FISHERY RESEARCH

WILD ADULT STEELHEAD AND CHINOOK SALMON ABUNDANCE AND COMPOSITION AT LOWER GRANITE DAM, SPAWN YEAR 2011

2011 ANNUAL REPORT

Photo: Allen Bartels

Prepared by:

William C. Schrader, Principal Fishery Research Biologist
Matthew P. Corsi, Regional Fisheries Biologist
Patrick Kennedy, Senior Fishery Research Biologist
Michael W. Ackerman, Fishery Research Biologist
Matthew R. Campbell, Fisheries Genetics Program Coordinator
Kristin K. Wright, Fishery Research Biologist
Timothy Copeland, Senior Fishery Research Biologist

IDFG Report Number 13-15
July 2013

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Matthew P. Corsi
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Michael W. Ackerman
Matthew R. Campbell
Kristin K. Wright
Timothy Copeland

Idaho Department of Fish and Game
600 South Walnut Street
P.O. Box 25
Boise, ID 83707

To

U.S. Department of Energy
Bonneville Power Administration
Division of Fish and Wildlife
P.O. Box 3621
Portland, OR 97283-3621

Project Numbers #1990-055-00, 1991-073-00, 2010-026-00
Contract Numbers 45642, 50973, 50975, 53239

IDFG Report Number 13-15
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ACKNOWLEDGEMENTS

Report Authors:

William C. Schrader (IDFG)

Matthew P. Corsi (IDFG)

Patrick Kennedy (IDFG)

Michael W. Ackerman (IDFG / PSMFC)

Matthew R. Campbell (IDFG)

Kristin K. Wright (IDFG / PSMFC)

Timothy Copeland (IDFG)

Report Contributors: Data, reviews, and other assistance (*alphabetical*)

IDFG

- Amber Barenberg
- Brett Bowersox
- Grant Bruner
- Alan Byrne
- Joe Dupont
- Robert Hand
- Pete Hassemer
- Lance Hebdon
- Chris McConnell
- Jamie Nelson
- Charlie Petrosky
- Scott Putnam
- Leslie Reinhardt
- Lynn Schrader
- Jesse McCane
- Laura Redfield
- Ron Roberts
- Craig Steele
- Thea Vanderwey
- Ninh Vu

IDFG / PSMFC

- Paul Bunn
- Carlos Camacho
- Tyler Gross
- Kala Hernandez
- Cliff Hohman
- Tyler Johnson
- Dylan Kovis

Columbia River Inter-Tribal Fish Commission

- Jon Hess
- Amanda Matala
- Andrew Matala
- Shawn Narum
- Jeff Stephenson

University of Idaho

- Kirk Steinhorst

NMFS Northwest Fisheries Science Center

- Vicky Brenner
- Shane Collier
- Jack Lyman
- Doug Marsh
- Ken McIntyre
- Darren Ogden
- Neil Paasch
- Ken Thomas

Quantitative Consultants, Inc.

- Allen Bartels
- Jody White

ACKNOWLEDGEMENTS (CONTINUED)

Project Administration: Funding and other assistance (*alphabetical*)

- Bonneville Power Administration (BPA); projects:
  1990-055-00 Idaho Steelhead Monitoring and Evaluation Studies
  1991-073-00 Idaho Natural Production Monitoring and Evaluation Program
  2010-026-00 Chinook and Steelhead Genotyping for Genetic Stock Identification (GSI) at Lower Granite Dam

- Idaho Office of Species Conservation (IOSC)

- Northwest Power and Conservation Council (NPCC)

- Pacific States Marine Fisheries Commission (PSMFC)

- Quantitative Consultants, Inc. (QCI)

- U. S. Fish and Wildlife Service, Lower Snake River Compensation Program (LSRCP)

Suggested citation:

Schrader, W. C., M. P. Corsi, P. Kennedy, M. W. Ackerman, M. R. Campbell, K. K. Wright, and T. Copeland. 2013. Wild adult steelhead and Chinook salmon abundance and composition at Lower Granite Dam, spawn year 2011. Idaho Department of Fish and Game Report 13-15. Annual report 2011, BPA Projects 1990-055-00, 1991-073-00, 2010-026-00.

DEDICATION

Dedicated to the memory of Danielle (Dani) J. Schiff and Lawrence (Larry) T. Barrett who died in a helicopter crash on August 31, 2010, in route to fly Chinook salmon spawning ground surveys in the Selway River. Both were Fisheries Biologists with the Idaho Department of Fish and Game. Dani had recently accepted a new assignment overseeing Lower Granite Dam sampling activities for the Department in the summer of 2010 (this report). They will both be missed.

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
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
MSA	Mixed Stock Analysis
MY	Smolt Migration Year
NMFS	National Marine Fisheries Service
PBT	Parentage Based Tagging
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, *U.S. v. Oregon*
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 2011. 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, 2010 and June 30, 2011, wild escapement was estimated to be 44,404 fish or 21.3% of the total run. Of these, 563 fish were from brood year (BY) 2008; 10,241 fish from BY2007; 21,519 fish from BY2006; 11,258 fish from BY2005; and 823 fish from BY2004. Total age at spawning ranged from three to seven years; freshwater age ranged from one to four years and saltwater age ranged from one to three years. Using a sex-specific genetic assay, we estimate 29,616 females and 14,788 males returned. Genetic stock abundance estimates were 6,717 fish for the upper Salmon River; 3,934 fish for the Middle Fork Salmon River; 2,357 fish for the South Fork Salmon River; 1,573 fish for the lower Salmon River; 4,179 fish for the upper Clearwater River; 4,377 fish for the South Fork Clearwater River; 1,809 fish for the lower Clearwater River; 2,496 fish for the Imnaha River; 7,212 fish for the Grande Ronde River; and 9,750 fish for the lower Snake River. The combined wild and hatchery steelhead escapement was 208,296 fish counted at the window by U.S. Army Corps of Engineers. We estimate that 163,892 of these fish were of hatchery origin, of which 13.5% were unclipped. For Chinook salmon between March 1 and August 17, 2011, wild escapement was estimated to be 26,608 fish or 19.8% of the total run. Of these, 160 fish were from BY2009; 3,980 fish from BY2008; 14,561 fish from BY2007; and 7,774 fish from BY2006; and 133 fish from BY2005. 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 three years. Using a sex-specific genetic assay, we estimate 9,154 females and 17,454 males returned. Genetic stock abundance estimates were 4,236 fish for the upper Salmon River; 3,929 fish for the Middle Fork Salmon River; 551 fish for Chamberlain Creek; 5,479 fish for the South Fork Salmon River; 11,050 fish for the Hells Canyon aggregate stock including the Clearwater, Little Salmon, lower Salmon, Grande Ronde, Imnaha, and lower Snake rivers; and 238 fish for the Tucannon River. In addition, 1,125 fish or 4.2% of the wild run were identified as fall Chinook salmon based on genetic data. The combined wild and hatchery Chinook salmon escapement was 134,594 fish counted at the window by U.S. Army Corps of Engineers. We estimate that 107,986 of these fish were of hatchery origin, of which 5.0% 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.

Authors:

William C. Schrader, Principal Fishery Research Biologist

Matthew P. Corsi, Regional Fisheries Biologist

Patrick Kennedy, Senior Fishery Research Biologist

Michael W. Ackerman, Fishery Research Biologist

Matthew R. Campbell, Fisheries Genetics Program Coordinator

Kristin K. Wright, Fishery Research Biologist

Timothy Copeland, Senior Fishery Research Biologist

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 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 goal, consistent with basinwide mitigation and recovery programs, is 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; Kennedy et al. 2011, 2012; Schrader et al. 2011, 2012). 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) designates jack Chinook salmon as fish between 30 and 56 cm (12 and 22 inches) in length, and 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) 2011. For steelhead, fish passing LGR during the summer and fall of 2010 comprise the bulk of the 2011 spawn year. There is one previous preliminary accounting of the data: Ackerman et al. (2012) reported initial genetic stock identification (GSI) results for both steelhead and Chinook salmon based on single nucleotide polymorphism (SNP) variation. 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 2011, 2012). 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 2010, the trap sample rate changed twice and ranged from 4% in early July to 12% in late August and early September (Table 2). The trap was closed from August 14 to August 21, 2010 due to high water temperatures. It was closed from November 19, 2010 to March 6, 2011 due to freezing water temperatures. The trap sample rate was 10% from March 7 to August 17, 2011; no trap closures occurred during this time period. The adult fish ladder was dewatered from January 4 to February 2, 2011; 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 2011, 2012; 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 parentage based tagging (PBT) genetic mark 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 genetic mark. Genotyping for PBT analysis was conducted post hoc. Fish determined to be phenotypically wild by the trap crew were sampled for scales and tissue. All captured wild fish were also PIT tagged for the Integrated Status and Effectiveness Monitoring Project (ISEMP, BPA project 2003-017-00; Beasley and White 2010; QCI 2011, 2012).

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 aging 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 SY2011 (Ogden 2011, 2012).

Valid Sample Selection

Not all trapped fish were deemed valid 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 Doug 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. No trapped steelhead was considered invalid for SY2011. There were fifty-nine trapped Chinook salmon that were considered invalid by these criteria – thirty-four were hatchery mini-jacks less than 30 cm (FL); fifteen were wild sort-by-code fish for the Lemhi River radio telemetry project (Bowersox and Biggs 2012); eight were wild and hatchery sort-by-code fish for the Lower Columbia River sonic tagging project (Rub et al. 2012); and two were missing data entry fields.

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 genetics 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 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 aging 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 aging 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 aging 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. (2012). 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).

Beginning in 2008 and continuing to present, 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. 2012). For steelhead in 2008 only, 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. 2013). For SY2011, 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 or classification 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 both likelihood and 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 SY2011 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. (2012) 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 also 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). Because the accuracy of assignments declines with decreased assignment probabilities, only individuals with ≥80% probability of assignment to a particular stock were considered assigned and 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 for SY2011 is evaluated fully in Ackerman et al. (2012) 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 to for BPA project 2010-026-00.

The accuracy of the sex-specific genetic assays is evaluated in Steele et al. (2012). Gender was not and generally cannot be reliably determined at the LGR adult trap; thus, a direct comparison was not attempted. Steele et al. (2012) found that the sex-specific genetic assay matched phenotypic sex in 94.4% and 100.0% of steelhead and Chinook salmon samples analyzed, respectively. 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/environment/fishdata.asp. Additional daily window and video operation information was obtained from COE annual fish passage reports (COE 2010, 2011).

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 2.5^{th} and 97.5^{th} 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,…, 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 2.5^{th} and 97.5^{th} 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 proportion 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) LSNAKE: 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. 2012); 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 and Age

After estimating the wild escapements by stock using MM, we used results from IA analyses to decompose the stock escapements by sex and age. As the accuracy of assignment declines with decreased assignment probabilities, only individuals that assigned with ≥80% probability to a particular genetic stock were used to calculate stock-by-sex-by-age proportions.

Calculated proportions from fish that assigned with ≥80% probability were then applied to the estimated stock escapements to obtain abundance for stock-by-sex-by-age.

RESULTS

Steelhead Escapement

For SY2011 – from July 1, 2010 to June 30, 2011 – a total of 208,296 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, 2010, and the last fish was counted on June 30, 2011. Of the total escapement, there were 4,482 fish or 2.2% of the run that passed during the August 14 to August 21, 2010 trap closure. Another 2,955 fish or 1.4% of the run passed during the November 19, 2010 to March 6, 2011 trap closure. The trap was operational during 96.4% of the run.

At the adult trap, a total of 22,716 wild and hatchery steelhead were captured and considered valid (Appendix Table C-1). Of these, 21,274 fish or 93.7% were trapped during fall 2010, and 1,442 fish or 6.3% were trapped during spring 2011. The adult trap sampled 10.9% of the window count overall (weekly range 2.9-13.9%).

Of the steelhead trapped, there were 1,073 large (≥78 cm, FL) wild fish; 3,599 large hatchery clipped fish; 462 large hatchery unclipped fish; 3,628 small (<78 cm, FL) wild fish; 12,079 small hatchery clipped fish; and 1,875 small hatchery unclipped fish (Appendix Table C-2). Combining large and small fish, a total of 7,038 unclipped and 15,678 clipped fish were trapped. These data are adjusted for 11 fish misidentified at the trap as small wild that were later reclassified to small hatchery unclipped as determined by PBT.

We estimate that 4.4% of the run was large wild; 15.0% was large hatchery clipped; 2.0% was large hatchery unclipped; 16.9% was small wild; 53.0% was small hatchery clipped; and 8.7% was small hatchery unclipped (Appendix Table C-3). Of all returning unclipped fish, we estimate 33.3% were of hatchery origin, which is a minimum estimate. Of all returning hatchery fish, we estimate 13.5% were unclipped, which is also a minimum estimate. We estimate that 20.6% of all large fish were wild compared to 21.5% of all small fish. Overall, 21.3% of the run was wild and 78.7% was of hatchery origin. However, the percentage of wild was not constant throughout the run and ranged from 15.6% in early March 2011 to 47.3% in May and June 2011.

Of the total steelhead escapement to LGR, we estimate that 9,195 fish (95% CI 8,648-9,764) were large wild; 31,245 fish (95% CI 30,335 -32,189) were large hatchery clipped; 4,100 fish (95% CI 3,734-4,479) were large hatchery unclipped; 35,209 fish (95% CI 34,091-36,318) were small wild; 110,481 fish (95% CI 109,057-111,951) were small hatchery clipped; and 18,066 fish (95% CI 17,208-18,942) were small hatchery unclipped (Figure 4; Appendix Table C-4). The large and small hatchery unclipped estimates are a minimum because not all of them have a hatchery mark or tag, i.e. a CWT, a ventral clip, dorsal or ventral fin erosion, or a PBT genetic mark. Overall, 44,404 wild (95% CI 43,164-45,642) and 163,892 hatchery (95% CI 162,683-165,116) steelhead returned to LGR after combining large, small, clipped, and unclipped fish (Figure 5). Our total estimate of 66,570 unclipped fish, wild and hatchery combined, is 106.0% of the COE reported window count of 62,773 unclipped fish.

Wild Steelhead Age, Sex, and Stock Composition

Of the 4,701 wild steelhead scale and genetics samples collected at the trap, we systematically subsampled 2,302 for aging and genotyping (Appendix Table C-5). The first sample was collected on July 6, 2010 and the last was collected on May 28, 2011. We were able to assign total age to 2,051 samples or 4.6% of the estimated run size (weekly range 3.2-5.5%). We were able to assign gender to 2,198 samples or 5.0% of the run size (weekly range 3.6-5.8%). We were able to obtain complete genotype data (≥90% of SNPs amplify successfully) for 2,267 samples or 5.1% of the run size (weekly range 3.7-6.0%).

We observed 16 different age classes from the 2,051 fish that we were able to assign a total age (Appendix Table C-6). Total age at spawning ranged from three to seven years, with freshwater age ranging from one to four years and saltwater age ranging from one to three years. We estimate that 25.9% of the wild return was from smolt migration year (MY) 2009; 72.5% from MY2008; 0.6% from MY2007; and 1.0% from repeat spawners (Appendix Table C-7). No more than one spawn check for each repeat spawner was observed. We estimate that 1.3% of the wild return was from brood year (BY) 2008; 23.1% from BY2007; 48.5% from BY2006; 25.4% from BY2005; and 1.9% from BY2004.

Estimated escapement to LGR by age class was 563 fish for age 1.1 (95% CI 225-1,285); 8,119 fish for age 2.1 (95% CI 4,575-14,312); 2,641 fish for age 3.1 (95% CI 1,355-4,995); 173 fish for age 4.1 (95% CI 40-491); 2,122 fish for age 1.2 (95% CI 1,063-4,067); 18,791 fish for age 2.2 (95% CI 10,997-31,872); 87 fish for age 2.1S (95% CI 13-286); 10,608 fish for age 3.2 (95% CI 6,043-18,406); 22 fish for age 3.1S (95% CI 0-106); 671 fish for age 4.2 (95% CI 279-1,455); 195 fish for age 2.3 (95% CI 53-549); 108 fish for age 2.1S1 (95% CI 14-349); 152 fish for age 2.2S (95% CI 27-429); 65 fish for age 3.3 (95% CI 0-243); 65 fish for age 3.1S1 (95% CI 0-241); and 22 fish for age 3.2S (95% CI 0-108; Figure 6). Estimated escapement to LGR by saltwater age was 11,496 one-saltwater fish (95% CI 9,821-13,359); 32,192 two-saltwater fish (95% CI 28,718-36,041); 260 three-saltwater fish (95% CI 120-446); and 456 fish that were repeat spawners (95% CI 256-712). Estimated escapement to LGR by total age at spawning was 563 fish from BY2008 (95% CI 343-842); 10,241 fish from BY2007 (95% CI 8,810-11,844); 21,519 fish from BY2006 (95% CI 19,100-24,181); 11,258 fish from BY2005 (95% CI 9,720-12,947); and 823 fish from BY2004 (95% CI 542-1,168; Figure 7).

Of the 2,198 fish for which gender was successfully determined using the sex-specific assay, 1,466 were female and 732 were male (Appendix Table C-8). The gender percentages for the entire run were 66.7% female and 33.3% male (Appendix Table C-9). The sex ratio was female-biased throughout the run and ranged from 58.9 to 75.2%. Expanding the overall percentages to the wild run gives 29,616 females (95% CI 28,002-31,284) and 14,788 males (95% CI 13,634-15,976; Figure 8). We estimate that 17.8% of the females and 42.8% of the males were one-saltwater, and that 1.4% of the females and none of the males were repeat spawners.

Based on MM results using the 2,267 fish with complete genotypes, we estimate that 15.1% of the wild return originated from UPSALM; 8.9% from MFSALM; 5.3% from SFSALM; 3.5% from LOSALM; 9.4% from UPCLWR; 9.9% from SFCLWR; 4.1% from the LOCLWR; 5.6% from IMNAHA; 16.2% from GRROND; and 22.0% from LSNAKE. Aggregating by MPGs, 32.8% of the wild return originated from the Salmon River; 23.3% from the Clearwater River; 5.6% from the Imnaha River; 16.2% from the Grande Ronde River; and 22.0% from the Lower Snake River.

Based on MM results, estimated escapement to LGR by genetic stock was 6,717 fish for UPSALM (95% CI 5,367-8,502); 3,934 fish for MFSALM (95% CI 3,063-4,969); 2,357 fish for SFSALM (95% CI 1,759-3,116); 1,573 fish for LOSALM (95% CI 776-2,234); 4,179 fish for UPCLWR (95% CI 3,311-5,312); 4,377 fish for SFCLWR (95% CI 3,412-5,457); 1,809 fish for LOCLWR (95% CI 1,086-2,532); 2,496 fish for IMNAHA (95% CI 1,655-3,339); 7,212 fish for GRROND (95% CI 5,706-9,059); and 9,750 fish for LSNAKE (95% CI 8,014-12,308; Figure 9). Estimated escapement was 14,581 fish for the Salmon River MPG (95% CI 12,721-16,529) which combines UPSALM, MFSALM, SFSALM, and LOSALM. Estimated escapement was 10,365 fish for the Clearwater River MPG (95% CI 8,924-11,752) which combines UPCLWR, SFCLWR, and LOCLWR.

