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

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

Project Progress 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 (sp/sum) Chinook salmon for the 01/01/2013 to 12/31/2013 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 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 sp/sum Chinook salmon passing Lower Granite Dam (LGR). For both species, panels of 192 SNPs have been identified and are being used 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 2.0 (v2) consists of 63 collections and 4,116 individuals. Chinook salmon baseline v2 consists of 39 collections and 3,327 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 2012 at LGR using v2 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 sp/sum 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 population productivity (i.e. recruits-per-female). Both abundance and productivity metrics provide indicators of the resiliency and viability 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 (sp/sum) 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 Snake 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 stocks are believed to exhibit differences in spawning distribution. A-run steelhead are thought to spawn throughout the Columbia basin, whereas B-run steelhead are believed to 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 have 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 by “A-run” or “B-run” designations.

The above issues and similar conservation and management questions relating to Snake River steelhead and spring/summer (sp/sum) 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). 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 objectives of the study. Section 1 addresses the evaluation and maintenance of single nucleotide polymorphism (SNP) panels 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 past LGR during the fall of the previous year and the spring of the current year (e.g., SY2012 steelhead are adults that migrated past LGR bewteen 7/1/11 - 6/30/12 and spawned in spring of 2012). 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: EVALUATE AND MAINTAIN SNP MARKER PANELS

INTRODUCTION

For GSI and parentage based tagging (PBT; Steele et al. 2012), it is important to evaluate SNP marker panels annually and document changes to ensure data integrity and consistency across collaborative laboratories. Data consistency among labs is especially important because genetic data produced as part of this project will be deposited and shared in an open, standardized database currently in development (FishGen.net) and scheduled for completion in 2014.

Ackerman et al. (2012) provides a detailed description of work done during the first two years of this project to screen and evaluate hundreds of SNPs available from CRITFC and collaborating agencies that were candidates for steelhead and Chinook salmon PBT and GSI programs. The goal of this work was to identify 96 easily scorable SNPs with high minor allele frequency (MAF) for PBT and an additional 96 SNPs for GSI. Ackerman et al. (2012) provides sequence (primer and probe) information and evaluates genetic diversity and divergence information for the 192 SNPs for each species using 63 steelhead collections and 39 Chinook salmon collections of natural-origin.

During this reporting period (third year), we initiated procedures to annually check SNP genotyping concordance among collaborating labs for the 192 steelhead and the 192 Chinook salmon SNPs used for this project. Five labs (Washington Department of Fish and Wildlife [WDFW], Northwest Fisheries Science Center [NWFSC], Columbia River Inter-Tribal Fish Commission [CRITFC], Idaho Department of Fish and Game [IDFG], and Abernathy Fish Technology Center [AFTC]) participated in the effort. The goal of this work is to ensure data integrity and to demonstrate that SNP genotype data is reproducible among labs.

We also initiated efforts to document additional information for all of the SNPs we use for our GSI and PBT projects. We have previously published the name and primer/probe sequences of each SNP (Ackerman et al. 2012 and MonitoringMethod.org [1356]), but more detailed information, including the DNA sequence adjacent to the SNP site, dbSNP cluster ID number, original literature documenting each SNP's discovery, and genome location information for each SNP was not summarized. Unfortunately, this information has been difficult to obtain; many different labs developed the original SNPs, and although all of the SNP markers have been rigorously tested, many have not been formally published. In addition, lab records (dating as far back as the 1990s) are often incomplete or difficult to obtain. While the lack of this more detailed information does not affect our ability to complete project objectives, we are motivated to contribute to regional efforts intended to improve documentation of protocols and methods and make them publicly available.

METHODS

SNP Standardization

In early 2013, we sent each collaborating lab an identical set of 93 DNA samples for both species. The samples were from adults sampled at Bonneville Dam, which ensured a variety of stocks was represented and that SNP genotypes would be highly variable. Of the five participating labs, three genotyped both species using the complete 192 SNP panels. AFTC only conducted steelhead PBT projects during the calendar year and therefore only genotyped the steelhead samples at the 96 PBT SNPs. The WDFW lab screened the steelhead samples at 192 SNPs; however, the panel used by WDFW only overlaps at 142 of our 192 SNPs. Consequently, comparisons with WDFW could only be made at those 142 SNPs. The CRITFC lab genotype scores were designated as the reference genotypes. Genotypes of each individual at each SNP for each lab were compared to the reference genotype.

SNP Documentation

Each SNP marker was first web searched for original publication and documentation in publically accessible databases. For SNPs not found through passive search, we contacted collaborating labs and independent researchers for information. These labs include but are not limited to Alaska Department of Fish & Game, WDFW, NWFSC, Southwest Fisheries Science Center (SWFSC), and AFTC. Independent researchers from academic institutions were also contacted, including: Washington State University-Gary H. Thorgaard, Washington State Vancouver University-Jennifer De Koning, Aarhus Universitet-Mette Hansen, among others. SNP markers with no source of information are noted and marked for future investigation.

SNP Evaluation

Allele frequencies across populations for each SNP were calculated using GENALEX v6.4 (Peakall and Smouse 2006). We report the range of MAF across all SNP baseline v2 collections for each SNP.

We tested for linkage disequilibrium (LD) between all locus pairs (excluding the Chinook salmon mitochondrial DNA [mtDNA] SNP *Ots_C3N3*) using simulated exact tests in GENEPOP v4.0 (Rousset 2008). A pair of loci was determined to be significantly out of linkage equilibrium if tests were significant ($\alpha = 0.05$) in more than one-half of baseline populations. If the test was significant between a pair of SNPs, the least informative of the SNP pair (according to F_{ST}) was removed to avoid violating the assumption of independence of loci in population genetics and GSI analyses.

For each SNP we calculated the number of baseline populations that the SNP deviated from Hardy-Weinberg expectation (HWE). The goal was to identify any SNPs that may exhibit null alleles (an allele that may not amplify due to a sequence mutation, etc.) or amplify poorly across Snake River populations for various reasons. We tested for deviations from HWE across all nuclear SNPs for each population using exact p-values calculated from the MC method in GENEPOP v4.0. 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 baseline collections exhibiting an excess or deficit of heterozygotes for any SNPs that deviated from HWE in >10% of baseline collections.

SNP-specific expected heterozygosity (H_E) and F_{ST} were calculated for each SNP using SNP baseline v2 samples and GENALEX v6.4.

RESULTS

SNP Standardization

The overall concordance among labs for steelhead was 99.8% (56,207 genotypes compared) and for Chinook salmon, 99.9% (51,710 genotypes compared). Discrepancies were isolated to 14 steelhead SNPs and 13 Chinook salmon SNPs. Labs were asked to check discrepancies and develop a scoring guide for these loci to reduce the potential for discrepancies in the future. Consistent SNP scoring guides among labs ensures data consistency. Allele nomenclature conflicts occurred in 3 out of 384 SNPs; these were resolved by relabeling allelic calls. This second effort resulted in the four labs sharing near identical genotyping methods, which provides confidence to the accuracy and consistency of genotypic data produced among collaborating labs.

SNP Documentation

Information for each SNP was documented on MonitoringMethods.org, Method: *O. mykiss* and *O. tshawytscha* SNP maker sets for PBT and GSI use in the Columbia River basin v1.0 (https://www.monitoringmethods.org/Method/Details/1356). Each SNP may contain information for the following fields:

1. SNP panel – PBT or GSI
2. SNP # - number given to a SNP as it is identify on Fluidigm SNP Genotyper
3. Well # - location of each SNP on Fluidigm chip
4. SNP Marker name
5. Allele A and B – designated allelic calls in FishGen.net database
6. Forward primer & Reverse primers
7. VIC & 6FAM probes
8. Citation – research paper documenting SNP discovery
9. National Center for Biotechnology Information (NCBI)
    a. dbSNP rs# - SNP Cluster Identifier
    b. dbSNP ss# - SNP Identifier
    c. GenBank acc. # - GenBank Accession number
    d. Gene name and or location

Approximately 25% of 384 SNPs have near complete information. However, only 59% of SNPs are currently documented in NCBI dbSNP repository, and of these, only 85% are also documented in GenBank repository. Over half of all SNPs (207) are not published. Only nine of 384 SNPs lack citation and/or a lab of origin. Gene name and/or genome location information is sparse, with only 26% of the SNPs having known associations with a gene or location.

SNP Evaluation

Tables 2 and 5 summarize SNPs screened for steelhead and sp/sum Chinook salmon, respectively. Summaries include MAF range, H_E, F_{ST}, HWE (heterozygote excess and deficit collections), and linkage disequilibrium. SNPs were analyzed using Snake River SNP baselines v2 (see section 2).

DISCUSSION

Our test of SNP genotyping standardization indicated greater than 99.8% data concordance for both species among collaborating labs. Nomenclature and discrepancy issues were resolved by advising lab(s) to make the necessary changes in their scoring methods. Three nomenclature issues arose and were resolved in similar fashion. We are confident that data produced with the latest SNP panels are highly consistent among labs. Consequently, depositing standardized data in our shared database, Fishgen.net, can proceed with great confidence.

Our effort to track and document additional information for all of the SNPs used in the GSI project was met with mixed success. A little more than half of the SNPs in our panels are documented in NCBI repositories, and nearly the same amount has been published in journals. Original sources for these unknown SNPs may materialize as we continue to search for them. However, as genomic data become readily available it is conceivable to account and fill in missing information about these SNPs. One of our hopes is to use primer and probe sequences as a starting point in the search for the gene and/or location of each SNP. The purpose of this exercise is to provide information for researchers to aid their research. It is work in progress, and we believe the relevant information we have gathered will be even more accessible now that it has become publicly available online at http://www.monitoringmethods.org/Method/Details/1356.

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 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. *In Review*) and returning adults (e.g. Schrader et al. 2013). 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 (reporting groups) are represented disproportionately. 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 were used to define genetic stocks (Ackerman et al. 2012). It is worth clarifying that in past reports, the term “reporting group” was used instead of “genetic stock.” They are synonymous; however, we wish to maintain consistency among IDFG technical reports. Hereafter “genetic stock” will be used exclusively. For baseline v2, work was focused on completing and verifying the four SNP panels (two panels [PBT & GSI] for each species), and more importantly, more samples from underrepresented areas were added to the baselines. For version 3 baselines, our primary focus will be on expanding samples included with the goal of having all Snake River TRT populations characterized.

METHODS

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*." 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 TRT 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 3 show the relationship between baseline collection, population, genetic stock, and MPG.

Sample Collection

Tissues for genetic analysis of juvenile collections were sampled from rayed fins. Tissues of adult collections were sampled from multiple sources: 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 agencies 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™ 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 FishGen.net easier in the future.

Statistical Analyses

Allele frequencies for baseline collections were calculated using GENALEX v6.4 (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. 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 v6.4. 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 v2 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 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 sp/sum 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 sp/sum 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.

We created a neighbor-joining (N-J) phylogram for steelhead and a N-J dendrogram for Chinook salmon to visualize the genetic relationship among baseline populations and to assist in the determination of genetic stocks to be used for GSI. The N-J phylogram was 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 phylogram and dendrogram topologies was estimated using 1,000 bootstrap replicates in SEQBOOT (PHYLIP v3.6.7). The final N-J phylogram and dendogram were constructed with FigTree (Rambaut 2012). Results from the N-J phylogram (steelhead) and N-J dendrogram (Chinook) gave an initial look at the genetic structure of baseline populations. This genetic structure was used to create the initial genetic stock structure prior to self-assignment tests.

RESULTS

Ackerman et al. (2012) presented initial results for SNP baselines v2 for both steelhead and Chinook salmon in the Snake River. A summary follows:

Steelhead: Baseline v2 consisted of 85 sample collections totaling 4,116 samples; temporal collections from geographically proximate locations were pooled resulting in 63 baseline collections (16 collections contained temporal collections). Samples were screened at 191 SNPs and a sex-specific assay (Campbell et al. 2012). Table 1 provides a description of each baseline collection; descriptions include TRT population, genetic stock, MPG, sample size, years collected, genotyping agency, latitude/longitude, life stage, and basic genetic diversity and structure metrics (H_E, F_{ST}, HWE). Table 2 summarizes SNPs screened for baseline collections including SNP-specific MAF range, H_E, F_{ST}, HWE deviations, and LD. Table 3 provides results of self-assignment tests; Table 3a shows results from all assignments (no probability threshold) and Table 3b shows only assignments made with ≥0.80 probability. Figure 1 is a map of collections and shows the relationship with TRT populations, genetic stocks, and major population groups. Figure 2 shows mean pairwise F_{ST} and the average F_{ST} for 63 collections. Results from STRUCTURE analysis with collections grouped by genetic stock (K cluster) are shown in Figure 3. Figure 4 is a N-J phylogram based on Nei's (1972) genetic distances, which is used as a framework for establishing genetic stocks.

Chinook salmon: Baseline v2 consisted of 110 sample collections totaling 3,327 samples; temporal collections from geographically proximate locations were pooled resulting in 39 baseline collections (20 collections contained temporal collections). Samples were screened at 191 SNPs and a sex-specific assay (Campbell et al. 2012). Table 4 provides a description of each baseline collection; descriptions include TRT population, genetic stock, MPG, sample size, years collected, genotyping agency, latitude/longitude, lineage, life stage, and basic genetic diversity and structure metrics (H_E, F_{ST}, HWE). Table 5 summarizes SNPs screened for baseline collections including SNP-specific MAF range, H_E, F_{ST}, HWE deviations, and LD. Table 6 provides results from self-assignment tests; Table 6a shows results from all assignments (no probability threshold) and Table 6b shows only assignments made with ≥0.80 probability. Figure 5 is a map and shows the relationship with TRT populations, genetic stocks, and major population groups. Figure 6 shows mean pairwise F_{ST} and the average F_{ST} for 36 collections. Results from STRUCTURE analysis with collections grouped by genetic stock (K cluster) are shown in Figure 7. Figure 8 is a N-J dendogram based on pairwise Cavalli-Sforza and Edwards (1967) genetic chord distances, which is used as a framework for establishing genetic stocks

For future versions of Snake River SNP baselines, our primary objective is to have collection representing all TRT populations (ICTRT 2003) within the Snake River basin. In addition, areas where sample numbers are low, we will focus our efforts to increase sample size. A proposed outline of our sampling strategy for the current and coming years is outlined in Table 7. Thus far, for 2013, we have added 4,592 and 3,057 samples for steelhead and Chinook salmon, respectively. Below is a tentative summary of these additions.

Steelhead: For baseline v3, approximately 4,700 new samples have been genotyped. They comprise 48 collections spanning from 2003 to 2013. Some collections will be pooled into existing collections. The remainder will form approximately 31 new collections. Sample types are adults and juveniles sampled at location, and returning adults that were PIT tagged and biosampled at LGR that were later detected at Instream PIT Tag Detection Systems (IPTDS) throughout the Snake River basin (Ackerman et al. *In Review*).

Chinook salmon: For baseline v3, approximately 3,400 new samples have been genotyped. They comprise 41 collections spanning from 2005 to 2012. Some collections will be pooled into existing collections. The remainder will form approximately 20 new collections. Sample types are adults and juveniles sampled at location, and returning adults that were PIT tagged and biosampled at LGR that were later detected at IPTDS throughout the Snake River basin (Ackerman et al. *In Review*).

DISCUSSION

For v3 baselines, we will complete similar suites of analyses used during the construction and testing of v2 (Ackerman et al 2012) to ensure continuity and for comparison. In addition to these standardized analyses, we also plan to complete more extensive testing of baseline configurations using self-assignment tests from gsi_sim (Anderson et al. 2008, Anderson 2010) and mixture simulations. Evaluations will be completed to assess whether additional samples and complete TRT population representation will improve assignment and accuracy rates. Additionally, we can also test whether removing older collections in favor of more contemporary collections will create more representative and contemporaneous baselines. Addressing these issues should help us develop sampling and genotyping plans for maintaining and improving GSI baselines into the future.

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.

We would like to thank the Integrated Status and Effectiveness Monitoring Project (ISEMP; BPA Project 2003-017-00) in advance for data contributed for SNP baselines v3; the PIT tagging of adults at the LGR adult trapping facility and subsequent detection data of those adults at IPTDS throughout the Snake River basin provides additional data that can be used in baselines. We will conduct evaluations of IPTDS detected fish during the upcoming year; detections from SY2010–2012 will be included in v3 baselines. Additionally, we would like to thank the Northwest Fisheries Science Center for genotyping a portion of new samples particularly from underrepresented areas in our baselines. These samples will be a welcome addition to the new baselines.

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, allows 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 evaluate life-history diversity (sex, length, age, migration timing) of individuals assigning to the various genetic stocks.

Mixtures of fish from LGR are analyzed and interpreted in the context of VSP monitoring with particular emphasis on evaluating life-history differences among genetic stocks. 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.

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, and 2013) 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. (*In review*) 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. (2013) for adults and Copeland et al. (*In review*) for juveniles (and citations within both reports). Fish captured at either 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. (2013). Scale aging protocols for juveniles are detailed in Copeland et al. (*In review*).

Genetics Laboratory Protocol

Laboratory protocols for DNA extraction, amplification, and SNP genotyping are detailed in Section 2. Samples were processed at either IDFG's Eagle Fish Genetics Lab in Eagle, Idaho or the CRITFC Genetics Lab in Hagerman, Idaho.

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. 2012, 2013). 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 SY2012 adults and MY2012 juveniles. All MY2012 hatchery juvenile cohorts were interrogated via PBT. For SY2012, 1-ocean and 2-ocean steelhead and spring/summer Chinook were interrogated via PBT (Steele et al. 2014). 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 SY2012 adults and MY2012 juveniles (both species) using the Snake River SNP baselines v2 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 individual (i.e. smolt) originates from a baseline population is calculated based on the likelihood that the individual's genotype belongs to that population, given baseline allele frequency estimates. Individual population estimates were first calculated and then summed into genetic stock estimates (allocate-sum procedure; Wood et al. 1987). Genetic stocks (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 for 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 sp/sum 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:

- SY2012 steelhead adults
- SY2012 Chinook adults
- MY2012 steelhead juveniles
- MY2012 Chinook juveniles

RESULTS

We inventoried 14,132 samples from SY2012 adults and MY2012 juveniles (Table 8). Of the samples inventoried, 9,118 were queued for genotyping. Of the 9,118 queued samples, 116 (1.3%) failed genotyping and 9,002 (98.7%) genotyped successfully (Table 8). All 9,002 samples had an intact adipose fin; of the 9,002 samples, 800 (8.8%) had a PBT. We performed IA on the remaining 8,202 samples. Samples are summarized below and in Table 8.

