



**WILD ADULT STEELHEAD AND CHINOOK SALMON
ABUNDANCE AND COMPOSITION AT
LOWER GRANITE DAM,
SPAWN YEAR 2012**

2012 ANNUAL REPORT



Photo: IDFG

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ABBREVIATIONS AND ACRONYMS

BPA	Bonneville Power Administration
BY	Brood Year
CI	Confidence Interval
COE	U. S. Army Corps of Engineers
CWT	Coded Wire Tag
DPS	Distinct Population Segment
ESA	Endangered Species Act
ESU	Evolutionarily Significant Unit
F	Female
FL	Fork Length
GSI	Genetic Stock Identification
IA	Individual Assignment
ICBTRT	Interior Columbia Basin Technical Recovery Team
IDFG	Idaho Department of Fish and Game
IOSC	Idaho Office of Species Conservation
IPC	Idaho Power Company
ISEMP	Integrated Status and Effectiveness Monitoring Project
LGR	Lower Granite Dam
LSRCP	Lower Snake River Compensation Plan
M	Male
MCMC	Markov Chain Monte Carlo
MM	Mixture Modeling
MPG	Major Population Group
MY	Smolt Migration Year
NMFS	National Marine Fisheries Service
PBT	Parentage Based Tag
PIT	Passive Integrated Transponder
PSMFC	Pacific States Marine Fisheries Commission
QCI	Quantitative Consultants, Inc.
SNP	Single Nucleotide Polymorphism
SY	Spawn Year
TAC	Technical Advisory Committee, <i>U.S. v. Oregon</i>
VSP	Viable Salmonid Population
WDFW	Washington Department of Fish and Wildlife

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ABSTRACT

This report summarizes the abundance and composition of wild adult steelhead and spring-summer Chinook salmon returning to Lower Granite Dam in spawn year 2012. We used a combination of window counts and systematic biological samples from the adult fish trap to decompose each run by origin, body size (steelhead only), age, gender, and stock. For steelhead between July 1, 2011 and June 30, 2012, wild escapement was estimated to be 39,504 fish or 21.9% of the total run. Of these, 892 fish were from brood year (BY) 2009; 9,332 fish from BY2008; 19,488 fish from BY2007; 8,572 fish from BY2006; 1,132 fish from BY2005; and 88 fish from BY2004. Total age at spawning ranged from three to eight years; freshwater age ranged from one to five years and saltwater age ranged from one to three years. Using a sex-specific genetic assay, we estimate 26,917 females and 12,587 males returned. Genetic stock abundance estimates were 7,015 fish for the upper Salmon River; 2,744 fish for the Middle Fork Salmon River; 960 fish for the South Fork Salmon River; 1,174 fish for the lower Salmon River; 2,514 fish for the upper Clearwater River; 2,959 fish for the South Fork Clearwater River; 2,010 fish for the lower Clearwater River; 2,285 fish for the Imnaha River; 6,866 fish for the Grande Ronde River; and 10,977 fish for the lower Snake River. The combined wild and hatchery steelhead escapement was 180,320 fish counted at the window by U.S. Army Corps of Engineers. We estimate that 140,816 of these fish were of hatchery origin, of which 7.1% were unclipped. For Chinook salmon between March 1 and August 17, 2012, wild escapement was estimated to be 21,733 fish or 25.6% of the total run. Of these, 22 fish were from BY2010; 1,136 fish from BY2009; 14,074 fish from BY2008; 6,263 fish from BY2007; and 238 fish from BY2006. Total age at spawning ranged from two to six years; freshwater age ranged from zero to two years and saltwater age ranged from zero (mini-jack) to four years. Using a sex-specific genetic assay, we estimate 10,974 females and 10,759 males returned. Genetic stock abundance estimates were 3,408 fish for the upper Salmon River; 3,325 fish for the Middle Fork Salmon River; 594 fish for Chamberlain Creek; 4,104 fish for the South Fork Salmon River; 9,425 fish for the Hells Canyon aggregate stock including the Clearwater, Little Salmon, lower Salmon, Grande Ronde, Imnaha, and lower Snake rivers; and 94 fish for the Tucannon River. In addition, 783 fish or 3.6% of the wild run were identified as fall Chinook salmon based on genetic data. The combined wild and hatchery Chinook salmon escapement was 84,771 fish counted at the window by U.S. Army Corps of Engineers. We estimate that 63,038 of these fish were of hatchery origin, of which 7.3% were unclipped. In the future, estimates of wild adult abundance and composition for these two species will be combined with similar information for smolts from the Lower Granite Dam juvenile facility. This will enable us to estimate productivity and other viable salmonid population parameters.

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INTRODUCTION

Populations of steelhead trout *Oncorhynchus mykiss* and Chinook salmon *O. tshawytscha* in the Snake River basin declined substantially following the construction of hydroelectric dams in the Snake and Columbia rivers. Raymond (1988) documented a decrease in survival of emigrating steelhead trout and Chinook salmon from the Snake River following the construction of dams on the lower Snake River during the late 1960s and early 1970s. Abundance rebounded slightly in the early 1980s, but then escapements over Lower Granite Dam into the Snake River basin declined again (Busby et al. 1996). In recent years, abundances in the Snake River basin have slightly increased. The increase has been dominated by hatchery fish, while the returns of naturally produced steelhead trout and Chinook salmon remain critically low. As a result, Snake River steelhead trout (hereafter steelhead) were classified as threatened under the Endangered Species Act (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; Figure 1; ICBTRT 2003, 2005; NMFS 2011). The Hells Canyon MPG is considered to have been extirpated. A total of 24 extant populations have been identified in the DPS. Snake River spring-summer Chinook salmon (hereafter Chinook salmon) were classified as threatened in 1992 under the ESA. 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; Figure 2). The Dry Clearwater River and Wet Clearwater River MPGs are considered to have been extirpated but have been refounded with stocks from other Snake River MPGs. A total of 28 extant populations have been identified in the ESU.

Anadromous fish management programs in the Snake River basin include large-scale hatchery programs – intended to mitigate for the impacts of hydroelectric dam construction and operation in the basin – and recovery planning and implementation efforts aimed at recovering ESA-listed wild steelhead and salmon stocks. The Idaho Department of Fish and Game's anadromous fish program long-range goals, consistent with basinwide mitigation and recovery programs, are to preserve Idaho's salmon and steelhead runs and recover them to provide benefit to all users (IDFG 2007). 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 measured at Lower Granite Dam (LGR), with the exception of the Tucannon River, Washington, population. Some of the wild fish are headed to Washington or Oregon tributaries to spawn, but the majority is destined for Idaho. Age, sex, and stock composition data are important for monitoring recovery of wild fish for both species. Age data collected at LGR are used to assign returning adults to specific brood years, for cohort analysis, and to estimate productivity and survival rates (Copeland et al. 2007; Copeland and Putnam 2009; Copeland et al. 2009; Copeland and Roberts 2010; Copeland et al. 2011, 2012, 2013a; Kennedy et al. 2011, 2012, 2013; Schrader et al. 2011, 2012, 2013). 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 (COE) counts fish at viewing windows and designates jack Chinook salmon as fish between 30 and 56 cm (12 and 22 inches)

in length; salmonids under 30 cm (12 inches) in length are not identified to species. Mini-jacks are precocious salmon generally under 30 cm in 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 less than 30 cm. For Chinook salmon, the run year at LGR is defined to be from March 1 to June 17 for the spring run, and from June 18 to August 17 for the summer run. For steelhead, the run year at LGR is defined to be from July 1 to June 30. 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.

This report summarizes the abundance and composition of wild adult steelhead and Chinook salmon returning to LGR during spawn year (SY) 2012. For steelhead, fish passing LGR during the summer and fall of 2011 comprise the bulk of the 2012 spawn year. There are two previous preliminary accountings of the data: Ackerman et al. (2012, 2014) reported initial genetic stock identification (GSI) results for both steelhead and Chinook salmon based on single nucleotide polymorphism (SNP) variation. Ackerman et al. (2014) provides individual assignments of SY2012 adults to genetic stocks and is duplicate reporting of Ackerman et al. (2012); reporting timelines for the GSI project were modified in 2013. Here we develop those analyses further and this report supersedes the earlier work. Because of the collaborative nature of the work at LGR, this report is a product of several Bonneville Power Administration (BPA) projects: Idaho Steelhead Monitoring and Evaluation Studies (1990-055-00), Idaho Natural Production Monitoring and Evaluation Program (1991-073-00), and Chinook and Steelhead Genotyping for Genetic Stock Identification at Lower Granite Dam (2010-026-00).

METHODS

Adult Trap Operations at Lower Granite Dam

Systematic samples of steelhead and Chinook salmon returning to LGR were collected during daily operation of the adult fish trap by National Marine Fisheries Service (NMFS; BPA project 2005-002-00, Lower Granite Dam Adult Trap Operations; Harmon 2003; Ogden 2012, 2013). The adult trap is located in the LGR fish ladder upstream from the fish counting window. The trap captures a systematic random sample of fish by operating a trap gate according to a predetermined sample rate. The sample rate determines how long the trap gate remains open four times per hour; the trap is operational 24 hours per day. Additional details on the adult trap can be found in Harmon (2003) and Steinhorst et al. (2010). During 2011, the trap sample rate remained constant at 10%; no trap closures occurred during this time period (Table 2). The trap was closed from November 21, 2011 to March 7, 2012 due to freezing water temperatures. The trap sample rate was 10% from March 8 to August 17, 2012, except the trap was closed July 27 to 29, August 6 to 9, and August 13 to 17 due to high water temperatures. The adult fish ladder was dewatered from January 4 to February 13, 2012; hence, there was no adult passage during this time period except through the navigation lock.

Standard methods were used by NMFS or Idaho Department of Fish and Game (IDFG) staff to process and biologically sample adult fish at the trap (Harmon 2003; Ogden 2012, 2013; Appendix A). All adult fish captured were anesthetized; examined for external marks, tags, and injuries; scanned for an internal coded wire tag (CWT) or passive integrated transponder (PIT) tag; and measured for fork length (FL, nearest cm). All fish were classified by origin (wild or hatchery) and the presence (hereafter unclipped) or absence (hereafter clipped) of the adipose fin. Wild fish have an unclipped adipose fin because they spend their entire life cycle in the

natural environment. Although most hatchery origin steelhead and Chinook salmon have a clipped adipose fin, some are released with an unclipped adipose fin for supplementation purposes. For unclipped steelhead, hatchery origin was determined primarily by the presence of dorsal or ventral fin erosion, which is assumed to occur only in hatchery-reared fish (Latremouille 2003). We also used the presence of a CWT, a ventral fin clip, or a genetic parentage based tag (PBT) to determine if an unclipped fish was of hatchery origin. For unclipped Chinook salmon, hatchery origin was determined solely by the presence of a CWT, a ventral fin clip, or a PBT. Genotyping for PBT analysis was conducted post hoc. In sum, final classification of hatchery origin fish was made using any of five marks or tags: adipose fin clip, CWT, ventral fin clip, dorsal or ventral fin erosion (steelhead only), and PBT (Table 3). Information from fish previously PIT tagged was not used to determine origin. Fish determined to be phenotypically wild by the trap crew were sampled for scales and tissue. All captured wild fish were also PIT tagged if not previously tagged for the Integrated Status and Effectiveness Monitoring Project (ISEMP, BPA project 2003-017-00; Beasley and White 2010; QCI 2011, 2012, 2013).

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 ageing laboratory in Nampa, Idaho. Tissue samples were taken from a small clip of the anal fin. Tissues were stored in a vial with 200-proof nondenatured ethyl alcohol for transport to the IDFG genetics laboratory in Eagle, Idaho.

After processing, all fish were returned to the adult fish ladder to resume their upstream migration. No trap mortalities for either species were observed during SY2012 (Ogden 2012, 2013).

Trap Data Management

Data collected at the LGR adult trap were historically recorded on paper data sheets. These data were then transcribed into Excel spreadsheets by NMFS and IDFG personnel, checked for transcription errors, reformatted, and uploaded into the IDFG Lower Granite Dam SQL server database. From May 24, 2012 forward, all data were entered directly into a new NMFS cloud-based database via new touch-screen computer systems located in the trap work area. Real Time Research, Inc. was contracted by NMFS to develop and manage the data collection system and cloud-based database (Ogden 2013). This new system allowed interested parties to access the data they need at the end of each day and eliminated transcription errors from paper data sheets to electronic form. The IDFG SQL server database automatically queries the NMFS database to populate tables used by IDFG for reporting purposes. Trap data can now be accessed by IDFG staff in almost real time, but there are no longer opportunities for broad electronic data quality assurance and control because there are no longer paper data sheets to reference.

Valid Sample Selection

Not all trapped fish were deemed valid by IDFG for sample selection or analysis. Trapped fish that were missing data entry records for any of the following five fields were considered invalid: date of collection, species, fork length, origin (hatchery or wild), or adipose fin status (clipped or unclipped). Trapped fish less than 30 cm (FL) were considered invalid as they are not identified to species at the COE fish-counting window. Further, the adult 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. Finally, any

sort-by-code PIT-tagged fish trapped outside the normal trap sampling timeframe were considered invalid. A computer program written by Tiffani Marsh (NMFS) was used to make this determination. Sort-by-code, or separation-by-code, is the process whereby PIT-tagged fish ascending the LGR fish ladder are diverted into the trap box using predetermined tag codes programmed into the trap gate computer. For SY2012, there were 226 trapped steelhead that were considered invalid by these criteria – 35 were wild sort-by-code repeat spawners for scale pattern validation (present study); 190 were sort-by-code fish for a Dworshak Hatchery length-at-age validation study (Alan Byrne, IDFG, personal communication); and one fish was missing data entry fields. There were 313 trapped Chinook salmon that were considered invalid by these criteria – four were hatchery mini-jacks less than 30 cm (FL); 12 were wild sort-by-code fish for the Lemhi River radio telemetry project (Bowersox and Biggs 2012); and 297 were McCall Hatchery and Rapid River Hatchery sort-by-code fish for a PIT tag retention study (Cassinelli et al. 2013).

Our goal was to age and genotype approximately 2,000 wild steelhead and 2,000 wild Chinook salmon. In collaboration with our work, the ISEMP goal was to PIT tag and collect scale and genetic tissue samples from approximately 4,000 wild steelhead and 4,000 wild Chinook salmon. We emphasize that IDFG and ISEMP sample goals are complimentary and not mutually exclusive. To achieve the IDFG goal, all trap samples 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 simple random sample (Kirk Steinhorst, University of Idaho, personal communication).

Scale Processing and Analysis

Technicians processed scale samples in the IDFG ageing laboratory. Scales were examined for regeneration and 6-10 nonregenerated scales were cleaned and mounted between two glass microscope slides. Scales were examined on a computer video monitor using a Leica DM4000B microscope and a Leica DC500 digital camera. A technician chose the best scales for ageing and saved them as digitized images. The entire scale was imaged using 12.5x magnification. In addition, the freshwater portion was imaged using 40x magnification. Two technicians independently viewed each image to assign ages without reference to fish length. If there was no age consensus among the readers, a third reader viewed the image and all readers collectively examined the image to resolve their differences before a final age was assigned. If a consensus age was not attained, the sample was excluded from further analysis.

Freshwater annuli were defined by pinching or cutting-over of circuli within the freshwater zone in the center of the scale. The criterion for a saltwater annulus was the crowding of circuli after the rapid saltwater growth had begun. We used only visible annuli formed on the scales, excluding time spent overwintering in fresh water prior to spawning. We identified steelhead repeat spawners by the presence of a spawn check. A spawn check appears as a ragged scar mark within the saltwater zone. Spawn checks are caused by resorption of circuli that occurs during their return to freshwater for spawning (Davis and Light 1985). After resorption occurs in freshwater, and when the fish returns to saltwater and scale growth resumes, a spawn check is formed (White and Medcof 1968). We also identified Chinook salmon ocean age-0 mini-jacks. Mini-jacks exhibit rapid saltwater growth after entering the ocean but lack a saltwater annulus (Johnson et al. 2012). Mini-jacks return to freshwater within the same year and stay in the ocean or estuary only three to five months. We use the European system to designate ages; freshwater age is separated from saltwater age by a

decimal. For steelhead repeat spawners, an 'S' is added to the saltwater age to designate the winter spent in freshwater while on a spawning run. Brood year, or total age at spawning, is the sum of freshwater and saltwater ages, plus 1. Fish lacking either a freshwater or saltwater determined age were not used for analysis.

Known ocean-age fish that were PIT tagged as juveniles were used for saltwater age validation. We currently do not have any validation methods for wild fish freshwater ages. Accuracy of age assignments was estimated by percent agreement between saltwater age and known emigration date, determined from juvenile PIT tag detection in the hydrosystem. Known ocean-age hatchery and wild fish were used to compute accuracy rate for Chinook salmon ages; only known ocean-age wild fish were used to compute accuracy rate for steelhead ages. The mean coefficient of variation was used to measure ageing precision between primary readers (formula from Chang 1982; see Copeland et al. 2007).

Genetics Tissue Processing and Analysis

Detailed methods for extraction of genomic DNA from tissue samples, DNA amplification, and SNP genotyping are described in Ackerman et al. (2014). For both species, all individuals were genotyped at 191 SNPs and a sex-specific genetic assay. The 191 steelhead SNPs include three SNPs used to identify putative *O. mykiss* x *O. clarki* hybrids. SNP amplification was performed using Fluidigm 96.96 Dynamic Array IFCs (chips). Chips were imaged on a Fluidigm EP1™ system and analyzed and scored using the Fluidigm SNP Genotyping Analysis Software. Samples were processed at either the IDFG genetics laboratory in Eagle, Idaho, or the Columbia River Inter-Tribal Fish Commission's genetics laboratory in Hagerman, Idaho (BPA project 2010-026-00).

Since 2008, fin tissue has been sampled from nearly all adult steelhead and spring-summer Chinook salmon broodstock returning to Snake River hatcheries in Idaho, Oregon, and Washington (Steele et al. 2013a). For steelhead in 2008, some Dworshak Hatchery early-arriving broodstock, most Lyons Ferry Hatchery broodstock, and all Oregon hatcheries broodstock were not sampled. The PBT project (BPA project 2010-031-00) genotypes the broodstock tissue samples at 95 SNPs (within the 191 described above for both species) and creates a parental database of the SNP genotypes. The genotyping of broodstock essentially "tags" all steelhead and spring-summer Chinook salmon smolts released in the Snake River basin. This allows researchers to identify the origin and age (brood year) of their offspring using parentage analysis (Steele et al. 2013b). For SY2012, parentage analysis was conducted on adults captured and biosampled at the LGR trap using a parental database of broodstock spawned in 2008 and 2009 to identify hatchery fish that were phenotypically wild. Parentage assignment using SNP genotypes was performed using the program SNPPIT (Anderson 2010a).

GSI is a form of mixed stock analysis that uses genetic data to estimate the stock of origin of individuals (or groups of individuals). Two assignment methods are used in GSI: 1) individual assignment (IA), and 2) mixture modeling (MM). Both IA and MM use allele frequency estimates from baseline populations as reference information to characterize potentially contributing stocks. Individual assignment methods assign each individual to the stock in which the probability of its genotype occurring is the greatest. The proportion of a particular stock can then be estimated by summing all of the individual assignments to that stock and dividing by the total sample size. In contrast, MM does not assign each individual to one specific stock. Instead, MM uses likelihood and/or Bayesian modeling to fractionally allocate individual samples within the mixture to each stock in proportion to the probability that it belongs to that stock. Mixture

modeling methods have been shown to be more accurate for estimating stock composition when all individual assignments cannot be made with high confidence (Manel et al. 2005, Koljonen et al. 2005).

Because we are interested in both estimating stock proportions and partitioning LGR wild escapement by stock, as well as estimating sex and age proportions using biological data from fish returning to individual stocks, we used a combination of both MM and IA for SY2012 genetic stock reconstruction. For both GSI methods, a genetic baseline is first established by sampling fish from discrete “reference” populations (i.e. wild Snake River spawning aggregations) that potentially contribute to the mixed population (i.e. aggregate wild escapement at LGR). Fish captured at LGR are then genotyped and assigned wholly (IA) or fractionally (MM) back to their genetic stock of origin (Pella and Milner 1987, Shaklee et al. 1999). Ackerman et al. (2014) provide a detailed description of the Snake River genetic baselines used for both steelhead and Chinook salmon GSI analyses (also see Figures 1 and 2, and Appendix B). Snake River genetic stocks used for both MM and IA at LGR were defined by Ackerman et al. (2012). Reporting groups (referred to here as genetic stocks) are assemblages of reference (baseline) populations grouped primarily by genetic and geographic similarities and secondarily by political boundaries and management units (Ackerman et al. 2011).

Mixture modeling using multi-locus SNP data was performed to estimate stock proportions of the wild escapement at LGR. Maximum likelihood stock proportion estimates are multiplied by the estimated total wild escapement at LGR to estimate abundance by stock. Mixture modeling of individuals genotyped from the LGR adult fish trap was done using the Bayesian version of the program *gsi_sim* (Anderson et al. 2008, Anderson 2010b). The Bayesian version of *gsi_sim* uses Markov chain Monte Carlo (MCMC) to compute posterior probabilities of stock membership conditional on the allele frequencies estimated from the baseline. The likelihood that a fish originates from a stock is computed using the compound Dirichlet-multinomial formulation of Rannala and Mountain (1997) conditional on the baseline samples; these likelihoods remain fixed throughout the MCMC simulation. To perform the MCMC, *gsi_sim* uses a Gibbs sampler (Casella and George 1992) which alternately: 1) updates the stock assignments of the fish in the mixture as a multinomial draw from their posterior probabilities given the current estimate of the stock proportions and the stock-likelihoods of the fish; and 2) updates the stock proportions as a draw from a Dirichlet distribution given a unit-information prior and the current values of the stock assignments of all the fish in the mixture. By sampling the current values of the stock proportions as the chain proceeds, a Monte Carlo estimator of the posterior mean and any desired quantiles can be computed. For estimating stock proportions, we ran 300,000 MCMC sweeps with a burn-in of 50,000 sweeps (leaving 250,000) and a thinning interval of 50 to obtain 5,000 Bayesian posterior estimates of stock proportions for each stock. The 5,000 Bayesian posterior estimates of stock proportions were used for subsequent calculation of confidence intervals (CI) for stock proportions and abundances. The maximum likelihood estimates of stock proportions were used to calculate stock abundance point estimates.

To estimate sex and age proportions within each stock, genotyped individuals were assigned to their “best-estimate” genetic stock-of-origin using *gsi_sim*; the “best-estimate” stock is the stock that each individual’s genotype data most likely originated from (i.e. highest probability of assignment). Fish that had a determined sex and total age, irrespective of assignment probability, were used to calculate stock-by-sex-by-age proportions.

The resolution of the Snake River genetic baselines used to perform both MM and IA analyses is evaluated in Ackerman et al. (2014) as part of BPA project 2010-026-00. The GSI

project will continue to update the genetic baselines periodically in an effort to improve resolution. Further, the GSI project will continue to develop methods and evaluate available tools to assess and improve the accuracy and precision of genetic stock proportion and abundance estimates in the future; these efforts will be reported in the annual progress reports for BPA project 2010-026-00.

The accuracy of the sex-specific genetic assays is evaluated in Steele et al. (2013a). Gender was not and generally cannot be reliably determined by personnel at the LGR adult trap; thus, a direct comparison was not attempted. The sex-determination assay for steelhead is 99.3% accurate and for Chinook is 99.0% accurate based on comparisons with known-sex individuals (C. Steele and J. McCane, PSMFC, personal communication). Campbell et al. (2012) and references therein describe in more detail the methods of sex-determination using genetic assays.

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

The COE daily window counts, which occur in the fish ladder downstream of the adult trap, were assumed to be the daily aggregate escapement to LGR for each species. Video counts were used by COE in lieu of window counts in November, December, and March (Table 2). Window count times were 0400-2000, whereas video count times were 0600-1600 Pacific Time. Count data were downloaded from the COE website:

<http://www.nwp.usace.army.mil/Missions/Environment/Fish/Counts.aspx>

Additional daily window and video operation information was obtained from COE annual fish passage reports (COE 2011, 2012). For Chinook salmon, the adult count was combined with the jack count to derive the total count on a daily basis.

To estimate escapement by origin or size, the daily window or video counts were combined with adult trap sample data on a statistical week basis to account for changes in the trapping rate and run characteristics through time. Statistical weeks started on Monday and ended on Sunday. If necessary, weeks were grouped to try to provide a minimum sample size of 100 trapped fish. In some time strata, we opted not to combine if adjacent strata were above the minimum or if there was a gap in sampling (e.g., summer sampling for steelhead). For steelhead, weekly proportions of wild, clipped hatchery, and unclipped hatchery fish were estimated for large fish (≥ 78 cm, FL) and small fish (< 78 cm, FL) using the trap data. These size criteria are used to inform management processes, particularly under the Technical Advisory Committee (TAC), *U.S. vs. Oregon*. For Chinook salmon, weekly proportions were estimated for wild, clipped hatchery, and unclipped hatchery fish irrespective of size. For both species, weekly escapement was estimated by multiplying the weekly window or video counts by the weekly trap proportions; the sum of the weekly escapement estimates was the total escapement to LGR by origin or size. In essence, the weekly proportions for origin (and size) are weighted by weekly run size of all fish as counted at the window or by video.

To estimate wild escapement by age, sex, or stock, the total wild escapement estimate was multiplied by the overall age, sex, or stock proportions from the trap biological samples of wild fish. Stock proportions were estimated based on MM using multi-locus SNP data. Because we systematically subsampled all wild fish trapped at LGR, and because this sample pool can be considered a simple random sample selected in proportion to abundance, time stratification was not necessary for the age, sex, or stock abundance point estimates (Kirk Steinhorst, University of Idaho, personal communication).

Confidence intervals for all point estimates were computed using a bootstrapping algorithm (Manly 1997). For origin – wild versus hatchery – the variation in trap sampling is accounted for by taking bootstrap samples of the trap data by week. This bootstrap proportion is then multiplied by the total weekly window count and summed over all weeks to produce 5,000 bootstrap values for number wild (or hatchery). The 95% confidence intervals were estimated by finding the 2.5th and 97.5th percentiles of the 5,000 ordered bootstrap values for each group.

When estimating abundance by age and by sex, there is additional variability due to scale (or genetic tissue) sampling. The scale (or genetic) database was sampled with replacement 5,000 times. This generates 5,000 bootstrap proportions for age (or sex). For each bootstrap iteration ($i = 1, 2, 3, \dots, 5000$) we multiply value i in the vector of 5,000 bootstrap wild estimates by value i in the vector of 5,000 bootstrap proportions for age (or sex) resulting in a vector of 5,000 bootstrap wild estimates by age (or sex). The one-at-a-time 95% confidence intervals were estimated by finding the 2.5th and 97.5th percentiles of the 5,000 ordered bootstrap values for each group. Simultaneous confidence intervals for the number of wild fish of different ages or sex were found by expanding the hypercube formed from the one-at-a-time bootstrap confidence intervals 0.5% in each dimension until 95% of all the bootstrap points were within the expanded hypercube. Separate bootstraps were performed for each grouping within a parameter (e.g., total age, ocean age, and brood year were separate runs of the age data). Confidence intervals for the origin group (e.g., wild versus hatchery) were determined from the vector of bootstrap abundances output after the first level of the bootstrapping routine was finished. The algorithm was written and implemented in the R programming environment (R Development Core Team 2008) by Kirk Steinhorst (University of Idaho).

