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

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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 01/01/2014 to 12/31/2014 reporting period. Three objectives for the GSI project are addressed in this report: 1) the maintenance and evaluation of single nucleotide polymorphism (SNP) panels for high-throughput genotyping of steelhead and Chinook salmon in the Snake and Columbia river basins; 2) the updating, maintenance, and testing of SNP baselines to describe genetic variation and for use as a reference in conducting GSI for both species in the basin; and 3) the implementation of GSI to estimate genetic stock composition and life-history diversity of steelhead and sp/sum Chinook salmon passing Lower Granite Dam (LGR). For both species, panels of 192 SNPs have been identified 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 (v3) consists of 68 collections and 8,028 individuals. Chinook salmon baseline v3 consists of 57 collections and 6,151 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 2013 at LGR using v3 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 steelheadare 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., SY2013 steelhead are adults that migrated past LGR bewteen 7/1/12 - 6/30/13 and spawned in spring of 2013). 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 to document changes and ensure data integrity and consistency across collaborating laboratories. Data consistency among labs is especially important because genetic data produced as part of this project are deposited and shared in an open, standardized database www.FishGen.net.

Ackerman et al. (2012 and 2013) provide a detailed description of work done during the first three years of this project screening and evaluating 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. They also provided sequence (primer and probe) information and evaluated genetic diversity and divergence information for the 192 SNPs for each species using 63 steelhead collections and 39 Chinook salmon collections of natural-origin from across the Snake River basin.

In the fourth reporting year, we accomplished three goals related to objective 1 of the GSI project: (1) evaluate data consistency among labs, (2) make available SNP marker primer and probe sequences on www.FishGen.net and (3) evaluate genetic variation across current SNPs based on baseline collections from the Snake River. In 2013, we performed an annual check for data consistency among collaborating labs for the 192 *O. mykiss* and 192 Chinook salmon SNP marker panels (Ackerman et al. 2012 and 2013) Chinook salmon concordance was evaluated using a plate of samples from spring-summer Chinook. For 2014, we perfomed a similar evaluation of data consistency for fall (ocean-type) Chinook salmon. The goal is to ensure data integrity and to demonstrate that SNP genotype data is reproducible among labs regardless of genotyping methods. For goal 3, we evaluated genetic variation among the current SNP marker panels using version 3 of our Snake River steelhead and Chinook salmon baselines (see Section 2).

METHODS

SNP Standardization

In late 2013, we provided five collaborating labs an identical set of 93 DNA samples from Fall Chinook broodstock spawned at Lyons Ferry Hatchery. Each lab genotyped these samples using the Chinook salmon PBT v5.1 and GSI v1.1 SNP panels and scored genotypes using their scoring guidelines. Each lab sent final genotypes to the lead author to evaluate consistency among genotypes. We define the standard or reference genotype as the most genotype found in at least three out of five labs. The five participating labs include Abernathy Fish Technology Center, Columbia River Inter-Tribal Fish Commission, Idaho Department of Fish and Game Eagle Fish Genetics Lab, NOAA Northwest Fisheries Science Center, and Washington Department of Fish and Wildlife.

SNP Documentation

Primer and probe sequences for both steelhead and Chinook salmon PBT and GSI SNP marker panels are online at http://www.fishgen.net/WebPages/CustomMarkerSet/MarkerExport.aspx.

SNP Evaluation

Allele frequencies across populations for each SNP are calculated using GENALEX v6.5 (Peakall and Smouse 2006). We report the range of minor allele frequency (MAF) across all SNP baseline v3 collections for each SNP marker.

We test 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 is determined to be significantly out of linkage equilibrium if tests are significant ($\alpha = 0.05$) in more than one-half of baseline collections. If the test is significant between a pair of SNPs, the least informative of the SNP pair (according to F_{ST}) is removed to avoid violating the assumption of independence of loci in population genetics and GSI analyses.

For each SNP we calculate the number of baseline collections that the SNP deviate from Hardy-Weinberg expectation (HWE). The goal is to identify 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 test 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 are used for the MC algorithm (dememorization = 1,000; batches = 20; iterations per batch = 5,000). Critical values are 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} are calculated for each SNP using SNP baseline v3 samples and GENALEX v6.5.

RESULTS

SNP Standardization

A total 17,472 (91 samples x 192 SNPs) genotypes were compared across the 5 labs. Two samples were excluded from analysis due to high level of missing data. Genotype concordance among labs for fall Chinook salmon was 99.76%. There were 41 discrepancies where at least two different genotypes were found. For these we encouraged each lab to review scoring guides to potentially correct any discrepancies identified. Eighteen of these 41 discrepancies had no majority genotype. All labs are asked to void data. For the remaining 23 discrepancies, all had a majority genotype. Labs with discrepant genotype are asked to change their calls to the standard genotype or void their scores. SNP-specific error rates are available from the primary author by request.

SNP Documentation

Primer and probe sequences for steelhead and Chinook salmon are now available on www.FishGen.net: CRITFC/IDFG Steelhead 192 GSI v4.1 + PBT v5.1 & CRITFC/IDFG Chinook salmon 192 GSI v1.1 + PBT v5.1). They can also be downloaded directly from http://www.fishgen.net/WebPages/CustomMarkerSet/MarkerExport.aspx

SNP Evaluation

SNP markers are analyzed using Snake River SNP baselines v3 (see section 2). Tables 1 and 2 summarize SNPs screened for steelhead and sp/sum Chinook salmon, respectively. Summaries for each SNP include minor allele frequency (MAF) range, heterozygosity (H_E), fixation index (F_{ST}), Hardy-Weinberg Equilibrum (HWE, heterozygote excess and deficit), and linkage disequilibrium (LD).

DISCUSSION

SNP Standardization

Our test of SNP genotyping standardization indicated greater than 99.76% data concordance for Fall Chinook salmon among the five collaborating labs. The genotype consistency observed for Fall Chinook salmon is similar to that observed for Spring/Summer Chinook observed from the previous year (99.9%).

SNP Documentation

Primer and probe sequences for Taqman assays used by our lab for *O. mykiss* and Chinook salmon genotyping are available on the new genetic data repository www.FishGen.net. They can be downloaded at http://www.fishgen.net/WebPages/CustomMarkerSet/MarkerExport.aspx. In addition, our DNA extraction and SNP genotyping protocols can be found at http://www.monitoringmethods.org/method/details/1356. Our goal is to be transparent in our methods and provide greater access of information on our genotyping methods to the broader research community.

SNP Evaluation

Steelhead: We use baseline v3 to screen 191 SNP markers (95 – PBTv5.1 & 96 – GSIv4.1) and a sex-specific assay (Campbell et al. 2012). Based on the same criteria established in prior reporting years, we chose a subset of the full panel, 185 SNP markers, to evaluate the baseline. Six markers are excluded to create the 185 SNP marker working panel. They include three hybrid markers (Omy_Omyclmk43896, Omy_myclarp404111 and Ocl_gshpx357), two lesser informative linked marker pairs (Omy_Il1b198 and Omy_mapK3103) and one poor performing marker (Omy_IL1b163).

Chinook salmon: We use baseline v3 to screen at 191 SNP markers (95 – PBTv5.1 & 96 – GSIv1.1) and a sex-specific assay (Campbell et al. 2012). Based on the same criteria established in prior reporting years, we chose a subset of the full panel to create the 180 SNP marker working panel. Eleven markers are excluded, and they include three lesser informative linked markers (Ots_Tnsf, Ots_FGF6A & Ots_hsc71-3'-488) and eight uninformative markers (Ots_CCR7, Ots_GST375, Ots_LWSop638, Ots_RAS1, Ots_TNF, Ots_u07-64.221,

Ots_unk8200-45 & Ots_zP3b-215). Note: the eight markers uninformative in the Snake River basin are variable and information elsewhere in the coastwide range of Chinook salmon.

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

INTRODUCTION

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

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

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

Maintaining and updating genetic baselines for GSI is critical to the power and accuracy of GSI, which can diminish if genetic stocks (reporting groups) are not represented accurately. 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 geneticstocks (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, TRT 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 www.FishGen.net easier in the future.

Statistical Analyses

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

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

We performed self-assignment tests using gsi_sim (Anderson et al. 2008, Anderson 2010) to evaluate the accuracy of the Snake River SNP baselines 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 created radial neighbor-joining (N-J) dendrograms for both steelhead and Chinook salmon to visualize the genetic relationship among baseline populations. The radial N-J dendrograms were based on pairwise Nei's (1972) genetic distances, and the N-J dendrogram was based on pairwise Cavalli-Sforza and Edwards (1967) genetic chord distances calculated using GENDIST (PHYLIP v3.6.7; Felsenstein 1993). Pairwise genetic distances were used to construct the trees in NEIGHBOR (PHYLIP v3.6.7). The consistency of the dendrogram

topologies was estimated using 1,000 bootstrap replicates in SEQBOOT (PHYLIP v3.6.7). The final N-J dendograms were constructed with FigTree (Rambaut 2012).

We used STRUCTURE 2.3.4 (Pritchard et al. 2000) to infer population structure using genetic clustering methods. Default model parameters of admixture and correlated allele frequencies were used; these parameters account for recent gene flow among populations and allow some flexibility for linkage disequilibrium within populations. These default settings are most flexible for dealing with real biological phenomena (Pritchard et al. 2010) and are likely most appropriate for steelhead and Chinook salmon. Within the admixture model, we used the LOCPRIOR option in STRUCTURE that allows the user to use sampling locations as prior information (Hubisz et al. 2009). The LOCPRIOR version of the admixture model works by modifying the prior distribution for each individual's population assignment; the new prior distributions allow the proportion of individuals assigned to a particular cluster to vary by location. In total, there were a total of 10 'sampling locations' for steelhead and six for 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.

RESULTS

Steelhead: Baseline v3 consists of 139 sample collections totaling 8,028 samples. Temporal collections from geographically proximate locations are pooled resulting in 68 baseline collections, of which 47 contain temporal collections. In total, 3,912 new samples from 57 sample collections are added, an increase of 95% compare to v2. Of these new additions, 1,878 samples (48%) are returning adults sampled at Lower Granite Dam in 2010, 2011, and 2012. These adults were last detected at an instream PIT tag detection array (IPTDS). They are assumed to spawn or reside in the stream of their last detection. For the first time, baseline v3 has at minimum of one collection representing all 23 TRT populations and covering all 5 MPGs (Table 3). The geographic distribution of these collections are shown in Figure 1 along with their TRT populations, genetic stocks, and MPGs. Note, not all samples from v2 were included in v3; we removed a small number of collections. We removed old collections, collections that did not appear to accurately reflect the true genetic structure of the populations, or collections from populations with low abundance that did not contribute greatly to the baseline. Removed collections include Whitebird Creek 2000 and 2001, Johns Creek 2000, and Cow Creek 2000, for a total of 183 samples.

Based on the 185 SNP marker panel, the mean pairwise F_{ST} across 68 collections is 0.020 (Figure 2), and the average heterozygosity is 29.7%. Average population-specific F_{ST} range from 0.013 (Asotin Cr) to 0.034 (Lake Cr - Salmon R). Heterozygosity range from the low of 27.4% (Crooked R - South Fork Clearwater R) to the high of 32.6% (upper Lemhi R/IPTDSs - HYC, KEN, and LRW). Thirty-one of 68 collections have 10% or more SNPs not in Hardy-Weinberg proportion, with all showing deficiency (Table 3). Collections from terminal drainages, on average, are more highly differentiated and possess lower heterozygosity relative to collections located further down the drainage or that have been affected by past fish management practices, a trend observed in both baseline v1 and v2.

Steelhead Genetic Stock Identification

For the new baseline, we choose to maintain the same genetic stocks established in v1 and v2 for continuity and for comparisons. Genetic distance and STRUCTURE analyses of v3 support our decision to maintain existing genetic stocks (Figure 3 & 4). In addition, we choose to pool geographically proximate collections with low genetic differentiation; e.g., Sawtooth/IPTDS (STL) and Valley Cr/IPTDS-VAL are pooled to become Sawtooth. The result is a reduction from 68 collections down to 47 collections. Below is a summary of steelhead GSI baseline v3.

Genetic Stock	# of TRT Population	# of collection	# of sample
UPSALM	5	6	847
MFSALM	4	7	1236
SFSALM	2	3	889
LOSALM	1	2	222
UPCLWR	2	6	942
SFCLWR	2	5	486
LOCLWR	1	5	773
IMNAHA	1	4	608
GRROND	3	6	1030
LSNAKE	2	3	808
Total	23	47	7841

Although v3 is nearly twice as large in term of sample size, self-assignment results suggest comparable scores to that of v2 (Table 4a & 5b). Assignments are most accurate for the upper Clearwater R (UPCLWR), followed by the Middle Fork Salmon R (MFSALM) and South Fork Salmon R (SFSALM). Assignments are least accurate for genetic stocks geographically located lower in the drainage (e.g. lower Snake R (LSNAKE) and lower Salmon R (LOSALM)).

Chinook salmon: Baseline v3 consists of 151 sample collections totaling 6,151 samples. Temporal collections from geographically proximate locations are pooled resulting in 57 baseline collections, of which 47 contain temporal collections. In total, 2,824 new samples from 41 collections are added, an increase of 85% compare to v2. Of these new additions, 1,547 samples (55%) are returning adults sampled at Lower Granite Dam in 2010, 2011, and 2012. These adults were last detected at an IPTDS. They are assumed to spawn or reside in the stream of their last detection. Baseline v3 has at least one collection in 31 out of 41 TRT populations (Table 5). For the remaining 10 unrepresented TRT populations, seven are in the functionally extirpated Clearwater R draingage. Lookingglass Creek and Middle Fork Salmon above and below Indian Creek (MFUMA & MFLMA) round out the remaining three unrepresented TRT populations. The geographic distribution of these collections is shown in Figure 5 along with their TRT populations, genetic stocks and MPGs. Not all samples in this baseline are additions, however. We choose to remove an old collection, Imnaha 1998 (92 samples), and replace it with a more contemporary collection, Imnaha 2010 (53 samples).

Based on the 180 SNP marker panel and excluding three fall Chinook collections, the mean pairwise F_{ST} across 54 collections is 0.014 (Figure 5), and the average heterozygosity is 22.8%. Average F_{ST} range from 0.009 (upper South Fork Salmon R) to 0.025 (Chamberlain Cr). Heterozygosity range from the low of 20.6% (Sulphur Cr) to the high of 26.4% (Wenaha R).

Thirteen of 57 collections have 10% or more markers not in Hardy-Weinberg proportion, with all showing deficiency (Table 5).

Chinook salmon Genetic Stock Identification

For the new baseline, we maintained the same genetic stocks established in v1 and v2 for continuity and for comparisons. Genetic distance and STRUCTURE analyses of v3 support our decision to maintain existing genetic stocks (Figure 7 & 8). In addition, we chose to pool geographically proximate collections with low genetic differentiation; e.g., Decker Flat, Sawtooth Weir, and Sawtooth/IPTDS (STL) are pooled to become Sawtooth. The result is a reduction from 57 collections down to 30 collections, which are now structured more similar to extant TRT populations. A summary of the GSI baseline v3 is below.

Genetic Stock	# of TRT population	# of Collection	# of sample
UPSALM	9	8	1240
MFSALM	6	7	1070
CHMBLN	1	1	219
SFSALM	3	3	1315
HELLSC	11	8	1638
TUCANO	1	1	81
FALL	N/A	2	318
Total	31	30	5881

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

DISCUSSION

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

Baseline v3 marks the fourth year in our effort to maintain and update the genetic composition of steelhead and Chinook salmon in the Snake R basin. For v3, we nearly double the number of samples available for each baseline, with 95% increase for steelhead and 85%

increase for Chinook salmon. Approximately 50% of all new samples are of returning adults sampled at Lower Granite Dam from 2010 to 2012 that were later detected at an IPTDS. We suspect that many contribute to the next generation; consequently, we want to include them in the baseline. Genetic structure analyses and GSI self-assignment tests confirm our decision. Regarding the geographic distribution for steelhead, all 23 TRT populations for the first time have at least a collection represented in the baseline. For Chinook salmon baseline, we added collections to 8 new TRT populations, which now accounts for 31 out of a total 41 TRT populations. Seven of 10 unrepresented TRT populations are in the functionally extirpated Clearwater R drainage above Dworshak Dam, a part of the HELLSC genetic stock. The remaining three TRT populations are located in the Grande Ronde drainage (Lookingglass Cr) and Middle Fork Salmon R (Middle Fork Salmon R above and below Indian Cr). We will attempt to include these populations in future baselines, particularly for the remaining three TRT populations. Although baseline v3 nearly double in size and are more geographically represented for both species, genetic analyses show high similarity to prior versions.

GSI baseline: For v3 baselines, we elected to pool many geographically proximate collections for GSI applications. These collections were not highly differentiated, and their F_{ST} are typically 3 to 4 times lower than geographically separated collections. Pooled collections better approximate the TRT populations outlined in ICTRT (2003). A pooled collection can consist of two or more temporal and/or adjacent creek collections. Pooling reduced the steelhead baseline collections from 68 to 47 and the Chinook salmon baseline collections from 57 to 30. Our decision to simplify the GSI baseline is confirmed by the self-assignment test scores, where both v2 and v3 scored comparably.

We would like to thank the Integrated Status and Effectiveness Monitoring Project (ISEMP; BPA Project 2003-017-00) 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. 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, allow estimation of population growth rates; and both abundance and productivity metrics provide indicators of the resiliency and viability of populations. Estimates of these metrics at the genetic stock or MPG level is information that fisheries managers can use to achieve sustainable harvest of larger populations, while protecting weaker stocks and the biodiversity within them.

However, population level or MPG assessments of abundance and productivity for ESA listed Snake River steelhead and spring/summer Chinook salmon can be particularly difficult (see Report Introduction). Specific data on Snake River steelhead and Chinook salmon MPGs and populations are lacking, particularly key parameters such as population abundance, age composition, genetic diversity, recruits per spawner, and survival rates (ICTRT 2003). GSI is one potential means for estimating these parameters at a finer-scale; perhaps at the level of MPG, genetic stock (reporting group), or population. GSI uses multi-locus genotype data from reference populations (representing potential contributing stocks) as a baseline and a complimentary set of genotype data from mixtures of fish of unknown origin to estimate stock proportions within the mixture and to estimate stock of origin of individual fish (Shaklee et al. 1999). In Section 2, we presented the SNP baselines used for GSI in the Snake River basin. In Section 3, we use complementary sets of genotype data from adults sampled at the Lower Granite Dam (LGR) adult trap and juveniles sampled at the LGR juvenile bypass facility to estimate the genetic stock of origin of upstream migrating adults and emigrating juveniles. We then evaluate life-history diversity (sex, length, age, migration timing) of individuals assigning to the various genetic stocks (e.g., Moran et al. 2014).

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. (2014) and citations within. The juvenile trap is located on the LGR juvenile bypass system. The trap captures a systematic sample of fish by operating two trap gates according to a pre-determined sample rate. The sample rate determines how long the trap gates remain open, up to six times per hour. The trap is operational 24 hours per day and fish are processed every morning. Sample rate is predetermined daily to collect 250-750 fish per day (all species combined) and is based on the expected number of fish entrained in the bypass system that day.

