FISHERY RESEARCH

WILD JUVENILE STEELHEAD AND CHINOOK SALMON ABUNDANCE AND COMPOSITION AT LOWER GRANITE DAM, MIGRATORY YEARS 2010 AND 2011

2010-2011 ANNUAL REPORT

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IDFG Report Number 13-17
August 2013

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2010-2011 Annual Report

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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, 45995, 48347, 50973, 50975, 59800

IDFG Report Number 13-17
August 2013

ACKNOWLEDGEMENTS

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ACKNOWLEDGEMENTS (CONTINUED)

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

- Bonneville Power Administration (via the following 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 at Lower Granite Dam

- Idaho Office of Species Conservation

- Pacific States Marine Fisheries Commission (PSMFC)

- Northwest Power and Conservation Council

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

Suggested citation:

Copeland, T., M. W. Ackerman, M. P. Corsi, P. Kennedy, K. K. Wright, M. R. Campbell, and W. C. Schrader. 2013. Wild juvenile steelhead and Chinook salmon abundance and composition at Lower Granite Dam, migratory years 2010 and 2011. Idaho Department of Fish and Game Report 13-17. Annual report 2010-2011, BPA Projects 1990-055-00, 1991-073-00, 2010-026-00.

ABBREVIATIONS AND ACRONYMS

BPA	Bonneville Power Administration
BY	Brood Year
CI	Confidence Interval
CWT	Coded Wire Tag
DPS	Distinct Population Segment
ESA	Endangered Species Act
ESU	Evolutionarily Significant Unit
FL	Fork Length
GSI	Genetic Stock Identification
IA	Individual Assignment
ICBTRT	Interior Columbia Basin Technical Recovery Team
IDFG	Idaho Department of Fish and Game
LGR	Lower Granite Dam
MPG	Major Population Group
MY	Smolt Migration Year
NMFS	National Marine Fisheries Service
PBT	Parentage Based Tagging
PIT	Passive Integrated Transponder
PSMFC	Pacific States Marine Fisheries Commission
SNP	Single Nucleotide Polymorphism
WDFW	Washington Department of Fish and Wildlife

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ABSTRACT

Juvenile production is one measure of the biological capacity of a population and is important for understanding the life cycle survival of ESA listed steelhead and Chinook salmon stocks. Using systematic sampling and genetic techniques, we sampled smolts at the Lower Granite Dam Juvenile Fish Facility and estimated the origin, genetic stock, and sex of steelhead and Chinook salmon smolts for migration years 2010 and 2011.

For migration year 2010, nearly 1 million steelhead smolts and 1.2 million Chinook salmon smolts emigrated past Lower Granite Dam. Two brood years (BYs) dominated the 2010 steelhead emigration: BY 2007 (50%) and BY 2008 (40%). Sex ratio was slightly skewed toward females for both species. Steelhead abundances were dominated by the Upper Salmon River (16%) and Grande Ronde River (15%) genetic stocks. The B-run steelhead genetic stocks (Middle Fork Salmon River, South Fork Salmon River, South Fork Clearwater River and Upper Clearwater River) contributed 35% of the migrants in 2010. The Chinook salmon smolt emigration was dominated (41%) by the Hells Canyon genetic stock (which includes Rapid, Clearwater, Imnaha, Grande Ronde, and lower Snake rivers) with the Upper Salmon River and Middle Fork Salmon River genetic stocks comprising 40%. Spring/summer Chinook genetic stocks comprised 6% of the subyearling smolt production through July 31).

Smolt abundances for migration year 2011 were similar to 2010 for both species. Two BYs accounted for almost 90% of the steelhead smolt emigration: BY 2009 (61%) and BY 2008 (28%). Steelhead sex ratios were again skewed toward females but Chinook salmon smolts were slightly male skewed. Steelhead abundances were dominated by the Grande Ronde River (17.5%) and Upper Salmon River (12.7%) genetic stocks. The B-run steelhead genetic stocks contributed 30% of the migrants in 2011. The Chinook salmon yearling smolt outmigration was again dominated (37%) by the Hells Canyon genetic stock, with the Upper Salmon and Middle Fork Salmon again comprising 40%. Spring/summer Chinook genetic stocks comprised 13% of subyearling smolt production.

This report is the first attempt at a complete stock assessment for the emigration of wild steelhead and spring/summer Chinook salmon smolts from the Snake River. Over time the information will allow us to estimate adult-to-juvenile and juvenile-to-adult productivity. Some patterns are emerging but data necessary to compute productivity accumulate over time and it will take 4-5 years before the first productivity estimate for steelhead is complete.

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INTRODUCTION

Populations of steelhead trout *Oncorhynchus mykiss* and Chinook salmon *O. tshawytscha* in the Snake River basin declined substantially following the construction of hydroelectric dams in the Snake and Columbia rivers. Raymond (1988) documented a decrease in survival of emigrating steelhead trout and Chinook salmon from the Snake River following the construction of dams on the lower Snake River during the late 1960s and early 1970s. Abundance rebounded slightly in the early 1980s, but then adult escapement over Lower Granite Dam (LGR) into the Snake River basin declined again (Busby et al. 1996). In recent years, abundances in the Snake River basin have slightly increased. However, the increase has been dominated by hatchery fish, while returns of naturally produced steelhead and Chinook salmon remain depressed.

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; ICBTRT 2003, 2005; NMFS 2011). The Hells Canyon MPG is considered to be extirpated. Twenty-four extant demographically independent populations have been identified within 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 five major population groups: Lower Snake River, Grande Ronde/Imnaha rivers, South Fork Salmon River, Middle Fork Salmon River, and Upper Salmon River. Twenty-nine extant demographically independent populations have been identified within 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 – and recovery planning and implementation efforts aimed at recovering ESA-listed wild steelhead and salmon stocks. The long-range goal of Idaho Department of Fish and Game's anadromous fish program, consistent with basin-wide mitigation and recovery programs, is to preserve Idaho's salmon and steelhead runs and recover them to provide benefit to all users (IDFG 2013). Management to achieve these goals requires an understanding of how salmonid populations function as well as regular status assessments (McElhany et al. 2000). However, specific data on Snake River steelhead and Chinook salmon populations are lacking, particularly key parameters such as population abundance, age composition, genetic diversity, recruits per spawner, and survival rates (ICBTRT 2003). The key metrics to assessing viability of salmonid populations are abundance, productivity, spatial structure, and diversity (McElhany et al. 2000).

Juvenile production is one measure of the biological capacity of a population and is important for understanding the life cycle survival of ESA listed steelhead and Chinook salmon stocks. The aggregate emigration of smolts from Snake River steelhead and spring/summer Chinook salmon populations is measured at LGR, with the exception of the Tucannon River (Washington) populations. Some wild fish originate from Washington or Oregon tributaries, but the majority are from Idaho. Age, sex, and genetic stock composition data obtained at the LGR Juvenile Fish Facility enables estimation of productivity and survival metrics that are important for monitoring recovery of wild fish for both species. Productivity is the generational replacement rate, defined as the number of progeny surviving to adulthood per parent (i.e. recruits per

spawner). Conversion of progeny to adulthood (smolt-to-adult return rate [SAR]) is an important survival metric to monitor. Estimates of wild smolt abundance and composition will be combined with similar information for adults (e.g. Schrader et al. 2012); enabling us to estimate adult-to-juvenile, juvenile-to-adult, and adult-to-adult productivity and survival metrics for each component of the aggregate populations sampled at LGR.

This report summarizes the abundance and composition of wild juvenile steelhead and spring/summer Chinook salmon emigrating past LGR during smolt migration years (MY) 2010 and 2011. Spring/summer Chinook smolts primarily emigrate as yearlings. However, some spring/summer Chinook populations produce subyearling smolts (Connor et al. 2001; Copeland and Venditti 2009); therefore, we also collected samples from subyearling Chinook to estimate that component of the ESU smolt production. 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

Juvenile Trap Operations at Lower Granite Dam

Samples of steelhead and Chinook salmon passing LGR were collected during daily operation of the Juvenile Fish Facility by Washington Department of Fish and Wildlife (WDFW; BPA project 1987-127-00, Smolt Monitoring Project; Mensik et al. 2010). The juvenile trap is located on the LGR juvenile bypass system. The trap captures a systematic sample of fish by operating two trap gates according to a predetermined sample rate. The sample rate determines how long the trap gates remain open, up to six times per hour. The trap is operational 24 hours per day and fish are processed every morning. Additional details on the juvenile trap can be found in Mensik et al. (2010). Sample rate is predetermined daily to collect 250-750 fish per day (all species combined) and is based on the expected number of fish entrained in the bypass system that day.

Standard methods were used by WDFW and Idaho Department of Fish and Game (IDFG) staff to process juvenile fish (see Mensik et al. 2010 and Appendix A). All fish captured were anesthetized; identified to species; examined for external marks, tags, and injuries; and scanned for an internal coded wire tag (CWT) or passive integrated transponder (PIT) tag. 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 population supplementation purposes. For unclipped steelhead, hatchery origin was additionally determined by the presence of dorsal or ventral fin erosion, which is assumed to occur only in hatchery-reared fish (Latremouille 2003). Captured fish determined to be potentially wild were subsampled for tissue (both species) and scales (steelhead only). The trap sample was sorted and processed by WDFW personnel and the subsample passed to IDFG technicians. Fish bearing PIT tags and/or diseased or injured fish were omitted from the subsample, as were Chinook deemed to be yearling fall Chinook based on external morphology (Tiffan et al. 2000). Target sample sizes were 2,000 per species for steelhead and yearling Chinook and 500 subyearling Chinook for the trapping season. All subsampled fish were

measured for fork length (FL, to the nearest millimeter). After processing, all fish were returned to the bypass system to resume downstream migration.

Scale samples were taken from steelhead smolts above the lateral line and posterior to the dorsal fin (Appendix A). Scales 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 caudal fin from both species. Tissues were stored in a vial with 200-proof non-denatured ethyl alcohol for transport to the IDFG Eagle Fish Genetics Laboratory (EFGL) in Eagle, Idaho.

Scale Processing and Analysis

Technicians processed scale samples in the IDFG Anadromous Aging Laboratory. Scales were examined for regeneration and 6-10 non-regenerated 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 the fish and saved them as digitized images. The entire scale 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.

Annuli were defined by pinching or cutting-over of circuli. We used only visible annuli formed on the scales. Fish lacking a determined age were not used for analysis. In this report, total age equals freshwater age, so we do not use the aging designations developed for anadromous salmonids and report age as an integer.

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 steelhead, all individuals were genotyped at 191 SNPs (including three SNPs that differentiate *O. mykiss* and *O. clarkii* and identify potential hybrids) and a sex-specific assay that differentiates sex in *O. mykiss*. For Chinook salmon, MY 2010 individuals were genotyped at 95 SNPs; MY 2011 individuals were genotyped at 191 SNPs. All individuals were genotyped using a sex-specific assay that differentiates sex in *O. tshawytscha*. Genotyping was performed using Fluidigm® 96.96 Dynamic Array™ IFCs (chips). Chips were imaged on a Fluidigm EP1™ and analyzed 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).

Individual assignment (IA) tests for MY 2010 steelhead and MY 2011 steelhead and Chinook smolts were done using Snake River genetic baselines v2.0 described in Ackerman et al. (2012). Steelhead and Chinook salmon populations throughout the Snake River basin potentially contributing to smolt emigration at LGR have previously been screened at the 191 *O. mykiss* and *O tshawytscha* SNP assays mentioned above (see Ackerman et al. 2012, their Objective 2). MY 2010 Chinook were analyzed using baseline samples in v2.0, but with only the 95 SNPs described in Snake River Chinook baseline v1.0 (Ackerman et al. 2011). SNP allele frequency estimates from baseline collections are the reference information for IA tests. Fish sampled at the LGR Juvenile Fish Facility were genotyped at the same SNPs and genotype data were used to assign individual fish back to their population of origin (Pella and Milner 1987,

Shaklee et al. 1999). In IA, the probability that each individual (i.e. smolt) originates from a baseline population is calculated based on the likelihood that the individual's genotype belongs to that population, given baseline allele frequency estimates. Individual population estimates were first calculated and then summed into genetic stock estimates (allocate-sum procedure; Wood et al. 1987). Genetic stocks are assemblages of reference (baseline) populations grouped primarily by genetic and geographic similarities and secondarily by political boundaries and/or management units (Ackerman et al. 2011). IA of smolts to the "best-estimate" genetic stock of origin is based on the genetic stock with the highest probability that the smolt's genotypes originated from for each particular fish. Ackerman et al. (2012) provide a thorough analysis of the resolution of the Snake River genetic baselines for both steelhead and Chinook salmon.

Ten wild steelhead genetic stocks were used during IA analyses (Figure 1; Appendix Table B-1). Genetic stocks include: 1) UPSALM: the upper Salmon River; 2) MFSALM: Middle Fork Salmon River (including Chamberlain and Bargamin creeks); 3) SFSALM: South Fork Salmon River; 4) LOSALM: lower Salmon River; 5) UPCLWR: upper Clearwater River (Lochsa and Selway rivers); 6) SFCLWR: South Fork Clearwater River (including Clear Creek); 7) LOCLWR: lower Clearwater River; 8) IMNAHA: Imnaha River; 9) GRROND: Grande Ronde River; and 10) LSNAKE: Asotin Creek and tributaries to the Snake River downstream of the Clearwater River confluence. Results from some genetic stocks are aggregated to report by Snake River steelhead MPGs (Appendix Table B-1).

Seven wild Chinook salmon genetic stocks were used during IA analyses (Figure 2; Appendix Table B-2). Genetic stocks include: 1) UPSALM: upper Salmon River; 2) MFSALM: Middle Fork Salmon River; 3) CHMBLN: Chamberlain Creek; 4) SFSALM: South Fork Salmon River; 5) HELLSC: an aggregate genetic stock that includes the Little Salmon, Clearwater, Grande Ronde, and Imnaha rivers; 6) TUCANO: Tucannon River, and 7) FALL: Snake River fall Chinook salmon. Results from CHMBLN and MFSALM are aggregated to report for the Middle Fork Salmon River MPG (Appendix Table B-2). The TUCANO genetic stock was included in the baseline to identify emigrants that may be progeny of adults originating from the Tucannon River that successfully spawned upstream of LGR. Three collections of Snake River fall Chinook salmon (see Table 2 in Ackerman et al. 2012) were included in the baseline (FALL genetic stock); our intention was to differentiate fall Chinook salmon from spring/summer Chinook salmon.

The sex of each individual was determined using sex-specific genetic assays for *O. mykiss* and *O. tshawytscha* (Ackerman et al. 2012, Steele et al. 2012). Individuals that amplify only at the autosomal control region are determined to be females. Individuals that amplify at both the autosomal control region and a region associated with the Y-chromosome are determined to be males (Campbell et al. 2012).

Emigration by Origin, Age, Sex, and Genetic Stock

Smolt production was estimated using daily counts of putative wild smolts collected in the LGR juvenile fish trap, the trap sample rate, and estimated daily collection efficiencies (probability of entrainment in the juvenile bypass system at the dam). The daily counts of all steelhead and Chinook smolts at LGR during March-July as well as the trap sample rates were obtained from the Fish Passage Center (Brandon Chockley, personal communication). The estimated daily smolt collection efficiencies were obtained from the Northwest Fisheries Science Center (Steve Smith, personal communication). Efficiencies for steelhead, yearling Chinook, and subyearling Chinook were estimated using procedures detailed in Sandford and Smith (2002). The total number of smolts was estimated as

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

where *s* is species (steelhead, yearling Chinook, subyearling Chinook), N_s is abundance by species, *d* is day of the year, c_{sd} is the daily count in the trap by species, t_d is the daily trapping rate, and e_{sd} is the estimated daily collection efficiency for each species. Total abundance for each species during a MY was estimated from the sums of daily estimates beginning at initiation of trapping until the end of July. Note that the population sampling rate is the product of t_d and e_{sd} and changes almost daily.

To estimate emigration by origin, age, sex, or stock, the daily abundance estimates were combined with trap sample data on a statistical week basis to account for changes in the trapping rate and bypass efficiency 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 approximately 100 sampled fish. The weekly proportions were applied to the estimated total emigration for each week. Because the actual population sampling rate changes almost daily, individual data points (fish) were weighted by the daily population sampling rate to calculate weekly proportions.

Confidence intervals for all point estimates were computed using a bootstrapping algorithm (Manly 1997). There are two sources of sampling error in the decomposed emigration estimates: variance in the estimated number of wild fish and variance in estimates of age, sex, and genetic stock proportions. To account for these sources of variability when estimating abundance by age, sex, and genetic stock, we used a compound bootstrap routine: a parametric bootstrap for the estimate of total wild abundance (by week) and a nonparametric bootstrap by week of the biological sample data (age, sex, and genetic stock). The number of smolts trapped per day was considered a series of Bernoulli trials, where N_i is the true number of smolts passing the trap for day *i* and each smolt is trapped with probability p_i. A bootstrap value of trap catch *c* for day *i* is generated by taking a random value from $c_i^* \sim Binomial(N_i, p_i)$, where $p_i = t_d \times e_{sd}$ as above. Given a bootstrap value for the number of smolts trapped on day *i*, we get a bootstrap value for the number of smolts arriving for day *i* using the equation within the summation above. Summing over days we get a bootstrap value for the total number of wild smolts. If we produce many bootstrap values and order them, then the 100(1-α)% confidence interval is found by moving in α/2 proportion of the way from either extreme.

Given the bootstrap values for total wild smolts, we can get bootstrap values for the *numbers* of smolts of each age, sex, and genetic stock if we can get bootstrap values for the *proportions* of smolts in each respective group. Proportions may change throughout the trapping season, which we address by grouping all the fish trapped by week (or a collection of weeks if very few fish are trapped and analyzed). Each of these periods is referred to as a "statistical week." We assume that the proportions are roughly stable for a week. We would like to know the true proportions, e.g., of ages 1 to 5 $(\pi_{1t}, \pi_{2t}, \pi_{3t}, \pi_{4t}, \pi_{5t})$ for t = 1,…, T where T is the number of statistical weeks. If the capture rate for fish of different groups was uniform, then we would estimate the proportions of fish of each age in period *t* by the proportion of fish of each age for that statistical week. However, we know from above that the capture rate, p_i, is changing every day. In addition, not all trapped fish are analyzed so the realized capture rate of a group of fish analyzed on day *i* is $p_i \times \frac{a_i}{c_i}$ where a_i is the number of smolts analyzed. If a_{ji} is the number

of fish of group *j* on day *i*, we get an estimate of the number of smolts of each group for statistical week t as

$$A_{jt} = \sum_{i \text{ in } t} \frac{a_{ji}}{p_i \times \frac{a_i}{c_i}} = \sum_{i \text{ in } t} \sum_{fish\ on\ day\ i} \frac{1}{p_i \times \frac{a_i}{c_i}}.$$

Note that the realized probability of capture is assumed to be the same for all of the fish aged on a given day. For each statistical week, we resample the fish aged for that week with replacement and with probabilities equal to the realized sample rate for each fish. For each iteration, proportions are multiplied by the bootstrap abundance for each statistical week to get estimates of the numbers of smolts in each group.

We conducted the compound bootstrap procedure 5,000 times. For each iteration, the number of wild fish and the numbers of wild fish of various ages, sex, or stock were computed. The one-at-a-time bootstrap intervals were found by finding the 2.5th and 97.5th percentiles of the 5,000 ordered bootstrap values for each group (i.e., $\alpha = 0.05$). 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. The algorithm was written and implemented in the R programming environment (R Development Core Team 2008) by Kirk Steinhorst (University of Idaho).