Variance in the wild fish escapement estimate was incorporated into variance in the genetic stock abundance estimates using a combination of bootstrapping (variance in wild fish escapement) and Monte Carlo methods (variance in stock proportions). The bootstrapping algorithm outlined above was used to create a vector of 5,000 bootstrap estimates of total wild escapement. The MCMC method implemented in *gsi_sim* was used to generate a vector of 5,000 Bayesian posterior estimates of stock proportion for each genetic stock. The bootstrap estimates of total wild escapement were then multiplied through the Bayesian posterior estimates of stock proportions for each genetic stock to obtain a vector of stock abundance. The one-at-a-time bootstrap intervals of stock abundance were estimated via the 2.5th and 97.5th percentiles of the 5,000 ordered “bootstrap” values for each group. Similar to age and sex calculations, simultaneous confidence intervals for each genetic stock’s abundance were found by expanding the hypercube formed from the one-at-a-time bootstrap confidence intervals 0.5% in each dimension until 95% of all the bootstrap points were within the expanded hypercube.

Ten wild steelhead genetic stocks were used during MM and IA analyses (Appendix Table B-1). 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 (primarily Potlatch River); 8) IMNAHA: Imnaha River; 9) GRROND: Grande Ronde River; and 10) LSSNAKE: tributaries of the lower Snake River both above (Alpowa and Asotin creeks) and below (primarily Tucannon River) LGR. Fish that originated below LGR 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 during MM and IA analyses (Appendix Table B-2). The genetic stocks include: 1) UPSALM: upper Salmon River (Lemhi River and upstream); 2) MFSALM: Middle Fork Salmon River; 3) CHMBLN: Chamberlain Creek; 4) SFSALM: South Fork Salmon River; 5) HELLSC: Hells Canyon stock, an aggregate genetic stock that includes the Clearwater, Little Salmon, lower Salmon, Grande Ronde, Imnaha, and lower Snake rivers; 6) TUCANO: Tucannon River; and 7) FALL: Snake River fall Chinook salmon. Chinook salmon populations in TUCANO can be distinguished from HELLSC in GSI analyses because they exhibit low levels of introgression with fall Chinook salmon (Narum et al. 2010). The TUCANO genetic stock was included in the baseline to represent fish that originated below LGR but ascend 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 individual or combined MPGs (Table 1); the MFSALM and CHMBLN genetic stock results are aggregated to report for 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 baseline (Ackerman et al. 2014); our purpose was to distinguish fall Chinook salmon from spring-summer Chinook salmon trapped prior to August 17 using genetic data.

Wild Stock Escapement by Sex, Age, and Size

After estimating the wild escapements by stock using MM, we used results from IA analyses to decompose the stock escapements by sex, age, and, for steelhead only, size. Fish that had a determined sex and total age, irrespective of assignment probability, were used to calculate stock-by-sex-by-age proportions. Calculated proportions were then applied to the estimated stock escapements to obtain abundance for stock-by-sex-by-age.

RESULTS

Steelhead Escapement

For SY2012 – from July 1, 2011 to June 30, 2012 – a total of 180,320 wild and hatchery steelhead were counted at the LGR window or by video (Figure 3; Appendix Table C-1). The first fish was counted on July 1, 2011, and the last fish was counted on June 30, 2012. Of the total escapement, there were 1,898 fish or 1.1% of the run that passed during the November 21, 2011 to March 7, 2012 trap closure. The trap was operational during 98.9% of the run.

At the adult trap, a total of 19,478 wild and hatchery steelhead were captured and considered valid (Appendix Table C-1). Of these, 18,569 fish or 95.3% were trapped during fall 2011, and 909 fish or 4.7% were trapped during spring 2012. The adult trap sampled 10.8% of the window count overall (weekly range 6.4-17.9%).

Of the steelhead trapped, there were 483 large (≥ 78 cm, FL) wild fish; 1,996 large hatchery clipped fish; 234 large hatchery unclipped fish; 3,663 small (< 78 cm, FL) wild fish; 12,239 small hatchery clipped fish; and 863 small hatchery unclipped fish (Appendix Table C-2). Combining large and small fish, a total of 5,243 unclipped and 14,235 clipped fish were trapped. These data are adjusted for 122 fish misidentified at the trap as large wild that were later reclassified to large hatchery unclipped, and 138 fish misidentified at the trap as small wild that were later reclassified to small hatchery unclipped, both as determined by PBT.

We estimate that 2.4% of the run was large wild; 9.8% was large hatchery clipped; 1.2% was large hatchery unclipped; 19.5% was small wild; 62.7% was small hatchery clipped; and 4.4% was small hatchery unclipped (Appendix Table C-3). Of all returning unclipped fish, we estimate 20.2% were of hatchery origin, which is a minimum estimate. Of all returning hatchery fish, we estimate 7.1% were unclipped, which is also a minimum estimate. Both are minimum estimates because not all hatchery unclipped fish have a distinguishing mark or tag, i.e. a CWT, a ventral clip, dorsal or ventral fin erosion, or a PBT. We estimate that 18.0% of all large fish were wild compared to 22.5% of all small fish. Overall, 21.9% of the run was wild and 78.1% was of hatchery origin. However, the percentage of wild was not constant throughout the run and ranged from 14.2% in early October 2011 to 58.9% in May and June 2012.

Of the total steelhead escapement to LGR, we estimate that 4,345 fish (95% CI 3,973-4,742) were large wild; 17,749 fish (95% CI 17,011 -18,486) were large hatchery clipped; 2,111 fish (95% CI 1,848-2,387) were large hatchery unclipped; 35,159 fish (95% CI 34,186-36,172) were small wild; 113,060 fish (95% CI 111,847-114,299) were small hatchery clipped; and 7,896 fish (95% CI 7,389-8,418) were small hatchery unclipped (Figure 4; Appendix Table C-4). Overall, 39,504 wild (95% CI 38,453-40,532) and 140,816 hatchery (95% CI 139,762-141,848) steelhead returned to LGR after combining large, small, clipped, and unclipped fish (Figure 5). Our total estimate of 49,511 unclipped fish, wild and hatchery combined, is 107.0% of the COE reported window count of 46,282 unclipped fish.

Wild Steelhead Age, Sex, and Stock Composition

Of the 4,146 wild steelhead scale and genetics samples collected at the trap, we systematically subsampled 2,017 for ageing and genotyping (Appendix Table C-5). The first sample was collected on July 7, 2011 and the last was collected on June 30, 2012. We were able to assign total age to 1,816 samples or 4.6% of the estimated run size (weekly range 3.5-5.2%). We were able to assign gender to 1,971 samples or 5.0% of the run size (weekly range 4.3-5.6%). We were able to obtain complete stock genotype data ($\geq 90\%$ of SNPs amplify successfully) for 2,004 samples or 5.1% of the run size (weekly range 4.3-5.6%).

We observed 22 different age classes from the 1,816 fish that we were able to assign a total age (Appendix Table C-6). Total age at spawning ranged from three to eight years, with freshwater age ranging from one to five years and saltwater age ranging from one to three years. We estimate that 36.2% of the wild return was from smolt migration year (MY) 2010; 61.7% from MY2009; 0.9% from MY2008; and 1.2% from repeat spawners (Appendix Table C-7). No more than one spawn check for each repeat spawner was observed. We estimate that 2.3% of the wild return was from brood year (BY) 2009; 23.6% from BY2008; 49.3% from BY2007; 21.7% from BY2006; 2.9% from BY2005; and 0.2% from BY2004.

Estimated escapement to LGR by age class, grouped by smolt migration year, was (Figure 6):

- For MY2010: 892 fish for age 1.1 (95% CI 397-1,868); 7,766 fish for age 2.1 (95% CI 4,393-13,654); 5,090 fish for age 3.1 (95% CI 2,787-9,138); 522 fish for age 4.1 (95% CI 204-1,178); and 44 fish for age 5.1 (95% CI 0-176).
- For MY2009: 1,566 fish for age 1.2 (95% CI 766-3,110); 14,289 fish for age 2.2 (95% CI 8,343-24,381); 65 fish for age 2.1S (95% CI 0-243); 7,701 fish for age 3.2 (95% CI 4,340-13,541); 783 fish for age 4.2 (95% CI 335-1,680); and 22 fish for age 5.2 (95% CI 0-105).

- For MY2008: 44 fish for age 1.2S (95% CI 0-176); 196 fish for age 2.3 (95% CI 52-529); 131 fish for age 2.1S1 (95% CI 27-388); 22 fish for age 2.2S (95% CI 0-105); 152 fish for age 3.3 (95% CI 27-441); 44 fish for age 3.1S1 (95% CI 0-176); 65 fish for age 3.2S (95% CI 0-243); and 22 fish for age 4.1S1 (95% CI 0-105).
- For MY2007: 44 fish for age 2.2S1 (95% CI 0-176); 22 fish for age 3.1S2 (95% CI 0-105); and 22 fish for age 3.2S1 (95% CI 0-105).

Estimated escapement to LGR by saltwater age was 14,314 one-saltwater fish (95% CI 12,474-16,365); 24,361 two-saltwater fish (95% CI 21,672-27,266); 348 three-saltwater fish (95% CI 182-560); and 481 fish that were repeat spawners (95% CI 268-736). Estimated escapement to LGR by total age at spawning was 892 fish from BY2009 (95% CI 571-1,301); 9,332 fish from BY2008 (95% CI 7,699-11,242); 19,488 fish from BY2007 (95% CI 16,591-22,799); 8,572 fish from BY2006 (95% CI 7,038-10,378); 1,132 fish from BY2005 (95% CI 757-1,601); and 88 fish from BY2004 (95% CI 19-198; Figure 7).

Of the 1,971 fish for which gender was successfully determined using the sex-specific assay, 1,343 were female and 628 were male (Appendix Table C-8). The gender percentages for the entire run were 68.1% female and 31.9% male (Appendix Table C-9). The sex ratio was female-biased throughout the run and ranged from 56.7 to 77.0%. Expanding the overall percentages to the wild run gives 26,917 females (95% CI 25,414-28,402) and 12,587 males (95% CI 11,569-13,680; Figure 8). We estimate that 25.6% of the females and 59.4% of the males were one-saltwater, and that 1.6% of the females and 0.2% of the males were repeat spawners. Conversely, we estimate that 48.8% of the one-saltwater fish were females and 51.2% were males, and that 95.2% of the repeat spawners were females and 4.8% were males.

Based on MM results using the 2,004 fish with complete genotypes, we estimate that 17.8% of the wild return originated from UPSALM; 6.9% from MFSALM; 2.4% from SFSALM; 3.0% from LOSALM; 6.4% from UPCLWR; 7.5% from SFCLWR; 5.1% from LOCLWR; 5.8% from IMNAHA; 17.4% from GRROND; and 27.8% from LSSNAKE. Aggregating by MPGs, 30.1% of the wild return originated from the Salmon River; 18.9% from the Clearwater River; 5.8% from the Imnaha River; 17.4% from the Grande Ronde River; and 27.8% from the Lower Snake River.

Based on MM results, estimated escapement to LGR by genetic stock was 7,015 fish for UPSALM (95% CI 5,600-8,995); 2,744 fish for MFSALM (95% CI 2,007-3,619); 960 fish for SFSALM (95% CI 619-1,418); 1,174 fish for LOSALM (95% CI 440-1,634); 2,514 fish for UPCLWR (95% CI 1,795-3,287); 2,959 fish for SFCLWR (95% CI 2,267-3,966); 2,010 fish for LOCLWR (95% CI 1,311-2,849); 2,285 fish for IMNAHA (95% CI 1,479-3,060); 6,866 fish for GRROND (95% CI 5,215-8,739); and 10,977 fish for LSSNAKE (95% CI 9,033-13,934; Figure 9). Estimated escapement was 11,893 fish for the Salmon River MPG (95% CI 10,204-13,500) which combines UPSALM, MFSALM, SFSALM, and LOSALM. Estimated escapement was 7,483 fish for the Clearwater River MPG (95% CI 6,366-8,691) which combines UPCLWR, SFCLWR, and LOCLWR.

Of the 2,004 fish with complete genotypes, 1,774 fish had both a determined sex and a total age which were used for genetic stock decomposition (Appendix Table C-10). Percentages of sex by age were calculated for each stock (Appendix Table C-11) and then applied to SY2012 stock escapement estimates (Appendix Table C-12). All 2,004 fish with complete genotypes had a length which was also used for genetic stock decomposition (Appendix Table C-13). Percentages of large and small fish were calculated for each stock (Appendix Table C-14) and then applied to SY2012 stock escapement estimates (Appendix Table C-15).

Chinook Salmon Escapement

For SY2011 – from March 1 to August 17, 2012 – a total of 84,771 wild and hatchery Chinook salmon were counted at the LGR window or by video (Figure 10; Appendix Table D-1). This total combines adult and jack counts. The first fish was counted on April 15 and the last fish was counted on August 17. Of the total escapement, there were 832 fish or 1.0% of the run that passed during the July 27-29, August 6-9, and August 13-17, 2012 trap closures. The trap was operational during 99.0% of the run.

At the adult trap, a total of 8,631 wild and hatchery Chinook salmon were captured and considered valid (Appendix Table D-1). The adult trap sampled 10.2% of the window count overall (weekly range 5.7-11.8%).

Of the Chinook salmon trapped, there were 2,191 wild fish, 5,972 hatchery clipped fish, and 468 hatchery unclipped fish (Appendix Table D-2). A total of 2,659 unclipped and 5,972 clipped fish were trapped. These data are adjusted for 153 fish misidentified at the trap as wild that were later reclassified to hatchery unclipped as determined by PBT.

We estimate that 25.6% of the run was wild, 68.9% was hatchery clipped, and 5.4% was hatchery unclipped (Appendix Table D-3). Of all returning unclipped fish, we estimate 17.5% were of hatchery origin, which is a minimum estimate. Of all returning hatchery fish, we estimate 7.3% were unclipped, which is also a minimum estimate. Both are minimum estimates because not all hatchery unclipped fish have a distinguishing mark or tag, i.e. a CWT, a ventral clip, or a PBT. Overall, 25.6% of the run was wild and 74.4% was of hatchery origin. However, the percentage of wild was not constant throughout the run and ranged from 12.3% in April and early May to 71.7% in early August 2012.

Of the total Chinook salmon escapement to LGR, we estimate that 21,733 fish (95% CI 20,968-22,507) were wild; 58,436 fish (95% CI 57,635-59,272) were hatchery clipped; and 4,602 fish (95% CI 4,198-5,010) were hatchery unclipped (Figure 11; Appendix Table D-4). Overall, 21,733 wild (95% CI 20,968-22,507) and 63,038 hatchery (95% CI 62,287-63,779) Chinook salmon returned to LGR after combining clipped and unclipped fish (Figure 12). Our total estimate of 26,335 unclipped fish, wild and hatchery combined, is 97.1% of the COE unreported window count of 27,135 unclipped fish (John Dalen, COE, personal communication).

Wild Chinook Salmon Age, Sex, and Stock Composition

Of the 2,191 wild Chinook salmon scale and genetics samples collected at the trap, we processed them all for ageing and genotyping (Appendix Table D-5). The first sample was collected on May 5 and the last was collected on August 12. We were able to assign total age to 2,009 samples or 9.2% of the estimated run size (weekly range 7.1-10.9%). We were able to assign gender to 2,123 samples or 9.8% of the run size (weekly range 7.5-11.3%). We were able to obtain complete stock genotype data ($\geq 90\%$ of SNPs amplify successfully) for 2,166 samples or 10.0% of the run size (weekly range 7.9-11.6%).

We observed ten different age classes from the 2,009 fish that we were able to assign a total age (Appendix Table D-6). Total age at spawning ranged from two to six years, with freshwater age ranging from zero to two years and saltwater age ranging from zero (mini-jack) to four years. We estimate that 0.2% of the wild return was from MY2012; 5.4% from MY2011; 65.3% from MY2010; 28.9% from MY2009; and 0.2% from MY2008 (Appendix Table D-7). We

estimate that 0.1% of the wild return was from BY2010; 5.2% from BY2009; 64.8% from BY2008; 28.8% from BY2007; and 1.1% from BY2006.

Estimated escapement to LGR by age class, grouped by smolt migration year, was (Figure 13):

- For MY2012: 22 fish for age 1.0 (95% CI 0-73), and 22 fish for age 2.0 (95% CI 0-73). These are mini-jacks ≥ 30 cm, FL.
- For MY2011: 1,103 fish for age 1.1 (95% CI 675-1,759), and 65 fish for age 2.1 (95% CI 16-161). These are jacks or jills.
- For MY2010: 11 fish for age 0.2 (95% CI 0-44); 14,009 fish for age 1.2 (95% CI 10,020-19,492); and 162 fish for age 2.2 (95% CI 65-331).
- For MY2009: 6,101 fish for age 1.3 (95% CI 4,230-8,798), and 184 fish for age 2.3 (95% CI 75-365).
- For MY2008: 54 fish for age 1.4 (95% CI 8-141).

Estimated escapement to LGR by saltwater age was 44 zero-saltwater fish (mini-jacks ≥ 30 cm, FL; 95% CI 10-98); 1,168 one-saltwater fish (jacks or jills; 95% CI 854-1,542); 14,182 two-saltwater fish (95% CI 12,138-16,519); 6,285 three-saltwater fish (95% CI 5,228-7,522); and 54 four-saltwater fish (95% CI 10-119). Estimated escapement to LGR by total age at spawning was 22 fish from BY2010 (95% CI 0-59); 1,136 fish from BY2009 (95% CI 863-1,450); 14,074 fish from BY2008 (95% CI 12,503-15,826); 6,263 fish from BY2007 (95% CI 5,385-7,246); and 238 fish from BY2006 (95% CI 131-367; Figure 14).

Of the 2,123 fish for which gender was successfully determined using the sex-specific assay, 1,072 were female and 1,051 were male (Appendix Table D-8). The gender percentages for the entire run were 50.5% female and 49.5% male (Appendix Table D-9). The sex ratio was not gender-biased throughout the run and ranged from 46.8 to 57.2% males. Expanding the overall percentages to the wild run gives 10,974 females (95% CI 10,223-11,759) and 10,759 males (95% CI 10,010-11,513; Figure 15). We estimate that 0.1% of the females were one-saltwater jills and 11.0% of the males were one-saltwater jacks, and that none of the females and 0.4% of the males were zero-saltwater mini-jacks ≥ 30 cm (FL). Conversely, we estimate that 0.9% of the one-saltwater fish were females and 99.1% were males, and that all of the zero-saltwater mini-jacks ≥ 30 cm (FL) were males.

Based on MM results using the 2,166 fish with complete genotypes, we estimate that 15.7% of the wild return originated from UPSALM; 15.3% from MFSALM; 2.7% from CHMBLN; 18.9% from SFSALM; 43.4% from HELLSC; and 0.4% from TUCANO. The remaining 3.6% of the wild return was identified as fall Chinook salmon based on multi-locus genotype data. Aggregating by MPG, 18.0% of the wild return originated from the Middle Fork Salmon River MPG (combining MFSALM and CHMBLN).

Based on MM results, estimated escapement to LGR by genetic stock was 3,408 fish for UPSALM (95% CI 2,744-4,203); 3,325 fish for MFSALM (95% CI 2,659-4,069); 594 fish for CHMBLN (95% CI 408-826); 4,104 fish for SFSALM (95% CI 3,349-5,075); 9,425 fish for HELLSC (95% CI 8,069-10,979); and 94 fish for TUCANO (95% CI 33-188; Figure 16). Estimated escapement was 3,919 fish for the Middle Fork Salmon River MPG (95% CI 3,232-4,653) which combines MFSALM and CHMBLN. In addition, an estimated 783 fish of the wild return were identified as fall Chinook salmon based on multi-locus SNP data (95% CI 568-1,051).

Of the 2,166 fish with complete genotypes, 1,945 fish had both a determined sex and a total age which were used for genetic stock decomposition (Appendix Table D-10). Percentages of sex by age were calculated for each stock (Appendix Table D-11) and then applied to SY2012 stock escapement estimates (Appendix Table D-12).

Age Validation

Readers accurately determined the ocean-age of 97.8% of the scale samples (n = 82) from known ocean-age PIT-tagged wild steelhead. The known ocean-age sample was 43.9% one-saltwater and 56.1% two-saltwater fish. There were no three- or four-saltwater fish in the known ocean-age sample. In addition, readers accurately identified spawn checks, and accurately determined age after spawn, whether zero or one-saltwater, in 87.5% of known repeat spawning scale samples (n = 32). This was the first year of known repeat spawner scale collection for validation purposes and these samples were collected using the sort-by-code program at LGR. Mean coefficient of variation between primary readers for wild fish analysis was 8.7% for freshwater age and 3.3% for saltwater age.

Readers accurately determined the ocean-age of 98.8% of the scale samples (n = 82) from known ocean-age PIT-tagged wild and hatchery Chinook salmon. The known ocean-age sample was 6.1% one-saltwater, 62.2% two-saltwater, and 31.7% three-saltwater fish. There were no four-saltwater fish in the known ocean-age sample. Mean coefficient of variation between primary readers for wild fish analysis was 2.0% for freshwater age and 1.5% for saltwater age.

DISCUSSION

This report continues the wild Snake River steelhead and Chinook salmon comprehensive stock assessments, exclusive of some Tucannon River fish, that began in SY2009 by Schrader et al. (2011). Our assessments are done at LGR before fish arrive at their spawning grounds, and they are more refined than those done prior to SY2009 because we use window counts that are adjusted by a variety of morphological, marking and tagging, ageing, and genetics data collected from fish captured at the adult trap. Previous assessments used window counts that are unadjusted by various stock parameters such as number of unclipped hatchery fish. Prior to the SY2009 runs, wild steelhead stock assessments were done for the aggregate A-run and B-run at LGR (e.g., Busby et al. 1996, Good et al. 2005; Ford et al. 2010), and wild Chinook salmon stock assessments were done using data collected from spawning ground surveys or from the aggregate at LGR (e.g., Good et al. 2005; Ford et al. 2010).

We continue to refine our stock assessments using parentage based tags (PBT) which began in SY2011 (Schrader et al. 2013). For both species we use PBT to better separate wild fish from unclipped hatchery fish. In this report, through PBT, we are able to identify age-3 and age-4 unclipped hatchery fish that returned from migration year 2011 and 2010 smolt releases, respectively – releases which were BY2008 and BY2009 progeny of hatchery broodstock added to the PBT baseline in SY2008 and SY2009, respectively (Steele et al. 2011). We also would have been able to identify Chinook salmon age-2 unclipped hatchery mini-jacks (≥ 30 cm, FL) – returning from migration year 2012 smolt releases or BY2010 – had any returned. Because hatchery cohort parents prior to BY2008 are not in the baseline, and because all phenotypically wild fish captured at the adult trap in SY2012 were not necessarily genotyped, there is only a “partial” correction to the SY2012 wild fish escapement estimates at LGR, i.e. phenotypic wild

fish that were corrected to be unclipped hatchery fish. In the future, as Snake River basin hatchery broodstocks continue to be added to the baseline, the LGR corrections will become more comprehensive. A mostly “complete” correction will be possible in SY2013 by identification of age-3 to age-5 unclipped hatchery fish (from BY2010, BY2009, and BY2008).

Ideally, the entire run at LGR would be counted accurately at the window or by video, and the entire run would be sampled in a completely systematic random manner at the adult trap. All passage would be through the fish ladder, and all fish passing once through the ladder would continue migrating upstream to spawn. It is well documented that this ideal scenario is not the case (e.g., Boggs et al. 2004; Steinhorst et al. 2010; Cassinelli and Rosenberger 2011; Cassinelli et al. 2012, 2013; Beasley and White 2010; QCI 2011, 2012, 2013). However, despite the imperfections, we discuss below why our estimates are reasonably accurate (unbiased) and relatively precise, and why IDFG has continued to use this same methodology for the last two decades for *U.S. vs. Oregon* TAC and other management forums (e.g., Table 4). Our hope is to make the reader aware of some issues related to counting and sampling fish at LGR in order to aid interpretation of our results, as well as to identify areas where improvement may be needed.

Our wild (and hatchery) escapement estimates are based on unadjusted window counts, i.e. we treat the counts as a complete census. However, there are a number of potential biases when estimating total adult escapement at LGR using unadjusted window counts. Fish may ascend the ladder, be counted, fall back, and reascend the ladder to be counted again, in which case the window count is an overestimate. Fish may fall back and die or go elsewhere downriver to spawn (overestimate). Fish may pass at night or through the navigation lock and not be counted at all (underestimate) Boggs et al. (2004) describe these issues in detail and they used radio telemetry to observe the fate of fish passing LGR during 1996-2001. Overall, they found that the LGR window counts were slightly and positively biased – of the window counts, 91.2-96.6% (n = 4 yr) of steelhead and 95.0-99.5% (n = 5 yr) of spring-summer Chinook salmon continued upriver presumably to spawn. Hydrosystem management currently includes more spill than during the Boggs et al. (2004) study, so these percentages are likely different today. There are no steelhead or Chinook salmon radio telemetry studies similar to Boggs et al. (2004) currently being conducted at LGR to estimate fish-count bias or provide the needed adjustment factors on a yearly basis. However, there are several studies that have attempted to do so, at least partially, using PIT tags (Cassinelli and Rosenberger 2011; Cassinelli et al. 2012, 2013) or a Bayesian modeling approach (Beasley and White 2010; QCI 2011, 2012, 2013).

Cassinelli and Rosenberger (2011) and Cassinelli et al. (2012, 2013) used PIT tags to: 1) adjust for the overestimation caused by double counting from fallback and reascension, and 2) adjust for the underestimation caused by after-hours passage. In general for hatchery spring-summer Chinook salmon, they have shown that the overestimation caused by fallback and reascension is greater than the underestimation caused by after-hours passage. For SY2012, the net difference between the two would have resulted in the adult count at the window being 2,881 fish or 3.3% high and the jack count being the same (Cassinelli et al. 2013). Higher net differences were reported for the SY2011 return (Cassinelli et al. 2012), possibly due to more spill in 2011. However, it is not possible to completely quantify alternate routes of passage or fallback and non-reascension using PIT tags due to incomplete coverage of PIT tag antennas at LGR and throughout the Columbia River basin. As many as 22.2% of radio-tagged steelhead and 28.6% of radio-tagged spring-summer Chinook salmon that fell back at LGR later entered tributaries or hatcheries downstream of LGR (Boggs et al. 2004). Further, not all spawning areas below LGR are currently monitored by PIT antenna arrays. Cassinelli and Rosenberger (2011) and Cassinelli et al. (2012, 2013) concluded that because PIT tags cannot be used for this direct assessment of fallback and non-reascension, their net differences of approximately 3-

11% overestimation is likely a minimum estimate for 2010-2012. Boggs et al. (2004), Cassinelli and Rosenberger (2011), and Cassinelli et al. (2012, 2013) do not report navigation lock passage at LGR, although Boggs et al. (2004) reports this passage at other lower Columbia River dams. There are currently no PIT antenna arrays on navigation locks or spillway bays. At the present time, any adjustments of escapement using PIT tag detections will be biased and incomplete to some unknown degree.