SY2012 Steelhead Adults

We summarize SY2012 unclipped steelhead adult samples from LGR that were inventoried and genotyped in Table 8. We inventoried 5,066 unclipped adult steelhead (no adipose, ventral, or pelvic fin clips). Of the 5,066 unclipped steelhead, 4,448 (87.8%) were phenotypically wild (no dorsal or ventral fin erosion); 2,902 were queued for genotyping and 2,853 were genotyped successfully. Of those genotyped successfully, 260 (9.1%) had a PBT and 2,593 (90.9%) were assigned a genetic stock via IA (Table 8).

Of the 5,066 unclipped steelhead, 618 (12.2%) were phenotypically identified as hatchery origin due to dorsal/ventral fin erosion; 389 were queued for genotyping and 379 were genotyped successfully. Of those genotyped successfully, 254 (67.0%) had a PBT and 125 (33.0%) were assigned a genetic stock via IA (Table 9).

We summarize life-history diversity information (sex, length, age, run-timing) for the 2,718 unclipped steelhead adults that were assigned a genetic stock (without a PBT) in Table 9. Of the 2,718 fish, 472 (17.4%) were assigned to UPSALM, 190 (7.0%) to MFSALM, 109 (4.0%) to SFSALM, 163 (6.0%) to LOSALM, 190 (7.0%) to UPCLWR, 231 (8.5%) to SFCLWR, 202 (7.4%) to LOCLWR, 228 (8.4%) to IMNAHA, 519 (19.1%) to GRROND, and 414 (15.2%) to LSNAKE.

MY2012 Steelhead Juveniles

We summarize MY2012 unclipped juvenile steelhead samples from LGR that were inventoried and genotyped in Table 8. We inventoried 1,274 unclipped steelhead juveniles, all of which were queued for genotyping. Of samples queued, 1,264 (99.2%) were genotyped successfully. Of those genotyped successfully, 64 (5.1%) had a PBT and 1,200 (94.9%) were assigned a genetic stock via IA.

Life-history diversity information for emigrating steelhead smolts that were assigned a genetic stock is summarized in Table 10. Of the 1,200 emigrating steelhead smolts that were assigned a genetic stock, 193 (16.1%) were assigned to UPSALM, 99 (8.3%) to MFSALM, 49 (4.1%) to SFSALM, 74 (6.2%) to LOSALM, 98 (8.2%) to UPCLWR, 92 (7.7%) to SFCLWR, 99 (8.3%) to LOCLWR, 80 (6.7%) to IMNAHA, 257 (21.4%) to GRROND, and 159 (13.3%) to LSNAKE.

SY2012 Chinook Adults

We summarize SY2012 unclipped Chinook salmon adult samples from LGR that were inventoried and genotyped in Table 8. We inventoried 2,358 unclipped adult Chinook salmon; all of them were queued for genotyping. Of samples queued, 2,331 (98.9%) were genotyped successfully. Of samples genotyped successfully, 155 (6.6%) had a PBT and 2,176 (93.3%) were assigned a genetic stock via IA.

We summarize life-history diversity information (sex, length, age, run-timing) for the 2,176 Chinook adults that were assigned a genetic stock (without a PBT) in Table 11. Of the 2,176 fish, 391 (18.0%) were assigned to UPSALM, 367 (16.9%) to MFSALM, 62 (2.8%) to CHMBLN, 296 (13.6%) to SFSALM, 968 (44.5%) to HELLSC, 14 (0.6%) to TUCANO, and 78 (3.6%) to FALL.

MY2012 Chinook Juveniles

We summarize SY2012 unclipped Chinook salmon juveniles from LGR that were inventoried and genotyped in Table 8. We inventoried 5,434 unclipped juvenile Chinook salmon. Of those inventoried, 2,772 were yearlings and 2,662 were sub-yearlings.

Of the 2,772 yearling Chinook salmon, 1,663 (60.0%) were queued for genotyping; 1,648 (99.1%) were genotyped successfully. Of the 1,648 genotyped, 66 (4.0%) had a PBT and 1,582 (96.0%) were assigned a genetic stock via IA.

Of the 2,662 subyearling Chinook salmon, 532 (20.0%) were queued for genotyping; 527 (99.1%) were genotyped successfully. Of the 527 genotyped, 1 (0.2%) had a PBT and 526 were assigned a genetic stock via IA.

Life-history diversity information for emigrating Chinook salmon smolts assigned a genetic stock is summarized in Table 12. In total, we assigned a genetic stock to 2,108 juvenile Chinook salmon emigrants (yearling and subyearling combined). Of the 2,108, 265 (12.6%) assigned to UPSALM, 251 (11.9%) to MFSALM, 28 (1.3%) to CHMBLN, 289 (13.7%) to SFSALM, 757 (35.9%) to HELLSC, 5 (0.2%) to TUCANO, and 513 (24.3% to FALL).

DISCUSSION

Adult steelhead and sp/sum 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 (BPA Project 2010-026-00) 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 patch occupancy model to provide reliable and unbiased estimates of abundance at the population level (QCI 2013; Ackerman et al. *In Review*). During this contract period, we have initiated collaboration between these two innovative technologies (SNP genotying for PBT and GSI & 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 sp/sum 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. A draft of the initial report "*Abundance, Life-History, and Genetic Data for VSP Monitoring of Snake River Steelhead DPS and Spring/Summer Chinook ESU using IPTDS, SY2010 – 2012*" has been completed and is in review (Ackerman et al. *In Review*).

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 information from fishery harvest 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.

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TABLES

Table 1. Sixty three collections of Snake River basin **steelhead (*Oncorhynchus mykiss*)** screened with the PBT and GSI SNP panels for **baseline v2**. 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, life stage, 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. Life stage codes are A – adult and J – Juvenile. All collections are summer-run, inland lineage, natural origin, and presumed to be of anadromous life-history.

														HWE	
Map #	**Super Collection**	**TRT Population**	**Genetic Stock**	**MPG**	**n**	**Year Collected**	**Genotype Agency**	**Baseline Version**	**Latitude**	**Longitude**	**Life Stage**	**HE**	**FST**	**Defic-ient**	**Excess**
1	Sawtooth Weir	SRUMA	UPSALM	Salmon	108	05, 10	IDFG	1.0	44.15058	-114.88509	A	30.0%	0.018		
2	Valley Cr	SRUMA	UPSALM	Salmon	45	05	NWFSC	2.0	44.30113	-115.04574	J	30.4%	0.020		
3	WF Yankee Fork SR	SRUMA	UPSALM	Salmon	117	04, 08	IDFG	1.0	44.34941	-114.72657	J	30.5%	0.018		
4	Morgan Cr	SREFS	UPSALM	Salmon	37	00	IDFG	1.0	44.67882	-114.23945	J	32.2%	0.023	7	5
5	Pahsimeroi Weir	SRPAH	UPSALM	Salmon	97	06, 10	IDFG	1.0	44.56767	-113.90717	A	32.1%	0.019	9	2
6	Hayden Cr	SRLEM	UPSALM	Salmon	86	09, 10	IDFG	2.0	44.78519	-113.70621	J	32.6%	0.019		
7	North Fork SR	SRNFS	UPSALM	Salmon	100	10	IDFG	1.0	45.50356	-113.95717	A	31.1%	0.015		
8	Marsh Cr	MFUMA	MFSALM	Salmon	59	00	NWFSC	1.0	44.41537	-115.18385	J	29.0%	0.032		
9	Sulphur Cr	MFUMA	MFSALM	Salmon	45	00	NWFSC	2.0	44.54370	-115.39566	J	28.9%	0.030		
10	Rapid R Middle Fork SR	MFUMA	MFSALM	Salmon	45	00	IDFG	1.0	44.64151	-115.05621	J	29.5%	0.031		
11	Pistol Cr	MFUMA	MFSALM	Salmon	23	00	IDFG	1.0	44.76347	-115.31469	J	29.2%	0.034		
12	Loon Cr	MFUMA	MFSALM	Salmon	57	99, 00	NWFSC	1.0	44.59829	-114.81164	J	29.3%	0.024		
13	Camas Cr	MFUMA	MFSALM	Salmon	84	00	NWFSC	1.0	44.82399	-114.49990	J	29.0%	0.024		
14	upper Big Cr	MFBIG	MFSALM	Salmon	46	00	NWFSC	1.0	45.15063	-115.29674	J	28.6%	0.032	5	10
15	lower Big Cr	MFBIG	MFSALM	Salmon	48	00	IDFG	1.0	45.10717	-114.80611	J	29.6%	0.027	6	4
16	Chamberlain Cr	SRCHA	MFSALM	Salmon	46	00	NWFSC	2.0	45.36865	-115.19689	J	29.7%	0.020		
17	Bargamin Cr	SRCHA	MFSALM	Salmon	32	00	IDFG	1.0	45.66604	-115.08712	J	31.3%	0.023		
18	EF South Fork SR	SFMAI	SFSALM	Salmon	45	00	IDFG	1.0	44.94642	-115.59941	J	29.3%	0.026		
19	Stolle Meadows	SFMAI	SFSALM	Salmon	47	00	CRITFC	1.0	44.60701	-115.68098	J	29.8%	0.028		
20	Lick Cr	SFSEC	SFSALM	Salmon	40	00	IDFG	2.0	45.05880	-115.86100	J	29.5%	0.026		
21	Secesh R	SFSEC	SFSALM	Salmon	45	10	NWFSC	1.0	45.12659	-115.77011	J	28.9%	0.029		
22	Boulder Cr	SRLSR	LOSALM	Salmon	47	00	IDFG	1.0	45.12183	-116.42752	J	30.8%	0.019	9	1
23	Rapid R	SRLSR	LOSALM	Salmon	100	03, 09	IDFG	1.0	45.31576	-116.41871	A	30.4%	0.019		
24	Slate Cr	SRLSR	LOSALM	Salmon	47	00	IDFG	1.0	45.63932	-116.12444	J	30.7%	0.018	8	2
25	Whitebird Cr	SRLSR	LOSALM	Salmon	62	00, 01	IDFG	1.0	45.79165	-116.23164	J	29.9%	0.017	9	1
26	Colt Killed Cr	CRLOC	UPCLWR	Clearwater	38	00	IDFG	2.0	46.43110	-114.53952	J	27.5%	0.027		
27	Storm Cr	CRLOC	UPCLWR	Clearwater	38	00	IDFG	1.0	46.53651	-114.46931	J	27.7%	0.030		
28	Crooked F Lochsa R	CRLOC	UPCLWR	Clearwater	44	00	IDFG	1.0	46.61523	-114.67046	J	28.3%	0.025		
29	Lake Cr	CRLOC	UPCLWR	Clearwater	47	00	IDFG	2.0	46.41437	-115.00679	J	28.0%	0.028		

Table 1. Continued.

Map #	Super Collection	TRT Population	Genetic Stock	MPG	n	Year Collected	Genotype Agency	Baseline Version	Latitude	Longitude	Life Stage	HE	FST	HWE Defic-ient	HWE Excess
30	Fish Cr	CRLOC	UPCLWR	Clearwater	100	10, 11	IDFG	2.0	46.35582	-115.39851	A	28.4%	0.023		
31	Canyon Cr	CRLOC	UPCLWR	Clearwater	46	11	IDFG	1.0	46.23909	-115.57909	J	28.0%	0.024		
32	Selway R	CRSEL	UPCLWR	Clearwater	78	08	IDFG	2.0	45.69208	-114.71753	J	28.6%	0.027		
33	Little Clearwater R	CRSEL	UPCLWR	Clearwater	59	08	IDFG	2.0	45.71018	-114.87330	J	28.9%	0.025		
34	Whitecap Cr	CRSEL	UPCLWR	Clearwater	76	08	IDFG	2.0	45.88777	-114.60935	J	28.9%	0.026	8	4
35	Bear Cr	CRSEL	UPCLWR	Clearwater	35	00	IDFG	1.0	46.03569	-114.75107	J	29.2%	0.028		
36	NF Moose Cr	CRSEL	UPCLWR	Clearwater	94	00, 04	IDFG	1.0	46.22329	-114.94754	J	28.5%	0.022	8	3
37	Three Links Cr	CRSEL	UPCLWR	Clearwater	47	00	IDFG	2.0	46.14508	-115.09495	J	27.9%	0.030		
38	Gedney Cr	CRSEL	UPCLWR	Clearwater	45	00	IDFG	1.0	46.09381	-115.29383	J	29.2%	0.022		
39	O'Hara Cr	CRSEL	UPCLWR	Clearwater	47	00	IDFG	1.0	46.04494	-115.51908	J	28.9%	0.020		
40	Crooked R	CRSFC	SFCLWR	Clearwater	106	07, 08	IDFG	3.0	45.76562	-115.54264	A	27.7%	0.025	9	4
41	Tenmile Cr	CRSFC	SFCLWR	Clearwater	47	00	IDFG	1.0	45.72703	-115.66138	J	28.0%	0.032		
42	John's Cr	CRSFC	SFCLWR	Clearwater	38	00	IDFG	1.0	45.72137	-115.88962	J	29.2%	0.023		
43	Clear Cr	CRLMA	SFCLWR	Clearwater	45	00	IDFG	1.0	46.04859	-115.78140	J	28.7%	0.025		
44	WF Potlatch R	CRLMA	LOCLWR	Clearwater	84	09, 10	IDFG	2.0	46.86420	-116.40160	A	30.4%	0.017		
45	EF Potlatch R	CRLMA	LOCLWR	Clearwater	158	08, 10, 11	IDFG	1.0	46.80991	-116.38142	A	30.2%	0.017	8	3
46	Big Bear Cr	CRLMA	LOCLWR	Clearwater	99	07, 08, 10, 11	IDFG	1.0	46.69415	-116.65593	A	31.5%	0.016		
47	Little Bear Cr	CRLMA	LOCLWR	Clearwater	151	07, 08, 10, 11	IDFG	1.0	46.71997	-116.70423	A	30.5%	0.016	10	1
48	Big Sheep Cr	IRMAI	IMNAHA	Imnaha	68	01	NWFSC	2.0	45.45693	-116.82688	J	29.5%	0.019		
49	Camp Cr	IRMAI	IMNAHA	Imnaha	24	01	CRITFC	1.0	45.55406	-116.87253	J	29.8%	0.026		
50	Lightning Cr	IRMAI	IMNAHA	Imnaha	44	00	CRITFC	1.0	45.65537	-116.72653	J	30.0%	0.018		
51	Cow Cr	IRMAI	IMNAHA	Imnaha	41	00	CRITFC	1.0	45.76814	-116.74956	J	29.3%	0.020		
52	Little Minam R	GRWAL	GRROND	Grande Ronde	53	00	CRITFC	1.0	45.34536	-117.65340	J	30.3%	0.017		
53	Lostine R	GRWAL	GRROND	Grande Ronde	97	00	CRITFC	1.0	45.42211	-117.42496	J	30.9%	0.018		
54	Wenaha R	GRLMT	GRROND	Grande Ronde	48	00	CRITFC	1.0	45.97269	-117.69367	J	30.0%	0.025		
55	Crooked Cr	GRLMT	GRROND	Grande Ronde	45	11	CRITFC	1.0	46.03905	-117.57340	J	28.9%	0.026	6	4
56	Menatchee Cr	GRLMT	GRROND	Grande Ronde	45	01	CRITFC	1.0	46.04457	-117.38550	J	31.0%	0.024		
57	Elk Cr Grande Ronde R	GRJOS	GRROND	Grande Ronde	73	99	CRITFC	1.0	45.67203	-117.18960	J	31.7%	0.019		
58	Joseph Cr	GRJOS	GRROND	Grande Ronde	94	01	IDFG	2.0	45.95606	-117.13746	A	30.2%	0.017	10	2
59	Captain John Cr	SRLSR	GRROND	Grande Ronde	56	00	IDFG	2.0	46.14595	-116.87108	J	30.0%	0.020		
60	Asotin Cr	SNASO	LSNAKE	Lower Snake	95	10	IDFG	2.0	46.32280	-117.13681	A	31.2%	0.016		
61	George Cr	SNASO	LSNAKE	Lower Snake	99	08, 10	IDFG	2.0	46.28326	-117.14434	A	31.5%	0.015	12	3
62	Alpowa Cr	SNTUC	LSNAKE	Lower Snake	98	10	IDFG	2.0	46.42479	-117.32812	A	31.4%	0.016		
63	Tucannon R	SNTUC	LSNAKE	Lower Snake	106	05, 09, 10	IDFG	1.0	46.50530	-118.01440	A	31.3%	0.015	14	2

Table 2. Summary of 185 SNPs (Appendix A and Hess et al. 2013) screened among 63 steelhead collections in Snake River baseline v2.0. SNPs designated as PBT are used for both the PBT (BPA Project #2010-031-00, Steele et al. 2012) and GSI projects. SNPs designated as GSI are used primarily for GSI applications. Summary statistics include minor-allele frequency (MAF) range, expected heterozygosity (H_E), mean of Weir and Cockerham (1984) F_{ST}, "HWE" designates the number of populations that a SNP deviated from Hardy-Weinberg expectation (deficient or in excess) for any SNP that deviated in greater than 10% of collections and "LD" signifies SNPs that exhibit linkage disequilibrium in more than half of the collections.

