

GENETIC ASSESSMENT OF COLUMBIA RIVER STOCKS

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Executive Summary

This project combines four inter-related studies from the Accords Agreement that address the following current and future objectives:

Objective 1) discover and evaluate SNP markers in salmon and steelhead and other anadromous fishes. In the current year of this project we have continued our use of GT-seq protocols for SNP discovery. Our laboratory has designed SNP panels for five study species (Chinook salmon [*Oncorhynchus tshawytscha*] – 299 loci; Steelhead trout [*O. mykiss*] – 390 loci; Sockeye salmon [*O. nerka*] – 382 loci; Coho salmon [*O. kisutch*] – 257 loci; and Pacific lamprey [*Entosphenus tridentata*] – 316 loci). The expanded panel for *O. mykiss* (from 379 to 390 markers) include markers associated with specific traits to enable identification of premature (early-arrival to spawning grounds, primarily summer-run) or mature (late-arrival to spawning grounds, primarily winter-run) steelhead.

Objective 2) expand and create genetic baselines for multiple species including Chinook Salmon (*Oncorhynchus tshawytscha*), steelhead trout (*O. mykiss*), Sockeye Salmon and kokanee (*O. nerka*), and Coho Salmon (*O. kisutch*). Objective two of this project describes efforts to evaluate genetic diversity among populations that will inform managers in the areas of harvest monitoring, and conservation monitoring. Our approach involves the collection, analysis, interpretation and distribution of genotypic data. These data are being compiled as species-specific reference baselines for characterizing Chinook salmon, steelhead trout, and *O. nerka* population structure specific to the Columbia River Basin. The collaborative, inter-agency application of genetic stock identification (GSI) tools continues to provide invaluable monitoring capabilities to understand relative stock proportions in sport, commercial and tribal harvests, as well as monitoring of stock specific run-timing at Bonneville Dam, Lower Granite Dam and other fish weirs in the basin. Moreover, GSI is being used in concert with parentage-based tagging (PBT; *O. tshawytscha*, *O. mykiss*, *O. kisutch*), providing the means to genetically assign individual fish to a hatchery broodstock-of-origin. PBT continues to be valuable for monitoring trends in hatchery production, harvest of hatchery fish, and population attributes of specific hatcheries (e.g., stray rates, survival/mortality, migratory behavior, hatchery/wild interactions). Major accomplishments in 2018 include expansion of our PBT baselines with the addition of several new hatcheries in the Columbia River Basin, both above and below Bonneville Dam. The GSI baseline for steelhead trout was substantially expanded from <200 SNP markers to 389 SNP markers after genotyping many of the original baseline collections with our newly expanded GT-seq panel of 390 SNP markers (includes 1 sex marker). Of this addition, approximately 40 SNPs were specifically designed for their ability to differentiate between 7 smaller reporting groups within the larger MGILCS reporting group spanning the middle Columbia and lower Snake rivers (Hasselman et al. 2018). It is not clear whether these 40 loci hold the power for discriminating among these MGILCS reporting groups from our initial results (Figure 1). The expansion also included 69 SNPs that displayed significant associations with environmental variables in landscape genetic analyses. Some SNPs were informative for both applications (i.e. differentiating MGILCS and landscape genetics). Lastly, the Omy 390 SNP panel also includes newly designed markers in the GREB1 gene region, which is involved in maturation and has been shown to be highly informative for differentiating between summer-run and winter-run steelhead ecotypes.

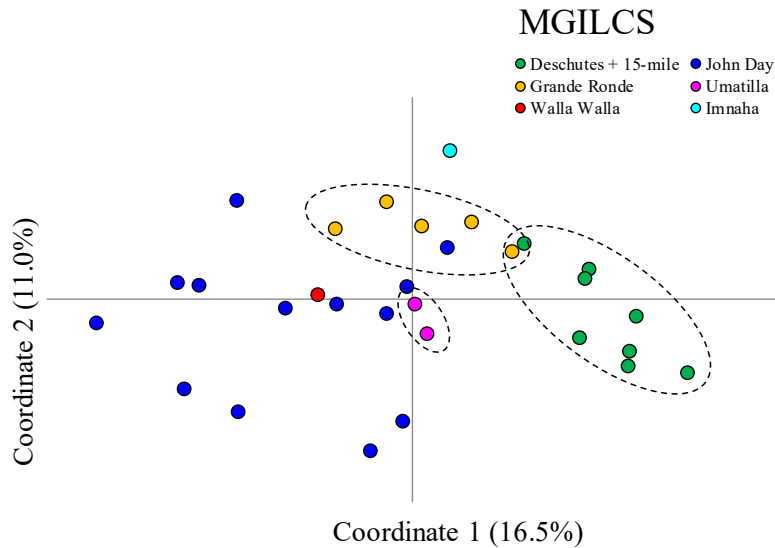


Figure 1. Principle Coordinates Analysis plot based on 40 loci used to differentiate between subbasins in the MGILCS reporting group.

There are three projects that have begun to characterize reference baselines of millions of SNPs for Chinook Salmon, Coho Salmon, and *O. mykiss*. These new projects utilize whole genome resequencing methods that barcode pools of individuals that represent different collections and can generate allele frequencies across millions of SNP loci. We expect that in the near future there will be no shortage of genetic markers that can be used for GSI and PBT applications anywhere in the species range of our fish of interest. Specific SNPs may be targeted to improve GSI and PBT by incorporating them into GT-seq panels for high-throughput genotyping. In addition, projects will be able to utilize these SNPs for a number of other applications that involve elucidation of genetic mechanisms underlying fitness traits of interest.

Objective 3) implement GSI programs for mainstem Chinook salmon, Sockeye salmon, and steelhead fisheries. In this section, we first evaluate the informativeness of the 299 SNP panel for PBT applications in Chinook salmon using the spawn year 2015 broodstocks that were genotyped with 299 SNPs. Results of this evaluation, demonstrated a subset of 268 SNPs that may be most likely to hold optimal information content across the three major lineages of Chinook Salmon in the Columbia River. These 268 SNPs would include 192, 217, and 195 SNPs with >10% observed heterozygosity for each of the major lineages stream-type, ocean-type, and Lower Columbia, respectively. We would recommend adopting this panel of SNPs for all PBT applications of Chinook Salmon in future years because it would effectively avoid crashing issues with SNPPIT, the software we use for PBT assignments and would allow higher accuracy in PBT assignments.

We used a combination of PBT and GSI analyses to determine stock composition of Chinook salmon harvested in 2017 in sport, commercial, and tribal fisheries in the mainstem Columbia River, and used GSI to estimate stock composition of sockeye salmon harvested above and below Bonneville Dam in commercial, sport, and tribal fisheries during the spring, summer, and fall management periods (Figure 2). We were unable to characterize the stock composition of a mark-selective sport fishery from the mouth of the Wind River (above Bonneville Dam) which had expanded its fishing boundary into the Columbia River mainstem. We had been

analyzing this bubble fishery each year since this boundary change, however, the Wind River sport fishery was not conducted and sampled in 2017.

Analysis of adipose-clipped Chinook salmon from multiple fishery mixtures in the spring management period (April to June 15th) identified relatively large proportions of individuals that assigned via PBT to Snake River and Columbia River hatcheries. Chinook salmon from Snake River hatcheries comprised 31-32% of fish harvested in Region B, 41% of fish harvested in Region A from sport and Test fisheries, and 46% of fish harvested in Zone 6 from Tribal Ceremonial fisheries (Figure 3). These proportions are broadly consistent with the proportion of hatchery origin Chinook salmon passing Bonneville Dam in 2017 that assigned via PBT to Snake River hatcheries (36%).

The closure of adipose-intact commercial fisheries during the spring management period of 2017 restricted comparisons of stock composition to the test fishery. Analysis of the adipose-intact test fishery revealed that 25% of fish assigned via PBT to Snake River (17%) and Columbia River (8%) hatcheries. This is consistent with the proportion of adipose intact fish at Bonneville Dam that assigned via PBT (22%) to Snake River (11%) and Columbia River (10%) hatcheries, and, as expected, is considerably lower than that observed for adipose-clipped fisheries (59-83%; Figure 3). The LC lineage comprised 26% of the test fishery, but only 1% of the fish encountered passing Bonneville Dam. The OT lineage was observed at Bonneville Dam (34%), but not in the test fishery due to the early-timed occurrence of the test fishery in March to April. The ST lineage comprised the greatest proportion of adipose-intact test fishery (28%), and matched that encountered at Bonneville Dam (28%) during the spring management period (Figure 4).

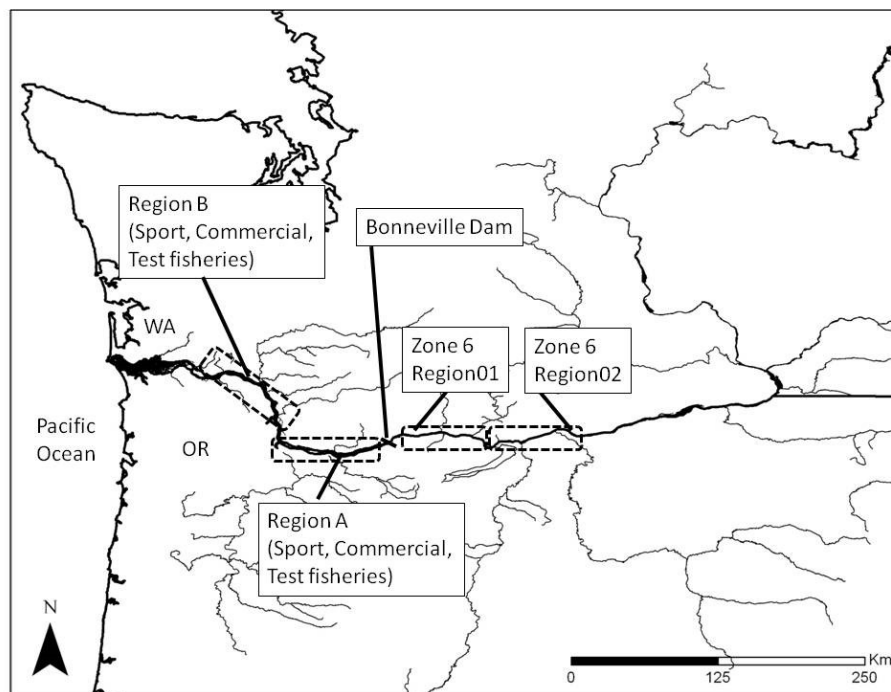


Figure 2. Sources of fishery mixtures in the lower Columbia River mainstem.

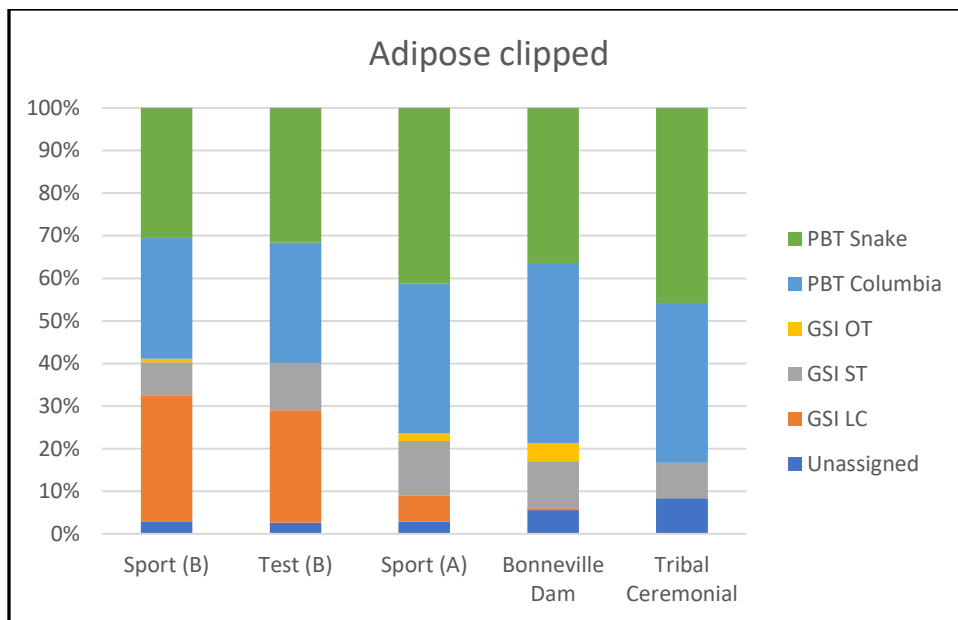


Figure 3. Stock composition of spring management period adipose-clipped Chinook salmon harvest mixtures in 2017. ‘PBT Snake’ and ‘PBT Columbia’ include assignments to all Snake River and Columbia River hatcheries that are in our PBT baseline. Interior ocean type (OT), interior stream type (ST), and lower Columbia lineage include GSI assignments to reporting groups within our GSI baseline.

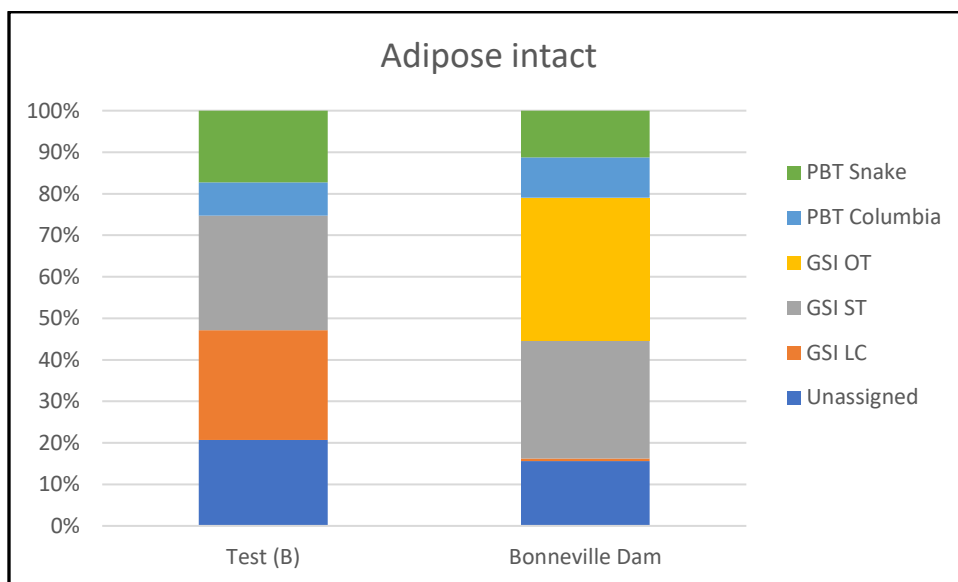


Figure 4. Stock composition of spring management period adipose-intact Chinook salmon harvest mixtures in 2017. ‘PBT Snake’ and ‘PBT Columbia’ include assignments to all Snake River and Columbia River hatcheries that are in our PBT baseline. Interior ocean type (OT), interior stream type (ST), and lower Columbia lineage include GSI assignments to reporting groups within our GSI baseline.

Analysis of Chinook salmon fisheries in the summer management period (June 16 – August 1) addressed the following objectives: 1) estimate stock composition for the mark selective sport fishery in Region B and Region A below Bonneville Dam, and 2) compare stock composition of adipose-clipped versus adipose-intact fish from the Tribal Zone 6 harvest above Bonneville Dam.

The stock composition of adipose-clipped sport fisheries in Region B and Region A were similar in the proportions of fish that assigned via PBT to Snake River hatcheries (11% for both), and the proportion of fish from the ST (2% for both) and OT (26-28%) lineages (Figure 5). However, PBT assignments to Columbia River hatcheries was greater for Region A (56%) than Region B (38%), while the LC lineage comprised a greater proportion of fish in Region B (21%) than Region A (2%).

We detected broad similarities in the stock composition of adipose-clipped fish from the sport fishery in Region A, with those sampled at Bonneville Dam and those taken in the Zone 6 Tribal harvest (Figure 5). We also observed broad similarities in the stock composition of adipose-intact mixture collections from Bonneville Dam and the Zone 6 tribal harvest.

We observed differences in the stock composition of adipose-intact and adipose-clipped fish taken in the Zone 6 tribal harvests. As observed in other comparisons of adipose-clipped vs. adipose-intact mixtures, a greater proportion of adipose-clipped fish assigned to Columbia River hatcheries (63%) vs. adipose-intact fish (12%) (Figure 5). We also detected a greater proportion of adipose-intact fish assigned to the OT lineage (77%) than adipose-clipped fish (28%).

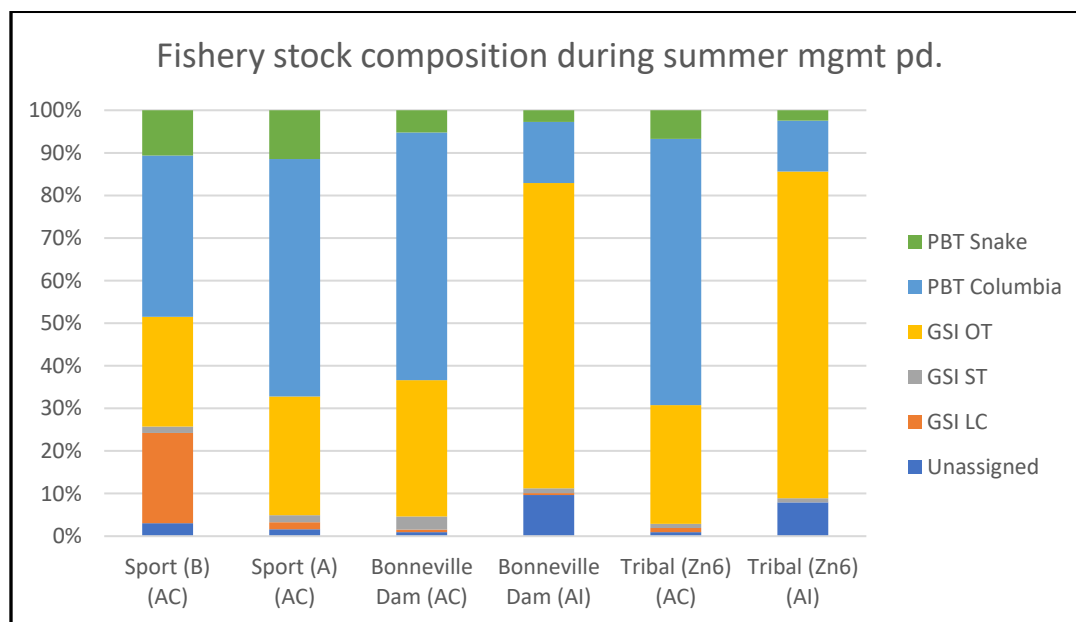


Figure 5. Stock composition of summer management period Chinook salmon fisheries and Bonneville Dam. ‘AC’ is adipose-clipped; ‘AI’ is adipose intact. ‘PBT Snake’ and ‘PBT Columbia’ include assignments to all Snake River and Columbia River hatcheries that are

in our PBT baseline. Interior ocean type (OT), interior stream type (ST), and lower Columbia lineage include GSI assignments to reporting groups within our GSI baseline.

Analysis of stock composition of sockeye salmon fisheries included those from the lower Columbia River sport fishery below Bonneville Dam and the Zone 6 tribal fishery collected in 2017. The overall stock composition of sockeye salmon in these fisheries are shown in Table 1. The proportion of each sockeye salmon stock encountered at Bonneville Dam and in the Zone 6 tribal fishery varied over time (Figure 6).

Table 1. Comparison of percent composition among sockeye salmon fisheries and Bonneville Dam in 2017.

Mixture source	Stock proportion			
	Okanagan	Wenatchee	Snake	Lake Billy Chinook
Sport	58.10%	41.90%	-	-
Zone 6	38.99%	59.19%	1.37%	0.45%
Total Harvest	41.08%	56.99%	1.62%	0.32%
Bonneville Dam*	58.27%	41.07%	0.58%	0.09%

Note: * Bonneville Dam abundance estimates only include the interval of weeks that coincide with sockeye salmon fisheries (statistical weeks 24-30).

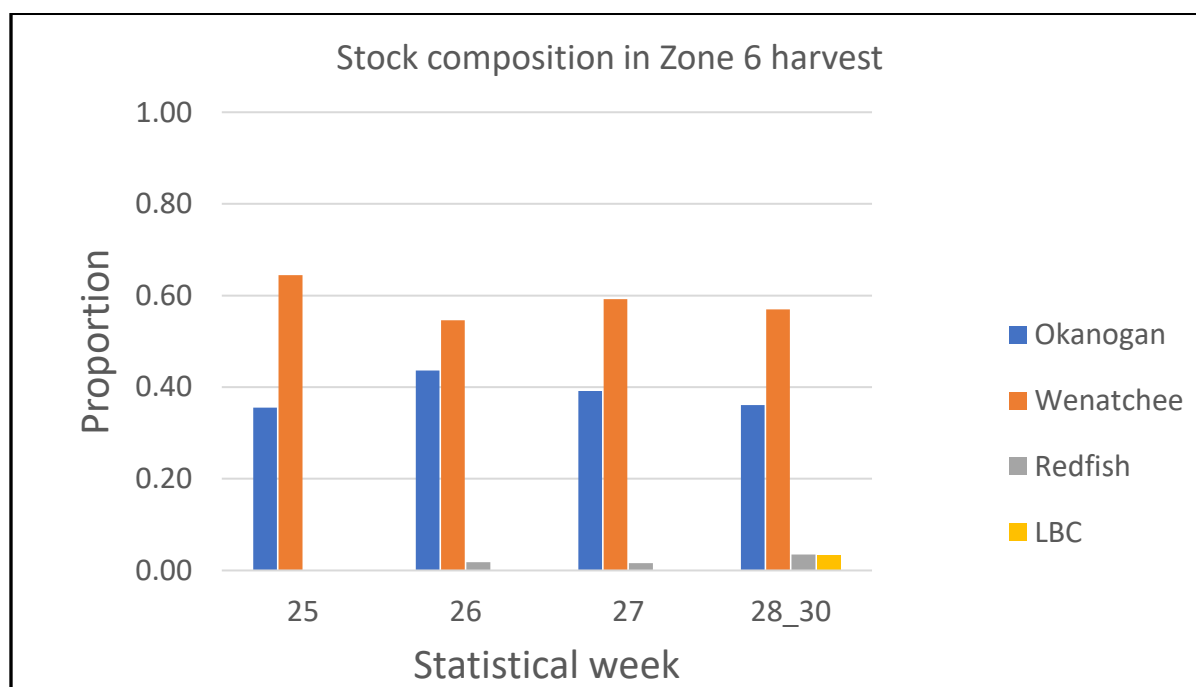
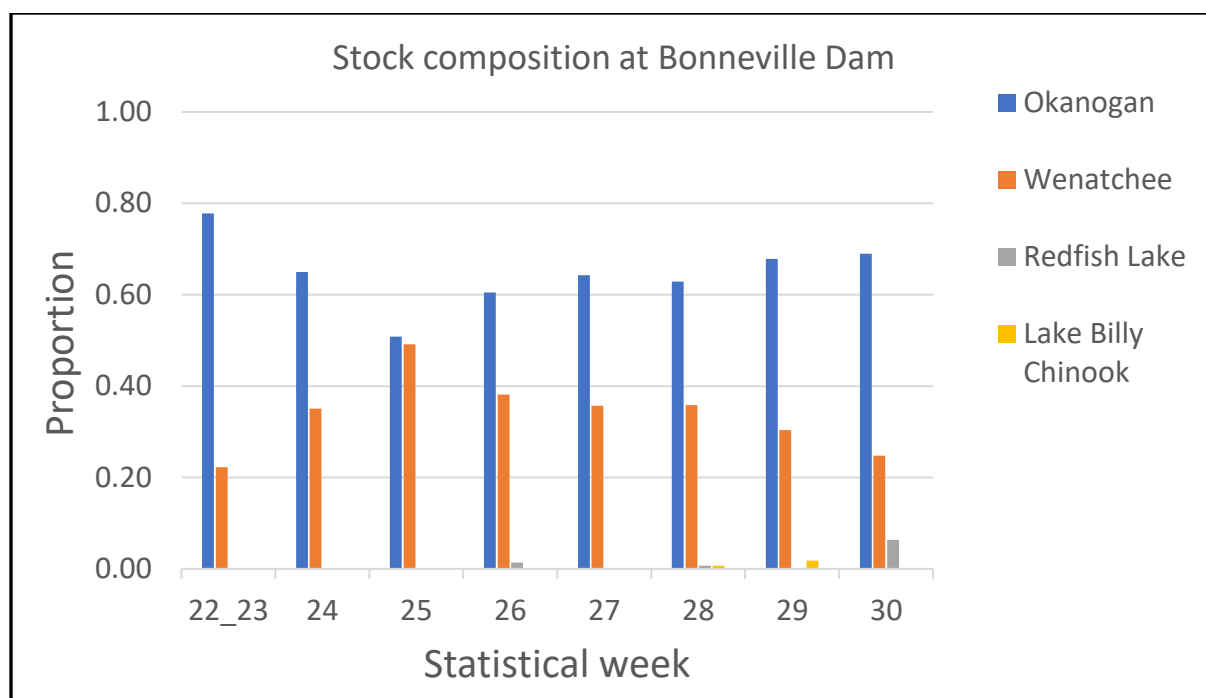


Figure 6. Stock composition of sockeye salmon at Bonneville Dam (top panel) and in the Zone 6 tribal harvest (bottom panel) across weekly strata in 2017.

Objective 4) Use PBT and GSI to estimate stock composition of fish passage at Bonneville Dam (steelhead, Sockeye salmon, and Chinook salmon). This section describes our efforts to determine the relative stock composition, abundance and migration run-timing distributions of hatchery and natural origin Chinook salmon, steelhead, and sockeye salmon passing Bonneville Dam. Fish were sampled as they migrated past Bonneville Dam. We sampled adult and jack Chinook and adult steelhead during the spring, summer, and fall management periods, and used a combination of GSI and PBT to estimate run-timing distributions and relative abundance of hatchery and wild Chinook salmon and steelhead stocks in 2017 (post-season analyses). Further, in-season analyses were completed for fish returning throughout 2018 and provided to regional fisheries managers such as the Technical Advisory Committee (TAC).

There were 14 major (i.e., abundance >1000 fish) hatchery origin Chinook salmon stocks represented in the total estimated relative abundance (N=318,060) of hatchery Chinook salmon passing Bonneville Dam in 2017 (Figure 7). These stocks in order of decreasing magnitude were 18_UCOLSF (112,391), 22_BONPOOLFA (43,065), 12_HELLSC (40,400), 19_SRFALL (38,112), 05_SPCRTU (14,955), 20_BONPOOLSP (14,694), 07_DESCP (11,965), 13_SFSALM (10,067), 21_UMATILLASP (9,837), 10_UCOLSP (6,860), 16_UPSALM (4,590), 06_KLICKR (3,252), 09_YAKIMA (3,010), and 23_UMATILLAFA (2,845). These estimates include relative abundance for PBT-assigned fish (adipose clipped and non-clipped) and adipose clipped fish that were assigned via GSI.

There were 11 major (i.e., abundance >1000 fish) Chinook salmon stocks represented in the total estimated relative abundance (N=229,732) of natural origin (i.e., adipose non-clipped fish that did not assign via PBT) Chinook salmon passing Bonneville Dam in 2017 (Figure 8). These non-clipped stocks in order of decreasing magnitude were 18_UCOLSF (162,406), 19_SRFALL (35,829), 05_SPCRTU (7,418), 17_DESCFA (5,908), 09_YAKIMA (3,604), 12_HELLSC (2,722), 10_UCOLSP (2,679), 13_SFSALM (2,549), 16_UPSALM (1,583), 08_JOHNDR (1,246) and 15_MFSALM (1,081).

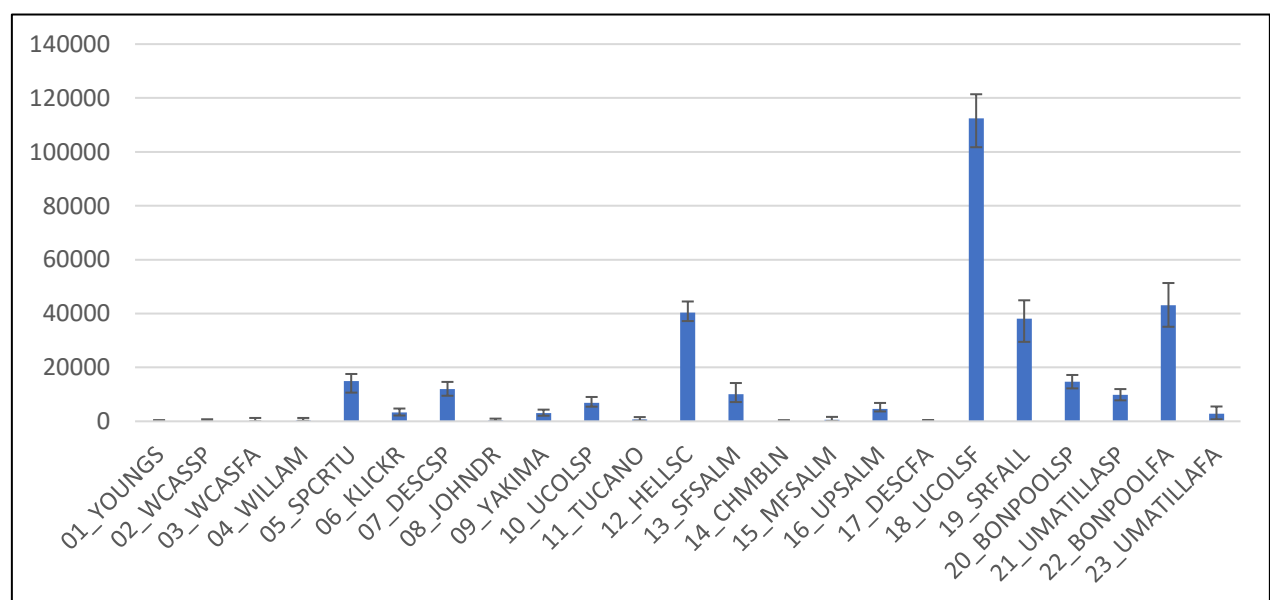


Figure 7. Relative abundance (\pm 95% CI) of hatchery origin Chinook (adipose clipped and non-clipped) assigned to genetic stock of origin that were sampled at Bonneville Dam in 2017.

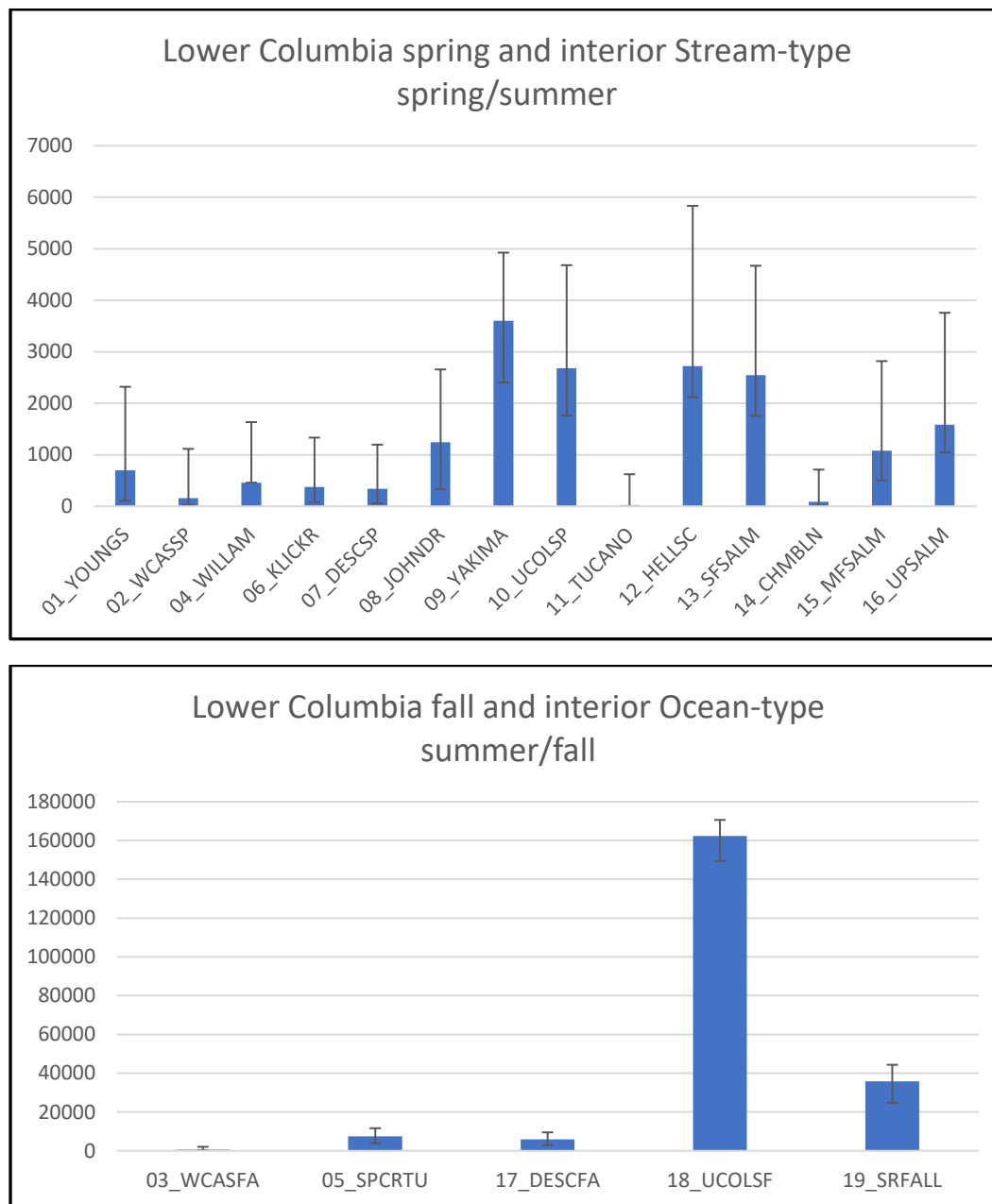


Figure 8. Relative abundance (\pm 95% CI) of natural origin (adipose non-clipped) Chinook sampled at Bonneville Dam in 2017 assigned to genetic stock of origin. Lower Columbia spring and interior stream-type spring/summer Chinook reporting groups (top panel), and lower Columbia fall and interior Ocean-type Chinook reporting groups (bottom panel) are shown.

We identified five stocks (abundance>1000) represented each in the total estimated relative abundance of hatchery origin (N=84,301) and natural origin (N=29,953) steelhead passing Bonneville Dam in 2017, respectively (Figure 9). The 07_MGILCS reporting group comprised the largest fraction of both hatchery origin fish (31,728), and natural origin fish (20,419) passing Bonneville Dam in 2017 (Figure 9).

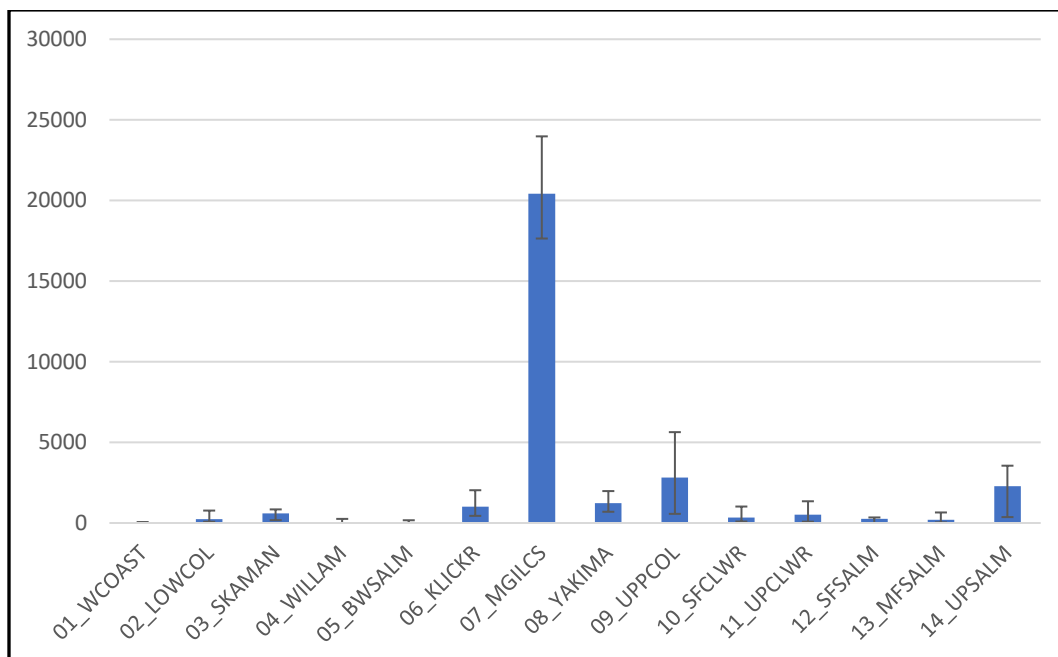
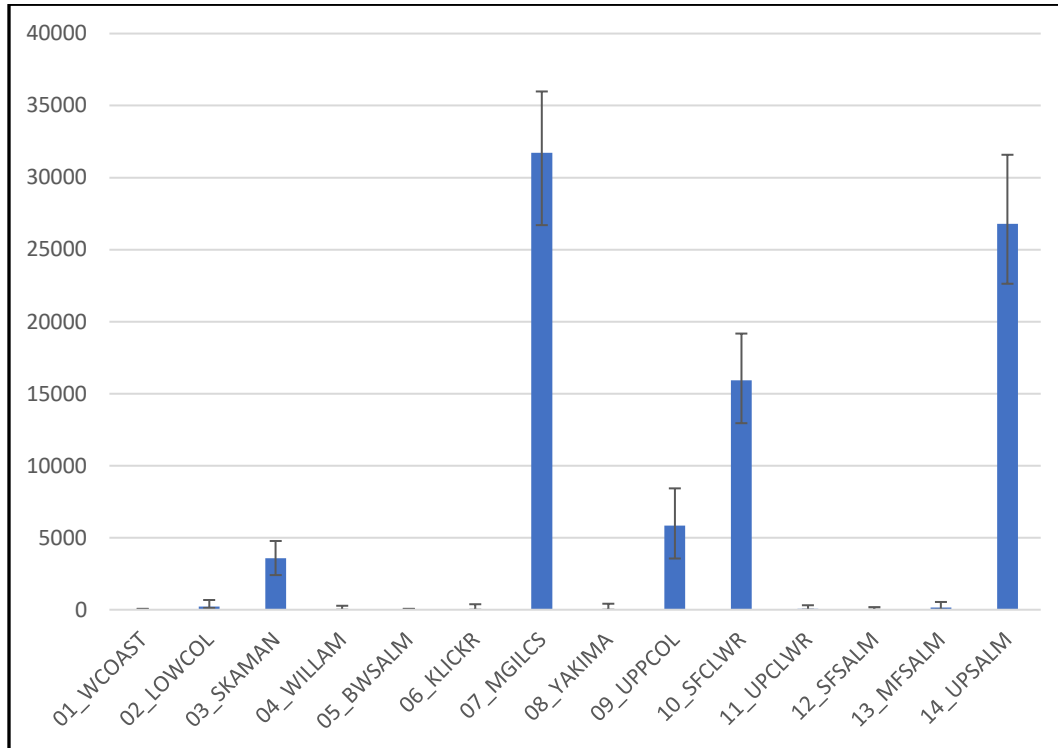


Figure 9. Relative abundance (\pm 95% CI) of hatchery origin steelhead (adipose clipped and non-clipped) (top panel), and natural origin (adipose non-clipped) steelhead (bottom panel) assigned to genetic stock of origin that were sampled at Bonneville Dam in 2017.

The greatest proportion of sockeye salmon passing Bonneville Dam in 2017 assigned to the Okanogan stock (51,943), followed by the Wenatchee (34,848; Figure 10). The Snake and Lake Billy Chinook stocks had estimated abundances < 500 , but were based on relatively few genetic assignments (<15).

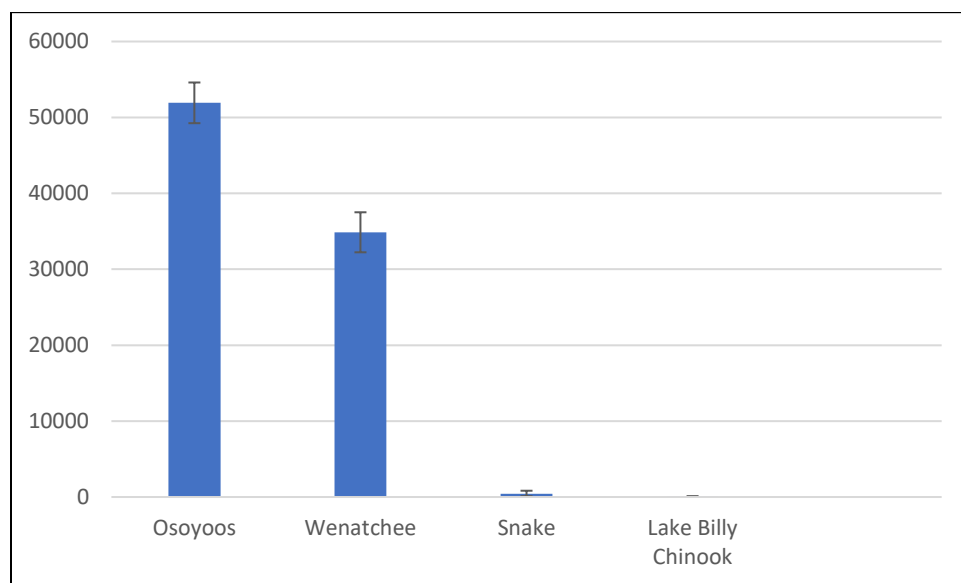


Figure 10. Relative abundance (\pm 95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2017.

While the run timing distributions of some hatchery origin and natural origin spring Chinook salmon stocks terminated within the spring management period, several spring Chinook salmon stocks extended well into the summer management period. The run timing distributions for hatchery origin and natural origin fall Chinook salmon stocks all had median dates on or after 9/3/17. For steelhead, we identified an early Skamania summer-run (median run-timing date 06/20/17), an intermediate run-timing category that contains most wild and hatchery steelhead stocks from the 09_UPPCOL, 07_MGILCS, and 14_UPPSALM reporting groups (median run-timing date range: 7/24/17 – 8/27/17), and a late run-timing category comprised of hatchery and natural origin stocks from the 10_SFCLWR reporting group with median run-timing dates on 09/18/17 – 09/19/17. Run timing distributions for sockeye salmon sampled at Bonneville Dam broadly overlapped in 2017, and we observed nearly identical run timing distributions for the Okanogan, Wenatchee, and Snake River stocks (median date: 06/24/17, 06/25/17, and 06/27/17, respectively).

Finally, we delivered reports to the U.S. v OR Technical Advisory Committee (TAC) on in-season and timely post-season analyses of several runs and fish species passing Bonneville Dam in 2018 (Table 2). The timely reporting of these preliminary analyses increased their usefulness to the fisheries managers of these Columbia River stocks because the results were available while the fishing seasons were being actively shaped or just prior to the TAC needing information to perform their annual analytical tasks.

Table 2. The in-season and post-season report timing and scope of the 2018 fish runs.

Species	Management Period	Data coverage	Report timing
Chinook	Spring	01/01/2018 - 05/04/2018	05/11/2018
		01/01/2018 - 05/18/2018	05/24/2018
		01/01/2018 - 06/02/2018	06/08/2018
	Summer	01/01/2018 - 06/15/2018	06/25/2018
		01/01/2018 - 07/07/2018	07/16/2018
	Fall	01/01/2018 - 07/31/2018	08/06/2018
Steelhead	Skamania	01/01/2018 - 11/25/2018	12/03/2018
	Summer A-/B-Index	04/01/2018 - 06/30/2018	07/16/2018
		07/01/2018 - 07/31/2018	08/07/2018
Steelhead	Summer A-/B-Index	07/01/2018 - 10/31/2018	11/19/2018
		07/01/2018 - 10/31/2018	11/19/2018
Sockeye	Total	01/01/2018 - 08/18/2018	08/21/2018

Note: The data were reported as cumulative abundance estimates for each genetic stock during the Chinook Salmon and Summer Steelhead A-/B-Index management periods. The report timing indicates the date these reports were provided to the USvOR TAC chair Stuart Ellis for distribution to TAC members.

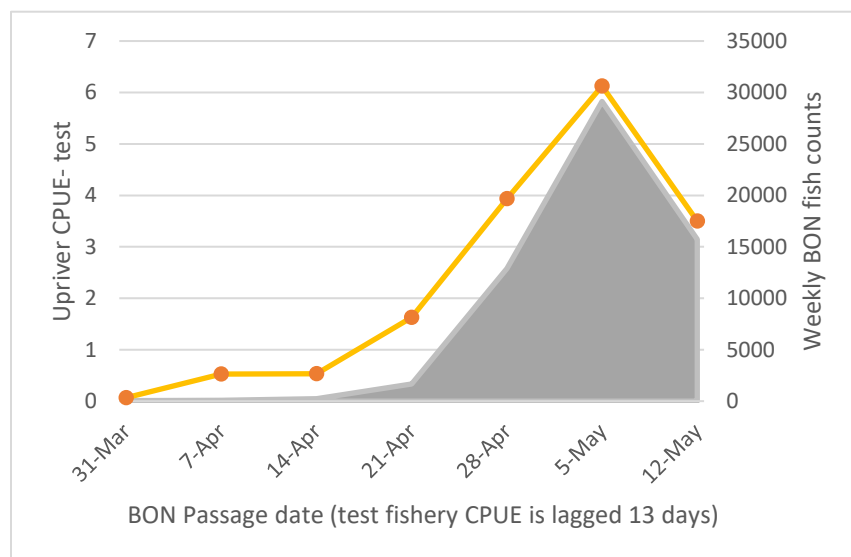


Figure 11. The relationship between the test fishery upriver Chinook Salmon CPUE (line) and weekly fish counts at Bonneville Dam (solid gray) in 2018.

One of the 2018 in-season analyses that compared PBT broodstock composition of the early spring Chinook Salmon test fishery to that of the first weeks of the run sampled at Bonneville Dam provided evidence that this test fishery has potential for predicting the timing and abundance of specific stocks of Chinook Salmon weeks in advance of their arrival at Bonneville Dam (Figure 11). This potential predictive ability of the combination of test fishery and genetic data was described in more detail in this section.

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Introduction

This project combines four inter-related studies from the Fish & Wildlife Program Accords that address the following current and future objectives: 1) discover and evaluate SNP markers in salmon, steelhead, and lamprey; 2) expand and create genetic baselines for multiple species (Chinook, steelhead, sockeye, and coho); 3) implement Genetic Stock Identification (GSI) sampling programs for mainstem Chinook salmon, sockeye salmon, and steelhead fisheries and 4) GSI of fish passing Bonneville Dam (salmon and steelhead). These four projects are highly related since SNP markers are needed to complete species-specific baselines, and these baselines are requisite to complete GSI. The results of these four objectives address needs for distinguishing specific stocks, determining genetic diversity, stock specific run timing, and estimating stock composition which can provide information for fisheries management.

Objective 1) SNP Discovery

One of the highest priorities in the full-scale implementation of SNPs for genetic applications of Columbia River fishes is the discovery and development of a sufficient number of markers to characterize population variability. These DNA sequence polymorphisms represent the most abundant variation in the genome of most organisms, and are spread throughout the entire genome at high density (Morin et al. 2004). We currently utilize panels of hundreds of SNP markers in six fish species including: Chinook salmon, Steelhead trout, Sockeye salmon, Coho salmon, Pacific lamprey, and White Sturgeon. Development of these panels of SNP markers has enabled several studies to investigate stock identification of unknown stocks of fish, parentage analysis, population structure, adaptive variation, and underlying genetic variation for specific traits. We also continue to improve our technology for genotyping to make it more cost effective and highly informative to evaluate genetic variation. Our lab developed a new method called GT-seq (Genotyping-in-Thousands by Sequencing) to genotype these SNP markers in large numbers of individuals (Campbell et al. 2015) for much lower costs (< 4 times) than previous technology. Over the past several years, our lab has contributed to the increasing numbers of SNP markers that are available for salmonids and lampreys, and we have reached a point where rigorous stock composition and assessment goals for timely management of fisheries and highly accurate, precise stock assignments can be achieved using panels of SNP markers.

Objective 2) Baseline Expansion

Development and maintenance of genetic baselines have created powerful resources for stock identification of both natural- and hatchery-origin fish. Genetic Stock Identification (GSI) baselines are used to identify the genetic stock of origin of natural-origin fish based on genetic similarity to one of the multiple distinct stocks that represent the Columbia River Basin. Hatchery-origin fish are identified directly to their hatchery of origin based on assignment to hatchery broodstock parents and their ages are inferred using the Parentage Based Tagging (PBT) baselines. PBT continues to be valuable for monitoring trends in hatchery production, harvest of hatchery fish, and population attributes of specific hatcheries (e.g., stray rates, survival/mortality, migratory behavior, hatchery/natural-origin interactions). GSI provides one of

the few ways to estimate the escapement of natural-origin stocks through run reconstruction of these stocks passing Bonneville Dam.

Objectives 3 & 4) Genetic Stock Identification

Genetic Stock Identification (GSI) methods have proven to be effective in determining the proportion of stock origin in several mixed stock applications (Narum et al. 2008b, Hess et al. 2011, Hess and Narum 2011). This study includes two GSI projects that will utilize genetic baselines: 1) GSI to provide information about harvest; and 2) GSI of fish passing Bonneville Dam.

This study includes GSI analysis of Chinook salmon and Sockeye salmon collected from commercial, recreational, and tribal fisheries in the Columbia River. Subsequent years of the study may include other species such as Coho salmon. Implementation of GSI technology could make monitoring individual production units in mixed stock areas possible. Tissues will be sampled annually from fisheries with existing programs in place with Washington Department of Fish and Wildlife (WDFW), Oregon Department of Fish and Wildlife (ODFW), Yakama Nation Fisheries Program (YNFP) and Confederated Tribes of the Warm Springs of Oregon (CTWSRO). We plan to genotype representative samples from fisheries of primary interest. The GSI estimates may help fill information gaps on natural-origin stocks.

The second application of GSI analysis in this study includes sampling unknown origin salmon and steelhead at Bonneville Dam for genetic analysis. Samples will be collected over the majority of the run on a weekly basis, and genetic baselines will be utilized to determine the stock composition of these runs. Few studies have been able to determine the extent of overlap among life history types of salmon and steelhead, but GSI of each life history type will allow us to determine the stock composition of the different runs through Bonneville Dam which can be compared to other methods such as using fish that were PIT-tagged as juveniles. Population genetic methods and statistical assignment models have advanced dramatically in recent years, and estimating stock composition is now possible using either Bayesian or Maximum Likelihood methods (Anderson et al. 2008). Therefore, we plan to estimate stock composition of multiple species passing Bonneville Dam and provide this information on a timely basis to fisheries managers in the form of an annual report.

Finally, we continue to utilize a new genetic technology, parentage based tagging (PBT), in combination with GSI to help augment and refine our stock identification results. PBT is an efficient approach for mass-tagging of fish. The method is carried out by first genotyping a set of potential parents which then provides the opportunity to assign a set of genotyped offspring to their true parent pair. PBT is currently being utilized on a broad scale in the Columbia River Basin to tag all Snake River Chinook salmon and steelhead hatchery broodstocks (Steele et al. 2011) and we now have a baseline that includes most Chinook salmon and steelhead hatcheries located above Bonneville Dam. This application has effectively tagged all hatchery Chinook salmon and steelhead above Bonneville Dam starting with the 2012 brood years. When parent pairs of a hatchery fish are identified with PBT, we can provide accurate information including age of the fish and the source hatchery in which its parents were spawned. We can now use PBT in both Chinook salmon and steelhead GSI applications to identify all hatchery-origin fish, and

then we estimate stock-of-origin of all other hatchery fish that were not assigned with PBT (i.e. the few hatcheries not in the PBT baseline) and all natural-origin fish using GSI. In this way PBT and GSI are complimentary, and using them in combination takes full advantage of the strengths of each method, while resolving or minimizing limitations. Exogenous stock transfers by hatcheries have made hatchery-origin fish challenging to assign with GSI and represents a main limitation that is addressed with PBT. Applications of PBT have been initiated in other species such as Pacific lamprey, and are being used to monitor translocations of lamprey throughout the interior of the Columbia River.

Report Structure

This report is divided into four sections, one for each of the objectives of the study. The first section reports on SNP discovery efforts and the second section on genotyping SNP markers in Chinook salmon, steelhead, and *O. nerka* to create genetic baselines. The third section contains stock composition estimates of Chinook salmon and Sockeye salmon sampled in mainstem fisheries in 2017. The fourth section includes analysis of run-timing distributions and estimated abundance of adult Chinook salmon, Sockeye salmon, and steelhead stocks migrating over Bonneville Dam in 2017. In addition, we have implemented in-season and timely post-season analysis of the runs of Chinook salmon, Sockeye salmon and steelhead migrating over Bonneville Dam in 2018. These in-season and post-season 2018 results were provided to fisheries managers that participate on the USvOR Technical Advisory Committee and are summarized in the fourth section of this report.

Section 1: SNP Discovery

Introduction

Population genetic studies examine variation within the genomes of individuals in order to gain insights into the nature of those populations. For instance, genetic similarities among groups of individuals can indicate relatedness, recent population collapse, or barriers to migration. In the context of salmon conservation, population genetics can answer important questions directly related to fisheries management such as stock exploitation rates, effective population size, and rate of return. Other demographic information such as stock abundance estimates can also be made through analysis of samples taken from fish as they enter the Columbia River through genetic stock identification (GSI). These studies require genotype data from a suitably large and informative set of genetic markers for analysis. Likewise, the number of genotyped individuals must be suitably large to provide accurate results.

Next generation sequencing instruments can provide both a means to identify genetic variation and provide a platform for high-throughput sequencing. In the past, we have used methods such as restriction-site associated DNA sequencing (RAD-seq: <https://www.monitoringmethods.org/Method/Details/4144>) to identify and genotype thousands of single nucleotide polymorphisms (SNPs) within and among study populations. Recently reference genome assemblies have become publicly available for both Chinook salmon and steelhead, and these genome resources has enabled whole genome resequencing for investigating adaptive variation across a large portion of the genome (50-80%) in these species (whole genome resequencing: [Whole Genome Resequencing: Poolseq Individual Barcode v1.0](#)). Whole genome resequencing methods include individually barcoded samples, or pools of samples (Pool-seq, [Whole Genome Resequencing: Poolseq Pooled v1.0](#); Schlotterer et al. 2014) depending on the study design. For both methods, sequence data is aligned to the reference genome assembly, and allele frequencies from millions of SNPs are analyzed to detect statistically significant regions of the genome associated with specific traits or adaptation to environmental factors. Putatively neutral regions of the genome are also useful for standard phylogeny and demographic analyses of populations. In most studies, allele frequencies are available for collections but sequencing depth is typically not high enough to provide individual genotypes. However, candidate SNPs may be developed into standard panels with Genotyping in Thousands by sequencing (GT-seq: <https://www.monitoringresources.org/Document/Method/Details/5446>) or other approaches to genotype many individuals to validate trait association, determine inheritance, and estimate linkage disequilibrium. GT-seq is a high throughput method that uses Illumina sequencers to rapidly genotype thousands of individual samples at hundreds of loci for less than ¼ the cost of previously used TaqMan assays (Campbell et al. 2015). Following the development of GT-seq, our laboratory has designed panels for 5 study species (Chinook salmon [*O. tshawytscha*] – 299 loci; Steelhead trout [*O. mykiss*] – 390 loci; Sockeye salmon [*O. nerka*] – 382 loci; Coho salmon [*O. kisutch*] – 257 loci; and Pacific lamprey [*E. tridentata*] – 316 loci). All of these GT-seq

panels have been designed to a maximum of 75bp to allow for inexpensive sequencing runs on Illumina NextSeq 500. Recent additions of 11 SNPs were made to increase GT-seq panels for *O. mykiss* to 390 SNPs (Table 3). The expanded panel for *O. mykiss* will improve our ability to identify specific traits of premature (summer-run) or mature (winter-run) steelhead (Micheletti et al. 2018).

Methods

For new SNP loci added to panels, the program Primer3 (Rozen and Skaletsky 2000) was used to design primers flanking the target SNP locus for inclusion in existing GT-seq panels. (GT-seq: <https://www.monitoringresources.org/Document/Method/Details/5446>) Parameters used for primer design are as follows (product size range: 50-80 bases, optimal annealing temperature: 60°C, primer size range: 18-24 bases, optimal GC content: 50%). The designed primers were then modified by including the Illumina sequencing primer sites. The primers were ordered from IDT (Integrated DNA technologies) at a concentration of 200µM at the 25nmole synthesis scale. Testing was done by combining primers from previous loci for each species that already worked for GT-seq with the newly designed primers. These new primer pools were then used to create test libraries containing 96 samples using the GT-seq protocol (Campbell et al. 2015). Test libraries were “spiked” into an Illumina HiSeq lane with another sequencing library such that each test library produced about 10 million reads of data for analysis. Since the test library uses only a small percentage of the total reads on the flow cell the new library can be sequenced very cheaply. The sequencing reads were analyzed for the presence of significant numbers of hetero-dimers produced in multiplex PCR using custom perl scripts (<https://github.com/GTseq/GTseq-Pipeline/>). Primers producing large numbers of sequencing artifact reads through primer hetero-dimer interactions were flagged and omitted from the next primer mix. Following this step the primer mix was used for full scale genotyping using GT-seq libraries containing up to 5,000 samples for a NextSeq flow cell.

Results

GT-seq primer pools are being used for all high throughput genotyping projects for 5 target species (Steelhead [*O. mykiss*] – 390 SNP loci including a sex determination marker, Chinook [*O. tshawytscha*]-299 SNP loci including a sex determination marker, Coho [*O. kisutch*]-257 SNP loci, Sockeye [*O. nerka*]-382 SNP loci, and Pacific Lamprey [*E. tridentata*]-316 SNP loci). The remaining primer pools remain unchanged from last year’s report but any additional SNPs from Pool-seq data will be under development in the coming year (Paired-end data assemblies, primer design, and testing). Our GT-seq panels have been used to genotype over 120,815 samples as of Dec. 18th in the 2018 calendar year (Figure 12).

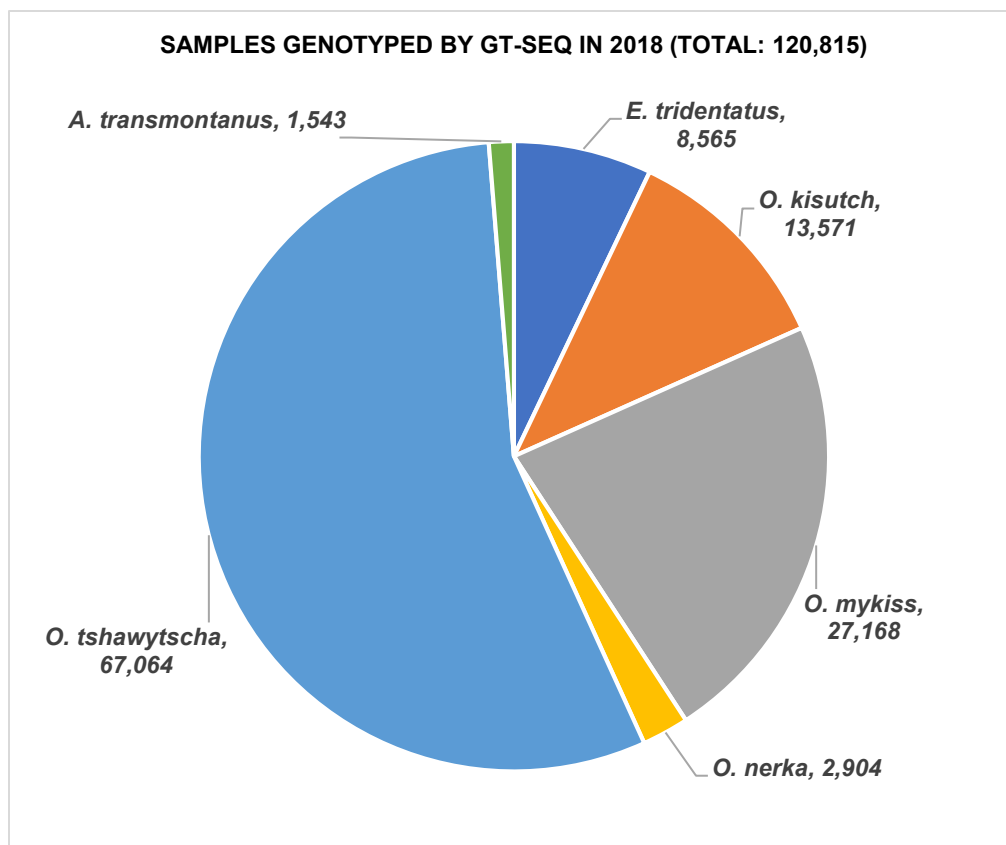


Figure 12. Summary of Columbia River fish samples genotyped using GT-seq in calendar year 2018.

Discussion

The GT-seq genotyping method has allowed for the genotyping of more samples in less time at more loci and at significantly cheaper cost than our previously used method (TaqMan genotyping assays). The total number of samples genotyped using this method has continued to increase from previous years but is expected to stay at a similar level in coming years of this project. The inclusion of more loci afforded by this method has also allowed for improved capabilities such as greater ability to discriminate between reporting groups in GSI and single parent assignments in PBT projects. Similarly, we can now take advantage of genetic markers associated with physical and behavioral traits of our study species by including them in our high-throughput panels. An example of this is our ability to distinguish between early- and late-spawning ground arrival timing in steelhead by including SNP loci found to be highly associated with this trait (Hess et al. 2016, Micheletti et al. 2018).

Expansion of our GT-seq panel for Sockeye salmon is also projected to greatly improve research capabilities in that species. The expanded panel contains 382 loci compared to the previous 93 loci, which should be sufficient for differentiation of Columbia River populations, but also provide statistical power for parentage analysis in this species.

In conclusion, the GT-seq method continues to produce quality genotyping data at a fraction of the cost of previous TaqMan genotyping assays. The technique uses only general laboratory instrumentation (Thermal cyclers, plate centrifuges, quantitative PCR instrument) for library preparation and the Illumina sequencers (either HiSeq or NextSeq500) can be used as high throughput genotyping platforms while maintaining utility for other sequencing studies (whole-genome shotgun, RAD-seq, transcriptome sequencing, synthetic long read, etc.). This is a key feature of the technique since it allows the multipurpose functionality of the laboratory without investment in specialized equipment. Overall, GT-seq is a valuable tool for conservation genetics studies allowing vastly improved statistical power, higher throughput, and prediction of heritable traits at a lower cost.

References

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Table 3. *Oncorhynchus mykiss* GT-seq panel (390 loci including one sex determining marker).

Assay	A 1	A 2	FWD	Reverse	A1-Probe	A2-Probe	Allele Correction s	Comments
Ocl_gshpx-357	T	G	GAGATCCTGAGGTCCTGAAGTAT	AAGTGGAAATTTGGGCTCAAAGC	ATCCGTCCAGGAAATG	TCCGTCCTCGGAAATG	0,0	GSI Panel - Species Marker, Campbell et a. 2009
Omy_myclarp404-111	T	G	GCTGTGGTGCTCATGGGTAA	CCAGGGCAGGGTTGTCTC	CAAAGCCATACGTGGC	AAGCCATCCGTGGC	0,0	GSI Panel - Species Marker, Campbell unpublished
Omy_Omyclm k438-96	A	C	CCCGACTCTACTTCACTACTTTCCT	GGCCTAGGACAATAGGACTGAAC	TACGCAAATTAGGTTAAAA	CGCAAATTAGGGTTAAA	0,0	GSI Panel - Species Marker, Sprowles et al. 2006
M09AAC.055	C	T	GTCTCCGACGTGTGGCT	TGGAACGAACCTGAGAACATAAGG	ACCTCCACGCTGTCC	ACCTCCACACTGTCC	0,0	GSI Panel - Presumed Neutral, S. Young unpubl.
OMGH1PRO	A	T	TCAAACCTGCATTTGATGGAACAAACAT	AGGACAATTCTAAGTGACCTCAAAC	TGCA	TAGTGTA	0,0	
M1-SNP1	A	T	TCAAACCTGCATTTGATGGAACAAACAT	AGGACAATTCTAAGTGACCTCAAAC	CA	TCA	0,0	GSI Panel - Presumed Neutral, (Abadia-Cardoso et al. 2011)
OMS00003	T	G	GTGCCACTGATGAGGATGAGATCA	GTAATAAAGCCCTTTTGTGAGGAAA	CTTTACTGTGCACATT	TACTGTGCGCCATTT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00008	A	T	CCCTTTAAGGAGGATTTAAATATGTGAG	AACTAAT	TTA	TACTGTGCGCCATTT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00013	A	G	ATAGAA	GGATACAGCGTTTGGAAATGAAACT	CTTCTTTTCCCTTGCT	CTTTCCCTCGCTAC	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00014	A	G	GCCTTTGTCTCCTTGGTGGTTA	AGAAAAGTGTGGACTGAGGTTGAG	ACTC	TC	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00015	T	C	CTTACACACAAGGGCTTCATTCTG	GATGTCTCTGGGTGGTTGTCA	TGATTTGATGAATTA	TTGATGAATTGAACT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00015	A	T	TCAGACCCTATTTTGGCACAAGT	GTCTAACTGATCCCACTTCTGCAT	AACCTC	TC	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00017	A	G	ATTAAGTTCATACAAAAGTTCATCATAAAT	GGAGAACAAAGGGAAGAGAAGAC	CAAGTCACACTTTTA	CAAGTCACACTTATA	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00017	A	G	ATTTTCCTTT	A	TAGACCTCGGTGCTG	ATGAA	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00018	T	G	AGAGTACATGTGTGGCTGCAA	GTCTAACTGATCCCACTTCTGCAT	TAG	CCTCGGCGCTGTAG	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_cd28-130	T	C	CACAACTCCACAGAGACAGTGA	GGATCAAAATCAACACAATTATCTTC	AACCACATAATTAAT	CCACATAATTCATAA	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00030	T	G	AGAGTACATGTGTGGCTGCAA	TTCACAGAA	AATTC	TTC	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00030	T	G	CCTCGTGA	GAGGACAAA	CCTGTTCATTACCC	CTGTTCGTTACCC	0,2,7	GSI Panel - Presumed Neutral, DeKoning upubl.
OMS00048	T	C	CCTCGTGA	GAGGACAAA	ATGAGGGTCCCTATA	ATGAGGGTCCCTCTA	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00048	T	C	CCTCGTGA	GAGGACAAA	CAGG	CAGG	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00052	T	G	GGAAGAGCTGGAGAACAACGT	GATCTGATCGGTGCGGAGAGA	CAGCTAAACTCAGCA	AGCTAAACTCGGCA	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00052	T	G	GGAAGAGCTGGAGAACAACGT	GATCTGATCGGTGCGGAGAGA	AAA	AAA	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00056	T	C	TGCGTTTTTCATCCCAATCATTAC	GGCATCAGGCTCTTCTTCCT	CTTCTTTTCCCTTGCT	CTTCTTTTCCCTTGCT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00056	T	C	TCAGGAAGTAAACTGAAAATTCCAATGTA	GGCATCAGGCTCTTCTTCCT	AT	CCTTTTGCGAATAAT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00056	T	C	TGA	CCCCAACCATGCTTGTATTGAAC	TAGCTTGACCAAATA	CTTGACCGAATAGC	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00061	T	C	AAGTGAGGGCTGACCTGTG	GCTGATGGCACCTGACAGTTAATT	GCA	A	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00092	A	C	TCTCCAGGTGTATCTTGAGAAGGT	AGGGTTCACACAGGGAAGATATCA	CATTGCCATTTACAG	TGCCATTTGCAGACT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00092	A	C	TCTCCAGGTGTATCTTGAGAAGGT	AGGGTTCACACAGGGAAGATATCA	ACTT	T	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00096	T	G	CATGAGAATGGATCAGTCTCCACAA	GATGAAATCTGAATGTGTGACACT	CAGCTGAGAATAGGT	AGCTGAGAAGAGGT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00096	T	G	CATGAGAATGGATCAGTCTCCACAA	GATGAAATCTGAATGTGTGACACT	TC	TC	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00087	A	G	GCAAAATTTACCCCTTAACGTGGTTT	ACAG	AAAGAGGAAGAGTCT	AAAGAGGAAGCGTC	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00087	A	G	GCAAAATTTACCCCTTAACGTGGTTT	ACAG	CG	TCG	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00119	A	T	AGCGGCAGTTGTGTTAATGAGA	GATTTGATGTGTGTATTACCTCCT	GTTA[CA]AACTGACA	GTTA[CA]AGCTGAC	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00119	A	T	AGCGGCAGTTGTGTTAATGAGA	CTTCTAAAGCCTGACAGTCTGT	AAGTGTG	AAAGTGT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00129	C	G	GGAGATGATGAAATAAAATTGAGGAAA	TGCTGTGTAATTATCGCAAATAAC	CCACACAGCTGCCTG	CACACAGCAGCCTG	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00129	C	G	AGATGA	CA	T	T	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00133	A	G	GACCACCTTCACTCATTCTCCTTTT	TCCGGTTTACACACTTCATGCA	TTGAACAACAAGAAA	TTGAACAACAACAA	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00133	A	G	GACCACCTTCACTCATTCTCCTTTT	TCCGGTTTACACACTTCATGCA	AA	AA	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00138	T	G	TCGGACCACATGAGCAGTTC	GTTCACACAGGTGCCACAC	CGCCTCCATCTTTGTG	CGCCTCCATCTCTGT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00149	T	G	GGATGATGCTGTGAGTCGAGAAG	ACCTTCGCCCACCATGTTTTATT	GT	GGT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00149	T	G	GGATGATGCTGTGAGTCGAGAAG	ACCTTCGCCCACCATGTTTTATT	CTAACAATAACCAA	CTAACAATAACCAC	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00151	A	G	TA	CAAT	GACTG	AGACTG	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00151	A	G	TA	CAAT	GACTG	AGACTG	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00095	A	T	CTCCAATGGCTGTCAACAATTAATATAA	CCTGGGAGGGTTATATCGGAGTAT	GCTAAATGCACAG	GCTAAAGGCACAG	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00095	A	T	GAC	ACCGTGGAATACAATTTTTATGCA	TC	ATGACCTCGATAATC	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00169	A	G	AGCACTTGACTCAAACCTCACATAAATCA	GTGTGCTGGTCTCTCTTTTATTCTC	AGGCAACTATATATT	AGGCAACTATATAT	1,5,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00169	A	G	AGCACTTGACTCAAACCTCACATAAATCA	GTGTGCTGGTCTCTCTTTTATTCTC	TTTT	ATTTTT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00173	T	C	TGGAAGTAGTACTTAACAGGAAATGG	CTGAGACAGGAAGAACAATGTTAA	CAAAAAGCATTGATA	AAAAGCATTGACAT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00176	T	G	GTTGGAAAGTTCGGGTGGTAGAG	CAAAA	TCAAT	CAAT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_impal-55	C	T	CGCTGAGAGGATTGTCAA	CGCAGGAGACGGATGCC	CATTAGCTTGTGTATG	ATTAGCTTGTGTGTG	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_103705-558	T	C	CTCCAATCGCAAATACCCAGACT	CGCAGGAGACGGATGCC	AACT	AACT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_105075-162	T	G	GGAGAAGGACAAGGACATTGGTAAT	CTGGGTCTGAAAGGAGCTT	TTCCAGCACTGCTGTC	CCAGCCCTGCTGTC	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_107031-704	C	T	GGCTTTCGGATACTGAGCAACAA	TTTCTTTGTTCAGTCTTCTGTCTCT	CGAGATGATGCGTCT	CGAGATGATGCATCT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_107285-69	C	G	GCCCTTGTGACAATGCACTGTTATA	G	ACA	ACA	0,0	GSI Panel - Presumed Neutral, Narum et al. 2010
Omy_110201-359	T	G	GGTAAGGCCTGTCTGACTATTTTGA	AGAGGTCAATGGATGCCAGTTT	AGACTTACCCAGAGT	ACTTACCCAGGGTG	0,0	GSI Panel - Presumed Neutral, (Abadia-Cardoso et al. 2011)
Omy_CRBF1-1	C	T	AGTTCGGTACGGTAGCCTATTCTA	CGCCCCGGGTGAGAGTAATTG	GAGAG	ACTTACCCAGGGTG	0,0	GSI Panel - Presumed Neutral, (Abadia-Cardoso et al. 2011)
OMS00114	T	G	GGATGATGCTGTGAGTCGAGAAG	ACCTTCGCCCACCATGTTTTATT	CTTTCTCTCCTACTTT	CTTTCTCTCCTCCTTT	0,0	GSI Panel - Presumed Neutral, (Abadia-Cardoso et al. 2011)
OMS00143	T	C	GGAGGCACGCCCCAAA	TTTGTAAAAATAGAGCCCTTAGTGG	CC	CTGGACATGATTACA	0,0	GSI Panel - Presumed Neutral, (Abadia-Cardoso et al. 2011)
OMS00174	A	C	TGACTAACTATGCAGCCTGAAAGG	GTTT	AGAC	TAGAC	0,0	GSI Panel - Presumed Neutral, (Abadia-Cardoso et al. 2011)
Omy_97077-73	T	A	GTGTAACAAAAATGACTCTGGGATTGAG	AGAAGTGGCAATGGTGTGAAGTAT	ATACGTTACTTTTGAC	ACGTTACTTTTCACC	0,0	GSI Panel - Presumed Neutral, (Abadia-Cardoso et al. 2011)
Omy_97865-196	A	G	TCCAGACTTCTGGTTTGTTCATT	CCAGCCCCTATATTCACAATTAAGT	CTTGT	CTTGT	0,0	GSI Panel - Presumed Neutral, (Abadia-Cardoso et al. 2011)
Omy_97954-618	C	T	GCTCTGCTTCCTCGGCAAATA	CACAATTGGTTTTTGCACAAAAGTA	TTGGCTATTGAAATT	TTGGCTATTGAAATT	0,0	GSI Panel - Presumed Neutral, (Abadia-Cardoso et al. 2011)
Omy_128996-481	T	G	CTCATCCACACTGTACAGTACAAGT	AAGTATT	ATACATT	CTACATT	0,0	GSI Panel - Presumed Neutral, (Abadia-Cardoso et al. 2011)
Omy_aromat-280	T	C	CTCCATTGATTGATGCCGAACATT	GGAGAGGTCAAACATAGCCTGGTA	CAGAGTCGCCAAAAT	CCAGAGTCACCAAAA	0,1	GSI Panel - Presumed Neutral, Aguilar and Garza 2008
Omy_aspAT-123	T	C	GCCCATTTCATGATGCTGTGA	AGGAGACCACTCCAAAGAGAACT	AAACGTTTCACATGC	AAACGTTTCACCTGC	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_b9-164	T	-	GCACAGAACACAGCCAATATTAACA	GCCTTGACTCTCCCTTCATGAC	ACC	ACC	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_BAC-F5.284	C	T	CCTCATTTACTGTAGGACCATGCA	ACAACGCCAACAACTTTCTCTTG	CCTGATCCAGAATCT	CCTGATCCAGAGTCT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_BAMBI2.312	G	T	CGAGCTCATGTCCGAAACTCAT	TTTGATGTAAGATTGCTTATAGCTA	AGA	AGA	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_carban1-264	G	A	GCAAAGCCTCATCTTCAATCATTTGT	TTTGATGTAAGATTGCTTATAGCTA	CAAGAACAGG[AC]TA	CAAGAACAGG[AC]G	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_cd59b-112	C	T	TGTGATAAGATTGCTTATAGCTA	GCCAAACGTCCTAGATATGGTGTAA	AATGT	AAATGT	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_cin-172	C	T	CGCATGGGACAGGTGTGT	GAGAAAGCCTGTAGAACCATGTCT	TGGTGCAATAGAAAT	CATGGTGCAATAGT	0,0	GSI Panel - Presumed Neutral, (Abadia-Cardoso et al. 2011)
Omy_cox2-335	T	G	AGCTGGGCTGTATTTGTCAATACTT	CAGCCCGCCACTGTCT	A	AATA	0,0	GSI Panel - Presumed Neutral, (Abadia-Cardoso et al. 2011)
Omy_e1-147	G	T	GCACTGACTGTTACCAGGAAAGAG	GTACTGCAAGTGTGAGGCTATATCA	ATTAATTAACAAGCT	ATTAATTAACAAGCT	0,0	GSI Panel - Presumed Neutral, (Abadia-Cardoso et al. 2011)
Omy_g1-103	T	C	AGTCGTGACAATGAGAAACAGTGTT	CTCAGCAAAAAAGAAACGTCCCTTT	C	CTTAAAGACAAAGA	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_G3PD_2-371	C	A	GCAGGTAAGGTACACCATAGAGACA	CTCCCCCTGCCTTACCAAAC	CTTTAT	CTTTAT	0,0	GSI Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_gadd45-332	T	C	AGAGAAGACTCACTGCTGTTTGC	AAATCAGTTCCACGCTATGCT	CCATCCTGAATCTGA	CCATCCTGAATATGA	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_gdh-271	C	T	AGGTCAGTCTACTTACAGTATAAAGCAGT	AAATCAGTTCCACGCTATGCT	TAA	TAA	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_gh-475	C	T	AAGTTACCAGAATTTTGCAAACCTCAACT	CTTCAAGTTCACAGAGTAACATAA	ATC	TC	0,0	GSI Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_GHSR-121	T	C	CTGTGTATAAGTTTATACAGTCAGCACAGT	G	AGACATGTGGATTGG	CAGACATGTGTATTG	0,0	GSI Panel - Presumed Neutral, CRITFC - N. Campbell unpubl.
Omy_GHSR-121	T	C	CTGTGTATAAGTTTATACAGTCAGCACAGT	G	CA	GCA	0,0	GSI Panel - Presumed Neutral, CRITFC - N. Campbell unpubl.