In order to estimate total abundance for each genetic stock and MPG, we used the genetic stock (or MPG) from which an individual's genotype most likely originated. However, when estimating sex (both species) and age (for steelhead) proportions within each genetic stock, we applied a probability threshold in order to be more conservative with the subdivided data. Because the accuracy of assignment declines with decreased assignment probabilities, only individuals with ≥80% probability of assignment to a particular genetic stock were considered 'assigned' and were used to calculate stock-by-sex-by-age proportions within each genetic stock. Individuals assigning with <80% probability were dropped from this analysis. We assumed that probability of assignment was equivalent between sexes and among ages. Sex and age proportions were calculated using all individuals (across the entire emigration) that assigned to each genetic stock with ≥80% probability; proportions were multiplied by abundance for each genetic stock (determined using all genotyped fish as on p. 6) to get abundance by age/sex group within each stock.

RESULTS

Migratory Year 2010

During 2010, the trap was operated from March 25 to October 31. Collection of biological samples for this project did not start until April 27 and concluded the week of July 4. The last unclipped yearling Chinook smolt passing through the juvenile trap was counted on July 2 and the last unclipped wild steelhead smolt on July 15. The trap sample rate started at 20% on April 1 and changed 14 times during the study period. The average trap rate for April – July was 8% and ranged from 1% to 20%.

Steelhead Emigration

For MY 2010 – from March 27, 2010 to July 31, 2010 – 11,341 steelhead were collected at the LGR Juvenile Fish Facility (Figure 1); of these, 1,899 fish were judged to be wild. The first wild steelhead was collected on March 27, 2010, and the last was collected on July 15, 2010. Daily efficiency estimates for steelhead smolts in the bypass system ranged from 8.1% to 73.9% and averaged 24.6% (Figure 2). The total estimated smolt abundance was 926,771 wild steelhead (95% CI 875,376-978,168 smolts; Figure 3).

Wild Steelhead Age, Sex, and Stock Composition

A total of 1,352 wild steelhead smolts were sampled and considered valid (Appendix Table C-1). The first sample was collected on April 27, 2010, and the last was collected on July 1, 2010. We assigned total age to 1,323 samples. We assigned sex to 1,262 samples. We obtained complete genotype data (≥90% of SNPs amplify successfully) for 1,233 samples.

We observed individuals aged 1 to 5 years from the 1,323 fish that we assigned a total age (Appendix Table C-2). We estimate that 1.1% of the wild return was from brood year (BY) 2009; 40.0% from BY2008; 50.1% from BY2007; 8.4% from BY2006; and 0.4% from BY2005 (Appendix Tables C-3-4).

Estimated emigration to LGR by age was 10,316 fish for BY2009 (95% CI 4,502-16,673); 370,765 fish for BY2008 (95% CI 304,173-436,133); 464,502 fish for BY2007 (95% CI 393,759-558,647); 77,556 fish for BY2006 (95% CI 53,660-106,257); and 3,632 fish for BY2005 (95% CI 0-10,766). Estimated emigration to LGR by age is shown in Figure 4 and Appendix Table C-4.

Of the 1,262 fish for which sex was successfully determined using the sex-specific genetic assay, 713 were female and 549 were male (Appendix Table C-4). Percentages for the entire run were 53.2% female and 46.8% male (Appendix Table C-5). Estimated wild smolt emigration was 493,445 females (95% CI 445,708-553,934) and 433,326 males (95% CI 382,203-480,610; Figure 5).

Based on IA results using the 1,233 fish with complete genotypes (Appendix Table C-6), we estimate that 16.0% of the wild emigration originated from the UPSALM genetic stock; 10.3% from MFSALM; 2.9% from SFSALM; 5.5% from LOSALM; 10.0% from UPCLWR; 11.4% from SFCLWR; 8.4% from LOCLWR; 7.5% from IMNAHA; 15.3% from GRROND; and 12.7% from LSNAKE (Appendix Tables C-7). Aggregating by MPG, 34.7% of the wild emigration originated from Salmon River; 29.8% from Clearwater River; 7.5% from Imnaha River; 15.3% from Grande Ronde River; and 12.7% from Lower Snake River.

Estimated smolt emigration to LGR by genetic stock was 147,822 smolts from the UPSALM genetic stock (95% CI 113,905 – 197,733); 95,388 smolts from MFSALM (95% CI 67,286 – 136,124); 26,774 smolts from SFSALM (95% CI 15,801 – 45,606); 51,427 smolts from LOSALM (95% CI 35,504 – 79,838); 92,261 smolts from UPCLWR (95% CI 67,721 – 135,420); 106,772 smolts from SFCLWR (95% CI 74,811 – 141,853); 77,687 smolts from LOCLWR (95% CI 50,300 – 105,262); 69,907 smolts from IMNAHA (95% CI 41,694 – 93,496); 141,485 smolts from GRROND (95% CI 103,220 – 179,975); and 117,248 smolts from LSNAKE (95% CI 86,243 – 157,815; Figure 6). Aggregating by MPG, estimated emigration to LGR was 321,411 smolts from Salmon River (95% CI 279,161 – 392,598); 276,720 smolts from Clearwater River

(95% CI 227,893 – 330,181); the Imnaha, Grande Ronde and Lower Snake MPGs are as above. Abundance estimates by statistical week are presented in Appendix Table C-8.

Of the 1,233 fish with complete genotypes, 578 (46.9%) assigned to a stock with ≥80% probability. Of the 578 assigned fish, 541 had both a determined sex and total age and were used for genetic stock decomposition (Appendix Table C-9). Percentages of sex by age were calculated for each stock (Appendix Table C-10) and were applied to the MY 2010 genetic stock emigration estimates (Appendix Table C-11).

Chinook Salmon Emigration

For MY 2010 – from March 27, 2010 to July 31, 2010 – a total of 12,584 yearling Chinook salmon were collected at the Juvenile Fish Facility (Figure 1); of these, 2,383 fish were judged to be wild. The first wild yearling was collected on March 28, 2010, and the last was collected on July 27, 2010. Daily efficiency estimates for yearling Chinook salmon smolts in the bypass system ranged from 3.6% to 54.3% and averaged 25.4% (Figure 2). The total estimated wild yearling smolt abundance was 1,212,407 fish (Figure 3).

During the same period, 18,552 subyearling Chinook salmon were collected Figure 1), of which 11,641 were judged to be wild. The first wild subyearling was collected on April 25, 2010 but most were collected in June and July. Daily efficiency estimates for subyearling Chinook salmon smolts in the bypass system ranged from 4.9% to 81.0% and averaged 12.3% (Figure 2). The total estimated wild subyearling smolt abundance was 3,036,829 fish (Figure 3).

Wild Chinook Salmon Age, Sex, and Stock Composition

Yearlings—A total of 1,419 yearling Chinook salmon smolts were sampled and considered valid (Appendix Table D-1). The first sample was collected on April 27, 2010, and the last was collected on July 2, 2010. We were able to assign sex to 1,322 samples. We were able to obtain complete genotype data (≥90% of SNPs amplify successfully) for 1,400 samples.

Of the 1,322 yearlings that sex was successfully determined using the sex-specific assay, 787 were female and 535 were male (Appendix Table D-2). Sex percentages for the entire run were 55.6% female and 44.4% male (Appendix Table D-3). Expanding the overall percentages to the wild run gives 674,361 females (95% CI 632,858-778,018) and 538,046 males (95% CI 444,474-574,911; Figure 7).

Based on IA results using the 1,400 fish with complete genotypes (Appendix Table D-4), we estimate that 21.9% of the wild yearling Chinook emigration originated from the UPSALM genetic stock; 18.8% from MFSALM; 4.7% from CHMBLN; 11.4% from SFSALM; 41.4% from HELLSC; and 0.9% from TUCANO (Appendix Table D-5). Aggregating the MFSALM and CHMBLN genetic stocks; 23.5% of the wild yearling Chinook smolt emigration originated from the Middle Fork Salmon River MPG. The remaining 0.9% of yearlings were identified as fall Chinook salmon based on multi-locus SNP data.

Estimated yearling smolt emigration to LGR by stock was 266,042 fish from the UPSALM genetic stock (95% CI 199,576 – 354,210); 228,454 smolts from MFSALM (95% CI 176,647 – 319,705); 57,063 smolts from CHMBLN (25,001 – 82,519); 137,702 smolts from SFSALM (95% CI 94,598 – 198,876); 501,724 smolts from HELLSC (95% CI 389,593 – 625,592); and 10,975 smolts from TUCANO (95% CI 2,775 – 23,277; Figure 8). Aggregating the MFSALM and CHMBLN genetic stocks; 285,517 wild yearling smolts (95% CI 221,983 –

369,782) originated from the Middle Fork Salmon River MPG. We estimate that 10,447 yearling smolts originated from fall Chinook salmon stocks (95% CI 7,463 – 21,962). Genetic stock emigration estimates by statistical week are presented in Appendix Table D-6.

Of the 1,400 yearling smolts with complete genotypes, 684 (48.9%) assigned to a stock with ≥80% probability. Of the 684 assigned fish, 652 had a determined sex and were used for estimates of sex ratios for each stock and were applied to the MY 2010 stock emigration estimates (Appendix Table D-7). Sufficient assignments were not made to the TUCANO genetic stock to estimate sex ratios and abundance.

Subyearlings—A total of 500 subyearling Chinook salmon smolts were sampled and considered valid (Appendix Table E-1). The first sample was collected on May 20, 2010, and the last was collected on July 8, 2010. We were able to assign sex to 462 samples. We were able to obtain complete genotype data (≥90% of SNPs amplify successfully) for 498 samples.

Of the 462 subyearlings that sex was successfully determined using the sex-specific assay, 257 were female and 205 were male (Appendix Table E-2). Sex percentages for the entire run were 50.5% female and 49.5% male (Appendix Table E-3). The sex ratio was male-biased at the beginning of the run but became female-biased during the latter half of sampling. Percentage of females ranged from 42.8% to 68.7%. Expanding the overall percentages to the wild run gives 1,533,690 females (95% CI 1,383,514-1,830,586) and 1,503,139 males (95% CI 1,218,779-1,658,949; Figure 9).

Of the 498 subyearling Chinook smolts with complete genotype data (Appendix Table E-4), 6.0% were estimated to originate from spring/summer stocks. Of those, we estimate that 20.6% originated from the UPSALM genetic stock; 4.9% from MFSALM; 4.4% from CHMBLN; 66.1% from HELLSC; and 1.5% from TUCANO (Appendix Table E-5). Aggregating the MFSALM and CHMBLN genetic stocks; 9.3% of the spring/summer subyearling smolt emigration originated from the Middle Fork Salmon River MPG. The remaining 94.0% of subyearlings were identified as fall Chinook salmon based on multi-locus SNP data.

Of the total estimated wild subyearling abundance of 3,036,829 smolts, we estimate that 182,375 originated from spring/summer stocks. Estimated subyearling smolt emigration to LGR by spring/summer stock was 37,592 fish from the UPSALM genetic stock; 8,925 smolts from MFSALM; 8,011 smolts from CHMBLN; 120,478 smolts from HELLSC; and 2,756 smolts from TUCANO (Figure 10). Aggregating the MFSALM and CHMBLN genetic stocks; 16,936 wild subyearling smolts originated from the Middle Fork Salmon River MPG. We estimate that 2,854,454 subyearling smolts originated from fall Chinook salmon stocks. Adequate genetic assignments were not made to spring/summer stocks to produce confidence intervals for estimates of abundance by genetic stocks or MPGs for subyearling smolts. Abundance estimates by statistical week are presented in Appendix Table E-6.

Of the 500 subyearling smolts sampled, we obtained complete genotype data from 498 fish. Of the 498 with complete genotype data, 478 (96.0%) assigned to a stock with ≥80% probability. Of the 478 assigned fish, 443 had a sex determined. However, there were not sufficient assignments to any spring/summer stocks for estimates of sex ratios within genetic stock (425 of 443 assignments were to FALL genetic stock).

Migratory Year 2011

During 2011, the trap was operated from March 26 to November 1. Collection of biological samples for this project started on March 29 and concluded July 9. The last unclipped yearling Chinook smolt passing through the juvenile trap was counted on July 16 and the last unclipped wild steelhead smolt on July 27. The trap sample rate started at 10% on April 1 and changed 18 times during the study period. The average trap rate was 3% and ranged from 0.5% to 20%.

Steelhead Emigration

For MY 2011 – from March 26, 2011 to July 31, 2011 – 20,728 steelhead were collected at the LGR Juvenile Fish Facility (Figure 11); of these, 2,494 fish were judged to be wild. The first wild steelhead was collected on March 26, 2011, and the last was collected on July 17, 2011. Daily efficiency estimates for steelhead smolts in the bypass system ranged from 21.7% to 76.4% and averaged 41.4% (Figure 12). The total estimated smolt abundance was 914,513 wild steelhead (95% CI 874,384-955,484 smolts; Figure 13).

Wild Steelhead Age, Sex, and Stock Composition

A total of 2,131 wild steelhead smolts were sampled and considered valid (Appendix Table F-1). The first sample was collected on March 29, 2011, and the last was collected on July 9, 2011. We were able to assign total age to 2,087 samples. We were able to assign sex to 1,987 samples. We were able to obtain complete genotype data (≥90% of SNPs amplify successfully) for 2,114 samples.

We observed individuals aged 1 to 5 years from the 2,087 fish that we were able to assign a total age (Appendix Table F-2). We estimate that 5.9% of the wild return was from brood year (BY) 2010; 60.8% from BY2009; 27.6% from BY2008; 5.4% from BY2007; and 0.3% from BY2006 (Appendix Table F-3).

Estimated emigration to LGR by age was 54,158 fish for BY2010 (95% CI 44,084-69,003); 556,218 fish for BY2009 (95% CI 498,811-627,318); 252,488 fish for BY2008 (95% CI 212,747-287,504); 49,342 fish for BY2007 (95% CI 36,375-63,141); and 2,307 fish for BY2006 (95% CI 0-5,016; Figure 14).

Of the 1,987 fish that sex was successfully determined using the sex-specific genetic assay, 1,105 were female and 882 were male (Appendix Table F-4). Percentages for the entire run were 55.0% female and 45.0% male (Appendix Table F-5). The sex ratio was female-biased for most of the run and ranged from 49.1% to 100.0%. Expanding overall percentages to the wild run gives 503,198 females (95% CI 462,934-541,265) and 411,315 males (95% CI 377,984-449,980; Figure 15).

Based on IA results using the 2,114 fish with complete genotype data (Appendix Table F-6), we estimate that 17.5% of the wild emigration originated from the UPSALM genetic stock; 7.3% from MFSALM; 4.1% from SFSALM; 6.5% from LOSALM; 9.6% from UPCLWR; 9.3% from SFCLWR; 7.4% from LOCLWR; 8.0% from IMNAHA; 17.7% from GRROND; and 12.7% from LSNAKE (Appendix Table F-7). Aggregating by MPG, 35.3% of the wild emigration originated from Salmon River; 26.3% from Clearwater River; 8.0% from Imnaha River; 17.7% from Grande Ronde River; and 12.7% from Lower Snake River.

Estimated smolt emigration to LGR by genetic stock was 159,675 fish from the UPSALM genetic stock (95% CI 130,415 – 193,127); 66,926 smolts from MFSALM (95% CI 50,101 – 87,231); 37,282 smolts from SFSALM (95% CI 24,761 – 49,714); 59,016 smolts from LOSALM (95% CI 45,025 – 78,402); 88,073 smolts from UPCLWR (95% CI 65,054 – 107,245); 84,756 smolts from SFCLWR (95% CI 65,339 – 107,288); 67,853 smolts from LOCLWR (95% CI 52,358 – 87,629); 73,557 smolts from IMNAHA (95% CI 57,339 – 93,660); 161,472 smolts from GRROND (95% CI 131,746 – 194,922); and 115,904 smolts from LSNAKE (95% CI 96,708 – 147,968; Figure 16). Aggregating by MPG, estimated smolt emigration to LGR was 322,898 smolts from Salmon River (95% CI 285,151 – 362,463); 240,681 smolts from Clearwater River (95% CI 206,877 – 270,596); the CIs for the Imnaha River, Grande Ronde River, and Lower Snake River MPGs are as above. Abundance estimates by statistical week are presented in Appendix Table F-8.

Of the 2,114 fish with complete genotypes, 957 (45.3%) assigned to a stock with ≥80% probability. Of the 957 assigned fish, 884 had both a determined sex and total age and were used for genetic stock decomposition (Appendix Table F-9). Percentages of sex by age were calculated for each stock (Appendix Table F-10) and were applied to the MY 2011 stock emigration estimates (Appendix Table F-11).

Chinook Salmon Emigration

For MY 2011 – from March 26, 2011 to July 31, 2011 – a total of 16,294 yearling Chinook salmon were collected at the Juvenile Fish Facility (Figure 11); of these, 3,209 fish were judged to be wild. The first wild yearling was collected on March 26, 2011, and the last was collected on July 16, 2011. Daily efficiency estimates for yearling Chinook salmon smolts in the bypass system ranged from 16.5% to 61.2% and averaged 39.0% (Figure 12). The total estimated wild yearling abundance was 1,192,923 smolts (95% CI 1,149,714-1,237,616; Figure 13).

During the same time period, 19,150 subyearling Chinook salmon were collected (Figure 11), of which 10,557 were judged to be wild. The first wild subyearling was collected on March 26, 2011 but most were collected in June and July. Daily efficiency estimates for subyearling Chinook salmon smolts in the bypass system ranged from 5.7% to 32.4% and averaged 16.3% (Figure 12). The total estimated wild subyearling abundance was 911,764 smolts (95% CI 885,826-938,730; Figure 13).

Wild Chinook Salmon Age, Sex, and Stock Composition

Yearlings—A total of 1,510 yearling Chinook salmon smolts were sampled and considered valid (Appendix Table G-1). The first sample was collected on March 29, 2011, and the last was collected on July 8, 2011. We were able to assign sex to 1,438 samples. We were able to obtain complete genotype data (≥90% of SNPs amplify successfully) for 1,507 samples.

Of the 1,438 yearlings that sex was successfully determined using the sex-specific assay, 687 were female and 751 were male (Appendix Table G-2). Sex percentages for the entire run were 48.1% female and 51.9% male (Appendix Table G-3). Expanding the overall percentages to the wild run gives 574,157 females (95% CI 528,777-627,852) and 618,766 males (95% CI 565,956-667,245; Figure 17).

Based on IA results using the 1,507 fish with complete genotypes (Appendix Table G-4), we estimate that 23.0% of the wild yearling Chinook emigration originated from the UPSALM genetic stock; 17.2% from MFSALM; 4.0% from CHMBLN; 16.5% from SFSALM; 37.2% from

HELLSC; and 0.7% from TUCANO (Appendix Table G-5). Aggregating the MFSALM and CHMBLN genetic stocks; 21.2% of the wild yearling Chinook smolt emigration originated from the Middle Fork Salmon River MPG. The remaining 1.3% of yearlings were identified as fall Chinook salmon based on multi-locus SNP data.

Estimated yearling smolt emigration to LGR by stock was 274,850 fish from the UPSALM genetic stock (95% CI 216,237 – 336,180); 205,370 smolts from MFSALM (95% CI 164,174 – 264,406); 47,949 smolts from CHMBLN (31,798 – 70,831); 197,097 smolts from SFSALM (95% CI 153,667 – 248,914); 443,528 smolts from HELLSC (95% CI 366,268 – 535,215); and 8,781 smolts from TUCANO (95% CI 3,433 – 16,138; Figure 18). Aggregating the MFSALM and CHMBLN genetic stocks; 253,320 wild yearling smolts (95% CI 210,492 – 315,859) originated from the Middle Fork Salmon River MPG. We estimate that 15,347 yearling smolts originated from fall Chinook salmon stocks (95% CI 8,355 – 21,015). Abundance estimates by statistical week are presented in Appendix Table G-6.

Of the 1,507 yearling smolts with complete genotypes, 1,062 (70.5%) assigned to a stock with ≥80% probability. Of the 1,062 assigned fish, 1,012 had a determined sex and were used for estimates of sex ratios for each stock (Appendix Table G-7) and were applied to the MY 2011 stock emigration estimates (Appendix Table G-7). We did not have sufficient assignments to estimate sex ratios for the TUCANO genetic stock.