					HWE		
SNP Marker	**Panel**	**MAF Range**	**H_E**	**F_{ST}**	**Deficient**	**Excess**	**LD**
M09AAD.076	PBT v5.1	(0.278 - 0.717)	48.6%	0.037			
M09AAE.082	PBT v5.1	(0.100 - 0.694)	34.3%	0.070			
M09AAJ.163	PBT v5.1	(0.044 - 0.564)	41.0%	0.047			
OmS00002	PBT v5.1	(0.289 - 0.557)	45.8%	0.024			
OmS00006	PBT v5.1	(0.224 - 0.628)	48.2%	0.040			
OmS00024	PBT v5.1	(0.167 - 0.663)	45.5%	0.062			
OmS00039	PBT v5.1	(0.277 - 0.656)	48.9%	0.029			
OmS00053	PBT v5.1	(0.319 - 0.669)	48.6%	0.032			
OmS00057	PBT v5.1	(0.156 - 0.671)	44.7%	0.061			
OmS00058	PBT v5.1	(0.096 - 0.689)	44.2%	0.093			
OmS00062	PBT v5.1	(0.128 - 0.490)	37.3%	0.030			
OmS00064	PBT v5.1	(0.098 - 0.713)	43.6%	0.082			
OmS00068	PBT v5.1	(0.170 - 0.565)	42.2%	0.046			
OmS00070	PBT v5.1	(0.239 - 0.739)	47.5%	0.059			
OmS00071	PBT v5.1	(0.263 - 0.713)	48.0%	0.041			
OmS00072	PBT v5.1	(0.263 - 0.656)	48.5%	0.033			
OmS00074	PBT v5.1	(0.065 - 0.649)	45.6%	0.077			
OmS00077	PBT v5.1	(0.244 - 0.556)	47.1%	0.031			
OmS00078	PBT v5.1	(0.156 - 0.457)	38.7%	0.028			
OmS00079	PBT v5.1	(0.181 - 0.609)	48.6%	0.037			
OmS00089	PBT v5.1	(0.079 - 0.454)	37.2%	0.044			
OmS00090	PBT v5.1	(0.200 - 0.713)	47.6%	0.049			
OmS00101	PBT v5.1	(0.131 - 0.750)	46.3%	0.060			
OmS00105	PBT v5.1	(0.128 - 0.566)	45.1%	0.044			
OmS00106	PBT v5.1	(0.068 - 0.411)	34.6%	0.037			
OmS00111	PBT v5.1	(0.075 - 0.533)	30.9%	0.064			
OmS00112	PBT v5.1	(0.000 - 0.297)	28.8%	0.056			
OmS00118	PBT v5.1	(0.133 - 0.620)	44.0%	0.076			
OmS00120	PBT v5.1	(0.000 - 0.489)	26.3%	0.089			
OmS00121	PBT v5.1	(0.273 - 0.670)	48.7%	0.027			
OmS00132	PBT v5.1	(0.184 - 0.581)	47.2%	0.031			
OmS00154	PBT v5.1	(0.074 - 0.422)	30.8%	0.037			
OmS00175	PBT v5.1	(0.182 - 0.609)	47.4%	0.038			
OmS00179	PBT v5.1	(0.083 - 0.500)	39.4%	0.039			
OmS00180	PBT v5.1	(0.119 - 0.467)	43.0%	0.037			
Omy_101832-195	PBT v5.1	(0.167 - 0.739)	47.0%	0.053			
Omy_101993-189	PBT v5.1	(0.067 - 0.605)	34.7%	0.079			
Omy_102505-102	PBT v5.1	(0.234 - 0.567)	45.9%	0.026			
Omy_104519-624	PBT v5.1	(0.053 - 0.578)	39.3%	0.086			
Omy_105105-448	PBT v5.1	(0.216 - 0.674)	47.1%	0.046			
Omy_105385-406	PBT v5.1	(0.243 - 0.652)	46.7%	0.034			
Omy_105714-265	PBT v5.1	(0.156 - 0.500)	42.7%	0.036			
Omy_107806-34	PBT v5.1	(0.078 - 0.606)	38.9%	0.088			

Table 2. Continued.

SNP Marker	Panel	MAF Range	H_E	F_{ST}	HWE Deficient	HWE Excess	LD
Omy_108007-193	PBT v5.1	(0.092 - 0.692)	44.4%	0.077			
Omy_109243-222	PBT v5.1	(0.000 - 0.304)	26.5%	0.036			
Omy_109894-185	PBT v5.1	(0.239 - 0.571)	45.3%	0.043			
Omy_110064-419	PBT v5.1	(0.076 - 0.592)	44.5%	0.074			
Omy_111383-51	PBT v5.1	(0.145 - 0.589)	46.6%	0.047			
Omy_113490-159	PBT v5.1	(0.198 - 0.725)	45.6%	0.075			
Omy_114315-438	PBT v5.1	(0.093 - 0.691)	44.4%	0.099			
Omy_114587-480	PBT v5.1	(0.085 - 0.500)	41.8%	0.055			
Omy_116733-349	PBT v5.1	(0.102 - 0.511)	39.5%	0.045			
Omy_128923-433	PBT v5.1	(0.197 - 0.729)	46.9%	0.069			
Omy_129870-756	PBT v5.1	(0.043 - 0.311)	28.3%	0.033			
Omy_130524-160	PBT v5.1	(0.241 - 0.600)	46.6%	0.028			
Omy_97660-230	PBT v5.1	(0.130 - 0.422)	43.7%	0.036			
Omy_99300-202	PBT v5.1	(0.093 - 0.500)	34.4%	0.044			
Omy_ada10-71	PBT v5.1	(0.072 - 0.320)	29.5%	0.035			
Omy_aldB-165	PBT v5.1	(0.160 - 0.434)	41.2%	0.021			
Omy_anp-17	PBT v5.1	(0.026 - 0.761)	39.0%	0.134			
Omy_arp-630	PBT v5.1	(0.313 - 0.638)	48.4%	0.037			
Omy_b1-266	PBT v5.1	(0.141 - 0.453)	39.7%	0.026			
Omy_BAC-B4-324	PBT v5.1	(0.266 - 0.600)	47.9%	0.030			
Omy_bcAKala-380rd	PBT v5.1	(0.106 - 0.518)	41.0%	0.049	6	1	
Omy_cd59-206	PBT v5.1	(0.084 - 0.500)	38.8%	0.042			
Omy_colla1-525	PBT v5.1	(0.118 - 0.447)	40.6%	0.026			
Omy_cox1-221	PBT v5.1	(0.171 - 0.641)	45.6%	0.051			
Omy_crb-106	PBT v5.1	(0.253 - 0.691)	46.8%	0.061	8		
Omy_g12-82	PBT v5.1	(0.276 - 0.656)	48.5%	0.038			
Omy_gluR-79	PBT v5.1	(0.211 - 0.717)	48.0%	0.041			
Omy_hsc715-80	PBT v5.1	(0.205 - 0.540)	46.1%	0.027			
Omy_hsf2-146	PBT v5.1	(0.071 - 0.628)	40.4%	0.085			
Omy_IL17-185	PBT v5.1	(0.200 - 0.625)	47.5%	0.047	2	8	
Omy_Il-1b_.028	PBT v5.1	(0.022 - 0.270)	25.6%	0.044			
Omy_Il1b-198	PBT v5.1	(0.136 - 0.698)	45.6%	0.055			
Omy_IL6-320	PBT v5.1	(0.066 - 0.400)	33.3%	0.036			
Omy_metA-161	PBT v5.1	(0.080 - 0.588)	36.8%	0.055			
Omy_NaKATPa3-50	PBT v5.1	(0.096 - 0.527)	39.6%	0.044			
Omy_nkef-241	PBT v5.1	(0.267 - 0.630)	47.1%	0.037			
Omy_ntl-27	PBT v5.1	(0.133 - 0.531)	42.8%	0.051			
Omy_Ogo4-212	PBT v5.1	(0.106 - 0.576)	46.6%	0.040			
Omy_Ots249-227	PBT v5.1	(0.136 - 0.400)	41.0%	0.028			
Omy_oxct-85	PBT v5.1	(0.000 - 0.245)	17.9%	0.043			
Omy_p53-262	PBT v5.1	(0.144 - 0.523)	34.1%	0.045			
Omy_rapd-167	PBT v5.1	(0.043 - 0.359)	29.7%	0.035			
Omy_rbm4b-203	PBT v5.1	(0.011 - 0.408)	30.0%	0.056			
Omy_redd1-410	PBT v5.1	(0.078 - 0.568)	33.7%	0.045			
Omy_srp09-37	PBT v5.1	(0.149 - 0.561)	41.7%	0.041			
Omy_stat3-273	PBT v5.1	(0.066 - 0.408)	34.1%	0.040			
Omy_txnip-343	PBT v5.1	(0.078 - 0.539)	36.4%	0.049			
Omy_u09-53.469	PBT v5.1	(0.174 - 0.660)	44.7%	0.102			
Omy_u09-54-311	PBT v5.1	(0.078 - 0.553)	41.0%	0.049			
Omy_U11_2b-154	PBT v5.1	(0.053 - 0.351)	32.3%	0.042			
Omy_vatf-406	PBT v5.1	(0.120 - 0.580)	42.3%	0.071			
OmY1011SNP	PBT v5.1	(0.096 - 0.459)	36.4%	0.038			
M09AAC.055	GSI v4.1	(0.000 - 0.272)	13.7%	0.050			
OmGH1PROM1-SNP1	GSI v4.1	(0.000 - 0.239)	17.3%	0.083			

Table 2. Continued.

SNP Marker	Panel	MAF Range	H_E	F_{ST}	HWE Deficient	HWE Excess	LD
OmS00003	GSI v4.1	(0.089 - 0.336)	24.5%	0.024			
OmS00008	GSI v4.1	(0.000 - 0.456)	26.1%	0.079			
OmS00013	GSI v4.1	(0.000 - 0.132)	12.4%	0.042			
OmS00014	GSI v4.1	(0.000 - 0.122)	2.8%	0.041			
OmS00015	GSI v4.1	(0.000 - 0.198)	10.9%	0.045			
OmS00017	GSI v4.1	(0.132 - 0.733)	38.7%	0.077			
OmS00018	GSI v4.1	(0.022 - 0.287)	17.9%	0.032			
OmS00030	GSI v4.1	(0.000 - 0.193)	15.0%	0.034			
OmS00048	GSI v4.1	(0.047 - 0.239)	20.2%	0.026			
OmS00052	GSI v4.1	(0.056 - 0.378)	28.6%	0.029			
OmS00056	GSI v4.1	(0.085 - 0.411)	34.3%	0.036			
OmS00061	GSI v4.1	(0.000 - 0.239)	10.5%	0.049			
OmS00087	GSI v4.1	(0.071 - 0.458)	29.3%	0.055	16		
OmS00092	GSI v4.1	(0.034 - 0.514)	27.2%	0.088			
OmS00095	GSI v4.1	(0.000 - 0.191)	11.3%	0.043			
OmS00096	GSI v4.1	(0.043 - 0.351)	30.1%	0.034			
OmS00114	GSI v4.1	(0.000 - 0.200)	15.6%	0.026			
OmS00119	GSI v4.1	(0.000 - 0.288)	21.7%	0.043			
OmS00129	GSI v4.1	(0.014 - 0.435)	27.0%	0.057	15		
OmS00133	GSI v4.1	(0.000 - 0.176)	4.6%	0.049			
OmS00138	GSI v4.1	(0.027 - 0.391)	21.2%	0.059			
OmS00143	GSI v4.1	(0.000 - 0.283)	18.5%	0.057			
OmS00149	GSI v4.1	(0.000 - 0.144)	7.8%	0.034			
OmS00151	GSI v4.1	(0.053 - 0.424)	30.5%	0.043			
OmS00169	GSI v4.1	(0.000 - 0.135)	1.8%	0.044			
OmS00173	GSI v4.1	(0.022 - 0.276)	21.0%	0.041			
OmS00174	GSI v4.1	(0.000 - 0.174)	9.1%	0.028			
OmS00176	GSI v4.1	(0.000 - 0.157)	11.6%	0.048			
Omy_103705-558	GSI v4.1	(0.021 - 0.242)	18.6%	0.029			
Omy_105075-162	GSI v4.1	(0.011 - 0.220)	15.0%	0.031			
Omy_107031-704	GSI v4.1	(0.056 - 0.391)	27.0%	0.050			
Omy_107285-69	GSI v4.1	(0.036 - 0.289)	27.3%	0.031			
Omy_110201-359	GSI v4.1	(0.033 - 0.297)	17.7%	0.039			
Omy_128996-481	GSI v4.1	(0.000 - 0.149)	12.6%	0.040	11		
Omy_97077-73	GSI v4.1	(0.000 - 0.149)	3.6%	0.048			
Omy_97865-196	GSI v4.1	(0.000 - 0.089)	7.3%	0.030			
Omy_97954-618	GSI v4.1	(0.107 - 0.419)	31.8%	0.056			
Omy_aromat-280	GSI v4.1	(0.060 - 0.446)	28.9%	0.030			
Omy_aspAT-123	GSI v4.1	(0.156 - 0.481)	39.5%	0.029			
Omy_b9-164	GSI v4.1	(0.000 - 0.457)	20.4%	0.118	8		
Omy_BAC-F5.284	GSI v4.1	(0.000 - 0.178)	9.4%	0.047			
Omy_BAMBI2.312	GSI v4.1	(0.000 - 0.367)	18.9%	0.064	7		
Omy_ca050-64	GSI v4.1	(0.152 - 0.541)	44.5%	0.034			
Omy_carban1-264	GSI v4.1	(0.000 - 0.355)	21.3%	0.059			
Omy_cd28-130	GSI v4.1	(0.000 - 0.064)	2.7%	0.028			
Omy_cd59b-112	GSI v4.1	(0.000 - 0.388)	18.1%	0.070			
Omy_cin-172	GSI v4.1	(0.044 - 0.464)	31.9%	0.047			
Omy_cox2-335	GSI v4.1	(0.043 - 0.375)	26.1%	0.047			
Omy_CRBF1-1	GSI v4.1	(0.000 - 0.186)	9.0%	0.033			
Omy_e1-147	GSI v4.1	(0.000 - 0.178)	9.3%	0.035			
Omy_g1-103	GSI v4.1	(0.000 - 0.162)	9.9%	0.047			
Omy_G3PD_2-371	GSI v4.1	(0.059 - 0.521)	28.4%	0.045			
Omy_gadd45-332	GSI v4.1	(0.011 - 0.478)	20.4%	0.094			
Omy_gdh-271	GSI v4.1	(0.034 - 0.401)	20.3%	0.061			

Table 2. Continued.

SNP Marker	Panel	MAF Range	H_E	F_{ST}	HWE Deficient	HWE Excess	LD
Omy_gh-475	GSI v4.1	(0.043 - 0.305)	23.0%	0.034			
Omy_GHSR-121	GSI v4.1	(0.000 - 0.207)	8.2%	0.064			a
Omy_hsf1b-241	GSI v4.1	(0.000 - 0.197)	15.3%	0.033			
Omy_hsp47-86	GSI v4.1	(0.033 - 0.391)	33.2%	0.028			
Omy_hsp70aPro-329	GSI v4.1	(0.000 - 0.115)	8.0%	0.113			
Omy_hus1-52	GSI v4.1	(0.000 - 0.125)	8.6%	0.057			
Omy_IL1b-163	GSI v4.1	(0.000 - 0.454)	17.3%	0.168			
Omy_impa1-55	GSI v4.1	(0.000 - 0.243)	17.3%	0.041			
Omy_inos-97	GSI v4.1	(0.000 - 0.271)	12.7%	0.058			
Omy_LDHB-1_i2	GSI v4.1	(0.016 - 0.170)	14.8%	0.026			
Omy_LDHB-2_e5	GSI v4.1	(0.026 - 0.349)	25.6%	0.029			
Omy_LDHB-2_i6	GSI v4.1	(0.000 - 0.068)	1.7%	0.021			
Omy_lpl-220	GSI v4.1	(0.078 - 0.311)	26.0%	0.021			
Omy_mapK3-103	GSI v4.1	(0.000 - 0.119)	5.1%	0.047			a
Omy_mcsf-268	GSI v4.1	(0.000 - 0.230)	3.6%	0.070			
Omy_metB-138	GSI v4.1	(0.000 - 0.357)	25.1%	0.037			
Omy_myoD-178	GSI v4.1	(0.000 - 0.359)	18.7%	0.056			
Omy_nach-200	GSI v4.1	(0.000 - 0.041)	1.5%	0.017			
Omy_ndk-152	GSI v4.1	(0.000 - 0.152)	4.7%	0.035			
Omy_nips-299	GSI v4.1	(0.004 - 0.217)	12.6%	0.039			
Omy_nxt2-273	GSI v4.1	(0.000 - 0.257)	12.7%	0.046	11		
Omy_OmyP9-180	GSI v4.1	(0.000 - 0.216)	16.5%	0.043			
Omy_pad-196	GSI v4.1	(0.000 - 0.200)	8.4%	0.036			
Omy_ppie-232	GSI v4.1	(0.000 - 0.232)	22.3%	0.043			
Omy_sast-264	GSI v4.1	(0.127 - 0.865)	30.2%	0.100			
Omy_SECC22b-88	GSI v4.1	(0.000 - 0.135)	2.7%	0.047			
Omy_sSOD-1	GSI v4.1	(0.000 - 0.041)	1.7%	0.017			
Omy_star-206	GSI v4.1	(0.000 - 0.129)	9.5%	0.043			
Omy_sys1-188	GSI v4.1	(0.000 - 0.394)	18.6%	0.075			
Omy_tlr3-377	GSI v4.1	(0.000 - 0.300)	15.8%	0.065			
Omy_tlr5-205	GSI v4.1	(0.000 - 0.140)	9.7%	0.030			
Omy_u07-79-166	GSI v4.1	(0.000 - 0.271)	15.9%	0.063			
Omy_u09-52.284	GSI v4.1	(0.000 - 0.103)	5.3%	0.036			
Omy_u09-56.119	GSI v4.1	(0.000 - 0.196)	15.7%	0.034			
Omy_UT16_2-173	GSI v4.1	(0.011 - 0.189)	12.7%	0.022			
Omy_vamp5-303	GSI v4.1	(0.043 - 0.407)	32.5%	0.052			
Omy_zg57-91	GSI v4.1	(0.000 - 0.243)	14.9%	0.056			

[a] *Omy_GHSR-121 and Omy_mapK3-103* exhibited linkage disequilibrium in 34 of 63 baseline collections. *Omy_mapK3-103* was the least informative of the locus pair and was dropped from baseline and GSI analyses.

