

GENETIC ASSESSMENT OF COLUMBIA RIVER STOCKS

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Executive Summary

This project combines multiple 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 seven SNP panels for the following species: Chinook salmon (*Oncorhynchus tshawytscha* – 351 loci including a sex determination marker), Steelhead trout (*O. mykiss* – 376 loci including a sex determination marker; Sockeye salmon (*O. nerka* – 363 loci); Coho salmon (*O. kisutch* – 235 loci including two sex determination markers), White sturgeon (*Acipenser transmontanus* – 325 loci), Pacific lamprey (*Entosphenus tridentatus* – 295 loci), and a species complex of lampreys in the genus *Lampetra* (*L. richardsoni*, *L. ayresii*, and *L. pacifica* – 384 loci). Additional SNPs from Pool-seq data will be under development in the coming year (Paired-end data assemblies, primer design, and testing).

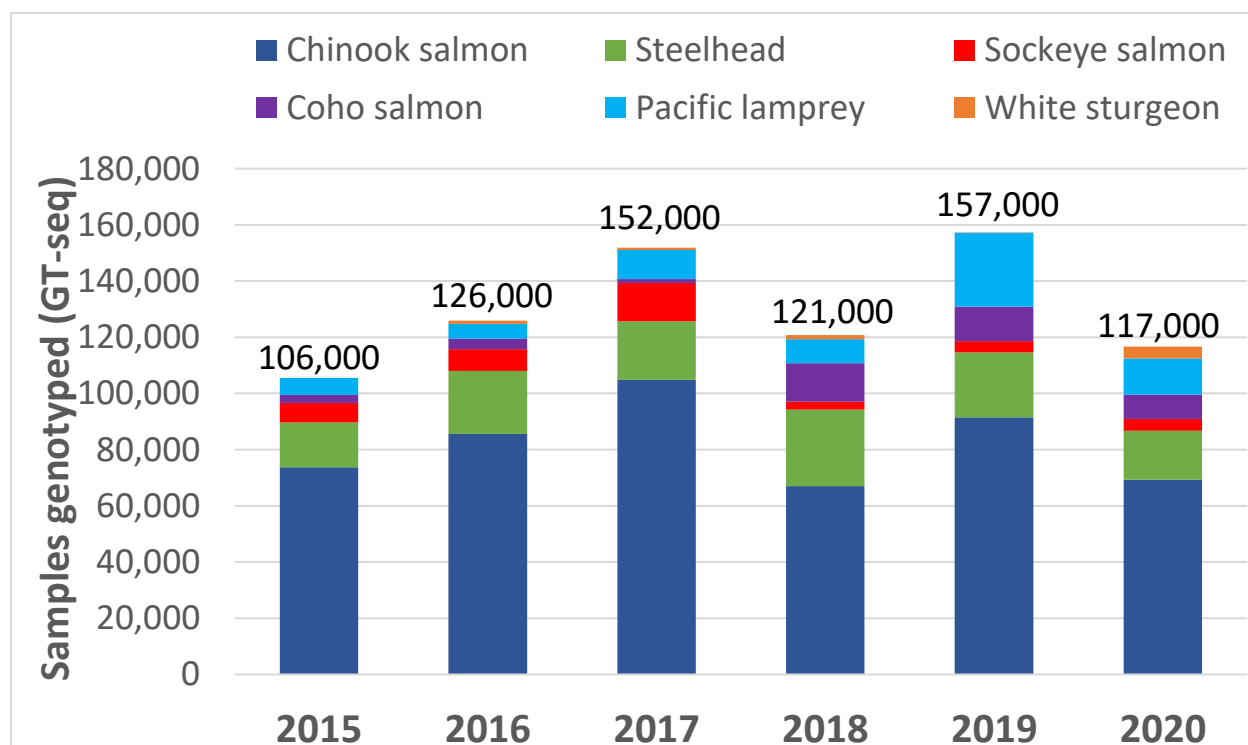


Figure 1. Summary of Columbia River fish samples genotyped using GT-seq (2015 – 2020).

In 2020, the total number of samples genotyped with GTseq was 116,655. The largest portion of samples were Chinook salmon (69,317), then steelhead (17,450), Pacific lamprey (12,876), coho (8,666), and sockeye (4,167) as shown in **Figure 1**.

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, Coho 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 2020 include expansion of the Coho salmon PBT baseline with the addition of two new hatcheries in the lower Columbia River. Additional work examining the neutral genomic population structure of Steelhead trout populations throughout the Columbia River basin had aided in defining population boundaries and expanding the PBT baseline to 368 SNP markers.

There are three projects that are in progress to characterize reference baselines of millions of SNPs for Chinook Salmon, Coho Salmon, and *O. mykiss*. These 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 for our study species in the Columbia River. Specific SNPs that are identified 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 described a new method for estimating abundance from catch estimates and at Bonneville Dam using functions that minimize bias from expansion of PBT tag rates. This method allowed us to take PBT tag rates into account, and accurately estimate attributes of natural-origin fish without being influenced by the attributes of unmarked hatchery-origin fish that were not assigned with PBT. We have continued implementing this approach in all our harvest estimates for 2019. We have switched to a larger panel of SNP loci (254) that are a subset of the most informative loci for PBT applications which we previously identified among a set of 299 SNPs in Chinook salmon. Results have demonstrated this subset of 254 SNPs improves accuracy of PBT assignments for all lineages of Chinook salmon and effectively avoids crashing issues with SNPPIT, the software used for PBT assignments.

We used a combination of PBT and GSI analyses to determine stock composition of Chinook salmon harvested in 2019 in test, sport, commercial, pound net, and Treaty fisheries in the mainstem Columbia River during the spring, summer, and fall management periods (Figure 2). PBT is a new application for Sockeye salmon and can identify fish that are part of the Yakima River reintroduction using a baseline of translocated adults.

There were 162 coded-wire tags (CWTs) recovered and identified to hatchery stock and broodyear (BY) among the snouts recovered from the lower river fisheries, and 113 of these CWTs also were PBT assigned (70%). Of the 113 fish with both CWT and PBT, there were 107 fish (95%) that appeared concordant with the PBT assignments according to both the hatchery source and the broodyear.

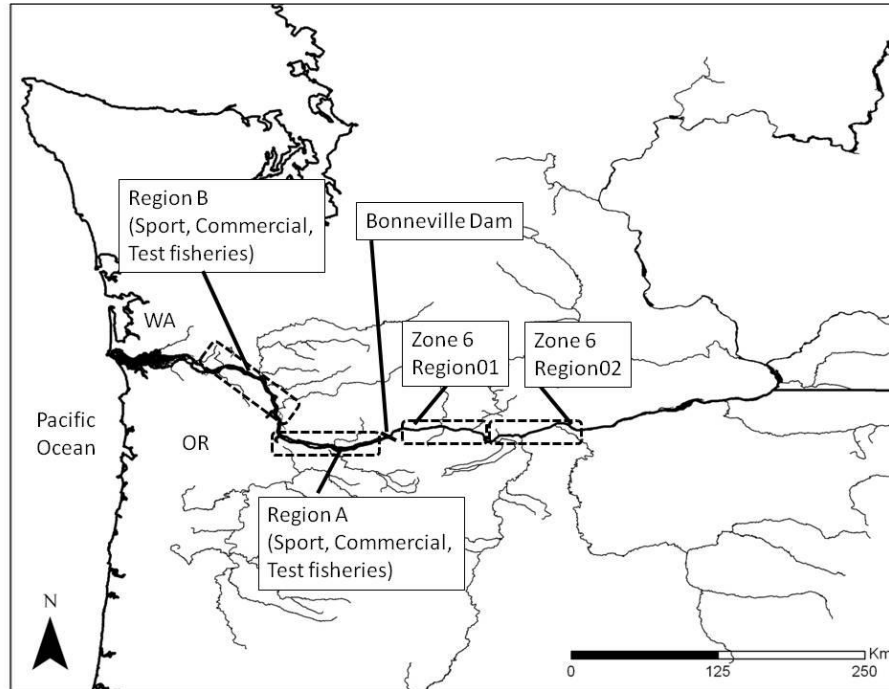


Figure 2. Sources of fishery mixtures in the lower Columbia River mainstem.

We examined one source of information that could potentially be useful to managers particularly on years when the spring Chinook Salmon run is delayed and passage data is not available from Bonneville Dam. There is a test fishery in the lower Columbia River that is typically conducted by WDFW on Sundays each week in the early spring (February – May). When the 2019 test fishery CPUE was compared to passage at Bonneville Dam for the same year, the peak in CPUE appears to correspond with a peak in Bonneville weekly counts with a lag of 13 days difference (Figure 3). This relationship between the test fishery and Bonneville passage is consistent with our previous results for the 2018 test fishery data (Hess et al. 2020). This result is an important finding that may be useful information for U.S. v OR managers to evaluate early season returns of Chinook salmon. Our analysis can add another valuable layer of information to this predictive relationship when we decompose the test fishery CPUE into units of hatchery and natural-origin stocks and predict the abundance of these stocks passing Bonneville Dam up to 2 weeks later.

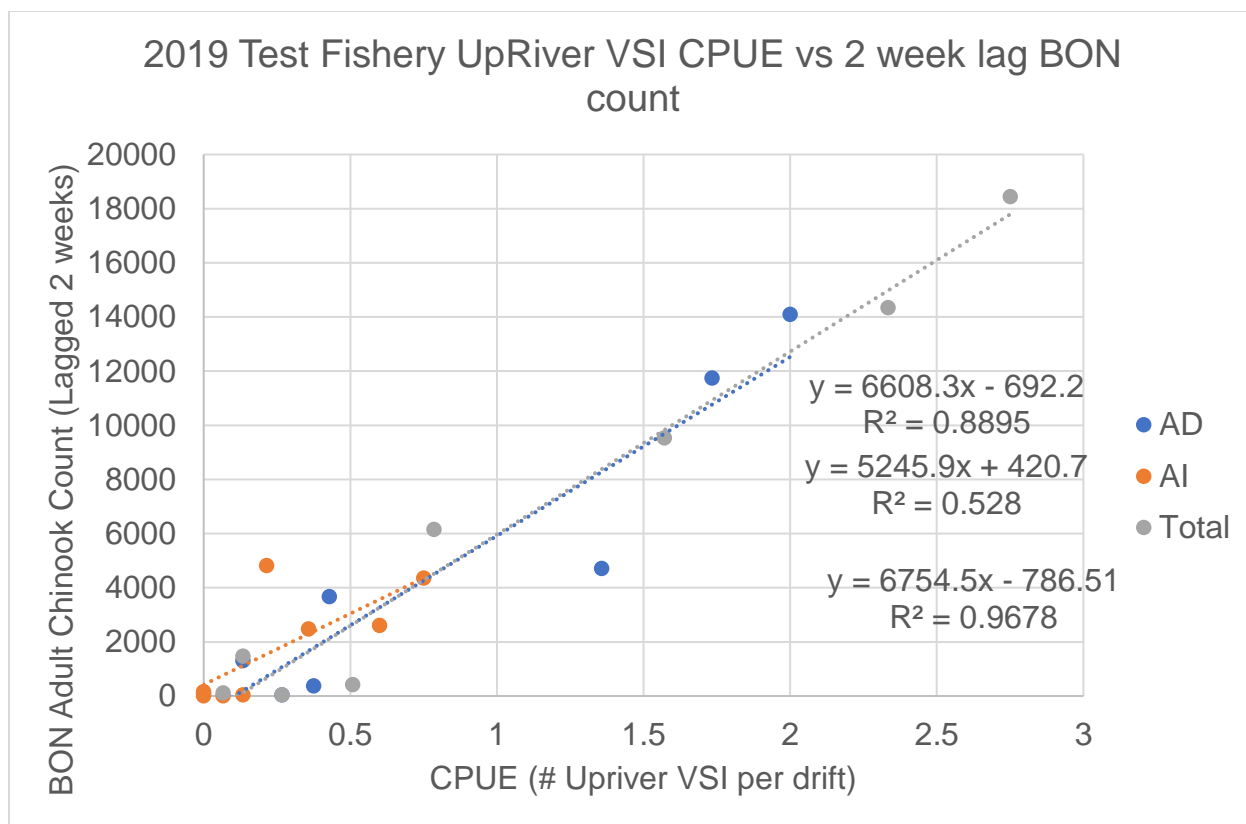


Figure 3. The relationship between the test fishery upriver Chinook Salmon CPUE and weekly fish counts at Bonneville Dam in 2019 with 2 week lag.

In 2019, the pound net was operated in the Cathlamet Channel (Region B) during each of the three Chinook salmon management periods. The Non-Treaty recreational and commercial fisheries were not conducted in the summer period (June 16 – July 31) in 2019, and so the data from the pound net was the only option to compare to stock composition of the Treaty Summer Chinook commercial fishery.

The largest difference in the composition of these two fisheries was the presence of lower river stocks (04_WILLAM) in the lower river pound net fishery compared to the zone 6 fishery (Figure 4). There were small but detectable abundances of Snake River spring stocks in the Treaty summer fishery, but not in the pound net adult sample likely due to low sample rates.

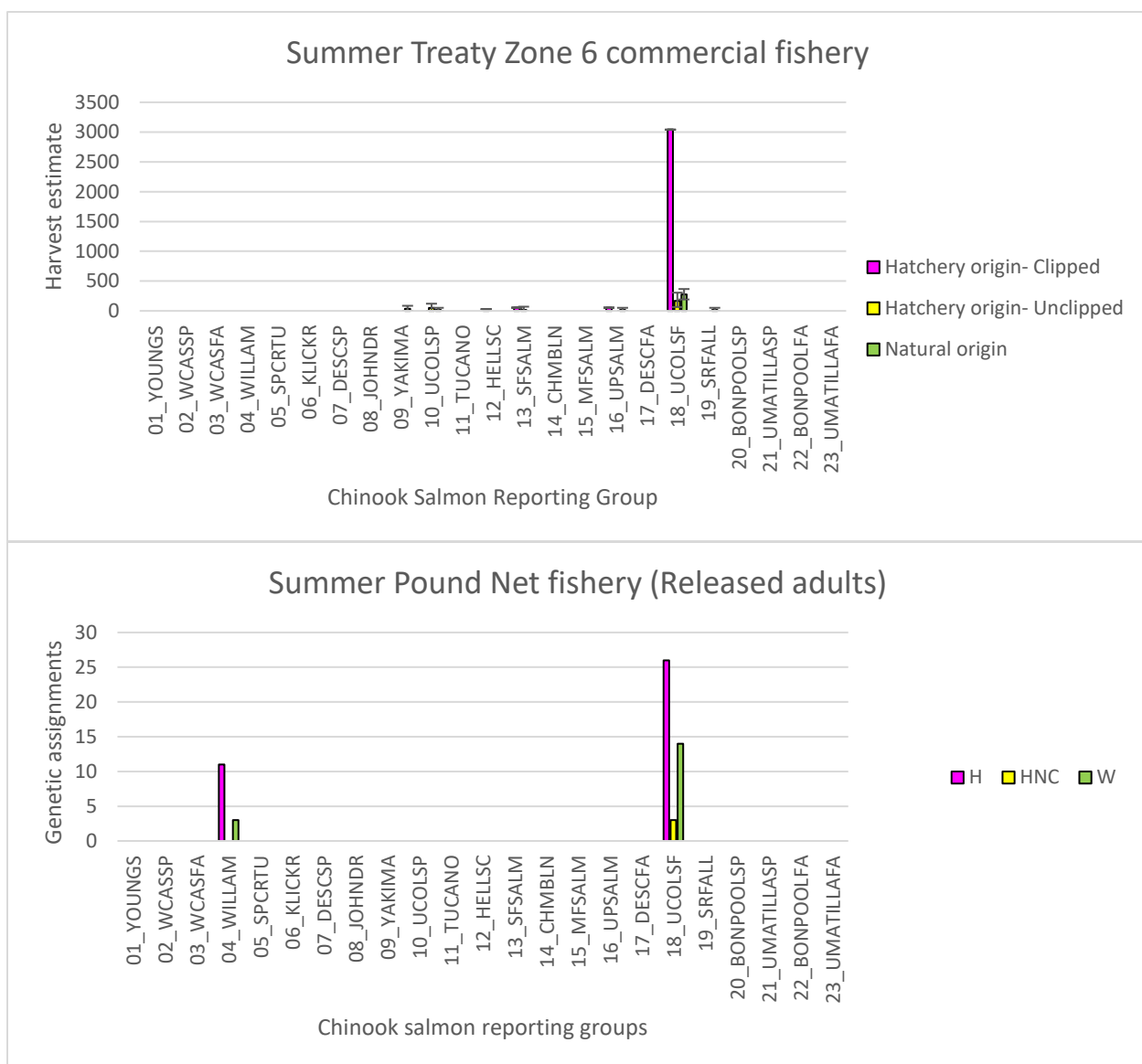


Figure 4. Genetic stock composition of the Treaty Zone 6 commercial Chinook salmon fishery and the pound net fishery during the summer period analyzed in 2019.

The composition of the stocks in the pound net fishery was also used to compare to other fall fisheries in the lower river. The compositions of the pound net fishery and the Non-Treaty commercial harvest showed a dramatically higher abundance of “tules” compared to the sport fishery harvests (Figure 5). This difference may largely be due to sport fishers preferentially keeping the VSI bright fish over the tule fish.

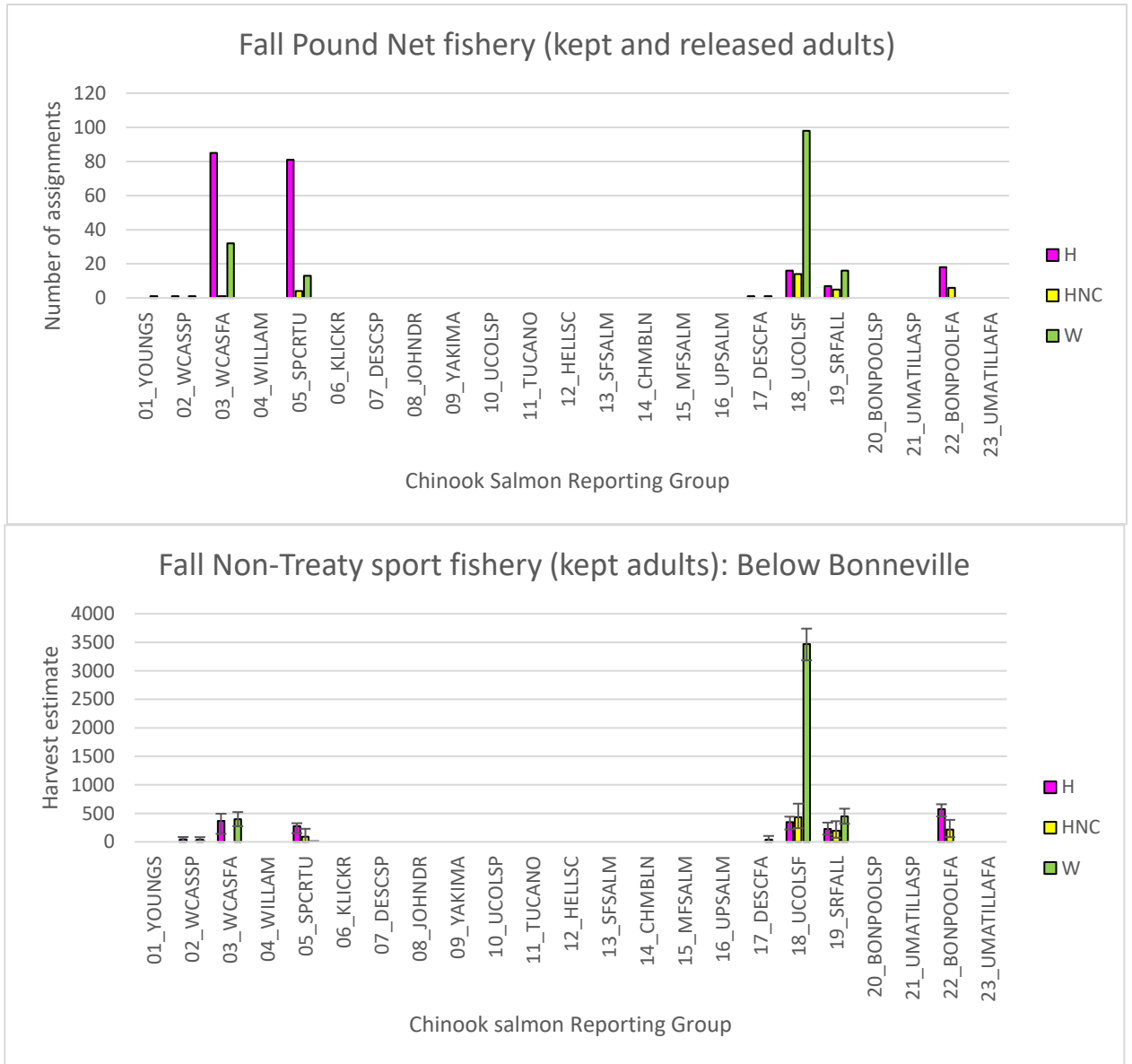


Figure 5. Genetic stock composition of the Non-Treaty fall pound net and sport Chinook salmon fisheries analyzed in 2019.

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-sized and jack-sized Chinook salmon during the spring, summer, and fall management periods and all steelhead during the A-/B-Index summer steelhead management period, and used a combination of GSI and PBT to estimate run-timing distributions and relative abundance of hatchery and natural-origin Chinook salmon and steelhead stocks in 2019 (post-season analyses). Further, in-season analyses were completed for fish returning throughout 2020 and provided to regional fisheries managers that serve the U.S. v OR Technical Advisory Committee (TAC).

In 2019, there were 8 major (i.e., abundance >1000 fish) Chinook salmon stocks represented in the total estimated relative abundance (N=158,337) of natural-origin (i.e., excluding unclipped hatchery-origin fish) Chinook salmon passing Bonneville Dam in 2019 (Figure 6). These natural-origin stocks in order of decreasing magnitude were 18_UCOLSF (123,635), 19_SRFALL (17,688), 12_HELLSC (4,217), 17_DESCFA (3,003), 10_UCOLSP (2,513), 05_SPCRTU (1,445), 03_WCASFA (1,358), and 13_SFSALM (1,129). These stock abundance estimates were generated using SCOBIDEUX and SPIBETR functions and the estimates of clipped and unclipped adults distributed by TAC.

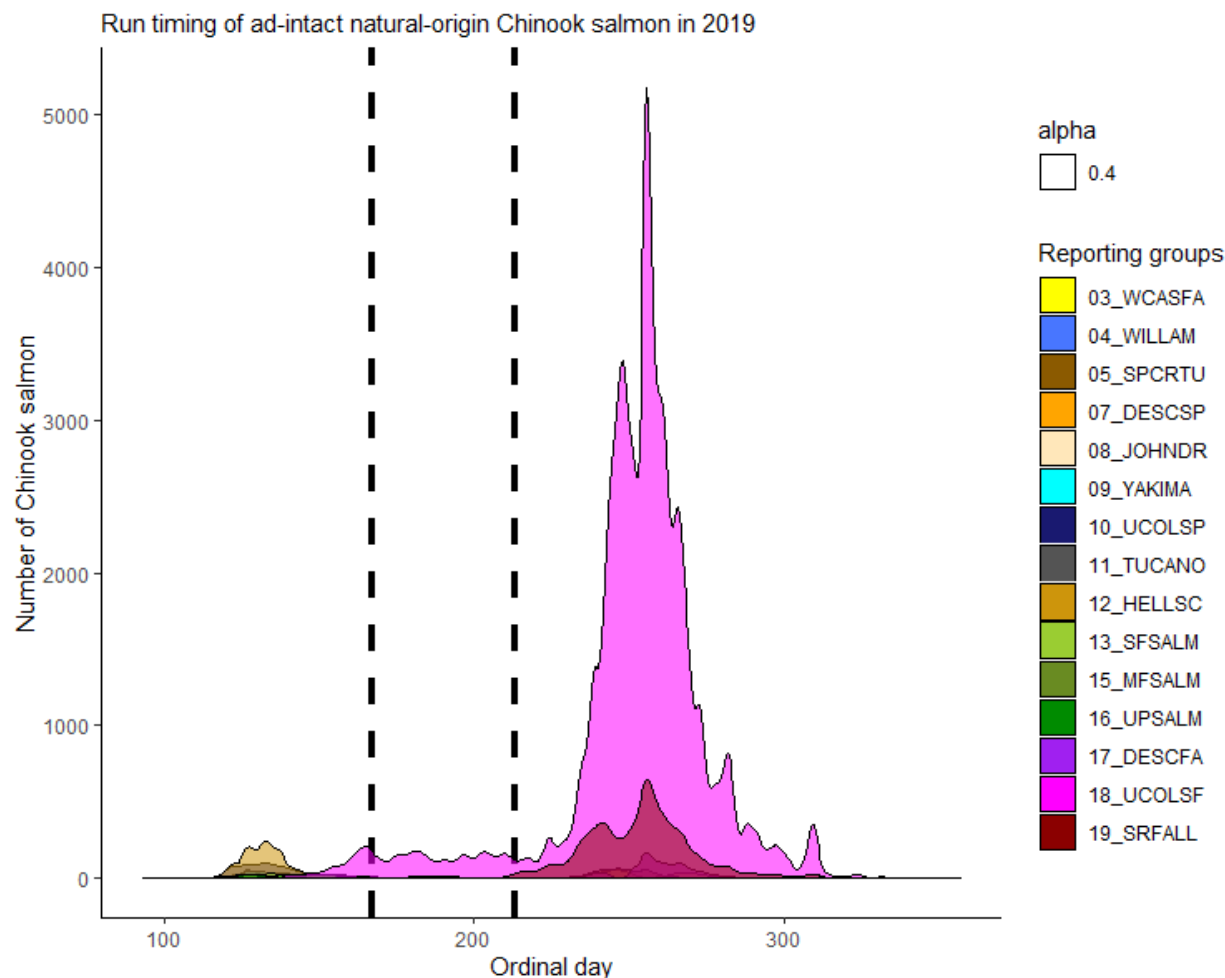


Figure 6. Estimated abundance of natural origin (excluding adipose-intact hatchery-origin fish) adult-sized Chinook salmon sampled at Bonneville Dam in 2019 assigned to genetic stock of origin. The dotted lines mark the beginning of the summer and fall management periods (June 16 = Ordinal day 167; Aug 1 = Ordinal day 213, respectively).

There were five major stocks (abundance >1000) represented in the total estimated relative abundance (N=40,469) of hatchery-origin steelhead passing Bonneville Dam in 2019. These stocks in order of decreasing magnitude were 07_MGILCS (14,548), 14_UPSALM (11,722), 10_SFCLWR (9,962), 03_SKAMAN (3,082), and 09_UPPCOL (1,087) (Figure 7). There were four major stocks (abundance >1000) represented in the total estimated relative abundance (N=31,997) of natural origin (excluding unclipped hatchery-origin fish) steelhead passing Bonneville Dam in 2019 (Figure 7). These stocks in order of decreasing magnitude were 07_MGILCS (20,210), 14_UPSALM (5,381), 08_YAKIMA (1,390), and 09_UPPCOL (1050). There were three stocks that were just below an estimated abundance of 1000: 03_SKAMAN (977), 10_SFCLWR (932), and 06_KLICKR (924). The results of the SCOBIDEUX SPIBETR function minimized bias from tag rate expansion of the unclipped hatchery-origin fish and represent a significant improvement for accuracies of natural-origin stock composition.

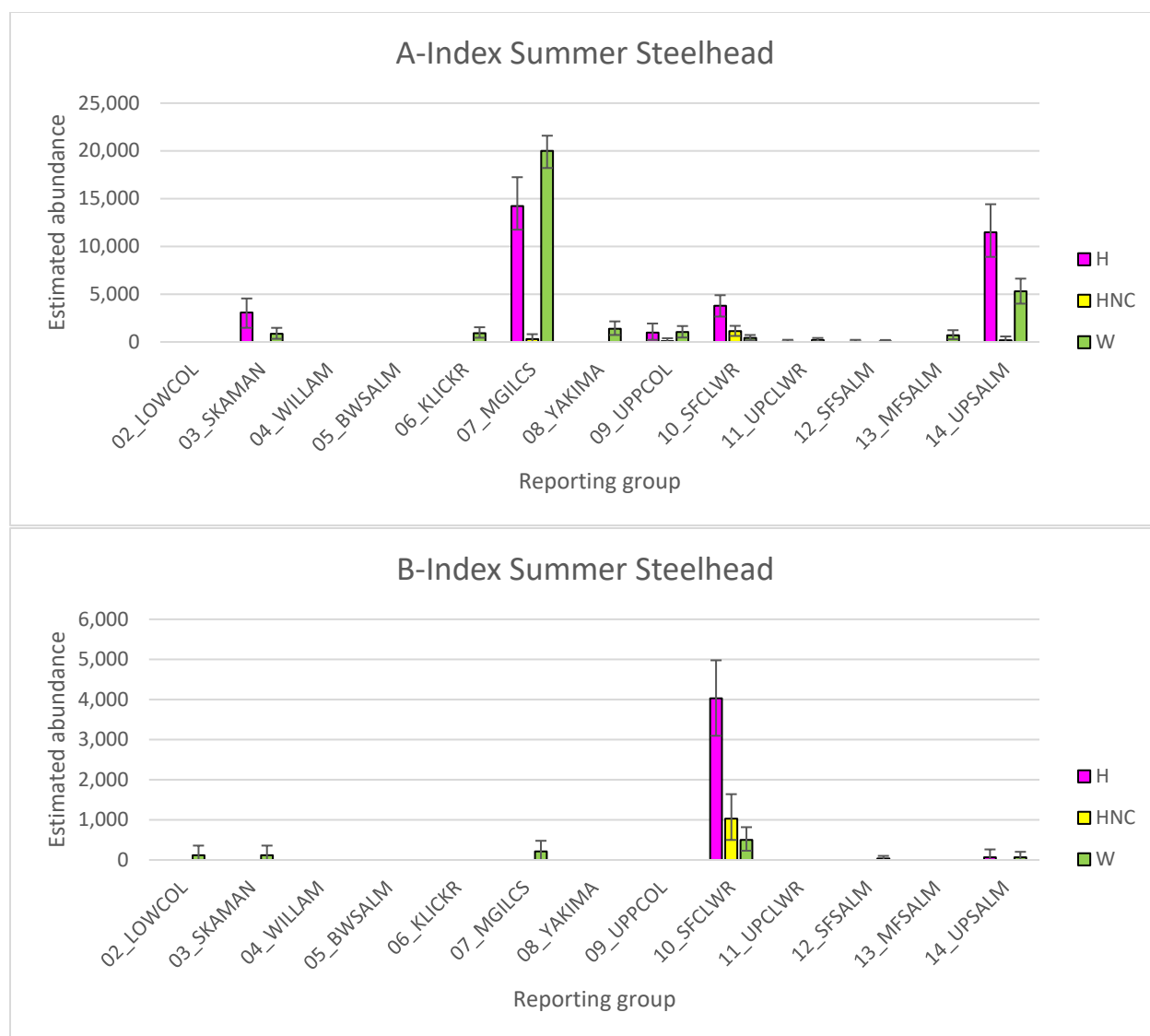


Figure 7. Estimated abundance (\pm 95% CI) of A-Index (<780mm FL, top) and B-Index (\geq 780mm FL, bottom) hatchery origin (clipped “H” and unclipped “HNC”) and natural-origin (“W”) steelhead assigned to genetic stock of origin that were sampled at Bonneville Dam in 2019.

Stock abundance for sockeye salmon was estimated over a course of 15 statistical weeks (i.e. weeks 22-36). A total of 971 sockeye salmon were sampled at Bonneville Dam in 2019 and were assigned to one of four genetic stocks (i.e., Okanogan, Wenatchee, Snake, and Lake Billy Chinook) using GSI and one reintroduced stock using PBT (Yakima R.). This year was the first year in which we identified zero assignments to the Snake River since 2012 when we initiated genetic monitoring on sockeye salmon at Bonneville Dam. In 2019, the Okanogan stock had the highest relative abundance (54,466), followed by the Wenatchee (8,052). The Lake Billy Chinook stock had estimated abundance < 500, but were based on relatively few genetic

assignments (N=10) (Figure 8) which reduces precision of the estimate. The reintroduced stock from Yakima River was also low sample size and was estimated at 265 fish in 2019.

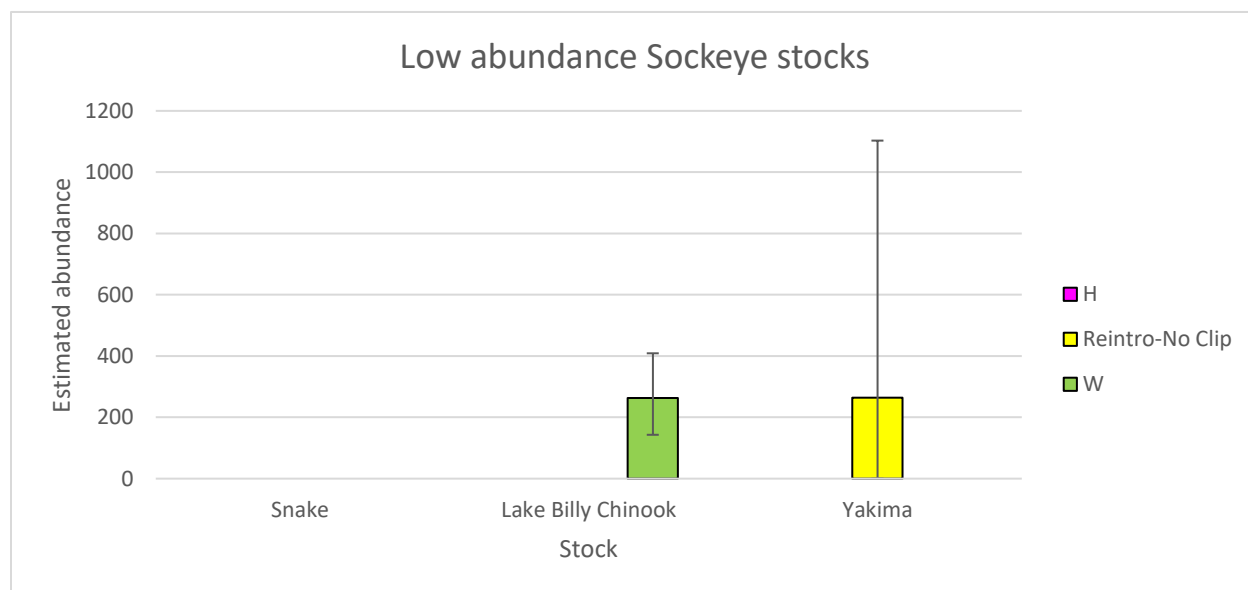
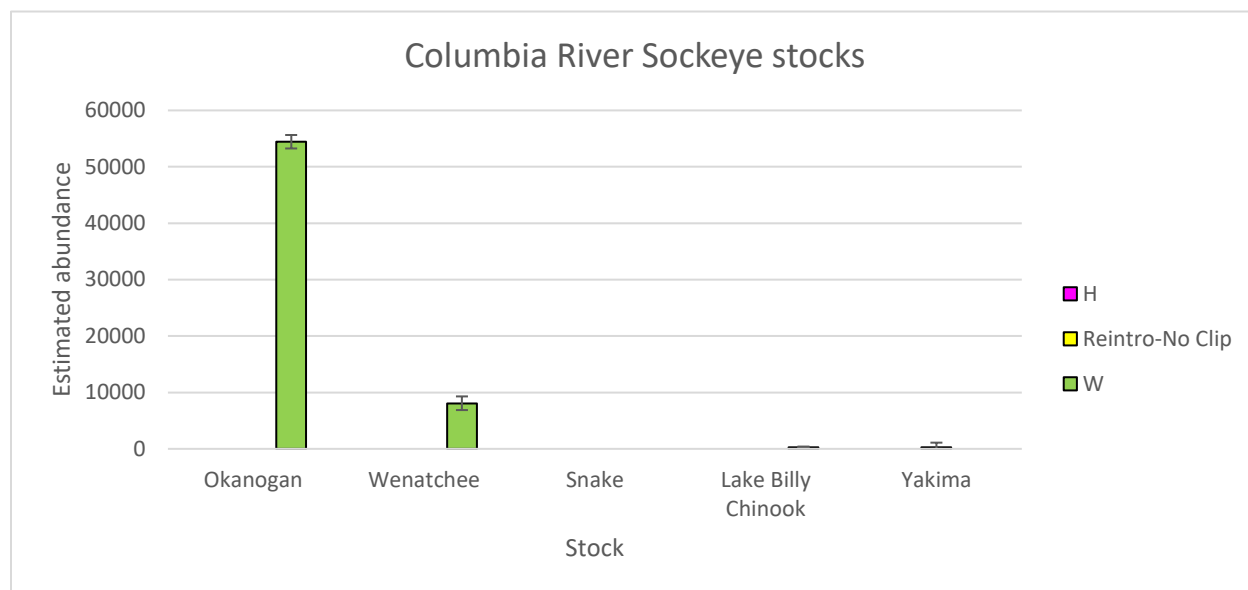


Figure 8. Estimated abundance (\pm 95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2019.

In 2019, run timing distributions of most spring-run hatchery- and natural-origin Chinook salmon stocks were found to terminate in the spring period (i.e., the 95th percentile of the run

passed before the summer period). However, the natural-origin summer-run stock from the upper Columbia River passed 25% of its abundance (2,300 fish) in the spring period and had the majority pass in the spring and summer periods combined (8,908 fish). For steelhead, the patterns generally are consistent with past years. The late arriving natural-origin stocks with median dates on or after August 25th were 10_SFCLWR, 11_UPCLWR, 12_SFSALM, and 14_UPSALM (Figure 9). We characterized run-timing by A-Index and B-Index categories for these stocks. For some stocks that had earlier run-timing as A-Index sizes, these stocks were later arriving as B-Index stocks. Run timing distributions for sockeye salmon sampled at Bonneville Dam broadly overlapped in 2019, and we observed nearly identical run timing distributions for the Okanogan and Wenatchee stocks (median date near 06/26/19).