Of the 2,267 fish with complete genotypes, 1,150 fish or 50.7% assigned to a stock with ≥80% probability (Ackerman et al. 2012). Of the 1,150 assigned fish, 974 fish had both a determined sex and a total age and 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 SY2011 stock escapement estimates (Appendix Table C-12).

Chinook Salmon Escapement

For SY2011 – from March 1 to August 17, 2011 – a total of 134,594 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 3 and the last fish was counted on August 17. The trap was operational during the entire run.

At the adult trap, a total of 14,068 wild and hatchery Chinook salmon were captured and considered valid (Appendix Table D-1). The adult trap sampled 10.5% of the window count overall (weekly range 7.4-11.2%).

Of the Chinook salmon trapped, there were 2,795 wild fish, 10,705 hatchery clipped fish, and 568 hatchery unclipped fish (Appendix Table D-2). A total of 3,363 unclipped and 10,705 clipped fish were trapped. These data are adjusted for 46 fish misidentified at the trap as wild that were later reclassified to hatchery unclipped as determined by PBT.

We estimate that 19.8% of the run was wild, 76.2% was hatchery clipped, and 4.0% was hatchery unclipped (Appendix Table D-3). Of all returning unclipped fish, we estimate 17.0% were of hatchery origin, which is a minimum estimate. Of all returning hatchery fish, we estimate 5.0% were unclipped, which is also a minimum estimate. Overall, 19.8% of the run was wild and 80.2% was of hatchery origin. However, the percentage of wild was not constant throughout the run and ranged from 10.6% in late May to 54.9% in mid-August 2011.

Of the total Chinook salmon escapement to LGR, we estimate that 26,608 fish (95% CI 25,739-27,465) were wild; 102,538 fish (95% CI 101,568-103,458) were hatchery clipped; and 5,448 fish (95% CI 5,021-5,911) were hatchery unclipped (Figure 11; Appendix Table D-4). The hatchery unclipped estimate is a minimum because not all of them have a hatchery mark or tag, i.e. a CWT, a ventral clip, or a PBT genetic mark. Overall, 26,608 wild (95% CI 25,739-27,465) and 107,986 hatchery (95% CI 107,094-108,841) Chinook salmon returned to LGR after combining clipped and unclipped fish (Figure 12). Our total estimate of 32,056 unclipped fish, wild and hatchery combined, is 94.9% of the COE unreported window count of 33,765 unclipped fish (John Dalen, COE, personal communication).

Wild Chinook Salmon Age, Sex, and Stock Composition

Of the 2,795 wild Chinook salmon scale and genetics samples collected at the trap, we systematically subsampled 2,104 for aging and genotyping (Appendix Table D-5). The first sample was collected on April 27 and the last was collected on August 17. We were able to assign total age to 1,999 samples or 7.5% of the estimated run size (weekly range 6.7-8.1%). We were able to assign gender to 2,023 samples or 7.6% of the run size (weekly range 6.8-8.1%). We were able to obtain complete genotype data (≥90% of SNPs amplify successfully) for 2,099 samples or 7.9% of the run size (weekly range 7.0-8.5%).

We observed nine different age classes from the 1,999 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 three years. We estimate that 0.7% of the wild return was from MY2011; 15.3% from MY2010; 55.5% from MY2009; and 28.5% from MY2008 (Appendix Table D-7). We estimate that 0.6% of the wild return was from BY2009; 15.0% from BY2008; 54.7% from BY2007; 29.2% from BY2006; and 0.5% from BY2005.

Estimated escapement to LGR by age class was 160 fish for age 1.0 (95% CI 60-333); 27 fish for age 2.0 (95% CI 0-88); 3,953 fish for age 1.1 (95% CI 2,694-5,743); 106 fish for age 2.1 (95% CI 31-243); 14,442 fish for age 1.2 (95% CI 10,435-19,871); 333 fish for age 2.2 (95% CI 162-615); 13 fish for age 0.3 (95% CI 0-54); 7,441 fish for age 1.3 (95% CI 5,236-10,533); and 133 fish for age 2.3 (95% CI 41-293; Figure 13). Estimated escapement to LGR by saltwater age was 187 zero-saltwater fish (mini-jacks ≥30 cm, FL; 95% CI 91-305); 4,059 one-saltwater fish (jacks; 95% CI 3,479-4,689); 14,775 two-saltwater fish (95% CI 13,489-16,134); and 7,587 three-saltwater fish (95% CI 6,744-8,512). Estimated escapement to LGR by total age at spawning was 160 fish from BY2009 (95% CI 73-280); 3,980 fish from BY2008 (95% CI 3,258-4,810); 14,561 fish from BY2007 (95% CI 12,706-16,656); 7,774 fish from BY2006 (95% CI 6,606-9,101); and 133 fish from BY2005 (95% CI 50-238; Figure 14).

Of the 2,023 fish for which gender was successfully determined using the sex-specific assay, 696 were female and 1,327 were male (Appendix Table D-8). The gender percentages for the entire run were 34.4% female and 65.6% male (Appendix Table D-9). The sex ratio was male-biased throughout the run and ranged from 57.4 to 76.9% males. Expanding the overall percentages to the wild run gives 9,154 females (95% CI 8,419-9,936) and 17,454 males (95% CI 16,431-18,552; Figure 15). We estimate that 0.7% of the females were one-saltwater jills, 22.5% of the males were one-saltwater jacks, and 1.1% of the males were zero-saltwater mini-jacks ≥30 cm (FL).

Based on MM results using the 2,099 fish with complete genotypes, we estimate that 15.9% of the wild return originated from UPSALM; 14.8% from MFSALM; 2.1% from CHMBLN; 20.6% from SFSALM; 41.5% from HELLSC; and 0.9% from TUCANO. The remaining 4.2% of the wild return was identified as fall Chinook salmon based on multi-locus genotype data. Aggregating by MPG, 16.9% 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 4,236 fish for UPSALM (95% CI 3,371-5,098); 3,929 fish for MFSALM (95% CI 3,188-4,799); 551 fish for CHMBLN (95% CI 364-794); 5,479 fish for SFSALM (95% CI 4,533-6,658); 11,050 fish for HELLSC (95% CI 9,560-12,804); and 238 fish for TUCANO (95% CI 125-397; Figure 16). Estimated escapement was 4,480 fish for the Middle Fork Salmon River MPG (95% CI 3,741-

5,320) which combines MFSALM and CHMBLN. In addition, an estimated 1,125 fish of the wild return were identified as fall Chinook salmon based on multi-locus SNP data (95% CI 1,004-1,257).

Of the 2,099 fish with complete genotypes, 1,496 fish or 71.3% assigned to a stock with ≥80% probability (Ackerman et al. 2012). Of the 1,496 assigned fish, 1,368 fish had both a determined sex and a total age and 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 SY2011 stock escapement estimates (Appendix Table D-12).

Age Validation

Readers accurately determined the ocean-age of 98.9% of the scale samples (n = 91) from known ocean-age PIT-tagged wild steelhead. The known ocean-age sample was 35.2% one-saltwater, 63.7% two-saltwater fish, and 1.1% 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 11.9% for freshwater age and 4.4% for saltwater age.

Readers accurately determined the ocean-age of 98.1% of the scale samples (n = 154) from known ocean-age PIT-tagged wild and hatchery Chinook salmon. The known ocean-age sample was 23.4% one-saltwater, 59.7% two-saltwater, and 16.9% 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 3.3% for freshwater age and 3.4% for saltwater age.

DISCUSSION

This report continues the wild Snake River steelhead and Chinook salmon comprehensive stock assessments, exclusive of some Tucannon River fish, begun 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, aging, 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 added one new refinement to our stock assessments in SY2011 (this report). For both species we used parentage based tagging (PBT) to better separate wild fish from unclipped hatchery fish. Through PBT we were able to identify age-3 unclipped hatchery fish that returned from migration year 2010 smolt releases – releases which were BY2008 progeny of hatchery broodstock added to the PBT baseline in SY2008 (Steele et al. 2012, 2013). Although none were detected, we were also able to identify Chinook salmon age-2 unclipped hatchery mini-jacks (≥30 cm, FL) that returned from migration year 2011 smolt releases and were BY2009. Because hatchery cohort parents prior to BY2008 are not in the baseline, and because all phenotypically wild fish captured at the adult trap in SY2011 were not necessarily genotyped, there is only a “slight” correction to the SY2011 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 "partial" correction will be possible in SY2012 by identification of age-3 and age-4 unclipped hatchery fish (from BY2009 and BY2008), and 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; Beasley and White 2010; QCI 2011, 2012). 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 3). 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 through the navigation lock or at night 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 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) or a Bayesian modeling approach (Beasley and White 2010; QCI 2011, 2012).

Cassinelli et al. (2012) 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 showed that the overestimation caused by fallback and reascension is greater than the underestimation caused by after-hours passage. The net difference between the two would have resulted in the adult count at the window being 7,952 fish or 8.3% high and the jack count being 4,157 fish or 10.8% high in 2011. Similar but smaller net differences were reported for the 2010 return (Cassinelli and Rosenberger 2011), possibly due to less spill in 2010. 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) concluded that because PIT tags cannot be used for this direct assessment of fallback and non-reascension, their net differences of approximately 3-10% overestimation is likely a minimum estimate for both 2010 and 2011. Boggs et al. (2004), Cassinelli and Rosenberger (2011), or Cassinelli et al. (2012) 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) 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 SY2011, our unadjusted LGR wild steelhead escapement estimate of 44,404 fish (95% CI 43,164-45,642; Figure 5) is significantly less than the estimate of 48,639 fish (95% CI 47,409-49,690) reported by the ISEMP project (QCI 2012). Our unadjusted wild Chinook salmon escapement estimate of 26,608 fish (95% CI 25,739-27,465; Figure 12) is less than but not significantly different from their estimate of 26,972 fish (95% CI 25,889-28,173).

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 SY2011, these included Lemhi River spring-summer Chinook salmon PIT tagged as juveniles (Bowersox and Biggs 2012); lower Columbia River spring-summer Chinook salmon sonic-tagged as adults (Rub et al. 2012); and Snake River fall Chinook salmon that were PIT tagged as juveniles (Doug 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 2012) 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 used our method of 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 (Table 3).

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 closure 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 26,608 wild Chinook salmon returning to LGR between March 1 and August 17, 2011, we estimate that 1,125 fish or 4.2% of the escapement during this period were actually fall Chinook salmon as determined by genetics, with the remaining 25,483 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. 2012). 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). This is the second year which we estimate repeat spawning steelhead as well as mini-jack Chinook salmon. Laboratory personnel continue to improve their aging 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 SY2012 we will 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). 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 using the two methods, we note that our genetic stock estimate for South Fork Salmon River steelhead in SY2011 was 2,357 fish at LGR (95% CI 1,759-3,116; Figure 9) which is less than but not statistically different from the ISEMP PIT-array escapement estimate of 2,540 fish (95% CI 2,447-2,633; QCI 2012). For South Fork Salmon River Chinook salmon, our genetic stock estimate of 5,479 fish at LGR (95% CI 4,533-6,658; Figure 16) is significantly greater than the ISEMP PIT-array escapement estimate of 3,318 fish (95% CI 2,895-3,741; QCI 2012). 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. 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. Lookinglass Creek (extirpated) [a]
South Fork Salmon River	11. Little Salmon River 12. South Fork Salmon River 13. Secesh River 14. East Fork South Fork Salmon River
Middle Fork Salmon River	15. Chamberlain Creek 16. Lower Middle Fork Salmon River 17. Big Creek 18. Camas Creek 19. Loon Creek 20. Upper Middle Fork Salmon River 21. Sulphur Creek 22. Bear Valley Creek 23. Marsh Creek
Upper Salmon River	24. North Fork Salmon River 25. Lemhi River 26. Upper Salmon River Lower Mainstem 27. Pahsimeroi River 28. East Fork Salmon River 29. Yankee Fork Salmon River 30. Valley Creek 31. Upper Salmon River Upper Mainstem 32. Panther Creek (extirpated) [a]
Dry Clearwater River (extirpated) [a]	33. Potlatch River (extirpated) [a] 34. Lapwai Creek (extirpated) [a] 35. Lawyer Creek (extirpated) [a] 36. Upper South Fork Clearwater River (extirpated) [a]
Wet Clearwater River (extirpated) [a]	37. Lower North Fork Clearwater River (extirpated) 38. Upper North Fork Clearwater River (extirpated) 39. Lolo Creek (extirpated) [a] 40. Lochsa River (extirpated) [a] 41. Meadow Creek (extirpated) [a] 42. Moose Creek (extirpated) [a] 43. Upper Selway River (extirpated) [a]

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

Table 2. Status of the fish ladder, the fish counting window and video, and the adult trap sample rate at Lower Granite Dam, 7/1/2010 to 8/17/2011 (COE 2010, 2011; Ogden 2011, 2012).

<table>
<tr><th>Sampling period 2010-11</th><th>Statistical week</th><th>Ladder open?</th><th>Window count?</th><th>Video count?</th><th>Adult trap sample rate</th></tr>
<tr><td>7/1-7/4</td><td>27</td><td rowspan="27">Yes, Start 7/1/10, End 1/3/11</td><td rowspan="18">Yes, 0400-2000, Start 7/1/10, End 10/31/10</td><td rowspan="13">Yes, 0200-0400, Start 7/1/10, End 9/30/10 (sockeye and lamprey only)</td><td rowspan="6">0.04 Rate, Start 7/1/10, End 8/13/10</td></tr>
<tr><td>7/5-7/11</td><td>28</td></tr>
<tr><td>7/12-7/18</td><td>29</td></tr>
<tr><td>7/19-7/25</td><td>30</td></tr>
<tr><td>7/26-8/1</td><td>31</td></tr>
<tr><td>8/2-8/8</td><td>32</td></tr>
<tr><td>8/9-8/15</td><td>33</td><td rowspan="2">Trap Closed, Start 8/14/10, End 8/21/10</td></tr>
<tr><td>8/16-8/22</td><td>34</td></tr>
<tr><td>8/23-8/29</td><td>35</td><td rowspan="4">0.12 Rate, Start 8/22/10, End 9/18/10</td></tr>
<tr><td>8/30-9/5</td><td>36</td></tr>
<tr><td>9/6-9/12</td><td>37</td></tr>
<tr><td>9/13-9/19</td><td>38</td></tr>
<tr><td>9/20-9/26</td><td>39</td><td rowspan="8">0.10 Rate, Start 9/19/10, End 11/18/10</td></tr>
<tr><td>9/27-10/3</td><td>40</td><td rowspan="5">No, Start 10/1/10, End 10/31/10</td></tr>
<tr><td>10/4-10/10</td><td>41</td></tr>
<tr><td>10/11-10/17</td><td>42</td></tr>
<tr><td>10/18-10/24</td><td>43</td></tr>
<tr><td>10/25-10/31</td><td>44</td></tr>
<tr><td>11/1-11/7</td><td>45</td><td rowspan="21">No, Start 11/1/10, End 3/31/11</td><td rowspan="8">Yes, 0600-1600, Start 11/1/10, End 12/31/10</td></tr>
<tr><td>11/8-11/14</td><td>46</td></tr>
<tr><td>11/15-11/21</td><td>47</td><td rowspan="16">Trap Closed, Start 11/19/10, End 3/6/11</td></tr>
<tr><td>11/22-11/28</td><td>48</td></tr>
<tr><td>11/29-12/5</td><td>49</td></tr>
<tr><td>12/6-12/12</td><td>50</td></tr>
<tr><td>12/13-12/19</td><td>51</td></tr>
<tr><td>12/20-12/26</td><td>52</td></tr>
<tr><td>12/27-1/2</td><td>53-1</td><td rowspan="9">No, Start 1/1/11, End 2/28/11</td></tr>
<tr><td>1/3-1/9</td><td>2</td><td rowspan="4">No, Start 1/4/11, End 2/2/11</td></tr>
<tr><td>1/10-1/16</td><td>3</td></tr>
<tr><td>1/17-1/23</td><td>4</td></tr>
<tr><td>1/24-1/30</td><td>5</td></tr>
<tr><td>1/31-2/6</td><td>6</td><td rowspan="29">Yes, Start 2/3/11, End 8/17/11</td></tr>
<tr><td>2/7-2/13</td><td>7</td></tr>
<tr><td>2/14-2/20</td><td>8</td></tr>
<tr><td>2/21-2/27</td><td>9</td></tr>
<tr><td>2/28-3/6</td><td>10</td><td rowspan="4">Yes, 0600-1600, Start 3/1/11, End 3/31/11</td></tr>
<tr><td>3/7-3/13</td><td>11</td><td rowspan="24">0.10 Rate, Start 3/7/11, End 8/17/11</td></tr>
<tr><td>3/14-3/20</td><td>12</td></tr>
<tr><td>3/21-3/27</td><td>13</td></tr>
<tr><td>3/28-4/3</td><td>14</td><td rowspan="21">Yes, 0400-2000, Start 4/1/11, End 8/17/11</td><td rowspan="11">No, Start 4/1/11, End 6/14/11</td></tr>
<tr><td>4/4-4/10</td><td>15</td></tr>
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<tr><td>6/6-6/12</td><td>24</td></tr>
<tr><td>6/13-6/19</td><td>25</td><td rowspan="10">Yes, 0200-0400, Start 6/15/11, End 8/17/11 (sockeye and lamprey only)</td></tr>
<tr><td>6/20-6/26</td><td>26</td></tr>
<tr><td>6/27-7/3</td><td>27</td></tr>
<tr><td>7/4-7/10</td><td>28</td></tr>
<tr><td>7/11-7/17</td><td>29</td></tr>
<tr><td>7/18-7/24</td><td>30</td></tr>
<tr><td>7/25-7/31</td><td>31</td></tr>
<tr><td>8/1-8/7</td><td>32</td></tr>
<tr><td>8/8-8/14</td><td>33</td></tr>
<tr><td>8/15-8/17</td><td>34</td></tr>
</table>

Table 3. Estimated annual total escapement, by fish size and origin, of steelhead at Lower Granite Dam (LGR), spawn years 1976-2011. 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 adjusted by NMFS adult trapping data (Alan Byrne, IDFG, personal communication; Schrader et al. 2011, 2012; present study). Estimates for 1986 and earlier are the COE window counts adjusted by an unknown method.

		Estimated number of steelhead at LGR that were:							
Spawn year	LGR window count(a)	Large wild	Large hatchery clipped	Large hatchery unclipped	Small wild	Small hatchery clipped	Small hatchery unclipped	Total hatchery	Total wild
1976	16,608	N/A(b)	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	13,538	8,963
1978	56,979	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	13,293	13,187
1980	28,778	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	16,208	21,850
1982	42,388	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	47,115	25,210
1984	89,296	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	80,107	24,554
1986	116,063	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

(a) Downloaded from COE link 5/17/13.
(b) N/A = trap data not available.

