REPORT TO NOAA FISHERIES FOR 5-YEAR ESA STATUS REVIEW: SNAKE RIVER BASIN STEELHEAD AND CHINOOK SALMON POPULATION ABUNDANCE, LIFE HISTORY, AND DIVERSITY METRICS CALCULATED FROM IN-STREAM PIT-TAG OBSERVATIONS (SY2010-SY2019)

January 2020

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Suggested citation:

IPTDSW (In-stream PIT-tag detection systems workgroup). 2020. Report to NOAA Fisheries for 5-Year ESA Status Review: Snake River Basin Steelhead and Chinook Salmon Population Abundance, Life History, and Diversity Metrics Calculated from In-stream PIT-Tag Observations (SY2010-SY2019). January 2020.

ABSTRACT

This report provides estimates of abundance, life history, and diversity metrics for populations of wild adult summer steelhead (*Oncorhynchus mykiss*) and spring/summer Chinook Salmon (*O. tshawytscha)* from the Snake River basin based on in-stream passive integrated transponder (PIT) tag observations paired with sex, age, and genetic data. This summary is being presented to the National Oceanic and Atmospheric Administration fisheries for their 2020, 5-Year Endangered Species Act (ESA) Status Review. In total, 34,915 steelhead and 21,515 spring/summer Chinook Salmon were sampled and PIT tagged at Lower Granite Dam (LGR) during spawn years 2010–2019. Of the fish tagged at LGR, 12,362 steelhead and 10,796 Chinook Salmon were subsequently identified at PIT tag detection sites located throughout the Snake River basin landscape that enabled the estimation of abundance, life history, and diversity metrics. First, the annual number of wild adult steelhead and Chinook Salmon crossing Lower Granite Dam and associated uncertainty were estimated using statistical models that account for varying rates of nighttime passage and reascension during the spawning run. In addition, a hierarchically structured branch occupancy model was utilized to estimate PIT tag transition probabilities to tributary PIT tag observation sites and partition the estimated abundance at LGR into estimates for individual populations of steelhead and Chinook Salmon. Using scale age data along with genetic sex data associated with each PIT tag, we described the proportion of returning females and age classes on a per population basis. In addition, we utilized single nucleotide polymorphism (SNP) genotypes generated by the 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, to detail levels of genetic diversity, effective population size, and genetic relatedness among individual steelhead and Chinook Salmon populations. Lastly, we detailed the genetic stock of origin for all adults sampled at LGR, adults detected at an in-stream PIT tag array, and those tagged but never detected at an array. Combined, the information presented here provides critical data for viable Salmonid population monitoring of the Snake River steelhead DPS and the Snake River spring/summer Chinook Salmon ESU.

INTRODUCTION

Across the Pacific Northwest of the United States, populations of anadromous salmonids (genus *Oncorhynchus*) have experienced significant declines (e.g., Heard et al. 2007) with many runs now listed as either threatened or endangered under the Endangered Species Act (ESA). In the Snake River basin, the abundance of spring/summer steelhead and Chinook Salmon has decreased significantly over the past five decades (Nehlsen et al. 1991; Williams 2020). In response to historic declines and future threats to survival, two Chinook Salmon Evolutionary Significant Units (ESUs) and one steelhead distinct population segment (DPS) in the basin were listed as threatened under the ESA (Godd et al. 2005).

In 2003, the Interior Columbia Technical Recovery Team (ICTRT) drafted population delineations for the Snake River steelhead DPS and spring/summer Chinook Salmon ESU (ICTRT 2003), which were subsequently adopted in the ESA Recovery Plan for Snake River steelhead and spring/summer Chinook Salmon (NMFS 2017). Hereafter, the use of the term populations refers to those described in the ESA Recovery Plan. Within the Snake River basin steelhead DPS, there are six major population groups (MPGs; five extant and one, Hells Canyon, with no associated independent populations) and 28 populations. Of the 28 steelhead populations, 24 are extant and four are considered extirpated due to blocked access (e.g., Dworshak Dam on the North Fork Clearwater River and Hells Canyon Dam restricting access to the Powder, Burnt, and Weiser rivers). The Snake River spring/summer Chinook Salmon (hereafter Chinook Salmon) ESU includes 5 MPGs and 32 populations (not including extirpated Clearwater River populations or populations from historically accessible areas). Of the 32 populations, 4 are considered extirpated (Panther Creek, Big Sheep Creek, Lookingglass Creek, Asotin Creek) and 28 are extant.

This document summarizes key information used to evaluate the viability of salmonid populations in the Snake River basin. The concept of a viable salmonid population (VSP) was proposed to advance recovery efforts of Pacific salmonids (McElhany et al. 2000) by identifying key metrics that could be used to perform salmonid conservation assessments. Four parameters were identified for establishing population viability: population size, growth rate and related parameters, spatial structure, and diversity (McElhany et al. 2000).

Research and monitoring efforts that track the abundance, distribution, and diversity of steelhead and Chinook Salmon in the Snake River basin through PIT tag observations are performed as part of multiple projects executed by a large number of state, federal, and tribal agencies. Trapping at LGR is coordinated by National Marine Fisheries Service (NMFS; BPA Project 2005-002-00; Harmon 2003; Ogden 2016). 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 parentage-based tagging (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 analyses. The Integrated Status and Effectiveness Monitoring Project (ISEMP; BPA Project 2003-017-00) developed and maintained much of the in-stream PIT tag detection infrastructure throughout the Snake River basin directed at monitoring populations. In addition, the ISEMP project also developed two critical run decomposition models that; 1) estimates the number of wild adults at LGR with uncertainty, and 2) partitions the LGR abundance into tributary level abundances with uncertainty based on PIT tag observations (BPA Project 2003-017-00, See et al. 2016). Many of the pit tag detection sites used in this study were installed, maintained, and operated by the Bonneville Power Administration under BPA project 2003-017-00 and currently under BPA Project 2018-002-00 (QCI 2013; Orme and Albee 2012; Orme and Albee 2013) for the purpose of detecting PIT-tagged adults and have operated with minimal downtime or equipment loss (Meier 2019).

In addition, the Snake Basin Steelhead Assessments project (BPA Project 2010-057-00) is currently tasked with executing and reporting results of the developed run decomposition models. For steelhead populations above LGR, the PIT tagged based run decomposition methodology is the only means available to estimate tributary escapement because high spring flows preclude other methodologies. Because PIT tag detection sites are not always aligned with established management boundaries, we pooled estimates and observations at PIT tag detection locations where appropriate to generate population estimates as defined by the Snake River basin steelhead and Snake River Spring/Summer Chinook Salmon recovery plans (NMFS 2017, Tables 1 and 2).

To facilitate the status evaluation of the steelhead DPS and spring/summer Chinook Salmon ESU in the Snake River basin, this report summarizes the following pieces of information: 1) wild adult escapement at Lower Granite Dam, 2) wild adult escapement at the population-level, 3) population-level estimates of life history characteristics (sex and age), 4) estimates of population genetic diversity and differentiation, 5) effective number of breeders, and 6) genetic origin of detected and non-detected fish.

METHODS

Study area and infrastructure

The PIT tag observation sites consisted of in-stream PIT tag detection systems (IPTDS), weirs, hatchery ladders, and carcass recovery sites that are operated and maintained by several different tribal, state, and federal management agencies (Tables 1 and 2, Figures 1 and 2). Adult PIT tag observations were not used to generate escapement estimates in cases where flow events, forest fires, and equipment loss or malfunctions limited reliable and consistent PIT tag observations during the migration period. Such failures were rare but did occur at site code USI and VC1 for Chinook Salmon in 2017 (high flows inundating equipment), at site code LC1 and LC2 for Chinook in 2013 and 2015 (forest fire), at site code LC2 for steelhead and Chinook Salmon 2019 (flood event), and at site code LTR for Chinook Salmon in 2018 and 2019. Additionally the lower most IPTDS in the Potlatch River (site code JUL) was removed by high flows in 2014 and not replaced. The loss of JUL in conjunction with low PIT tag observations at upstream sites prevented estimates for the entire Potlatch River after 2014.

The number of PIT tag observation sites were variable within individual populations (Tables 1 and 2, Figures 1 and 2). Some populations did not have PIT tag detection infrastructure and were therefore not included in this report. Some populations were monitored by weir infrastructure (Tables 1 and 2) and estimates were based solely on reported PIT tag observations and therefore may not accurately represent actual weir operations. Some populations were monitored for PIT tags with just a single set of observation sites (two independent single pass sites or a single site with a dual span). Other populations covered a much larger geographic area or multiple tributaries and required pooling estimates from several observation sites (Figures 1 and 2). In addition, some IPTDS were located well upstream of the population boundary and may have monitored only a fraction of the population. Therefore, as a measure of population coverage, the proportion of the population monitored was estimated and reported relative to population habitat area (intrinsic potential; ICTRT 2007). This measure assumes or implies a relationship between the amount of habitat and adult abundance which may not be realized or consistent across populations. However, the annual population estimates reported here were based on a consistent monitoring effort through time within individual populations. As such, the population abundance estimates and trends reported here were not influenced by the addition or removal of observation sites over time within an individual population. As an example, abundance estimates from the Potlatch River were only available for a portion of the study period and therefore all estimates were excluded from the CRLMA-s population abundance estimates to maintain consistency through time.

1) Adult escapement at Lower Granite Dam

Total adult escapement of steelhead and Chinook Salmon (including jacks) crossing Lower Granite dam (LGR) was estimated using the STate space Adult Dam Escapement Model (STADEM). This model incorporates fish ladder window counts, data from fish sampled at the LGR adult trap (trap data), and observations of PIT-tagged fish within the LGR adult fish trap and ladder. Total escapement generated using this model includes estimates of uncertainty, parsed into weekly strata, and decomposed into three origin groups; wild, hatchery and hatchery no-clip. However, only annual estimates of wild origin abundance are reported here.

Data sources

Window count data generated by the US Army Corps of Engineers (USACE) at LGR was used in STADEM to estimate of the number of fish ascending and passing LGR each season. Window counts were made for each species observed using video monitoring and direct visual monitoring methods during daytime hours. Video monitoring was conducted during the beginning and tail ends of fish runs for 10 hours a day (0600-1600 hours); March 1-March 31 and November 1-December 31. Direct visual monitoring occurred during peak run times and operated for 16 hours a day (0400-2000 hours); April 1-October 31 (USACE 2015). Visual observers recorded each species they saw crossing the window for 50 minutes of each 16 hours of operation. The sum of the daily 50-minute counts were then multiplied by 1.2 to account for the missing 10 minutes each hour. Daytime fish counts were not expanded for fish ascending the ladder outside of operational hours (nighttime passage) (USACE 2015). Window counts were accessed through the Columbia Basin Research Data Access in Real Time (DART) website, using their window count query. Counts were provided for each day the fish ladder was open to fish passage. Although window counts were assumed to be a census of every fish passing LGR, nighttime and reascending fish were ignored as sources of potential observational error.

Systematic random samples of adult steelhead and Chinook Salmon returning to LGR were collected as part of daily operation at the adult trap located within the fish ladder. Sampling at the adult fish trap provided biological information (e.g., origin, genetic stock, age, sex) to allow the decomposition of total escapement into specific groups (Schrader 2013). The trap randomly and systematically sampled the daily run by opening four times each hour of the day for a length of time that was determined by the daily trap rate. The trap rate was determined using forecasted abundances for target species, runs, rear types, and research projects with associated sample size needs or requirements. Adult fish trap operation dates varied annually as a result of environmental conditions or changes to run forecast. For example, trap operations ceased or were modified due to high (≥21°C) and low (below freezing) water temperatures. Additionally, trap operations were reduced seasonally (closed weekends from March 1 to August 17) and may have been modified in-season to accommodate limitations at the trapping facility, changes to run forecasts, or sample size modifications. Fish captured in the trap were identified to species, examined for external marks and tags, scanned for a coded wire tag (CWT) and passive integrated transponder (PIT) tag, and measured for fork length (FL) to the nearest centimeter. Prior to release, sampled fish with an intact adipose fin and no PIT tag were PIT-tagged. Wild, hatchery, and hatchery no-clip (HNC) origins were assigned to each fish using a post-hoc analysis of marks, tags, and genetic information. Trap data included in the model was accessed from the Lower Granite Dam trapping database (Schrader 2013).

PIT-tag observations at the LGR adult trap and detections within the adult ladder provided a trap rate estimate and weekly nighttime and reascension passage rates. Adults tagged at the LGR adult trap were excluded from this analysis. Data was provided through a DART web access (Data Access in Real Time: www.cbr.washington.edu/dart) and the adult ladder PIT tag query. We previously examined the difference in night passage and reascension rates estimated by using only wild fish, versus combining hatchery and wild fish together, and found little difference. Therefore, we combined all PIT tagged fish (tagged prior to reaching LGR) to estimate common nighttime and reascension passage rates to increase the sample size.

A trap rate estimate was derived using mark-recapture methods where the “mark” group included PIT tags detected in the trap and the “capture” group included PIT tags observed within the LGR adult fish ladder. Using a mark-recapture model with differing capture probabilities, we estimated the trap rate on a weekly basis. Those estimates, with the associated uncertainties, were then incorporated into the model as informed priors, while the model estimated the “true” trap rate based on all the data, including trap and window counts.

Total and weekly escapement estimates

Escapement at LGR was estimated by combining two independent observations, trap catches and window counts, of the true number of fish crossing LGR in a state-space model with a weekly time-step. Both were assumed to be corrupted observations of the true unknown number of fish crossing LGR each week. The log of the true number of fish crossing (X_t), was modeled as a random walk process (Shumway and Stoffer 2010):

$$\begin{aligned} \log(X_t) &= \log(X_{t-1}) + e_t \\ e_t &\sim \mathcal{N}(0, \sigma_X^2) \end{aligned}$$

The number of fish caught in the trap, Y_t^T, for week t was modeled as a binomial process based on the unknown true trap rate that week, ν_t, and the unknown true number of fish crossing the dam that week, X_t. The true trap rate was estimated from a beta distribution with previously estimated parameters, $\widehat{\alpha_t}$ and $\widehat{\beta}_t$, informed by the mark-recapture estimate of the trap rate:

$$\begin{aligned} Y_t^T &\sim \mathrm{Bin}(\nu_t, X_t) \\ \nu_t &\sim \mathrm{Beta}\left(\widehat{\alpha_t}, \widehat{\beta}_t\right) \end{aligned}$$

The number of fish counted at the window, Y_t^W, was modeled as a (potentially) over-dispersed negative binomial process, with an expected value of X_t^{day}, the number of fish crossing the dam while the window is open. In the formula below, p_t is the proportion of fish observed at the window and r is the shape parameter. If r is estimated to be small this provides evidence for over-dispersion, and as it grows very large, the negative binomial distribution behaves like a Poisson distribution. The parameter θ_t is the proportion of fish crossing the dam during the hours when the window is open for counting:

$$
\begin{aligned}
Y_t^W &\sim \text{NegBin}(p_t, r) \\
p_t &= \frac{r}{\left(r + X_t^{day}\right)} \\
X_t^{day} &= X_t * \theta_t
\end{aligned}
$$

Nighttime passage and re-ascension rates

Two other processes were accounted for, first, the proportion of fish that cross the dam while the window is closed for counting (nighttime passage rate), and the second, the proportion of fish that are crossing the dam multiple times (reascension rate) and therefore potentially double-counted. Both rates can be estimated from previously PIT-tagged fish that are crossing the dam each week.

The proportion of fish passing the window during non-operational hours, nighttime passage rate, was just the complement of the rate of fish passing during the day when the window was operating. The daytime passage rate for week t, θ_t, was modeled as a random walk process and estimated from a binomial distribution based on the number of PIT tags observed to cross the dam during operational hours, y_t^{day}, and the total number of PIT tags observed to cross the dam at any point that week, N_t (Shumway and Stoffer 2010):

$$
\begin{aligned}
y_t^{day} &\sim \text{Bin}(\theta_t, N_t) \\
\text{logit}(\theta_t) &= \text{logit}(\theta_{t-1}) + g_t \\
g_t &\sim \mathcal{N}(0, \sigma_\theta^2)
\end{aligned}
$$

The number of total fish crossing LGR differs from the number of unique fish crossing LGR because some fish fall back and re-ascend the dam. These fish are potentially double-counted at the window, and have the potential to be caught in the fish trap more than once. The number of tags known to be re-ascending the dam each week, y_t^{reasc}, was modeled as a binomial process based on the estimated re-ascension rate, η_t, and the total number of tags crossing the dam that week, N_t. The logit of the reascension rate was modeled as a random walk process similar to daytime passage (Shumway and Stoffer 2010):

$$
\begin{aligned}
y_t^{reasc} &\sim \text{Bin}(\eta_t, N_t) \\
\text{logit}(\eta_t) &= \text{logit}(\eta_{t-1}) + f_t \\
f_t &\sim \mathcal{N}(0, \sigma_\eta^2)
\end{aligned}
$$

Origin proportions

After estimating the total number of fish to have crossed LGR each week, X_t, the total must be further refined into the number of wild fish, $X_{w,t}$, hatchery fish, $X_{h,t}$ and hatchery no-clip fish, $X_{hnc,t}$. This was done by estimating a weekly origin proportion vector, ω_t based on the stratified random sample of fish caught in trap that week, Y_t^T. The observed number of wild, $Y_{w,t}^T$, hatchery, $Y_{h,t}^T$, and hatchery no-clip, $Y_{hnc,t}^T$, fish caught in the trap that week was assumed to come from a multinomial distribution with probability vector ω_t. The log-odds ratio of the proportions in ω_t, in relation to the proportion of hatchery fish, $\omega_{h,t}$ was modeled as a random walk, so it can change through time. This allow the proportions of wild, hatchery, and hatchery no-clip fish to shift throughout the season, based on the data available from the fish trap.

$$
\begin{aligned}
\left(Y_{w,t}^{T}, Y_{h,t}^{T}, Y_{hnc,t}^{T}\right) &\sim \text{Multinom}(\omega_t, Y_t^T) \\
\omega_t &= \frac{\exp(\phi_t)}{\sum \exp(\phi_t)} \\
\phi_{w,t} &= \log\left(\frac{\omega_{w,t}}{\omega_{h,t}}\right) \\
\phi_{hnc,t} &= \log\left(\frac{\omega_{hnc,t}}{\omega_{h,t}}\right) \\
\phi_{h,t} &= 0 \\
\phi_{w,t} &= \phi_{w,t-1} + d_{w,t} \\
\phi_{hnc,t} &= \phi_{hnc,t-1} + d_{hnc,t} \\
d_t &\sim \mathcal{N}(0, \sigma_\omega^2)
\end{aligned}
$$

Finally, the number of unique fish crossing LGR each week, $X_{w,t}$, is the product of the total fish crossing that week, X_t multiplied by one minus the re-ascension rate, $(1-\eta_t)$, and the origin proportion vector, ω_t.

$$
\begin{bmatrix} X_{w,t} \\ X_{h,t} \\ X_{hnc,t} \end{bmatrix} = X_t * (1-\eta_t) * \begin{bmatrix} \omega_{w,t} \\ \omega_{h,t} \\ \omega_{hnc,t} \end{bmatrix}
$$

The model was fit using the JAGS program (Plummer 2009), run with R software (R Core Team 2019). Uninformative priors were used for $\sigma_X, \sigma_\eta, \sigma_\theta, \sigma_\omega$ and $\log(X_1)$ (Uniform(0,10)), as well as logit(η_1) and logit(θ_1) ($\mathcal{N}(0{,}1000)$), and finally $\phi_{w,1}$ and $\phi_{hnc,1}$ ($\mathcal{N}(0{,}100)$).

2) Adult escapement at the population-level

Estimates of wild adult escapement for steelhead and spring/summer Chinook Salmon (jacks included) populations to various tributary locations above Lower Granite Dam (LGR) were generated utilizing the observations of PIT tags from the systematic random sample of all wild adults migrating over LGR. To accomplish this goal, the probability that a fish moved along certain paths of the stream network and escaped to a given location was estimated and combined with the total wild escapement of fish above LGR. To this end, the DABOM model (Lower Granite Dam Adult Branch Occupancy Model) was developed to estimate movement probabilities of fish traveling the stream network above LGR and the subsequent tributary escapement estimates with uncertainty.

The DABOM model estimates tributary escapement at in-stream PIT-tag detection systems (IPTDS) or other types of PIT tag detection sites such as hatchery weirs. PIT tag detections are required upstream of estimation sites to generate valid and unbiased estimates of detection probabilities, and ultimately movement probabilities and escapement estimates. Estimates at terminal sites (such as single arrays or weirs) can still be obtained if PIT-tag detection probabilities can be generated using other independent methods (e.g., mark-recapture weir efficiencies). If the detection probability is unknown, a value of 1.0 is assumed and provides a minimum estimate of escapement. Estimates at terminal sites, however, may by highly variable and subject to positive or negative bias depending on the accuracy of estimated or supplied detection probabilities. For this study all terminal observations sites were assigned a detection probability of 1.0.

Data sources

As mentioned in the STADEM model description (see above), returning steelhead and adult Chinook Salmon were systematically and randomly collected at the adult fish trap. As part of this process, fish were assigned an origin [hatchery, wild, or hatchery no clip (HNC)] based on the presence of marks, tags, and parentage-based tagging. All adipose intact adult steelhead and Chinook Salmon were PIT-tagged (if a PIT tag was not already present) and scales and genetic samples were collected prior to release. For steelhead, the annual tag group was composed of fish captured in the trap beginning July 1 through June 30 of the following year. For Chinook Salmon, the annual PIT tag group was composed of fish captured in the trap from March 1 (or start of trapping operations) through August 17. The regional PIT tag database PTAGIS, was queried for the Complete Tag History (Interrogations, Recaptures, and Mortalities) for all tags within the list. Detection histories were then constructed and individual spawn sites were determined with the R package PITcleanr (available at https://github.com/KevinSee/PITcleanr) as described in Orme and Kinzer (2019). The PITcleanr package filtered the complete PIT tag histories into site-specific passage events for each consecutive DABOM observation site encountered beginning at LGR. A site passage event for a PIT tag was defined as a tag observation or consecutive multiple observations all at the same observation site or individual instream array (model node). The PITcleanr package provided the minimum and maximum observation date for each event, thus filtering out consecutive or repetitive non-informative observations. Movement to a different observation site or instream array would initiate a new passage event.

As a rule, each observed PIT tag can only follow a single branch in the stream network and must be assigned a final spawning location. The observation dates and the farthest upstream observations were the primary variables used to define and assign spawn locations. However, if a tag was observed in multiple branches or tributaries (dip-in or post-spawn behavior), the tag was assigned a spawn location based on the complete detection history. A comparison of the minimum and maximum observation dates between sites along with the observed residency time above or between observation sites was used to assign a final spawn location. After each tag detection history was reviewed, a capture history file consisting of ones (i.e., detected at the site) and zeros (i.e., not detected at the site) was created. The capture history file was then filtered to exclude, 1) all fish captured during separation by code events (targeted trap capture) and 2) hatchery no clip fish as determined by genetic parentage assignment.

Because the stream network can be observed as a hierarchy of rivers and tributaries (e.g., branched spatial arrangement) the spatial distribution of spawning salmonids can be modeled using a hierarchical patch occupancy model (Royle and Dorazio 2008). These types of models are ideal for estimating hierarchical transition probabilities that are used to represent movement of individuals through river networks. Because detection efficiencies typically are less than 100% for IPTDS, we must model both the probability that a fish has passed a certain point, ψ, as well as the probability that it is detected there, p. This model is a series of nested patch-occupancy models where the nested structure mimics the branching nature of the stream network and the locations of the detection infrastructure (see Orme et al. 2019 for detection site schematics).

Initial movement probabilities

The probability that a fish, i, has moved to branch j is:

$$\psi_j = Pr(z_{i,j} = 1),$$

where $z_{i,j}$ is 1 if fish i has moved to branch j, and 0 if it hasn't.

Estimation of movement probabilities for initial branches is complicated because the LGR trap rate can vary within a season or the trap may shut down completely for extended periods of time. Inconsistent trap rates combined with different population run-timings leads to a non-representative sample of fish within the valid tag list (Orme 2016). For example, if the trap rate changes from 7% early in the Chinook run to 15% later in the run, the trap will sample late-run stocks twice as much as early-run stocks. Associated movement probabilities to mainstem branches based on the season-wide sample would then be negatively biased for early run stocks and positively biased for later run stocks (Orme 2016).

To account for the potential under- or oversampling, initial movement probabilities were allowed to vary through time. Initial movement of fish crossing LGR in week t and then escaping to various mainstem branches was modeled from a multinomial distribution with probability vector ψ_t. Each week, the valid PIT-tagged fish were assumed to be a representative sample of the fish crossing LGR that week. The log-odds ratio of moving to the j^{th} branch in relation to the probability of going to the initial black box (unseen), $\phi_{j,t}$, was modeled as a random walk. The actual movement probabilities, $\psi_{j,t}$ were then recovered through exponentiating.

$$\begin{aligned}
\phi_{j,t} &= \log\left(\frac{\psi_{j,t}}{\psi_{J,t}}\right) \\
\phi_{j,t} &= \phi_{j,t-1} + e_{j,t} \\
e_{j,t} &\sim \mathcal{N}(0, \sigma^2) \\
\psi_{j,t} &= \frac{\exp(\phi_{j,t})}{\sum \exp(\phi_{.,t})}
\end{aligned}$$

The above approach allows for time-varying movement probabilities. After that initial branch, movement probabilities within each branch were assumed to be constant through the season (e.g., once a fish gets to the South Fork Salmon, it has the same probability of going to the Secesh as any other fish that has gotten to the South Fork Salmon, regardless of when each fish crossed Lower Granite).

Other movement probabilities

For a single branch confluence within a tributary with J upstream branches, the unknown state of fish i, $z_{i,j}$ (i.e., whether it is in branch j or not), was modeled from a multinomial distribution with probability ψ_j. The ψ vector was constrained by a Dirichlet distribution so that the probabilities sum to one above that confluence. A Dirichlet vector specified with 1 for each tributary represented an uninformative prior on transition probabilities. If no tags were detected in a particular tributary in a given year the Dirichlet vector was given a prior of 0 for that tributary to indicate that no fish escaped there. In addition, upstream of each confluence contains a "not seen" patch, or "black box", $(J + 1)$ that represents fish that may have "dropped out" or did not migrate past the next upstream observation and estimation site. Drop outs are likely fish that may have spawned between detection sites, either in the mainstem or a non-monitored tributary. Drop outs may also include fish that fell back and were undetected elsewhere or experienced prespawn mortality.

$$\begin{aligned} z_{i,j} &\sim \mathrm{MultiNom}(1, \psi), \\ \psi_{j,\ldots,J,J+1} &\sim \mathrm{Dir}(1,1,\ldots,1) \end{aligned}$$

There are some detection sites with only a single upstream observation site. Fish reaching these points can then follow one of two branches: reach the upstream site, or not. This ψ vector of length 2 was modeled as a binomial, with a single ψ parameter, with an uninformative prior of $\mathrm{Beta}(1,1)$, representing the probability that a fish reaches that upstream site.

Detection probabilities

Observations at each antenna, $y_{i,j,k}$, were modeled from Bernoulli distributions and the function of the unknown state, $z_{i,j}$, and the detection probability, $p_{j,k}$, of antenna k at each IPTDS.

$$\begin{aligned} y_{i,j,k} &\sim \mathrm{Bern}(z_{i,j} * p_{j,k}) \\ p_{j,k} &= Pr(y_{i,j,k} = 1 \mid z_{i,j} = 1) \end{aligned}$$

To simultaneously estimate occurrence and detection the model requires at least two observation sites. Several IPTDS sites have two or more stream spanning antenna arrays. For sites with three antenna arrays, detections from the middle array were combined with detections from the upstream array, and for sites with four arrays, the two downstream arrays were combined, as were the two upstream arrays. This minimized the number of detection probabilities that the model must estimate, while still utilizing all observations.

If multiple antenna arrays or upstream detections were unavailable, the probability of detection cannot be estimated and can either be fixed at 100%, or an independent estimate of detection probability can be provided and passed to the model as an informative beta prior. For this study a detection probability of 100% was used at terminal observation sites.

While informed priors are preferable to assuming 100% detection, there are several potential issues with passing informed priors to the model for these locations. For example, there may have been an underestimate of escapement if all the detected tags were not uploaded to PTAGIS, or if weir efficiency was significantly different from the probability of detecting a PIT tag (e.g., due to hand scanning).

Escapement estimates at individual detection sites

To estimate escapement at each detection site, movement probability estimates from the above described branch occupancy model were combined with escapement estimates from STADEM (described above). To estimate wild escapement to various tributary detection sites, samples from the posterior of total weekly wild escapement past Lower Granite Dam, $X_{w,t}$, were multiplied by appropriate combinations of movement probabilities. For example, the estimate of fish moving to Webb Creek (past the WEB PIT array) was the sum across all weeks of the product of the weekly LGR escapement and the probability of moving along the Lapwai branch (past LAP), multiplied by the probability of moving along the Sweetwater branch (past SWT) and into Webb Creek (past WEB).

$$\left(\sum_{t=1}^{T}\left(X_{w,t} * \psi_{LAP,t}\right)\right) * \psi_{SWT} * \psi_{WEB}$$

Model assumptions

A series of assumptions were made when constructing the above described model. It was assumed that tagged and untagged fish had similar behavior patterns and that a representative random sample of the fish escaping to each main branch was tagged. Mortality was assumed to be the same between tagged and untagged fish (i.e., tagging mortality was equal to zero), and the last place a fish was detected or the furthest upstream (accounting for observations of steelhead kelts) was assumed to be the spawning location (e.g., they did not fall back undetected and spawn somewhere else). Tags were assumed to have functioned properly until spawning, that tag loss was zero, and there was no decrease in tag efficiency through time. Lastly, all fish returning to the same branch were assumed to have similar run timing.

The model was fit using the JAGS program (Plummer 2009) run with R software (R Core Team 2009) Uninformative priors were used for all ψ's (Dirichlet(1,1…,1) or Beta(1,1)) and p's (Beta(1,1)). The prior for σ was Uniform(0,10).

3) Population-level estimates of life history characteristics (sex and age)

Proportion of females

Female escapement to each branch and population considered in the DABOM model was estimated using genetic sex data evaluated in a hierarchical model. Sex was determined post hoc using a sex-specific allelic discrimination assay (Campbell et al. 2012). Genomic DNA extraction and SNP genotyping (which includes sex-specific assays for steelhead and Chinook Salmon) are described in Section 3 of Powell et al. (2018). The most current concordance check of the sex-determination assay using known-sex broodstock spawned in 2016 at Snake River hatcheries indicated 99.1% accuracy for steelhead and 99.7% accuracy for Chinook Salmon (Steele et al. 2018).

Because branches differed in the number of returning fish, a hierarchical model was developed to allow for some borrowing of information from larger branches to smaller branches. The purpose of information borrowing was to avoid skewing the sex ratio due solely to small sample sizes in some branches. The proportion of females at the population scale was estimated using the following model:

$$f_i \sim Bin\ (p_{pop_i}, N_i\ )$$

$$p_{pop_i} \sim N(\mu, \sigma^2)$$

where f_i is the number of females observed in a branch, N_i is the total number of sexed tags observed in that branch, and p_{pop_i} is the proportion of females for the population containing model branch i (the quantity of interest). Hierarchy was imposed by assuming that the logit of p_{pop_i} comes from a normal distribution centered around a value, μ, that represents the overall female proportion for the entire DPS/ESU. The variation between populations is captured by σ^2.

Age proportion model

Similar to estimation of female proportions, a model was developed to estimate escapement by brood year to each branch and population. The age of fish distributed across the landscape was determined via the ageing of scales collected as part of biological sampling at LGR. Protocols for determining freshwater, saltwater, and total age are detailed in Wright et al. (2015). Escapement by brood year to each branch and population was estimated via hierarchical model of the form:

$$A_i \sim Multinomial(\pi_{pop_i}, N_i)$$

where A_i is the vector of age classes observed in a branch, N_i is the total number of aged tags observed in that branch, and π_{pop_i} is the vector of proportion of ages for the population containing model branch i (the quantity of interest).

We then imposed some hierarchy by assuming that the vector of age proportions for each branch, π_{pop_i}, is drawn from a multivariate logistic normal distribution, with mean vector μ and covariance matrix Σ. Steelhead in the upriver Columbia River basin are managed as two stocks based on size (A-run are <78-cm FL and B-run as ≥78-cm FL) with A-run steelhead typically spending 1 or 2 years at sea, while B-run fish typically spend 2 or 3 years at sea (Busby et al. 1996; Copeland et al. 2017). To account for the potential differences in age proportions between A-run and the generally older B-run populations (steelhead only), we used two different μ_{run} vectors, one for each type of population:

$$\mathrm{alr}\left(\pi_{pop_i}\right) \sim MVN(\mu_{run}, \Sigma),$$

where the additive log ratio transformation is

$$\mathrm{alr}(\pi_{pop_i}) = \left(\log(\frac{p_{i,a_2}}{p_{i,a_1}}), \ldots, \log(\frac{p_{i,a_{max}}}{p_{i,a_1}})\right).$$

This formulation requires the choice of a reference age, so that the length of μ is one less than the total number of ages observed. We chose to use the smallest age, age 2, as the reference age for steelhead.

4) Estimates of genetic diversity and differentiation

Protocols for genetic laboratory procedures (e.g., DNA extraction and SNP amplification) can be found in Section 3 of Powell et al. (2018) and references therein. Briefly, steelhead and Chinook Salmon were screened at panels of up to 368 SNP markers. Because older collections of fish (i.e., SY2010) were not typed at the most recent and largest panels, estimates of diversity and differentiation (described below) were made using a subset of markers common to all collections (steelhead = 174 markers; Chinook Salmon = 167 markers).

The observed and expected heterozygosity and the percent of SNPs that were polymorphic were calculated for each population as a proxy measure of genetic diversity. Observed heterozygosity directly measures the percentage of detected fish in a population that were heterozygotes (carry both alleles). The overall observed heterozygosity was calculated as 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 population. Unlike genetic metrics such as effective population size, there is currently no specified value of expected heterozygosity that is used to assess whether a population is at elevated risk. Nonetheless, genetic diversity represents a fundamental population genetic parameter, and significant changes to levels of genetic diversity may reflect changes in population size (e.g., population bottlenecks; Peery et al. 2012) or be driven by changes in gene flow between populations (Slatkin 1995). Estimates of genetic diversity were made for populations with a minimum sample size of twenty individuals.

Tests for deviation from Hardy-Weinberg expectation (HWE) were performed across all SNPs for each population 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 (174 for steelhead and 167 for Chinook Salmon) following Bonferroni correction (Rice 1989). We report the number of SNPs exhibiting an excess or deficit of heterozygotes for any location.

A neighbor-joining (NJ) tree was created for each species. These trees include detections from all years (SY2010-2019), as well as all samples included in the steelhead and Chinook Salmon GSI baseline versions 3.1. Samples from the GSI baselines were first pooled into populations to assist in comparison. Neighbor-joining trees are based on pairwise Cavalli-Sforza Edwards chord distance (Cavalli-Sforza and Edwards 1967) 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 using Figtree v1.3.0 (https://github.com/rambaut/figtree/) and manually edited in Inkscape v0.92.3 (https://inkscape.org/).

5) Effective number of breeders (N_b)

Effective population size (N_e) represents a measure of the relative contribution of individuals in a population that contribute offspring to the next generation, and when individuals from a single brood year are analyzed N_e is the same as N_b. Minimum effective population sizes of 50 and 500 have been proposed as goals to prevent short-term inbreeding and to maintain sufficient long-term genetic diversity, respectively (Franklin 1980).

