FISHERY RESEARCH

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

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Prepared by:

John H. Powell, Fishery Biologist 2
Ninh Vu, Fishery Biologist 2
Jesse McCane, Data Management Specialist 2
Michael W. Ackerman, Fishery Biologist 2
Kristin K. Wright, Fishery Biologist 2
Matthew R. Campbell, Fisheries Genetics Program Coordinator

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Project Progress Report

2016 Annual Report

By

John H. Powell
Ninh Vu
Jesse McCane
Michael W. Ackerman
Kristin K. Wright
Matthew R. Campbell

Idaho Department of Fish and Game
600 South Walnut Street
P.O. Box 25
Boise, ID 83707

and

Daniel J. Hasselman
Shawn R. Narum

Columbia River Inter-Tribal Fish Commission
Hagerman Fish Culture Experiment Station
3059-F National Fish Hatchery Road
Hagerman, ID 83332

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ABSTRACT

This report summarizes progress in the development and implementation of genetic stock identification (GSI) in the Snake River basin for natural origin steelhead and spring/summer (spring/summer) Chinook Salmon for the 01/01/2015 to 12/31/2015 reporting period. Four objectives for the GSI project are addressed in this report: 1) the maintenance and evaluation of single nucleotide polymorphism (SNP) panels for high-throughput genotyping of steelhead and Chinook Salmon in the Snake and Columbia river basins; 2) the updating, maintenance, and testing of SNP baselines to describe genetic variation and for use as a reference in conducting GSI for both species; 3) the implementation of GSI to estimate genetic stock composition and life history diversity of steelhead and spring/summer Chinook Salmon passing Lower Granite Dam (LGR); and 4) summarize the life history and genetic diversity information for steelhead and spring/summer Chinook Salmon detected at Instream PIT Tag Detection Systems (IPTDS). For both species, panels of up to 191 SNPs have been in use for GSI and parentage based tagging (PBT) at both Idaho Department of Fish and Game's Eagle Fish Genetics Lab, and its collaborating laboratory, the Columbia River Inter-Tribal Fish Commission's Hagerman Genetics Lab. Steelhead SNP baseline version 3.1 (v3.1) consists of 66 collections and 6,150 individuals. Chinook Salmon SNP baseline v3.1 consists of 46 collections and 4,604 individuals. SNP baselines are used to describe genetic diversity and structure of natural-origin populations throughout the Snake River. Based on population structure we have defined 10 genetic stocks for steelhead and 7 genetic stocks for Chinook Salmon for GSI analysis at LGR. We summarize GSI results for returning adults and emigrating juveniles during 2015 at LGR using v3.1 baselines as reference. Finally, we describe the life history variation and genetic diversity of steelhead and Chinook Salmon detected at IPTDS. The information presented in this report provides critical data for viable Salmonid population (VSP) monitoring of the Snake River steelhead DPS and the Snake River spring/summer Chinook Salmon ESU.

Authors:

John H. Powell, Fishery Biologist 2

Ninh Vu, Fishery Biologist 2

Jesse McCane, Data Management Specialist 2

Michael W. Ackerman, Fishery Biologist 2

Kristin K. Wright, Ageing Laboratory Coordinator

Matthew R. Campbell, Fisheries Genetics Program Coordinator

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INTRODUCTION

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

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

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

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

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

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

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

REPORT STRUCTURE

This report contains four sections, one for each of the study objectives. Section 1 addresses the development of GT-Seq (Genotyping in Thousands by Sequencing) for more efficient and cheaper high-throughput genotyping for GSI in the Snake River basin. Section 2 summarizes efforts to update, maintain, and test SNP baselines for both Snake River steelhead and spring/summer Chinook Salmon. These baselines are used to monitor genetic diversity and structure of natural-origin populations and are the reference for GSI at LGR. Section 3 addresses the use of GSI to estimate genetic stock proportions and life history diversity for wild stocks (both juveniles and adults) at LGR. Section 4 summarizes life history and genetic diversity of steelhead and spring/summer Chinook Salmon that are detected using Instream PIT tag Detection Systems (IPTDS).

In this report, we refer to adult steelhead and Chinook Salmon migrating past LGR using spawn years (SY). For steelhead, a spawn year refers to adults that migrate upstream past LGR during the fall of the previous calendar year and the spring of the current calendar year (e.g., SY2015 steelhead are adults that migrated past LGR between 7/1/14 - 6/30/15 and spawned in spring of 2015). For spring/summer Chinook Salmon, a spawn year refers to adults that migrate past the dam prior to August 17 and spawn that same fall. We refer to juveniles of both species

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

SECTION 1: EVALUATE AND MAINTAIN SNP MARKER PANELS

INTRODUCTION

Transition from Fluidigm to GT-seq (Genotyping-in-Thousands by Sequencing) genotyping platform was completed in 2015. SNP markers genotyped using the GT-seq platform included a subset of the original 192 SNPs genotyped with the Fluidigm platform for both steelhead and Chinook Salmon. For both species, all 96 SNP markers from the PBT panels were consistent across genotyping platforms. For steelhead 179 of 191 SNP markers from the GSI panel were consistent across platforms, and for Chinook Salmon 173 of 191 SNP markers from the GSI panel were consistent across genotyping platforms. For 2016, we began testing an expanded panel for both species. These additional markers have the potential to improve GSI and PBT applications. We are in the process of evaluating these additional markers' utility and power. Results will be in the upcoming annual progress report.

DISCUSSION

Up to 2015, both steelhead and Chinook Salmon GSI SNP panels contain 191 SNP markers. The PBT panels are a subset of these panels with 96 SNP markers each. For 2016, we began adding additional markers to both steelhead and Chinook Salmon GSI SNP panels. For the steelhead panel, we added 77 markers for a new total of 268. For the Chinook Salmon panel, we added 106 additional markers for a new total of 298. We are currently evaluating each panel for genotyping accuracy and their utility in GSI and PBT applications. Results will be reported in next year's annual report.

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

INTRODUCTION

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

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

Second, the Snake River SNP baselines serve as a reference for GSI conducted at LGR to estimate genetic stock composition of out-migrating smolts (e.g. Stark et al. 2016) and returning adults (e.g. Schrader et al. 2014). Genetic stock composition estimates of adults and juveniles at LGR, combined with sex and age data, will allow us to estimate abundance, productivity, and life history diversity of genetic stocks over time for VSP monitoring. For GSI, our objective is to periodically update and maintain the SNP baselines to accurately estimate contemporary allele frequencies (genetic structure) of wild populations throughout the Snake River contributing to production at LGR.

For this year, we chose to keep steelhead and Chinook Salmon baselines as is, with no changes to the last reporting year, 2015. As such, methods, results and in depth analyses can be found in Vu et al. (2015).

DISCUSSION

We chose to keep the same baselines from the previous year, 2015. Steelhead baseline v3.1 consists of 6,150 samples in 66 pooled collections. These collections represent all 23 TRT populations and all 6 major population groups. These collections were pooled into 45 GSI populations encompassing 10 genetic stocks. Chinook Salmon v3.1 consists of 4,604 samples in 46 pooled collections. These collections represent 31 of 41 TRT populations and all 5 major population groups. These collections were further pooled into 30 GSI populations encompassing seven genetic stocks. Methods, results and analyses of both baselines can be found in Vu et al. (2015).

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

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

However, population level or MPG assessments of abundance and productivity for ESA-listed Snake River steelhead and spring/summer Chinook Salmon can be particularly difficult (see Report Introduction). Specific data on Snake River steelhead and Chinook Salmon MPGs and populations are lacking, particularly key parameters such as population abundance, age composition, genetic diversity, recruits per spawner, and survival rates (ICTRT 2003). GSI is one potential means for estimating these parameters at a finer-scale (e.g., MPG, genetic stock [reporting group], or population). GSI uses multilocus genotype data from reference populations (representing potential contributing stocks) as a baseline and a complimentary set of genotype data from mixtures of fish of unknown origin to estimate stock proportions within the mixture and to estimate stock of origin of individual fish (Shaklee et al. 1999). Section 2 of Vu et al. (2015) presents the SNP baselines used for GSI in the Snake River basin. In Section 3, we use complementary sets of genotype data from adults sampled at the Lower Granite Dam (LGR) adult trap and juveniles sampled at the LGR juvenile bypass facility to estimate the genetic stock of origin of upstream migrating adults and emigrating juveniles. We then provide life history diversity (sex, length, age, migration timing) information of individuals assigning to the various Snake River genetic stocks.

In this report, we present individual genetic assignments and life history diversity information for SY2015 adults and MY2015 juveniles (both steelhead and Chinook Salmon) sampled at LGR.

METHODS

Sampling at Lower Granite Dam

Adult Trap Operations

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

Juvenile Trap Operations

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

Fish Handling Protocols (Adults and Juveniles)

Fish handling procedures are detailed in Schrader et al. (2014) for adults and Copeland et al. (2014) for juveniles (and citations within both reports). Fish captured at the LGR adult or juvenile trap are anesthetized; identified to species; examined for external marks, tags, and injuries; scanned for an internal CWT or PIT tag; and measured for fork length (FL). All fish are examined for the presence (unclipped) or absence (clipped) of the adipose fin and classified to putative origin (hatchery or wild). All wild fish have an unclipped adipose fin because they spend their entire life cycle in the natural environment. Most hatchery-origin fish have a clipped adipose fin. However, some hatchery fish may be released with an unclipped adipose fin for supplementation or tribal harvest opportunities. Thus, unclipped fish are also examined for a CWT or a PIT tag. The presence of a CWT definitively identifies an unclipped fish as hatchery origin. For unclipped steelhead, hatchery origin may also be determined by the presence of dorsal and/or ventral fin erosion, which is assumed to occur only in hatchery-reared steelhead (Latremouille 2003). Captured fish determined to be putatively wild or unclipped hatchery with no CWT (steelhead ‘stubbies’) are sampled for scales (for age; except juvenile Chinook) and tissue (for sex and genotype data). For juveniles, fish bearing PIT tags and/or diseased or injured fish were omitted from the subsample, as were Chinook deemed to be yearling fall Chinook based on external morphology (Tiffan et al. 2000).

Scales were taken from above the lateral line and posterior to the dorsal fin. Samples were stored in coin envelopes for transport to the IDFG ageing laboratory in Nampa, Idaho. Tissue samples were taken from a small clip of the anal fin. Tissues were stored in a vial with 200-proof non-denatured ethyl alcohol for transport to the IDFG Eagle Fish Genetics Laboratory. Gender was not visually determined at the trap, but was assessed using Y-specific genetic assays (Campbell et al. 2012). After processing, all fish were returned to the fish ladder to resume upstream migration (adults) or the bypass system to resume downstream migration (juveniles).

Scale Age Protocol

Protocols for determining an adult fish’s age from scales are detailed in Schrader et al. (2014). Protocols for determining a juvenile fish’s age from scales are detailed in Copeland et al. (2014).

Genetics Laboratory Protocol

Laboratory protocols for DNA extraction, amplification, and SNP genotyping are detailed in Section 2 (Vu et al. 2015). MY2015 steelhead juveniles were processed at the CRITFC Genetics Lab in Hagerman, Idaho. SY2015 steelhead adults were processed at IDFG’s Eagle

Fish Genetics Lab (EFGL) in Eagle, Idaho. SY2015 Chinook Salmon adults and MY2015 Chinook Salmon juveniles were processed at EFGL.

Parentage-Based Tagging

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

We conducted PBT analysis for both SY2015 adults and MY2015 juveniles. All MY2015 hatchery juvenile cohorts were interrogated via PBT. For SY2015, 1-ocean, 2-ocean, and 3-ocean steelhead and spring/summer Chinook were interrogated via PBT. In using PBT to evaluate all the fish, we are better able to identify putative natural-origin (unclipped, unmarked) fish that are truly of hatchery origin. Any individuals identified as unmarked hatchery origin adults with a PBT were removed from the dataset before performing GSI and evaluating life history diversity of genetic stocks.

Genetic Stock Identification

Individual assignment (IA) tests were conducted for SY2015 adults and MY2015 juveniles (both species) using the Snake River SNP baselines v3.1 described in Section 2 of Vu et al. (2015). SNP allele frequency estimates from baseline collections are the reference information for IA tests. Fish sampled at the LGR adult and juvenile trapping facilities were genotyped at the same SNPs and multilocus genotype data were used to assign individual fish back to their estimated population (and genetic stock) of origin (Pella and Milner 1987; Shaklee et al. 1999). In IA, the probability that each fish originates from a baseline population is calculated based on the likelihood that the individual's genotype belongs to that population, given baseline allele frequency estimates. Individual population estimates were first calculated and then summed into genetic stock estimates (allocate-sum procedure; Wood et al. 1987). Genetic stocks (aka reporting groups) are assemblages of reference (baseline) populations grouped primarily by genetic and geographic similarities and secondarily by political boundaries and/or management units (Ackerman et al. 2011). IA procedures assign an individual's genotype to the reporting group from which it is most likely to have originated.

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

Seven wild Chinook Salmon genetic stocks were used during IA analyses. Genetic stocks include: 1) UPSALM: upper Salmon River; 2) MFSALM: Middle Fork Salmon River; 3) CHMBLN: Chamberlain Creek; 4) SFSALM: South Fork Salmon River; 5) HELLSC: an aggregate reporting group that includes the Little Salmon, Clearwater, Grande Ronde, and Imnaha rivers; 6) TUCANO: Tucannon River, and 7) FALL: Snake River fall Chinook Salmon.

Three collections of Snake River fall Chinook Salmon (see Table 2 in Ackerman et al. 2012) are included in the SNP baselines (FALL genetic stock); we are able to identify fall Chinook within mixtures of spring/summer Chinook with 100% accuracy.

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

- SY2015 steelhead adults
- SY2015 Chinook adults
- MY2015 steelhead juveniles
- MY2015 Chinook juveniles

RESULTS

We inventoried a total of 9,406 samples from SY2015 adults and MY2015 juveniles from LGR (Table 1). Of the samples inventoried, 9,404 were queued for genotyping. Of queued samples, 87 (0.9%) failed to genotype successfully. All samples were from fish with intact adipose fins; however, 1,896 (20.3%) assigned back to hatchery parents in our PBT baseline. We performed IA on the remaining 7,421 samples; results for those samples are summarized below and in Tables 1-5.

SY2015 Steelhead Adults

We inventoried 4,936 unclipped adult steelhead samples for SY2015. Of those, 4,287 (86.9%) were phenotypically wild (no dorsal or ventral fin erosion) and all were queued for genotyping; 4,264 (99.5%) were genotyped successfully. Of samples genotyped successfully, 257 (6%) assigned to hatchery parents and the remaining 4,007 (94%) were assigned back to a genetic stock via IA.

Of the 4,936 unclipped adult steelhead samples, 649 (13.1%) were phenotypically identified as hatchery origin due to dorsal and/or ventral fin erosion. Of these 649 samples one was not queued for genotyping and 644 (99.4%) were genotyped successfully. Of those genotyped successfully, 525 (81.5%) assigned back to hatchery parents and the remaining 119 (18.5%) were assigned back to a genetic stock via IA.

Life history diversity information (sex, length, and ocean age) for the 4,126 unclipped steelhead adults that were assigned a genetic stock is summarized in Table 2. Of the 4,126 assigned a genetic stock, 631 (15.3%) assigned to UPSALM, 365 (8.8%) to MFSALM, 210 (5.1%) to SFSALM, 157 (3.8%) to LOSALM, 451 (10.9%) to UPCLWR, 247 (6%) to SFCLWR, 404 (9.8%) to LOCLWR, 306 (7.4%) to IMNAHA, 878 (21.2%) to GRROND, and 477 (11.6%) to LSNAKE.

MY2015 Steelhead Juveniles

We inventoried 666 unclipped juvenile steelhead samples for MY2015 (Table 1); all but one sample was queued for genotyping and 653 (98.2%) were genotyped successfully. Of samples genotyped, four (0.6%) were assigned back to hatchery parents and the remaining 649 (99.4%) were assigned a genetic stock via IA.

Life history diversity information for the 649 emigrating steelhead smolts that were assigned a genetic stock is summarized in Table 3. Of the 649 steelhead smolts assigned a genetic stock, 101 (15.6%) assigned to UPSALM, 58 (8.9%) to MFSALM, 35 (5.4%) to SFSALM, 29 (4.4%) to LOSALM, 70 (10.8%) to UPCLWR, 44 (6.8%) to SFCLWR, 65 (10%) to LOCLWR, 50 (7.7%) to IMNAHA, 142 (21.9%) to GRROND, and 55 (8.5%) to LSNAKE.

SY2015 Chinook Salmon Adults

We inventoried 3,192 unclipped adult Chinook Salmon samples for SY2015 and all of them were queued for genotyping (Table 1). Of those, 3,147 (98.6%) were genotyped successfully, of which 1,010 (32.1%) were assigned back to hatchery parents and 2,137 (67.9%) were assigned back to a genetic stock via IA.

Life history diversity information for the 2,137 Chinook Salmon adults that were assigned to a genetic stock is summarized in Table 4. Of the 2,137 samples, 440 (20.6%) assigned to UPSALM, 469 (21.9%) to MFSALM, 40 (1.9%) to CHMBLN, 183 (8.6%) to SFSALM, 901 (42.2%) to HELLSC, 19 (0.9%) to TUCANO, and 85 (4%) to FALL.

MY2015 Chinook Salmon Juveniles

We inventoried 612 unclipped juvenile Chinook Salmon for MY2015. Of the 612 juvenile Chinook Salmon inventoried, all were queued for genotyping and 609 (99.5%) of those genotyped successfully (Table 1). Of the juveniles genotyped, 100 (16.4%) were assigned back to hatchery parents and the remaining 509 (83.6%) were assigned a genetic stock via IA.

Life history diversity information for the 509 Chinook Salmon smolts assigned a genetic stock is summarized in Table 5. Of the 509 Chinook Salmon smolts assigned a genetic stock, 82 (16.1%) assigned to UPSALM, 87 (17.1%) to MFSALM, 10 (2%) to CHMBLN, 67 (13.2%) to SFSALM, 245 (48.1%) to HELLSC, 5 (1%) to TUCANO, and 13 (2.6%) to FALL.

DISCUSSION

Adult steelhead and spring/summer Chinook Salmon are intercepted at the LGR adult trapping facility at approximately 10-20% trapping rate. Tissue samples are taken from trapped fish as part of this project to estimate abundance and life history diversity metrics at the genetic stock and/or MPG scale. Trapped adult fish are also PIT tagged by the Integrated Status And Effectiveness Monitoring Project (ISEMP; BPA Project 2003-017-00). Detection of these PIT tagged adults at Instream PIT Tag Detection Systems (IPTDS) throughout the Snake River basin are used in a Bayesian branching model to provide reliable and unbiased estimates of abundance at the arrays (QCI 2013; See et al. 2016). A multi-agency collaboration has been initiated to utilize information generated from these two innovative technologies (SNP genotyping for PBT and GSI and IPTDS infrastructure for array based abundance estimates). The goal of this collaboration is to synthesize available data regarding abundance, life history diversity, and genetic structure and diversity of Snake River steelhead and spring/summer Chinook Salmon that is available from the PIT tagging and biological sampling of adults at LGR and the subsequent detection of those adults at IPTDS throughout the Snake River basin. We present results of this collaboration relating to life history and genetic diversity in Section 4.

GSI at LGR estimates the origin of fish and provides abundance estimates at the genetic stock and/or MPG level; PIT tagging at LGR estimates the final spawning destination of fish and

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

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

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

SECTION 4: SUMMARIZE LIFE HISTORY AND GENETIC DIVERSITY OF WILD STEELHEAD AND SPRING/SUMMER CHINOOK SALMON THAT ARE DETECTED AT INSTREAM PIT TAG DETECTIONS SYSTEMS IN THE SNAKE RIVER BASIN SY2010-2015

INTRODUCTION

In this section, we synthesize life history and genetic diversity of 15 of the 24 extant Snake River steelhead DPS populations (5/12 populations in Salmon River MPG, 4/5 in Clearwater River MPG, 1/1 in Imnaha River MPG, 3/4 in Grande Ronde River MPG, 2/2 in Lower Snake River MPG). We provide similar information for 17 of the 28 extant Snake River spring/summer Chinook Salmon populations (6/8 in Upper Salmon River MPG, 2/9 in Middle Fork Salmon River MPG, 4/4 in South Fork Salmon River MPG, 5/6 in Grande Ronde / Imnaha Rivers MPG, 0/1 in Lower Snake River MPG). For spring/summer Chinook Salmon, we also report on 4 extirpated populations including Big Sheep Creek and 3 populations from the Clearwater River (Lolo Creek and lower and upper South Fork Clearwater).

