FISHERY RESEARCH

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

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

## Project Progress Report

**2011 Annual Report**

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## ABSTRACT

This report summarizes progress in development and implementation of genetic stock identification (GSI) within the Snake River basin for natural origin steelhead and spring/summer Chinook salmon for the 07/01/2011 to 06/30/2012 reporting periood. Three objectives for the project are addressed in this report: 1) the evaluation and maintenance of single nucleotide polymorphism (SNP) panels for high-throughput genotyping of steelhead and Chinook salmon in the Snake and Columbia river basins; 2) the updating, maintenance, and testing of SNP baselines to describe genetic variation and for use as a reference in GSI methods for both species in the basin; and 3) the implementation of GSI to estimate the stock composition and biological parameters of steelhead and spring/summer Chinook salmon passing Lower Granite Dam. For both species, panels of 192 SNPs have been identified and are being used for GSI 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 updates to and testing of SNP baselines for steelhead and Chinook salmon; steelhead baseline v2.0 consists of 63 populations represented by a total of 83 collections and 4,145 individuals. Chinook salmon baseline v2.0 consists of 39 populations represented by a total of 111 collections and 3,392 individuals. Baselines were used to describe genetic variation and population structure throughout the Snake River baseline. Using that information, we define 10 reporting groups for steelhead and 7 reporting groups for Chinook salmon for GSI analysis at Lower Granite Dam. Finally, we summarize three years of GSI results at Lower Granite Dam using the new v2.0 baselines as reference; SY2009, SY2010, and SY2011 adults and MY2010 and MY2011 juveniles. The information presented within should greatly assist managers in achieving sustainable harvest of larger populations, while protecting weaker stocks and the biodiversity present within them. Further, GSI monitoring at Lower Granite Dam provides crucial data for VSP monitoring of the Snake River steelhead DPS and the Snake River spring/summer Chinook salmon ESU.



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## INTRODUCTION

Abundance (i.e. number of adults on spawning grounds) is a primary metric needed for monitoring the status of steelhead and salmon populations in the Columbia River basin (McElhany et al. 2000). Estimates of abundance combined with age and sex information over time allows estimation of population growth rates. Both abundance and productivity metrics provide indicators of the resiliency and viability of populations, and allows assessments of extinction risk. Estimates of these metrics at the stock or population level 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 steelhead populations with fall and winter adult migration, 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 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 Salmon 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) are not available for most Snake River stocks (Busby et al. 1996; Good et al. 2005).

In lieu of more detailed basin-level and stock-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 do not exhibit a bimodal passage distribution and A-run and B-run adults are enumerated based on length (A-run, ≤78 cm; B-run, >78 cm) as a proxy for ocean age. In addition to run timing at Bonneville Dam and size differences, the two stocks are believed to exhibit differences in spawning distribution. A-run steelhead are thought to spawn throughout the Columbia basin, whereas B-run steelhead are believed to originate primarily from the Clearwater, Middle Fork Salmon, and South Fork Salmon rivers in Idaho. The putative differences in migration timing, morphology, and life history characteristics have been used as a surrogate for biodiversity in conservation planning for Snake River steelhead. However, the relationship between the morphological and life history characteristics to time of passage at Bonneville Dam is uncertain (Good et al. 2005). Further, the bimodal passage distribution at Bonneville Dam has become unimodal in recent years (Robards and Quinn 2002).

Two main 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 ESU, 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 Snake River tributaries in Idaho exhibit a complicated pattern of genetic structure with populations grouping genetically according to drainage locality, not by "A-run" or "B-run" designations.

The above issues and similar biological and management questions relating to Snake River steelhead and 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 technologies have 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 stock origin of kelt steelhead at Lower Granite Dam (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. 2011a; Schrader et al. 2011; Campbell et al. 2012) at Lower Granite Dam.

The results of the studies summarized above demonstrate the utility of GSI technology to obtain stock abundance estimates for steelhead and Chinook salmon in the Snake River basin. Continuation of GSI efforts at Lower Granite Dam will allow us to 1) monitor genetic structure throughout the basin over time, and 2) estimate productivity parameters and related biological information for genetic stocks throughout the Snake River basin. Sustained development and evaluation of this management tool 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 SNP panels for GSI in the Snake River basin. Section 2 summarizes efforts to update and maintain genetic baselines for both steelhead and Chinook salmon in the basin to monitor genetic diversity and for use as a reference for GSI. Section 3 addresses the use of GSI to estimate proportions, abundance, and biological parameters for wild stocks (both juveniles and adults) at Lower Granite Dam.

In this report, we refer to adult steelhead and Chinook salmon migrating past Lower Granite Dam using spawn years (SY). For steelhead, a spawn year refers to adults that migrate past Lower Granite Dam in the previous year's fall and the current year's spring (e.g. SY2010 steelhead are adults that migrated past during fall 2009 through spring 2010 and spawned in spring of 2010). For Chinook salmon, a spawn year refers to adults that migrate past the dam in the summer and spawn that same fall (e.g. SY2010 Chinook salmon migrated above the dam during summer 2010 and spawned later that year). We refer to juveniles of both species migrating past Lower Granite Dam using migratory years (MY). A migratory year refers to juveniles migrating downstream past Lower Granite Dam during that year's spring.

## SECTION 1: EVALUATE AND MAINTAIN SNP MARKER PANELS

### INTRODUCTION

GSI requires the use of an informative suite of genetic markers to quantify genetic variation among contributing populations and to ascertain the origin of individuals (or groups of individuals). One of the top priorities in the full-scale implementation of SNPs for GSI is the selection and evaluation of a sufficient number of SNP loci to characterize genetic variability among populations within the study area. The current genotyping platform used at IDFG and CRITFC can screen 96 samples with 96 genetic assays (9,216 data points) at a time; ideally, our laboratories would screen multiples of 96 assays to maximize the amount of data obtained per sample and to decrease cost per data point. Ultimately, the goal of IDFG and CRITFC is to identify 192 SNPs each for steelhead and Chinook salmon to discriminate populations throughout the Snake River basin (and mid- to lower-Columbia River). For both species, the 192 SNPs would be organized into two 96 SNP panels as such:

- **PBT:** 96 SNPs would be identified for parentage based tagging (PBT; BPA project #2010-031-00; Steele et al. 2012) applications throughout the Snake and Columbia rivers. PBT requires highly variable genetic markers (high minor allele frequency) to infer the parents of unknown origin offspring using parentage analyses (assuming the parents have been genotyped). Anderson and Garza (2006) and Steele at al. (*In Review*) have demonstrated that 60-100 SNPs are sufficient to perform PBT.

- **GSI:** In addition to the 96 PBT SNPs, 96 additional SNPs would be screened for both species for GSI. In typical PBT applications, all parents (or a large fraction of parents) are sampled and genotyped, so parentage analyses based on Mendelian inheritance can be performed to ascertain the origin (parents) of individuals. In GSI applications (especially in wild populations) it is impractical to genotype a large fraction of the population (i.e. the parent generation) and thus populations are characterized by estimating allele frequencies based on a sample of the population. In general, greater numbers of variable SNPs to estimate the allele frequencies of reference populations provides greater resolution and accuracy of GSI analyses (although there is a point at which adding more SNPs results in diminishing returns). IDFG and CRITFC screened 96 GSI SNPs (in addition to the 96 PBT SNPs) for GSI applications in the Snake River basin and mid- to lower-Columbia River for a total of 192.

During the first year of this project, we presented the initial SNP panels used to characterize genetic variation among natural origin Snake River steelhead and spring/summer Chinook salmon populations (Ackerman et al. 2011a). A brief synopsis of the initial baselines follows:

#### Steelhead

The first SNP panels for steelhead included 192 assays (96 for PBT, additional 96 for GSI; see Appendix A from Ackerman et al. 2011a). The 192 steelhead assays were screened across 49 natural origin steelhead populations from throughout the Snake River basin to form Snake River steelhead baseline v1.0 (see Section 2 from Ackerman et al. 2011a).

### Chinook salmon

The initial SNP panel used for Chinook salmon included only 96 assays. Within this initial 96 panel, 50 assays were also part of the PBT panel (Steele et al. 2012, Steele et al. *In Review*); the remaining 46 assays were unique to the "GSI" panel. This resulted in 142 unique Chinook salmon assays that were in use at the IDFG and CRITFC laboratories for both PBT and GSI. The incomplete panels allowed us to add an additional 50 Chinook assays during the 2nd year of the project.

During the first year of this project, the 96 original Chinook GSI assays were screened across 32 spring/summer Chinook salmon populations from throughout the Snake River basin to form Snake River Chinook salmon baseline v1.0 (see Section 2 from Ackerman et al. 2011a). In the 2nd year of the project we have screened additional collections for both steelhead and Chinook salmon resulting in a total of 63 populations screened for steelhead (Figure 1, Table 1) and 39 populations screened for Chinook salmon (Figure 2, Table 2). All populations (including Chinook salmon) have now been screened with 192 assays (191 SNP assays and 1 Y-specific allelic discrimination assay; Tables 3 and 4). Below, we summarize two achievements that occurred during the second year of the GSI project: 1) the addition of 50 new SNP assays to the Chinook salmon GSI panel, and 2) our evaluation of the ability of each of the SNPs to discriminate natural origin steelhead and spring/summer Chinook salmon populations throughout the Snake River Basin.

## METHODS

### SNP Selection and Addition

### Steelhead

During year two of the project, only two minor changes were made to the *O. mykiss* SNP panels. Within the PBT panel, the initial Y-specific sex determination assay (*Omy_SEXY1*) was replaced by a redesigned Y-specific assay *OmyY1_2SEXY* (Table 5). Further, within the GSI panel, the hybrid marker *Ocl_calT7RT2* was replaced by another hybrid marker *Ocl_gshpx-357* (Table 5). *Ocl_calT7RT2* was found to perform poorly in identifying *O. mykiss* and cutthroat trout *O. clarkii* hybrids.

### Chinook salmon

Starting in 2010, Washington Department of Fish and Wildlife (WDFW), University of Washington (UW), and Alaska Department of Fish and Game (ADFG) initiated a project funded by the Pacific Salmon Commission's Chinook Technical Committee. The intent of the study was to identify standardized Chinook salmon SNP panels that could be used by laboratories involved in the Genetic Analysis of Pacific Salmonids (GAPS) consortium (Moran et al. 2005). As part of that project, 288 Chinook salmon SNPs available among the GAPS laboratories were evaluated and reduced to 192 SNPs. These 192 SNPs were screened among 40 "core" populations that were intended to represent the northern Pacific range of Chinook salmon and were contributed by GAPS laboratories. The overlying goal was to identify a high-resolution panel of 96 SNPs for Pacific Salmon Commission and coastwide fisheries analysis. Of the 192 assays identified and screened across the 40 core populations, 134 were already in use at the IDFG and CRITFC laboratories. This left 58 "unique" SNPs that were not in use at IDFG and CRITFC.

During the 2nd year of the GSI project, we evaluated the 58 unique SNPs above from the GAPS laboratories to identify the 50 best SNPs for addition to the IDFG/CRITFC Chinook salmon GSI panel. Screening of the 58 potential SNP loci was done by genotyping 537 samples from 10 collections from throughout the Snake and Columbia rivers including both spring/summer (stream-type) and fall (ocean-type) lineages (Hess et al. 2012). Genotypes were obtained using the laboratory protocols outlined below. Loci were evaluated by plot quality, minor allele frequency, population differentiation ($G_{ST}$), deviations from HWE, and linkage disequilibrium (Hess et al. 2012). The program GENEPOP was used to evaluate deviation from HWE and to test for statistically significant LD. Allele frequencies and $G_{ST}$ were calculated using GENALEX. The 50 SNPS (out of 58) that were of highest quality and were most informative were added to the IDFG/CRITFC Chinook salmon GSI panel (Table 6). As part of this report, these 50 SNPs were analyzed among the full complement of 192 SNPs for population differentiation and diversity within Snake River Chinook salmon baseline v2.0 populations as described below.

Beyond the addition of 50 SNPs described above, only one additional change was made to the Chinook salmon SNP panels. Within the PBT panel, we replaced the initial Y-specific sex determination assay (*Ots_SEXY1*) with a redesigned Y-specific assay *Ots_SEXY3-1* (Table 6) to increase accuracy in sex determination.

**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 cool down 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 EFGL. 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 GAPS and SPAN 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 will promote seamless sharing of data among labs in the future.

**Statistical Analyses**

SNP analyses described below were conducted using Snake River baselines v2.0 for both steelhead and Chinook salmon (see Section 2) to evaluate each SNP for within-population diversity and among population differentiation. For steelhead, 188 SNPs (192 assays minus *OmyY1_2SEXY* and the 3 SNPs used to identify *O. mykiss* and *O. clarkii* hybridization) were available for analysis. For Chinook salmon, analyses were conducted starting with 191 SNPS (192 assays minus *Ots_SEXY3-1*). As the GSI project is primarily focused on stream-type (spring/summer) Chinook salmon, analyses concerning population differentiation in Section 1 were conducted using only stream-type collections within Snake River Chinook salmon baseline v2.0 (36 of 39 collections; Table 2). Hardy-Weinberg equilibrium (HWE) and linkage disequilibrium (LD) analyses were conducted using all 39 baseline collections.

Allele frequencies across populations for each SNP were calculated using GENALEX v6.4 (Peakall and Smouse 2006). Minimally variable SNPs (i.e. <5% minor allele frequency in all Snake River populations) were removed from subsequent analyses. These SNPs provide little/no information in population genetics or GSI analyses.

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

For each SNP, we calculated the number of baseline populations that the SNP deviated from Hardy-Weinberg equilibrium (HWE). The goal was to identify any SNPs that may exhibit null alleles (an allele that may not amplify due to a sequence mutation, etc.) or amplify poorly across Snake River populations for various reasons. We tested for deviation from HWE across all nuclear SNPs for each population using exact p-values calculated from the MC method in GENEPOP v4.0. Default parameters were used for the MC algorithm (dememorization = 1,000; batches = 20; iterations per batch = 5,000). Critical values were not adjusted using corrections for multiple tests. We report any SNPs that deviated from HWE in >10% of baseline populations (Tables 3 and 4).

For both species, each SNP was evaluated for within-population diversity and among-population information content (i.e. its ability to differentiate populations) across Snake River baseline v2.0 populations (see Section 2; Tables 1 and 2). The minor allele frequency (MAF) range, expected heterozygosity ($H_E$), and the Weir and Cockerham (1984) $F_{ST}$ statistic for each SNP were calculated using GENALEX v6.4. Further, we calculated the informativeness for assignment ($I_N$) and the optimal rate of correct assignment (ORCA) for each SNP to evaluate the information content of each locus for use in inference of population of origin of individuals. $I_N$ and ORCA calculations were calculated using equations from Rosenberg et al. (2003) (Tables 3 & 4). The following is a brief explanation of each summary statistic:

- **Minor allele frequency (MAF) range**: MAF is the estimated frequency that the minor allele (allele present in lower frequency) is present in a population based on

the sample/collection. The MAF range among populations is an indication of the amount of variability a locus exhibits among the study populations.

- **Expected heterozygosity ($H_E$)**: An estimate of the amount of genetic variability among baseline populations (averaged across populations) for each SNP. A weighted average that estimates the proportion of baseline individuals that are heterozygotes calculated from allele frequency estimates using the equation $p^2 + 2pq + q^2$ where p and q are allele frequencies and 2pq is the estimated proportion of heterozygotes.

- **Fixation Index ($F_{ST}$)**: A measure of population differentiation often expressed as the proportion of genetic diversity due to allele frequency differences among populations.

- **Informativeness for Assignment ($I_N$)**: A measure of the potential of assignment for one allele to one population compared to that of an "average" population (a population whose allele frequencies are calculated using all baseline individuals; Rosenberg et al. 2003).

- **Optimal Rate of Correct Assignment (ORCA)**: The probability of correct assignment of an allele using a decision rule with lowest risk (Rosenberg et al. 2003).

The $I_N$ and ORCA for each SNP is a sum of allele-specific $I_N$s and ORCAs, respectively. The $I_N$ and ORCA statistics are generally highly correlated to $F_{ST}$, but provide an advantage over $F_{ST}$ in that they are designed specifically for estimating the information content of a locus for estimation of population of origin of individuals (Rosenberg et al. 2003). Finally, we ranked each SNP according to $F_{ST}$, $I_N$, and ORCA and then averaged those rankings to obtain a final "Informativeness" rank for each SNP. Tables 3 (steelhead) and 4 (Chinook salmon) are sorted according to "Informativeness" with the most informative SNPs sorted to the top.

Finally, we used the program LOSITAN (Antao et al. 2008) to test neutrality of nuclear SNP loci ($\alpha = 0.01$). LOSITAN evaluates the relationship between $F_{ST}$ and $H_E$ across all loci in an island model to identify outlier loci having excessively high or low $F_{ST}$ compared to neutral expectation. Results were based on 50,000 data simulations using an infinite alleles model and a false discovery rate of 0.1. SNPs lying above or below the given criteria (outliers) are candidates for directional or balancing selection, respectively.

## RESULTS

### SNP Selection and Addition

#### Steelhead

Summarized in Methods. See Table 5 for changes made to the *O. mykiss* SNP panels during the second year of the project. Primer and probe sequence information for the *O. mykiss* PBT and GSI SNP panels are summarized in Appendix A.

### Chinook salmon

We evaluated the 58 SNPs mentioned in METHODS that were available from GAPs laboratories by screening them across a set of 537 samples including both fall (ocean-type) and spring/summer (stream-type) lineages. The 10 collections from throughout the Snake and Columbia river drainages included Wenaha River, Shitike River, Lostine River, Johnson Creek, Clearwater River, Lolo Creek, Upper Deschutes River, Yakima River, Lyons-Ferry National Fish Hatchery, and Cowlitz National Fish Hatchery. Genotyping was completed at the CRITFC laboratory and analysis was performed by CRITFC personnel (Hess et al. 2012). Results revealed that three assays were monomorphic in all 10 collections screened and four assays exhibited poor plot quality. This left only a single assay that could be dropped before adding 50 SNPs to the GSI panel to generate the full 192 SNP set. The last assay dropped was *Ots_IsoT* due to deviations from HWE in several collections. The remaining 50 assays (Table 6) were added to the 46 SNPs included in baseline v1.0, which replaced the 50 assays that were redundant between the PBT and GSI panels (Table 6; Hess et al. 2012). Primer and probe sequence information for the Chinook salmon PBT and GSI SNP panels are in Appendix B.

## Statistical Analyses

### Steelhead

Of the 192 assays that were screened across 63 natural origin steelhead populations, one (*OmyY1_2SEXY*) is a Y-specific allelic discrimination assay that differentiates sex in *O. mykiss*. Further, three SNP assays (*Ocl_gshpx-357*, *Omy_myclarp404-111*, and *Omy_Omyclmk438-96*) identify putative O. *mykiss* x O. *clarkii* hybrids. These four assays were removed from subsequent population genetics and GSI analyses.

We tested for linkage disequilibrium across all pairwise comparisons (17,578 pairwise comparisons) for the 188 nuclear SNPs. Among all pairwise comparisons, only one locus pair (*Omy_GHSR-121* and *Omy_mapK3-013*) exhibited linkage disequilibrium in more than one-half of baseline populations (34 of 63). *Omy_mapK3-013* was the less informative of the pair and was removed to maintain independence of loci in population structure and GSI analyses (Table 3).

Of the remaining 187 steelhead SNPs, 10 (5%) deviated from HWE in >10% of baseline populations (Table 3). The worst offenders were *OMS00129* and *OMS00087*, which both deviated from HWE in 16 of the 63 (25%) baseline populations. Further evaluation of these SNP assays will be necessary to determine whether deviations result from genotyping errors or Wahlund effects (i.e. grouping multiple populations). Three other SNPs (*Omy_IL17-185*, *Omy_nxt2-273*, and *Omy_128996-481*) deviated from HWE in 11 (17%) of the baseline populations. No other SNPs deviated from HWE in more than nine baseline populations.

Among SNPs, *Omy_sast-264* (an A-G variant SNP) exhibited the largest range in minor allele frequency among Snake River steelhead populations (Table 3). The A allele was present at a frequency of 6.8% and 86.5% in the Cow Creek (GRROND) and the lower Big Creek (MFSALM) populations, respectively. Alternatively, *Omy_sSOD-1* (a G-T SNP) exhibited the smallest range in minor allele frequency among Snake River steelhead populations. *Omy_sSOD-1* was absent for the G allele in 34 of 63 baseline populations; and the highest frequency of the G allele was 4.5% in the Cow Creek (GRROND) population. Despite its low MAF, *Omy_sSOD-1* is a very informative SNP for identifying introgression among interior

redband *O. mykiss gairdneri* and coastal *O. mykiss irideus* lineages of rainbow trout and thus was retained for subsequent analyses.

*OMS00039* had the greatest $H_E$ (48.4%) when averaged across populations. Conversely, *Omy_nach-200* had the lowest $H_E$ (1.5%). As a side note, the 3 SNPs that ranked lowest according to "informativeness" (*Omy_LDHB-2_i6*, *Omy_sSOD-1*, *Omy_nach-200*; see Table 3) also exhibited the lowest $H_E$ (1.5 – 1.6%) among all *O. mykiss* SNPs. These three SNPs are highly variable among coastal rainbow trout (see Appendix C) and are useful for identifying introgression among interior redband and coastal lineages of rainbow trout.

*Omy_anp-17* was determined to be the most informative of the 187 *O. mykiss* SNPs for GSI applications in the Snake River (Table 3). *Omy_anp-17* ranked second most informative according to all three of the measures estimated ($F_{ST}$, $I_N$, ORCA), but ranked first when averaged across the three measures. Three SNPs (*Omy_sast-264*, *Omy_114315-438*, and *Omy_u09-53.469*) tied for second most informative according to the three measures. Again, *Omy_LDHB-2_i6*, *Omy_sSOD-1*, and *Omy_nach-200* tied as the least informative of the SNPs when used for GSI applications of interior redband steelhead in the Snake River; each of these three SNPs were nearly fixed across Snake River steelhead collections.

Twenty-five *O. mykiss* SNPs were candidates for directional selection and five SNPs were candidates for balancing selection (Table 3, Figure 3). Directional selection is a form of natural selection in which an allele (and its corresponding phenotype) is favored, causing the allele frequency in a population to shift continuously in one direction. If the environment (and selection) acts on populations differently, the minor allele frequency divergence among populations will become larger than expected under neutral selection conditions. Conversely, balancing selection is a form of natural selection in which multiple alleles are actively maintained in populations. SNPs influenced by directional selection are of interest to the GSI project as they can be particularly useful for GSI applications (Ackerman et al. 2011b, Russello et al. 2011). Seven of the more divergent candidate SNPs for directional selection are identified in Figure 3.

**Chinook salmon**

Of the 192 assays that were screened across 39 natural origin Chinook salmon populations, one (*Ots_SEXY3-1*) is a Y-specific allelic discrimination assay that differentiates sex in Chinook salmon. *Ots_SEXY3-1* was removed from subsequent baseline and GSI analyses. In addition, 16 of the remaining 191 SNPs were considered monomorphic (<5% minor allele frequency) among all 36 Snake River spring/summer collections included in baseline v2.0 (Table 4). These SNPs were removed from subsequent analyses conducted in Section 1. Of the 16 monomorphic SNPs, eight were variable among the three fall Chinook collections included in baseline v2.0; these eight SNPs will be included in baseline and GSI analyses in Sections 2 and 3 where we are concerned with differentiating or identifying fall Chinook vs. spring/summer Chinook lineages. After removing *Ots_SEXY3-1* and the 16 invariable SNPs, 175 SNPs were included in subsequent analyses in Section 1.

We tested for linkage disequilibrium across all pairwise comparisons (15,051) for the remaining 174 nuclear SNPs (*Ots_C3N3*, a mitochondrial DNA SNP, was removed from linkage analyses). Among all pairwise comparisons, three pairs of loci exhibited linkage disequilibrium in more than one-half of baseline populations (Table 4). *Ots_Tnsf* and *Ots_OTSF1-SNP* exhibited linkage disequilibrium in 37 of 39 baseline populations. *Ots_FGF6A* and *Ots_FGF6B_1* exhibited linkage disequilibrium in all 39 baseline populations. *Ots_hsc71-5'-453* and *Ots_hsc71-3'-488* exhibited linkage disequilibrium in 26 of 39 baseline populations. *Ots_Tnsf*,

*Ots_FGF6A*, and *Ots_hsc71-3'-488* were the less informative of the respective locus pairs and were removed from subsequent baseline and GSI analyses. This leaves a panel of 172 SNPs that can be used in stream-type Chinook salmon baseline and GSI analyses and a panel of 180 SNPs that can be used in analyses concerning both spring/summer (stream-type) and fall (ocean-type) Chinook salmon in the Snake River basin.

Out of 174 nuclear SNPs (*Ots_C3N3* removed), 19 (11%) deviated from HWE in >10% of baseline populations (Table 4). The worst offender was *Ots_ZR-575, which* deviated from HWE in 11 of the 39 (28%) baseline populations. Further evaluation of this SNP will be necessary to determine if a null allele is present among Snake River populations or to evaluate potential amplification issues. No other SNPs deviated from HWE in greater than six of the baseline populations.

Among SNPs, *Ots_TAPBP* (a C-T variant SNP) exhibited the largest range in minor allele frequency among Snake River stream-type Chinook salmon populations (Table 4). The C allele was present at a frequency of 0.5% in the Elk Creek (MFSALM) collection; the C allele was present at a frequency of 61.9% in the Lostine River (HELLSC) collections. As mentioned above, 16 SNPs were monomorphic among Snake River stream-type collections (Table 4). Note: Table 4 shows three SNPs (*Ots_GPDH-338*, *Ots_u1007-124*, and *Ots_CRB211*) with minor allele frequencies of <5% among all natural origin spring/summer (stream-type) Snake River collections; these SNPs were not considered monomorphic as they exhibited a frequency of >5% in one or more of the hatchery collections screened (see Section 2, Table 8).

*Ots_unk1832-39* had the greatest $H_E$ (48.8%) when averaged across populations. Conversely, Ots_GPDH-338 had the lowest $H_E$ (0.5%) of the polymorphic SNPs. Of the 96 SNPs exhibiting the greatest $H_E$ among natural origin populations, 80 are within the Chinook salmon PBT panel.

*Ots_TAPBP* was determined to be the most informative of the 175 Chinook salmon SNPs for differentiating spring/summer populations in the Snake River (Table 4). Ots_TAPBP ranked as the most informative according to all three of the measures estimated ($F_{ST}$, $I_N$, ORCA). *Ots_MHC2*, *Ots_110495-380*, *Ots_OTSF1-SNP1*, and *Ots_117432-409* rounded out the top 5 most informative SNPs for spring/summer Chinook salmon in the Snake River basin (Table 4).

Eight Chinook salmon SNPs were candidates for directional selection (Table 4); none were candidates for balancing selection. Four of the more divergent candidate SNPs for directional selection are identified in Figure 4.

## DISCUSSION

With the addition of 50 Chinook salmon SNP assays to the GSI panel, the IDFG and CRITFC laboratories are now operating using 96 SNPs for PBT and 192 SNPs for GSI for both steelhead and Chinook salmon throughout the Snake (and mid- to low-Columbia) River basin. Both Anderson and Garza (2006) and Steele et al. (*In Review*) have demonstrated that 96 SNPs are sufficient to perform PBT. Further, Hess et al. (2012) and this report (see Sections 2 and 3) demonstrate the utility of the current 192 SNP panels to characterize genetic variability throughout the Snake and Columbia rivers and to perform GSI analyses at Lower Granite Dam, Bonneville Dam, and in lower Columbia River mixed fisheries. The continued use of these SNP panels over time will 1) allow us to monitor genetic diversity for both steelhead and Chinook

salmon throughout the region over time, and 2) provide valuable long-term datasets for the estimation of viable salmonid parameters (VSP; McElhany et al. 2000).

Starting in SY2010, the Integrated Status and Effectiveness Monitoring Program (ISEMP; BPA Project Number 2003-017-00) began PIT tagging a proportion of natural origin adult steelhead and Chinook salmon sampled at the LGD adult trap. Described in Section 2, we genotyped and analyzed 1,034 Chinook salmon that were detected at PIT-tag arrays (or hatchery traps) located in tributaries throughout the Snake River. Of the 1,034 fish analyzed, we were able to assign 63% of the individuals to a GSI reporting group with ≥80% probability; of those, 80% had concordant results between PIT detection location and genetic assignment location using 192 SNPs. This dataset was re-analyzed using the reduced 96 SNP panel used for Chinook salmon baseline v1.0 (Ackerman et al. 2011a). We analyzed 1,305 fish (including the 1,034 that were genotyped using 192 SNPs) using the 96 SNPs. Of the 1,305 fish analyzed, only 34% of individuals were assigned to a reporting group; of those, 68% had concordant results between PIT detection location and genetic assignment location. The simultaneous increase in assignment rate from 34% to 63% and the increase in concordance rate from 68% to 80% demonstrate the benefit of adding 50 SNPs to the Chinook salmon panels.

We analyzed exclusively interior redband steelhead populations represented in Snake River baseline v2.0. A large number of the SNPs contained within our 192 panel are also highly variable in coastal lineages of *O. mykiss*. In Appendix C, we demonstrate the utility of our SNP panels to 1) differentiate interior redband *O. mykiss* from coastal *O. mykiss*, and 2) evaluate introgression occurring between the two lineages. Results in Appendix C suggest that the 192 SNP panels developed by CRITFC and IDFG will be useful in assessments of intraspecific introgression.

Of the 191 Chinook salmon SNP assays (*Ots_SEXY3-1* excluded), 16 were considered monomorphic in spring/summer collections and eight were considered monomorphic in both spring/summer and fall collections from throughout the Snake River basin. These SNPs will be retained in IDFG's SNP panels because 1) they may be variable in populations elsewhere in the Columbia River (Hess et al. 2012) and 2) a number SNPs considered monomorphic in the Snake basin are also being used by other agencies involved in Chinook salmon GSI outside the Snake River (i.e. ADFG, Northwest Fisheries Science Center [NWFSC], Southwest Fisheries Science Center [SWFSC], UW, WDFW, USFWS) because they are variable in Chinook salmon outside the Columbia River. The standardization of SNP panels among agencies is currently a priority of the GAPS consortium. Standardization among laboratories is important to allow GSI to be performed across large geographic scales (i.e. coastwide) and on the high seas.

Currently, the SNP panels in use at IDFG and CRITFC for both steelhead and Chinook salmon are being used to track stock proportions (this report, Hess et al. 2012) and abundances (Schrader et al. 2011), track hatchery straying rates (Steele et al. 2012), estimate reproductive success, estimate effective population sizes (Steele et al. 2012), and estimate parameters for VSP analysis (this report, Hess et al. 2012). These studies provide critical information that is likely to affect conservation efforts and hatchery management practices throughout the Snake and Columbia river basins.

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

### INTRODUCTION

The high fidelity of Pacific salmon (*Oncorhynchus* spp.) to their natal streams allows adaptation to local spawning and rearing environments, resulting in a range of life history characteristics and genetic variation among discrete populations (Taylor 1991; Dittman and Quinn 1996; Quinn 2005). Marked population differentiation among steelhead and salmon populations allows researchers to estimate the population of origin of individuals or mixtures of individuals using GSI (Shaklee et al. 1999). Initially, fish from discrete "reference" populations that might contribute to a mixed fishery are sampled. Reference populations are then genotyped to characterize genetic variation among contributing populations, establishing a genetic baseline. For objective 2 of the GSI project, we describe efforts that have occurred over the past year to update and evaluate the Snake River baselines for both steelhead and Chinook salmon. Efforts were conducted to 1) describe genetic diversity and population structure among Snake River populations, and 2) establish a reference for GSI applications at Lower Granite Dam. We refer to the updated baselines as Snake River baselines v2.0 (version will be updated annually as baseline expansion efforts occur).

In the 1st year of the GSI project, we described the transition from genetic baselines based on microsatellite markers to baselines based on SNP markers (Ackerman et al. 2011a). This transition has been completed. The transfer from microsatellites to SNPs was initiated because 1) SNPs represent the most abundant form of variation in the genome of most organisms; 2) SNPs can be discovered throughout the genome of non-model organisms with relative ease; 3) The bi-allelic nature of SNPs allows for highly-automated and rapid genotyping, low genotyping error rates, and easy standardization for transferring data among laboratories; and 4) SNPs may be characterized in coding regions of the genome potentially influenced by selection. A brief summary of the baselines generated in the 1st year of this project are described below (Ackerman et al. 2011a):

- **Steelhead**: Baseline v1.0 consisted of 2,514 samples from 52 collections representing 49 populations (3 populations had temporal collections). Samples were screened at 192 assays.

- **Chinook salmon**: Baseline v1.0 consisted of 2,390 samples from 54 collections representing 32 populations (12 populations had temporal collections). Samples were screened at 96 assays.

Collections genotyped for the initial SNP baselines (v1.0) were primarily chosen to complement or overlap collections previously submitted to the standardized SPAN or GAPS microsatellite consortiums for steelhead and Chinook salmon, respectively. The genotyping of overlapping collections/populations with both microsatellites and SNPs allowed us to evaluate and compare the resolutions of the baselines created using both genetic markers (see Ackerman et al. 2011a for a brief comparison).

In year 2 of the GSI project, our focus shifted towards increasing geographic coverage so that all major contributing populations in the Snake River basin are well represented. Ideally, our long-term goals for the Snake River baselines for these species are to ensure the following:

- All major contributing populations in the Snake River basin are represented; with an attempt to include all 'populations' designated by the Interior Columbia Basin Technical Recovery Team (ICTRT 2003).
- All populations are represented by temporal collections (sampled in more than one year).
- All populations are represented by collections obtained within at minimum the previous 5 generations (15 - 20 years).
- All populations are represented by adequate sample sizes (i.e. >50 fish) to accurately estimate allele frequencies.

Collections genotyped over the past project year were chosen to contribute to the above goals.

Section 2 is structured to follow three subobjectives related to the updating and maintenance of Snake River baselines for steelhead and Chinook salmon in the Snake River basin:

**Subobjective 1.** First, we describe current and ongoing efforts to generate and evaluate the Snake River baselines v2.0. We document collections/samples that have been added during the 2nd year of this project. Using the expanded multilocus SNP baselines, we characterize genetic variation among steelhead and spring/summer Chinook salmon populations in the Snake River. Both within-population diversity and among-population differentiation are evaluated. Finally, we compare differentiation between natural origin baseline populations genotyped as part of the GSI project and hatchery stocks that have been genotyped as part of IDFG's PBT project (BPA project #2010-031-00).

**Subobjective 2.** After characterizing genetic variation among wild populations, we use that information to define Snake River reporting groups for GSI applications at Lower Granite Dam (see Section 3). Reporting groups are assemblages of reference (baseline) populations grouped primarily according to genetic and geographic similarities and in some cases political boundaries and/or management units (Ackerman et al. 2011a).

**Subobjective 3.** Finally, using the defined reporting groups, we predict the accuracy of Snake River baselines v2.0 for GSI analyses. The accuracy of GSI given the baselines and reporting groups are evaluated by assigning individuals (either simulated or real) of known origin back to the reporting groups.

## METHODS

### 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 2011 annual report for BPA Project 2008-97-00 (Hess et al. 2012).

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

**Laboratory Protocol**

Laboratory methods follow those in Section 1. Steelhead were genotyped at 191 SNPs (including three SNPs that were designed to differentiate *O. mykiss* and *O. clarkii* hybrids) and a Y-specific assay that differentiates sex in *O. mykiss*. Chinook salmon were genotyped at 191 SNPs (including one mtDNA SNP) and a Y-specific allelic discrimination assay that differentiates sex in *O. tshawytscha*.

**Statistical Analyses – Baseline Evaluation**

Allele frequencies for baseline collections were calculated using GENALEX v6.4 (see Section 1). Collections taken at geographically proximate locations across multiple years were tested for genetic differentiation across all loci using pairwise exact tests in GENEPOP v4.0 (Rousset 2008) and were pooled as suggested by Waples (1990) if temporal collections failed to demonstrate significant departures from genetic homogeneity ($\alpha = 0.05$). Temporal pooling of collections allows for increased sample sizes, and thus, generally better estimates of population allele frequencies. Markov chain (MC) parameters for pairwise exact tests in GENEPOP v4.0 were as follows: dememorization = 10,000; batches = 100; iterations per batch = 5,000. Pooled collections were defined as “populations” in all subsequent analyses.

Tests for deviation from Hardy-Weinberg expectation (HWE) were performed across all loci for each population (methods in Section 1). For each population, we counted the number of loci that deviated from HWE. Deviations from HWE may be indicative of kinship bias (heterozygote excess) or Wahlund effect (heterozygote deficit; sample resembles more than one population).

Baseline populations were evaluated for expected heterozygosity ($H_E$), allelic richness (AR), and population-specific $F_{ST}$ using GENALEX v6.4 and FSTAT v2.9.3.2 (Goudet 1995, 2001). Higher $H_E$ and AR indicates increased levels of genetic variability within a population; lower $H_E$ and AR may indicate decreased genetic variability attributable to various factors (population bottlenecks, reduced meta-population dynamics). Population-specific $F_{ST}$ is an indicator of the level of differentiation a population exhibits relative to all other baseline populations.

In year 2, we screened collections of Snake River hatchery stocks (Tables 7 and 8) using the full complement of SNPs so that natural origin populations represented in the Snake River baselines could be directly compared to hatchery stocks spawned in the basin. For each hatchery stock, we identified a representative sample of parents that had previously been genotyped for IDFG’s PBT project (BPA Project 2010-031-00) using the 96 PBT SNPs and genotyped identified individuals using the additional 96 panel of GSI SNPs. For each natural origin population in the baseline, we estimated its genetic differentiation ($F_{ST}$) from each of the Snake River hatchery stocks using GENALEX v6.4. To visually evaluate differentiation of

natural origin populations and hatchery stocks, pairwise $F_{ST}$ estimates were imported into ArcGIS 10 for analysis. For each hatchery stock, an analysis was conducted in which we spatially interpolated observed differentiation ($F_{ST}$) with natural populations across the basin using the kriging (Isaaks and Srivastava 1989) function under Spatial Analyst, Interpolation in ArcToolbox. The goal was to visually evaluate at a broad-scale differentiation among natural-origin populations and hatchery stocks throughout the Snake River basin.

For steelhead, we show results from comparisons with Pahsimeroi Hatchery and Dworshak Hatchery broodstocks. The Pahsimeroi Hatchery comparison is important because the upper Salmon River (upstream of the confluence of the Middle Fork Salmon River) is managed primarily for harvest, based on the assumption that steelhead were not historically abundant in this part of the Salmon River drainage as they were in the Middle Fork and South Fork Salmon River drainages (HSRG 2009). The expectation is that given the long history of stocking hatchery steelhead from the Pahsimeroi and Sawtooth hatcheries in the upper Salmon River, extant steelhead populations would look genetically similar to these stocks. The Pahsimeroi Hatchery stock was initiated with progeny of adult steelhead trapped at Oxbow and Hells Canyon dams from 1966 through 1968, and the Sawtooth Fish Hatchery broodstock was founded with adults that returned from hatchery-origin smolt releases from the Pahsimeroi Hatchery. Dworshak Dam was constructed in 1972 and eliminated access to one of the most productive systems for anadromous steelhead in the subbasin.

For Chinook salmon, we show results from comparisons with Rapid River Hatchery broodstock. Indigenous Chinook salmon in the Clearwater River subbasin were likely eliminated by Lewiston Dam. However, naturally reproducing populations of spring Chinook salmon have been reestablished in Lolo Creek and mainstem/tributary reaches of the Lochsa, Selway, and South Fork Clearwater rivers. Founding hatchery stocks used for spring Chinook salmon reintroductions were primarily obtained from the Rapid River Hatchery.

**Statistical Analyses – Defining Reporting Groups**

After characterizing within-population diversity and among-population differentiation for populations included in baselines v2.0, we then defined reporting groups for GSI applications at Lower Granite Dam. Determination of reporting groups was completed using multiple sources of information:

1. **N-J phylograms and dendrograms:** We created a neighbor-joining (N-J) phylogram for steelhead and a N-J dendrogram for Chinook salmon to visualize the genetic relationship among baseline populations and to assist in the determination of reporting groups to be used for GSI. The N-J phylogram was based on pairwise Nei's (1972) genetic distances, and the N-J dendrogram was based on pairwise Cavalli-Sforza and Edwards (1967) genetic chord distances calculated using GENDIST (PHYLIP v3.5; Felsenstein 1993). Pairwise genetic distances were used to construct the trees in NEIGHBOR (PHYLIP v3.5). The consistency of the phylogram and dendrogram topologies was estimated using 1,000 bootstrap replicates in SEQBOOT (PHYLIP v3.5). The final N-J phylogram was constructed using TREEGRAPH2 (Stover and Muller 2010). The final N-J dendrogram was constructed using TREEVIEW (Page 1996). Nodes that were identified in greater than 50% of bootstrap iterations are noted. Results from the N-J phylogram (steelhead) and N-J dendrogram (Chinook) gave an initial look at the genetic structure of baseline populations. This genetic structure was used to create the initial reporting group structure prior to 100% simulations and self-assignment tests.

2. **Principal Coordinate Analysis (PCA):** We performed a principal coordinates analysis (PCA) analysis based on a pairwise $F_{ST}$ table in GENALEX v6.4 to evaluate differentiation among fall (ocean-type) and spring/summer (stream-type) Chinook salmon collections in Snake River baseline v2.0.

3. **100% Simulations:** Detailed methods described below. Simulated mixtures were generated from each population represented in the baseline and then assigned back to the baseline using mixture modeling. We examined where simulated mixtures mis-assigned to and pooled populations according to that information. Several iterations of reporting group formations were analyzed to optimize allocation back to correct reporting groups.

4. **Self-Assignment Tests:** Detailed methods described below. Each individual in the baseline was sequentially removed from the baseline and then assigned back to the baseline (with that individual removed). Similar to 100% simulations, we examined where individuals mis-assigned to and modified reporting groups accordingly to reduce the mis-assignment.

5. **Population Clustering Analysis (BAPS):** Baseline collections were analyzed with the software program Bayesian Analysis of Population Structure (BAPS 5.3; Corander et al. 2008). BAPS assigned collections to k clusters using a partition-based mixture model that minimized deviations from Hardy Weinberg and linkage equilibria within each cluster of collections. We used the "clustering groups of individuals" option with the predefined maximum of K = 20. We repeated the run 10 times to check stability of results. The best clustering solution was chosen based on the largest value of the log of marginal likelihood from all runs. The optimal BAPS clustering was considered when modifying reporting groups to reduce mis-allocation. Results from BAPS clustering are not presented here.

6. **MPG Designations:** Finally, in some cases MPG designations were considered when modifying reporting groups to accommodate management needs and to allow evaluation of GSI results at the MPG scale for VSP monitoring.

NOTE: Several iterations of 100% simulations and self-assignment tests using various reporting group designations were performed when trying to optimize reporting groups for GSI at Lower Granite Dam. Results from the multiple iterations are not presented here to maintain simplicity in reporting. The goal of the multiple iterations was to optimize allocation of known-origin individuals to the correct reporting group while simultaneously considering management and conservation needs for VSP monitoring.

**Statistical Analyses – Predicting the Accuracy of Defined Reporting Groups for GSI**

Two types of genetic classification techniques are generally used for mixed stock analyses (MSA) and both use allele frequencies from baseline populations as reference information to characterize potentially contributing stocks. Individual assignment (IA) methods assign each individual to the stock in which the probability of its genotype occurring is the greatest. The proportion of a particular stock can then be estimated by summing all of the individual assignments to that stock and dividing by the total sample size. In contrast, mixture modeling (MM) does not assign each individual to a specific stock. Instead, MM uses likelihood or Bayesian modeling methods to fractionally allocate individual samples within the mixture to

each stock in proportion to the probability that it belongs to that stock. Mixture modeling methods have been shown to be more accurate for estimating stock contributions when all individual assignments cannot be made with high confidence (Manel et al. 2005, Koljonen et al. 2005). Because we are interested in estimating both stock proportions (and abundance) of the wild escapement as a whole, as well as evaluating life-history information within each genetic stock (based on biological data from individual fish), we used a combination of both MM and IA techniques for genetic stock reconstruction at Lower Granite Dam.

Prior to performing MM and IA of mixtures from Lower Granite Dam, we first needed to evaluate the accuracy of Snake River baselines v2.0 (for steelhead and Chinook salmon) to determine whether the spatial resolution of the reporting groups was appropriate for performing MM and IA. Four separate analyses were performed:

1. We performed 100% simulations in the program ONCOR (Kalinowski 2007) to evaluate the accuracy of the baselines for MM.

2. We performed self-assignment tests in the program gsi_sim to evaluate the accuracy of IA.

3. We performed MM on mixtures of "known-origin" fish to estimate accuracy of the baselines for MM.

4. We conducted IA on fish that were PIT tagged at Lower Granite Dam and later detected upstream in tributary PIT-tag arrays to evaluate concordance between "genetic assignments" and "PIT-tag assignments."

Methods for each of these four analyses are described below.

To evaluate the accuracy of the Snake River genetic baselines v2.0 for MM, we performed 100% simulations in the program ONCOR using the final designated reporting groups. An analysis was run for each of the baseline populations in which the baseline and mixture genotypes were randomly generated using estimated baseline allele frequencies and the leave-one-out cross validation method (Anderson et al. 2008). The mixture (n = 300) for each population's analysis contained 100% individuals simulated from the baseline population being tested. The simulated mixture was then proportionally assigned back to the resampled baseline to evaluate the proportion of the simulated mixture that assigned back to the correct reporting group and the proportion of the simulated mixture that assigned back to incorrect reporting groups. This procedure was repeated 200 times for each population. A population is generally considered acceptably identifiable if ≥90% (mean estimate from bootstrap resamples) of the mixture assigns back to the correct reporting group (Seeb et al. 2007).

To evaluate the accuracy of the Snake River genetic baselines v2.0 for IA, we performed self-assignment tests in the program gsi_sim using the final designated reporting groups presented in Section 2. In self-assignment tests, each individual from the baseline is removed (one at a time) and the population (and reporting group) of origin of that individual is then estimated using the method of Rannala and Mountain (1997). For each baseline population, we calculated the proportion of individuals that assigned to a reporting group with ≥80% probability (we refer to this proportion as the individual assignment detection rate); and of those, we calculated the proportion of assigned individuals that assigned to their reporting group of origin (correct allocation).

The accuracy of the baselines was further tested for MM by estimating the composition of three mixtures (for each species) of known origin individuals using gsi_sim. The known mixtures were generated by randomly sampling 30 individual fish from each reporting group within the baseline and placing the sampled individuals into a mixture. For each mixture analysis, the baseline was reconstructed with the mixture individuals removed. For steelhead, each mixture consisted of 300 individuals (10 reporting groups) and for Chinook salmon each mixture consisted of 210 individuals (7 reporting groups). As there were 10 reporting groups for steelhead, each reporting group had an expected allocation of 10%; for Chinook salmon the expected allocation to each reporting group was 14.3% (7 reporting groups). We then compared the expected allocation to the observed allocation to examine for potential bias in stock composition estimates.

Starting in SY2010, the Integrated Status and Effectiveness Monitoring Program (ISEMP; BPA Project Number 2003-017-00) began PIT tagging a proportion of natural origin adult steelhead and Chinook salmon sampled at the LGD adult trap with the goal of decomposing the run-at-large past LGD into population and/or tributary escapement estimates. In the past year, we received from ISEMP personnel a list of adults that were PIT tagged at Lower Granite Dam that were later detected at tributary PIT-tag arrays or hatchery traps:

- SY2010 steelhead n = 245
- SY2011 steelhead n = 1,104
- SY2010 Chinook salmon n = 350
- SY2011 Chinook salmon n = 955

Of these samples, we genotyped and analyzed 134 steelhead and 79 Chinook salmon from SY2010 and 886 steelhead and 955 Chinook salmon for SY2011 using 192 SNPs to 1) estimate sex-ratios of fish detected an these arrays and traps (see Ellsworth and Ackerman 2012 for example), and 2) to evaluate concordance between array and trap detection locations and the estimated genetic origin of these adults using IA. Only fish that assigned with ≥80% probability using IA were considered genetically assigned. We used caution when interpreting PIT versus IA assignments since the two methods measure fundamentally different things. Individual genetic assignments are used to estimate the genetic stock *origin* of adults that return to Lower Granite Dam. PIT tags attempt to identify the final *destination* of adults sampled at Lower Granite Dam (with the assumption that homing returns adults to the stream in which they were born). While we expected to see similarities between IAs and PIT tag assignments, we recognized that wandering adults, straying adults, and genetic misassignments could lead to discordancy between the two methods.

## RESULTS

### Baseline Evaluation

#### Steelhead

In total, steelhead baseline v2.0 consists of 63 populations represented by a total of 83 collections (15 populations consist of temporal collections) and 4,145 individuals (Table 1). For

the 15 populations with collections from multiple years, collections failed to demonstrate significant departures ($\alpha = 0.05$) from homogeneity. Of the 63 populations in baseline v2.0:

- 32 populations originated from baseline v1.0
- 13 populations originated from baseline v1.0, but samples sizes were increased or collections were added as part of v2.0 expansion efforts
- 18 populations were added as part of baseline v2.0 expansion efforts

Average sample size across the 63 populations was 66 individuals with a minimum of 23 for Pistol Cr. (Middle Fork Salmon River).

Within steelhead baseline v2.0, 500 out of 10,799 (4.6%) tests for deviation from HWE (across loci and populations) were significant (540 would be expected by chance at $\alpha = 0.05$). Of the 63 baseline populations, 16 deviated from HWE in greater than 5% of SNPs (Table 1). The worst offenders were the WF Yankee F Salmon (Upper Salmon; heterozygote deficiency) and Asotin Cr (tributary of mainstem Lower Snake; heterozygote deficiency) populations, which both deviated from HWE in 19 of 187 (10.2%) SNPs analyzed.

Populations from within the Middle and South forks of the Salmon River and from the upper Clearwater (Lochsa and Selway rivers) and South Fork Clearwater River generally exhibited the greatest among-population genetic distinctness. Populations within the Middle Fork Salmon River had an average pairwise $F_{ST}$ of 0.030 when compared pairwise to all other steelhead baseline v2.0 populations (Table 1, Figure 5); within the Middle Fork, Pistol Creek exhibited the greatest pairwise $F_{ST}$ (0.036). Populations within the South Fork Salmon River had an average pairwise $F_{ST}$ of 0.028, followed closely by Lochsa River (0.027), Selway River (0.027), and South Fork Clearwater River (0.027). Outside of the above-mentioned drainages, Camp Cr (0.027) within the Imnaha River and Little Minam R (0.026), Lostine R (0.025), and Elk Cr (0.027) from within the Grande Ronde River exhibited increased levels of genetic distinctness. Populations originating in the lower Salmon (including Little Salmon River) and lower Clearwater (Potlatch River) and below the confluence of the two rivers in the lower Snake River generally exhibited the lowest levels of genetic distinctness, ranging from 0.016 to 0.020. Average pairwise $F_{ST}$ estimates for each baseline population are shown in Table 1 and Figure 5.

Upper Clearwater populations generally had the lowest within-population genetic diversity. Averaged across populations, populations in the Lochsa River had an $H_E$ of 27.6% and an AR of 1.86; Selway populations had an $H_E$ of 28.4% and an AR of 1.87. Populations in the Middle and South forks of the Salmon River also exhibited decreased within-population diversity. Averaged across populations, Middle Fork Salmon River populations had an $H_E$ of 28.5% and an AR of 1.85; South Fork Salmon River populations had an $H_E$ of 28.7% and an AR of 1.88. In contrast, populations from the upper Salmon (North Fork Salmon River and above) and lower Salmon (Little Salmon River and below) and from the lower Clearwater (Potlatch River) and lower Snake River had increased levels of within-population genetic diversity. Populations originating from Lower Snake River tributaries had an $H_E$ of 30.9% and an AR of 1.96, followed by upper Salmon River (30.8% $H_E$; 1.95 AR), Potlatch River (30.4% $H_E$; 1.94 AR), and lower Salmon River (29.9% $H_E$; 1.93 AR). Table 1 shows $H_E$ and AR for each baseline population.

Figures 6 and 7 demonstrate differentiation between natural origin steelhead collections represented in Snake River baseline v2.0 and collections from Pahsimeroi Hatchery and

Dworshak Hatchery broodstock, respectively, that were screened using the full complement of SNPs. Areas of the map shaded red represent regions where collections were more highly differentiated ($F_{ST}$ ~ 0.025 – 0.045) from the respective hatchery collection. Areas shaded blue represent regions that were less differentiated ($F_{ST}$ ~ 0.005 – 0.015).

When compared to the Pahsimeroi Hatchery collection (Figure 6), collections from the Lochsa, Selway, and South Fork Clearwater rivers and from the Middle and South forks of the Salmon River were generally more highly differentiated. Alternatively, collections from the upper and lower Salmon River, Imnaha River, Grande Ronde River, and tributaries to the Lower Snake generally exhibited less levels of differentiation from the Pahsimeroi Hatchery broodstock.

Compared to the Dworshak Hatchery collection (Figure 7), collections from the Middle and South forks of the Salmon River were the most highly differentiated, and collections from the upper and lower Salmon River, upper Clearwater, Imnaha River, Grande Ronde River, and lower Snake River exhibited intermediate levels of differentiation. Collections from the South Fork Clearwater River and Potlatch River exhibited lower levels of differentiation from the Dworshak hatchery collection.

**Chinook salmon**

In total, Chinook salmon baseline v2.0 consists of 39 populations represented by a total of 111 collections (27 populations consist of temporal collections) and 3,392 individuals (Table 2). Among the 27 populations with collections from multiple years, collections failed to demonstrate significant departures ($\alpha = 0.05$) from homogeneity. Of the 39 populations in baseline v2.0:

- 17 populations originated from baseline v1.0
- 12 populations originated from baseline v1.0, but sample sizes were increased or collections were added as part of v2.0 expansion efforts
- 10 populations were added as part of baseline v2.0 expansion efforts

Average sample size across the 39 populations was 87 individuals with a minimum of 29 for Crooked Fork Lochsa River (upper Clearwater River).

Within Chinook salmon baseline v2.0, 293 out of 5,894 (5.0%) tests for deviation from HWE were significant (295 would be expected by chance at $\alpha = 0.05$) among 175 SNPs. Of the 39 baseline populations, 11 deviated from HWE in greater than 5% of SNPs (Table 2). The population with the highest deviation was the Lolo Cr (Clearwater River; heterozygote deficiency) collection, which departed from HWE in 17 of 175 (9.7%) SNPs analyzed. Two collections, upper Lemhi River (upper Salmon River; heterozygote excess and deficiency) and Minam River (Grande Ronde River; heterozygote deficiency), deviated from HWE in 15 of 175 (8.6%) SNPs; all other collections deviated from HWE in 14 or less SNPs (Table 2).

The two collections from the Chamberlain Creek population (pre- and post-2008) and the Tucannon River population exhibited the greatest among-population genetic distinctness (Table 2, Figure 10); Chamberlain Cr (post-2008) had an average pairwise $F_{ST}$ of 0.027 followed by Tucannon R (0.025) and Chamberlain Cr (pre-2008; 0.021). Outside of the above-mentioned drainages, Hayden Cr (0.020) from the Lemhi R, upper Salmon River and Sulphur Cr (0.021)

and Camas Cr (0.020) from the Middle Fork Salmon River also exhibited increased genetic distinctness. Remaining populations from the Middle Fork Salmon River and populations from the upper Salmon River exhibited intermediate levels of differentiation. Populations from the South Fork Salmon River, Little Salmon River, Clearwater River, Imnaha River, and Grande Ronde River exhibited relatively lower levels of differentiation. Averaged across populations, pairwise $F_{ST}$ estimates for various regions of the Snake River were: upper Salmon River (Lemhi and above; 0.016), Middle Fork Salmon River (0.018), Chamberlain Creek (0.024), South Fork Salmon River (0.015), Rapid River (Little Salmon; 0.015), Lochsa River (0.015), South Fork Clearwater River (0.013), Lolo Cr (Clearwater; 0.012), Imnaha River (0.014), Grande Ronde River (0.015), and Tucannon River (0.025). Average pairwise $F_{ST}$ estimates for each baseline population are shown in Table 2 and Figure 10.

Chamberlain Creek and Middle Fork Salmon River populations generally had the lowest within-population genetic diversity. Averaged across populations, Chamberlain Creek had an $H_E$ of 21.2% and an AR of 1.52; Middle Fork Salmon River populations also had an $H_E$ of 21.2% and an AR of 1.52. Populations from the South Fork Salmon River (22.3% $H_E$; 1.55 AR) and the upper Salmon River (22.8% $H_E$; 1.56 AR) exhibited intermediate within-population diversity. In contrast, the Tucannon River population exhibited the greatest within-population diversity (26.0% $H_E$; 1.64 AR). Populations from the Little Salmon River (23.0% $H_E$; 1.57 AR), Lochsa River (23.7% $H_E$; 1.59 AR), South Fork Clearwater River (23.9% $H_E$; 1.59 AR), Lolo Creek (24.0% $H_E$; 1.59 AR), Imnaha River (23.8% $H_E$; 1.59 AR), and Grande Ronde River (24.8% $H_E$; 1.61 AR) also had higher levels of within-population diversity (Table 2).

Figure 11 displays the genetic differentiation observed between natural origin spring/summer Chinook salmon collections represented in Snake River baseline v2.0 and Rapid River Hatchery broodstock that were screened using the full complement of SNPs. Areas of the map shaded red represent regions where collections were more highly differentiated ($F_{ST}$ ~ 0.02 – 0.03) from the respective hatchery collection. Areas shaded blue represent regions that were less differentiated ($F_{ST}$ ~ 0.005 – 0.015). Regions of the upper Salmon River, Middle Fork Salmon River, Chamberlain Creek, South Fork Salmon River, and Tucannon River are relatively more differentiated from Rapid River broodstock. Conversely, the Little Salmon, Clearwater, Imnaha, and Grande Ronde rivers are less differentiated from Rapid River broodstock relative to other wild collections from the Snake River.

## Defining Reporting Groups

### Steelhead

Genetic variation among Snake River steelhead populations represented in baseline v2.0 was visualized using a N-J phylogram (Figure 8); the genetic structure observed was used (in combination with other information) in designating the final reporting groups for GSI analyses at Lower Granite Dam. Following multiple iterations of 100% simulations and self-assignments tests, we identified 10 reporting groups for GSI applications at Lower Granite Dam:

1) **UPSALM**: upper Salmon River, North Fork Salmon River and upstream

2) **MFSALM**: Middle Fork Salmon River, Chamberlain Creek

3) **SFSALM**: South Fork Salmon River

4) **LOSALM**: Little Salmon River and tributaries of the lower Salmon River

5) **UPCLWR**: Lochsa River and Selway River

6) **SFCLWR**: South Fork Clearwater River; includes Clear Creek, a tributary of the main-stem Clearwater River

7) **LOCLWR**: Currently represented by collections from the Potlatch River

8) **IMNAHA**: Imnaha River

9) **GRROND**: Grande Ronde River

10) **LSNAKE**: Tributaries of the lower Snake River both below (Tucannon River) and above (Alpowa and Asotin) Lower Granite Dam

Table 1 summarizes the populations representing each reporting group (including the TRT populations designation for each baseline population). The NJ-phylogram shows that the genetic structure of populations corresponds closely to the reporting groups designated for GSI; reporting groups are designated by brackets in Figure 8. Of note is that populations from the Salmon River MPG (UPSALM, MFSALM, SFSALM, and LOSALM reporting groups) are significantly and highly differentiated from populations from the Clearwater River MPG (UPCLWR, SFCLWR, and LOCLWR reporting groups) and that populations from the IMNAHA, GRROND, and LSNAKE reporting groups are intermediate of Salmon River and Clearwater River groups. Figure 9 shows the pairwise $F_{ST}$ as a function of $H_E$ (averaged across populations) for each reporting group; individuals originating from reporting groups with higher average $F_{ST}$ are expected to be more easily identifiable in GSI analyses.

Cumulatively, the UPSALM, MFSALM, SFSALM, and LOSALM reporting groups represent the Salmon River MPG. The UPCLWR, SFCLWR, and LOCLWR reporting groups cumulatively represent the Clearwater River MPG. The IMNAHA, GRROND, and LSNAKE reporting groups directly correspond to the Imnaha River, Grande Ronde River, and Lower Snake River MPGs, respectively. The extant Hells Canyon Tributaries MPG (SNHCT TRT population) is currently not represented in the Snake River steelhead baseline. Note that the Lower Snake River MPG also contains populations within the Tucannon River, Washington, whose confluence with the Snake River occurs downstream of Lower Granite Dam. Thus, GSI estimates for the LSNAKE reporting group at LGD represent fish that 1) originate from tributaries of the Lower Snake River above Lower Granite Dam (i.e. Alpowa and Asotin Creeks), and 2) originate from tributaries of the Lower Snake River below Lower Granite Dam (including the Tucannon River) that may ascend Lower Granite Dam and perhaps fall back downstream or continue an upstream migration.

The changes that were made between steelhead baseline v1.0 and steelhead baseline v2.0 are summarized below:

- BLWLGD was changed to LSNAKE reporting group. Further, Asotin Creek (a tributary of the mainstem lower Snake River) was moved from the GRROND to the LSNAKE reporting group. We replaced samples collected in 2000 from Asotin Creek with two more recent collections made in 2008 and 2010 (Table 1). Further, we added collections from George Creek (a tributary of Asotin Creek) and Alpowa Creek (a tributary of the mainstem Snake River downstream of the town of Clarkston). After adding these

collections, the genetic structure in the region indicated that Asotin and George creeks and Alpowa Creek are genetically similar, and further, that they are more similar to the Tucannon River collection than they are to collections from the Grande Ronde River. The LSNAKE reporting group now represents populations from both above and below Lower Granite Dam.

- The SALMON reporting group (see Schrader et al. 2011) was split into two reporting groups, UPSALM and LOSALM (Table 1).

**Chinook salmon**

Genetic variation among Snake River spring/summer Chinook salmon populations represented in baseline v2.0 was visualized using an unrooted N-J dendrogram (Figure 12); the genetic structure observed in the N-J dendrogram was used (in conjunction with other information) in designating the final reporting groups for GSI analyses at Lower Granite Dam. Further, PCA results (Figure 13) demonstrate high levels of differentiation among fall Chinook and spring/summer Chinook collections in the Snake River basin; thus, a reporting group was designated to represent fall Chinook. Using GSI we expect to be able to identify fall Chinook individuals at Lower Granite Dam with 100% accuracy (see Section 3). Following multiple iterations of 100% simulations and self-assignments tests, we identified seven reporting groups for GSI applications at Lower Granite Dam:

1. **UPSALM**: upper Salmon River, Lemhi River and upstream
2. **MFSALM**: Middle Fork Salmon River
3. **CHMBLN**: Chamberlain Creek
4. **SFSALM**: South Fork Salmon River
5. **HELLSC**: Little Salmon River, Clearwater River, Imnaha River, and Grande Ronde River
6. **TUCANO**: Tucannon River
7. **FALL**: Fall (ocean-type) Chinook

Table 2 summarizes the collections representing each reporting group (including the TRT population designation for each baseline population). The N-J dendrogram shows that the genetic structure of populations generally corresponds to the reporting groups designated for GSI; reporting groups are designated by gray shading in Figure 12. Of note are those populations from the CHMBLN and TUCANO reporting groups are highly differentiated relative to collections from other regions in the Snake River basin. Further, Figure 12 shows that there is high bootstrap support (>50%) for each reporting group's primary node. Figure 14 shows the pairwise $F_{ST}$ as a function of $H_E$ (averaged across populations) for each reporting group; individuals originating from reporting groups with higher average $F_{ST}$ are expected to be more easily identifiable in GSI analyses.

For Chinook salmon, the UPSALM and SFSALM reporting groups directly correspond to the Upper Salmon River and South Fork Salmon River MPGs within the Snake River Spring/Summer Chinook salmon ESU. The Middle Fork Salmon River MPG is broken into two

reporting groups: CHMBLN and MFSALM. The HELLSC reporting group encompasses the Rapid River population (Little Salmon River drainage), the Imnaha/Grande Ronde rivers MPG, and also unlisted populations originating from the Clearwater River drainage. We did not observe enough genetic population structure to separate populations from these areas into discrete reporting groups. The genetic similarities observed between populations from these areas are clearly displayed in the spatial interpolation of pairwise $F_{ST}$ estimates (Figure 11). The TUCANO reporting group is within the Lower Snake River tributaries MPG; Asotin Creek within the Lower Snake River tributaries MPG is not represented in Snake River Chinook salmon baseline v2.0. Populations in the FALL reporting group are representative of the Snake River fall Chinook Salmon ESU.

The changes that were made between Chinook salmon baseline v1.0 and Chinook salmon baseline v2.0 are summarized below:

- CHMBLN reporting group was added. The Chamberlain Creek collection included in baseline v1.0 exhibited high levels of differentiation (Ackerman et al. 2011a). To validate this we added further samples from Chamberlain Creek for baseline v2.0 and results from new samples were consistent with genetic patterns observed in baseline v1.0 (Figure 12). The high level of differentiation of the Chamberlain Creek population has also been observed using allozyme data (ICTRT 2003).

- FALL reporting group was added. For baseline v2.0, we added 3 collections of fall (ocean-type) Chinook (Table 2). In doing so, we are able to differentiate spring/summer (stream-type) fall Chinook at Lower Granite Dam with 100% expected accuracy (Figures 13 and 16).

## Predicting the Accuracy of Defined Reporting Groups for GSI

### Steelhead

Of the 63 populations represented in Snake River steelhead baseline v2.0, 53 (84%) exhibited greater than 90% mean correct allocation to the correct reporting group during 100% simulations (Table 11). That is, when a mixture of fish was simulated based on the population's estimated allele frequencies, greater than 90% of the mixture (mean across 200 simulations) was allocated back to the correct reporting group for 53 of 63 populations. Among the reporting groups, the SFSALM exhibited the greatest mean correct allocation; 99% of mixtures simulated from SFSALM populations assigned back to the SFSALM reporting group. Other reporting groups with greater than 90% mean correct allocation include UPCLWR (99%), MFSALM (98%), SFCLWR (97%), LOCLWR (97%), UPSALM (96%), and GRROND (92%). The LOSALM reporting group exhibited the lowest mean correct allocation; 87% of mixtures simulated from LOSALM populations assigned back to the LOSALM reporting group. Other groups with less than 90% mean correct allocation include IMNAHA (89%) and LSNAKE (89%).

Of the 63 populations in steelhead baseline v2.0, 52 (83%) had greater than 80% of assigned baseline individuals (individuals that assigned to a reporting group with >80% probability) assign back to the correct reporting group during self-assignment tests performed in gsi_sim (Table 12). Among reporting groups, MFSALM, SFSALM, and UPCLWR had the highest assignment rates and the greatest assignment to the correct reporting group. Of 487 baseline individuals from the MFSALM reporting group, 416 (85%) assigned with greater than 80% probability; of those, 406 (98%) assigned back to the MFSALM reporting group. Of 176 baseline individuals from SFSALM, 155 (88%) assigned; of those 152 (98%) assigned back to

SFSALM. Of 796 individuals originating from the UPCLWR reporting group, 728 (91%) assigned; of those 716 (98%) assigned back to UPCLWR. The LSNAKE performed poorest among reporting groups. Of 401 baseline individuals originating from LSNAKE, only 104 (26%) assigned with greater than 80% probability; of those 45 (43%) assigned back to LSNAKE. Overall, of the 4,145 individuals in the baseline, 2,617 (63%) assigned with greater than 80% probability; of those 2,371 (91%) assigned back to the correct reporting group (Table 12). Figure 15 summarizes the expected resolution of steelhead baseline v2.0 for both MM and IA based on 100% simulations and self-assignment tests, respectively.

The mean observed allocation (averaged across three mixtures) for 9 out of 10 steelhead reporting groups was not significantly different from the expected allocation (10%) when we analyzed mixtures comprised of "known origin" individuals removed from the baseline (Table 14). Further, 7 out of 10 reporting groups had a mean observed allocation within ±2% of the expected allocation. The reporting group with the nearest mean observed allocation relative to the expected allocation was UPCLWR (+0.2%) followed by MFSALM (+0.2%), LOCLWR (+0.9%), GRROND (-1.0%), LOSALM (-1.1%), SFCLWR (-1.2%), and SFSALM (-1.4%). The reporting group where the mean observed allocation deviated most from the expected allocation was IMNAHA (-4.6%) followed by LSNAKE (+4.5%) and UPSALM (+3.4%). The IMNAHA reporting group was the only group where the mean observed allocation among the three mixtures generated from "known origin" individuals was significantly different from the expected allocation (Table 14).

We genotyped and analyzed 1,020 adult steelhead (from SY2010 and SY2011) that were PIT tagged during their upstream migration at the Lower Granite Dam adult trap and were later detected at a tributary PIT tag array (Table 15). Of all 1,020 steelhead, 515 (50.5%) assigned to a reporting group with greater than 80% probability. Of the 515 that assigned, 421 (81.7%) had a genetic assignment that "matched" the location of the PIT tag array that the fish was detected at (Table 15). Individual location summaries are provided below:

- **Valley Creek Array:** Of the 30 fish that were detected at PIT tag arrays located in Valley Creek in the upper Salmon River; 17 (57%) assigned and 16 (94%) assigned to the UPSALM reporting group.

- **Lemhi River arrays:** Of the 60 fish that were detected at PIT tag arrays located within the Lemhi River (BTC = Big Timber Creek, HYC = Hayden Creek, KEN = Kenny Creek, LLR = Lower Lemhi River, LRW = Lemhi River Bjornn Weir); 37 (62%) assigned and 32 (86%) assigned to the UPSALM reporting group.

- **Big Creek Array:** Of the 75 fish that were detected at the PIT tag arrays located at Taylor Ranch on Big Creek, Middle Fork Salmon River, 62 (83%) assigned and 58 (94%) assigned to the MFSALM reporting group.