Table 3. Steelhead results from self-assignment tests performed in gsi_sim (Anderson et al. 2008, Anderson 2010). For each baseline collection represented in baseline v2.0, 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 3a is results for all individuals that assigned to a genetic stock, and Table 3b is for individuals that assigned to a genetic stock with ≥80% probability. For example, n = 108 individuals represent the Sawtooth Weir collection. Of the 108 individuals in the baseline, 50 (46%) assigned back to a genetic stock with ≥80% probability. Of the 50 that assigned, 48 (98%) assigned to the correct UPSALM reporting group. Shaded boxes represent the correct genetic stock of origin for each population.

Table 3a:

		Number Assigned	Assigned Genetic Stock (No Threshhold)									
Collection of Origin	**n**	**(Proportion)**	**UPSALM**	**MFSALM**	**SFSALM**	**LOSALM**	**UPCLWR**	**SFCLWR**	**LOCLWR**	**IMNAHA**	**GRROND**	**LSNAKE**
Sawtooth Weir	108	108 (1.00)	0.77			0.05			0.02	0.04	0.08	0.05
Valley Cr	45	45 (1.00)	0.73			0.02	0.02			0.02	0.13	0.07
WF Yankee Fork SR	117	117 (1.00)	0.77	0.03	0.01	0.05			0.01	0.03	0.07	0.04
Morgan Cr	37	37 (1.00)	0.92								0.08	
Pahsimeroi Weir	97	97 (1.00)	0.75	0.01		0.04			0.02	0.04	0.07	0.06
Hayden Cr	86	86 (1.00)	0.77	0.06		0.03					0.07	0.07
North Fork SR	100	100 (1.00)	0.56	0.02		0.17	0.01	0.01	0.04	0.07	0.02	0.10
Marsh Cr	59	59 (1.00)		1.00								
Sulphur Cr	45	45 (1.00)		0.96	0.04							
Rapid R Middle Fork SR	45	45 (1.00)		0.98					0.02			
Pistol Cr	23	23 (1.00)		1.00								
Camas Cr	57	57 (1.00)	0.02	0.98								
Loon Cr	84	84 (1.00)	0.01	0.93		0.05						0.01
upper Big Cr	46	46 (1.00)	0.04	0.93		0.02						
lower Big Cr	48	48 (1.00)	0.04	0.92			0.02				0.02	
Chamberlain Cr	46	46 (1.00)	0.09	0.72		0.07				0.07	0.02	0.04
Bargamin Cr	32	32 (1.00)	0.16	0.63	0.03	0.03					0.09	0.06
EF South Fork SR	47	47 (1.00)		0.06	0.85	0.09						
Secesh R	45	45 (1.00)		0.02	0.91	0.04						0.02
Lick Cr	40	40 (1.00)	0.03	0.05	0.78	0.10			0.03		0.03	
Stolle Meadows	45	45 (1.00)	0.02		0.96						0.02	
Boulder Cr	47	47 (1.00)	0.15	0.02		0.60	0.04	0.06	0.04	0.02		0.06
Rapid R	100	100 (1.00)	0.14	0.06	0.04	0.65			0.02	0.01	0.03	0.05
Slate Cr	47	47 (1.00)	0.19	0.02		0.62			0.04	0.02	0.02	0.09
Whitebird Cr	62	62 (1.00)	0.18	0.06		0.45		0.02	0.05	0.08	0.08	0.08
Colt Cr	38	38 (1.00)					1.00					
Storm Cr	38	38 (1.00)				0.03	0.97					
Crooked F Lochsa R	44	44 (1.00)				0.02	0.89	0.09				
Fish Cr	100	100 (1.00)	0.01				0.91	0.04	0.02		0.01	0.01

Table 3a. Continued.

Collection of Origin	n	Number Assigned (Proportion)	Assigned Genetic Stock (No Threshhold)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
Canyon Cr	46	46 (1.00)					0.87	0.11	0.02			
Selway R	78	78 (1.00)					0.99	0.01				
Little Clearwater R	59	59 (1.00)					0.98		0.02			
Whitecap Cr	76	76 (1.00)					1.00					
Bear Cr	35	35 (1.00)					1.00					
NF Moose Cr	94	94 (1.00)					0.96	0.02	0.01			0.01
Three Links Cr	47	47 (1.00)					1.00					
Gedney Cr	45	45 (1.00)					0.93	0.02	0.04			
O'Hara Cr	47	47 (1.00)				0.04	0.77	0.15	0.02			0.02
Crooked R	106	106 (1.00)					0.12	0.85	0.02		0.01	
Tenmile Cr	47	47 (1.00)				0.02	0.15	0.83				
John's Cr	38	38 (1.00)					0.13	0.71	0.16			
Clear Cr	45	45 (1.00)				0.02	0.16	0.80	0.02			
WF Potlatch R	84	84 (1.00)	0.02			0.06	0.05	0.04	0.71	0.01	0.06	0.05
EF Potlatch R	158	158 (1.00)	0.01		0.01	0.01	0.06	0.02	0.77		0.06	0.08
Big Bear Cr	99	99 (1.00)	0.05			0.01	0.02	0.02	0.64	0.03	0.06	0.17
Little Bear Cr	151	151 (1.00)	0.04			0.03	0.02	0.03	0.71	0.02	0.07	0.09
Big Sheep Cr	68	68 (1.00)	0.09	0.06		0.04			0.04	0.63	0.09	0.04
Camp Cr	24	24 (1.00)	0.13		0.04	0.04				0.58	0.08	0.13
Cow Cr	44	44 (1.00)	0.11	0.05		0.05	0.02		0.09	0.50	0.09	0.09
Lightning Cr	41	41 (1.00)	0.12						0.10	0.59	0.12	0.07
Joseph Cr	53	53 (1.00)	0.04		0.02	0.04			0.06	0.06	0.55	0.25
Crooked Cr	97	97 (1.00)	0.04	0.02		0.03			0.05	0.07	0.64	0.14
Elk Cr	45	45 (1.00)	0.02						0.07	0.02	0.84	0.04
Little Minam R	48	48 (1.00)	0.02						0.08		0.71	0.19
Lostine R	45	45 (1.00)							0.02	0.02	0.91	0.04
Menatchee Cr	73	73 (1.00)	0.07	0.01		0.03		0.01	0.01	0.05	0.60	0.21
Wenaha R	94	94 (1.00)	0.03	0.01	0.01	0.02	0.01		0.02	0.07	0.66	0.16
Captain John Cr	56	56 (1.00)	0.11			0.02			0.04		0.73	0.11
George Cr	95	95 (1.00)	0.17	0.02	0.01	0.02			0.09	0.04	0.15	0.49
Asotin Cr	99	99 (1.00)	0.08	0.02		0.14	0.02		0.11	0.04	0.14	0.44
Alpowa Cr	98	98 (1.00)	0.11			0.03	0.01	0.03	0.07	0.01	0.20	0.53
Tucannon R	106	106 (1.00)	0.08	0.03		0.04			0.12	0.03	0.20	0.50

Table 3b

Collection of Origin	n	Number Assigned (Proportion)	Assigned Genetic Stock (≥80% Probability)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
Sawtooth Weir	108	50 (0.46)	0.98							0.02		
Valley Cr	45	22 (0.49)	0.82				0.05				0.14	
WF Yankee Fork SR	117	64 (0.55)	0.91	0.02		0.05					0.02	0.02
Morgan Cr	37	27 (0.73)	0.96								0.04	
Pahsimeroi Weir	97	58 (0.60)	0.91	0.02		0.03			0.02	0.02		
Hayden Cr	86	51 (0.59)	0.94	0.04							0.02	
North Fork SR	100	34 (0.34)	0.76			0.18	0.03					0.03
Marsh Cr	59	59 (1.00)		1.00								
Sulphur Cr	45	43 (0.96)		1.00								
Rapid R Middle Fork SR	45	44 (0.98)		1.00								
Pistol Cr	23	23 (1.00)		1.00								
Camas Cr	57	53 (0.93)	0.02	0.98								
Loon Cr	84	77 (0.92)		0.97		0.03						
upper Big Cr	46	42 (0.91)		1.00								
lower Big Cr	48	41 (0.85)		0.95			0.02				0.02	
Chamberlain Cr	46	32 (0.70)	0.03	0.88		0.03				0.03	0.03	
Bargamin Cr	32	21 (0.66)	0.14	0.76							0.05	0.05
EF South Fork SR	47	41 (0.87)			0.98	0.02						
Secesh R	45	40 (0.89)		0.03	0.95	0.03						
Lick Cr	40	32 (0.80)	0.03		0.88	0.06			0.03			
Stolle Meadows	45	44 (0.98)	0.02		0.95						0.02	
Boulder Cr	47	28 (0.60)	0.11			0.71	0.04	0.07	0.04	0.04		
Rapid R	100	69 (0.69)	0.19	0.07	0.03	0.70					0.01	
Slate Cr	47	23 (0.49)	0.13			0.83						0.04
Whitebird Cr	62	24 (0.39)	0.17			0.63				0.08	0.04	0.08
Colt Cr	38	38 (1.00)					1.00					
Storm Cr	38	38 (1.00)				0.03	0.97					
Crooked F Lochsa R	44	37 (0.84)					1.00					
Lake Cr	47	46 (0.98)					1.00					
Fish Cr	100	89 (0.89)					0.99	0.01				
Canyon Cr	46	33 (0.72)					0.94	0.06				
Selway R	78	77 (0.99)					1.00					
Little Clearwater R	59	57 (0.97)					0.98		0.02			
Whitecap Cr	76	75 (0.99)					1.00					
Bear Cr	35	33 (0.94)					1.00					
NF Moose Cr	94	87 (0.93)					0.99	0.01				
Three Links Cr	47	47 (1.00)					1.00					

Table 3b. Continued.

Collection of Origin	n	Number Assigned (Proportion)	Assigned Genetic Stock (≥80% Probability)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
Gedney Cr	45	41 (0.91)					0.95	0.02	0.02			
O'Hara Cr	47	31 (0.66)					0.84	0.13	0.03			
Crooked R	106	84 (0.79)					0.06	0.94				
Tenmile Cr	47	35 (0.74)					0.06	0.94				
John's Cr	38	20 (0.53)					0.20	0.80				
Clear Cr	45	33 (0.73)					0.18	0.82				
WF Potlatch R	84	57 (0.68)				0.04	0.02	0.02	0.86	0.02	0.04	0.02
EF Potlatch R	158	103 (0.65)			0.01		0.04	0.01	0.91		0.01	0.02
Big Bear Cr	99	42 (0.42)						0.02	0.81		0.05	0.12
Little Bear Cr	151	95 (0.63)					0.01	0.02	0.87		0.05	0.04
Big Sheep Cr	68	37 (0.54)	0.03	0.03		0.08				0.81	0.03	0.03
Camp Cr	24	13 (0.54)			0.08					0.92		
Cow Cr	44	21 (0.48)	0.14	0.05			0.05		0.05	0.62	0.10	
Lightning Cr	41	17 (0.41)	0.12							0.88		
Joseph Cr	53	11 (0.21)				0.09					0.91	
Crooked Cr	97	50 (0.52)	0.02	0.04		0.02			0.02	0.06	0.78	0.06
Elk Cr	45	34 (0.76)							0.03		0.97	
Little Minam R	48	30 (0.63)							0.07		0.87	0.07
Lostine R	45	29 (0.64)									1.00	
Menatchee Cr	73	26 (0.36)				0.04					0.85	0.12
Wenaha R	94	37 (0.39)	0.05			0.03	0.03				0.86	0.03
Captain John Cr	56	38 (0.68)	0.03			0.03			0.05		0.79	0.11
George Cr	95	20 (0.21)	0.15						0.15	0.05	0.15	0.50
Asotin Cr	99	30 (0.30)	0.07			0.10			0.07	0.03	0.07	0.67
Alpowa Cr	98	33 (0.34)	0.06			0.06		0.09	0.03		0.21	0.55
Tucannon R	106	38 (0.36)	0.11	0.03		0.05			0.13	0.05	0.13	0.50

Table 4. Thirty-nine 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, life stage, 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. Lineages are ST – stream type, OC – ocean type. Life stage codes are A – adult, C – carcass, J – Juvenile. 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	Latitude	Longitude	Lineage	Life Stage	HE	FST	HWE Deficient	HWE Excess
1	Sawtooth Weir	SRUMA	UPSALM	Upper Salmon	91	09, 10	IDFG	1.0	44.15058	-114.88509	ST	A	22.0%	0.013		
2	Valley Cr	SRVAL	UPSALM	Upper Salmon	56	07, 08, 09, 10	IDFG	2.0	44.30113	-115.04574	ST	C	22.9%	0.015		
3	WF Yankee Fork SR	SRYFS	UPSALM	Upper Salmon	75	05	CRITFC	1.0	44.34941	-114.72657	ST	J	22.3%	0.019		
4	EF Salmon R	SREFS	UPSALM	Upper Salmon	187	04, 05, 11	IDFG/CRITFC	1.0	44.11542	-114.42998	ST	A	22.4%	0.014		
5	Pahsimeroi R	SRPAH	UPSALM	Upper Salmon	92	07, 08, 09, 10	IDFG	1.0	44.56767	-113.90717	ST	A, C	22.9%	0.016		
6	Hayden Cr	SRLEM	UPSALM	Upper Salmon	79	09, 10	IDFG	1.0	44.78519	-113.70621	ST	C, J	23.5%	0.019		
7	upper Lemhi R	SRLEM	UPSALM	Upper Salmon	96	09, 10	IDFG	1.0	44.86917	-113.62510	ST	C, J	21.5%	0.017	7	8
8	lower Lemhi R	SRLEM	UPSALM	Upper Salmon	90	09, 10	IDFG	1.0	45.15296	-113.81357	ST	J	23.6%	0.014	9	3
9	Elk Cr Middle Fork SR	MFBEA	MFSALM	MF Salmon	84	07, 08, 09, 10	IDFG	1.0	44.43041	-115.47107	ST	C, J	21.2%	0.017		
10	Bear Valley Cr	MFBEA	MFSALM	MF Salmon	80	07, 08, 09, 10	IDFG	1.0	44.37328	-115.39501	ST	C	21.5%	0.015		
11	Capehorn Cr	MFMAR	MFSALM	MF Salmon	112	05, 06, 07, 09, 10	IDFG/CRITFC	1.0	44.35864	-115.22362	ST	C, J	21.5%	0.018	8	6
12	Marsh Cr	MFMAR	MFSALM	MF Salmon	66	07, 08, 09, 10	IDFG	1.0	44.41537	-115.18385	ST	C	21.5%	0.015		
13	Sulphur Cr	MFSUL	MFSALM	MF Salmon	35	08, 09, 10	IDFG	1.0	44.54370	-115.39566	ST	C, J	20.2%	0.021		
14	Camas Cr	MFCAM	MFSALM	MF Salmon	57	06, 09	CRITFC	1.0	44.82399	-114.49990	ST	J	20.5%	0.020	5	5
15	Big Cr	MFBIG	MFSALM	MF Salmon	95	01, 10	IDFG/CRITFC	1.0	45.15063	-115.29674	ST	C, A	21.3%	0.015	10	4
16	Chamberlain Cr (post-2008)	SRCHA	CHMBLN	MF Salmon	55	09, 10	IDFG/CRITFC	1.0	45.39781	-115.19339	ST	C, J	21.2%	0.027		
17	Chamberlain Cr (pre-2008)	SRCHA	CHMBLN	MF Salmon	70	03, 04, 06, 07	IDFG	2.0	45.36865	-115.19689	ST	C, J	21.1%	0.021		
18	Johnson Cr	SFMAI	SFSALM	SF Salmon	92	02	CRITFC	1.0	44.90445	-115.48689	ST	A	22.3%	0.014		
19	SF Salmon R	SFMAI	SFSALM	SF Salmon	140	09, 10	IDFG	1.0	44.66676	-115.70292	ST	A, C	22.9%	0.011		
20	Lake Cr, Summit Cr	SFSEC	SFSALM	SF Salmon	74	07, 08, 09, 10	IDFG	1.0	45.27881	-115.92169	ST	C	21.6%	0.017		
21	Secesh R	SFSEC	SFSALM	SF Salmon	130	01, 07, 08, 09, 10	IDFG/CRITFC	1.0	45.12659	-115.77011	ST	C, J	21.9%	0.015		
22	Rapid R	SRLSR	HELLSC	SF Salmon	91	06	IDFG	1.0	45.31576	-116.41871	ST	A	22.8%	0.014	7	3
23	Crooked F Lochsa R	CRLOC	HELLSC	N/A	26	07, 08, 09, 10	IDFG	2.0	46.61523	-114.67046	ST	C	24.3%	0.015		
24	Powell Weir	CRLOL	HELLSC	N/A	31	09	IDFG	1.0	46.50561	-114.68718	ST	A	23.4%	0.013		
25	Red R	SCUMA	HELLSC	N/A	72	07, 08, 09, 10	IDFG	1.0	45.70979	-115.34389	ST	A, C	24.1%	0.012		
26	Crooked R Weir	SCUMA	HELLSC	N/A	67	09, 10	IDFG	1.0	45.76562	-115.54264	ST	A	24.1%	0.012		

Table 4. Continued.