Subyearlings—A total of 587 subyearling Chinook salmon smolts were sampled and considered valid (Appendix Table H-1). The first sample was collected on May 21, 2011, and the last was collected on July 9, 2011. We were able to assign sex to 545 samples. We were able to obtain complete genotype data (≥90% of SNPs amplify successfully) for all 587 samples.

Of the 545 subyearlings that sex was successfully determined using the sex-specific assay, 250 were female and 295 were male (Appendix Table H-2). Sex percentages for the entire run were 42.2% female and 57.8% male (Appendix Table H-3). The sex ratio was male-biased most of the run and ranged from 49.6% to 63.3%. Expanding the overall percentages to the wild run gives 384,560 females (95% CI 321,703-473,403) and 527,204 males (95% CI 429,954-596,784; Figure 19).

Based on IA results using the 587 subyearling Chinook smolts with complete genotype data (Appendix Table H-4), we estimate 12.9% originated from spring/summer stocks. Of those, we estimate that 23.6% originated from the UPSALM genetic stock; 8.5% from MFSALM; 3.9% from CHMBLN; 61.3% from HELLSC; and 0.3% from TUCANO (Appendix Table H-5). Aggregating the MFSALM and CHMBLN genetic stocks; 12.4% of the spring/summer subyearling smolt emigration originated from the Middle Fork Salmon River MPG. The remaining 87.1% of subyearlings were identified as fall Chinook salmon based on multi-locus SNP data.

Of the total estimated wild subyearling abundance of 911,764 smolts, we estimate that 117,988 smolts originated from spring/summer stocks. The latter was composed of 27,896 fish from the UPSALM genetic stock; 9,972 smolts from MFSALM; 4,607 smolts from CHMBLN; 72,297 smolts from HELLSC; and 406 smolts from TUCANO (Figure 20). Aggregating the MFSALM and CHMBLN genetic stocks; 14,579 wild subyearling smolts originated from the Middle Fork Salmon River MPG. We estimate that 793,776 subyearling smolts originated from fall Chinook salmon stocks. We did not have adequate genetic assignments to spring/summer stocks to produce confidence intervals around estimates of abundance for genetic stocks or

MPGs for subyearling smolts of those groups. Abundance estimates by statistical week are presented in Appendix Table H-6.

Of the 587 subyearling smolts sampled, we obtained complete genotype data from 587 fish. Of the 587 smolts with complete genotype data, 573 smolts (97.6%) assigned to a stock with ≥80% probability. Of the 587 assigned fish, 533 had a sex determined. However, there were not sufficient assignments to any spring/summer stocks for estimates of sex ratios (480 of 533 assignments were to FALL genetic stock).

DISCUSSION

This report is the first attempt at a stock assessment for natural smolt emigration from the Snake River steelhead DPS and spring/summer Chinook ESU, exclusive of the Tucannon River, using genetic stock identification. Previous stock assessments were done on the aggregate smolt emigration without identifying the component units (e.g., Raymond 1979, 1988; Copeland et al. 2009). In the following discussion, we focus primarily on caveats for the interpretation of the present results and improvements that should be made in future analyses.

In this analysis, we assumed that the realized sampling rate adequately describes the probability that any fish passing LGR can be sampled. There are four possible exceptions to this assumption. First, we assume there is no size bias in collection (i.e., larger smolts are less likely to enter the juvenile by-pass system). Second, PIT-tagged fish were not sampled; therefore, populations in which there is a high rate of tagging may be under-represented in the analysis. We have no data to address these concerns at this time. Third, we extrapolated the subyearling composition estimates based on the final week of sampling to the full month of July. Inspection of sex and stock frequencies suggests that composition does not change appreciably between the last two weeks of sampling. Lastly, yearling fall Chinook salmon that were phenotypically distinguishable from spring/summer Chinook smolts (Tiffan et al. 2000) were not subsampled at the trap. Consequently, our estimates of the abundance of yearling fall Chinook are biased low. In 2012, these fish were included in the subsample and future estimates will be more accurate.

The ultimate goal of this program is to develop productivity relationships at the level of genetic stock and MPG, requiring stock-specific information relative to sex and age. There are three issues related to stock-specific estimates of abundance, sex ratio, and age composition. First, only individuals assigning with a probability of ≥0.80 were used to decompose stock abundance. For steelhead, 45.8% of individuals with complete genotype data analyzed in this study were assigned to a stock with ≥0.80 probability. For Chinook, 71.7% of yearlings and 98.5% of subyearlings were assigned to a stock with high confidence. In applying a threshold of 0.80 for assignment, the likelihood that an assigned individual truly originated from the estimated genetic stock is increased. Thus, we believe estimates of sex ratio and age structure (for steelhead) are more accurate when using a conservative standard. However, applying a threshold effectively decreases the data available for genetic stock decomposition, decreasing the precision of various age/sex estimates within each stock. Gerritsen and McGrath (2007) suggested a rule-of-thumb sample size of 10 times the number of classes. Thompson (1987) suggested a sample size of 510 individuals would be sufficient given a worst-case scenario, regardless of the number of classes. Even under Gerritsen and McGrath's more liberal criteria, sufficient data were not available to develop confidence intervals for genetic-stock specific sex/age estimates for either species, and further, sufficient data were not available to estimate sex-specific point estimates for subyearling spring/summer Chinook. Second, we assumed there were no temporal changes of sex ratio/age structure within each stock (i.e. data are not

broken into time strata); this was also due to insufficient data available within time strata. We made the assumption that sex ratios and age structure within each genetic stock were consistent throughout the emigration. The final assumption was that we assumed that no bias was generated by dropping unassigned (fish that assign with <0.80 probability) individuals from the analysis, i.e., there was no correlation between life history patterns and genetic uncertainty within a stock. In other words, we assumed that fish of various sexes and ages assigned with equal probability; we have informally tested this third assumption and believe it holds true.

The vast majority of Snake River stocks spawn upstream of Lower Granite Dam with a notable exception. We report smolt emigration estimates from the TUCANO (Tucannon River) genetic stock for both yearling and subyearling Chinook salmon. These estimates represent the number of offspring that were produced from adults originating from the Tucannon River and successfully strayed and reproduced above LGR. Tucannon River populations demonstrate slight evidence for introgression (5.3%) with fall Chinook (Narum et al. 2010) and are generally highly identifiable in mixed stock analysis (Ackerman et al. 2012). The present estimates are not intended to be used to calculate productivity metrics for Tucannon River populations, given that the majority of this group spawns downstream from LGR. Similarly, some wild steelhead belonging to the LSNAKE genetic stock spawn in Asotin Creek 61 rkm upstream from LGR and many steelhead from the Tucannon River stray extensively above LGR (Bumgarner and Dedloff 2011). Accounting of production by steelhead and Chinook salmon populations that do not spawn exclusively upstream of LGR will be incomplete in this report but they must be identified for accurate assessment of the other Snake River stocks.

Beginning in MY 2012, we anticipate further refinement to our total wild smolt emigration estimate by using parentage based tagging (PBT; Steele et al. 2012). PBT will allow us to identify unclipped hatchery fish that are otherwise indistinguishable from wild fish. For MY 2010 and MY 2011 analyses, we did not remove fish that were genetically identified as hatchery origin based on PBT. These fish were a small minority (during MY 2011, 2.0% of analyzed steelhead, 3.4% of yearling and 9.8% of subyearling Chinook); therefore, we do not expect composition results reported here will be biased. Note that unclipped smolts with CWTs or eroded dorsal fins (steelhead only) were already excluded in the present analyses. Beginning with brood year 2009, all steelhead and spring/summer hatchery stocks in the Snake River basin will be PBT-tagged (Steele et al. 2011); only 8 of 12 steelhead stocks were PBT-tagged during BY2009. MY 2013 will be the first year that almost all hatchery steelhead smolts emigrating from the Snake River basin will be PBT tagged. PBT analysis will be incorporated during MY 2012 analyses to better address the unclipped hatchery portion of the emigration.

Although there are only two years of results, there are a few patterns in the data that have interesting implications regarding life history and demography. Steelhead age structure appears to be older earlier in the migration and in populations generally defined as having a B-run life history, despite these populations being farther from LGR than many A-run populations. Anadromy in salmonids should have greater benefits for females (Hendry et al. 2004); therefore, we may expect a female bias in emigrating smolts. This appears true for steelhead (53.2% and 55.0% for MY 2010 and MY 2011, respectively) but was more variable for Chinook salmon. The fitness of a particular life history strategy may vary with density, frequency of other types, and condition of individuals (Hendry et al. 2004), all of which change with time and location. Certainly sex ratio in smolts varies a lot among stocks, which may be influenced by the habitats that they rear in. For example, some tributaries can produce more female emigrants than others even within the same watershed (Mills et al. 2012). Life history and demographic patterns in data presented here may suggest smaller-scale investigations to determine causes and they

also provide the means to test predictions at the smolt stage, which is convenient and meaningful stage to consider recruitment (Solomon 1985).

In conclusion, the wild smolt abundance and composition estimates reported here will be used to evaluate the status of wild populations relative to three viable salmonid population criteria: abundance, productivity, and diversity. We directly estimate juvenile abundance at LGR as well as elements of diversity such as sex ratio, age at emigration, and emigration 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. This work will enable us to estimate adult-to-juvenile and juvenile-to-adult productivity. For steelhead, the data necessary to compute productivity accumulate over time will take 4-5 years before the first productivity estimate is complete. For spring/summer Chinook, productivity tables may commence once we are confident in our methodology.

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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)	

Snake River spring/summer Chinook salmon ESU	
Major population group	Population name
Lower Snake River	1. Tucannon River 2. Asotin Creek (extirpated)
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) 10. Lookinglass Creek
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)

FIGURES

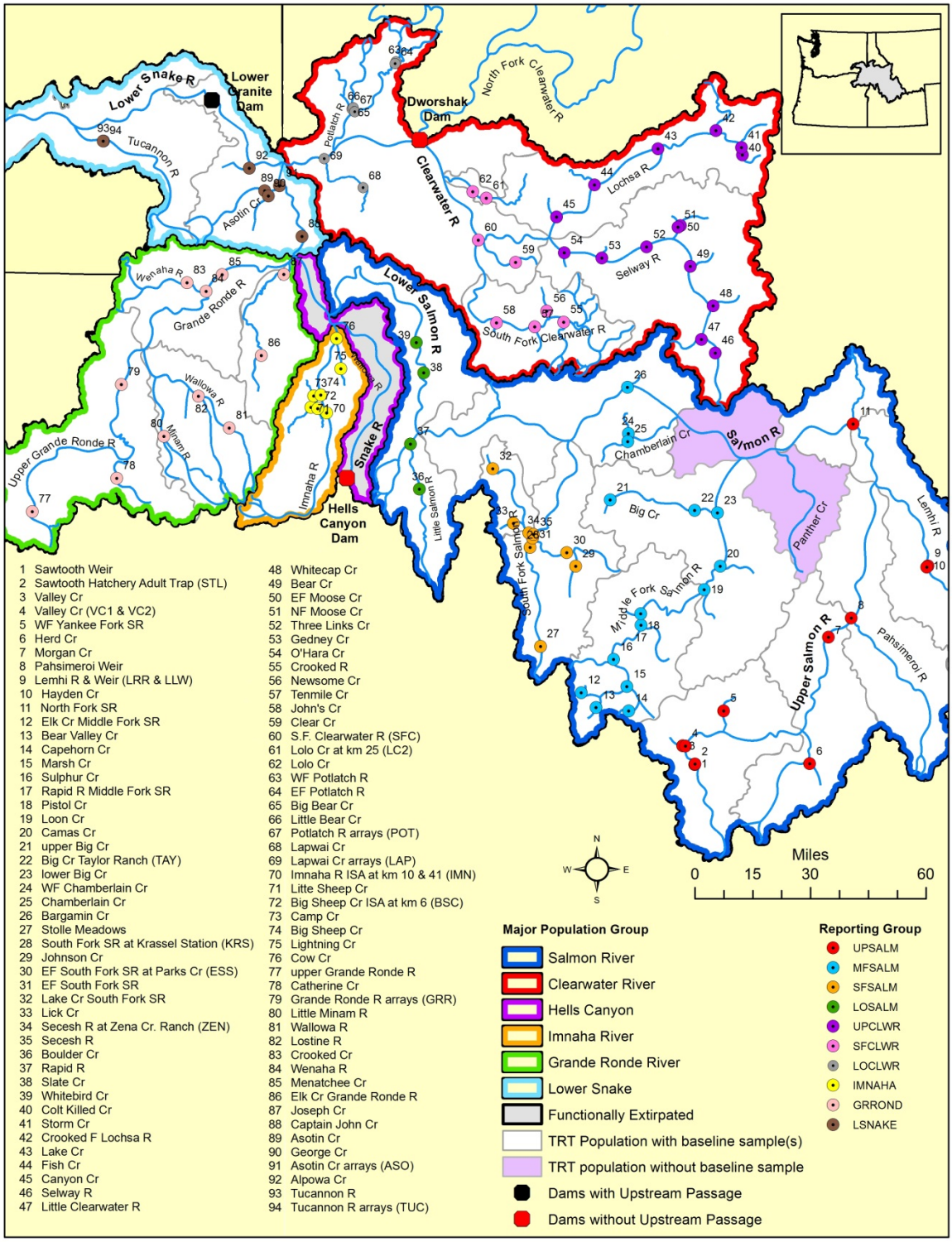


Figure 1. Genetic stocks and baseline collections used for steelhead mixed stock analysis at Lower Granite Dam, spawn year 2011 (Ackerman et al. 2012). The Hells Canyon Tributaries MPG (shaded gray) does not support independent populations and is considered extirpated (NMFS 2011).

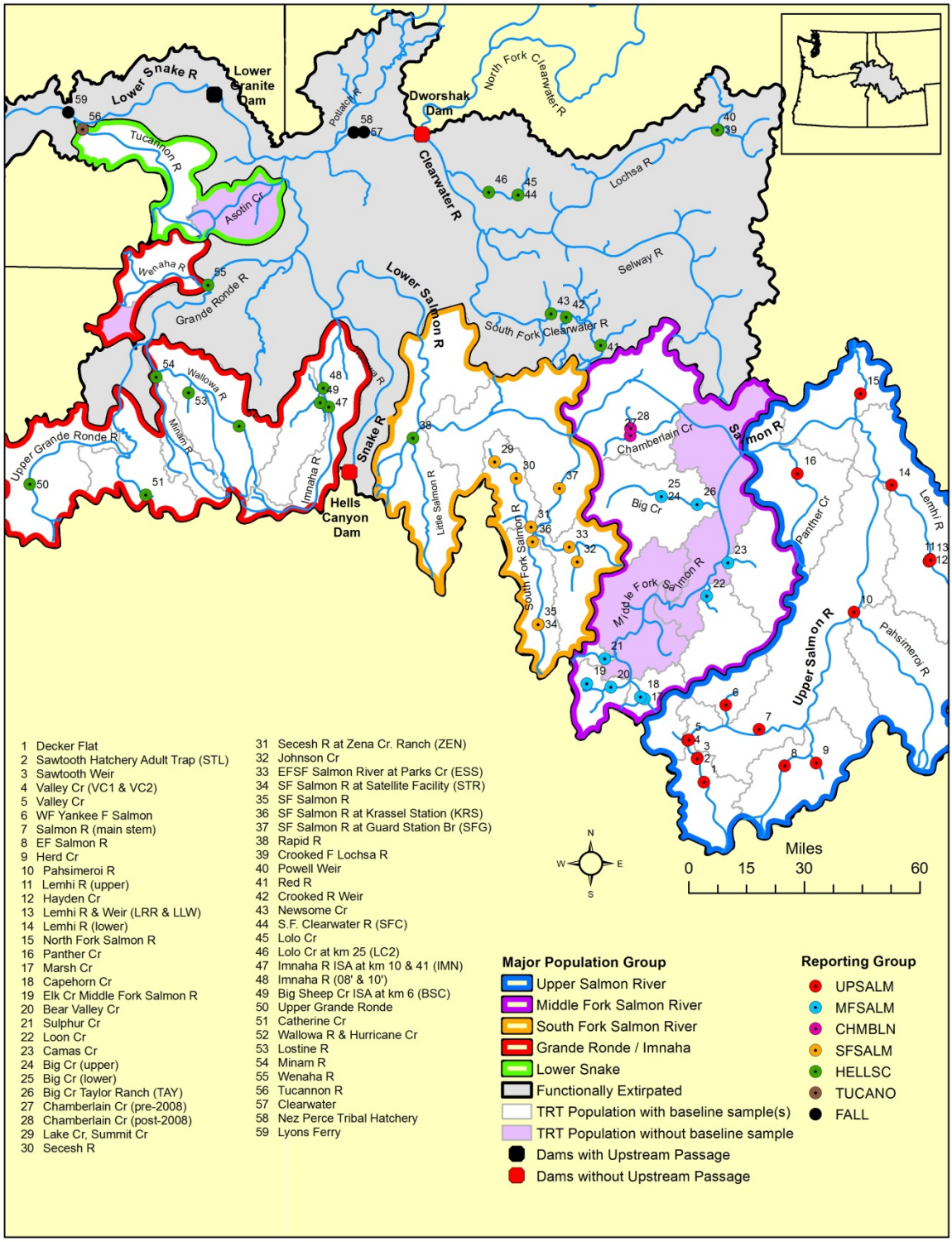


Figure 2. Genetic stocks and baseline collections used for Chinook salmon mixed stock analysis at Lower Granite Dam, spawn year 2011 (Ackerman et al. 2012). Reintroduced fish exist in functionally extirpated TRT populations as mapped.

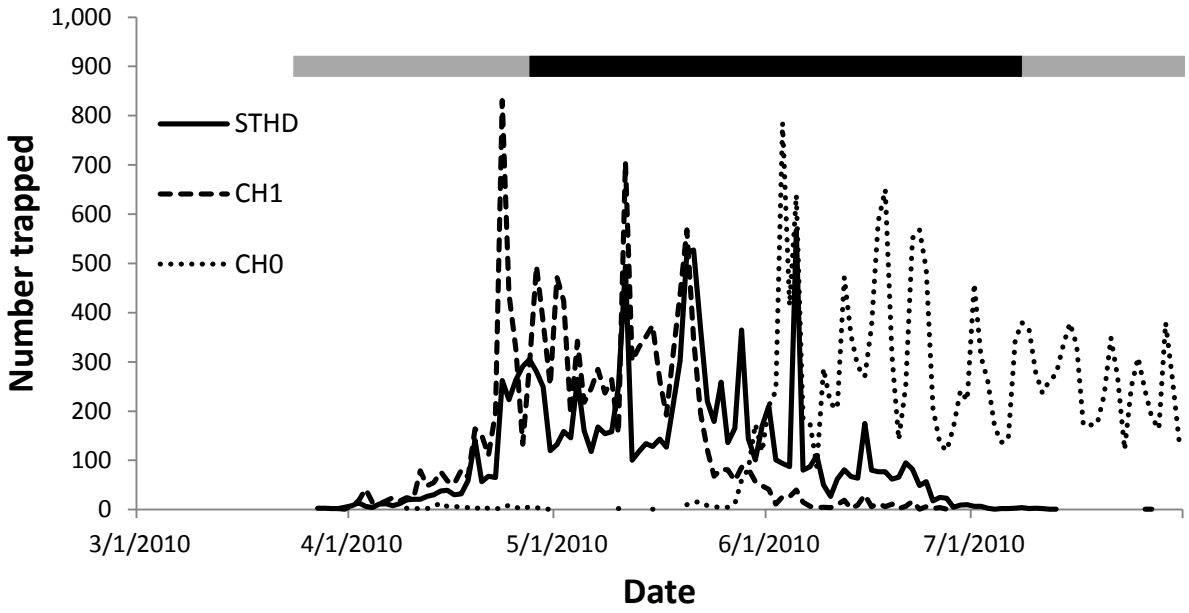


Figure 3. Daily number of smolts trapped at the Lower Granite Dam juvenile fish facility, migratory year 2010. Horizontal bar indicates when the trap was open (gray) and when biological samples were taken (black). Species are steelhead (STHD), yearling Chinook (CH1), and subyearling Chinook (CH0).