Beasley and White (2010; see also QCI 2011, 2012, 2013) used a Bayesian modeling approach to adjust for sampling inconsistencies in trap operation and fish ladder counts, such as trap closures and missing nighttime counts. For SY2012, our unadjusted LGR wild steelhead escapement estimate of 39,504 fish (95% CI 38,453-40,532; Figure 5) is significantly more than the estimate of 34,799 fish (95% CI 33,539-35,203) reported by the ISEMP project (QCI 2013). Our unadjusted wild Chinook salmon escapement estimate of 21,733 fish (95% CI 20,968-22,507; Figure 12) is slightly less than but not significantly different from their estimate of 21,746 fish (95% CI 19,738-23,754).

Another issue that may potentially bias our wild escapement and composition estimates is related to the sort-by-code process. There are two sampling processes or events that occur at the adult fish trap: systematic random sampling and sort-by-code. For the latter, the computer guiding the trap gate is programmed with a series of predetermined PIT tag codes. In SY2012, these steelhead codes included: fish that were previously trapped and PIT tagged at LGR then returned as repeat spawners (present study), and Dworshak hatchery fish that were PIT tagged as juveniles (Alan Byrne, IDFG, personal communication). These Chinook salmon codes included: Lemhi River wild fish that were PIT tagged as juveniles (Bowersox and Biggs 2013); McCall and Rapid River hatchery fish that were PIT tagged as juveniles (Cassinelli et al. 2013); and Snake River fall Chinook salmon that were PIT tagged as juveniles (Tiffani Marsh, NMFS; personal communication). If one of these tags is detected in the ladder, the computer opens the trap gate and diverts the tagged fish into the trap. Although sort-by-code is assumed to be an independent sampling process or event, a potential problem arises because fish frequently migrate in groups; therefore, untagged "by-catch" fish may accompany the tagged individual. One result is that the percent of the run actually trapped is often higher than the desired trap rate (Appendix Tables C-1 and D-1). This is especially problematic for estimates based on trap expansions (e.g., Steinhorst et al. 2010; QCI 2013) and leads to overestimation. To address this issue, our wild (and hatchery) escapement estimate is stratified over time (statistical weeks) and partitions the trap data into time groups along with the window counts. We assume that these extra by-catch fish are random and do not differ from the systematic sample in terms of origin or size. If true, the only effect of the sort-by-code by-catch is to increase the sample size for any particular time stratum. Due to the various issues affecting the true trapping rate, our escapement estimates based on window counts should be more accurate than estimates based on trap expansions.

It is possible that our wild escapement estimates at LGR are slightly positively biased, and this has some potential to impact management as they and estimates at other dams in the hydrosystem are used to plan fishing seasons. However, our estimates are still more accurate than estimates based solely on window counts due to our accounting and removal of unclipped hatchery fish from wild fish estimates. This ensures for risk-averse planning in regards to harvest impacts on ESA-listed populations. Given greater scrutiny on steelhead in the Columbia River basin, our estimate will allow for a fishing season planning process similar to that for Chinook salmon. We note that IDFG managers have been estimating wild steelhead escapement at LGR for several decades, and these estimates have been used in *U.S. vs. Oregon TAC* and other management forums (e.g., Table 4).

Time stratification is not necessary for our composition estimates because we can systematically subsample all wild fish trapped at LGR and because this sample pool can be considered a simple random sample selected in proportion to abundance (Kirk Steinhorst, University of Idaho, personal communication). The effective result is that the percent of the run actually aged and genotyped for sex and stock was approximately constant over time (Appendix Tables C-5 and D-5). It was not exactly constant over time because scale and tissue samples of wild fish were taken inconsistently from some portions of the run. This was due to trap closure, extra sort-by-code “by-catch” fish, and perhaps other unknown reasons. The trap typically closes in late summer due to high water temperatures and in early winter due to freezing water temperatures. We recommend that COE in conjunction with NMFS explore fixing the high water temperature issue, which is caused by the surface location of the fish ladder water intake. This would also likely result in more attractive fish ladder entrance water temperatures. In the meantime, adequate sampling prior to and after short closures should allow valid interpolation of the data.

Abundance and stock composition estimation for spring-summer Chinook salmon at LGR could potentially be confounded by the short period of overlap in migration timing with fall-run Chinook salmon. Of the 21,733 wild Chinook salmon returning to LGR between March 1 and August 17, 2012, we estimate that 783 fish or 3.6% of the escapement during this period were actually fall Chinook salmon as determined by genetics, with the remaining 20,950 fish being spring-summer Chinook salmon. However, in addition to fall Chinook salmon identified within the spring-summer Chinook salmon escapement time period, it is also likely that some summer Chinook salmon arrive at LGR after the August 17 cutoff date. Several summer Chinook salmon individuals, based on phenotypic characteristics, were recorded by the trap crew after this date (Darren Ogden, NMFS, personal communication). Individual assignment testing of known origin genetic samples indicates 100% accuracy in our ability to differentiate spring-summer Chinook salmon from fall Chinook salmon (Ackerman et al. 2014). In the future, we may use genetic individual assignment to assess the accuracy of these phenotypic characteristics to discriminate between the two run types.

We provide age composition estimates of steelhead and Chinook salmon adults at LGR based on scale analysis in this report and the previous reports (Schrader et al. 2011, 2012, 2013). This is the third year which we estimate repeat spawning steelhead as well as mini-jack Chinook salmon. Laboratory personnel continue to improve their ageing techniques and validate their readings for fish that display these unusual life history strategies. As our reference baseline for these unusual types of fish continues to grow as LGR samples are added, accuracy in age assignment should continue to improve. In addition, in SY2013 we will continue to use the sort-by-code feature at LGR to sample known repeat spawning steelhead as determined by PIT tags. Another study to define life histories of Chinook salmon based on scales, including mini-jacks, was recently completed by Johnson et al. (2012).

Ackerman et al. (2012) and Schrader et al. (2012) estimated there were genetic individual assignment concordance rates of 92.0% for steelhead and 92.6% for Chinook salmon using tributary PIT-tag array or hatchery trap PIT-tag detections in SY2010. However, caution should be used when interpreting these comparisons since the two methods measure fundamentally different things at different locations and at different scales. Genetic individual assignments are used to estimate the stock of *origin* for adults that return to LGR (Ackerman et al. 2012). The tributary PIT-tag arrays and hatchery traps attempt to estimate the final *destination* of adults that are sampled at LGR, with the assumption that their homing instinct returns most fish to their natal streams to spawn (Beasley and White 2010; QCI 2011, 2012,

2013). While we expect to see similarities between genetic assignments and location of PIT-tag detections, we also expect that wandering adults, straying adults, or genetic misassignments could lead to some discordance between the two methods. In the larger context, and for the only location that is directly comparable for both species using the two methods, we note that our genetic stock estimate for South Fork Salmon River steelhead in SY2012 was 960 fish at LGR (95% CI 619-1,418; Figure 9), which is less than but not statistically different from the ISEMP PIT-array escapement estimate of 1,510 fish (95% CI 1,244-1,776; QCI 2013). For South Fork Salmon River Chinook salmon, our genetic stock estimate of 4,104 fish at LGR (95% CI 3,349-5,075; Figure 16) is significantly greater than the ISEMP PIT-array escapement estimate of 1,592 fish (95% CI 1,374-1,810; QCI 2013). The latter discrepancy needs to be investigated but is beyond the scope of this report. However, we emphasize that both methods for both species are highly dependent on the wild escapement estimates generated at LGR, which is also calculated using different methods. In addition, Ackerman et al. (2012) concluded that stock composition estimates based on genetic stock identification for both South Fork Salmon River genetic stocks may slightly underestimate the true compositions based on mixture modeling of known origin individuals. A third independent method to estimate South Fork Salmon River Chinook salmon spawner abundance based on redd count expansions is currently being developed by IDFG and the Nez Perce Tribe.

The wild escapement and composition estimates reported here will be used to evaluate the status of wild populations relative to three viable salmonid population (VSP) criteria: abundance, productivity, and diversity. We directly estimate adult abundance at LGR as well as elements of diversity such as sex ratio, life history variations, and run timing. We estimate abundance by brood year through use of age data, and these estimates are necessary for productivity analyses. Productivity is the generational replacement rate, defined as the number of progeny per parent. In the future, estimates of wild adult abundance and composition will be combined with similar information for smolts from the LGR juvenile facility (e.g., Copeland et al. 2013b). This will enable us to estimate adult-to-adult, adult-to-juvenile, and juvenile-to-adult productivity. The data necessary to compute productivity accumulate over time. In general, it will take 4-5 years before the first productivity data are complete.

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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; Ford et al. 2010; NMFS 2011).

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 and Rapid Rivers 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. Lookingglass 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

Reintroduced fish exist in extirpated areas except the North Fork Clearwater River.

Table 2. Status of the fish ladder, the fish counting window and video, and the adult trap sample rate at Lower Granite Dam, 7/1/2011 to 8/17/2012 (COE 2011, 2012; Ogden 2012, 2013).

Sampling period 2011-12	Statistical week	Ladder open?	Window count?	Video count?	Adult trap sample rate	
7/1-7/3	27	Yes, Start 7/1/11, End 1/3/12	Yes, 0400-2000, Start 7/1/11, End 10/31/11	Yes, 0200-0400, Start 7/1/11, End 9/30/11 (sockeye and lamprey only)	0.10 Rate, Start 7/1/11, End 11/20/11	
7/4-7/10	28					
7/11-7/17	29					
7/18-7/24	30					
7/25-7/31	31					
8/1-8/7	32					
8/8-8/14	33					
8/15-8/21	34					
8/22-8/28	35					
8/29-9/4	36					
9/5-9/11	37					
9/12-9/18	38					
9/19-9/25	39					
9/26-10/2	40					
10/3-10/9	41		No, Start 10/1/11, End 10/31/11			
10/10-10/16	42					
10/17-10/23	43					
10/24-10/30	44					
10/31-11/6	45					
11/7-11/13	46					
11/14-11/20	47					
11/21-11/27	48					
11/28-12/4	49					
12/5-12/11	50					
12/12-12/18	51	No, Start 11/1/11, End 3/31/12				
12/19-12/25	52					
12/26-1/1	53-1					
1/2-1/8	2					
1/9-1/15	3					
1/16-1/22	4					
1/23-1/29	5					
1/30-2/5	6					
2/6-2/12	7					
2/13-2/19	8					
2/20-2/26	9	Yes, 0600-1600, Start 3/1/12, End 3/31/12				
2/27-3/4	10					
3/5-3/11	11					
3/12-3/18	12					
3/19-3/25	13					
3/26-4/1	14					
4/2-4/8	15					
4/9-4/15	16					
4/16-4/22	17					
4/23-4/29	18					
4/30-5/6	19	No, Start 4/1/12, End 6/14/12				
5/7-5/13	20					
5/14-5/20	21					
5/21-5/27	22					
5/28-6/3	23					
6/4-6/10	24					
6/11-6/17	25					
6/18-6/24	26					
6/25-7/1	27					
7/2-7/8	28					
7/9-7/15	29	Yes, 0400-2000, Start 4/1/12, End 8/17/12				
7/16-7/22	30					
7/23-7/29	31					
7/30-8/5	32					
8/6-8/12	33					
8/13-8/17	34					
						0.10 Rate, Start 3/8/12, End 8/12/12 (except closed 7/27 to 7/29, and 8/6 to 8/9)
						Trap Closed

Table 3. External mark and internal tag key used to determine hatchery origin steelhead and Chinook salmon at Lower Granite Dam (LGR), spawn year 2012.

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	Hatchery	Hatchery	Hatchery
Coded wire tag (CWT)	N/A(a)	Hatchery	Hatchery
Ventral fin clip	N/A	Hatchery	Hatchery
Dorsal/ventral fin erosion (steelhead only)	N/A	Hatchery	Hatchery
Parentage based tag (PBT)	N/A	N/A	Hatchery(b)
Passive integrated transponder (PIT)	N/A	N/A	N/A(c)

(a) N/A = not applicable.

(b) Started in SY2011 with complete coverage by SY2013.

(c) Needs resolution due to minor discrepancies between PIT-tag database (PTAGIS) and LGR trap databases (LGTrappingDB, Biosamples, and Progeny).

Table 4. Estimated annual total escapement, by fish size and origin, of steelhead at Lower Granite Dam (LGR), spawn years 1976-2012. Large fish are greater than or equal to 78 cm (FL) and small fish are less than 78 cm (FL). Clipped and unclipped refer to the adipose fin. Estimates for 1987 and later were generated by IDFG and are the COE window counts decomposed using NMFS adult trap data (Alan Byrne, IDFG, personal communication; Schrader et al. 2011, 2012, 2013; present study). Estimates for 1986 and earlier are the COE window counts decomposed using an unknown method.

Spawn year	LGR window count(a)	Estimated number of steelhead at LGR that were:								Total hatchery	Total wild
		Large wild(b)	Large hatchery clipped	Large hatchery unclipped(b)	Small wild(b)	Small hatchery clipped	Small hatchery unclipped(b)				
1976	16,608	N/A(c)	N/A	N/A	N/A	N/A	N/A	N/A	3,934	12,674	
1977	22,501	N/A	N/A	N/A	N/A	N/A	N/A	N/A	13,538	8,963	
1978	56,979	N/A	N/A	N/A	N/A	N/A	N/A	N/A	34,754	22,225	
1979	26,480	N/A	N/A	N/A	N/A	N/A	N/A	N/A	13,293	13,187	
1980	28,778	N/A	N/A	N/A	N/A	N/A	N/A	N/A	12,343	16,435	
1981	38,058	N/A	N/A	N/A	N/A	N/A	N/A	N/A	16,208	21,850	
1982	42,388	N/A	N/A	N/A	N/A	N/A	N/A	N/A	24,470	17,918	
1983	72,325	N/A	N/A	N/A	N/A	N/A	N/A	N/A	47,115	25,210	
1984	89,296	N/A	N/A	N/A	N/A	N/A	N/A	N/A	70,807	18,489	
1985	104,661	N/A	N/A	N/A	N/A	N/A	N/A	N/A	80,107	24,554	
1986	116,063	N/A	N/A	N/A	N/A	N/A	N/A	N/A	89,417	26,646	
1987	129,945	5,463	36,969	0	16,613	70,900	0	107,869	22,076		
1988	71,402	5,347	13,473	0	20,164	32,418	0	45,891	25,511		
1989	87,063	4,614	22,006	0	15,700	44,743	0	66,749	20,314		
1990	131,348	8,042	39,866	0	16,937	66,503	0	106,369	24,979		
1991	56,881	4,483	22,015	0	4,806	25,577	0	47,592	9,289		
1992	99,085	3,182	11,883	0	14,135	69,885	0	81,768	17,317		
1993	128,380	5,777	25,566	0	13,617	83,420	0	108,986	19,394		
1994	59,674	1,790	15,895	0	7,332	34,657	0	50,552	9,122		
1995	47,238	2,231	7,178	0	5,873	31,956	0	39,134	8,104		
1996	79,145	1,334	8,317	0	6,721	62,773	0	71,090	8,055		
1997	86,911	1,645	12,211	0	5,980	67,075	0	79,286	7,625		
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	5,729	39,887	6,933	20,035	93,380	12,906	153,106	25,764		
2010	323,382	4,330	16,309	2,634	38,443	231,167	30,499	280,609	42,773		
2011	208,296	9,195	31,245	4,100	35,209	110,481	18,066	163,892	44,404		
2012	180,320	4,345	17,749	2,111	35,159	113,060	7,896	140,816	39,504		

(a) Downloaded from COE link 7/2/13.

(b) Spawn year 2011 was first year of adult PBT returns used to adjust unclipped estimates.

(c) N/A = trap data not available.

FIGURES

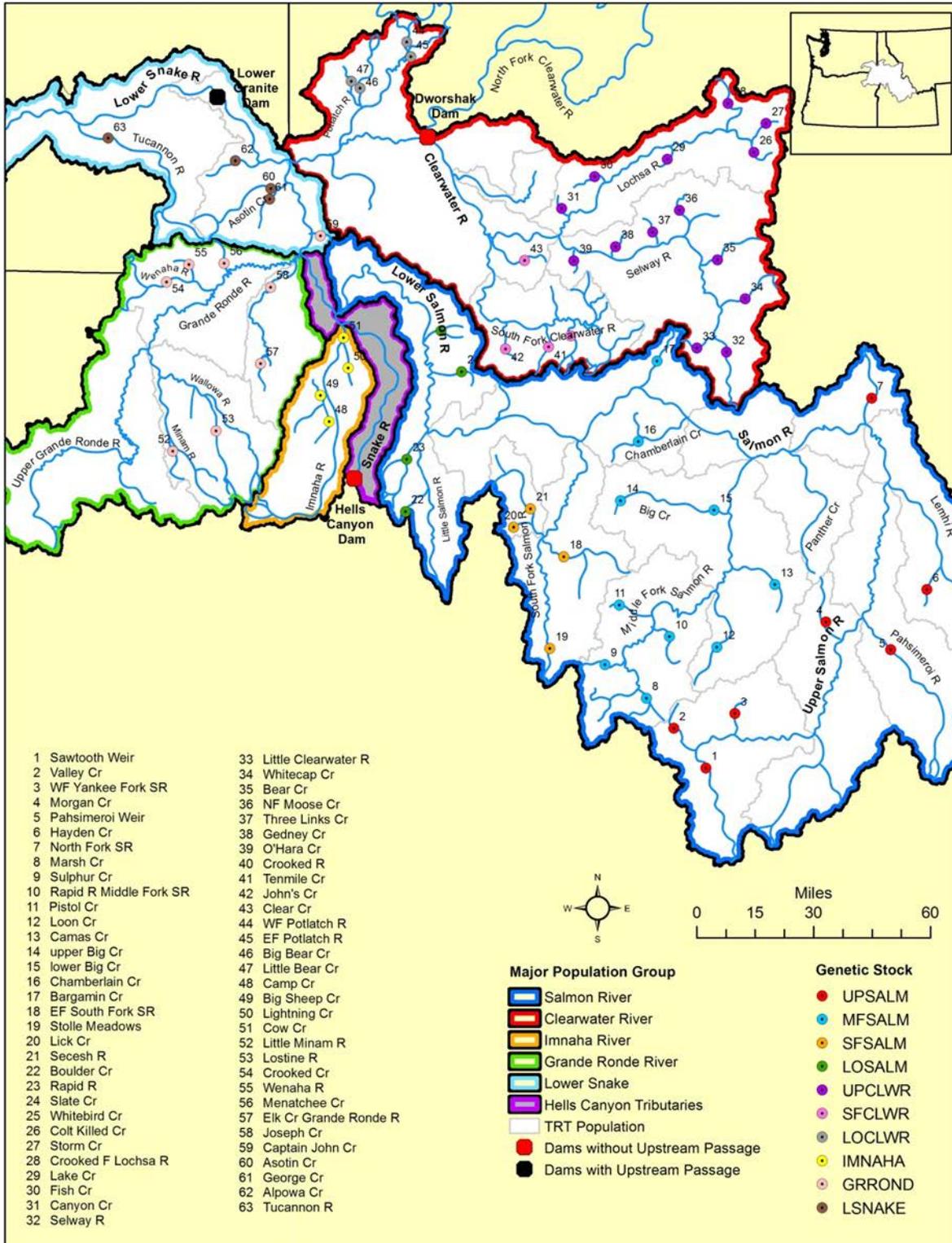


Figure 1. Genetic stocks and baseline collections used for steelhead mixed stock analysis at Lower Granite Dam, spawn year 2012 (Ackerman et al. 2014). The Hells Canyon Tributaries MPG (shaded gray) does not support independent populations and is considered extirpated (NMFS 2011).

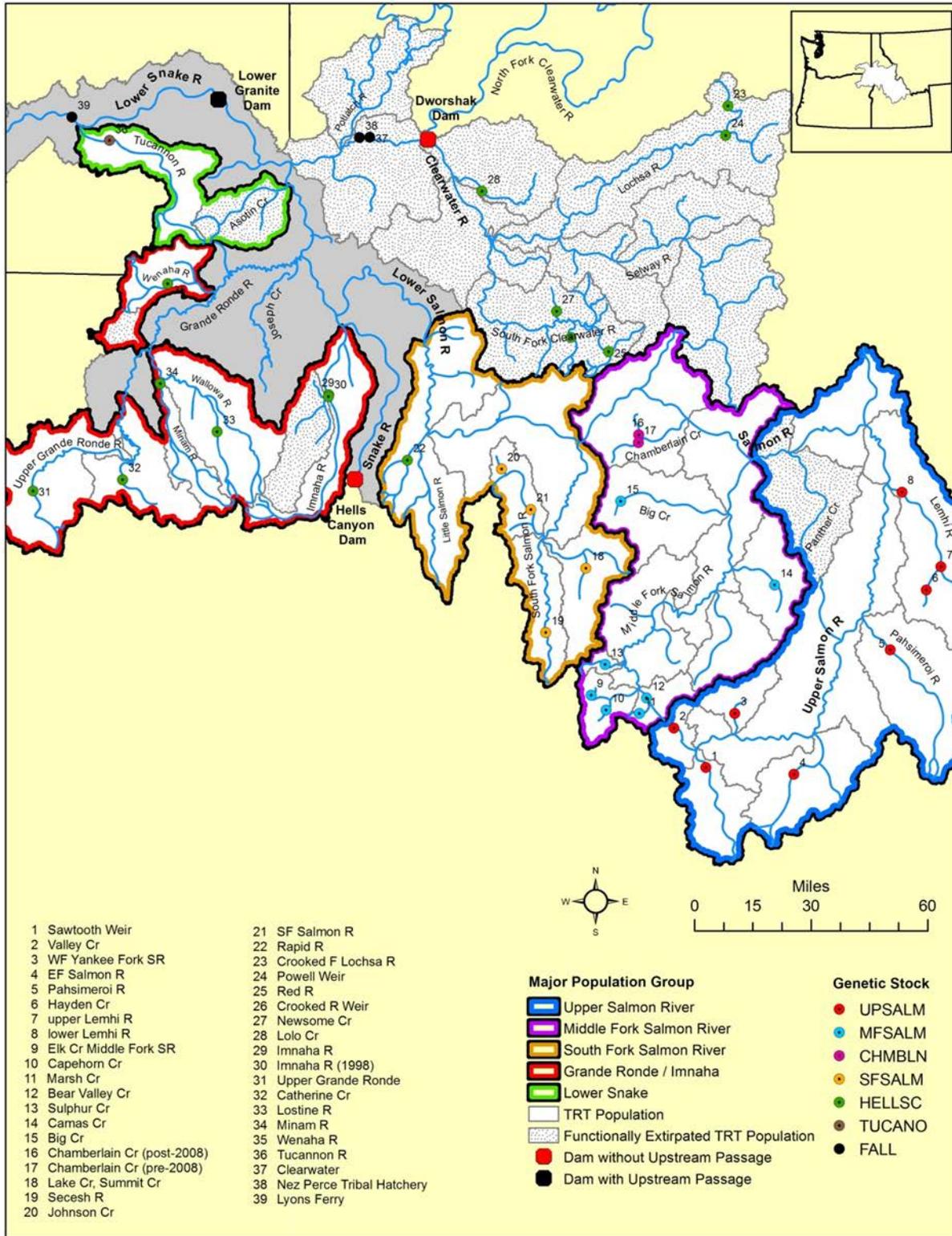


Figure 2. Genetic stocks and baseline collections used for Chinook salmon mixed stock analysis at Lower Granite Dam, spawn year 2012 (Ackerman et al. 2014). Reintroduced fish exist in functionally extirpated TRT populations as mapped.

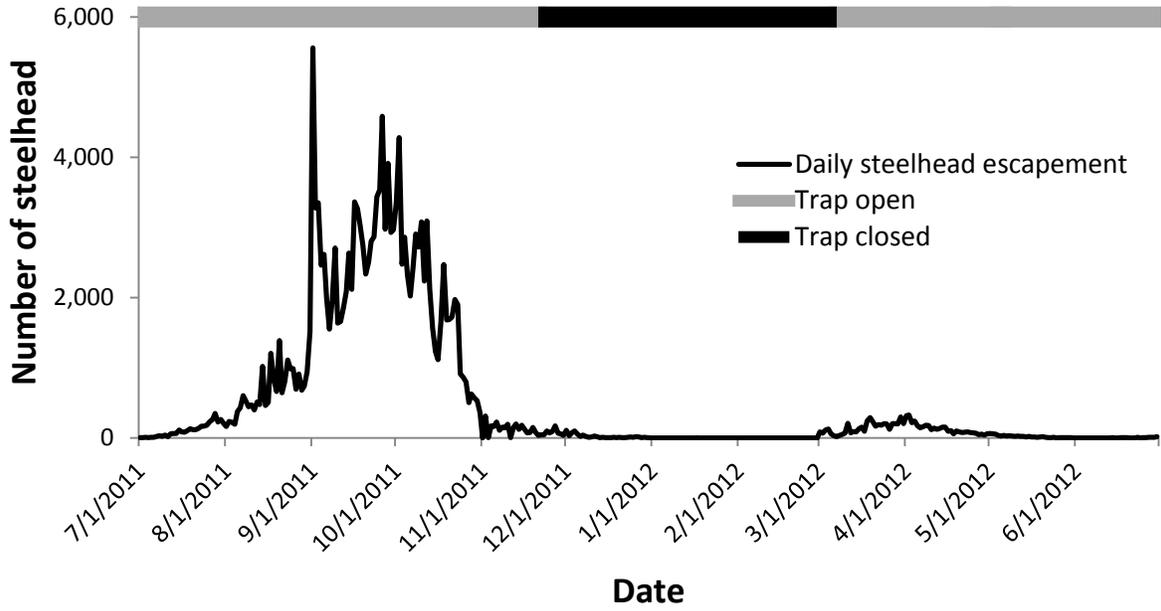


Figure 3. Daily number of steelhead counted at the Lower Granite Dam window or by video, spawn year 2012. Horizontal bar indicates when the adult trap was open or closed; overall, it was open during 98.9% of the total run (n = 180,320).