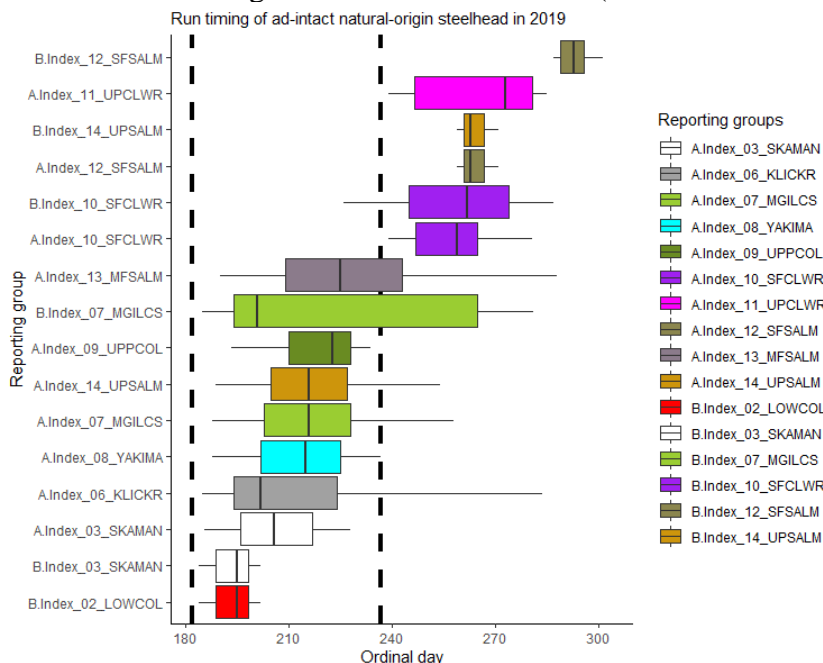


Figure 9. Reporting group level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for natural-origin steelhead (unclipped hatchery-origin fish excluded) that were sampled at Bonneville Dam in 2019 and split by A-Index and B-Index size category. August 25th is dashed line at ordinal day 237.

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 2020 (**Table 1**). 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. One of the notable results was the observation that nearly 12,000 Sockeye salmon returned to Bonneville Dam in 2020 originating from the Yakama Nation reintroduction program in the Yakima River basin. This relatively large return was comprised of a mixture of both Okanagan and Wenatchee genetic stocks (Figure 10), with the Wenatchee stock comprising 58% of the total abundance estimate which is reversed from the proportions in which these stocks are observed at Priest Rapids Dam where they were translocated from.

Table 1. The in-season and post-season report timing and scope of the 2020 fish runs for Chinook salmon, steelhead, and Sockeye salmon.

Species	Management Period	Data coverage	Samples Arrive	Analysis begins	Report distributed
Chinook	Spring	01/01/2020 – 05/01/2020	5/4/2020	5/7/2020	5/11/2020
		01/01/2020 – 05/15/2020	5/18/2020	5/21/2020	5/26/2020
		01/01/2020 – 05/29/2020	6/1/2020	6/4/2020	6/8/2020
		01/01/2020 – 06/15/2020	6/16/2020	6/22/2020	6/24/2020
	Summer	06/16/2020 – 07/03/2020	7/6/2020	7/9/2020	7/13/2020
		06/16/2020 – 07/31/2020	8/3/2020	8/6/2020	8/10/2020
	Fall	08/01/2020 – 8/28/2020	8/31/2020	9/3/2020	9/8/2020
		08/01/2020 – 10/30/2020	11/2/2020	11/5/2020	11/9/2020
Steelhead	Skamania	04/01/2020 – 06/30/2020	7/6/2020	7/9/2020	7/13/2020
	Summer A-/B-Index	07/01/2020 – 07/31/2020	8/3/2020	8/6/2020	8/10/2020
		07/01/2020 – 08/28/2020	8/31/2020	9/3/2020	9/8/2020
		07/01/2020 – 10/30/2020	11/2/2020	11/5/2020	11/9/2020
Sockeye	Total	01/01/2020 – 07/31/2020	8/3/2020	8/6/2020	8/10/2020

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 U.S. v OR TAC members Stuart Ellis and Kate Self for distribution to TAC members.

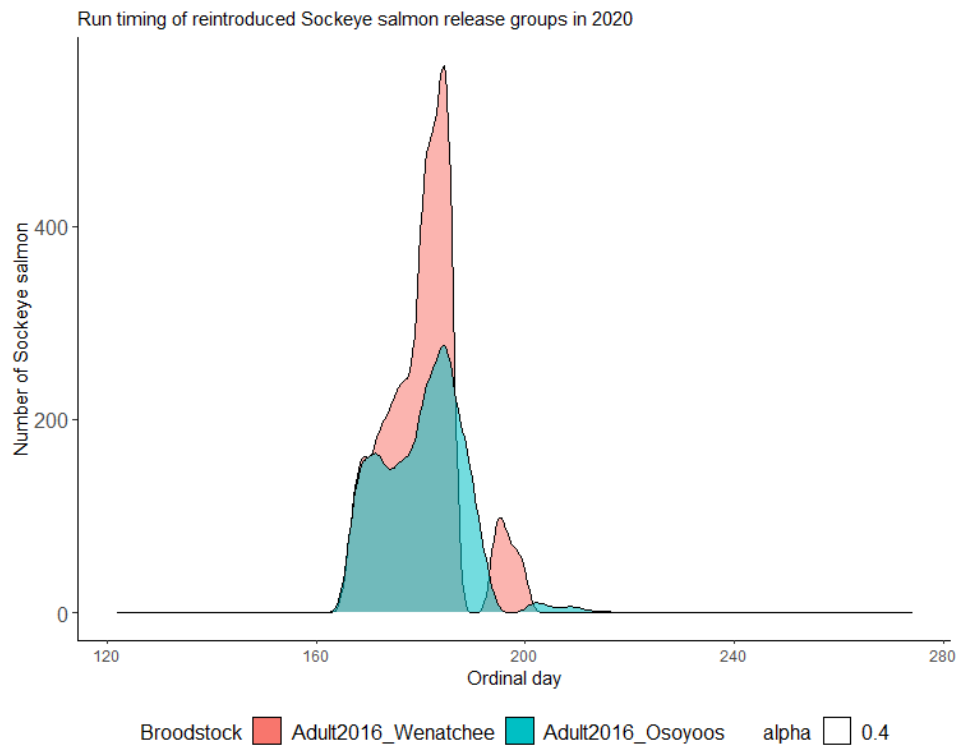


Figure 10. In-season analysis estimated a relatively large return of reintroduced Yakima River sockeye salmon in 2020 comprised of a mixture of Wenatchee and Osoyoos genetic stocks.

Objective 5) Adaptive Genetic Variation associated with environment, landscape, and phenotypic traits

For Objective 5, work has progressed on sequencing Chinook salmon and steelhead throughout the Columbia River Basin to evaluate neutral and adaptive genetic variation related to environmental features. Our recent results indicate that environmental features are strong drivers of adaptive genomic divergence in salmonid species and provide a foundation to investigate how populations might respond to global environmental change (Matala et al. 2014; Hand et al. 2015; Hecht et al. 2015; Micheletti et al. 2018a; Collins et al. 2020). Broad geographic patterns of neutral and non-neutral variation demonstrated in these studies can be used to accommodate priorities for regional management and inform long-term conservation of Chinook salmon and steelhead in the Columbia River. Results from these studies indicate that temperature and precipitation are consistently the main environmental factors influencing genetic variation in salmonids, but other variables may also contribute for specific populations. Recent results also emphasize that environmental conditions through the migratory corridor are stronger drivers of selection than those at natal sites for steelhead in the Columbia River Basin (Micheletti et al. 2018a).

Empirical studies have been implemented to advance our understanding of multiple traits related to recovery of salmonids in the Columbia River. Work has focused on genomic regions associated with resident vs. anadromous *O. mykiss* life histories (Narum et al. 2008; Hecht et al. 2013), run-timing for steelhead (Hess et al. 2016; Micheletti et al. 2018c; Willis et al. 2020) and Chinook salmon (Narum et al. 2018; Koch and Narum 2020), age at maturity in Chinook salmon (Micheletti and Narum 2018b) and steelhead (Willis et al. 2020), disease resistance in *O. mykiss* (Campbell and Narum 2015), and thermally adapted strains of redband trout under heat stress (Narum et al. 2010; Narum et al. 2013; Garvin et al. 2015; Narum et al. 2015, Chen et al. 2018a; Chen et al. 2018b; Chen and Narum 2020). Candidate markers have been confirmed for adult migration/maturation timing in both steelhead and Chinook salmon and are being monitored broadly in large numbers of individuals throughout the Columbia River. Studies are also in progress investigating the genomic basis for age-at-maturity in Chinook salmon, and development of studies to investigate thermal adaptation in anadromous stocks of *O. mykiss* and age/size at maturity in steelhead (A vs. B run; Willis et al. 2020). As candidate genes for these traits have begun to be identified, SNP markers from these regions are being incorporated in standard genotyping panels with GTseq in order to validate and monitor genetic variation for these traits in large numbers of individuals.

Objective 6) White Sturgeon Genetics

The research for this section is specific to genetic monitoring of white sturgeon (*Acipenser transmontanus*). The monitoring began in 2008 and has been focused on populations in the impoundments upstream of four middle Columbia River dams: Bonneville, The Dalles, John Day, and McNary. We have also incorporated collections from the lower Columbia River Below Bonneville Dam and from several reaches of the Snake River Basin (Matala et al. 2017). Our monitoring objectives are aimed at providing answers for uncertainties that will inform long-term conservation and management of the species. Some ways this is being achieved is through evaluating the amount of spatial and temporal genetic differentiation among sub-populations or population aggregates to gain a better understanding of the extent of migration (gene flow), relatedness, and effective number of breeders within and between locations. In addition, we are working with the Yakama Nation to genotype supplementation broodstocks utilized for translocation efforts in the middle Columbia but also in several PUDs in the Columbia River above Priest Rapids Dam. Thus far, our analyses suggest there is a limited amount of genetic differentiation between the Middle Columbia impoundments, including hatchery broodstocks. Therefore, hatchery reared fish are not genetically distinct from the wild populations. Isolation by distance indicates a downstream cline in genetic similarity from the upper Snake River down to the Lower Columbia River below Bonneville Dam. This is likely the result of downstream juvenile passage at the dams and a lack of upstream migration through fish ladders by larger adult fish. Recently, we developed a suite of 325 Single Nucleotide Polymorphism (SNP) markers that are being used to evaluate population structure, estimate individual ploidy levels, and test the efficacy of the panel in parentage applications. Recent efforts also include progress towards assembly of a draft genome for white sturgeon that will enable further investigation into a sex-linked marker that is intended to allow white sturgeon of any age to be identified by genetic sex. Overall, these efforts are intended to provide an improved understanding of connectivity between adjacent populations (i.e. gene flow), and demographic trends (e.g. age structure) that will be vital in managing for population viability. The contemporary status and temporal trends in genetic diversity are likely to aid managers in understanding the impacts of

782 limited habitat in the confines of the mid-Columbia impoundments that may be exacerbated by
783 further anthropogenic influences.

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Introduction

This project combines multiple 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, 4) GSI of fish passing Bonneville Dam (salmon and steelhead), 5) characterize adaptive genetic variation associated with environment, landscape, and phenotypic traits, 6) genetic diversity and structure of white sturgeon. These 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 six 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 more than seven fish species including: Chinook salmon, Steelhead trout, Sockeye salmon, Coho salmon, White Sturgeon, Pacific lamprey, and the Genus *Lampetra* Species Complex (includes Western Brook lamprey and Western River lamprey). 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, Narum et al. 2010, Hess et al. 2011, Hess et al. 2016, Hargrove et al. 2020, Jensen et al. 2020). 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. 2013, Steele et al. 2019) 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 Sockeye salmon and Pacific lamprey, and are being used to monitor translocations of lamprey throughout the interior of the Columbia River and Sockeye salmon in the Yakima River basin.

Objective 5) Adaptive Genetic Variation

With increasing genomic information available for non-model organisms, single nucleotide polymorphisms (SNPs) have begun to see increased use as genetic markers for population genetic studies (e.g., Morin et al. 2004). These sequence polymorphisms are densely scattered throughout the genome of most organisms, and are commonly observed in both coding and non-coding regions of functional genes making them ideal markers to study adaptive molecular variation (e.g., Akey et al. 2002). In a large suite of SNPs that are distributed across the genome (e.g., Narum et al. 2018), it is possible to utilize both functionally neutral and adaptive markers within a single study. This combination of information provides a powerful approach to study questions in ecological genetics since both demographic processes (i.e., gene flow and genetic drift) and local adaptation (i.e., selection) may be inferred. Thus, genome scans with large numbers of SNP markers (e.g., RAD sequencing, Baird et al. 2008; Pool-seq, Schlotterer et al. 2014) and gene expression (e.g., RNA-seq) approaches may be effective tools for identifying the genetic architecture underlying specific traits such as thermal tolerance, run-timing/maturation, disease resistance, anadromy, and age-at-maturity. Underlying genomic regions for these traits continue to be investigated and once identified, they can be broadly screened in populations throughout the Columbia River Basin to facilitate management for long term conservation and recovery of salmonids.

Objective 6) White Sturgeon Genetics

The research for this section is specific to genetic monitoring of white sturgeon (*Acipenser transmontanus*). The monitoring began in 2008 and has been focused on populations in the impoundments upstream of four middle Columbia River dams: Bonneville, The Dalles, John Day, and McNary. We have also incorporated collections from the lower Columbia River Below Bonneville Dam and from several reaches of the Snake River Basin (Matala et al. 2017). This research project directly addresses the following uncertainties: 1) What approaches to population recovery and habitat restoration are most effective in regaining meta-population structure and diversity that will increase viability of fish and wildlife in the Columbia River Basin?, 2) How do artificial production and supplementation impact the maintenance or restoration of an

ecologically functional metapopulation structure?, and 3) What is the relationship between genetic diversity and ecological and evolutionary performance, and to what extent does the loss of stock diversity reduce the fitness, and hence survival rate and resilience of remaining populations? Our monitoring objectives are aimed at providing answers for these uncertainties that will inform long-term conservation and management of the species.

Report Structure

This report is divided into six 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 2019. 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 2019. 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 2020. These in-season and post-season 2020 results were provided to fisheries managers that participate on the USvOR Technical Advisory Committee and are summarized in the fourth section of this report. The fifth section reports on progress to identify adaptive variation associated with landscape, environment, and phenotypes. The sixth section reports on updates to genetic analyses of white sturgeon.

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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). GT-seq panels have been designed to a maximum of 75bp to allow for inexpensive sequencing runs on Illumina NextSeq 500.

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 200 μ M 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 3,000-4,000 samples for a NextSeq flow cell.

Results

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). GT-seq primer pools are being used for all high throughput genotyping projects for seven SNP panels for the following species: Chinook salmon (*Oncorhynchus tshawytscha* – 351 loci including a sex determination marker), Steelhead trout (*O. mykiss* – 376 loci including a sex determination marker; Sockeye salmon (*O. nerka* – 363 loci); Coho salmon (*O. kisutch* – 235 loci including two sex determination markers), White sturgeon (*Acipenser transmontanus* – 325 loci), Pacific lamprey (*Entosphenus tridentatus* – 295 loci), and a species complex of lampreys in the genus *Lampetra* (*L. richardsoni*, *L. ayresii*, and *L. pacifica* – 384 loci). 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 116,655 samples in 2020 (Figure 11). The largest portion of samples were Chinook salmon (69,317), then Steelhead (17,450), Pacific lamprey (12,876), Coho (8,666), White sturgeon (4,179) and Sockeye (4,167).

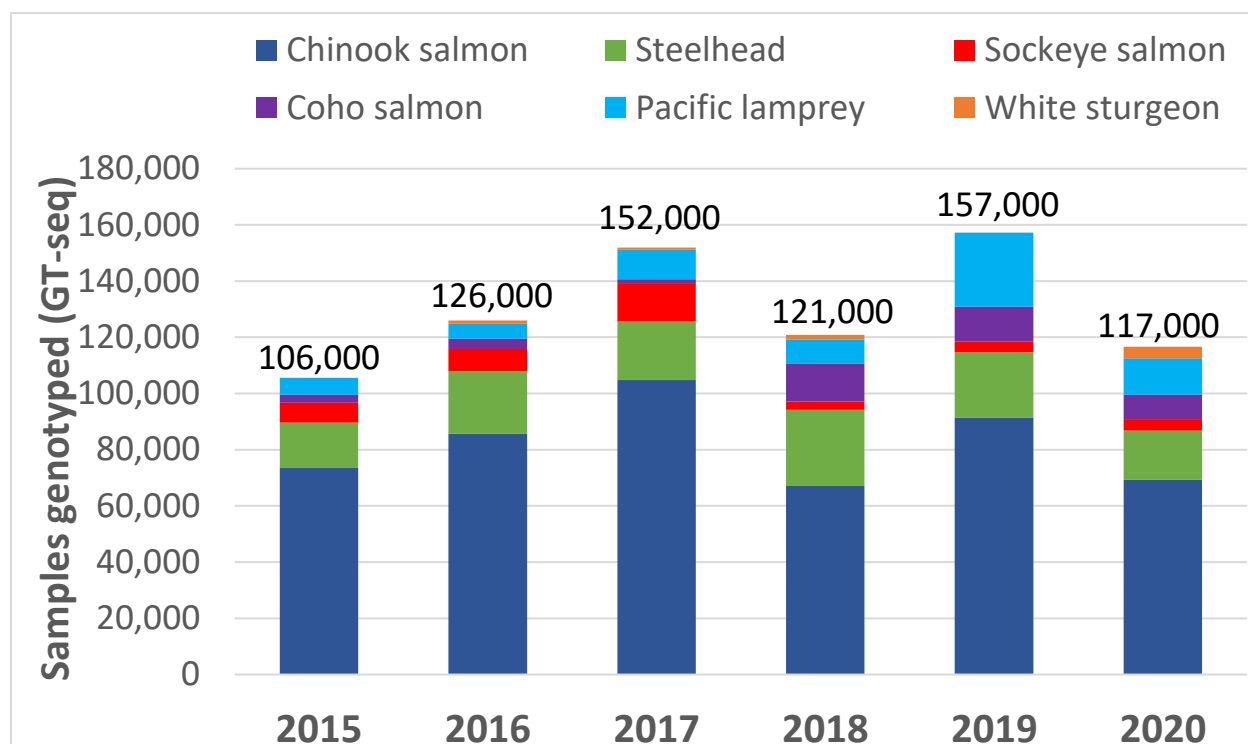


Figure 11. Summary of Columbia River fish samples genotyped using GT-seq in calendar year 2020.

The Chinook panel underwent multiple changes in 2020. We added nine markers from Micheletti and Narum 2018 (CHI06027687_143477, CHI06035945_4547, CHI06048618_5222, CHI06105101_16717, CHI06105101_18523, Ots17_1066109_C6, Ots17_1345774_C6, Ots17_1486479_C6, Ots17_1488679_C6; Appendix 2). Eight Markers from McKinney et al. 2020 were tested and nine added to the panel. Ots_wenYhap_106664_9, Ots_wenYhap_25067_92, Ots_wenYhap_33126, Ots_wenYhap_71572.

The Steelhead panel underwent minor changes with testing of 26 markers from Chen and Narum 2020. Eight markers were integrated into the steelhead panel (Omy4_8260712, Omy4_8261223, Omy4_8269484, Omy4_8272302, Omy4_8325040, Omy4_8327140, Omy4_8343709, Omy4_8345868; Appendix 1).

The Sockeye panel had a single marker added (One_LRRC9_68810) from Veale and Russello 2017. Twenty additional poor performing, or low diversity loci were dropped from the panel. The Coho panel had 24 poor performing or low diversity loci removed. No changes were made to the pre-existing Pacific lamprey panel or the sturgeon panel. The new panel for the species complex of lampreys in the genus *Lampetra* is described in further detail in the Lamprey BPA report.

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. 2016b, Micheletti et al. 2018).

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 (e.g. 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.

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1157 **Appendix 1. *GT-seq* SNP panel for steelhead trout.**

Assay	A	A	Forward	Reverse	A1-Probe	A2-Probe	Allele	GCF_0	GCF_0
	1	2					Correctio	201634	021634
							ns	95.1	SNP
								chromo	Coordi
								some	nate
OmyY1_2SEX Y	X	Y	GCGCATTTGTATGGTGAAAA	GCCTGGCATATGAGTGT TGA	NA	ATGTGTTCAT ATGCCAG	NA		
Omy_R AD7252 8-44	A	T	TGATGATCCGGACCCTCTCT	CCCGGATTCCCTCCACA GTT	TTGGAACAAA CTGT	TTGGAACTAA CTGT	0,0	omy01	7354513
OMS00 078	T	C	GAGGGAAGCAGCCATAAAC AGAATA	GTCTCACTATGGTCCAT ATCTGTGTAGA	TTCACATGCAT AAGAGTG	TCACATGCAT GAGAGTG	0,0	omy01	10499333
Omy_R AD6580 8-68	T	G	TCCTTCACTCTCGATCGGGA	TCAAACCTGGGCCACTAC TGT	ATCGGGATTCT ACTT	ATCGGGAGTC ACTT	0,0	omy01	12187698
Omy_ga dd45-332	T	C	AGAGAAGACTCACTGCTGTT TGC	AAATCAGTTCCCACGCT ATGCT	TTGCTCCAAA ATGG	TTGCTCCGAA ATGG	0,0	omy01	12240053
Omy_10 7031-704	C	T	GGCTTTCGGATACTGAGCAA CAA	TGAACTCACTGTTGGTA TGGACTAGA	TGGACATGAT TGCATAGAC	CTGGACATGA TTACATAGAC	0,0	omy01	18131799
Omy_R AD7396 3-73	T	A	CCCTCTCAGGAAAGTGACCA C	GGATCATGTCAATCTGA TGAGTTGG	TTTCTTTTGGA	TTTCTATTGG A	0,0	omy01	23729539
Omy_m etA-161	T	G	CGCATGCACCAGTTGTAAGA AAG	AGTGCCACCAGCGATAA GAAAA	CAAGTAAGTG GTTATATTCT	CAAGTAAGTG GTTCTATTCT	0,0	omy01	24257340
Omy_R AD5063 2-21	C	T	CCTGCAGGCTGGGTCATTAT	GAGCCAGCTGTACCTTC TCC	TCAGCACCTC CAGCC	TCAGTACCTC CAGCC	0,0	omy01	38986533
Omy_R AD5791 6-29	A	C	GCAGGGCCTTAGAAACAGAC T	TACACGCCTCACTGTTC TGC	CAGGGGCAAAA ACGG	CAGGGGCCAA ACGG	0,0	omy01	44429931
OMS00 070	T	C	CGTTCCTGCGGGACAGT	GTTTCTCTCACGTCCAC AGATCT	CAAAATACGG AAATGCAG	AAATACGGGA ATGCAG	0,0	omy01	55279296
OMS00 003	T	G	GTGCCACTGATGAGGATGAG ATCA	GTAATAAAGCCCTTTTG TGAGGAAAACTAAT	CTTTACTGTCTG ACATTTTA	TACTGTCTGCC ATTTTA	0,0	omy01	59464348

Omy_gd h-271	C	T	AGGTCAGTCTACTTACAGTA TAAAGCAGT	GTCATGTCAACAGAGTA ACATAATAAATCTGC	TCACCCTGAA GTGTAGAC	TCACCCTGAA ATGTAGAC	0,0	omy01	637384 13
Omy_cy p17-153	C	T	GCCCTCCAAGTTCCAAGTGA AAA	CAGGTCATTGATGAAAC GTCAGAAC	ATACCTGAGT GTCATCG	ATACCTGAGT ATCATCG	0,0	omy01	645098 89
OMGH1 PROM1 -SNP1	A	T	TCAAACCTGCATTTGATGGAA ACAAACAT	AGGACAATTCTAAGTGA CCTCAAACCTG	TAGTGTTCACT GACTTCA	TAGTGACAC TGACTTCA	0,0	omy01	704664 74
Omy_G HIP1_2	C	T	TGCATTTGATGGAAACAAAC ATAT-TTATAATGTGT	CAAAAACAAGGACAAT TCTAAGTGACCTC	AAACTGTTGA ACGGTAGTG	AAACTGTTGA ACAGTAGTG	0,0	omy01	704664 83
OMS00 008	A	T	CCCTTTAAGGAGGATTTTAA ATATGTGAGATAGAA	GGATACAGCGTTTTGGA ATGAAACT	CTTCAAATATC CATAATTATAT C	TCAAATATCC ATAATAATAT C	0,0	omy01	773840 35
Omy_10 5385- 406	T	C	GTAACCTACCCTCACCTGAA CTTCA	GTCGCTCTTCTGGGCGT ATCG	CTTGGAACCA TTGCTAC	TTGGAACCGT TGCTAC	0,0	omy01	774461 33
Omy_st at3-273	G	-	CAGACCTCCTCTATCTCCCTA TGAG	ACCTCCTTTAAATTGTG CCCAAGAA	CCAGTTTG	TCAGTTTG	0,0	omy01	79XXX XXX
Omy_G 3PD_2- 371	C	A	GCAGGTAAGGTACACCATAG AGACA	CTCCCCCTGCCTTACCA AAC	AGACATGTGG ATTGGCA	CAGACATGTG TATTGGCA	0,0	omy02	608394 6
Omy_G 3PD_2.2 46	C	T	TCATGTATCAATTAAGGCAT TGTCTTGTCT	GTTAGACACAGTGACCA CCTCTTT	AGTAAAGCCC ATTGTTGAGT	AGTAAAGCCC ATTATTGAGT	0,0	omy02	608407 1
Omy_98 683-165	A	C	GCCATTGCCAGAGAATTTGG TTAA	AACACACGCACCATCTT AAAGC	AGCCAGATAC ATATTTGT	CCAGATACAG ATTTGT	0,0	omy02	855514 0
OMS00 156	A	T	GAGCAGAACACATAGAGGA AAGACT	GTAATCACCTCTTAGC CTGTATGG	TGTGTGTCCTG CTGTAACA	TGTGTCCTGC AGTAACA	0,0	omy02	123971 97
Omy_11 4587- 480	T	G	CAGATTACGTTATTACGTTTG GGAAATTTTAAAGT	GTGAAAGAGTGGGAAA TATAATTATAAGGTCAG A	CCTGTCCAAA ATTGT	CCTGTCCACA ATTGT	0,0	omy02	162045 63
OMS00 138	T	G	TCGGACCACATGAGCAGTTC	GTTCAACAGGTGCCCCAC AC	CTAACAATAA CCAAAGACTG	CTAACAATAA CCACAGACTG	0,0	omy02	223184 48
Omy_N aKATPa 3-50	A	C	GTTGAGCGTGTTATGGGAAA AGAG	TTGCATCGGCTTTCTGA AAACC	CACTCTGTTTC CTTTCTTT	TCTGTTTCCG TTCTTT	0,0	omy02	238931 57
Omy_R AD2504 2-68	G	T	GCTGCTGAAACTGGTTTGCA	TCATGCAGATGAGCTTC CCTG	AATTTCTGCCC AAA	AATTTCTTCC CAA	0,0	omy02	327931 23

Omy_cd 59b-112	C	T	TTTGGATAAGATTGTCTTATA TGACTAAAATGTCATGT	GCCAACGTCCTAGATAT GGTGTAAT	CTAAAAGCCT ATAGCAAACCT	CTAAAAGCCT ATAACAAACCT	0,0,6	omy02	389226 11
Omy_R AD2774 0-55	A	T	TCGGCCTGTACTAGTCTCACT	GCCTAAAATGGCCACTT TCATCA	TAACTTTTAAA AAAA	TAACTTTTAA AAAA	0,0	omy02	427459 63
Omy_u0 9-53,469	T	C	ACAGCCTGAGCGTTTGCA	GGAAACTGGGAGAGAT CAAAGGA	TTGCAGCCCTT ATTGTG	TTGCAGCCCT TGTTGTG	0,0	omy02	488598 83
Omy_R AD2091 7-11	T	C	CGTTGTCGTCTCCAATCAGG A	ACCAGCTCGATGCCATT GC	AGGTTGCGAG GTC	AGGTCGCGAG GTC	0,0	omy02	523844 97
Omy_m etB-138	T	A	TCTGTCCCTGACGCTATAAA AACG	GAAGTATTTTCAGCTTAA TTTCACTGTTGAGTT	TTCGCCAAAG AGAAAT	TTCGCCAAAG TGAAAT	0,0	omy02	537920 50
Omy_R AD9004 -13	G	A	TATACCACGCCTTCCCTGGA	CAGAGAGAAATCCCCCA CCC	TCATCTGAAG GGGG	TCATCTAAAG GGGG	0,0	omy02	540448 36
Omy_lpl -220	C	G	TGACAATCACTGAGCAACTG AACTC	GTCCAGTCTTGCTTCAA CTCATTCT	AGTGACAGTC A	AGTCACAGTC A	0,0	omy02	600228 13
Omy_R AD1610 4-20	A	G	ATTCCAAAACCTGCAGGGGT	TCAGGATTTGGTAAGGT GGCC	AGGGCAAAG[AT]CAAAGG	AGGGCAAGG[AT]CAAAGG	0,0	omy02	671193 13
Omy_R AD3781 6-68	A	T	CTCATTCCTGGCCGTCTG	CCACTCACACTGGCTTA TGC	GCGGCGTAAA AATG	GCGGCGTTAA AATG	0,0	omy02	735000 31
Omy_R AD4631 4-35	A	G	ACTGCATCTTTTCCCCTGCA	TGAAGATACCCAGAGAC ACCA	TAGCAATGGT	TAGCGATGGT	0,0	omy02	784801 58
Omy_R AD7320 4-63	G	C	CCTGGGCAATGACCTCCAC	AGCTCCCTTCTCTCTCCC TC	GTGCCCGCTCT CCACCG	GTGCCCCCTC TCCACCG	0,0	omy03	246702 64
OMS00 096	T	G	CATGAGAATGGATCAGTCTC CACAA	GATGAAATCTGAATGTG TTGACACTACAG	AAAGAGGAAG AGTCTCG	AAAGAGGAA GCGTCTCG	0,0	omy03	291093 94
Omy_11 2301- 202	T	G	GTAAACCCTGCCCACATAAT TAGGT	CTGAGACACTGCTCCAA GGT	AATGCGAAGA CAAACCT	AATGCGAAGC CAAACCT	0,0	omy03	375905 54
Omy_R AD3379 8-24	T	C	CAGGAGGGTCAAGTGGAGTC	TTGGGCCCTCTCTTTTTG GG	GAGTCTATCA AGAT	GAGTCTACCA AGAT	1,4,0	omy03	383366 51

Omy_R AD1349 9-13	T	C	GTTACCTGACGACCAAGGT	GCTGGGGGAGCTTTACA TGA	CGCCCTGTCC GCCA	CGCCCTGCCC GCCA	0,0	omy03	384089 41
Omy_u0 9-54- 311	C	T	GTGGCTCCCCAGGAACAAG	AAGTTTCATGTCACATT CCAGTTACCT	TGGTAATTATT CAACAGATCA GT	TGGTAATTAT TCAACAAATC AGT	0,0	omy03	429205 02
Omy_R AD5883 5-15	G	T	GTCTGCTAAGGTCCTGCAGG	GCCGACCATGAGAGACC TG	ATAGCTGCTG GGACCCA	ATAGCTTCTG GGACCCA	0,0.2	omy03	537353 38
Omy_u0 7-79- 166	G	T	CCCGCTATATTATTTGATCAC CCTTGA	ATTTAAATCCATTTCTA AAAATAAGCAAACCTA ACCA	ACTTGGGAAT ACCCAGCC	CTTGGGAATA ACCCAGCC	0,0	omy03	575236 76
Omy_11 7815-81	C	T	CTGCTTTATGCACACCACATT GT	GCTCTTTCTGGAGAACA AGGTACTG	CTATACGGAG ACCAGC	CTATACGGAA ACCAGC	0,0	omy03	678942 57
Omy_11 8654-91	A	G	CAGCGTAGACCGTTTCCTCA TTAT	GCGCCGATGAGCAGCTT	TCAGCTTGTCT TGCCGC	CAGCTTGTCC TGCCGC	0,0	omy03	754580 69
Omy_ar omat- 280	T	C	CTCCATTGATTCATGCCGAA CATT	GGAGAGGTCAAACATA GCCTGGTA	TCTTGCAAAC TCC	TCTTGCGAAC TCC	1,0	omy04	339146 9
Omy_10 5075- 162	T	G	GGAGAAGGACAAGGACATT GGTAAT	AAAGCAGACCACACCAT ACTTCTC	CTTTCTCTCCT ACTTTCC	CTTTCTCTCCT CCTTTCC	0,0	omy04	763533 4
Omy_m yoD-178	A	C	GGTCAAATATTTCAATTTACG ATTACACTTAGGC	TGGCAAAGCTGTCATTC CTTCTAAT	TTTTATGAGAT ATAATTTCC	TTTTATGAGA TATCATTTCC	0,0	omy04	105207 93
Omy_12 8923- 433	T	C	CTATGTCCTTGGCAGAAGTC TACA	ACGTTTCTTTGGGCTGA GACTTATT	CTTCATTTTCA TTCAGTGT	CATTTTCATT CGCTGTTTT	0,0	omy04	164362 34
Omy_13 0524- 160	C	G	CGAAGGTAGCGATTGGTCGT T	TGTCTGTTCTGCTGTGTG CTT	ATGGCTTGAT CCTCA	ATGGCTTCAT CCTCA	0,0	omy04	288890 24
Omy_R AD7778 9-54	T	C	AGACAAAACCTGCAGGGGA C	AGCACGTTAAAACCAAA CTGTCA	TAAATTATATT TGACAG	TAAATTACAT TTGACAG	0,0	omy04	309761 38
Omy_11 7286- 374	A	T	GTAACATTATGAATCTATCA GTTTCCCTAGCT	ACCTGCAACGTTAGAGC TGTTTATT	CTACTTTTCAC AGTAACACAG	CTACTTTTCA CAGTGACACA G	0,0	omy04	352504 73
					CTTTCCTCATC ATACTCTATG G	TCCTCATCAT ACACTATGG	0,0	omy04	523101 65

Oms00 087	A	G	GCAAATTTTACCCTTAACGT GGTTT	GATTTGATGTGTGTGTA TTACCTCCTCTA	GTTA[CA]AAC TGACAAAGTG TG	GTTA[CA]AGC TGACAAAGTG T	0,0	omy04	525119 64
Oms00 111	T	C	CATGCGGACCTGCATAGCT	GCTTAGCCATTGACAGA GCATATCA	CAACCAGACT ACCATTC	AACCAGACTG CCATTC	0,0	omy04	630315 81
Omy_R AD9248 5-64	T	A	CCAGTCAGTCTTGCCTCAGG	GGTCACCACAGGATTGG AGG	GTGTAGATAT ACAT	GTGTAGAAAT ACAT	0,0	omy04	683184 64
Oms00 116	T	A	GCCTTTCTCCCATATCACATT CGA	AAACGCATCTTACACTG TGTTGTG	CTTTTACATTT TCAATATTCTG	TTTACATTTTC AATTTTCTG	0,0	omy05	113417 54
Omy_R AD1307 3-16	G	A	GTGAGGGATCACACCTGCAG	GCACCCATTTCGTAATGT CCC	AAAGGGGACA TTACG	AAAAGGGAC ATTACG	0,0	omy05	139545 98
Omy_11 0362- 585	G	A	GCAGCCAAGATGAACGAAA ACTTC	CCGGCCTGGGTCTCAAT G	CACCGCCCTG CCCGT	CACCGCCTTG CCCGT	0,0	omy05	143072 79
OmyR2 4370	G	A	TCATTACCTACGCAGTGGAG	ATCTCTGGGCCTGAACA AT	ATTTAGCAGG AGGCCTCTCC A	ATTTAGCAGA AGGCCTCTCC A	0,0	omy05	285793 73
OmyR4 0252	T	A	ACTCTGAATTCCTCAGGCTT	TCGAACCAGCTGTCTTT CT	AATGCTATATT GAACCTTAA	AATGCTAAAT TGAACCTTAA	0,0	omy05	316752 78
OmyR1 9198	T	A	GTAACCATGACATCCACCAA TC	CCTATGCACAAAGCCTT CAC	ATCCCTGTTAT CTAATCATT	ATCCCTGTAA TCTAATCATT	0,0	omy05	349734 85
Omy_R AD2389 4-58	A	T	TGCAGAAAGGCTGTGTGGAT	TCTTAACACAGTCCTCA TGGAACA	GTGGATTAGG GG	GTGGATTTGG GG	0,0	omy05	409271 21
OmyR3 3562	G	A	CAGGAGTAATGCATCCCAAT G	CAAGTTGATAACGAGAC ATAAGGG	TAAGACTTGG CATAAGCATG	TAAGACTTAG CATAAGCATG	0,0	omy05	473375 40
Omy_bc AKala- 380rd	G	A	TTGCTCTCTTCTGGTTGCCTT A	CTTCAGGAGAAAGCGCT ACTGT	CATACCCATC CTATGTCAG	CATACTCATC CTATGTCAG	0,0	omy05	534692 95
OmyR1 4589	A	G	GGTGACTGAGCTGGATGT	TTTAGAGAATTTGGCAG TACGTC	GTGGTTACAA AGGGTCTGCA	GTGGTTACAA GGGGTCTGCA	0,0	omy05	561627 85
Omy_u0 9-61.043	A	T	TAGTCACATCCATAGTAATA CTTCC	TGTTTCAGAAGCAGAAAA CCAATCTCT	CACTTGCTCCT TTTTCA	CTTGGTCCAT TTTTCA	0,0.4	omy05	588408 10
Omy_R AD3039 2-17	T	C	CCACTACTCACAGACCTGCA	GCTCAAGGACCAACAA AAAGCT	CTGAGACTGT GTGT	CTGAGACCGT GTGT	0,0	omy05	617726 69