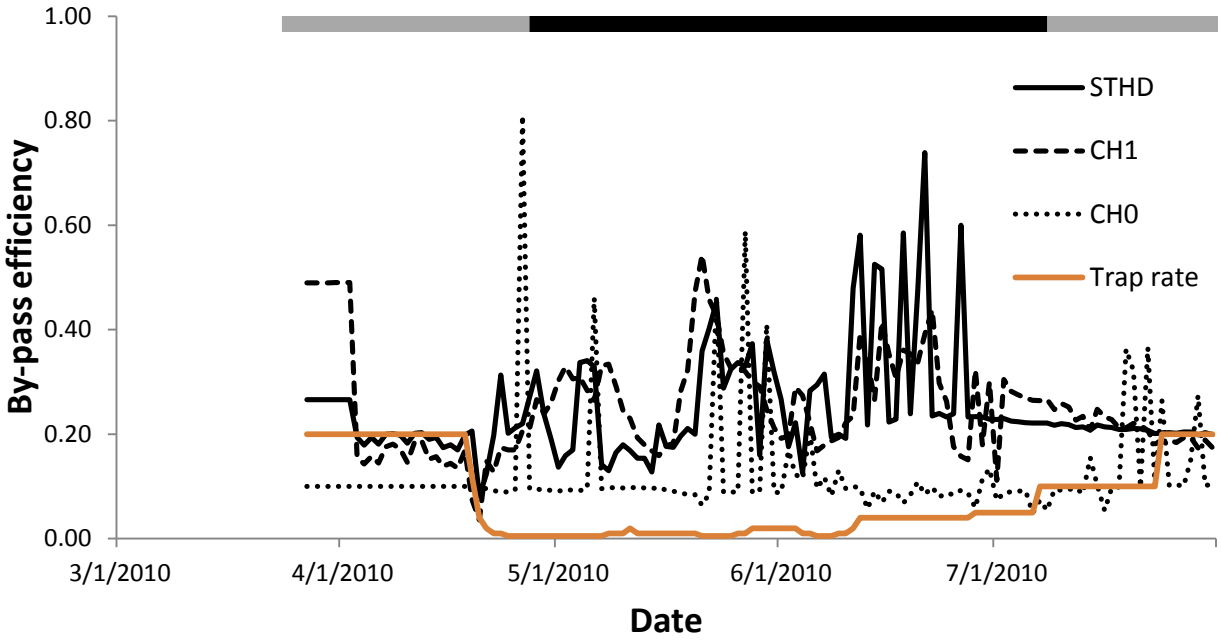


Figure 4. Daily trap rate and by-pass efficiency, by species, of smolts trapped at the Lower Granite Dam juvenile fish facility, migratory year 2010. Horizontal bar indicates when the trap was open (gray) and when biological samples were taken (black).

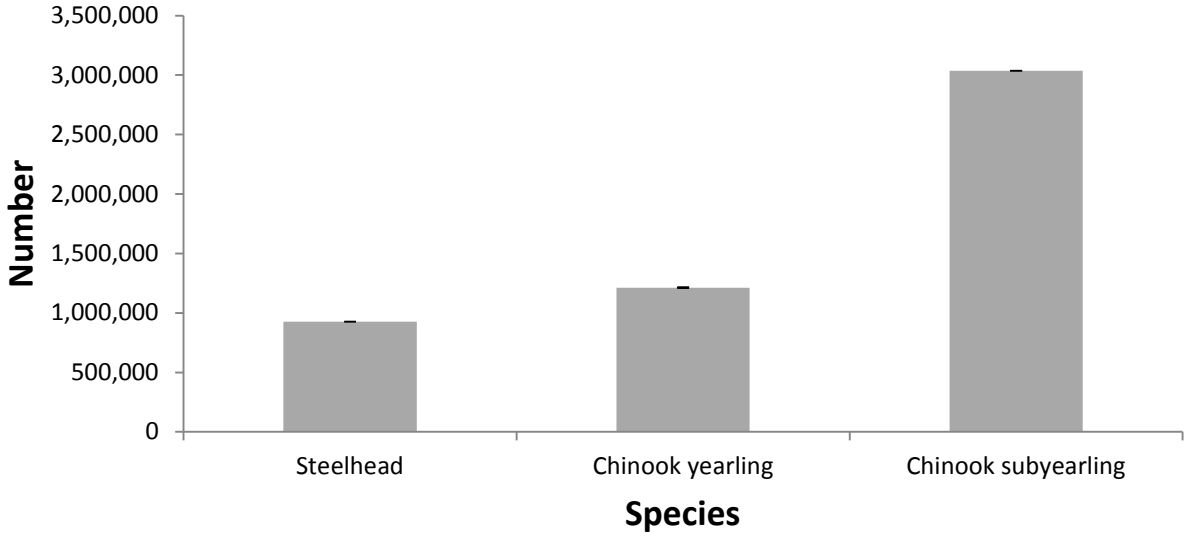


Figure 5. Abundance by species of wild smolts at Lower Granite Dam, migratory year 2010 (March 27 – July 31). Confidence intervals are at 95%.

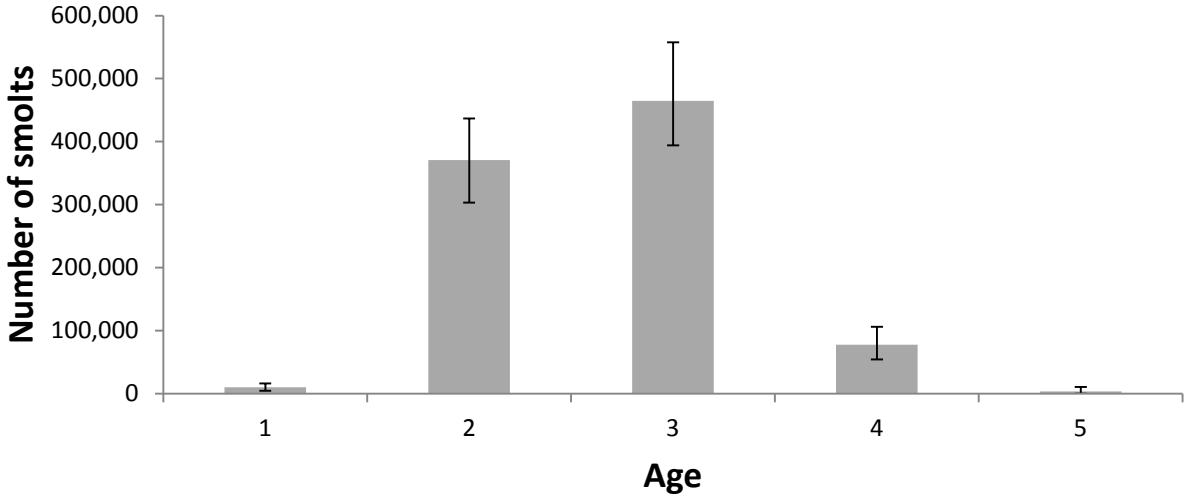


Figure 6. Abundance by age of wild steelhead smolts at Lower Granite Dam, migratory year 2010. Confidence intervals are at 95%.

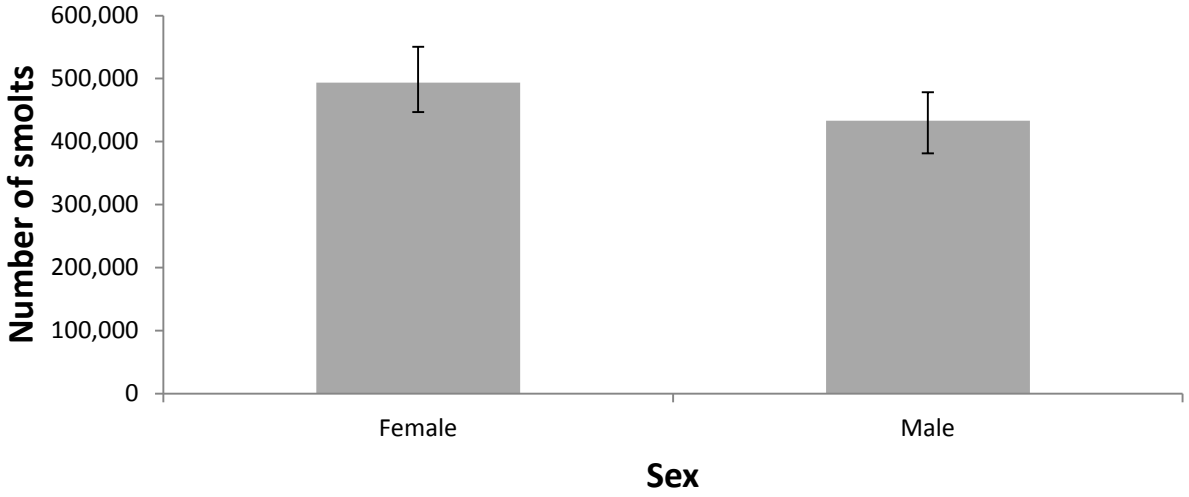


Figure 7. Abundance by sex of wild steelhead smolts at Lower Granite Dam, migratory year 2010. Confidence intervals are at 95%.

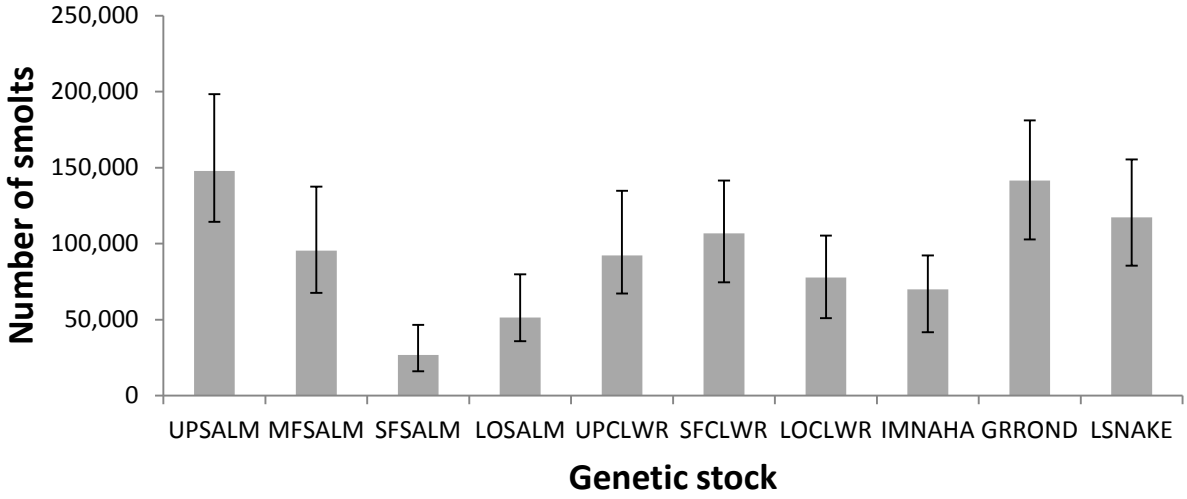


Figure 8. Abundance by genetic stock of wild steelhead smolts at Lower Granite Dam, migratory year 2010. Confidence intervals are at 95%. See Appendix Table B-1 for stock abbreviations.

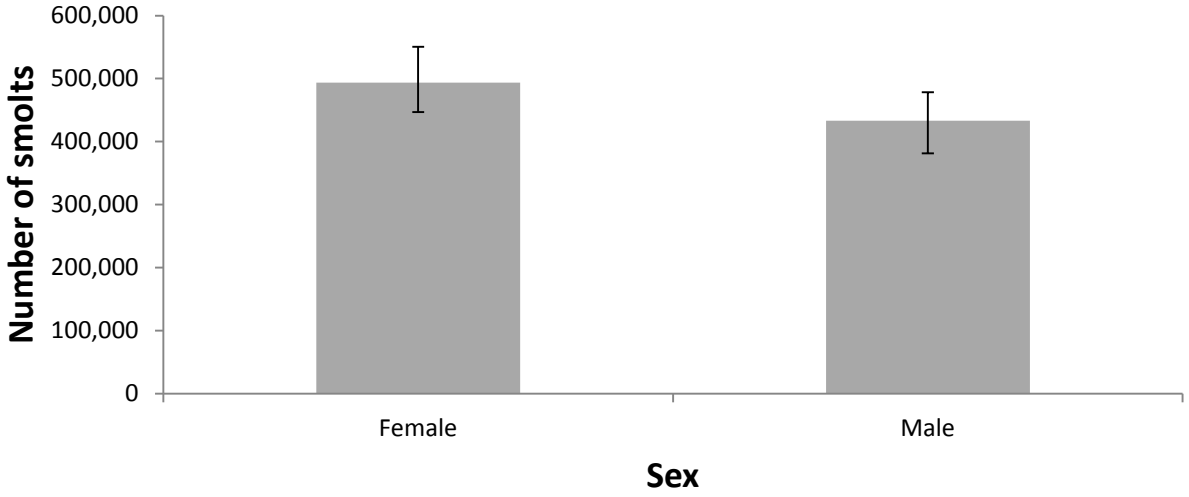


Figure 9. Abundance by sex of wild Chinook salmon yearling smolts at Lower Granite Dam, migratory year 2010. Confidence intervals are at 95%.

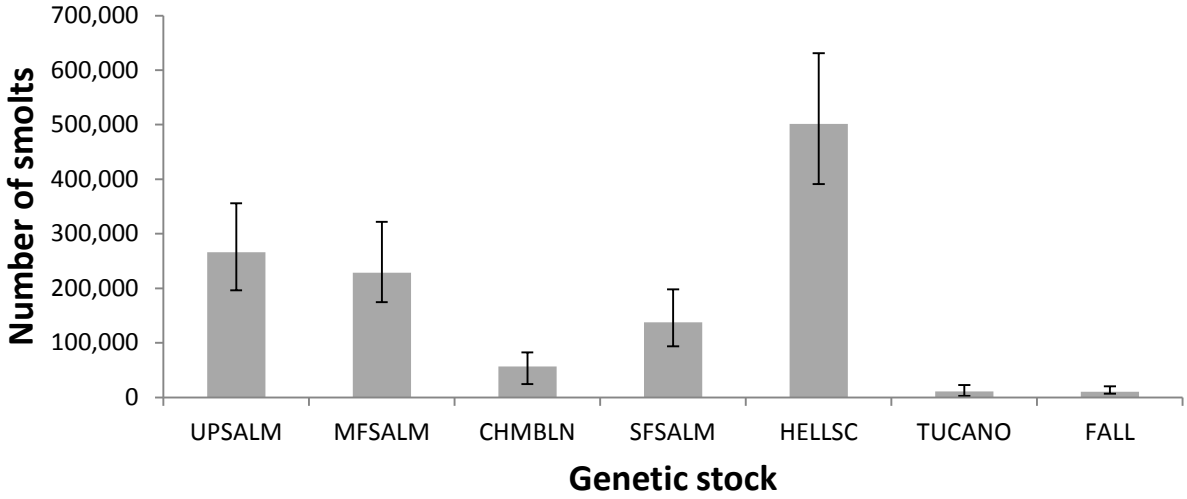


Figure 10. Abundance by genetic stock of wild yearling Chinook salmon smolts at Lower Granite Dam, migratory year 2010. Confidence intervals are at 95%. See Appendix Table B-2 for stock abbreviations.

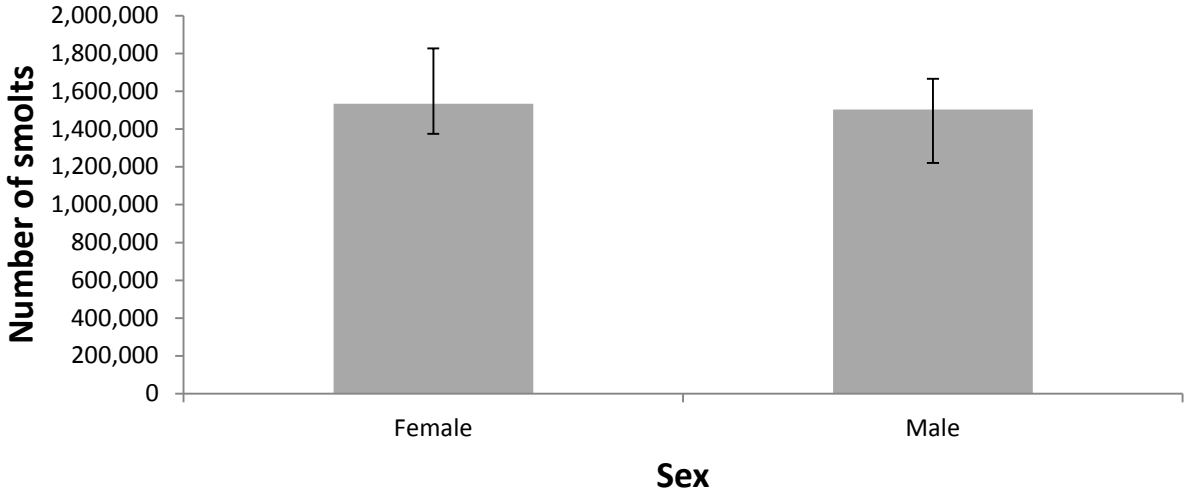


Figure 11. Abundance by sex of wild subyearling Chinook salmon smolts at Lower Granite Dam, migratory year 2010. Confidence intervals are at 95%.

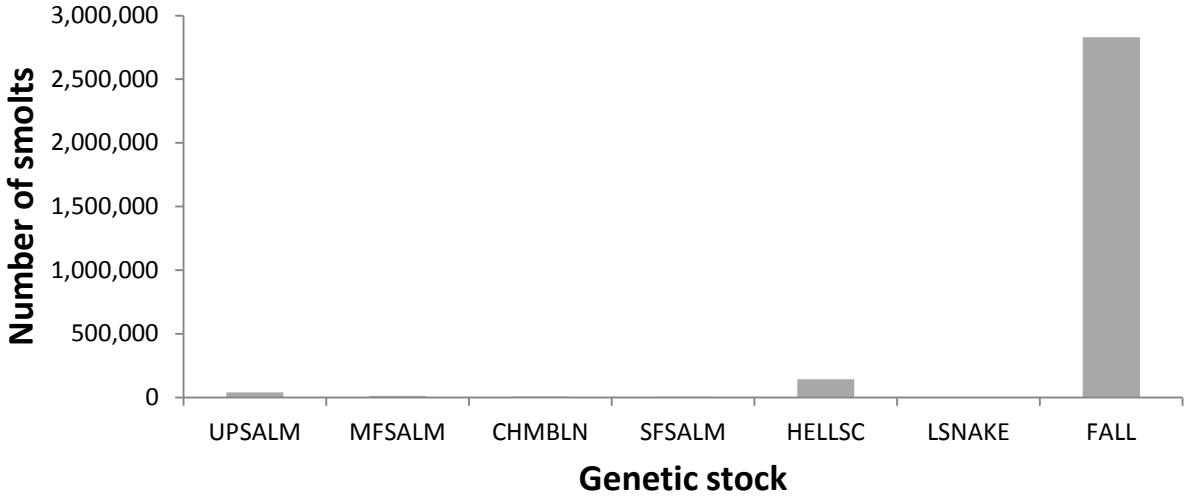


Figure 12. Abundance by genetic stock of wild subyearling Chinook salmon smolts at Lower Granite Dam, migratory year 2010. Sufficient genetic assignments were not made to spring/summer stocks; thus no confidence intervals were calculated. See Appendix Table B-2 for stock abbreviations.