We used two programs to estimate the effective number of breeders (N_b) by parental brood year (BY) for each population. 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 version 2.1 (Do et al. 2014) to estimate N_b using the bias corrected linkage disequilibrium (LD) method of Waples (2006) excluding all alleles with frequencies less than 0.03. The LD method is the most widely used method for estimating N_e from a single collection (Waples and England 2011), and 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 fish detected at a PIT tag array back to a brood year. Offspring from the same population and BY were then analyzed as a single sample to estimate N_b. 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 were calculated. Because the unweighted harmonic mean is the sample size divided by the sum of the reciprocal values, infinite estimates of N_b were replaced with the limit of the reciprocal of N_b, as N_b approaches infinity in the calculation of the harmonic mean N_b within a BY. The SA and LD methods were combined to increase precision of the estimated N_b (Waples and Do 2010).

6) Genetic origin of detected and non-detected fish

Each fish PIT tagged at Lower Granite Dam was also sampled for genetic tissue. All fish sampled at Lower Granite Dam were assigned to a genetic reporting unit based on the highest probability maximum likelihood individual assignment (Smouse et al. 1990) calculated with the Expectation-Maximization algorithm (Dempster et al. 1977) in the program *gsi_sim* (Anderson et al. 2008, Anderson 2010). We provide a summary of the proportion of returning adults assigned to different reporting groups for three sets of samples. Specifically, all adults sampled at Lower Granite Dam, adults that were detected at a population-specific PIT tag arrays, and adults that were never detected at an array. Because a significant number of fish PIT-tagged at Lower Granite Dam are never detected at a PIT tag array (Table 3), we present these data to assess whether PIT-tagged adults that were detected at arrays varied systematically from a genetic stock perspective relative to the overall population.

Unless otherwise stated all analyses were performed in the statistical computing package R version 3.5.1 (R Core Team 2019).

RESULTS

Steelhead

1) Adult escapement at Lower Granite Dam

The estimated wild steelhead abundance at Lower Granite Dam resulting from the STADEM model runs (Table 3) ranged from a high of 47,816 (45,058-51,592, 95% CI) adults in spawn year 2015 to a low of 10,096 (9,376-10,888) adults in spawn year 2018. Total wild steelhead abundance at LGR averaged nearly 38,000 adults from spawn year 2010 through 2016 but only averaged roughly 12,000 individuals between spawn year 2017 through 2019 (Table 3).

The number of PIT tags within each annual tag group varied based on the adult trap rate and the actual abundance of wild fish passing LGR. The number of PIT-tagged wild adult steelhead released from the LGR adult trap averaged nearly 4,000 individuals annually from spawn year 2010 through 2016 but only averaged approximately 2,400 individuals from spawn year 2017 through 2019 (Table 3). The annual proportion of tagged wild adult steelhead released from the LGR adult trap increased over time resulting from lower run sizes and a subsequent increase in the LGR adult sampling rate. The mean annual proportion of tagged individuals was approximately 0.11 for spawn years 2010-2016 and 0.20 for spawn years 2017-2019 (Table 3).

The proportion of the adult steelhead LGR tag group detected at observation sites used within the DABOM model increased through time (Table 3), a product of the installation of additional observation sites over time to monitor additional populations. The proportion of the annual tag groups observed ranged from a low of 0.19 for the spawn year 2010 tag group to a high of 0.53 for the spawn year 2019 tag group with an overall mean proportion observed of 0.37 at sties used within the DABOM model (Table 3).

2) Adult escapement at the population-level

DABOM model estimates of abundance using NMFS designated population delineation for natural-origin steelhead exhibited declines in population abundance throughout the study period (Figure 3; Appendix A). All populations also exhibited a high degree of annual synchronicity in terms of annual adult abundance trends (Figure 4) regardless of geographic spawning locations. In addition, estimates showed that populations were composed of both consistently large and consistently small populations (Table 4). For example, the Imnaha River population (IRMAI-s) was on average the largest population and annually accounted for 6.7% (range 5.5%-8.9%, n = 9) of all wild steelhead ascending LGR. The Joseph Creek population (GRJOS-s) within the Grande Ronde River was the second largest population averaging 5.7% (range 3.8%-7.4%, n = 9) of the total annual wild abundance at LGR (Table 4). In contrast, estimates for the entire upper Salmon River (Lemhi River and mainstem Salmon River sites LLR and USE) accounted for less than 3% (range 1.7% to 5.0%) of the annual estimate over LGR. Similarly, the entire South Fork Salmon River (populations SFMAI-s and SFSEC-s) on average accounted for just 3.3% (range 1.8% to 5.6%) of the annual returning wild steelhead adults (Table 4). The current PIT tag detection infrastructure within the Grande Ronde River accounted for nearly 12% (range 3.8% to 18.5%) of all wild steelhead crossing LGR (Table 4). It is interesting to note that the estimated escapement into the Tucannon River (SNTUC-s) represents a minimum estimate of the LGR adult fallback. On average and at a minimum, 2.2% (range 1.6% to 4.7%) of the annual estimated wild steelhead abundance at LGR falls back over LGR and enters the Tucannon River (Table 4).

3) Population-level estimates of life history characteristics (sex and age)

Female adult steelhead population proportions varied little, both between years and between populations within a single year (Figure 5). Overall, 64% of all wild steelhead observed at DABOM PIT tag observation sites were female. Annual averages ranged from a low of 53% in spawn year 2014 to a high of 72.6% in spawn year 2017. The variability in female proportion between populations was greatest for spawn years 2010 and 2019 although both spawn years had the fewest PIT tag observations and therefore the smallest sample sizes. Conversely, spawn years 2012, 2016, and 2018 had the least variability between populations (Figure 6). Population and year specific female proportion, variance, and sample sizes are presented in Appendix B.

Total age at return for wild steelhead observed at DABOM PIT tag observation sites spanned 6 age classes, ages 3 to 8. The annual age proportions within individual populations were fairly consistent between years (Figure 7). However, age proportions between populations within a single spawn year showed more variability at least though spawn year 2017 (Figure 8), after which the age class proportions between populations appeared to become more synchronous. Differences in mean age at return were observed between groups generally referred to as “A” run and “B” run fish (Figure 8). Steelhead populations within the Middle Fork and South Fork Salmon rivers, and those in the upper Clearwater River (B run) on average were primarily composed of individuals of age 5 or older whereas all other population were primarily composed of individuals age 5 or younger. Proportion, variance, and sample size by age, by spawn year, and by population are presented in Appendix B.

4) Estimates of Genetic Diversity and Differentiation

Overall, we observed variation in levels of expected heterozygosity at the MPG- and population-level. Averaging across all years, expected heterozygosity was lowest among populations in the Clearwater River MPG (H_e = 29.0%; Figure 9; Table 5) and highest in the Lower Snake River (31.0%). Intermediate values of expected heterozygosity were observed for the Salmon (30.1%), Imnaha (30.2%), and Grande Ronde (30.6%) rivers. The levels of heterozygosity within MPGs remained generally consistent through time (Table 5; Appendix C) and the patterns we observed were similar to previous microsatellite-based estimates from the Snake River basin (Nielsen et al. 2009).

In addition to observing differences among MPGs, we also observed variation within MPGs. Levels of genetic diversity in dendritic landscapes are known to vary hierarchically, with elevated genetic diversity common in downstream reaches (Selkoe et al 2016). We observed evidence of hierarchical genetic structure in the Snake River basin. For example, the lower Clearwater population (CRLMA-s), which is low in the Clearwater River basin, had higher levels of heterozygosity than the most upriver populations, the Selway (CRSEL-s) and Lochsa rivers (Lochsa-s, Figure 9, Table 5). This pattern contrasted with rivers in northeast Oregon, where minimal difference were noted in levels of genetic diversity among populations in the Grande Ronde River MPG (Figure 9, Appendix C). In the Salmon River, we observed similar levels of genetic diversity across populations, with the exception of the Lemhi River (SRLEM-s). As was noted previously with patterns across MPGs, we failed to observed marked variation in diversity levels within populations through time.

We observed minimal genetic differentiation between PIT-tagged fish assigned to populations on the landscape and reference collections (genetic baseline) from those same areas (Figure 10). Within each genetic stock, collections of PIT tag detected fish grouped by population were most closely related to baseline samples collected from the same population.

5) Effective number of breeders (N_b)

Using data from spawn years 2010-2019, we were able to estimate the effective number of breeders for 17 steelhead populations. With few exceptions there were multiple estimates per population (Table 6, Figure 11). Mean estimates of N_b (i.e., values averaged across populations and brood years) at the MPG level were highest for the Imnaha River (459) and lowest for the Salmon River MPG (234; Table 6). Mean values of N_b for the Grande Ronde River (345) and Lower Snake River MPG (350) were intermediate relative to the other MPGs. In general, values of N_b at the MPG level varied in sync through time (Figure 11).

At the population level, N_b ranged from a low of 41 in the South Fork Clearwater River (CRSFC-s) in spawn year 2012 to a high of 632 in the Imnaha River (IRMAI-s) in spawn year 2007. Similar to the MPG level, we observed fluctuations in N_b estimates at the population level through time (Figure 11); however there was greater variation among populations than among MPGs (Table 6, Figure 11).

6) Genetic origin of detected and non-detected fish

We assessed the genetic origin of returning adults sampled at Lower Granite Dam, adults detected at a PIT tag array, and adults that were never detected at a PIT tag array. The Grande Ronde reporting unit represented the largest contribution to sampled at Lower Granite Dam

(0.268) and the Lower Salmon reporting unit represented the smallest proportion (0.026, Table 7, Figure 12).

Across all spawn years, the proportions of different genetic stocks observed at Lower Granite Dam were highly similar to the stock proportions detected at PIT tag arrays (Table 7, Figure 12). The greatest number of steelhead that were tagged at Lower Granite Dam and detected at a PIT tag array was from the Grande Ronde River (0.260) genetic stock (Table 7, Figure 12). The smallest average contributions to PIT detections were from the Lower Salmon River (0.026). Through time, the number of detections increased for the Grande Ronde River and Upper Clearwater River genetic stocks (Figure 12). In contrast, fewer observations through time were noted for the Imnaha River, Lower Clearwater River, Lower Salmon River, Middle Fork Salmon River, and South Fork Salmon River.

The genetic stock of origin for adults never detected at an array were generally similar with a couple of exceptions. The proportions of fish assigned to the Imnaha River and South Fork Salmon that were never detected were lower relative to the proportions observed at PIT tag arrays or at Lower Granite Dam. A greater proportion of fish assigned to the Middle Fork Salmon River and Upper Salmon River reporting units were never detected relative to observations at PIT tag arrays or at Lower Granite Dam (Table 7, Figure 12).

Chinook Salmon

1) Adult escapement at Lower Granite Dam

The estimated wild spring/summer Chinook Salmon abundance (jacks included) at LGR from the STADEM model runs (Table 8) ranged from a high of 28,491 (26,423–30,484, 95% CI) adults in spawn year 2014 to a low of 4,668 (3,942–6,090) adults in spawn year 2019. Total Chinook Salmon abundance at LGR averaged over 23,000 adults from spawn year 2010 through 2016 but only averaged roughly 5,600 individuals between spawn year 2017 and 2019 (Table 8).

The number of PIT tags within each annual tag group varied based on the adult trap rate and the actual abundance of wild fish passing LGR. The number of PIT-tagged wild adult Chinook Salmon released from the LGR adult trap averaged nearly 2,500 individuals annually from spawn year 2010 through 2016 but only averaged approximately 1,300 individuals from spawn year 2017 through 2019 (Table 8). The proportion of tagged wild adult Chinook Salmon released from the LGR adult trap increased through time as a result of lower run sizes and a subsequent increase in the sampling rate. The mean annual proportion of tagged adults was approximately 0.11 for spawn years 2010-2016 and 0.23 for spawn years 2017 through 2019.

The proportion of the wild adult Chinook Salmon LGR tag group detected at observation sites used within the DABOM model increased through time (Table 8), a product of the installation of additional observation sites over time to monitor additional populations. The proportion of the annual tag groups observed ranged from a low of 0.33 for the 2010 tag group to 0.63 for the 2019 tag group with an overall mean proportion observed of 0.50 at sties used within the DABOM model.

2) Adult escapement at the population-level

DABOM model estimates of abundance by the NMFS population delineation for wild Chinook Salmon (jacks included) by spawn year are presented in Figure 13 and in Appendix

Table D. Overall, all populations exhibited declines in population abundance throughout the time frame of this study (Figure 13). All populations also exhibited a high degree of annual synchronicity in terms of annual adult abundance trends regardless of geographic spawning location (Figure 14). In addition, estimates show that populations are composed of both consistently large and consistently small populations (Table 9). For example, the Lemhi River population (SRLEM) on average accounted for 2.0% (range 0.5%-4.6%, n = 10) of all wild Chinook Salmon ascending Lower Granite Dam. In contrast the South Fork Salmon mainstem population (SFMAI) accounted for an average of 6.4% (range 3.4%-13.8%, n = 10) of the total wild abundance at Lower Granite Dam (Table 9). The three largest contributions of the total annual wild Chinook Salmon abundance at Lower Granite Dam was the South Fork Salmon River populations (SFMAI, SFEFS, SFSEC), which accounted for an average of 14.5% (range 9.4%-21.3%, n = 10), followed by the upper Salmon populations (average 10.0%, range 6.4%-13.9%), and the Grande Ronde and Imnaha populations (average 14.3%, range 7.3%-22.9%; Table 9).

3) Population-level estimates of life history characteristics

Wild Chinook Salmon female population proportions varied widely, both between years and between populations within a single year (Figure 15). However, the annual change in female proportions both in magnitude and direction were highly synchronized between populations (Figure 16). Overall, 41% of all wild Chinook Salmon at DABOM PIT tag observation sites were female. Annual averages ranged from a low of 26% in spawn year 2011 to a high of 54.3% in spawn year 2016. Population and year specific female proportion, variance, and sample sizes are presented in Appendix Table E.

Total age at return for wild Chinook Salmon observed at DABOM sites spanned 5 age classes, ages 2 to 6. However the vast majority were ages 3 through 5 with a small proportion of age 2 mini-jacks observed in several basins in spawn year 2017. The annual age proportions were highly variable between years within individual populations (Figure 17). In contrast, very little variability was observed in age 3 and age 4 proportion between populations within any single spawn year (Figure 18). Proportion, variance, and sample size by age, by spawn year, and by population are presented in Appendix Table E.

4) Estimates of genetic diversity and differentiation

Values of expected heterozygosity quantified for Chinook Salmon varied at the MPG and population level. Averaged across years, mean levels of expected heterozygosity were very similar for the Middle Fork Salmon River (22.1%), South Fork Salmon River (22.5%), and Upper Salmon River (22.9%) MPGs (Table 10, Figure 19). The Grande Ronde/Imnaha MPG had a mean heterozygosity of 24.6% average across spawn years. We did not observe appreciable variation in heterozygosity at the MPG level through time (Appendix F).

Patterns in heterozygosity for Chinook Salmon did not appear to display a hierarchical structure throughout the Snake River basin. Populations in the Grande Ronde displayed varying levels of diversity across relatively small spatial scales. For example, the highest average levels of heterozygosity of any population were observed in the Wenaha River (GRWEN, 30.1%), which was much higher than the nearby Lostine River (GRLOS, 23.5%, Figure 19). Additionally, populations highest up in the Salmon River (e.g., SRYFS, SRVAL, SRUMA) had levels of heterozygosity similar to populations in the South Fork Salmon River and Middle Fork Salmon Rivers (Table 10, Figure 19)

We observed minimal genetic differentiation between fish from the same geographic areas regardless of collection source (PIT vs baseline sampling). In general, genetic stocks fell out as well supported clades (Figure 20) with a few exceptions. Collections from the Little Salmon River grouped most closely with Upper South Fork Clearwater River, which was unexpected. PIT tag collections were generally most closely related to baseline samples collected from the same population.

5) Effective number of breeders (N_b)

Across all spawn years, estimates of effective number of breeders were produced for a total of 22 Chinook Salmon populations. With few exceptions, multiple estimates of N_b were made per population. Mean estimates of N_b (i.e., values averaged across populations and brood years) at the MPG level were highest for the South Fork Salmon River (215) and lowest for the Grande Ronde/Imnaha River MPG (182, Table 11). Mean values of N_b for the Upper Salmon River (185) and Middle Fork Salmon River MPG (201) were intermediate relative to the other MPGs. Synchrony varied temporally among values of N_b at the MPG level, with some populations displaying increases in N_b while others decreased (Figure 21).

Among extant populations, mean estimates of N_b (i.e., values averaged across multiple brood years) ranged from a low of 99 in Big Sheep Creek (IRBSH) to a high of 255 in the South Fork Salmon River mainstem (SFMAI, Figure 21). Estimates of N_b fluctuated considerably through time within individual populations (Figure 21). For example, the difference between the largest and smallest estimate of N_b in the South Fork Salmon River mainstem (SFMAI) population was 331.

6) Genetic origin of detected and non-detected fish

We assessed the genetic origin of returning adults sampled at Lower Granite Dam, adults detected at a PIT tag array, and adults that were never detected at a PIT tag array. The Hells Canyon reporting unit represented the largest contribution to samples at Lower Granite Dam (0.417). Chamberlain Creek, (0.009), Tucannon (0.007) represented the smallest proportion of spring/summer Chinook sampled at Lower Granite Dam (Table 12, Figure 22).

Across all spawn years, the proportions of different genetic stocks observed at Lower Granite Dam were highly similar to the stock proportions detected at PIT tag arrays (Table 12, Figure 22). Through time, the number of detections increased for the Fall Chinook genetic stock (Figure 12). In contrast, fewer observations through time were noted for the Middle Fork Salmon River and Upper Salmon River.

The genetic stock of origin for adults never detected at an array were generally similar with a couple of exceptions. The proportions of fish assigned to Chamberlain Creek and Middle Fork Salmon River at Lower Granite Dam that were never detected was higher relative to the proportions observed at PIT tag arrays or at Lower Granite Dam. In contrast, a small proportion of fish assigned to the Middle Fork Salmon River were never detected relative to observations at PIT tag arrays or at Lower Granite Dam (Table 12, Figure 22).

ACKNOWLEDGEMENTS

The authors would like to thank the many individuals who contributed time and expertise towards implementing this project (alphabetical):

Biomark
- Chris Beasley
- Mike Ackerman
- Steve Anglea

Bonneville Power Administration
- Barbara Shields
- David Burns
- Rick Golden
- Brady Allen

Columbia River Inter-Tribal Fish Commission:
- Rishi Sharma
- Shawn Narum
- Jon Hess
- Stephanie Harmon
- Vanessa Jacobson
- Rebeka Horn
- Jeff Stephenson

Pacific States Marine Fisheries Commission:
- John Tenney
- Nichol Tacreto
- Kristin Wright

Idaho Department of Fish and Game:
- Bill Schrader
- Tim Copeland
- J. Lance Hebdon
- Carlos Camacho

IDFG Eagle Fish Genetics Lab:
- Amanda Boone (PSMFC)
- Grant Bruner (IDFG)
- Dan Eardley (PSMFC)
- Kelly Heindel (PSMFC)
- Dylan Kovis (PSMFC)
- Lynn Schrader (PSMFC)

NOAA Northwest Fisheries Science Center:
- Darren Ogden
- Tiffani Marsh
- Chris Jordan
- Gordon Axel
- Sandy Downing

NOAA NMFS/FE Electronics Shop:
- Gabriel Brooks

Nez Perce Tribe:
- Jay Hesse
- Jason Vogel
- Cameron Albee

Quantitative Consultants:
- Jody White
- Bryce Semmens

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Table 1. A description of PIT tag arrays in the Snake River basin used for estimation of abundance, life history characteristics, and genetic diversity for steelhead. The genetic stock, major population group (MPG), population, site code (Array ID), and site description including GPS data are shown. Fish detected at locations denoted NA* in column may belong to more than one population and as a result detections at these arrays were excluded from genetic diversity summaries.

Genetic Stock	MPG	Population	Array ID	Site Description	Spawn Years Operational	Latitude	Longitude
LOCLWR	Clearwater R	CRLMA-s	CLC	Clear Creek near Kooskia NFH	2015-2018	-115.950184	46.132739
LOCLWR	Clearwater R	CRLMA-s	HLM	Potlatch River near Helmer	<2010-present	-116.428412	46.799006
LOCLWR	Clearwater R	CRLMA-s	JUL	Potlatch River near Juliaetta	2008-2014	-116.709318	46.565323
LOCLWR	Clearwater R	CRLMA-s	KHS	Big Bear Cr. @ Kendrick HS	<2010-present	-116.646846	46.619115
LOCLWR	Clearwater R	CRLMA-s	LAP	Lapwai Creek, near its mouth	2015-present	-116.812535	46.443273
LOCLWR	Clearwater R	CRLMA-s	MIS	Mission Creek	<2010-2019	-116.735597	46.367062
LOCLWR	Clearwater R	CRLMA-s	PCM	Pine Creek Mouth, Potlatch R.	2015-present	-116.596836	46.630673
LOCLWR	Clearwater R	CRLMA-s	SWT	Sweetwater Cr. near its mouth	<2010-present	-116.795757	46.369217
LOCLWR	Clearwater R	CRLMA-s	WEB	Webb Creek	2010-present	-116.831974	46.325992
LOCLWR	Clearwater R	CRLMA-s	BIGBEC	Big Bear Creek, Potlatch River	2010-2016	-116.621142	46.730007
LOCLWR	Clearwater R	CRLMA-s	LBEARC	Little Bear Creek, Potlatch River watershed	2010-2012	-116.707271	46.674010
LOCLWR	Clearwater R	CRLMA-s	POTREF	East Fork Potlatch River	2010-2019	-116.349116	46.847724
LOCLWR	Clearwater R	CRLMA-s	POTRWF	West Fork Potlatch River	2010	-116.451557	46.923856
SFCLWR	Clearwater R	CRSFC-s	CRT	Crooked River Satellite Fac.	2012-2015	-115.527782	45.820931
SFCLWR	Clearwater R	CRSFC-s	RRT	Red River Satellite Facility	2012-2015	-115.347147	45.711179
SFCLWR	Clearwater R	CRSFC-s	CROTRP	Crooked River Trap	2013-2016	-115.527745	45.821205
SFCLWR	Clearwater R	CRLOL-s	LC1	Lower Lolo Creek at rkm 21	2012-present	-115.976159	46.294360
SFCLWR	Clearwater R	CRLOL-s	LC2	Upper Lolo Creek at rkm 25	2012-present	-115.933747	46.290498
SFCLWR	Clearwater R	CRSFC-s	SC1	Lower SF Clearwater R at rkm 1	2012-present	-115.981313	46.137022
SFCLWR	Clearwater R	CRSFC-s	SC2	Lower SF Clearwater R at rkm 2	2012-present	-115.977760	46.127209
SFCLWR	Clearwater R	CRSFC-s	REDTRP	Red River Trap	2010-2019	-115.434575	45.793850
UPCLWR	Clearwater R	CRSEL-s	SW1	Lower Selway River Array	2017-present	-115.565886	46.110318
UPCLWR	Clearwater R	CRSEL-s	SW2	Upper Selway River Array	2018-present	-115.515533	46.085934
UPCLWR	Clearwater R	CRLOC-s	LRL	Lower Lochsa River Array Site	2017-present	-115.596497	46.145727
UPCLWR	Clearwater R	CRLOC-s	LRU	Lochsa River Upper Site	2018-present	-115.589663	46.163821
UPCLWR	Clearwater R	CRLOC-s	FISTRP	Fish Creek Trap	2010-2019	-115.355127	46.340115
GRROND	Grande Ronde R	GRJOS-s	JOC	Joseph Creek ISA @ km 3	2011-present	-117.016408	46.030237
GRROND	Grande Ronde R	GRJOS-s	JOSEPC	Joseph Creek, Grande Ronde R. Basin	2011-present	-117.209152	45.899793
GRROND	Grande Ronde R	GRLMT-s	WEN	Wenaha River Mouth	2019-present	-117.454124	45.946151
GRROND	Grande Ronde R	GRUMA-s	CCW	Catherine Creek Ladder/Weir	2015-present	-117.828617	45.190964
GRROND	Grande Ronde R	GRUMA-s	UGR	Upper Grande Ronde at rkm 155	2013-present	-117.903379	45.593520
GRROND	Grande Ronde R	GRUMA-s	UGS	Upper Grande Ronde Starkey	2018-present	-118.388958	45.248955
GRROND	Grande Ronde R	GRUMA-s	CATHEW	Catherine Creek Weir	2010-2019	-117.828617	45.190964

Table 1. Continued

Genetic Stock	MPG	Population	Array ID	Site Description	Spawn Years Operational	Latitude	Longitude
GRROND	Grande Ronde R	GRUMA-s	LOOKGC	Lookingglass Creek	2010-2019	-117.960012	45.757199
GRROND	Grande Ronde R	GRWAL-s	WR1	Wallowa River at river km 14	2014-present	-117.733757	45.633679
GRROND	Grande Ronde R	GRWAL-s	WR2	Wallowa River at rkm 32	2019-present	-117.579223	45.594466
GRROND	Grande Ronde R	GRWAL-s	BCANF	Big Canyon Facility	2010-2017	-117.698633	45.61904
GRROND	Grande Ronde R	GRWAL-s	LOSTIW	Lostine River Weir	2011-2019	-117.484500	45.543266
GRROND	Grande Ronde R	GRWAL-s	WALH	Wallowa Hatchery	2011-2018	-117.301573	45.417567
IMNAHA	Imnaha R	IRMAI-s	BSC	Big Sheep Creek ISA at km 6	2011-present	-116.850735	45.506482
IMNAHA	Imnaha R	IRMAI-s	CMP	Camp Creek at rkm 2 - Imnaha	2013-present	-116.866939	45.551819
IMNAHA	Imnaha R	IRMAI-s	COC	Cow Creek ISA @ stream mouth	2011-present	-116.744037	45.76774
IMNAHA	Imnaha R	IRMAI-s	CZY	Crazyman Creek at 0.6 km	2014-present	-116.844780	45.22930
IMNAHA	Imnaha R	IRMAI-s	IR1	Lower Imnaha R. ISA @ km 7	2011-present	-116.750231	45.761052
IMNAHA	Imnaha R	IRMAI-s	IR2	Lower Imnaha R. ISA @ km 10	2011-present	-116.764304	45.742702
IMNAHA	Imnaha R	IRMAI-s	IR3	Upper Imnaha R. ISA @ km 41	2011-present	-116.804096	45.489957
IMNAHA	Imnaha R	IRMAI-s	IR4	Imnaha Weir Downstream Array	2017-present	-116.868774	45.194460
IMNAHA	Imnaha R	IRMAI-s	IR5	Imnaha Weir Upstream Array	2017-present	-116.868593	45.193188
IMNAHA	Imnaha R	IRMAI-s	DRY2C	Dry Creek - tributary to Imnaha R.	2014-2016	-116.867075	45.121790
IMNAHA	Imnaha R	IRMAI-s	FREEZC	Freezeout Creek - tributary to Imnaha R.	2014-2019	-116.762169	45.350411
IMNAHA	Imnaha R	IRMAI-s	GUMBTC	Gumboot Creek, Imnaha R. Basin	2012-2017	-116.941111	45.155719
IMNAHA	Imnaha R	IRMAI-s	HORS3C	Horse Creek, Imnaha R. Basin	2010-2013	-116.727273	45.549508
IMNAHA	Imnaha R	IRMAI-s	LSHEEF	Little Sheep Facility	2011-2018	-116.930252	45.477819
IMNAHA	Imnaha R	IRMAI-s	MAHOGC	Mahogany Creek, Imnaha R. Basin	2011-2013	-116.899988	45.200210
MFSALM	Salmon R	MFBIG-s	TAY	Big Creek at Taylor Ranch	<2010-present	-114.853817	45.103532
SFSALM	Salmon R	SFMAI-s	ESS	EFSF Salmon R. at Parks Cr.	2010-present	-115.533150	44.956205
SFSALM	Salmon R	SFMAI-s	KRS	SF Salmon R. at Krassel Cr.	2009-present	-115.726994	44.978472
SFSALM	Salmon R	NA*	SFG	SF Salmon at Guard Station Br.	2010-present	-115.579712	45.175659
SFSALM	Salmon R	SFMAI-s	YPP	Yellow Pine Pit Lake	2019-present	-115.333883	44.928995
SFSALM	Salmon R	SFSEC-s	ZEN	Secesh River at Zena Cr. Ranch	2010-present	-115.733020	45.033300
LSNAKE	Lower Snake R	SNASO-s	ACB	Asotin Cr. at Cloverland Brdg.	2010-present	-117.108679	46.325584
LSNAKE	Lower Snake R	SNASO-s	ACM	Asotin Creek near mouth	2012-present	-117.055707	46.341368
LSNAKE	Lower Snake R	SNASO-s	AFC	No./So. Fk Asotin Cr. Jct. ISA	2010-present	-117.292147	46.272487
LSNAKE	Lower Snake R	SNASO-s	CCA	Lower Charley Creek ISA	2010-present	-117.282497	46.288458
LSNAKE	Lower Snake R	SNASO-s	ALMOTC	Almota Creek - tributary to Snake River	2011-2016	-117.359348	46.701606
LSNAKE	Lower Snake R	SNASO-s	ALPOWC	Alpowa Creek, Lower Snake R. River	2010-2019	-117.398266	46.402354
LSNAKE	Lower Snake R	SNASO-s	ASOTIC	Asotin Creek, Snake River above Clarkston, WA	2010-2019	-117.181953	46.330643
LSNAKE	Lower Snake R	SNASO-s	GEORGC	George Creek, Asotin Creek watershed	2010-2019	-117.198841	46.192301
LSNAKE	Lower Snake R	SNASO-s	TENMC2	Tenmile Creek, tributary to Snake River	2010-11, 2014-15,2018-19	-117.041854	46.195250

Table 1. Continued

Genetic Stock	MPG	Population	Array ID	Site Description	Spawn Years Operational	Latitude	Longitude
LSNAKE	Lower Snake R	SNTUC-s	LTR	Lower Tucannon River	<2010-present	118.162901	46.544192
LSNAKE	Lower Snake R	SNTUC-s	MTR	Middle Tucannon River	2012-present	118.016274	46.505239
LSNAKE	Lower Snake R	SNTUC-s	UTR	Upper Tucannon River	2012-present	117.738342	46.415922
LSNAKE	Lower Snake R	SNTUC-s	PENAWC	Penawawa Creek - tributary to Snake River	2013-2019	117.541357	46.747772
LSNAKE	Lower Snake R	SNTUC-s	TUCH	Tucannon River Hatchery	2010-2018	117.662840	46.320108
UPSALM	Salmon R	SREFS-s	SALEFT	East Fork Salmon R. Trap	2011-2019	114.428956	44.118413
UPSALM	Salmon R	SRLEM-s	18M	Eighteenmile Creek	2018-present	113.353660	44.682795
UPSALM	Salmon R	SRLEM-s	BHC	Bohannon Creek Lemhi R Basin	2012-present	113.746897	45.112189
UPSALM	Salmon R	SRLEM-s	BTL	Lower Big Timber, Lemhi Basin	2014-present	113.374118	44.697568
UPSALM	Salmon R	SRLEM-s	BTM	Big Timber Creek - Middle	2015-2018	113.377624	44.660444
UPSALM	Salmon R	SRLEM-s	BTU	Big Timber Creek - Upper	2016-2018	113.397036	44.613860
UPSALM	Salmon R	SRLEM-s	CAC	Canyon Creek ISA @ km 1	2011-present	113.365281	44.691090
UPSALM	Salmon R	SRLEM-s	CRC	Carmen Creek, Salmon R. Basin	2014-2017	113.893466	45.246485
UPSALM	Salmon R	SRLEM-s	HYC	Hayden Creek In-stream Array	2010-present	113.631937	44.861654
UPSALM	Salmon R	SRLEM-s	KEN	Kenney Creek In-stream Arrays	2011-present	113.654847	45.026792
UPSALM	Salmon R	SRLEM-s	LB8	Big Eightmile Creek	2016-2018	113.462458	44.738218
UPSALM	Salmon R	SRLEM-s	LBS	Big Springs Creek	2015-2019	113.433214	44.727349
UPSALM	Salmon R	SRLEM-s	LCL	Lee Creek, Lemhi R. Basin	2015-2018	113.474641	44.747074
UPSALM	Salmon R	SRLEM-s	LLR	Lower Lemhi River	2010-present	113.885278	45.176475
UPSALM	Salmon R	SRLEM-s	LLS	Lemhi Little Springs Instream	2012-present	113.545027	44.780552
UPSALM	Salmon R	SRLEM-s	LRW	Lemhi River Weir	2010-present	113.624721	44.865960
UPSALM	Salmon R	SRLEM-s	WPC	Wimpey Creek, Lemhi R. Basin	2014-2018	113.720497	45.097938
LOSALM	Salmon R	SRLSR-s	RAPH	Rapid River Hatchery	2010-2019	116.394575	45.353681
UPSALM	Salmon R	SRNFS-s	NFS	North Fork Salmon R.	2017-present	113.992002	45.408645
UPSALM	Salmon R	NA*	USE	Upper Salmon R. at rkm 437	2013-present	113.916319	45.028530
UPSALM	Salmon R	NA*	USI	Upper Salmon R. at rkm 460	2013-present	113.964145	44.889763
UPSALM	Salmon R	SRPAH-s	PAHH	Pahsimeroi Hatchery	2011-2019	114.039471	44.684139
UPSALM	Salmon R	SRPAN-s	PCA	Panther Creek Array	2018-present	114.358101	45.295253
UPSALM	Salmon R	SRUMA-s	RFL	Redfish Lake Creek	2019-present	114.905043	44.164727
UPSALM	Salmon R	SRUMA-s	STL	Sawtooth Hatchery Adult Trap	2010-2018	114.883772	44.153369
UPSALM	Salmon R	SRUMA-s	VC1	Valley Creek, Upstream Site	<2010-present	114.942150	44.218672
UPSALM	Salmon R	SRUMA-s	VC2	Valley Creek, Downstream Site	<2010-present	114.931460	44.221900
UPSALM	Salmon R	SRUMA-s	YFK	Yankee Fork Salmon R.	2012-present	114.720453	44.287737

Table 2. A description of PIT tag arrays in the Snake River basin used for estimation of abundance, life history characteristics, and genetic diversity for Chinook Salmon. The genetic stock, major population group (MPG), population, site code (Array ID), and site description including GPS data are shown. Fish detected at locations denoted NA* in population column belong to more than one population and as a result individuals detected at these locations were excluded from genetic diversity summaries.