The data produced in this report are the product of multiple projects and agencies and are generated from the PIT tagging and biological sampling of adult steelhead and Chinook Salmon as they migrate through the LGR fish ladder and the subsequent detection of PIT-tagged adults at upstream Instream PIT Tag Detection Systems (IPTDS) throughout the Snake River basin. The Integrated Status and Effectiveness Monitoring Project (ISEMP; BPA Project 2003-017-00) PIT tags adults at LGR, develops and maintains much of the IPTDS infrastructure throughout the Snake River Basin, and developed models for abundance estimation at these arrays. The Idaho Steelhead Monitoring and Evaluation Studies (ISMES; BPA Project 1990-055-00) and the Idaho Natural Production Monitoring and Evaluation Program (INPMEP; BPA Project 1991-073-00) have coordinated biological sampling of adults at LGR and have provided length, age, and passage timing data. The Snake River Chinook and Steelhead Parental Based Tagging (BPA Project 2010-031-00) has provided PBT baselines within the Snake River basin, and the Snake River Genetic Stock Identification (BPA Project 2010-026-00) has provided SNP genotype data for population-level genetic diversity and structure analysis. Trapping at LGR is coordinated by National Marine Fisheries Service (NMFS; BPA Project 2005-002-00; Harmon 2003; Ogden 2010, 2011).

METHODS

Adult Trap Operations and Sample Processing

Adult steelhead and Chinook Salmon were sampled at the LGR adult trap as described in Section 3 of this report. Protocols for determining age from scales and genetic laboratory protocols for these samples can also be found in Section 3 of this report and references therein.

IPTDS Spawning Site Estimation

The “PtagisEventLastSpawnSite” field in the Lower Granite adult trap database (http://lgradulttrap.rtrdatacloud.com) is derived by first querying PTAGIS using the Advanced Reporting -> New Query Builder2 Report -> Complete Tag History template for all events in the Snake River Basin (RKM>522.*) using the metric “Event Time Max” and “Event Time Min”. Tag codes of interest selected from the Lower Granite adult trap database are then uploaded to this PTAGIS template to create the intersection. Interrogations (at dams, arrays, etc.), recaptures, recoveries, and mortalities are all considered events in this query template. The mark events of

the fish are not needed because we are only looking for adult detections, so those records are filtered out using the “Event Type” filter. The “Event Site RKM”, “Event Site Code”, “Event Site Type” and “Event Type” attribute fields are selected at this point so that they are included in the query results. The results from this initial query are then exported from PTAGIS and imported into an IDFG SQL server for aggregation queries and database joins.

Once in the IDFG SQL server, the next step is to filter out events not needed such as the mainstem adult/juvenile interrogations and lower Snake hatchery recaptures (i.e. GRJ, GRA, Oxbow, and Dworshak). A couple of nested maximum aggregation queries on the RKM total and event date fields with joins back to the original list narrow the records down to just one event site for each tag. Some event sites have the same RKM total as other sites nearby (i.e. JOC and JOSEPC). For these records, a second aggregation query is used to select the single event site with the greater event date. Rarely are event site recaptures uploaded to PTAGIS from field personnel without a RKM or event date data. When this happens a similar aggregation query is used to select a single event site based on its last event date. A few records had juvenile array interrogations without any accompanying adult event detections. These records are filtered out using SQL case statements to compare dates. Because repeat spawning steelhead with the same tag code could potentially have multiple last spawn sites across multiple years, a manual inspection of these records is necessary. These records are assigned a last spawn site individually using a “manual override” table. The final list of unique tag codes with the associated event site are then joined to the Lower Granite adult trap database.

LGR Valid Tag List Query

Records of “valid” PIT tags implanted into, or detected in, putative natural-origin steelhead and spring/summer Chinook Salmon at the LGR adult trap were downloaded from the Lower Granite adult trap database on the 26th of October 2016. For these downloads all wild steelhead and Chinook Salmon with a valid PIT-tag sampled in return years 2010-2015 were exported. Variables included were LGDNumPIT, BioSamplesID, and PtagisEventLastSpawnSite. In total, records were downloaded for 38,193 valid tags; 23,525 and 14,668 tags for steelhead and Chinook salmon, respectively (Table 6).

Genetic and phenotypic data (fork length, scale age, and sample date at Lower Granite Dam) for each individual was downloaded from the Eagle Fish Genetic Lab Progeny database along with an individual’s PIT-tag number and BioSamplesID. The two datasets were joined using BioSamplesID numbers.

Pooling Arrays into Reporting Locations

We pooled IPTDS into reporting locations (Table 7) so the life history and genetic information generated in this report would correspond to abundance estimates being generated with a Bayesian patch-occupancy model (See et al. 2016).

Life History (Sex, Length, Age, Run Timing)

Sex determination is not based on phenotypic characteristics observed at the LGR adult trap; rather sex is determined post hoc using a sex-specific allelic discrimination assay. Campbell et al. (2012) described sex determination using sex-specific allelic discrimination assays. Genomic DNA extraction and SNP genotyping (which includes sex-specific assays for both O. mykiss and O. tshawytscha) are described in Section 3 of this report. The most current

concordance check of the sex-determination assay using known-sex broodstock spawned in 2015 at Snake River hatcheries indicated 99.2% accuracy for steelhead and 99.4% accuracy for Chinook salmon (Steele et al. 2017).

We summarize fork length (cm), freshwater age, ocean (saltwater) age, and total age by location and spawn year. For steelhead, we also summarize the frequency and percentage of fish that meet small or A-run (<78 cm FL) and large or B-run (≥78 cm FL) length criteria; these size criteria are used to inform management processes and were defined by the Technical Advisory Committee, U.S. vs. Oregon (NMFS 2008). Length at ocean age was also summarized by location.

Passage timing at LGR for fish detected at upstream IPTDS were summarized by location and year for steelhead and Chinook salmon. We calculated the 5th, 25th, 50th (median), 75th, and 95th quantile dates of passage for each group.

Genetic Diversity and Structure

The observed and expected heterozygosity and the percent of SNPs that were polymorphic were calculated for each location and year as a proxy measure of genetic diversity. Observed heterozygosity directly measures the percentage of IPTDS detected fish that were heterozygotes (carry both alleles); the overall observed heterozygosity is the average across all SNPs. Expected heterozygosity is an estimate of the percentage of individuals in the population that are heterozygotes (average across SNPs) based on the allele frequency estimates from the sample (i.e. IPTDS detections).

Tests for deviation from Hardy-Weinberg expectation (HWE) were performed across all SNPs for each location/year with at least 20 samples. Exact tests were performed for all nuclear SNPs in the R package Hardy-Weinberg version 1.5.6 (Graffelman and Morales-Camarena 2008, Graffelman 2015). Critical values were adjusted using corrections for multiple tests (185 for steelhead and 180 for Chinook Salmon) following the false discovery rate correction procedure of Benjamini and Yekutieli (2001), described in Narum (2006). We report the number of SNPs exhibiting an excess or deficit of heterozygotes for any location/year. An excess of heterozygotes may indicate kinship bias (sample contains a significant number of half-sibs or full-sibs). A deficit of heterozygotes may suggest that the sample contains individuals from multiple populations (Wahlund effect; Wahlund 1928).

Genotypic differentiation was tested across years and location for all pooled locations with greater than 20 PIT-tag detections using the R package hierfstat version 0.04-22 (Goudet and Jombart 2015). Tests were performed within years, across locations, for all samples containing more than 20 individuals when genotypic differentiation was observed. Critical values for each test were adjusted for all possible comparisons (114 for steelhead and 116 for Chinook Salmon) following the false discovery rate correction procedure of Benjamini and Yekutieli (2001), described in Narum (2006). Only those sites with statistically homogenous genotypic distributions were used in subsequent genetic analyses.

Pairwise F_{ST} was estimated for each location using the method of Weir and Cockerham (1984) in the R package hierfstat version 0.04-22 (Goudet and Jombart 2015).

One neighbor-joining (NJ) tree was created for IPTDS detections for each species. NJ-trees include detections from all six years, SY2010-2015, as well as all samples included in the steelhead and Chinook Salmon GSI baseline versions 3.1. NJ trees are based on pairwise Nei's

standard distance (Nei 1972) calculated using GENDIST (PHYLIP v3,5; Felsenstein 1993). Pairwise genetic distances were used to construct NJ trees in NEIGHBOR (PHYLIP v3.5). NJ trees were visualized and exported using FigTree v1.4.0 developed by Andrew Rambaut (Rambaut 2012, http://tree.bio.ed.ac.uk/software/figtree/).

Genetic clustering of individuals detected at PIT-tag array locations was examined using discriminant analysis of principal components (Jombart et al. 2008) using the R package adegenet version 1.3-1 (Jombart 2008, Jombart and Ahmed 2011). This method provides a multivariate based analysis of genetic clustering that is free of underlying genetic models.

Effective Number of Breeders (N_b)

We used two programs to estimate the effective number of breeders (N_b) by parental brood year (BY) for each location. The program COLONY 2 (Jones and Wang 2010) implements the sibship assignment (SA) method for calculating effective population size (N_e) and N_b proposed by Wang (2009). The SA method is a single-sample approach that uses sibship assignments to determine full-sibling and half-sibling relationships within the sample; estimates of N_e are then acquired from frequencies of full- and half-sibling dyads. The SA method has been shown to perform well both with simulated and empirical data (Wang 2005, Beebee 2009, Barker 2011, Phillipsen et al. 2011, Skrbinsek et al. 2012, Ackerman et al. 2016). When offspring from the same cohort (brood year) are analyzed as a single sample, estimates of N_e from the SA method are equivalent to N_b. We also used the program NeEstimator (Do et al. 2014) to estimate N_b using the bias corrected linkage disequilibrium (LD) method of Waples (2006). The LD method is the most widely used method for estimating N_e from a single collection (Waples and England 2011). The LD method also provides estimates of N_b in a population when used on a single BY (Waples 2005).

We used scale age data (methods described above) to assign each IPTDS detection back to a brood year. Offspring from the same location and BY were than analyzed as a single sample to estimate N_b for that location and the parental BY. Because steelhead and Chinook Salmon reproductive strategies fall on a spectrum between monogamy and random mating, we calculated N_b assuming random mating. The unweighted harmonic mean of the SA and LD estimates of N_b within a BY was then calculated. The SA and LD methods were combined to increase precision of the estimated N_b (Waples and Do 2010). Finally, the unweighted harmonic mean was taken across BY for each location.

Genetic Origin of Detected and Non-Detected Fish

Each fish had been assigned a genetic reporting unit based on the highest probability scaled likelihood individual assignment using gsi_sim (Anderson et al. 2008, Anderson 2010). Individual assignments were used to examine concordance between genetic stock and PIT-tag array detection. The proportions of fish from a genetic reporting unit within a return year that were not detected at an upstream array were also calculated. A resampling test was used to determine if the proportion of non-detected fish was homogenous with the proportion of fish from that reporting unit that passed LGR. For this test we randomly sampled the same number of undetected fish from the entire collection at LGR without replacement 9999 times. The p-value of this test was calculated as the number of random samples whose proportion of fish from a reporting unit was greater than or equal to what was observed. This test was developed to investigate whether non-detection was a random process across the landscape.

Unless otherwise stated all analyses were performed in the statistical computing package R version 3.3.2 (R Core Team 2016).

RESULTS

Steelhead

We present life history and genetic diversity information for 15 of the 24 extant Snake River steelhead DPS populations (Figure 1). Supplemental information contained in the appendices referenced in this document can be found online at https://collaboration.idfg.idaho.gov/Appendices/Forms/AllItems.aspx.

IPTDS Detection Query in PTAGIS

Records were downloaded for 23,525 valid PIT tags that were implanted into adult steelhead for SY2010-2015 at the LGR trapping facility (Table 6). Of these fish, 7,684 steelhead were subsequently detected at an upstream location and 15,841 were undetected. In total, 7,337 of the detected steelhead were genotyped, and 11,068 of the steelhead not detected at an upstream location were also genotyped.

Life History (Sex, Length, Age, Run Timing)

Life history diversity information including sex ratios, mean length (including A- vs. B-run proportions), ocean (saltwater) age, total age, and LGR passage timing information for steelhead populations (by year) are summarized in Appendix A.

Including IPTDS detections across all years, the locations with the highest average annual percentage of females was Clear Creek and the East Fork Salmon River (77.8%). The location with the lowest average annual percentage of females was Penawawa Creek (44.4%). Appendix A and Figure 2 summarize annual sex ratios for steelhead by location and spawn year.

The locations with the largest adult steelhead (mean FL, cm) averaging across all years were the South Fork Clearwater River and the South Fork Salmon River mainstem (77.4 cm). The locations with the smallest adult steelhead (mean FL, cm) averaging across all years was Tenmile Creek (59.6 cm). The location with the highest average annual percentage of B-run length (≥78 cm) IPTDS detections was the South Fork Salmon River mainstem (56.3%). Mean length (cm FL) and percentage of A-run versus B-run fish by location and year are summarized in Appendix A. Appendix B summarizes length frequencies (by ocean age) of IPTDS detections by location; detections from all six years (SY2010-2015) are plotted together.

We observed freshwater ages ranging from age-1 to age-5, and ocean ages ranging from age-1 to age-3. Repeat spawners were observed at 58.3% of the IPTDS array locations (Appendix A). Excluding all repeat spawning IPTDS detections across all years, the locations with the highest average annual ocean (saltwater) ages were the South Fork Clearwater River and Clear Creek (2.0 years). The location with the lowest average annual ocean age was Almota Creek (1.0 year). Appendix A and Figure 3 summarize the percentage of returning steelhead of a given ocean- and total-age for IPTDS detections by location and year. Appendix C provides a complete summary of age structure by sex for each IPTDS location and spawn year.

The date of median passage at LGR ranged from September 3 for the Pahsimeroi River in spawn year 2012 to March 19 for Penawawa Creek in spawn year 2013. Median passage date within a location across years ranged as little as 6 days in Clear Creek and the East Fork Salmon River to as long as 177 days in Penawawa Creek. Valley Creek had the earliest median passage date at LGR (including IPTDS collections from all years) with a median passage 9.3 days before the median passage date for the entire run. Fish Creek had the latest median passage date at LGR with median passage 18.2 days after the median passage date for the entire run. Appendix A summarizes the distribution of LGR passage date by location and year, and Figure 4 summarizes the distribution of LGR passage date by GSI reporting unit across all years.

Genetic Diversity and Structure

Expected heterozygosity for locations with a minimum sample size of 20 ranged from a high of 32.3% in the Lemhi River in spawn years 2010 and 2012 to a low of 27.1% in Fish Creek in spawn year 2015. The location with the highest expected heterozygosity averaged across years was the Lemhi River (H_E = 31.8%), and the location with the lowest expected heterozygosity was Fish Creek (H_E = 27.1%). The percent polymorphic SNPs were high across all locations and years with a maximum of 100% in the Imnaha River from spawn year 2011 to spawn year 2015 and a minimum of 88.6% in Fish Creek in spawn year 2015. Appendix A summarizes observed and expected heterozygosity and percentage of polymorphic SNPs by location and year.

We analyzed samples from 97 different IPTDS location/year combinations (Appendix A). Of those, none deviated from HWE in ≥10% of SNPs analyzed. There were 162 single locus/collection deviations from HWE, 136 of which were due to a deficit of heterozygotes (Appendix A).

A NJ tree based on Nei's standard distances displays the genetic structure of steelhead PIT tagged at LGR and later detected at upstream IPTDS throughout the Snake River basin (Figure 5). Largely, when locations had genotypic differentiation across time, temporal collections for each location still clustered together inferring temporal stability in genetic structure. Collections from IPTDS locations also clustered with baseline sample locations across the basin.

Patterns of genetic divergence, estimated by mean pairwise F_{ST} across IPTDS locations, mirrored patterns observed across baseline samples (Figure 6). Collections in the Middle Fork Salmon River, South Fork Salmon River, upper Clearwater River, and South Fork Clearwater River reporting units were the most differentiated, whereas samples from the Imnaha River, Grande Ronde River, and lower Snake River reporting units all exhibited low levels of genetic differentiation (Figure 6).

Discriminant analysis of principal components (DAPC) indicated the presence of eight genetic clusters in the steelhead detected at upstream IPTDS. Retaining the first 78 principal components we assigned individuals detected at IPTDS to these eight clusters. In general, we saw replication of the clustering patterns represented in the GSI reporting units (Figure 7). However, the upper Clearwater and South Fork Clearwater river reporting units were combined into a single cluster in the DAPC analysis (Figure 7), a fact that may be driven by the reduced sample size and geographic range of upper Clearwater River IPTDS locations.

Effective Number of Breeders

We were able to estimate N_b for 20 locations for at least a single parental BY (Table 8). Again, N_b for a single BY is an estimate of the number of parent spawners in a given BY that successfully generated offspring that survived to adulthood and returned to the spawning grounds. Most N_b estimates reported here are the harmonic mean across multiple BY, and in all cases estimates of N_b were greater than 50. Franklin (1980) proposed a minimum N_e of 50 to prevent short-term inbreeding; and N_e size of 50 corresponds to an inbreeding rate of 1% per generation.

Genetic Origin of Detected and Non-Detected Fish

Overall we observed high concordance between IPTDS detections and individual GSI reporting unit assignments (Table 9). Concordance was highest in the upper Clearwater River reporting unit with greater than 93.7% of fish detected in Fish Creek assigned to the upper Clearwater River reporting unit. We observed the lowest concordance in the lower Snake River with only 37.2% of fish detected at an array within this reporting unit assigning to the lower Snake River reporting unit. We report assignment concordance at individual IPTDS detection locations in Table 9.

We estimated the genetic stock of origin for all fish that were PIT tagged and were NOT later detected at upstream IPTDS using individual assignment and Snake River steelhead SNP baseline v3.1 (Vu et al. 2015, Figure 8). We consistently observed fewer undetected steelhead than expected by random chance in the South Fork Salmon River, South Fork Clearwater River, and Imnaha River reporting units (Figure 9). Alternatively, the Middle Fork Salmon River and Upper Clearwater River reporting units have consistently more undetected fish than expected by random chance alone (Figure 9).

Chinook Salmon

We present life history and genetic diversity information for 17 of the 28 extant Snake River spring/summer Chinook salmon populations (Figure 10). In addition, we also provide information for four extirpated populations including Big Sheep Creek (Imnaha River) and three populations from the Clearwater River (Lolo Creek and the lower and upper South Fork Clearwater). Supplemental information contained in the appendices referenced in this document can be found online at https://collaboration.idfg.idaho.gov/Appendices/Forms/AllItems.aspx.

IPTDS Detection Query in PTAGIS

Records were downloaded for 14,668 valid PIT tags that were implanted into adult Chinook Salmon for SY2010-2015 at the LGR trapping facility (Table 6). Of these fish, 7,077 Chinook Salmon were subsequently detected at an upstream location. In total, 6,883 of the detected Chinook Salmon were genotyped, and 7,005 of the Chinook Salmon not detected at an upstream location were also genotyped.

Life History (Sex, Length, Age, Run Timing)

Life history diversity information including sex ratios, mean length (both including and excluding jacks), ocean (saltwater) age, total age, and LGR passage timing information for Chinook Salmon populations (by year) are summarized in Appendix D.

Including IPTDS detections across all years with a minimum sample size of 20, the location with the highest average annual percentage of females was Marsh Creek (61.8%). The location with the lowest average annual percentage of females was Valley Creek (24.4%). Appendix D and Figure 11 summarize annual sex ratios for Chinook Salmon by location and spawn year.

The location with the largest average annual adult (minimum sample size = 20, jacks excluded) Chinook Salmon (mean FL, cm) was the upper Salmon River from Pahsimeroi to the headwaters (83.5 cm). The location with the smallest adult Chinook Salmon (mean FL, cm) was the Grande Ronde River (71 cm). Appendix D summarizes mean lengths by location and year, and Appendix E summarizes length frequencies (by ocean age) of IPTDS detections by locations; detections from all 6 years (SY2010-2015) are plotted together.

We observed freshwater ages ranging from age-0 to age-1, and ocean ages ranging from age-1 to age-4. Including IPTDS detections across all years (minimum sample size = 20) the location with the greatest average ocean (saltwater) ages was the upper Salmon River from Pahsimeroi to the headwaters (2.4 years). The location with the smallest average ocean ages was Chamberlain Creek (1.8 years). Appendix D and Figure 12 summarize the percentage of returning Chinook Salmon of a given ocean- and total-age for IPTDS detections by location and year. Appendix F provides a complete summary of age structure by sex for each location and spawn year.

