FISHERY RESEARCH

CHINOOK SALMON AND STEELHEAD GENOTYPING FOR GENETIC STOCK IDENTIFICATION AT LOWER GRANITE DAM

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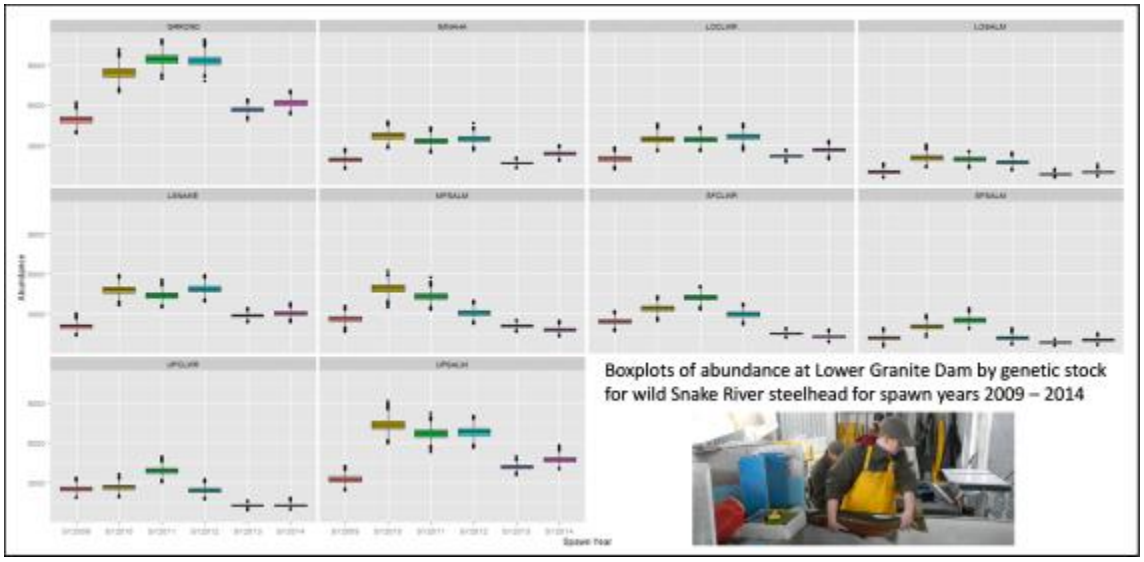

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Project Progress Report

2015 Annual Report

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ABSTRACT

This report summarizes progress in the development and implementation of genetic stock identification (GSI) in the Snake River basin for natural origin Steelhead and spring/summer (spring/summer) Chinook Salmon for the 01/01/2015 to 12/31/2015 reporting period. Three objectives for the GSI project are addressed in this report: 1) the maintenance and evaluation of single nucleotide polymorphism (SNP) panels for high-throughput genotyping of Steelhead and Chinook Salmon in the Snake and Columbia river basins; 2) the updating, maintenance, and testing of SNP baselines to describe genetic variation and for use as a reference in conducting GSI for both species in the basin; and 3) the implementation of GSI to estimate genetic stock composition and life-history diversity of Steelhead and spring/summer Chinook Salmon passing Lower Granite Dam (LGR). For both species, panels of 192 SNPs have been in use for GSI and parentage based tagging (PBT) at both Idaho Department of Fish and Game's Eagle Fish Genetics Lab, and its collaborating laboratory, the Columbia River Inter-Tribal Fish Commission's Hagerman Genetics Lab. We describe SNP baselines for Steelhead and Chinook Salmon. Steelhead baseline version 3.1 (v3.1) consists of 66 collections and 6,150 individuals. Chinook Salmon baseline v3.1 consists of 46 collections and 4,604 individuals. SNP baselines are used to describe genetic diversity and structure of natural-origin populations throughout the Snake River. Based on population structure we have defined 10 genetic stocks for Steelhead and 7 genetic stocks for Chinook Salmon for GSI analysis at LGR. Finally, we summarize GSI results for returning adults and emigrating juveniles during 2014 at LGR using v3.1 baselines as reference. The information presented in this report provides critical data for viable Salmonid population (VSP) monitoring of the Snake River Steelhead DPS and the Snake River spring/summer Chinook Salmon ESU.

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INTRODUCTION

Abundance (i.e. number of adults on spawning grounds) is a primary metric needed for monitoring the status of Steelhead and Salmon populations in the Columbia River basin (McElhany et al. 2000). Estimates of abundance combined with age and sex information over time allows estimation of productivity (e.g. recruits-per-female). Both abundance and productivity metrics provide indicators of the resiliency of populations and allow assessments of extinction risk. Estimates of these metrics at the population or major population group (MPG) scale is information that fisheries managers can use to achieve sustainable harvest of larger populations, while protecting weaker stocks and the biodiversity present within them.

Population level assessments of abundance and productivity for ESA threatened Snake River Steelhead and Chinook Salmon can be particularly difficult due to the wide distribution and location of spawning areas (many populations are present in remote or wilderness areas). Additionally, environmental conditions at the time of spawning, especially for Snake River Steelhead, often prevent the use of traditional counting methodologies (weirs, rotary screw traps, and redd-count surveys). This is less of a problem for spring/summer (spring/summer) Chinook Salmon, although turbid water conditions resulting from storms and forest fires have impacted the ability to estimate adult abundance using redd-based surveys in the Middle Fork and South Fork Salmon rivers (Thurow 2000). Snake River Steelhead monitoring is further hampered due to high turbidity and changing flow conditions during the time of spawning (Thurow 1985). As a result, escapement estimates (and other demographic information) have not been available for most Snake River populations (Busby et al. 1996; Good et al. 2005) until recently.

In lieu of more detailed basin-level and population-specific information, Steelhead in the Columbia River basin have traditionally been assigned to two groups (A-run and B-run), based on life history characteristics and bimodal timing of passage at Bonneville Dam in the mid-Columbia River (Busby et al. 1996). By definition, A-run Steelhead pass Bonneville Dam before August 25 and tend to return after one year in the ocean. B-run Steelhead pass Bonneville Dam after August 25, tend to return after two years in the ocean, and are thought to be larger at age than A-run Steelhead. Upstream migrating Steelhead adults at Lower Granite Dam (LGR) do not exhibit a bimodal passage distribution and A-run and B-run adults are enumerated based on length (A-run, ≤78 cm; B-run, >78 cm) as a proxy for ocean age. In addition to run timing at Bonneville Dam and size differences, the two groups exhibit differences in spawning distribution. A-run Steelhead spawn throughout the Columbia basin, whereas the majority of B-run Steelhead originate primarily from the Clearwater, Middle Fork Salmon, and South Fork Salmon rivers in Idaho. The putative differences in migration timing, morphology, and life history characteristics have been used as a surrogate for biodiversity in conservation planning for Snake River Steelhead. However, the relationship between the morphological and life history characteristics to time of passage at Bonneville Dam is uncertain (Good et al. 2005). Further, the bimodal passage distribution at Bonneville Dam has become unimodal in recent years (Robards and Quinn 2002).

Two management concerns regarding Snake River Steelhead have arisen in the last several years. First, populations classified as B-run do not appear to be self-sustaining (NMFS 2007) and their presence in the basin has affected operation of the Columbia River hydrosystem and fisheries management in the lower Columbia River. In particular, harvest of fall Chinook Salmon is constrained in order to limit impacts to B-run Steelhead concurrently present in the Columbia River fishery. Secondly, there are substantial data needs to refine population delineations and conservation assessments (ICTRT 2003), but data have been lacking.

Although Snake River “B-run” Steelhead are currently identified as a biologically significant and distinct component of the Snake River DPS, their management is confounded by the lack of a clear and detailed understanding of their actual spawning distribution and population structure. Nielsen et al. (2009) found that Steelhead in Idaho Snake River tributaries exhibit a complicated pattern of genetic structure with populations clustering according to drainage locality, not simply by “A-run” or “B-run” designations.

The above issues and similar conservation and management questions relating to Snake River Steelhead and spring/summer (spring/summer) Chinook Salmon may be addressed through genetic stock identification (GSI). GSI uses multilocus genotype data from reference populations (representing the contributing stocks) as a baseline and complimentary genotype data from mixtures of fish of unknown origin to estimate stock proportions within the mixture (Shaklee et al. 1999; Anderson et al. 2008). GSI has been used extensively to understand and manage mixed stock fisheries for a variety of Pacific Salmonids including Chinook Salmon (Smith et al. 2005), sockeye Salmon (Habicht et al. 2010), coho Salmon (Beacham et al. 2001) and Steelhead (Beacham et al. 2000). In the Snake River basin, studies have indicated that both Steelhead and Chinook Salmon exhibit significant genetic structuring at the watershed (or subbasin) level (Moran 2003; Narum et al. 2007; Nielsen et al. 2009, Matala et al. 2014). Previously, researchers have made use of this genetic structure to identify the genetic stock origin of kelt Steelhead at LGR (Narum et al. 2008) and to estimate the stock composition of wild and hatchery Chinook Salmon (Smith 2007) and wild Steelhead and Chinook Salmon (Ackerman et al. 2012; Schrader et al. 2011, 2012, 2013; Campbell et al. 2012) at LGR.

The results of the studies summarized above demonstrate the utility of GSI to obtain genetic stock abundance estimates for Steelhead and Chinook Salmon in the Snake River basin. Continuation of GSI at LGR will allow us to 1) monitor genetic structure throughout the basin over time, and 2) estimate abundance, productivity, and life-history diversity for genetic stocks throughout the Snake River. Sustained development and evaluation of GSI has been strongly recommended by regional RME workgroups. Similar work initiated at Bonneville Dam and in the lower Columbia River has been supported by the Independent Scientific Review Panel (http://www.nwcouncil.org/library/isrp/isrp2008-15.pdf).

REPORT STRUCTURE

This report contains three sections, one for each of the study objectives. Section 1 addresses the development of GT-seq (genotyping in thousands by sequencing) for more efficient and cheaper high-throughput genotyping for GSI in the Snake River basin. Section 2 summarizes efforts to update, maintain, and test SNP baselines for both Snake River Steelhead and spring/summer Chinook Salmon to monitor genetic diversity and structure of natural-origin populations and to use as a reference for GSI at LGR. Section 3 addresses the use of GSI to estimate genetic stock proportions and life-history diversity for wild stocks (both juveniles and adults) at LGR.

In this report, we refer to adult Steelhead and Chinook Salmon migrating past LGR using spawn years (SY). For Steelhead, a spawn year refers to adults that migrate upstream past LGR during the fall of the previous year and the spring of the current year (e.g., SY2014 Steelhead are adults that migrated past LGR between 7/1/13 - 6/30/14 and spawned in spring of 2014). For spring/summer Chinook Salmon, a spawn year refers to adults that migrate past the dam prior to August 17 and spawn that same fall. We refer to juveniles of both species migrating

past LGR using migratory years (MY). A migratory year refers to juveniles migrating downstream past LGR during spring that year.

SECTION 1: ADOPTING NEW GENOTYPING PLATFORM: GT-SEQ (GENOTYPING-IN-THOUSANDS BY SEQUENCING)

INTRODUCTION

In past reports, our focus has been on evaluating and maintaining separate SNP marker panels for PBT and GSI in the Snake River basin. In addition, we have performed concordance exercises to assess genotyping error rates between collaborating laboratories and have demonstrated continually that genotypes are highly standardized among laboratories, which ensures genotyping accuracy and data compatibility. However, since the beginning of this project, all genotyping efforts have been performed on the Fluidigm genotyping platform. In fall of 2015, we began a transition to a more efficient and cost-effective platform for high-throughput genotyping - Genotyping-in-Thousands by Sequencing (GT-seq; Campbell et al. 2015). Here, we elect to focus briefly and exclusively on documenting our transition to GT-seq.

There are many advantages to switching to GT-seq. For example, laboratory consumable cost is significantly less per sample. GT-seq has the potential to increase throughput capacity beyond the Fluidigm platform or other traditional methods. In addition, genotype scoring using GT-seq is automated, thus avoiding human error in the genotype scoring process. Finally, it has been demonstrated that GT-seq genotyping accuracy is comparable to the Fluidigm platform (Campbell et al. 2015).

METHODS

During the fall 2015, we adapted GT-seq methods described in Campbell et al. (2015). We made minor adjustments to the protocol to run on the NextSeq 500 (Illumina, USA) a next generation sequencing instrument. For our initial test project, we genotyped 2,046 Steelhead (combination of adults and juveniles) from the Pahsimeroi and Rapid River weirs and screw traps. In addition, to test for concordance of genotypes between GT-seq and the Fluidigm platform, we selected a subset of 93 samples to genotype on the Fluidigm platform using both PBT and GSI panels. We compared the genotypes generated by both platforms.

RESULTS

Genotyping success rate for the trial run was 95%, a rate comparable to the Fluidigm platform. A sample is considered successfully genotyped if it is assigned a genotype for at least 90% (173 out of 192) of the SNP markers. Overall genotype concordance for the subset of 93 samples was 99.8%, which was comparable to comparisons reported by Campbell et al. (2015). Of the 17,305 total comparisons (192 SNPs X 93 samples), there were 34 discrepancies. Locus *Omy_carban1-264* accounting for the majority of those discrepancies (29/34 = 85.3% and will either be redesigned or removed from the panel for future projects.

DISCUSSION

Our transition to GT-seq has been very successful. Genotyping concordance of 99.8% indicates that GT-seq is highly accurate in comparison to the Fluidigm platform. Reduction in material cost savings and reduction in human error associated with the scoring process strongly favors GT-seq as the preferred genotyping platform. Transition to GT-seq is near completion, but we will continue to evaluate genotyping accuracy and consistency within and between collaborating laboratories over the next year.. For Lower Granite Dam samples, SY2016 adults and MY2016 juveniles will be the first groups screened using GT-seq. For PBT broodstock, all SY2015 adults will be screened using GT-seq.

SECTION 2: UPDATE, MAINTAIN, AND TEST SNP BASELINES FOR STEELHEAD AND CHINOOK SALMON IN THE SNAKE RIVER

INTRODUCTION

The Snake River SNP baselines for Steelhead and Chinook Salmon serve two primary purposes: 1) to monitor genetic structure and diversity of wild Snake River populations both spatially and temporally, and 2) to serve as a reference for GSI work at LGR.

First, the monitoring of genetic structure over time and space provides insight regarding gene flow, both historic and contemporary, from natural (successful straying) and manmade (i.e. out-of-basin hatchery stocking) causes. Monitoring genetic diversity of populations provides information about gain or loss in genetic diversity over time and provides insight into the adaptive potential of populations. In this section, we provide genetic structure and diversity information for 23 extant Steelhead TRT populations and 28 extant Chinook Salmon TRT populations throughout the Snake River basin to aid in viable Salmonid population (VSP; McElhany et al. 2000) monitoring of the Snake River Steelhead DPS and spring/summer Chinook ESU.

Second, the Snake River SNP baselines serve as a reference for GSI conducted at LGR to estimate genetic stock composition of outmigrating smolts (e.g. Copeland et al. 2014) and returning adults (e.g. Schrader et al. 2014). Genetic stock composition estimates of adults and juveniles at LGR, combined with sex and age data, will allow us to estimate abundance, productivity, and life history diversity of genetic stocks over time for VSP monitoring. For GSI, our objective is to periodically update and maintain the SNP baselines to accurately estimate contemporary allele frequencies (genetic structure) of wild populations throughout the Snake River contributing to production at LGR.

Maintaining and updating genetic baselines for GSI is critical to the power and accuracy of GSI, which can diminish if genetic stocks are not accurately represented. For example, estimates of stock proportion of adults returning to their natal spawning area may be biased if the SNP baseline does not accurately characterize the current genetic diversity of the region. To this end, our goal is to maintain the most complete genetic representation for all genetic stocks within the Snake River basin. Adequate sample sizes and contemporary collections are two primary criteria that have been and will continue to be used in construction and maintenance of baselines. Results of the genetic structure of Snake River populations are used to define genetic stocks (Ackerman et al. 2012). For baseline v2, work was focused on completing and validating the four SNP panels (two panels: PBT and GSI for each species). Additionally, more samples from underrepresented areas were added to the baselines compared to v1. Version 3 baselines were greatly expanded to include returning adults that were PIT tagged at Lower Granite Dam and later detected at an instream PIT tag detection system (IPTDS). For this report and for baseline v3.1, we chose to remove LGT PIT-tagged adults later detected at IPTDS. Inclusion of IPTDS detected adults in the GSI baselines was problematic for a number of reasons. First, in many cases, it was difficult to confirm whether an adult detected at a particular IPTDS truly originated from that drainage and was not a ‘dip-in’ or stray. Second (and more importantly), their inclusion in the baselines when performing retrospective GSI analyses would bias stock mixture analyses, because some adults were and have been part of the stock mixture analyses (i.e. some adults would be included in both the baseline and the mixture).

METHODS

We made the first change of nomenclature in v3, but it is worth reiterating this change as it will benefit and inform new readers. In past reports, we have generally been consistent in how we defined different groups of tissue samples and followed nomenclature common to genetic population structure studies. However, we recognize the advantages of adopting a nomenclature similar to that used by the Interior Columbia Technical Recovery Team (ICTRT 2003). Hereafter, a sample collection refers to a set of tissue samples collected at a specific location and time (i.e. one sampling event). A baseline collection may consist of one or more sample collections (i.e. from separate sampling events at different times and/or geographically proximate areas). We refer to a population in the same context as the ICTRT. McElhany et al. (2000) defined a population as

> *a group of fish of the same species that spawns in a particular lake or stream (or portion thereof) at a particular season and which, to a substantial degree, does not interbreed with fish from any other group spawning in a different place or in the same place at a different season*.