FIGURES

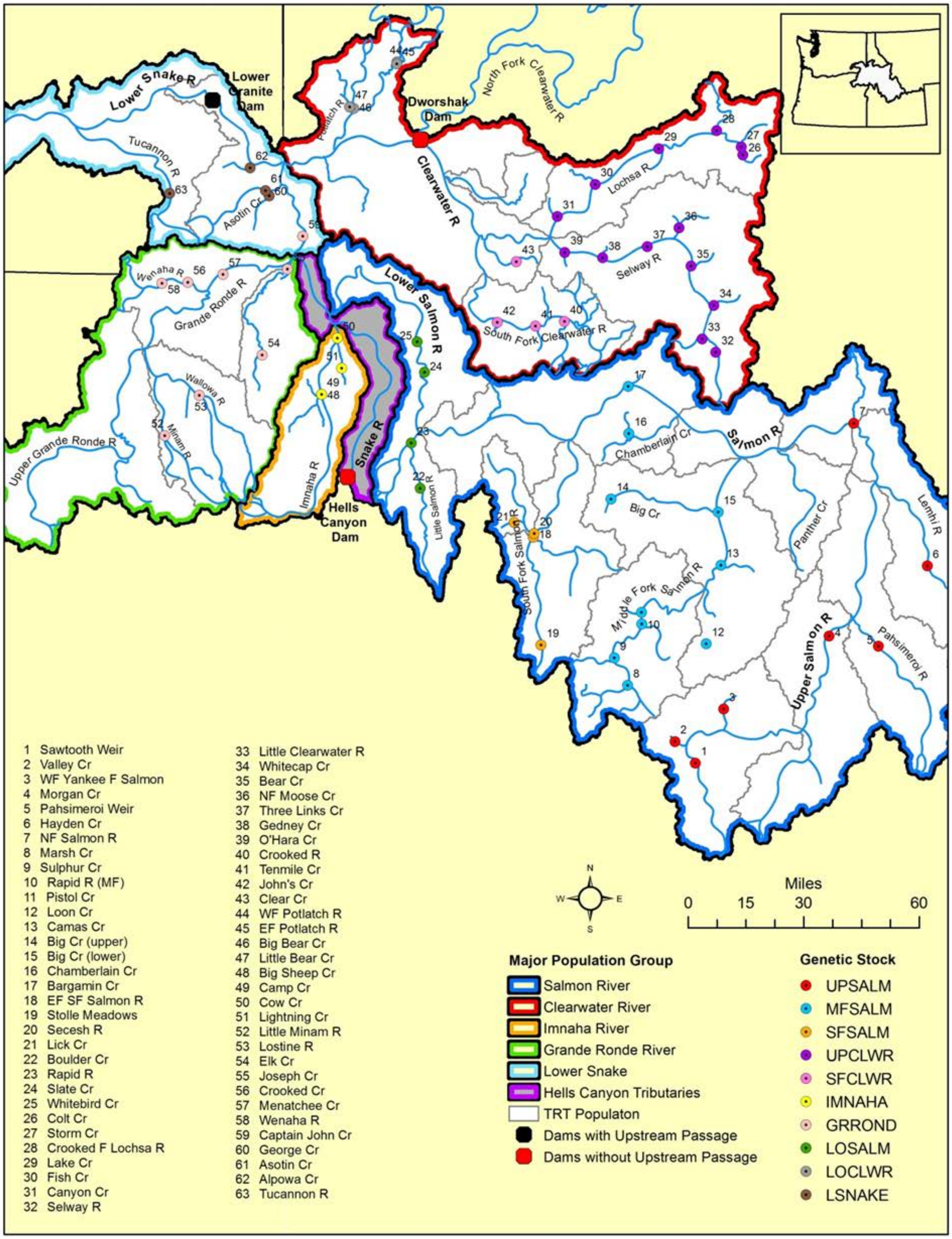


Figure 1. Genetic stocks and baseline collections used for steelhead mixed stock analysis at Lower Granite Dam, spawn year 2011 (Ackerman et al. 2012). The Hells Canyon Tributaries MPG (shaded gray) does not support independent populations and is considered extirpated (NMFS 2011).

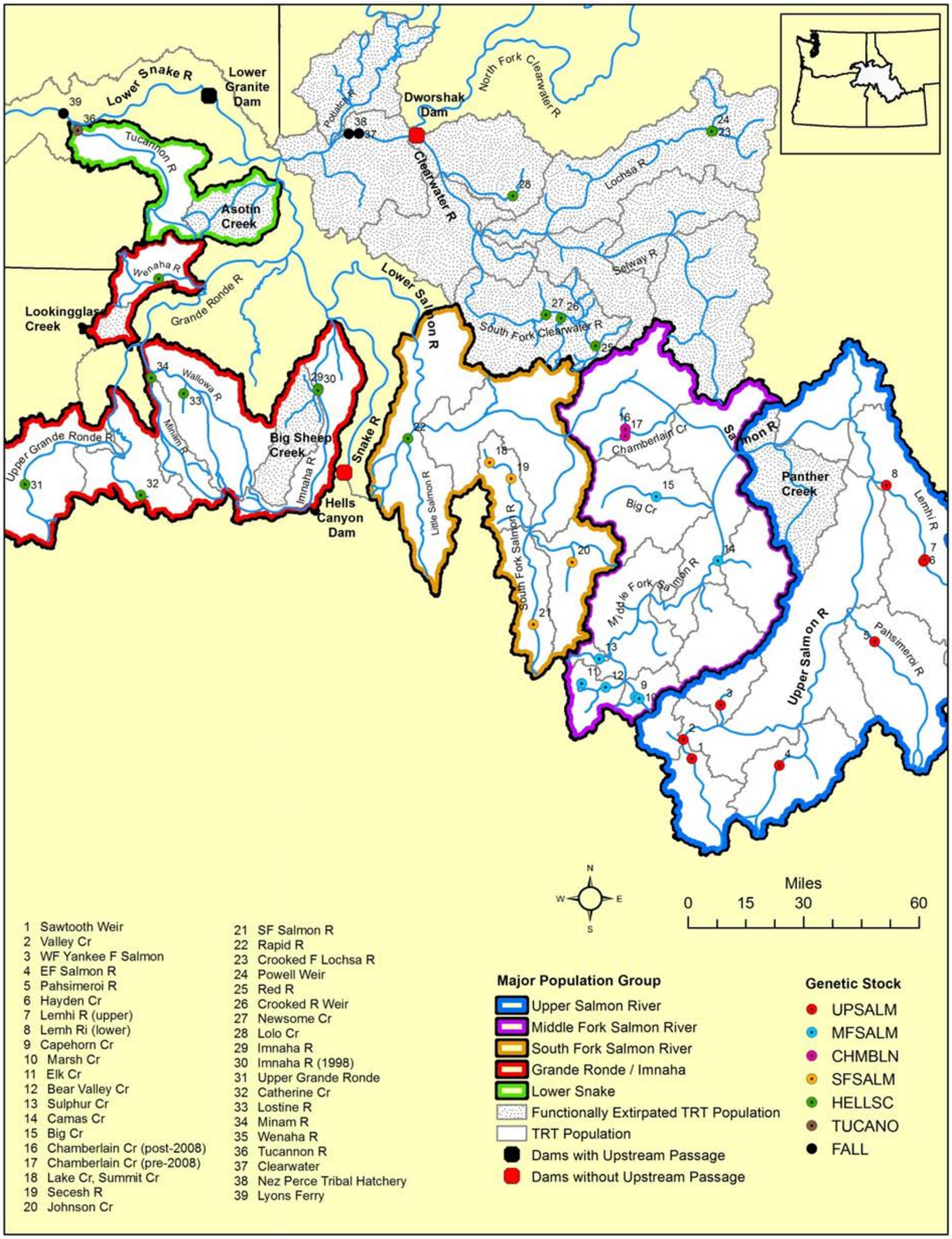


Figure 2. Genetic stocks and baseline collections used for Chinook salmon mixed stock analysis at Lower Granite Dam, spawn year 2011 (Ackerman et al. 2012). Reintroduced fish exist in functionally extirpated TRT populations as mapped.

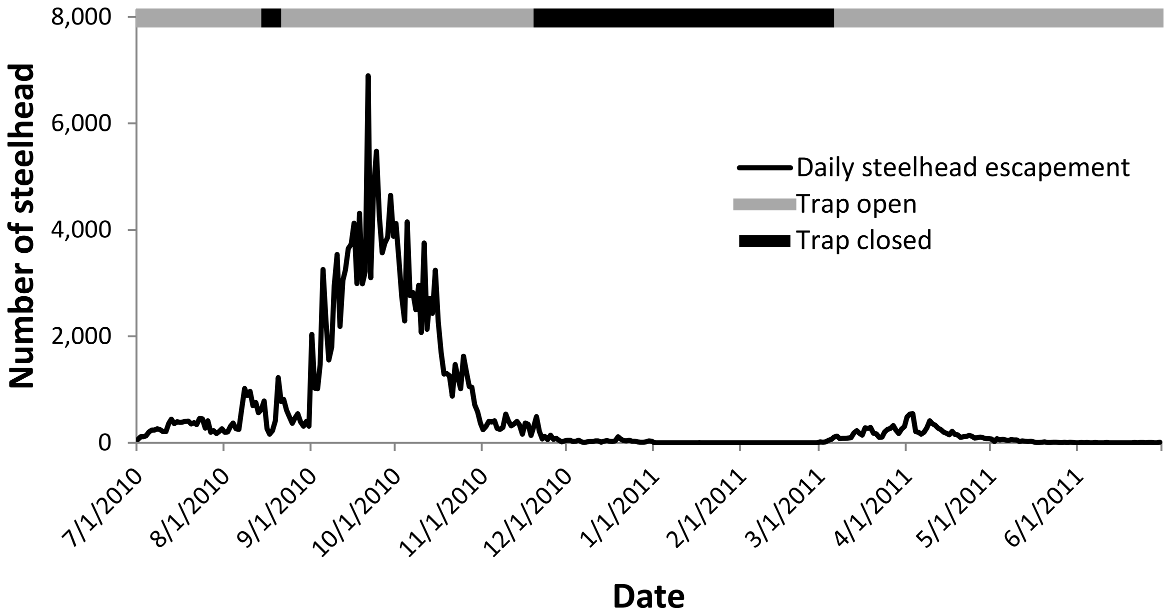


Figure 3. Daily number of steelhead counted at the Lower Granite Dam window or by video, spawn year 2011. Horizontal bar indicates when the adult trap was open or closed; overall, it was open during 96.4% of the total run (n = 208,296).

Figure 4. Estimated escapement, by fish size and origin, of steelhead at Lower Granite Dam, spawn year 2011. 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%.

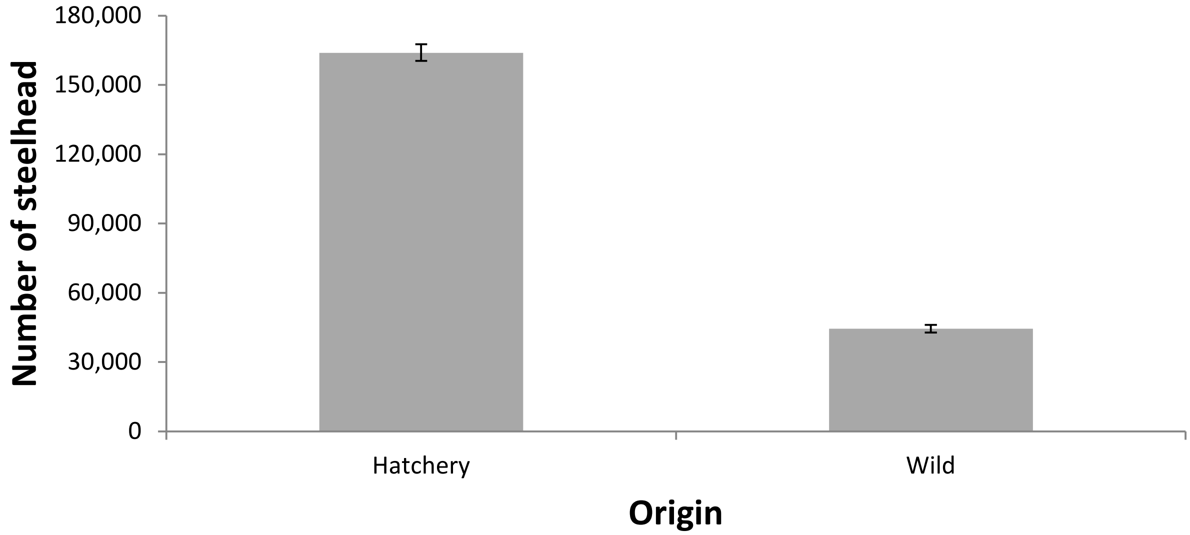


Figure 5. Estimated hatchery and wild steelhead escapement at Lower Granite Dam, spawn year 2011. Confidence intervals are at 95%.

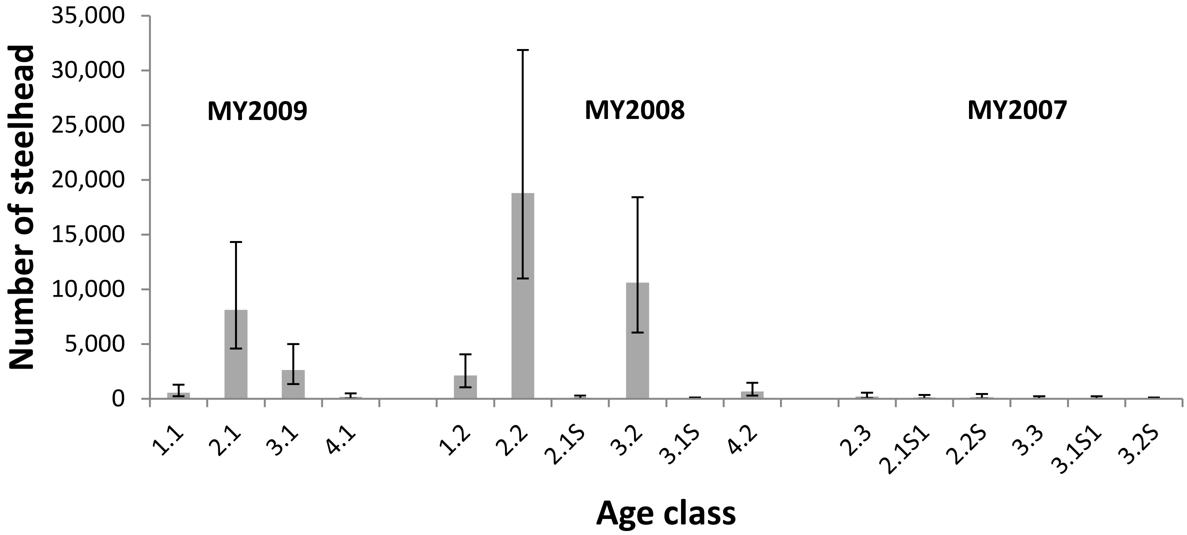


Figure 6. Estimated escapement by age class, grouped by smolt migration year (MY), of wild adult steelhead at Lower Granite Dam, spawn year 2011. Large and small fish were combined. Confidence intervals are at 95%.

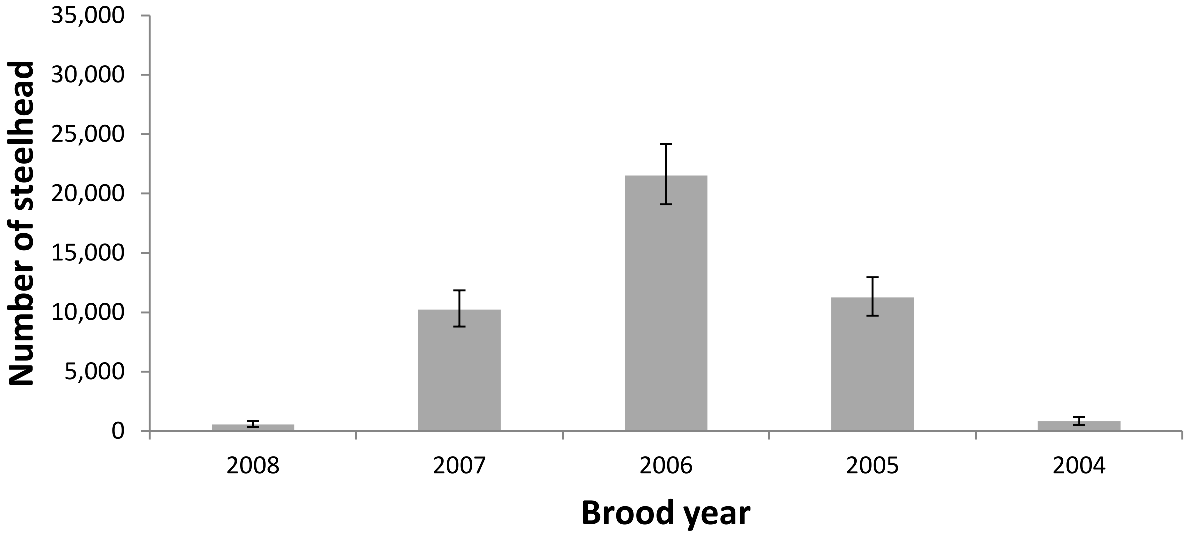


Figure 7. Estimated escapement by brood year of wild adult steelhead at Lower Granite Dam, spawn year 2011. Large and small fish were combined. Confidence intervals are at 95%.

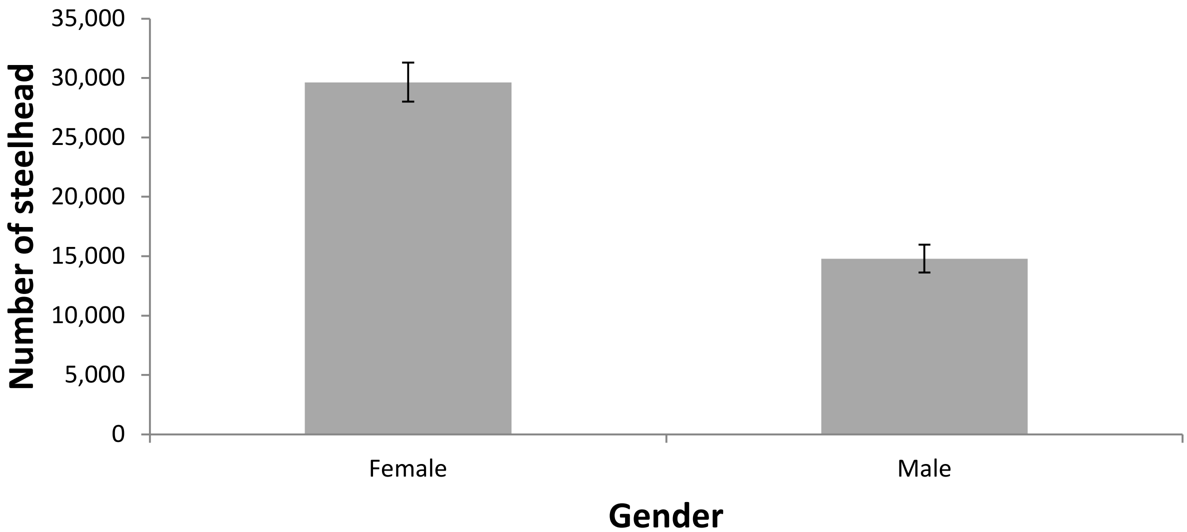


Figure 8. Estimated escapement by gender of wild adult steelhead at Lower Granite Dam, spawn year 2011. Large and small fish were combined. Confidence intervals are at 95%.