Genetic Stock	MPG	Population	Array ID	Site Description	Spawn Years Operational	Latitude	Longitude
HELLSC	Clearwater R - Dry	CRLAP	LAP	Lapwai Creek, near its mouth	<2010-present	-116.812535	46.443273
HELLSC	Clearwater R - Dry	CRLAP	MIS	Mission Creek	2010-present	-116.735597	46.367062
HELLSC	Clearwater R - Dry	CRLAP	SWT	Sweetwater Cr. near its mouth	<2010-present	-116.795757	46.369217
HELLSC	Clearwater R - Dry	CRLAP	WEB	Webb Creek	2010-present	-116.831974	46.325992
HELLSC	Clearwater R - Dry	SCLAW	CLC	Clear Creek near Kooskia NFH	2015-2018	-115.950184	46.132739
HELLSC	Clearwater R - Dry	SCLAW	KOOS	Kooskia National Fish Hatchery	2011-2013, 2017, 2018	-115.946826	46.129706
HELLSC	Clearwater R - Dry	SCUMA	SC1	Lower SF Clearwater R at rkm 1	2012-present	-115.981313	46.137022
HELLSC	Clearwater R - Dry	SCUMA	SC2	Lower SF Clearwater R at rkm 2	2012-present	-115.977760	46.127209
HELLSC	Clearwater R - Dry	SCUMA	CRT	Crooked River Satellite Fac.	2012-2015	-115.527782	45.820931
HELLSC	Clearwater R - Dry	SCUMA	RRT	Red River Satellite Facility	2012-2015	-115.347147	45.711179
HELLSC	Clearwater R - Dry	SCUMA	CROTRP	Crooked River Trap	2010-2019	-115.527745	45.821205
HELLSC	Clearwater R - Dry	SCUMA	REDR	Red River	2010-2019	-115.354049	45.710066
HELLSC	Clearwater R - Dry	CRPOT	HLM	Potlatch River near Helmer	<2010-present	-116.428412	46.799006
HELLSC	Clearwater R - Dry	CRPOT	JUL	Potlatch River near Juliaetta	<2010-2014	-116.709318	46.565323
HELLSC	Clearwater R - Dry	CRPOT	KHS	Big Bear Cr. @ Kendrick HS	<2010-present	-116.646846	46.619115
HELLSC	Clearwater R - Dry	CRPOT	PCM	Pine Creek Mouth, Potlatch R.	<2010-present	-116.596836	46.630673
HELLSC	Clearwater R - Wet	CRLOC	LRL	Lower Lochsa River Array Site	2017-present	-115.596497	46.145727
HELLSC	Clearwater R - Wet	CRLOC	LRU	Lochsa River Upper Site	2018-present	-115.589663	46.163821
HELLSC	Clearwater R - Wet	CRLOL	LC1	Lower Lolo Creek at rkm 21	2012-present	-115.976160	46.294360
HELLSC	Clearwater R - Wet	CRLOL	LC2	Upper Lolo Creek at rkm 25	2012-present	-115.933747	46.290498
HELLSC	Clearwater R - Wet	SEMEA	SW1	Lower Selway River Array	2017-present	-115.565886	46.110318
HELLSC	Clearwater R - Wet	SEMEA	SW2	Upper Selway River Array	2018-present	-115.515533	46.085934
HELLSC	Grande Ronde R	GRCAT	CCW	Catherine Creek Ladder/Weir	2015-present	-117.828617	45.190964
HELLSC	Grande Ronde R	GRCAT	CATHEW	Catherine Creek Weir	2010-2019	-117.828617	45.190964
HELLSC	Grande Ronde R	GRLOO	LOOKGC	Lookingglass Creek	2010-2019	-117.960012	45.757199
HELLSC	Grande Ronde R	NA*	WR1	Wallowa River at river km 14	2014-present	-117.733757	45.633679
HELLSC	Grande Ronde R	GRLOS	WR2	Wallowa River at rkm 32	2019-present	-117.579223	45.594466
HELLSC	Grande Ronde R	GRLOS	LOSTIW	Lostine River Weir	2010-2019	-117.484500	45.543266

Table 2. Continued

Genetic Stock	MPG	Population	Array ID	Site Description	Spawn Years Operational	Latitude	Longitude
HELLSC	Grande Ronde R	GRUMA	UGS	Upper Grande Ronde Starkey	2018-present	-118.388958	45.248955
HELLSC	Grande Ronde R	GRUMA	GRANDW	Grande Ronde River Weir	2012-2019	-118.388983	45.248961
HELLSC	Grande Ronde R	GRWEN	WEN	Wenaha River Mouth	2019-present	-117.454124	45.946151
HELLSC	Imnaha R	IRBSH	BSC	Big Sheep Creek ISA at km 6	2011-present	-116.850735	45.506482
HELLSC	Imnaha R	IRBSH	CMP	Camp Creek at rkm 2 - Imnaha	2013-present	-116.866939	45.551819
HELLSC	Imnaha R	IRMAI	COC	Cow Creek ISA @ stream mouth	2011-present	-116.744037	45.767740
HELLSC	Imnaha R	IRMAI	IML	Imnaha River Weir Adult Ladder	2015-present	-116.868663	45.194276
HELLSC	Imnaha R	IRMAI	IR1	Lower Imnaha River ISA @ km 7	2011-present	-116.750231	45.761052
HELLSC	Imnaha R	IRMAI	IR2	Lower Imnaha River ISA @ km 10	2011-present	-116.764304	45.742702
HELLSC	Imnaha R	IRMAI	IR3	Upper Imnaha River ISA @ km 41	2011-present	-116.804096	45.489957
HELLSC	Imnaha R	IRMAI	IR4	Imnaha Weir Downstream Array	2017-present	-116.868774	45.194460
HELLSC	Imnaha R	IRMAI	IR5	Imnaha Weir Upstream Array	2017-present	-116.868593	45.193188
HELLSC	Imnaha R	IRMAI	DRY2C	Dry Creek - tributary to Imnaha River		-116.867075	45.121790
HELLSC	Imnaha R	IRMAI	IMNAHW	Imnaha River Weir	2010-2019	-116.868664	45.194276
TUCANO	Lower Snake R	SNASO	ACB	Asotin Cr. at Cloverland Brdg.	2010-present	-117.108679	46.325584
TUCANO	Lower Snake R	SNASO	ACM	Asotin Creek near mouth	2012-present	-117.055707	46.341368
TUCANO	Lower Snake R	SNASO	AFC	No./So. Fk Asotin Cr. Jct. ISA	2010-present	-117.292147	46.272487
TUCANO	Lower Snake R	SNASO	CCA	Lower Charley Creek ISA	2010-present	-117.282497	46.288458
TUCANO	Lower Snake R	SNASO	ASOTIC	Asotin Creek, Snake River above Clarkston, WA	2010, 2014	-117.181953	46.330643
TUCANO	Lower Snake R	SNTUC	LTR	Lower Tucannon River	<2010-present	-118.162901	46.544192
TUCANO	Lower Snake R	SNTUC	MTR	Middle Tucannon River	2012-present	-118.016274	46.505239
TUCANO	Lower Snake R	SNTUC	UTR	Upper Tucannon River	2012-present	-117.738342	46.415922
TUCANO	Lower Snake R	SNTUC	TUCH	Tucannon River Hatchery	2016-2018	-117.662840	46.320108
MFSALM	Middle Fork Salmon R	MFBEA	BRC	Bear Valley Adult Video Weir	2014-present	-115.284171	44.427939
MFSALM	Middle Fork Salmon R	MFBIG	TAY	Big Creek at Taylor Ranch	<2010-present	-114.853817	45.103532
HELLSC	South Fork Salmon R	SRLSR	RAPH	Rapid River Hatchery	2010-2019	-116.394575	45.353681
SFSALM	South Fork Salmon R	SFEFS	ESS	EFSF Salmon River at Parks Cr.	2010-present	-115.533150	44.956205
SFSALM	South Fork Salmon R	SFEFS	YPP	Yellow Pine Pit Lake	2019-present	-115.333883	44.928995
SFSALM	South Fork Salmon R	SFEFS	JOHNSC	Johnson Creek	2010-2019	-115.548602	44.733928
SFSALM	South Fork Salmon R	SFMAI	KRS	SF Salmon River at Krassel Cr.	<2010-present	-115.726994	44.978472
SFSALM	South Fork Salmon R	SFMAI	SFG	SF Salmon at Guard Station Br.	2010-present	-115.579712	45.175659
SFSALM	South Fork Salmon R	SFMAI	STR	SF Salmon Satellite Facility	2011-present	-115.702953	44.666874
SFSALM	South Fork Salmon R	SFSEC	ZEN	Secesh River at Zena Cr. Ranch	2010-present	-115.733020	45.033300
UPSALM	Upper Salmon R	SREFS	SALEFT	East Fork Salmon River Trap		-114.428956	44.118413

Table 2. Continued

Genetic Stock	MPG	Population	Array ID	Site Description	Spawn Years Operational	Latitude	Longitude
UPSALM	Upper Salmon R	SRLEM	18M	Eighteenmile Creek	2018-present	-113.353660	44.682795
UPSALM	Upper Salmon R	SRLEM	AGC	Agency Creek, Lemhi R. Basin	2014-2016	-113.639543	44.956739
UPSALM	Upper Salmon R	SRLEM	BHC	Bohannon Creek Lemhi R Basin	2012-present	-113.746897	45.112189
UPSALM	Upper Salmon R	SRLEM	BTL	Lower Big Timber, Lemhi Basin	2014-present	-113.374118	44.697568
UPSALM	Upper Salmon R	SRLEM	BTM	Big Timber Creek - Middle	2015-2018	-113.377624	44.660444
UPSALM	Upper Salmon R	SRLEM	BTU	Big Timber Creek - Upper	2016-2018	-113.397036	44.613860
UPSALM	Upper Salmon R	SRLEM	CAC	Canyon Creek ISA @ km 1	2011-present	-113.365281	44.691090
UPSALM	Upper Salmon R	SRLEM	CRC	Carmen Creek, Salmon R. Basin	2014-2017	-113.893466	45.246485
UPSALM	Upper Salmon R	SRLEM	HEC	Hawley Cr/18 Mile Cr Array	2014-2015	-113.311550	44.668594
UPSALM	Upper Salmon R	SRLEM	HYC	Hayden Creek In-stream Array	2010-present	-113.631937	44.861654
UPSALM	Upper Salmon R	SRLEM	KEN	Kenney Creek In-stream Arrays	2011-present	-113.654847	45.026792
UPSALM	Upper Salmon R	SRLEM	LB8	Big Eightmile Creek	2016-2018	-113.462458	44.738218
UPSALM	Upper Salmon R	SRLEM	LBS	Big Springs Creek	2015-2019	-113.433214	44.727349
UPSALM	Upper Salmon R	SRLEM	LCL	Lee Creek, Lemhi R. Basin	2015-2018	-113.474641	44.747074
UPSALM	Upper Salmon R	SRLEM	LLR	Lower Lemhi River	2010-present	-113.885278	45.176475
UPSALM	Upper Salmon R	SRLEM	LLS	Lemhi Little Springs Instream	2012-present	-113.545027	44.780552
UPSALM	Upper Salmon R	SRLEM	LRW	Lemhi River Weir	2010-present	-113.624721	44.865960
UPSALM	Upper Salmon R	SRLEM	WPC	Wimpey Creek, Lemhi R. Basin	2014-2018	-113.720497	45.097938
UPSALM	Upper Salmon R	SRLMA	USE	Upper Salmon River at rkm 437	2013-present	-113.916319	45.028530
UPSALM	Upper Salmon R	SRLMA	USI	Upper Salmon River at rkm 460	2013-present	-113.964145	44.889763
UPSALM	Upper Salmon R	SRNFS	NFS	North Fork Salmon River	2017-present	-113.992002	45.408645
UPSALM	Upper Salmon R	SRPAH	PAHH	Pahsimeroi Hatchery	2010-2019	-114.039471	44.684139
UPSALM	Upper Salmon R	SRPAN	PCA	Panther Creek Array	2018-present	-114.358101	45.295253
UPSALM	Upper Salmon R	SRUMA	RFL	Redfish Lake Creek	2018-present	-114.905043	44.164727
UPSALM	Upper Salmon R	SRUMA	STL	Sawtooth Hatchery Adult Trap	2010-2018	-114.883772	44.153369
UPSALM	Upper Salmon R	SRVAL	VC1	Valley Creek, Upstream Site	<2010-present	-114.942150	44.218672
UPSALM	Upper Salmon R	SRVAL	VC2	Valley Creek, Downstream Site	<2010-present	-114.931461	44.221900
UPSALM	Upper Salmon R	SRYFS	YFK	Yankee Fork Salmon River	2012-present	-114.720453	44.287737

Table 3. STADEM model estimates of total passage and 95% confidence intervals of wild adult steelhead passing above Lower Granite Dam for spawn years 2010-2019. Additionally, the total number of wild PIT-tagged adult steelhead released at the LGR adult trap, and the subsequent number and proportion of the tag group detected at sites used within the DABOM model by spawn year are presented. Lastly, the number of PIT-tagged adult steelhead that were observed (detected) and genotyped is reported.

Spawn Year	Wild Abundance	Lower CI	Upper CI	PIT Tags Released	Observed PIT Tags (proportion of released tags)	Observed and Genotyped PIT Tags (proportion of observed tags)
2010	45,093	42,515	49,185	4,011	744 (0.19)	625 (0.84)
2011	45,866	42,625	49,528	4,648	1,243 (0.27)	1,150 (0.93)
2012	40,373	38,613	42,879	4,111	1,343 (0.33)	1,249 (0.93)
2013	25,049	23,416	27,511	3,391	1,371 (0.40)	1,367 (0.99)
2014	28,107	24,760	32,228	3,436	1,388 (0.40)	1,385 (0.99)
2015	47,816	45,058	51,592	3,929	1,522 (0.39)	1,509 (0.99)
2016	36,082	33,829	38,642	4,302	1,558 (0.36)	1,532 (0.98)
2017	15,433	14,470	16,716	3,017	1,178 (0.39)	1,172 (0.99)
2018	10,096	9,376	10,888	2,306	1,080 (0.47)	1,025 (0.95)
2019	10,389	8,366	18,348	1,764	935 (0.53)	905 (0.97)

Table 4. The average, minimum and maximum proportion of the steelhead population abundance as a proportion of the total wild adult run at large over Lower Granite Dam including the number of spawn years with abundance estimates and the estimated monitoring coverage of the population.

MPG	ICTRT Population	Description	Mean Proportion of LGR	Minimum Proportion	Maximum Proportion	Number of Spawn Years	Population Coverage (%)
Lower Snake	SNASO-s	Asotin Creek	0.032	0.020	0.041	10	52
	SNTUC-s*	Tucannon River	0.022*	0.016*	0.047*	10	-
Clearwater	CRLMA-s	lower mainstem	0.023	0.012	0.031	10	13
	CRLOC-s	Lochsa	0.039	0.035	0.043	2	99
	CRLOL-s	Lolo Creek	0.012	0.008	0.016	7	95
	CRSEL-s	Selway River	0.028	0.026	0.030	2	99
	CRSFC-s	South Fork Clearwater	0.023	0.012	0.032	8	100
Grande Ronde River	GRJOS-s	Joseph Creek	0.057	0.038	0.074	9	99
	GRLMT-s	lower mainstem	0.040	0.040	0.040	1	99
	GRUMA-s	upper mainstem	0.044	0.037	0.051	7	88
	GRWAL-s	Wallowa River	0.031	0.019	0.061	6	95
Imnaha	IRMAI-s	Imnaha River	0.067	0.055	0.090	9	99
Salmon River	MFBIG-s	Big, Camas, Loon creeks	0.011	0.004	0.018	9	37
	SFMAI-s	South Fork Salmon River	0.028	0.015	0.048	10	84
	SFSEC-s	Secesh River	0.004	0.002	0.008	10	99
	SREFS-s	East Fork Salmon River	0.001	0.001	0.003	4	99
	SRLEM-s	Lemhi River	0.010	0.006	0.015	10	96
	SRLSR-s	Little Salmon, Rapid River	0.001	0.000	0.003	10	-
	SRNFS-s	North Fork Salmon River	0.011	0.004	0.021	3	78
	SRPAH-s	Pahsimeroi	0.003	0.001	0.005	8	99
	SRPAN-s	Panther Creek	0.009	0.008	0.010	2	76
	SRUMA-s	upper mainstem	0.008	0.004	0.013	10	47

Table 5. Mean, minimum, and maximum values of H_e for steelhead in the Snake River basin summarized by MPG and population. Only populations with greater than 20 samples detected in a given year are reported. Values represent mean estimates averaged across spawn years. The number of years for which there is an estimate of H_e is identified in the column *n*.

MPG	**Population**	***n***	**Avg H_e**	**Min H_e**	**Max H_e**
Clearwater R	CRLMA-s	10	30.8%	30.3%	31.1%
	CRLOC-s	4	28.0%	27.6%	28.3%
	CRLOL-s	7	28.0%	27.2%	28.4%
	CRSEL-s	3	28.5%	28.3%	28.7%
	CRSFC-s	7	28.3%	27.8%	28.7%
Grande Ronde R	GRJOS-s	9	30.3%	30.1%	30.6%
	GRLMT-s	1	30.2%	-	-
	GRUMA-s	9	30.6%	29.7%	31.0%
	GRWAL-s	7	30.9%	30.6%	31.4%
Imnaha R	IRMAI-s	9	30.2%	30.0%	30.4%
Lower Snake R	SNASO-s	10	30.9%	29.8%	31.4%
	SNTUC-s	10	31.1%	30.5%	31.8%
Salmon R	MFBIG-s	8	29.3%	28.9%	30.3%
	SFMAI-s	10	29.7%	29.4%	30.0%
	SFSEC-s	2	28.7%	28.6%	28.7%
	SRLEM-s	9	31.9%	31.5%	32.5%
	SRNFS-s	1	30.7%	-	-
	SRPAN-s	1	29.6%	-	-
	SRUMA-s	6	29.6%	29.1%	29.9%

Table 6. Values of N_b for steelhead in the Snake River basin summarized by MPG and population. Only populations with greater than 20 samples for a given brood year are reported upon.

MPG	Population	Brood Year	N_b
Clearwater	CRLMA-s	2005	532
		2006	301
		2007	258
		2008	254
		2009	207
		2010	230
		2011	348
		2012	267
		2013	166
		2014	197
	CRLOC-s	2010	319
		2011	311
		2012	251
		2013	265
		2014	183
	CRLOL-s	2007	131
		2008	144
		2009	111
		2010	225
		2011	291
	CRSEL-s	2013	207
		2014	442
	CRSFC-s	2006	296
		2007	214
		2008	130
		2009	209
		2010	277
		2011	200
		2012	41
Grande Ronde	GRJOS-s	2006	342
		2007	364
		2008	410
		2009	396
		2010	563
		2011	601
		2012	266
		2013	263
		2014	364

Table 6. Continued

MPG	Population	Brood Year	N_b
Grande Ronde	GRJOS-s	2015	162
	GRLMT-s	2014	284
		2015	421
	GRUMA-s	2006	264
		2007	254
		2008	349
		2009	379
		2010	499
		2011	463
		2012	380
		2013	291
		2014	272
		2015	229
	GRWAL-s	2009	414
		2010	330
		2011	308
		2012	339
		2013	286
		2014	273
		2015	250
Imnaha	IRMAI-s	2005	424
		2006	490
		2007	632
		2008	382
		2009	496
		2010	574
		2011	542
		2012	508
		2013	394
		2014	408
		2015	195
Salmon River	MFBIG-s	2005	206
		2006	154
		2007	96
		2008	133
		2009	179
		2010	214
		2013	265
	SFMAI-s	2004	284
		2005	431
		2006	311

Table 6. Continued

MPG	Population	Brood Year	N_b
Salmon River	SFMAI-s	2007	226
		2008	308
		2009	195
		2010	303
		2011	255
		2013	219
	SFSEC-s	2005	108
Lower Snake River	SNASO-s	2005	330
		2006	400
		2007	270
		2008	304
		2009	316
		2010	381
		2011	404
		2012	281
		2013	552
		2014	302
	SNTUC-s	2005	616
		2006	363
		2007	272
		2008	154
		2009	186
		2010	334
		2011	373
		2012	272
		2013	520
		2014	359
		2015	352
	SRLEM-s	2006	161
		2007	199
		2008	241
		2009	163
		2010	293
		2011	202
		2012	206
	SRUMA-s	2006	229
		2007	236
		2008	154
		2010	404
		2011	336

Table 7. The genetic composition of steelhead that were sampled at Lower Granite Dam, detected at a PIT tag array in the Snake River basin, and never detected at a PIT tag array determined via genetic stock identification (GSI). Average, minimum, and maximum values cover spawn years 2010 – 2019.

	GSI at Lower Granite Dam		GSI and detected at PIT array		GSI and never detected at PIT array	
Genetic Stock	**Average**	**Range**	**Average**	**Range**	**Average**	**Range**
GRROND	0.268	(0.155-0.405)	0.260	(0.151-0.398)	0.263	(0.192-0.422)
IMNAHA	0.127	(0.045-0.196)	0.123	(0.043-0.192)	0.049	(0.034-0.096)
LOCLWR	0.088	(0.036-0.130)	0.085	(0.035-0.127)	0.085	(0.061-0.110)
LOSALM	0.026	(0.010-0.040)	0.026	(0.009-0.040)	0.037	(0.011-0.049)
LSNAKE	0.132	(0.101-0.192)	0.129	(0.098-0.190)	0.128	(0.091-0.200)
MFSALM	0.043	(0.019-0.083)	0.044	(0.019-0.087)	0.102	(0.082-0.123)
SFCLWR	0.062	(0.005-0.116)	0.060	(0.006-0.114)	0.067	(0.026-0.146)
SFSALM	0.090	(0.024-0.194)	0.096	(0.027-0.208)	0.016	(0.009-0.023)
UPCLWR	0.057	(0.010-0.160)	0.056	(0.010-0.152)	0.093	(0.020-0.158)
UPSALM	0.108	(0.049-0.163)	0.121	(0.069-0.159)	0.160	(0.081-0.208)

Table 8. STADEM model estimated total passage and 95% confidence intervals of wild Chinook Salmon passing above Lower Granite Dam for spawn years 2010-2019. Additionally, the total number of wild PIT-tagged adult Chinook Salmon released at the LGR adult trap, and the subsequent number and proportion of the tag group observed at sites used within the DABOM model by spawn year are presented. Lastly, the number of PIT-tagged adult Chinook Salmon that were observed (detected) and genotyped is reported.

Spawn Year	Wild Abundance	Lower CI	Upper CI	PIT Tags Released	Observed PIT Tags (proportion of released tags)	Observed and Genotyped PIT Tags (proportion of observed tags)
2010	26,948	24,274	30,005	1,197	391 (0.33)	383 (0.99)
2011	24,694	23,346	26,058	2,758	1,023 (0.37)	1,005 (0.98)
2012	21,329	19,667	23,787	2,167	940 (0.43)	932 (0.99)
2013	19,051	17,972	20,433	2,997	1,514 (0.51)	1,494 (0.99)
2014	28,491	26,423	30,484	3,380	1,939 (0.57)	1,897 (0.98)
2015	23,829	21,981	26,053	2,170	1,197 (0.55)	1,104 (0.92)
2016	17,244	16,366	18,567	3,051	1,623 (0.53)	1,594 (0.98)
2017	5,159	4,716	5,670	1,200	556 (0.46)	555 (0.99)
2018	6,997	6,408	7,656	1,467	907 (0.62)	897 (0.99)
2019	4,668	3,942	6,090	1,128	706 (0.62)	701 (0.99)

Table 9. The average, minimum and maximum proportion of the wild Chinook Salmon population abundance as a proportion of the total wild adult run at large over Lower Granite Dam including the number of spawn years with abundance estimates and the estimated monitoring coverage of the population. * denotes populations that are pooled together. (Two blank rows were deleted)

MPG	Population	Description	Mean Proportion of LGR	Minimum Proportion	Maximum Proportion	Number of Spawn Years	Population Coverage
Dry Clearwater	SCUMA	Upper S. Fork Clearwater	0.027	0.012	0.050	8	100
	CRLAP	Lapwai/Big Canyon	0.000	0.000	0.000	10	39
Wet Clearwater	CRLOC	Lochsa River	0.035	0.029	0.042	2	100
	CRLOL	Lolo Creek	0.009	0.005	0.015	7	54
	SEMEA*	Meadow Creek					
	SEMOO*	Moose Creek	0.047*	0.036*	0.058*	2*	100*
	SEUMA*	Upper Selway River					
Lower Snake	SNTUC	Tucannon River	0.005	0.001	0.012	9	-
Grande Ronde - Imnaha	GRCAT	Catherine Creek	0.017	0.006	0.033	10	25
	GRLOO	Lookingglass Creek	0.010	0.003	0.017	10	-
	GRLOS	Lostine River	0.041	0.041	0.041	1	99
	GRLOS/ GRMIN	Lostine and Minam rivers	0.051	0.063	0.086	6	100
	GRUMA	Grande Ronde upper mainstem	0.006	0.001	0.020	7	32
	GRWEN	Wenaha River	0.025	0.025	0.025	1	99
	IRBSH	Big Sheep Creek	0.005	0.002	0.013	9	52
	IRMAI	Imnaha River mianstem	0.046	0.031	0.076	9	100

Table 9. Continued

MPG	Population	Description	Mean Proportion of LGR	Minimum Proportion	Maximum Proportion	Number of Spawn Years	Population Coverage
South Fork Salmon River	SFEFS	East Fork South Fork Salmon	0.038	0.024	0.053	10	98
	SFMAI	South Fork Salmon mainstem	0.064	0.034	0.138	10	65
	SFSEC	Secesh River	0.043	0.027	0.063	10	99
	SRLSR	Little Salmon River	0.002	0.000	0.004	6	-
Middle Fork Salmon	MFBEA	Bear Valley Creek	0.031	0.005	0.059	5	96
	MFBIG	Big Creek	0.038	0.015	0.048	9	99
Upper Salmon	SREFS	East Fork Salmon River	0.009	0.001	0.018	7	-
	SRLEM	Lemhi	0.020	0.005	0.046	10	99
	SRLMA	mainstem below Redfish Lake	0.019	0.001	0.034	7	-
	SRNFS	North Fork Salmon	0.005	0.003	0.008	4	83
	SRPAH	Pahsimeroi River	0.010	0.006	0.014	8	99
	SRPAN	Panther Creek	0.020	0.018	0.022	2	96
	SRUMA	mainstem above Redfish Lake	0.021	0.003	0.046	10	87
	SRVAL	Valley Creek	0.019	0.014	0.024	10	100
	SRYFS	Yankee Fork	0.009	0.005	0.015	8	98

Table 10. Mean, minimum, and maximum values of H_e for Chinook Salmon in the Snake River Basin summarized by MPG and population. Only populations with greater than 20 samples detected in a given year are reported upon. Values represent mean estimates averaged across spawn years. The number of years for which there is an estimate of H_e is identified in the column *n*.

MPG	Population	*n*	Avg H_e	Min H_e	Max H_e
Dry Clearwater	SCUMA	7	25.0%	23.6%	27.9%
Wet Clearwater	CRLOC	2	24.5%	24.2%	24.8%
	CRLOL	3	24.6%	24.4%	24.9%
	SEMEA	2	25.4%	24.8%	25.9%
Grande Ronde	GRCAT	6	25.3%	25.1%	25.7%
	GRLOO	6	25.0%	24.3%	26.1%
	GRLOS	8	23.5%	22.6%	24.2%
	GRUMA	1	24.2%	-	-
	GRWEN	1	30.1%	-	-
Imnaha	IRBSH	1	24.3%	-	-
	IRMAI	9	24.1%	23.5%	24.8%
Middle Fork Salmon River	MFBEA	4	21.4%	21.1%	21.9%
	MFBIG	9	22.4%	21.9%	22.8%
South Fork Salmon River	SFEFS	10	22.5%	20.4%	23.3%
	SFMAI	10	23.0%	22.5%	23.5%
	SFSEC	10	22.0%	20.9%	22.4%
Upper Salmon River	SREFS	2	23.0%	23.0%	23.0%
	SRLEM	7	23.1%	22.6%	23.7%
	SRPAH	4	23.1%	22.8%	23.4%
	SRPAN	2	22.5%	22.3%	22.7%
	SRUMA	7	22.9%	22.3%	24.2%
	SRVAL	8	22.8%	22.2%	23.4%
	SRYFS	4	22.4%	22.0%	23.1%

Table 11. Mean, minimum, and maximum values of N_b for Chinook Salmon in the Snake River Basin summarized by MPG and population. Only populations with greater than 20 samples for a given brood year are reported upon. Values represent mean estimates averaged across brood years. The number of years for which there is an estimate of N_b is identified in the column *n*.

MPG	Population	Brood Year	N_b
Grande Ronde River	GRCAT	2008	167
		2009	155
		2010	205
		2011	221
		2012	100
		2015	153
	GRLOO	2008	164
		2011	147
		2012	119
		2014	240
	GRLOS	2008	187
		2010	166
		2011	268
		2012	183
		2014	176
		2015	216
	GRUMA	2014	252
Imnaha River	IRBSH	2007	99
	IRMAI	2006	93
		2007	321
		2008	239
		2009	9
		2010	308
		2011	257
		2012	307
		2013	183
		2014	200
		2015	173
Middle Fork Salmon River	MFBEA	2011	218
		2012	140
		2014	164
	MFBIG	2007	127
		2008	151
		2009	174
		2010	242
		2011	249

Table 11. Continued

MPG	Population	Brood Year	N_b
Middle Fork Salmon River	MFBIG	2012	207
		2014	296
		2015	380
South Fork Salmon River	SFEFS	2006	65
		2007	121
		2008	219
		2009	270
		2010	259
		2011	188
		2012	226
		2014	220
		2015	198
	SFMAI	2006	299
		2007	332
		2008	225
		2009	262
		2010	438
		2011	254
		2012	239
		2013	138
		2014	255
		2015	107
	SFSEC	2006	61
		2007	103
		2008	228
		2009	238
		2010	242
		2011	235
		2012	224
		2013	118
		2014	243
		2015	266
Upper Salmon River	SREFS	2010	179
	SRLEM	2007	96
		2009	134
		2010	107
		2011	104
		2014	153
		2015	174

Table 11. Continued

MPG	Population	Brood Year	N_b
Upper Salmon River	SRPAH	2009	161
		2010	230
		2011	154
	SRPAN	2014	250
	SRUMA	2006	120
		2007	202
		2008	220
		2009	41
		2010	277
		2011	198
		2012	164
	SRVAL	2007	114
		2008	187
		2009	129
		2010	182
		2011	163
		2012	144
		2014	153
	SRYFS	2008	210
		2009	175
		2010	168
		2014	380
Wet Clearwater River	CRLOC	2014	238
		2015	218
	CRLOL	2008	71
		2011	228
		2012	105
	SEMEA	2014	45
		2015	99
Dry Clearwater River	SCUMA	2007	229
		2008	324
		2009	158
		2010	261
		2011	213
		2012	16
		2014	37

Table 12. The genetic composition of Chinook Salmon that were and were not detected at PIT tag arrays in the Snake River basin. The final column displays the average genetic composition of Chinook Salmon crossing over Lower Granite Dam as determined via genetic stock identification (GSI). Average, minimum, and maximum values cover spawn years 2010–2019.

	GSI at Lower Granite Dam		Detected at PIT array		Never detected at PIT array	
Genetic Stock	**Average**	**Range**	**Average**	**Range**	**Average**	**Range**
CHMBLN	0.009	(0.002-0.034)	0.009	(0.002-0.034)	0.048	(0.032-0.074)
FALL	0.003	(0.000-0.012)	0.002	(0.000-0.007)	0.108	(0.037-0.239)
HELLSC	0.417	(0.252-0.496)	0.390	(0.240-0.486)	0.383	(0.299-0.440)
MFSALM	0.139	(0.070-0.226)	0.132	(0.065-0.199)	0.238	(0.162-0.343)
SFSALM	0.232	(0.109-0.277)	0.224	(0.101-0.294)	0.067	(0.056-0.100)
TUCANO	0.007	(0.001-0.012)	0.006	(0.001-0.011)	0.006	(0.000-0.018)
UPSALM	0.193	(0.131-0.236)	0.238	(0.181-0.290)	0.150	(0.114-0.234)

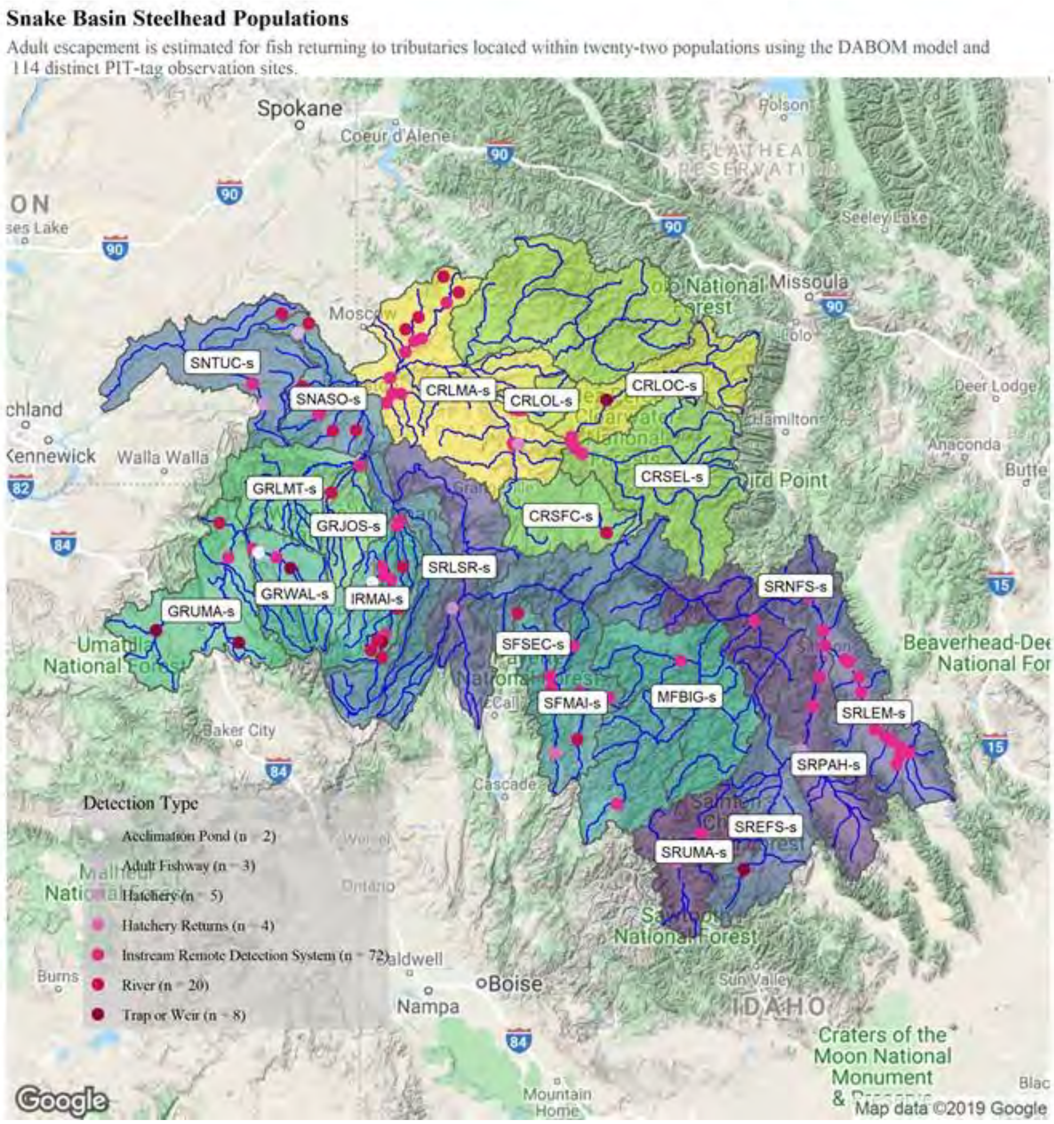

Figure 1. A map displaying populations of steelhead (color coded) within the Snake River basin along with the number and type of PIT tag detection sites within each population.