- **S.F. Salmon Arrays:** Of the 361 fish that were detected at PIT tag arrays within the South Fork Salmon River (ZEN = Secesh River, Zena, ESS = East Fork South Fork Salmon, KRS = South Fork Salmon, Krassel, SFG = South Fork Salmon, Guard Station); 245 (68%) assigned and 217 (89%) assigned to the SFSALM.

- **Imnaha River Arrays:** Of the 330 fish that were detected at PIT tag arrays within the Imnaha River (BSC = Big Sheep Creek, COC = Cow Creek, IR1 = Imnaha River, IR2 =

Imnaha River, IR3 = Imnaha River); 105 (32%) assigned and 63 (60%) assigned to the IMNAHA reporting group.

- **Joseph Creek Array:** Of the 164 fish that were detected at the Joseph Creek PIT tag array within the Grande Ronde River; 50 (30%) assigned and 35 (70%) assigned to the GRROND reporting group.

**Chinook salmon**

Of the 39 populations represented in Snake River Chinook salmon baseline v2.0, all 39 exhibited greater than 90% mean correct allocation to the correct reporting group during 100% simulations (Table 16). That is, when a mixture of fish was simulated based on the population's allele frequencies, greater than 90% of the mixture (mean across 200 simulations) was allocated back to the correct reporting group for every collection in the baseline. Among the reporting groups, the CHMBLN, TUCANO, and FALL groups exhibited 100% allocation back to the correct reporting group followed closely by UPSALM (99%), MFSALM (99%), SFSALM (98%), and HELLSC (98%).

Of the 39 populations represented in Chinook salmon baseline v2.0, 38 (97%) had greater than 80% of assigned baseline individuals (individuals that assigned to a reporting group with ≥80% probability) assign back to the correct reporting group during self-assignment tests (Table 17). Among the reporting groups representing spring/summer Chinook salmon, five of the six had greater than 75% of baseline individuals assign with greater than 80% probability; all six reporting groups had greater than 80% of assigned individuals assign to the correct reporting group (Table 17). Of 776 baseline individuals from the UPSALM reporting group, 597 (77%) assigned with ≥80% probability; of those, 562 (94%) assigned back to UPSALM. Of the 549 baseline individuals from the MFSALM reporting group, 454 (83%) assigned with ≥80% probability; of those, 426 (94%) assigned back to MFSALM. Of 126 baseline individuals from the CHMBLN reporting group, 111 (88%) assigned with ≥80% probability; of those, 105 (95%) assigned back to CHMBLN. Of the 448 baseline individuals from the SFSALM reporting group, 287 (64%) assigned with ≥80% probability; of those, 239 (83%) assigned back to SFSALM. Of the 1,086 baseline individuals from the HELLSC reporting group, 897 (83%) assigned with ≥80% probability; of those, 864 (96%) assigned back to HELLSC. Of the 81 baseline individuals from the TUCANO reporting group, 74 (91%) assigned with ≥80% probability; of those, 74 (85%) assigned back to TUCANO. Further, of the 327 fall Chinook representing the FALL reporting group, all 327 (100%) assigned with ≥80% probability; of those, all 327 (100%) assigned back to the FALL reporting group. Overall, of the 3,393 individuals in the baseline, 2,747 (81%) assigned with ≥80% probability; of those 2,586 (94%) assigned back to the correct reporting group (Table 18). Figure 16 summarizes the expected resolution of Chinook salmon baseline v2.0 for both MM and IA based on 100% simulations and self-assignment tests, respectively.

The mean observed allocation (averaged across 3 mixtures) for all seven Chinook salmon reporting groups was not significantly different from the expected allocation (14.3%) when we analyzed mixtures comprised of "known origin" individuals removed from the baseline (Table 19). Further, six out of seven reporting groups had a mean observed allocation within ± 2% of the expected allocation. The reporting group with the nearest mean observed allocation relative to the expected allocation was FALL (±0.0%) followed by UPSALM (-0.1%), MFSALM (-0.3%), CHMBLN (-0.3%), SFSALM (-1.0%) and TUCANO (-1.6%). The reporting group where the mean observed allocation most deviated from the expected allocation was HELLSC (+3.3%) although the difference was not significant (Table 19).

We genotyped and analyzed 1,034 adult Chinook salmon (from SY2010 and SY2011) that were PIT tagged during their upstream migration at the Lower Granite Dam adult trap and were later detected at a tributary PIT tag array (Table 20). Overall, of the 1,034 detected fish analyzed, 649 (63%) assigned with ≥80% probability; of those 518 (80%) had a genetic assignment that "matched" the location of the PIT tag array that the fish was detected at (Table 20). Individual location summaries are provided below:

- **Sawtooth Trap:** Of 113 fish detected at the Sawtooth Fish Hatchery trap, 71 (63%) assigned with ≥80%; of those, 65 (92%) assigned to the UPSALM reporting group.

- **Valley Cr. Array:** Of 44 fish detected at the Valley Cr PIT tag array, 32 (73%) assigned with ≥80%; of those, 30 (94%) assigned to the UPSALM reporting group.

- **Pahsimeroi Trap:** Of 7 fish detected at the Pahsimeroi Fish Hatchery trap, 6 (86%) assigned with ≥80%; of those, 6 (100%) assigned to the UPSALM reporting group.

- **Hayden Cr. Array:** Of 12 fish detected at the Hayden Cr PIT tag array, 6 (50%) assigned with ≥80%; of those, 4 (67%) assigned to the UPSALM reporting group.

- **Lemhi R. (Bjornn Weir) Array:** Of 16 fish detected at the Lemhi R (Bjornn Weir) PIT tag array, 10 (63%) assigned with ≥80%; of those, 7 (70%) assigned to the UPSALM reporting group.

- **Lower Lemhi R. Array:** Of 4 fish detected at the lower Lemhi R PIT tag array, 4 (100%) assigned with ≥80%; of those, 3 (75%) assigned to the UPSALM reporting group.

- **Big Cr. Array:** Of 34 fish detected at the Big Cr PIT tag array, 23 (68%) assigned with ≥80%; of those, 9 (39%) assigned to the MFSALM reporting group.

- **Secesh R. (Zena Cr.) Array:** Of 87 fish detected at the Secesh R (Zena Cr) PIT tag array, 66 (76%) assigned with ≥80%; of those, 59 (89%) assigned to the SFSALM reporting group.

- **EFSF Salmon R. Array:** Of 70 fish detected at the East Fork South Fork Salmon R PIT tag array, 46 (66%) assigned with ≥80%; of those, 33 (72%) assigned to the SFSALM reporting group.

- **South Fork Salmon R. Trap:** Of 14 fish detected at the South Fork Salmon River trap, 7 (50%) assigned with ≥80%; of those, 6 (86%) assigned to the SFSALM reporting group.

- **South Fork Salmon River (Krassel) Array:** Of 302 fish detected at the South Fork Salmon River (Krassel) PIT tag array, 138 (46%) assigned with ≥80%; of those, 75 (54%) assigned to the SFSALM reporting group.

- **South Fork Salmon River (Guard Station) Array:** Of 26 fish detected at the South Fork Salmon River (Guard Station) PIT tag array, 20 (77%) assigned with ≥80%; of those, 15 (75%) assigned to the SFSALM reporting group.

- **Big Sheep Cr. Array:** Of 35 fish detected at the Big Sheep Cr PIT tag array, 24 (69%) assigned with ≥80%; of those, 21 (88%) assigned to the HELLSC reporting group.

- **Imnaha R. Weir:** Of 19 fish detected at the Imnaha R weir, 15 (79%) assigned with ≥80%; of those, 15 (100%) assigned to the HELLSC reporting group.

- **Imnaha River (IR1, IR3) Arrays:** Of 215 fish detected at Imnaha R (IR1, IR3) PIT tag arrays, 150 (70%) assigned with ≥80%; of those, 141 (94%) assigned to the HELLSC reporting group.

- **Lookingglass Trap:** Of 36 fish detected at the Lookingglass Hatchery trap, 31 (86%) assigned with ≥80%; of those, 29 (94%) assigned to the HELLSC reporting group.

## DISCUSSION

Substantial achievements were made over the last year to increase the resolution of genetic baselines for steelhead and Chinook salmon in the Snake River basin and assess their accuracy for GSI.

### Steelhead

The Snake River steelhead distinct population segment (DPS) includes 26 populations distributed among six MPGs in southeastern Washington, northeastern Oregon, and central Idaho (ICTRT 2003). Of those, the Hells Canyon MPG and the North Fork Clearwater River population within the Clearwater River MPG are currently blocked from their historic habitat and are considered extirpated (ICTRT 2003). Of the 24 remaining extant populations, 21 are currently represented in steelhead baseline v2.0. The three populations not represented include Panther Creek (SRPAN, Salmon River MPG), Lolo Creek (CRLOL, Clearwater River MPG), and Upper Grande Ronde (GRUMA, Grande Ronde River MPG). With the assistance of collaborating agencies, we anticipate the collection and/or genotyping of samples from each of these populations in the upcoming project year so that all extant populations will be represented.

For steelhead, sample sizes were increased for 13 of the existing sample collections and 18 new sample collections were added to the baseline. We discerned 10 reporting groups that closely follow the geographic boundaries of major subbasins or drainages in the Snake River basin using the updated v2.0 baseline. Importantly, we were able to provide a finer scale of resolution in the mainstem Salmon River corridor, splitting it into two reporting groups corresponding to the upper and lower Salmon River. Populations in these sections had been combined into one group for reporting purposes in Schrader et al. (2011).

Use of the 10 steelhead reporting groups for GSI is supported by the testing of our baselines using several different methods. Results of 100% simulation testing reinforced the use of these reporting groups for MM analyses. It has been recommended that reporting groups meet a threshold of 90% correct assignment in 100% simulation analyses to be useful for fishery management applications (Beacham et al. 2006; Seeb et al. 2007). All but three of the steelhead reporting groups exhibited greater than 90% mean correct allocation, and the remaining three all exhibited values approaching 90% (87% - 89%).

Mixture modeling tests using known origin fish randomly sampled from the baseline yielded generally positive results as well. Of the 10 reporting groups, seven exhibited observed mean allocation within +/-2% of the expected mixture proportion. The remaining three reporting groups exhibited observed mean allocation within +/-5% of the expected proportion and only one (IMNAHA) had a mean observed allocation significantly different than expected. Of note was the IMNAHA reporting group, which consistently yielded mixture proportions less than expected (-4.6%) and the LSNAKE reporting group, which consistently yielded mixture proportions greater than expected (+4.5%). Over the next year we plan to investigate statistical procedures for incorporating these estimated misclassification rates during stock abundance estimation.

Results from self-assignment tests supported the use of the baseline for IA analyses for 8 of the 10 reporting groups. The highest accuracy was observed in the three reporting groups comprising populations from areas managed exclusively for wild spawning steelhead (UPCLWR, SFSALM, and MFSALM) with all exhibiting 98% correct individual assignment. The two reporting groups that exhibited the lowest correct individual assignments were LOSALM (68%) and LSNAKE (43%). Both of these reporting groups have either had direct hatchery releases of juveniles or have had straying hatchery adults identified, and have likely received hatchery introgression.

Because all adult steelhead PIT tagged at Lower Granite Dam are also sampled for fin tissue, we have a unique opportunity to assess concordance between the two methods (PIT array detections versus genetic identifications). Of the adults detected at arrays and genetically assigned, 82% yielded concordant location results. The highest concordance was observed at the Valley Creek, Lemhi River, Big Creek, and S.F. Salmon arrays (86% - 94%). For example, of the 75 adults detected at the Big Creek array in 2010 and 2011 that were analyzed, 62 (82.7%) assigned to a reporting group with high probabililty. Of 62 assigned adults, 58 (93.5%) assigned to MFSALM. We observed less concordance at arrays on the Imnaha River (60.0%) and Joseph Creek (70.0%) in the Grande Ronde River drainage, reflective of genetic mis-assignment, increased current levels of roaming and straying, mixed ancestry, or a comibination of the three.

**Chinook salmon**

The Snake River spring/summer Chinook salmon evolutionary significant unit (ESU) includes 31 independent populations among five MPGs spanning Idaho, Oregon, and Washington (ICTRT 2003, 2005). Of the 31 populations, three are considered functionally extirpated including Panther Creek (SRPAN, Upper Salmon River MPG), Big Sheep Creek (IRBSH, Grande Ronde / Imnaha MPG), and Asotin Creek (SNASO, Lower Snake River MPG). Of the remaining 28 extant populations, 23 are currently represented in Chinook baseline v2.0. The five populations not represented include Salmon River lower main stem (SRLMA, Upper Salmon River MPG), North Fork Salmon River (SRNFS, Upper Salmon River MPG), Middle Fork upper main stem (MFUMA, Middle Fork Salmon River MPG), Loon Creek (MFLOO, Middle Fork Salmon River MPG), and Middle Fork lower main stem (MFLMA, Middle Fork Salmon River MPG). Currently, samples have been made available for Loon Creek by the Northwest Fisheries Science Center and we will attempt to identify samples from the remaining populations not represented so that all extant population will be represented in the future.

Sample sizes were increased for 12 of the existing sample collections and 10 new sample collections were added to the baseline. Using this updated v2.0 baseline along with the increase in the number of SNP markers genotyped, we were able to discern seven reporting

groups. The majority (>60%) of the Chinook salmon within the Snake River ESU come from the Salmon River basin and its major tributaries. Importantly populations within this basin are well represented in baseline v2.0 and cluster into four reporting groups: UPSALM, MFSALM, CHMBLN, and SFSALM. These are critical stocks in the Snake River ESU for VSP monitoring because three of them reside primarily in wilderness areas, or in habitats with minimal anthropogenic impacts, and most have not had the level out of basin stock transfers that has occurred through the rest of the ESU.

Despite increasing the number of SNP loci screened and increasing the number of sample collections, we did not observe sufficient genetic population structure between populations from the Clearwater River drainage, Imnaha and Grande Ronde Rivers and Rapid River, to separate these areas into discrete reporting groups. The genetic similarities observed between populations from these areas are clearly displayed in the spatial interpolation of pairwise $F_{ST}$ estimates. The Rapid River hatchery stock originated from stream-type Chinook salmon stocks from the mid-Snake River above Hells Canyon. Subsequently, the entire Clearwater River drainage was reestablished with stocks from both within the ESU (50 million Rapid River Hatchery outplants since 1968) and outside of the ESU (9 million Carson Hatchery outplants since 1968; LSRCP 1998; Myers et al. 1998). Both the Imnaha and Grande Ronde Rivers have also directly received Rapid River hatchery outplants or supplementation from stocks founded from Rapid River Hatchery stock (Narum et al. 2007; and references within). Due to the genetic similarities from shared ancestry, all of the populations from these areas were combined into a single reporting group (HELLSC). Although, we cannot currently provide a finer level of resolution for the HELLSC reporting group, we observed some genetic structuring within this group. For example, the NJ-dendogram clusters the Clearwater River populations and Rapid River, independently from the other populations within this reporting group. Over the next year, we will continue to add collections to the Chinook salmon baseline to determine if there are opportunities to provide finer levels of resolution for GSI.

The Tucannon River collection (TUCANO) exhibited increased levels of genetic distinctness and increased population diversity (Figure 14). Narum et al. (2007) showed that Tucannon River spring Chinook cluster closely with fall Chinook collections resulting from introgression (~5%) with proximate fall Chinook populations (Narum et al. 2010). Introgression between the two lineages has resulted in the observed increase in genetic diversity in Tucannon River populations, and further, the genetic distinction that identified TUCANO as an independent reporting group for GSI at Lower Granite Dam.

Similar to the steelhead results, the use of the seven reporting groups we have resolved for Snake River Chinook salmon for GSI purposes is clearly supported by the testing of our baselines using several methods. Results of 100% simulation testing reinforced the use of these reporting groups for MM analyses. All reporting groups exhibited mean correct allocation at 98% or greater.

Mixture modeling tests, using known origin fish randomly sampled from the baseline, indicated that of the seven reporting groups, six exhibited observed mean allocation within +/- 2% of the expected mixture proportion. The only reporting group exceeding this was the HELLSC reporting group, which consistently yielded mixture proportions higher than expected (3.3%).

Results from self- assignment tests supported the use of the baseline for IA analyses for all reporting groups. All spring/summer Chinook salmon reporting groups exhibited greater than

80% average correct individual assignment, with the highest accuracy observed in the HELLSC (96%), CHMBLM (95%), UPSALM (94%), and MFSALM (94%).

As was available for steelhead, all adult Chinook salmon PIT tagged at Lower Granite Dam are also sampled for fin tissue, allowing us the opportunity to assess concordance between the two methods. We observed high concordance between the two methods, with 80% of the adults detected at arrays and genetically assigned yielding concordant results. The highest concordance was observed at the Sawtooth, Valley, Pahsimeroi, Secesh, Imnaha, and Lookingglass traps or arrays (89% - 100%). For example, of the 113 adults detected at the Sawtooth Hatchery trap in 2010 and 2011, 71 (62.8%) assigned to a reporting group. Of the 71 assigned fish, 65 (91.5%) assigned to the UPSALM reporting group. Interestingly, we observed low concordance at the array on Big Creek (39.0%), despite self-assignment tests indicating 88% predicted accuracy to the MFSALM reporting group. This potentially indicates increased levels of roaming or straying into Big Creek relative to other regions in the Middle Fork Salmon River. In addition, we observed highly variable concordance across array locations within the S.F. Salmon River drainage. For example, we observed an average concordance of 89.4% at the array on the Secesh River (Zena) in 2010 and 2011, but the average concordance for the array at Krassel during those two years was only 54.3%. The lower concordance observed at this array may be due to a combination of factors including increased levels of genetic mis-assignment. The genetic sample collection from the adult weir located on the mainstem South Fork Salmon River, located approximately 30-40 km upstream of the array, exhibits only 59% accuracy in self-assignment tests despite tributary collections (Secesh River and Johnson Creek) exhibiting increased accuracy (84% - 97%).

## CONCLUSION

For the purposes of VSP monitoring and run reconstruction efforts, our intent is to maintain consistency in reporting groups over time. However, in cases where reporting groups have to be modified over time, we do have the ability to re-analyze past years data using updated baselines to ensure consistency in reporting (as was done here; SY2009 and SY2010 steelhead adults and SY2009 Chinook adults were re-analyzed using updated baselines v2.0). Further, some plasticity in reporting group structure will be necessary; as baselines are updated annually as part of the GSI project the increase in available data may highlight genetic structure that conflicts with current reporting group structure.

The IDFG Eagle Fish Genetic Lab and the CRITFC Hagerman Genetics Lab are highly collaborative laboratories; the Snake River SNP baselines will annually be transferred to and duplicated in CRITFC's Progeny database. Vice-versa, mid- and lower-Columbia River baseline data is available to IDFG EFGL staff. This collaboration and data sharing is important for management and conservation of steelhead and Chinook salmon throughout the Columbia basin. Currently, IDFG is pursuing VSP monitoring of steelhead and Chinook salmon in the Snake River basin and is beginning run reconstruction efforts (in collaboration with multiple agencies) of steelhead in the basin. In addition to GSI efforts at Lower Granite Dam (this project), CRITFC conducts GSI at Bonneville Dam. Consistency in data and collaboration will allow run reconstruction efforts in the Snake River basin to extend downstream to Bonneville Dam and may enable evaluation of harvest and survival between Bonneville Dam and Lower Granite Dam.

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

### INTRODUCTION

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 provide benefit to 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 age and sex information over time allows estimation of population growth rates; and both abundance and productivity metrics provide indicators of the resiliency and viability of populations. Estimates of these metrics at the genetic stock or MPG level is information that fisheries managers can use to achieve sustainable harvest of larger populations, while protecting weaker stocks and the biodiversity within them.

However, population level or MPG assessments of abundance and productivity for ESA listed Snake River steelhead and spring/summer Chinook salmon can be particularly difficult (see Report Introduction for explanation). Specific data on Snake River steelhead and Chinook salmon populations are lacking, particularly key parameters such as population abundance, age composition, genetic diversity, recruits per spawner, and survival rates (ICTRT 2003). GSI is one potential means for estimating these parameters at a finer-scale; perhaps at the level of MPG, genetic reporting group, or population. GSI uses multilocus genotype data from reference populations (representing potential contributing stocks) as a baseline (Snake River baselines presented in Section 2) and a complimentary set of genotype data from mixtures of fish of unknown origin to estimated stock proportions within the mixture and to estimate the stock of origin of individual fish. In Section 2, we presented the baselines to be used for GSI in the Snake River baseline. Using the v2.0 baselines, we documented the genetic structure of natural origin steelhead and Chinook salmon within the basin, and based on the genetic structure, established reporting groups for GSI in the basin. In Section 3 we use complementary sets of genotype data from adults sampled at the Lower Granite Dam adult trap and juveniles samples at the Lower Granite Dam juvenile bypass facility to estimate reporting group proportions of mixtures and to estimate the reporting group of origin of individuals.

Below, we summarize three years of GSI efforts at Lower Granite Dam, including:

- Steelhead adults: SY2009, SY2010, and SY2011
- Steelhead juveniles: MY2010 and MY2011
- Chinook adults: SY2009, SY2010, and SY2011
- Chinook juveniles: MY2010 and MY2011

All fishery mixtures were analyzed using the Snake River v2.0 baselines. In the first year's annual report (Ackerman et al. 2011a), we analyzed steelhead adults from SY2009 and SY2010 and Chinook salmon adults from SY2009; the analyses presented here using baselines v2.0 supersede those analyses using baselines v1.0. Note: Chinook salmon mixtures from SY2010 and MY2010 and prior were only genotyped and analyzed using the 96 SNP panel described in the 1$^{st}$ year's annual report as the full complement of 192 SNPs were not available when these samples were processed at the IDFG and CRITFC laboratories. All Chinook salmon

mixtures from SY2011 and MY2011 and subsequent are genotyped and analyzed using the full complement of 192 SNPs described for Snake River Chinook salmon baseline v2.0.

Fishery mixtures from LGD are analyzed and interpreted in the context of VSP monitoring with particular emphasis on evaluating life-history differences among reporting groups. Continuation of GSI efforts at Lower Granite Dam will allow us to 1) monitor genetic structure throughout the basin over time, and 2) estimate productivity parameters and related biological information for genetic stocks throughout the Snake River basin.

## METHODS

### Sampling at Lower Granite Dam

#### Adult Trap Operations

Methods for operation of the adult trap at Lower Granite Dam are adapted from Schrader et al. (2011). Systematic samples of steelhead and Chinook salmon returning to LGD were collected during daily operation of the adult fish trap by National Marine Fisheries Service (NMFS; BPA project 2005-002-00, Lower Granite Dam Adult Trap Operations; Harmon 2003; Harmon 2009; Ogden 2010). The adult trap is located in the LGD fish ladder upstream from the fish counting window. The trap captures a systematic random sample of fish by operating a trap gate according to a predetermined sample rate. The sample rate determines how long the trap gate remains open four times per hour; the trap is operational 24 hours per day. Additional details on the trap can be found in Harmon (2003) and Steinhorst et al. (2010). Additional operation information as it pertains to data analysis for SY2009 is available in Schrader et al. (2011) and will be published for subsequent spawn years annually in similar reports.

Standard methods were used by NMFS or IDFG staff to process and biologically sample adult fish (Harmon 2003; Harmon 2009; Ogden 2010). All adult fish captured were anesthetized; examined for external marks, tags, and injuries; scanned for an internal coded wire tag (CWT) or passive integrated transponder (PIT) tag; and measured for fork length (FL, nearest cm). All fish were classified by origin (wild or hatchery) and the presence or absence of the adipose fin. Wild fish have an unclipped adipose fin because they spend their entire lifecycle in the natural environment. Although most hatchery origin steelhead and Chinook salmon have a clipped adipose fin, some are released with an unclipped adipose fin for supplementation purposes. For unclipped steelhead, hatchery origin was determined primarily by the presence of dorsal or ventral fin erosion, which is assumed to occur only in hatchery-reared fish (Latremouille 2003). We also used the presence of a CWT to determine if an unclipped fish was of hatchery origin. For unclipped Chinook salmon, hatchery origin was determined solely by the presence of a CWT. Captured fish determined to be wild were subsampled for scales and tissue.

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. Tissues 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 (Steele et al. 2012). After processing, all fish were returned to the adult fish ladder to resume their upstream migration.

**Juvenile Trap Operations**

Detailed methods for operation of the juvenile adult trap will become available in annual reports similar to Schrader et al. (2011). Additional information regarding operation of the juvenile trap is also available in past annual reports from the Lower Granite Dam Smolt Monitoring Program (see Mensik et al. 2006 for example) and on the Fish Passage Center's Smolt Monitoring Program website: http://www.fpc.org/smolt_home.html.

Briefly, a sample of naturally produced juvenile steelhead and Chinook salmon are shunted into a trough for biological sampling. Only adipose fin intact, putative naturally produced juveniles are sampled. Juveniles falling under any of the following categories are excluded from biological sampling:

- Juveniles with a coded wire tag (CWT)
- Juveniles that are de-scaled or otherwise injured
- Juveniles with a PIT tag (to avoid confounding other research studies)

All sampled fish were measured to the nearest millimeter (fork length) and a scale sample (for age) and tissue sample (for genetic analysis) was taken. A piece of fin tissue was generally taken from the top of the caudal fin (approximately one-half the size of a pencil eraser). Tissues were stored in a vial with 200-proof non-denatured ethyl alcohol for transport to the IDFG Eagle Fish Genetics Laboratory.

**Valid Sample Selection**

Methods for valid sample selection are adapted from Schrader et al. (2011). Not all trapped fish were deemed valid for sample selection or analysis. Trapped fish that were missing data entry records for any of the following five fields were considere invalid: date of collection, species, fork length, origin (hatchery or wild), or adipose fin status (clipped or unclipped). Trapped fish less than 30 cm (FL) were considered invalid as they are not identified to species at the COE fish-counting window. Further, the adult trap was not designed to efficiently trap smaller fish (Darren Ogden, NMFS, personal communication); for Chinook salmon this includes all mini-jacks less than 30 cm. Finally, any sort by code PIT-tagged fish that were trapped outside the normal trap sampling timeframe were considered invalid. A computer program written by Doug Marsh (NMFS) was used to make this determination. Invalid samples for SY2009 adults are described in Schrader et al. (2011); invalid samples from subsequent years will be describe in similar reports.

For the first year of this study (SY2009), our goal was to age and genotype approximately 1,000 wild steelhead and 1,000 wild Chinook salmon. After the first year (for SY2010 and SY2011), our goals were increased for both species to age and genotype approximately 2,000 wild steelhead and 2,000 Chinook salmon to obtain desired coefficients of variation (CV) for stock composition estimates. When necessary, trap samples were systematically subsampled to reach this goal. The result was a pool of samples collected systematically across the spawning run of each species and generally in constant proportion to their abundance. Hence, the sample pool can be considered a simple random sample (Kirk Steinhorst, University of Idaho, personal communication).

### Laboratory Protocol

Laboratory methods follow those in Sections 1 and 2. For steelhead, all adults (SY2009, SY2010, SY2011) and all juveniles (MY2010, MY2011) were screened using the full complement of 192 *O. mykiss* assays. For Chinook salmon, all adults (SY2009, SY010) and all juveniles (MY2010) sampled prior to 2011 were only screened at the original 96 assays that comprised Snake River Chinook baseline v1.0 (see Ackerman et al. 2011a). Adults (SY2011) and juveniles (MY2011) sampled post-2010 were screened using the full complement of 192 Chinook salmon assays.

## GSI at Lower Granite Dam

### SY2009 through SY2011 GSI Analyses of Lower Granite Dam Adults

Mixture modeling using multilocus genotype data was performed to estimate genetic stock proportions of the wild escapement at LGD. Genetic stock proportions are then applied to estimated escapement at Lower Granite Dam to estimate abundance for each genetic stock (see Schrader et al. 2011). Mixture modeling of individuals genotyped from LGD was done using the Bayesian version of the program gsi_sim (Anderson et al. 2008, Anderson 2010). The Bayesian version of gsi_sim uses Markov chain Monte Carlo (MCMC) to computer posterior probabilities of stock membership conditional on the allele frequencies estimated from the baseline. The likelihood that a fish originates from a stock is computed using the compound Dirichlet-multinomial formulation of Rannala and Mountain (1997) conditional on the baseline samples and these likelihoods remain fixed throughout the MCMC simulation. To perform the MCMC, gsi_sim uses a Gibbs sampler (Casella and George 1992) in which alternately, 1) the stock assignments of the fish in the mixture are updated as a multinomial draw from their posterior probabilities given the current estimate of the stock proportions and the stock-likelihoods of the fish; and 2) the stock proportions are updated as a draw from a Dirichlet distribution given a unit-information prior and the current values of the stock assignments of all the fish in the mixture. By sampling the current values of the stock proportions as the chain proceeds, a Monte Carlo estimator of the posterior mean and any desired quantiles can be computed. For estimating stock proportions, we ran 300,000 MCMC sweeps with a burn-in of 50,000 sweeps and a thinning interval of 50 to obtain 5,000 Bayesian posterior estimates of stock proportions for each stock. The 5,000 Bayesian posterior estimates of stock proportions were used for subsequent calculation of confidence intervals (CI) for stock proportions. The maximum likelihood estimates of stock proportions were considered the point estimates.

The coefficient of variation (CV) for each reporting group's composition estimate was calculated from the 5,000 Bayesian posterior estimates obtained from the MCMC chain above. The CV was calculated as the standard deviation of the 5,000 Bayesian posterior estimates divided by the mean of the 5,000 Bayesian posterior estimates and was expressed as a percentage. CV's were calculated for each reporting group for SY2009 through SY2011.

Once MM had been completed to estimate stock proportion and abundance for each genetic stock, the next step was to decompose each stock by sex, age, length, time-of-passage, etc., using biological information taken from individual fish sampled at Lower Granite Dam. To accomplish this, we use IA; the advantage of IA over MM is that fish are assigned wholly back to a genetic stock; thus, biological information from each fish can be tracked to genetic stock. IA was performed using the program gsi_sim. Maximum likelihood estimates of probability of assignment to each reporting group were obtained using the full expectation-maximization algorithm implemented in gsi_sim. For IA, we only used biological information from fish that

assigned to a reporting group with ≥80% probability. A fish that assigned with <80% probability was considered unassigned. In performing IA to evaluate life-history information for each reporting group, we made the assumptions that fish of different sexes, lengths, age classes, and run-timing (early vs. late) assign with equal probabilities. We believe these assumptions hold true and each assumption will be tested in the future for further validaton.

The sex of each individual was determined using a Y-specific assay for steelhead or for Chinook salmon (Steele et al. 2012). Individuals that amplify only at the autosomal control region are determined to be females. Individuals that amplify at both the autosomal control region and the Y-specific region are determined to be males. The accuracy of the Y-specific sex assays for both steelhead and Chinook salmon were estimated by comparing sex estimated from the assay to phenotypic sex of PBT broodstock obtained during spawning during SY2010 (Steele et al. 2012). For steelhead, the *OmyY1_2SEXY* assay was estimated to be 94.4% accurate when compared to known-sex broodstock (n = 3,110). For Chinook salmon, the *Ots_SEXY3-1* assay was estimated to be 100% accurate (n = 275).

**MY2010 through MY2011 GSI Analyses of Lower Granite Dam Juveniles**

Similar as for adults, the sex of each individual was determined using a Y-specific sex assay (Steele et al. 2012). Results from the Y-specific sex assays were used to estimate sex ratios of sampled individuals for each genetic reporting group using individuals that assigned to a reporting group with ≥80% probability.

Finally, for individuals that assigned to a reporting group with ≥80% probability we used age and length data to evaluate life-history information for each reporting group. Length data was obtained as individuals were sampled at the Lower Granite Dam juvenile trapping facility. Steelhead age was obtained from a scale sample aged at the Nampa Research aging lab (see Schrader et al. 2011 for methods). Chinook age (yearling vs. subyearling) was based on phenotype.

## RESULTS

### GSI at Lower Granite Dam

#### Steelhead

##### *Adults (SY2009 through SY2011)*

Table 21 and Figure 17 summarize the reporting group composition of the natural origin steelhead adult escapement at Lower Granite Dam for SY2009 through SY2011. The LSNAKE reporting group comprised the largest percentage of the adult escapement across all three spawn years (SY2009 = 18.9%, SY2010 = 23.1%, SY2011 = 22.5%), and was followed by the GRROND (SY2009 = 16.4%, SY2010 = 16.2%, SY2011 = 16.2%) and the UPSALM (SY2009 = 12.1%, SY2010 = 18.2%, SY2011 = 15.4%). The three reporting groups that comprised the smallest percentage of the adult escapement were SFSALM (SY2009 = 3.4%, SY2010 = 3.6%, SY2011 = 4.7%), LOSALM (SY2009 = 7.9%, SY2010 = 3.4%, SY2011 = 4.1%), and LOCLWR (SY2009 = 5.7%, SY2010 = 3.9%, SY2011 = 3.9%). Interestingly, the UPSALM and MFSALM comprised a larger portion of the escapement in SY2010 than each of the other years while the UPCLWR and SFCLWR reporting groups comprised a smaller portion in SY2010 (Table 21, Figure 17). From SY2009 through SY2010, the estimated allocation to populations in the

Salmon River major population group (MPG) was 31.6%, 35.7%, and 32.6%, respectively. The estimated allocation to populations in the Clearwater River MPG was 27.3%, 18.1%, and 23.4% across the 3 years.

Coefficients of variation (CV) for stock composition estimates for steelhead adults across the three years ranged from 5.8% (SY2011 LSNAKE) to 26.3% (SY2010 LOSALM; Table 21, Figure 18). The LSNAKE reporting group had the lowest average CV (SY2009 = 9.6%, SY2010 = 6.0%, SY2011 = 5.8%) across the three years. The LOSALM reporting group had the highest average CV (SY2009 = 15.1%, SY2010 = 26.3%, SY2011 = 19.1%). Of the 10 reporting groups, eight had a CV of less than 15% when averaged across years; LSNAKE (7.1%), UPSALM (8.0%), GRROND (8.3%), SFCLWR (8.4%), UPCLWR (8.7%), MFSALM (8.8%), IMNAHA (13.8%), and SFSALM (13.9%). The LOCLWR (17.7%) and LOSALM (20.2%) reporting groups had the highest CV averaged across years (Table 21, Figure 18).

For SY2009, we analyzed 1,057 natural origin adult steelhead from the Lower Granite Dam adult trap; of those 537 (50.8%) assigned back to a reporting group with ≥80% probability and were determined to originate from that reporting group. For SY2010, 1,918 adult steelhead were analyzed of which 957 (49.9%) assigned to a reporting group. For SY2011, 2,264 adult steelhead were analyzed of which 1,152 (50.8%) assigned (Table 22). Biological information taken from these fish as they were sampled at the Lower Granite Dam adult trap were used to examine various life-history traits for each of the reporting groups.

Across three years (SY2009 – SY2011), 67% of assigned adult steelhead were estimated to be females (SY2009 = 70%, SY2010 = 63%, SY2011 = 68%) based on the Y-specific allelic discrimination assay (Table 23, Figure 19). Among the reporting groups, MFSALM exhibited the most heavily skewed female sex ratios (SY2009 = 77%, SY2010 = 75%, SY2011 = 75%, average = 75%). The MFSALM was followed closely by UPCLWR (across years = 70%) and SFSALM (71%) as the highest percentage of females. The reporting group with the lowest percentage of females across years was LOSALM (55%) followed by LSNAKE (57%) and SFCLWR (61%). All reporting groups had a larger percentage of females than males in all years with one exception (SY2010 LSNAKE = 47% females). Sex ratios are shown in Table 23 and Figure 19.

Adult steelhead assigning to the UPCLWR, SFCLWR, and SFSALM reporting groups were among the largest and oldest, whereas adult assigning to the UPSALM, IMNAHA, GRROND, and LSNAKE were the smallest and youngest (Tables 24 and 25, Figures 20 and 21). Average across years, adults originating from the UPCLWR reporting group had a mean fork length of 78 cm and were primarily 2-ocean fish (1-ocean = 13%, 2-ocean = 82%, 3-ocean = 5%). Adults originating from the SFCLWR also had a mean fork length of 78 cm and were primarily 2-ocean (1-ocean = 11%, 2-ocean = 82%, 3-ocean = 7%). Adult steelhead originating from the SFSALM had a mean fork length of 77 cm and were primarily 2-ocean (1-ocean = 13%, 2-ocean = 82%, 3-ocean = 5%). Conversely, adults originating from the UPSALM reporting group had a mean fork length of 63 cm and were primarily 1-ocean (1-ocean = 58%, 2-ocean = 42%, 3-ocean = 0%). Adults from IMNAHA had a mean fork length of 64 cm and were primarily 1-ocean (1-ocean = 62%, 2-ocean = 38%, 3-ocean = 0%). Adults from GRROND had a mean fork length of 65 cm and were a split of 1-ocean and 2-ocean (1-ocean = 49%, 2-ocean = 51%, 3-ocean = 0%). Adults from the LSNAKE reporting group had a mean fork length of 65 cm and were primarily 1-ocean (1-ocean = 58%, 2-ocean = 41%, 3-ocean = 1%). Figure 20 summarizes length information for all reporting groups, SY2009 through SY2011. Tables 24 and 25 and Figure 21 summarizes age information for all reporting groups, SY2009 through SY2011.

Steelhead adults assigning to the MFSALM reporting group generally had the earliest date of passage at Lower Granite Dam in all three years (Figure 22). In general, adults assigning to the UPSALM and SFSALM reporting groups also had an earlier data of passage. Conversely, adults assigning to the UPCLWR and SFCLWR reporting groups generally had a latest date of passage. Figure 22 shows the cumulative proportion of fish that assigned to each reporting group over time for SY2009 through SY2011.

***Juveniles (MY2010 and MY2011)***

For MY2010, we analyzed 1,233 natural origin steelhead smolts from the Lower Granite Dam juvenile facility; of those 578 (46.9%) assigned to a reporting group with ≥80% probability and were determined to originate from that reporting group. For MY2011, we analyzed 2,115 steelhead smolts of which 957 (45.2%) assigned with ≥80% probability (Table 22). Biological information obtained from these fish as they were sampled at the Lower Granite Dam juvenile facility was used to examine life-history traits for each of the reporting groups.

Across two years (MY2010 – MY2011), 57% of assigned juvenile steelhead were estimated to be females (MY2010 = 58%, MY2011 = 56%) based on the Y-specific allelic discrimination assay (Table 23, Figure 19). Among reporting groups, MFSALM had the most heavily skewed female sex ratios (MY2010 = 67%, MY2011 = 60%). MFSALM was followed by GRROND (MY2010 = 67%, MY2011 = 57%) and UPSALM (MY2010 = 61%, MY2011 = 61%). In contrast, UPCLWR (MY2010 = 47%, MY2011 = 53%) and LOCLWR (MY2010 = 44%, MY2011 = 55%) had approximately a 1:1 sex ratio across years. Sex ratios are shown in Table 23 and Figure 19.

Of juveniles sampled at Lower Granite Dam, three reporting groups in particular produced older outmigrants (Table 26); a majority of juveniles from MFSALM, SFSALM, and UPCLWR had freshwater ages of 3 and 4. In MY2010, greater than 75% of juveniles originating from these reporting groups had a freshwater age of 3 or greater; MFSALM (2-freshwater = 16%, 3-freshwater = 68%, 4-freshwater = 14%), SFSALM (2-freshwater = 15%, 3-freshwater = 69%, 4-freshwater = 14%), UPCLWR (2-freshwater = 22%, 3-freshwater = 62%, 4-freshwater = 14%, 5-freshwater = 3%). In MY2011, all reporting groups produced younger migrants, but MFSALM (1-freshwater = 1%, 2-freshwater = 27%, 3-freshwater = 54%, 4-freshwater = 18%), SFSALM (2-freshwater = 25%, 3-freshwater = 50%, 4-freshwater = 23%, 5-freshwater = 2%), and UPCLWR (1-freshwater = 4%, 2-freshwater = 42%, 3-freshwater = 41%, 4-freshwater = 11%, 5-freshwater = 1%) still had the oldest migrants within the migratory year. In contrast, a larger proportion of juveniles from the remaining seven reporting groups had a freshwater age of 2 (Table 26) in both years relative to MFSALM, SFSALM, and UPCLWR. Juveniles assigning to the MFSALM and SFSALM reporting groups were also generally larger (mean FL) at time of sampling (Figure 23).

**Chinook salmon**

***Adults (SY2009 through SY2011)***

Table 27 and Figure 24 summarize the reporting group composition of the natural origin Chinook salmon escapement at Lower Granite Dam for SY2009 through SY2011. The HELLSC reporting group comprised the largest percentage of the adult escapement across all three spawn years (SY2009 = 35.9%, SY2010 = 31.8%, SY2011 = 41.5%). HELLSC was followed by SFSALM (SY2009 = 27.1%, SY2010 = 27.9%, SY2011 = 20.4%), UPSALM (SY2009 = 19.5%,

SY2010 = 16.8%, SY2011 = 16.1%), and MFSALM (SY2009 = 11.0%, SY2010 = 16.4%, SY2011 = 14.8%). The three reporting groups comprising the smallest percentage of the adult escapement were CHMBLN (SY2009 = 4.6%, SY2010 = 4.2%, SY2011 = 2.1%), FALL (SY2009 = 1.5%, SY2010 = 2.8%, SY2011 = 4.2%), and TUCANO (SY2009 = 0.5%, SY2010 = 0.2%, SY2011 = 0.9%).

CVs for stock composition estimates for natural origin Chinook salmon adults across the three years ranged from 2.9% (SY2011 HELLSC) to 72.4% (SY2009 TUCANO; Table 27, Figure 25). The HELLSC reporting group had the lowest average CV (SY2009 = 6.3%, SY2010 = 5.7%, SY2011 = 2.9%) across the three years. The TUCANO reporting group had the highest average CV (SY2009 = 72.4%, SY2010 = 48.6%, SY2011 = 24.8%). Of the six reporting groups where CVs were calculated, four had a CV of less than 15% when averaged across years; HELLSC (5.0%), SFSALM (7.5%), UPSALM (8.6%), and MFSALM (10.3%). The CHMBLN (18.6%) and TUCANO (48.6%) reporting groups had the highest CV averaged across years (Table 27, Figure 25).

For SY2009, we analyzed 825 natural origin adult Chinook salmon from the Lower Granite Dam adult trap; of those 375 (45.5%) assigned back to a reporting group with ≥80% probability and were determined to originate from that reporting group. For SY2010, 1,176 adult Chinook salmon were analyzed of which 553 (47.0%) assigned with ≥80%, and for SY2011, 2,104 adult Chinook salmon were analyzed of which 1,499 (71.2%) assigned with ≥80% (Table 28). Biological information taken from these fish as they were sampled at the Lower Granite Dam adult trap were used to examine various life-history traits for each of the reporting groups.

Across three years (SY2009 – SY2011), 98% of assigned 1-ocean adult Chinook salmon (SY2009 = 99%, SY2010 = 95%, SY2011 = 98%) and 58% of 2- and 3-ocean adult Chinook salmon (SY2009 = 52%, SY2010 = 53%, SY2011 = 61%) were estimated to be males based on the Y-specific allelic discrimination assay (Table 29). Among the reporting groups, five of the seven had a male-skewed sex ratio when averaged across years. UPSALM exhibited the most heavily skewed male sex ratio (SY2009 = 62%, SY2010 = 61%, SY2011 = 68%), and was followed by MFSALM (across years = 59%), FALL (57%), SFSALM (56%), and HELLSC (56%). The two reporting groups with female-skewed sex ratios were CHMBLN (48% male) and TUCANO (40% male). Sex ratios for each reporting group across years are shown in Table 29.

Among the spring/summer Chinook salmon reporting groups originating from above Lower Granite Dam, individuals assigning to the UPSALM reporting group were the largest and oldest (Tables 30 and 31, Figures 26 and 27); individuals assigning to UPSALM had a mean fork length (FL) of 76.3 cm and 91% had an ocean age of 2 (68%) or 3 (23%). UPSALM was followed by SFSALM (mean FL = 75.1 cm, 2-ocean = 63%, 3-ocean = 23%) and HELLSC (mean FL = 72.9 cm, 2-ocean = 69%, 3-ocean = 17%) as the next largest and oldest reporting groups. Individuals assigning to the MFSALM (mean FL = 72.9 cm, 2-ocean = 60%, 3-ocean = 23%) and the CHMBLN (mean FL = 71.6 cm, 2-ocean = 66%, 3-ocean = 10%) reporting groups had the smallest mean fork length and highest proportion of 1-ocean individuals among reporting groups. Figure 26 summarizes length information for all reporting groups, SY2009 through SY2011. Tables 30 and 31 and Figure 27 summarize age information for all reporting groups, SY2009 through SY2011.

Among the reporting groups representing spring/summer Chinook salmon originating from above Lower Granite Dam, individuals from the MFSALM and HELLSC generally had the earliest date of passage at Lower Granite Dam (Figure 28). Conversely, adults assigning to the SFSALM and CHMBLN reporting groups generally had a later date of passage. UPSALM

generally had an intermediate mean date of passage. Figure 28 shows the cumulative proportion of fish that assigned to each reporting group over time, SY2009 through SY2011.

***Juveniles (MY2010 and MY2011)***

For MY2010, we analyzed 1,914 natural origin juvenile Chinook salmon from the Lower Granite Dam juvenile facility; of those 1,169 (61.1%) assigned to a reporting group with ≥80% probability and were determined to originate from that reporting group. For MY2011, 2,103 juvenile Chinook salmon were analyzed of which 1,642 (78.1%) assigned with ≥80% probability (Table 28). Biological information obtained from these fish as they were sampled at the Lower Granite Dam juvenile facility was used to examine life-history traits for each of the reporting groups.

Across two years (MY2010 – MY2011), 48% of assigned juvenile Chinook salmon were estimated to be males (MY2010 = 42%, MY2011 = 53%). The UPSALM (50% males), MFSALM (51%), CHMBLN (51%), and FALL (50%) reporting groups has sex ratios near 1:1. Worth noting, the HELLSC reporting group was the only reporting group that had a female-biased sex ratio in both years (MY2010 = 35% male, MY2011 = 48% male). Sex ratios for Chinook salmon are shown in Table 29 in Figure 19.

A vast majority of individuals for the six spring/summer Chinook salmon reporting groups (UPSALM, MFSALM, CHMBLN, SFSALM, HELLSC, and TUCANO) were phenotypic yearlings. Conversely, a majority (95%) of juveniles assigning to the FALL reporting group were phenotypic subyearlings (Table 32). Of the reporting groups representing spring/summer Chinook salmon from above Lower Granite Dam, individuals assigning to UPSALM and HELLSC were generally larger (mean FL); individuals assigning to MFSALM, CHMBLN, and SFSALM were of similar sizes to each other and were slightly smaller (Figure 29).

## DISCUSSION

Reporting group composition estimates reported here will be multiplied by estimates of total wild excapement at Lower Granite Dam (see Schrader et al. 2011 for example) to assess wild escapement for each of the defined genetic reporting groups. Wild escapement estimates for each of the 'genetic stocks' will be used to evaluate the status of wild populations; particularly related to viable salmonid population (VSP) monitoring (McElhany et al. 2000) parameters including abundance, productivity, and diversity. We directly estimate adult abundance for each genetic stock at LGD; abundance estimates are combined with sex, age, and date of collection data obtained at the LGD trapping facility to further decompose abundance. We can estimate abundance by sex and by brood year through use of the sex and age data, and these estimates are necessary to generate brood tables and for productivity analyses. Productivity is the generational replacement rate, defined as the number of progeny per parent (or female). In the future, estimates of wild adult abundance will be combined with related data for smolts from the LGD juvenile facility. This will enable us to estimate adult-to-adult, adult-to-juvenile, and juvenile-to-adult productivity. GSI will allow for unprecedented monitoring of productivity of natural populations for both steelhead and spring/summer Chinook salmon in the Snake River basin.

Crawford and Rumsey (2011) suggest that agencies and tribes should strive to have adult abundance estimates with a CV on average of 15% or less for all ESA populations. Acknowledging that our GSI estimates are made at the scale of genetic reporting group (similar

geographic scale to MPG), we have achieved average CVs of 15% or less for eight of ten steelhead reporting groups (excluding LOSALM and LOCLWR; Table 21) and four of the five spring/summer Chinook reporting groups (excluding CHMBLN; Table 27) that originate from above Lower Granite Dam. Results suggest that current trapping rates at the LGD adult trapping facility are appropriate to achieve desired levels of CV levels for adult estimates at the scale of reporting group. We will continue to evaluate the accuracy and precision of GSI estimates in the future, and further, we intend to perform power analyses to evaluate precision of productivity estimates.

Accurate estimates of adult abundance for each reporting group rely on accurate estimation of wild escapement at Lower Granite Dam. Starting in SY2012, we will further refine estimates of wild escapement using PBT (Steele et al. *In Review*); PBT will be used to identify unclipped hatchery fish thus providing more accurate estimates of wild versus hatchery proportions throughout the run at LGD. For both species, SY2012 will be the first year that two-ocean hatchery fish will return from hatchery broodstock collections that began in SY2008.

CRITFC conducts 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 LGD 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 greatly assist run reconstruction efforts.

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**TABLES**

Table 1. *Oncorhynchus mykiss* populations screened with 192 assays for Snake River steelhead baseline v2.0. Reporting unit used for genetic stock identification at Lower Granite Dam, major population group (MPG), TRT population designation (ICBTRT 2003), sample size (*n*), years collected, genotyping agency, baseline version, latitude, longitude, life stage, mean pairwise fixation indices ($F_{ST}$), expected heterozygosity ($H_E$), mean allelic richness (AR), and number of loci with HWE deviations (for any population deviating from HWE in >5% of SNPs) are shown. Map # corresponds to numbers in Figures 1, 8, and 9. Agency indicates the laboratory where samples were genotyped. Life stage codes: A – adult, J – juvenile, K – kelt. All collections are summer-run, of natural origin, and presumed to be of anadromous lineage.

| Map # | Population | Reporting Group | MPG | TRT Population | *n* | Years Collected | Genotype Agency | Baseline Version | Latitude | Longitude | Life Stage | $F_{ST}$ | $H_E$ | AR | HWE |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Sawtooth Weir | UPSALM | Salmon | SRUMA | 108 | 05, 10 | IDFG | 1.0, 2.0 | 44.151 | -114.885 | A | 0.019 | 29.5% | 1.93 | |
| 2 | Valley Cr | UPSALM | Salmon | SRUMA | 45 | 05 | IDFG | 2.0 | 44.223 | -114.927 | J | 0.020 | 29.8% | 1.94 | 17 |
| 3 | WF Yankee F Salmon | UPSALM | Salmon | SRUMA | 117 | 04, 08 | IDFG | 1.0, 2.0 | 44.351 | -114.730 | J | 0.019 | 30.1% | 1.93 | 19 |
| 4 | Morgan Cr | UPSALM | Salmon | SREFS | 37 | 00 | IDFG | 1.0 | 44.613 | -114.164 | J | 0.024 | 31.5% | 1.95 | |
| 5 | Pahsimeroi Weir | UPSALM | Salmon | SRPAH | 99 | 06, 10 | IDFG | 1.0, 2.0 | 44.682 | -114.040 | A | 0.020 | 31.7% | 1.97 | 11 |
| 6 | Hayden Cr | UPSALM | Salmon | SRLEM | 90 | 09, 10 | IDFG | 2.0 | 44.862 | -113.632 | J | 0.020 | 32.3% | 1.98 | |
| 7 | NF Salmon R | UPSALM | Salmon | SRNFS | 102 | 10 | IDFG | 1.0, 2.0 | 45.409 | -113.992 | A, K | 0.016 | 30.6% | 1.95 | |
| 8 | Marsh Cr | MFSALM | Salmon | MFUMA | 59 | 00 | IDFG | 1.0 | 44.449 | -115.230 | J | 0.033 | 28.5% | 1.85 | |
| 9 | Sulphur Cr | MFSALM | Salmon | MFUMA | 46 | 00 | IDFG | 2.0 | 44.553 | -115.297 | J | 0.031 | 28.3% | 1.85 | |
| 10 | Rapid R (MF) | MFSALM | Salmon | MFUMA | 45 | 00 | IDFG | 1.0 | 44.679 | -115.149 | J | 0.032 | 28.8% | 1.87 | |
| 11 | Pistol Cr | MFSALM | Salmon | MFUMA | 23 | 00 | IDFG | 1.0 | 44.722 | -115.149 | J | 0.036 | 28.2% | 1.84 | |
| 12 | Loon Cr | MFSALM | Salmon | MFUMA | 84 | 99, 00 | CRITFC | 1.0, 2.0 | 44.598 | -114.812 | J | 0.025 | 28.5% | 1.87 | |
| 13 | Camas Cr | MFSALM | Salmon | MFBIG | 57 | 00 | IDFG | 1.0 | 44.892 | -114.722 | J | 0.025 | 28.7% | 1.88 | 15 |
| 14 | Big Cr (upper) | MFSALM | Salmon | MFBIG | 46 | 00 | IDFG | 1.0 | 45.151 | -115.297 | J | 0.033 | 28.0% | 1.81 | |
| 15 | Big Cr (lower) | MFSALM | Salmon | MFBIG | 48 | 00 | CRITFC | 1.0 | 45.092 | -114.730 | J | 0.028 | 28.9% | 1.88 | |
| 16 | Chamberlain Cr | MFSALM | Salmon | SRCHA | 47 | 00 | IDFG | 2.0 | 45.452 | -114.931 | J | 0.020 | 29.3% | 1.94 | 11 |
| 17 | Bargamin Cr | MFSALM | Salmon | SRCHA | 32 | 00 | IDFG | 1.0 | 45.572 | -115.192 | J | 0.024 | 30.5% | 1.93 | |
| 18 | EF SF Salmon R | SFSALM | Salmon | SFMAI | 47 | 00 | IDFG | 1.0 | 45.013 | -115.713 | J | 0.029 | 29.2% | 1.87 | |
| 19 | Stolle Meadows | SFSALM | Salmon | SFMAI | 45 | 00 | CRITFC | 1.0 | 44.607 | -115.681 | J | 0.030 | 28.3% | 1.88 | |
| 20 | Secesh R | SFSALM | Salmon | SFSEC | 45 | 00 | IDFG | 1.0 | 45.027 | -115.708 | J | 0.027 | 28.7% | 1.90 | |
| 21 | Lick Cr | SFSALM | Salmon | SFSEC | 39 | 10 | IDFG | 2.0 | 45.069 | -115.814 | J | 0.027 | 28.6% | 1.87 | |
| 22 | Boulder Cr | LOSALM | Salmon | SRLSR | 47 | 00 | IDFG | 1.0 | 45.202 | -116.311 | J | 0.020 | 30.2% | 1.92 | |
| 23 | Rapid R | LOSALM | Salmon | SRLSR | 101 | 03, 09 | IDFG | 1.0, 2.0 | 45.372 | -116.356 | A | 0.019 | 29.9% | 1.93 | 12 |
| 24 | Slate Cr | LOSALM | Salmon | SRLSR | 47 | 00 | IDFG | 1.0 | 45.638 | -116.283 | J | 0.018 | 30.1% | 1.94 | |
| 25 | Whitebird Cr | LOSALM | Salmon | SRLSR | 62 | 00, 01 | IDFG | 1.0, 2.0 | 45.752 | -116.320 | J | 0.018 | 29.3% | 1.92 | |
| 26 | Colt Cr | UPCLWR | Clearwater | CRLOC | 38 | 00 | IDFG | 2.0 | 46.431 | -114.540 | J | 0.029 | 27.1% | 1.85 | |
| 27 | Storm Cr | UPCLWR | Clearwater | CRLOC | 38 | 00 | IDFG | 1.0 | 46.461 | -114.547 | J | 0.031 | 27.3% | 1.85 | |
| 28 | Crooked F Lochsa R | UPCLWR | Clearwater | CRLOC | 44 | 00 | IDFG | 1.0 | 46.525 | -114.679 | J | 0.026 | 27.9% | 1.87 | 12 |
| 29 | Lake Cr | UPCLWR | Clearwater | CRLOC | 47 | 00 | IDFG | 2.0 | 46.463 | -114.997 | J | 0.029 | 27.6% | 1.85 | |
| 30 | Fish Cr | UPCLWR | Clearwater | CRLOC | 100 | 10, 11 | IDFG | 2.0 | 46.334 | -115.347 | A | 0.024 | 28.2% | 1.87 | |
| 31 | Canyon Cr | UPCLWR | Clearwater | CRLOC | 47 | 11 | IDFG | 1.0 | 46.216 | -115.556 | J | 0.025 | 27.7% | 1.89 | |
| 32 | Selway R | UPCLWR | Clearwater | CRSEL | 78 | 08 | IDFG | 2.0 | 45.692 | -114.718 | J | 0.029 | 28.3% | 1.87 | 13 |
| 33 | Little Clearwater R | UPCLWR | Clearwater | CRSEL | 59 | 08 | IDFG | 2.0 | 45.744 | -114.789 | J | 0.027 | 28.6% | 1.86 | |
| 34 | Whitecap Cr | UPCLWR | Clearwater | CRSEL | 76 | 08 | IDFG | 2.0 | 45.869 | -114.721 | J | 0.028 | 28.7% | 1.87 | 12 |
| 35 | Bear Cr | UPCLWR | Clearwater | CRSEL | 36 | 00 | IDFG | 1.0 | 46.019 | -114.838 | J | 0.029 | 28.7% | 1.87 | |
| 36 | NF Moose Cr | UPCLWR | Clearwater | CRSEL | 94 | 00, 04 | IDFG | 1.0, 2.0 | 46.163 | -114.897 | J | 0.023 | 28.2% | 1.85 | 11 |

| Map # | Population | Reporting Group | MPG | TRT Population | *n* | Years Collected | Genotype Agency | Baseline Version | Latitude | Longitude | Life Stage | $F_{ST}$ | $H_E$ | AR | HWE |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 37 | Three Links Cr | UPCLWR | Clearwater | CRSEL | 47 | 00 | IDFG | 2.0 | 46.096 | -115.072 | J | 0.031 | 27.5% | 1.86 | |
| 38 | Gedney Cr | UPCLWR | Clearwater | CRSEL | 45 | 00 | IDFG | 1.0 | 46.058 | -115.314 | J | 0.023 | 28.8% | 1.87 | |
| 39 | O'Hara Cr | UPCLWR | Clearwater | CRSEL | 47 | 00 | IDFG | 1.0 | 46.081 | -115.518 | J | 0.022 | 28.6% | 1.90 | 13 |
| 40 | Crooked R | SFCLWR | Clearwater | CRSFC | 109 | 07, 08 | IDFG | 1.0, 2.0 | 45.821 | -115.527 | A | 0.026 | 27.5% | 1.87 | |
| 41 | Tenmile Cr | SFCLWR | Clearwater | CRSFC | 47 | 00 | IDFG | 1.0 | 45.806 | -115.683 | J | 0.033 | 27.5% | 1.88 | |
| 42 | John's Cr | SFCLWR | Clearwater | CRSFC | 40 | 00 | IDFG | 1.0 | 45.822 | -115.889 | J | 0.024 | 28.8% | 1.92 | 10 |
| 43 | Clear Cr | SFCLWR | Clearwater | CRLMA | 45 | 00 | IDFG | 1.0 | 46.049 | -115.781 | J | 0.026 | 28.2% | 1.90 | |
| 44 | WF Potlatch R | LOCLWR | Clearwater | CRLMA | 85 | 09, 10 | IDFG | 2.0 | 46.805 | -116.418 | A | 0.018 | 30.0% | 1.93 | |
| 45 | EF Potlatch R | LOCLWR | Clearwater | CRLMA | 160 | 08, 10, 11 | IDFG | 1.0, 2.0 | 46.798 | -116.419 | A | 0.018 | 30.0% | 1.94 | 12 |
| 46 | Big Bear Cr | LOCLWR | Clearwater | CRLMA | 99 | 07, 08, 10, 11 | IDFG | 1.0, 2.0 | 46.631 | -116.656 | A | 0.017 | 31.2% | 1.95 | |
| 47 | Little Bear Cr | LOCLWR | Clearwater | CRLMA | 151 | 07, 08, 10, 11 | IDFG | 1.0, 2.0 | 46.637 | -116.678 | A | 0.017 | 30.2% | 1.94 | |
| 48 | Big Sheep Cr | IMNAHA | Imnaha | IRMMT | 69 | 01 | CRITFC | 1.0 | 45.557 | -116.834 | J | 0.020 | 29.0% | 1.91 | |
| 49 | Camp Cr | IMNAHA | Imnaha | IRMMT | 24 | 01 | CRITFC | 1.0 | 45.557 | -116.835 | J | 0.027 | 28.8% | 1.88 | |
| 50 | Cow Cr | IMNAHA | Imnaha | IRMMT | 44 | 00 | CRITFC | 1.0 | 45.768 | -116.750 | J | 0.019 | 29.4% | 1.92 | |
| 51 | Lightning Cr | IMNAHA | Imnaha | IRMMT | 39 | 00 | CRITFC | 1.0 | 45.655 | -116.727 | J | 0.021 | 28.6% | 1.92 | |
| 52 | Little Minam R | GRROND | Grande Ronde | GRWAL | 48 | 00 | CRITFC | 1.0 | 45.400 | -117.672 | J | 0.026 | 29.5% | 1.93 | |
| 53 | Lostine R | GRROND | Grande Ronde | GRWAL | 45 | 00 | CRITFC | 1.0 | 45.552 | -117.490 | J | 0.025 | 30.4% | 1.95 | 12 |
| 54 | Elk Cr | GRROND | Grande Ronde | GRJOS | 45 | 00 | CRITFC | 1.0 | 45.705 | -117.153 | J | 0.027 | 28.3% | 1.86 | |
| 55 | Joseph Cr | GRROND | Grande Ronde | GRJOS | 60 | 11 | IDFG | 2.0 | 46.028 | -117.018 | A | 0.018 | 29.9% | 1.94 | |
| 56 | Crooked Cr | GRROND | Grande Ronde | GRLMT | 97 | 01 | CRITFC | 1.0 | 45.977 | -117.555 | J | 0.018 | 30.5% | 1.95 | |
| 57 | Menatchee Cr | GRROND | Grande Ronde | GRLMT | 73 | 99 | CRITFC | 1.0 | 46.007 | -117.365 | J | 0.019 | 31.2% | 1.95 | |
| 58 | Wenaha R | GRROND | Grande Ronde | GRLMT | 94 | 01 | CRITFC | 1.0 | 45.945 | -117.451 | J | 0.018 | 29.8% | 1.93 | |
| 59 | Captain John Cr | GRROND | Lower Snake | GRLMT | 56 | 00 | IDFG | 2.0 | 46.151 | -116.934 | J | 0.021 | 29.5% | 1.93 | 15 |
| 60 | George Cr | LSNAKE | Lower Snake | SNASO | 96 | 10 | IDFG | 2.0 | 46.303 | -117.117 | A | 0.016 | 30.7% | 1.96 | |
| 61 | Asotin Cr | LSNAKE | Lower Snake | SNASO | 99 | 08, 10 | IDFG | 2.0 | 46.323 | -117.137 | A | 0.016 | 31.1% | 1.97 | 19 |
| 62 | Alpowa Cr | LSNAKE | Lower Snake | SNTUC | 98 | 10 | IDFG | 2.0 | 46.408 | -117.220 | A | 0.016 | 31.0% | 1.97 | |
| 63 | Tucannon R | LSNAKE | Lower Snake | SNTUC | 108 | 05, 09, 10 | IDFG | 1.0, 2.0 | 46.310 | -117.657 | A | 0.016 | 31.0% | 1.96 | |

Table 2. *Oncorhynchus tshawytscha* populations screened with 192 assays for Snake River Chinook salmon baseline v2.0. Reporting unit used for genetic stock identification at Lower Granite Dam, major population group (MPG), TRT population designation (ICBTRT 2003), sample size (*n*), years collected, genotyping agency, baseline version, latitude, longitude, lineage, life stage, mean pairwise fixation indices ($F_{ST}$), expected heterozygosity ($H_E$), mean allelic richness (AR), and number of loci with HWE deviations (for any population deviating from HWE in >5% of SNPs) are shown. Map # corresponds to numbers in Figures 2 and 11. Agency indicates the laboratory where samples were genotyped. Life stage codes: A – adult, C – carcass, J – juvenile. Lineage codes: ST – stream-type, OT – ocean-type. All spring/summer (stream-type) collections are of natural origin, fall (ocean-type) collections are of hatchery origin.

| Map # | Population | Reporting Group | MPG | TRT Population | *n* | Years Collected | Genotype Agency | Baseline Version | Latitude | Longitude | Lineage | Life Stage | $F_{ST}$ | $H_E$ | AR | HWE |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Sawtooth Weir | UPSALM | Upper Salmon | SRUMA | 92 | 09, 10 | IDFG | 1.0 | 44.151 | -114.885 | ST | A | 0.013 | 22.2% | 1.54 | |
| 2 | Valley Cr | UPSALM | Upper Salmon | SRVAL | 59 | 07, 08, 09, 10 | IDFG | 2.0 | 44.223 | -114.927 | ST | C | 0.015 | 23.0% | 1.56 | |
| 3 | WF Yankee F Salmon | UPSALM | Upper Salmon | SRYFS | 75 | 05 | CRITFC | 1.0 | 44.349 | -114.727 | ST | J | 0.019 | 22.5% | 1.55 | |
| 4 | EF Salmon R | UPSALM | Upper Salmon | SREFS | 187 | 04, 05, 11 | IDFG/CRITFC | 1.0, 2.0 | 44.115 | -114.430 | ST | A | 0.014 | 22.6% | 1.55 | |
| 5 | Pahsimeroi R | UPSALM | Upper Salmon | SRPAH | 97 | 07, 08, 09, 10 | IDFG | 1.0, 2.0 | 44.682 | -114.039 | ST | A, C | 0.017 | 22.9% | 1.56 | |
| 6 | Hayden Cr | UPSALM | Upper Salmon | SRLEM | 80 | 09, 10 | IDFG | 1.0, 2.0 | 44.862 | -113.632 | ST | C, J | 0.020 | 23.6% | 1.57 | |
| 7 | Lemhi (upper) | UPSALM | Upper Salmon | SRLEM | 96 | 09, 10 | IDFG | 1.0, 2.0 | 44.869 | -113.625 | ST | C, J | 0.017 | 21.7% | 1.53 | 15 |
| 8 | Lemhi (lower) | UPSALM | Upper Salmon | SRLEM | 90 | 09, 10 | IDFG | 1.0 | 45.153 | -113.814 | ST | J | 0.014 | 23.8% | 1.58 | 11 |
| 9 | Capehorn Cr | MFSALM | MF Salmon | MFMAR | 113 | 05, 06, 07, 09, 10 | IDFG/CRITFC | 1.0, 2.0 | 44.388 | -115.174 | ST | C, J | 0.018 | 21.7% | 1.53 | 13 |
| 10 | Marsh Cr | MFSALM | MF Salmon | MFMAR | 67 | 07, 08, 09, 10 | IDFG | 1.0 | 44.381 | -115.153 | ST | C | 0.015 | 21.6% | 1.54 | |
| 11 | Elk Cr | MFSALM | MF Salmon | MFBEA | 91 | 07, 08, 09, 10 | IDFG | 1.0, 2.0 | 44.442 | -115.454 | ST | C, J | 0.016 | 21.4% | 1.53 | |
| 12 | Bear Valley Cr | MFSALM | MF Salmon | MFBEA | 85 | 07, 08, 09, 10 | IDFG | 1.0 | 44.427 | -115.328 | ST | C | 0.015 | 21.6% | 1.53 | |
| 13 | Sulphur Cr | MFSALM | MF Salmon | MFSUL | 37 | 08, 09, 10 | IDFG | 1.0, 2.0 | 44.534 | -115.358 | ST | C, J | 0.021 | 20.2% | 1.51 | |
| 14 | Camas Cr | MFSALM | MF Salmon | MFCAM | 61 | 06, 09 | CRITFC | 1.0, 2.0 | 44.892 | -114.721 | ST | J | 0.020 | 20.8% | 1.51 | 11 |
| 15 | Big Cr | MFSALM | MF Salmon | MFBIG | 95 | 01, 10 | IDFG/CRITFC | 1.0, 2.0 | 45.138 | -115.038 | ST | C, A | 0.016 | 21.4% | 1.53 | 13 |
| 16 | Chamberlain Cr (post-2008) | CHMBLN | MF Salmon | SRCHA | 56 | 09, 10 | IDFG/CRITFC | 1.0, 2.0 | 45.452 | -114.931 | ST | C, J | 0.027 | 21.2% | 1.52 | |
| 17 | Chamberlain Cr (pre-2008) | CHMBLN | MF Salmon | SRCHA | 70 | 03, 04, 06, 07 | IDFG | 2.0 | 45.454 | -114.933 | ST | C, J | 0.021 | 21.2% | 1.52 | |
| 18 | Lake Cr, Summit Cr | SFSALM | SF Salmon | SFSEC | 78 | 07, 08, 09, 10 | IDFG | 1.0 | 45.279 | -115.922 | ST | C | 0.018 | 21.7% | 1.54 | |
| 19 | Secesh R | SFSALM | SF Salmon | SFSEC | 134 | 01, 07, 08, 09, 10 | IDFG/CRITFC | 1.0 | 45.217 | -115.808 | ST | C, J | 0.015 | 22.0% | 1.54 | |
| 20 | Johnson Cr | SFSALM | SF Salmon | SFEFS | 92 | 02 | CRITFC | 1.0 | 44.899 | -115.492 | ST | A | 0.015 | 22.4% | 1.55 | |
| 21 | SF Salmon R | SFSALM | SF Salmon | SFMAI | 143 | 09, 10 | IDFG | 1.0, 2.0 | 44.667 | -115.703 | ST | A, C | 0.011 | 23.1% | 1.57 | |
| 22 | Rapid R | HELLSC | SF Salmon | SRLSR | 91 | 06 | IDFG | 1.0 | 45.372 | -116.356 | ST | A | 0.015 | 23.0% | 1.57 | 10 |
| 23 | Crooked F Lochsa R | HELLSC | N/A | N/A | 29 | 07, 08, 09, 10 | IDFG | 2.0 | 46.506 | -114.681 | ST | C | 0.016 | 24.2% | 1.60 | |
| 24 | Powell Weir | HELLSC | N/A | N/A | 32 | 09 | IDFG | 1.0 | 46.506 | -114.687 | ST | A | 0.014 | 23.3% | 1.58 | |
| 25 | Red R | HELLSC | N/A | N/A | 73 | 07, 08, 09, 10 | IDFG | 1.0, 2.0 | 45.710 | -115.344 | ST | A, C | 0.013 | 24.3% | 1.60 | |
| 26 | Crooked R Weir | HELLSC | N/A | N/A | 67 | 09, 10 | IDFG | 1.0 | 45.817 | -115.527 | ST | A | 0.012 | 24.2% | 1.60 | |
| 27 | Newsome Cr | HELLSC | N/A | N/A | 82 | 01 | CRITFC | 1.0 | 45.831 | -115.608 | ST | A | 0.015 | 23.1% | 1.57 | |
| 28 | Lolo Cr | HELLSC | N/A | N/A | 89 | 01, 02 | IDFG/CRITFC | 1.0 | 46.279 | -115.775 | ST | J | 0.012 | 24.0% | 1.59 | 17 |
| 29 | Imnaha R | HELLSC | Grande Ronde / Imnaha | IRMAI | 46 | 08 | IDFG/NOAA | 2.0 | 45.620 | -116.845 | ST | J | 0.014 | 23.8% | 1.59 | |
| 30 | Imnaha R (1998) | HELLSC | Grande Ronde / Imnaha | IRMAI | 91 | 98 | CRITFC | 1.0 | 45.561 | -116.834 | ST | A | 0.013 | 23.8% | 1.58 | |
| 31 | Upper Grande Ronde | HELLSC | Grande Ronde / Imnaha | GRUMA | 46 | 08 | IDFG/NOAA | 2.0 | 45.132 | -118.365 | ST | J | 0.015 | 24.7% | 1.61 | |
| 32 | Catherine Cr | HELLSC | Grande Ronde / Imnaha | GRCAT | 94 | 04, 06 | IDFG/CRITFC | 2.0 | 45.158 | -117.779 | ST | A | 0.013 | 24.8% | 1.61 | |
| 33 | Lostine R | HELLSC | Grande Ronde / Imnaha | GRLOS | 177 | 03, 05, 09 | IDFG/CRITFC/NOAA | 2.0 | 45.542 | -117.555 | ST | J | 0.015 | 23.3% | 1.58 | 12 |
| 34 | Minam R | HELLSC | Grande Ronde / Imnaha | GRMIN | 81 | 94, 02 | IDFG/CRITFC | 1.0 | 45.600 | -117.729 | ST | J | 0.014 | 25.4% | 1.63 | 15 |
| 35 | Wenaha R | HELLSC | Grande Ronde / Imnaha | GRWEN | 88 | 02, 06 | IDFG/CRITFC | 1.0 | 45.946 | -117.455 | ST | J | 0.014 | 25.8% | 1.63 | |
| 36 | Tucannon R | TUCANO | Lower Snake Tribs | SNTUC | 81 | 03 | CRITFC | 1.0 | 46.526 | -118.142 | ST | A | 0.025 | 26.0% | 1.64 | 9 |
| 37 | Clearwater | FALL | FALL ESU | FALL ESU | 152 | 08 | IDFG/CRITFC | 2.0 | 46.520 | -116.610 | OC | A | n/a | 29.6% | 1.70 | 14 |
| 38 | Nez Perce Tribal Hatchery | FALL | FALL ESU | FALL ESU | 85 | 03 | CRITFC | 2.0 | 46.519 | -116.665 | OC | A | n/a | 29.0% | 1.69 | |
| 39 | Lyons Ferry | FALL | FALL ESU | FALL ESU | 90 | 00 | CRITFC | 2.0 | 46.589 | -118.220 | OC | A | n/a | 29.0% | 1.69 | |