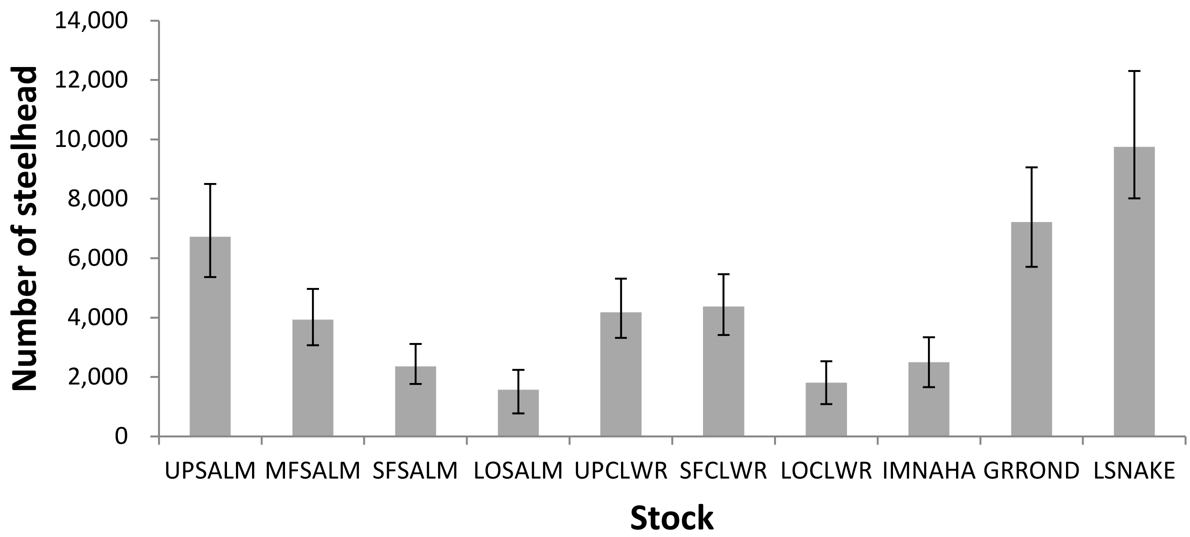


Figure 9. Estimated escapement by genetic stock of wild adult steelhead at Lower Granite Dam, spawn year 2011. Large and small fish were combined. Confidence intervals are at 95%. See Appendix Table B-1 for stock abbreviations.

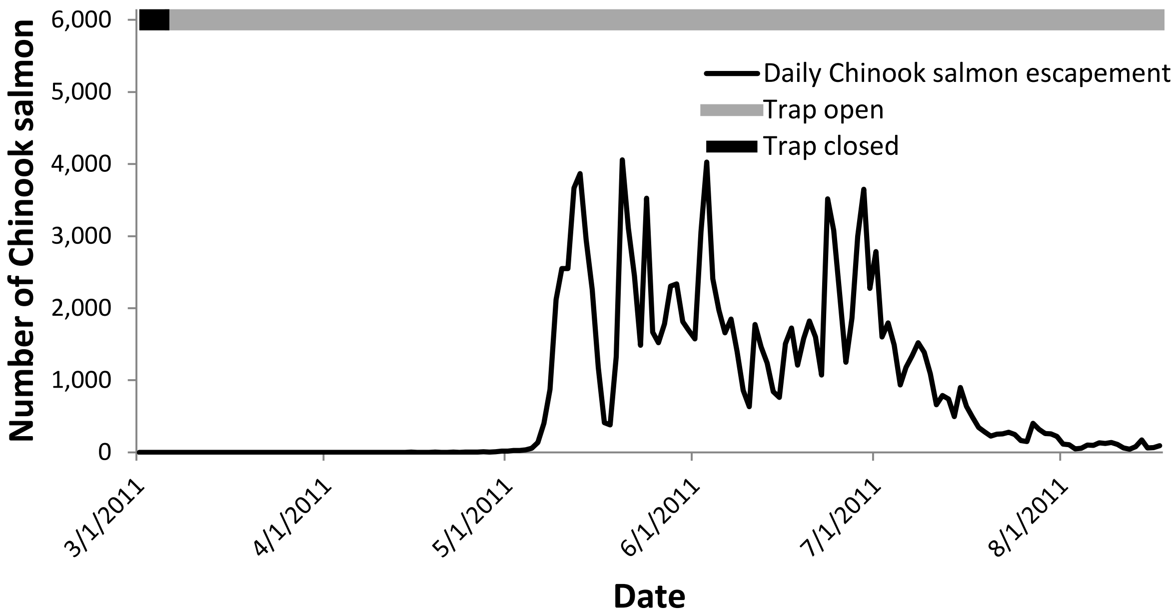


Figure 10. Daily number of Chinook salmon counted at the Lower Granite Dam window or by video, spawn year 2011. Horizontal bar indicates when the adult trap was open or closed; overall, it was open during 100.0% of the total run (n = 134,594).

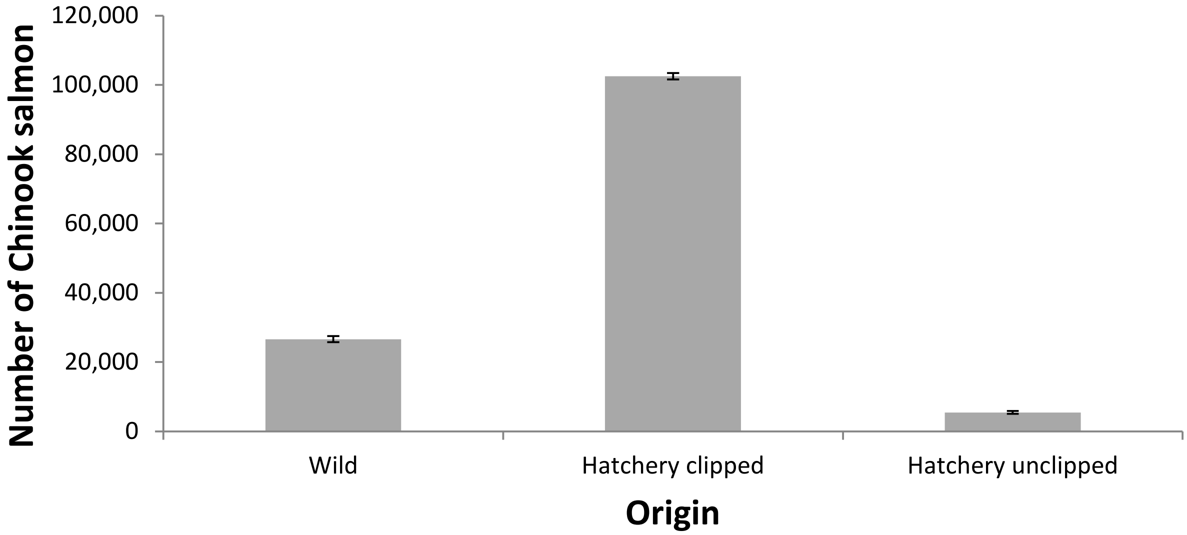


Figure 11. Estimated escapement by origin of Chinook salmon at Lower Granite Dam, spawn year 2011. Clipped and unclipped refer to the adipose fin. Confidence intervals are at 95%.

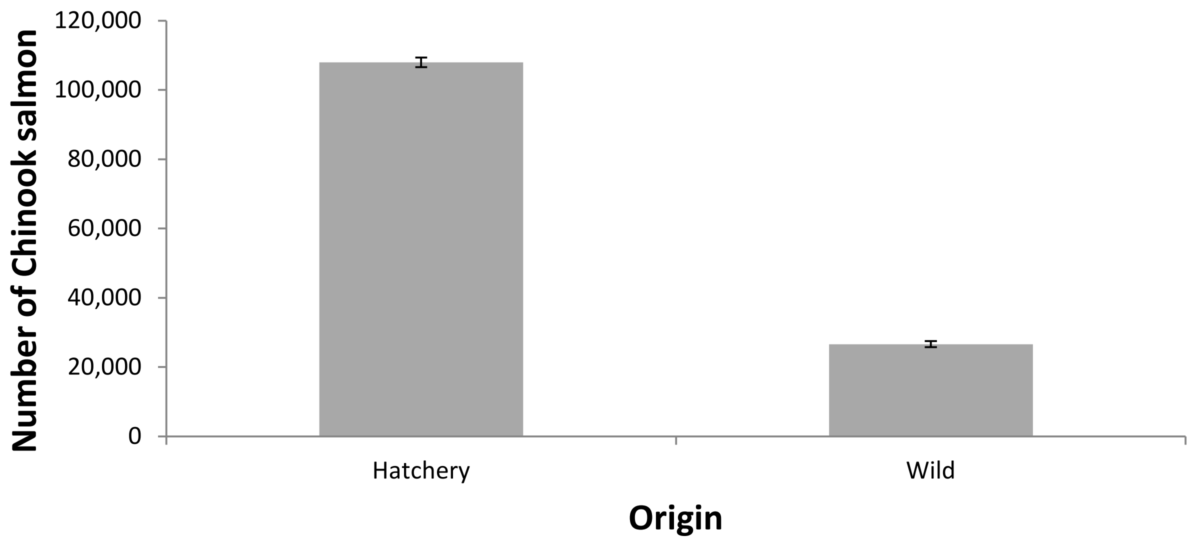


Figure 12. Estimated hatchery and wild Chinook salmon escapement at Lower Granite Dam, spawn year 2011. Confidence intervals are at 95%.

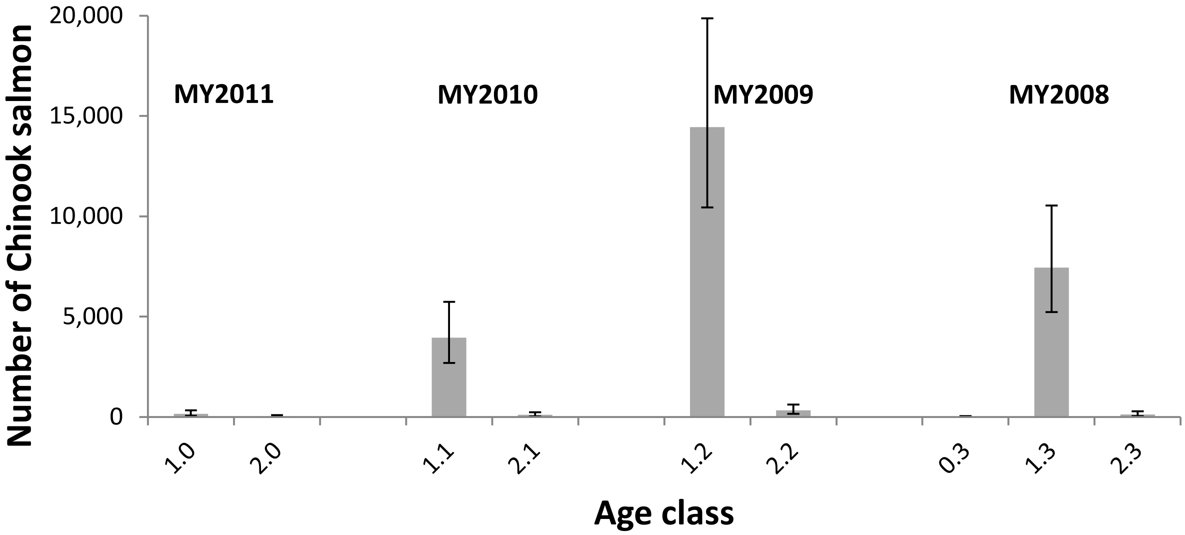


Figure 13. Estimated escapement by age class, grouped by smolt migration year (MY), of wild adult Chinook salmon at Lower Granite Dam, spawn year 2011. Confidence intervals are at 95%.

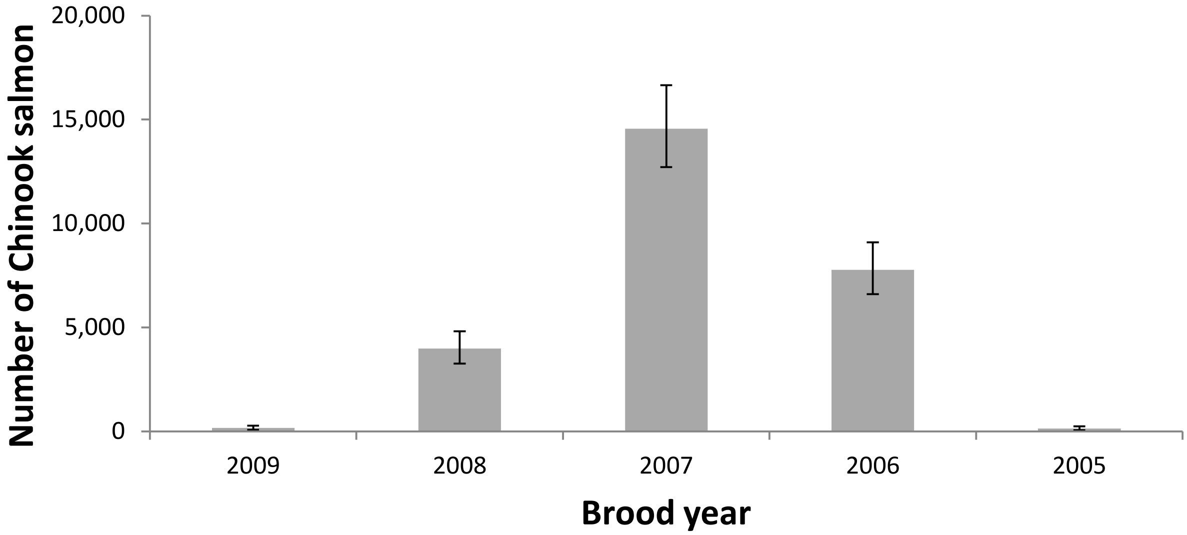


Figure 14. Estimated escapement by brood year of wild adult Chinook salmon at Lower Granite Dam, spawn year 2011. Confidence intervals are at 95%.

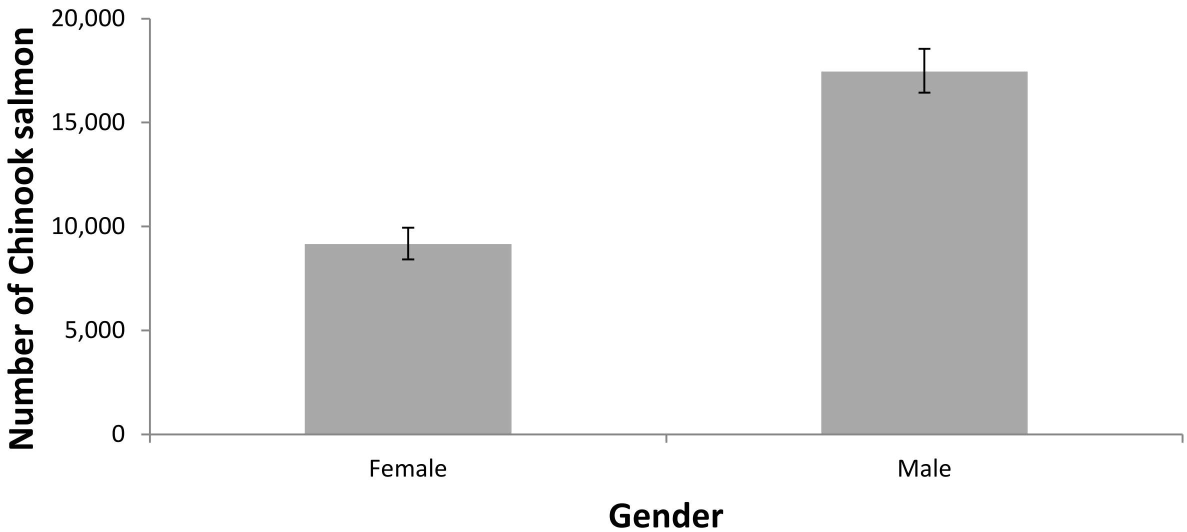


Figure 15. Estimated escapement by gender of wild adult Chinook salmon at Lower Granite Dam, spawn year 2011. Confidence intervals are at 95%.

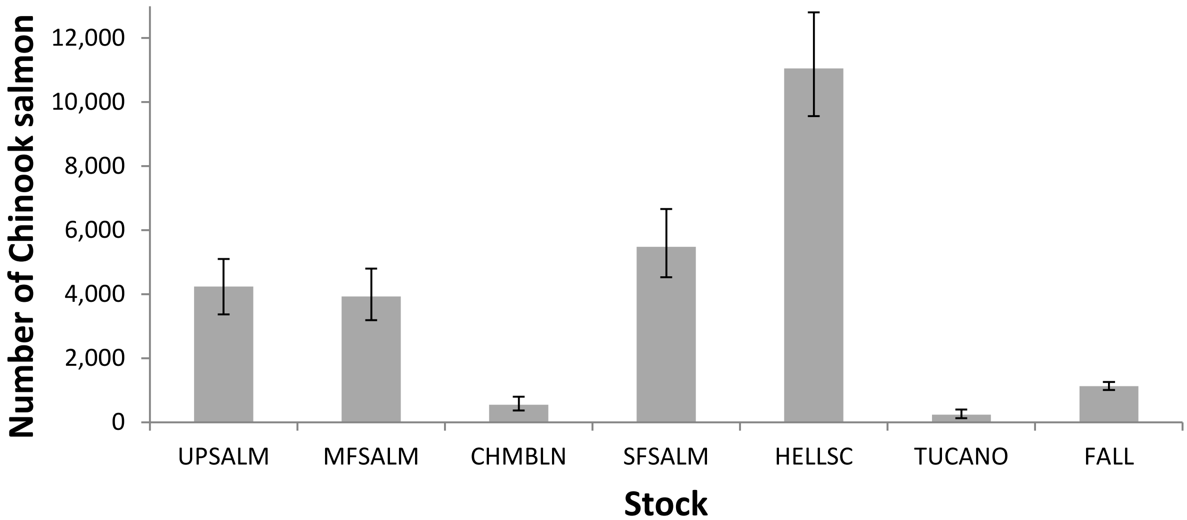


Figure 16. Estimated escapement by genetic stock of wild adult Chinook salmon at Lower Granite Dam, spawn year 2011. Confidence intervals are at 95%. See Appendix Table B-2 for stock abbreviations.