Omy_S ECC22b -88	T	C	GGATCCCTCCTTTTAACACA AGACT	CTACAGGATGACTACCT AATTGCTAATAAAACA	CTGTCTGTCCA TATATC	CTGTCTGTCC GTATATC	0,0	omy05	618289 03
OmyR4 0319	C	T	AAAGATTGCTGCGATGTCTA AT	CGCAGAGAACAGAGGA TGA	TGCAAGTGC[T A]GCCCTTTTA T	TGCAAGTGC[TA]GCCTTTTT AT	0,0	omy05	631589 19
OMS00 169	A	G	AGCACTTGACTCAAACAC ATAAATCA	CTGAGACAGGAAGAAC AATGTTAACAAAA	CAAAAAGCAT TGATATCAAT	AAAAGCATTG ACATCAAT	0,0	omy05	675681 74
Omy_R AD8513 1-35	T	C	TTCAATAACTACAGGCAGAT GGT	AGTTCCCAAATGCACTG TACA	GATGGTATGG TGAG	GATGGTACGG TGAG	0,0	omy05	755346 97
Omy_10 9525- 403	A	G	CCTCATTCTCATTGGTGAGTT GTCT	TGTAAGATCTGACCACA TGAGTATAACCA	CCTACACCTCT TTTTTCCACA	CCTACACCTC TTTTCTCCAC A	0,0	omy05	842248 92
Omy_R AD4357 3-37	A	G	TGCAGGGAACGATGAAACCA	ACAGACACAGCATTGGC CAA	GAAAGAGAGA GTTT	GAAAGAGGG AGTTT	0,0	omy06	174595 4
Omy_10 5714- 265	C	T	CCACTCAGTGCAAGCATGGA	GCTTTCAATCCTTGGCT CCAATATC	CTGTTGTTTGA GGTTCAG	TGTTGTTTGA GATTCAG	0,0	omy06	759484 7
Omy_10 7285-69	C	G	GCCCTTGTGACAATGCACTG TTATA	AGGTCTAGACAGTGTGC CATTTG	ATACGTTACTT TTGACCTTGT	ACGTTACTTT TCACCTTGT	0,0	omy06	980915 6
OMS00 013	A	G	GCCTTTGTTCTCCTTGGTGGT TA	AGAAAAGTGTGGACTG AGGTTGAG	CTTCTTTTCCC TTGCTACTC	CTTTTCCCTC GCTACTC	0,0	omy06	103252 71
Omy_R AD3541 7-9	G	A	GCACTTGACCACATAGCTGG	ACTCCACACTCCACAAA GCA	TGCAGGACGT GCTTTGT	TGCAGGACAT GCTTTGT	0,0	omy06	158675 14
Omy_b9 -164	T	-	GCACAGAACACAGCCAATAT TAACA	GCCTTGACTCTCCCTTC ATGAC	CCTACAACCTT GATCTAACGT G	CCTACAACCTT GATCTACGTG	0,0	omy06	175997 31
Omy_R AD4795 5-51	G	T	AGTGTGCTAGAATGGGCCTG	ACCATGGGCAGTTCATT TCA	TTGGAATAGA ATCTATA	TTGGAATATA ATCTATA	0,0	omy06	231917 48
Omy_va mp5- 303	A	-	CTGCTTCCCAATTCAGTATCG TCTT	AGGCTGAAGCATTTCTG AGTATGAA	TGGCCGTAGT AGTTGGTCA	TGGCCGTAGT TGGTCA	0,0	omy06	336251 38
Omy_st ar-206	A	G	CGTGTGCCAGCCCTTCT	GACCACTGAGATCATTG CTGTGA	TCTTTGGCACT ATATCT	TTTGGCACCA TATCT	0,0	omy06	366248 63

Omy_R AD6863 4-40	A	C	TGCAGGACTCCTTTGAAACG T	TAACGCCAGCTGCATGA TGA	CCTCTAAACT GAAT	CCTCTAACCT GAAT	0,0	omy06	402608 00
Omy_R AD3695 2-53	C	A	TGTACGTCATTGGGGCTGAG	CCTACCAGACCACACGA TGA	AGGACATCTT CATC	AGGACATATT CATC	0,0	omy06	402609 70
Omy_IL 1b-163	T	G	GGAACAACAGGATTAAGCCT ACTCT	CCTAAAGGCCTAGGAAA CTAAACTTCA	CTGAGGTCAT AAAAATA	CTGAGGTCAT ACAAATA	0,0	omy06	423131 29
Omy_R AD7016 -31	C	A	GCAGGAATATTCACTGTTGC CA	TCTAAAATGTCGTTGGC GGC	ATAATTTTCATT TAA	ATAATTTAAT TTAA	0,0	omy06	514907 60
Omy_R AD6013 5-12	C	G	AGCATACACACCTGCAGGAA	TGGTAGGAGGAGATGCT CTGT	GAACATACCG GAAC	GAACATAGCG GAAC	0,0	omy06	561100 72
Omy_R AD3514 9-9	G	A	GAGTCAATAGAGCCCCCTGC	TGGTTAGCAGGAGCAAT CTCA	GCGCGCTTAT GTC	GCGCACTTAT GTC	0,0	omy06	601825 01
Omy_R AD3915 6-33	T	C	GGGTGTGACATGTGTGCAGA	ACTGCTTGTCCCCACCA AG	ACCGTAATGG AGAG	ACCGTAACGG AGAG	0,0	omy06	468XX XXX
Omy_R AD366- 7	C	A	ACCAAATTAGAGCCTGCAGG A	GGAGAGGCCTTTCCGTG ATC	CAGGACTTGC TTTT	CAGGAATTGC TTTT	0,1.4	omy07	623006 6
Omy_m apK3- 103	A	T	GAAGTCATTACTGGTCAGTG GTCAA	GCACAAAACATGAGGA AAGTTGAGA	AATTATTAAG CCTATTTTTTT	ATTATTAAGC CTAATTTTTTT	0,0	omy07	109757 16
Omy_O myclmk 438-96	A	C	CCCGACTCTACTTCACTACTT TCCT	GGCCTAGGACAATAGG ACTGAAC	TACGCAAATT AGGTTTAAA	CGCAAATTAG GGTTAAA	0,0	omy07	109760 28
OMS00 176	T	G	GTTGGAAGTTCCGGTGGTAG AG	CTGGGTCCTGAAGGAGC TT	TTCCAGCACT GCTGTC	CCAGCCCTGC TGTC	0,0	omy07	110291 67
Omy_13 1460- 646	C	T	GTGAAAAGGAATGGAGGAG TACAGT	TGCTAGGACAGGAAGAT CATTTGTG	AATAAAGCAG AATTTGTTACT G	AAAGCAGAAT TTATTACTG	0,0	omy07	366000 38
Omy_R AD3061 9-61	T	A	CTGCAGGTCAATGGGTGCTA	ACACTGATCACATTTTT GTCACACT	CACTGTAAAA	CACTGTAAAA	0,0	omy07	427104 19

Omy_R AD2567-8	A	T	CTGTCTGGATAGCCTTGCCC	TCTATCTCTGGGGAAAA TAGCCC	GCAATGGGCT ATTT	GCATTGGGCT ATTT	0,0	omy07	437932 41
Omy_p ad-196	C	T	CAAACAACCACAGTAGTCCT CCAAT	GCTTTTCACCCTTTTGTA AATTAAGCCAAA	AAGACAAAGG TGTAATACC	AAGACAAAG GTATAATACC	0,0	omy07	444706 19
Omy_R AD1243 9-64	G	A	GGAACTTTTCACATCATGTT GACTG	GCACAGAGAACTCCAG GCAA	CTTCTCCGATG TCA	CTTCTCCAAT GTCA	0,0	omy07	445378 93
OMS00 064	T	G	GTGGATATGTAGTTCGATGG AACAGT	TTTACAACAATCTTCTTT TAATAAAAAATATAGCCA CTTAT	CAGGCAACAT TTTATATAACT A	CAGGCAACAT TTTATCTAAC TA	0,0	omy07	452277 50
Omy_R AD6259 6-38	A	T	GCAGGACACTGGTTCCCAAA	CCTGAGATTTGAGATCA CTGGCT	TTAAAAAATA TATATTA	TTAAAATATA TATATTA	0,5,0	omy07	499777 94
OMS00 154	A	T	GATGTTGGCTGGAGGTGTAG T	TGGGAACACTTTGCCTA CCC	ACAGGGCTTC TGATTGA	AGGGCTTCAG ATTGA	0,0	omy07	562345 73
Omy_sy s1-188	C	A	CTTAAATGGTGCTGGTTGCT GTATT	AGTGATATCTTAGTGGG TCGAGGAAA	AAACATGTAC GACCTGTC	TGTAAACATG TACTACCTGT C	0,0	omy07	564287 76
Omy_ar p-630	G	A	CTGCACAACCTGTTTCCTGCT ATT	ACCAAGTGTCCTGTAA GCC	CCGCTCCGTCT GCT	CCGCTCTGTC TGCT	0,0	omy07	572397 51
Omy_m yclarp40 4-111	T	G	GCTGTGGTGCTCATGGGTAA A	CCAGGGCAGGGTTGTTC TC	CAAAGCCATA CGTGGCC	AAGCCATCCG TGGCC	0,0	omy07	572399 57
Omy_R AD2976 -26	G	A	AGGACTGTGATCCTCTCAGC T	AGCTCTGCTGAAACATC AGTCT	CAGCTGGGTT GAGA	CAGCTGGATT GAGA	0,0	omy07	583371 26
Omy_97 077-73	T	A	GTGTAAACAAAATGACTCTG GGATTGAG	AGAAGTGGCAATGGTGT GAAGTAT	TGGTGCAATA GAAATA	CATGGTGCAA TAGTAATA	0,0	omy07	618754 65
Omy_R AD7384 -50	T	C	GACACGCCCTCAGCCAG	CTGGTACCTTCCTGCTG TGG	GCCTCTGGCA G	GCCTCCGGCA G	0,0	omy07	652417 84
OMS00 057	T	G	GAGAAAGGGAGCATGAGAC AGA	GTTGGGCTCCGGTACGA T	CTCCACAGAA CCTTG	CTCCACAGCA CCTTG	0,0	omy07	679081 35
Omy_10 5105- 448	C	T	CAATTTGCAAGCAGGGAAAG GTTAT	GTGATGGGCTGCAATTG CTT	AAGGAGAATG CATAATC	TGAAAGGAG AATACATAAT C	0,0	omy07	683035 84
Omy_cd 28-130	T	C	CACAACTCCACAGAGACAGT GA	GAGGACAAAACCTGACC GTATGGT	CCTGTTTCATTC ACCC	CTGTTTCGTTT ACCC	0,2,7	omy07	190XX XXX

OMS00 132	A	T	GTTTATGACTCCATTGCCGA AATGATT	ACGCGACCTGCAATTCA TCAATA	CAGCAGTCCT CTGTGTGG	AGCAGTCCTC AGTGTGG	0,0	omy08	945135 0
Omy_hs p90BA- 193	C	T	GGAATCGATGACGACGAAGT GATC	TTCCTCCATGCGTGATG CA	CCTCCGCGCCT GC	CCTCCGCACC TGC	0.5,0	omy08	106673 61
OMS00 153	T	G	ACTTTGCACCATAGGCTTGA CAT	TGATAAGGATGATCAAA AAGCTGAAGTATGTA	ACAAAATGTA ATTTTCC	CAAAAATGTCA TTTTCC	0,0	omy08	163033 16
Omy_hs f2-146	A	-	CCAACAATTGCAGCCTCATC TTAAT	GGAGCAGAAAAAAGGAT TGGACCTT	ATAATCTACT A	ATAATCTAAC A	0,0	omy08	174703 64
OMS00 068	A	G	GCACTAACTGGACAACATTT TTAAGAATGA	GGCAGTTGAGCATTTTG GGATATT	AATATGCCTC CTTCGTCTC	TATGCCTCCT CCGTCTC	0,0	omy08	174880 38
Omy_sr p09-37	C	T	TAGTTGTATTAACCTCTTCTTT GAGTCTAGA	TCATTCCAGCTCCGTTCT CTTC	TTGTGCTATTG ACGCCACAG	TTGTGCTATT GACACCACAG	0,0	omy08	214268 23
OMS00 151	A	G	CTAACGTCTTCCCAATGATA TTTCACAAGATA	ACCGTGGAATACAATT TTTTATGCCAAT	TCATGACCTTG ATAATC	ATGACCTCGA TAATC	0,0	omy08	239492 30
OMS00 179	A	C	GTCATAACAAAATCAGGGCT TTCCAA	TGGGAGATTTGGGCTGC TTTAAA	TGCCTCTTCTC TTTTCTCAT	CCTCTTCTCTT GTCTCAT	0,0	omy08	255399 30
Omy_R AD2428 7-74	A	G	ATTGTCTGTCTGCCGAGGTG	TGGCGACCTGTCACTAA TGC	GGTCACTACC TCCC	GGTCACTGCC TCCC	0,0	omy08	280357 34
Omy_12 0255- 332	A	T	GCTAGCTAACATTGAAGGGT GGAAT	GGCTACAGGGACTTTAC AATGGG	ACTATGCCAT GAAGTTA	ACTATGCCAA GAAGTTA	0,0	omy08	291028 20
Omy_R AD2823 6-38	T	C	GGCACACATCTGTCCCGTAG	GCACTAAGGTCTAGGAG CACG	ATCTGTCTTCG TGC	ATCTGTCCTC GTGC	0,0	omy08	403994 99
Omy_R AD8670 6-72	C	T	TTCCCTGTAACTGTCACGCC	CCACATCACACCCTGAC CTC	TACGTTTCATT TCT	TACGTTTTAT TTCT	0,0	omy08	404794 21
Omy_10 4519- 624	T	C	CGTGTGAGTTTGCGGTAAAG AC	TGACGAGTCCGTCTTAT CATCCT	CAGCAGGATA CATCCGACT	AGCAGGATAC GTCCGACT	0,0	omy08	427641 23
Omy_10 8007- 193	A	G	GTGAATACCACCCAGGCTTG T	GTCCCTTCCCCAGTTTC ACTTAATT	ATGTTTTCTCC CTACTTAAC	TTTTCTCCCC ACTTAAC	0,0	omy08	436719 91
Omy_co x2-335	T	G	AGCTGGGCTGTATTTGTCAA TACTT	CAGCCCGCCACTGTCT	CTTTAAAGAC AAAGACTTTA T	TTTAAAGACA AAGCCTTTAT	0,0	omy08	508226 29

Omy_R AD1890 3-48	A	G	GGGGATGAGTTCTTCGGTGG	CCACCAAATCCCCGAA GAA	AGGAGACACC A	AGGAGGCACC A	0,0	omy08	610392 08
Omy_nk ef-241	C	A	AGTGTCATTGATGTCGGCCT ATTTT	AAACGAATGTCCACCTC AGATGTT	CTTCTGTATCA TTTTTG	TCTTCTGTAT AATTTTTG	0,0	omy08	694270 37
Omy_97 865-196	A	G	TCCAGACTTCTGGTTTGTTC ATT	CCAGCCCCATATTCAC AATTAAGTGT	ATTAATTAAC AAGCTC	ATTAATTGAC AAGCT	0,0	omy08	825133 44
Omy_rb m4b- 203	-	T	CTGAAATTTGATGAATGGAA GCTGCA	CGTATTCAAGTCGATAT ACAGTCACGAT	CACGTTATTAT GAAAAGGATG T	ACGTTATTAT GAAAAAGGA TGT	0,0	omy09	124851 17
Omy_11 2820-82	G	A	CCTTTCCTTTTGCATTTCTC TACTTATTTATTT	AAATGAACTCACGTTGA CCTCTGA	CGCCGCCAAG TTA	CGCCGCTAAG TTA	0,0	omy09	218612 64
Omy_R AD6595 9-69	G	A	ACATTTTGGTGTAAACAACC CTGT	GCTAGCGAAGACCCTGA AGG	TTTTGTCTGTT CTT	TTTTGTCATTC CTT	0,0	omy09	363384 72
OMS00 103	A	T	GAGATCACTGTAGGATTGGC TGTTT	CCTCAGAGCAGCTCACA ATGGCATC	CTCCACAGTA ATTTTTTTTT	CCACAGTAAT TATTTTTT	0,0	omy09	383356 92
OMS00 056	T	C	TCAGGAAGTAAACTGAAAAT TCCAATGTATGA	CCCCAACCATGCTTGTT ATTGAAC	TAGCTTGACC AAATAGCA	CTTGACCGAA TAGCA	0,0	omy09	437713 25
OMS00 175	T	C	TTGCGATATGGGACTGTATA CATTTATTCC	ACTACCTCCAGTTAAAA TAGTGTGGGAAA	ATCACTAGTTC AAATACAA	ATCACTAGTT CAGATACAA	0,0	omy09	503817 07
Omy_tlr 5-205	T	A	GAGCGTATCTGGTATGGTAA CAACA	CTCCAGCAGCTTTAGAG AGTTTACA	CAGTAATATTT CAGTGCCCG	CAGTAATATT TCTGTGCCCCG	0,0	omy09	605104 83
Omy_11 4315- 438	T	G	CCTCACCGATCTAGTCAACT TCATC	AGGAGGCTGAGGGAGA TTCTAG	TTATGGGCTTA AGGGTC	TTATGGGCTT ACGGGTC	0,0	omy09	645645 08
Omy_gl uR-79	C	T	GACTGTCTATAGCTATTCTTC TCAAACGTGT	AGAAACTACCATTGTGA TTAACAGATAGAAAATA CAT	CAAGTATTTTG CGTAGGAAT	CAAGTATTTT GCATAGGAAT	0,0	omy10	750822 1
Omy_R AD3213 9-58	G	A	GCAGGAAACAGGTACAAAG GA	TGGCTTCTTCCTTGCTGA GC	TCGACATGAC CTGA	TCGACATAAC CTGA	0,1	omy10	107738 03
Omy_10 9894- 185	T	C	GGGAGGAATTGGAATGACA GATTAAC	CGGTGTCATTATGGTTG TCATTGTG	CTCCCTGATCC CCC	CTCCCTGGTC CCCC	0,0.5	omy10	108522 82
Omy_R AD6640 2-36	T	C	GGTGTGATACCTCAGAGCTC TG	CGTCTCCGGATCGTTCA GAG	AACCACTTCTC TG	AACCACCTCT CTG	0,2	omy10	303720 84

M09AA E.082	T	G	CTATGTGCAGTGCCCTTCTCA	GGCTTACAAGTATGCAT GACTAGCT	AGGTTGTTTTA CAAATTTAA	AGGTTGTTTT ACACATTTAA	0,0	omy10	328727 04
OMS00 095	A	T	CTCCAATGGCTGTCAACAAT TAAATATAAGAC	GTGTGCTGGTCTCTTCTT TTATTCTCA	AGGCAACTAT ATATTTTTTT	AGGCAACTAT ATATATTTTT	0,7,0	omy10	387046 54
Omy_R AD2608 0-69	G	A	TGTGGGACAGCACATACTCC	CCAGGACACCAGTGGA GAAG	ATTAGTAGCA TCATCGAG	ATTAGTAACA TCATCGAG	0,0	omy10	404866 18
Omy_R AD1073 3-10	A	G	TATAGACCCCCTGCCAGTCA	ACAGAGAAACCCCCGTC ATT	AGGGTGAAGA ACTG	AGGGTGAGG AACTG	0,0	omy10	414117 54
Omy_ftz f1-217	A	T	ACAGGGATGGGCAACTTTGT T	GGATGACCCACGTGACA CT	TCATGACGAG TTCTGATTT	TGACGAGTTC AGATTT	0,0	omy10	440609 19
Omy_p5 3-262	T	A	CCCCAACATCCAGTATACAG TTTCA	CCCAAATTGGCAATTTT AATAGGATTCAGA	CAAGTAGTAT GGAGCTCTAT	AAGTAGTATG GTGCTCTAT	0,0	omy10	461908 22
Omy_tlr 3-377	C	T	GTCGCTCCGGGTGCTT	GGCCCAAACACTTCCTT CCT	CGTGATTAGG TTCTTC	CGTGATTAGA TTCTTC	0,0	omy10	564470 78
OMS00 106	T	G	CGTGTAGCATTCTTGAGGAA GCTT	TTTCCAACAGATGCCAG AATCCT	TCTGATGGAA ACTTTC	TGATGGCAAC TTTC	0,0	omy10	598556 97
OMS00 030	T	G	CCTCGTGACTACAGAGCTAT ACAAC	GATCTGATCGGTCGGGA GAGA	ATGAGGGTCC CTATACAGG	ATGAGGGTCC CTCTACAGG	0,0	omy10	604014 05
Omy_U T16_2- 173	C	T	ATTGACTCATTATCACCTTAG TTGTAGCTTCA	GCAGCTACTTGCTGTAT CACATGTTTGT	ACAGTCAACA AGGGACTTAA	ACAGTCAATA AGGGACTTAA	0,0	omy10	614962 64
Omy_R AD3684 8-7	G	A	CGAGGACGTTCATAGGGAGC	TCGATAAGTCCACCAGC TGG	TGCAGGGACA CCACCCT	TGCAGGAACA CCACCCT	0,5,0	omy10	636507 47
Omy_R AD5374 -56	A	C	GCTGTTACCGTGTGATGTTG A	AGAGTTCTGGCCTCTCC CTC	AGAGGGAAAAG AGAG	AGAGGGACA GAGAG	0,0	omy11	618693 7
Omy_g1 2-82	T	C	GATCAATTTCGATCGCTCATG AAACTT	CTTCTCTCGTTCTCATTG TGTCTCA	CAAACCTCTCA GGATTAG	AAACTCTCGG GATTAG	0,0	omy11	147648 07
Omy_B AMBI4. 238	T	C	CATGATGAGGAGGACCAAG ATGAG	AGGTGTGGTTCAGGGCA G	CACCGCAATC ACCG	ACCGCGATCA CCG	0,0	omy11	244110 85
Omy_M YC_2	T	C	CGGTTGCAGAACTCTCATGT TTG	CACGCCATGTCTTAACT TGCATTA	CATAGACTTTT TGACCTTAT	CATAGACTTT TTGGCCTTAT	0,0	omy11	338412 60

Omy_R AD7850 2-57	T	G	GAGAGGCATCCTGTCTAGGG	ACCATGCTCTTTCTGTG GGTGT	GGAAATATCA CACA	GGAAATAGCA CACA	0,0	omy11	370317 57
Omy_B AC- F5.284	C	T	CCTCATTTACTGTAGGACCA TGCA	ACAACGCCAACAACCTTT CTCTTG	CAGTAGGGCG GCAAG	ACAGTAGGAC GGCAAG	0,0	omy11	427893 02
Omy_co x1-221	T	A	CACTGAACTGTAAGCCATTG TGATT	GCAACATGGGAATGATT CATAAATGCA	CGGTAAGACC ATTAAAA	CGGTAAGACC ATTTAAA	0,0	omy11	470523 10
OMS00 120	A	G	GGCAGAAGAGGAGAGAGAT ATGATTG	CCTCAAATACCTCTGAC ATTGAAGGTT	C[GA]CCCAC AAAAC	C[GA]CCCACC AAAAC	0,0	omy11	510131 77
Omy_R AD4279 3-59	T	C	CACGGCTAGTGGCATGTACC	CCACACCTGCATCAGTC TGT	CAGAGAATGC CAACAGA	CAGAGAACGC CAACAGA	0,0	omy11	514085 22
Omy_10 2867- 443	T	G	CATTTGTTTAATTTGATTTGG CACAACCTCA	CCCTAGTTCTGTAACAC AAGACGTAA	TTTGGGTACAT AATTTTT	TGGGTACATC ATTTTT	0,0	omy11	559343 32
Omy_ox ct-85	A	T	CGTCACTGAAACATTACTGT AACATCCA	CATCATCACGCTGTTGG TTTCTTAA	CATCGCTTATT TATGC	CATCGCTAAT TTATGC	0,0	omy11	684058 94
Omy_11 7540- 259	T	G	GGCAGGTTAACACAGTCATC TACTATAAA	CAGCATGTTGCTTTAAT CCTTCACA	TGTCACTTCAA AGTTTG	TGTCACTTCA ACGTTTG	0,0	omy12	507937 1
Omy_11 0201- 359	T	G	GGTAAGGCCTGTCTGACTAT TTTGA	AGAGGTCAATGGATGCC AGTTT	TTTGGCTATTG AAATTATACA TT	TTGGCTATTG AAATTCTACA TT	0,0	omy12	287279 52
OMS00 074	T	G	CCTGTTTATTCATCTAAACCA GTTCTTTAAAAT	AACTTAATTTAGCAAAC AAATGTCTGAACAGAA	TGAAACAAAA CAAATGTTCC	AAACAAAAC ACATGTTCC	0,0	omy12	311047 27
Omy_hs c715-80	C	A	CCGGTCTACCCTATAGCTGTT G	AGTCAGTCAATTAGTGG TTTGAAATACTATCA	AACTGTATTTG GGAAAAT	ATAAACTGTA TTTGTGAAAA T	0,0	omy12	401363 09
Omy_R AD2669 1-36	A	G	TGCAGGAAACCGTCAATCTA CA	CAGGAATTAATTGTATG GCCGGA	TCTCCTAACA GAAC	TCTCCTAGCA GAAC	0,0	omy12	472849 87
Omy_R AD3840 6-19	T	A	CTGCAGGGGTATTAGGAGGC	AATGAGTTGTGGCGGTG AGT	AGGCTTTATAT GGCC	AGGCATTATA TGGCC	0,0	omy12	481811 30
OMS00 077	C	G	AATACCATCTTGAGCTCATT AGTAATTATTCAA	CCAGACTTTACACACTC TTGACTGA	TTCCGGTGGT GAAGTT	CCGGTGCTGA AGTT	0,0	omy12	488619 50

Omy_R AD1919-22	A	G	CAGGTCACAGACACACAGGG	CTACACCACCCACGTTCTG	CAGGGAGGAGG	CAGGGGGGAGG	0,0	omy12	53383757
Omy_ndk-152	A	G	AAGAATTGAGGGATAAAAA CAAAATAATATATAAACATGA	CAAACCTACATTCATTA AAGTCCAGTTTTGT	ACCCACTTTCAAAAC	ACCCACTCTCAAAAC	0,0	omy12	56277959
Omy_R AD76570-62	T	G	GCAGGTAGGTAGGAAGGAAAGC	TCTGACTGGTATTGAAA GGACCA	AGAGGTGTTCTGGT	AGAGGTGGTCTGGT	0,0	omy12	56297752
Omy_gh-475	C	T	AAGTTACCAGAATTTTGCAA ACTCAACT	CCATATTTTGAGGTGTA GCTTTACCCT	CTGAAACTCATGGTATACA	CTGAAACTCATGATATACA	0,0	omy12	62308122
Omy_R AD33122-47	G	C	CAGGCTTTGTGGACATGTGC	GTGCTCTATCTTGCTCTTGGC	CCACAGGGTG GTGC	CCACAGGCTG GTGC	0,0.6	omy12	66078752
Omy_hsp70aPro-329	A	G	TGCGTATTATTGTTTTTCAAG GACTTTCAAA	TGAATATTTTCAAATAC ATGCCAATTCTTTCCAA	ACATTCCAATATTCAACTAT	CATTCCAATATCCAACTAT	0,0	omy12	66828836
OMS00053	T	C	GGAGCCAGGTCAAGGTGATC	GGATGTCTGGTGTGGCTGTAAA	ATTTATATGTATCAATCA	ATTTATACGTATCAATCA	0,0	omy12	66917868
OMS00112	A	T	TGGCAGCAAAAAGGGATGCA	TCCTGAGCAACCAGTCAACATT	CCGGTTTCAA GTTTACTTGT	CGGTTTCAAGTATACTTGT	0,0	omy12	68382081
Omy_111666-301	T	A	GGGTGAAAAGAGTGGGACATTTACA	GTCAATTTCAAGGCACCAGACAAT	AGTATAACACAGTAAGACAA T	AGTATAACACAGTTAGACAA T	0,0	omy12	70990844
OMS00149	T	G	GGCATCATTGTTCTTGCTCTGTTTA	CCTGGGAGGGTTTATATCGGAGTAT	GCTAAATGCACAG	GCTAAAGGCACAG	0,0	omy12	6589XXX
Omy_R AD66834-17	C	T	CTCCTGCAGGTCATCTCTGG	CTGTCTTGCTCAATGCTG	TCTGGCTGACACCTTTA	TCTGGTTGACACCTTTA	0,0	omy13	10112620
Omy_118175-396	T	A	AGGCTTCACACACACATGCA	GACGCGCAACCTCTAGATTATACTT	CTCTTGACAGATACCCGTA	CTCTTGACAGATTCCCGTA	0,0	omy13	20282478
Omy_129870-756	C	T	TCGTTATTTTGCTCGCGGTA	TCCCATGAAGATGTATACATGTTTGTGA	ACAGGTATTTCTGAAATG	CAGGTATTTATGAAATG	0,0	omy13	22915161
Omy_113490-159	C	T	CATAGTACATTTACAGATAATGTTTTAAAGTGCATGT	CGAGATACCAAAATGCCACAGTTACAT	CATCTGTTTTGTGTTAGC	CATCTGTTTTAGTTTAGC	0,0	omy13	26494831

Omy_nach-200	A	T	CTCATGAAAAACGGGAGAGCAAAG	CAGCGGCTCTTCAGTAGTCT	AACTGACAGAGTCACAAC	CTGACAGAGACACAAC	0,0	omy13	30001796
OMS00180	T	G	GCGCCGAATGGCATTAGG	CACATTGCTGTCGTTTAGTTGACT	CTAAAAGTGCATTAAGCC	CTAAAAGTGCCTTAAGCC	0,0	omy13	32462775
Omy_110064-419	T	G	GTGCAAGGGACCTAGCTAATCC	TCTGAACTGACACTGAA GAACAAAGAA	ACGTTAGCTTTTAATTTTC	AACGTTAGCTTTTCATTTTC	0,0	omy13	36272850
Omy_g1-103	T	C	AGTCGTGACAATGAGAAACAGTGTT	CTCAGCAAAAAAGAAACGTCCCTTT	CCTTTTACAATGAAGATC	CTTTTACAGTGAAGATC	0,0	omy13	39287232
Omy_IL6-320	C	T	CGACTGATCTCCTGCAGACATG	CTTGTTCCCTCGTTGTCTTCCTTCTA	CTATAGGAGAGAGGACAACA	ATAGGAGAGAAGACAACA	0,0	omy14	7102407
OMS00089	A	G	GCACCATTTGAATAAAAAATCTGCTTTGT	GCAACCCAATTCAATATTAAGCACATGAT	ATGAATCCCAATAAGAAC	AATCCCAAACAAGAAC	0,0	omy14	13150534
Omy_hsf1b-241	A	-	AGCCCGAACTATCCTAAAGCATTTT	AAATCAATAGCTCAGAGATAATGAACACCA	CAGTGTTTTGTTTTTGTGTCATT	AGTGTTTTGTTTTTGTGTCATT	0,0	omy14	14516742
Omy_116733-349	C	T	GAAATGGACATGCCTACAAATTGCT	GATGTGATCAGTTTAGGCAAGGC	AGAGAATCTGATAGTATTTTC	AGAGAATCTGATAATATTTTC	0,0	omy14	18498042
Omy_ntl-27	G	A	GGTGTGTTACTGTAGTTGTGTCCTT	TGTGTAGCTAGTGATCC TGATTGTCT	CAGACAAGAGTACCCCAAGAC	CAGACAAGAGTACTCCAAGAC	0,0	omy14	22071034
Omy_txnip-343	T	C	CCTTCAAACCTAACGCATCATAGACATG	GGTCACTTGGCTAATCCCTTAT	AACTGAAGAGATCTG	AACTGAAGGGATCTG	0,0	omy14	24435825
Omy_UBA3b	A	T	GCCACTCAATGCATGTGTTTTCTAG	CAGCTAGCTTAAGTGGGATGCAA	TGGAGATAACGCTAACTATT	AGATAACGCATAACTATT	0,0	omy14	28552649
Omy_RAD55404-54	C	T	GCAGGGTGTCCACTACAGAC	AGGAGTCCTGAGAGTTGGC	ATTGTTTCTGAGG	ATTGTTTTTGAAGG	0,0	omy14	43876869
Omy_RAD12566-14	C	T	GTGGACATTCCTGCAGGGAT	TCCCACAAATATTTTCATACGCACA	ATGTAAACAAATTG	ATGTAAATAAATTG	0,0	omy14	44125336
Omy_RAD3926-22	T	C	CGTTCCTGCAGGCTTTTCAC	TTGGCACAGAGAGTACGCAG	TTCACTTTTCCCTG	TTCACTTCTCCCTG	0,0	omy14	45345547
Omy_mcsf-268	T	C	CCAGCATTCGTTCCCATTTCC	CTTTTAATGTAGATTATATTCTTCTGTAGCCACTATGG	AAATAATAGATAAA[CT]CCT	AAATAACAGATAAA[CT]CCT	0,0	omy14	48758470

Omy_10 1554-306	T	C	GCCTGTATTTCTCCTGTATGT GCAT	TCAACTTTTGCAAACCTT TTTTATTCTTTGTCAATTT	TGCTTCTCAC TTTTTA	TGCTTCTCAC GTTTTTA	0,0	omy14	536601 17
Omy_R AD4744 4-53	C	T	GTCGTCTGGAGGAGCTGAAG	GGGTGACGTTTTTCCTTC AGC	GGCGAGCTTG GCCCCAAA	GGCGAGTTTG GCCCCAAA	0,0	omy14	560519 17
Omy_R AD1763 2-23	C	T	AAGCTCCTGCAGGTCATCTC	TCTGTGAACTGTCTTCT GCAAGT	CATGTGAGAC CTTTGCA	CATGTGAGAT CTTTGCA	0,0	omy14	560744 85
OMS00 072	A	G	GTGGGAGAGCTCGTCTATGG	ACAACAGGTCATTGGAT GTGATCAG	TAGAAGGTCC ATGTATCTC	AAGGTCCATG CATCTC	0,0	omy14	599717 80
Omy_re dd1-410	C	T	GTACTCCCACTAACATACAG TAGACTCA	GGCACCATTGTGTTTTA GGATGTAG	AAAATATCCT GCAAGGAAT	AATATCCTGC AAGAAAT	0,0	omy14	690441 21
Omy_nx t2-273	C	T	CTTTAGAAAAGCCAAGGTAT ATTTTAACATACTTCT	CTGCTGCCCTCTAATGG TAAGATAG	AAGGCAC	AAGGCAT	0,0	omy14	719697 84
Omy_11 0689-148	A	C	GTGTGTGGCAGAGAACTAAC TGAT	GGTTAAGACATTAACAT AACACTGGACTCT	CAAATGAACA CATTATTTATC	ATGAACACAT GATTTATC	0,0	omy14	7235X XXX
Omy_R AD8802 8-7	G	A	TAGCCCAGTTCGGTTCCAAC	AGTGTCTTTGGTGCGTC CTC	TGCAGGGGCT GG	TGCAGGAGCT GG	0,0	omy15	567666 4
Omy_O go4-212	T	C	TGAAAGGTTTTATGCAGGTT ATTTTCT	GTGTGTGTTAAATAAGC ATTTGATGA	CATTTGATGA GACATCTT	ATTTGATGAG GCATCTT	0,0	omy15	125958 06
Omy_hu s1-52	G	A	CTTGCCGGAGGGTAGCT	CCACAACCTTCTCAAATG AATGGAATGT	CCCATCCCTCC TCCTGG	CCCATCCCTT CTCCTGG	0,0.5	omy15	130422 22
Omy_11 1084-526	A	C	CACCACACCAAGCAACTATT TCATT	ACCCAACACTGTCCCA TTTTTCAT	CCAGTGAAAT TTATTTTT	CAGTGAAATG TATTTTT	0,0	omy15	173008 50
Omy_11 1383-51	C	T	CACGCGCAATCTCTCGTTTTA C	TCTTTAGGCAACAAGCG TGTCAC	AGCAAGCGCA CT[AG]GGT	AGCAAGTGCA CT[AG]GGT	0,0	omy15	212397 68
Omy_ca rban1-264	G	A	GCAAAGCCTCATCTTCAATC ATTTGT	GCAAAACACAAGTCAG GAATCACTTA	CATTAATATTG CTAATAACAC CAAG	ATTAATATTG CTAATAACAC TAAG	0,0	omy15	214540 64
Omy_96 222-125	T	C	GTAAGGAACTAATTGGCGCA ACATT	CAGTTTGTCTAACACCC AGGCATAT	AACTACAAC GTAGCTAATT	CAACTGTGGC TAATT	0,0	omy15	240411 11
Omy_R AD2357 7-43	T	C	AATAGGAACCAAGCCCCAGC	CAGAGCCTGAACCCATG GAG	TCTGGCTCTGT CGGTCT	TCTGGCTCCG TCGGTCT	0,0	omy15	269722 88