Table 3. Summary of 187 SNPs (Appendix A and Hess et al. 2012) screened among 63 steelhead populations in Snake River baseline v2.0. SNPs designated as PBT are used for both the PBT (BPA Project #2010-031-00, Steele et al. 2012) and GSI projects. SNPs designated as GSI are used primarily for GSI applications. Summary statistics include minor-allele frequency (MAF) range, expected heterozygosity ($H_E$), Weir and Cockerham (1984) $F_{ST}$, informativeness for assignment ($I_N$), and optimal rate of correct assignment (ORCA). Each SNP was ranked (1 = most informative) according to $F_{ST}$, $I_N$, and ORCA. "Informativeness" rank is based on average across the three ranks. "HWE" designates the number of populations that a SNP deviated from Hardy-Weinberg expectation for any SNP that deviated in greater than 10% of populations. "LD" signifies SNPs that exhibit linkage disequilibrium in more than half of the populations. "CS" indicates a locus that was designated as a candidate for divergent (+) or balancing (-) selection. SNPs are ranked according to "Informativeness."

| SNP | Panel | MAF Range | $H_E$ | $F_{ST}$ | $I_N$ | ORCA | $F_{ST}$ Rank | $I_N$ Rank | ORCA Rank | "Informativeness" Rank | HWE | LD | CS |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Omy_anp-17* | PBT | .026 - .761 | 38.7% | 0.134 | 0.032 | 0.028 | 2 | 2 | 2 | 1 | | | + |
| *Omy_sast-264* | GSI | .068 - .865 | 30.0% | 0.099 | 0.018 | 0.029 | 6 | 13 | 1 | 2 | | | + |
| *Omy_114315-438* | PBT | .093 - .691 | 44.0% | 0.099 | 0.023 | 0.025 | 6 | 4 | 11 | 2 | | | + |
| *Omy_u09-53.469* | PBT | .174 - .756 | 44.3% | 0.104 | 0.023 | 0.025 | 5 | 4 | 11 | 2 | | | + |
| *OMS00058* | PBT | .096 - .689 | 43.8% | 0.092 | 0.022 | 0.025 | 9 | 6 | 11 | 5 | | | + |
| *OMS00064* | PBT | .098 - .705 | 43.3% | 0.081 | 0.018 | 0.026 | 16 | 13 | 4 | 6 | | | + |
| *Omy_107806-34* | PBT | .078 - .656 | 38.7% | 0.087 | 0.019 | 0.025 | 12 | 10 | 11 | 6 | | | + |
| *OMS00074* | PBT | .065 - .729 | 45.1% | 0.078 | 0.018 | 0.026 | 19 | 13 | 4 | 8 | | | + |
| *Omy_hsf2-146* | PBT | .069 - .628 | 40.0% | 0.085 | 0.019 | 0.025 | 14 | 10 | 11 | 8 | | | + |
| *Omy_104519-624* | PBT | .053 - .578 | 39.0% | 0.088 | 0.020 | 0.024 | 11 | 7 | 21 | 10 | | | + |
| *OMS00120* | PBT | .000 - .489 | 26.1% | 0.090 | 0.020 | 0.024 | 10 | 7 | 21 | 10 | | | + |
| *Omy_110064-419* | PBT | .076 - .755 | 44.1% | 0.073 | 0.017 | 0.027 | 25 | 18 | 3 | 12 | | | + |
| *Omy_113490-159* | PBT | .167 - .802 | 45.2% | 0.075 | 0.017 | 0.026 | 24 | 18 | 4 | 12 | | | + |
| *Omy_101993-189* | PBT | .056 - .605 | 34.3% | 0.080 | 0.017 | 0.025 | 17 | 18 | 11 | 12 | | | + |
| *OMS00092* | GSI | .021 - .514 | 27.2% | 0.087 | 0.018 | 0.024 | 12 | 13 | 21 | 12 | | | + |
| *Omy_IL1b-163* | GSI | .000 - .454 | 17.2% | 0.169 | 0.037 | 0.023 | 1 | 1 | 43 | 12 | | | + |
| *OMS00017* | GSI | .100 - .733 | 38.4% | 0.077 | 0.016 | 0.026 | 20 | 24 | 4 | 17 | | | + |
| *Omy_b9-164* | GSI | .000 - .457 | 20.3% | 0.118 | 0.025 | 0.023 | 3 | 3 | 43 | 17 | 9 | | + |
| *Omy_108007-193* | PBT | .092 - .692 | 44.1% | 0.076 | 0.017 | 0.025 | 22 | 18 | 11 | 19 | | | + |
| *OMS00118* | PBT | .133 - .691 | 43.6% | 0.076 | 0.017 | 0.025 | 22 | 18 | 11 | 19 | | | + |
| *Omy_gadd45-332* | GSI | .000 - .478 | 20.3% | 0.094 | 0.019 | 0.023 | 8 | 10 | 43 | 21 | | | + |
| *M09AAE.082* | PBT | .083 - .694 | 33.9% | 0.070 | 0.014 | 0.026 | 28 | 31 | 4 | 22 | | | |
| *OMS00008* | GSI | .000 - .446 | 25.9% | 0.080 | 0.020 | 0.023 | 17 | 7 | 43 | 23 | | | + |
| *Omy_128923-433* | PBT | .197 - .729 | 46.5% | 0.070 | 0.016 | 0.024 | 28 | 24 | 21 | 24 | | | |
| *Omy_vatf-406* | PBT | .074 - .604 | 41.8% | 0.071 | 0.016 | 0.024 | 26 | 24 | 21 | 24 | | | + |
| *Omy_hsp70aPro-329* | GSI | .000 - .450 | 7.9% | 0.114 | 0.016 | 0.023 | 4 | 24 | 43 | 24 | | | + |
| *OMS00101* | PBT | .131 - .745 | 46.0% | 0.058 | 0.013 | 0.026 | 42 | 38 | 4 | 27 | | | |
| *OMS00024* | PBT | .167 - .750 | 45.1% | 0.061 | 0.013 | 0.025 | 36 | 38 | 11 | 27 | | | |
| *OMS00111* | PBT | .042 - .533 | 30.6% | 0.066 | 0.014 | 0.024 | 31 | 31 | 21 | 27 | | | |
| *OMS00057* | PBT | .156 - .671 | 44.2% | 0.061 | 0.013 | 0.024 | 36 | 38 | 21 | 30 | | | |

| SNP | Panel | MAF Range | $H_E$ | $F_{ST}$ | $I_N$ | ORCA | $F_{ST}$ Rank | $I_N$ Rank | ORCA Rank | "Informativeness" Rank | HWE | LD | CS |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *OMS00070* | PBT | .213 - .761 | 47.0% | 0.059 | 0.013 | 0.024 | 41 | 38 | 21 | 31 | | | |
| *Omy_101832-195* | PBT | .125 - .739 | 46.6% | 0.053 | 0.012 | 0.026 | 56 | 47 | 4 | 32 | | | |
| *Omy_Il1b-198* | PBT | .136 - .698 | 45.1% | 0.055 | 0.012 | 0.025 | 51 | 47 | 11 | 32 | | | |
| *Omy_sys1-188* | GSI | .000 - .394 | 18.3% | 0.077 | 0.018 | 0.022 | 20 | 13 | 75 | 32 | | | |
| *OMGH1PROM1-SNP1* | GSI | .000 - .375 | 17.0% | 0.083 | 0.017 | 0.022 | 15 | 18 | 75 | 32 | | | + |
| *Omy_crb-106* | PBT | .256 - .691 | 46.4% | 0.061 | 0.014 | 0.023 | 36 | 31 | 43 | 36 | 7 | | |
| *Omy_metA-161* | PBT | .080 - .590 | 36.4% | 0.055 | 0.012 | 0.024 | 51 | 47 | 21 | 37 | | | |
| *Omy_97954-618* | GSI | .023 - .521 | 31.4% | 0.055 | 0.012 | 0.024 | 51 | 47 | 21 | 37 | | | |
| *OMS00112* | PBT | .000 - .456 | 28.5% | 0.056 | 0.013 | 0.023 | 47 | 38 | 43 | 39 | | | |
| *Omy_cd59b-112* | GSI | .000 - .397 | 17.8% | 0.071 | 0.015 | 0.022 | 26 | 29 | 75 | 39 | | | |
| *Omy_u09-54-311* | PBT | .078 - .589 | 40.6% | 0.050 | 0.011 | 0.024 | 61 | 57 | 21 | 41 | | | |
| *OMS00129* | GSI | .014 - .435 | 26.6% | 0.056 | 0.012 | 0.023 | 47 | 47 | 43 | 41 | 16 | | |
| *Omy_BAMBI2.312* | GSI | .000 - .370 | 18.9% | 0.066 | 0.014 | 0.022 | 31 | 31 | 75 | 41 | 7 | | |
| *OMS00090* | PBT | .205 - .708 | 47.2% | 0.048 | 0.011 | 0.024 | 65 | 57 | 21 | 44 | | | |
| *Omy_ntl-27* | PBT | .128 - .577 | 42.4% | 0.051 | 0.012 | 0.023 | 58 | 47 | 43 | 45 | | | |
| *OMS00087* | GSI | .023 - .458 | 29.0% | 0.055 | 0.011 | 0.023 | 51 | 57 | 43 | 46 | 16 | | |
| *Omy_carban1-264* | GSI | .000 - .355 | 21.0% | 0.060 | 0.013 | 0.022 | 40 | 38 | 75 | 47 | | | |
| *OMS00068* | PBT | .056 - .565 | 41.8% | 0.045 | 0.011 | 0.024 | 80 | 57 | 21 | 48 | | | |
| *Omy_cox1-221* | PBT | .171 - .643 | 45.2% | 0.051 | 0.011 | 0.023 | 58 | 57 | 43 | 48 | | | |
| *Omy_rbm4b-203* | PBT | .011 - .408 | 29.7% | 0.056 | 0.013 | 0.022 | 47 | 38 | 75 | 48 | | | |
| *Omy_myoD-178* | GSI | .000 - .311 | 18.4% | 0.052 | 0.014 | 0.022 | 57 | 31 | 75 | 51 | | | |
| *Omy_txnip-343* | PBT | .076 - .539 | 35.9% | 0.048 | 0.011 | 0.023 | 65 | 57 | 43 | 52 | | | |
| *Omy_bcAKala-380rd* | PBT | .089 - .544 | 40.6% | 0.048 | 0.011 | 0.023 | 65 | 57 | 43 | 52 | 7 | | |
| *OMS00138* | GSI | .013 - .391 | 21.2% | 0.058 | 0.012 | 0.022 | 42 | 47 | 75 | 52 | | | |
| *Omy_tlr3-377* | GSI | .000 - .300 | 15.8% | 0.065 | 0.016 | 0.021 | 33 | 24 | 107 | 52 | | | |
| *M09AAJ.163* | PBT | .044 - .564 | 40.7% | 0.046 | 0.010 | 0.024 | 74 | 72 | 21 | 56 | | | |
| *Omy_114587-480* | PBT | .085 - .500 | 41.4% | 0.054 | 0.013 | 0.022 | 55 | 38 | 75 | 56 | | | |
| *Omy_gdh-271* | GSI | .022 - .401 | 20.2% | 0.060 | 0.011 | 0.022 | 39 | 57 | 75 | 58 | | | |
| *Omy_116733-349* | PBT | .100 - .604 | 39.2% | 0.045 | 0.010 | 0.024 | 80 | 72 | 21 | 59 | | | |
| *Omy_111383-51* | PBT | .145 - .604 | 46.2% | 0.046 | 0.011 | 0.023 | 74 | 57 | 43 | 59 | | | |
| *Omy_vamp5-303* | GSI | .032 - .422 | 32.2% | 0.051 | 0.012 | 0.022 | 58 | 47 | 75 | 61 | | | |
| *Omy_109894-185* | PBT | .100 - .583 | 44.9% | 0.043 | 0.010 | 0.024 | 92 | 72 | 21 | 62 | 7 | | |
| *Omy_cin-172* | GSI | .044 - .464 | 31.5% | 0.047 | 0.010 | 0.023 | 71 | 72 | 43 | 63 | | | |
| *Omy_105105-448* | PBT | .216 - .674 | 46.6% | 0.046 | 0.010 | 0.023 | 74 | 72 | 43 | 64 | | | |
| *Omy_IL17-185* | PBT | .208 - .656 | 47.1% | 0.046 | 0.010 | 0.023 | 74 | 72 | 43 | 64 | 11 | | |
| *Omy_107031-704* | GSI | .035 - .391 | 26.9% | 0.050 | 0.011 | 0.022 | 61 | 57 | 75 | 66 | | | |
| *OMS00105* | PBT | .128 - .583 | 44.7% | 0.045 | 0.010 | 0.023 | 80 | 72 | 43 | 67 | | | |
| *Omy_redd1-410* | PBT | .078 - .568 | 33.2% | 0.044 | 0.009 | 0.024 | 86 | 91 | 21 | 68 | | | |
| *Omy_u07-79-166* | GSI | .000 - .271 | 15.7% | 0.063 | 0.015 | 0.020 | 34 | 29 | 134 | 68 | | | |
| *Omy_NaKATPa3-50* | PBT | .096 - .527 | 39.2% | 0.044 | 0.010 | 0.023 | 86 | 72 | 43 | 70 | | | |
| *OMS00089* | PBT | .056 - .513 | 36.8% | 0.043 | 0.010 | 0.023 | 92 | 72 | 43 | 71 | | | |
| *Omy_G3PD_2-371* | GSI | .059 - .521 | 28.4% | 0.045 | 0.009 | 0.023 | 80 | 91 | 43 | 72 | | | |
| *Omy_zg57-91* | GSI | .000 - .243 | 14.7% | 0.056 | 0.014 | 0.020 | 47 | 31 | 134 | 72 | | | |
| *Omy_gluR-79* | PBT | .211 - .717 | 47.6% | 0.041 | 0.009 | 0.024 | 104 | 91 | 21 | 74 | | | |

| SNP | Panel | MAF Range | $H_E$ | $F_{ST}$ | $I_N$ | ORCA | $F_{ST}$ Rank | $I_N$ Rank | ORCA Rank | "Informativeness" Rank | HWE | LD | CS |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *OMS00071* | PBT | .255 - .737 | 47.6% | 0.041 | 0.009 | 0.024 | 104 | 91 | 21 | 74 | | | |
| *Omy_p53-262* | PBT | .044 - .523 | 33.8% | 0.044 | 0.009 | 0.023 | 86 | 91 | 43 | 76 | | | |
| *Omy_GHSR-121* | GSI | .000 - .206 | 8.0% | 0.062 | 0.014 | 0.019 | 35 | 31 | 154 | 76 | | a | |
| *OMS00143* | GSI | .000 - .287 | 18.4% | 0.057 | 0.012 | 0.020 | 44 | 47 | 134 | 78 | | | |
| *Omy_inos-97* | GSI | .000 - .264 | 12.5% | 0.057 | 0.012 | 0.020 | 44 | 47 | 134 | 78 | | | |
| *Omy_cd59-206* | PBT | .084 - .533 | 38.6% | 0.042 | 0.009 | 0.023 | 101 | 91 | 43 | 80 | | | |
| *Omy_ppie-232* | GSI | .000 - .500 | 22.3% | 0.042 | 0.008 | 0.024 | 101 | 116 | 21 | 81 | | | |
| *Omy_hus1-52* | GSI | .000 - .193 | 8.5% | 0.057 | 0.013 | 0.019 | 44 | 38 | 154 | 81 | | | |
| *Omy_Ogo4-212* | PBT | .106 - .576 | 46.1% | 0.040 | 0.009 | 0.023 | 108 | 91 | 43 | 83 | | | |
| *Omy_srp09-37* | PBT | .122 - .561 | 41.4% | 0.040 | 0.009 | 0.023 | 108 | 91 | 43 | 83 | | | |
| *OMS00176* | GSI | .000 - .351 | 11.5% | 0.048 | 0.010 | 0.021 | 65 | 72 | 107 | 83 | | | |
| *Omy_mcsf-268* | GSI | .000 - .230 | 3.5% | 0.070 | 0.009 | 0.020 | 28 | 91 | 134 | 86 | | | |
| *Omy_99300-202* | PBT | .093 - .500 | 34.1% | 0.043 | 0.009 | 0.022 | 92 | 91 | 75 | 87 | | | |
| *OMS00151* | GSI | .053 - .424 | 30.4% | 0.043 | 0.009 | 0.022 | 92 | 91 | 75 | 87 | | | |
| *Omy_cox2-335* | GSI | .028 - .362 | 25.8% | 0.045 | 0.010 | 0.021 | 80 | 72 | 107 | 87 | | | |
| *OMS00061* | GSI | .000 - .239 | 10.3% | 0.047 | 0.011 | 0.020 | 71 | 57 | 134 | 90 | | | |
| *Omy_arp-630* | PBT | .156 - .679 | 48.0% | 0.036 | 0.008 | 0.024 | 127 | 116 | 21 | 91 | | | |
| *OMS00079* | PBT | .181 - .700 | 48.2% | 0.036 | 0.008 | 0.024 | 127 | 116 | 21 | 91 | | | |
| *Omy_Il-1b_.028* | PBT | .022 - .339 | 25.4% | 0.044 | 0.010 | 0.021 | 86 | 72 | 107 | 91 | | | |
| *Omy_oxct-85* | PBT | .000 - .296 | 17.6% | 0.044 | 0.010 | 0.021 | 86 | 72 | 107 | 91 | | | |
| *M09AAC.055* | GSI | .000 - .272 | 13.7% | 0.050 | 0.010 | 0.020 | 61 | 72 | 134 | 95 | | | |
| *Omy_U11_2b-154* | PBT | .053 - .375 | 31.9% | 0.043 | 0.010 | 0.021 | 92 | 72 | 107 | 96 | | | |
| *Omy_g12-82* | PBT | .244 - .724 | 48.1% | 0.038 | 0.008 | 0.023 | 114 | 116 | 43 | 97 | | | |
| *OMS00180* | PBT | .119 - .571 | 42.5% | 0.038 | 0.008 | 0.023 | 114 | 116 | 43 | 97 | | | |
| *OMS00175* | PBT | .189 - .609 | 47.0% | 0.038 | 0.008 | 0.023 | 114 | 116 | 43 | 97 | | | |
| *OMS00006* | PBT | .224 - .628 | 47.7% | 0.040 | 0.009 | 0.022 | 108 | 91 | 75 | 97 | | | |
| *M09AAD.076* | PBT | .267 - .722 | 48.1% | 0.037 | 0.008 | 0.023 | 121 | 116 | 43 | 101 | | | |
| *Omy_97660-230* | PBT | .130 - .563 | 43.2% | 0.037 | 0.008 | 0.023 | 121 | 116 | 43 | 101 | | | |
| *OMS00179* | PBT | .083 - .489 | 39.1% | 0.038 | 0.009 | 0.022 | 114 | 91 | 75 | 101 | | | |
| *Omy_metB-138* | GSI | .000 - .362 | 24.8% | 0.038 | 0.009 | 0.022 | 114 | 91 | 75 | 101 | | | |
| *Omy_nxt2-273* | GSI | .000 - .250 | 12.5% | 0.046 | 0.010 | 0.020 | 74 | 72 | 134 | 101 | 11 | | |
| *Omy_BAC-F5.284* | GSI | .000 - .174 | 9.3% | 0.047 | 0.011 | 0.019 | 71 | 57 | 154 | 106 | | | |
| *Omy_g1-103* | GSI | .000 - .170 | 9.7% | 0.046 | 0.011 | 0.019 | 74 | 57 | 154 | 107 | | | |
| *Omy_OmyP9-180* | GSI | .000 - .284 | 16.4% | 0.044 | 0.010 | 0.020 | 86 | 72 | 134 | 108 | | | |
| *OMS00119* | GSI | .000 - .288 | 21.5% | 0.043 | 0.010 | 0.020 | 92 | 72 | 134 | 109 | | | |
| *Omy_star-206* | GSI | .000 - .178 | 9.4% | 0.043 | 0.011 | 0.019 | 92 | 57 | 154 | 110 | | | |
| *OMY1011SNP* | PBT | .096 - .459 | 36.0% | 0.038 | 0.008 | 0.022 | 114 | 116 | 75 | 111 | | | |
| *OMS00133* | GSI | .000 - .176 | 4.5% | 0.049 | 0.009 | 0.019 | 64 | 91 | 154 | 112 | | | |
| *Omy_nkef-241* | PBT | .234 - .630 | 46.6% | 0.037 | 0.008 | 0.022 | 121 | 116 | 75 | 113 | | | |
| *OMS00106* | PBT | .056 - .423 | 34.3% | 0.037 | 0.008 | 0.022 | 121 | 116 | 75 | 113 | | | |
| *Omy_stat3-273* | PBT | .066 - .409 | 33.9% | 0.039 | 0.009 | 0.021 | 113 | 91 | 107 | 113 | | | |
| *OMS00013* | GSI | .000 - .202 | 12.1% | 0.041 | 0.011 | 0.019 | 104 | 57 | 154 | 116 | | | |
| *Omy_105714-265* | PBT | .100 - .500 | 42.3% | 0.036 | 0.008 | 0.022 | 127 | 116 | 75 | 117 | | | |
| *OMS00095* | GSI | .000 - .255 | 11.2% | 0.043 | 0.009 | 0.020 | 92 | 91 | 134 | 117 | | | |

| SNP | Panel | MAF Range | $H_E$ | $F_{ST}$ | $I_N$ | ORCA | $F_{ST}$ Rank | $I_N$ Rank | ORCA Rank | "Informativeness" Rank | HWE | LD | CS |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *OMS00015* | GSI | .000 - .198 | 10.9% | 0.043 | 0.010 | 0.019 | 92 | 72 | 154 | 117 | | | |
| *OMS00056* | GSI | .042 - .411 | 34.1% | 0.035 | 0.008 | 0.022 | 134 | 116 | 75 | 120 | | | |
| *Omy_109243-222* | PBT | .000 - .342 | 26.2% | 0.036 | 0.009 | 0.021 | 127 | 91 | 107 | 120 | | | |
| *Omy_110201-359* | GSI | .000 - .240 | 17.4% | 0.036 | 0.009 | 0.021 | 127 | 91 | 107 | 120 | | | |
| *OMS00173* | GSI | .022 - .313 | 20.7% | 0.042 | 0.009 | 0.020 | 101 | 91 | 134 | 123 | | | |
| *Omy_105385-406* | PBT | .211 - .652 | 46.3% | 0.033 | 0.007 | 0.023 | 144 | 144 | 43 | 124 | | | |
| *Omy_ca050-64* | GSI | .152 - .541 | 44.1% | 0.034 | 0.008 | 0.022 | 140 | 116 | 75 | 124 | | | |
| *Omy_97077-73* | GSI | .000 - .149 | 3.6% | 0.048 | 0.009 | 0.018 | 65 | 91 | 175 | 124 | | | |
| *Omy_impa1-55* | GSI | .000 - .243 | 17.0% | 0.040 | 0.009 | 0.020 | 108 | 91 | 134 | 127 | | | |
| *OMS00053* | PBT | .213 - .681 | 48.1% | 0.031 | 0.007 | 0.023 | 152 | 144 | 43 | 128 | | | |
| *OMS00154* | PBT | .074 - .422 | 30.8% | 0.037 | 0.008 | 0.021 | 121 | 116 | 107 | 129 | | | |
| *Omy_128996-481* | GSI | .000 - .214 | 12.5% | 0.040 | 0.009 | 0.019 | 108 | 91 | 154 | 130 | 11 | | |
| *Omy_IL6-320* | PBT | .066 - .400 | 33.0% | 0.035 | 0.008 | 0.021 | 134 | 116 | 107 | 131 | | | |
| *Omy_ada10-71* | PBT | .042 - .364 | 29.2% | 0.035 | 0.008 | 0.021 | 134 | 116 | 107 | 131 | | | |
| *Omy_rapd-167* | PBT | .043 - .359 | 29.4% | 0.035 | 0.008 | 0.021 | 134 | 116 | 107 | 131 | | | |
| *Omy_SECC22b-88* | GSI | .000 - .135 | 2.7% | 0.048 | 0.008 | 0.018 | 65 | 116 | 175 | 131 | | | |
| *OMS00072* | PBT | .244 - .656 | 48.0% | 0.033 | 0.007 | 0.022 | 144 | 144 | 75 | 135 | | | |
| *OMS00096* | GSI | .043 - .351 | 29.8% | 0.034 | 0.008 | 0.021 | 140 | 116 | 107 | 135 | | | |
| *OMS00132* | PBT | .184 - .588 | 46.8% | 0.031 | 0.007 | 0.022 | 152 | 144 | 75 | 137 | | | |
| *Omy_aromat-280* | GSI | .060 - .446 | 28.6% | 0.031 | 0.007 | 0.022 | 152 | 144 | 75 | 137 | | | |
| *OMS00030* | GSI | .000 - .193 | 14.8% | 0.035 | 0.009 | 0.019 | 134 | 91 | 154 | 139 | | | |
| *Omy_nips-299* | GSI | .000 - .217 | 12.7% | 0.038 | 0.008 | 0.019 | 114 | 116 | 154 | 140 | | | |
| *Omy_u09-52.284* | GSI | .000 - .111 | 5.3% | 0.037 | 0.009 | 0.018 | 121 | 91 | 175 | 141 | | | |
| *OMS00062* | PBT | .128 - .495 | 37.0% | 0.030 | 0.006 | 0.022 | 156 | 160 | 75 | 142 | | | |
| *OMS00039* | PBT | .277 - .678 | 48.4% | 0.029 | 0.006 | 0.022 | 160 | 160 | 75 | 143 | | | |
| *Omy_129870-756* | PBT | .043 - .367 | 28.1% | 0.033 | 0.007 | 0.021 | 144 | 144 | 107 | 143 | | | |
| *Omy_pad-196* | GSI | .000 - .200 | 8.3% | 0.036 | 0.008 | 0.019 | 127 | 116 | 154 | 143 | | | |
| *Omy_e1-147* | GSI | .000 - .178 | 9.1% | 0.036 | 0.008 | 0.019 | 127 | 116 | 154 | 143 | | | |
| *OMS00078* | PBT | .156 - .521 | 38.3% | 0.028 | 0.006 | 0.022 | 166 | 160 | 75 | 147 | | | |
| *Omy_hsp47-86* | GSI | .033 - .391 | 32.8% | 0.028 | 0.006 | 0.022 | 166 | 160 | 75 | 147 | | | |
| *OMS00077* | PBT | .227 - .576 | 46.7% | 0.032 | 0.007 | 0.021 | 150 | 144 | 107 | 147 | | | |
| *Omy_102505-102* | PBT | .234 - .596 | 45.4% | 0.027 | 0.006 | 0.022 | 171 | 160 | 75 | 150 | | | |
| *Omy_LDHB-2_e5* | GSI | .026 - .349 | 25.3% | 0.030 | 0.007 | 0.021 | 156 | 144 | 107 | 151 | | | |
| *OMS00121* | PBT | .273 - .670 | 48.3% | 0.026 | 0.006 | 0.022 | 175 | 160 | 75 | 152 | | | |
| *Omy_BAC-B4-324* | PBT | .266 - .608 | 47.5% | 0.029 | 0.007 | 0.021 | 160 | 144 | 107 | 152 | | | |
| *OMS00052* | GSI | .056 - .378 | 28.5% | 0.029 | 0.007 | 0.021 | 160 | 144 | 107 | 152 | | | |
| *Omy_u09-56.119* | GSI | .000 - .202 | 15.6% | 0.033 | 0.008 | 0.019 | 144 | 116 | 154 | 155 | | | |
| *Omy_hsf1b-241* | GSI | .000 - .197 | 15.2% | 0.033 | 0.008 | 0.019 | 144 | 116 | 154 | 155 | | | |
| *Omy_CRBF1-1* | GSI | .000 - .186 | 9.0% | 0.033 | 0.008 | 0.019 | 144 | 116 | 154 | 155 | | | |
| *OMS00169* | GSI | .000 - .135 | 1.8% | 0.045 | 0.006 | 0.018 | 80 | 160 | 175 | 155 | | | |
| *Omy_gh-475* | GSI | .043 - .305 | 22.6% | 0.034 | 0.007 | 0.020 | 140 | 144 | 134 | 159 | | | |
| *OMS00014* | GSI | .000 - .122 | 2.8% | 0.041 | 0.007 | 0.018 | 104 | 144 | 175 | 160 | | | |
| *Omy_aspAT-123* | GSI | .146 - .481 | 39.1% | 0.029 | 0.006 | 0.021 | 160 | 160 | 107 | 161 | | | |
| *Omy_107285-69* | GSI | .036 - .313 | 27.0% | 0.031 | 0.007 | 0.020 | 152 | 144 | 134 | 162 | | | |

| SNP | Panel | MAF Range | $H_E$ | $F_{ST}$ | $I_N$ | ORCA | $F_{ST}$ Rank | $I_N$ Rank | ORCA Rank | "Informativeness" Rank | HWE | LD | CS |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *OMS00018* | GSI | .022 - .287 | 17.6% | 0.032 | 0.007 | 0.020 | 150 | 144 | 134 | 162 | | | |
| *Omy_130524-160* | PBT | .250 - .597 | 46.2% | 0.028 | 0.006 | 0.021 | 166 | 160 | 107 | 164 | | | |
| *Omy_Ots249-227* | PBT | .136 - .477 | 40.6% | 0.028 | 0.006 | 0.021 | 166 | 160 | 107 | 164 | | | |
| *OMS00149* | GSI | .000 - .144 | 7.7% | 0.034 | 0.008 | 0.018 | 140 | 116 | 175 | 164 | | | |
| *Omy_hsc715-80* | PBT | .205 - .540 | 45.7% | 0.027 | 0.006 | 0.021 | 171 | 160 | 107 | 167 | | | |
| *Omy_colla1-525* | PBT | .114 - .447 | 40.2% | 0.026 | 0.006 | 0.021 | 175 | 160 | 107 | 168 | | | |
| *Omy_b1-266* | PBT | .141 - .421 | 39.4% | 0.024 | 0.006 | 0.021 | 179 | 160 | 107 | 169 | | | - |
| *Omy_97865-196* | GSI | .000 - .116 | 7.2% | 0.030 | 0.008 | 0.018 | 156 | 116 | 175 | 169 | | | |
| *Omy_105075-162* | GSI | .000 - .233 | 15.0% | 0.030 | 0.006 | 0.020 | 156 | 160 | 134 | 171 | | | |
| *Omy_ndk-152* | GSI | .000 - .152 | 4.7% | 0.035 | 0.007 | 0.018 | 134 | 144 | 175 | 172 | | | |
| *OMS00002* | PBT | .229 - .556 | 45.4% | 0.023 | 0.005 | 0.021 | 180 | 179 | 107 | 173 | | | - |
| *OMS00003* | GSI | .033 - .336 | 24.3% | 0.023 | 0.005 | 0.021 | 180 | 179 | 107 | 173 | | | - |
| *OMS00048* | GSI | .007 - .239 | 20.2% | 0.025 | 0.006 | 0.020 | 178 | 160 | 134 | 175 | | | |
| *Omy_103705-558* | GSI | .021 - .240 | 18.5% | 0.029 | 0.006 | 0.019 | 160 | 160 | 154 | 176 | | | |
| *Omy_tlr5-205* | GSI | .000 - .139 | 9.6% | 0.029 | 0.007 | 0.018 | 160 | 144 | 175 | 177 | | | |
| *OMS00114* | GSI | .000 - .205 | 15.5% | 0.027 | 0.006 | 0.019 | 171 | 160 | 154 | 178 | | | |
| *OMS00174* | GSI | .000 - .174 | 9.1% | 0.027 | 0.006 | 0.019 | 171 | 160 | 154 | 178 | | | |
| *Omy_LDHB-1_i2* | GSI | .000 - .182 | 14.6% | 0.026 | 0.006 | 0.019 | 175 | 160 | 154 | 180 | | | |
| *Omy_aldB-165* | PBT | .160 - .434 | 40.9% | 0.020 | 0.005 | 0.020 | 184 | 179 | 134 | 181 | | | - |
| *Omy_lpl-220* | GSI | .056 - .311 | 25.9% | 0.020 | 0.004 | 0.020 | 184 | 184 | 134 | 182 | | | - |
| *Omy_UT16_2-173* | GSI | .000 - .189 | 12.8% | 0.022 | 0.005 | 0.019 | 182 | 179 | 154 | 183 | | | |
| *Omy_cd28-130* | GSI | .000 - .116 | 2.8% | 0.028 | 0.005 | 0.018 | 166 | 179 | 175 | 184 | | | |
| *Omy_LDHB-2_i6* | GSI | .000 - .068 | 1.6% | 0.021 | 0.004 | 0.017 | 183 | 184 | 185 | 185 | | | |
| *Omy_sSOD-1* | GSI | .000 - .045 | 1.6% | 0.017 | 0.004 | 0.017 | 186 | 184 | 185 | 186 | | | |
| *Omy_nach-200* | GSI | .000 - .051 | 1.5% | 0.017 | 0.003 | 0.017 | 186 | 187 | 185 | 187 | | | |

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

Table 4. Summary of 191 SNPs (Appendix B and Hess et al. 2012) screened across 36 stream-type Chinook salmon populations in Snake River baseline v2.0 (Note: fall Chinook collections were excluded from analyses below). SNPs designated as PBT are used for both the PBT (BPA Project #2010-031-00, Steele et al. 2012) and GSI projects. SNPs designated as GSI are used primarily for GSI applications. Summary statistics include minor-allele frequency (MAF) range, expected heterozygosity ($H_E$), Weir and Cockerham (1984) $F_{ST}$, informativeness for assignment ($I_N$), and optimal rate of correct assignment (ORCA). Each SNP was ranked (1 = most informative) according to $F_{ST}$, $I_N$, and ORCA. "Informativeness" rank is based on the average across the three ranks. "HWE" designates the number of populations that a SNP deviated from Hardy-Weinberg expectation for any SNP that deviated in greater than 10% of populations. "LD" signifies SNPs that exhibit linkage disequilibrium in more than half of the populations. "CS" indicates a locus that was designated as a candidate for divergent (+) or balancing (-) selection. SNPs are ranked according to "Informativeness."

| SNP | Panel | MAF Range | $H_E$ | $F_{IS}$ | $F_{ST}$ | $F_{ST}$ Rank | $I_N$ | $I_N$ Rank | ORCA | ORCA Rank | "Informativeness" Rank | HWE | LD | CS | Comments |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Ots_TAPBP* | PBT | .005 - .619 | 0.345 | 0.047 | 0.167 | 1 | 0.069 | 1 | 0.041 | 1 | 1 | 6 | | + | |
| *Ots_MHC2* | PBT | .185 - .763 | 0.420 | -0.023 | 0.112 | 2 | 0.055 | 2 | 0.040 | 2 | 2 | | | + | |
| *Ots_110495-380* | PBT | .032 - .593 | 0.223 | -0.019 | 0.098 | 4 | 0.048 | 4 | 0.040 | 2 | 3 | | | + | |
| *Ots_OTSTF1-SNP1* | PBT | .101 - .673 | 0.440 | -0.025 | 0.063 | 11 | 0.045 | 6 | 0.040 | 2 | 4 | | a | + | |
| *Ots_117432-409* | PBT | .127 - .611 | 0.408 | -0.019 | 0.072 | 8 | 0.047 | 5 | 0.038 | 7 | 5 | | | + | |
| *Ots_Tnsf* | GSI | .111 - .675 | 0.422 | -0.033 | 0.059 | 12 | 0.044 | 8 | 0.040 | 2 | 6 | 6 | a | | |
| *Ots_ppie-245* | PBT | .009 - .437 | 0.263 | -0.036 | 0.080 | 7 | 0.049 | 3 | 0.037 | 13 | 7 | | | + | |
| *Ots_108820-336* | PBT | .154 - .700 | 0.462 | 0.015 | 0.050 | 22 | 0.043 | 11 | 0.040 | 2 | 8 | | | | |
| *Ots_118938-325* | PBT | .033 - .471 | 0.337 | 0.003 | 0.054 | 17 | 0.043 | 11 | 0.037 | 13 | 9 | | | | |
| *Ots_TLR3* | PBT | .102 - .506 | 0.379 | -0.046 | 0.064 | 10 | 0.045 | 6 | 0.036 | 25 | 9 | 4 | | + | |
| *Ots_u07-07.161* | PBT | .114 - .593 | 0.446 | -0.045 | 0.047 | 29 | 0.042 | 17 | 0.038 | 7 | 11 | | | | |
| *Ots_unk3513-49* | GSI | .103 - .600 | 0.355 | -0.008 | 0.048 | 27 | 0.041 | 23 | 0.038 | 7 | 12 | 4 | | | |
| *Ots_u07-25.325* | PBT | .264 - .700 | 0.476 | 0.022 | 0.048 | 27 | 0.042 | 17 | 0.037 | 13 | 12 | | | | |
| *Ots_94857-232R* | PBT | .223 - .698 | 0.477 | 0.038 | 0.046 | 31 | 0.041 | 23 | 0.038 | 7 | 14 | | | | |
| *Ots_102414-395* | PBT | .230 - .643 | 0.474 | -0.039 | 0.049 | 24 | 0.042 | 17 | 0.036 | 25 | 15 | | | | |
| *Ots_U2446-123* | GSI | .109 - .593 | 0.430 | 0.014 | 0.042 | 38 | 0.041 | 23 | 0.038 | 7 | 16 | 6 | | | |
| *Ots_101704-143* | PBT | .015 - .357 | 0.231 | 0.029 | 0.058 | 13 | 0.044 | 8 | 0.034 | 47 | 16 | | | | |
| *Ots_106747-239* | GSI | .220 - .659 | 0.461 | 0.010 | 0.045 | 34 | 0.041 | 23 | 0.037 | 13 | 18 | | | | |
| *Ots_SClkF2R2-135* | PBT | .205 - .625 | 0.463 | 0.007 | 0.047 | 29 | 0.042 | 17 | 0.036 | 25 | 19 | | | | |
| *Ots_mapK-3'-309* | PBT | .125 - .586 | 0.451 | 0.024 | 0.043 | 37 | 0.041 | 23 | 0.037 | 13 | 20 | | | | |
| *Ots_pigh-105* | PBT | .194 - .625 | 0.473 | 0.003 | 0.042 | 38 | 0.041 | 23 | 0.037 | 13 | 21 | | | | |
| *Ots_105407-117* | PBT | .247 - .615 | 0.462 | -0.022 | 0.049 | 24 | 0.042 | 17 | 0.035 | 34 | 22 | 4 | | | |
| *Ots_cox1-241* | PBT | .013 - .344 | 0.239 | 0.014 | 0.051 | 21 | 0.043 | 11 | 0.034 | 47 | 23 | | | | |
| *Ots_FARSLA-220* | GSI | .000 - .306 | 0.067 | -0.027 | 0.084 | 6 | 0.044 | 8 | 0.033 | 65 | 23 | | | + | |
| *Ots_P450-288* | GSI | .170 - .667 | 0.447 | 0.028 | 0.040 | 43 | 0.040 | 39 | 0.038 | 7 | 25 | | | | |
| *Ots_112876-371* | PBT | .000 - .357 | 0.244 | -0.041 | 0.042 | 38 | 0.041 | 23 | 0.035 | 34 | 26 | | | | |
| *Ots_txnip-321* | PBT | .031 - .303 | 0.243 | 0.015 | 0.053 | 20 | 0.043 | 11 | 0.033 | 65 | 27 | | | | |
| *Ots_u1002-75* | PBT | .033 - .397 | 0.350 | -0.038 | 0.041 | 42 | 0.041 | 23 | 0.035 | 34 | 28 | | | | |
| *Ots_FGF6B_1* | PBT | .170 - .614 | 0.477 | -0.054 | 0.037 | 54 | 0.040 | 39 | 0.037 | 13 | 29 | | b | | |

| SNP | Panel | MAF Range | $H_E$ | $F_{IS}$ | $F_{ST}$ | $F_{ST}$ Rank | $I_N$ | $I_N$ Rank | ORCA | ORCA Rank | "Informativeness" Rank | HWE | LD | CS | Comments |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Ots_100884-287* | PBT | .095 - .433 | 0.333 | 0.004 | 0.044 | 36 | 0.041 | 23 | 0.034 | 47 | 29 | | | | |
| *Ots_P53* | PBT | .069 - .449 | 0.361 | 0.001 | 0.040 | 43 | 0.040 | 39 | 0.035 | 34 | 31 | | | | |
| *Ots_103122-180* | PBT | .021 - .389 | 0.240 | 0.002 | 0.040 | 43 | 0.040 | 39 | 0.035 | 34 | 31 | | | | |
| *Ots_Prl2* | PBT | .091 - .458 | 0.373 | -0.002 | 0.040 | 43 | 0.040 | 39 | 0.035 | 34 | 31 | | | | |
| *Ots_E2-275* | PBT | .125 - .480 | 0.398 | -0.016 | 0.040 | 43 | 0.040 | 39 | 0.035 | 34 | 31 | | | | |
| *Ots_u211-85* | PBT | .180 - .588 | 0.460 | 0.017 | 0.037 | 54 | 0.040 | 39 | 0.036 | 25 | 35 | | | | |
| *Ots_Est1363* | GSI | .000 - .247 | 0.074 | 0.064 | 0.054 | 17 | 0.041 | 23 | 0.032 | 83 | 36 | | | | |
| *Ots_C3N3* | GSI | .000 - .203 | 0.074 | 1.000 | 0.055 | 15 | 0.043 | 11 | 0.031 | 98 | 37 | | | | mtDNA |
| *Ots_112820-284* | PBT | .025 - .321 | 0.226 | -0.032 | 0.042 | 38 | 0.041 | 23 | 0.033 | 65 | 38 | | | | |
| *Ots_107806-821* | GSI | .172 - .633 | 0.471 | -0.005 | 0.036 | 60 | 0.039 | 56 | 0.037 | 13 | 39 | | | | |
| *Ots_unk9480-51* | GSI | .019 - .315 | 0.261 | -0.021 | 0.040 | 43 | 0.041 | 23 | 0.033 | 65 | 40 | | | | |
| *Ots_il-1racp-166* | GSI | .171 - .630 | 0.469 | -0.016 | 0.034 | 66 | 0.039 | 56 | 0.037 | 13 | 41 | | | | |
| *Ots_u07-53.133* | GSI | .009 - .286 | 0.126 | 0.006 | 0.046 | 31 | 0.040 | 39 | 0.033 | 65 | 41 | | | | |
| *Ots_109693-392* | GSI | .000 - .216 | 0.054 | 0.029 | 0.057 | 14 | 0.041 | 23 | 0.031 | 98 | 41 | | | | |
| *Ots_GDH-81x* | PBT | .090 - .429 | 0.357 | 0.015 | 0.039 | 50 | 0.040 | 39 | 0.034 | 47 | 44 | 4 | | | |
| *Ots_GPH-318* | PBT | .051 - .373 | 0.310 | 0.020 | 0.039 | 50 | 0.040 | 39 | 0.034 | 47 | 44 | | | | |
| *Ots_102213-210* | GSI | .000 - .179 | 0.022 | -0.033 | 0.100 | 3 | 0.042 | 17 | 0.030 | 116 | 44 | | | | |
| *Ots_pop5-96* | PBT | .113 - .500 | 0.381 | -0.047 | 0.036 | 57 | 0.039 | 56 | 0.036 | 25 | 47 | | | | |
| *Ots_OTDESMIN19-SNP1* | PBT | .235 - .557 | 0.466 | -0.014 | 0.038 | 53 | 0.040 | 39 | 0.034 | 47 | 48 | | | | |
| *Ots_IL11* | GSI | .000 - .185 | 0.080 | 0.019 | 0.055 | 15 | 0.043 | 11 | 0.030 | 116 | 49 | | | | |
| *Ots_FGF6A* | GSI | .127 - .571 | 0.457 | -0.043 | 0.033 | 74 | 0.039 | 56 | 0.037 | 13 | 50 | | b | | |
| *Ots_96500-180* | PBT | .235 - .671 | 0.471 | 0.021 | 0.033 | 74 | 0.039 | 56 | 0.037 | 13 | 50 | | | | |
| *Ots_mapKpr-151* | PBT | .089 - .407 | 0.370 | -0.011 | 0.036 | 57 | 0.040 | 39 | 0.034 | 47 | 50 | | | | |
| *Ots_nkef-192* | PBT | .203 - .607 | 0.471 | -0.010 | 0.034 | 66 | 0.039 | 56 | 0.036 | 25 | 53 | | | | |
| *Ots_101554-407* | PBT | .238 - .626 | 0.480 | -0.004 | 0.034 | 66 | 0.039 | 56 | 0.036 | 25 | 53 | 5 | | | |
| *Ots_94903-99R* | PBT | .176 - .617 | 0.475 | -0.026 | 0.032 | 79 | 0.039 | 56 | 0.037 | 13 | 55 | | | | |
| *Ots_unk526* | PBT | .022 - .261 | 0.205 | 0.005 | 0.040 | 43 | 0.041 | 23 | 0.032 | 83 | 56 | | | | |
| *Ots_129458-451* | PBT | .000 - .281 | 0.202 | -0.015 | 0.039 | 50 | 0.040 | 39 | 0.033 | 65 | 57 | | | | |
| *Ots_u07-57.120* | GSI | .000 - .185 | 0.068 | 0.006 | 0.049 | 24 | 0.041 | 23 | 0.030 | 116 | 58 | | | | |
| *Ots_mybp-85* | PBT | .000 - .240 | 0.187 | 0.056 | 0.035 | 61 | 0.041 | 23 | 0.032 | 83 | 59 | | | | |
| *Ots_110689-218* | PBT | .071 - .445 | 0.338 | -0.022 | 0.032 | 79 | 0.039 | 56 | 0.035 | 34 | 60 | | | | |
| *Ots_109525-816* | PBT | .062 - .429 | 0.302 | 0.013 | 0.032 | 79 | 0.039 | 56 | 0.035 | 34 | 60 | | | | |
| *Ots_115987-325* | PBT | .150 - .459 | 0.396 | -0.005 | 0.034 | 66 | 0.039 | 56 | 0.034 | 47 | 60 | | | | |
| *Ots_GCSH* | PBT | .005 - .245 | 0.184 | -0.004 | 0.037 | 54 | 0.040 | 39 | 0.032 | 83 | 63 | | | | |
| *Ots_122414-56* | GSI | .000 - .173 | 0.019 | 0.005 | 0.087 | 5 | 0.039 | 56 | 0.030 | 116 | 64 | | | | |
| *Ots_u6-75* | PBT | .019 - .307 | 0.206 | 0.061 | 0.036 | 57 | 0.039 | 56 | 0.033 | 65 | 65 | 4 | | | |
| *Ots_nramp-321* | GSI | .000 - .167 | 0.022 | 0.089 | 0.071 | 9 | 0.039 | 56 | 0.030 | 116 | 66 | | | | |
| *Ots_GTH2B-550* | PBT | .267 - .609 | 0.482 | -0.010 | 0.032 | 79 | 0.039 | 56 | 0.034 | 47 | 67 | 4 | | | |
| *Ots_102457-132* | GSI | .000 - .181 | 0.050 | -0.050 | 0.046 | 31 | 0.040 | 39 | 0.030 | 116 | 68 | | | | |
| *Ots_ARNT* | PBT | .042 - .329 | 0.287 | -0.007 | 0.034 | 66 | 0.039 | 56 | 0.033 | 65 | 69 | | | | |
| *Ots_IGF-I.1-76* | PBT | .074 - .359 | 0.294 | 0.022 | 0.034 | 66 | 0.039 | 56 | 0.033 | 65 | 69 | | | | |
| *Ots_SL* | GSI | .000 - .160 | 0.034 | 0.027 | 0.050 | 22 | 0.039 | 56 | 0.030 | 116 | 71 | | | | |
| *Ots_u07-18.378* | PBT | .000 - .212 | 0.177 | -0.015 | 0.035 | 61 | 0.040 | 39 | 0.031 | 98 | 72 | | | | |
| *Ots_RAG3* | PBT | .033 - .285 | 0.211 | 0.007 | 0.035 | 61 | 0.039 | 56 | 0.032 | 83 | 73 | | | | |

| SNP | Panel | MAF Range | $H_E$ | $F_{IS}$ | $F_{ST}$ | $F_{ST}$ Rank | $I_N$ | $I_N$ Rank | ORCA | ORCA Rank | "Informativeness" Rank | HWE | LD | CS | Comments |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Ots_110064-383* | PBT | .089 - .500 | 0.428 | 0.020 | 0.029 | 101 | 0.038 | 83 | 0.036 | 25 | 73 | | | | |
| *Ots_S7-1* | PBT | .164 - .569 | 0.440 | -0.011 | 0.029 | 101 | 0.038 | 83 | 0.036 | 25 | 73 | | | | |
| *Ots_110201-363* | PBT | .182 - .537 | 0.434 | -0.045 | 0.030 | 92 | 0.038 | 83 | 0.035 | 34 | 73 | | | | |
| *Ots_108735-302* | GSI | .016 - .315 | 0.161 | 0.073 | 0.035 | 61 | 0.038 | 83 | 0.033 | 65 | 73 | 6 | | | |
| *Ots_105105-613* | PBT | .157 - .494 | 0.434 | 0.022 | 0.031 | 88 | 0.038 | 83 | 0.034 | 47 | 78 | | | | |
| *Ots_tpx2-125* | PBT | .010 - .246 | 0.181 | -0.027 | 0.032 | 79 | 0.039 | 56 | 0.032 | 83 | 78 | | | | |
| *Ots_123921-111* | PBT | .027 - .274 | 0.229 | -0.022 | 0.031 | 88 | 0.039 | 56 | 0.032 | 83 | 80 | | | | |
| *Ots_128757-61R* | PBT | .006 - .195 | 0.157 | -0.034 | 0.032 | 79 | 0.039 | 56 | 0.031 | 98 | 81 | | | | |
| *Ots_hsc71-5'-453* | GSI | .000 - .167 | 0.071 | 0.011 | 0.035 | 61 | 0.039 | 56 | 0.030 | 116 | 81 | | c | | |
| *Ots_96222-525* | GSI | .000 - .150 | 0.068 | 0.029 | 0.034 | 66 | 0.040 | 39 | 0.029 | 132 | 83 | | | | |
| *Ots_112419-131* | PBT | .000 - .255 | 0.179 | -0.008 | 0.029 | 101 | 0.039 | 56 | 0.032 | 83 | 84 | | | | |
| *Ots_CirpA* | PBT | .007 - .219 | 0.189 | -0.018 | 0.030 | 92 | 0.039 | 56 | 0.031 | 98 | 85 | | | | |
| *Ots_AldB1-122* | GSI | .000 - .203 | 0.128 | 0.063 | 0.030 | 92 | 0.039 | 56 | 0.031 | 98 | 85 | 4 | | | |
| *Ots_myoD-364* | GSI | .005 - .205 | 0.116 | -0.020 | 0.033 | 74 | 0.038 | 83 | 0.031 | 98 | 87 | | | | |
| *Ots_96899-357R* | PBT | .009 - .283 | 0.222 | 0.001 | 0.028 | 110 | 0.038 | 83 | 0.033 | 65 | 88 | | | | |
| *Ots_117242-136* | GSI | .005 - .205 | 0.113 | -0.062 | 0.032 | 79 | 0.038 | 83 | 0.031 | 98 | 89 | | | | |
| *Ots_131460-584* | GSI | .000 - .146 | 0.073 | 0.010 | 0.033 | 74 | 0.039 | 56 | 0.029 | 132 | 90 | | | | |
| *Ots_u07-17.135* | PBT | .036 - .253 | 0.206 | 0.001 | 0.030 | 92 | 0.038 | 83 | 0.031 | 98 | 91 | | | | |
| *Ots_104569-86* | GSI | .033 - .246 | 0.204 | -0.043 | 0.030 | 92 | 0.038 | 83 | 0.031 | 98 | 91 | | | | |
| *Ots_Ikaros-250* | PBT | .022 - .227 | 0.176 | -0.008 | 0.030 | 92 | 0.038 | 83 | 0.031 | 98 | 91 | | | | |
| *Ots_vatf-251* | PBT | .017 - .259 | 0.165 | -0.040 | 0.028 | 110 | 0.038 | 83 | 0.032 | 83 | 94 | | | | |
| *Ots_OTSMTA-SNP1* | GSI | .000 - .117 | 0.018 | 0.057 | 0.045 | 34 | 0.037 | 112 | 0.029 | 132 | 95 | | | | |
| *Ots_myo1a-384* | GSI | .000 - .130 | 0.048 | -0.013 | 0.034 | 66 | 0.038 | 83 | 0.029 | 132 | 96 | | | | |
| *Ots_hsc71-3'-488* | PBT | .054 - .294 | 0.267 | -0.010 | 0.027 | 116 | 0.038 | 83 | 0.032 | 83 | 97 | | c | | |
| *Ots_Thio* | PBT | .084 - .434 | 0.383 | 0.010 | 0.023 | 138 | 0.037 | 112 | 0.035 | 34 | 98 | | | | |
| *Ots_AsnRS-60* | PBT | .045 - .299 | 0.295 | -0.008 | 0.026 | 119 | 0.038 | 83 | 0.032 | 83 | 99 | | | | |
| *Ots_redd1-187* | PBT | .074 - .396 | 0.374 | 0.008 | 0.025 | 128 | 0.037 | 112 | 0.034 | 47 | 100 | | | | |
| *Ots_GnRH-271* | GSI | .000 - .146 | 0.058 | -0.009 | 0.033 | 74 | 0.038 | 83 | 0.029 | 132 | 101 | | | | |
| *Ots_DDX5-171* | GSI | .006 - .197 | 0.137 | 0.017 | 0.028 | 110 | 0.038 | 83 | 0.031 | 98 | 102 | | | | |
| *Ots_NFYB-147* | PBT | .047 - .286 | 0.287 | -0.013 | 0.025 | 128 | 0.038 | 83 | 0.032 | 83 | 103 | | | | |
| *Ots_IL8R_C8* | PBT | .213 - .513 | 0.464 | -0.019 | 0.026 | 119 | 0.037 | 112 | 0.033 | 65 | 104 | | | | |
| *Ots_unk1832-39* | GSI | .328 - .656 | 0.488 | -0.006 | 0.023 | 138 | 0.037 | 112 | 0.034 | 47 | 105 | | | | |
| *Ots_112301-43* | PBT | .043 - .258 | 0.238 | 0.040 | 0.027 | 116 | 0.038 | 83 | 0.031 | 98 | 105 | 4 | | | |
| *Ots_ZR-575* | GSI | .000 - .167 | 0.106 | 0.206 | 0.029 | 101 | 0.038 | 83 | 0.030 | 116 | 107 | 11 | | | |
| *Ots_127236-62* | GSI | .000 - .117 | 0.042 | -0.026 | 0.031 | 88 | 0.038 | 83 | 0.029 | 132 | 108 | | | | |
| *Ots_104415-88* | PBT | .337 - .633 | 0.485 | 0.038 | 0.025 | 128 | 0.037 | 112 | 0.033 | 65 | 109 | | | | |
| *Ots_GST-207* | GSI | .000 - .098 | 0.010 | 0.186 | 0.054 | 17 | 0.036 | 142 | 0.028 | 147 | 110 | | | | |
| *Ots_118205-61* | PBT | .090 - .330 | 0.313 | 0.004 | 0.026 | 119 | 0.037 | 112 | 0.032 | 83 | 111 | 4 | | | |
| *Ots_ETIF1A* | PBT | .158 - .443 | 0.411 | -0.032 | 0.023 | 138 | 0.037 | 112 | 0.033 | 65 | 112 | 5 | | | |
| *Ots_113457-40R* | GSI | .013 - .188 | 0.153 | -0.017 | 0.026 | 119 | 0.038 | 83 | 0.030 | 116 | 113 | 4 | | | |
| *Ots_105385-421* | PBT | .300 - .650 | 0.483 | 0.027 | 0.022 | 144 | 0.036 | 142 | 0.035 | 34 | 114 | | | | |
| *Ots_hsp27b-150* | GSI | .005 - .160 | 0.082 | 0.011 | 0.030 | 92 | 0.037 | 112 | 0.030 | 116 | 114 | | | | |
| *Ots_NOD1* | PBT | .143 - .414 | 0.391 | -0.023 | 0.022 | 144 | 0.037 | 112 | 0.033 | 65 | 116 | | | | |
| *Ots_112208-722* | GSI | .000 - .138 | 0.084 | 0.004 | 0.028 | 110 | 0.038 | 83 | 0.029 | 132 | 117 | | | | |

| SNP | Panel | MAF Range | $H_E$ | $F_{IS}$ | $F_{ST}$ | $F_{ST}$ Rank | $I_N$ | $I_N$ Rank | ORCA | ORCA Rank | "Informativeness" Rank | HWE | LD | CS | Comments |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Ots_hnRNPL-533* | GSI | .283 - .667 | 0.487 | 0.009 | 0.021 | 152 | 0.036 | 142 | 0.035 | 34 | 118 | | | | |
| *Ots_Hsp90a* | GSI | .000 - .068 | 0.025 | -0.047 | 0.032 | 79 | 0.038 | 83 | 0.027 | 166 | 118 | | | | |
| *Ots_HSP90B-100* | PBT | .080 - .308 | 0.288 | -0.014 | 0.026 | 119 | 0.037 | 112 | 0.031 | 98 | 120 | | | | |
| *Ots_EndoRB1-486* | GSI | .000 - .111 | 0.055 | -0.037 | 0.029 | 101 | 0.038 | 83 | 0.028 | 147 | 121 | | | | |
| *Ots_u07-49.290* | PBT | .164 - .500 | 0.420 | 0.013 | 0.022 | 144 | 0.036 | 142 | 0.034 | 47 | 122 | | | | |
| *Ots_nelfd-163* | GSI | .000 - .087 | 0.024 | 0.040 | 0.032 | 79 | 0.037 | 112 | 0.028 | 147 | 123 | | | | |
| *Ots_ntl-255* | PBT | .214 - .549 | 0.449 | 0.004 | 0.021 | 152 | 0.036 | 142 | 0.034 | 47 | 124 | | | | |
| *Ots_Est740* | PBT | .289 - .621 | 0.479 | -0.050 | 0.021 | 152 | 0.036 | 142 | 0.034 | 47 | 124 | | | | |
| *Ots_Cath_D141* | GSI | .000 - .069 | 0.024 | 0.161 | 0.030 | 92 | 0.038 | 83 | 0.027 | 166 | 124 | | | | |
| *Ots_108007-208* | GSI | .000 - .123 | 0.067 | -0.018 | 0.025 | 128 | 0.038 | 83 | 0.029 | 132 | 127 | | | | |
| *Ots_HMGB1-73* | PBT | .059 - .265 | 0.246 | -0.003 | 0.024 | 134 | 0.037 | 112 | 0.031 | 98 | 128 | | | | |
| *Ots_105132-200* | PBT | .067 - .313 | 0.329 | -0.017 | 0.021 | 152 | 0.037 | 112 | 0.032 | 83 | 129 | | | | |
| *Ots_99550-204* | GSI | .000 - .099 | 0.030 | -0.007 | 0.031 | 88 | 0.037 | 112 | 0.028 | 147 | 129 | | | | |
| *Ots_unk1104-38* | GSI | .263 - .607 | 0.484 | -0.017 | 0.020 | 159 | 0.036 | 142 | 0.034 | 47 | 131 | | | | |
| *Ots_130720-99* | GSI | .000 - .114 | 0.087 | 0.035 | 0.024 | 134 | 0.038 | 83 | 0.029 | 132 | 132 | | | | |
| *Ots_97077-179R* | GSI | .000 - .088 | 0.049 | 0.047 | 0.026 | 119 | 0.038 | 83 | 0.028 | 147 | 132 | | | | |
| *Ots_SWS1op-182* | PBT | .190 - .505 | 0.411 | 0.029 | 0.019 | 163 | 0.036 | 142 | 0.034 | 47 | 134 | | | | |
| *Ots_110551-64* | PBT | .098 - .322 | 0.327 | -0.021 | 0.022 | 144 | 0.037 | 112 | 0.031 | 98 | 135 | | | | |
| *Ots_131906-141* | GSI | .000 - .149 | 0.087 | -0.004 | 0.028 | 110 | 0.037 | 112 | 0.029 | 132 | 135 | | | | |
| *Ots_OTALDBINT1-SNP1* | PBT | .027 - .202 | 0.161 | 0.071 | 0.025 | 128 | 0.037 | 112 | 0.030 | 116 | 137 | 6 | | | |
| *Ots_106499-70* | GSI | .143 - .444 | 0.377 | -0.009 | 0.021 | 152 | 0.036 | 142 | 0.033 | 65 | 138 | | | | |
| *Ots_CD59-2* | PBT | .284 - .562 | 0.467 | -0.010 | 0.021 | 152 | 0.036 | 142 | 0.033 | 65 | 138 | 4 | | | |
| *Ots_zn593-346* | GSI | .000 - .111 | 0.034 | 0.000 | 0.029 | 101 | 0.037 | 112 | 0.028 | 147 | 140 | | | | |
| *Ots_U2362-227* | GSI | .000 - .109 | 0.030 | 0.015 | 0.029 | 101 | 0.037 | 112 | 0.028 | 147 | 140 | | | | |
| *Ots_EP-529* | GSI | .000 - .098 | 0.039 | -0.051 | 0.029 | 101 | 0.037 | 112 | 0.028 | 147 | 140 | | | | |
| *Ots_128302-57* | GSI | .000 - .133 | 0.079 | -0.011 | 0.026 | 119 | 0.037 | 112 | 0.029 | 132 | 143 | | | | |
| *Ots_unk7936-50* | GSI | .000 - .151 | 0.123 | 0.030 | 0.022 | 144 | 0.037 | 112 | 0.030 | 116 | 144 | | | | |
| *Ots_GH2* | GSI | .000 - .125 | 0.083 | -0.043 | 0.025 | 128 | 0.037 | 112 | 0.029 | 132 | 144 | | | | |
| *Ots_PGK-54* | GSI | .000 - .075 | 0.029 | 0.078 | 0.027 | 116 | 0.037 | 112 | 0.028 | 147 | 146 | | | | |
| *Ots_CD63* | GSI | .000 - .141 | 0.098 | -0.011 | 0.024 | 134 | 0.037 | 112 | 0.029 | 132 | 147 | | | | |
| *Ots_118175-479* | GSI | .000 - .080 | 0.039 | 0.026 | 0.026 | 119 | 0.037 | 112 | 0.028 | 147 | 147 | | | | |
| *Ots_brp16-64* | PBT | .052 - .277 | 0.234 | 0.013 | 0.022 | 144 | 0.036 | 142 | 0.031 | 98 | 149 | | | | |
| *Ots_U2362-330* | GSI | .278 - .586 | 0.484 | -0.062 | 0.015 | 172 | 0.035 | 167 | 0.034 | 47 | 150 | | | | |
| *Ots_102801-308* | PBT | .100 - .329 | 0.336 | -0.008 | 0.019 | 163 | 0.036 | 142 | 0.032 | 83 | 151 | | | | |
| *Ots_107285-93* | GSI | .000 - .088 | 0.041 | 0.022 | 0.024 | 134 | 0.037 | 112 | 0.028 | 147 | 152 | | | | |
| *Ots_107074-284* | GSI | .000 - .080 | 0.050 | 0.005 | 0.023 | 138 | 0.037 | 112 | 0.028 | 147 | 153 | | | | |
| *Ots_parp3-286* | PBT | .055 - .261 | 0.283 | -0.027 | 0.020 | 159 | 0.036 | 142 | 0.031 | 98 | 154 | | | | |
| *Ots_123048-521* | GSI | .000 - .086 | 0.018 | -0.038 | 0.028 | 110 | 0.036 | 142 | 0.028 | 147 | 154 | | | | |
| *Ots_il13Ra2B-37* | GSI | .269 - .544 | 0.461 | -0.011 | 0.016 | 168 | 0.035 | 167 | 0.033 | 65 | 156 | 5 | | | |
| *Ots_u4-92* | PBT | .000 - .111 | 0.069 | 0.005 | 0.022 | 144 | 0.037 | 112 | 0.028 | 147 | 157 | | | | |
| *Ots_111681-657* | GSI | .017 - .181 | 0.149 | -0.018 | 0.021 | 152 | 0.036 | 142 | 0.030 | 116 | 158 | | | | |
| *Ots_113242-216* | PBT | .011 - .178 | 0.181 | -0.020 | 0.019 | 163 | 0.036 | 142 | 0.030 | 116 | 159 | | | | |
| *Ots_unk8200-45* | GSI | .000 - .054 | 0.006 | -0.034 | 0.030 | 92 | 0.035 | 167 | 0.027 | 166 | 160 | | | | |
| *Ots_124774-477* | PBT | .004 - .167 | 0.143 | -0.022 | 0.016 | 168 | 0.036 | 142 | 0.030 | 116 | 161 | | | | |

| SNP | Panel | MAF Range | $H_E$ | $F_{IS}$ | $F_{ST}$ | $F_{ST}$ Rank | $I_N$ | $I_N$ Rank | ORCA | ORCA Rank | "Informativeness" Rank | HWE | LD | CS | Comments |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Ots_TCTA-58* | GSI | .000 - .102 | 0.050 | -0.004 | 0.023 | 138 | 0.036 | 142 | 0.028 | 147 | 162 | | | | |
| *Ots_arp-436* | GSI | .000 - .056 | 0.012 | -0.033 | 0.026 | 119 | 0.036 | 142 | 0.027 | 166 | 162 | | | | |
| *Ots_u202-161* | GSI | .000 - .136 | 0.075 | -0.026 | 0.020 | 159 | 0.036 | 142 | 0.029 | 132 | 164 | | | | |
| *Ots_GPDH-338* | GSI | .000 - .049 | 0.005 | -0.033 | 0.029 | 101 | 0.034 | 175 | 0.027 | 166 | 165 | | | | |
| *Ots_102867-609* | GSI | .000 - .069 | 0.024 | 0.004 | 0.023 | 138 | 0.036 | 142 | 0.027 | 166 | 166 | | | | |
| *Ots_HFABP-34* | GSI | .000 - .093 | 0.052 | -0.009 | 0.019 | 163 | 0.036 | 142 | 0.028 | 147 | 167 | | | | |
| *Ots_117259-271* | GSI | .000 - .066 | 0.019 | 0.003 | 0.022 | 144 | 0.036 | 142 | 0.027 | 166 | 167 | | | | |
| *Ots_aldb-177M* | GSI | .000 - .111 | 0.115 | -0.004 | 0.015 | 172 | 0.036 | 142 | 0.028 | 147 | 169 | | | | |
| *Ots_MHC1* | PBT | .019 - .167 | 0.112 | -0.007 | 0.016 | 168 | 0.035 | 167 | 0.029 | 132 | 170 | | | | |
| *Ots_P450* | GSI | .000 - .062 | 0.032 | 0.085 | 0.020 | 159 | 0.036 | 142 | 0.027 | 166 | 170 | | | | |
| *Ots_128693-461* | GSI | .000 - .106 | 0.065 | -0.019 | 0.015 | 172 | 0.035 | 167 | 0.028 | 147 | 172 | | | | |
| *Ots_TGFB* | PBT | .011 - .109 | 0.103 | 0.039 | 0.014 | 175 | 0.035 | 167 | 0.028 | 147 | 173 | | | | |
| *Ots_u1007-124* | GSI | .000 - .039 | 0.016 | -0.025 | 0.017 | 167 | 0.035 | 167 | 0.027 | 166 | 174 | | | | |
| *Ots_CRB211* | GSI | .000 - .041 | 0.012 | -0.023 | 0.016 | 168 | 0.035 | 167 | 0.027 | 166 | 175 | | | | |
| *Ots_zP3b-215* | GSI | .000 - .000 | 0.000 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic |
| *Ots_RAS1* | GSI | .000 - .000 | 0.000 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic |
| *Ots_TNF* | GSI | .000 - .012 | 0.001 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic |
| *Ots_RFC2-558* | GSI | .000 - .038 | 0.014 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic[d] |
| *Ots_aspat-196* | GSI | .000 - .011 | 0.002 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic[d] |
| *Ots_GST-375* | GSI | .000 - .005 | 0.000 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic |
| *Ots_LWSop-638* | GSI | .000 - .003 | 0.000 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic |
| *Ots_u07-20.332* | GSI | .000 - .017 | 0.001 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic[d] |
| *Ots_Ots311-101x* | GSI | .000 - .037 | 0.007 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic[d] |
| *Ots_u07-64.221* | GSI | .000 - .034 | 0.002 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic |
| *Ots_Myc-366* | GSI | .000 - .036 | 0.005 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic |
| *Ots_CCR7* | GSI | .000 - .000 | 0.000 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic |
| *Ots_101119-381* | GSI | .000 - .019 | 0.002 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic[d] |
| *Ots_129144-472* | GSI | .000 - .025 | 0.009 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic[d] |
| *Ots_stk6-516* | GSI | .000 - .000 | 0.000 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic[d] |
| *Ots_108390-329* | GSI | .000 - .019 | 0.003 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | | | | monomorphic[d] |

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

[b] Ots_FGF6A and Ots_FGF6B_1 exhibited linkage disequilibrium in 39 of 39 baseline collections. Ots_FGF6A was the less 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] These markers were variable in the 3 fall Chinook collections included in Snake River baseline v2.0 and will be included in analyses baseline and GSI analyses concerning differentiating spring/summer and fall lineages.