Map #	Collection	TRT Population	Genetic Stock	MPG	n	Years Collected	Genotype Agency	Baseline Version	Latitude	Longitude	Lineage	Life Stage	HE	FST	HWE Deficient	HWE Excess
27	Newsome Cr	SCUMA	HELLSC	N/A	82	01	CRITFC	1.0	45.86383	-115.61725	ST	A	22.9%	0.014		
28	Lolo Cr	CRLOL	HELLSC	N/A	89	01, 02	IDFG/CRITFC	1.0	46.31500	-116.00741	ST	J	23.9%	0.012	12	4
29	Imnaha R	IRMAI	HELLSC	Grande Ronde / Imnaha	43	08	IDFG/NOAA	2.0	45.56100	-116.83400	ST	J	23.7%	0.014		
30	Imnaha R (1998)	IRMAI	HELLSC	Grande Ronde / Imnaha	91	98	CRITFC	1.0	45.55400	-116.83474	ST	A	23.7%	0.013		
31	Upper Grande Ronde	GRUMA	HELLSC	Grande Ronde / Imnaha	43	08	IDFG/NOAA	2.0	45.19319	-118.39458	ST	J	24.6%	0.015		
32	Catherine Cr	GRCAT	HELLSC	Grande Ronde / Imnaha	93	04, 06	IDFG/CRITFC	2.0	45.24062	-117.92199	ST	A	24.6%	0.013		
33	Lostine R	GRLOS	HELLSC	Grande Ronde / Imnaha	176	03, 05, 09	IDFG/CRITFC/NOAA	2.0	45.42211	-117.42496	ST	J	23.0%	0.014		
34	Minam R	GRMIN	HELLSC	Grande Ronde / Imnaha	80	94, 02	IDFG/CRITFC	1.0	45.60000	-117.72900	ST	J	25.2%	0.014	13	2
35	Wenaha R	GRWEN	HELLSC	Grande Ronde / Imnaha	88	02, 06	IDFG/CRITFC	1.0	45.97269	-117.69367	ST	J	25.7%	0.014		
36	Tucannon R	SNTUC	TUCANO	Lower Snake Tribs	81	03	CRITFC	1.0	46.50530	-118.01440	ST	A	26.1%	0.024	6	4
37	Clearwater	N/A	FALL	FALL ESU	143	08	IDFG/CRITFC	2.0	46.52000	-116.60950	OC	A	30.0%	N/A	8	6
38	Nez Perce Tribal Hatchery	N/A	FALL	FALL ESU	85	03	CRITFC	2.0	46.51910	-116.66460	OC	A	29.4%	N/A		
39	Lyons Ferry	N/A	FALL	FALL ESU	90	00	CRITFC	2.0	46.58940	-118.21950	OC	A	29.4%	N/A		

Table 5. Summary of 190 SNPs (Appendix B and Hess et al. 2013) screened across 36 stream-type Chinook salmon collections in Snake River baseline v2.0. (Note: fall Chinook collections were excluded from analyses below.) SNPs designated as PBT are used for both the PBT (BPA Project #2010-031-00, Steele et al. 2012) and GSI projects. SNPs designated as GSI are used primarily for GSI applications. Summary statistics include minor-allele frequency (MAF) range, expected heterozygosity (H_E), mean Weir and Cockerham (1984) F_{ST}, "HWE" designates the number of collections that a SNP deviated from Hardy-Weinberg expectation (deficient or in excess) for any SNP that deviated in greater than 10% of collections. "LD" signifies SNPs that exhibit linkage disequilibrium in more than half of the collections.

					HWE			
SNP Marker	**Panel**	**MAF Range**	**H_E**	**F_{ST}**	**Deficient**	**Excess**	**LD**	**Comment**
Ots_101554-407	PBT v5.1	(0.118 - 0.626)	46.4%	0.034	2	2		
Ots_101704-143	PBT v5.1	(0.015 - 0.355)	24.9%	0.059				
Ots_102414-395	PBT v5.1	(0.224 - 0.643)	47.5%	0.049				
Ots_102801-308	PBT v5.1	(0.071 - 0.329)	32.5%	0.019				
Ots_103122-180	PBT v5.1	(0.021 - 0.389)	24.7%	0.039				
Ots_104415-88	PBT v5.1	(0.086 - 0.633)	46.4%	0.025				
Ots_105105-613	PBT v5.1	(0.101 - 0.494)	41.9%	0.031				
Ots_105132-200	PBT v5.1	(0.031 - 0.314)	31.0%	0.021				
Ots_105385-421	PBT v5.1	(0.028 - 0.650)	45.4%	0.022				
Ots_105407-117	PBT v5.1	(0.247 - 0.614)	46.8%	0.049	1	3		
Ots_108820-336	PBT v5.1	(0.050 - 0.698)	43.9%	0.050				
Ots_109525-816	PBT v5.1	(0.062 - 0.427)	30.4%	0.033				
Ots_110064-383	PBT v5.1	(0.082 - 0.488)	42.1%	0.028				
Ots_110201-363	PBT v5.1	(0.178 - 0.537)	43.3%	0.030				
Ots_110495-380	PBT v5.1	(0.034 - 0.593)	24.2%	0.098				
Ots_110551-64	PBT v5.1	(0.100 - 0.316)	33.3%	0.022				
Ots_110689-218	PBT v5.1	(0.077 - 0.445)	34.4%	0.033				
Ots_112301-43	PBT v5.1	(0.043 - 0.262)	23.9%	0.028	4			
Ots_112419-131	PBT v5.1	(0.000 - 0.255)	20.5%	0.029				
Ots_112820-284	PBT v5.1	(0.026 - 0.327)	24.5%	0.043				
Ots_112876-371	PBT v5.1	(0.000 - 0.357)	26.0%	0.041				
Ots_113242-216	PBT v5.1	(0.011 - 0.178)	20.6%	0.018				
Ots_115987-325	PBT v5.1	(0.065 - 0.471)	37.9%	0.034				
Ots_117432-409	PBT v5.1	(0.128 - 0.614)	41.0%	0.072				
Ots_118205-61	PBT v5.1	(0.091 - 0.330)	31.7%	0.027	1	3		
Ots_118938-325	PBT v5.1	(0.026 - 0.471)	35.1%	0.055				
Ots_123921-111	PBT v5.1	(0.027 - 0.275)	23.5%	0.031				
Ots_124774-477	PBT v5.1	(0.004 - 0.167)	16.7%	0.016				
Ots_128757-61R	PBT v5.1	(0.006 - 0.195)	18.4%	0.033				
Ots_129458-451	PBT v5.1	(0.000 - 0.277)	22.7%	0.039				
Ots_94857-232R	PBT v5.1	(0.218 - 0.698)	48.1%	0.047				
Ots_94903-99R	PBT v5.1	(0.186 - 0.624)	47.8%	0.032				
Ots_96500-180	PBT v5.1	(0.237 - 0.679)	46.9%	0.032				
Ots_96899-357R	PBT v5.1	(0.000 - 0.295)	20.9%	0.028				
Ots_ARNT	PBT v5.1	(0.000 - 0.329)	26.8%	0.034				
Ots_AsnRS-60	PBT v5.1	(0.045 - 0.301)	29.8%	0.026				
Ots_brp16-64	PBT v5.1	(0.052 - 0.273)	25.5%	0.021				
Ots_CD59-2	PBT v5.1	(0.286 - 0.562)	46.9%	0.021	3	1		
Ots_CirpA	PBT v5.1	(0.007 - 0.229)	19.3%	0.030				
Ots_cox1-241	PBT v5.1	(0.014 - 0.352)	23.7%	0.053				
Ots_E2-275	PBT v5.1	(0.051 - 0.480)	38.0%	0.041				

Table 5. Continued.

SNP Marker	Panel	MAF Range	H_E	F_{ST}	HWE Deficient	HWE Excess	LD	Comment
Ots_Est740	PBT v5.1	(0.289 - 0.622)	48.4%	0.020				
Ots_GCSH	PBT v5.1	(0.005 - 0.241)	17.4%	0.036				
Ots_GDH-81x	PBT v5.1	(0.069 - 0.436)	37.0%	0.041				
Ots_GPH-318	PBT v5.1	(0.014 - 0.373)	29.1%	0.040				
Ots_GTH2B-550	PBT v5.1	(0.006 - 0.615)	44.9%	0.034	2	3		
Ots_HMGB1-73	PBT v5.1	(0.060 - 0.265)	24.9%	0.025				
Ots_hsc71-3'-488	PBT v5.1	(0.044 - 0.297)	26.5%	0.028			c	
Ots_HSP90B-100	PBT v5.1	(0.080 - 0.308)	28.4%	0.024				
Ots_IGF-I.1-76	PBT v5.1	(0.000 - 0.359)	27.4%	0.034				
Ots_Ikaros-250	PBT v5.1	(0.000 - 0.231)	16.4%	0.030				
Ots_IL8R_C8	PBT v5.1	(0.030 - 0.524)	43.7%	0.027				
Ots_mapK-3'-309	PBT v5.1	(0.121 - 0.582)	44.9%	0.043				
Ots_mapKpr-151	PBT v5.1	(0.053 - 0.404)	35.5%	0.036				
Ots_MHC1	PBT v5.1	(0.019 - 0.167)	13.3%	0.017				
Ots_MHC2	PBT v5.1	(0.171 - 0.772)	42.1%	0.114				
Ots_mybp-85	PBT v5.1	(0.000 - 0.240)	21.2%	0.035				
Ots_NFYB-147	PBT v5.1	(0.000 - 0.286)	26.6%	0.025				
Ots_nkef-192	PBT v5.1	(0.017 - 0.621)	44.1%	0.034				
Ots_NOD1	PBT v5.1	(0.006 - 0.414)	36.6%	0.023				
Ots_ntl-255	PBT v5.1	(0.218 - 0.549)	45.2%	0.021				
Ots_OTALDBINT1-SNP1	PBT v5.1	(0.026 - 0.199)	18.6%	0.024	6			
Ots_OTDESMIN19-SNP1	PBT v5.1	(0.159 - 0.557)	45.6%	0.038				
Ots_OTSTF1-SNP1	PBT v5.1	(0.078 - 0.673)	42.2%	0.063			a	
Ots_P53	PBT v5.1	(0.074 - 0.449)	37.1%	0.041				
Ots_parp3-286	PBT v5.1	(0.006 - 0.261)	26.3%	0.020				
Ots_pigh-105	PBT v5.1	(0.200 - 0.633)	46.8%	0.041				
Ots_pop5-96	PBT v5.1	(0.006 - 0.491)	35.7%	0.035				
Ots_ppie-245	PBT v5.1	(0.009 - 0.437)	25.3%	0.080				
Ots_Prl2	PBT v5.1	(0.091 - 0.474)	38.6%	0.041				
Ots_RAG3	PBT v5.1	(0.035 - 0.285)	21.9%	0.035				
Ots_redd1-187	PBT v5.1	(0.012 - 0.396)	35.3%	0.026				
Ots_S7-1	PBT v5.1	(0.164 - 0.582)	44.7%	0.030				
Ots_SClkF2R2-135	PBT v5.1	(0.200 - 0.631)	46.5%	0.048				
Ots_SWS1op-182	PBT v5.1	(0.184 - 0.505)	41.7%	0.019				
Ots_TAPBP	PBT v5.1	(0.006 - 0.619)	35.8%	0.169	5			
Ots_TGFB	PBT v5.1	(0.011 - 0.108)	11.7%	0.013				
Ots_Thio	PBT v5.1	(0.084 - 0.434)	39.5%	0.023				
Ots_TLR3	PBT v5.1	(0.103 - 0.506)	37.3%	0.064				
Ots_tpx2-125	PBT v5.1	(0.010 - 0.250)	17.5%	0.034				
Ots_txnip-321	PBT v5.1	(0.000 - 0.300)	22.7%	0.053				
Ots_u07-07.161	PBT v5.1	(0.118 - 0.593)	44.9%	0.047				
Ots_u07-17.135	PBT v5.1	(0.017 - 0.256)	19.7%	0.030				
Ots_u07-18.378	PBT v5.1	(0.000 - 0.212)	19.9%	0.035				
Ots_u07-25.325	PBT v5.1	(0.045 - 0.695)	45.4%	0.047				
Ots_u07-49.290	PBT v5.1	(0.164 - 0.522)	42.4%	0.023				
Ots_u1002-75	PBT v5.1	(0.026 - 0.397)	35.2%	0.040				
Ots_u211-85	PBT v5.1	(0.006 - 0.582)	43.0%	0.037				
Ots_u4-92	PBT v5.1	(0.000 - 0.105)	7.1%	0.022				
Ots_u6-75	PBT v5.1	(0.006 - 0.307)	19.4%	0.037				
Ots_unk526	PBT v5.1	(0.024 - 0.261)	21.2%	0.040				
Ots_vatf-251	PBT v5.1	(0.018 - 0.259)	18.4%	0.028				
Ots_101119-381	GSI v1.1	(0.000 - 0.019)	0.7%	0.015				
Ots_102213-210	GSI v1.1	(0.000 - 0.182)	3.2%	0.101				
Ots_102457-132	GSI v1.1	(0.000 - 0.181)	8.4%	0.046				

Table 5. Continued.

SNP Marker	Panel	MAF Range	H_E	F_{ST}	HWE Deficient	HWE Excess	LD	Comment
Ots_102867-609	GSI v1.1	(0.000 - 0.074)	4.5%	0.024				
Ots_104569-86	GSI v1.1	(0.033 - 0.239)	22.6%	0.029				
Ots_106499-70	GSI v1.1	(0.143 - 0.444)	39.0%	0.021				
Ots_106747-239	GSI v1.1	(0.220 - 0.644)	46.0%	0.044				
Ots_107074-284	GSI v1.1	(0.000 - 0.082)	8.1%	0.025				
Ots_107285-93	GSI v1.1	(0.000 - 0.088)	4.9%	0.024				
Ots_107806-821	GSI v1.1	(0.161 - 0.633)	46.7%	0.036				
Ots_108007-208	GSI v1.1	(0.000 - 0.125)	10.0%	0.027				
Ots_108390-329	GSI v1.1	(0.000 - 0.019)	2.2%	0.014				
Ots_108735-302	GSI v1.1	(0.016 - 0.318)	18.7%	0.037	6			
Ots_109693-392	GSI v1.1	(0.000 - 0.216)	7.3%	0.057				
Ots_111681-657	GSI v1.1	(0.017 - 0.183)	16.3%	0.021				
Ots_112208-722	GSI v1.1	(0.000 - 0.127)	11.6%	0.027				
Ots_113457-40R	GSI v1.1	(0.013 - 0.190)	18.0%	0.027				
Ots_117242-136	GSI v1.1	(0.005 - 0.189)	14.1%	0.032				
Ots_117259-271	GSI v1.1	(0.000 - 0.066)	4.6%	0.022				
Ots_118175-479	GSI v1.1	(0.000 - 0.082)	5.7%	0.026				
Ots_122414-56	GSI v1.1	(0.000 - 0.173)	4.8%	0.087				
Ots_123048-521	GSI v1.1	(0.000 - 0.086)	3.2%	0.028				
Ots_127236-62	GSI v1.1	(0.000 - 0.117)	7.1%	0.030				
Ots_128302-57	GSI v1.1	(0.000 - 0.133)	9.8%	0.026				
Ots_128693-461	GSI v1.1	(0.000 - 0.106)	9.6%	0.015				
Ots_129144-472	GSI v1.1	(0.000 - 0.025)	4.4%	0.009				
Ots_130720-99	GSI v1.1	(0.000 - 0.114)	12.0%	0.024				
Ots_131460-584	GSI v1.1	(0.000 - 0.146)	10.5%	0.034				
Ots_131906-141	GSI v1.1	(0.000 - 0.140)	9.6%	0.024				
Ots_96222-525	GSI v1.1	(0.000 - 0.129)	9.8%	0.031				
Ots_97077-179R	GSI v1.1	(0.000 - 0.088)	7.9%	0.026				
Ots_99550-204	GSI v1.1	(0.000 - 0.100)	4.0%	0.033				
Ots_AldB1-122	GSI v1.1	(0.000 - 0.210)	14.1%	0.031				
Ots_aldb-177M	GSI v1.1	(0.000 - 0.109)	13.5%	0.015				
Ots_arp-436	GSI v1.1	(0.000 - 0.058)	4.9%	0.027				
Ots_aspat-196	GSI v1.1	(0.000 - 0.011)	2.2%	0.008				
Ots_C3N3	GSI v1.1	(0.000 - 0.192)	10.7%	0.054				mtDNA
Ots_Cath_D141	GSI v1.1	(0.000 - 0.054)	2.7%	0.024				
Ots_CCR7	GSI v1.1	(0.000 - 0.000)	0.0%	N/A				monomorphic
Ots_CD63	GSI v1.1	(0.000 - 0.145)	12.9%	0.026				
Ots_CRB211	GSI v1.1	(0.000 - 0.038)	1.9%	0.013				
Ots_DDX5-171	GSI v1.1	(0.006 - 0.197)	16.6%	0.028				
Ots_EndoRB1-486	GSI v1.1	(0.000 - 0.111)	8.3%	0.029				
Ots_EP-529	GSI v1.1	(0.000 - 0.105)	4.7%	0.027				
Ots_Est1363	GSI v1.1	(0.000 - 0.247)	6.7%	0.052				
Ots_FARSLA-220	GSI v1.1	(0.000 - 0.306)	6.4%	0.084				
Ots_FGF6A	GSI v1.1	(0.054 - 0.571)	43.8%	0.033	1	3	b	
Ots_GH2	GSI v1.1	(0.000 - 0.127)	7.7%	0.026				
Ots_GnRH-271	GSI v1.1	(0.000 - 0.147)	5.4%	0.034				
Ots_GPDH-338	GSI v1.1	(0.000 - 0.049)	1.9%	0.031				
Ots_GST-207	GSI v1.1	(0.000 - 0.105)	2.7%	0.058				
Ots_GST-375	GSI v1.1	(0.000 - 0.000)	0.1%	N/A				monomorphic
Ots_HFABP-34	GSI v1.1	(0.000 - 0.093)	8.6%	0.019				
Ots_hnRNPL-533	GSI v1.1	(0.007 - 0.667)	45.7%	0.022				
Ots_hsc71-5'-453	GSI v1.1	(0.000 - 0.169)	10.1%	0.036			c	
Ots_hsp27b-150	GSI v1.1	(0.005 - 0.160)	11.5%	0.030				
Ots_Hsp90a	GSI v1.1	(0.000 - 0.070)	6.0%	0.033				

Table 5. Continued.