Omy_R AD5281 2-28	C	G	AGGAGTCCTGTCCCATGTCA	GCTTAAGGCTGTGGTAT GTGG	CAACCTC[TC] ATTCCACAT	CAACCTG[TC] ATTCCACAT	0,0	omy15	286237 29
OMS00 061	T	C	AAGTGGAGGCTGACCTGTTG	GCTGATGGCACCTGACA GTTAATT	CATTGCCATTT ACAGACTT	TGCCATTTGC AGACTT	0,0	omy15	312319 75
Omy_ni ps-299	T	-	GACAGGATAGGAACGGTTTC TCAAT	ATCAGAAGTTTAATTCA ATATGTACACGATCCT	CTGGATTTCAC ATGTAATAC	CTGGATTTC CGTAATAC	0,0	omy15	397887 84
Omy_L DHB- 1_i2	C	T	ACGCACACTTATCCTTGACA ATGTT	ACTGTGACAACAAATTC GGTGACA	ATGGGCAGTC ATTCA	TGGGCAATCA TTCA	0,0	omy15	440944 40
OMS00 143	T	C	GGAGGCACGCCCCAAA	TTTGTAAAAATAGAGCC CTTAGTGGGTTT	CCTGATCCAG AATCTAGA	CCTGATCCAG AGTCTAGA	0,0	omy15	592330 15
Omy_97 954-618	C	T	GCTCTGCTTCCTCGGCAAAT A	CACAATTGGTTTTTGCA CAAAAGTAAAGTATT	CAACGCTTAC CGGTGTGT	CAACGCTTAC CAGTGTGT	0,0	omy16	114334 35
Omy_11 7370- 400	A	G	TGCAAACACAGAGGAAAGG GATTT	GGCTTATTTGTTCCGTA CTTGCAAT	CAACTCCAAT GAATTAA	AACTCCAACG AATTAA	0,0	omy16	148539 62
OMS00 062	T	C	ACCCTGGGAAGGCTACTGTA C	TGAACAGAGATCTGGAG AGTTGGAT	TTGACCAGCA GATGGTGTA	ACCAGCAGGT GGTGTA	0,0	omy16	148580 81
Omy_R AD8812 2-32	G	A	TCAGTGGATGGAGTGTCCT	GGTCTTTGGCCTTGTTG CTG	GCTGTGGAGA TCAT[CT]CG	GCTGTGAAA TCAT[CT]CG	0,0	omy16	163340 74
Omy_R AD4064 1-58	T	C	GGCAAACCTGGCTTGTGAGTG	AAGGCTCTGCTTCTGCT TGA	AGTGATATCA AGTG	AGTGATACCA AGTG	0,0	omy16	178582 78
OMS00 041	G	C	GATTCTGTTCCATCCTCTTTC TGTCA	AAACATAAAAAAGGGC ATGAAGGTGTC	CCACTCTATGC CTGCCCT	CACTCTATGC GTGCCCT	0,0	omy16	182791 74
OMS00 119	A	T	AGCGGCAGTTGTGTTAATGA GA	CTTCCTAAAGCCTGACA GTCTGT	CCACACAGCT GCCTGT	CACACAGCAG CCTGT	0,0	omy16	275060 18
Omy_R AD116- 59	T	C	GGAAGAAGTGAGAGCCCTG G	CTGTAGTCCACGATCCG CTC	CCACAATGTC AAC	CCACAACGTC AAC	0,0	omy16	330748 66
Omy_R AD1784 9-16	G	C	GACTCCACAGCCTACATGGG	CCGTAAATGCCAGGGGA GTC	AGACGGACTC CCC	AGACCGACTC CCC	1,1,0	omy16	441164 56
M09AA J.163	G	A	TCCCATGGCCCTTACTCTATC AA	TTGAGGTGTATGTTGAA AAGTAACTT	AACAAAGTGA AAGTGCCT	CAAAGTGAAA GTGTCTT	0,0	omy16	448434 40

OMS00 018	T	G	AGAGTACATGTGTGGCTGCA A	GTCATAAATCAACACAA TTATCTTCTTCACAGAA	AACCACATAA TTAATAATTC	CCACATAATT CATAATTC	0,0	omy16	464324 62
OMS00 134	A	G	GAAACTGAAATGATCCCATC GTGTT	GCTAGCATAACAGCATT GCCATAT	TCTATAGCTGC AGTATATTA	TAGCTGCAGC ATATTA	0,0	omy16	477436 37
Omy_R AD3140 8-67	T	C	CAACCCTGCAGGCTACAGAA	TGGAGTGCCAACAAAA GAAGC	ACAGAATGCA GAAA	ACAGAACGCA GAAA	0,0	omy16	483410 10
Omy_R AD7931 4-58	C	T	CACACTGACTCATCCCTCGC	GAGTGTCTTACCGAGCT GCC	AGACCTTGTC	AGACTTTGTC	0,0	omy16	627284 32
Omy_R AD4013 2-55	A	C	TGCAGGGCCTGTATATTGCT	TCAAAGGACTGGGGAG AGGA	TCTGTGCAGTC CTC	TCTGTGCCGT CCTC	0,0	omy16	627847 79
OMS00 006	T	C	TCCACGTAGGACATAGTTTG AGCTA	TGTGGTGTGTCATGTTTGC CCTAC	CACTTACAAA TACAAAATT	CTTACAAATG CAAAATT	0,0	omy16	632479 44
Omy_an p-17	C	A	GGTAATGCCACATGCGGTAA ATT	GGCGAAATCTGAAAATG TGCTGTTA	CTCTCATTGGT ATAGTAACC	CTCATTGGTA TATTAACC	0,0	omy16	3072X XXX
Omy_10 3705- 558	T	C	CTCCAATCGCAAATACCCAG ACT	CGCAGGAGACGGATGC C	AGACTTACCC AGAGTGAGAG	ACTTACCCAG GGTGAGAG	0,0	omy17	706598 6
Omy_11 6938- 264	A	G	GTTCAATTCATGTTGAAGTGC GACAT	CTCTGCATGCTCCCATC CT	CCTTGTCTCAA TTTTCTCTCT	CTTGTCTCAA TTTCTCCTCT	0,0	omy17	715446 3
OMS00 128	T	G	ATGAAAGAACTCCCAGACAC GTATTTT	ACATTTTAACACAGTAA CACTAATACACACCA	ACTCTCAGAA TTAATTATG	CACTCTCAGA ATTCATTATG	0,0	omy17	144885 87
Omy_10 1832- 195	A	C	TGGCTCTGGACCTGTTGAGA	CGTCACAGCTATTTTAG GCGTAGT	TGTAGTCTTTC AGAGTAGTAT G	TAGTCTTTCA GAGGAGTATG	0,0	omy17	170156 58
Omy_R AD4510 4-18	A	G	TGGTGCTTCAGTGCTGTCAA	AGAGTGAAAACGTGTGTG CGG	CAAGACACCG CACACAG	CAAGACGCCG CACACAG	0,0	omy17	206937 54
Omy_10 1993- 189	A	T	ACAAAACACAGTGGAATTAC AATTAACGTT	GGAAGTTAAATTTTCGCT TCGTCAGAA	CTTGATTGCA GCTTGTCAA	TGATTGTCAG CATGTCAA	0,0	omy17	214912 90
Omy_R AD2212 3-69	T	C	TGGGAAAGCATAGGAGGGG A	TGTGTGCCTGTCTTATA GCCC	CCAAAGATGT CAGA	CCAAAGACGT CAGA	0,0	omy17	237569 20

Omy_11 4976- 223	T	G	GACAAACAGCACTTCATTGC AGTAA	GTTGCTCCAGCACCAGG T	ACCGATGGAA CAATC	CCGATGGCAC AATC	0,0	omy17	414629 73
Omy_u0 9-56.119	T	C	CCAAGGTGGACCCACCAG	GCTGAGTTTATAGGTCA GTCATTATACATATTGA	AGTGAGCTGA AACAGAGCA	TGAGCTGAAG CAGAGCA	0,0	omy17	416909 56
Omy_ca 050-64	T	G	GTCATACAGAACTGTTTTGTT GTGTCAA	ACCTTGAATTGGTTCCT AATGCTATTGT	CAGTTTGAAG AATATACTC	CAGTTTGAAG ACTATACTC	0,0	omy17	486517 93
Omy_R AD4369 4-41	A	C	CCCCCTCTCCCTGGCTAGAAT	TCAGGGGGTGTGCTTTT CC	AGGGAAGAGC GGAG	AGGGAAGCG CGGAG	0,1.1	omy17	577285 49
Omy_R AD4667 2-27	C	G	TGCAGGAGGTCTTTTTCCTTG T	AACACATTCTTATTTGC AATGATGG	GTGGTAGCCC ATCA	GTGGTAGGCC ATCA	0,0	omy17	582563 53
Omy_R AD5821 3-70	A	T	CCTGATGGGTGCTCTTCTCTC	AAACAGCATCATTATCC ATAGTGTT	TTTTTT[TA]AA AATATACT	TTTTTT[AT]TA AATATACT	0,0	omy17	582662 27
Omy_U 11_2b- 154	T	C	GGGAAGCAGAAAACTGGA AGTT	CCCTCTGTGGGCTTGAT ATTCA	AATGATACTTT TCAGATTGTA AC	TGATACTTTT CAGGTTGTAA C	0,0	omy17	594666 96
Ocl_gsh px-357	T	G	GAGATCCTGAGGTCCCTGAA GTAT	AAGTGGAAATTTGGGCT CAAAGC	ATCCGTCCAG GAAATG	TCCGTCCCGG AAATG	0,0	omy17	646977 03
Omy_G HSR- 121	T	C	CTGTGTATAAGTTTATACAG TCAGCACAGT	TTCAGAGAGAGAAATG GCAGAAAGG	CCTAATAACC ATGATAACAG C	AATAACCATG GTAACAGC	0,0	omy18	116628 01
Omy_R AD5995 0-44	G	A	GGAGCTCATATCGCCGATGG	GAACTCTGTCACCCTGC CC	GGAGGGGAAG GG	GAAGGGGAA GGG	0,0	omy18	172929 64
Omy_R AD4246 5-32	G	T	GTGGATCTTGGA CTCCAGGC	TAGACATCGGCCCTCAC AGA	CCAGGCTGGA AGAA	CCAGGCTTGA AGAA	0,0	omy18	250342 87
Omy_R AD7877 6-10	T	C	CACAGCTTCCTGCAGGGTAA	GCTTGCATGGTCTCGCT AGT	GGGTAATCCT GGCT	GGGTAACCCT GGCT	0,0	omy18	250343 26
Omy_sa st-264	G	A	GAAGTAGGGTTTGTGACCA TGTGA	TGGATTCCATTTTAGGC TGTAATACATCTT	CTAGCCAATG CGTCTAA	ATCTAGCCAA TGTGTCTAA	0,0	omy18	282520 83
Omy_R AD4361 2-42	T	C	GTGGAGAGGGATTTTGGGGG	TGACAGGACAAACACA AGCCA	AAATGTGTAT TTGTGTA	AAATGTGCAT TTGTGTA	0,0	omy18	291187 77

Omy_12 8996- 481	T	G	CTCATCCACACTGTACAGTA CAAGT	CATGCCTTCGTCTCATC AATAACAC	CAAACCTCAA CCAC	CAAACCGCAA CCAC	0,0	omy18	308021 01
OMS00 121	T	C	GGAAGGAGGTCCAGTGTGAG T	AAAATATGCAACACCAC TAAAACTGGAAAA	ACAGCGTGAT AAATT	CAGCGTGGTA AATT	0,0	omy18	342329 91
OMS00 127	T	G	CACCTTTCTCTCTCTCTCCAT CTCA	AGTGTGCTACACAACCT TAAAAAATATATATCTA TT	CACACACCCA AATGTA	ACACACCCCA ATGTA	0,0	omy18	362684 23
OMS00 118	T	G	GCTTATTTAGAGTGCATGCC AGATG	TGGAACCAATGGGACA GTCCTA	GCGGGGTGTG C[AG]CATT	GCGGGGGGTG C[AG]CATT	0,0	omy18	422122 99
Omy_R AD7210 -8	C	A	ACACCACACTCCACAAAGCA	GCGCCTTGGTCTCCTTC ATA	TGCAGGACTT GCTTTGT	TGCAGGAATT GCTTTGT	0,0	omy18	425586 54
Omy_R AD1934 0-24	A	G	GCAGGGAGCAGCATATACAT G	TGGGGTGATTTGAGTGA CAC	CATGGAAATA CATA	CATGGAGATA CATA	0,0	omy18	427018 41
Omy_R AD3209 -10	A	G	CGGAGGAGTTTGAGCAGTCT	CTTCTACCACCACCTCG CTG	CGGTATCCCT GGC	CGGTGTCCCT GGC	0,0	omy18	509849 53
M09AA D.076	T	C	ACTGTTACCACTCTCTCATCA ACCT	GGGTCCAGGAGGTTTTT AAACAACAT	CACCAACCAC TGGTGAA	CCAACCGCTG GTGAA	0,0	omy18	537175 12
Omy_II- 1b_028	T	C	ACTGTCTGGCTAGAGCACAT TG	ATCTTCTACCACCGCAC TGTTTTAA	CTGAGGCAAC TTTTGT	TGAGGCAGCT TTTGT	0,0	omy19	103295 30
OMS00 092	A	C	TCTCCAGGTGTATCTTGAGA AGGT	AGGGTTCACACAGGGA AGATATCAT	CAGCTGAGAA TAGGTTC	AGCTGAGAAG AGGTTC	0,0	omy19	125185 51
OMS00 017	A	G	ATTAAGTTCATACAAAAGTT CATCATAAATATTTTCCTTT	GGAGAACAAAGGGAAA GAGAAGACA	TAGACCTCGG TGCTGTAG	CCTCGGCGCT GTAG	0,0	omy19	191115 91
OMS00 105	T	G	ACATTTGAAGTCAGTATGGG TGTTGAG	GAACCTCACCACAGTAC TAAATGCA	CTGCTATTCAA ATTGCT	CTGCTATTCA CATTGCT	0,0	omy19	202649 68
OMS00 133	A	G	GACCACTTCACTCATTCCTCC TTTT	TCCGGTTTACACACTTC ATGCA	CGCCTCCATCT TTGTGGT	CGCCTCCATC TCTGTGGT	0,0	omy19	237020 93
Omy_ra pd-167	G	T	CCCAACATGCTCTATTGCAG CTA	AGTTGCATAAGATGAAT CAATAAATTAAAAACAC AGAT	AAACAATCCC CCCCAAA	AAACAATCCC ACCCAAA	0,0	omy19	273624 24
Omy_12 8693- 455	T	C	GCCTGCAGGAGAAGGTAGA GTTA	GAAATGGAATGGACCCC AATCCT	CACTCAACTG ATACCC	CTCAGCTGAT ACCC	0,1.4	omy19	328900 59

Omy_R AD4911 1-35	T	C	GCAGGCTTAGCATTGCTGAC	GGAACCTGGGTGGGAG AATG	TTTCTTATATT TGA	TTTCTTACATT TGA	0,0	omy19	400501 11
Omy_R AD739- 59	C	G	ACGAGGCTTGTAATGCAGT	TGCCTTTATACCAATGT CTGCTG	GAGTTGGCTA TTTT	GAGTTGGGTA TTTT	0,0	omy19	529237 02
M09AA C.055	C	T	GTCTCCGACGTGTGGCT	TGGAACGAACCTGAGA ACATAAGG	ACCTCCACGC TGTCC	ACCTCCACAC TGTCC	0,0	omy19	538551 67
OMY10 11SNP	C	A	AGGCTGGTTTGGGATTCACT G	CGCCAAACACTAACTCT CTGTCT	CTTTACCTCGA AGACAAT	ACTTTACCTC TAAGACAAT	0,0,6	omy19	544462 25
Omy_B AMBI2. 312	G	T	CGAGCTCATGTCCGAAACTC AT	TTTGACAGCCTCAACTT CTAGGG	CCGAAAGTTC AACTTT	CCGAAAGTTA AACTTT	2,1,0	omy19	611XX XX
Omy_R AD2970 0-18	C	A	AATGGAATTGGCCCCAACCC	TCTCCATTGTGTGTAAT CATGGT	ACAATTCAAA TGATTTA	ACAATTAAAA TGATTTA	0,0	omy20	167319 6
OMS00 039	A	G	GTCAGTACTGTGTGTGTCTGT GT	CCATCTACATTGTCAGC AGTGTGA	GTACGTGTCTC TGACC	GTGCGTGTCT CTGACC	0,0	omy20	480049 5
OMS00 114	T	G	GGATGATGCTGTGAGTCGAG AAG	ACCTTCGCCACCCATGT TTTATT	AAACGTTTCA CATGCACC	AAACGTTTCA CCTGCACC	0,0	omy21	110354 95
Omy_99 300-202	T	A	CAGTTTGACCCGATGGTGTG A	GATTATGGCGTGGCCTT TTGG	TCAGGCATGA GAGAAA	ATCAGGCATG TGAGAAA	0,0	omy21	146970 73
Omy_ci n-172	C	T	CGCATGGGACAGGTGTGT	GAGAAAGCCTGTAGAA CCATGTCT	CGCTCACCGT GGTTAC	CGCTCACCAT GGTTAC	0,0	omy21	216026 18
Omy_va tf-406	T	C	TTGCTTCATTTTGTGATAACC TTGGG	TGCATGCTCTGACAAAT GTTACACT	ATGACTATCC ACA	ATGACTGTCC ACA	0,0	omy21	238062 20
Omy_L DHB- 2_e5	T	C	TGCTAGGTGAGTCAGAGGTA CATATT	GA CTGGAAGGCCACCCA TAAG	TTTACCTGTCA AC	CCTGTGCGAC	0,0	omy21	241299 07
Omy_L DHB- 2_i6	G	T	TCCTCGCCAATACCATACAT GTC	AGAGTGAAGCTAACAC ACACATTCT	CTGTGTTTTGC TTCCCCA	CTGTGTTTTG ATTCCCCA	0,0,5	omy21	241305 59
Omy_10 4569- 114	A	C	CCGAGGCCGACGTGATC	GCGCCTCGCTCATCATC A	CGCCACTCCG ACGCC	CCACGCCGAC GCC	0,5,0	omy21	321785 17
Omy_zg 57-91	C	A	CACTCATACACTCACTCACA AAGGA	AGCAGATAAGCCTTGTG AGTGAATCTT	CACAGACTGC ACAGCC	CCACAGACTT CACAGCC	0,0	omy21	327667 40

Omy_R AD3500 5-13	C	T	TGGTCAAAGTTGAGGGTGGT	CAGGGCCCTGATTAACC ACT	CCAACTCCCG ACGG	CCAACTCTCG ACGG	0,0	omy21	371884 35
Omy_b1 -266	G	T	TCATGTGAACTTTAATTGACT AGGAAGTCG	GATATGAAAATATCTGA AGAGTTATATTTGGGAA ATTGAC	TCTATAAACA ACATTTTTC	TCTATAAACA AAATTTTTC	0,0	omy21	412557 73
Omy_10 04	A	T	GAGAATCGGAGCTAATCTTA GTTATTGTGA	CACTTTATTGAGCTACA TGGCAAATCTG	CATGTGATGTT TTTTTGC	ATGTGATGAT TTTTGC	0,0	omy21	419442 18
Omy_10 2505- 102	A	G	CTGCAAACCTGACATGGTAGC AAAA	TGCTTGCTTTTTTAAAAA CAATCTCCCA	AACAGGATGT TTTTGC	CAGGATGCTT TTGC	0,0	omy22	775932 8
OMS00 173	T	C	TGGAAGTAGCTACTTAACAG GAAATGG	AACACGTGTGCTTGTTT TGTCAA	CATTAGCTTGT GTATGAACT	ATTAGCTTGT GTGTGAACT	0,0	omy22	910589 1
Omy_Ot s249- 227	C	T	CTATCTATCTATCTATCTATC TATCTATCTATCTATCTACTT ACTGAGA	CCCCTAGATTAAACCTG TCCAGTCT	CCCTCTGAGA ACTAC	CCTCTGAAAA CTAC	0,0	omy22	189174 30
OMS00 058	A	G	GTGACATTTGGAGCCACTGC	GCTAGGAGACAGAGGG TGAAAG	CAACACTTTGT ACCCCTC	CACTTTGCAC CCCTC	0,0	omy22	199221 39
Omy_R AD9358 0-37	T	G	AGGCAGAGGAGGGTTGTTTG	TGCAGAAAGTCAAATCAC GAACA	AGTCACCTGG GATT	AGTCACCGGG GATT	0,0	omy22	242478 65
Omy_IL 17-185	G	A	CCACCACACTCTGCAGCTT	TTGACGGGAATCCGAGA CTTC	AAGAATCTCA CCTGCCCCAT	AAGAATCTCA CTTGCCCCAT	0,0	omy22	272260 63
Omy_R AD1033 59-45	C	T	GGAGAAGGATGTGCTCCCTG	ATTTGGAGGTGGAGGGT CCA	CCTGTAACGC ACAG	CCTGTAATGC ACAG	0.4,0	omy22	405024 75
Omy_R AD4848 -14	G	T	TGTCCCTCTTCTGCACGATG	AGTTGGTAGCTCACTCT CTGT	GAGACAAGGA CAGA	GAGACAATGA CAGA	0,0	omy23	549364 8
Omy_10 7806-34	C	T	TCTTTGTCCATGCACATTGAT ATT	AGCACATTTAGTTAGCA GTGATGGA	ATTGGATGTC AGTGTCATT	ATTGGATGTC AATGTCATT	0,0	omy23	100954 18
Omy_R AD4879 9-69	A	G	GCTGAGCCACCTACACACAG	GTCTAACACTCGCAGCA GGT	CATCCTAGAA TAGAAGT	CATCCTGGAA TAGAAGT	0,0	omy23	215810 80
Omy_18 7760- 385	A	T	CGGCTATTCTCGCGTAAAAG CT	AAATGCAACCAGAAAC GGAATGTC	TCCTTATCCAA AATTATTGTGC	CTTATCCAAA ATAATTGTGC	0,0	omy23	236597 37

OMS00 024	T	G	CACATACAACCATCACCCCTT CCTAA	AGCATTGAGCGAAATTA CCAAGAGT	AA[AC]CCCAA ATTTTAC	AA[CA]CCCAA TTTTAC	0,0	omy23	314183 39
Omy_R AD3651 -48	G	T	GAGTACAGTGCAGTGTGGGG	CCTTCCTCTTGCCACCAT CA	GTTGGGAGAA CTTT	GTTGGGATAA CTTT	0,0	omy23	320298 60
OMS00 048	T	C	GGAAGAGCTGGAGAACAAC GT	TGCAGTTGACAGAGGCT TTCTTT	CAGCTAAACT CAGCAAAA	AGCTAAACTC GGCAAAA	0,0	omy23	371256 68
Omy_e1 -147	G	T	GCACTGACTGTTACCAGGAA AGAG	GTACTGCAGTGTGAGG CTATATCA	CCATCCTGAA TCTGATTAA	CCATCCTGAA TATGATTAA	0,0	omy23	383133 38
Omy_10 9243- 222	A	C	ATGTGCACCTCTTAAATTGT AAGTAAAATGT	ACCCTATATTCAGTGGC AAGATTGC	TGTTTCATTAAA TTGACTTTTT	TTCATTAAAT GGACTTTTT	0,0	omy24	700968 7
OMS00 101	A	G	GCGTGTTCGTGGGTCAGTTAA ATA	GTGCAATCCAACCTATT AGTAGATATGCT	CTCTAGTAGC CTTATAGAAA G	CTAGTAGCCT TACAGAAAG	0,0	omy24	104754 51
Omy_in os-97	C	A	GATGGACAGGGTCTCTTCA C	CCTGTAGATAAAACATG GTACCAGGTC	CCTTTCTTGAT GGTATCC	TCCTTTCTTG ATTGTATCC	0,0	omy24	245476 87
Omy_R AD5599 7-10	A	C	CATTTTCTACCTGCAGGCTGC	AGCCTACATACATAAAG CCAACA	AGGCTGCAAT GTTT	AGGCTGCCAT GTTT	1.5,0	omy24	274058 86
OMS00 052	T	G	TGCGTTTTTCATCCCAATCAT TCAC	GGCATCAGGCTCTTCTT CCT	CTTCCTTTTGA GAATAAT	CCTTTTGCGA ATAAT	0,0	omy24	281749 67
Omy_10 7336- 170	C	G	GCCCTCTCACTCATGACATC AAC	GCTCCAGCCACTCGCA	CACTCCTGGG TGCAGAA	ACTCCTGCGT GCAGAA	0,0	omy25	300174 55
Omy_R AD5975 8-41	T	C	GGCCCCCTTCTTTTCAGGAAT	CACACACTCAACGGGTC AGT	TGATTGCTACT GAC	TGATTGCCAC TGAC	0,0	omy25	402193 56
OMS00 174	A	C	TGACTAACTATGCAGCCTGA AAGG	GGGATACTCTTGTAATA AACTGTTGGTTAGTA	CAAGAACAGG [AC]TAAATGT	CAAGAACAG G[AC]GAAATG T	0,0	omy25	473253 93
OMS00 071	A	G	CCGGAGTGACCTCACATTTG G	GCATCGTACAGTTCACC TACCT	CTTGTTTGAGC TTTTTCT	TTGTTTGAGC CTTTTCT	0,0	omy25	482484 74
Omy_pp ie-232	C	T	CTGTTTTAGATTAGAATGTTT TTGGTCAGGT	CTGAACATAGGCTTTCA TTTCAGACAT	AAATAGCGGA GAAAAT	AAAATAGCAG AGAAAAT	0,0	omy25	549909 25

Omy_R AD1403 3-46	A	G	GCAGGAGATTTATTTGGCCC C	ACCCTTGTGATCACATA CTGTCT	ATAGAGGAAT AGAC	ATAGAGGGAT AGAC	0,0	omy25	600640 21
Omy_R AD1186 -59	A	G	CACAGCCTGGATGTGGTTCT	ACAAGTTCCGGGAGTTT CCT	CCAGGACATC CAGG	CCAGGACGTC CAGG	0,0	omy25	702523 14
OMS00 002	A	C	TTTGATTTGATTTGTATCTGC TTCTT	CCAACATGCCTCACACA AAA	TGTTTTGCAGC GCTC	TGTTTGGCAG CGCT	0,0	omy25	823663 95
Omy_R AD4159 4-34	A	G	TGCAGGGTTATAATGTGTCT TTGT	AAATCTCGGGCTGAGGA ACG	CAGAGATACG TTCC	CAGAGATGCG TTCC	0,0	omy26	560047 5
Omy_cd 59-206	C	T	CGATTGGCCCAGATGTTTCC AT	GCTCCGTTGCATAGGTG ACT	CAACAATCGA AGGTAAAT	CAACAATCAA AGGTAAAT	0,0	omy26	802832 2
Omy_R AD1303 4-67	A	C	GAGTGATTCCCAGCCCTCC	TCTCTCCGTTGGCCAGA AAC	ATAAATCACA A	CTAAATCACA A	0,0	omy26	125370 39
Omy_ad a10-71	C	T	TCTTTGAGCGACAAAGTCCT TGT	ACCCACACATGAACGCA AAAG	CTTCCTGCGTC CAA	CTTCCTGCAT CCAA	0,0	omy26	183154 20
Omy_as pAT- 123	T	C	GCCCATTTCACTGATGCTGT GA	AGGAGACCACTCCAAA GAGAACT	CCTTCCTAGGC AGTCAG	TTCCTGGGCA GTCAG	0,0	omy26	192895 82
OMS00 014	T	C	CTTACACACAAGGGCTTCAT TCTG	GATGTCTCTGGGTGGTT GTCA	TGATTTGATG AATTAACTT C	TTGATGAATT GAACTTC	0,0	omy27	629752 6
OMS00 015	A	T	TCAGACCCTATTTTGGCAC AAGT	GTCTAACTGATCCCACT TCTGCAT	CAAGTCACAC TTTAATGAA	CAAGTCACAC TTATAATGAA	0,0	omy27	237309 45
Omy_hs p47-86	T	A	CACATTAAGCACTCCCAGGG A	TTGCAAAGGCCAAACAG CATT	CAGGAGTGTA AATGTTT	ACAGGAGTGT ATATGTTT	0,0	omy27	279444 94
OMS00 090	T	C	AGGGCACAACACCACTCTAA ATT	TCGAAAAGCAACATCTG TCTCAGT	ACAACCACAC AAGATT	AACCACGCAA GATT	0,0	omy28	424599 7
Omy28_ 1160795 4	G	A	TGACACTGATCACAATGGTG AAAT	TAAACTGGAAGGAGAG AGCAAAAT	TGTGGGCTGC GAACATACTC A	TGTGGGCTGC AAACATACTC A	0,0	omy28	116079 54
Omy_R AD5245 8-17	C	A	ACGTGTCCCTGAGGATGGTA	AGCTCTAGGTCTGGGTC CTG	ATGGCCCC[CT]AAGAACCC	ATGGCCCA[C T]AAGAACCC	0,0	omy28	116097 94

Omy_G REB1_0 5	T	G	TGGGCAGATATGGAAGAACG G	ACCTTCTAAATGGCCTC TGTGT	CGGTGGCTCT C	CGGTGGCTCG C	0,0	omy28	116180 27
Omy28_ 1162524 1	A	G	CAACATTTAGGGAGAGGTTG CTAT	ATCATCAAGTTTGCCTA CGACAC	CCTCCTCCCTA TGGTTGTCTC	CCTCCTCCCT GTGGTTGTCT C	0,0	omy28	116252 41
Omy28_ 1163259 1	G	A	GTAGAGGCCAAAGGCTTGAG	TGCTCTTATTACCTTCCA GACTCC	TGAGAAGAAC ACAGAGG	TGAGAAAAAC ACAGAGG	0,0	omy28	116325 91
Omy_G REB1_0 9	T	G	CCAGTGGCAACCTCAGGTAG	GACTCCAGTCACCCAAG TCA	TCAATGGAGA	TCAAGGGAGA	0,0	omy28	116416 23
Omy28_ 1165885 3	A	C	CAACATATGACCACTCGAAA ACTC	ATTAATCACACCGTGAG ACTCCTC	TGGTACAGAC ACGCACTAGC A	TGGTACAGAC CCGCACTAGC A	0,0	omy28	116588 53
Omy28_ 1166757 8	T	C	ACAGTAAACCCATTTCAGGCA TAGT	TTATCCTCTCAATCCAC ATCAAGA	GTATTGATCCT GTGGGAGACA	GTATTGATCC CGTGGGAGAC A	0,0	omy28	116675 78
Omy_R AD4708 0-54	A	G	TCAAAACCTGCAGGACTTGG A	TGGTTATATCTACAGTA CAGTTCGT	TGCAAGACTT AAAACGA	TGCAAGGCTT AAAACGA	0,0	omy28	116679 15
Omy_R AD1570 9-53	G	A	TGCAGGACTTGGATAACACA GA	TGGTTATATCTACAGTA CAGTTCGT	ATGCAAGGCT TAAA	ATGCAAGACT TAAA	0,0	omy28	116679 15
Omy28_ 1167111 6	C	T	AATTTCCCCAAATTTGAAAC TCTT	GTGTACATTGTCAGGCA GAAACAT	CTGGTGAGAA CAGGAATTAC C	CTGGTGAGAA TAGGAATTAC C	0,0	omy28	116711 16
Omy28_ 1167662 2	T	G	CGAATGCACTGTAGCTCATT CTAA	GCAGTAGAATGTCTCGC AAATACA	ACATGTCATTT ATTGTTATCT	ACATGTCATT GATTGTTATC T	0,0	omy28	116766 22
Omy28_ 1168320 4	G	T	CAAGAAAGAAACAGATGTTG TCCA	TTGTGACTCAAATCTGC AACCTAT	ATGTAAAAAA GGGCAGAAAA	ATGTAAAAAA TGGCAGAAAA	0,0	omy28	116832 04
Omy28_ 1177319 4	A	T	AGTTTGACACCCCTGTACTA GAGC	GTCTAACAAGCTCTGGG TGATTTA	GCAATTTTTTA AAATTACCGC	GCAATTTTTT TAAATTACCG C	0,0	omy28	117731 94
Omy_R AD7606 0-20	C	T	TGCAGGGTGTCTAGTATTGGG	TCCCATGCAAATTCCAA ATGCT	GGGCGCTGTA GGCAA	GGGTGCTGTA GGCAA	0,0	omy28	215613 03

OMS00 129	C	G	GGAGATGATGAAATAAAAAAT TGAGGAAAAGATGA	TGTCTGGTGAATTATCG CAAATAACCA	TTGAACAACA AGAAAAA	TTGAACAACA ACAAAAA	0,0	omy28	225311 25
Omy_R AD4645 2-51	A	G	TGCAGGTAAGACTTGATCTG GA	TGACTCCAACCTAAGTG CATGT	TGAAGTCAGA AGTT	TGAAGTCGGA AGTT	0,0	omy28	275166 10
Omy_97 660-230	C	G	TCAGTTATGTGTAATCTCATT ACCTCTCCAA	AACAGAAAAGGTCTCA ATGTATTTTTTGCA	ACGTAACCTTG TAGCGTTTT	ACGTAACCTTG TACCGTTTT	0,0	omy28	357429 46
Omy_im pal-55	C	T	CGCTGAGAGGATTGTCAA	TTTTCTTTGTTTCAGTCTT CTGTCTCTG	CGAGATGATG CGTCTACA	CGAGATGATG CATCTACA	0,0	omy28	363905 09
Omy_B AC-B4- 324	G	T	CGTACTTTTCTTTTACAAAAT TAAGTGGAGGAT	GCCTAATATTGGCCTAA TGTCCTTCA	CATTGCCAAA TACG	TACATTGACA AATACG	0,0	omy29	145286 35
Omy_O myP9- 180	C	G	CTGGATGTGTAGTATCGGTG GAAAA	CACTGGGCACCTCTGAT CTC	CTGTAGTAGT CCCCATTGT	CTGTAGTAGT CCGCATTGT	0,0	omy29	156734 14
OMS00 164	T	G	CAGAGGAGAGGAGAGCAAA ATACTT	ACAACCTACTCATTGAA ACTCATTGGA	CCAGATTCAA TTAAATTTA	CAGATTCAAT TCAATTTA	0,0	omy29	172496 54
Omy_cr b-106	G	T	GCTCAAAAAGATTCTGCCAA ATTCACA	ATTACAATGAAAGTACT TGAGTGTTTATGCAAA	TTGCAATGCG TCTTT	TTGCAATGAG TCTTT	0,0	omy29	307013 74
Omy_11 8205- 116	A	G	CTGCGGTGGGCTACACA	CGCAGCTGCGGATGAG	CTACTGAGGC TGAGTGCT	TACTGAGGCC GAGTGCT	0,0	omy29	332671 27
Omy_sS OD-1	T	G	GCCGGACCCCACTTCAA	CAGACTAACCGAACAGC ATCAGTGG	CCACAACAAG ACCC	CCACAACCAG ACCC	0,0	omy29	398022 21
Omy_R AD1957 8-59	A	G	GGTTGGACACCTCCTGGTTA	TCAACCAAGCAACAGAT TATAGCT	GGTTAAGAGT ATTC	GGTTAAGGGT ATTC	0,1.8	NA	NA
Omy_R AD4052 0-48	T	G	TGTTTCATCTGATCAGCTGTCA G	ACACGTCGGTCTTCTTC TCC	GTCAGATTGC GCTG	GTCAGATGGC GCTG	0,0	NA	NA
Omy_R AD7814 7-27	C	T	GCATTTTAGCCCTCCCAAAG TC	CCTTCTTCCAGTTGTAA AACCCA	CAAAGTCCCA GAGA	CAAAGTCTCA GAGA	0,2.6	NA	NA
Omy_R AD619- 59	T	C	CATGGAGAAACAGACCCGCT	TGCTGTGTGTGTATCTG GGG	TGCTGGATCC CCCA	TGCTGGACCC CCCA	0,0	NA	NA

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Assay	A1	A2	Forward	Reverse	A1-Probe	A2-Probe	Allele Corrections	Koop GCA_ 00287 2995.1 chromosome	Koop GCA_ 00287 2995.1 snpcordinate	Chi6 GCA_ 00283 1465.1 chromosome	Chi6 GCA_ 00283 1465.1 snpcordinate
Ots_SEXY3-1	X	Y	GGTCTTGCAGTCAGGA GAGG	CCAGGTGGTGAAG GTAGGAA	NA	TCAGCGAA GTGGAGAT	NA	NA	NA	NA	NA
Ots_myoD-364	T	G	GTGTGTGTGTGTGTGT GTCATCGT	TTTACACATATACA AAAATGGTCCTCTA TTGTCAT	TCATCTTTT GTTATTTCC TTG	ATCTTTTGT TCTTTCCTT G	0,7, 0	Ots01	10134 698	Ots01	72997 84
Ots_u07-25.325	T	C	AGACAATCATGGTGTT TTGAGTCTTTCT	GCCTAGGCTTGATG GAGTCA	CCGCTTGAA AGTTTGA	CGCTTGAA GGTTTGA	0,0	Ots01	12626 231	Ots01	91987 21
Ots_110689-218	T	G	GTATAAACTAGAGTCC AGTGTTATGTTAATGT CTT	CATGGCAGACAAC AGTAGAGAATATG A	CACCAATCA ATTAATTAT T	ACCAATCA ATTCATTAT T	0,0	Ots01	15276 095	NA	NA
Ots_129458-451	T	C	TGGGACCCACATAAAG CAACTG	GACATAAGACCCAT TTAGCCCCTTTT	CATCTGGCA ATGCCTT	CATCTGGC AGTGCCTT	0,0	Ots01	15863 134	Ots01	11080 640
Ots_crRAD21115-24	C	T	TGCAGGTGGGACTTAA ACACA	ACCTGTGGCAACGG TTGA	CACACACAT GCACG	CACACATA TGCACG	0,0	Ots01	27727 076	Ots01	23499 747
Ots_Prl2	A	G	CCTGGTCTGTTTGTGAT CAAGATG	GGTTAACTCAAATA GAACATACTCTGAC ACA	ATGTATTGT TCATTTAAT G	TGTATTGTT CGTTTAAT G	0,0	Ots01	46840 237	Ots01	40924 770
Ots_Ikaros-250	G	A	GAGGCTGACTTGGA TTGC	GGCCTGTCAGCCAA GGA	ACAGAAGA TTTTCGGCT GC	ACAGAAGA TTTTCGACT GC	0,0	Ots01	50283 457	Ots01	45385 098
Ots_107806-821	T	A	TGCAGTGCTGAATTAG AGATTAATTTTGTG	CTCCCTTGCTTTTG GTCATTGG	CAAAGAAA ATCAAAATT T	CAAAGAAA ATCTAAAT TT	0,0	Ots01	56999 741	Ots01	51993 828
Ots_127760-569	C	T	CTGCTGGCGCAGACAT G	CGTTATAGAGGATA GTTTGGAGGAAGG A	CCGGTTTAC CGATTTG	CGGTTTAC CAATTTG	0,0	Ots01	70642 723	Ots01	65444 532
Ots_crRAD23631-48	G	A	GCCATATCCCGGGGCT TG	TGCCTCTGAGCACT GACTG	GGGCTTGGG GGCAT	GGGCTTAG GGGCAT	0,0	Ots01	73494 810	Ots01	68018 794