Table 5. SNPs that were added (left) or removed (right) from the *O. mykiss* SNP panels during the second year of the GSI project. SNP panel is noted.

| SNP/Comments | Panel | SNP/Comments | Panel |
|---|---|---|---|
| ***Added*** | | ***Removed*** | |
| OmyY1_2SEXY | PBT | Omy_SEXY1 | PBT |
| Ocl_gshpx-357: *O. clarkii* hybrid marker | GSI | Ocl_calT7RT2: *O. clarkii* hybrid marker | GSI |

Table 6. SNPs that were added (left) and removed (right) from the Chinook salmon SNP panels during the second year of the GSI project. SNP panel is noted.

| SNP/Comments | Panel | SNP/Comments | Panel |
|---|---|---|---|
| ***Added*** | | ***Removed*** | |
| Ots_SEXY3-1 | PBT | Ots_SEXY1 | GSI/PBT |
| Ots_101119-381 | GSI | | |
| Ots_107074-284 | GSI | | |
| Ots_111681-657 | GSI | | |
| Ots_128693-461 | GSI | | |
| Ots_HFABP-34 | GSI | | |
| Ots_OTSMTA-SNP1 | GSI | | |
| Ots_U2362-330 | GSI | | |
| Ots_102213-210 | GSI | | |
| Ots_107285-93 | GSI | | |
| Ots_112208-722 | GSI | | |
| Ots_129144-472 | GSI | | |
| Ots_hnRNPL-533 | GSI | | |
| Ots_P450-288 | GSI | | |
| Ots_U2446-123 | GSI | | |
| Ots_zn593-346 | GSI | | |
| Ots_107806-821 | GSI | | |
| Ots_117242-136 | GSI | | |
| Ots_130720-99 | GSI | | |
| Ots_Hsp90a | GSI | | |
| Ots_stk6-516 | GSI | | |
| Ots_unk1104-38 | GSI | | |
| Ots_102457-132 | GSI | | |
| Ots_108007-208 | GSI | | |
| Ots_117259-271 | GSI | | |
| Ots_131460-584 | GSI | | |
| Ots_il13Ra2B-37 | GSI | | |
| Ots_TCTA-58 | GSI | | |
| Ots_unk1832-39 | GSI | | |
| Ots_102867-609 | GSI | | |
| Ots_108390-329 | GSI | | |
| Ots_118175-479 | GSI | | |
| Ots_131906-141 | GSI | | |
| Ots_il-1racp-166 | GSI | | |
| Ots_unk3513-49 | GSI | | |
| Ots_108735-302 | GSI | | |
| Ots_122414-56 | GSI | | |
| Ots_99550-204 | GSI | | |

| SNP/Comments | Panel | SNP/Comments | Panel |
|---|---|---|---|
| ***Added*** | | ***Removed*** | |
| Ots_unk7936-50 | GSI | | |
| Ots_104569-86 | GSI | | |
| Ots_109693-392 | GSI | | |
| Ots_127236-62 | GSI | | |
| Ots_DDX5-171 | GSI | | |
| Ots_nelfd-163 | GSI | | |
| Ots_u1007-124 | GSI | | |
| Ots_unk8200-45 | GSI | | |
| Ots_106499-70 | GSI | | |
| Ots_128302-57 | GSI | | |
| Ots_Est1363 | GSI | | |
| Ots_U2362-227 | GSI | | |
| Ots_unk9480-51 | GSI | | |

Table 7. Steelhead hatchery broodstock collections screened with 192 assays to allow direct comparison with natural origin populations. Sample size (*n*), years collected, latitude, longitude, expected heterozygosity ($H_E$), and mean allelic richness (AR) are shown.

| Hatchery | *n* | Years Collected | Latitude | Longitude | $H_E$ | AR |
|---|---|---|---|---|---|---|
| Sawtooth | 93 | 08, 09 | 44.151 | -114.885 | 29.6% | 1.94 |
| Pahsimeroi | 165 | 08, 09 | 44.682 | -114.040 | 30.4% | 1.95 |
| Oxbow | 93 | 08, 09 | 44.520 | -116.855 | 30.2% | 1.94 |
| Dworshak | 115 | 05, 08, 09 | 46.502 | -116.321 | 27.6% | 1.88 |
| Wallowa | 93 | 09 | 45.418 | -117.301 | 30.0% | 1.94 |
| Lyons Ferry, Tucannon, Touchet | 92 | 09 | 46.038 | -117.295 | 30.8% | 1.96 |

Table 8. Chinook salmon hatchery broodstock collections screened with 192 assays to allow direct comparison with natural origin populations. Sample size (*n*), years collected, latitude, longitude, expected heterozygosity ($H_E$), and mean allelic richness (AR) are shown. All hatchery collections are stream-type lineage.

| Hatchery | *n* | Years Collected | Latitude | Longitude | $H_E$ | AR |
|---|---|---|---|---|---|---|
| Sawtooth | 92 | 10 | 44.151 | -114.885 | 0.229 | 1.55 |
| Pahsimeroi | 91 | 10 | 44.682 | -114.040 | 0.231 | 1.56 |
| McCall | 94 | 10 | 44.890 | -116.103 | 0.227 | 1.56 |
| Rapid | 92 | 10 | 45.372 | -116.356 | 0.232 | 1.57 |
| Powell | 92 | 10 | 46.506 | -114.687 | 0.241 | 1.59 |
| Dworshak | 93 | 10 | 46.502 | -116.321 | 0.242 | 1.60 |
| Lookingglass | 94 | 10 | 45.735 | -117.863 | 0.249 | 1.61 |
| Tucannon | 91 | 10 | 46.310 | -117.657 | 0.256 | 1.64 |

Table 9. Pairwise fixation indices ($F_{ST}$) between natural origin steelhead populations represented in baseline v2.0 (Table 1) and hatchery broodstock collections (Table 7) using 187 SNPs (Table 3). Cells shaded red represent comparisons with greater differentiation (max = 0.050, Pistol Creek vs Dworshak hatchery); cells shaded green represent comparisons of lower differentiation (min = 0.003, Alpowa Creek vs Lyons Ferry hatchery). Reporting group of each population is noted. Average pairwise $F_{ST}$ is averaged across hatchery collections.

| | | | Hatchery | | | | | |
|---|---|---|---|---|---|---|---|---|
| **Wild Population** | **Reporting Group** | **Avg. Pairwise $F_{ST}$** | **Sawtooth** | **Pahsimeroi** | **Oxbow** | **Dworshak** | **Wallowa** | **Lyons Ferry** |
| 1. Sawtooth Weir | UPSALM | 0.010 | | | | | | |
| 2. Valley Cr | UPSALM | 0.012 | | | | | | |
| 3. WF Yankee F Salmon | UPSALM | 0.010 | | | | | | |
| 4. Morgan Cr | UPSALM | 0.017 | | | | | | |
| 5. Pahsimeroi Weir | UPSALM | 0.011 | | | | | | |
| 6. Hayden Cr | UPSALM | 0.012 | | | | | | |
| 7. NF Salmon R | UPSALM | 0.010 | | | | | | |
| 8. Marsh Cr | MFSALM | 0.033 | | | | | | |
| 9. Sulphur Cr | MFSALM | 0.031 | | | | | | |
| 10. Rapid R (MF) | MFSALM | 0.031 | | | | | | |
| 11. Pistol Cr | MFSALM | 0.036 | | | | | | |
| 12. Camas Cr | MFSALM | 0.024 | | | | | | |
| 13. Loon Cr | MFSALM | 0.024 | | | | | | |
| 14. Big Cr (upper) | MFSALM | 0.031 | | | | | | |
| 15. Big Cr (lower) | MFSALM | 0.027 | | | | | | |
| 16. Chamberlain Cr | MFSALM | 0.018 | | | | | | |
| 17. Bargamin Cr | MFSALM | 0.020 | | | | | | |
| 18. EF SF Salmon R | SFSALM | 0.028 | | | | | | |
| 19. Secesh R | SFSALM | 0.026 | | | | | | |
| 20. Lick Cr | SFSALM | 0.027 | | | | | | |
| 21. Stolle Meadows | SFSALM | 0.030 | | | | | | |
| 22. Boulder Cr | LOSALM | 0.015 | | | | | | |
| 23. Rapid R | LOSALM | 0.015 | | | | | | |
| 24. Slate Cr | LOSALM | 0.013 | | | | | | |
| 25. Whitebird Cr | LOSALM | 0.013 | | | | | | |
| 26. Colt Cr | UPCLWR | 0.029 | | | | | | |
| 27. Storm Cr | UPCLWR | 0.032 | | | | | | |
| 28. Crooked F Lochsa R | UPCLWR | 0.026 | | | | | | |
| 29. Lake Cr | UPCLWR | 0.031 | | | | | | |
| 30. Fish Cr | UPCLWR | 0.025 | | | | | | |
| 31. Canyon Cr | UPCLWR | 0.024 | | | | | | |
| 32. Selway R | UPCLWR | 0.031 | | | | | | |
| 33. Little Clearwater R | UPCLWR | 0.027 | | | | | | |
| 34. Whitecap Cr | UPCLWR | 0.029 | | | | | | |
| 35. Bear Cr | UPCLWR | 0.031 | | | | | | |
| 36. NF Moose Cr | UPCLWR | 0.024 | | | | | | |
| 37. Three Links Cr | UPCLWR | 0.032 | | | | | | |
| 38. Gedney Cr | UPCLWR | 0.024 | | | | | | |
| 39. O'Hara Cr | UPCLWR | 0.020 | | | | | | |
| 40. Clear Cr | SFCLWR | 0.023 | | | | | | |
| 41. Crooked R | SFCLWR | 0.021 | | | | | | |
| 42. Tenmile Cr | SFCLWR | 0.031 | | | | | | |
| 43. John's Cr | SFCLWR | 0.021 | | | | | | |
| 44. WF Potlatch R | LOCLWR | 0.013 | | | | | | |
| 45. EF Potlatch R | LOCLWR | 0.014 | | | | | | |
| 46. Big Bear Cr | LOCLWR | 0.012 | | | | | | |
| 47. Little Bear Cr | LOCLWR | 0.012 | | | | | | |
| 48. Big Sheep Cr | IMNAHA | 0.015 | | | | | | |
| 49. Camp Cr | IMNAHA | 0.021 | | | | | | |
| 50. Cow Cr | IMNAHA | 0.014 | | | | | | |
| 51. Lightning Cr | IMNAHA | 0.017 | | | | | | |
| 52. Joseph Cr | GRROND | 0.013 | | | | | | |
| 53. Crooked Cr | GRROND | 0.012 | | | | | | |
| 54. Elk Cr | GRROND | 0.022 | | | | | | |
| 55. Little Minam R | GRROND | 0.020 | | | | | | |

| Wild Population | Reporting Group | Avg. Pairwise $F_{ST}$ | Hatchery | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | Sawtooth | Pahsimeroi | Oxbow | Dworshak | Wallowa | Lyons Ferry |
| 56. Lostine R | GRROND | 0.018 | | | | | | |
| 57. Menatchee Cr | GRROND | 0.012 | | | | | | |
| 58. Wenaha R | GRROND | 0.013 | | | | | | |
| 59. Captain John Cr | GRROND | 0.015 | | | | | | |
| 60. George Cr | LSNAKE | 0.010 | | | | | | |
| 61. Asotin Cr | LSNAKE | 0.009 | | | | | | |
| 62. Alpowa Cr | LSNAKE | 0.010 | | | | | | |
| 63. Tucannon R | LSNAKE | 0.010 | | | | | | |

Table 10. Pairwise fixation indices ($F_{ST}$) between natural origin Chinook salmon populations represented in baseline v2.0 (Table 2) and hatchery broodstock collections (Table 8). Cells shaded red represent comparisons with greater differentiation (max = 0.036, Chamberlain Creek [post-2008] vs Pahsimeroi hatchery); cells shaded green represent comparisons of lower differentiation (min = 0.003, Rapid River vs Rapid River hatchery). Reporting group of each population is noted. Average pairwise $F_{ST}$ is averaged across hatchery collections.

| Wild Population | Reporting Group | Avg. Pairwise $F_{ST}$ | Hatchery | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Sawtooth | Pahsimeroi | McCall | Rapid | Powell | Dworshak | Lookingglass | Tucannon |
| 1. Sawtooth Weir | UPSALM | 0.013 | | | | | | | | |
| 2. Valley Cr | UPSALM | 0.014 | | | | | | | | |
| 3. WF Yankee F Salmon | UPSALM | 0.020 | | | | | | | | |
| 4. EF Salmon R | UPSALM | 0.014 | | | | | | | | |
| 5. Pahsimeroi R | UPSALM | 0.015 | | | | | | | | |
| 6. Hayden Cr | UPSALM | 0.020 | | | | | | | | |
| 7. Lemhi (upper) | UPSALM | 0.017 | | | | | | | | |
| 8. Lemhi (lower) | UPSALM | 0.013 | | | | | | | | |
| 9. Capehorn Cr | MFSALM | 0.020 | | | | | | | | |
| 10. Marsh Cr | MFSALM | 0.017 | | | | | | | | |
| 11. Elk Cr | MFSALM | 0.019 | | | | | | | | |
| 12. Bear Valley Cr | MFSALM | 0.017 | | | | | | | | |
| 13. Sulphur Cr | MFSALM | 0.023 | | | | | | | | |
| 14. Camas Cr | MFSALM | 0.021 | | | | | | | | |
| 15. Big Cr | MFSALM | 0.017 | | | | | | | | |
| 16. Chamberlain Cr (post-2008) | CHMBLN | 0.030 | | | | | | | | |
| 17. Chamberlain Cr (pre-2008) | CHMBLN | 0.024 | | | | | | | | |
| 18. Lake Cr, Summit Cr | SFSALM | 0.018 | | | | | | | | |
| 19. Secesh R | SFSALM | 0.016 | | | | | | | | |
| 20. Johnson Cr | SFSALM | 0.016 | | | | | | | | |
| 21. SF Salmon R | SFSALM | 0.011 | | | | | | | | |
| 22. Rapid R | HELLSC | 0.014 | | | | | | | | |
| 23. Crooked F Lochsa R | HELLSC | 0.014 | | | | | | | | |
| 24. Powell Weir | HELLSC | 0.013 | | | | | | | | |
| 25. Red R | HELLSC | 0.011 | | | | | | | | |
| 26. Crooked R Weir | HELLSC | 0.011 | | | | | | | | |
| 27. Newsome Cr | HELLSC | 0.014 | | | | | | | | |
| 28. Lolo Cr | HELLSC | 0.010 | | | | | | | | |
| 29. Imnaha R | HELLSC | 0.014 | | | | | | | | |
| 30. Imnaha R (1998) | HELLSC | 0.012 | | | | | | | | |
| 31. Upper Grande Ronde | HELLSC | 0.015 | | | | | | | | |
| 32. Catherine Cr | HELLSC | 0.011 | | | | | | | | |
| 33. Lostine R | HELLSC | 0.015 | | | | | | | | |
| 34. Minam R | HELLSC | 0.012 | | | | | | | | |
| 35. Wenaha R | HELLSC | 0.012 | | | | | | | | |
| 36. Tucannon R | TUCANO | 0.021 | | | | | | | | |

Table 11. Steelhead results from 100% simulations performed in ONCOR (Kalinowski et al. 2007). For each population represented in steelhead baseline v2.0, 200 mixtures were generated each containing 100% of individuals simulated from that population; simulated mixtures were then allocated back to the baseline. Rows represent population where simulated individuals originated. Columns represent reporting groups where simulated mixtures assigned. Shaded boxes represent the correct reporting group of origin for each population.

| | Assigned Reporting Group | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **Population of Origin** | **UPSALM** | **MFSALM** | **SFSALM** | **LOSALM** | **UPCLWR** | **SFCLWR** | **LOCLWR** | **IMNAHA** | **GRROND** | **LSNAKE** |
| Sawtooth Weir | 0.98 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Valley Cr | 0.95 | 0.00 | 0.00 | 0.02 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | 0.01 |
| WF Yankee F Salmon | 0.98 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 |
| Morgan Cr | 0.97 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 |
| Pahsimeroi Weir | 0.97 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.02 |
| Hayden Cr | 0.97 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.02 |
| NF Salmon R | 0.87 | 0.01 | 0.00 | 0.03 | 0.00 | 0.00 | 0.01 | 0.01 | 0.01 | 0.07 |
| Marsh Cr | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Sulphur Cr | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Rapid R (MF) | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Pistol Cr | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Camas Cr | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Loon Cr | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Big Cr (upper) | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Big Cr (lower) | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Chamberlain Cr | 0.02 | 0.91 | 0.00 | 0.04 | 0.00 | 0.00 | 0.00 | 0.01 | 0.01 | 0.00 |
| Bargamin Cr | 0.08 | 0.88 | 0.00 | 0.01 | 0.00 | 0.00 | 0.00 | 0.01 | 0.01 | 0.01 |
| EF SF Salmon R | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Secesh R | 0.00 | 0.00 | 0.99 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Lick Cr | 0.00 | 0.00 | 0.99 | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Stolle Meadows | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Boulder Cr | 0.07 | 0.00 | 0.00 | 0.90 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.02 |
| Rapid R | 0.01 | 0.01 | 0.00 | 0.97 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Slate Cr | 0.15 | 0.01 | 0.00 | 0.72 | 0.00 | 0.00 | 0.01 | 0.01 | 0.03 | 0.07 |
| Whitebird Cr | 0.06 | 0.00 | 0.00 | 0.88 | 0.00 | 0.00 | 0.00 | 0.01 | 0.01 | 0.03 |
| Colt Cr | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Storm Cr | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Crooked F Lochsa R | 0.00 | 0.00 | 0.00 | 0.00 | 0.99 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Lake Cr | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Fish Cr | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Canyon Cr | 0.00 | 0.00 | 0.00 | 0.00 | 0.98 | 0.02 | 0.00 | 0.00 | 0.00 | 0.00 |
| Selway R | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Little Clearwater R | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Whitecap Cr | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Bear Cr | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |

| | Assigned Reporting Group | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **Population of Origin** | **UPSALM** | **MFSALM** | **SFSALM** | **LOSALM** | **UPCLWR** | **SFCLWR** | **LOCLWR** | **IMNAHA** | **GRROND** | **LSNAKE** |
| NF Moose Cr | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Three Links Cr | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Gedney Cr | 0.00 | 0.00 | 0.00 | 0.00 | 0.99 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| O'Hara Cr | 0.00 | 0.00 | 0.00 | 0.00 | 0.92 | 0.07 | 0.01 | 0.00 | 0.00 | 0.00 |
| Clear Cr | 0.00 | 0.00 | 0.00 | 0.00 | 0.02 | 0.98 | 0.01 | 0.00 | 0.00 | 0.00 |
| Crooked R | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.99 | 0.00 | 0.00 | 0.00 | 0.00 |
| Tenmile Cr | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| John's Cr | 0.00 | 0.00 | 0.00 | 0.00 | 0.07 | 0.89 | 0.03 | 0.00 | 0.00 | 0.00 |
| WF Potlatch R | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.98 | 0.00 | 0.01 | 0.01 |
| EF Potlatch R | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.99 | 0.00 | 0.00 | 0.00 |
| Big Bear Cr | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.92 | 0.00 | 0.01 | 0.06 |
| Little Bear Cr | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.97 | 0.00 | 0.00 | 0.01 |
| Big Sheep Cr | 0.01 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | 0.00 | 0.95 | 0.02 | 0.00 |
| Camp Cr | 0.03 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | 0.00 | 0.93 | 0.02 | 0.01 |
| Cow Cr | 0.07 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | 0.01 | 0.79 | 0.08 | 0.03 |
| Lightning Cr | 0.02 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | 0.00 | 0.91 | 0.04 | 0.01 |
| Joseph Cr | 0.01 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | 0.01 | 0.01 | 0.77 | 0.19 |
| Crooked Cr | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.90 | 0.08 |
| Elk Cr | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 |
| Little Minam R | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.97 | 0.02 |
| Lostine R | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | 0.97 | 0.02 |
| Menatchee Cr | 0.02 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.87 | 0.10 |
| Wenaha R | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.93 | 0.05 |
| Captain John Cr | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | 0.94 | 0.04 |
| George Cr | 0.06 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | 0.03 | 0.00 | 0.05 | 0.85 |
| Asotin Cr | 0.03 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | 0.04 | 0.00 | 0.03 | 0.88 |
| Alpowa Cr | 0.02 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | 0.01 | 0.00 | 0.05 | 0.91 |
| Tucannon R | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | 0.01 | 0.00 | 0.05 | 0.92 |

Table 12. Steelhead results from self-assignment tests performed in gsi_sim (Anderson et al. 2008, Anderson 2010). For each baseline population represented in baseline v2.0, each individual was sequentially removed from the baseline and then assigned back to the baseline. Rows represent population where individual originated. Columns represent reporting groups that individuals assigned. Results are using exclusively individuals that assigned to a reporting group with ≥80% probability. For example, n = 108 individuals represent the Sawtooth Weir population. Of the 108 individuals in the baseline, 48 (44%) assigned back to a reporting group with ≥80% probability during self-assignment tests. Of the 48 that assigned, 47 (98%) assigned to the correct UPSALM reporting group. Shaded boxes represent the correct reporting group of origin for each population.

| Population | *n* | Number Assigned (Proportion) | UPSALM | MFSALM | SFSALM | LOSALM | UPCLWR | SFCLWR | LOCLWR | IMNAHA | GRROND | LSNAKE |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Sawtooth Weir | 108 | 48 (0.44) | 0.98 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.02 | 0.00 | 0.00 |
| Valley Cr | 45 | 20 (0.44) | 0.80 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.05 | 0.15 | 0.00 |
| WF Yankee F Salmon | 117 | 61 (0.52) | 0.95 | 0.02 | 0.00 | 0.03 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Morgan Cr | 37 | 30 (0.81) | 0.93 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.03 | 0.03 | 0.00 |
| Pahsimeroi Weir | 99 | 54 (0.55) | 0.89 | 0.02 | 0.00 | 0.04 | 0.00 | 0.00 | 0.02 | 0.04 | 0.00 | 0.00 |
| Hayden Cr | 90 | 56 (0.62) | 0.95 | 0.04 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.02 | 0.00 |
| NF Salmon R | 102 | 32 (0.31) | 0.75 | 0.00 | 0.00 | 0.19 | 0.03 | 0.00 | 0.00 | 0.03 | 0.00 | 0.00 |
| Marsh Cr | 59 | 56 (0.95) | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Sulphur Cr | 46 | 44 (0.96) | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Rapid R (MF) | 45 | 44 (0.98) | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Pistol Cr | 23 | 22 (0.96) | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Camas Cr | 57 | 52 (0.91) | 0.02 | 0.98 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Loon Cr | 84 | 74 (0.88) | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Big Cr (upper) | 46 | 35 (0.76) | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Big Cr (lower) | 48 | 42 (0.88) | 0.00 | 0.95 | 0.00 | 0.00 | 0.02 | 0.00 | 0.00 | 0.00 | 0.02 | 0.00 |
| Chamberlain Cr | 47 | 28 (0.60) | 0.04 | 0.89 | 0.00 | 0.04 | 0.00 | 0.00 | 0.00 | 0.00 | 0.04 | 0.00 |
| Bargamin Cr | 32 | 19 (0.59) | 0.21 | 0.79 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| EF SF Salmon R | 47 | 40 (0.85) | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Secesh R | 45 | 39 (0.87) | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Lick Cr | 39 | 31 (0.79) | 0.03 | 0.00 | 0.97 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Stolle Meadows | 45 | 45 (1.00) | 0.02 | 0.00 | 0.96 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.02 | 0.00 |
| Boulder Cr | 47 | 21 (0.45) | 0.10 | 0.00 | 0.05 | 0.67 | 0.05 | 0.10 | 0.05 | 0.00 | 0.00 | 0.00 |
| Rapid R | 101 | 63 (0.62) | 0.17 | 0.08 | 0.06 | 0.65 | 0.00 | 0.00 | 0.00 | 0.02 | 0.02 | 0.00 |
| Slate Cr | 47 | 17 (0.36) | 0.18 | 0.00 | 0.00 | 0.82 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Whitebird Cr | 62 | 22 (0.35) | 0.09 | 0.00 | 0.00 | 0.68 | 0.00 | 0.00 | 0.00 | 0.09 | 0.05 | 0.09 |
| Colt Cr | 38 | 38 (1.00) | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Storm Cr | 38 | 36 (0.95) | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Crooked F Lochsa R | 44 | 39 (0.89) | 0.00 | 0.00 | 0.00 | 0.00 | 0.97 | 0.03 | 0.00 | 0.00 | 0.00 | 0.00 |
| Lake Cr | 47 | 46 (0.98) | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Fish Cr | 100 | 91 (0.91) | 0.00 | 0.00 | 0.00 | 0.01 | 0.98 | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 |
| Canyon Cr | 47 | 33 (0.70) | 0.00 | 0.00 | 0.00 | 0.00 | 0.97 | 0.03 | 0.00 | 0.00 | 0.00 | 0.00 |
| Selway R | 78 | 76 (0.97) | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Little Clearwater R | 59 | 57 (0.97) | 0.00 | 0.00 | 0.00 | 0.00 | 0.98 | 0.00 | 0.02 | 0.00 | 0.00 | 0.00 |
| Whitecap Cr | 76 | 76 (1.00) | 0.00 | 0.00 | 0.00 | 0.00 | 0.99 | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 |
| Bear Cr | 36 | 33 (0.92) | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |

| Population | *n* | Number Assigned (Proportion) | UPSALM | MFSALM | SFSALM | LOSALM | UPCLWR | SFCLWR | LOCLWR | IMNAHA | GRROND | LSNAKE |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NF Moose Cr | 94 | 84 (0.89) | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Three Links Cr | 47 | 45 (0.96) | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Gedney Cr | 45 | 42 (0.93) | 0.00 | 0.00 | 0.00 | 0.00 | 0.95 | 0.02 | 0.02 | 0.00 | 0.00 | 0.00 |
| O'Hara Cr | 47 | 32 (0.68) | 0.00 | 0.00 | 0.00 | 0.00 | 0.88 | 0.09 | 0.03 | 0.00 | 0.00 | 0.00 |
| Clear Cr | 45 | 32 (0.71) | 0.00 | 0.00 | 0.00 | 0.00 | 0.16 | 0.84 | 0.00 | 0.00 | 0.00 | 0.00 |
| Crooked R | 109 | 87 (0.80) | 0.01 | 0.00 | 0.00 | 0.00 | 0.07 | 0.92 | 0.00 | 0.00 | 0.00 | 0.00 |
| Tenmile Cr | 47 | 15 (0.32) | 0.00 | 0.00 | 0.00 | 0.00 | 0.13 | 0.87 | 0.00 | 0.00 | 0.00 | 0.00 |
| John's Cr | 40 | 23 (0.58) | 0.00 | 0.00 | 0.00 | 0.00 | 0.17 | 0.83 | 0.00 | 0.00 | 0.00 | 0.00 |
| WF Potlatch R | 85 | 52 (0.61) | 0.00 | 0.00 | 0.00 | 0.02 | 0.00 | 0.00 | 0.90 | 0.02 | 0.04 | 0.02 |
| EF Potlatch R | 160 | 105 (0.66) | 0.00 | 0.00 | 0.01 | 0.00 | 0.06 | 0.01 | 0.90 | 0.00 | 0.01 | 0.01 |
| Big Bear Cr | 99 | 37 (0.37) | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.03 | 0.84 | 0.03 | 0.05 | 0.05 |
| Little Bear Cr | 151 | 88 (0.58) | 0.01 | 0.01 | 0.00 | 0.00 | 0.00 | 0.02 | 0.86 | 0.00 | 0.03 | 0.06 |
| Big Sheep Cr | 69 | 41 (0.59) | 0.02 | 0.00 | 0.00 | 0.02 | 0.00 | 0.00 | 0.00 | 0.93 | 0.00 | 0.02 |
| Camp Cr | 24 | 13 (0.54) | 0.00 | 0.00 | 0.08 | 0.00 | 0.00 | 0.00 | 0.00 | 0.92 | 0.00 | 0.00 |
| Cow Cr | 44 | 19 (0.43) | 0.16 | 0.05 | 0.00 | 0.00 | 0.00 | 0.00 | 0.05 | 0.63 | 0.11 | 0.00 |
| Lightning Cr | 39 | 17 (0.44) | 0.06 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.94 | 0.00 | 0.00 |
| Joseph Cr | 60 | 22 (0.37) | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.05 | 0.95 | 0.00 |
| Crooked Cr | 97 | 50 (0.52) | 0.04 | 0.02 | 0.00 | 0.00 | 0.00 | 0.00 | 0.02 | 0.08 | 0.76 | 0.08 |
| Elk Cr | 45 | 32 (0.71) | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.03 | 0.00 | 0.97 | 0.00 |
| Little Minam R | 48 | 26 (0.54) | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.12 | 0.00 | 0.81 | 0.08 |
| Lostine R | 45 | 32 (0.71) | 0.00 | 0.00 | 0.03 | 0.00 | 0.00 | 0.00 | 0.03 | 0.00 | 0.94 | 0.00 |
| Menatchee Cr | 73 | 30 (0.41) | 0.03 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.03 | 0.80 | 0.13 |
| Wenaha R | 94 | 37 (0.39) | 0.03 | 0.00 | 0.00 | 0.03 | 0.00 | 0.00 | 0.00 | 0.00 | 0.95 | 0.00 |
| Captain John Cr | 56 | 32 (0.57) | 0.00 | 0.00 | 0.00 | 0.03 | 0.00 | 0.00 | 0.03 | 0.00 | 0.88 | 0.06 |
| George Cr | 96 | 18 (0.19) | 0.22 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.17 | 0.06 | 0.17 | 0.39 |
| Asotin Cr | 99 | 23 (0.23) | 0.13 | 0.00 | 0.00 | 0.04 | 0.00 | 0.00 | 0.04 | 0.09 | 0.17 | 0.52 |
| Alpowa Cr | 98 | 28 (0.29) | 0.14 | 0.00 | 0.04 | 0.07 | 0.00 | 0.11 | 0.04 | 0.00 | 0.18 | 0.43 |
| Tucannon R | 108 | 35 (0.32) | 0.09 | 0.06 | 0.00 | 0.09 | 0.00 | 0.00 | 0.14 | 0.09 | 0.14 | 0.40 |

Table 13. Steelhead results from self-assignment tests performed in gsi_sim (Anderson et al. 2008, Anderson 2010) summarized by reporting group.

| Reporting Group | *n* | Number Assigned >80% Probability | Number Assigned to Correct Reporting Group | Percent Assigned >80% Probability | Percent Assigned to Correct Reporting Group |
|---|---|---|---|---|---|
| UPSALM | 598 | 301 | 274 | 50% | 91% |
| MFSALM | 487 | 416 | 406 | 85% | 98% |
| SFSALM | 176 | 155 | 152 | 88% | 98% |
| LOSALM | 257 | 123 | 84 | 48% | 68% |
| UPCLWR | 796 | 728 | 716 | 91% | 98% |
| SFCLWR | 241 | 157 | 139 | 65% | 89% |
| LOCLWR | 495 | 282 | 249 | 57% | 88% |
| IMNAHA | 176 | 90 | 78 | 51% | 87% |
| GRROND | 518 | 261 | 228 | 50% | 87% |
| LSNAKE | 401 | 104 | 45 | 26% | 43% |
| Total: | 4,145 | 2,617 | 2,371 | 63% | 91% |

Table 14. Steelhead mixture modeling results performed in gsi_sim (Anderson et al. 2008, Anderson 2010) for mixtures of known origin fish randomly sampled and removed from the baseline. Results are averaged across three iterations. Expected allocation reflects that mixture contained n = 30 fish from each reporting group. Observed mean allocation, mean allocation +/-, mean lower 95% CI, and mean upper 95% CI are results from gsi_sim.

| | | Observed | | | |
|---|---|---|---|---|---|
| Reporting Group | Expected Allocation | Mean Allocation | Mean Allocation +/- | Mean Lower 95% CI | Mean Upper 95% CI |
| UPSALM | 10.0% | 13.4% | 3.4% | 9.2% | 19.8% |
| MFSALM | 10.0% | 10.2% | 0.2% | 6.7% | 14.0% |
| SFSALM | 10.0% | 8.6% | -1.4% | 5.6% | 12.2% |
| LOSALM | 10.0% | 8.9% | -1.1% | 4.4% | 12.7% |
| UPCLWR | 10.0% | 10.2% | 0.2% | 6.6% | 13.7% |
| SFCLWR | 10.0% | 8.8% | -1.2% | 5.7% | 12.7% |
| LOCLWR | 10.0% | 10.9% | 0.9% | 7.1% | 16.0% |
| IMNAHA | 10.0% | 5.4% | -4.6% | 2.0% | 8.9% |
| GRROND | 10.0% | 9.0% | -1.0% | 3.8% | 13.7% |
| LSNAKE | 10.0% | 14.5% | 4.5% | 9.6% | 22.3% |

Table 15. Evaluation of location of PIT-tag detection and genetic individual assignment for natural origin steelhead that were PIT-tagged at the Lower Granite Dam adult trapping facility (Integrated Status and Effectiveness Monitoring Program, ISEMP; BPA Project Number 2003-017-00) and were later detected at a PIT-tag array within the Snake River basin. Individuals detected at PIT-tag arrays were screened using the full 192 SNP panel and reporting group of origin was estimated using gsi_sim (Anderson et al. 2008, Anderson 2010). Row represents location of PIT-tag detection. Columns represent reporting groups that individuals assigned. Results are using exclusively individuals that assigned to a reporting group with ≥80% probability. For example, seven fish that were detected at the Valley Creek array in 2010 were analyzed via individual assignment; of those four (57%) assigned to a reporting group with ≥80% probability. Of the four, all four (100%) assigned to the UPSALM reporting group. In total, 82% of the individuals that assigned with ≥80% probability had concordant results between location of PIT-tag detection and genetic assignment.

| | | | | Reporting Unit | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PIT-Tag Array** | **# Analyzed** | **# Assigned (Proportion)** | **Array Concordance Rate** | **UPSALM** | **MFSALM** | **SFSALM** | **LOSALM** | **UPCLWR** | **SFCLWR** | **LOCLWR** | **IMNAHA** | **GRROND** | **LSNAKE** |
| Valley Cr '10 | 7 | 4 (.57) | 0.94 | 4 | | | | | | | | | |
| Valley Cr '11 | 23 | 13 (.57) | | 12 | | | | | | | | 1 | |
| Lemhi R '10 | 27 | 13 (.48) | 0.86 | 11 | | | 1 | | | 1 | | | |
| Lemhi R '11 | 33 | 24 (.73) | | 21 | 1 | | | | | | 1 | | 1 |
| Big Cr '10 | 19 | 16 (.84) | 0.94 | | 16 | | | | | | | | |
| Big Cr '11 | 56 | 46 (.82) | | 1 | 42 | | 2 | 1 | | | | | |
| SF Salmon R '10 | 81 | 54 (.67) | 0.89 | 1 | 3 | 49 | | | | | | | 1 |
| SF Salmon R '11 | 280 | 191 (.68) | | | 12 | 168 | 6 | | | 1 | 4 | | |
| Imnaha R '11 | 330 | 105 (.32) | 0.60 | 12 | 6 | 2 | 3 | | 1 | 2 | 63 | 11 | 5 |
| Joseph Cr '11 | 164 | 50 (.30) | 0.70 | 3 | 2 | | | | | 1 | 2 | 35 | 7 |
| Total | 1020 | 516 (.51) | 0.82 | | | | | | | | | | |

Table 16. Chinook salmon results from 100% simulations performed in ONCOR (Kalinowski et al. 2007). For each population represented in Chinook v2.0, 200 mixtures were generated each containing 100% of individuals simulated from that population; simulated mixtures were then allocated back to the baseline. Rows represent population where simulated individuals originated. Columns represent reporting groups where simulated mixtures assigned. Shaded boxes represent the correct reporting group of origin for each population.

| | Assigned Reporting Group | | | | | | |
|---|---|---|---|---|---|---|---|
| **Population of Origin** | **UPSALM** | **MFSALM** | **CHMBLN** | **SFSALM** | **HELLSC** | **TUCANO** | **FALL** |
| Sawtooth Weir | 0.98 | 0.00 | 0.00 | 0.02 | 0.00 | 0.00 | 0.00 |
| Valley Cr | 0.99 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| WF Yankee F Salmon | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| EF Salmon R | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Pahsimeroi R | 0.99 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Hayden Cr | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Lemhi (upper) | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Lemhi (lower) | 0.98 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 |
| Capehorn Cr | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Marsh Cr | 0.00 | 0.97 | 0.00 | 0.02 | 0.00 | 0.00 | 0.00 |
| Elk Cr | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Bear Valley Cr | 0.00 | 0.99 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Sulphur Cr | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Camas Cr | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Big Cr | 0.00 | 0.99 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Chamberlain Cr (post-2008) | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Chamberlain Cr (pre-2008) | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Lake Cr, Summit Cr | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 |
| Secesh R | 0.00 | 0.00 | 0.00 | 0.99 | 0.00 | 0.00 | 0.00 |
| Johnson Cr | 0.00 | 0.01 | 0.00 | 0.98 | 0.00 | 0.00 | 0.00 |
| SF Salmon R | 0.02 | 0.01 | 0.00 | 0.96 | 0.02 | 0.00 | 0.00 |
| Rapid R | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 |
| Crooked F Lochsa R | 0.01 | 0.00 | 0.00 | 0.00 | 0.98 | 0.00 | 0.00 |
| Powell Weir | 0.01 | 0.02 | 0.00 | 0.02 | 0.95 | 0.00 | 0.00 |
| Red R | 0.00 | 0.00 | 0.00 | 0.00 | 0.99 | 0.00 | 0.00 |
| Crooked R Weir | 0.01 | 0.00 | 0.00 | 0.00 | 0.98 | 0.00 | 0.00 |
| Newsome Cr | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 |
| Lolo Cr | 0.01 | 0.00 | 0.00 | 0.01 | 0.99 | 0.00 | 0.00 |
| Imnaha R | 0.02 | 0.00 | 0.00 | 0.03 | 0.95 | 0.00 | 0.00 |
| Imnaha R (1998) | 0.01 | 0.00 | 0.00 | 0.01 | 0.98 | 0.00 | 0.00 |
| Upper Grande Ronde | 0.01 | 0.00 | 0.00 | 0.01 | 0.98 | 0.00 | 0.00 |
| Catherine Cr | 0.00 | 0.00 | 0.00 | 0.00 | 0.99 | 0.00 | 0.00 |
| Lostine R | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 |
| Minam R | 0.00 | 0.00 | 0.00 | 0.00 | 0.99 | 0.00 | 0.00 |
| Wenaha R | 0.00 | 0.00 | 0.00 | 0.00 | 0.99 | 0.00 | 0.00 |
| Tucannon R | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 |
| Clearwater | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 |
| Nez Perce Tribal Hatchery | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 |
| Lyons Ferry | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 |

Table 17. Chinook salmon results from self-assignment tests performed in gsi_sim (Anderson et al. 2008, Anderson 2010). For each baseline population represented in baseline v2.0, each individual was sequentially removed from the baseline and then assigned back to the baseline. Rows represent population where individual originated. Columns represent reporting groups that individuals assigned. Results are using exclusively individuals that assigned to a reporting group with ≥80% probability. For example, n = 92 individuals represent the Sawtooth Weir population. Of the 92 individuals in the baseline, 53 (58%) assigned back to a reporting group with ≥80% probability during self-assignment tests. Of the 53, 50 (94%) assigned to the UPSALM reporting group. Shaded boxes represent the correct reporting group of origin for each population.

| | | | Assigned Reporting Group | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| **Population of Origin** | **n** | **Number Assigned (Proportion)** | **UPSALM** | **MFSALM** | **CHMBLN** | **SFSALM** | **HELLSC** | **TUCANO** | **FALL** |
| Sawtooth Weir | 92 | 53 (0.58) | 0.94 | 0.02 | 0.00 | 0.02 | 0.02 | 0.00 | 0.00 |
| Valley Cr | 59 | 46 (0.78) | 0.93 | 0.00 | 0.02 | 0.00 | 0.04 | 0.00 | 0.00 |
| WF Yankee F Salmon | 75 | 62 (0.83) | 0.98 | 0.00 | 0.00 | 0.00 | 0.02 | 0.00 | 0.00 |
| EF Salmon R | 187 | 146 (0.78) | 0.95 | 0.02 | 0.00 | 0.01 | 0.03 | 0.00 | 0.00 |
| Pahsimeroi R | 97 | 79 (0.81) | 0.97 | 0.00 | 0.00 | 0.01 | 0.01 | 0.00 | 0.00 |
| Hayden Cr | 80 | 70 (0.88) | 0.91 | 0.00 | 0.00 | 0.00 | 0.09 | 0.00 | 0.00 |
| Lemhi (upper) | 96 | 75 (0.78) | 0.92 | 0.03 | 0.00 | 0.01 | 0.04 | 0.00 | 0.00 |
| Lemhi (lower) | 90 | 66 (0.73) | 0.91 | 0.00 | 0.00 | 0.00 | 0.09 | 0.00 | 0.00 |
| Capehorn Cr | 113 | 95 (0.84) | 0.00 | 0.98 | 0.00 | 0.01 | 0.01 | 0.00 | 0.00 |
| Marsh Cr | 67 | 50 (0.75) | 0.04 | 0.92 | 0.00 | 0.02 | 0.02 | 0.00 | 0.00 |
| Elk Cr | 91 | 70 (0.77) | 0.00 | 0.94 | 0.01 | 0.03 | 0.01 | 0.00 | 0.00 |
| Bear Valley Cr | 85 | 65 (0.76) | 0.00 | 0.95 | 0.00 | 0.03 | 0.02 | 0.00 | 0.00 |
| Sulphur Cr | 37 | 35 (0.95) | 0.00 | 0.94 | 0.00 | 0.03 | 0.03 | 0.00 | 0.00 |
| Camas Cr | 61 | 55 (0.90) | 0.02 | 0.95 | 0.00 | 0.02 | 0.02 | 0.00 | 0.00 |
| Big Cr | 95 | 84 (0.88) | 0.04 | 0.88 | 0.01 | 0.01 | 0.06 | 0.00 | 0.00 |
| Chamberlain Cr (post-'08) | 56 | 52 (0.93) | 0.00 | 0.00 | 0.98 | 0.00 | 0.02 | 0.00 | 0.00 |
| Chamberlain Cr (pre-'08) | 70 | 59 (0.84) | 0.00 | 0.00 | 0.92 | 0.02 | 0.07 | 0.00 | 0.00 |
| Lake Cr, Summit Cr | 78 | 64 (0.82) | 0.00 | 0.03 | 0.00 | 0.97 | 0.00 | 0.00 | 0.00 |
| Secesh R | 135 | 102 (0.76) | 0.00 | 0.03 | 0.00 | 0.89 | 0.08 | 0.00 | 0.00 |
| Johnson Cr | 92 | 58 (0.63) | 0.00 | 0.05 | 0.00 | 0.84 | 0.10 | 0.00 | 0.00 |
| SF Salmon R | 143 | 63 (0.44) | 0.16 | 0.10 | 0.02 | 0.59 | 0.14 | 0.00 | 0.00 |
| Rapid R | 91 | 80 (0.88) | 0.04 | 0.00 | 0.00 | 0.01 | 0.95 | 0.00 | 0.00 |
| Crooked F Lochsa R | 29 | 23 (0.79) | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 |
| Powell Weir | 32 | 23 (0.72) | 0.04 | 0.04 | 0.00 | 0.00 | 0.91 | 0.00 | 0.00 |
| Red R | 73 | 60 (0.82) | 0.03 | 0.00 | 0.00 | 0.02 | 0.95 | 0.00 | 0.00 |
| Crooked R Weir | 67 | 59 (0.88) | 0.02 | 0.02 | 0.00 | 0.00 | 0.95 | 0.02 | 0.00 |
| Newsome Cr | 82 | 70 (0.85) | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 |
| Lolo Cr | 89 | 71 (0.80) | 0.04 | 0.00 | 0.00 | 0.00 | 0.96 | 0.00 | 0.00 |
| Imnaha R | 46 | 30 (0.65) | 0.03 | 0.00 | 0.00 | 0.00 | 0.97 | 0.00 | 0.00 |
| Imnaha R ('98) | 91 | 68 (0.75) | 0.03 | 0.00 | 0.01 | 0.01 | 0.94 | 0.00 | 0.00 |
| upper Grande Ronde | 46 | 36 (0.78) | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 |
| Catherine Cr | 94 | 75 (0.80) | 0.03 | 0.00 | 0.00 | 0.01 | 0.96 | 0.00 | 0.00 |
| Lostine R | 177 | 156 (0.88) | 0.03 | 0.00 | 0.00 | 0.00 | 0.97 | 0.01 | 0.00 |
| Minam R | 81 | 69 (0.85) | 0.00 | 0.00 | 0.00 | 0.00 | 0.99 | 0.01 | 0.00 |
| Wenaha R | 88 | 77 (0.88) | 0.00 | 0.00 | 0.00 | 0.00 | 0.95 | 0.05 | 0.00 |
| Tucannon R | 81 | 74 (0.91) | 0.00 | 0.01 | 0.00 | 0.00 | 0.12 | 0.85 | 0.01 |
| Clearwater | 152 | 152 (1.00) | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 |
| Nez Perce Tribal Hatchery | 85 | 85 (1.00) | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 |
| Lyons Ferry | 90 | 90 (1.00) | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 1.00 |

Table 18. Chinook salmon results from self-assignment tests performed in gsi_sim (Anderson et al. 2008, Anderson 2010) summarized by reporting group.

| Reporting Group | n | Number Assigned >80% Probability | Number Assigned to Correct Reporting Group | Percent Assigned >80% Probability | Percent Assigned to Correct Reporting Group |
|---|---|---|---|---|---|
| UPSALM | 776 | 597 | 562 | 77% | 94% |
| MFSALM | 549 | 454 | 426 | 83% | 94% |
| CHMBLN | 126 | 111 | 105 | 88% | 95% |
| SFSALM | 448 | 287 | 239 | 64% | 83% |
| HELLSC | 1086 | 897 | 864 | 83% | 96% |
| TUCANO | 81 | 74 | 63 | 91% | 85% |
| FALL | 327 | 327 | 327 | 100% | 100% |
| Total: | 3,393 | 2,747 | 2,586 | 81% | 94% |

Table 19. Chinook salmon mixture modeling results performed in gsi_sim (Anderson et al. 2008, Anderson 2010) for mixtures of known origin fish randomly sampled and removed from the baseline. Results are averaged across three iterations. Expected allocation reflects that mixture contained n = 30 fish from each reporting group. Observed mean allocation, mean allocation +/-, mean lower 95% CI, and mean upper 95% CI are results from gsi_sim.

| | | Observed | | | |
|---|---|---|---|---|---|
| Reporting Group | Expected Allocation | Mean Allocation | Mean Allocation +/- | Mean Lower 95% CI | Mean Upper 95% CI |
| UPSALM | 14.3% | 14.2% | -0.1% | 9.3% | 20.0% |
| MFSALM | 14.3% | 14.0% | -0.3% | 8.8% | 19.2% |
| CHMBLN | 14.3% | 14.0% | -0.3% | 9.5% | 19.1% |
| SFSALM | 14.3% | 13.3% | -1.0% | 8.5% | 20.0% |
| HELLSC | 14.3% | 17.6% | 3.3% | 12.0% | 23.4% |
| TUCANO | 14.3% | 12.7% | -1.6% | 8.5% | 17.7% |
| FALL | 14.3% | 14.3% | 0.0% | 9.8% | 19.2% |

Table 20. Evaluation of location of PIT-tag detection and genetic individual assignment for natural origin Chinook salmon that were PIT-tagged at the Lower Granite Dam adult trapping facility (Integrated Status and Effectiveness Monitoring Program, ISEMP; BPA Project Number 2003-017-00) and were later detected at a PIT-tag array within the Snake River basin. Individuals detected at PIT-tag arrays were screened using the full 192 SNP panel and reporting group of origin was estimated using gsi_sim (Anderson et al. 2008, Anderson 2010). Row represents location of PIT-tag detection. Columns represent reporting groups that individuals assigned. Results are using exclusively individuals that assigned to a reporting group with ≥80% probability. For example, 27 fish that were detected at the Sawtooth Hatchery trap in 2010 were analyzed via individual assignment; of those 18 (67%) assigned to a reporting group with ≥80% probability. Of the 18, all 18 (100%) assigned to the UPSALM reporting group. In total, 80% of the individuals that assigned with ≥80% probability had concordant results between location of PIT-tag detection and genetic assignment.

| SY2010 & SY2011 | | | | Assigned Reporting Group | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **Detection Site** | **# Analyzed** | **# Assigned (Proportion)** | **Proportion Concordant Assignment** | **UPSALM** | **MFSALM** | **CHMBLN** | **SFSALM** | **HELLSC** | **TUCANO** | **FALL** |
| Sawtooth Trap '10 | 27 | 18 (.67) | 1.00 | 18 | | | | | | |
| Sawtooth Trap '11 | 86 | 53 (.62) | 0.89 | 47 | 2 | | 1 | 3 | | |
| Valley Cr '11 | 44 | 32 (.73) | 0.94 | 30 | 1 | | | 1 | | |
| Pahsimeroi Trap '10 | 7 | 6 (.86) | 1.00 | 6 | | | | | | |
| Hayden Cr '11 | 12 | 6 (.50) | 0.67 | 4 | | | 1 | 1 | | |
| Lemhi R (Bjornn Weir) '11 | 16 | 10 (.63) | 0.70 | 7 | | | 1 | 2 | | |
| Lower Lemhi '11 | 4 | 4 (1.00) | 0.75 | 3 | | | | 1 | | |
| Big Creek '11 | 34 | 23 (.68) | 0.39 | 6 | 9 | 1 | | 7 | | |
| Secesh River (Zena) '10 | 2 | 1 (.50) | 1.00 | | | | 1 | | | |
| Secesh River (Zena) '11 | 85 | 65 (.76) | 0.89 | 3 | 2 | | 58 | 1 | 1 | |
| EFSF Salmon '10 | 3 | 2 (.67) | 1.00 | | | | 2 | | | |
| EFSF Salmon '11 | 67 | 44 (.66) | 0.70 | 1 | 1 | | 31 | 11 | | |
| SF Salmon Trap '10 | 14 | 7 (.50) | 0.86 | | | | 6 | 1 | | |
| SF Salmon (Krassel) '10 | 4 | 2 (.50) | 0.50 | | | | 1 | 1 | | |
| SF Salmon (Krassel) '11 | 298 | 136 (.46) | 0.54 | 13 | 18 | | 74 | 31 | | |
| SF Salmon (Guard Station) '10 | 3 | 3 (1.00) | 0.33 | 1 | 1 | | 1 | | | |
| SF Salmon (Guard Station) '11 | 23 | 17 (.74) | 0.82 | | | | 14 | 2 | | 1 |
| Big Sheep Creek '11 | 35 | 24 (.69) | 0.88 | 1 | | | 1 | 21 | 1 | |
| Imnaha Weir '10 | 19 | 15 (.79) | 1.00 | | | | | 15 | | |
| Imnaha (IR1) '11 | 22 | 16 (.73) | 1.00 | | | | | 16 | | |
| Imnaha (IR3) '11 | 193 | 134 (.69) | 0.93 | 3 | 2 | 1 | 2 | 125 | | 1 |
| Lookingglass Hatchery '11 | 36 | 31 (.86) | 0.94 | 1 | | | | 29 | 1 | |
| Total | 1034 | 649 (.63) | 0.80 | | | | | | | |

Table 21. Mixture modeling results for natural origin adult steelhead mixtures from the Lower Granite Dam adult trap, SY2009 through SY2011. Reporting groups within the Salmon River MPG and Clearwater MPG are grouped for each respective MPG. All results are shown as percentages.

| | Stock Composition | | | Coefficient of Variation | | | Lower 95% CI | | | Upper 95% CI | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Reporting Unit** | **SY2009** | **SY2010** | **SY2011** | **SY2009** | **SY2010** | **SY2011** | **SY2009** | **SY2010** | **SY2011** | **SY2009** | **SY2010** | **SY2011** |
| UPSALM | 12.1 | 18.2 | 15.4 | 11.1 | 6.3 | 6.6 | 9.8 | 16.4 | 13.8 | 15.2 | 21.2 | 17.8 |
| MFSALM | 8.1 | 10.6 | 8.4 | 11.5 | 7.3 | 7.6 | 6.2 | 9.0 | 7.1 | 9.8 | 12.0 | 9.5 |
| SFSALM | 3.4 | 3.6 | 4.7 | 18.4 | 13.2 | 10.2 | 2.3 | 2.7 | 3.9 | 4.6 | 4.6 | 5.7 |
| LOSALM | 7.9 | 3.4 | 4.1 | 15.1 | 26.3 | 19.1 | 5.6 | 1.4 | 2.4 | 10.2 | 4.1 | 5.2 |
| **Salmon MPG** | **31.6** | **35.7** | **32.6** | **5.6** | **3.9** | **3.8** | **28.0** | **32.7** | **30.1** | **35.0** | **38.2** | **35.0** |
| UPCLWR | 10.9 | 6.7 | 9.3 | 9.7 | 9.4 | 7.1 | 8.7 | 5.4 | 8.0 | 12.8 | 7.8 | 10.6 |
| SFCLWR | 10.7 | 7.6 | 10.1 | 9.4 | 8.9 | 6.9 | 8.9 | 6.3 | 8.7 | 12.8 | 8.9 | 11.5 |
| LOCLWR | 5.7 | 3.9 | 3.9 | 18.3 | 18.0 | 16.9 | 3.8 | 2.5 | 2.6 | 7.8 | 5.1 | 5.0 |
| **Clearwater MPG** | **27.3** | **18.1** | **23.4** | **6.5** | **5.6** | **4.3** | **24.2** | **15.9** | **21.2** | **30.2** | **19.8** | **25.1** |
| IMNAHA | 5.9 | 6.9 | 5.3 | 16.6 | 11.6 | 13.3 | 3.7 | 5.2 | 3.8 | 7.2 | 8.2 | 6.4 |
| GRROND | 16.4 | 16.2 | 16.2 | 10.2 | 7.7 | 6.9 | 13.3 | 13.7 | 14.1 | 20.0 | 18.6 | 18.5 |
| LSNAKE | 18.9 | 23.1 | 22.5 | 9.6 | 6.0 | 5.8 | 15.9 | 21.2 | 20.5 | 23.2 | 26.9 | 25.8 |

Table 22. Number of individuals analyzed and number of individuals that assigned to each Snake River reporting group with ≥80% probability for natural origin adult (SY2009 – SY2011) and juvenile (MY2010 – MY2011) steelhead mixtures from the Lower Granite Dam adult and juvenile trapping facilities. Of the 8,587 natural origin steelhead analyzed, 4,181 (48.7%) assigned to a reporting group with ≥80% probability. Individuals assigning with <80% probability were considered unassigned. Biological data obtained from assigned individuals were used to examine life-history information for each reporting group.

| | Number Assigned | | | | |
|---|---|---|---|---|---|
| | Adults | | | Juveniles | |
| **Reporting Group** | **SY2009** | **SY2010** | **SY2011** | **MY2010** | **MY2011** |
| *Total Analyzed:* | *1057* | *1918* | *2264* | *1233* | *2115* |
| UPSALM | 61 | 171 | 172 | 104 | 181 |
| MFSALM | 76 | 179 | 164 | 63 | 89 |
| SFSALM | 35 | 62 | 93 | 26 | 48 |
| LOSALM | 29 | 24 | 39 | 16 | 32 |
| UPCLWR | 111 | 121 | 200 | 65 | 143 |
| SFCLWR | 76 | 99 | 160 | 95 | 140 |
| LOCLWR | 29 | 28 | 50 | 39 | 52 |
| IMNAHA | 31 | 58 | 58 | 36 | 60 |
| GRROND | 60 | 134 | 149 | 89 | 135 |
| LSNAKE | 29 | 81 | 67 | 45 | 77 |
| Total Assigned With ≥80% Probability: | 537 (50.8%) | 957 (49.9%) | 1152 (50.8%) | 578 (46.9%) | 957 (45.2%) |

Table 23. Estimated sex (frequency and proportion) for individuals assigning to a reporting group with ≥80% probability based on the Y-specific assay (*OmyY1_2SEXY*) for natural origin adult (SY2009 – SY2011) and juvenile (MY2010 – MY2011) steelhead mixtures from the Lower Granite Dam adult and juvenile trapping facilities.

| Reporting Group | SY / MY | # Females | # Males | # Unknown | % Females | % Males |
|---|---|---|---|---|---|---|
| UPSALM | SY2009 | 42 | 19 | 0 | 69% | 31% |
| | SY2010 | 102 | 61 | 8 | 63% | 37% |
| | SY2011 | 99 | 69 | 4 | 59% | 41% |
| | MY2010 | 61 | 39 | 4 | 61% | 39% |
| | MY2011 | 102 | 65 | 14 | 61% | 39% |
| MFSALM | SY2009 | 57 | 17 | 2 | 77% | 23% |
| | SY2010 | 130 | 44 | 5 | 75% | 25% |
| | SY2011 | 114 | 39 | 11 | 75% | 25% |
| | MY2010 | 39 | 19 | 5 | 67% | 33% |
| | MY2011 | 50 | 33 | 6 | 60% | 40% |
| SFSALM | SY2009 | 28 | 7 | 0 | 80% | 20% |
| | SY2010 | 37 | 23 | 2 | 62% | 38% |
| | SY2011 | 66 | 25 | 2 | 73% | 27% |
| | MY2010 | 14 | 9 | 3 | 61% | 39% |
| | MY2011 | 22 | 25 | 1 | 47% | 53% |
| LOSALM | SY2009 | 15 | 14 | 0 | 52% | 48% |
| | SY2010 | 15 | 9 | 0 | 63% | 38% |
| | SY2011 | 19 | 18 | 2 | 51% | 49% |
| | MY2010 | 10 | 6 | 0 | 63% | 38% |
| | MY2011 | 16 | 13 | 3 | 55% | 45% |
| UPCLWR | SY2009 | 81 | 27 | 3 | 75% | 25% |
| | SY2010 | 74 | 38 | 9 | 66% | 34% |
| | SY2011 | 151 | 41 | 8 | 79% | 21% |
| | MY2010 | 28 | 32 | 5 | 47% | 53% |
| | MY2011 | 71 | 62 | 10 | 53% | 47% |
| SFCLWR | SY2009 | 49 | 26 | 1 | 65% | 35% |
| | SY2010 | 58 | 39 | 2 | 60% | 40% |
| | SY2011 | 91 | 65 | 4 | 58% | 42% |
| | MY2010 | 49 | 43 | 3 | 53% | 47% |
| | MY2011 | 70 | 63 | 7 | 53% | 47% |
| LOCLWR | SY2009 | 23 | 5 | 1 | 82% | 18% |
| | SY2010 | 13 | 11 | 4 | 54% | 46% |
| | SY2011 | 31 | 18 | 1 | 63% | 37% |
| | MY2010 | 17 | 22 | 0 | 44% | 56% |
| | MY2011 | 27 | 22 | 3 | 55% | 45% |
| IMNAHA | SY2009 | 18 | 13 | 0 | 58% | 42% |
| | SY2010 | 35 | 21 | 2 | 63% | 38% |
| | SY2011 | 41 | 16 | 1 | 72% | 28% |
| | MY2010 | 19 | 15 | 2 | 56% | 44% |
| | MY2011 | 32 | 25 | 3 | 56% | 44% |
| GRROND | SY2009 | 39 | 21 | 0 | 65% | 35% |
| | SY2010 | 79 | 50 | 5 | 61% | 39% |
| | SY2011 | 101 | 43 | 5 | 70% | 30% |
| | MY2010 | 56 | 28 | 5 | 67% | 33% |
| | MY2011 | 73 | 55 | 7 | 57% | 43% |
| LSNAKE | SY2009 | 18 | 10 | 1 | 64% | 36% |
| | SY2010 | 37 | 41 | 3 | 47% | 53% |
| | SY2011 | 38 | 26 | 3 | 59% | 41% |
| | MY2010 | 24 | 20 | 1 | 55% | 45% |
| | MY2011 | 40 | 33 | 4 | 55% | 45% |

Table 24. Estimated scale age (frequency) for individuals assigning to a reporting group with ≥80% probability for natural origin adult (SY2009 – SY2011) steelhead mixtures from the Lower Granite Dam adult trapping facility.

| **SY2009** | **Total age and age class (frequency)** | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Reporting Group** | **3 1.1** | **4 1.2** | **4 2.1** | **5 2.2** | **5 3.1** | **6 2.3** | **6 3.2** | **6 4.1** | **7 3.3** | **7 4.2** | **7 5.1** | **Total** |
| UPSALM | 1 | 1 | 24 | 13 | 16 | - | 4 | - | - | 1 | - | 60 |
| MFSALM | - | - | 4 | 9 | 18 | 1 | 20 | 6 | 3 | 11 | - | 72 |
| SFSALM | - | - | - | 5 | 1 | 1 | 17 | - | 2 | 2 | - | 28 |
| LOSALM | - | - | 7 | 10 | 5 | 1 | 1 | 1 | - | 1 | - | 26 |
| UPCLWR | 1 | - | 4 | 40 | 9 | 5 | 37 | - | 3 | 1 | - | 100 |
| SFCLWR | - | - | 3 | 40 | 4 | 7 | 9 | - | 4 | - | - | 67 |
| LOCLWR | - | - | 4 | 11 | 3 | 1 | 4 | 1 | 1 | - | - | 25 |
| IMNAHA | - | - | 9 | 4 | 9 | - | 2 | 3 | - | - | - | 27 |
| GRROND | - | - | 19 | 15 | 13 | - | 6 | 1 | - | 1 | - | 55 |
| LSNAKE | - | - | 8 | 8 | 6 | 1 | 3 | - | - | - | - | 26 |
| Total | 2 | 1 | 82 | 155 | 84 | 17 | 103 | 12 | 13 | 17 | | 486 |

| **SY2010** | **Total age and age class (frequency)** | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Reporting Group** | **3 1.1** | **4 1.2** | **4 2.1** | **5 2.2** | **5 3.1** | **6 2.3** | **6 3.2** | **6 4.1** | **7 3.3** | **7 4.2** | **7 5.1** | **Total** |
| UPSALM | 2 | 3 | 72 | 29 | 30 | - | 14 | 2 | - | - | - | 152 |
| MFSALM | - | - | 15 | 11 | 53 | 1 | 40 | 23 | 5 | 11 | - | 159 |
| SFSALM | 1 | - | 2 | 3 | 10 | - | 19 | 2 | 4 | 8 | 2 | 51 |
| LOSALM | - | - | 7 | 5 | 5 | - | 6 | - | - | - | - | 23 |
| UPCLWR | 2 | 1 | 5 | 29 | 20 | 3 | 35 | 5 | 4 | 5 | - | 109 |
| SFCLWR | 2 | 2 | 8 | 41 | 11 | 7 | 12 | - | 1 | 2 | - | 86 |
| LOCLWR | 1 | 2 | 11 | 9 | 3 | - | 2 | - | - | - | - | 28 |
| IMNAHA | 2 | 1 | 16 | 7 | 22 | - | 5 | - | - | - | - | 53 |
| GRROND | 2 | 1 | 53 | 31 | 26 | - | 11 | 1 | - | 1 | - | 126 |
| LSNAKE | 2 | - | 38 | 19 | 12 | - | 5 | - | - | 1 | - | 77 |
| Total | 14 | 10 | 227 | 184 | 192 | 11 | 149 | 33 | 14 | 28 | 2 | 864 |

| **SY2011** | **Total age and age class (frequency)** | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Reporting Group** | **3 1.1** | **4 1.2** | **4 2.1** | **5 2.2** | **5 3.1** | **6 2.3** | **6 3.2** | **6 4.1** | **7 3.3** | **7 4.2** | **7 5.1** | **Total** |
| UPSALM | 5 | 10 | 49 | 60 | 10 | - | 18 | - | - | - | - | 172 |
| MFSALM | - | 2 | - | 36 | 7 | - | 84 | 2 | - | 11 | - | 164 |
| SFSALM | - | - | 1 | 20 | 1 | - | 52 | - | 1 | 3 | - | 93 |
| LOSALM | 1 | - | 3 | 17 | 5 | - | 9 | - | - | - | - | 39 |
| UPCLWR | 1 | 3 | 1 | 53 | 1 | 5 | 107 | 1 | - | 5 | - | 200 |
| SFCLWR | - | 4 | 4 | 100 | - | - | 29 | - | 1 | 2 | - | 160 |
| LOCLWR | 1 | 3 | 8 | 23 | 2 | - | 6 | - | - | 1 | - | 50 |
| IMNAHA | - | - | 15 | 22 | 6 | - | 9 | - | - | - | - | 58 |
| GRROND | 1 | 7 | 27 | 72 | 8 | - | 14 | 1 | - | - | - | 149 |
| LSNAKE | 2 | 2 | 19 | 26 | 6 | - | 1 | - | - | - | - | 67 |
| Total | 11 | 31 | 127 | 429 | 46 | 5 | 329 | 4 | 2 | 22 | | 1152 |

Table 25. Estimated scale age (proportion) for individuals assigning to a reporting group with ≥80% probability for natural origin adult (SY2009 – SY2011) steelhead mixtures from the Lower Granite Dam adult trapping facility.