Omy_hsp47-86	T	A	CACATTAAGCACTCCCAGGGA	TTGCAAAGGCCAAACAGCATT	CAGGAGTGTAATGT	ACAGGAGTGATAT	0,0	GSI Panel - Presumed Neutral, Campbell and Narum 2009
Omy_hsp70APro-329	A	G	TGCGTATTATTGTTTTTCAAGGACTTTCAA	TGAATATTTTCAAATACATGCCAAT	ACATTCCAATATTCA	GTTT	0,0	GSI Panel - Presumed Neutral, Campbell and Narum 2009
Omy_IL1b-163	T	G	A	TC1TTTCCAA	ACTAT	CTAT	0,0	GSI Panel - Presumed Neutral, Campbell and Narum 2009
			GGAACAACAGGATTAAGCCTACTCT	CCTAAAGGCCTAGGAACTAAACTTCA	CTGAGGTCATAAAAA	CTGAGGTCATACAA	0,0	GSI Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
				CA	TA	ATA	0,0	GSI Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_inos-97	C	A	GATGGACAGGGTCCTCTTCAC	CCTGTAGATAAAACATGGTACCAGG	CCTTTCTTGATGGTAT	TCCTTCTTGATTGT	0,0	GSI Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_LDHB-1_i2	C	T		TC	CC	ATCC	0,0	GSI Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_LDHB-2_e5	C	T	ACGCACACTTATCCTTGACAATGTT	ACTGTGACAACAAATTCGGTGACA	ATGGGCAGTCATTCA	TGGGCAATCATTCA	0,0	GSI Panel - Presumed Neutral, Aguilar and Garza 2008
Omy_LDHB-2_i6	T	C	TGCTAGGTGAGTCAGAGGTACATATT	GACTGGAAGGCCACCCATAAG	TTTACCTGTCAAC	CCTGTGCGAC	0,0	GSI Panel - Presumed Neutral, (Aguilar and Garza 2008)
Omy_LDHB-2_i6	G	T	TCCTCGCCAATACCATACATGTG	AGAGTGAAGCTAACACACACATTTC	CTGTGTTTTGCTTCCC	CTGTGTTTTGATTCC	0,0	GSI Panel - Presumed Neutral, Aguilar and Garza 2008
Omy_lpl-220	C	G	TGACAATCACTGAGCAACTGAACTC	T	CA	CA	0,0	GSI Panel - Presumed Neutral, Narum et al. 2010
Omy_mapK3-103	A	T	GAAGTCATTACTGGTCAGTGGTCAA	GTCCAGTCTTGCTTCAACTCATTCT	AGTGACAGTCA	AGTCACAGTCA	0,0	GSI Panel - Presumed Neutral, CRITFC - N. Campbell unpubl.
Omy_mcsf-268	T	C	CCAGCATTCGTTCCCATTTCC	GCACAAAACATGAGGAAAGTTGAG	AATTATTAAGCCTATT	ATTATTAAGCCTAAT	0,0	GSI Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_metB-138	T	A	TCTGTCCCTGACGCTATAAAAAACG	CTTTTAATGTAGATTATATTCTTCTG	AAATAATAGATAAA[CT]CCT	AAATAACAGATAAAA[CT]CCT	0,0	GSI Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_myoD-178	A	C	GGTCAAATATTTCAATTACGATTACACTTA	GAAGTATTTCAAGCTTAATTTCACTG	TTCGCCAAAGAGAAAA	TTCGCCAAAGTGAA	0,0	GSI Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_nach-200	A	T	CTCATGAAAAACGGGAGAGCAAAG	TTGAGTT	T	AT	0,0	GSI Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_nxt2-273	C	T	CTTAGAAAAAGCCAAGGTATATTTTAACAT	TGGCAAAGCTGTCAATTCCTCTAAT	TITTTATGAGATATAAT	TITTTATGAGATATCA	0,0	GSI Panel - Presumed Neutral, (Campbell et al. 2009)
Omy_OmyP9-180	C	G	ACTTCT	CAGCGGCTCTTCAGTAGTCT	TTC	TTCC	0,0	GSI Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
				CTGCTGCCCTCTAATGGTAAGATAG	AAGGCAC	AAGGCAT	0,0	GSI Panel - Presumed Neutral, (Campbell et al. 2009)
					CTGTAGTAGTCCCCA	CTGTAGTAGTCCGCA	0,0	GSI Panel - Presumed Neutral, (Campbell et al. 2009)
Omy_pad-196	C	T	CAAACAACCACAGTAGTCTCTCAAT	CACTGGGACCTCTGATCTC	TTGT	TGTT	0,0	GSI Panel - Presumed Neutral, Campbell unpubl.
Omy_ppic-232	C	T	CTGTTTTAGATTAGAATGTTTTTGGTCAGG	GCTTTTACCCTTTTGTAAATTAAGC	AAGACAAAGGTGTAA	AAGACAAAGGTATA	0,0	GSI Panel - Presumed Neutral, Campbell unpubl.
Omy_ca050-64	T	G	T	CTAAACATAGGCTTTCAATTCAGAC	TACC	ATACC	0,0	GSI Panel - Presumed Neutral, Narum et al. 2010
				AT	T	AAT	0,0	GSI Panel - Presumed Neutral, Narum et al. 2010
				ACCTTGAATTGGTTCCTAATGCTAT	CAGTTTGAAGAATAT	CAGTTTGAAGACTAT	0,0	GSI Panel - Presumed Neutral, Narum et al. 2010
				TGT	ACTC	ACTC	0,0	GSI Panel - Presumed Neutral, Narum et al. 2010
				TGGATTCCATTTAGGCTGTAATAC	CTAGCCAATGCGTCT	ATCTAGCCAATGTGT	0,0	GSI Panel - Presumed Neutral, Narum et al. 2010
Omy_sast-264	G	A	GAAGTAGGGTTGTTGACCATGTGA	ATCTT	AA	CTAA	0,0	GSI Panel - Presumed Neutral, Narum et al. 2010
Omy_SECC22b-88	T	C	GGATCCCTCCTTTTAACACAAGACT	CTACAGGATGACTACCTAATTGCTA	CTGTCTGTCCATATAT	CTGTCTGTCCGTATA	0,0	GSI Panel - Presumed Neutral, Campbell unpubl.
				ATAAAACA	C	TC	0,0	GSI Panel - Presumed Neutral, Campbell unpubl.
Omy_sSOD-1	T	G	GCCGGACCCCACTTCAA	CAGACTAACCGAACAGCATCAGTG	G		0,0	GSI Panel - Presumed Neutral, Brunelli et al. 2008
				G			0,0	GSI Panel - Presumed Neutral, Brunelli et al. 2008
Omy_star-206	A	G	CGTGTGCCAGCCCTTCT	GACCACTGAGATCATTGCTGTGA	T	TTTGGCACCATATCT	0,0	GSI Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_sys1-188	C	A	CTTAAATGGTGCTGGTTGCTGTATT	AGTGATATCTTAGTGGGTCGAGGAA	AAACATGTACGACCT	TGTAAACATGTACTA	0,0	GSI Panel - Presumed Neutral, Narum et al. 2010
				A	GTC	CCTGTC	0,0	GSI Panel - Presumed Neutral, Narum et al. 2010
						CGTGATTAGATTCTT	0,0	GSI Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_tlr3-377	C	T	GTCGCTCCGGGTGCTT	GGCCCAAACACTTCCTTCCT	CGTGATTAGGTTCTTC	C	0,0	GSI Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
					CAGTAATATTTCTGT	CAGTAATATTTCTGT	0,0	GSI Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_tlr5-205	T	A	GAGCGTATCTGGTATGGTAACAACA	CTCCAGCAGCTTTAGAGAGTTTACA	GCCCG	GCCCG	0,0	GSI Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_hsflb-241	A	-	AGCCCGAACTATCCTAAAGCATTTT	AAATCAATAGCTCAGAGAATAATG	CAGTGTTTTGTTTTT	AGTGTTTTGTTTTT	0,0	GSI Panel - Presumed Neutral, Campbell and Narum 2009
Omy_u07-79-166	G	T	CCCGCTATATTATTTGATCACCCTTGA	AACACCA	GTCATT	TCATT	0,0	GSI Panel - Presumed Neutral, (Limborg et al. 2012)
Omy_u09-52.284	T	G	TTTGTGTGTATTGTTGTGACTTG	ATTTAAATCCATTTCTAAAAATAAG	ACTTGGGAATACCCC	CTTGGGAATAACCC	0,0	GSI Panel - Presumed Neutral, (Limborg et al. 2012)
				CAAACCTAACCA	AGCC	AGCC	0,0	GSI Panel - Presumed Neutral, (Limborg et al. 2012)
					ACTGCATTGTTGTAG	CTGCATTGTTGTGCG	0,0	GSI Panel - Presumed Neutral, (Limborg et al. 2012)
Omy_hus1-52	G	A	CTTGCCGGAGGGTAGCT	TGATGTTATTGCAGGTCTAGCGAAA	CTAG	TAG	0,0	GSI Panel - Presumed Neutral, Narum et al. 2010
Omy_u09-56.119	T	C	CCAAGGTGGACCCACCAG	CCACAACCTCTCAAATGAATGGAAT	CCCATCCCCTCCTCGT	CCCATCCCCTCTCCT	0,1	GSI Panel - Presumed Neutral, Narum et al. 2010
				GT	G	GG	0,0	GSI Panel - Presumed Neutral, (Limborg et al. 2012)
				GCTGAGTTTATAGGTCAGTCATTAT	AGTGAGCTGAAACAG	TGAGCTGAAGCAGA	0,0	GSI Panel - Presumed Neutral, (Limborg et al. 2012)
				ACATATTGA	AGCA	GCA	0,0	GSI Panel - Presumed Neutral, (Campbell et al. 2009)
Omy_nips-299	T	-	GACAGGATAGGAACGGTTTCTCAAT	ATCAGAAGTTTAATTCATATGTAC	CTGGATTTACATGT	CTGGATTTACGTAA	0,0	GSI Panel - Presumed Neutral, (Campbell et al. 2009)
Omy_UT16_2-173	C	T	ATTGACTCATTATCACCTTAGTTGTAGCTT	ACGATCCT	AATAC	TAC	0,0	GSI Panel - Presumed Neutral, Young unpubl.
Omy_vamp5-303	A	-	CTGCTTCCCAATTCAGTATCGTCTT	GCAGTACTTGCTGTATCACATGTT	ACAGTCAACAAGGGA	ACAGTCAATAAGGG	0,0	GSI Panel - Presumed Neutral, Young unpubl.
				TGT	CTTAA	ACTTAA	0,0	GSI Panel - Presumed Neutral, Young unpubl.
					TGGCCGTAGTAGTTG	TGGCCGTAGTTGGTC	0,0	GSI Panel - Presumed Neutral, Narum et al. 2010
Omy_zg57-91	C	A	CACTCATACACTCACTCACAAAGGA	AGGCTGAAGCATTCTGAGTATGAA	GTC	A	0,0	GSI Panel - Presumed Neutral, Narum et al. 2010
				AAGAATTGAGGGATAAAAAACAAAATAATA	CACAGACTGCACAGC	CCACAGACTTCACA	0,0	GSI Panel - Presumed Neutral, Narum et al. 2010
Omy_ndk-152	A	G	TATAAACATGA	TT	C	GCC	0,0	GSI Panel - Presumed Neutral, Narum et al. 2010
				CAAACCTACATTCAATAAAGTCCAG	ACCCACTTTCAAAAC	ACCCACTCTCAAAAC	0,0	GSI Panel - Presumed Neutral, Campbell unpubl.
M09AAD.076	T	C	ACTGTTACCACTCTCTCATCAACCT	TTTTGT	CACCAACCACTGGTG	CCAACCGCTGGTGA	0,0	PBT Panel - Presumed Neutral, Young Unpubl.
M09AAJ.163	G	A	TCCCATGGCCCTTACTCTATCAA	GGGTCCAGGAGGTTTTTAAACAACA	AA	A	0,0	PBT Panel - Presumed Neutral, Young Unpubl.
				TTGAGGTGTATGTTGAAAAGTAAAC	AACAAAGTGAAAGTG	CAAAGTGAAAGTGT	0,0	PBT Panel - Presumed Neutral, Young Unpubl.
				TT	TCCTTA	CTTTA	0,0	PBT Panel - Presumed Neutral, Young Unpubl.
M09AAE.082	T	G	CTATGTGCAGTGCCCTTCTCA	AGGTTGTTTTACAAA	AGGTTGTTTTACAAA	AGGTTGTTTTACACA	0,0	PBT Panel - Presumed Neutral, Young Unpubl.
OMS00002	A	C	TTTGATTTGATTGTATCTGCTTCTT	TTTAA	TTTAA	TTTAA	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
				GGCTTACAAGTATGCATGACTAGCT	TGTTTTGCAGCGCTC	TGTTTTGGCAGCGCT	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
				CCAACATGCCTCACACAAAA	CATTACAAATACAA	CTTACAAATGCAAA	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00006	T	C	TCCACGTAGGACATAGTTTGAGCTA	TGTGGTGCATGTTTGCCCTAC	AATT	ATT	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00024	T	G	CACATACAACCATCACCCCTTCTAA	AGCATTGAGCGAAATTACCAAGAG	AA[AC]CCCAAATTTT	AA[CA]CCCAAATTTTA	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
				T	AC	GTGCGTGTCTCTGAC	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
					GTACGTGTCTCTGAC	CT	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00039	A	G	GTCAGTACTGTGTGTCTGTGT	CCATCTACATTGTCAGCAGTGTGA	ATTTATATGTATCAAT	ATTTATACGTATCAA	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00053	T	C	GGAGCCAGGTCAAGGTGATC	GGATGTCTGGTGTGGCTGTAAA	CA	TCA	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00057	T	G	GAGAAAGGGAGCATGAGACAGA	GTTGGGCTCCGGTACGAT	CTCCACAGAACCTTG	CTCCACAGCACCTTG	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
					CAACACTTTGTACCC		0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00058	A	G	GTGACATTTGGAGCCACTGC	GCTAGGAGACAGAGGGTGAAAG	CTC	CACTTTGCACCCCTC	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
				TGAACAGAGATCTGGAGAGTTGGA	TTGACCAGCAGATGG	ACCAGCAGGTGGTG	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00062	T	C	ACCCTGGGAAGGCTACTGTAC	T	TGTA	TA	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
				TTTACAACAATCTTCTTTAATAAAA	CAGGCAACATTTTAT	CAGGCAACATTTTAT	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00064	T	G	GTGGATATGTAGTTGCATGGAACAGT	AATATAGCCACTTAT	ATAACTA	CTAACTA	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00068	A	G	A	GGCAGTTGAGCATTTTGGGATATT	AATATGCCTCCTTCGT	TATGCCTCTCCGTC	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
					CTC	TC	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
					CAAAATACGGAAATG	AAATACGGGAATGC	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00070	T	C	CGTTCTCGGGGACAGT	GTTTCTCTCACGTCCACAGATCT	CAG	AG	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
					CTTGTTGAGCTTTTT	TGTGTTGAGCCTTTT	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00071	A	G	CCGGAGTGACCTCACATTTGG	GCATCGTACAGTTCACCTACCT	CT	CT	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
					TAGAAGGTCCATGTA	AAGGTCCATGCATCT	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00072	A	G	CTGGGAGAGCTCGTCTATGG	ACAACAGGTCAATTGGATGTGATCAG	TCTC	C	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
				CACTTAATTTAGCAACAAATGTCT	TGAAACAAAACAAAT	AAACAAAACACATG	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00074	T	G	AAT	GAACAGAA	GTTCC	TTCC	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
					TTCCGGTGGTGAAGT		0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00077	C	G	CAA	CCAGACTTTACACACTCTTGACTGA	T	CCGGTGTGAAGTT	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
				GTCTCACTATGGTCCATATCTGTGT	TTCACATGCATAAGA	TCACATGCATGAGA	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00078	T	C	GAGGGAAGCAGCCATAAACAGAATA	AGA	GTG	GTG	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00079	T	C	CT	ACCTGCAACGTTAGAGCTGTTTATT	CTACTTTTCACAGTAA	CTACTTTTCACAGTG	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
					CACAG	ACACAG	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
					CAACCAGACTACCAT	AACCAGACTGCCATT	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00111	T	C	CATGCGGACCTGCATAGCT	GCTTAGCCATTGACAGAGCATATCA	TC	C	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
				GCAACCCAATTCAATATTAAGCACA	ATGAATCCCAATAA	AATCCCAACAAGA	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00089	A	G	GCACCATTTGAATAAAAAATCTGCTTTGT	TGAT	GAAC	AC	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
					ACAACCACACAAGAT		0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00090	T	C	AGGGCACAAACCACTCTAAATT	TCGAAAAGCAACATCTGTCTCAGT	T	AACCACGCAAGATT	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
				GTGCAATCCAACCTATTAGTAGATA	CTCTAGTAGCCTTATA	CTAGTAGCCTTACAG	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00101	A	G	GCGTGTGCTGGGTGAGTTAAATA	TGCT	GAAAG	AAAG	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
					CTGCTATTCAAATTGC	CTGCTATTACATTG	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00105	T	G	ACATTTGAAGTCAGTATGGGTGTTGAG	GAACCTCACCACAGTACTAAATGCA	T	CT	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
					TCTGATGGAACTTT		0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00106	T	G	CGTGTAGCATTCTTGAGGAAGCTT	TTTCCAACAGATGCCAGAATCCT	C	TGATGGCAACTTTC	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
					ACAGGGCTTCTGATT	AGGGCTTCAGATTG	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00154	A	T	GATGTTGGCTGGAGGTGTAGT	TGGGAACACTTTGCGCTACCC	GA	A	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
					CCGGTTTCAAGTTTAC	CGGTTTCAAGTATAC	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00112	A	T	TGGCAGCAAAAGGGATGCA	TCCTGAGCAACCAAGTCAACATT	TTGT	TTGT	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)

OMS00118	T	G	GCTTATTTAGAGTGCATGCCAGATG	TGGAACCAATGGGACAGTCCTA CCTCAAATACCTCTGACATTGAAGG	GCGGGGTGTGC[AG]C ATT	GCGGGGGTGC[AG] CATT C[GA]CCCACCAAAA C	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00120	A	G	GGCAGAAGAGGAGAGAGATATGATTG	TT AAAATATGCAACACCACTAAAACT GGAAAA	C[GA]CCCACCTAAAAAC		0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00121	T	C	GGAAGGAGGTCCAGTGTGAGT	ACGCGACCTGCAATTCATCAATA ACTACCTCCAGTTAAAATAGTGTGG GAAA	ACAGCGTGATAAAATT CAGCAGTCCTCTGTG TGG ATCACTAGTTCAAAT ACAA TGCCTCTTCTCTTTTC TCAT CTAAAAAGTGCATTAA GCC TGTAGTCTTTCAGAGT AGTATG CTTGATTTGCAGCTTG TCAA AACAGGATGTTTTTG C CAGCAGGATACATCC GACT AAGGAGAATGCATAA TC CTTGAACCATTGCT AC CTGTTGTTTGAGGTTG AG ATTGGATGTCAAGTGT CATT ATGTTTCTCCCTACT TAAC TGTTTCATTAAATTGAC TTTT	CAGCGTGGTAAATT AGCAGTCCTCAGTGT GG ATCACTAGTTCAGAT ACAA CCTCTTCTTGTCT CAT CTAAAAAGTGCCTTAA GCC TAGTCTTTCAGAGGA GTATG CCTTTGCAGCATGT CAA	0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00132	A	T	GTTTATGACTCCATTGCCGAAATGATT				0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00175	T	C	TTGCGATATGGGACTGTATACATTTATTC				0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00179	A	C	GTCATAACAAAATCAGGGCTTTCCAA	TGGGAGATTGGGCTGCTTTAAA			0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
OMS00180	T	G	GCGCCGAATGGCATTAGG	CACATTGCTGTCGTTTAGTTGACT			0,0	PBT Panel - Presumed Neutral, (Sánchez et al. 2009)
Omy_101832-195	A	C	TGGCTCTGGACCTGTTGAGA	CGTCACAGCTATTTTAGGCGTAGT			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_101993-189	A	T	ACAAAACACAGTGGAAATACAATTAACGT	GGAAGTTAAATTTTCGCTTCGTCAGA A			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_102505-102	A	G	CTGCAAACTGACATGGTAGCAAAA	TGCTTGCTTTTTAAAAACAATCTCC CA			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_104519-624	T	C	CGTGTGAGTTTGCGGTAAAGAC	TGACGAGTCCGCTTATCATCCT			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_105105-448	C	T	CAATTTGCAAGCAGGGAAAGGTTAT	GTGATGGGCTGCAATTGCTT			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_105385-406	T	C	GTAACCTACCCTCACCTGAACCTCA	GTCGCTCTTCTGGGCGTATCG			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_105714-265	C	T	CCACTCAGTGCAAGCATGGA	GCTTTCATCCTTGGCTCCAATATC			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_107806-34	C	T	TCTTTGTCATGCACATTGATATT	AGCACATTTAGTTAGCAGTGATGGA			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_108007-193	A	G	GTGAATACCAACCCAGGCTTGT	GTCCCTTCCCCAGTTTCACTTAATT			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_109243-222	A	C	ATGTGCACCTCTTAAATTGTAAGTAAAATG	ACCCTATATTCAAGTGGCAAGATTGC			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_109894-185	T	C	GGGAGGAATTGGAATGACAGATTAAC	CGGTGTCATTATGGTTGTCATTGTG TCTGAACTGACACTGAAGAACAAA GAA	CTCCCTGATCCCC ACGTTAGCTTTTAATT TC AGCAAGCGCACT[AG] GGT CATCTGTTTTGGTTTA GC TTATGGGCTTAAGGG TC	CTCCCTGGTCCCC AACGTTAGCTTTTCA TTTC AGCAAGTGCCT[AG] JGGT CATCTGTTTTAGTTT AGC TTATGGGCTTACGGG TC	0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_110064-419	T	G	GTGCAAGGGACCTAGCTAATCC				0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_111383-51	C	T	CACGCGCAATCTCTCGTTTTAC	TCTTTAGGCAACAAGCGTGTC			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_113490-159	C	T	CATAGTACATTTACAGATAATGTTTTAAAG	CGAGATACCAAAATGCCACAGTTAC AT			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_114315-438	T	G	CCTCACCGATCTAGTCAACTTCATC	AGGAGGCTGAGGGAGATTCTAG			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_114587-480	T	G	CAGATTACGTTATTACGTTTGGGAAATTTT	GTGAAAGAGTGGGAAATATAATTA TAAGT			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_129870-756	C	T	TCGTTATTTGCGCTCGCGGTA	TCCCATGAAGATGTATACATGTTTT GTGA			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_116733-349	C	T	GAAATGGACATGCCTACAAAATTGCT	GATGTGATCAGTTTAGGCAAGGC			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_128923-433	T	C	CTATGTCCTTGGCAGAAAGTCTACA	ACGTTTCTTTGGGCTGAGACTTATT			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_130524-160	C	G	CGAAGGTAGCGATTGGTCGTT	TGCTGTCTGCTGTGTGCTT			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_97660-230	C	G	TCAGTTATGTGAATCTCATTACCTCTCCA	AACAGAAAAGGTCTCAATGTATTTT TTGCA			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_99300-202	T	A	CAGTTTGACCCGATGGTGTGA	GATTATGGCGTGGCCTTTTGG			0,0	PBT Panel - Presumed Neutral, (Abadía-Cardoso et al. 2011)
Omy_aldB-165	C	G	GGGTTAGGTGGATTGAAGGAGTAA	AGGAAGGTGATGCCTGAGAGA			0,0	PBT Panel - Presumed Neutral, (Campbell et al. 2009)
Omy_anp-17	C	A	GGTAATGCCACATGCGGTAAATT	GGCGAAATCTGAAAATGTGCTGTTA			0,0	PBT Panel - Presumed Neutral, Narum et al. 2010
Omy_arp-630	G	A	CTGCACAATTGTTTCTGCTATT	ACCAAGTGTCCCTGTAAGCC GATATGAAAATATCTGAAGAGTTAT ATTTGGGAAATTGAC GCCTAATATTGGCCTAATGTCTTTC A			0,0	PBT Panel - Presumed Neutral, (Campbell et al. 2009)
Omy_b1-266	G	T	TCATGTGAACTTTAATTGACTAGGAAGTCG				0,0	PBT Panel - Presumed Neutral, Sprowles et al. 2006
Omy_BAC-B4-324	G	T	CGTACTTTTCTTTTACAAAATTAAGTGGAG				0,0	PBT Panel - Presumed Neutral, Sprowles et al. 2006
Omy_ada10-71	C	T	TCTTTGAGCGACAAAGTCTTGT	ACCCACACATGAACGCAAAAAG			0,0	PBT Panel - Presumed Neutral, Narum et al. 2010
Omy_redd1-410	C	T	GTACTCCCACTAACATACAGTAGACTCA	GGCACCATTGTGTTTTAGGATGTAG			0,0	PBT Panel - Presumed Neutral, Narum et al. 2010
Omy_cd59-206	C	T	CGATTGGCCAGATGTTTCCAT	GCTCCGTTGCATAGGTGACT			0,0	PBT Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_colla1-525	C	T	CCTCGGCGTGACAACCT	CCCAGAGAATGGTGCGATTAGG GCAACATGGGAATGATTCAAAATG CA ATTACAATGAAAGTACTTGAGTGTT TATGCAAA			0,0	PBT Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_cox1-221	T	A	CACTGAACTGTAAGCCATTGTGATT				0,0	PBT Panel - Presumed Neutral, (Campbell et al. 2009)
Omy_crb-106	G	T	GCTCAAAAAGATTCTGCCAAATTCACA				0,0	PBT Panel - Presumed Neutral, Sprowles et al. 2006
Omy_g12-82	T	C	GATCAATTCGATCGCTCATGAAACTT	CTTCTCTCGTTCTCATTGTGCTCA AGAACTACCAATTGTGATTAAACAGA TAGAAAATACAT AGTCAGTCAATTAGTGGTTTGAAAT ACTATCA			0,0	PBT Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_gluR-79	C	T	GACTGTCTATAGCTATTCTTCTCAAACGTG				0,0	PBT Panel - Presumed Neutral, Campbell unpubl.
Omy_hsc715-80	C	A	CCGGTCTACCCTATAGCTGTTG				0,0	PBT Panel - Presumed Neutral, Campbell and Narum 2009
Omy_hsf2-146	A	-	CCAACAATTGCAGCCTCATCTTAAT	GGAGCAGAAAAAGGATTGGACCTT			0,0	PBT Panel - Presumed Neutral, Campbell and Narum 2009
Omy_IL17-185	G	A	CCACCACACTCTGCAGCTT	TTGACGGGAATCCGAGACTTC			0,0	PBT Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_Il-1b_028	T	C	ACTGTCTGGCTAGAGCACATTG	ATCTTCTACCACCGCACTGTTTTAA			0,0	PBT Panel - Presumed Neutral, Young Unpubl.
Omy_Il1b-198	A	T	CAAGCAAAATTGACTCCAGCCATTA	TTTAATCTCGGTGCTGAGCTAGTG			0,0	PBT Panel - Presumed Neutral, Young Unpubl.
Omy_IL6-320	C	T	CGACTGATCTCCTGCAGACATG	CTTGTTCTCGTTGTCTTCCTTCTA			0,0	PBT Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_metA-161	T	G	CGCATGCACCAAGTTGAAGAAAG	AGTGCCACCAGCGATAAGAAAA			0,0	PBT Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_NaKATPa3-50	A	C	GTTGAGCGTGTATTGGGAAAAGAG	TTGCATCGGCTTCTGAAAACC			0,0	PBT Panel - Presumed Neutral, (Campbell et al. 2009)
Omy_txnip-343	T	C	CCTTCAAACCTAACGCATCATAGACATG	GGTCACCTTGGCTAATCCCCTTAT			0,0	PBT Panel - Presumed Neutral, Narum et al. 2010
Omy_nkef-241	C	A	AGTGTCAATTGATGTGGCCTATTTT	AAACGAATGTCCACCTCAGATGTT TGTGTAGCTAGTGATCCTGATTGTG T GTGTGTGTTAAATAAGCATTTGATG A			0,0	PBT Panel - Presumed Neutral, (Campbell et al. 2009)
Omy_ntl-27	G	A	GGTGTGTTACTGTAGTTGTGTCCTT				0,0	PBT Panel - Presumed Neutral, (Campbell et al. 2009)
Omy_Ogo4-212	T	C	TGAAAGGTTTTATGCAGGTTATTTTCT				0,0	PBT Panel - Presumed Neutral, Campbell unpubl.
Omy_bcAKal a-380rd	G	A	TTGCTCTCTTCTGGTTGCCTTA	CTTCAGGAGAAAAGCGCTACTGT			0,0	PBT Panel - Presumed Neutral, Narum et al. 2010
Omy_Ots249-227	C	T	CTATCTATCTATCTATCTATCTATCTA	CCCCTAGATTAACCTGTCCAGTCT			0,0	PBT Panel - Presumed Neutral, (Campbell et al. 2009)
Omy_oxct-85	A	T	CGTCACTGAAACATTACTGTAACATCCA	CATCATCACGCTGTGGTTTCTTAA CCCCAAATTGGCAATTTTAATAGGAT TCAGA AGTTGCATAAGATGAATCAATAAAT TAAAAACACAGAT CGTATTCAAGTCGATATACAGTCAC GAT			0,0	PBT Panel - Presumed Neutral, WSU - J. DeKoning unpubl.
Omy_p53-262	T	A	CCCCAACATCCAGTATACAGTTTCA				0,0	PBT Panel - Presumed Neutral, Campbell unpubl.
Omy_rapd-167	G	T	CCCAACATGCTCTATTGCAGCTA				0,0	PBT Panel - Presumed Neutral, Sprowles et al. 2006
Omy_rbm4b-203	-	T	CTGAAATTTGATGAATGGAAGCTGCA				0,0	PBT Panel - Presumed Neutral, Narum et al. 2010
Omy_srp09-37	C	T	TAGTTGTATTAACTCTTCTTGAGTCTAGA	TCATTCCAGCTCCGTTCTCTTC			0,0	PBT Panel - Presumed Neutral, Narum et al. 2010
Omy_stat3-273	G	-	CAGACCTCTCTATCTCCCTATGAG	ACCTCCTTTAAATTGTGCCAAGAA			0,0	PBT Panel - Presumed Neutral, WSU - J. DeKoning unpubl.

Omy_u09-53.469	T	C	ACAGCCTGAGCGTTTGCA	GGAAACTGGGAGAGATCAAAGGA	TTGCAGCCCTTATTGT	TTGCAGCCCTTGTGTG	0,0	PBT Panel - Presumed Neutral, Limborg et al. 2012
Omy_u09-54-311	C	T	GTGGCTCCCCAGGAACAAG	AAGTTTCATGTCACATTCCAGTTACCT	G TGGTAATTATTCAACAGATCAGT	TG	0,0	PBT Panel - Presumed Neutral, Young Unpubl.
Omy_U11_2b-154	T	C	GGGAAGCAGAAAACTGGAAGTT	CCCTCTGTGGGCTTGATATTCA	AATGATACTTTTCAGATTGTAAC	AAATCAGT	0,0	PBT Panel - Presumed Neutral, Young Unpubl.
Omy_vatf-406 OMY1011SNP	T	C	TTGCTTCATTTTGTCTATAACCTTGGG	TGCATGCTCTGACAAATGTTACACT	ATGACTATCCACA	TGTAAC	0,0	PBT Panel - Presumed Neutral, Narum et al. 2010
	C	A	AGGCTGGTTTGGGATTCACTG	CGCCAAACACTAACTCTCTGTCT	CTTTACCTCGAAGAC	ATGACTGTCCACA	0,0	PBT Panel - Presumed Neutral, Hansen et al. 2011
OMS00041	G	C	GATTCTGTTCCATCCTCTTTCTGTCA	AAACATAAAAAAGGGCATGAAGGTGTC	AATCCACTCTATGCCTGCCCT	CAAT	0,0	Existing WDFW Panel, Sánchez et al. 2009
OMS00103	A	T	GAGATCACTGTAGGATTGGCTGTTT	CCTCAGAGCAGCTCACAATGGCATC	CTCCACAGTAATTTTTTTT	CT	0,0	Existing WDFW Panel, Sánchez et al. 2009
OMS00116	T	A	GCCTTTCTCCCATATCACATTCTGA	AAACGCATCTTACACTGTGTTGTG	TTTTCTTTACATTTTCAAT	TTT	0,0	Existing WDFW Panel, Sánchez et al. 2009
OMS00127	T	G	CACCTTTCTCTCTCTCTCCATCTCA	AGTGTGCTACACAACCTTAAAAAATATATATCTATT	ATTCTGCACACACCCCAAAATGTA	TTCTG	0,0	Existing WDFW Panel, Sánchez et al. 2009
OMS00128	T	G	ATGAAAGAACTCCAGACACGTATTTT	ACATTTTAACACAGTAACACTAATACACCA	ACTCTCAGAATTAAT	A	0,0	Existing WDFW Panel, Sánchez et al. 2009
OMS00134	A	G	GAAACTGAAATGATCCCATCGTGTT	GCTAGCATAACAGCATTGCCATAT	TATGTCTATAGCTGCAGTATATTA	TTATG	0,0	Existing WDFW Panel, Sánchez et al. 2009
OMS00153	T	G	ACTTTCACCATAGGCTTGACAT	TGATAAGGATGATCAAAAAGCTGAGTATGTA	ACAAAATGTAATTTTCC	A	0,0	Existing WDFW Panel, Sánchez et al. 2009
OMS00156	A	T	GAGCAGAACACATAGAGGAAAGACT	GTAATCACCCCTCTTAGCCTGTATGG	TGTGTGTCCTGCTGTACA	CA	0,0	Existing WDFW Panel, Sánchez et al. 2009
OMS00164	T	G	CAGAGGAGAGGAGAGCAAAATACTTGAGAATCGGAGCTAATCTTAGTTATTGTG	ACAACCTACTCATTGAAACTCATTGGA	CCAGATTCAATTAAATTTA	CAGATTCAATTCAATTTA	0,0	Existing WDFW Panel, Sánchez et al. 2009
Omy_1004	A	T	A	CACCTTTATTGAGCTACATGGCAAATCTG	CATGTGATGTTTTTTTGC	ATGTGATGATTTTTTG	0,0	Existing WDFW Panel, Hansen et al. 2011
Omy_101554-306	T	C	GCCTGTATTTCTCCTGTATGTGCAT	TCAACTTTTGCAAACCTTTTTTATTCTTTGTCAATT	TGCTTCTCACATTTTTA	TGCTTCTCACGTTTTTA	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_102867-443	T	G	A	CCCTAGTTCTGTAACACAAGACGTAA	TTTGGGTACATAATTTT	T	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_104569-114	A	C	CCGAGGCCGACGTGATC	GCGCCTCGCTCATCATCA	CGCCACTCCGACGCC	CCACGCCGACGCC	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_107336-170	C	G	GCCCTCTCACTCATGACATCAAC	GCTCCAGCCACTCGCA	CACTCCTGGGTGCAGAA	ACTCCTGCGTGCAGAA	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_109525-403	A	G	CCTCATTCTCATTGGTGAGTTGTCT	TGTAAGATCTGACCACATGAGTATAACCA	CCTACACCTCTTTTTTCCACA	CCTACACCTCTTTTCTCCACA	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_110362-585	G	A	GCAGCCAAGATGAACGAAAACTTC	CCGGCCTGGGTCTCAATG	CACCGCCTGCCCGT	CACCGCCTTGCCCGT	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_110689-148	A	C	GTGTGTGGCAGAGAACTAAGTAT	GGTTAAGACATTAACATAACACTGGACTCT	CAAATGAACACATTTATATC	ATGAACACATGATTTATC	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_111084-526	A	C	CACCACACCAAGCAACTATTTTCATT	ACCCAACTACTGTCCATTTTTTCAT	CCAGTGAAATTTATTTT	CAGTGAAATGTATTTT	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_111666-301	T	A	GGGTGAAAAGAGTGGGACATTTTACA	GTCAATTTCAAGGCACCAGACAAT	TTAGTATAACACAGTAA	AGTATAACACAGTT	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_112301-202	T	G	GTAACCCCTGCCACATAATTAGGT	CTGAGACACTGCTCCAAGGT	GACAAT	AGACAAT	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_112820-82	G	A	TTT	AAATGAACTCACGTTGACCTCTGA	AATGCGAAGACAAAAC	AATGCGAAGCCAAA	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_114976-223	T	G	GACAAACAGCACTTCATTGCAGTAA	GTTGCTCCAGCACCAGGT	CGCCGCCAAGTTA	CGCCGCTAAGTTA	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_116938-264	A	G	GTTTCATTTCATGTTGAAGTGCACAT	CTCTGCATGCTCCCATCCT	ACCGATGGAACAATC	CCGATGGCACAATC	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_117286-374	A	T	TGATGTGTGTTCCCTCATGGCTTA	CTGTGCATTTATTCTGTGATGCTAGG	CCTTGCTCAATTTTTCTCT	CTTGCTCAATTTTCT	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_117370-400	A	G	TGCAAAACACAGAGGAAAGGGATTT	GGCTTATTTGTTCCGTACTTGCATT	CTTTCCTCATCATACT	TCCTCATCATACT	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_117540-259	T	G	GGCAGGTTAACACAGTCATCTACTATAAA	CAGCATGTTGCTTTAATCCTTCACA	CTATGGCAACTCCAATGAATTAA	AACTCCAACGAATTAA	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_117815-81	C	T	CTGCTTTATGCACACCACATTGT	GCTCTTTCTGGAGAACAAGGTACTG	TGTCACCTCAAGTTTG	TG	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_118175-396	T	A	AGGCTTCACACACACATGCA	GACGCGCAACCTCTAGATTATACTT	CTATACGGAGACCAGC	CTATACGGAAACCA	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_118205-116	A	G	CTGCGGTGGGCTACACA	CGCAGCTCGCGATGAG	CTCTTGACAGACATAC	CTCTTGACAGATTTC	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_118654-91	A	G	CAGCGTAGACCGTTTCCTCATTAT	GCGCCGATGAGCAGCTT	CCGTA	CCGTA	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_120255-332	A	T	GCTAGCTAACATTGAAGGGTGAAT	GGCTACAGGGACTTTACAATGGG	CTACTGAGGCTGAGTGCT	TACTGAGGCCGAGTGCT	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_128693-455	T	C	GCCTGCAGGAGAAGGTAGAGTTA	GAAATGGAATGGACCCCAATCCT	TCAGCTTGCTTGCCCGC	CAGCTTGCTCTGCCGC	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_131460-646	C	T	GTGAAAAGGAATGGAGGAGTACAGT	TGCTAGGACAGGAAGATCATTGTG	ACTATGCCATGAAGTTA	ACTATGCCAAGAAGTTA	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_187760-385	A	T	CGGCTATTCTCGCGTAAAAGCT	AAATGCAACCAGAAACGGAATGTC	CACTCAACTGATACC	CTCAGCTGATACCC	0,1,8	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_96222-125	T	C	GTAAGGAACTAATTGGCGCAACATT	CAGTTTGTCTAACACCCAGGCATAT	C	AAAGCAGAAATTTACTG	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_98683-165	A	C	GCCATTGCCAGAGAATTTGGTTAA	AACACACGCACCATCTTAAAGC	TCCTTATCCAAAATA	CTTATCCAAAATAAT	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_BAMBI 4.238	T	C	CATGATGAGGAGGACCAAGATGAG	AGGTGTGGTTCAAGGGCAG	TTGTGC	TGTGC	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_cyp17-153	C	T	GCCCTCCAAGTTCCAAGTGAAAA	CAGGTCATTGATGAAACGTCAGAAC	AACTACAACGTAGCTAATT	CAACTGTGGCTAATT	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_ftzfl-217	A	T	ACAGGGATGGGCAACTTTGTT	GGATGACCACGTGACACT	AGCCAGATACATATT	CCAGATACAGATTTG	0,0	Existing WDFW Panel, Abadía-Cardoso et al. 2011
Omy_G3PD_2.246	C	T	TCATGTATCAATTAAGGCATTGTCTTGCTTGCATTTGATGGAAACAAACATATTATAAATGTGT	GTTAGACACAGTGACCACCTCTTCAAAAACAAGGACAATTCTAAGTGACCTC	CACCGCAATCACCG	ACCGGATCACCG	0,0	Existing WDFW Panel, Existing WDFW Panel - S. Young unpubl.
Omy_GH1P1_2	C	T	GCATGGAACCAAGTTCTCTACAAAAG	TTCTCCATGCGTGATGCA	ATACCTGAGTGTCA	ATACCTGAGTATCAT	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
Omy_gsd-291	T	C	GATGGAACCAAGTTCTCTACAAAAG	TTCTCCATGCGTGATGCA	TCATGACGAGTTCTG	TGACGAGTTGAGATT	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
Omy_hsp90B A-193	C	T	GGAATCGATGACGACGAAGTGATC	TTCCTCCATGCGTGATGCA	ATTT	T	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
Omy_MYC_2	T	C	CGGTTGCAGAACTCTCATGTTTG	CACGCCATGTCTTAACTTGCAATTA	AGTAAAGCCCATTGT	AGTAAAGCCCATTAT	0,0	Existing WDFW Panel, Existing WDFW Panel - S. Young unpubl.
Omy_u09-61.043	A	T	TAGTCACATCCATAGTAATACTTCC	TGTTTCAGAAAGCAGAAAAACCAATCTCT	TGAGT	TGAGT	0,0	Existing WDFW Panel, Existing WDFW Panel - S. Young unpubl.
Omy_UBA3b	A	T	GCCACTCAATGCATGTGTTTTCTAG	CAGCTAGCTTAAAGTGGGATGCAA	AAACTGTTGAACGGT	AAACTGTTGAACAG	0,0	Existing WDFW Panel, Aguilar and Garza 2008
Omy_RAD17	C	T	AAGCTCCTGCAGGTCATCTC	TCTGTGAACTGTCTTCTGCAAGT	CATGTCAGACCTTTG	TAGT	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
Omy_RAD23	T	C	AATAGGAACCAAGCCCCAGC	CAGAGCCTGAACCCATGGAG	CA	CA	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
Omy_RAD26	G	A	TGTGGGACAGCACATACTCC	CCAGGACACCAGTGGAGAAG	TCTGGCTCTGTGCGTCT	TCTGGCTCCGTCGGT	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
Omy_RAD29	C	A	AATGGAATTGGCCCCAACCC	TCTCCATTGTGTGTAATCATGGT	ATTAGTAGCATCATC	ATTAGTAACATCATC	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
Omy_RAD36	G	A	CGAGGACGTTCATAGGGAGC	TCGATAAGTCCACCAGCTGG	GAG	GAG	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
Omy_RAD38	C	A	AAGCCACACCGTTCAACTGA	TGGCTTATCGCGCTCTAGTG	ACAATTCAAATGATT	ACAATTAAAATGATT	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
Omy_RAD43	T	C	GTGGAGAGGGATTTTGGGGG	TGACAGGACAAAACACAAGCCA	TA	TA	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
Omy_RAD45	A	G	TGGTGCTTCAGTGCTGTCAA	AGAGTGAAAACTGTGTGCGG	TGCAGGGACACCACC	TGCAGGAACACCAC	1,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
Omy_RAD47	A	G	TCAAAACCTGCAGGACTTGGA	TGGTTATATCTACAGTACAGTTTCGT	CT	CCT	0,5,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
Omy_RAD47	C	T	GTCGTCTGGAGGAGCTGAAG	GGGTGACGTTTTCTCTCAGC	CGC	CGC	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
Omy_RAD48	A	G	GCTGAGCCACCTACACACAG	GTCTAACACTCGCAGCAGGT	AAATGTGTATTTGTGT	AAATGTGCATTTGTG	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
					A	CAAGACCCGCACAC	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
					AG	TGCAAGACTTAAAA	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
					GA	GGCGAGCTTGGCCCA	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
					AA	AAA	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
					CATCCTAGAATAGAA	CATCCTGGAATAGAA	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.
					GT	AGT	0,0	Existing WDFW Panel, WSU - J. DeKoning unpubl.

Omy_RAD52 458-17	C	A	ACGTGTCCCTGAGGATGGTA	AGCTCTAGGTCTGGGCTCTG	ATGGCCCC[CT]AAGA ACCC	ATGGCCCA[CT]AAG AACCC	0,0	greb1L SNP from Hess et al 2016, ProcB
Omy_RAD52 812-28	C	G	AGGAGTCCTGTCCCATGTCA	GCTTAAGGCTGTGGTATGTGG	CAACCTC[TC]ATTCCA CAT	CAACCTG[TC]ATTCC ACAT	0,0	Omy269
Omy_RAD58 213-70	A	T	CCTGATGGGTGCTCTTCTCTC	AAACAGCATCATTATCCATAGTGTT	TTTTTT[TA]AAAATAT ACT	TTTTTT[AT]TAAATA TACT	0,0	Omy269
Omy_RAD58 835-15	G	T	GTCTGCTAAGGTCTGCAGG	GCCGACCATGAGAGACCTG	ATAGCTGCTGGGACC CA	ATAGCTTCTGGGACC CA	0,0	Omy269
Omy_RAD62 596-38	A	T	GCAGGACACTGGTTCCCAAA	CCTGAGATTGGAGATCACTGGCT	TAAAAAATATATAT TA	TAAAAATATATATAT TA	0,5,0	Omy269
Omy_RAD66 834-17	C	T	CTCCTGCAGGTCATCTCTGG	CTGTCTTGTGCTCAATGCCTG	TCTGGCTGACACCTTT A	TCTGGTTGACACCTT TA	0,0	Omy269. Added by Jon Hess as run timing selection in the Klickitat
Omy_RAD69 583-33	C	T	GACTCTAGACTGCTCCCTGC	GGCCTCAGTCTCCTTCCAGA	CCGGAGACATT[CT]C GCGT	CCGGAGATATT[CT]C GCGT	0,1	Omy269
Omy_RAD72 10-8	C	A	ACACCACACTCCACAAAGCA	GCGCCTTGGTCTCCTTCATA	TGCAGGACTTGCTTT GT	TGCAGGAATTGCTTT GT	0,0	Omy269
Omy_RAD74 691-49	A	G	CATCTCAGATCAGCCACCCG	AGCACAAATTCTTCTGTTGTGCA	ACTGTGGATTGCAC AA	ACTGTGGGTTGCAC AA	0,3	Omy269
Omy_RAD77 789-54	T	C	AGACAAAACCTGCAGGGGAC	AGCACGTTAAAACCAAAGTGTCA	TAAATTATATTGAC AG	TAAATTACATTGAC AG	0,0	Omy269. greb1L SNP from Hess et al 2016, ProcB
Omy_RAD88 122-32	G	A	TCAGTGGATGGAGTGTCCCT	GGTCTTTGGCCTTGTGTCTG	GCTGTGGAGATCAT[C T]CG	GCTGTGGAATCAT[C T]CG	0,0	Omy269
Omy_RAD16 104-20	A	G	ATTCCAAAACCTGCAGGGGT	TCAGGATTTGGTAAGGTGGCC	AGGGCAAAG[AT]CAA AGG	AGGGCAAAG[AT]CA AAGG	0,0	Omy269. Added by Jon Hess as run timing selection in the Klickitat
Omy_RAD35 417-9	G	A	GCACTTGACCACATAGCTGG	ACTCCACACTCCACAAAGCA	TGCAGGACGTGCTTT GT	TGCAGGACATGCTTT GT	0,0	Omy269. Added by Jon Hess as run timing selection in the Klickitat
Omy_RAD42 793-59	T	C	CACGGCTAGTGGCATGTACC	CCACACCTGCATCAGTCTGT	CAGAGAATGCCAAC GA	CAGAGAACGCCAAC AGA	0,0	Omy269. Added by Jon Hess as run timing selection in the Klickitat
Omy_RAD47 955-51	G	T	AGTGTGCTAGAATGGGCCTG	ACCATGGGCAGTTCATTTC	TTGGAATAGAATCTA TA	TTGGAATATAATCTA TA	0,0	Omy269. Added by Jon Hess as run timing selection in the Klickitat
Omy_RAD66 218-58	T	C	CTGTGCAGGGAGACAGCTAG	GTGGTATCGTAGCATCGGGG	CTTGGAGTGTGTTGG TA	CTTGGAGCGTGTGG TA	0,0	Omy269
Omy_RAD73 204-63	G	C	CCTGGGCAATGACCTCCAC	AGTCCCTTCTCTCTCCCTC	GTGCCCCTCTCCAC CG	GTGCCCCCTCTCCAC CG	0,0	Omy269. Added by Jon Hess as run timing selection in the Klickitat
Omy_RAD76 882-63	A	T	GGTGGGGGCAAACCTCAGTA	TGTCTCAGCTTAGAATGACAGATT	CAAATGAAACTATG TA	CAAATGAAATCTAT GTA	0,0	Omy269. Added by Jon Hess as run timing selection in the Klickitat
Omy_RAD88 028-7	G	A	TAGCCCAAGTTCGGTTCCAAC	AGTGTCTTTGGTGCGTCCCTC	TGCAGGGGCTGG	TGCAGGAGCTGG	0,0	Omy269. Added by Jon Hess as run timing selection in the Klickitat
Omy_GREB1 _03	T	C	CACCAGCCTCCAAGAG	AAATTGCTGCCCCCTATCCC	TTTGGGATAGG	TTCCGGATAGG	0,0	Top GREB1 marker, FST = 0.93; null allele problem-drop
Omy_GREB1 _05	T	G	TGGGCAGATATGGAAGAACGG	ACCTTCTAAATGGCCTCTGTGT	CGGTGGCTCTC	CGGTGGCTCGC	0,0	Top GREB1 marker, FST = 1
Omy_GREB1 _06	G	T	GCATAGAGCCAGTGCAAAACA	TCATCAAATGGTACCCGGA	CAAGGTAAA	CAAGTTAAA	2,75,0	Top GREB1 marker, FST = 0.93; null allele problem-drop
Omy_GREB1 _07	T	C	AGGGCCTTCTCTGACACTA	GTACATCACTGGGGGCGAAC	CTGGTATAG	CCGGTATAG	0,0	Top GREB1 marker, FST = 1; null allele problem-drop
Omy_GREB1 _09	T	G	CCAGTGGCAACCTCAGGTAG	GACTCCAGTCACCCAAGTCA	TCAATGGAGA	TCAAGGGAGA	0,0	Top GREB1 marker, FST = 0.95
Omy_GREB1 _10	T	G	GTTCTTAGTGTAAGAGAGACTGAGA	TCTCAGAAAGAAAATATGCCACA	AAGATACAATGT	AAGAGACAATGT	0,0	Top GREB1 marker, FST = 0.93; null allele problem-drop
Omy_RAD11 6-59	T	C	GGAAGAAGTGAGAGCCCTGG	CTGTAGTCCACGATCCGCTC	CCACAATGTCAAC	CCACAACGTCAAC	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD19 19-22	A	G	CAGGTACAGACACACAGGG	CTACACCACCCACGTTCTG	CAGGGAGGAGG	CAGGGGGGAGG	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD22 77-7	G	T	CATCTGTCCAAACCTGCAGG	ACTGACATGTTGTCCACCCA	TGCAGGTGCTGGCT	TGCAGGTTCTGGCT	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD36 51-48	G	T	GAGTACAGTGCAGTGTGGGG	CCTTCCTCTTGCCACCATCA	GTTGGGAGAACTTT	GTTGGGATAACTTT	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD39 26-22	T	C	CGTTCCTGCAGGCTTTTCAC	TTGGCACAGAGAGTACGCAG	TTCACTTTCCCTG	TTCACTTCTCCCTG	0,0	Basin-wide, precipitation-related; Micheletti et al 2018 Mol Ecol
Omy_RAD48 48-14	G	T	TGTCCCTTCTGCACGATG	AGTTGGTAGTCACTCTCTGT	GAGACAAGGACAGA	GAGACAATGACAGA	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD53 74-56	A	C	GCTGTTACCGTGTGATGTTGA	AGAGTTCTGGCCTCTCCCTC	AGAGGGAAAGAGAG	AGAGGGACAGAGAG	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD90 04-13	G	A	TATACCACGCCTTCCCTGGA	CAGAGAGAAATCCCCACCC	TCATCTGAAGGGGG	TCATCTAAAGGGGG	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD10 733-10	A	G	TATAGACCCCTGCCAGTCA	ACAGAGAAACCCCGTCATT	AGGGTGAAGAACTG	AGGGTGAGGAACTG	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD10 945-51	T	A	GCAGGCGTTCCATTTGGATG	AGATCGACGAAATCGGTGCA	AATGCGCTTTAACG	AATGCGCATTAAACG	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD12 566-14	C	T	GTGGACATTCTGCAGGGAT	TCCCAAAATATTTCATACGCACA	ATGTAAACAAATTG	ATGTAAATAAATTG	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD13 499-13	T	C	GTTCACTGACGACCAAGGT	GCTGGGGGAGCTTTACATGA	CGCCCTGTCCGCCA	CGCCCTGCCCGCCA	0,0	Basin-wide, precipitation-related; Micheletti et al 2018 Mol Ecol
Omy_RAD14 033-46	A	G	GCAGGAGATTATTGCCCCC	ACCCTTGTGATCACATACTGTCT	ATAGAGGAATAGAC	ATAGAGGGATAGAC	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD19 578-59	A	G	GGTTGGACACCTCCTGGTTA	TCAACCAAGCAACAGATTATAGCT	GGTTAAGAGTATTC	GGTTAAGGGTATTC	0,1,25	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD22 123-69	T	C	TGGGAAAGCATAGGAGGGGA	TGTGTGCCTGTCTTATAGCCC	CCAAAGATGTCAGA	CCAAAGACGTCAGA	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD26 691-36	A	G	TGCAGGAAACCGTCAATCTACA	CAGGAATTAATGTATGGCCGGA	TCTCTAACAGAAC	TCTCTAGCAGAAC	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD27 740-55	A	T	TCGGCCTGTACTAGTCTCACT	GCCTAAAAATGGCCACTTTCATCA	TAACTTTAAAAAAA	TAACTTTAAAAAAA	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD29 559-69	G	T	TGGGCATCAGAGGCATCAAG	TCAATTGTACTCACTGCTCCGT	CTGGCTTGTATATC	CTGGCTTTTATATC	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD30 230-25	C	T	ATGCTTTCCTGCAGGTTGT	CCTGTAAGTGTAAGGGATCTGGG	ACGTGTGCTGTAGC	ACGTGTGTTGTAGC	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD30 392-17	T	C	CCACTACTCACAGACCTGCA	GCTCAAGGACCAACAAAAAGCT	CTGAGACTGTGTGT	CTGAGACCGTGTGT	0,0	Basin-wide, temperature-related; Micheletti et al 2018 Mol Ecol
Omy_RAD31 079-58	G	T	CGCGCAAAGTGCAGTGATAG	CGCCATGTATTTTCGGACCC	CGATCAGGGCCCTA	CGATCAGTGCCTA	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD31 408-67	T	C	CAACCCTGCAGGCTACAGAA	TGGAGTGCCAACAAAAGAAGC	ACAGAATGCAGAAA	ACAGAACGCAGAAA	0,0	Basin-wide, top-outlier; Stacks Locus ID is 31408_14
Omy_RAD33 798-24	T	C	CAGGAGGGTCAAGTGAGTC	TTGGGCCCTCTCTTTTGGG	GAGTCTATCAAGAT	GAGTCTACCAAGAT	1,5,0	Basin-wide, temperature-related; Micheletti et al 2018 Mol Ecol
Omy_RAD35 005-13	C	T	TGGTCAAAGTTGAGGGTGGT	CAGGGCCCTGATTAACCACT	CCAACTCCCGACGG	CCAACTCTCGACGG	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD36 952-53	C	A	TGTACGTCATTGGGGCTGAG	CCTACCAGACCACACGATGA	AGGACATCTTCATC	AGGACATATTCATC	0,0	Basin-wide, temperature-related; Micheletti et al 2018 Mol Ecol
Omy_RAD37 492-53	G	T	AGTTAGACCGGAGCCGTCT	ACTGACAGTAGATTTACCATGCCT	GTGGCTTGTTAGGT	GTGGCTTTTLAGGT	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD39 156-33	T	C	GGGTGTGACATGTGTGCAGA	ACTGCTTGTCCCCACCAAG	ACCGTAATGGAGAG	ACCGTAACGGAGAG	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD40 132-55	A	C	TGCAGGGCCTGTATATTGCT	TCAAAGGACTGGGGAGAGGA	TCTGTGCAGTCCCTC	TCTGTGCCGTCCCTC	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD40 520-48	T	G	TGTTCATCTGATCAGCTGTCAG	ACACGTGCGTCTTCTTCTCC	GTCAGATTGCGCTG	GTCAGATGGCGCTG	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD42 465-32	G	T	GTGGATCTTGACTCCAGGC	TAGACATCGCCCTCACAGA	CCAGGCTGGAAGAA	CCAGGCTTGAAGAA	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD45 246-10	G	A	GCCACAAACATTGCAGCCT	TGCAGACAGGCCATGCATAG	AGGTAGAGAATATC	AGGTAGAAAATATC	0,2	Basin-wide, migration-related; Micheletti et al 2018 Mol Ecol
Omy_RAD46 452-51	A	G	TGCAGGTAAGACTTGATCTGGA	TGACTCCAACCTAAGTGCATGT	TGAAGTCAGAAAGTT	TGAAGTCGGAAGTT	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD49 637-74	C	G	TGGGGAACGGTCATTGGATC	ACTCCGGTTGTTGCTAGCTT	CGGCTGGCTCCGGC	CGGCTGGGTCCGGC	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD54 441-29	T	G	TGTCTGAGGAGGAGAGGCG	GCCAGATCCAGCCAATCAGA	AGGCGGGTGCTGAG	AGGCGGGGGCTGAG	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD55 404-54	C	T	GCAGGGTGCTCACTACAGAC	AGGAGTCCTGAGAGTTGGGC	ATTGTTTCTGAAGG	ATTGTTTTTGAAGG	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD55 997-10	A	C	CATTTTCTACCTGCAGGCTGC	AGCCTACATACATAAAGCCAACA	AGGCTGCAATGTTT	AGGCTGCCATGTTT	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD59 758-41	T	C	GGCCCCCTTCTTTCAGGAAT	CACACACTCAACGGGTCAGT	TGATTGCTACTGAC	TGATTGCCACTGAC	0,0	Basin-wide, precipitation-related; Micheletti et al 2018 Mol Ecol

Omy_RAD60 135-12	C	G	AGCATACACACCTGCAGGAA	TGGTAGGAGGAGATGCTCTGT	GAACATACCGGAAC	GAACATAGCGGAAC	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD65 808-68	T	G	TCCTTCACTCTCGATCGGGA	TCAAACCTGGGCCACTACTGT	ATCGGGATTCACTT	ATCGGGAGTCACTT	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD66 402-36	T	C	GGTGTGATACCTCAGAGCTCTG	CGTCTCCGGATCGTTCAGAG	AACCACTTCTCTG	AACCACCTCTCTG	0,1.5	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD68 634-40	A	C	TGCAGGACTCCTTTGAAACGT	TAACGCCAGCTGCATGATGA	CCTCTAAACTGAAT	CCTCTAACCTGAAT	0,0	Basin-wide, temperature-related; Micheletti et al 2018 Mol Ecol
Omy_RAD72 528-44	A	T	TGATGATCCGGACCCTCTCT	CCCGGATTCCCTCCACAGTT	TTGGAACAACTGT	TTGGAACTAACTGT	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD76 570-62	T	G	GCAGGTAGGTAGGAAGGAAAGC	TCTGACTGGTATTGAAAGGACCA	AGAGGTGTTCTGGT	AGAGGTGGTCTGGT	0,0	Basin-wide, precipitation-related; Micheletti et al 2018 Mol Ecol
Omy_RAD78 147-27	C	T	GCATTTTAGCCCTCCCAAAGTC	CCTTCTTCCAGTTGTTAAAACCCA	CAAAGTCCCAGAGA	CAAAGTCTCAGAGA	0,2.75	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD78 502-57	T	G	GAGAGGCATCCTGTCTAGGG	ACCATGCTCTTTCTGTAGGTGT	GGAAATATCACACA	GGAAATAGCACACA	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD78 776-10	T	C	CACAGCTTCTGCAGGGTAA	GCTTGCATGGTCTCGCTAGT	GGGTAATCCTGGCT	GGGTAACCCTGGCT	0,0	Basin-wide, temperature-related; Micheletti et al 2018 Mol Ecol
Omy_RAD85 131-35	T	C	TTCAATAACTACAGGCAGATGGT	AGTTCCCAAAATGCACTGTACA	GATGGTATGGTGAG	GATGGTACGGTGAG	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD92 485-64	T	A	CCAGTCAGTCTTGCCCTCAGG	GGTCACCACAGGATTGGAGG	GTGTAGATATACAT	GTGTAGAAATACAT	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD98 715-53	T	G	CGTAACGGGGAGCTGATCTG	GCTGGTAAATGCTGAGGGG	CAGGACTTCTCCCC	CAGGACTGCTCCCC	0,1.75	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD10 3359-45	C	T	GGAGAAGGATGTGCTCCCTG	ATTTGGAGGTGGAGGGTCCA	CCTGTAACGCACAG	CCTGTAATGCACAG	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD36 6-7	C	A	ACCAAATTAGAGCCTGCAGGA	GGAGAGGCCTTTC CGTGATC	CAGGACTTGCTTTT	CAGGAATTGCTTTT	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD61 9-59	T	C	CATGGAGAAACAGACCCGCT	TGCTGTGTGTATCTGGGG	TGCTGGATCCCCCA	TGCTGGACCCCCCA	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD73 9-59	C	G	ACGAGGCTTGTAATGCAGT	TGCCTTTATACCAATGTCTGCTG	GAGTTGGCTATTTT	GAGTTGGGTATTTT	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD11 86-59	A	G	CACAGCCTGGATGTGGTTCT	ACAAGTTCGGGGAGTTTCCT	CCAGGACATCCAGG	CCAGGACGTCCAGG	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD17 51-18	T	G	TCCATGTTCTGCAGGAGTG	TGAATGGACTGGTGAACCACA	GGAGGTGTACACCT	GGAGGGGTACACCT	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, Immune related
Omy_RAD25 67-8	A	T	CTGTCTGGATAGCCTTGCCC	TCTATCTCTGGGGAAATAGCCC	GCAATGGGCTATTT	GCATTGGGCTATTT	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD29 76-26	G	A	AGGACTGTGATCCTCTCAGCT	AGCTCTGCTGAAACATCAGTCT	CAGCTGGGTTGAGA	CAGCTGGATTGAGA	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD32 09-10	A	G	CGGAGGAGTTTGAGCAGTCT	CTTCTACCACCACCTCGCTG	CGGTATCCCTGGC	CGGTGTCCCTGGC	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD70 16-31	C	A	GCAGGAATATTCACTGTTGCCA	TCTAAATGTCTGTTGGCGGC	ATAATTTCATTTAA	ATAATTTAATTTAA	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD94 08-71	G	T	TGCACATATGGCGGGGAAAT	TGTGTGTGATGAGCTTCCAAC	GCCAGGGGGACAGG	GCCAGGGTGACAGG	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, stream order - related
Omy_RAD12 439-64	G	A	GGAACTTTTCACATCATGTTGACTG	GCACAGAGAACTCCAGGCAA	CTTCTCCGATGTCA	CTTCTCCAATGTCA	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD13 073-16	G	A	GTGAGGGATCACACCTGCAG	GCACCCATTCTGTAATGTCCC	AAAGGGGACATTACG	AAAAGGGACATTAC G	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD14 269-30	C	T	TGCAGGTTCACTTCTCTACAACAGT	CTGGATTAGGACCTGAGCCG	TAGAGTACGACCCT	TAGAGTATGACCCT	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD14 541-72	A	T	ACGCAACGTGACGGTCTTAT	ACAGCCGATGACATGAGACA	CTTATAGAGTTTTA	CTTATAGTGTTTTA	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD15 709-53	G	A	TGCAGGACTTGGATAACACAGA	TGGTTATATCTACGTACAGTTCTG	ATGCAAGGCTTAAA	ATGCAAGACTTAAA	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, run-time - related
Omy_RAD17 849-16	G	C	GACTCCACAGCCTACATGGG	CCGTTAATGCCAGGGGAGTC	AGACGGACTCCCC	AGACCGACTCCCC	1.25,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD19 340-24	A	G	GCAGGGAGCAGCATATACATG	TGGGGTGATTTGAGTGACAC	CATGGAATACATA	CATGGAGATACATA	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD20 917-11	T	C	CGTTGTCGTCTCCAATCAGGA	ACCAGCTCGATGCCATTGC	AGGTTGCGAGGTC	AGGTCGCGAGGTC	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD23 354-66	A	C	CTGCTAGTCAAGTCCACCGG	CCTCCAGTAGTAAGGGCTGC	AGCCTGAATGAGGT	AGCCTGACTGAGGT	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD24 287-74	A	G	ATTGTCTGTCTGCCGAGGTG	TGGCGACCTGTCACTAATGC	GGTCACTACCTCCC	GGTCACTGCCTCCC	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD24 343-29	A	G	TGCAGGCAAGATTGGTAGACT	AGGAATGTGAGTCTTATTCAGTACA	TAGAAATACAAGCA	TAGAAATGCAAGCA	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, temperature-related
Omy_RAD25 042-68	G	T	GCTGCTGAAACTGGTTTGCA	TCATGCAGATGAGCTTCCCTG	AATTTCTGCCAAA	AATTTCTTCCCAA	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD25 266-23	G	T	TTTGAGAGTGGTGCCTGCAG	GGGGACAGCACATGGAGAC	GCAGGGGTAGATACC	GCAGGTGTAGATAC C	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD25 907-57	T	C	TCGTAATCGCTCCTCCTTCA	CGTCTCCGTAATCTAGCATGTGT	TCCTTCATGCCAGC	TCCTTCACGCCAGC	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD28 236-38	T	C	GGCACACATCTGTCCCGTAG	GCACTAAGGTCTAGGAGCACG	ATCTGTCTTCGTGC	ATCTGTCCTCGTGC	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, migration-related
Omy_RAD29 352-6	A	G	TGTGAGAAAGCGCCTCAAGA	GCCTTACAGTGGTGTGTCTGA	GAGAGTAAATA	GGGAGTAAATA	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD30 243-74	C	G	TCTTCTTTCTCCTGCCCCAG	ACACTGCCTTTAGCCATCGG	GGACCGGCCCTCTA	GGACCGGGCCTCTA	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD32 139-58	G	A	GCAGGAAACAGGTACAAAGGA	TGGCTTCTTCCTTGCTGAGC	TCGACATGACCTGA	TCGACATAACCTGA	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD33 122-47	G	C	CAGGCTTTGTGGACATGTGC	GTGCTCTATCTTGCTCTTGGC	CCACAGGGTGGTGC	CCACAGGCTGGTGC	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD35 149-9	G	A	GAGTCAATAGAGCCCCCTGC	TGGTTAGCAGGAGCAATCTCA	GCGCGTTATGTC	GCGCACTTATGTC	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD37 816-68	A	T	CTCATTCCTGGCCGTCTG	CCACTCACACTGGCTTATGC	GCGGCGTAAAAATG	GCGGCGTTAAAAATG	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD38 406-19	T	A	CTGCAGGGGTATTAGGAGGC	AATGAGTTGTGGCGGTGAGT	AGGCTTTATATGGCC	AGGCATTATATGGCC	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, temperature-related
Omy_RAD40 641-58	T	C	GGCAAACCTGGCTTGTGAGTG	AAGGCTCTGCTTCTGCTTGA	AGTGATATCAAGTG	AGTGATACCAAGTG	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD41 594-34	A	G	TGCAGGGTTAATAATGTGTCTTTGT	AAATCTCGGGCTGAGGAACG	CAGAGATACGTTCC	CAGAGATGCGTTCC	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, temperature-related
Omy_RAD43 573-37	A	G	TGCAGGGAACGATGAAACCA	ACAGACACAGCATTGGCCAA	GAAAGAGAGAGTTT	GAAAGAGGGAGTTT	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD43 694-41	A	C	CCCCTCTCCCTGGCTAGAAT	TCAGGGGGTGTGCTTTTCC	AGGGAAGAGCGGAG	AGGGAAGCGCGGAG	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD46 672-27	C	G	TGCAGGAGGTCTTTTCCCTTGT	AACACATTCTTATTGCAATGATGG	GTGGTAGCCCATCA	GTGGTAGGCCATCA	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD49 111-35	T	C	GCAGGCTTAGCATTGCTGAC	GGAACCTGGGTGGGAGAATG	TTTCTTATATTGA	TTTCTTACATTGA	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD49 827-67	A	G	CCTGTGGTCCAACCTCAGAGAC	ATGGTTGTGGCGGAATCTC	TGTCTTCAGATGCC	TGTCTTCGGATGCC	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD50 632-21	C	T	CCTGCAGGCTGGGTCAATTAT	GAGCCAGCTGTACCTTCTCC	TCAGCACCTCCAGCC	TCAGTACCTCCAGCC	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD57 916-29	A	C	GCAGGGCCTTAGAAACAGACT	TACACGCCTCACTGTTCTGC	CAGGGGCAAAACGG	CAGGGGCCAAACGG	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD59 950-44	G	A	GGAGCTCATATCGCCGATGG	GAACTCTGTCAACCCTGCCC	GGAGGGGAAGGG	GAAGGGGAAGGG	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD65 959-69	G	A	ACATTTTGGTGTTAACAACCTGT	GCTAGCGAAGACCTGAAGG	TTTTGTGTTCTCTT	TTTTGTCA TTCCTT	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD73 963-73	T	A	CCCTCTCAGGAAAGTGACCAC	GGATCATGTCAATCTGATGAGTTGG	TTTCTTTTGGA	TTTCTATTGGA	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD76 060-20	C	T	TGCAGGGTGTGAGTATTGGG	TCCCATGCAAATCCAAATGCT	GGGCGCTG TAGGCAA	GGGTGCTGTAGGCA A	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD86 706-72	C	T	TTCCTGTAACTGTACGCC	CCACATCACACCCTGACCTC	TACGTTTCATTCT	TACGTTTTATTCT	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, elevation-related
Omy_RAD93 580-37	T	G	AGGCAGAGGAGGGTTGTTTG	TGCAGAAGTCAAAATCAGGAACA	AGTCACCTGGGATT	AGTCACCGGGGATT	0,0	MGILCS GSI locus (Gen Assess BPA report 2017); Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD23 894-58	A	T	TGCAGAAAGGCTGTGTGGAT	TCTTAACACAGTCTCATGGAACA	GTGGATTAGGGG	GTGGATTG GGGG	0,0	thermal adaptation (Chen et al. 2018, MEC); Basin-wide, top-outlier (Micheletti et al. 2018, MEC)
Omy_RAD18 903-48	A	G	GGGGATGAGTTCTTCGGTGG	CCACCAAATCCCCGAAGAA	AGGAGACACCA	AGGAGGCACCA	0,0	thermal adaptation (Chen et al. 2018, MEC); Basin-wide, top-outlier (Micheletti et al. 2018, MEC)

Omy_RAD79 314-58	C	T	CACACTGACTCATCCCTCGC	GAGTGTCTTACCGAGCTGCC	AGACCTTGTC	AGACTTTGTC	0,0	thermal adaptation (Chen et al. 2018, MEC); Basin-wide, top-outlier (Micheletti et al. 2018, MEC)
Omy_RAD73 84-50	T	C	GACACGCCCTCAGCCAG	CTGGTACCTTCCTGCTGTGG	GCCTCTGGCAG	GCCTCCGGCAG	0,0	thermal adaptation (Chen et al. 2018, MEC); Basin-wide, top-outlier (Micheletti et al. 2018, MEC)
Omy_RAD46 314-35	A	G	ACTGCATCTTTTCCCTGCA	TGAAGATACCCAGAGACACCA	TAGCAATGGT	TAGCGATGGT	0,0	thermal adaptation (Chen et al. 2018, MEC); Basin-wide, top-outlier (Micheletti et al. 2018, MEC)
Omy_RAD13 034-67	A	C	GAGTGATTCCCAGCCCTCC	TCTCTCCGTTGGCCAGAAAC	ATAAATCACAA	CTAAATCACAA	0,0	thermal adaptation (Chen et al. 2018, MEC); Basin-wide, top-outlier (Micheletti et al. 2018, MEC)
Omy_RAD43 117-55	A	G	CGGTCACCAGTTGAACCTGT	CTCATCACCCGCCAGCTTAA	CCTCTAACACATT	CCTCTGACACATT	0,0	Basin-wide, top-outlier; Micheletti et al 2018 Mol Ecol
Omy_RAD30 619-61	T	A	CTGCAGGTCAATGGGTGCTA	ACACTGATCACATTTTGTACACT	CACTGTATAA	CACTGTAAAA	0,0	thermal adaptation (Chen et al. 2018, MEC); Basin-wide, top-outlier (Micheletti et al. 2018, MEC)
Chr28_116079 54	G	A	TGACACTGATCACAATGGTGAAAT	TAAACTGGAAGGAGAGAGCAAAAT	TGTGGGCTGCGAACA	TGTGGGCTGCAAAAC	0,0	greb1L; non-synon (Micheletti et al. 2018, BMC Evol Biol)
Chr28_116252 41	A	G	CAACATTTAGGGAGAGGTTGCTAT	ATCATCAAGTTTGCCTACGACAC	TACTCA	ATACTCA	0,0	greb1L (Micheletti et al. 2018, BMC Evol Biol)
Chr28_116325 91	G	A	GTAGAGGCCAAAGGCTTGAG	TGCTCTTATTACCTTCCAGACTCC	CCTCCTCCCTATGGTT	CCTCCTCCCTGTGGT	0,0	greb1L; non-synon (Micheletti et al. 2018, BMC Evol Biol)
Chr28_116588 53	A	C	CAACATATGACCACTCGAAAACTC	ATTAATCACACCGTGAGACTCCTC	GTCTC	TGCTCTC	0,0	greb1L (Micheletti et al. 2018, BMC Evol Biol)
Chr28_116675 78	T	C	ACAGTAAACCCATTCAGGCATAGT	TTATCCTCTCAATCCACATCAAGA	TGAGAAAGAACACAGA	TGAGAAAAACACAG	0,0	greb1L; non-synon (Micheletti et al. 2018, BMC Evol Biol)
Chr28_116711 16	C	T	AATTTCCCAAAATTTGAAACTCTT	GTGTACATTGTCAGGCAGAAACAT	GG	AGG	0,0	greb1L; non-synon (Micheletti et al. 2018, BMC Evol Biol)
Chr28_116766 22	T	G	CGAATGCACTGTAGCTCATTCTAA	GCAGTAGAATGTCTCGCAAATACA	TGGTACAGACACGCA	TGGTACAGACCCGC	0,0	intergenic region (Micheletti et al. 2018, BMC Evol Biol)
Chr28_116832 04	G	T	CAAGAAAGAAACAGATGTTGTCCA	TTGTGACTCAAATCTGCAACCTAT	CTAGCA	ACTAGCA	0,0	intergenic region (Micheletti et al. 2018, BMC Evol Biol)
Chr28_116978 34	A	G	CATTCAATACAATGTCATCCTCGT	ATTCACAAATGAAAGCATCCAAAC	GTATTGATCCTGTGG	GTATTGATCCCGTGG	0,0	intergenic region (Micheletti et al. 2018, BMC Evol Biol)
Chr28_117022 10	T	G	CGATCCAGAGTATAACAAACATGC	GATCTGTACACAATTCCTGGAAGC	GAGACA	GAGACA	0,0	intergenic region (Micheletti et al. 2018, BMC Evol Biol)
Chr28_117731 94	A	T	AGTTTGACACCCCTGTACTAGAGC	GTCTAACAAGCTCTGGGTGATTTA	CTGGTGAGAACAGGA	CTGGTGAGAAATAGG	0,0	intergenic region (Micheletti et al. 2018, BMC Evol Biol)
OmyY1_2SE XY	X	Y	GCGCATTTGTATGGTGAAAA	GCCTGGCATATGAGTGTTGA	ATTACC	AATTACC	0,0	intergenic region (Micheletti et al. 2018, BMC Evol Biol)
					ACATGTCATTTATTGT	ACATGTCATTGATTG	0,0	intergenic region (Micheletti et al. 2018, BMC Evol Biol)
					TATCT	TTATCT	0,0	intergenic region (Micheletti et al. 2018, BMC Evol Biol)
					ATGTAAAAAAGGGCA	ATGTAAAAAATGGC	0,0	intergenic region (Micheletti et al. 2018, BMC Evol Biol)
					GAAAA	AGAAAA	0,0	intergenic region (Micheletti et al. 2018, BMC Evol Biol)
					TGCCCTACACAT	TGCCCTACACGT	0,0	intergenic region; fixed marker in all pops, drop (Micheletti et al. 2018, BMC Evol Biol)
					GTGGTGGCATTTCTG	GTGGTGGCATGTCTG	0,0	intergenic region (Micheletti et al. 2018, BMC Evol Biol)
					GTGT	GTGT	0,0	intergenic region (Micheletti et al. 2018, BMC Evol Biol)
					GCAATTTTTTAAAATT	GCAATTTTTTTAAAT	0,0	rock1 (Micheletti et al. 2018, BMC Evol Biol)
					ACCGC	TACCGC	0,0	rock1 (Micheletti et al. 2018, BMC Evol Biol)
						ATGTGTTCATATGCC	NA	Brunelli et al. 2008, Genome
						AG	NA	Brunelli et al. 2008, Genome

Note: This table contains the primer sequences, in-silico probe sequences for each allele, and correction values for each allele for each SNP locus included in the *O. mykiss* GT-seq primer pool. Each forward primer is modified with a 5' ‘small RNA’ sequencing primer site (CGACAGGTTCAGAGTTCTACAGTCCGACGATC) and each reverse primer is modified with a 5' standard paired-end sequencing primer site (GTGACTGGAGTTCAGACGTGTGCTCTCCGATCT).