The date of median passage at LGR ranged from March 28th for the Potlatch River in spawn year 2014 to July 31st for the Lyons Ferry Hatchery weir spawn year 2012. Median passage date within a location across years ranged as little as 2 days in Knapp Creek to as long as 52 days in the Upper Salmon river from Pahsimeroi to the headwaters. Lookingglass Creek had the earliest average median passage date at LGR (including IPTDS collections from all years, minimum sample size of 20) with a median passage 28.9 days before the median passage date for the entire run. The Pahsimeroi River had the latest median passage date at LGR with median passage 10.8 days after the median passage date for the entire run. Appendix D summarizes the distribution of LGR passage date by location and year, and Figure 13 summarizes the distribution of LGR passage date by GSI reporting unit across all years.

Genetic Diversity and Structure

Expected heterozygosity for locations with a minimum sample size of 20 ranged from a high of 25.4% in Catherine Creek in spawn year 2015 to a low of 19.9% in the Secesh River in spawn year 2010. The location with the highest expected heterozygosity averaged across years was Catherine Creek (H_E = 24.9%). The location with the lowest expected heterozygosity was Bear Valley Creek (H_E = 20.8%). The percent polymorphic SNPs were high across all locations and years with a minimum of 79.4% in Bear Valley Creek and a maximum of 95.5% in the Imnaha River. Appendix D summarizes observed and expected heterozygosity and percentage of polymorphic SNPs by location and year.

We analyzed samples from 70 different IPTDS location/year combinations (Appendix D). Of those, none deviated from HWE in ≥10% of SNPs analyzed. There were 155 single locus/collection deviations from HWE, only 11 of which were due to a deficit of heterozygotes (Appendix D).

A NJ tree based on Nei's standard distances displays the genetic structure of Chinook Salmon PIT tagged at LGR and later detected at upstream IPTDS throughout the Snake River

basin (Figure 14). Largely, when locations had genotypic differentiation across time, temporal collections for each location still clustered together temporal stability in genetic structure. Collections from IPTDS locations also clustered with baseline sample locations across the basin.

Patterns of genetic divergence, estimated by mean pairwise F_{ST} across IPTDS locations, mirrored patterns observed across baseline samples (Figure 15). Collections in Chamberlain Creek, the Pahsimeroi River, and the Secesh River were the most differentiated, whereas samples from the South Fork Salmon River mainstem and Hells Canyon reporting units all exhibited low levels of genetic differentiation (Figure 15).

Discriminant analysis of principal components (DAPC) indicated the presence of nine genetic clusters in the Chinook Salmon detected at upstream IPTDS. Retaining the first 75 principal components we assigned individuals detected at IPTDS to these nine clusters. We saw a general weak replication of the clustering patterns represented in the GSI reporting units (Figure 16), with many of the genetic clusters having members spread across multiple reporting units (Figure 16).

Effective Number of Breeders

We were able to estimate N_b for 20 locations for at least a single parental BY (Table 10). Again, N_b for a single BY is an estimate of the number of parent spawners in a given BY that successfully generated offspring that survived to adulthood and returned to the spawning grounds. Most N_b estimates reported here are the harmonic mean across multiple BY. The only estimated N_b less than 50 was in the Imnaha River (Table 10). A single BY estimate in the Sawtooth Hatchery weir was below 50, but the overall estimate was not less than 50 (Table 10). Franklin (1980) proposed a minimum N_e of 50 to prevent short-term inbreeding; and N_e size of 50 corresponds to an inbreeding rate of 1% per generation.

Genetic Origin of Non-Detected Fish

Overall we observed high concordance between IPTDS detections and individual GSI reporting unit assignments (Table 11). Concordance was highest in the Fall reporting unit with all fish detected assigning to to this reporting unit. We observed the lowest concordance in the Tucannon River with only 50.7% of fish detected in this location assigning to the Tucannon River reporting unit. We report assignment concordance at individual IPTDS detection locations in Table 11.

We estimated the genetic stock of origin for all fish that were PIT tagged and were NOT later detected at upstream IPTDS using individual assignment and Snake River Chinook Salmon SNP baseline v3.1 (Vu et al. 2015, Figure 17). We consistently observed fewer undetected Chinook Salmon than expected by random chance in the South Fork Salmon River, and later upper Salmon River reporting unit collections (Figure 18). Alternatively, Chamberlain Creek, the Middle Fork Salmon River, and the Fall reporting units have consistently more undetected fish than expected by random chance alone (Figure 18).

DISCUSSION

Monitoring the life history variation and genetic diversity of populations of Snake River steelhead and spring/summer Chinook Salmon is important for determining their viability. McElhany et al. (2000) defined a viable salmonid population (VSP) as:

> An independent population of any Pacific salmonid (genus Oncorhynchus) that has a negligible risk of extinction due to threats from demographic variation (random or directional), local environmental variation, and genetic diversity changes (random or directional) over a 100-year time frame.

Four parameters were identified for determining whether a population is a VSP: population size, growth rate and related parameters, spatial structure, and diversity (McElhany et al. 2000). To assess the risk to population viability caused by the spatial structure and diversity of populations the ICTRT developed 12 metrics, seven of which relate to maintaining natural patterns of phenotypic and genetic variation and gene flow (ICTRT 2007). Therefore, understanding the current and past patterns of life history diversity and genetic variation within a population is essential to assessing whether the population meets these metrics.

In this section, we summarized the sex-ratios and distributions of age, length, and run-timing of Snake River steelhead and Chinook Salmon populations. We also described genetic diversity in, and summarized patterns of genetic divergence among, these populations.

Life history (Sex, Length, Age, Run Timing)

We observed a large range of variation in life histories across the genetic stocks in the Snake River basin. For example, a greater proportion of steelhead returned to the South Fork Salmon River after two years in the ocean than to the Imnaha River (Figure 3 and Appendix B). In addition, the average size of these two-ocean fish was also different between these two populations (Appendix B). Similarly, while there was annual variation in the median passage date of Chinook Salmon at LGR, fish returning to the Lemhi River always had a median passage date earlier than fish returning to the Secesh River (Appendix D).

With the wealth of life history data collected on fish sampled at LGR, we can also begin to test the utility of incorporating phenotypic characteristics into the current methods for genetic stock identification.

Genetic Diversity and Structure

Overall we observed high levels of genetic diversity within populations (Appendix A and Appendix D), and similarity between patterns of genetic divergence among adult returns and baseline collections in both species (Figure 5 and Figure 14). Steelhead populations in the upper Clearwater River, South Fork Clearwater River, and South Fork Salmon River showed increased genetic divergence relative to other populations (Figure 6), and Chinook Salmon in Chamberlain Creek, the Pahsimeroi River, the East Fork South Fork Salmon River, and the Secesh River exhibited increased genetic divergence (Figure 15).

Effective Number of Breeders

Effective population size is an important parameter to estimate because it is a measure of the relative contribution of individuals in a population that contribute offspring to the next

generation. Effective population size is almost always smaller than census size (which biologists have traditionally attempted to measure) and summarizes the magnitude of genetic drift and increase in inbreeding occurring in a population (Wright 1931). Genetic drift refers to changes due to random sampling effects. Inbreeding refers to the mating of relatives. Theoretically, as a population decreases in size, inbreeding and genetic drift increase, resulting in the loss of genetic variation. Franklin (1980) proposed minimum effective population sizes of 50 and 500 to prevent short-term inbreeding and to maintain sufficient long-term genetic diversity, respectively. An effective population size of 50 corresponds to an inbreeding rate of 1% per generation. An effective population size of 500 is aimed at maintaining genetic variation within a population by balancing the rate of loss of variation from genetic drift with the increase in variation from genetic mutations.

It is known that estimates of N_e and N_b are biased downwards when N_e is large, sample size is much smaller than NE, and when number of loci is low (Wang 2009). We expect estimates of N_b reported in this paper, if biased, are likely biased low, especially in cases where sample size is low relative to true effective population size.

We are now generating estimates of N_b in brood years where abundance has also been estimated from IPTDS detections. These estimates could be directly compared to provide insight into a population's productivity. For example, a high N_b/N would suggest that most fish present for spawning are successful at producing returning adults. This may be suggestive of low density-dependent effects. A low N_b/N would suggest that few fish present on the spawning grounds are successful at producing returning adults.

Genetic Origin of Non-Detected Fish

While detection rates have been increasing for both Snake River steelhead and spring/summer Chinook Salmon between SY2010 and SY2015 (Table 6), the year with the highest detection rates (SY2014) still had 58.9% of PIT-tagged steelhead and 41.3% of PIT-tagged Chinook Salmon not subsequently detected at upstream arrays. These undetected fish might fall back, die, or return to areas that do not have arrays. For example, steelhead in both the South Fork Salmon River and upper Clearwater River reporting units show increased genetic divergence (Figure 2) and high self-assignment rates (Table 3) relative to other reporting units. The South Fork Salmon River has two PIT tag arrays and a weir in the mainstem that covers a large portion of the drainage (Figure 1), whereas PIT-tagged steelhead from the upper Clearwater River reporting unit were only detected at a weir in Fish Creek. As expected, the South Fork Salmon River steelhead reporting unit observes fewer non-detected fish than expected by random chance alone, while the upper Clearwater River reporting unit observes more non-detected fish than expected by random chance alone (Figure 9). These differences highlight a benefit of the GSI analysis, in that it is capable of estimating abundance and diversity for all genetic stocks that return to the Snake River basin above LGR regardless of array coverage. However, there are specific management and conservation monitoring needs (fish-in/fish-out) that require collection of data at the scale of individual populations within genetic stocks. The results presented in this report hopefully demonstrate the strength of combining both technologies for providing VSP information at the multiple spatial scales needed for ESA status assessments.

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TABLES

Table 1. Summary of SY2015 adult and MY2015 juvenile steelhead and Chinook Salmon samples from Lower Granite Dam (LGR). Summary includes the number of samples that arrived from LGR (inventoried) and the number inventoried that were queued for genotyping. Of queued samples, we show the number that genotyped successfully and the number that failed genotyping. For samples that genotyped successfully, we show the number that had a parentage based tag (PBT) and the number that were assigned a genetic stock based on individual assignment (IA) using SNP baselines v3.1

Sample Group	Total Samples Inventoried	Samples Queued for Genotyping	Failed Genotyping (NG)	Successfully Genotyped	PBT Assignments	GSI Assignments
Steelhead						
SY2015 Adults (Wild Phenotype)	4287	4287	23 (0.5%)	4264 (99.5%)	257 (6%)	4007 (94%)
SY2015 Adults (Stubbies)	649	648	4 (0.6%)	644 (99.4%)	525 (81.5%)	119 (18.5%)
MY2015 Juveniles	666	665	12 (1.8%)	653 (98.2%)	4 (0.6%)	649 (99.4%)
Chinook						
SY2015 Adults	3192	3192	45 (1.4%)	3147 (98.6%)	1010 (32.1%)	2137 (67.9%)
MY2015 Juveniles	612	612	3 (0.5%)	609 (99.5%)	100 (16.4%)	509 (83.6%)
TOTAL:	9406	9404	87 (0.9%)	9317 (99.1%)	1896 (20.3%)	7421 (79.7%)

Table 2. Summary of 4,126 Lower Granite Dam (LGR) adult steelhead samples from SY2015 assigned to a genetic stock using individual assignment based on Snake River steelhead SNP baseline v3.1. Summaries of life history diversity information (sex, length, and ocean age) for each genetic stock are shown. The 'Other' saltwater age category includes fish that were not queued to be aged, fish that could not be aged, and fish with spawn checks.

			Sex					Length							Ocean (Saltwater) Age						
			Frequency			Percentage		Mean Length (cm FL) by Ocean Age			Frequency		Percentage		Frequency				Percentage		
Genetic Stock	Total Assignments	% Stock Composition	F	M	U	F	M	1	2	3	A-Run	B-Run	A-Run	B-Run	1	2	3	Other	1	2	3
UPSALM	631	15%	394	230	7	63%	37%	57	69.1	-	614	17	97%	3%	189	227	0	215	45%	55%	0%
MFSALM	365	9%	253	108	4	70%	30%	57.9	74.6	82.5	273	92	75%	25%	44	160	6	155	21%	76%	3%
SFSALM	210	5%	159	50	1	76%	24%	62.2	77.8	81	113	97	54%	46%	9	165	8	28	5%	91%	4%
LOSALM	157	4%	105	47	5	69%	31%	58.1	71	82	141	16	90%	10%	35	65	1	56	35%	64%	1%
UPCLWR	451	11%	330	117	4	74%	26%	60.1	77.9	89	213	237	47%	53%	19	240	2	190	7%	92%	1%
SFCLWR	247	6%	163	83	1	66%	34%	60.8	78	85.8	115	132	47%	53%	10	155	8	74	6%	90%	5%
LOCLWR	404	10%	247	151	6	62%	38%	57.6	71	89	369	35	91%	9%	95	157	1	151	38%	62%	0%
IMNAHA	306	7%	190	113	3	63%	37%	55.7	68.8	-	302	4	99%	1%	109	128	0	69	46%	54%	0%
GRROND	878	21%	608	262	8	70%	30%	57.2	68.6	79.5	871	7	99%	1%	213	386	2	277	35%	64%	0%
LSNAKE	477	12%	316	159	2	67%	33%	57.3	69.1	-	467	10	98%	2%	119	187	0	171	39%	61%	0%
Total:	4,126		2,765	1,320	41	68%	32%	57	72	83	3,478	647	84%	16%	842	1,870	28	1,386	31%	68%	1%

Table 3. Summary of 649 Lower Granite Dam (LGR) juvenile steelhead samples from MY2015 assigned to a genetic stock using individual assignment based on Snake River steelhead SNP baseline v3.1. Summaries of life history diversity information (sex, length, and freshwater age) for each genetic stock are shown. The 'Other' freshwater age category includes fish that were not queued to be aged or could not be aged.

			Sex					Length	Freshwater Age										
			Frequency			Percentage			Frequency						Percentage				
Genetic Stock	Total Assignments	% Stock Composition	F	M	U	F	M	Mean Length (mm FL)	1	2	3	4	5	Other	1	2	3	4	5
UPSALM	101	16%	69	32	0	68%	32%	181	18	47	33	0	0	3	18%	48%	34%	0%	0%
MFSALM	58	9%	36	22	0	62%	38%	188	1	10	35	5	1	6	2%	19%	67%	10%	2%
SFSALM	35	5%	25	10	0	71%	29%	186	0	7	21	4	0	3	0%	22%	66%	12%	0%
LOSALM	29	4%	18	11	0	62%	38%	193	2	8	11	2	0	6	9%	35%	48%	9%	0%
UPCLWR	70	11%	48	22	0	69%	31%	180	1	13	37	16	0	3	1%	19%	55%	24%	0%
SFCLWR	44	7%	30	14	0	68%	32%	175	6	23	12	0	0	3	15%	56%	29%	0%	0%
LOCLWR	65	10%	41	23	1	64%	36%	180	8	42	11	1	0	3	13%	68%	18%	2%	0%
IMNAHA	50	8%	34	16	0	68%	32%	187	3	19	24	0	0	4	7%	41%	52%	0%	0%
GRROND	142	22%	91	51	0	64%	36%	190	17	73	44	3	0	5	12%	53%	32%	2%	0%
LSNAKE	55	8%	33	22	0	60%	40%	188	10	29	11	0	0	5	20%	58%	22%	0%	0%
Total:	649		425	223	1	66%	34%	185	66	271	239	31	1	41	11%	45%	39%	5%	0%

Table 4. Summary of 2,137 Lower Granite Dam (LGR) adult Chinook Salmon samples from SY2015 assigned to a genetic stock using individual assignment based on Snake River Chinook Salmon SNP baseline v3.1. Summaries of life history diversity information (sex, length, and ocean age) for each genetic stock are shown. MJ = minijack.

			Sex					Ocean (Saltwater) Age									Length		
			Frequency			Percentage		Frequency					Percentage				Mean Length (cm FL) by Ocean Age		
Genetic Stock	Total Assignments	% Stock Composition	F	M	U	F	M	MJ	1	2	3	U	MJ	1	2	3	1	2	3
UPSALM	440	21%	180	258	2	41%	59%	0	19	316	50	55	0%	5%	82%	13%	54.6	73.1	87.4
MFSALM	470	22%	156	312	2	33%	67%	0	18	278	45	129	0%	5%	82%	13%	54.3	73.1	90.6
CHMBLN	40	2%	22	18	0	55%	45%	0	1	24	4	11	0%	3%	83%	14%	53	71.6	88.2
SFSALM	180	8%	83	97	0	46%	54%	0	12	117	22	29	0%	8%	77%	15%	57.2	74.3	88.7
HELLSC	903	42%	438	462	3	49%	51%	0	45	574	106	178	0%	6%	79%	15%	53.1	72.2	84.6
TUCANO	19	1%	5	14	0	26%	74%	0	3	11	1	4	0%	20%	73%	7%	50.7	68.9	80
FALL	85	4%	28	57	0	33%	67%	2	18	31	7	27	3%	31%	53%	12%	60.3	75.3	83.6
Total:	2137		912	1218	7	43%	57%	2	116	1351	235	433	0%	7%	79%	14%	55	72.8	86.7

Table 5. Summary of 509 Lower Granite Dam (LGR) juvenile Chinook Salmon samples from MY2015 assigned to a genetic stock using individual assignment based on Snake River Chinook Salmon SNP baseline v3.1. Summaries of life history diversity information (sex and length) by genetic stock are shown. Freshwater age is not summarized because scales were not collected from juvenile Chinook Salmon at Lower Granite Dam.

			Sex					Length
			Frequency			Percentage		
Genetic Stock	Total Assignments	% Stock Composition	F	M	U	F	M	Mean Length (mm FL)
UPSALM	82	16%	33	48	1	41%	59%	115
MFSALM	87	17%	41	46	0	47%	53%	113
CHMBLN	10	2%	7	3	0	70%	30%	109
SFSALM	67	13%	32	35	0	48%	52%	111
HELLSC	245	48%	122	123	0	50%	50%	116
TUCANO	5	1%	3	2	0	60%	40%	120
FALL	13	3%	6	7	0	46%	54%	124
Total:	509		244	264	1	48%	52%	115

Table 6. Summary of total valid PIT-tags implanted into adult steelhead and Chinook Salmon at the Lower Granite Dam (LGR) trapping facility and subsequent upstream detection of valid tags at Instream PIT Tag Detection Systems (IPTDS). Genotyped Unique Valid Tags Detected are genotyped fish that were subsequently detected at an IPTDS. Genotyped Unique Valid Tags NOT Detected are genotyped fish that were NOT detected at Snake River IPTDS.

Species	Spawn Year	LGR Total Valid Tags	Unique Valid Tags Detected Upstream	Unique Valid Tags NOT Detected Upstream	Genotyped Unique Valid Tags Detected Upstream	Genotyped Unique Valid Tags NOT Detected Upstream
Steelhead	SY2010	4,011	747 (18.6%)	3,264 (81.4%)	624 (27.2%)	1,673 (72.8%)
	SY2011	4,648	1,254 (27%)	3,394 (73%)	1,156 (41.1%)	1,658 (58.9%)
	SY2012	4,111	1,368 (33.3%)	2,743 (66.7%)	1,261 (48.8%)	1,321 (51.2%)
	SY2013	3,391	1,376 (40.6%)	2,015 (59.4%)	1,373 (40.5%)	2,013 (59.5%)
	SY2014	3,436	1,412 (41.1%)	2,024 (58.9%)	1,408 (41.1%)	2,014 (58.9%)
	SY2015	3,928	1,527 (38.9%)	2,401 (61.1%)	1,515 (38.8%)	2,389 (61.2%)
Steelhead Total		23,525	7,684 (32.7%)	15,841 (67.3%)	7,337 (39.9%)	11,068 (60.1%)
Chinook	SY2010	1,197	413 (34.5%)	784 (65.5%)	409 (34.8%)	765 (65.2%)
	SY2011	2,758	1,098 (39.8%)	1,660 (60.2%)	1,058 (45.8%)	1,253 (54.2%)
	SY2012	2,167	956 (44.1%)	1,211 (55.9%)	949 (44.3%)	1,193 (55.7%)
	SY2013	2,996	1,548 (51.7%)	1,448 (48.3%)	1,530 (51.7%)	1,432 (48.3%)
	SY2014	3,380	1,983 (58.7%)	1,397 (41.3%)	1,939 (58.5%)	1,377 (41.5%)
	SY2015	2,170	1,079 (49.7%)	1,091 (50.3%)	998 (50.3%)	985 (49.7%)
Chinook Total		14,668	7,077 (48.2%)	7,591 (51.8%)	6,883 (49.6%)	7,005 (50.4%)
Grand Total		38,193	14,761 (38.6%)	23,432 (61.4%)	14,220 (44%)	18,073 (56%)

Table 7. PIT-tag detection locations in the Snake River basin. The alphanumeric site code, site description, and location are shown. Steelhead Population and Chinook Population represent the ICTRT delineated population (ICTRT 2003) within the Snake River Basin steelhead DPS and Snake River Spring/Summer Chinook Salmon ESU that each IPTDS falls within geographically. Please note that fish detected at some IPTDS may belong to more than one population.