| SY2009 | Total age and age class (frequency) | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | 3 | 4 | 4 | 5 | 5 | 6 | 6 | 6 | 7 | 7 | 7 |
| Reporting Group | 1.1 | 1.2 | 2.1 | 2.2 | 3.1 | 2.3 | 3.2 | 4.1 | 3.3 | 4.2 | 5.1 |
| UPSALM | 0.02 | 0.02 | 0.40 | 0.22 | 0.27 | - | 0.07 | - | - | 0.02 | - |
| MFSALM | - | - | 0.06 | 0.13 | 0.25 | 0.01 | 0.28 | 0.08 | 0.04 | 0.15 | - |
| SFSALM | - | - | - | 0.18 | 0.04 | 0.04 | 0.61 | - | 0.07 | 0.07 | - |
| LOSALM | - | - | 0.27 | 0.38 | 0.19 | 0.04 | 0.04 | 0.04 | - | 0.04 | - |
| UPCLWR | 0.01 | - | 0.04 | 0.40 | 0.09 | 0.05 | 0.37 | - | 0.03 | 0.01 | - |
| SFCLWR | - | - | 0.04 | 0.60 | 0.06 | 0.10 | 0.13 | - | 0.06 | - | - |
| LOCLWR | - | - | 0.16 | 0.44 | 0.12 | 0.04 | 0.16 | 0.04 | 0.04 | - | - |
| IMNAHA | - | - | 0.33 | 0.15 | 0.33 | - | 0.07 | 0.11 | - | - | - |
| GRROND | - | - | 0.35 | 0.27 | 0.24 | - | 0.11 | 0.02 | - | 0.02 | - |
| LSNAKE | - | - | 0.31 | 0.31 | 0.23 | 0.04 | 0.12 | - | - | - | - |
| Total | 0.00 | 0.00 | 0.17 | 0.32 | 0.17 | 0.03 | 0.21 | 0.02 | 0.03 | 0.03 | 0.00 |

| SY2010 | Total age and age class (frequency) | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | 3 | 4 | 4 | 5 | 5 | 6 | 6 | 6 | 7 | 7 | 7 |
| Reporting Group | 1.1 | 1.2 | 2.1 | 2.2 | 3.1 | 2.3 | 3.2 | 4.1 | 3.3 | 4.2 | 5.1 |
| UPSALM | 0.01 | 0.02 | 0.47 | 0.19 | 0.20 | - | 0.09 | 0.01 | - | - | - |
| MFSALM | - | - | 0.09 | 0.07 | 0.33 | 0.01 | 0.25 | 0.14 | 0.03 | 0.07 | - |
| SFSALM | 0.02 | - | 0.04 | 0.06 | 0.20 | - | 0.37 | 0.04 | 0.08 | 0.16 | 0.04 |
| LOSALM | - | - | 0.30 | 0.22 | 0.22 | - | 0.26 | - | - | - | - |
| UPCLWR | 0.02 | 0.01 | 0.05 | 0.27 | 0.18 | 0.03 | 0.32 | 0.05 | 0.04 | 0.05 | - |
| SFCLWR | 0.02 | 0.02 | 0.09 | 0.48 | 0.13 | 0.08 | 0.14 | - | 0.01 | 0.02 | - |
| LOCLWR | 0.04 | 0.07 | 0.39 | 0.32 | 0.11 | - | 0.07 | - | - | - | - |
| IMNAHA | 0.04 | 0.02 | 0.30 | 0.13 | 0.42 | - | 0.09 | - | - | - | - |
| GRROND | 0.02 | 0.01 | 0.42 | 0.25 | 0.21 | - | 0.09 | 0.01 | - | 0.01 | - |
| LSNAKE | 0.03 | - | 0.49 | 0.25 | 0.16 | - | 0.06 | - | - | 0.01 | - |
| Total | 0.02 | 0.01 | 0.26 | 0.21 | 0.22 | 0.01 | 0.17 | 0.04 | 0.02 | 0.03 | 0.00 |

| SY2011 | Total age and age class (frequency) | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | 3 | 4 | 4 | 5 | 5 | 6 | 6 | 6 | 7 | 7 | 7 |
| Reporting Group | 1.1 | 1.2 | 2.1 | 2.2 | 3.1 | 2.3 | 3.2 | 4.1 | 3.3 | 4.2 | 5.1 |
| UPSALM | 0.03 | 0.06 | 0.28 | 0.35 | 0.06 | - | 0.10 | - | - | - | - |
| MFSALM | - | 0.01 | - | 0.22 | 0.04 | - | 0.51 | 0.01 | - | 0.07 | - |
| SFSALM | - | - | 0.01 | 0.22 | 0.01 | - | 0.56 | - | 0.01 | 0.03 | - |
| LOSALM | 0.03 | - | 0.08 | 0.44 | 0.13 | - | 0.23 | - | - | - | - |
| UPCLWR | 0.01 | 0.02 | 0.01 | 0.27 | 0.01 | 0.03 | 0.54 | 0.01 | - | 0.03 | - |
| SFCLWR | - | 0.03 | 0.03 | 0.63 | - | - | 0.18 | - | 0.01 | 0.01 | - |
| LOCLWR | 0.02 | 0.06 | 0.16 | 0.46 | 0.04 | - | 0.12 | - | - | 0.02 | - |
| IMNAHA | - | - | 0.26 | 0.38 | 0.10 | - | 0.16 | - | - | - | - |
| GRROND | 0.01 | 0.05 | 0.18 | 0.48 | 0.05 | - | 0.09 | 0.01 | - | - | - |
| LSNAKE | 0.03 | 0.03 | 0.28 | 0.39 | 0.09 | - | 0.01 | - | - | - | - |
| Total | 0.01 | 0.03 | 0.11 | 0.37 | 0.04 | 0.00 | 0.29 | 0.00 | 0.00 | 0.02 | 0.00 |

Table 26. Estimated scale age (frequency and proportion) for individuals assigning to a reporting group with ≥80% probability for natural origin juvenile (MY2010 – MY2011) steelhead mixtures from the Lower Granite Dam juvenile trapping facility.

| MY2010 Reporting Group | Freshwater Age | | | | | | |
|---|---|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 | U | Total |
| UPSALM | 4 | 53 | 36 | 6 | - | 5 | 104 |
| MFSALM | - | 10 | 43 | 9 | - | 1 | 63 |
| SFSALM | - | 4 | 18 | 4 | - | - | 26 |
| LOSALM | - | 9 | 5 | 1 | 1 | - | 16 |
| UPCLWR | - | 14 | 40 | 9 | 2 | - | 65 |
| SFCLWR | 2 | 46 | 42 | 4 | - | 1 | 95 |
| LOCLWR | - | 15 | 23 | 1 | - | - | 39 |
| IMNAHA | - | 16 | 15 | 5 | - | - | 36 |
| GRROND | 3 | 34 | 45 | 6 | - | 1 | 89 |
| LSNAKE | 1 | 21 | 16 | 5 | - | 2 | 45 |
| Total | 10 | 222 | 283 | 50 | 3 | 10 | 578 |

| MY2010 Reporting Group | Freshwater Age | | | | | |
|---|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 | U |
| UPSALM | 0.04 | 0.51 | 0.35 | 0.06 | 0.00 | 0.05 |
| MFSALM | 0.00 | 0.16 | 0.68 | 0.14 | 0.00 | 0.02 |
| SFSALM | 0.00 | 0.15 | 0.69 | 0.15 | 0.00 | 0.00 |
| LOSALM | 0.00 | 0.56 | 0.31 | 0.06 | 0.06 | 0.00 |
| UPCLWR | 0.00 | 0.22 | 0.62 | 0.14 | 0.03 | 0.00 |
| SFCLWR | 0.02 | 0.48 | 0.44 | 0.04 | 0.00 | 0.01 |
| LOCLWR | 0.00 | 0.38 | 0.59 | 0.03 | 0.00 | 0.00 |
| IMNAHA | 0.00 | 0.44 | 0.42 | 0.14 | 0.00 | 0.00 |
| GRROND | 0.03 | 0.38 | 0.51 | 0.07 | 0.00 | 0.01 |
| LSNAKE | 0.02 | 0.47 | 0.36 | 0.11 | 0.00 | 0.04 |
| Total | 0.02 | 0.38 | 0.49 | 0.09 | 0.01 | 0.02 |

| MY2011 Reporting Group | Freshwater Age | | | | | | |
|---|---|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 | U | Total |
| UPSALM | 26 | 117 | 30 | 6 | - | 2 | 181 |
| MFSALM | 1 | 24 | 48 | 16 | - | - | 89 |
| SFSALM | - | 12 | 24 | 11 | 1 | - | 48 |
| LOSALM | 2 | 16 | 13 | 1 | - | - | 32 |
| UPCLWR | 6 | 60 | 58 | 16 | 1 | 2 | 143 |
| SFCLWR | 7 | 94 | 29 | 5 | - | 5 | 140 |
| LOCLWR | 4 | 36 | 11 | 1 | - | - | 52 |
| IMNAHA | - | 40 | 19 | 1 | - | - | 60 |
| GRROND | 11 | 85 | 31 | 5 | - | 3 | 135 |
| LSNAKE | 11 | 47 | 15 | - | - | 4 | 77 |
| Total | 68 | 531 | 278 | 62 | 2 | 16 | 957 |

| MY2011 Reporting Group | Freshwater Age | | | | | |
|---|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 | U |
| UPSALM | 0.14 | 0.65 | 0.17 | 0.03 | 0.00 | 0.01 |
| MFSALM | 0.01 | 0.27 | 0.54 | 0.18 | 0.00 | 0.00 |
| SFSALM | 0.00 | 0.25 | 0.50 | 0.23 | 0.02 | 0.00 |
| LOSALM | 0.06 | 0.50 | 0.41 | 0.03 | 0.00 | 0.00 |
| UPCLWR | 0.04 | 0.42 | 0.41 | 0.11 | 0.01 | 0.01 |
| SFCLWR | 0.05 | 0.67 | 0.21 | 0.04 | 0.00 | 0.04 |
| LOCLWR | 0.08 | 0.69 | 0.21 | 0.02 | 0.00 | 0.00 |
| IMNAHA | 0.00 | 0.67 | 0.32 | 0.02 | 0.00 | 0.00 |
| GRROND | 0.08 | 0.63 | 0.23 | 0.04 | 0.00 | 0.02 |
| LSNAKE | 0.14 | 0.61 | 0.19 | 0.00 | 0.00 | 0.05 |
| Total | 0.07 | 0.55 | 0.29 | 0.06 | 0.00 | 0.02 |

Table 27. Mixture modeling results for natural origin adult Chinook salmon mixtures from the Lower Granite Dam adult trap, SY2009 through SY2011. All results are shown as percentages.

| Reporting Unit | Stock Composition | | | C.V. | | | Lower 95% CI | | | Upper 95% CI | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | SY2009 | SY2010 | SY2011 | SY2009 | SY2010 | SY2011 | SY2009 | SY2010 | SY2011 | SY2009 | SY2010 | SY2011 |
| UPSALM | 19.5 | 16.8 | 16.1 | 10.4 | 9.3 | 6.1 | 14.6 | 13.9 | 14.0 | 22.6 | 19.9 | 17.9 |
| MFSALM | 11.0 | 16.4 | 14.8 | 15.6 | 9.2 | 6.2 | 7.3 | 12.7 | 13.0 | 14.0 | 18.7 | 16.6 |
| CHMBLN | 4.6 | 4.2 | 2.1 | 21.3 | 18.7 | 15.8 | 2.8 | 2.7 | 1.5 | 6.6 | 5.7 | 2.8 |
| SFSALM | 27.1 | 27.9 | 20.4 | 9.6 | 7.4 | 5.4 | 23.5 | 24.5 | 18.4 | 33.7 | 32.6 | 22.7 |
| HELLSC | 35.9 | 31.8 | 41.5 | 6.3 | 5.7 | 2.9 | 31.8 | 28.6 | 39.2 | 40.8 | 35.7 | 44.0 |
| TUCANO | 0.5 | 0.2 | 0.9 | 72.4 | 48.6 | 24.8 | 0.0 | 0.0 | 0.5 | 1.1 | 0.3 | 1.4 |
| FALL | 1.5 | 2.8 | 4.2 | 0.0 | 0.0 | 0.0 | n/a | n/a | n/a | n/a | n/a | n/a |

Table 28. Number of individuals analyzed and number of individuals that assigned to each Snake River reporting group with ≥80% probability for natural origin adult (SY2009 – SY2011) and juvenile (MY2010 – MY2011) Chinook salmon mixtures from the Lower Granite Dam adult and juvenile trapping facilities. Of the 8,122 natural origin Chinook salmon analyzed, 5,238 (64.5%) assigned to a reporting group with ≥80% probability. Individuals assigning with <80% probability were considered unassigned. Biological data obtained from assigned individuals were used to examine life-history information for each reporting group. NOTE: Mixtures from 2010 and prior were analyzed using the SNP panel from Snake River Chinook salmon baseline v1.0 resulting in the decreased assignment rate.

| | **Number Assigned** | | | | |
|---|---|---|---|---|---|
| | **Adults** | | | **Juveniles** | |
| **Reporting Group** | **SY2009** | **SY2010** | **SY2011** | **MY2010** | **MY2011** |
| *Total Analyzed:* | *825* | *1,176* | *2,104* | *1,914* | *2,103* |
| UPSALM | 67 | 92 | 234 | 100 | 226 |
| MFSALM | 42 | 100 | 237 | 101 | 161 |
| CHMBLN | 20 | 28 | 41 | 18 | 47 |
| SFSALM | 41 | 58 | 181 | 36 | 138 |
| HELLSC | 189 | 239 | 700 | 421 | 515 |
| TUCANO | 4 | 3 | 17 | 6 | 11 |
| FALL | 12 | 33 | 89 | 487 | 544 |
| Total Assigned With ≥80% Probability: | 375 (45.5%) | 553 (47.0%) | 1,499 (71.2%) | 1,169 (61.1%) | 1,642 (78.1%) |

Table 29. Estimated sex (frequency and proportion) for individuals assigning to a reporting group with ≥80% probability based on the Y-specific assay (*Ots_SEXY3-1*) for natural origin adult (SY2009 – SY2011) and juvenile (MY2010 – MY2011) Chinook salmon mixtures from the Lower Granite Dam adult and juvenile trapping facilities. For adult mixtures, individuals were split into 1-ocean ("jacks") and 2- and 3-ocean age groups.

| Reporting Group | Spawn Year / Migratory Year | Ocean Age | # Females | # Males | # Unknown | % Females | % Males |
|---|---|---|---|---|---|---|---|
| UPSALM | SY2009 | 1 | 0 | 10 | 0 | 0% | 100% |
| | | 2 & 3 | 20 | 33 | 1 | 38% | 62% |
| | SY2010 | 1 | 0 | 2 | 0 | 0% | 100% |
| | | 2 & 3 | 34 | 54 | 2 | 39% | 61% |
| | SY2011 | 1 | 3 | 23 | 0 | 12% | 88% |
| | | 2 & 3 | 62 | 131 | 10 | 32% | 68% |
| | MY2010 | | 55 | 42 | 3 | 57% | 43% |
| | MY2011 | | 92 | 124 | 10 | 43% | 57% |
| MFSALM | SY2009 | 1 | 0 | 14 | 0 | 0% | 100% |
| | | 2 & 3 | 16 | 12 | 0 | 57% | 43% |
| | SY2010 | 1 | 1 | 2 | 0 | 33% | 67% |
| | | 2 & 3 | 36 | 55 | 6 | 40% | 60% |
| | SY2011 | 1 | 1 | 46 | 0 | 2% | 98% |
| | | 2 & 3 | 68 | 109 | 8 | 38% | 62% |
| | MY2010 | | 56 | 40 | 5 | 58% | 42% |
| | MY2011 | | 60 | 92 | 9 | 39% | 61% |
| CHMBLN | SY2009 | 1 | 0 | 7 | 0 | 0% | 100% |
| | | 2 & 3 | 8 | 4 | 1 | 67% | 33% |
| | SY2010 | 1 | 0 | 0 | 0 | | |
| | | 2 & 3 | 15 | 12 | 1 | 56% | 44% |
| | SY2011 | 1 | 0 | 13 | 0 | 0% | 100% |
| | | 2 & 3 | 11 | 16 | 1 | 41% | 59% |
| | MY2010 | | 9 | 9 | 0 | 50% | 50% |
| | MY2011 | | 22 | 23 | 2 | 49% | 51% |
| SFSALM | SY2009 | 1 | 0 | 7 | 0 | 0% | 100% |
| | | 2 & 3 | 15 | 18 | 1 | 45% | 55% |
| | SY2010 | 1 | 0 | 0 | 1 | | |
| | | 2 & 3 | 28 | 26 | 1 | 52% | 48% |
| | SY2011 | 1 | 0 | 31 | 0 | 0% | 100% |
| | | 2 & 3 | 57 | 83 | 7 | 41% | 59% |
| | MY2010 | | 16 | 17 | 3 | 48% | 52% |
| | MY2011 | | 73 | 56 | 9 | 57% | 43% |
| HELLSC | SY2009 | 1 | 1 | 34 | 1 | 3% | 97% |
| | | 2 & 3 | 74 | 70 | 4 | 51% | 49% |
| | SY2010 | 1 | 0 | 12 | 0 | 0% | 100% |
| | | 2 & 3 | 111 | 105 | 7 | 51% | 49% |
| | SY2011 | 1 | 1 | 98 | 0 | 1% | 99% |
| | | 2 & 3 | 224 | 346 | 22 | 39% | 61% |
| | MY2010 | | 253 | 144 | 24 | 64% | 36% |
| | MY2011 | | 258 | 235 | 22 | 52% | 48% |
| TUCANO | SY2009 | 1 | 0 | 2 | 0 | 0% | 100% |
| | | 2 & 3 | 1 | 0 | 1 | 100% | 0% |
| | SY2010 | 1 | 0 | 0 | 0 | | |
| | | 2 & 3 | 1 | 2 | 0 | 33% | 67% |
| | SY2011 | 1 | 0 | 6 | 0 | 0% | 100% |
| | | 2 & 3 | 7 | 4 | 0 | 64% | 36% |
| | MY2010 | | 3 | 3 | 0 | 50% | 50% |
| | MY2011 | | 4 | 6 | 1 | 40% | 60% |
| FALL | SY2009 | 1 | 0 | 2 | 0 | 0% | 100% |
| | | 2 & 3 | 2 | 8 | 0 | 20% | 80% |
| | SY2010 | 1 | 0 | 4 | 0 | 0% | 100% |
| | | 2 & 3 | 12 | 14 | 2 | 46% | 54% |
| | SY2011 | 1 | 0 | 9 | 0 | 0% | 100% |
| | | 2 & 3 | 28 | 34 | 4 | 45% | 55% |
| | MY2010 | | 246 | 207 | 34 | 54% | 46% |
| | MY2011 | | 227 | 280 | 37 | 45% | 55% |

Table 30. Estimated scale age (frequency) for individuals assigning to a reporting group with ≥80% probability for natural origin adult (SY2009 – SY2011) Chinook salmon mixtures from the Lower Granite Dam adult trapping facility.

| **SY2009** | **Total age and age class (frequency)** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| **Reporting Group** | **3 0.2** | **3 1.1** | **4 0.3** | **4 1.2** | **4 2.1** | **5 1.3** | **5 2.2** | **6 2.3** | **Total** |
| UPSALM | - | 7 | - | 46 | 2 | 7 | - | - | 62 |
| MFSALM | - | 14 | - | 22 | - | 5 | - | - | 41 |
| CHMBLN | - | 7 | - | 11 | - | 2 | - | - | 20 |
| SFSALM | - | 7 | - | 28 | - | 5 | 1 | - | 41 |
| HELLSC | - | 30 | - | 111 | 2 | 31 | - | - | 174 |
| TUCANO | - | 2 | - | - | - | 2 | - | - | 4 |
| FALL | 3 | 1 | - | 1 | 1 | 5 | 1 | - | 12 |
| Total | 3 | 68 | 0 | 219 | 5 | 57 | 2 | 0 | 354 |

| **SY2010** | **Total age and age class (frequency)** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| **Reporting Group** | **3 0.2** | **3 1.1** | **4 0.3** | **4 1.2** | **4 2.1** | **5 1.3** | **5 2.2** | **6 2.3** | **Total** |
| UPSALM | - | 1 | - | 75 | 1 | 13 | - | - | 90 |
| MFSALM | - | 3 | - | 90 | - | 4 | - | - | 97 |
| CHMBLN | - | - | - | 26 | - | - | - | - | 26 |
| SFSALM | - | 1 | - | 52 | - | - | - | - | 53 |
| HELLSC | - | 12 | - | 202 | - | 10 | 3 | - | 227 |
| TUCANO | - | - | - | 2 | - | 1 | - | - | 3 |
| FALL | 1 | 1 | 1 | 8 | 3 | 2 | 16 | - | 32 |
| Total | 1 | 18 | 1 | 455 | 4 | 30 | 19 | 0 | 528 |

| **SY2011** | **Total age and age class (frequency)** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| **Reporting Group** | **3 0.2** | **3 1.1** | **4 0.3** | **4 1.2** | **4 2.1** | **5 1.3** | **5 2.2** | **6 2.3** | **Total** |
| UPSALM | - | 22 | - | 127 | 1 | 65 | 3 | - | 218 |
| MFSALM | - | 44 | - | 105 | 1 | 74 | - | - | 224 |
| CHMBLN | - | 13 | - | 20 | - | 7 | - | - | 40 |
| SFSALM | - | 29 | - | 84 | 1 | 55 | 1 | - | 170 |
| HELLSC | - | 96 | - | 418 | 2 | 145 | 7 | 1 | 669 |
| TUCANO | - | 5 | - | 4 | 1 | 6 | - | - | 16 |
| FALL | - | 7 | 1 | 17 | 2 | 15 | 21 | 10 | 73 |
| Total | 0 | 216 | 1 | 775 | 8 | 367 | 32 | 11 | 1,410 |

Table 31. Estimated scale age (proportion) for individuals assigning to a reporting group with ≥80% probability for natural origin adult (SY2009 – SY2011) Chinook salmon mixtures from the Lower Granite Dam adult trapping facility.

| **SY2009** | **Total age and age class (proportion)** | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | **3** | **3** | **4** | **4** | **4** | **5** | **5** | **6** |
| **Reporting Group** | **0.2** | **1.1** | **0.3** | **1.2** | **2.1** | **1.3** | **2.2** | **2.3** |
| UPSALM | - | 0.11 | - | 0.74 | 0.03 | 0.11 | - | - |
| MFSALM | - | 0.34 | - | 0.54 | - | 0.12 | - | - |
| CHMBLN | - | 0.35 | - | 0.55 | - | 0.10 | - | - |
| SFSALM | - | 0.17 | - | 0.68 | - | 0.12 | 0.02 | - |
| HELLSC | - | 0.17 | - | 0.64 | 0.01 | 0.18 | - | - |
| TUCANO | - | 0.50 | - | - | - | 0.50 | - | - |
| FALL | 0.25 | 0.08 | - | 0.08 | 0.08 | 0.42 | 0.08 | - |
| Total | 0.01 | 0.19 | 0.00 | 0.62 | 0.01 | 0.16 | 0.01 | 0.00 |

| **SY2010** | **Total age and age class (proportion)** | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | **3** | **3** | **4** | **4** | **4** | **5** | **5** | **6** |
| **Reporting Group** | **0.2** | **1.1** | **0.3** | **1.2** | **2.1** | **1.3** | **2.2** | **2.3** |
| UPSALM | - | 0.01 | - | 0.83 | 0.01 | 0.14 | - | - |
| MFSALM | - | 0.03 | - | 0.93 | - | 0.04 | - | - |
| CHMBLN | - | - | - | 1.00 | - | - | - | - |
| SFSALM | - | 0.02 | - | 0.98 | - | - | - | - |
| HELLSC | - | 0.05 | - | 0.89 | - | 0.04 | 0.01 | - |
| TUCANO | - | - | - | 0.67 | - | 0.33 | - | - |
| FALL | 0.03 | 0.03 | 0.03 | 0.25 | 0.09 | 0.06 | 0.50 | - |
| Total | 0.00 | 0.03 | 0.00 | 0.86 | 0.01 | 0.06 | 0.04 | 0.00 |

| **SY2011** | **Total age and age class (proportion)** | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | **3** | **3** | **4** | **4** | **4** | **5** | **5** | **6** |
| **Reporting Group** | **0.2** | **1.1** | **0.3** | **1.2** | **2.1** | **1.3** | **2.2** | **2.3** |
| UPSALM | - | 0.10 | - | 0.58 | 0.00 | 0.30 | 0.01 | - |
| MFSALM | - | 0.20 | - | 0.47 | 0.00 | 0.33 | - | - |
| CHMBLN | - | 0.33 | - | 0.50 | - | 0.18 | - | - |
| SFSALM | - | 0.17 | - | 0.49 | 0.01 | 0.32 | 0.01 | - |
| HELLSC | - | 0.14 | - | 0.62 | 0.00 | 0.22 | 0.01 | 0.00 |
| TUCANO | - | 0.31 | - | 0.25 | 0.06 | 0.38 | - | - |
| FALL | - | 0.10 | 0.01 | 0.23 | 0.03 | 0.21 | 0.29 | 0.14 |
| Total | 0.00 | 0.15 | 0.00 | 0.55 | 0.01 | 0.26 | 0.02 | 0.01 |

Table 32. Phenotypic age (frequency and proportion) for individuals assigning to a reporting group with ≥80% probability for natural origin juvenile (MY2010 – MY2011) Chinook salmon mixtures from the Lower Granite Dam juvenile trapping facility.

| MY2010 | Phenotypic Age | | |
|---|---|---|---|
| Reporting Group | Subyearling | Yearling | Total |
| UPSALM | 2 | 98 | 100 |
| MFSALM | - | 101 | 101 |
| CHMBLN | - | 18 | 18 |
| SFSALM | - | 36 | 36 |
| HELLSC | 17 | 404 | 421 |
| TUCANO | 1 | 5 | 6 |
| FALL | 458 | 29 | 487 |
| Total | 478 | 691 | 1,169 |

| MY2010 | Phenotypic Age | |
|---|---|---|
| Reporting Group | Subyearling | Yearling |
| UPSALM | 0.02 | 0.98 |
| MFSALM | 0.00 | 1.00 |
| CHMBLN | 0.00 | 1.00 |
| SFSALM | 0.00 | 1.00 |
| HELLSC | 0.04 | 0.96 |
| TUCANO | 0.17 | 0.83 |
| FALL | 0.94 | 0.06 |
| Total | 0.41 | 0.59 |

| MY2011 | Phenotypic Age | | |
|---|---|---|---|
| Reporting Group | Subyearling | Yearling | Total |
| UPSALM | 13 | 213 | 226 |
| MFSALM | 4 | 157 | 161 |
| CHMBLN | 3 | 44 | 47 |
| SFSALM | 4 | 134 | 138 |
| HELLSC | 35 | 480 | 515 |
| TUCANO | 1 | 10 | 11 |
| FALL | 515 | 28 | 543 |
| Total | 575 | 1,066 | 1,641 |

| MY2011 | Phenotypic Age | |
|---|---|---|
| Reporting Group | Subyearling | Yearling |
| UPSALM | 0.06 | 0.94 |
| MFSALM | 0.02 | 0.98 |
| CHMBLN | 0.06 | 0.94 |
| SFSALM | 0.03 | 0.97 |
| HELLSC | 0.07 | 0.93 |
| TUCANO | 0.09 | 0.91 |
| FALL | 0.95 | 0.05 |
| Total | 0.35 | 0.65 |

**FIGURES**

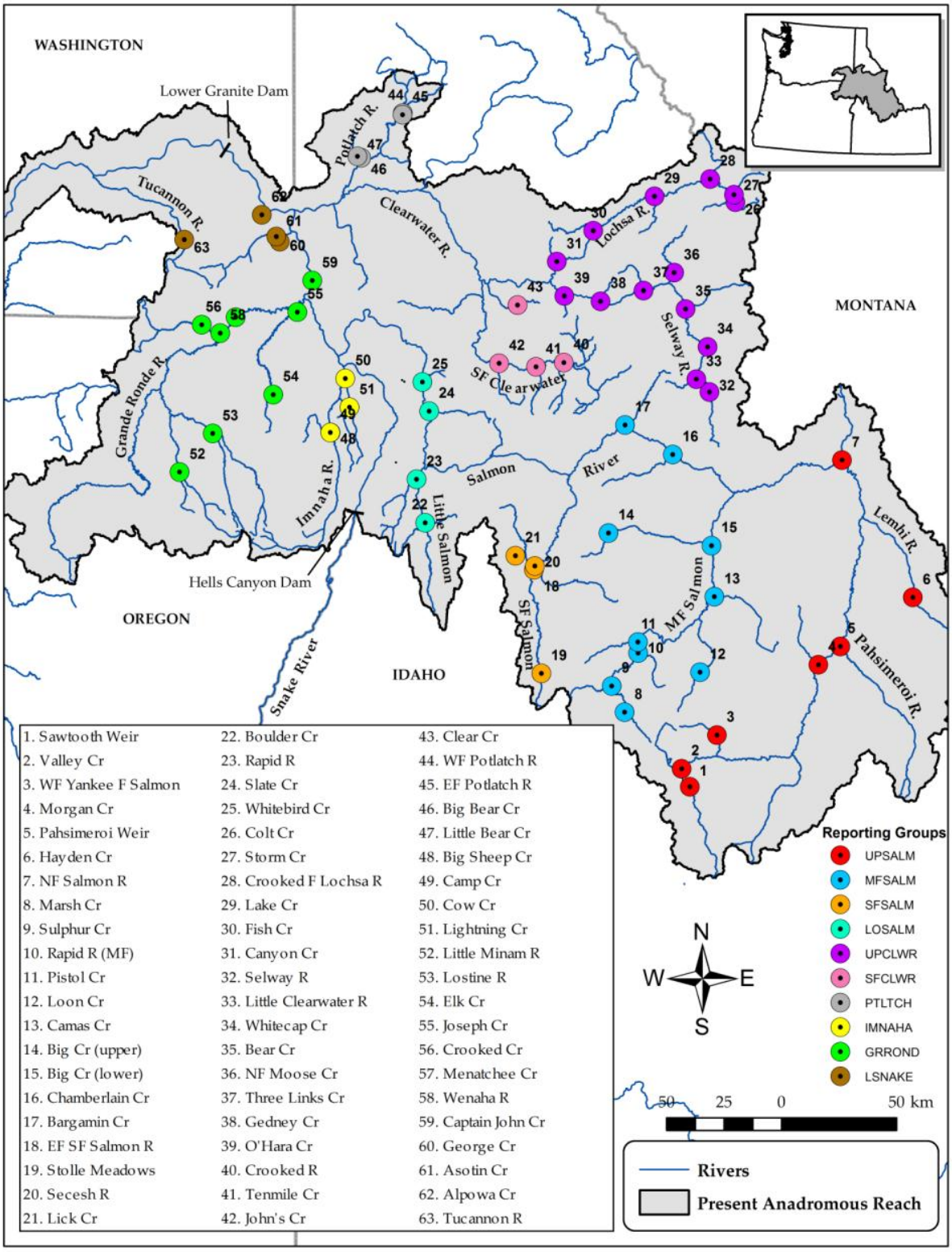


Figure 1. Collections representing Snake River steelhead baseline v2.0. Numbers correspond to "Map #" in Table 1. Reporting groups for GSI at Lower Granite Dam are noted. All collections are of natural origin individuals. Note that PTLTCH reporting group is equivalent to LOCLWR.

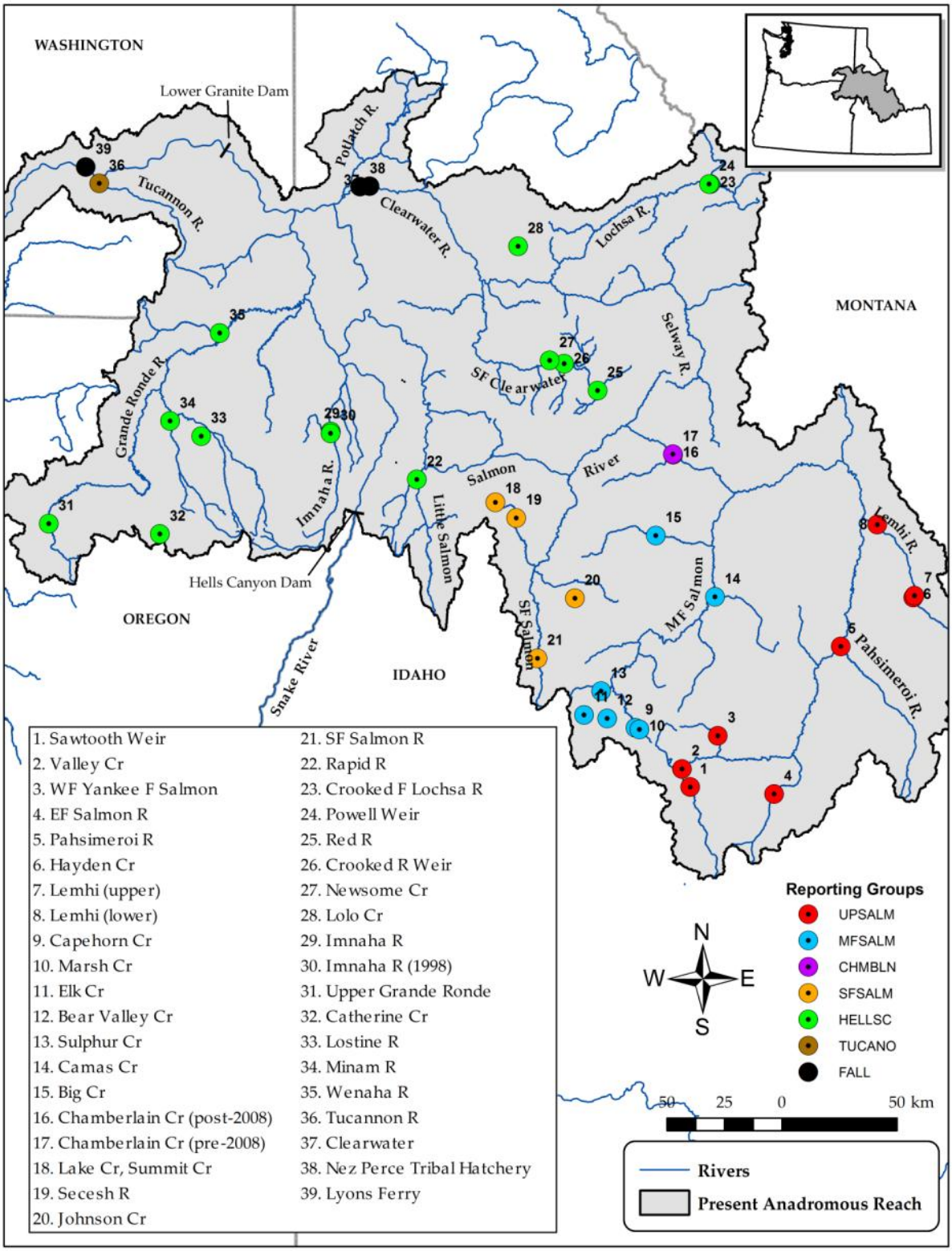


Figure 2. Collections representing Snake River Chinook salmon baseline v2.0. Numbers correspond to "Map #" in Table 2. Reporting groups for GSI at Lower Granite Dam are noted. All stream-type collections (excluding FALL reporting group) are of natural origin individuals. FALL collections are hatchery origin.

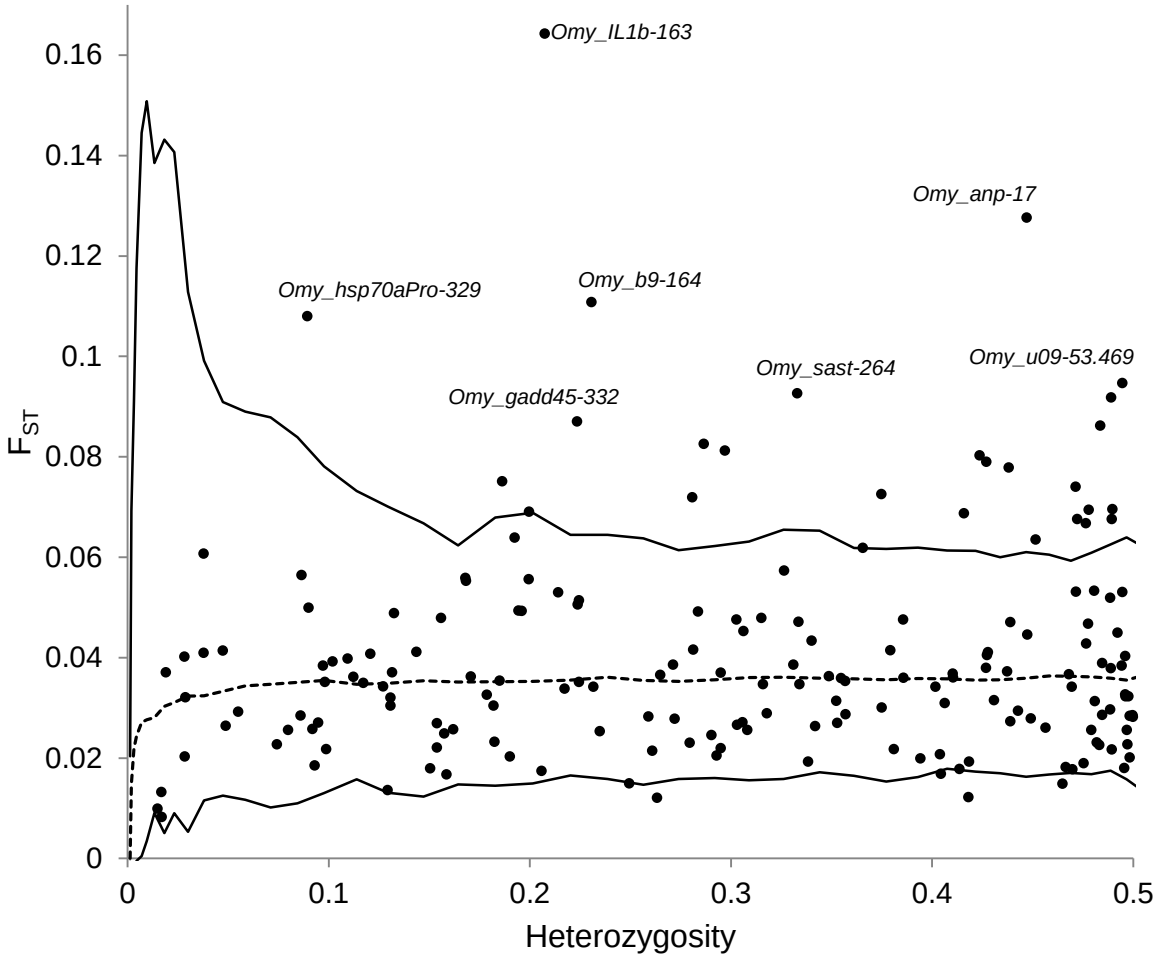


Figure 3. $F_{ST}$ as a function of heterozygosity (LOSITAN; Beaumont and Nichols 1996; Antao et al. 2008) for 187 *O. mykiss* SNP loci evaluated among Snake River steelhead baseline v2.0. The dashed line represents the median and the solid lines represent the 99% confidence interval boundaries based on 50,000 simulations and using an infinite alleles model. The seven most divergent candidate SNPs for directional selection are identified.

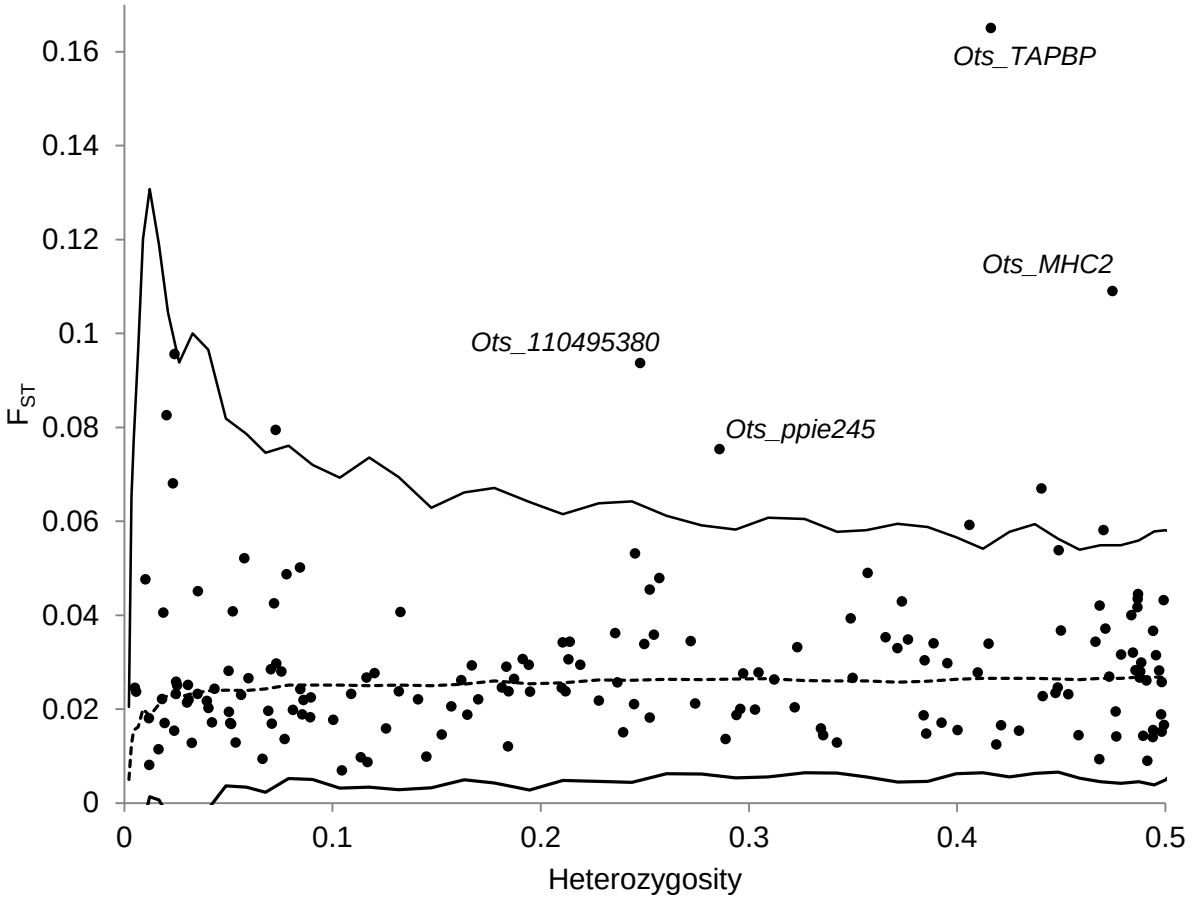


Figure 4. $F_{ST}$ as a function of heterozygosity (LOSITAN; Beaumont and Nichols 1996; Antao et al. 2008) for 174 Chinook salmon SNP loci evaluated among Snake River spring/summer Chinook salmon baseline v2.0 (fall Chinook collections were removed from analysis). The dashed line represents the median and the solid lines represent the 99% confidence interval boundaries based on 50,000 simulations and using an infinite alleles model. The four most divergent candidate SNPs for directional selection are identified.

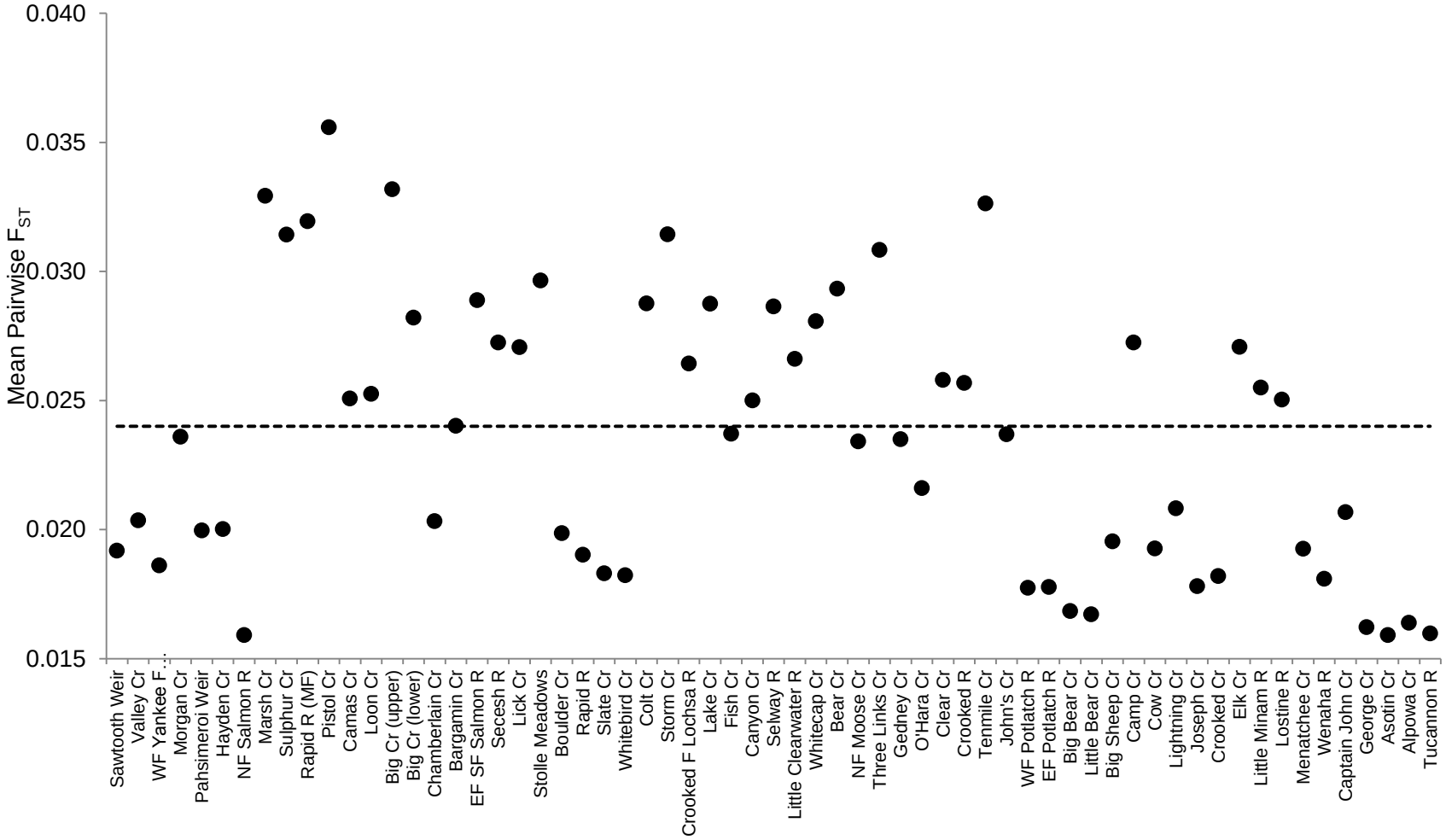


Figure 5. Mean pairwise $F_{ST}$ estimates for Snake River steelhead baseline v2.0 collections. The dashed line represents the average pairwise $F_{ST}$ estimate across all populations. High mean pairwise $F_{ST}$ estimates suggest high levels of genetic differentiation relative to other baseline populations.

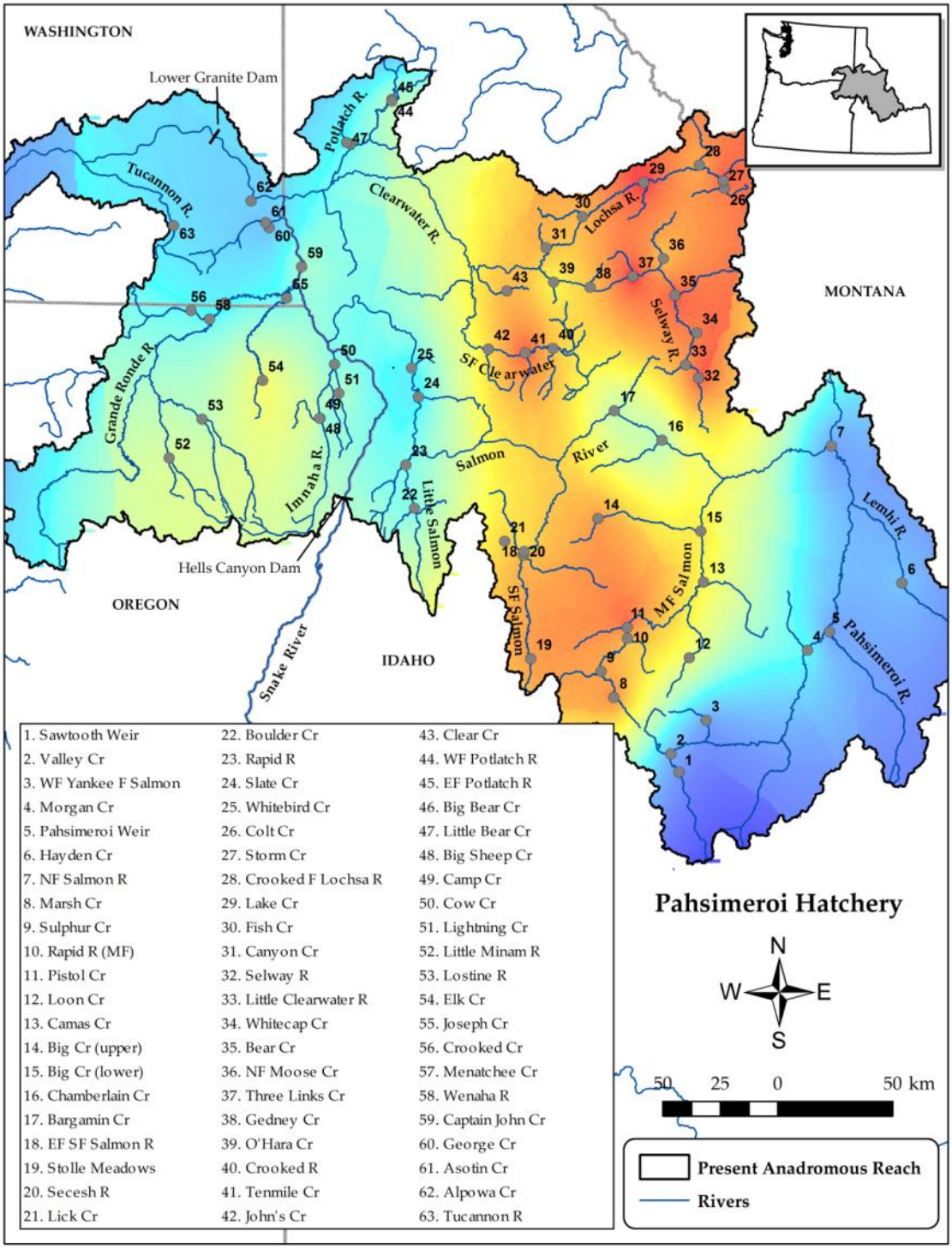


Figure 6. Results from spatial interpolation of pairwise $F_{ST}$ estimates for each natural origin collection in Snake River steelhead baseline v2.0 relative to the Pahsimeroi Hatchery broodstock collection (Table 9) using the kriging function under Spatial Analyst, Interpolation in ArcToolbox, ArcGIS 10. Regions shaded red represent comparisons with greater differentiation (max = 0.034, Lake Cr); regions shaded dark blue represent comparisons with lower differentiation (min = 0.004, Sawtooth Weir).

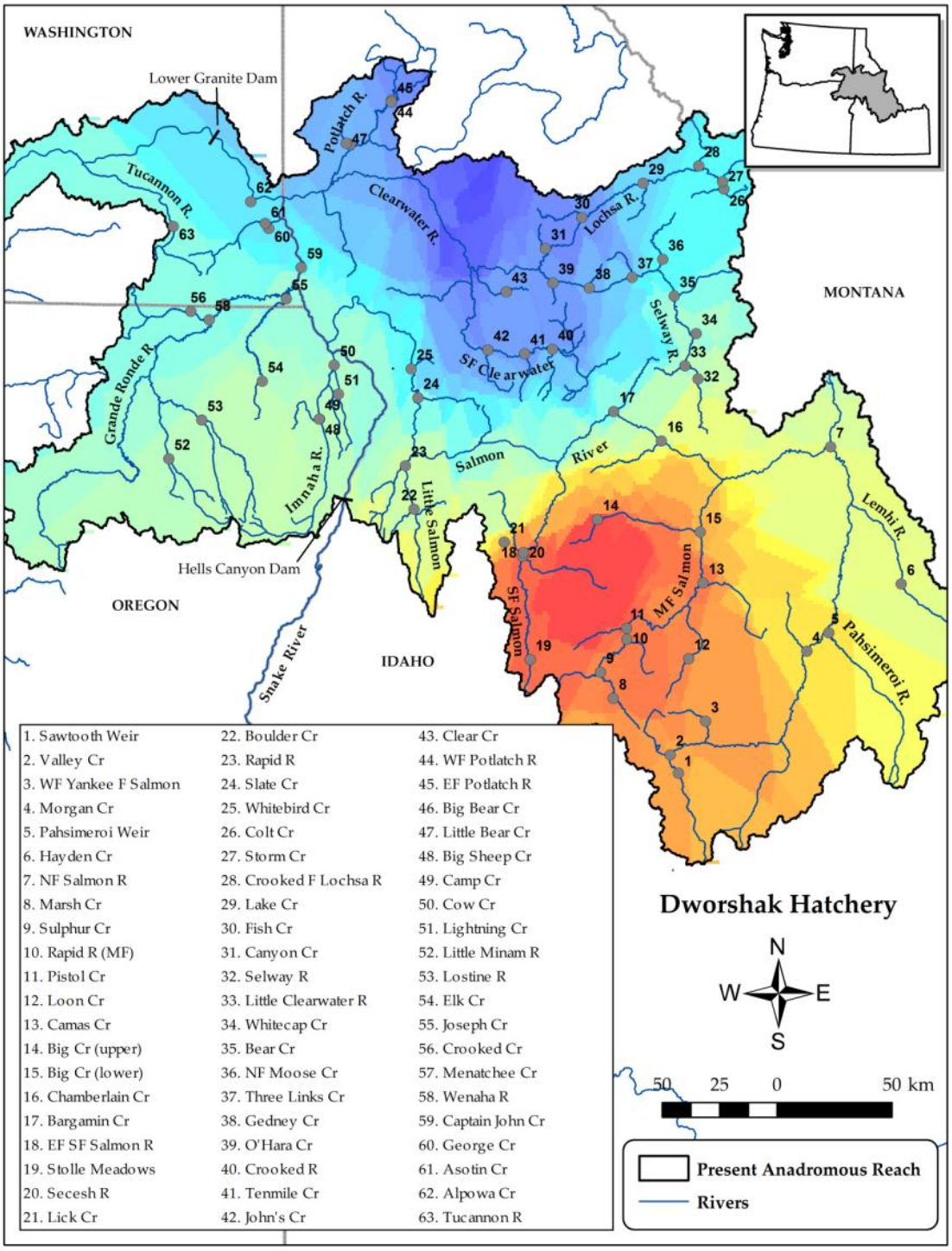


Figure 7. Results from spatial interpolation of pairwise $F_{ST}$ estimates for each natural origin collection in Snake River steelhead baseline v2.0 relative to the Dworshak Hatchery broodstock collection (Table 9) using the kriging function under Spatial Analyst, Interpolation in ArcToolbox, ArcGIS 10. Regions shaded red represent comparisons with greater differentiation (max = 0.050, Pistol Cr); regions shaded dark blue represent comparisons with lower differentiation (min = 0.004, Crooked R).

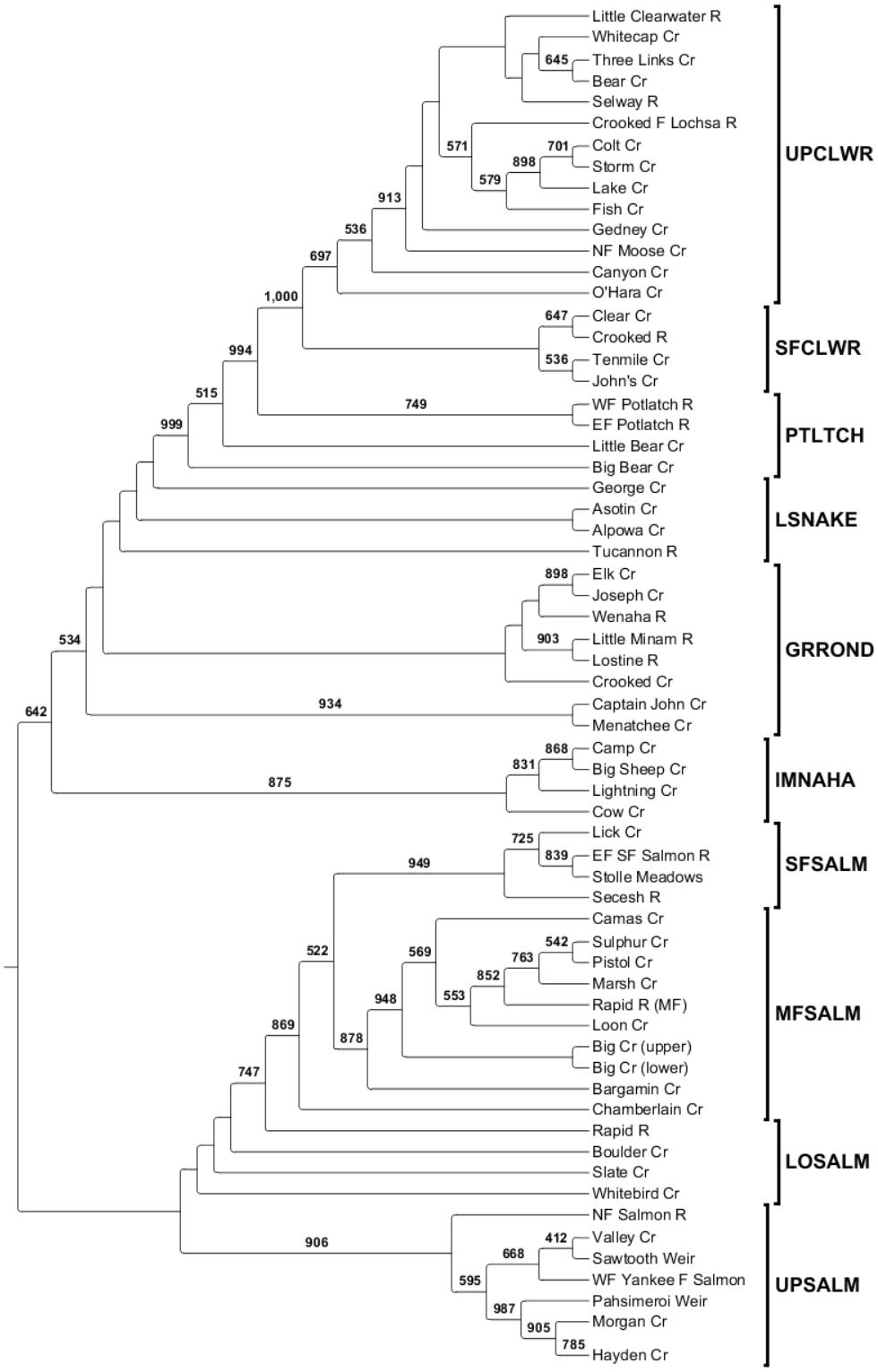


Figure 8. NJ-phylogram based on Nei's (1972) distance for Snake River steelhead baseline v2.0. Brackets designate reporting regions used for genetic stock identification at Lower Granite Dam. Nodes that were identified in greater than 50% of 1,000 bootstrap iterations are shown. Note that PTLTCH reporting group is equivalent to LOCLWR.

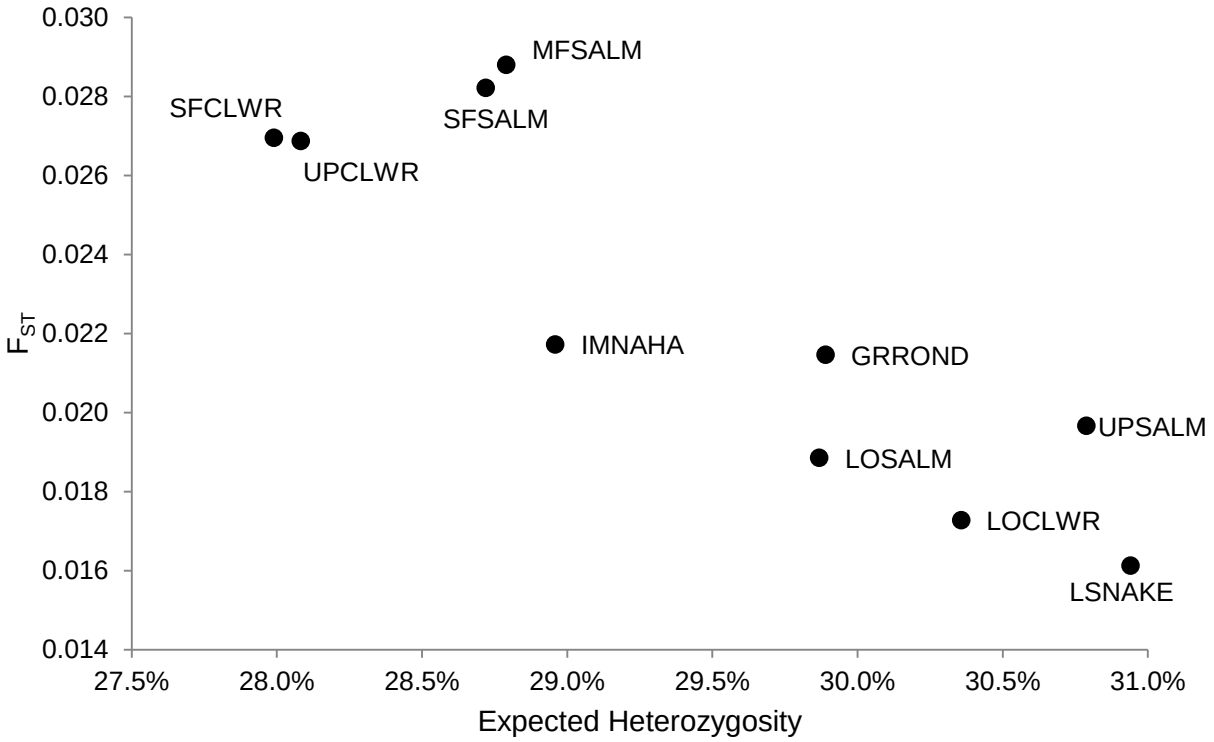


Figure 9. $F_{ST}$ as a function of expected heterozygosity for each of the reporting groups (averaged across collections within the reporting group) in Snake River steelhead baseline v2.0. In theory, the relationship between $F_{ST}$ and $H_E$ is inverse; increased gene flow among populations increases within-population diversity and decreases differentiation. Conversely, decreased gene flow among populations decreases within-population diversity over time and increases differentiation.

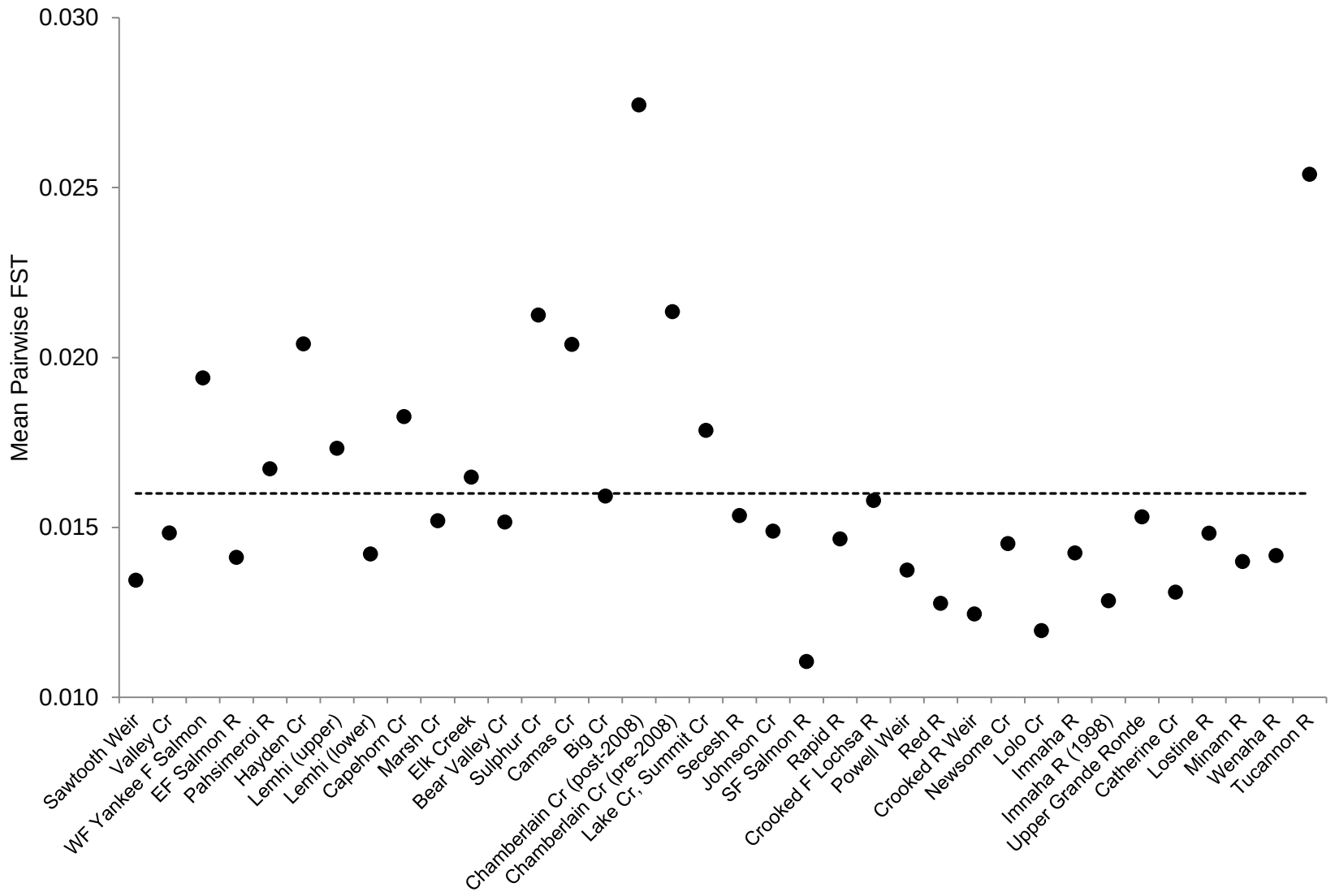


Figure 10. Mean pairwise $F_{ST}$ estimates for Snake River Chinook salmon baseline v2.0 collections. The dashed line represents the average pairwise $F_{ST}$ estimate across all populations. High mean pairwise $F_{ST}$ estimates suggest high levels of genetic differentiation relative to other baseline populations. The FALL reporting group was excluded.

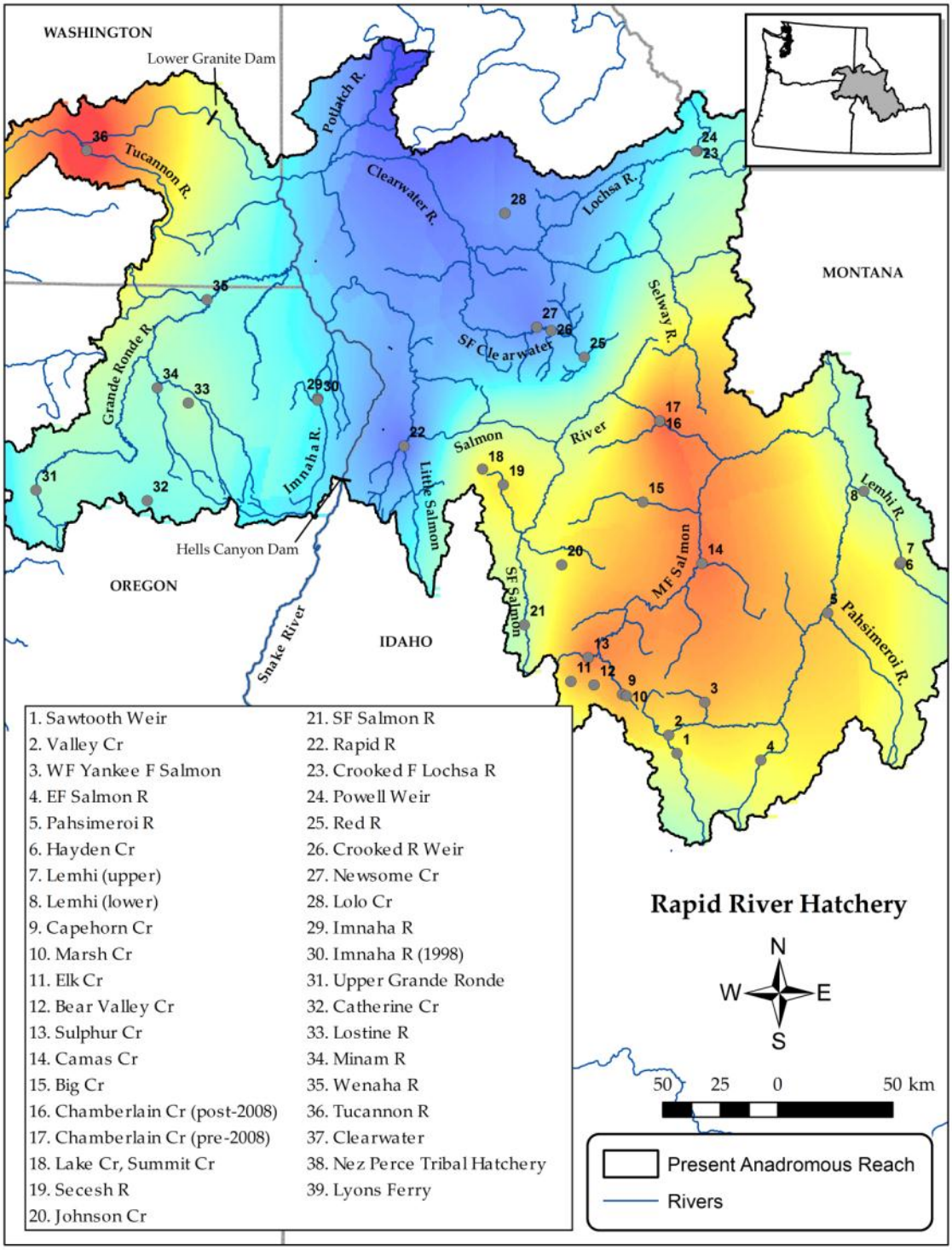


Figure 11. Results from spatial interpolation of pairwise $F_{ST}$ estimates for each natural origin collection in Snake River Chinook salmon baseline v2.0 relative to the Rapid River Hatchery broodstock collection (Table 10) using the kriging function under Spatial Analyst, Interpolation in ArcToolbox, ArcGIS 10. Regions shaded red represent comparisons with greater differentiation (max = 0.027, Tucannon R); regions shaded dark blue represent comparisons with lower differentiation (min = 0.003, Rapid R).