The ICTRT (2003) delineated populations for the Snake River Steelhead DPS and spring/summer Chinook Salmon ESU. A genetic stock (reporting group) is made of one or more ICTRT populations and is defined based on the genetic structure among natural-origin baseline collections documented by this project (Ackerman et al. 2012). Finally, a major population group (MPG) may consist of one or more genetic stocks; genetic stock and MPG may slightly overlap. Figures 1 and 5 show the relationship between baseline collection, TRT population, genetic stock, and MPG for Steelhead and spring/summer Chinook Salmon, respectively.

Sample Collection

Tissues for genetic analysis of juvenile collections were sampled from rayed fins. Tissues from adults were sampled from multiple structures: 1) rayed fins, 2) opercle punches (generally fish passed above a weir), or 3) carcass tissue (from adult Chinook Salmon carcass surveys). In general, tissues genotyped at the IDFG lab were originally stored in individually labeled vials containing 200-proof denatured ethyl alcohol. For collections genotyped at the CRITFC lab, samples were generally stored using a dry Whatman paper medium (Lahood et al. 2008). For further details on sample storage and genotyping of samples at the CRITFC lab, see the 2012 annual report for BPA Project 2008-97-00 (Hess et al. 2013).

Baseline samples were contributed from multiple collaborating entities including CRITFC, IDFG, Nez Perce Tribe (NPT), NWFSC, Oregon Department of Fish and Wildlife (ODFW), Quantitative Consultants, Inc. (QCI), Shoshone-Bannock Tribes (SBT), US Fish and Wildlife Service (USFWS), and WDFW.

Laboratory Protocol

DNA was extracted using the Nexttec^{TM} Genomic DNA Isolation Kit from XpressBio (Thurmont, Maryland) or QIAGEN DNeasy Tissue Kits (Valencia, California). Prior to DNA amplification of SNP loci using primer-probe sets (fluorescent tags), an initial polymerase chain reaction (PCR) “pre-amp” was implemented using whole genomic DNA to jumpstart SNP amplification via increased copy number of target DNA regions. The PCR conditions for the pre-amp step were as follows: an initial denaturation of 95°C for 15 min, followed by 14 cycles of 95°C for 15 seconds and 60°C for four minutes, ending with a final 4°C dissociation step. For

Steelhead, all individuals were genotyped at 191 SNPs (including three SNPs that identify potential *O. mykiss* and *O. clarkii* hybrids) and a Y-specific assay that differentiates sex in *O. mykiss*. For Chinook Salmon, all individuals were genotyped at 191 SNPs (including one mtDNA SNP) and a Y-specific allelic discrimination assay that differentiates sex in *O. tshawytscha*. Genotyping was performed using Fluidigm® 96.96 Dynamic Array™ IFCs (chips). For each genotyping run, 96 samples (including an extraction negative control, a PCR negative control, and a PCR positive control) and 96 TaqMan® SNP assays were hand-pipetted onto the 96.96 chips. Sample cocktail and SNP assay cocktail recipes are available by request from the primary author (mike.ackerman@idfg.idaho.gov). Each 96.96 chip was pressurized to load the sample mixture and SNP assays into the chip using a Fluidigm IFC Controller HX. SNP amplification on the 96.96 chips were performed using the Fluidigm FC1™ Cycler (protocol: thermal mixing step of 70°C for 30 min and 25°C for 10 min, a hot-start step of 95°C for 60 sec, followed by 50 cycles of 95°C for 5 sec and 58°C for 25 sec, and a final cooldown step of 25°C for 10 sec). Chips were imaged on a Fluidigm EP1™ and analyzed and scored using the Fluidigm SNP Genotyping Analysis Software v3.1.1. The laboratory methods/protocols in use at the IDFG and CRITFC genetics laboratories are similar.

Standardized genotypes were stored on a Progeny database server housed at Eagle Fish Genetics Laboratory. All genotypes are also transferred to and stored in the CRITFC Progeny database. Progeny software (http://www.progenygenetics.com/) is currently in use by a large number of Genetic Analysis of Pacific Salmonids (GAPS; Moran et al. 2005) and Stephen Phelps Allele Nomenclature (SPAN; Blankenship et al. 2011, Stephenson et al. 2009) labs throughout the Pacific Northwest: Idaho Department of Fish and Game, UW, WDFW, CRITFC, and U.S. Fish and Wildlife Service (USFWS). The commonality of database software promotes seamless sharing of data among labs and will make the transfer of data to www.FishGen.net easier in the future.

Statistical Analyses

Allele frequencies for baseline collections were calculated using GENALEX v6.5 (Peakall and Smouse 2006). We performed tests for deviation from HWE across all loci for each population; tests were conducted across all nuclear SNPs for each population using exact p-values calculated from the MC method in GENEPOP v4.0 (Rousset 2008). Default parameters were used for the MC algorithm (dememorization = 1,000; batches = 20; iterations per batch = 5,000). Critical values were not adjusted using corrections for multiple tests. We report the number of SNPs exhibiting an excess or deficit of heterozygotes for any baseline collection that deviated from HWE in >10% of SNPs analyzed. Deviations from HWE may be indicative of kinship bias (heterozygote excess) or Wahlund effect (heterozygote deficit; sample resembles more than one population).

Baseline collections were evaluated for expected heterozygosity (H_E) and population-specific F_{ST} using GENALEX v6.5. Higher H_E indicates increased levels of genetic variability within a population; lower H_E may indicate decreased genetic diversity attributable to various factors (population bottlenecks, reduced meta-population dynamics). Population-specific F_{ST} (Weir and Cockerham 1984) is an indicator of the level of differentiation a population exhibits relative to all other baseline populations.

We performed self-assignment tests using gsi_sim (Anderson et al. 2008, Anderson 2010) to evaluate the accuracy of the Snake River SNP baselines v3.1 for individual assignment (IA). In self-assignment tests, each individual from the baseline is removed (one at a time), baseline allele frequencies are re-calculated with that individual removed, and the population

(and genetic stock) of origin of that individual is then estimated using the method of Rannala and Mountain (1997). For each baseline collection, we calculated the proportion of individuals that assigned to each genetic stock; results are summarized using both a 0.80 probability of assignment threshold and no threshold.

We created radial neighbor-joining (N-J) dendrograms for both Steelhead and Chinook Salmon to visualize the genetic relationship among baseline populations. The radial N-J dendrograms were based on pairwise Nei's (1972) genetic distances, and the N-J dendrogram was based on pairwise Cavalli-Sforza and Edwards (1967) genetic chord distances calculated using GENDIST (PHYLIP v3.6.7; Felsenstein 1993). Pairwise genetic distances were used to construct the trees in NEIGHBOR (PHYLIP v3.6.7). The consistency of the dendrogram topologies was estimated using 1,000 bootstrap replicates in SEQBOOT (PHYLIP v3.6.7). The final N-J dendrograms were constructed with FigTree (Rambaut 2012).

We used STRUCTURE 2.3.4 (Pritchard et al. 2000) to infer population structure using genetic clustering methods. Default model parameters of admixture and correlated allele frequencies were used; these parameters account for recent gene flow among populations and allow some flexibility for linkage disequilibrium within populations. These default settings are most flexible for dealing with real biological phenomena (Pritchard et al. 2010) and are likely most appropriate for Steelhead and Chinook Salmon. Within the admixture model, we used the LOCPRIOR option in STRUCTURE that allows the user to use sampling locations as prior information (Hubisz et al. 2009). The LOCPRIOR version of the admixture model works by modifying the prior distribution for each individual's population assignment; the new prior distributions allow the proportion of individuals assigned to a particular cluster to vary by location. In total, there were a total of 10 'sampling locations' for Steelhead and six for spring/summer Chinook Salmon; equal to the number of genetic stocks identified in Ackerman et al. (2012); the number of inferred clusters (*K*) was set to 10 and 6 for Steelhead and spring/summer Chinook Salmon, respectively. A burn-in length of 50,000 with 100,000 repeats of the Monte Carlo Markov Chain (MCMC) was used to capture structure in the data.

RESULTS

Steelhead: Baseline v3.1 consists of 136 sample collections totaling 6,150 samples. Temporal collections from geographically proximate locations are pooled resulting in 66 baseline collections, of which 47 contain temporal collections. Baseline v3.1 has a minimum of one collection representing all 23 TRT populations and covering all 5 MPGs (Table 1). The geographic distribution of these collections is shown in Figure 1 along with their TRT populations, genetic stocks, and MPGs. Not all samples from v3 were included in v3.1. We removed 1,878 adults PIT tagged at Lower Granite Dam that were later detected at an IPTDS. A summary of the number of collections and samples in the steelhead GSI baseline v3.1 is shown in Table 2.

Based on the 185 SNP marker panel, the mean pairwise F_{ST} across 66 collections is 0.021 (Figure 2), and the average heterozygosity is 29.4%. Average population-specific F_{ST} ranges from 0.014 (Asotin Cr) to 0.034 (Lake Cr - Salmon R). Heterozygosity ranges from the low of 27.3% (Crooked R - South Fork Clearwater R) to the high of 32.1%. Twenty-three of 66 collections have 10% or more SNPs not in Hardy-Weinberg proportion, with all showing deficiency (Table 1). Collections from terminal drainages, on average, are more highly differentiated and possess lower heterozygosity relative to collections located further down the

drainage or those that have been affected by past fish management practices, a trend observed in previous baselines (v1, v2 and v3).

Steelhead Genetic Stock Identification

For the new baseline, we choose to maintain the same genetic stocks established in v1, v2 and v3 for continuity and for comparisons. Genetic distance and STRUCTURE analyses of v3.1 support our decision to maintain existing genetic stocks (Figure 3 & 4). Finally, we maintained the same pooling of collections as established in v3.

Although v3.1 is 48% larger in term of sample size in comparison to v2, self-assignment results reveal comparable scores to that of v2 and v3 (Table 3a & 3b). Assignments are most accurate for the upper Clearwater R (UPCLWR), followed by the Middle Fork Salmon R (MFSALM) and South Fork Salmon R (SFSALM). Assignments are least accurate for genetic stocks geographically located lower in the drainage (e.g. lower Snake R [LSNAKE] and lower Salmon R [LOSALM]).

Chinook Salmon: Baseline v3.1 consists of 148 sample collections totaling 4,604 samples. Temporal collections from geographically proximate locations are pooled resulting in 46 baseline collections, of which 36 contain temporal collections. Baseline v3.1 has at least one collection in 31 out of 41 TRT populations (Table 4). For the remaining 10 unrepresented TRT populations, 7 are in the functionally extirpated Clearwater R drainage. Lookingglass Creek and Middle Fork Salmon above and below Indian Creek (MFUMA and MFLMA) round out the remaining three unrepresented TRT populations. The geographic distribution of these collections is shown in Figure 5 along with their TRT populations, genetic stocks and MPGs. Not all samples from v3 were included in v3.1. We removed 1,547 adults PIT tagged at Lower Granite Dam that were later detected at an IPTDS. A summary of the number of collections and samples in the Chinook Salmon GSI baseline v3.1 is shown in Table 5.

Based on the 180 SNP marker panel and excluding three fall Chinook collections, the mean pairwise F_{ST} across 54 collections is 0.016 (Figure 6), and the average heterozygosity is 22.7%. Average F_{ST} range from 0.011 (upper South Fork Salmon R) to 0.025 (Chamberlain Cr). Heterozygosity range from the low of 20.5% (Sulphur Cr) to the high of 26.4% (Wenaha R). Thirteen of 57 collections have 10% or more markers not in Hardy-Weinberg proportion, with all showing deficiency (Table 4).

Chinook Salmon Genetic Stock Identification

For the new baseline, we maintained the same genetic stocks established in v1, v2, and v3 for continuity and for comparisons. Genetic distance and STRUCTURE analyses of v3.1 support our decision to maintain existing genetic stocks (Figure 7 and 8). We maintained the same pooling of collections established in v3. The result is a reduction from 57 sample collections down to 30 baseline collections, which is now structured more similar to extant TRT populations. A summary of the GSI baseline v3.1 is below.

Although v3.1 is larger in term of sample size in comparison to v2, self-assignment results reveal comparable scores to that of v2 (Table 6a & 6b). Assignments are most accurate for fall Chinook (FALL) follow by Chamberlain Cr (CHMBLN). Assignments are least accurate for historically managed South Fork Salmon R (SFSALM) and for the lower Snake R drainage genetic stock, Tucannon R (TUCANO).

DISCUSSION

Having the most contemporary representation of Steelhead and Chinook Salmon within the Snake River basin has been and continues to be the primary goal of maintaining genetic baselines. The Snake River SNP baselines for Steelhead and Chinook Salmon serve two primary purposes: 1) to monitor genetic structure and diversity of wild Snake River populations both spatially and temporally, and 2) to serve as a reference for GSI at LGR. Both Steelhead and Chinook Salmon in the Snake River basin are listed as threatened under the Endangered Species Act (71 FR 834 and 70 FR 37160 respectively). McElhany et al. (2000) established four major criteria for VSP monitoring objectives: abundance, growth rate/productivity, spatial structure, and diversity. The SNP baselines presented here provide essential information to assess genetic diversity and population structure. To this end, we aim to provide accurate and contemporary genetic data and periodic updating and evaluations of our baselines are a necessary and important part of this larger VSP monitoring effort.

Baseline v3.1 marks the fifth year in our effort to maintain and update the genetic baselines for Steelhead and Chinook Salmon in the Snake R basin. Version 3.1 shares many similarities to v3, and we view it as a refinement to v3. We made only one change. We chose to exclude all adults PIT tagged at Lower Granite Dam that were later detected at an IPTDS. By excluding these fish, we saw reduction in the total number of collections (Steelhead 68 to 66 and Chinook Salmon 57 to 46). We believe including them in the baselines has the potential to bias stock mixture analyses. Furthermore, due to inherent limitation of IPTDS ability to detect fish 100% of the time, we are not certain that all fish finish their journeys where they were last detected. Consequently, their spawning grounds are uncertain. Based on all population genetic metrics we used to evaluate all past baselines, we saw no marked change from the exclusion of these fish in comparison to v3.

GSI baseline: For v3.1 baselines, we kept the identical pooled collections established in v3. These geographically separated collections showed approximately the same level of genetic differentiation seen in v3, when PIT-tagged adults were included. To reiterate, pooling reduced the Steelhead baseline collections from 66 to 47 and the Chinook Salmon baseline collections from 57 to 30. Our decision to simplify the GSI baseline is supported by similar self-assignment test scores found in all three baseline versions (v2, v3, and v3.1).

SECTION 3. IMPLEMENT GSI METHODS TO ESTIMATE PROPORTIONS AND BIOLOGICAL PARAMETERS OF WILD STOCKS AT LOWER GRANITE DAM

The IDFG's long-range goal of its anadromous fish program, consistent with basinwide mitigation and recovery efforts, is to preserve Idaho's Salmon and Steelhead runs and recover them to benefit all users (IDFG 2007). Fisheries management to achieve these goals requires an understanding of how Salmonid populations function as well as regular status assessments (McElhany et al. 2000). Estimates of abundance, combined with sex and age information over time, allow estimation of population growth rates; and both abundance and productivity metrics provide indicators of the resiliency and viability of populations. Estimates of these metrics at the genetic stock or MPG level is information that fisheries managers can use to achieve sustainable harvest of larger populations, while protecting weaker stocks and the biodiversity within them.

However, population level or MPG assessments of abundance and productivity for ESA-listed Snake River Steelhead and spring/summer Chinook Salmon can be particularly difficult (see Report Introduction). Specific data on Snake River Steelhead and Chinook Salmon MPGs and populations are lacking, particularly key parameters such as population abundance, age composition, genetic diversity, recruits per spawner, and survival rates (ICTRT 2003). GSI is one potential means for estimating these parameters at a finer-scale; perhaps at the level of MPG, genetic stock (reporting group), or population. GSI uses multi-locus genotype data from reference populations (representing potential contributing stocks) as a baseline and a complimentary set of genotype data from mixtures of fish of unknown origin to estimate stock proportions within the mixture and to estimate stock of origin of individual fish (Shaklee et al. 1999). In Section 2, we presented the SNP baselines used for GSI in the Snake River basin. In Section 3, we use complementary sets of genotype data from adults sampled at the Lower Granite Dam (LGR) adult trap and juveniles sampled at the LGR juvenile bypass facility to estimate the genetic stock of origin of upstream migrating adults and emigrating juveniles. We then provide life-history diversity (sex, length, age, migration timing) information of individuals assigning to the various Snake River genetic stocks.

In this report, we present individual genetic assignments and life-history diversity information for SY2014 adults and MY2014 juveniles (both Steelhead and Chinook Salmon) sampled at LGR.

In spring of 2015 we re-analyzed all SY2009 – 2013 adults and MY2010 – 2013 juveniles using our v3.1baseline presented in Section 2. Now all adults and all juveniles collected from our LGR program have been analyzed using the same GSI baselines to provide consistency among all years. Those genetic results have all been uploaded to IDFG's Lower Granite Dam trapping database (LGTrappingDB). Moreover, SY2014 marks the sixth year of GSI results for returning Snake River adults at LGR. We provide brief and preliminary summaries from work completed for SY2009 through 2014 adults.