APPENDICES

Appendix A. Lower Granite Dam trap sampling protocols, SY2011.

Field Sampling Protocol for Steelhead and Spring/Summer Chinook Salmon at the Lower Granite Dam Adult Trap, August 18 to December 31, 2010

By:
IDFG, QCI, PSMFC, NOAAF

Specific Data Requirements for 2010 Season

This protocol outlines specific Lower Granite Dam (LGR) adult trap sampling and 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 and a sub-sample of hatchery origin fish to estimate age composition, length at age, etc;
4) Tissue collections from all natural origin fish and all 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 to estimate tributary specific escapement.

Once adult fish are trapped, all information from sampled fish will be recorded on the Field Data Entry Form, 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 and steelhead 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 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 unclipped hatchery steelhead.

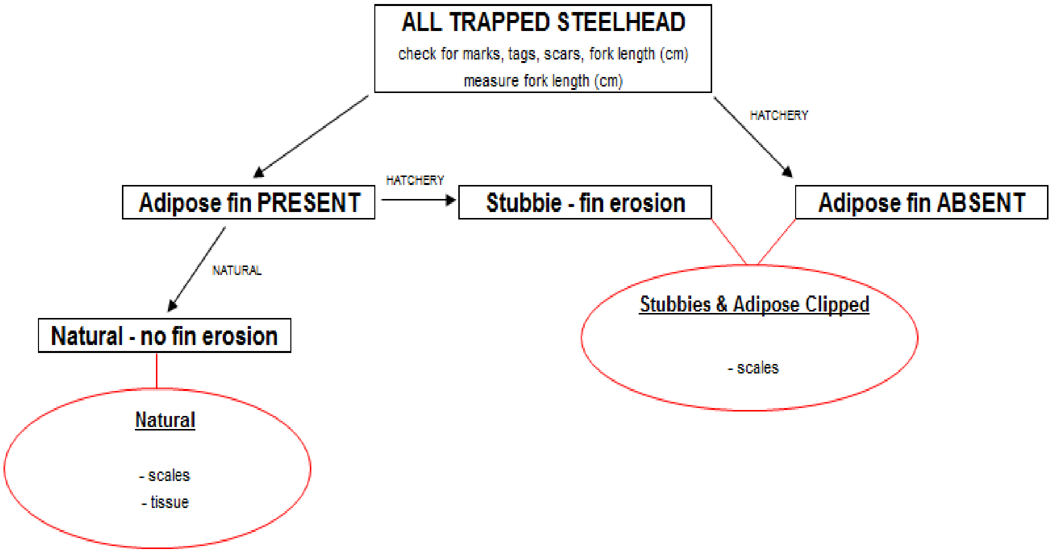
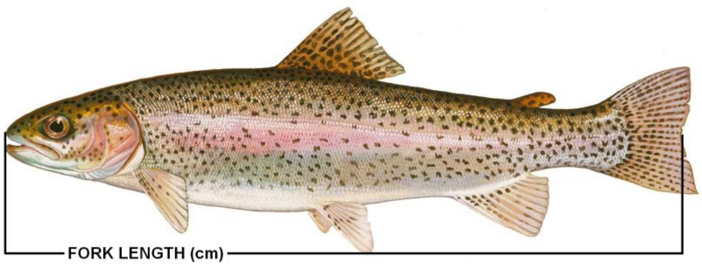


Figure 1. Steelhead wild/natural determination process.

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 both right and left sides of the fish, for a total of ten to twelve 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 from the trap will have scale samples taken.
    b. A subsample, to be determined, of 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 and stored in a closed vial with 100% 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 from the trap will have tissue samples taken.
    b. **Do not** take genetics tissues from hatchery fish unless it is PIT tagged.

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 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 5 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 recaptured PIT-tagged fish.** 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 2010 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
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)
2” x 4” Mailing labels (Avery 5163) (same # as coin envelopes)

Species, Adult YY-00000
Location

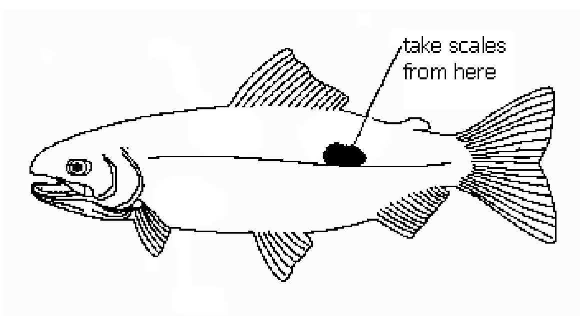
Date:__________ male female unknown (circle one)
Markings: None AD LV RV OP (circle one)
Fork Length: _____cm MEHP Length _____cm
Tags: None PIT CWT Other (circle one)
Tag Number: ______________________________
Comments:________________________________
Collector (full name): _________________________

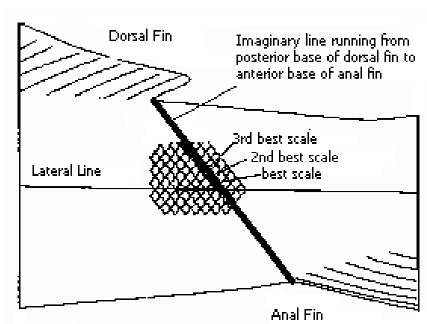
1. Species, life stage (Adult), sample number (**<u>matches that on data form</u>**), and location will be filled out for you.
2. The date requested is the day you are taking the sample.
3. Circle appropriate marks
4. Fill in Fork length
5. Fill in the PIT tag number.
6. In the comment line, put anything you feel may be of interest; for example, scars or deformities on the fish.

<u>Scale Sample Collection Method</u>

Supplies:
Forceps or tweezers
Knife
Rags or paper towels
Collection packet

1. Take any measurements requested (instructions for filling out the collection packet are above).
2. Clear away dirt from the area located on both sides 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.





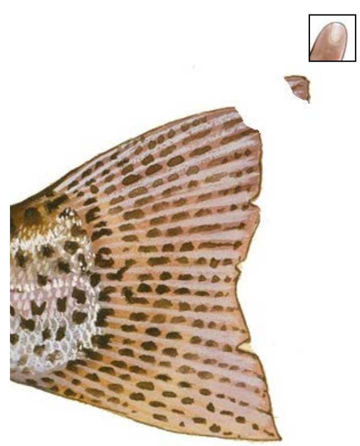
3. The preferred collection method is to use forceps or tweezers to remove individual scales. However, a knife may be used to remove scales if several fish need to be handled in a very short amount of time.
   Forceps/Tweezers
   a. Inspect for and remove from the forceps any scales from the previous 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. Hold the scale up to the light checking to see if the scale is regenerated. A scale is regenerated if, when holding it up to the light, you do not see a small distinct focal point in the center of the scale. If you do not understand this, please ask. It is very important. If the scale is regenerated discard it and select another.
5. Wipe scales onto one side of the folded strip of paper found in the collection packet.

6. Repeat steps 2 through 5 on the opposite side of the fish until there are at least 10 scales on the paper.
7. Refold the strip of paper over the scales and place the strip of paper directly into the collection packet it was removed from.
8. **<u>Make sure that all information requested is filled out on the collection packet.</u>**
9. Seal the collection packet.
10. Wipe the forceps/knife with rag or paper towel and inspect for any scales remaining. If necessary rinse with water.
11. 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 2010 Season

Supplies:
Labeled sample vials filled with 100% ethyl alcohol
100% ethyl alcohol (for cleaning scissors)
Paper towels
Scissors

1. Rinse the scissors and wipe with a paper towel to prevent cross contamination.
2. Clip a small tissue sample, about the size of your small fingernail, from the top of the caudal fin. Do not remove too much tissue. Too much tissue will overwhelm the sample vial alcohol.



3. Place the tissue sample in an alcohol-filled vial. Record the vial number on the data sheet.
4. Replace the alcohol in each sample vial at the end of the field season.

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, 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:

6) 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;
7) Length measurements of all fish to determine length distribution, length at age, A/B partition, etc;
8) 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;
9) 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;
10) Passive integrated tag (PIT) placement in all natural origin fish to estimate tributary specific escapement.

Once adult fish are trapped, all information from sampled fish will be recorded on the Field Data Entry Form, 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:

9. All spring/summer Chinook salmon and steelhead 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 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 unclipped hatchery steelhead (stubbies).

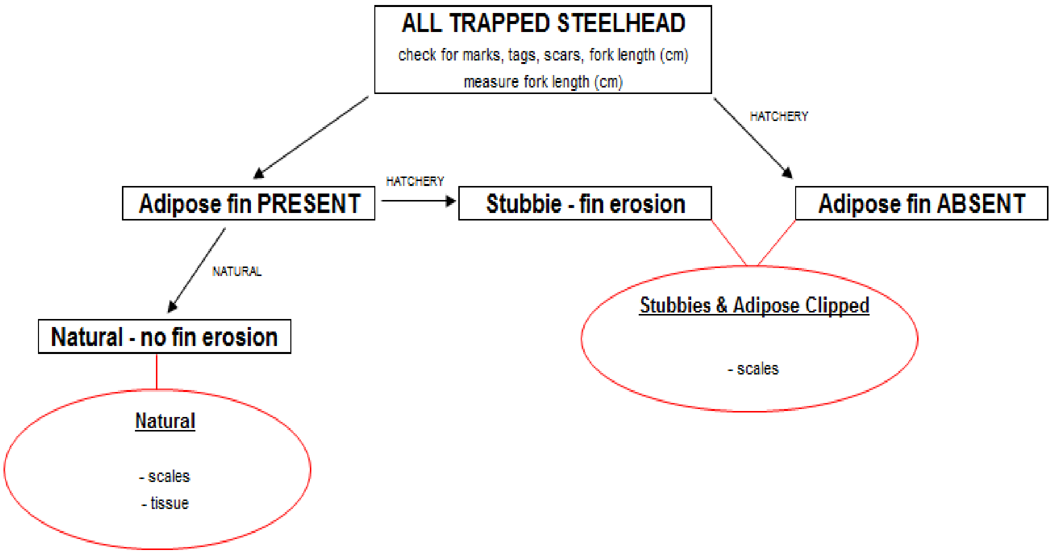
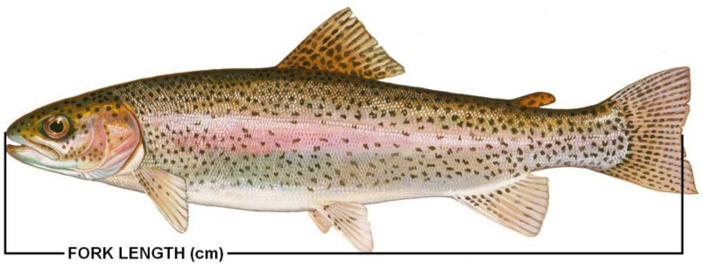


Figure 2. Steelhead wild/natural determination process.

10. 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.**

11. Any significant injuries will be noted in the comment column.

12. All spring/summer Chinook salmon and steelhead from the trap will be measured to the nearest centimeter (fork length).



13. For all spring/summer Chinook salmon and steelhead that are sampled, five to six scales will be removed from the preferred area on both right and left sides of the fish, for a total of ten to twelve 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 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.

14. 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% 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 from the trap will have tissue samples taken.
    b. All previously PIT tagged hatchery origin fish will have tissue samples taken.

15. 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 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 5 digits of the PIT tag code, and time of placement – record in the appropriate columns on the field data.

16. **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), collection date and sample number.

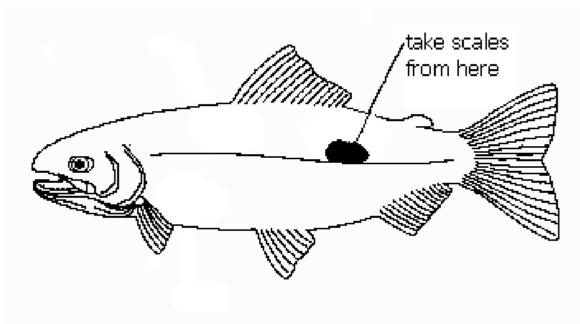
Scale Sample Collection Method

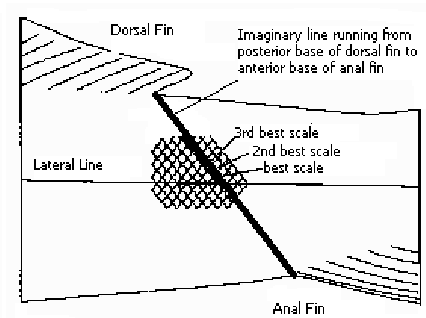
Supplies:

- Forceps or tweezers
- Knife
- Rags or paper towels

- Collection packets (sample envelopes)

12. Take any measurements requested.
13. Clear away dirt from the area located on both sides 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.





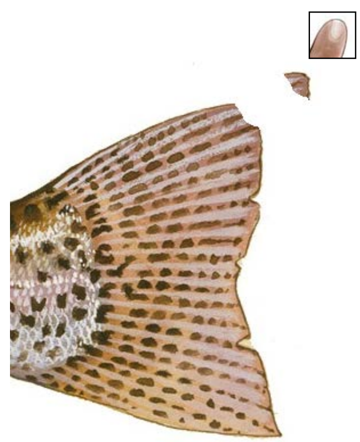
14. The preferred collection method is to use forceps or tweezers to remove individual scales. However, a knife may be used to remove scales if several fish need to be handled in a very short amount of time.
    Forceps/Tweezers
    a. Inspect for and remove from the forceps any scales from the previous 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.
15. Hold the scale up to the light checking to see if the scale is regenerated. A scale is regenerated if, when holding it up to the light, you do not see a small distinct focal point in the center of the scale. If you do not understand this, please ask. It is very important. If the scale is regenerated discard it and select another.
16. Wipe scales onto one side of the folded strip of paper found in the collection packet.
17. Repeat steps 2 through 5 on the opposite side of the fish until there are at least 10 scales on the paper.
18. Refold the strip of paper over the scales and place the strip of paper directly into the collection packet it was removed from.
19. Seal the collection packet.
20. Wipe the forceps/knife with rag or paper towel and inspect for any scales remaining. If necessary rinse with water.
21. 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 200 proof NON-DENATURED ethanol (denatured alcohol will disrupt DNA preservation and extraction)
- Squeeze bottle with 200 proof NON-DENATURED ethanol
- Paper towels
- Scissors

5. 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.
6. On vial collection boxes (100 vials per box), record species, origin (wild/hatchery), collection date range and sample number range.
7. 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.
8. 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.
9. 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.



10. Place the tissue sample in an alcohol-filled vial. Record the vial number on the data sheet.
11. Vials should be topped off with alcohol before shipping to Nampa Research. Vials should be checked every two weeks for proper alcohol level.
12. Contact Kristin Ellsworth (208-465-8404x233; kristin.ellsworth@idfg.idaho.gov) or Mike Ackerman (208-939-6713; mike.ackerman@idfg.idaho.gov) if questions.

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:

Appendix B: Snake River genetic baselines v2.0 (Ackerman et al. 2012) used for stock identification at Lower Granite Dam, spawn year 2011.

Appendix Table B-1. Genetic stocks and baseline collections used for steelhead mixed stock analysis at Lower Granite Dam, spawn year 2011 (Ackerman et al. 2012). MPG = major population group.

Genetic stock / Collection name		*n*	Years collected	Latitude	Longitude	MPG
UPSALM (Upper Salmon River)						
1	Sawtooth Weir	108	05, 10	44.151	-114.885	Salmon
2	Valley Cr	45	05	44.223	-114.927	Salmon
3	WF Yankee F Salmon	117	04, 08	44.351	-114.730	Salmon
4	Morgan Cr	37	00	44.613	-114.164	Salmon
5	Pahsimeroi Weir	99	06, 10	44.682	-114.040	Salmon
6	Hayden Cr	90	09, 10	44.862	-113.632	Salmon
7	NF Salmon R	102	10	45.409	-113.992	Salmon
MFSALM (Middle Fork Salmon River)						
8	Marsh Cr	59	00	44.449	-115.230	Salmon
9	Sulphur Cr	46	00	44.553	-115.297	Salmon
10	Rapid R (MF)	45	00	44.679	-115.149	Salmon
11	Pistol Cr	23	00	44.722	-115.149	Salmon
12	Loon Cr	84	99, 00	44.598	-114.812	Salmon
13	Camas Cr	57	00	44.892	-114.722	Salmon
14	Big Cr (upper)	46	00	45.151	-115.297	Salmon
15	Big Cr (lower)	48	00	45.092	-114.730	Salmon
16	Chamberlain Cr	47	00	45.452	-114.931	Salmon
17	Bargamin Cr	32	00	45.572	-115.192	Salmon
SFSALM (South Fork Salmon River)						
18	EF SF Salmon R	47	00	45.013	-115.713	Salmon
19	Stolle Meadows	45	00	44.607	-115.681	Salmon
20	Secesh R	45	00	45.027	-115.708	Salmon
21	Lick Cr	39	10	45.069	-115.814	Salmon
LOSALM (Lower Salmon River)						
22	Boulder Cr	47	00	45.202	-116.311	Salmon
23	Rapid R	101	03, 09	45.372	-116.356	Salmon
24	Slate Cr	47	00	45.638	-116.283	Salmon
25	Whitebird Cr	62	00, 01	45.752	-116.320	Salmon
UPCLWR (Upper Clearwater River)						
26	Colt Cr	38	00	46.431	-114.540	Clearwater
27	Storm Cr	38	00	46.461	-114.547	Clearwater
28	Crooked F Lochsa R	44	00	46.525	-114.679	Clearwater
29	Lake Cr	47	00	46.463	-114.997	Clearwater
30	Fish Cr	100	10, 11	46.334	-115.347	Clearwater
31	Canyon Cr	47	11	46.216	-115.556	Clearwater
32	Selway R	78	08	45.692	-114.718	Clearwater
33	Little Clearwater R	59	08	45.744	-114.789	Clearwater
34	Whitecap Cr	76	08	45.869	-114.721	Clearwater
35	Bear Cr	36	00	46.019	-114.838	Clearwater
36	NF Moose Cr	94	00, 04	46.163	-114.897	Clearwater
37	Three Links Cr	47	00	46.096	-115.072	Clearwater
38	Gedney Cr	45	00	46.058	-115.314	Clearwater
39	O'Hara Cr	47	00	46.081	-115.518	Clearwater
SFCLWR (South Fork Clearwater River)						
40	Crooked R	109	07, 08	45.821	-115.527	Clearwater
41	Tenmile Cr	47	00	45.806	-115.683	Clearwater
42	John's Cr	40	00	45.822	-115.889	Clearwater
43	Clear Cr	45	00	46.049	-115.781	Clearwater

Appendix Table B-1, continued.