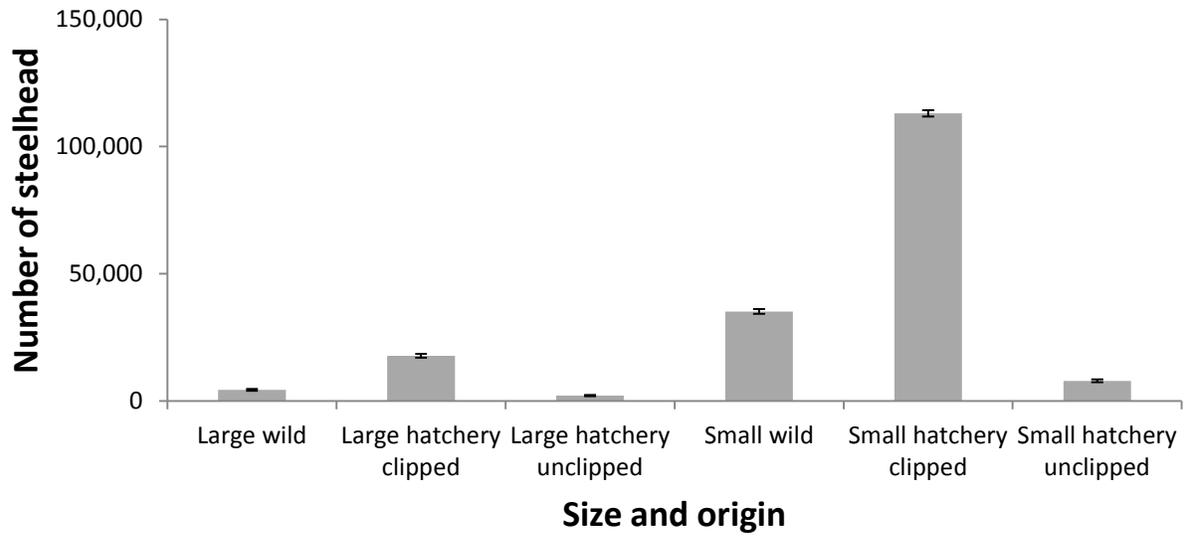


Figure 4. Estimated escapement, by fish size and origin, of steelhead at Lower Granite Dam, spawn year 2012. Large fish are greater than or equal to 78 cm (FL) and small fish are less than 78 cm (FL). Clipped and unclipped refer to the adipose fin. Confidence intervals are at 95%.

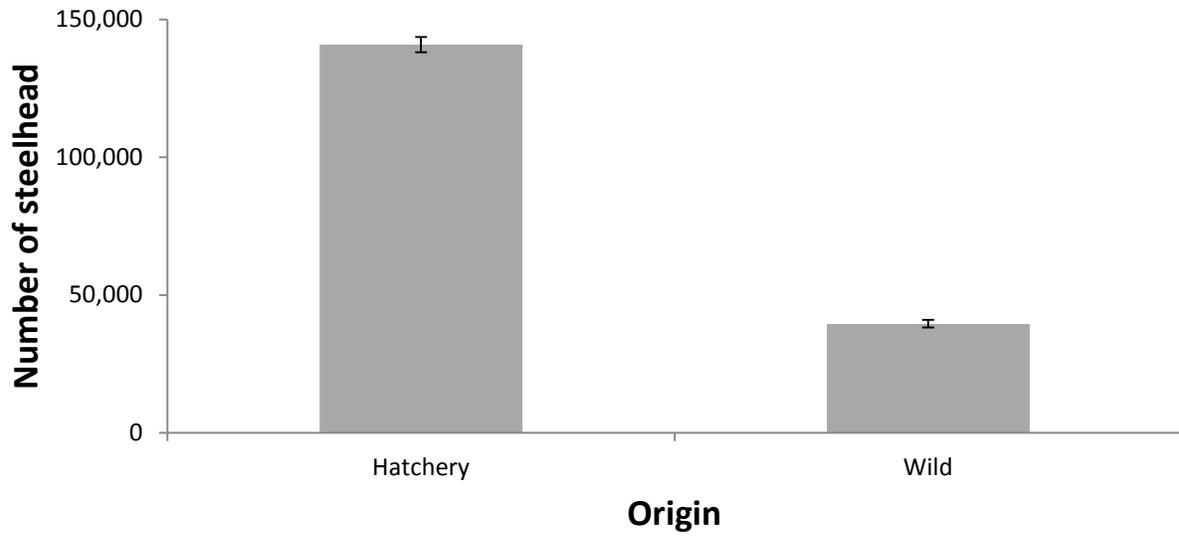


Figure 5. Estimated hatchery and wild steelhead escapement at Lower Granite Dam, spawn year 2012. Confidence intervals are at 95%.

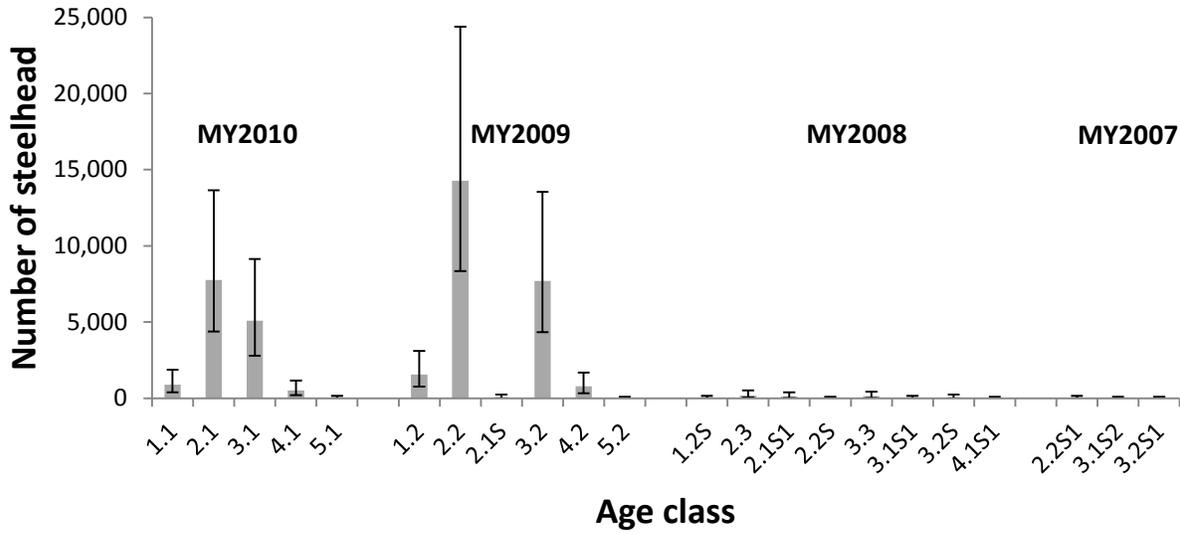


Figure 6. Estimated escapement by age class, grouped by smolt migration year (MY), of wild adult steelhead at Lower Granite Dam, spawn year 2012. Large and small fish were combined. Confidence intervals are at 95%.

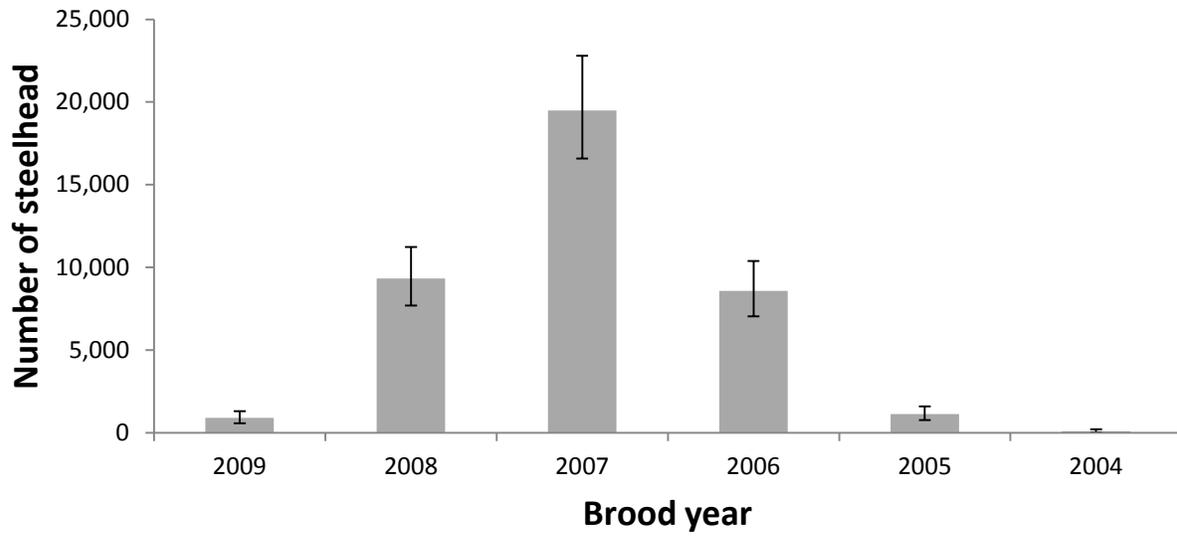


Figure 7. Estimated escapement by brood year of wild adult steelhead at Lower Granite Dam, spawn year 2012. Large and small fish were combined. Confidence intervals are at 95%.

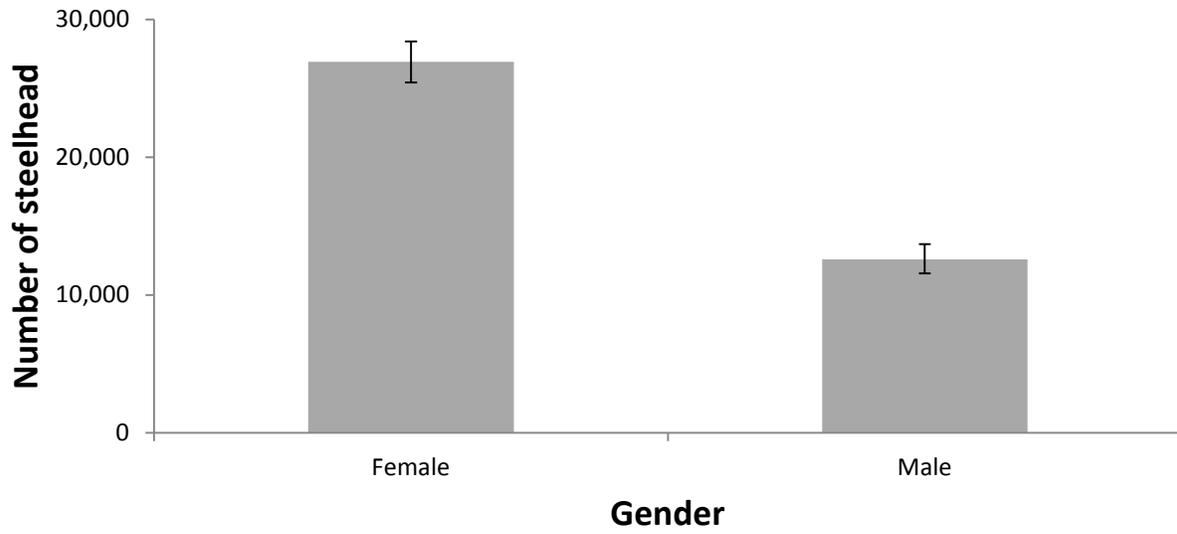


Figure 8. Estimated escapement by gender of wild adult steelhead at Lower Granite Dam, spawn year 2012. Large and small fish were combined. Confidence intervals are at 95%.

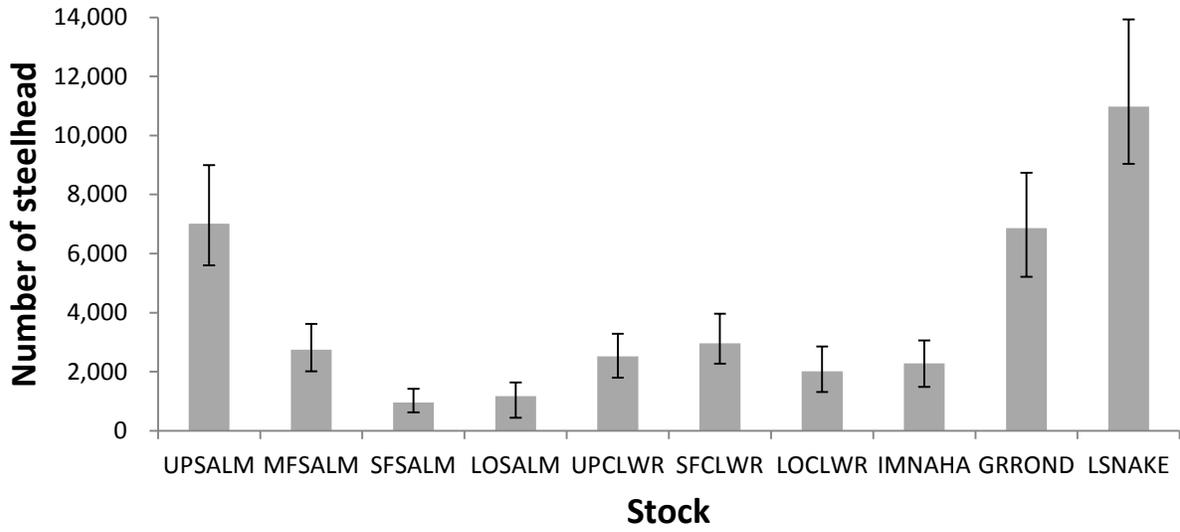


Figure 9. Estimated escapement by genetic stock of wild adult steelhead at Lower Granite Dam, spawn year 2012. Large and small fish were combined. Confidence intervals are at 95%. See Appendix Table B-1 for stock abbreviations.

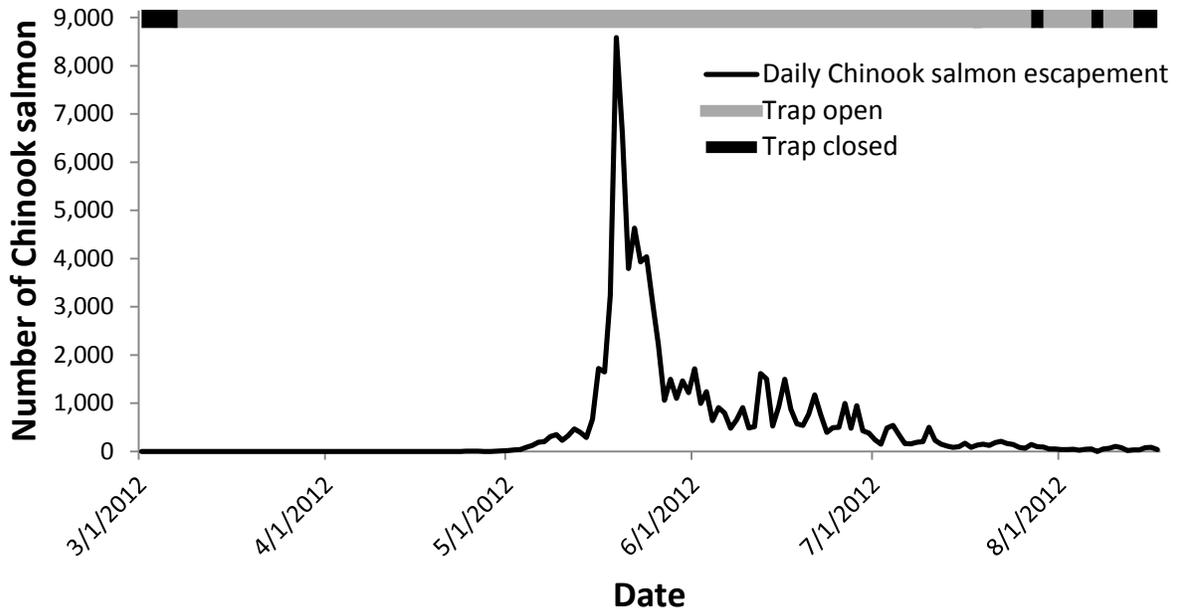


Figure 10. Daily number of Chinook salmon counted at the Lower Granite Dam window or by video, spawn year 2012. Horizontal bar indicates when the adult trap was open or closed; overall, it was open during 99.0% of the total run (n = 84,771).

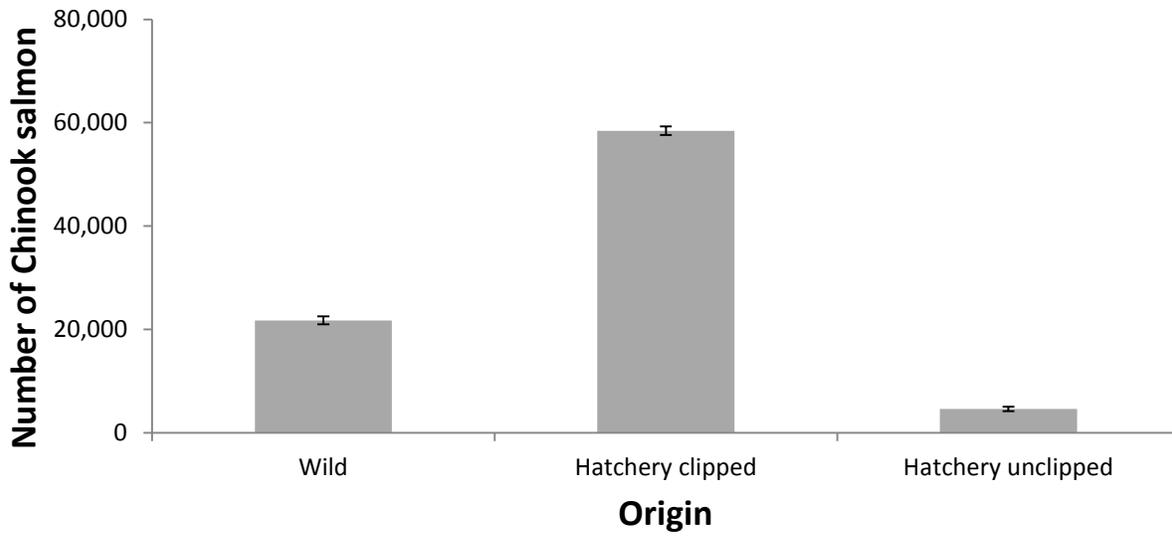


Figure 11. Estimated escapement by origin of Chinook salmon at Lower Granite Dam, spawn year 2012. Clipped and unclipped refer to the adipose fin. Confidence intervals are at 95%.

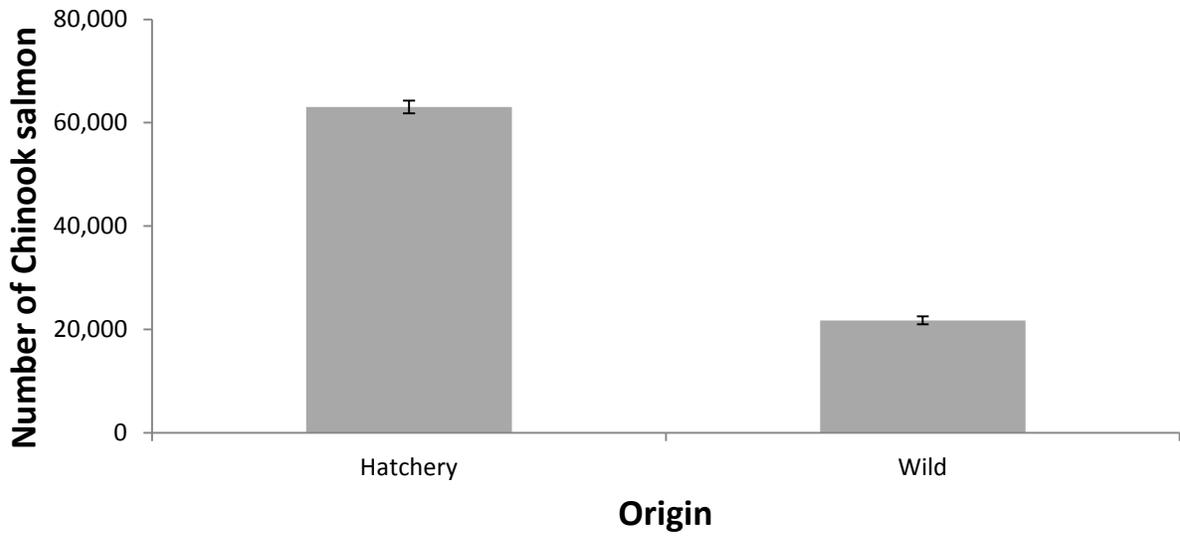


Figure 12. Estimated hatchery and wild Chinook salmon escapement at Lower Granite Dam, spawn year 2012. Confidence intervals are at 95%.

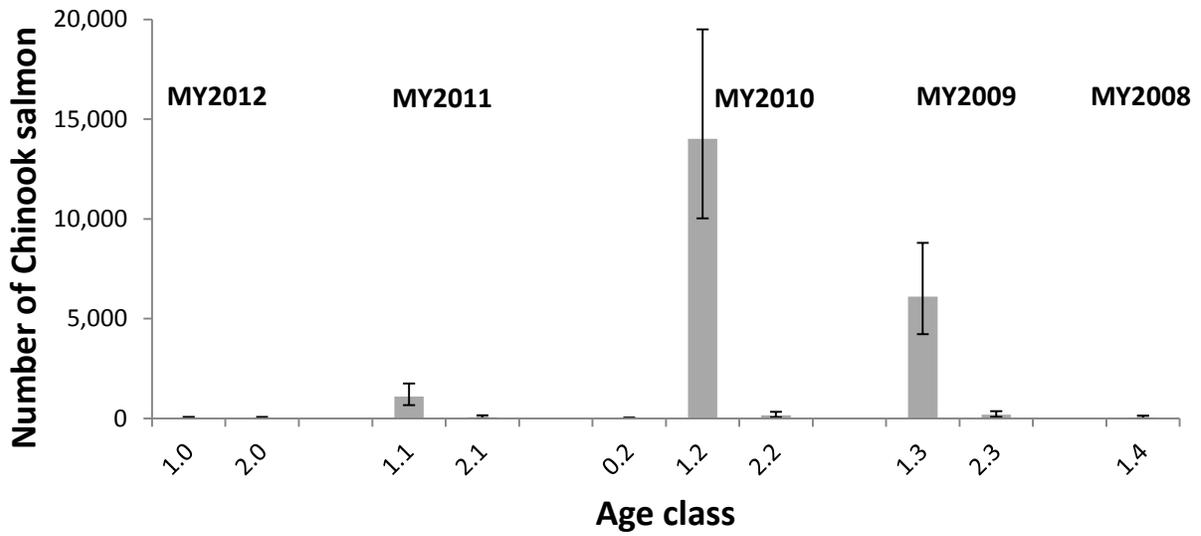


Figure 13. Estimated escapement by age class, grouped by smolt migration year (MY), of wild adult Chinook salmon at Lower Granite Dam, spawn year 2012. Confidence intervals are at 95%.

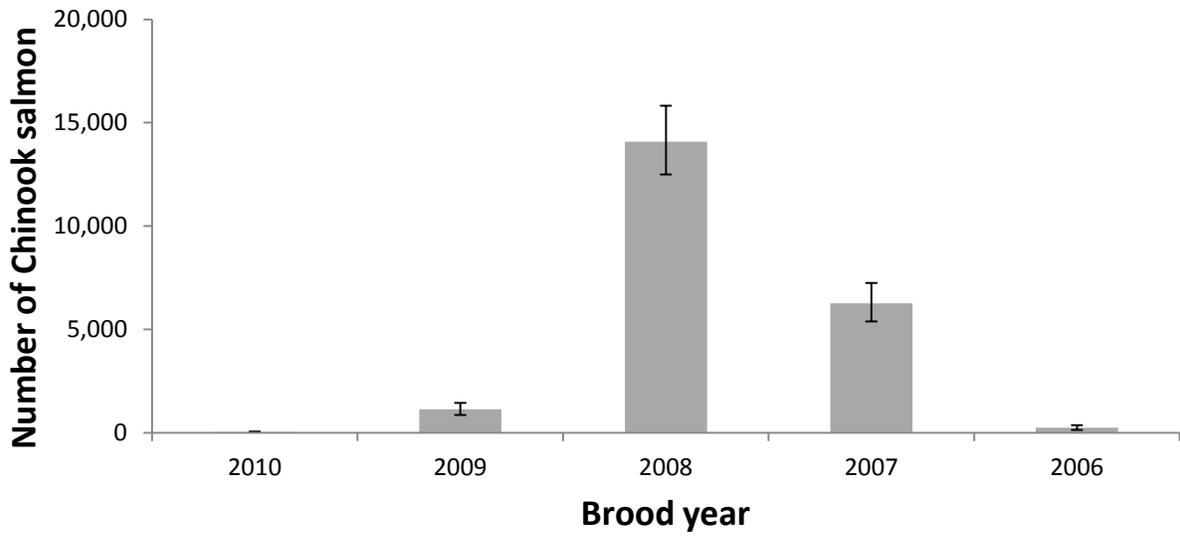


Figure 14. Estimated escapement by brood year of wild adult Chinook salmon at Lower Granite Dam, spawn year 2012. Confidence intervals are at 95%.

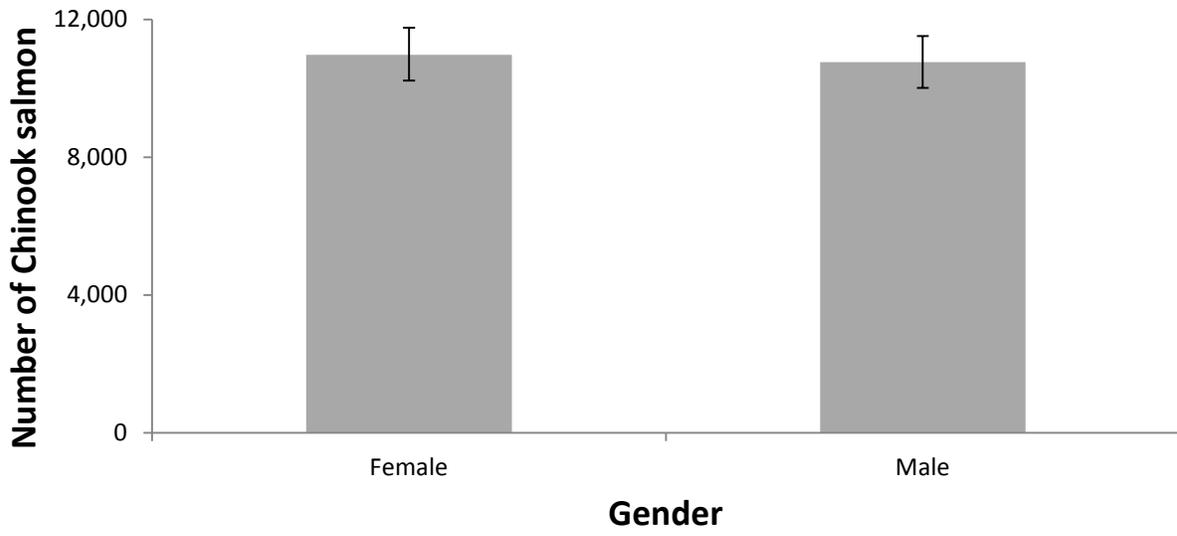


Figure 15. Estimated escapement by gender of wild adult Chinook salmon at Lower Granite Dam, spawn year 2012. Confidence intervals are at 95%.