Site Code	Site Description	Latitude	Longitude	Steelhead Population	Chinook Population
Alturas Lake Creek					
ALTULC	Alturas Lake Creek	43.91135	-114.86168	SRUMA-s	SRUMA
Beaver Creek (upper Salmon River)					
BEAVEC	Beaver Creek	43.88419	-114.85996	SRUMA-s	SRUMA
Sawtooth Hatchery					
STL	Sawtooth Hatchery	44.15317	-114.88347	SRUMA-s	SRUMA
SAWT	Sawtooth Hatchery	44.15068	-114.88366	SRUMA-s	SRUMA
SAWTRP	Sawtooth Trap	44.14800	-114.88370	SRUMA-s	SRUMA
Valley Creek					
VC1	Valley Cr, lower site	44.22178	-114.93154	SRUMA-s	SRVAL
VC2	Valley Cr, upper site	44.21860	-114.94216	SRUMA-s	SRVAL
East Fork Salmon River					
SALEFT	East Fork Salmon River	44.12878	-114.41867	SREFS-s	SREFS
Pahsimeroi River					
PAHH	Pahsimeroi Hatchery	44.68414	-114.03947	SRPAH-s	SRPAH
PAHTRP	Pahsimeroi River Trap	44.68453	-114.04044	SRPAH-s	SRPAH
PAHSIR	Pahsimeroi River	44.45445	-113.80791	SRPAH-s	SRPAH
Lemhi River					
LLR	Lower Lemhi R	45.17635	-113.88512	SRLEM-s	SRLEM
KEN	Kenney Cr	45.02703	-113.65801	SRLEM-s	SRLEM
AGC	Agency Creek, Lemhi R. Basin	44.95674	-113.63954	SRLEM-s	SRLEM
LRW	Lemhi River Weir	44.86612	-113.62475	SRLEM-s	SRLEM
HYC	Hayden Cr	44.86159	-113.63215	SRLEM-s	SRLEM
WPC	Wimpey Creek, Lemhi R. Basin	45.09794	-113.72050	SRLEM-s	SRLEM
WIMPYC	Wimpey Creek, Lemhi River Basin	45.13571	-113.66249	SRLEM-s	SRLEM
BHC	Bohannon Cr	45.11777	-113.74130	SRLEM-s	SRLEM
LLS	Lemhi Little Springs	44.77865	-113.54208	SRLEM-s	SRLEM
BTC	Big Timber Cr	44.68811	-113.37041	SRLEM-s	SRLEM
HEC	Hawley Cr/18 Mile Cr Array	44.66859	-113.31155	SRLEM-s	SRLEM
CAC	Canyon Cr	44.69197	-113.35468	SRLEM-s	SRLEM
HAYDNC	Hayden Creek, Lemhi River Basin	44.75277	-113.71298	SRLEM-s	SRLEM
LEMHIR	Lemhi River	44.91055	-113.62504	SRLEM-s	SRLEM
Carmen Creek					
CRC	Carmen Creek, Salmon R. Basin	45.24648	-113.89347	SRLEM-s	SRLEM
CARMEC	Carmen Creek - tributary to Salmon River	45.30850	-113.80428	SRLEM-s	SRLEM
Yankee Fork Salmon River					
YFK	Yankee F Salmon R	44.28761	-114.72075	SRUMA-s	SRYFS
YANKFRK	Yankee Fork Salmon River	44.41217	-114.63615	SRUMA-s	SRYFS

Table 7. Continued.

Site Code	Site Description	Latitude	Longitude	Steelhead Population	Chinook Population
Upper Salmon River					
USE	Upper Salmon R, rkm 437	45.02894	-113.91589	SRUMA-s, SREFS-s, SRPAH-s	SRUMA, SRVAL, SRYFS, SREFS, SRPAH
USI	Upper Salmon R, rkm 460	44.89038	-113.96258	SRUMA-s, SREFS-s, SRPAH-s	SRUMA, SRVAL, SRYFS, SREFS, SRPAH
North Fork Salmon River					
SALRNF	North Fork Salmon River	45.54903	-113.93657	SRNFS-s	SRNFS
Upper Salmon River, Pahsimeroi to the headwaters					
SALR4	Salmon River - Pahsimeroi River to headwaters (km 489-650)	44.25448	-114.61050	SRUMA-s, SREFS-s	SRUMA, SRVAL, SRYFS, SREFS
Chamberlain Creek					
CHAMBC	Chamberlain Creek	45.37391	-115.12965	SRCHA-s	SRCHA
CHAMWF	West Fork Chamberlain Creek	45.43024	-115.19718	SRCHA-s	SRCHA
Sulphur Creek					
SULFUC	Sulphur Creek, Middle Fork Salmon River	44.54785	-115.40215	MFUMA-s	MFSUL
Marsh Creek					
MARSHC	Marsh Creek	44.39026	-115.16326	MFUMA-s	MFMAR
Knapp Creek					
KNAPPC	Knapp Creek	44.41870	-115.03850	MFUMA-s	MFMAR
Capehorn Creek					
CAPEHC	Capehorn Creek	44.35683	-115.21968	MFUMA-s	MFMAR
Bear Valley Creek					
BRC	Bear Valley Adult Video Weir*	522.303.319.170.006		MFUMA-s	MFBEA
BEARVC	Bear Valley Creek	44.37421	-115.39612	MFUMA-s	MFBEA
ELKC	Elk Creek	44.41567	-115.46876	MFUMA-s	MFBEA
Middle Fork Salmon River, Loon Creek to the headwaters					
SALMF2	Middle Fork Salmon River - Loon Creek to headwaters (km 73-170)	44.69847	-115.14967	MFUMA-s	MFSUL, MFMAR, MFBEA
Loon Creek					
LOONC	Loon Creek	44.62360	-114.76017	MFBIG-s	MFLOO
Camas Creek					
CAMASC	Camas Creek, Middle Fork Salmon River	44.80691	-114.47671	MFBIG-s	MFCAM
Beaver Creek (Middle Fork Salmon River)					
BEAV4C	Beaver Creek, Big Creek watershed, MF Salmon River	45.22554	-115.29957	MFBIG-s	MFBIG
Big Creek					
TAY	Big Cr	45.10387	-114.84970	MFBIG-s	MFBIG
BIG2C	Big Creek, Middle Fork Salmon River	45.15776	-115.12014	MFBIG-s	MFBIG
McCall Hatchery					
MCCA	McCall Hatchery	44.90777	-116.11650	SFMAI-s	SFMAI
KNOXB	Knox Bridge, SF Salmon River	44.65552	-115.70240	SFMAI-s	SFMAI
STR	SF Salmon Hatchery Satellite	44.66661	-115.70292	SFMAI-s	SFMAI

* River km of the interrogation site

Table 7. Continued

Site Code	Site Description	Latitude	Longitude	Steelhead Population	Chinook Population
South Fork Salmon River mainstem					
KRS	SF Salmon R, Krassel	44.97840	-115.72700	SFMAI-s	SFMAI
SALRSF	South Fork Salmon River	44.92815	-115.74330	SFMAI-s	SFMAI
East Fork South Fork Salmon River					
ESS	EFSF Salmon R	44.95621	-115.53315	SFMAI-s	SFEFS
JOHNSC	Johnson Creek	44.73393	-115.54860	SFMAI-s	SFEFS
BURNLC	Burnt Log Creek	44.71577	-115.49444	SFMAI-s	SFEFS
SAEFSF	East Fork South Fork Salmon River	44.96969	-115.47706	SFMAI-s	SFEFS
Secesh River					
ZEN	Secesh River near Zena Creek Ranch	45.03330	-115.73302	SFSEC-s	SFSEC
LAKEC	Lake Creek	45.32906	-115.94920	SFSEC-s	SFSEC
SECESR	Secesh River	45.15195	-115.79685	SFSEC-s	SFSEC
Grouse Creek					
GROUSC	Grouse Creek, Secesh River Basin	45.29016	-115.82851	SFSEC-s	SFSEC
South Fork Salmon River					
SFG	South Fork Salmon R, near Guard Station Road Bridge	45.17575	-115.57998	SFMAI-s, SFSEC-s	SFMAI, SFEFS, SFSEC
Rapid River					
RAPH	Rapid River Hatchery	45.35368	-116.39458	SRLSR-s	SRLSR
RPDTRP	Rapid River Smolt Trap	45.35841	-116.38804	SRLSR-s	SRLSR
Fish Creek					
FISTRP	Fish Creek Trap	46.34011	-115.35513	CRLOC-s	CRLOC‡
Crooked Fork Creek					
CROOKC	Crooked Fork Creek	46.59497	-114.65018	CRLOC-s	CRLOC‡
Powell Hatchery					
POWP	Powell Rearing Pond	46.50807	-114.68086	CRLOC-s	CRLOC‡
Moose Creek					
MOOS2C	Moose Creek (Selway River)	46.14218	-114.91268	CRSEL-s	SEMOO‡
Selway River, Moose Creek to the headwaters					
SELWY2	Selway River - Moose Creek to headwaters (km 65-147)	45.81005	-114.75804	CRSEL-s	SEUMA‡
Bear Creek					
BEARC	Bear Creek	46.09149	-114.67845	CRSEL-s	SEUMA‡
Potlatch River					
HLM	Potlatch R, Helmer	46.79921	-116.42869	CRLMA-s	CRPOT‡
POTREF	East Fork Potlatch River	46.84772	-116.34912	CRLMA-s	CRPOT‡
POTRWF	West Fork Potlatch River	46.92386	-116.45156	CRLMA-s	CRPOT‡
KHS	Big Bear Cr	46.61912	-116.64685	CRLMA-s	CRPOT‡
LBEARC	Little Bear Creek, Potlatch River watershed	46.67401	-116.70727	CRLMA-s	CRPOT‡
BIGBEC	Big Bear Creek, Potlatch River	46.73001	-116.62114	CRLMA-s	CRPOT‡
JUL	Potlatch R, Juliaetta	46.56574	-116.70954	CRLMA-s	CRPOT‡

* River km of the interrogation site

‡ The TRT population that this IPTDS is geographically located within is considered functionally extirpated.

Table 7. Continued

Site Code	Site Description	Latitude	Longitude	Steelhead Population	Chinook Population
Lapwai Creek					
LAP	Lapwai Cr	46.44327	-116.81254	CRLMA-s	CRLAP‡
SWT	Sweetwater Cr	46.36979	-116.79508	CRLMA-s	CRLAP‡
WEB	Webb Cr	46.32599	-116.83197	CRLMA-s	CRLAP‡
MIS	Mission Cr	46.36706	-116.73560	CRLMA-s	CRLAP‡
Lolo Creek					
LC1	Lolo Cr, rkm 21	46.29443	-115.97612	CRLOL-s	CRLOL‡
LC2	Lolo Cr, rkm 25	46.29056	-115.93415	CRLOL-s	CRLOL‡
LOLOC	Lolo Creek	46.26807	-115.81539	CRLOL-s	CRLOL‡
Clear Creek					
CLC	Clear Creek near Kooskia National Fish Hatchery*	522.224.120.004.001		CRLMA-s	SCLAW‡
KOOS	Kooskia National Fish Hatchery	46.12971	-115.94683	CRLMA-s	SCLAW‡
South Fork Clearwater River					
SC1	SF Clearwater, rkm 1	46.13685	-115.98091	CRLMA-s, CRSFC-s	SCLAW‡, SCUMA‡
SC2	SF Clearwater, rkm 2	46.12749	-115.97730	CRLMA-s, CRSFC-s	SCLAW‡, SCUMA‡
CLWRSF	South Fork Clearwater River	45.82815	-115.95471	CRSFC-s	SCUMA‡
NEWSOC	Newsome Creek	45.90833	-115.62971	CRSFC-s	SCUMA‡
AMERR	American River	45.87372	-115.44146	CRSFC-s	SCUMA‡
REDR	Red River	45.71007	-115.35405	CRSFC-s	SCUMA‡
RRT	Red River Satellite Facility	45.71118	-115.34715	CRSFC-s	SCUMA‡
REDTRP	Red River Trap	45.79385	-115.43457	CRSFC-s	SCUMA‡
REDP	Red River Rearing Pond	45.71066	-115.34650	CRSFC-s	SCUMA‡
CRT	Crooked River Satellite Fac.	45.82093	-115.52778	CRSFC-s	SCUMA‡
CROTRP	Crooked River Trap	45.82120	-115.52775	CRSFC-s	SCUMA‡
CROOKR	Crooked River	45.76266	-115.54144	CRSFC-s	SCUMA‡
Cow Creek					
COC	Cow Cr	45.76774	-116.74404	IRMAI-s	IRMAI
Big Sheep Creek					
BSC	Big Sheep Cr	45.50649	-116.85067	IRMAI-s	IRBSH‡

* River km of the interrogation site

‡ The TRT population that this IPTDS is geographically located within is considered functionally extirpated.

Table 7. Continued

Site Code	Site Description	Latitude	Longitude	Steelhead Population	Chinook Population
Imnaha River					
IR1	Imnaha R, rkm 7	45.76112	-116.75066	IRMAI-s	IRMAI
IR2	Imnaha R, rkm 10	45.74284	-116.76456	IRMAI-s	IRMAI
HORS3C	Horse Creek, Imnaha River Basin	45.54951	-116.72727	IRMAI-s	IRMAI
CMP	Camp Creek at rkm 2 - Imnaha	45.55182	-116.86694	IRMAI-s	IRBSH‡
LSHEEF	Little Sheep Facility	45.47782	-116.93025	IRMAI-s	IRBSH‡
IR3	Imnaha R, rkm 41	45.49004	-116.80393	IRMAI-s	IRMAI
CZY	Crazyman Creek at 0.6 km	45.22930	-116.84478	IRMAI-s	IRMAI
IMNAHW	Imnaha River Weir	45.19428	-116.86866	IRMAI-s	IRMAI
FREEZC	Freezeout Creek - tributary to Imnaha River	45.35041	-116.76217	IRMAI-s	IRMAI
GUMBTC	Gumboot Creek, Imnaha River Basin	45.15572	-116.94111	IRMAI-s	IRMAI
MAHOGC	Mahogany Creek, Imnaha River Basin	45.20021	-116.89999	IRMAI-s	IRMAI
Catherine Creek					
CATHEC	Catherine Creek	45.20967	-117.88785	GRUMA-s	GRCAT
CATHEW	Catherine Creek Weir	45.19096	-117.82862	GRUMA-s	GRCAT
CCW	Catherine Creek Ladder/Weir*	522.271.232.032		GRUMA-s	GRCAT
Upper Grande Ronde River					
UGR	Upper Grande Ronde R	45.59334	-117.90312	GRUMA-s	GRUMA, GRCAT
GRANDW	Grande Ronde River Weir	45.24896	-118.38898	GRUMA-s	GRUMA
GRAND2	Grande Ronde River - Wallowa River to headwaters (km 131-325)	45.32564	-117.92053	GRUMA-s	GRUMA
GRNTRP	Grande Ronde River Trap	46.07001	-116.98481	GRUMA-s	GRUMA
Lookingglass Creek					
LOOH	Lookingglass Hatchery	45.73154	-117.86441	GRUMA-s	GRLOO‡
LOOKGC	Lookingglass Creek	45.75720	-117.96001	GRUMA-s	GRLOO‡
Wallowa River					
WR1	Wallowa River at river km 14	45.63368	-117.73376	GRWAL-s	GRMIN, GRLOS
WALH	Wallowa Hatchery	45.41757	-117.30157	GRWAL-s	GRLOS
LOSTIW	Lostine River Weir	45.54327	-117.48450	GRWAL-s	GRLOS
LOSTIR	Lostine River	45.37281	-117.42359	GRWAL-s	GRLOS
BCANF	Big Canyon Facility	45.61904	-117.69863	GRWAL-s	GRLOS
MINAMR	Minam River	45.33888	-117.60018	GRWAL-s	GRMIN
WALLOR	Wallowa River	45.54922	-117.45906	GRWAL-s	GRLOS
Joseph Creek					
JOC	Joseph Cr	46.03002	-117.01604	GRJOS-s	
JOSEPC	Joseph Creek, Grande Ronde River Basin	45.89979	-117.20915	GRJOS-s	

* River km of the interrogation site

‡ The TRT population that this IPTDS is geographically located within is considered functionally extirpated.

Table 7. Continued

Site Code	Site Description	Latitude	Longitude	Steelhead Population	Chinook Population
Asotin					
ACM	Asotin Cr, Mouth	46.34137	-117.05571	SNASO-s	SNASO‡
GEORGC	George Creek, Asotin Creek watershed	46.19230	-117.19884	SNASO-s	SNASO‡
ASOTIC	Asotin Creek, Snake River above Clarkston, WA	46.33064	-117.18195	SNASO-s	SNASO‡
ACB	Asotin Cr, Cloverland	46.32545	-117.10852	SNASO-s	SNASO‡
AFC	Asotin Cr, NF/SF Junction	46.27230	-117.29243	SNASO-s	SNASO‡
CCA	Charley Cr	46.28846	-117.28250	SNASO-s	SNASO‡
CHARLC	Charley Creek, Asotin Creek watershed	46.27241	-117.43662	SNASO-s	SNASO‡
Alpowa Creek					
ALPOWC	Alpowa Creek, lower Snake River	46.40235	-117.39827	SNASO-s	
Almota Creek					
ALMOTC	Almota Creek - tributary to Snake River	46.70161	-117.35935	SNASO-s	
Penawawa Creek					
PENAWC	Penawawa Creek - tributary to Snake River	46.74777	-117.54136	SNASO-s	
Tucannon River					
LTR	Lower Tucannon R	46.54419	-118.16290	SNTUC-s	SNTUC
MTR	Middle Tucannon R	46.50526	-118.01628	SNTUC-s	SNTUC
UTR	Upper Tucannon R	46.41584	-117.73832	SNTUC-s	SNTUC
TUCR	Tucannon River	46.39572	-117.71120	SNTUC-s	SNTUC
TUCH	Tucannon River Hatchery	46.32011	-117.66284	SNTUC-s	SNTUC
TFH	Tucannon Hatchery	46.30965	-117.65715	SNTUC-s	SNTUC
PATAHC	Patah Creek - tributary to Tucannon River	46.47285	-117.54508	SNTUC-s	
Tenmile Creek					
TENMC2	Tenmile Creek, tributary to Snake River	46.19525	-117.04185	GRLMT-s	
Lyons Ferry Hatchery					
LYFE	Lyons Ferry Hatchery	46.59692	-118.22873		

* River km of the interrogation site

‡ The TRT population that this IPTDS is geographically located within is considered functionally extirpated.

Table 8. Effective number of breeders (N_b) for steelhead detected at IPTDS locations tested assuming random mating. Harmonic means and ranges across BY collections with more than 20 individuals are reported.