Genetic stock / Collection name		*n*	Years collected	Latitude	Longitude	MPG
LOCLWR (Lower Clearwater River)						
44	WF Potlatch R	85	09, 10	46.805	-116.418	Clearwater
45	EF Potlatch R	160	08, 10, 11	46.798	-116.419	Clearwater
46	Big Bear Cr	99	07, 08, 10, 11	46.631	-116.656	Clearwater
47	Little Bear Cr	151	07, 08, 10, 11	46.637	-116.678	Clearwater
IMNAHA (Imnaha River)						
48	Big Sheep Cr	69	01	45.557	-116.834	Imnaha
49	Camp Cr	24	01	45.557	-116.835	Imnaha
50	Cow Cr	44	00	45.768	-116.750	Imnaha
51	Lightning Cr	39	00	45.655	-116.727	Imnaha
GRROND (Grande Ronde River)						
52	Little Minam R	48	00	45.400	-117.672	Grande Ronde
53	Lostine R	45	00	45.552	-117.490	Grande Ronde
54	Elk Cr	45	00	45.705	-117.153	Grande Ronde
55	Joseph Cr	60	11	46.028	-117.018	Grande Ronde
56	Crooked Cr	97	01	45.977	-117.555	Grande Ronde
57	Menatchee Cr	73	99	46.007	-117.365	Grande Ronde
58	Wenaha R	94	01	45.945	-117.451	Grande Ronde
LSNAKE (Lower Snake River)						
59	Captain John Cr	56	00	46.151	-116.934	Grande Ronde
60	George Cr	96	10	46.303	-117.117	Lower Snake
61	Asotin Cr	99	08, 10	46.323	-117.137	Lower Snake
62	Alpowa Cr	98	10	46.408	-117.220	Lower Snake
63	Tucannon R	108	05, 09, 10	46.310	-117.657	Lower Snake

Appendix Table B-2. Genetic stocks and baseline collections used for Chinook salmon mixed stock analysis at Lower Granite Dam, spawn year 2011 (Ackerman et al. 2012). MPG = major population group.

Genetic stock / Collection name	*n*	Years collected	Latitude	Longitude	MPG
UPSALM (Upper Salmon River)					
1 Sawtooth Weir	92	09, 10	44.151	-114.885	Upper Salmon
2 Valley Cr	59	07, 08, 09, 10	44.223	-114.927	Upper Salmon
3 WF Yankee F Salmon	75	05	44.349	-114.727	Upper Salmon
4 EF Salmon R	187	04, 05, 11	44.115	-114.430	Upper Salmon
5 Pahsimeroi R	97	07, 08, 09, 10	44.682	-114.039	Upper Salmon
6 Hayden Cr	80	09, 10	44.862	-113.632	Upper Salmon
7 Lemhi (upper)	96	09, 10	44.869	-113.625	Upper Salmon
8 Lemhi (lower)	90	09, 10	45.153	-113.814	Upper Salmon
MFSALM (Middle Fork Salmon River)					
9 Capehorn Cr	113	05, 06, 07, 09, 10	44.388	-115.174	MF Salmon
10 Marsh Cr	67	07, 08, 09, 10	44.381	-115.153	MF Salmon
11 Elk Cr	91	07, 08, 09, 10	44.442	-115.454	MF Salmon
12 Bear Valley Cr	85	07, 08, 09, 10	44.427	-115.328	MF Salmon
13 Sulphur Cr	37	08, 09, 10	44.534	-115.358	MF Salmon
14 Camas Cr	61	06, 09	44.892	-114.721	MF Salmon
15 Big Cr	95	01, 10	45.138	-115.038	MF Salmon
CHMBLN (Chamberlain Creek)					
16 Chamberlain Cr (post-2008)	56	09, 10	45.452	-114.931	MF Salmon
17 Chamberlain Cr (pre-2008)	70	03, 04, 06, 07	45.454	-114.933	MF Salmon
SFSALM (South Fork Salmon River)					
18 Lake Cr, Summit Cr	78	07, 08, 09, 10	45.279	-115.922	SF Salmon
19 Secesh R	134	01, 07, 08, 09, 10	45.217	-115.808	SF Salmon
20 Johnson Cr	92	02	44.899	-115.492	SF Salmon
21 SF Salmon R	143	09, 10	44.667	-115.703	SF Salmon
HELLSC (Hells Canyon Stock)					
22 Rapid R	91	06	45.372	-116.356	SF Salmon
23 Crooked F Lochsa R	29	07, 08, 09, 10	46.506	-114.681	Wet Clearwater
24 Powell Weir	32	09	46.506	-114.687	Wet Clearwater
25 Red R	73	07, 08, 09, 10	45.710	-115.344	Dry Clearwater
26 Crooked R Weir	67	09, 10	45.817	-115.527	Dry Clearwater
27 Newsome Cr	82	01	45.831	-115.608	Dry Clearwater
28 Lolo Cr	89	01, 02	46.279	-115.775	Wet Clearwater
29 Imnaha R	46	08	45.620	-116.845	Grande Ronde / Imnaha
30 Imnaha R (1998)	91	98	45.561	-116.834	Grande Ronde / Imnaha
31 Upper Grande Ronde	46	08	45.132	-118.365	Grande Ronde / Imnaha
32 Catherine Cr	94	04, 06	45.158	-117.779	Grande Ronde / Imnaha
33 Lostine R	177	03, 05, 09	45.542	-117.555	Grande Ronde / Imnaha
34 Minam R	81	94, 02	45.600	-117.729	Grande Ronde / Imnaha
35 Wenaha R	88	02, 06	45.946	-117.455	Grande Ronde / Imnaha
TUCANO (Tucannon River)					
36 Tucannon R	81	03	46.526	-118.142	Lower Snake
FALL (Fall Chinook ESU)					
37 Clearwater	152	08	46.520	-116.610	FALL ESU
38 Nez Perce Tribal Hatchery	85	03	46.519	-116.665	FALL ESU
39 Lyons Ferry	90	00	46.589	-118.220	FALL ESU

Appendix C: Wild adult steelhead at Lower Granite Dam, spawn year 2011.

Appendix Table C-1. Weekly window or video counts and adult valid trap samples of steelhead at Lower Granite Dam (LGR), spawn year 2011.

Statistical week(a)	Sampling period 2010-11	Number of days	LGR window count(b)	LGR adult valid trap sample(c)	LGR adult trap sample rate (%)	Percent of run trapped
			Fall 2010			
27-28(d)	7/1-7/11	11	2,038	89	4	4.4
29	7/12-7/18	7	2,740	116	4	4.2
30	7/19-7/25	7	2,665	108	4	4.1
31	7/26-8/1	7	1,695	76	4	4.5
32	8/2-8/8	7	3,076	95	4	3.1
33(e)	8/9-8/15	7	5,284	159	0-4	3.0
34-35(e)	8/16-8/29	14	7,065	491	0-12	6.9
36	8/30-9/5	7	9,517	1,183	12	12.4
37	9/6-9/12	7	17,378	2,132	12	12.3
38	9/13-9/19	7	25,054	3,280	10-12	13.1
39	9/20-9/26	7	31,309	3,799	10	12.1
40	9/27-10/3	7	26,462	3,139	10	11.9
41	10/4-10/10	7	19,560	2,207	10	11.3
42	10/11-10/17	7	18,259	1,999	10	10.9
43	10/18-10/24	7	8,459	975	10	11.5
44	10/25-10/31	7	6,730	751	10	11.2
45	11/1-11/7	7	2,284	296	10	13.0
46	11/8-11/14	7	2,655	272	10	10.2
47-53(d,g)	11/15-12/31	47	3,703	107	0-10	2.9
Fall total:		184	195,933	21,274	0-12	10.9
			Spring 2011			
1-10(d,h)	1/1-2/28	59	ND(i)	ND	ND	ND
10-11(d,h)	3/1-3/13	13	1,027	90	0-10	8.8
12	3/14-3/20	7	1,579	219	10	13.9
13	3/21-3/27	7	1,436	189	10	13.2
14	3/28-4/3	7	2,548	266	10	10.4
15	4/4-4/10	7	1,827	244	10	13.4
16	4/11-4/17	7	1,601	186	10	11.6
17	4/18-4/24	7	896	100	10	11.2
18-27(d)	4/25-6/30	67	1,449	148	10	10.2
Spring total:		181	12,363	1,442	0-10	11.7
Run total:		365	208,296	22,716	0-12	10.9

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 trapped fish.
(b) Downloaded from COE link 1/12/13.
(c) From Darren Ogden (NMFS, personal communication).
(d) Includes partial beginning or ending week.
(e) The trap was closed 8/14/10 to 8/21/10 due to high water temperatures.
(g) The trap was closed 11/19/10 to 12/31/10 due to freezing water temperatures.
(h) The trap was closed 1/1/11 to 3/6/11; the window was closed 1/1/11 to 2/28/11; the fish ladder was closed 1/4/11 to 2/2/11 and fish passage was only by navigation lock.
(i) ND = no data.

Appendix Table C-2. Number of steelhead captured in the adult trap, by fish size and origin, at Lower Granite Dam (LGR), spawn year 2011. 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.

		LGR	Number of trapped fish that were(c):							
Statistical week(a)	Sample period ending(b)	adult valid trap sample(c)	Large wild	Large hatchery clipped	Large hatchery unclipped	Small wild	Small hatchery clipped	Small hatchery unclipped	Total hatchery	Total wild
					Fall 2010					
27-28	7/11	89	0	2	0	24	57	6	65	24
29	7/18	116	1	1	1	29	61	23	86	30
30	7/25	108	0	0	1	29	62	16	79	29
31	8/1	76	0	0	0	23	42	11	53	23
32	8/8	95	0	0	0	29	56	10	66	29
33	8/15	159	1	0	0	52	84	22	106	53
34-35	8/29	491	5	3	0	106	313	64	380	111
36	9/5	1,183	37	34	4	261	759	88	885	298
37	9/12	2,132	76	96	5	383	1,426	146	1,673	459
38	9/19	3,280	134	317	36	465	2,076	252	2,681	599
39	9/26	3,799	194	551	51	510	2,179	314	3,095	704
40	10/3	3,139	177	633	63	431	1,611	224	2,531	608
41	10/10	2,207	120	554	61	269	1,026	177	1,818	389
42	10/17	1,999	116	536	55	298	872	122	1,585	414
43	10/24	975	55	228	39	145	431	77	775	200
44	10/31	751	43	179	31	133	306	59	575	176
45	11/7	296	24	58	9	50	128	27	222	74
46	11/14	272	7	50	10	55	126	24	210	62
47-53	12/31	107	3	17	4	20	51	12	84	23
Fall total:		21,274	993	3,259	370	3,312	11,666	1,674	16,969	4,305
					Spring 2011					
1-10	2/28	ND(d)	ND	ND	ND	ND	ND	ND	ND	ND
10-11	3/13	90	3	34	12	11	19	11	76	14
12	3/20	219	7	68	15	33	70	26	179	40
13	3/27	189	7	62	11	30	55	24	152	37
14	4/3	266	24	71	8	66	75	22	176	90
15	4/10	244	20	63	17	46	67	31	178	66
16	4/17	186	8	35	22	39	55	27	139	47
17	4/24	100	4	6	3	28	30	29	68	32
18-27	6/30	148	7	1	4	63	42	31	78	70
Spring total:		1,442	80	340	92	316	413	201	1,046	396
Run total:		22,716	1,073	3,599	462	3,628	12,079	1,875	18,015	4,701

(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); small hatchery unclipped includes 11 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 2011. 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): Large wild	Large hatchery clipped	Large hatchery unclipped	Small wild	Small hatchery clipped	Small hatchery unclipped	Total hatchery	Total wild
Fall 2010										
27-28	7/11	89	0.0	2.2	0.0	27.0	64.0	6.7	73.0	27.0
29	7/18	116	0.9	0.9	0.9	25.0	52.6	19.8	74.1	25.9
30	7/25	108	0.0	0.0	0.9	26.9	57.4	14.8	73.1	26.9
31	8/1	76	0.0	0.0	0.0	30.3	55.3	14.5	69.7	30.3
32	8/8	95	0.0	0.0	0.0	30.5	58.9	10.5	69.5	30.5
33	8/15	159	0.6	0.0	0.0	32.7	52.8	13.8	66.7	33.3
34-35	8/29	491	1.0	0.6	0.0	21.6	63.7	13.0	77.4	22.6
36	9/5	1,183	3.1	2.9	0.3	22.1	64.2	7.4	74.8	25.2
37	9/12	2,132	3.6	4.5	0.2	18.0	66.9	6.8	78.5	21.5
38	9/19	3,280	4.1	9.7	1.1	14.2	63.3	7.7	81.7	18.3
39	9/26	3,799	5.1	14.5	1.3	13.4	57.4	8.3	81.5	18.5
40	10/3	3,139	5.6	20.2	2.0	13.7	51.3	7.1	80.6	19.4
41	10/10	2,207	5.4	25.1	2.8	12.2	46.5	8.0	82.4	17.6
42	10/17	1,999	5.8	26.8	2.8	14.9	43.6	6.1	79.3	20.7
43	10/24	975	5.6	23.4	4.0	14.9	44.2	7.9	79.5	20.5
44	10/31	751	5.7	23.8	4.1	17.7	40.7	7.9	76.6	23.4
45	11/7	296	8.1	19.6	3.0	16.9	43.2	9.1	75.0	25.0
46	11/14	272	2.6	18.4	3.7	20.2	46.3	8.8	77.2	22.8
47-53	12/31	107	2.8	15.9	3.7	18.7	47.7	11.2	78.5	21.5
Fall total(d):		21,274	4.3	14.5	1.7	16.6	54.6	8.3	79.1	20.9
Spring 2011										
1-10	2/28	ND(e)	ND	ND	ND	ND	ND	ND	ND	ND
10-11	3/13	90	3.3	37.8	13.3	12.2	21.1	12.2	84.4	15.6
12	3/20	219	3.2	31.1	6.8	15.1	32.0	11.9	81.7	18.3
13	3/27	189	3.7	32.8	5.8	15.9	29.1	12.7	80.4	19.6
14	4/3	266	9.0	26.7	3.0	24.8	28.2	8.3	66.2	33.8
15	4/10	244	8.2	25.8	7.0	18.9	27.5	12.7	73.0	27.0
16	4/17	186	4.3	18.8	11.8	21.0	29.6	14.5	74.7	25.3
17	4/24	100	4.0	6.0	3.0	28.0	30.0	29.0	68.0	32.0
18-27	6/30	148	4.7	0.7	2.7	42.6	28.4	20.9	52.7	47.3
Spring total(d):		1,442	5.6	23.2	6.4	22.4	28.4	14.0	72.0	28.0
Run total(d):		22,716	4.4	15.0	2.0	16.9	53.0	8.7	78.7	21.3

(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); small hatchery unclipped includes 11 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 2011. 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.

			Estimated number of steelhead at LGR that were:							
Statistical week(a)	**Sample period ending(b)**	**LGR window count(c)**	**Large wild**	**Large hatchery clipped**	**Large hatchery unclipped**	**Small wild**	**Small hatchery clipped**	**Small hatchery unclipped**	**Total hatchery**	**Total wild**
					Fall 2010					
27-28	7/11	2,038	0	46	0	550	1,305	137	1,488	550
29	7/18	2,740	24	24	24	685	1,440	543	2,031	709
30	7/25	2,665	0	0	25	716	1,529	395	1,949	716
31	8/1	1,695	0	0	0	513	937	245	1,182	513
32	8/8	3,076	0	0	0	939	1,813	324	2,137	939
33	8/15	5,284	33	0	0	1,728	2,792	731	3,523	1,761
34-35	8/29	7,065	72	43	0	1,525	4,504	921	5,468	1,597
36	9/5	9,517	298	274	32	2,100	6,105	708	7,119	2,398
37	9/12	17,378	619	782	41	3,122	11,624	1,190	13,637	3,741
38	9/19	25,054	1,024	2,421	275	3,552	15,857	1,925	20,478	4,576
39	9/26	31,309	1,599	4,541	420	4,203	17,958	2,588	25,507	5,802
40	10/3	26,462	1,492	5,336	531	3,633	13,582	1,888	21,337	5,125
41	10/10	19,560	1,064	4,910	541	2,384	9,092	1,569	16,112	3,448
42	10/17	18,259	1,060	4,896	502	2,722	7,965	1,114	14,477	3,782
43	10/24	8,459	477	1,978	338	1,258	3,740	668	6,724	1,735
44	10/31	6,730	385	1,604	278	1,192	2,742	529	5,153	1,577
45	11/7	2,284	185	448	69	386	988	208	1,713	571
46	11/14	2,655	68	488	98	537	1,230	234	2,050	605
47-53	12/31	3,703	104	588	138	692	1,766	415	2,907	796
Fall total:		195,933	8,504	28,379	3,312	32,437	106,969	16,332	154,992	40,941
					Spring 2011					
1-10	2/28	ND(d)	ND	ND	ND	ND	ND	ND	ND	ND
10-11	3/13	1,027	34	388	137	126	216	126	867	160
12	3/20	1,579	50	490	108	238	506	187	1,291	288
13	3/27	1,436	53	471	84	228	418	182	1,155	281
14	4/3	2,548	230	680	77	632	718	211	1,686	862
15	4/10	1,827	150	472	127	344	502	232	1,333	494
16	4/17	1,601	69	301	189	336	474	232	1,196	405
17	4/24	896	36	54	27	251	268	260	609	287
18-27	6/30	1,449	69	10	39	617	410	304	763	686
Spring total:		12,363	691	2,866	788	2,772	3,512	1,734	8,900	3,463
Run total:		208,296	9,195	31,245	4,100	35,209	110,481	18,066	163,892	44,404
95% CI:			(8,648-9,764)	(30,335-32,189)	(3,734-4,479)	(34,091-36,318)	(109,057-111,951)	(17,208-18,942)	(162,683-165,116)	(43,164-45,642)

(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 1/12/13.
(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 2011. Large and small fish were combined.

						Scale samples:		Genetics samples:			
Statistical week(a)	Sampling period 2010-11	Number of days	Wild run size(b)	Number of scale and genetics samples collected(c)	Number of scale and genetics systematic subsamples(d)	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 2010											
27-32(f)	7/1-8/8	39	3,427	135	135	111	3.2	129	3.8	129	3.8
33-36(g)	8/9-9/5	28	5,756	462	216	193	3.4	207	3.6	213	3.7
37	9/6-9/12	7	3,741	459	183	168	4.5	170	4.5	182	4.9
38	9/13-9/19	7	4,576	599	246	219	4.8	242	5.3	246	5.4
39	9/20-9/26	7	5,802	704	351	322	5.5	327	5.6	351	6.0
40	9/27-10/3	7	5,125	608	304	263	5.1	279	5.4	288	5.6
41	10/4-10/10	7	3,448	389	195	177	5.1	190	5.5	193	5.6
42	10/11-10/17	7	3,782	414	207	189	5.0	201	5.3	207	5.5
43	10/18-10/24	7	1,735	200	100	96	5.5	100	5.8	100	5.8
44-53(f,h)	10/25-12/31	68	3,549	335	167	156	4.4	162	4.6	165	4.6
Fall total:		184	40,941	4,305	2,104	1,894	4.6	2,007	4.9	2,074	5.1
Spring 2011											
1-10(f,i)	1/1-2/28	59	ND(j)	ND	ND	ND	ND	ND	ND	ND	ND
10-27(f,i)	3/1-6/30	122	3,463	396	198	157	4.5	191	5.5	193	5.6
Spring total:		181	3,463	396	198	157	4.5	191	5.5	193	5.6
Run total:		365	44,404	4,701	2,302	2,051	4.6	2,198	5.0	2,267	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 11 fish misidentified as wild at the trap and later determined to be unclipped hatchery by PBT.