Section 2: Genetic Baseline Expansion

Introduction

Distinct population aggregates of Chinook Salmon (*Oncorhynchus tshawytscha*), steelhead trout (*O. mykiss*), and the species *O. nerka* (Sockeye Salmon and kokanee), have evolved through the cumulative effects of selection and genetic drift (Waples 1991). The homing behavior (philopatry) displayed by Pacific Salmon means that fish typically return to spawn in their natal rearing sites or stream of origin. This distinctive life history attribute can significantly restrict gene flow, shape regional variation, and influence demographics among naturally reproducing populations (Hasler and Scholz 1983; McIssac and Quinn 1988; Quinn *et al.* 1991). Genetic differentiation is most easily resolved among populations that are geographically distant, where degree of gene flow is generally correlated with relative migration distances and adjacency in stream networks. However, local adaptations and the distribution of suitable spawning habitat within stream networks may influence finer (regional) scale genetic structure among watersheds in close proximity (Beacham *et al.* 2006; Matala *et al.* 2012). The natural phenomenon of immigration or straying (a homing miscue) buffers the loss of genetic diversity in salmon populations (Milner and Bailey 1989), but the rate of straying exhibited by wild fish is generally low (Quinn 1993; Heard *et al.* 1995) and genetic structure between populations may persist despite moderate gene flow from straying (e.g., Neville *et al.* 2007). Some evidence indicates that hatchery-origin fish exhibit a higher rate of straying which may be affected by changes in fish passage protocols, transport through the hydro system, artificial rearing practices, or inadequate acclimation (imprinting to natal waters by juvenile salmon). An elevated rate of immigration between populations may erode local adaptations, and lead to changes in spatial and temporal variability within and/or among populations (Hess and Matala 2013; Hess *et al.* 2016a; Matala *et al.* 2017).

In the Columbia River Basin, Chinook Salmon have been studied extensively (e.g., Waples *et al.* 2004; Beacham *et al.* 2006; Narum *et al.* 2008b; Matala *et al.* 2011; Hecht *et al.* 2015), as have steelhead trout (Winans *et al.* 2004; Currens *et al.* 2009; Blankenship *et al.* 2011; Narum *et al.* 2011; Matala *et al.* 2016). The scope of Sockeye Salmon and Coho Salmon genetic monitoring has been comparatively limited but has received greater attention in recent years (Gustafson *et al.* 1997; Kozfkay *et al.* 2008; Iwamoto *et al.* 2012; Galbreath *et al.* 2014). Continued monitoring and evaluation of the genetic structure among salmon populations in the Columbia River Basin has guided managers in establishing and maintaining primary conservation units to protect fisheries resources. The delineation of such conservation units, including distinct population segment (DPS), evolutionarily significant unit (ESU), major population group (MPG), and viable salmonid population (VSP) is guided by a core set of criteria, including population ecology and viability, ancestry and descent, reproductive isolation, and genetic structure and local adaptation (Fraser and Bernatchez 2001; Fraser *et al.* 2011). Although an understanding of adaptive variation is critical to proper salmon management, the majority of genetic information available to managers is based on neutral genetic variation. Landscape genetics is an approach aimed at describing population differentiation relative to features in an organism's environment (Segelbacher 2010; Latch *et al.* 2011; Sepulveda-villet & Stepien 2012; Matala *et al.* 2014). Landscape genetics explores population differentiation relative to features in the environment such as migratory barriers (e.g., dams), or heterogeneous

habitats such as variation in local climates or temperatures (Dionne et al. 2008; Narum et al. 2008a; Micheletti et al. 2017). Although local adaptation may be inferred from landscape genetics (Olsen et al. 2010; Blankenship et al. 2011), inferences based primarily on neutral genetic differentiation risk incorrectly identifying the underlying processes affecting population distinctions (Funk et al. 2012; Landguth & Balkenhol 2012). Techniques such as outlier detection methods, and genome wide association studies (GWAS) based on DNA sequence variation provide evidence of non-neutral population structure or adaptive variation (markers associated with run timing; Hess et al. 2016b). Such applications in genetic monitoring allow a more resolved understanding of genetic differentiation beyond what can be concluded from neutral loci alone (Narum et al. 2010b; Matala et al. 2011; Ackerman et al. 2012, Bourret et al. 2013). Putative non-neutral population differentiation can then be interpreted in the context of contemporary risks and vulnerabilities (e.g., climate change) for salmonid populations in the Columbia River Basin, revealing highly correlative relationships between genetic variation and the physical environment (see Limborg et al 2011). This additional information may ultimately influence conservation criteria for delineating populations across diverse landscapes.

Project objectives, time line and harvest management questions:

Objective two of project #2008-907-00 (Genetic Assessment of Columbia River Stocks) describes efforts to evaluate genetic diversity among populations that will inform managers in the areas of harvest monitoring, and conservation monitoring. Our approach involves the collection, analysis, interpretation and distribution of genotypic data. These data are being compiled as species-specific reference baselines for characterizing Chinook Salmon, steelhead trout, and *O. nerka* population structure specific to the Columbia River Basin. Baselines were initially created from genotypes at single nucleotide polymorphism (SNP) loci, which are highly prolific in the genome and provide substantial coverage for linkage analyses (Moen et al. 2008). SNPs are amenable to superior high throughput capabilities and are relatively easily amplified and scored compared to other types of genetic markers, even with poor quality tissue (DNA) sources (Campbell and Narum 2008). Because SNPs are commonly found within or adjacent to coding and regulatory regions of a genome, corresponding allelic diversity and allele frequency variation are likely to be informative for understanding non-neutral influences (i.e. selection and local adaptation) on observed population structure. Large numbers of highly informative SNP loci have been discovered through our ongoing efforts using a next generation sequencing methods known as restriction-site associated DNA (RAD) sequencing (Miller et al. 2007; Baird et al. 2008; Hecht et al. 2013) and whole genome resequencing ([Whole Genome Resequencing: Poolseq Individual Barcode v1.0](#)). Our two primary objectives for utilizing SNP baselines to monitor salmon species in the Columbia River are 1) genetic stock identification (GSI) of natural-origin stocks, and 2) parentage based tagging (PBT), a large-scale, non-lethal tagging technology for monitoring and evaluating hatchery stocks. The collaborative, inter-agency application of GSI continues to provide invaluable monitoring capabilities to understand relative stock proportions in sport, commercial and tribal harvests, as well as monitoring of stock specific run-timing at Bonneville Dam, Lower Granite Dam and other fish weirs in the basin. Moreover, GSI is being used concordantly with PBT to monitor trends in hatchery production, harvest of hatchery fish, and population attributes of specific hatcheries (e.g., stray rates, survival/mortality, migratory behavior, hatchery/wild interactions). Additionally, our genetic baselines are being used to characterize populations in archival studies, to inform efforts to reintroduce fish into extirpated regions within historic ranges, and in domestication studies. In step with technological

advancements, further geographic coverage, and continuing marker development, our efforts continue to expand. Our most recent results will be reported on an annual basis, and data will be routinely uploaded to the FishGen.net database (<http://www.fishgen.net/home.aspx>) as a repository for data sharing and collaboration.

Methods

Baseline sampling and protocols:

Our previously established baselines, comprised of putatively neutral SNPs (e.g. 180 loci for *O. mykiss*), have been well characterized and have been used extensively for genetic stock identification (GSI) as described in Hess et al. (2015) and Hasselman et al. (2016). Our most recent efforts focus on expanding genetic characterizations throughout the basin that will provide information about adaptive potentials and natural selective forces contributing to stock structure. Next generation sequencing technologies in genotyping (RAD) continue to be employed by the CRITFC genetics lab in order to expand SNP panels for Chinook Salmon, Coho Salmon, Sockeye Salmon, steelhead trout and Pacific lamprey (Hess et al. 2016c). Methods for genotyping by sequencing (GT-seq) are described in Campbell et al. (2015), and for RAD sequencing (SbfI restriction enzyme protocol) see Monitoring Methods #4144, owner: Nathan Campbell. SNP discovery using the RAD sequencing technique is described in Chapter-1 of this report. Detailed laboratory methods are available in Monitoring Methods: <https://www.monitoringmethods.org/Protocol/Details/230> (ID#230; owner Matthew Campbell) and Hess et al. (2012). The program STACKS was used to identify and quality-filter SNPs from raw Illumina sequence data (Catchen et al. 2011). Methods for whole genome resequencing ([Whole Genome Resequencing: Poolseq Individual Barcode v1.0](#)) utilize PoolParty v0.8 (Micheletti and Narum 2018), a bioinformatic pipeline based on bash and R to identify and process SNPs. High-quality SNPs were then used to assess population structure based on principal component analyses (PCA) and pairwise genetic distance displayed in neighbor joining (NJ) trees using the ‘adeget’ package in R (Jombart & Ahmed 2011) or in GenAlEx v6.5 (Peakall and Smouse 2006).

Expansion and status of reference baselines for GSI:

Our three primary goals for expanding, maintaining, and evaluating each species-specific baseline are threefold. First, we used genetic stock identification (GSI) analyses for monitoring of fishery returns through the migratory corridor of the Columbia River, including harvest GSI in the lower Columbia River, and fish passage GSI at Bonneville and Lower Granite dams (see sections 3 & 4 of this report). Second, PBT broodstock sampling and genotyping of Columbia River Basin hatcheries has been updated to include return year 2017 for continued evaluation of hatchery stock composition in various fisheries and to more accurately account for abundance of natural-origin stocks by identifying unmarked hatchery fish. Third, the sequence/genotypic data are also being applied in various analyses to evaluate selection, including investigations of landscape genetics, and adaptive differentiation among populations.

The GT-seq primer pools developed from RAD-seq data are currently being used for all high throughput genotyping projects, including 5 target species: steelhead trout – 389 SNP loci plus sex determination marker, Chinook Salmon -298 SNP loci plus sex determination marker, Coho Salmon - 257 SNP loci, Sockeye Salmon - 363 SNP loci, and Pacific Lamprey - 308 SNP loci (Hasselman et al. 2016). Currently we do not utilize reference baselines for GSI of either

Coho Salmon or Pacific Lamprey, and in 2018 there were no updates to the reference populations in our GSI baseline for Chinook Salmon and Sockeye Salmon. The most up to date GSI marker panel used for stock assessment of Chinook Salmon is described in Hess et al. (2016c). For *O. nerka*, the most up to date GSI marker panel (363 SNPs) and baseline used for stock assessment of Sockeye Salmon is described in Hasselman et al. 2018. Updates to the reference baseline for GSI based on the expanded SNP marker panel for steelhead trout is described in this section.

In addition, we are using whole genome resequencing methods that pool samples (Pool-seq; Schlotterer et al. 2014) to generate reference baselines with millions of SNPs for several species, Chinook Salmon (Table 4), Coho Salmon (Table 5), and *O. mykiss* (Table 6). Allele frequencies from millions of SNPs will be analyzed to detect statistically significant regions of the genome associated with specific traits or adaptation to environmental factors. Putatively neutral regions of the genome are also useful for standard phylogeny and demographic analyses of populations. Therefore, there are multiple objectives that can be accomplished with these Pool-seq reference baselines including identifying novel SNPs that can be used for improved accuracy and precision of future GSI and PBT applications. These reference baselines comprised of millions of SNPs thus fit two of the main objectives for this project: SNP discovery AND expand and create baselines.

Table 4. Creation of a Chinook Salmon SNP baseline by whole genome resequencing of pools of samples

Pool Seq Library ID	Number of reads (R1)	ID	Collection	(n)	Lineage	Reporting Groups
L-0730	764426428	OTS01	Big Creek Tule	71	Rogue	01_YOUNGS
L-0731	812304568	OTS03	Kalama R spring-run	93	LC	02_WCASSP
L-1037	815599916	OTS05	Elochoman R fall-run	86	LC	03_WCASFA
L-0732	967452852	OTS06	Lewis R fall-run	68	LC	03_WCASFA
L-1067	857684796	OTS12	White Salmon fall-run	78	LC	05_SPCRTU
L-0736/L-0736_2	1829616180	OTS13	Spring Creek NFH tule fall-run	47	LC	05_SPCRTU
L-0737	992124812	OTS16	Warm Springs R spring-run	190	ST	07_DESCSP
L-0756	593717960	OTS17	John Day North Fork-Main Stem	52	ST	08_JOHNDR
L-0739	886633952	OTS18	Middle Fork John Day R spring-run	36	ST	08_JOHNDR
L-0740	556776700	OTS19	North Fork John Day R spring-run	39	ST	08_JOHNDR
L-0741_A	784672092	OTS20	American R spring-run	62	ST	09_YAKIMA
L-0742	708185484	OTS22	Winthrop NFH spring-run	83	ST	10_UCOLSP
L-0743	1110957296	OTS24	Wenatchee R spring-run	51	ST	10_UCOLSP
L-1038	822422724	OTS28	Lostine R spring-run	41	ST	12_HELLSC
L-0747	1116650532	OTS29	Grande Ronde R spring-run	30	ST	12_HELLSC
L-1069	783838616	OTS32	Red R spring-run	45	ST	12_HELLSC
L-0749	864235488	OTS33	Powell R spring-run	94	ST	12_HELLSC
L-1070	869926808	OTS35	South Forth Salmon R spring-run	45	ST	13_SFSALM
L-0751	994944104	OTS37	Secesh R spring-run	90	ST	13_SFSALM
L-0752	1007223828	OTS38	Chamberlain Cr spring-run	78	ST	14_CHMBLN

L-0753	953068680	OTS39	Big Cr spring-run	139	ST	15_MFSALM
L-1059	995254852	OTS41	Loon Cr spring-run	42	ST	15_MFSALM
L-0754	757118500	OTS43	Bear Valley Cr spring-run	33	ST	15_MFSALM
L-0755	874750408	OTS45	Marsh Cr spring-run	44	ST	15_MFSALM
L-0757	753567604	OTS47	Lemhi R spring-run	95	ST	16_UPSALM
L-0758	565547400	OTS48	Pahsimeroi R spring-run	92	ST	16_UPSALM
L-1057	815540824	OTS49	East Fork Salmon R spring-run	96	ST	16_UPSALM
L-1080	973129248	OTS50	Salmon R spring-run	61	ST	16_UPSALM
L-1060	958890180	OTS51	West Fork Yankee Fork spring-run	93	ST	16_UPSALM
L-0760	1106804140	OTS53	Sawtooth Hatchery weir spring-run	91	ST	16_UPSALM
L-0761	1055033180	OTS55	lower Yakima R fall-run	46	OT	18_UCOLSF
L-0762/L-0966/L-0967	1905181788	OTS57	Wenatchee R summer-run	61	OT	18_UCOLSF
L-0763/L-0877/L-0897/L-0904	1930607120	OTS59	Methow R summer-run	68	OT	18_UCOLSF
L-0764	861913556	OTS60	Lyons Ferry weir fall-run	92	OT	19_SRFALL
L-0906/L-0733/L-0733_Test/L-0876	832164948		Methow R spring-run	87	ST	10_UCOLSP

Table 5. Creation of a Coho Salmon SNP baseline by whole genome resequencing of pools of samples

Stock	n	Location	Region (BPA subbasin)	Lineage
Wenatchee	282	Leavenworth NFH	Wenatchee	Oki-Lower Columbia
Bonneville Dam	175	Bonneville Dam	Mixed	Mixed

Table 6. Creation of *O. mykiss* SNP baseline by whole genome resequencing of pools of samples

Pool Seq Library ID	ID#	Abbreviation	Name	(n)	Lineage	Subbasin
L-0983	29	LICK	Lick Creek	70	IN	Salmon
L-0781	52	WFYF	West Fork Yankee Fork	58	IN	Salmon
L-0782	2	ASOT	Asotin	60	IN	Asotin
L-0925	49	TUCN	Tucannon	42	IN	Tucannon
L-1001	11	EAGL	Eagle	61	C	Willamette
L-1002	46	SKAM	Skamania Stock	60	C	Willamette
L-0786	51	UMAT	Umatilla	70	IN	Umatilla

L-0787	37	NACH	Naches -Nile Creek	38	IN	Yakima
L-0788	35	MINT	Minthorn	74	IN	Umatilla
L-0789	30	LOON	Loon	51	IN	Salmon
L-1022	13	ELEW	East Fork Lewis	78	C	Lewis
L-0916	55	WNFH	Winthrop	93	IN	Methow
L-1020	31	LSHE	LittleSheep	76	IN	Imnaha
L-0908	50	UGRT	Upper Grande Ronde	58	IN	Grande Ronde
L-0924	6	CATH	Catherine	91	IN	Grande Ronde
L-0971	43	SATU	Satus	67	IN	Yakima
L-0972	53	WHIT	Whitebird	50	IN	Salmon
L-1023	16	FIFT	Fifteen	92	IN	Fifteenmile Creek
L-0973	42	ROCK	Rock	91	IN	Lower Mid-Columbia
L-0974	21	JOSE	Joseph	88	IN	Grande Ronde
L-1017	8	CHIW	Chiwaukum	54	IN	Wenatchee
L-1018	34	MILL	Mill Creek	96	IN	Columbia Gorge
L-1021	45	SFJD	South Fork John Day	96	IN	John Day
L-0984	40	NSAN	Little Rock	50	C	Willamette
L-0985	20	JDMA	John Day Main Fork	69	IN	John Day
L-1000	38	MFJD	Middle North Fork JD	67	IN	John Day
L-0909	54	WHOO	West Fork Hood	79	C	Hood
L-0928	12	EFHJ	East Fork Hood	48	C	Hood
L-0929	18	HOOH	Pakdale Fish Hatchery	83	C	Hood

Oncorhynchus mykiss GT-seq SNP panel expansion

The ability to genetically assign individual fish to geographic region-of-origin facilitates better management of distinct groups or populations. In past years, our marker panels (180 SNPs) for *O. mykiss* have been employed to successfully assigned individual steelhead to 13 distinct reporting groups in the Columbia River Basin: Quinault, Lower Columbia, Skamania, Willamette, Big White Salmon, Klickitat, Yakima, Upper Columbia, South Fork Clearwater, Upper Clearwater, Middle Fork Salmon, South Fork Salmon, Upper Salmon (Hasselman et al. 2018, Figure 13). However, the 14th reporting group, termed Mid Columbia-Grande Ronde-Imnaha-Lower Snake-Lower Clearwater-Lower Salmon (MGILCS), is less distinct because it spans multiple sub-basins (Hess et al. 2016). Thus, any genetic assignments to MGILCS are less informative than other reporting groups since individuals may have originated from one of many far-off or non-adjacent tributaries within MGILCS. Efforts to expand the reference baseline for *O. mykiss* in 2017 were focused on discovery of additional genetic markers that would provide better resolution of the populations within MGILCS, allowing separation of smaller reporting groups. This was achieved by employing a Restriction site-associated DNA (RAD) method (Micheletti et al. 2017). Populations representing 21 localities within the MGILCS reporting group were scrutinized as groups based on adjacency in the stream network and greatest genetic similarity (*i.e.*, those with high F_{ST} and greatest allele frequency differences) using 24,526 single nucleotide polymorphisms (Micheletti et al. 2017). To select the most informative SNPs, a

principle component analysis (PCA) was iterated in the R package *adeigenet* (Jombart 2008) with different combinations of candidate SNPs from the 24,526 RAD markers, until sufficient (i.e. greatest) differentiation was observed between spatially distinct tributaries within MGILCS.

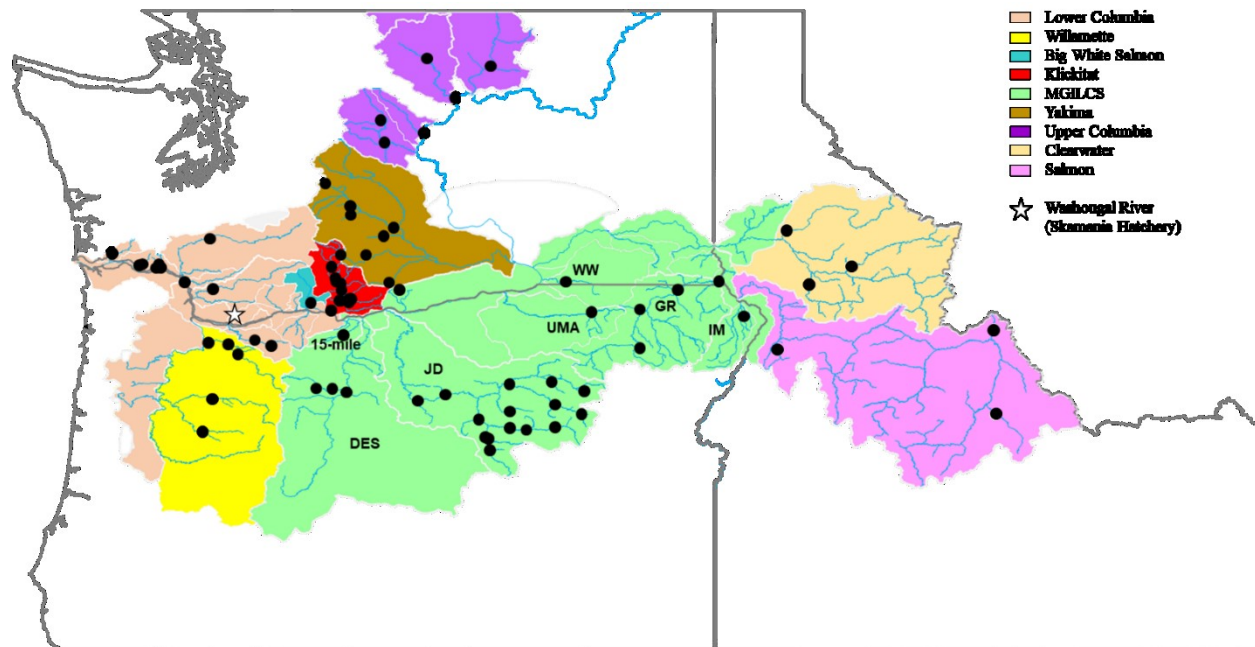


Figure 13. Map of reporting groups and sampled populations (see Appendix 1) included in the current reference baseline for Steelhead Trout. Individual subbasins with the MGILCS reporting group are: 15-mile – Fifteenmile, DES – Deschutes, JD – John Day, UMA – Umatilla, WW – Walla Walla, GR – Grande Ronde, and IM – Imnaha. Note that the Clearwater River and Salmon River subbasins are each represented by a single reporting group due to limited coverage in the expanded baseline.

To ensure that the newly developed 63 markers could successfully identify the reporting group of origin, genotypes were simulated for 56 localities in the Columbia River Basin, representing 14 reporting groups (Micheletti *et al.* 2017), among which the MGILCS reporting group was broken up into 7 smaller reporting groups. After PCA iterations, a group of 63 SNPs were shown to produce high-resolution differentiation between 7 reporting groups within the larger MGILCS reporting group.

Run-timing marker expansion

Populations of *O. mykiss* from across the Columbia River Basin experience regionally and/or locally variable environmental (e.g., habitat) conditions, such as air temperature, water temperature, precipitation, stream flow, elevation, and migration distance (Matala *et al.* 2014; Micheletti *et al.* 2017). Variation in environmental conditions can be strongly correlated with specific alleles at specific loci, where certain alleles favor survival under certain habitat conditions. Environment also influences run timing phenotypes among *O. mykiss* populations. Run timing is a distinct trait involving maturation of fish as they return to freshwater to spawn (Hess *et al.* 2016b). Winter-run fish, referred to as ocean maturing, often cannot be easily or

reliably differentiated from summer-run fish (stream maturing) based on physical appearance alone.

This is largely due to the protracted return time of summer-run fish, which may reside in the freshwater environment for up to a year as they undergo reproductive maturation (e.g., gonadal development). Run-timing associated markers have been incorporated into our SNP panel (Hasselman et al. 2018), which display large allele frequency differences between fish with differing maturation schedules (e.g. summer-run and winter-run fish of the coastal genetic lineage). Of these previously discovered SNPs, several failed to produce quality genotypes, prompting the need to develop additional run-timing markers identified through previous sequencing and discovery efforts using pooled sequencing (Pool-seq) of individuals sampled from the Klickitat and Kalama rivers, where “known” winter-run or summer-run origin of fish was based on documented spawn time (Hasselman et al. 2018; Micheletti *et al.* 2018).

Statistical Analysis:

We evaluated the distinctiveness of each population in the reference baseline using assignment tests. Individual assignment likelihood scores (LS) were generated using GENECLASS2 (Piry et al. 2004), implementing the Bayesian method of Rannala and Mountain (1997) in a leave-one-out jackknife procedure. The assigned origin of each individual was the population with highest corresponding GSI likelihood score from among the top five ranked scores. The rate of self-assignment was defined as the proportion of fish of known origin that genetically assigned to that specific population. The program ARLEQUIN version 3.5 (Excoffier et al. 2010) was used to calculate pairwise population F_{ST} to evaluate among group variation. A pairwise matrix of Nei’s standard genetic distance (Nei 1972) and an un-rooted neighbor-joining (NJ) tree were generated using PHYLIP version 3.68 (Felsenstein 1993). Pairwise genetic distances generated in GenAIEx version 6.5 were used to display population clustering patterns in a principal coordinate analysis (PCoA) plot.

Results

O. mykiss baseline: reporting group and marker expansion

The current SNP panel now includes 11 loci (Table 7) developed from a genome region on Chromosome 28 that is associated with run-time (i.e. maturation gene region; Micheletti *et al.* 2018). Ultimately, a total of 349 loci were retained from the original 389 loci following quality control screening measures employed to omit marker failing to successfully amplify with acceptable coverage (i.e. greater than 85% of samples). Further, only 40 of the original 63 SNPs developed to differentiate among reporting groups in the larger MGILCS reporting group were retained. This was largely a result of primer interactions that precluded the ability to successfully generate genotypic data. Seven of the 63 loci exhibited fixed allele frequencies across all populations in the expanded reference population baseline.

Table 7. Sixty-three SNP loci determined to show power to differentiate among subbasins in the MGILCS reporting group based on RAD-seq data (Hasselman et al. 2017).

Omy_RAD2674-44	Omy_RAD1186-59	Omy_RAD24287-74	Omy_RAD43694-41
Omy_RAD12871-35	Omy_RAD1751-18	Omy_RAD24343-29	Omy_RAD46672-27

Omy_RAD12925-52	Omy_RAD2567-8	Omy_RAD25042-68	Omy_RAD49111-35
Omy_RAD14666-65	Omy_RAD2976-26	<i>Omy_RAD25266-23</i>	<i>Omy_RAD49827-67</i>
Omy_RAD14881-63	Omy_RAD3209-10	Omy_RAD25907-57	Omy_RAD50632-21
Omy_RAD16027-52	Omy_RAD7016-31	Omy_RAD28236-38	Omy_RAD57916-29
Omy_RAD30503-56	<i>Omy_RAD9408-71</i>	Omy_RAD29352-6	Omy_RAD59950-44
Omy_RAD34844-68	Omy_RAD12439-64	<i>Omy_RAD30243-74</i>	Omy_RAD65959-69
Omy_RAD39254-12	Omy_RAD13073-16	Omy_RAD32139-58	Omy_RAD73963-73
Omy_RAD42888-53	Omy_RAD14269-30	Omy_RAD33122-47	Omy_RAD76060-20
Omy_RAD63808-66	<i>Omy_RAD14541-72</i>	Omy_RAD35149-9	Omy_RAD86706-72
Omy_RAD62138-53	Omy_RAD15709-53	Omy_RAD37816-68	Omy_RAD93580-37
Omy_RAD95256-58	Omy_RAD17849-16	Omy_RAD38406-19	Omy_RAD70874-8
Omy_RAD366-7	Omy_RAD19340-24	Omy_RAD40641-58	Omy_RAD81818-40
Omy_RAD619-59	Omy_RAD20917-11	Omy_RAD41594-34	Omy_RAD92398-62
Omy_RAD739-59	<i>Omy_RAD23354-66</i>	Omy_RAD43573-37	*Chr28_11607954
*Chr28_11625241	*Chr28_11632591	*Chr28_11658853	*Chr28_11667578
*Chr28_11671116	*Chr28_11676622	*Chr28_11683204	*Chr28_11697834
*Chr28_11702210	*Chr28_11773194		

Note: Primers development to incorporate loci into the current reference baseline panel of SNPs produced deficient or spurious genotypic data for some loci (gray fill). These loci are not represented in the current baseline. Seven additional SNP loci (bold italics) among the original 63 were found to be uninformative (i.e. fixed at a common allele) among all reference baseline populations. The current SNP panel includes 11 additional loci (*) developed to differentiate among run timing or maturation phenotypes based on Pool-seq data from Klickitat and Kalama summer-run and winter-run populations.

Although RAD sequence data for the 63 MGILCS-markers initially differentiated 7 spatial clusters within the reporting group based on simulation tests, SNP genotypes for the 40 markers retained in the current baseline proved to be less informative. This was evidenced by the low assignment rates observed among subbasins in the MGILCS reporting group (Table 9), and in cluster analyses based on genetic distances which showed non-discrete clustering patterns between collections from different subbasins (Figure 14). However, collections from subbasins within the MGILCS reporting group continue to exhibit accurate assignment to the larger reporting group as has been previously reported. Ultimately, the goal for the reference baseline in

GSI application to fisheries harvest and management is accurate reporting group assignment. Only three populations in the inland lineage *O. mykiss* baseline failed to reach an 80% accuracy threshold (Fifteenmile, Entiat and Methow; Table 9). Overall population grouping in a dendrogram based on pairwise genetic distances shows clustering based on geographic proximity (e.g. reporting group origin) and distinctions among regions (Figure 15). Branch lengths identify the Klickitat, Yakima, and Clearwater River subbasins as the most highly distinct (i.e. most genetically distant groups) as has been previously reported (Hess et al. 2016; Hasselman et al. 2018).

Table 8. Genetic assignment results generated in GENECLASS for the *O. mykiss* coastal lineage reference baseline.

POP	RG	n	self (POP)		LC		WILL		BWS		SKA	
			%	LS	%	LS	%	LS	%	LS	%	LS
Abernathy	LC	71	0.77	94.5	0.99	100.0					0.01	96.0
Elochoman	LC	44	0.50	78.4	0.98	99.9			0.02	58.1		
Germany	LC	35	0.31	82.8	1.00	99.9						
Grays	LC	31	0.32	80.9	1.00	99.8						
Kalama (SUM)	LC	36	0.64	88.7	0.83	96.9	0.08	60.0			0.08	91.0
Kalama (WIN)	LC	39	0.51	88.4	1.00	99.4						
Lewis	LC	77	0.75	94.5	1.00	99.8						
Mill	LC	30	0.47	79.8	0.97	99.4			0.03	51.5		
Sandy	LC	12	0.17	87.2	1.00	98.2						
Washougal	LC	38	0.29	88.2	0.84	97.7	0.13	84.7			0.03	46.6
Cowlitz	LC	91	0.89	97.4	1.00	100.0						
Clackamas (WIN)	WILL	219	0.87	88.2	0.03	82.0	0.97	99.6				
Eagle	WILL	45	0.53	81.2	0.07	87.9	0.93	96.1				
Clackamas (SUM)	WILL	25	0.92	96.4	0.08	91.3	0.92	96.4				
N. Santiam	WILL	22	0.27	99.3	0.14	84.6	0.82	99.3	0.05	99.8		
S. Santiam	WILL	55	0.58	95.0	0.05	84.9	0.91	98.5			0.04	78.7
mainstem BWS	BWS	177	0.59	96.1	0.14	83.5	0.08	87.2	0.68	99.1	0.10	98.2
Rattlesnake	BWS	60	0.97	94.2					1.00	100.0		
Skamania	SKA	40	0.93	99.3	0.05	90.2	0.03	99.6			0.93	99.3

Note: For each baseline population the rate of assignment accuracy is identified by a proportion of the total sample (%) that assigned to known origin, and a corresponding statistical likelihood score (LS 1-100). Assignments exhibiting greater than 80% accuracy are shaded gray. Assignments were evaluated hierarchically, at the level of known population (pop), known subbasin, and known reporting group (RG) of origin. Assignments are based on multilocus genotypes across 349 SNPs.

Table 9. Genetic assignment results generated in GENECLASS for the *O. mykiss* inland lineage reference baseline.

pop	n	subbasin	RG	self (pop)			subbasin			RG		
				#	%	LS	#	%	LS	#	%	LS
Deschutes	231	DES	MGILCS	171	0.74	95.5	117	0.51	74.8	217	0.94	97.3
15_Fifteenmile	85	FIF	MGILCS	46	0.54	91.3	33	0.39	84.8	66	0.78	93.7
Catherine	228	GR	MGILCS	157	0.69	82.9	76	0.48	88.4	221	0.97	96.1
GR_Joseph	45	GR	MGILCS	16	0.36	84.8	16	0.45	85.6	40	0.89	92.7
GR_Upper	42	GR	MGILCS	14	0.33	85.9	21	0.49	91.0	41	0.98	97.2
GR_Wenaha	77	GR	MGILCS	37	0.48	87.1	39	0.41	90.7	68	0.88	95.2
IM_Lightning	72	IM	MGILCS	54	0.75	91.4	48	0.67	70.0	66	0.92	96.1
JohnDay	169	JD	MGILCS	113	0.67	87.7	70	0.41	52.9	162	0.96	97.5
Umatilla	144	UMA	MGILCS	63	0.44	77.2	36	0.25	47.0	126	0.88	94.4
WW_Touchet	57	WW	MGILCS	42	0.74	90.6	30	0.53	63.6	57	1.00	99.3
klickitat	607	KLICK	KLICK	534	0.88	99.1	534	0.88	99.1	534	0.88	99.1
YAK_Ahtanum	56	YAK	YAK	38	0.68	92.2	56	1.00	72.7	56	1.00	72.7
YAK_Cowiche	68	YAK	YAK	58	0.85	98.2	68	1.00	96.8	68	1.00	96.8
YAK_Naches	310	YAK	YAK	291	0.94	96.6	310	1.00	93.1	310	1.00	93.1
YAK_Satus	435	YAK	YAK	414	0.95	98.3	435	1.00	94.3	435	1.00	94.3
YAK_Toppenish	111	YAK	YAK	107	0.96	99.4	110	0.99	99.9	110	0.99	99.9
ENT_Entiat	43	ENT	UC	8	0.19	76.9	8	0.19	76.9	24	0.56	83.6
Methow	73	MET	UC	34	0.47	80.8	34	0.47	80.8	57	0.78	92.4
OKN_Omak	115	OKN	UC	62	0.54	90.3	62	0.54	90.3	92	0.80	93.6
Wenatchee	40	WEN	UC	13	0.33	90.5	13	0.33	90.5	33	0.83	91.7
NFSALM	100	SALM	SALM	76	0.76	91.3	93	0.93	95.9	93	0.93	95.9
PAH	100	SALM	SALM	79	0.79	94.3	95	0.95	98.7	95	0.95	98.7
rapid	100	SALM	SALM	86	0.86	98.2	98	0.98	99.2	98	0.98	99.2
DWOR	100	CLWTR	CLWTR	100	1.00	99.1	100	1.00	100.0	100	1.00	100.0
Lochsa	100	CLWTR	CLWTR	99	0.99	100.0	100	1.00	100.0	100	1.00	100.0
SFCLWR	11	CLWTR	CLWTR	0	na	na	11	1.00	100.0	11	1.00	100.0

Note: For each baseline population the rate of assignment accuracy is identified by a proportion of the total sample (%) that assigned to known origin, and a corresponding statistical likelihood score (LS 1-100). Assignments exhibiting greater than 80% accuracy are shaded gray. Assignments were evaluated hierarchically, at the level of known population (pop), known subbasin, and known reporting group (RG) of origin. Assignments are based on multilocus genotypes across 349 SNPs with the exception of subbasin assignments within MGILCS, which are based on the 40 loci (*) specifically developed to differentiate between those subbasins.

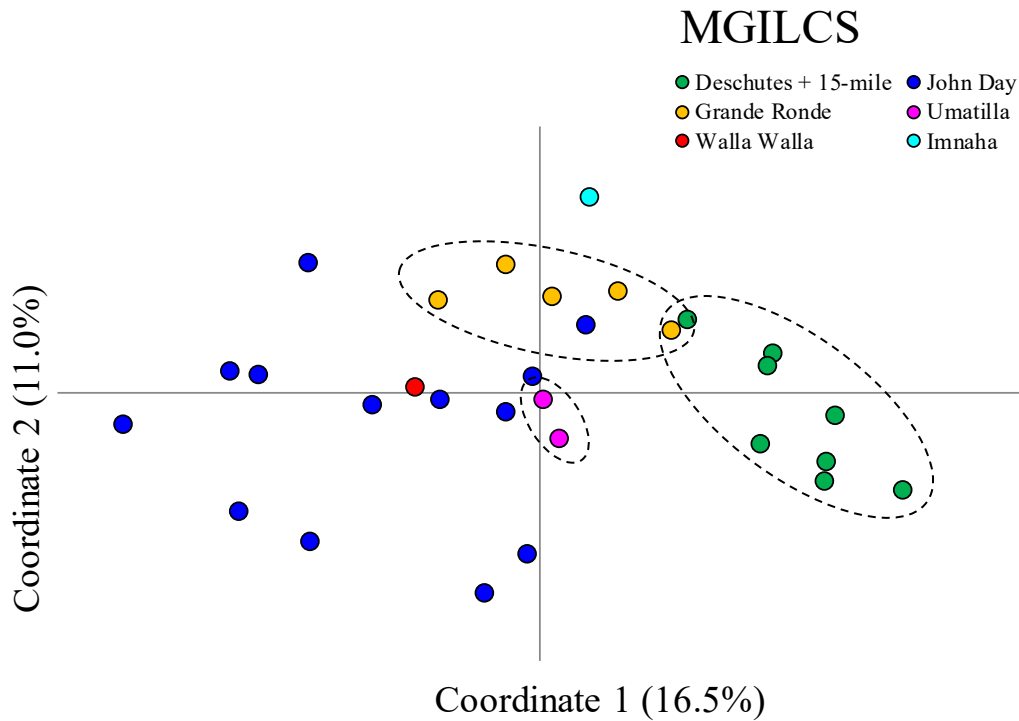


Figure 14. Principle Coordinates Analysis plot based on 40 loci used to differentiate between subbasins in the MGILCS reporting group. Clustering is based on pairwise genetic distances. The amount of total variation described by the first two coordinates are shown in parentheses.

Coastal lineage *O. mykiss* populations exhibited highly accurate genetic assignments among reporting groups with the exception of the mainstem collection from the Big White Salmon River (Table 8). The subbasin is located on the eastern edge of the range of the coastal genetic lineage, downstream of most steelhead populations inhabiting the Columbia River Basin. Prior to removal of Condit Dam in 2014, the Big White Salmon River had limited available habitat below the impassable barrier, and a natural spawning steelhead population of limited abundance. The nondescript or mixed-origin appearance of the population inferred from assignment results may indicate significant colonization of the river (natural straying) by fish originating from multiple source populations since dam removal. Population clustering based on pairwise genetic distances among reference baseline populations shows a pattern among reporting groups that is consistent with assignment results (Figure 16).

- Klickitat
- MGLCS
- Yakima
- Upper Columbia
- Clearwater
- Salmon

- 1 Klickitat
- 2 Fifteenmile
- 3 Deschutes
- 4 Entiat
- 5 Catherine
- 6 Joseph
- 7 Upper Grande Ronde
- 8 Wenaha
- 9 Lightning
- 10 John Day
- 11 Methow
- 12 Omak
- 13 Umatilla
- 14 Wenatchee
- 15 Touchet
- 16 Altanum
- 17 Cowiche
- 18 Naches
- 19 Satus
- 20 Toppenish
- 21 Dworshak
- 22 Lochsa
- 23 N. F. Salmon
- 24 Pahsimeroi
- 25 Rapid
- 26 S. F. Clearwater

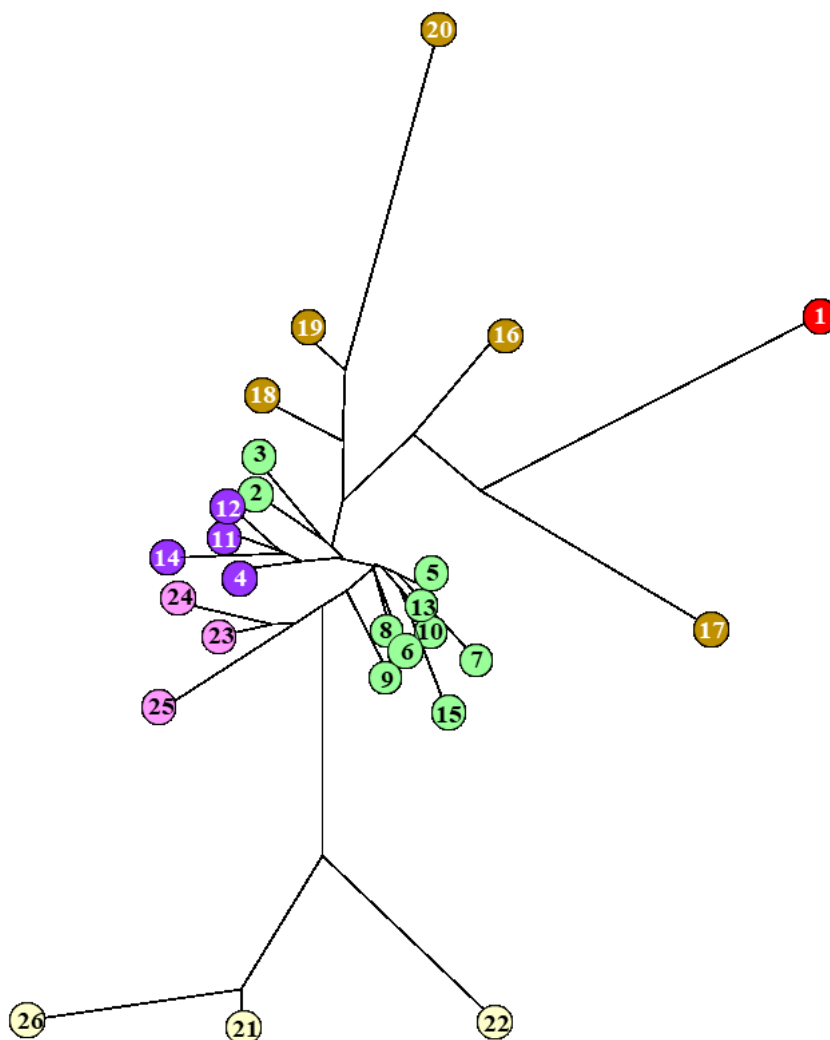


Figure 15. Neighbor joining tree for the inland lineage reference baseline.

Most clustering among the lower Columbia River collections is highly influenced by geographic proximity of the basins. One exception to this observation was apparent among three summer-run populations (Skamania, Kalama, and Clackamas). The clustering pattern among these summer-run collections reveals that they share recent common ancestry, and each collection is distinct from other collections obtained from the same basins but displaying winter-run phenotype (Figure 16).

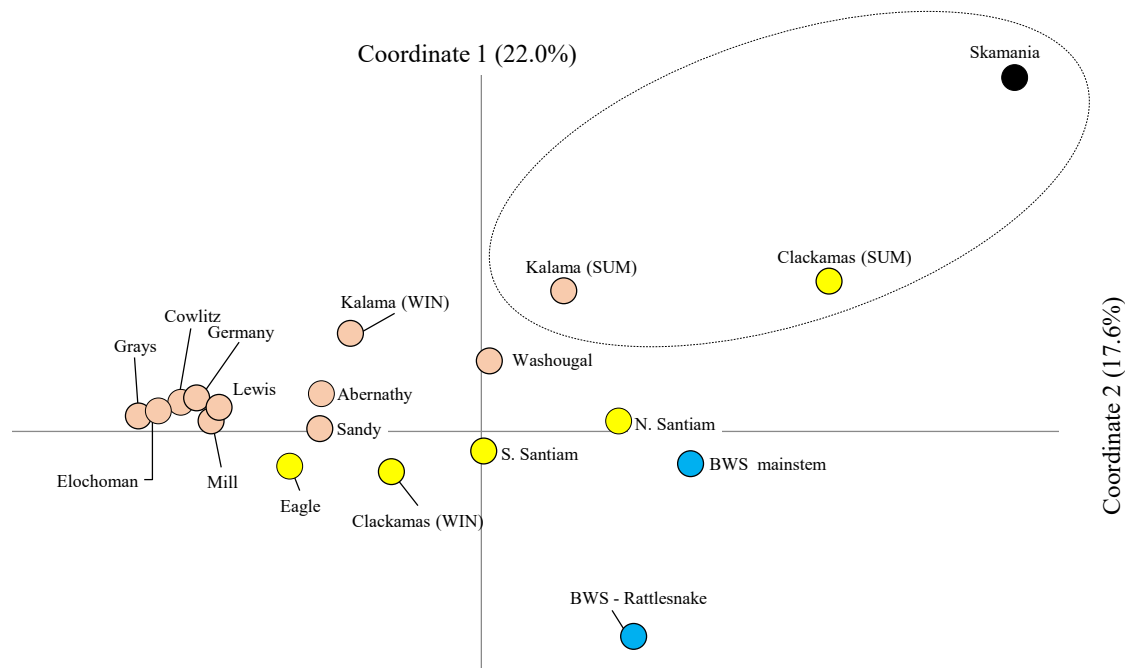


Figure 16. Principle Coordinates Analysis plot based on 349 loci used to differentiate between reporting groups of the coastal genetic lineage. The ellipse highlights the ordination of three summer-run populations. Skamania is a summer-run hatchery stock originating from the Washougal River that has been used pervasively in supplementation efforts in the Lower Columbia River region.

Parentage Based Tagging (PBT) update

PBT began with Chinook Salmon and steelhead hatchery stocks in the Snake River basin of Idaho (2008-present; Steele et al., 2013; Steele et al., 2015). However, we have expanded PBT coverage (Figure 17, Appendix 4, Appendix 5, and Appendix 6) to include Chinook Salmon, steelhead, and Coho Salmon broodstocks in all hatcheries above Bonneville Dam using expanded SNP panels of 299 loci for Chinook Salmon, 379 loci for steelhead trout and 257 loci for Coho Salmon. Each year the expansion effort is integrated with existing PBT baselines as data comes available (e.g., Chinook salmon, Appendix 2).

Adopting PBT to the broader Col. River basin facilitates our ability to genetically track millions of salmonids and provide opportunities to address a variety of parentage-based research and management questions, including stock contributions to fisheries (Byrne et al., 2015), estimates of stock-specific abundance and run-timing at dams (Hess et al., 2016c; Vu et al. 2015), and use of thermal refugia during migration (Hess et al., 2016a).

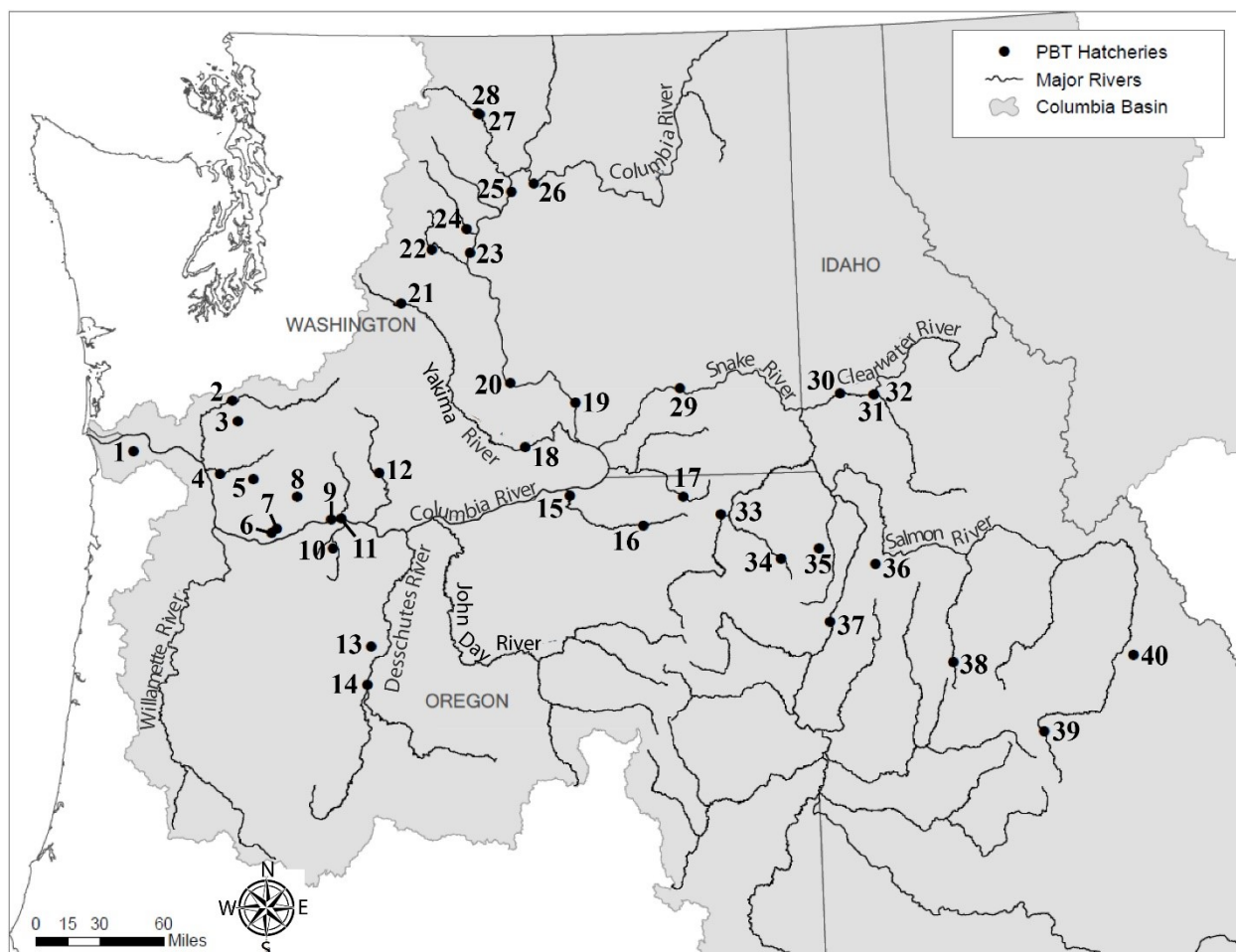


Figure 17. Chinook Salmon, steelhead, and Coho Salmon PBT hatcheries. Numbers correspond to map ID and hatchery descriptions (Appendix 4, Appendix 5, Appendix 6).

The PBT tagging technology has been implemented through annual hatchery broodstock sampling to create a temporally structured parental genotype baseline. As adult fish return to participating hatcheries in the Columbia River basin, broodstock are sampled by collection of fin tissue during hatchery spawning. Required data for PBT sampling includes a hatchery record of phenotypic sex and spawn date. Additional and optional information was collected at some hatcheries when resources allowed, including fork length, and mated cross records of male and female broodstock individuals. The PBT baseline expansion during the 2018 report period included spawn years 2015 to 2016 for some lower Columbia River hatcheries, but primarily broodyear 2017 was genotyped for most hatcheries. The total numbers of fish genotyped for PBT baselines in 2018 included $n=15,377$ spring Chinook Salmon, $n=3,028$ upper Columbia summer Chinook Salmon, $n=32,246$ fall Chinook Salmon (Appendix 2), $n=4,232$ steelhead trout (Appendix 3), and $n=11,106$ Coho Salmon (Appendix 3). DNA was extracted using modified Chelex extractions and Qiagen DNeasy 96 kits. Extracted genomic DNA was genotyped at 299 SNP loci for Chinook Salmon, 390 SNP loci for steelhead trout, and 257 SNP loci for Coho Salmon using a GTseq protocol: (<https://www.monitoringresources.org/Document/Method/Details/5446>).

Hatchery offspring that are subsequently sampled either as juveniles or adults (e.g., in a fishery) are then PBT assigned back to spawned parents which provides the individual age and specific hatchery of origin for each offspring.

Discussion

Large datasets produced by genomic sequencing techniques may contain informative markers for population assignment. An original *O. mykiss* marker panel being used prior to 2017 could not effectively assign fish to basins within MGILCS; however, mining the RAD dataset from Micheletti *et al.* (2017) using population genetic tools identified a small set of 63 markers that increased assignment success while breaking MGILCS into 7 smaller reporting groups. Unfortunately these results gleaned from sequence data and simulated allele frequencies did not produce the same level of informativeness when incorporated into a SNP panel containing 40 of the original 63 markers. Nevertheless, annual monitoring efforts based on sequential marker and reference population expansions is likely to provide insight into how environmental conditions are changing and how populations are reacting on a genetic level (i.e. changing allele frequencies). For example, the addition of markers that can differentiate summer and winter-run *O. mykiss* will increase the confidence of determining an individual's run timing phenotype regardless of origin. In our current analyses these markers were undoubtedly valuable and informative. Pilot studies are currently underway to assess the utility of the specific group of run type markers (comprised of GREB1 and Chromosome28 loci) for management application. These include an effort between the Confederated Tribes of the Warm Springs Reservation, Oregon Department of Fish and Wildlife, and CRIFTC to conduct in-season screening of fish returning to Hood River for the purpose of collecting winter-run broodstock fish. This location is unique in that Hood River supports both a natural spawning summer-run and winter-run populations. Results to-date suggest a high degree of accuracy in differentiating between phenotypes in Hood River such that the multilocus genotypic data used to identify specific summer-run and winter-run genotypes may be sufficient to evaluate larger geographic regions (e.g. reporting groups within our larger GSI baseline).

Over the course of the 10 year genetic assessment project we have compiled extensive data sets of SNP genotypes for Chinook Salmon steelhead trout and *O. nerka*, and to a lesser degree for Coho Salmon and Pacific Lamprey. The populations we have evaluated span diverse regions in the Columbia River Basin (including the Snake River Basin). In some years our directed efforts are focused on one or a few particular species. Although we did not address expansions for Sockeye Salmon or Chinook Salmon in the 2018 project year, we continue to update and maintain SNP reference baselines for evaluation of these species in future generations. This long-term strategy informs harvest management and assures the greatest likelihood of discerning temporal variation among reproductively distinct species aggregates (Waples 1991), while monitoring population viability related to demographic trends that occur locally and/or regionally. Philopatry (Quinn *et al.* 1991, Hendry *et al.* 2003) and hatchery supplementation activities (Ford *et al.* 2006; Hard & Heard 1999) play a major role in how genetic divergence and differentiation is distributed geographically. For managing sustainable fisheries, it is necessary to understand the magnitude of influence that these and other factors have on our ability to differentiate populations, both qualitatively (phenotypes; landscapes) and quantitatively (e.g., genetic stock identification). This becomes particularly important where mixed stock fisheries may consist of both ESA listed and unlisted populations, and where differential harvest may have the greatest impact on specific populations. Our current efforts have largely focused on expanding numbers of markers and non-neutral markers associated with maturation. However, loci for adaptive divergence (landscape genetics) remains as one of our primary objectives for strengthening our understanding of non-neutral genetic variation among

populations. Data collected through RAD sequencing and GT-seq techniques has yield tens of thousands of potential SNPs, and demonstrated their utility for characterizing adaptive variation, and identifying environmental and life history related variables that are likely to have significant influence on allele frequencies (e.g., precipitation, temperature, run-timing.; Hecht et al. 2015, Hess et al. 2016b; Micheletti et al. 2017). The expansion efforts reported here also provided improved ability to differentiate stocks on regional and local scales through application of GSI and PBT methods. The continued expansion of SNP panels and updating of baseline that include a more geographically broad set of collections/populations is imperative, and will help us achieve a greater level of resolution in such applications as GSI (e.g. the MGILCS reporting group).

Collections of *O. tshawytscha*, *O. mykiss*, and *O. nerka* have been chosen for baseline expansion based on availability, novelty, and in accordance with our goal of reaching complete coverage of extant stocks within the Columbia River Basin. Priority collections for all three species have been identified as those important to basin-wide harvest and hatchery management, particularly in tribal fisheries. This includes major supplementation stocks for all three species: lower Columbia, ocean-type, and stream-type lineages of Chinook Salmon, inland and coastal lineages and summer-run and winter-run ecotypes of steelhead trout, and the anadromous (Sockeye Salmon) and land-locked (kokanee) forms of *O. nerka*. Species-specific reference baselines may include life history variants such as potentially distinct populations of resident *O. mykiss* (Narum et al. 2008a; Narum et al. 2011). The application of GSI in fisheries continues to inform managers on several fronts, including: harvest management, abundance estimates, life history distinctions and conservation needs. Moreover, PBT is being used for multiple purposes including validation of assigned origins using GSI. In fact, PBT frequently reveals substantial numbers of unmarked hatchery-origin fish that are incorrectly identified as wild in the field. Future efforts for baseline expansion include compiling marker “banks” that can be drawn from at any time should the need for more markers be necessary. An example of such need is basin-wide coverage to account for stock transfers or reintroductions throughout the basin (e.g., *O. nerka* in Cle Elum Lake).

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Appendix 1. Populations represented in the expanded GT-seq SNP panel for steelhead trout.

pop	subbasin	location	latitude	longitude	origin	(n)
<u>Coastal Lineage</u>						
Grays	Grays	Gray R.	46.2121	-123.3634	NOR	31
Elochoman	Elochoman	Elochoman R.	46.2267	-123.3304	NOR	42
Mill	Elochoman	Mill Cr.	46.1885	-123.1773	NOR	29
Abernathy	Elochoman	AFTC weir	46.2256	-123.1481	NOR	65
Germany	Elochoman	Germany Cr.	46.1901	-123.1238	NOR	34
Cowlitz	Cowlitz	Cowlitz R. at Barrier Dam	46.5026	-122.5881	NOR	91
Kalama (SUM)	Kalama	Kalama R.	46.0329	-122.8703	NOR	38
Kalama (WIN)	Kalama	Kalama R.	46.0329	-122.8703	NOR	36
Lewis	Lewis	North Fork Lewis @ Merwin Dam	45.9568	-122.5551	NOR	76
Eagle Clackamas (SUM)	Willamette	Clackamas R. - Eagle Cr.	45.3514	-122.3840	NOR	25
Clackamas (WIN)	Willamette	Clackamas R. - North Fork Dam	45.2417	-122.2817	HAT	25
	Willamette	Clackamas R. - Eagle Cr.	45.3514	-122.3840	NOR	22
	Willamette	Clackamas R. - Timber Park	45.2994	-122.3506	NOR	170
	Willamette	Columbia R. - mainstem	45.3724	-122.6044	NOR	48
N. Santiam	Willamette	Rock Cr.	44.7467	-122.3953	NOR	20
S. Santiam	Willamette	Wiley Cr.	44.4150	-122.6739	NOR	45
Sandy	Sandy	Still Cr.	45.3309	-121.9158	NOR	12
Washougal	Washougal	Washougal R.	45.3909	-122.0960	NOR	38
BWS Rattlesnake	Big White Salmon	Rattlesnake Cr.	45.7993	-121.4843	NOR	82
	Big White Salmon	BWS screw trap	45.7476	-121.5211	NOR	30
BWS mainstem	Big White Salmon	mainstem (Dam6 relocation)	45.7993	-121.4843	NOR	24
	Big White Salmon	BWS screw trap	45.7476	-121.5211	NOR	9
Skamania	Washougal	Skamania Hatchery	45.6227	-122.2175	HAT	40
<u>Inland Lineage</u>						
Fifteenmile	Fifteenmile	Fifteenmile Cr.	45.4509	-121.1244	NOR	85
Deschutes	Deschutes	Deschutes R. - Trout Cr.	44.8214	-121.0872	NOR	14
	Deschutes	Warm Springs R.	44.8609	-121.2444	NOR	82
	Deschutes	Warm Springs R. - Mill Cr.	44.8647	-121.4222	NOR	135
Klickitat	Klickitat	Dillacort Cr.	45.7414	-121.2222	NOR	24
	Klickitat	Wheeler Cr.	45.7951	-121.1928	NOR	4
	Klickitat	Swale Cr.	45.8091	-121.0652	NOR	87
	Klickitat	Snyder Cr.	45.8247	-121.1565	NOR	101
	Klickitat	Little Klickitat R.	45.8271	-120.8181	NOR	81
	Klickitat	Bowman Cr.	45.8452	-121.0421	NOR	84
	Klickitat	Dead Canyon	45.9423	-121.1439	NOR	34
	Klickitat	Summit Cr.	45.9876	-121.1255	NOR	36
	Klickitat	White Cr.	46.0133	-121.1500	NOR	31
	Klickitat	Trout Cr.	46.0378	-121.1994	NOR	125
JohnDay	John Day	Beech Cr.	44.4113	-119.1160	NOR	29
	John Day	Black Canyon Cr.	44.3314	-119.5657	NOR	35
	John Day	Murderer's Cr.	44.3173	-119.5310	NOR	18
	John Day	Deer Cr.	44.1890	-119.5139	NOR	21
	John Day	Middle Fork John Day	44.9129	-119.2964	NOR	6
	John Day	Fox Cr.	44.6156	-119.2941	NOR	9
	John Day	Belshaw Cr.	44.4370	-119.2930	NOR	7
	John Day	Desolation Cr.	44.9397	-118.8379	NOR	5
	John Day	Camp Cr.	44.6891	-118.7966	NOR	15
	John Day	Clear Cr.	44.5888	-118.5068	NOR	15
	John Day	Granite Cr.	44.8383	-118.4770	NOR	9
Umatilla	Umatilla	Iskuulpa Cr.	45.6994	-118.3965	HAT	144
Ahtanum	Yakima	Ahtanum R.	46.5318	-120.6815	NOR	56
Cowiche	Yakima	Cowiche Cr.	46.6288	-120.5708	NOR	68
Naches	Yakima	Little Rattlesnake Cr.	46.7680	-121.0464	NOR	69
	Yakima	N.F. Little Naches R.	47.1090	-121.3201	NOR	58
	Yakima	Pile Up Cr.	46.3274	-121.1537	NOR	5
	Yakima	Nile Cr.	46.8618	-121.0489	NOR	90

	Yakima	Quartz Cr.	45.9457	-120.5097	NOR	88
Satus	Yakima	Dry Cr.	46.1929	-120.6138	NOR	50
	Yakima	Satus Cr.	46.0432	-120.5716	NOR	385
Toppenish	Yakima	Toppenish Cr.	46.3227	-120.8749	NOR	111
Wenatchee	Wenatchee	Levenworth NFH	47.5591	-120.6742	HAT	10
	Wenatchee	Nason Cr.	47.8019	-120.7150	NOR	19
	Wenatchee	Wells Hatchery (LNFH Stock)	47.5591	-120.6742	HAT	11
Methow	Methow	Methow R.	48.0495	-119.9012	NOR/HAT	73
Entiat	Entiat	Entiat R. - screw trap	47.6641	-120.2417	NOR	43
Omak	Okanogan	Omak Cr. Adult Weir	48.3957	-119.5043	NOR	115
Touchet	Walla Walla	Touchet R.	46.0340	-118.6836	NOR	57
Dworshak	Clearwater	Dworshak National Fish Hatchery	46.5025	-116.3205	HAT	100
Lochsa	Clearwater	Fish Cr.	46.3316	-115.3461	NOR	100
S. F. Clearwater	Clearwater	South Fork Clearwater R.	46.5061	-116.5491	NOR	11
Catherine	Grande Ronde	Catherine Cr.	45.3070	-117.8660	NOR	228
Joseph	Grande Ronde	Joseph Cr.	46.0416	-117.0017	NOR	45
UpperGR	Grande Ronde	Upper Grande Ronde Adult Trap	45.7314	-117.8640	NOR	42
Wenaha	Grande Ronde	Wenaha R.	45.9453	-117.4513	NOR	77
Lightning	Imnaha	Lightning Cr. Weir	45.6554	-116.7265	NOR	72
Rapid	Salmon	Little Salmon R. - Rapid R.	45.3547	-116.3915	NOR	100
N. F. Salmon	Salmon	North Fork Salmon R.	45.4099	-113.9919	NOR	100
Pahsimeroi	Salmon	Pahsimeroi Fish Hatchery	44.6845	-114.0404	HAT	100
total						4549

Note: Each locality is identified by the lineage, subbasin- specific location (e.g. tributary) with geographic coordinates, origin, and sample size (n).

Appendix 2. Chinook Salmon hatchery broodstock sampled for PBT baselines.