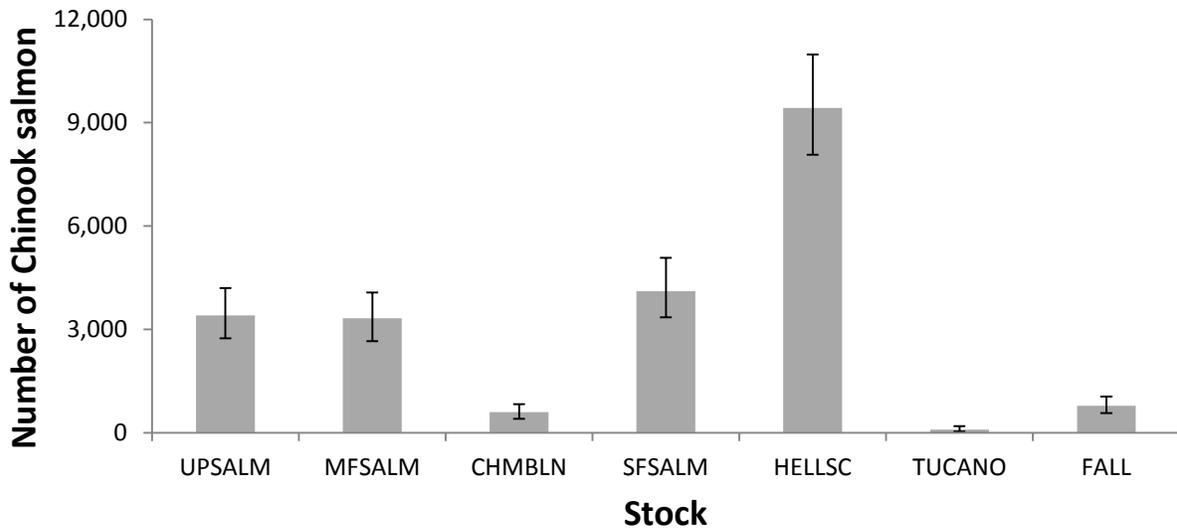


Figure 16. Estimated escapement by genetic stock of wild adult Chinook salmon at Lower Granite Dam, spawn year 2012. Confidence intervals are at 95%. See Appendix Table B-2 for stock abbreviations.

APPENDICES



Field Sampling Protocol for Steelhead and Spring/Summer Chinook Salmon at the Lower Granite Dam Adult Trap, July 1 to November 30, 2011

By:
IDFG, QCI, PSMFC, NOAAF

Specific Data Requirements for 2011 Season

This protocol outlines specific Lower Granite Dam (LGR) adult trap sampling and field data management procedures for:

- 1) Documentation of marks, tags, fin clips, and fin erosion for all fish to determine the proportion by origin, the proportion of adipose intact fish that are unmarked fish of hatchery origin, etc;
- 2) Length measurements of all fish to determine length distribution, length at age, A/B partition, etc;
- 3) Scale collections from all natural origin fish, all previously PIT tagged hatchery origin fish, and a 1,000 fish subsample of non-PIT tagged hatchery origin fish to estimate age composition, length at age, etc;
- 4) Tissue collections from all natural origin fish and all previously PIT tagged hatchery origin fish to estimate contribution rates and sex ratios of fish migrating to specific Snake River genetic reporting groups;
- 5) Passive integrated tag (PIT) placement in all natural origin fish and unclipped hatchery steelhead (stubbies) to estimate tributary specific escapement.

Once adult fish are trapped, all information from sampled fish will be recorded on the Field Data Entry Forms, in the FS2001 PIT tag reader (set up FS2001 PIT tag reader correctly and header information is completed for each day of sampling; see FS2001 Reader Use Section), and on the associated scale collection packets and genetic tissue vials. An individual sampled fish must have an identical, corresponding number placed on the Field Data Entry Form, scale sample packets and/or tissue sample vial. Each fish will have a unique sample number. Below are the required elements of field data and the field data form:

1. All spring/summer Chinook salmon (July 1- August 17) and steelhead (July 1 – November 30) from the trap will be classified as to species and whether adipose fin clipped hatchery fish; unclipped hatchery fish (see **Figure 1** – steelhead determined by fin erosion, other external marks, or CWT's; Chinook determined by other external marks or CWT's); or unclipped natural origin fish. Clipped and unclipped hatchery fish (with CWT's) will be lumped together for sampling scales. All trapped fish will be visually

scanned for the presence or absence of an adipose fin, and all unclipped steelhead will be visually scanned for the presence of fin erosion that typifies stubbies.

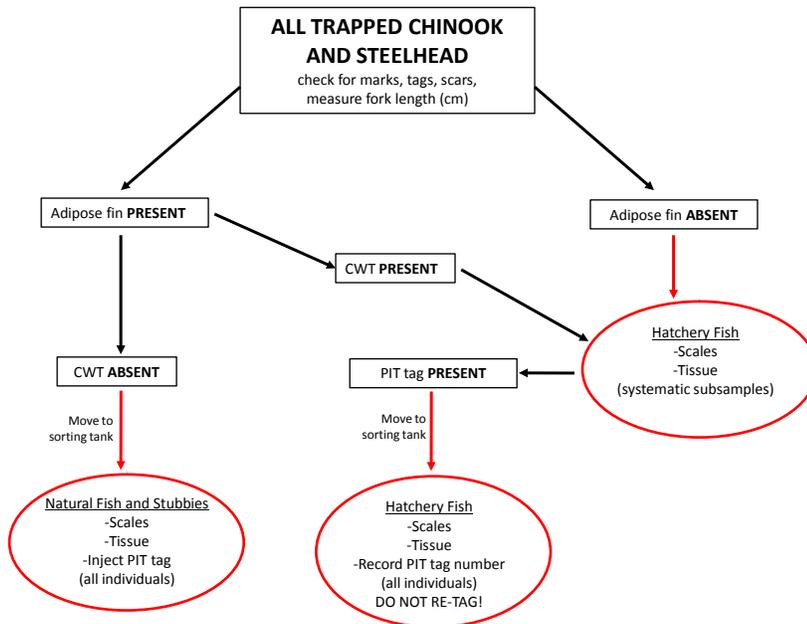
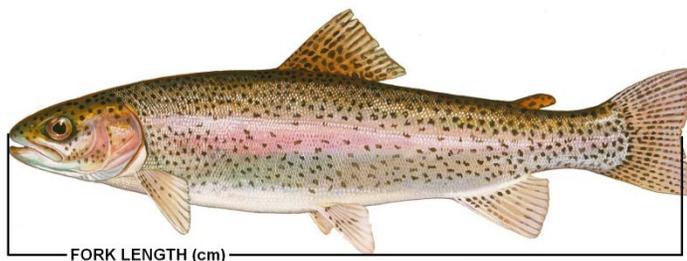


Figure 1. Chinook and steelhead natural/hatchery determination process and sorting procedure. Stubbie steelhead will be treated in the same manner as natural fish. Data collected from natural fish, stubbies, and recaptured PIT tagged fish will be recorded on a separate datasheet at the natural fish sorting tank.

2. All spring/summer Chinook salmon and steelhead from the trap will be examined for other fin clips (pelvic, pectoral, etc.), external marks (brands, elastomer, VIE, etc.), external tags (floy tags, jaw tags, etc.) and internal tags (PIT, CWT, radio tags) and noted in the appropriate columns on the field form.
 - a. If a PIT tag is detected, note on the form that it is a **recapture**, write down the entire PIT tag number and **continue with the tissue/scale sampling; however do not place another PIT tag into the fish.**
3. Any significant injuries will be noted in the comment column.
4. All spring/summer Chinook salmon and steelhead from the trap will be measured to the nearest centimeter (fork length).



5. For all spring/summer Chinook salmon and steelhead that are sampled, five to six scales will be removed from the preferred area on one side of the fish, for a total of 15 to 20 scales per sample. Scales should be left un-cleaned and stored in paper envelopes. Care should be taken to store envelopes in such a manner that they can dry quickly. Sample number from the field form must correspond to the same number on the sample packet.
 - a. All natural origin fish and stubbies from the trap will have scale samples taken.
 - b. All previously PIT tagged hatchery origin fish will have scale samples taken.
 - c. A scale subsample of ~1,000 hatchery fish will be taken systematically across the run.

6. For all spring/summer Chinook salmon and steelhead that are sampled, a piece of tissue should be taken from the top of the caudal fin or the bottom of the anal fin and stored in a closed vial with 100% non-denatured ethanol for future genetics analysis. Sample number from the field form must correspond to the same number on the sample vial.
 - a. All natural origin fish and stubbies from the trap will have tissue samples taken.
 - b. All previously PIT tagged hatchery origin fish will have tissue samples taken.

7. For all spring/summer Chinook salmon and steelhead that are sampled, a 12 mm PIT tag should be placed in the pelvic girdle location using the provided pre-loaded PIT tag needles.
 - a. All natural origin fish and stubbies from the trap will be released with a single PIT tag, either newly tagged at the trap or from a previous tagging event (e.g. recaptured from juvenile PIT tagging, Bonneville PIT tagging, etc).
 - b. **Do not** PIT tag the fish if it is already PIT tagged, i.e. no double tagging.
 - c. After tagging, wand the fish with the FS2001 to ensure the PIT tag is placed appropriately in the fish.
 - d. Note the last 10 digits of the PIT tag code, and time of placement – record in the appropriate columns on the field data.

8. **Make sure tissue/scale samples are collected from every new PIT-tagged fish and every previously PIT-tagged fish (recaptures).** The only exception to this rule is PIT tagged fallback fish when previous tissue/scale sample collection is obvious. Please record PIT numbers for fallbacks.

Scale Sample Collection for 2011 Season

Collection of scale samples requires following only a few simple steps. The two most important things to remember are to guard against cross contamination of samples and to make sure that all information is filled out on the sample envelopes. At every step of the collection process, care must be taken to keep individual samples separate.

Collection Packets (Sample Envelopes)

2 ½" x 4 ¼" (6.4 x 10.8 cm) Coin envelopes (as many as needed)

2" x 8" strips of paper (same # as coin envelopes)

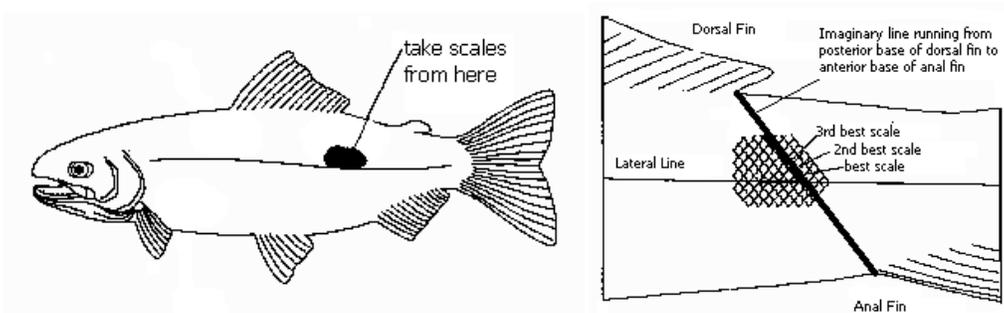
On collection packets record species, origin (wild/hatchery/stubbie), collection date and sample number.

Scale Sample Collection Method

Supplies:

- Forceps or tweezers
- Knife
- Rags or paper towels
- Collection packets (sample envelopes)

1. Take any measurements requested.
2. Clear away dirt from one side of the fish, within six scales on either side of an imaginary line running from the posterior base of the dorsal fin to the anterior base of the anal fin and two to three scale rows above the lateral line.



3. The preferred collection method is to use forceps or tweezers to remove individual scales. However, in most situations, a knife will be used because several fish need to be handled in a very short amount of time.

Forceps/Tweezers

- a. Inspect for and remove from the forceps any scales from the previous sample collected.
- b. Five to six scales should be removed. Grasp a scale within the appropriate area and pull the scale from the fish.

Knife

- a. Inspect for and remove from the knife any scales from the previous sample collected.
- b. Five to six scales should be removed. Use the knife point to scrape with the grain in the preferred area.

4. Wipe scales onto one side of the folded strip of paper found in the collection packet.
5. Refold the strip of paper over the scales and place the strip of paper directly into the collection packet it was removed from.
6. Seal the collection packet.
7. Wipe the forceps/knife with rag or paper towel and inspect for any scales remaining. If necessary rinse with water.
8. Place the collection packets on the drying rack at the end of your shift. Provide adequate space between the packets to promote air flow.

Genetic Sample Collection for 2011 Season

Supplies:

- Labeled sample vials filled with 100% NON-DENATURED ethanol (denatured alcohol will disrupt DNA preservation and extraction)
 - Squeeze bottle with 100% NON-DENATURED ethanol
 - Paper towels
 - Scissors
1. Label sample vials with sample numbers. The vial sample number should match the scale sample number for each fish. Sample numbers should be consecutive integers throughout the season.
 2. On vial collection boxes (100 vials per box), record species, origin (wild/hatchery), collection date range and sample number range.
 3. Check and fill all vials to ensure they are full of alcohol at the start of each day. Fill the vials to the bottom of the threads.
 4. Rinse the scissors with water and wipe with a paper towel between samples to prevent cross contamination. Periodically replace paper towel, approximately every 20 samples.
 5. Clip a small tissue sample, about the size of your small fingernail, from the top of the caudal fin or the bottom of the anal fin. Do not remove too much tissue. Too much tissue will overwhelm the sample vial alcohol.



6. Place the tissue sample in an alcohol-filled vial. Record the vial number on the data sheet.
7. Vials should be topped off with alcohol before shipping to Nampa Research. Vials should be checked every two weeks for proper alcohol level.
8. Contact Mike Ackerman (208-939-6713; mike.ackerman@idfg.idaho.gov) with questions regarding tissue sample collection.

FS 2001 Operational Instructions

Note: all tag files will be emailed, daily if possible, to Jody White (QCI) at jody@qcinc.org

Jody will be responsible for uploading all PIT tag information to PTAGIS daily from the LGD adult trapping operation.

Required Header information:

File Title: JSWyyddd.LGD (note: <yyddd> = year and Julian date of day of tagging)

Tag Date: MM/DD/YY hh:mm (note: usually filled in by software)

Tagger: Ogden D

Hatchery Site:

Stock:

Brood YR:

Migratory YR: 10

Tag Site: LGRLDR

Raceway/Transect:

Capture Method: LADDER

Tagging Temp: nn.n (note: <nnn> = 18.5, the starting daily temp in C)

Post Tagging Temp:

Release Water Temp:

Tagging Method: HAND

Organization: QCI

Coordinator ID: JSW

Release Date:

Release site:

Release River KM:



Field Sampling Protocol for Steelhead and Spring/Summer Chinook Salmon at the Lower Granite Dam Adult Trap, March 1 to June 30, 2012

By:
IDFG, QCI, PSMFC, NOAAF

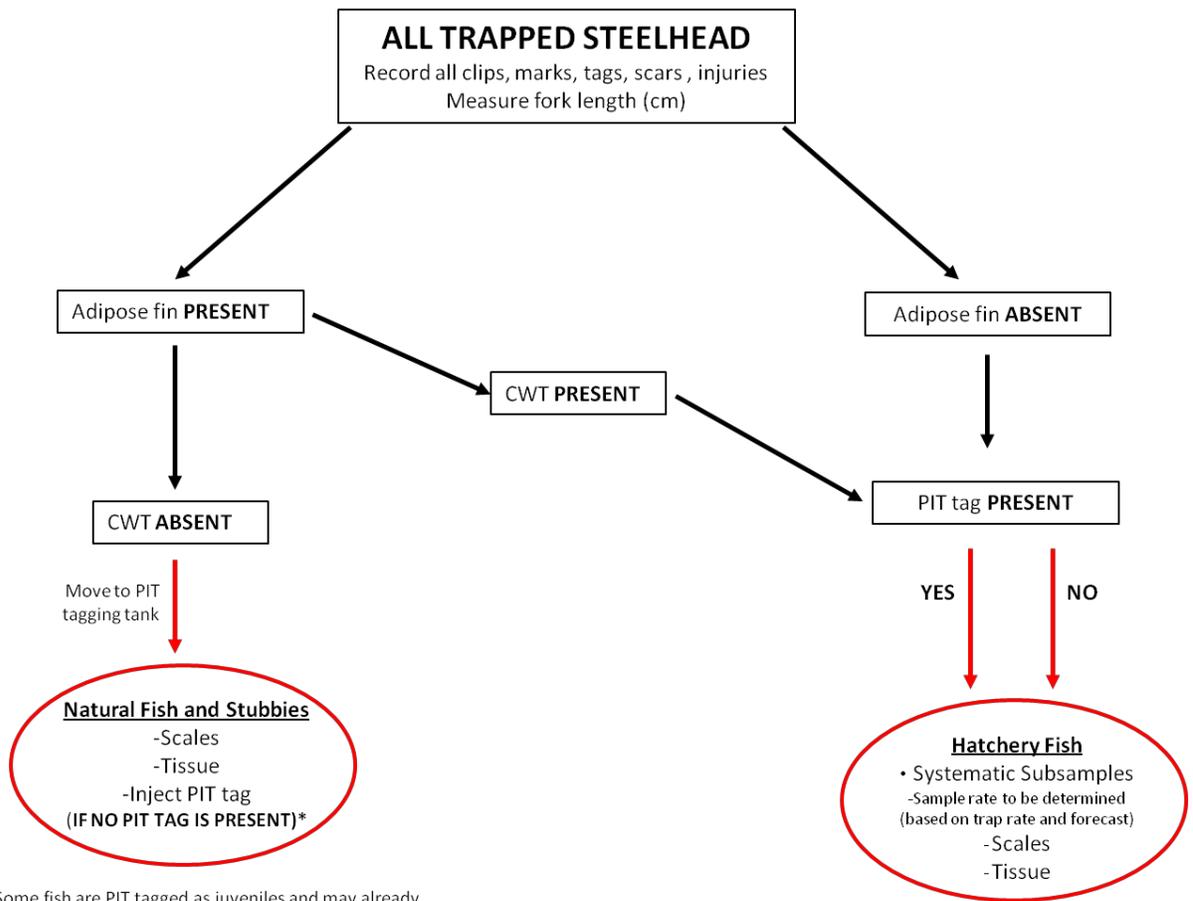
Specific Data Requirements for 2012 Season

This protocol outlines specific Lower Granite Dam (LGR) adult trap sampling and field data management procedures for:

- 1) Documentation of marks, tags, fin clips, and fin erosion for all fish to determine the proportion by origin, the proportion of adipose intact fish that are unmarked fish of hatchery origin, etc;
- 2) Length measurements of all fish to determine length distribution, length at age, A/B partition, etc;
- 3) Scale collections from all natural origin fish, all previously PIT tagged hatchery origin fish, and a subsample (goal 1000 fish) of non-PIT tagged hatchery origin fish (steelhead only) to estimate age composition, length at age, etc;
- 4) Tissue collections from all natural origin fish and a subsample (goal 1000 fish) of non-PIT tagged hatchery origin fish to estimate contribution rates, sex ratios, and ages of fish migrating to specific Snake River genetic reporting groups and hatchery stocks;
- 5) Passive integrated tag (PIT) placement in all natural origin fish and unclipped hatchery steelhead (stubbies) to estimate tributary specific escapement.

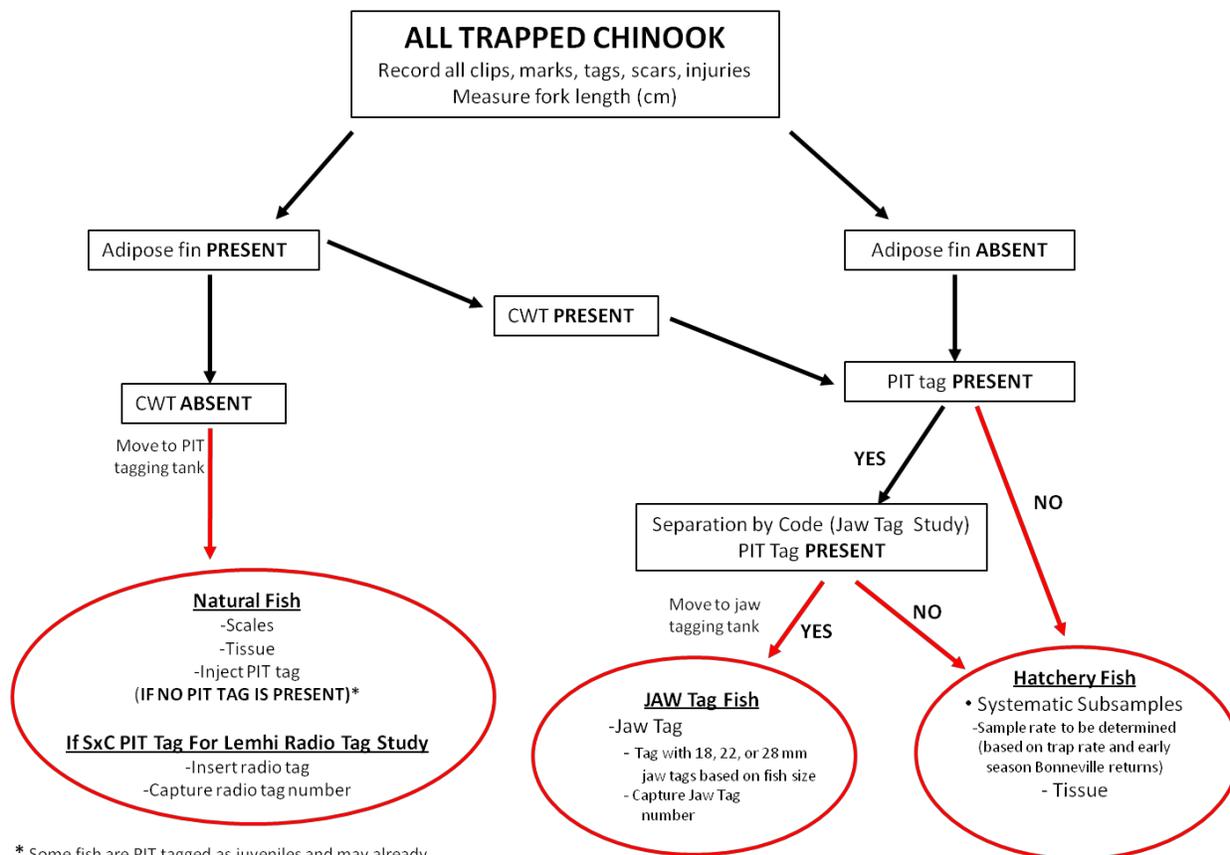
Once adult fish are trapped, all information from sampled fish will be recorded on the Field Data Entry Forms, in the FS2001 PIT tag reader (set up FS2001 PIT tag reader correctly and header information is completed for each day of sampling; see FS2001 Reader Use Section), and on the associated scale collection packets and genetic tissue vials. An individual sampled fish must have an identical, corresponding number placed on the Field Data Entry Form, scale sample packets and/or tissue sample vial. Each fish will have a unique sample number. Below are the required elements of field data and the field data form:

1. All spring/summer Chinook salmon (April 15- June 30) and steelhead (March 1 – June 30) from the trap will be classified as to species and whether adipose fin clipped hatchery fish; unclipped hatchery fish (see **Figure 1** – steelhead determined by fin erosion, other external marks, or CWT's; see **Figure 2** – Chinook determined by other external marks or CWT's); or unclipped natural origin fish. Clipped and unclipped hatchery fish (with CWT's and PIT tags) will be lumped together for sampling scales and/or tissue (unless for a specific sort-by-code study, see **Figure 2**). All trapped fish will be visually scanned for the presence or absence of an adipose fin, and all unclipped steelhead will be visually scanned for the presence of fin erosion that typifies stubbies.



* Some fish are PIT tagged as juveniles and may already have a PIT tag when encountered at the trap

Figure 2. Steelhead natural/hatchery determination process and sorting procedure. Stubbie steelhead will be treated in the same manner as natural fish. Data collected from natural fish and stubbies will be recorded on a separate datasheet at the natural fish/PIT tagging sorting tank.



* Some fish are PIT tagged as juveniles and may already have a PIT tag when encountered at the trap

Figure 2. Chinook natural/hatchery determination process and sorting procedure. Wild/natural fish will be sorted into the PIT tagging tank where data collected will be recorded on a separate datasheet or computer terminal. Separation by code fish for jaw or radio tag studies will be sorted into an additional tank where data will be recorded on a separate datasheet or computer terminal.

2. All spring/summer Chinook salmon and steelhead from the trap will be examined for other fin clips (pelvic, pectoral, etc.), external marks (brands, elastomer, VIE, etc.), external tags (floy tags, jaw tags, etc.) and internal tags (PIT, CWT, radio tags) and noted in the appropriate columns on the field form.
 - a. If a PIT tag is detected, note on the form that it is a **recapture**, write down the entire PIT tag number and, **if wild/natural, continue with the tissue/scale sampling; however do not place another PIT tag into the fish.**
3. Any significant injuries will be noted in the comment column.
4. All spring/summer Chinook salmon and steelhead from the trap will be measured to the nearest centimeter (fork length, **Figure 3**).

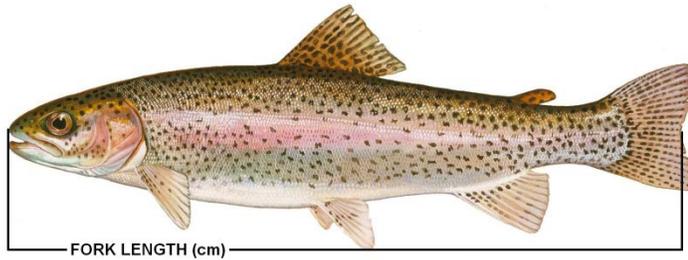


Figure 3. Appropriate points on a fish for determining fork length.

5. For natural Sp/Su Chinook and steelhead, scales will be removed from the preferred area on one side of the fish (see scale collection instruction below), for a total of 15 to 20 scales per sample. Scales should be left un-cleaned and stored on Rite-in-the-Rain sheets in paper envelopes. Care should be taken to store envelopes in such a manner that they can dry quickly. Sample number from the field form must correspond to the same number on the sample packet. For sampling natural and hatchery steelhead prior to 6/30/2012, please follow these instructions:
 - a. All natural origin steelhead and stubbies from the trap will have scale samples taken.
 - b. All previously PIT tagged hatchery origin steelhead will have scale samples taken.
 - c. A scale subsample of ~1,000 hatchery steelhead will be taken systematically across the run.