(d) Does not include 7 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 8/14/10 to 8/21/10 due to high water temperatures.

(h) The trap was closed 11/19/10 to 12/31/10 due to freezing water temperatures.

(i) The trap was closed 1/1/11 to 3/6/11; the window was closed 1/1/11 to 2/28/11; the fish ladder was closed 1/4/11 to 2/2/11 and fish passage was only by navigation lock.

(j) 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 2011. Large and small fish were combined.

			Smolt migration year (MY), brood year (BY), and age class (frequency):																
	Sample	Number	MY2009				MY2008						MY2007					
Statistical	period	of samples	BY08	BY07	BY06	BY05	BY07	BY06	BY06	BY05	BY05	BY04	BY05	BY05	BY05	BY04	BY04	BY04
week(a)	ending(b)	aged	1.1	2.1	3.1	4.1	1.2	2.2	2.1S	3.2	3.1S	4.2	2.3	2.1S1	2.2S	3.3	3.1S1	3.2S
								Fall 2010										
27-32	8/8	111	2	27	6	-	12	44	-	18	-	2	-	-	-	-	-	-
33-36	9/5	193	4	36	9	-	9	90	-	40	-	2	1	2	-	-	-	-
37	9/12	168	3	23	11	1	6	71	-	48	-	4	-	1	-	-	-	-
38	9/19	219	2	33	8	-	9	97	1	61	-	7	-	-	1	-	-	-
39	9/26	322	2	49	16	2	14	141	-	86	-	6	2	-	3	-	1	-
40	10/3	263	3	48	15	1	17	99	3	70	-	5	-	-	1	-	1	-
41	10/10	177	4	32	12	1	8	67	-	45	-	1	3	-	1	2	1	-
42	10/17	189	2	37	10	1	7	91	-	38	-	1	1	-	-	-	-	1
43	10/24	96	1	20	4	-	1	43	-	24	-	2	-	-	-	1	-	-
44-53	12/31	156	3	29	17	1	10	61	-	31	-	1	1	1	1	-	-	-
Fall total:		1,894	26	334	108	7	93	804	4	461	0	31	8	4	7	3	3	1
								Spring 2011										
1-10	2/28	ND(c)	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
10-27	6/30	157	-	41	14	1	5	64	-	29	1	-	1	1	-	-	-	-
Spring total:		157	0	41	14	1	5	64	0	29	1	0	1	1	0	0	0	0
Run total:		2,051	26	375	122	8	98	868	4	490	1	31	9	5	7	3	3	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 2011. Large and small fish were combined. Percentages may not sum to 100.0% due to rounding error.

			Smolt migration year (MY), brood year (BY), and age class (percent):															
	Sample	Number	MY2009				MY2008						MY2007					
Statistical	period	of samples	BY08	BY07	BY06	BY05	BY07	BY06	BY06	BY05	BY05	BY04	BY05	BY05	BY05	BY04	BY04	BY04
week(a)	ending(b)	aged	1.1	2.1	3.1	4.1	1.2	2.2	2.1S	3.2	3.1S	4.2	2.3	2.1S1	2.2S	3.3	3.1S1	3.2S
								Fall 2010										
27-32	8/8	111	1.8	24.3	5.4	-	10.8	39.6	-	16.2	-	1.8	-	-	-	-	-	-
33-36	9/5	193	2.1	18.7	4.7	-	4.7	46.6	-	20.7	-	1.0	0.5	1.0	-	-	-	-
37	9/12	168	1.8	13.7	6.5	0.6	3.6	42.3	-	28.6	-	2.4	-	0.6	-	-	-	-
38	9/19	219	0.9	15.1	3.7	-	4.1	44.3	0.5	27.9	-	3.2	-	-	0.5	-	-	-
39	9/26	322	0.6	15.2	5.0	0.6	4.3	43.8	-	26.7	-	1.9	0.6	-	0.9	-	0.3	-
40	10/3	263	1.1	18.3	5.7	0.4	6.5	37.6	1.1	26.6	-	1.9	-	-	0.4	-	0.4	-
41	10/10	177	2.3	18.1	6.8	0.6	4.5	37.9	-	25.4	-	0.6	1.7	-	0.6	1.1	0.6	-
42	10/17	189	1.1	19.6	5.3	0.5	3.7	48.1	-	20.1	-	0.5	0.5	-	-	-	-	0.5
43	10/24	96	1.0	20.8	4.2	-	1.0	44.8	-	25.0	-	2.1	-	-	-	1.0	-	-
44-53	12/31	156	1.9	18.6	10.9	0.6	6.4	39.1	-	19.9	-	0.6	0.6	0.6	0.6	-	-	-
Fall total:		1,894	1.4	17.6	5.7	0.4	4.9	42.4	0.2	24.3	0.0	1.6	0.4	0.2	0.4	0.2	0.2	0.1
								Spring 2011										
1-10	2/28	ND(c)	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
10-27	6/30	157	-	26.1	8.9	0.6	3.2	40.8	-	18.5	0.6	-	0.6	0.6	-	-	-	-
Spring total:		157	0.0	26.1	8.9	0.6	3.2	40.8	0.0	18.5	0.6	0.0	0.6	0.6	0.0	0.0	0.0	0.0
Run total:		2,051	1.3	18.3	5.9	0.4	4.8	42.3	0.2	23.9	0.0	1.5	0.4	0.2	0.3	0.1	0.1	0.0

(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 2011. Large and small fish were combined.

Statistical week(a)	Sample period ending(b)	Number of samples genotyped for gender	Gender (frequency):	
			Female	Male
		Fall 2010		
27-32	8/8	129	97	32
33-36	9/5	207	138	69
37	9/12	170	107	63
38	9/19	242	181	61
39	9/26	327	225	102
40	10/3	279	182	97
41	10/10	190	112	78
42	10/17	201	134	67
43	10/24	100	59	41
44-53	12/31	162	99	63
Fall total:		2,007	1,334	673
		Spring 2011		
1-10	2/28	ND(c)	ND	ND
10-27	6/30	191	132	59
Spring total:		191	132	59
Run total:		2,198	1,466	732

(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 2011. 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 2010		
27-32	8/8	129	75.2	24.8
33-36	9/5	207	66.7	33.3
37	9/12	170	62.9	37.1
38	9/19	242	74.8	25.2
39	9/26	327	68.8	31.2
40	10/3	279	65.2	34.8
41	10/10	190	58.9	41.1
42	10/17	201	66.7	33.3
43	10/24	100	59.0	41.0
44-53	12/31	162	61.1	38.9
Fall total:		2,007	66.5	33.5
		Spring 2011		
1-10	2/28	ND(c)	ND	ND
10-27	6/30	191	69.1	30.9
Spring total:		191	69.1	30.9
Run total:		2,198	66.7	33.3

(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 2011. Large and small fish were combined. Only individual fish whose assignment probability was ≥0.80 and had both a determined sex and a total age are included (n = 974); fish whose assignment probability was <0.80 are excluded. See Appendix Table B-1 for stock abbreviations.

		Smolt migration year (MY), brood year (BY), and age class (frequency):															
		MY2009				**MY2008**						**MY2007**					
Genetic stock	**Sex**	**BY08 1.1**	**BY07 2.1**	**BY06 3.1**	**BY05 4.1**	**BY07 1.2**	**BY06 2.2**	**BY06 2.1S**	**BY05 3.2**	**BY05 3.1S**	**BY04 4.2**	**BY05 2.3**	**BY05 2.1S1**	**BY05 2.2S**	**BY04 3.3**	**BY04 3.1S1**	**Total sample**
UPSALM	F	1	18	4	0	6	45	2	14	0	0	0	0	0	0	1	91
	M	4	27	5	0	5	13	0	4	0	0	0	0	0	0	0	58
	Total:	5	45	9	0	11	58	2	18	0	0	0	0	0	0	1	149
MFSALM	F	0	0	2	0	1	25	0	58	1	10	0	0	0	0	0	97
	M	0	0	5	2	1	8	0	20	0	1	0	0	0	0	0	37
	Total:	0	0	7	2	2	33	0	78	1	11	0	0	0	0	0	134
SFSALM	F	0	1	1	0	0	15	0	38	0	3	0	0	1	0	0	59
	M	0	0	0	0	0	4	0	13	0	0	0	0	0	1	0	18
	Total:	0	1	1	0	0	19	0	51	0	3	0	0	1	1	0	77
LOSALM	F	1	0	1	0	0	8	0	6	0	0	0	0	0	0	0	16
	M	0	3	4	0	0	8	0	2	0	0	0	0	0	0	0	17
	Total:	1	3	5	0	0	16	0	8	0	0	0	0	0	0	0	33
UPCLWR	F	0	0	1	0	3	42	0	79	0	3	3	0	0	0	0	131
	M	1	0	0	1	0	11	0	21	0	2	2	0	0	0	0	38
	Total:	1	0	1	1	3	53	0	100	0	5	5	0	0	0	0	169
SFCLWR	F	0	0	0	0	1	62	0	13	0	2	0	0	1	1	0	80
	M	0	3	0	0	3	35	0	15	0	0	0	0	0	0	0	56
	Total:	0	3	0	0	4	97	0	28	0	2	0	0	1	1	0	136
LOCLWR	F	0	4	2	0	1	16	0	4	0	0	0	0	1	0	0	28
	M	1	4	0	0	2	6	0	2	0	1	0	0	0	0	0	16
	Total:	1	8	2	0	3	22	0	6	0	1	0	0	1	0	0	44
IMNAHA	F	0	5	5	0	0	19	0	9	0	0	0	1	0	0	0	39
	M	0	8	1	0	0	4	0	0	0	0	0	0	0	0	0	13
	Total:	0	13	6	0	0	23	0	9	0	0	0	1	0	0	0	52
GRROND	F	1	14	3	1	6	50	0	14	0	0	0	0	2	0	1	92
	M	0	11	4	0	1	19	0	1	0	0	0	0	0	0	0	36
	Total:	1	25	7	1	7	69	0	15	0	0	0	0	2	0	1	128
LSNAKE	F	0	9	5	0	2	18	0	1	0	0	0	0	0	0	0	35
	M	2	10	0	0	0	5	0	0	0	0	0	0	0	0	0	17
	Total:	2	19	5	0	2	23	0	1	0	0	0	0	0	0	0	52
	Grand total:	11	117	43	4	32	413	2	314	1	22	5	1	5	2	2	974

Appendix Table C-11. Percentage of wild adult steelhead sampled at Lower Granite Dam by gender by age for each genetic stock, spawn year 2011. Large and small fish were combined. Only individual fish whose assignment probability was ≥0.80 and had both a determined sex and a total age are included (n = 974); fish whose assignment probability was <0.80 are excluded. See Appendix Table B-1 for stock abbreviations.

		Smolt migration year (MY), brood year (BY), and age class (percent):															
		MY2009				MY2008						MY2007					
Genetic		BY08	BY07	BY06	BY05	BY07	BY06	BY06	BY05	BY05	BY04	BY05	BY05	BY05	BY04	BY04	Sex
stock	Sex	1.1	2.1	3.1	4.1	1.2	2.2	2.1S	3.2	3.1S	4.2	2.3	2.1S1	2.2S	3.3	3.1S1	ratio
UPSALM	F	1.1	19.8	4.4	0.0	6.6	49.5	2.2	15.4	0.0	0.0	0.0	0.0	0.0	0.0	1.1	61.1
	M	6.9	46.6	8.6	0.0	8.6	22.4	0.0	6.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	38.9
	Total:	3.4	30.2	6.0	0.0	7.4	38.9	1.3	12.1	0.0	0.0	0.0	0.0	0.0	0.0	0.7	100.0
MFSALM	F	0.0	0.0	2.1	0.0	1.0	25.8	0.0	59.8	1.0	10.3	0.0	0.0	0.0	0.0	0.0	72.4
	M	0.0	0.0	13.5	5.4	2.7	21.6	0.0	54.1	0.0	2.7	0.0	0.0	0.0	0.0	0.0	27.6
	Total:	0.0	0.0	5.2	1.5	1.5	24.6	0.0	58.2	0.7	8.2	0.0	0.0	0.0	0.0	0.0	100.0
SFSALM	F	0.0	1.7	1.7	0.0	0.0	25.4	0.0	64.4	0.0	5.1	0.0	0.0	1.7	0.0	0.0	76.6
	M	0.0	0.0	0.0	0.0	0.0	22.2	0.0	72.2	0.0	0.0	0.0	0.0	0.0	5.6	0.0	23.4
	Total:	0.0	1.3	1.3	0.0	0.0	24.7	0.0	66.2	0.0	3.9	0.0	0.0	1.3	1.3	0.0	100.0
LOSALM	F	6.3	0.0	6.3	0.0	0.0	50.0	0.0	37.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	48.5
	M	0.0	17.6	23.5	0.0	0.0	47.1	0.0	11.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	51.5
	Total:	3.0	9.1	15.2	0.0	0.0	48.5	0.0	24.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
UPCLWR	F	0.0	0.0	0.8	0.0	2.3	32.1	0.0	60.3	0.0	2.3	2.3	0.0	0.0	0.0	0.0	77.5
	M	2.6	0.0	0.0	2.6	0.0	28.9	0.0	55.3	0.0	5.3	5.3	0.0	0.0	0.0	0.0	22.5
	Total:	0.6	0.0	0.6	0.6	1.8	31.4	0.0	59.2	0.0	3.0	3.0	0.0	0.0	0.0	0.0	100.0
SFCLWR	F	0.0	0.0	0.0	0.0	1.3	77.5	0.0	16.3	0.0	2.5	0.0	0.0	1.3	1.3	0.0	58.8
	M	0.0	5.4	0.0	0.0	5.4	62.5	0.0	26.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	41.2
	Total:	0.0	2.2	0.0	0.0	2.9	71.3	0.0	20.6	0.0	1.5	0.0	0.0	0.7	0.7	0.0	100.0
LOCLWR	F	0.0	14.3	7.1	0.0	3.6	57.1	0.0	14.3	0.0	0.0	0.0	0.0	3.6	0.0	0.0	63.6
	M	6.3	25.0	0.0	0.0	12.5	37.5	0.0	12.5	0.0	6.3	0.0	0.0	0.0	0.0	0.0	36.4
	Total:	2.3	18.2	4.5	0.0	6.8	50.0	0.0	13.6	0.0	2.3	0.0	0.0	2.3	0.0	0.0	100.0
IMNAHA	F	0.0	12.8	12.8	0.0	0.0	48.7	0.0	23.1	0.0	0.0	0.0	2.6	0.0	0.0	0.0	75.0
	M	0.0	61.5	7.7	0.0	0.0	30.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	25.0
	Total:	0.0	25.0	11.5	0.0	0.0	44.2	0.0	17.3	0.0	0.0	0.0	1.9	0.0	0.0	0.0	100.0
GRROND	F	1.1	15.2	3.3	1.1	6.5	54.3	0.0	15.2	0.0	0.0	0.0	0.0	2.2	0.0	1.1	71.9
	M	0.0	30.6	11.1	0.0	2.8	52.8	0.0	2.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	28.1
	Total:	0.8	19.5	5.5	0.8	5.5	53.9	0.0	11.7	0.0	0.0	0.0	0.0	1.6	0.0	0.8	100.0
LSNAKE	F	0.0	25.7	14.3	0.0	5.7	51.4	0.0	2.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	67.3
	M	11.8	58.8	0.0	0.0	0.0	29.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	32.7
	Total:	3.8	36.5	9.6	0.0	3.8	44.2	0.0	1.9	0.0	0.0	0.0	0.0	0.0	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 2011. Large and small fish were combined. Only individual fish whose assignment probability was ≥0.80 and had both a determined sex and a total age were used (n = 974); fish whose assignment probability was <0.80 were excluded. See Appendix Table B-1 for stock abbreviations.

		Smolt migration year (MY), brood year (BY), and age class (abundance):															
		MY2009				MY2008						MY2007					
Genetic stock	**Sex**	**BY08 1.1**	**BY07 2.1**	**BY06 3.1**	**BY05 4.1**	**BY07 1.2**	**BY06 2.2**	**BY06 2.1S**	**BY05 3.2**	**BY05 3.1S**	**BY04 4.2**	**BY05 2.3**	**BY05 2.1S1**	**BY05 2.2S**	**BY04 3.3**	**BY04 3.1S1**	**Total abundance**
UPSALM	F	45	811	180	0	270	2,030	90	631	0	0	0	0	0	0	45	4,102
	M	180	1,217	225	0	225	588	0	180	0	0	0	0	0	0	0	2,615
	Total:	225	2,028	405	0	495	2,618	90	811	0	0	0	0	0	0	45	6,717
MFSALM	F	0	0	59	0	29	734	0	1,703	29	294	0	0	0	0	0	2,848
	M	0	0	147	59	29	235	0	587	0	29	0	0	0	0	0	1,086
	Total:	0	0	206	59	58	969	0	2,290	29	323	0	0	0	0	0	3,934
SFSALM	F	0	31	31	0	0	459	0	1,162	0	92	0	0	31	0	0	1,806
	M	0	0	0	0	0	122	0	398	0	0	0	0	0	31	0	551
	Total:	0	31	31	0	0	581	0	1,560	0	92	0	0	31	31	0	2,357
LOSALM	F	48	0	48	0	0	381	0	286	0	0	0	0	0	0	0	763
	M	0	143	191	0	0	381	0	95	0	0	0	0	0	0	0	810
	Total:	48	143	239	0	0	762	0	381	0	0	0	0	0	0	0	1,573
UPCLWR	F	0	0	25	0	74	1,039	0	1,953	0	74	74	0	0	0	0	3,239
	M	25	0	0	25	0	272	0	520	0	49	49	0	0	0	0	940
	Total:	25	0	25	25	74	1,311	0	2,473	0	123	123	0	0	0	0	4,179
SFCLWR	F	0	0	0	0	32	1,997	0	418	0	64	0	0	32	32	0	2,575
	M	0	97	0	0	97	1,125	0	483	0	0	0	0	0	0	0	1,802
	Total:	0	97	0	0	129	3,122	0	901	0	64	0	0	32	32	0	4,377
LOCLWR	F	0	164	82	0	41	659	0	164	0	0	0	0	41	0	0	1,151
	M	41	164	0	0	82	248	0	82	0	41	0	0	0	0	0	658
	Total:	41	328	82	0	123	907	0	246	0	41	0	0	41	0	0	1,809
IMNAHA	F	0	240	240	0	0	912	0	432	0	0	0	48	0	0	0	1,872
	M	0	384	48	0	0	192	0	0	0	0	0	0	0	0	0	624
	Total:	0	624	288	0	0	1,104	0	432	0	0	0	48	0	0	0	2,496
GRROND	F	56	789	169	56	338	2,818	0	789	0	0	0	0	113	0	56	5,184
	M	0	620	225	0	56	1,071	0	56	0	0	0	0	0	0	0	2,028
	Total:	56	1,409	394	56	394	3,889	0	845	0	0	0	0	113	0	56	7,212
LSNAKE	F	0	1,688	938	0	375	3,374	0	188	0	0	0	0	0	0	0	6,563
	M	375	1,875	0	0	0	937	0	0	0	0	0	0	0	0	0	3,187
	Total:	375	3,563	938	0	375	4,311	0	188	0	0	0	0	0	0	0	9,750

Appendix D: Wild adult Chinook salmon at Lower Granite Dam, spawn year 2011.