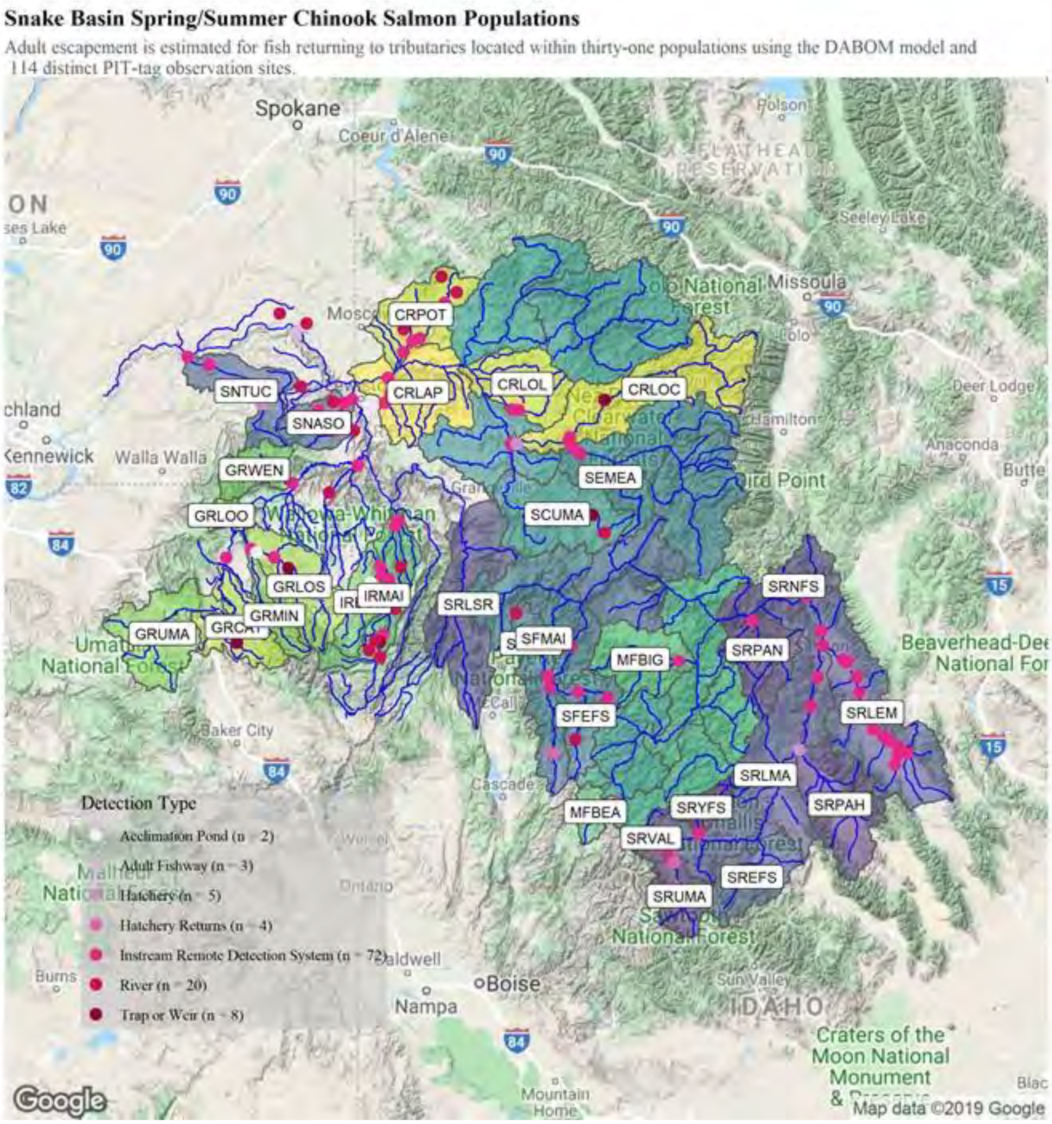

Figure 2. A map displaying populations of Chinook Salmon (color coded) within the Snake River basin along with the number and type of PIT tag detection sites within each population.

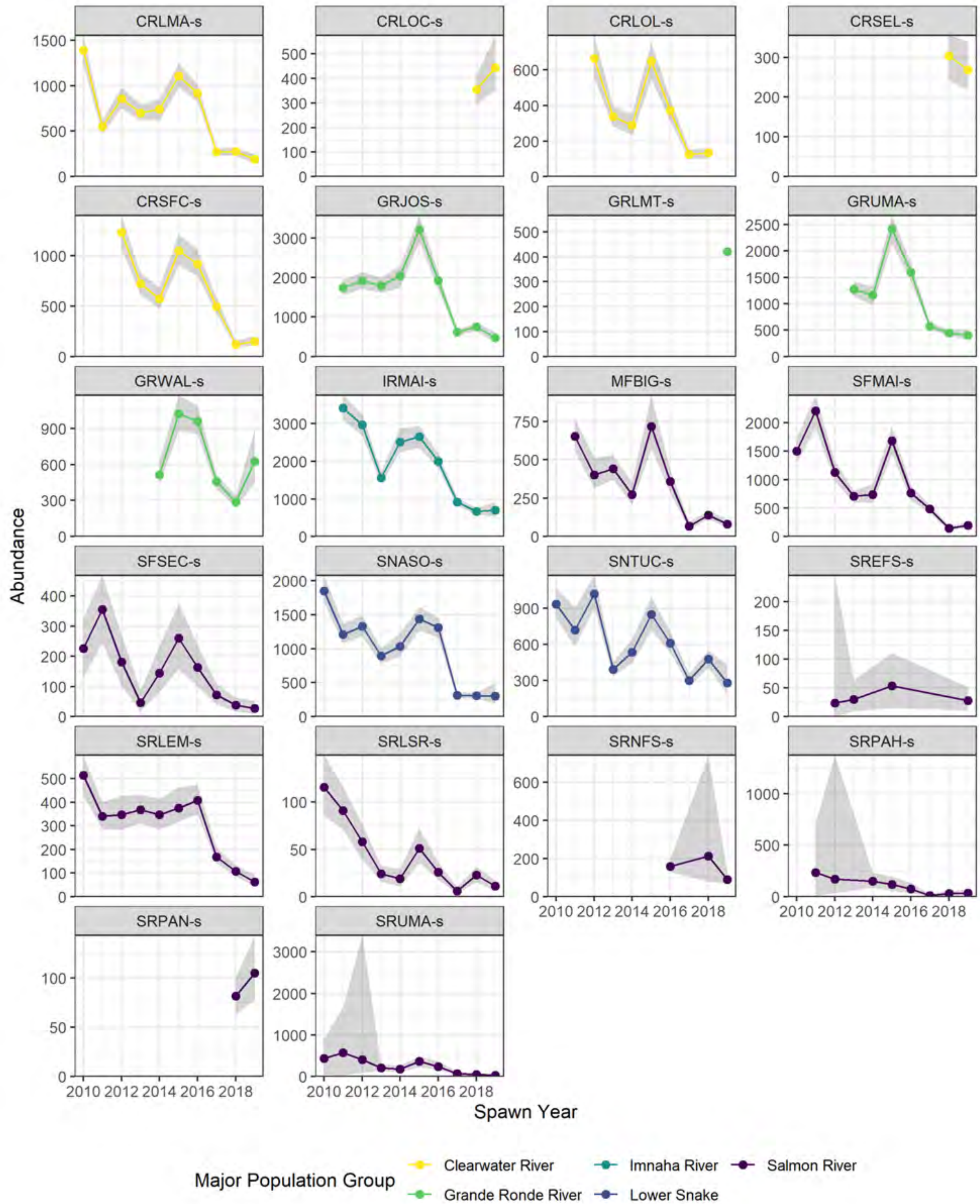

Figure 3. Estimated abundance of adult steelhead and 95% confidence intervals (gray shading) from DABOM model runs by spawn year and population.

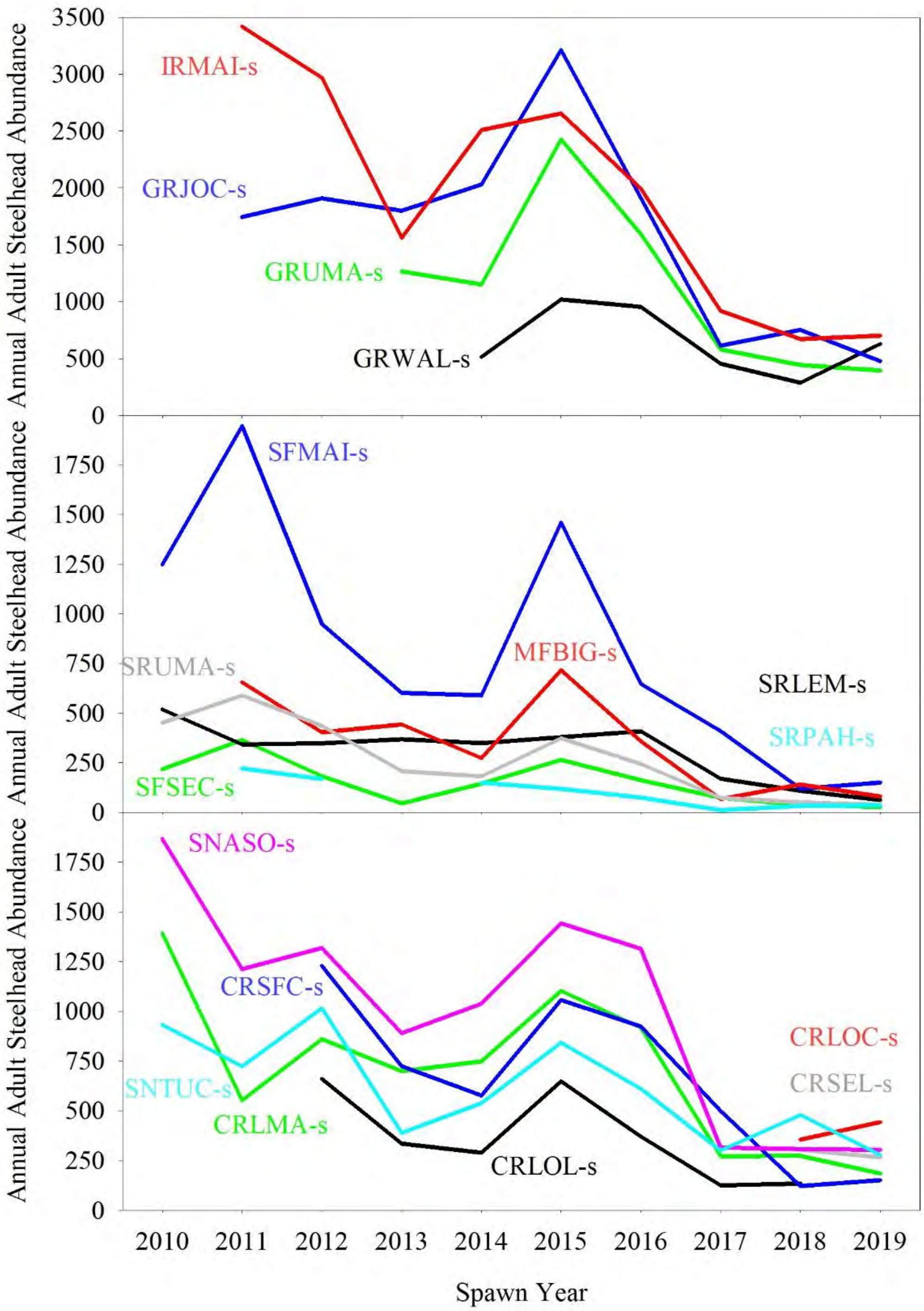

Figure 4. Estimated trends in wild adult steelhead abundance by spawn year for population roughly grouped by geographic location.

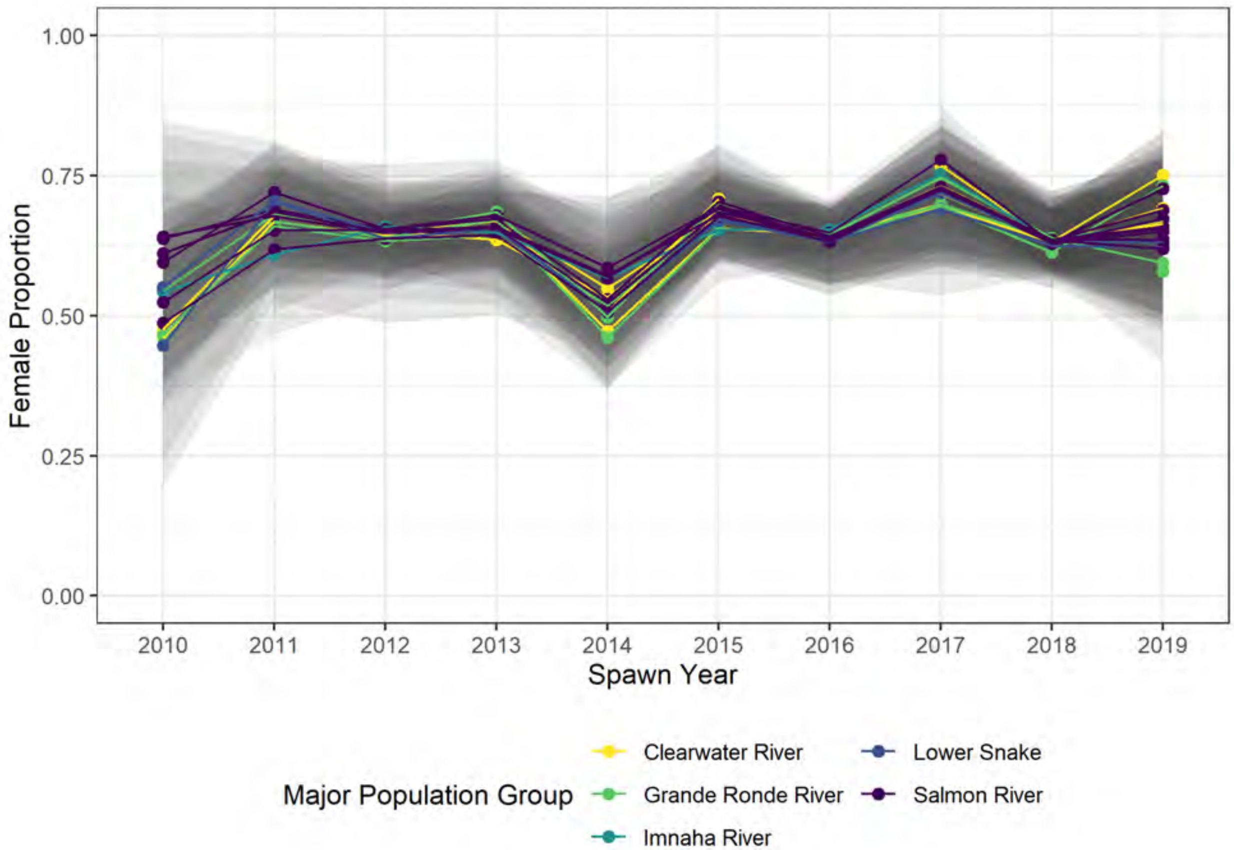

Figure 5. Returning wild adult steelhead female population proportion by spawn year and individual population grouped by Major Population Group (MPG).

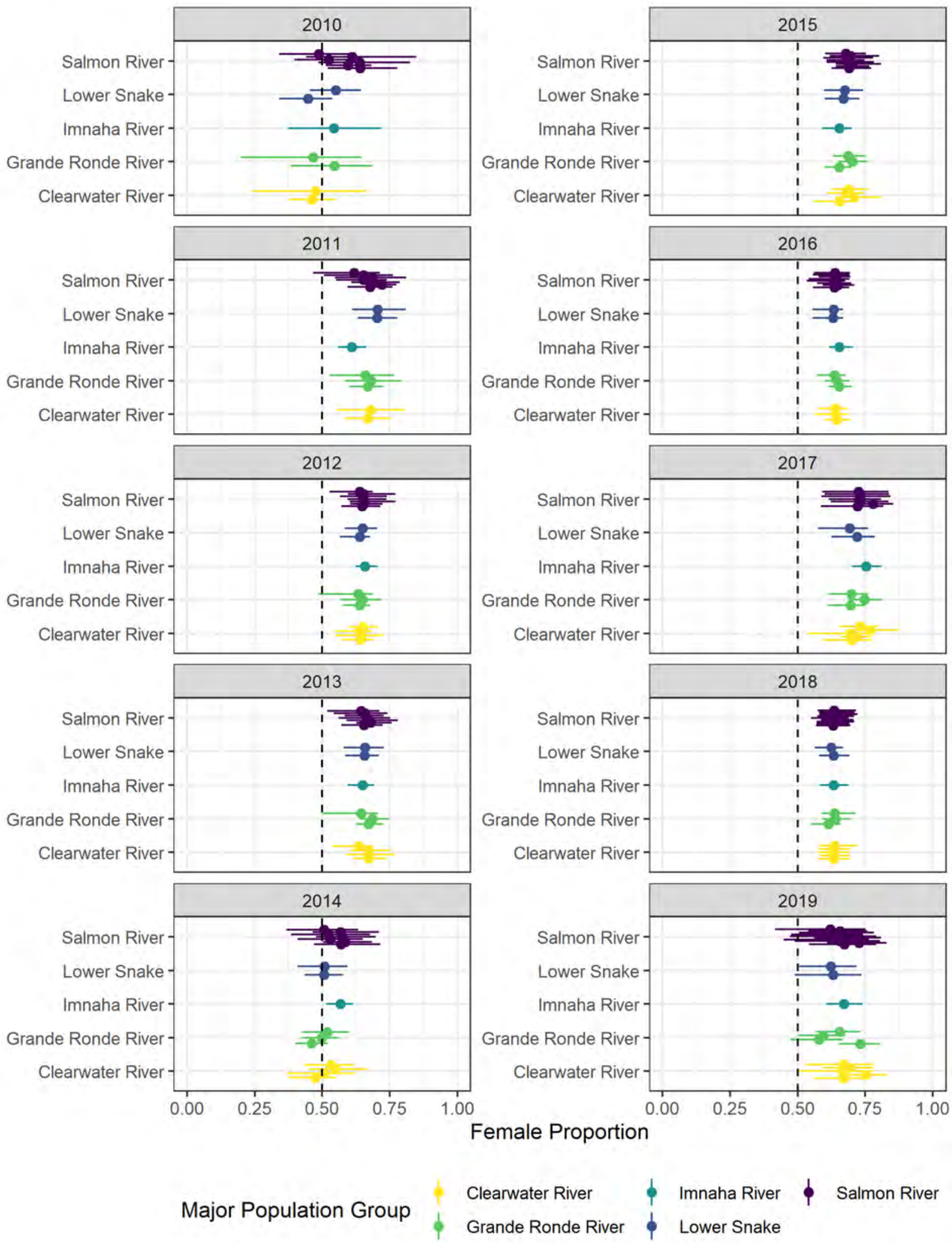

Figure 6. Estimated female proportions and 95% confidence intervals for individual populations of wild adult steelhead by spawn years 2010 through 2019 and grouped by Major Population Group (MPG).

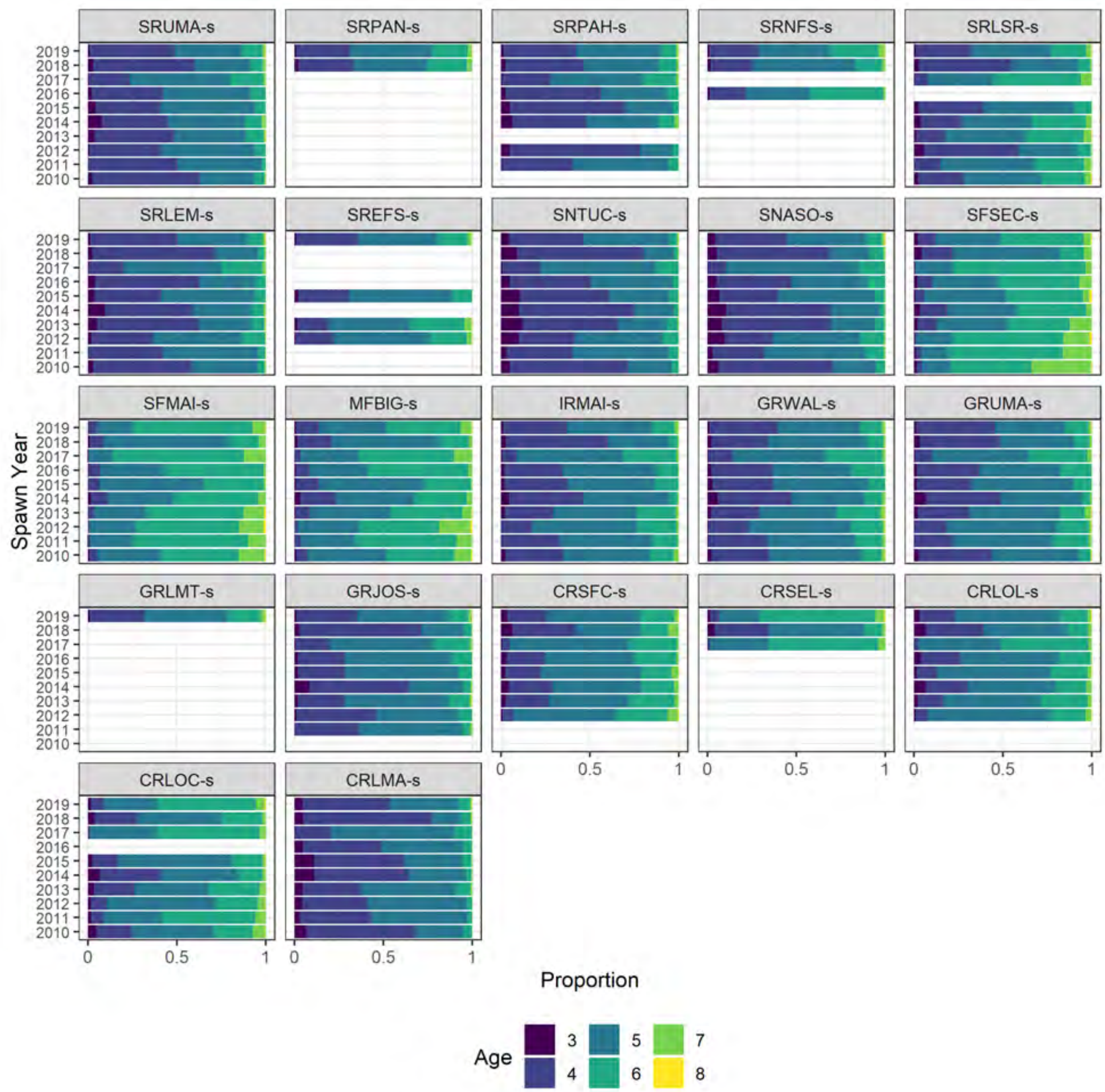

Figure 7. Estimated age proportions of returning wild adult steelhead by spawn year and population.

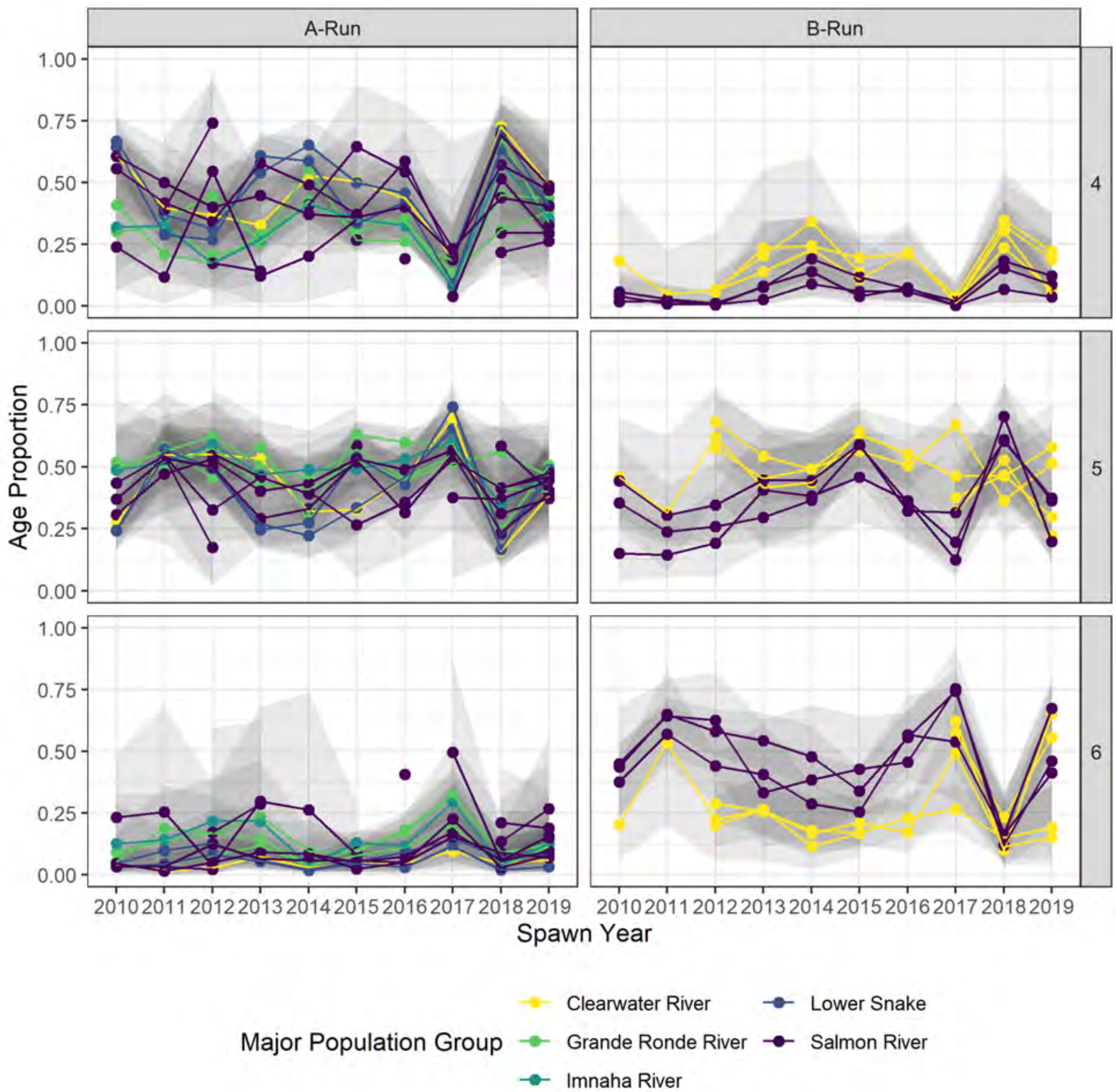

Figure 8. Estimated proportions and 95% confidence intervals of age class of returning wild adult steelhead by individual population and spawn year, grouped by Major Population Group (MPG), by “A” run (left panel) and “B” run (right panel) populations, and by age (age 4 top, age 5 middle, age 6 bottom).

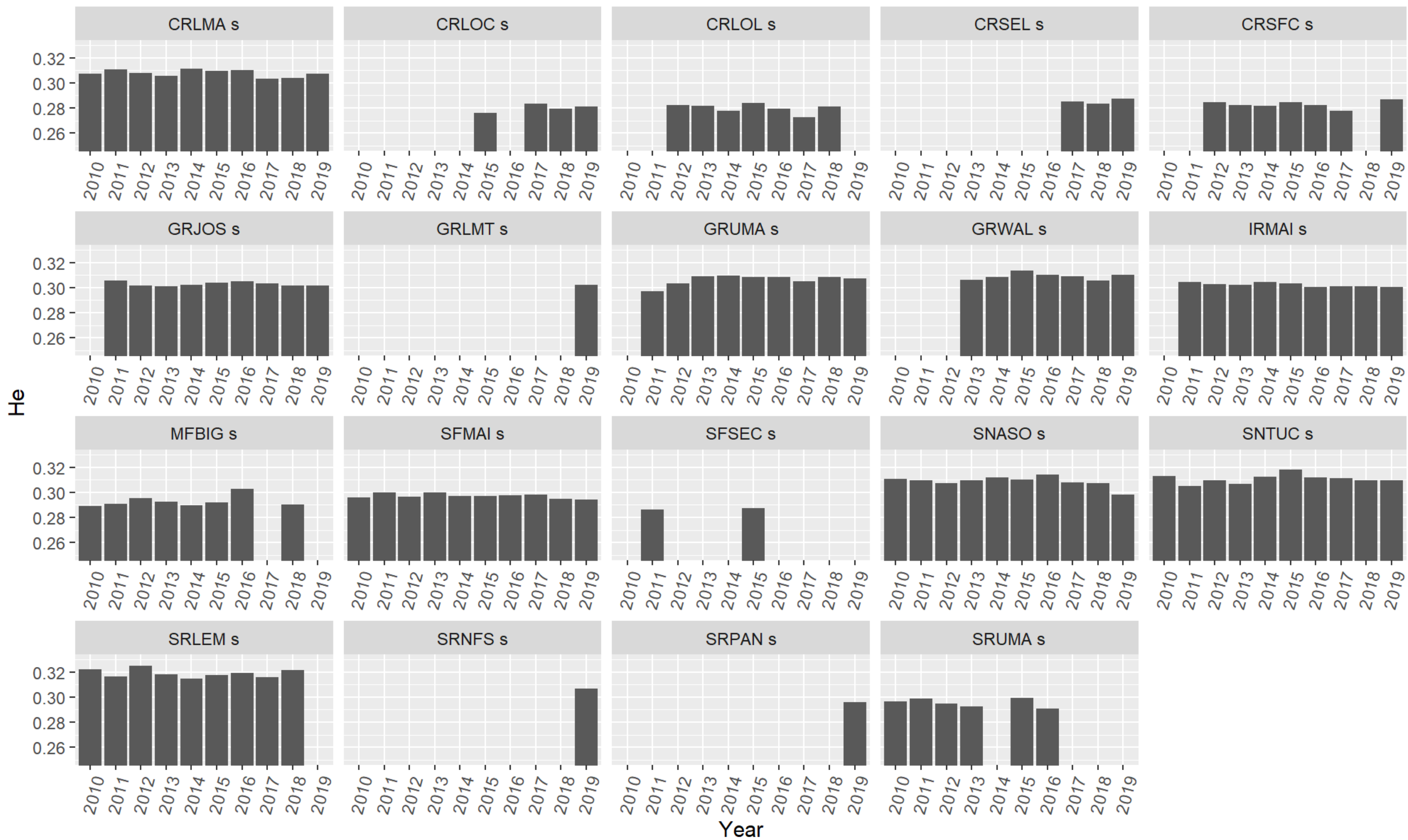

Figure 9. Levels of expected heterozygosity (H_e) calculated for steelhead populations in the Snake River basin by spawn year. Only populations with more than 20 observations within a given year are presented.

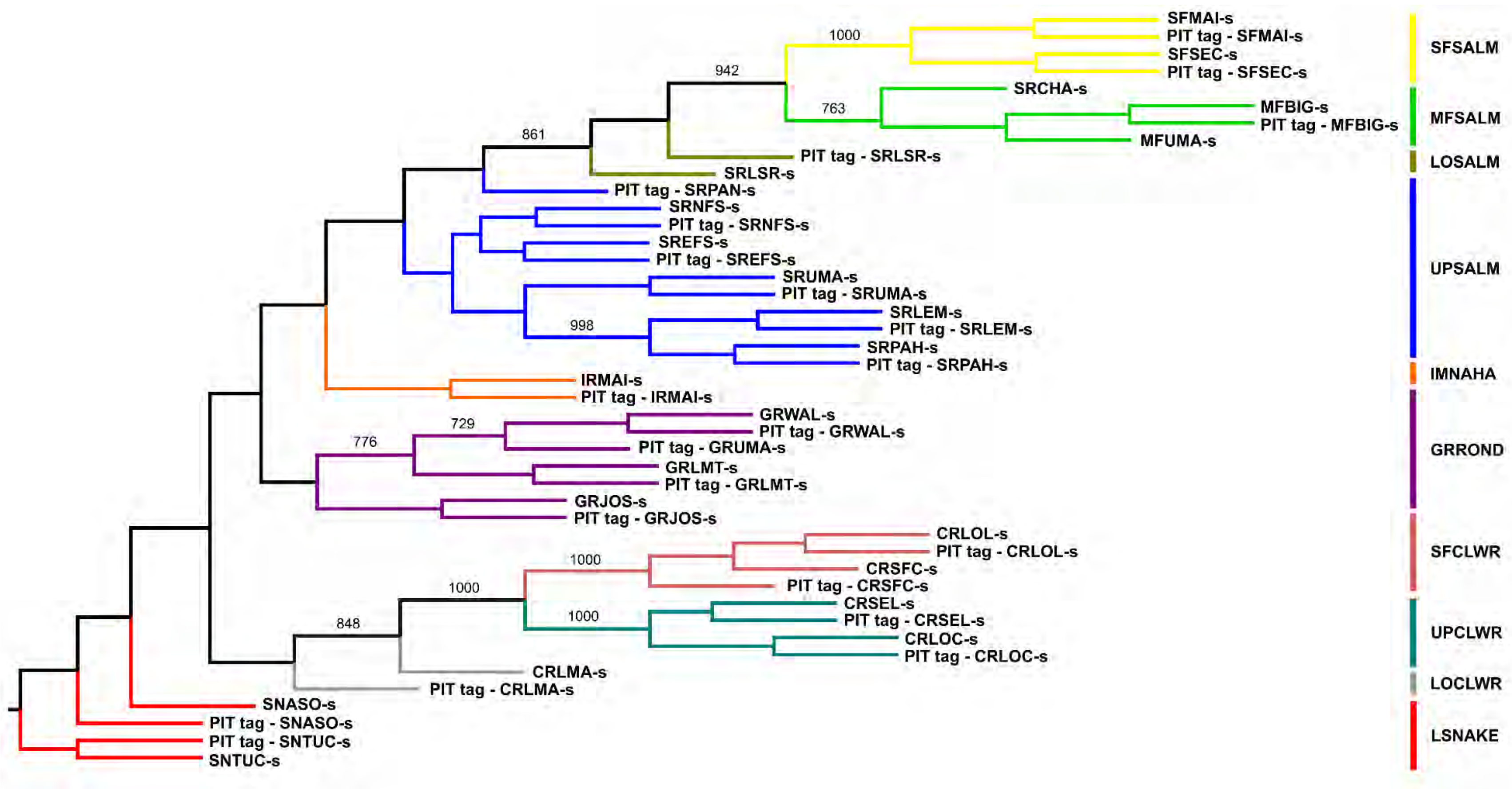

Figure 10. A neighbor-joining tree based on Cavalli-Sforza Edwards chord distance for Snake River steelhead populations included in the GSI baseline version 3.1 and collections of PIT tagged returning adults for SY2010-2019 (indicated with prefix PIT tag). Bootstrap support greater than 70% based on 1,000 replicated are reported.