Location	BY	Harmonic Mean	Range
Upper Salmon	2006-2010	531.0	285.4, 1252.7
Upper Salmon mainstem	2006-2008, 2010	778.4	264.1, ∞
Valley	2006-2007	∞	11073.4, ∞
Lemhi	2006-2010	298.1	229.7, 590.8
Big	2005-2008	306.5	193.3, 462.6
SF Salmon	2003-2010	599.4	395.7, 1271.6
SF Salmon mainstem	2004-2010	481.4	312.4, 681.5
Secesh	2005	184.4	184.4449573
SF Clearwater	2006-2010	430.0	205.6, 1358.8
Lolo	2007-2010	238.0	164.4, 826.2
Potlatch	2005-2010	325.9	129.4, 10435.9
Potlatch above KHS	2006-2007	187.3	142, 275.2
Lapwai	2006-2011	544.8	328.7, ∞
Imnaha	2005-2011	796.7	688.6, 922.1
Big Sheep	2006-2010	441.9	248.9, 1243
Grande Ronde	2007-2011	849.4	490.7, 2420
Wallowa	2009-2011	968.1	598.7, 5517.4
Joseph	2006-2011	645.5	478.6, 1018.9
Asotin	2005-2011	866.0	531.5, ∞
Tucannon	2005-2011	726.4	247.9, ∞

Table 9. Assignment concordance between IPTDS locations and GSI reporting units for PIT-tagged steelhead from SY2010-2015. The GSI reporting unit of each IPTDS location is highlighted in gray.

	n	UPSALM	MFSALM	SFSALM	LOSALM	UPCLWR	SFCLWR	LOCLWR	IMNAHA	GRROND	LSNAKE
Upper Salmon River	424	0.724	0.012	0.000	0.042	0.012	0.021	0.052	0.024	0.064	0.050
Sawtooth Hatchery Weir	47	0.723	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.149	0.064
Upper Salmon River mainstem	173	0.751	0.006	0.000	0.040	0.017	0.006	0.023	0.029	0.087	0.040
Valley Creek	105	0.743	0.000	0.000	0.057	0.019	0.010	0.038	0.019	0.076	0.038
Yankee Fork Salmon River	21	0.857	0.048	0.000	0.048	0.048	0.000	0.000	0.000	0.000	0.000
East Fork Salmon River	9	0.333	0.111	0.000	0.000	0.000	0.000	0.556	0.000	0.000	0.000
Pahsimeroi River	54	0.815	0.000	0.000	0.037	0.000	0.000	0.019	0.019	0.056	0.056
Lemhi River	228	0.759	0.013	0.000	0.035	0.000	0.004	0.022	0.031	0.079	0.057
Carmen Creek	8	0.500	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.250	0.250
Big Creek	244	0.029	0.881	0.016	0.041	0.004	0.000	0.004	0.012	0.000	0.012
South Fork Salmon River	950	0.012	0.057	0.836	0.028	0.001	0.002	0.012	0.009	0.028	0.015
South Fork Salmon River mainstem	737	0.012	0.050	0.847	0.024	0.001	0.001	0.014	0.009	0.024	0.016
Secesh River	118	0.000	0.042	0.864	0.051	0.000	0.000	0.000	0.000	0.034	0.008
Rapid River	22	0.182	0.091	0.000	0.545	0.000	0.045	0.045	0.000	0.045	0.045
Fish Creek	79	0.000	0.000	0.000	0.000	0.937	0.063	0.000	0.000	0.000	0.000
Lolo Creek	196	0.005	0.000	0.000	0.005	0.077	0.770	0.117	0.005	0.015	0.005
South Fork Clearwater	332	0.024	0.000	0.000	0.006	0.105	0.768	0.084	0.000	0.006	0.006
Clear Creek	18	0.000	0.000	0.000	0.000	0.278	0.611	0.056	0.000	0.056	0.000
Lapwai Creek	240	0.092	0.000	0.008	0.025	0.025	0.029	0.262	0.075	0.262	0.221
Potlatch River	253	0.047	0.008	0.004	0.008	0.032	0.032	0.704	0.032	0.051	0.083
Potlatch above HLM	73	0.014	0.000	0.000	0.014	0.027	0.055	0.822	0.027	0.014	0.027
Potlatch above KHS	98	0.051	0.020	0.000	0.000	0.041	0.010	0.673	0.020	0.082	0.102
Imnaha River	1325	0.072	0.025	0.005	0.035	0.005	0.002	0.052	0.608	0.131	0.065
Cow Creek	76	0.237	0.026	0.000	0.092	0.013	0.000	0.053	0.263	0.237	0.079
Big Sheep Creek	321	0.047	0.040	0.003	0.022	0.000	0.000	0.044	0.720	0.084	0.040
Grande Ronde River upper mainstem	529	0.106	0.021	0.004	0.034	0.004	0.000	0.089	0.055	0.533	0.155
Lookingglass Creek	66	0.076	0.015	0.000	0.045	0.000	0.000	0.121	0.061	0.621	0.061
Wallowa River	203	0.074	0.005	0.000	0.025	0.000	0.015	0.089	0.044	0.631	0.118
Joseph Creek	1091	0.071	0.015	0.007	0.022	0.007	0.005	0.124	0.053	0.544	0.152
Asotin Creek	566	0.154	0.018	0.004	0.046	0.004	0.012	0.122	0.028	0.260	0.353
Almota Creek	5	0.000	0.000	0.000	0.200	0.000	0.000	0.200	0.000	0.200	0.400
Alpowa Creek	77	0.221	0.000	0.000	0.026	0.000	0.013	0.091	0.039	0.182	0.429
Tucannon River	373	0.110	0.019	0.003	0.029	0.011	0.008	0.118	0.048	0.268	0.386
Tucannon Hatchery Weir	31	0.065	0.032	0.000	0.032	0.000	0.032	0.065	0.065	0.194	0.516
Penawawa Creek	18	0.167	0.000	0.000	0.000	0.000	0.000	0.111	0.056	0.389	0.278
Tenmile Creek	11	0.091	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.273	0.636

Table 10. Effective number of breeders (N_b) for Chinook Salmon detected at IPTDS locations tested assuming random mating. Harmonic means and ranges across BY collections with more than 20 individuals are reported.

Location	BY	Harmonic Mean	Range
Upper Salmon	2006-2011	364.7	194.8, 733.6
Sawtooth Hatchery Weir	2006-2011	92.4	21.8, 560.1
Valley	2007-2011	207.7	152.8, 287.2
Yankee Fork	2008-2010	237.9	155.5, 360
EF Salmon	2010	299.6	299.6
Pahsimeroi	2010	563.6	563.6
Lemhi	2007, 2009-2011	154.5	136.6, 188.3
Big	2007-2011	250.5	176, 308
McCall Hatchery Weir	2006-2010	247.9	140.4, 1866.2
SF Salmon	2006-2011	507.5	377.9, 774.1
SF Salmon mainstem	2006-2011	361.4	251.4, 586.2
Secesh	2006-2011	173.8	63.7, 381.9
EFSF Salmon	2006-2011	175.7	89.3, 396.5
Lolo	2008	97.3	97.3
SF Clearwater	2007-2011	268.7	126.4, 538.4
Imnaha	2006-2011	47.1	15.3, 519.7
Catherine	2008-2010	237.3	212.7, 306.1
Grande Ronde	2008-2011	371.0	249.8, 536.7
Lookingglass	2008	208.6	208.6
Wallowa	2008-2011	509.9	323.9, 20134.4

Table 11. Assignment concordance between IPTDS locations and GSI reporting units for PIT-tagged Chinook Salmon from SY2010-2015. The GSI reporting unit of each IPTDS location is highlighted in gray.

	n	UPSALM	CHMBLN	MFSALM	SFSALM	HELLSC	TUCANO	FALL
Upper Salmon River	1407	0.816	0.006	0.062	0.038	0.077	0.001	0.001
Sawtooth Hatchery Weir	345	0.762	0.006	0.087	0.049	0.093	0.000	0.003
Valley Creek	257	0.883	0.000	0.039	0.027	0.047	0.004	0.000
Yankee Fork Salmon River	93	0.753	0.000	0.075	0.054	0.118	0.000	0.000
East Fork Salmon River	123	0.732	0.024	0.049	0.041	0.154	0.000	0.000
Pahsimeroi River	68	0.868	0.000	0.074	0.029	0.029	0.000	0.000
Lemhi River	263	0.551	0.000	0.091	0.042	0.312	0.004	0.000
Alturas Creek	1	1.000	0.000	0.000	0.000	0.000	0.000	0.000
UPSALM Beaver Creek	9	0.111	0.000	0.667	0.000	0.222	0.000	0.000
North Fork Salmon River	3	1.000	0.000	0.000	0.000	0.000	0.000	0.000
UPSALM Pahsimeroi to Headwaters	24	0.875	0.000	0.083	0.042	0.000	0.000	0.000
Chamberlain Creek	26	0.077	0.846	0.038	0.000	0.038	0.000	0.000
Big Creek	473	0.131	0.038	0.588	0.059	0.184	0.000	0.000
Sulfur Creek	11	0.091	0.000	0.818	0.091	0.000	0.000	0.000
Marsh Creek	34	0.176	0.000	0.647	0.118	0.059	0.000	0.000
MFSALM Loon to Headwaters	1	0.000	0.000	1.000	0.000	0.000	0.000	0.000
Loon Creek	4	0.250	0.000	0.500	0.250	0.000	0.000	0.000
Knapp Creek	2	0.000	0.000	1.000	0.000	0.000	0.000	0.000
Capehorn Creek	9	0.222	0.000	0.667	0.000	0.111	0.000	0.000
Camas Creek	4	0.000	0.000	0.500	0.000	0.500	0.000	0.000
Beaver Creek	5	0.200	0.000	0.800	0.000	0.000	0.000	0.000
Bear Valley Creek	36	0.111	0.000	0.806	0.000	0.083	0.000	0.000
McCall Hatchery Weir	270	0.193	0.007	0.181	0.359	0.252	0.007	0.000
South Fork Salmon River	2245	0.109	0.010	0.151	0.584	0.144	0.001	0.001
South Fork Salmon River mainstem	1007	0.148	0.012	0.197	0.428	0.212	0.003	0.001
Secesh River	614	0.059	0.003	0.085	0.803	0.050	0.000	0.000
EFSF Salmon River	514	0.076	0.012	0.148	0.636	0.128	0.000	0.000
Grouse Creek	2	0.000	0.000	0.000	1.000	0.000	0.000	0.000
Rapid River	11	0.182	0.000	0.000	0.000	0.818	0.000	0.000
Selway Moose to Headwaters	1	0.000	0.000	0.000	0.000	1.000	0.000	0.000
Moose Creek	2	0.500	0.000	0.000	0.000	0.500	0.000	0.000
Bear Creek	1	0.000	0.000	0.000	0.000	1.000	0.000	0.000
Crooked Fork Creek	1	0.000	0.000	0.000	0.000	1.000	0.000	0.000
Powell Hatchery	3	0.000	0.000	0.000	0.000	1.000	0.000	0.000
Potlatch River	2	0.000	0.000	0.000	0.000	1.000	0.000	0.000
Lolo Creek	89	0.112	0.000	0.056	0.022	0.809	0.000	0.000
Clear Creek	9	0.111	0.000	0.111	0.000	0.778	0.000	0.000
South Fork Clearwater	349	0.072	0.003	0.046	0.026	0.848	0.003	0.003
Big Sheep Creek	68	0.074	0.015	0.044	0.059	0.794	0.015	0.000
Imnaha River	684	0.076	0.010	0.037	0.051	0.813	0.004	0.009
Catherine Creek	248	0.056	0.004	0.052	0.016	0.863	0.008	0.000
Grande Ronde River upper mainstem	475	0.061	0.002	0.053	0.038	0.842	0.004	0.000
Lookingglass Creek	121	0.050	0.000	0.050	0.008	0.876	0.017	0.000
Wallowa River	510	0.043	0.000	0.027	0.027	0.896	0.004	0.002
Joseph Creek	1	0.000	0.000	0.000	0.000	0.000	1.000	0.000
Asotin Creek	24	0.083	0.000	0.000	0.083	0.292	0.500	0.042
Tucannon River	45	0.044	0.000	0.000	0.044	0.378	0.511	0.022
Lyons Hatchery	1	0.000	0.000	0.000	0.000	0.000	0.000	1.000

FIGURES

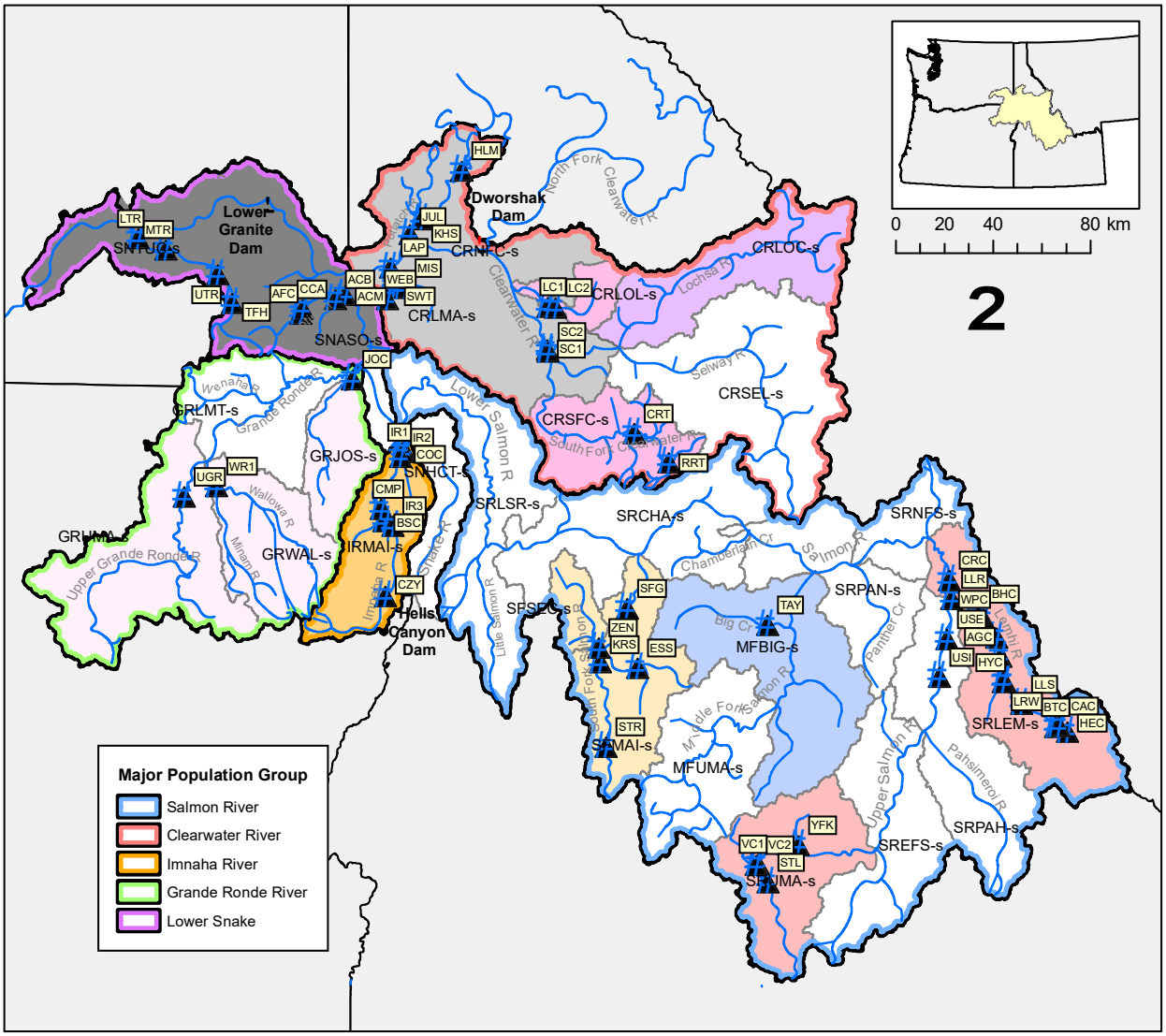

Figure 1. Map showing Snake River steelhead ESU major population groups (MPG) and ICTRT (2003) delineated populations. The locations of IPTDS are shown. We report life history characteristics for all locations, and genetic structure and diversity information for locations with more than 20 individuals detected in a single year. TRT populations where genetic structure and diversity information was reported are shaded. The location of Lower Granite Dam, Dworshak Dam, and Hells Canyon Dam are noted; dams with no anadromous passage are shaded red.

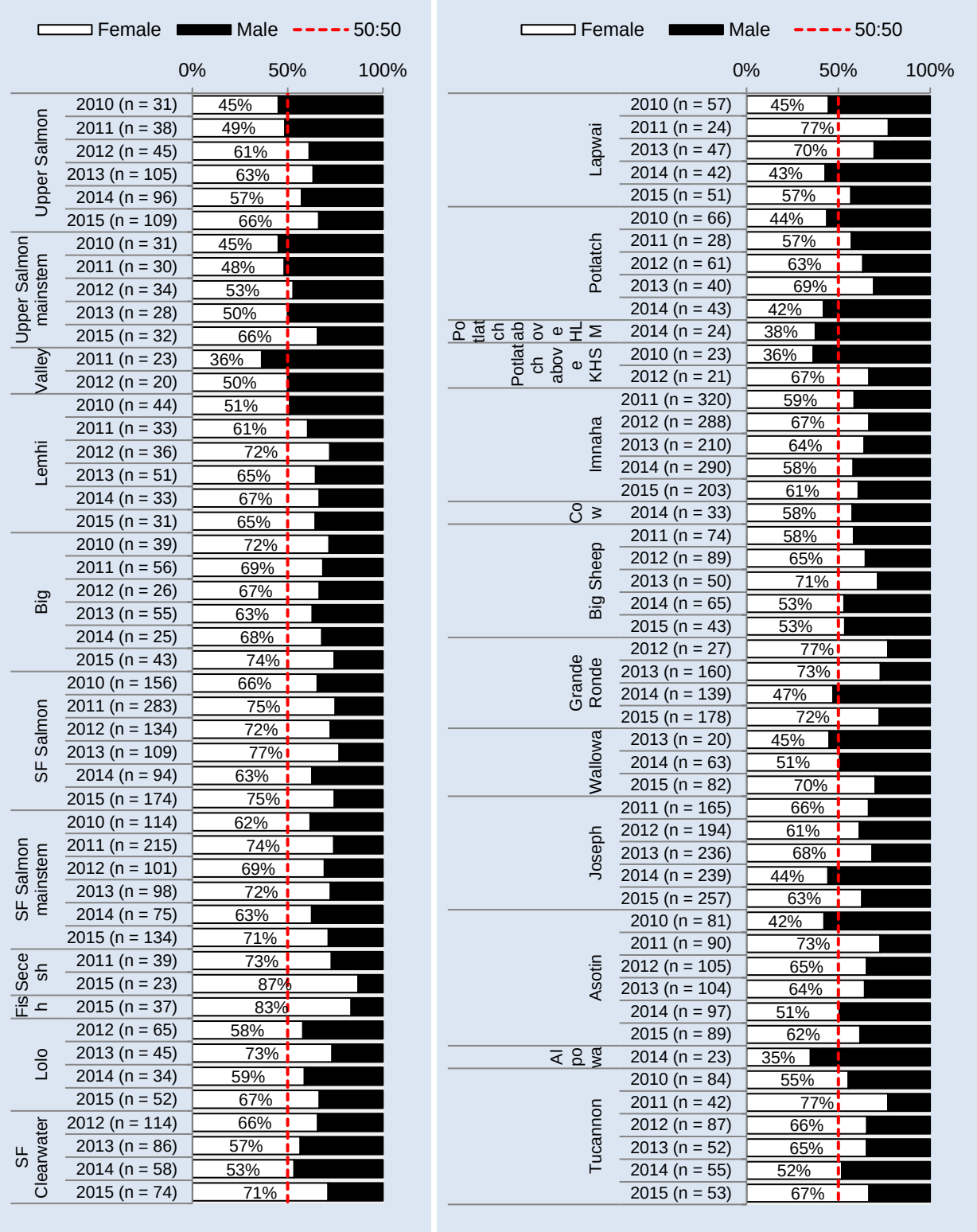

Figure 2. Sex ratios for adult steelhead PIT-tagged at Lower Granite Dam and later detected at Snake River Instream PIT Tag Detection Systems by location and year. Sample sizes are shown in y-axis labels. The dotted vertical red line indicates a 50:50 sex ratio.

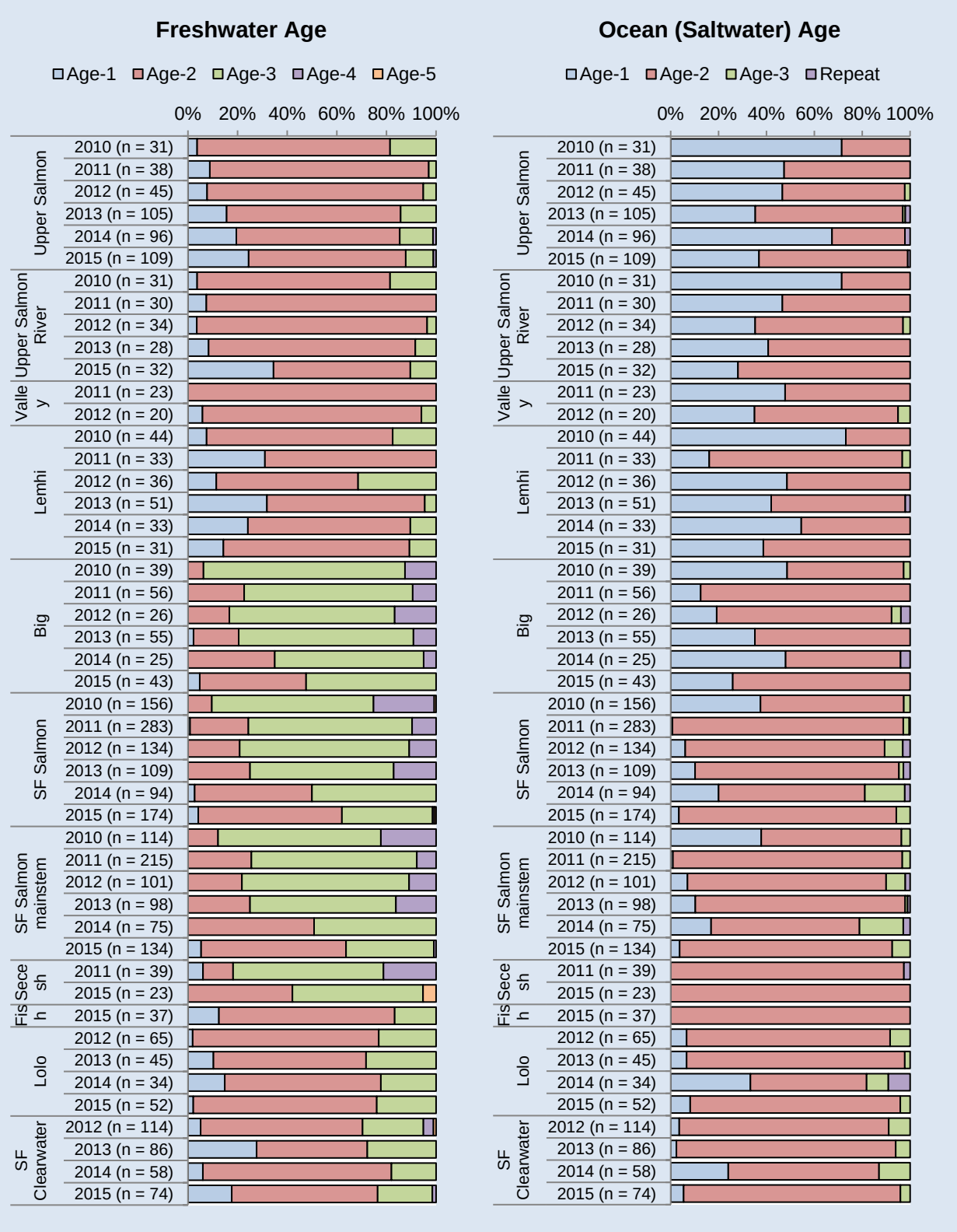

Figure 3. Distribution of freshwater and ocean (saltwater) ages for adult steelhead PIT tagged at Lower Granite Dam and later detected at Snake River Instream PIT Tag Detection Systems by location and year. Sample sizes are shown in y-axis labels.