									2018 genotyping
Map ID	Spawning hatchery	Run type	Lineage	Region	Latitude	Longitude	Year	Sampled	Completed
1	Klaskanine (NF brood)	fall (tule)	LC	Col.	46.09000	-123.71800	na	na	na
	Klaskanine (SF brood)	fall (tule)	LC	Col.	46.09000	-123.71800	na	na	na
	Big Creek	fall (tule)	LC	Col.	46.14616	-123.58102	2015	2017	1884
	Cowlitz Salmon	fall (tule)	LC	Col.	46.51145	-122.62935	2015	2015-2016	3578
	Cowlitz Salmon	spring	LC	Col.	46.51145	-122.62935	2015	2015-2016	2495
	Toutle	fall (tule)	LC	Col.	46.37464	-122.57200	2015	2015-2016	1465
	Kalama Falls	fall (tule)	LC	Col.	46.01624	-122.73284	2016	2016	3257
	Kalama Falls	spring	LC	Col.	46.01624	-122.73284	2015	2015-2016	743
	Lewis River	spring	LC	Col.	45.98849	-122.40618	2015	2015-2016	831
	Clackamas	spring	LC	Col.	45.29600	-122.36200	na	na	na
	Marion Forks	spring	LC	Col.	44.61200	-121.94800	na	na	na
	South Santiam	spring	LC	Col.	44.41600	-122.67500	na	na	na
	McKenzie	spring	LC	Col.	44.11800	-122.63700	na	na	na
	Willamette	spring	LC	Col.	43.74500	-122.44400	na	na	na
	Washougal	fall (tule)	LC	Col.	45.65344	-122.16910	2015	2015-2016	4019
11	Bonneville, Tanner Cr.	fall (tule)	LC	Col.	45.63300	-121.95700	na	na	na
	Spring Creek NFH	fall (tule)	LC	Col.	45.72779	-121.54529	2015	2017	4240
9	Little White Salmon NFH	fall	IOT	Col.	45.72226	-121.64010	2013	2017	5474
15	Umatilla	fall	IOT	Col.	45.88172	-119.32256	2012	2017	*
18	Prosser	fall	IOT	Col.	46.21512	-119.75962	2012	2017	189
19	Ringold Springs	fall	IOT	Col.	46.51401	-119.25926	2016	2017	1641
20	Priest Rapids	fall	IOT	Col.	46.64728	-119.89895	2012	2017	5121
29	Lyons Ferry	fall	IOT	Snake	46.59725	-118.22823	2011	2017	581
30	Nez Perce Tribal	fall	IOT	Snake	46.51954	-116.66010	2011	2017	797
23	Eastbank	summer	IOT	Col.	47.53367	-120.28911	2012	2016-2017	1407
24	Entiat NFH	summer	IOT	Col.	47.69806	-120.32310	2013	2017	299
25	Wells	summer	IOT	Col.	47.94582	-119.87115	2012	2017	566
26	Chief Joseph	summer	IOT	Col.	48.00060	-119.64510	2013	2017	756
9	Little White Salmon NFH	spring	IST	Col.	45.72226	-121.64010	2013	2017	576
15	Umatilla	spring	IST	Col.	45.88172	-119.32256	2012	2017	511
29	Lyons Ferry	spring	IST	Snake	46.59725	-118.22823	2008	2017	IDFG
30	Nez Perce Tribal	spring	IST	Snake	46.51954	-116.66010	2008	2017	428
23	Eastbank	spring	IST	Col.	47.53367	-120.28911	2012	2016-2017	604
26	Chief Joseph	spring	IST	Col.	48.00060	-119.64510	2014	2017	545
8	Carson NFH	spring	IST	Col.	45.86826	-121.97417	2012	2017	1001
10	Parkdale	spring	IST	Col.	45.52439	-121.62157	2012	2017	185
12	Klickitat	spring	IST	Col.	46.04236	-121.18232	2008	2017	491
13	Warm Springs NFH	spring	IST	Col.	44.86201	-121.24503	2012	2017	748
14	Round Butte	spring	IST	Col.	44.60503	-121.27784	2012	2017	904
21	Cle Elum SRF	spring	IST	Col.	47.18679	-120.97618	2012	2017	522
22	Leavenworth NFH	spring	IST	Col.	47.55842	-120.67383	2013	2017	802
27	Methow	spring	IST	Col.	48.47703	-120.20513	2012	2017	145
28	Winthrop NFH	spring	IST	Col.	48.47366	-120.18910	2013	2017	426
33	Lookingglass	spring	IST	Snake	45.73136	-117.86397	2008	2017	693
31	Dworshak NFH	spring	IST	Snake	46.50206	-116.32324	2008	2017	IDFG
32	Clearwater	spring	IST	Snake	46.50429	-116.32773	2008	2017	IDFG
36	Rapid River	spring/summer	IST	Snake	45.35411	-116.39381	2008	2017	2727
38	SF Salmon, McCall	spring/summer	IST	Snake	44.65554	-115.70245	2008	2017	IDFG
40	Pahsimeroi	spring/summer	IST	Snake	44.62284	-113.98627	2008	2017	IDFG
39	Sawtooth	spring/summer	IST	Snake	44.15174	-114.88429	2008	2017	IDFG

* In 2017 adult broodstock for Umatilla were collected/spawned at Ringold Springs.
Note: The Map ID indicates the sites of the hatcheries corresponding to Figure 17. Genetic lineage is lower Col. (LC), interior ocean-type (IOT), and interior stream-type (IST). Year refers to the first year of PBT sampling for each hatchery: na – not currently a PBT hatchery. For some hatchery PBT samples, genotyping efforts have begun to backdate collections that were initially archived- the “sampled” field indicates which collection years were genotyped in 2018. The project collaborators at Idaho Department of Fish and Game (IDFG) were responsible for genotyping of Snake River hatcheries (see “completed” column).

Appendix 3. Steelhead and Coho Salmon hatchery broodstock sampled for PBT baselines.

Map ID	Spawning hatchery	Run type	Lineage	Region	Latitude	Longitude	Year	2018 Genotyping	
								Sampled	Completed
Steelhead									
1	Big Creek	winter	coastal	Col.	46.14616	-123.58102	na	na	na
	Abernathy FTC	winter	coastal	Col.	46.22600	-123.15300	2012	archived	0
	Cowlitz Trout	winter	coastal	Col.	46.48769	-122.72702	na	na	na
4	Kalama Falls	winter	coastal	Col.	46.01624	-122.73284	na	na	na
	Merwin	winter	coastal	Col.	45.95400	-122.56400	na	na	na
	Clackamas	winter	coastal	Col.	45.29600	-122.36200	na	na	na
	Eagle Creek NFH	winter	coastal	Col.	45.27600	-122.20200	na	na	na
	Sandy	winter	coastal	Col.	45.40700	-122.25400	na	na	na
7	Skamania	summer/winter	coastal	Col.	45.62179	-122.21734	2013	2017	393
10	Parkdale	winter	coastal	Col.	45.52439	-121.62157	2012	2017	47
14	Round Butte	summer	inland	Col.	44.60503	-121.27784	2013	2017	992
	Umatilla	summer	inland	Col.	45.91300	-119.55200	2012	2017	75
23	Eastbank	summer	inland	Col.	47.53367	-120.28911	2012	2016-2017	232
25	Wells	summer	inland	Col.	47.94582	-119.87115	2013	2017	156
27	Methow (Twisp)	summer	inland	Col.	48.47703	-120.20513	2013	2017	na*
28	Winthrop NFH	summer	inland	Col.	48.47366	-120.18910	2012	2017	106
29	Lyons Ferry	summer	inland	Snake	46.59725	-118.22823	2009	2017	IDFG
34	Wallowa	summer	inland	Snake	45.41778	-117.30042	2009	2017	471
37	Oxbow	summer	inland	Snake	44.97272	-116.85475	2008	2017	IDFG
31	Dworshak NFH	summer	inland	Snake	46.50206	-116.32324	2008	2017	1626
40	Pahsimeroi	summer	inland	Snake	44.62284	-113.98627	2008	2017	IDFG
39	Sawtooth	summer	inland	Snake	44.15174	-114.88429	2008	2017	IDFG
35	Little Sheep Creek	summer	inland	Snake	45.47769	-116.93059	2008	2017	134
Coho									
	Umatilla	na	na	Col.	45.91300	-119.55200	2012	2015-2017	1939
18	Prosser	na	na	Col.	46.21512	-119.75962	2016	2016-2017	1172
22	Leavenworth NFH	na	na	Col.	47.55842	-120.67383	2012	2015-2018	2152
28	Winthrop NFH	na	na	Col.	48.47366	-120.18910	2012	2015-2018	2153
31	Dworshak NFH	na	na	Snake	46.50206	-116.32324	2012	2015-2017	3690

* Steelhead Methow Hatchery Twisp stock spawned at Winthrop NFH starting in 2017; not distinguished from Winthrop stock.

Note: The map ID indicates site locations corresponding with Figure 17. Genetic lineage is coastal or inland. Year refers to the first year of PBT sampling for each hatchery: na – not currently a PBT hatchery. Some 2017 PBT samples have been archived awaiting shipment to the Hagerman Genetics Laboratory as of the

drafting of this report. The project collaborators at Idaho Department of Fish and Game (IDFG) were responsible for genotyping of Snake River hatcheries (see “completed” column). All Coho broodstocks sampled for PBT broodstock were designated for release of fish upstream of Bonneville Dam.

Appendix 4. Checklist of PBT broodstock collections that comprise the PBT baselines for Chinook salmon from 2008 through 2017.

Map num.	Hatchery	Species	Code	Run type	Lineage	Year									
						2008	2009	2010	2011	2012	2013	2014	2015	2016	2017
32	Clearwater Fish Hatchery	Chinook	OtsCLWH	Spring	Interior stream type	X	X	X	X	X	X	X	X	X	X
32	Clearwater Fish Hatchery - Powell Facility	Chinook	OtsPOWP	Spring	Interior stream type	X	X	X	X	X	X	X	X	X	
31	Dworshak National Fish Hatchery	Chinook	OtsDWOR	Spring	Interior stream type	X	X	X	X	X	X	X	X	X	
33	Lookingglass Fish Hatchery - Catherine Creek	Chinook	OtsCTHW	Spring/Summer	Interior stream type	X	X	X	X	X	X	X	X	X	X
33	Lookingglass Fish Hatchery - Grande Ronde	Chinook	OtsGRUW	Spring	Interior stream type	X	X	X	X	X	X	X	X	X	X
33	Lookingglass Fish Hatchery - Imnaha River	Chinook	OtsIMNW	Spring/Summer	Interior stream type	X	X	X	X	X	X	X	X	X	X
33	Lookingglass Fish Hatchery - Lookingglass Creek	Chinook	OtsLOOK	Spring	Interior stream type	X	X	X	X	X	X	X	X	X	X
33	Lookingglass Fish Hatchery - Lostine River	Chinook	OtsLSTW	Spring	Interior stream type	X	X	X	X	X	X	X	X	X	X
29	Lyons Ferry Fish Hatchery	Chinook	OtsLYON	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X
29	Lyons Ferry Fish Hatchery - Tucannon River	Chinook	OtsTUCW a	Spring	Interior stream type	X	X	X	X	X	X	X	X	X	X
29	Lyons Ferry Fish Hatchery	Chinook	OtsLYON 1	Fall	Interior ocean type	*	*	*	X	X	X	X	X	X	X
38	McCall Fish Hatchery - Johnson Creek	Chinook	OtsJHNW	Spring/Summer	Interior stream type	X	X	X	X	X	X	X	X	X	X
38	McCall Fish Hatchery - South Fork Salmon	Chinook	OtsMCCA	Spring	Interior stream type	X	X	X	X	X	X	X	X	X	X
30	Nez Perce Tribal Fish Hatchery (Fall)	Chinook	OtsNPFH 1	Fall	Interior ocean type	*	*	*	X	X	X	X	X	X	X
30	Nez Perce Tribal Fish Hatchery (Spring)	Chinook	OtsNPFH	Spring	Interior stream type	X	X	X	X	X	X	X	X	X	X
40	Pahsimeroi Fish Hatchery	Chinook	OtsPAHH	Spring	Interior stream type	X	X	X	X	X	X	X	X	X	X
36	Rapid River Fish Hatchery	Chinook	OtsRAPH	Spring	Interior stream type	X	X	X	X	X	X	X	X	X	X
39	Sawtooth Fish Hatchery	Chinook	OtsSAWT	Spring	Interior stream type	X	X	X	X	X	X	X	X	X	X
1	Big Creek Hatchery	Chinook	OtsBIG Tule	Fall	Lower Columbia	*	*	*	*	*	*	*	X	X	X
8	Carson National Fish Hatchery	Chinook	OtsCAR	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X
26	Chief Joseph Hatchery (Spring)	Chinook	OtsCJH sp	Spring	Interior stream type	*	*	*	*	*	*	X	X	X	X
26	Chief Joseph Hatchery (Summer/Fall) - Integrated	Chinook	OtsCJHint sufa	Summer	Interior ocean type	*	*	*	*	*	X	X	X	X	X
26	Chief Joseph Hatchery (Summer/Fall) - Segregated	Chinook	OtsCJHseg sufa	Summer	Interior ocean type	*	*	*	*	*	X	X	X	X	X
2	Cowlitz Salmon	Chinook	OtsCOW sp	Spring	Interior stream type	*	*	*	*	*	*	*	X	X	**
2	Cowlitz Salmon	Chinook	OtsCOW sufa	Fall	Interior stream type	*	*	*	*	*	*	*	X	X	**
23	Eastbank Fish Hatchery (Spring)	Chinook	OtsEASTBK sp	Spring	Interior stream type	*	*	*	*	*	X	X	X	X	X
23	Eastbank Fish Hatchery (Summer)	Chinook	OtsEASTBK su	Summer	Interior ocean type	*	*	*	*	X	X	X	X	X	X
24	Entiat National Fish Hatchery	Chinook	OtsENFH	Summer	Interior ocean type	*	*	*	*	*	X	X	X	X	X
4	Kalama Falls	Chinook	OtsKAL sp	Spring	Interior stream type	*	*	*	*	*	*	*	X	X	**
4	Kalama Falls	Chinook	OtsKAL sufa	Fall	Interior stream type	*	*	*	*	*	*	*	**	X	**
12	Klickitat State Fish Hatchery	Chinook	OtsKH	Spring	Interior stream type	X	X	X	X	X	X	X	X	X	X
22	Leavenworth National Fish Hatchery	Chinook	OtsLNFH	Spring	Interior stream type	*	*	*	*	*	X	X	X	X	X
5	Speelyai Hatchery	Chinook	OtsLEW	Spring	Interior stream type	*	*	*	*	*	*	*	X	X	**
9	Little White Salmon National Fish Hatchery (Fall)	Chinook	OtsLWS sufa	Fall	Interior ocean type	*	*	*	*	*	X	X	X	X	X
9	Little White Salmon National Fish Hatchery (Spring)	Chinook	OtsLWS sp	Spring	Interior stream type	*	*	*	*	*	X	X	X	X	X
27	Methow State Fish Hatchery	Chinook	OtsMETH	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X
10	Parkdale Fish Facility	Chinook	OtsPFF	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X
20	Priest Rapids Hatchery	Chinook	OtsPRH	Fall	Interior ocean type	*	*	*	*	X	X	X	X	X	X
14	Round Butte Fish Hatchery	Chinook	OtsRB	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X
19	Ringold Springs State Hatchery	Chinook	OtsRGS	Fall	Interior ocean type	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	X	X
11	Spring Creek National Fish Hatchery	Chinook	OtsSPCR Tule	Fall	Lower Columbia	*	*	*	*	*	*	*	X	X	X
3	Toutle	Chinook	OtsTOU	Fall	Interior ocean type	*	*	*	*	*	*	*	X	X	**
15	Three mile dam, Umatilla River (Fall)	Chinook	OtsUMA sufa b	Fall	Interior ocean type	*	*	*	*	X	X	X	~	~	~
17	South Fork Walla Walla facility	Chinook	OtsUMA sp	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X
6	Washougal	Chinook	OtsWAS	Fall	Interior ocean type	*	*	*	*	*	*	*	X	X	**
13	Warm Springs National Fish Hatchery	Chinook	OtsWSNFH h	Spring	Interior stream type	*	*	*	*	X	X	X	~	~	~
25	Wells Fish Hatchery	Chinook	OtsWELLS	Summer	Interior ocean type	*	*	*	*	X	X	X	X	X	X
28	Winthrop National Fish Hatchery	Chinook	OtsWTP	Spring	Interior stream type	*	*	*	*	*	X	X	X	X	X
18	Yakima Nation Prosser Hatchery	Chinook	OtsPRO	Fall	Interior ocean type	*	*	*	*	X	X	*	X	X	X
21	Levi George/Cle Elum (Integrated)	Chinook	OtsYRint	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X
21	Levi George/Cle Elum (Segregated)	Chinook	OtsYRseg	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X

Note: Species-specific collections code along with run type and genetic lineage are provided for both species. Map numbers correspond with

- Figure 17.
- X

Chinook tissues genotyped using 298 SNPs
- X

Chinook tissues genotyped using 96 SNPs
- Chinook broodstock sampled, spawned at another hatchery and genotyped using 298 SNPs
- a

Chinook Lyons Ferry stock consolidated under 'OtsLYON' starting in 2012
- b

Chinook Umatilla fall stock spawned at Little White Salmon Hatchery in 2015 & 2016; not distinguished from LWS stock. Broodstock collected/spawned at Ringold Springs in 2017; not distinguished from Ringold stock.
- h

Chinook Warm Springs NFH spring stock spawned at Little White Salmon Hatchery starting in 2015-2017.
- N/A

Stock discontinued/non-existent
- *

Broodstock not sampled
- **

Broodstock sampled, tissues archived until funding identified for processing

Appendix 5. Checklist of PBT broodstock collections that comprise the PBT baselines for steelhead from 2008 through 2018.

Map num.	Hatchery	Species	Code	Run type	Lineage	Year											
						2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	
31	Dworshak National Fish Hatchery	Steelhead	OmyDWOR	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	
35	Little Sheep Creek Hatchery	Steelhead	OmyLSCR	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	
29	Lyons Ferry Fish Hatchery- Touchet	Steelhead	OmyTOUW c	Summer	Interior	*	X	X	X	X	X	X	X	X	X	X	
29	Lyons Ferry Fish Hatchery	Steelhead	OmyLYON d	Summer	Interior	*	X	X	X	X	N/A	N/A	N/A	N/A	N/A	N/A	
29	Lyons Ferry Fish Hatchery - Grande Ronde	Steelhead	OmyCGRW c	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	
29	Lyons Ferry Fish Hatchery - Tucannon	Steelhead	OmyTUCW c	Summer	Interior	*	X	X	X	X	X	X	X	X	X	X	
29	Lyons Ferry Fish Hatchery - Wallowa	Steelhead	OmyWALW	Summer	Interior	N/A	N/A	N/A	N/A	N/A	N/A	N/A	X	N/A	N/A	N/A	
37	Oxbow	Steelhead	OmyOXBO	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	
39	Sawtooth Fish Hatchery	Steelhead	OmySAWT	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	
39	Sawtooth Fish Hatchery - East Fork Salmon	Steelhead	OmyEFSW e	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	
39	Sawtooth Fish Hatchery - Squaw Creek	Steelhead	OmySQUW f	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	
40	Pahsimeroi Fish Hatchery	Steelhead	OmyPAHH	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	
34	Wallowa Fish Hatchery	Steelhead	OmyWALL	Summer	Interior	*	X	X	X	X	X	X	X	X	X	X	
23	Eastbank Hatchery	Steelhead	OmyEASTBK	Summer	Interior	*	*	*	*	X	X	X	X	X	X		
27	Methow Hatchery (Twisp)	Steelhead	OmyTWP i	Summer	Interior	*	*	*	*	*	X	X	X	X	~		
10	Parkdale Fish Facility	Steelhead	OmyPFF	Winter	Coastal	*	*	*	*	X	X	X	X	X	X		
14	Round Butte Fish Hatchery	Steelhead	OmyRB	Summer	Interior	*	*	*	*	*	X	X	X	X	X		
7	Skamania Hatchery (Summer)	Steelhead	OmySKH su g	Summer	Coastal	*	*	*	*	*	X	X	X	X	X		
7	Skamania Hatchery (Winter)	Steelhead	OmySKH wi g	Winter	Coastal	*	*	*	*	*	X	X	X	X	X		
16	Minthorn Springs	Steelhead	OmyUMA	Summer	Interior	*	*	*	*	X	X	X	X	X	X		
25	Wells Hatchery - On Station	Steelhead	Omy WEL	Summer	Interior	*	*	*	*	*	X	X	X	X	X		
25	Wells Hatchery - Okanogan stock	Steelhead	OmyWEL OKA	Summer	Interior	*	*	*	*	*	X	X	X	X	X		
25	Wells Hatchery - Omak stock	Steelhead	OmyWEL OMA	Summer	Interior	*	*	*	*	*	X	X	X	X	X		
25	Wells Hatchery - Methow stock	Steelhead	OmyWEL MET	Summer	Interior	*	*	*	*	*	X	X	X	X	X		
28	Winthrop National Fish Hatchery	Steelhead	OmyWTP	Summer	Interior	*	*	*	*	X	X	X	X	X	X		

Note map numbers correspond to sites in

Figure 17.

- XSteelhead tissues genotyped using 96 SNPs
- XSteelhead tissues genotyped using 379 SNPs
- XSteelhead tissues genotyped using 269 SNPs
- XSteelhead tissues genotyped using 192 SNPs
- XSteelhead tissues genotyped using 390 SNPs
- XSteelhead broodstock sampled, spawned at another hatchery and genotyped using 379 SNPs
- cSteelhead Lyons Ferry stock consolidated under 'OmyLYON' starting in 2012
- dSteelhead Lyons Ferry stock discontinued starting in 2013
- eSteelhead Sawtooth stock consolidated under 'OmySAWT' from 2012-2013
- fSteelhead Sawtooth stock consolidated under 'OmySAWT' in 2012; renamed 'Upper Salmon B-run' (YFLW) and consolidated under 'OmyPAHH' starting in 2013; spawned at Yankee Fork Weir by Shoshone-Bannock tribe beginning in 2017
- gSteelhead Skamania stock is collected late in calendar year, and is designated for the following broodyear (i.e., late 2012 collections are part of BY2013). Skamania winter Steelhead stock changed from Chambers Creek stock to Big Creek stock starting with SY2018.
- iSteelhead Methow Hatchery Twisp stock spawned at Winthrop NFH starting in 2017; not distiguished from Withrop stock
- N/AStock discontinued/non-existent
- *Broodstock not sampled
- **Broodstock sampled, tissues archived until funding identified for processing

Appendix 6. Checklist of PBT broodstock collections that comprise the PBT baselines for Coho Salmon from 2008 through 2017.

Map num.	Hatchery	Species	Code	Run type	Lineage	Year									
						2008	2009	2010	2011	2012	2013	2014	2015	2016	2017
15	Three mile dam, Umatilla River	Coho	OkiUMA	Fall	Lower Columbia								X	X	X
22	Leavenworth National Fish Hatchery	Coho	OkiLNFH	Fall	Lower Columbia				X	X	X	X	X	X	X
30	Nez Perce Tribal Fish Hatchery	Coho	OkiNPT	Fall	Lower Columbia						*	*	X	X	X
18	Yakima Nation Prosser Hatchery	Coho	OkiPRO	Fall	Lower Columbia									X	X
28	Winthrop National Fish Hatchery	Coho	OkiWTP, OkiMET	Fall	Lower Columbia					X	X	X	X	X	X
33	Lookingglass Fish Hatchery - Lostine River	Coho	OkiLSTW	Fall	Lower Columbia										

Note: map numbers correspond to sites in

Figure 17.

- XCoho tissues genotyped at 257 loci
- *Samples received, but not genotype.

Section 3: Genetic Stock Identification of Chinook Salmon, Sockeye Salmon, and Steelhead Harvest Mixtures in the Mainstem Columbia River

Introduction

Genetic Stock Identification (GSI) methods have proven to be effective in determining the proportion of stock origin in mixed stock applications of salmonids (Shaklee et al. 1999, Winans et al. 2004, Beacham et al. 2006, and Beacham et al. 2011). These methods have been demonstrated to be useful even at relatively fine geographic scales within the Columbia River Basin (CRB) (Hess et al. 2011, Hess and Narum 2011, Hess et al. 2014). Within the CRB, Chinook salmon consist of three major genetic lineages and steelhead consist of two major genetic lineages that can be further divided into populations that are genetically structured on a finer spatial scale (e.g., Waples et al. 2004; Narum et al. 2010; Blankenship et al. 2011). In this study, we used separate groups of SNP markers to discriminate 19 reporting groups for Chinook salmon, 14 reporting groups for steelhead, and four reporting groups for sockeye salmon.

Despite continuous improvements of the power of our Chinook salmon and steelhead baselines in GSI applications (Hess et al. 2014), we have determined that further improvement in the detail of data and accuracy of stock assignments could be made by utilizing a recently developed genetic technology (i.e., parentage based tagging (PBT)), in combination with GSI, in a tiered approach for stock identification (Hess et al. 2016). PBT is an efficient approach for mass tagging of fish. The method is carried out by first genotyping a set of potential parents which then provides the opportunity to assign a set of genotyped offspring to their true parent pair. PBT is currently being utilized on a broad scale in the Columbia River Basin, and was recently (i.e., 2012-present) expanded beyond Snake River hatcheries (Steele et al. 2011) to tag all Chinook salmon and steelhead hatchery broodstock from hatcheries in the CRB above Bonneville Dam. This application has effectively tagged all Snake River hatchery Chinook salmon and steelhead starting with the 2008 brood years, and elsewhere in the CRB above Bonneville Dam beginning with the 2012 brood year. When parent pairs of hatchery fish are identified with PBT, we can provide accurate information including age of the fish and the source hatchery in which its parents were spawned (Steele et al. 2011). We use PBT in this harvest study to identify hatchery-origin fish, and then use GSI to estimate stock-of-origin of all other hatchery fish that were not assigned with PBT and for all natural-origin fish. For sockeye salmon, we rely solely on GSI to determine stock of origin since PBT is not necessary to identify stocks. For the 2017 Chinook harvest, multiple age classes (3-, 4-, and 5-year old fish) can be identified from Snake River stocks using PBT (Appendix 4).

We continue to employ the genotyping-in-thousands by sequencing (GT-seq) approach that has been developed in our laboratory (Campbell et al. 2015). This approach has increased the cost-effectiveness for genotyping moderate numbers of SNP loci (100s) for relatively large numbers of individuals (1000s), which allows us to run all SNP loci regardless of whether we

intend to use primarily PBT analyses or a combination of PBT and GSI. Thus, our projects now benefit from the additional data that comes from genotyping with all available markers (i.e., increased power for statistical assignment of individuals).

Fisheries conducted in the mainstem of the lower and middle Columbia River provide an important application of genetic stock analyses because the fish harvested consist of mixtures of stocks throughout the CRB. Further, mainstem Chinook salmon fisheries represent a majority of the CRB harvest of this species taken by the commercial, sport, and tribal fishermen. In order to help support sustainable fisheries, PBT and GSI can be used to address two primary questions: 1) how are Chinook salmon stocks temporally and spatially distributed in the mainstem Columbia River; and 2) how are these stocks temporally and spatially distributed in the harvests of fisheries.

Project objectives and higher-level harvest management questions

Our study had two primary objectives: 1) utilize a combination of PBT and GSI analyses to determine stock composition of Chinook salmon harvested in sport, commercial, and tribal fisheries in the mainstem Columbia River, and 2) utilize GSI to estimate stock composition of sockeye salmon harvested above and below Bonneville Dam in commercial, sport, and tribal fisheries. Results from these objectives were used to address:

Harvest RM&E: F&W Program Management Question: What are your in-river monitoring results and what are your estimates of stock composition and stock-specific abundance, escapement, catch, and age distribution?

Increasingly, we are tailoring our analyses to address specific questions that fisheries managers have presented to us. For example, in 2012 managers proposed extending the geographic boundary of one of the mark selective spring-run Chinook salmon sport fisheries above Bonneville Dam that occurs at the mouth of the Wind River. This extension created a larger “bubble” boundary at the mouth of the Wind River and was intended to increase Columbia River mainstem fishing access while maintaining targeted focus on Wind River spring-run Chinook salmon. For 2012-2016, we examined the stock composition of the Wind River sport harvest and provided context by comparing stock proportions among the various samples from other fisheries and Bonneville Dam that were analyzed that same year. The Wind River sport fishery was not sampled in 2017 and could not be included in analyses. We include in this report the 5th year of analysis of sockeye salmon fisheries in the Columbia River mainstem. Differences in relative abundance of the three main stocks (Okanagan, Wenatchee, and Snake) present challenges to managing lower river harvest, because of the desire to harvest the highly abundant Okanagan stock around the much less abundant Snake River stock and moderately abundant Wenatchee River stock. Stock composition estimates are expected to help determine how harvest is impacting these various stocks.

Time line for completion of objectives

Objectives will be ongoing and PBT/GSI results updated each year for harvest analyses of salmonids throughout the accords-funding. As new genetic techniques are developed they

will be applied to this project and results will be compared between years to determine the extent of improvements.

Our study was not designed to address the following question:

Harvest RM&E: F&W Program Management Question: Can selective fisheries targeting hatchery fish or healthy populations reduce impacts on ESA-listed populations?

Accuracy testing of PBT and GSI baselines

Prior to conducting analyses for fisheries harvest collections and mixture samples encountered at Bonneville Dam (Section 4), we assessed the accuracy of our PBT and GSI baselines in assigning Chinook salmon and steelhead to their hatchery brood or reporting group of origin (see Results section).

Methods

Methods for estimating stock composition are available at (<https://www.monitoringmethods.org/Protocol/Details/229>). The Monitoring Methods Protocol is entitled Snake River steelhead and Chinook salmon stock composition estimates (2010-026-00) v1.0.

Tissue collection of Chinook salmon and Sockeye salmon

Tissues were sampled from Chinook salmon in 2017 from a total of 8 different mixture sources: the spring-run seasons of the following fisheries: 1) lower river sport, 2) lower river test, and 3) Zone 6 tribal ceremonial, the summer management period harvests of the following fisheries: 4) lower river sport, and 5) Zone 6 tribal summer, and the fall-run harvest from 6) the lower river commercial, 7) lower river sport, and 8) Zone 6 tribal fall fishery. Tissues are also collected from steelhead, Chinook salmon, and sockeye salmon at Bonneville Dam for stock ID (see Section 4). Drano Lake samples from the spring sport fishery were not provided to us in 2017. While fisheries generally harvest jack sized Chinook salmon at low rates and do not have specific harvest limits on jacks, jacks do comprise part of the harvest and may be sampled if encountered. Jacks are sampled at the Bonneville AFF trap in the proportion that they are encountered in the sampling. Sampling restrictions at the AFF can result in biases in the size of fish sampled compared to the run at large. Harvest tissues were collected in coordination with existing monitoring programs led by Washington Department of Fish and Wildlife (WDFW) and Oregon Department of Fish and Wildlife (ODFW) and the Yakama Nation. The spring management period Chinook salmon fisheries were sampled below Bonneville Dam in the sport and test fishery and sampled above Bonneville Dam in Zone 6 as tribal ceremonial fishery (

Figure 18; Table 10). The summer management period fisheries were sampled below Bonneville Dam in the sport fishery, and above Bonneville Dam in the Zone 6 tribal commercial fishery. Due to limited funds, we analyzed a subset of samples obtained from the various fisheries sampled above and below Bonneville Dam. For all fisheries in which we had to

subsample the harvest, we selected fish randomly and with a balanced design across spatial regions.

Stock proportions were calculated for some groupings within each fishery source, such that stock proportions could be compared across geographic regions as well as adipose-clipped versus non-adipose-clipped categories for particular fisheries. We use the following four main geographic regions (

Figure 18): Region A corresponds to our grouping of pre-existing Oregon and Washington state sport fishing zones 1-4 (or commercial zones 4-5), Region B corresponds to our grouping of sport zones 5-10 (or commercial zones 1-3). Here, we do not discriminate between Region 01 and Region 02 in the Zone 6 fishery, because that information did not accompany the samples we received. These sets of groupings were established for this study in order to achieve balanced sampling for analysis of these fishery datasets, as well as to set an appropriate spatial scale of analysis to minimize variance of our estimates of stock proportions over temporal strata.

Non-tribal fisheries during the spring management period for Chinook salmon are mark-selective based on absence or presence of the adipose fin to distinguish hatchery fish from natural origin fish, respectively. These adipose markings make it possible to have a mark-selective sport and commercial fishery in which only fish with missing adipose fins (hatchery-origin) are legally retained. Fish with intact adipose fins that are caught in these fisheries are released, but mortality rates are unknown from these releases. In addition to sampling hatchery-origin fish from the mark selective commercial and sport fisheries, we were able to obtain samples from non-clipped hatchery and natural origin fish from Bonneville Dam and the tribal Zone 6 fishery above Bonneville Dam.

Tissues were sampled from sockeye salmon in 2017 from three fishery mixture sources: 1) lower river sport, 2) Bonneville Dam (see Section 4), and 3) the tribal fishery in Zone 6. All samples obtained from these fisheries were analyzed.

Molecular data

Methods for DNA extraction, DNA amplification, and genotyping of SNP assays using genotyping-in-thousands by sequencing (GT-seq) are available at (<https://www.monitoringresources.org/Document/Method/Details/5446>). Additional details regarding how 192 SNPs were reduced to 186 SNPs can be found in Hess et al. (2012, 2013). Subsequently, we have reduced our Chinook salmon GSI baseline from 186 SNPs to 179 SNPs, because we were unable to transition the full set of 186 SNPs to GT-seq protocols. These 179 SNP markers were used for GSI, and for PBT analyses, we used 93 of the SNPs. We used 364 SNP markers for GSI of sockeye mixtures.

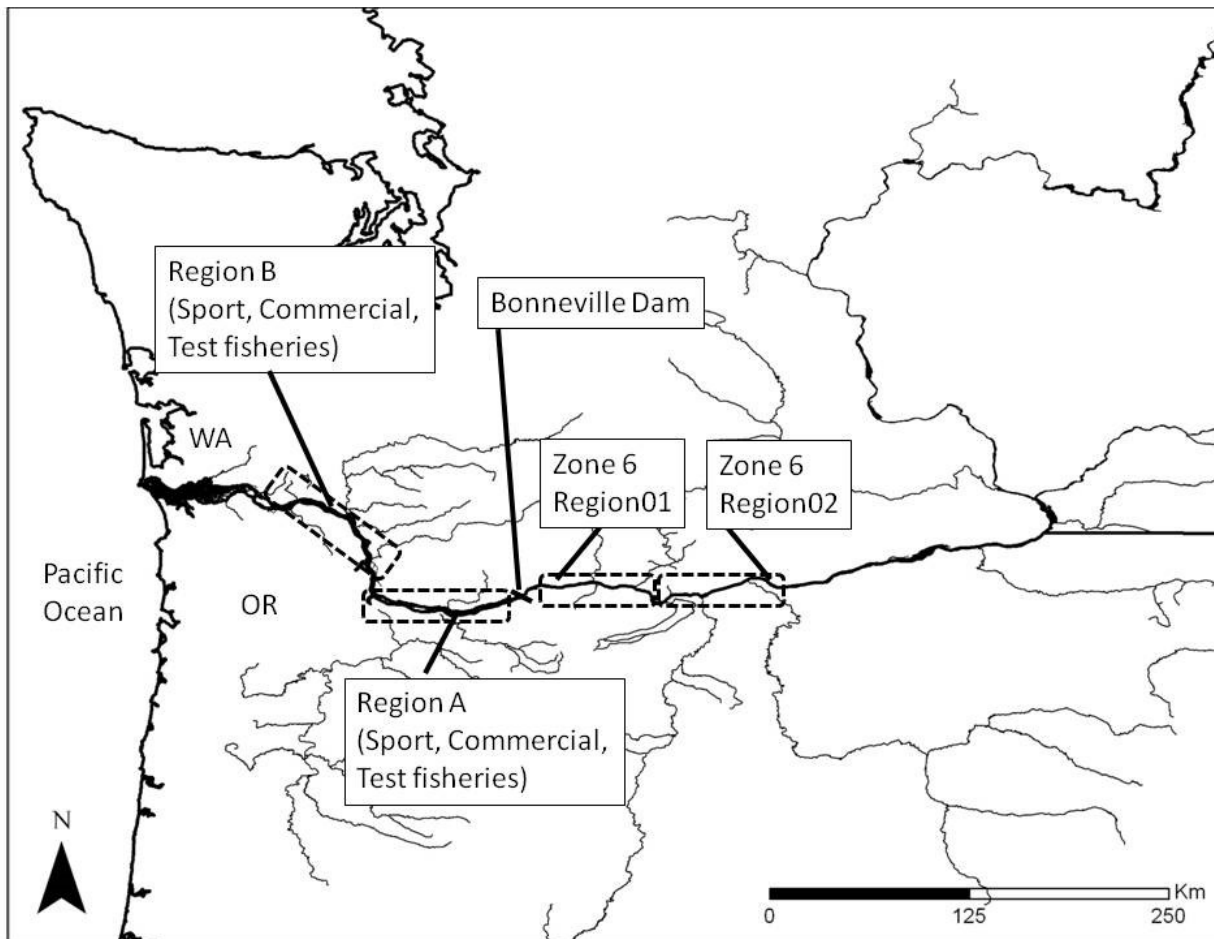


Figure 18. Project scope showing sources of Chinook salmon and sockeye salmon harvest mixtures that were analyzed using PBT/GSI.

GSI baselines for Chinook salmon, sockeye salmon, and steelhead

Chinook salmon GSI analyses were performed using the updated baseline referred to as “Columbia River Basin Chinook salmon GSI baseline version 3.1” and is available on the FishGen website (<https://www.fishgen.net>). This baseline consists of 61 collections that are delineated into the following 19 reporting groups: Columbia Rogue “01_YOUNGS”, West Cascade spring-run “02_WCASSP”, West Cascade fall-run “03_WCASFA”, Willamette River spring-run “04_WILLAM”, Spring Creek Group Tule fall-run “05_SPCRTU”, Klickitat River spring-run “06_KLICKR”, Deschutes River spring-run “07_DESCSP”, John Day River spring-run “08_JOHNDR”, Yakima River spring-run “09_YAKIMA”, upper Columbia River spring-run “10_UCOLSP”, Tucannon River spring-run “11_TUCANO”, Hells Canyon spring-run “12_HELLSC”, South Fork Salmon River spring-run “13_SFSALM”, Chamberlain Creek spring-run “14_CHMBLN”, Middle Fork Salmon River spring-run “15_MFSALM”, upper Salmon River spring-run “16_UPSALM”, Deschutes River fall-run “17_DESCFA”, upper Columbia River summer-/fall-run “18_UCOLSF”, and Snake River fall-run “19_SRFALL” (Table 13; Figure 19). Reporting groups were primarily determined by the relative genetic similarity among populations according to a phylogenetic analysis, and our previous results demonstrate sufficient power to discern three reporting groups (17_DESCFA, 18_UCOLSF, and 19_SRFALL) among the interior ocean-type collections. In one year, we had grouped all interior ocean-type collections into a single reporting group “Interior_Columbia_R_su/fa” (Hess et al. 2013). Genetic distances were computed from allele frequencies based on Nei’s (1972) genetic distance, with the PHYLIP v 3.69 (Felsenstein 1989) and 1000 bootstrap replicates were performed. Distances were clustered using the Neighbor – Joining method (Saitou and Nei, 1987), and a consensus tree was constructed (<http://evolution.genetics.washington.edu/phylip/>) (Figure 20). The clusters are labeled with names of reporting groups used to aggregate the collections based on a combination of factors including genetic similarity, life history, and geographic proximity. Bootstrap support is shown with shaded ovals (Source: Hess et al. 2015).

The 10_UCOLSP reporting group includes the following Bonneville pool hatchery stocks: Carson stock (Ots22), and Little White Salmon R. (Ots23) because they are genetically indistinguishable from Upper Columbia R. spring Chinook salmon (includes Walla Walla and Umatilla River stocks). This composite group is notable because inclusion of these Bonneville pool stocks explains why a large proportion of fish from the Wind R. sport fishery should assign to this 10_UCOLSP reporting group. However, the PBT baseline is now able to specifically identify fish from Carson Hatchery and Little White Salmon Hatchery allowing them to be distinguished from fish returning to the upper Columbia R. The 01_YOUNGS reporting group represents an out-of-basin genetic stock (originating from the Rogue R., OR) that is reared within the Columbia R. at Youngs Bay. Basic QAQC was performed to remove duplicate individuals and strays from the reference populations in the baseline. The baseline and reporting group data is available on FishGen.

GSI analyses for *O. nerka* utilized a baseline that included sockeye salmon and kokanee populations from throughout the Columbia River basin. This baseline included sockeye populations from the Osoyoos (i.e., Okanogan), Wenatchee, and Redfish Lake (i.e., Snake), and a kokanee population from Lake Whatcom that were included in “Sockeye GSI baseline v1.0, and were shown to accurately discriminate among these major stock (Hess et al 2013). We updated our baseline to included additional kokanee populations from Alturas Lake, Fishhook

Creek, Lake Billy Chinook, Meadow Creek, Suttle Creek, Cougar, Gold, North Fork Tieton, Odell, Speylai, Stanley, Warm, Wizard, Wallowa River, and Wallowa Lake, and refer to this as “Sockeye GSI baseline v3.0”. The transition to GT-seq required omission of a few loci due to poor genotyping quality with the new protocols. A total of 364 SNPs was used for these analyses.

For steelhead, we used GSI baseline version 3.3 that comprises 116 collections from throughout the Columbia River basin that are partitioned into the following 14 reporting groups: 01_WCOAST (Quinault River), 02_LOWCOL (lower Columbia River), 03_SKAMAN (Skamania hatchery releases at three sites in lower Columbia River, Willamette River, and Klickitat River), 04_WILLAM (Willamette River), 05_BWSALM (Big White Salmon River), 06_KLICKR (Klickitat River), 07_MGILCS (middle Columbia River, Grande Ronde River, Imnaha River, lower Snake River, lower Clearwater River, and lower Salmon River), 08_YAKIMA (Yakima River), 09_UPPCOL (upper Columbia River), 10_SFCLWR (South Fork Clearwater River), 11_UPCLWR (upper Clearwater River), 12_SFSALM (South Fork Salmon River), 13_MFSALM (Middle Fork Salmon River), and 14_UPSALM (upper Salmon River) (see Table 15; Figure 21). Genetic distances were computed from allele frequencies based on Nei’s (1972) genetic distance, with the PHYLIP v 3.69 (Felsenstein 1989) and 1000 bootstrap replicates were performed. Distances were clustered using the Neighbor – Joining method (Saitou and Nei, 1987), and a consensus tree was constructed (<http://evolution.genetics.washington.edu/phylip/>) (Figure 22).

Combined application of PBT and GSI

We combined PBT and GSI results together by first accepting all confident PBT assignments to hatchery broodstock for interior stream-type (i.e., $\text{LOD} \geq 14$ & $\text{FDR} \leq 0.1$) and interior ocean-type (i.e., $\text{LOD} \geq 14$ & $\text{FDR} \leq 3.0$) Chinook salmon (See methods for [Parentage assignments using SNPPIT software v1.0](#), ID: 1341). For the remaining individuals, we used the best estimate of GSI assignments (probability of assignment ≥ 0.80) provided by the program ONCOR to determine likely reporting group of origin (Method: [Assigning individual samples using Individual Assignment \(IA\) genetic methods v1.0](#), ID: 1334). For the assignment of sockeye, GSI via ONCOR was used. For Chinook salmon, all age classes (3-, 4-, and 5-year old fish) can be identified from Snake River and Columbia River stocks using PBT.

Results

We first present results from our assessment of PBT and GSI baseline accuracy, and then address results from the assignment of the 2017 harvest samples.

Information content of the 299 SNPs for PBT applications

The 93 SNPs that have been used since the beginning of PBT applications in the Columbia River basin were originally optimized for Spring Chinook Salmon broodstocks. One issue that has recently become problematic is that there are individual genotypes that have been causing the software SNPPIT to crash. We rely on this software for our PBT analyses and so resolving this problem is critical to the effectiveness of PBT applications in the long term. We examined the entire set of 299 SNPs in the GT-seq panel for information content (observed heterozygosity) in each of the three major lineages of Chinook Salmon represented by a set of broodstocks collected in 2015 that were genotyped with the full panel of SNPs (Table 11). We first

discovered that among the original 93 SNPs, there were 92 that were found above an observed heterozygosity of 10% for the stream-type lineage broodstocks of spawn year 2015 (Table 12). In contrast, there were 72 and 64 SNPs with observed heterozygosities >10% for the ocean-type and Lower Columbia lineages, respectively (Table 12). According to Steele et al. (2013), less than 72 highly polymorphic SNPs is the point at which accuracy for PBT was observed to decline. We suspect that it is the lack of sufficient numbers of SNP markers with high information content (i.e. observed heterozygosity) that has been causing SNPPIT to crash when we analyze parent-offspring pairs from ocean-type and Lower Columbia River broodstocks with low polymorphism at these 93 SNPs.

To resolve this issue, we recommend the use of a larger set of SNP markers (~200) that have greater than 10% observed heterozygosity in each of the major lineages of Chinook Salmon. Our evaluation of the broodstocks from SY2015 indicated a set of 269 SNP loci that had >10% observed heterozygosity for at least 1 major lineage, and within this panel of 269 loci there were 193, 218, and 195 SNPs with >10% observed heterozygosity for each of the major lineages stream-type, ocean-type, and Lower Columbia, respectively (Table 12). Therefore, this single panel of 269 loci may help achieve higher accuracy and power for PBT applications across all three lineages. We applied this panel of 269 loci to our last in-season analysis of Chinook salmon at Bonneville Dam in 2018 and report on results in Section 4. Evaluation of mismatches among these loci revealed that there was at least a single locus (Ots_crRAD506127) among these 269 loci that were found mismatched in more than 5% of all the crosses identified (N=1284 unique crosses). If this locus were also excluded from this PBT panel, then the remaining 268 highly informative loci would include 192, 217, and 195 SNPs with >10% observed heterozygosity for each of the major lineages stream-type, ocean-type, and Lower Columbia, respectively (Table 12).

Application of the 268 SNP panel to the Chinook Salmon passing Bonneville Dam in 2018 revealed that the use of this expanded panel fully resolved the crashing issue with SNPPIT. All eleven individuals that caused the program to crash were possible to analyze in SNPPIT to completion and eight of those individuals were observed with highly confident assignments (LOD>23, FDR<0.001) to ocean-type broodstocks. This result confirmed that the source of the crashing issue was likely related to the lack of sufficient numbers of SNPs with high information content that is primarily affecting ocean-type broodstocks.

Table 11. List of PBT broodstock collections from spawn year 2015 that were evaluated with 299 SNPs to estimate observed heterozygosity for three major genetic lineages of Columbia River Chinook Salmon.

Stream-type	Ocean-type	Lower Columbia
OtsCAR15	OtsLWS15_sufa	OtsBIG_Tule15
OtsCLWH15S	OtsLYON15S_1	OtsSPCR_Tule15
OtsCJH15_sp	OtsNPFH15S_1	
OtsCTHW15S	OtsCJH15int_sufa	
OtsDWOR15S	OtsCJH15seg_sufa	
OtsGRUW15S	OtsEASTBK15_su	
OtsIMNW15S	OtsENFH15	
OtsLOOK15S	OtsPRH15	
OtsLSTW15S	OtsPRO15	
OtsJHNW15S	OtsWELLS15	
OtsKH15		
OtsLNFH15		
OtsLWS15_sp		
OtsMCCA15S		
OtsMETH15		
OtsPAHH15S		
OtsPFF15		
OtsPOWP15S		
OtsRB15		
OtsRAPH15S		
OtsSAWT15S		
OtsWSNFH15		
OtsWTP15		
OtsYR15int		
OtsYR15seg		
OtsLYON15S		
OtsNPFH15S		
OtsEASTBK15_sp		
OtsUMA15_sp		

Note: The broodstock codes correspond to the hatchery names in Appendix 4. All broodstock collections were pooled within each lineage (stream-type, ocean-type, and lower Columbia) to estimate observed heterozygosities reported in Table 12.

Table 12. The informativeness of a panel of 299 SNP loci for PBT applications of the three major genetic lineages of Columbia River Chinook salmon based on observed heterozygosity across broodstocks from spawn year 2015.

SNP93 order	Best 269	Locus	Stream-type broodstock 2015					Ocean-type broodstock 2015					Lower Columbia (tule) broodstock 2015				
			k	N	Total N	% success	H Obs.	k	N	Total N	% success	H Obs.	k	N	Total N	% success	H Obs.
1	SNP269	Ots_100884287	2	16078	16112	99.8%	0.295	2	18346	18356	99.9%	0.186	2	6212	6223	99.8%	0.431
2	SNP269	Ots_101554407	2	16094	16112	99.9%	0.473	2	18351	18356	100.0%	0.186	2	6223	6223	100.0%	0.091
3	SNP269	Ots_101704143	2	16099	16112	99.9%	0.178	2	18228	18356	99.3%	0.415	2	6216	6223	99.9%	0.464
4	SNP269	Ots_102414395	2	16037	16112	99.5%	0.483	2	18310	18356	99.7%	0.420	2	6196	6223	99.6%	0.486
5	SNP269	Ots_102801308	2	16089	16112	99.9%	0.332	2	18321	18356	99.8%	0.177	2	6212	6223	99.8%	0.276
6	SNP269	Ots_103122180	2	16101	16112	99.9%	0.261	2	18345	18356	99.9%	0.250	2	6223	6223	100.0%	0.135
7	SNP269	Ots_10441588	2	16078	16112	99.8%	0.482	2	18347	18356	100.0%	0.233	2	6223	6223	100.0%	0.000
8	SNP269	Ots_105105613	2	16054	16112	99.6%	0.444	2	18335	18356	99.9%	0.260	2	6218	6223	99.9%	0.053
9	SNP269	Ots_105132200	2	16096	16112	99.9%	0.361	2	18355	18356	100.0%	0.131	2	6223	6223	100.0%	0.006
10	SNP269	Ots_105385421	2	16083	16112	99.8%	0.482	2	18352	18356	100.0%	0.051	2	6222	6223	100.0%	0.049
11	SNP269	Ots_105407117	2	16072	16112	99.8%	0.430	2	18278	18356	99.6%	0.492	2	6208	6223	99.8%	0.345
12	SNP269	Ots_108820336	2	16082	16112	99.8%	0.503	2	18350	18356	100.0%	0.103	2	6205	6223	99.7%	0.429
13	SNP269	Ots_109525816	2	16100	16112	99.9%	0.311	2	18353	18356	100.0%	0.257	2	6223	6223	100.0%	0.001
14	SNP269	Ots_110064383	2	16072	16112	99.8%	0.463	2	18349	18356	100.0%	0.343	2	6222	6223	100.0%	0.149
15	SNP269	Ots_110201363	2	16042	16112	99.6%	0.416	2	18203	18356	99.2%	0.417	2	6132	6223	98.5%	0.451
16	SNP269	Ots_110495380	2	15776	16112	97.9%	0.202	2	18037	18356	98.3%	0.474	2	6154	6223	98.9%	0.372
17	SNP269	Ots_11055164	2	16099	16112	99.9%	0.304	2	18339	18356	99.9%	0.350	2	6219	6223	99.9%	0.293
18	SNP269	Ots_110689218	2	15770	16112	97.9%	0.345	2	16893	18356	92.0%	0.336	2	5802	6223	93.2%	0.377
19	SNP269	Ots_11230143	2	16099	16112	99.9%	0.243	2	18239	18356	99.4%	0.239	2	6213	6223	99.8%	0.497
20	SNP269	Ots_112419131	2	16095	16112	99.9%	0.244	2	18317	18356	99.8%	0.494	2	6205	6223	99.7%	0.501
21	SNP269	Ots_112820284	2	16101	16112	99.9%	0.279	2	18340	18356	99.9%	0.457	2	6214	6223	99.9%	0.463
22	SNP269	Ots_112876371	2	16087	16112	99.8%	0.337	2	18341	18356	99.9%	0.468	2	6214	6223	99.9%	0.510
23	SNP269	Ots_113242216	2	16100	16112	99.9%	0.238	2	18341	18356	99.9%	0.494	2	6211	6223	99.8%	0.496
24	SNP269	Ots_115987325	2	16095	16112	99.9%	0.369	2	18353	18356	100.0%	0.169	2	6219	6223	99.9%	0.418
25	SNP269	Ots_117432409	2	16099	16112	99.9%	0.396	2	18334	18356	99.9%	0.459	2	6216	6223	99.9%	0.499
26	SNP269	Ots_11820561	2	16104	16112	100.0%	0.276	2	18346	18356	99.9%	0.307	2	6220	6223	100.0%	0.269
27	SNP269	Ots_118938325	2	16093	16112	99.9%	0.410	2	18340	18356	99.9%	0.478	2	6218	6223	99.9%	0.492

28	SNP269	Ots_123921111	2	16097	16112	99.9%	0.287	2	18217	18356	99.2%	0.332	2	6187	6223	99.4%	0.107
29	SNP269	Ots_124774477	2	16016	16112	99.4%	0.153	2	18283	18356	99.6%	0.445	2	6139	6223	98.7%	0.191
30	SNP269	Ots_12875761R	2	16108	16112	100.0%	0.194	2	18335	18356	99.9%	0.498	2	6217	6223	99.9%	0.457
31	SNP269	Ots_129458451	2	16106	16112	100.0%	0.236	2	18333	18356	99.9%	0.484	2	6219	6223	99.9%	0.369
32	SNP269	Ots_94857232R	2	15985	16112	99.2%	0.475	2	18334	18356	99.9%	0.489	2	6221	6223	100.0%	0.155
33	SNP269	Ots_9490399R	2	16090	16112	99.9%	0.483	2	18335	18356	99.9%	0.492	2	6215	6223	99.9%	0.439
34	SNP269	Ots_96500180	2	16041	16112	99.6%	0.484	2	18094	18356	98.6%	0.373	2	6150	6223	98.8%	0.197
35	SNP269	Ots_96899357R	2	16081	16112	99.8%	0.233	2	18345	18356	99.9%	0.014	1	6223	6223	100.0%	0.000
36	SNP269	Ots_ARNT	2	16093	16112	99.9%	0.365	2	18355	18356	100.0%	0.028	2	6223	6223	100.0%	0.002
37	SNP269	Ots_AsnRS60	2	16087	16112	99.8%	0.335	2	18335	18356	99.9%	0.284	2	6217	6223	99.9%	0.189
38	SNP269	Ots_brp1664	2	15911	16112	98.8%	0.257	2	18335	18356	99.9%	0.499	2	6213	6223	99.8%	0.494
39	SNP269	Ots_CD592	2	16033	16112	99.5%	0.477	2	18172	18356	99.0%	0.446	2	6168	6223	99.1%	0.495
40	SNP269	Ots_CirpA	2	16106	16112	100.0%	0.205	2	18352	18356	100.0%	0.240	2	6218	6223	99.9%	0.320
41	SNP269	Ots_cox1241	2	16057	16112	99.7%	0.306	2	18353	18356	100.0%	0.145	2	6215	6223	99.9%	0.403
42	SNP269	Ots_E2275	2	15921	16112	98.8%	0.436	2	18349	18356	100.0%	0.150	2	6221	6223	100.0%	0.305
43	SNP269	Ots_Est740	2	16077	16112	99.8%	0.487	2	18322	18356	99.8%	0.469	2	6208	6223	99.8%	0.476
44	SNP269	Ots_ETIF1A	2	16085	16112	99.8%	0.427	2	18294	18356	99.7%	0.241	2	6217	6223	99.9%	0.092
45	SNP269	Ots_FGF6B_1	2	16098	16112	99.9%	0.467	2	18325	18356	99.8%	0.467	2	6135	6223	98.6%	0.113
46	SNP269	Ots_GCSH	2	16104	16112	100.0%	0.190	2	18354	18356	100.0%	0.047	2	6219	6223	99.9%	0.178
47	SNP269	Ots_GDH81x	2	16095	16112	99.9%	0.349	2	18321	18356	99.8%	0.498	2	6216	6223	99.9%	0.421
48	SNP269	Ots_GPH318	2	16101	16112	99.9%	0.301	2	18356	18356	100.0%	0.048	2	6223	6223	100.0%	0.060
49	SNP269	Ots_GTH2B550	2	16067	16112	99.7%	0.480	2	18327	18356	99.8%	0.058	2	6204	6223	99.7%	0.258
50	SNP269	Ots_HMGB173	2	16103	16112	99.9%	0.218	2	18337	18356	99.9%	0.324	2	6215	6223	99.9%	0.428
51	SNP269	Ots_hsc713488	2	16093	16112	99.9%	0.300	2	18330	18356	99.9%	0.238	2	6219	6223	99.9%	0.048
52	SNP269	Ots_HSP90B100	2	16105	16112	100.0%	0.290	2	18352	18356	100.0%	0.185	2	6223	6223	100.0%	0.118
53	SNP269	Ots_IGFI176	2	16089	16112	99.9%	0.304	2	18349	18356	100.0%	0.003	1	6222	6223	100.0%	0.000
54	SNP269	Ots_Ikaros250	2	15868	16112	98.5%	0.141	2	17972	18356	97.9%	0.004	2	6223	6223	100.0%	0.032
55	SNP269	Ots_IL8R_C8	2	16022	16112	99.4%	0.485	2	18350	18356	100.0%	0.052	2	6223	6223	100.0%	0.007
56	SNP269	Ots_mapK3309	2	16090	16112	99.9%	0.435	2	18268	18356	99.5%	0.430	2	6201	6223	99.6%	0.490
57	SNP269	Ots_mapKpr151	2	16101	16112	99.9%	0.404	2	18354	18356	100.0%	0.152	2	6222	6223	100.0%	0.133
58	SNP269	Ots_MHC2	2	15886	16112	98.6%	0.381	2	18125	18356	98.7%	0.481	2	6213	6223	99.8%	0.027
59	SNP269	Ots_mybp85	2	16094	16112	99.9%	0.176	2	18285	18356	99.6%	0.479	2	6199	6223	99.6%	0.501

60	SNP269	Ots_NFYB147	2	16077	16112	99.8%	0.301	2	18343	18356	99.9%	0.007	1	6223	6223	100.0%	0.000
61	SNP269	Ots_nkef192	2	16085	16112	99.8%	0.481	2	18353	18356	100.0%	0.015	1	6223	6223	100.0%	0.000
62	SNP269	Ots_NOD1	2	16094	16112	99.9%	0.404	2	18177	18356	99.0%	0.055	2	6216	6223	99.9%	0.062
63	SNP269	Ots_ntl255	2	16095	16112	99.9%	0.468	2	18344	18356	99.9%	0.421	2	6214	6223	99.9%	0.456
64	SNP269	Ots_OTALDBINT1SNP1	2	16078	16112	99.8%	0.168	2	18254	18356	99.4%	0.431	2	6218	6223	99.9%	0.506
65	SNP269	Ots_OTDESMIN19SNP1	2	16100	16112	99.9%	0.469	2	18346	18356	99.9%	0.347	2	6223	6223	100.0%	0.165
66	SNP269	Ots_OTSTF1SNP1	2	16094	16112	99.9%	0.446	2	18355	18356	100.0%	0.161	2	6219	6223	99.9%	0.310
67	SNP269	Ots_P53	2	16091	16112	99.9%	0.359	2	18346	18356	99.9%	0.405	2	6212	6223	99.8%	0.483
68	SNP269	Ots_parp3286	2	16093	16112	99.9%	0.313	2	18355	18356	100.0%	0.112	2	6223	6223	100.0%	0.064
69	SNP269	Ots_pop596	2	16097	16112	99.9%	0.368	2	18353	18356	100.0%	0.065	2	6219	6223	99.9%	0.369
70	SNP269	Ots_ppie245	2	16086	16112	99.8%	0.391	2	18345	18356	99.9%	0.077	2	6223	6223	100.0%	0.023
71	SNP269	Ots_Prl2	2	16080	16112	99.8%	0.368	2	18324	18356	99.8%	0.441	2	6212	6223	99.8%	0.489
72	SNP269	Ots_RAG3	2	16090	16112	99.9%	0.240	2	18316	18356	99.8%	0.324	2	6212	6223	99.8%	0.312
73	SNP269	Ots_redd1187	2	16093	16112	99.9%	0.425	2	18355	18356	100.0%	0.072	2	6223	6223	100.0%	0.018
74	SNP269	Ots_S71	2	16049	16112	99.6%	0.474	2	18267	18356	99.5%	0.421	2	6186	6223	99.4%	0.457
75	SNP269	Ots_SClkF2R2135	2	16092	16112	99.9%	0.447	2	18342	18356	99.9%	0.420	2	6212	6223	99.8%	0.499
76	SNP269	Ots_SWS1op182	2	16068	16112	99.7%	0.403	2	18224	18356	99.3%	0.478	2	6216	6223	99.9%	0.050
77	SNP269	Ots_TAPBP	2	16089	16112	99.9%	0.437	2	18347	18356	100.0%	0.365	2	6220	6223	100.0%	0.030
78	SNP269	Ots_TGFB	2	16110	16112	100.0%	0.104	2	18348	18356	100.0%	0.272	2	6176	6223	99.2%	0.394
79	SNP269	Ots_Thio	2	15548	16112	96.5%	0.406	2	17793	18356	96.9%	0.493	2	6063	6223	97.4%	0.468
80	SNP269	Ots_TLR3	2	16066	16112	99.7%	0.431	2	18317	18356	99.8%	0.305	2	6211	6223	99.8%	0.345
81	SNP269	Ots_tpx2125	2	16107	16112	100.0%	0.165	2	18356	18356	100.0%	0.062	2	6223	6223	100.0%	0.000
82	SNP269	Ots_txnip321	2	16108	16112	100.0%	0.195	2	18343	18356	99.9%	0.006	2	6221	6223	100.0%	0.080
83	SNP269	Ots_u0707161	2	16079	16112	99.8%	0.464	2	18301	18356	99.7%	0.493	2	6198	6223	99.6%	0.294
84	SNP269	Ots_u0717135	2	16104	16112	100.0%	0.199	2	18336	18356	99.9%	0.054	2	6222	6223	100.0%	0.003
85	SNP269	Ots_u0718378	2	16100	16112	99.9%	0.216	2	18296	18356	99.7%	0.496	2	6200	6223	99.6%	0.504
86	SNP269	Ots_u0725325	2	15724	16112	97.6%	0.477	2	16762	18356	91.3%	0.060	1	5853	6223	94.1%	0.000
87	SNP269	Ots_u0749290	2	16094	16112	99.9%	0.429	2	18331	18356	99.9%	0.440	2	6215	6223	99.9%	0.456
88	SNP269	Ots_u100275	2	16096	16112	99.9%	0.391	2	18351	18356	100.0%	0.289	2	6220	6223	100.0%	0.427
89	SNP269	Ots_u21185	2	16089	16112	99.9%	0.468	2	18356	18356	100.0%	0.024	2	6223	6223	100.0%	0.069
90	SNP269	Ots_u492	2	16085	16112	99.8%	0.056	2	18351	18356	100.0%	0.102	2	6221	6223	100.0%	0.208
91	SNP269	Ots_u675	2	15806	16112	98.1%	0.168	2	17940	18356	97.7%	0.042	2	6220	6223	100.0%	0.091

92	SNP269	Ots_unk526	2	16022	16112	99.4%	0.283	2	18242	18356	99.4%	0.280	2	6211	6223	99.8%	0.218
93	SNP269	Ots_vatf251	2	16105	16112	100.0%	0.151	2	18341	18356	99.9%	0.383	2	6216	6223	99.9%	0.508
	SNP269	Ots_unk183239	2	16059	16112	99.7%	0.492	2	18340	18356	99.9%	0.327	2	6218	6223	99.9%	0.300
	SNP269	Ots_unk110438	2	16086	16112	99.8%	0.490	2	18355	18356	100.0%	0.167	2	6216	6223	99.9%	0.380
	SNP269	Ots_crRAD5768734	2	15793	16112	98.0%	0.486	2	17981	18356	98.0%	0.119	2	6069	6223	97.5%	0.196
	SNP269	Ots_crRAD7558170	2	16082	16112	99.8%	0.482	2	18315	18356	99.8%	0.292	2	6201	6223	99.6%	0.442
	SNP269	Ots_crRAD1654050	2	16087	16112	99.8%	0.480	2	18355	18356	100.0%	0.235	2	6219	6223	99.9%	0.338
	SNP269	Ots_106747239	2	16080	16112	99.8%	0.476	2	18347	18356	100.0%	0.375	2	6215	6223	99.9%	0.494
	SNP269	Ots_crRAD2867765	2	15888	16112	98.6%	0.475	2	17955	18356	97.8%	0.260	2	6091	6223	97.9%	0.407
	SNP269	Ots_crRAD6062051	2	16078	16112	99.8%	0.467	2	18351	18356	100.0%	0.237	2	6217	6223	99.9%	0.416
	SNP269	Ots_SEXY31	2	13717	16112	85.1%	0.465	2	18232	18356	99.3%	0.431	2	6209	6223	99.8%	0.446
	SNP269	Ots_107806821	2	15993	16112	99.3%	0.463	2	17890	18356	97.5%	0.451	2	6092	6223	97.9%	0.381
	SNP269	Ots_crRAD5752066	2	16088	16112	99.9%	0.461	2	18347	18356	100.0%	0.243	2	6220	6223	100.0%	0.387
	SNP269	Ots_U2446123	2	16085	16112	99.8%	0.458	2	18340	18356	99.9%	0.367	2	6222	6223	100.0%	0.106
	SNP269	Ots_crRAD1162055	2	16086	16112	99.8%	0.453	2	18335	18356	99.9%	0.378	2	6222	6223	100.0%	0.138
	SNP269	Ots_10649970	2	16080	16112	99.8%	0.440	2	18258	18356	99.5%	0.497	2	6209	6223	99.8%	0.504
	SNP269	Ots_Ostm1	2	16092	16112	99.9%	0.440	2	18327	18356	99.8%	0.484	2	6219	6223	99.9%	0.428
	SNP269	Ots_crRAD7651228	2	16012	16112	99.4%	0.433	2	18017	18356	98.2%	0.401	2	6051	6223	97.2%	0.161
	SNP269	Ots_crRAD3305462	2	16087	16112	99.8%	0.430	2	18347	18356	100.0%	0.251	2	6218	6223	99.9%	0.344
	SNP269	Ots_FGF6A	2	16035	16112	99.5%	0.429	2	18292	18356	99.7%	0.156	2	6184	6223	99.4%	0.373
	SNP269	Ots_crRAD1203739	2	16050	16112	99.6%	0.418	2	18269	18356	99.5%	0.495	2	6193	6223	99.5%	0.481
	SNP269	Ots_NAML12SNP1	2	14320	16112	88.9%	0.401	2	17893	18356	97.5%	0.285	2	6209	6223	99.8%	0.460
	SNP269	Ots_110381164	2	16085	16112	99.8%	0.392	2	18341	18356	99.9%	0.445	2	6212	6223	99.8%	0.327
	SNP269	Ots_crRAD7382360	2	16092	16112	99.9%	0.386	2	18335	18356	99.9%	0.476	2	6215	6223	99.9%	0.519
	SNP269	Ots_unk351349	2	16096	16112	99.9%	0.378	2	18307	18356	99.7%	0.372	2	6174	6223	99.2%	0.223
	SNP269	Ots_U230563	2	14786	16112	91.8%	0.378	2	17237	18356	93.9%	0.188	2	6096	6223	98.0%	0.208
	SNP269	Ots_crRAD4205848	2	15316	16112	95.1%	0.363	2	13005	18356	70.8%	0.431	2	5049	6223	81.1%	0.395
	SNP269	Ots_crRAD3034148	2	15166	16112	94.1%	0.360	2	16313	18356	88.9%	0.331	2	5595	6223	89.9%	0.283
	SNP269	Ots_crRAD6152371	2	15693	16112	97.4%	0.332	2	18301	18356	99.7%	0.352	2	6207	6223	99.7%	0.330
	SNP269	Ots_crRAD2536750	2	16088	16112	99.9%	0.328	2	18309	18356	99.7%	0.492	2	6190	6223	99.5%	0.169
	SNP269	Ots_U5049250	2	16102	16112	99.9%	0.277	2	18337	18356	99.9%	0.411	2	6220	6223	100.0%	0.284
	SNP269	Ots_crRAD5547526	2	15350	16112	95.3%	0.274	2	17204	18356	93.7%	0.375	2	5556	6223	89.3%	0.430

SNP269	Ots_cgo2422	2	16107	16112	100.0%	0.266	2	18341	18356	99.9%	0.364	2	6217	6223	99.9%	0.416
SNP269	Ots_10304152	2	16093	16112	99.9%	0.262	2	18334	18356	99.9%	0.497	2	6210	6223	99.8%	0.470
SNP269	Ots_crRAD5753724	2	15846	16112	98.3%	0.260	2	17759	18356	96.7%	0.451	2	6040	6223	97.1%	0.474
SNP269	Ots_crRAD2037666	2	16100	16112	99.9%	0.252	2	18332	18356	99.9%	0.418	2	6208	6223	99.8%	0.499
SNP269	Ots_unk948051	2	16107	16112	100.0%	0.247	2	18351	18356	100.0%	0.274	2	6219	6223	99.9%	0.290
SNP269	Ots_DDX5171	2	16102	16112	99.9%	0.245	2	18340	18356	99.9%	0.499	2	6215	6223	99.9%	0.468
SNP269	Ots_108735302	2	15806	16112	98.1%	0.233	2	17450	18356	95.1%	0.490	2	5847	6223	94.0%	0.470
SNP269	Ots_crRAD4729755	2	16093	16112	99.9%	0.226	2	18343	18356	99.9%	0.455	2	6214	6223	99.9%	0.506
SNP269	Ots_crRAD2026246	2	16106	16112	100.0%	0.218	2	18342	18356	99.9%	0.413	2	6218	6223	99.9%	0.429
SNP269	Ots_IL11	2	16103	16112	99.9%	0.218	2	18340	18356	99.9%	0.124	2	6213	6223	99.8%	0.182
SNP269	Ots_126619400	2	15894	16112	98.6%	0.214	2	17405	18356	94.8%	0.325	2	5749	6223	92.4%	0.403
SNP269	Ots_crRAD961569	2	16105	16112	100.0%	0.207	2	18338	18356	99.9%	0.427	2	6219	6223	99.9%	0.306
SNP269	Ots_unk793650	2	16088	16112	99.9%	0.199	2	18160	18356	98.9%	0.316	2	5803	6223	93.3%	0.550
SNP269	Ots_U512134	2	15993	16112	99.3%	0.199	2	18340	18356	99.9%	0.295	2	6188	6223	99.4%	0.191
SNP269	Ots_crRAD4458867	2	16063	16112	99.7%	0.198	2	18319	18356	99.8%	0.396	2	6200	6223	99.6%	0.477
SNP269	Ots_PEMT	2	16107	16112	100.0%	0.194	2	18319	18356	99.8%	0.478	2	6213	6223	99.8%	0.432
SNP269	Ots_AldB1122	2	15819	16112	98.2%	0.193	2	18242	18356	99.4%	0.211	2	6150	6223	98.8%	0.295
SNP269	Ots_11345740R	2	16088	16112	99.9%	0.191	2	18324	18356	99.8%	0.494	2	6223	6223	100.0%	0.225
SNP269	Ots_crRAD2296032	2	16102	16112	99.9%	0.190	2	18348	18356	100.0%	0.168	2	6221	6223	100.0%	0.239
SNP269	Ots_111681657	2	16094	16112	99.9%	0.162	2	18335	18356	99.9%	0.307	2	6207	6223	99.7%	0.498
SNP269	Ots_104048194	2	16066	16112	99.7%	0.159	2	18057	18356	98.4%	0.405	2	6047	6223	97.2%	0.156
SNP269	Ots_myoD364	2	16100	16112	99.9%	0.151	2	17967	18356	97.9%	0.452	2	6101	6223	98.0%	0.462
SNP269	Ots_CD63	2	16101	16112	99.9%	0.142	2	18339	18356	99.9%	0.477	2	6220	6223	100.0%	0.507
SNP269	Ots_117242136	2	16109	16112	100.0%	0.139	2	18333	18356	99.9%	0.504	2	6214	6223	99.9%	0.489
SNP269	Ots_120950417	2	16107	16112	100.0%	0.131	2	18345	18356	99.9%	0.435	2	6223	6223	100.0%	0.103
SNP269	Ots_108007208	2	16107	16112	100.0%	0.130	2	18329	18356	99.9%	0.498	2	6218	6223	99.9%	0.401
SNP269	Ots_96222525	2	16108	16112	100.0%	0.126	2	18337	18356	99.9%	0.495	2	6220	6223	100.0%	0.363
SNP269	Ots_myo1a384	2	16109	16112	100.0%	0.122	2	18354	18356	100.0%	0.193	2	6219	6223	99.9%	0.499
SNP269	Ots_131460584	2	16107	16112	100.0%	0.117	2	18312	18356	99.8%	0.467	2	6220	6223	100.0%	0.233
SNP269	Ots_u0753133	2	16076	16112	99.8%	0.114	2	18035	18356	98.3%	0.494	2	6152	6223	98.9%	0.190
SNP269	Ots_aldb177M	2	16096	16112	99.9%	0.113	2	17437	18356	95.0%	0.440	2	6084	6223	97.8%	0.415
SNP269	Ots_131906141	2	16108	16112	100.0%	0.113	2	18352	18356	100.0%	0.236	2	6216	6223	99.9%	0.378

SNP269	Ots_crRAD2088770	2	16111	16112	100.0%	0.109	2	18351	18356	100.0%	0.264	2	6203	6223	99.7%	0.500
SNP269	Ots_13072099	2	16110	16112	100.0%	0.106	2	18342	18356	99.9%	0.475	2	6215	6223	99.9%	0.395
SNP269	Ots_TCTA58	2	16109	16112	100.0%	0.103	2	18340	18356	99.9%	0.443	2	6217	6223	99.9%	0.389
SNP269	Ots_9766056	2	16112	16112	100.0%	0.102	2	18353	18356	100.0%	0.152	2	6219	6223	99.9%	0.246
SNP269	Ots_crRAD25559	2	16074	16112	99.8%	0.501	2	18343	18356	99.9%	0.124	2	6217	6223	99.9%	0.079
SNP269	Ots_pigh105	2	15020	16112	93.2%	0.472	2	14928	18356	81.3%	0.313	2	5364	6223	86.2%	0.029
SNP269	Ots_crRAD506127	2	16029	16112	99.5%	0.458	2	15118	18356	82.4%	0.138	2	1745	6223	28.0%	0.034
SNP269	Ots_crRAD280642	2	15960	16112	99.1%	0.444	2	18351	18356	100.0%	0.138	2	6218	6223	99.9%	0.064
SNP269	Ots_95442b204	2	16096	16112	99.9%	0.428	2	18355	18356	100.0%	0.128	2	6223	6223	100.0%	0.055
SNP269	Ots_Tnsf	2	16090	16112	99.9%	0.425	2	18356	18356	100.0%	0.109	2	6223	6223	100.0%	0.042
SNP269	Ots_crRAD6932753	2	16098	16112	99.9%	0.213	2	18355	18356	100.0%	0.110	2	6221	6223	100.0%	0.098
SNP269	Ots_crRAD2480774	2	15841	16112	98.3%	0.186	2	17889	18356	97.5%	0.161	2	6167	6223	99.1%	0.040
SNP269	Ots_ZR575	2	15590	16112	96.8%	0.179	2	17742	18356	96.7%	0.221	2	6170	6223	99.1%	0.019
SNP269	Ots_crRAD3531366	2	15621	16112	97.0%	0.170	2	17781	18356	96.9%	0.176	2	6122	6223	98.4%	0.059
SNP269	Ots_crRAD3607229	2	16084	16112	99.8%	0.146	2	16268	18356	88.6%	0.344	2	6214	6223	99.9%	0.050
SNP269	Ots_u1008108	2	16079	16112	99.8%	0.120	2	18305	18356	99.7%	0.161	2	6211	6223	99.8%	0.059
SNP269	Ots_u0717373	2	16048	16112	99.6%	0.120	2	18202	18356	99.2%	0.107	2	6169	6223	99.1%	0.070
SNP269	Ots_u202161	2	15635	16112	97.0%	0.112	2	17470	18356	95.2%	0.449	2	6139	6223	98.7%	0.054
SNP269	Ots_crRAD3349171	2	16077	16112	99.8%	0.479	2	18354	18356	100.0%	0.073	2	6220	6223	100.0%	0.260
SNP269	Ots_111084b619	2	16064	16112	99.7%	0.349	2	18332	18356	99.9%	0.074	2	6213	6223	99.8%	0.198
SNP269	Ots_104063132	2	15720	16112	97.6%	0.333	2	18334	18356	99.9%	0.049	2	6054	6223	97.3%	0.287
SNP269	Ots_U2567104	2	16101	16112	99.9%	0.192	2	18355	18356	100.0%	0.069	2	6221	6223	100.0%	0.229
SNP269	Ots_Est1363	2	15967	16112	99.1%	0.108	2	18258	18356	99.5%	0.033	2	6158	6223	99.0%	0.381
SNP269	Ots_hnRNPL533	2	16062	16112	99.7%	0.481	2	18254	18356	99.4%	0.069	2	5370	6223	86.3%	0.064
SNP269	Ots_P450288	2	16064	16112	99.7%	0.477	2	18069	18356	98.4%	0.076	2	6223	6223	100.0%	0.074
SNP269	Ots_crRAD5540059	2	16051	16112	99.6%	0.475	2	18355	18356	100.0%	0.035	1	6222	6223	100.0%	0.000
SNP269	Ots_U2362330	2	16085	16112	99.8%	0.461	2	18356	18356	100.0%	0.069	2	6223	6223	100.0%	0.032
SNP269	Ots_crRAD2654147	2	15850	16112	98.4%	0.460	2	18092	18356	98.6%	0.070	2	6088	6223	97.8%	0.022
SNP269	Ots_127760569	2	16061	16112	99.7%	0.434	2	18070	18356	98.4%	0.035	2	2124	6223	34.1%	0.003
SNP269	Ots_crRAD2751569	2	16093	16112	99.9%	0.376	2	18356	18356	100.0%	0.050	2	6223	6223	100.0%	0.000
SNP269	Ots_RAD454352	2	16090	16112	99.9%	0.336	2	18293	18356	99.7%	0.077	2	6223	6223	100.0%	0.027
SNP269	Ots_crRAD5737668	2	16018	16112	99.4%	0.312	2	18108	18356	98.6%	0.052	2	6162	6223	99.0%	0.007