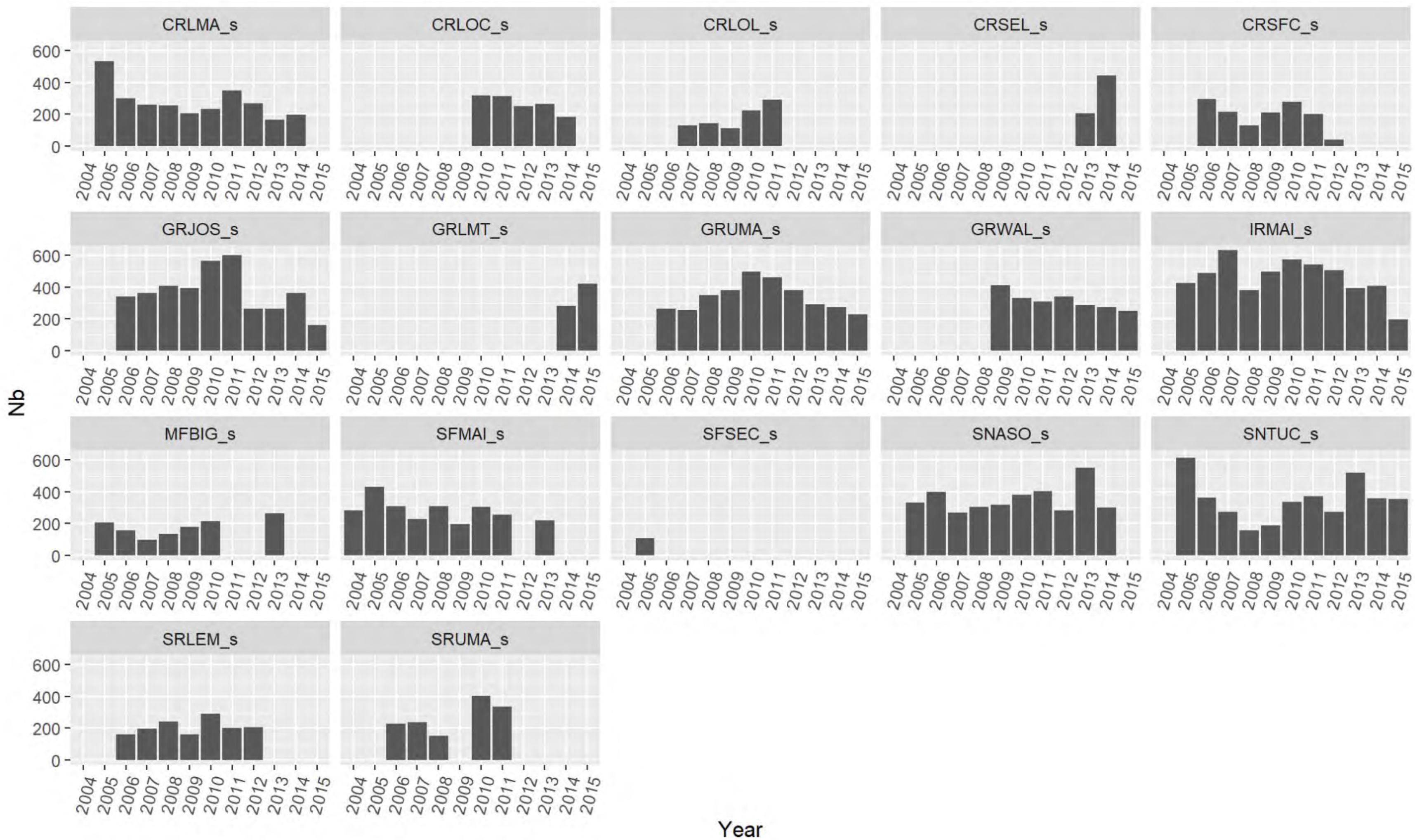

Figure 11. The number of breeders (N_b) estimated for steelhead populations in the Snake River basin by spawn year. Only populations with more than 20 observations within a given year are presented.

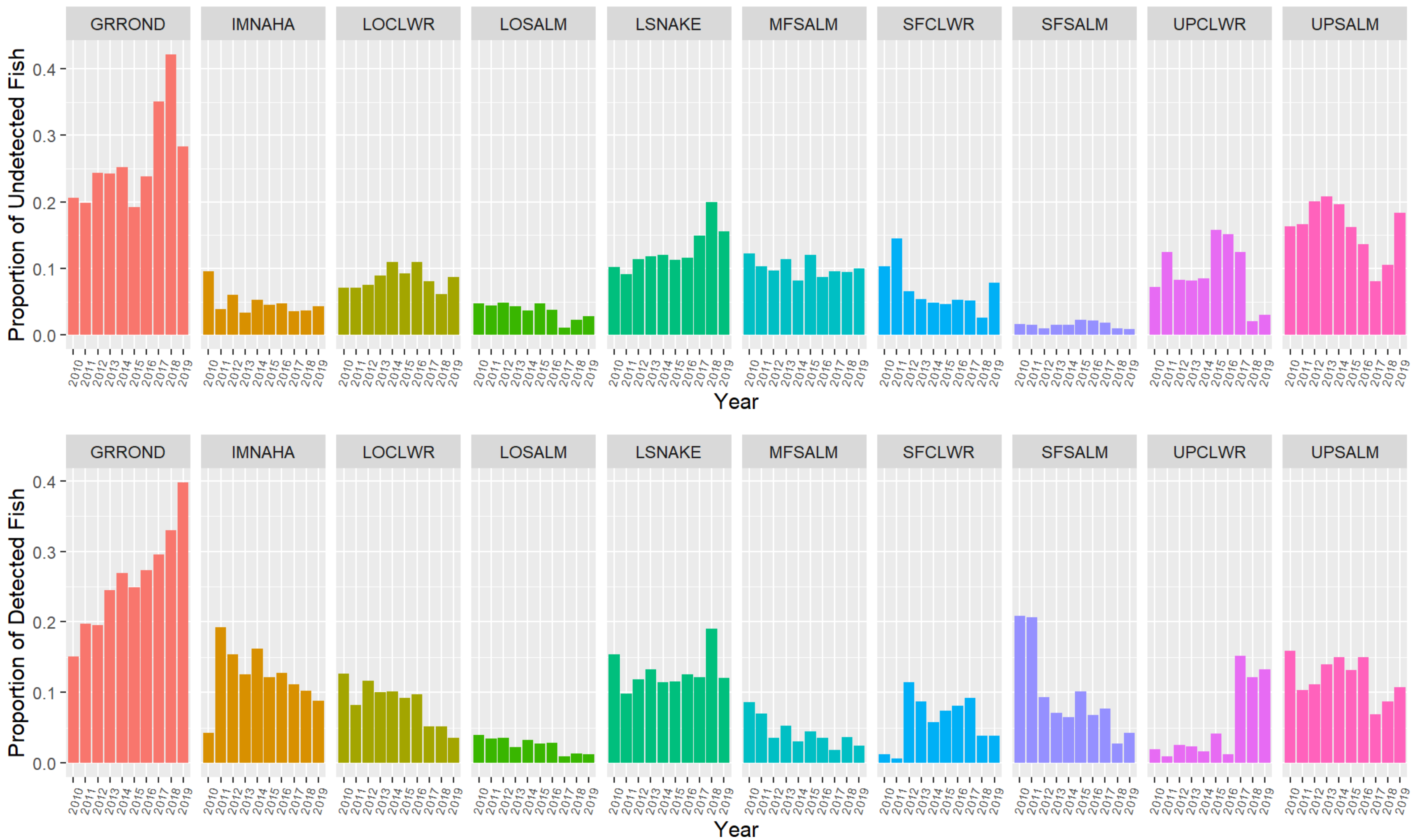

Figure 12. The relative contribution of different steelhead genetic stocks that were undetected (top) or detected (bottom) at PIT tag arrays following passage of Lower Granite Dam in the Snake River basin. Shown are proportions of fish by genetic stock by year for spawn years 2010–2019.

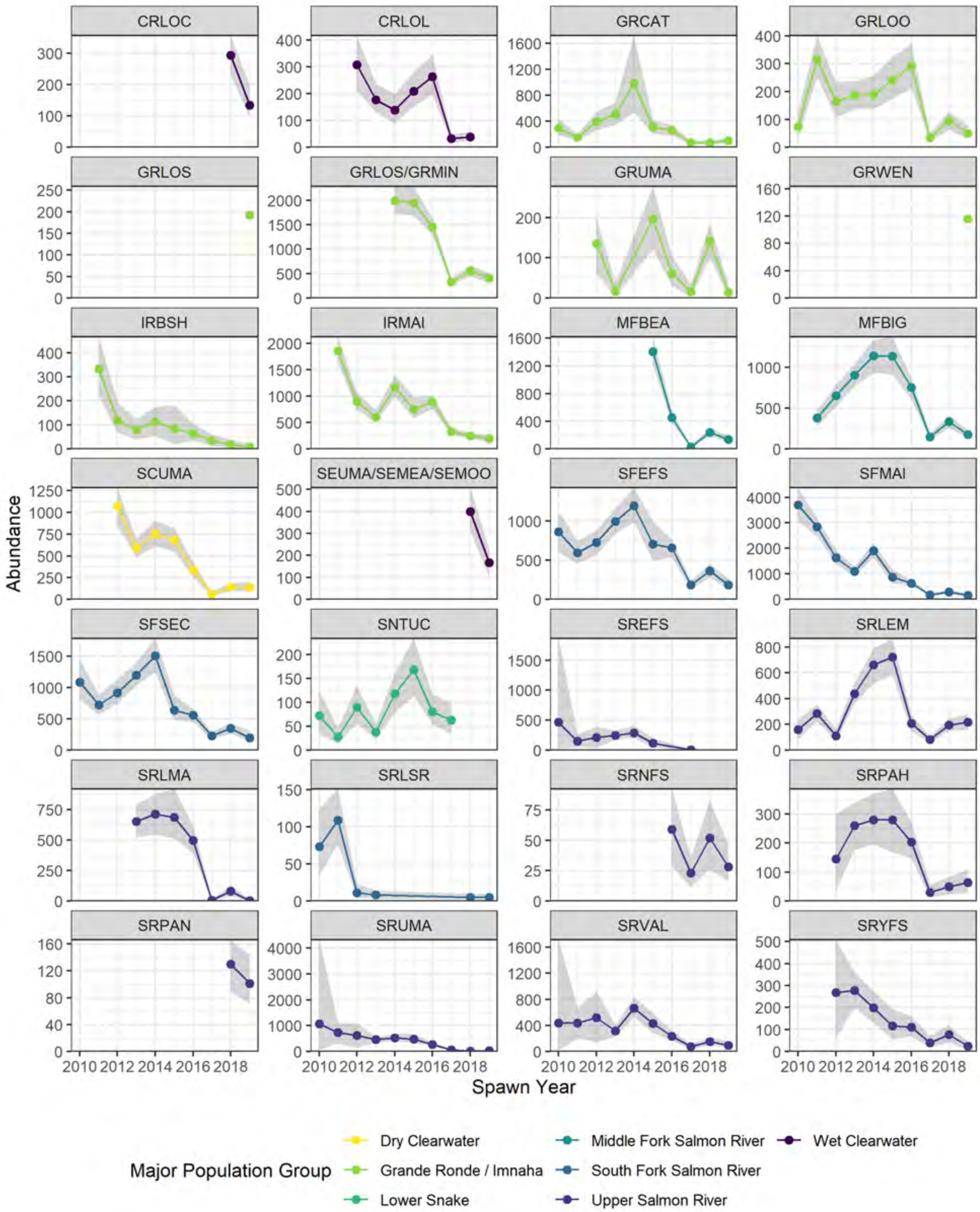

Figure 13. Estimated wild adult Chinook Salmon abundance and 95% confidence intervals (gray shading) from DABOM model runs by spawn year and population.

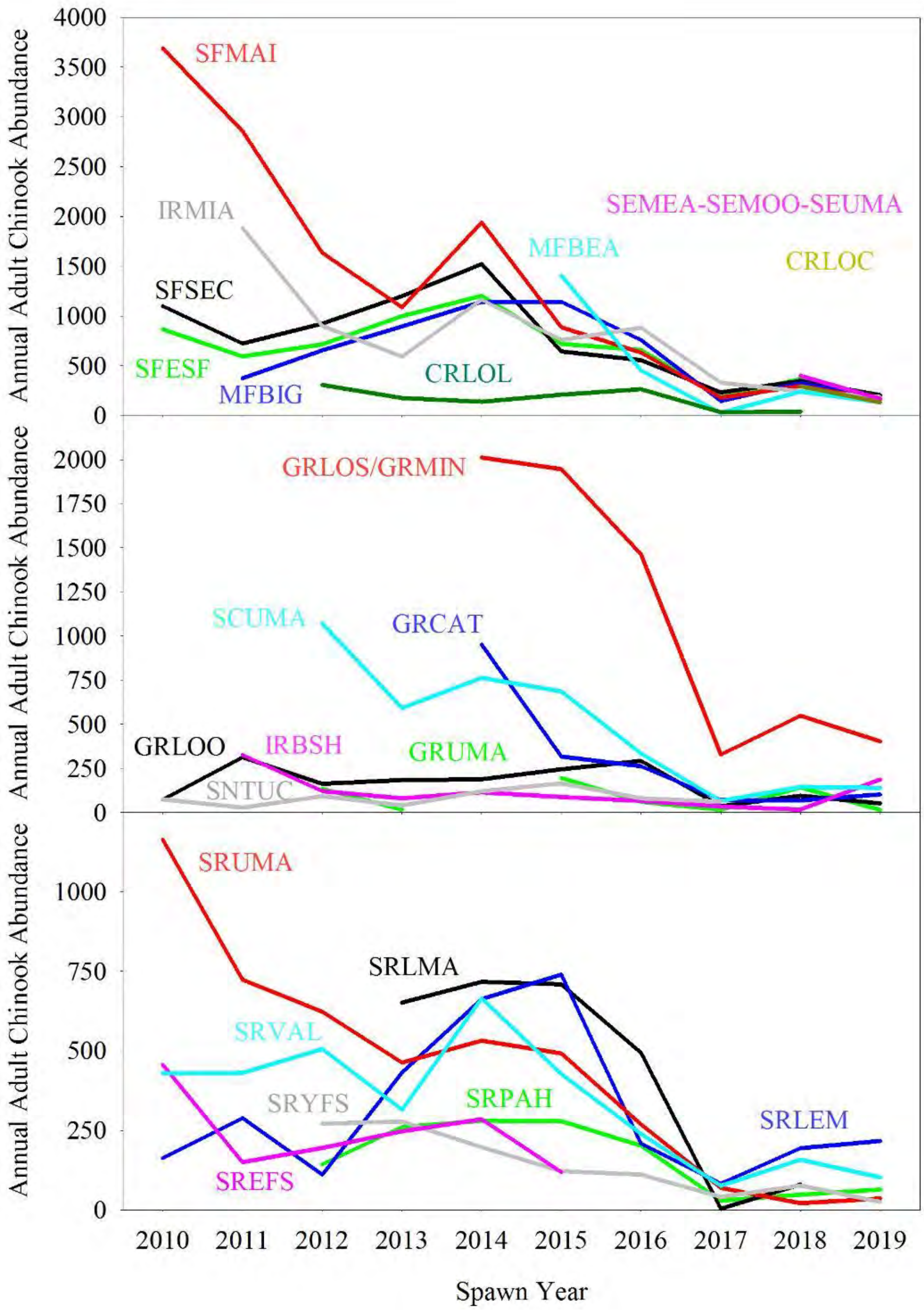

Figure 14. Estimated wild adult Chinook Salmon abundance trends by spawn year and population roughly grouped by geographic location showing the highly synchronous annual abundance trends.

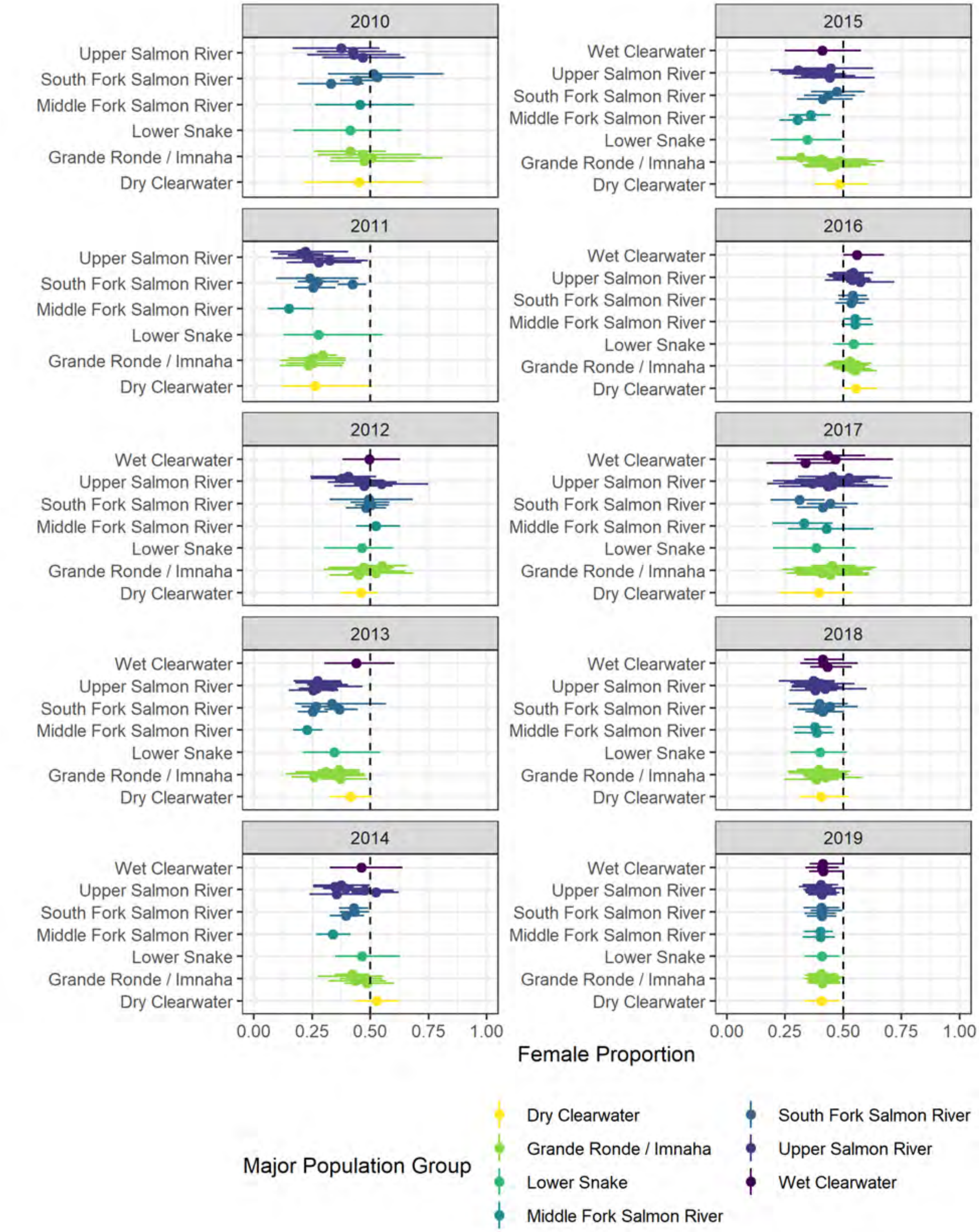

Figure 15. Estimated female proportions and 95% confidence intervals for wild adult Chinook Salmon by spawn years 2010-2019 and by population.

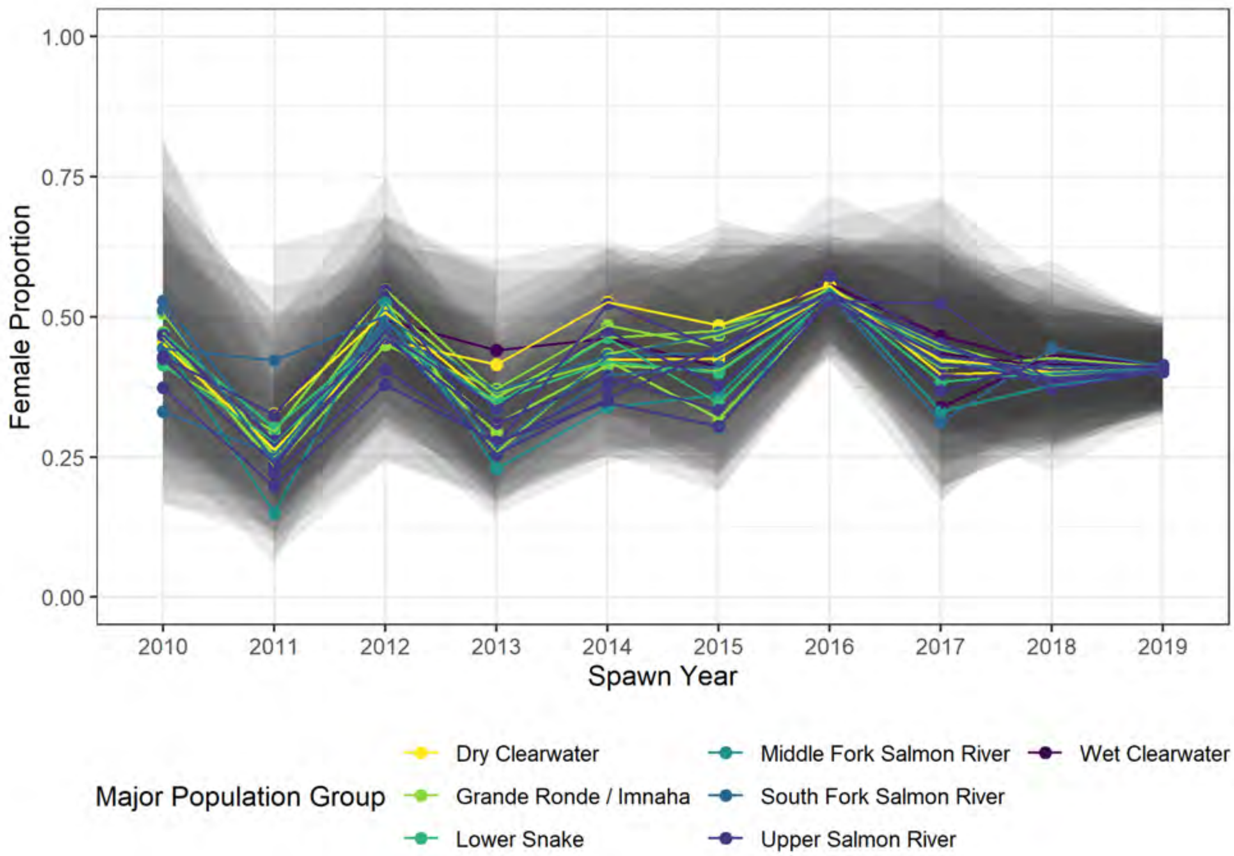

Figure 16. Returning wild adult Chinook Salmon female population proportion and 95% confidence interval (gray shading) by spawn year and individual population grouped by Major Population Group (MPG).

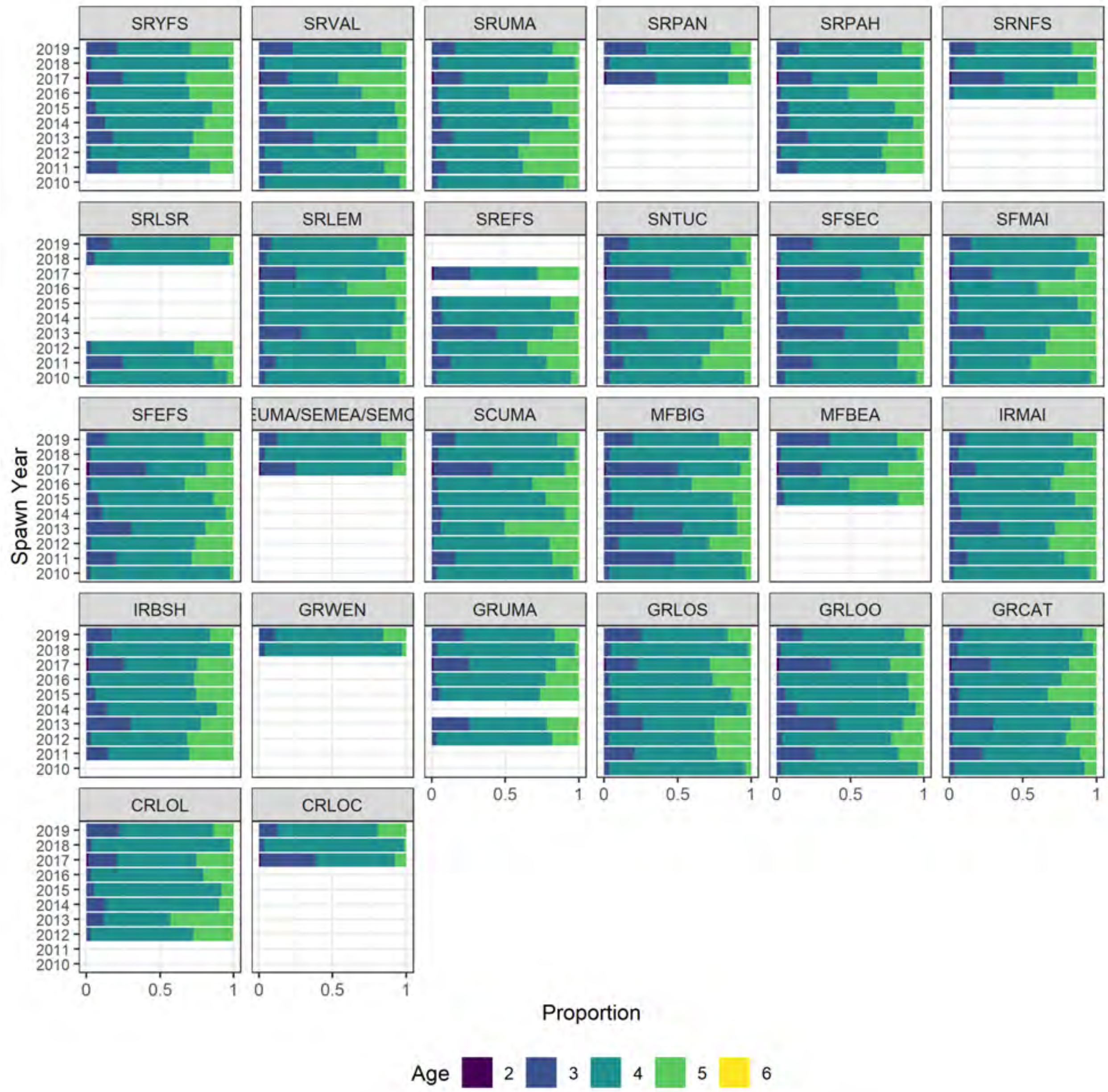

Figure 17. Estimated age proportions of returning wild adult Chinook Salmon by spawn year and population.

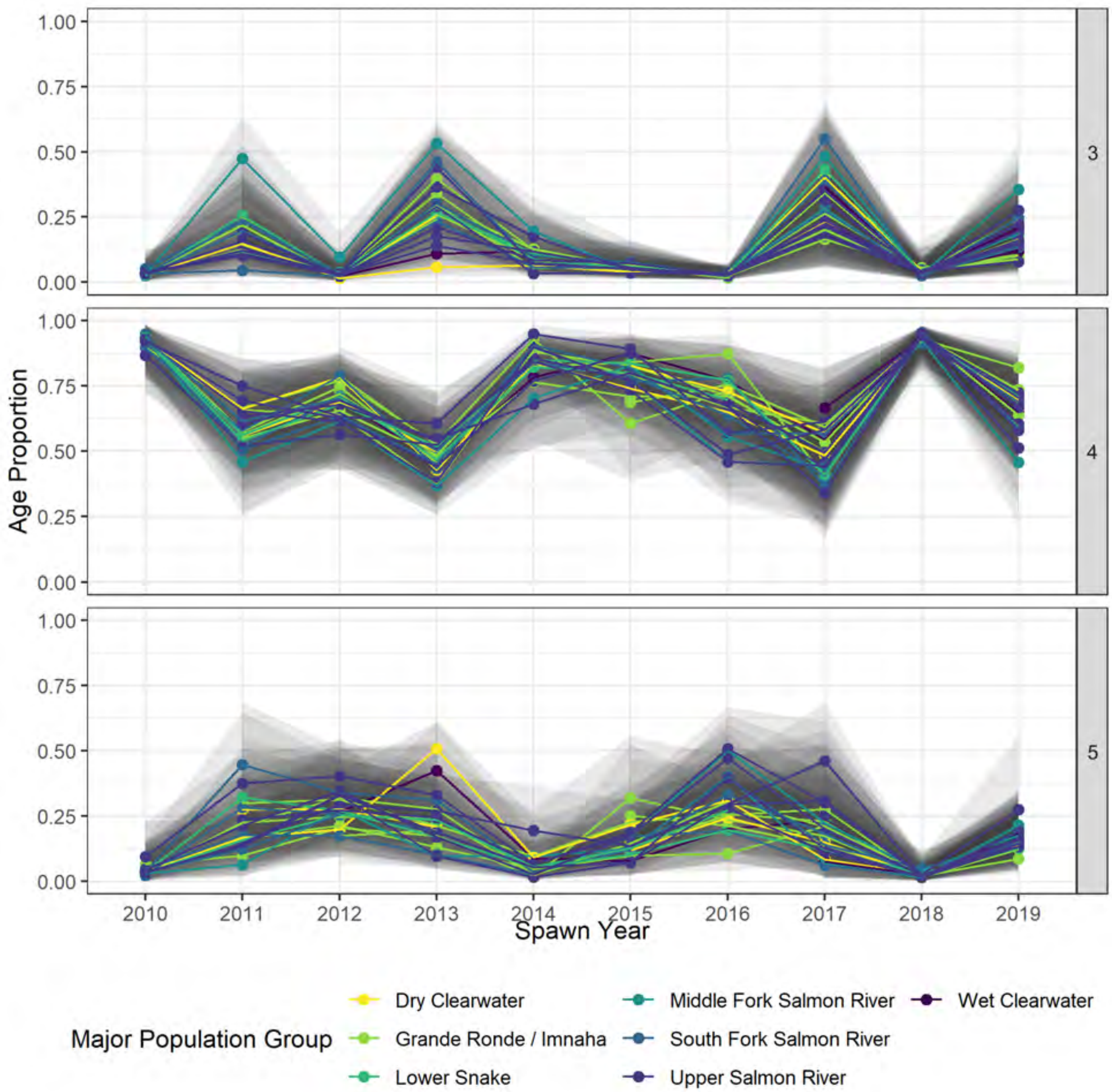

Figure 18. Estimated age class proportions and 95% confidence intervals (gray shading) of returning wild adult Chinook Salmon by individual population and by spawn year and grouped by age and Major Population Group (MPG).

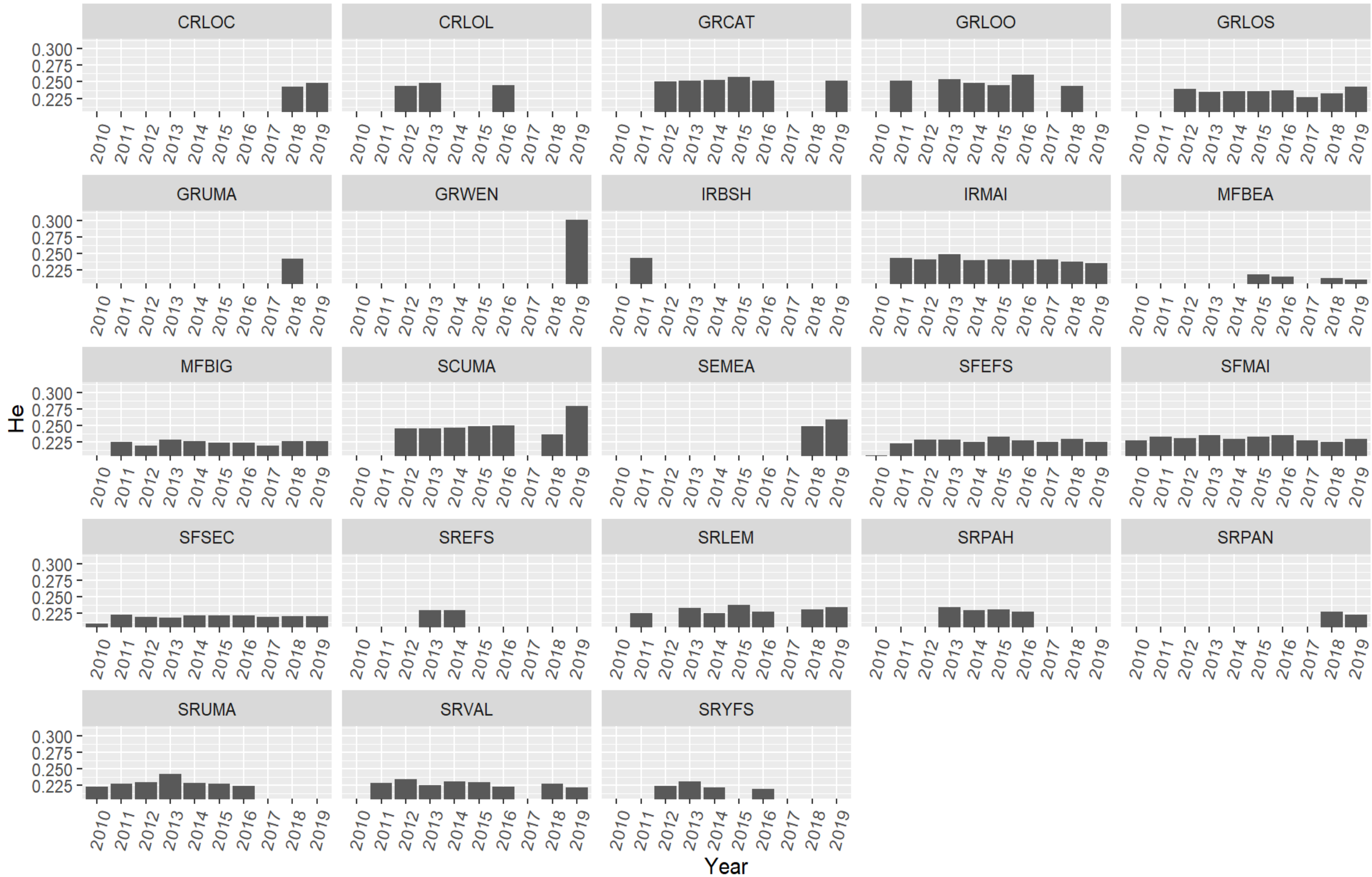

Figure 19. Levels of expected heterozygosity (H_e) calculated for Chinook Salmon populations in the Snake River basin by spawn year. Only populations with more than 20 observations within a given year are presented.

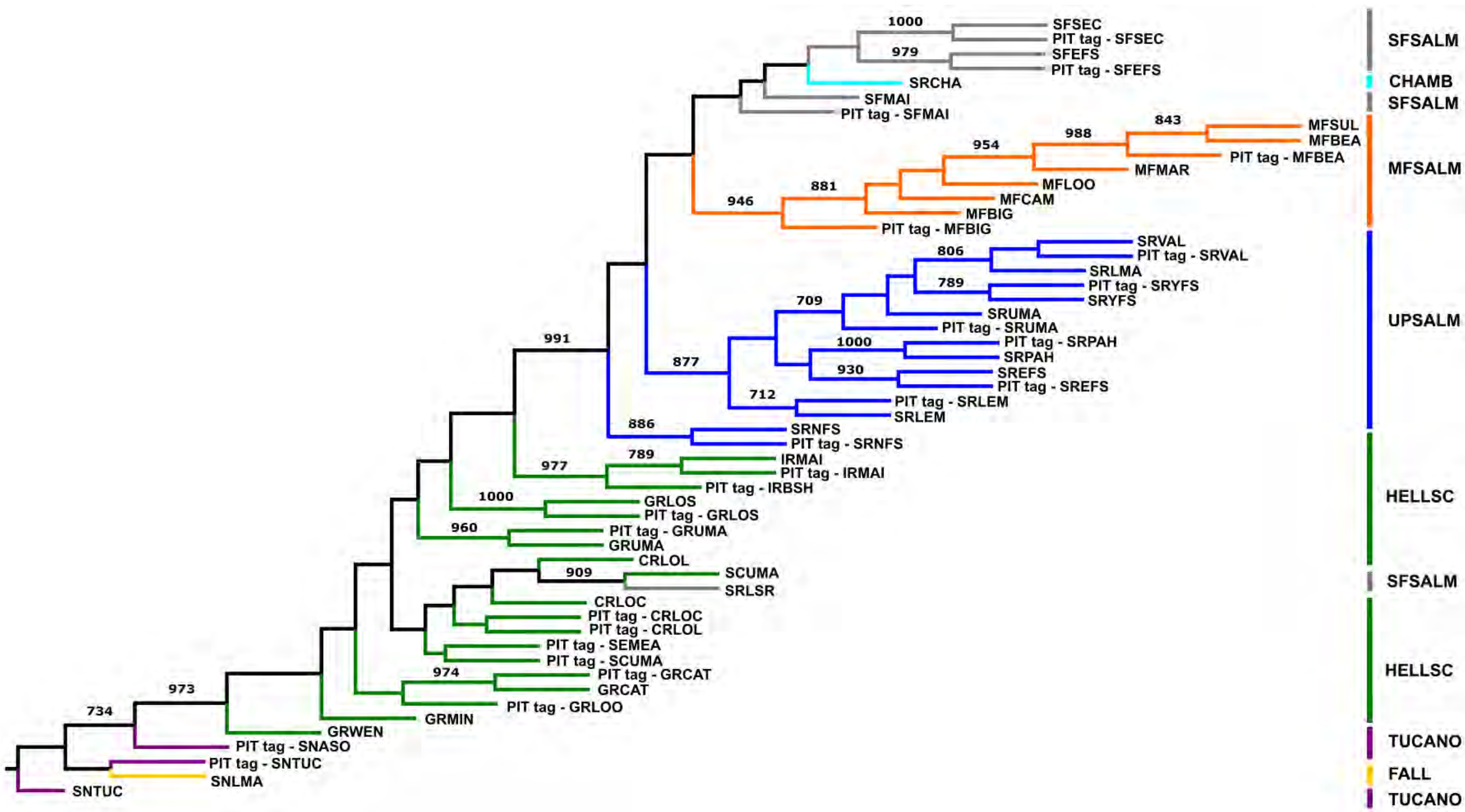

Figure 20. A neighbor-joining tree based on Cavalli-Sforza Edwards chord distance for Snake River Chinook Salmon populations included in the GSI baseline version 3.1 and collections of PIT tagged returning adults for SY2010-2019 (indicated with prefix PIT tag). Bootstrap support greater than 70% based on 1,000 replicated are reported.