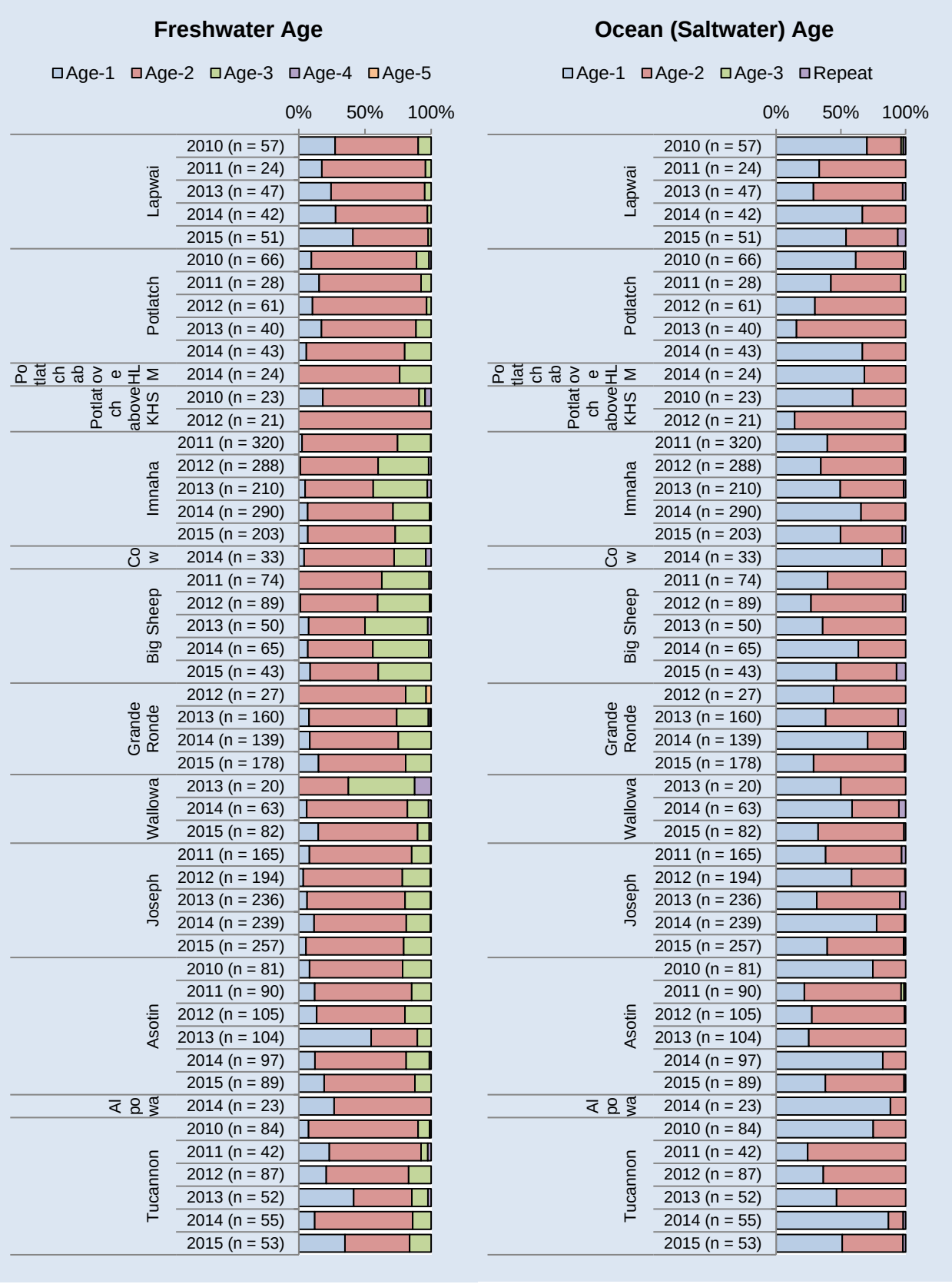

Figure 3. continued.

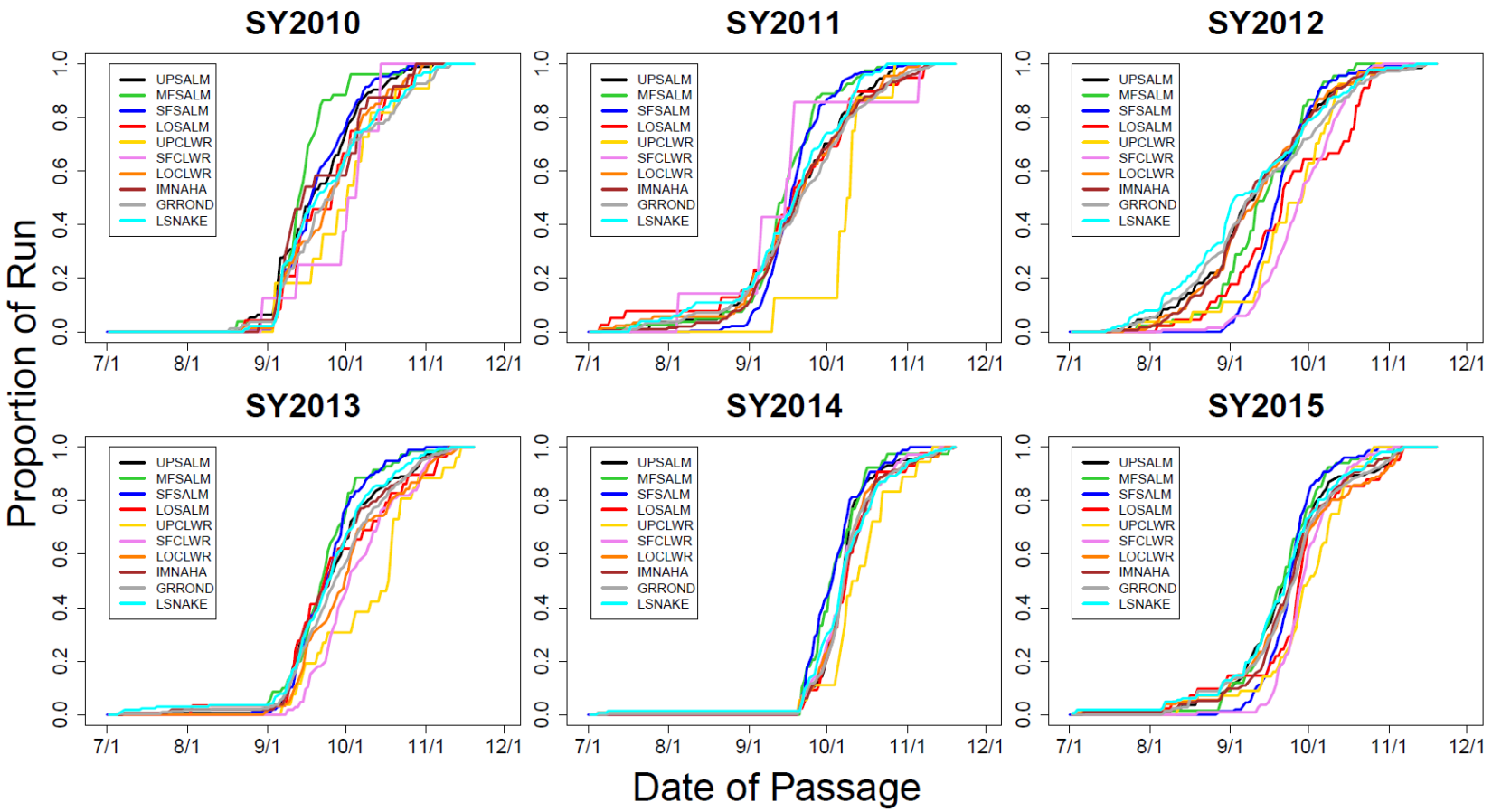

Figure 4. Date of passage for adult steelhead PIT tagged at Lower Granite Dam (LGR) and later detected at Snake River Instream PIT Tag Detection Systems by GSI reporting unit and year. Steelhead migrating past LGR during the spring portion of the migration were removed from the analysis.

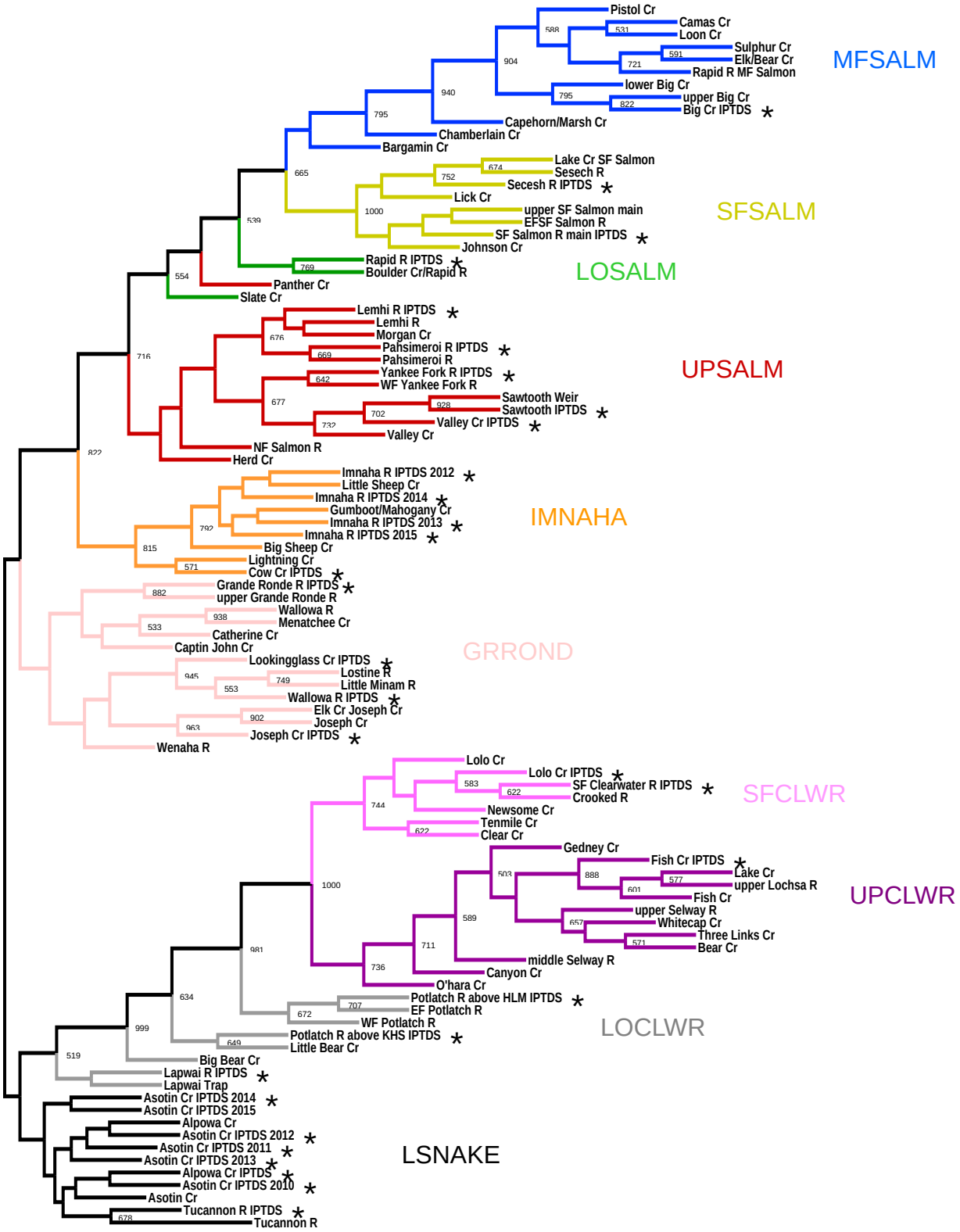

Figure 5. Neighbor-joining (NJ) Tree based on Nei's standard distances for steelhead GSI baseline version 3 collections and fish PIT tagged at Lower Granite Dam and subsequently detected at IPTDS. IPTDS locations are labeled with an asterisk, and GSI reporting units are color coded.

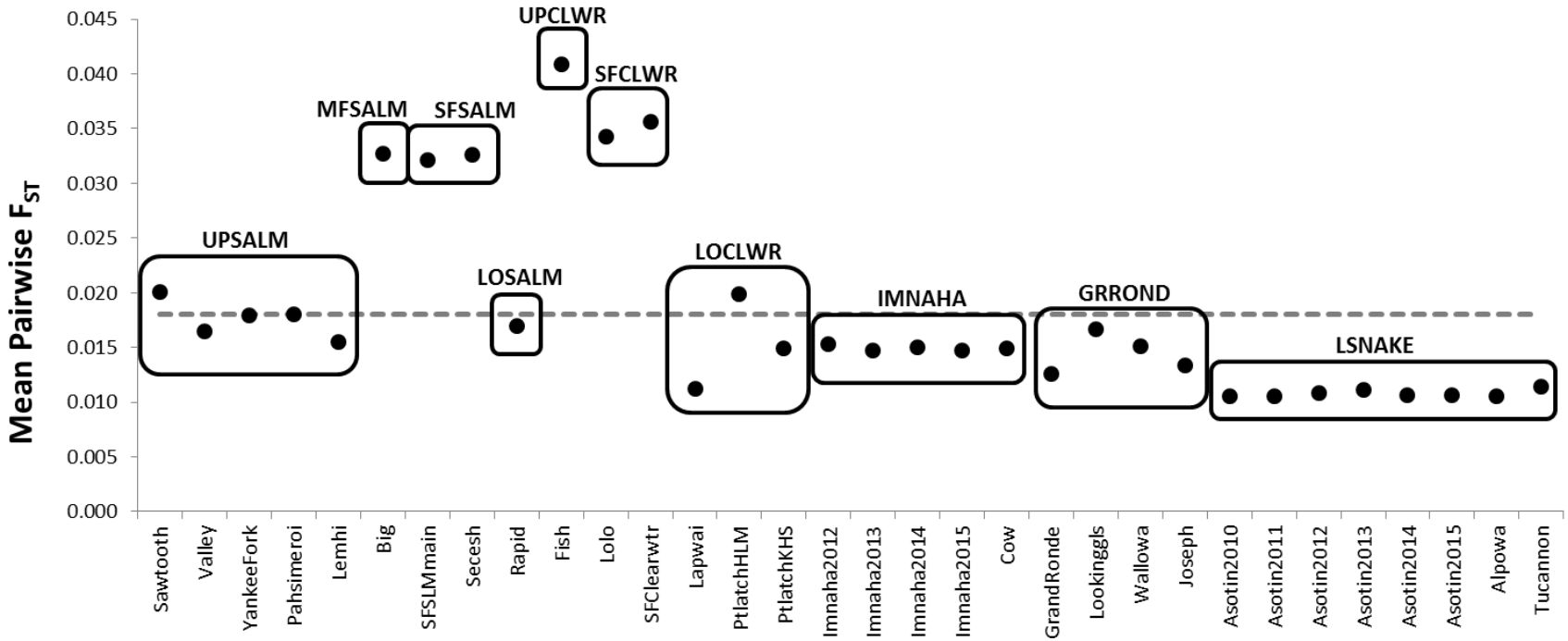

Figure 6. Mean pairwise F_{ST} estimates for Snake River steelhead IPTDS locations. The dashed line is the average pairwise F_{ST} estimate across all locations. High mean F_{ST} estimates suggest high genetic differentiation relative to other locations. Each genetic stock is circumscribed.

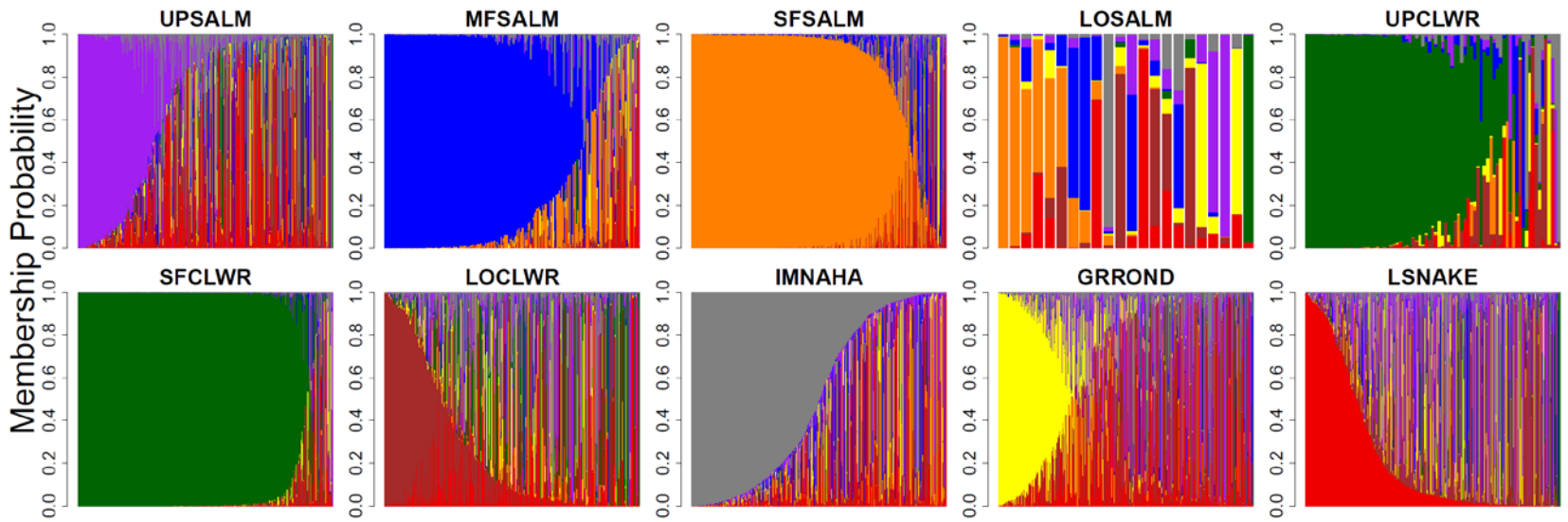

Figure 7. Bar charts of individual membership probability to the eight genetic clusters identified in a discriminant analysis of principal components. Each individual is plotted as a single vertical line, and each genetic cluster is color coded. Individuals are grouped based on the location of the IPTDS within a GSI reporting unit, and have been sorted based on cluster membership probability.