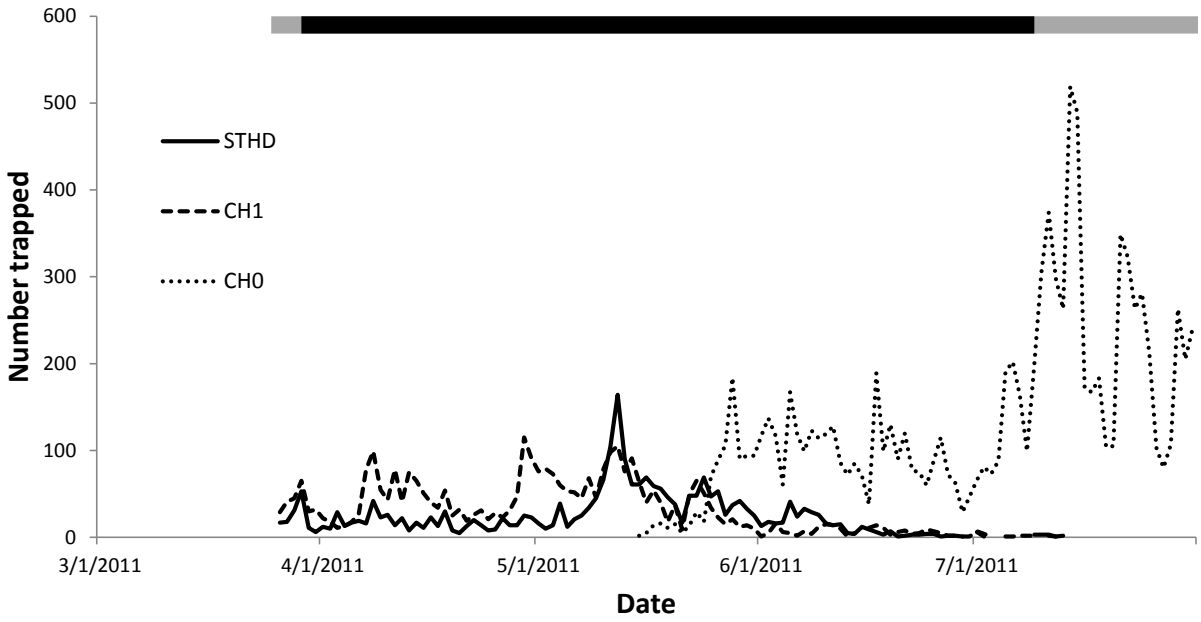


Figure 13. Daily number of smolts trapped at the Lower Granite Dam juvenile fish facility, migratory year 2011. Horizontal bar indicates when the trap was open (gray) and when biological samples were taken (black). Species are steelhead (STHD), yearling Chinook (CH1), and subyearling Chinook (CH0).

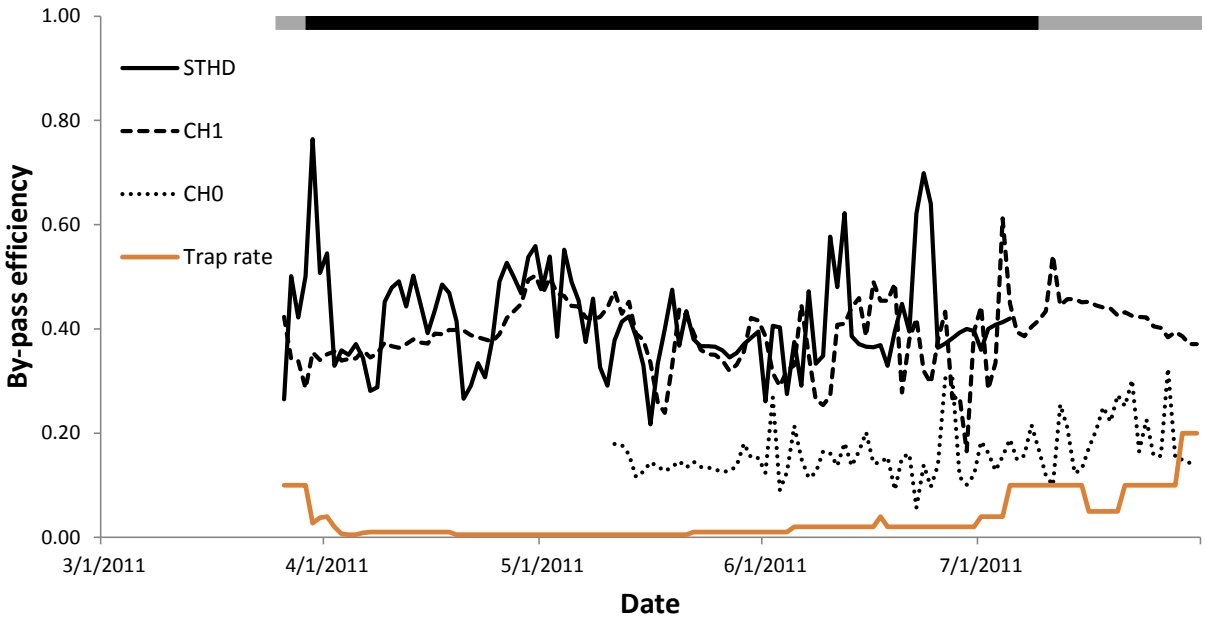


Figure 14. Daily trap rate and by-pass efficiency, by species, of smolts trapped at the Lower Granite Dam juvenile fish facility, migratory year 2011. Horizontal bar indicates when the trap was open (gray) and when biological samples were taken (black).

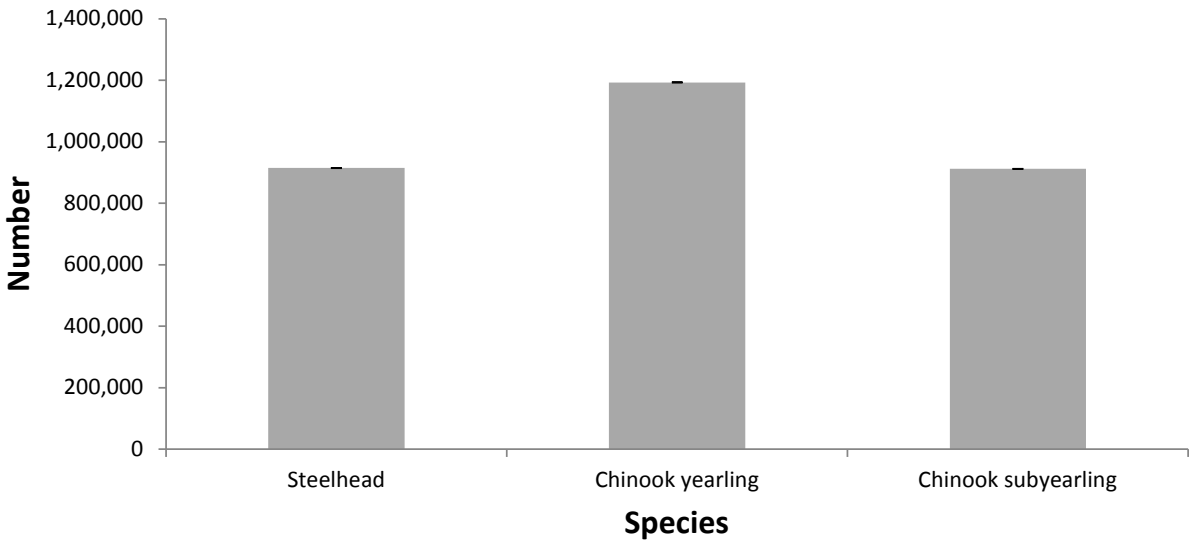


Figure 15. Abundance by species, of wild smolts at Lower Granite Dam, migratory year 2011 (March 26 – July 31). Confidence intervals are at 95%.

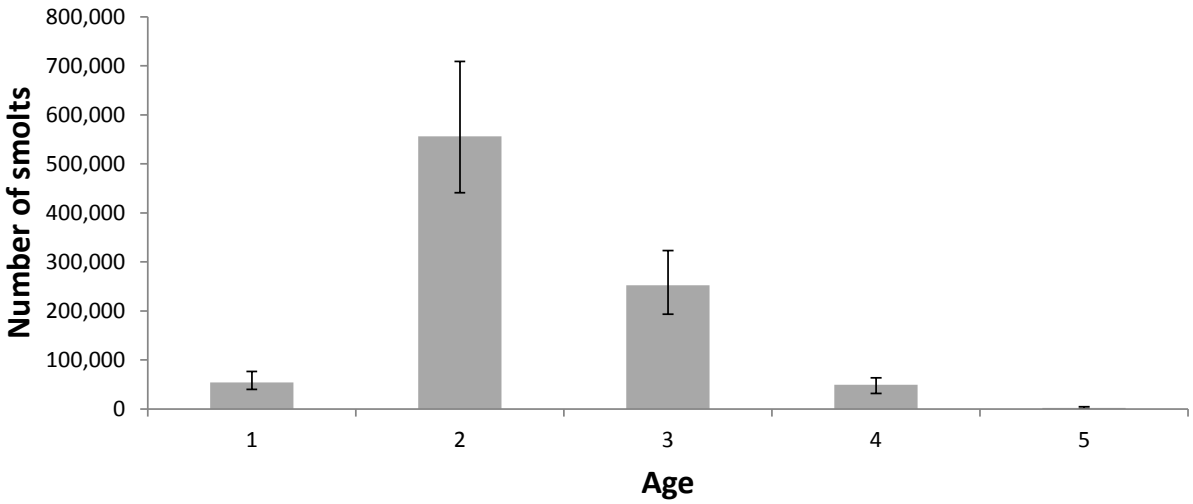


Figure 16. Abundance by age of wild steelhead smolts at Lower Granite Dam, migratory year 2011. Confidence intervals are at 95%.

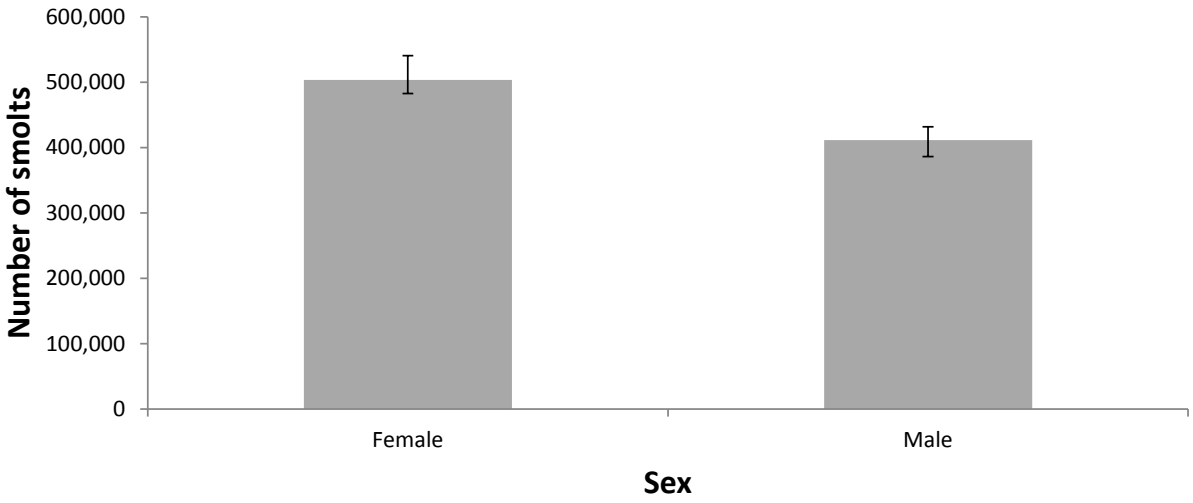


Figure 17. Abundance by sex of wild steelhead smolts at Lower Granite Dam, migratory year 2011. Confidence intervals are at 95%.

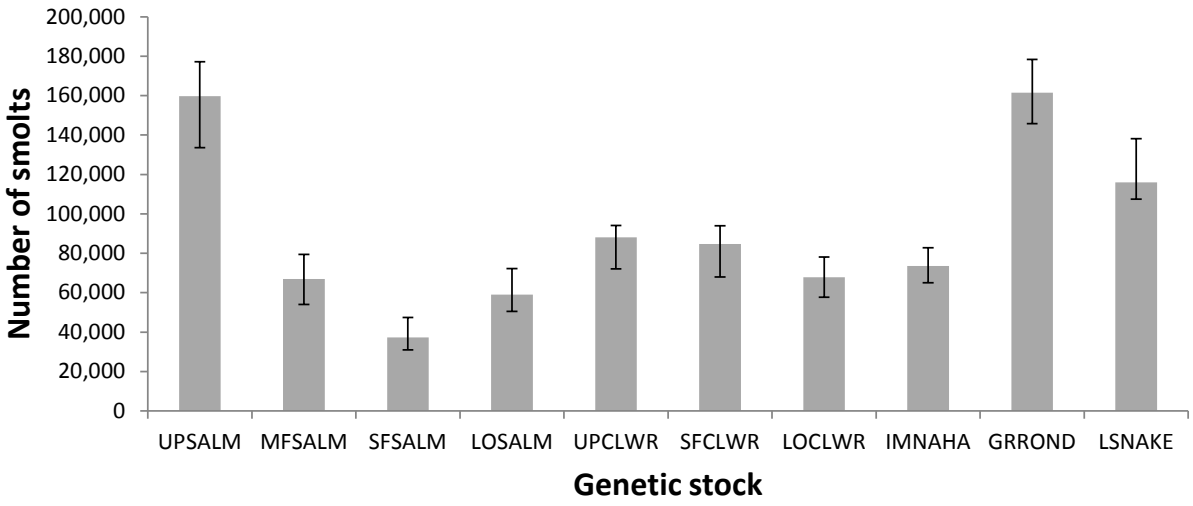


Figure 18. Abundance by genetic stock of wild steelhead smolts at Lower Granite Dam, migratory year 2011. Confidence intervals are at 95%. See Appendix Table B-1 for stock abbreviations.

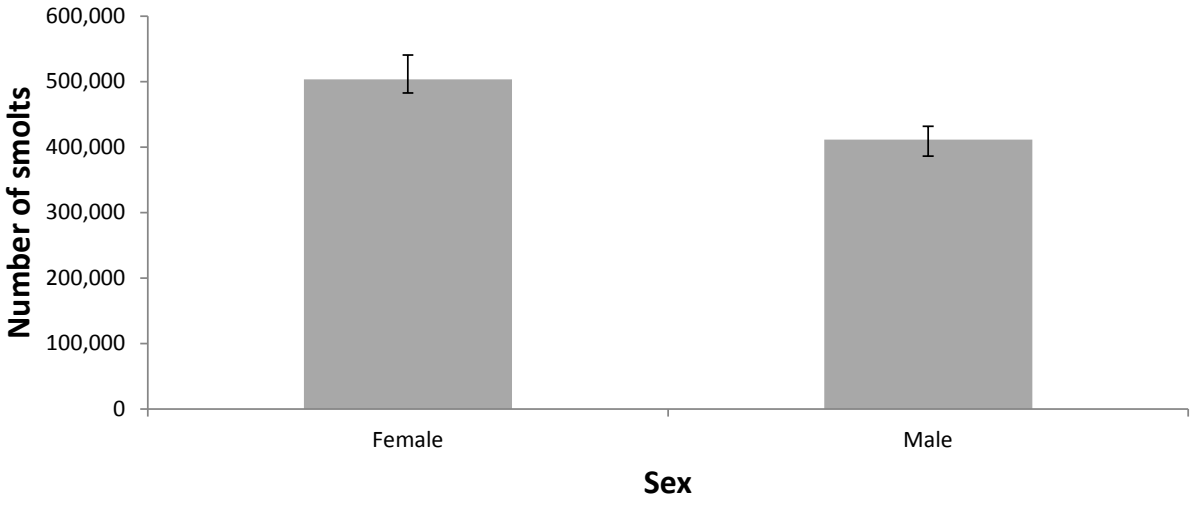


Figure 19. Abundance by sex of wild Chinook salmon yearling smolts at Lower Granite Dam, migratory year 2011. Confidence intervals are at 95%.

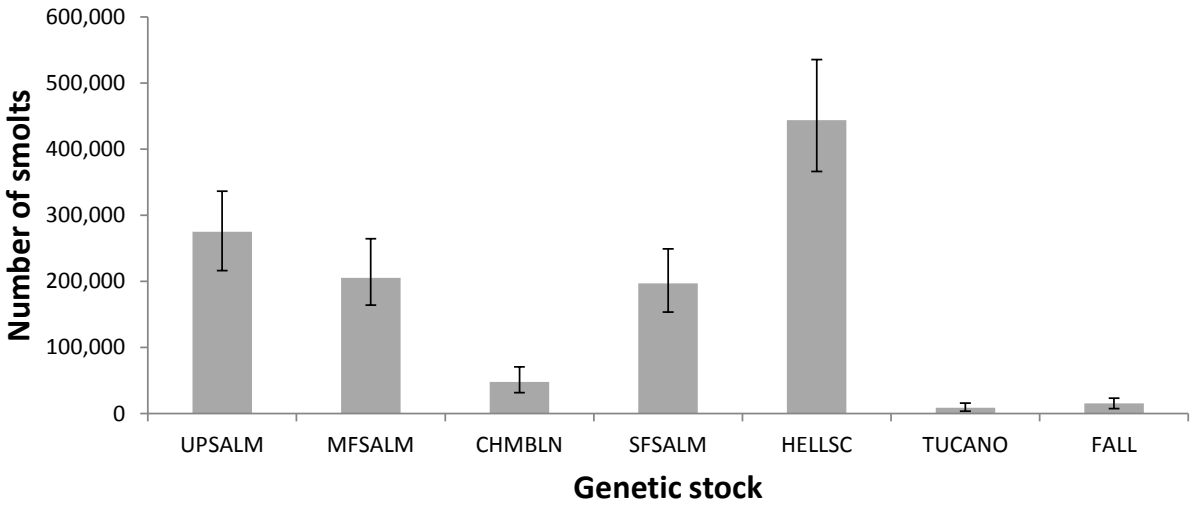


Figure 20. Abundance by genetic stock of wild yearling Chinook salmon smolts at Lower Granite Dam, migratory year 2011. Confidence intervals are at 95%. See Appendix Table B-2 for stock abbreviations.

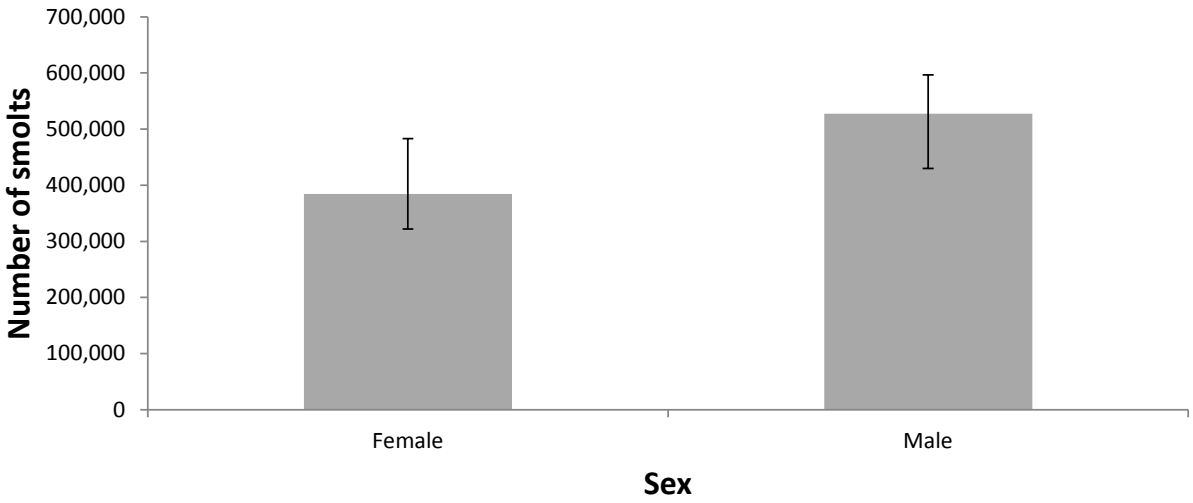


Figure 21. Abundance by sex of wild subyearling Chinook salmon smolts at Lower Granite Dam, migratory year 2011. Confidence intervals are at 95%.