METHODS

Sampling at Lower Granite Dam

Adult Trap Operations

Detailed methods for operation of the LGR adult trap can be found in Schrader et al. (2011, 2012, 2013, and 2014) and citations within. Briefly, adult Steelhead and spring/summer Chinook Salmon migrating upstream past LGR may be intercepted at a trapping facility, located on the adult fish ladder above the counting window, according to a predetermined sampling rate. Trap sampling rates are determined by a committee of co-managers in an attempt to achieve sample requirements for multiple projects and to balance fish handling concerns; sample rates are typically 10–20%. The sample rate determines how long a trap gate remains open four times per hour; the trap is operational 24 hours per day.

Juvenile Trap Operations

Detailed methods for operation of the LGR juvenile trap can be found in Copeland et al. (2014) and citations within. 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 pre-determined 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. 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.

Fish Handling Protocols (Adults and Juveniles)

Fish handling procedures are detailed in Schrader et al. (2014) for adults and Copeland et al. (2014) for juveniles (and citations within both reports). Fish captured at the LGR adult or juvenile trap are anesthetized; identified to species; examined for external marks, tags, and injuries; scanned for an internal CWT or PIT tag; and measured for fork length (FL). All fish are examined for the presence (unclipped) or absence (clipped) of the adipose fin and classified to putative origin (hatchery or wild). All wild fish have an unclipped adipose fin because they spend their entire life cycle in the natural environment. Most hatchery-origin fish have a clipped adipose fin. However, some hatchery fish may be released with an unclipped adipose fin for supplementation or tribal harvest opportunities. Thus, unclipped fish are also examined for a CWT or a PIT tag. The presence of a CWT definitively identifies an unclipped fish as hatchery origin. For unclipped Steelhead, hatchery origin may also be determined by the presence of dorsal and/or ventral fin erosion, which is assumed to occur only in hatchery-reared Steelhead (Latremouille 2003). Captured fish determined to be putatively wild or unclipped hatchery with no CWT (Steelhead ‘stubbies’) are sampled for scales (for age; except juvenile Chinook) and tissue (for sex and genotype data). For juveniles, 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).

Scales were taken from above the lateral line and posterior to the dorsal fin. Samples were stored in coin envelopes for transport to the IDFG aging laboratory in Nampa, Idaho. Tissue samples were taken from a small clip of the anal fin. Tissues were stored in a vial with 200-proof non-denatured ethyl alcohol for transport to the IDFG Eagle Fish Genetics Laboratory. Gender was not visually determined at the trap, but was assessed using Y-specific

genetic assays (Campbell et al. 2012). After processing, all fish were returned to the fish ladder to resume upstream migration (adults) or the bypass system to resume downstream migration (juveniles).

Scale Aging Protocol

Scale aging protocols for adults are detailed in Schrader et al. (2014). Scale aging protocols for juveniles are detailed in Copeland et al. (2014).

Genetics Laboratory Protocol

Laboratory protocols for DNA extraction, amplification, and SNP genotyping are detailed in Section 2. SY2014 Chinook Salmon adults and MY2014 Chinook Salmon juveniles were processed at the CRITFC Genetics Lab in Hagerman, Idaho. SY2014 Steelhead adults were processed at both CRITFC (fall individuals) and IDFG's Eagle Fish Genetics Lab (EFGL) (spring individuals) in Eagle, Idaho. MY2014 Steelhead juveniles were processed at EFGL.

Parentage-Based Tagging

Beginning in 2008, parentage-based tagging (PBT; Anderson and Garza 2005) has been used to genetically tag nearly all hatchery-origin Steelhead in the Snake River Basin (Steele et al. 2013, 2014). PBT is accomplished by genotyping all parental broodstock each spawn year, thereby allowing any offspring to be assigned back to their parents and identifying the hatchery of origin and age of offspring. PBT has been implemented primarily as an alternative to coded-wire tags (CWT) for identifying the origin and age of fish harvested in mixed-stock fisheries or that stray into natural spawning areas.

We conducted PBT analysis for both SY2013 adults and MY2013 juveniles. All MY2013 hatchery juvenile cohorts were interrogated via PBT. For SY2013, 1-ocean, 2-ocean, and 3-ocean Steelhead and spring/summer Chinook were interrogated via PBT. In using PBT to evaluate all the fish, we are better able to identify putative natural-origin (unclipped, unmarked) fish that are truly of hatchery origin. Any individuals identified as unmarked hatchery origin adults with a PBT were removed from the dataset before performing GSI and evaluating life-history diversity of genetic stocks.

Genetic Stock Identification

Individual assignment (IA) tests were conducted for SY2013 adults and MY2013 juveniles (both species) using the Snake River SNP baselines v3.1 described in Section 2. SNP allele frequency estimates from baseline collections are the reference information for IA tests. Fish sampled at the LGR adult and juvenile trapping facilities were genotyped at the same SNPs and multi-locus genotype data were used to assign individual fish back to their estimated population (and genetic stock) of origin (Pella and Milner 1987, Shaklee et al. 1999). In IA, the probability that each fish 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 (aka reporting groups) 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 procedures assign an individual's genotype to the reporting group from which it is most likely to have originated.

Ten genetic stocks were used for Steelhead IA analyses. Genetic stocks include: 1) UPSALM: 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.

Seven wild Chinook Salmon genetic stocks were used during IA analyses (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 reporting group that includes the Little Salmon, Clearwater, Grande Ronde, and Imnaha rivers; 6) TUCANO: Tucannon River, and 7) FALL: Snake River fall Chinook Salmon. Three collections of Snake River fall Chinook Salmon (see Table 2 in Ackerman et al. 2012) are included in the SNP baselines (FALL genetic stock); we are able to identify fall Chinook within mixtures of spring/summer Chinook with 100% accuracy.

After performing IA, we estimated genetic stock compositions of all samples analyzed and evaluated life-history diversity for each genetic stock. We summarize results for four sample groups:

- SY2014 Steelhead adults
- SY2014 Chinook adults
- MY2014 Steelhead juveniles
- MY2014 Chinook juveniles

RESULTS

We inventoried a total of 13,596 samples from SY2014 adults and MY2014 juveniles from LGR (Table 7). Of the samples inventoried, 12,413 were queued for genotyping. Of queued samples, 164 (1.3%) failed to genotype successfully. All samples were from fish with intact adipose fins; however, 2,140 (17.5%) assigned back to hatchery parents in our PBT baseline. We performed IA on the remaining 10,109 samples; results for those samples are summarized below and in Tables 8-10.

SY2014 Steelhead Adults

We inventoried 4,589 unclipped adult Steelhead samples for SY2014. Of those, 3,712 (80.9%) were phenotypically wild (no dorsal or ventral fin erosion) and all were queued for genotyping; 3,697 (99.6%) were genotyped successfully. Of samples genotyped successfully, 226 (6.1%) assigned to hatchery parents and the remaining 3,471 (93.9%) were assigned back to a genetic stock via IA.

Of the 4,589 unclipped adult Steelhead samples, 877 (19.1%) were phenotypically identified as hatchery origin due to dorsal and/or ventral fin erosion and all were queued for genotyping and 873 (99.5%) were genotyped successfully. Of those genotyped successfully, 757 (86.7%) assigned back to hatchery parents and the remaining 116 (13.3%) were assigned back to a genetic stock via IA.

Life-history diversity information (sex, length, and ocean age) for the 3,587 unclipped Steelhead adults that were assigned a genetic stock is summarized in Table 8. Of the 3,587 assigned a genetic stock, 636 (17.7%) assigned to UPSALM, 212 (5.9%) to MFSALM, 122 (3.4%) to SFSALM, 130 (3.6%) to LOSALM, 200 (5.6%) to UPCLWR, 199 (5.5%) to SFCLWR, 386 (10.8%) to LOCLWR, 336 (9.4%) to IMNAHA, 917 (25.6%) to GRROND, and 449 (12.5%) to LSNAKE.

MY2014 Steelhead Juveniles

We inventoried 1,387 unclipped juvenile Steelhead samples for MY2014 (Table 7); all samples were queued for genotyping and 1,383 (99.7%) were genotyped successfully. Of samples genotyped, 12 (0.9%) were assigned back to hatchery parents and the remaining 1,371 (99.1%) were assigned a genetic stock via IA.

Life-history diversity information for the 1,371 emigrating Steelhead smolts that were assigned a genetic stock is summarized in Table 9. Of the 1,371 Steelhead smolts assigned a genetic stock, 223 (16.3%) assigned to UPSALM, 132 (9.6%) to MFSALM, 65 (4.7%) to SFSALM, 50 (3.6%) to LOSALM, 162 (11.8%) to UPCLWR, 117 (8.5%) to SFCLWR, 118 (8.6%) to LOCLWR, 106 (7.7%) to IMNAHA, 274 (20.0%) to GRROND, and 124 (9.0%) to LSNAKE.

SY2014 Chinook Salmon Adults

We inventoried 4,529 unclipped adult Chinook Salmon samples for SY2014 and all of them were queued for genotyping (Table 7). Of those, 4,461 (98.5%) were genotyped successfully of which 1,076 (24.1%) were assigned back to hatchery parents and 3,385 (75.9%) were assigned back to a genetic stock via IA.

Life-history diversity information for the 3,385 Chinook Salmon adults that were assigned to a genetic stock is summarized in Table 10. Of the 3,385 samples, 690 (20.4%) assigned to UPSALM, 708 (20.9%) to MFSALM, 105 (3.1%) to CHMBLN, 500 (14.8%) to SFSALM, 1,291 (38.1%) to HELLSC, 15 (0.4%) to TUCANO, and 76 (2.2%) to FALL.

MY2014 Chinook Salmon Juveniles

We inventoried 3,091 unclipped juvenile Chinook Salmon for MY2014; 2,184 were yearlings and 907 were subyearlings (Table 7).

Of the 2,184 yearling Chinook Salmon inventoried, 1,455 were queued for genotyping and 1,393 (95.7%) of those genotyped successfully. Of the yearlings genotyped, 66 (4.7%) were assigned back to hatchery parents and the remaining 1,327 were assigned a genetic stock via IA.

Of the 907 subyearlings inventoried, 453 were queued for genotyping and 442 (97.6%) of those genotyped successfully. Of the subyearlings genotyped, 3 (0.7%) were assigned back to hatchery parents and the remaining 439 were assigned a genetic stock via IA.

Life-history diversity information for the 1,766 Chinook Salmon smolts assigned a genetic stock is summarized in Table 11. Of the 1,766 Chinook Salmon smolts assigned a genetic stock, 206 (11.7%) assigned to UPSALM, 200 (11.3%) to MFSALM, 19 (1.1%) to

CHMBLN, 150 (8.5%) to SFSALM, 717 (40.6%) to HELLSC, 12 (0.7%) to TUCANO, and 462 (26.2%) to FALL.

SY2009 – 2014 Abundance by Genetic Stock

Figures 9 and 10 are boxplots of abundance at Lower Granite Dam by genetic stock for Snake River Steelhead and spring/summer Chinook Salmon, respectively for SY2009 – 2014.

DISCUSSION

Adult Steelhead and spring/summer Chinook Salmon are intercepted at the LGR adult trapping facility at approximately 10-20% trapping rate; each fish is implanted with a PIT tag and tissue and scale samples are taken. Tissue samples are taken as part of this project to estimate abundance and life-history diversity metrics at the genetic stock and/or MPG scale. PIT tagging of adults is conducted by the Integrated Status And Effectiveness Monitoring Project (ISEMP; BPA Project 2003-017-00); detection data of those adults at Instream PIT Tag Detection Systems (IPTDS) throughout the Snake River basin are used in a Bayesian branching model to provide reliable and unbiased estimates of abundance at the population level (QCI 2013; Ackerman In Prep). A multi-agency collaboration has recently been initiated to utilize information generated from these two innovative technologies (SNP genotyping for PBT and GSI and IPTDS infrastructure for population level abundance estimates). PBT analysis of fish PIT tagged at LGR allows us to identify phenotypically natural origin fish that are truly of hatchery origin; these fish can then be removed from analysis prior to estimating abundance of the natural origin population. Further, SNP genotyping provides sex information (via a sex-specific allelic discrimination assay; Campbell et al. 2012) and genetic structure and diversity information for detected fish and scale age analysis provides age structure information. The goal of this collaboration is to synthesize available data regarding abundance, life-history diversity, and genetic structure and diversity of Snake River Steelhead and spring/summer Chinook Salmon that is available from the PIT tagging and biological sampling of adults at LGR and the subsequent detection of those adults at IPTDS throughout the Snake River basin.

GSI at LGR estimates the origin of fish and provides abundance estimates at the genetic stock and/or MPG level; PIT tagging at LGR estimates the final spawning destination of fish and provides abundance estimates at the population or subpopulation level. We intend to contribute abundance estimates from both GSI and PIT tagging to stock assessment efforts in the Snake and Columbia River basins; estimates of abundance combined with harvest information can be used in run reconstruction (see Copeland et al. 2013 for example) and provide unprecedented monitoring of Snake River populations. Information from GSI (particularly genetic assignment of individuals) combined with PIT tag detection data may also provide information on straying.

CRITFC conducts PBT and GSI of adult Steelhead and Chinook Salmon at Bonneville Dam to estimate stock composition and abundance and to evaluate life-history information for stocks migrating above Bonneville Dam. In the future, we intend to combine information from GSI at both LGR and Bonneville Dam to evaluate straying and survival between the two dams for both species. Further, we will evaluate adults captured in the Zone 6 fishery (between Bonneville Dam and McNary Dam) using a combination of PBT and GSI. The above information combined will also greatly assist run reconstruction efforts.

Continuation of GSI efforts at LGR will allow us to 1) monitor genetic structure and diversity throughout the basin over time, and 2) estimate productivity parameters and related life-history diversity information for genetic stocks throughout the Snake River basin.

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TABLES

Table 1. Sixty-six collections of Snake River basin Steelhead (*Oncorhynchus mykiss*) screened with the PBT and GSI SNP panels for baseline v3.1. Each collection is identified by its TRT population, genetic stock, major population group (MPG), sample size (n), year collected, genotyping agency, baseline version in which it first appeared, latitude, longitude, expected heterozygosity (H_E), mean pairwise fixation indices (F_{ST}), and number of loci out of Hardy–Weinberg expectation (deficient or excess in ≥10% of SNPs). Map # corresponds to numbers in Figure 1. Agency indicates the laboratory where samples were genotyped. All collections are summer-run, inland lineage, natural origin, and presumed to be of anadromous life history.

Map#	Collection Name	TRT population	Genetic Stock	MPG	n	Year Collected	Genotype Agency	Baseline Version	Latitude	Longitude	He	Fst	HWE Deficient	HWE Excess
1	Sawtooth	SRUMA	UPSALM	Salmon River	108	05, 10	IDFG	1	44.1506	-114.8849	29.6%	0.018		
2	Valley Cr	SRUMA	UPSALM	Salmon River	94	00, 10	IDFG/NWFSC	3	44.2181	-114.9338	30.2%	0.017		
3	WF Yankee Fork	SRUMA	UPSALM	Salmon River	117	00	IDFG	2	44.3494	-114.7295	30.1%	0.017		
4	Herd Cr	SREFS	UPSALM	Salmon River	85	10, 11	NWFSC	3	44.1091	-114.2595	30.1%	0.018		
5	Morgan Cr	SREFS	UPSALM	Salmon River	61	00, 12	IDFG	3	44.6611	-114.2265	32.1%	0.020	8	5
6	Pahsimeroi R	SRPAH	UPSALM	Salmon River	97	06, 10	IDFG	2	44.6823	-114.0396	31.7%	0.018	9	2
7	upper Lemhi R	SRLEM	UPSALM	Salmon River	86	09, 10	IDFG	2	44.8675	-113.6281	32.1%	0.019		
8	NF Salmon R	SRNFS	UPSALM	Salmon River	100	10	IDFG	1	45.4094	-113.9918	30.7%	0.014		
9	Panther Cr	SRPAN	N/A	Salmon River	53	13	IDFG	3	45.0349	-114.3016	30.5%	0.018		
10	Capehorn/Marsh Cr	MFUMA	MFSALM	Salmon River	195	00, 09, 10	IDFG/NWFSC	3	44.3949	-115.1709	30.2%	0.019	10	5
11	Elk/Bear Cr	MFUMA	MFSALM	Salmon River	173	10, 11	IDFG/NWFSC	3	44.4104	-115.4685	29.2%	0.024		
12	Sulphur Cr	MFUMA	MFSALM	Salmon River	94	00, 11	IDFG/NWFSC	3	44.5437	-115.3034	29.2%	0.024		
13	Rapid R (MF Salmon R)	MFUMA	MFSALM	Salmon River	75	00, 12	IDFG	3	44.6790	-115.1490	29.4%	0.026		
14	Pistol Cr	MFUMA	MFSALM	Salmon River	58	00, 12	IDFG	3	44.7635	-115.1565	30.0%	0.023		
15	Loon Cr	MFUMA	MFSALM	Salmon River	131	00, 11	IDFG/NWFSC/CRITFC	3	44.5983	-114.8083	28.4%	0.023		
16	Camas Cr	MFBIG	MFSALM	Salmon River	97	00, 10	IDFG/NWFSC	3	44.8240	-114.7194	28.7%	0.023	12	1
17	upper Big Cr	MFBIG	MFSALM	Salmon River	87	00, 11	IDFG/NWFSC	3	45.1506	-115.3070	28.3%	0.028	6	4
18	lower Big Cr	MFBIG	MFSALM	Salmon River	137	00, 11	IDFG/NWFSC	3	45.1072	-114.7429	29.5%	0.019		
19	Chamberlain Cr	SRCHA	MFSALM	Salmon River	189	00, 10, 11	IDFG/NWFSC	3	45.3877	-115.1896	28.2%	0.021	14	3
20	Bargamin Cr	SRCHA	N/A	Salmon River	32	00	IDFG	1	45.6660	-115.1875	30.6%	0.022		
21	upper SF Salmon R mainstem	SFMAI	SFSALM	Salmon River	45	00	IDFG/CRITFC	1	44.6069	-115.6799	28.4%	0.025		
22	Johnson Cr	SFMAI	SFSALM	Salmon River	89	10, 11	IDFG/NWFSC	3	44.9341	-115.4867	29.6%	0.022		
23	EFSF Salmon R	SFMAI	SFSALM	Salmon River	46	00	IDFG	1	44.9553	-115.7127	29.3%	0.027		
24	Lake Cr (SF Salmon R)	SFSEC	SFSALM	Salmon River	50	10, 11	IDFG	3	45.2756	-115.9184	28.3%	0.034	6	4
25	Lick Cr	SFSEC	SFSALM	Salmon River	63	10, 11	IDFG	3	45.0591	-115.8510	28.6%	0.023		
26	Secesh R	SFSEC	SFSALM	Salmon River	95	00, 11	IDFG/NWFSC	3	45.2188	-115.8076	29.0%	0.023		
27	Boulder Cr/Rapid R	SRLSR	LOSALM	Salmon River	147	00, 03, 09	IDFG	1	45.3546	-116.3907	30.3%	0.016	9	1
28	Slate Cr	SRLSR	LOSALM	Salmon River	75	00, 13	IDFG	3	45.6392	-116.2804	30.3%	0.016		
29	upper Lochsa R	CRLOC	UPCLWR	Clearwater River	129	00	IDFG	2	46.5082	-114.6775	27.8%	0.025		
30	Lake Cr	CRLOC	UPCLWR	Clearwater River	47	00	IDFG	2	46.4144	-114.9943	27.5%	0.029		