SNP269	Ots_crRAD1752758	2	14387	16112	89.3%	0.264	2	17135	18356	93.3%	0.068	2	5920	6223	95.1%	0.022
SNP269	Ots_U212158	2	16043	16112	99.6%	0.225	2	18288	18356	99.6%	0.029	2	6217	6223	99.9%	0.020
SNP269	Ots_IsoT	2	15854	16112	98.4%	0.191	2	18289	18356	99.6%	0.001	1	6223	6223	100.0%	0.000
SNP269	Ots_AldoB4183	2	16094	16112	99.9%	0.150	2	18332	18356	99.9%	0.051	2	6222	6223	100.0%	0.000
SNP269	Ots_u0757120	2	16053	16112	99.6%	0.145	2	18141	18356	98.8%	0.087	2	6202	6223	99.7%	0.061
SNP269	Ots_crRAD4675142	2	16109	16112	100.0%	0.129	2	18338	18356	99.9%	0.024	1	6223	6223	100.0%	0.000
SNP269	Ots_crRAD1044725	2	15673	16112	97.3%	0.101	2	18154	18356	98.9%	0.029	2	6216	6223	99.9%	0.014
SNP269	Ots_112208722	2	15657	16112	97.2%	0.097	2	18006	18356	98.1%	0.477	2	6118	6223	98.3%	0.431
SNP269	Ots_117259271	2	16105	16112	100.0%	0.097	2	18344	18356	99.9%	0.333	2	6221	6223	100.0%	0.136
SNP269	Ots_U2362227	2	16110	16112	100.0%	0.097	2	18318	18356	99.8%	0.217	2	6020	6223	96.7%	0.303
SNP269	Ots_hsc715453	2	16080	16112	99.8%	0.096	2	17943	18356	97.8%	0.455	2	6134	6223	98.6%	0.353
SNP269	Ots_128693461	2	16109	16112	100.0%	0.094	2	18332	18356	99.9%	0.441	2	6222	6223	100.0%	0.280
SNP269	Ots_hsp27b150	2	16105	16112	100.0%	0.093	2	18340	18356	99.9%	0.501	2	6223	6223	100.0%	0.116
SNP269	Ots_P450	2	15864	16112	98.5%	0.087	2	18277	18356	99.6%	0.142	2	6216	6223	99.9%	0.151
SNP269	Ots_crRAD6633060	2	16097	16112	99.9%	0.086	2	18321	18356	99.8%	0.270	2	6219	6223	99.9%	0.265
SNP269	Ots_118175479	2	16105	16112	100.0%	0.084	2	18347	18356	100.0%	0.236	2	6219	6223	99.9%	0.320
SNP269	Ots_106419b618	2	16100	16112	99.9%	0.083	2	18291	18356	99.6%	0.336	2	6219	6223	99.9%	0.368
SNP269	Ots_109693392	2	16111	16112	100.0%	0.079	2	18354	18356	100.0%	0.217	2	6210	6223	99.8%	0.509
SNP269	Ots_Hsp90a	2	16088	16112	99.9%	0.077	2	17852	18356	97.3%	0.473	2	6090	6223	97.9%	0.388
SNP269	Ots_102457132	2	16092	16112	99.9%	0.076	2	18305	18356	99.7%	0.484	2	6208	6223	99.8%	0.443
SNP269	Ots_EndoRB1486	2	16112	16112	100.0%	0.072	2	18300	18356	99.7%	0.436	2	6215	6223	99.9%	0.459
SNP269	Ots_97077179R	2	16111	16112	100.0%	0.065	2	18339	18356	99.9%	0.462	2	6211	6223	99.8%	0.421
SNP269	Ots_crRAD2716455	2	16112	16112	100.0%	0.060	2	18308	18356	99.7%	0.387	2	6222	6223	100.0%	0.205
SNP269	Ots_Ots311101x	2	16111	16112	100.0%	0.057	2	18350	18356	100.0%	0.247	2	6214	6223	99.9%	0.492
SNP269	Ots_99550204	2	16111	16112	100.0%	0.057	2	18353	18356	100.0%	0.183	2	6214	6223	99.9%	0.448
SNP269	Ots_crRAD7476628	2	16112	16112	100.0%	0.055	2	18284	18356	99.6%	0.490	2	6214	6223	99.9%	0.306
SNP269	Ots_sept978	2	16052	16112	99.6%	0.054	2	16592	18356	90.4%	0.364	2	6089	6223	97.8%	0.416
SNP269	Ots_crRAD9242025	2	16106	16112	100.0%	0.054	2	18332	18356	99.9%	0.253	2	6222	6223	100.0%	0.201
SNP269	Ots_107074284	2	16108	16112	100.0%	0.052	2	18318	18356	99.8%	0.483	2	6217	6223	99.9%	0.444
SNP269	Ots_SL	2	16112	16112	100.0%	0.052	2	18351	18356	100.0%	0.214	2	6216	6223	99.9%	0.349
SNP269	Ots_HFABP34	2	16111	16112	100.0%	0.050	2	18344	18356	99.9%	0.356	2	6211	6223	99.8%	0.496
SNP269	Ots_10728593	2	16111	16112	100.0%	0.047	2	18350	18356	100.0%	0.121	2	6213	6223	99.8%	0.374

SNP269	Ots_crRAD1849265	2	16060	16112	99.7%	0.044	2	18301	18356	99.7%	0.122	2	6180	6223	99.3%	0.505
SNP269	Ots_107607315	2	16111	16112	100.0%	0.043	2	18354	18356	100.0%	0.204	2	6213	6223	99.8%	0.457
SNP269	Ots_PGK54	2	16110	16112	100.0%	0.042	2	18335	18356	99.9%	0.483	2	6220	6223	100.0%	0.261
SNP269	Ots_129144472	2	16110	16112	100.0%	0.042	2	18341	18356	99.9%	0.455	2	6220	6223	100.0%	0.352
SNP269	Ots_crRAD2111524	2	16082	16112	99.8%	0.041	2	18340	18356	99.9%	0.143	2	6217	6223	99.9%	0.326
SNP269	Ots_12723662	2	16102	16112	99.9%	0.040	2	18275	18356	99.6%	0.486	2	6208	6223	99.8%	0.309
SNP269	Ots_106313729	2	16107	16112	100.0%	0.039	2	17852	18356	97.3%	0.302	2	5851	6223	94.0%	0.404
SNP269	Ots_crRAD4608156	2	16109	16112	100.0%	0.038	2	18151	18356	98.9%	0.410	2	6219	6223	99.9%	0.240
SNP269	Ots_102867609	2	16112	16112	100.0%	0.035	2	18346	18356	99.9%	0.293	2	6223	6223	100.0%	0.101
SNP269	Ots_crRAD3615244	2	15092	16112	93.7%	0.033	2	17652	18356	96.2%	0.324	2	6064	6223	97.4%	0.407
SNP269	Ots_arp436	2	16000	16112	99.3%	0.030	2	17180	18356	93.6%	0.480	2	5956	6223	95.7%	0.322
SNP269	Ots_u1007124	2	16112	16112	100.0%	0.030	2	18346	18356	99.9%	0.301	2	6223	6223	100.0%	0.159
SNP269	Ots_12987055	2	16084	16112	99.8%	0.029	2	18298	18356	99.7%	0.282	2	6186	6223	99.4%	0.381
SNP269	Ots_afmid196	2	15973	16112	99.1%	0.028	2	17319	18356	94.4%	0.294	2	5967	6223	95.9%	0.201
SNP269	Ots_crRAD3439733	2	16107	16112	100.0%	0.025	2	17388	18356	94.7%	0.371	2	5879	6223	94.5%	0.473
SNP269	Ots_12241456	2	16112	16112	100.0%	0.025	2	18340	18356	99.9%	0.350	2	6212	6223	99.8%	0.485
SNP269	Ots_105401325	2	13445	16112	83.4%	0.022	2	18318	18356	99.8%	0.306	2	6210	6223	99.8%	0.392
SNP269	Ots_nelfd163	2	16111	16112	100.0%	0.021	2	18334	18356	99.9%	0.455	2	6217	6223	99.9%	0.311
SNP269	Ots_aspat196	2	16108	16112	100.0%	0.021	2	18346	18356	99.9%	0.248	2	6218	6223	99.9%	0.121
SNP269	Ots_123048521	2	16112	16112	100.0%	0.020	2	18351	18356	100.0%	0.265	2	6223	6223	100.0%	0.178
SNP269	Ots_OTSMASNP1	2	16111	16112	100.0%	0.017	2	18345	18356	99.9%	0.256	2	6220	6223	100.0%	0.311
SNP269	Ots_GST207	2	16112	16112	100.0%	0.015	2	18346	18356	99.9%	0.237	2	6216	6223	99.9%	0.171
SNP269	Ots_RFC2558	2	16111	16112	100.0%	0.014	2	18332	18356	99.9%	0.494	2	6213	6223	99.8%	0.503
SNP269	Ots_101119381	2	16112	16112	100.0%	0.008	2	18338	18356	99.9%	0.125	2	6217	6223	99.9%	0.130
SNP269	Ots_117370471	2	16110	16112	100.0%	0.007	2	18298	18356	99.7%	0.139	2	6212	6223	99.8%	0.142
SNP269	Ots_108390329	2	16112	16112	100.0%	0.006	2	18345	18356	99.9%	0.308	2	6216	6223	99.9%	0.313
SNP269	Ots_12830257	2	16057	16112	99.7%	0.086	2	18302	18356	99.7%	0.331	2	6210	6223	99.8%	0.015
SNP269	Ots_crRAD1372551	2	16111	16112	100.0%	0.085	2	18338	18356	99.9%	0.264	2	6222	6223	100.0%	0.076
SNP269	Ots_EP529	2	16111	16112	100.0%	0.067	2	18353	18356	100.0%	0.230	2	6222	6223	100.0%	0.094
SNP269	Ots_crRAD4845974	2	15079	16112	93.6%	0.066	2	15771	18356	85.9%	0.396	2	6219	6223	99.9%	0.032
SNP269	Ots_crRAD1893760	2	16093	16112	99.9%	0.052	2	18257	18356	99.5%	0.259	2	6223	6223	100.0%	0.010
SNP269	Ots_129170683	2	13275	16112	82.4%	0.044	2	17128	18356	93.3%	0.168	2	6040	6223	97.1%	0.088

SNP269	Ots_trnaulap86	2	16110	16112	100.0%	0.043	2	18312	18356	99.8%	0.235	2	6222	6223	100.0%	0.072
SNP269	Ots_slc7a271	2	16111	16112	100.0%	0.024	2	18347	18356	100.0%	0.218	2	6223	6223	100.0%	0.041
SNP269	Ots_Cath_D141	2	16089	16112	99.9%	0.024	2	18254	18356	99.4%	0.114	2	6220	6223	100.0%	0.003
SNP269	Ots_131802393	2	16112	16112	100.0%	0.006	2	18302	18356	99.7%	0.184	2	6222	6223	100.0%	0.016
SNP269	Ots_CRB211	2	16112	16112	100.0%	0.005	2	18355	18356	100.0%	0.149	2	6219	6223	99.9%	0.076
SNP269	Ots_crRAD2616569	2	16112	16112	100.0%	0.004	2	18330	18356	99.9%	0.270	2	6221	6223	100.0%	0.005
SNP269	Ots_102213210	2	16038	16112	99.5%	0.002	2	18275	18356	99.6%	0.221	2	6217	6223	99.9%	0.093
SNP269	Ots_crRAD6061446	2	16111	16112	100.0%	0.001	2	18339	18356	99.9%	0.267	2	6223	6223	100.0%	0.053
SNP269	Ots_stk6516	2	16112	16112	100.0%	0.001	2	18355	18356	100.0%	0.104	2	6223	6223	100.0%	0.001
SNP269	Ots_FARSLA220	2	16110	16112	100.0%	0.066	2	18355	18356	100.0%	0.033	2	6217	6223	99.9%	0.262
SNP269	Ots_crRAD1828933	2	16102	16112	99.9%	0.035	2	18348	18356	100.0%	0.071	2	6219	6223	99.9%	0.119
SNP269	Ots_nramp321	2	16076	16112	99.8%	0.034	2	18311	18356	99.8%	0.034	2	6223	6223	100.0%	0.167
SNP269	Ots_crRAD7896846	2	16112	16112	100.0%	0.026	2	18353	18356	100.0%	0.089	2	6216	6223	99.9%	0.353
SNP269	Ots_MetA	2	16052	16112	99.6%	0.019	2	9736	18356	53.0%	0.085	2	5665	6223	91.0%	0.209
SNP269	Ots_BMP2SNP1	2	16112	16112	100.0%	0.001	2	18356	18356	100.0%	0.084	2	6222	6223	100.0%	0.104
SNP269	Ots_u0720332	2	15880	16112	98.6%	0.001	2	18324	18356	99.8%	0.079	2	6185	6223	99.4%	0.274
SNP269	Ots_GST375	2	16112	16112	100.0%	0.001	2	18356	18356	100.0%	0.022	2	6223	6223	100.0%	0.114
SNP269	Ots_LWSop638	2	16112	16112	100.0%	0.000	2	18355	18356	100.0%	0.010	2	6221	6223	100.0%	0.177
	Ots_111312435	2	16076	16112	99.8%	0.087	2	18204	18356	99.2%	0.046	2	4969	6223	79.8%	0.003
	Ots_GH2	2	16105	16112	100.0%	0.083	2	18356	18356	100.0%	0.003	2	6223	6223	100.0%	0.000
	Ots_MHC1	2	15593	16112	96.8%	0.077	2	15701	18356	85.5%	0.040	2	4695	6223	75.4%	0.000
	Ots_zn593346	2	16112	16112	100.0%	0.056	2	18356	18356	100.0%	0.002	1	6223	6223	100.0%	0.000
	Ots_GnRH271	2	16047	16112	99.6%	0.036	2	18336	18356	99.9%	0.006	1	6211	6223	99.8%	0.000
	Ots_105897124	2	15939	16112	98.9%	0.010	2	18296	18356	99.7%	0.031	2	6220	6223	100.0%	0.001
	Ots_GPDH338	2	15146	16112	94.0%	0.004	2	17285	18356	94.2%	0.040	2	6161	6223	99.0%	0.002
	Ots_98683796	2	16112	16112	100.0%	0.003	2	18354	18356	100.0%	0.010	2	6223	6223	100.0%	0.031
	Ots_crRAD1271137	2	16112	16112	100.0%	0.002	2	18355	18356	100.0%	0.053	2	6223	6223	100.0%	0.027
	Ots_crRAD375851	2	16104	16112	100.0%	0.001	2	18125	18356	98.7%	0.047	2	6193	6223	99.5%	0.035
	Ots_TNF	2	16112	16112	100.0%	0.001	2	18355	18356	100.0%	0.044	2	6223	6223	100.0%	0.016
	Ots_CCR7	2	16112	16112	100.0%	0.001	2	18356	18356	100.0%	0.009	2	6223	6223	100.0%	0.093
	Ots_u0764221	1	16112	16112	100.0%	0.000	2	18356	18356	100.0%	0.023	1	6223	6223	100.0%	0.000
	Ots_Myc366	2	16112	16112	100.0%	0.000	2	18351	18356	100.0%	0.016	1	6223	6223	100.0%	0.000

Ots_10177082	1	16112	16112	100.0%	0.000	2	18353	18356	100.0%	0.011	1	6223	6223	100.0%	0.000
Ots_u0719260	1	16111	16112	100.0%	0.000	2	18353	18356	100.0%	0.007	2	6223	6223	100.0%	0.014
Ots_RAS1	2	15990	16112	99.2%	0.000	2	18262	18356	99.5%	0.002	2	6221	6223	100.0%	0.038
Ots_zP3b215	1	16106	16112	100.0%	0.000	1	18353	18356	100.0%	0.000	1	6223	6223	100.0%	0.000
Ots_SERPC1209	1	16099	16112	99.9%	0.000	1	18351	18356	100.0%	0.000	1	6223	6223	100.0%	0.000
Ots_98409850	1	16112	16112	100.0%	0.000	2	18356	18356	100.0%	0.000	1	6223	6223	100.0%	0.000
Ots_Chin30up211	1	16084	16112	99.8%	0.000	1	18304	18356	99.7%	0.000	1	6222	6223	100.0%	0.000
Ots_crRAD2363148	1	16112	16112	100.0%	0.000	1	18323	18356	99.8%	0.000	1	6223	6223	100.0%	0.000
Ots_crRAD2608128	1	16112	16112	100.0%	0.000	1	18356	18356	100.0%	0.000	1	6223	6223	100.0%	0.000
Ots_crRAD29221	1	16081	16112	99.8%	0.000	1	18300	18356	99.7%	0.000	1	5974	6223	96.0%	0.000
Ots_crRAD3809529	1	16089	16112	99.9%	0.000	1	18356	18356	100.0%	0.000	1	6223	6223	100.0%	0.000
Ots_crRAD3874636	1	16107	16112	100.0%	0.000	1	18355	18356	100.0%	0.000	1	6223	6223	100.0%	0.000
Ots_LEI292	1	16112	16112	100.0%	0.000	2	18356	18356	100.0%	0.000	1	6223	6223	100.0%	0.000
Ots_u1004117	1	16112	16112	100.0%	0.000	1	18356	18356	100.0%	0.000	1	6223	6223	100.0%	0.000
Ots_u1006171	1	16102	16112	99.9%	0.000	1	18349	18356	100.0%	0.000	1	6223	6223	100.0%	0.000
Ots_USMG567	1	16112	16112	100.0%	0.000	1	18356	18356	100.0%	0.000	1	6223	6223	100.0%	0.000

Note: The loci are sorted by their order in the original panel of 93SNPs used for PBT applications, and “SNP269” indicates the group of 269 SNPs that were observed with a heterozygosity >10% for at least one of the major genetic lineages based on hatchery broodstock of spawn year 2015. For each lineage (Stream-type , Ocean-type, and Lower Columbia tule), we provide information on how many alleles (k) were observed across broodstock,, the number (N) and percentage (% success) of fish that were successfully genotyped, the total number of SY2015 broodstock adults that represent each lineage and were evaluated (Total N), and the observed Heterozygosity (H Obs.).

Accuracy testing of the PBT baseline

Chinook (93 SNPs)

To test the accuracy of the Chinook salmon PBT baseline (93 SNPs) in assigning known samples to their hatchery brood of origin, we selected six hatchery collections from 2016 and one hatchery collection from 2015, and converted them to unknown samples (Hasselman et al. 2018).

Table 13. Sample sizes and reporting groups of Chinook salmon baseline populations. Lineages: ST (stream type), OT (ocean type), LC (Lower Columbia).

ID	Collection	(n)	Lineage	Reporting Groups	Reporting Group description
OTS01	Youngs Bay fall-run	91	Rogue	01_YOUNGS	Youngs Bay- Columbia Rogue stock
OTS02	Cowlitz R spring-run	90	LC	02_WCASSP	West Cascade spring-run
OTS03	Kalama R spring-run	83	LC	02_WCASSP	West Cascade spring-run
OTS04	Cowlitz R fall-run	82	LC	03_WCASFA	West Cascade fall-run
OTS05	Elochoman R fall-run	86	LC	03_WCASFA	West Cascade fall-run
OTS06	Lewis R fall-run	93	LC	03_WCASFA	West Cascade fall-run
OTS07	NF Lewis fall-run	178	LC	03_WCASFA	West Cascade fall-run
OTS08	Sandy R fall-run	83	LC	03_WCASFA	West Cascade fall-run
OTS09	McKenzie R spring-run	78	LC	04_WILLAM	Willamette River spring-run
OTS10	N Santiam R spring-run	79	LC	04_WILLAM	Willamette River spring-run
OTS11	Sandy R spring-run	48	LC	04_WILLAM	Willamette River spring-run
OTS12	White Salmon fall-run	77	LC	05_SPCRTU	Spring Creek tule fall-run
OTS13	Spring Creek NFH tule fall-run	49	LC	05_SPCRTU	Spring Creek tule fall-run
OTS14	Klickitat R spring-run	84	ST	06_KLICKR	Klickitat River spring-run
OTS15	Shitike R spring-run	93	ST	07_DESCSP	Deschutes River spring-run
OTS16	Warm Springs R spring-run	90	ST	07_DESCSP	Deschutes River spring-run
OTS17	John Day R spring-run	78	ST	08_JOHNDR	John Day River spring-run
OTS18	Middle Fork John Day R spring-run	47	ST	08_JOHNDR	John Day River spring-run
OTS19	North Fork John Day R spring-run	42	ST	08_JOHNDR	John Day River spring-run
OTS20	American R spring-run	76	ST	09_YAKIMA	Yakima River spring-run
OTS21	Cle-Elum spring-run	88	ST	09_YAKIMA	Yakima River spring-run
OTS22	Winthrop NFH spring-run	82	ST	10_UCOLSP	upper Columbia River spring-run/ Carson Hatchery spring-run
OTS23	little White Salmon R spring-run	93	ST	10_UCOLSP	upper Columbia River spring-run/ Carson Hatchery spring-run
OTS24	Wenatchee R spring-run	109	ST	10_UCOLSP	upper Columbia River spring-run/ Carson Hatchery spring-run
OTS25	Entiat R spring-run	98	ST	10_UCOLSP	upper Columbia River spring-run/ Carson Hatchery spring-run
OTS26	Tucannon R spring-run	81	ST	11_TUCANO	Tucannon River spring-run
OTS27	Wenaha R spring-run	179	ST	12_HELLSC	Hells Canyon spring-run
OTS28	Lostine R spring-run	212	ST	12_HELLSC	Hells Canyon spring-run
OTS29	Grande Ronde R spring-run	314	ST	12_HELLSC	Hells Canyon spring-run
OTS30	Imnaha R spring-run	96	ST	12_HELLSC	Hells Canyon spring-run
OTS31	Lolo Cr spring-run	89	ST	12_HELLSC	Hells Canyon spring-run
OTS32	Red R spring-run	221	ST	12_HELLSC	Hells Canyon spring-run
OTS33	Powell R spring-run	56	ST	12_HELLSC	Hells Canyon spring-run
OTS34	Red R weir spring-run	91	ST	12_HELLSC	Hells Canyon spring-run
OTS35	South Forth Salmon R spring-run	139	ST	13_SFSALM	South Fork Salmon River spring/summer-run
OTS36	Johnson Cr spring-run	137	ST	13_SFSALM	South Fork Salmon River spring/summer-run
OTS37	Secesh R spring-run	252	ST	13_SFSALM	South Fork Salmon River spring/summer-run
OTS38	Chamberlain Cr spring-run	219	ST	14_CHMBLN	Chamberlain Creek spring/summer-run
OTS39	Big Cr spring-run	139	ST	15_MFSALM	Middle Fork Salmon River spring/summer-run
OTS40	Camas Cr spring-run	55	ST	15_MFSALM	Middle Fork Salmon River spring/summer-run
OTS41	Loon Cr spring-run	107	ST	15_MFSALM	Middle Fork Salmon River spring/summer-run
OTS42	Sulphur Cr spring-run	94	ST	15_MFSALM	Middle Fork Salmon River spring/summer-run
OTS43	Bear Valley Cr spring-run	135	ST	15_MFSALM	Middle Fork Salmon River spring/summer-run
OTS44	Capehorn Cr spring-run	214	ST	15_MFSALM	Middle Fork Salmon River spring/summer-run
OTS45	Marsh Cr spring-run	228	ST	15_MFSALM	Middle Fork Salmon River spring/summer-run
OTS46	North Fork Salmon R spring-run	55	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS47	Lemhi R spring-run	96	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS48	Pahsimeroi R spring-run	92	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS49	East Fork Salmon R spring-run	286	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS50	Salmon R spring-run	83	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS51	West Fork Yankee Fork spring-run	75	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS52	Valley Cr spring-run	100	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS53	Sawtooth Hatchery weir spring-run	186	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS54	upper Deschutes R fall-run	252	OT	17_DESCFA	Deschutes River fall-run
OTS55	lower Yakima R fall-run	62	OT	18_UCOLSF	upper Columbia River summer/fall-run
OTS56	Hanford Reach fall-run	93	OT	18_UCOLSF	upper Columbia River summer/fall-run
OTS57	Wenatchee R summer-run	92	OT	18_UCOLSF	upper Columbia River summer/fall-run

OTS58	Entiat R summer-run	51	OT	18_UCOLSF	upper Columbia River summer/fall-run
OTS59	Methow R summer-run	87	OT	18_UCOLSF	upper Columbia River summer/fall-run
OTS60	Lyons Ferry weir fall-run	90	OT	19_SRFALL	Snake River fall-run
OTS61	Clearwater R fall-run	228	OT	19_SRFALL	Snake River fall-run

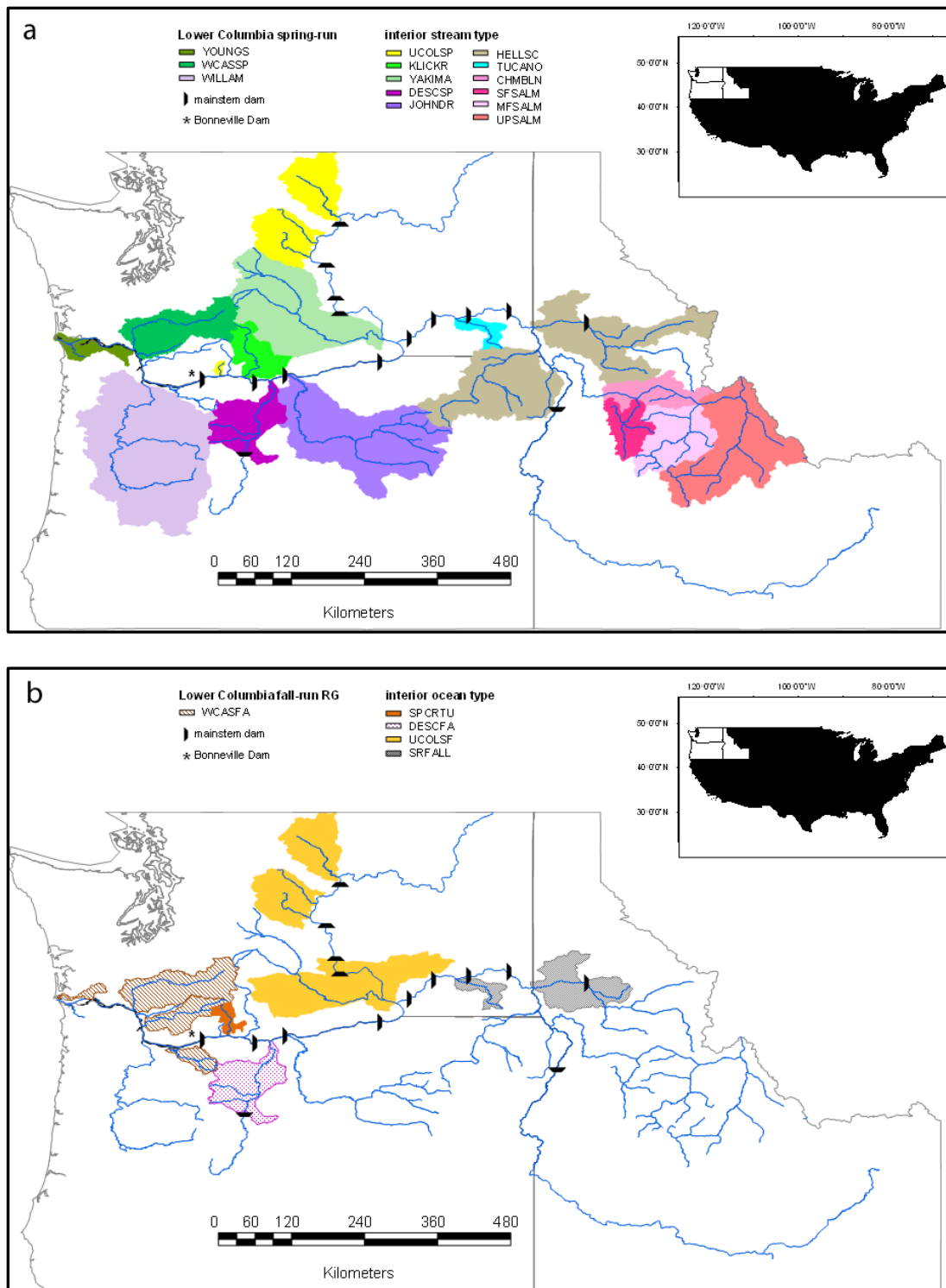


Figure 19. Map of Chinook salmon GSI reporting groups for a) Lower Columbia (LC) and interior stream type (ST) lineage, and b) interior ocean type (OT) lineage.

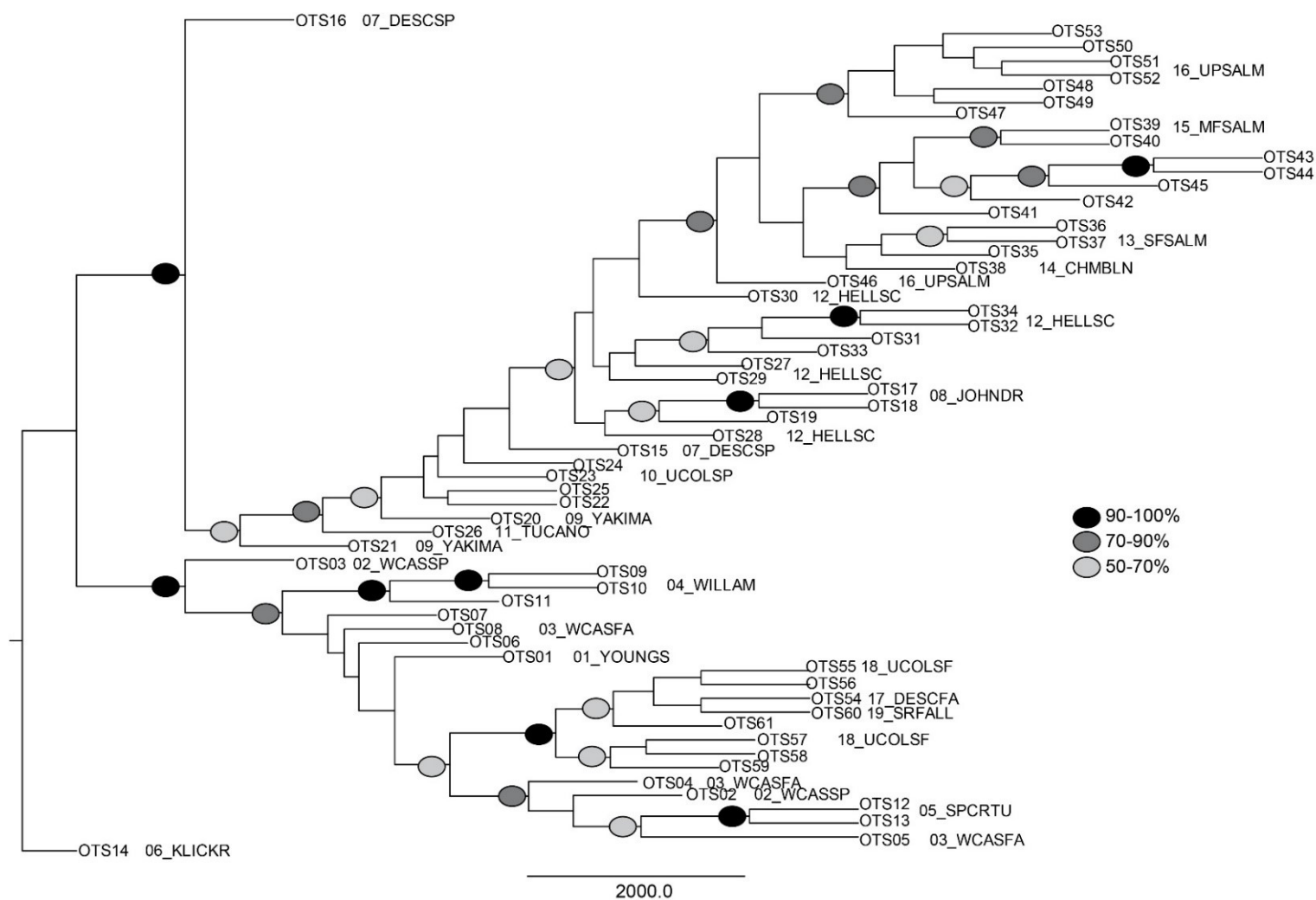


Figure 20. Neighbor-joining tree of Chinook salmon baseline populations using Nei's 1972 genetic distance of 179 SNP loci.

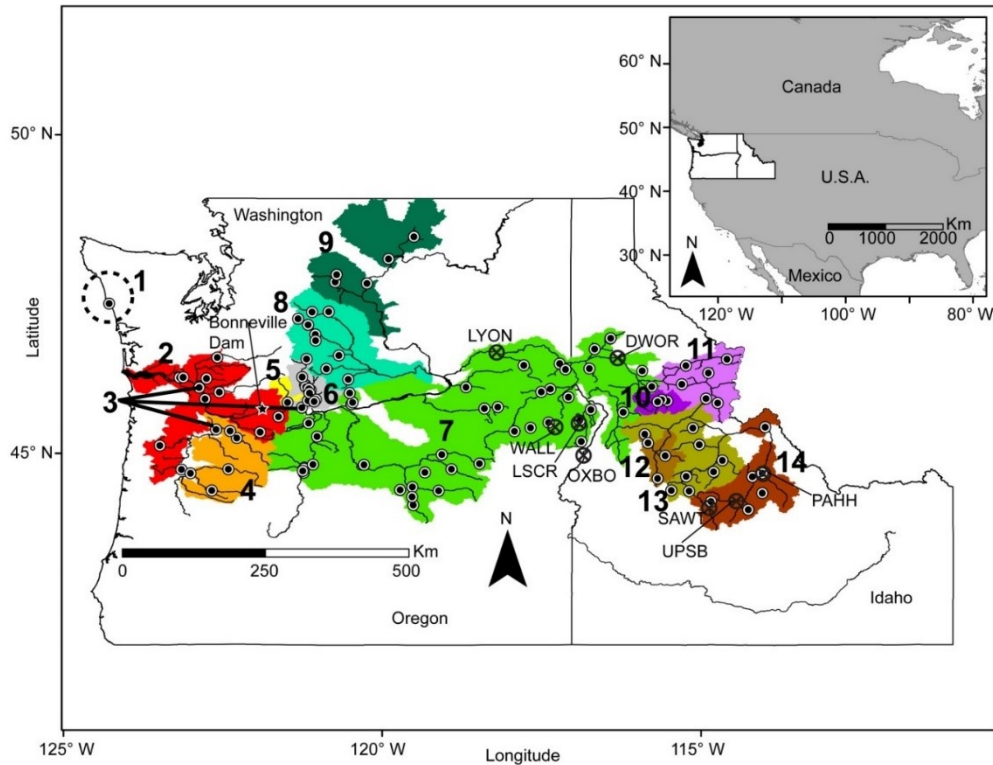


Figure 21. Geographic distribution of collections represented in the Columbia River steelhead GSI and PBT genetic baselines.

In Figure 21, the shape overlay represents the geographic extent of the following 14 reporting groups in the GSI baseline: 1) Quinault (WCOAST), 2) lower Columbia River (LOWCOL), 3) Skamania hatchery releases at three sites in lower Columbia River, Willamette River, and Klickitat River (SKAMAN), 4) Willamette River (WILLAM), 5) Big White Salmon River (BWSALM), 6) Klickitat River (KLICKR), 7) middle Columbia River, Grande Ronde River, Imnaha River, lower Snake River, lower Clearwater River, and lower Salmon River (MGILCS), 8) Yakima River (YAKIMA), 9) upper Columbia River (UPPCOL), 10) South Fork Clearwater River (SFCLWR), 11) upper Clearwater River (UPCLWR), 12) South Fork Salmon River (SFSALM), 13) Middle Fork Salmon River (MFSALM), and 14) upper Salmon River (UPSALM). There are 116 collections (filled circles) categorized into reporting groups. The PBT baseline is indicated as 8 stocks (crossed circles) corresponding to the following sites where fish are collected and spawned for broodstock: Lyons Ferry Hatchery (LYON), Wallowa (WALL), Little Sheep Creek (LSCR), Oxbow Hatchery (OXBO), Dworshak Hatchery (DWOR), upper Salmon River B-run (UPSB), Sawtooth Hatchery (SAWT), and Pahsimeroi Hatchery (PAHH). Bonneville Dam (star) is the site where fish were non-lethally sampled for the mixed-stock analysis.

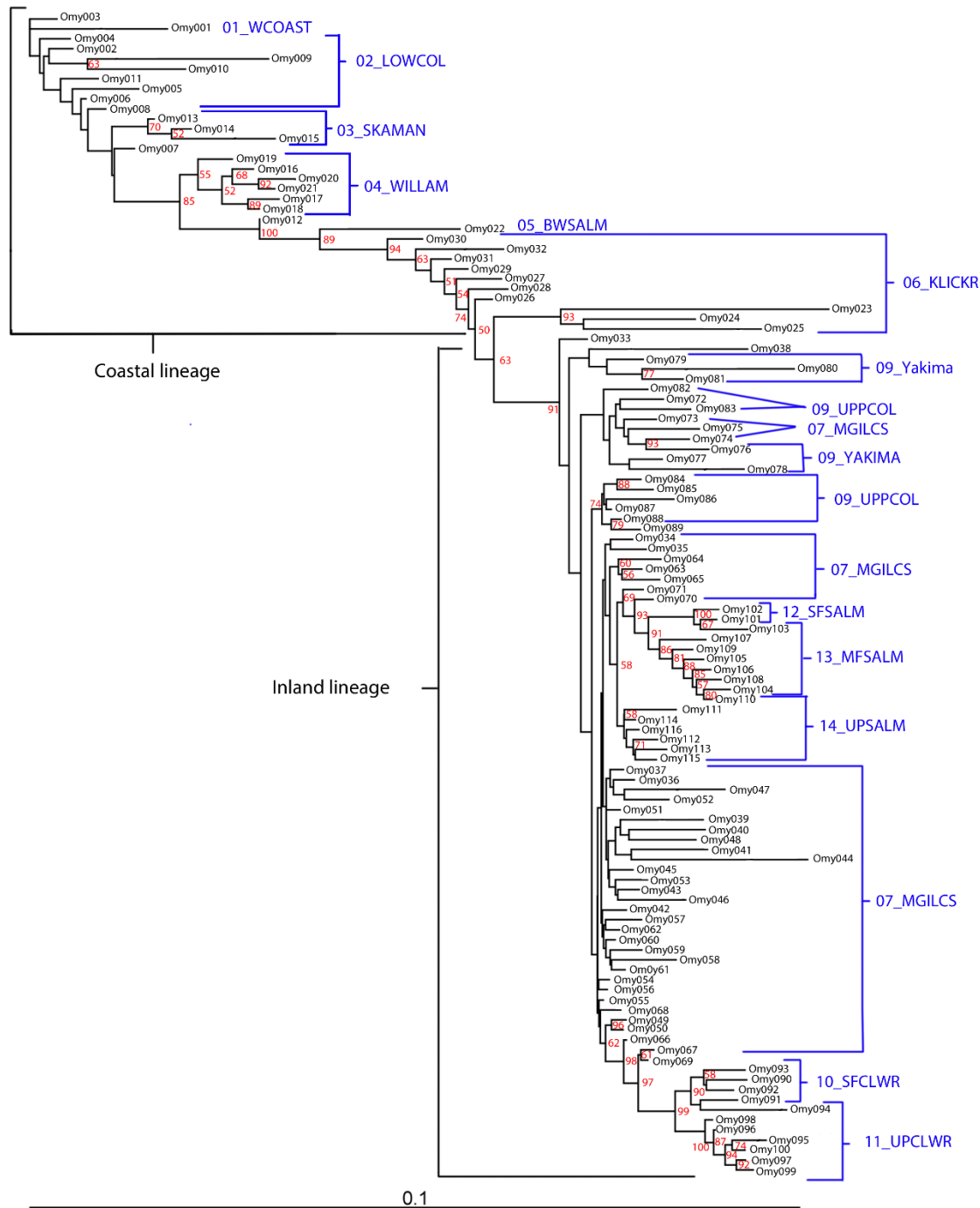


Figure 22. Neighbor-joining tree of steelhead baseline populations in GSI baseline v.3.3 (186 SNPs) using Nei's 1972 genetic distance.

In **Figure 22**, the bootstrap values (in red) $\geq 50\%$ (based on 1000 bootstraps) are shown and reporting group names (in blue) are provided and are clustered by lineage (i.e, coastal or inland).

Chinook (94 SNPs vs 298 SNPs)

We compared the PBT assignment accuracy of the 93 SNP and the 298 SNP panels using the 2016 broodstock collections for the Lyons Ferry and Nez Perce programs (Hasselman et al. 2018). The 298 SNP panel did appear to assign additional fall Chinook salmon via PBT, and provide greater confidence in PBT assignment over the 94 SNP panel, as reflected in higher LOD-scores and lower FDR values. This test will need to be repeated on collections from the interior stream type lineage as the 298 SNP panel is genotyped for additional programs in the future.

Steelhead (95 SNPs)

To test the accuracy of the steelhead PBT baseline (95 SNPs) in assigning known samples to their hatchery brood of origin, we selected five hatchery collections from 2016 and converted them to unknown samples (Hasselman et al. 2018).

Steelhead (95 SNPs vs 186 SNPs)

We compared the PBT assignment accuracy of the 95 SNP and the 186 SNP panels using the 2016 broodstock collections for the Umatilla, Winthrop and Parkdale programs (Hasselman et al. 2018). The 186 SNP panel did appear to provide greater confidence in PBT assignment over the 95 SNP panel, as reflected in higher LOD-scores, but this test will need to be repeated as the 186 SNP panel is genotyped for additional programs in the future.

Accuracy testing of the GSI baseline

To test the accuracy of the GSI baselines for Chinook salmon and steelhead, we conducted the self-assignment procedure implemented in GeneClass v.2.0 (Piry et al. 2004) using the ‘leave-one-out’ approach and the Bayesian resampling procedure of Rannala and Mountain (1997) to evaluate how well individuals could be assigned to their population and reporting group of origin. We examined the proportion of self-assignments for all individuals, but also examined how implementing a self-assignment probability threshold of ≥ 0.80 influenced overall self-assignments to reporting group of origin.

Chinook (179 SNPs)

For Chinook salmon, we used GSI baseline v3.1 that comprises 61 collections from throughout the Columbia River basin that are partitioned into 19 reporting groups (N=7083) (Figure 19). When considering the assignment of all individuals in the GSI baseline, 5820 (82%) of the 7083 individuals correctly assigned to their reporting group of origin (Table 14). Across all reporting groups, the proportion of correct assignments ranged from 0.52 (08_JOHNDR) to 1.0 (01_YOUNGS) (Figure 23a). Employing a self-assignment probability threshold of ≥ 0.80 reduced the number of fish assigned to 3000 individuals, but increased the proportion of correct assignments to 0.94 (n=2808). When implementing this threshold, the proportion of correct assignments across all reporting groups ranged from 0.79 (12_HELLSC) to 1.0 (01_YOUNGS, 04_WILLAM, 07_DECSP)(Figure 23b).

The highest proportion of correct assignments when considering all individuals was observed for Lower Columbia (LC) lineage reporting groups, and ranged from 0.83 (02_WCASSP) to 1.0 (01_YOUNGS) (Table 14; Figure 23a). Incorrect assignments for LC lineage populations were typically to other reporting groups within this lineage with the most common incorrect assignments to reporting groups that included collections from the same river (i.e., Cowlitz spring and fall run). However, six individuals were incorrectly assigned to the Interior Ocean Type (OT) lineage (18_UCOLSF; 19_SRFALL), and 12 individuals were assigned incorrectly to the Interior Stream Type (ST) lineage (06_KLICKR; 09_YAKIMA) (Table 14). Incorrect assignments to the 06_KLICKR reporting group are likely due introgression that has occurred between lineages in the Klickitat sub-basin (Hess et al. 2014).

The proportion of correct assignments for OT lineage reporting groups ranged from 0.74 (19_SRFALL) to 0.90 (17_DESCFA) (Table 14; Figure 23a). Incorrect assignments for OT lineage populations when considering all individuals were typically to other reporting groups within this lineage, or to LC lineage reporting groups (i.e., OTS54 – Upper Deschutes River fall run to 01_YOUNGS, 02_WCASSP, 03_WCASFA, and 04_WILLAM, and OTS55 Lower Yakima River fall run to 02_WCASSP). A single individual from OTS57 – Wenatchee River summer run incorrectly assigned to 06_KLICKR, and one individuals from OTS59 – Methow River summer run incorrectly assigned to 02_WCASSP (Table 14). These types of incorrect assignments were not as common as those to reporting group of the same run type.

The proportion of correct assignments for ST lineage reporting groups ranged from 0.52 (08_JOHNDR) to 0.94 (09_YAKIMA) (Table 14; Figure 23a). Incorrect assignments were typically to other reporting groups within this lineage. However, we did observe instances where ST lineage samples were assigned incorrectly to a LC lineage reporting group (i.e., OTS17 – John Day River spring run to 02_WCASSP; OTS26 – Tucannon River spring run to 02_WCASSP; OTS27 – Wenaha River spring run to 01_YOUNGS and 02_WCASSP; OTS28 – Lostine River spring run to 01_YOUNGS) (Table 14).

Table 14. Results of the leave-one-out analysis for the Chinook salmon GSI v3.1 baseline. Lineage, run type, reporting group, population ID, population name and samples size used in analysis are provided for each collection in the baseline. The number of correct assignments to reporting group for each population in the baseline are reported (gray shading) and are tallied to provide the number of correct assignments for the reporting group overall (yellow shading). The proportion of correct assignments to reporting group for each population and reporting group (yellow shading) in the baseline is provided.

Lineage	Run type	RepGrp	PopI D	Pop Name	N	Number assigned to reporting group																		Proportion assigned correct			
						01_YOUNG S	02_WCASS P	03_WCASF A	04_WILLA M	05_SPCRT U	06_KLICK R	07_DESCS P	08_JOHND R	09_YAKIM A	10_UCOLS P	11_TUCAN O	12_HELLS C	13_SFSAL M	14_CHMBL N	15_MFSAL M	16_UPSAL M	17_DESCF A	18_UCOLS F		19_SRFAL L		
Lower Columbi a	Spring	01_YOUNG S	OTS0 1	Youngs Bay fall-run	91	91																		1.0000			
			Reporting Group total			91	91	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.0000		
Lower Columbi a	Spring	02_WCASS P	OTS0 2	Cowlitz R spring-run	90		80	9		1														0.8889			
			OTS0 3	Kalama R spring-run	83		63	2	6		11			1											0.7590		
			Reporting Group total			173	0	143	11	6	1	11	0	0	1	0	0	0	0	0	0	0	0	0	0.8266		
Lower Columbi a	Fall	03_WCASF A	OTS0 4	Cowlitz R fall-run	82		8	73	1															0.8902			
			OTS0 5	Elochoman R fall-run	86	8	1	61		15												1		0.7093			
			OTS0 6	Lewis R fall-run	93		2	91																	0.9785		
			OTS0 7	NF Lewis fall-run	178			178																	1.0000		
			OTS0 8	Sandy R fall-run	83			79	1													3			0.9518		
			Reporting Group total			522	8	11	482	2	15	0	0	0	0	0	0	0	0	0	0	0	4	0	0.9234		
Lower Columbi a	Spring	04_WILLA M	OTS0 9	McKenzie R spring-run	78				78															1.0000			
			OTS1 0	N Santiam R spring-run	79				79																1.0000		
			OTS1 1	Sandy R spring-run	48		1	4	43																0.8958		
			Reporting Group total			205	0	1	4	200	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.9756		
Lower Columbi a	Fall	05_SPCRT U	OTS1 2	White Salmon fall-run	77			2		75														0.9740			
			OTS1 3	Spring Creek NFH tule fall-run	49					47													2		0.9592		
			Reporting Group total			126	0	0	2	0	122	0	0	0	0	0	0	0	0	0	0	0	0	2	0.9683		
Interior stream type	Spring	06_KLICKR	OTS1 4	Klickitat R spring-run	84						76			5	1		2							0.9048			
					Reporting Group total			84	0	0	0	0	76	0	0	5	1	0	2	0	0	0	0	0.9048			
Interior stream type	Spring	07_DESCSP	OTS1 5	Shitike R spring-run	93					1	80	1			6		1	2		1	1				0.8602		
			OTS1 6	Warm Springs R spring-run	90						88				1		1									0.9778	
					Reporting Group total			183	0	0	0	0	0	1	168	1	0	7	0	2	2	0	1	1	0	0	0.9180
Interior stream type	Spring	08_JOHND R	OTS1 7	John Day R spring-run	78		1					42	3	5		20	2		1	4					0.5385		
			OTS1 8	Middle Fork John Day R spring-run	47						1	32			1		12	1								0.6809	
			OTS1 9	North Fork John Day R spring-run	42								12		1	8	1	12	5		3					0.2857	
			Reporting Group total			167	0	1	0	0	0	0	1	86	4	14	1	44	8	0	4	4	0	0	0	0.5150	
Interior stream type	Spring	09_YAKIM A	OTS2 0	American R spring-run	76								76												1.0000		
			OTS2 1	Cle-Elum spring-run	88								1	78	3	2	3			1						0.8864	
			Reporting Group total			164	0	0	0	0	0	0	0	1	154	3	2	3	0	0	1	0	0	0	0	0.9390	
Interior stream type	Spring	10_UCOLS P	OTS2 2	Winthrop NFH spring-run	82							6			55		11	4		2	4				0.6707		
			OTS2 3	little White Salmon R spring-run	93						1	2				74		9	3			4				0.7957	
			OTS2 4	Wenatchee R spring-run	109											85		14	3		2	5				0.7798	
			OTS2 5	Entiat R spring-run	98					1			5	2		64	1	16	1		2	6				0.6531	
			Reporting Group total			382	0	0	0	0	0	1	1	13	2	278	1	50	11	0	6	19	0	0	0	0.7277	
Interior stream type	Spring	11_TUCAN O	OTS2 6	Tucannon R spring-run	81		1						2	2	65	9	1		1						0.8025		
			Reporting Group total			81	0	1	0	0	0	0	0	2	2	65	9	1	0	1	0	0	0	0	0.8025		
Interior stream type	Spring	12_HELLS C	OTS2 7	Wenaha R spring-run	179	3	1				5	1	17	2	14	4	121	5		1	5				0.6760		
			OTS2 8	Lostine R spring-run	213	1							19	2	5	1	171	3		4	7					0.8028	
			OTS2 9	Grande Ronde R spring-run	313						4	2	33	2	26	2	207	11		10	16					0.6613	
			OTS3 0	Imnaha R spring-run	96							1	1			3		69	5		6	11				0.7188	
			OTS3 1	Lolo Cr spring-run	89								4			14	1	58	3	1	1	7				0.6517	
			OTS3 2	Red R spring-run	221					1	1	9				22		161	4		6	17				0.7285	
			OTS3 3	Powell R spring-run	56								1			12		35	1		4	3				0.6250	
			OTS3 4	Red R weir spring-run	91											1		84	2		1	3				0.9231	
			Reporting Group total			1258	4	1	0	0	0	10	5	84	6	97	8	906	34	1	33	69	0	0	0	0.7202	
Interior stream type	Spring	13_SFSAL M	OTS3 5	South Forth Salmon R spring-run	139							4		4		16	74	3	16	22				0.5324			
			OTS3 6	Johnson Cr spring-run	137						1					6	106	1	12	11					0.7737		
			OTS3 7	Secesh R spring-run	252								1		6		13	208	1	16	7					0.8254	
			Reporting Group total			528	0	0	0	0	0	0	1	5	0	10	0	35	388	5	44	40	0	0	0	0.7348	
Interior stream type	Spring	14_CHMBL N	OTS3 8	Chamberlain Cr spring-run	219							1		1		12	5	188	5	6					0.8584		
			Reporting Group total			219	0	0	0	0	0	0	0	1	0	1	0	12	5	188	5	6	0	0	0	0.8584	
Interior stream type	Spring	15_MFSAL M	OTS3 9	Big Cr spring-run	139							3					13	5	2	105	11				0.7554		
			OTS4 0	Camas Cr spring-run	55												2	1	3	48	1					0.8727	
			OTS4 1	Loon Cr spring-run	107							1	1			1		4	4	2	93	1				0.8692	
			OTS4 2	Sulphur Cr spring-run	94								1			1		3	2		80	7				0.8511	
			OTS4 3	Bear Valley Cr spring-run	135												1	1		128	5					0.9481	
			OTS4 4	Capehorn Cr spring-run	214								1			2		6	10	2	189	4				0.8832	
			OTS4 5	Marsh Cr spring-run	228								2			3		3	11		196	13				0.8596	
			Reporting Group total			972	0	0	0	0	0	0	1	8	0	7	0	32	34	9	839	42	0	0	0	0.8632	
Interior stream type	Spring/Summer	16_UPSAL M	OTS4 6	North Fork Salmon R spring-run	55									1		7	1		2	44					0.8000		
			OTS4 7	Lemhi R spring-run	96								1				7	4		8	76				0.7917		
			OTS4 8	Pahsimeroi R spring-run	92										1		1	6		3							

			OTS5 1	West Fork Yankee Fork spring-run	75							1					1		1	72				0.9600
			OTS5 2	Valley Cr spring-run	100							1	7				1	1	3	87				0.8700
			OTS5 3	Sawtooth Hatchery weir spring-run	186							1		1		10	13	1	15	146				0.7849
			Reporting Group total		973	0	0	0	0	0	0	4	7	8	0	36	33	2	52	832	0	0	0	0.8551
Interior ocean type	Fall	17_DESCF A	OTS5 4	upper Deschutes R fall-run	252	4	1	2	1												227	10	7	0.9008
			Reporting Group total		252	4	1	2	1	0	0	0	0	0	0	0	0	0	0	0	227	10	7	0.9008
Interior ocean type	Summer/Fall	18_UCOLS F	OTS5 5	lower Yakima R fall-run	62		1														1	44	16	0.7097
			OTS5 6	Hanford Reach fall-run	93																	76	17	0.8172
			OTS5 7	Wenatchee R summer-run	92					1												87	4	0.9457
			OTS5 8	Entiat R summer-run	51																	50	1	0.9804
			OTS5 9	Methow R summer-run	87		1															82	4	0.9425
			Reporting Group total		385	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	1	339	42	0.8805
			OTS6 0	Lyons Ferry weir fall-run	90																1	13	76	0.8444
Interior ocean type	Fall	19_SRFALL	OTS6 1	Clearwater R fall-run	228																7	61	160	0.7018
			Reporting Group total		318	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	74	236	0.7421

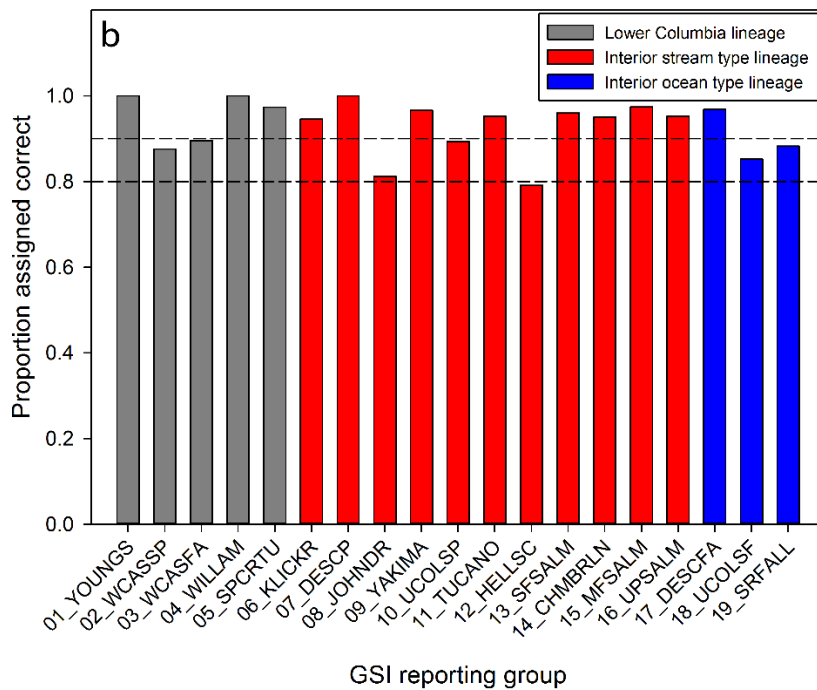
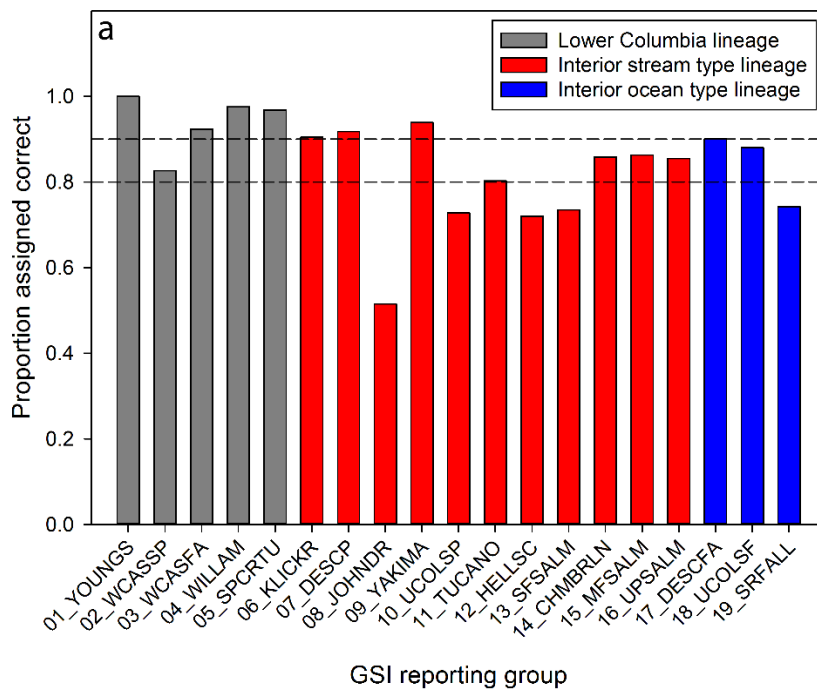


Figure 23. Proportion of Chinook salmon in leave-one-out tests that assigned correctly for each reporting group by lineage using a) all data, and b) $\geq 80\%$ self-assignment probability threshold. The dashed lines indicate 80% and 90% thresholds for correct assignment.

Steelhead (180 SNPs)

For steelhead, we used GSI baseline v3.3 that comprises 116 collections from throughout the Columbia River basin that are partitioned into 14 reporting groups (N= 9991) (Figure 21). When considering the assignment of all individuals in the GSI baseline, 8364 (84%) of the 9991 individuals correctly assigned to their reporting group of origin (Table 15). Across all reporting groups, the proportion of correct assignments ranged from 0.55 (09_UPPCOL) to 0.99 (01_WCOAST) (Figure 24a). Employing a self-assignment probability threshold of ≥ 0.80 reduced the number of fish assigned to 3989 individuals, but increased the proportion of correct assignments to 0.94 (n=3758). When implementing this threshold, the proportion of correct assignments across all reporting groups ranged 0.77 (09_UPPCOL) to 1.00 (01_WCOAST) (Figure 24b). When considering all individuals, the proportion of correct assignments for most reporting groups was >0.80 ; the two exceptions being 09_UPPCOL (0.55) and 14_UPSALM (0.66) (Table 15; Figure 24a) with the majority of incorrect assignments to the 07_MGILCS reporting group. The proportion of correct assignments for inland lineage reporting groups ranged from 0.55 (09_UPPCOL) to 0.93 (11_UPCLWR) (Table 15). These results support the inclusion of a hierarchical approach to improve stock ID results by resolving assignment to the MGILCS reporting group with more markers as discussed in Section 2.

We detected samples (n=28, 1.5%) from the coastal lineage (i.e., 01_WCOAST – 06_KLICKR reporting groups) that were incorrectly assigned to reporting groups of the inland lineage (i.e., 07_MGILCS – 14_UPSALM reporting groups (Table 15). We similarly detected samples (n=29, 0.34%) from reporting groups from the inland lineage were incorrectly assigned to coastal lineage reporting groups (Table 15). Incorrect assignments were typically distributed across multiple reporting groups, but the largest proportion of incorrect assignments were consistently to three reporting groups (07_MGILCS, 06_KLICKR, and 05_BWSALM). Samples from the geographically large 07_MGILCS reporting group were incorrectly assigned to every reporting group except 01_WCOAST, 03_SKAMAN, and 04_WILLAM (Table 15).

Table 15. Results of the leave-one-out analysis for the steelhead GSI v3.3 baseline. Reporting group, population ID, population name and samples size used in analysis are provided for each collection in the baseline. The number of correct assignments to reporting group for each population in the baseline are reported (gray shading) and are tallied to provide the number of correct assignments for the reporting group overall (yellow shading). The proportion of correct assignments to reporting group for each population and reporting group (yellow shading) in the baseline is provided.

Lineage	Reporting Group	PopID	Pop Name	N	Number assigned to reporting group														Proportion assigned correct
					01_WCOAST	02_LOWCOL	03_SKAMAN	04_WILLAM	05_BWSALM	06_KLICKR	07_MGILCS	08_YAKIMA	09_UPPCOL	10_SFCLWR	11_UPCLWR	12_SFSALM	13_MFSALM	14_UPSALM	
Coastal	01_WCOAST	OMY001	Quinalt River	89	88	1													0.989
		Reporting Group total		89	88	1	0	0	0	0	0	0	0	0	0	0	0	0	0.989
Coastal	02_LOWCOL	OMY002	Mill Creek	43	3	40													0.930
		OMY003	Germany Creek	47	1	43	1	2											0.915
		OMY004	Coweeaman River	45		42	3												0.933
		OMY005	Cowliltz River	94		93	1												0.989
		OMY006	Kalama River - winter run	94		80	12	1			1								0.851
		OMY007	East Fork Lewis River	77		57	14	5						1					0.740
		OMY008	North Fork Lewis River	94	1	88	2	2	1										0.936
		OMY009	Luckiamute River	26		25		1											0.962
		OMY010	Willamina Creek	30		27		3											0.900
		OMY011	Still Creek	28		20	4	4											0.714
		OMY012	East Fork Hood River	52		33	1	6		12									0.635
		Reporting Group total		630	5	548	38	24	1	12	1	0	0	1	0	0	0	0	0.870
Coastal	03_SKAMAN	OMY013	Kalama River - summer run	94	1	29	64												0.681
		OMY014	Clackamas River - summer run	59		3	55	1											0.932
		OMY015	Klickitat-Skamanian - summer run	249			249												1.000
		Reporting Group total		402	1	32	368	1	0	0	0	0	0	0	0	0	0	0	0.915
Coastal	04_WILLAM	OMY016	Clackamas River - winter run	92		3	3	84		1	1								0.913
		OMY017	North Fork Eagle River	43		9		34											0.791
		OMY018	Eagle River	47		7		40											0.851
		OMY019	Little Rock/Mad River	50		1	7	41	1										0.820
		OMY020	North Fork Santiam River	39		1		38											0.974
		OMY021	South Fork Santiam River/Wiley	93		2	10	81											0.871
		Reporting Group total		364	0	23	20	318	1	1	1	0	0	0	0	0	0	0	0.874
Coastal	05_BWSALM	OMY022	Big White Salmon River	78		3			72	3									0.923
		Reporting Group total		78	0	3	0	0	72	3	0	0	0	0	0	0	0	0	0.923
Coastal	06_KLICKR	OMY023	Upper Trout Creek	31						30				1					0.968
		OMY024	Suveyors Creek	25		1				24									0.960
		OMY025	Snyder Creek	26						25				1					0.962
		OMY026	Lower Summit Creek	37		1	1			29	3		1			1		1	0.784
		OMY027	Lower Trout Creek	22		1	1			17	3								0.773
		OMY028	Lower White Creek	29		1				22	4		1	1					0.759
		OMY029	Little Klickitat River	30		2			1	25	2								0.833
		OMY030	Dead Canyon Creek	20			5			14	1								0.700
		OMY031	Bowman Creek	37		3	1			29	2							2	0.784
		OMY032	Swale Creek	21		1		1		18								1	0.857
		Reporting Group total		278	0	10	8	1	1	233	15	0	2	3	0	1	0	4	0.838
Inland	07_MGILCS	OMY033	Fifteenmile Creek	91		1				4	75	4	4					3	0.824
		OMY034	Pelton	45					1		27	3	2	1		2	2	7	0.600
		OMY035	Shitike Creek	31						1	27		1					2	0.871
		OMY036	Buck Hollow Creek	63							51	2	4					6	0.810
		OMY037	Deschutes River-Trout Creek	57							47	1	4				1	4	0.825
		OMY038	Deschutes River-upper mainstem	61							59				1		1		0.967
		OMY039	Beech	21							19		1					1	0.905
		OMY040	John Day River - upper mainstem	34							33		1						0.971
		OMY041	Baldy	25							25								1.000
		OMY042	John Day River - lower mainstem	44							36	1	1	1	1			4	0.818
		OMY043	John Day River - upper middle fork	107							102	1	2				2		0.953
		OMY044	Granite	18							18								1.000
		OMY045	North Fork John Day River	56							50	2	2			1		1	0.893
		OMY046	Big Wall	22							20		1			1			0.909
		OMY047	Deer Creek	18							18								1.000
		OMY048	Murderers Creek	18							18								1.000
		OMY049	Rock Creek	126							105	2	4	2	3		1	9	0.833
		OMY050	Squaw Creek	136						1	103	3	7	5	2		2	13	0.757
		OMY051	Iskuilpa Creek	148						1	124	7	6			1		9	0.838
		OMY052	Umatilla River	34							30	1	1		1		1		0.882
		OMY053	Touchet River	86							84						1	1	0.977
		OMY054	Alpowa Creek	98						1	67	4	18	4	1			3	0.684
		OMY055	Asotin Creek	194							134	9	28	2	1	1	2	17	0.691
		OMY056	Tucannon River	106							79	5	12	1		1	2	6	0.745
		OMY057	Joseph Creek	97							89		4		1		1	2	0.918
		OMY058	Little Minam River	48							43	3	1					1	0.896
		OMY059	Menatchee Creek	73							67	2	1					3	0.918
		OMY060	Upper Grand Ronde River	156							134	1	8			1	4	8	0.859
		OMY061	Wallowa River	117		1			2		98	4	4			1		7	0.838
		OMY062	Wenaha River	191						1	160		19			1		2	0.838
		OMY063	Big Sheep Creek	184							166	1	5				5	7	0.902
		OMY065	Lightning Creek	39							30	1	2		1		1	4	0.769
		OMY066	Upper Imnaha River	53							43		4	1			3	2	0.811
		OMY067	Big Bear Creek	250							217	1	11	5	6			10	0.868
		OMY068	East Fork Potlatch River	158						1	136		4	10	4	2		1	0.861
		OMY069	Lapwai Creek	158							134	2	11		2			9	0.848
		OMY072	West Fork Potlatch River	84							72		3	7		1		1	0.857
		OMY073	Little Salmon River	147							103	2	1	5		5	10	21	0.701
		OMY074	Slate Creek	75							52		3			3	3	14	0.693
		Reporting Group total		3469	0	2	0	0	3	10	2895	62	180	44	24	21	44	184	0.835
Inland	08_YAKIMA	OMY075	Naches River - Rattlesnake Creek	36							7	27	2						0.750
		OMY076	Naches River - Nile Creek	59							6	50	2				1		0.847
		OMY077	Naches River - Pileup Creek	26							2	23						1	0.885
		OMY078	Naches River - Quartz Creek	26							3	23							0.885
		OMY079	North Fork Little Naches River	21							2	18	1						0.857
		OMY080	Satus Creek	46							6	38				1		1	0.826
		OMY081	Toppenish Creek	34							1	33							0.971
		OMY081.2	Ahtanum Creek	40							11	28						1	0.700
		OMY081.3	Yakima River - Big Creek	38					1		1	36							0.947
		OMY081.4	Cowiche River - Crow Creek	38					1	1	5	31							0.816
		OMY081.5	Teanaway River	65						1	9	54	1						0.831
		OMY081.6	Little Rattlesnake Creek	36							5	29	1					1	0.806
		Reporting Group total		465	0	0	0	0	2	2	58	390	7	0	0	1	1	4	0.839
Inland	09_UPPCOL	OMY082	Chiwaukum Creek	54						1	14	2	36					1	0.667

		OMY083	Upper Chiwaukum Creek	29						8		15					3	3	0.517
		OMY084	Nason River	21						6		15							0.714
		OMY085	Entiat River	193				1		82	6	90	1	4	1		2	6	0.466
		OMY086	Methow River	90						37	2	44		1				6	0.489
		OMY088	Omak River	94				1		19	2	64			1			7	0.681
		Reporting Group total		481	0	0	0	0	2	1	166	12	264	1	5	2	5	23	0.549
Inland	10_SFCLWR	OMY070	Lolo Creek	94						2		1	84	6				1	0.894
		OMY090	Clear Creek	45					1	5			36	3					0.800
		OMY091	Crooked River	136						4			125	7					0.919
		OMY092	Newsome Creek	99									94	4				1	0.949
		OMY093	Tenmile Creek	47						4			34	9					0.723
		Reporting Group total		421	0	0	0	0	0	1	15	0	1	373	29	0	0	2	0.886
Inland	11_UPCLWR	OMY094	Bear Creek	70						1				68				1	0.971
		OMY095	Lower Selway River	211						9		2	22	178					0.844
		OMY096	Middle Lochsa River	147						6			4	136				1	0.925
		OMY097	Middle Selway River	138						3		1	5	128	1				0.928
		OMY098	Upper Lochsa River	129						1			6	122					0.946
		OMY099	Upper Selway River	247						2		1	2	242					0.980
		Reporting Group total		942	0	0	0	0	0	0	22	0	4	39	874	1	0	2	0.928
Inland	12_SFSLM	OMY100	East Fork South Fork Salmon River	135						9			1			121	4		0.896
		OMY101	Secesh River	208						13			1			188	1	5	0.904
		OMY102	South Fork Salmon River	45						2	1					42			0.933
		Reporting Group total		388	0	0	0	0	0	0	24	1	2	0	0	351	5	5	0.905
Inland	13_MFSALM	OMY103	Bear Valley Creek	173						6						1	166		0.960
		OMY104	Big Creek	224						11			1		2	203	7		0.906
		OMY105	Camas Creek	97						3	1				3	90			0.928
		OMY106	Chamberlain Creek	189						16		1			1	166	5		0.878
		OMY107	Loon Creek	131						6				1		123	1		0.939
		OMY108	Marsh Creek	195						16	3	5		1	2	151	17		0.774
		OMY109	Middle Fork Salmon River	227						15	1	1			2	201	7		0.885
		Reporting Group total		1236	0	0	0	0	0	0	73	5	7	1	2	11	1100	37	0.890
Inland	14_UPSALM	OMY110	Herd Creek	85					1	19			4			2	59		0.694
		OMY111	Lemhi River	86				1	1	13	4	3				3	61		0.709
		OMY112	Morgan Creek	61				1		9			1		1		49		0.803
		OMY113	North Fork Salmon River	100						44			4	1	1	3	47		0.470
		OMY114	Pahsimeroi River	97				2		29	2		1			1	62		0.639
		OMY115	Sawtooth Hatchery	319						100	1		4			2	212		0.665
		Reporting Group total		748	0	0	0	0	4	2	214	7	17	0	1	2	11	490	0.655

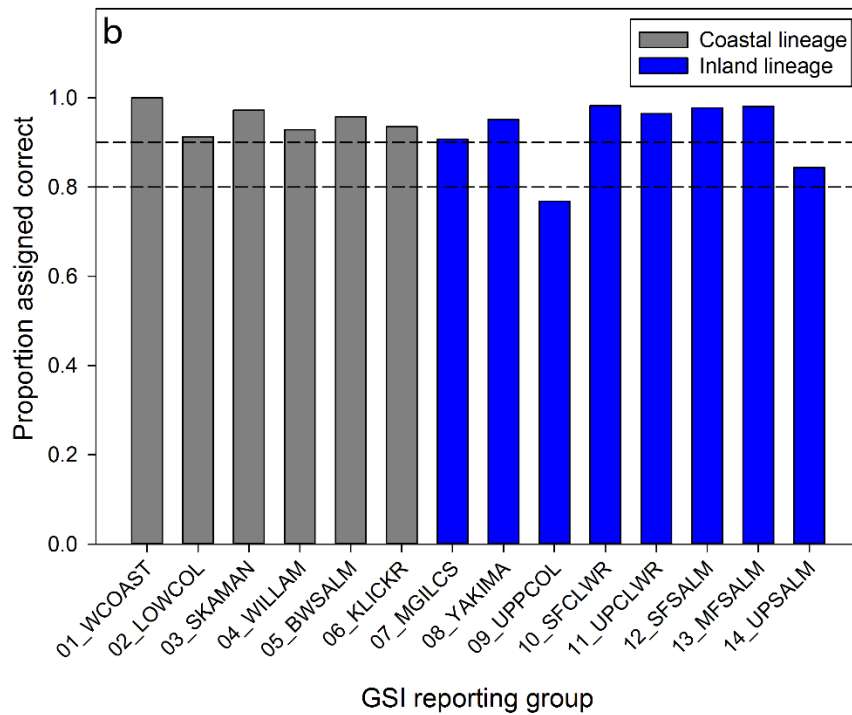
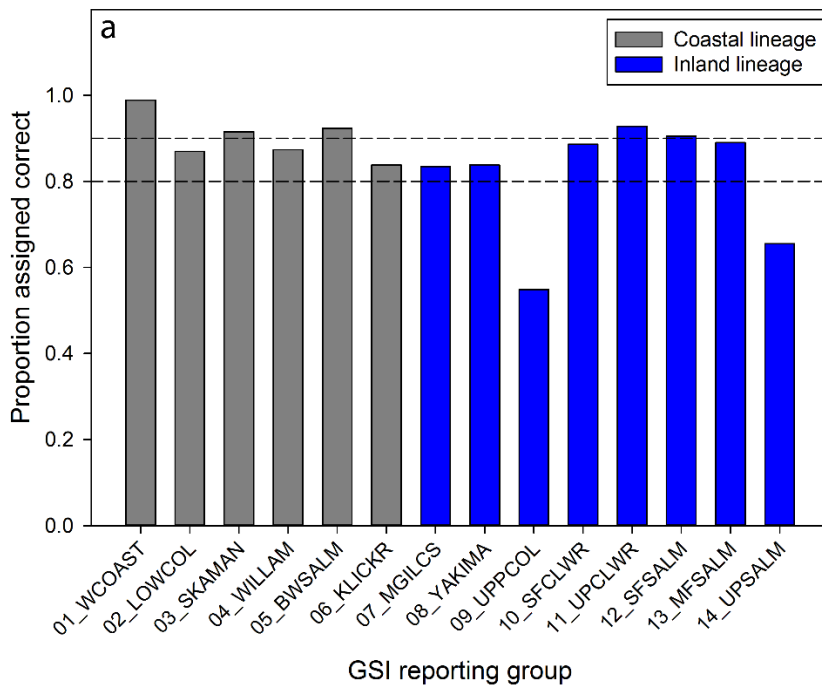


Figure 24. Proportion of steelhead in leave-one-out tests that assigned correctly for each reporting group by lineage using a) all data, and b) $\geq 80\%$ self-assignment probability threshold. The dashed lines indicate 80% and 90% thresholds for correct assignment.