Ots1_728 58599	A	G	AACCATTGTTCTTGTAT TCCTGCT	GTAAAAAGACGAA TGAAAGGATGG	GGTGGAGG GAAAAAGC AGTG	GGTGGAGG GGAAAAAGC AGTG	0,0	Ots01	78671 220	Ots01	72858 599
Ots_unk3 513-49	C	T	TTTGAGTGAGTCACTG CACCAA	CAGCTCCACAGTGT CACCAT	AGTGCGAA GAACC	AGTGCAAA GAACC	0,0	Ots01	81595 603	NA	NA
Ots_crRA D74766- 28	G	A	GCTGACCACCGACCAC AG	AGCTCTGCAGTAAC AATGGGA	AGACTGGTA AAAG[AT]	AGACTGAT AAAAG[AT]	0,0	Ots01	88530 200	NA	NA
Ots_crRA D57376- 68	T	C	TGCAGGCATCATGCTT AATAACT	ACGTGACACAGGTC TGGG	ATAAAGTGT GTTAT	ATAAAGCG TGTTAT	0,0	Ots02	99375 16	Ots02	54571 149
Ots2_424 05643	G	T	GAGAGAGTGCATTCTT CATCAAGTT	TCAGTACAGGGTTT TTCCCAAT	CAGGTTGTT GGTTGTT	CAGGTTGT TGTTTGTT	0,0	Ots02	19918 478	Ots02	42405 643
Ots_crRA D75581- 70	A	G	ACACATGGCTCGTCTG CA	GGAGCTCAGGGTGC AGGA	GAAC TTAAA ACACT	GAAC TTGA AACACT	0,0	Ots02	20994 028	Ots03	27546 510
Ots_crRA D46081- 56	C	T	GCAGGGTCTGTGTGGG TT	ATGAGGACACTCCG CCCA	GCACCACTG GACCC	GCACCATT GGACCC	0,0	Ots02	24120 152	Ots02	34735 614
Ots_nelfd -163	A	G	CTCACTGCAAATCCAA CTTCATCAT	CCACTACATCCTCA TCCAAGGTT	ACCCACCAG TGTCATT	CCACCAGC GTCATT	0,0	Ots02	27801 414	Ots02	31069 128
Ots_crRA D27515- 69	T	A	CAGATGGTGCAGGCCG AA	ACTCGTTGTGATTC CAGCCA	GCATTTTAA AAATC	GCATTTTAA AAAATC	0,0	Ots02	31417 111	Ots02	27211 812
Ots_1283 02-57	C	T	GGTTGCAGGGCAGAAC TGT	ACCCATCCAATAAC CCATTTTCCTT	CCTGCAATA CGACCAAC	CTGCAATA CAACCAAC	0,0	Ots02	34870 376	Ots02	23632 129
Ots_crRA D78968- 46	C	T	CCTGCTCTGTGTCTGG GC	GTGAAGACGACCCC GGTG	AG[CA]AATC [CA]CACAGC	AG[CA]AAT T[CA]CACA GC	0,0	Ots02	35362 682	Ots02	23276 932
Ots_crRA D11620- 55	C	T	TGGGATAGAACAGGA GCTTAAACA	TGTCTTGGTCGCGC AGTT	AGAAGCCC AGCTCC	AGAAGCTC AGCTCC	0,0	Ots02	36061 414	Ots07	43120 003
Ots_1054 07-117	T	A	TGTGTACATCCGCGTA AATATTGAAGATAA	CTGTGAGCTGCTGC AAACC	CAGGTTAGG AATGGTTG	CAGGTTAG GATTGGTT G	0,0. 2	Ots02	37138 862	NA	NA
Ots_LWS op-638	T	C	CAATTACTCTTTCTCAG CCCTGTGT	GCGGTAAGATGCA GTTTTACATGGA	TTTAACAAG AAAATTATA CATTTTC	CAAGAAAAG TTATACATT TC	0,0	Ots02	44036 657	Ots02	13620 416

Ots_crRA D69327- 53	G	T	GCCATTTGACCAACGG AGC	ACTCATACAGTATT TCCGCCTGT	ATAGGAGA ATTGGA	ATAGGATA ATTGGA	0,0	Ots02	52051 529	Ots02	47082 99
Ots_stk6- 516	C	A	TGTGTTTtaggATTGAA CTGACCATGTT	GTAAACTCCACCTG CAAGAAGGA	AACATAAC GGACTCCC	TAGAACAT AACTGACT CCC	0,0	Ots02	53397 399	Ots02	38145 27
Ots_cgo2 4-22	T	C	AGGTCCTCTGTCGCAC CTA	GGAGGCGAGGTCT GGTG	CCAGATGA ACAACCTCA C	CCAGATGA GCAACTTC AC	0,0	Ots03	95886 38	Ots03	12326 537
Ots_NOD 1	C	G	GTGCTGCAGGAACCAT GTG	CTGTGTGGACTGCT GTCTAAGG	CCAACGGC GACTTG	CCAACGCC GACTTG	0,0	Ots03	95985 76	Ots12	23568 768
Ots_1134 57-40R	C	T	CCCAAGTGGTGAGTGT CAGT	ACTACAACAGGTGT TGATAATAGAATCA TTCTC	CCCT[AG]TT CTCCAATCC ATAT	CCCT[AG]TT CTCTAATCC ATATG	0,0	Ots03	17561 381	Ots23	94474 90
Ots_TNF	C	T	CCAAATCCTCATCCCA CACACT	CCGTTGCACTTGAC CCTAAAC	CTGGCTGTA AACGAAGA	TGGCTGTA AACAAAGA	2,0	Ots03	20344 952	Ots03	21402 560
Ots_1123 01-43	T	C	GCATGGCTGCCCTAGA ACA	TCAGAACATTTTCCT TCAGCTTCGT	CGTCGCATT CAGC	CGTCGCGT TCAGC	0,0	Ots03	33896 915	Ots03	284X XXXX
Ots_u07- 20.332	A	C	CGCGAGTTAGCTCGAA TATTATGATTTC	TCAAGCTAGCATAG CAACTTCATCAA	ACCATTTGA TATAACTGC GTTAG	CATTTGAT ATAACGGC GTTAG	0,0	Ots03	39126 796	Ots03	33660 993
Ots3_348 94254	T	C	TGATATATTTTGCTGC AATGATCTG	AGAGGGAAGGTGG ACAATGTT	TAAC TTACA GTC	TAAC TTAC AGCC	0,0	Ots03	40436 224	Ots03	34894 254
Ots_1189 38-325	C	T	ATTTTCAAACAGGCAT TTATCATTGGTGAA	GGTCTGTCCCTCAT TCTTTGCA	AGAGATGC AAAGTGGA GTT	AGAGATGC AAAATGGA GTT	0,0	Ots03	48430 243	Ots03	43610 834
Ots3_570 55518	T	C	TTAGCAGGCGATCTAA TTCTGATT	ACACGCTAACTGCT GTATTCTCTG	TGATCATAT CTCGTTCAG T	TGATCATA CCTCGTTCA GT	0,0	Ots03	61138 782	Ots03	57055 518
Ots_1008 84-287	T	C	CGGAAGACCAGATTCT CCAAGAGTA	CGACCAAGTAGCG GCACTT	ATAGAACTA CAATTCACA TATAT	AACTACAA TTCGCATAT AT	0,0	Ots03	72097 697	Ots09	34802 127
Ots_9485 7-232R	T	C	GGCACTCTCCCTGGCT AGA	CCCCATCACTTCTC TGGCTTTAAAT	CAGGATAAT AACAAACA AG	CAGGATAA TAACGAAC AAG	0,0	Ots03	2XXX XXXX	Ots03	27503 532
Ots_1072 85-93	T	A	GCCCTTGTGACAATGC ACTGTTATA	AACATACACCAATA CTTAGGTCTAGACA GT	AAGTAACGT ATCAAATGG C	AAAGTAAC GTATCATA TGGC	0,0	Ots04	66909 09	Ots04	58529 87

Ots_Ots3 11-101x	A	-	AAATGAGGCCGTCCTT TACACT	GCAATACAAGCCCT TGATAATGAAGT	CTGAGATCA CTTTGAGCA C	ACTGAGAT CACTGAGC AC	0,0	Ots04	20118 827	Ots04	40706 52
Ots_1031 22-180	T	C	CAAACGCGCACTCACA CACA	TCACAATGGTACGA TTTTACGACTCAA	CATCAACAC AATCTGC	CATCAACA CGATCTGC	0,0	Ots04	22443 878	Ots04	16781 457
Ots4_409 42276	G	A	ATTAGTGCATATGAAT CGGGCTAT	CCAAAAGGTTGAAC GTACATATTG	GGAGTCAG ATAC	GAAGTCAG ATAC	0,0	Ots04	48716 473	Ots04	40942 276
Ots4_416 38710	G	A	CAGCAGCTGTTTATGA CTGACTTC	CTCGTGTAACCGAT GTGAAATG	CCTGAGATT AGG	CCTGAGAT TAAG	0,0	Ots04	49353 548	Ots04	41638 710
Ots4_423 78741	C	T	CAGTTTAAGTGTTACC ACCACGAG	GTGCAGGTGAGCGT TAACG	AGATGAAC ACCAACTGG CCGG	AGATGAAC ACTAACTG GCCGG	0,0	Ots04	50072 182	Ots04	42378 741
Ots_9650 0-180	G	T	CAGGTCTGGTCTACAT CGAACAC	GATCATGTCAGATA GGATGCTGAAAGT	AAAACAAA TCATTTTTC G	AAAAACAA ATAATTTTT CG	0,0	Ots04	53468 710	Ots04	45636 897
Ots4_649 78818	C	A	AGAACCCATGCTTTCA GTACACTT	AAAATGGACAGAA ATGTATCGCTC	TCAAGTGTT TCCTTTATT TTG	TCAAGTGT TTACTTTAT TTTG	0,0	Ots04	71212 183	Ots04	64978 818
Ots11_11 925999	G	T	TTTATATTCAGACATTC GCCAAAA	GATTGTCACAGTAA CATAGAAATGGTTT	CATTTAAAA TGGTAAAA ATCA	CATTTAAA ATTGTAAA AATCA	0,0	Ots04	71231 942	Ots11	11925 999
Ots_1054 01-325	G	T	GAAGTGGCGGCTGCT G	CGCCTCCTGGTGTC TATCCT	CCCGGACA AGATGAGA CAG	CCCGGACA AGATGAGA CCG	0,0	Ots04	1XXX XXXX	Ots04	12543 170
Ots_HSP 90B-100	C	T	CACCTTAGTTCCACGC AACATG	CTGCGTGTATTGTA GTGGTGACA	TCTATGGTG TGATTCAAT	TTCTATGGT GTAATTCA TT	0,0	Ots05	76415 77	Ots05	68666 92
Ots_1116 81-657	G	T	CTGAGCTTTTTCAACTT ACTTGTTGGA	GGCGCAGCAGCAA CTG	TAGCGCAA ACCCCGAAC C	CGCAAACA CCGAACC	0,0	Ots05	94397 42	Ots05	85399 47
Ots_1286 93-461	C	T	TCAATGTTTCATCAATG CACTTCCTGTA	GCCTGCAGGAGAA GGTAGAGTTA	CTGGTACCC A	CTGATACC CA	0,0	Ots05	15919 055	Ots11	29099 828
Ots_crRA D66330- 60	G	T	ACTCTCCAGAAAGGAT TCAGAGA	TCCCAAAGCATCCT GCCA	AGAGAGGG GTCAAA	AGAGAGTG GTCAAA	0,0	Ots05	17933 258	Ots05	14208 918
Ots_u211 -85	C	T	TGGTGAGAGCAGCTTT AAATGTCTT	ACCCATTCTTCTGT CTGGTTTAAGC	TCCCAAAGT CGAGTGTG	CCCAAAGT CAAGTGTG	0,0	Ots05	29079 237	Ots05	34253 781

Ots_1209 50-417	A	T	CAGACAGGTCACCATC ACACT	TGGTGAAGCTGTAG GAGAAGGA	CTGGACCAG AACTCTGA	CTGGACCA GATCTCTG A	0,0	Ots05	31561 077	Ots05	18867 357
Ots_HM GB1-73	G	T	TGCTTCAGTGAAAATA AGCGTGAGA	GTCGAGCGGTATGA ATACTTTCTGA	ACTGTATAT GTTACGTTT TC	ACTGTATA TGTTAAGTT TTC	0,0	Ots05	39590 504	Ots05	27531 907
Ots_BMP 2-SNP1	C	T	ACTGCCACAGACACGA ACTC	GCCACTATCCACTC GTTCCA	CCCACCTCG CTGAAGT	CCCACCTC ACTGAAGT	0,0	Ots05	42344 711	Ots05	30442 475
Ots5_447 95073	C	T	GCACTGTATACAAAAT CGTGTGGT	CATTAAGACAGACA ATGCCCAATA	TTTTTGTGT CCGCCATGA ATT	TTTTTGTGT CTGCCATG AATT	0,0	Ots05	54248 412	Ots05	44795 073
Ots_Cirp A	C	T	GCTGTGATTGTGCTCT AAAGACATG	CTCCCACCTTAGCAT TCCTACCTT	CAGTTCTGT AATGCATT	CAGTTTTGT AATGCATT	0,0	Ots05	56708 050	Ots05	47621 841
Ots_1272 36-62	T	A	TGGAGAACTTGCCTG AATGTGAAA	GCTGTTGGACCTTG ACTTTAACAAATT	TCTCTTATC TGAGTTCTG C	CTCTTATCT GTGTTCTGC	0,0	Ots05	61558 078	Ots05	52450 716
Ots_u4- 92	T	C	ATCCAAGGAGCCCCAT TAAAGATTT	CGTACCAGAGTTGT AGAAGCATCT	CTGTGTTGA ATTTAACAT AAT	TCTGTGTTG AATTTAAC GTAAT	0,0	Ots05	62235 849	Ots05	49324 631
Ots_unk9 480-51	G	C	CAAATCAGAACAAAAC CTCCCACAA	GGAAGTCTGTCTGA ATGGTTGTCTT	CTCCCACAA ACCC	TCCCAGAA ACCC	0,0	Ots05	68359 607	Ots05	58885 154
Ots_1095 25-816	C	T	GCCAGATAGTAGCGTA CATCATGAG	CTCCCCATGTCCCT GAGTCT	CATGAGGC GTTCCGGC	ATGAGGCA TTCGGC	0,0	Ots05	86382 977	Ots05	70296 658
Ots_crRA D47297- 55	T	C	CTCCCTGTTCGCTAGC CG	GGACGACCAAAGG TAGAACCC	TAGCCGTCA CCGAT	TAGCCGCC ACCGAT	0,0	Ots05	91281 495	Ots12	48785 08
Ots_SClk F2R2-135	A	T	CCAAATACAGACCAGC TACTTGTGT	CTTCAAGTCCCTGA ATAATGGTACGT	ATTCAAAGT CAAATTTT	ATTCAAAG TCTAATTTT	0,0	Ots05	XXXX XXXX	Ots05	60109 411
Ots_crRA D13725- 51	C	A	TGCAGGAGGAGGAAG GCA	AGAGCTGCCAGGTG GAGT	GAGGCCCC AGATTC	GAGGCCAC AGATTC	0,0	Ots06	12958 480	Ots06	10662 607
Ots6_109 04949	C	T	AAATCACCCCATTCT TTTGTG	GTAGAAAGGTGAT GTGCATAAGCA	CCTTTGTCA CCGCTCATC AGC	CCTTTGTCA CTGCTCATC AGC	0,0	Ots06	13203 375	Ots06	10904 949
Ots6_335 05144	T	A	CCCACCATACAATAAA GGCATGT	ATCTCTCCCATAAA CAAATACCCA	AACATATGA GTTGTAATG CCC	AACATATG AGATGTAA TGCCC	0,0	Ots06	14379 077	Ots06	33505 144
Ots_OTS MTA- SNP1	C	T	GCCGAAAAATAAGCG ATTAGTGATGA	GCCCCATGGTAAAC CTAATTAACCT	AATTGCCTC ATTGGGTG	AATTGCCT CATTAGGT G	0,0	Ots06	21997 348	Ots06	20396 609

Ots_Met A	T	A	GATCATTTATCAAGAC TATAGGCTATGGATAC G	AGTTGAGTTAAGTA ATTGGTAATTAGCC TGTT	CCTTAAGCA TATTTCT	CCTTAAGC GTATTTCT	1,6, 0	Ots06	21997 591	Ots06	20396 849
Ots_ZR- 575	G	A	GCCTACCAGAAAGTAC CAATTGTGA	ACTTTTCACTGTCC TATTACAATTAGTA TTTGTGATAT	CC[GA]ACAC AATTTTGT	CC[GA]ACA TAATTTTGT	0,0	Ots06	29177 962	Ots06	27576 884
Ots_crRA D46751- 42	C	T	CAGGAACCTGCTTTAA TGCTCT	GCTTCTGCAGGGGG ACAA	TTTCTACTT AGTAA	TTTCTATTT AGTAA	0,0	Ots06	35130 855	NA	NA
Ots_9490 3-99R	G	T	CCGTCTGAGTAGGAGG ATCAATACA	TTTGGATCCAGCTC TCCGTATAGA	CAAACCAG CAAACAT	ACAAACCA GAAAACAT	0,0	Ots06	36076 090	Ots06	35539 172
Ots_1076 07-315	A	C	GTGATGAGAGGTTTCC GGAAAATCT	GTGTTCTGGATTCC ATTGTGCAAA	ATGGGAGA CAGATAACT	ATGGGAGA CATATAAC T	0,0	Ots06	36480 917	Ots06	36761 804
Ots_FGF 6B_1	A	C	GAGACAAAGGTTTGCA GGTTCATG	GGGAGCCATGCACT AATATATTGGA	CCTGTTATC AGACCCAA AT	CTGTTATCA GCCCCAAA T	0,0	Ots06	37585 917	Ots06	37250 687
Ots_u6- 75	C	T	GAAAAAGTAAAGTAA AAGTAAAGTATTATAC CACTAAAGACAAT	GATCCACACTGTTG GTCTACTACAA	TTAGTCAAC TGTTGTTTT T	TTAGTCAA CTGTTATTT TT	0,0	Ots06	50534 743	NA	NA
Ots_crRA D73823- 60	T	A	GCAGGAAGCAAAGTTC GGTG	AGCAACTCATCGCG TGGT	GCACGATG[CT]AGAAC	GCACGAAG [CT]AGAAC	0,0	Ots06	52896 472	Ots06	53325 628
Ots14_54 53033	G	A	ATTATTCAAACAGAGA TGGCGAAA	GAGGAGGTTTGCAT AGAACATGAT	TCTCTAAAA AGGTACAGT ATA	TCTCTAAA AAAGTACA GTATA	0,0	Ots06	55710 320	Ots14	54530 33
Ots_u07- 53.133	C	T	AGCTAGGCTGTAAATG CAAGGAT	CAGTGCTTTCAATT CATGCTGTCAA	TAACACATG TTGGAGGTC	AACACATG TTAGAGGT C	0,0	Ots06	58232 274	NA	NA
Ots_GDH -81x	C	-	CTTTTCTGAATTAGTGC TGTGCTTGT	CCAACCTTCTTCAAC TCTGTCACTGA	TGTTACGGG ACATACT	TCTGTTACG GACATACT	0,0	Ots06	58688 462	Ots06	585X XXXX
Ots_GnR H-271	C	T	CAGATGAAAAATAAAT AATTGGGCCATTAGGA A	CAGAGAGACTGAG ACCATATGATGTAG T	CAATGAATA CAATATCTA ACCTAAT	AATGAATA CAATATCT AATCTAAT	0,0	Ots06	65879 558	Ots06	65660 176
Ots_1159 87-325	T	G	GGAGGTGTAGTGAAAT GGGAAGAT	GCATTCACTGAACC AGTAGTGCTAT	ATGCATAAA AGGTAATTG TG	ATGCATAA AAGGTCAT TGTG	0,0	Ots06	66387 317	Ots06	66193 572
Ots_1053 85-421	A	G	GACTGTCTTGGAACCG TTGCTA	TCCCGGAACACACC AATGTC	CCTCCTGGG TATATCG	CTCCTGGG CATATCG	0,0	Ots06	73075 541	Ots06	73012 849

Ots_map Kpr-151	A	T	TGTTGTCTCGGACTGC ATGAC	GAAGGCACAGAGA TGAAGGACAT	CGTATGTGC AATGCATG	CGTATGTG CATTGCAT G	0,0	Ots07	35931 75	Ots07	54601 43
Ots_map K-3'-309	T	G	GGCCACTGTCATAGAA TTAGGCATT	CGTGACCCTTGTA CTGAAAAGC	ATGCTATTA AATGAATAT TC	ATGCTATT AAATGACT ATTC	0,0	Ots07	36086 28	Ots07	54800 42
Ots_1287 57-61R	A	-	CGTGTCCGGCTTCTTTT ATTCATT	GATGGGTATGTTAA TCATATTACCAGCG TAA	TTGTGCATT TTCCCC	TGTGCATTT CCCCC	0,0	Ots07	66438 30	NA	NA
Ots_1318 02-393	C	T	TGATTGTCTCATGGCC AATTGTCA	TGTAAATTCCACTT GGCAATCTTTGG	TGTTTCGAGA ATGAAGAT GAGTAA	TCGAGAAT GAAGGTGA GTAA	0,0	Ots07	35733 706	Ots07	25665 994
Ots_1314 60-584	T	C	CCTATTTTTGATAGGTC ATAGTGAATGGGATAG	CTGTACTCCTCCAT TCCTTTTCACT	CTATCAAAG CAATACATT G	CTATCAAA GCAGTACA TTG	0,0	Ots07	42945 148	Ots07	31130 645
Ots_CHI 06048618 _5222	T	G	GCAATTACCCATGACT CTGTGA	GCCAAAAAGAGAC CGAATCA	ATTGTGCTT ATCACA	ATTGTGCTT AGCACA	0,0	Ots07	50130 039	Ots07	38043 969
Ots7_509 97124	G	T	AGATCAAGCTTGCTGA CTTCG	CATACACCACACTG TATTTTGCTG	GGGCCTTCG GGGTGCCTG TCC	GGGCCTTC GGTGTGCC TGTC	0,0	Ots07	62901 252	Ots07	50997 124
Ots_nram p-321	G	A	GGCCATCTTTCAGGAC GTACAG	GCATGCTCTGCAAT ACGTTGAG	AAC[GT]GGC ATGAACGA CTT	AAC[GT]GG CATGAATG ACTT	0,0	Ots07	63847 460	Ots07	51336 125
Ots7_514 09415	T	C	ACAACTAGTCATCGTG GAATCTGA	ACATGCTAAAAGA AAGGAATGAGG	TGGTCTACT TTGTGC	TGGTCTACT TCGTGC	0,0	Ots07	63921 389	Ots07	51409 415
Ots9_289 75221	A	T	GCCTGCCCTACTTATCT CTTATCA	ACCTCTTCACTGTA AAATTTGCTG	TTTGCCAAA GAGTTCAGA TAC	TTTGCCAA AGTGTTC GATAC	0,0	Ots07	64709 638	Ots09	28975 221
Ots_arp- 436	A	T	GCCCTGGAGAAGTACG TTTTAACTAA	GCAACCATGTCAAC ATTGCACATAA	CTAGGTGAA ACTTTTTTT AAA	CTAGGTGA AACTTTTTA AAAA	0,0	Ots07	65259 187	Ots07	52672 820
Ots7_532 91035	G	A	TCAAATTGAATGTAGA CAGATGGAA	AAATAGCTCGCAAA GCTAACATTA	GCTAGCAA ACGTCGCCA	GCTAGCAA ACATCGCC A	0,0	Ots07	66039 124	Ots07	53291 035
Ots7_536 31522	A	G	CTTATCTCAAAGGAAT GGGAATGA	CTACAGTATTTGGA TGCAGCTTTG	TGAGTTTTT AAGGGGTT	TGAGTTTTT AGGGGGTT	0,0	Ots07	66362 189	Ots07	53631 522
Ots7_542 12944	T	A	AAACCACGGTATCCTT TATTCATC	TTCTAACCCCAAA ATATGTCTAAA	AATATATTT TTTATAGGC	AATATATA TTTTATAGG C	0,0	Ots07	66905 811	Ots07	54212 944

Ots_9707 7-179R	G	T	CCTGAACAAATACTTA ACGCTCCAGTT	GTAATAATACTTCA CACCATTGCCACTT C	TCACAAATG TATCCTAAA GC	CACAAATG TATACTAA AGC	0,0	Ots07	70085 972	Ots07	5632X XXX
Ots_1051 05-613	C	G	AGTACAAGTGCAGAGA ATGACATCATG	GGTGTTTTATTTTCC CATATATCTTTTAA CTTTAAGCT	CCGAGCTTG AGTTAGGA	CCGAGCTT GACTTAGG A	0,0	Ots07	77202 120	Ots07	63322 755
Ots_slc7a 2-71	G	T	CCATTCCCATCGGCAT CGT	GCAGCAGACACAC CGAAGTA	GTCTCTGAC GGTGTGCTT TC	GTCTCTGA CTGTGTGCT TTC	0,0	Ots08	86683 69	Ots08	61099 332
Ots_crRA D34397- 33	C	G	TGCCTAAACACTCCCA AGGT	GTTCCGTTTTTGTTC CGCGA	AA[GA]GTG CCTTCCCC	AA[GA]GTG GCTTCCCC	0,4, 0	Ots08	10116 544	Ots08	60161 043
Ots_u07- 64.221	G	C	GAGGATGACACTGTCC GTTTGT	CACAGTCCTTCGTA TTCACCTTGAT	ATCGACCCT GTCATTAG	CGACCCTG TGATTAG	0,0	Ots08	12242 337	Ots08	57998 143
Ots_1030 41-52	G	A	ACCACCCACCTCCTCA GA	AGACAGAGAAAGT CGGGACACT	CATCCTGCT GGACCC	CATCCTGTT GGACCC	0,0	Ots08	15518 130	Ots08	55669 454
Ots_OTA LDBINT 1-SNP1	T	C	CGCTGGGCATGGATGA GT	GGCCAACACTGCTA CTTCCT	CTACTGTTG TATTTTCTC	CTGTTGTGT TTTCTC	0,0	Ots08	16275 426	NA	NA
Ots_1017 04-143	T	G	ACTTCTTGAGCCAATC GGATGATG	CCAGAGATAAACTA GTGGAGGAGATCA	CTTAGACGT CAGAGGTC	CTTAGACG TCCGAGGT C	0,0	Ots08	21039 383	Ots08	51040 180
Ots_1022 13-210	A	G	CATTCCATGACAATGA TTGAAATCTAAAAACA C	GAGTATCTCAATTG CAACACTATGGTAT GT	CTGTATACA GTAAGAGT ATTAAT	ACAGTAAG AGCATTAA T	0,0	Ots08	26477 291	Ots08	45XX XXXX
Ots_1291 70-683	C	A	AACCCTATGGGAACTC GTAGAACT	GCTAGGAGTTCTCA AAAGGGTTCT	ATTAGAAGT CGTAGAACT AT	ATATTAGA ACTCGTAT AACTAT	0,6, 0	Ots08	47390 818	Ots17	11485 501
Ots_ppie- 245	C	A	TGTTTTTGGTCATGTAT TTTCTCTGCTATTTTT	GGACTGGAGCTGCT GAACATA	ATGTCTGAA ATGAAAGC C	AATGTCTG AAATTAAA GCC	0,0	Ots08	50220 193	Ots08	23260 130
Ots_Asn RS-60	T	C	CCGACGCCTCACTGAG T	TGGTTTTTCAGGTC ATGGTTTCCA	TGAGTCCCT GACCAGC	AGTCCCCG ACCAGC	0,0	Ots09	28000 47	Ots20	41784 960
Ots_u100 7-124	A	G	CGAAATAAGGGCCTGG TGTTTAAAA	TGTACCAGGTGGAA GCTTTGG	TGTCCTGTC CTCAGATCA CCAGTGAG	TCCTGTCCC CAGATCA CCAGTGAG	0,0	Ots09	11679 141	Ots09	94303 81
Ots9_161 15048	G	A	ATAGAGCTTTTGGTGT TTCATTCC	AGTGTGTGTACTGT GTACTGGCCT	ATGCTGTGT TGCA	ATACTGTG TTGCA	0,0	Ots09	19855 559	Ots09	16115 048

Ots_P450-288	A	G	ATGTCAATATATTTCA CTATAATGATTGGAAG CCA	CACTGAACTCGAAG CTGTTAGGA	CTATAAAGT TGGACAGTT GG	AAAGTTGG GCAGTTGG	0,0	Ots09	23147 965	Ots09	19138 835
Ots_102457-132	A	G	CCAGCAGAGACTGGGT TCAC	TTCCCTACCGGCGA AACC	TGGGGCAA CGCACAATT GGCT	TGGGGCGA CGCACAAT TGGCT	0,0	Ots09	26992 696	Ots09	23XX XXXX
Ots_110201-363	A	T	TTTTGGCTATTGAAAT TATACATTAAAACATG TAGCT	CCATGGCATCCTGT AAAGAACAACA	TTTTAAAA+ CTGGCATCC A	TTTTTAAAC TGGCATCC A	0,0	Ots09	29017 362	Ots09	25990 000
Ots_hsp27b-150	G	A	TAGGAGTTGGAAAGAC TGCACA	CCCATTGGTTCTTT GGTGTT	[CT]GATCTG GACCAGGCT	[CT]GATTTG GACCAGGC T	0,0	Ots09	67075 478	Ots09	52471 033
Ots_u1008-108	T	A	GGATGACTCCTACTAA TAGACGGATGT	AGGACAGGAAAGA AGCAGCAAATA	TTGGTAAAC CTGTTTATT GGTA	TGGTAAAC CTGTTTTTT GGTA	0,0	Ots09	75362 394	Ots09	62354 402
Ots_FARSLA-220	G	A	GTTCGTGGGATTGTTC AATGTTTCAT	CTTGGACAGGCTCA CATTACCATA	CCTTGGATG GGA	CCTTGGAT AGGA	0,0	Ots09	82809 166	Ots09	68274 964
Ots_hsc71-3'-488	C	T	TGCATCCATTCCATACC TGACCAATT	TTTGGTTAGGCACA CGATAATTTGC	TTTCCAATG GTATAGATA TGA	TTTCCAATG ATATAGAT ATGA	0,0	Ots09	XXXX XXXX	Ots09	37358 812
Ots_Thio	T	C	TTTTAAAAATGGAGAT AAACTCCTGACCTGAA	AATACCAAACCATG CCACTAATACCT	CAGTGTATT AGTCATTCT TA	CAGTGTAT TAGTCGTTT TTA	0,0	Ots10	71448 61	Ots10	56253 22
Ots_112820-284	C	T	CATAGATGTTTATATG AAAAACCTCCCACTGT	GCATCCAAAAAGA CGTGTGTGTTT	ACTCACACT CGAGTGACT	ACTCACAC TCAAGTGA CT	0,0	Ots10	18438 064	Ots10	16907 470
Ots_102414-395	A	G	GCCTACTGATAAATGT ATGACAGTAATGGA	CAATAACAAACAA GCTAGGAACAAAA GTGT	CACATAGTG TAGCTTTAC TAC	CACATAGT GTAGCTCT ACTAC	0,0	Ots10	21873 207	Ots10	20097 469
Ots_108007-208	A	T	CAGGCTTGTGTAAAGT AGGGAGAAA	CATTGGACAAGACC GGGTAGTC	CAGTTTCAC TTAATTTTA AAATG	TTTCACTTA ATTTAAAA ATG	0,0	Ots10	25247 839	Ots20	49711 42
Ots_129144-472	C	A	CTGTTAGTGCAGAAGA CGTAGCT	GCAGAGCTATTGAG CCAAGTTACAA	TGGGTCTCG AGCCTGTA	TGGGTCTC GATCCTGT A	0,0	Ots10	30541 697	Ots10	30704 018
Ots_crRAD10447-25	C	T	CCGTTGCAGGACTCAT CAGT	GCGTGGTTCAACAG CAGTG	AGCTAGCGC TCCTC	AGCTAGTG CTCCTC	0,0	Ots10	36392 206	Ots10	36699 634

Ots_crRA D18937- 60	G	A	GGCACAGCGACAGGA GTT	TGAGCTGGTGCCTC TGAG	CTCCTCAGG TGGGC	CTCCTCAA GTGGGC	0,0	Ots10	50635 181	Ots10	51017 984
Ots_nkef- 192	C	T	CATTTAGCAGACACTC TTATCTTAGTGTCA	CGAATGTCCACCTC AGATGTTACAA	AATAGGCC GACATCAA	AAATAGGC CAACATCA A	0,0	Ots10	51361 376	Ots10	51394 567
Ots_crRA D26165- 69	C	T	GGGCCACGGGGTTGTA AA	TCCCAGGATGCAAT GGGA	CTCT[GA]CC CCTGGAC	CTCT[GA]CT CCTGGAC	0,0	Ots10	52149 501	Ots16	20109 332
Ots_u07- 57.120	A	T	GGTTTGAGCCAATCAG TTGTGTT	CGGTCTAATGTCCA TTGCTCATGTT	GTGACAAG GTAGGGGT G	GTGACATG GTAGGGGT TG	0,0	Ots11	12974 126	Ots11	16346 192
Ots_1063 13-729	A	G	TTGTTCAATGGGCATT AATGCATGTT	TGCTTATGTGCAGA TACTTGAGACAAA	AAGAGTCC AGCGTTACT T	AAGAGTCC AGTGTTAC TT	0,0	Ots11	16517 829	NA	NA
Ots_1087 35-302	C	T	CCTTTTTCTTATTAGTT TTACTTCCCCAGAGA	CAATTCCATTCTTG ATTCTGTTTAACGG T	AAACAAAC AACGCCTCA TG	AACAAACA ACACCTCA TG	0,0	Ots11	17583 626	Ots11	21337 974
Ots_crRA D76512- 28	A	T	GCAGGGACAGGGCCCT	TGGTGCTGGGTGCT GTAC	TAAAAAAA TATAAA	TAAAAATA TATAAA	0,3, 0	Ots11	25425 413	Ots11	32328 258
Ots11_32 418659	A	T	CAATTGTAGCCCTCTA ACTTTTCC	ATACGACACACAA AGCCAATTGTA	AGCCAATTG TAGCCTTAG TGC	AGCCAATT GTTGCCTTA GTGC	0,0	Ots11	25519 430	Ots11	32418 659
Ots11_32 468959	G	C	AACACAGATCAAATGT TTTCACAC	AACACAGGAAAAA CAGAATGTTGA	GTGATAGTT TGATAGTTT TAT	GTGATAGT TTCATAGTT TTAT	0,0	Ots11	25588 829	NA	NA
Ots_crRA D9615-69	T	C	GAATGCAGGGCCAGG GAG	ACTCCCAGACCATC CAGCT	TATTGGTCA GGGAA	TATTGGCC AGGGAA	0,0	Ots11	25656 094	NA	NA
Ots_crRA D36072- 29	T	C	TGCAGGACCAACTTTC TCAT	GGCTGACTGGTGAA GGGG	AACCTGTGT GATTT	AACCTGCG TGATTT	0,0	Ots11	29147 224	Ots11	36019 633
Ots_crRA D61523- 71	A	G	GCCAAGTGATCAAGTG CTTGT	CCAGCAGTTCAGTT GCGG	CAGAGCAT GTGCTG	CAGAGCGT GTGCTG	0,2, 0	Ots11	35352 564	Ots11	41149 096
Ots_GPH -318	C	T	GGTGATAACAGGTGTT GCACCAA	TCAGGTGGTGGTGG ACAAC	ATCAAGCTG ACGAACCA	CAAGCTGA CAAACCA	0,0	Ots11	40844 253	Ots11	46176 184
Ots_crRA D20376- 66	G	A	GGGAGGCAGGCAAAA GGT	GGTTCACCACCAGC CTTCT	GGGA[TA]G GAGTATTT	GGGA[TA]G AAGTATTT	0,0	Ots11	41283 424	Ots11	46457 753

Ots_zn59 3-346	A	T	CTACGCGAGAAATAAC ACTTTTCAAAACT	GGCGAGTTTATTAC GGTGTTATGAC	TCTTGCAAT CATTTTTTAA C	CTTGCAAT CATATTTA AC	0,0	Ots11	41292 800	Ots11	46464 971
Ots_IsoT	T	C	GACTCAGGTAAGGAAA CATCAATGTCA	GAAAGCAAAGCAT TTTATCCACCACTA	AACCAGTA GAATAACC CTAACCCGG	CAGTGGAA TAACC CTAACCTG	0.5, 0	Ots12	10323 252	Ots12	91214 89
Ots_crRA D55400- 59	C	T	CGCAATGAGCCAACCC CT	CTGGTTTGTTCCTG GGCT	A[CA][GA]A C	GA[CA][GA] AC	0,0	Ots12	18236 712	Ots12	17250 308
Ots_1028 67-609	A	G	CTCTGCCATTCATTTGG GCTTTG	GTCTAAAGTGGTCC CCTTGGAT	ACAGAGAG AAGTCCCAG GTG	AGAGAGAA GCCCCAGG TG	0,0	Ots12	21101 745	Ots12	204X XXXX
Ots_1319 06-141	A	T	GGCTCGAACCACCCAG TTTA	TGCCCAACTGGTTT GCAATC	CACGGTTTA CACTCCTAT TA	ACGGTTTA CACTCCAA TTA	0,0	Ots12	21773 920	NA	NA
Ots12_23 066874	A	G	CTCTTTTCAGTTGTCTTT GCTCTTG	ATTATGAAAAGGCA TGAACAGGGT	TCCCCACCA AAATTAAGC AAA	TCCCCACC AAGATTAA GCAAA	0,0	Ots12	25387 620	Ots12	23066 874
Ots_pop5 -96	T	C	CTCTTGCTACTTGCAGT GTATCTCA	AGTTTGAGGGCTCT ATTCTGTCATG	TTCTGTTAC TGGAC	CTGTTACTG GGC	0,0	Ots12	29307 827	Ots12	27353 346
Ots_u07- 49.290	G	A	GCTGAGGAAGGATTCT GTATTTGCT	TCGGACAGAGCGC ATCC	CTTTCCCCG TGTTGGT	ACTTTCCCT GTGTTGGT	0,0	Ots12	31470 258	Ots12	30314 171
Ots_cox1 -241	C	T	CACTGAAGTGTAAAGCC ATTGTGATT	GTAAATGTAGTATA CAGTATAGGCATCG TAGGT	CACTACGGT AAGACCAT	CACTACAG TAAGACCA T	0,0	Ots12	31570 301	Ots12	30421 258
Ots_ETIF 1A	A	C	TCTGAAGTCAACAAAG GAACACTTG	GAGAGAAAAGGAG AAATGATTGCCATT	CAACTGAA GAAAATAA TATG	CTGAAGAA AAGAATAT G	0,0	Ots12	38462 855	Ots12	34678 104
Ots_GCS H	C	T	GTTCTTTTTTAATGATGA CTACAGGTCTTTTCAC	GCTACTTTACATAA TACCATTTGAGCTG AGA	TATCTGGGC GGGCTG	CTATCTGG ACGGGCTG	0,0	Ots12	65634 622	Ots12	58052 588
Ots_9689 9-357R	T	A	TCTCCTGAAGTAATTT AGACCTCTGAATGT	CCTCATATTGCTTT CATCTGAAGAGAG A	CTGAATGTT TTTTTTAAT CTTT	CTGAATGT TTTTTTTTTA TCTTT	0,0	Ots12	67888 781	Ots15	21523 451
Ots_aspat -196	G	C	CCTGAACAGGTACACA CAAACGA	TCCAAGTATGAAT ATGACCAACATGAA T	CACTCTTTA TATCCACAC C[GA]	CAGTCTTTA TATCCACA CC[GA]	0,0	Ots12	68043 508	Ots12	60406 597
Ots_P450	T	A	TGAGCGAGATTTATCA AACTGTCAAAGA	CCCAAGCGGGAGA ACTTACAG	CCCCGAAGT ACTTTT	CCCGAAGA ACTTTT	0,0	Ots12	72832 053	Ots12	65154 384
Ots_brp1 6-64	T	C	ACTCTGGGTCCAGGAG GTTTT	CTGACGAGACCATG CACCAA	AAGTCAGC ATCTTTCA	AGTCAGCG TCTTTCA	0,0	Ots13	42932 54	Ots13	43839 23