Table 1. Continued

Map#	Collection Name	TRT population	Genetic Stock	MPG	n	Year Collected	Genotype Agency	Baseline Version	Latitude	Longitude	He	Fst	HWE	
													Deficient	Excess
31	Fish Cr	CRLOC	UPCLWR	Clearwater River	100	10, 11	IDFG	2	46.3558	-115.3483	28.1%	0.023	10	
32	Canyon Cr	CRLOC	N/A	Clearwater River	46	04	IDFG	1	46.2391	-115.5619	27.5%	0.024		
33	upper Selway R	CRSEL	UPCLWR	Clearwater River	137	08	IDFG	2	45.6921	-114.7175	28.7%	0.024	10	1
34	Whitecap Cr	CRSEL	UPCLWR	Clearwater River	110	11, 12	IDFG	3	45.8689	-114.7205	28.7%	0.026	13	5
35	Bear Cr	CRSEL	UPCLWR	Clearwater River	70	00, 12	IDFG	3	46.0357	-114.8376	28.7%	0.026		
36	middle Selway R	CRSEL	UPCLWR	Clearwater River	138	00, 12	IDFG	2	46.0978	-114.8842	28.2%	0.021	9	3
37	Three Links Cr	CRSEL	UPCLWR	Clearwater River	81	00, 12	IDFG	3	46.1451	-115.0720	28.0%	0.026		
38	Gedney Cr	CRSEL	UPCLWR	Clearwater River	45	00	IDFG	1	46.0583	-115.3141	28.7%	0.023		
39	O'Hara Cr	CRSEL	UPCLWR	Clearwater River	85	00, 13	IDFG	3	46.0449	-115.5177	28.4%	0.019		
40	Crooked R	CRSFC	SFCLWR	Clearwater River	136	07, 08, 11	IDFG	3	45.7656	-115.5280	27.3%	0.025	11	
41	Newsome Cr	CRSFC	SFCLWR	Clearwater River	99	12	IDFG	3	45.8345	-115.6164	27.5%	0.026	7	5
42	Tenmile Cr	CRSFC	SFCLWR	Clearwater River	47	00	IDFG	1	45.8057	-115.6833	27.5%	0.032		
43	Clear Cr	CRLMA	SFCLWR	Clearwater River	45	00	IDFG	1	46.0486	-115.7737	28.1%	0.025		
44	Lolo Cr	CRLMA	SFCLWR	Clearwater River	94	12	IDFG	3	46.2906	-115.9228	27.4%	0.027		
45	WF Potlatch R	CRLMA	LOCLWR	Clearwater River	84	09, 10	IDFG	2	46.8638	-116.4190	29.9%	0.016		
46	EF Potlatch R	CRLMA	LOCLWR	Clearwater River	158	08, 10, 11	IDFG	2	46.8049	-116.4247	29.9%	0.017	8	3
47	Little Bear Cr	CRLMA	LOCLWR	Clearwater River	151	07, 08, 10, 11	IDFG	2	46.6532	-116.6594	30.1%	0.015	10	1
48	Big Bear Cr	CRLMA	LOCLWR	Clearwater River	99	07, 08, 10, 11	IDFG	2	46.6752	-116.6595	31.1%	0.015		
49	Lapwai Cr	CRLMA	LOCLWR	Clearwater River	158	13	IDFG	3	46.6191	-116.6316	30.1%	0.016	13	6
50	Gumboot/Mahogany Cr	IRMAI	IMNAHA	Imnaha River	53	11, 12, 13	IDFG	3	45.2033	-116.8773	28.3%	0.019		
51	Little Sheep Cr	IRMAI	IMNAHA	Imnaha River	93	00	IDFG	3	45.4723	-116.9572	29.6%	0.020		
52	Big Sheep Cr	IRMAI	IMNAHA	Imnaha River	91	00	IDFG/CRITFC	1	45.5551	-116.8391	29.3%	0.017		
53	Lightning Cr	IRMAI	IMNAHA	Imnaha River	39	00	NWFSC	1	45.6847	-116.7265	28.7%	0.019		
54	upper Grande Ronde R	GRWAL	GRROND	Grande Ronde River	65	09, 10, 11	CRITFC	3	45.5065	-117.9330	30.2%	0.017		
55	Catherine Cr	GRWAL	GRROND	Grande Ronde River	91	11	CRITFC	3	45.2406	-117.9223	30.3%	0.015	9	2
56	Little Minam R	GRWAL	GRROND	Grande Ronde River	48	00	NWFSC	1	45.3991	-117.6740	29.5%	0.024		
57	Wallowa R	GRWAL	GRROND	Grande Ronde River	72	00, 09, 11	NWFSC	3	45.4360	-117.3319	31.6%	0.017	9	4
58	Lostine R	GRWAL	GRROND	Grande Ronde River	45	00	CRITFC	1	45.5508	-117.4892	30.5%	0.023		
59	Wenaha R	GRLMT	GRROND	Grande Ronde River	191	00	NWFSC	1	45.9455	-117.4516	30.3%	0.015	15	2
60	Menatchee Cr	GRLMT	GRROND	Grande Ronde River	73	00	CRITFC	1	46.0081	-117.3655	31.2%	0.018		
61	Elk Cr (Joseph Cr)	GRJOS	GRROND	Grande Ronde River	45	00	CRITFC	1	45.9727	-117.1534	28.3%	0.025	6	4
62	Joseph Cr	GRJOS	GRROND	Grande Ronde River	52	11	CRITFC	2	46.0446	-117.0177	29.8%	0.017		
63	Captain John Cr	SRLSR	N/A	NA	56	00	CRITFC	2	45.6720	-116.9264	29.5%	0.019		
64	Asotin Cr	SNASO	LSNAKE	LSNAKE	194	08, 10	IDFG	2	46.3224	-117.1379	31.0%	0.014	11	2
65	Alpowa Cr	SNTUC	LSNAKE	LSNAKE	98	10	IDFG	2	46.4076	-117.2198	31.0%	0.015		
66	Tucannon R	SNTUC	LSNAKE	LSNAKE	106	05, 09, 10	IDFG	2	46.3228	-117.6557	31.0%	0.014	14	2

Table 2. Steelhead results from self-assignment tests performed in gsi_sim (Anderson et al. 2008, Anderson 2010). For each baseline collection represented in baseline v3.1, each individual was sequentially removed from the baseline and then assigned back to the baseline. Rows represent collection of origin and columns represent genetic stock to which individuals assigned. Table 2a is results for all individuals that assigned to a genetic stock, and Table 2b is for individuals that assigned to a genetic stock with ≥80% probability. For example, n = 319 individuals represent the upper Salmon collection. Of the 319 individuals in the baseline, 149 (47%) assigned back to a genetic stock with ≥80% probability. Of the 149 that assigned, 138 (92%) assigned to the correct UPSALM genetic stock. Shaded boxes represent the correct genetic stock of origin for each population.

Table 2a.

			Genetic Stock (No Threshold)									
Collection of origin	**n**	**Number Assigned (Proportion)**	**UPSALM**	**MFSALM**	**SFSALM**	**LOSALM**	**UPCLWR**	**SFCLWR**	**LOCLWR**	**IMNAHA**	**GRROND**	**LSNAKE**
Sawtooth	319	319 (1.00)	241 (0.76)	2 (0.01)		18 (0.06)			6 (0.02)	9 (0.03)	34 (0.11)	9 (0.03)
Herd Cr	85	85 (1.00)	60 (0.71)		1 (0.01)	1 (0.01)		1 (0.01)	12 (0.14)	3 (0.04)	4 (0.05)	3 (0.04)
Morgan Cr	61	61 (1.00)	51 (0.84)		1 (0.02)	1 (0.02)			1 (0.02)	3 (0.05)	2 (0.03)	2 (0.03)
Pahsimeroi R	97	97 (1.00)	74 (0.76)	1 (0.01)			1 (0.01)		4 (0.04)	4 (0.04)	5 (0.05)	8 (0.08)
Lemhi R	86	86 (1.00)	71 (0.83)	3 (0.03)		1 (0.01)					7 (0.08)	4 (0.05)
NF Salmon R	100	100 (1.00)	61 (0.61)		2 (0.02)	15 (0.15)	1 (0.01)	1 (0.01)	5 (0.05)	6 (0.06)	5 (0.05)	4 (0.04)
Marsh Cr	195	195 (1.00)	26 (0.13)	155 (0.79)		5 (0.03)	1 (0.01)			3 (0.02)	2 (0.01)	3 (0.02)
Bear Valley Cr	173	173 (1.00)		167 (0.97)	1 (0.01)	1 (0.01)					3 (0.02)	1 (0.01)
MF Salmon R	227	227 (1.00)	7 (0.03)	202 (0.89)	2 (0.01)	4 (0.02)			2 (0.01)	4 (0.02)	4 (0.02)	2 (0.01)
Loon Cr	131	131 (1.00)	1 (0.01)	125 (0.95)		3 (0.02)	1 (0.01)				1 (0.01)	
Camas Cr	97	97 (1.00)	1 (0.01)	95 (0.98)						1 (0.01)		
Big Cr	224	224 (1.00)	8 (0.04)	205 (0.92)		3 (0.01)		1 (0.00)	2 (0.01)	2 (0.01)	1 (0.00)	2 (0.01)
Chamberlain Cr	189	189 (1.00)	6 (0.03)	166 (0.88)	1 (0.01)	3 (0.02)			2 (0.01)	3 (0.02)	5 (0.03)	3 (0.02)
SF Salmon R	45	45 (1.00)	1 (0.02)		42 (0.93)					1 (0.02)	1 (0.02)	
EFSF Salmon R	135	135 (1.00)		4 (0.03)	122 (0.90)	2 (0.01)			2 (0.01)		4 (0.03)	1 (0.01)
Secesh R	208	208 (1.00)	4 (0.02)	3 (0.01)	192 (0.92)	3 (0.01)	1 (0.00)		1 (0.00)		2 (0.01)	2 (0.01)
Little Salmon R	147	147 (1.00)	23 (0.16)	12 (0.08)	3 (0.02)	85 (0.58)		5 (0.03)	4 (0.03)	4 (0.03)	6 (0.04)	5 (0.03)
Slate Cr	75	75 (1.00)	13 (0.17)	3 (0.04)	2 (0.03)	38 (0.51)			4 (0.05)	3 (0.04)	5 (0.07)	7 (0.09)
upper Lochsa R	129	129 (1.00)				1 (0.01)	122 (0.95)	6 (0.05)				
middle Lochsa R	147	147 (1.00)	1 (0.01)				138 (0.94)	4 (0.03)	1 (0.01)		2 (0.01)	1 (0.01)
upper Selway R	247	247 (1.00)					242 (0.98)	2 (0.01)	2 (0.01)			1 (0.00)
Bear Cr	70	70 (1.00)					69 (0.99)		1 (0.01)			
middle Selway R	138	138 (1.00)					131 (0.95)	5 (0.04)	1 (0.01)	1 (0.01)		
lower Selway R	211	211 (1.00)	1 (0.00)				180 (0.85)	20 (0.09)	7 (0.03)		1 (0.00)	2 (0.01)

Collection of origin	n	Number Assigned (Proportion)	Genetic Stock (No Threshold)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
Crooked R	136	136 (1.00)					7 (0.05)	125 (0.92)	3 (0.02)		1 (0.01)	
Newsome Cr	99	99 (1.00)	1 (0.01)				5 (0.05)	93 (0.94)				
Tenmile Cr	47	47 (1.00)					7 (0.15)	38 (0.81)	2 (0.04)			
Clear Cr	45	45 (1.00)			1 (0.02)		6 (0.13)	36 (0.80)	2 (0.04)			
Lolo Cr	94	94 (1.00)	1 (0.01)				7 (0.07)	83 (0.88)	3 (0.03)			
WF Potlatch R	84	84 (1.00)	3 (0.04)			4 (0.05)	1 (0.01)	7 (0.08)	58 (0.69)	1 (0.01)	5 (0.06)	5 (0.06)
EF Potlatch R	158	158 (1.00)	1 (0.01)		2 (0.01)		5 (0.03)	8 (0.05)	120 (0.76)	1 (0.01)	10 (0.06)	11 (0.07)
Big Bear Cr	250	250 (1.00)	12 (0.05)			4 (0.02)	6 (0.02)	3 (0.01)	161 (0.64)	8 (0.03)	26 (0.10)	30 (0.12)
Lapwai Cr	158	158 (1.00)	13 (0.08)			5 (0.03)	3 (0.02)		90 (0.57)	4 (0.03)	24 (0.15)	19 (0.12)
upper Imnaha R	53	53 (1.00)	5 (0.09)	1 (0.02)		2 (0.04)		1 (0.02)	2 (0.04)	37 (0.70)	4 (0.08)	1 (0.02)
Big Sheep Cr	184	184 (1.00)	10 (0.05)	4 (0.02)		7 (0.04)			7 (0.04)	139 (0.76)	7 (0.04)	10 (0.05)
Lightning Cr	39	39 (1.00)	5 (0.13)	1 (0.03)		1 (0.03)			3 (0.08)	20 (0.51)	7 (0.18)	2 (0.05)
upper Grande Ronde R	156	156 (1.00)	11 (0.07)	4 (0.03)	1 (0.01)	6 (0.04)			18 (0.12)	5 (0.03)	92 (0.59)	19 (0.12)
Little Minam R	48	48 (1.00)	1 (0.02)						6 (0.13)		35 (0.73)	6 (0.13)
Wallowa R	117	117 (1.00)	18 (0.15)	1 (0.01)	1 (0.01)	1 (0.01)	1 (0.01)		6 (0.05)	4 (0.03)	79 (0.68)	6 (0.05)
Wenaha R	191	191 (1.00)	8 (0.04)	3 (0.02)	2 (0.01)	6 (0.03)			10 (0.05)	14 (0.07)	125 (0.65)	23 (0.12)
Menatchee Cr	73	73 (1.00)	4 (0.05)	1 (0.01)		2 (0.03)					55 (0.75)	11 (0.15)
Joseph Cr	97	97 (1.00)	3 (0.03)	1 (0.01)		2 (0.02)	1 (0.01)		9 (0.09)	2 (0.02)	68 (0.70)	11 (0.11)
Asotin Cr	194	194 (1.00)	26 (0.13)	2 (0.01)	1 (0.01)	10 (0.05)	1 (0.01)	2 (0.01)	33 (0.17)	6 (0.03)	38 (0.20)	75 (0.39)
Alpowa Cr	98	98 (1.00)	13 (0.13)		1 (0.01)	2 (0.02)	1 (0.01)	5 (0.05)	5 (0.05)	4 (0.04)	22 (0.22)	45 (0.46)
Tucannon R	106	106 (1.00)	8 (0.08)	3 (0.03)	1 (0.01)	2 (0.02)	1 (0.01)		15 (0.14)	7 (0.07)	26 (0.25)	43 (0.41)