Appendix Table D-1. Weekly window or video counts and adult valid trap samples of Chinook salmon at Lower Granite Dam (LGR), spawn year 2011.

Statistical week(a)	Sampling period 2011	Number of days	LGR window count(b)	LGR adult valid trap sample(c)	LGR adult trap sample rate (%)	Percent of run trapped
10-19(d)	3/1-5/8	69	1,650	122	10	7.4
20	5/9-5/15	7	19,965	1,919	10	9.6
21	5/16-5/22	7	12,902	1,440	10	11.2
22	5/23-5/29	7	14,630	1,497	10	10.2
23	5/30-6/5	7	16,546	1,687	10	10.2
24	6/6-6/12	7	9,638	1,027	10	10.7
25	6/13-6/19	7	8,861	921	10	10.4
26	6/20-6/26	7	14,508	1,594	10	11.0
27	6/27-7/3	7	16,975	1,894	10	11.2
28	7/4-7/10	7	8,946	929	10	10.4
29	7/11-7/17	7	4,706	496	10	10.5
30	7/18-7/24	7	1,890	179	10	9.5
31	7/25-7/31	7	1,773	188	10	10.6
32-34(d)	8/1-8/17	17	1,604	175	10	10.9
Run total:		170	134,594	14,068	10	10.5

(a) Statistical weeks were grouped to try to provide a minimum sample size of 100 trapped fish.
(b) Downloaded from COE link 1/5/13.
(c) From Darren Ogden (NMFS, personal communication).
(d) Includes partial beginning or ending week.

Appendix Table D-2. Number of Chinook salmon captured in the adult trap, by origin, at Lower Granite Dam (LGR), spawn year 2011. Clipped and unclipped refer to the adipose fin.

		LGR	Number of trapped fish that were(c):				
Statistical week(a)	**Sample period ending(b)**	**LGR adult valid trap sample(c)**	**Wild**	**Hatchery clipped**	**Hatchery unclipped**	**Total hatchery**	**Total wild**
10-19	5/8	122	38	78	6	84	38
20	5/15	1,919	322	1,517	80	1,597	322
21	5/22	1,440	170	1,219	51	1,270	170
22	5/29	1,497	159	1,278	60	1,338	159
23	6/5	1,687	199	1,420	68	1,488	199
24	6/12	1,027	140	847	40	887	140
25	6/19	921	150	730	41	771	150
26	6/26	1,594	411	1,121	62	1,183	411
27	7/3	1,894	548	1,276	70	1,346	548
28	7/10	929	274	610	45	655	274
29	7/17	496	163	313	20	333	163
30	7/24	179	54	117	8	125	54
31	7/31	188	71	110	7	117	71
32-34	8/17	175	96	69	10	79	96
Run total:		14,068	2,795	10,705	568	11,273	2,795

(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 46 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 2011. 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
10-19	5/8	122	31.1	63.9	4.9	68.9	31.1
20	5/15	1,919	16.8	79.1	4.2	83.2	16.8
21	5/22	1,440	11.8	84.7	3.5	88.2	11.8
22	5/29	1,497	10.6	85.4	4.0	89.4	10.6
23	6/5	1,687	11.8	84.2	4.0	88.2	11.8
24	6/12	1,027	13.6	82.5	3.9	86.4	13.6
25	6/19	921	16.3	79.3	4.5	83.7	16.3
26	6/26	1,594	25.8	70.3	3.9	74.2	25.8
27	7/3	1,894	28.9	67.4	3.7	71.1	28.9
28	7/10	929	29.5	65.7	4.8	70.5	29.5
29	7/17	496	32.9	63.1	4.0	67.1	32.9
30	7/24	179	30.2	65.4	4.5	69.8	30.2
31	7/31	188	37.8	58.5	3.7	62.2	37.8
32-34	8/17	175	54.9	39.4	5.7	45.1	54.9
Run total(d):		14,068	19.8	76.2	4.0	80.2	19.8

(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 46 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 2011. 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
10-19	5/8	1,650	514	1,055	81	1,136	514
20	5/15	19,965	3,350	15,783	832	16,615	3,350
21	5/22	12,902	1,523	10,922	457	11,379	1,523
22	5/29	14,630	1,554	12,490	586	13,076	1,554
23	6/5	16,546	1,952	13,927	667	14,594	1,952
24	6/12	9,638	1,314	7,949	375	8,324	1,314
25	6/19	8,861	1,443	7,024	394	7,418	1,443
26	6/26	14,508	3,741	10,203	564	10,767	3,741
27	7/3	16,975	4,911	11,437	627	12,064	4,911
28	7/10	8,946	2,639	5,874	433	6,307	2,639
29	7/17	4,706	1,547	2,969	190	3,159	1,547
30	7/24	1,890	570	1,236	84	1,320	570
31	7/31	1,773	670	1,037	66	1,103	670
32-34	8/17	1,604	880	632	92	724	880
Run total:		134,594	26,608	102,538	5,448	107,986	26,608
95% CI:			(25,739-27,465)	(101,568-103,458)	(5,021-5,911)	(107,094-108,841)	(25,739-27,465)

(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 1/5/13.

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 2011.

						Scale samples:		Genetics samples:			
Statistical week(a)	**Sampling period 2011**	**Number of days**	**Wild run size(b)**	**Number of scale and genetics samples collected(c)**	**Number of scale and genetics systematic subsamples(d)**	**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**
10-20(f)	3/1-5/15	76	3,864	360	271	258	6.7	263	6.8	270	7.0
21	5/16-5/22	7	1,523	170	130	123	8.1	123	8.1	129	8.5
22	5/23-5/29	7	1,554	159	119	117	7.5	114	7.3	119	7.7
23	5/30-6/5	7	1,952	199	151	143	7.3	145	7.4	151	7.7
24	6/6-6/12	7	1,314	140	104	99	7.5	95	7.2	103	7.8
25	6/13-6/19	7	1,443	150	116	112	7.8	108	7.5	115	8.0
26	6/20-6/26	7	3,741	411	308	295	7.9	302	8.1	308	8.2
27	6/27-7/3	7	4,911	548	410	378	7.7	394	8.0	409	8.3
28	7/4-7/10	7	2,639	274	206	195	7.4	198	7.5	206	7.8
29	7/11-7/17	7	1,547	163	122	118	7.6	119	7.7	122	7.9
30-34(f)	7/18-8/17	31	2,120	221	167	161	7.6	162	7.6	167	7.9
Run total:		170	26,608	2,795	2,104	1,999	7.5	2,023	7.6	2,099	7.9

(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 46 fish misidentified as wild at the trap and later determined to be unclipped hatchery by PBT.

(d) Does not include 39 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.

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 2011.

Statistical week(a)	Sample period ending(b)	Number of samples aged	Smolt migration year (MY), brood year (BY), and age class (frequency):								
			MY2011		MY2010		MY2009		MY2008		
			BY09 1.0	BY08 2.0	BY08 1.1	BY07 2.1	BY07 1.2	BY06 2.2	BY07 0.3	BY06 1.3	BY05 2.3
10-20	5/15	258	-	-	3	-	142	1	-	112	-
21	5/22	123	-	-	7	1	79	-	-	36	-
22	5/29	117	-	-	15	1	77	1	-	23	-
23	6/5	143	-	-	14	1	79	2	-	47	-
24	6/12	99	-	-	20	1	57	1	-	20	-
25	6/19	112	-	-	22	1	65	-	-	24	-
26	6/26	295	-	-	43	1	176	2	-	73	-
27	7/3	378	-	-	57	-	195	1	-	125	-
28	7/10	195	-	-	52	-	93	2	-	47	1
29	7/17	118	1	-	34	1	59	6	-	17	-
30-34	8/17	161	11	2	30	1	63	9	1	35	9
Run total:		1,999	12	2	297	8	1,085	25	1	559	10

(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 2011. Percentages may not sum to 100.0% due to rounding error.

			Smolt migration year (MY), brood year (BY), and age class (percent):								
	Sample	Number	MY2011		MY2010		MY2009		MY2008		
Statistical week(a)	period ending(b)	of samples aged	BY09 1.0	BY08 2.0	BY08 1.1	BY07 2.1	BY07 1.2	BY06 2.2	BY07 0.3	BY06 1.3	BY05 2.3
10-20	5/15	258	-	-	1.2	-	55.0	0.4	-	43.4	-
21	5/22	123	-	-	5.7	0.8	64.2	-	-	29.3	-
22	5/29	117	-	-	12.8	0.9	65.8	0.9	-	19.7	-
23	6/5	143	-	-	9.8	0.7	55.2	1.4	-	32.9	-
24	6/12	99	-	-	20.2	1.0	57.6	1.0	-	20.2	-
25	6/19	112	-	-	19.6	0.9	58.0	-	-	21.4	-
26	6/26	295	-	-	14.6	0.3	59.7	0.7	-	24.7	-
27	7/3	378	-	-	15.1	-	51.6	0.3	-	33.1	-
28	7/10	195	-	-	26.7	-	47.7	1.0	-	24.1	0.5
29	7/17	118	0.8	-	28.8	0.8	50.0	5.1	-	14.4	-
30-34	8/17	161	6.8	1.2	18.6	0.6	39.1	5.6	0.6	21.7	5.6
Run total:		1,999	0.6	0.1	14.9	0.4	54.3	1.3	0.1	28.0	0.5

(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-8. Weekly gender frequencies of wild adult Chinook salmon sampled at Lower Granite Dam, spawn year 2011.

Statistical week(a)	Sample period ending(b)	Number of samples genotyped for gender	Gender (frequency):	
			Female	Male
10-20	5/15	263	112	151
21	5/22	123	40	83
22	5/29	114	36	78
23	6/5	145	61	84
24	6/12	95	27	68
25	6/19	108	25	83
26	6/26	302	105	197
27	7/3	394	148	246
28	7/10	198	46	152
29	7/17	119	42	77
30-34	8/17	162	54	108
Run total:		2,023	696	1,327

(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 2011. 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
10-20	5/15	263	42.6	57.4
21	5/22	123	32.5	67.5
22	5/29	114	31.6	68.4
23	6/5	145	42.1	57.9
24	6/12	95	28.4	71.6
25	6/19	108	23.1	76.9
26	6/26	302	34.8	65.2
27	7/3	394	37.6	62.4
28	7/10	198	23.2	76.8
29	7/17	119	35.3	64.7
30-34	8/17	162	33.3	66.7
Run total:		2,023	34.4	65.6

(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 2011. Only individual fish whose assignment probability was ≥0.80 and had both a determined sex and a total age are included (n = 1,368); fish whose assignment probability was <0.80 are excluded. See Appendix Table B-2 for stock abbreviations.

		Smolt migration year (MY), brood year (BY), and age class (frequency)									
		MY2011		MY2010		MY2009		MY2008			
Genetic stock	Sex	BY09 1.0	BY08 2.0	BY08 1.1	BY07 2.1	BY07 1.2	BY06 2.2	BY07 0.3	BY06 1.3	BY05 2.3	Total sample
UPSALM	F	0	0	2	1	22	0	0	36	0	61
	M	0	0	20	0	99	1	0	27	0	147
	Total:	0	0	22	1	121	1	0	63	0	208
MFSALM	F	0	0	1	0	20	0	0	45	0	66
	M	0	0	43	1	80	0	0	25	0	149
	Total:	0	0	44	1	100	0	0	70	0	215
CHMBLN	F	0	0	0	0	8	0	0	3	0	11
	M	0	0	13	0	11	0	0	4	0	28
	Total:	0	0	13	0	19	0	0	7	0	39
SFSALM	F	0	0	0	0	25	0	0	30	0	55
	M	0	0	30	0	56	1	0	21	0	108
	Total:	0	0	30	0	81	1	0	51	0	163
HELLSC	F	0	0	1	0	139	2	0	77	0	219
	M	0	0	95	2	269	1	0	60	0	427
	Total:	0	0	96	2	408	3	0	137	0	646
TUCANO	F	0	0	0	0	3	0	0	3	0	6
	M	0	0	5	1	1	0	0	3	0	10
	Total:	0	0	5	1	4	0	0	6	0	16
FALL	F	0	0	0	0	5	4	0	11	8	28
	M	12	2	5	2	12	14	1	3	2	53
	Total:	12	2	5	2	17	18	1	14	10	81
	Grand total:	12	2	215	7	750	23	1	348	10	1,368

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 2011. Only individual fish whose assignment probability was ≥0.80 and had both a determined sex and a total age are included (n = 1,368); fish whose assignment probability was <0.80 are excluded. See Appendix Table B-2 for stock abbreviations.

		Smolt migration year (MY), brood year (BY), and age class (percent)									
		MY2011		**MY2010**		**MY2009**		**MY2008**			
Genetic stock	**Sex**	**BY09 1.0**	**BY08 2.0**	**BY08 1.1**	**BY07 2.1**	**BY07 1.2**	**BY06 2.2**	**BY07 0.3**	**BY06 1.3**	**BY05 2.3**	**Sex ratio**
UPSALM	F	0.0	0.0	3.3	1.6	36.1	0.0	0.0	59.0	0.0	29.3
	M	0.0	0.0	13.6	0.0	67.3	0.7	0.0	18.4	0.0	70.7
	Total:	0.0	0.0	10.6	0.5	58.2	0.5	0.0	30.3	0.0	100.0
MFSALM	F	0.0	0.0	1.5	0.0	30.3	0.0	0.0	68.2	0.0	30.7
	M	0.0	0.0	28.9	0.7	53.7	0.0	0.0	16.8	0.0	69.3
	Total:	0.0	0.0	20.5	0.5	46.5	0.0	0.0	32.6	0.0	100.0
CHMBLN	F	0.0	0.0	0.0	0.0	72.7	0.0	0.0	27.3	0.0	28.2
	M	0.0	0.0	46.4	0.0	39.3	0.0	0.0	14.3	0.0	71.8
	Total:	0.0	0.0	33.3	0.0	48.7	0.0	0.0	17.9	0.0	100.0
SFSALM	F	0.0	0.0	0.0	0.0	45.5	0.0	0.0	54.5	0.0	33.7
	M	0.0	0.0	27.8	0.0	51.9	0.9	0.0	19.4	0.0	66.3
	Total:	0.0	0.0	18.4	0.0	49.7	0.6	0.0	31.3	0.0	100.0
HELLSC	F	0.0	0.0	0.5	0.0	63.5	0.9	0.0	35.2	0.0	33.9
	M	0.0	0.0	22.2	0.5	63.0	0.2	0.0	14.1	0.0	66.1
	Total:	0.0	0.0	14.9	0.3	63.2	0.5	0.0	21.2	0.0	100.0
TUCANO	F	0.0	0.0	0.0	0.0	50.0	0.0	0.0	50.0	0.0	37.5
	M	0.0	0.0	50.0	10.0	10.0	0.0	0.0	30.0	0.0	62.5
	Total:	0.0	0.0	31.3	6.3	25.0	0.0	0.0	37.5	0.0	100.0
FALL	F	0.0	0.0	0.0	0.0	17.9	14.3	0.0	39.3	28.6	34.6
	M	22.6	3.8	9.4	3.8	22.6	26.4	1.9	5.7	3.8	65.4
	Total:	14.8	2.5	6.2	2.5	21.0	22.2	1.2	17.3	12.3	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 2011. Only individual fish whose assignment probability was ≥0.80 and had both a determined sex and a total age (n = 1,368) were used; fish whose assignment probability was <0.80 were excluded. See Appendix Table B-2 for stock abbreviations.

		Smolt migration year (MY), brood year (BY), and age class (abundance)									
		MY2011		MY2010		MY2009		MY2008			
Genetic stock	Sex	BY09 1.0	BY08 2.0	BY08 1.1	BY07 2.1	BY07 1.2	BY06 2.2	BY07 0.3	BY06 1.3	BY05 2.3	Total abundance
UPSALM	F	0	0	41	20	448	0	0	733	0	1,242
	M	0	0	407	0	2,017	20	0	550	0	2,994
	Total:	0	0	448	20	2,465	20	0	1,283	0	4,236
MFSALM	F	0	0	18	0	366	0	0	822	0	1,206
	M	0	0	786	18	1,462	0	0	457	0	2,723
	Total:	0	0	804	18	1,828	0	0	1,279	0	3,929
CHMBLN	F	0	0	0	0	113	0	0	42	0	155
	M	0	0	184	0	155	0	0	57	0	396
	Total:	0	0	184	0	268	0	0	99	0	551
SFSALM	F	0	0	0	0	840	0	0	1,009	0	1,849
	M	0	0	1,008	0	1,882	34	0	706	0	3,630
	Total:	0	0	1,008	0	2,722	34	0	1,715	0	5,479
HELLSC	F	0	0	17	0	2,378	34	0	1,317	0	3,746
	M	0	0	1,625	34	4,602	17	0	1,026	0	7,304
	Total:	0	0	1,642	34	6,980	51	0	2,343	0	11,050
TUCANO	F	0	0	0	0	45	0	0	44	0	89
	M	0	0	75	15	15	0	0	44	0	149
	Total:	0	0	75	15	60	0	0	88	0	238
FALL	F	0	0	0	0	69	56	0	153	111	389
	M	167	28	69	28	167	193	14	42	28	736
	Total:	167	28	69	28	236	249	14	195	139	1,125

Prepared by:

William C. Schrader
Principal Fishery Research Biologist

Matthew P. Corsi
Regional Fisheries Biologist

Patrick Kennedy
Senior Fishery Research Biologist

Michael W. Ackerman
Fishery Research Biologist

Matthew R. Campbell
Fisheries Genetics Program Coordinator

Kristin K. Wright
Fishery Research Biologist

Timothy Copeland
Senior Fishery Research Biologist

Approved by:

IDAHO DEPARTMENT OF FISH AND GAME

Peter F. Hassemer
Anadromous Fisheries Manager

Edward B. Schriever, Chief
Bureau of Fisheries