Parentage based tagging assignments of Chinook salmon in harvest mixtures

A summary of the Chinook harvest samples that were genotyped (derived from Table 10) is presented in Table 16. Of the 4,169 harvest Chinook analyzed, PBT identified 1,558 hatchery-origin individuals that could be confidently assigned back to 70 hatchery broodstock sources (i.e., 32 Snake River hatchery broodstocks and 38 Columbia River hatchery broodstocks) spawned in 2012-2014 (Table 17). The majority of PBT assigned individuals (74.13%) were from the 2013 brood year (i.e., 4-years-old), with a smaller fraction represented by 3-year-old (brood year 2014; 11.49%) and 5-year-old (brood year 2012; 14.38%) fish. Of the 4-year-old fish, the majority (23.12%) were assigned to the Rapid River Fish Hatchery, followed by the Umatilla Fish Hatchery (spring stock) (10.91%), and Priest Rapids Fish Hatchery (8.66%). The majority of 4-year-old fish assigned to Columbia River hatchery broodstocks (58.86%), while 41.04% of PBT assigned 4-year-old fish assigned to Snake River hatchery broodstocks.

Table 16. Summary of the Chinook salmon harvest samples by fishery, region, and origin in 2017.

Fishery	Harvest Region	Origin	Management period		
			Spring	Summer	Fall
Lower River Test	Region B	Hatchery	779	0	0
		Wild	100	0	0
Lower River Sport	Region A	Hatchery	244	0	0
	Region B	Hatchery	786	0	0
Tribal Ceremonial	Zone 6	Hatchery	35	0	0
Tribal Harvest	Zone 6	Hatchery	0	229	0
		Wild	0	222	0
Lower River Sport	Region A	Hatchery	0	104	0
	Region B	Hatchery	0	130	0
Tribal Harvest	Zone 6	Hatchery	0	0	276
		Wild	0	0	313
Lower River Commercial	Region A	Hatchery	0	0	194
Sport	Region A	Hatchery	0	0	298
	Region B	Wild	0	0	459

Comparison of stock composition among spring management period Chinook salmon fisheries

The majority of adipose-clipped Chinook salmon from fishery mixtures during the spring management period (April to June 15th) were assigned via PBT. Across fishery mixtures the proportion of fish assigned via PBT ranged from 59-83%, and we identified relatively large proportions of individuals that assigned via PBT to Snake River and Columbia River hatcheries. Chinook salmon from Snake River hatcheries comprised 31-32% of fish harvested in Region B, 41% of fish harvested in Region A from sport and Test fisheries, and 46% of fish harvested in Zone 6 from Tribal Ceremonial fisheries (Figure 25). These proportions are broadly consistent with the proportion of hatchery origin Chinook salmon passing Bonneville Dam in 2017 that assigned via PBT to Snake River hatcheries (36%). PBT assignments to Columbia River hatcheries ranged from 28-38%, broadly consistent with the proportion of hatchery origin Chinook passing Bonneville Dam in 2017 (42%), and reflects the continued expansion of our PBT baseline for Columbia River hatchery broodstocks (i.e., in 2016 we were able to assign 10-19% of harvest samples to Columbia River broodstocks). This is consistent with, albeit slightly lower than, the overall proportion of fish that assigned to Columbia River hatchery broodstocks (59%) (Table 17).

The proportion of adipose-clipped Chinook salmon from fishery mixtures during the spring management period that were assigned via GSI ranged from 8-38%. Chinook salmon from the interior ocean type lineage (OT) comprised a small fraction (0-2%) of Chinook salmon taken in spring harvests, and was similar to the proportion passing Bonneville Dam (4%) during the spring management period (Figure 25). Chinook salmon from the interior stream type lineage (ST) comprised 8-13% of harvest samples; consistent with that observed at Bonneville Dam (11%). As in 2015 and 2016, we observed a decrease in the proportion of harvests comprised of the lower Columbia (LC) Chinook lineage up to Bonneville Dam (Figure 25). The proportion of LC lineage Chinook in Region B fisheries was 26-30%. This decreased to 6% for the Region A sport fishery, and to 0% at Bonneville Dam and in the Zone 6 Tribal Ceremonial fishery. The proportion of fish that could not be assigned using either PBT or GSI represented a small fraction of the harvest samples analyzed, and ranged from 3-8%; consistent with that observed at Bonneville Dam (6%) (Figure 25).

The closure of adipose-intact commercial fisheries during the spring management period of 2017 restricted comparisons of stock composition to the test fishery. Analysis of the adipose-intact test fishery revealed that 25% of fish assigned via PBT to Snake River (17%) and Columbia River (8%) hatcheries. This is consistent with the proportion of adipose intact fish at Bonneville Dam that assigned via PBT (22%) to Snake River (11%) and Columbia River (10%) hatcheries, and is considerably lower than that observed for adipose-clipped fisheries (59-83%; Figure 25) (as expected). A greater proportion of adipose-intact fish in the test fishery assigned to Snake River hatcheries (17%) relative to those at Bonneville Dam (11%). The LC lineage comprised 26% of the test fishery, but only 1% of the fish encountered passing Bonneville Dam. The OT lineage was observed at Bonneville Dam (34%), but not in the test fishery due to the early-timed occurrence of the test fishery in March to April. The ST lineage comprised the greatest proportion of adipose-intact test fishery (28%), and matched that encountered at Bonneville Dam (28%) during the spring management period (Figure 26). Interestingly, 21% of adipose-intact fish in the test fishery and 16% of adipose intact fish at Bonneville Dam could not be assigned either via PBT or GSI with our assignment thresholds.

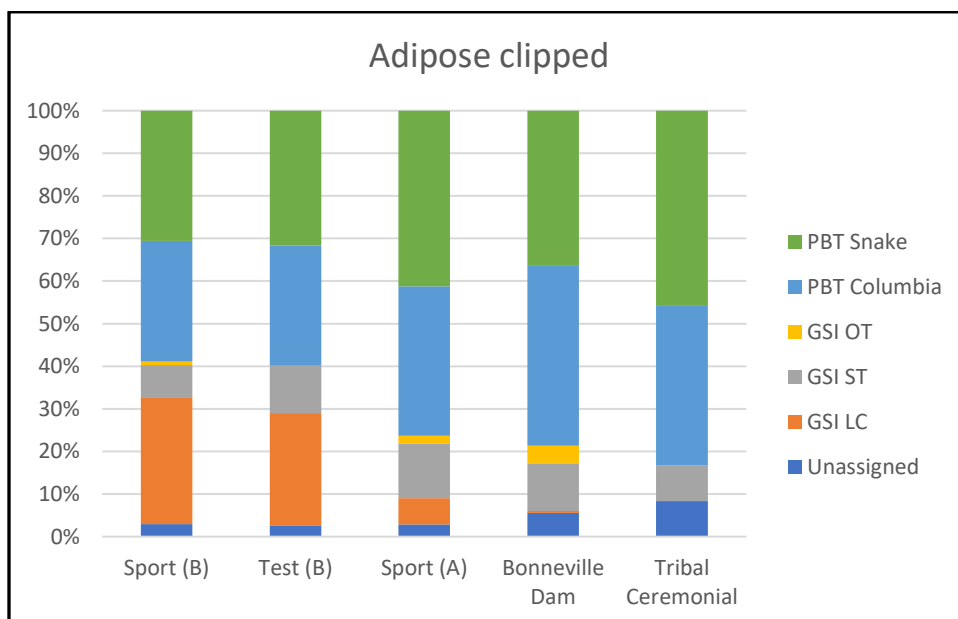


Figure 25. Stock composition of spring management period adipose-clipped Chinook salmon harvest mixtures. ‘PBT Snake’ and ‘PBT Columbia’ include assignments to all Snake River and Columbia River hatcheries that are in our PBT baseline. Interior ocean type (OT), interior stream type (ST), and lower Columbia lineage include GSI assignments to reporting groups within our GSI baseline.

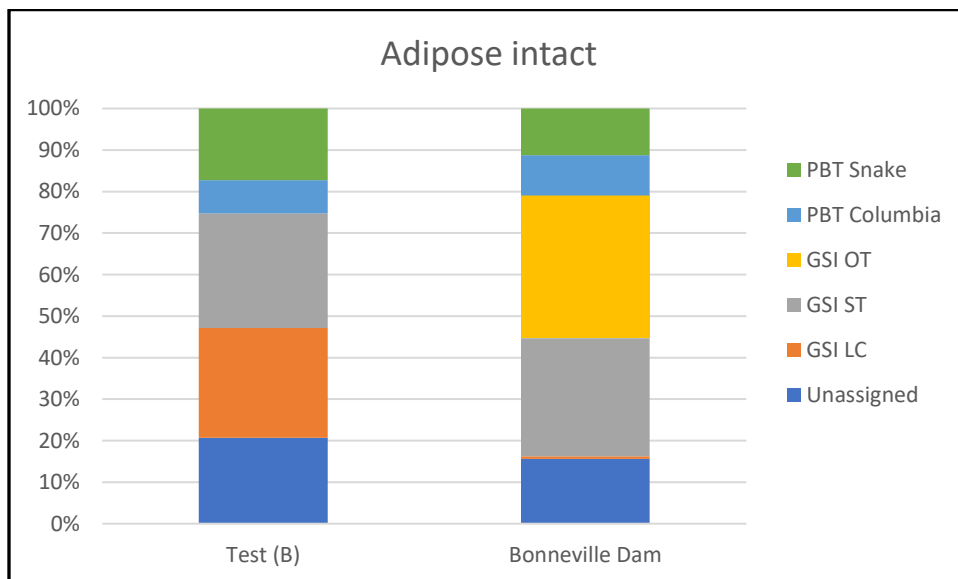


Figure 26. Stock composition of spring management period adipose-intact Chinook salmon harvest mixtures. ‘PBT Snake’ and ‘PBT Columbia’ include assignments to all Snake River and Columbia River hatcheries that are in our PBT baseline. Interior ocean type (OT), interior stream type (ST), and lower Columbia lineage include GSI assignments to reporting groups within our GSI baseline.

Comparison of percent stock composition of upriver spring Chinook salmon stocks (ST) among summer-management period Chinook salmon fisheries

Analysis of Chinook salmon fisheries in the summer management period (June 16 – August 1) addressed the following objectives: 1) estimate stock composition for the mark selective sport fishery in Region B and Region A below Bonneville Dam, and 2) compare stock composition of adipose-clipped versus adipose-intact fish from the Tribal Zone 6 harvest above Bonneville Dam. Due to closure of the commercial fishery during the summer management period in 2017, we could not estimate the stock composition of this harvest or characterize temporal changes in stock composition of the commercial fishery across the season. While jack Chinook salmon are not harvested at high rates in fisheries and there are no specific harvest limits for them, jack Chinook salmon if sampled could have been incorporated into this analysis.

The stock composition of adipose-clipped sport fisheries in Region B and Region A were similar in the proportions of fish that assigned via PBT to Snake River hatcheries (11% for both), and the proportion of fish from the ST (2% for both) and OT (26-28%) lineages (Figure 27). However, PBT assignments to Columbia River hatcheries was greater for Region A (56%) than Region B (38%), while the LC lineage comprised a greater proportion of fish in Region B (21%) than Region A (2%).

We detected broad similarities in the stock composition of adipose-clipped fish from the sport fishery in Region A, with those sampled at Bonneville Dam and those taken in the Zone 6 Tribal harvest (Figure 27). The proportion of fish from these mixtures that assigned via PBT ranged from 63-70%, with a greater proportion assigned to Columbia River hatcheries (56-63%) than Snake River hatcheries (5-11%). The OT lineage comprised the greatest proportion of GSI assignments (28-32%) for these mixtures, while the LC lineage (1-2%) and ST lineage (1-3%) were relatively minor by comparison (Figure 27).

We also observed broad similarities in the stock composition of adipose-intact mixture collections from Bonneville Dam and the Zone 6 tribal harvest. The OT lineage comprised the greatest proportion of these mixtures (72-77%), followed by PBT assignments to Columbia River hatcheries (12-14%) (Figure 27). Snake River hatcheries comprised a relatively small proportion of assignments (2-3%), as did assignments to the ST lineage (1% for both).

We observed differences in the stock composition of adipose-intact and adipose-clipped fish taken in the Zone 6 tribal harvests. As observed in other comparisons of adipose-clipped vs. adipose-intact mixtures, a greater proportion of adipose-clipped fish assigned to Columbia River hatcheries (63%) vs. adipose-intact fish (12%) (Figure 27). A greater proportion of adipose-clipped fish assigned to Snake River hatcheries (7%) than adipose-intact fish (2%). We also detected a greater proportion of adipose-intact fish assigned to the OT lineage (77%) than adipose-clipped fish (28%). Across all comparisons, the proportion of fish that could not be assigned using either PBT or GSI was low, and ranged from 1-10% (Figure 27).

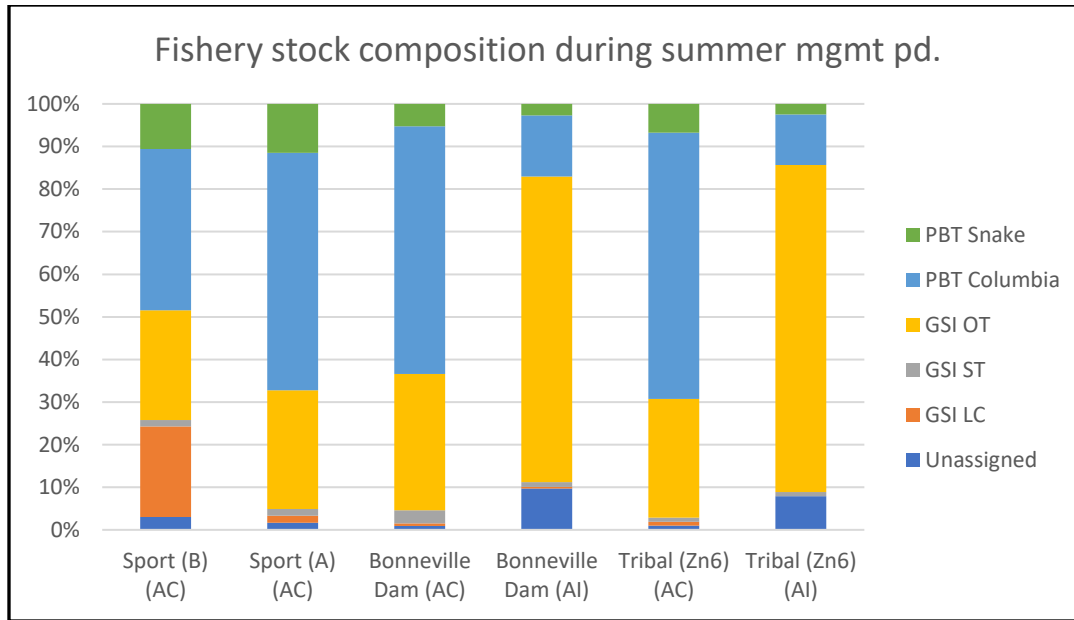


Figure 27. Stock composition of summer management period Chinook salmon fisheries and Bonneville Dam. ‘AC’ is adipose-clipped; ‘AI’ is adipose intact. ‘PBT Snake’ and ‘PBT Columbia’ include assignments to all Snake River and Columbia River hatcheries that are in our PBT baseline. Interior ocean type (OT), interior stream type (ST), and lower Columbia lineage include GSI assignments to reporting groups within our GSI baseline.

Stock composition of the fall-run mark-selective Chinook salmon sport fishery

We estimated stock composition of the mark selective sport fishery in the lower Columbia River in 2017. Major reporting groups in order of decreasing proportion were: 18_UCOLSF (72%), 19_SRFALL (13%), and 03_WCASFA (10%) (Figure 28). These results are broadly consistent with the composition of the fall sport harvest from previous years.

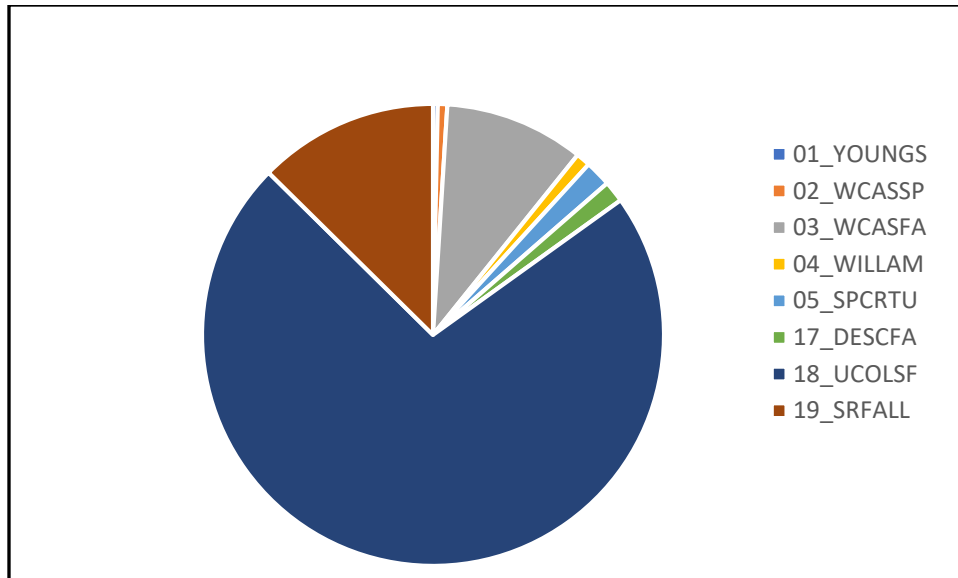


Figure 28. Genetic stock composition of the lower Columbia River fall-run mark-selective Chinook salmon sport harvest in 2017. Note: the assignment of West Cascade spring stock (02_WCASSP) may owe to misassignment between the spring and fall runs from that region, strays from the net pen rearing at Youngs Bay, or other unknown reasons.

Comparison of stock composition among sockeye salmon fisheries

Sockeye salmon were sampled from the lower Columbia River below Bonneville Dam in the lower river sport and above Bonneville Dam in the Zone 6 tribal fishery, and were assigned to four Columbia River genetic stocks (Table 18). The lower river commercial harvest did not occur in 2017, and the Zone 6 sport fishery was not sampled in 2017. Low sample numbers of *O. nerka* make it difficult to estimate narrow confidence intervals for abundance estimates of the Snake River and Lake Billy Chinook stocks (Table 19).

The timing of the sockeye salmon fisheries may influence the harvested proportion of each stock, and is consistent with run-timing distributions observed at Bonneville Dam; particularly that the Okanogan and Wenatchee stocks had nearly identical run-timing distributions in 2017, but migrated past Bonneville Dam earlier than other stocks. The Snake River stock (i.e., Redfish Lake) was only represented by 10 fish in the Zone 6 tribal fishery sample (Table 18) making run-timing estimates imprecise for this stock. Of the 10 Snake River fish identified with GSI, the largest number (n=5) was sampled in week 26 (Figure 29). The highest proportions of Okanogan stock (44%) and Wenatchee stock (64%) in the Zone 6 tribal fishery occurred during statistical weeks 26 and 25, respectively (Figure 29). Notable difference in stock proportions between Bonneville Dam and the Zone 6 tribal harvest were observed for the Okanogan stock (58% vs. 39%) and for the Wenatchee stock (41% vs. 59%) in the harvest vs. Bonneville Dam mixture samples, respectively (Table 19).

Table 18. Summary of sample sizes and stock assignments for sockeye salmon fisheries by weekly strata.

Fishery	Stock	Statistical week						
		24	25	26	27	28	29	30
Sport	Okanogan		8	3				
	Wenatchee	3	4	1				
Zone 6	Okanogan		27	123	72	18	2	1
	Wenatchee		49	154	109	29	3	1
	Snake			5	3	2		
	Lake Billy Chinook					2		

Table 19. Comparison of stock-specific abundance and percent composition among sockeye salmon fisheries. The mean stock abundance estimate is provided for each fishery harvest and includes 95% confidence intervals.

Mixture source	Mean (95% C.I.)				Stock proportion			
	Okanagan	Wenatchee	Snake	Lake Billy Chinook	Okanagan	Wenatchee	Snake	Lake Billy Chinook
Sport	153 (97 – 208)	111 (56 – 167)	-	-	58.10%	41.90%	-	-
Zone 6	1,716 (1,520 – 1,924)	2,604 (2,397 – 2,799)	60 (25 – 104)	20 (0 – 49)	38.99%	59.19%	1.37%	0.45%
Total Harvest	1,950 (1,764 – 2,132)	2,706 (2,524 – 2,892)	77 (31 – 130)	15 (0 – 38)	41.08%	56.99%	1.62%	0.32%
Bonneville Dam*	43,606 (41,050 – 46,102)	30,739 (28,278 – 33,267)	431 (108 – 2829)	65 (0 – 169)	58.27%	41.07%	0.58%	0.09%

* Bonneville Dam abundance estimates shown here differ from those in Table 35 (Chp 4) since they only include the interval of weeks that coincide with sockeye salmon fisheries (statistical weeks 24-30).

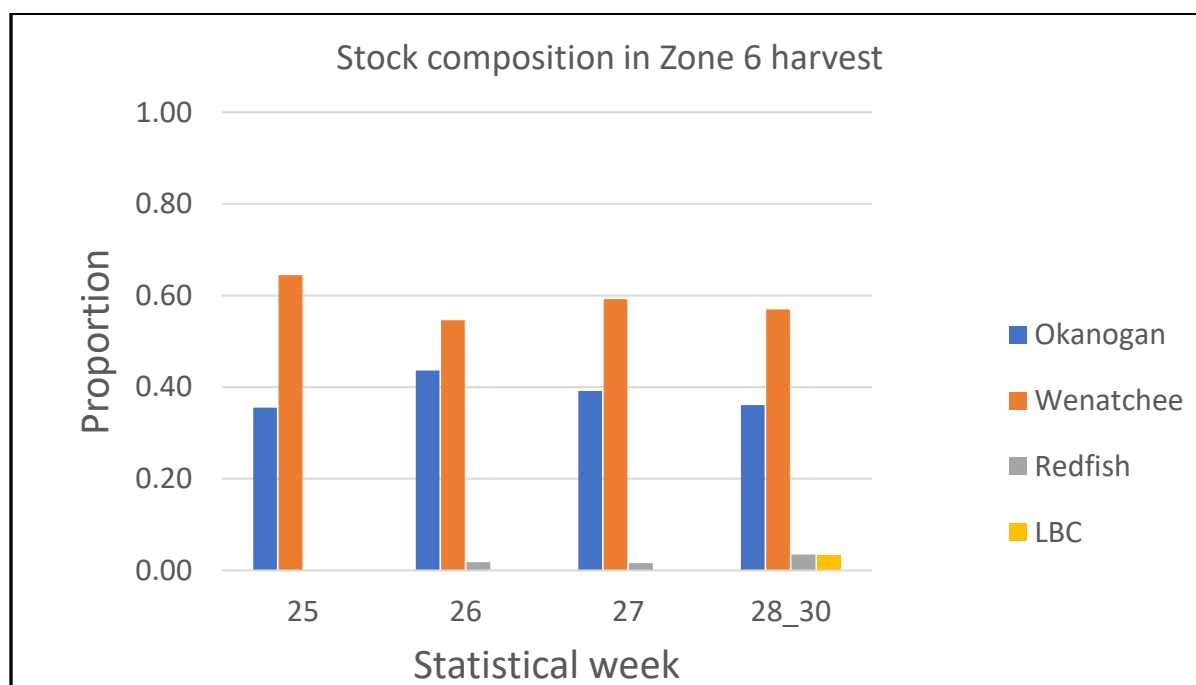
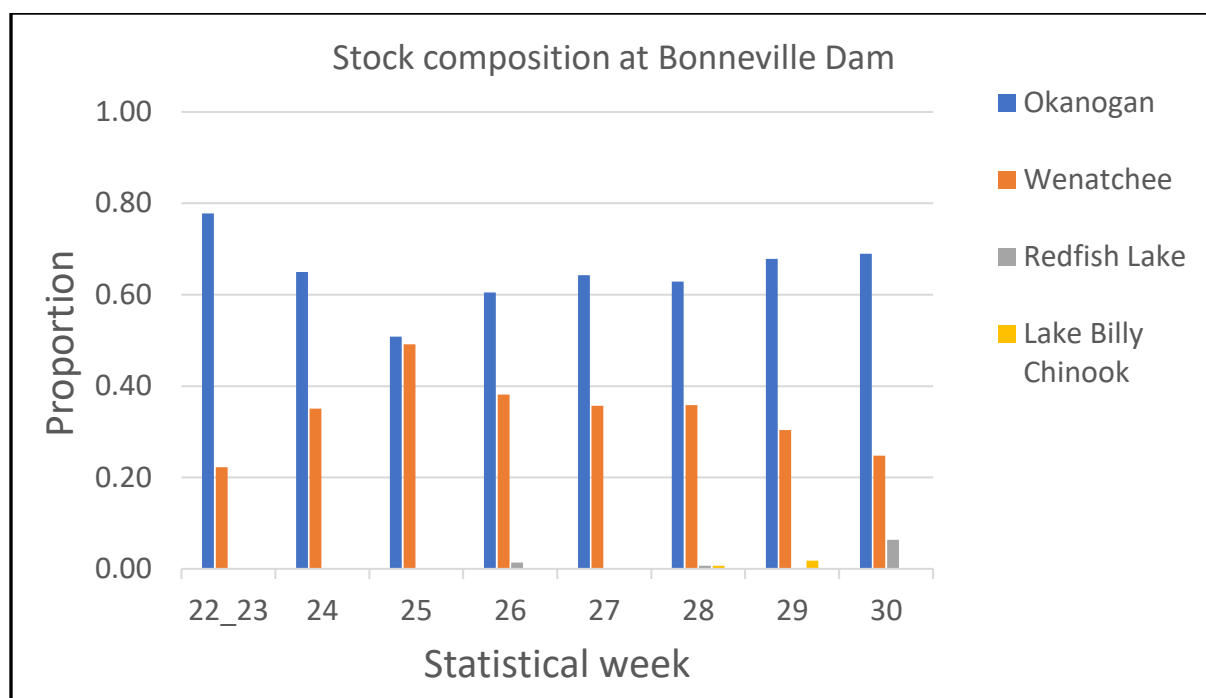


Figure 29. Stock composition of sockeye salmon at Bonneville Dam (top panel) and in the Zone 6 tribal harvest (bottom panel) across weekly strata.

Discussion

Management implications

This study utilized both genetic stock identification (GSI) and parentage based tagging (PBT) in combination to estimate stock composition of mainstem Columbia River Chinook salmon and sockeye fisheries. This is the fifth year in which we were able to assign all three major age classes of spring Chinook from Snake River hatcheries and the first year in which we could assign 3-, 4-, and 5-year old fish to Columbia River hatcheries as a consequence of our expanded PBT baseline. Ongoing expansion of the PBT baseline will allow us the ability to assign Snake River hatchery jacks of the fall-run Chinook salmon as well as all other hatchery jacks originating above Bonneville Dam (migration year 2018), and so future years of analyses will include more emphasis on fall-run harvest. Expansion of the PBT baseline to include not only hatcheries of Chinook salmon and steelhead above Bonneville Dam, but also hatcheries throughout the range of these species could eventually lead to replacing the coded wire tag program for monitoring of in-river harvest stock composition of these species if increases in funding were available and fishery managers thought it were needed. We understand there will be benefit to not only increasing the number of broodstocks represented in the baseline but also expanding the number of SNP loci that we use for PBT applications. A new subset of 268 SNP loci was identified in this report as having optimal information content across the three major genetic lineages of Chinook Salmon found in the Columbia River Basin. This report includes the fifth genetic analysis on sockeye salmon harvest. Our results demonstrated differences in stock composition of the sockeye salmon harvest as compared to the total run estimated at Bonneville Dam, but there are questions about the validity of the estimates especially at Bonneville given the potential for sampling error around rare stocks like Snake River sockeye salmon. We will continue to perform GSI on sockeye salmon harvest in the future to gain further insight into these patterns.

One higher level management question was possible to address in this section:

- 1) Harvest RM&E: F&W Program Management Question: What are your in-river monitoring results and what are your estimates of stock composition and stock-specific abundance, escapement, catch, and age distribution?**

The in-river estimates of stock composition, stock-specific abundance, escapement, catch, and age distribution were addressed for part of the treaty mainstem spring-management period fisheries Chinook salmon harvests above Bonneville Dam along with fisheries below Bonneville Dam, the non-treaty summer-management fisheries below Bonneville Dam which are a portion of the total non-treaty summer fisheries, and the mainstem treaty sockeye salmon harvests above and non-treaty harvest below Bonneville Dam. For the spring management period of Chinook salmon, we continue to observe a spatial pattern for the stock composition of lower Columbia River stocks which appear more abundant downstream from the Willamette River mouth as compared to upstream of this point which is consistent with a long history of CWT data. We observed differences in the composition of hatchery stocks represented in spring vs. summer management period harvest of Chinook salmon, and run-timing plays an important role in this difference (i.e., late-running stocks appear more abundant among the upriver spring-type lineage that are caught in the summer management period). This pattern is consistent when compared to known origin PIT tagged adult and jack fish tagged as juveniles. Known origin

adult age upriver spring and Snake River spring Chinook salmon are almost all past Bonneville by June 15 in most years. However, specific conclusions relative to the harvest impacts on spring run Chinook salmon cannot be made from this genetic analysis as jacks are included in the current study.

The sockeye salmon tribal fishery is managed in a way that attempts to harvest as many harvestable sockeye salmon as possible under the allowed harvest rate schedule in the U.S. v. Oregon Management Agreement. This 2017 year of analysis of the sockeye salmon harvest corroborates harvest analyses from previous years, which suggested there may be some over representation of the Wenatchee sockeye stocks in the Zone 6 harvest as compared to the stock proportions that are present at Bonneville Dam. The results for Snake River sockeye salmon are dependent upon representative sampling at Bonneville Dam, but low sample rate and the rarity of this stock led to uncertainty and high variation around estimates of Snake River sockeye salmon from Bonneville Dam. Sampling protocols at Bonneville Dam may have higher representation of young fish as compared to harvest mixtures. Timing of the fishery may also influence the proportion of each stock, and is consistent with run-timing distributions we observed in previous reports; the Wenatchee stock has relatively early run-timing but the timing of the Snake River stock is uncertain due to inconsistent results between PIT-tag and GSI methods. Future analysis will be needed to examine these patterns for consistency and delve into explanations.

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Section 4: Characterization of Chinook salmon, sockeye salmon, and steelhead run-timing and abundance at Bonneville Dam

Introduction

The Columbia River Basin supports ESA listed natural-origin stocks of Chinook salmon and steelhead as well as hatchery supplemented populations. Both Chinook salmon and steelhead have been declining in the Columbia River Basin for several reasons including climate change, habitat degradation, hydropower, hatchery practices, and over-harvesting. Along with abundance estimates, basic information related to the way in which stocks of salmonids are spatiotemporally distributed are needed by fisheries managers to achieve sustainable fisheries.

As evident from the genetic stock identification (GSI and PBT) analyses of Chinook and sockeye salmon fisheries harvests in Section 3, certain stocks seem to have strong spatial and temporal associations. However, because the type of fishing gear, harvest regulations, and the locations targeted varies considerably among fisheries, samples from a representative mixture of all hatchery- and natural-origin stocks at a fixed location is expected to more accurately estimate relative abundance and characterize run-timing distributions of stocks. One potentially ideal fixed location for such sampling is Bonneville Dam, but trapping limitations at this location continue to pose a major challenge for sampling. In addition to information on abundance and run-timing, biological data including fork length and age can be examined with estimated stock of origin to characterize life history differences among stocks. This type of examination is especially important for steelhead, which has been managed using two life-history categories (i.e., A- and B-run). These life-history categories have been observed to be differentially characterized by run-timing at Bonneville Dam (e.g., B-run typically arrives after Aug. 25th), fork length (e.g., by definition, B-run fish are ≥ 78 cm), and ocean age (e.g., most B-run fish tend to spend 2 or more years in saltwater) and all of these types of data have been collected for steelhead in this study.

Project objectives and higher level harvest management questions

Here we analyze fish across the entire run of steelhead, Chinook and sockeye salmon from April to October to estimate temporally stratified proportions of stocks and extrapolate abundance using a daily census that is conducted at the Bonneville Dam fish counting window. We examine steelhead, Chinook salmon, and Sockeye salmon using sets of species-specific SNP assays for up to 390 loci per species. Although there are some methodological differences among these species-specific applications (e.g., different temporal strata), the general approach to estimating abundance and characterizing run-timing distributions was applied consistently post-season across species in 2017. For all three species, we have demonstrated that these genetic baselines are generally accurate for assigning fish of unknown origin, but the genetic similarity of some stocks requires large reporting groups comprised of broad geographic areas (i.e., mid-Columbia R. and lower Snake R. for spring Chinook salmon). Since Bonneville Dam is the most downstream dam on the Columbia River, the mixture samples obtained here represent the majority of upriver/interior Columbia River Basin stocks. This ongoing study offers a rare opportunity to monitor populations of multiple species of salmonids from a broad geographic range over several years. This long-term study will allow us to characterize trends in run timing and abundance of steelhead, Chinook and sockeye salmon and provide this data to fisheries managers. However, the genetic stock units ('reporting groups') are not the same units that

groups of fish are currently managed for due to levels of genetic differentiation that can be detected among baseline stocks (see results under Objective 2 for details). Thus, fisheries managers continue to explore how to best incorporate genetic monitoring results with more traditional monitoring/tagging programs.

One of the newest features of our analyses is an in-season analysis that was first conducted on Chinook Salmon during the 2017 spring and summer management periods. We have continued offering in-season reports for Chinook Salmon on an approximately bi-weekly report timing schedule during the 2018 spring and summer management periods. Other species and runs have been reported to U.S. v OR Technical Advisory Committee (TAC) members on a timely basis near the end of each management period. Specifically, in 2018, we provided timely post-season reports for steelhead after the Skamania Management Period and the Summer A-/B-Index Management Period, Sockeye Salmon, and Chinook Salmon after the Fall Management Period (see Table 20 for the number and timing of reports for each species and run that were delivered in-season and post-season in 2018).

Harvest RM&E: F&W Program Management Questions:

- i) What are the status and trend of adult productivity of fish populations?**
- ii) What are your in-river monitoring results and what are your estimates of stock composition and stock-specific abundance, escapement, catch, and age distribution?**

Analysis of the 2011 dataset by Hess et al. (2012) was the first year we were able to apply Parentage Based Tagging (PBT) to assign a portion of Snake River hatchery-origin spring-run Chinook salmon and summer-run steelhead back to their hatchery parents (Steele et al. 2011). This powerful genetic tool provides the opportunity to obtain additional types of data including accurate age of fish, quantification of the number of non-adipose clipped hatchery-origin fish, and precise assignments of fish to their hatchery broodstock (Steele et al. 2013). The ability of PBT to assign fish to their hatchery broodstock has been shown to be equally accurate as traditional tags (e.g., CWTs; Steele et al. 2013), and PBT provides assignments to specific hatchery broodstocks rather than larger reporting groups used in GSI methods. However, these tools can provide the greatest benefit when applied in combination, as GSI has the ability to provide information on natural-origin fish throughout the Columbia River basin, while PBT is most effective for hatchery-origin fish. The current PBT baseline was recently expanded beyond Snake River hatcheries to include others above Bonneville Dam. However, this effort is ongoing, and while hatcheries continue to be added to our PBT baseline annually, GSI remains a necessary tool for both hatchery- and natural-origin fish that originate from outside the Snake River basin. This report is the 5th year in which all major age classes of steelhead (i.e. 1-, 2-, and 3- ocean ages) and Chinook salmon (3-, 4-, and 5-year olds) can be assigned using the PBT baseline of Snake River hatcheries, and the 3rd year in which these can be assigned to some Columbia River hatcheries. This study integrates PBT and GSI results to provide the greatest amount of stock-specific information available for hatchery- and natural-origin steelhead and Chinook salmon passing Bonneville Dam.

Time line for completion of objectives

Objectives will be ongoing and GSI results updated each year for analyses of salmon and steelhead throughout the accords-funding. This report that is written in January 2019 features the final analyses of 2017, as well as the preliminary in-season and post-season analyses of 2018. As new genetic techniques are developed they will be applied to this project and results will be compared between years to determine the extent of improvements.

Table 20. The in-season and post-season report timing and scope of the 2018 fish runs.

Species	Management Period	Data coverage	Report timing
Chinook	Spring	01/01/2018 - 05/04/2018	05/11/2018
		01/01/2018 - 05/18/2018	05/24/2018
		01/01/2018 - 06/02/2018	06/08/2018
		01/01/2018 - 06/15/2018	06/25/2018
	Summer	01/01/2018 - 07/07/2018	07/16/2018
		01/01/2018 - 07/31/2018	08/06/2018
	Fall	01/01/2018 - 11/25/2018	12/03/2018
Steelhead	Skamania	04/01/2018 - 06/30/2018	07/16/2018
	Summer A-/B-Index	07/01/2018 - 07/31/2018	08/07/2018
		07/01/2018 - 10/31/2018	11/19/2018
Sockeye	Total	01/01/2018 - 08/18/2018	08/21/2018

Note: The data were reported as cumulative abundance estimates for each genetic stock during the Chinook Salmon and Summer Steelhead A-/B-Index management periods. The report timing indicates the date these reports were provided to the USvOR TAC chair Stuart Ellis for distribution to TAC members.

Methods

Sample Collection

Tissue samples were obtained from adult steelhead (n=838), Chinook (n=2,783) and sockeye salmon (n=1,077) adults in 2017 during migration runs at Bonneville Dam. This sampling effort is covered under the 2008 – 2017 U.S. vs. Oregon harvest biological opinion for sampling at Bonneville Dam.

Sampling for Chinook salmon at Bonneville Dam began during statistical week 16 (04/16/17) and was completed on 10/21/17 (statistical week 42). Sampling occurred at the Adult Fish Facility (AFF) located on the northern end of Bonneville Dam. Fish were sampled 4–5 d per statistical week (except when reduced due to restrictions on trap use or low run size at the beginning and end of the run) and for 4–6 h per day. A picket weir was used to divert migrating fish ascending the Washington shore fish ladder into the AFF collection pool. An attraction flow was used to draw fish through a false weir where they were selected for sampling. After sampling was completed and fish recovered from the anesthetic, they were returned to the Washington shore fish ladder above the picket weir. Only 0.4% of the total Spring management period (i.e., January 1-June 15) adult Chinook salmon count had passed Bonneville by the sampling start date (April 16). In previous years, 2.0-2.5% of the total Spring management period adult Chinook salmon count had passed Bonneville by the sampling start date. However, delayed migration passed Bonneville Dam in the spring of 2017 (Figure 30) resulted in a lower proportion of unsampled fish. Nonetheless, some early timed stocks may be slightly under-

estimated in the results. Restrictions imposed by USACE and NMFS on sampling at the Bonneville AFF result in sample rates for Chinook, sockeye, and steelhead that are often low. The average sample rate for the adult and jack spring Chinook run in 2017 for the spring and summer management periods was 0.96%, whereas the average sample rate for adult and jack fall Chinook was 0.40% (Table 21).

Based on numbers of fish collected, samples were pooled into weekly strata for Chinook (Table 21), monthly strata for steelhead (Table 22), or a combination thereof for sockeye salmon (Table 23) spanning the majority of the run-year from April to October. We followed a similar protocol as the Monitoring Methods [Protocol "Snake River steelhead and Chinook salmon stock composition estimates \(2010-026-00\) v1.0"](#).

Molecular markers

Expanded panels of genetic markers for steelhead (379 SNPs) and sockeye salmon (382 SNPs) are provided in Section 1, while the GT-seq panel of 298 SNPs for Chinook salmon is provided in Hasselman et al. (2017).

Statistical analyses

Snake River Chinook salmon and steelhead were analyzed for [Parentage assignments using SNPPIT software v1.0](#) (ID: 1341) (Published). The program ONCOR was used to estimate the most likely population-of-origin for the sockeye salmon samples. Individuals were assigned using a ‘best estimate’ approach [Assigning individual samples using Individual Assignment \(IA\) genetic methods v1.0](#) (ID: 1334) (Published). We used GSIsim for [Mixture modeling to estimate stock proportions v1.0](#) (ID: 1333) (Published) to estimate stock composition of Bonneville Dam

mixture strata for Chinook salmon and steelhead. Additional detail regarding the specific application to Bonneville Dam are published in Hess et al. (2013).

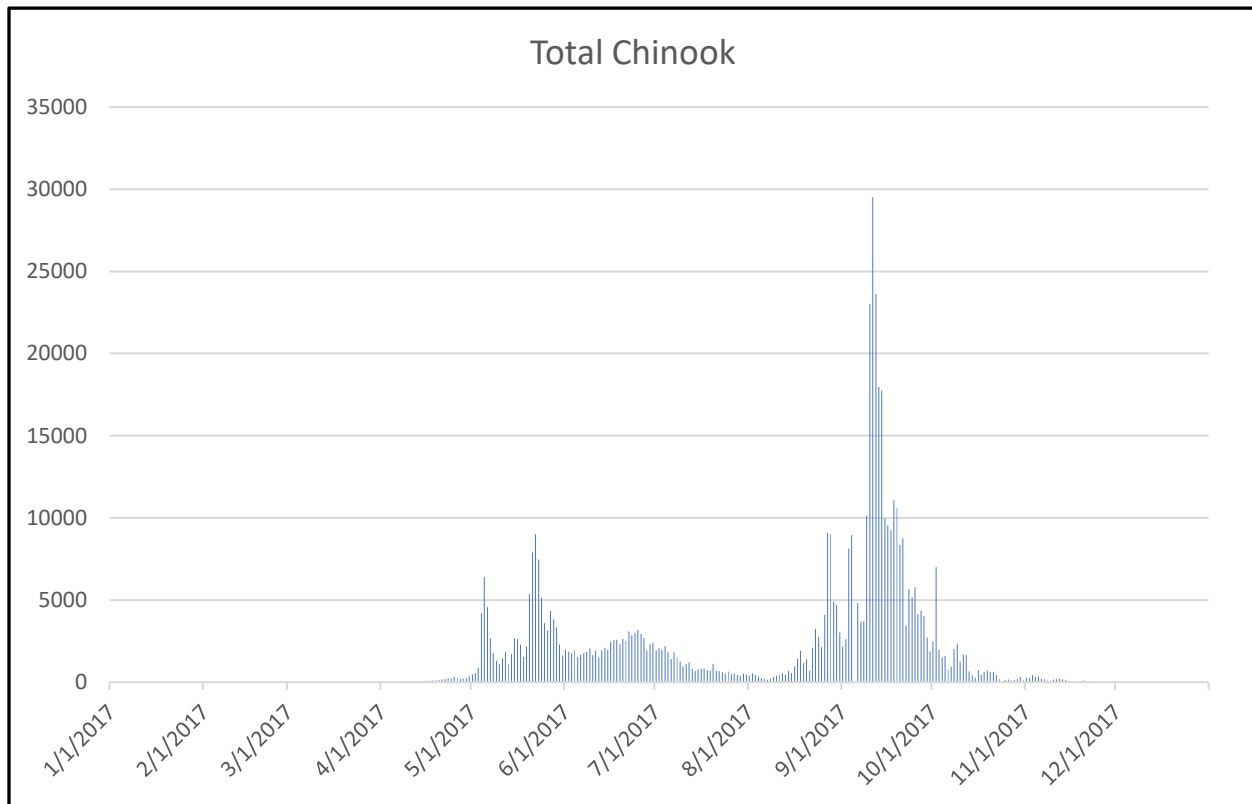


Figure 30. Daily passage of Chinook salmon (adults and jacks) at Bonneville Dam in 2017 (source: www.fpc.org).

Table 21. Sample numbers by weekly strata for Chinook salmon that were DNA sampled or tallied for abundance at Bonneville Dam in 2017.

		Statistical week	Bonneville dam fish window count	Sample (N)					
				Clipped		Non-clipped		Sample	
				GSI	PBT	GSI	PBT	Total	Rate
Management period	Spring	1-16	1273	1	2	0	0	3	0.24%
		17	1731	1	9	0	0	10	0.58%
		18	17439	9	111	10	4	134	0.77%
		19	11285	19	156	10	7	192	1.70%
		20	18348	17	93	10	6	126	0.69%
		21	40572	36	140	46	20	242	0.60%
		22	16696	47	94	57	11	209	1.25%
		23	12453	31	66	54	10	161	1.29%
		24sp	9419	31	38	66	9	144	1.53%
	Summer	24su	5020	2	4	6	2	14	0.28%
		25	18992	26	47	35	4	112	0.59%
		26	17352	25	37	43	11	116	0.67%
		27	12809	19	34	55	12	120	0.94%
		28	6860	17	31	30	9	87	1.27%
		29	5559	17	25	22	3	67	1.21%
		30	3638	10	25	18	2	55	1.51%
		31su	980	3	3	5	1	12	1.22%
	Fall	31fa	1963	0	2	4	0	6	0.31%
		32	2235	0	0	0	0	0	0.00%
		33	7177	1	2	11	5	19	0.26%
		34	16413	5	7	9	8	29	0.18%
		35	35485	15	12	33	9	69	0.19%
		36	39411	6	9	29	3	47	0.12%
		37	131357	31	45	106	38	220	0.17%
38		57194	13	12	58	13	96	0.17%	
39		28025	11	27	147	29	214	0.76%	
40		16273	17	16	112	25	170	1.04%	
41		10022	4	8	47	13	72	0.72%	
42		4043	2	3	29	3	37	0.92%	
		Total	550024	416	1058	1052	257	2783	0.51%

Note: Statistical weeks 1-16 are 1/1/17–4/22/17 and 42 is 10/15/16–10/21/16. ‘Fish count’ is based on tallies of Chinook salmon adults and jacks provided by the Fish Passage Center (<http://www.fpc.org>) observed by the Corps of Engineers at their fish counting window. The total sum of all samples for a given week was used to calculate sample rate. The management periods approximate the date ranges from April to June 15th (Spring management period), June 16th to July 31st (Summer management period), and August 1st to December 31 (Fall management period) which are used to categorize spring-, summer-, and fall-run Chinook salmon, respectively. The number of sampled fish that were assigned via PBT or GSI are shown.

Table 22. Sample numbers by monthly strata for steelhead that were DNA sampled or tallied for abundance at Bonneville Dam in 2017.

Management Period	Statistical month (4 week strata)	Bonneville dam fish window count			Sample (N)				Sample	
					Clipped		Non- clipped			
		Total	Clipped	Non-clipped	GSI	PBT	GSI	PBT	Total	rate
Skamania Summer	16 19	487	347	140	4	9	7	0	20	4.1%
	20 23	966	749	217	1	18	5	0	24	2.5%
	24 26	1508	860	648	1	3	4	0	8	0.5%
Summer A/B Index	27 30	15559	6980	8579	34	73	199	1	307	2.0%
	31 34	46804	31913	14891	37	75	61	3	176	0.4%
	35 38	38893	32268	6625	27	66	26	8	127	0.3%
	39 42	10036	8056	1980	31	87	29	16	163	1.6%
	Total	114253	81173	33080	135	331	331	28	825	0.7%

Note: Statistical week 16 is 4/16/17–4/22/17 and 42 is 10/15/17–10/21/17 ‘Fish count’ is based on tallies of adipose-clipped and non-clipped adult steelhead provided by the Fish Passage Center (<http://www.fpc.org>) observed by the Corps of Engineers at their fish counting window. The total sum of all samples for a given week was used to calculate sample rate. The management periods approximate the date ranges from April 1st-June 30th and July 1st-October 31st which are used to categorize Skamania and summer steelhead, respectively. The sample numbers were split into two categories according to whether samples had been taken from fish that were adipose clipped or non-clipped, and then further split according to the number of samples that were either assigned via PBT or GSI.

Table 23. Sample numbers for genetic stock assignments of sockeye salmon that passed Bonneville Dam in 2017.

Statistical week grouping	Bonneville dam fish window count	OKA	WEN	RED	LBC	Total	Sample rate (%)
22_23	1971	28	8			36	1.83
24	10475	87	47			134	1.28
25	25975	126	122			248	0.95
26	26669	179	113	4		296	1.11
27	14499	92	51			143	0.99
28	5646	93	53	1	1	148	2.62
29	1539	38	17		1	56	3.64
30	513	11	4	1		16	3.12
Total	87287	654	415	6	2	1077	1.23

Note: Statistical week 22 is 5/28/17–6/3/2107 and 30 is 7/23/17–7/29/2107. ‘Fish count’ is based on tallies of sockeye salmon adults provided by the Fish Passage Center (<http://www.fpc.org>) observed by the Corps of Engineers at their fish counting window. GSI stocks are Okanagan (OKA), Wenatchee (WEN), Snake River (RED), and Lake Billy Chinook (LBC). The number of samples for a given statistical week or grouping was used to calculate sample rate. Relatively few sockeye salmon were sampled from the RED and LBC stocks, and limits inference regarding run-timing and abundance of these stocks.

Results

Estimated relative abundance of Chinook salmon stocks in 2017

In previous years the 10_UCOLSP reporting group included Carson Hatchery for estimates of relative abundance due to genetic similarity in GSI assignments, so the abundance estimates for this reporting group did not represent actual returns specifically to the upper Columbia River. Beginning in 2017, we have categorized several hatcheries as their own reporting groups to alleviate this issue and so that a more accurate assessment of the number of Chinook returning to the upper Columbia River can be determined. To that end, we have included the following reporting groups that are comprised of collections from our PBT baseline. The 20_BONPOOLSP reporting group includes spring Chinook from Caron Hatchery and Little White Salmon Hatchery. The 21_UMATILLASP reporting group includes spring Chinook from the Umatilla Hatchery. The 22_BONPOOLFA reporting group includes fall Chinook from the Little White Salmon Hatchery. The 22_UMATILLFA reporting group includes fall Chinook from the Umatilla Hatchery.

There were 14 major (i.e., abundance >1000 fish) hatchery origin Chinook salmon stocks represented in the total estimated relative abundance (N=318,060) of hatchery Chinook salmon passing Bonneville Dam in 2017 (Table 24; Figure 31). These stocks in order of decreasing magnitude were 18_UCOLSF (112,391), 22_BONPOOLFA (43,065), 12_HELLSC (40,400), 19_SRFALL (38,112), 05_SPCRTU (14,955), 20_BONPOOLSP (14,694), 07_DESCP (11,965), 13_SFSALM (10,067), 21_UMATILLASP (9,837), 10_UCOLSP (6,860), 16_UPSALM (4,590), 06_KLICKR (3,252), 09_YAKIMA (3,010), and 23_UMATILLAFA (2,845) (Table 24; Figure 31). One stock (13_MFSALM) that was considered major in 2016 did not meet the abundance threshold (>1000) to be considered a major stock in 2017 (Table 24).

With the exception of reporting groups 20_BONPOOLSP, 21_UMATILLASP, 22_BONPOOLFA, and 23_UMATILLAFA, abundance estimates include relative abundance for PBT-assigned fish (adipose clipped and non-clipped) and adipose clipped fish that were assigned via GSI. PBT assignments improved our ability to accurately identify hatchery origin fish and estimate total stock abundance (Table 24). Further, using PBT assignments we can now provide relative abundance and run-timing estimates for particular hatchery broodstocks (Table 25; Figure 32; Figure 35) which will allow for much improved abundance estimates.

Table 24. Stock-specific relative abundance and run-timing distribution of hatchery origin (adipose clipped and non-clipped) Chinook salmon passing Bonneville Dam in 2017.

Reporting Group	Estimated abundance					Run-timing distribution						
	Mean	95% CI	Management Period			Ordinal day						Interquartile
			Spring	Summer	Fall	Median	1st	3rd	5th	95th	Median	
			Jan. 1-Jun. 15	Jun. 16-Jul. 31	Aug. 1-Dec. 1		quartile	quartile	percentile	percentile	date	
01_YOUNGS¶	0	0 – 450	0	0	0	-	-	-	-	-	-	-
02_WCASSP¶	28	13 – 765	28	0	0	-	-	-	-	-	-	-
03_WCASFA¶	0	0 – 1246	0	0	0	-	-	-	-	-	-	-
04_WILLAM¶	343	189 – 1245	190	153	0	-	-	-	-	-	-	-
05_SPCRTU	14955	10651 – 17568	0	0	14955	247	239	254	236	262	9/4/17	15
06_KLICKR	3252*	2161 – 4739	2908	344	0	144	140	152	126	181	5/24/17	12
07_DESCSP	11965*	9495 – 14632	10829	1136	0	143	140	153	127	172	5/23/17	13
08_JOHNDR¶	277	14 – 1007	277	0	0	-	-	-	-	-	-	-
09_YAKIMA	3010*	2085 – 4334	2954	56	0	143	140	150	134	165	5/23/17	10
10_UCOLSP	6860*	5441 – 9042	6860	0	0	140	129	146	118	159	5/20/17	17
11_TUCANO	706*	190 – 1576	706	0	0	141	131	143	123	146	5/21/17	12
12_HELLSC	40400*	37207 – 44481	39518	882	0	138	126	142	122	158	5/18/17	16
13_SFSALM	10067*	7146 – 14217	5563	4504	0	162	148	178	141	196	6/11/17	30
14_CHMBLN¶	0	0 – 431	0	0	0	-	-	-	-	-	-	-
15_MFSALM¶	536	127 – 1646	536	0	0	-	-	-	-	-	-	-
16_UPSALM	4590*	3674 – 6818	3776	814	0	152	144	166	138	240	6/1/17	22
17_DESCFA	128	0 – 477	0	0	128	-	-	-	-	-	-	-
18_UCOLSF	112391*	101731 – 121394	6927	34999	70465	251	183	255	163	270	9/9/17	72
19_SRFALL	38112*	29494 – 44917	260	510	37342	251	239	255	229	270	9/9/17	16
20_BONPOOLSP	14694	12227 – 17204	14447	248	0	135	125	141	118	151	5/15/17	16
21_UMATILLASP	9837	7793 – 11967	9765	72	0	135	125	142	123	146	5/15/17	17
22_BONPOOLFA	43065	35089 – 51333	137	2025	40904	253	248	260	209	273	9/11/17	12
23_UMATILLAFA	2845	756 – 5501	0	0	2845	253	250	265	245	283	9/11/17	15
Total	318060*		105679	45742	166639							

*Combined GSI and PBT estimated abundance

¶Run-timing distributions were not estimated for stocks where the combined number of PBT and GSI assignments to reporting group was n<5.

Note: These summary statistics of run-timing distributions were calculated using a method to estimate abundance of each stock based on weekly stock proportions and total numbers of Chinook salmon that were observed passing Bonneville Dam at the fish counting window. The run-timing distributions are characterized by ordinal days for the median date, inter-quartile range (days), and 5th and 95th percentile. The distributions were based on the weekly estimated reporting group proportions that were applied to the daily tallies of Chinook salmon at the Bonneville Dam fish counting window. This method for estimating run-timing distributions minimizes bias imposed by uneven sampling. Run-timing distributions for hatchery-origin fish include stock abundance estimated from PBT and GSI assignments.

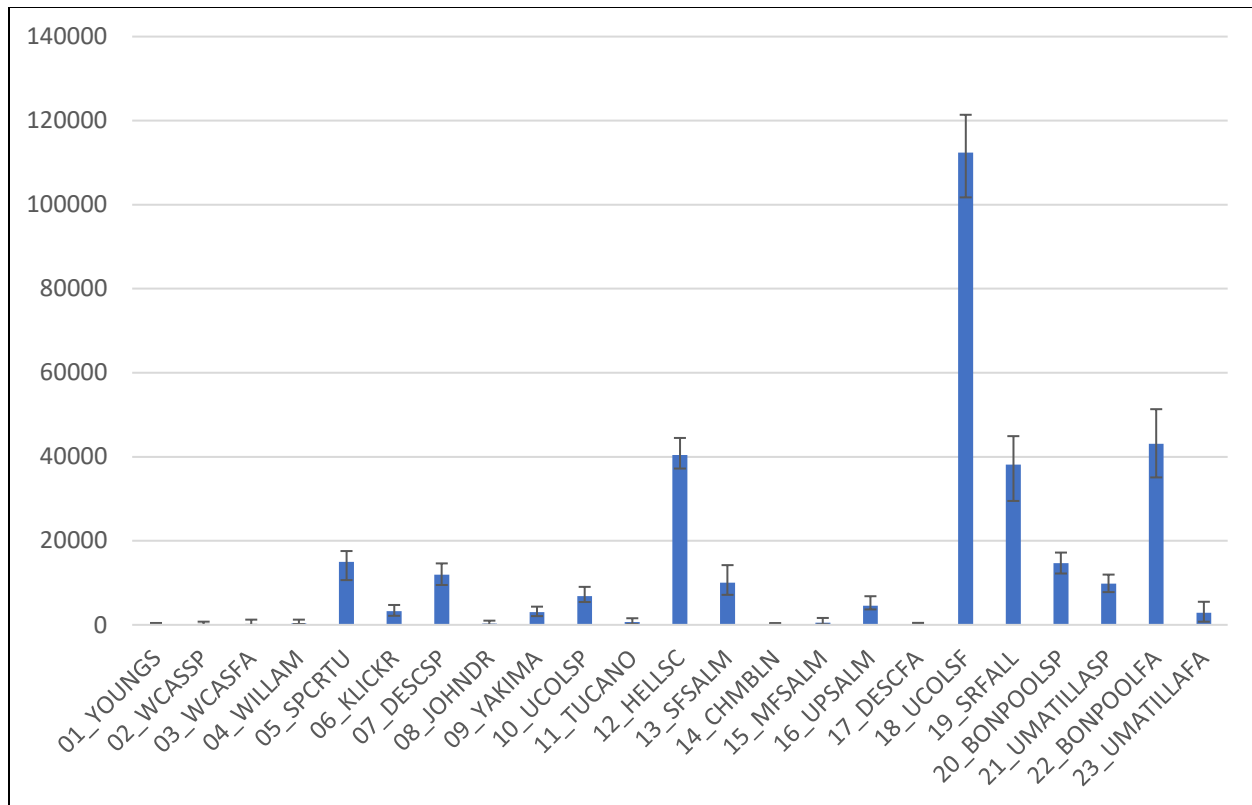


Figure 31. Relative abundance (± 95% CI) of hatchery origin Chinook (adipose clipped and non-clipped) assigned to genetic stock of origin that were sampled at Bonneville Dam in 2017.

In Figure 31, there are several new reporting groups that have been created and are populated based on hatchery fish assigned via PBT, which were subsequently categorized into higher level groups to complement the GSI reporting groups. For example, 20_BONPOOLSP reporting group includes PBT assignments of spring Chinook to Carson Hatchery and Little White Salmon Hatchery. The 21_UMATILLASP reporting group includes PBT assignments of spring Chinook to the Umatilla Hatchery. The 22_BONPOOLFA reporting group includes PBT assignments of fall Chinook to the Little White Salmon Hatchery. The 22_UMATILLAFA reporting group includes PBT assignments of fall Chinook to the Umatilla Hatchery. These reporting groups serve the purpose of distinguishing these hatchery broodstocks apart from other reporting groups that share genetic affinity with these hatcheries but are part of ESA listed groups. For example, 20_BONPOOLSP broodstocks share genetic similarity with upper Columbia River spring Chinook Salmon, but only hatchery fish from the latter group are ESA listed.

We detected PBT assignments for 19.6% (257/1309) of adipose non-clipped (i.e., presumed natural-origin) Chinook salmon sampled at Bonneville Dam in 2017. There were 11 major (i.e., abundance >1000 fish) Chinook salmon stocks represented in the total estimated relative abundance (N=229,732) of natural origin (i.e., adipose non-clipped fish that did not assign via PBT) Chinook salmon passing Bonneville Dam in 2017 (Table 26; Figure 33). These non-clipped stocks in order of decreasing magnitude were 18_UCOLSF (162,406), 19_SRFALL

(35,829), 05_SPCRTU (7,418), 17_DESCFA (5,908), 09_YAKIMA (3,604), 12_HELLSC (2,722), 10_UCOLSP (2,679), 13_SFSALM (2,549), 16_UPSALM (1,583), 08_JOHNDR (1,246) and 15_MFSALM (1,081). These stock abundance estimates were based on the stock proportions that were estimated in GSI_sim across weekly strata, and were multiplied by the total abundance of Chinook salmon that was tallied on a daily basis at the Bonneville Dam fish counting window (Table 21).

Table 25. Hatchery broodstock-specific relative abundance and run-timing distributions of adipose clipped and non-clipped PBT-assigned Chinook salmon passing Bonneville Dam in 2017.

Reporting Group	Broodstock collection	Tagging rate (%)	Estimated abundance					Run-timing distribution						
			Mean	95% CI	Management Period			Ordinal day					Median date	Interquartile range (days)
					Spring	Summer	Fall	Median	1st quartile	3rd quartile	5th percentile	95th percentile		
					Jan. 1-Jun. 15	Jun. 16-Jul. 31	Aug. 1-Dec. 1		percentile	percentile	percentile	percentile		
06_KLICKR	OtsKH12	0.83	466	0 – 1109	466	0	0	141	140	143	127	146	5/21/17	3
	OtsKH13	0.98	2322	1382 – 3377	2193	128	0	145	139	152	125	175	5/25/17	13
	OtsKH14	0.95	248	0 – 678	248	0	0	143	141	147	140	152	5/23/17	6
07_DESCSP†	OtsPFF13	0.68	178	0 – 469	178	0	0	152	149	163	147	165	6/1/17	14
	OtsPFF14	1.00	1279	579 – 2125	961	318	0	149	142	160	140	173	5/29/17	18
	OtsRB13	0.94	3094	1882 – 4450	2924	170	0	142	141	146	131	168	5/22/17	5
	OtsRB14	0.96	2274	1247 – 3445	1945	329	0	143	140	158	134	172	5/23/17	18
	OtsWSNFH13	0.76	2690	1521 – 4026	2690	0	0	139	130	144	124	157	5/19/17	14
	OtsWSNFH14	0.27	1258	196 – 2827	1258	0	0	143	140	157	127	164	5/23/17	17
09_YAKIMA	OtsYRint14	1.00	1193	509 – 2024	1193	0	0	143	141	151	136	160	5/23/17	10
10_UCOLSP	OtsLNFH13	0.88	1294	573 – 2179	1294	0	0	125	123	129	114	143	5/5/17	6
	OtsLNFH14	0.78	601	0 – 1378	601	0	0	141	139	143	134	146	5/21/17	4
	OtsMETH14*	1.00	539	68 – 1160	539	0	0	-	-	-	-	-	-	-
	OtsWTP13	0.85	1069	402 – 1869	1069	0	0	139	131	146	123	152	5/19/17	15
	OtsWTP14	0.94	148	0 – 386	148	0	0	153	149	157	147	160	6/2/17	8
11_TUCANO	OtsTUCW13S	1.00	514	58 – 1106	514	0	0	141	125	143	123	146	5/21/17	18
	OtsTUCW14S	0.85	192	0 – 593	192	0	0	142	141	144	140	146	5/22/17	3
12_HELLSC•	OtsCLWH13S	0.97	3962	2598 – 5426	3962	0	0	136	125	141	119	148	5/16/17	16
	OtsCLWH14S	0.98	2821	1706 – 4041	2660	161	0	141	137	146	131	168	5/21/17	9
	OtsCTHW13S*	0.93	204	0 – 557	204	0	0	-	-	-	-	-	-	-
	OtsCTHW14S*	0.79	292	0 – 809	292	0	0	-	-	-	-	-	-	-
	OtsDWOR12S	0.99	388	58 – 841	388	0	0	125	124	129	121	159	5/5/17	5
	OtsDWOR13S	0.95	3441	2188 – 4837	3441	0	0	136	125	141	123	146	5/16/17	16
	OtsDWOR14S	0.99	759	201 – 1456	759	0	0	141	139	144	130	157	5/21/17	5
	OtsGRUW13S	0.96	709	234 – 1318	709	0	0	140	129	143	126	149	5/20/17	14
	OtsGRUW14S	0.97	223	0 – 601	223	0	0	139	135	148	133	152	5/19/17	13
	OtsIMNW13S	0.98	598	201 – 1124	598	0	0	149	145	153	140	159	5/29/17	8
	OtsIMNW14S	0.88	138	0 – 368	138	0	0	160	157	163	154	165	6/9/17	6
	OtsLOOK13S*	0.95	74	0 – 238	74	0	0	-	-	-	-	-	-	-
	OtsLOOK14S*	0.97	59	0 – 183	59	0	0	-	-	-	-	-	-	-
	OtsLSTW13S*	0.95	151	0 – 392	151	0	0	-	-	-	-	-	-	-
	OtsLSTW14S*	0.71	223	0 – 709	0	223	0	-	-	-	-	-	-	-
	OtsNPFH13S*	0.99	191	0 – 512	191	0	0	-	-	-	-	-	-	-
	OtsPOWP12S	0.99	130	0 – 397	130	0	0	124	123	125	121	125	5/4/17	2
	OtsPOWP13S	1.00	887	320 – 1569	887	0	0	135	127	140	123	148	5/15/17	13
	OtsPOWP14S	0.93	951	297 – 1787	951	0	0	141	131	143	123	146	5/21/17	12
	OtsRAPH12S	0.95	821	250 – 1523	745	75	0	131	123	137	113	191	5/11/17	14
	OtsRAPH13S	0.99	16131	13717 – 18670	16131	0	0	131	124	140	116	148	5/11/17	16
	OtsRAPH14S	0.78	5017	3341 – 6811	4735	282	0	141	138	145	126	169	5/21/17	7
13_SFSALM	OtsJHNW14S*	0.91	331	53 – 741	193	138	0	-	-	-	-	-	-	-
	OtsMCCA12S	1.00	71	0 – 227	71	0	0	149	148	151	147	153	5/29/17	3
	OtsMCCA14S	0.20	7779	4460 – 11158	3639	4140	0	170	152	180	142	194	6/19/17	28
16_UPSALM	OtsPAHH13S	1.00	606	216 – 1078	480	126	0	152	148	163	147	180	6/1/17	15
	OtsPAHH14S	1.00	670	209 – 1227	141	528	0	176	169	210	149	211	6/25/17	41
	OtsSAWT12S	1.00	162	0 – 504	162	0	0	142	141	144	140	146	5/22/17	3
	OtsSAWT13S	1.00	145	0 – 441	145	0	0	136	135	139	133	139	5/16/17	4
	OtsSAWT14S	1.00	1523	781 – 2393	1363	160	0	146	141	159	130	171	5/26/17	18
18_UCOLSF	OtsCJH13_sufa	0.90	5625	4161 – 7213	234	5211	179	186	177	200	166	210	7/5/17	23
	OtsCJH14_sufa	0.99	2782	1442 – 4481	0	1658	1124	203	190	229	174	237	7/22/17	39
	OtsEASTBK12_sufa	0.96	8444	6576 – 10428	1258	7186	0	175	168	186	156	199	6/24/17	18
	OtsENFH14*	0.76	463	70 – 1025	69	394	0	-	-	-	-	-	-	-
	OtsPRH12	0.63	15054	8954 – 21764	0	756	14298	253	251	257	195	270	9/11/17	6
	OtsPRH13	0.79	30721	23513 – 38128	66	1054	29601	254	251	259	238	274	9/12/17	8
	OtsPRH14	0.87	6005	2940 – 9577	0	289	5715	258	252	263	224	273	9/16/17	11
	OtsWELLS12	0.99	4010	2779 – 5379	1470	2540	0	172	159	178	143	192	6/21/17	19
	OtsWELLS13	0.98	5120	2599 – 6799	1402	3718	0	170	164	178	150	192	6/19/17	14
OtsWELLS14	0.98	726	234 – 1321	0	556	169	197	183	208	169	215	7/16/17	25	
19_SRFALL	OtsLYON12S_1	0.99	2860	773 – 5300	124	96	2640	236	232	241	183	255	8/24/17	9
	OtsLYON13S_1	0.92	10397	6169 – 15209	0	0	10397	253	246	258	238	279	9/11/17	12
	OtsLYON14S_1	0.97	15468	10107 – 21281	0	0	15468	251	241	254	234	257	9/9/17	13
	OtsNPFH12S_1	0.98	2596	688 – 5001	72	238	2286	237	234	243	170	262	8/25/17	9
	OtsNPFH13S_1	0.99	2663	1031 – 4644	0	74	2589	237	229	268	225	282	8/25/17	39
	OtsNPFH14S_1	0.98	827	0 – 2238	0	0	827	254	252	265	251	273	9/12/17	13
20_BONPOOLSP	OtsCAR13	0.95	6144	4500 – 7883	5976	168	0	135	125	139	117	152	5/15/17	14
	OtsCAR14	0.90	370	64 – 810	370	0	0	135	130	139	126	151	5/15/17	9
	OtsLWS13_sp	0.90	7477	5645 – 9422	7398	80	0	134	124	141	118	151	5/14/17	17
	OtsLWS14_sp	0.87	703	147 – 1418	703	0	0	142	141	145	129	158	5/22/17	4
21_UMATILLASP	OtsUMA12_sp	0.92	157	0 – 478	157	0	0	136	135	139	133	139	5/16/17	4
	OtsUMA13_sp	0.96	6281	4713 – 7952	6281	0	0	126	124	139	122	145	5/6/17	15
	OtsUMA14_sp	1.00	3399	2165 – 4788	3327	72	0	142	140	144	130	149	5/22/17	4
22_BONPOOLFA	OtsLWS13_sufa	0.88	35953	28210 – 43852	81	1707	34165	253	250	259	224	273	9/11/17	9
	OtsLWS14_sufa	0.93	7113	3796 – 10899	57	317	6739	253	241	263	207	281	9/11/17	22
23_UMATILLAFA	OtsUMA12_sufa	0.99	1534	0 – 3852	0	0	1534	250	247	253	245	273	9/8/17	6
	OtsUMA13_sufa	0.94	1162	140 – 2724	0	0	1162	256	253	268	251	289	9/14/17	15
	OtsUMA14_sufa	0.91	149	0 – 465	0	0	149	281	280	283	279	284	10/9/17	3
		Total	253019		91081	32896	129042							

*Run-timing distributions were not estimated for hatchery broodstocks where the number of PBT assignments was n<5.

†This reporting groups includes fish from Hood River.

•This reporting group includes Clearwater River locations.

Note: These summary statistics of run-timing distributions were calculated using a method to estimate abundance of each stock based on stock proportions and total numbers of Chinook salmon that were observed passing Bonneville Dam at the fish counting window. Key to broodstock collection is presented in Appendix 4.