Ots_1064 19b-618	G	T	CAAGGGCACATTGGCA GATTTT	ACCGGACCAAAGC ACACA	CAATGATTA ATGATTAAT CCTTC	TGATTAAT GATTCATC CTTC	0,0	Ots13	11736 968	Ots13	11463 845
Ots_HFA BP-34	C	T	CAAGAACACCGAGATC TCCTTCA	TCGGCGGTGGTCTC G	TCGAACTCC GCTCCTAG	TCGAACTC CACTCCTA G	0,0	Ots13	12380 464	NA	NA
Ots_TAP BP	C	T	TTTCTCATCCTTCTCTC TTCCAGTCT	GGACAAACCAGCA CTCCAGAA	CAGCTGTCC AGTTCTG	CAGTTGTC CAGTTCTG	0,0	Ots13	26128 999	Ots30	34770 823
Ots_crRA D27164- 55	A	T	GGAGGCTCTACGTAGG CCT	ACAATATCTGACAC TGACTTGGTCA	AATTTGAAT GACCA	AATTTGTAT GACCA	0,0	Ots13	27591 014	Ots13	25285 990
Ots_myb p-85	C	T	CAAGGGATGTGACAAA TTAATCAAACACATAA	AAGAGGTCTAATAA ATCTCCAATGTAAA AACGT	AGAGCATGT AGTTTTG	AGCATGTA ATTTTTG	0,0	Ots13	31784 059	Ots13	29231 079
Ots_crRA D17527- 58	C	T	TGCCGCTGGATTTATT GACA	GCGTCAGATCAGCT GGTCT	TAGCTCCGA GCTAA	TAGCTCTG AGCTAA	0,0	Ots13	36124 810	Ots11	37324 165
Ots_1124 19-131	A	T	GTGGGTAATCGATGCC AAAGAGAT	TGGCAGTGTTTTCA ACTAGCTTTG	AAGCGACTT GATTATC	AGCGACAT GATTATC	0,0	Ots13	45350 303	Ots32	78532 51
Ots_hnR NPL-533	A	T	TCTTTGATATTGAGCTC ATAAAAGCAAGGT	TCCTTGTTTCATCCA TCAGGCATAAAA	CATTTACCA GTTCTCACA CAC	TTTACCAGT TCACACAC AC	0,0	Ots13	46418 615	Ots13	46705 374
Ots_SL	A	G	AATATTGGCTTTCTGA GAATGCATTTGG	CCAAGATACTTCCT TTAACTTCTCTGTC A	TCAAAGATA TGATTCAAT TAA	AAGATATG GTTCAATT AA	0,0	Ots13	62174 556	NA	NA
Ots_crRA D35313- 66	A	G	TGCAGGAAGAGTTCAG AGAAATCT	GCTCGTTGCAGGTA GAAATGT	TTTAAGATG TAGTT	TTTAAGGT GTAGTT	0,0	Ots13	70298 983	Ots13	65139 272
Ots_U25 67-104	G	A	CATAGTATAGTGATTC GAGTCTGGAGTCT	CGGGCTTTCTTAGG ATATTTTCCTGA	GAGACTGTT GAGAC	GAGACTAT TGAGAC	0,0	Ots13	73139 521	Ots13	68622 537
Ots_IL8R _C8	C	T	CGTGGTGTTGCGCTTC CT	TGTCGGCCATCACT GTCATG	CTGGACGCC GTTACA	TGGACGCC ATTACA	0,5, 0	Ots14	14298 70	NA	NA
Ots_GPD H-338	G	A	CACTAAATATTCCTTA TCATTTCTACTAAGT CTGAAGAA	AGCTGATACACAAT CAAAACACAAAAC AT	CCACTACTT AACGTGCTT T	CCACTACTT AACATGCT TT	1,0	Ots14	79965 96	Ots14	11576 466
Ots_CHI 06035945 _4547	C	T	AGCGAGGCTTGCGTTT TACT	GTGCAGTCTGGGCT TGCTCT	CCGCAACA GATC	CTGCAACA GATC	0,0	Ots14	87879 79	Ots14	12373 492

Ots_U50 49-250	G	T	CAATGTCTAAAGTAAT GGTGGTATTCTTGC	TCTTTGACACACCA TCTGCCAATT	TGGAATGG GTAAGGTGT A	TGGAATGT GTAAGGTG TA	0,0	Ots14	21359 050	Ots14	2257X XXX
Ots_crRA D18492- 65	C	T	GCAGGGCGCAAAGTTC TT	CAGTGAGCGACTGT AATCTGA	TTATGGCTA TTATT	TTATGGTTA TTATT	0,0	Ots14	43620 612	Ots14	424X XXXX
Ots_crRA D57687- 34	T	G	TGCAGGGACGGGGCT	TGCTGTTGTCTTGG GTCTCTC	ACAAATTAA TTAAA	ACAAATGA ATTAAA	0,0, 7	Ots14	3XXX XXXX	Ots14	31889 864
Ots_1040 63-132	C	T	GCGTTACTGGTGTTAT AAACGTTAGC	GTTTATTTAATTAT GAAGGACGATGTTG AAGTCA	CTTTCGTCC TTAGCACAT AG	CTTTCGTCC TTAACACA TAG	0,5, 0	Ots15	27472 51	NA	NA
Ots_NFY B-147	C	T	CAGATGATAGCTTCAG TAAGTGGTTCA	CCGTCCACAGCACA AGACTATAATA	TGTTCCAAT GTAAAATGT ATGC	TTCCAATGT AAAATATA TGC	0,0	Ots15	53130 10	NA	NA
Ots_1247 74-477	T	C	AGTTGTTCTTTTTATAT TGTGTTTTTATTCCATT CCA	GCCAAATAAAAAC AAAGCATGAACAC A	CCACCGCCA TCTGATA	CACCGCCG TCTGATA	0,0	Ots15	10921 418	Ots15	15167 502
Ots_vatf- 251	G	-	CTTTTCGGGTTATTCAT GCTGTTGT	GCAAGCATTTGAAA AACAGACTGGAT	AGACCACA AGATACAGT ACC	AGACCACA AGATAGTA CC	0,0	Ots15	13005 607	Ots17	76640 45
Ots_1122 08-722	C	A	CTGCATGAACGTTAAC TCAAATAAAAGGT	AATGAGTTCTACTG ACATTGTATACTAG AATAAGTATCA	TGTGAGGGC GGTCTT	ATGTGAGG TCGGTCTT	0,0	Ots15	13348 552	Ots15	17637 330
Ots15_18 157381	C	T	TCTCAATGTGATTGAA ATGGATGT	TGTCTGTAGTTTGT GTGTACGGTG	CCCTGGAGA TCT	CTCTGGAG ATCT	0,0	Ots15	13993 075	Ots15	18157 381
Ots_crRA D20887- 70	G	A	CTGCTTGTAGCCGTTC AGC	AGAACACATCTGGC CAGGT	GAAGTCGTC GTTGG	GAAGTCAT CGTTGG	0,0	Ots15	17832 008	Ots20	73780 67
Ots_CHI 06027687 _143477	G	A	GCGAGTGTTAAAAGGG TCAAA	TCTCAAGCCATAAG ACGGGTA	GGAGATAG TCAGGG	GGAAATAG TCAGGG	0,0	Ots15	17999 857	Ots01	34155 766
Ots_1028 01-308	C	A	TGGGACAGAGGTGGG AATTGA	CCCAAAGATGCTTA ACTGAAGATGTG	AGGGACAG TTTCGCAG CG	AAGGGACA GTTTCTCAG ACG	0,0	Ots15	19904 397	Ots15	19971 476
Ots5_709 08626	T	C	TACGGTAGGAAGACTG AATGAGTG	CCCTACCTCTCCAG ATAGCTTGTA	AGCCTCTTC CTCTCTG	AGCCTCTTC CCCTCTG	0,0	Ots15	36201 712	Ots05	70908 626
Ots_1172 59-271	T	G	ACACCCACTTCAACCT CCATAAC	GCCTCAGAGCTTAG CTTGGA	CTCTCCTGA TCACTCTGT	CTCTCCTGA TCCCTCTGT	0,0	Ots16	11947 135	Ots16	11458 685

Ots_1172 42-136	A	G	GTGACAGGAGACAGA AAGAGACATT	TGGTCCTCCCTGTC TCTATCTACTA	CAGCACATA ACTTGACCT C	AGCACATA ACCTGACC TC	0,0	Ots16	29941 952	Ots16	29333 295
Ots_unk5 26	A	G	TCAAGACTGTGCTGTA GTTGTCTAC	CCTCCCCCTTTTCC ACATCAG	CAACATTCC AGTCTGAAA C	CATTCCAG CCTGAAAC	0,0	Ots16	30269 244	Ots16	29699 840
Ots_Myc- 366	T	C	CCTTAGCTGCTCTTTGA AGTTGACT	GGCTATAGAGTGTA TTTACAGCATGCA	TCTCTGCTC ATCTGTC	CTCTGCTCG TCTGTC	0,0	Ots16	30269 853	Ots16	29700 449
Ots_unk1 832-39	C	T	GAAACGTCTATGCTGT CCCCTTTAA	CTGCAGTATTAGCT CTAGTTGAATCCA	CACCACTAG AACTCTC	CACCACTA AAACTCTC	0,0	Ots16	37061 421	NA	NA
Ots17_88 5364	C	A	GTAAAGAAACATGACC TTTTCTGAG	CAGGTTATGGCCAT CATAGTTAAA	TAGCCTTAA GCGCTTCCT GCC	TAGCCTTA AGAGCTTC CTGCC	0,0	Ots17	14052 57	Ots17	88536 4
Ots_1044 15-88	C	T	CCTGAGCATCCCAGTT GAACT	TGTTTTCAATACAC TGCAATTTAGTTTT GGT	TCCTGAAAA ACGACATCC	CTGAAAAA CAACATCC	0,0	Ots17	59936 49	Ots17	55123 67
Ots_SWS 1op-182	T	A	TCAAAGACATCGAACA CAAGAACGA	GCAGGTAAATTCAA ACGTCATCATAAGA A	ATGTACTTT AACGATTCA TTT	ATGTACTTT AACGTTTC ATTT	0,0	Ots17	86561 75	Ots17	73656 88
Ots_crRA D16540- 50	C	T	TGTGTATTCGTCGACC GGA	TCACCTGACCAAAG CACTGG	ATTAAACGT [CA]TGGA	ATTAAATG T[CA]TGGA	0,0	Ots17	11570 673	Ots17	97284 18
Ots_crRA D2806-42	C	A	GCAGGGGCAGACTGA AGG	ACTTCATGCCAATC TCACTAAACA	GTTTGGCAT AAAGT	GTTTGGA TAAAGT	0,0	Ots17	15937 591	Ots17	14222 969
Ots_crRA D22960- 32	C	T	ATCAGGTCTGGGGCGA CA	TTCACCTCTGCCAT CGCC	CGACACCAC TTACA	CGACACTA CTTACA	0,0	Ots17	15937 659	Ots17	14223 038
Ots_IGF- I.1-76	A	T	GGTAGGCCGTCAGTGT AAAATAAGT	GATGGAGGCCACTG TGTTCTTA	CTGCCTAGT TAAATAAA ATA	CTGCCTAG TTAAATTA AATA	0,0	Ots17	17781 778	Ots18	41507 43
Ots18_35 41813	T	C	CCCCAAAAACATCAAG AAGTCTAA	ACATGGTGAGGAA AAGGTAGACTAA	CTACCTACC TTAGTGCTC	CTACCTAC CTCAGTGC TC	0,0	Ots18	45874 5	Ots18	35418 13
Ots18_35 50047	A	G	ATCATCTCTGCTCAGA GGCTATTC	AGAGTGGAAGGAA CGTCTTACACT	TCATTTTTG CAGAGAGA GAAT	TCATTTTTG CGGAGAGA GAAT	0,0	Ots18	46766 1	Ots18	35500 47
Ots_crRA D92420- 25	G	T	AGTGCAGGTCTCCAGA TTTACA	ACCGAAGTGTATGT AAACTTCCGA	CAATCGGA AGTCGG	CAATCGTA AGTCGG	0,0	Ots18	24234 32	Ots18	66951 98

Ots_crRA D33491- 71	C	T	CAGTTCGCTTCTCCAG GGA	TGTGGGTAGCAGAC TGACG	GAGAGCCG AGCTTT	GAGAGCTG AGCTTT	0,0	Ots18	61008 51	Ots18	26993 87
Ots_crRA D12037- 39	A	G	TGCAGGAACTTGCTAT GCT	TGTGGAAAAAGTCA AGGGGTCT	CATTCAAAA AGTAT	CATTCAGA AAGTAT	0,0	Ots18	97703 15	Ots18	10327 070
Ots_crRA D55475- 26	T	G	TGCAGGGTTGGGGACA ATT	AGTCTATTTCCCGA TTTGACTGGA	CCATTTTAA TTCCA	CCATTTGA ATTCCA	0,0	Ots18	17529 243	Ots18	17929 277
Ots18_29 943476	A	G	GTTCATTTTGAAATAA CTGCATCG	CTCTACAAGGTCCA TGCACATTAG	GCCTGACTG GACAACCAT TTG	GCCTGACT GGGCAACC ATTTG	0,0	Ots18	30949 170	Ots18	29943 476
Ots18_30 099101	C	T	CAAATGTAAGGATACG CTTGAATG	GAGTTGCAAGCGAT TACATGTATT	ATTGCATAC TCGAGTCAT CCA	ATTGCATA CTTGAGTC ATCCA	0,0	Ots18	32296 859	Ots18	30099 101
Ots_Hsp9 0a	G	C	GTCGTTTTTCATAGAA AATAGCTCACAGTT	ACAGTATACCGGCT GCCTATTCTATA	ATTTGACTT GTCTTTTT TACAGGAG	ATTTGACTT GTCTTTTT CAGGAGAT	0,0	Ots18	32303 237	Ots18	30105 519
Ots_S7-1	T	C	TGCCATCATAAACAAC CTAACAAGTAACT	CCTGGTTTAAAAAC GGCCAACCTG	ATAAGGTCG CA	AGGGTCGC A	0,0	Ots18	33195 644	Ots18	31651 991
Ots18_32 088284	T	C	CATGAGACACCTGGA GAAAA	ATTTTGATAGTACC TTCTTGGGGC	ATGTTACAT GTA	ACGTTACA TGTA	0,0	Ots18	33781 780	Ots18	32088 284
Ots_pigh- 105	A	-	GCATTACTAAAACTG GTGTGTGGAA	GTTTGGAATGTTTC TCTGATTGTGTAA CAA	TGACCTGAA AATA[TC]AT ATTTTT	ACCTGAAA ATA[TC]ATT TTTTT	0,0	Ots18	38228 583	Ots18	35641 063
Ots_CD5 9-2	G	A	CATGTTACCCAGCTAA AAGTCTATAGCA	TGTTTATCTCTGAG TGAAAAAGGTGTGT	CTAAAATGT CATGTAAAT AT	ACTAAAAT GTCATATA AATAT	0.5, 0	Ots19	95507 12	Ots19	93127 96
Ots_RAG 3	C	T	CATTTCCACGAAAAGC CAGATGAC	ACAGAATAAAGTAT CTTCCTCTTACATC ACTACTAAT	CTCTACAGT ATG	CTCTACAA TATG	0,0	Ots19	36242 326	Ots19	34427 967
Ots_1103 81-164	A	G	CTCTTGTTTGCTATGGG AGATGTAGT	CCGTATCCTAAACC CTTCACTGTT	ATTTGCGTC TTCTCCC	TTGCGTCCT CTCCC	0,0	Ots19	36960 028	Ots19	35228 582
Ots_RAS 1	C	T	TCATAAACATGGTGTC TTTCAGTCAGTT	CTGACATGTGAAAC TACTAAAGCATTTA ATCAC	CAATCTATC ATCGACCAG C	CAATCTAT CATCAACC AGC	0,0	Ots19	37925 628	Ots19	36275 840
Ots_9544 2b-204	A	T	GTCTCTCTCTTTTGCA TCATTACACT	GGACTCTTGAGCTG TCTGGCTATAT	TGGTTCCCC AAATTT	TGATGGTT CCCCTAATT T	0,0	Ots19	40912 881	Ots19	39212 513

Ots19_46 172133	C	T	CACATGGCTCTTTGCT CAAAAT	GCCTACCATTATGT GTTGAATGTT	GCAAATCTC CGATGTAAA GT	GCAAATCT CTGATGTA AAGT	1,0	Ots19	47135 055	Ots19	46172 133
Ots19_46 172427	G	A	CAGTTCCTGACATTCA CCAAAATA	GCAAACAACCCATC ACTAATACAG	TATTCAAAA GGAGCAGTT CAT	TATTCAAAA AGAAGCAG TTCAT	0,8, 0	Ots19	47135 348	Ots19	46172 427
Ots_crRA D20262- 46	A	G	CCTCTGCTGAGTTTGA GGGG	TGAGCAGAGCCTAT GAGGACT	GGTTACA[T C]CCCCAAA	GGTTACG[T C]CCCCAAA	0,0	Ots19	47358 507	Ots19	46397 112
Ots10_21 244146	A	C	CTTCCAGGAGGTATTG TTGGTTAT	TGAACGTAGGTTTG CCATATACAG	CCATTATCA TTAT	CCCTTATCA TTAT	0,0	Ots19	53906 684	Ots10	21244 146
Ots_Est7 40	T	C	GGACTCGTGCTTGAGG AAGATG	TGCATGGCTCCAAC TCCTT	TCTGGATGG AACCGTTAG	CTGGATGG AGCCGTTA G	0,0	Ots20	37510 56	Ots20	39254 576
Ots_crRA D44588- 67	C	T	CGCAAGTCAGCAGGGT GA	TGGGGTTTTAGGCT GGGT	GTGA[AG]CC AATCAAT	GTGA[AG]C TAATCAAT	0,0	Ots20	20333 782	Ots20	25774 788
Ots_Aldo B4-183	T	A	TTTGTGCGTAAAGTCA GGTAGTGT	GTGCATGCCATGAG AACTTTGTTT	CTGTGTGTC TAAGACAAT	CTGTGTGTC TATGACAA T	0,0	Ots21	64771 38	Ots21	52520 21
Ots_AldB 1-122	C	T	GCCATGGAGGACTGGA TGA	GCCACCACTACTTG CTGAGAAAATA	TGTTGGCGA AGTG[GT]GT	TGTTGGTG AAGTG[GT] GT	0,0	Ots21	64801 72	Ots21	52550 56
Ots_1051 32-200	G	T	CGATGTACTGAGGGCA GTGT	GAGTGGAGTTCCTT AATAATCATTGACC TT	CAAGAGTG GCATAAAA	CAAGAGTG GAATAAAA	0,0	Ots21	11799 043	Ots21	95853 79
Ots_1015 54-407	C	G	TGAAAGATATCAATTG TAGTAGTGGTGGTG	ACACGCCAGTCCAC AAGT	ATGGAGGA TTGTGGTTG T	ATGGAGGA TTCTGGTTG T	0,0	Ots21	12050 017	Ots21	97841 11
Ots_GST -375	C	T	CAGCCCGTCCCAAAAT CAAG	CAGGAATATCACTG TTTGCCATTGC	TTTCTTGTA GGCGTCAG AG	TCTTGTAG GCATCAGA G	0,0	Ots21	20087 626	Ots21	18672 650
Ots_GST -207	G	A	GGAGAACATGCATCAC CATTCAAG	TCAGCAAACGAAG GCTATGTAGAAT	ATGAGAGA GTCTTTCTC TGTT	ATGAGAGA GTCTTTTTC TGTT	0,0	Ots21	20087 794	Ots21	18672 818
Ots_redd 1-187	A	G	TTCTGGGTTGCCATAC TCTTTCAAT	AGTTGAGACCTTCA GTTCTTAGGGTAT	ATTCTGACA GCTGTTTTG	CTGACAGC CGTTTTG	0,0	Ots21	27483 610	Ots01	99393 18

Ots_E2-275	A	G	GGTGCCACTTTAGTAT AGCTGCTTA	CCCTACCCCCTGTG TTCCA	CCCCCATAT TGCTG	CCCCACAT TGCTG	0,0	Ots22	64192 64	Ots22	54570 12
Ots_123048-521	A	C	CTCAACAGTGCACCTC CCTTAATT	CCAAACACACCCTT CCATAATCTCT	TCACATCCA ACTCAGTACT	CATCCAAC GCAGTACT	0,0	Ots22	94784 78	Ots22	80333 23
Ots_parp3-286	A	G	AGTCAGTGTTGGTGTA GTGAAGAGA	CATTTGTGGAGTGT TTATTGAACAGTAA CA	AGTTACAAG TGGTGTTTC A	ACAAGTGG CGTTTCA	0,0	Ots22	10728 055	Ots22	95051 20
Ots_u07-17.135	A	G	CTCGCCTCTGTCATTGT ATTACCTT	TGACACACGAGCCA TTTTGATGAT	AAAATGTAC CACATACTT GT	AAATGTAC CACATACT CGT	0,0	Ots22	12134 293	Ots22	11164 448
Ots_CD63	A	C	TGCATGTTTTCTAACTG TGTTTTTGTTG	TGAATGCCCCCAT CAACA	AGATCATGG GAATCATAT	ATCATGGG CATCATAT	0,0	Ots22	14629 707	Ots22	13378 891
Ots_110551-64	C	A	GAGTGGTCAAGGTTTC AGTTTCTG	GAAATGGACAGAC ACAAGGTCAAAC	ACGCTCGGA ACATT	ACGCTCTG AACATT	0,0	Ots22	15838 315	Ots22	14420 914
Ots_u1002-75	T	C	CCGCCTTTCCCACCTTC TC	TCAAACGAGAACA CACTAAGGTTGT	ATGGCCCTT ACACTATC	TGGCCCTT ACGCTATC	0,0	Ots22	16981 803	Ots22	15468 014
Ots_tpx2-125	C	T	TGTTGTAATCTTTCTGA ATATTTGCTTGCTT	TCTTCCAAATTGAG CACAAAAGCAT	CAGGCGGTT CTCC	CAGGCAGT TCTCC	0,0	Ots22	21879 673	Ots22	20362 912
Ots22_32650802	G	A	AAGGAGCAGGAGATG TTATTGAAG	ACTAGGTACTTCAC TGGTCCACTG	GGGAGAGG AGGCCTGTC TTTA	GGGAGAGG AGACCTGT CTTTA	0,0	Ots22	34412 033	Ots22	32650 802
Ots_CHI06105101_16717	C	T	AAGGCCGTGAACATCT GTG	ATCGCAGGCTAGCT TTTCAA	CCTCACATA CTCCCTT	CCTCATAT ACTCCCTT	0,0	Ots23	18000 122	Ots23	51243 25
Ots_CHI06105101_18523	A	G	GCGGTGGGATACCTCC TCTA	GCGAGAAAAGCAC TGAATGA	GGCGGCTCG GAAAATTAT TTT	GGCGGCTC GGGAAATT ATTTT	0,0	Ots23	18003 825	NA	NA
Ots_106747-239	C	A	ATCGAGGATGCCTCAA AGACATC	GTTAGACCCACCAC CAGTCATC	CCCGCGGTG AGTAT	CCCGCTGT GAGTAT	0,0	Ots24	95681 30	Ots24	17321 046
Ots_PEMT	C	T	AGAGCATTC AATTTAA AAGCTGAAAACGA	CTTTGATCCCTGCT TGCAGTATTTT	TGC[AT]TTG CTAAGACTT G	TGC[AT]TTG TTAAGACT TG	0,0	Ots24	10785 871	Ots24	15921 271
Ots_117370-471	G	T	GTTGGCTCCTTCAATTC AATTTGGA	TGCAAACACAGAG GAAAGGGATTT	ACGGAACA AATAAGAC ATTT	CGGAACAA ATAAGCCA TTT	0,0	Ots24	12157 474	Ots24	14581 248
Ots_107074-284	A	T	CCCACTTCCAGAGCCT GAA	TTTTCCATGGCTGT GTGTA CTGT	ACCGTAGCT GCACCTG	CGTAGCAG CACCTG	0,0	Ots25	81428 48	Ots11	16750 220

Ots_GTH 2B-550	C	G	CACAGGAAGGACGTGT TTTGATG	TGACTACCCGTTGT ACCAATGAAC	ATAACATCT GCAGCATTAA	ATAACATG TGCAGCAT TAA	0,0	Ots25	26054 245	Ots25	27327 552
Ots_myo 1a-384	A	C	CTCCCCCTGGACTTT GG	GCTCTATTGCACCG TGTTCTG	ACAGATCCA TCCACCACT	AGATCCAG CCACCACT CACATCAC	0,0	Ots26	10237 957	Ots03	39283 854
Ots_1128 76-371	C	A	GCCTACAGCAAATTCA GCTACACAT	TGGACCTTCAATCA TCACAGCTT	CATCACAAC GATGTGTG	AACTATGT GTG	0,0	Ots26	30XX XXXX	Ots26	29108 047
Ots17_22 360456	T	G	ATGGTTAAATTGACTC CTCCCTAT	GCCTACTACTGTTC TGTCATCTGC	AGTCTGTCTG TTGT	AGGCTGTC GTTGT	0,0	Ots27	14067 908	Ots17	22360 456
Ots_RAD 4543-52	T	C	TCTTTGGACTGTGTAT ACCAGGTGTA	GCCAGATGCTGTGT GTGTTT	TACATATGA CTAATGAAA	TACATACG ACTAATGA AA	0,0	Ots27	17341 235	Ots27	12866 217
Ots_Endo RB1-486	G	A	CCTTTGGGTCTGCTTG AGGTT	GGAGCCAAATCCTA ATGCTGAAGTA	TCCTTCTCA CGCTTCT	CTCCTTCTC ATGCTTCT	0,0	Ots28	93101 15	Ots28	81874 90
Ots_1088 20-336	G	A	TGAAATAAATTGTTCT GTTGATATGTGAATTT TGGA	CAACGACACACCA ACAACGT	ATTGCCCAT CTCAGAATA	AATTGCCC ATCTTAGA ATA	0,0	Ots28	12014 613	Ots28	10815 622
Ots28_11 023212	A	G	AGAAAGCCATCATCAT GAGACC	ACAAACAAACAAA AATGGTCAGAA	AACGTGAC ACAAT	AACGTGAC ACGAT	0,0	Ots28	12231 157	Ots28	11023 212
Ots28_11 025336	A	C	TGCAATATAGAACAAA TCCGAAAA	AATAACCCTTGGCT TCACATACAT	CAATGAAGT TAATTTAAT TGG	CAATGAAG TTCATTTAA TTGG	0,0	Ots28	12233 225	Ots28	11025 336
Ots28_11 033282	G	A	GGCTTTCTGATGATCTT GAACCTT	AGTGTGAGAGAGA GGAAGTCCCTA	TAAAAATG GTTGATATG TA	TAAAAATG ATTGATAT GTA	0,0	Ots28	12241 662	Ots28	11033 282
Ots28_11 062192	C	G	AGATGATATGGATTG CTGTGTGT	TTGAACATAACGAT CAGAGAAAGA	TTCTCAAGT CCTACTCAA CTG	TTCTCAAGT CGTACTCA ACTG	0,0	Ots28	12266 158	Ots28	11062 192
Ots28_11 070757	A	G	TTTTGGAACCCTTTTAA CTACGAG	ACATCAGTATAGCA GAGGAGAGGG	ACCCATGAA TAAGGACG AGAG	ACCCATGA ATGAGGAC GAGAG	0,0	Ots28	12274 804	Ots28	11070 757
Ots28_11 071377	T	C	ATTTGCTGTGTGTGGA GTGAAT	GTAGTGACAGATGC TCTTGGAGG	CATCTTAGC CTCTCTGAC CCC	CATCTTAG CCCCTCTG ACCCC	0,0	Ots28	12275 402	Ots28	11071 377
Ots28_11 072994	C	T	GGGAGACTTAAAAACAA CCTCAAAA	ACCTGCAACCTTCT ATTCAACAGT	CCATATGTC GCTTGT	CCATATGT CGTTTGT	0,0	Ots28	12277 000	Ots28	11072 994
Ots28_11 073102	T	A	GGTGAGCCATTTCATAA CAATCTT	TGTTATCCTGGATC ATTCAAGAGA	ACATTACTT TTCAAAAAT ATT	ACATTACTT TACAAAAA TATT	0,0	Ots28	12277 108	Ots28	11073 102

Ots28_11 073668	T	A	CCTAAGAGGAGACGA GCATTACAG	GGTAAATCAACATA TGACCACTCG	TACAGTTTC CTGTCTGA	TACAGTTTC CAGTCTGA	0,0	Ots28	12277 674	Ots28	11073 668
Ots28_11 075348	G	A	CATTTCAAAATTAGGA GGTTAGGG	AGATGAGAGCTGTG GCCTGT	GTGTGAAA GGGGAGAA GGGCT	GTGTGAAA GGAGAGAA GGGCT	0,0	Ots28	12279 292	Ots28	11075 348
Ots28_11 075712	C	T	GCTTAAACAGCTGCTA TTAGGACA	TAAGGATTTGTTGC CAGCTCTAAT	GAAAACTCT GCCCTG	GAAAACTC TGTCCTG	0,0	Ots28	12279 656	Ots28	11075 712
Ots28_11 077016	C	T	AAAATATGTGCAACAT CCAATGTC	ACACAAGCTGGCTG AAGCTAAT	GTCAAACCA ACTTTGCCA AGG	GTCAAACC AATTTTGCC AAGG	0,0	Ots28	12280 918	Ots28	11076 976
Ots28_11 077172	G	A	GTTTTGCCAGAGAGAA TGTACAAA	TAGTGGTTAGAGCA TTGGACTAGC	ACACACAC AAGAGACA CCCAC	ACACACAC AAAAGACA CCCAC	0,0 4	Ots28	12281 112	Ots28	11077 172
Ots28_11 077576	A	G	TGTGCGGAATTACTGA TAATTGAC	GCTCTGCATTTTAC AACACTGCT	GAAGGCCA AATAAAATT G	GAAGGCCG AATAAAAT TG	0,0	Ots28	12281 512	Ots28	11077 576
Ots28_11 095755	A	T	CCAATGGTGATTTTAG AACCATTAC	AAAACAGAGTATG GATCAACAGCA	AGAGTTGA ATGGC	AGTGTGTA ATGGC	0,0	Ots28	12299 996	Ots28	11095 755
Ots28_11 143508	G	A	ACCTTTTAGCCAGTGA CAACATTT	ATGCAAGAACTCT CGACGATAG	TTCACGTAC GGCCCAT	TTCACATA CGGCCCAT	0,0	Ots28	12341 541	Ots28	11143 508
Ots28_11 160599	G	T	GTGCATATTTTACGTG GTTGAAGT	ATTCCATTTACCC ATATGAATTT	CTCTCTGCT TGC GTT	CTCTCTGCT TTC GTT	0,0	Ots28	12359 222	Ots28	11160 599
Ots28_11 164637	C	A	TGATTTGACTTTTTGTG GTGTTTT	GTTCCAATCTGTTT TTGCTCTCTT	CTGGCGGG GTCTGGG	CTGGCGGG GTATGGG	0,0	Ots28	12363 212	Ots28	11164 637
Ots28_11 186543	A	T	GGCTTGCCTTTAGATA GAATCTTG	AAATCTCACAGTC CAAAAACAAA	AAAGCTGAT TAAAAA	AAAGCTGA TTTAAAA	0,0	Ots28	12385 919	Ots28	11186 543
Ots28_11 201129	T	G	TGCGAGATTTATCTAC TTGTCCAG	GGTAGTTTTGTACG CAATTGCTAA	ACTGAAGG AATTTAAC	ACTGAAGG AAGTTAAC	0,0	Ots28	12400 459	Ots28	11201 129
Ots28_11 202190	T	C	GCTAAATGTAAATCGA GTGGCTGT	TACATGGGTCCTCT CAGTGTTCTA	CAAAAGTCT GTATTTTCA AAA	CAAAAGTC TGCATTTTC AAAA	0,0	Ots28	12401 520	Ots28	11202 190
Ots28_11 202400	C	T	CCCTCCAAAAAGAAAA CATTTGAT	AAATTGGCTAATCA AACACTGGTT	GACACACTC ACGA	GACACACT CATGA	0,0	Ots28	12401 729	Ots28	11202 400
Ots28_11 202863	C	A	GAGGATGGATGAGACT TTTCAGAT	GCTCTTTACCGGGT TTATATGAAG	ATAAAAAA TTCTGCGTG AATG	ATAAAAAA TTATGCGT GAATG	0,0	Ots28	12402 193	Ots28	11202 863

Ots28_11 205423	A	G	TTAAATCACCCAGAGC TTGTTAGA	ACCTGACCTAGATA ACAACCACAA	CCTGCACAC ATGTCAAAC CG	CCTGCACA CGTGTCAA ACCG	0,0	Ots28	12404 734	Ots28	11205 423
Ots28_11 205993	C	T	GCTGCTATTTCCGACC TTACAATA	ATCAAGACAAAAC ACTCACCAGAA	GCTATTAAA AGG	GTTATTAA AAGG	0,0	Ots28	12405 298	Ots28	11205 993
Ots28_11 206740	T	C	ACTTTGAGGACTTACT CCTGTCCT	CTGGAGAAAGACA AGATGATGATC	CCTTCCCTC CTAGGGCA ACGT	CCTTCCCTC CCAGGGCA ACGT	0,0	Ots28	12406 045	Ots28	11206 740
Ots28_11 207428	T	G	TATACCTTTGTAGCAT CCCTCTCC	CATATAAAGTGGAC AGCGTTTGAC	GTTGGGAGC GTCCCAAAA TGG	GTTGGGAG CGGCCCAA AATGG	0,5, 0	Ots28	12406 663	Ots28	11207 428
Ots_trnau 1ap-86	G	T	GGACAAGTTGAAACAG ATCAGGAAGT	GCCACTGGATACCA TCACTTCAAA	AATCCCTCC TTTTTCC	TCCCTCATT TTCC	0,0	Ots28	18849 666	Ots28	17646 942
Ots_OTS TF1- SNP1	G	T	CGGACAAAGAGCTACA GAAATGC	CGTCCCTCTTCACG CATGA	CCGCCACCT TGGCT	CGCCACAT TGGCT	0,0	Ots28	27509 692	Ots28	25845 386
Ots_1224 14-56	C	T	GCACCGTATCAACGAG CTCAT	TGCATGGATTTCCT TTGTGTTGTTG	TGTATGACC TCTGACCTG T	TGTATGAC CTCTAACCT GT	0,0	Ots28	28489 780	Ots28	26647 710
Ots_CCR 7	C	T	CTGCTCACCTGCATCA GTGT	CCATGGTGGTCTGG ACGAT	CCACGTAGC GATCG	ACCACATA GCGATCG	0,0	Ots28	37080 463	Ots28	34762 262
Ots_9766 0-56	A	T	TTCCCTAATCTGACGT ACTACCAACT	CGCCACTGACGTTC ATTCCA	ACGAGACA GATATTC	ACGAGACT GATATTC	0,0	Ots28	37155 946	Ots28	34830 271
Ots_crRA D18289- 33	T	C	GCAGGGAAAACTGGTC AGGA	AGGTGAACCTCCGT CCCA	GAATGGTGT TAAAT	GAATGGCG TTAAAT	0,0	Ots29	78932 96	Ots34	89707 78
Ots29_23 344676	T	C	GAACTATCCTGACTCC CATTGAAA	CTGAGTTCCTCCTG GTTGTTATG	TGCAAGTCC TTCAAAGGC TCA	TGCAAGTC CTCCAAAG GCTCA	0,0	Ots29	12582 492	Ots29	23344 676
Ots_1110 84b-619	C	A	TTGTGGAATTACACCT TCAGAGTTCAAT	GCCTGTTTGGCTTT CTTAAACTGAT	TCCATGG[A T]AACGGAC AAT	TCCATGG[A T]AACTGAC AAT	0,0	Ots29	16022 207	Ots29	19749 885
Ots29_18 791740	T	G	GTTTTGGTGTGGTCTC AAATCC	CGGCACCTGGAAAC AGTC	CCTATGAAG TT	CCGATGAA GTT	0,0	Ots29	17054 573	Ots29	18791 748
Ots_1083 90-329	G	C	GAGGTTTGTACTGTC ACCCATAGA	CCTGCTGTAGCAAA CTGTCTCAAA	CTACTTATG TAGCATTTT AA	CTACTTATG TAGGATTTT AA	0,0	Ots29	19105 883	Ots29	16533 976