6. For all spring/summer Chinook salmon and steelhead from which biological samples are collected, a piece of tissue should be taken from the top of the caudal fin or the bottom of the anal fin and stored in a closed vial with 100% non-denatured ethanol for future genetics analysis. Sample number from the field form must correspond to the same number on the sample vial.
 - a. All natural origin fish and stubbies from the trap will have tissue samples taken.
 - b. All previously PIT tagged hatchery origin fish will have tissue samples taken.
 - c. A genetics subsample of ~1,000 hatchery fish will be taken systematically across the run; these will be the same fish and have the same sample number as those selected for scale samples.

7. For all natural/wild spring/summer Chinook salmon and steelhead (including stubbies) that are sampled, a 12 mm PIT tag should be placed in the pelvic girdle location using the provided pre-loaded PIT tag needles.
 - a. All natural origin fish and stubbies from the trap will be released with a single PIT tag, either newly tagged at the trap or from a previous tagging event (e.g. recaptured from juvenile PIT tagging, Bonneville PIT tagging, etc).
 - b. **Do not** PIT tag the fish if it is already PIT tagged, i.e. no double tagging.
 - c. After tagging, wand the fish with the FS2001 to ensure the PIT tag is placed appropriately in the fish.
 - d. Note the last 10 digits of the PIT tag code, and time of placement – record in the appropriate columns on the field data.

8. **Make sure tissue/scale samples are collected from every new PIT-tagged fish and every previously PIT-tagged fish (natural recaptures only).** The only exception to

this rule is PIT tagged fallback fish when previous tissue/scale sample collection is obvious. Please record PIT numbers for fallbacks.

Scale Sample Collection for 2012 Season

Collection of scale samples requires following only a few simple steps. The two most important things to remember are to guard against cross contamination of samples and to make sure that the appropriate sample number is filled out on the sample envelopes. At every step of the collection process, care must be taken to keep individual samples separate.

Collection Packets (Sample Envelopes)

2 ½" x 4 ¼" (6.4 x 10.8 cm) Coin envelopes (as many as needed)
2" x 8" strips of Rite-in-the-Rain paper (same # as coin envelopes)

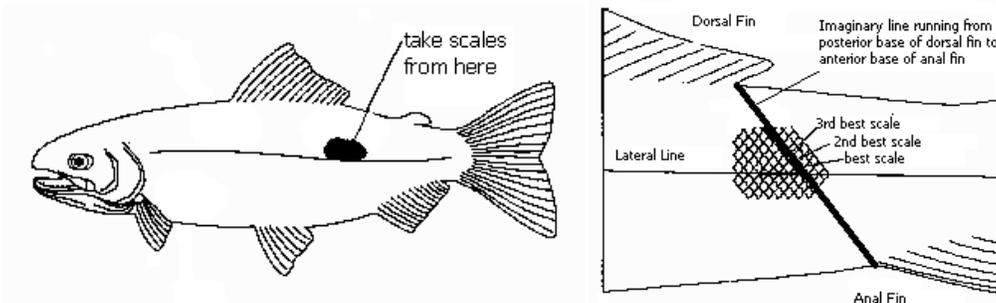
Ensure proper sample number is recorded on all packets.

Scale Sample Collection Method

Supplies:

- Forceps or tweezers
- Knife
- Rags or paper towels
- Collection packets (sample envelopes)

1. Take any measurements requested.
2. Clear away dirt from one side of the fish, within six scales on either side of an imaginary line running from the posterior base of the dorsal fin to the anterior base of the anal fin and two to three scale rows above the lateral line.



3. The preferred collection method is to use forceps or tweezers to remove individual scales. However, in most situations, a knife will be used because several fish need to be handled in a very short amount of time.

Forceps/Tweezers

- a. Inspect for and remove from the forceps any scales from the previous sample collected.
- b. Five to six scales should be removed. Grasp a scale within the appropriate area and pull the scale from the fish.

Knife

- c. Inspect for and remove from the knife any scales from the previous sample collected.

- d. Five to six scales should be removed. Use the knife point to scrape with the grain in the preferred area.
4. Wipe scales onto one side of the folded strip of paper found in the collection packet.
5. Refold the strip of paper over the scales and place the strip of paper directly into the collection packet it was removed from.
6. Seal the collection packet.
7. Wipe the forceps/knife with rag or paper towel and inspect for any scales remaining. If necessary rinse with water.
8. Place the collection packets on the drying rack at the end of your shift. Provide adequate space between the packets to promote air flow.
9. Contact Kristin Ellsworth (208-465-8404; kristin.ellsworth@idfg.idaho.gov) with questions regarding scale sample collection.

Genetic Sample Collection for 2012 Season

Supplies:

- Labeled sample vials filled with 100% NON-DENATURED ethanol (denatured alcohol will disrupt DNA preservation and extraction)
 - Squeeze bottle with 100% NON-DENATURED ethanol
 - Paper towels
 - Scissors
1. Label sample vials with sample numbers. The vial sample number should match the scale sample number for each fish. Sample numbers should be consecutive integers throughout the season.
 2. On vial collection boxes (100 vials per box), record species, origin (wild/hatchery), collection date range and sample number range.
 3. Check and fill all vials to ensure they are full of alcohol at the start of each day. Fill the vials to the bottom of the threads.
 4. Rinse the scissors with water and wipe with a paper towel between samples to prevent cross contamination. Periodically replace paper towel, approximately every 20 samples.
 5. Clip a small tissue sample, about the size of your small fingernail, from the top of the caudal fin or the bottom of the anal fin. Do not remove too much tissue. Too much tissue will overwhelm the sample vial alcohol.





6. Place the tissue sample in an alcohol-filled vial. Record the vial number on the data sheet.
7. Vials should be topped off with alcohol before shipping to Nampa Research. Vials should be checked every two weeks for proper alcohol level.
8. Contact Mike Ackerman (208-939-6713; mike.ackerman@idfg.idaho.gov) with questions regarding tissue sample collection.

FS 2001 Operational Instructions

Note: all tag files will be emailed, daily if possible, to Jody White (QCI) at jody@gcinc.org

Jody will be responsible for uploading all PIT tag information to PTAGIS daily from the LGD adult trapping operation.

Required Header information:

File Title: JSWyyddd.LGD (note: <yyddd> = year and Julian date of day of tagging)

Tag Date: MM/DD/YY hh:mm (note: usually filled in by software)

Tagger: Ogden D

Hatchery Site:

Stock:

Brood YR:

Migratory YR: 12

Tag Site: LGRLDR

Raceway/Transect:

Capture Method: LADDER

Tagging Temp: nn.n (note: <nnn> = 18.5, the starting daily temp in C)

Post Tagging Temp:

Release Water Temp:

Tagging Method: HAND

Organization: QCI

Coordinator ID: JSW

Release Date:
Release site:
Release River KM:

Appendix B: Snake River genetic baselines v2.0 (Ackerman et al. 2014) used for stock identification at Lower Granite Dam, spawn year 2012.

Appendix Table B-1. Genetic stocks and baseline collections used for steelhead mixed stock analysis at Lower Granite Dam, spawn year 2012 (Ackerman et al. 2014). MPG = major population group.

Reporting Group / Collection Name	n	Years Collected	Latitude	Longitude	MPG
UPSALM (Upper Salmon River)					
1 Sawtooth Weir	108	05, 10	44.15058	-114.88509	Salmon
2 Valley Cr	45	05	44.30113	-115.04574	Salmon
3 WF Yankee F Salmon	117	04, 08	44.34941	-114.72657	Salmon
4 Morgan Cr	37	00	44.67882	-114.23945	Salmon
5 Pahsimeroi Weir	97	06, 10	44.68448	-114.04036	Salmon
6 Hayden Cr	86	09, 10	44.78519	-113.70621	Salmon
7 NF Salmon R	100	10	45.50356	-113.95717	Salmon
MFSALM (Middle Fork Salmon River)					
8 Marsh Cr	59	00	44.41537	-115.18385	Salmon
9 Sulphur Cr	45	00	44.54370	-115.39566	Salmon
10 Rapid R (MF)	45	00	44.64151	-115.05621	Salmon
11 Pistol Cr	23	00	44.76347	-115.31469	Salmon
12 Loon Cr	84	99, 00	44.59829	-114.81164	Salmon
13 Camas Cr	57	00	44.82399	-114.49990	Salmon
14 Big Cr (upper)	46	00	45.15063	-115.29674	Salmon
15 Big Cr (lower)	48	00	45.10717	-114.80611	Salmon
16 Chamberlain Cr	46	00	45.36865	-115.19689	Salmon
17 Bargamin Cr	32	00	45.66604	-115.07812	Salmon
SFSALM (South Fork Salmon River)					
18 EF SF Salmon R	45	00	44.94642	-115.59941	Salmon
19 Stolle Meadows	47	00	44.60701	-115.68098	Salmon
20 Lick Cr	40	10	45.05880	-115.86100	Salmon
21 Secesh R	45	00	45.12659	-115.77011	Salmon
LOSALM (Lower Salmon River)					
22 Boulder Cr	47	00	45.12183	-116.42752	Salmon
23 Rapid R	100	03, 09	45.31576	-116.41871	Salmon
24 Slate Cr	47	00	45.63932	-116.12444	Salmon
25 Whitebird Cr	62	00, 01	45.79165	-116.23164	Salmon
UPCLWR (Upper Clearwater River)					
26 Colt Killed Cr	38	00	46.43110	-114.53952	Clearwater
27 Storm Cr	38	00	46.53651	-114.46931	Clearwater
28 Crooked F Lochsa R	44	00	46.61523	-114.67046	Clearwater
29 Lake Cr	47	00	46.41437	-115.00679	Clearwater
30 Fish Cr	100	10, 11	46.35582	-115.39851	Clearwater
31 Canyon Cr	46	11	46.23909	-115.57909	Clearwater
32 Selway R	78	08	45.69208	-114.71753	Clearwater
33 Little Clearwater R	59	08	45.71018	-114.87330	Clearwater
34 Whitecap Cr	76	08	45.88777	-114.60935	Clearwater
35 Bear Cr	35	00	46.03569	-114.75107	Clearwater
36 NF Moose Cr	94	00, 04	46.22329	-114.94754	Clearwater
37 Three Links Cr	47	00	46.14508	-115.09495	Clearwater
38 Gedney Cr	45	00	46.09381	-115.29383	Clearwater
39 O'Hara Cr	47	00	46.04494	-115.51908	Clearwater
SFCLWR (South Fork Clearwater River)					
40 Crooked R	106	07, 08	45.76562	-115.54264	Clearwater
41 Tenmile Cr	47	00	45.72703	-115.66138	Clearwater
42 John's Cr	38	00	45.72137	-115.88962	Clearwater
43 Clear Cr	45	00	46.04859	-115.78140	Clearwater
LOCLWR (Lower Clearwater River)					
44 WF Potlatch R	84	09, 10	46.86420	-116.40160	Clearwater
45 EF Potlatch R	158	08, 10, 11	46.80991	-116.38142	Clearwater
46 Big Bear Cr	99	07, 08, 10, 11	46.69415	-116.65593	Clearwater
47 Little Bear Cr	151	07, 08, 10, 11	46.71997	-116.70423	Clearwater

Appendix Table B-1, continued.

Reporting Group / Collection Name	<i>n</i>	Years Collected	Latitude	Longitude	MPG
IMNAHA (Imnaha River)					
48 Big Sheep Cr	68	01	45.45693	-116.82688	Imnaha
49 Camp Cr	24	01	45.55406	-116.87253	Imnaha
50 Lightning Cr	44	00	45.65537	-116.72653	Imnaha
51 Cow Cr	41	00	45.76814	-116.74956	Imnaha
GRROND (Grande Ronde River)					
52 Little Minam R	48	00	45.34536	-117.65340	Grande Ronde
53 Lostine R	45	00	45.42211	-117.42496	Grande Ronde
54 Wenaha R	94	01	45.97269	-117.69367	Grande Ronde
55 Crooked Cr	97	01	46.03905	-117.57340	Grande Ronde
56 Menatchee Cr	45	01	45.04457	-117.38550	Grande Ronde
57 Elk Cr - Grande Ronde	45	00	45.67203	-117.18960	Grande Ronde
58 Joseph Cr	60	11	45.95606	-117.13746	Grande Ronde
59 Captain John Cr	56	00	46.14595	-116.87108	Lower Snake
LSNAKE (Lower Snake River)					
60 Asotin Cr	95	08, 10	46.32280	-117.13681	Lower Snake
61 George Cr	99	10	46.28326	-117.14434	Lower Snake
62 Alpowa Cr	98	10	46.42479	-117.32812	Lower Snake
63 Tucannon R	106	05, 09, 10	46.50530	-118.01440	Lower Snake

Appendix Table B-2. Genetic stocks and baseline collections used for Chinook salmon mixed stock analysis at Lower Granite Dam, spawn year 2012 (Ackerman et al. 2014). MPG = major population group.

Reporting Group / Collection Name	<i>n</i>	Years Collected	Latitude	Longitude	MPG
UPSALM (Upper Salmon River)					
1 Sawtooth Weir	91	09, 10	44.15058	-114.88509	Upper Salmon
2 Valley Cr	56	07, 08, 09, 10	44.30113	-115.04574	Upper Salmon
3 WF Yankee F Salmon	75	05	44.34941	-114.72657	Upper Salmon
4 EF Salmon R	187	04, 05, 11	44.11542	-114.42998	Upper Salmon
5 Pahsimeroi R	92	07, 08, 09, 10	44.68448	-114.04037	Upper Salmon
6 Hayden Cr	79	09, 10	44.78519	-113.70621	Upper Salmon
7 Lemhi (upper)	96	09, 10	44.86917	-113.62510	Upper Salmon
8 Lemhi (lower)	90	09, 10	45.15296	-113.81357	Upper Salmon
MFSALM (Middle Fork Salmon River)					
9 Elk Cr	84	07, 08, 09, 10	44.43041	-115.47107	MF Salmon
10 Bear Valley Cr	80	07, 08, 09, 10	44.37328	-115.39501	MF Salmon
11 Capehorn Cr	112	05, 06, 07, 09, 10	44.35864	-115.22362	MF Salmon
12 Marsh Cr	66	07, 08, 09, 10	44.41537	-115.18385	MF Salmon
13 Sulphur Cr	35	08, 09, 10	44.54370	-115.39566	MF Salmon
14 Camas Cr	57	06, 09	44.82399	-114.49990	MF Salmon
15 Big Cr	95	01, 10	45.15063	-115.29674	MF Salmon
CHMBLN (Chamberlain Creek)					
16 Chamberlain Cr (post-2008)	55	09, 10	45.39781	-115.19339	MF Salmon
17 Chamberlain Cr (pre-2008)	70	03, 04, 06, 07	45.36865	-114.19689	MF Salmon
SFSALM (South Fork Salmon River)					
18 Johnson Cr	92	02	44.90445	-115.48689	SF Salmon
19 SF Salmon R	140	09, 10	44.66676	-115.70292	SF Salmon
20 Lake Cr, Summit Cr	74	07, 08, 09, 10	45.27881	-115.92169	SF Salmon
21 Secesh R	130	01, 07, 08, 09, 10	45.12659	-115.77011	SF Salmon
HELLSC (Hells Canyon Stock)					
22 Rapid R	91	06	45.31576	-116.41871	SF Salmon
23 Crooked F Lochsa R	26	07, 08, 09, 10	46.61523	-114.67046	Wet Clearwater
24 Powell Weir	31	09	46.50561	-114.68718	Wet Clearwater
25 Red R	72	07, 08, 09, 10	45.70979	-115.34389	Dry Clearwater
26 Crooked R Weir	67	09, 10	45.76562	-115.54264	Dry Clearwater
27 Newsome Cr	82	01	45.86383	-115.61725	Dry Clearwater
28 Lolo Cr	89	01, 02	46.31500	-116.00741	Wet Clearwater
29 Imnaha R	43	08	45.56100	-116.83400	Grande Ronde / Imnaha
30 Imnaha R (1998)	91	98	45.55400	-116.83474	Grande Ronde / Imnaha
31 Upper Grande Ronde	43	08	45.19319	-118.39458	Grande Ronde / Imnaha
32 Catherine Cr	93	04, 06	45.24062	-117.92199	Grande Ronde / Imnaha
33 Lostine R	176	03, 05, 09	45.42211	-117.42496	Grande Ronde / Imnaha
34 Minam R	80	94, 02	45.60000	-117.72900	Grande Ronde / Imnaha
35 Wenaha R	88	02, 06	45.97269	-117.69367	Grande Ronde / Imnaha
TUCANO (Tucannon River)					
36 Tucannon R	81	03	46.50530	-118.01440	Lower Snake
FALL (Fall Chinook ESU)					
37 Clearwater	143	08	46.52000	-116.60950	FALL ESU
38 Nez Perce Tribal Hatchery	85	03	46.51910	-116.66460	FALL ESU
39 Lyons Ferry	90	00	46.58940	-118.21950	FALL ESU

Appendix C: Wild adult steelhead at Lower Granite Dam, spawn year 2012.

Appendix Table C-1. Weekly window or video counts and adult valid trap samples of steelhead at Lower Granite Dam (LGR), spawn year 2012.

Statistical week(a)	Sampling period 2011-12	Number of days	LGR window count(b)	LGR adult valid trap sample(c)	LGR adult trap sample rate (%)	Percent of run trapped
Fall 2011						
27-30(d)	7/1-7/24	24	1,585	145	10	9.1
31	7/25-7/31	7	1,724	168	10	9.7
32	8/1-8/7	7	2,225	193	10	8.7
33	8/8-8/14	7	3,844	315	10	8.2
34	8/15-8/21	7	5,709	584	10	10.2
35	8/22-8/28	7	6,182	646	10	10.4
36	8/29-9/4	7	17,856	1,725	10	9.7
37	9/5-9/11	7	14,132	1,420	10	10.0
38	9/12-9/18	7	18,362	2,114	10	11.5
39	9/19-9/25	7	20,223	2,335	10	11.5
40	9/26-10/2	7	24,992	2,862	10	11.5
41	10/3-10/9	7	17,756	2,066	10	11.6
42	10/10-10/16	7	14,434	1,666	10	11.5
43	10/17-10/23	7	13,080	1,355	10	10.4
44	10/24-10/30	7	4,807	554	10	11.5
45	10/31-11/6	7	1,232	220	10	17.9
46-53(d,e)	11/7-12/31	55	3,142	201	0-10	6.4
Fall total:		184	171,285	18,569	0-10	10.8
Spring 2012						
1-10(d,f)	1/1-2/29	60	ND(g)	ND	ND	ND
10-12(d,f)	3/1-3/18	18	1,752	125	0-10	7.1
13	3/19-3/25	7	1,465	183	10	12.5
14	3/26-4/1	7	1,550	172	10	11.1
15	4/2-4/8	7	1,436	128	10	8.9
16	4/9-4/15	7	1,001	107	10	10.7
17-18	4/16-4/29	14	1,050	104	10	9.9
19-27(d,h)	4/30-6/30	62	781	90	10	11.5
Spring total:		182	9,035	909	0-10	10.1
Run total:		366	180,320	19,478	0-10	10.8

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 trapped fish.

(b) Downloaded from COE link 7/2/13.

(c) From Darren Ogden (NMFS, personal communication).

(d) Includes partial beginning or ending week.

(e) The trap was closed 11/21/11 to 12/31/11 due to freezing water temperatures.

(f) The trap was closed 1/1/12 to 3/7/12 due to freezing water temperatures; the window was closed 1/1/12 to 2/29/12; the fish ladder was closed 1/4/12 to 2/13/12 and fish passage was only by navigation lock.

(g) ND = no data.

(h) All trapped fish data are from new NMFS database from 5/24/12 forward.

Appendix Table C-2. Number of steelhead captured in the adult trap, by fish size and origin, at Lower Granite Dam (LGR), spawn year 2012. Large fish are greater than or equal to 78 cm (FL) and small fish are less than 78 cm (FL). Clipped and unclipped refer to the adipose fin.

Statistical week(a)	Sample period ending(b)	LGR adult valid trap sample(c)	Number of trapped fish that were(c):							Total hatchery	Total wild
			Large wild	Large hatchery clipped	Large hatchery unclipped	Small wild	Small hatchery clipped	Small hatchery unclipped			
Fall 2011											
27-30	7/24	145	0	0	0	50	91	4	95	50	
31	7/31	168	0	1	0	69	93	5	99	69	
32	8/7	193	1	2	0	92	95	3	100	93	
33	8/14	315	0	0	0	136	173	6	179	136	
34	8/21	584	1	6	0	199	357	21	384	200	
35	8/28	646	5	7	0	202	414	18	439	207	
36	9/4	1,725	8	39	0	483	1,149	46	1,234	491	
37	9/11	1,420	17	38	4	328	975	58	1,075	345	
38	9/18	2,114	58	183	10	338	1,438	87	1,718	396	
39	9/25	2,335	58	282	28	303	1,557	107	1,974	361	
40	10/2	2,862	92	454	47	313	1,834	122	2,457	405	
41	10/9	2,066	62	314	32	245	1,312	101	1,759	307	
42	10/16	1,666	50	294	35	221	983	83	1,395	271	
43	10/23	1,355	51	206	24	193	797	84	1,111	244	
44	10/30	554	25	63	14	89	333	30	440	114	
45	11/6	220	5	36	7	31	131	10	184	36	
46-53	12/31	201	5	19	5	50	116	6	146	55	
Fall total:		18,569	438	1,944	206	3,342	11,848	791	14,789	3,780	
Spring 2012											
1-10	2/29	ND(d)	ND	ND	ND	ND	ND	ND	ND	ND	
10-12	3/18	125	4	11	7	25	70	8	96	29	
13	3/25	183	8	17	9	48	83	18	127	56	
14	4/1	172	11	10	9	56	71	15	105	67	
15	4/8	128	5	10	2	49	50	12	74	54	
16	4/15	107	13	2	0	35	48	9	59	48	
17-18	4/29	104	1	2	1	58	35	7	45	59	
19-27	6/30	90	3	0	0	50	34	3	37	53	
Spring total:		909	45	52	28	321	391	72	543	366	
Run total:		19,478	483	1,996	234	3,663	12,239	863	15,332	4,146	

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 trapped fish.

(b) See Appendix Table C-1 for inclusive dates and other notes regarding statistical weeks and LGR operations.

(c) From Darren Ogden (NMFS, personal communication); large hatchery unclipped includes 122 fish misidentified at the trap as wild as determined by PBT; small hatchery unclipped includes 138 fish misidentified at the trap as wild as determined by PBT.

(d) ND = no data.

Appendix Table C-3. Percentage of steelhead captured in the adult trap, by fish size and origin, at Lower Granite Dam (LGR), spawn year 2012. Large fish are greater than or equal to 78 cm (FL) and small fish are less than 78 cm (FL). Clipped and unclipped refer to the adipose fin. Percentages may not sum to 100.0% due to rounding error.

Statistical week(a)	Sample period ending(b)	LGR adult valid trap sample(c)	Percentage of trapped fish that were(c):						Total hatchery	Total wild
			Large wild	Large hatchery clipped	Large hatchery unclipped	Small wild	Small hatchery clipped	Small hatchery unclipped		
Fall 2011										
27-30	7/24	145	0.0	0.0	0.0	34.5	62.8	2.8	65.5	34.5
31	7/31	168	0.0	0.6	0.0	41.1	55.4	3.0	58.9	41.1
32	8/7	193	0.5	1.0	0.0	47.7	49.2	1.6	51.8	48.2
33	8/14	315	0.0	0.0	0.0	43.2	54.9	1.9	56.8	43.2
34	8/21	584	0.2	1.0	0.0	34.1	61.1	3.6	65.8	34.2
35	8/28	646	0.8	1.1	0.0	31.3	64.1	2.8	68.0	32.0
36	9/4	1,725	0.5	2.3	0.0	28.0	66.6	2.7	71.5	28.5
37	9/11	1,420	1.2	2.7	0.3	23.1	68.7	4.1	75.7	24.3
38	9/18	2,114	2.7	8.7	0.5	16.0	68.0	4.1	81.3	18.7
39	9/25	2,335	2.5	12.1	1.2	13.0	66.7	4.6	84.5	15.5
40	10/2	2,862	3.2	15.9	1.6	10.9	64.1	4.3	85.8	14.2
41	10/9	2,066	3.0	15.2	1.5	11.9	63.5	4.9	85.1	14.9
42	10/16	1,666	3.0	17.6	2.1	13.3	59.0	5.0	83.7	16.3
43	10/23	1,355	3.8	15.2	1.8	14.2	58.8	6.2	82.0	18.0
44	10/30	554	4.5	11.4	2.5	16.1	60.1	5.4	79.4	20.6
45	11/6	220	2.3	16.4	3.2	14.1	59.5	4.5	83.6	16.4
46-53	12/31	201	2.5	9.5	2.5	24.9	57.7	3.0	72.6	27.4
Fall total(d):		18,569	2.3	10.1	1.1	18.7	63.7	4.2	79.0	21.0
Spring 2012										
1-10	2/29	ND(e)	ND	ND	ND	ND	ND	ND	ND	ND
10-12	3/18	125	3.2	8.8	5.6	20.0	56.0	6.4	76.8	23.2
13	3/25	183	4.4	9.3	4.9	26.2	45.4	9.8	69.4	30.6
14	4/1	172	6.4	5.8	5.2	32.6	41.3	8.7	61.0	39.0
15	4/8	128	3.9	7.8	1.6	38.3	39.1	9.4	57.8	42.2
16	4/15	107	12.1	1.9	0.0	32.7	44.9	8.4	55.1	44.9
17-18	4/29	104	1.0	1.9	1.0	55.8	33.7	6.7	43.3	56.7
19-27	6/30	90	3.3	0.0	0.0	55.6	37.8	3.3	41.1	58.9
Spring total(d):		909	4.8	5.9	3.1	34.7	43.7	7.8	60.5	39.5
Run total(d):		19,478	2.4	9.8	1.2	19.5	62.7	4.4	78.1	21.9

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 trapped fish.

(b) See Appendix Table C-1 for inclusive dates and other notes regarding statistical weeks and LGR operations.

(c) From Darren Ogden (NMFS, personal communication); large hatchery unclipped includes 122 fish misidentified at the trap as wild as determined by PBT; small hatchery unclipped includes 138 fish misidentified at the trap as wild as determined by PBT.

(d) Run total percentages for each fish size and origin class were calculated from escapement estimates in Appendix Table C-4.

(e) ND = no data.

Appendix Table C-4. Estimated weekly escapement, by fish size and origin, of steelhead at Lower Granite Dam (LGR), spawn year 2012. Large fish are greater than or equal to 78 cm (FL) and small fish are less than 78 cm (FL). Clipped and unclipped refer to the adipose fin.