Fish Handling Protocols (Adults and Juveniles)

Fish handling procedures are detailed in Schrader et al. (2013) for adults and Copeland et al. (2014) 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. (2014).

Genetics Laboratory Protocol

Laboratory protocols for DNA extraction, amplification, and SNP genotyping are detailed in Section 2. SY2013 steelhead adults and MY2013 steelhead juveniles were processed at the CRITFC Genetics Lab in Hagerman, Idaho. SY2013 Chinook adults and MY2013 Chinook juveniles were processed at IDFG's Eagle Fish Genetics Lab in Eagle, 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. 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 SY2013 adults and MY2013 juveniles. All MY2013 hatchery juvenile cohorts were interrogated via PBT. For SY2013, 1-ocean, 2-ocean, and 3-ocean steelhead and spring/summer Chinook were interrogated via PBT. In using PBT to evaluate all the fish, we are better able to identify putative natural-origin (unclipped, unmarked) fish that are truly of hatchery origin. Any individuals identified as unmarked hatchery origin adults with a PBT were removed from the dataset before performing GSI and evaluating life-history diversity of genetic stocks.

Genetic Stock Identification

Individual assignment (IA) tests were conducted for SY2013 adults and MY2013 juveniles (both species) using the Snake River SNP baselines v3 described in Section 2. SNP allele frequency estimates from baseline collections are the reference information for IA tests. Fish sampled at the LGR adult and juvenile trapping facilities were genotyped at the same SNPs and multi-locus genotype data were used to assign individual fish back to their estimated population (and genetic stock) of origin (Pella and Milner 1987, Shaklee et al. 1999). In IA, the probability that each fish originates from a baseline population is calculated based on the likelihood that the individual's genotype belongs to that population, given baseline allele frequency estimates. Individual population estimates were first calculated and then summed into genetic stock estimates (allocate-sum procedure; Wood et al. 1987). Genetic stocks (aka reporting groups) are assemblages of reference (baseline) populations grouped primarily by genetic and geographic similarities and secondarily by political boundaries and/or management units (Ackerman et al. 2011). IA procedures assign an individual's genotype to the reporting group from which it is most likely to have originated.

Ten genetic stocks were used for steelhead 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:

- SY2013 steelhead adults
- SY2013 Chinook adults
- MY2013 steelhead juveniles
- MY2013 Chinook juveniles

RESULTS

We inventoried 12,911 samples from SY2013 adults and MY2013 juveniles (Table 7). Of samples inventoried, 11,797 were queued for genotyping. Of queued samples, 69 (0.6%) failed genotyping and 11,728 (99.4%) genotyped successfully (Table 7). The 11,728 samples all had an intact adipose fin; however, 1,643 (14.0%) had a PBT. We performed IA on the remaining, 10,085 samples. Those samples are summarized below and in Table 7.

SY2013 Steelhead Adults

We inventoried 4,482 unclipped (no adipose, ventral, or pelvic fin clips) adult steelhead samples for SY2013 (Table 7). Of the 4,482 unclipped steelhead, 3,878 (86.5%) were phenotypically wild (no dorsal or ventral fin erosion); 3,876 were queued for genotyping and 3,873 were genotyped successfully. Of those genotyped, 452 (11.7%) had a PBT and 3,418 (88.3%) were assigned a genetic stock via IA. Three fish were not assigned a PBT or genetic stock.

Of the 4,482 steelhead, 604 (13.5%) were phenotypically identified as hatchery origin due to dorsal/ventral fin erosion; 603 were queued for genotyping and 602 were genotyped successfully. Of those genotyped, 512 (85.0%) had a PBT and 90 (15.0%) were assigned a genetic stock via IA (Table 7).

Life-history diversity information (sex, length, age, passage timing) for the 3,508 unclipped steelhead adults that were assigned a genetic stock (without a PBT) is summarized in Table 8. Of the 3,508 fish, 581 (16.6%) were assigned to UPSALM, 302 (8.6%) to MFSALM, 143 (4.1%) to SFSALM, 107 (3.1%) to LOSALM, 202 (5.8%) to UPCLWR, 260 (7.4%) to SFCLWR, 355 (10.1%) to LOCLWR, 308 (8.8%) to IMNAHA, 830 (23.7%) to GRROND, and 420 (12.0%) to LSNAKE.

MY2013 Steelhead Juveniles

We inventoried 1,807 unclipped juvenile steelhead samples for MY2013 (Table 7); all samples were queued for genotyping. Of samples queued, 1,803 (99.8%) were genotyped

successfully. Of those genotyped, 48 (2.7%) had a PBT and 1,755 (97.3%) were assigned a genetic stock via IA.

Life-history diversity information for the 1,755 emigrating steelhead smolts that were assigned a genetic stock is summarized in Table 9. Of the 1,755 steelhead smolts assigned a genetic stock, 296 (16.9%) were assigned to UPSALM, 137 (7.8%) to MFSALM, 62 (3.5%) to SFSALM, 64 (3.6%) to LOSALM, 186 (10.6%) to UPCLWR, 186 (10.6%) to SFCLWR, 166 (9.5%) to LOCLWR, 165 (9.4%) to IMNAHA, 338 (19.3%) to GRROND, and 155 (8.8%) to LSNAKE.

SY2013 Chinook Adults

We inventoried 3,494 unclipped adult Chinook salmon samples for SY2013 (Table 7); 3,490 were queued for genotyping and 3,461 (99.2%) were genotyped successfully. Of those genotyped, 456 (13.2%) had a PBT and 3,005 (86.8%) were assigned a genetic stock via IA.

Life-history diversity information for the 3,005 Chinook adults that were assigned a genetic stock (without a PBT) is summarized in Table 10. Of the 3,005 adult Chinook salmon assigned a genetic stock, 624 (20.8%) assigned to UPSALM, 603 (20.1%) to MFSALM, 121 (4.0%) to CHMBLN, 492 (16.4%) to SFSALM, 1,086 (36.1%) to HELLSC, 17 (0.6%) to TUCANO, and 62 (2.1%) to FALL.

MY2013 Chinook Juveniles

We inventoried 3,128 unclipped juvenile Chinook salmon for MY2013; 1,468 were yearlings and 1,660 were subyearlings (Table 7).

All 1,468 yearling Chinook salmon were queued for genotyping and 1,439 (98.0%) of those were genotyped successfully. Of the 1,439 genotyped, 174 (12.1%) had a PBT and 1,265 were assigned a genetic stock via IA.

Of the 1,660 subyearlings inventoried, 553 were queued for genotyping and 550 (99.5%) of those were genotyped successfully. Of the 550 genotyped, 1 (0.2%) had a PBT and 549 (99.8%) were assigned a genetic stock via IA.

Life-history diversity information for the 1,814 Chinook salmon smolts assigned a genetic stock is summarized in Table 11. Of the 1,814 Chinook salmon smolts assigned a genetic stock, 236 (13.0%) assigned to UPSALM, 174 (9.6%) to MFSALM, 11 (0.6%) to CHMBLN, 116 (6.4%) to SFSALM, 579 (31.9%) to HELLSC, 4 (0.2%) to TUCANO, and 694 (38.3%) 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 to estimate abundance and life-history diversity metrics at the genetic stock and/or MPG scale. PIT tagging of adults is conducted by the Integrated Status And Effectiveness Monitoring Project (ISEMP; BPA Project 2003-017-00); detection data of those adults at Instream PIT Tag Detection Systems (IPTDS) throughout the Snake River basin are used in a Bayesian branching model to provide reliable and unbiased estimates of abundance at the population level (QCI 2013;

Ackerman et al. 2014). A multi-agency collaboration has recently been initiated to utilize information generated from these two innovative technologies (SNP genotyping for PBT and GSI and IPTDS insfrastructure 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.

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. Summary of 185 SNPs (Appendix A and Hess et al. 2013) screened among 68 steelhead collections in Snake River baseline v3.0. 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		
Locus	**Panel**	**MAF Range**	**He**	**Fst**	**Deficient**	**Excess**	**LD**
M09AAC.055	GSI v4.1	(0.000 - 0.232)	13.7%	0.043			
M09AAD.076	PBT v5.1	(0.267 - 0.710)	48.7%	0.030	6	1	
M09AAE.082	PBT v5.1	(0.083 - 0.543)	34.1%	0.048			
M09AAJ.163	PBT v5.1	(0.116 - 0.564)	41.2%	0.041			
OMGH1PROM1-SNP1	GSI v4.1	(0.000 - 0.370)	16.6%	0.085			
OMS00002	PBT v5.1	(0.258 - 0.640)	45.9%	0.022			
OMS00003	GSI v4.1	(0.033 - 0.276)	26.3%	0.016	4	3	
OMS00006	PBT v5.1	(0.264 - 0.624)	48.7%	0.028			
OMS00008	GSI v4.1	(0.000 - 0.424)	28.2%	0.072			
OMS00013	GSI v4.1	(0.000 - 0.202)	13.5%	0.036			
OMS00014	GSI v4.1	(0.000 - 0.098)	2.8%	0.032			
OMS00015	GSI v4.1	(0.000 - 0.178)	11.0%	0.034			
OMS00017	GSI v4.1	(0.080 - 0.620)	39.2%	0.065			
OMS00018	GSI v4.1	(0.035 - 0.318)	19.1%	0.041			
OMS00024	PBT v5.1	(0.215 - 0.750)	45.3%	0.055			
OMS00030	GSI v4.1	(0.000 - 0.182)	14.9%	0.030			
OMS00039	PBT v5.1	(0.279 - 0.678)	49.0%	0.021			
OMS00048	GSI v4.1	(0.013 - 0.310)	20.5%	0.031			
OMS00052	GSI v4.1	(0.047 - 0.353)	29.8%	0.022			
OMS00053	PBT v5.1	(0.213 - 0.681)	48.1%	0.036			
OMS00056	GSI v4.1	(0.042 - 0.388)	33.1%	0.030			
OMS00057	PBT v5.1	(0.197 - 0.628)	44.7%	0.049			
OMS00058	PBT v5.1	(0.117 - 0.656)	45.6%	0.073			
OMS00061	GSI v4.1	(0.000 - 0.207)	10.8%	0.039			
OMS00062	PBT v5.1	(0.061 - 0.490)	37.1%	0.027	7	1	
OMS00064	PBT v5.1	(0.098 - 0.651)	44.2%	0.068			
OMS00068	PBT v5.1	(0.056 - 0.500)	42.3%	0.036			
OMS00070	PBT v5.1	(0.261 - 0.733)	47.6%	0.053			
OMS00071	PBT v5.1	(0.255 - 0.720)	48.1%	0.037			
OMS00072	PBT v5.1	(0.254 - 0.638)	48.6%	0.026			
OMS00074	PBT v5.1	(0.141 - 0.726)	46.1%	0.062			
OMS00077	PBT v5.1	(0.208 - 0.561)	46.8%	0.034			
OMS00078	PBT v5.1	(0.144 - 0.521)	38.4%	0.024			
OMS00079	PBT v5.1	(0.140 - 0.737)	48.3%	0.038	5	2	
OMS00087	GSI v4.1	(0.023 - 0.520)	30.1%	0.059	33		
OMS00089	PBT v5.1	(0.056 - 0.580)	38.0%	0.044			
OMS00090	PBT v5.1	(0.183 - 0.698)	47.6%	0.050			
OMS00092	GSI v4.1	(0.019 - 0.521)	25.6%	0.079			
OMS00095	GSI v4.1	(0.000 - 0.283)	11.8%	0.044			
OMS00096	GSI v4.1	(0.028 - 0.359)	30.5%	0.029			
OMS00101	PBT v5.1	(0.185 - 0.750)	46.5%	0.054			
OMS00105	PBT v5.1	(0.130 - 0.561)	44.0%	0.043			
OMS00106	PBT v5.1	(0.056 - 0.423)	35.1%	0.033			

Table 1. Continued.

Locus	Panel	MAF Range	He	Fst	HWE		LD
					Deficient	Excess	
OMS00111	PBT v5.1	(0.042 - 0.494)	31.0%	0.055			
OMS00112	PBT v5.1	(0.013 - 0.456)	29.5%	0.060			
OMS00114	GSI v4.1	(0.006 - 0.183)	15.4%	0.024			
OMS00118	PBT v5.1	(0.092 - 0.691)	43.5%	0.068	6	1	
OMS00119	GSI v4.1	(0.011 - 0.290)	22.8%	0.034			
OMS00120	PBT v5.1	(0.012 - 0.489)	28.2%	0.076			
OMS00121	PBT v5.1	(0.278 - 0.674)	48.6%	0.026			
OMS00129	GSI v4.1	(0.029 - 0.345)	28.7%	0.041	17		
OMS00132	PBT v5.1	(0.223 - 0.600)	48.1%	0.022			
OMS00133	GSI v4.1	(0.000 - 0.148)	4.3%	0.039			
OMS00138	GSI v4.1	(0.013 - 0.286)	21.1%	0.045			
OMS00143	GSI v4.1	(0.013 - 0.278)	17.7%	0.042			
OMS00149	GSI v4.1	(0.000 - 0.208)	8.7%	0.033			
OMS00151	GSI v4.1	(0.054 - 0.356)	29.7%	0.036			
OMS00154	PBT v5.1	(0.059 - 0.366)	31.4%	0.038			
OMS00169	GSI v4.1	(0.000 - 0.066)	1.8%	0.027			
OMS00173	GSI v4.1	(0.029 - 0.313)	20.8%	0.032			
OMS00174	GSI v4.1	(0.000 - 0.128)	8.9%	0.019			
OMS00175	PBT v5.1	(0.240 - 0.591)	47.2%	0.031			
OMS00176	GSI v4.1	(0.000 - 0.351)	11.5%	0.045			
OMS00179	PBT v5.1	(0.085 - 0.515)	39.2%	0.038			
OMS00180	PBT v5.1	(0.131 - 0.571)	43.7%	0.036			
Omy_101832-195	PBT v5.1	(0.165 - 0.734)	47.4%	0.039			
Omy_101993-189	PBT v5.1	(0.056 - 0.559)	33.9%	0.064			
Omy_102505-102	PBT v5.1	(0.173 - 0.596)	45.8%	0.028			
Omy_103705-558	GSI v4.1	(0.010 - 0.330)	18.5%	0.034			
Omy_104519-624	PBT v5.1	(0.065 - 0.575)	40.2%	0.068			
Omy_105075-162	GSI v4.1	(0.003 - 0.233)	15.5%	0.026			
Omy_105105-448	PBT v5.1	(0.182 - 0.638)	47.5%	0.036			
Omy_105385-406	PBT v5.1	(0.211 - 0.664)	46.2%	0.033			
Omy_105714-265	PBT v5.1	(0.100 - 0.505)	42.7%	0.035			
Omy_107031-704	GSI v4.1	(0.029 - 0.383)	25.5%	0.048			
Omy_107285-69	GSI v4.1	(0.053 - 0.302)	26.7%	0.022			
Omy_107806-34	PBT v5.1	(0.069 - 0.656)	40.2%	0.076			
Omy_108007-193	PBT v5.1	(0.193 - 0.675)	45.5%	0.060			
Omy_109243-222	PBT v5.1	(0.011 - 0.342)	26.5%	0.029			
Omy_109894-185	PBT v5.1	(0.100 - 0.650)	45.1%	0.040	6	2	
Omy_110064-419	PBT v5.1	(0.075 - 0.755)	44.5%	0.064			
Omy_110201-359	GSI v4.1	(0.000 - 0.297)	16.4%	0.036			
Omy_111383-51	PBT v5.1	(0.175 - 0.640)	46.8%	0.044			
Omy_113490-159	PBT v5.1	(0.200 - 0.795)	45.9%	0.069			
Omy_114315-438	PBT v5.1	(0.146 - 0.691)	45.0%	0.081			
Omy_114587-480	PBT v5.1	(0.124 - 0.597)	43.6%	0.047			
Omy_116733-349	PBT v5.1	(0.130 - 0.465)	39.7%	0.033			
Omy_128923-433	PBT v5.1	(0.222 - 0.713)	47.9%	0.049			
Omy_128996-481	GSI v4.1	(0.000 - 0.214)	12.7%	0.035	21		
Omy_129870-756	PBT v5.1	(0.057 - 0.367)	28.4%	0.028			
Omy_130524-160	PBT v5.1	(0.212 - 0.600)	46.0%	0.026			
Omy_97077-73	GSI v4.1	(0.000 - 0.098)	3.5%	0.036			
Omy_97660-230	PBT v5.1	(0.173 - 0.551)	43.8%	0.033			
Omy_97865-196	GSI v4.1	(0.000 - 0.116)	6.9%	0.026			
Omy_97954-618	GSI v4.1	(0.037 - 0.454)	31.3%	0.050			
Omy_99300-202	PBT v5.1	(0.100 - 0.640)	35.5%	0.055			
Omy_ada10-71	PBT v5.1	(0.042 - 0.364)	29.8%	0.028			

Table 1. Continued.