SNP Marker	Panel	MAF Range	H_E	F_{ST}	HWE Deficient	HWE Excess	LD	Comment
Ots_IL11	GSI v1.1	(0.000 - 0.174)	8.7%	0.055				
Ots_il13Ra2B-37	GSI v1.1	(0.116 - 0.544)	44.5%	0.016	3	2		
Ots_il-1racp-166	GSI v1.1	(0.147 - 0.616)	45.8%	0.033				
Ots_LWSop-638	GSI v1.1	(0.000 - 0.003)	0.1%	0.003				
Ots_Myc-366	GSI v1.1	(0.000 - 0.037)	0.6%	0.021				
Ots_myo1a-384	GSI v1.1	(0.000 - 0.132)	6.1%	0.035				
Ots_myoD-364	GSI v1.1	(0.005 - 0.209)	14.5%	0.033				
Ots_nelfd-163	GSI v1.1	(0.000 - 0.070)	5.7%	0.028				
Ots_nramp-321	GSI v1.1	(0.000 - 0.167)	2.2%	0.072				
Ots_Ots311-101x	GSI v1.1	(0.000 - 0.038)	2.1%	0.016				
Ots_OTSMTA-SNP1	GSI v1.1	(0.000 - 0.117)	4.2%	0.045				
Ots_P450	GSI v1.1	(0.000 - 0.062)	4.0%	0.020				
Ots_P450-288	GSI v1.1	(0.101 - 0.667)	43.1%	0.041				
Ots_PGK-54	GSI v1.1	(0.000 - 0.076)	6.6%	0.028				
Ots_RAS1	GSI v1.1	(0.000 - 0.000)	0.0%	N/A				monomorphic
Ots_RFC2-558	GSI v1.1	(0.000 - 0.036)	5.0%	0.011				
Ots_SL	GSI v1.1	(0.000 - 0.160)	4.9%	0.051				
Ots_stk6-516	GSI v1.1	(0.000 - 0.000)	1.4%	N/A				monomorphic[d]
Ots_TCTA-58	GSI v1.1	(0.000 - 0.102)	7.2%	0.021				
Ots_TNF	GSI v1.1	(0.000 - 0.012)	0.2%	0.010				
Ots_Tnsf	GSI v1.1	(0.039 - 0.671)	40.1%	0.059	3	2	a	
Ots_u07-20.332	GSI v1.1	(0.000 - 0.000)	0.7%	N/A				monomorphic
Ots_u07-53.133	GSI v1.1	(0.009 - 0.282)	15.5%	0.045				
Ots_u07-57.120	GSI v1.1	(0.000 - 0.185)	6.9%	0.046				
Ots_u07-64.221	GSI v1.1	(0.000 - 0.019)	0.3%	0.015				
Ots_u1007-124	GSI v1.1	(0.000 - 0.039)	4.6%	0.016				
Ots_u202-161	GSI v1.1	(0.000 - 0.136)	10.9%	0.020				
Ots_U2362-227	GSI v1.1	(0.000 - 0.116)	4.1%	0.032				
Ots_U2362-330	GSI v1.1	(0.006 - 0.586)	45.4%	0.016				
Ots_U2446-123	GSI v1.1	(0.109 - 0.593)	43.5%	0.043	4	1		
Ots_unk1104-38	GSI v1.1	(0.045 - 0.607)	45.7%	0.021				
Ots_unk1832-39	GSI v1.1	(0.090 - 0.661)	47.3%	0.024				
Ots_unk3513-49	GSI v1.1	(0.105 - 0.611)	35.7%	0.049	3	1		
Ots_unk7936-50	GSI v1.1	(0.000 - 0.153)	13.9%	0.022				
Ots_unk8200-45	GSI v1.1	(0.000 - 0.055)	0.6%	0.031				
Ots_unk9480-51	GSI v1.1	(0.019 - 0.316)	26.7%	0.041				
Ots_zn593-346	GSI v1.1	(0.000 - 0.111)	3.0%	0.031				
Ots_zP3b-215	GSI v1.1	(0.000 - 0.000)	0.0%	N/A				monomorphic
Ots_ZR-575	GSI v1.1	(0.000 - 0.169)	12.3%	0.030	11			

[a] Ots_Tnsf and Ots_OTSF1-SNP exhibited linkage disequilibrium in 37 of 39 baseline collections. Ots_Tnsf was the least informative of the locus pair and was dropped from baseline and GSI analyses.

[b] Ots_FGF6A and Ots_FGF6B_1 exhibited linkage disequilibrium in 39 of 39 baseline collections. Ots_FGF6A was the least informative of the locus pair and was dropped from baseline and GSI analyses.

[c] Ots_hsc71-5'-453 and Ots_hsc71-3'-488 exhibited linkage disequilibrium in 29 of 39 baseline collections. Ots_hsc71-3'-488 was the less informative of the locus pair and was dropped from baseline and GSI analyses.

[d] This marker was variable in the 3 fall Chinook collections included in Snake River baseline v2.0 and will be included in analyses baseline and GSI analyses concerning differentiating spring/summer and fall lineages.

Table 6. 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 v2.0, 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 6a is results for all individuals that assigned to a genetic stock, and Table 6b is for individuals that assigned to a genetic stock with ≥80% probability. For example, n = 91 individuals represent the Sawtooth Weir collection. Of the 91 individuals in the baseline, 53 (58%) assigned back to a genetic stock with ≥80% probability. Of the 53 that assigned, 49 (54%) assigned to the correct UPSALM reporting group. Shaded boxes represent the correct genetic stock of origin for each population.

Table 6a.

		Number Assigned	Assigned Genetic Stock (No Threshhold)						
Collection of Origin	**n**	**(Proportion)**	**UPSALM**	**MFSALM**	**CHMBLN**	**SFSALM**	**HELLSC**	**TUCANO**	**FALL**
Sawtooth Weir	91	91 (1.00)	0.77	0.08	0.01	0.07	0.08		
Valley Cr	56	56 (1.00)	0.84	0.02	0.02	0.04	0.09		
WF Yankee F Salmon	75	75 (1.00)	0.95			0.03	0.03		
EF Salmon R	187	187 (1.00)	0.88	0.03		0.02	0.06		
Pahsimeroi R	92	92 (1.00)	0.86	0.02		0.05	0.07		
Hayden Cr	79	79 (1.00)	0.76			0.01	0.23		
Capehorn Cr	112	112 (1.00)	0.02	0.91		0.04	0.03		
Marsh Cr	66	66 (1.00)	0.09	0.79		0.08	0.05		
Elk Cr	84	84 (1.00)	0.05	0.87	0.01	0.05	0.02		
Bear Valley Cr	80	80 (1.00)		0.91		0.05	0.04		
Sulphur Cr	35	35 (1.00)	0.03	0.94		0.03			
Camas Cr	57	57 (1.00)	0.02	0.93		0.02	0.04		
Big Cr	95	95 (1.00)	0.04	0.84	0.01	0.02	0.08		
Chamberlain Cr post	55	55 (1.00)		0.02	0.95	0.02	0.02		
Chamberlain Cr pre	70	70 (1.00)		0.04	0.84	0.03	0.09		
Lake Cr and Summit Cr	74	74 (1.00)	0.01	0.04		0.88	0.07		
Secesh R	130	130 (1.00)		0.07		0.85	0.08		
Johnson Cr	92	92 (1.00)	0.04	0.09		0.73	0.14		
SF Salmon R	140	140 (1.00)	0.16	0.11	0.02	0.50	0.20		
Rapid R	91	91 (1.00)	0.03	0.01		0.01	0.95		
Crooked F Lochsa R	26	26 (1.00)	0.08			0.04	0.88		
Powell Weir	31	31 (1.00)	0.03	0.06			0.90		
Red R	72	72 (1.00)	0.03			0.01	0.96		
Crooked R Weir	67	67 (1.00)	0.01	0.03		0.01	0.93	0.01	
Newsome Cr	82	82 (1.00)	0.01	0.01		0.02	0.95		
Lolo Cr	89	89 (1.00)	0.04	0.02	0.01	0.02	0.89	0.01	
Imnaha R recent	43	43 (1.00)	0.09	0.02		0.05	0.84		
Imnaha R older	91	91 (1.00)		0.04	0.01	0.04	0.90		
Upper Grande Ronde	43	43 (1.00)	0.09	0.02			0.88		
Catherine Cr	93	93 (1.00)	0.05	0.02		0.03	0.89		
Lostine R	176	176 (1.00)	0.03	0.01		0.02	0.94	0.01	
Minam R	80	80 (1.00)	0.01	0.01		0.03	0.94	0.01	
Wenaha R	88	88 (1.00)				0.02	0.92	0.06	
Tucannon R	81	81 (1.00)	0.01	0.01			0.17	0.79	0.01
Clearwater	143	143 (1.00)							1.00
Nez Perce Tribal Hatchery	85	85 (1.00)							1.00
Lyons Ferry	90	90 (1.00)							1.00

Table 6b.

Collection of Origin	n	Number Assigned (Proportion)	Assigned Genetic Stock (≥ 80% Probability)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
Sawtooth Weir	91	53 (0.58)	0.54	0.02			0.02		
Valley Cr	56	43 (0.77)	0.71		0.02		0.04		
WF Yankee F Salmon	75	62 (0.83)	0.81				0.01		
EF Salmon R	187	144 (0.77)	0.73	0.02		0.01	0.02		
Pahsimeroi R	92	75 (0.82)	0.79			0.01	0.01		
Hayden Cr	79	67 (0.85)	0.71				0.14		
Capehorn Cr	112	94 (0.84)		0.82		0.01	0.01		
Marsh Cr	66	49 (0.74)	0.02	0.68		0.02	0.03		
Elk Cr	84	67 (0.80)		0.76	0.01	0.01	0.01		
Bear Valley Cr	80	65 (0.81)		0.79		0.01	0.01		
Sulphur Cr	35	33 (0.94)		0.91		0.03			
Camas Cr	57	47 (0.82)		0.81		0.02			
Big Cr	95	81 (0.85)	0.01	0.77	0.01	0.01	0.05		
Chamberlain Cr post	55	52 (0.95)			0.93		0.02		
Chamberlain Cr pre	70	59 (0.84)			0.77	0.01	0.06		
Lake Cr and Summit Cr	74	61 (0.82)		0.03		0.80			
Secesh R	130	101 (0.78)		0.02		0.71	0.05		
Johnson Cr	92	61 (0.66)		0.04		0.53	0.09		
SF Salmon R	140	61 (0.44)	0.07	0.04	0.01	0.24	0.07		
Rapid R	91	83 (0.91)	0.02			0.01	0.88		
Crooked F Lochsa R	26	20 (0.77)					0.77		
Powell Weir	31	23 (0.74)	0.03	0.03			0.68		
Red R	72	64 (0.89)	0.01			0.01	0.86		
Crooked R Weir	67	61 (0.91)		0.01			0.88	0.01	
Newsome Cr	82	72 (0.88)					0.88		
Lolo Cr	89	75 (0.84)	0.03				0.81		
Imnaha R recent	43	30 (0.70)					0.70		
Imnaha R older	91	74 (0.81)			0.01	0.01	0.79		
Upper Grande Ronde	43	34 (0.79)		0.02			0.77		
Catherine Cr	93	76 (0.82)	0.01	0.01		0.01	0.78		
Lostine R	176	157 (0.89)	0.02				0.87	0.01	
Minam R	80	69 (0.86)					0.85	0.01	
Wenaha R	88	79 (0.90)					0.85	0.05	
Tucannon R	81	74 (0.91)		0.01			0.11	0.78	0.01
Clearwater	143	143 (1.00)							1.00
Nez Perce Tribal Hatchery	85	85 (1.00)							1.00
Lyons Ferry	90	90 (1.00)							1.00

Table 7. Proposed sampling strategy and baseline reporting schedule of upcoming years for steelhead and Chinook salmon in the Snake River basin.

STHD baseline report		2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
			baseline v3.0		baseline v4.0		baseline v5.0		baseline v6.0		baseline v7.0
UPSALM	TRT Population fillins					sample year					sample year
MFSALM							sample year				
SFSALM				sample year					sample year		
UPCLWR							sample year				
SFCLWR					sample year					sample year	
GRROND					sample year					sample year	
IMNAHA			sample year					sample year			
LOSALM			sample year					sample year			
LOCLWR						sample year					sample year
LSNAKE				sample year					sample year		

CHNK baseline report		2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
			baseline v3.0		baseline v4.0		baseline v5.0		baseline v6.0		baseline v7.0
UPSALM	TRT Population fillins					sample year					sample year
MFSALM					sample year					sample year	
CHMBLN				sample year					sample year		
SFSALM							sample year				
HELLSC			sample year					sample year			
TUCANO			sample year					sample year			
FALL				sample year					sample year		

Table 8. Summary of SY2012 adult and MY2012 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 v2.

Sample Group	**Total Samples Inventoried**	**Samples Queued for Genotyping**	**Failed Genotyping (NG)**	**Successfully Genotyped**	**PBT Assignments**	**GSI Assignments**
Steelhead						
SY2012 Adults (Wild Phenotype)	4,448	2,902	49 (1.7%)	2,853 (98.3%)	260 (9.1%)	2,593 (90.9%)
SY2012 Adults (Stubbies)	618	389	10 (2.6%)	379 (97.4%)	254 (67.0%)	125 (33.0%)
MY2012 Juveniles	1,274	1,274	10 (0.8%)	1,264 (99.2%)	64 (5.1%)	1,200 (94.9%)
Chinook						
SY2012 Adults	2,358	2,358	27 (1.1%)	2,331 (98.9%)	155 (6.6%)	2,176 (93.4%)
MY2012 Juveniles (Yearling)	2,772	1,663	15 (0.9%)	1,648 (99.1%)	66 (4.0%)	1,582 (96.0%)
MY2012 Juveniles (Sub-yearling)	2,662	532	5 (0.9%)	527 (99.1%)	1 (0.2%)	526 (99.8%)
TOTAL:	14,132	9,118	116 (1.3%)	9,002	800 (8.8%)	8,202

Table 9. Summary of 2,718 Lower Granite Dam (LGR) **adult steelhead** samples from **SY2012** assigned to a genetic stock using individual assignment based on **Snake River steelhead SNP baseline v2**. Summaries of life-history diversity information (sex, length, saltwater age, and passage timing at LGR) 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							Passage Timing				
			Frequency			Percentage			Frequency		Percentage		Frequency				Percentage			Quantiles				
Genetic Stock	Total Assignments	% Stock Composition	F	M	U	F	M	Mean Length (cm FL)	A-Run	B-Run	A-Run	B-Run	1	2	3	Other	1	2	3	5th	25th	Med	75th	95th
UPSALM	472	17.4%	304	163	5	65%	35%	63.9	468	4	99%	1%	191	238	1	42	44%	55%	0%	8/6	9/1	9/13	10/2	10/22
MFSALM	190	7.0%	143	45	2	76%	24%	69.1	164	26	86%	14%	54	123	5	8	30%	68%	3%	8/17	9/3	9/14	9/26	10/18
SFSALM	109	4.0%	74	35	-	68%	32%	76.0	58	51	53%	47%	8	86	9	6	8%	83%	9%	9/6	9/16	9/24	10/5	10/17
LOSALM	163	6.0%	115	43	5	73%	27%	65.7	160	3	98%	2%	40	108	-	15	27%	73%	-	8/4	9/2	9/21	10/6	10/24
UPCLWR	190	7.0%	136	54	-	72%	28%	75.8	108	82	57%	43%	18	143	7	22	11%	85%	4%	9/4	9/22	10/2	10/14	10/26
SFCLWR	231	8.5%	143	84	4	63%	37%	77.0	113	118	49%	51%	8	167	14	42	4%	88%	7%	9/8	9/22	10/2	10/13	10/29
LOCLWR	202	7.4%	135	65	2	68%	33%	68.1	181	21	90%	10%	57	129	2	14	30%	69%	1%	8/6	9/1	9/18	10/9	10/23
IMNAHA	228	8.4%	154	68	6	69%	31%	64.4	224	4	98%	2%	85	128	1	14	40%	60%	0%	8/8	9/1	9/12	10/1	10/27
GRROND	519	19.1%	342	168	9	67%	33%	64.0	512	7	99%	1%	218	269	-	32	45%	55%	-	8/6	8/25	9/9	10/2	10/26
LSNAKE	414	15.2%	264	145	5	65%	35%	64.3	406	8	98%	2%	165	222	1	26	43%	57%	0%	7/30	8/27	9/11	10/5	10/26
Total	**2718**		**1810**	**870**	**38**	**68%**	**32%**	**67.2**	**2394**	**324**	**88%**	**12%**	**844**	**1613**	**40**	**221**	**34%**	**65%**	**2%**	**8/7**	**9/2**	**9/18**	**10/5**	**10/24**

Table 10. Summary of 1,200 Lower Granite Dam (LGR) **juvenile steelhead** samples from **MY2012** assigned to a genetic stock using individual assignment based on **Snake River steelhead SNP baseline v2**. Summaries of life-history diversity information (sex, length, freshwater age, and emigration timing at LGR) 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											Emigration Timing				
			Frequency			Percentage			Frequency						Percentage					Quantiles				
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	5th	25th	Med	75th	95th
UPSALM	193	16.1%	109	83	1	57%	43%	178	20	123	43	3	-	4	11%	65%	23%	2%	-	4/5	4/27	5/14	5/23	6/7
MFSALM	99	8.3%	57	39	3	59%	41%	184	3	19	56	17	-	4	3%	20%	59%	18%	-	4/5	4/17	4/30	5/16	5/26
SFSALM	49	4.1%	29	20	-	59%	41%	190	1	6	31	7	2	2	2%	13%	66%	15%	4%	3/27	4/6	4/17	5/13	5/23
LOSALM	74	6.2%	43	30	1	59%	41%	182	3	42	20	4	-	5	4%	61%	29%	6%	-	4/1	4/30	5/17	5/25	6/8
UPCLWR	98	8.2%	59	34	5	63%	37%	173	3	29	51	10	-	5	3%	31%	55%	11%	-	4/3	4/15	4/27	5/15	5/25
SFCLWR	92	7.7%	53	38	1	58%	42%	168	10	57	18	1	-	6	12%	66%	21%	1%	-	3/29	4/30	5/17	5/24	6/7
LOCLWR	99	8.3%	59	38	2	61%	39%	178	9	63	21	1	-	5	10%	67%	22%	1%	-	3/27	4/14	5/14	5/23	6/4
IMNAHA	80	6.7%	55	25	-	69%	31%	181	5	42	25	1	-	7	7%	58%	34%	1%	-	4/3	4/28	5/12	5/21	6/5
GRROND	257	21.4%	145	110	2	57%	43%	179	13	141	88	3	-	12	5%	58%	36%	1%	-	3/28	4/12	5/17	5/24	6/9
LSNAKE	159	13.3%	96	63	-	60%	40%	175	14	104	36	1	-	4	9%	67%	23%	1%	-	3/27	4/14	5/13	5/22	6/7
Total	**1200**		**705**	**480**	**15**	**59%**	**41%**	**178**	**81**	**626**	**389**	**48**	**2**	**54**	7%	55%	34%	4%	0%	**3/29**	**4/19**	**5/13**	**5/23**	**6/7**

Table 11. Summary of 2,176 Lower Granite Dam (LGR) **adult Chinook salmon** samples from **SY2012** assigned to a genetic stock using individual assignment based on **Snake River Chinook salmon SNP baseline v2**. Summaries of life-history diversity information (sex, length, saltwater age, and passage timing at LGR) for each genetic stock are shown. MJ = minijack.