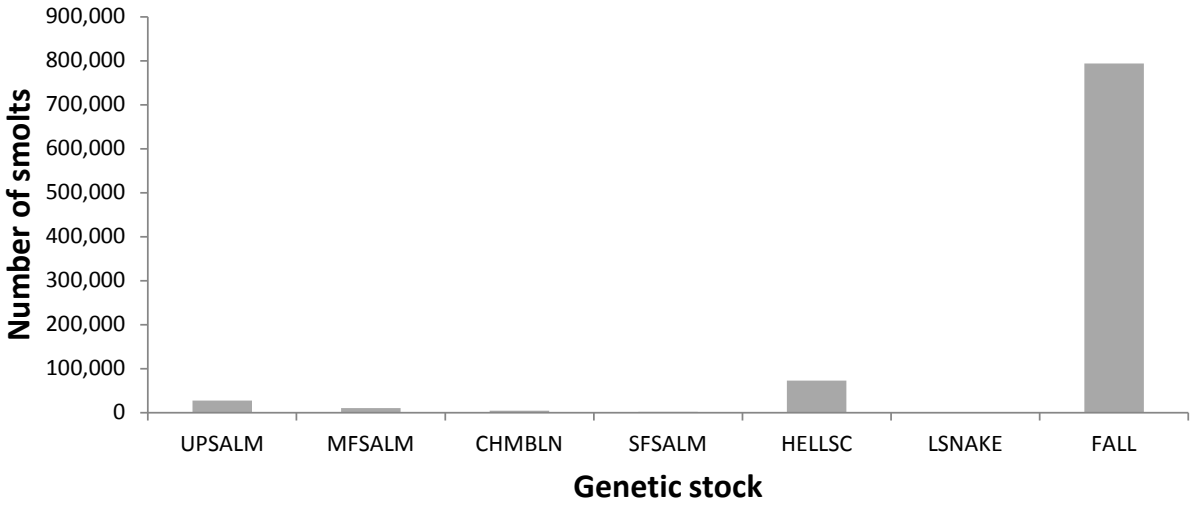


Figure 22. Abundance by genetic stock of wild subyearling Chinook salmon smolts at Lower Granite Dam, migratory year 2011. Sufficient genetic assignments were not made to spring/summer stocks; thus no confidence intervals were calculated. See Appendix Table B-2 for stock abbreviations.

APPENDICES

Appendix A. Lower Granite Dam juvenile sampling protocol, spring 2010.

Sampling Protocol for Juvenile Spring-Summer Chinook Salmon and Steelhead at the Lower Granite Dam Juvenile Fish Facility April 26 through July 10, 2010

Adapted from the LGR Adult Sampling Protocol Developed 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:

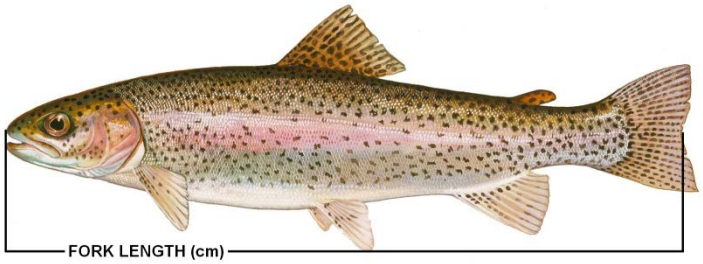
1) Length measurements of a sub-sample of natural origin juvenile Chinook (CHN) salmon and steelhead trout (STH) to determine length distribution and length at age;
2) Tissue collections from a sub-sample of natural origin juvenile CHN and STH for genetic stock identification (GSI);
3) Scale collections from a sub-sample of natural origin juvenile STH to estimate age composition.

Only adipose fin intact, naturally produced, juvenile CHN and STH should be sub-sampled. No fish with PIT tags or coded wire tags (CWT) should be included in this sub-sample. All data should be recorded and retained on paper data sheets (Data Entry Form), on the associated scale collection packets, and genetic tissue vials. An individually 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 previously be identified to species and if it was naturally produced. Naturally produced fish are defined as non-adipose-clipped, non-CWT-bearing, non-PIT-tag-bearing, without dorsal fin erosion.

2. A sub-sample of all naturally produced juvenile CHN or STH will be shunted into a trough for this project. A minimum of 2,000 and a maximum of 4,000 yearling samples, and a minimum of 500 and a maximum of 1,500 sub-yearling are desired. Two out of three naturally produced yearling and sub-yearling CHN salmon will be sub-sampled. A minimum of 2,000 and a maximum of 4,000 yearling STH are desired. Two out of three naturally produced yearling STH will also be sub-sampled.

3. All spring/summer CHN salmon and STH sub-sampled will be measured to the nearest millimeter (fork length).



4. For all STH that are sub-sampled, six to twelve scales will be removed from immediately behind the dorsal fin and above the lateral line. Scales will 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.

5. 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 (pencil eraser sized) 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.

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.

<u>Collection Packets</u>
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)

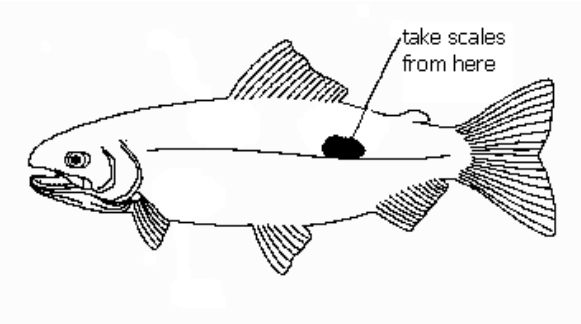
On the Coin envelope:
1. Identify life stage (Juvenile) and sample number (**<u>matches that on data form</u>**).
2. Enter the date (XX/XX/XXXX)
3. Circle appropriate marks
4. Fill in Fork length (mm)
5. In the comment line, put anything you feel may be of interest; for example, scars or deformities on the fish.

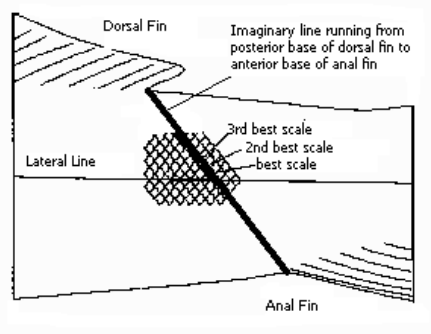
<u>Scale Sample Collection Method</u>

Supplies:
Forceps, tweezers, or scissors
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. A knife is used to remove scales.
    a. Inspect for and remove from the knife any scales from the previous sample collected.
    b. Six to twelve scales should be removed. Use the knife point to scrape with the grain in the preferred area.
4. Wipe scales onto one side of the folded strip of paper found in the collection packet.
5. Refold the strip of paper over the scales and place the strip of paper directly into the collection packet it was removed from.
6. **Make sure that all information requested is filled out on the collection packet.**
7. Seal the collection packet.
8. Wipe the forceps/knife with rag or paper towel and inspect for any scales remaining. If necessary rinse with water.
9. 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 half a pencil eraser, 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.

Need HELP or Have Questions?

Contact Patrick Kennedy or Tim Copeland at IDFG Fishery Research in Nampa, Idaho (208.465.8404 or pat.kennedy@idfg.idaho.gov or tim.copeland@idfg.idaho.gov)

Appendix B: Snake River genetic baselines v2.0 (Ackerman et al. 2012) used for mixed stock analysis at Lower Granite Dam, migratory years 2010 and 2011.

Appendix Table B-1. Genetic stocks and baseline collections used for steelhead mixed stock analysis at Lower Granite Dam (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 (Ackerman et al. 2012). MPG = major population group. Note: Samples/collections listed here were used to analyze both MY 2010 and MY 2011. However, MY 2010 individuals were only genotyped using the initial 96 Chinook SNP assays that were available during the time of genotyping (Ackerman et al. 2011); thus individual assignment was performed using a reduced number of SNPs.

	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 steelhead smolts at Lower Granite Dam, migratory year 2010.

Appendix Table C-1. Number of wild steelhead smolt scale and genetics samples collected at Lower Granite Dam and subsequently aged or genotyped, migratory year 2010.

Statistical week(a)	Sample period ending	Weekly Run Size	Total Samples	Aged Samples	Sexed Samples	Genotyped Samples
18	5/2	217,596	188	183	171	180
19	5/9	123,639	140	139	128	133
20	5/16	99,565	175	174	170	164
21	5/23	194,208	355	346	319	316
22	5/30	75,445	188	185	186	164
23	6/6	65,712	177	172	167	161
24	6/13	16,594	54	53	51	46
25	6/20	4,234	47	45	44	43
26	6/27	2,059	25	23	23	23
27	7/4	347	3	3	3	3
Total			1,352	1,323	1,262	1,233

Appendix Table C-2. Weekly age frequencies of wild steelhead smolts sampled at Lower Granite Dam, migratory year 2010.

Statistical week	Sample period ending	Weekly Run Size	Brood year and age class (frequency)				
			BY2009 1	BY2008 2	BY2007 3	BY2006 4	BY2005 5
18	5/2	217,596	-	46	116	19	2
19	5/9	123,639	3	62	63	11	-
20	5/16	99,565	-	75	87	12	-
21	5/23	194,208	7	174	140	24	1
22	5/30	75,445	5	100	75	5	-
23	6/6	65,712	2	79	71	20	-
24	6/13	16,594	1	26	24	2	-
25	6/20	4,234	-	23	16	6	-
26	6/27	2,059	-	12	8	3	-
27	7/4	347	-	2	1	-	-
24-27	7/8	23,235	1	63	49	11	-
Total			18	599	601	102	3

Appendix Table C-3. Weekly age proportions of wild steelhead smolts sampled at Lower Granite Dam, migratory year 2010. Proportions may not sum to 1 due to rounding error.

Statistical week	Sample period ending	Weekly Run Size	Brood year and age class (proportion)				
			BY2009 1	BY2008 2	BY2007 3	BY2006 4	BY2005 5
18	5/2	217,596	-	0.263	0.621	0.108	0.009
19	5/9	123,639	0.020	0.451	0.459	0.070	-
20	5/16	99,565	-	0.440	0.489	0.070	-
21	5/23	194,208	0.020	0.499	0.410	0.068	0.003
22	5/30	75,445	0.031	0.547	0.392	0.029	-
23	6/6	65,712	0.022	0.479	0.374	0.125	-
24	6/13	16,594	0.003	0.463	0.528	0.006	-
25	6/20	4,234	-	0.488	0.351	0.162	-
26	6/27	2,059	-	0.500	0.394	0.106	-
27	7/8	347	-	0.747	0.253	-	-
24-27	7/8	23,235	0.002	0.475	0.480	0.043	-

Appendix Table C-4. Weekly sex frequencies of wild steelhead smolts sampled at Lower Granite Dam, migratory year 2010.

Statistical week	Sample period ending	Weekly Run Size	Sex (number)	
			Female	Male
18	5/2	217,596	91	80
19	5/9	123,639	53	75
20	5/16	99,565	100	70
21	5/23	194,208	172	147
22	5/30	75,445	114	72
23	6/6	65,712	95	72
24	6/13	16,594	33	18
25	6/20	4,234	33	11
26	6/27	2,059	20	3
27	7/4	347	2	1
28	7/11	0	-	-
24-28	7/8	23,235	88	33
Total:			713	549

Appendix Table C-5. Weekly sex proportions of wild steelhead smolts sampled at Lower Granite Dam, migratory year 2010. Proportions may not sum to 1 due to rounding error.

Statistical week	Sample period ending	Weekly Run Size	Sex (proportion)	
			Female	Male
18	5/2	217,596	0.534	0.466
19	5/9	123,639	0.394	0.606
20	5/16	99,565	0.604	0.396
21	5/23	194,208	0.523	0.477
22	5/30	75,445	0.584	0.416
23	6/6	65,712	0.561	0.439
24	6/13	16,594	0.749	0.251
25	6/20	4,234	0.757	0.243
26	6/27	2,059	0.844	0.156
27	7/8	347	0.505	0.495
24-27	7/8	23,235	0.755	0.245

Appendix Table C-6. Weekly individual assignment frequencies of wild steelhead smolts sampled at Lower Granite Dam, migratory year 2010.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (estimated number)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
18	5/2	217,596	23	32	7	13	30	18	12	14	16	15
19	5/9	123,639	18	13	4	2	14	22	21	6	16	17
20	5/16	99,565	32	6	3	10	9	19	14	10	32	29
21	5/23	194,208	54	17	10	22	25	34	16	26	61	51
22	5/30	75,445	39	13	5	8	5	22	11	7	31	23
23	6/6	65,712	34	8	2	10	8	12	15	10	41	21
24	6/13	16,594	9	1	1	1	1	4	8	3	9	9
25	6/20	4,234	13	2	1	3	-	3	3	4	6	8
26	6/27	2,059	9	1	-	1	-	1	-	3	4	4
27	7/4	347	1	-	-	-	-	1	1	-	-	-
28	7/8	0	-	-	-	-	-	-	-	-	-	-
24-28	7/8	23,235	32	4	2	5	1	9	12	10	19	21
Total			232	93	33	70	92	136	101	83	216	177

Appendix Table C-7. Weekly stock proportions of wild steelhead smolts sampled at Lower Granite Dam, migratory year 2010. Proportions may not sum to 1 due to rounding error.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (proportion)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
18	5/2	217,596	0.127	0.172	0.035	0.068	0.152	0.097	0.077	0.088	0.092	0.091
19	5/9	123,639	0.144	0.106	0.026	0.010	0.101	0.155	0.142	0.052	0.124	0.138
20	5/16	99,565	0.191	0.031	0.018	0.057	0.056	0.109	0.089	0.055	0.203	0.191
21	5/23	194,208	0.170	0.054	0.033	0.067	0.078	0.107	0.054	0.083	0.196	0.159
22	5/30	75,445	0.204	0.080	0.031	0.041	0.032	0.175	0.056	0.045	0.226	0.109
23	6/6	65,712	0.213	0.042	0.010	0.060	0.047	0.091	0.097	0.084	0.237	0.119
24	6/13	16,594	0.150	0.004	0.007	0.045	0.060	0.173	0.194	0.109	0.151	0.107
25	6/20	4,234	0.331	0.038	0.019	0.094	-	0.064	0.070	0.114	0.117	0.153
26	6/27	2,059	0.357	0.052	-	0.020	-	0.051	-	0.130	0.208	0.182
27	7/8	347	0.495	-	-	-	-	0.253	0.253	-	-	-
24-27	7/8	23,235	0.206	0.014	0.008	0.051	0.043	0.144	0.156	0.110	0.148	0.120

Appendix Table C-8. Weekly stock abundance of wild steelhead smolts sampled at Lower Granite Dam, migratory year 2010. Percentages in bottom row may not sum to 100.0% due to rounding error.

Statistical week	Time period ending	Weekly Run Size	Genetic stock (estimated abundance)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
13-18	5/2	344,875	43,668	59,462	12,195	23,356	52,489	33,408	26,567	30,453	31,832	31,444
19	5/9	123,639	17,862	13,165	3,197	1,225	12,513	19,210	17,597	6,462	15,335	17,073
20	5/16	99,565	19,005	3,122	1,762	5,673	5,566	10,807	8,882	5,494	20,232	19,020
21	5/23	194,208	33,065	10,513	6,385	12,923	15,182	20,852	10,395	16,029	38,014	30,849
22	5/30	75,445	15,428	6,032	2,367	3,105	2,430	13,187	4,239	3,361	17,048	8,249
23	6/6	65,712	13,978	2,762	676	3,962	3,073	5,956	6,379	5,545	15,573	7,808
24	6/13	16,594	2,496	63	114	741	1,000	2,870	3,223	1,804	2,511	1,772
25	6/20	4,234	1,401	161	78	399	-	272	298	481	497	648
26	6/27	2,059	735	107	-	42	-	105	-	268	428	375
27	7/8	347	172	-	-	-	-	88	88	-	-	-
24-27	7/8	23,235	4,797	330	192	1,179	1,002	3,338	3,614	2,553	3,437	2,793
28-31	7/31	93	19	1	1	5	4	13	14	10	14	11
Run total:		926,771	147,822	95,388	26,774	51,427	92,261	106,772	77,687	69,907	141,485	117,248
Percent of total:			16.0%	10.3%	2.9%	5.5%	10.0%	11.5%	8.4%	7.5%	15.3%	12.7%

Appendix Table C-9. Frequencies of natural origin juvenile steelhead sampled at Lower Granite Dam by sex and age for each genetic stock, migratory year 2010. Only individual fish whose probability of assignment was ≥0.80 (n = 541) are included for decomposition.

		Brood year and age class (frequency)					
Genetic stock	**Sex**	**BY2009 1**	**BY2008 2**	**BY2007 3**	**BY2006 4**	**BY2005 5**	**Total**
UPSALM	F	0	29	24	6	0	59
	M	4	21	11	0	0	36
MFSALM	F	0	6	26	7	0	39
	M	0	3	14	2	0	19
SFSALM	F	0	1	10	3	0	14
	M	0	3	6	0	0	9
LOSALM	F	0	6	2	1	1	10
	M	0	3	3	0	0	6
UPCLWR	F	0	5	19	3	1	28
	M	0	8	18	5	1	32
SFCLWR	F	0	27	18	3	0	48
	M	2	18	22	1	0	43
LOCLWR	F	0	5	11	1	0	17
	M	0	10	12	0	0	22
IMNAHA	F	0	6	9	4	0	19
	M	0	10	5	0	0	15
GRROND	F	2	16	31	6	0	55
	M	1	15	12	0	0	28
LSNAKE	F	0	12	8	3	0	23
	M	1	8	8	2	0	19

Appendix Table C-10. Percentages of natural origin juvenile steelhead sampled at Lower Granite Dam by gender by age for each genetic stock, migratory year 2010. Age percentages are computed within each sex. Only individual fish whose probability of assignment was ≥0.80 (n = 541) are included for decomposition.

		Brood year and age class (percentage)					
Genetic stock	**Sex**	**BY2009 1**	**BY2008 2**	**BY2007 3**	**BY2006 4**	**BY2005 5**	**Total**
UPSALM	F	0.0	49.2	40.7	10.2	0.0	62.1
	M	11.1	58.3	30.6	0.0	0.0	37.9
MFSALM	F	0.0	15.4	66.7	17.9	0.0	67.2
	M	0.0	15.8	73.7	10.5	0.0	32.8
SFSALM	F	0.0	7.1	71.4	21.4	0.0	60.9
	M	0.0	33.3	66.7	0.0	0.0	39.1
LOSALM	F	0.0	60.0	20.0	10.0	10.0	62.5
	M	0.0	50.0	50.0	0.0	0.0	37.5
UPCLWR	F	0.0	17.9	67.9	10.7	3.6	46.7
	M	0.0	25.0	56.3	15.6	3.1	53.3
SFCLWR	F	0.0	56.3	37.5	6.3	0.0	52.7
	M	4.7	41.9	51.2	2.3	0.0	47.3
LOCLWR	F	0.0	29.4	64.7	5.9	0.0	43.6
	M	0.0	45.5	54.5	0.0	0.0	56.4
IMNAHA	F	0.0	31.6	47.4	21.1	0.0	55.9
	M	0.0	66.7	33.3	0.0	0.0	44.1
GRROND	F	3.6	29.1	56.4	10.9	0.0	66.3
	M	3.6	53.6	42.9	0.0	0.0	33.7
LSNAKE	F	0.0	52.2	34.8	13.0	0.0	54.8
	M	5.3	42.1	42.1	10.5	0.0	45.2

Appendix Table C-11. Estimated abundance of natural origin juvenile steelhead sampled at Lower Granite Dam by gender by age for each genetic stock, migratory year 2010. Only individual fish whose probability of assignment was ≥0.80 (n = 541) are included for decomposition.