Table 2b

Collection of origin	n	Number Assigned (Proportion)	Genetic Stock (≥80% Probability)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
Sawtooth	319	319 (0.47)	138 (0.92)	1 (0.01)		4 (0.03)			1 (0.01)	1 (0.01)	4 (0.03)	1 (0.01)
Herd Cr	85	85 (0.59)	45 (0.90)						1 (0.02)	3 (0.06)	1 (0.02)	
Morgan Cr	61	61 (0.72)	42 (0.95)		1 (0.02)						1 (0.02)	
Pahsimeroi R	97	97 (0.59)	53 (0.93)	1 (0.02)						3 (0.05)		
Lemhi R	86	86 (0.64)	51 (0.93)	3 (0.05)							1 (0.02)	
NF Salmon R	100	100 (0.33)	26 (0.79)			4 (0.12)	1 (0.03)			1 (0.03)	1 (0.03)	
Marsh Cr	195	195 (0.77)	7 (0.05)	144 (0.95)								
Bear Valley Cr	173	173 (0.95)		164 (1.00)								
MF Salmon R	227	227 (0.85)	1 (0.01)	189 (0.98)	1 (0.01)	1 (0.01)				1 (0.01)		
Loon Cr	131	131 (0.92)		120 (1.00)								
Camas Cr	97	97 (0.97)	1 (0.01)	92 (0.98)						1 (0.01)		
Big Cr	224	224 (0.91)	5 (0.02)	194 (0.96)				1 (0.00)		1 (0.00)	1 (0.00)	1 (0.00)
Chamberlain Cr	189	189 (0.85)	1 (0.01)	158 (0.99)		1 (0.01)						

Collection of origin	n	Number Assigned (Proportion)	Genetic Stock (≥80% Probability)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
SF Salmon R	45	45 (0.96)	1 (0.02)		40 (0.93)					1 (0.02)	1 (0.02)	
EFSF Salmon R	135	135 (0.87)		4 (0.03)	114 (0.97)							
Secesh R	208	208 (0.85)	3 (0.02)		172 (0.98)	1 (0.01)						
Little Salmon R	147	147 (0.53)	16 (0.21)	6 (0.08)	1 (0.01)	51 (0.65)		2 (0.03)	1 (0.01)		1 (0.01)	
Slate Cr	75	75 (0.40)	2 (0.07)		2 (0.07)	23 (0.77)				1 (0.03)	1 (0.03)	1 (0.03)
upper Lochsa R	129	129 (0.93)					118 (0.98)	2 (0.02)				
middle Lochsa R	147	147 (0.93)					133 (0.97)	3 (0.02)			1 (0.01)	
upper Selway R	247	247 (0.96)					237 (1.00)		1 (0.00)			
Bear Cr	70	70 (0.96)					67 (1.00)					
middle Selway R	138	138 (0.91)					124 (0.98)	1 (0.01)		1 (0.01)		
lower Selway R	211	211 (0.84)					161 (0.90)	15 (0.08)	2 (0.01)			
Crooked R	136	136 (0.90)					4 (0.03)	118 (0.97)				
Newsome Cr	99	99 (0.88)						87 (1.00)				
Tenmile Cr	47	47 (0.74)					3 (0.09)	32 (0.91)				
Clear Cr	45	45 (0.71)					2 (0.06)	30 (0.94)				
Lolo Cr	94	94 (0.83)					1 (0.01)	77 (0.99)				
WF Potlatch R	84	84 (0.61)						2 (0.04)	46 (0.90)	1 (0.02)	2 (0.04)	
EF Potlatch R	158	158 (0.65)			1 (0.01)		2 (0.02)	1 (0.01)	95 (0.92)		2 (0.02)	2 (0.02)
Big Bear Cr	250	250 (0.52)	2 (0.02)			1 (0.01)	2 (0.02)	2 (0.02)	111 (0.85)	1 (0.01)	6 (0.05)	5 (0.04)
Lapwai Cr	158	158 (0.36)	5 (0.09)						44 (0.77)	1 (0.02)	5 (0.09)	2 (0.04)
upper Imnaha R	53	53 (0.58)								29 (0.94)	2 (0.06)	
Big Sheep Cr	184	184 (0.51)	1 (0.01)	1 (0.01)		2 (0.02)			2 (0.02)	83 (0.89)	1 (0.01)	3 (0.03)
Lightning Cr	39	39 (0.49)	2 (0.11)							17 (0.89)		
upper Grande Ronde R	156	156 (0.29)	4 (0.09)	3 (0.07)					2 (0.04)	1 (0.02)	34 (0.74)	2 (0.04)
Little Minam R	48	48 (0.65)							1 (0.03)		28 (0.90)	2 (0.06)
Wallowa R	117	117 (0.37)	5 (0.12)						1 (0.02)	1 (0.02)	36 (0.84)	
Wenaha R	191	191 (0.40)	3 (0.04)	1 (0.01)	1 (0.01)				1 (0.01)	4 (0.05)	63 (0.82)	4 (0.05)
Menatchee Cr	73	73 (0.41)				1 (0.03)					29 (0.97)	
Joseph Cr	97	97 (0.48)					1 (0.02)		2 (0.04)		43 (0.91)	1 (0.02)
Asotin Cr	194	194 (0.19)	5 (0.14)			3 (0.08)			4 (0.11)	2 (0.05)	7 (0.19)	16 (0.43)
Alpowa Cr	98	98 (0.27)	2 (0.08)			1 (0.04)	1 (0.04)	3 (0.12)	1 (0.04)		5 (0.19)	13 (0.50)
Tucannon R	106	106 (0.29)	3 (0.10)	2 (0.06)		1 (0.03)			6 (0.19)	1 (0.03)	7 (0.23)	11 (0.35)

Table 3. Forty-six collections of Snake River basin Chinook Salmon *Oncorhynchus tshawytscha* were screened with the PBT and GSI SNP panels. Each collection is identified by its TRT population, genetic stock, major population group (MPG), sample size (n), years collected, genotyping agency, baseline version in which it first appeared, latitude, longitude, lineage, expected heterozygosity (H_E), mean pairwise fixation indices (F_{ST}), and number of loci out of Hardy–Weinberg expectation (deficient (def.) or excess (ex). in ≥10% of SNPs). Map # corresponds to numbers in Figure 1. Agency indicates the laboratory where samples were genotyped. Lineages are ST – stream type, OC – ocean type. All collections are summer-run, of natural origin and presumed to be of anadromous lineage.

Map #	Collection	TRT population	Genetic Stock	MPG	n	Years Collected	Genotype Agency	Baseline version	Lineage	Latitude	Longitude	H_E	F_{ST}	HWE D	HWE E
1	Decker Flat	SRUMA	UPSALM	Upper Salmon	95	10, 11	NWFSC	3	ST	44.0654	-114.8558	22.6%	0.013		
2	Sawtooth Weir	SRUMA	UPSALM	Upper Salmon	91	09, 10	IDFG	1	ST	44.1507	-114.8855	21.9%	0.013		
3	Valley Cr	SRVAL	UPSALM	Upper Salmon	100	07, 08, 09, 10, 11	IDFG	3	ST	44.2408	-115.0016	22.8%	0.014	7	6
4	WF Yankee Fork	SRYFS	UPSALM	Upper Salmon	75	05	CRITFC	1	ST	44.3448	-114.7252	22.1%	0.019		
5	upper Salmon mainstem	SLRMA	UPSALM	Upper Salmon	83	05, 06, 07, 08, 09, 10	IDFG	3	ST	44.2557	-114.5648	22.3%	0.014		
6	Herd Cr	SREFS	UPSALM	Upper Salmon	99	10, 11	NWFSC	3	ST	44.1232	-114.2664	21.5%	0.016		
7	East Fork SR	SREFS	UPSALM	Upper Salmon	187	04, 05, 11	IDFG/CRITFC	2	ST	44.2002	-114.2861	22.3%	0.013		
8	Pahsimeroi R	SRPAH	UPSALM	Upper Salmon	92	07, 08, 09, 10	IDFG	2	ST	44.5630	-113.9124	22.7%	0.016		
9	Hayden Cr	SRLEM	N/A	Upper Salmon	79	09, 10	IDFG	2	ST	44.7854	-113.7059	23.4%	0.020	9	0
10	upper Lemhi R	SRLEM	UPSALM	Upper Salmon	96	09, 10	IDFG	2	ST	44.8267	-113.6068	21.4%	0.017	7	8
11	lower Lemhi R	SRLEM	N/A	Upper Salmon	90	09, 10	IDFG	1	ST	45.1664	-113.8614	23.5%	0.014	9	3
12	NF Salmon R	SRNFS	UPSALM	Upper Salmon	55	05, 06, 07, 08, 09, 10	IDFG	3	ST	45.5010	-113.9631	22.4%	0.016		
13	Panther Cr	SRPAN	N/A	Upper Salmon	86	10, 11	IDFG	3	ST	45.2067	-114.3201	22.2%	0.013		
14	Marsh Cr	MFMAR	MFSALM	Middle Fork Salmon	116	07, 08, 09, 10, 11	IDFG	3	ST	44.4153	-115.1842	21.5%	0.014		
15	Capehorn Cr	MFMAR	MFSALM	Middle Fork Salmon	112	05, 06, 07, 09, 10	IDFG/CRITFC	2	ST	44.3586	-115.2236	21.4%	0.018	7	6
16	Elk Cr (MF Salmon R)	MFBEA	MFSALM	Middle Fork Salmon	134	07, 08, 09, 10, 11	IDFG/NWFSC	3	ST	44.4304	-115.4711	21.1%	0.016		
17	Bear Valley Cr	MFBEA	MFSALM	Middle Fork Salmon	80	07, 08, 09, 10	IDFG	1	ST	44.3735	-115.3954	21.3%	0.015		
18	Sulphur Cr	MFSUL	MFSALM	Middle Fork Salmon	135	08, 09, 10, 11	IDFG/NWFSC	3	ST	44.5433	-115.3962	20.5%	0.019	6	3
19	Loon Cr	MFLOO	MFSALM	Middle Fork Salmon	94	10, 11	IDFG	3	ST	44.5982	-114.8110	21.5%	0.016		
20	Camas Cr	MFCAM	MFSALM	Middle Fork Salmon	107	06, 09, 10	IDFG/CRITFC	3	ST	44.8255	-114.4996	20.9%	0.017		
21	upper Big Cr	MFBIG	MFSALM	Middle Fork Salmon	55	10, 11	IDFG/CRITFC	3	ST	45.1530	-115.2961	21.3%	0.017		

Table 3. Continued

Map #	Collection	TRT population	Genetic Stock	MPG	n	Years Collected	Genotype Agency	Baseline version	Lineage	Latitude	Longitude	H_E	F_{ST}	HWE D	HWE E
22	lower Big Cr	MFBIG	MFSALM	Middle Fork Salmon	139	01, 11	CRITFC/NWFSC	3	ST	45.1072	-114.8061	21.6%	0.012	12	1
23	Chamberlain Cr (pre-2008)	SRCHA	CHMBLN	Middle Fork Salmon	70	03, 04, 06, 07	IDFG	2	ST	45.3936	-115.1944	20.9%	0.022		
24	Chamberlain Cr (post-2008)	SRCHA	CHMBLN	Middle Fork Salmon	149	09, 10	IDFG/CRITFC	3	ST	45.3708	-115.1967	21.0%	0.023	8	1
25	Summit and Lake Cr	SFSEC	SFSALM	South Fork Salmon	122	07, 08, 09, 10, 11	IDFG	3	ST	45.2712	-115.9141	21.7%	0.017		
26	Sesech R	SFSEC	SFSALM	South Fork Salmon	130	01, 07, 08, 09, 10	IDFG/CRITFC	1	ST	45.2172	-115.8086	21.9%	0.015		
27	Johnson Cr	SFMAI	SFSALM	South Fork Salmon	137	02, 11	CRITFC/NWFSC	3	ST	44.9059	-115.4867	22.2%	0.015		
28	SF Salmon R mainstem	SFMAI	SFSALM	South Fork Salmon	139	09, 10	IDFG	2	ST	44.6666	-115.7029	22.9%	0.011		
29	Rapid R	SRLSR	HELLSC	N/A	91	06	IDFG	1	ST	45.3163	-116.4180	22.7%	0.015	8	3
30	Crooked F (Lochsa R)	CRLOC	HELLSC	N/A	26	07, 08, 09, 10	IDFG	2	ST	46.6188	-114.6671	23.8%	0.016		
31	Powell Weir	CRLOC	HELLSC	N/A	30	09	IDFG	1	ST	46.5070	-114.6874	22.9%	0.014		
32	Red R	SCUMA	HELLSC	N/A	72	07, 08, 09, 10	IDFG	2	ST	45.7094	-115.3399	24.0%	0.013		
33	Crooked R Weir	SCUMA	HELLSC	N/A	67	09, 10	IDFG	1	ST	45.7655	-115.5438	23.9%	0.013		
34	Newsome Cr	SCUMA	HELLSC	N/A	82	01	CRITFC	1	ST	45.8338	-115.6112	22.8%	0.015		
35	Lolo Cr	CRLOL	HELLSC	N/A	89	01, 02	IDFG/CRITFC	1	ST	46.2802	-115.7727	23.7%	0.012	14	3
36	Imnaha R	IRMAI	HELLSC	Grande Ronde / Imnaha	96	08, 10	IDFG/NOAA	2	ST	45.4900	-116.8039	23.5%	0.012		
37	upper Grande Ronde R	GRUMA	HELLSC	Grande Ronde / Imnaha	43	08	IDFG/NOAA	2	ST	45.1932	-118.3944	24.4%	0.015		
38	Catherine Cr	GRCAT	HELLSC	Grande Ronde / Imnaha	140	04, 06, 11	IDFG/CRITFC/ NWFSC	3	ST	45.1549	-117.7793	24.8%	0.013	10	2
39	Minam R	GRMIN	HELLSC	Grande Ronde / Imnaha	131	94, 02, 10	IDFG/CRITFC/ NWFSC	3	ST	45.3476	-117.6534	25.1%	0.013	11	1
40	Wallowa R & Hurricane Cr	GRLOS	HELLSC	Grande Ronde / Imnaha	37	11	IDFG	3	ST	45.4241	-117.2927	25.4%	0.019		
41	Lostine R	GRLOS	HELLSC	Grande Ronde / Imnaha	175	03, 05, 09	IDFG//NOAA	2	ST	45.4736	-117.4257	23.0%	0.015	11	0
42	Wenaha R	GRWEN	HELLSC	Grande Ronde / Imnaha	179	02, 06, 09, 10	CRITFC	3	ST	45.9689	-117.6956	26.4%	0.014	14	3
43	Tucannon R	SNTUC	TUCANO	Tucannon	81	03	CRITFC	1	ST	46.5053	-118.0144	26.0%	0.025	6	3
44	Clearwater R	FALL ESU	FALL	Snake R	143	08	IDFG/CRITFC	2	OC	46.5229	-116.6152	NA	NA	NA	
45	Nez Perce Tribal H.	FALL ESU	FALL	Snake R	85	03	CRITFC	2	OC	46.5191	-116.6646	NA	NA	NA	
46	Lyons Ferry H.	FALL ESU	FALL	Snake R	90	00	CRITFC	2	OC	46.5894	-118.2195	NA	NA	NA	

Table 4. Chinook Salmon results from self-assignment tests performed in gsi_sim (Anderson et al. 2008, Anderson 2010). For each baseline super collection represented in baseline v3.1, each individual was sequentially removed from the baseline and then assigned back to the baseline. Rows represent collection of origin and columns represent genetic stock to which individuals assigned. Table 4a is results for all individuals that assigned to a genetic stock, and Table 4b is for individuals that assigned to a genetic stock with ≥80% probability. For example, n = 186 individuals represent the Sawtooth collection. Of the 186 individuals in the baseline, 129 (69%) assigned back to a genetic stock with ≥80% probability. Of the 129 that assigned, 123 (95%) assigned to the correct UPSALM reporting group. Shaded boxes represent the correct genetic stock of origin for each population

Table 4a.

Collection of Origin	n	Number Assigned (Proportion)	Assigned Generic Stock (No Threshold)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
Sawtooth	186	186 (1.00)	158 (0.85)	14 (0.08)		5 (0.03)	9 (0.05)		
Valley Cr	100	100 (1.00)	91 (0.91)	2 (0.02)	1 (0.01)	1 (0.01)	5 (0.05)		
WF Yankee Fork	75	75 (1.00)	69 (0.92)			2 (0.03)	4 (0.05)		
upper Salmon mainstem	83	83 (1.00)	76 (0.92)	4 (0.05)		1 (0.01)	2 (0.02)		
Herd Cr	286	286 (1.00)	259 (0.91)	10 (0.03)		5 (0.02)	12 (0.04)		
Pahsimeroi R	92	92 (1.00)	84 (0.91)	1 (0.01)		3 (0.03)	4 (0.04)		
upper Lemhi R	96	96 (1.00)	77 (0.80)	8 (0.08)		3 (0.03)	8 (0.08)		
NF Salmon R	55	55 (1.00)	42 (0.76)	3 (0.05)	1 (0.02)	1 (0.02)	8 (0.15)		
Marsh Cr	228	228 (1.00)	11 (0.05)	196 (0.86)		13 (0.06)	8 (0.04)		
Elk Cr (MF Salmon R)	214	214 (1.00)	5 (0.02)	192 (0.90)	1 (0.00)	9 (0.04)	7 (0.03)		
Sulphur Cr	135	135 (1.00)	3 (0.02)	130 (0.96)		1 (0.01)	1 (0.01)		
Loon Cr	94	94 (1.00)	5 (0.05)	82 (0.87)			7 (0.07)		
Camas Cr	107	107 (1.00)	1 (0.01)	94 (0.88)	1 (0.01)	5 (0.05)	6 (0.06)		
upper Big Cr	55	55 (1.00)	4 (0.07)	48 (0.87)	2 (0.04)		1 (0.02)		
lower Big Cr	139	139 (1.00)	8 (0.06)	102 (0.73)	2 (0.01)	6 (0.04)	21 (0.15)		
Chamberlain Cr	219	219 (1.00)	4 (0.02)	6 (0.03)	195 (0.89)	2 (0.01)	12 (0.05)		
Summit and Lake Cr	252	252 (1.00)	6 (0.02)	15 (0.06)	1 (0.00)	213 (0.85)	17 (0.07)		
Johnson Cr	137	137 (1.00)	6 (0.04)	12 (0.09)		109 (0.80)	10 (0.07)		
SF Salmon R mainstem	139	139 (1.00)	25 (0.18)	17 (0.12)	4 (0.03)	75 (0.54)	18 (0.13)		
Rapid R	91	91 (1.00)	4 (0.04)	1 (0.01)		2 (0.02)	84 (0.92)		
Crooked F (Lochsa R)	56	56 (1.00)	5 (0.09)	4 (0.07)		2 (0.04)	44 (0.79)	1 (0.02)	
Red R	221	221 (1.00)	10 (0.05)	5 (0.02)		5 (0.02)	201 (0.91)		
Lolo Cr	89	89 (1.00)	8 (0.09)	2 (0.02)	1 (0.01)	2 (0.02)	75 (0.84)	1 (0.01)	
Imnaha R	96	96 (1.00)	9 (0.09)	8 (0.08)		5 (0.05)	74 (0.77)		
upper Grande Ronde R	314	314 (1.00)	13 (0.04)	10 (0.03)		10 (0.03)	280 (0.89)	1 (0.00)	
Wallowa R & Hurricane Cr	212	212 (1.00)	5 (0.02)	4 (0.02)		6 (0.03)	196 (0.92)	1 (0.00)	
Wenaha R	179	179 (1.00)	7 (0.04)	1 (0.01)	1 (0.01)	3 (0.02)	157 (0.88)	6 (0.03)	4 (0.02)
Tucannon R	81	81 (1.00)	1 (0.01)	1 (0.01)		1 (0.01)	11 (0.14)	66 (0.81)	1 (0.01)
Clearwater R	228	228 (1.00)							228 (1.00)
Lyons Ferry H.	90	90 (1.00)							90 (1.00)

Table 4b.