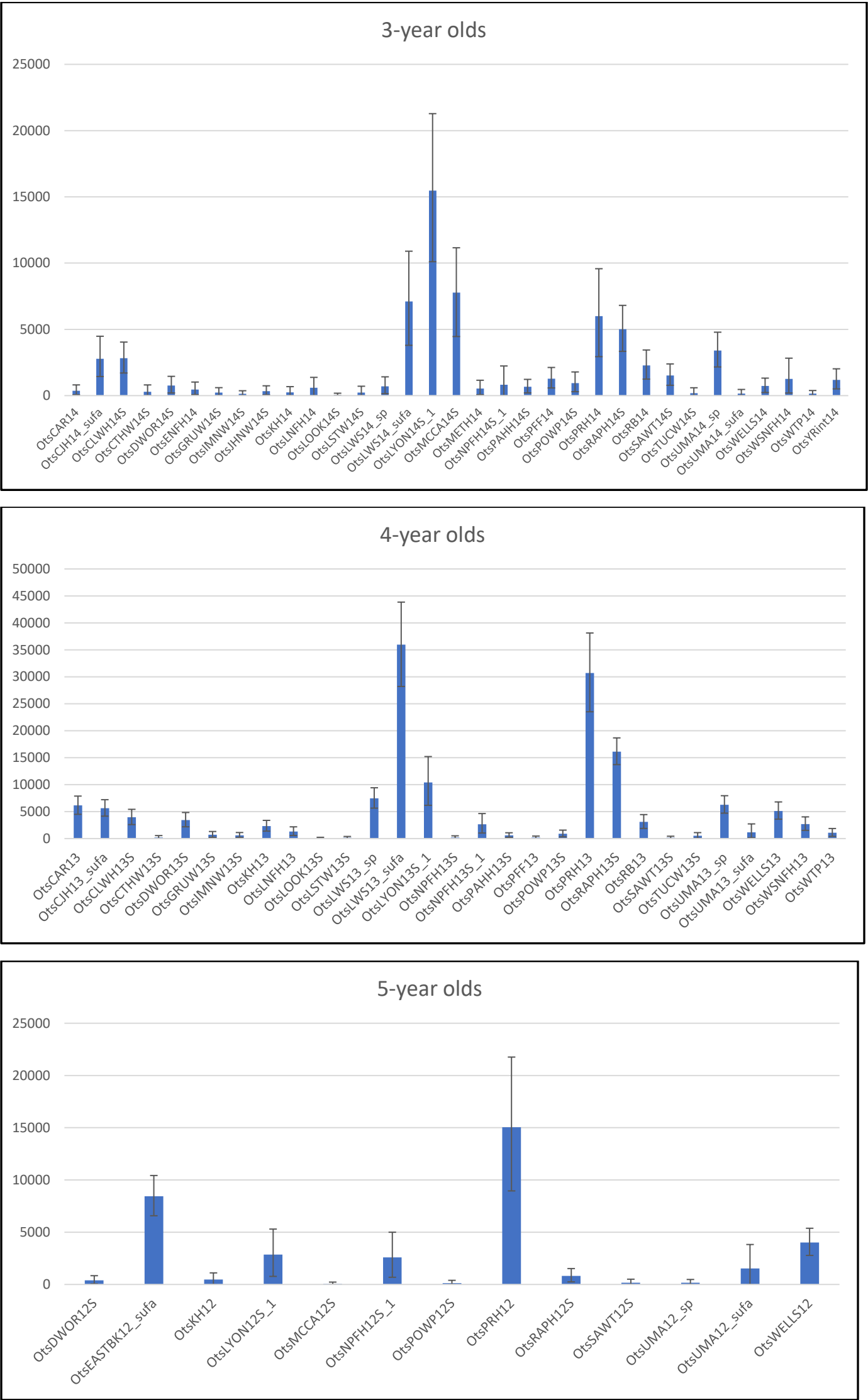


Figure 32. Relative abundance (\pm 95% CI) of hatchery origin Chinook (adipose clipped and non-clipped) sampled at Bonneville Dam in 2017 that assigned via PBT to 75 hatchery broodstocks of origin by age class. The 2014 age-class (3-year old fish; top panel), 2013 age class (4-year old fish), 2012 age class (5-year old fish) are shown. Key to broodstock collection is presented in Appendix 4.

Table 26. Relative abundance and run-timing distributions of natural origin (adipose non-clipped) Chinook salmon stocks passing Bonneville Dam in 2017.

Reporting Group	Estimated abundance					Run-timing distribution						
	Mean	95% CI	Management Period			Ordinal day					Median date	Interquartile range (days)
			Spring	Summer	Fall	Median	1st quartile	3rd quartile	5th percentile	95th percentile		
			Jan. 1-Jun. 15	Jun. 16-Jul. 31	Aug. 1-Dec. 1							
01_YOUNGS*	701	108 – 2320	0	0	701	-	-	-	-	-	-	-
02_WCASSP*	160	91 – 1115	160	0	0	-	-	-	-	-	-	-
03_WCASFA*	561	191 – 2067	144	0	418	-	-	-	-	-	-	-
04_WILLAM*	459	170 – 1634	58	82	319	-	-	-	-	-	-	-
05_SPCRTU	7418	3962 – 11624	0	0	7418	246	243	250	235	255	09/03/17	7
06_KLICKR*	373	82 – 1333	373	0	0	-	-	-	-	-	-	-
07_DESCSP*	342	58 – 1197	342	0	0	-	-	-	-	-	-	-
08_JOHNDR*	1246	330 – 2657	1246	0	0	-	-	-	-	-	-	-
09_YAKIMA	3604	2401 – 4925	3604	0	0	142	139	148	124	170	05/22/17	9
10_UCOLSP	2679	1763 – 4681	2303	376	0	144	140	164	124	245	05/24/17	24
11_TUCANO*	24	0 – 622	24	0	0	-	-	-	-	-	-	-
12_HELLSC	2722	2117 – 5832	2722	0	0	146	141	153	134	252	05/26/17	12
13_SFSALM	2549	1755 – 4671	2335	213	0	149	142	160	138	233	05/29/17	18
14_CHMBLN*	88	10 – 713	88	0	0	-	-	-	-	-	-	-
15_MFSALM*	1081	502 – 2818	690	391	0	-	-	-	-	-	-	-
16_UPSALM	1583	1047 – 3758	1441	143	0	150	143	197	140	259	05/30/17	54
17_DESCFA	5908	2871 – 9508	0	203	5705	259	254	263	251	283	09/17/17	9
18_UCOLSF	162406	149412 – 170622	7905	23019	131482	253	244	261	166	277	09/11/17	17
19_SRFALL	35829	24719 – 44334	102	1041	34685	252	239	257	226	273	09/10/17	18
Total	229732		23537	25468	180727							

* Run-timing distributions were not estimated for stocks where the number of GSI assignments was n<5

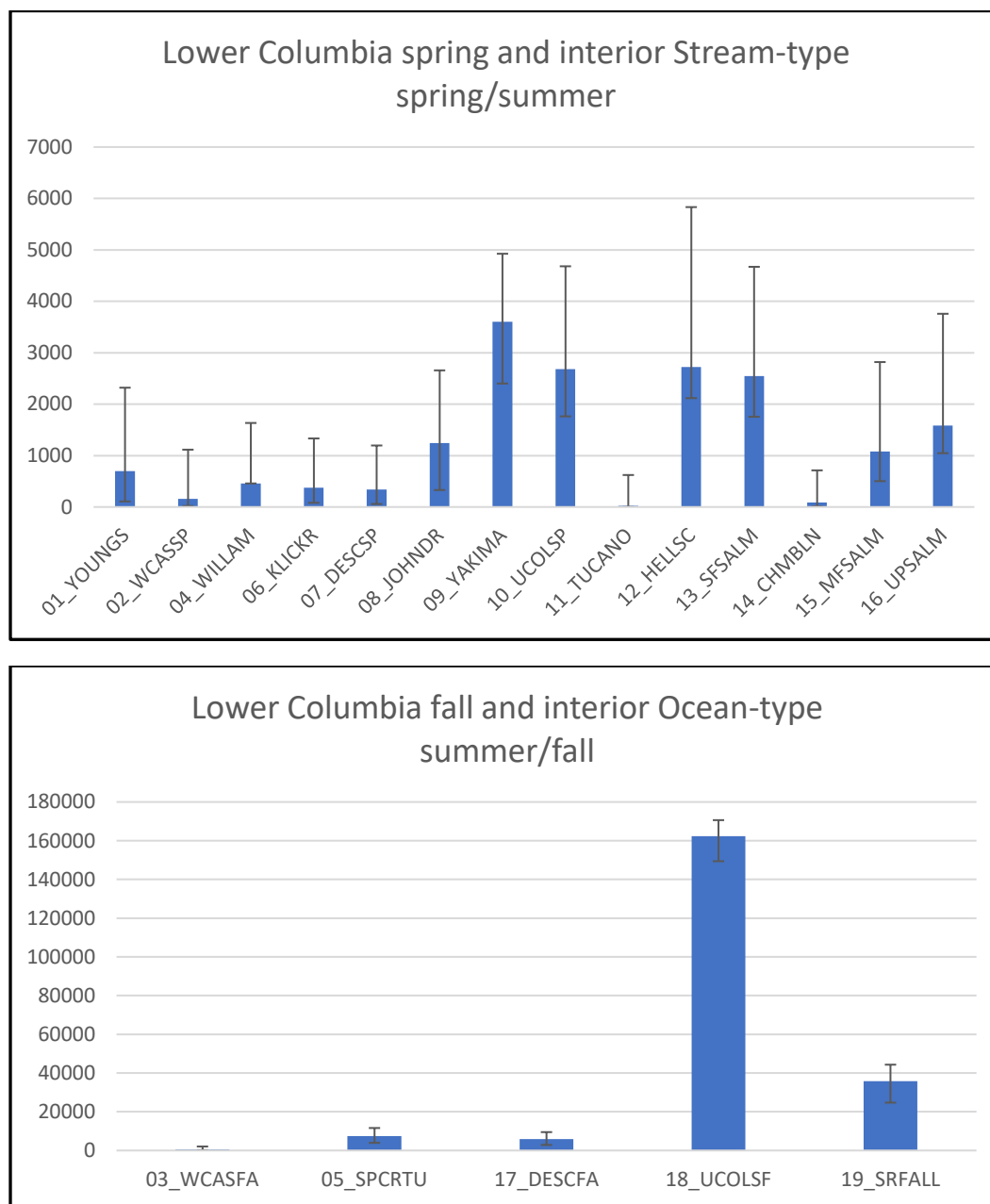


Figure 33. Relative abundance (\pm 95% CI) of natural origin (adipose non-clipped) Chinook sampled at Bonneville Dam in 2017 assigned to genetic stock of origin. Lower Columbia spring and interior stream-type spring/summer Chinook reporting groups (top panel), and lower Columbia fall and interior Ocean-type Chinook reporting groups (bottom panel) are shown.

Run-timing of Chinook salmon stocks in 2017

We obtained a sufficient number of PBT and GSI assignments to characterize the run-timing distributions of 15 hatchery-origin (adipose clipped and non-clipped) Chinook salmon stocks (Table 24; Figure 34). The run timing of six hatchery-origin spring Chinook stocks (i.e., 09_YAKIMA, 10_UCOLSP, 11_TUCANO, 12_HELLSC, 20_BONPOOLSP, and 21_UMATILLASP) were found to terminate within the spring management period (i.e., the 95th percentile of their run distribution occurred on or before June 15th; ordinal day 166). The run timing for three hatchery-origin spring Chinook stocks (i.e., 06_KLICKR, 07_DESCP, and 13_SFSALM) were found to terminate within the summer management period (i.e., the 95th percentile of their run distribution occurred on or before July 31st; ordinal day 212). Although the median date of passage for hatchery spring/summer Chinook from 16_UPSALM was 06/01/17, two PBT assignments to the Pahsimeroi Hatchery on 7/18/17 and 8/1/17 extended the run-timing distribution of this reporting group into the fall management period. The run-timing for the remaining hatchery summer/fall Chinook (i.e., 18_UCOLSF) and hatchery fall Chinook stocks (i.e., 05_SPCRTU, 19_SRFALL, 22_BONPOOLFA, and 23_UMATILLAFA) all had median dates on or after 9/3/17 (Table 24).

We obtained a sufficient number of GSI assignments to characterize the run-timing distributions of 9 natural-origin (adipose non-clipped) Chinook salmon stocks (Table 26; Figure 34). While the median date of passage for all natural-origin spring Chinook stocks (09_YAKIMA, 10_UCOLSP, 12_HELLSC, 13_SFSALM) and one spring/summer Chinook stock (16_UPSALM) occurred on or before 5/30/17 (ordinal day 150), the run-timing for all of these stocks was found to extend beyond the spring management period (i.e., the 95th percentile of their run distribution occurred on or after 6/19/17; ordinal day 170). The run-timing for one natural-origin summer/fall Chinook stock (i.e., 18_UCOLSF) and three natural-origin fall Chinook salmon stocks (i.e., 05_SPCRTU, 17_DESCFA, and 19_SRFALL) all had median dates on or after 9/3/17 (Table 26).

Using the PBT-assigned Chinook salmon, we also characterized the run timing distributions for hatchery broodstocks in our PBT baseline (Table 25; Figure 35). Among major broodstock sources (mean estimated abundance ≥ 1000 fish) for which we had a sufficient number of PBT assignments (i.e. $n > 5$), the run-timing of 12 spring Chinook broodstocks (i.e., OtsCAR13, OtsCLWH13S, OtsDWOR13S, OtsLNFH13, OtsLWS13_sp, OtsRAPH13S, OtsUMA13_sp, OtsUMA14S, OtsWSNFH13, OtsWSNFH14, OtsWTP13, OtsYRint14) were found to terminate within the spring management (i.e., the 95th percentile of their run distribution occurred on or before June 15th; ordinal day 166). The run-timing for eight spring Chinook broodstocks (i.e., OtsPFF14, OtsSAWT14S, OtsRB13, OtsRB14, OtsKH13, OtsCLWH14S, OtsRAPH14S, and OtsMCCA14S) and four summer Chinook broodstocks (OtsWELLS12, OtsWELLS13, OtsCJH13_sufa, and OtsEASTBK12_sufa) were found to terminate within the summer management period (i.e., the 95th percentile of their run distribution occurred on or before July 31st; ordinal day 212). While the median date of passage for the OtsCJH14_sufa broodstock occurred on 7/22/17, the run timing of this summer Chinook broodstock was found to extend beyond the summer management period (i.e., the 95th percentile of the run distribution for this broodstock occurred on 8/25/17; ordinal day 237). The run-timing for 12 fall Chinook broodstocks (OtsLWS13_sufa, OtsLWS14_sufa, OtsLYON12S_1, OtsLYON13S_1,

OtsLYON14S_1, OtsNPFH12S_1, OtsNPFH13S_1, OtsPRH12, OtsPRH13, OtsPRH14, OtsUMA12_sufa, OtsUMA13_sufa) all had median dates on or after 8/24/17 (Table 25).

PBT and GSI assignments for Chinook salmon in 2017

We were able to assign 1315 adult and jack Chinook salmon sampled at Bonneville Dam in 2017 to 75 different hatchery broodstock sources from 2012-2014. The majority (i.e., 851; 64.7%) assigned to 37 Columbia River hatchery broodstock sources, while the remaining 464 fish assigned to 38 Snake River hatchery broodstock sources (Table 27). This is the first year in which the majority of PBT-assigned fish have been assigned to Columbia River hatchery broodstocks, and reflects the expansion of our PBT baseline. The Snake River and Columbia River hatchery broodstock sources were aggregated into appropriate GSI reporting groups in order to integrate the relative abundance estimates from this analysis with relative abundance from GSI analyses. Tagging rates varied across hatchery brood stock sources from 19.62% (OtsMCCA14S) to 100%, with 42 hatchery broodstock sources having tagging rates $\geq 95\%$ (Table 27).

Using GSI, we were able to assign 882 natural-origin and 355 hatchery-origin adult and jack Chinook salmon (that could not be assigned via PBT) sampled at Bonneville Dam in 2017 to 17 reporting groups throughout the Columbia River basin (Table 28). The majority (79%) of these assignments were to the interior Ocean-type lineage (dominated by assignments to 18_UCOLSF; 96%), followed by assignment to the interior Stream-type lineage (16%), and lower Columbia lineage (5%) (Table 28).

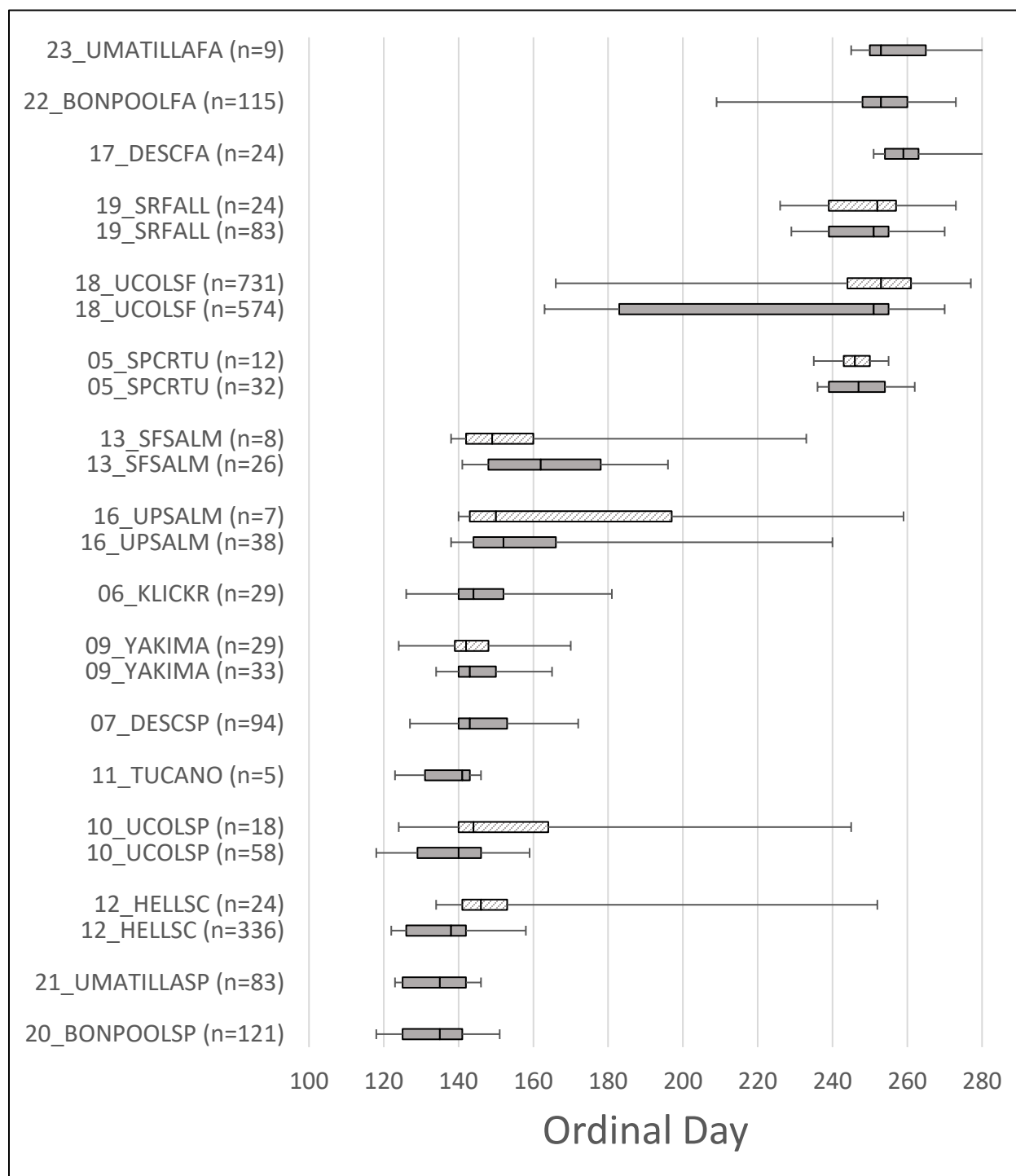


Figure 34. Run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for hatchery origin Chinook (adipose clipped and non-clipped; solid filled) and natural origin Chinook (adipose non-clipped; hash-marked) that were sampled at Bonneville Dam in 2017 and assigned to stock of origin. The number of PBT and/or GSI assignments used in the relative stock abundance expansion procedure from which these run-timing distributions are derived are shown.

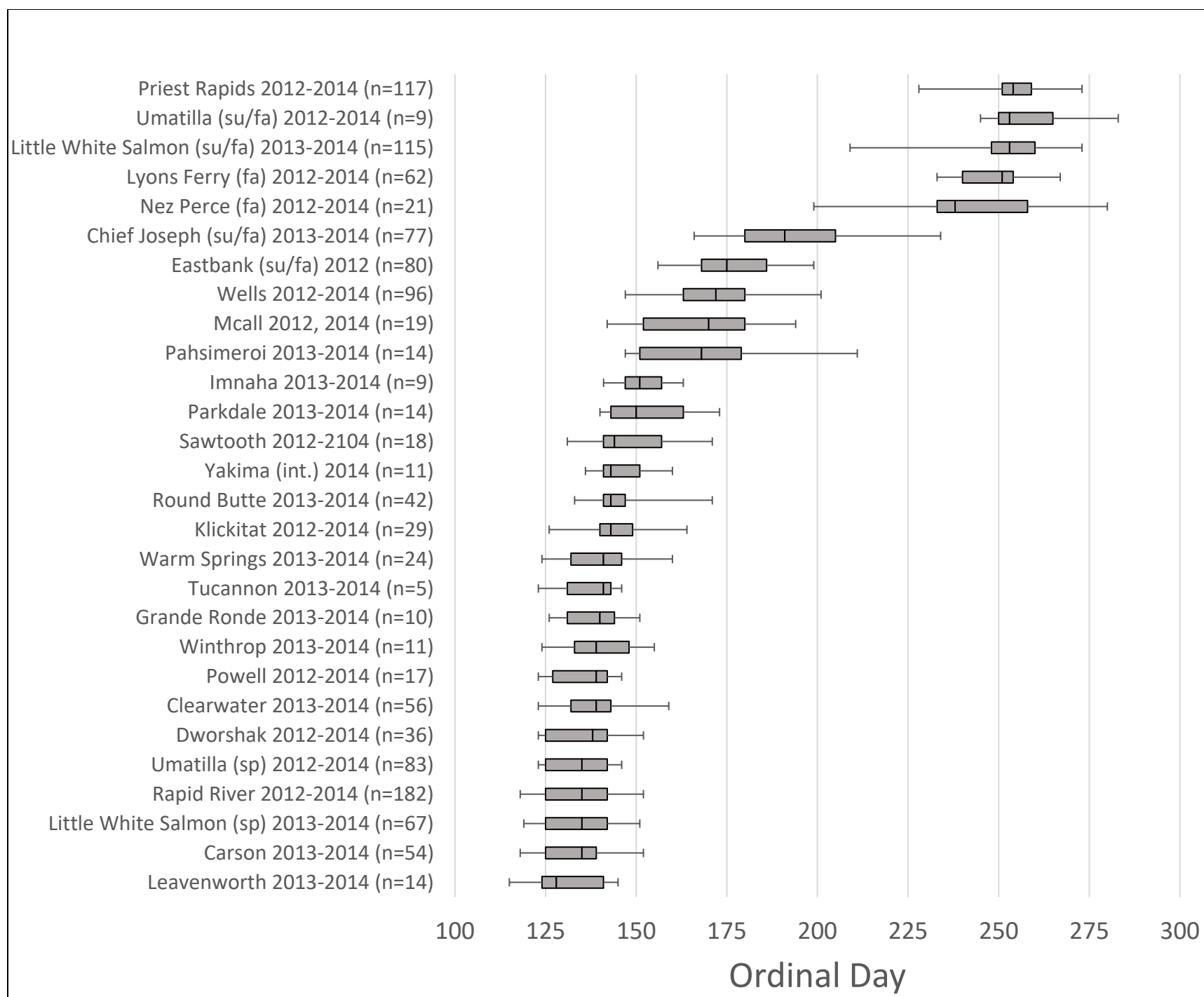


Figure 35. Run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for hatchery origin Chinook (adipose clipped and non-clipped) assigned to PBT broodstock of origin that were sampled at Bonneville Dam in 2017. Hatcheries and their broodyears are ordered from earliest to latest median run-timing, with fall Chinook hatchery stocks at the top. The number of PBT assignments used in the relative stock abundance expansion procedure from which these run-timing distributions are derived are shown.

Table 27. Summary information about the PBT Chinook salmon hatchery broodstock sources and number of assignments.

Broodstock collection	Basin	Reporting Group	Tagging rate (%)	Age	Adipose fin		Total
					Clipped	Non-clipped	
OtsCAR13	Columbia	20 BONPOOLSP	95.47	4	47	3	50
OtsCAR14	Columbia	20 BONPOOLSP	89.87	3	4		4
OtsCJH13_sufa	Columbia	18 UCOLSF	89.87	4	46	8	54
OtsCJH14_sufa	Columbia	18 UCOLSF	99.14	3	22	1	23
OtsEASTBK12_sufa	Columbia	18 UCOLSF	96.19	5	75	5	80
OtsENFH14	Columbia	18 UCOLSF	76.19	3	4		4
OtsKH12	Columbia	06 KCLICKR	83.00	5	3		3
OtsKH13	Columbia	06 KCLICKR	97.88	4	24		24
OtsKH14	Columbia	06 KCLICKR	94.74	3	2		2
OtsLNFH13	Columbia	10 UCOLSP	88.03	4	11		11
OtsLNFH14	Columbia	10 UCOLSP	78.40	3	3		3
OtsLWS13_sp	Columbia	20 BONPOOLSP	90.49	4	57	5	62
OtsLWS13_sufa	Columbia	22 BONPOOLFA	87.63	4	51	40	91
OtsLWS14_sp	Columbia	20 BONPOOLSP	87.15	3	5		5
OtsLWS14_sufa	Columbia	22 BONPOOLFA	92.92	3	10	14	24
OtsMETH14	Columbia	10 UCOLSP	100.00	3		4	4
OtsPFF13	Columbia	07 DESCSP	68.00	4	2		2
OtsPFF14	Columbia	07 DESCSP	100.00	3	12		12
OtsPRH12	Columbia	18 UCOLSF	62.64	5	10	15	25
OtsPRH13	Columbia	18 UCOLSF	79.12	4	32	42	74
OtsPRH14	Columbia	18 UCOLSF	86.77	3	7	11	18
OtsRB13	Columbia	07 DESCSP	94.00	4	23	1	24
OtsRB14	Columbia	07 DESCSP	96.24	3	18		18
OtsUMA12_sp	Columbia	21 UMATILLASP	92.00	5	1		1
OtsUMA12_sufa	Columbia	23 UMATILLAFA	99.00	5	2	1	3
OtsUMA13_sp	Columbia	21 UMATILLASP	96.00	4	53	3	56
OtsUMA13_sufa	Columbia	23 UMATILLAFA	93.60	4	5		5
OtsUMA14_sp	Columbia	21 UMATILLASP	99.55	3	23	3	26
OtsUMA14_sufa	Columbia	23 UMATILLAFA	91.30	3	1		1
OtsWELLS12	Columbia	18 UCOLSF	99.47	5	38	3	41
OtsWELLS13	Columbia	18 UCOLSF	97.69	4	42	6	48
OtsWELLS14	Columbia	18 UCOLSF	97.61	3	6	1	7
OtsWSNFH13	Columbia	07 DESCSP	75.66	4	19	1	20
OtsWSNFH14	Columbia	07 DESCSP	26.57	3	3	1	4
OtsWTP13	Columbia	10 UCOLSP	85.17	4	8	1	9
OtsWTP14	Columbia	10 UCOLSP	94.09	3	1	1	2
OtsYRint14	Columbia	09 YAKIMA	100.00	3	10	1	11
OtsCLWH13S	Snake	12 HELLSC	97.48	4	29	3	32
OtsCLWH14S	Snake	12 HELLSC	98.37	3	18	6	24
OtsCTHW13S	Snake	12 HELLSC	93.14	4	2		2
OtsCTHW14S	Snake	12 HELLSC	79.01	3	2		2
OtsDWOR12S	Snake	12 HELLSC	99.26	5	4		4
OtsDWOR13S	Snake	12 HELLSC	95.18	4	25	1	26
OtsDWOR14S	Snake	12 HELLSC	99.38	3	6		6
OtsGRUW13S	Snake	12 HELLSC	96.07	4	6	2	8
OtsGRUW14S	Snake	12 HELLSC	97.22	3	1	1	2
OtsIMNW13S	Snake	12 HELLSC	97.89	4	7		7
OtsIMNW14S	Snake	12 HELLSC	87.97	3	2		2
OtsJHNW14S	Snake	13 SFSALM	90.84	3		4	4
OtsLOOK13S	Snake	12 HELLSC	95.02	4	1		1
OtsLOOK14S	Snake	12 HELLSC	96.94	3	1		1
OtsLSTW13S	Snake	12 HELLSC	95.18	4	2		2
OtsLSTW14S	Snake	12 HELLSC	71.22	3	1		1
OtsLYON12S_1	Snake	19 SRFALL	98.52	5	5	3	8
OtsLYON13S_1	Snake	19 SRFALL	92.38	4	9	16	25
OtsLYON14S_1	Snake	19 SRFALL	96.96	3	16	13	29
OtsMCCA12S	Snake	13 SFSALM	100.00	5		1	1
OtsMCCA14S	Snake	13 SFSALM	19.62	3	14	4	18
OtsNPFH12S_1	Snake	19 SRFALL	97.51	5	2	5	7
OtsNPFH13S	Snake	12 HELLSC	99.48	4		2	2
OtsNPFH13S_1	Snake	19 SRFALL	99.06	4	3	8	11
OtsNPFH14S_1	Snake	19 SRFALL	98.03	3	1	2	3
OtsPAHH13S	Snake	16 UPSALM	99.55	4	6	2	8
OtsPAHH14S	Snake	16 UPSALM	99.74	3	5	1	6
OtsPOWP12S	Snake	12 HELLSC	99.15	5	1		1
OtsPOWP13S	Snake	12 HELLSC	100.00	4	8	1	9
OtsPOWP14S	Snake	12 HELLSC	93.37	3	7		7
OtsRAPH12S	Snake	12 HELLSC	95.36	5	7		7
OtsRAPH13S	Snake	12 HELLSC	98.61	4	138	4	142
OtsRAPH14S	Snake	12 HELLSC	78.16	3	33		33
OtsSAWT12S	Snake	16 UPSALM	99.80	5	1		1
OtsSAWT13S	Snake	16 UPSALM	99.77	4	1		1
OtsSAWT14S	Snake	16 UPSALM	100.00	3	14	2	16
OtsTUCW13S	Snake	11 TUCANO	100.00	4		4	4
OtsTUCW14S	Snake	11 TUCANO	84.75	3		1	1
				Total	1058	257	1315

Note: Key to broodstock collection is presented in Appendix 4.

Table 28. Summary of the number of GSI assignments by reporting group for hatchery-origin Chinook salmon that did not assign via PBT, and natural-origin Chinook salmon that assigned via GSI.

Reporting group	Run type	Lineage	Adipose fin		Total
			Clipped	Non-clipped	
01_YOUNGS	Spring	Lower Columbia		2	2
02_WCASSP	Spring	Lower Columbia	1	1	2
03_WCASFA	Fall	Lower Columbia		1	1
04_WILLAM	Spring	Lower Columbia	5	3	8
05_SPCRTU	Fall	Lower Columbia	32	12	44
06_KLICKR	Spring	Interior stream type	2	2	4
07_DESCSP	Spring	Interior stream type	14	4	18
08_JOHNDR	Spring	Interior stream type			0
09_YAKIMA	Spring	Interior stream type	22	29	51
10_UCOLSP	Spring	Interior stream type	33	18	51
11_TUCANO	Spring	Interior stream type			0
12_HELLSC	Spring	Interior stream type	26	24	50
13_SFSALM	Spring	Interior stream type	7	8	15
14_CHMBLN	Spring	Interior stream type		1	1
15_MFSALM	Spring	Interior stream type		1	1
16_UPSALM	Spring/Summer	Interior stream type	6	7	13
17_DESCFA	Fall	Interior ocean type		14	14
18_UCOLSF	Summer/Fall	Interior ocean type	204	731	935
19_SRFALL	Fall	Interior ocean type	3	24	27
		Total	355	882	1237

Estimated relative abundance of steelhead stocks in 2017

Daily passage of steelhead at Bonneville Dam in 2017 is provided in Figure 36. There were five major stocks (abundance >1000) represented in the total estimated relative abundance (N=84,301) of hatchery origin steelhead passing Bonneville Dam in 2017 (Table 29). These stocks in order of decreasing magnitude were 07_MGILCS (31,728), 14_UPSALM (26,782), 10_SFCLWR (15,938), 09_UPPCOL (5,833), and 03_SKAMAN (3,576) (Table 29; Figure 37). These same stocks were identified as being of major abundance in 2016. These estimates include relative abundance estimated from PBT-assigned fish that were mostly adipose clipped; however, a portion of the PBT-assigned fish were found to be non-clipped. Therefore, PBT assignments improved our ability to accurately identify hatchery-origin steelhead and estimate total stock relative abundance. Further, using PBT assignments we can now provide relative abundance (Table 30; Figure 38) and run-timing estimates for particular hatchery broodstocks (Table 30). There were 14 major hatchery broodstock sources (abundance >1000) represented in the total estimated relative abundance of hatchery-origin steelhead passing Bonneville Dam in 2017 (Table 30). These stocks in order of decreasing magnitude were OmyLYON15S (9,874), OmyWALL15S (7,835), OmyDWOR15S (7,261), OmyDWOR14S (6,120), OmyPAHH15S (5,704), OmySAWT15S (4,321), OmyWEL_OKA (3,423), OmyLYON14S (2,743), OmyOXBO15S (2,432), OmySKH13_su (2,066), OmyLSCR15s (1,605), OmyRB15 (1,555), OmyRB14 (1,013), and OmyPAHH14S (1,004). Skamania broodstock are spawned earlier in the year than other broodstock collections, and are designated for the following brood year (e.g., OmySKH12_su are spawned in 2013 and are 3-ocean fish).

We detected PBT assignments for 7.8% (28/359) of adipose non-clipped (i.e., presumed natural-origin) steelhead sampled at Bonneville Dam in 2017. There were five major stocks (abundance >1000) represented in the total estimated relative abundance (N=29,953) of natural origin (i.e., adipose non-clipped fish that did not assign via PBT) steelhead passing Bonneville Dam in 2017 (Table 31; Figure 39). These stocks in order of decreasing magnitude were 07_MGILCS (20,419), 09_UPPCOL (2,815), 14_UPSALM (2,286), 08_YAKIMA (1,236), and 06_KLICKR (1,013).

Table 29. Stock-specific relative abundance and run-timing distribution of hatchery origin (adipose clipped and non-clipped) steelhead passing Bonneville Dam in 2017.

Reporting Group	Estimated abundance				Run-timing distribution						
	Mean	95% CI	Management Period		Ordinal day					Median date	Interquartile range (days)
			Skamania	Summer	Median	1st quartile	3rd quartile	5th percentile	95th percentile		
			Apr. 1-Jun. 30	July 1- Oct. 31							
01_WCOAST	0	0 – 63	0	0	-	-	-	-	-	-	-
02_LOWCOL	214*	1236 – 676	214	0	124	113	130	107	154	05/04/17	17
03_SKAMAN	3576*	2404 – 4772	1727	1849	186	161	223	134	252	07/05/17	62
04_WILLAM [¶]	15	0 – 275	15	0	-	-	-	-	-	-	-
05_BWSALM	0	0 – 62	0	0	-	-	-	-	-	-	-
06_KLICKR	0	0 – 380	0	0	-	-	-	-	-	-	-
07_MGILCS	31728*	26700 – 35981	0	31728	234	219	247	200	263	08/22/17	28
08_YAKIMA	0	0 – 416	0	0	-	-	-	-	-	-	-
09_UPPCOL	5833*	3556 – 8425	0	5833	235	224	249	204	263	08/23/17	25
10_SFCLWR	15938*	12950 – 19173	0	15938	260	247	268	235	282	09/18/17	21
11_UPCLWR [¶]	56	0 – 311	0	56	-	-	-	-	-	-	-
12_SFSALM	0	0 – 181	0	0	-	-	-	-	-	-	-
13_MFSALM [¶]	159	0 – 538	0	159	-	-	-	-	-	-	-
14_UPSALM	26782*	22631 – 31587	0	26782	238	231	254	209	264	08/26/17	23
Total	84301										

*Combined with PBT estimated abundance

[¶]Run-timing distributions were not estimated for stocks where the combined number of PBT and GSI assignments to reporting group was n<5.

Note: These summary statistics of run-timing distributions were calculated using a method to estimate abundance of each stock based on weekly stock proportions and total numbers of steelhead that were observed passing Bonneville Dam at the fish counting window. The run-timing distributions are characterized by ordinal days for the median date, inter-quartile range (days), and 5th and 95th percentile. The distributions were based on the weekly estimated reporting group proportions that were applied to the daily tallies of steelhead at the Bonneville Dam fish counting window. This method for estimating run-timing distributions minimizes bias imposed by uneven sampling. Run-timing distributions for hatchery-origin fish include stock abundance estimated from PBT and GSI assignments.

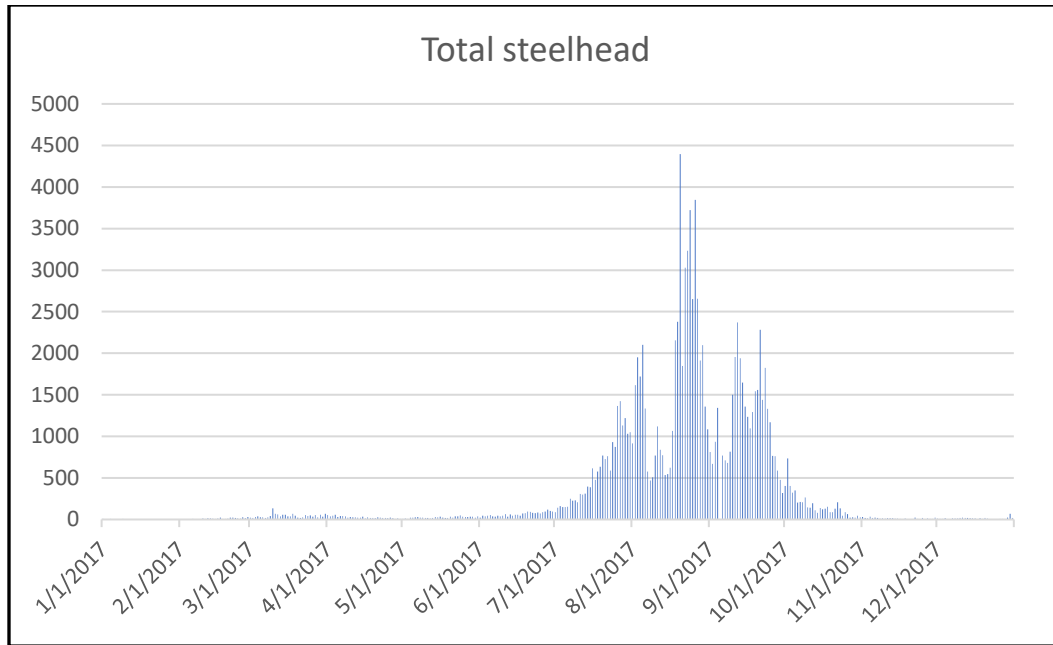


Figure 36. Daily passage of steelhead at Bonneville Dam in 2017 (source: www.fpc.org).

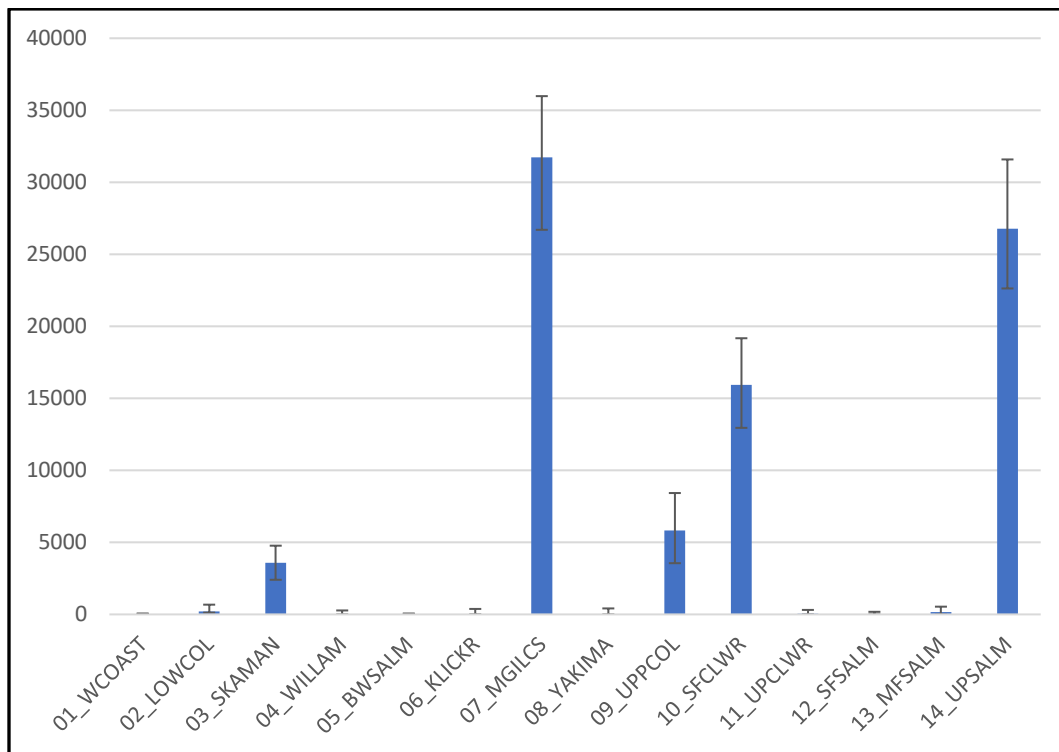


Figure 37. Relative abundance (\pm 95% CI) of hatchery origin steelhead (adipose clipped and non-clipped) assigned to genetic stock of origin that were sampled at Bonneville Dam in 2017.

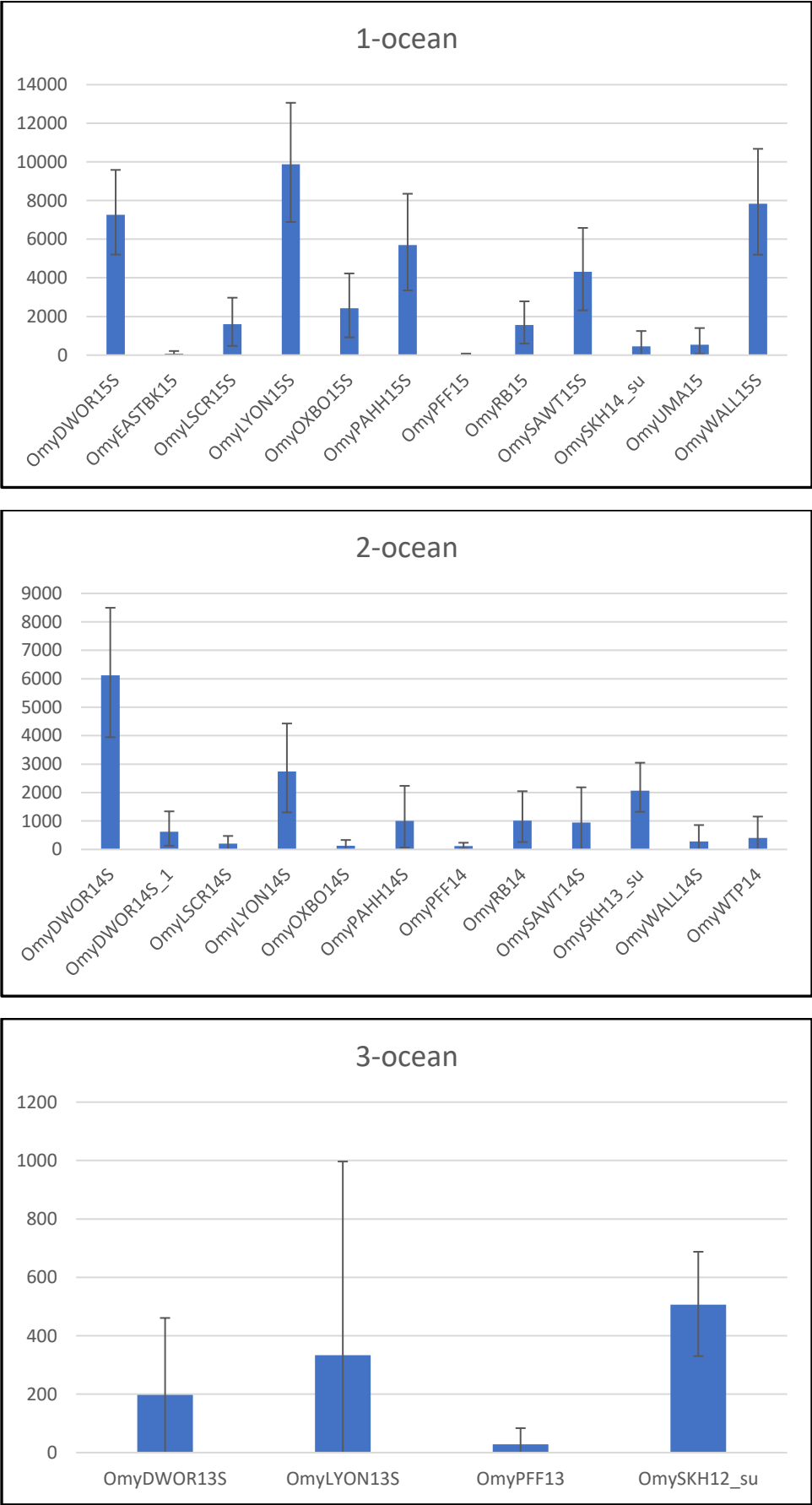


Figure 38. Relative abundance (\pm 95% CI) of hatchery origin steelhead (adipose clipped and non-clipped) sampled at Bonneville Dam in 2017 that assigned via PBT to 31 hatchery broodstocks of origin. The 2015 age-class (1-ocean fish; top panel), 2014 age-class (2-ocean fish), and 2013 age class (3-ocean fish) are shown. Key to broodstock collection is presented in Appendix 4. Skamania broodstock are spawned earlier in the year and are designated for the following brood year.

Table 30. Hatchery broodstock-specific relative abundance and run-timing distributions of adipose clipped and non-clipped PBT-assigned steelhead passing Bonneville Dam in 2017.

Reporting Group	Broodstock collection	Tagging rate	Estimated abundance				Run-timing distribution						
			Mean	95% CI	Management Period		Ordinal day					Median date	Interquartile range (days)
					Skamania	Summer	Median	1st quartile	3rd quartile	5th percentile	95th percentile		
					Apr. 1-Jun. 30	July 1- Oct. 31							
02_LOWCOL	OmyPFF13*	95.3%	28	0 – 84	28	0	-	-	-	-	-	-	-
	OmyPFF14*	95.2%	124	28 – 235	124	0	-	-	-	-	-	-	-
	OmyPFF15*	100.0%	27	0 – 81	27	0	-	-	-	-	-	-	-
03_SKAMAN	OmySKH12 su ^a	99.2%	507	330 – 688	507	0	144	134	153	111	159	05/24/17	19
	OmySKH13 su ^b	100.0%	2066	1323 – 3048	920	1146	193	169	213	145	235	07/12/17	44
	OmySKH14 su ^{c*}	100.0%	461	0 – 1249	0	461	-	-	-	-	-	-	-
07_MGILCS	OmyLSCR14S*	95.5%	204	0 – 474	0	204	-	-	-	-	-	-	-
	OmyLSCR15S	86.7%	1605	477 – 2973	0	1605	229	213	234	197	237	08/17/17	21
	OmyLYON13S*	100.0%	333	0 – 997	0	333	-	-	-	-	-	-	-
	OmyLYON14S	99.4%	2743	1302 – 4427	0	2743	232	215	240	197	264	08/20/17	25
	OmyLYON15S	93.2%	9874	6891 – 13064	0	9874	236	228	251	207	263	08/24/17	23
	OmyRB14	99.1%	1013	261 – 2047	0	1013	230	206	243	192	261	08/18/17	37
	OmyRB15	98.2%	1555	597 – 2785	0	1555	230	207	241	193	268	08/18/17	34
	OmyUMA15*	97.8%	535	65 – 1401	0	535	-	-	-	-	-	-	-
	OmyWALL14S*	99.6%	281	0 – 857	0	281	-	-	-	-	-	-	-
	OmyWALL15S	94.3%	7835	5201 – 10680	0	7835	235	226	246	208	262	08/23/17	20
	OmyWALW15S	96.3%	827	67 – 1864	0	827	240	231	259	205	274	08/28/17	28
	09_UPPCOL	OmyEASTBK15*	91.3%	71	0 – 214	0	71	-	-	-	-	-	-
OmyWEL_OKA15		96.6%	3423	1689 – 5392	0	3423	239	231	254	211	265	08/27/17	23
OmyWEL_OMA15*		96.6%	581	0 – 1466	0	581	-	-	-	-	-	-	-
OmyWTP14*		97.1%	408	0 – 1156	0	408	-	-	-	-	-	-	-
10_SFCLWR	OmyDWOR13S*	96.4%	198	0 – 461	0	198	-	-	-	-	-	-	-
	OmyDWOR14S	96.9%	6120	3945 – 8495	0	6120	257	247	265	239	279	09/15/17	18
	OmyDWOR14S_1	96.9%	619	131 – 1338	0	619	233	213	266	196	280	08/21/17	53
	OmyDWOR15S	88.7%	7261	5205 – 9589	0	7261	264	252	270	238	283	09/22/17	18
14_UPSALM	OmyOXBO14S*	97.0%	132	0 – 332	0	132	-	-	-	-	-	-	-
	OmyOXBO15S	92.8%	2432	921 – 4230	0	2432	251	239	259	208	269	09/09/17	20
	OmyPAHH14S*	100.0%	1004	65 – 2234	0	1004	-	-	-	-	-	-	-
	OmyPAHH15S	84.5%	5704	3351 – 8355	0	5704	234	227	240	213	262	08/22/17	13
	OmySAWT14S	99.4%	949	0 – 2184	0	949	238	230	253	207	264	08/26/17	23
	OmySAWT15S*	94.2%	4321	2319 – 6587	0	4321	-	-	-	-	-	-	-
Total			63241		1606	61631							

*Run-timing distributions were not estimated for hatchery broodstocks where the number of PBT assignments was n<5.

^a OmySKH12_su are 3-ocean

^b OmySKH13_su are 2-ocean

^c OmySKH14_su are 1-ocean

Note: These summary statistics of run-timing distributions were calculated using a method to estimate abundance of each stock based on stock proportions and total numbers of steelhead that were observed passing Bonneville Dam at the fish counting window. The date ranges listed under “Skamania” and “Summer” management period were chosen by steelhead fishery managers, and for each hatchery source stock we provide the abundance that has passed within these time periods. Key to broodstock collection is presented in Appendix 5. Skamania broodstock are spawned earlier in the year and are designated for the following brood year.

Table 31. Relative abundance and run-timing distributions of natural origin (adipose non-clipped) steelhead stocks passing Bonneville Dam in 2017.

Reporting Group	Estimated abundance				Run-timing distribution						
	Mean	95% CI	Management Period		Ordinal day					Median date	Interquartile range (days)
			Skamania	Summer	Median	1st	3rd	5th	95th		
			Apr. 1-Jun. 30	July 1- Oct. 31		quartile	quartile	percentile	percentile		
01_WCOAST	0	0 – 59	0	0	-	-	-	-	-	-	-
02_LOWCOL*	232	77 – 771	38	194	-	-	-	-	-	-	-
03_SKAMAN	599	175 – 843	508	91	171	156	179	117	268	06/20/17	23
04_WILLAM*	27	0 – 255	27	0	-	-	-	-	-	-	-
05_BWSALM*	43	0 – 170	0	43	-	-	-	-	-	-	-
06_KLICKR	1013	443 – 2032	65	948	218	205	235	153	258	08/06/17	30
07_MGILCS	20419	17642 – 23978	367	20052	220	206	235	190	262	08/08/17	29
08_YAKIMA	1236	696 – 1980	0	1236	205	199	214	188	267	07/24/17	15
09_UPPCOL	2815	567 – 5634	0	2815	223	213	232	198	265	08/11/17	19
10_SFCLWR	327	91 – 1020	0	327	261	250	268	239	286	09/19/17	18
11_UPCLWR*	507	81 – 1347	0	507	-	-	-	-	-	-	-
12_SFSALM*	258	0 – 343	0	258	-	-	-	-	-	-	-
13_MFSALM*	191	37 – 652	0	191	-	-	-	-	-	-	-
14_UPSALM	2286	365 – 3554	0	2286	239	219	253	199	263	08/27/17	34
Total	29953										

* Run-timing distributions were not estimated for stocks where the number of GSI assignments was n<5.

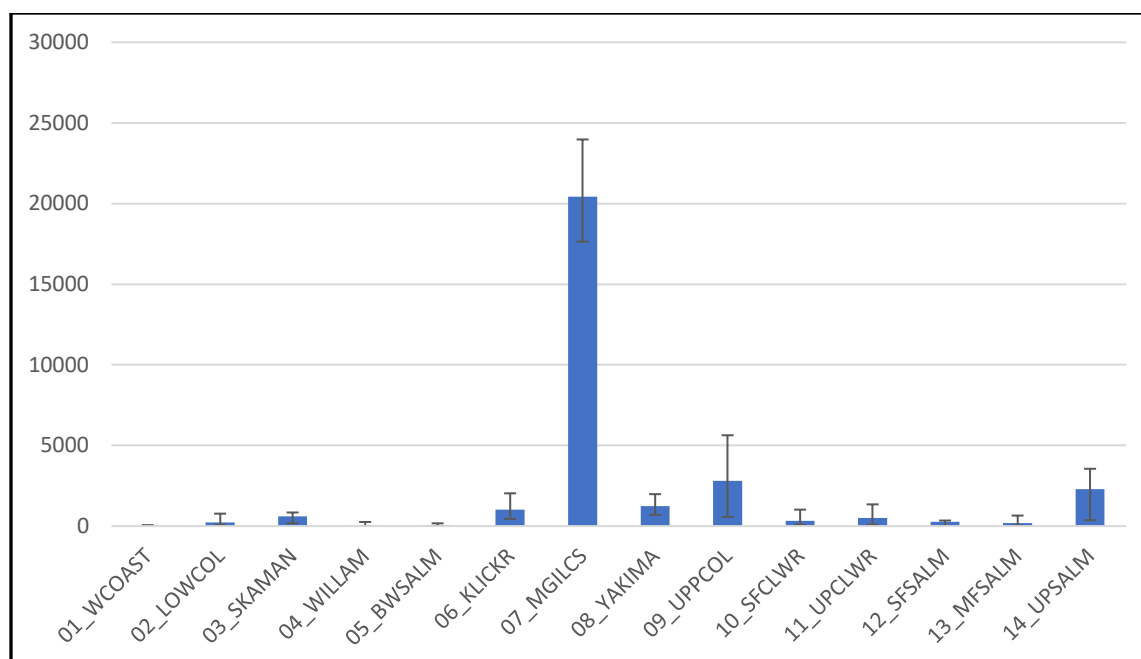


Figure 39. Relative abundance (\pm 95% CI) of natural origin (adipose non-clipped) steelhead sampled at Bonneville Dam in 2017 assigned to genetic stock of origin.

Run-timing of steelhead stocks in 2017

We were able to characterize the run-timing distributions for six hatchery origin steelhead stocks (Table 29; Figure 40). Very few winter-run steelhead stocks exist above Bonneville Dam and our sampling program at Bonneville AFF does not trap or collect fish between December and March when winter-run steelhead would be most likely to occur. Thus, winter-run stocks are expected to be rare in our samples from Bonneville Dam, but could occur from hatchery-origin fish from PFF in the Hood River (winter-run broodstock) or natural-origin fish from sub-basins nearest upstream such as Klickitat, Hood, and Fifteenmile rivers. Indeed, we observed an early run-timing distribution for the 02_LOWCOL hatchery stock comprised of PBT assigned fish to PFF (i.e. winter-run broodstock) (Figure 40). The 02_LOWCOL hatchery stock had a median run-timing date of 05/04/2017 (ordinal day 124). The 03_SKAMAN hatchery stock has previously been characterized as part of an early run-timing category, and in 2017 had a median run-timing date of 07/05/17 (ordinal day 186). This is somewhat later than the median run timing observed for this hatchery stock in 2016 (i.e., 06/22/2016; ordinal day 173), and may be attributable to delayed migration passed Bonneville Dam in 2017 (Figure 36). An intermediate run-timing category has also been described, and includes the following steelhead stocks (ordered by median date): 07_MGILCS (08/22/16; ordinal day 234), 09_UPPCOL (08/23/17; ordinal day 235), and 14_UPSALM (08/26/17; ordinal day 238). Finally, a late run-timing category consists of the 10_SFCLWR stock (09/18/17; ordinal day 260), and is typically thought to be characteristic of B-run steelhead that return after August 25th at Bonneville Dam (Table 29; Figure 40).

Using the PBT-assigned steelhead, we also characterized the run-timing distributions for major broodstock sources (mean estimated abundance \geq 1000 fish) in our PBT baseline (Table 30; Figure 41). For this analysis, we grouped the 14 major hatchery broodstock sources (abundance >1000) into categories according to their median run-timing date.

Only one broodstock source (i.e. OmySKH13_su) had a median run-timing date before August 1st. Ten broodstock sources had median run-timing dates from August 1 – August 31

(i.e., OmyLSCR15S, OmyRB14, OmyRB15, OmyLYON14S, OmyLYON15S, Omy PAHH14S, OmyPAHH15S, OmyWALL15S, OmySAWT15S, and OmyWEL_OKA15). Three broodstock sources had median run-timing distributions after September 1st: OmyOXBO15S, OmyDWOR14S, OmyDWRO15S (Table 30). Relative to our findings for 2016, these results demonstrate a shift to later run-timing distributions for hatchery stocks, and may reflect delayed migration at Bonneville Dam in 2017 (Figure 36).

We were able to characterize the run-timing distributions for seven natural-origin steelhead stocks (Table 31; Figure 40); patterns generally fit the same run-timing categories as characterized for hatchery-origin steelhead. The seven natural origin stocks ordered by median run-timing date were: 03_SKAMAN (06/20/17; ordinal day 171), 08_YAKIMA (07/24/17; ordinal day 205), 06_KLICKR (08/06/17; ordinal day 218), 07_MGILCS (08/08/17; ordinal day 220), 09_UPPCOL (08/11/17; ordinal day 223), 14_UPSALM (08/27/17; ordinal day 239), and 10_SFCLWR (09/19/17; ordinal day 261) (Table 31; Figure 40). Natural-origin stocks from 06_KLICKR and 07_MGILCS had later run-timing distributions relative to that observed in 2016, and may reflect delayed migration at Bonneville Dam in 2017 (Figure 36).

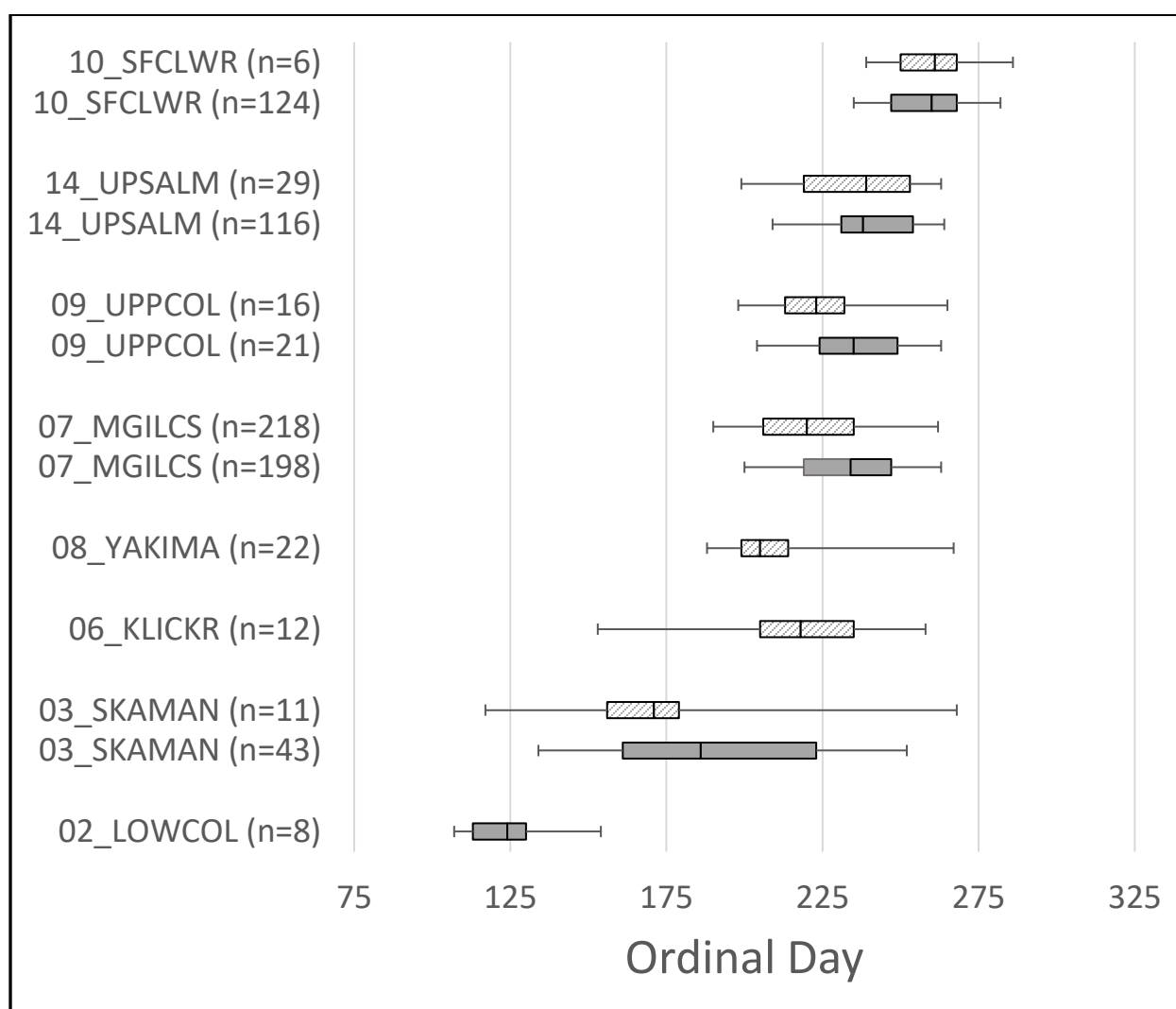


Figure 40. Run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for hatchery-origin steelhead (adipose clipped and non-clipped; solid filled) and natural-origin steelhead (adipose non-clipped; hash-marked) that were sampled at Bonneville Dam in 2017 and assigned to stock of origin. The number of PBT and/or GSI assignments used in the relative stock abundance expansion procedure from which these run-timing distributions are derived are shown.

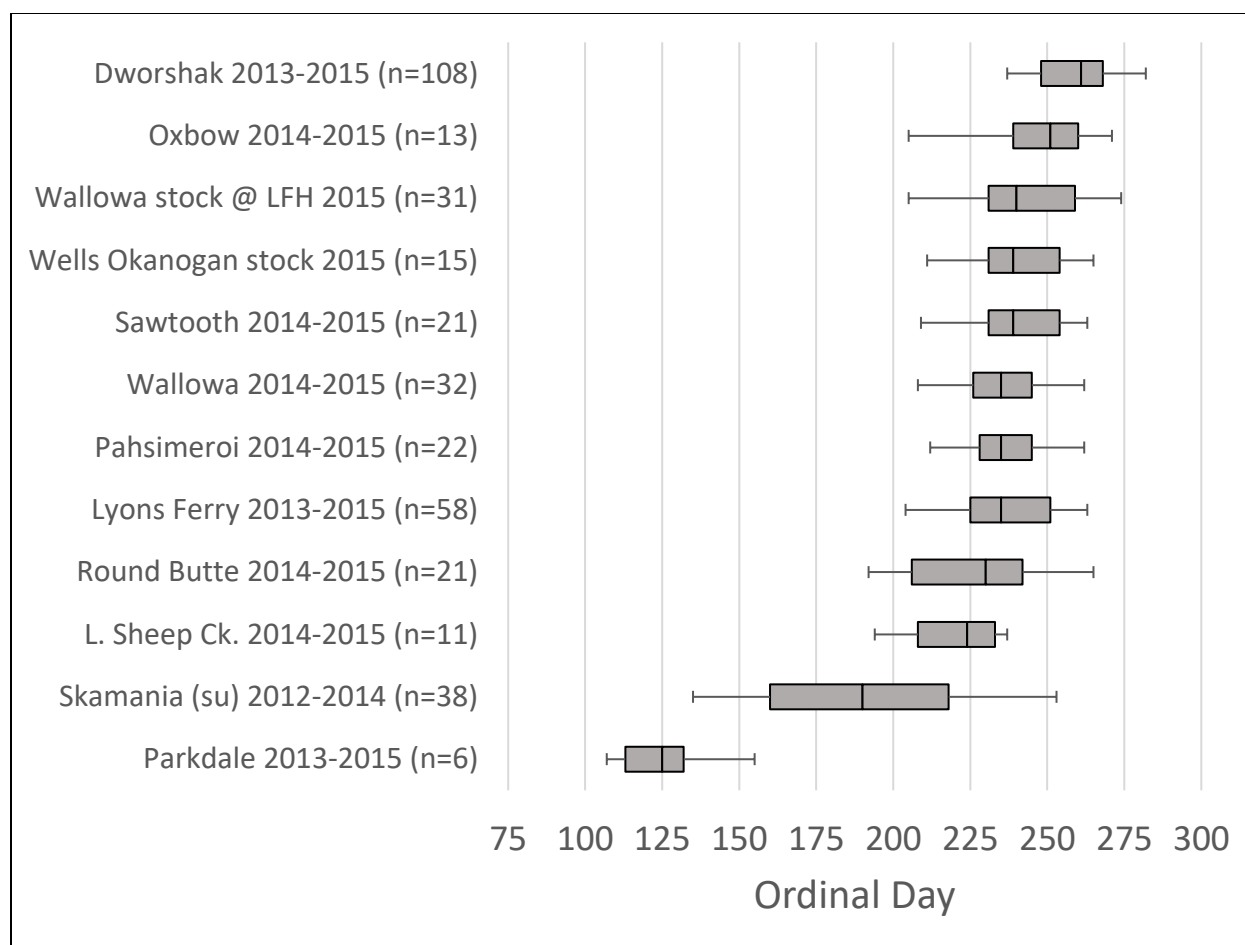


Figure 41. Run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for hatchery origin steelhead (adipose clipped and non-clipped) assigned to PBT broodstock of origin that were sampled at Bonneville Dam in 2017. Hatcheries and their broodyears are ordered from earliest to latest run-timing. Key to broodstock collection is presented in Appendix 5. The number of PBT assignments used in the relative stock abundance expansion procedure from which these run-timing distributions are derived are shown.

PBT and GSI assignments for steelhead in 2017

We were able to assign 44% (359/825) of steelhead sampled at Bonneville Dam in 2017 to 31 hatchery broodstock sources (2013-2015) throughout the Columbia River basin (Table 30, Table 32). The largest portion of the PBT-assigned fish originated from the Dworshak Hatchery (n=108; 30%), followed by Lyons Ferry (n=58; 16%), Skamania (summer) (n=38; 11%), and Wallowa (n=32; 9%) hatcheries. Using these known hatchery-of-origin steelhead, we compared the individual assignments from GSI analysis, and used these assignments to help classify them into reporting groups (Table 32). Those groupings were used to combine results of PBT-hatchery abundance estimates with the GSI estimated abundance of hatchery stocks (Table 30). Tagging rates varied across source hatcheries from 84.48% (OmyPAHH15S) to 100% (OmyLYON13S, OmyPAHH14S OmySKH13_su, OmySKH14_su, and OmyPFF15) (Table 30, Table 32).

Using GSI, we were able to assign 331 natural-origin and 135 hatchery-origin steelhead (that could not be assigned via PBT) sampled at Bonneville Dam in 2017 to 14 reporting groups throughout the Columbia River basin (Table 33). The majority (94%) of these assignments were to the inland lineage (dominated by assignments to 07_MGILCS; 60%); 6% assigned to the coastal lineage (dominated by assignments to 03_SKAMAN; 62%) (Table 33).

We examined which of the hatchery sources contributed to the size range of fish typically classified as B-run steelhead (Table 34). Fish with a fork length ≥ 78 cm were found to primarily originate from the Dworshak broodstock sources, and most of these were from the 2014 (2-ocean age) spawn year (Table 34). The 2-ocean age is typical of B-run life history. Further, the regions of the South Fork and Upper Clearwater R. and Middle Fork and South Fork Salmon R. are generally thought to be the largest sources of B-run steelhead. Dworshak broodstock fit within the South Fork Clearwater R. genetic stock and so are expected to produce large, older steelhead. We also observed that 71% (10/14) of the steelhead that assigned to 2013 Skamania broodstock (OmySKH12_su) had fork lengths ≥ 78 cm (Table 34); this is feasible given their age (3-ocean age) (Table 34).

Table 32. Summary information about the PBT steelhead hatchery broodstock sources and number of assignments.

Broodstock collection	Basin	Reporting Group	Tagging rate (%)	Age	Clipped	Non-clipped	Total
OmyPFF13	Columbia	02 LOWCOL	0.9529	3-ocean	1		1
OmyPFF15	Columbia	02 LOWCOL	1.0000	1-ocean	1		1
OmyPFF14	Columbia	02 LOWCOL	0.9518	2-ocean	4		4
OmySKH12 su	Columbia	03 SKAMAN	0.9915	3-ocean	14		14
OmySKH13 su	Columbia	03 SKAMAN	1.0000	2-ocean	21		21
OmySKH14 su	Columbia	03 SKAMAN	1.0000	1-ocean	3		3
OmyLSCR14S	Snake	07 MGILCS	0.955	2-ocean	3		3
OmyLYON13S	Snake	07 MGILCS	1.0000	3-ocean	1		1
OmyLYON14S	Snake	07 MGILCS	0.9939	2-ocean	17		17
OmyRB14	Columbia	07 MGILCS	0.9913	2-ocean	8		8
OmyWALL14S	Snake	07 MGILCS	0.9959	2-ocean	1		1
OmyWALL15S	Snake	07 MGILCS	0.9428	1-ocean	31		31
OmyRB15	Columbia	07 MGILCS	0.9824	1-ocean	13		13
OmyUMA15	Columbia	07 MGILCS	0.9777	1-ocean	4		4
OmyLYON15S	Snake	07 MGILCS	0.9322	1-ocean	38	2	40
OmyLSCR15S	Snake	07 MGILCS	0.8673	1-ocean	8		8
OmyWALW15S	Snake	07 MGILCS	0.963	1-ocean	5		5
OmyWTP14	Columbia	09 UPPCOL	0.9712	2-ocean	2		2
OmyWEL OKA15	Columbia	09 UPPCOL	0.9658	1-ocean	11	4	15
OmyEASTBK15	Columbia	09 UPPCOL	0.9134	1-ocean	1		1
OmyWEL OMA15	Columbia	09 UPPCOL	0.9658	1-ocean	1	1	2
OmyDWOR13S	Snake	10 SFCLWR	0.9642	3-ocean	3		3
OmyDWOR14S	Snake	10 SFCLWR	0.9689	2-ocean	30	9	39
OmyDWOR14S 1	Snake	10 SFCLWR	0.9689	2-ocean	6		6
OmyDWOR15S	Snake	10 SFCLWR	0.887	1-ocean	49	11	60
OmyOXBO14S	Snake	14 UPSALM	0.9701	2-ocean	1	1	2
OmyPAHH14S	Snake	14 UPSALM	1.0000	2-ocean	4		4
OmySAWT14S	Snake	14 UPSALM	0.9942	2-ocean	3		3
OmySAWT15S	Snake	14 UPSALM	0.9415	1-ocean	18		18
OmyPAHH15S	Snake	14 UPSALM	0.8448	1-ocean	18		18
OmyOXBO15S	Snake	14 UPSALM	0.9278	1-ocean	11		11

Note: Key to broodstock collection is presented in Appendix 5. Skamania broodstock are spawned earlier in the year and are designated for the following brood year.

Table 33. Summary of the number of GSI assignments by reporting group for hatchery-origin steelhead passing Bonneville in 2017 that did not assign via PBT, and natural-origin steelhead that assigned via GSI.

Reporting group	Lineage	Adipose fin		Total
		Clipped	Non-clipped	
01_WCOAST	Coastal			0
02_LOWCOL	Coastal	2	6	8
03_SKAMAN	Coastal	5	11	16
04_WILLAM	Coastal		1	1
05_BWSALM	Coastal		1	1
06_KLICKR	Inland		12	12
07_MGILCS	Inland	45	218	263
08_YAKIMA	Inland		22	22
09_UPPCOL	Inland	6	16	22
10_SFCLWR	Inland	16	5	21
11_UPCLWR	Inland	1	3	4
12_SFSALM	Inland		3	3
13_MFSALM	Inland		4	4
14_UPSALM	Inland	60	29	89
	Total	135	331	466

Table 34. Summary information for Columbia River and Snake River hatchery broodstock sources for steelhead sampled at Bonneville Dam in 2017. The percent of steelhead that were identified to be B-run fish (i.e., ≥ 78 cm fork length) by sex from each broodstock are shown. Skamania broodstock are spawned earlier in the year and are designated for the following brood year.