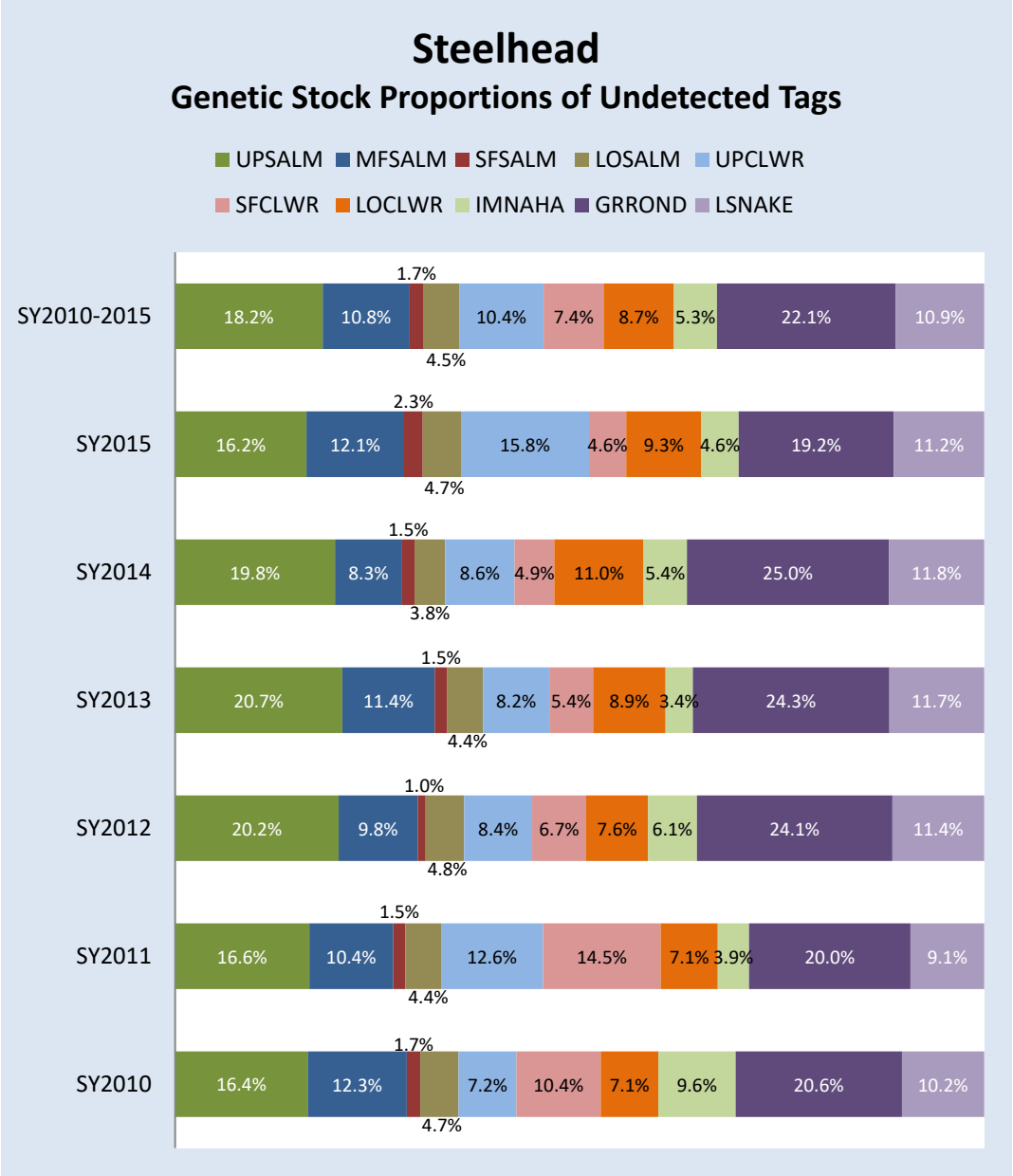

Figure 8. Genetic stock proportions of steelhead PIT tagged at Lower Granite Dam and NOT detected at Snake River Instream PIT Tag Detection Systems.

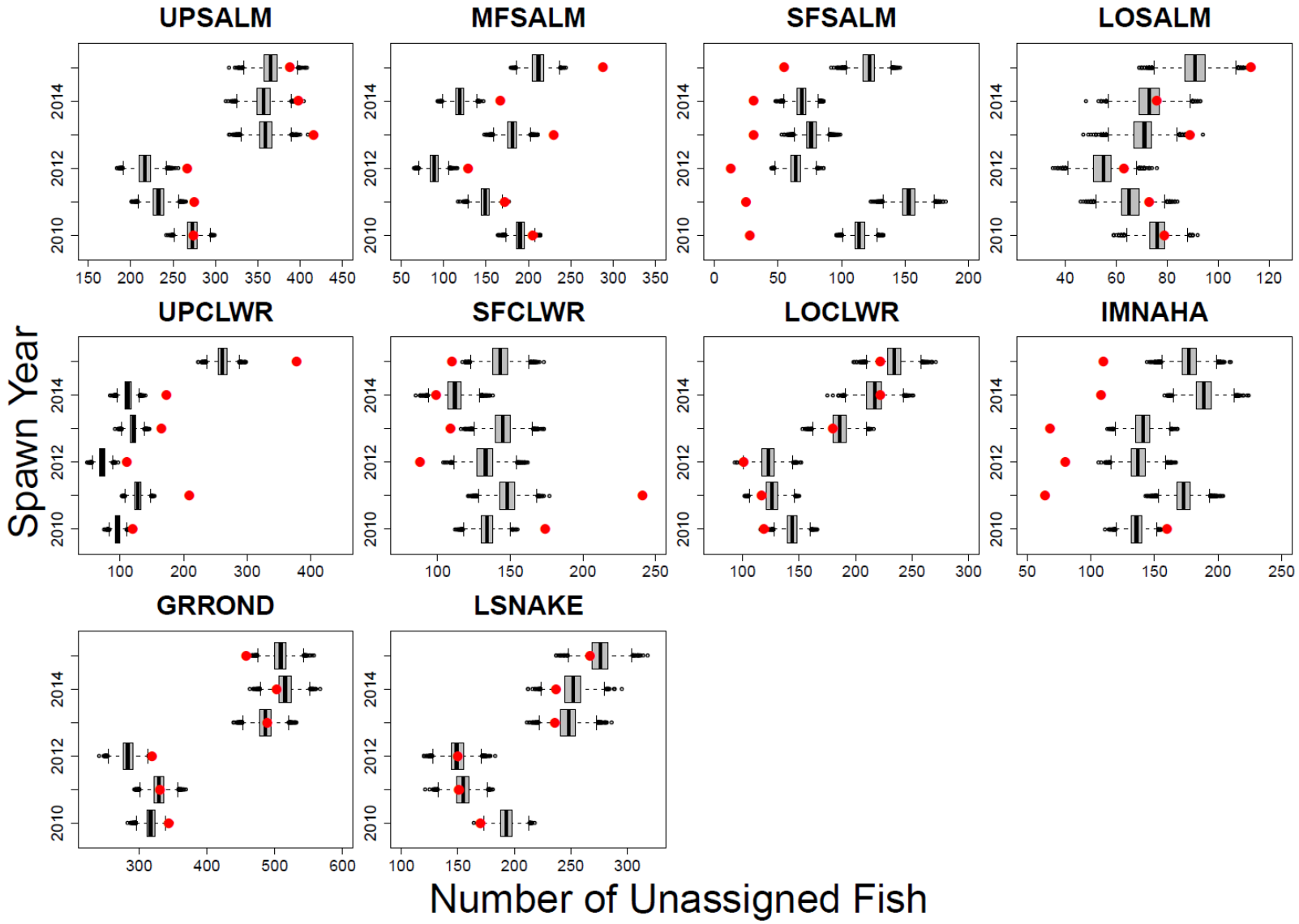

Figure 9. Resampling distributions of the expected number of undetected steelhead from each GSI reporting unit in a given year. The actual number of unobserved steelhead each year is plotted with a red point.

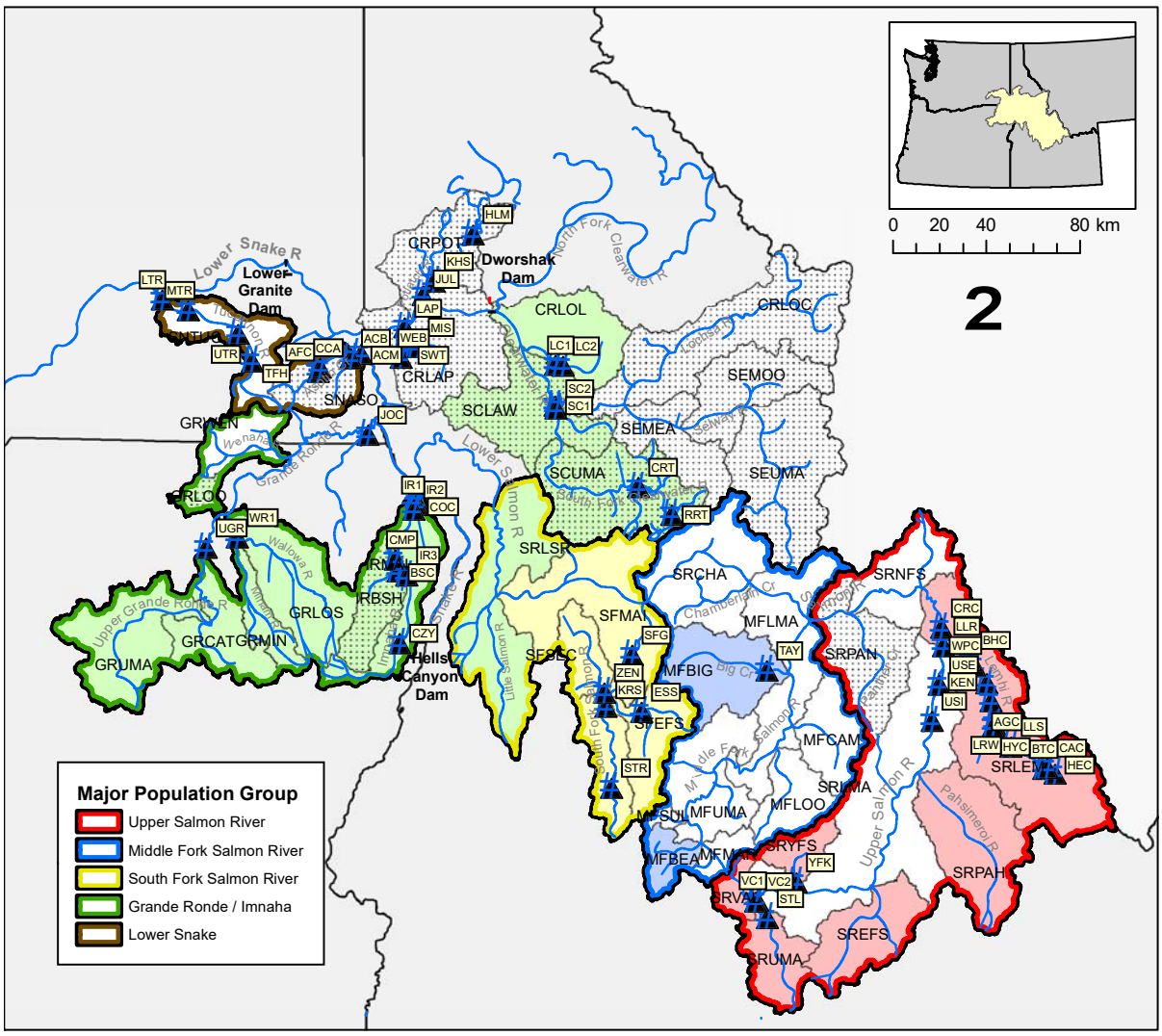

Figure 10. Map showing Snake River Spring/Summer Chinook Salmon ESU major population groups (MPG) and ICTRT (2003) delineated populations. The locations of IPTDS are shown. We report life history characteristics for all locations, and genetic structure and diversity information for locations with more than 20 individuals detected in a single year. TRT populations where genetic structure and diversity information was reported are shaded. The location of Lower Granite Dam, Dworshak Dam, and Hells Canyon Dam are noted; dams with no anadromous passage are shaded red. Populations shaded with dots are considered functionally extirpated.

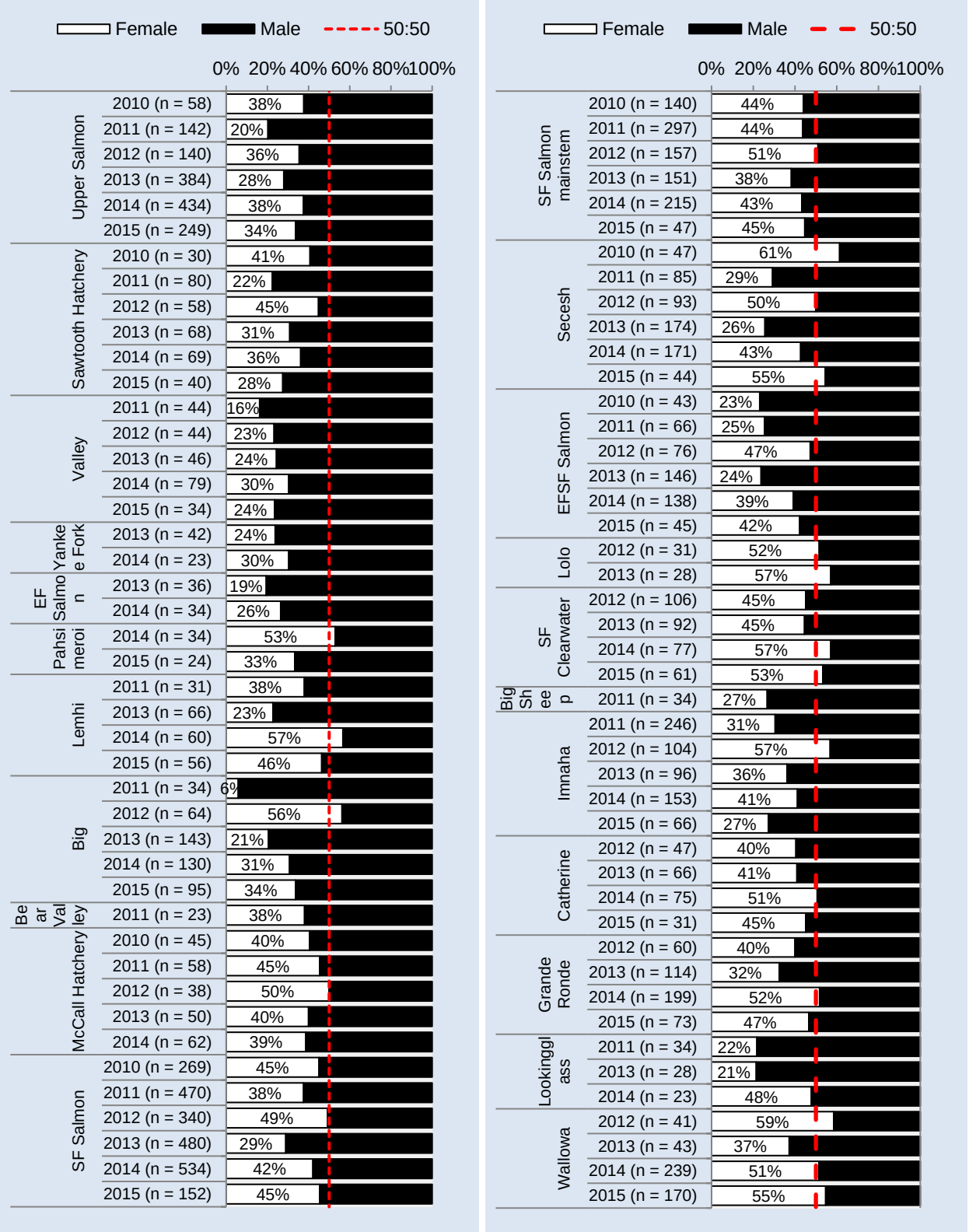

Figure 11. Sex ratios for adult sp/sum Chinook salmon PIT-tagged at Lower Granite Dam and later detected at Snake River Instream PIT Tag Detection Systems by location and year. Sample sizes are shown in y-axis labels. The dotted vertical red line indicates a 50:50 sex ratio.

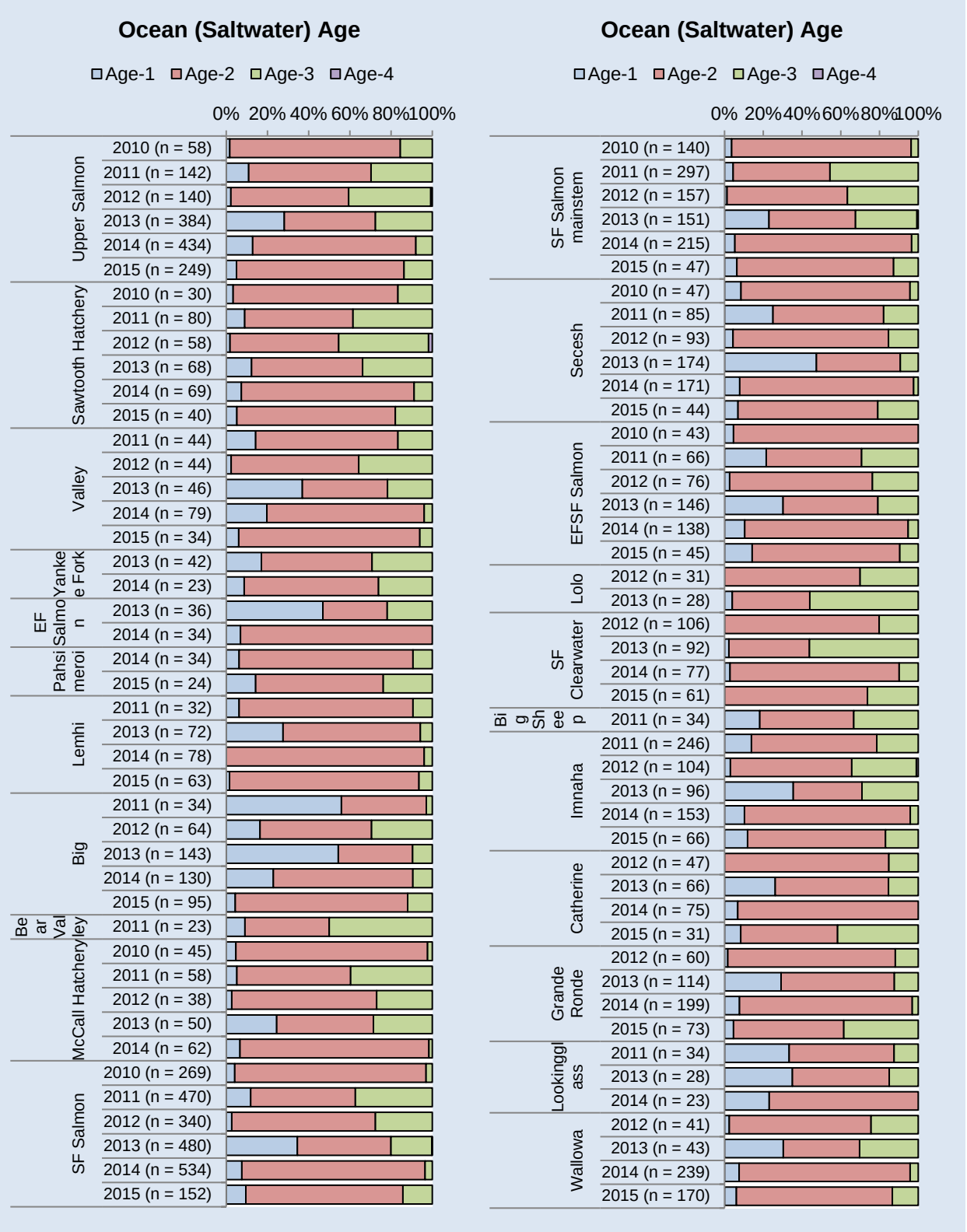

Figure 12. Distribution of ocean (saltwater) ages for sp/sum Chinook salmon PIT tagged at Lower Granite Dam and later detected at Snake River Instream PIT Tag Detection Systems by location and year. Sample sizes are shown in y-axis labels.