Collection of Origin	n	Number Assigned (Proportion)	Assigned Generic Stock (≥80% Probability)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
Sawtooth	186	129 (0.69)	123 (0.95)	2 (0.02)		1 (0.01)	3 (0.02)		
Valley Cr	100	85 (0.85)	81 (0.95)		1 (0.01)		3 (0.04)		
WF Yankee Fork	75	64 (0.85)	63 (0.98)				1 (0.02)		
upper Salmon mainstem	83	70 (0.84)	68 (0.97)	2 (0.03)					
Herd Cr	286	236 (0.83)	225 (0.95)	5 (0.02)		1 (0.00)	5 (0.02)		
Pahsimeroi R	92	75 (0.82)	74 (0.99)			1 (0.01)			
upper Lemhi R	96	69 (0.72)	63 (0.91)	4 (0.06)			2 (0.03)		
NF Salmon R	55	36 (0.65)	33 (0.92)			1 (0.03)	2 (0.06)		
Marsh Cr	228	173 (0.76)	4 (0.02)	163 (0.94)		4 (0.02)	2 (0.01)		
Elk Cr (MF Salmon R)	214	179 (0.84)		170 (0.95)	1 (0.01)	3 (0.02)	5 (0.03)		
Sulphur Cr	135	123 (0.91)		122 (0.99)		1 (0.01)			
Loon Cr	94	78 (0.83)	3 (0.04)	75 (0.96)					
Camas Cr	107	89 (0.83)		83 (0.93)	1 (0.01)	1 (0.01)	4 (0.04)		
upper Big Cr	55	45 (0.82)		42 (0.93)	2 (0.04)		1 (0.02)		
lower Big Cr	139	101 (0.73)	6 (0.06)	81 (0.80)		1 (0.01)	13 (0.13)		
Chamberlain Cr	219	192 (0.88)	2 (0.01)	1 (0.01)	180 (0.94)		9 (0.05)		
Summit and Lake Cr	252	191 (0.76)		2 (0.01)		181 (0.95)	8 (0.04)		
Johnson Cr	137	92 (0.67)	3 (0.03)	2 (0.02)		84 (0.91)	3 (0.03)		
SF Salmon R mainstem	139	53 (0.38)	9 (0.17)	3 (0.06)		36 (0.68)	5 (0.09)		
Rapid R	91	80 (0.88)	1 (0.01)			1 (0.01)	78 (0.98)		
Crooked F (Lochsa R)	56	33 (0.59)	1 (0.03)	1 (0.03)			31 (0.94)		
Red R	221	191 (0.86)	8 (0.04)	2 (0.01)		1 (0.01)	180 (0.94)		
Lolo Cr	89	72 (0.81)	3 (0.04)	1 (0.01)	1 (0.01)	1 (0.01)	65 (0.90)	1 (0.01)	
Imnaha R	96	66 (0.69)	3 (0.05)	1 (0.02)			62 (0.94)		
upper Grande Ronde R	314	249 (0.79)	5 (0.02)	2 (0.01)		3 (0.01)	238 (0.96)	1 (0.00)	
Wallowa R & Hurricane Cr	212	180 (0.85)	3 (0.02)	1 (0.01)		1 (0.01)	174 (0.97)	1 (0.01)	
Wenaha R	179	151 (0.84)	2 (0.01)			1 (0.01)	141 (0.93)	3 (0.02)	4 (0.03)
Tucannon R	81	72 (0.89)		1 (0.01)			7 (0.10)	63 (0.88)	1 (0.01)
Clearwater R	228	228 (1.00)							228 (1.00)
Lyons Ferry H.	90	90 (1.00)							90 (1.00)

Table 5. Summary of SY2014 adult and MY2014 juvenile Steelhead and Chinook Salmon samples from Lower Granite Dam (LGR). Summary includes the number of samples that arrived from LGR (inventoried) and the number inventoried that were queued for genotyping. Of queued samples, we show the number that genotyped successfully and the number that failed genotyping. For samples that genotyped successfully, we show the number that had a parentage based tag (PBT) and the number that were assigned a genetic stock based on individual assignment (IA) using SNP baselines v3.1

Sample Group	Total Samples Inventoried	Samples Queued for Genotyping	Failed Genotyping (NG)	Successfully Genotyped	PBT Assignments	GSI Assignments
Steelhead						
SY2014 Adults (Wild Phenotype)	3,712	3,712	15 (0.4%)	3,697 (99.6%)	226 (6.1%)	3,471 (93.9%)
SY2014 Adults (Stubbies)	877	877	4 (0.5%)	873 (99.5%)	757 (86.7%)	116 (13.3%)
MY2014 Juveniles	1,387	1,387	4 (0.3%)	1,383 (99.7%)	12 (0.9%)	1,371 (99.1%)
Chinook						
SY2014 Adults	4,529	4,529	68 (1.5%)	4,461 (98.5%)	1,076 (24.1%)	3,385 (75.9%)
MY2014 Juveniles (Yearling)	2,184	1,455	62 (4.3%)	1,393 (95.7%)	66 (4.7%)	1,327 (95.3%)
MY2014 Juveniles (Sub-yearling)	907	453	11 (2.4%)	442 (97.6%)	3 (0.7%)	439 (99.3%)
TOTAL:	13,596	12,413	164 (1.3%)	12,249 (98.7%)	2,140 (17.5%)	10,109 (82.5%)

Table 6. Summary of 3,587 Lower Granite Dam (LGR) **adult Steelhead** samples from **SY2014** assigned to a genetic stock using individual assignment based on **Snake River Steelhead SNP baseline v3.1**. Summaries of life-history diversity information (sex, length, and ocean age) for each genetic stock are shown. The 'Other' saltwater age category includes fish that were not queued for scale aging, fish that could not be aged, and fish with spawn checks.

			Sex					Length							Ocean (Saltwater) Age						
			Frequency			Percentage		Mean Length (cm FL) by Ocean Age			Frequency		Percentage		Frequency				Percentage		
Genetic Stock	Total Assignments	% Stock Composition	F	M	U	F	M	1	2	3	A-Run	B-Run	A-Run	B-Run	1	2	3	Other	1	2	3
UPSALM	636	17.7%	352	282	2	56%	44%	57.5	68.6	-	629	7	99%	1%	340	145	-	151	70%	30%	0%
MFSALM	212	5.9%	131	81	-	62%	38%	60.2	73.7	77.0	182	30	86%	14%	86	75	2	49	53%	46%	1%
SFSALM	122	3.4%	80	42	-	66%	34%	61.3	77.2	82.8	63	59	52%	48%	27	63	16	16	25%	59%	15%
LOSALM	130	3.6%	70	60	-	54%	46%	57.4	71.3	-	125	5	96%	4%	75	24	-	31	76%	24%	0%
UPCLWR	200	5.6%	113	87	-	57%	44%	61.1	77.3	82.3	118	82	59%	41%	45	74	7	74	36%	59%	6%
SFCLWR	199	5.5%	104	95	-	52%	48%	62.4	77.9	81.6	115	84	58%	42%	49	82	14	54	34%	57%	10%
LOCLWR	386	10.8%	209	177	-	54%	46%	57.7	71.1	86.0	371	15	96%	4%	189	86	1	110	68%	31%	0%
IMNAHA	336	9.4%	188	147	1	56%	44%	57.0	68.0	-	335	1	100%	0%	206	84	-	46	71%	29%	0%
GRROND	917	25.6%	480	434	3	53%	47%	56.9	69.4	-	905	12	99%	1%	491	192	-	234	72%	28%	0%
LSNAKE	449	12.5%	231	217	1	52%	48%	57.0	69.2	-	443	6	99%	1%	231	85	-	133	73%	27%	0%
Total:	**3,587**		**1,958**	**1,622**	**7**	**55%**	**45%**	**57.6**	**71.6**	**82.1**	**3,286**	**301**	**92%**	**8%**	**1,739**	**910**	**40**	**898**	**65%**	**34%**	**1%**

Table 7. Summary of 1,371 Lower Granite Dam (LGR) **juvenile Steelhead** samples from **MY2014** assigned to a genetic stock using individual assignment based on **Snake River Steelhead SNP baseline v3.1**. Summaries of life-history diversity information (sex, length, and freshwater age) for each genetic stock are shown. The 'Other' freshwater age category includes fish that were not queued for scale aging or could not be aged.

			Sex					Length	Freshwater Age										
			Frequency			Percentage			Frequency						Percentage				
Genetic Stock	Total Assignments	% Stock Composition	F	M	U	F	M	Mean Length (mm FL)	1	2	3	4	5	Other	1	2	3	4	5
UPSALM	223	16.3%	130	90	3	59%	41%	178	13	145	43	6	-	16	6%	70%	21%	3%	0%
MFSALM	132	9.6%	85	45	2	65%	35%	181	-	29	72	20	-	11	0%	24%	60%	17%	0%
SFSALM	65	4.7%	44	21	-	68%	32%	184	-	11	38	12	-	4	0%	18%	62%	20%	0%
LOSALM	50	3.6%	40	6	4	87%	13%	179	1	21	19	8	-	1	2%	43%	39%	16%	0%
UPCLWR	162	11.8%	101	59	2	63%	37%	177	1	36	95	16	3	11	1%	24%	63%	11%	2%
SFCLWR	117	8.5%	66	50	1	57%	43%	169	1	84	23	5	-	4	1%	74%	20%	4%	0%
LOCLWR	118	8.6%	66	52	-	56%	44%	181	8	70	25	6	-	9	7%	64%	23%	6%	0%
IMNAHA	106	7.7%	68	36	2	65%	35%	181	3	60	34	1	-	8	3%	61%	35%	1%	0%
GRROND	274	20.0%	179	90	5	67%	33%	183	14	153	86	7	-	14	5%	59%	33%	3%	0%
LSNAKE	124	9.0%	83	39	2	68%	32%	182	7	82	22	5	-	8	6%	71%	19%	4%	0%
Total:	**1,371**		**862**	**488**	**21**	**64%**	**36%**	**180**	**48**	**691**	**457**	**86**	**3**	**86**	**4%**	**54%**	**36%**	**7%**	**0%**

Table 8. Summary of 3,385 Lower Granite Dam (LGR) **adult Chinook Salmon** samples from **SY2014** assigned to a genetic stock using individual assignment based on **Snake River Chinook Salmon SNP baseline v3.1**. Summaries of life-history diversity information (sex, length, and ocean age) for each genetic stock are shown. MJ = minijack.

			Sex				Ocean (Saltwater) Age									Length		
			Frequency		Percentage		Frequency					Percentage				Mean Length (cm FL) by Ocean Age		
Genetic Stock	Total Assignments	% Stock Composition	F	M	F	M	MJ	1	2	3	U	MJ	1	2	3	1	2	3
UPSALM	690	20.4%	275	415	40%	60%	-	63	485	43	99	0%	11%	82%	7%	51.2	74.4	88.1
MFSALM	708	20.9%	284	424	40%	60%	-	61	376	18	253	0%	13%	83%	4%	51.5	75.1	85.6
CHMBLN	105	3.1%	52	53	50%	50%	-	6	49	1	49	0%	11%	88%	2%	62.8	74.1	82.0
SFSALM	500	14.8%	228	272	46%	54%	-	40	386	16	58	0%	9%	87%	4%	56.3	75.4	89.1
HELLSC	1,291	38.1%	624	667	48%	52%	-	85	814	48	344	0%	9%	86%	5%	54.4	73.2	85.6
TUCANO	15	0.4%	10	5	67%	33%	-	2	9	-	4	0%	18%	82%	0%	62.0	70.6	-
FALL	76	2.2%	24	52	32%	68%	2	12	14	10	38	5%	32%	37%	26%	55.2	80.7	85.9
Total:	**3,385**		**1497**	**1888**	**44%**	**56%**	**2**	**269**	**2133**	**136**	**845**	**0%**	**11%**	**84%**	**5%**	**53.5**	**74.3**	**86.8**

Table 9. Summary of 1,766 Lower Granite Dam (LGR) **juvenile Chinook Salmon** samples from **MY2014** assigned to a genetic stock using individual assignment based on **Snake River Chinook Salmon SNP baseline v3.1**. Summaries of life-history diversity information (sex, length, freshwater age, and emigration timing at LGR) by genetic stock are shown.

Genetic Stock	Total Assignments	% Stock Composition	Sex				Length	Freshwater Age	
			Frequency		Percentage		Mean Length (mm FL)	Frequency	
			F	M	F	M		0	1
UPSALM	206	11.7%	126	80	61%	39%	108	6	200
MFSALM	200	11.3%	114	86	57%	43%	105	7	193
CHMBLN	19	1.1%	8	11	42%	58%	104	1	18
SFSALM	150	8.5%	75	75	50%	50%	105	-	150
HELLSC	717	40.6%	398	319	56%	44%	112	19	698
TUCANO	12	0.7%	8	4	67%	33%	111	-	12
FALL	462	26.2%	242	220	52%	48%	101	406	56
Total:	**1,766**		**971**	**795**	**55%**	**45%**	**107.5**	**439**	**1327**

FIGURES

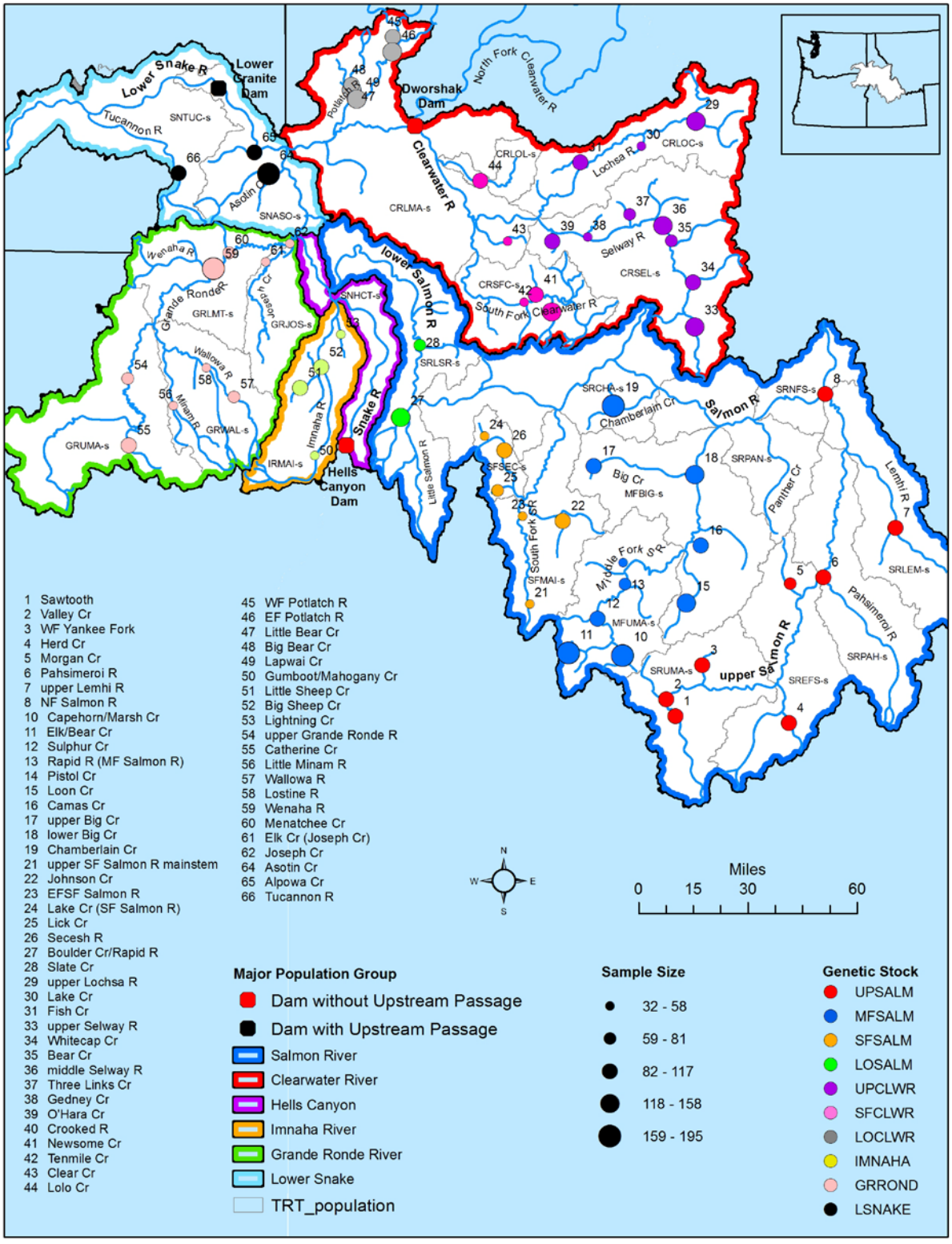

Figure 1. Natural origin Steelhead baseline v3.1 consists of 68 collections located within 23 TRT populations. TRT populations are grouped into 10 Genetic Stocks spanning across 6 Major Population Groups. Collections are described in detail in Table 1.