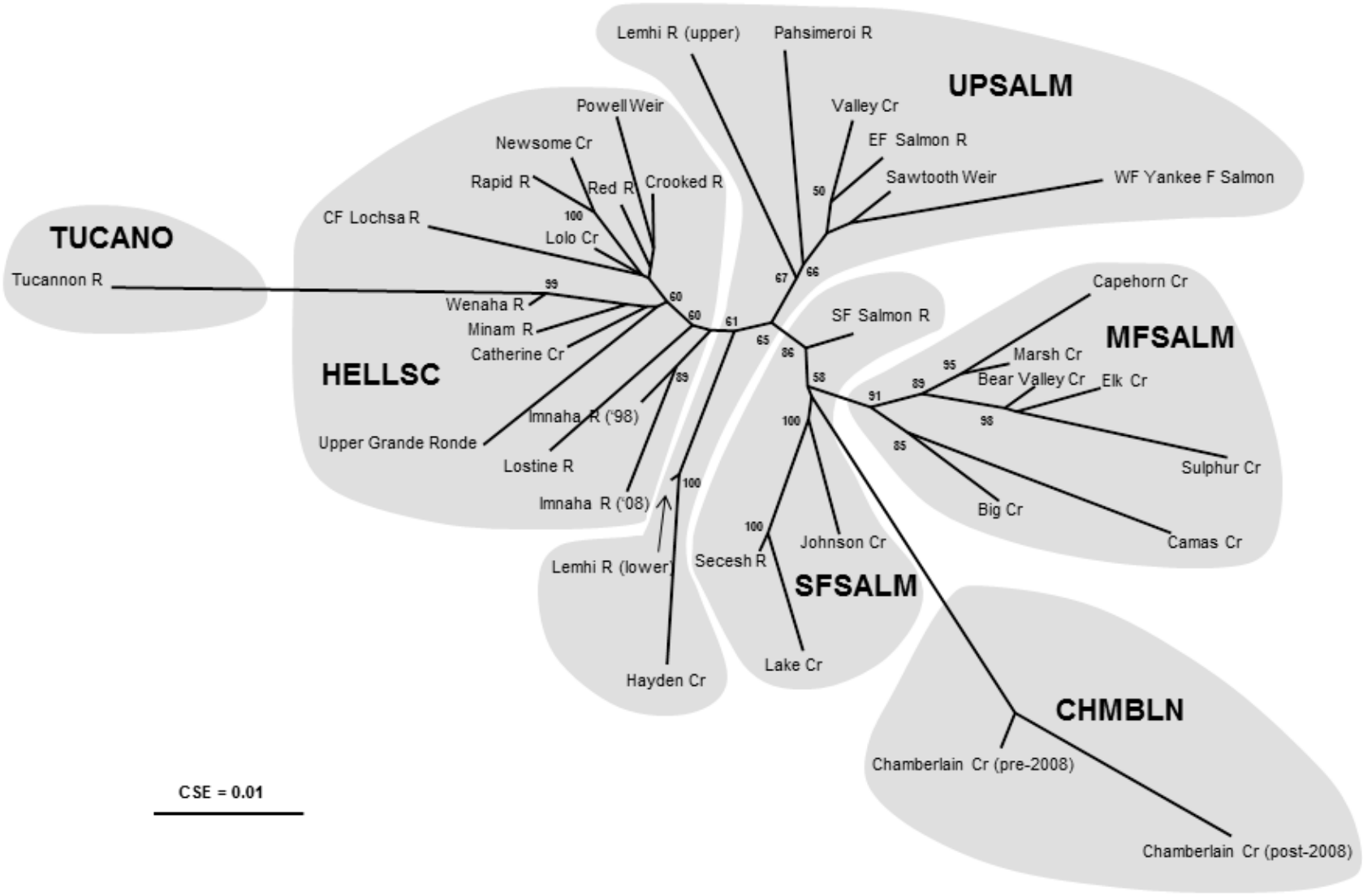


Figure 12. NJ-dendrogram of populations represented in Chinook salmon baseline v2.0 based on Cavalli-Sforza and Edwards (1967) genetic chord distances. Support for nodes that were identified in greater than 50 percent of 1,000 bootstrap iterations are shown. Gray shading corresponds to reporting groups used for genetic stock identification at Lower Granite Dam. FALL collections are excluded.

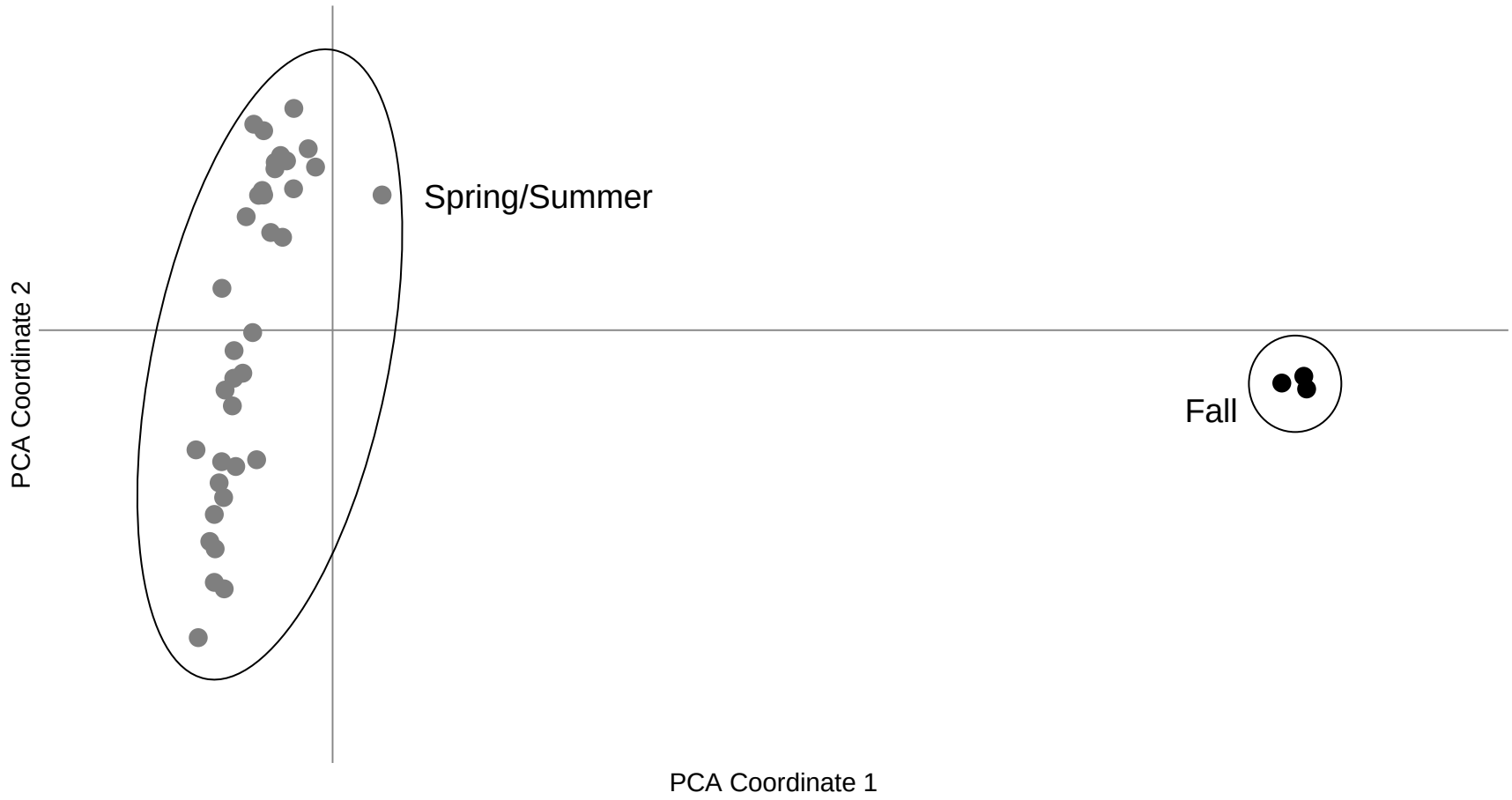


Figure 13. Principal coordinates analysis (PCA) based on pairwise $F_{ST}$ values for Snake River Chinook salmon baseline v2.0 including both spring/summer (stream-type) and fall (ocean-type) collections. PCA Coordinate 1 explains 79.9% of the variation in the table.

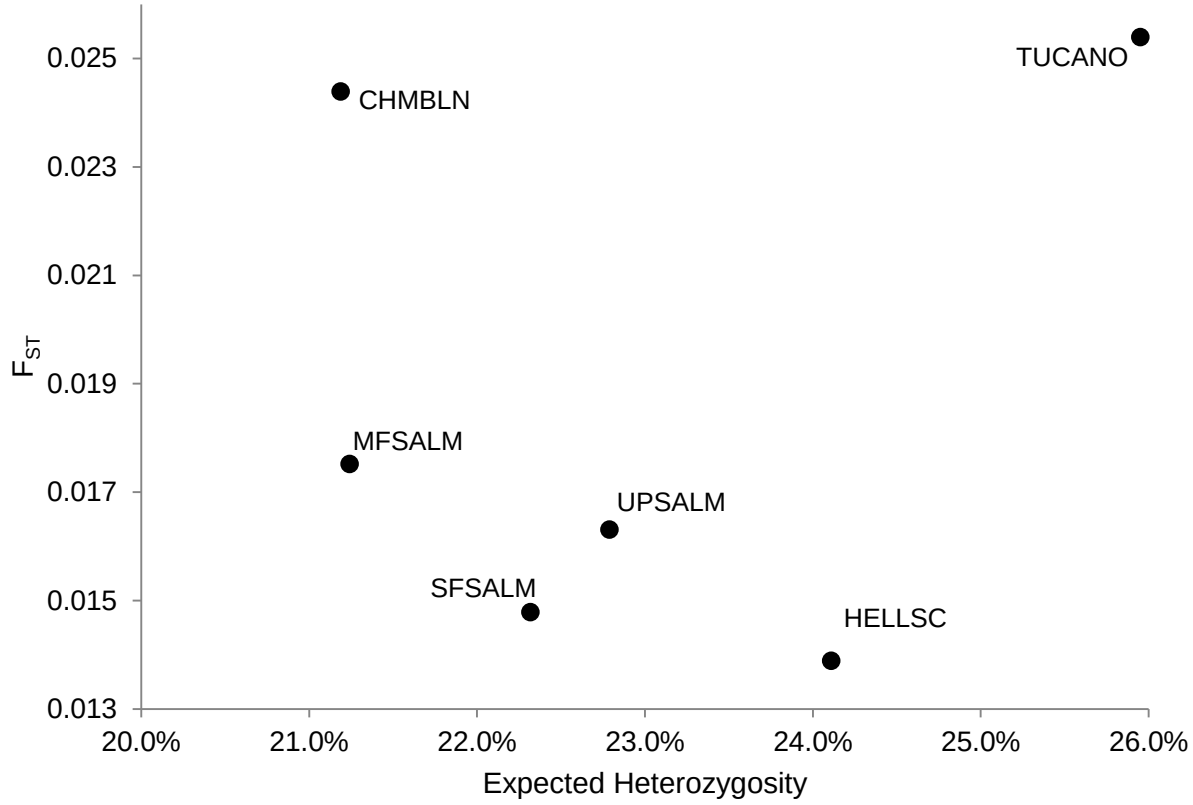


Figure 14. $F_{ST}$ as a function of expected heterozygosity for each of the reporting groups (averaged across collections within the reporting group) in Snake River Chinook salmon baseline v2.0. The FALL reporting group was excluded. In theory, the relationship between $F_{ST}$ and $H_E$ is inverse; increased gene flow among populations increases within-population diversity and decreases differentiation. Conversely, decreased gene flow among populations decreases within-population diversity over time and increases differentiation.

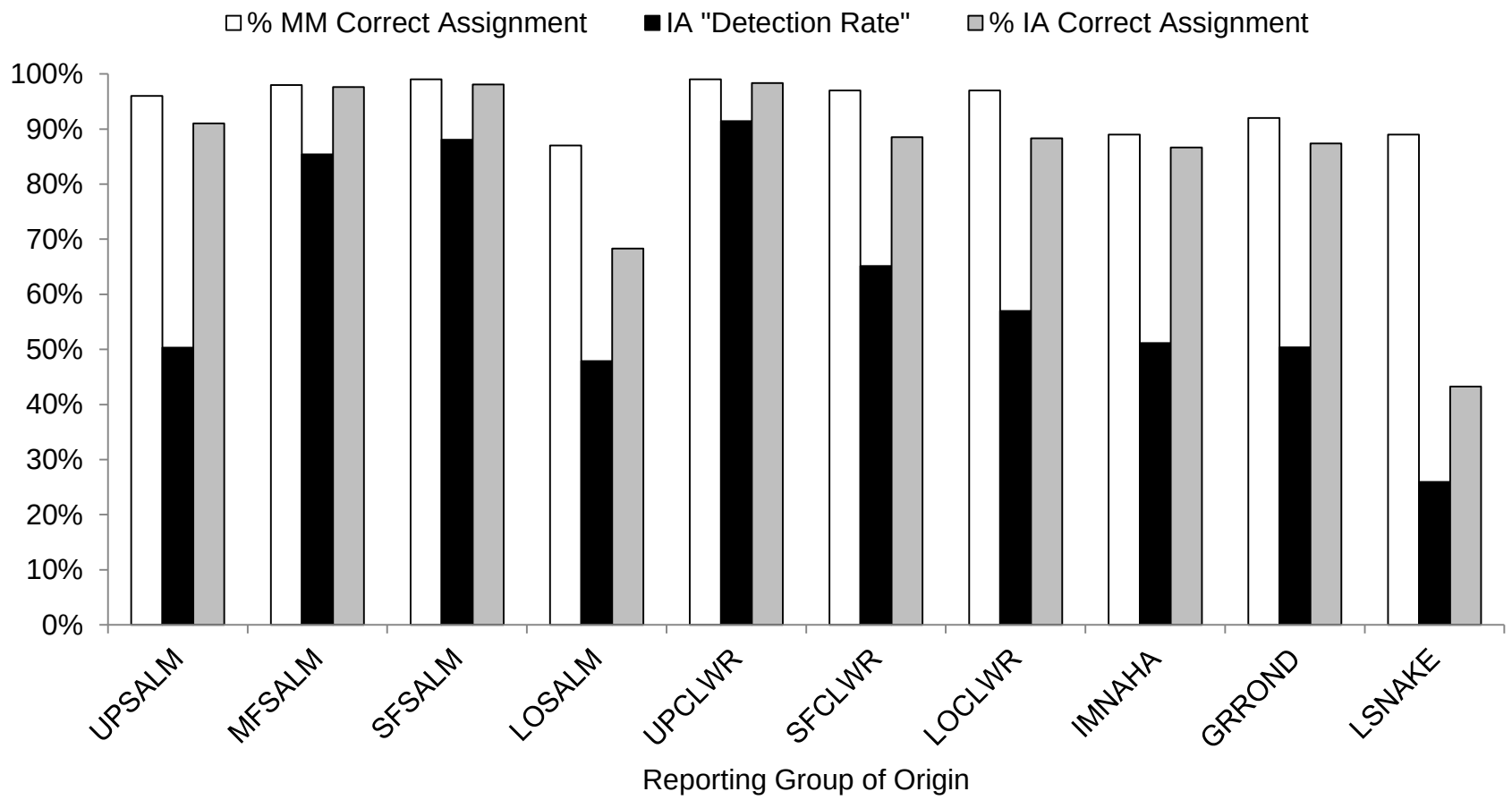


Figure 15. Summary of results from 100% simulations (ONCOR; Kalinowski et al. 2007) and self-assignment tests (gsi_sim; Anderson et al. 2008, Anderson 2010) for Snake River steelhead baseline v2.0 by reporting group. “Percent MM Correct Assignment” is the percentage of simulated mixtures (simulated from a population within that reporting group) that correctly assigned back to that reporting group of origin (averaged across popualtions). “IA Detection Rate” is the percentage of individuals from the baseline, that when removed and assigned back to the baseline, assigned back to any reporting group with ≥80% probability. “Percent IA Correct Assignment” is the percentage of assigned individuals that assigned back to the correct reporting group of origin.

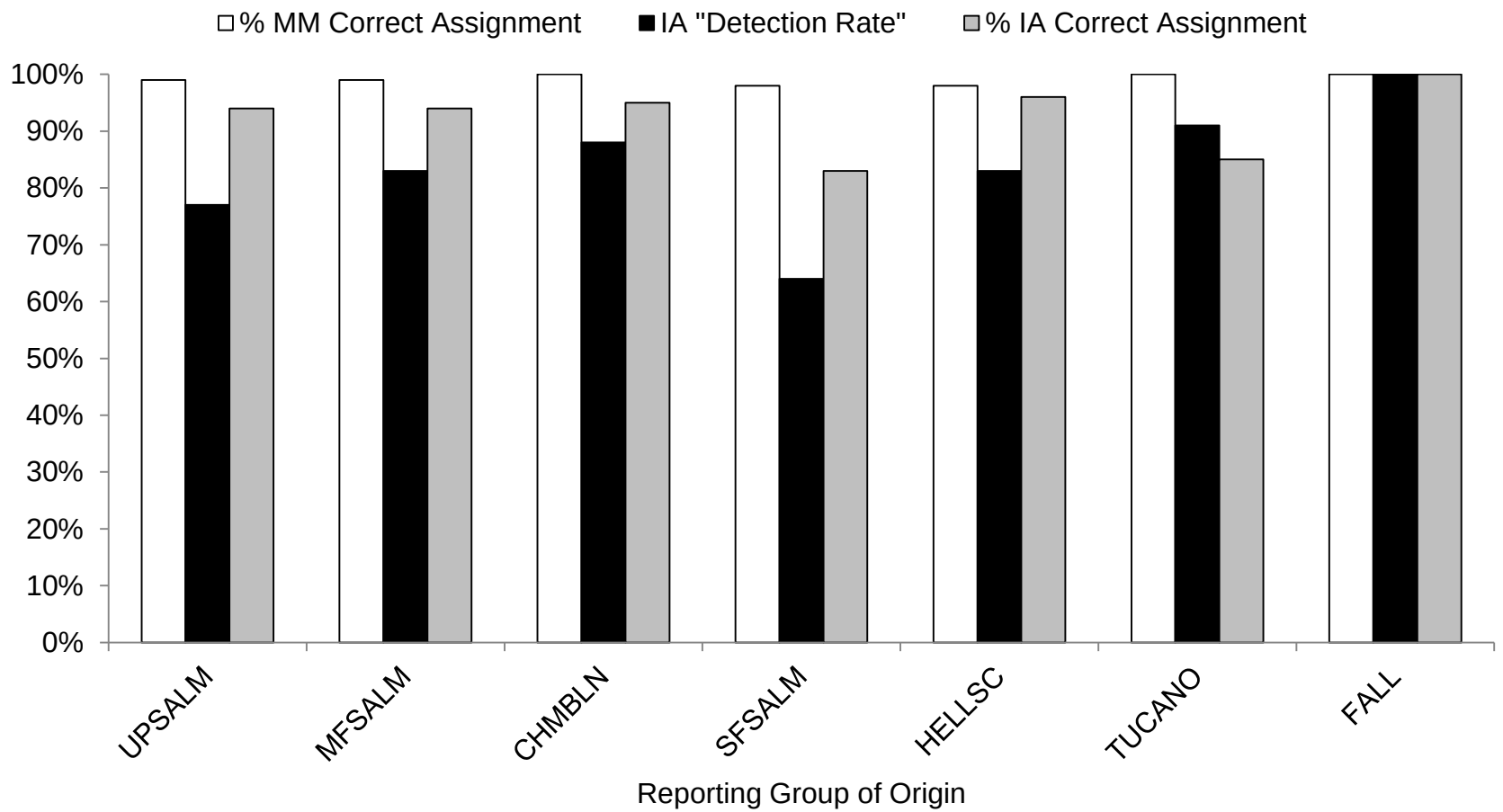


Figure 16. Summary of results from 100% simulations (ONCOR; Kalinowski et al. 2007) and self-assignment tests (gsi_sim; Anderson et al. 2008, Anderson 2010) for Snake River Chinook salmon baseline v2.0 by reporting group. “Percent MM Correct Assignment” is the percentage of simulated mixtures (simulated from a population within that reporting group) that correctly assigned back to that reporting group of origin (averaged across popualtions). “IA Detection Rate” is the percentage of individuals from the baseline, that when removed and assigned back to the baseline, assigned back to any reporting group with ≥80% probability. “Percent IA Correct Assignment” is the percentage of assigned individuals that assigned back to the correct reporting group of origin.

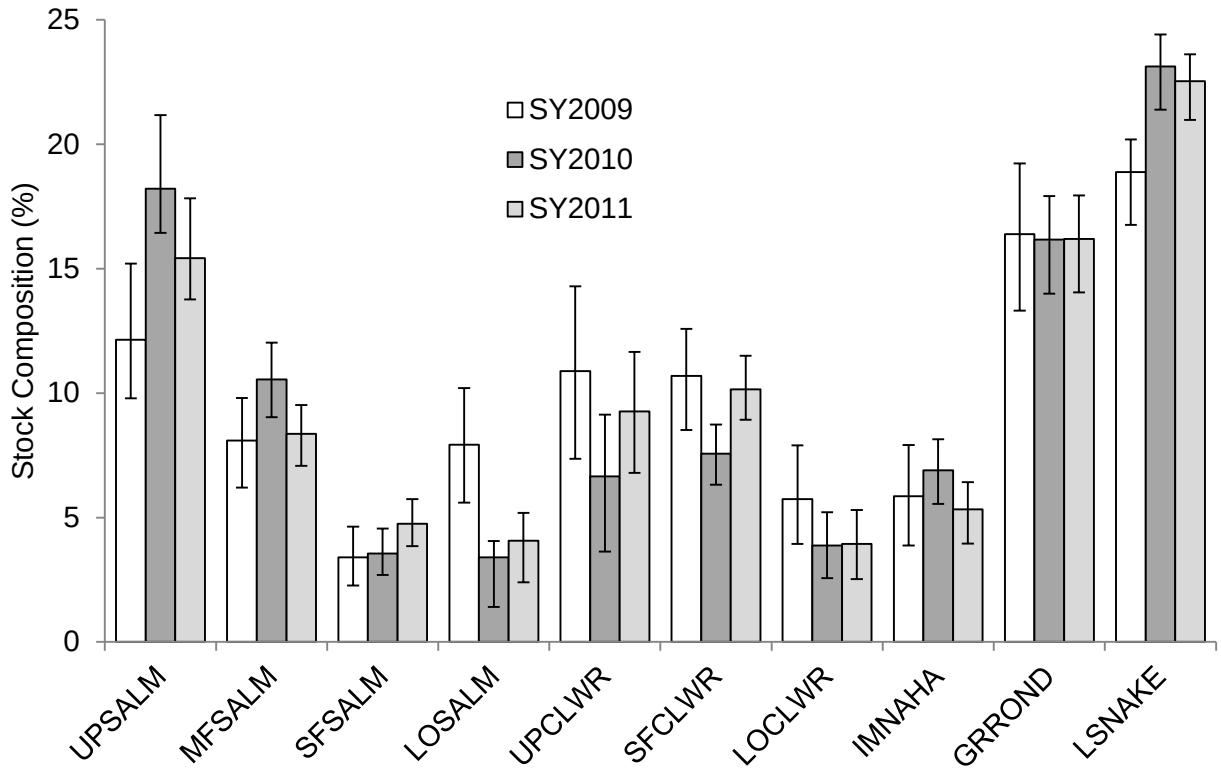


Figure 17. Mixture modeling results for natural origin adult steelhead mixtures from the Lower Granite Dam adult trap, SY2009 through SY2011.

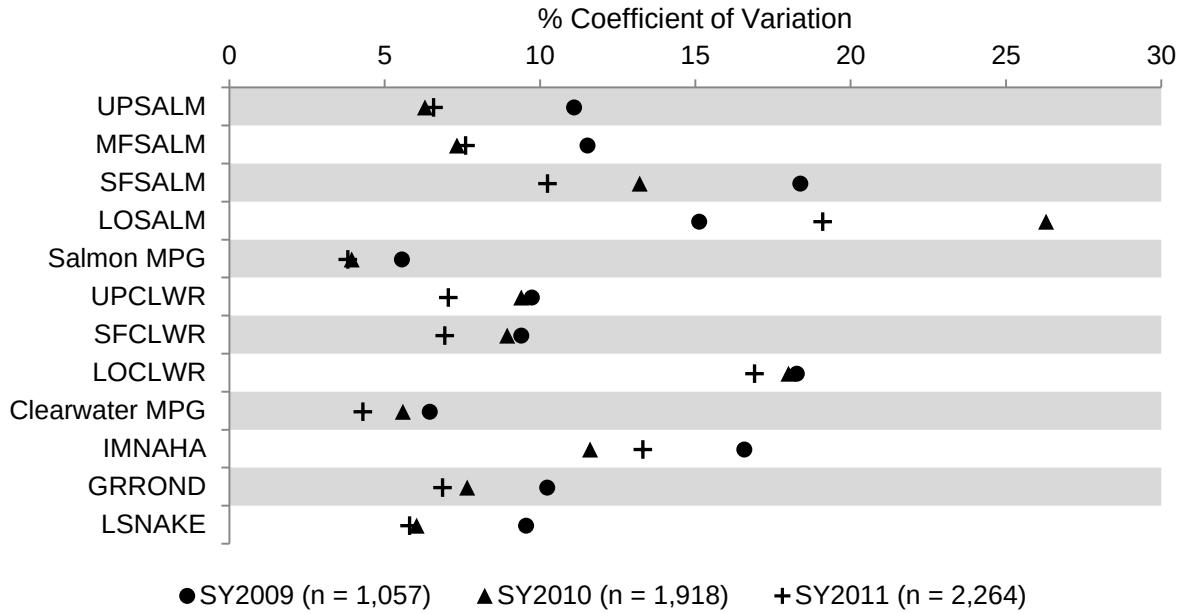


Figure 18. Coefficients of variation (CV) for stock composition estimates for natural origin steelhead mixtures from the Lower Granite Dam adult trap, SY2009 through SY2011 (Figure 17).

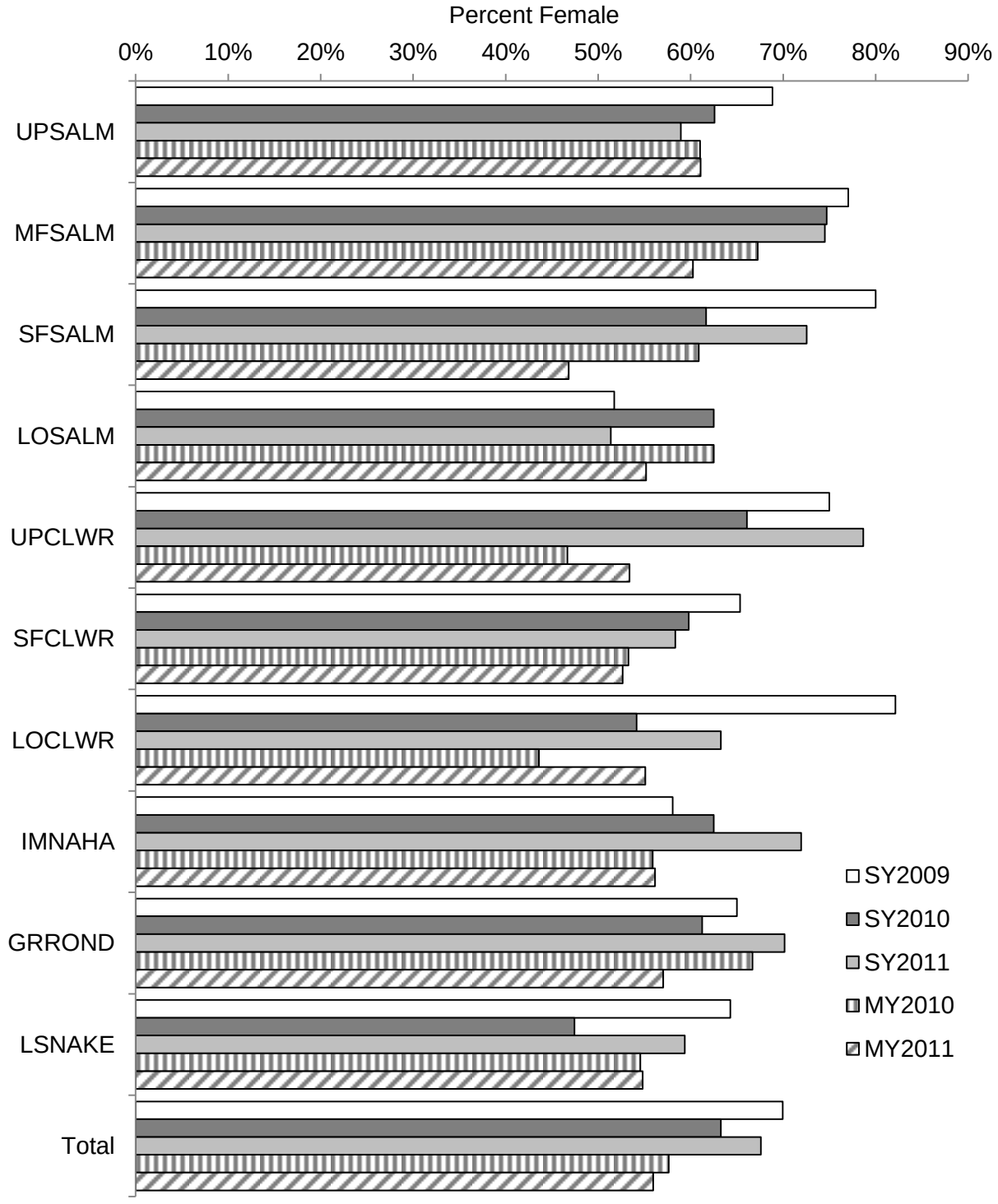


Figure 19. Estimated percentage of females based on individuals assigning to a reporting group with ≥80% probability using the Y-specific assay (*OmyY1_2SEXY*) for natural origin adult (SY2009 – SY2011) and juvenile (MY2010 – MY2011) steelhead mixtures from the Lower Granite Dam adult and juvenile trapping facilities.

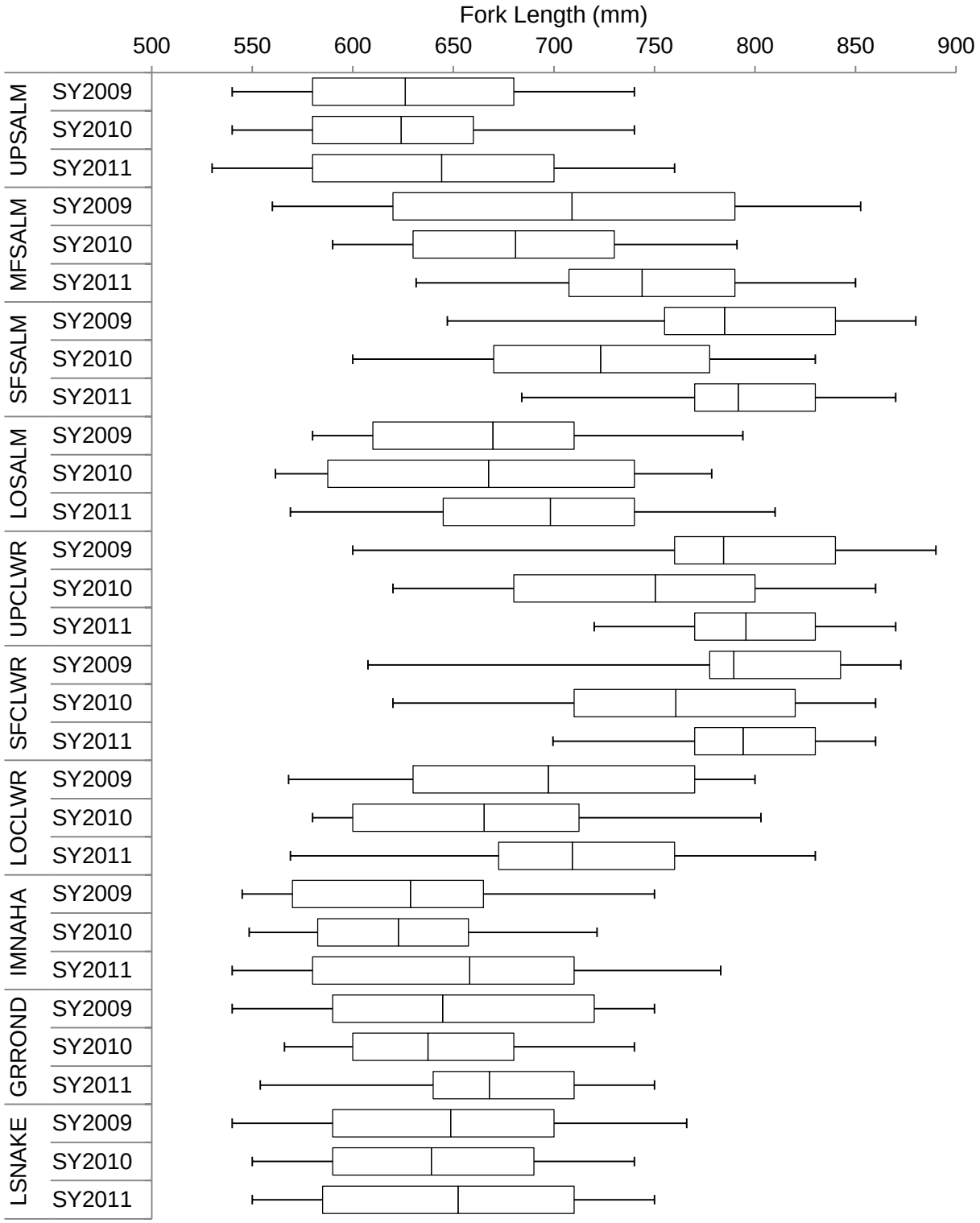


Figure 20. Box and whisker plots of length frequency for individuals assigning to a reporting group with ≥80% probability for natural origin adult (SY2009 – SY2011) steelhead mixtures from the Lower Granite Dam adult trapping facility. Intervals are 5$^{th}$, 25$^{th}$, Mean, 75$^{th}$, and 95$^{th}$ percentiles.

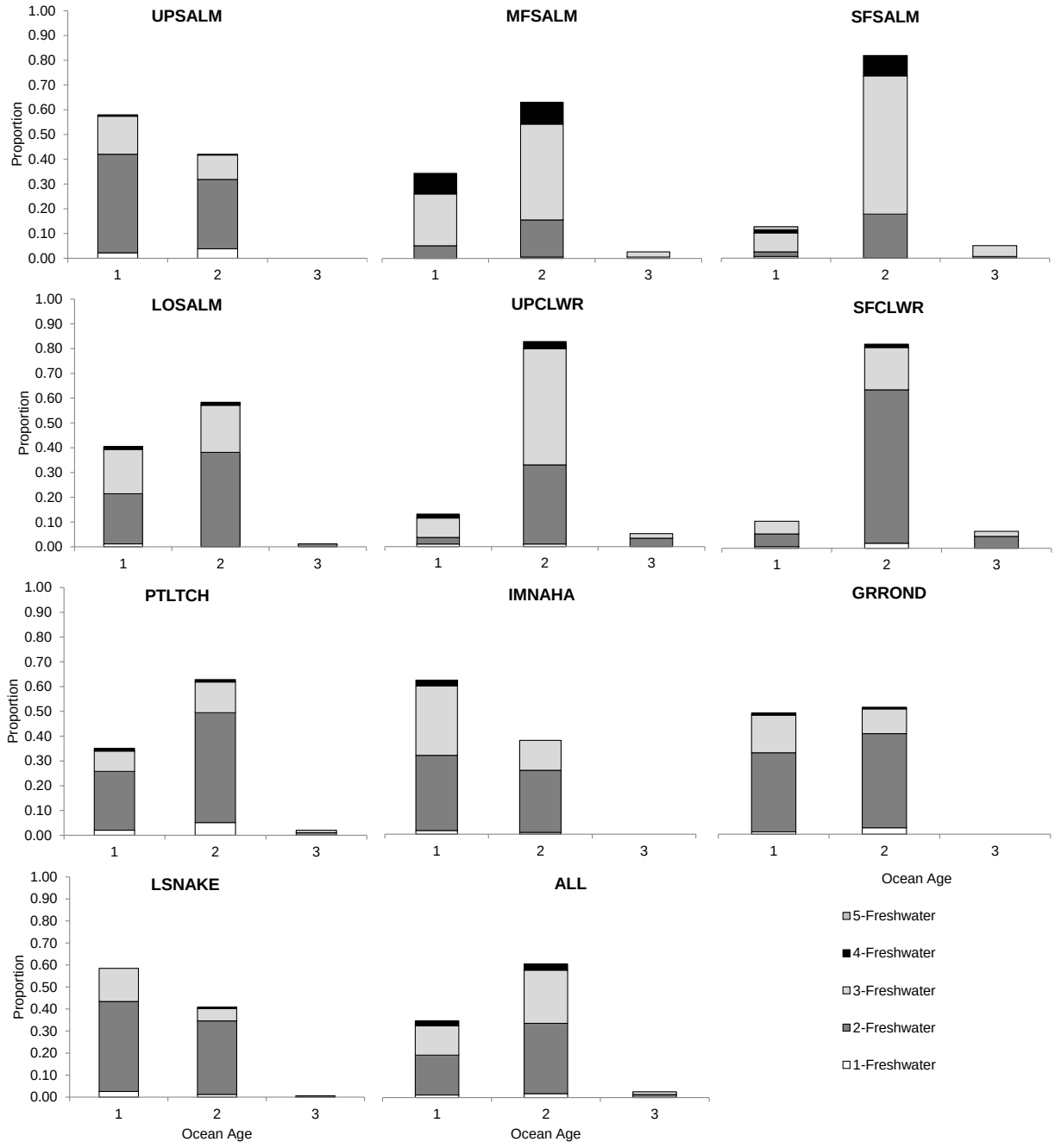


Figure 21. Estimated ocean age (proportion) for individuals assigning to a reporting group with ≥80% probability for natural origin adult (SY2009 – SY2011) steelhead mixtures from the Lower Granite Dam adult trapping facility. Freshwater age proportions are shown within ocean-age histograms.

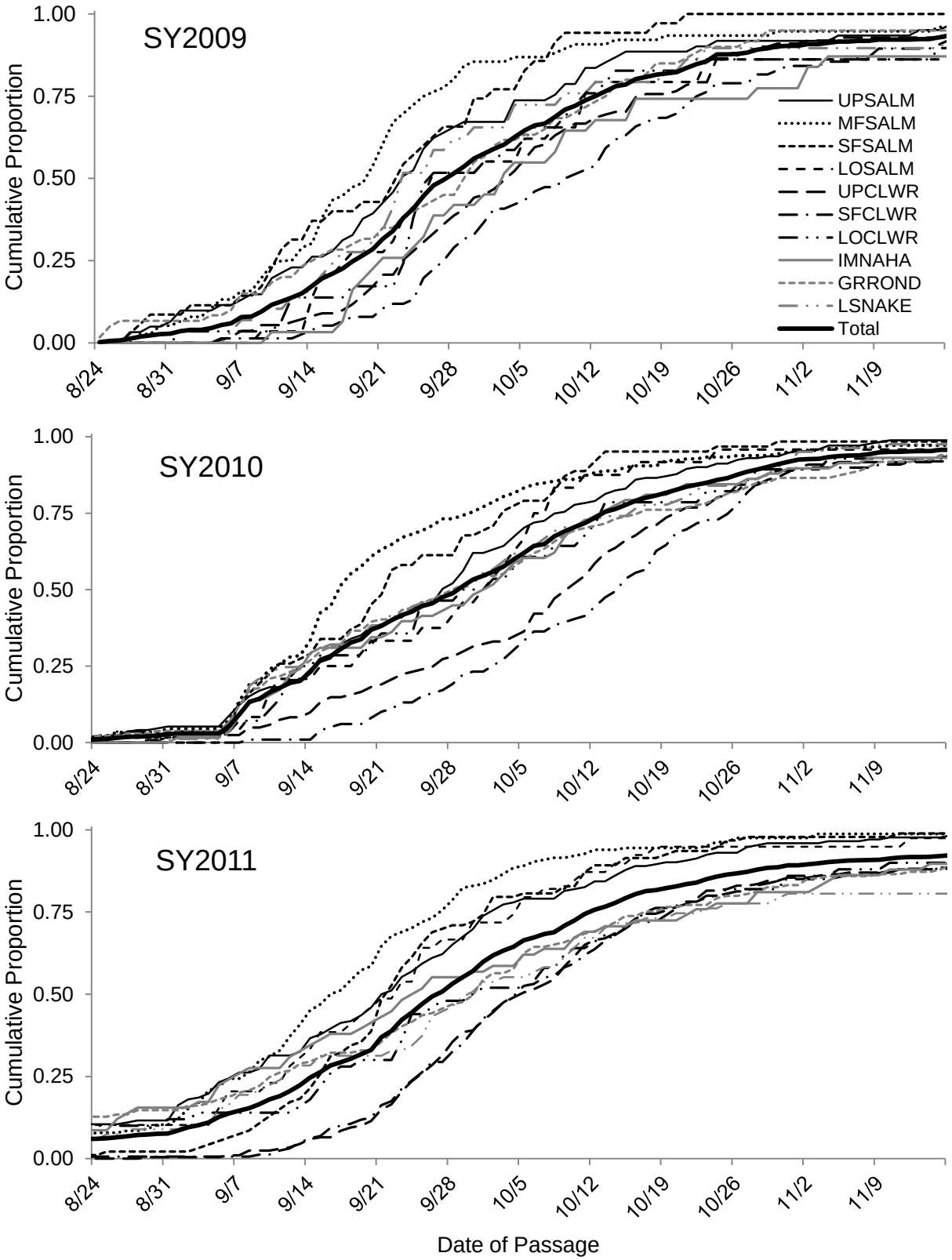


Figure 22. Cumulative proportion of individuals assigning to each reporting group with ≥80% probability and date of passage for natural origin adult (SY2009 – SY2011) steelhead mixtures from the Lower Granite Dam adult trapping facility.

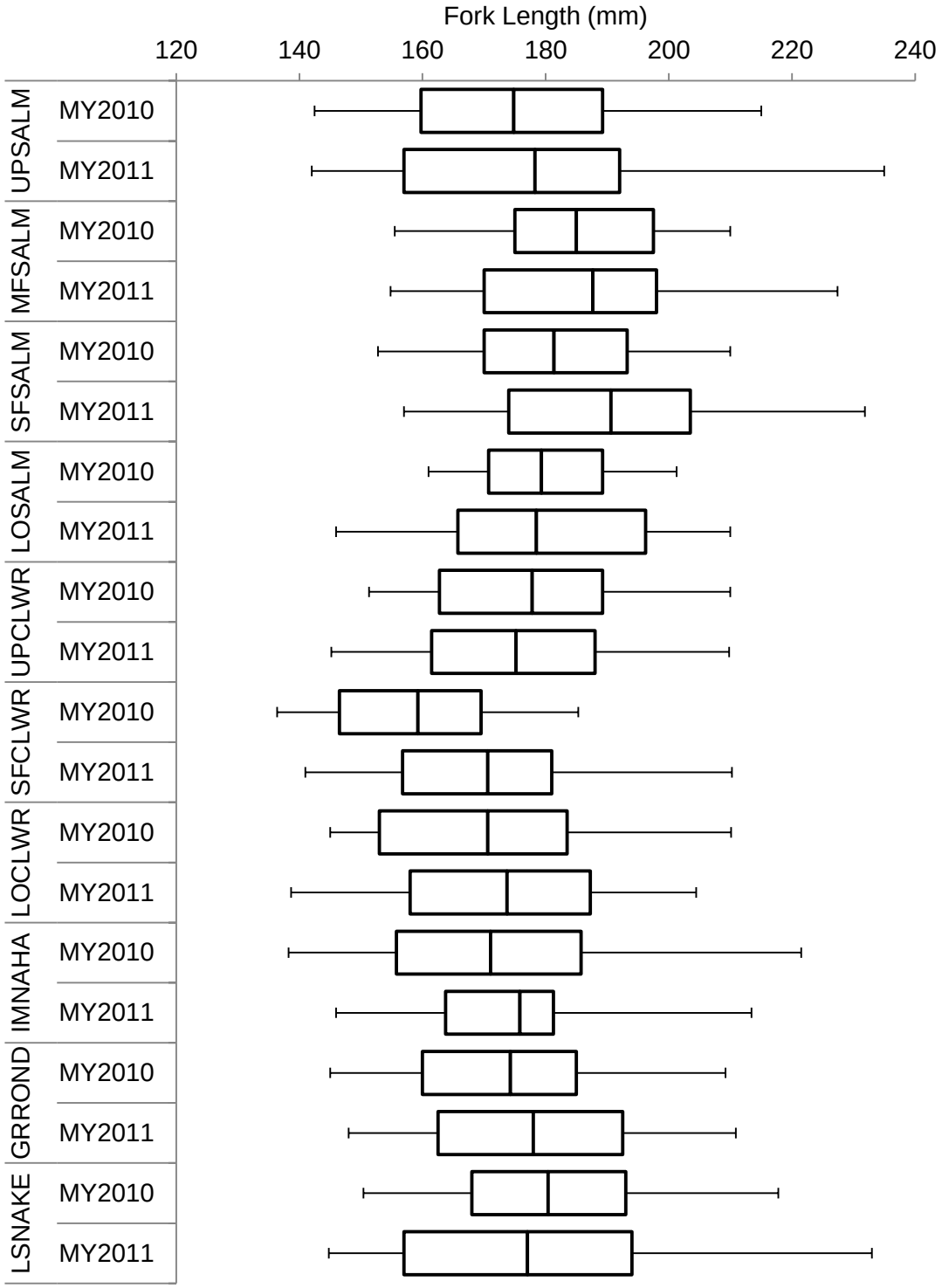


Figure 23. Box and whisker plots of length frequency for individuals assigning to a reporting group with ≥80% probability for natural origin juvenile (MY2010 – MY2011) steelhead mixtures from the Lower Granite Dam adult trapping facility. Intervals are 5$^{th}$, 25$^{th}$, Mean, 75$^{th}$, and 95$^{th}$ percentiles.

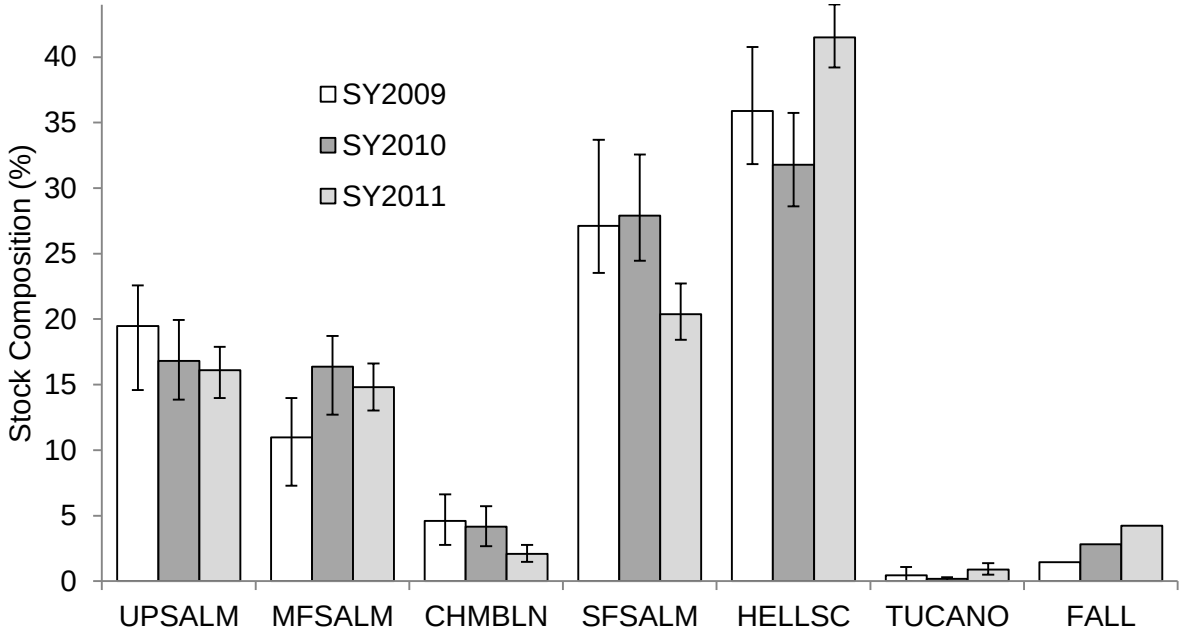


Figure 24. Mixture modeling results for natural origin adult Chinook salmon mixtures from the Lower Granite Dam adult trap, SY2009 through SY2011. Composition estimates for the FALL reporting group are via individual assignment.

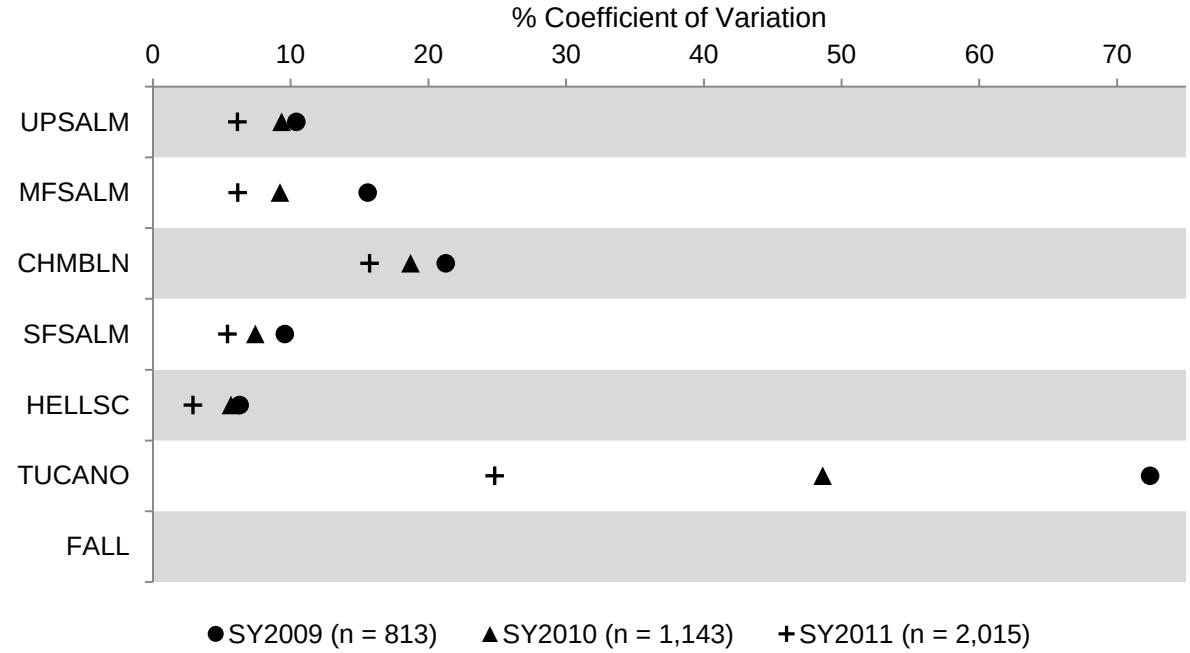


Figure 25. Coefficients of variation (CV) for stock composition estimates for natural origin Chinook salmon mixtures from the Lower Granite Dam adult trap, SY2009 through SY2011 (Figure 24). FALL composition estimates are via individual assignment, thus no CVs are calculated for FALL.

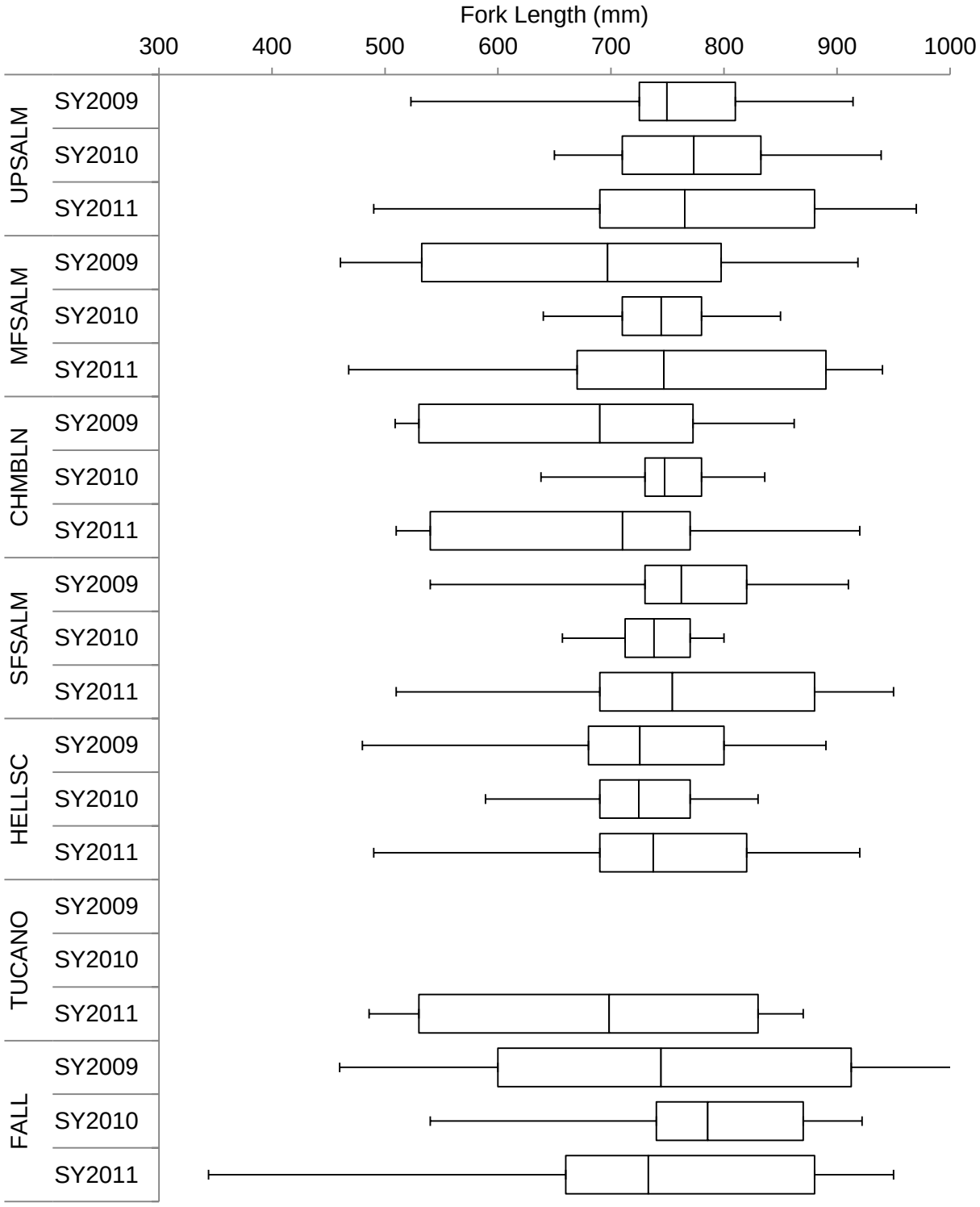


Figure 26. Box and whisker plots of length frequency for individuals assigning to a reporting group with ≥80% probability for natural origin adult (SY2009 – SY2011) Chinook salmon mixtures from the Lower Granite Dam adult trapping facility. Intervals are 5$^{th}$, 25$^{th}$, Mean, 75$^{th}$, and 95$^{th}$ percentiles. TUCANO SY2009 and SY2010 were excluded due to low sample sizes.

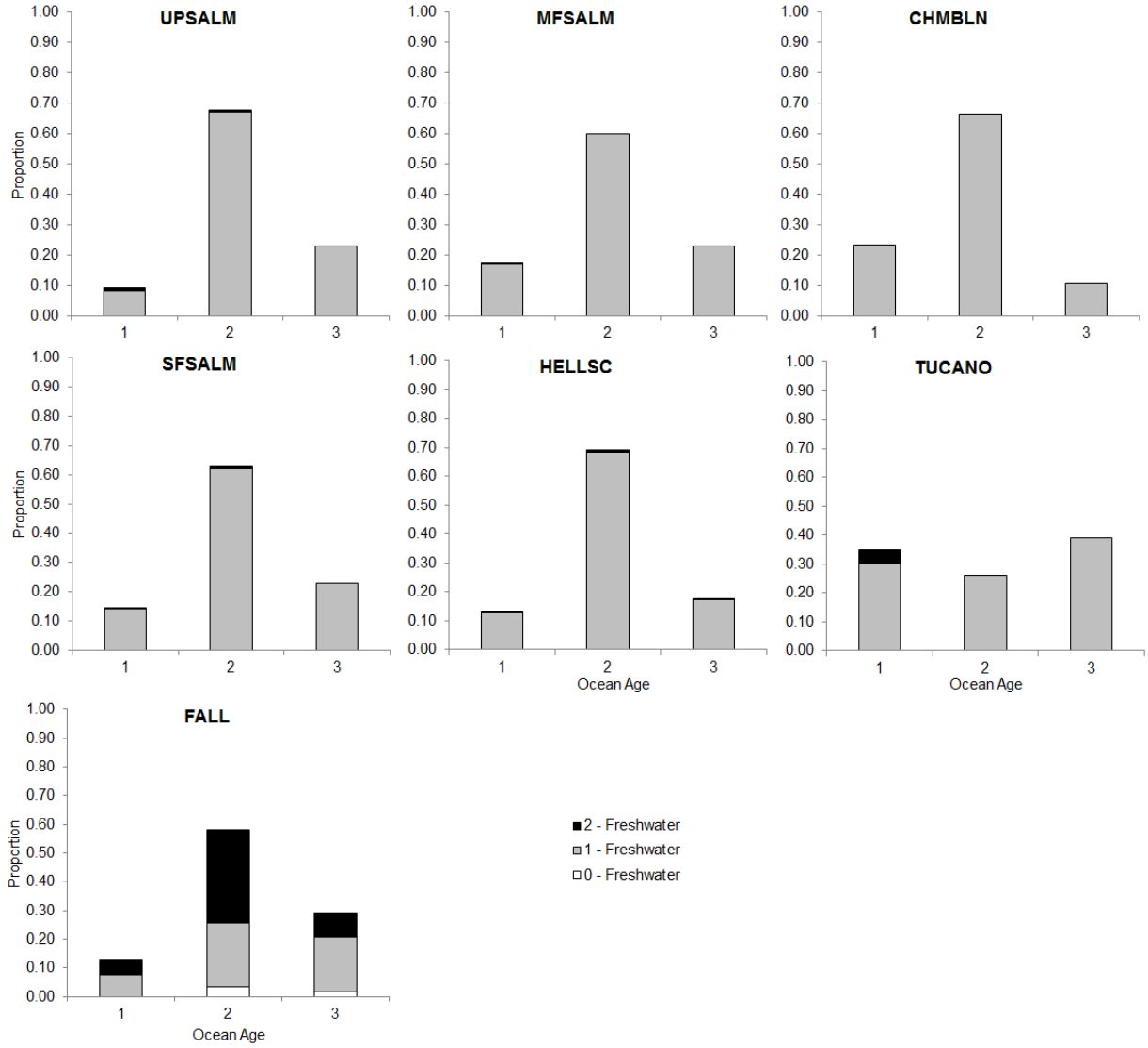


Figure 27. Estimated ocean age (proportion) for individuals assigning to a reporting group with ≥80% probability for natural origin adult (SY2009 – SY2011) Chinook salmon mixtures from the Lower Granite Dam adult trapping facility. Freshwater age proportions are shown within ocean-age histograms.

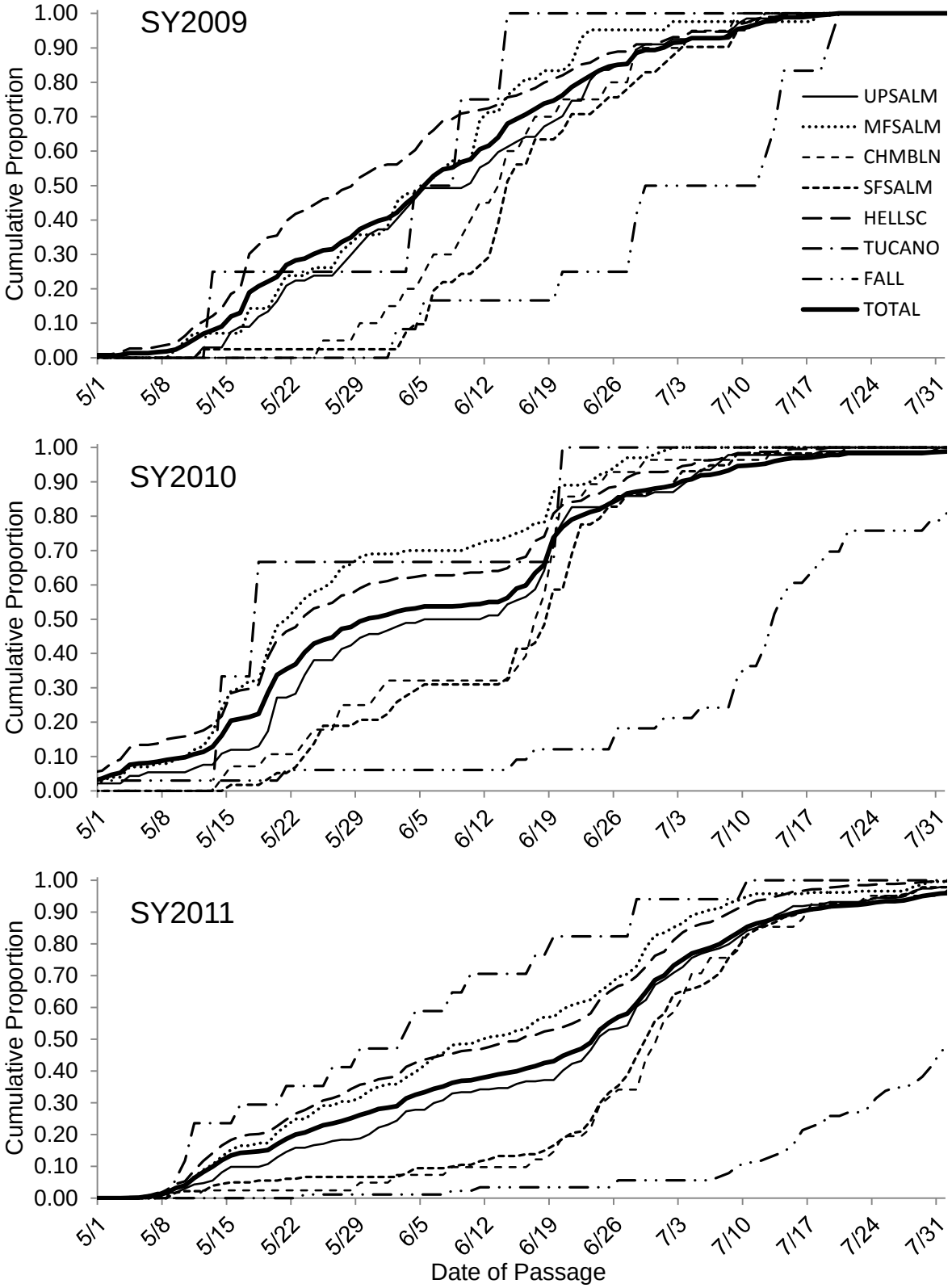


Figure 28. Cumulative proportion of individuals assigning to each reporting group with ≥80% probability and date of passage for natural origin adult (SY2009 – SY2011) Chinook salmon mixtures from the Lower Granite Dam adult trapping facility.

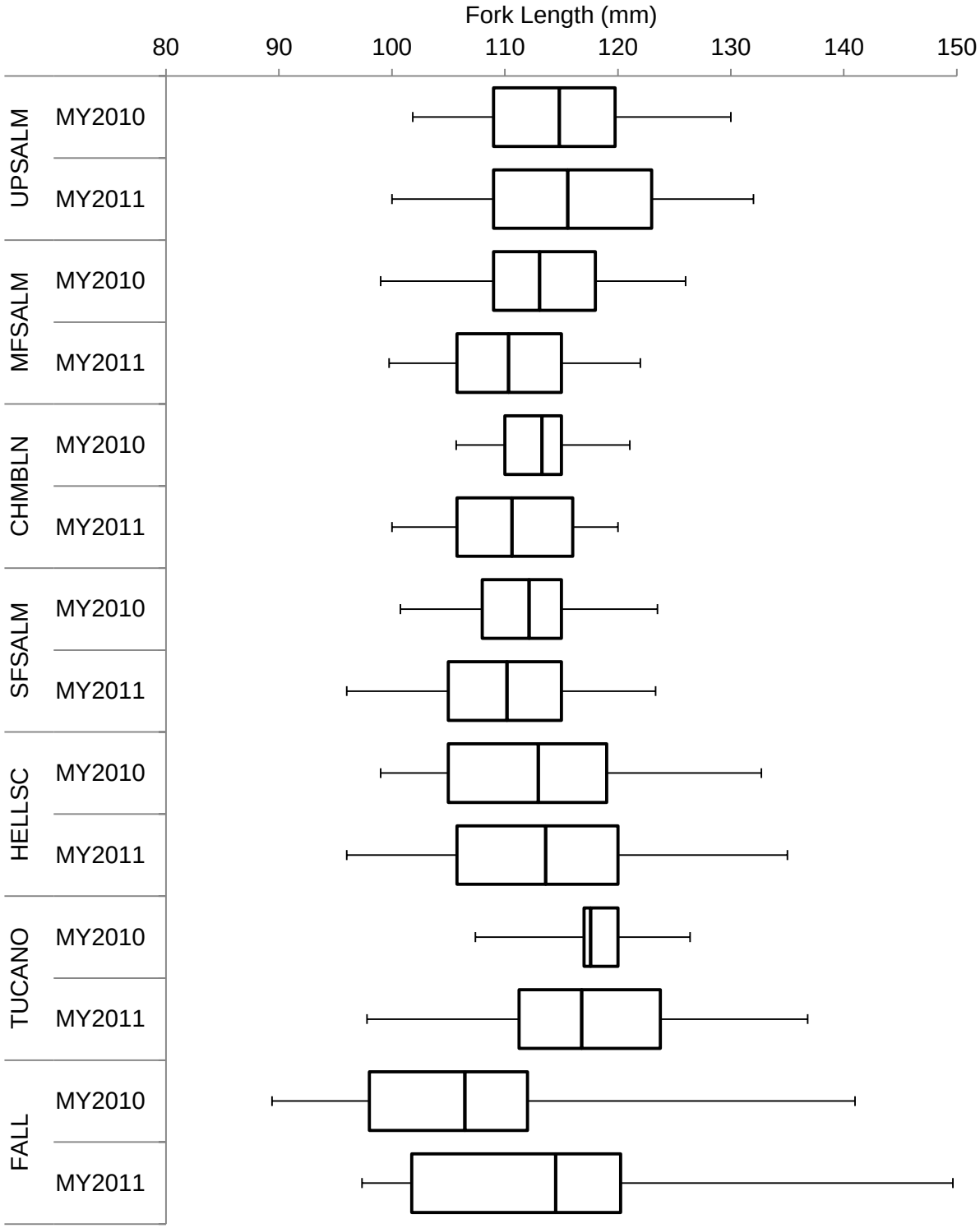


Figure 29. Box and whisker plots of length frequency for individuals assigning to a reporting group with ≥80% probability for natural origin juvenile (MY2010 – MY2011) Chinook salmon mixtures from the Lower Granite Dam adult trapping facility. Intervals are 5$^{th}$, 25$^{th}$, Mean, 75$^{th}$, and 95$^{th}$ percentiles.