			Sex					Length		Ocean (Saltwater) Age											Passage Timing				
			Frequency			Percentage				Frequency						Percentage					Quantiles				
Genetic Stock	Total Assignments	% Stock Composition	F	M	U	F	M	Mean Length All (cm FL)	Mean Length Exc. Jacks (cm FL)	MJ	1	2	3	4	U	MJ	1	2	3	4	5th	25th	Med	75th	95th
UPSALM	391	18.0%	176	200	15	47%	53%	78.9	79.5	-	35	187	148	1	20	-	9.4%	50.4%	39.9%	0.3%	5/19	5/25	6/10	6/24	7/15
MFSALM	367	16.9%	184	179	4	51%	49%	78.2	79.7	-	55	172	131	-	9	-	15.4%	48.0%	36.6%	-	5/18	5/21	5/28	6/14	7/6
CHMBLN	62	2.8%	25	36	1	41%	59%	69.4	72.1	-	8	48	5	-	1	-	13.1%	78.7%	8.2%	-	5/23	5/30	6/12	6/24	7/11
SFSALM	296	13.6%	144	147	5	49%	51%	75.4	76.9	-	16	198	80	-	2	-	5.4%	67.3%	27.2%	-	5/20	6/3	6/16	6/26	7/16
HELLSC	968	44.5%	498	451	19	52%	48%	73.0	73.7	-	135	617	175	1	40	-	14.5%	66.5%	18.9%	0.1%	5/16	5/20	5/26	6/13	7/4
TUCANO	14	0.6%	8	6	-	57%	43%	69.6	70.1	-	1	10	3	-	-	-	7.1%	71.4%	21.4%	-			-		
FALL	78	3.6%	37	34	7	52%	48%	75.0	84.8	4	15	23	29	3	4	5.4%	20.3%	31.1%	39.2%	4.1%			-		
Total	**2176**		**1072**	**1053**	**51**	**50%**	**50%**	**75.0**	**76.5**	**4**	**265**	**1255**	**571**	**5**	**76**	**0.2%**	**12.6%**	**59.8%**	**27.2%**	**0.2%**	**5/18**	**5/22**	**6/1**	**6/18**	**7/10**

Table 12. Summary of 2,108 Lower Granite Dam (LGR) **juvenile Chinook salmon** samples from **MY2012** assigned to a genetic stock using individual assignment based on **Snake River Chinook salmon SNP baseline v2**. Summaries of life-history diversity information (sex, length, freshwater age, and emigration timing at LGR) by genetic stock are shown.

			Sex Frequency			Sex Percentage		Length	Freshwater Age Frequency		Emigration Timing Quantiles				
Genetic Stock	**Total Assignments**	**% Stock Composition**	**F**	**M**	**U**	**F**	**M**	**Mean Length (mm FL)**	**0**	**1**	**5th**	**25th**	**Med**	**75th**	**95th**
UPSALM	265	12.6%	145	116	4	56%	44%	111.9	8	257	3/27	4/2	4/19	5/17	6/3
MFSALM	251	11.9%	128	120	3	52%	48%	108.0	6	245	3/27	4/10	4/27	5/18	5/27
CHMBLN	28	1.3%	17	10	1	63%	37%	107.4	-	28			-		
SFSALM	289	13.7%	151	137	1	52%	48%	107.9	6	283	3/27	4/3	4/21	5/18	5/28
HELLSC	757	35.9%	392	351	14	53%	47%	112.7	31	726	3/26	3/27	4/6	5/17	6/3
TUCANO	5	0.2%	4	1	-	80%	20%	110.2	-	5			-		
FALL	513	24.3%	252	244	17	51%	49%	102.2[a]	475	38	5/28	6/7	6/20	6/30	7/6
Total	**2108**		**1089**	**979**	**40**	53%	47%	**110.8[b]**	**526**	**1582**	**3/26[c]**	**3/30**	**4/18**	**5/18**	**6/1**

[a] Mean length for FALL genetic stock was calculated using Freshwater Age 0 smolts only.
[b] Mean length for Total was calculated using only sp/sum lineage genetic stocks (excludes FALL), both Freshwater Age 0 and 1.
[c] Emigration timing for Total was calculated using only sp/sum lineage genetic stocks (excluded FALL).

FIGURES

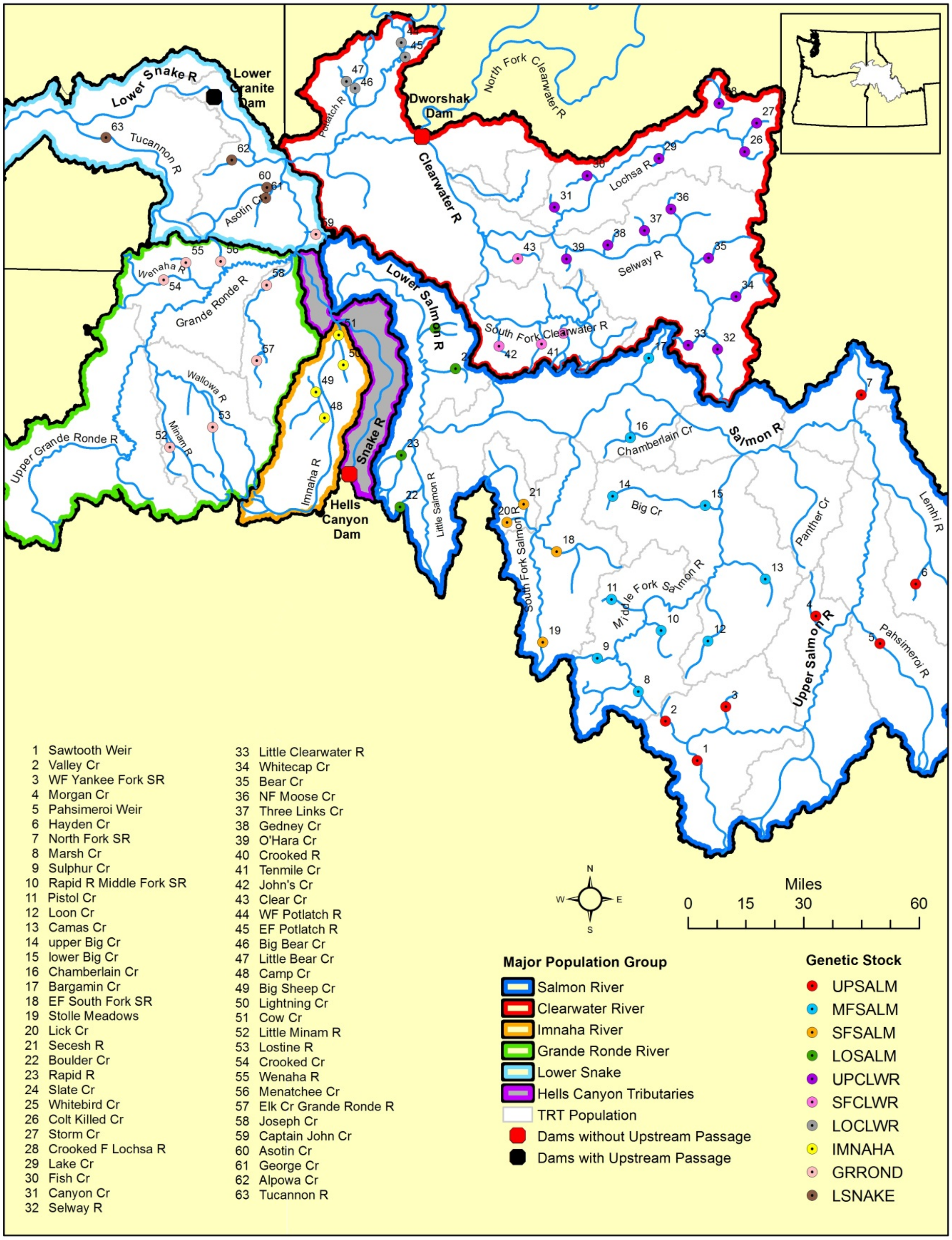

Figure 1. Natural origin steelhead baseline v2.0 consists of 63 collections located within 22 TRT populations. TRT populations are grouped into 10 Genetic Stocks spanning across 6 Major Population Groups. Collections are described in greater detail in Table 1.

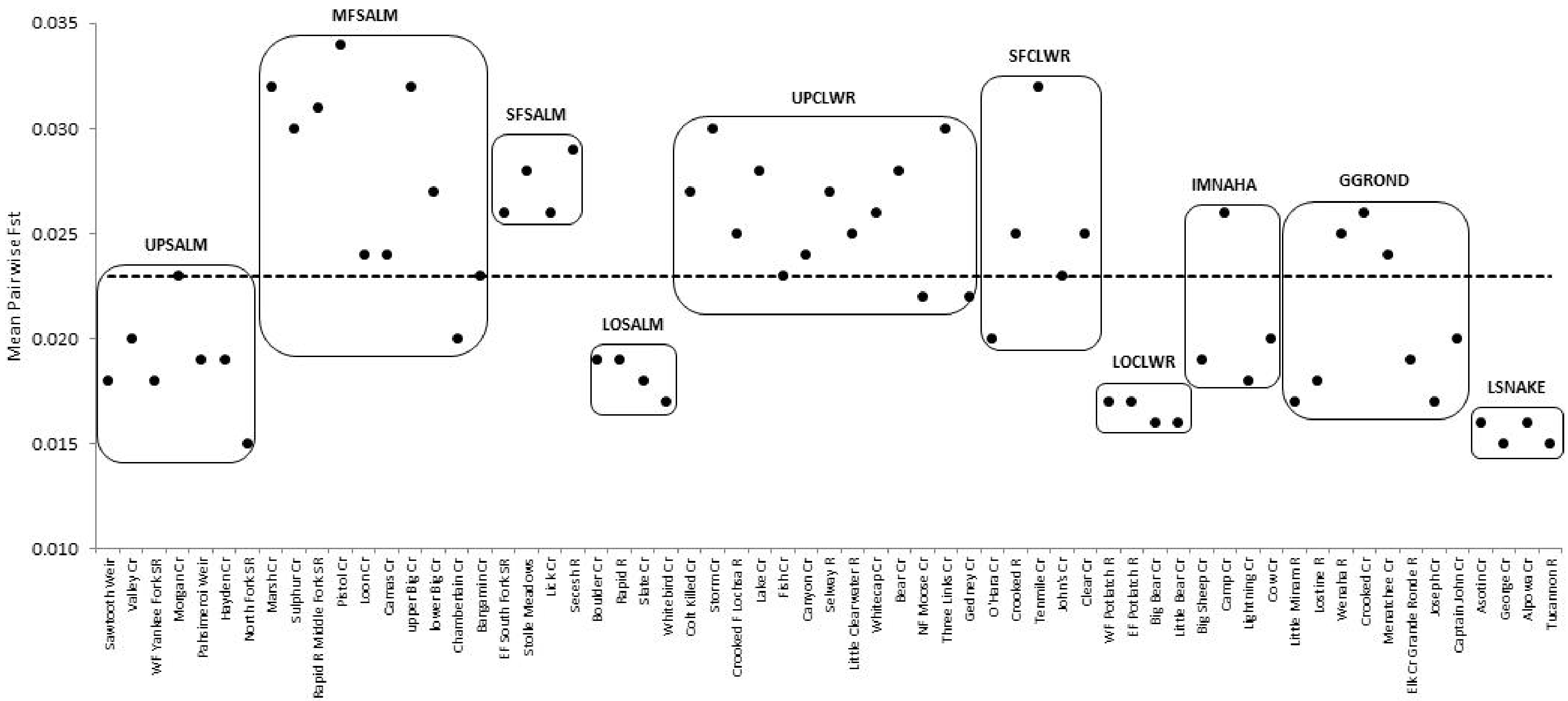

Figure 2. Mean pairwise F_{ST} estimates for Snake River steelhead baseline v2.0 collections. The dashed line is the average pairwise F_{ST} estimate across all collections. High mean F_{ST} estimates suggest high genetic differentiation relative to other collections in the baseline. Each genetic stock is circumscribed.

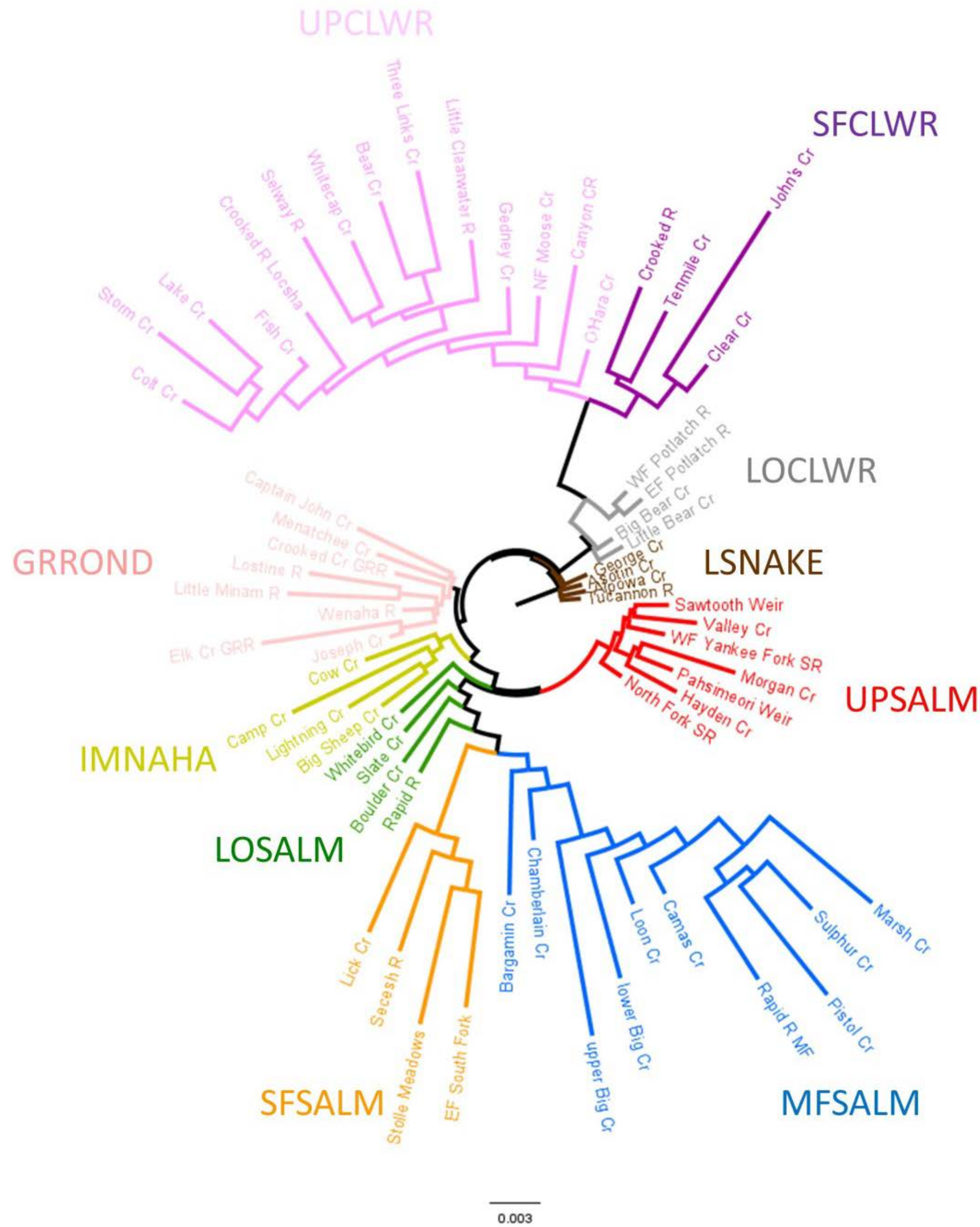

Figure 3. NJ-phylogram of Snake River basin steelhead baseline 2 collections based on Nei (1972) genetic distances.