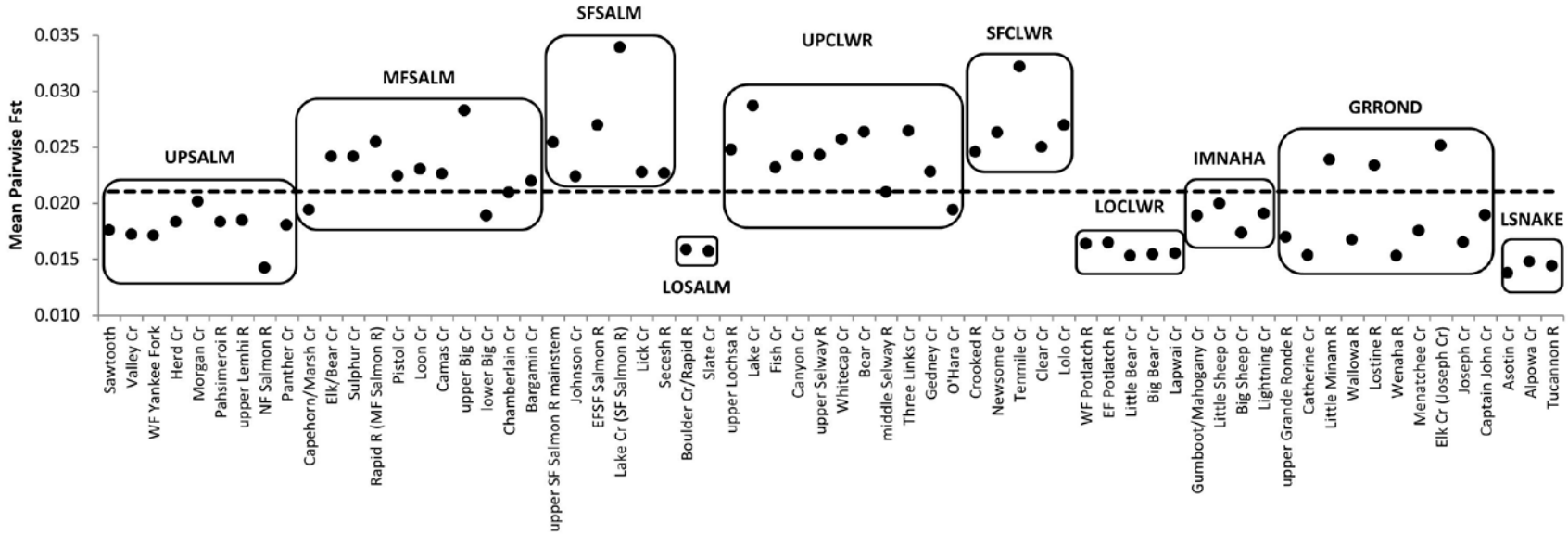

Figure 2. Mean pairwise F_{ST} estimates for Snake River Steelhead baseline v3.1 collections. The dashed line is the average pairwise F_{ST} estimate across all collections. High mean F_{ST} estimates suggest high genetic differentiation relative to other collections in the baseline. Each genetic stock is circumscribed.

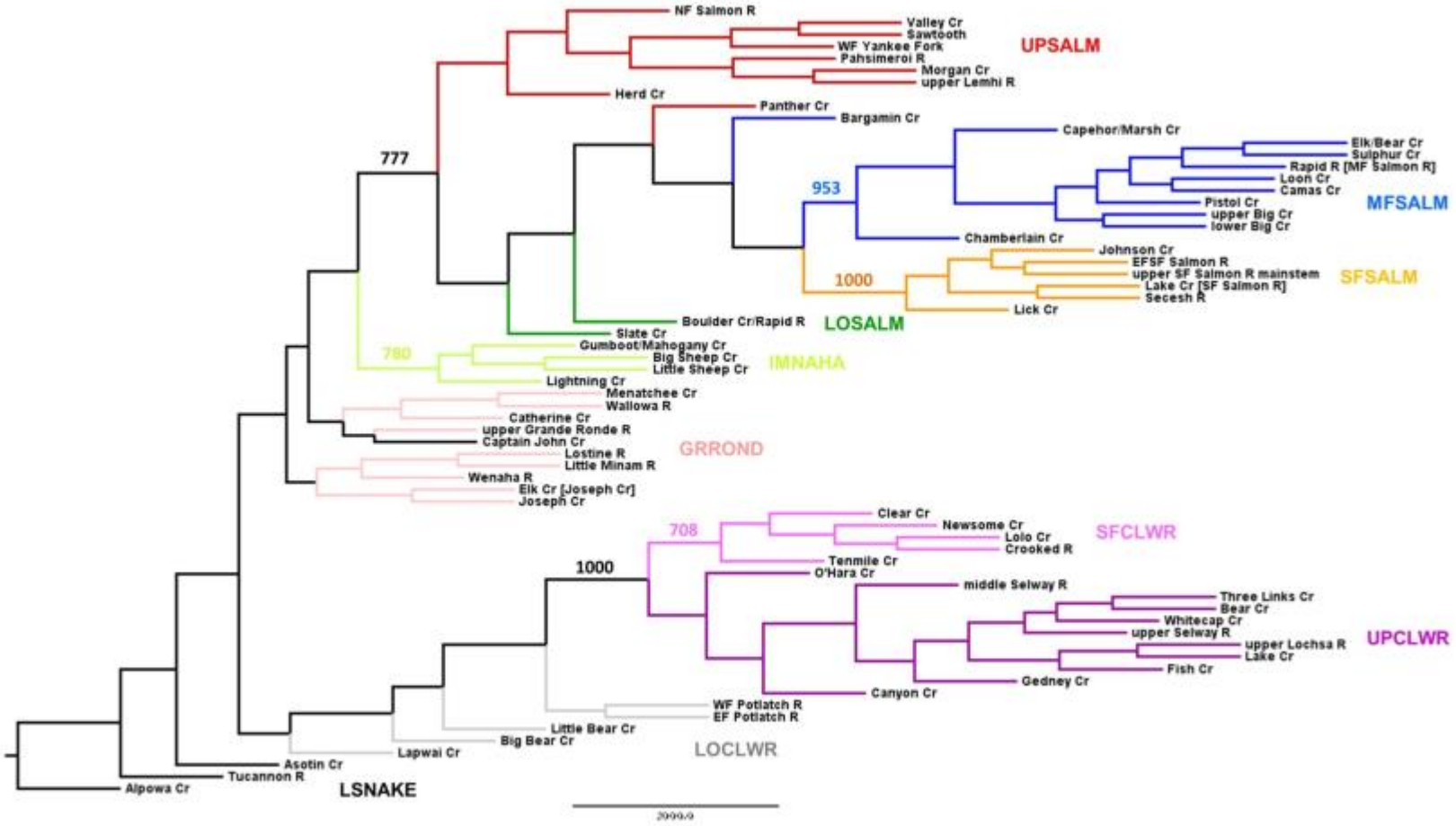

Figure 3. NJ-phylogram of Snake River basin Steelhead baseline v3.1 collections based on Nei (1972) genetic distances. Numbers above branches are bootstrap support based on 1000 replicates.

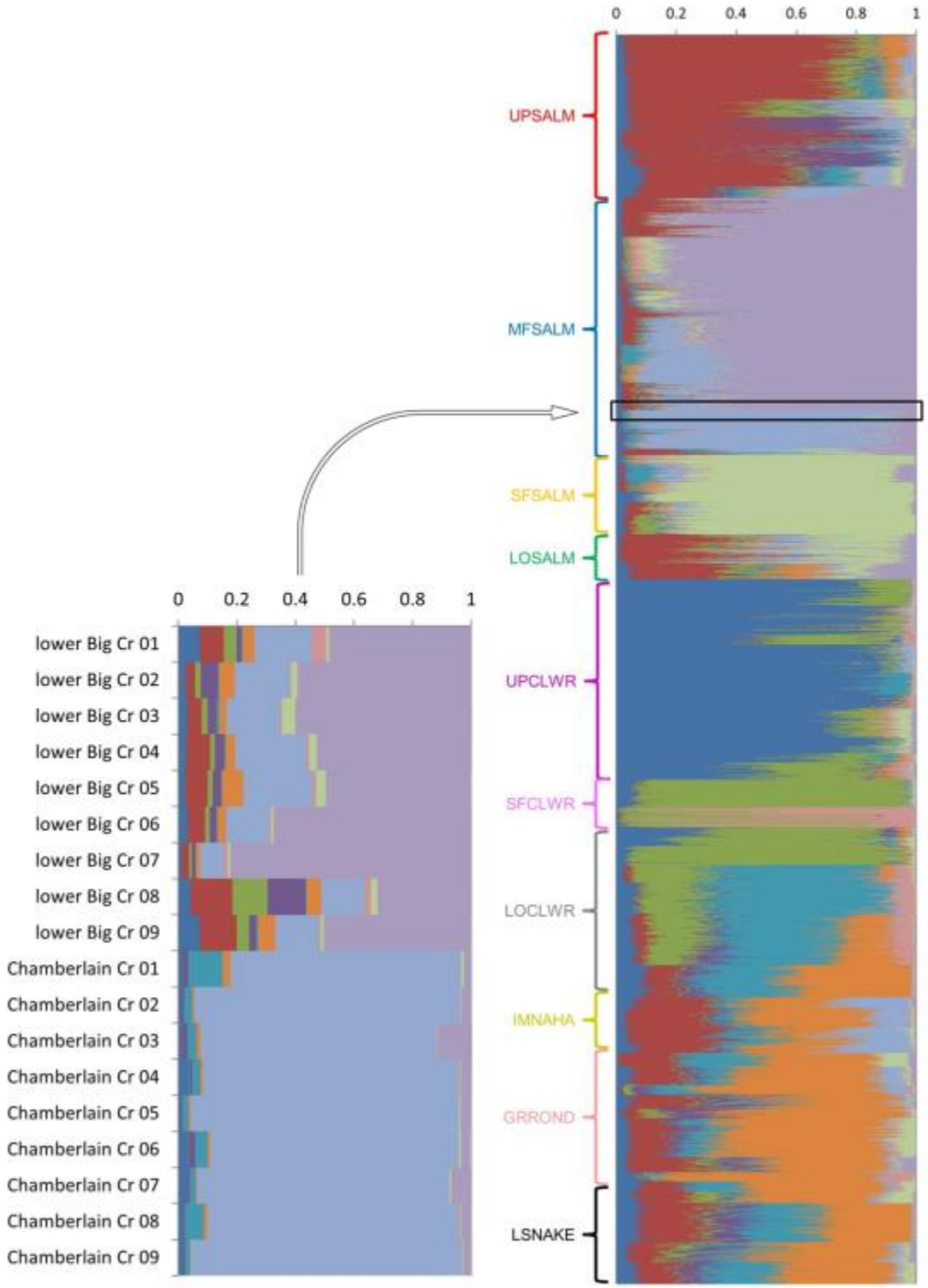

Figure 4. Histogram of STRUCTURE results for natural origin Steelhead (K = 10). Results are based on admixture ancestral model. Each individual is represented by a single horizontal line divided into K colored segments that is proportional to each K inferred clusters. Individuals are arranged by genetic stock.

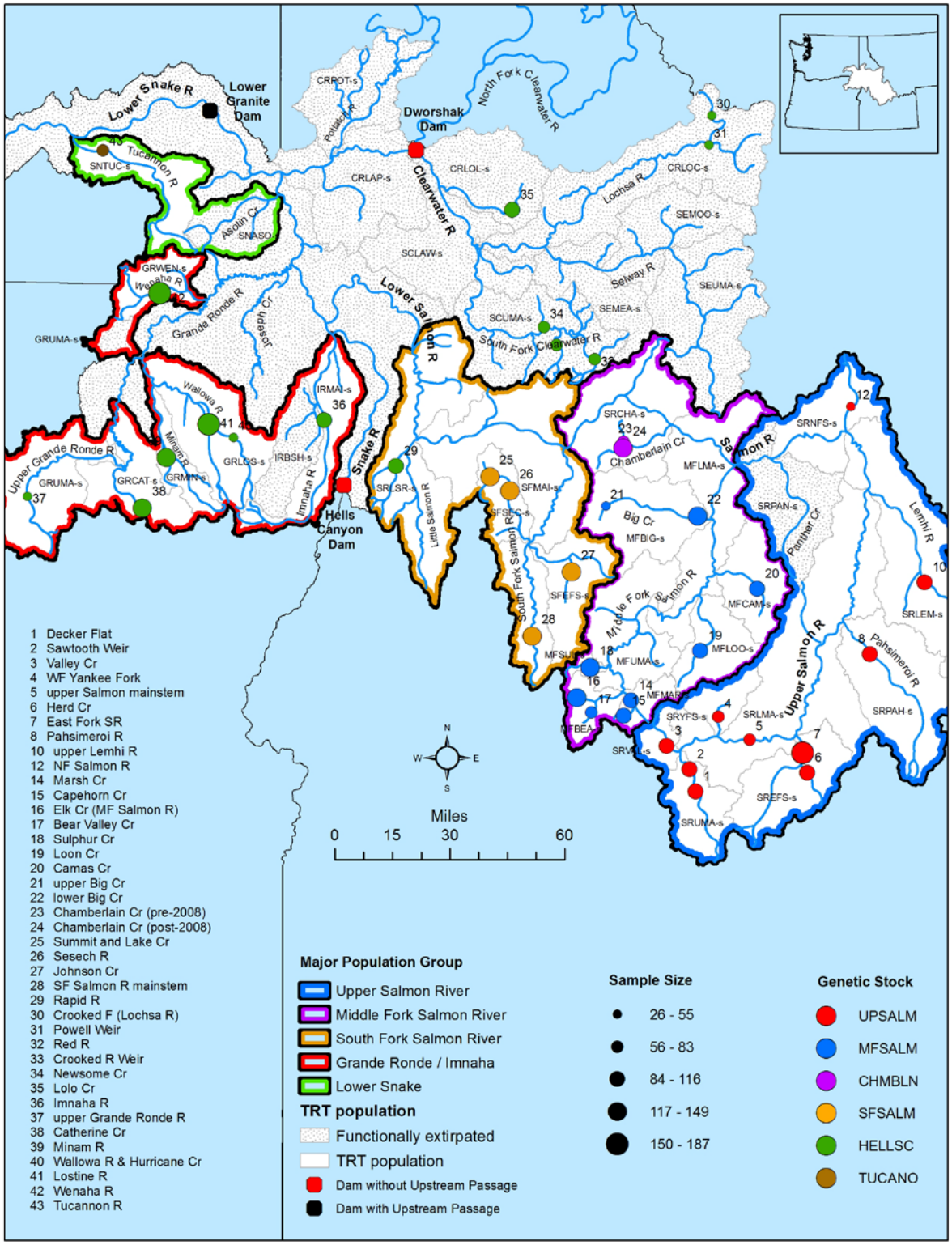

Figure 5. Natural origin Chinook Salmon baseline version 3.1 consists of 43 collections within 25 TRT populations. TRT populations are grouped into six Genetic Stocks spanning across five Major Population Groups. Collections are described in details in Table 5.