Locus	Panel	MAF Range	He	Fst	HWE		LD
					Deficient	Excess	
Omy_aldB-165	PBT v5.1	(0.150 - 0.438)	40.8%	0.019			
Omy_anp-17	PBT v5.1	(0.053 - 0.698)	40.6%	0.112			
Omy_aromat-280	GSI v4.1	(0.076 - 0.343)	30.5%	0.029	8		
Omy_arp-630	PBT v5.1	(0.156 - 0.662)	47.8%	0.043			
Omy_aspAT-123	GSI v4.1	(0.146 - 0.438)	39.0%	0.024			
Omy_b1-266	PBT v5.1	(0.130 - 0.486)	39.4%	0.022			
Omy_b9-164	GSI v4.1	(0.011 - 0.457)	18.8%	0.102	16		
Omy_BAC-B4-324	PBT v5.1	(0.247 - 0.610)	48.4%	0.022			
Omy_BAC-F5.284	GSI v4.1	(0.000 - 0.187)	9.9%	0.040			
Omy_BAMBI2.312	GSI v4.1	(0.000 - 0.307)	20.3%	0.060			
Omy_bcAKala-380rd	PBT v5.1	(0.089 - 0.544)	42.3%	0.042			
Omy_ca050-64	GSI v4.1	(0.167 - 0.536)	43.9%	0.031			
Omy_carban1-264	GSI v4.1	(0.009 - 0.353)	19.5%	0.055			
Omy_cd28-130	GSI v4.1	(0.000 - 0.116)	3.0%	0.022			
Omy_cd59-206	PBT v5.1	(0.121 - 0.533)	40.8%	0.027	6	2	
Omy_cd59b-112	GSI v4.1	(0.000 - 0.380)	19.2%	0.060			
Omy_cin-172	GSI v4.1	(0.064 - 0.469)	31.8%	0.048			
Omy_colla1-525	PBT v5.1	(0.116 - 0.450)	40.8%	0.025			
Omy_cox1-221	PBT v5.1	(0.178 - 0.643)	46.0%	0.045			
Omy_cox2-335	GSI v4.1	(0.037 - 0.375)	26.4%	0.035			
Omy_crb-106	PBT v5.1	(0.239 - 0.753)	46.7%	0.057	20		
Omy_CRBF1-1	GSI v4.1	(0.000 - 0.146)	9.7%	0.021			
Omy_e1-147	GSI v4.1	(0.000 - 0.190)	8.6%	0.036			
Omy_g1-103	GSI v4.1	(0.000 - 0.170)	10.9%	0.044			
Omy_g12-82	PBT v5.1	(0.240 - 0.756)	48.4%	0.037			
Omy_G3PD_2-371	GSI v4.1	(0.073 - 0.522)	29.1%	0.040			
Omy_gadd45-332	GSI v4.1	(0.011 - 0.399)	21.1%	0.090			
Omy_gdh-271	GSI v4.1	(0.022 - 0.409)	20.0%	0.049	7		
Omy_gh-475	GSI v4.1	(0.053 - 0.300)	23.5%	0.028			
Omy_GHSR-121	GSI v4.1	(0.000 - 0.207)	8.1%	0.057			b
Omy_gluR-79	PBT v5.1	(0.150 - 0.621)	48.2%	0.036			
Omy_hsc715-80	PBT v5.1	(0.222 - 0.520)	46.4%	0.017	5	2	
Omy_hsf1b-241	GSI v4.1	(0.000 - 0.181)	15.4%	0.026			
Omy_hsf2-146	PBT v5.1	(0.084 - 0.670)	41.4%	0.084			
Omy_hsp47-86	GSI v4.1	(0.077 - 0.400)	33.0%	0.023			
Omy_hsp70aPro-329	GSI v4.1	(0.000 - 0.450)	8.1%	0.086			
Omy_hus1-52	GSI v4.1	(0.000 - 0.210)	9.6%	0.060			
Omy_IL17-185	PBT v5.1	(0.221 - 0.656)	48.2%	0.039	1	10	
Omy_Il-1b_.028	PBT v5.1	(0.000 - 0.339)	26.0%	0.044			a
Omy_Il1b-198	PBT v5.1	(0.204 - 0.605)	46.3%	0.040			a
Omy_IL6-320	PBT v5.1	(0.096 - 0.398)	33.9%	0.031			
Omy_impa1-55	GSI v4.1	(0.012 - 0.236)	16.2%	0.032			
Omy_inos-97	GSI v4.1	(0.000 - 0.186)	11.2%	0.042			
Omy_LDHB-1_i2	GSI v4.1	(0.000 - 0.182)	15.1%	0.024	9		
Omy_LDHB-2_e5	GSI v4.1	(0.053 - 0.400)	26.8%	0.031			
Omy_LDHB-2_i6	GSI v4.1	(0.000 - 0.090)	1.9%	0.020			
Omy_lpl-220	GSI v4.1	(0.050 - 0.302)	25.5%	0.020			
Omy_mapK3-103	GSI v4.1	(0.000 - 0.138)	5.0%	0.043			b
Omy_mcsf-268	GSI v4.1	(0.000 - 0.172)	3.2%	0.046			
Omy_metA-161	PBT v5.1	(0.086 - 0.489)	36.7%	0.046			
Omy_metB-138	GSI v4.1	(0.018 - 0.306)	25.3%	0.033			
Omy_myoD-178	GSI v4.1	(0.000 - 0.359)	19.2%	0.054			
Omy_nach-200	GSI v4.1	(0.000 - 0.051)	1.6%	0.017			
Omy_NaKATPa3-50	PBT v5.1	(0.096 - 0.505)	39.8%	0.046			

Table 1. Continued.

Locus	Panel	MAF Range	He	Fst	HWE		LD
					Deficient	Excess	
Omy_ndk-152	GSI v4.1	(0.000 - 0.130)	4.8%	0.028			
Omy_nips-299	GSI v4.1	(0.000 - 0.202)	12.6%	0.028			
Omy_nkef-241	PBT v5.1	(0.234 - 0.621)	47.6%	0.029			
Omy_ntl-27	PBT v5.1	(0.127 - 0.577)	42.9%	0.051			
Omy_nxt2-273	GSI v4.1	(0.000 - 0.245)	11.8%	0.044	16		
Omy_Ogo4-212	PBT v5.1	(0.191 - 0.570)	46.8%	0.035			
Omy_OmyP9-180	GSI v4.1	(0.011 - 0.284)	17.2%	0.035	8		
Omy_Ots249-227	PBT v5.1	(0.144 - 0.479)	40.6%	0.024			
Omy_oxct-85	PBT v5.1	(0.000 - 0.348)	18.3%	0.050			
Omy_p53-262	PBT v5.1	(0.044 - 0.506)	34.4%	0.045			
Omy_pad-196	GSI v4.1	(0.000 - 0.135)	8.0%	0.029			
Omy_ppie-232	GSI v4.1	(0.043 - 0.500)	22.6%	0.034			
Omy_rapd-167	PBT v5.1	(0.043 - 0.395)	29.1%	0.033			
Omy_rbm4b-203	PBT v5.1	(0.015 - 0.407)	28.8%	0.055			
Omy_redd1-410	PBT v5.1	(0.067 - 0.446)	32.6%	0.031			
Omy_sast-264	GSI v4.1	(0.075 - 0.300)	29.5%	0.018			
Omy_SECC22b-88	GSI v4.1	(0.000 - 0.100)	2.8%	0.037			
Omy_srp09-37	PBT v5.1	(0.122 - 0.505)	41.2%	0.035			
Omy_sSOD-1	GSI v4.1	(0.000 - 0.049)	1.7%	0.015			
Omy_star-206	GSI v4.1	(0.000 - 0.178)	8.5%	0.037			
Omy_stat3-273	PBT v5.1	(0.080 - 0.389)	35.5%	0.028			
Omy_sys1-188	GSI v4.1	(0.000 - 0.394)	18.0%	0.068			
Omy_tlr3-377	GSI v4.1	(0.000 - 0.233)	16.7%	0.046			
Omy_tlr5-205	GSI v4.1	(0.000 - 0.148)	10.5%	0.024			
Omy_txnip-343	PBT v5.1	(0.074 - 0.511)	35.9%	0.040			
Omy_u07-79-166	GSI v4.1	(0.000 - 0.279)	15.0%	0.060			
Omy_u09-52.284	GSI v4.1	(0.000 - 0.118)	5.3%	0.036			
Omy_u09-53.469	PBT v5.1	(0.241 - 0.756)	45.5%	0.081			
Omy_u09-54-311	PBT v5.1	(0.081 - 0.589)	40.7%	0.039			
Omy_u09-56.119	GSI v4.1	(0.017 - 0.328)	16.8%	0.037			
Omy_U11_2b-154	PBT v5.1	(0.071 - 0.415)	32.6%	0.042			
Omy_UT16_2-173	GSI v4.1	(0.000 - 0.167)	12.0%	0.023			
Omy_vamp5-303	GSI v4.1	(0.032 - 0.422)	33.3%	0.036			
Omy_vatf-406	PBT v5.1	(0.085 - 0.562)	42.6%	0.063			
Omy_zg57-91	GSI v4.1	(0.000 - 0.217)	14.9%	0.044			
OMY1011SNP	PBT v5.1	(0.110 - 0.438)	36.6%	0.031			

[a] Omy_Il1b-198 and Omy_Il-1b_.028 exhibited linkage disequilibrium in 38 of 68 baseline collections. Omy_Il1b-198 was the lesser informative of the pair and was dropped from baseline and GSI analyses.

[b] Omy_mapK3-103 and Omy_GHSR-121 exhibited linkage disequilibrium in 41 of 68 baseline collections. Omy_mapK3-103 was the lesser informative of the pair and was dropped from baseline and GSI analyses.

Table 2. Summary of 191 SNPs (Appendix B and Hess et al. 2013) screened across 54 stream-type Chinook salmon collections in Snake River baseline v3.0. (Note: fall Chinook collections were excluded from analyses below.) SNPs designated as PBT are used for both 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 all collections.

					HWE		
SNP Marker	**Panel**	**MAF Range**	**HE**	**FST**	**Deficient**	**Excess**	**LD**
Ots_100884-287	PBT v5.1	(0.073 - 0.463)	34.0%	0.044	4	2	
Ots_101554-407	PBT v5.1	(0.118 - 0.717)	47.2%	0.061	3	3	
Ots_101704-143	PBT v5.1	(0.009 - 0.685)	21.8%	0.144			
Ots_102414-395	PBT v5.1	(0.201 - 0.679)	47.7%	0.048			
Ots_102801-308	PBT v5.1	(0.071 - 0.340)	33.1%	0.023			
Ots_103122-180	PBT v5.1	(0.036 - 0.843)	23.2%	0.188			
Ots_104415-88	PBT v5.1	(0.082 - 0.633)	47.2%	0.049			
Ots_105105-613	PBT v5.1	(0.101 - 0.835)	42.0%	0.090			
Ots_105132-200	PBT v5.1	(0.032 - 0.313)	31.8%	0.027			
Ots_105385-421	PBT v5.1	(0.028 - 0.650)	46.5%	0.049			
Ots_105407-117	PBT v5.1	(0.194 - 0.614)	47.1%	0.043			
Ots_108820-336	PBT v5.1	(0.050 - 0.832)	45.5%	0.089			
Ots_109525-816	PBT v5.1	(0.061 - 0.426)	29.7%	0.026			
Ots_110064-383	PBT v5.1	(0.121 - 0.835)	43.2%	0.066			
Ots_110201-363	PBT v5.1	(0.163 - 0.574)	42.9%	0.037			
Ots_110495-380	PBT v5.1	(0.045 - 0.756)	23.1%	0.167			
Ots_110551-64	PBT v5.1	(0.104 - 0.358)	35.1%	0.022			
Ots_110689-218	PBT v5.1	(0.080 - 0.445)	35.8%	0.029			
Ots_112301-43	PBT v5.1	(0.043 - 0.250)	23.6%	0.019	5	1	
Ots_112419-131	PBT v5.1	(0.000 - 0.461)	20.3%	0.076			
Ots_112820-284	PBT v5.1	(0.026 - 0.378)	24.3%	0.045			
Ots_112876-371	PBT v5.1	(0.019 - 0.733)	24.4%	0.129			
Ots_113242-216	PBT v5.1	(0.000 - 0.536)	20.0%	0.082			
Ots_115987-325	PBT v5.1	(0.065 - 0.864)	39.3%	0.111			
Ots_117432-409	PBT v5.1	(0.129 - 0.733)	41.0%	0.083			
Ots_118205-61	PBT v5.1	(0.091 - 0.329)	31.0%	0.019			
Ots_118938-325	PBT v5.1	(0.061 - 0.474)	33.5%	0.053			
Ots_123921-111	PBT v5.1	(0.028 - 0.308)	24.0%	0.037			
Ots_124774-477	PBT v5.1	(0.004 - 0.676)	16.5%	0.176			
Ots_128757-61R	PBT v5.1	(0.006 - 0.596)	16.9%	0.112			
Ots_129458-451	PBT v5.1	(0.013 - 0.600)	22.0%	0.099			
Ots_94857-232R	PBT v5.1	(0.238 - 0.698)	48.4%	0.037			
Ots_94903-99R	PBT v5.1	(0.200 - 0.647)	48.2%	0.030			
Ots_96500-180	PBT v5.1	(0.237 - 0.744)	47.4%	0.044			
Ots_96899-357R	PBT v5.1	(0.000 - 0.295)	22.1%	0.026			
Ots_ARNT	PBT v5.1	(0.000 - 0.958)	26.7%	0.225			
Ots_AsnRS-60	PBT v5.1	(0.043 - 0.318)	29.6%	0.024			
Ots_brp16-64	PBT v5.1	(0.052 - 0.494)	24.6%	0.055			
Ots_CD59-2	PBT v5.1	(0.257 - 0.574)	47.3%	0.022			
Ots_CirpA	PBT v5.1	(0.007 - 0.861)	18.8%	0.241			
Ots_cox1-241	PBT v5.1	(0.011 - 0.959)	23.7%	0.225			

Table 2. Continued.

SNP Marker	Panel	MAF Range	H_E	F_{ST}	HWE Deficient	HWE Excess	LD
Ots_E2-275	PBT v5.1	(0.051 - 0.854)	38.4%	0.122			
Ots_Est740	PBT v5.1	(0.289 - 0.620)	48.5%	0.023			
Ots_ETIF1A	PBT v5.1	(0.144 - 0.847)	40.9%	0.082			
Ots_FGF6B_1	PBT v5.1	(0.245 - 0.657)	48.3%	0.031			b
Ots_GCSH	PBT v5.1	(0.005 - 0.972)	17.5%	0.314			
Ots_GDH-81x	PBT v5.1	(0.104 - 0.600)	36.2%	0.057			
Ots_GPH-318	PBT v5.1	(0.014 - 0.373)	31.3%	0.042			
Ots_GTH2B-550	PBT v5.1	(0.006 - 0.745)	46.0%	0.085			
Ots_HMGB1-73	PBT v5.1	(0.030 - 0.856)	23.9%	0.184			
Ots_hsc71-3'-488	PBT v5.1	(0.044 - 0.897)	27.1%	0.170			c
Ots_HSP90B-100	PBT v5.1	(0.056 - 0.917)	29.0%	0.162			
Ots_IGF-I.1-76	PBT v5.1	(0.000 - 0.359)	28.3%	0.039			
Ots_Ikaros-250	PBT v5.1	(0.000 - 0.209)	16.4%	0.029			
Ots_IL8R_C8	PBT v5.1	(0.031 - 0.777)	44.9%	0.087			
Ots_mapK-3'-309	PBT v5.1	(0.117 - 0.771)	45.4%	0.064			
Ots_mapKpr-151	PBT v5.1	(0.053 - 0.415)	35.7%	0.036			
Ots_MHC1	PBT v5.1	(0.005 - 0.772)	13.0%	0.279			
Ots_MHC2	PBT v5.1	(0.156 - 0.759)	42.7%	0.110			
Ots_mybp-85	PBT v5.1	(0.000 - 0.596)	19.7%	0.118			
Ots_NFYB-147	PBT v5.1	(0.000 - 0.300)	26.0%	0.033			
Ots_nkef-192	PBT v5.1	(0.017 - 0.760)	45.9%	0.081			
Ots_NOD1	PBT v5.1	(0.006 - 0.875)	37.9%	0.136			
Ots_ntl-255	PBT v5.1	(0.208 - 0.678)	45.5%	0.034			
Ots_OTALDBINT1-SNP1	PBT v5.1	(0.005 - 0.597)	17.9%	0.137	8		
Ots_OTDESMIN19-SNP1	PBT v5.1	(0.159 - 0.765)	46.5%	0.060			
Ots_OTSTF1-SNP1	PBT v5.1	(0.078 - 0.897)	43.5%	0.109			a
Ots_P53	PBT v5.1	(0.077 - 0.480)	37.3%	0.034			
Ots_parp3-286	PBT v5.1	(0.006 - 0.265)	27.4%	0.027			
Ots_pigh-105	PBT v5.1	(0.210 - 0.633)	47.3%	0.042			
Ots_pop5-96	PBT v5.1	(0.006 - 0.453)	36.9%	0.045			
Ots_ppie-245	PBT v5.1	(0.015 - 0.956)	24.4%	0.243			
Ots_Prl2	PBT v5.1	(0.077 - 0.550)	38.4%	0.047			
Ots_RAG3	PBT v5.1	(0.025 - 0.833)	21.0%	0.203			
Ots_redd1-187	PBT v5.1	(0.012 - 0.396)	36.5%	0.037			
Ots_S7-1	PBT v5.1	(0.178 - 0.582)	44.6%	0.026			
Ots_SClkF2R2-135	PBT v5.1	(0.247 - 0.631)	47.0%	0.036			
Ots_SWS1op-182	PBT v5.1	(0.169 - 0.744)	41.6%	0.057			
Ots_TAPBP	PBT v5.1	(0.011 - 0.736)	35.5%	0.155	5	1	
Ots_TGFB	PBT v5.1	(0.000 - 0.211)	11.5%	0.029			
Ots_Thio	PBT v5.1	(0.084 - 0.522)	39.4%	0.029			
Ots_TLR3	PBT v5.1	(0.103 - 0.867)	37.9%	0.118			
Ots_tpx2-125	PBT v5.1	(0.010 - 0.226)	16.6%	0.033			
Ots_txnip-321	PBT v5.1	(0.000 - 0.336)	24.5%	0.056			
Ots_u07-07.161	PBT v5.1	(0.149 - 0.694)	45.7%	0.050			
Ots_u07-17.135	PBT v5.1	(0.017 - 0.256)	20.9%	0.026			
Ots_u07-18.378	PBT v5.1	(0.010 - 0.725)	18.8%	0.170			
Ots_u07-25.325	PBT v5.1	(0.046 - 0.736)	46.3%	0.078			
Ots_u07-49.290	PBT v5.1	(0.164 - 0.759)	42.0%	0.052			
Ots_u1002-75	PBT v5.1	(0.055 - 0.394)	34.9%	0.035			
Ots_u211-85	PBT v5.1	(0.006 - 0.820)	43.8%	0.106			
Ots_u4-92	PBT v5.1	(0.000 - 0.105)	7.4%	0.020			
Ots_u6-75	PBT v5.1	(0.006 - 0.307)	20.5%	0.034	7		
Ots_unk526	PBT v5.1	(0.000 - 0.261)	18.8%	0.046			
Ots_vatf-251	PBT v5.1	(0.018 - 0.728)	17.4%	0.202			

Table 2. Continued.