		Brood year and age class (abundance)					
Genetic stock	**Sex**	**BY2009 1**	**BY2008 2**	**BY2007 3**	**BY2006 4**	**BY2005 5**	**Total**
UPSALM	F	-	45,125	37,345	9,336	-	91,805
	M	6,224	32,676	17,116	-	-	56,017
	Total:	6,224	77,801	54,461	9,336	-	147,822
MFSALM	F	-	9,868	42,760	11,512	-	64,140
	M	-	4,934	23,025	3,289	-	31,248
	Total:	-	14,802	65,785	14,802	-	95,388
SFSALM	F	-	1,164	11,641	3,492	-	16,297
	M	-	3,492	6,985	-	-	10,477
	Total:	-	4,656	18,625	3,492	-	26,774
LOSALM	F	-	19,285	6,428	3,214	3,214	32,142
	M	-	9,643	9,643	-	-	19,285
	Total:	-	28,928	16,071	3,214	3,214	51,427
UPCLWR	F	-	7,688	29,216	4,613	1,538	43,055
	M	-	12,301	27,678	7,688	1,538	49,206
	Total:	-	19,990	56,894	12,301	3,075	92,261
SFCLWR	F	-	31,680	21,120	3,520	-	56,319
	M	2,347	21,120	25,813	1,173	-	50,453
	Total:	2,347	52,799	46,933	4,693	-	106,772
LOCLWR	F	-	9,960	21,912	1,992	-	33,864
	M	-	19,920	23,904	-	-	43,823
	Total:	-	29,880	45,815	1,992	-	77,687
IMNAHA	F	-	12,337	18,505	8,224	-	39,066
	M	-	20,561	10,280	-	-	30,841
	Total:	-	32,897	28,785	8,224	-	69,907
GRRON D	F	3,409	27,274	52,844	10,228	-	93,755
	M	1,705	25,570	20,456	-	-	47,730
	Total:	5,114	52,844	73,299	10,228	-	141,485
LSNAKE	F	-	33,499	22,333	8,375	-	64,207
	M	2,792	22,333	22,333	5,583	-	53,041
	Total:	2,792	55,832	44,666	13,958	-	117,248

Appendix D: Wild yearling Chinook salmon smolts at Lower Granite Dam, migratory year 2010.

Appendix Table D-1. Number of wild yearling Chinook salmon smolt samples collected at Lower Granite Dam and subsequently genotyped, migratory year 2010.

Statistical week	Sample period ending	Weekly Run Size	Total Samples	Sexed Samples	Genotyped Samples
18	5/2	371,260	267	246	265
19	5/9	160,451	205	197	205
20	5/16	139,949	252	230	244
21	5/23	172,531	403	375	396
22	5/30	72,138	177	168	176
23	6/6	28,058	67	64	66
24	6/13	13,302	22	18	22
25	6/20	3,061	17	15	17
26	6/27	1,309	8	8	8
27	7/4	66	1	1	1
28	7/11	0	-	-	
Total:			1,419	1,322	1,400

Appendix Table D-2. Weekly sex frequencies of wild yearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2010.

Statistical week	Sample period ending	Weekly Run Size	Sex (number)	
			Female	Male
18	5/2	371,260	137	109
19	5/9	160,451	114	83
20	5/16	139,949	157	73
21	5/23	172,531	224	151
22	5/30	72,138	92	76
23	6/6	28,058	39	25
24	6/13	13,302	11	7
25	6/20	3,061	10	5
26	6/27	1,309	2	6
27	7/4	66	1	-
28	7/11	0	-	-
23-28	7/11	45,795	63	43
Total:			787	535

Appendix Table D-3. Weekly sex proportions of wild yearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2010.

Statistical week	Sample period ending	Weekly Run Size	Sex (proportion)	
			Female	Male
18	5/2	371,260	0.529	0.471
19	5/9	160,451	0.486	0.514
20	5/16	139,949	0.708	0.292
21	5/23	172,531	0.591	0.409
22	5/30	72,138	0.555	0.445
23	6/6	28,058	0.489	0.511
24	6/13	13,302	0.782	0.218
25	6/20	3,061	0.663	0.337
26	6/27	1,309	0.348	0.652
27	7/4	66	1.000	-
23-27	7/4	45,795	0.576	0.424

Appendix Table D-4. Weekly individual assignment frequencies of wild yearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2010.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (number)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
18	5/2	371,260	68	60	14	36	85	2	-
19	5/9	160,451	42	31	6	22	103	1	-
20	5/16	139,949	38	38	4	24	134	4	2
21	5/23	172,531	71	74	10	32	203	3	3
22	5/30	72,138	33	33	8	17	80	-	5
23	6/6	28,058	15	10	-	4	19	2	16
24	6/13	13,302	1	2	-	1	17	-	1
25	6/20	3,061	4	2	1	1	9	-	-
26	6/27	1,309	1	3	-	-	3	-	1
27	7/4	66	-	-	-	-	1	-	-
28	7/11	0	-	-	-	-	-	-	-
23-28	7/11	45,795	21	17	1	6	49	2	18
Total:			273	253	43	137	654	12	28

Appendix Table D-5. Weekly genetic stock proportions of wild yearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2010.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (proportion)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
18	5/2	371,260	0.231	0.215	0.070	0.139	0.335	0.010	-
19	5/9	160,451	0.329	0.125	0.020	0.100	0.425	0.002	-
20	5/16	139,949	0.154	0.157	0.015	0.090	0.560	0.017	0.008
21	5/23	172,531	0.169	0.196	0.024	0.081	0.516	0.007	0.007
22	5/30	72,138	0.188	0.156	0.056	0.090	0.486	-	0.023
23	6/6	28,058	0.159	0.209	-	0.061	0.331	0.037	0.204
24	6/13	13,302	0.006	0.054	-	0.006	0.915	-	0.017
25	6/20	3,061	0.257	0.118	0.050	0.078	0.497	-	-
26	6/27	1,309	0.106	0.480	-	-	0.307	-	0.106
27	7/4	66	-	-	-	-	1.000	-	-
23-27	7/4	45,795	0.118	0.168	0.002	0.045	0.503	0.024	0.140

Appendix Table D-6. Weekly genetic stock abundance of wild yearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2010.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (abundance)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
13-18	5/2	621,441	143,581	133,676	43,574	86,546	208,079	5,986	-
19	5/9	160,451	52,748	19,982	3,161	16,065	68,145	350	-
20	5/16	139,949	21,612	21,972	2,058	12,539	78,316	2,312	1,140
21	5/23	172,531	29,087	33,828	4,123	13,985	89,020	1,229	1,260
22	5/30	72,138	13,592	11,264	4,051	6,516	35,081	-	1,633
23	6/6	28,058	4,449	5,852	-	1,716	9,291	1,036	5,713
24	6/13	13,302	85	723	-	85	12,176	-	232
25	6/20	3,061	786	360	153	240	1,521	-	-
26	6/27	1,309	139	629	-	-	402	-	139
27	7/4	66	-	-	-	-	66	-	-
23-27	7/4	45,795	5,410	7,715	95	2,047	23,033	1,096	6,400
28-31	7/31	101	12	17	0	5	51	2	14
Run total:		1,212,407	266,042	228,454	57,063	137,702	501,724	10,975	10,447

Appendix Table D-7. Frequencies of wild yearling Chinook smolts sampled at Lower Granite Dam by sex for each genetic stock, migratory year 2010. Only individual fish whose probability of assignment was ≥0.80 (n = 541) are included for decomposition.

Genetic	Number			Proportion		Abundance		
stock	Female	Male	Total	F	M	F	M	Total
UPSALM	53	42	95	55.8	44.2	148,423	117,618	266,042
MFSALM	56	40	96	58.3	41.7	133,265	95,189	228,454
CHMBLN	9	9	18	50.0	50.0	28,531	28,531	57,063
SFSALM	16	17	33	48.5	51.5	66,765	70,938	137,702
HELLSC	242	136	378	64.0	36.0	321,210	180,514	501,724
TUCANO	2	3	5	n/a	n/a	n/a	n/a	n/a
FALL	9	18	27	33.3	66.7	3,482	6,965	10,447

Appendix E: Wild subyearling Chinook salmon smolts at Lower Granite Dam, migratory year 2010 (March-July).

Appendix Table E-1. Number of wild subyearling Chinook salmon smolt samples collected at Lower Granite Dam and subsequently genotyped, migratory year 2010.

Statistical week	Sample period ending	Weekly Run Size	Total Samples	Sexed Samples	Genotyped Samples
21	5/23	53,093	1	1	1
22	5/30	59,347	4	4	4
23	6/6	839,077	56	53	56
24	6/13	658,987	53	50	53
25	6/20	347,919	95	92	95
26	6/27	311,330	117	113	116
27	7/4	222,458	105	88	104
28	7/11	222,334	69	61	69
Total:			500	462	498

Appendix Table E-2. Weekly sex frequencies of wild subyearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2010.

Statistical week	Sample period ending	Weekly Run Size	Sex (number)	
			Female	Male
21	5/23	53,093	1	-
22	5/30	59,347	3	1
23	6/6	839,077	27	26
24	6/13	658,987	20	30
25	6/20	347,919	42	50
26	6/27	311,330	74	39
27	7/4	222,458	60	28
28	7/11	222,334	30	31
27-28	7/11	444,793	90	59
Total:			257	205

Appendix Table E-3. Weekly sex proportions of wild subyearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2010.

Statistical week	Sample period ending	Weekly Run Size	Sex (proportion)	
			Female	Male
21-24	6/13	1,610,504	0.428	0.572
25	6/20	347,919	0.462	0.538
26	6/27	311,330	0.676	0.324
27	7/4	222,458	0.687	0.313
28	7/11	222,334	0.511	0.489
27-28	7/11	762,819	0.617	0.383

Appendix Table E-4. Weekly genetic stock frequencies of wild subyearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2010.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (number)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
21	5/23	53,093	-	-	-	-	-	-	1
22	5/30	59,347	-	-	-	-	-	-	4
23	6/6	839,077	-	-	-	-	1	-	55
24	6/13	658,987	2	-	1	-	1	-	49
25	6/20	347,919	-	1	-	-	7	-	87
26	6/27	311,330	1	-	-	2	13	-	100
27	7/4	222,458	1	1	-	-	8	-	94
28	7/11	222,334	-	-	-	-	-	1	68
27-28	7/31	444,793	1	1	-	-	8	1	162
Total:			4	2	1	2	30	1	458

Appendix Table E-5. Weekly genetic stock frequencies of wild subyearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2010.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (proportion)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
21-24	6/13	711,468	0.019	-	0.005	-	0.017	-	0.959
25	6/20	347,919	-	0.012	-	-	0.083	-	0.905
26	6/27	311,330	0.007	-	-	0.015	0.099	-	0.880
27	7/4	222,458	0.010	0.010	-	-	0.073	-	0.907
28	7/11	222,334	-	-	-	-	-	0.009	0.991
27-28	7/11	444,793	0.006	0.006	-	-	0.044	0.004	0.940

Appendix Table E-6. Weekly genetic stock abundance of wild subyearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2010.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (abundance)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
13-24	6/13	711,468	30,799	-	8,011	-	27,460	-	1,548,491
25	6/20	347,919	-	4,328	-	-	28,838	-	314,753
26	6/27	311,330	2,196	-	-	4,613	30,670	-	273,851
27-31	7/11	444,793	4,597	4,597	-	-	33,510	2,756	717,359
Run total		**3,036,829**	**37,592**	**8,925**	**8,011**	**4,613**	**120,478**	**2,756**	**2,854,454**

Appendix F: Wild steelhead smolts at Lower Granite Dam, migratory year 2011.

Appendix Table F-1. Number of wild steelhead smolt scale and genetics samples collected at Lower Granite Dam and subsequently aged or genotyped, migratory year 2011.

Statistical week(a)	Sample period ending	Weekly Run Size	Total Samples	Aged Samples	Sexed Samples	Genotyped Samples
14	4/3	16,822	109	104	99	107
15	4/10	49,841	147	145	138	146
16	4/17	23,712	102	98	96	99
17	4/24	48,121	84	83	80	83
18	5/1	47,865	108	106	104	108
19	5/8	74,448	146	143	139	146
20	5/15	333,393	464	451	441	462
21	5/22	159,058	314	311	268	307
22	5/29	88,669	302	298	295	302
23	6/5	42,998	149	147	135	148
24	6/12	18,652	133	131	122	133
25	6/19	5,700	37	36	34	37
26	6/26	1,955	18	18	18	18
27	7/3	1,212	8	8	8	8
28	7/10	424	10	9	10	10
Total			2,131	2,088	1,987	2,114

Appendix Table F-2. Weekly age frequencies of wild steelhead smolts sampled at Lower Granite Dam, migratory year 2011.

Statistical week	Sample period ending	Weekly Run Size	Brood year and age class (number)				
			BY2010 1	BY2009 2	BY2008 3	BY2007 4	BY2006 5
14	4/3	16,822	2	69	28	4	-
15	4/10	49,841	4	87	46	8	-
16	4/17	23,712	3	61	31	3	-
17	4/24	48,121	3	51	25	4	-
18	5/1	47,865	2	72	28	4	-
19	5/8	74,448	3	107	24	9	-
20	5/15	333,393	10	250	160	29	2
21	5/22	159,058	24	196	72	18	1
22	5/29	88,669	50	190	49	9	-
23	6/5	42,998	26	93	22	6	-
24	6/12	18,652	32	75	20	4	-
25	6/19	5,700	9	23	3	1	-
26	6/26	1,955	5	8	4	1	-
27	7/3	1,212	-	6	2	-	-
28	7/10	424	3	4	2	-	-
25-28	7/10	9,290	17	41	11	2	-
Total			176	1,292	516	100	3

Appendix Table F-3. Weekly age proportions of wild steelhead smolts sampled at Lower Granite Dam, migratory year 2011. Proportions may not sum to 1 due to rounding error.

Statistical week	Sample period ending	Weekly Run Size	Brood year and age class (proportion)				
			BY2010 1	BY2009 2	BY2008 3	BY2007 4	BY2006 5
14	4/3	16,822	0.002	0.683	0.297	0.018	-
15	4/10	49,841	0.017	0.575	0.364	0.044	-
16	4/17	23,712	0.035	0.611	0.324	0.030	-
17	4/24	48,121	0.029	0.608	0.311	0.052	-
18	5/1	47,865	0.020	0.679	0.262	0.039	-
19	5/8	74,448	0.021	0.749	0.167	0.063	-
20	5/15	333,393	0.022	0.553	0.356	0.065	0.005
21	5/22	159,058	0.073	0.624	0.237	0.062	0.004
22	5/29	88,669	0.169	0.636	0.165	0.031	-
23	6/5	42,998	0.180	0.628	0.146	0.046	-
24	6/12	18,652	0.245	0.567	0.158	0.030	-
25	6/19	5,700	0.244	0.622	0.107	0.027	-
26	6/26	1,955	0.290	0.488	0.153	0.069	-
27	7/3	1,212	-	0.767	0.233	-	-
28	7/10	424	0.333	0.417	0.250	-	-
25-28	7/10	9,290	0.231	0.601	0.135	0.032	-

Appendix Table F-4. Weekly sex frequencies of wild steelhead smolts sampled at Lower Granite Dam, migratory year 2011.

Statistical week	Sample period ending	Weekly Run Size	Sex (number)	
			Female	Male
14	4/3	16,822	57	42
15	4/10	49,841	70	68
16	4/17	23,712	54	42
17	4/24	48,121	45	35
18	5/1	47,865	61	43
19	5/8	74,448	77	62
20	5/15	333,393	231	210
21	5/22	159,058	157	111
22	5/29	88,669	146	149
23	6/5	42,998	83	52
24	6/12	18,652	76	46
25	6/19	5,700	23	11
26	6/26	1,955	11	7
27	7/3	1,212	8	0
28	7/10	424	6	4
25-28	7/10	9,290	48	22
Total:			1,105	882

Appendix Table F-5. Weekly sex proportions of wild steelhead smolts sampled at Lower Granite Dam, migratory year 2011. Proportions may not sum to 1 due to rounding error.

Statistical week	Sample period ending	Weekly Run Size	Sex (proportion)	
			Female	Male
14	4/3	16,822	0.581	0.419
15	4/10	49,841	0.491	0.509
16	4/17	23,712	0.572	0.428
17	4/24	48,121	0.575	0.425
18	5/1	47,865	0.576	0.424
19	5/8	74,448	0.584	0.416
20	5/15	333,393	0.527	0.473
21	5/22	159,058	0.581	0.419
22	5/29	88,669	0.493	0.507
23	6/5	42,998	0.604	0.396
24	6/12	18,652	0.608	0.392
25	6/19	5,700	0.692	0.308
26	6/26	1,955	0.600	0.400
27	7/3	1,212	1.00	-
28	7/10	424	0.625	0.375
25-28	7/10	9,290	0.702	0.298

Appendix Table F-6. Weekly individual assignment frequencies of wild steelhead smolts sampled at Lower Granite Dam, migratory year 2011.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (estimated number)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
14	4/3	16,822	10	3	1	3	12	18	12	3	22	23
15	4/10	49,841	11	6	2	5	39	24	7	2	36	14
16	4/17	23,712	14	2	2	4	20	10	7	5	24	11
17	4/24	48,121	11	3	4	5	8	8	11	3	18	12
18	5/1	47,865	18	6	4	2	6	7	15	9	21	20
19	5/8	74,448	14	6	5	6	14	26	14	18	24	19
20	5/15	333,393	79	61	29	39	50	47	28	40	47	42
21	5/22	159,058	67	14	9	21	18	16	22	18	74	48
22	5/29	88,669	65	8	6	20	10	12	24	31	67	59
23	6/5	42,998	33	5	2	10	3	10	9	23	32	21
24	6/12	18,652	43	7	1	15	2	5	4	13	24	19
25	6/19	5,700	8	1	1	2	-	1	2	3	8	11
26	6/26	1,955	7	-	-	-	-	1	-	2	7	1
27	7/3	1,212	2	2	-	-	-	-	-	-	3	1
28	7/10	424	-	-	-	2	1	1	3	-	2	1
25-28	7/10	9,290	17	3	1	4	1	3	5	5	20	14
Total			382	124	66	134	183	186	158	170	409	302

Appendix Table F-7. Weekly stock proportions of wild steelhead smolts sampled at Lower Granite Dam, migratory year 2011. Proportions may not sum to 1 due to rounding error.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (proportion)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
14	4/3	16,822	0.093	0.037	0.005	0.010	0.234	0.217	0.047	0.037	0.208	0.113
15	4/10	49,841	0.081	0.032	0.009	0.031	0.275	0.182	0.052	0.013	0.228	0.097
16	4/17	23,712	0.146	0.018	0.024	0.043	0.195	0.099	0.070	0.053	0.242	0.110
17	4/24	48,121	0.132	0.036	0.050	0.059	0.098	0.082	0.139	0.044	0.229	0.132
18	5/1	47,865	0.166	0.054	0.036	0.019	0.058	0.066	0.142	0.080	0.192	0.188
19	5/8	74,448	0.094	0.045	0.032	0.042	0.093	0.184	0.095	0.123	0.169	0.125
20	5/15	333,393	0.172	0.132	0.067	0.082	0.109	0.100	0.061	0.087	0.102	0.088
21	5/22	159,058	0.216	0.048	0.030	0.067	0.067	0.052	0.069	0.055	0.243	0.153
22	5/29	88,669	0.215	0.026	0.020	0.067	0.033	0.040	0.079	0.103	0.221	0.195
23	6/5	42,998	0.228	0.031	0.013	0.069	0.017	0.058	0.066	0.151	0.223	0.146
24	6/12	18,652	0.333	0.048	0.005	0.109	0.016	0.038	0.028	0.100	0.180	0.142
25	6/19	5,700	0.211	0.013	0.024	0.081	-	0.041	0.056	0.085	0.223	0.265
26	6/26	1,955	0.448	-	-	-	-	0.070	-	0.111	0.333	0.037
27	7/3	1,212	0.165	0.233	-	-	-	-	-	-	0.503	0.100
28	7/10	424	-	-	-	0.167	0.083	0.125	0.292	-	0.250	0.083
25-28	7/10	9,290	0.252	0.033	0.015	0.057	0.003	0.046	0.045	0.079	0.278	0.192

Appendix Table F-8. Weekly stock abundance of wild steelhead smolts sampled at Lower Granite Dam, migratory year 2011. Percentages in bottom row may not sum to 100.0% due to rounding error.