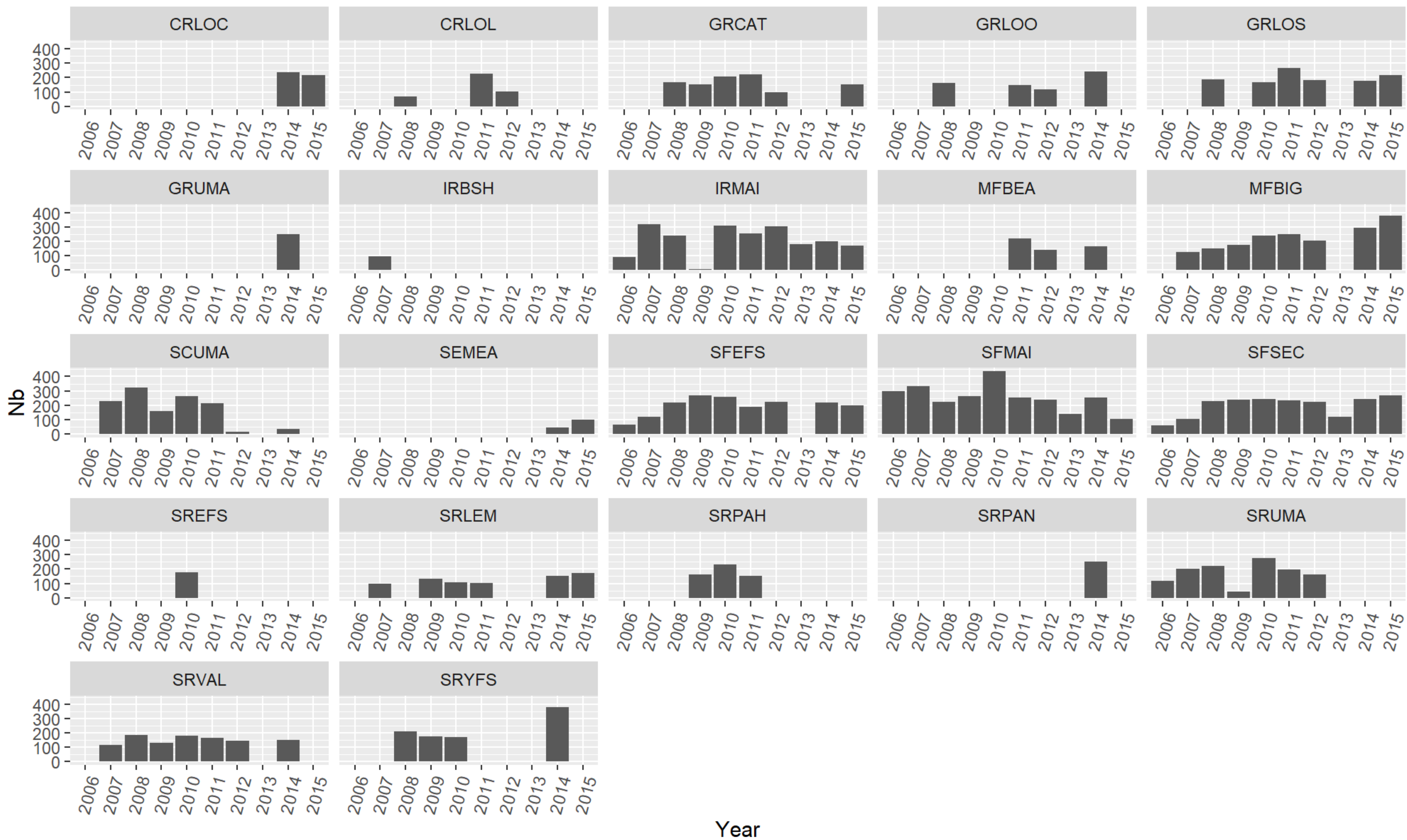

Figure 21. The number of breeders (N_b) estimated for Chinook Salmon populations in the Snake River basin by spawn year. Only populations with more than 20 observations within a given year are presented.

Figure 22. The relative contribution of different Chinook Salmon genetic stocks that were undetected (top) or detected (bottom) at PIT tag arrays following passage of Lower Granite Dam in the Snake River basin. Shown are proportions of fish by genetic stock by year for spawn years 2010–2019.

Appendix A. Wild adult steelhead abundance by spawn year and population including the lower and upper confidence intervals and the annual number of unique PIT tags from the Lower Granite Dam adult PIT tag group observed within the population and available to estimate age and sex (N-tags not corrected for detection probability).

MPG	Population	Spawn Year	Escapement	Lower CI	Upper CI	N-Tags
Lower Snake	SNASO-s	2010	1,851	1,668	2,090	166
		2011	1,205	1,089	1,351	114
		2012	1,320	1,184	1,478	133
		2013	889	777	981	116
		2014	1,030	885	1,212	110
		2015	1,443	1,274	1,631	100
		2016	1,315	1,191	1,476	153
		2017	313	267	356	60
		2018	307	265	348	61
		2019	299	194	517	33
	SNTUC-s*	2010	936	809	1,061	84
		2011	724	556	889	53
		2012	1,021	885	1,159	96
		2013	390	329	452	54
		2014	536	448	632	59
		2015	850	714	1,013	66
		2016	609	539	717	73
		2017	302	259	363	49
		2018	471	410	554	105
		2019	279	187	434	44
Clearwater	CRLMA-s	2010	1,395	1,236	1,555	123
		2011	549	477	616	54
		2012	861	757	982	86
		2013	697	615	787	89
		2014	741	620	858	86
		2015	1,100	980	1,254	86
		2016	914	814	1,030	106
		2017	272	237	316	52
		2018	274	238	320	61
		2019	190	143	249	38
	CRLOC-s	2018	354	294	406	74
		2019	446	364	583	77
	CRLOL-s	2012	664	542	777	65
		2013	336	286	395	45
		2014	288	233	359	34
		2015	643	539	765	52

Appendix A. Continued

MPG	Population	Spawn Year	Escapement	Lower CI	Upper CI	N-Tags
Clearwater	CRLOL-s	2016	370	308	429	43
		2017	126	102	155	23
		2018	134	108	170	30
	CRSEL-s	2018	304	256	361	63
		2019	269	211	337	50
	CRSFC-s	2012	1,226	1,043	1,377	114
		2013	724	617	840	86
		2014	575	474	693	58
		2015	1,054	881	1,196	78
		2016	922	807	1,051	98
		2017	501	438	591	81
		2018	121	95	157	20
		2019	152	111	211	26
Grande Ronde River	GRJOS-s	2011	1,731	1,553	1,943	167
		2012	1,914	1,696	2,119	193
		2013	1,797	1,630	1,979	237
		2014	2,032	1,771	2,301	239
		2015	3,202	2,842	3,527	258
		2016	1,918	1,730	2,138	221
		2017	617	546	706	118
		2018	744	657	842	169
		2019	479	376	597	100
	GRLMT-s	2019	420	329	551	86
	GRUMA-s	2013	1,268	1,128	1,410	173
		2014	1,161	994	1,341	147
		2015	2,414	2,143	2,700	183
		2016	1,599	1,460	1,775	190
		2017	578	510	646	115
		2018	445	387	512	101
		2019	395	318	491	82
	GRWAL-s	2014	520	419	615	63
		2015	1,011	867	1,165	82
		2016	957	853	1,085	115
		2017	457	395	515	86
		2018	288	246	337	66
		2019	634	481	901	105

Appendix A. Continued

MPG	Population	Spawn Year	Escapement	Lower CI	Upper CI	N-Tags
Imnaha	IRMAI-s	2011	3,429	3,117	3,758	339
		2012	2,960	2,704	3,275	302
		2013	1,560	1,428	1,778	217
		2014	2,521	2,248	2,879	323
		2015	2,654	2,383	2,956	215
		2016	2,001	1,808	2,213	241
		2017	924	820	1,018	187
		2018	673	587	763	155
		2019	704	528	932	118
Salmon River	MFBIG-s	2011	658	561	796	57
		2012	402	309	513	27
		2013	446	365	519	55
		2014	274	207	358	25
		2015	719	564	897	43
		2016	357	286	440	29
		2017	68	49	99	9
		2018	138	109	166	32
		2019	80	55	104	17
	SFMAI-s	2010	1,494	1,289	1,701	114
		2011	2,210	1,913	2,498	216
		2012	1,128	965	1,303	102
		2013	716	617	819	98
		2014	718	592	915	74
		2015	1,688	1,461	1,925	138
		2016	767	654	898	64
		2017	486	397	552	84
		2018	147	110	186	30
		2019	194	150	256	36
	SFSEC-s	2010	219	128	324	18
		2011	354	259	478	39
		2012	181	114	275	18
		2013	45	17	84	6
		2014	146	76	224	15
		2015	262	170	375	23
		2016	162	102	245	19
		2017	72	43	112	14
		2018	36	18	64	8

Appendix A. Continued

MPG	Population	Spawn Year	Escapement	Lower CI	Upper CI	N-Tags
	SFSEC-s	2019	28	9	50	5
	SREFS-s	2012	27	2	251	2
		2013	31	7	61	4
		2015	56	16	114	5
		2019	29	8	54	7
	SRLEM-s	2010	519	436	616	45
		2011	342	284	402	34
		2012	348	283	423	36
		2013	367	307	427	51
		2014	349	297	428	41
		2015	378	311	458	32
		2016	408	352	479	49
		2017	168	144	204	34
		2018	107	87	133	25
Salmon River		2019	62	45	92	13
	SRLSR-s	2010	115	85	148	10
		2011	90	70	113	9
		2012	58	40	81	6
		2013	23	16	33	3
		2014	19	12	29	2
		2015	52	34	71	4
		2016	27	18	37	3
		2017	6	4	10	1
		2018	23	16	31	5
		2019	11	6	18	2
	SRNFS-s	2016	160	124	195	19
		2018	214	75	708	12
		2019	92	66	124	21

Appendix A. Continued

MPG	Population	Spawn Year	Escapement	Lower CI	Upper CI	N-Tags
Salmon River	SRPAH-s	2011	221	10	746	12
		2012	177	40	1,356	18
		2014	151	90	242	18
		2015	121	53	196	11
		2016	74	29	126	9
		2017	12	1	27	2
		2018	32	14	60	8
		2019	36	16	63	9
	SRPAN-s	2018	81	63	101	19
		2019	105	76	137	25
	SRUMA-s	2010	444	47	979	31
		2011	619	18	1,647	30
		2012	406	95	3,394	44
		2013	206	137	296	28
		2014	179	103	281	18
		2015	373	234	506	33
		2016	245	152	344	28
		2017	74	34	120	12
		2018	50	22	84	11
		2019	40	16	76	8

Appendix B. Wild adult steelhead total age at return (1 S.E.) and female proportions (F*p*)(1 S.E.) (n = unique PIT tags observed and used to estimate value) by spawn year and population.

Spawn Year	Age 3	Age 4	Age 5	Age 6	Age 7	n Aged	F*p*	n F*p*
				CRLMA-s				
2010	0.06 (0.02)	0.61 (0.04)	0.27 (0.04)	0.04 (0.02)	0 (0)	114	0.46 (0.05)	120
2011	0.03 (0.01)	0.4 (0.07)	0.55 (0.06)	0.02 (0.02)	0 (0)	49	0.67 (0.04)	50
2012	0.04 (0.02)	0.37 (0.05)	0.55 (0.05)	0.03 (0.02)	0 (0)	80	0.64 (0.03)	79
2013	0.04 (0.02)	0.33 (0.05)	0.53 (0.05)	0.08 (0.03)	0.01 (0.01)	77	0.67 (0.03)	86
2014	0.11 (0.03)	0.53 (0.05)	0.32 (0.05)	0.03 (0.02)	0.01 (0.01)	75	0.47 (0.05)	85
2015	0.11 (0.03)	0.5 (0.06)	0.33 (0.05)	0.05 (0.02)	0 (0.01)	67	0.66 (0.04)	83
2016	0.05 (0.02)	0.44 (0.05)	0.46 (0.05)	0.05 (0.02)	0 (0)	85	0.64 (0.03)	104
2017	0.01 (0.01)	0.19 (0.06)	0.7 (0.06)	0.1 (0.04)	0 (0)	46	0.7 (0.04)	51
2018	0.05 (0.02)	0.73 (0.06)	0.16 (0.04)	0.05 (0.02)	0.01 (0.01)	52	0.63 (0.03)	58
2019	0.04 (0.02)	0.49 (0.08)	0.39 (0.07)	0.06 (0.04)	0.01 (0.01)	33	0.67 (0.06)	38
				CRLOC-s				
2010	0.04 (0.03)	0.18 (0.11)	0.46 (0.12)	0.2 (0.1)	0.05 (0.06)	8	0.48 (0.11)	7
2011	0.02 (0.02)	0.05 (0.06)	0.31 (0.15)	0.53 (0.17)	0.04 (0.05)	6	0.68 (0.06)	5
2012	0.01 (0.02)	0.07 (0.08)	0.62 (0.12)	0.23 (0.12)	0.03 (0.05)	5	0.65 (0.04)	8
2013	0.03 (0.03)	0.2 (0.14)	0.42 (0.12)	0.27 (0.15)	0.02 (0.04)	4	0.67 (0.04)	10
2014	0.06 (0.03)	0.34 (0.13)	0.44 (0.11)	0.12 (0.09)	0.01 (0.02)	6	0.51 (0.06)	11
2015	0.02 (0.02)	0.14 (0.06)	0.64 (0.07)	0.17 (0.06)	0.01 (0.01)	24	0.71 (0.04)	36
2017	0 (0)	0.01 (0.01)	0.37 (0.04)	0.58 (0.04)	0.03 (0.01)	151	0.72 (0.03)	164
2018	0.04 (0.02)	0.24 (0.05)	0.47 (0.06)	0.23 (0.05)	0.02 (0.01)	62	0.63 (0.03)	72

Appendix B. Continued

Spawn Year	Age 3	Age 4	Age 5	Age 6	Age 7	n Aged	F*p*	n F*p*
				CRLOC-s				
2019	0.02 (0.01)	0.07 (0.03)	0.3 (0.05)	0.56 (0.06)	0.05 (0.02)	67	0.75 (0.04)	75
				CRLOL-s				
2012	0.01 (0.01)	0.06 (0.03)	0.68 (0.06)	0.2 (0.05)	0.03 (0.02)	52	0.63 (0.04)	62
2013	0.02 (0.01)	0.14 (0.05)	0.54 (0.07)	0.26 (0.06)	0.02 (0.02)	39	0.67 (0.04)	45
2014	0.06 (0.03)	0.23 (0.07)	0.49 (0.07)	0.17 (0.06)	0.03 (0.02)	27	0.55 (0.05)	34
2015	0.01 (0.01)	0.11 (0.04)	0.63 (0.06)	0.21 (0.05)	0.02 (0.02)	47	0.68 (0.03)	51
2016	0.04 (0.02)	0.22 (0.06)	0.55 (0.07)	0.17 (0.06)	0.01 (0.01)	37	0.64 (0.03)	42
2017	0 (0)	0.02 (0.02)	0.46 (0.1)	0.49 (0.1)	0.02 (0.02)	19	0.69 (0.06)	21
2018	0.06 (0.03)	0.33 (0.08)	0.46 (0.08)	0.11 (0.05)	0.02 (0.02)	25	0.63 (0.03)	29
2019	0.03 (0.02)	0.19 (0.08)	0.58 (0.09)	0.15 (0.08)	0.02 (0.01)	11	0.66 (0.07)	9
				CRSEL-s				
2017	0 (0)	0.01 (0.01)	0.32 (0.1)	0.62 (0.1)	0.03 (0.03)	17	0.77 (0.05)	19
2018	0.04 (0.02)	0.31 (0.06)	0.53 (0.06)	0.1 (0.04)	0.02 (0.01)	56	0.63 (0.03)	63
2019	0.01 (0.01)	0.05 (0.03)	0.22 (0.06)	0.65 (0.07)	0.04 (0.02)	42	0.69 (0.05)	50
				CRSFC-s				
2012	0.01 (0.01)	0.06 (0.02)	0.58 (0.05)	0.29 (0.04)	0.05 (0.02)	98	0.65 (0.03)	114
2013	0.02 (0.01)	0.24 (0.05)	0.45 (0.06)	0.26 (0.05)	0.02 (0.01)	65	0.64 (0.04)	83

Appendix B. Continued

Spawn Year	Age 3	Age 4	Age 5	Age 6	Age 7	n Aged	F*p*	n F*p*
				CRSFC-s				
2014	0.04 (0.02)	0.24 (0.06)	0.49 (0.06)	0.18 (0.05)	0.02 (0.02)	50	0.53 (0.05)	58
2015	0.02 (0.01)	0.2 (0.04)	0.56 (0.05)	0.17 (0.04)	0.03 (0.02)	71	0.69 (0.03)	73
2016	0.03 (0.01)	0.21 (0.04)	0.51 (0.05)	0.23 (0.05)	0.01 (0.01)	82	0.64 (0.03)	94
2017	0 (0)	0.04 (0.02)	0.67 (0.05)	0.27 (0.05)	0.01 (0.01)	74	0.73 (0.03)	78
2018	0.06 (0.03)	0.35 (0.1)	0.36 (0.09)	0.15 (0.06)	0.05 (0.04)	19	0.63 (0.03)	19
2019	0.03 (0.02)	0.22 (0.07)	0.51 (0.08)	0.19 (0.07)	0.02 (0.01)	24	0.67 (0.06)	25
				GRJOS-s				
2011	0 (0)	0.36 (0.04)	0.58 (0.04)	0.04 (0.02)	0.01 (0.01)	151	0.67 (0.03)	161
2012	0.01 (0.01)	0.45 (0.04)	0.46 (0.04)	0.08 (0.02)	0 (0)	178	0.64 (0.02)	191
2013	0.02 (0.01)	0.26 (0.03)	0.58 (0.03)	0.12 (0.02)	0.01 (0.01)	195	0.67 (0.02)	234
2014	0.08 (0.02)	0.56 (0.03)	0.31 (0.03)	0.04 (0.01)	0.01 (0.01)	207	0.46 (0.03)	239
2015	0.02 (0.01)	0.27 (0.03)	0.63 (0.03)	0.08 (0.02)	0 (0)	223	0.65 (0.03)	253
2016	0.02 (0.01)	0.26 (0.03)	0.6 (0.03)	0.11 (0.02)	0 (0)	195	0.65 (0.02)	219
2017	0.01 (0.01)	0.19 (0.03)	0.59 (0.04)	0.2 (0.04)	0.01 (0.01)	110	0.7 (0.04)	115
2018	0.03 (0.01)	0.68 (0.04)	0.25 (0.03)	0.04 (0.01)	0.01 (0.01)	148	0.61 (0.03)	162
2019	0.01 (0.01)	0.34 (0.04)	0.51 (0.05)	0.12 (0.03)	0.02 (0.01)	97	0.73 (0.04)	99

Appendix B. Continued

Spawn Year	Age 3	Age 4	Age 5	Age 6	Age 7	n Aged	F*p*	n F*p*
				GRLMT-s				
2019	0.01 (0.01)	0.3 (0.05)	0.47 (0.05)	0.18 (0.04)	0.02 (0.01)	80	0.58 (0.05)	84
				GRUMA-s				
2010	0.02 (0.01)	0.41 (0.1)	0.49 (0.09)	0.05 (0.04)	0 (0.01)	18	0.55 (0.08)	18
2011	0 (0)	0.21 (0.07)	0.56 (0.08)	0.19 (0.07)	0.02 (0.02)	22	0.68 (0.05)	21
2012	0 (0)	0.17 (0.07)	0.62 (0.08)	0.17 (0.06)	0.01 (0.01)	27	0.65 (0.04)	28
2013	0.02 (0.01)	0.29 (0.04)	0.51 (0.04)	0.14 (0.03)	0.03 (0.01)	149	0.69 (0.03)	172
2014	0.06 (0.02)	0.43 (0.04)	0.45 (0.04)	0.04 (0.02)	0.01 (0.01)	127	0.5 (0.04)	144
2015	0.01 (0.01)	0.31 (0.04)	0.57 (0.04)	0.1 (0.02)	0 (0)	164	0.7 (0.03)	182
2016	0.02 (0.01)	0.35 (0.04)	0.45 (0.04)	0.17 (0.03)	0 (0)	151	0.65 (0.02)	187
2017	0.01 (0)	0.09 (0.03)	0.55 (0.05)	0.32 (0.04)	0.03 (0.01)	99	0.75 (0.03)	111
2018	0.03 (0.01)	0.45 (0.05)	0.42 (0.05)	0.08 (0.03)	0.01 (0.01)	91	0.64 (0.03)	100
2019	0.01 (0.01)	0.44 (0.05)	0.4 (0.05)	0.13 (0.03)	0.01 (0.01)	81	0.59 (0.05)	82
				GRWAL-s				
2010	0.02 (0.01)	0.3 (0.16)	0.52 (0.13)	0.09 (0.09)	0.01 (0.03)	4	0.47 (0.11)	6
2011	0 (0)	0.32 (0.1)	0.5 (0.09)	0.14 (0.08)	0.01 (0.02)	16	0.66 (0.06)	18
2012	0 (0.01)	0.21 (0.11)	0.57 (0.1)	0.17 (0.09)	0.01 (0.02)	10	0.63 (0.05)	12
2013	0.02 (0.02)	0.26 (0.11)	0.43 (0.1)	0.24 (0.1)	0.02 (0.02)	9	0.64 (0.05)	20

Appendix B. Continued

Spawn Year	Age 3	Age 4	Age 5	Age 6	Age 7	n Aged	F*p*	n F*p*
				GRWAL-s				
2014	0.06 (0.02)	0.42 (0.06)	0.41 (0.06)	0.1 (0.04)	0.02 (0.01)	50	0.52 (0.04)	63
2015	0.03 (0.01)	0.34 (0.05)	0.53 (0.05)	0.09 (0.03)	0 (0)	68	0.68 (0.03)	80
2016	0.02 (0.01)	0.34 (0.04)	0.45 (0.04)	0.18 (0.04)	0.01 (0)	104	0.63 (0.03)	114
2017	0.01 (0)	0.13 (0.04)	0.51 (0.05)	0.32 (0.05)	0.01 (0.01)	75	0.7 (0.04)	84
2018	0.02 (0.01)	0.31 (0.06)	0.56 (0.06)	0.09 (0.03)	0.01 (0.01)	57	0.64 (0.03)	62
2019	0.01 (0.01)	0.38 (0.05)	0.46 (0.05)	0.12 (0.03)	0.01 (0.01)	98	0.66 (0.04)	99
				IRMAI-s				
2010	0.02 (0.01)	0.32 (0.11)	0.49 (0.1)	0.13 (0.07)	0.02 (0.03)	13	0.54 (0.09)	14
2011	0 (0)	0.32 (0.03)	0.52 (0.03)	0.14 (0.02)	0.01 (0)	303	0.61 (0.03)	326
2012	0 (0)	0.17 (0.02)	0.59 (0.03)	0.22 (0.02)	0.01 (0.01)	279	0.66 (0.02)	297
2013	0.02 (0.01)	0.27 (0.03)	0.47 (0.04)	0.22 (0.03)	0.02 (0.01)	172	0.65 (0.03)	213
2014	0.05 (0.01)	0.41 (0.03)	0.49 (0.03)	0.04 (0.01)	0.01 (0)	278	0.57 (0.03)	322
2015	0.02 (0.01)	0.35 (0.03)	0.49 (0.04)	0.13 (0.02)	0 (0)	173	0.66 (0.03)	211
2016	0.02 (0.01)	0.33 (0.03)	0.53 (0.03)	0.12 (0.02)	0 (0)	217	0.65 (0.02)	238
2017	0 (0)	0.08 (0.02)	0.6 (0.04)	0.3 (0.04)	0.01 (0.01)	167	0.75 (0.03)	184
2018	0.03 (0.01)	0.58 (0.04)	0.35 (0.04)	0.04 (0.02)	0.01 (0.01)	134	0.63 (0.02)	151
2019	0.01 (0.01)	0.36 (0.05)	0.48 (0.05)	0.13 (0.03)	0.02 (0.01)	99	0.67 (0.04)	114

Appendix B. Continued

Spawn Year	Age 3	Age 4	Age 5	Age 6	Age 7	n Aged	F*p*	n F*p*
				SNASO-s				
2010	0.06 (0.02)	0.64 (0.05)	0.24 (0.04)	0.05 (0.02)	0 (0)	94	0.45 (0.05)	82
2011	0.03 (0.01)	0.29 (0.05)	0.57 (0.05)	0.1 (0.03)	0.01 (0.01)	82	0.7 (0.04)	96
2012	0.09 (0.03)	0.27 (0.04)	0.49 (0.05)	0.13 (0.03)	0.01 (0.01)	111	0.64 (0.03)	116
2013	0.08 (0.03)	0.61 (0.05)	0.25 (0.04)	0.06 (0.02)	0 (0)	92	0.66 (0.03)	113
2014	0.1 (0.03)	0.59 (0.05)	0.27 (0.04)	0.02 (0.01)	0 (0)	89	0.5 (0.04)	110
2015	0.06 (0.02)	0.33 (0.05)	0.54 (0.05)	0.06 (0.02)	0 (0.01)	84	0.67 (0.03)	100
2016	0.05 (0.02)	0.42 (0.04)	0.43 (0.04)	0.09 (0.02)	0 (0)	129	0.63 (0.03)	149
2017	0 (0.01)	0.09 (0.04)	0.74 (0.05)	0.15 (0.05)	0 (0)	52	0.72 (0.04)	57
2018	0.05 (0.02)	0.63 (0.06)	0.23 (0.05)	0.07 (0.03)	0.01 (0.01)	53	0.63 (0.03)	59
2019	0.04 (0.02)	0.4 (0.07)	0.44 (0.07)	0.08 (0.04)	0.01 (0.01)	32	0.63 (0.06)	28
				SNTUC-s				
2010	0.05 (0.02)	0.67 (0.05)	0.24 (0.04)	0.03 (0.02)	0 (0)	81	0.55 (0.05)	83
2011	0.03 (0.01)	0.37 (0.07)	0.54 (0.06)	0.05 (0.03)	0 (0.01)	49	0.7 (0.05)	39
2012	0.1 (0.03)	0.31 (0.05)	0.5 (0.05)	0.08 (0.03)	0 (0)	88	0.65 (0.03)	87
2013	0.11 (0.05)	0.54 (0.07)	0.27 (0.06)	0.06 (0.03)	0.01 (0.01)	43	0.66 (0.04)	54
2014	0.1 (0.03)	0.65 (0.06)	0.22 (0.05)	0.02 (0.02)	0 (0.01)	51	0.51 (0.05)	58
2015	0.1 (0.04)	0.5 (0.06)	0.33 (0.06)	0.05 (0.02)	0 (0.01)	51	0.68 (0.04)	64

Appendix B. Continued

Spawn Year	Age 3	Age 4	Age 5	Age 6	Age 7	n Aged	F*p*	n F*p*
				SNTUC-s				
2016	0.05 (0.02)	0.46 (0.06)	0.46 (0.06)	0.03 (0.02)	0 (0)	63	0.63 (0.03)	72
2017	0.01 (0.01)	0.2 (0.06)	0.65 (0.06)	0.12 (0.04)	0 (0)	44	0.69 (0.05)	49
2018	0.09 (0.03)	0.71 (0.05)	0.17 (0.04)	0.02 (0.01)	0.01 (0.01)	90	0.62 (0.03)	103
2019	0.04 (0.03)	0.41 (0.07)	0.49 (0.07)	0.03 (0.03)	0 (0.01)	38	0.62 (0.06)	42
				MFBIG-s				
2010	0.01 (0.01)	0.06 (0.03)	0.44 (0.08)	0.38 (0.07)	0.09 (0.05)	32	0.65 (0.07)	39
2011	0 (0)	0.03 (0.02)	0.3 (0.06)	0.57 (0.06)	0.08 (0.04)	54	0.68 (0.04)	54
2012	0 (0)	0.01 (0.02)	0.34 (0.08)	0.44 (0.08)	0.17 (0.07)	25	0.65 (0.03)	24
2013	0.01 (0.01)	0.08 (0.03)	0.45 (0.06)	0.41 (0.07)	0.05 (0.02)	44	0.66 (0.04)	54
2014	0.03 (0.02)	0.19 (0.07)	0.44 (0.08)	0.29 (0.09)	0.03 (0.02)	20	0.57 (0.06)	25
2015	0.01 (0.01)	0.12 (0.06)	0.59 (0.08)	0.26 (0.08)	0.01 (0.01)	21	0.69 (0.04)	43
2016	0.01 (0.01)	0.07 (0.04)	0.32 (0.08)	0.57 (0.09)	0.02 (0.02)	25	0.64 (0.03)	29
2017	0 (0)	0.02 (0.03)	0.32 (0.11)	0.54 (0.12)	0.09 (0.07)	9	0.72 (0.06)	9
2018	0.02 (0.01)	0.18 (0.07)	0.6 (0.08)	0.16 (0.06)	0.01 (0.01)	29	0.63 (0.03)	30
2019	0.01 (0.01)	0.12 (0.06)	0.37 (0.09)	0.41 (0.11)	0.05 (0.04)	15	0.67 (0.06)	17
				SFMAI-s				
2010	0.01 (0.01)	0.04 (0.02)	0.35 (0.05)	0.44 (0.05)	0.15 (0.04)	99	0.59 (0.04)	110

Appendix B. Continued

Spawn Year	Age 3	Age 4	Age 5	Age 6	Age 7	n Aged	F*p*	n F*p*
				SFMAI-s				
2011	0 (0)	0.01 (0.01)	0.24 (0.03)	0.65 (0.03)	0.1 (0.02)	181	0.72 (0.03)	209
2012	0 (0)	0.01 (0.01)	0.26 (0.04)	0.58 (0.05)	0.13 (0.03)	92	0.65 (0.03)	101
2013	0 (0)	0.03 (0.02)	0.29 (0.05)	0.54 (0.06)	0.11 (0.04)	68	0.68 (0.04)	98
2014	0.02 (0.01)	0.09 (0.03)	0.36 (0.06)	0.48 (0.06)	0.04 (0.02)	60	0.58 (0.05)	74
2015	0 (0)	0.06 (0.02)	0.58 (0.04)	0.34 (0.04)	0.01 (0.01)	117	0.69 (0.03)	135
2016	0.01 (0.01)	0.06 (0.03)	0.36 (0.06)	0.56 (0.06)	0.01 (0.01)	57	0.65 (0.03)	63
2017	0 (0)	0 (0.01)	0.12 (0.04)	0.74 (0.05)	0.12 (0.04)	76	0.78 (0.04)	83
2018	0.01 (0.01)	0.07 (0.05)	0.7 (0.08)	0.16 (0.06)	0.03 (0.03)	25	0.63 (0.03)	29
2019	0 (0)	0.04 (0.03)	0.2 (0.06)	0.67 (0.08)	0.07 (0.04)	34	0.72 (0.06)	36
				SFSEC-s				
2010	0.01 (0.02)	0.02 (0.03)	0.15 (0.08)	0.45 (0.11)	0.33 (0.11)	16	0.64 (0.09)	17
2011	0.01 (0.01)	0.02 (0.02)	0.14 (0.06)	0.64 (0.08)	0.16 (0.06)	33	0.69 (0.05)	37
2012	0 (0.01)	0.01 (0.01)	0.19 (0.09)	0.63 (0.11)	0.13 (0.08)	14	0.65 (0.04)	18
2013	0.01 (0.02)	0.08 (0.09)	0.41 (0.13)	0.33 (0.14)	0.09 (0.11)	4	0.67 (0.05)	6
2014	0.03 (0.03)	0.14 (0.08)	0.38 (0.11)	0.39 (0.14)	0.02 (0.03)	9	0.53 (0.06)	15
2015	0.01 (0.01)	0.04 (0.04)	0.46 (0.09)	0.43 (0.1)	0.03 (0.03)	19	0.7 (0.04)	23
2016	0.02 (0.02)	0.07 (0.05)	0.36 (0.09)	0.46 (0.11)	0.06 (0.06)	18	0.64 (0.03)	19

Appendix B. Continued

Spawn Year	Age 3	Age 4	Age 5	Age 6	Age 7	n Aged	F*p*	n F*p*
				SFSEC-s				
2017	0 (0)	0 (0.01)	0.2 (0.1)	0.75 (0.1)	0.03 (0.03)	11	0.73 (0.05)	12
2018	0.04 (0.03)	0.15 (0.11)	0.61 (0.12)	0.12 (0.08)	0.03 (0.04)	7	0.64 (0.03)	8
2019	0.02 (0.02)	0.09 (0.07)	0.36 (0.12)	0.46 (0.16)	0.03 (0.03)	5	0.66 (0.08)	5
				SREFS-s				
2012	0 (0.01)	0.18 (0.18)	0.55 (0.16)	0.17 (0.16)	0.01 (0.05)	1	0 (0)	0
2013	0.01 (0.02)	0.14 (0.14)	0.46 (0.12)	0.29 (0.15)	0.03 (0.04)	2	0.66 (0.05)	4
2014	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0 (0)	0
2015	0.02 (0.02)	0.27 (0.14)	0.59 (0.13)	0.09 (0.08)	0 (0.01)	4	0.69 (0.05)	5
2016	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0 (0)	0
2017	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0 (0)	0
2018	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0 (0)	0
2019	0.01 (0.01)	0.33 (0.13)	0.45 (0.1)	0.15 (0.1)	0.02 (0.02)	6	0.64 (0.08)	7
				SRLEM-s				
2010	0.03 (0.02)	0.56 (0.07)	0.37 (0.07)	0.03 (0.02)	0 (0)	40	0.52 (0.06)	43
2011	0 (0)	0.42 (0.08)	0.53 (0.08)	0.03 (0.03)	0 (0.01)	30	0.65 (0.05)	33
2012	0.01 (0.02)	0.34 (0.07)	0.5 (0.07)	0.12 (0.05)	0 (0.01)	35	0.66 (0.03)	36
2013	0.05 (0.02)	0.58 (0.07)	0.29 (0.06)	0.07 (0.03)	0 (0.01)	44	0.66 (0.04)	51