Ots_9622 2-525	C	T	GCTCTTGCCCATCTGT AGGAT	GGCGCAACATATGT ATTAAGCAACT	TGTAGCTAA TTTTAAGTT CTC	AGCTAATT TTAAATTCT C	0,0	Ots29	23142 347	Ots29	12489 280
Ots_U24 46-123	C	A	CTGGTCTGTGACGTCA AAATGATG	AGCTAGACCAGGCC ATTTGAG	CTGCAACTC GACGCAAG	ACTGCAAC TCTACGCA AG	0,0	Ots29	23877 989	Ots29	11728 129
Ots_1174 32-409	A	G	TCATCAAAACATGCCT CTTCTGTGT	TGTTGAACCTGTCA CTCTGTCTTC	TTTAGACTT TGCTCTATA ACAG	ACTTTGCTC CATAACAG	0,0	Ots29	25338 465	Ots29	10328 032
Ots_crRA D255-59	T	C	TGCAGGAGCTGTGATG GG	GTACGGAGCGTCAC TGCT	AACTGTTCA AACCC	AACTGTCC AAACCC	0,0	Ots30	69759 04	Ots30	40093 591
Ots_RFC 2-558	A	-	AAGGTCTACTCCGGTT GTATTCGGT	CAATACGACAGTAC CGGTGTTAAACT	TGCATGTAA CAAATAAC AT	TGCATGTA ACATAACA T	0,0	Ots30	17770 066	Ots07	27438 208
Ots_PGK -54	T	A	CTCATACTTTGTACCTG TGTGTTCCA	CGACCCAAGTGGCT CATCAG	CCACCATCA AGCACTG	CCACCATC ATGCACTG	0,0	Ots30	19962 166	Ots30	23782 920
Ots_1307 20-99	A	G	CGGTCAATTGTAAATGT CAACGGTTT	TGCTTGCATGTTCT TGGTGTAGTAA	CCTGTCTCA TTCCC	CTGTCCCAT TCCC	0,0	Ots30	24569 258	Ots30	17928 099
Ots30_17 330688	T	C	CTGACAAAAGTGATCT GCCTGA	TGCTTGGTTACACA GTTTGACA	TGTGTCTGA GA	TGTGTCCG AGA	0,0	Ots30	25291 039	Ots30	17330 706
Ots30_17 330452	G	C	CACAAATGTGACCGTT TTCATC	TTGAACCAGGGTGT CTGTAGTG	CATGTCAGT GC	CATGTCAC TGC	0,0	Ots30	25291 293	Ots30	17330 452
Ots_EP- 529	A	G	GCCCTGCCTGCAACTT C	GAAACCAACGTCTT GATGTAGACCTA	CAGTGTCA TTTCGGC	ATCAGTGT CATCTTCG GC	0,0	Ots30	26852 592	NA	NA
Ots_crRA D25367- 50	T	G	ACTGCAGGCGTCATGC TT	TGGACAAAAGACC ACAGGCT	GTATATTTA GAATG	GTATATGT AGAATG	0,0	Ots30	34187 799	Ots30	80425 26
Ots_u07- 18.378	A	T	GGAAACCAGCTAGGAT TCAGGAA	CGTTATATGGTTTG CTTGTGCGATA	ATATGGTAT GTAGAGGCT AGTTA	TATGTAGA GGCAAGTT A	0,0	Ots30	36420 567	Ots30	61306 60
Ots_U23 62-227	A	T	TCGTGGATTGTGGCTT ACGT	GGGTGTTTAAACAAG TAGTCCCTTCA	AAGAAGCA TTTTTT[GT][GT]	AAGAAGCA TTTATTTT	0,0	Ots30	38784 785	Ots06	14700 070
Ots_U23 62-330	A	G	AATGGGTAACAAAGA AATAGCTAGCTACTT	GACAGACCACAGT GAAGGTGAAA	ACTGGGAA GATTGTTTG	CTGGGAAG ACTGTTTG	0,0	Ots30	38784 886	Ots06	14699 971

Ots_crRA D57520- 66	T	G	ACAGAGCTGTGTCTAC CAGA	ACCCTCTCTTGGCC TTGC	TTTTTGTTT AAAAG	TTTTTGGTC AAAAG	0,0	Ots30	39954 606	Ots30	13323 75
Ots_P53	G	A	GGAACCTCCTCTCCCG TTCTG	GCACACACACGCAC CTCAA	CTGGGTCGG CGCT	TGGGTCTGA CGCTC	0,0	Ots30	40916 627	Ots30	24175 91
Ots_1096 93-392	T	G	TCTCCCTCATTCCCATG TCATATCA	GGGAACGTATCAG GTGAGTGT	TCCGTTAGT TCATCCTGG	TCCGTTAGT TCCTCCTGG	0,0	Ots31	93693 78	Ots13	74025 50
Ots_unk1 104-38	C	T	TAACCATGACTTCTAT CAATCACCCC	CCTCCATACATCGT CAAAGCTGTA	CCACTAAGG ATTACGTTA CG	CACTAAGG ATTACATT ACG	0,0	Ots31	14800 538	Ots31	21291 286
Ots_ntl- 255	T	A	TGCAGTTACAAGCCTA AGACAATCT	CAACTAAAGTAACA CACCAGCAACTG	ATTCTTCCT C[TC]ACAAT TG	ATACTTCCT C[TC]ACAA TTG	0,0	Ots31	20616 326	Ots31	15370 000
Ots_1011 19-381	T	C	TTTTCTAGGACAGGTT GCTTGCA	CCAGGTTTCTTTAG CCTACTTATTCTTTA CA	TGCCACATG ATAATTGA	CCACATGG TAATTGA	0,0	Ots31	21772 790	Ots02	58361 347
Ots_txnip -321	T	C	CCTTCAAACCTAACACA TCATAGACATGCTT	TTATCAAACCTGAAG GCGGATTTACTGA	TCTGGCGGA TTTACA	CTGGCGGG TTTACA	0,0	Ots31	23141 496	Ots31	13146 728
Ots_1132 42-216	C	T	GAGGCCTAATGTCTCT TGTGACT	GACATCTTCAACAA GTGTTCAATCACC	ATTACCAAC GGAGAACC	TTACCAAC AGAGAACC	0,0	Ots31	31397 037	NA	NA
Ots_sept9 -78	G	A	GTCGATTACCGTTAGC TTCATCCT	ATTCTCCTGTGTCT CTCTCTGTCT	CTCTTCGAT GTCTAGACA	CTCTTCAAT GTCTAGAC A	0,0	Ots32	55431 76	Ots32	93903 57
Ots_DDX 5-171	C	T	ATGACCAATTGAAGAG TTCTTCCGT	CAAAGCCAAACGTC ACATTTACACT	TTCATAATT GAACGATTT CA	CATAATTG AACAATTT CA	0,0	Ots32	71833 41	Ots32	59485 80
Ots_1181 75-479	C	T	TGCGCGTCTCATTCAA CCAT	ACCTTACGTCCTAG GTAGGAAACA	AGAATGAA GTGAAAAG AA	AGAATGAA GTAAAAAG AA	0,0	Ots32	76315 74	Ots32	54361 60
Ots_1298 70-55	A	T	GCATGTAACACATTAT TTGGCATATGTACT	CAGTACACTGGAGA TTTGCAATGTT	ATGCATTCA CCTGTATTA T	TGCATTCA CCAGTATT AT	0,0	Ots32	10246 920	Ots32	29798 52
Ots_Ostm 1	C	G	CCAGCCCCGTAACACA CAT	GAGAGGAAGCAGA AAGGTCGTTTAA	CCGTGGTAT TGTTTCAA	CCGTGGTA TTCTTTCAA	0,0	Ots33	27432 27	Ots33	45699 55
Ots_NA ML12- SNP1	A	G	TGCCACCTCAGTTTTA GTGTTATATCC	AGCGCCAACCTGTC ACT	AAACCATTT TCATTCTTT TG	CCATTTTCA CTCTTTTG	0,0	Ots33	85237 57	Ots33	97778 02
Ots_CRB 211	A	C	CAACGCGGGAATGGCT TTTAA	GCCAGAGTCGCCAA AATAGTAGAAT	CTACCGTAC TGAATCTC	CCGTACGG AACTC	0,0	Ots33	28420 240	Ots33	29785 703

Ots_TGF B	C	T	GCCTCACATTTTACTG ATGTCACTTC	GAGCAGATCTCTTC AGTAGTGGTTT	AGCCTAGCT CTCGGAAG	AGCCTAGT TCTCGGAAG	0,0	Ots33	28445 695	Ots33	29760 263
Ots_1064 99-70	C	G	ACTCTATCATCGGCAG GACCAT	ACCGTAAGTGTGGT TGTGTTTCATTA	CATTTTTCA GAATTGTAT TC	CATTTTTCA GAATTCTA TTC	0,0	Ots33	37411 470	NA	NA
Ots_TLR 3	C	T	TGCACCTGCGAGAGCA T	CTGGCGTTTGTTC GTTTCAG	CTGTGGTTT GTGGCGTG	CTGTGGTTT GTAGCGTG	0,0	Ots34	72341 89	Ots34	73652 14
Ots_crRA D24807- 74	A	T	TGCAGGAGAGCAGGGT AGA	CGTGCCTAACATCA TGTGCA	ATGATAAT	ATGATATT	0,8, 0	Ots4	44035 017	Ots04	36172 590
Ots_crRA D36152- 44	C	T	CAAAGTGCAGGTGCTG GC	CCAGCCAGGTGTTG AGCA	CTGCCACCC TTTGA	CTGCCATC CTTTGA	0,0	NA	NA	Ots12	13203 734
Ots_afmi d-196	G	C	CGTGGAGTAGGTGGTT ACAGTTTAT	CTCGTAACAAGCTA CTGTAGTGTACT	CAAAGTCA AAGATCCTA TAAA	AAGTCAAA GATCGTAT TAAA	2,0	NA	NA	Ots32	17096 334
Ots_1266 19-400	C	T	GGATGGTTGTCATTTT TCTGCAAA	CCGGGATACAATAA TAATATTTGGTTAA GAGTTTTTT	AGAAAGTTC TAGAAATA ATT	AAAGTTCT AGGAATAA TT	2,0	NA	NA	NA	NA
Ots_Est1 363	A	T	GGTGATTTTGCCACAG AGTAGAGAT	AGTGTTAAATGTAA CTTGCATATACAGG CAAT	CCATCCTGT CTTGTCTG	CATCCTGTC ATGTCTG	0,0	NA	NA	Ots03	82923 51
Ots_U23 05-63	T	-	TGTCATCTCTATTGCA ATCTCAGTAGATTTCT AT	CCAGGTCGTCTTTA TTGCAGATTATCA	AATGTCATA TAGAAATCT AC	AATGTCAT AGAAATCT ACTG	2,0	NA	NA	Ots14	398X XXX
Ots_u07- 07.161	C	T	GTCAACAAATGCAGGT AACATAAATGGT	GATGCAAACACCTG TGAAATTGTGA	ATCAGTGAC ATAAGTTGT CCA	TCAGTGAC ATAAATTG TCCA	0,0	NA	NA	Ots04	37799 853
Ots_u202 -161	T	A	CACTTTTGACTTTACAT GGAACTTAACTCAT	GGGACTTCACTTTC TACAAACATGTCA	AGCTAGTGC TTAGCAGCT A[AC]	AGCTAGTG CATAGCAG CTA[AC]	1,5, 0	NA	NA	NA	NA
Ots_Cath _D141	T	C	CACTTGTTCTGCACAC TACTTGTC	CACACATGGATTTT GCCTGTCTAAA	TGGGAAGC AATCAA	AATTGGGA AGCAGTCA A	0,2	NA	NA	NA	NA
Ots_1104 95-380	G	C	GCCTAGGTATGTACGA AACTTCACA	AGGCTTTTTTCAGAT GGTCGTATGA	CATAGAC[A G]GGGGCCA T	CATACAC[A G]GGGGCC AT	1,9, 0	NA	NA	NA	NA
Ots18_34 17174	A	C	TGAGGTATTACTTGCT GAGTTTGC	CAAGAAGATGTGA ACTAATTCCCA	CTGAATCCT GTAAG	CTGCATCCT GTAAG	0,0	NA	NA	Ots18	34171 74

Ots_1239 21-111	A	G	TCGCTAGGCAGAAATA TAGGGTTCT	GAGCATGGCGCTTG CA	TGCTAAATG GCATATATT AT	CTAAATGG CACATATT AT	0,0	NA	NA	Ots18	25247 852
Ots_unk7 936-50	C	G	ATGGGTTGGGATTATG GTTTCATTGT	CAAAATGGTTACTT GCATAGTCTTTTGT	AGACATGTA GCTATGTAG GTAA	AGACATGT AGCTATCT AGGTAA	0,0	NA	NA	NA	NA
Ots_9955 0-204	C	T	TGACAGATTTTCACCTT TAACTAGCTAAGC	GCAACCTCTTTCAC ACTTCAGTAAC	AAGGCTTTG GTTGTTTG	AAGGCTTT GATTGTTTG	0,0	NA	NA	NA	NA
Ots_crRA D60614- 46	G	T	TGCCGTGAGAACTGG TCA	TTTCCTCCTCTCTGC CTCA	AAGATGGT ATGTAT	AAGATGTT ATGTAT	0,0	NA	NA	Ots12	72156 356
Ots_OTD ESMIN1 9-SNP1	C	A	GGTCTGTCTGTCTGTCT ATCTGTCAATG	TGTGTGTCTTTGTTC ATTCCTACCA	CCAGTCATG GGTCATT	TCCAGTCA TTGGTCATT	0,0	NA	NA	NA	NA
Ots_TCT A-58	C	T	ACCAGTACCTAAACGT TAGAAAGCAA	CGTTAGTTAGCTAT GTCTGAAAGGCA	CTGCCATGA AGTGCTAG	TGCCATGA AATGCTAG	0,0	NA	NA	Ots02	89930 26
Ots_MH C2	T	G	GTCCTCAGCTGGGTCA AGAG	GTAGTGGAGAGCA GCGTTAGG	CTGGAGCGT TTCTGTA	CTGGAGCG TGTCTGTA	0,5, 0	NA	NA	NA	NA
Ots_1100 64-383	C	T	AACAAAGAATGTTAAA CACCAAACAGGAA	GTGCAAGGGACCTA GCTAATCC	CTACGTAAT GAACGTTAG CT	ACGTAATG AACATTAG CT	0,0	NA	NA	Ots27	81410 61
Ots_U21 2-158	G	A	CCCCATATGAGACGCT ACAGTAATG	CAAATGCCCTCTAA GCAGACCTT	CTGGAAGA AGGCCTC	CTGGAAAA AGGCCTC	1,5, 0	NA	NA	Ots27	14522 192
Ots33_19 359879	T	C	AGCGCCTGTTTTACAT AAACACTT	GTGAGTACCGTAAA GACTGAGCAA	AAATAAAC GCTGGGTCT AATT	AAATAAAC GCCGGGTC TAATT	0,0	NA	NA	Ots33	19359 879
Ots2_382 64269	A	C	GTATGAGTTGTGTGGT TGCAATGT	CTCTAGCCTATTGC ACAATGTCC	TCCCTTGTC TATGGTATA TCT	TCCCTTGTC TCTGGTAT ATCT	0,0	NA	NA	Ots02	38264 269
Ots18_34 26299	T	A	TTATTTTGGGCTTCATA TGGTTCT	GGTCATGATGTTGA TATTTTGGGA	AATGCCATT TTGT	AAAGCCAT TTTGT	0,0	NA	NA	Ots18	34262 99
Ots_U51 21-34	A	G	CCAGAGGTTAGATGGC CCTTT	CTGAGCCAGAACCA CAAATTGAATT	AGGGTCTCA TGCTCCCT	AGGGTCTC GTGCTCCCT	0,0	NA	NA	Ots05	20893 356
Ots_crRA D60620- 51	A	G	CAGGCAGTCACTGAGT CCG	TTTGAGCACCGTTT CCGA	GTACGGAA AAAACA	GTACGGGA AAAACA	0,0	NA	NA	Ots21	24004 835
Ots_ARN T	G	T	CCACTGGCTGTGGAGC TT	GGGTTTCAGTGATAG TTGGGCAAAT	TACAGATGT CATTTTAC	CTACAGAT GTAATTTTA C	2,2, 0	NA	NA	Ots23	24857 375

Ots_GH2	A	T	GCGTACTGAGCCTGGA TGACA	CCCCCAGGTTCTGG TAGTAGTTC	TGACTCTCA GCA[TA]CTG	TGACTCTCT GCA[TA]CT G	1,8, 0	NA	NA	NA	NA
Ots_IL11	T	C	CCTCCAGATGAGACCC ACTCT	CAAAATGGTGCTCA AACGACTTCA	AGCTCCATG CGGACT	AGCTCCAC GCGGACT	0,0	NA	NA	Ots20	20625 334
Ots_1182 05-61	T	C	CCATACAGCCAGTCCA GGTG	ACTGGACAGGGCTG GGT	TAGTAGCCC CTACACCTC	TAGCCCCT GCACCTC	0,0. 4	NA	NA	Ots33	32594 959
Ots_crRA D26081- 28	T	G	GGGAGAGGGAGACGT GGA	TCACCAGCTCCTCC TCCTC	TGGAGGTG GAGGAG	TGGAGGGG GAGGAG	0,0	NA	NA	NA	NA
Ots28_11 210919	C	T	AGTGCTCCATGCTGGA GTTT	GATGAAGCAGAAG GAGAGGCT	GACCTCAAG CAGTCAG	GACCTTAA GCAGTCAG	0,0	NA	NA	Ots28	11210 919

1160
1161

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, timeline 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, Coho Salmon, 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

Neutral steelhead population structure across the Columbia River basin:

Putatively neutral markers were assessed using a combination of multivariate methods to detect underlying population structure, which we expected to coincide with coastal and inland lineages described in previous studies (Blankenship et al., 2011; Matala et al., 2014; Micheletti et al., 2018). All neutral markers were mapped to their physical location on the *O. mykiss* genome assembly available in NCBI (accession number GCF_002163495.1) and multiple markers were found on all chromosomes with physical distance ranging from 194 KB to 39 MB. All markers had physical distance greater than 194 KB which would be greater than expected linkage decay in this species and thus were expected to be in linkage disequilibrium (LD). This expectation was tested with pairwise LD estimates in GenePop for a representative subsample of 25 collections. In cases where markers were consistently significant for LD tests in multiple populations, one in each significant pair was removed leaving a total of 226 markers for all subsequent analyses with neutral markers.

A principal component analysis (PCA) was plotted for all populations based on allele frequencies of putatively neutral markers determined to be without LD. A discriminant analysis of principal components (DAPC) was conducted with the R package adegenet 2.1.0 to assign probability of individual membership to genetic groups (K) (Jombart, 2008; Jombart & Ahmed, 2011). The DAPC recovers maximum genetic variation between groups, while minimizing genetic variation within groups (Jombart, 2008; Jombart & Ahmed, 2011). The adegenet package was used to identify clusters with successive K -means and ran for 25 instances for $K=1$ through $K=10$. The Bayesian information criterion (BIC) was averaged and scaled by the standard deviation for each K value. The most appropriate number of genetic groups was determined with the greatest ΔK value as described in Evanno et al. (2005). The LEA 2.0 R package was used to estimate population structure through sparse nonnegative matrix factorization (Frichot & François, 2015).

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 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 protocols for whole genome resequencing are shown below. 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). 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 GenAIEx 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 the most recent years 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, Chinook Salmon, Coho Salmon, Sockeye Salmon, and Pacific Lamprey. Currently we do not utilize reference baselines for GSI of either Coho Salmon or Pacific Lamprey, and in 2020 there were no updates to the reference populations in our GSI baseline for Chinook Salmon and Sockeye Salmon. The most recent marker panels are described in Section 1. Testing of the reference baseline for GSI based on the expanded SNP marker panel for steelhead trout is described in Section 3.

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 2), Coho Salmon (Table 3), and *O. mykiss* (Table 4). 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 2. Creation of a Chinook Salmon SNP baseline by whole genome resequencing of pools of samples

Pool Seq Library ID	Number of reads (R1)	Mean Coverage	ID	Collection	(n)	Lineage	Reporting Groups
L-0730	438,161,235	35.02	OTS01	Big Creek Tule	71	Rogue	01_YOUNGS

L-0731	203,076,142	16.26	OTS03	Kalama R spring-run	93	LC	02_WCASSP
L-1037	203,899,979	16.07	OTS05	Elochoman R fall-run	86	LC	03_WCASFA
L-0732	241,863,213	14.64	OTS06	Lewis R fall-run	68	LC	03_WCASFA
L-1067	214,421,199	19.45	OTS12	White Salmon fall-run	78	LC	05_SPCRTU
L-0736/L-0736_2	751,365,978	64.28	OTS13	Spring Creek NFH tule fall-run	94	LC	05_SPCRTU
L-0737	248,031,203	21.27	OTS16	Warm Springs R spring-run	93	ST	07_DESCSP
L-0756	148,429,490	11.86	OTS17	John Day North Fork-Main Stem	52	ST	08_JOHNDR
L-0739	479,879,641	36.47	OTS18	Middle Fork John Day R spring-run	36	ST	08_JOHNDR
L-0740	139,194,175	9.99	OTS19	North Fork John Day R spring-run	39	ST	08_JOHNDR
L-0741_A	196,168,023	12.61	OTS20	American R spring-run	62	ST	09_YAKIMA
L-0906/L-0733/L-0733_Test/L-0876	208,041,237	16.89	-	Methow R spring-run	87	ST	10_UCOLSP
L-0742	340,007,427	14.54	OTS22	Winthrop NFH spring-run	83	ST	10_UCOLSP
L-0743	277,739,324	24.25	OTS24	Wenatchee R spring-run	51	ST	10_UCOLSP
L-0745	221,784,271	16.25	OTS26	Tucannon River spring-run	52	ST	11_TUCANO
L-1038	205,605,681	17.82	OTS28	Lostine R spring-run	41	ST	12_HELLSC
L-0747	279,162,633	21.60	OTS29	Grande Ronde R spring-run	30	ST	12_HELLSC
L-1069	195,959,654	16.30	OTS32	Red R spring-run	45	ST	12_HELLSC
L-0749	468,738,121	36.61	OTS33	Powell R spring-run	94	ST	12_HELLSC
L-0748	212,015,624	18.42	OTS30	Imnaha R spring-run	76	ST	12_HELLSC
L-1068	200,911,545	15.92	OTS31	Lolo Cr spring-run	48	ST	12_HELLSC
L-1087	194,515,174	17.94	OTS34	Rapid R Hatchery	96	ST	12_HELLSC
L-1070	217,481,702	19.89	OTS35	South Forth Salmon R spring-run	45	ST	13_SFSALM
L-0751	248,736,026	18.17	OTS37	Secesh R spring-run	90	ST	13_SFSALM
L-0752	570,363,043	49.47	OTS38	Chamberlain Cr spring-run	78	ST	14_CHMBLN
L-0753	238,267,170	10.02	OTS39	Big Cr spring-run	48	ST	15_MFSALM
L-1059	248,813,713	21.73	OTS41	Loon Cr spring-run	42	ST	15_MFSALM
L-0754	189,279,625	14.94	OTS43	Bear Valley Cr spring-run	33	ST	15_MFSALM
L-0755	218,687,602	20.14	OTS45	Marsh Cr spring-run	44	ST	15_MFSALM
L-1085	207,691,679	14.92	OTS40	Camas Cr spring-run	60	ST	15_MFSALM
L-1086	608,135,302	54.51	OTS42	Sulphur Cr spring-run	35	ST	15_MFSALM
L-1105	210,570,014	18.39	OTS44	Capehorn Cr spring-run	60	ST	15_MFSALM
L-0757	188,391,901	17.82	OTS47	Lemhi R spring-run	95	ST	16_UPSALM
L-0758	141,386,850	9.71	OTS48	Pahsimeroi R spring-run	92	ST	16_UPSALM
L-1057	203,885,206	18.56	OTS49	East Fork Salmon R spring-run	96	ST	16_UPSALM

L-1080	243,282,312	20.16	OTS50	Salmon R spring-run	61	ST	16_UPSALM
L-1060	239,722,545	14.02	OTS51	West Fork Yankee Fork spring-run	93	ST	16_UPSALM
L-0760	276,701,035	18.50	OTS53	Sawtooth Hatchery weir spring-run	91	ST	16_UPSALM
L-1106	208,349,688	20.87	OTS52	Valley Cr spring-run	42	ST	16_UPSALM
L-0761	503,337,440	32.75	OTS55	lower Yakima R fall-run	46	OT	18_UCOLSF
L-0762/L-0966/L-0967	476,295,447	32.01	OTS57	Wenatchee R summer-run	122	OT	18_UCOLSF
L-0763/L-0877/L-0897/L-0904	482,651,780	24.78	OTS59	Methow R summer-run	136	OT	18_UCOLSF
L-0764	215,478,389	17.03	OTS60	Lyons Ferry weir fall-run	92	OT	19_SRFALL

Table 3. 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 4. Creation of *O. mykiss* SNP baseline by whole genome resequencing of pools of samples

Lineage	Reporting Group	Major Subbasin	Subbasin	Reach	Sites	N	Mapped Reads	*Genome Proportion
Coastal	02_LOWCOL	L. Columbia	Cowlitz	Cowlitz	Cowlitz R, Coweeman R	95	257,455,270	0.61
Coastal	02_LOWCOL	L. Columbia	Lewis	Lewis	EF Lewis R	78	325,463,369	0.65
Coastal	02_LOWCOL	L. Columbia	Columbia Gorge	Columbia Gorge	Mill Cr	96	232,750,154	0.56
Coastal	02_LOWCOL	L. Columbia	Columbia Gorge	Sandy Cr	Sandy Cr	87	291,529,099	0.64
Coastal	02_LOWCOL	L. Columbia	Hood	EF Hood	EF Hood R	48	260,113,702	0.62
Coastal	02_LOWCOL	L. Columbia	Hood	EF Hood	Parkdale Fish Facility	83	219,546,080	0.51
Coastal	02_LOWCOL	L. Columbia	Hood	WF Hood	WF Hood R	79	212,615,249	0.45
Coastal	03_SKAMAN	L. Columbia	Washougal	Washougal	Skamania Hatchery Stock	60	250,089,125	0.58
Coastal	04_WILLAM	L. Columbia	Willamette	Willamette	Eagle Cr	61	254,529,741	0.58

Coastal	04_WILLAM	L. Columbia	Willamette	Willamette	Little Rock, Mad Crks	50	265,050,782	0.55
Coastal	05_BWSALM	L. Columbia	Big White Salmon	Big White Salmon	Big White Salmon R	95	194,626,391	0.48
Inter-mediate	06_KLICKR	L. Columbia	Klickitat	Klickitat	Swale, Brush, Dead Canyon, Synder, White, Tepee, Fish Lake Crks	95	227,020,456	0.52
Inland	07_MGILCS	L. Columbia	Middle Columbia	Middle Columbia	Rock, Squaw Crks	91	216,427,544	0.61
Inland	07_MGILCS	L. Columbia	Middle Columbia	Fifteen Mile Cr	Fifteenmile Cr	92	520,699,926	0.72
Inland	07_MGILCS	L. Columbia	John Day	John Day	MF John Day R, Granite, Rudio, Wall, Trail Crks	95	285,409,446	0.58
Inland	07_MGILCS	L. Columbia	John Day	MF John Day	Upper John Day R, Beech, Belshaw, Canyon Crks	69	246,704,439	0.57
Inland	07_MGILCS	L. Columbia	John Day	SF John Day	Murderers, Deer, Black Canyon Crks	96	224,529,764	0.57
Inland	07_MGILCS	L. Columbia	Deschutes	Deschutes	Deschutes R, Warm Springs R, Trout Cr	95	262,227,329	0.61
Inland	07_MGILCS	L. Columbia	Umatilla	Umatilla	Minthorn Springs	74	222,263,607	0.54
Inland	07_MGILCS	L. Columbia	Umatilla	Umatilla	Umatilla R	70	236,157,293	0.54
Inland	07_MGILCS	L. Columbia	Walla Walla	Walla Walla	Walla Walla R, Touchet R, Yellowhawk Cr	95	380,515,222	0.69
Inland	07_MGILCS	Snake	Tucannon	Tucannon	Tucannon R	42	214,476,660	0.55
Inland	07_MGILCS	Snake	Lower Snake	Lower Snake	Alpowa Cr	53	287,842,645	0.63
Inland	07_MGILCS	Snake	Asotin	Asotin	George Creek	58	321,868,839	0.66
Inland	07_MGILCS	Snake	Asotin	Asotin	Asotin Cr	60	227,071,819	0.57
Inland	07_MGILCS	Snake	Clearwater	L Clearwater	Lapwai, Mission Crks	119	310,700,629	0.73
Inland	07_MGILCS	Snake	Clearwater	L Clearwater	Little Bear Cr	46	267,109,802	0.60
Inland	07_MGILCS	Snake	Clearwater	L Clearwater	Sweetwater Cr	51	224,853,521	0.53
Inland	07_MGILCS	Snake	Clearwater	L Clearwater	Potlatch R	50	217,298,385	0.51
Inland	07_MGILCS	Snake	Clearwater	NF Clearwater	Dworshak Hatchery	68	699,424,228	0.71
Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	Big Canyon Cr	95	251,726,901	0.59
Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	Catherine Cr	91	199,865,574	0.53
Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	Joseph Cr	88	240,989,824	0.52
Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	upper Grande Ronde R	58	190,569,290	0.61
Inland	07_MGILCS	Snake	Imnaha	Imnaha	Gumboot Cr	38	233,911,089	0.54
Inland	07_MGILCS	Snake	Imnaha	Imnaha	Lightning Cr	95	319,903,348	0.66
Inland	07_MGILCS	Snake	Imnaha	Imnaha	Little Sheep Cr	76	235,566,015	0.53

Inland	07_MGILCS	Snake	Salmon	L Salmon	Little Salmon R, Hazard, Boulder Crks	95	248,041,850	0.59
Inland	07_MGILCS	Snake	Salmon	L Salmon	Rapid River	78	337,982,422	0.73
Inland	07_MGILCS	Snake	Salmon	L Salmon	White Bird Cr	50	200,302,136	0.46
Inland	08_YAKIMA	U. Columbia	Yakima	Yakima	Naches R, Nile Cr	38	402,080,355	0.62
Inland	08_YAKIMA	U. Columbia	Yakima	Yakima	Satus R	67	208,951,362	0.49
Inland	08_YAKIMA	U. Columbia	Yakima	Yakima	Toppenish Cr	95	295,948,341	0.63
Inland	08_YAKIMA	U. Columbia	Yakima	Yakima	Teanaway R, Big Cr, Roza Dam	95	384,909,116	0.69
Inland	09_UPPCOL	U. Columbia	Entiat	Entiat	Entiat R	43	336,470,474	0.65
Inland	09_UPPCOL	U. Columbia	Methow	Methow	Winthrop NFH	93	180,992,366	0.46
Inland	09_UPPCOL	U. Columbia	Okanogan	Okanogan	Bonaparte, Salmon, Omak Crks	95	278,354,930	0.58
Inland	09_UPPCOL	U. Columbia	Wenatchee	Wenatchee	Chiwaukum Cr	54	227,418,107	0.56
Inland	10_SFCLWR	Snake	Clearwater	SF Clearwater	Clear Cr	61	243,826,940	0.59
Inland	10_SFCLWR	Snake	Clearwater	SF Clearwater	Crooked R	86	216,426,527	0.51
Inland	10_SFCLWR	Snake	Clearwater	SF Clearwater	Lolo Cr	68	159,912,565	0.59
Inland	10_SFCLWR	Snake	Clearwater	SF Clearwater	Tenmile Cr	60	288,038,275	0.64
Inland	11_UPCLWR	Snake	Clearwater	Lochsa	Canyon, Deadman Crks	68	285,197,311	0.61
Inland	11_UPCLWR	Snake	Clearwater	Lochsa	upper Lochsa R	72	295,662,531	0.72
Inland	11_UPCLWR	Snake	Clearwater	Selway	Hell's Half Acre	55	307,760,209	0.72
Inland	11_UPCLWR	Snake	Clearwater	Selway	Little Clearwater R	65	236,963,840	0.55
Inland	11_UPCLWR	Snake	Clearwater	Selway	upper Selway R	51	246,349,248	0.69
Inland	11_UPCLWR	Snake	Clearwater	Selway	White Cap Cr	72	264,031,261	0.60
Inland	12_SFSALM	Snake	Salmon	SF Salmon	Johnson Cr	95	201,270,498	0.48
Inland	12_SFSALM	Snake	Salmon	SF Salmon	Lick Cr	70	200,066,360	0.56
Inland	12_SFSALM	Snake	Salmon	SF Salmon	Secesh R	30	263,042,376	0.60
Inland	12_SFSALM	Snake	Salmon	SF Salmon	East Fork SF Salmon R	53	363,259,811	0.73
Inland	12_SFSALM	Snake	Salmon	SF Salmon	Stolle Meadows	42	366,401,888	0.68
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Bargamin Cr	60	189,953,336	0.53
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Big, Rush Crks	95	328,230,174	0.67
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Camas Cr	70	268,890,213	0.70
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Loon Cr	51	320,069,394	0.65
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Marsh Cr	60	334,274,383	0.72
Inland	14_UPSALM	Snake	Salmon	NF Salmon	EF Salmon R	51	304,068,477	0.64
Inland	14_UPSALM	Snake	Salmon	NF Salmon	Yankee Fork Salmon R	58	191,268,742	0.52
Inland	14_UPSALM	Snake	Salmon	NFSalmon	Lemhi R, Bear Valley Cr	95	225,800,707	0.51
Inland	14_UPSALM	Snake	Salmon	NF Salmon	Morgan Cr	39	337,843,016	0.73

Inland	14_UPSALM	Snake	Salmon	NF Salmon	Pahsimeroi Hatchery	56	284,569,935	0.70
Inland	14_UPSALM	Snake	Salmon	NF Salmon	Sawtooth Hatchery	47	241,483,030	0.57

*proportion of draft genome covered at a minimum depth of 10X:

Results

Neutral steelhead population structure across the Columbia River basin:

After aligning markers in common for all samples and accounting for LD, 226 neutral markers (Hess et al., 2016b) were included for further analyses. A total of 9,471 individuals from 113 populations met inclusion criteria (>90% loci successfully genotyped and had an estimated <0.5% genotyping error based on replicate genotyping) and were included in this study.

Population structure as visualized by PCA of allelic frequencies of neutral markers indicated genetic divergence by geographic locations (Figure 12). The DAPC with neutral markers assigned steelhead to two clusters ($K=2$); 25 putative coastal collections grouped into one cluster and 90 putative inland collections grouped into the second cluster (Figure 13). Additionally, DAPC and ΔK exposed hierarchical structure with a smaller peak at $K = 6$ (Figure 13). The hierarchical population structure includes well known population structure within the coastal and inland regions (Blankenship et al., 2011; Matala et al., 2014; Micheletti et al., 2018) and admixture coefficient analyses were plotted for $K=6$ with LEA to visualize the genetic mixing within finer scale geographic groupings (Figure 14). These finer scale geographic groupings are also represented by shapes in Figure 12. Most coastal collections, except for Mill Creek and Indian Creek, exhibited non-overlapping allele frequencies relative to all inland collections. The Klickitat River which is located between coastal and inland populations formed a cluster intermediate of the two population types. Inland collections from the Yakima and Clearwater rivers clustered distinctly from others in study (Figure 12). Neutral structure was consistent with previous studies with various marker types that largely correspond to geographic population structure and significant heterogeneity in environmental conditions (Blankenship et al., 2011; Matala et al., 2014; Micheletti et al., 2018).

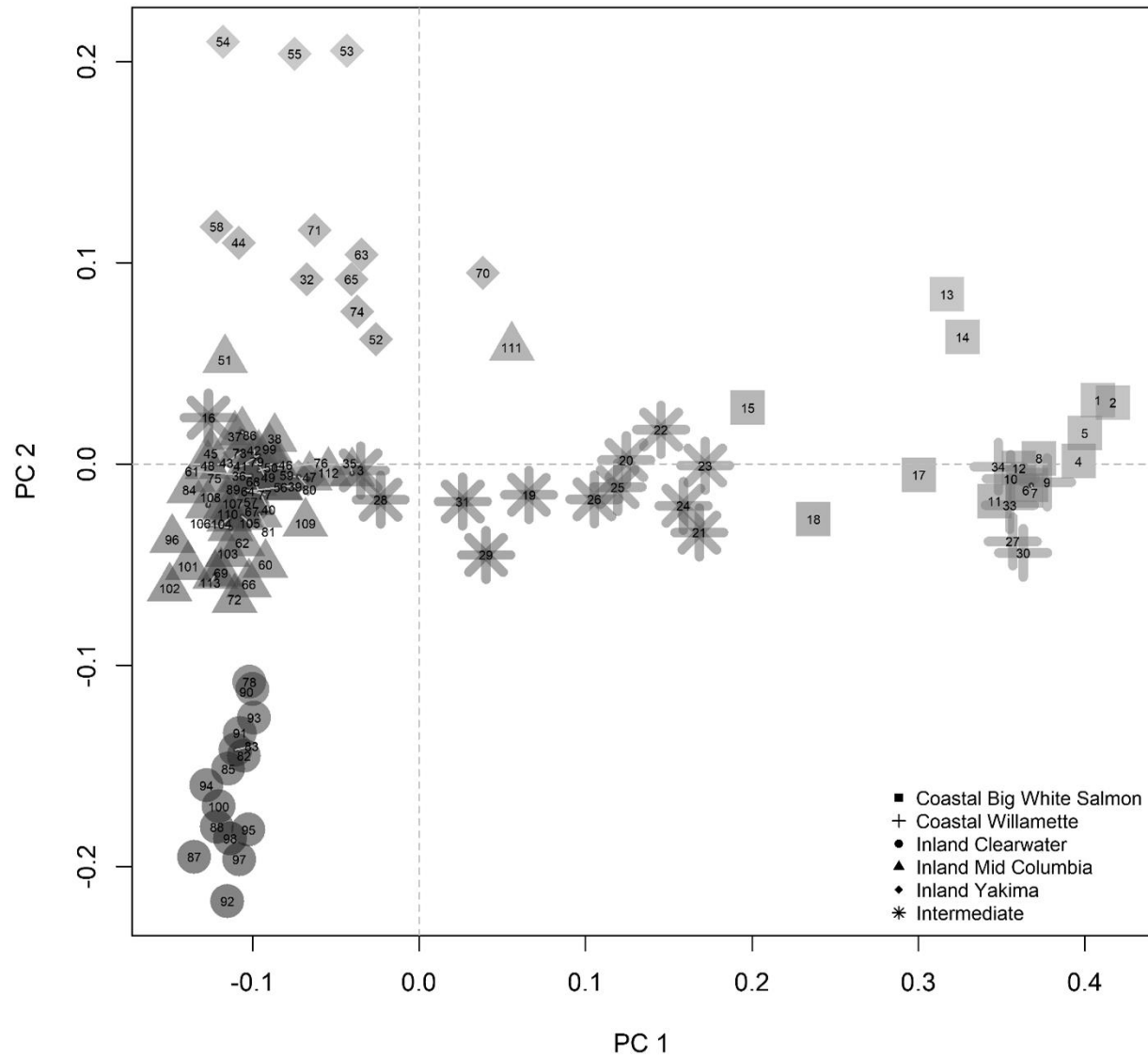


Figure 12. Neutral marker PCA plot for all steelhead populations. Shapes indicate the geographic region of the population.