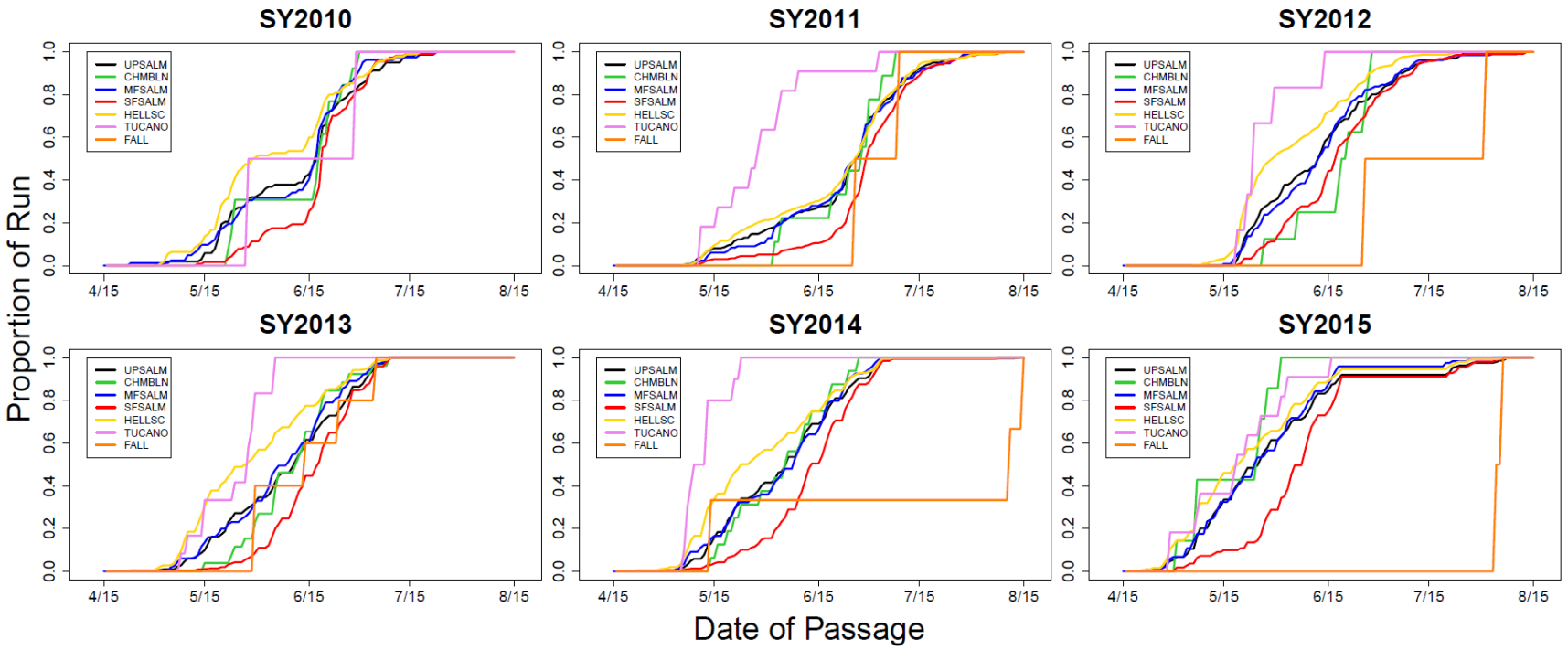

Figure 13. Date of passage for adult Chinook Salmon PIT tagged at Lower Granite Dam (LGR) and later detected at Snake River Instream PIT Tag Detection Systems by GSI reporting unit and year.

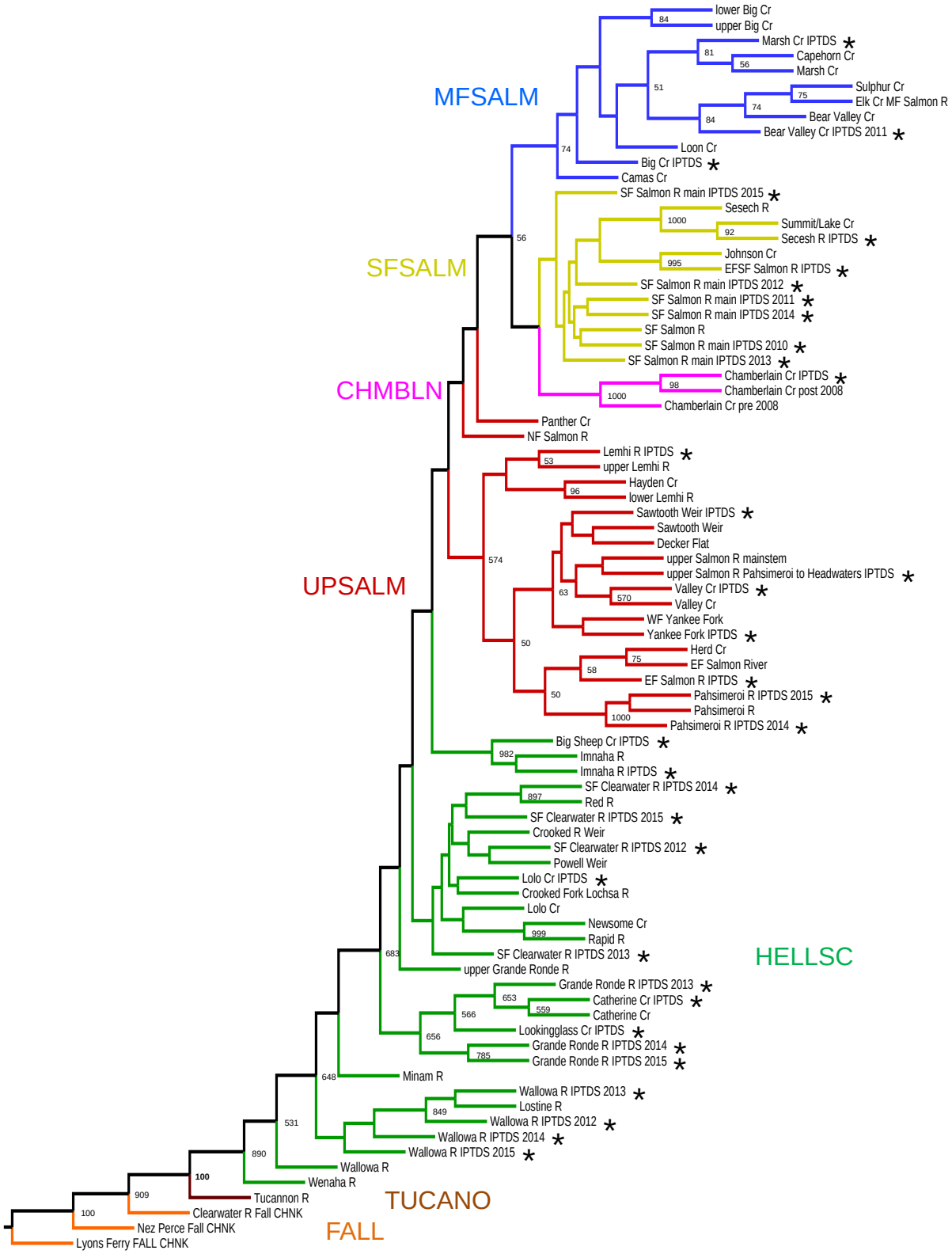

Figure 14. Neighbor-joining (NJ) Tree based on Nei's standard distances for Chinook Salmon GSI baseline version 3 collections and fish PIT tagged at Lower Granite Dam and subsequently detected at IPTDS. IPTDS locations are labeled with an asterisk, and GSI reporting units are color-coded.

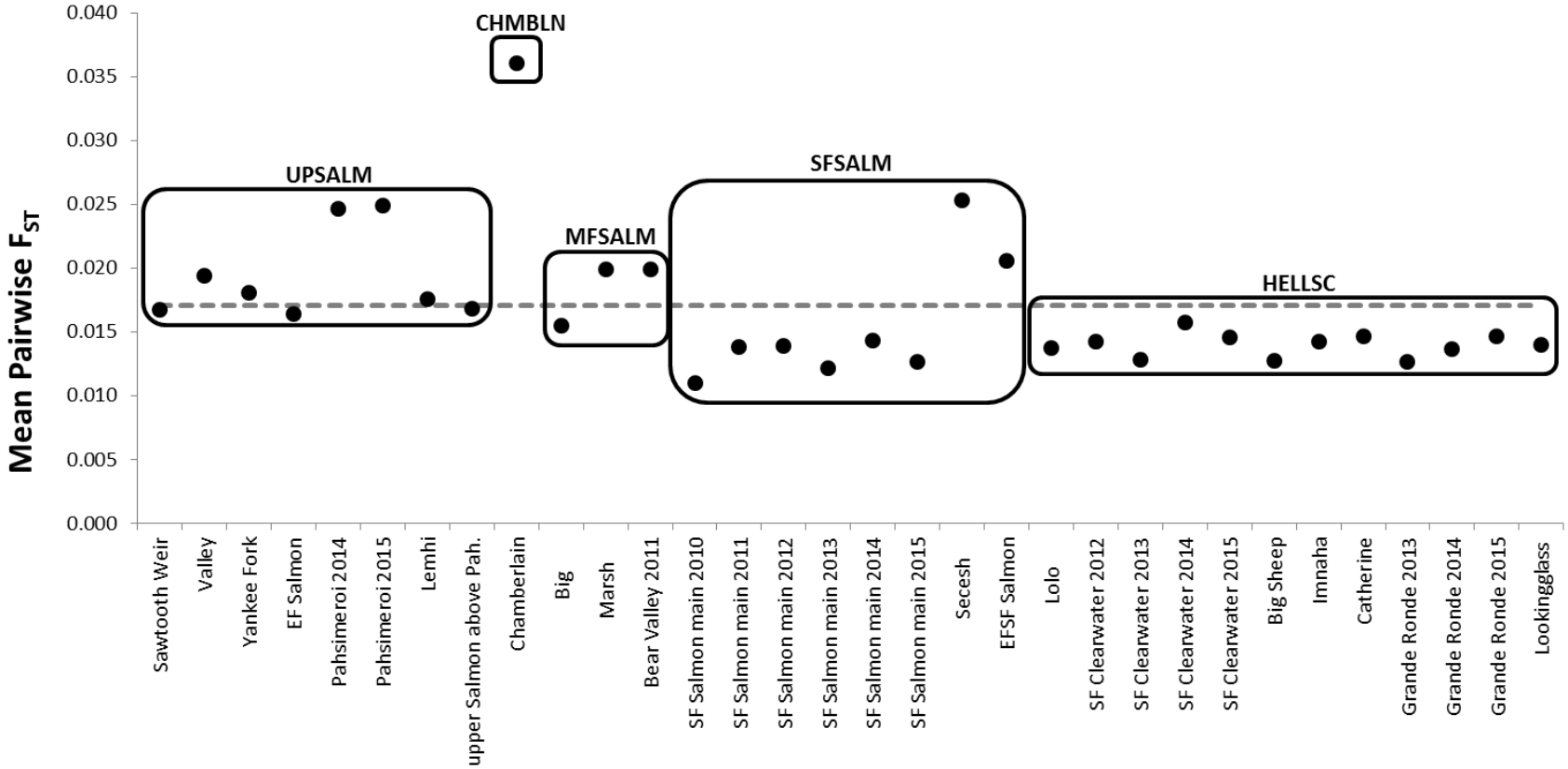

Figure 15. Mean pairwise F_{ST} estimates for Snake River Chinook Salmon IPTDS locations. The dashed line is the average pairwise F_{ST} estimate across all locations. High mean F_{ST} estimates suggest high genetic differentiation relative to other locations. Each genetic stock is circumscribed.

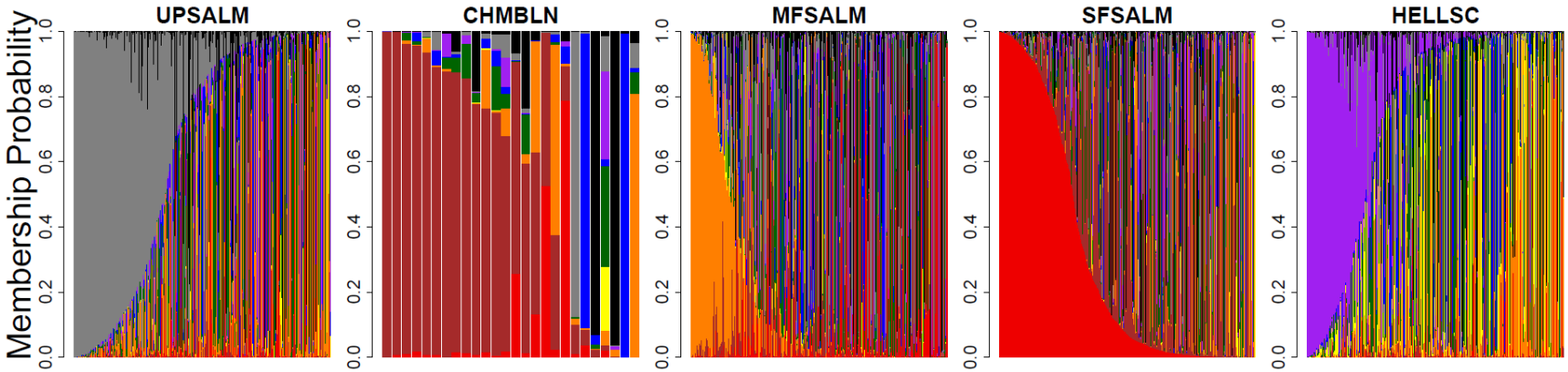

Figure 16. Bar charts of individual membership probability to the nine genetic clusters identified in a discriminant analysis of principal components. Each individual is plotted as a single vertical line, and each genetic cluster is color coded. Individuals are grouped based on the location of the IPTDS within a GSI reporting unit, and have been sorted based on cluster membership probability.

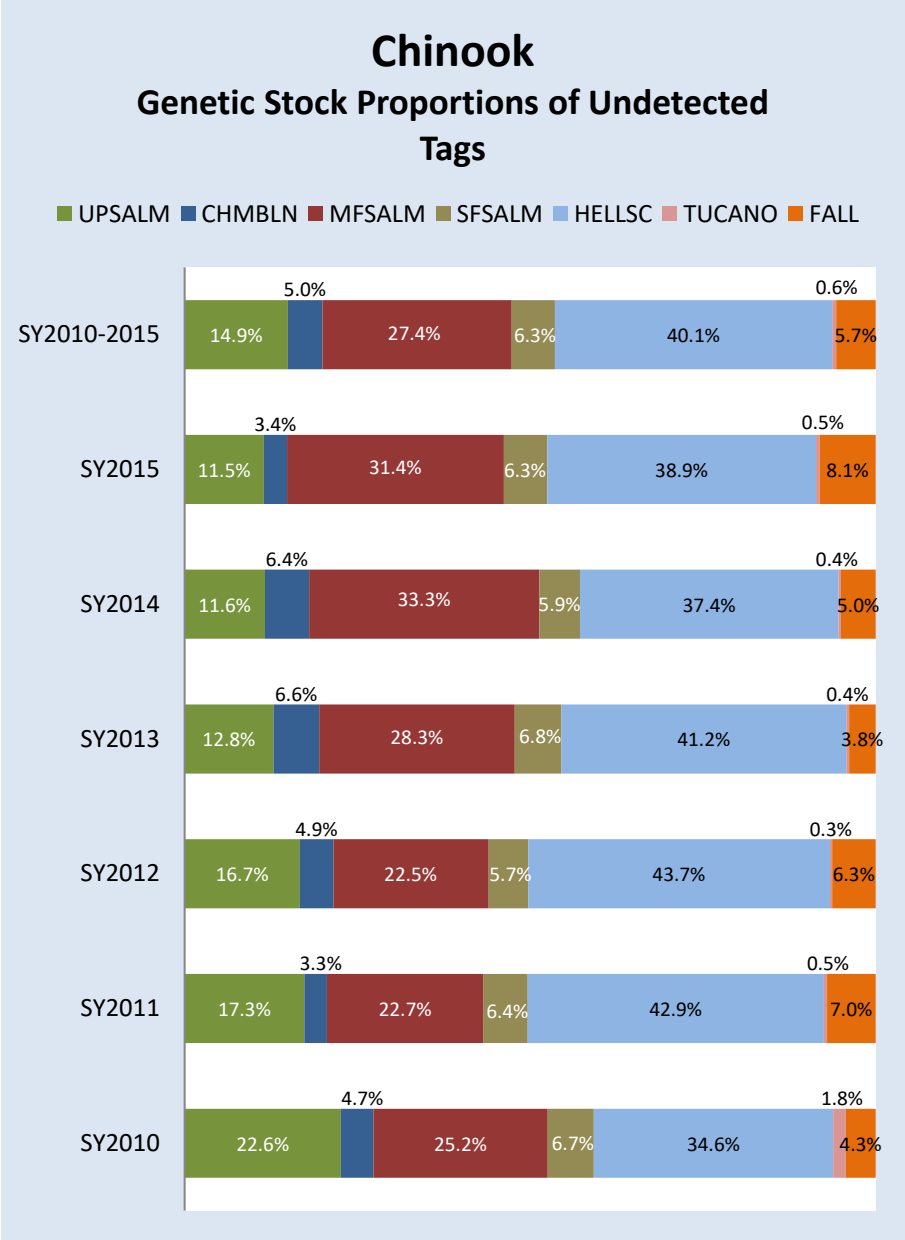

Figure 17. Genetic stock proportions of Chinook Salmon PIT tagged at Lower Granite Dam and NOT detected at Snake River Instream PIT Tag Detection Systems.

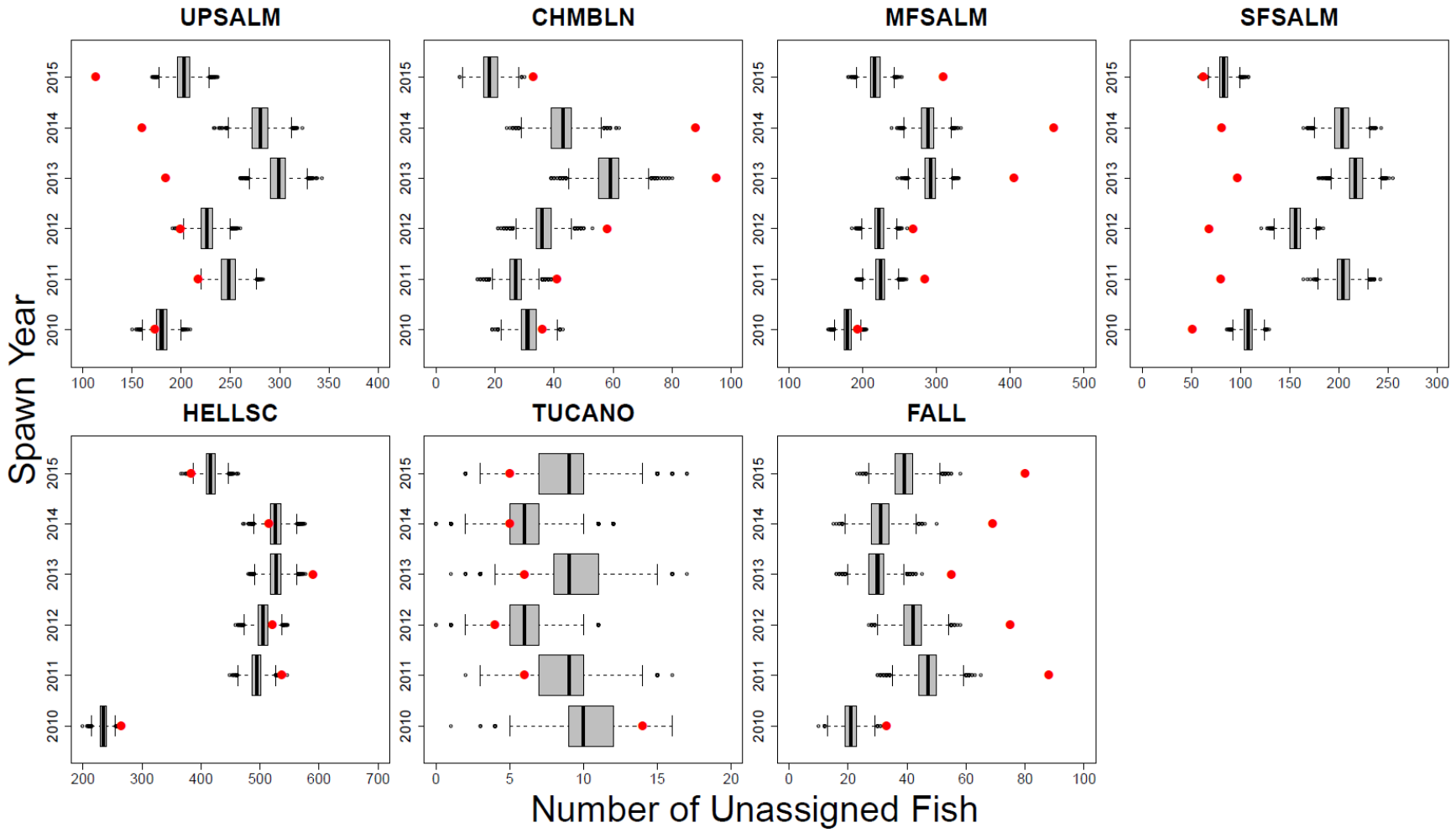

Figure 18. Resampling distributions of the expected number of undetected Chinook Salmon from each GSI reporting unit in a given year. The actual number of unobserved Chinook Salmon each year is plotted with a red point.

Prepared by:

John H. Powell
Fishery Biologist 2

Ninh Vu
Fishery Biologist 2

Matthew R. Campbell
Fisheries Genetics Program Coordinator

Approved by:
IDAHO DEPARTMENT OF FISH AND GAME

Daniel J. Schill
Fisheries Research Manager

James P. Fredericks, Chief
Bureau of Fisheries