**APPENDICES**

Appendix A. 192 Taqman™ assays used for *O. mykiss* genotyping. All forward and reverse primers are unlabeled and probes contain a 5' fluorophore and a 3' quencher and minor groove binder. SNP panel (PBT or GSI) is noted.

| SNP/Comments | Panel | Primers | Probes |
|---|---|---|---|
| OmyY1_2SEXY | PBT | F - GCGCATTTGTATGGTGAAAA | |
| | | R - GCCTGGCATATGAGTGTTGA | 6FAM - CTGGCATATGAACACAT |
| OmyY1_2SEXY AC | PBT | F - CCTCTCATTTTGCCCTGAAA | VIC - AGTAGGTTTCCATATTGGT |
| | | R - ACTGCCATCTGGAGGAACTG | |
| M09AAD.076 | PBT | F - ACTGTTACCACTCTCTCATCAACCT | VIC - CACCAACCACTGGTGAA |
| | | R - GGGTCCAGGAGGTTTTTAAACAACAT | 6FAM - CCAACCGCTGGTGAA |
| M09AAJ.163 | PBT | F - TCCCATGGCCCTTACTCTATCAA | VIC - AACAAAGTGAAAGTGTCCTTA |
| | | R - TTGAGGTGTATGTTGAAAAGTAAACTT | 6FAM - CAAAGTGAAAGTGTCTTTA |
| M09AAE.082 | PBT | F - CTATGTGCAGTGCCCTTCTCA | VIC - AGGTTGTTTTACAAATTTAA |
| | | R - GGCTTACAAGTATGCATGACTAGCT | 6FAM - AGGTTGTTTTACACATTTAA |
| OMS00002 | PBT | F - TTTGATTTGATTTGTATCTGCTTCTT | VIC - TGTTTTGCAGCGCTC |
| | | R - CCAACATGCCTCACACAAAA | 6FAM - TGTTTGGCAGCGCT |
| OMS00006 | PBT | F - TCCACGTAGGACATAGTTTGAGCTA | VIC - CACTTACAAATACAAAATT |
| | | R - TGTGGTGTCATGTTTGCCCTAC | 6FAM - CTTACAAATGCAAAATT |
| OMS00024 | PBT | F - CACATACAACCATCACCCTTCCTAA | VIC - AAAAACCCAAATTTTAC |
| | | R - AGCATTGAGCGAAATTACCAAGAGT | 6FAM - AACCCCAATTTTAC |
| OMS00039 | PBT | F - GTCAGTACTGTGTGTCTGTGT | VIC - CAGAGACACGTACGCACA |
| | | R - CCATCTACATTGTCAGCAGTGTGA | 6FAM - AGACACGCACGCACA |
| OMS00053 | PBT | F - GGAGCCAGGTCAAGGTGATC | VIC - TGTGTGATTGATACATATAAAT |
| | | R - GGATGTCTGGTGTGGCTGTAAA | 6FAM - TGTGATTGATACGTATAAAT |
| OMS00057 | PBT | F - GAGAAAGGGAGCATGAGACAGA | VIC - CTCCACAGAACCTTG |
| | | R - GTTGGGCTCCGGTACGAT | 6FAM - CTCCACAGCACCTTG |
| OMS00058 | PBT | F - GTGACATTTGGAGCCACTGC | VIC - CAACACTTTGTACCCCTC |
| | | R - GCTAGGAGACAGAGGGTGAAAG | 6FAM - CACTTTGCACCCCTC |
| OMS00062 | PBT | F - ACCCTGGGAAGGCTACTGTAC | VIC - TTGACCAGCAGATGGTGTA |
| | | R - TGAACAGAGATCTGGAGAGTTGGAT | 6FAM - ACCAGCAGGTGGTGTA |
| OMS00064 | PBT | F - GTGGATATGTAGTTCGATGGAACAGT | VIC - CAGGCAACATTTTATATAACTA |
| | | R - TTTACAACAATCTTCTTTTAATAAAAATATAGCCACTTAT | 6FAM - CAGGCAACATTTTATCTAACTA |
| OMS00068 | PBT | F - GCACTAACTGGACAACATTTTTAAGAATGA | VIC - AATATGCCTCCTTCGTCTC |
| | | R - GGCAGTTGAGCATTTTGGGATATT | 6FAM - TATGCCTCCTCCGTCTC |
| OMS00070 | PBT | F - CGTTCCTGCGGGACAGT | VIC - CAAAATACGGAAATGCAG |
| | | R - GTTTCTCTCACGTCCACAGATCT | 6FAM - AAATACGGGAATGCAG |
| OMS00071 | PBT | F - CCGGAGTGACCTCACATTTGG | VIC - CTTGTTTGAGCTTTTTCT |
| | | R - GCATCGTACAGTTCACCTACCT | 6FAM - TTGTTTGAGCCTTTTCT |
| OMS00072 | PBT | F - GTGGGAGAGCTCGTCTATGG | VIC - TAGAAGGTCCATGTATCTC |
| | | R - ACAACAGGTCATTGGATGTGATCAG | 6FAM - AAGGTCCATGCATCTC |
| OMS00074 | PBT | F - CCTGTTTATTCATCTAAACCAGTTCTTTAAAAT | VIC - TGAAACAAAACAAATGTTCC |
| | | R - AACTTAATTTAGCAAACAAATGTCTGAACAGAA | 6FAM - AAACAAAACACATGTTCC |
| OMS00077 | PBT | F - AATACCATCTTGAGCTCATTAGTAATTATTCAA | VIC - TTCCGGTGGTGAAGTT |
| | | R - CCAGACTTTACACACTCTTGACTGA | 6FAM - CCGGTGCTGAAGTT |
| OMS00078 | PBT | F - GAGGGAAGCAGCCATAAACAGAATA | VIC - TTCACATGCATAAGAGTG |
| | | R - GTCTCACTATGGTCCATATCTGTGTAGA | 6FAM - TCACATGCATGAGAGTG |
| OMS00079 | PBT | F - GTAACATTATGAATCTATCAGTTTCCCTAGCT | VIC - CTACTTTTCACAGTAACACAG |
| | | R - ACCTGCAACGTTAGAGCTGTTTATT | 6FAM - CTACTTTTCACAGTGACACAG |
| OMS00111 | PBT | F - CATGCGGACCTGCATAGCT | VIC - CAACCAGACTACCATTC |
| | | R - GCTTAGCCATTGACAGAGCATATCA | 6FAM - AACCAGACTGCCATTC |
| OMS00089 | PBT | F - GCACCATTTGAATAAAAAATCTGCTTTGT | VIC - ATGAATCCCAAATAAGAAC |
| | | R - GCAACCCAATTCAATATTAAGCACATGAT | 6FAM - AATCCCAAACAAGAAC |
| OMS00090 | PBT | F - AGGGCACAACACCACTCTAAATT | VIC - ACAACCACACAAGATT |
| | | R - TCGAAAAGCAACATCTGTCTCAGT | 6FAM - AACCACGCAAGATT |
| OMS00101 | PBT | F - GCGTGTCGTGGGTCAGTTAAATA | VIC - CTCTAGTAGCCTTATAGAAAG |
| | | R - GTGCAATCCAACCTATTAGTAGATATGCT | 6FAM - CTAGTAGCCTTACAGAAAG |
| OMS00105 | PBT | F - ACATTTGAAGTCAGTATGGGTGTTGAG | VIC - CTGCTATTCAAATTGCT |
| | | R - GAACCTCACCACAGTACTAAATGCA | 6FAM - CTGCTATTCACATTGCT |
| OMS00106 | PBT | F - CGTGTAGCATTCTTGAGGAAGCTT | VIC - TCTGATGGAAACTTTC |
| | | R - TTTCCAACAGATGCCAGAATCCT | 6FAM - TGATGGCAACTTTC |
| OMS00154 | PBT | F - GATGTTGGCTGGAGGTGTAGT | VIC - ACAGGGCTTCTGATTGA |
| | | R - TGGGAACACTTTGCCTACCC | 6FAM - AGGGCTTCAGATTGA |
| OMS00112 | PBT | F - TGGCAGCAAAAGGGATGCA | VIC - CCGGTTTCAAGTTTACTTGT |
| | | R - TCCTGAGCAACCAGTCAACATT | 6FAM - CGGTTTCAAGTATACTTGT |
| OMS00118 | PBT | F - GCTTATTTAGAGTGCATGCCAGATG | VIC - AATGTGCACACCCCGC |
| | | R - TGGAACCAATGGGACAGTCCTA | 6FAM - AATGTGCACCCCCCGC |
| OMS00120 | PBT | F - GGCAGAAGAGGAGAGAGATATGATTG | VIC - TCGCCCACTAAAAC |
| | | R - CCTCAAATACCTCTGACATTGAAGGTT | 6FAM - CGCCCACCAAAAC |
| OMS00121 | PBT | F - GGAAGGAGGTCCAGTGTGAGT | VIC - ACAGCGTGATAAATT |
| | | R - AAAATATGCAACACCACTAAAACTGGAAAA | 6FAM - CAGCGTGGTAAATT |
| OMS00132 | PBT | F - GTTTATGACTCCATTGCCGAAATGATT | VIC - CAGCAGTCCTCTGTGTGG |
| | | R - ACGCGACCTGCAATTCATCAATA | 6FAM - AGCAGTCCTCAGTGTGG |
| OMS00175 | PBT | F - TTGCGATATGGGACTGTATACATTTATTCC | VIC - CATCACTAGTTCAAATACAA |
| | | R - ACTACCTCCAGTTAAAATAGTGTGGGAAA | 6FAM - CATCACTAGTTCAGATACAA |
| OMS00179 | PBT | F - GTCATAACAAAATCAGGGCTTTCCAA | VIC - TGCCTCTTCTCTTTTCTCAT |
| | | R - TGGGAGATTTGGGCTGCTTTAAA | 6FAM - CCTCTTCTCTTGTCTCAT |

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|---|---|---|---|
| OMS00180 | PBT | F - GCGCCGAATGGCATTAGG | VIC - CTAAAAGTGCATTAAGCC |
| | | R - CACATTGCTGTCGTTTAGTTTGACT | 6FAM - CTAAAAGTGCCTTAAGCC |
| Omy_101832-195 | PBT | F - TGGCTCTGGACCTGTTGAGA | VIC - TGTAGTCTTTCAGAGTAGTATG |
| | | R - CGTCACAGCTATTTTAGGCGTAGT | 6FAM - TAGTCTTTCAGAGGAGTATG |
| Omy_101993-189 | PBT | F - ACAAAACACAGTGGAATTACAATTAACGTT | VIC - CTTGATTTGCAGCTTGTCAA |
| | | R - GGAAGTTAAATTTCGCTTCGTCAGAA | 6FAM - TGATTTGCAGCATGTCAA |
| Omy_102505-102 | PBT | F - CTGCAAACTGACATGGTAGCAAAA | VIC - AACAGGATGTTTTTGC |
| | | R - TGCTTGCTTTTTAAAAACAATCTCCCA | 6FAM - CAGGATGCTTTTGC |
| Omy_104519-624 | PBT | F - CGTGTGAGTTTGCGGTAAAGAC | VIC - CAGCAGGATACATCCGACT |
| | | R - TGACGAGTCCGTCTTATCATCCT | 6FAM - AGCAGGATACGTCCGACT |
| Omy_105105-448 | PBT | F - CAATTTGCAAGCAGGGAAAGGTTAT | VIC - AAGGAGAATGCATAATC |
| | | R - GTGATGGGCTGCAATTGCTT | 6FAM - TGAAAGGAGAATACATAATC |
| Omy_105385-406 | PBT | F - ACCTACCCTCACCTGAACTTCA | VIC - CTTGGAACCATTGCTAC |
| | | R - CGCTCTTCTGGGCGTATCG | 6FAM - TTGGAACCGTTGCTAC |
| Omy_105714-265 | PBT | F - CCACTCAGTGCAAGCATGGA | VIC - CTGTTGTTTGAGGTTCAG |
| | | R - GCTTTCAATCCTTGGCTCCAATATC | 6FAM - TGTTGTTTGAGATTCAG |
| Omy_107806-34 | PBT | F - TCTTTGTCCATGCACATTGATATT | VIC - ATTGGATGTCAGTGTCATT |
| | | R - AGCACATTTAGTTAGCAGTGATGGA | 6FAM - ATTGGATGTCAATGTCATT |
| Omy_108007-193 | PBT | F - GTGAATACCACCCAGGCTTGT | VIC - ATGTTTTCTCCCTACTTAAC |
| | | R - GTCCCTTCCCCAGTTTCACTTAATT | 6FAM - TTTTCTCCCCACTTAAC |
| Omy_109243-222 | PBT | F - ATGTGCACCTCTTAAATTGTAAGTAAAATGT | VIC - TGTTCATTAAATTGACTTTTT |
| | | R - ACCCTATATTCAGTGGCAAGATTGC | 6FAM - TTCATTAAATGGACTTTTT |
| Omy_109894-185 | PBT | F - CGGTGTCATTATGGTTGTCATTGTG | VIC - CTCCCTGATCCCCC |
| | | R - GGGAGGAATTGGAATGACAGATTAAC | 6FAM - CTCCCTGGTCCCCC |
| Omy_110064-419 | PBT | F - GTGCAAGGGACCTAGCTAATCC | VIC - ACGTTAGCTTTTAATTTC |
| | | R - TCTGAACTGACACTGAAGAACAAAGAA | 6FAM - AACGTTAGCTTTTCATTTC |
| Omy_111383-51 | PBT | F - CACGCGCAATCTCTCGTTTTAC | VIC - ACCTAGTGCGCTTGCT |
| | | R - TCTTTAGGCAACAAGCGTGTCA | 6FAM - ACCTAGTGCACTTGCT |
| Omy_113490-159 | PBT | F - CATAGTACATTTACAGATAATGTTTTAAAGTGCATGT | VIC - CATCTGTTTTGGTTTAGC |
| | | R - CGAGATACCAAAATGCCACAGTTACAT | 6FAM - CATCTGTTTTAGTTTAGC |
| Omy_114315-438 | PBT | F - CCTCACCGATCTAGTCAACTTCATC | VIC - TTATGGGCTTAAGGGTC |
| | | R - AGGAGGCTGAGGGAGATTCTAG | 6FAM - TTATGGGCTTACGGGTC |
| Omy_114587-480 | PBT | F - CAGATTACGTTATTACGTTTGGGAAATTTTTAAGT | VIC - CCTGTCCAAAATTGT |
| | | R - GTGAAAGAGTGGGAAATATAATTATAAGGTCAGA | 6FAM - CCTGTCCACAATTGT |
| Omy_129870-756 | PBT | F - TCGTTATTTTGCCTCGCGGTA | VIC - ACAGGTATTTCGTGAAATG |
| | | R - TCCCATGAAGATGTATACATGTTTTGTGA | 6FAM - CAGGTATTTCATGAAATG |
| Omy_116733-349 | PBT | F - GAAATGGACATGCCTACAAATTGCT | VIC - AGAGAATCTGATAGTATTTC |
| | | R - GATGTGATCAGTTTAGGCAAGGC | 6FAM - AGAGAATCTGATAATATTTC |
| Omy_128923-433 | PBT | F - ACGTTTCTTTGGGCTGAGACTTATT | VIC - CTTCATTTTCATTCACTGTTTT |
| | | R - CTATGTCCTTGGCAGAAGTCTACA | 6FAM - CATTTTCATTCGCTGTTTT |
| Omy_130524-160 | PBT | F - CGAAGGTAGCGATTGGTCGTT | VIC - ATGGCTTGATCCTCA |
| | | R - TGTCTGTTCTGCTGTGTGCTT | 6FAM - ATGGCTTCATCCTCA |
| Omy_97660-230 | PBT | F - TCAGTTATGTGTAATCTCATTACCTCTCCAA | VIC - ACGTAACTTGTAGCGTTTT |
| | | R - AACAGAAAAGGTCTCAATGTATTTTTTGCA | 6FAM - ACGTAACTTGTACCGTTTT |
| Omy_99300-202 | PBT | F - CAGTTTGACCCGATGGTGTGA | VIC - TCAGGCATGAGAGAAA |
| | | R - GATTATGGCGTGGCCTTTTGG | 6FAM - ATCAGGCATGTGAGAAA |
| Omy_aldB-165 | PBT | F - GGGTTAGGTGGATTTGAAGGAGTAA | VIC - ATGCTAAAATGAACTCCCCACCA |
| | | R - AGGAAGGTGATGCCTGAGAGA | 6FAM - CTAAAATGAACTCGCCACCA |
| Omy_anp-17 | PBT | F - GGTAATGCCACATGCGGTAAATT | VIC - CTCTCATTGGTATAGTAACC |
| | | R - GGCGAAATCTGAAAATGTGCTGTTA | 6FAM - CTCATTGGTATATTAACC |
| Omy_arp-630 | PBT | F - CTGCACAACTTGTTTCCTGCTATT | VIC - CCGCTCCGTCTGCT |
| | | R - ACCAAGTGTCCCTGTAAGCC | 6FAM - CCGCTCTGTCTGCT |
| Omy_b1-266 | PBT | F - TCATGTGAACTTTAATTGACTAGGAAGTCG | VIC - TCTATAAACAACATTTTTC |
| | | R - GATATGAAAATATCTGAAGAGTTATATTTGGGAAATTGAC | 6FAM - TCTATAAACAAAATTTTTC |
| Omy_BAC-B4-324 | PBT | F - GCCTAATATTGGCCTAATGTCCTTCA | VIC - CATTGCCAAATACG |
| | | R - CGTACTTTTCTTTTACAAAATTAAGTGGAGGAT | 6FAM - TACATTGACAAATACG |
| Omy_ada10-71 | PBT | F - TCTTTGAGCGACAAAGTCCTTGT | VIC - CTTCCTGCGTCCAATT |
| | | R - ACCCACACATGAACGCAAAAG | 6FAM - CTTCCTGCATCCAATT |
| Omy_redd1-410 | PBT | F - GTACTCCCACTAACATACAGTAGACTCA | VIC - AAAATATCCTGCAAGGAAT |
| | | R - GGCACCATTGTGTTTTAGGATGTAG | 6FAM - AATATCCTGCAAGAAAT |
| Omy_cd59-206 | PBT | F - CGATTGGCCCAGATGTTTCCAT | VIC - CAACAATCGAAGGTAAAT |
| | | R - GCTCCGTTGCATAGGTGACT | 6FAM - CAACAATCAAAGGTAAAT |
| Omy_colla1-525 | PBT | F - CCTCGGCGTGACAACCT | VIC - CTGTTGGGAGAAGAG |
| | | R - CCCAGAGAATGGTGCGATTAGG | 6FAM - TGTTGGGAAAAGAG |
| Omy_cox1-221 | PBT | F - CACTGAACTGTAAGCCATTGTGATT | VIC - CGGTAAGACCATTAAAA |
| | | R - GCAACATGGGAATGATTCATAAATGCA | 6FAM - CGGTAAGACCATTTAAA |
| Omy_crb-106 | PBT | F - GCTCAAAAAGATTCTGCCAAATTCACA | VIC - TTGCAATGCGTCTTT |
| | | R - ATTACAATGAAAGTACTTGAGTGTTTATGCAAA | 6FAM - TTGCAATGAGTCTTT |
| Omy_g12-82 | PBT | F - GATCAATTCGATCGCTCATGAAACTT | VIC - CAAACTCTCAGGATTAG |
| | | R - CTTCTCTCGTTCTCATTGTGTCTCA | 6FAM - AAACTCTCGGGATTAG |
| Omy_gluR-79 | PBT | F - GACTGTCTATAGCTATTCTTCTCAAACTGT | VIC - CAAGTATTTTGCGTAGGAAT |
| | | R - AGAAACTACCATTGTGATTAACAGATAGAAAATACAT | 6FAM - CAAGTATTTTGCATAGGAAT |
| Omy_hsc715-80 | PBT | F - CCGGTCTACCCTATAGCTGTTG | VIC - AACTGTATTTGGGAAAAT |
| | | R - AGTCAGTCAATTAGTGGTTTGAAATACTATCA | 6FAM - ATAAACTGTATTTGTGAAAAT |
| Omy_hsf2-146 | PBT | F - GGAGCAGAAAAAGGATTGGACCTT | VIC - CAGCTGTTAGTAGATTAT |
| | | R - CCAACAATTGCAGCCTCATCTTAAT | 6FAM - ACAGCTGTTAGATTAT |
| Omy_IL17-185 | PBT | F - CCACCACACTCTGCAGCTT | VIC - AAGAATCTCACCTGCCCAT |
| | | R - TTGACGGGAATCCGAGACTTC | 6FAM - AAGAATCTCACTTGCCCAT |
| Omy_Il-1b_.028 | PBT | F - ACTGTCTGGCTAGAGCACATTG | VIC - CTGAGGCAACTTTTGT |

| SNP/Comments | Panel | Primers | Probes |
|---|---|---|---|
| | | R - ATCTTCTACCACCGCACTGTTTTAA | 6FAM - TGAGGCAGCTTTTGT |
| Omy_Il1b-198 | PBT | F - TTTAATCTCGGTGCTGAGCTAGTG | VIC - ACCTTAGTTGTTGCTTCAT |
| | | R - CAAGCAAAATTGACTCCAGCCATTA | 6FAM - ACCTTAGTTGTAGCTTCAT |
| Omy_IL6-320 | PBT | F - CTTGTTCCTCGTTGTCTTCCTTCTA | VIC - CTATAGGAGAGAGGACAACA |
| | | R - CGACTGATCTCCTGCAGACATG | 6FAM - ATAGGAGAGAAGACAACA |
| Omy_metA-161 | PBT | F - CGCATGCACCAGTTGTAAGAAAG | VIC - CAAGTAAGTGGTTATATTCT |
| | | R - AGTGCCACCAGCGATAAGAAAA | 6FAM - CAAGTAAGTGGTTCTATTCT |
| Omy_NaKATPa3-50 | PBT | F - GTTGAGCGTGTTATGGGAAAAGAG | VIC - CACTCTGTTTCCTTTCTTT |
| | | R - TTGCATCGGCTTTCTGAAAACC | 6FAM - TCTGTTTCCGTTCTTT |
| Omy_txnip-343 | PBT | F - CCTTCAAACTAACGCATCATAGACATG | VIC - CCAACTGAAGAGATCTG |
| | | R - GGTCACTTGGCTAATCCCCTTAT | 6FAM - CAACTGAAGGGATCTG |
| Omy_nkef-241 | PBT | F - AGTGTCATTGATGTCGGCCTATTTT | VIC - CTTCTGTATCATTTTTG |
| | | R - AAACGAATGTCCACCTCAGATGTT | 6FAM - TCTTCTGTATAATTTTTG |
| Omy_ntl-27 | PBT | F - GGTGTGTTACTGTAGTTGTGTCCTT | VIC - CAGACAAGAGTACCCCAAGAC |
| | | R - TGTGTAGCTAGTGATCCTGATTGTCT | 6FAM - CAGACAAGAGTACTCCAAGAC |
| Omy_Ogo4-212 | PBT | F - TCCTCTCTCCCATTCAATCACTAATGA | VIC - CATTTGATGAGACATCTT |
| | | R - AGACAGTAACAAAGCCTCAAACTTGA | 6FAM - ATTTGATGAGGCATCTT |
| Omy_bcAKala-380rd | PBT | F - TTGCTCTCTTCTGGTTGCCTTA | VIC - CATACCCATCCTATGTCAG |
| | | R - CTTCAGGAGAAAGCGCTACTGT | 6FAM - CATACTCATCCTATGTCAG |
| Omy_Ots249-227 | PBT | F - CCCCTAGATTAAACCTGTCCAGTCT | VIC - CCCTCTGAGAACTAC |
| | | R - CTATCTATCTATCTATCTATCTATCTATCTATCTACTTACT GAGA | 6FAM - CCTCTGAAAACTAC |
| Omy_oxct-85 | PBT | F - CGTCACTGAAACATTACTGTAACATCCA | VIC - CATCGCTTATTTATGC |
| | | R - CATCATCACGCTGTTGGTTTCTTAA | 6FAM - CATCGCTAATTTATGC |
| Omy_p53-262 | PBT | F - CCCCAACATCCAGTATACAGTTTCA | VIC - CAAGTAGTATGGAGCTCTAT |
| | | R - CCCAAATTGGCAATTTTAATAGGATTCAGA | 6FAM - AAGTAGTATGGTGCTCTAT |
| Omy_rapd-167 | PBT | F - CCCAACATGCTCTATTGCAGCTA | VIC - ATTAAAACAATCCCCCCCAAAA |
| | | R - AGTTGCATAAGATGAATCAATAAATTAAAAACACAGAT | 6FAM - TTAAAACAATCCCACCCAAAA |
| Omy_rbm4b-203 | PBT | F - CTGAAATTTGATGAATGGAAGCTGCA | VIC - CACGTTATTATGAAAAGGATGT |
| | | R - CGTATTCAAGTCGATATACAGTCACGAT | 6FAM - ACGTTATTATGAAAAAGGATGT |
| Omy_srp09-37 | PBT | F - TAGTTGTATTAACTCTTCTTTGAGTCTAGA | VIC - TTGTGCTATTGACGCCACAG |
| | | R - TCATTCCAGCTCCGTTCTCTTC | 6FAM - TTGTGCTATTGACACCACAG |
| Omy_stat3-273 | PBT | F - CAGACCTCCTCTATCTCCCTATGAG | VIC - TTTTCCAGACTCCAGTTTG |
| | | R - ACCTCCTTTAAATTGTGCCCAAGAA | 6FAM - TTTTCCAGACTCAGTTTG |
| Omy_u09-53.469 | PBT | F - ACAGCCTGAGCGTTTGCA | VIC - TTGCAGCCCTTATTGTG |
| | | R - GGAAACTGGGAGAGATCAAAGGA | 6FAM - TTGCAGCCCTTGTTGTG |
| Omy_u09-54-311 | PBT | F - GTGGCTCCCCAGGAACAAG | VIC - TGGTAATTATTCAACAGATCAGT |
| | | R - AAGTTTCATGTCACATTCCAGTTACCT | 6FAM - TGGTAATTATTCAACAAATCAGT |
| Omy_U11_2b-154 | PBT | F - GGGAAGCAGAAAAACTGGAAGTT | VIC - AATGATACTTTTCAGATTGTAAC |
| | | R - CCCTCTGTGGGCTTGATATTCA | 6FAM - TGATACTTTTCAGGTTGTAAC |
| Omy_vatf-406 | PBT | F - TTGCTTCATTTTGTCATAACCTTGGG | VIC - TTGCAGATGACTATCCACA |
| | | R - TGCATGCTCTGACAAATGTTACACT | 6FAM - TGCAGATGACTGTCCACA |
| OMY1011SNP | PBT | F - GAGGCTGGTTTGGGATTCACT | VIC - CTTTACCTCGAAGACAAT |
| | | R - CGCCAAACACTAACTCTCTGTCT | 6FAM - ACTTTACCTCTAAGACAAT |
| Ocl_gshpx-357 *O. clarkii* hybrid marker | GSI | F - GAGATCCTGAGGTCCCTGAAGTAT | VIC - ATCCTTCC**A**GGAAATG |
| | | R - AAGTGGAAATTTGGGCTCAAAGC | 6FAM - TCCTTCC**C**GGAAATG |
| Omy_myclarp404-111 *O. clarkii* hybrid marker | GSI | F - GCTGTGGTGCTCATGGGTAAA | VIC - CAAAGCCATACGTGGCC |
| | | R - CCAGGGCAGGGTTGTTCTC | 6FAM - AAGCCATCCGTGGCC |
| Omy_Omyclmk438-96 *O. clarkii* hybrid marker | GSI | F - CCCGACTCTACTTCACTACTTTCCT | VIC - TACGCAAATTAGGTTTAAA |
| | | R - GGCCTAGGACAATAGGACTGAAC | 6FAM - CGCAAATTAGGGTTAAA |
| M09AAC.055 | GSI | F - GTCTCCGACGTGTGGCT | VIC - ACCTCCACGCTGTCC |
| | | R - TGGAACGAACCTGAGAACATAAGG | 6FAM - ACCTCCACACTGTCC |
| OMGH1PROM1-SNP1 | GSI | F - TCAAACTGCATTTGATGGAAACAAACAT | VIC - TAGTGTTCACTGACTTCA |
| | | R - AGGACAATTCTAAGTGACCTCAAACTG | 6FAM - TAGTGTACACTGACTTCA |
| OMS00003 | GSI | F - GTGCCACTGATGAGGATGAGATC | VIC - CTTTACTGTCGACATTTTA |
| | | R - GTAATAAAGCCCTTTTGTGAGGAAAAACTAAT | 6FAM - TACTGTCGCCATTTTA |
| OMS00008 | GSI | F - CCCTTTAAGGAGGATTTTAAATATGTGAGATAGAA | VIC - CTTCAAATATCCATAATTATATC |
| | | R - GGATACAGCGTTTTGGAATGAAACT | 6FAM - TCAAATATCCATAATAATATC |
| OMS00013 | GSI | F - GCCTTTGTTCTCCTTGGTGGTTA | VIC - CTTCTTTTCCCTTGCTACTC |
| | | R - AGAAAAGTGTGGACTGAGGTTGAG | 6FAM - CTTTTCCCTCGCTACTC |
| OMS00014 | GSI | F - CTTACACACAAGGGCTTCATTCTG | VIC - TGATTTGATGAATTAAACTTC |
| | | R - GATGTCTCTGGGTGGTTGTCA | 6FAM - TTGATGAATTGAACTTC |
| OMS00015 | GSI | F - TCAGACCCTATTTTTGGCACAAGT | VIC - CAAGTCACACTTTTAATGAA |
| | | R - GTCTAACTGATCCCACTTCTGCAT | 6FAM - CAAGTCACACTTATAATGAA |
| OMS00017 | GSI | F - ATTAAGTTCATACAAAAGTTCATCATAAATATTTTCCTTT | VIC - TAGACCTCGGTGCTGTAG |
| | | R - GGAGAACAAAGGGAAAGAGAAGACA | 6FAM - CCTCGGCGCTGTAG |
| OMS00018 | GSI | F - AGAGTACATGTGTGGCTGCAA | VIC - AACCACATAATTAATAATTC |
| | | R - GTCATAAATCAACACAATTATCTTCTTCACAGAA | 6FAM - CCACATAATTCATAATTC |
| Omy_cd28-130 | GSI | F - CACAACTCCACAGAGACAGTGA | VIC - CCTGTTCATTCACCC |
| | | R - GAGGACAAAACTGACCGTATGGT | 6FAM - CTGTTCGTTCACCC |
| OMS00030 | GSI | F - CCTCGTGACTACAGAGCTATACAAC | VIC - ATGAGGGTCCCTATACAGG |
| | | R - GATCTGATCGGTCGGGAGAGA | 6FAM - ATGAGGGTCCCTCTACAGG |
| OMS00048 | GSI | F - GGAAGAGCTGGAGAACAACGT | VIC - CAGCTAAACTCAGCAAAA |
| | | R - TGCAGTTGACAGAGGCTTTCTTT | 6FAM - AGCTAAACTCGGCAAAA |
| OMS00052 | GSI | F - TGCGTTTTTCATCCCAATCATTCAC | VIC - CTTCCTTTTGAGAATAAT |

| SNP/Comments | Panel | Primers | Probes |
|---|---|---|---|
| | | R - GGCATCAGGCTCTTCTTCCT | 6FAM - CCTTTTGCGAATAAT |
| OMS00056 | GSI | F - TCAGGAAGTAAACTGAAAATTCCAATGTATGA | VIC - TAGCTTGACCAAATAGCA |
| | | R - CCCCAACCATGCTTGTTATTGAAC | 6FAM - CTTGACCGAATAGCA |
| OMS00061 | GSI | F - AAGTGGAGGCTGACCTGTTG | VIC - CATTGCCATTTACAGACTT |
| | | R - GCTGATGGCACCTGACAGTTAATT | 6FAM - TGCCATTTGCAGACTT |
| OMS00092 | GSI | F - TCTCCAGGTGTATCTTGAGAAGGT | VIC - CAGCTGAGAATAGGTTC |
| | | R - AGGGTTCACACAGGGAAGATATCAT | 6FAM - AGCTGAGAAGAGGTTC |
| OMS00096 | GSI | F - CATGAGAATGGATCAGTCTCCACAA | VIC - AAAGAGGAAGAGTCTCG |
| | | R - GATGAAATCTGAATGTGTTGACACTACAG | 6FAM - AAAGAGGAAGCGTCTCG |
| OMS00087 | GSI | F - GCAAATTTCACCCTTAACGTGGTTT | VIC - CACACTTTGTCAGTTGTAAC |
| | | R - GATTTGATGTGTGTGTATTACCTCCTCTA | 6FAM - ACACTTTGTCAGCTGTAAC |
| OMS00119 | GSI | F - AGCGGCAGTTGTGTTAATGAGA | VIC - CCACACAGCTGCCTGT |
| | | R - CTTCCTAAAGCCTGACAGTCTGT | 6FAM - CACACAGCAGCCTGT |
| OMS00129 | GSI | F - GGAGATGATGAAATAAAAATTGAGGAAAAGATGA | VIC - TTGAACAACAAGAAAAA |
| | | R - TGTCTGGTGAATTATCGCAAATAACCA | 6FAM - TTGAACAACAACAAAAA |
| OMS00133 | GSI | F - GACCACTTCACTCATTCCTCCTTTT | VIC - CGCCTCCATCTTTGTGGT |
| | | R - TCCGGTTTACACACTTCATGCA | 6FAM - CGCCTCCATCTCTGTGGT |
| OMS00138 | GSI | F - TCGGACCACATGAGCAGTTC | VIC - CTAACAATAACCAAAGACTG |
| | | R - GTTCAACAGGTGCCCACAC | 6FAM - CTAACAATAACCACAGACTG |
| OMS00149 | GSI | F - GGCATCATTGTTCTTGCTCTGTTTA | VIC - CAACTGTGCATTTAGC |
| | | R - CCTGGGAGGGTTTATATCGGAGTAT | 6FAM - CAACTGTGCCTTTAGC |
| OMS00151 | GSI | F - CTAACGTCTTCCCAATGATATTTCACAAGATA | VIC - TCATGACCTTGATAATC |
| | | R - ACCGTGGAAATACAATTTTTTATGCCAAT | 6FAM - ATGACCTCGATAATC |
| OMS00095 | GSI | F - CTCCAATGGCTGTCAACAATTAAATATAAGAC | VIC - AGGCAACTATATATTTTTTT |
| | | R - GTGTGCTGGTCTCTTCTTTTATTCTCA | 6FAM - AGGCAACTATATATATTTTT |
| OMS00169 | GSI | F - AGCACTTGACTCAAACTCACATAAATCA | VIC - CAAAAAGCATTGATATCAAT |
| | | R - CTGAGACAGGAAGAACAATGTTAACAAAA | 6FAM - AAAAGCATTGACATCAAT |
| OMS00173 | GSI | F - TGGAAGTAGCTACTTAACAGGAAATGG | VIC - CATTAGCTTGTGTATGAACT |
| | | R - AACACGTGTGCTTGTTTTGTCAA | 6FAM - ATTAGCTTGTGTGTGAACT |
| OMS00176 | GSI | F - GTTGGAAGTTCCGGTGGTAGAG | VIC - TTCCAGCACTGCTGTC |
| | | R - CTGGGTCCTGAAGGAGCTT | 6FAM - CCAGCCCTGCTGTC |
| Omy_impa1-55 | GSI | F - CGCTGAGAGGATTGTCAA | VIC - CGAGATGATGCGTCTACA |
| | | R - ATTTTTCTTTGTTCAGTCTTCTGTCTC | 6FAM - CGAGATGATGCATCTACA |
| Omy_103705-558 | GSI | F - CTCCAATCGCAAATACCCAGACT | VIC - AGACTTACCCAGAGTGAGAG |
| | | R - CGCAGGAGACGGATGCC | 6FAM - ACTTACCCAGGGTGAGAG |
| Omy_105075-162 | GSI | F - GGAGAAGGACAAGGACATTGGTAAT | VIC - CTTTCTCTCCTACTTTCC |
| | | R - AAAGCAGACCACACCATACTTCTC | 6FAM - CTTTCTCTCCTCCTTTCC |
| Omy_107031-704 | GSI | F - GGCTTTCGGATACTGAGCAACAA | VIC - TGGACATGATTGCATAGAC |
| | | R - TGAACTCACTGTTGGTATGGACTAGA | 6FAM - CTGGACATGATTACATAGAC |
| Omy_107285-69 | GSI | F - GCCCTTGTGACAATGCACTGTTATA | VIC - ATACGTTACTTTTGACCTTGT |
| | | R - AGGTCTAGACAGTGTGCCATTTG | 6FAM - ACGTTACTTTTCACCTTGT |
| Omy_110201-359 | GSI | F - GGTAAGGCCTGTCTGACTATTTTGA | VIC - TTTGGCTATTGAAATTATACATT |
| | | R - AGAGGTCAATGGATGCCAGTTT | 6FAM - TTGGCTATTGAAATTCTACATT |
| Omy_CRBF1-1 | GSI | F - AGTTCCGTACGGTAGCCTATTCTA | VIC - CAGAGTCGCCAAAAT |
| | | R - CGCCCGGGTGAGAGTAATTG | 6FAM - CCAGAGTCACCAAAAT |
| OMS00114 | GSI | F - GGATGATGCTGTGAGTCGAGAAG | VIC - AAACGTTTCACATGCACC |
| | | R - ACCTTCGCCACCCATGTTTTATT | 6FAM - AAACGTTTCACCTGCACC |
| OMS00143 | GSI | F - GGAGGCACGCCCCAAA | VIC - CCTGATCCAGAATCTAGA |
| | | R - TTTGTTAAAATAGAGCCCTTAGTGGGTTT | 6FAM - CCTGATCCAGAGTCTAGA |
| OMS00174 | GSI | F - TGACTAACTATGCAGCCTGAAAGG | VIC - CAAGAACAGGATAAATGT |
| | | R - GGGATACTCTTGTAATAAACTGTTGGTTAGTA | 6FAM - AAGAACAGGAGAAATGT |
| Omy_97077-73 | GSI | F - GTGTAAACAAAATGACTCTGGGATTCAG | VIC - TGGTGCAATAGAAATA |
| | | R - AGAAGTGGCAATGGTGTGAAGTAT | 6FAM - CATGGTGCAATAGTAATA |
| Omy_97865-196 | GSI | F - TCCAGACTTCTGGTTTGTTCCATT | VIC - ATGAGCTTGTTAATTAAT |
| | | R - CCAGCCCCTATATTCACAATTAAGTGT | 6FAM - AGCTTGTCAATTAAT |
| Omy_97954-618 | GSI | F - GCTCTGCTTCCTCGGCAAATA | VIC - CAACGCTTACCGGTGTGT |
| | | R - CACAATTGGTTTTTGCACAAAAGTAAAGTATT | 6FAM - CAACGCTTACCAGTGTGT |
| Omy_128996-481 | GSI | F - CTCATCCACACTGTACAGTACAAGT | VIC - CTTGTGGTTGAGGTTTG |
| | | R - CATGCCTTCGTCTCATCAATAACAC | 6FAM - TTGTGGTTGCGGTTTG |
| Omy_aromat-280 | GSI | F - CTCCATTGATTCATGCCGAACATT | VIC - TCTTGCAAACTCC |
| | | R - GGAGAGGTCAAACATAGCCTGGTA | 6FAM - TCTTGCGAACTCC |
| Omy_aspAT-123 | GSI | F - GTTTGCCCATTTCACTGATGCT | VIC - CCTTCCTAGGCAGTCAG |
| | | R - AGGAGACCACTCCAAAGAGAACT | 6FAM - TTCCTGGGCAGTCAG |
| Omy_b9-164 | GSI | F - GCACAGAACACAGCCAATATTAACA | VIC - CCTACAACTTGATCTAACGTG |
| | | R - GCCTTGACTCTCCCTTCATGAC | 6FAM - CCTACAACTTGATCTACGTG |
| Omy_BAC-F5.284 | GSI | F - ACAACGCCAACAACTTTCTCTTG | VIC - CAGTAGGGCGGCAAG |
| | | R - CCTCATTTACTGTAGGACCATGCA | 6FAM - ACAGTAGGACGGCAAG |
| Omy_BAMBI2.312 | GSI | F - CGAGCTCATGTCCGAAACTCAT | VIC - CCGAAAGTTCAACTTT |
| | | R - TTTGACAGCCTCAACTTCTAGGG | 6FAM - CCGAAAGTTAAACTTT |
| Omy_carban1-264 | GSI | F - GCAAAGCCTCATCTTCAATCATTTGT | VIC - CATTAATATTGCTAATAACACCAAG |
| | | R - GCAAAACACAAGTCAGGAATCACTTA | 6FAM - ATTAATATTGCTAATAACACTAAG |
| Omy_cd59b-112 | GSI | F - TTTGGATAAGATTGTCTTATATGACTAAAATGTCATGT | VIC - CTAAAAGCCTATAGCAAACT |
| | | R - GCCAACGTCCTAGATATGGTGTAAT | 6FAM - CTAAAAGCCTATAACAAACT |
| Omy_cin-172 | GSI | F - CGCATGGGACAGGTGTGT | VIC - CGCTCACCGTGGTTAC |
| | | R - GAGAAAGCCTGTAGAACCATGTCT | 6FAM - CGCTCACCATGGTTAC |
| Omy_cox2-335 | GSI | F - AGCTGGGCTGTATTTGTCAATACTT | VIC - CTTTAAAGACAAAGACTTTAT |
| | | R - CAGCCCGCCACTGTCT | 6FAM - TTTAAAGACAAAGCCTTTAT |
| Omy_e1-147 | GSI | F - GCACTGACTGTTACCAGGAAAGAG | VIC - CCATCCTGAATCTGATTAA |
| | | R - GTACTGCAGTGTTGAGGCTATATCA | 6FAM - CCATCCTGAATATGATTAA |

| SNP/Comments | Panel | Primers | Probes |
|---|---|---|---|
| Omy_g1-103 | GSI | F - CTCAGCAAAAAAGAAACGTCCCTTT | VIC - CCTTTTACAATGAAGATC |
| | | R - AGTCGTGACAATGAGAAACAGTGTT | 6FAM - CTTTTACAGTGAAGATC |
| Omy_G3PD_2-371 | GSI | F - GCAGGTAAGGTACACCATAGAGACA | VIC - AGACATGTGGATTGGCA |
| | | R - CTCCCCCTGCCTTACCAAAC | 6FAM - CAGACATGTGTATTGGCA |
| Omy_gadd45-332 | GSI | F - AGAGAAGACTCACTGCTGTTTGC | VIC - TTGCTCCAAAATGG |
| | | R - AAATCAGTTCCCACGCTATGCT | 6FAM - TTGCTCCGAAATGG |
| Omy_gdh-271 | GSI | F - AGGTCAGTCTACTTACAGTATAAAGCAGT | VIC - TCACCCTGAAGTGTAGAC |
| | | R - GTCATGTCAACAGAGTAACATAATAAATCTGC | 6FAM - TCACCCTGAAATGTAGAC |
| Omy_gh-475 | GSI | F - AAGTTACCAGAATTTTGCAAACTCAACT | VIC - CTGAAACTCATGGTATACA |
| | | R - CCATATTTTGAGGTGTAGCTTTACCCT | 6FAM - CTGAAACTCATGATATACA |
| Omy_GHSR-121 | GSI | F - CTGTGTATAAGTTTATACAGTCAGCACAGT | VIC - CCTAATAACCATGATAACAGC |
| | | R - TTCAGAGAGAGAAATGGCAGAAAGG | 6FAM - AATAACCATGGTAACAGC |
| Omy_hsp47-86 | GSI | F - CACATTAAGCACTCCCAGGGA | VIC - CAGGAGTGTAAATGTTT |
| | | R - TTGCAAAGGCCAAACAGCATT | 6FAM - ACAGGAGTGTATATGTTT |
| Omy_hsp70aPro-329 | GSI | F - TGCGTATTATTGTTTTTCAAGGACTTTCAAA | VIC - ACATTCCAATATTCAACTAT |
| | | R - TGAATATTTTCAAATACATGCCAATTCTTTCCAA | 6FAM - CATTCCAATATCCAACTAT |
| Omy_IL1b-163 | GSI | F - GGAACAACAGGATTAAGCCTACTCT | VIC - CTGAGGTCATAAAAATA |
| | | R - CCTAAAGGCCTAGGAAACTAAACTTCA | 6FAM - CTGAGGTCATACAAATA |
| Omy_inos-97 | GSI | F - GATGGACAGGGTCCTCTTCAC | VIC - CCTTTCTTGATGGTATCC |
| | | R - CCTGTAGATAAAACATGGTACCAGGTC | 6FAM - TCCTTTCTTGATTGTATCC |
| Omy_LDHB-1_i2 | GSI | F - ACGCACACTTATCCTTGACAATGTT | VIC - ATGGGCAGTCATTCA |
| | | R - ACTGTGACAACAAATTCGGTGACA | 6FAM - TGGGCAATCATTCA |
| Omy_LDHB-2_e5 | GSI | F - TGCTAGGTGAGTCAGAGGTACATATT | VIC - TTTACCTGTCAACCACTTC |
| | | R - GACTGGAAGGCCACCCATAAG | 6FAM - CCTGTCGACCACTTC |
| Omy_LDHB-2_i6 | GSI | F - TCCTCGCCAATACCATACATGTC | VIC - CTGTGTTTTGCTTCCCCA |
| | | R - AGAGTGAAGCTAACACACACATTTCT | 6FAM - CTGTGTTTTGATTCCCCA |
| Omy_lpl-220 | GSI | F - TGACAATCACTGAGCAACTGAACTC | VIC - AGTTACTCAGTGACAGTCA |
| | | R - GTCCAGTCTTGCTTCAACTCATTCT | 6FAM - AGTTACTCAGTCACAGTCA |
| Omy_mapK3-103 | GSI | F - GAAGTCATTACTGGTCAGTGGTCAA | VIC - AATTATTAAGCCTATTTTTTT |
| | | R - GCACAAAACATGAGGAAAGTTGAGA | 6FAM - ATTATTAAGCCTAATTTTTT |
| Omy_mcsf-268 | GSI | F - CCAGCATTCGTTCCCATTTCC | VIC - TGAGGGTTTATCTATTATTT |
| | | R - CTTTTAATGTAGATTATATTCTTCTGTAGCCACTATGG | 6FAM - AGGGTTTATCTGTTATTT |
| Omy_metB-138 | GSI | F - TCTGTCCCTGACGCTATAAAAACG | VIC - TTCGCCAAAGAGAAAT |
| | | R - GAAGTATTTCAGCTTAATTTCACTGTTGAGTT | 6FAM - TTCGCCAAAGTGAAAT |
| Omy_myoD-178 | GSI | F - TGGCAAAGCTGTCATTCCTTCTAAT | VIC - TTTTATGAGATATAATTTCC |
| | | R - GGTCAAATATTTCATTTACGATTACACTTAGGC | 6FAM - TTTTATGAGATATCATTTCC |
| Omy_nach-200 | GSI | F - CTCATGAAAAACGGGAGAGCAAAG | VIC - AACTGACAGAGTCACAAC |
| | | R - CAGCGGCTCTTCAGTAGTCT | 6FAM - CTGACAGAGACACAAC |
| Omy_nxt2-273 | GSI | F - CTTTAGAAAAGCCAAGGTATATTTTAACATACTTCT | VIC - ATCGACATTTACTGTGCCTT |
| | | R - CTGCTGCCCTCTAATGGTAAGATAG | 6FAM - ATCGACATTTACTATGCCTT |
| Omy_OmyP9-180 | GSI | F - CTGGATGTGTAGTATCGGTGGAAAA | VIC - CTGTAGTAGTCCCCATTGT |
| | | R - CACTGGGCACCTCTGATCTC | 6FAM - CTGTAGTAGTCCGCATTGT |
| Omy_pad-196 | GSI | F - CAAACAACCACAGTAGTCCTCCAAT | VIC - AAGACAAAGGTGTAATACC |
| | | R - GCTTTTCACCCTTTTGTAAATTAAGCCAAA | 6FAM - AAGACAAAGGTATAATACC |
| Omy_ppie-232 | GSI | F - CTGTTTTAGATTAGAATGTTTTTGGTCAGGT | VIC - AAATAGCGGAGAAAAT |
| | | R - CTGAACATAGGCTTTCATTTCAGACAT | 6FAM - AAAATAGCAGAGAAAAT |
| Omy_ca050-64 | GSI | F - GTCATACAGAACTGTTTTGTTGTGTCAA | VIC - CAGTTTGAAGAATATACTC |
| | | R - ACCTTGAATTGGTTCCTAATGCTATTGT | 6FAM - CAGTTTGAAGACTATACTC |
| Omy_sast-264 | GSI | F - GAAGTAGGGTTTGTTGACCATGTGA | VIC - CTAGCCAATGCGTCTAA |
| | | R - TGGATTCCATTTTAGGCTGTAATACATCTT | 6FAM - ATCTAGCCAATGTGTCTAA |
| Omy_SECC22b-88 | GSI | F - GGATCCCTCCTTTTAACACAAGACT | VIC - CTGTCTGTCCATATATC |
| | | R - CTACAGGATGACTACCTAATTGCTAATAAAACA | 6FAM - CTGTCTGTCCGTATATC |
| Omy_sSOD-1 | GSI | F - GCCGGACCCCACTTCAA | VIC - CCACAACAAGACCC |
| | | R - CAGACTAACCGAACAGCATCAGT | 6FAM - CCACAACCAGACCC |
| Omy_star-206 | GSI | F - CGTGTGCCAGCCCTTCT | VIC - TCTTTGGCACTATATCT |
| | | R - GACCACTGAGATCATTGCTGTGA | 6FAM - TTTGGCACCATATCT |
| Omy_sys1-188 | GSI | F - CTTAAATGGTGCTGGTTGCTGTATT | VIC - AAACATGTACGACCTGTC |
| | | R - AGTGATATCTTAGTGGGTCGAGGAAA | 6FAM - TGTAAACATGTACTACCTGTC |
| Omy_tlr3-377 | GSI | F - GTCGCTCCGGGTGCTT | VIC - CGTGATTAGGTTCTTC |
| | | R - GGCCCAAACACTTCCTTCCT | 6FAM - CGTGATTAGATTCTTC |
| Omy_tlr5-205 | GSI | F - GAGCGTATCTGGTATGGTAACAACA | VIC - CAGTAATATTTCAGTGCCCG |
| | | R - CTCCAGCAGCTTTAGAGAGTTTACA | 6FAM - CAGTAATATTTCTGTGCCCG |
| Omy_hsf1b-241 | GSI | F - AGCCCGAACTATCCTAAAGCATTTT | VIC - CAGTGTTTTGTTTTTTGTCATT |
| | | R - AAATCAATAGCTCAGAGAATAATGAACACCA | 6FAM - AGTGTTTTGTTTTTGTCATT |
| Omy_u07-79-166 | GSI | F - CCCGCTATATTATTTGATCACCCTTGA | VIC - ACTTGGGAATACCCCAGCC |
| | | R - ATTTAAATCCATTTCTAAAAATAAGCAAACCTAACCA | 6FAM - CTTGGGAATAACCCAGCC |
| Omy_u09-52.284 | GSI | F - TTTGTGTGTATTGTTGTGACTTG | VIC - ACTGCATTGTTGTAGCTAG |
| | | R - TGATGTTATTGCAGGTCTAGCGAAA | 6FAM - CTGCATTGTTGTCGCTAG |
| Omy_hus1-52 | GSI | F - CTTGCCGGAGGGTAGCT | VIC - CCCATCCCTCCTCCTGG |
| | | R - CCACAACTTCTCAAATGAATGGAATGT | 6FAM - CCCATCCCTTCTCCTGG |
| Omy_u09-56.119 | GSI | F - CCAAGGTGGACCCACCAG | VIC - AGTGAGCTGAAACAGAGCA |
| | | R - GCTGAGTTTATAGGTCAGTCATTATACATATTGA | 6FAM - TGAGCTGAAGCAGAGCA |
| Omy_nips-299 | GSI | F - GACAGGATAGGAACGGTTTCTCAAT | VIC - CTGGATTTCACATGTAATAC |
| | | R - ATCAGAAGTTTAATTCAATATGTACACGATCCT | 6FAM - CTGGATTTCACGTAATAC |
| Omy_UT16_2-173 | GSI | F - GACTCATTATCACCTTAGTTGTAGCTTCA | VIC - AGTTAAGTCCCTTGTTGACTG |
| | | R - AGCTACTTGCTGTATCACATGTTTGT | 6FAM - AGTTAAGTCCCTTATTGACTG |
| Omy_vamp5-303 | GSI | F - CTGCTTCCCAATTCAGTATCGTCTT | VIC - TGGCCGTAGTAGTTGGTCA |
| | | R - AGGCTGAAGCATTTCTGAGTATGAA | 6FAM - TGGCCGTAGTTGGTCA |
| Omy_zg57-91 | GSI | F - CACTCATACACTCACTCACAAAGGA | VIC - CACAGACTGCACAGCC |

| SNP/Comments | Panel | Primers | Probes |
|---|---|---|---|
| | | R - AGCAGATAAGCCTTGTGAGTGAATC | 6FAM - CCACAGACTTCACAGCC |
| Omy_ndk-152 | GSI | F - AAGAATTGAGGGATAAAAACAAAATAATATATAAACATGA | VIC - CACCCACTTTCAAAAC |
| | | R - CAAACCTACATTCATTAAAGTCCAGTTTTGT | 6FAM - ACCCACTCTCAAAAC |

Appendix B. 192 Taqman™ assays used for Chinook salmon genotyping. All forward and reverse primers are unlabeled and probes contain a 5' fluorophore and a 3' quencher and minor groove binder. SNP panel (PBT or GSI) is noted.

| SNP/Comments | Panel | Primers | Probes |
|---|---|---|---|
| Ots_100884-287 | PBT | F - CGGAAGACCAGATTCTCCAAGAGTA | VIC - ATAGAACTACAATTCACATATAT |
| | | R - CGACCAAGTAGCGGCACTT | 6FAM - AACTACAATTCGCATATAT |
| Ots_105132-200 | PBT | F - CGATGTACTGAGGGCAGTGT | VIC - CAAGAGTGGCATAAAA |
| | | R - GAGTGGAGTTCCTTAATAATCATTGACCTT | 6FAM - CAAGAGTGGAATAAAA |
| Ots_110551-64 | PBT | F - GAGTGGTCAAGGTTTCAGTTTCTG | VIC - ACGCTCGGAACATT |
| | | R - GAAATGGACAGACACAAGGTCAAAC | 6FAM - ACGCTCTGAACATT |
| Ots_117432-409 | PBT | F - TCATCAAAACATGCCTCTTCTGTGT | VIC - TTTAGACTTTGCTCTATAACAG |
| | | R - TGTTGAACCTGTCACTCTGTCTTC | 6FAM - ACTTTGCTCCATAACAG |
| Ots_94903-99R | PBT | F - CCGTCTGAGTAGGAGGATCAATACA | VIC - CAAACCAGCAAACAT |
| | | R - TTTGGATCCAGCTCTCCGTATAGA | 6FAM - ACAAACCAGAAAACAT |
| Ots_cox1-241 | PBT | F - CACTGAACTGTAAGCCATTGTGATT | VIC - CACTACGGTAAGACCAT |
| | | R - GTAAATGTAGTATACAGTATAGGCATCGTAGGT | 6FAM - CACTACAGTAAGACCAT |
| Ots_GTH2B-550 | PBT | F - TGACTACCCGTTGTACCAATGAAC | VIC - TTAATGCTGCAGATGTTAT |
| | | R - CACAGGAAGGACGTGTTTTGATG | 6FAM - ATGCTGCACATGTTAT |
| Ots_pr-151 | PBT | F - TGTTGTCTCGGACTGCATGAC | VIC - CATGCATTGCACATAC |
| | | R - GAAGGCACAGAGATGAAGGACAT | 6FAM - CATGCAATGCACATAC |
| Ots_OTALDBINT1-SNP1 | PBT | F - CGCTGGGCATGGATGAGT | VIC - CTACTGTTGTATTTTCTC |
| | | R - GGCCAACACTGCTACTTCCT | 6FAM - CTGTTGTGTTTTCTC |
| Ots_Prl2 | PBT | F - CCTGGTCTGTTTGTGATCAAGATG | VIC - ATGTATTGTTCATTTAATG |
| | | R - GGTTAACTCAAATAGAACATACTCTGACACA | 6FAM - TGTATTGTTCGTTTAATG |
| Ots_TGFB | PBT | F - GCCTCACATTTTACTGATGTCACTTC | VIC - CTTCCGAGAGCTAGGCT |
| | | R - GAGCAGATCTCTTCAGTAGTGGTTT | 6FAM - CTTCCGAGAACTAGGCT |
| Ots_u07-25.325 | PBT | F - AGACAATCATGGTGTTTTGAGTCTTTCT | VIC - CCGCTTGAAAGTTTGA |
| | | R - GCCTAGGCTTGATGGAGTCA | 6FAM - CGCTTGAAGGTTTGA |
| Ots_101554-407 | PBT | F - TGAAAGATATCAATTGTAGTAGTGGTGGTG | VIC - ATGGAGGATTGTGGTTGT |
| | | R - ACACGCCAGTCCACAAGT | 6FAM - ATGGAGGATTCTGGTTGT |
| Ots_105385-421 | PBT | F - GACTGTCTTGGAACCGTTGCTA | VIC - CCTCCTGGGTATATCG |
| | | R - TCCCGGAACACACCAATGTC | 6FAM - CTCCTGGGCATATCG |
| Ots_110689-218 | PBT | F - GTATAAACTAGAGTCCAGTGTTATGTTAATGTCTT | VIC - CACCAATCAATTAATTATT |
| | | R - CATGGCAGACAACAGTAGAGAATATGA | 6FAM - ACCAATCAATTCATTATT |
| Ots_118205-61 | PBT | F - CCATACAGCCAGTCCAGGTG | VIC - TAGTAGCCCCTACACCTC |
| | | R - ACTGGACAGGGCTGGGT | 6FAM - TAGCCCCTGCACCTC |
| Ots_96500-180 | PBT | F - GATCATGTCAGATAGGATGCTGAAAGT | VIC - AAAACAAATCATTTTTCG |
| | | R - CAGGTCTGGTCTACATCGAACAC | 6FAM - AAAAACAAATAATTTTTCG |
| Ots_E2-275 | PBT | F - GGTGCCACTTTAGTATAGCTGCTTA | VIC - CCCCCATATTGCTG |
| | | R - CCCTACCCCCTGTGTTCCA | 6FAM - CCCCACATTGCTG |
| Ots_HMGB1-73 | PBT | F - TGCTTCAGTGAAAATAAGCGTGAGA | VIC - ACTGTATATGTTACGTTTTC |
| | | R - GTCGAGCGGTATGAATACTTTCTGA | 6FAM - ACTGTATATGTTAAGTTTTC |
| Ots_MHC1 | PBT | F - GTCCACATTCTCCAGTACATGTATGG | VIC - CATCATCCCGTGAGCAG |
| | | R - CAAACCCCTCTGTCTGTTCAGT | 6FAM - TCATCATCCCATGAGCAG |
| Ots_OTDESMIN19-SNP1 | PBT | F - GGTCTGTCTGTCTGTCTATCTGTCA | VIC - CCAGTCATGGGTCATT |
| | | R - TGTGTGTCTTTGTTCATTCCTACCA | 6FAM - TCCAGTCATTGGTCATT |
| Ots_RAG3 | PBT | F - CATTTCCACGAAAAGCCAGATGAC | VIC - CTCTACAGTATGAACTATG |
| | | R - ACAGAATAAAGTATCTTCCTCTTACATCACTACTAAT | 6FAM - CTCTACAATATGAACTATG |
| Ots_Thio | PBT | F - TTTTAAAAATGGAGATAAACTCCTGACCTGAA | VIC - CAGTGTATTAGTCATTCTTA |
| | | R - AATACCAAACCATGCCACTAATACCT | 6FAM - CAGTGTATTAGTCGTTCTTA |
| Ots_u07-49.290 | PBT | F - GCTGAGGAAGGATTCTGTATTTGCT | VIC - CTTTCCCCGTGTTGGT |
| | | R - TCGGACAGAGCGCATCC | 6FAM - ACTTTCCCTGTGTTGGT |
| Ots_101704-143 | PBT | F - ACTTCTTGAGCCAATCGGATGATG | VIC - CTTAGACGTCAGAGGTC |
| | | R - CCAGAGATAAACTAGTGGAGGAGATCA | 6FAM - CTTAGACGTCCGAGGTC |
| Ots_105407-117 | PBT | F - TGTGTACATCCGCGTAAATATTGAAGATAA | VIC - CAGGTTAGGAATGGTTG |
| | | R - CTGTGAGCTGCTGCAAACC | 6FAM - CAGGTTAGGATTGGTTG |
| Ots_112301-43 | PBT | F - GCATGGCTGCCCTAGAACA | VIC - CGTCGCATTCAGC |
| | | R - TCAGAACATTTCCTTCAGCTTCGT | 6FAM - CGTCGCGTTCAGC |
| Ots_118938-325 | PBT | F - ATTTTCAAACAGGCATTTATCATTGGTGAA | VIC - AGAGATGCAAAGTGGAGTT |
| | | R - GGTCTGTCCCTCATTCTTTGCA | 6FAM - AGAGATGCAAAATGGAGTT |
| Ots_96899-357R | PBT | F - TCTCCTGAACTAATTTAGACCTCTGAATGT | VIC - CTGAATGTTTTTTTTTAATCTTT |
| | | R - CCTCATATTGCTTTCATCTGAAGAGAGA | 6FAM - CTGAATGTTTTTTTTTATCTTT |
| Ots_Est740 | PBT | F - GGACTCGTGCTTGAGGAAGATG | VIC - TCTGGATGGAACCGTTAG |
| | | R - TGCATGGCTCCAACTCCTT | 6FAM - CTGGATGGAGCCGTTAG |
| Ots_hsc71-3'-488 | PBT | F - TGCATCCATTCATACCTGACCAATT | VIC - TTTCCAATGGTATAGATATGA |
| | | R - TTTGGTTAGGCACACGATAATTTGC | 6FAM - TTTCCAATGATATAGATATGA |
| Ots_MHC2 | PBT | F - GTCCTCAGCTGGGTCAAGAG | VIC - CTGGAGCGTTTCTGTA |
| | | R - GTAGTGGAGAGCAGCGTTAGG | 6FAM - CTGGAGCGTGTCTGTA |
| Ots_OTSTF1-SNP1 | PBT | F - CGGACAAAGAGCTACAGAAATGC | VIC - CCGCCACCTTGGCT |
| | | R - CGTCCCTCTTCACGCATGA | 6FAM - CGCCACATTGGCT |
| Ots_redd1-187 | PBT | F - TTCTGGGTTGCCATACTCTTTCAAT | VIC - ATTCTGACAGCTGTTTTG |
| | | R - AGTTGAGACCTTCAGTTCTTAGGGTAT | 6FAM - CTGACAGCCGTTTTG |
| Ots_TLR3 | PBT | F - TGCACCTGCGAGAGCAT | VIC - CTGTGGTTTGTGGCGTG |
| | | R - CTGGCGTTTGTTCCGTTCAG | 6FAM - CTGTGGTTTGTAGCGTG |
| Ots_u1002-75 | PBT | F - CCGCCTTTCCCACCTTCTC | VIC - ATGGCCCTTACACTATC |
| | | R - TCAAACGAGAACACACTAAGGTTGT | 6FAM - TGGCCCTTACGCTATC |
| Ots_102414-395 | PBT | F - GCCTACTGATAAATGTATGACAGTAATGGA | VIC - CACATAGTGTAGCTTTACTAC |

| SNP/Comments | Panel | Primers | Probes |
|---|---|---|---|
| | | R - CAATAACAAACAAGCTAGGAACAAAAGTGT | 6FAM - CACATAGTGTAGCTCTACTAC |
| Ots_108820-336 | PBT | F - TGAAATAAATTGTTCTGTTGATATGTGAATTTTGGA | VIC - ATTGCCCATCTCAGAATA |
| | | R - CAACGACACACCAACAACGT | 6FAM - AATTGCCCATCTTAGAATA |
| Ots_112419-131 | PBT | F - GTGGGTAATCGATGCCAAAGAGAT | VIC - AAGCGACTTGATTATC |
| | | R - TGGCAGTGTTTTCAACTAGCTTTG | 6FAM - AGCGACATGATTATC |
| Ots_123921-111 | PBT | F - TCGCTAGGCAGAAATATAGGGTTCT | VIC - TGCTAAATGGCATATATTAT |
| | | R - GAGCATGGCGCTTGCA | 6FAM - CTAAATGGCACATATTAT |
| Ots_ARNT | PBT | F - CCACTGGCTGTGGAGCTT | VIC - TACAGATGTCATTTTAC |
| | | R - GGGTTCAGTGATAGTTGGGCAAAT | 6FAM - CTACAGATGTAATTTTAC |
| Ots_ETIF1A | PBT | F - TCTGAACTCACCAAAGGAACACTTG | VIC - CAACTGAAGAAAATAATATG |
| | | R - GAGAGAAAAGGAGAAATGATTGCCATT | 6FAM - CTGAAGAAAAGAATATG |
| Ots_HSP90B-100 | PBT | F - CACCTTAGTTCCACGCAACATG | VIC - TCTATGGTGTGATTCATT |
| | | R - CTGCGTGTATTGTAGTGGTGACA | 6FAM - TTCTATGGTGTAATTCATT |
| Ots_mybp-85 | PBT | F - CAAGGGATGTGACAAATTAATCAAACACATAA | VIC - AGAGCATGTAGTTTTG |
| | | R - AAGAGGTCTAATAAATCTCCAATGTAAAAACGT | 6FAM - AGCATGTAATTTTG |
| Ots_P53 | PBT | F - GGAACTTCCTCTCCCGTTCTG | VIC - CTGGGTCGGCGCT |
| | | R - GCACACACACGCACCTCAA | 6FAM - TGGGTCGACGCTC |
| Ots_S7-1 | PBT | F - TGCCATCATAAACAACCTAACAAGTAACT | VIC - TACAGGAGATAAGGTCGCA |
| | | R - CCTGGTTTAAAAACGGCCAACTG | 6FAM - CAGGAGATAGGGTCGCA |
| Ots_tpx2-125 | PBT | F - TGTTGTAATCTTTCTGAATATTTGCTTGCTT | VIC - CAGGCGGTTCTCC |
| | | R - TCTTCCAAATTGAGCACAAAAGCAT | 6FAM - CAGGCAGTTCTCC |
| Ots_u211-85 | PBT | F - TGGTGAGAGCAGCTTTAAATGTCTT | VIC - TCCCAAAGTCGAGTGTG |
| | | R - ACCCATTCTTCTGTCTGGTTTAAGC | 6FAM - CCCAAAGTCAAGTGTG |
| Ots_102801-308 | PBT | F - TGGGACAGAGGTGGGAATTGA | VIC - AGGGACAGTTTCGCAGACG |
| | | R - CCCAAAGATGCTTAACTGAAGATGTG | 6FAM - AAGGGACAGTTTCTCAGACG |
| Ots_109525-816 | PBT | F - GCCAGATAGTAGCGTACATCATGAG | VIC - CATGAGGCGTTCGGC |
| | | R - CTCCCCATGTCCCTGAGTCT | 6FAM - ATGAGGCATTCGGC |
| Ots_112820-284 | PBT | F - CATAGATGTTTATATGAAAAACCTCCCACTGT | VIC - ACTCACACTCGAGTGACT |
| | | R - GCATCCAAAAAGACGTGTGTGTTT | 6FAM - ACTCACACTCAAGTGACT |
| Ots_124774-477 | PBT | F - AGTTGTTCTTTTTATATTGTGTTTTTATTCCATTCCA | VIC - CCACCGCCATCTGATA |
| | | R - GCCAAATAAAAACAAAGCATGAACACA | 6FAM - CACCGCCGTCTGATA |
| Ots_AsnRS-60 | PBT | F - CCGACGCCTCACTGAGT | VIC - TGAGTCCCTGACCAGC |
| | | R - TGGTTTTTCAGGTCATGGTTTCCA | 6FAM - AGTCCCCGACCAGC |
| Ots_FGF6B_1 | PBT | F - GAGACAAAGGTTTGCAGGTTCATG | VIC - CCTGTTATCAGACCCAAAT |
| | | R - GGGAGCCATGCACTAATATATTGGA | 6FAM - CTGTTATCAGCCCCAAAT |
| Ots_IGF-I.1-76 | PBT | F - GGTAGGCCGTCAGTGTAAAATAAGT | VIC - CTGCCTAGTTAAATAAAATA |
| | | R - GATGGAGGCCACTGTGTTCTTA | 6FAM - CTGCCTAGTTAAATTAAATA |
| Ots_NFYB-147 | PBT | F - CCGTCCACAGCACAAGACTATAATA | VIC - TGTTCCAATGTAAAATGTATGC |
| | | R - CAGATGATAGCTTCAGTAAGTGGTTCA | 6FAM - TTCCAATGTAAAATATATGC |
| Ots_parp3-286 | PBT | F - AGTCAGTGTTGGTGTAGTGAAGAGA | VIC - AGTTACAAGTGGTGTTTCA |
| | | R - CATTTGTGGAGTGTTTATTGAACAGTAACA | 6FAM - ACAAGTGGCGTTTCA |
| Ots_SClkF2R2-135 | PBT | F - CCAAATACAGACCAGCTACTTGTGT | VIC - ATTCAAAGTCAAATTTT |
| | | R - CTTCAAGTCCCTGAATAATGGTACGT | 6FAM - ATTCAAAGTCTAATTTT |
| Ots_txnip-321 | PBT | F - CCTTCAAACTAACACATCATAGACATGCTT | VIC - TCTGGCGGATTTACA |
| | | R - TTATCAAACTGAAGGCGGATTTACTGA | 6FAM - CTGGCGGGTTTACA |
| Ots_u4-92 | PBT | F - ATCCAAGGAGCCCCATTAAAGATTT | VIC - CTGTGTTGAATTTAACATAAT |
| | | R - CGTACCAGAGTTGTAGAAGCATCT | 6FAM - TCTGTGTTGAATTTAACGTAAT |
| Ots_103122-180 | PBT | F - CAAACGCGCACTCACACA | VIC - CATCAACACAATCTGC |
| | | R - TCACAATGGTACGATTTTACGACTCAA | 6FAM - CATCAACACGATCTGC |
| Ots_110064-383 | PBT | F - AACAAAGAATGTTAAACACCAAACAGGAA | VIC - CTACGTAATGAACGTTAGCT |
| | | R - GTGCAAGGGACCTAGCTAATCC | 6FAM - ACGTAATGAACATTAGCT |
| Ots_112876-371 | PBT | F - GCCTACAGCAAATTCAGCTACACAT | VIC - CATCACAACGATGTGTG |
| | | R - TGGACCTTCAATCATCACAGCTT | 6FAM - CACATCACAACTATGTGTG |
| Ots_128757-61R | PBT | F - CGTGTCCGGCTTCTTTTATTTCATT | VIC - TTGTGCATTTTCCCC |
| | | R - GATGGGTATGTTAATCATATTACCAGCGTAA | 6FAM - TGTGCATTTCCCCC |
| Ots_brp16-64 | PBT | F - ACTCTGGGTCCAGGAGGTTTT | VIC - AAGTCAGCATCTTTCA |
| | | R - CTGACGAGACCATGCACCAA | 6FAM - AGTCAGCGTCTTTCA |
| Ots_GCSH | PBT | F - GTTCTTTTTAATGATGACTACAGGTCTTTCAC | VIC - TATCTGGGCGGGCTG |
| | | R - GCTACTTTACATAATACCATTTGAGCTGAGA | 6FAM - CTATCTGGACGGGCTG |
| Ots_Ikaros-250 | PBT | F - GAGGCTGACTTGGACTTTGC | VIC - ACAGAAGATTTTCGGCTGC |
| | | R - GGCCTGTCAGCCAAGGA | 6FAM - ACAGAAGATTTTCGACTGC |
| Ots_nkef-192 | PBT | F - CATTTAGCAGACACTCTTATCTTAGTGTCA | VIC - AATAGGCCGACATCAA |
| | | R - CGAATGTCCACCTCAGATGTTACAA | 6FAM - AAATAGGCCAACATCAA |
| Ots_pigh-105 | PBT | F - GTTTGGAATGTTTCTCTGATTGTGTTAACAA | VIC - TGACCTGAAAATATATATTTTTT |
| | | R - GCATTACTAAAAACTGGTGTGTGGAA | 6FAM - ACCTGAAAATATATTTTTTT |
| Ots_SEXY3-1 | PBT | F - GGTCTTGCAGTCAGGAGAGG | VIC - CAGAATTAGCTTTGGACATT |
| Ots_SEXY3-1 AC | | R - CCAGGTGGTGAAGGTAGGAA | 6FAM - ATCTCCACTTCGCTGA |
| Ots_u07-07.161 | PBT | F - GTCAACAAATGCAGGTAACATAAATGGT | VIC - ATCAGTGACATAAGTTGTCCA |
| | | R - GATGCAAACACCTGTGAAATTGTGA | 6FAM - TCAGTGACATAAATTGTCCA |
| Ots_u6-75 | PBT | F - GAAAAAGTAAAGTAAAAGTAAAGTATTATACCACTAAAGACAAT | VIC - TTAGTCAACTGTTGTTTTT |
| | | R - GATCCACACTGTTGGTCTACTACAA | 6FAM - TTAGTCAACTGTTATTTTT |
| Ots_104415-88 | PBT | F - CCTGAGCATCCCAGTTGAACT | VIC - TCCTGAAAAACGACATCC |
| | | R - TGTTTTCAATACACTGCAATTTAGTTTTGGT | 6FAM - CTGAAAAACAACATCC |
| Ots_110201-363 | PBT | F - GTTTGGCTATTGAAATTATACATTAAAACATGTAGCT | VIC - TGGATGCCAGTTTTAAAA |
| | | R - CCATGGCATCCTGTAAAGAACAACA | 6FAM - TGGATGCCAGTTTAAAAA |
| Ots_113242-216 | PBT | F - GAGGCCTAATGTCTCTTGTGACT | VIC - ATTACCAACGGAGAACC |
| | | R - GACATCTTCAACAAGTGTTCATTCACC | 6FAM - TTACCAACAGAGAACC |
| Ots_129458-451 | PBT | F - TGGGACCCACATAAAGCAACTG | VIC - CATCTGGCAATGCCTT |
| | | R - GACATAAGACCCATTTAGCCCCTTTT | 6FAM - CATCTGGCAGTGCCTT |