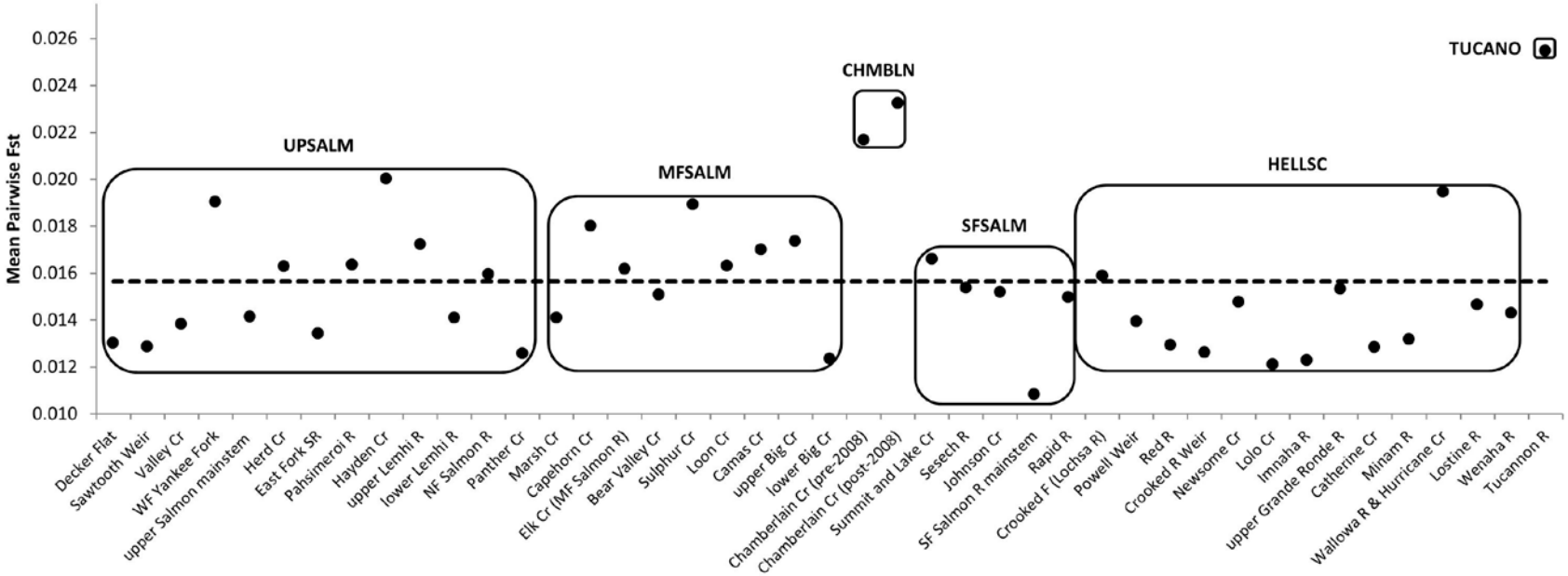

Figure 6. Mean pairwise F_{ST} estimates of Snake River Chinook Salmon baseline v3.1 collections. The dashed line is the average pairwise F_{ST} estimates suggest high genetic differentiation relative to other collections in the baseline. Each genetic stock is circumscribed.

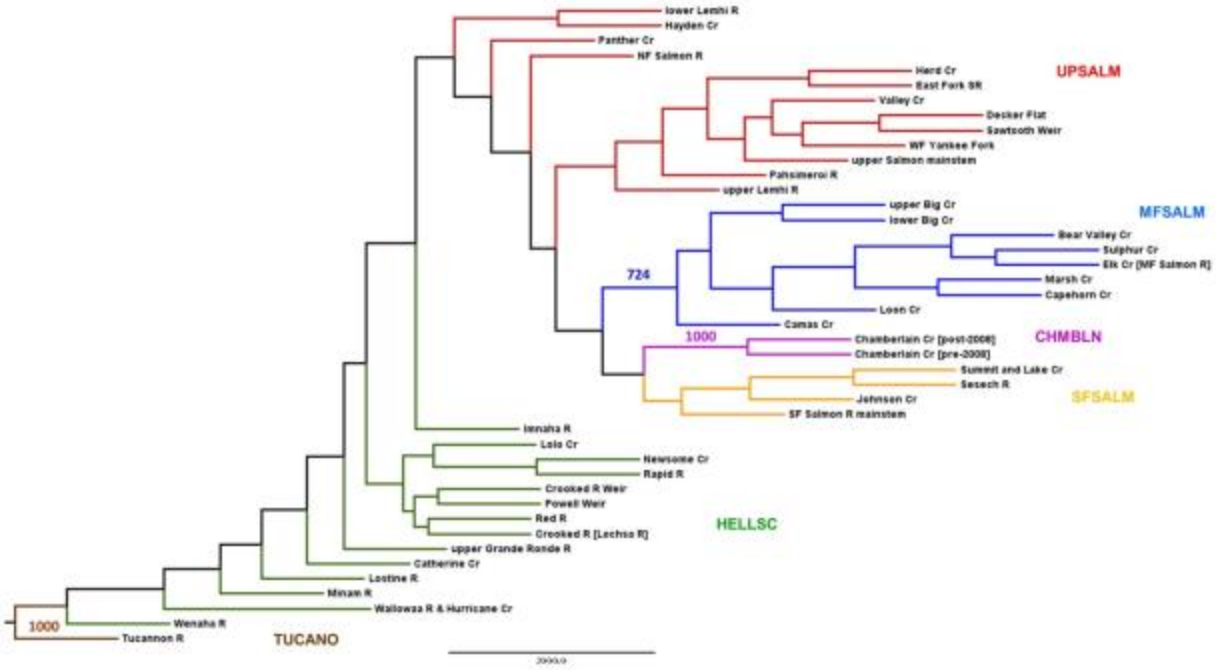

Figure 7. NJ-dendrogram of Snake River basin Chinook Salmon baseline v3.1 based on Cavalli-Sforza and Edwards (1967) genetic chord distances. Numbers above branches are bootstrap support based on 1000 replicates.

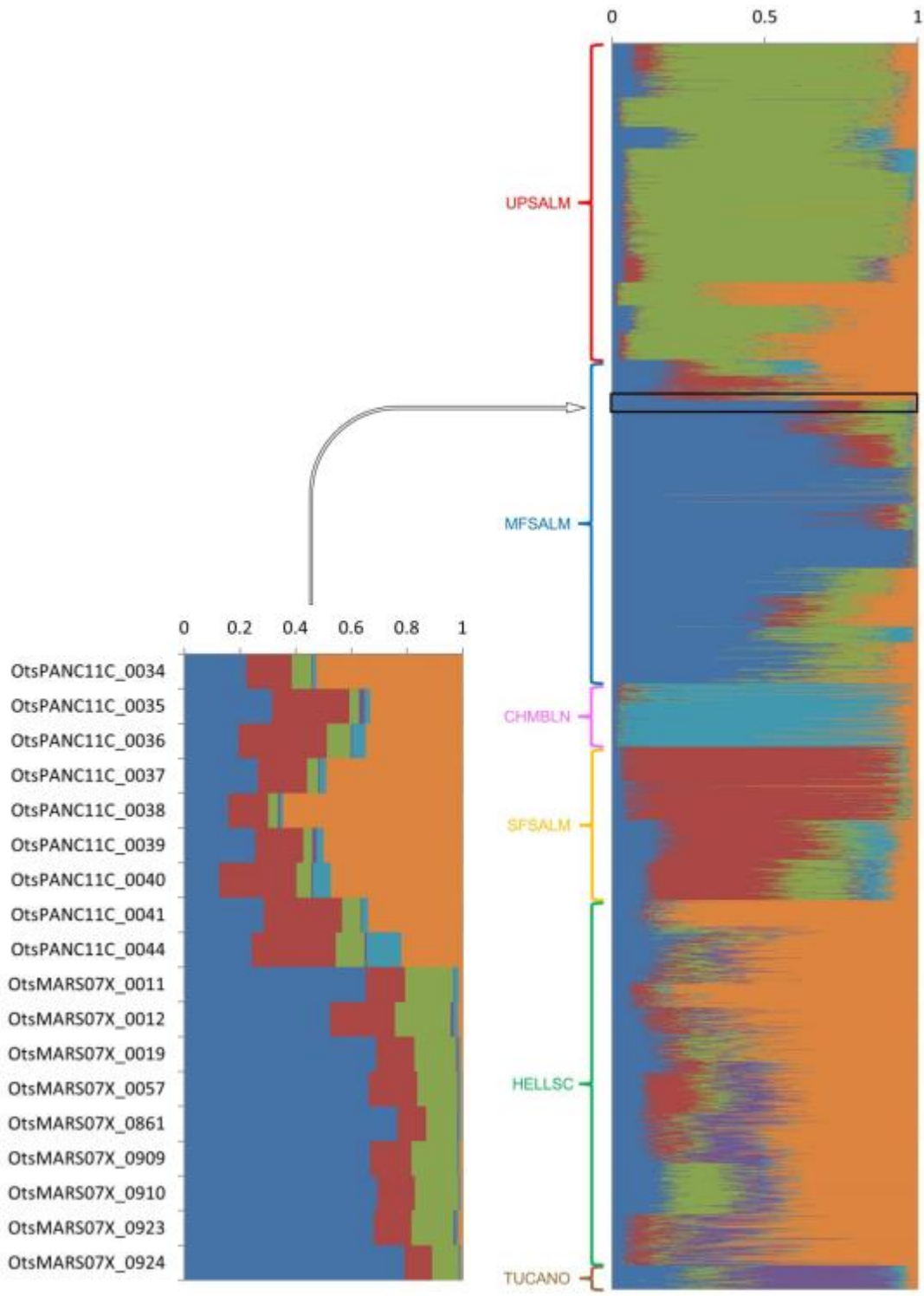

Figure 8. Histogram of STRUCTURE results for natural origin Chinook Salmon (K = 6). Results are based on admixture ancestral model. Each individual is represented by a single horizontal line divided into K colored segments that is proportional to each K inferred clusters. Individuals are arranged by genetic stock.

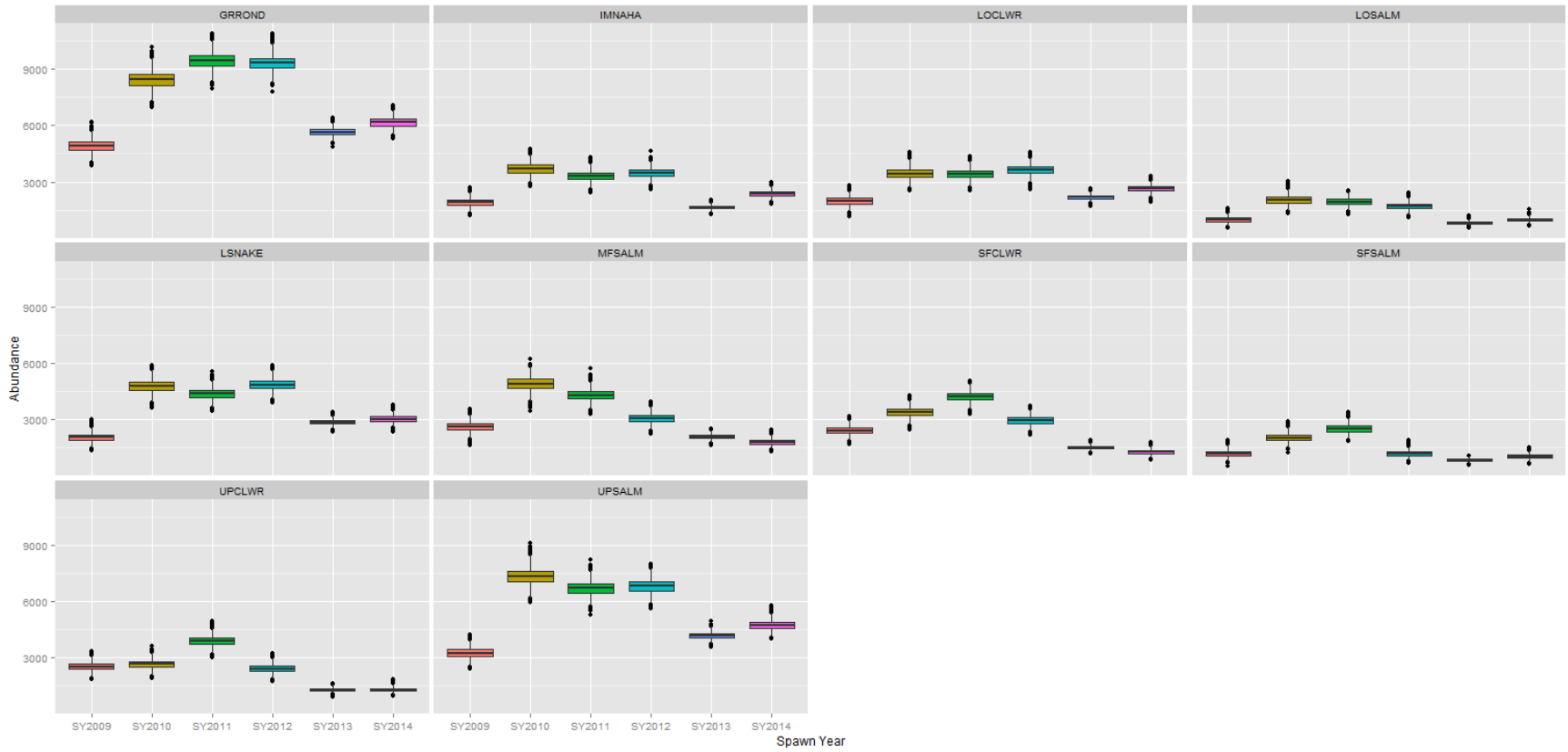

Figure 9. Boxplot of abundance at Lower Granite Dam by genetic stock for Snake River Steelhead, SY2009 – 2014. The box contains the inter-quartile range (IQR) and the median. The upper whisker extends from the IQR to the highest value within 1.5 times the IQR. The lower whisker extends from the IQR to the lowest value within 1.5 times the IQR. Data beyond the end of the whiskers are outliers and plotted as points. Estimates for each box and whisker are from 5,000 bootstrap estimates from SCOBI.r (Steinhorst et al. *unpublished*).

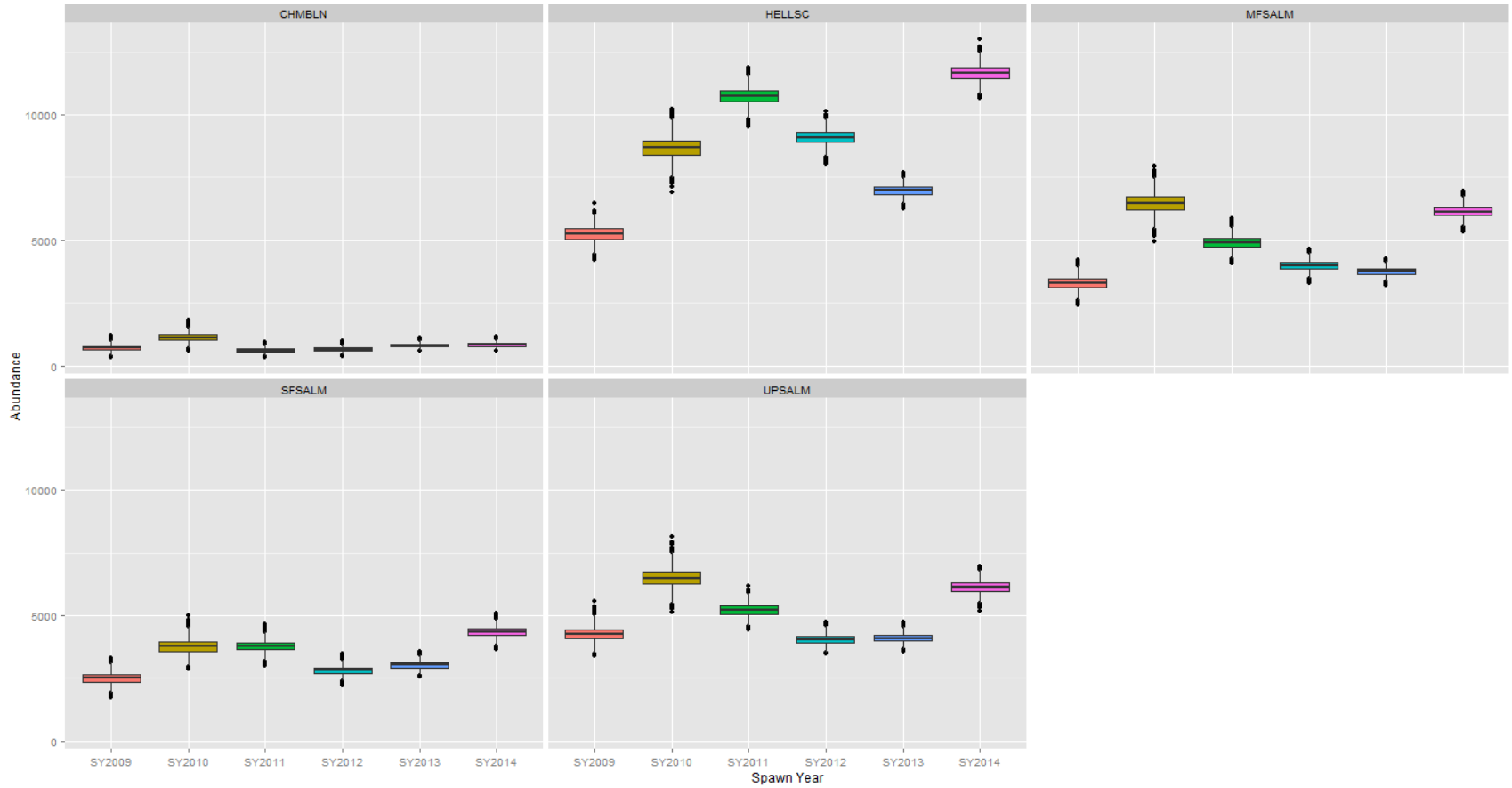

Figure 10. Boxplot of abundance at Lower Granite Dam by genetic stock for Snake River spring/summer Chinook Salmon, SY2009 – 2014. The box contains the inter-quartile range (IQR) and the median. The upper whisker extends from the IQR to the highest value within 1.5 times the IQR. The lower whisker extends from the IQR to the lowest value within 1.5 times the IQR. Data beyond the end of the whiskers are outliers and plotted as points. Estimates for each box and whisker are from 5,000 bootstrap estimates from SCOBI.r (Steinhorst et al. *unpublished*).

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