Appendix B. Continued

Spawn Year	Age 3	Age 4	Age 5	Age 6	Age 7	n Aged	F*p*	n F*p*
				SRLEM-s				
2014	0.09 (0.03)	0.49 (0.07)	0.33 (0.06)	0.06 (0.03)	0.01 (0.01)	36	0.57 (0.05)	41
2015	0.03 (0.02)	0.37 (0.08)	0.53 (0.08)	0.06 (0.03)	0 (0)	29	0.68 (0.04)	32
2016	0.03 (0.02)	0.59 (0.07)	0.31 (0.06)	0.05 (0.03)	0 (0)	43	0.63 (0.03)	49
2017	0.01 (0.01)	0.19 (0.06)	0.55 (0.07)	0.23 (0.06)	0.02 (0.02)	32	0.73 (0.05)	34
2018	0.02 (0.01)	0.69 (0.1)	0.24 (0.09)	0.03 (0.03)	0 (0.01)	17	0.64 (0.03)	24
2019	0.01 (0.01)	0.49 (0.11)	0.39 (0.09)	0.08 (0.06)	0.01 (0.01)	12	0.69 (0.06)	13
				SRLSR-s				
2010	0.02 (0.01)	0.24 (0.12)	0.43 (0.11)	0.23 (0.11)	0.02 (0.04)	8	0.61 (0.1)	7
2011	0 (0)	0.12 (0.11)	0.54 (0.16)	0.25 (0.18)	0.02 (0.05)	3	0.69 (0.06)	3
2012	0.01 (0.11)	0.55 (0.24)	0.33 (0.2)	0.04 (0.11)	0 (0.02)	1	0.65 (0.04)	2
2013	0.01 (0.01)	0.12 (0.13)	0.46 (0.13)	0.3 (0.16)	0.03 (0.05)	2	0.66 (0.05)	3
2014	0.03 (0.03)	0.2 (0.15)	0.39 (0.13)	0.26 (0.19)	0.03 (0.04)	1	0.52 (0.07)	2
2015	0.02 (0.03)	0.35 (0.17)	0.52 (0.15)	0.08 (0.08)	0 (0)	2	0.69 (0.04)	4
2016	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0.64 (0.04)	3
2017	0 (0)	0.04 (0.1)	0.38 (0.18)	0.5 (0.21)	0.04 (0.07)	1	0.73 (0.06)	1
2018	0.02 (0.02)	0.52 (0.16)	0.37 (0.14)	0.06 (0.05)	0.01 (0.01)	5	0.63 (0.03)	5
2019	0.01 (0.01)	0.29 (0.16)	0.45 (0.12)	0.16 (0.15)	0.02 (0.03)	1	0.65 (0.08)	2

Appendix B. Continued

Spawn Year	Age 3	Age 4	Age 5	Age 6	Age 7	n Aged	F*p*	n F*p*
				SRNFS-s				
2016	0.01 (0.01)	0.19 (0.08)	0.36 (0.09)	0.41 (0.11)	0.01 (0.01)	16	0.64 (0.03)	19
2017	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0 (0)	0
2018	0.02 (0.01)	0.22 (0.11)	0.58 (0.1)	0.14 (0.07)	0.01 (0.02)	11	0.63 (0.03)	11
2019	0.01 (0.01)	0.26 (0.08)	0.4 (0.08)	0.27 (0.09)	0.03 (0.02)	20	0.63 (0.06)	21
				SRPAH-s				
2011	0 (0)	0.39 (0.14)	0.54 (0.12)	0.03 (0.06)	0 (0.01)	7	0.65 (0.06)	8
2012	0.03 (0.06)	0.74 (0.11)	0.17 (0.1)	0.02 (0.04)	0 (0)	11	0.65 (0.04)	10
2013	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0 (0)	0
2014	0.06 (0.03)	0.41 (0.1)	0.4 (0.09)	0.09 (0.06)	0.02 (0.02)	14	0.57 (0.06)	18
2015	0.04 (0.04)	0.65 (0.15)	0.26 (0.13)	0.02 (0.03)	0 (0)	5	0.69 (0.05)	10
2016	0.02 (0.01)	0.54 (0.14)	0.36 (0.12)	0.05 (0.06)	0 (0)	7	0.64 (0.03)	9
2017	0.01 (0.01)	0.23 (0.17)	0.53 (0.13)	0.15 (0.14)	0.01 (0.02)	2	0.73 (0.06)	2
2018	0.02 (0.01)	0.44 (0.15)	0.41 (0.13)	0.09 (0.06)	0.01 (0.01)	6	0.64 (0.03)	7
2019	0.01 (0.01)	0.4 (0.12)	0.48 (0.1)	0.07 (0.06)	0.01 (0.01)	8	0.66 (0.07)	9
				SRPAN-s				
2018	0.02 (0.01)	0.3 (0.11)	0.42 (0.11)	0.21 (0.09)	0.02 (0.03)	13	0.63 (0.03)	19
2019	0.01 (0.01)	0.3 (0.08)	0.46 (0.07)	0.19 (0.07)	0.02 (0.02)	23	0.66 (0.06)	25

Appendix B. Continued

Spawn Year	Age 3	Age 4	Age 5	Age 6	Age 7	n Aged	F*p*	n F*p*
				SRUMA-s				
2010	0.02 (0.01)	0.61 (0.09)	0.31 (0.08)	0.05 (0.04)	0 (0.01)	27	0.48 (0.07)	31
2011	0 (0)	0.5 (0.09)	0.47 (0.08)	0.01 (0.02)	0 (0)	27	0.62 (0.06)	29
2012	0.01 (0.01)	0.4 (0.08)	0.53 (0.07)	0.05 (0.03)	0 (0)	37	0.64 (0.04)	34
2013	0.03 (0.02)	0.45 (0.09)	0.4 (0.08)	0.09 (0.05)	0.01 (0.01)	24	0.64 (0.05)	28
2014	0.07 (0.03)	0.37 (0.09)	0.43 (0.09)	0.08 (0.05)	0.02 (0.02)	17	0.51 (0.07)	18
2015	0.04 (0.03)	0.36 (0.07)	0.53 (0.08)	0.05 (0.03)	0 (0)	30	0.68 (0.04)	32
2016	0.02 (0.01)	0.4 (0.09)	0.49 (0.08)	0.07 (0.05)	0 (0)	24	0.64 (0.03)	28
2017	0.01 (0.01)	0.21 (0.1)	0.57 (0.09)	0.17 (0.09)	0.01 (0.01)	12	0.72 (0.05)	11
2018	0.03 (0.02)	0.57 (0.13)	0.31 (0.11)	0.06 (0.04)	0.01 (0.02)	9	0.64 (0.03)	10
2019	0.01 (0.01)	0.47 (0.13)	0.37 (0.1)	0.1 (0.08)	0.01 (0.02)	8	0.62 (0.08)	8

Appendix C. Summary of genetic diversity by spawn year and population for steelhead in the Snake River basin. Reported are observed (H_o) and expected heterozygosity (H_e) along with deviations from Hardy-Weinberg equilibrium (HWE) for collections with more than 20 samples.

Array Group	Spawn Year (sample size)	H_o	H_e	% Polymorphic	HWE Het Deficiency	HWE Het Excess
SRPAN-s	2019 (n = 25)	29.6%	29.6%	96.6%	0	0
SRNFS-s	2019 (n = 21)	30.5%	30.7%	94.8%	0	0
SRLEM-s	2010 (n = 44)	31.9%	32.2%	99.4%	2	0
SRLEM-s	2011 (n = 33)	31.1%	31.7%	99.4%	0	0
SRLEM-s	2012 (n = 35)	32.5%	32.5%	98.9%	2	0
SRLEM-s	2013 (n = 50)	31.7%	31.8%	100.0%	3	0
SRLEM-s	2014 (n = 39)	31.3%	31.5%	98.9%	1	2
SRLEM-s	2015 (n = 32)	30.5%	31.7%	98.9%	1	0
SRLEM-s	2016 (n = 49)	31.8%	31.9%	100.0%	1	0
SRLEM-s	2017 (n = 34)	30.9%	31.6%	100.0%	3	0
SRLEM-s	2018 (n = 24)	31.1%	32.2%	98.3%	1	0
SRUMA-s	2010 (n = 31)	31.2%	29.7%	98.9%	0	1
SRUMA-s	2011 (n = 30)	30.3%	29.9%	97.1%	1	0
SRUMA-s	2012 (n = 34)	29.3%	29.5%	96.0%	1	0
SRUMA-s	2013 (n = 28)	28.9%	29.3%	97.1%	0	0
SRUMA-s	2015 (n = 32)	30.8%	29.9%	98.3%	1	0
SRUMA-s	2016 (n = 28)	28.9%	29.1%	97.7%	1	0
MFBIG-s	2010 (n = 39)	28.9%	28.9%	93.7%	1	0
MFBIG-s	2011 (n = 56)	29.1%	29.1%	94.8%	1	0
MFBIG-s	2012 (n = 26)	29.1%	29.5%	90.2%	4	0
MFBIG-s	2013 (n = 55)	28.8%	29.3%	94.3%	1	0
MFBIG-s	2014 (n = 25)	29.7%	29.0%	90.8%	1	1
MFBIG-s	2015 (n = 43)	29.2%	29.2%	94.8%	1	0
MFBIG-s	2016 (n = 29)	31.6%	30.3%	91.4%	0	0
MFBIG-s	2018 (n = 30)	28.2%	29.0%	95.4%	0	0
SFSEC-s	2011 (n = 39)	28.0%	28.6%	93.7%	0	0
SFSEC-s	2015 (n = 23)	29.0%	28.7%	90.8%	0	1
SFMAI-s	2010 (n = 114)	29.5%	29.6%	97.7%	1	0
SFMAI-s	2011 (n = 214)	29.8%	30.0%	98.9%	1	0
SFMAI-s	2012 (n = 101)	29.4%	29.6%	94.3%	0	0
SFMAI-s	2013 (n = 98)	30.7%	30.0%	98.3%	1	1
SFMAI-s	2014 (n = 74)	29.7%	29.7%	92.0%	1	0
SFMAI-s	2015 (n = 136)	29.6%	29.7%	97.1%	2	0
SFMAI-s	2016 (n = 63)	30.2%	29.8%	92.0%	0	0
SFMAI-s	2017 (n = 83)	29.6%	29.8%	96.6%	3	0
SFMAI-s	2018 (n = 29)	28.7%	29.5%	92.5%	2	1

Appendix C. Continued

Array Group	Spawn Year (sample size)	H_o	H_e	% Polymorphic	HWE Het Deficiency	HWE Het Excess
SFMAI-s	2019 (n = 36)	30.0%	29.4%	92.5%	0	0
CRLOC-s	2015 (n = 37)	27.9%	27.6%	89.7%	0	0
CRLOC-s	2017 (n = 171)	27.8%	28.3%	96.6%	7	0
CRLOC-s	2018 (n = 71)	27.1%	27.9%	91.4%	2	0
CRLOC-s	2019 (n = 75)	27.5%	28.1%	93.7%	4	0
CRSEL-s	2017 (n = 20)	28.3%	28.5%	87.9%	1	0
CRSEL-s	2018 (n = 59)	27.6%	28.3%	90.8%	3	0
CRSEL-s	2019 (n = 50)	27.8%	28.7%	91.4%	4	0
CRLOL-s	2012 (n = 65)	28.2%	28.2%	94.8%	1	0
CRLOL-s	2013 (n = 45)	28.7%	28.1%	92.5%	1	0
CRLOL-s	2014 (n = 34)	28.0%	27.8%	93.1%	0	1
CRLOL-s	2015 (n = 52)	28.5%	28.4%	94.8%	0	0
CRLOL-s	2016 (n = 42)	26.7%	27.9%	91.4%	2	0
CRLOL-s	2017 (n = 23)	26.2%	27.2%	90.2%	3	0
CRLOL-s	2018 (n = 29)	27.4%	28.1%	93.7%	2	0
CRSFC-s	2012 (n = 114)	28.3%	28.5%	96.0%	1	1
CRSFC-s	2013 (n = 86)	28.0%	28.2%	96.6%	5	0
CRSFC-s	2014 (n = 58)	27.8%	28.2%	94.8%	1	0
CRSFC-s	2015 (n = 74)	28.3%	28.5%	96.6%	0	1
CRSFC-s	2016 (n = 94)	27.9%	28.2%	97.7%	6	0
CRSFC-s	2017 (n = 80)	28.6%	27.8%	94.3%	2	2
CRSFC-s	2019 (n = 25)	29.4%	28.7%	91.4%	1	0
CRLMA-s	2010 (n = 123)	30.1%	30.7%	99.4%	2	0
CRLMA-s	2011 (n = 52)	30.6%	31.1%	99.4%	3	0
CRLMA-s	2012 (n = 80)	30.4%	30.8%	99.4%	1	0
CRLMA-s	2013 (n = 88)	30.2%	30.6%	98.9%	0	0
CRLMA-s	2014 (n = 85)	31.2%	31.1%	100.0%	1	0
CRLMA-s	2015 (n = 84)	30.3%	31.0%	100.0%	3	0
CRLMA-s	2016 (n = 104)	30.7%	31.0%	99.4%	2	0
CRLMA-s	2017 (n = 52)	29.8%	30.3%	98.3%	1	0
CRLMA-s	2018 (n = 59)	28.7%	30.4%	100.0%	3	0
CRLMA-s	2019 (n = 38)	30.4%	30.7%	97.1%	0	0
IRMAI-s	2011 (n = 335)	30.1%	30.4%	100.0%	7	0
IRMAI-s	2012 (n = 300)	30.0%	30.3%	100.0%	4	0
IRMAI-s	2013 (n = 217)	30.1%	30.2%	100.0%	3	0
IRMAI-s	2014 (n = 323)	30.6%	30.4%	100.0%	1	3
IRMAI-s	2015 (n = 213)	30.1%	30.3%	100.0%	1	1
IRMAI-s	2016 (n = 238)	29.8%	30.0%	100.0%	5	0
IRMAI-s	2017 (n = 185)	29.1%	30.1%	99.4%	4	0

Appendix C. Continued

Array Group	Spawn Year (sample size)	H_o	H_e	% Polymorphic	HWE Het Deficiency	HWE Het Excess
IRMAI-s	2018 (n = 145)	29.3%	30.1%	100.0%	6	0
IRMAI-s	2019 (n = 114)	29.6%	30.1%	98.9%	5	0
GRLMT-s	2019 (n = 84)	29.3%	30.2%	99.4%	4	0
GRJOS-s	2011 (n = 165)	30.0%	30.6%	100.0%	2	0
GRJOS-s	2012 (n = 193)	30.0%	30.1%	99.4%	2	0
GRJOS-s	2013 (n = 236)	29.7%	30.1%	100.0%	1	0
GRJOS-s	2014 (n = 239)	30.0%	30.2%	99.4%	2	0
GRJOS-s	2015 (n = 257)	30.4%	30.4%	98.9%	2	1
GRJOS-s	2016 (n = 219)	29.9%	30.5%	100.0%	8	0
GRJOS-s	2017 (n = 118)	30.3%	30.3%	100.0%	5	1
GRJOS-s	2018 (n = 162)	29.3%	30.2%	98.3%	8	0
GRJOS-s	2019 (n = 99)	29.4%	30.2%	97.1%	1	0
GRWAL-s	2013 (n = 20)	31.2%	30.6%	97.7%	0	0
GRWAL-s	2014 (n = 63)	30.9%	30.9%	99.4%	2	0
GRWAL-s	2015 (n = 82)	31.0%	31.4%	99.4%	2	0
GRWAL-s	2016 (n = 114)	30.5%	31.0%	100.0%	2	0
GRWAL-s	2017 (n = 86)	29.6%	30.9%	99.4%	5	0
GRWAL-s	2018 (n = 61)	29.5%	30.6%	99.4%	6	0
GRWAL-s	2019 (n = 99)	30.5%	31.0%	100.0%	2	0
GRUMA-s	2011 (n = 22)	30.1%	29.7%	96.0%	1	0
GRUMA-s	2012 (n = 29)	31.3%	30.3%	98.9%	1	0
GRUMA-s	2013 (n = 173)	30.9%	30.9%	99.4%	3	0
GRUMA-s	2014 (n = 145)	30.9%	31.0%	99.4%	2	1
GRUMA-s	2015 (n = 183)	30.5%	30.8%	100.0%	3	0
GRUMA-s	2016 (n = 187)	30.6%	30.8%	100.0%	2	0
GRUMA-s	2017 (n = 114)	29.7%	30.5%	100.0%	2	0
GRUMA-s	2018 (n = 99)	30.1%	30.9%	98.9%	4	0
GRUMA-s	2019 (n = 82)	30.1%	30.7%	99.4%	1	1
SNTUC-s	2010 (n = 84)	31.4%	31.3%	99.4%	1	0
SNTUC-s	2011 (n = 42)	29.6%	30.5%	100.0%	2	0
SNTUC-s	2012 (n = 87)	30.1%	31.0%	100.0%	3	0
SNTUC-s	2013 (n = 54)	30.6%	30.7%	98.9%	0	0
SNTUC-s	2014 (n = 59)	31.0%	31.2%	100.0%	0	0
SNTUC-s	2015 (n = 66)	31.6%	31.8%	100.0%	1	0
SNTUC-s	2016 (n = 72)	30.7%	31.2%	100.0%	2	0
SNTUC-s	2017 (n = 49)	29.9%	31.1%	100.0%	4	0
SNTUC-s	2018 (n = 99)	30.3%	31.0%	99.4%	4	0
SNTUC-s	2019 (n = 42)	30.3%	30.9%	99.4%	0	0

Appendix C. Continued

Array Group	Spawn Year (sample size)	H_o	H_e	% Polymorphic	HWE Het Deficiency	HWE Het Excess
SNASO-s	2010 (n = 93)	30.8%	31.1%	99.4%	2	0
SNASO-s	2011 (n = 98)	30.6%	30.9%	100.0%	2	1
SNASO-s	2012 (n = 117)	30.8%	30.7%	99.4%	1	0
SNASO-s	2013 (n = 116)	30.7%	31.0%	100.0%	1	1
SNASO-s	2014 (n = 110)	31.1%	31.2%	100.0%	1	0
SNASO-s	2015 (n = 100)	31.0%	31.0%	100.0%	2	0
SNASO-s	2016 (n = 149)	31.0%	31.4%	100.0%	4	0
SNASO-s	2017 (n = 60)	30.8%	30.8%	98.3%	2	0
SNASO-s	2018 (n = 55)	30.1%	30.7%	97.1%	2	0
SNASO-s	2019 (n = 28)	30.3%	29.8%	96.6%	0	0

Appendix D. Wild adult Chinook Salmon abundance by spawn year and population including the lower and upper confidence intervals and the annual number of unique PIT tags from the annual Lower Granite Dam PIT tag group observed within the population and available to estimate age and sex (tags not corrected for detection probability).

MPG	Population	Spawn Year	Escapement	Lower CI	Upper CI	N-Tags
Dry Clearwater	SCUMA	2012	1,058	824	1,291	101
		2013	591	499	712	90
		2014	766	613	941	81
		2015	696	548	841	67
		2016	336	255	432	48
		2017	64	44	88	14
		2018	144	104	198	26
		2019	139	90	193	24
Wet Clearwater	CRLOC	2018	293	232	365	59
		2019	134	90	183	26
	CRLOL	2012	312	222	417	31
		2013	177	133	236	28
		2014	138	85	189	14
		2015	212	151	285	20
		2016	264	191	340	39
		2017	33	20	49	7
		2018	39	24	59	8
	SEMEA	2018	404	312	498	65
		2019	169	117	233	29
Lower Snake	SNTUC	2010	72	35	131	3
		2011	27	15	46	3
		2012	92	60	142	9
		2013	38	24	55	6
		2014	119	78	163	14
		2015	167	108	234	14
		2016	81	55	117	13
		2017	63	32	101	8
		2019	33	18	52	7
Grande Ronde/Imnaha	GRCAT	2010	293	171	410	13
		2011	153	113	201	18
		2012	389	275	536	40
		2013	514	356	679	67
		2014	930	479	1,677	66
		2015	313	215	416	32

Appendix D. Continued

MPG	Population	Spawn Year	Escapement	Lower CI	Upper CI	N-Tags
Grande Ronde / Imnaha	GRCAT	2016	259	189	350	41
		2017	71	42	110	16
		2018	69	39	105	15
		2019	102	60	144	24
	GRLOO	2010	71	32	127	3
		2011	311	250	397	35
		2012	162	104	240	16
		2013	186	136	239	30
		2014	189	127	263	22
		2015	245	169	318	25
		2016	292	219	381	45
		2017	35	22	52	8
		2018	95	68	129	20
		2019	51	29	75	11
	GRLOS	2019	193	138	252	47
	GRLOS-GRMIN	2014	1,999	1,738	2,279	189
		2015	1,950	1,625	2,245	164
		2016	1,463	1,284	1,640	215
		2017	326	260	393	61
		2018	549	458	654	86
		2019	403	326	509	64
	GRUMA	2012	132	61	204	13
		2013	16	3	37	2
		2015	187	115	277	19
		2016	61	30	101	9
		2017	17	4	35	3
		2018	143	99	191	31
		2019	14	2	38	2
	GRWEN	2019	115	77	159	24
	IRBSH	2011	326	214	455	35
		2012	117	66	191	12
		2013	81	36	122	11
		2014	112	55	177	13
		2015	83	22	195	4
		2016	67	36	104	11
		2017	31	14	61	7
		2018	17	4	38	3
		2019	8	1	23	1
	IRMAI	2011	1,867	1,636	2,149	191
		2012	896	753	1,095	91

Appendix D. Continued

MPG	Population	Spawn Year	Escapement	Lower CI	Upper CI	N-Tags
Grande Ronde / Imnaha	IRMAI	2013	596	471	715	85
		2014	1,171	956	1,385	137
		2015	752	544	942	54
		2016	881	769	1,013	144
		2017	332	265	397	74
		2018	242	176	294	49
		2019	187	135	258	46
South Fork Salmon River	SFEFS	2010	873	627	1,190	41
		2011	592	465	762	66
		2012	722	553	884	75
		2013	1,006	818	1,174	148
		2014	1,198	985	1,433	143
		2015	713	507	971	52
		2016	660	540	781	127
		2017	185	135	244	45
		2018	364	279	454	73
		2019	185	118	273	49
	SFMAI	2010	3,706	3,052	4,379	140
		2011	2,857	2,493	3,171	296
		2012	1,649	1,405	1,932	156
		2013	1,095	910	1,294	152
		2014	1,938	1,658	2,241	219
		2015	880	648	1,139	48
		2016	635	504	741	88
		2017	179	130	241	42
		2018	292	216	376	57
		2019	159	98	224	39
	SFSEC	2010	1,084	780	1,442	49
		2011	719	572	886	78
		2012	923	721	1,131	95
		2013	1,194	1,027	1,409	177
		2014	1,513	1,256	1,794	180
		2015	654	453	853	47
		2016	560	451	658	107
		2017	231	181	296	56
		2018	352	277	446	69
		2019	205	136	297	54
South Fork Salmon River	SRLSR	2010	74	42	129	3
		2011	110	75	153	12
		2012	11	4	24	1
		2013	8	4	14	1

Appendix D. Continued

MPG	Population	Spawn Year	Escapement	Lower CI	Upper CI	N-Tags
South Fork Salmon River	SRLSR	2018	5	1	10	1
		2019	5	2	10	1
Middle Fork Salmon	MFBEA	2015	1,404	1,210	1,644	143
		2016	448	363	552	75
		2017	26	14	39	6
		2018	241	188	307	51
		2019	133	93	183	30
	MFBIG	2011	374	280	466	34
		2012	657	525	802	64
		2013	899	774	1,041	144
		2014	1,143	962	1,374	130
		2015	1,133	922	1,374	96
		2016	752	648	902	121
		2017	146	111	190	30
		2018	331	259	409	62
		2019	176	126	230	39
Upper Salmon	SREFS	2010	490	26	1,752	12
		2011	153	54	276	16
		2012	209	44	394	18
		2013	245	163	326	37
		2014	285	204	394	35
		2015	120	57	203	10
		2017	6	0	19	1
	SRLEM	2010	159	99	248	7
		2011	290	220	356	32
		2012	114	71	168	11
		2013	431	367	524	73
		2014	664	533	807	81
		2015	735	577	879	71
		2016	208	153	274	34
		2017	82	58	107	19
		2018	194	146	247	41
		2019	217	158	277	50

Appendix D. Continued

MPG	Population	Spawn Year	Escapement	Lower CI	Upper CI	N-Tags
Upper Salmon	SRLMA	2013	653	525	793	N/A
		2014	718	556	886	N/A
		2015	711	488	905	N/A
		2016	492	387	612	N/A
		2018	80	45	133	N/A
	SRNFS	2016	58	31	90	8
		2017	24	14	40	4
		2018	53	26	85	8
		2019	29	16	47	6
	SRPAH	2012	140	27	284	13
		2013	262	188	345	39
		2014	279	195	380	35
		2015	278	160	380	24
		2016	205	141	277	37
		2017	29	11	56	7
		2018	48	19	82	10
		2019	64	33	106	16
	SRPAN	2017	9	4	16	2
		2018	128	95	171	27
		2019	102	70	139	25
	SRUMA	2010	1,236	93	4,238	30
		2011	716	271	1,090	78
		2012	608	155	1,128	55
		2013	465	354	567	70
		2014	535	411	668	67
		2015	493	341	662	43
		2016	271	200	354	50
		2017	66	32	102	17
		2018	22	5	44	4
		2019	36	13	68	10
Upper Salmon	SRVAL	2010	406	18	1,791	11
		2011	416	154	665	46
		2012	507	149	947	46
		2013	317	222	420	47
		2014	665	533	841	83
		2015	429	294	590	36
		2016	238	170	317	43
		2017	76	43	118	19
		2018	154	105	229	32

Appendix D. Continued

MPG	Population	Spawn Year	Escapement	Lower CI	Upper CI	N-Tags
Upper Salmon	SRVAL	2019	102	60	157	26
	SRYFS	2012	270	78	520	24
		2013	279	202	370	42
		2014	196	127	283	24
		2015	121	57	207	10
		2016	112	68	165	20
		2017	41	17	72	10
		2018	77	44	120	16
		2019	25	7	47	6

Appendix E. Wild adult Chinook Salmon total age at return (1 S.E.) and Female proportions (F*p*) (1 S.E.)(n = unique PIT tags observed and used to estimate value) by spawn year and population.

Spawn Year	Age 2	Age 3	Age 4	Age 5	Age 6	n Aged	F*p*	n F*p*
CRPOT								
2014	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0.42 (0.08)	1
2015	0 (0)	0.05 (0.03)	0.81 (0.1)	0.14 (0.09)	0 (0)	1	0.43 (0.11)	1
SCUMA								
2010	0 (0)	0.03 (0.02)	0.93 (0.05)	0.03 (0.04)	0 (0)	3	0.45 (0.12)	2
2011	0 (0)	0.15 (0.09)	0.66 (0.11)	0.17 (0.1)	0 (0)	3	0.27 (0.1)	3
2012	0 (0)	0.02 (0.01)	0.78 (0.04)	0.2 (0.04)	0 (0)	98	0.46 (0.04)	97
2013	0 (0)	0.06 (0.03)	0.43 (0.05)	0.51 (0.05)	0 (0)	77	0.41 (0.05)	89
2014	0 (0)	0.06 (0.02)	0.84 (0.04)	0.09 (0.03)	0 (0)	71	0.53 (0.05)	76
2015	0 (0)	0.04 (0.02)	0.74 (0.05)	0.22 (0.05)	0 (0)	54	0.48 (0.06)	57
2016	0 (0)	0.03 (0.01)	0.65 (0.07)	0.31 (0.06)	0 (0)	40	0.55 (0.04)	48
2017	0.01 (0.01)	0.4 (0.11)	0.48 (0.11)	0.08 (0.06)	0 (0)	10	0.4 (0.07)	14
2018	0 (0)	0.04 (0.02)	0.93 (0.03)	0.03 (0.02)	0 (0)	25	0.4 (0.05)	26
2019	0 (0)	0.16 (0.06)	0.7 (0.08)	0.14 (0.05)	0 (0)	18	0.41 (0.04)	24
GRCAT								
2010	0 (0)	0.03 (0.02)	0.9 (0.06)	0.07 (0.05)	0 (0)	12	0.47 (0.09)	13
2011	0 (0)	0.22 (0.09)	0.67 (0.09)	0.1 (0.06)	0 (0)	13	0.23 (0.07)	15
2012	0 (0)	0.02 (0.01)	0.77 (0.06)	0.21 (0.05)	0 (0)	38	0.45 (0.06)	40
2013	0 (0)	0.3 (0.05)	0.53 (0.05)	0.17 (0.04)	0 (0)	61	0.37 (0.05)	66
2014	0 (0)	0.05 (0.02)	0.93 (0.03)	0.02 (0.01)	0 (0)	61	0.49 (0.05)	65
2015	0 (0)	0.07 (0.03)	0.61 (0.09)	0.32 (0.09)	0 (0)	21	0.45 (0.07)	29

Appendix E. Continued

Spawn Year	Age 2	Age 3	Age 4	Age 5	Age 6	n Aged	F*p*	n F*p*
				GRCAT				
2016	0 (0)	0.03 (0.01)	0.73 (0.06)	0.24 (0.06)	0 (0)	38	0.55 (0.04)	41
2017	0.01 (0.01)	0.26 (0.08)	0.53 (0.09)	0.18 (0.08)	0 (0)	16	0.44 (0.08)	16
2018	0 (0)	0.05 (0.03)	0.93 (0.04)	0.02 (0.02)	0 (0)	15	0.39 (0.06)	15
2019	0 (0)	0.09 (0.04)	0.82 (0.06)	0.09 (0.04)	0 (0)	22	0.41 (0.03)	24
				GRLOO				
2010	0 (0)	0.03 (0.02)	0.93 (0.05)	0.03 (0.04)	0 (0)	3	0.5 (0.13)	3
2011	0 (0)	0.25 (0.07)	0.58 (0.08)	0.17 (0.06)	0 (0)	24	0.25 (0.06)	24
2012	0 (0)	0.03 (0.02)	0.75 (0.07)	0.21 (0.07)	0 (0)	15	0.53 (0.07)	15
2013	0 (0)	0.4 (0.09)	0.45 (0.08)	0.13 (0.06)	0 (0)	20	0.26 (0.06)	30
2014	0 (0)	0.12 (0.06)	0.82 (0.08)	0.05 (0.04)	0 (0)	12	0.43 (0.07)	22
2015	0 (0)	0.06 (0.03)	0.84 (0.06)	0.1 (0.05)	0 (0)	21	0.47 (0.08)	20
2016	0 (0)	0.02 (0.01)	0.87 (0.05)	0.11 (0.04)	0 (0)	39	0.54 (0.04)	44
2017	0.01 (0.01)	0.34 (0.12)	0.4 (0.12)	0.21 (0.11)	0 (0)	6	0.41 (0.09)	8
2018	0 (0)	0.03 (0.02)	0.95 (0.02)	0.02 (0.01)	0 (0)	19	0.43 (0.06)	20
2019	0 (0)	0.17 (0.07)	0.7 (0.09)	0.12 (0.06)	0 (0)	9	0.41 (0.04)	11
				GRLOS				
2010	0 (0)	0.03 (0.02)	0.93 (0.05)	0.03 (0.04)	0 (0)	5	0.47 (0.11)	5
2011	0 (0)	0.2 (0.08)	0.56 (0.09)	0.23 (0.09)	0 (0)	11	0.24 (0.08)	11
2012	0 (0)	0.03 (0.02)	0.72 (0.06)	0.25 (0.06)	0 (0)	41	0.52 (0.06)	41
2013	0 (0)	0.26 (0.07)	0.48 (0.07)	0.24 (0.07)	0 (0)	30	0.36 (0.06)	41
2014	0 (0)	0.09 (0.03)	0.88 (0.04)	0.03 (0.02)	0 (0)	42	0.46 (0.05)	67

Appendix E. Continued

Spawn Year	Age 2	Age 3	Age 4	Age 5	Age 6	n Aged	F*p*	n F*p*
				GRLOS				
2015	0 (0)	0.04 (0.02)	0.83 (0.05)	0.13 (0.05)	0 (0)	28	0.47 (0.07)	32
2016	0 (0)	0.03 (0.01)	0.71 (0.05)	0.25 (0.05)	0 (0)	61	0.54 (0.04)	77
2017	0.01 (0.01)	0.2 (0.07)	0.5 (0.09)	0.28 (0.09)	0 (0)	18	0.42 (0.07)	20
2018	0 (0)	0.04 (0.02)	0.94 (0.02)	0.02 (0.01)	0 (0)	37	0.41 (0.04)	39
2019	0 (0)	0.24 (0.06)	0.59 (0.06)	0.16 (0.04)	0 (0)	46	0.41 (0.03)	47
				GRUMA				
2012	0 (0)	0.03 (0.03)	0.79 (0.07)	0.17 (0.07)	0 (0)	12	0.46 (0.07)	13
2013	0 (0)	0.24 (0.13)	0.52 (0.11)	0.2 (0.11)	0 (0)	2	0.29 (0.09)	2
2014	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0 (0)	0
2015	0 (0)	0.05 (0.02)	0.69 (0.09)	0.25 (0.09)	0 (0)	16	0.49 (0.09)	16
2016	0 (0)	0.02 (0.01)	0.75 (0.1)	0.21 (0.09)	0 (0)	8	0.53 (0.04)	9
2017	0.01 (0.01)	0.23 (0.12)	0.59 (0.13)	0.13 (0.1)	0 (0)	3	0.42 (0.09)	3
2018	0 (0)	0.04 (0.02)	0.94 (0.03)	0.02 (0.02)	0 (0)	30	0.41 (0.05)	31
2019	0 (0)	0.19 (0.1)	0.64 (0.13)	0.15 (0.07)	0 (0)	2	0.41 (0.04)	2
				GRWEN				
2018	0 (0)	0.03 (0.03)	0.94 (0.04)	0.02 (0.03)	0 (0)	1	0.4 (0.06)	1
2019	0 (0)	0.1 (0.05)	0.74 (0.07)	0.15 (0.05)	0 (0)	23	0.41 (0.04)	24
				IRBSH				
2011	0 (0)	0.14 (0.05)	0.55 (0.07)	0.3 (0.07)	0 (0)	33	0.25 (0.06)	31
2012	0 (0)	0.03 (0.02)	0.66 (0.09)	0.31 (0.09)	0 (0)	10	0.47 (0.07)	12
2013	0 (0)	0.29 (0.1)	0.48 (0.09)	0.21 (0.09)	0 (0)	9	0.31 (0.07)	11
2014	0 (0)	0.13 (0.06)	0.76 (0.09)	0.1 (0.06)	0 (0)	11	0.42 (0.07)	13