Reporting Group	Broodstock collection	Tagging rate	Age	Sex and size				
				Females		Males		Total
				N	%B-run (≥ 78 cm FL)	N	%B-run (≥ 78 cm FL)	N
02_LOWCOL	OmyPFF13	95.3%	3-ocean	1	0.0%	0	0.0%	1
	OmyPFF14	95.2%	2-ocean	4	0.0%	0	0.0%	4
	OmyPFF15	100.0%	1-ocean	0	0.0%	1	0.0%	1
03_SKAMAN	OmySKH12_su	99.2%	3-ocean	2	50.0%	12	75.0%	14
	OmySKH13_su	100.0%	2-ocean	12	0.0%	8	0.0%	20
	OmySKH14_su	100.0%	1-ocean	0	0.0%	2	0.0%	2
07_MGILCS	OmyLSCR14S	95.5%	2-ocean	3	0.0%	0	0.0%	3
	OmyLSCR15S	86.7%	1-ocean	4	0.0%	3	0.0%	7
	OmyLYON13S	100.0%	3-ocean	1	0.0%	0	0.0%	1
	OmyLYON14S	99.4%	2-ocean	15	0.0%	2	0.0%	17
	OmyLYON15S	93.2%	1-ocean	23	0.0%	16	0.0%	39
	OmyRB14	99.1%	2-ocean	6	0.0%	2	0.0%	8
	OmyRB15	98.2%	1-ocean	2	0.0%	10	0.0%	12
	OmyUMA15	97.8%	1-ocean	3	0.0%	1	0.0%	4
	OmyWALL14S	99.6%	2-ocean	0	0.0%	1	0.0%	1
	OmyWALL15S	94.3%	1-ocean	15	0.0%	14	0.0%	29
	OmyWALW15S	96.3%	1-ocean	2	0.0%	3	0.0%	5
09_UPPCOL	OmyEASTBK15	91.3%	1-ocean	1	0.0%	0	0.0%	1
	OmyWEL_OKA15	96.6%	1-ocean	5	0.0%	9	0.0%	14
	OmyWEL_OMA15	96.6%	1-ocean	0	0.0%	2	0.0%	2
	OmyWTP14	97.1%	2-ocean	0	0.0%	2	0.0%	2
10_SFCLWR	OmyDWOR13S	96.4%	3-ocean	1	100.0%	2	0.0%	3
	OmyDWOR14S	96.9%	2-ocean	24	41.7%	15	66.7%	39
	OmyDWOR14S_1	96.9%	2-ocean	4	0.0%	2	100.0%	6
	OmyDWOR15S	88.7%	1-ocean	16	0.0%	44	0.0%	60
14_UPSALM	OmyOXBO14S	97.0%	2-ocean	0	0.0%	2	0.0%	2
	OmyOXBO15S	92.8%	1-ocean	6	0.0%	5	0.0%	11
	OmyPAHH14S	100.0%	2-ocean	2	0.0%	2	0.0%	4
	OmyPAHH15S	84.5%	1-ocean	9	0.0%	9	0.0%	18
	OmySAWT14S	99.4%	2-ocean	3	0.0%	0	0.0%	3
	OmySAWT15S	94.2%	1-ocean	10	0.0%	8	0.0%	18

Estimated relative abundance and run-timing of sockeye salmon stocks in 2017

Daily passage of sockeye at Bonneville Dam in 2017 is provided in Figure 42. Relative stock abundance for sockeye salmon was estimated over a course of nine statistical weeks (i.e. weeks 22-30). A total of 1,077 sockeye salmon were sampled at Bonneville Dam in 2017 and were assigned to one of four genetic stocks (i.e., Okanogan, Wenatchee, Snake, and Lake Billy Chinook) (Table 35). The Okanogan stock had the highest relative abundance (51,943), followed by the Wenatchee (34,848) (Figure 43). The Snake and Lake Billy Chinook stocks had estimated abundances < 500, but were based on relatively few genetic assignments (<15) (Table 35).

We characterized the run-timing distributions for three sockeye salmon stocks (Table 35, Figure 44). The Wenatchee and Okanogan stocks had nearly identical run timing distributions (median date: 06/24/17 and 06/25/17, respectively), while the median run-timing for the Snake stock occurred slightly later on 06/27/17 (Figure 44).

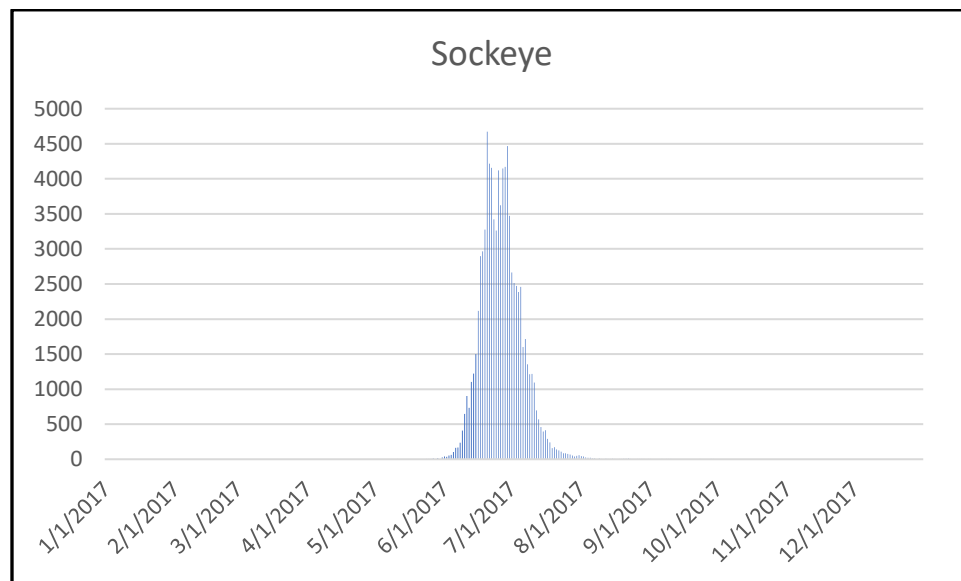


Figure 42. Daily passage of sockeye at Bonneville Dam in 2017 (source: www.fpc.org).

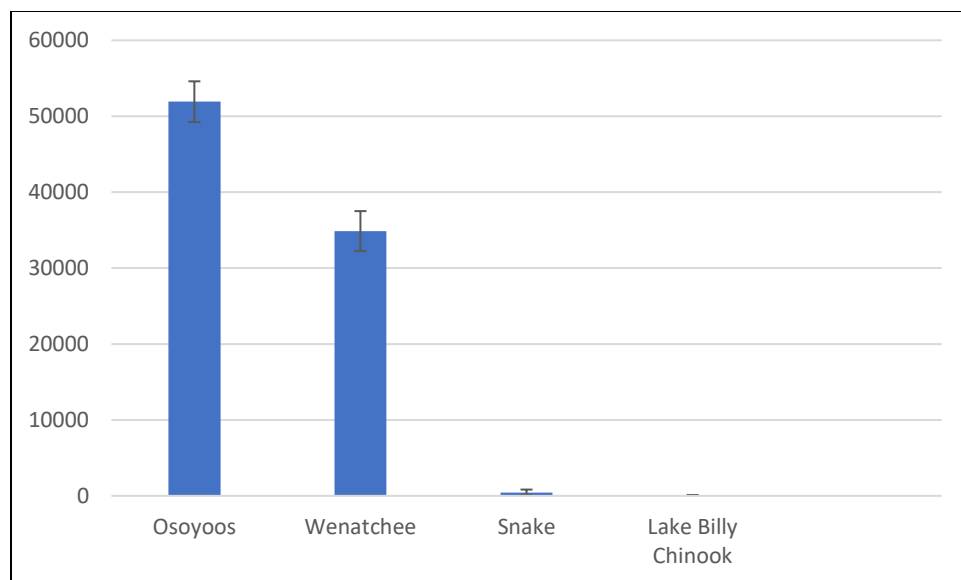


Figure 43. Relative abundance (\pm 95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2017.

Table 35. Relative abundance and run-timing distributions of sockeye salmon stocks passing Bonneville Dam in 2017.

Reporting group	N	Estimated abundance		Run -timing distributions						
		Mean	95% CI	Ordinal day					Median date	Interquartile range
				Median	1st quartile	3rd quartile	5th percentile	95th percentile		
Okanogan	654	51,943	49,241 – 54,600	176	163	182	163	192	06/25/17	19
Wenatchee	415	34,848	32,233 – 37,505	175	164	181	164	191	06/24/17	17
Snake	6	431	108 – 829	178	175	180	175	204	06/27/17	5
Lake Billy Chinook*	2	65	0 – 114	-	-	-	-	-	-	-
Total	1,077	87,287								

* Run-timing distributions were not estimated for stocks where the number of GSI assignments was n<5

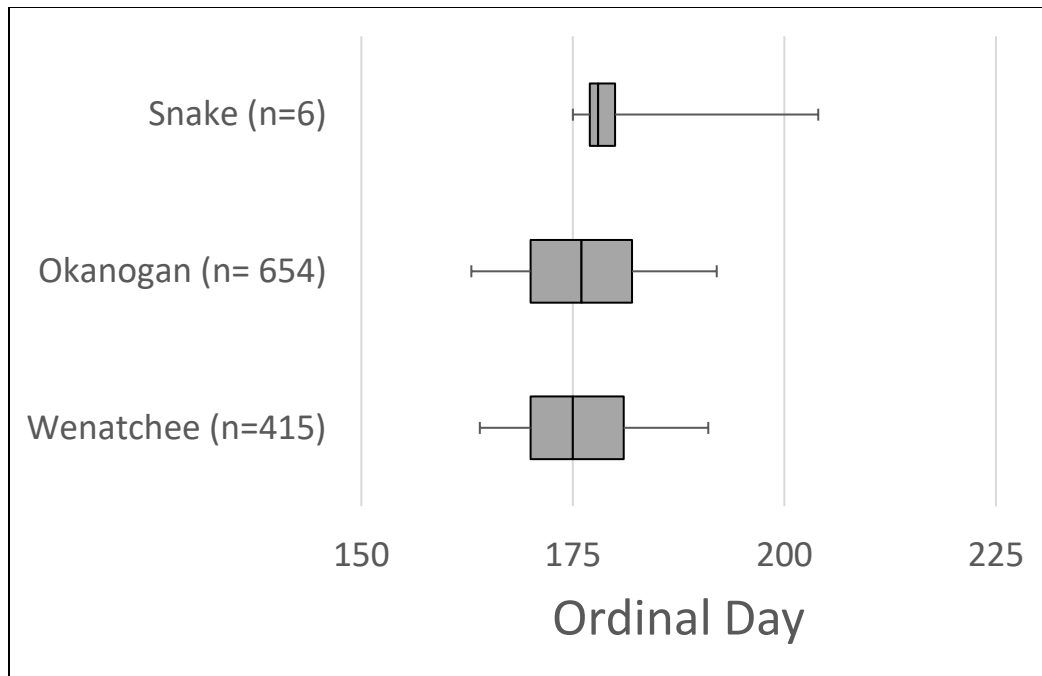


Figure 44. Run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for sockeye salmon that were sampled at Bonneville Dam in 2017 and assigned to stock of origin.

In-season analysis of Chinook salmon passing Bonneville Dam in 2018

There were four in-season reports covering data on Chinook Salmon that passed Bonneville Dam during the Spring Management Period (Table 20), and a total of seven in-season reports for Chinook Salmon in 2018 across all management periods (Table 36). The first report was distributed to members of the USvOR TAC on May 11, 2018 and included an analysis of data on Chinook Salmon sampled at the Bonneville Dam AFF from the date on which the first Chinook Salmon was sampled (April 25, 2018) until May 4, 2018 (Table 20). We had originally planned to offer reports on approximately a bi-weekly reporting schedule after mid-April when sampling typically begins at the Bonneville Dam AFF, however, the 2018 run of Spring Chinook Salmon was delayed relative to the 10 year average-timed run. The goal for analysis is to have at least two weeks of sample sizes greater than 50 fish per week before in-season reporting is initiated. Each report used an analysis similar to the methods and reporting for the Bonneville Dam post-season report for run year 2017. However, there was one important change to the post-season methods that we implemented in-season to improve the suitability of the results for managers. Specifically, we used window counts of only the adult-sized fish in order to estimate stock-specific abundances of adult-size Chinook Salmon. In the past, our BPA reports included stock-specific abundance and run-timing estimates of all Chinook Salmon, including jack-sized fish. Management of Chinook Salmon fisheries in the Columbia River is based solely on adult-sized Chinook Salmon (>560 mm fork length), and so we restricted our sample to this fork length threshold for our in-season analysis.

A total of 3,019 adult-sized Chinook Salmon were collected and analyzed for the 2018 in-season reports (Table 36). Estimates of stock-specific abundances of natural-origin stocks (i.e., those fish that were adipose unclipped and did not have a PBT-assignment) and hatchery-origin stocks (i.e. adipose-clipped fish and/or those fish that were PBT-assigned) were provided in each in-season report. Each subsequent report provided cumulative stock-specific abundances and the final report issued on December 3, 2018 provided sub-totals for each stock that were broken out by management period (hatchery-origin stocks, Table 37; natural-origin stocks, Table 38). Two of the stocks that were of particular interest this year were the natural-origin Snake River spring/summer run (Reporting groups 11_TUCANO, 12_HELLSC, 13_SFSALM, 14_CHMBLN, 15_MFSALM, and 16_UPSALM; Table 38) and upper Columbia River spring Chinook Salmon stocks (Reporting group 10_UCOLSP, Table 38). These ESA listed stocks can affect the overall harvest rates that pertain to the Treaty and Non-Treaty fisheries on the mainstem Columbia River. Another aspect of this in-season analysis that was useful to managers was the ability to determine the approximate abundance of stream-type lineage stocks (the spring-run and Snake River spring/summer run stocks) that continue to pass Bonneville Dam during the summer management period. Further, there are non-ESA listed upper Columbia River summer-run (reporting group 18_UCOLSF) that can pass Bonneville Dam before the summer management period. The delineation of these management periods is known by managers to not provide complete separation of these mixed stocks (i.e., interior Columbia River stream-type versus ocean-type genetic lineages), however the dates of the management periods are the result of policy decisions that in part consider a trade-off between over- and under-utilization of ESA and non-ESA listed Chinook Salmon stocks. This in-season genetic analysis can be used in addition to other data by managers to help evaluate options for shaping the fisheries in a way that balances objectives of the USvOR Management Agreement.

PBT assignments during the Chinook Salmon management periods allowed classification of 64 unique hatchery broodstocks in 2018 (Table 40). These broodstocks were comprised of 35% of hatcheries from the Snake River and 65% of hatcheries from the rest of the Columbia River above Bonneville Dam (Figure 45). Similar to the natural- and hatchery-origin abundance estimates, the subtotals of these hatchery broodstock abundances were provided to USvOR TAC for each management period and bi-weekly strata for the in-season reporting in 2018. We observed that this run year of Chinook Salmon at Bonneville Dam was one of the best in terms of coverage of hatchery broodstock in the PBT baseline. One measure of the level of coverage of the PBT baseline is the percentage of clipped adult-sized Chinook Salmon that were estimated to belong to a PBT hatchery broodstock. If all hatchery broodstock above Bonneville Dam are included in the PBT baseline AND our estimated tag rates are accurate for each hatchery broodstock, then this percentage is expected to be 100% across all strata in the all the management periods (Table 39). In fact, in 2018, the percentage of adipose-clipped fish abundance that were estimated to be PBT broodstock ranged from 90-100%, 95-100%, and 76-97% in the spring, summer, and fall management periods, respectively. One reason that the early fall management period had some of the lowest estimated percentages of PBT-assigned clipped fish was likely due to the fact that a major hatchery component of the run during this time, Spring Creek Hatchery, has only recently been added to the PBT baseline and not all broodyears are covered yet (Appendix 4). We expect that even the fall management period will have higher percentages in the future.

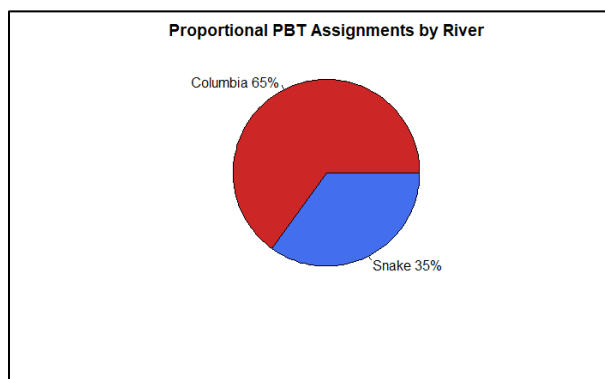


Figure 45. Proportion of hatchery broodstocks from the Snake River versus the rest of the Columbia River above Bonneville Dam in 2018.

Table 36. The sample sizes of Chinook salmon at the Bonneville Dam AFF during the spring, summer, and fall management periods of 2018.

		Sample (N)							
		Statistical week	Fish count	Clipped		Non- clipped		Sample rate	
				GSI	PBT	GSI	PBT		Total
Management period	Spring	1-17	3,439	4	52	4	2	62	1.80%
		18	16,943	9	142	32	18	201	1.19%
		19	24,587	9	186	39	26	260	1.06%
		20	16,385	10	158	43	12	223	1.36%
		21	20,501	24	181	82	22	309	1.51%
		22	8,511	15	64	33	15	127	1.49%
		23	9,132	18	81	37	13	149	1.63%
		24	8,546	13	48	26	7	94	1.10%
	Summer	25	14,637	11	45	14	1	71	0.49%
		26	9,518	12	38	13	3	66	0.69%
		27	6,363	4	17	4	2	27	0.42%
		28	4,385	5	37	13	4	59	1.35%
		29	2,856	8	34	19	3	64	2.24%
		30-31	3,147	3	25	9	2	39	1.24%
	Fall	31-34	20,521	6	18	49	19	92	0.45%
		35	35,966	23	69	138	30	260	0.72%
		36	40,722	8	30	99	19	156	0.38%
		37	30,088	19	48	174	24	265	0.88%
		38	23,164	6	33	121	23	183	0.79%
		39	17,317	7	28	101	16	152	0.88%
		40	9,779	3	20	81	10	114	1.17%
		41-48	9,429	1	5	35	5	46	0.49%
Total		335,936	218	1,359	1,166	276	3,019	0.90%	

Note: The fish counts indicate the number of adult-sized Chinook Salmon at the fish ladder windows at Bonneville Dam and the sample (N) indicates the numbers of adult-sized Chinook Salmon (>560 mm fork length) that were collected at the AFF. The AFF sample is broken into adipose-clipped and non-clipped categories and then further indicate whether a PBT assignment (PBT) was confirmed or if it was not assigned with PBT (GSI). Sample rate relates the total sample for a particular stratum to the total fish counted at the window. The alternating gray and clear rows indicate the breakpoints in the weekly strata at which time one of the seven total in-season analyses was performed (Table 20).

Table 37. Preliminary in-season reporting of hatchery-origin stock-specific abundance estimates of Chinook Salmon passing Bonneville Dam across all management periods in 2018.

			Hatchery origin	Spring		Summer		Fall		Cumulative total date Nov 25	
Reporting Group name	Run type	Reporting Group Code	Estimated abundance		Estimated abundance		Estimated abundance		Estimated abundance		
			Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI	
Youngs Bay	Spring	01_YOUNGS	2	0 – 21	1	0 – 16	12	0 – 118	15	0 – 124	
West Cascade Spring	Spring	02_WCASSP	3	0 – 34	2	0 – 27	23	0 – 178	30	0 – 186	
West Cascade Fall*	Fall	03_WCASFA	9	0 – 59	7	0 – 45	11605*	9060 – 14214	11,622	9080 – 14231	
Willamette	Spring	04_WILLAM	82	18 – 181	73	11 – 181	36	0 – 232	192	67 – 408	
Spring Creek Tule	Fall	05_SPCRTU	3	0 – 34	2	0 – 27	4538	3601 – 5436	4,544	3606 – 5439	
Klickitat	Spring	06_KLICKR	764	349 – 1249	1	0 – 14	11	0 – 108	777	357 – 1270	
Deschutes spring	Spring	07_DESCSP	3,531	2579 – 4566	2	0 – 27	23	0 – 175	3,557	2600 – 4592	
John Day	Spring	08_JOHNDR	54	0 – 187	4	0 – 34	35	0 – 224	95	1 – 307	
Yakima	Spring	09_YAKIMA	2,684	1840 – 3591	2	0 – 26	23	0 – 180	2,711	1860 – 3616	
Upper Columbia spring	Spring	10_UCOLSP	5,760	4508 – 7080	5	0 – 39	171	125 – 389	5,937	4673 – 7286	
Tucannon	Spring	11_TUCANO	670	249 – 1174	1	0 – 14	12	0 – 123	683	254 – 1195	
Hells Canyon	Spring/Summer	12_HELLSC	33,738	31305 – 36143	56	0 – 171	94	1 – 389	33,889	31421 – 36320	
South Fork Salmon	Spring/Summer	13_SFSALM	3,843	2806 – 4960	402	0 – 976	35	0 – 232	4,282	3138 – 5519	
Chamberlain Creek	Spring/Summer	14_CHMBLN	1	0 – 18	1	0 – 16	12	0 – 119	15	0 – 125	
Middle Fork Salmon	Spring/Summer	15_MFSALM	43	0 – 147	24	0 – 116	83	0 – 367	151	18 – 454	

Upper Salmon	Spring/Summer	16 UPSALM	6,679	5422 – 8003	404	0 – 1014	96	1 – 396	7,181	5802 – 8635
Deschutes fall	Fall	17 DESCFA	2	0 – 22	1	0 – 14	97	3 – 300	101	5 – 302
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	9,645	8589 – 10699	31358	30408 – 32156	20404	17368 – 23476	61,408	58027 – 64704
Snake River fall	Fall	19 SRFALL	8	0 – 74	268	46 – 552	17889	15002 – 20828	18,166	15282 – 21110
Bonneville Pool spring	Spring	20_BONPOOL SP	12,348	10543 – 14175	207	0 – 657	0	0 – 0	12,556	10726 – 14448
Umatilla spring	Spring	21_UMATILL ASP	6,915	5605 – 8282	0	0 – 0	0	0 – 0	6,915	5605 – 8282
Bonneville Pool fall	Fall	22_BONPOOL FA	0	0 – 0	0	0 – 0	17166	14504 – 19999	17,166	14504 – 19999
Umatilla fall	Fall	23_UMATILL AFA	0	0 – 0	0	0 – 0	0	0 – 0	0	0 – 0
Total			86,784		32,821		72,365		191,993	

Note: the sub-total estimates for each stock are provided for the spring (jan 1 – jun 15), summer (jun 16 – jul 31), and fall (aug 1 – nov 25) management periods and the cumulative total through the window counts on Nov 25, 2018 are provided. The fall period extends until Dec 31 but only window counts through Nov 25 were available at the time of reporting.

*West Cascade Fall stock was mistakenly labeled and actually represents Spring Creek Tule Chinook Salmon.

Table 38. Preliminary in-season reporting of natural-origin stock-specific abundance estimates of Chinook Salmon passing Bonneville Dam across all management periods in 2018

Reporting Group name	Run type	Reporting Group Code	Natural origin		Spring		Summer		Fall		Cumulative total date Nov 25
			Estimated abundance		Estimated abundance		Estimated abundance		Estimated abundance		Estimated abundance
			Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI	
Youngs Bay	Spring	01 YOUNGS	0	0 – 77	71	2 – 266	111	0 – 283	183	6 – 425	

West Cascade Spring	Spring	02 WCASSP	0	0 – 119	0	0 – 175	0	0 – 284	0	0 – 375
West Cascade Fall	Fall	03 WCASFA	0	0 – 202	0	0 – 350	135	3 – 696	135	38 – 864
Willamette	Spring	04 WILLAM	0	0 – 157	0	0 – 228	219	17 – 883	219	40 – 970
Spring Creek Tule	Fall	05 SPCRTU	0	0 – 114	0	0 – 177	923	333 – 2013	923	364 – 2074
Klickitat	Spring	06 KCLICKR	64	0 – 242	0	0 – 108	0	0 – 169	64	0 – 344
Deschutes spring	Spring	07 DESCSP	880	471 – 1420	0	0 – 167	0	0 – 278	880	506 – 1532
John Day	Spring	08 JOHNDR	1,584	402 – 1755	0	0 – 229	0	0 – 347	1,584	462 – 1884
Yakima	Spring	09 YAKIMA	2,818	2087 – 3727	0	0 – 177	0	0 – 270	2,818	2136 – 3812
Upper Columbia spring	Spring	10 UCOLSP	2,584	1733 – 3632	0	0 – 261	0	0 – 394	2,584	1818 – 3803
Tucannon	Spring	11 TUCANO	315	20 – 554	0	0 – 113	0	0 – 179	315	30 – 623
Hells Canyon	Spring/Summer	12 HELLSC	5,628	5066 – 7700	0	0 – 417	0	4 – 604	5,628	5233 – 8029
South Fork Salmon	Spring/Summer	13 SFSALM	1,319	753 – 2116	632	114 – 1240	0	0 – 363	1,952	1181 – 3038
Chamberlain Creek	Spring/Summer	14 CHMBLN	399	96 – 689	0	0 – 114	0	0 – 186	399	112 – 754
Middle Fork Salmon	Spring/Summer	15 MFSALM	1,211	614 – 1827	0	0 – 398	0	2 – 543	1,211	760 – 2167
Upper Salmon	Spring/Summer	16 UPSALM	1,096	445 – 1605	44	4 – 534	0	4 – 601	1,140	640 – 2078
Deschutes fall	Fall	17 DESCFA	0	0 – 86	41	0 – 151	2,044	1254 – 3252	2,085	1282 – 3280
Upper Columbia summer/fall	Summer/Fall	18 UCOLSF	3,295	2718 – 3834	6,722	5386 – 6963	88,221	82828 – 92761	98,238	92233 – 102410
Snake River fall	Fall	19 SRFALL	53	0 – 187	560	241 – 909	22,953	17542 – 27141	23,568	18100 – 27743
Total			21,246		8,070		114,606		143,926	

Note: the sub-total estimates for each stock are provided for the spring (jan 1 – jun 15), summer (jun 16 – jul 31), and fall (aug 1 – nov 25) management periods and the cumulative total through the window counts on Nov 25, 2018 are provided. The fall period extends until Dec 31 but only window counts through Nov 25 were available at the time of reporting.

Table 39. Expanded abundance of PBT-assigned Chinook Salmon stocks across management periods in 2018

		Sample (Tag-rate-Corrected abundance)				% PBT of Clipped fish	
	Statistical	Clipped		Non-clipped			
	week	GSI	PBT	GSI	PBT		
Management period	Spring	1-17	0	3,106	207	126	100.0%
		18	0	12,728	2,642	1,573	100.0%
		19	0	18,440	3,481	2,666	100.0%
		20	0	12,344	3,125	916	100.0%
		21	638	12,963	5,326	1,574	95.3%
		22	526	4,768	2,069	1,148	90.1%
		23	549	5,518	2,109	955	90.9%
		24	455	5,091	2,293	708	91.8%
	Summer	25	478	11,066	2,880	212	95.9%
		26	129	7,081	1,818	490	98.2%
		27	144	4,805	886	528	97.1%
		28	0	3,122	930	333	100.0%
		29	90	1,784	843	139	95.2%
		30-31	0	2,259	716	172	100.0%
	Fall	31-34*	1,227	4,127	10,755	4,413	77.1%
35*		2,698	10,028	18,796	4,444	78.8%	
36*		1,713	8,206	25,479	5,324	82.7%	

37*	1,815	5,792	19,481	3,000	76.1%
38	516	4,420	14,930	3,297	89.5%
39	537	3,451	11,307	2,023	86.5%
40	65	1,908	6,870	936	96.7%
41-48	125	1,104	6,993	1,206	89.8%
Total	11,707	144,113	143,935	36,181	

Note: The % PBT of Clipped fish indicates the percentage of adipose clipped fish that are accounted for by PBT after tag rate expansions. If all hatchery broodstock above Bonneville Dam are included in the PBT baseline AND our estimated tag rates are accurate for each hatchery broodstock, then this percentage is expected to be 100% across all strata.

*The early strata of the fall management period may have relatively low “% PBT of clipped fish” due to the fact that a major hatchery component of the run during this time, Spring Creek Hatchery, has only recently been added to the PBT baseline and not all broodyears are covered yet.

Table 40. The estimated abundances of the PBT hatchery broodstock that passed Bonneville Dam in 2018 (1/1/2018 – 11/25/2018)

BON18 by hatchery brood year (01/01/18-11/25/18)										
Order	Expected Run Time	Hatchery	Broodstock	Brood year	MLE	95% CI	Lineage	GSI RepGrp	Snake.Columbia	Percent
22	01Spring	Klickitat State Fish Hatchery	OtsKH13	2013	135	0 – 346	Interior stream type	06_KLICK_R	Columbia	0.1
23	01Spring	Klickitat State Fish Hatchery	OtsKH14	2014	627	266 – 1071	Interior stream type	06_KLICK_R	Columbia	0.4
42	01Spring	Parkdale Fish Facility	OtsPFF14	2014	1,969	1277 – 2729	Interior stream type	07_DESCS_P	Columbia	1.1
50	01Spring	Round Butte Fish Hatchery	OtsRB14	2014	1,229	685 – 1859	Interior stream type	07_DESCS_P	Columbia	0.7
60	01Spring	Warm Springs National Fish Hatchery	OtsWSNFH14	2014	183	0 – 545	Interior stream type	07_DESCS_P	Columbia	0.1
63	01Spring	Levi George/Cle Elum (Integrated)	OtsYR14int	2014	2,259	1512 – 3068	Interior stream type	09_YAKI_MA	Columbia	1.3
64	01Spring	Levi George/Cle Elum (Segregated)	OtsYR14seg	2014	421	96 – 886	Interior stream type	09_YAKI_MA	Columbia	0.2

5	01Spring	Chief Joseph Hatchery (Spring)	OtsCJH14 sp	2014	611	183 – 1107	Interior stream type	10_UCOL SP	Columbia	0.3
14	01Spring	Eastbank Fish Hatchery (Spring)	OtsEASTB K14 sp	2014	963	404 – 1626	Interior stream type	10_UCOL SP	Columbia	0.5
16	01Spring	Eastbank Fish Hatchery (Spring)	OtsEASTB K15 sp	2015	100	0 – 309	Interior stream type	10_UCOL SP	Columbia	0.1
24	01Spring	Leavenworth National Fish Hatchery	OtsLNFH1 4	2014	1,1 10	581 – 1709	Interior stream type	10_UCOL SP	Columbia	0.6
36	01Spring	Methow State Fish Hatchery	OtsMETH 14	2014	325	67 – 682	Interior stream type	10_UCOL SP	Columbia	0.2
61	01Spring	Winthrop National Fish Hatchery	OtsWTP13	2013	118	0 – 349	Interior stream type	10_UCOL SP	Columbia	0.1
62	01Spring	Winthrop National Fish Hatchery	OtsWTP14	2014	2,2 31	1460 – 3098	Interior stream type	10_UCOL SP	Columbia	1.2
53	01Spring	Lyons Ferry Fish Hatchery - Tucannon River	OtsTUCW 14S	2014	668	249 – 1170	Interior stream type	11_TUCA NO	Snake	0.4
9	01Spring	Clearwater Fish Hatchery	OtsCLWH1 4S	2014	8,0 69	6608 – 9595	Interior stream type	12_HELLS C	Snake	4.5
43	01Spring	Clearwater Fish Hatchery - Powell Facility	OtsPOWP 13S	2013	97	0 – 289	Interior stream type	12_HELLS C	Snake	0.1
44	01Spring	Clearwater Fish Hatchery - Powell Facility	OtsPOWP1 4S	2014	4,0 08	2949 – 5145	Interior stream type	12_HELLS C	Snake	2.2
11	01Spring	Dworshak National Fish Hatchery	OtsDWOR 14S	2014	3,6 39	2653 – 4716	Interior stream type	12_HELLS C	Snake	2.0
10	01Spring	Lookingglass Fish Hatchery - Catherine Creek	OtsCTHW 14S	2014	252	0 – 571	Interior stream type	12_HELLS C	Snake	0.1
19	01Spring	Lookingglass Fish Hatchery - Grande Ronde	OtsGRUW 14S	2014	862	373 – 1435	Interior stream type	12_HELLS C	Snake	0.5
25	01Spring	Lookingglass Fish Hatchery - Lookingglass Creek	OtsLOOK1 4S	2014	579	185 – 1044	Interior stream type	12_HELLS C	Snake	0.3
26	01Spring	Lookingglass Fish Hatchery - Lostine River	OtsLSTW1 4S	2014	248	0 – 577	Interior stream type	12_HELLS C	Snake	0.1
38	01Spring	Nez Perce Tribal Fish Hatchery (Spring)	OtsNPFH1 4S	2014	167	0 – 433	Interior stream type	12_HELLS C	Snake	0.1

48	01Spring	Rapid River Fish Hatchery	OtsRAPH1 3S	2013	66	0 – 202	Interior stream type	12_HELLS C	Snake	0.0
49	01Spring	Rapid River Fish Hatchery	OtsRAPH1 4S	2014	15, 009	12965 – 17122	Interior stream type	12_HELLS C	Snake	8.3
51	01Spring	Sawtooth Fish Hatchery	OtsSAWT 14S	2014	4,9 99	3884 – 6177	Interior stream type	16_UPSAL M	Snake	2.8
1	01Spring	Carson National Fish Hatchery	OtsCAR13	2013	110	0 – 335	Interior stream type	20_BONP OOLSP	Columbia	0.1
2	01Spring	Carson National Fish Hatchery	OtsCAR14	2014	4,1 25	3023 – 5300	Interior stream type	20_BONP OOLSP	Columbia	2.3
27	01Spring	Little White Salmon National Fish Hatchery (Spring)	OtsLWS13 _sp	2013	235	0 – 542	Interior stream type	20_BONP OOLSP	Columbia	0.1
29	01Spring	Little White Salmon National Fish Hatchery (Spring)	OtsLWS14 sp	2014	8,0 87	6616 – 9636	Interior stream type	20_BONP OOLSP	Columbia	4.5
54	01Spring	South Fork Walla Walla facility	OtsUMA1 3 sp	2013	211	0 – 490	Interior stream type	21_UMAT ILLASP	Columbia	0.1
55	01Spring	South Fork Walla Walla facility	OtsUMA1 4 sp	2014	6,7 04	5412 – 8062	Interior stream type	21_UMAT ILLASP	Columbia	3.7
20	02Spring/Su mmer	Lookingglass Fish Hatchery - Imnaha River	OtsIMNW 14S	2014	581	216 – 1009	Interior stream type	12_HELLS C	Snake	0.3
21	02Spring/Su mmer	McCall Fish Hatchery - Johnson Creek	OtsJHNW 14S	2014	204	0 – 473	Interior stream type	13_SFSAL M	Snake	0.1
35	02Spring/Su mmer	McCall Fish Hatchery - South Fork Salmon	OtsMCCA 14S	2014	3,8 76	2769 – 5059	Interior stream type	13_SFSAL M	Snake	2.2
41	02Spring/Su mmer	Pahsimeroi Fish Hatchery	OtsPAHH1 4S	2014	2,0 10	1218 – 2897	Interior stream type	16_UPSAL M	Snake	1.1
3	03Summer	Chief Joseph Hatchery (Summer/Fall) - Integrated	OtsCJH13i nt_sufa	2013	934	270 – 1782	Interior ocean type	18_UCOL SF	Columbia	0.5
6	03Summer	Chief Joseph Hatchery (Summer/Fall) - Integrated	OtsCJH14i nt_sufa	2014	5,1 32	3603 – 6819	Interior ocean type	18_UCOL SF	Columbia	2.9
8	03Summer	Chief Joseph Hatchery (Summer/Fall) - Integrated	OtsCJH15in t_sufa	2015	292	0 – 876	Interior ocean type	18_UCOL SF	Columbia	0.2
4	03Summer	Chief Joseph Hatchery (Summer/Fall) - Segregated	OtsCJH13s eg_sufa	2013	2,0 56	1139 – 3133	Interior ocean type	18_UCOL SF	Columbia	1.1

7	03Summer	Chief Joseph Hatchery (Summer/Fall) - Segregated	OtsCJH14seg_sufa	2014	8,3 64	5793 – 11089	Interior ocean type	18_UCOL SF	Columbia	4.6
12	03Summer	Eastbank Fish Hatchery (Summer)	OtsEASTBK12_su	2012	506	86 – 1146	Interior ocean type	18_UCOL SF	Columbia	0.3
13	03Summer	Eastbank Fish Hatchery (Summer)	OtsEASTBK13_su	2013	2,2 58	1211 – 3482	Interior ocean type	18_UCOL SF	Columbia	1.3
15	03Summer	Eastbank Fish Hatchery (Summer)	OtsEASTBK14_su	2014	5,4 95	3999 – 7090	Interior ocean type	18_UCOL SF	Columbia	3.1
17	03Summer	Entiat National Fish Hatchery (Summer)	OtsENFH13	2013	300	0 – 771	Interior ocean type	18_UCOL SF	Columbia	0.2
18	03Summer	Entiat National Fish Hatchery (Summer)	OtsENFH14	2014	6,5 10	4528 – 8662	Interior ocean type	18_UCOL SF	Columbia	3.6
56	03Summer	Wells Fish Hatchery (Summer)	OtsWELLS12	2012	60	0 – 186	Interior ocean type	18_UCOL SF	Columbia	0.0
57	03Summer	Wells Fish Hatchery (Summer)	OtsWELLS13	2013	1,8 85	1171 – 2683	Interior ocean type	18_UCOL SF	Columbia	1.1
58	03Summer	Wells Fish Hatchery (Summer)	OtsWELLS14	2014	5,7 21	3992 – 7614	Interior ocean type	18_UCOL SF	Columbia	3.2
59	03Summer	Wells Fish Hatchery (Summer)	OtsWELLS15	2015	200	0 – 550	Interior ocean type	18_UCOL SF	Columbia	0.1
52	04Fall	Spring Creek National Fish Hatchery	OtsSPCR_Tule15	2015	11, 547	9000 – 14150	Lower Columbia	03_WCAS FA	Columbia	6.4
45	04Fall	Priest Rapids Fish Hatchery	OtsPRH13	2013	2,0 62	1006 – 3266	Interior ocean type	18_UCOL SF	Columbia	1.1
46	04Fall	Priest Rapids Fish Hatchery	OtsPRH14	2014	6,6 43	4666 – 8794	Interior ocean type	18_UCOL SF	Columbia	3.7
47	04Fall	Priest Rapids Fish Hatchery	OtsPRH15	2015	8,3 97	6360 – 10545	Interior ocean type	18_UCOL SF	Columbia	4.7
32	04Fall	Lyons Ferry Fish Hatchery (Fall)	OtsLYON13S_1	2013	1,3 06	479 – 2317	Interior ocean type	19_SRFAL L	Snake	0.7
33	04Fall	Lyons Ferry Fish Hatchery (Fall)	OtsLYON14S_1	2014	6,5 31	4688 – 8447	Interior ocean type	19_SRFAL L	Snake	3.6
34	04Fall	Lyons Ferry Fish Hatchery (Fall)	OtsLYON15S_1	2015	5,1 30	3435 – 6960	Interior ocean type	19_SRFAL L	Snake	2.9

37	04Fall	Nez Perce Tribal Fish Hatchery (Fall)	OtsNPFH1 3S_1	2013	259	0 – 794	Interior ocean type	19_SRFAL L	Snake	0.1
39	04Fall	Nez Perce Tribal Fish Hatchery (Fall)	OtsNPFH1 4S_1	2014	2,3 20	1141 – 3653	Interior ocean type	19_SRFAL L	Snake	1.3
40	04Fall	Nez Perce Tribal Fish Hatchery (Fall)	OtsNPFH1 5S_1	2015	2,1 40	995 – 3526	Interior ocean type	19_SRFAL L	Snake	1.2
28	04Fall	Little White Salmon National Fish Hatchery (Fall)	OtsLWS13 _sufa	2013	4,4 29	2850 – 6210	Interior ocean type	22_BONP OOLFA	Columbia	2.5
30	04Fall	Little White Salmon National Fish Hatchery (Fall)	OtsLWS14 _sufa	2014	7,1 94	5369 – 9142	Interior ocean type	22_BONP OOLFA	Columbia	4.0
31	04Fall	Little White Salmon National Fish Hatchery (Fall)	OtsLWS15 _sufa	2015	5,5 44	4044 – 7200	Interior ocean type	22_BONP OOLFA	Columbia	3.1

In-season analysis of the test fishery in the Chinook Salmon Spring Management Period of 2018

We examined one source of information that could potentially be useful to managers particularly on years when the spring Chinook Salmon run is delayed. There is a test fishery that is typically conducted by WDFW on Sundays each week in the early spring (February – May). Four boats are contracted to perform a series of drifts (typically four drifts per boat) through the commercial zones 1-3 near the mouth of the Columbia River. The drifts are targeted for Spring Chinook and biodata and a tissue for genetic analysis is collected. Visual Stock ID classifies fish as lower river (West Cascade Spring and Willamette River stocks) versus upriver (all stocks destined above Bonneville Dam). Genetic Analysis can refine the initial Visual Stock ID calls and more accurately classify these fish into lower and upriver stocks. We use a catch per unit effort (CPUE) metric in the test fishery that is based on the number of upriver Chinook handled per test fishery drift. If the test fishery CPUE were lagged 13 days the peak in CPUE appears to correspond with a peak in Bonneville weekly counts (Figure 46). So if the in-season genetic analysis includes the data from the test fishery, our report may be able to predict the abundance of particular hatchery and natural-origin stocks that we can expect to pass Bonneville Dam up to 2 weeks later which would be useful information for USvOR managers. In fact, comparison of the relative proportions of the hatchery broodstocks that were estimated in the test fishery and Bonneville Dam showed that these samples from these two sources have very similar compositions of stocks (Figure 47). Further, there is high correlation between the estimated CPUE of each hatchery broodstock in the test fishery and the estimated abundance of the same broodstocks passing Bonneville Dam in weeks lagged 13 days after the test fishery.

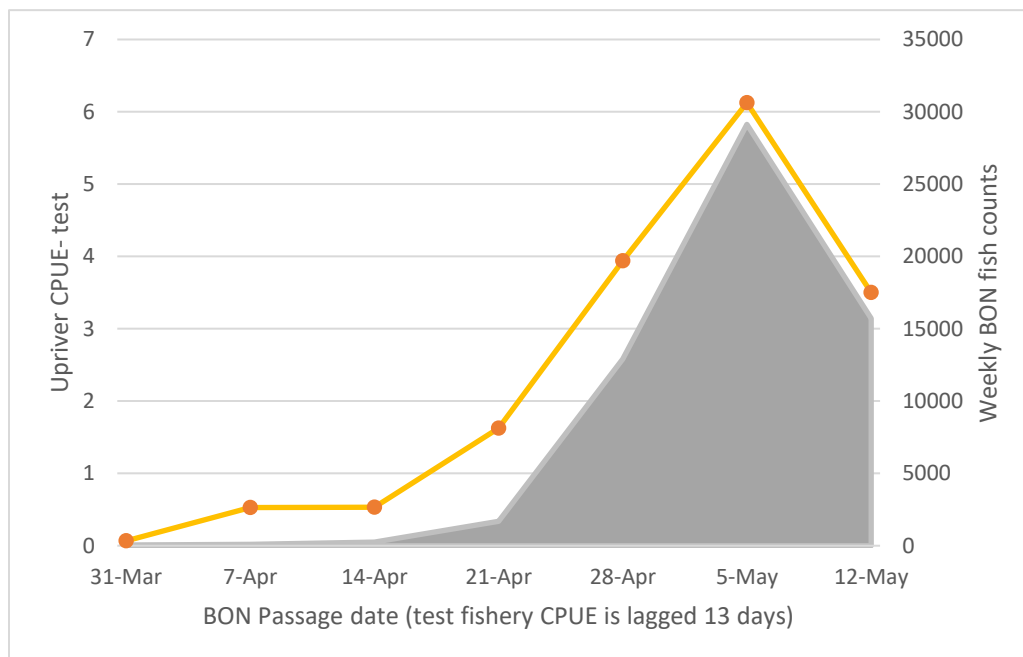


Figure 46. The relationship between the test fishery upriver Chinook Salmon CPUE (line) and weekly fish counts at Bonneville Dam (solid gray) in 2018.

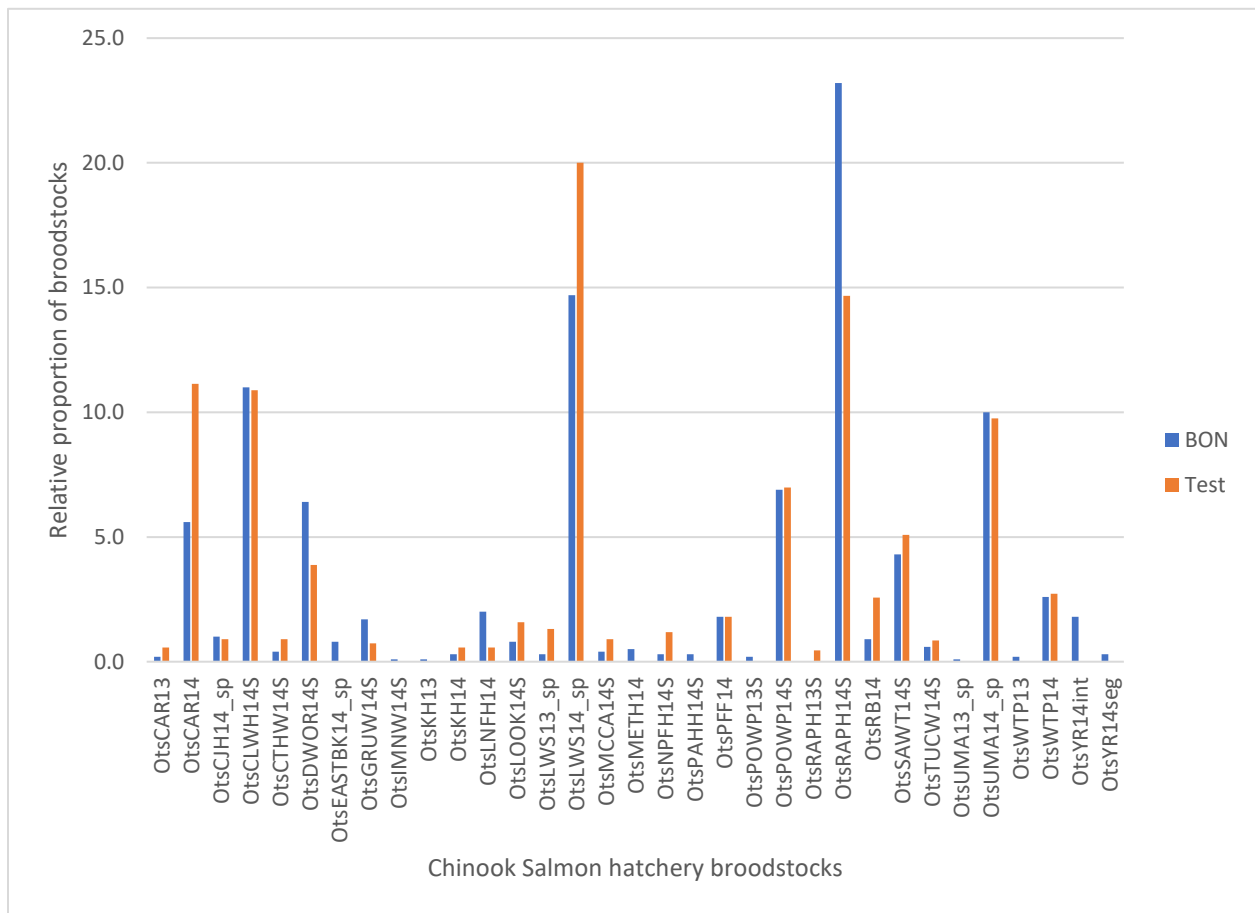


Figure 47. Relative proportions of hatchery broodstocks of upriver Chinook Salmon caught in the test fishery (March 18 – April 29) compared to Chinook Salmon that passed Bonneville Dam in corresponding weeks lagged 13 days from the test fishery (March 31 – May 12) in 2018.

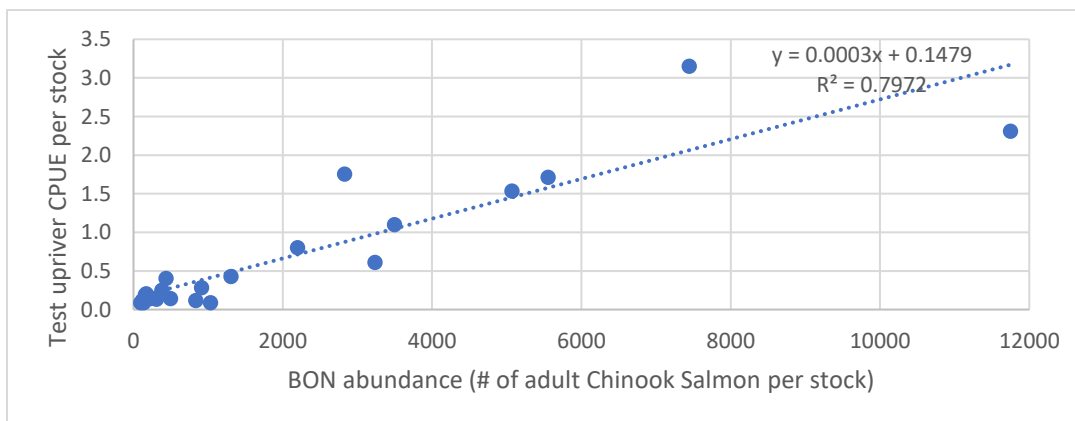


Figure 48. Correlation of the test fishery CPUE with the estimated abundance passing Bonneville Dam of hatchery broodstocks identified by PBT analysis in 2018.

Concordance of ages derived by PBT and scale reading

The analysis of the Chinook Salmon sampled at the Bonneville Dam AFF in 2018 took advantage of a larger number of SNP markers than had previously been available for PBT (Table 12). As mentioned in Section 3, it is critical to have a sufficient level of variation among SNP markers to discriminate highly related broodstock parents, and the original 93 SNPs designed for interior stream-type broodstocks were not variable enough for the interior ocean-type broodstocks. As evidence, we demonstrate the fact that most of the Chinook Salmon passing Bonneville Dam in 2018 that could not be assigned using 93 SNPs with strict LOD and FDR thresholds (i.e., $LOD > 14$, $FDR < 0.1$) were from the interior ocean-type lineage (Table 41). Many of the PBT assignments that were borderline in confidence levels (i.e. passed the $LOD > 14$ threshold but failed the $FDR < 0.1$ threshold) nonetheless appeared to be highly confidence assignments when using higher numbers of SNPs (see “PBT2” and “PBT3” assignments, Table 41). Therefore, using 268 or 299 SNP panels, we are able to pick up a large number of assignments that would have otherwise failed to meet strict confidence thresholds (i.e., $LOD > 14$, $FDR < 0.1$) using the original 93 SNP panel, and many of these assignment pick-ups involve interior ocean-type broodstocks. We also find that we cannot simply lower the assignment confidence thresholds and expect to get accurate results using the 93 SNP panel. Assignments that fall below the strict confidence thresholds using 93 SNPs, tended to show more discordant assignments when compared to the larger SNP panes (e.g. categories “PBT3” and “PBT4”, Table 41).

Table 41. PBT assignment concordance between 93 SNP and 268/299 SNP panels using Chinook Salmon passing Bonneville Dam in 2018.

93SNP LOD>14;FDR<0.1		93SNP LOD>14;FDR>0.1			93SNP LOD<14 (Unassigned)		Total
Broodstock Rep. Gr.	PBT	PBT2	PBT3*	PBT5	PBT4*	Unassign.	
Interior ocean type	333	277	14	223	19		866
18_UCOLSF	239	146	9	91	15		500
19_SRFALL	68	36	3	9	1		117
22_BONPOOLFA	26	95	2	122	3		248
23_UMATILLAFA				1			1
Interior stream type	929	10		6			945
06_KLICKR	13						13
07_DESCSP	46						46
09_YAKIMA	35	1					36
10_UCOLSP	62	4		1			67
11_TUCANO	7	1					8
12_HELLSC	387	1		5			393
13_SFSALM	42	2					44
16_UPSALM	97						97
20_BONPOOLSP	150	1					151
21_UMATILLASP	90						90

Lower Columbia	52	10	2	1	65
03 WCASFA	52	10	2	1	65
Unassigned.					1173
Total	1314	297	14	231	20
					1173
					3049

Note: The assignments are broken into three different threshold categories based on the results from the original 93 SNP PBT panel: Passing both the “93 SNP” LOD score and FDR criteria (>14 and <0.1 , respectively), Passing only the “93 SNP” LOD score criterium but NOT the FDR, and failing both criteria (i.e. >14 and >0.1 for the LOD and FDR, respectively). These three threshold categories were further broken into five categories based on whether the 268 and 299 SNP panels were assigned with LOD score >14 , $FDR < 0.1$ and whether their assignments were concordant with the assignments from the original 93 SNP panel. Specifically “PBT” indicates all confident assignments identified by the 93 SNP panel and none of the results from the 268/299 SNP panels were discordant. “PBT2” indicates that of these assignments not passing the FDR threshold for the 93 SNPs, these assignments were all highly confident assignments and concordant with the 268/299 SNP panels. “PBT3” indicates that of the assignments not passing the FDR threshold for the 93 SNPs, these assignments were all highly confident assignments but **discordant** with the 268/299 SNP panels. “PBT5” indicates that of the assignments not passing the FDR threshold for the 93 SNPs, none of these were confident assignments based on the other panels. Finally, “PBT4” indicates that of the fish that were not assigned with 93 SNPs due to low LOD scores, these fish were confident assignments based on the other panels and most assignments were discordant from the 93 SNP panel results. The hatchery broodstocks that were assigned to these fish are classified into the GSI reporting group and lineage to which they belong. Subtotals of assignments for each lineage are provided in grayed rows in the Table.

We compared parentage results from the Bonneville Dam 2018 dataset using 94, 268, and 299 SNPs and examined concordance of ages from PBT assigned fish versus ages estimated by scale reading (J. Fryer, CRITFC). We found that the PBT assignments meeting high confidence thresholds using the 93SNP and 268/299 SNP panels that were referred to as “PBT” and “PBT2” were the ones with the highest concordance rates with the ages derived by scale-reading (Table 42). The age concordance rates were 99.4% (1009 concordant out of 1015 total comparisons) and 99.2% (237 out of 239 comparisons) for the two categories of confident PBT assignments (“PBT” and “PBT2” categories, respectively; Table 42). In contrast, PBT assignments that had been assigned using $LOD > 14$ for 93 SNPs, but did not meet $FDR < 0.1$ and did not have confirmed assignments with the 268/299 SNP Panels (i.e. category “PBT5”) had the lowest concordance rate with scale-ages (43.6%, 79 out of 181 comparisons). The other PBT categories (“PBT3” and “PBT4”) had too few samples to make rigorous comparisons with the scale ages. These results further support the need to increase the number of SNPs to a panel of at least 268 SNPs in order to recover accurate PBT assignments that may otherwise have failed strict confidence thresholds using the original 93 SNP panel.

Table 42. Comparison of ages derived by PBT or scale-reading of Chinook Salmon passing Bonneville Dam in 2018

PBT age versus Scale Age

PBT assignment category	Concordant	Discordant	Not compared	Total
PBT	1009	6	248	1263
PBT2	237	2	49	288
PBT3*	4	1	9	14
PBT4*	5		14	19
PBT5	79	102	47	228
Total	1334	111	367	1812

In-season analysis of steelhead passing Bonneville Dam in 2018

There were three reports provided to USvOR TAC during the steelhead management periods: Skamania Management Period (4/1/2018 – 6/30/2018) and summer A-/B-Index Management Period (7/1/2018 – 10/31/2018, Table 20). There were a total of 604 adipose clipped and 274 adipose unclipped steelhead that were sampled at the Bonneville Dam AFF and genotyped in 2018 (Table 43). The methods described for the analysis of the 2017 sample of steelhead at Bonneville Dam are not as useful to fisheries managers that serve on USvOR TAC because the size groups (A-/B-Index) have not been fully integrated into the results. Therefore, we revised these methods and provided a breakdown of those A-/B-Index groups in addition to the adipose clipped and unclipped categories (Table 43). One of the important features of the genetic analyses of steelhead at Bonneville Dam is that they can identify unmarked hatchery fish via PBT assignments. The identification of unmarked hatchery fish is critical for accurate calculations of ESA impacts on steelhead stocks. The methods we are using provide a means to estimate the abundance of six categories of steelhead; i.e., clipped hatchery (H), unclipped hatchery (HNC), and natural-origin (W) for A-Index and B-Index fish (Table 44). We also incorporate tag rate expansion to account for the percentage of each hatchery stock that has been successfully genotyped. Tag rate expansions have been used previously in all of our genetic analyses for Chinook Salmon and steelhead. However, one feature that has been missing from our tag rate expansion methods in the past is a way to balance the numbers of fish that are expanded in the PBT broodstock categories by subtracting an equal set of fish from the sample. This is a problem that is difficult to address and can potentially cause bias in our abundance estimates. To illustrate the issue, imagine that one of the hatchery broodstocks had an extremely low tag rate (~50%), and we identified 10 out of our total sample of 100 fish that were PBT-assigned to this hatchery broodstock. After expanding for tag rates, we estimate that there were actually 20 fish in our sample that should be assigned to that hatchery (10 raw PBT assignments / 0.5 tag rate = 20 expanded PBT assignments). We know that we need to account for another 10 fish from our sample and place them into the hatchery category, but we have no perfect way to identify which fish among our data to subtract. The result is that any attempts to use the remaining 90 PBT-unassigned fish to characterize natural-origin fish (e.g. composition of GSI reporting groups, ages, lengths, etc) are being biased by inclusion of the characteristics of the 10 fish that were inferred hatchery-origin based on tag-rate expansion. For these in-season analyses, we employed a basic solution to this problem. We subtracted fish from the sample based on the metadata of the fish that were tag-rate expanded. For example, if 10 fish were adipose-unclipped, B-Index-sized fish and were identified to a PBT broodstock that had a tag-rate of 50%, we

increased that category by 10 fish and subtracted 10 fish from the other unclipped B-Index-sized fish that did not have PBT assignments. This balancing step is fairly easy to implement when using six metadata categories (Table 44), but there needs to be a more sophisticated approach when attempting to break the sample into greater numbers of categories, e.g. GSI reporting groups and ages. In the future we will work toward an automated step that will balance tag-rate expanded fish in the sample by subtracting an almost “equal” fish from the PBT-unassigned fish based on the same characteristics that we want to estimate (e.g., GSI assignment, length, and age).

Table 43. The sample sizes of Summer Steelhead at the Bonneville Dam AFF during the Skamania and A-/B-Index management periods of 2018

Sample (N)																

	34	2	3536	1,313	5	28	11			1		33	12	0.93%	0.91%	
	35	3	6286	1,862	5	36	10	1		11	2	2	52	15	0.83%	0.81%
	36	3	7802	1,822	4	23	3	1	1	21	3	2	49	9	0.63%	0.49%
	37	4	6179	1,676	1	18	4	1	2	33	5	5	54	15	0.87%	0.89%
	38	4	5447	1,358		16	1	1	4	34	2	5	54	9	0.99%	0.66%
	39	5	4120	1,130		13	3	4	3	37	4	11	53	22	1.29%	1.95%
	40	5	2533	868		13	3	2	6	48	2	9	67	16	2.65%	1.84%
	41	6	1548	598	2	27	8	8	7	39	5	13	75	34	4.84%	5.69%
	42	6	804	320											0.00%	0.00%
	43	6	341	134											0.00%	0.00%
	44	6	143	145											0.00%	0.00%
	Skamania subtotal		3,629	2,854	7	43	29	0	0	4	3	0	54	32	1.49%	1.12%
	Summer A-/B-Index subtotal		64,486	29,514	41	260	149	21	23	226	25	47	550	242	0.85%	0.82%
	Total		68,115	32,368	48	303	178	21	23	230	28	47	604	274	0.89%	0.85%

Note: The clipped and non-clipped counts indicate the number of adipose clipped and unclipped steelhead at the fish ladder windows at Bonneville Dam and the sample (N) indicates the numbers of A- and B-sized (<580 mm and ≥580 mm fork length, respectively) that were collected at the AFF. The AFF sample is broken into A- and B-sized and adipose-clipped and non-clipped categories and then further indicate whether a PBT assignment (PBT) was confirmed or if it was not assigned with PBT (GSI). Sample rate relates the total sample for a particular stratum to the total fish counted at the window. The alternating gray and clear rows indicate the breakpoints in the weekly strata at which time one of the three total in-season analyses was performed (Table 20).

Table 44. Estimated abundance of six categories of Summer Steelhead that passed Bonneville Dam in 2018 during the Skamania and A-/B-Index Management Periods.

	Weeks	Strata	Estimated abundance							
			Clipped count	Non-Clipped count	A-Index			B-Index		
					H	HNC	W	H	HNC	W
Skamania	14-26	1	3,629	2,854	3,360	0	2,586	269	0	268

A-/B-Index	27-29	1	7,515	6,999	7,173	117	6,766	342	0	117
	30-34	2	21,768	12,602	21,768	511	11,887	0	0	203
	35-36	3	14,088	3,684	9,485	338	1,964	4,603	676	705
	37-38	4	11,626	3,034	3,768	273	612	7,858	1,364	785
	39-40	5	6,653	1,998	1,441	358	273	5,212	1,194	173
	41-44	6	2,836	1,197	1,097	310	253	1,739	504	130
Summer A-/B-Index subtotal										
	27-44		64,486	29,514	44,732	1,907	21,756	19,754	3,737	2,114

Note: Based on the sample data described in Table 43 we estimated abundances of six categories of steelhead; i.e., clipped hatchery (H), unclipped hatchery (HNC), and natural-origin (W) for A-Index and B-Index fish. The sample was divided into the most strata possible maintaining a minimum sample of 100 clipped and unclipped steelhead per stratum in the A-/B-Index period. All weeks were pooled into a single stratum in the Skamania period.

Post-season analysis of Sockeye Salmon passing Bonneville Dam in 2018

We provided a timely post-season analysis of Sockeye Salmon once the majority of samples had been collected at the Bonneville Dam AFF in mid-August and distributed the report to USvOR TAC on August 21, 2018 (Table 20). In recent years, the results of our genetic analysis have become an official component of the post-season run reconstruction and pre-season forecasting that TAC performs in November of each year. Therefore, timely reporting of the individual assignments of the Bonneville Dam sample of Sockeye Salmon to GSI reporting groups is critical for efficient execution of fisheries management of this species in the Columbia River. In 2018, there were 1,860 Sockeye Salmon that were sampled at the AFF and genotyped for this analysis (Table 45). The abundance estimate of the ESA listed stock (Redfish Lake Sockeye Salmon from the Snake River) was 351 (95% C.I.: 28 – 790) fish (Table 45, Figure 49). The genetic analyses provide additional information that cannot be obtained by conventional tagging methods. For example, PIT-tags placed in adults at the Bonneville Dam AFF can identify the stock-of-origin only for fish that survive and are detected at upstream dams. However, the genetic analysis can provide stock-of-origin on most fish regardless of whether they survive further upstream of Bonneville Dam. This ability has allowed greater numbers of fish to be detected from the relatively rare ESA listed Snake River stock, which improves accuracy and precision of abundance estimates. In addition, the Lake Billy Chinook stock from the Deschutes River is rare and difficult to detect with PIT-tags because of limited arrays in the Deschutes River. Therefore, the ability for the genetic baseline to identify individuals from this stock provides the only way to effectively monitor this stock's abundance in the mainstem Columbia River. In 2018, we estimated the Lake Billy Chinook stock was 79 (95% C.I.: 0 – 184) fish.

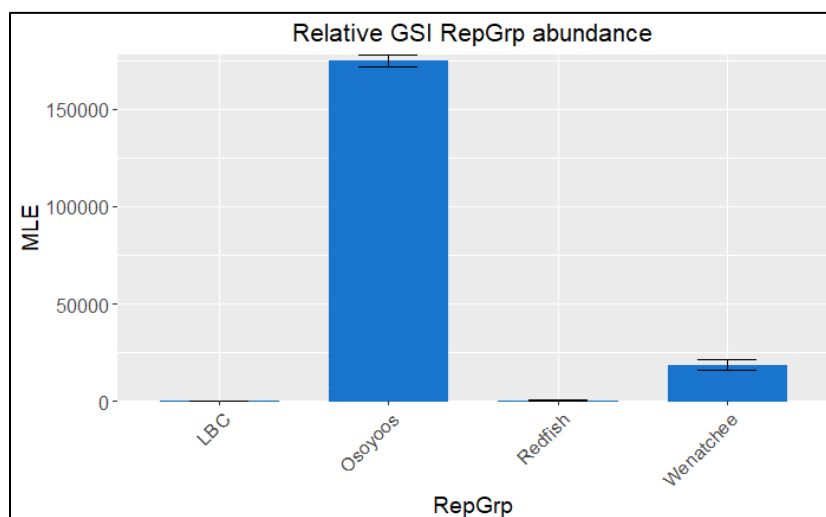


Figure 49. Abundance estimates of Sockeye Salmon stocks passing Bonneville Dam in 2018.

Table 45. Estimated abundance of Sockeye Salmon genetic stocks that passed Bonneville Dam in 2018.

Statistical week	Fish count	GSI assignment				Total	Sample rate	Abundance estimate			
		Lake Billy Chinook	Osoyoos	Redfish	Wenatchee			Lake Billy Chinook	Osoyoos	Redfish	Wenatchee
1_23	3,158		84		1	85	2.69%	0	3,121	0	37
18	17,831		217		14	231	1.30%	0	16,750	0	1,081
19	59,289		314		37	351	0.59%	0	53,039	0	6,250
20	62,984		414	2	44	460	0.73%	0	56,686	274	6,025
21	34,044		277		33	310	0.91%	0	30,420	0	3,624
22	10,880		200	1	20	221	2.03%	0	9,846	49	985
23	3,201	1	103	1	8	113	3.53%	28	2,918	28	227
30_33	2,264	2	75		12	89	3.93%	51	1,908	0	305
Total	193,651	3	1,684	4	169	1,860	0.96%	79	174,688	351	18,533

Note: The fish counts indicate the number of Sockeye Salmon at the fish ladder windows at Bonneville Dam and the GSI assignment pertains to the sample collected at the AFF. The AFF sample is broken into four GSI stocks based on individual assignments to the baseline. Sample rate relates the total sample for a particular stratum to the total fish counted at the window. The abundance estimates are based on the stock proportions of the sample and the window counts of each stratum.

Discussion

Parentage based tagging (PBT) and genetic stock identification (GSI) may be considered as methods that could replace the central functions of the coded wire tag program and could be a replacement for adipose fin marking to identify hatchery origin fish. However, this replacement would be contingent on continued genotyping of hatchery broodstock, fish passing Bonneville Dam, and harvested fish. For ocean fisheries management, additional hatcheries throughout the range of Chinook salmon would have to contribute broodstock samples to this PBT baseline in order for the method to serve ocean fisheries management and the need to monitor total fishery impacts for stocks including Columbia River stocks of fall Chinook (tules and upriver brights) harvested in ocean fisheries. The genetic methods provide a substantial amount of information when they are combined and used to analyze Columbia River Chinook salmon and steelhead passing Bonneville Dam. PBT improves the accuracy for defining hatchery-origin and by subtraction, total natural-origin stocks. Expansion of our PBT baseline to include hatcheries in the Columbia River has increased the proportion of hatchery origin fish passing Bonneville Dam that can be assigned to their broodstock source. We were able to assign 71% of hatchery-origin steelhead sampled at Bonneville Dam in 2017 to 31 broodstock sources. As this effort continues to expand, we anticipate a corresponding increase in the proportion of hatchery origin fish that can be confidently assigned to their hatchery broodstock source. We have observed at least one sign of improved PBT coverage based upon our in-season analyses of Chinook Salmon that passed Bonneville Dam in 2018. Namely, the percentage of adipose-clipped fish abundance that was identified as PBT broodstock ranged from 90-100%, 95-100%, and 76-97% in the spring, summer, and fall management periods, respectively. We would expect these percentages to be high (~100%) only if all hatchery broodstock above Bonneville Dam are included in the PBT baseline AND our estimated tag rates are accurate for each hatchery broodstock. The fact that the management periods mostly attained high percentages gives us confidence that the PBT baseline coverage is nearly complete for Chinook Salmon above Bonneville Dam.

Genetic monitoring combining PBT and GSI is one of a number of possible tools that can be used to identify hatchery and natural fish at various resolutions. Other methods include, CWTs, PIT tags, VIE tags, and otolith marks. Adipose fin clips can be used to differentiate hatchery fish from wild fish either when fish are clipped at 100% or through expansions if stocks are not clipped at 100%. PBT can further discriminate among hatchery stocks within the reporting groups that we use for GSI analyses, and so we can now characterize different age-classes from particular hatcheries by run-timing distributions and estimate their abundance at Bonneville Dam. GSI continues to provide information that would not be possible with PBT, especially for natural-origin stocks.

This long-term study will allow us to characterize trends in run timing and abundance of steelhead and Chinook and sockeye salmon and provide this data to fisheries managers. We were able to address the following **F&W Program Management Questions:**

What are the status and trend of adult productivity of fish populations?

What are your in-river monitoring results and what are your estimates of stock composition and stock-specific abundance, escapement, catch, and age distribution?

Trapping at Bonneville Dam can only be done at very low rates due to restrictions placed on trap operations by USACE and NFMS. Low sample rates inhibit getting a representative sample of various stocks of fish. Higher sample rates would improve the precision of the estimates of fish at Bonneville Dam. Some fisheries were also sampled at very low rates.

We identified 14 Chinook salmon hatchery-origin stocks (75 hatchery broodstock sources) and 11 natural-origin stocks estimated to have relative abundances $\geq 1,000$ fish passing Bonneville Dam in 2017. The migratory delays observed at Bonneville Dam in the spring of 2017 appear to have affected the run-timing distributions for several hatchery-origin and natural-origin stocks. These delays likely contributed to the broad overlap in the temporal distributions of spring, summer/fall, and fall Chinook stocks, and our detection of spring stocks passing Bonneville Dam well into the summer management period.

We identified five steelhead hatchery-origin stocks (31 hatchery broodstock sources) and five natural-origin stocks estimated to have relative abundances $\geq 1,000$ fish passing Bonneville Dam in 2017. We found that genetic stocks seemed to fit well into the historical management categories, particularly the hatchery-origin stocks. Migratory delays at Bonneville Dam in the spring of 2017 shifted the median passage date for several stocks. For instance, the Skamania summer-run has previously been characterized as part of an early run-timing category, and in 2016 had a median run-timing of 06/22/2016. However, in 2017 this stock had a median run-timing of 07/05/17. Natural-origin stocks from the Klickitat River and the 07_MGILCS reporting group also exhibited later run-timing distributions relative to that observed in 2016. Characteristics of steelhead that assigned to Snake River hatchery broodstock sources generally support the typical A-run and B-run steelhead life history categories. The relatively large (≥ 78 cm) steelhead were found primarily to originate from Dworshak hatchery broodstock. These fish were also relatively old (2- and 3-ocean-age) and were derived from the Clearwater R., which is one of the regions expected to produce “B-run” steelhead. It is notable that the MGILCS reporting group represents some fish both within and outside the Snake River steelhead DPS, but does not represent all of the fish within the Snake River DPS.

This was the sixth year that we were able to analyze sockeye salmon using GSI, but for 2017 we used a GSI baseline that included kokanee samples from the Deschutes River drainage, Wallowa Lake, and other locations on the Snake River. We estimated relative stock composition and stock abundance for sockeye passing Bonneville Dam in 2017, and found that the Okanogan stock has the greatest relative abundance followed by the Wenatchee stock. We found fewer fish from the Snake River stock compared to previous years, and identified fish from Lake Billy Chinook that previously would have assigned to the ‘Whatcom’ stock. We also found that the migratory run timing for the Okanogan and Wenatchee stocks overlaps broadly at Bonneville Dam, with the Snake stock migrating slightly later in the year.

This year (2018) we have increased the frequency of in-season reporting during the Chinook Salmon spring and summer management periods, and we have offered timely post-season reports for the fall management period of Chinook Salmon, as well as Skamania and A-/B-Index Summer Steelhead Management Periods, and Sockeye Salmon. For steelhead and sockeye, our genetic analyses have become officially integrated into the routine analyses that

U.S. v OR TAC performs. In all cases, the genetic analyses are a complement to the data that fisheries managers have available to gain insights into the biological characteristics of fisheries. The genetic analysis of the Spring Chinook Salmon test fishery data may begin to play a particularly important role in the in-season analyses because of its potential predictive power for stock abundance and timing at Bonneville Dam weeks in advance of the arrival of the run.

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Overall Conclusion

This project combines four inter-related studies from the Fish & Wildlife Program Accords that address the following current and future objectives: 1) discover and evaluate SNP markers in salmon and steelhead and other anadromous fishes; 2) expand and create genetic baselines for multiple species including Chinook salmon, steelhead, sockeye salmon and kokanee, and coho salmon; 3) implement Genetic Stock Identification (GSI)/PBT programs for mainstem Chinook salmon, sockeye salmon, and steelhead fisheries and 4) GSI/PBT of fish passing Bonneville Dam (steelhead, sockeye, and Chinook salmon).

As described in Section 1, SNP panels continue to be expanded with GTseq that enables genotyping large sample sizes (>120,000 fish genotyped in 2018). This new genotyping protocol has greatly increased our laboratory's efficiency by allowing large numbers of fish to be genotyped with large numbers of SNP loci but at lower costs. For genetic baseline expansion (Objective 2), PBT hatcheries above Bonneville were genotyped to enable more thorough assignment of hatchery origin fish. In addition, GSI baselines are being genotyped to include newly developed SNP loci from RAD-seq projects that were intended to improve resolution for steelhead populations in the Columbia River Basin. SNPs identified through these previous RAD-seq efforts and current efforts involving whole genome resequencing will be useful in characterizing genetic diversity of hatchery and wild Chinook salmon and steelhead stocks. This study included two broad applications of stock identification; namely, stock composition of fisheries for Chinook salmon, sockeye salmon, and steelhead (Objective 3), and stock composition of Chinook salmon, sockeye salmon, and steelhead passing Bonneville Dam (Objective 4). Chinook salmon and steelhead fishery applications of GSI were integrated with the new genetic technology of parentage based tagging (PBT). The challenge imposed by long histories of exogenous stock transfers from specific hatchery programs often prevents effective application of GSI in assigning hatchery fish. However, as the role of PBT is expanding to tag all hatchery fish, the role of GSI will be focused on identifying stocks of natural-origin fish.

Our GSI analyses of harvest included stock composition results for the spring, summer, and fall management periods of Chinook salmon fisheries in the lower Columbia River mainstem. Sockeye salmon fisheries were analyzed and our stock composition results will provide additional information to managers of these fisheries. However, the sockeye salmon results indicate an increase in sample size may be warranted to make accurate estimates of rare stocks such as Snake River sockeye salmon. Although it was possible to estimate stock proportions of Snake River sockeye salmon, the low sample sizes precluded our ability to conclude whether there are significant differences in proportions of this stock among fisheries and at Bonneville Dam.

For Objective 4, we used a combination of GSI and PBT to estimate run-timing distributions and relative abundance of hatchery and wild Chinook salmon and steelhead stocks in 2016. For sockeye salmon, we used GSI to estimate relative stock abundance and run-timing distributions. The stock-specific data on abundance and run-timing of these species were used as a context for interpreting harvest stock composition. We have also begun timely post-season reporting of genetic analysis of steelhead and Sockeye Salmon at Bonneville Dam in 2018, and approximately bi-weekly in-season reporting of genetic analyses during the spring and summer management periods of Chinook Salmon in 2018. The timely updates of the genetic analyses for these runs and species of Columbia River fishes improves their utility for fisheries managers.