SNP Marker	Panel	MAF Range	H_E	F_{ST}	HWE		LD
					Deficient	Excess	
Ots_101119-381	GSI v1.1	(0.000 - 0.091)	0.9%	0.048			
Ots_102213-210	GSI v1.1	(0.000 - 0.121)	2.7%	0.059			
Ots_102457-132	GSI v1.1	(0.000 - 0.567)	6.7%	0.315			
Ots_102867-609	GSI v1.1	(0.000 - 0.183)	4.7%	0.063	11		
Ots_104569-86	GSI v1.1	(0.033 - 0.577)	21.9%	0.092			
Ots_106499-70	GSI v1.1	(0.143 - 0.467)	39.1%	0.027			
Ots_106747-239	GSI v1.1	(0.220 - 0.644)	46.5%	0.050			
Ots_107074-284	GSI v1.1	(0.000 - 0.404)	7.7%	0.139			
Ots_107285-93	GSI v1.1	(0.000 - 0.100)	5.0%	0.029			
Ots_107806-821	GSI v1.1	(0.229 - 0.633)	47.4%	0.034			
Ots_108007-208	GSI v1.1	(0.000 - 0.477)	8.5%	0.170			
Ots_108390-329	GSI v1.1	(0.000 - 0.172)	1.8%	0.117			
Ots_108735-302	GSI v1.1	(0.016 - 0.476)	18.1%	0.091	8		
Ots_109693-392	GSI v1.1	(0.000 - 0.216)	6.3%	0.070			
Ots_111681-657	GSI v1.1	(0.028 - 0.250)	15.9%	0.029			
Ots_112208-722	GSI v1.1	(0.000 - 0.453)	11.1%	0.136			
Ots_113457-40R	GSI v1.1	(0.011 - 0.611)	17.4%	0.138			
Ots_117242-136	GSI v1.1	(0.000 - 0.539)	13.4%	0.155			
Ots_117259-271	GSI v1.1	(0.000 - 0.818)	4.2%	0.572			
Ots_118175-479	GSI v1.1	(0.000 - 0.196)	4.7%	0.057			
Ots_122414-56	GSI v1.1	(0.000 - 0.336)	3.6%	0.198			
Ots_123048-521	GSI v1.1	(0.000 - 0.129)	2.9%	0.048			
Ots_127236-62	GSI v1.1	(0.000 - 0.717)	5.9%	0.444			
Ots_128302-57	GSI v1.1	(0.000 - 0.850)	9.0%	0.401			
Ots_128693-461	GSI v1.1	(0.000 - 0.394)	8.6%	0.122			
Ots_129144-472	GSI v1.1	(0.000 - 0.412)	3.1%	0.298			
Ots_130720-99	GSI v1.1	(0.000 - 0.515)	11.8%	0.153			
Ots_131460-584	GSI v1.1	(0.000 - 0.615)	9.3%	0.264			
Ots_131906-141	GSI v1.1	(0.000 - 0.139)	8.7%	0.023			
Ots_96222-525	GSI v1.1	(0.000 - 0.429)	8.1%	0.160			
Ots_97077-179R	GSI v1.1	(0.000 - 0.340)	6.5%	0.132			
Ots_99550-204	GSI v1.1	(0.000 - 0.119)	3.8%	0.031			
Ots_AldB1-122	GSI v1.1	(0.000 - 0.200)	13.2%	0.030			
Ots_aldb-177M	GSI v1.1	(0.000 - 0.279)	12.9%	0.038			
Ots_arp-436	GSI v1.1	(0.000 - 0.641)	3.6%	0.460			
Ots_aspat-196	GSI v1.1	(0.000 - 0.188)	1.6%	0.144			
Ots_C3N3	GSI v1.1	(0.000 - 0.435)	9.4%	0.177	na		
Ots_Cath_D141	GSI v1.1	(0.000 - 0.084)	2.4%	0.029			
Ots_CCR7	GSI v1.1	(0.000 - 0.004)	0.0%	0.003			
Ots_CD63	GSI v1.1	(0.000 - 0.478)	11.4%	0.127			
Ots_CRB211	GSI v1.1	(0.000 - 0.084)	1.3%	0.037			
Ots_DDX5-171	GSI v1.1	(0.006 - 0.530)	15.7%	0.121			
Ots_EndoRB1-486	GSI v1.1	(0.000 - 0.322)	8.0%	0.099			
Ots_EP-529	GSI v1.1	(0.000 - 0.122)	4.7%	0.031			
Ots_Est1363	GSI v1.1	(0.000 - 0.994)	6.6%	0.587			
Ots_FARSLA-220	GSI v1.1	(0.000 - 0.994)	5.7%	0.622			
Ots_FGF6A	GSI v1.1	(0.054 - 0.599)	44.8%	0.047			b
Ots_GH2	GSI v1.1	(0.000 - 0.127)	8.1%	0.023			
Ots_GnRH-271	GSI v1.1	(0.000 - 0.147)	5.8%	0.031			
Ots_GPDH-338	GSI v1.1	(0.000 - 0.116)	1.3%	0.081			
Ots_GST-207	GSI v1.1	(0.000 - 0.151)	1.9%	0.090			
Ots_GST-375	GSI v1.1	(0.000 - 0.012)	0.1%	0.010			
Ots_HFABP-34	GSI v1.1	(0.000 - 0.420)	7.4%	0.155			
Ots_hnRNPL-533	GSI v1.1	(0.007 - 0.732)	46.6%	0.073			

Table 2. Continued.

SNP Marker	Panel	MAF Range	H_E	F_{ST}	HWE		LD
					Deficient	Excess	
Ots_hsc71-5'-453	GSI v1.1	(0.000 - 0.363)	9.0%	0.113			c
Ots_hsp27b-150	GSI v1.1	(0.000 - 0.472)	9.9%	0.157			
Ots_Hsp90a	GSI v1.1	(0.000 - 0.699)	4.9%	0.410			
Ots_IL11	GSI v1.1	(0.000 - 0.920)	8.9%	0.482			
Ots_il13Ra2B-37	GSI v1.1	(0.120 - 0.527)	45.1%	0.029			
Ots_il-1racp-166	GSI v1.1	(0.147 - 0.760)	46.5%	0.058			
Ots_LWSop-638	GSI v1.1	(0.000 - 0.028)	0.3%	0.016			
Ots_Myc-366	GSI v1.1	(0.000 - 0.038)	0.4%	0.020			
Ots_myo1a-384	GSI v1.1	(0.000 - 0.132)	5.4%	0.040			
Ots_myoD-364	GSI v1.1	(0.005 - 0.641)	14.0%	0.190			
Ots_nelfd-163	GSI v1.1	(0.000 - 0.653)	4.9%	0.457			
Ots_nramp-321	GSI v1.1	(0.000 - 0.994)	2.1%	0.824			
Ots_Ots311-101x	GSI v1.1	(0.000 - 0.108)	1.6%	0.065			
Ots_OTSMTA-SNP1	GSI v1.1	(0.000 - 0.212)	3.3%	0.119			
Ots_P450	GSI v1.1	(0.000 - 0.940)	4.2%	0.666			
Ots_P450-288	GSI v1.1	(0.101 - 0.843)	43.7%	0.090			
Ots_PGK-54	GSI v1.1	(0.000 - 0.561)	5.2%	0.348			
Ots_RAS1	GSI v1.1	(0.000 - 0.279)	0.0%	#N/A			
Ots_RFC2-558	GSI v1.1	(0.000 - 0.433)	4.0%	0.305			
Ots_SL	GSI v1.1	(0.000 - 0.889)	4.2%	0.635			
Ots_stk6-516	GSI v1.1	(0.000 - 0.261)	1.1%	0.186			
Ots_TCTA-58	GSI v1.1	(0.000 - 0.259)	6.5%	0.073			
Ots_TNF	GSI v1.1	(0.000 - 0.012)	0.2%	0.009			
Ots_Tnsf	GSI v1.1	(0.039 - 0.671)	40.3%	0.069	4	3	a
Ots_u07-20.332	GSI v1.1	(0.000 - 0.078)	0.5%	0.051			
Ots_u07-53.133	GSI v1.1	(0.013 - 0.536)	15.3%	0.128			
Ots_u07-57.120	GSI v1.1	(0.000 - 0.974)	6.5%	0.576			
Ots_u07-64.221	GSI v1.1	(0.000 - 0.019)	0.3%	0.011			
Ots_u1007-124	GSI v1.1	(0.000 - 0.328)	3.6%	0.187			
Ots_u202-161	GSI v1.1	(0.000 - 0.603)	10.4%	0.206			
Ots_U2362-227	GSI v1.1	(0.000 - 0.116)	3.4%	0.039			
Ots_U2362-330	GSI v1.1	(0.006 - 0.734)	46.6%	0.070			
Ots_U2446-123	GSI v1.1	(0.102 - 0.593)	43.6%	0.037	4	2	
Ots_unk1104-38	GSI v1.1	(0.045 - 0.739)	46.7%	0.070			
Ots_unk1832-39	GSI v1.1	(0.090 - 0.650)	47.6%	0.044			
Ots_unk3513-49	GSI v1.1	(0.102 - 0.618)	34.5%	0.041			
Ots_unk7936-50	GSI v1.1	(0.000 - 0.229)	13.2%	0.027			
Ots_unk8200-45	GSI v1.1	(0.000 - 0.030)	0.4%	0.014			
Ots_unk9480-51	GSI v1.1	(0.019 - 0.831)	26.3%	0.156			
Ots_zn593-346	GSI v1.1	(0.000 - 0.111)	2.9%	0.025			
Ots_zP3b-215	GSI v1.1	(0.000 - 0.129)	0.0%	#N/A			
Ots_ZR-575	GSI v1.1	(0.000 - 0.815)	11.6%	0.333	13		

[a] Ots_Tnsf and Ots_OTSTF1-SNP1 exhibited linkage disequilibrium in 55 of 57 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 57 of 57 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.
It will be included in analyses baseline and GSI analyses concerning differentiating spring/summer and fall lineages.

Table 3. Sixty-eight collections of Snake River basin steelhead (*Oncorhynchus mykiss*) screened with the PBT and GSI SNP panels for baseline v3.0. 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.

Map #	Collection	TRT Population	Genetic Stock	MPG	n	Year Collected	Genotype Agency	Baseline Version	Latitude	Longitude	uHe	Fst	Deficient	Excess
1	Sawtooth/IPTDS (STL)	SRUMA	UPSALM	Salmon River	129	05, 10, 11, 12	IDFG	3	44.15058	-114.88509	29.8%	0.017	7	4
2	Valley Cr/IPTDS (VAL)	SRVAL	UPSALM	Salmon River	147	05, 10, 11, 12	IDFG/NWFSC	3	44.30113	-115.04574	30.1%	0.016		
3	WF Yankee Fork	SRUMA	UPSALM	Salmon River	117	04, 08	IDFG	1	44.34941	-114.72657	30.3%	0.017		
4	Herd Cr	SREFS	UPSALM	Salmon River	85	10, 11	NWFSC	3	44.10907	-114.25680	30.3%	0.018		
5	Morgan Cr	SREFS	UPSALM	Salmon River	61	00, 12	IDFG	1	44.64527	-114.21089	32.3%	0.020	8	5
6	Pahsimeroi R	SRPAH	UPSALM	Salmon River	97	06, 10	IDFG	1	44.61844	-113.98106	31.9%	0.018	9	2
7	upper Lemhi R/IPTDSs (HYC,KEN and LRW)	SRLEM	UPSALM	Salmon River	111	09, 10, 11, 12	IDFG	2	44.86983	-113.62648	32.6%	0.017	10	2
8	NF Salmon R	SRNFS	UPSALM	Salmon River	100	10	IDFG	1	45.50356	-113.95717	30.8%	0.014		
9	Panther Cr	SRPAN	N/A	Salmon River	53	13	IDFG	3	45.03494	-114.29949	30.8%	0.018		
10	Capehorn/Marsh Cr	MFUMA	MFSALM	Salmon River	195	00, 09, 10	IDFG/NWFSC	3	44.39488	-115.16905	30.3%	0.019	10	5
11	Elk/Bear Cr	MFUMA	MFSALM	Salmon River	173	10, 11	IDFG/NWFSC	3	44.41043	-115.37264	29.3%	0.024		
12	Sulphur Cr	MFUMA	MFSALM	Salmon River	94	00, 11	IDFG/NWFSC	2	44.54370	-115.39566	29.4%	0.024		
13	Rapid R (MF Salmon R)	MFUMA	MFSALM	Salmon River	75	00, 12	IDFG	1	44.64151	-115.05621	29.6%	0.025		
14	Pistol Cr	MFUMA	MFSALM	Salmon River	58	00, 12, 11	IDFG	1	44.76347	-115.31469	30.2%	0.022		
15	Loon Cr	MFUMA	MFSALM	Salmon River	131	99, 00	IDFG/NWFSC/CRITFC	2	44.59829	-114.81164	28.5%	0.023		
16	Camas Cr	MFBIG	MFSALM	Salmon River	97	00, 10	IDFG/NWFSC	1	44.82399	-114.49990	28.9%	0.022	12	1
17	upper Big Cr	MFBIG	MFSALM	Salmon River	87	00, 11	IDFG/NWFSC	1	45.15063	-115.29674	28.5%	0.028	6	4
18	lower Big Cr	MFBIG	MFSALM	Salmon River	137	00, 11	IDFG/NWFSC	1	45.10717	-114.80611	29.6%	0.019		
19	Chamberlain Cr	SRCHA	MFSALM	Salmon River	189	00, 10, 11	IDFG/NWFSC	2	45.36865	-115.19689	28.3%	0.021	14	3
20	Bargamin Cr	SRCHA	N/A	Salmon River	32	00	IDFG	1	45.66604	-115.08712	31.0%	0.022		
21	upper SF Salmon R mainstem	SFMAI	SFSALM	Salmon River	319	00, 10, 11, 12	IDFG/CRITFC	3	44.60691	-115.68021	29.4%	0.020	8	2
22	Johnson Cr	SFMAI	SFSALM	Salmon River	242	10, 11, 12	IDFG/NWFSC	3	44.93412	-115.48313	29.8%	0.020	12	4
23	EFSF Salmon R	SFMAI	SFSALM	Salmon River	46	00, 10, 11, 12	IDFG	1	44.95531	-115.53915	29.6%	0.027		
24	Lake Cr (SF Salmon R)	SFSEC	SFSALM	Salmon River	50	10, 11	IDFG	3	45.26611	-115.90920	28.6%	0.034	6	4
25	Lick Cr	SFSEC	SFSALM	Salmon River	63	10, 11	IDFG	2	45.05909	-115.86062	28.9%	0.022		
26	Secesh R/IPTDS (ZEN)	SFSEC	SFSALM	Salmon River	169	00, 10, 11, 12	IDFG/NWFSC	3	45.04116	-115.74806	29.2%	0.020	9	3
27	Boulder Cr/Rapid R	SRLSR	LOSALM	Salmon River	147	00, 03, 09	IDFG	1	45.25792	-116.33809	30.4%	0.015	9	1
28	Slate Cr	SRLSR	LOSALM	Salmon River	75	00, 13	IDFG	1	45.63918	-116.12441	30.5%	0.015		
29	upper Lochsa R	CRLOC	UPCLWR	Clearwater River	129	00	IDFG	1	46.50821	-114.68161	27.9%	0.024		
30	Lake Cr	CRLOC	UPCLWR	Clearwater River	47	00	IDFG	2	46.41437	-115.00679	27.8%	0.028		

Table 3. Continued.

Map #	Collection	TRT Population	Genetic Stock	MPG	n	Year Collected	Genotype Agency	Baseline Version	Latitude	Longitude	uHe	Fst	Deficient	Excess
31	Fish Cr	CRLOC	UPCLWR	Clearwater River	100	10, 11	IDFG	2	46.35582	-115.39851	28.2%	0.023	10	
32	Canyon Cr	CRLOC	N/A	Clearwater River	46	04	IDFG	1	46.23909	-115.57909	27.8%	0.024		
33	upper Selway R	CRSEL	UPCLWR	Clearwater River	137	08	IDFG	2	45.70726	-114.71946	28.8%	0.024	10	1
34	Whitecap Cr	CRSEL	UPCLWR	Clearwater River	110	08, 12	IDFG	2	45.88777	-114.60935	28.9%	0.025	12	5
35	Bear Cr	CRSEL	UPCLWR	Clearwater River	70	08, 12	IDFG	1	46.03569	-114.75107	28.9%	0.026		
36	middle Selway R	CRSEL	UPCLWR	Clearwater River	138	00, 04, 12	IDFG	3	46.09781	-115.07257	28.3%	0.021	9	3
37	Three Links Cr	CRSEL	UPCLWR	Clearwater River	81	00, 12	IDFG	2	46.14508	-115.09495	28.2%	0.026		
38	Gedney Cr	CRSEL	UPCLWR	Clearwater River	45	00	IDFG	1	46.09381	-115.29383	29.0%	0.022		
39	O'Hara Cr	CRSEL	UPCLWR	Clearwater River	85	00, 13	IDFG	1	46.04494	-115.51908	28.6%	0.019		
40	Crooked R	CRSFC	SFCLWR	Clearwater River	136	07, 08, 11	IDFG	1	45.76562	-115.54264	27.4%	0.024	11	
41	Newsome Cr	CRSFC	SFCLWR	Clearwater River	99	12	IDFG	3	45.83447	-115.61216	27.6%	0.026	7	5
42	Tenmile Cr	CRSFC	SFCLWR	Clearwater River	47	00	IDFG	1	45.72703	-115.66138	27.7%	0.032		
43	Clear Cr	CRLMA	SFCLWR	Clearwater River	45	00	IDFG	1	46.04859	-115.78140	28.4%	0.025		
44	Lolo Cr	CRLMA	SFCLWR	Clearwater River	159	12	IDFG	3	46.29056	-115.93415	27.9%	0.023		
45	WF Potlatch R	CRLMA	LOCLWR	Clearwater River	84	09, 10	IDFG	2	46.86382	-116.40197	30.1%	0.016		
46	EF Potlatch R	CRLMA	LOCLWR	Clearwater River	158	08, 10, 11	IDFG	1	46.80491	-116.40605	29.9%	0.016	8	3
47	Little Bear Cr	CRLMA	LOCLWR	Clearwater River	151	07, 08, 10, 11	IDFG	1	46.65323	-116.69004	30.2%	0.015	10	1
48	Big Bear Cr	CRLMA	LOCLWR	Clearwater River	99	07, 08, 10, 11	IDFG	1	46.67517	-116.66099	31.3%	0.015		
49	Potlatch R IPTDS (POT)	CRLMA	LOCLWR	Clearwater River	123	10, 11, 12	IDFG	3	46.61911	-116.64685	30.6%	0.014	9	1
50	Lapwai Cr	CRLMA	LOCLWR	Clearwater River	158	13	IDFG	3	46.37267	-116.70478	30.2%	0.015	13	6
51	Gumboot/Mahogany Cr	IRMAI	IMNAHA	Imnaha River	53	11, 12, 13	IDFG	3	45.18838	-116.87077	28.6%	0.018		
52	Imnaha R IPTDS (IR3)	IRMAI	IMNAHA	Imnaha River	190	10, 11, 12	IDFG/CRITFC	3	45.49004	-116.80393	29.7%	0.015	12	
53	Little Sheep Cr	IRMAI	IMNAHA	Imnaha River	93	11	NWFSC	3	45.47842	-116.92658	29.8%	0.019		
54	Big Sheep Cr/IPTDS (BSC)	IRMAI	IMNAHA	Imnaha River	233	01, 10, 11, 12	CRITFC	1	45.50649	-116.85067	29.7%	0.016		
55	Lightning Cr	IRMAI	IMNAHA	Imnaha River	39	00	CRITFC	1	45.65537	-116.72653	29.1%	0.019		
56	upper Grande Ronde R	GRWAL	GRROND	Grande Ronde River	65	09, 10, 11	NWFSC	3	45.59333	-117.90312	30.4%	0.017		
57	Catherine Cr	GRWAL	GRROND	Grande Ronde River	91	11	NWFSC	3	45.24062	-117.92199	30.5%	0.015	9	2
58	Little Minam R	GRWAL	GRROND	Grande Ronde River	48	00	CRITFC	1	45.34536	-117.65340	29.8%	0.023		
59	Wallowa R	GRWAL	GRROND	Grande Ronde River	72	09, 10, 11	NWFSC	3	45.43254	-117.32342	31.9%	0.016	9	4
60	Lostine R	GRWAL	GRROND	Grande Ronde River	45	00	CRITFC	1	45.42211	-117.42496	30.8%	0.023		
61	Wenaha R	GRLMT	GRROND	Grande Ronde River	191	01	CRITFC	1	45.97269	-117.69367	30.4%	0.015	15	2
62	Menatchee Cr	GRLMT	GRROND	Grande Ronde River	73	99	CRITFC	1	46.04457	-117.38550	31.4%	0.017		
63	Elk Cr (Joseph Cr)	GRJOS	GRROND	Grande Ronde River	45	00	CRITFC	1	45.67203	-117.18960	28.6%	0.025	6	4
64	Joseph Cr/IPTDS (JOC)	GRJOS	GRROND	Grande Ronde River	400	11, 12	IDFG	2	46.03001	-117.01604	30.1%	0.014	10	1
65	Captain John Cr	SRLSR	N/A	Grande Ronde River	56	00	IDFG	2	46.14595	-116.87108	29.8%	0.019		
66	Asotin Cr	SNASO	LSNAKE	Lower Snake River	387	08, 10, 11, 12	IDFG	2	46.32280	-117.13681	31.0%	0.013	13	4
67	Alpowa Cr	SNTUC	LSNAKE	Lower Snake River	98	10	IDFG	2	46.42479	-117.32812	31.1%	0.014		
68	Tucannon R	SNTUC	LSNAKE	Lower Snake River	323	05, 09, 10, 11, 12	IDFG	3	46.41584	-117.73832	31.1%	0.013	17	1

Table 4. Steelhead results from self-assignment tests performed in gsi_sim (Anderson et al. 2008, Anderson 2010). For each baseline collection represented in baseline v3.0, 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 4a is results for all individuals that assigned to a genetic stock, and Table 4b is for individuals that assigned to a genetic stock with ≥80% probability. For example, n = 371 individuals represent the upper Salmon/IPTDS (STL & VAL) collection. Of the 371 individuals in the baseline, 188 (51%) assigned back to a genetic stock with ≥80% probability. Of the 188 that assigned, 170 (90%) assigned to the correct UPSALM genetic stock. Shaded boxes represent the correct genetic stock of origin for each population.