| SNP/Comments | Panel | Primers | Probes |
|---|---|---|---|
| Ots_CD59-2 | PBT | F - TGTTTATCTCTGAGTGAAAAAGGTGTGT | VIC - CTAAAATGTCATGTAAATAT |
| | | R - CATGTTACCCAGCTAAAAGTCTATAGCA | 6FAM - ACTAAAATGTCATATAAATAT |
| Ots_GDH-81x | PBT | F - CTTTTCTGAATTAGTGCTGTGCTTGT | VIC - TGTTACGGGACATACT |
| | | R - CCAACTTCTTCAACTCTGTCAGTGA | 6FAM - TCTGTTACGGACATACT |
| Ots_IL8R_C8 | PBT | F - CGTGGTGTTCGCCTTCCT | VIC - CTGGACGCCGTTACA |
| | | R - TGTCGGCCATCACTGTCATG | 6FAM - TGGACGCCATTACA |
| Ots_NOD1 | PBT | F - GTGCTGCAGGAACCATGTG | VIC - CCAACGGCGACTTG |
| | | R - CTGTGTGGACTGCTGTCTAAGG | 6FAM - CCAACGCCGACTTG |
| Ots_pop5-96 | PBT | F - CTCTTGCTACTTGCAGTGTATCTCA | VIC - TTCTGTTACTGGACTGATG |
| | | R - AGTTTGAGGGCTCTATTCTGTCATG | 6FAM - CTGTTACTGGGCTGATG |
| Ots_SWS1op-182 | PBT | F - TCAAAGACATCGAACACAAGAACGA | VIC - ATGTACTTTAACGATTCATTT |
| | | R - GCAGGTAAATTCAAACGTCATCATAAGAA | 6FAM - ATGTACTTTAACGTTTCATTT |
| Ots_u07-17.135 | PBT | F - CTCGCCTCTGTCATTGTATTACCTT | VIC - AAAATGTACCACATACTTGT |
| | | R - TGACACACGAGCCATTTTGATGAT | 6FAM - AAATGTACCACATACTCGT |
| Ots_unk526 | PBT | F - TCAAGACTGTGCTGTAGTTGTCTAC | VIC - CAACATTCCAGTCTGAAAC |
| | | R - CCTCCCCCTTTTCCACATCAG | 6FAM - CATTCCAGCCTGAAAC |
| Ots_105105-613 | PBT | F - AGTACAAGTGCAGAGAATGACATCATG | VIC - CCGAGCTTGAGTTAGGA |
| | | R - GGTGTTTTATTTTCCCATATATCTTTTAACTTTAAGCT | 6FAM - CCGAGCTTGACTTAGGA |
| Ots_110495-380 | PBT | F - GCCTAGGTATGTACGAAACTTCACA | VIC - ATGGCCCCTGTCTATG |
| | | R - AGGCTTTTTCAGATGGTCGTATGA | 6FAM - ATGGCCCCTGTGTATG |
| Ots_115987-325 | PBT | F - GGAGGTGTAGTGAAATGGGAAGAT | VIC - ATGCATAAAAGGTAATTGTG |
| | | R - GCATTCAGTGAACCAGTAGTGCTAT | 6FAM - ATGCATAAAAGGTCATTGTG |
| Ots_94857-232R | PBT | F - GGCACTCTCCCTGGCTAGA | VIC - CAGGATAATAACAAACAAG |
| | | R - CCCCATCACTTCTCTGGCTTTAAAT | 6FAM - CAGGATAATAACGAACAAG |
| Ots_CirpA | PBT | F - GCTGTGATTGTGCTCTAAAGACATG | VIC - AATGCATTACAGAACTGA |
| | | R - CTCCCACTTAGCATTCCTACCTT | 6FAM - AATGCATTACAAAACTGA |
| Ots_GPH-318 | PBT | F - GGTGATAACAGGTGTTGCACCAA | VIC - ATCAAGCTGACGAACCA |
| | | R - TCAGGTGGTGGTGGACAAC | 6FAM - CAAGCTGACAAACCA |
| Ots_mapK-3'-309 | PBT | F - CGTGACCCTTGTAACTGAAAAGC | VIC - ATGCTATTAAATGAATATTC |
| | | R - GGCCACTGTCATAGAATTAGGCATT | 6FAM - ATGCTATTAAATGACTATTC |
| Ots_ntl-255 | PBT | F - TGCAGTTACAAGCCTAAGACAATCT | VIC - TTGTAGAGGAAGAATATTC |
| | | R - CAACTAAAGTAACACACCAGCAACTG | 6FAM - TTGTAGAGGAAGTATATTC |
| Ots_ppie-245 | PBT | F - TGTTTTTGGTCATGTATTTTCTCTGCTATTTTT | VIC - ATGTCTGAAATGAAAGCC |
| | | R - GGACTGGAGCTGCTGAACATA | 6FAM - AATGTCTGAAATTAAAGCC |
| Ots_TAPBP | PBT | F - TTTCTCATCCTTCTCTCTTCCAGTCT | VIC - CTGGACAGCTGGTCC |
| | | R - GGACAAACCAGCACTCCAGAA | 6FAM - CTGGACAACTGGTCC |
| Ots_u07-18.378 | PBT | F - GGAAACCAGCTAGGATTCAGGAA | VIC - ATATGGTATGTAGAGGCTAGTTA |
| | | R - CGTTATATGGTTTGCTTGTTTGCGATA | 6FAM - TATGTAGAGGCAAGTTA |
| Ots_vatf-251 | PBT | F - CTTTTCGGGTTATTCATGCTGTTGT | VIC - AGACCACAAGATACAGTACC |
| | | R - GCAAGCATTTGAAAAACAGACTGGAT | 6FAM - AGACCACAAGATA--GTACC |
| Ots_101119-381 | GSI | F - TTTTCTAGGACAGGTTGCTTGCA | VIC - TGCCACATGATAATTGA |
| | | R - CCAGGTTTCTTTAGCCTACTTATTCTTTACA | 6FAM CCACATGGTAATTGA |
| Ots_107074-284 | GSI | F - CCCACTTCCAGAGCCTGAA | VIC - ACCGTAGCTGCACCTG |
| | | R - TTTTCCATGGCTGTGTGTACTGT | 6FAM CGTAGCAGCACCTG |
| Ots_111681-657 | GSI | F - CTGAGCTTTTTCAACTTACTTGTTGGA | VIC - TAGCGCAAACCCCGAACC |
| | | R - GGCGCAGCAGCAACTG | 6FAM CGCAAACACCGAACC |
| Ots_128693-461 | GSI | F - TCAATGTTCATCAATGCACTTCCTGTA | VIC - CACTCAGCTGGTACCCA |
| | | R - GCCTGCAGGAGAAGGTAGAGTTA | 6FAM ACTCAGCTGATACCCA |
| Ots_HFABP-34 | GSI | F - CAAGAACACCGAGATCTCCTTCA | VIC - TCGAACTCCGCTCCTAG |
| | | R - TCGGCGGTGGTCTCG | 6FAM TCGAACTCCACTCCTAG |
| Ots_OTSMTA-SNP1 | GSI | F - GCCGAAAAATAAGCGATTAGTGATGA | VIC - AATTGCCTCATTGGGTG |
| | | R - GCCCCATGGTAAACCTAATTAACCT | 6FAM AATTGCCTCATTAGGTG |
| Ots_U2362-330 | GSI | F - AATGGGTAACAAAGAAATAGCTAGCTACTT | VIC - ACTGGGAAGATTGTTTG |
| | | R - GACAGACCACAGTGAAGGTGAAA | 6FAM CTGGGAAGACTGTTTG |
| Ots_hsp27b-150 | GSI | F - TAGGAGTTGGAAAGACTGCACA | VIC - YGATCTGGACCAGGCT |
| | | R - CCCATTGGTTCTTTGGTGTT | 6FAM YGATTTGGACCAGGCT |
| Ots_aspat-196 | GSI | F - CCTGAACAGGTACACACAAACGA | VIC - CACACCCACTCTTTAT |
| | | R - TCCAACTGATGAATATGACCAACATGAAT | 6FAM CACACCCAGTCTTTAT |
| Ots_GnRH-271 | GSI | F - CAGATGAAAAATAAATAATTGGGCCATTAGGAA | VIC - CAATGAATACAATATCTAACCTAAT |
| | | R - CAGAGAGACTGAGACCATATGATGTAGT | 6FAM AATGAATACAATATCTAATCTAAT |
| Ots_Ots311-101x | GSI | F - AAATGAGGCCGTCCTTTACACT | VIC - CTGAGATCACTTTGAGCAC |
| | | R - GCAATACAAGCCCTTGATAATGAAGT | 6FAM ACTGAGATCACTGAGCAC |
| Ots_u202-161 | GSI | F - CACTTTTGACTTTACATGGAACTTAACTCAT | VIC - ATTAGCTGCTAAGCACTAG |
| | | R - GGGACTTCACTTTCTACAAACATGTCA | 6FAM ATTAGCTGCTATGCACTAG |
| Ots_102213-210 | GSI | F - CATTCCATGACAATGATTGAAATCTAAAAACAC | VIC - CTGTATACAGTAAGAGTATTAAT |
| | | R - GAGTATCTCAATTGCAACACTATGGTATGT | 6FAM ACAGTAAGAGCATTAAT |
| Ots_107285-93 | GSI | F - GCCCTTGTGACAATGCACTGTTATA | VIC - AAGTAACGTATCAAATGGC |
| | | R - AACATACACCAATACTTAGGTCTAGACAGT | 6FAM AAAGTAACGTATCATATGGC |
| Ots_112208-722 | GSI | F - CTGCATGAACGTTAACTCAAATAAAAGGT | VIC - TGTGAGGGCGGTCTT |
| | | R - AATGAGTTCTACTGACATTGTATACTAGAATAAGTATCA | 6FAM ATGTGAGGTCGGTCTT |
| Ots_129144-472 | GSI | F - CTGTTAGTGCAGAAGACGTAGCT | VIC - TGGGTCTCGAGCCTGTA |
| | | R - GCAGAGCTATTGAGCCAAGTTACAA | 6FAM TGGGTCTCGATCCTGTA |
| Ots_hnRNPL-533 | GSI | F - TCTTTGATATTGAGCTCATAAAAGCAAGGT | VIC - CATTTACCAGTTCTCACACAC |
| | | R - TCCTTGTTCATCCATCAGGCATAAAA | 6FAM TTTACCAGTTCACACACAC |
| Ots_P450-288 | GSI | F - ATGTCAATATATTTCACTATAATGATTGGAAGCCA | VIC - CTATAAAGTTGGACAGTTGG |
| | | R - CACTGAACTCGAAGCTGTTAGGA | 6FAM AAAGTTGGGCAGTTGG |
| Ots_U2446-123 | GSI | F - CTGGTCTGTGACGTCAAAATGATG | VIC - CTGCAACTCGACGCAAG |
| | | R - AGCTAGACCAGGCCATTTGAG | 6FAM ACTGCAACTCTACGCAAG |
| Ots_zn593-346 | GSI | F - CTACGCGAGAAATAACACTTTTCAAAACT | VIC - TCTTGCAATCATTTTTAAC |

| SNP/Comments | Panel | Primers | Probes |
|---|---|---|---|
| | | R - GGCGAGTTTATTACGGTGTTATGAC | 6FAM CTTGCAATCATATTTAAC |
| Ots_C3N3 | GSI | F - CCGGATTCCATGGCCTACAC | VIC - CTAGAAAGGTTGATCCAATAA |
| | | R - GCCAAAATGATGTTCGGATGTAAAGT | 6FAM AAAGGTTGAGCCAATAA |
| Ots_GPDH-338 | GSI | F - CACTAAATATTCCTTATCATTTCATACTAAGTCTGAAGAA | VIC - CCACTACTTAACGTGCTTT |
| | | R - AGCTGATACACAATCAAAACACAAAACAT | 6FAM CCACTACTTAACATGCTTT |
| Ots_P450 | GSI | F - TGAGCGAGATTTATCAAACTGTCAAAGA | VIC - CCCCGAAGTACTTTT |
| | | R - CCCAAGCGGGAGAACTTACAG | 6FAM CCCGAAGAACTTTT |
| Ots_zP3b-215 | GSI | F - TGCTGAGGACCATCTGCAATTC | VIC - CCAAATATCCTACCCGTGATG |
| | | R - AGGTCCATGAATAACTGAAAATGTACAAGT | 6FAM CAAATATCCTACCAGTGATG |
| Ots_106747-239 | GSI | F - ATCGAGGATGCCTCAAAGACATC | VIC - CCCGCGGTGAGTAT |
| | | R - GTTAGACCCACCACCAGTCATC | 6FAM CCCGCTGTGAGTAT |
| Ots_107806-821 | GSI | F - CTCCCTTGCTTTTGGTCATTGG | VIC - CAAAGAAAATCAAAATTT |
| | | R - TGCAGTGCTGAATTAGAGATTAATTTTTGTG | 6FAM CAAAGAAAATCTAAATTT |
| Ots_117242-136 | GSI | F - GTGACAGGAGACAGAAAGAGACATT | VIC - CAGCACATAACTTGACCTC |
| | | R - TGGTCCTCCCTGTCTCTATCTACTA | 6FAM AGCACATAACCTGACCTC |
| Ots_130720-99 | GSI | F - CGGTCATTGTAAATGTCAACGGTTT | VIC - CCTGTCTCATTCCC |
| | | R - TGCTTGCATGTTCTTGGTGTAGTAA | 6FAM CTGTCCCATTCCC |
| Ots_Hsp90a | GSI | F - ACAGTATACCGGCTGCCTATTCATA | VIC - ATTTGACTTGTCTTTTTG |
| | | R - GTCGTTTTTCATAGAAAATAGCTCACAGTT | 6FAM TTTGACTTGTGTTTTTG |
| Ots_stk6-516 | GSI | F - TGTGTTTAGGATTGAACTGACCATGTT | VIC - AACATAACGGACTCCC |
| | | R - GTAAACTCCACCTGCAAGAAGGA | 6FAM TAGAACATAACTGACTCCC |
| Ots_unk1104-38 | GSI | F - TAACCATGACTTCTATCAATCACCCC | VIC - CCACTAAGGATTACGTTACG |
| | | R - CCTCCATACATCGTCAAAGCTGTA | 6FAM CACTAAGGATTACATTACG |
| Ots_113457-40R | GSI | F - CCCAAGTGGTGAGTGTCAGT | VIC - ATATGGATTGGAGAATAG |
| | | R - ACTACAACAGGTGTTGATAATAGAATCATTCTC | 6FAM CATATGGATTAGAGAATAG |
| Ots_CD63 | GSI | F - TGCATGTTTTCTAACTGTGTTTTTGTGT | VIC - AGATCATGGGAATCATAT |
| | | R - TGAATGCCCCCCATCAACA | 6FAM ATCATGGGCATCATAT |
| Ots_GST-375 | GSI | F - CAGCCCGTCCCAAAATCAAG | VIC - TTTCTTGTAGGCGTCAGAG |
| | | R - CAGGAATATCACTGTTTGCCATTGC | 6FAM TCTTGTAGGCATCAGAG |
| Ots_PGK-54 | GSI | F - CTCATACTTTGTACCTGTGTGTTCCA | VIC - CCACCATCAAGCACTG |
| | | R - CGACCCAAGTGGCTCATCAG | 6FAM CCACCATCATGCACTG |
| Ots_ZR-575 | GSI | F - GCCTACCAGAAAGTACCAATTGTGA | VIC - CCGACACAATTTTGT |
| | | R - ACTTTTCACTGTCCTATTACAATTAGTATTTGTGATAT | 6FAM CCGACATAATTTTGT |
| Ots_102457-132 | GSI | F - CCAGCAGAGACTGGGTTCAC | VIC - CAATTGTGCGTTGCCCCA |
| | | R - TTCCCTACCGGCGAAACC | 6FAM ATTGTGCGTCGCCCCA |
| Ots_108007-208 | GSI | F - CAGGCTTGTGTTAAGTAGGGAGAAA | VIC - CAGTTTCACTTAATTTTAAAATG |
| | | R - CATTGGACAAGACCGGGTAGTC | 6FAM TTTCACTTAATTTAAAAATG |
| Ots_117259-271 | GSI | F - ACACCCACTTCAACCTCCATAAC | VIC - CTCTCCTGATCACTCTGT |
| | | R - GCCTCAGAGCTTAGCTTGGA | 6FAM CTCTCCTGATCCCTCTGT |
| Ots_131460-584 | GSI | F - CCTATTTTTGATAGGTCATAGTGAATGGGATAG | VIC - CTATCAAAGCAATACATTG |
| | | R - CTGTACTCCTCCATTCCTTTTCACT | 6FAM CTATCAAAGCAGTACATTG |
| Ots_il13Ra2B-37 | GSI | F - AGGACTGGCTGCACATTCA | VIC - CCAGGGAATCTATCCCAG |
| | | R - GAGGAGCTGTTCACACATATGTTG | 6FAM CCAGGGAATCTCTCCCAG |
| Ots_TCTA-58 | GSI | F - ACCAGTACCTAAACGTTAGAAAGCAA | VIC - CTGCCATGAAGTGCTAG |
| | | R - CGTTAGTTAGCTATGTCTGAAAGGCA | 6FAM TGCCATGAAATGCTAG |
| Ots_unk1832-39 | GSI | F - GAAACGTCTATGCTGTCCCCTTTAA | VIC - CACCACTAGAACTCTC |
| | | R - CTGCAGTATTAGCTCTAGTTGAATCCA | 6FAM CACCACTAAAACTCTC |
| Ots_123048-521 | GSI | F - CTCAACAGTGCACCTCCCTTAATT | VIC - TCACATCCAACTCAGTACT |
| | | R - CCAAACACACCCTTCCATAATCTCT | 6FAM CATCCAACGCAGTACT |
| Ots_EndoRB1-486 | GSI | F - CCTTTGGGTCTGCTTGAGGTT | VIC - TCCTTCTCACGCTTCT |
| | | R - GGAGCCAAATCCTAATGCTGAAGTA | 6FAM CTCCTTCTCATGCTTCT |
| Ots_IL11 | GSI | F - CCTCCAGATGAGACCCACTCT | VIC - AGTCCGCATGGAGCT |
| | | R - CAAAATGGTGCTCAAACGACTTCA | 6FAM TCCGCGTGGAGCT |
| Ots_RFC2-558 | GSI | F - GTAAGGTCTACTCCGGTTGTATTCG | VIC - TGCATGTAACAAATAACAT |
| | | R - CAATACGACAGTACCGGTGTTAAACT | 6FAM TGCATGTAACATAACAT |
| Ots_nramp-321 | GSI | F - GGCCATCTTTCAGGACGTACAG | VIC - TCGTTCATGCCCGTTAG |
| | | R - GCATGCTCTGCAATACGTTGAG | 6FAM TCATTCATGCCCGT |
| Ots_102867-609 | GSI | F - CTCTGCCATTCATTTGGGCTTTG | VIC - ACAGAGAGAAGTCCCAGGTG |
| | | R - GTCTAAAGTGGTCCCCTTGGAT | 6FAM AGAGAGAAGCCCCAGGTG |
| Ots_108390-329 | GSI | F - GAGGTTTGTTACTGTCACCCATAGA | VIC - CTACTTATGTAGCATTTTAA |
| | | R - CCTGCTGTAGCAAACTGTCTCAAA | 6FAM CTACTTATGTAGGATTTTAA |
| Ots_118175-479 | GSI | F - TGCGCGTCTCATTCAACCAT | VIC - AGAATGAAGTGAAAAGAA |
| | | R - ACCTTACGTCCTAGGTAGGAAACA | 6FAM AGAATGAAGTAAAAAGAA |
| Ots_131906-141 | GSI | F - GGCTCGAACCACCCAGTTTA | VIC - CACGGTTTACACTCCTATTA |
| | | R - TGCCCAACTGGTTTGCAATC | 6FAM ACGGTTTACACTCCAATTA |
| Ots_il-1racp-166 | GSI | F - GCCAAGAAAGTGTAGCTCCAACATA | VIC - CCACATTCGTTTTTC |
| | | R - AAGCAGAAACCCAGTAAGAAGGAAA | 6FAM ACCACATTAGTTTTTC |
| Ots_GST-207 | GSI | F - GGAGAACATGCATCACCATTCAAG | VIC - ATGAGAGAGTCTTTCTCTGTT |
| | | R - TCAGCAAACGAAGGCTATGTAGAAT | 6FAM ATGAGAGAGTCTTTTTCTGTT |
| Ots_unk3513-49 | GSI | F - TTTGAGTGAGTCACTGCACCAA | VIC - AGTGCGAAGAACC |
| | | R - CAGCTCCACAGTGTCACCAT | 6FAM AGTGCAAAGAACC |
| Ots_96222-525 | GSI | F - GCTCTTGCCCATCTGTAGGAT | VIC - TGTAGCTAATTTTAAGTTCTC |
| | | R - GGCGCAACATATGTATTAAGCAACT | 6FAM AGCTAATTTTAAATTCTC |
| Ots_EP-529 | GSI | F - GCCCTGCCTGCAACTTC | VIC - CAGTGTCATTTTCGGC |
| | | R - GAAACCAACGTCTTGATGTAGACCTA | 6FAM ATCAGTGTCATCTTCGGC |
| Ots_LWSop-638 | GSI | F - CAATTACTCTTTCTCAGCCCTGTGT | VIC - TTTAACAAGAAAATTATACATTTC |
| | | R - GCGGTAAGATGCAGTTTTACATGGA | 6FAM CAAGAAAGTTATACATTTC |
| Ots_SL | GSI | F - AATATTGGCTTTCTGAGAATGCATTTGG | VIC - TCAAAGATATGATTCAATTAA |
| | | R - CCAAGATACTTCCTTTAACTTCTCTGTCA | 6FAM AAGATATGGTTCAATTAA |

| SNP/Comments | Panel | Primers | Probes |
|---|---|---|---|
| Ots_RAS1 | GSI | F - TCATAAACATGGTGTCTTTCAGTCAGTT | VIC - CAATCTATCATCGACCAGC |
| | | R - CTGACATGTGAAACTACTAAAGCATTTAATCAC | 6FAM CAATCTATCATCAACCAGC |
| Ots_arp-436 | GSI | F - GCCCTGGAGAAGTACGTTTTAAACTAA | VIC - CTAGGTGAAACTTTTTTTAAA |
| | | R - GCAACCATGTCAACATTGCACATAA | 6FAM CTAGGTGAAACTTTTTAAAAA |
| Ots_108735-302 | GSI | F - CCTTTTTCTTATTAGTTTTACTTCCCCAGAGA | VIC - AAACAAACAACGCCTCATG |
| | | R - CAATTCCATTCTTGATTCTGTTTAACGGT | 6FAM AACAAACAACACCTCATG |
| Ots_122414-56 | GSI | F - GCACCGTATCAACGAGCTCAT | VIC - TGTATGACCTCTGACCTGT |
| | | R - TGCATGGATTTCCTTTGTGTTGTTG | 6FAM TGTATGACCTCTAACCTGT |
| Ots_99550-204 | GSI | F - TGACAGATTTCACCTTTAACTAGCTAAGC | VIC - AAGGCTTTGGTTGTTTG |
| | | R - GCAACCTCTTTCACACTTCAGTAAC | 6FAM AAGGCTTTGATTGTTTG |
| Ots_CCR7 | GSI | F - CTGCTCACCTGCATCAGTGT | VIC - CCACGTAGCGATCG |
| | | R - CCATGGTGGTCTGGACGAT | 6FAM ACCACATAGCGATCG |
| Ots_hsc71-5'-453 | GSI | F - TTGAGAACATGTGGTAATTAACTACAATGACTAA | VIC - CTGAGGTGGCAAAAT |
| | | R - GTACGAAGTTGCGCCTTGTC | 6FAM TGAGGTGACAAAAT |
| Ots_unk7936-50 | GSI | F - ATGGGTTGGGATTATGGTTCATTGT | VIC - AGACATGTAGCTATGTAGGTAA |
| | | R - CAAAATGGTTACTTGCATAGTCTTTTGT | 6FAM AGACATGTAGCTATCTAGGTAA |
| Ots_97077-179R | GSI | F - CCTGAACAAATACTTAACGCTCCAGTT | VIC - TCACAAATGTATCCTAAAGC |
| | | R - GTAATAATACTTCACACCATTGCCACTTC | 6FAM CACAAATGTATACTAAAGC |
| Ots_FARSLA-220 | GSI | F - GTTCGTGGGATTGTTCAATGTTCAT | VIC - CCTTGGATGGGATGTG |
| | | R - CTTGGACAGGCTCACATTACCATA | 6FAM CCTTGGATAGGATGTG |
| Ots_Myc-366 | GSI | F - CCTTAGCTGCTCTTTGAAGTTGACT | VIC - TCTCTGCTCATCTGTC |
| | | R - GGCTATAGAGTGTATTTACAGCATGCA | 6FAM CTCTGCTCGTCTGTC |
| Ots_Tnsf | GSI | F - GCCAATACGGGTTCTGAACTGT | VIC - TGCTCCAGATCTC |
| | | R - CGGAATAGTCATAGTAGGGCTCGTT | 6FAM TGCTCCAGGTCTC |
| Ots_TNF | GSI | F - CCAAATCCTCATCCCACACACT | VIC - CTGGCTGTAAACGAAGA |
| | | R - CCGTTGCACTTGACCCTAAAC | 6FAM TGGCTGTAAACAAAGA |
| Ots_104569-86 | GSI | F - CCTGCATGTTGTTCACGTTGTC | VIC - TGGTCGCAGATGCC |
| | | R - CGGCCGGAGGGATCAC | 6FAM TGGTCGCCGATGCC |
| Ots_109693-392 | GSI | F - TCTCCCTCATTCCCATGTCATATCA | VIC - TCCGTTAGTTCATCCTGG |
| | | R - GGGAACGTATCAGGTGAGTGT | 6FAM TCCGTTAGTTCCTCCTGG |
| Ots_127236-62 | GSI | F - TGGAGAACTTGCACTGAATGTGAAA | VIC - TCTCTTATCTGAGTTCTGC |
| | | R - GCTGTTGGACCTTGACTTTAACAAATT | 6FAM CTCTTATCTGTGTTCTGC |
| Ots_DDX5-171 | GSI | F - ATGACCAATTGAAGAGTTCTTCCGT | VIC - TTCATAATTGAACGATTTCA |
| | | R - CAAAGCCAAACGTCACATTTACACT | 6FAM CATAATTGAACAATTTCA |
| Ots_nelfd-163 | GSI | F - CTCACTGCAAATCCAACTTCATCAT | VIC - ACCCACCAGTGTCATT |
| | | R - CCACTACATCCTCATCCAAGGTT | 6FAM CCACCAGCGTCATT |
| Ots_u1007-124 | GSI | F - CGAAATAAGGGCCTGGTGTTTAAAA | VIC - TGTCCTGTCCTCAGATCA |
| | | R - TGTACCAGGTGGAAGCTTTGG | 6FAM TCCTGTCCCCAGATCA |
| Ots_unk8200-45 | GSI | F - TCAGGAGTGAAGCTGGTCTCT | VIC - CAGTTTAAAGTGTATTCTCC |
| | | R - TTCCATAGTAACTGACCTCAGTGTCT | 6FAM TTTAAAGTGCATTCTCC |
| Ots_AldB1-122 | GSI | F - GCCATGGAGGACTGGATGA | VIC - ACCCACTTCGCCAACA |
| | | R - GCCACCACTACTTGCTGAGAAAATA | 6FAM ACCCACTTCACCAACA |
| Ots_FGF6A | GSI | F - TCAAAAATGTCTATCCAACAAATACTCTGAAAAATATTG | VIC - CACGATTAGCAATGAACAA |
| | | R - CTTGTGCGCACCTTGCA | 6FAM CACGATTAGCAATTAACAA |
| Ots_myo1a-384 | GSI | F - CTCCCCCCTGGACTTTGG | VIC - ACAGATCCATCCACCACT |
| | | R - GCTCTATTGCACCGTGTTCTG | 6FAM AGATCCAGCCACCACT |
| Ots_u07-53.133 | GSI | F - AGCTAGGCTGTAAATGCAAGGAT | VIC - TAACACATGTTGGAGGTC |
| | | R - CAGTGCTTTCAATTCATGCTGTCAA | 6FAM AACACATGTTAGAGGTC |
| Ots_u07-20.332 | GSI | F - CGCGAGTTAGCTCGAATATTATGATTTC | VIC - ACCATTTGATATAACTGCGTTAG |
| | | R - TCAAGCTAGCATAGCAACTTCATCAA | 6FAM CATTTGATATAACGGCGTTAG |
| Ots_106499-70 | GSI | F - ACTCTATCATCGGCAGGACCAT | VIC - CTCATTTTTCAGAATTGTATTC |
| | | R - ACCGTAAGTGTGGTTGTGTTCATTA | 6FAM CTCATTTTTCAGAATTCTATTC |
| Ots_Cath_D141 | GSI | F - CACTTGTTCTGCACACTACTTGTC | VIC - TGGGAAGCAATCAA |
| | | R - CACACATGGATTTTGCCTGTCTAAA | 6FAM AATTGGGAAGCAGTCAA |
| Ots_128302-57 | GSI | F - GGTTGCAGGGCAGAACTGT | VIC - CCTGCAATACGACCAAC |
| | | R - ACCCATCCAATAACCCATTTTCCTT | 6FAM CTGCAATACAACCAAC |
| Ots_Est1363 | GSI | F - GGTGATTTTGCCACAGAGTAGAGAT | VIC - CCATCCTGTCTTGTCTG |
| | | R - AGTGTTAAATGTAACTTGCATATACAGGCAAT | 6FAM CATCCTGTCATGTCTG |
| Ots_CRB211 | GSI | F - CAACGCGGGAATGGCTTTTAA | VIC - CTACCGTACTGAACTC |
| | | R - GCCAGAGTCGCCAAAATAGTAGAAT | 6FAM CCGTACGGAACTC |
| Ots_U2362-227 | GSI | F - TCGTGGATTGTGGCTTACGT | VIC - CTTAAGAAGCATTTTTTTG |
| | | R - GGGTGTTTAACAAGTAGTCCCTTCA | 6FAM AAGAAGCATTTATTTTTG |
| Ots_unk9480-51 | GSI | F - CAAATCAGAACAAAACCTCCCACAA | VIC - CTCCCACAAACCC |
| | | R - GGAAGTCTGTCTGAATGGTTGTCTT | 6FAM TCCCAGAAACCC |
| Ots_aldb-177M | GSI | F - GCGATCAGGTGACGCTAAAATGA | VIC - CCAAATTGCTTAACCC |
| | | R - AGGAAGGTGATGCCTGAGAGA | 6FAM CCAAATTGCTTTATCC |
| Ots_GH2 | GSI | F - GCGTACTGAGCCTGGATGACA | VIC - TGACTCTCAGCATCT |
| | | R - CCCCCAGGTTCTGGTAGTAGTTC | 6FAM TGACTCTCTGCATCTG |
| Ots_myoD-364 | GSI | F - GTGTGTGTGTGTGTGTCATC | VIC - TCATCTTTTGTTATTTCCTTG |
| | | R - TTTACACATATACAAAAATGGTCCTCTATTGTCAT | 6FAM ATCTTTTGTTCTTTCCTTG |
| Ots_u07-57.120 | GSI | F - GGTTTGAGCCAATCAGTTGTGTT | VIC - CAACCCCTACCTTGTCAC |
| | | R - CGGTCTAATGTCCATTGCTCATGTT | 6FAM CCCCTACCATGTCAC |
| Ots_u07-64.221 | GSI | F - GAGGATGACACTGTCCGTTTGT | VIC - ATCGACCCTGTCATTAG |
| | | R - CACAGTCCTTCGTATTCACCTTGAT | 6FAM CGACCCTGTGATTAG |

Appendix C. Assessing Intraspecific hybridization between Interior redband and coastal lineages of *oncorhynchus mykiss.*

## Introduction

Hatchery rainbow trout strains *Oncorhynchus mykiss sp.,* of predominantly California origin, have been stocked throughout the Pacific Northwest to provide increased fishing opportunities and to supplement wild populations for over 100 years. Within the last 30 years, emphasis has also been placed on stocking hatchery rainbow trout to mitigate for anadromous and resident fish losses as a result of the development and operation of the Columbia River hydrosystem (NWPPC 2000). In Idaho alone, over 500 million rainbow trout, comprising twenty different hatchery strains, were stocked throughout the State between 1967 and 1999 (IDFG historical stocking database). Both intraspecific hybridization (hatchery rainbow trout breeding with native interior redband trout and interspecific hybridization (hatchery rainbow trout breeding with native westslope cutthroat trout *O. clarkii lewisi*) have been cited as major threats to the persistence of these species (Williams et al. 1996; Behnke 1992; Leary et al., 1984; Deeds et al. 1999). Subsequently, introgressive hybridization and the resulting loss of pure populations has been cited as primary reasons in petitions to list both resident redband trout and westslope cutthroat trout as threatened under the ESA (Federal Register: August 7, 2003 (Volume 68, Number 152); Federal Register: August 8, 1995 (Volume 60, Number 152); Federal Register: November 16, 1998 (Volume 63, Number 220). While sufficient diagnostic genetic markers are readily available to assess interspecific hybridization between westslope cutthroat trout and *O. mykiss* (Baker et al. 2002; Campbell et al. 2002; Ostberg and Rodriguez 2002), few are available to assess intraspecific hybridization between the diverse group of hatchery strains that have been used for stocking and native redband trout over their broad geographic range in the Columbia River basin.

While few genetic markers have been identified to assess intraspecific hybridization, it is expected that with new genetic technologies, expanded screening would identify additional markers diagnostic between hatchery rainbow trout and redband trout native to the interior Columbia River basin. For the *O. mykiss* species, there is a major evolutionary break at the Cascade Mountain crest where populations residing to the west of the break are considered to be a “coastal” subspecies (*O. m. irideus*) and those residing to the east of the break are considered to be an “inland” subspecies (i.e. redband trout, *O. m. gairdneri*), regardless of whether they exhibit an anadromous or resident life-history (Behnke 1992; Currens 2009). All *O. mykiss* native to the Snake River basin are considered redband trout. Hatchery strains stocked throughout the Pacific Northwest were primarily derived from the coastal subspecies (Williams et al. 1996; and references within).

Single nucleotide polymorphic markers (SNPs) are a promising type of genetic marker for intraspecific hybridization studies, because they are abundant in the genomes of most organisms, and are easily detected with recently developed DNA sequencing technologies (Metzker 2010). In addition, they are generally bi-allelic, which allows them to be screened quickly on many samples using highly automated, rapid genotyping instruments. In the first year of this project, hundreds of SNP markers were developed and/or screened to identify two 96 sets of highly variable markers for Genetic Stock Identification and Parentage Based Tagging studies throughout the Columbia River basin (Ackerman et al 2011). During the past year, we screened these two sets of SNP markers on reference coastal hatchery rainbow trout populations and reference resident redband trout populations to assess their utility for intraspecific hybridization studies. We were particularly interested in completing screening this year because of previous research that had indicated that *O. mykiss* in the Pahsimeroi and

Lemhi Rivers might have been impacted from the past stocking of non-native hatchery rainbow trout. This was hypothesized because samples of *O. mykiss* collected from these rivers were genetically distinct from other populations in the upper Salmon River (Figure 1 from Nielsen et al 2004) and in recent years, fluvial resident *O. mykiss* (Figure C2) have been observed migrating upstream past the Pahsimeroi adult weir at the same time as anadromous steelhead (Figure C3). It is important to adequately describe the genetic variation in these Pahsimeroi River and Lemhi River populations for genetic stock identification purposes and it important to understand the origin, life-history, and genetic structure of these populations for VSP reporting.

## Methods

We screened 8 reference pure resident redband trout populations and 13 reference hatchery rainbow trout populations (Table C1), representing a diversity of strains that have been stocked throughout the Pacific Northwest (National Fish Strain Registry;https://sds.fws.gov/nfsr). All samples were genotyped with both panels of SNP markers (PBT; N = 96 and GSI; N = 96). Three of the genetic markers are hybrid markers to differentiate *O. mykiss* from cutthroat trout and one marker is a Y-chromosome specific assay that differentiates sex in *O. mykiss*. These four markers were genotyped but not included in subsequent analyses. For comparison purposes and to assess intraspecific hybridization, we included previously genotyped samples of anadromous steelhead passed above the adult weirs on the Pahsimeroi River and at the Sawtooth Hatchery on the upper mainstem Salmon River. We also included fluvial resident *O. mykiss* samples captured at the Pahsimeroi River adult weir and juvenile *O. mykiss* samples captured via electroshocking or screw traps in the Lemhi River drainage.

To summarize the relative power of each SNP as an intraspecific hybridization marker, we compared the allele frequencies of each marker between reference redband trout populations and reference hatchery rainbow trout populations using the software program Genalex. We also calculated the Polymorphic Information Content (PIC; Botstein et al 1980) of each SNP marker for both redband trout and hatchery rainbow trout populations, averaged those values across populations, and then subtracted these averages to estimate a statistic for each SNP marker we refer to as Total Information Content (TIC). For SNPs, we expect TIC values to range from negative 0.50 to positive 0.50, with increasing negative values observed in SNP loci that exhibit variation in reference redband trout populations, but not in reference hatchery rainbow trout populations and increasing positive values observed in SNP loci that exhibit variation in reference hatchery rainbow trout populations, but not in reference redband trout populations.

The Bayesian method of STRUCTURE 2.1 was used to provide an overall assessment of the 188 SNP loci for differentiating reference redband trout populations and reference hatchery rainbow trout populations, and to assess the origin of *O. mykiss* in the Pahsimeroi and Lemhi River drainages. Structure was run with the predefined number of clusters (K) set to 2 using the admixture model, and correlated allele frequencies with a running length of 5,000 burn-in and 5,000 MCMC repetitions. A K = 2 was set under the assumption that that samples would partition into “redband” and “hatchery” clusters and hybrids would share ancestry in both clusters.

## Results and Discussion

Screening of the 188 loci (PBT/GSI) identified many that exhibited large allele frequency differences between the 8 reference pure resident redband trout populations and 13 reference hatchery rainbow trout populations (Table C1 and Figure C4). In particular, 21 loci appear to be

very diagnostic between the two groups. Of these 21 loci, 9 had TIC values $\geq$ -0.20 indicating that they are polymorphic in reference redband trout populations, but not in reference hatchery rainbow trout populations (Table C1). All of these loci are present in the PBT SNP panel. The remaining 12 loci had TIC values $\geq$ 0.20 indicating that they are polymorphic in in reference hatchery rainbow trout populations, but not in reference redband trout populations (Table C1). All of these loci are present in the GSI SNP panel.

As expected, given the large number of diagnostic markers identified, the Bayesian analysis in STRUCTURE was clearly able to delineate reference populations into redband trout and hatchery rainbow trout clusters (K = 2) allowing an assessment of intraspecific hybridization and introgression in *O. mykiss* populations in the Upper Salmon River (Table C2). All but two of the reference hatchery rainbow trout populations had greater than 95% ancestry in one cluster (designated "hatchery"). All of the reference redband trout populations had greater than 95% ancestry in the second cluster (designated "redband").

Of the anadromous steelhead populations that we had previously genotyped, all four collections of steelhead from the adult weir at the Sawtooth hatchery exhibited "redband" ancestry (97%-99%). The two sample collections of steelhead from the Pahsimeroi River exhibited predominantly "redband" ancestry (92% - 94%), but higher levels of "hatchery" ancestry than observed in reference redband trout populations or in the steelhead collections from the Sawtooth weir (Table C2).

Samples of fluvial resident *O. mykiss* samples captured at the Pahsimeroi River adult weir exhibited predominantly "hatchery" ancestry (75% - 86%). High levels of "hatchery" ancestry were also observed in collections of juvenile samples from the Lemhi River screw trap and from the upper mainstem Lemhi River (59% - 72%). In contrast, while juvenile sample collections from Hayden Creek (screw trap and electroshocking) still displayed evidence of intraspecific introgression, they had predominantly "redband" ancestries (90% - 92%).

Results from this study suggest that the two SNP panels developed by CRITFC/IDFG for GSI and PBT programs will be powerful for assessments of intraspecific hybridization between hatchery rainbow trout and native interior redband trout. The identification of non-native rainbow trout and introgression within samples of presumed steelhead juveniles may confound ongoing efforts to estimate abundance and productivity of anadromous *O. mykiss* in the Pahsimeroi and Lemhi rivers and further research is warranted to better understand the origin and distribution of populations in these drainages. As a start, the sampling of adult steelhead that return to the Lemhi River could assess whether introgressed smolts successfully complete an anadromous life cycle. Additional tributary sampling in these drainages also may assist in identify the source of introgressed juveniles.

## APPENDIX C. LITERATURE CITED


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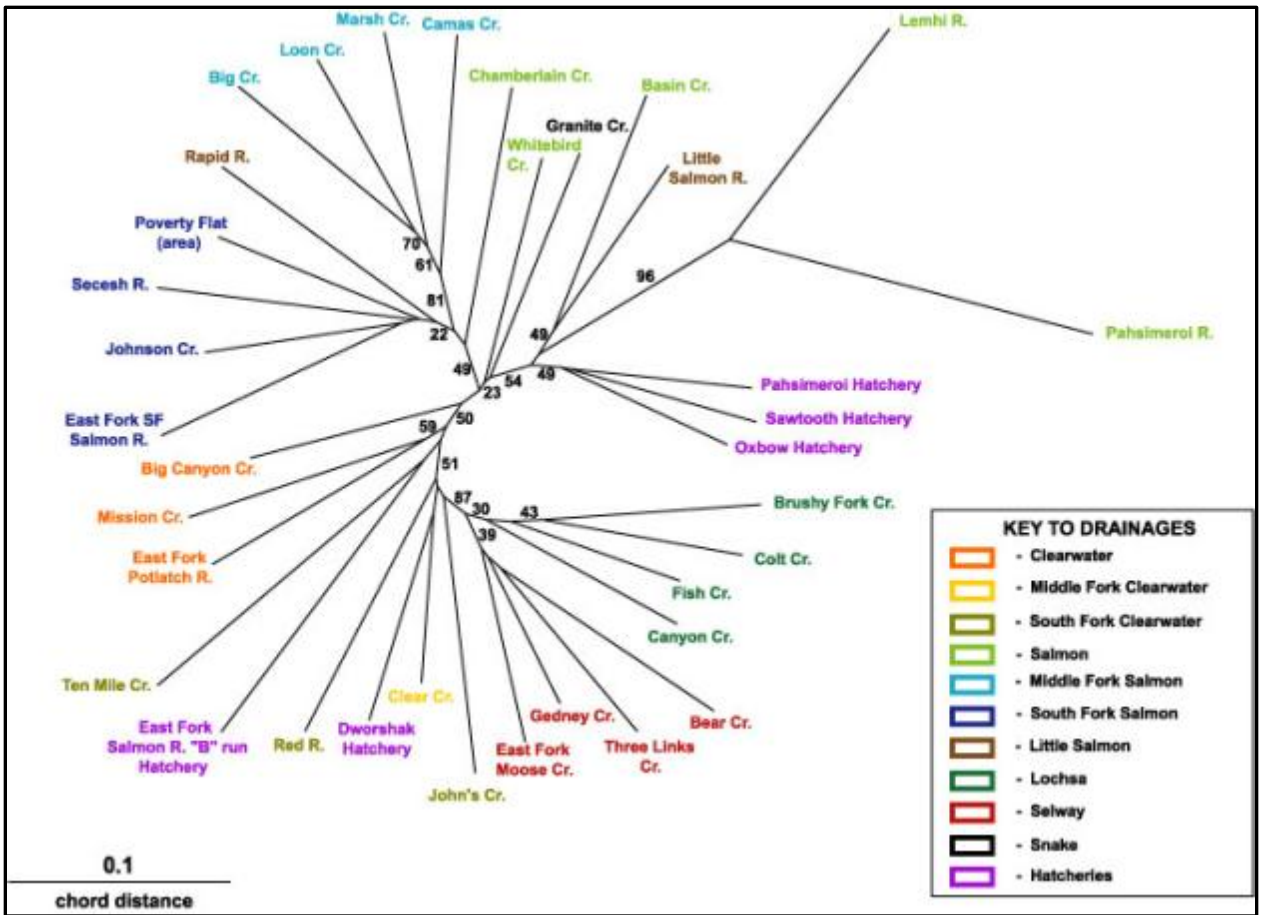


Figure C1. Figure originally published in Nielsen et al (2004) (Figure 2, page 17). Unrooted Neighbor-Joining tree based on Cavalli-Sforza and Edwards (1968) chord distance calculated from microsatellite DNA data, for steelhead populations sampled in the Snake River drainage, Idaho. Bootstrap values (% of 2,000 replicate trees) are given for major branches. Note the long branch lengths and high bootstrap support of samples from the Lemhi and Pahsimeroi Rivers.

Figure C2. Wild resident fluvial rainbow trout capture at the Pahsimeroi River adult weir (photo from Todd Garlie).

Figure C3. Wild anadromous steelhead captured at the Pahsimeroi River adult weir (photo from Todd Garlie).

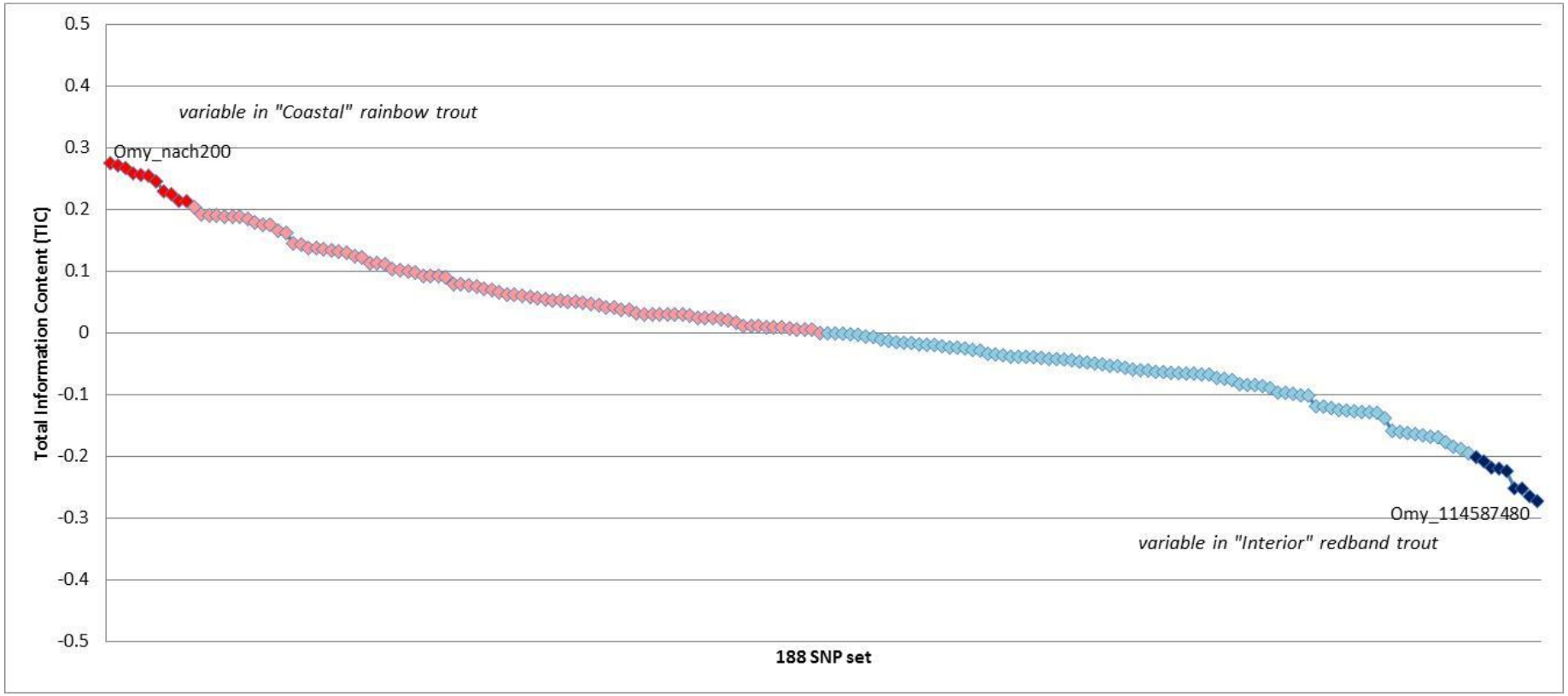


Figure C4. Distribution of TIC values for the 188 SNPs screened on reference “coastal” hatchery rainbow trout samples and reference “interior” redband trout samples. Loci with increasing negative values (blue) exhibit variation in reference redband trout populations, but not in reference hatchery rainbow trout populations. Loci with increasing positive values (pink) exhibit variation in reference hatchery rainbow trout populations, but not in reference redband trout populations. Dark red diamonds are SNP loci that exhibited TIC values of 0.2 or greater. Dark blue diamonds are SNP loci that exhibited TIC values of -0.2 or greater.

Table C1. Population, disposition, sample size (N), unbiased heterozygosity, observed heterozygosity, number of alleles observed and proportion of membership (q-value) to each cluster ("Redband" or "Hatchery").

| Population | Disposition | N | Unbiased Hz | Obs Hz | No Alleles | Cluster "Redband" | Cluster "Hatchery" |
|---|---|---|---|---|---|---|---|
| Hat Creek | Reference Redband | 24 | 0.25 | 0.25 | 1.8 | 1.00 | 0.01 |
| Big Jacks Creek | Reference Redband | 25 | 0.29 | 0.28 | 1.9 | 0.98 | 0.02 |
| Bennett Creek | Reference Redband | 24 | 0.28 | 0.28 | 1.9 | 0.96 | 0.04 |
| N.F. Owyhee Creek | Reference Redband | 25 | 0.24 | 0.24 | 1.7 | 1.00 | 0.00 |
| Rice Creek | Reference Redband | 26 | 0.19 | 0.19 | 1.7 | 0.99 | 0.01 |
| Shack Creek | Reference Redband | 25 | 0.27 | 0.29 | 1.8 | 0.97 | 0.03 |
| Wolf Creek | Reference Redband | 23 | 0.28 | 0.29 | 1.9 | 0.99 | 0.01 |
| Doby George Creek | Reference Redband | 46 | 0.26 | 0.26 | 1.9 | 0.99 | 0.01 |
| Shepherd of the Hills Hatchery | Reference Hatchery | 86 | 0.31 | 0.29 | 1.9 | 0.03 | 0.98 |
| Hofer Strain CDOW | Reference Hatchery | 32 | 0.20 | 0.22 | 1.6 | 0.01 | 0.99 |
| Eagle Lake | Reference Hatchery | 47 | 0.27 | 0.27 | 1.9 | 0.02 | 0.98 |
| Ennis-Fish | Reference Hatchery | 47 | 0.30 | 0.31 | 1.9 | 0.05 | 0.95 |
| Ennis-Shasta | Reference Hatchery | 46 | 0.28 | 0.27 | 1.8 | 0.02 | 0.98 |
| Ennis-Erwin | Reference Hatchery | 47 | 0.24 | 0.25 | 1.7 | 0.01 | 1.00 |
| Ennis-Arlee | Reference Hatchery | 47 | 0.28 | 0.28 | 1.8 | 0.00 | 1.00 |
| Ennis-McConaughy | Reference Hatchery | 25 | 0.28 | 0.27 | 1.8 | 0.01 | 0.99 |
| Ennis-Harrison Lake (D) | Reference Hatchery | 26 | 0.33 | 0.32 | 1.9 | 0.21 | 0.79 |
| Ennis-Harrison Lake (L) | Reference Hatchery | 28 | 0.33 | 0.33 | 1.9 | 0.20 | 0.81 |
| Mt. Lassen | Reference Hatchery | 93 | 0.28 | 0.28 | 1.9 | 0.01 | 0.99 |
| Mt. Whitney | Reference Hatchery | 42 | 0.30 | 0.28 | 1.9 | 0.18 | 0.82 |
| Nampa | Reference Hatchery | 47 | 0.25 | 0.31 | 1.8 | 0.01 | 1.00 |
| Sawtooth (adult weir)-05 | Anadromous Above | 29 | 0.30 | 0.29 | 2.0 | 0.99 | 0.01 |
| Sawtooth (adult weir)-10 | Anadromous Above | 80 | 0.30 | 0.30 | 2.0 | 0.99 | 0.01 |
| Sawtooth (adult weir)-08 | Anadromous Above | 48 | 0.29 | 0.29 | 2.0 | 0.98 | 0.02 |
| Sawtooth (adult weir)-09 | Anadromous Above | 45 | 0.30 | 0.31 | 2.0 | 0.97 | 0.03 |
| Pahsimeroi River (adult weir)-06 | Anadromous Above | 45 | 0.31 | 0.32 | 2.0 | 0.94 | 0.06 |
| Pahsimeroi River (adult weir)-10 | Anadromous Above | 52 | 0.32 | 0.32 | 2.0 | 0.92 | 0.08 |
| Hayden Creek-09 | Juvenile-ES | 57 | 0.32 | 0.32 | 2.0 | 0.92 | 0.09 |
| Hayden Creek-10 | Juvenile-ST | 32 | 0.32 | 0.32 | 2.0 | 0.90 | 0.10 |
| Lemhi River (screw trap) | Juvenile-ST | 62 | 0.36 | 0.34 | 2.0 | **0.41** | **0.59** |
| Lemhi River (screw trap) | Juvenile-ES | 39 | 0.34 | 0.34 | 2.0 | **0.28** | **0.72** |
| Pahsimeroi River (adult weir; RES)-09 | Resident Above | 36 | 0.35 | 0.34 | 2.0 | **0.25** | **0.75** |
| Pahsimeroi River (adult weir; RES)-10 | Resident Above | 57 | 0.34 | 0.32 | 2.0 | **0.14** | **0.86** |

Table C2. Allele frequencies and TIC values of 21 SNP loci diagnostic between reference redband trout and reference hatchery rainbow trout.

| Locus | TIC | Allele | Hat Creek | Big Jacks Creek | Bennet Creek | N.F. Owy. Creek | Rice Creek | Shack Creek | Wolf Creek | Doby G. Creek | Shepherd Hatchery | Hofer CDOW | Eagle Lake | Ennis Fish | Ennis Shasta | Ennis-Erwin | Ennis Ennis | Ennis McCon. | Ennis Harr. (D) | Ennis Harr. (L) | Mt. Lassen | Mt. Whitney | Nampa Hatchery |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| OMS00070 | -0.22 | 2 | 50.0 | 74.0 | 60.9 | 24.0 | 11.5 | 36.0 | 69.6 | 45.7 | 94.8 | 100.0 | 100.0 | 95.7 | 100.0 | 100.0 | 100.0 | 84.0 | 86.5 | 64.3 | 100.0 | 94.0 | 100.0 |
| | | 4 | 50.0 | 26.0 | 39.1 | 76.0 | 88.5 | 64.0 | 30.4 | 54.3 | 5.2 | 0.0 | 0.0 | 4.3 | 0.0 | 0.0 | 0.0 | 16.0 | 13.5 | 35.7 | 0.0 | 6.0 | 0.0 |
| OMS00090 | -0.25 | 2 | 58.3 | 50.0 | 43.8 | 52.0 | 32.7 | 70.0 | 41.3 | 72.8 | 100.0 | 100.0 | 100.0 | 86.2 | 100.0 | 100.0 | 100.0 | 100.0 | 90.4 | 96.4 | 82.3 | 88.1 | 100.0 |
| | | 4 | 41.7 | 50.0 | 56.3 | 48.0 | 67.3 | 30.0 | 58.7 | 27.2 | 0.0 | 0.0 | 0.0 | 13.8 | 0.0 | 0.0 | 0.0 | 0.0 | 9.6 | 3.6 | 17.7 | 11.9 | 0.0 |
| Omy_114587480 | -0.27 | 3 | 25.0 | 54.0 | 23.8 | 50.0 | 57.7 | 66.0 | 43.5 | 41.3 | 0.0 | 0.0 | 0.0 | 0.0 | 2.2 | 0.0 | 0.0 | 0.0 | 0.0 | 23.2 | 1.1 | 0.0 | 0.0 |
| | | 4 | 75.0 | 46.0 | 76.2 | 50.0 | 42.3 | 34.0 | 56.5 | 58.7 | 100.0 | 100.0 | 100.0 | 100.0 | 97.8 | 100.0 | 100.0 | 100.0 | 100.0 | 76.8 | 98.9 | 100.0 | 100.0 |
| Omy_anp17 | -0.22 | 1 | 87.5 | 52.0 | 77.1 | 46.0 | 17.3 | 40.0 | 41.3 | 63.0 | 91.3 | 100.0 | 100.0 | 91.5 | 100.0 | 100.0 | 98.9 | 86.0 | 96.2 | 100.0 | 100.0 | 97.6 | 75.5 |
| | | 2 | 12.5 | 48.0 | 22.9 | 54.0 | 82.7 | 60.0 | 58.7 | 37.0 | 8.7 | 0.0 | 0.0 | 8.5 | 0.0 | 0.0 | 1.1 | 14.0 | 3.8 | 0.0 | 0.0 | 2.4 | 24.5 |
| Omy_BACB4324 | -0.26 | 4 | 60.4 | 66.0 | 64.6 | 76.0 | 3.8 | 62.0 | 56.5 | 41.3 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 98.9 | 100.0 | 90.4 | 96.4 | 100.0 | 97.6 | 100.0 |
| | | 3 | 39.6 | 34.0 | 35.4 | 24.0 | 96.2 | 38.0 | 43.5 | 58.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.1 | 0.0 | 9.6 | 3.6 | 0.0 | 0.0 | 0.0 |
| Omy_crb106 | -0.21 | 3 | 83.3 | 66.0 | 78.3 | 66.0 | 76.9 | 70.0 | 76.1 | 96.7 | 84.8 | 100.0 | 100.0 | 95.6 | 100.0 | 100.0 | 100.0 | 100.0 | 79.2 | 96.4 | 92.9 | 94.4 | 97.9 |
| | | 4 | 16.7 | 34.0 | 21.7 | 34.0 | 23.1 | 30.0 | 23.9 | 3.3 | 15.2 | 0.0 | 0.0 | 4.4 | 0.0 | 0.0 | 0.0 | 0.0 | 20.8 | 3.6 | 7.1 | 5.6 | 2.1 |
| Omy_hsf2146 | -0.22 | 1 | 54.2 | 88.0 | 54.2 | 68.0 | 98.1 | 90.0 | 78.3 | 82.6 | 98.3 | 100.0 | 100.0 | 91.5 | 100.0 | 100.0 | 100.0 | 100.0 | 92.3 | 98.2 | 100.0 | 91.7 | 100.0 |
| | | 5 | 45.8 | 12.0 | 45.8 | 32.0 | 1.9 | 10.0 | 21.7 | 17.4 | 1.7 | 0.0 | 0.0 | 8.5 | 0.0 | 0.0 | 0.0 | 0.0 | 7.7 | 1.8 | 0.0 | 8.3 | 0.0 |
| Omy_nkef241 | -0.25 | 2 | 33.3 | 68.0 | 21.7 | 52.0 | 28.8 | 46.0 | 50.0 | 52.2 | 80.2 | 68.8 | 100.0 | 97.9 | 100.0 | 98.9 | 98.9 | 100.0 | 100.0 | 94.6 | 96.8 | 97.6 | 100.0 |
| | | 1 | 66.7 | 32.0 | 78.3 | 48.0 | 71.2 | 54.0 | 50.0 | 47.8 | 19.8 | 31.3 | 0.0 | 2.1 | 0.0 | 1.1 | 1.1 | 0.0 | 0.0 | 5.4 | 3.2 | 2.4 | 0.0 |
| Omy_bcAKala380rd | -0.20 | 3 | 93.8 | 72.0 | 52.1 | 26.0 | 53.8 | 66.0 | 63.0 | 41.3 | 82.9 | 96.9 | 93.6 | 86.2 | 100.0 | 100.0 | 92.6 | 100.0 | 61.5 | 85.7 | 100.0 | 83.3 | 100.0 |
| | | 1 | 6.3 | 28.0 | 47.9 | 74.0 | 46.2 | 34.0 | 37.0 | 58.7 | 17.1 | 3.1 | 6.4 | 13.8 | 0.0 | 0.0 | 7.4 | 0.0 | 38.5 | 14.3 | 0.0 | 16.7 | 0.0 |
| OMS00014 | 0.27 | 2 | 100.0 | 100.0 | 93.8 | 100.0 | 100.0 | 100.0 | 100.0 | 98.9 | 47.7 | 71.9 | 69.1 | 41.5 | 4.3 | 19.1 | 19.1 | 32.0 | 53.8 | 48.2 | 33.9 | 38.1 | 43.6 |
| | | 4 | 0.0 | 0.0 | 6.3 | 0.0 | 0.0 | 0.0 | 0.0 | 1.1 | 52.3 | 28.1 | 30.9 | 58.5 | 95.7 | 80.9 | 80.9 | 68.0 | 46.2 | 51.8 | 66.1 | 61.9 | 56.4 |
| OMS00133 | 0.25 | 1 | 100.0 | 96.0 | 89.6 | 100.0 | 98.1 | 100.0 | 100.0 | 100.0 | 32.1 | 87.5 | 67.0 | 31.7 | 19.6 | 45.7 | 50.0 | 36.0 | 48.1 | 60.7 | 72.8 | 81.0 | 65.2 |
| | | 3 | 0.0 | 4.0 | 10.4 | 0.0 | 1.9 | 0.0 | 0.0 | 0.0 | 67.9 | 12.5 | 33.0 | 68.3 | 80.4 | 54.3 | 50.0 | 64.0 | 51.9 | 39.3 | 27.2 | 19.0 | 34.8 |
| OMS00149 | 0.26 | 3 | 100.0 | 98.0 | 87.5 | 100.0 | 100.0 | 100.0 | 71.7 | 100.0 | 41.3 | 54.7 | 47.9 | 46.8 | 75.0 | 67.0 | 59.6 | 86.0 | 55.8 | 71.4 | 74.2 | 48.8 | 25.5 |
| | | 4 | 0.0 | 2.0 | 12.5 | 0.0 | 0.0 | 0.0 | 28.3 | 0.0 | 58.7 | 45.3 | 52.1 | 53.2 | 25.0 | 33.0 | 40.4 | 14.0 | 44.2 | 28.6 | 25.8 | 51.2 | 74.5 |
| OMS00169 | 0.26 | 1 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 92.0 | 100.0 | 100.0 | 80.8 | 67.2 | 73.4 | 44.7 | 52.2 | 60.6 | 67.0 | 34.0 | 98.1 | 78.6 | 78.5 | 77.4 | 92.6 |
| | | 3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 8.0 | 0.0 | 0.0 | 19.2 | 32.8 | 26.6 | 55.3 | 47.8 | 39.4 | 33.0 | 66.0 | 1.9 | 21.4 | 21.5 | 22.6 | 7.4 |
| Omy_IL1b163 | 0.23 | 3 | 0.0 | 4.5 | 4.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 23.8 | 85.9 | 43.6 | 22.3 | 16.3 | 35.1 | 60.6 | 36.0 | 11.5 | 25.0 | 28.5 | 0.0 | 40.4 |
| | | 4 | 100.0 | 95.5 | 95.8 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 76.2 | 14.1 | 56.4 | 77.7 | 83.7 | 64.9 | 39.4 | 64.0 | 88.5 | 75.0 | 71.5 | 100.0 | 59.6 |
| Omy_LDHB2_i6 | 0.27 | 3 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 96.0 | 100.0 | 97.8 | 61.6 | 35.9 | 69.1 | 28.7 | 65.2 | 75.5 | 56.4 | 88.0 | 65.4 | 66.1 | 47.8 | 45.0 | 92.6 |
| | | 4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 4.0 | 0.0 | 2.2 | 38.4 | 64.1 | 30.9 | 71.3 | 34.8 | 24.5 | 43.6 | 12.0 | 34.6 | 33.9 | 52.2 | 55.0 | 7.4 |
| Omy_mcsf268 | 0.21 | 2 | 0.0 | 2.0 | 0.0 | 0.0 | 3.8 | 4.0 | 0.0 | 1.1 | 20.0 | 21.9 | 54.3 | 16.0 | 38.0 | 8.5 | 22.3 | 12.0 | 36.5 | 51.8 | 60.8 | 2.4 | 66.0 |
| | | 4 | 100.0 | 98.0 | 100.0 | 100.0 | 96.2 | 96.0 | 100.0 | 98.9 | 80.0 | 78.1 | 45.7 | 84.0 | 62.0 | 91.5 | 77.7 | 88.0 | 63.5 | 48.2 | 39.2 | 97.6 | 34.0 |
| Omy_nach200 | 0.28 | 1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 4.0 | 0.0 | 0.0 | 40.7 | 66.1 | 36.2 | 37.2 | 46.7 | 8.5 | 79.8 | 48.0 | 40.4 | 37.5 | 33.7 | 31.7 | 14.1 |
| | | 4 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 96.0 | 100.0 | 100.0 | 59.3 | 33.9 | 63.8 | 62.8 | 53.3 | 91.5 | 20.2 | 52.0 | 59.6 | 62.5 | 66.3 | 68.3 | 85.9 |
| Omy_SECC22b88 | 0.21 | 2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 8.0 | 0.0 | 0.0 | 71.5 | 79.7 | 33.0 | 85.1 | 73.9 | 77.7 | 91.5 | 94.0 | 25.0 | 69.6 | 97.8 | 77.4 | 55.3 |
| | | 4 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 92.0 | 100.0 | 100.0 | 28.5 | 20.3 | 67.0 | 14.9 | 26.1 | 22.3 | 8.5 | 6.0 | 75.0 | 30.4 | 2.2 | 22.6 | 44.7 |
| Omy_sSOD1 | 0.23 | 3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 33.7 | 40.6 | 20.2 | 31.9 | 12.0 | 43.6 | 19.1 | 2.0 | 30.8 | 17.9 | 58.6 | 21.4 | 66.0 |
| | | 4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 66.3 | 59.4 | 79.8 | 68.1 | 88.0 | 56.4 | 80.9 | 98.0 | 69.2 | 82.1 | 41.4 | 78.6 | 34.0 |
| Omy_tlr5205 | 0.20 | 1 | 95.8 | 68.0 | 100.0 | 74.0 | 100.0 | 100.0 | 95.7 | 95.7 | 54.1 | 17.2 | 80.9 | 71.3 | 37.0 | 63.8 | 69.1 | 81.3 | 88.5 | 64.3 | 73.7 | 42.9 | 39.4 |
| | | 4 | 4.2 | 32.0 | 0.0 | 26.0 | 0.0 | 0.0 | 4.3 | 4.3 | 45.9 | 82.8 | 19.1 | 28.7 | 63.0 | 36.2 | 30.9 | 18.8 | 11.5 | 35.7 | 26.3 | 57.1 | 60.6 |
| Omy_ndk152 | 0.25 | 1 | 100.0 | 98.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 39.3 | 23.4 | 38.3 | 89.4 | 70.7 | 31.9 | 67.0 | 2.0 | 55.8 | 55.4 | 73.7 | 76.2 | 11.7 |
| | | 3 | 0.0 | 2.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 60.7 | 76.6 | 61.7 | 10.6 | 29.3 | 68.1 | 33.0 | 98.0 | 44.2 | 44.6 | 26.3 | 23.8 | 88.3 |

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