Statistical week(a)	Sample period ending(b)	LGR window count(c)	Estimated number of steelhead at LGR that were:							
			Large wild	Large hatchery clipped	Large hatchery unclipped	Small wild	Small hatchery clipped	Small hatchery unclipped	Total hatchery	Total wild
Fall 2011										
27-30	7/24	1,585	0	0	0	547	994	44	1,038	547
31	7/31	1,724	0	10	0	708	955	51	1,016	708
32	8/7	2,225	12	23	0	1,061	1,094	35	1,152	1,073
33	8/14	3,844	0	0	0	1,660	2,111	73	2,184	1,660
34	8/21	5,709	10	59	0	1,945	3,490	205	3,754	1,955
35	8/28	6,182	48	67	0	1,933	3,962	172	4,201	1,981
36	9/4	17,856	83	404	0	5,000	11,893	476	12,773	5,083
37	9/11	14,132	169	378	40	3,264	9,704	577	10,699	3,433
38	9/18	18,362	504	1,590	87	2,936	12,489	756	14,922	3,440
39	9/25	20,223	502	2,442	243	2,624	13,485	927	17,097	3,126
40	10/2	24,992	803	3,964	410	2,733	16,017	1,065	21,456	3,536
41	10/9	17,756	533	2,699	275	2,106	11,275	868	15,117	2,639
42	10/16	14,434	433	2,547	303	1,915	8,517	719	12,086	2,348
43	10/23	13,080	492	1,989	232	1,863	7,693	811	10,725	2,355
44	10/30	4,807	217	547	121	772	2,890	260	3,818	989
45	11/6	1,232	28	202	39	174	733	56	1,030	202
46-53	12/31	3,142	78	297	78	782	1,813	94	2,282	860
Fall total:		171,285	3,912	17,218	1,828	32,023	109,115	7,189	135,350	35,935
Spring 2012										
1-10	2/29	ND(d)	ND	ND	ND	ND	ND	ND	ND	ND
10-12	3/18	1,752	56	154	98	350	982	112	1,346	406
13	3/25	1,465	64	136	72	384	665	144	1,017	448
14	4/1	1,550	99	90	81	505	640	135	946	604
15	4/8	1,436	56	112	22	550	561	135	830	606
16	4/15	1,001	122	19	0	327	449	84	552	449
17-18	4/29	1,050	10	20	10	586	353	71	454	596
19-27	6/30	781	26	0	0	434	295	26	321	460
Spring total:		9,035	433	531	283	3,136	3,945	707	5,466	3,569
Run total:		180,320	4,345	17,749	2,111	35,159	113,060	7,896	140,816	39,504
95% CI:			(3,973-4,742)	(17,011-18,486)	(1,848-2,387)	(34,186-36,172)	(111,847-114,299)	(7,389-8,418)	(139,762-141,848)	(38,453-40,532)

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 trapped fish.

(b) See Appendix Table C-1 for inclusive dates and other notes regarding statistical weeks and LGR operations.

(c) Downloaded from COE link 7/2/13.

(d) ND = no data.

Appendix Table C-5. Number of wild adult steelhead scale and genetics samples collected at Lower Granite Dam and subsequently aged or genotyped, spawn year 2012. Large and small fish were combined.

Statistical week(a)	Sampling period 2011-12	Number of days	Wild run size(b)	Number of scale and genetics samples collected(c)	Number of scale and genetics systematic subsamples(d)	Scale samples:		Genetics samples:			
						Number of samples aged(e)	Percent of run aged	Number of samples genotyped for gender(e)	Percent of run genotyped for gender	Number of samples genotyped for stock(e)	Percent of run genotyped for stock
Fall 2011											
27-33(f)	7/1-8/14	45	3,988	348	172	160	4.0	170	4.3	171	4.3
34-35	8/15-8/28	14	3,936	407	200	183	4.6	193	4.9	199	5.1
36	8/29-9/4	7	5,083	491	240	226	4.4	233	4.6	238	4.7
37	9/5-9/11	7	3,433	345	172	163	4.7	165	4.8	170	5.0
38	9/12-9/18	7	3,440	396	194	175	5.1	191	5.6	193	5.6
39	9/19-9/25	7	3,126	361	171	149	4.8	165	5.3	170	5.4
40	9/26-10/2	7	3,536	405	194	183	5.2	190	5.4	194	5.5
41	10/3-10/9	7	2,639	307	150	130	4.9	149	5.6	149	5.6
42	10/10-10/16	7	2,348	271	130	121	5.2	126	5.4	129	5.5
43	10/17-10/23	7	2,355	244	119	108	4.6	118	5.0	119	5.1
44-53(f,g)	10/24-12/31	69	2,051	205	99	92	4.5	97	4.7	98	4.8
Fall total:		184	35,935	3,780	1,841	1,690	4.7	1,797	5.0	1,830	5.1
Spring 2012											
1-10(f,h)	1/1-2/29	60	ND(i)	ND	ND	ND	ND	ND	ND	ND	ND
10-27(f,h)	3/1-6/30	122	3,569	366	176	126	3.5	174	4.9	174	4.9
Spring total:		182	3,569	366	176	126	3.5	174	4.9	174	4.9
Run total:		366	39,504	4,146	2,017	1,816	4.6	1,971	5.0	2,004	5.1

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 aged or genotyped fish.

(b) From Appendix Table C-4.

(c) Does not include 260 fish misidentified as wild at the trap and later determined to be unclipped hatchery by PBT.

(d) Does not include 186 fish misidentified as wild at the trap and later determined to be unclipped hatchery by PBT.

(e) Some subsamples were not aged or genotyped due to missing scales or fin clips; other subsamples were not able to be aged (freshwater and saltwater) or successfully genotyped; neither are included here. Misidentified wild fish later determined to be unclipped hatchery by PBT are not included.

(f) Includes partial beginning or ending week.

(g) The trap was closed 11/21/11 to 12/31/11 due to freezing water temperatures.

(h) The trap was closed 1/1/12 to 3/7/12 due to freezing water temperatures; the window was closed 1/1/12 to 2/29/12; the fish ladder was closed 1/4/12 to 2/13/12 and fish passage was only by navigation lock.

(i) ND = no data.

Appendix Table C-6. Weekly age frequencies by smolt migration year, brood year, and age class of wild adult steelhead sampled at Lower Granite Dam, spawn year 2012. Large and small fish were combined.

Statistical week(a)	Sample period ending(b)	Number of samples aged	Smolt migration year (MY), brood year (BY), and age class (frequency):																					
			MY2010					MY2009					MY2008					MY2007						
			BY09	BY08	BY07	BY06	BY05	BY08	BY07	BY07	BY06	BY05	BY04	BY07	BY06	BY06	BY06	BY05	BY05	BY05	BY04	BY05	BY04	BY04
			1.1	2.1	3.1	4.1	5.1	1.2	2.2	2.1S	3.2	4.2	5.2	1.2S	2.3	2.1S1	2.2S	3.3	3.1S1	3.2S	4.1S1	2.2S1	3.1S2	3.2S1
Fall 2011																								
27-33	8/14	160	2	26	20	2	-	8	59	-	40	1	1	-	1	-	-	-	-	-	-	-	-	-
34-35	8/28	183	1	41	40	2	1	4	61	-	28	4	-	-	-	1	-	-	-	-	-	-	-	-
36	9/4	226	4	50	31	6	1	7	71	-	46	6	-	-	-	1	-	2	-	1	-	-	-	-
37	9/11	163	6	27	32	4	-	7	54	-	24	6	-	-	2	-	-	1	-	-	-	-	-	-
38	9/18	175	2	23	29	2	-	11	60	-	38	6	-	-	-	-	-	3	-	-	-	1	-	-
39	9/25	149	6	28	13	1	-	4	51	1	37	2	-	1	1	-	-	1	2	-	-	-	-	1
40	10/2	183	7	48	15	-	-	5	71	-	26	5	-	1	3	1	-	-	-	1	-	-	-	-
41	10/9	130	4	25	15	-	-	8	48	-	24	2	-	-	2	2	-	-	-	-	-	-	-	-
42	10/16	121	1	23	14	1	-	7	45	1	27	-	-	-	-	1	-	-	-	-	-	1	-	-
43	10/23	108	3	18	4	3	-	4	48	-	25	1	-	-	-	-	-	-	-	-	-	1	1	-
44-53	12/31	92	3	21	10	-	-	5	38	1	14	-	-	-	-	-	-	-	-	-	-	-	-	-
Fall total:		1,690	39	330	223	21	2	70	606	3	329	33	1	2	9	5	1	7	2	2	1	2	1	1
Spring 2012																								
1-10	2/29	ND(c)	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
10-27	6/30	126	2	27	11	3	-	2	51	-	25	3	-	-	-	1	-	-	-	1	-	-	-	-
Spring total:		126	2	27	11	3	0	2	51	0	25	3	0	0	0	1	0	0	0	1	0	0	0	0
Run total:		1,816	41	357	234	24	2	72	657	3	354	36	1	2	9	6	1	7	2	3	1	2	1	1

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 aged fish.

(b) See Appendix Table C-5 for inclusive dates and other notes regarding statistical weeks and LGR operations.

(c) ND = no data.

Appendix Table C-7. Weekly age percentages by smolt migration year, brood year, and age class of wild adult steelhead sampled at Lower Granite Dam, spawn year 2012. Large and small fish were combined. Percentages may not sum to 100.0% due to rounding error.

Statistical week(a)	Sample period ending(b)	Number of samples aged	Smolt migration year (MY), brood year (BY), and age class (percent):																					
			MY2010					MY2009					MY2008						MY2007					
			BY09 1.1	BY08 2.1	BY07 3.1	BY06 4.1	BY05 5.1	BY08 1.2	BY07 2.2	BY07 2.1S	BY06 3.2	BY05 4.2	BY04 5.2	BY07 1.2S	BY06 2.3	BY06 2.1S1	BY06 2.2S	BY05 3.3	BY05 3.1S1	BY05 3.2S	BY04 4.1S1	BY05 2.2S1	BY04 3.1S2	BY04 3.2S1
Fall 2011																								
27-33	8/14	160	1.3	16.3	12.5	1.3	-	5.0	36.9	-	25.0	0.6	0.6	-	0.6	-	-	-	-	-	-	-	-	-
34-35	8/28	183	0.5	22.4	21.9	1.1	0.5	2.2	33.3	-	15.3	2.2	-	-	-	0.5	-	-	-	-	-	-	-	-
36	9/4	226	1.8	22.1	13.7	2.7	0.4	3.1	31.4	-	20.4	2.7	-	-	-	0.4	-	0.9	-	0.4	-	-	-	-
37	9/11	163	3.7	16.6	19.6	2.5	-	4.3	33.1	-	14.7	3.7	-	-	1.2	-	-	0.6	-	-	-	-	-	-
38	9/18	175	1.1	13.1	16.6	1.1	-	6.3	34.3	-	21.7	3.4	-	-	-	-	-	1.7	-	-	0.6	-	-	-
39	9/25	149	4.0	18.8	8.7	0.7	-	2.7	34.2	0.7	24.8	1.3	-	0.7	0.7	-	-	0.7	1.3	-	-	-	-	0.7
40	10/2	183	3.8	26.2	8.2	-	-	2.7	38.8	-	14.2	2.7	-	0.5	1.6	0.5	-	-	-	0.5	-	-	-	-
41	10/9	130	3.1	19.2	11.5	-	-	6.2	36.9	-	18.5	1.5	-	-	1.5	1.5	-	-	-	-	-	-	-	-
42	10/16	121	0.8	19.0	11.6	0.8	-	5.8	37.2	0.8	22.3	-	-	-	-	0.8	-	-	-	-	0.8	-	-	-
43	10/23	108	2.8	16.7	3.7	2.8	-	3.7	44.4	-	23.1	0.9	-	-	-	-	-	-	-	-	0.9	0.9	-	-
44-53	12/31	92	3.3	22.8	10.9	-	-	5.4	41.3	1.1	15.2	-	-	-	-	-	-	-	-	-	-	-	-	-
Fall total:		1,690	2.3	19.5	13.2	1.2	0.1	4.1	35.9	0.2	19.5	2.0	0.1	0.1	0.5	0.3	0.1	0.4	0.1	0.1	0.1	0.1	0.1	0.1
Spring 2012																								
1-10	2/29	ND(c)	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
10-27	6/30	126	1.6	21.4	8.7	2.4	-	1.6	40.5	-	19.8	2.4	-	-	-	0.8	-	-	-	0.8	-	-	-	-
Spring total:		126	1.6	21.4	8.7	2.4	0.0	1.6	40.5	0.0	19.8	2.4	0.0	0.0	0.0	0.8	0.0	0.0	0.0	0.8	0.0	0.0	0.0	0.0
Run total:		1,816	2.3	19.7	12.9	1.3	0.1	4.0	36.2	0.2	19.5	2.0	0.1	0.1	0.5	0.3	0.1	0.4	0.1	0.2	0.1	0.1	0.1	0.1

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 aged fish.

(b) See Appendix Table C-5 for inclusive dates and other notes regarding statistical weeks and LGR operations.

(c) ND = no data.

Appendix Table C-8. Weekly gender frequencies of wild adult steelhead sampled at Lower Granite Dam, spawn year 2012. Large and small fish were combined.

Statistical week(a)	Sample period ending(b)	Number of samples genotyped for gender	Gender (frequency):	
			Female	Male
Fall 2011				
27-33	8/14	170	125	45
34-35	8/28	193	123	70
36	9/4	233	170	63
37	9/11	165	104	61
38	9/18	191	136	55
39	9/25	165	118	47
40	10/2	190	127	63
41	10/9	149	98	51
42	10/16	126	97	29
43	10/23	118	73	45
44-53	12/31	97	55	42
Fall total:		1,797	1,226	571
Spring 2012				
1-10	2/29	ND(c)	ND	ND
10-27	6/30	174	117	57
Spring total:		174	117	57
Run total:		1,971	1,343	628

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 genotyped fish.

(b) See Appendix Table C-5 for inclusive dates and other notes regarding statistical weeks and LGR operations.

(c) ND = no data.

Appendix Table C-9. Weekly gender percentages of wild adult steelhead sampled at Lower Granite Dam, spawn year 2012. Large and small fish were combined. Percentages may not sum to 100.0% due to rounding error.

Statistical week(a)	Sample period ending(b)	Number of samples genotyped for gender	Gender (percent):	
			Female	Male
Fall 2011				
27-33	8/14	170	73.5	26.5
34-35	8/28	193	63.7	36.3
36	9/4	233	73.0	27.0
37	9/11	165	63.0	37.0
38	9/18	191	71.2	28.8
39	9/25	165	71.5	28.5
40	10/2	190	66.8	33.2
41	10/9	149	65.8	34.2
42	10/16	126	77.0	23.0
43	10/23	118	61.9	38.1
44-53	12/31	97	56.7	43.3
Fall total:		1,797	68.2	31.8
Spring 2012				
1-10	2/29	ND(c)	ND	ND
10-27	6/30	174	67.2	32.8
Spring total:		174	67.2	32.8
Run total:		1,971	68.1	31.9

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 genotyped fish.

(b) See Appendix Table C-5 for inclusive dates and other notes regarding statistical weeks and LGR operations.

(c) ND = no data.

Appendix Table C-10. Frequencies of wild adult steelhead sampled at Lower Granite Dam by gender by age for each genetic stock, spawn year 2012. Large and small fish were combined. Only individual fish that had both a determined sex and a total age, and irrespective of assignment probability, are included (n = 1,774). See Appendix Table B-1 for stock abbreviations.

Genetic stock	Sex	Smolt migration year (MY), brood year (BY), and age class (frequency):																							Total sample
		MY2010					MY2009						MY2008						MY2007						
		BY09 1.1	BY08 2.1	BY07 3.1	BY06 4.1	BY05 5.1	BY08 1.2	BY07 2.2	BY07 2.1S	BY06 3.2	BY05 4.2	BY04 5.2	BY07 1.2S	BY06 2.3	BY06 2.1S1	BY06 2.2S	BY05 3.3	BY05 3.1S1	BY05 3.2S	BY04 4.1S1	BY05 2.2S1	BY04 3.1S2	BY04 3.2S1		
UPSALM	F	2	47	26	0	0	12	92	2	40	1	0	0	0	2	1	0	0	1	0	0	0	0	226	
	M	6	51	20	0	0	6	24	0	10	0	0	0	0	0	0	0	0	0	0	0	0	117		
	Total:	8	98	46	0	0	18	116	2	50	1	0	0	0	2	1	0	0	1	0	0	0	343		
MFSALM	F	0	5	20	5	1	0	21	0	47	12	0	0	1	0	0	0	0	1	0	0	1	114		
	M	0	6	8	4	0	0	2	0	11	2	0	0	2	0	0	0	0	0	0	0	0	35		
	Total:	0	11	28	9	1	0	23	0	58	14	0	0	3	0	0	0	0	1	0	0	1	149		
SFSALM	F	0	0	0	0	0	0	4	0	20	2	0	0	0	0	0	1	1	1	0	0	0	29		
	M	0	0	3	0	0	0	2	0	8	1	0	0	0	0	0	0	0	0	0	0	0	14		
	Total:	0	0	3	0	0	0	6	0	28	3	0	0	0	0	0	1	1	1	0	0	0	43		
LOSALM	F	0	12	5	1	0	4	40	0	13	1	0	0	0	0	0	0	1	0	0	0	0	77		
	M	1	6	4	2	0	2	5	0	2	0	0	0	0	0	0	0	0	0	0	0	0	22		
	Total:	1	18	9	3	0	6	45	0	15	1	0	0	0	0	0	0	1	0	0	0	0	99		
UPCLWR	F	0	3	0	2	0	2	37	0	45	3	0	0	1	0	0	3	0	0	0	1	0	97		
	M	2	3	3	0	0	1	10	0	7	1	0	0	1	0	0	0	0	0	0	1	0	29		
	Total:	2	6	3	2	0	3	47	0	52	4	0	0	2	0	0	3	0	0	0	1	0	126		
SFCLWR	F	0	1	0	0	0	7	48	0	8	1	0	0	2	0	0	2	0	1	0	0	0	70		
	M	0	1	0	0	0	2	29	0	4	0	0	0	2	0	0	0	0	0	0	0	0	38		
	Total:	0	2	0	0	0	9	77	0	12	1	0	0	4	0	0	2	0	1	0	0	0	108		
LOCLWR	F	1	12	7	0	0	7	50	0	12	1	0	0	0	1	0	0	0	0	0	0	0	91		
	M	3	10	4	0	0	2	14	0	6	1	0	0	0	0	0	0	0	0	0	0	0	40		
	Total:	4	22	11	0	0	9	64	0	18	2	0	0	0	1	0	0	0	0	0	0	0	131		
IMNAHA	F	1	12	14	1	0	1	35	0	23	1	0	0	0	0	0	0	0	0	0	0	0	88		
	M	0	14	16	1	0	0	7	0	3	0	0	0	0	0	0	1	0	0	0	0	0	42		
	Total:	1	26	30	2	0	1	42	0	26	1	0	0	0	0	0	1	0	0	0	0	0	130		
GRROND	F	4	42	28	3	1	9	95	0	51	2	0	1	0	3	0	0	0	0	0	0	0	239		
	M	5	51	34	1	0	3	19	0	4	3	0	0	0	0	0	0	0	0	0	0	0	120		
	Total:	9	93	62	4	1	12	114	0	55	5	0	1	0	3	0	0	0	0	0	0	0	359		
LSNAKE	F	2	35	17	3	0	11	87	1	32	1	1	0	0	0	0	0	0	0	1	0	0	191		
	M	11	39	18	1	0	3	20	0	2	1	0	0	0	0	0	0	0	0	0	0	0	95		
	Total:	13	74	35	4	0	14	107	1	34	2	1	0	0	0	0	0	0	0	1	0	0	286		
Grand total:		38	350	227	24	2	72	641	3	348	34	1	1	9	6	1	7	2	3	1	2	1	1	1,774	

Appendix Table C-11. Percentage of wild adult steelhead sampled at Lower Granite Dam by gender by age for each genetic stock, spawn year 2012. Large and small fish were combined. Only individual fish that had both a determined sex and a total age, and irrespective of assignment probability, are included (n = 1,774). See Appendix Table B-1 for stock abbreviations.

Genetic stock	Sex	Smolt migration year (MY), brood year (BY), and age class (percent):																							Sex ratio
		MY2010					MY2009						MY2008						MY2007						
		BY09 1.1	BY08 2.1	BY07 3.1	BY06 4.1	BY05 5.1	BY08 1.2	BY07 2.2	BY07 2.1S	BY06 3.2	BY05 4.2	BY04 5.2	BY07 1.2S	BY06 2.3	BY06 2.1S1	BY06 2.2S	BY05 3.3	BY05 3.1S1	BY05 3.2S	BY04 4.1S1	BY05 2.2S1	BY04 3.1S2	BY04 3.2S1		
UPSALM	F	0.9	20.8	11.5	0.0	0.0	5.3	40.7	0.9	17.7	0.4	0.0	0.0	0.0	0.9	0.4	0.0	0.0	0.4	0.0	0.0	0.0	0.0	65.9	
	M	5.1	43.6	17.1	0.0	0.0	5.1	20.5	0.0	8.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	34.1	
	Total:	2.3	28.6	13.4	0.0	0.0	5.2	33.8	0.6	14.6	0.3	0.0	0.0	0.0	0.6	0.3	0.0	0.0	0.3	0.0	0.0	0.0	0.0	100.0	
MFSALM	F	0.0	4.4	17.5	4.4	0.9	0.0	18.4	0.0	41.2	10.5	0.0	0.0	0.9	0.0	0.0	0.0	0.0	0.0	0.9	0.0	0.0	0.0	76.5	
	M	0.0	17.1	22.9	11.4	0.0	0.0	5.7	0.0	31.4	5.7	0.0	0.0	5.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	23.5	
	Total:	0.0	7.4	18.8	6.0	0.7	0.0	15.4	0.0	38.9	9.4	0.0	0.0	2.0	0.0	0.0	0.0	0.0	0.0	0.7	0.0	0.0	0.0	100.0	
SFSALM	F	0.0	0.0	0.0	0.0	0.0	0.0	13.8	0.0	69.0	6.9	0.0	0.0	0.0	0.0	0.0	3.4	3.4	3.4	0.0	0.0	0.0	0.0	67.4	
	M	0.0	0.0	21.4	0.0	0.0	0.0	14.3	0.0	57.1	7.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	32.6	
	Total:	0.0	0.0	7.0	0.0	0.0	0.0	14.0	0.0	65.1	7.0	0.0	0.0	0.0	0.0	0.0	2.3	2.3	2.3	0.0	0.0	0.0	0.0	100.0	
LOSALM	F	0.0	15.6	6.5	1.3	0.0	5.2	51.9	0.0	16.9	1.3	0.0	0.0	0.0	0.0	0.0	0.0	1.3	0.0	0.0	0.0	0.0	0.0	77.8	
	M	4.5	27.3	18.2	9.1	0.0	9.1	22.7	0.0	9.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	22.2	
	Total:	1.0	18.2	9.1	3.0	0.0	6.1	45.5	0.0	15.2	1.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	100.0	
UPCLWR	F	0.0	3.1	0.0	2.1	0.0	2.1	38.1	0.0	46.4	3.1	0.0	0.0	1.0	0.0	0.0	3.1	0.0	0.0	0.0	1.0	0.0	0.0	77.0	
	M	6.9	10.3	10.3	0.0	0.0	3.4	34.5	0.0	24.1	3.4	0.0	0.0	3.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.4	0.0	23.0	
	Total:	1.6	4.8	2.4	1.6	0.0	2.4	37.3	0.0	41.3	3.2	0.0	0.0	1.6	0.0	0.0	2.4	0.0	0.0	0.0	0.8	0.8	0.0	100.0	
SFCLWR	F	0.0	1.4	0.0	0.0	0.0	10.0	68.6	0.0	11.4	1.4	0.0	0.0	2.9	0.0	0.0	2.9	0.0	1.4	0.0	0.0	0.0	0.0	64.8	
	M	0.0	2.6	0.0	0.0	0.0	5.3	76.3	0.0	10.5	0.0	0.0	0.0	5.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	35.2	
	Total:	0.0	1.9	0.0	0.0	0.0	8.3	71.3	0.0	11.1	0.9	0.0	0.0	3.7	0.0	0.0	1.9	0.0	0.9	0.0	0.0	0.0	0.0	100.0	
LOCLWR	F	1.1	13.2	7.7	0.0	0.0	7.7	54.9	0.0	13.2	1.1	0.0	0.0	0.0	1.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	69.5	
	M	7.5	25.0	10.0	0.0	0.0	5.0	35.0	0.0	15.0	2.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	30.5	
	Total:	3.1	16.8	8.4	0.0	0.0	6.9	48.9	0.0	13.7	1.5	0.0	0.0	0.0	0.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	
IMNAHA	F	1.1	13.6	15.9	1.1	0.0	1.1	39.8	0.0	26.1	1.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	67.7	
	M	0.0	33.3	38.1	2.4	0.0	0.0	16.7	0.0	7.1	0.0	0.0	0.0	0.0	0.0	0.0	2.4	0.0	0.0	0.0	0.0	0.0	0.0	32.3	
	Total:	0.8	20.0	23.1	1.5	0.0	0.8	32.3	0.0	20.0	0.8	0.0	0.0	0.0	0.0	0.0	0.8	0.0	0.0	0.0	0.0	0.0	0.0	100.0	
GRROND	F	1.7	17.6	11.7	1.3	0.4	3.8	39.7	0.0	21.3	0.8	0.0	0.4	0.0	1.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	66.6	
	M	4.2	42.5	28.3	0.8	0.0	2.5	15.8	0.0	3.3	2.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	33.4	
	Total:	2.5	25.9	17.3	1.1	0.3	3.3	31.8	0.0	15.3	1.4	0.0	0.3	0.0	0.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	
LSNAKE	F	1.0	18.3	8.9	1.6	0.0	5.8	45.5	0.5	16.8	0.5	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	66.8	
	M	11.6	41.1	18.9	1.1	0.0	3.2	21.1	0.0	2.1	1.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	33.2	
	Total:	4.5	25.9	12.2	1.4	0.0	4.9	37.4	0.3	11.9	0.7	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	100.0	

Appendix Table C-12. Estimated escapement of wild adult steelhead sampled at Lower Granite Dam by gender by age for each genetic stock, spawn year 2012. Large and small fish were combined. Only individual fish that had both a determined sex and a total age, and irrespective of assignment probability, were used (n = 1,774). See Appendix Table B-1 for stock abbreviations.