Appendix E. Continued

Spawn Year	Age 2	Age 3	Age 4	Age 5	Age 6	n Aged	F*p*	n F*p*
				IRBSH				
2015	0 (0)	0.06 (0.03)	0.71 (0.13)	0.23 (0.13)	0 (0)	3	0.41 (0.1)	3
2016	0 (0)	0.03 (0.01)	0.71 (0.1)	0.26 (0.1)	0 (0)	11	0.54 (0.04)	11
2017	0.01 (0.01)	0.23 (0.1)	0.5 (0.12)	0.23 (0.12)	0 (0)	6	0.44 (0.09)	7
2018	0 (0)	0.04 (0.02)	0.94 (0.04)	0.02 (0.02)	0 (0)	3	0.4 (0.06)	3
2019	0 (0)	0.15 (0.09)	0.69 (0.12)	0.15 (0.07)	0 (0)	1	0.41 (0.04)	1
				IRMAI				
2010	0 (0)	0.03 (0.02)	0.93 (0.04)	0.04 (0.03)	0 (0)	19	0.41 (0.07)	19
2011	0 (0)	0.13 (0.02)	0.66 (0.03)	0.21 (0.03)	0 (0)	181	0.29 (0.03)	186
2012	0 (0)	0.04 (0.02)	0.64 (0.05)	0.32 (0.05)	0 (0)	82	0.55 (0.05)	87
2013	0 (0)	0.34 (0.05)	0.38 (0.05)	0.28 (0.05)	0 (0)	80	0.36 (0.05)	82
2014	0 (0)	0.08 (0.02)	0.89 (0.03)	0.02 (0.01)	0 (0)	124	0.42 (0.04)	135
2015	0 (0)	0.06 (0.03)	0.79 (0.05)	0.15 (0.05)	0 (0)	43	0.32 (0.06)	52
2016	0 (0)	0.03 (0.01)	0.67 (0.04)	0.31 (0.04)	0 (0)	124	0.53 (0.03)	141
2017	0.01 (0.01)	0.17 (0.04)	0.61 (0.05)	0.21 (0.05)	0 (0)	68	0.45 (0.05)	74
2018	0 (0)	0.06 (0.03)	0.92 (0.03)	0.02 (0.02)	0 (0)	47	0.4 (0.04)	48
2019	0 (0)	0.11 (0.04)	0.73 (0.06)	0.15 (0.04)	0 (0)	41	0.41 (0.03)	46
				SNASO				
2010	0 (0)	0.03 (0.02)	0.94 (0.04)	0.03 (0.03)	0 (0)	6	0.46 (0.11)	5
2011	0 (0)	0.26 (0.11)	0.56 (0.1)	0.16 (0.09)	0 (0)	7	0.3 (0.09)	7
2012	0 (0)	0.03 (0.03)	0.71 (0.11)	0.25 (0.1)	0 (0)	1	0.47 (0.09)	1
2013	0 (0)	0.27 (0.13)	0.47 (0.1)	0.24 (0.12)	0 (0)	3	0.35 (0.09)	3

Appendix E. Continued

Spawn Year	Age 2	Age 3	Age 4	Age 5	Age 6	n Aged	F*p*	n F*p*
				SNASO				
2014	0 (0)	0.11 (0.07)	0.82 (0.11)	0.06 (0.06)	0 (0)	2	0.43 (0.08)	3
2015	0 (0)	0.06 (0.04)	0.8 (0.1)	0.13 (0.09)	0 (0)	3	0.4 (0.1)	3
2016	0 (0)	0.03 (0.02)	0.7 (0.13)	0.27 (0.13)	0 (0)	1	0.54 (0.04)	1
				SNTUC				
2010	0 (0)	0.03 (0.02)	0.93 (0.05)	0.04 (0.04)	0 (0)	2	0.41 (0.12)	2
2011	0 (0)	0.12 (0.08)	0.54 (0.13)	0.32 (0.14)	0 (0)	3	0.28 (0.11)	2
2012	0 (0)	0.04 (0.03)	0.68 (0.1)	0.27 (0.09)	0 (0.01)	8	0.47 (0.08)	9
2013	0 (0)	0.29 (0.12)	0.52 (0.11)	0.17 (0.09)	0 (0)	4	0.35 (0.08)	6
2014	0 (0)	0.09 (0.04)	0.85 (0.07)	0.05 (0.04)	0 (0)	13	0.46 (0.07)	14
2015	0 (0)	0.05 (0.03)	0.84 (0.07)	0.1 (0.06)	0 (0)	8	0.34 (0.07)	11
2016	0 (0)	0.03 (0.01)	0.77 (0.09)	0.2 (0.08)	0 (0)	12	0.55 (0.04)	13
2017	0.01 (0.01)	0.43 (0.12)	0.41 (0.11)	0.12 (0.08)	0 (0)	8	0.38 (0.09)	8
2018	0 (0)	0.04 (0.02)	0.93 (0.04)	0.03 (0.03)	0 (0)	6	0.4 (0.06)	6
2019	0 (0)	0.15 (0.08)	0.71 (0.1)	0.13 (0.06)	0 (0)	6	0.41 (0.04)	7
				MFBEA				
2015	0 (0)	0.05 (0.02)	0.78 (0.04)	0.17 (0.04)	0 (0)	98	0.3 (0.04)	127
2016	0 (0)	0.03 (0.01)	0.46 (0.07)	0.5 (0.07)	0 (0)	44	0.55 (0.03)	73
2017	0.01 (0.01)	0.28 (0.11)	0.45 (0.11)	0.22 (0.12)	0 (0)	6	0.43 (0.09)	6
2018	0 (0)	0.03 (0.02)	0.92 (0.03)	0.04 (0.02)	0 (0)	50	0.39 (0.04)	51
2019	0 (0)	0.36 (0.08)	0.46 (0.08)	0.18 (0.06)	0 (0)	28	0.4 (0.04)	28
				MFBIG				
2010	0 (0)	0.03 (0.02)	0.94 (0.04)	0.03 (0.03)	0 (0)	7	0.46 (0.1)	6

Appendix E. Continued

Spawn Year	Age 2	Age 3	Age 4	Age 5	Age 6	n Aged	F*p*	n F*p*
				MFBIG				
2011	0 (0)	0.47 (0.08)	0.46 (0.08)	0.06 (0.04)	0 (0)	34	0.15 (0.05)	34
2012	0 (0)	0.1 (0.04)	0.61 (0.06)	0.28 (0.05)	0 (0.01)	58	0.52 (0.05)	64
2013	0 (0)	0.53 (0.04)	0.37 (0.04)	0.1 (0.02)	0 (0)	132	0.23 (0.03)	141
2014	0 (0)	0.2 (0.03)	0.7 (0.04)	0.1 (0.03)	0 (0)	122	0.34 (0.04)	130
2015	0 (0)	0.04 (0.02)	0.83 (0.04)	0.13 (0.03)	0 (0)	85	0.36 (0.04)	94
2016	0 (0)	0.04 (0.01)	0.56 (0.04)	0.4 (0.04)	0 (0)	111	0.55 (0.03)	117
2017	0.01 (0.01)	0.48 (0.08)	0.43 (0.08)	0.07 (0.04)	0 (0)	29	0.33 (0.07)	30
2018	0 (0)	0.04 (0.02)	0.95 (0.02)	0.01 (0.01)	0 (0)	60	0.38 (0.04)	61
2019	0 (0)	0.19 (0.06)	0.59 (0.07)	0.21 (0.06)	0 (0)	31	0.4 (0.04)	39
				SFEFS				
2010	0 (0)	0.03 (0.02)	0.95 (0.03)	0.02 (0.02)	0 (0)	40	0.34 (0.07)	37
2011	0 (0)	0.2 (0.05)	0.52 (0.06)	0.28 (0.05)	0 (0)	64	0.25 (0.05)	63
2012	0 (0)	0.03 (0.01)	0.71 (0.05)	0.26 (0.05)	0 (0)	70	0.48 (0.04)	73
2013	0 (0)	0.3 (0.04)	0.5 (0.04)	0.19 (0.03)	0 (0)	135	0.25 (0.03)	144
2014	0 (0)	0.1 (0.02)	0.84 (0.03)	0.05 (0.02)	0 (0)	128	0.39 (0.04)	137
2015	0 (0)	0.08 (0.03)	0.79 (0.05)	0.13 (0.04)	0 (0)	44	0.41 (0.06)	45
2016	0 (0)	0.03 (0.01)	0.64 (0.04)	0.33 (0.04)	0 (0)	124	0.54 (0.03)	124
2017	0.02 (0.01)	0.39 (0.07)	0.4 (0.07)	0.18 (0.05)	0 (0)	42	0.41 (0.05)	45
2018	0 (0)	0.03 (0.01)	0.95 (0.02)	0.02 (0.01)	0 (0)	72	0.41 (0.04)	72
2019	0 (0)	0.13 (0.04)	0.67 (0.06)	0.19 (0.05)	0 (0)	44	0.41 (0.03)	49

Appendix E. Continued

Spawn Year	Age 2	Age 3	Age 4	Age 5	Age 6	n Aged	F*p*	n F*p*
				SFMAI				
2010	0 (0)	0.03 (0.01)	0.93 (0.02)	0.04 (0.01)	0 (0)	134	0.44 (0.04)	134
2011	0 (0)	0.05 (0.01)	0.51 (0.03)	0.45 (0.03)	0 (0)	285	0.42 (0.03)	285
2012	0 (0)	0.02 (0.01)	0.63 (0.04)	0.34 (0.04)	0 (0)	138	0.5 (0.04)	152
2013	0 (0)	0.24 (0.03)	0.45 (0.04)	0.31 (0.04)	0 (0)	146	0.36 (0.04)	149
2014	0 (0)	0.06 (0.01)	0.91 (0.02)	0.03 (0.01)	0 (0)	195	0.43 (0.03)	215
2015	0 (0)	0.05 (0.02)	0.82 (0.05)	0.12 (0.04)	0 (0)	44	0.43 (0.06)	46
2016	0 (0)	0.03 (0.01)	0.57 (0.05)	0.4 (0.05)	0 (0)	84	0.54 (0.03)	80
2017	0.01 (0.01)	0.27 (0.06)	0.57 (0.07)	0.14 (0.05)	0 (0)	36	0.44 (0.06)	42
2018	0 (0)	0.04 (0.02)	0.91 (0.03)	0.05 (0.03)	0 (0)	55	0.39 (0.04)	57
2019	0 (0)	0.14 (0.05)	0.72 (0.06)	0.13 (0.04)	0 (0)	35	0.41 (0.03)	39
				SFSEC				
2010	0 (0)	0.05 (0.03)	0.9 (0.04)	0.05 (0.03)	0 (0)	48	0.53 (0.07)	46
2011	0 (0)	0.24 (0.04)	0.58 (0.05)	0.18 (0.04)	0 (0)	77	0.28 (0.04)	75
2012	0 (0)	0.03 (0.02)	0.79 (0.04)	0.17 (0.04)	0 (0)	88	0.49 (0.04)	94
2013	0 (0)	0.46 (0.04)	0.43 (0.04)	0.1 (0.02)	0 (0)	168	0.27 (0.03)	171
2014	0 (0)	0.07 (0.02)	0.9 (0.02)	0.03 (0.01)	0 (0)	170	0.43 (0.04)	172
2015	0 (0)	0.06 (0.02)	0.76 (0.06)	0.17 (0.05)	0 (0)	43	0.47 (0.06)	47
2016	0 (0)	0.02 (0.01)	0.78 (0.04)	0.19 (0.03)	0 (0)	103	0.54 (0.03)	105
2017	0.02 (0.01)	0.55 (0.06)	0.36 (0.06)	0.06 (0.03)	0 (0)	54	0.32 (0.06)	56
2018	0 (0)	0.02 (0.01)	0.95 (0.02)	0.02 (0.01)	0 (0)	69	0.44 (0.05)	68
2019	0 (0)	0.25 (0.05)	0.59 (0.06)	0.16 (0.04)	0 (0)	50	0.41 (0.03)	53

Appendix E. Continued

Spawn Year	Age 2	Age 3	Age 4	Age 5	Age 6	n Aged	F*p*	n F*p*
				SRLSR				
2010	0 (0)	0.03 (0.02)	0.93 (0.05)	0.04 (0.04)	0 (0)	3	0.52 (0.13)	3
2011	0 (0)	0.23 (0.11)	0.61 (0.11)	0.12 (0.08)	0 (0)	6	0.24 (0.09)	6
2012	0 (0)	0.03 (0.03)	0.7 (0.11)	0.26 (0.1)	0 (0)	1	0.49 (0.09)	1
2013	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0.34 (0.1)	1
2014	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0 (0)	0
2015	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0 (0)	0
2016	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0 (0)	0
2017	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0 (0)	0
2018	0 (0)	0.05 (0.05)	0.93 (0.06)	0.02 (0.03)	0 (0)	1	0.4 (0.07)	1
2019	0 (0)	0.15 (0.08)	0.69 (0.12)	0.15 (0.08)	0 (0)	1	0.41 (0.04)	1
				SREFS				
2010	0 (0)	0.03 (0.02)	0.92 (0.05)	0.04 (0.04)	0 (0)	12	0.47 (0.09)	10
2011	0 (0)	0.12 (0.06)	0.65 (0.09)	0.21 (0.08)	0 (0)	14	0.28 (0.08)	13
2012	0 (0)	0.03 (0.03)	0.61 (0.09)	0.35 (0.08)	0 (0)	17	0.48 (0.06)	18
2013	0 (0)	0.44 (0.08)	0.38 (0.06)	0.17 (0.06)	0 (0)	32	0.25 (0.05)	36
2014	0 (0)	0.07 (0.03)	0.9 (0.04)	0.03 (0.02)	0 (0)	28	0.35 (0.06)	34
2015	0 (0)	0.05 (0.03)	0.77 (0.09)	0.17 (0.09)	0 (0)	7	0.44 (0.08)	9
2016	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0 (0)	0
2017	0.01 (0.01)	0.23 (0.13)	0.46 (0.14)	0.25 (0.16)	0 (0)	1	0.43 (0.11)	1
2018	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0 (0)	0
2019	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0	0 (0)	0
				SRLEM				
2010	0 (0)	0.04 (0.03)	0.92 (0.05)	0.04 (0.04)	0 (0)	6	0.43 (0.1)	6
2011	0 (0)	0.11 (0.05)	0.75 (0.06)	0.13 (0.05)	0 (0)	32	0.33 (0.07)	29
2012	0 (0)	0.03 (0.02)	0.63 (0.1)	0.33 (0.1)	0 (0)	9	0.55 (0.08)	11

Appendix E. Continued

Spawn Year	Age 2	Age 3	Age 4	Age 5	Age 6	n Aged	F*p*	n F*p*
				SRLEM				
2013	0 (0)	0.29 (0.05)	0.61 (0.05)	0.1 (0.03)	0 (0)	68	0.27 (0.04)	73
2014	0 (0)	0.03 (0.02)	0.95 (0.02)	0.02 (0.01)	0 (0)	73	0.52 (0.05)	78
2015	0 (0)	0.04 (0.02)	0.89 (0.03)	0.07 (0.03)	0 (0)	59	0.45 (0.05)	62
2016	0 (0)	0.03 (0.01)	0.57 (0.08)	0.4 (0.08)	0 (0)	30	0.57 (0.05)	33
2017	0.01 (0.01)	0.24 (0.08)	0.61 (0.08)	0.13 (0.06)	0 (0)	19	0.46 (0.08)	19
2018	0 (0)	0.04 (0.02)	0.94 (0.03)	0.02 (0.01)	0 (0)	41	0.38 (0.05)	40
2019	0 (0)	0.08 (0.03)	0.72 (0.06)	0.19 (0.05)	0 (0)	47	0.41 (0.03)	49
				SRNFS				
2016	0 (0)	0.03 (0.01)	0.69 (0.11)	0.28 (0.1)	0 (0)	7	0.54 (0.05)	8
2017	0.01 (0.01)	0.35 (0.13)	0.5 (0.12)	0.11 (0.09)	0 (0)	4	0.37 (0.1)	4
2018	0 (0)	0.03 (0.02)	0.94 (0.03)	0.02 (0.02)	0 (0)	8	0.43 (0.07)	8
2019	0 (0)	0.16 (0.08)	0.67 (0.11)	0.16 (0.07)	0 (0)	6	0.41 (0.04)	6
				SRPAH				
2011	0 (0)	0.13 (0.09)	0.6 (0.12)	0.24 (0.12)	0 (0)	3	0.23 (0.09)	3
2012	0 (0)	0.03 (0.02)	0.7 (0.09)	0.27 (0.09)	0 (0)	10	0.48 (0.07)	12
2013	0 (0)	0.21 (0.06)	0.54 (0.07)	0.24 (0.07)	0 (0)	32	0.34 (0.06)	39
2014	0 (0)	0.08 (0.03)	0.84 (0.05)	0.07 (0.03)	0 (0)	32	0.48 (0.06)	34
2015	0 (0)	0.07 (0.03)	0.73 (0.08)	0.19 (0.07)	0 (0)	19	0.38 (0.07)	24
2016	0 (0)	0.03 (0.01)	0.46 (0.08)	0.51 (0.08)	0 (0)	32	0.54 (0.04)	36
2017	0.01 (0.01)	0.22 (0.1)	0.44 (0.12)	0.3 (0.13)	0 (0)	6	0.42 (0.09)	7
2018	0 (0)	0.03 (0.02)	0.95 (0.03)	0.02 (0.02)	0 (0)	10	0.4 (0.05)	10
2019	0 (0)	0.15 (0.06)	0.7 (0.08)	0.14 (0.05)	0 (0)	15	0.41 (0.03)	15

Appendix E. Continued

Spawn Year	Age 2	Age 3	Age 4	Age 5	Age 6	n Aged	F*p*	n F*p*
				SRPAN				
2017	0.01 (0.01)	0.32 (0.14)	0.5 (0.13)	0.13 (0.11)	0 (0)	2	0.4 (0.1)	2
2018	0 (0)	0.03 (0.02)	0.95 (0.03)	0.02 (0.01)	0 (0)	27	0.39 (0.05)	27
2019	0 (0)	0.28 (0.08)	0.58 (0.08)	0.13 (0.05)	0 (0)	24	0.4 (0.04)	25
				SRUMA				
2010	0 (0)	0.03 (0.02)	0.87 (0.05)	0.09 (0.05)	0 (0)	29	0.42 (0.08)	27
2011	0 (0)	0.1 (0.03)	0.52 (0.05)	0.38 (0.05)	0 (0)	73	0.24 (0.05)	56
2012	0 (0)	0.03 (0.02)	0.56 (0.06)	0.4 (0.06)	0 (0)	48	0.46 (0.05)	55
2013	0 (0)	0.14 (0.04)	0.52 (0.06)	0.33 (0.06)	0 (0)	61	0.31 (0.05)	68
2014	0 (0)	0.07 (0.03)	0.86 (0.04)	0.07 (0.03)	0 (0)	65	0.39 (0.05)	65
2015	0 (0)	0.05 (0.02)	0.77 (0.06)	0.18 (0.05)	0 (0)	39	0.33 (0.06)	39
2016	0 (0)	0.04 (0.01)	0.49 (0.07)	0.47 (0.07)	0 (0)	46	0.53 (0.04)	48
2017	0.01 (0.01)	0.19 (0.08)	0.58 (0.09)	0.2 (0.09)	0 (0)	14	0.43 (0.07)	17
2018	0 (0)	0.04 (0.03)	0.93 (0.04)	0.02 (0.03)	0 (0)	3	0.41 (0.06)	4
2019	0 (0)	0.15 (0.07)	0.67 (0.1)	0.17 (0.07)	0 (0)	9	0.41 (0.04)	10
				SRVAL				
2010	0 (0)	0.03 (0.03)	0.93 (0.04)	0.03 (0.03)	0 (0)	11	0.38 (0.1)	10
2011	0 (0)	0.16 (0.05)	0.69 (0.06)	0.14 (0.05)	0 (0)	41	0.2 (0.05)	45
2012	0 (0)	0.03 (0.02)	0.63 (0.06)	0.33 (0.06)	0 (0)	42	0.38 (0.07)	45
2013	0 (0)	0.37 (0.06)	0.44 (0.06)	0.19 (0.05)	0 (0)	46	0.27 (0.05)	45
2014	0 (0)	0.18 (0.04)	0.77 (0.04)	0.05 (0.02)	0 (0)	77	0.35 (0.05)	83
2015	0 (0)	0.05 (0.02)	0.87 (0.05)	0.07 (0.04)	0 (0)	34	0.31 (0.06)	35
2016	0 (0)	0.03 (0.01)	0.67 (0.07)	0.3 (0.06)	0 (0)	42	0.53 (0.04)	43

Appendix E. Continued

Spawn Year	Age 2	Age 3	Age 4	Age 5	Age 6	n Aged	F*p*	n F*p*
				SRVAL				
2017	0.01 (0.01)	0.18 (0.07)	0.34 (0.09)	0.46 (0.11)	0 (0)	17	0.53 (0.09)	19
2018	0 (0)	0.04 (0.02)	0.94 (0.03)	0.02 (0.02)	0 (0)	29	0.38 (0.05)	32
2019	0 (0)	0.22 (0.07)	0.61 (0.08)	0.16 (0.05)	0 (0)	25	0.4 (0.03)	26
				SRYFS				
2011	0 (0)	0.19 (0.11)	0.63 (0.11)	0.15 (0.09)	0 (0)	4	0.22 (0.09)	4
2012	0 (0)	0.02 (0.02)	0.68 (0.08)	0.29 (0.08)	0 (0)	21	0.41 (0.08)	24
2013	0 (0)	0.18 (0.05)	0.55 (0.06)	0.27 (0.06)	0 (0)	40	0.27 (0.05)	42
2014	0 (0)	0.12 (0.05)	0.68 (0.09)	0.19 (0.07)	0 (0)	23	0.38 (0.06)	24
2015	0 (0)	0.06 (0.03)	0.8 (0.08)	0.13 (0.07)	0 (0)	9	0.45 (0.09)	9
2016	0 (0)	0.03 (0.01)	0.67 (0.09)	0.3 (0.08)	0 (0)	19	0.54 (0.04)	20
2017	0.01 (0.01)	0.22 (0.09)	0.43 (0.11)	0.31 (0.12)	0 (0)	9	0.45 (0.09)	10
2018	0 (0)	0.03 (0.02)	0.94 (0.03)	0.03 (0.02)	0 (0)	15	0.37 (0.06)	16
2019	0 (0)	0.2 (0.09)	0.51 (0.13)	0.28 (0.11)	0 (0)	5	0.4 (0.03)	6
				CRLOC				
2017	0.01 (0.01)	0.37 (0.09)	0.54 (0.09)	0.07 (0.05)	0 (0)	17	0.34 (0.08)	17
2018	0 (0)	0.03 (0.01)	0.95 (0.02)	0.01 (0.01)	0 (0)	59	0.43 (0.04)	59
2019	0 (0)	0.12 (0.05)	0.68 (0.07)	0.19 (0.06)	0 (0)	26	0.41 (0.04)	26
				CRLOL				
2012	0 (0)	0.02 (0.02)	0.71 (0.07)	0.27 (0.07)	0 (0)	25	0.5 (0.06)	31
2013	0 (0)	0.11 (0.05)	0.45 (0.08)	0.43 (0.09)	0 (0)	22	0.44 (0.08)	28
2014	0 (0)	0.12 (0.05)	0.78 (0.08)	0.09 (0.06)	0 (0)	13	0.46 (0.08)	14
2015	0 (0)	0.04 (0.02)	0.87 (0.05)	0.08 (0.04)	0 (0)	19	0.41 (0.08)	17

Appendix E. Continued

Spawn Year	Age 2	Age 3	Age 4	Age 5	Age 6	n Aged	F*p*	n F*p*
				CRLOL				
2016	0 (0)	0.03 (0.01)	0.77 (0.06)	0.2 (0.05)	0 (0)	37	0.56 (0.04)	39
2017	0.01 (0.01)	0.18 (0.09)	0.54 (0.12)	0.23 (0.12)	0 (0)	6	0.46 (0.1)	7
2018	0 (0)	0.03 (0.02)	0.94 (0.03)	0.02 (0.02)	0 (0)	6	0.41 (0.06)	6
2019	0 (0)	0.21 (0.09)	0.65 (0.1)	0.13 (0.06)	0 (0)	8	0.41 (0.04)	9
				SEMEA				
2017	0.01 (0.01)	0.23 (0.08)	0.67 (0.09)	0.08 (0.05)	0 (0)	16	0.43 (0.08)	17
2018	0 (0)	0.04 (0.02)	0.93 (0.02)	0.02 (0.01)	0 (0)	63	0.41 (0.04)	63
2019	0 (0)	0.12 (0.05)	0.71 (0.07)	0.16 (0.05)	0 (0)	26	0.41 (0.04)	29

Appendix F. Summary of genetic diversity by spawn year and population for Chinook Salmon in the Snake River basin. Reported are observed (H_o) and expected heterozygosity (H_e) along with deviations from Hardy-Weinberg equilibrium (HWE) for collections with more than 20 samples.

Array Group	Spawn Year (sample size)	H_o	H_e	% Polymorphic	HWE Het Deficiency	HWE Het Excess
SRPAN	2018 (n = 27)	23.0%	22.7%	82.0%	1	1
SRPAN	2019 (n = 25)	22.7%	22.3%	82.0%	1	1
SRLEM	2011 (n = 32)	23.5%	22.6%	82.6%	0	1
SRLEM	2013 (n = 72)	23.6%	23.4%	86.2%	1	1
SRLEM	2014 (n = 78)	22.4%	22.6%	85.0%	0	1
SRLEM	2015 (n = 63)	23.5%	23.7%	88.0%	2	1
SRLEM	2016 (n = 34)	22.9%	22.8%	85.6%	0	1
SRLEM	2018 (n = 40)	22.4%	23.2%	84.4%	2	1
SRLEM	2019 (n = 50)	23.3%	23.4%	85.0%	0	1
SRPAH	2013 (n = 39)	24.1%	23.4%	79.6%	0	1
SRPAH	2014 (n = 34)	24.3%	23.0%	81.4%	0	1
SRPAH	2015 (n = 24)	24.3%	23.1%	76.6%	0	1
SRPAH	2016 (n = 36)	23.1%	22.8%	81.4%	0	1
SREFS	2013 (n = 36)	23.0%	23.0%	80.8%	0	1
SREFS	2014 (n = 34)	23.3%	23.0%	80.2%	0	1
SRYFS	2012 (n = 24)	23.8%	22.5%	78.4%	0	1
SRYFS	2013 (n = 42)	22.9%	23.1%	83.8%	0	1
SRYFS	2014 (n = 24)	23.7%	22.1%	76.6%	0	2
SRYFS	2016 (n = 20)	22.4%	22.0%	75.4%	0	1
SRVAL	2011 (n = 46)	22.9%	22.9%	82.0%	3	1
SRVAL	2012 (n = 46)	23.9%	23.4%	85.0%	1	1
SRVAL	2013 (n = 46)	23.2%	22.5%	85.0%	0	1
SRVAL	2014 (n = 83)	23.7%	23.1%	85.0%	0	2
SRVAL	2015 (n = 35)	23.4%	23.0%	82.0%	0	1
SRVAL	2016 (n = 43)	22.9%	22.3%	85.0%	1	1
SRVAL	2018 (n = 32)	22.8%	22.7%	79.0%	1	2
SRVAL	2019 (n = 26)	22.0%	22.2%	76.0%	1	1
SRUMA	2010 (n = 29)	22.7%	22.3%	78.4%	1	1
SRUMA	2011 (n = 78)	22.8%	22.8%	86.2%	1	1
SRUMA	2012 (n = 55)	23.2%	23.0%	85.6%	0	1
SRUMA	2013 (n = 68)	23.2%	24.2%	94.0%	4	1
SRUMA	2014 (n = 65)	23.0%	22.9%	83.8%	0	1
SRUMA	2015 (n = 39)	23.7%	22.8%	82.6%	0	1
SRUMA	2016 (n = 49)	22.3%	22.4%	85.6%	1	1
MFBIG	2011 (n = 34)	22.4%	22.4%	83.2%	0	1
MFBIG	2012 (n = 64)	22.6%	21.9%	86.8%	2	1
MFBIG	2013 (n = 143)	22.6%	22.8%	95.2%	3	2

Appendix F. Continued.

Array Group	Spawn Year (sample size)	H_o	H_e	% Polymorphic	HWE Het Deficiency	HWE Het Excess
MFBIG	2014 (n = 130)	22.9%	22.6%	91.6%	2	1
MFBIG	2015 (n = 94)	22.4%	22.4%	89.8%	1	1
MFBIG	2016 (n = 117)	22.2%	22.3%	92.8%	3	1
MFBIG	2017 (n = 30)	22.2%	21.9%	83.2%	0	1
MFBIG	2018 (n = 61)	22.3%	22.6%	89.2%	2	1
MFBIG	2019 (n = 39)	22.4%	22.6%	86.8%	1	1
MFBEA	2015 (n = 129)	22.3%	21.9%	87.4%	1	1
MFBEA	2016 (n = 73)	21.7%	21.5%	83.8%	0	1
MFBEA	2018 (n = 51)	21.6%	21.3%	77.2%	3	1
MFBEA	2019 (n = 29)	21.3%	21.1%	74.9%	0	1
SFMAI	2010 (n = 140)	23.4%	22.7%	85.0%	0	1
SFMAI	2011 (n = 296)	23.3%	23.2%	95.8%	3	1
SFMAI	2012 (n = 155)	23.5%	23.1%	93.4%	0	2
SFMAI	2013 (n = 151)	23.2%	23.5%	95.2%	2	1
SFMAI	2014 (n = 215)	23.1%	23.0%	94.6%	1	1
SFMAI	2015 (n = 46)	23.7%	23.3%	88.6%	1	1
SFMAI	2016 (n = 82)	23.8%	23.5%	90.4%	1	1
SFMAI	2017 (n = 42)	23.0%	22.7%	84.4%	1	1
SFMAI	2018 (n = 57)	22.4%	22.5%	89.2%	1	1
SFMAI	2019 (n = 39)	23.7%	22.9%	85.6%	1	1
SFSEC	2010 (n = 49)	24.2%	20.9%	58.1%	2	1
SFSEC	2011 (n = 78)	22.1%	22.4%	90.4%	2	1
SFSEC	2012 (n = 95)	22.3%	22.0%	84.4%	0	2
SFSEC	2013 (n = 173)	22.2%	21.9%	91.0%	0	1
SFSEC	2014 (n = 172)	22.6%	22.2%	85.6%	2	3
SFSEC	2015 (n = 47)	22.2%	22.2%	86.2%	0	1
SFSEC	2016 (n = 105)	22.1%	22.2%	86.2%	2	2
SFSEC	2017 (n = 56)	22.5%	22.0%	82.6%	0	1
SFSEC	2018 (n = 68)	21.7%	22.1%	86.2%	2	1
SFSEC	2019 (n = 53)	21.9%	22.1%	82.6%	1	1
SFEFS	2010 (n = 41)	25.4%	20.4%	53.9%	0	1
SFEFS	2011 (n = 66)	21.9%	22.2%	86.8%	1	1
SFEFS	2012 (n = 75)	23.2%	22.9%	88.0%	1	2
SFEFS	2013 (n = 146)	23.1%	22.8%	92.8%	1	1
SFEFS	2014 (n = 137)	22.7%	22.5%	90.4%	0	1
SFEFS	2015 (n = 45)	23.6%	23.3%	89.2%	4	2
SFEFS	2016 (n = 124)	23.0%	22.8%	92.2%	0	1
SFEFS	2017 (n = 45)	22.5%	22.4%	83.8%	1	1
SFEFS	2018 (n = 72)	22.6%	23.0%	88.6%	3	1

Appendix F. Continued.

Array Group	Spawn Year (sample size)	H_o	H_e	% Polymorphic	HWE Het Deficiency	HWE Het Excess
SFEFS	2019 (n = 49)	23.0%	22.5%	84.4%	0	1
GRWEN	2019 (n = 24)	28.5%	30.1%	96.4%	2	1
GRLOO	2011 (n = 35)	24.9%	25.1%	90.4%	1	1
GRLOO	2013 (n = 30)	25.8%	25.4%	89.8%	0	1
GRLOO	2014 (n = 22)	25.4%	24.8%	86.8%	0	1
GRLOO	2015 (n = 20)	25.0%	24.4%	84.4%	1	1
GRLOO	2016 (n = 44)	26.8%	26.1%	91.6%	0	1
GRLOO	2018 (n = 20)	24.8%	24.3%	82.6%	1	1
GRUMA	2018 (n = 31)	24.4%	24.2%	84.4%	1	1
GRCAT	2012 (n = 40)	25.9%	25.1%	89.2%	1	1
GRCAT	2013 (n = 66)	26.0%	25.2%	92.8%	1	2
GRCAT	2014 (n = 65)	25.9%	25.2%	89.2%	2	1
GRCAT	2015 (n = 29)	25.7%	25.7%	88.6%	1	1
GRCAT	2016 (n = 41)	25.7%	25.2%	89.2%	0	1
GRCAT	2019 (n = 24)	25.7%	25.2%	85.6%	0	1
GRLOS	2012 (n = 41)	24.8%	23.9%	86.8%	0	1
GRLOS	2013 (n = 41)	23.6%	23.5%	87.4%	0	1
GRLOS	2014 (n = 67)	23.4%	23.6%	90.4%	2	1
GRLOS	2015 (n = 32)	23.7%	23.6%	86.8%	0	1
GRLOS	2016 (n = 77)	24.2%	23.7%	89.8%	0	1
GRLOS	2017 (n = 20)	22.8%	22.6%	77.8%	0	1
GRLOS	2018 (n = 39)	22.6%	23.3%	85.0%	1	1
GRLOS	2019 (n = 47)	24.7%	24.2%	91.0%	0	1
IRBSH	2011 (n = 35)	24.9%	24.3%	89.2%	0	1
IRMAI	2011 (n = 191)	24.4%	24.3%	96.4%	6	1
IRMAI	2012 (n = 88)	24.8%	24.1%	92.2%	0	1
IRMAI	2013 (n = 84)	24.2%	24.8%	97.6%	11	1
IRMAI	2014 (n = 135)	24.4%	24.0%	94.0%	1	1
IRMAI	2015 (n = 52)	24.1%	24.1%	88.6%	1	1
IRMAI	2016 (n = 141)	24.2%	24.0%	95.8%	1	1
IRMAI	2017 (n = 74)	24.3%	24.1%	91.6%	2	1
IRMAI	2018 (n = 48)	23.7%	23.8%	88.0%	1	2
IRMAI	2019 (n = 46)	23.7%	23.5%	89.8%	1	1
SCUMA	2012 (n = 101)	24.9%	24.5%	93.4%	2	2
SCUMA	2013 (n = 89)	25.0%	24.5%	95.2%	1	1
SCUMA	2014 (n = 76)	25.6%	24.7%	92.8%	0	1
SCUMA	2015 (n = 57)	24.2%	24.9%	91.6%	0	1
SCUMA	2016 (n = 48)	23.8%	24.9%	94.6%	1	1
SCUMA	2018 (n = 26)	24.3%	23.6%	83.8%	0	1

Appendix F. Continued.

Array Group	Spawn Year (sample size)	H_o	H_e	% Polymorphic	HWE Het Deficiency	HWE Het Excess
SCUMA	2019 (n = 24)	25.0%	27.9%	96.4%	9	1
CRLOL	2012 (n = 31)	24.2%	24.4%	81.4%	1	1
CRLOL	2013 (n = 28)	25.2%	24.9%	86.8%	2	1
CRLOL	2016 (n = 39)	25.2%	24.5%	89.2%	0	1
CRLOC	2018 (n = 59)	24.3%	24.2%	90.4%	1	1
CRLOC	2019 (n = 26)	25.3%	24.8%	83.8%	1	1
SEMEA	2018 (n = 63)	24.3%	24.8%	95.2%	3	1
SEMEA	2019 (n = 29)	24.8%	25.9%	92.8%	3	2