4a.

			Genetic Stock (No Threshold)									
Collection of origin	**n**	**Number Assigned (Proportion)**	**UPSALM**	**MFSALM**	**SFSALM**	**LOSALM**	**UPCLWR**	**SFCLWR**	**LOCLWR**	**IMNAHA**	**GRROND**	**LSNAKE**
Sawtooth	393	393 (1.00)	288 (0.73)	1 (0.00)	2 (0.01)	19 (0.05)	1 (0.00)	1 (0.00)	14 (0.04)	16 (0.04)	36 (0.09)	15 (0.04)
Herd Cr	85	85 (1.00)	59 (0.69)		1 (0.01)	1 (0.01)		1 (0.01)	12 (0.14)	5 (0.06)	4 (0.05)	2 (0.02)
Morgan Cr	61	61 (1.00)	53 (0.87)		1 (0.02)	1 (0.02)			1 (0.02)	2 (0.03)	2 (0.03)	1 (0.02)
Pahsimeroi R	97	97 (1.00)	76 (0.78)	1 (0.01)			1 (0.01)		4 (0.04)	4 (0.04)	5 (0.05)	6 (0.06)
Lemhi R	111	111 (1.00)	91 (0.82)	3 (0.03)		2 (0.02)				1 (0.01)	8 (0.07)	6 (0.05)
NF Salmon R	100	100 (1.00)	58 (0.58)		1 (0.01)	14 (0.14)	1 (0.01)	1 (0.01)	5 (0.05)	8 (0.08)	6 (0.06)	6 (0.06)
Marsh Cr	195	195 (1.00)	29 (0.15)	155 (0.79)		3 (0.02)	1 (0.01)		1 (0.01)	2 (0.01)	2 (0.01)	2 (0.01)
Bear Valley Cr	173	173 (1.00)		165 (0.95)	4 (0.02)	1 (0.01)					3 (0.02)	
MF Salmon R	227	227 (1.00)	7 (0.03)	202 (0.89)		3 (0.01)			1 (0.00)	7 (0.03)	4 (0.02)	3 (0.01)
Loon Cr	131	131 (1.00)		125 (0.95)		3 (0.02)	1 (0.01)			2 (0.02)		
Camas Cr	97	97 (1.00)	1 (0.01)	93 (0.96)	2 (0.02)					1 (0.01)		
Big Cr	224	224 (1.00)	8 (0.04)	204 (0.91)	1 (0.00)	3 (0.01)		1 (0.00)	2 (0.01)	2 (0.01)	1 (0.00)	2 (0.01)
Chamberlain Cr	189	189 (1.00)	5 (0.03)	166 (0.88)	1 (0.01)	4 (0.02)			2 (0.01)	5 (0.03)	5 (0.03)	1 (0.01)
SF Salmon R	319	319 (1.00)	2 (0.01)	3 (0.01)	289 (0.91)	5 (0.02)			5 (0.02)	4 (0.01)	8 (0.03)	3 (0.01)
EFSF Salmon R	288	288 (1.00)	3 (0.01)	9 (0.03)	262 (0.91)	3 (0.01)			3 (0.01)	1 (0.00)	4 (0.01)	3 (0.01)
Secesh R	282	282 (1.00)	5 (0.02)	6 (0.02)	261 (0.93)	4 (0.01)	1 (0.00)		1 (0.00)		3 (0.01)	1 (0.00)
Little Salmon R	147	147 (1.00)	22 (0.15)	9 (0.06)	12 (0.08)	79 (0.54)		4 (0.03)	5 (0.03)	6 (0.04)	5 (0.03)	5 (0.03)
Slate Cr	75	75 (1.00)	13 (0.17)	2 (0.03)	2 (0.03)	37 (0.49)			4 (0.05)	4 (0.05)	7 (0.09)	6 (0.08)
upper Lochsa R	129	129 (1.00)				1 (0.01)	121 (0.94)	7 (0.05)				
middle Lochsa R	147	147 (1.00)	1 (0.01)				134 (0.91)	4 (0.03)	5 (0.03)		2 (0.01)	1 (0.01)
upper Selway R	247	247 (1.00)					241 (0.98)	1 (0.00)	4 (0.02)			1 (0.00)
Bear Cr	70	70 (1.00)	1 (0.01)				68 (0.97)		1 (0.01)			
middle Selway R	138	138 (1.00)					130 (0.94)	4 (0.03)	2 (0.01)	2 (0.01)		
lower Selway R	211	211 (1.00)	1 (0.00)				178 (0.84)	21 (0.10)	7 (0.03)	1 (0.00)	1 (0.00)	2 (0.01)

Collection of origin	n	Number Assigned (Proportion)	Genetic Stock (No Threshold)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
Crooked R	136	136 (1.00)					7 (0.05)	124 (0.91)	4 (0.03)		1 (0.01)	
Newsome Cr	99	99 (1.00)	1 (0.01)				3 (0.03)	93 (0.94)	2 (0.02)			
Tenmile Cr	47	47 (1.00)					5 (0.11)	38 (0.81)	4 (0.09)			
Clear Cr	45	45 (1.00)			1 (0.02)		4 (0.09)	37 (0.82)	3 (0.07)			
Lolo Cr	159	159 (1.00)				1 (0.01)	7 (0.04)	139 (0.87)	11 (0.07)			1 (0.01)
WF Potlatch R	84	84 (1.00)	3 (0.04)		1 (0.01)	1 (0.01)		6 (0.07)	62 (0.74)	2 (0.02)	5 (0.06)	4 (0.05)
EF Potlatch R	158	158 (1.00)			2 (0.01)		5 (0.03)	9 (0.06)	118 (0.75)	2 (0.01)	12 (0.08)	10 (0.06)
Big Bear Cr	250	250 (1.00)	12 (0.05)			2 (0.01)	6 (0.02)	3 (0.01)	177 (0.71)	8 (0.03)	24 (0.10)	18 (0.07)
Potlatch R	123	123 (1.00)	7 (0.06)	2 (0.02)	1 (0.01)	1 (0.01)	2 (0.02)	3 (0.02)	86 (0.70)	6 (0.05)	6 (0.05)	9 (0.07)
Lapwai Cr	158	158 (1.00)	12 (0.08)		1 (0.01)	3 (0.02)	3 (0.02)		86 (0.54)	7 (0.04)	28 (0.18)	18 (0.11)
upper Imnaha R	53	53 (1.00)	1 (0.02)	1 (0.02)		2 (0.04)		1 (0.02)	1 (0.02)	39 (0.74)	6 (0.11)	2 (0.04)
Imnaha R	190	190 (1.00)	9 (0.05)	3 (0.02)	1 (0.01)	6 (0.03)		1 (0.01)	13 (0.07)	137 (0.72)	12 (0.06)	8 (0.04)
Big Sheep Cr	326	326 (1.00)	19 (0.06)	9 (0.03)		10 (0.03)			14 (0.04)	252 (0.77)	11 (0.03)	11 (0.03)
Lightning Cr	39	39 (1.00)	5 (0.13)	1 (0.03)	1 (0.03)	1 (0.03)			4 (0.10)	20 (0.51)	5 (0.13)	2 (0.05)
upper Grande Ronde R	156	156 (1.00)	11 (0.07)	4 (0.03)		6 (0.04)			18 (0.12)	9 (0.06)	90 (0.58)	18 (0.12)
Little Minam R	48	48 (1.00)	1 (0.02)						6 (0.13)		35 (0.73)	6 (0.13)
Wallowa R	117	117 (1.00)	16 (0.14)	1 (0.01)	1 (0.01)	1 (0.01)	1 (0.01)		6 (0.05)	5 (0.04)	79 (0.68)	7 (0.06)
Wenaha R	191	191 (1.00)	9 (0.05)	3 (0.02)	3 (0.02)	6 (0.03)			12 (0.06)	18 (0.09)	121 (0.63)	19 (0.10)
Menatchee Cr	73	73 (1.00)	5 (0.07)	1 (0.01)		2 (0.03)				3 (0.04)	54 (0.74)	8 (0.11)
Joseph Cr	445	445 (1.00)	22 (0.05)	9 (0.02)	2 (0.00)	5 (0.01)	5 (0.01)		42 (0.09)	23 (0.05)	282 (0.63)	55 (0.12)
Asotin Cr	387	387 (1.00)	57 (0.15)	4 (0.01)	1 (0.00)	21 (0.05)	3 (0.01)	4 (0.01)	67 (0.17)	15 (0.04)	86 (0.22)	129 (0.33)
Alpowa Cr	98	98 (1.00)	7 (0.07)			2 (0.02)	1 (0.01)	4 (0.04)	7 (0.07)	6 (0.06)	25 (0.26)	46 (0.47)
Tucannon R	323	323 (1.00)	33 (0.10)	6 (0.02)	1 (0.00)	7 (0.02)	2 (0.01)	1 (0.00)	50 (0.15)	19 (0.06)	89 (0.28)	115 (0.36)

4b.

Collection of origin	n	Number Assigned (Proportion)	Genetic Stock (≥80% Probability)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
Sawtooth	393	188 (0.48)	170 (0.90)	1 (0.01)		4 (0.02)			2 (0.01)	4 (0.02)	7 (0.04)	
Herd Cr	85	54 (0.64)	46 (0.85)		1 (0.02)			1 (0.02)	2 (0.04)	3 (0.06)	1 (0.02)	
Morgan Cr	61	43 (0.70)	41 (0.95)							1 (0.02)	1 (0.02)	
Pahsimeroi R	97	57 (0.59)	53 (0.93)	1 (0.02)						3 (0.05)		
Lemhi R	111	64 (0.58)	62 (0.97)	2 (0.03)								
NF Salmon R	100	31 (0.31)	24 (0.77)			4 (0.13)	1 (0.03)		1 (0.03)			1 (0.03)
Marsh Cr	195	149 (0.76)	6 (0.04)	143 (0.96)								

Collection of origin	n	Number Assigned (Proportion)	Genetic Stock (≥80% Probability)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
Bear Valley Cr	173	163 (0.94)		163 (1.00)								
MF Salmon R	227	193 (0.85)	1 (0.01)	190 (0.98)		1 (0.01)				1 (0.01)		
Loon Cr	131	121 (0.92)		120 (0.99)						1 (0.01)		
Camas Cr	97	91 (0.94)	1 (0.01)	89 (0.98)						1 (0.01)		
Big Cr	224	198 (0.88)	3 (0.02)	192 (0.97)				1 (0.01)			1 (0.01)	1 (0.01)
Chamberlain Cr	189	158 (0.84)	1 (0.01)	155 (0.98)		1 (0.01)				1 (0.01)		
SF Salmon R	319	280 (0.88)	1 (0.00)	3 (0.01)	273 (0.98)					1 (0.00)	1 (0.00)	1 (0.00)
EFSF Salmon R	288	250 (0.87)	1 (0.00)	5 (0.02)	243 (0.97)					1 (0.00)		
Secesh R	282	241 (0.85)	3 (0.01)	1 (0.00)	237 (0.98)							
Little Salmon R	147	77 (0.52)	16 (0.21)	5 (0.06)	4 (0.05)	49 (0.64)		2 (0.03)			1 (0.01)	
Slate Cr	75	26 (0.35)	2 (0.08)		2 (0.08)	20 (0.77)				1 (0.04)	1 (0.04)	
upper Lochsa R	129	117 (0.91)					115 (0.98)	2 (0.02)				
middle Lochsa R	147	136 (0.93)					131 (0.96)	4 (0.03)	1 (0.01)			
upper Selway R	247	236 (0.96)					235 (1.00)		1 (0.00)			
Bear Cr	70	67 (0.96)					67 (1.00)					
middle Selway R	138	125 (0.91)					123 (0.98)	1 (0.01)		1 (0.01)		
lower Selway R	211	173 (0.82)					157 (0.91)	14 (0.08)	2 (0.01)			
Crooked R	136	121 (0.89)					2 (0.02)	119 (0.98)				
Newsome Cr	99	86 (0.87)						86 (1.00)				
Tenmile Cr	47	35 (0.74)					3 (0.09)	32 (0.91)				
Clear Cr	45	32 (0.71)					2 (0.06)	30 (0.94)				
Lolo Cr	159	137 (0.86)					3 (0.02)	132 (0.96)	2 (0.01)			
WF Potlatch R	84	47 (0.56)						2 (0.04)	43 (0.91)		2 (0.04)	
EF Potlatch R	158	102 (0.65)					2 (0.02)	2 (0.02)	96 (0.94)		1 (0.01)	1 (0.01)
Big Bear Cr	250	134 (0.54)	2 (0.01)			1 (0.01)	1 (0.01)	2 (0.01)	120 (0.90)	1 (0.01)	4 (0.03)	3 (0.02)
Potlatch R	123	57 (0.46)	3 (0.05)				2 (0.04)	1 (0.02)	46 (0.81)	1 (0.02)	2 (0.04)	2 (0.04)
Lapwai Cr	158	45 (0.28)	4 (0.09)						36 (0.80)	1 (0.02)	4 (0.09)	
upper Imnaha R	53	33 (0.62)								32 (0.97)	1 (0.03)	
Imnaha R	190	94 (0.49)	2 (0.02)	2 (0.02)		2 (0.02)			1 (0.01)	85 (0.90)	2 (0.02)	
Big Sheep Cr	326	182 (0.56)	2 (0.01)	2 (0.01)		1 (0.01)			3 (0.02)	172 (0.95)	1 (0.01)	1 (0.01)
Lightning Cr	39	17 (0.44)	1 (0.06)							16 (0.94)		
upper Grande Ronde R	156	43 (0.28)	4 (0.09)	3 (0.07)					2 (0.05)	3 (0.07)	30 (0.70)	1 (0.02)
Little Minam R	48	27 (0.56)							1 (0.04)		26 (0.96)	
Wallowa R	117	40 (0.34)	5 (0.13)						1 (0.03)	1 (0.03)	33 (0.83)	
Wenaha R	191	66 (0.35)	3 (0.05)	1 (0.02)					2 (0.03)	5 (0.08)	53 (0.80)	2 (0.03)
Menatchee Cr	73	27 (0.37)									27 (1.00)	
Joseph Cr	445	147 (0.33)	3 (0.02)	2 (0.01)			2 (0.01)		7 (0.05)	5 (0.03)	125 (0.85)	3 (0.02)
Asotin Cr	387	63 (0.16)	12 (0.19)	1 (0.02)		2 (0.03)			14 (0.22)	4 (0.06)	12 (0.19)	18 (0.29)

Collection of origin	n	Number Assigned (Proportion)	Genetic Stock (≥80% Probability)									
			UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
Alpowa Cr	98	28 (0.29)	3 (0.11)			1 (0.04)		3 (0.11)	1 (0.04)		8 (0.29)	12 (0.43)
Tucannon R	323	82 (0.25)	10 (0.12)	3 (0.04)		1 (0.01)		1 (0.01)	13 (0.16)	5 (0.06)	19 (0.23)	30 (0.37)

Table 5. Fifty-seven 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–Weinbe.rg 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	GS	MPG	n	Years Collected	Genotype Agency	Baseline version	Lineage	Latitude	Longitude	He	Fst	HWE	
														Deficient	Excess
1	Decker Flat	SRUMA	UPSALM	Upper Salmon River	95	10, 11	NWFSC	3.0	ST	44.06537	-114.85580	22.7%	0.012		
2	Sawtooth Weir	SRUMA	UPSALM	Upper Salmon River	91	09, 10	IDFG	1.0	ST	44.15066	-114.88545	22.0%	0.012		
3	Sawtooth/IPTDS (STL)	SRUMA	UPSALM	Upper Salmon River	159	10, 11, 12	IDFG/CRITFC	3.0	ST	44.15327	-114.88371	22.4%	0.011		
4	Valley Cr	SRVAL	UPSALM	Upper Salmon River	100	07, 08, 09, 10, 11	IDFG	2.0	ST	44.24084	-115.00155	22.9%	0.013	7	6
5	Valley Cr/IPTDS (VAL)	SRVAL	UPSALM	Upper Salmon River	87	10, 11, 12	IDFG/CRITFC	3.0	ST	44.22259	-114.93051	22.8%	0.013		
6	WF Yankee Fork	SRYFS	UPSALM	Upper Salmon River	75	05	CRITFC	3.0	ST	44.34484	-114.72517	22.3%	0.018		
7	upper Salmon mainstem	SLRMA	UPSALM	Upper Salmon River	83	05, 06, 07, 08, 09, 10	IDFG	3.0	ST	44.25568	-114.56477	22.5%	0.013		
8	Herd Cr	SREFS	UPSALM	Upper Salmon River	99	10, 11	NWFSC	3.0	ST	44.12319	-114.26642	21.6%	0.016		
9	East Fork SR	SREFS	UPSALM	Upper Salmon River	187	04, 05, 11	IDFG/CRITFC	1.0	ST	44.20019	-114.28613	22.4%	0.013		
10	Pahsimeroi R	SRPAH	UPSALM	Upper Salmon River	92	07, 08, 09, 10	IDFG	1.0	ST	44.56296	-113.91237	22.9%	0.016		
11	Hayden Cr	SRLEM	UPSALM	Upper Salmon River	79	09, 10	IDFG	1.0	ST	44.78536	-113.70588	23.5%	0.019		
12	upper Lemhi R	SRLEM	UPSALM	Upper Salmon River	96	09, 10	IDFG	1.0	ST	44.82673	-113.60684	21.5%	0.017	7	8
13	Lemhi R/IPTDSs (HYC & LRW)	SRLEM	UPSALM	Upper Salmon River	36	10, 11, 12	IDFG/CRITFC	3.0	ST	44.86612	-113.62475	22.8%	0.013		
14	lower Lemhi R	SRLEM	UPSALM	Upper Salmon River	90	09, 10	IDFG	1.0	ST	45.16639	-113.86137	23.6%	0.013	9	3
15	NF Salmon R	SRNFS	UPSALM	Upper Salmon River	55	05, 06, 07, 08, 09, 10	IDFG	3.0	ST	45.50104	-113.96306	22.6%	0.015		
16	Panther Cr	SRPAN	UPSALM	Upper Salmon River	86	10, 11	IDFG	3.0	ST	45.20673	-114.32009	22.4%	0.012		
17	Marsh Cr	MFMAR	MFSALM	Middle Fork Salmon River	116	07, 08, 09, 10, 11	IDFG	1.0	ST	44.41532	-115.18423	21.6%	0.013		
18	Capehorn Cr	MFMAR	MFSALM	Middle Fork Salmon River	112	05, 06, 07, 09, 10	IDFG/CRITFC	1.0	ST	44.35864	-115.22362	21.5%	0.017	7	6
19	Elk Cr (MF Salmon R)	MFBEA	MFSALM	Middle Fork Salmon River	134	07, 08, 09, 10, 11	IDFG/NWFSC	1.0	ST	44.43041	-115.47107	21.2%	0.016		
20	Bear Valley Cr	MFBEA	MFSALM	Middle Fork Salmon River	80	07, 08, 09, 10	IDFG	1.0	ST	44.37347	-115.39544	21.5%	0.014		
21	Sulphur Cr	MFSUL	MFSALM	Middle Fork Salmon River	135	08, 09, 10, 11	IDFG/NWFSC	1.0	ST	44.54330	-115.39615	20.6%	0.018		
22	Loon Cr	MFLOO	MFSALM	Middle Fork Salmon River	94	10, 11	IDFG	3.0	ST	44.59815	-114.81104	21.6%	0.016		
23	Camas Cr	MFCAM	MFSALM	Middle Fork Salmon River	107	06, 09, 10	IDFG/CRITFC	1.0	ST	44.82550	-114.49964	21.0%	0.016		
24	upper Big Cr	MFBIG	MFSALM	Middle Fork Salmon River	55	10, 11	IDFG/CRITFC	1.0	ST	45.15304	-115.29609	21.5%	0.017		
25	lower Big Cr	MFBIG	MFSALM	Middle Fork Salmon River	139	01, 11	CRITFC/NWFSC	1.0	ST	45.10717	-114.80611	21.7%	0.012	11	1
26	Big Cr/IPTDS (TAY)	MFBIG	MFSALM	Middle Fork Salmon River	98	10, 11, 12	IDFG/CRITFC	3.0	ST	45.10401	-114.85018	22.0%	0.011		
27	Chamberlain Cr (pre-2008)	SRCHA	CHMBLN	Middle Fork Salmon River	70	03, 04, 06, 07	IDFG	2.0	ST	45.39364	-115.19440	21.1%	0.021		
28	Chamberlain Cr (post-2008)	SRCHA	CHMBLN	Middle Fork Salmon River	149	09, 10	IDFG/CRITFC	1.0	ST	45.37078	-115.19671	21.0%	0.023		
29	Summit and Lake Cr	SFSEC	SFSALM	South Fork Salmon River	122	07, 08, 09, 10, 11	IDFG	1.0	ST	45.27121	-115.91413	21.8%	0.016		

Table 5. Continued.