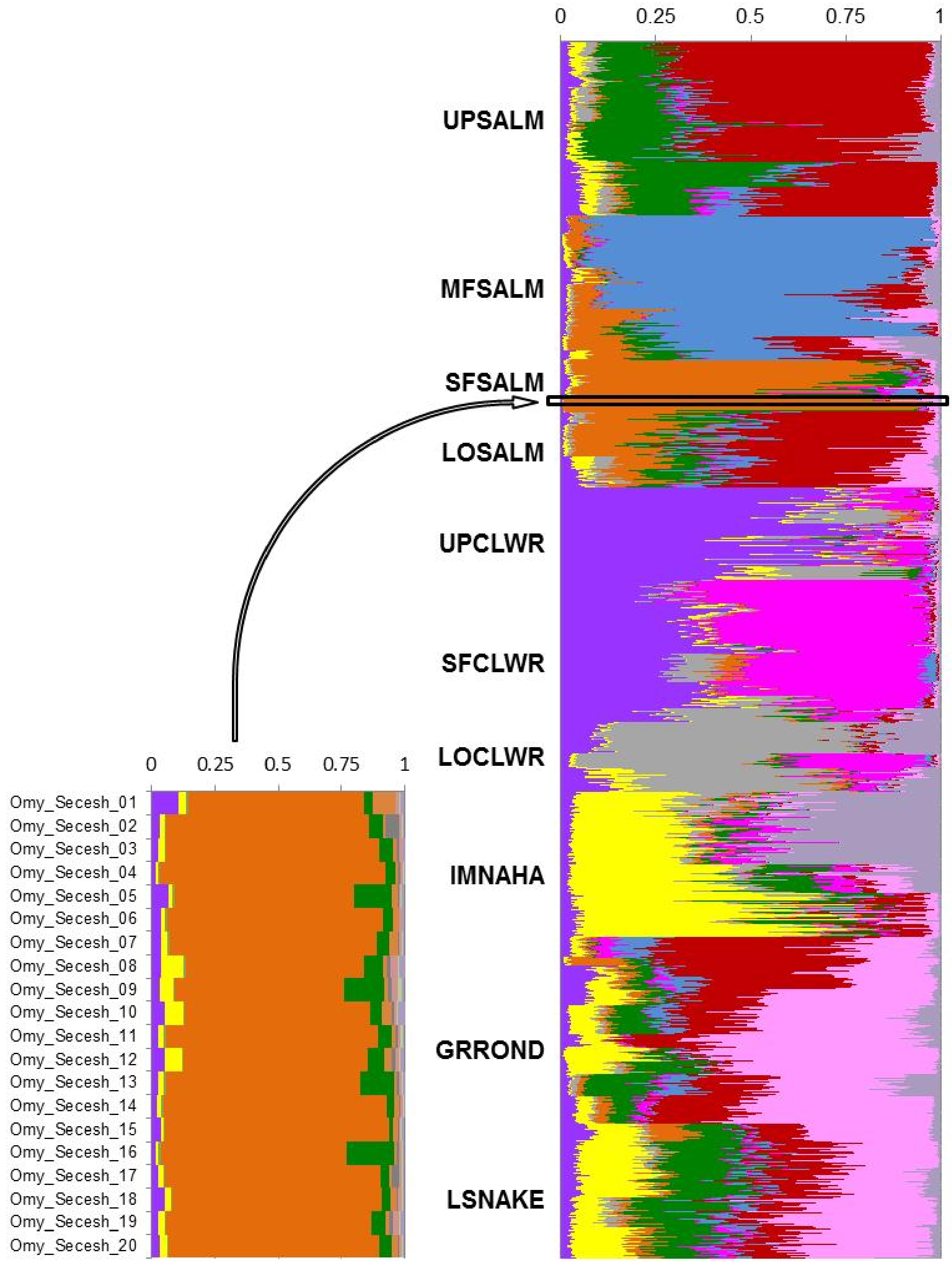

Figure 4 Histogram of STRUCTURE results for natural origin steelhead (K = 10). Results are based on admixture ancestral model. Each individual is represented by a single horizontal line divided into K colored segments that is proportional to each K inferred clusters. Individuals are arranged by genetic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

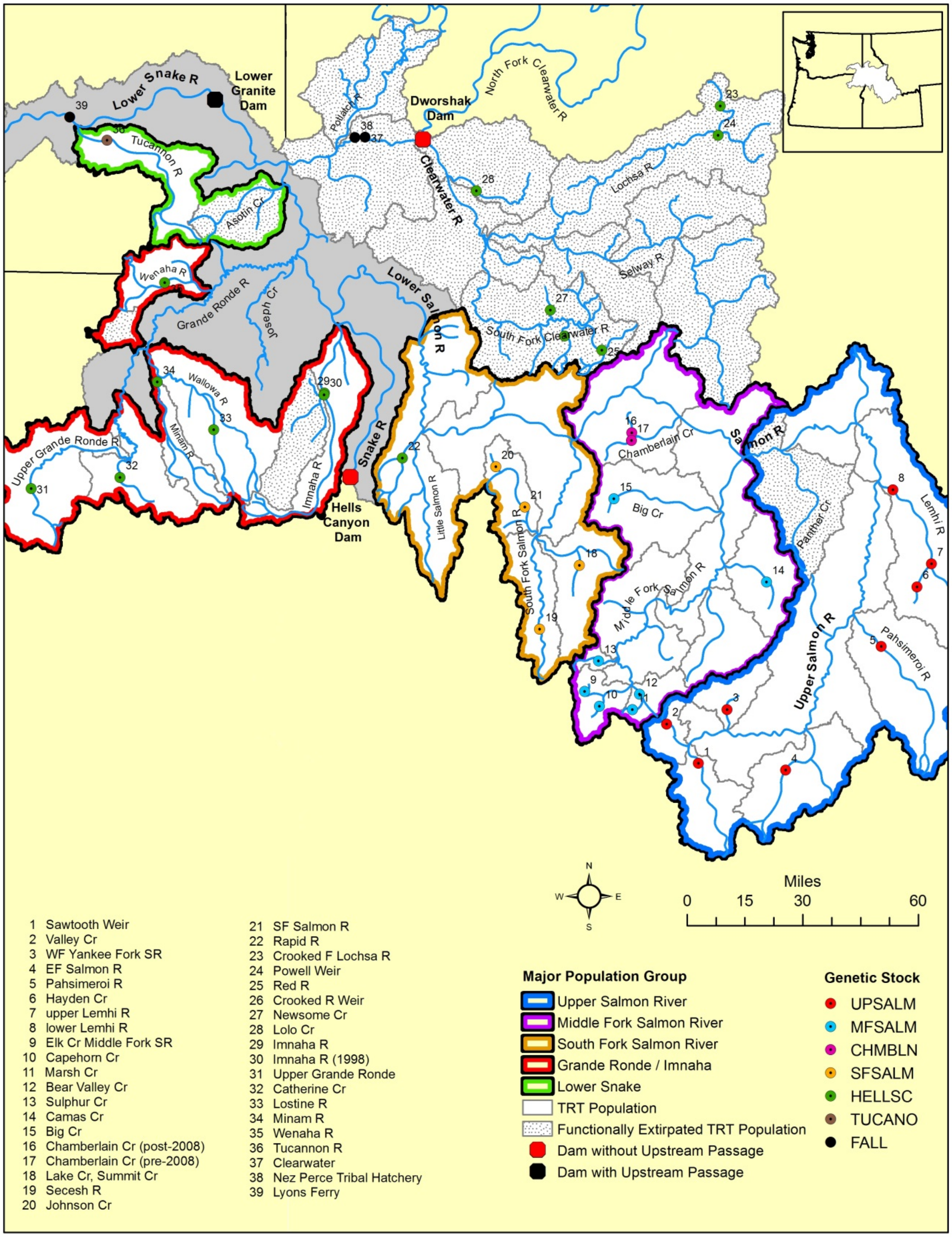

Figure 5. Natural origin Chinook salmon baseline version 2.0 consists of 39 collections within 24 TRT populations. TRT populations are grouped into 6 Genetic Stocks spanning across 5 Major Population Groups. Collections are described in greater details in Table 4.

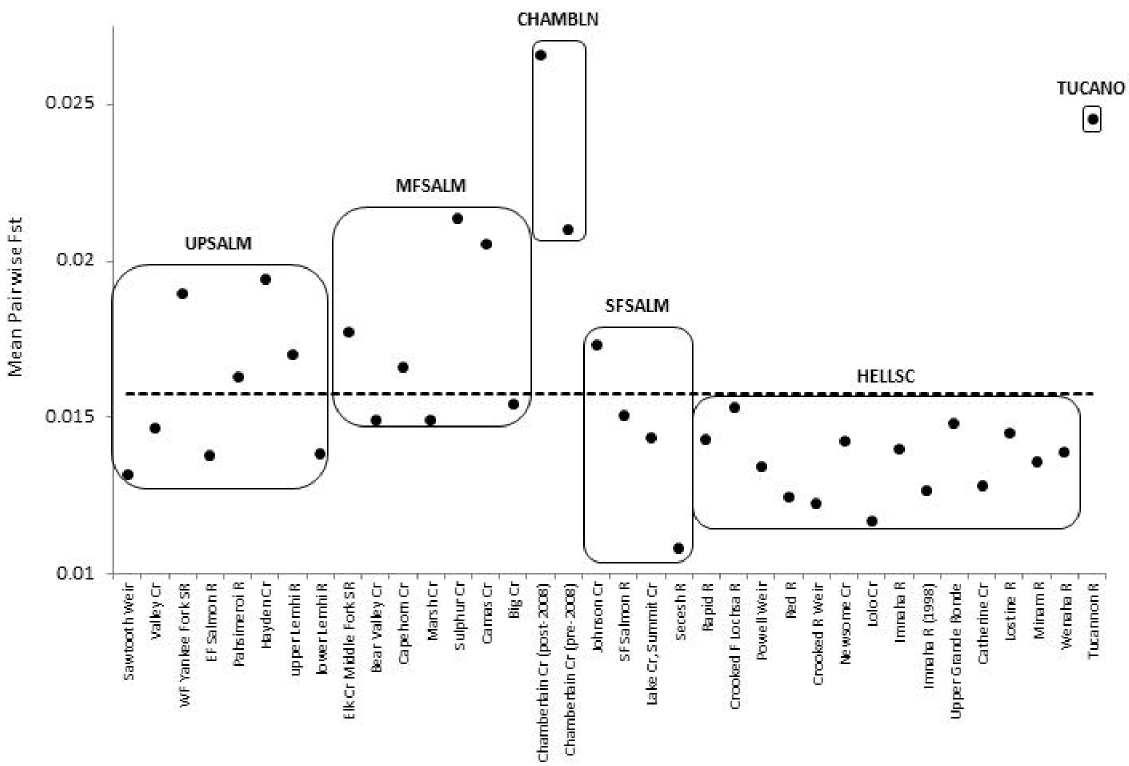

Figure 6. Mean pairwise F_{ST} estimates for Snake River Chinook salmon baseline v2.0 collections. The dashed line is the average pairwise F_{ST} estimate across all collections. High mean F_{ST} estimates suggest high genetic differentiation relative to other collections in the baseline. Each genetic stock is circumscribed.

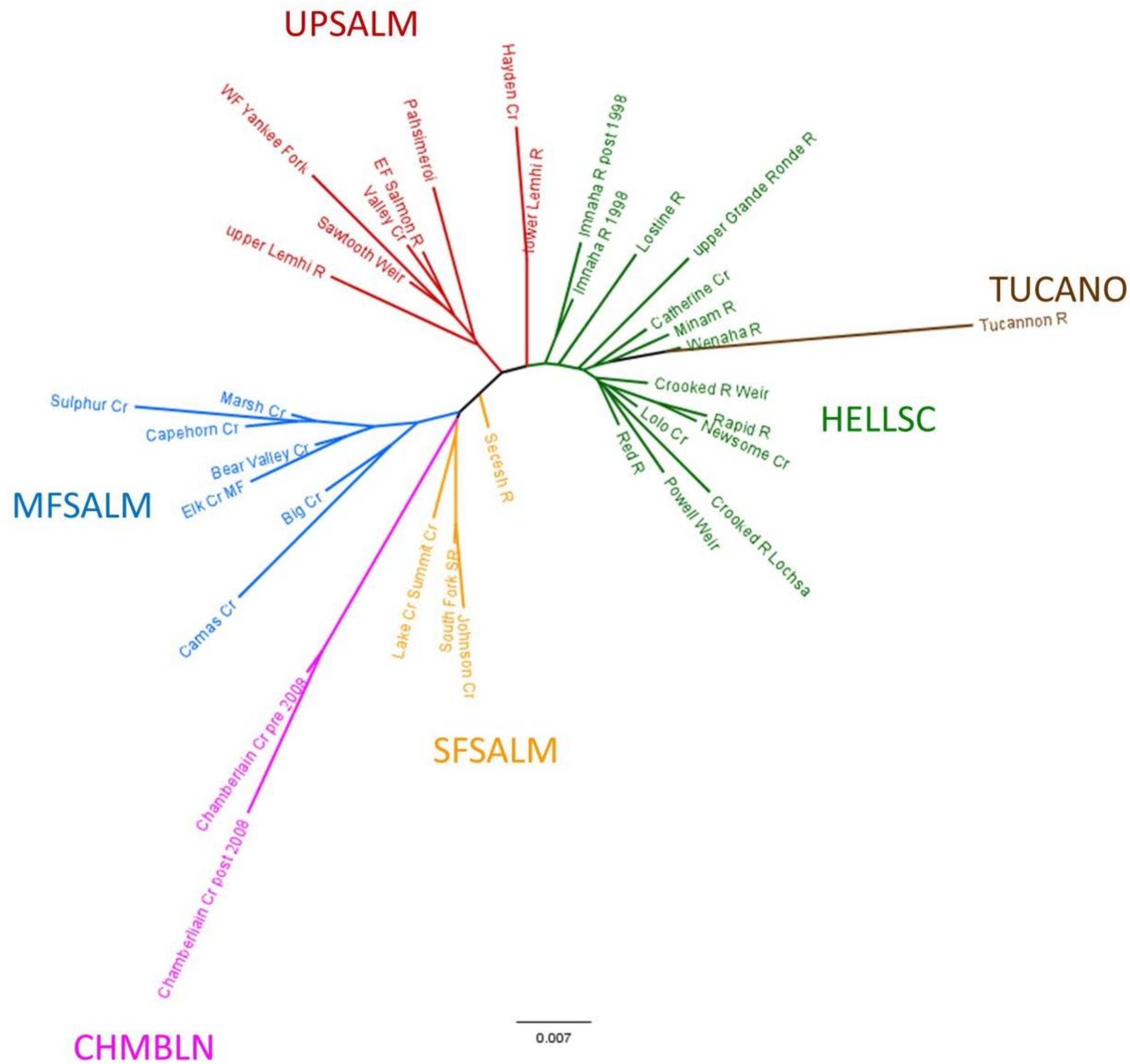

Figure 7. NJ-dendogram of Snake River basin Chinook salmon baseline v2 based on Cavalli-Sforza and Edwards (1967) genetic chord distances.

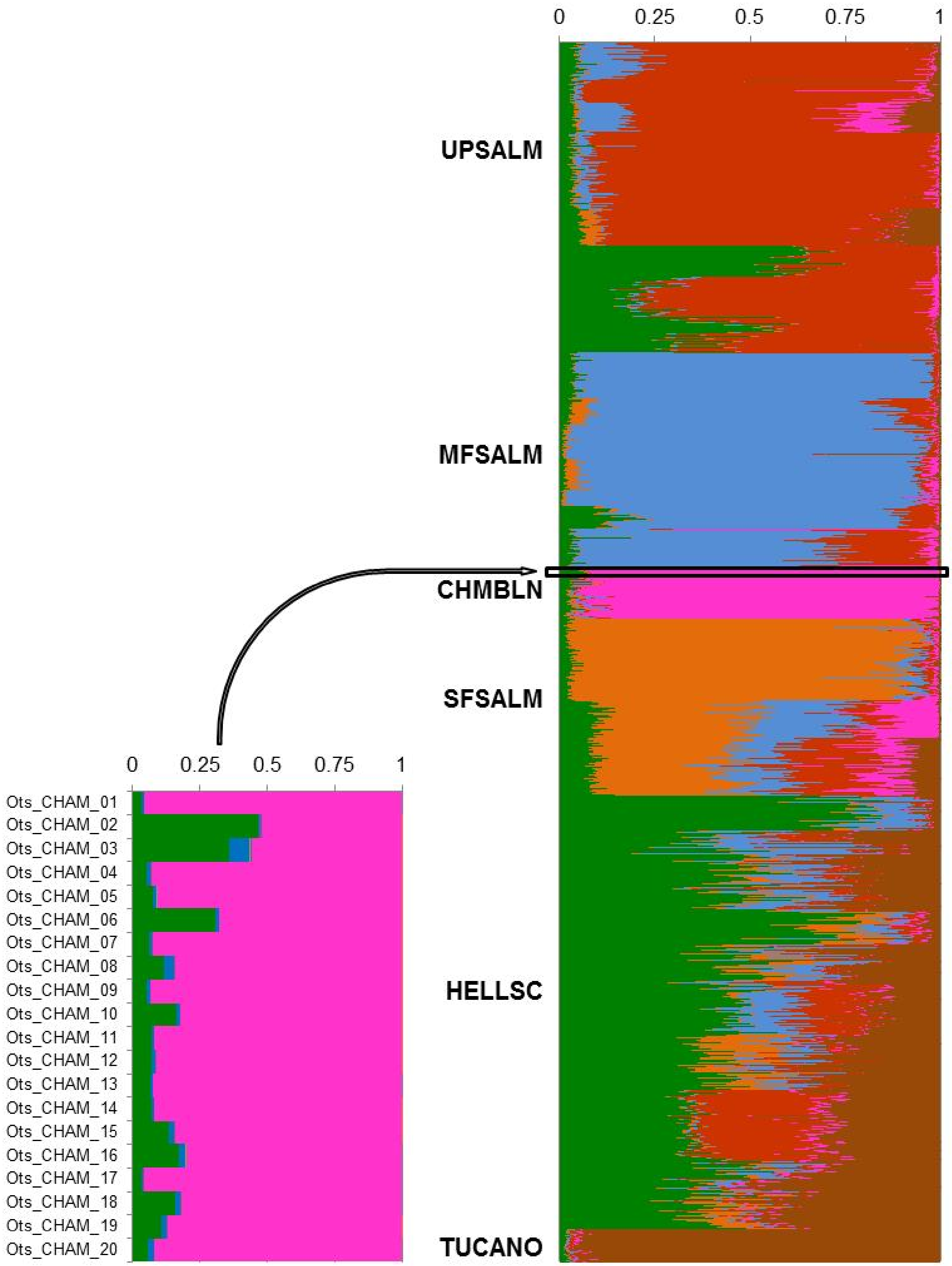

Figure 8 Histogram of STRUCTURE results for natural origin Chinook salmon (K = 6). Results are based on admixture ancestral model. Each individual is represented by a single horizontal line divided into K colored segments that is proportional to each K inferred clusters. Individuals are arranged by genetic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

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