Statistical week	Time period ending	Weekly Run Size	Genetic stock (estimated abundance)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
13	3/28	1,385	128	51	6	14	324	300	65	51	288	156
14	4/3	16,822	1,560	622	76	171	3,940	3,646	794	619	3,495	1,899
15	4/10	49,841	4,060	1,588	457	1,523	13,730	9,060	2,598	629	11,361	4,834
16	4/17	23,712	3,453	432	578	1,013	4,633	2,343	1,655	1,263	5,733	2,608
17	4/24	48,121	6,347	1,726	2,386	2,818	4,736	3,934	6,680	2,120	11,030	6,345
18	5/1	47,865	7,929	2,587	1,709	904	2,787	3,146	6,795	3,841	9,170	8,999
19	5/8	74,448	6,985	3,320	2,405	3,094	6,898	13,699	7,039	9,140	12,570	9,298
20	5/15	333,393	57,443	44,108	22,321	27,224	36,306	33,282	20,490	**28,944**	33,965	29,309
21	5/22	159,058	34,357	7,573	4,795	10,729	10,704	8,206	10,960	8,713	38,614	24,407
22	5/29	88,669	19,072	2,329	1,760	5,975	2,940	3,513	6,993	9,160	19,597	17,331
23	6/5	42,998	9,785	1,319	550	2,971	747	2,481	2,818	6,479	9,573	6,274
24	6/12	18,652	6,208	904	98	2,035	293	707	514	1,874	3,366	2,653
25	6/19	5,700	1,205	76	136	459	-	235	318	486	1,272	1,513
26	6/26	1,955	876	-	-	-	-	137	-	218	652	72
27	7/3	1,212	200	282	-	-	-	-	-	-	610	121
28	7/10	424	-	-	-	71	35	53	124	-	106	35
25-28	7/10	9,290	2,340	308	142	530	25	426	418	737	2,582	1,781
29-31	7/31	258	65	9	4	15	1	12	12	20	72	49
Run total:		914,513	**159,675**	**66,926**	**37,282**	**59,016**	**88,073**	**84,756**	**67,853**	**73,557**	**161,472**	**115,904**
Percent of total:			17.5%	7.3%	4.1%	6.5%	9.6%	9.3%	7.4%	8.0%	17.7%	12.7%

Appendix Table F-9. Frequencies of natural origin juvenile steelhead sampled at Lower Granite Dam by sex and age for each genetic stock, migratory year 2011. Only individual fish whose probability of assignment was ≥0.80 (n = 884) are included for decomposition.

		Brood year and age class (frequency)					
Genetic stock	**Sex**	**BY2010 1**	**BY2009 2**	**BY2008 3**	**BY2007 4**	**BY2006 5**	**Total**
UPSALM	F	14	67	15	5	-	101
	M	10	41	13	-	-	64
MFSALM	F	1	12	28	9	-	50
	M	-	10	17	6	-	33
SFSALM	F	-	7	11	4	-	22
	M	-	5	12	7	1	25
LOSALM	F	-	8	7	1	-	16
	M	2	6	5	-	-	13
UPCLWR	F	2	23	35	9	1	70
	M	3	34	20	4	-	61
SFCLWR	F	1	46	17	2	-	66
	M	5	44	11	2	-	62
LOCLWR	F	3	18	5	1	-	27
	M	1	15	6	-	-	22
IMNAHA	F	-	20	11	1	-	32
	M	-	18	7	-	-	25
GRROND	F	5	45	18	3	-	71
	M	4	39	11	1	-	55
LSNAKE	F	5	22	10	-	-	37
	M	6	21	5	-	-	32

Appendix Table F-10. Percentage of natural origin juvenile steelhead sampled at Lower Granite Dam by gender by age for each genetic stock, migratory year 2011. Only individual fish whose probability of assignment was ≥0.80 (n = 884) are included for decomposition.

		Brood year and age class (percentage)					
Genetic stock	**Sex**	**BY2009 1**	**BY2008 2**	**BY2007 3**	**BY2006 4**	**BY2005 5**	**Total**
UPSALM	F	13.9	66.3	14.9	5.0	0.0	61.2
	M	15.6	64.1	20.3	0.0	0.0	38.8
MFSALM	F	2.0	24.0	56.0	18.0	0.0	60.2
	M	0.0	30.3	51.5	18.2	0.0	39.8
SFSALM	F	0.0	31.8	50.0	18.2	0.0	46.8
	M	0.0	20.0	48.0	28.0	4.0	53.2
LOSALM	F	0.0	50.0	43.8	6.3	0.0	55.2
	M	15.4	46.2	38.5	0.0	0.0	44.8
UPCLWR	F	2.9	32.9	50.0	12.9	1.4	53.4
	M	4.9	55.7	32.8	6.6	0.0	46.6
SFCLWR	F	1.5	69.7	25.8	3.0	0.0	51.6
	M	8.1	71.0	17.7	3.2	0.0	48.4
LOCLWR	F	11.1	66.7	18.5	3.7	0.0	55.1
	M	4.5	68.2	27.3	0.0	0.0	44.9
IMNAHA	F	0.0	62.5	34.4	3.1	0.0	56.1
	M	0.0	72.0	28.0	0.0	0.0	43.9
GRROND	F	7.0	63.4	25.4	4.2	0.0	56.3
	M	7.3	70.9	20.0	1.8	0.0	43.7
LSNAKE	F	13.5	59.5	27.0	0.0	0.0	53.6
	M	18.8	65.6	15.6	0.0	0.0	46.4

Appendix Table F-11. Estimated abundance of natural origin juvenile steelhead sampled at Lower Granite Dam by gender by age for each genetic stock, migratory year 2011. Only individual fish whose probability of assignment was ≥0.80 (n = 884) are included for decomposition.

		Brood year and age class (abundance)					
Genetic stock	**Sex**	**BY2009 1**	**BY2008 2**	**BY2007 3**	**BY2006 4**	**BY2005 5**	**Total**
UPSALM	F	13,548	64,838	14,516	4,839	-	97,740
	M	9,677	39,677	12,580	-	-	61,935
	Total:	23,225	104,515	27,096	4,839	-	159,675
MFSALM	F	806	9,676	22,577	7,257	-	40,317
	M	-	8,063	13,708	4,838	-	26,609
	Total:	806	17,739	36,285	12,095	-	66,926
SFSALM	F	-	5,553	8,726	3,173	-	17,451
	M	-	3,966	9,519	5,553	793	19,831
	Total:	-	9,519	18,244	8,726	793	37,282
LOSALM	F	-	16,280	14,245	2,035	-	32,561
	M	4,070	12,210	10,175	-	-	26,455
	Total:	4,070	28,490	24,420	2,035	-	59,016
UPCLWR	F	1,345	15,463	23,531	6,051	672	47,062
	M	2,017	22,859	13,446	2,689	-	41,011
	Total:	3,362	38,322	36,977	8,740	672	88,073
SFCLWR	F	662	30,459	11,257	1,324	-	43,702
	M	3,311	29,135	7,284	1,324	-	41,054
	Total:	3,973	59,594	18,540	2,649	-	84,756
LOCLWR	F	4,154	24,926	6,924	1,385	-	37,388
	M	1,385	20,771	8,309	-	-	30,465
	Total:	5,539	45,697	15,232	1,385	-	67,853
IMNAHA	F	-	25,809	14,195	1,290	-	41,295
	M	-	23,229	9,033	-	-	32,262
	Total:	-	49,038	23,229	1,290	-	73,557
GRRON D	F	6,408	57,669	23,067	3,845	-	90,988
	M	5,126	49,979	14,097	1,282	-	70,484
	Total:	11,534	107,648	37,164	5,126	-	161,472
LSNAKE	F	8,399	36,955	16,798	-	-	62,151
	M	10,079	35,275	8,399	-	-	53,753
	Total:	18,477	72,230	25,197	-	-	115,904

Appendix G: Wild yearling Chinook salmon smolts at Lower Granite Dam, migratory year 2011.

Appendix Table G-1. Number of wild yearling Chinook salmon smolt samples collected at Lower Granite Dam and subsequently genotyped, migratory year 2011.

Statistical week	Sample period ending	Weekly Run Size	Total Samples	Sexed Samples	Genotyped Samples
14	4/3	18,277	87	84	87
15	4/10	104,078	169	165	167
16	4/17	102,254	194	189	194
17	4/24	93,073	97	91	97
18	5/2	175,846	206	202	206
19	5/9	190,054	215	202	215
20	5/16	261,549	215	206	214
21	5/23	143,837	115	104	115
22	5/30	63,492	110	97	110
23	6/6	15,725	24	24	24
24	6/13	10,047	31	31	31
25	6/20	4,071	21	21	21
26	6/27	6,415	19	17	19
27	7/4	1,998	5	3	5
28	7/11	197	2	2	2
Total:			1,510	1,438	1,507

Appendix Table G-2. Weekly sex frequencies of wild yearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2011.

Statistical week	Sample period ending	Weekly Run Size	Sex (number)	
			Female	Male
14	4/3	18,277	39	45
15	4/10	104,078	60	105
16	4/17	102,254	93	96
17	4/24	93,073	34	57
18	5/2	175,846	90	112
19	5/9	190,054	109	93
20	5/16	261,549	103	103
21	5/23	143,837	59	45
22	5/30	63,492	47	50
23	6/6	15,725	11	13
24	6/13	10,047	17	14
25	6/20	4,071	11	10
26	6/27	6,415	11	6
27	7/4	1,998	2	1
28	7/11	197	1	1
23-28	7/11	38,256	53	45
Total:			687	751

Appendix Table G-3. Weekly sex proportions of wild yearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2011.

Statistical week	Sample period ending	Weekly Run Size	Sex (proportion)	
			Female	Male
14	4/3	18,277	0.498	0.502
15	4/10	104,078	0.364	0.636
16	4/17	102,254	0.491	0.509
17	4/24	93,073	0.376	0.624
18	5/2	175,846	0.446	0.554
19	5/9	190,054	0.540	0.460
20	5/16	261,549	0.498	0.502
21	5/23	143,837	0.548	0.452
22	5/30	63,492	0.487	0.513
23	6/6	15,725	0.430	0.570
24	6/13	10,047	0.626	0.374
25	6/20	4,071	0.516	0.484
26	6/27	6,415	0.571	0.429
27	7/4	1,998	0.758	0.242
28	7/11	285	0.690	0.310
23-28	7/4	38,540	0.525	0.475

Appendix Table G-4. Weekly individual assignment frequencies of wild yearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2011.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (number)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
14	4/3	18,277	5	2	-	9	68	1	2
15	4/10	104,078	37	20	-	28	77	4	1
16	4/17	102,254	43	24	4	36	86	1	-
17	4/24	93,073	20	14	4	20	38	1	-
18	5/2	175,846	52	50	12	39	49	2	2
19	5/9	190,054	51	39	12	27	86	-	-
20	5/16	261,549	48	48	9	33	74	2	-
21	5/23	143,837	31	16	7	21	39	-	1
22	5/30	63,492	20	18	3	19	41	-	9
23	6/6	15,725	4	2	-	5	8	-	5
24	6/13	10,047	4	4	1	2	16	1	3
25	6/20	4,071	4	2	-	1	14	-	-
26	6/27	6,415	3	3	1	1	10	-	1
27	7/4	1,998	-	-	-	1	2	-	2
28	7/11	197	1	-	-	-	1	-	-
23-28	7/11	38,453	16	11	2	10	51	1	11
Total:			323	242	53	242	609	12	26

Appendix Table G-5. Weekly genetic stock proportions of wild yearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2011.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (proportion)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
14	4/3	18,277	0.047	0.063	-	0.115	0.739	0.015	0.022
15	4/10	104,078	0.211	0.122	-	0.175	0.466	0.021	0.005
16	4/17	102,254	0.227	0.123	0.020	0.189	0.436	0.006	-
17	4/24	93,073	0.193	0.125	0.040	0.223	0.405	0.013	-
18	5/2	175,846	0.256	0.244	0.061	0.187	0.232	0.010	0.010
19	5/9	190,054	0.245	0.178	0.054	0.126	0.397	-	-
20	5/16	261,549	0.226	0.219	0.045	0.154	0.346	0.009	-
21	5/23	143,837	0.305	0.132	0.049	0.166	0.339	-	0.009
22	5/30	63,492	0.173	0.157	0.029	0.174	0.390	-	0.078
23	6/6	15,725	0.160	0.110	-	0.186	0.279	-	0.264
24	6/13	10,047	0.097	0.150	0.024	0.064	0.554	0.038	0.073
25	6/20	4,071	0.183	0.096	-	0.046	0.675	-	-
26	6/27	6,415	0.124	0.074	0.029	0.074	0.580	-	0.118
27	7/4	1,998	-	-	-	0.141	0.441	-	0.418
28	7/11	197	0.690	-	-	-	0.310	-	-
23-28	7/11	38,256	0.135	0.109	0.012	0.116	0.453	0.010	0.165

Appendix Table G-6. Weekly genetic stock abundance of wild yearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2011.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (abundance)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
13-14(b.)	4/3	20,162	947	1,262	-	2,310	14,898	308	438
15	4/10	104,078	21,924	12,716	-	18,237	48,528	2,139	533
16	4/17	102,254	23,177	12,531	2,008	19,312	44,590	637	-
17	4/24	93,073	17,988	11,680	3,724	20,786	37,730	1,165	-
18	5/2	175,846	44,981	42,887	10,780	32,873	40,839	1,722	1,764
19	5/9	190,054	46,576	33,777	10,326	23,918	75,458	-	-
20	5/16	261,549	59,163	57,317	11,811	40,357	90,484	2,418	-
21	5/23	143,837	43,889	19,006	7,044	23,827	48,771	-	1,300
22	5/30	63,492	10,990	9,980	1,811	11,018	24,740	-	4,953
23	6/6	15,725	2,522	1,733	-	2,924	4,390	-	4,155
24	6/13	10,047	977	1,507	245	640	5,563	379	736
25	6/20	4,071	745	391	-	187	2,748	-	-
26	6/27	6,415	797	474	185	476	3,723	-	760
27	7/4	1,998	-	-	-	282	881	-	835
28	7/11	197	136	-	-	-	61	-	-
23-28(c.)	7/11	38,453	5,198	4,201	445	4,445	17,433	391	6,339
29-31(d.)	7/31	126	17	14	1	15	57	1	21
Run total:		1,192,923	274,850	205,370	47,949	197,097	443,528	8,781	15,347

Appendix Table G-7. Frequency, proportion, and abundance of wild yearling Chinook smolts sampled at Lower Granite Dam by sex for each genetic stock, migratory year 2011. Only individual fish whose probability of assignment was ≥0.80 (n = 1,012) are included for decomposition.

Genetic	Number			Proportion		Abundance		
stock	Female	Male	Total	F	M	F	M	Total
UPSALM	89	115	204	43.6	56.4	119,910	154,940	274,850
MFSALM	59	90	149	39.6	60.4	81,321	124,049	205,370
CHMBLN	20	22	42	47.6	52.4	22,833	25,116	47,949
SFSALM	72	52	124	58.1	41.9	114,444	82,654	197,097
HELLSC	238	221	459	51.9	48.1	229,977	213,550	443,528
TUCANO	3	6	9	33.3	66.7	2,927	5,854	8,781
FALL	10	15	25	40.0	60.0	6,139	9,208	15,347

Appendix H: Wild subyearling Chinook salmon smolts at Lower Granite Dam, migratory year 2011 (March-July).

Appendix Table H-1. Number of wild subyearling Chinook salmon smolt samples collected at Lower Granite Dam and subsequently genotyped, migratory year 2011.

Statistical week	Sample period ending	Weekly Run Size	Total Samples	Sexed Samples	Genotyped Samples
21	5/22	46,620	3	3	3
22	5/29	173,465	11	10	11
23	6/5	203,437	30	25	30
24	6/12	121,350	97	92	97
25	6/19	65,155	104	93	104
26	6/26	87,953	119	109	119
27	7/3	56,233	76	73	76
28	7/10	31,460	147	140	147
Total:			587	545	587

Appendix Table H-2. Weekly sex frequencies of wild subyearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2011.

Statistical week	Sample period ending	Weekly Run Size	Sex (number)	
			Female	Male
21	5/22	46,620	2	1
22	5/29	173,465	5	5
23	6/5	203,437	9	16
24	6/12	121,350	43	49
25	6/19	65,155	39	54
26	6/26	87,953	54	55
27	7/3	56,233	33	40
28	7/10	31,460	65	75
Total:			250	295

Appendix Table H-3. Weekly sex proportions of wild subyearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2011.

Statistical week	Sample period ending	Weekly Run Size	Sex (proportion)	
			Female	Male
21-24	6/13	544,872	0.397	0.603
25	6/20	65,155	0.367	0.633
26	6/27	87,953	0.504	0.496
27	7/4	56,233	0.465	0.535
28	7/11	31,460	0.469	0.531

Appendix Table H-4. Weekly genetic stock frequencies of wild subyearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2011.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (number)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
21	5/22	46,620	-	-	-	-	-	-	3
22	5/29	173,465	-	-	-	-	-	-	11
23	6/5	203,437	1	-	-	-	2	-	27
24	6/12	121,350	3	4	3	-	8	-	79
25	6/19	65,155	1	-	1	3	8	-	91
26	6/26	87,953	4	-	-	-	7	-	108
27	7/3	56,233	3	1	-	-	5	-	67
28	7/10	31,460	7	1	-	1	8	1	129
27-28	7/10	87,693	10	2	-	1	13	1	196
Total:			19	6	4	4	38	1	515

Appendix Table H-5. Weekly genetic stock proportions of wild subyearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2011.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (proportion)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
21-24	6/12	544,872	0.028	0.013	0.007	-	0.090	-	0.863
25	6/19	65,155	0.005	-	0.012	0.033	0.085	-	0.865
26	6/26	87,953	0.034	-	-	-	0.056	-	0.909
27	7/3	56,233	0.043	0.017	-	-	0.063	-	0.876
28	7/10	31,460	0.053	-	-	0.014	0.053	-	0.880
27-28	7/10	87,693	0.044	0.014	-	0.003	0.060	0.002	0.877

Appendix Table H-6. Weekly genetic stock abundance of wild subyearling Chinook salmon smolts sampled at Lower Granite Dam, migratory year 2011.

Statistical week	Sample period ending	Weekly Run Size	Genetic stock (abundance)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
13-24	6/12	546,432	15,215	6,997	3,841	-	49,064	-	471,315
25	6/19	65,155	325	-	766	2,179	5,507	-	56,377
26	6/26	87,953	3,012	-	-	-	4,964	-	79,978
27-31	7/31	212,224	9,344	2,975	-	631	12,763	406	186,107
Run total		**911,764**	**27,896**	**9,972**	**4,607**	**2,810**	**72,297**	**406**	**793,776**

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