Map #	Collection	TRT	GS	MPG	n	Years Collected	Genotype Agency	Baseline version	Lineage	Latitude	Longitude	He	Fst	HWE Deficient	HWE Excess
30	Secesh R/IPTDS (ZEN)	SFEFS	SFSALM	South Fork Salmon River	174	10, 11, 12	IDFG/CRITFC/NWFSC	3.0	ST	45.03397	-115.73627	21.8%	0.014		
31	Sesech R	SFSEC	SFSALM	South Fork Salmon River	130	01, 07, 08, 09, 10	IDFG/CRITFC	1.0	ST	45.21723	-115.80862	21.9%	0.014		
32	EFSF Salmon R/IPTDS (ESS)	SFMAI	SFSALM	South Fork Salmon River	143	10, 11, 12	IDFG/CRITFC	3.0	ST	44.95620	-115.53255	22.4%	0.012		
33	Johnson Cr	SFMAI	SFSALM	South Fork Salmon River	137	02, 11	CRITFC/NWFSC	1.0	ST	44.90585	-115.48672	22.3%	0.014		
34	upper SF Salmon R/IPTDS (KRS)	SFMAI	SFSALM	South Fork Salmon River	349	10, 11, 12	IDFG/CRITFC	3.0	ST	44.97852	-115.72739	22.8%	0.009		
35	SF Salmon R mainstem	SFMAI	SFSALM	South Fork Salmon River	139	09, 10	IDFG	1.0	ST	44.66661	-115.70292	22.9%	0.010		
36	SF Salmon R/IPTDS (STR)	SFMAI	SFSALM	South Fork Salmon River	121	10, 11, 12	IDFG/CRITFC	3.0	ST	44.66853	-115.70537	22.8%	0.010		
37	Rapid R	SRLSR	HELLSC	N/A	91	06	IDFG	1.0	ST	45.31630	-116.41804	22.8%	0.014	7	3
38	Crooked F (Lochsa R)	CRLOC	HELLSC	N/A	26	07, 08, 09, 10	IDFG	2.0	ST	46.61875	-114.66711	24.3%	0.015		
39	Powell Weir	CRLOC	HELLSC	N/A	30	09	IDFG	1.0	ST	46.50701	-114.68739	23.3%	0.013		
40	Red R	SCUMA	HELLSC	N/A	72	07, 08, 09, 10	IDFG	1.0	ST	45.70942	-115.33989	24.1%	0.012		
41	Crooked R Weir	SCUMA	HELLSC	N/A	67	09, 10	IDFG	1.0	ST	45.76553	-115.54375	24.1%	0.012		
42	Newsome Cr	SCUMA	HELLSC	N/A	82	01	CRITFC	1.0	ST	45.83376	-115.61115	22.9%	0.014		
43	Lolo Cr/IPTDS (LC2)	CRLOL	HELLSC	N/A	31	10, 11, 12	IDFG/CRITFC	3.0	ST	46.29079	-115.92267	24.3%	0.015		
44	Lolo Cr	CRLOL	HELLSC	N/A	89	01, 02	IDFG/CRITFC	1.0	ST	46.28015	-115.77274	23.9%	0.012	12	3
45	Imnaha R/IPTDS (IR2 & IR3)	IRMAI	HELLSC	Grande Ronde / Imnaha	302	10, 11, 12	IDFG/CRITFC	3.0	ST	45.49004	-116.80393	24.1%	0.011	13	2
46	Imnaha R (08' & 10')	IRMAI	HELLSC	Grande Ronde / Imnaha	96	08, 10	IDFG/NOAA	2.0	ST	45.49004	-116.80393	23.6%	0.012		
47	Big Sheep Cr/IPTDS (BSC)	IRBSH	HELLSC	Grande Ronde / Imnaha	47	10, 11, 12	IDFG/CRITFC	3.0	ST	45.51062	-116.85369	24.0%	0.013	7	3
48	upper Grande Ronde R	GRUMA	HELLSC	Grande Ronde / Imnaha	43	08	IDFG/NOAA	2.0	ST	45.19318	-118.39441	24.6%	0.015		
49	Catherine Cr	GRCAT	HELLSC	Grande Ronde / Imnaha	140	04, 06, 11	IDFG/CRITFC/NWFSC	2.0	ST	45.15485	-117.77926	24.9%	0.012	9	2
50	Minam R	GRMIN	HELLSC	Grande Ronde / Imnaha	131	94, 02, 10	IDFG/CRITFC/NWFSC	1.0	ST	45.34755	-117.65335	25.2%	0.013	11	1
51	Wallowa R & Hurricane Cr	GRLOS	HELLSC	Grande Ronde / Imnaha	37	11	IDFG	3.0	ST	45.42408	-117.29267	25.8%	0.019		
52	Lostine R	GRLOS	HELLSC	Grande Ronde / Imnaha	175	03, 05, 09	IDFG//NOAA	2.0	ST	45.47359	-117.42573	23.0%	0.014		
53	Wenaha R	GRWEN	HELLSC	Grande Ronde / Imnaha	179	02, 06, 09, 10	CRITFC	1.0	ST	45.96890	-117.69559	26.4%	0.014	9	3
54	Tucannon R	SNTUC	TUCANO	Tucannon river	81	03	CRITFC	1.0	ST	46.50530	-118.01440	26.1%	0.025		
55	Clearwater R	FALL ESU	FALL	Snake River	143	08	IDFG/CRITFC	2.0	OC	46.52285	-116.61520	30.0%	N/A	7	6
56	Nez Perce Tribal H.	FALL ESU	FALL	Snake River	85	03	CRITFC	2.0	OC	46.51910	-116.66460	29.4%	N/A		
57	Lyons Ferry H.	FALL ESU	FALL	Snake River	90	00	CRITFC	2.0	OC	46.58940	-118.21950	29.4%	N/A		

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 v3.0, 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 = 345 individuals represent the Sawtooth/IPTDS (STL) collection. Of the 345 individuals in the baseline, 248 (72%) assigned back to a genetic stock with ≥80% probability. Of the 248 that assigned, 232 (94%) assigned to the correct UPSALM reporting group. Shaded boxes represent the correct genetic stock of origin for each population

6a.

Collection of Origin	n	Number Assigned (Proportion)	Assigned Generic Stock (No Threshold)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
Sawtooth	345	345 (1.00)	286 (0.83)	29 (0.08)		10 (0.03)	20 (0.06)		
Valley Cr	187	187 (1.00)	169 (0.90)	7 (0.04)	1 (0.01)	2 (0.01)	7 (0.04)	1 (0.01)	
WF Yankee Fork	75	75 (1.00)	69 (0.92)			2 (0.03)	4 (0.05)		
upper Salmon R	83	83 (1.00)	76 (0.92)	4 (0.05)		1 (0.01)	2 (0.02)		
EF Salmon R	286	286 (1.00)	263 (0.92)	9 (0.03)		3 (0.01)	11 (0.04)		
Pahsimeroi R	92	92 (1.00)	85 (0.92)	1 (0.01)		2 (0.02)	4 (0.04)		
Lemhi R	117	117 (1.00)	93 (0.79)	9 (0.08)		5 (0.04)	10 (0.09)		
NF Salmon R	55	55 (1.00)	42 (0.76)	3 (0.05)	1 (0.02)	2 (0.04)	7 (0.13)		
Marsh Cr	228	228 (1.00)	12 (0.05)	192 (0.84)		17 (0.07)	7 (0.03)		
Bear Valley Cr	214	214 (1.00)	6 (0.03)	194 (0.91)	1 (0.00)	7 (0.03)	6 (0.03)		
Sulphur Cr	135	135 (1.00)	2 (0.01)	129 (0.96)		3 (0.02)	1 (0.01)		
Loon Cr	94	94 (1.00)	5 (0.05)	82 (0.87)			7 (0.07)		
Camas Cr	107	107 (1.00)	2 (0.02)	94 (0.88)	1 (0.01)	4 (0.04)	6 (0.06)		
upper Big Cr	55	55 (1.00)	4 (0.07)	48 (0.87)	2 (0.04)		1 (0.02)		
lower Big Cr	237	237 (1.00)	30 (0.13)	159 (0.67)	6 (0.03)	8 (0.03)	34 (0.14)		
Chamberlain Cr	219	219 (1.00)	3 (0.01)	5 (0.02)	194 (0.89)	4 (0.02)	13 (0.06)		
Sesech R	426	426 (1.00)	12 (0.03)	25 (0.06)	1 (0.00)	371 (0.87)	17 (0.04)		
EFSF Salmon R	280	280 (1.00)	11 (0.04)	27 (0.10)		216 (0.77)	26 (0.09)		
SF Salmon R	609	609 (1.00)	82 (0.13)	96 (0.16)	6 (0.01)	329 (0.54)	96 (0.16)		
Rapid R	91	91 (1.00)	4 (0.04)	1 (0.01)		3 (0.03)	83 (0.91)		
upper Lochsa R	56	56 (1.00)	6 (0.11)	4 (0.07)		1 (0.02)	44 (0.79)	1 (0.02)	
SF Clearwater R	221	221 (1.00)	10 (0.05)	5 (0.02)		3 (0.01)	203 (0.92)		
Lolo Cr	120	120 (1.00)	11 (0.09)	4 (0.03)	1 (0.01)	3 (0.03)	100 (0.83)	1 (0.01)	
Imnaha R	420	420 (1.00)	30 (0.07)	19 (0.05)	5 (0.01)	20 (0.05)	343 (0.82)	2 (0.00)	1 (0.00)
upper Grande Ronde R	339	339 (1.00)	16 (0.05)	10 (0.03)	1 (0.00)	9 (0.03)	302 (0.89)	1 (0.00)	
Wallowa R	212	212 (1.00)	8 (0.04)	4 (0.02)		4 (0.02)	195 (0.92)	1 (0.00)	
Wenaha R	179	179 (1.00)	7 (0.04)		1 (0.01)	5 (0.03)	156 (0.87)	6 (0.03)	4 (0.02)
Tucannon R	81	81 (1.00)	1 (0.01)	1 (0.01)		1 (0.01)	11 (0.14)	66 (0.81)	1 (0.01)
Clearwater R	228	228 (1.00)							228 (1.00)
Lyons Ferry	90	90 (1.00)							90 (1.00)

6b.

Collection of Origin	n	Number Assigned (Proportion)	Assigned Generic Stock (≥80% Probability)						
			UPSALM	MFSALM	CHMBLN	SFSALM	HELLSC	TUCANO	FALL
Sawtooth	345	248 (0.72)	232 (0.94)	8 (0.03)		2 (0.01)	6 (0.02)		
Valley Cr	187	150 (0.80)	142 (0.95)	4 (0.03)	1 (0.01)		2 (0.01)	1 (0.01)	
WF Yankee Fork	75	65 (0.87)	63 (0.97)			1 (0.02)	1 (0.02)		
upper Salmon R	83	68 (0.82)	66 (0.97)	2 (0.03)					
EF Salmon R	286	234 (0.82)	223 (0.95)	5 (0.02)		1 (0.00)	5 (0.02)		
Pahsimeroi R	92	77 (0.84)	76 (0.99)			1 (0.01)			
Lemhi R	117	83 (0.71)	75 (0.90)	4 (0.05)		1 (0.01)	3 (0.04)		
NF Salmon R	55	36 (0.65)	32 (0.89)			2 (0.06)	2 (0.06)		
Marsh Cr	228	164 (0.72)	4 (0.02)	154 (0.94)		4 (0.02)	2 (0.01)		
Bear Valley Cr	214	172 (0.80)		165 (0.96)	1 (0.01)	2 (0.01)	4 (0.02)		
Sulphur Cr	135	120 (0.89)		119 (0.99)		1 (0.01)			
Loon Cr	94	75 (0.80)	2 (0.03)	73 (0.97)					
Camas Cr	107	84 (0.79)		80 (0.95)		1 (0.01)	3 (0.04)		
upper Big Cr	55	45 (0.82)	1 (0.02)	42 (0.93)	2 (0.04)				
lower Big Cr	237	150 (0.63)	13 (0.09)	112 (0.75)	4 (0.03)	2 (0.01)	19 (0.13)		
Chamberlain Cr	219	191 (0.87)	1 (0.01)	1 (0.01)	181 (0.95)		8 (0.04)		
Sesech R	428	329 (0.77)	3 (0.01)	7 (0.02)	1 (0.00)	310 (0.94)	8 (0.02)		
EFSF Salmon R	284	176 (0.62)		10 (0.06)		154 (0.88)	12 (0.07)		
SF Salmon R	610	261 (0.43)	32 (0.12)	27 (0.10)		160 (0.61)	42 (0.16)		
Rapid R	91	79 (0.87)				1 (0.01)	78 (0.99)		
upper Lochsa R	56	35 (0.63)	1 (0.03)	1 (0.03)			33 (0.94)		
SF Clearwater R	221	184 (0.83)	8 (0.04)	2 (0.01)		1 (0.01)	173 (0.94)		
Lolo Cr	120	94 (0.78)	4 (0.04)	1 (0.01)	1 (0.01)		87 (0.93)	1 (0.01)	
Imnaha R	420	286 (0.68)	8 (0.03)	4 (0.01)	2 (0.01)	3 (0.01)	267 (0.93)	1 (0.00)	1 (0.00)
upper Grande Ronde R	339	263 (0.78)	4 (0.02)	2 (0.01)	1 (0.00)	2 (0.01)	253 (0.96)	1 (0.00)	
Wallowa R	213	175 (0.82)	3 (0.02)	1 (0.01)		2 (0.01)	168 (0.96)	1 (0.01)	
Wenaha R	183	148 (0.81)	1 (0.01)			1 (0.01)	139 (0.94)	3 (0.02)	4 (0.03)
Tucannon R	82	72 (0.88)		1 (0.01)		1 (0.01)	7 (0.10)	62 (0.86)	1 (0.01)
Clearwater R	228	228 (1.00)							228 (1.00)
Lyons Ferry	90	90 (1.00)							90 (1.00)

Table 7. Summary of SY2013 adult and MY2013 juvenile steelhead and Chinook salmon samples from Lower Granite Dam (LGR). Summary includes the number of samples that arrived from LGR (inventoried) and the number inventoried that were queued for genotyping. Of queued samples, we show the number that genotyped successfully and the number that failed genotyping. For samples that genotyped successfully, we show the number that had a parentage based tag (PBT) and the number that were assigned a genetic stock based on individual assignment (IA) using SNP baselines v3.