Genetic stock	Sex	Smolt migration year (MY), brood year (BY), and age class (abundance):																							Total abundance
		MY2010					MY2009					MY2008					MY2007								
		BY09 1.1	BY08 2.1	BY07 3.1	BY06 4.1	BY05 5.1	BY08 1.2	BY07 2.2	BY07 2.1S	BY06 3.2	BY05 4.2	BY04 5.2	BY07 1.2S	BY06 2.3	BY06 2.1S1	BY06 2.2S	BY05 3.3	BY05 3.1S1	BY05 3.2S	BY04 4.1S1	BY05 2.2S1	BY04 3.1S2	BY04 3.2S1		
UPSALM	F	41	961	532	0	0	245	1,883	41	818	20	0	0	41	20	0	0	20	0	0	0	0	0	0	4,622
	M	123	1,043	409	0	0	123	490	0	205	0	0	0	0	0	0	0	0	0	0	0	0	0	2,393	
	Total:	164	2,004	941	0	0	368	2,373	41	1,023	20	0	0	41	20	0	0	20	0	0	0	0	0	7,015	
MFSALM	F	0	92	368	92	18	0	388	0	866	221	0	18	0	0	0	0	0	18	0	0	18	0	2,099	
	M	0	110	147	74	0	0	37	0	203	37	0	37	0	0	0	0	0	0	0	0	0	0	645	
	Total:	0	202	515	166	18	0	425	0	1,069	258	0	55	0	0	0	0	18	0	0	18	0	0	2,744	
SFSALM	F	0	0	0	0	0	0	89	0	447	45	0	0	0	22	22	22	0	0	0	0	0	0	647	
	M	0	0	67	0	0	0	45	0	179	22	0	0	0	0	0	0	0	0	0	0	0	0	313	
	Total:	0	0	67	0	0	0	134	0	626	67	0	0	0	22	22	22	0	0	0	0	0	0	960	
LOSALM	F	0	142	59	12	0	47	475	0	154	12	0	0	0	0	12	0	0	0	0	0	0	0	913	
	M	12	71	47	24	0	24	59	0	24	0	0	0	0	0	0	0	0	0	0	0	0	0	261	
	Total:	12	213	106	36	0	71	534	0	178	12	0	0	0	0	12	0	0	0	0	0	0	0	1,174	
UPCLWR	F	0	60	0	40	0	40	737	0	898	60	0	20	0	0	60	0	0	0	20	0	0	0	1,935	
	M	40	60	60	0	0	20	199	0	140	20	0	20	0	0	0	0	0	0	0	20	0	0	579	
	Total:	40	120	60	40	0	60	936	0	1,038	80	0	40	0	0	60	0	0	0	20	20	0	0	2,514	
SFCLWR	F	0	27	0	0	0	192	1,316	0	219	27	0	55	0	0	55	0	27	0	0	0	0	0	1,918	
	M	0	27	0	0	0	55	794	0	110	0	0	55	0	0	0	0	0	0	0	0	0	0	1,041	
	Total:	0	54	0	0	0	247	2,110	0	329	27	0	110	0	0	55	0	27	0	0	0	0	0	2,959	
LOCLWR	F	15	184	107	0	0	107	769	0	184	15	0	0	15	0	0	0	0	0	0	0	0	0	1,396	
	M	46	153	61	0	0	31	216	0	92	15	0	0	0	0	0	0	0	0	0	0	0	0	614	
	Total:	61	337	168	0	0	138	985	0	276	30	0	0	15	0	0	0	0	0	0	0	0	0	2,010	
IMNAHA	F	18	211	246	18	0	18	614	0	404	18	0	0	0	0	0	0	0	0	0	0	0	0	1,547	
	M	0	246	281	18	0	0	122	0	53	0	0	0	0	18	0	0	0	0	0	0	0	0	738	
	Total:	18	457	527	36	0	18	736	0	457	18	0	0	0	18	0	0	0	0	0	0	0	0	2,285	
GRROND	F	77	803	536	57	19	172	1,818	0	975	38	0	19	0	57	0	0	0	0	0	0	0	0	4,571	
	M	96	975	650	19	0	57	364	0	77	57	0	0	0	0	0	0	0	0	0	0	0	0	2,295	
	Total:	173	1,778	1,186	76	19	229	2,182	0	1,052	95	0	19	0	57	0	0	0	0	0	0	0	0	6,866	
LSNAKE	F	77	1,343	652	115	0	422	3,342	38	1,228	38	38	0	0	0	0	0	0	0	38	0	0	0	7,331	
	M	422	1,497	691	38	0	115	768	0	77	38	0	0	0	0	0	0	0	0	0	0	0	0	3,646	
	Total:	499	2,840	1,343	153	0	537	4,110	38	1,305	76	38	0	0	0	0	0	0	0	38	0	0	0	10,977	

Appendix Table C-13. Frequencies of wild adult steelhead sampled at Lower Granite Dam by size for each genetic stock, spawn year 2012. Large fish are greater than or equal to 78 cm (FL) and small fish are less than 78 cm (FL). All individual fish irrespective of assignment probability are included (n = 2,004). See Appendix Table B-1 for stock abbreviations.

Genetic stock	Large	Small	Total sample
UPSALM	3	379	382
MFSALM	23	145	168
SFSALM	24	25	49
LOSALM	2	112	114
UPCLWR	72	79	151
SFCLWR	70	63	133
LOCLWR	15	129	144
IMNAHA	3	137	140
GRROND	7	390	397
LSNAKE	4	322	326
Total:	223	1,781	2,004

Appendix Table C-14. Percentage of wild adult steelhead sampled at Lower Granite Dam by size for each genetic stock, spawn year 2012. Large fish are greater than or equal to 78 cm (FL) and small fish are less than 78 cm (FL). All individual fish irrespective of assignment probability are included (n = 2,004). See Appendix Table B-1 for stock abbreviations.

Genetic stock	Large	Small	Total percent
UPSALM	0.8	99.2	100.0
MFSALM	13.7	86.3	100.0
SFSALM	49.0	51.0	100.0
LOSALM	1.8	98.2	100.0
UPCLWR	47.7	52.3	100.0
SFCLWR	52.6	47.4	100.0
LOCLWR	10.4	89.6	100.0
IMNAHA	2.1	97.9	100.0
GRROND	1.8	98.2	100.0
LSNAKE	1.2	98.8	100.0
Total:	11.1	88.9	100.0

Appendix Table C-15. Estimated escapement of wild adult steelhead sampled at Lower Granite Dam by size for each genetic stock, spawn year 2012. Large fish are greater than or equal to 78 cm (FL) and small fish are less than 78 cm (FL). All individual fish irrespective of assignment probability were used (n = 2,004). See Appendix Table B-1 for stock abbreviations.

Genetic stock	Large	Small	Total abundance
UPSALM	55	6,960	7,015
MFSALM	376	2,368	2,744
SFSALM	470	490	960
LOSALM	21	1,153	1,174
UPCLWR	1,199	1,315	2,514
SFCLWR	1,557	1,402	2,959
LOCLWR	209	1,801	2,010
IMNAHA	49	2,236	2,285
GRROND	121	6,745	6,866
LSNAKE	135	10,842	10,977
Total:	4,192	35,312	39,504

Appendix D: Wild adult Chinook salmon at Lower Granite Dam, spawn year 2012.

Appendix Table D-1. Weekly window or video counts and adult valid trap samples of Chinook salmon at Lower Granite Dam (LGR), spawn year 2012.

Statistical week(a)	Sampling period 2012	Number of days	LGR window count(b)	LGR adult valid trap sample(c)	LGR adult trap sample rate (%)	Percent of run trapped
10-20(d)	3/1-5/13	74	2,807	292	0-10	10.4
21	5/14-5/20	7	22,732	2,057	10	9.0
22(e)	5/21-5/27	7	22,756	2,555	10	11.2
23	5/28-6/3	7	9,243	886	10	9.6
24	6/4-6/10	7	4,884	577	10	11.8
25	6/11-6/17	7	7,469	788	10	10.6
26	6/18-6/24	7	4,709	469	10	10.0
27	6/25-7/1	7	3,969	431	10	10.9
28	7/2-7/8	7	2,026	216	10	10.7
29	7/9-7/15	7	1,377	147	10	10.7
30	7/16-7/22	7	1,062	114	10	10.7
31-34(d,f)	7/23-8/17	26	1,737	99	0-10	5.7
Run total:		170	84,771	8,631	0-10	10.2

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 trapped fish.

(b) Downloaded from COE link 4/10/14.

(c) From Darren Ogden (NMFS, personal communication).

(d) Includes partial beginning or ending week.

(e) All trapped fish data are from new NMFS database from 5/24/12 forward.

(f) The trap was closed 7/27/12 to 7/29/12, 8/6/12 to 8/9/12, and 8/13/12 to 8/17/12 due to high water temperatures.

Appendix Table D-2. Number of Chinook salmon captured in the adult trap, by origin, at Lower Granite Dam (LGR), spawn year 2012. Clipped and unclipped refer to the adipose fin.

Statistical week(a)	Sample period ending(b)	LGR adult valid trap sample(c)	Number of trapped fish that were(c):				
			Wild	Hatchery clipped	Hatchery unclipped	Total hatchery	Total wild
10-20	5/13	292	36	247	9	256	36
21	5/20	2,057	375	1,574	108	1,682	375
22	5/27	2,555	475	1,937	143	2,080	475
23	6/3	886	229	599	58	657	229
24	6/10	577	173	376	28	404	173
25	6/17	788	299	441	48	489	299
26	6/24	469	167	273	29	302	167
27	7/1	431	154	255	22	277	154
28	7/8	216	101	107	8	115	101
29	7/15	147	62	79	6	85	62
30	7/22	114	49	61	4	65	49
31-34	8/17	99	71	23	5	28	71
Run total:		8,631	2,191	5,972	468	6,440	2,191

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 trapped fish.

(b) See Appendix Table D-1 for inclusive dates and other notes regarding statistical weeks and LGR operations.

(c) From Darren Ogden (NMFS, personal communication); hatchery unclipped includes 153 fish misidentified at the trap as wild as determined by PBT.

Appendix Table D-3. Percentage of Chinook salmon captured in the adult trap, by origin, at Lower Granite Dam (LGR), spawn year 2012. Clipped and unclipped refer to the adipose fin. Percentages may not sum to 100.0% due to rounding error.

Statistical week(a)	Sample period ending(b)	LGR adult valid trap sample(c)	Percentage of trapped fish that were:				
			Wild	Hatchery clipped	Hatchery unclipped	Total hatchery	Total wild
10-20	5/13	292	12.3	84.6	3.1	87.7	12.3
21	5/20	2,057	18.2	76.5	5.3	81.8	18.2
22	5/27	2,555	18.6	75.8	5.6	81.4	18.6
23	6/3	886	25.8	67.6	6.5	74.2	25.8
24	6/10	577	30.0	65.2	4.9	70.0	30.0
25	6/17	788	37.9	56.0	6.1	62.1	37.9
26	6/24	469	35.6	58.2	6.2	64.4	35.6
27	7/1	431	35.7	59.2	5.1	64.3	35.7
28	7/8	216	46.8	49.5	3.7	53.2	46.8
29	7/15	147	42.2	53.7	4.1	57.8	42.2
30	7/22	114	43.0	53.5	3.5	57.0	43.0
31-34	8/17	99	71.7	23.2	5.1	28.3	71.7
Run total(d):		8,631	25.6	68.9	5.4	74.4	25.6

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 trapped fish.

(b) See Appendix Table D-1 for inclusive dates and other notes regarding statistical weeks and LGR operations.

(c) From Darren Ogden (NMFS, personal communication); hatchery unclipped includes 153 fish misidentified at the trap as wild as determined by PBT.

(d) Run total percentages for each origin class were calculated from escapement estimates in Appendix Table D-4.

Appendix Table D-4. Estimated weekly escapement, by origin, of Chinook salmon at Lower Granite Dam (LGR), spawn year 2012. Clipped and unclipped refer to the adipose fin.

Statistical week(a)	Sample period ending(b)	LGR window count(c)	Estimated number of Chinook salmon at LGR that were:				
			Wild	Hatchery clipped	Hatchery unclipped	Total hatchery	Total wild
10-20	5/13	2,807	346	2,374	87	2,461	346
21	5/20	22,732	4,144	17,394	1,194	18,588	4,144
22	5/27	22,756	4,231	17,251	1,274	18,525	4,231
23	6/3	9,243	2,389	6,249	605	6,854	2,389
24	6/10	4,884	1,464	3,183	237	3,420	1,464
25	6/17	7,469	2,834	4,180	455	4,635	2,834
26	6/24	4,709	1,677	2,741	291	3,032	1,677
27	7/1	3,969	1,418	2,348	203	2,551	1,418
28	7/8	2,026	947	1,004	75	1,079	947
29	7/15	1,377	581	740	56	796	581
30	7/22	1,062	456	569	37	606	456
31-34	8/17	1,737	1,246	403	88	491	1,246
Run total:		84,771	21,733	58,436	4,602	63,038	21,733
95% CI:			(20,968-22,507)	(57,635-59,272)	(4,198-5,010)	(62,287-63,779)	(20,968-22,507)

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 trapped fish.

(b) See Appendix Table D-1 for inclusive dates and other notes regarding statistical weeks and LGR operations.

(c) Downloaded from COE link 4/10/14.

Appendix Table D-5. Number of wild adult Chinook salmon scale and genetics samples collected at Lower Granite Dam and subsequently aged or genotyped, spawn year 2012.

Statistical week(a)	Sampling period 2012	Number of days	Wild run size(b)	Number of scale and genetics samples collected(c)	Number of scale and genetics systematic subsamples(c)	Scale samples:		Genetics samples:			
						Number of samples aged(d)	Percent of run aged	Number of samples genotyped for gender(d)	Percent of run genotyped for gender	Number of samples genotyped for stock(d)	Percent of run genotyped for stock
10-21(e)	3/1-5/20	81	4,490	411	411	380	8.5	398	8.9	406	9.0
22	5/21-5/27	7	4,231	475	475	442	10.4	462	10.9	469	11.1
23	5/28-6/3	7	2,389	229	229	218	9.1	227	9.5	228	9.5
24	6/4-6/10	7	1,464	173	173	160	10.9	165	11.3	170	11.6
25	6/11-6/17	7	2,834	299	299	267	9.4	288	10.2	294	10.4
26	6/18-6/24	7	1,677	167	167	147	8.8	162	9.7	167	10.0
27	6/25-7/1	7	1,418	154	154	141	9.9	152	10.7	154	10.9
28	7/2-7/8	7	947	101	101	93	9.8	98	10.3	98	10.3
29-34(e)	7/9-8/17	40	2,283	182	182	161	7.1	171	7.5	180	7.9
Run total:		170	21,733	2,191	2,191	2,009	9.2	2,123	9.8	2,166	10.0

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 aged or genotyped fish.

(b) From Appendix Table D-4.

(c) Does not include 153 fish misidentified as wild at the trap and later determined to be unclipped hatchery by PBT.

(d) Some subsamples were not aged or genotyped due to missing scales or fin clips; other subsamples were not able to be aged (freshwater and saltwater) or successfully genotyped; neither are included here. Misidentified wild fish later determined to be unclipped hatchery by PBT are not included.

(e) Includes partial beginning or ending week.

Appendix Table D-6. Weekly age frequencies by smolt migration year, brood year, and age class of wild adult Chinook salmon sampled at Lower Granite Dam, spawn year 2012.

Statistical week(a)	Sample period ending(b)	Number of samples aged	Smolt migration year (MY), brood year (BY), and age class (frequency):									
			MY2012		MY2011		MY2010			MY2009		MY2008
			BY10 1.0	BY09 2.0	BY09 1.1	BY08 2.1	BY09 0.2	BY08 1.2	BY07 2.2	BY07 1.3	BY06 2.3	BY06 1.4
10-21	5/20	380	-	-	7	-	-	248	-	124	1	-
22	5/27	442	-	-	7	-	-	303	-	131	1	-
23	6/3	218	-	-	8	-	-	133	-	77	-	-
24	6/10	160	-	-	10	-	-	104	-	45	-	1
25	6/17	267	-	-	10	-	-	183	-	73	-	1
26	6/24	147	-	-	8	-	-	98	1	39	1	-
27	7/1	141	-	-	18	1	1	92	1	26	2	-
28	7/8	93	-	-	10	1	-	61	1	19	-	1
29-34	8/17	161	2	2	24	4	-	73	12	30	12	2
Run total:		2,009	2	2	102	6	1	1,295	15	564	17	5

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 aged fish.

(b) See Appendix Table D-5 for inclusive dates and other notes regarding statistical weeks and LGR operations.

Appendix Table D-7. Weekly age percentages by smolt migration year, brood year, and age class of wild adult Chinook salmon sampled at Lower Granite Dam, spawn year 2012. Percentages may not sum to 100.0% due to rounding error.

Statistical week(a)	Sample period ending(b)	Number of samples aged	Smolt migration year (MY), brood year (BY), and age class (percent):										
			MY2012		MY2011		MY2010			MY2009		MY2008	
			BY10 1.0	BY09 2.0	BY09 1.1	BY08 2.1	BY09 0.2	BY08 1.2	BY07 2.2	BY07 1.3	BY06 2.3	BY06 1.4	
10-21	5/20	380	-	-	1.8	-	-	-	65.3	-	32.6	0.3	-
22	5/27	442	-	-	1.6	-	-	-	68.6	-	29.6	0.2	-
23	6/3	218	-	-	3.7	-	-	-	61.0	-	35.3	-	-
24	6/10	160	-	-	6.3	-	-	-	65.0	-	28.1	-	0.6
25	6/17	267	-	-	3.7	-	-	-	68.5	-	27.3	-	0.4
26	6/24	147	-	-	5.4	-	-	-	66.7	0.7	26.5	0.7	-
27	7/1	141	-	-	12.8	0.7	-	0.7	65.2	0.7	18.4	1.4	-
28	7/8	93	-	-	10.8	1.1	-	-	65.6	1.1	20.4	-	1.1
29-34	8/17	161	1.2	1.2	14.9	2.5	-	-	45.3	7.5	18.6	7.5	1.2
Run total:		2,009	0.1	0.1	5.1	0.3	-	0.0	64.5	0.7	28.1	0.8	0.2

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 aged fish.

(b) See Appendix Table D-5 for inclusive dates and other notes regarding statistical weeks and LGR operations.

Appendix Table D-8. Weekly gender frequencies of wild adult Chinook salmon sampled at Lower Granite Dam, spawn year 2012.

Statistical week(a)	Sample period ending(b)	Number of samples genotyped for gender	Gender (frequency):	
			Female	Male
10-21	5/20	398	204	194
22	5/27	462	245	217
23	6/3	227	116	111
24	6/10	165	80	85
25	6/17	288	148	140
26	6/24	162	76	86
27	7/1	152	65	87
28	7/8	98	47	51
29-34	8/17	171	91	80
Run total:		2,123	1,072	1,051

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 genotyped fish.

(b) See Appendix Table D-5 for inclusive dates and other notes regarding statistical weeks and LGR operations.

Appendix Table D-9. Weekly gender percentages of wild adult Chinook salmon sampled at Lower Granite Dam, spawn year 2012. Percentages may not sum to 100.0% due to rounding error.

Statistical week(a)	Sample period ending(b)	Number of samples genotyped for gender	Gender (percent):	
			Female	Male
10-21	5/20	398	51.3	48.7
22	5/27	462	53.0	47.0
23	6/3	227	51.1	48.9
24	6/10	165	48.5	51.5
25	6/17	288	51.4	48.6
26	6/24	162	46.9	53.1
27	7/1	152	42.8	57.2
28	7/8	98	48.0	52.0
29-34	8/17	171	53.2	46.8
Run total:		2,123	50.5	49.5

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 genotyped fish.

(b) See Appendix Table D-5 for inclusive dates and other notes regarding statistical weeks and LGR operations.

Appendix Table D-10. Frequencies of wild adult Chinook salmon sampled at Lower Granite Dam by gender by age for each genetic stock, spawn year 2012. Only individual fish that had both a determined sex and a total age, and irrespective of assignment probability, are included (n = 1,945). See Appendix Table B-2 for stock abbreviations.

		Smolt migration year (MY), brood year (BY), and age class (frequency)										Total sample
Genetic stock	Sex	MY2012		MY2011		MY2010			MY2009		MY2008	
		BY10 1.0	BY09 2.0	BY09 1.1	BY08 2.1	BY09 0.2	BY08 1.2	BY07 2.2	BY07 1.3	BY06 2.3	BY06 1.4	
UPSALM	F	0	0	0	0	0	65	0	93	0	1	159
	M	0	0	15	0	0	126	1	34	0	0	176
	Total:	0	0	15	0	0	191	1	127	0	1	335
MFSALM	F	0	0	0	0	0	69	0	97	0	0	166
	M	0	0	26	0	0	101	0	35	0	0	162
	Total:	0	0	26	0	0	170	0	132	0	0	328
CHMBLN	F	0	0	0	0	0	19	0	4	0	0	23
	M	0	0	8	0	0	26	0	1	0	0	35
	Total:	0	0	8	0	0	45	0	5	0	0	58
SFSALM	F	0	0	0	0	0	72	0	60	0	0	132
	M	0	0	14	0	0	116	0	12	0	0	142
	Total:	0	0	14	0	0	188	0	72	0	0	274
HELLSC	F	0	0	1	0	0	335	0	120	1	1	458
	M	0	0	27	0	0	320	0	66	0	0	413
	Total:	0	0	28	0	0	655	0	186	1	1	871
TUCANO	F	0	0	0	0	0	6	0	1	0	0	7
	M	0	0	0	0	0	4	0	2	0	0	6
	Total:	0	0	0	0	0	10	0	3	0	0	13
FALL	F	0	0	0	0	0	3	10	8	12	2	35
	M	2	2	9	6	1	4	3	1	2	1	31
	Total:	2	2	9	6	1	7	13	9	14	3	66
Grand total:		2	2	100	6	1	1,266	14	534	15	5	1,945

Appendix Table D-11. Percentage of wild adult Chinook salmon sampled at Lower Granite Dam by gender by age for each genetic stock, spawn year 2012. Only individual fish that had both a determined sex and a total age, and irrespective of assignment probability, are included (n = 1,945). See Appendix Table B-2 for stock abbreviations.

		Smolt migration year (MY), brood year (BY), and age class (percent)										Sex ratio
Genetic stock	Sex	MY2012		MY2011		MY2010			MY2009		MY2008	
		BY10 1.0	BY09 2.0	BY09 1.1	BY08 2.1	BY09 0.2	BY08 1.2	BY07 2.2	BY07 1.3	BY06 2.3	BY06 1.4	
UPSALM	F	0.0	0.0	0.0	0.0	0.0	40.9	0.0	58.5	0.0	0.6	47.5
	M	0.0	0.0	8.5	0.0	0.0	71.6	0.6	19.3	0.0	0.0	52.5
	Total:	0.0	0.0	4.5	0.0	0.0	57.0	0.3	37.9	0.0	0.3	100.0
MFSALM	F	0.0	0.0	0.0	0.0	0.0	41.6	0.0	58.4	0.0	0.0	50.6
	M	0.0	0.0	16.0	0.0	0.0	62.3	0.0	21.6	0.0	0.0	49.4
	Total:	0.0	0.0	7.9	0.0	0.0	51.8	0.0	40.2	0.0	0.0	100.0
CHMBLN	F	0.0	0.0	0.0	0.0	0.0	82.6	0.0	17.4	0.0	0.0	39.7
	M	0.0	0.0	22.9	0.0	0.0	74.3	0.0	2.9	0.0	0.0	60.3
	Total:	0.0	0.0	13.8	0.0	0.0	77.6	0.0	8.6	0.0	0.0	100.0
SFSALM	F	0.0	0.0	0.0	0.0	0.0	54.5	0.0	45.5	0.0	0.0	48.2
	M	0.0	0.0	9.9	0.0	0.0	81.7	0.0	8.5	0.0	0.0	51.8
	Total:	0.0	0.0	5.1	0.0	0.0	68.6	0.0	26.3	0.0	0.0	100.0
HELLSC	F	0.0	0.0	0.2	0.0	0.0	73.1	0.0	26.2	0.2	0.2	52.6
	M	0.0	0.0	6.5	0.0	0.0	77.5	0.0	16.0	0.0	0.0	47.4
	Total:	0.0	0.0	3.2	0.0	0.0	75.2	0.0	21.4	0.1	0.1	100.0
TUCANO	F	0.0	0.0	0.0	0.0	0.0	85.7	0.0	14.3	0.0	0.0	53.8
	M	0.0	0.0	0.0	0.0	0.0	66.7	0.0	33.3	0.0	0.0	46.2
	Total:	0.0	0.0	0.0	0.0	0.0	76.9	0.0	23.1	0.0	0.0	100.0
FALL	F	0.0	0.0	0.0	0.0	0.0	8.6	28.6	22.9	34.3	5.7	53.0
	M	6.5	6.5	29.0	19.4	3.2	12.9	9.7	3.2	6.5	3.2	47.0
	Total:	3.0	3.0	13.6	9.1	1.5	10.6	19.7	13.6	21.2	4.5	100.0

Appendix Table D-12. Estimated escapement of wild adult Chinook salmon sampled at Lower Granite Dam by gender by age for each genetic stock, spawn year 2012. Only individual fish that had both a determined sex and a total age, and irrespective of assignment probability, were used (n = 1,945). See Appendix Table B-2 for stock abbreviations.

		Smolt migration year (MY), brood year (BY), and age class (abundance)										Total abundance
Genetic stock	Sex	MY2012		MY2011		MY2010			MY2009		MY2008	
		BY10 1.0	BY09 2.0	BY09 1.1	BY08 2.1	BY09 0.2	BY08 1.2	BY07 2.2	BY07 1.3	BY06 2.3	BY06 1.4	
UPSALM	F	0	0	0	0	0	661	0	947	0	10	1,618
	M	0	0	153	0	0	1,281	10	346	0	0	1,790
	Total:	0	0	153	0	0	1,942	10	1,293	0	10	3,408
MFSALM	F	0	0	0	0	0	700	0	983	0	0	1,683
	M	0	0	264	0	0	1,023	0	355	0	0	1,642
	Total:	0	0	264	0	0	1,723	0	1,338	0	0	3,325
CHMBLN	F	0	0	0	0	0	195	0	41	0	0	236
	M	0	0	82	0	0	266	0	10	0	0	358
	Total:	0	0	82	0	0	461	0	51	0	0	594
SFSALM	F	0	0	0	0	0	1,078	0	899	0	0	1,977
	M	0	0	210	0	0	1,737	0	180	0	0	2,127
	Total:	0	0	210	0	0	2,815	0	1,079	0	0	4,104
HELLSC	F	0	0	11	0	0	3,624	0	1,299	11	11	4,956
	M	0	0	292	0	0	3,463	0	714	0	0	4,469
	Total:	0	0	303	0	0	7,087	0	2,013	11	11	9,425
TUCANO	F	0	0	0	0	0	44	0	7	0	0	51
	M	0	0	0	0	0	29	0	14	0	0	43
	Total:	0	0	0	0	0	73	0	21	0	0	94
FALL	F	0	0	0	0	0	36	119	95	141	24	415
	M	24	24	106	71	12	47	36	12	24	12	368
	Total:	24	24	106	71	12	83	155	107	165	36	783

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