Sample Group	Total Samples Inventoried	Samples Queued for Genotyping	Failed Genotyping (NG)	Successfully Genotyped	PBT Assignments	GSI Assignments
Steelhead						
SY2013 Adults (Wild Phenotype)	3,878	3,876	3 (0.1%)	3,873 (99.9%)	452 (11.7%)	3,418 (88.3%)
SY2013 Adults (Stubbies)	604	603	1 (0.2%)	602 (99.8%)	512 (85.0%)	90 (15.0%)
MY2013 Juveniles	1,807	1,807	4 (0.2%)	1,803 (99.8%)	48 (2.7%)	1,755 (97.3%)
Chinook						
SY2013 Adults	3,494	3,490	29 (0.8%)	3,461 (99.2%)	456 (13.2%)	3,005 (86.8%)
MY2013 Juveniles (Yearling)	1,468	1,468	29 (2.0%)	1,439 (98.0%)	174 (12.1%)	1,265 (87.9%)
MY2013 Juveniles (Sub-yearling)	1,660	553	3 (0.5%)	550 (99.5%)	1 (0.2%)	549 (99.8%)
TOTAL:	12,911	11,797	69 (0.6%)	11,728 (99.4%)	1,643 (14.0%)	10,085 (86.0%)

Table 8. Summary of 3,508 Lower Granite Dam (LGR) **adult steelhead** samples from **SY2013** assigned to a genetic stock using individual assignment based on **Snake River steelhead SNP baseline v3**. 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	581	16.6%	370	203	8	65%	35%	65.0	570	11	98%	2%	186	230	1	164	45%	55%	0%	9/5	9/15	9/26	10/6	11/4
MFSALM	302	8.6%	222	76	4	74%	26%	70.6	222	80	74%	26%	67	149	1	85	31%	69%	0%	9/2	9/13	9/21	9/30	10/23
SFSALM	143	4.1%	106	37	0	74%	26%	76.3	66	77	46%	54%	20	102	2	19	16%	82%	2%	9/8	9/16	9/25	10/3	10/20
LOSALM	107	3.1%	66	41	0	62%	38%	65.8	96	11	90%	10%	35	42	0	30	45%	55%	0%	9/6	9/17	9/26	10/12	11/8
UPCLWR	202	5.8%	153	47	2	77%	24%	78.3	75	127	37%	63%	11	111	3	77	9%	89%	2%	9/13	9/25	10/3	10/16	11/1
SFCLWR	260	7.4%	160	96	4	63%	38%	78.6	100	160	38%	62%	9	157	9	85	5%	90%	5%	9/13	9/26	10/5	10/21	11/7
LOCLWR	355	10.1%	238	111	6	68%	32%	69.7	314	41	88%	12%	66	202	2	85	24%	75%	1%	9/7	9/18	10/2	10/17	11/11
IMNAHA	308	8.8%	216	89	3	71%	29%	64.1	304	4	99%	1%	114	132	0	62	46%	54%	0%	9/7	9/15	9/25	10/8	11/3
GRROND	830	23.7%	568	257	5	69%	31%	66.1	814	16	98%	2%	215	352	0	263	38%	62%	0%	9/7	9/17	9/29	10/17	11/6
LSNAKE	420	12.0%	278	134	8	67%	33%	66.4	408	12	97%	3%	108	201	0	111	35%	65%	0%	9/2	9/15	9/26	10/7	11/2
Total:	**3,508**		**2,377**	**1,091**	**40**	**69%**	**31%**	**68.5**	**2,969**	**539**	**85%**	**15%**	**831**	**1,678**	**18**	**981**	**33%**	**66%**	**1%**	**9/6**	**9/17**	**9/28**	**10/11**	**11/5**

Table 9. Summary of 1,755 Lower Granite Dam (LGR) **juvenile steelhead** samples from **MY2013** assigned to a genetic stock using individual assignment based on **Snake River steelhead SNP baseline v3**. 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	296	16.9%	176	119	1	60%	40%	180	51	153	77	9	1	5	18%	53%	26%	3%	0%	4/18	5/10	5/16	5/27	6/4
MFSALM	137	7.8%	93	44	0	68%	32%	183	1	36	74	22	1	3	1%	27%	55%	16%	1%	4/16	5/7	5/13	5/22	5/30
SFSALM	62	3.5%	48	13	1	79%	21%	185	0	5	40	16	0	1	0%	8%	66%	26%	0%	4/9	4/15	5/10	5/19	5/30
LOSALM	64	3.6%	41	23	0	64%	36%	184	4	26	27	6	0	1	6%	41%	43%	10%	0%	4/26	5/9	5/15	5/27	6/4
UPCLWR	186	10.6%	109	76	1	59%	41%	176	3	46	106	23	0	8	2%	26%	60%	13%	0%	4/9	4/16	5/6	5/13	5/29
SFCLWR	186	10.6%	105	79	2	57%	43%	173	29	94	55	4	0	4	16%	52%	30%	2%	0%	4/6	4/30	5/10	5/22	5/31
LOCLWR	166	9.5%	94	71	1	57%	43%	176	40	81	34	3	0	8	25%	51%	22%	2%	0%	4/10	5/3	5/14	5/21	5/31
IMNAHA	165	9.4%	108	57	0	65%	35%	180	12	76	67	5	0	5	8%	48%	42%	3%	0%	4/24	5/13	5/16	5/28	6/5
GRROND	338	19.3%	215	120	3	64%	36%	181	30	182	102	13	0	11	9%	56%	31%	4%	0%	4/4	5/9	5/15	5/23	6/11
LSNAKE	155	8.8%	81	74	0	52%	48%	179	36	78	29	4	1	7	24%	53%	20%	3%	1%	4/4	5/8	5/16	5/27	6/7
Total:	**1,755**		**1,070**	**676**	**9**	**61%**	**39%**	**179**	**206**	**777**	**611**	**105**	**3**	**53**	**12%**	**46%**	**36%**	**6%**	**0%**	**4/9**	**5/6**	**5/14**	**5/24**	**6/4**

Table 10. Summary of 3,005 Lower Granite Dam (LGR) **adult Chinook salmon** samples from **SY2013** assigned to a genetic stock using individual assignment based on **Snake River Chinook salmon SNP baseline v3**. 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												Emigration 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	U	5th	25th	Med	75th	95th
UPSALM	624	20.8%	188	433	3	30%	70%	68.8	76.8	0	156	250	137	0	81	0%	29%	46%	25%	0%		5/9	5/22	6/7	6/24	7/5
MFSALM	603	20.1%	144	453	6	24%	76%	65.3	76.9	0	194	165	90	0	154	0%	43%	37%	20%	0%		5/8	5/20	5/31	6/13	7/2
CHMBLN	121	4.0%	39	81	1	33%	68%	65.5	74.2	0	39	44	9	0	29	0%	42%	48%	10%	0%		5/16	6/4	6/11	6/19	7/5
SFSALM	492	16.4%	146	340	6	30%	70%	67.8	76.6	0	174	187	81	0	50	0%	39%	42%	18%	0%		5/20	6/5	6/17	6/26	7/5
HELLSC	1,086	36.1%	413	664	9	38%	62%	69.4	75.8	0	211	374	244	1	256	0%	25%	45%	29%	0%		5/7	5/14	5/24	6/13	7/2
TUCANO	17	0.6%	9	8	0	53%	47%	65.6	73.5	0	4	7	3	0	3	0%	29%	50%	21%	0%		-	-	-	-	-
FALL	62	2.1%	24	36	2	40%	60%	66.6	78.1	2	12	12	12	1	23	5%	31%	31%	31%	3%		-	-	-	-	-
Total:	**3,005**		**963**	**2,015**	**27**	**32%**	**68%**	**68.0**	**76.3**	**2**	**790**	**1,039**	**576**	**2**	**596**	**0%**	**33%**	**43%**	**24%**	**0%**		**5/8**	**5/20**	**6/5**	**6/19**	**7/4**

Table 11. Summary of 1,814 Lower Granite Dam (LGR) **juvenile Chinook salmon** samples from **MY2013** assigned to a genetic stock using individual assignment based on **Snake River Chinook salmon SNP baseline v3**. Summaries of life-history diversity information (sex, length, freshwater age, and emigration timing at LGR) by genetic stock are shown.

			Sex					Length	Freshwater Age		Emigration Timing				
			Frequency			Percentage			Frequency		Quantiles				
Genetic Stock	Total Assignments	% Stock Composition	F	M	U	F	M	Mean Length (mm FL)	0	1	5th	25th	Med	75th	95th
UPSALM	236	13.0%	131	103	2	56%	44%	115.7	4	232	4/2	4/17	4/30	5/20	5/29
MFSALM	174	9.6%	79	92	3	46%	54%	110.9	1	173	4/8	4/19	5/7	5/21	5/29
CHMBLN	11	0.6%	5	5	1	50%	50%	107.3	0	11	-	-	-	-	-
SFSALM	116	6.4%	61	53	2	54%	46%	108.7	3	113	4/2	4/15	4/24	5/14	5/24
HELLSC	579	31.9%	316	259	4	55%	45%	117.4	15	564	3/28	4/3	4/16	5/13	5/31
TUCANO	4	0.2%	3	1	0	75%	25%	124.3	0	4	-	-	-	-	-
FALL	694	38.3%	320	369	5	46%	54%	100	526	168	5/22	5/30	6/6	6/23	7/3
Total:	**1,814**		**915**	**882**	**17**	**51%**	**49%**	**115**	**549**	**1,265**	**3/29**	**4/9**	**4/24**	**5/17**	**5/30**

FIGURES

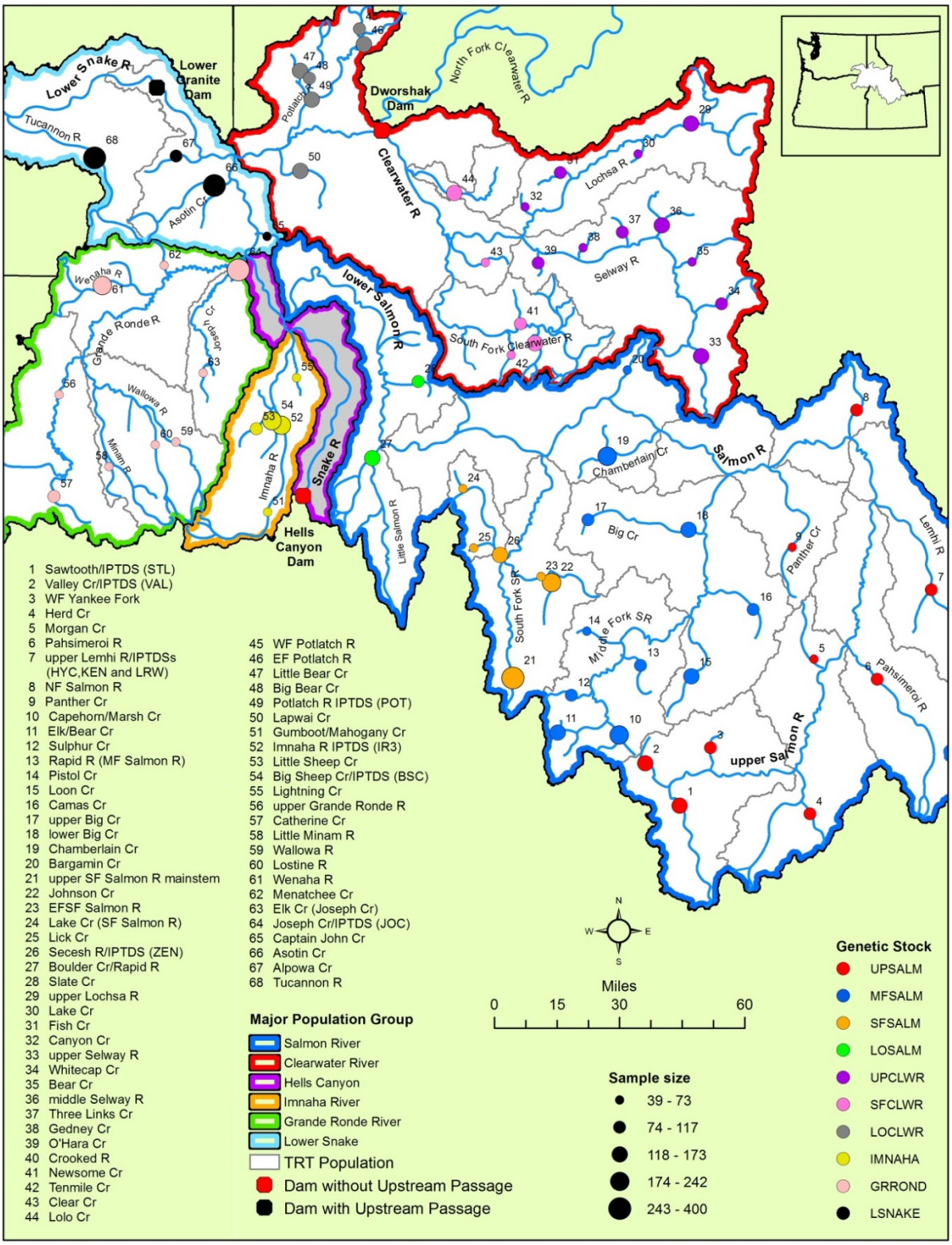

Figure 1. Natural origin steelhead baseline v3 consists of 68 collections located within 23 TRT populations. TRT populations are grouped into 10 Genetic Stocks spanning across 6 Major Population Groups. Collections are described in greater detail in Table 3.

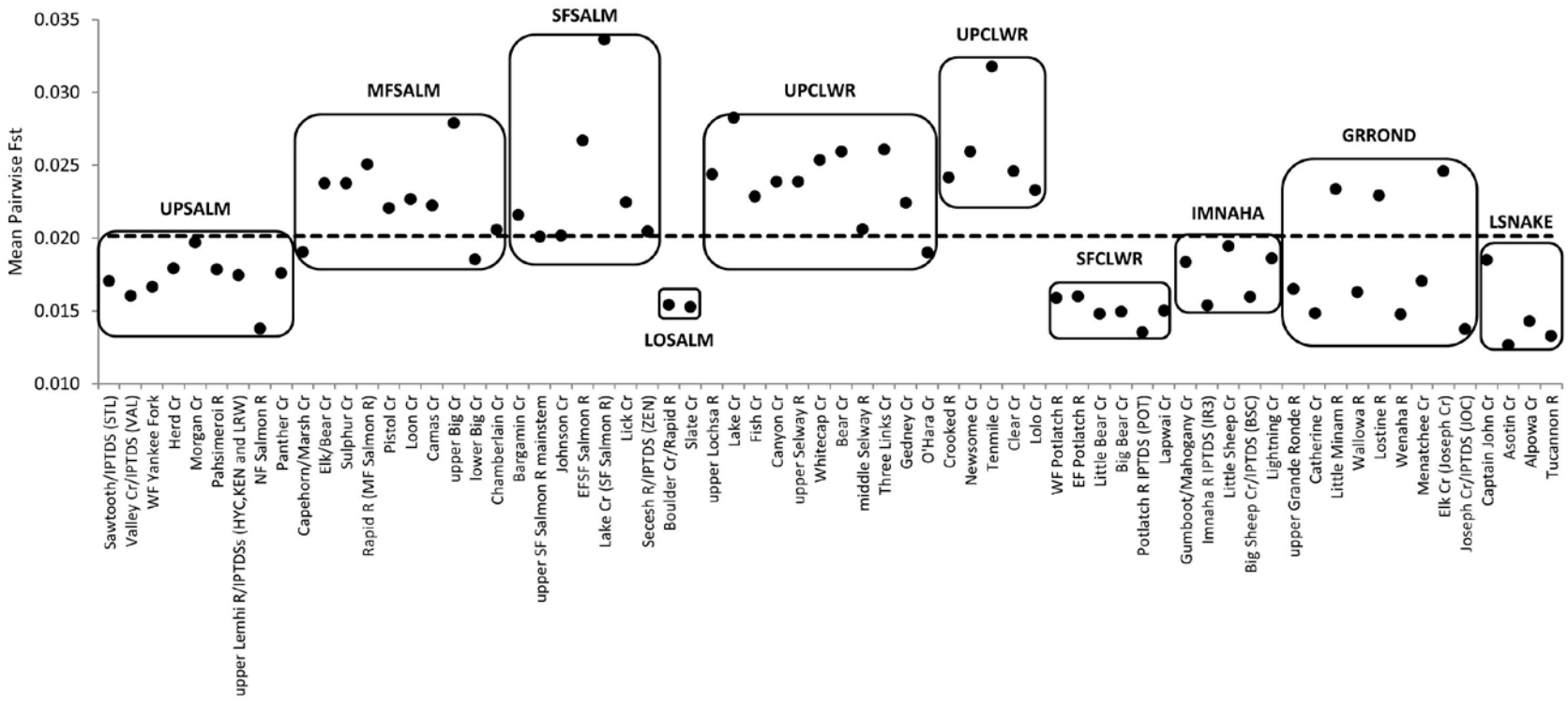

Figure 2. Mean pairwise F_{ST} estimates for Snake River steelhead baseline v3 collections. The dashed line is the average pairwise F_{ST} estimate across all collections. High mean F_{ST} estimates suggest high genetic differentiation relative to other collections in the baseline. Each genetic stock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

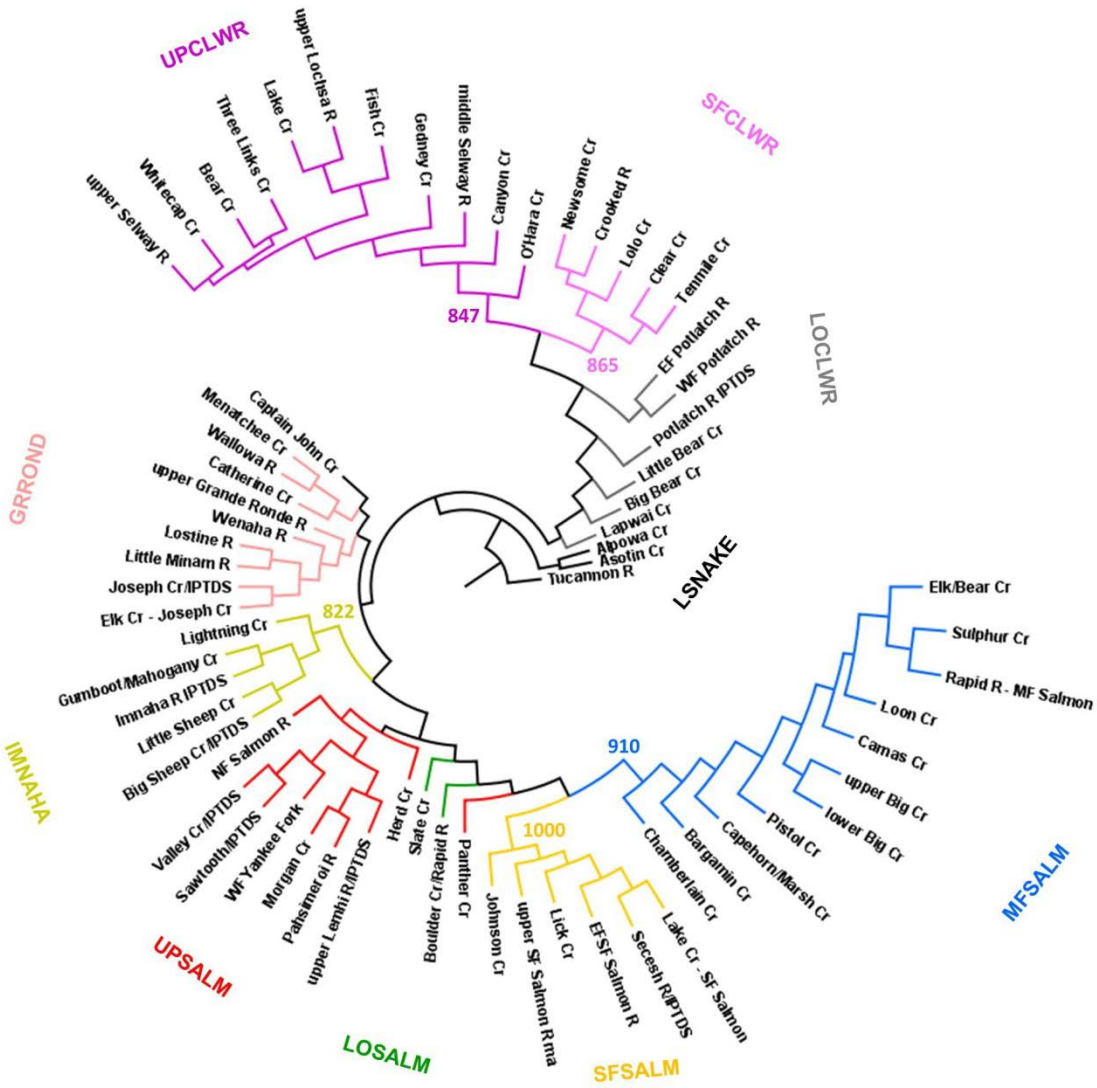

Figure 3. NJ-phylogram of Snake River basin steelhead baseline v3 collections based on Nei (1972) genetic distances.

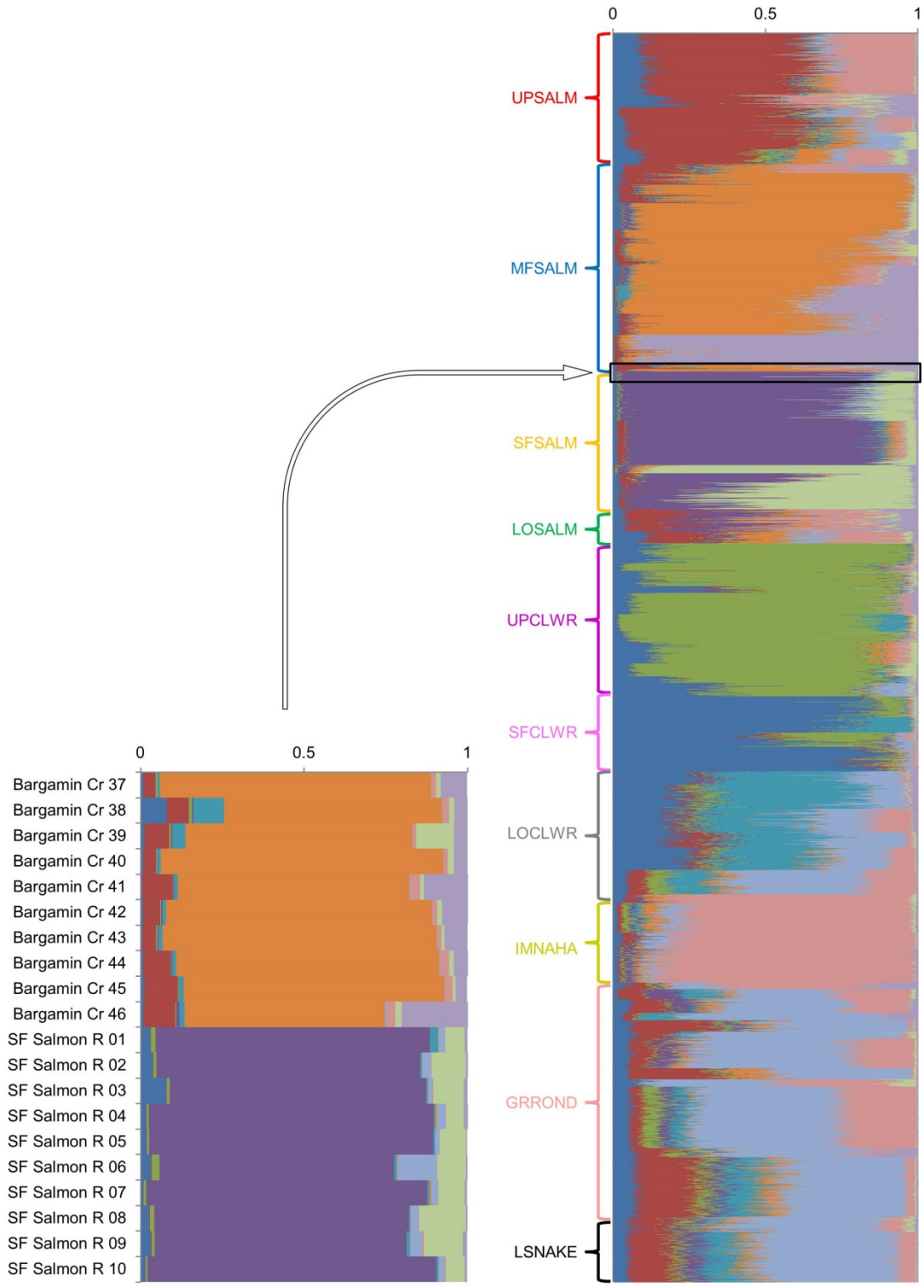

Figure 4 Histogram of STRUCTURE results for natural origin steelhead (K = 10). Results are based on admixture ancestral model. Each individual is represented by a single horizontal line divided into K colored segments that is proportional to each K inferred clusters. Individuals are arranged by genetic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

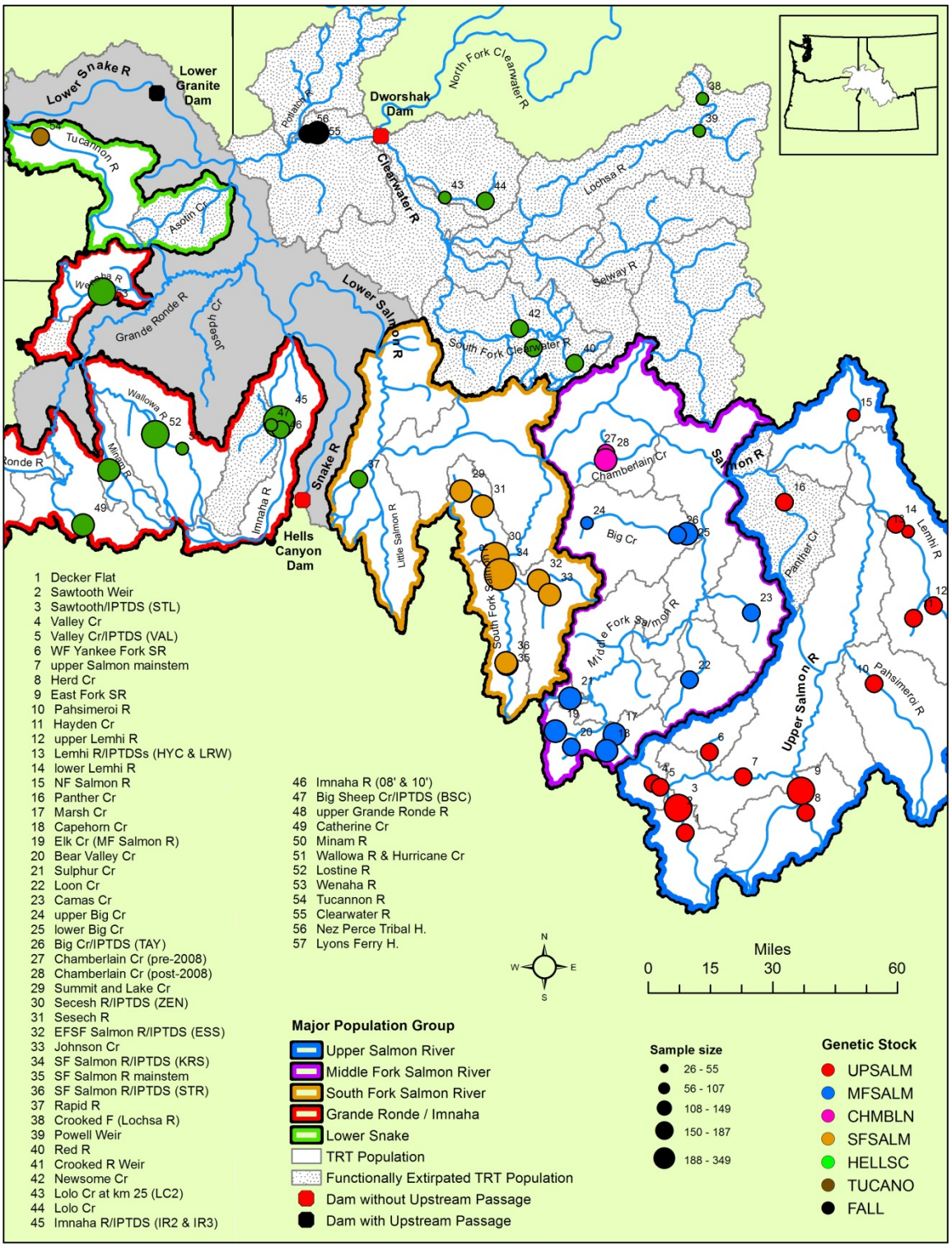

Figure 5. Natural origin Chinook salmon baseline version 3 consists of 54 collections within 25 TRT populations. TRT populations are grouped into six Genetic Stocks spanning across five Major Population Groups. Collections are described in greater details in Table 5.

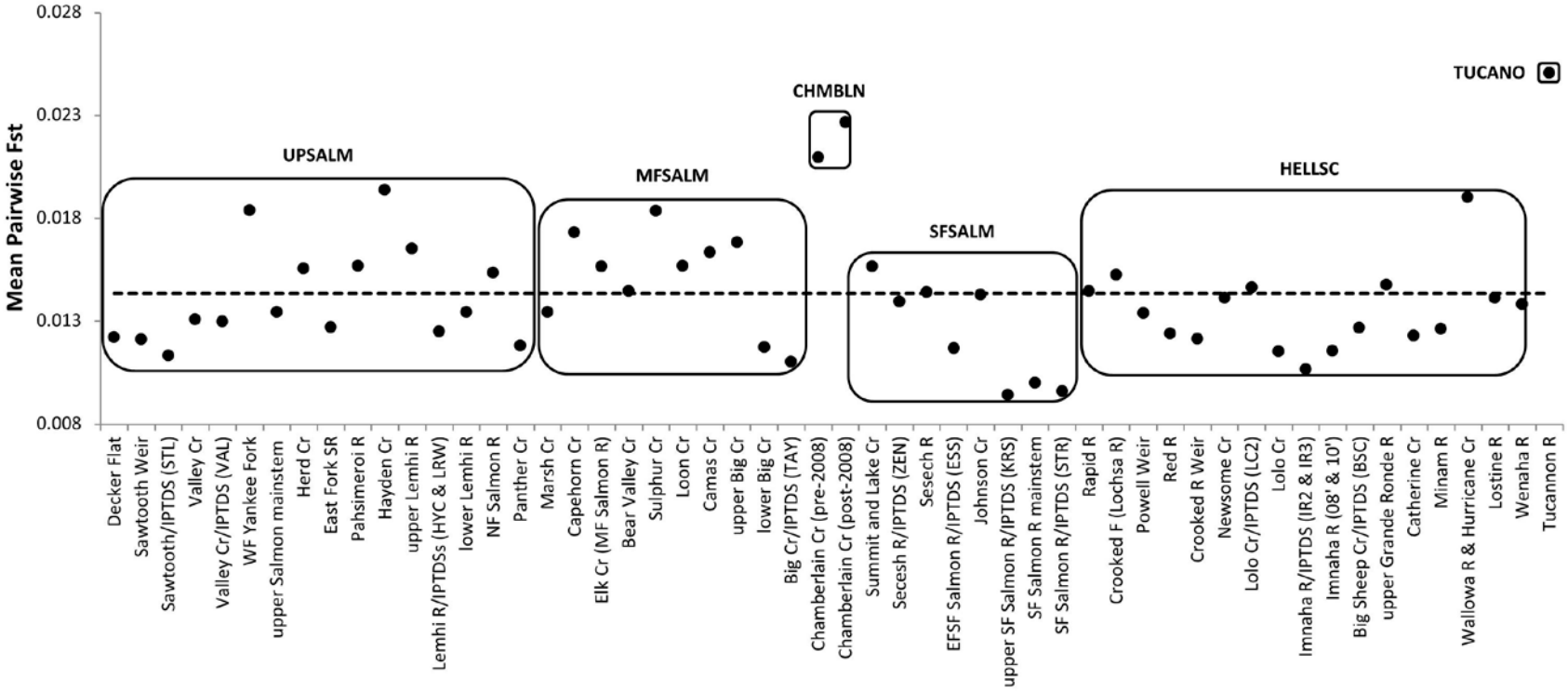

Figure 6. Mean pairwise F_{ST} estimates for Snake River Chinook salmon baseline v3 collections. The dashed line is the average pairwise F_{ST} estimate across all collections. High mean F_{ST} estimates suggest high genetic differentiation relative to other collections in the baseline. Each genetic stock is circumscribed.

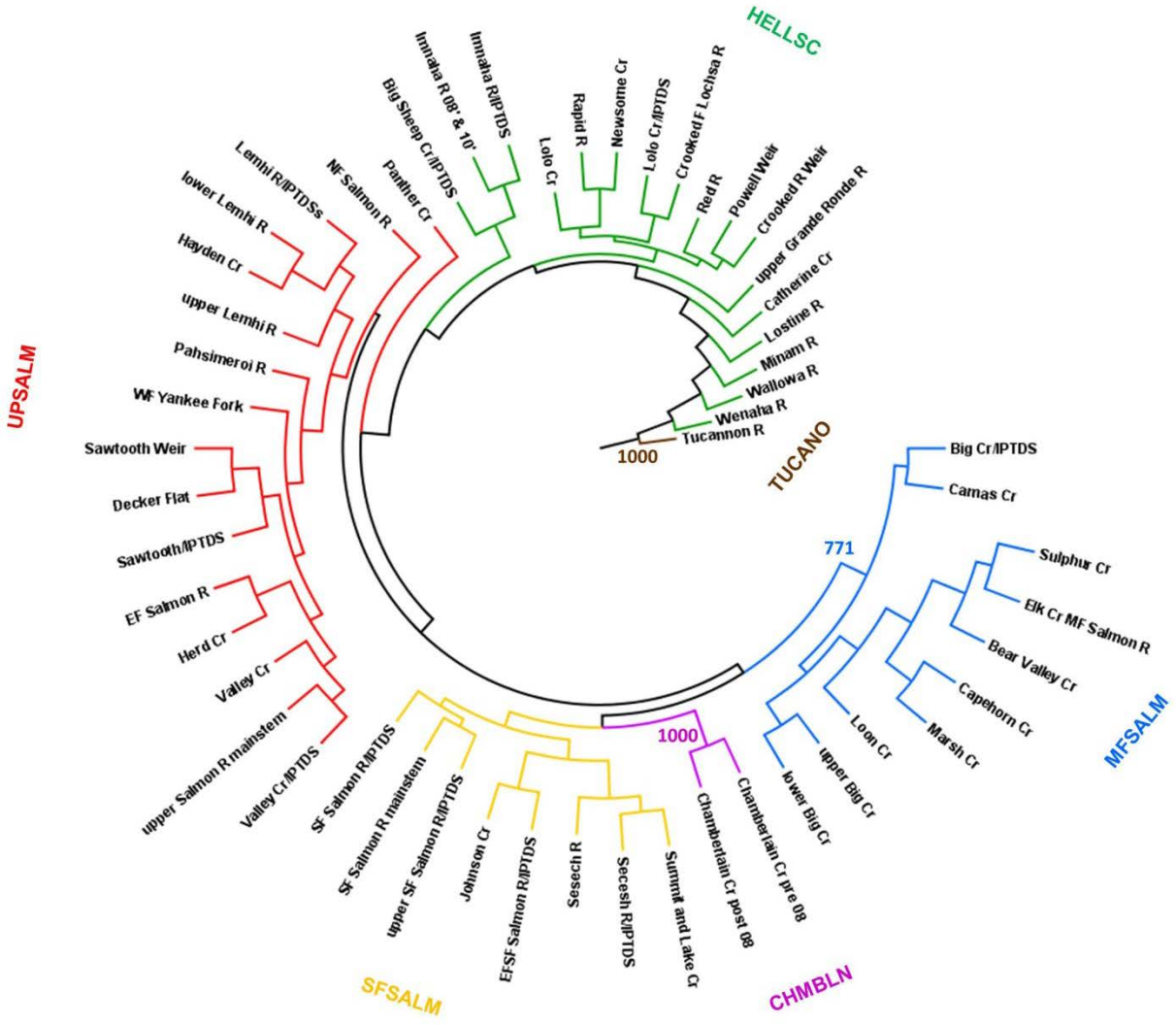

Figure 7. NJ-dendogram of Snake River basin Chinook salmon baseline v3 based on Cavalli-Sforza and Edwards (1967) genetic chord distances.

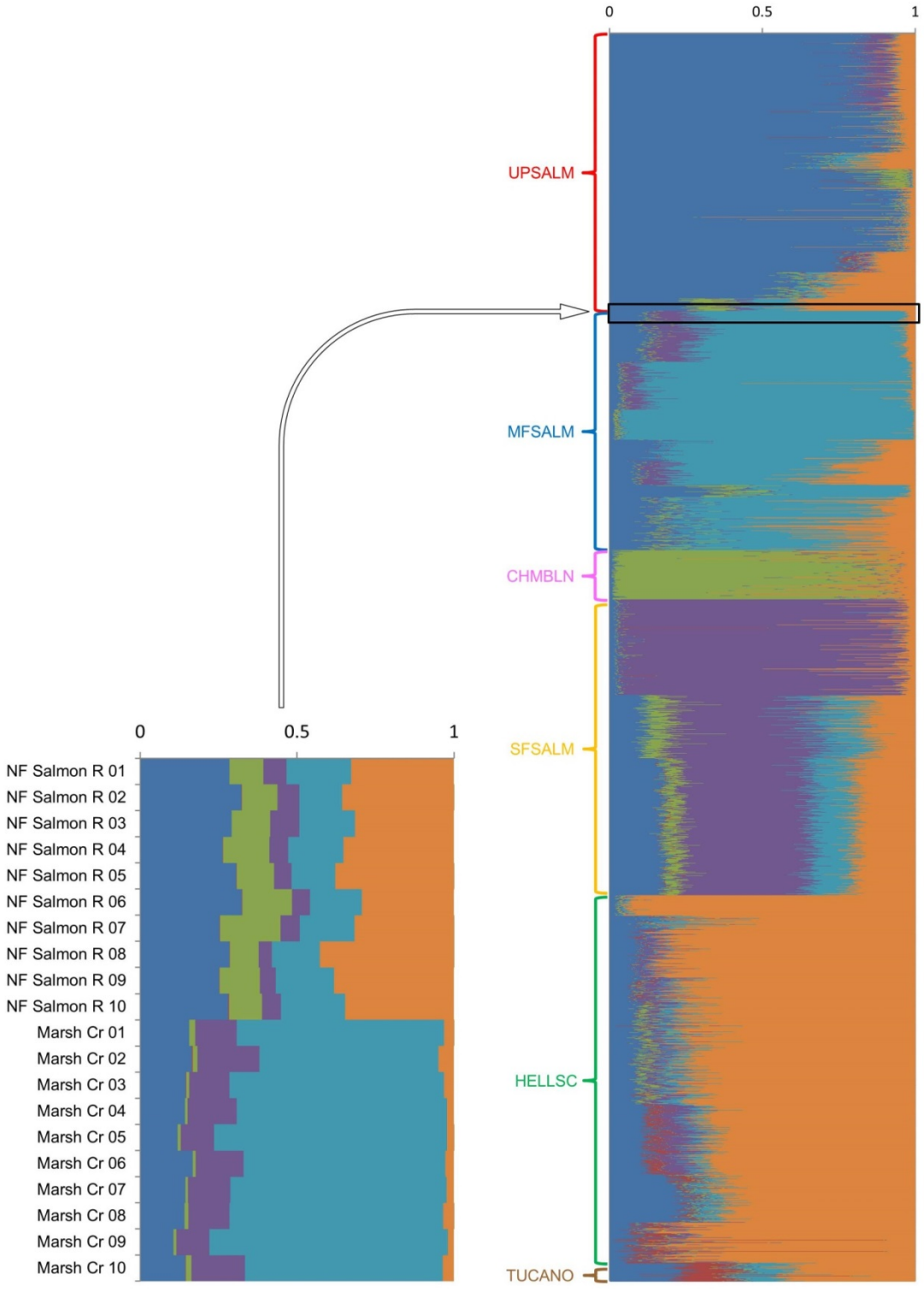

Figure 8. Histogram of STRUCTURE results for natural origin Chinook salmon (K = 6). Results are based on admixture ancestral model. Each individual is represented by a single horizontal line divided into K colored segments that is proportional to each K inferred clusters. Individuals are arranged by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

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