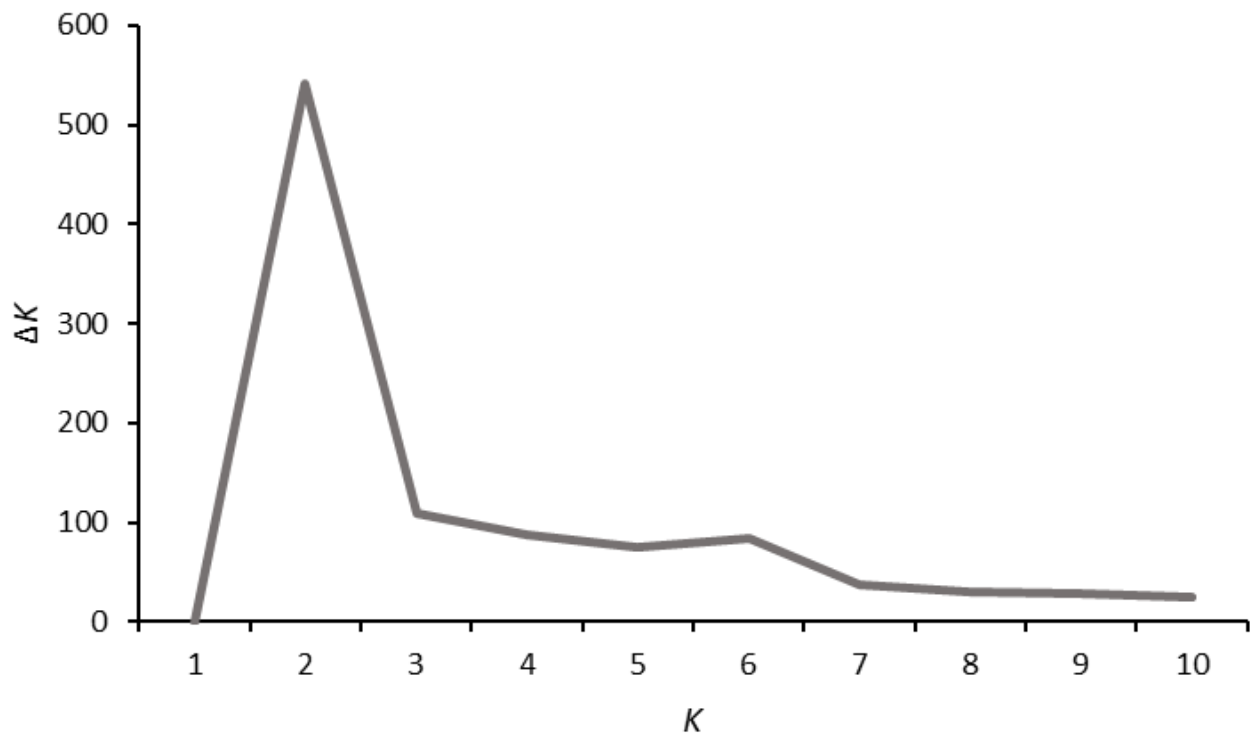


Figure 13. Delta K results based on DAPC Bayesian Information Criterion (BIC) values averaged over 25 iterations and divided by the standard deviation for K values 1-10.

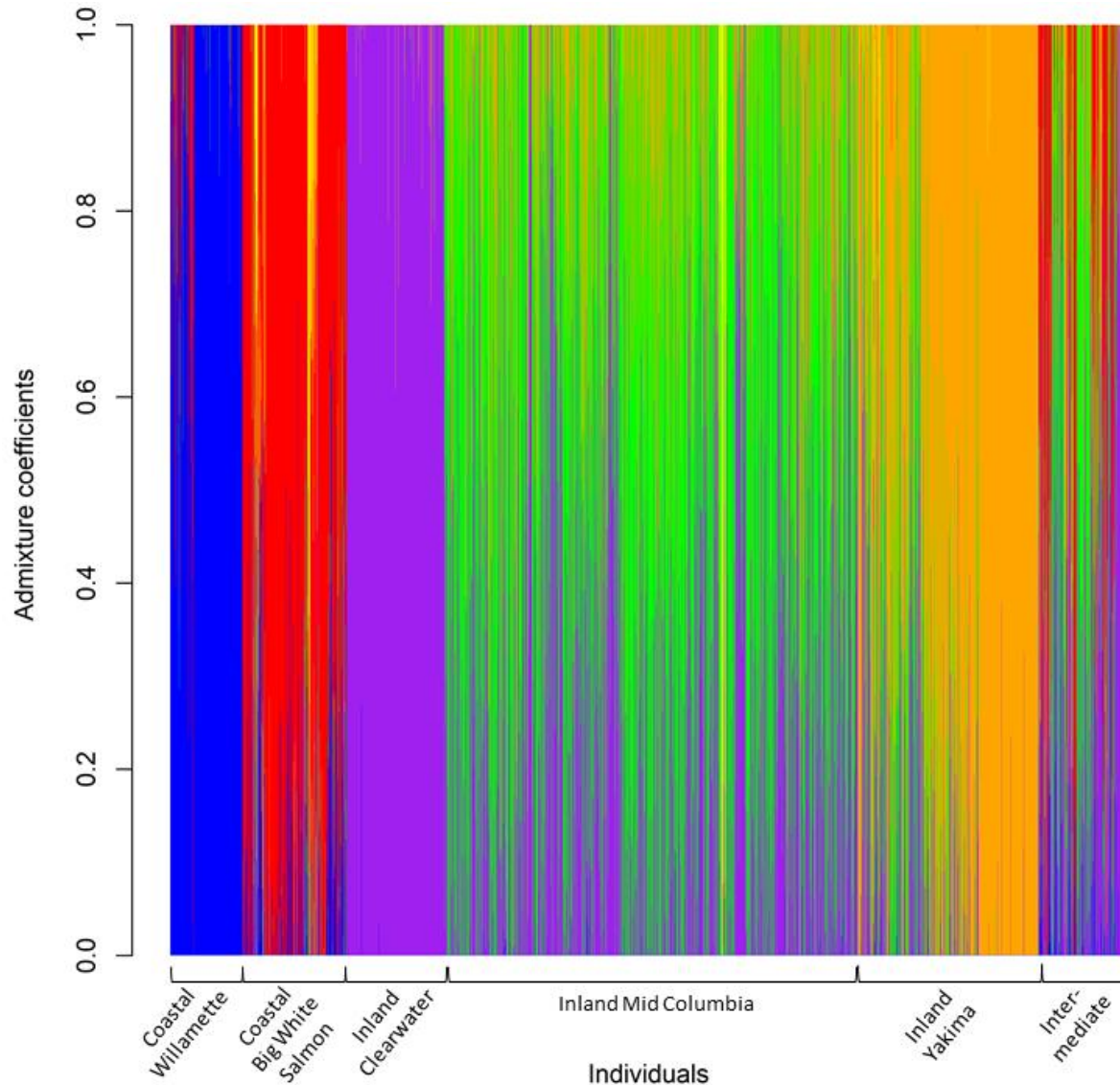


Figure 14. Admixture coefficients for each individual based on sparse non-negative matrix factorization least-squares optimizations to estimate hierarchical population structure at $K=6$ for steelhead collections.

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 15, Figure 16, Appendix 5, Appendix 6, and Appendix 7) to include Chinook Salmon, steelhead, and Coho Salmon broodstocks in all hatcheries above Bonneville Dam using expanded SNP panels of 343 loci for Chinook Salmon, 368 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 3).

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).

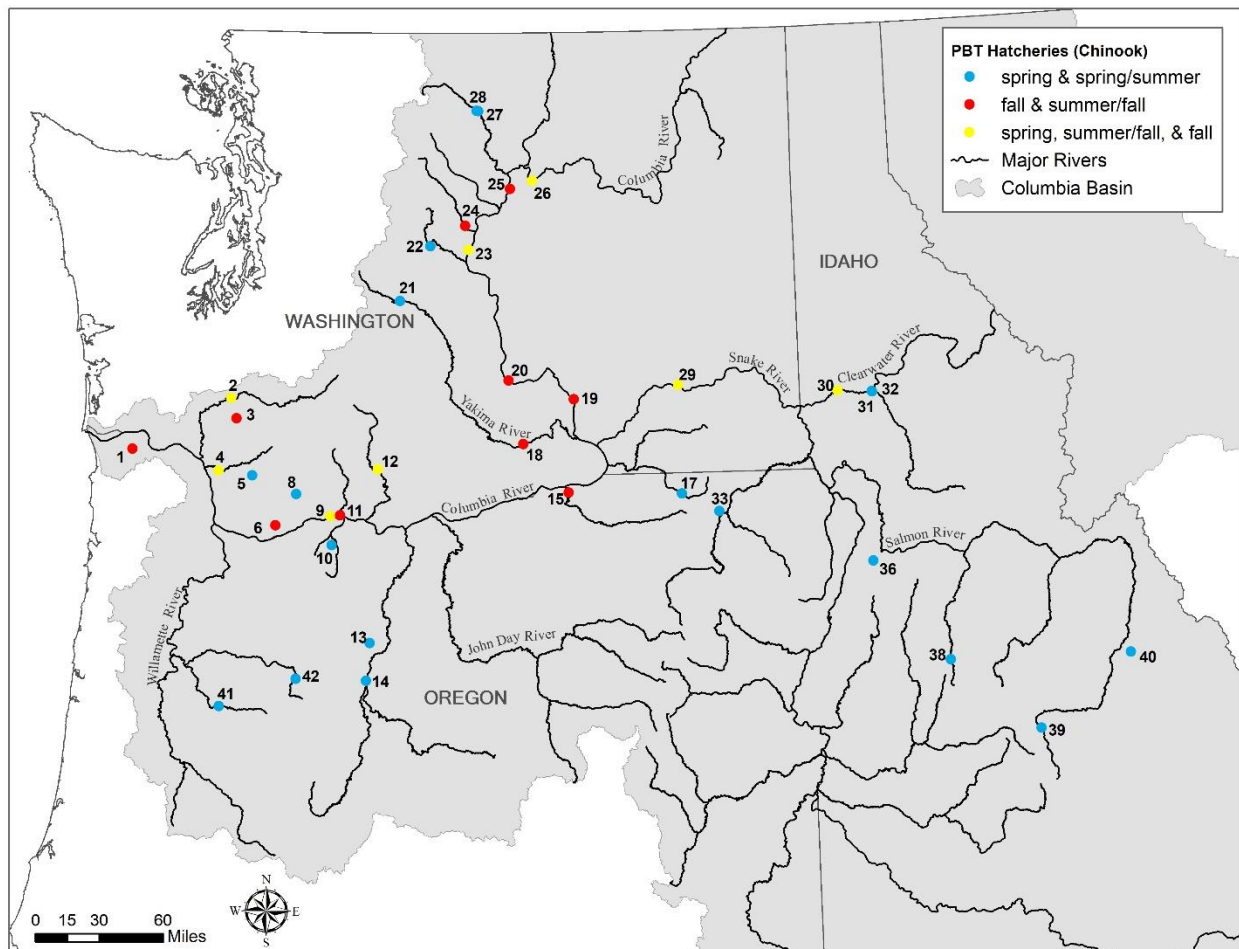


Figure 15. Chinook Salmon, PBT hatcheries. Numbers correspond to map ID and hatchery descriptions (Appendix 5).

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 2020 report period included spawn year 2018 for some lower Columbia River hatcheries, but primarily broodyear 2019 was genotyped for most hatcheries. The total numbers of fish genotyped for PBT baselines in 2020 included n=10,107 spring Chinook Salmon, n=2,473 upper Columbia summer Chinook Salmon, n=28,877 fall Chinook Salmon (Appendix 3), n=2,278 steelhead trout (Appendix 4), and n=6,732 Coho Salmon (Appendix 4). DNA was extracted using modified Chelex extractions and Qiagen DNeasy 96 kits. Extracted genomic DNA was genotyped at 343 SNP loci for Chinook Salmon, 368 SNP loci for steelhead trout, and 257 SNP loci for Coho Salmon using a GTseq protocol: (<https://www.monitoringresources.org/Document/Method/Details/5446>).

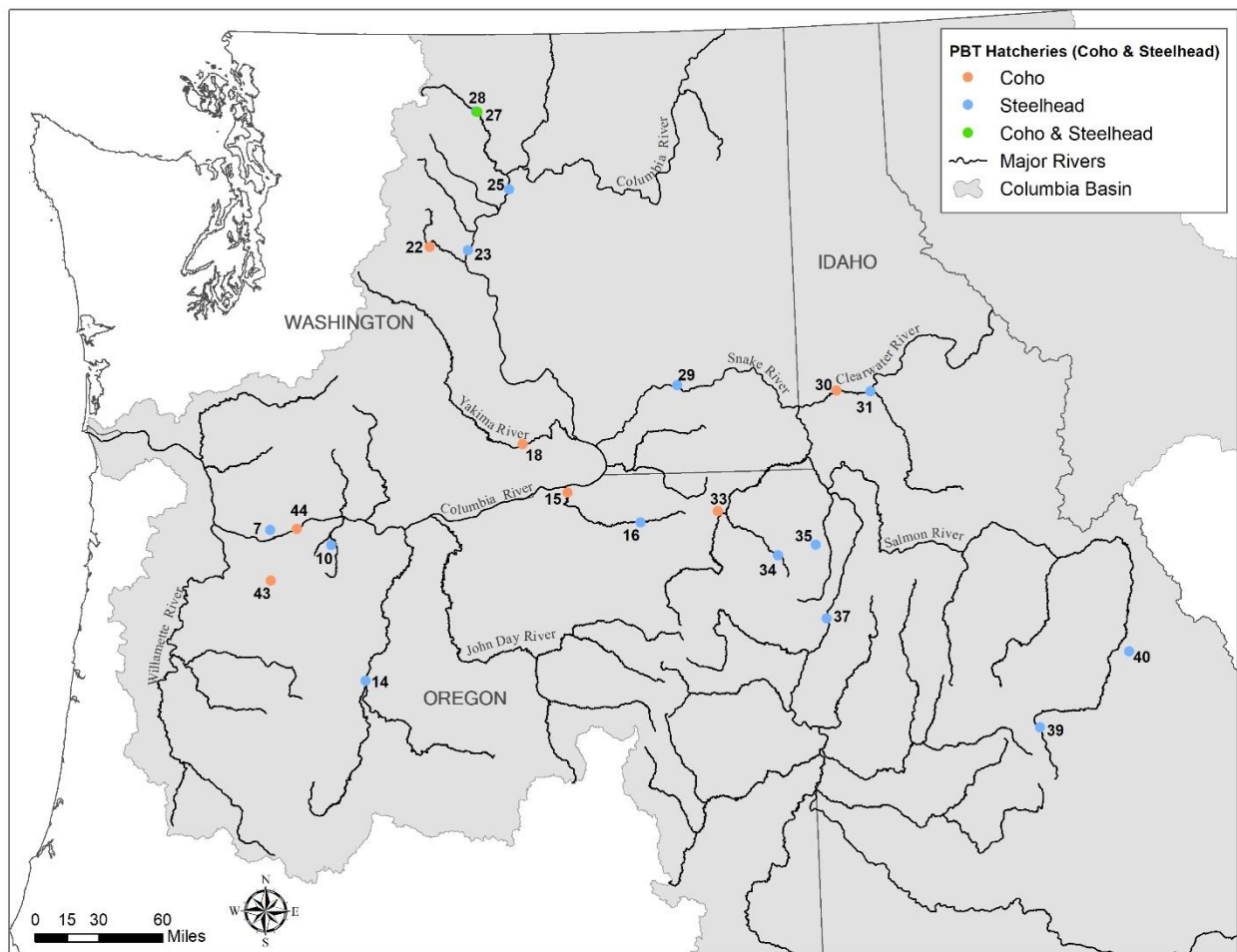


Figure 16. Steelhead and Coho Salmon, PBT hatcheries. Numbers correspond to map ID and hatchery descriptions (Appendix 6, Appendix 7).

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

Over the course of the Genetic Assessment project we have compiled extensive data sets of SNP genotypes for Chinook salmon, steelhead trout and *O. nerka*, and continue to improve resources for Coho Salmon and Pacific Lamprey. The populations we have evaluated span diverse regions in the Columbia River Basin (including the Snake River Basin). 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 whole genome resequencing and GT-seq techniques has yielded large numbers 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; Narum et al. 2018; Micheletti et al. 2018; Collins et al. 2020). The expansion efforts reported here also provided improved ability to differentiate stocks on regional and local scales through application of GSI and PBT methods.

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 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 allele frequencies for millions of SNPs from whole genome resequencing 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.

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Appendix 3. Chinook Salmon hatchery broodstock sampled for PBT baselines.

Map ID	Spawning hatchery	Run type	Lineage	Region	Latitude	Longitude	Year	2020 genotyping	
								Sampled	Completed
	Klaskanine (NF brood)	fall (tule)	LC	Col.	46.09	-123.718	na	na	na
	Klaskanine (SF brood)	fall (tule)	LC	Col.	46.09	-123.718	na	na	na
1	Big Creek	fall (tule)	LC	Col.	46.14616	-123.581	2015	2019	947
2	Cowlitz Salmon	fall (tule)	LC	Col.	46.51145	-122.6294	2015	2019	1106
2	Cowlitz Salmon	spring	LC	Col.	46.51145	-122.6294	2015	2019	1015
3	Toutle	fall (tule)	LC	Col.	46.37464	-122.572	2015	2018	na
4	Kalama Falls	fall (tule)	LC	Col.	46.01624	-122.7328	2016	2019	3119
4	Kalama Falls	spring	LC	Col.	46.01624	-122.7328	2015	2019	579
5	Lewis River	spring	LC	Col.	45.98849	-122.4062	2015	na	na
	Clackamas	spring	LC	Col.	45.296	-122.362	na	na	na
	Marion Forks	spring	LC	Col.	44.612	-121.948	na	na	na
	South Santiam	spring	LC	Col.	44.416	-122.675	2015	2019	797
	McKenzie	spring	LC	Col.	44.118	-122.637	na	na	na
	Willamette	spring	LC	Col.	43.745	-122.444	na	na	na
6	Washougal	fall (tule)	LC	Col.	45.65344	-122.1691	2015	2019	1554
	Bonneville, Tanner Cr.	fall (tule)	LC	Col.	45.633	-121.957	2019	2019	515
11	Spring Creek NFH	fall (tule)	LC	Col.	45.72779	-121.5453	2015	2019	4773
9	Little White Salmon NFH	fall	IOT	Col.	45.72226	-121.6401	2013	2019	6236
15	Umatilla	fall	IOT	Col.	45.88172	-119.3226	2012	2019	179
18	Prosser	fall	IOT	Col.	46.21512	-119.7596	2012	2019	121
19	Ringold Springs	fall	IOT	Col.	46.51401	-119.2593	2016	2019	839
20	Priest Rapids	fall	IOT	Col.	46.64728	-119.899	2012	2019	6328
29	Lyons Ferry	fall	IOT	Snake	46.59725	-118.2282	2011	2019	WDFW
30	Nez Perce Tribal	fall	IOT	Snake	46.51954	-116.6601	2011	2019	687
23	Eastbank	summer	IOT	Col.	47.53367	-120.2891	2012	2019	951
24	Entiat NFH	summer	IOT	Col.	47.69806	-120.3231	2013	2019	310
25	Wells	summer	IOT	Col.	47.94582	-119.8712	2012	2019	95
26	Chief Joseph	summer	IOT	Col.	48.0006	-119.6451	2013	2019	1117
9	Little White Salmon NFH	spring	IST	Col.	45.72226	-121.6401	2013	2019	1247
15	Umatilla	spring	IST	Col.	45.88172	-119.3226	2012	2019	271
29	Lyons Ferry	spring	IST	Snake	46.59725	-118.2282	2008	2019	85
30	Nez Perce Tribal	spring	IST	Snake	46.51954	-116.6601	2008	2019	837
23	Eastbank	spring	IST	Col.	47.53367	-120.2891	2012	2019	194
26	Chief Joseph	spring	IST	Col.	48.0006	-119.6451	2014	2019	525
8	Carson NFH	spring	IST	Col.	45.86826	-121.9742	2012	2019	412
10	Parkdale	spring	IST	Col.	45.52439	-121.6216	2012	2019	195
12	Klickitat	spring	IST	Col.	46.04236	-121.1823	2008	2019	96
13	Warm Springs NFH	spring	IST	Col.	44.86201	-121.245	2012	na	na
14	Round Butte	spring	IST	Col.	44.60503	-121.2778	2012	na	na
21	Cle Elum SRF	spring	IST	Col.	47.18679	-120.9762	2012	2019	127
22	Leavenworth NFH	spring	IST	Col.	47.55842	-120.6738	2013	2019	545
27	Methow	spring	IST	Col.	48.47703	-120.2051	2012	2019	103
28	Winthrop NFH	spring	IST	Col.	48.47366	-120.1891	2013	2019	363
33	Lookingglass	spring	IST	Snake	45.73136	-117.864	2008	2019	817
31	Dworshak NFH	spring	IST	Snake	46.50206	-116.3232	2008	2019	1899
32	Clearwater	spring	IST	Snake	46.50429	-116.3277	2008	2019	IDFG
36	Rapid River	spring/summer	IST	Snake	45.35411	-116.3938	2008	2019	IDFG
38	SF Salmon, McCall	spring/summer	IST	Snake	44.65554	-115.7025	2008	2019	IDFG
40	Pahsimeroi	spring/summer	IST	Snake	44.62284	-113.9863	2008	2019	IDFG
39	Sawtooth	spring/summer	IST	Snake	44.15174	-114.8843	2008	2019	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 15. 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).

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321 **Appendix 4. Steelhead and Coho Salmon hatchery broodstock sampled for PBT baselines.**

Map ID	Spawning hatchery	Run type	Lineage	Region	Latitude	Longitude	Year	2020 Genotyping	
								Sampled	Completed
	Steelhead								
1	Big Creek	winter	coastal	Col.	46.1462	-123.581	na	na	na
	Abernathy FTC	winter	coastal	Col.	46.226	-123.153	2012	na	na
	Cowlitz Trout	winter	coastal	Col.	46.4877	-122.727	na	na	na
4	Kalama Falls	winter	coastal	Col.	46.0162	-122.7328	na	na	na
	Merwin	winter	coastal	Col.	45.954	-122.564	na	na	na
	Clackamas	winter	coastal	Col.	45.296	-122.362	na	na	na
	Eagle Creek NFH	winter	coastal	Col.	45.276	-122.202	na	na	na
	Sandy	winter	coastal	Col.	45.407	-122.254	na	na	na
7	Skamania	summer/winter	coastal	Col.	45.6218	-122.2173	2013	2019	347
10	Parkdale	winter	coastal	Col.	45.5244	-121.6216	2012	2019	46
14	Round Butte	summer	inland	Col.	44.605	-121.2778	2013	2019	808
	Umatilla	summer	inland	Col.	45.913	-119.552	2012	2019	0
23	Eastbank	summer	inland	Col.	47.5337	-120.2891	2012	2019	na
25	Wells	summer	inland	Col.	47.9458	-119.8712	2013	2019	176
27	Methow (Twisp)	summer	inland	Col.	48.477	-120.2051	2013	2019	na
28	Winthrop NFH	summer	inland	Col.	48.4737	-120.1891	2012	2019	121
29	Lyons Ferry	summer	inland	Snake	46.5973	-118.2282	2009	2019	IDFG
34	Wallowa	summer	inland	Snake	45.4178	-117.3004	2009	2019	655
37	Oxbow	summer	inland	Snake	44.9727	-116.8548	2008	2019	IDFG
31	Dworshak NFH	summer	inland	Snake	46.5021	-116.3232	2008	2019	IDFG
40	Pahsimeroi	summer	inland	Snake	44.6228	-113.9863	2008	2019	IDFG
39	Sawtooth	summer	inland	Snake	44.1517	-114.8843	2008	2019	IDFG
35	Little Sheep Creek	summer	inland	Snake	45.4777	-116.9306	2008	2019	125
	Coho								
15	Umatilla	na	na	Col.	45.913	-119.552	2012	2019	438
18	Prosser	na	na	Col.	46.2151	-119.7596	2016	2019	1001
22	Leavenworth NFH	na	na	Col.	47.5584	-120.6738	2012	2019	1188
28	Winthrop NFH	na	na	Col.	48.4737	-120.1891	2012	2019	1165
31	Dworshak NFH	na	na	Snake	46.5021	-116.3232	2012	2019	na
43	Eagle Creek NFH	na	na	Col.	45.276	-122.202	2019	2019	1757
44	Bonneville	na	na	Col.	45.633	-121.957	2019	2019	1183

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

323 Note: The map ID indicates site locations corresponding with Figure 15. Genetic lineage is coastal or inland. Year refers to the first year of PBT sampling for
324 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
325 drafting of this report. The project collaborators at Idaho Department of Fish and Game (IDFG) were responsible for genotyping of Snake River hatcheries (see
326 “completed” column). All Coho broodstocks sampled for PBT broodstock were designated for release of fish upstream of Bonneville Dam.
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Map num.	Hatchery	Species	Code	Run type	Lineage	Year												
						2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	
32	Clearwater Fish Hatchery	Chinook	OtsCLWH	Spring	Interior stream type	X	X	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	X	X	X	
31	Dworshak National Fish Hatchery	Chinook	OtsDWOR	Spring	Interior stream type	X	X	X	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	X	X	
33	Lookingglass Fish Hatchery - Grande Ronde	Chinook	OtsGRUW	Spring	Interior stream type	X	X	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	X	X	
33	Lookingglass Fish Hatchery - Lookingglass Creek	Chinook	OtsLOOK	Spring	Interior stream type	X	X	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	X	X	
29	Lyons Ferry Fish Hatchery	Chinook	OtsLYON	Spring	Interior stream type	*	*	*	*	X	X	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	X	X	
29	Lyons Ferry Fish Hatchery	Chinook	OtsLYON_1	Fall	Interior ocean type	*	*	*	X	X	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	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	X	X	
30	Nez Perce Tribal Fish Hatchery	Chinook	OtsNPFH_1	Fall	Interior ocean type	*	*	*	X	X	X	X	X	X	X	X	X	
30	Nez Perce Tribal Fish Hatchery	Chinook	OtsNPFH	Spring	Interior stream type	X	X	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	X	X	
36	Rapid River Fish Hatchery	Chinook	OtsRAPH	Spring	Interior stream type	X	X	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	X	X	
1	Big Creek Hatchery	Chinook	OtsBIG_fa	Fall	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	X	
8	Carson National Fish Hatchery	Chinook	OtsCAR_sp	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X	X	X	
26	Chief Joseph Hatchery	Chinook	OtsCJH_sp	Spring	Interior stream type	*	*	*	*	*	*	X	X	X	X	X	X	
26	Chief Joseph Hatchery - Integrated	Chinook	OtsCJHint_su	Summer	Interior ocean type	*	*	*	*	*	X	X	X	X	X	X	X	
26	Chief Joseph Hatchery - Segregated	Chinook	OtsCJHseg_su	Summer	Interior ocean type	*	*	*	*	*	X	X	X	X	X	X	X	
2	Cowlitz Salmon	Chinook	OtsCOW_sp	Spring	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	**	
2	Cowlitz Salmon	Chinook	OtsCOW_fa	Fall	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	**	
23	Eastbank Fish Hatchery	Chinook	OtsEASTBK_sp	Spring	Interior stream type	*	*	*	*	*	X	X	X	X	X	X	X	
23	Eastbank Fish Hatchery	Chinook	OtsEASTBK_su	Summer	Interior ocean type	*	*	*	*	X	X	X	X	X	X	X	X	
24	Entiat National Fish Hatchery	Chinook	OtsENFH_su	Summer	Interior ocean type	*	*	*	*	*	X	X	X	X	X	X	X	
4	Kalama Falls	Chinook	OtsKAL_sp	Spring	Lower Columbia	*	*	*	*	*	*	*	X	X	X	XX	**	
4	Kalama Falls	Chinook	OtsKAL_fa	Fall	Lower Columbia	*	*	*	*	*	*	*	*	X	X	XX	**	
12	Klickitat State Fish Hatchery	Chinook	OtsKH_sp	Spring	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	
12	Klickitat State Fish Hatchery	Chinook	OtsKH_fa c	Fall	Interior ocean type	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	X	X	
22	Leavenworth National Fish Hatchery	Chinook	OtsLNFH_sp	Spring	Interior stream type	*	*	*	*	*	X	X	X	X	X	X	X	
5	Speelyai Hatchery	Chinook	OtsLEW_sp	Spring	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	**	
9	Little White Salmon National Fish Hatchery	Chinook	OtsLWS_fa	Fall	Interior ocean type	*	*	*	*	*	X	X	X	X	X	X	X	
9	Little White Salmon National Fish Hatchery	Chinook	OtsLWS_sp	Spring	Interior stream type	*	*	*	*	*	X	X	X	X	X	X	X	
9	Little White Salmon National Fish Hatchery - Touchet River	Chinook	OtsTOUCH_sp	Spring	Interior stream type	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	X	*	
42	Marion Forks Hatchery	Chinook	OtsNSANT_sp	Spring	Lower Columbia	*	*	*	*	*	*	*	*	*	*	X	X	
27	Methow State Fish Hatchery	Chinook	OtsMETH_sp	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X	X	X	
10	Parkdale Fish Facility	Chinook	OtsPFF_sp	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X	X	X	
20	Priest Rapids Hatchery	Chinook	OtsPRH_fa	Fall	Interior ocean type	*	*	*	*	X	X	X	X	X	X	X	X	
14	Round Butte Fish Hatchery	Chinook	OtsRB_sp	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X	X	**	
19	Ringold Springs State Hatchery	Chinook	OtsRG_fa	Fall	Interior ocean type	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	X	X	X	X	
41	South Santiam Hatchery	Chinook	OtsSSANT_sp	Spring	Lower Columbia	*	*	*	*	*	*	*	X	X	*	X	X	
11	Spring Creek National Fish Hatchery	Chinook	OtsSPCR_fa	Fall	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	X	
3	North Toutle Hatchery	Chinook	OtsTOU_fa	Fall	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	**	
15	Three mile dam, Umatilla River	Chinook	OtsUMA_fa b	Fall	Interior ocean type	*	*	*	*	X	X	X	~	~	~	X	X	
17	South Fork Walla Walla facility	Chinook	OtsUMA_sp	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X	X	X	
6	Washougal	Chinook	OtsWAS_fa	Fall	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	**	
13	Warm Springs National Fish Hatchery	Chinook	OtsWSNFH_sp h	Spring	Interior stream type	*	*	*	*	X	X	X	~	~	~	X	**	
25	Wells Fish Hatchery	Chinook	OtsWELLS_su	Summer	Interior ocean type	*	*	*	*	X	X	X	X	X	X	X	X	
28	Winthrop National Fish Hatchery	Chinook	OtsWTP_sp	Spring	Interior stream type	*	*	*	*	*	X	X	X	X	X	X	X	
18	Yakima Nation Prosser Hatchery	Chinook	OtsPRO_fa	Fall	Interior ocean type	*	*	*	*	X	X	*	X	X	X	X	X	
21	Levi George/Cle Elum (Integrated)	Chinook	OtsYRint_sp	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X	X	X	
21	Levi George/Cle Elum (Segregated)	Chinook	OtsYRseg_sp	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X	X	X	

- 330
- Note: Species-specific collections code along with run type and genetic lineage are provided for both species. Map numbers correspond with Figure 15.
- 331
- X Chinook tissues genotyped using 351 SNPs
- 332
- X Chinook tissues genotyped using 343 SNPs
- 333
- X Chinook tissues genotyped using 298 SNPs
- 334
- X Chinook tissues genotyped using 96 SNPs
- 335
- Chinook broodstock sampled, spawned at another hatchery and genotyped using 298 SNPs
- 336
- a Chinook Lyons Ferry stock consolidated under 'OtsLYON' starting in 2012
- 337
- 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 distiguished from
- 338
- Ringold stock.
- 339
- c Chinook typically spawned at Little White Salmon NFH, but due to low returns in 2018 they were spawned at Klickitat Hatchery .
- 340
- h Chinook Warm Springs NFH spring stock spawned at Little White Salmon Hatchery starting in 2015-2017.
- 341
- N/A Stock discontinued/non-existent
- 342
- * Broodstock not sampled
- 343
- ** Broodstock sampled, tissues archived until funding identified for processing

Map num.	Hatchery	Species	Code	Run type	Lineage	Year											
						2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019
31	Dworshak National Fish Hatchery	Steelhead	OmyDWOR	Summer	Interior	X	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	X
29	Lyons Ferry Fish Hatchery- Touchet	Steelhead	OmyTOUW c	Summer	Interior	*	X	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	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	X
29	Lyons Ferry Fish Hatchery - Tucannon	Steelhead	OmyTUCW c	Summer	Interior	*	X	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	N/A
37	Oxbow	Steelhead	OmyOXBO	Summer	Interior	X	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	X
39	Sawtooth Fish Hatchery - East Fork Salmon	Steelhead	OmyEFSW e	Summer	Interior	X	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	X
40	Pahsimeroi Fish Hatchery	Steelhead	OmyPAHH	Summer	Interior	X	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	X
23	Eastbank Hatchery	Steelhead	OmyEASTBK	Summer	Interior	*	*	*	*	X	X	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	X	X
14	Round Butte Fish Hatchery	Steelhead	OmyRB	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X	X
7	Skamania Hatchery (Summer)	Steelhead	OmySKH_su g	Summer	Coastal	*	*	*	*	*	X	X	X	X	X	X	X
7	Skamania Hatchery (Winter)	Steelhead	OmySKH_wi g	Winter	Coastal	*	*	*	*	*	X	X	X	X	X	X	X
16	Minthorn Springs	Steelhead	OmyUMA	Summer	Interior	*	*	*	*	X	X	X	X	X	X	X	*
25	Wells Hatchery - On Station	Steelhead	Omy_WEL	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X	X
25	Wells Hatchery - Okanogan stock	Steelhead	OmyWEL_OKA	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X	*
25	Wells Hatchery - Omak stock	Steelhead	OmyWEL_OMA	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X	*
25	Wells Hatchery - Methow stock	Steelhead	OmyWEL_MET	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X	*
28	Winthrop National Fish Hatchery	Steelhead	OmyWTP	Summer	Interior	*	*	*	*	X	X	X	X	X	X	X	X

- 345
- Note map numbers correspond to sites in Figure 15.
- 346
- X Steelhead tissues genotyped using 96 SNPs
- 347
- X Steelhead tissues genotyped using 379 SNPs
- 348
- X Steelhead tissues genotyped using 269 SNPs
- 349
- X Steelhead tissues genotyped using 192 SNPs
- 350
- X Steelhead tissues genotyped using 390 SNPs
- 351
- Steelhead tissues genotyped using 368 SNPs
- 352
- Steelhead broodstock sampled, spawned at another hatchery and genotyped using 379 SNPs
- 353
- Steelhead broodstock sampled, spawned at another hatchery and genotyped using 368 SNPs
- 354
- c Steelhead Lyons Ferry stock consolidated under 'OmyLYON' starting in 2012
- 355
- d Steelhead Lyons Ferry stock discontinued starting in 2013
- 356
- e Steelhead Sawtooth stock consolidated under 'OmySAWT' from 2012-2013
- 357
- f Steelhead 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
- 358
- Shoshone-Bannock tribe beginning in 2017
- 359
- g Steelhead 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
- 360
- Chambers Creek stock to Big Creek stock starting with SY2018.
- 361
- i Steelhead Methow Hatchery Twisp stock spawned at Winthrop NFH starting in 2017; not distiguished from Withrop stock
- 362
- N/A Stock discontinued/non-existent
- 363
- * Broodstock not sampled
- 364
- ** Broodstock sampled, tissues archived until funding identified for processing

Map num.	Hatchery	Species	Code	Run type	Lineage	Year											
						2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019
15	Three mile dam, Umatilla River	Coho	OkiUMA	Fall	Lower Columbia								X	X	X	X	X
22	Leavenworth National Fish Hatchery	Coho	OkiLNFH	Fall	Lower Columbia				X	X	X	X	X	X	X	X	X
30	Nez Perce Tribal Fish Hatchery	Coho	OkiNPT	Fall	Lower Columbia						*	*	X	X	X	X	**
18	Yakima Nation Prosser Hatchery	Coho	OkiPRO	Fall	Lower Columbia									X	X	X	X
28	Winthrop National Fish Hatchery	Coho	OkiWTP, OkiMET	Fall	Lower Columbia					X	X	X	X	X	X	X	X
33	Lookingglass Fish Hatchery - Lostine River	Coho	OkiLSTW	Fall	Lower Columbia											X	**
43	Eagle Creek National Fish Hatchery	Coho	OkiEGLC	Fall	Lower Columbia												X
44	Bonneville Hatchery	Coho	OkiBONN	Fall	Lower Columbia												X

366
367 Note: map numbers correspond to sites in Figure 15.
368 X Coho tissues genotyped at 257 loci
369 * Samples received, but not genotyped.
370 ** Samples collected, but not received.
371

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, Hargrove et al. 2020, Jensen et al. 2020). 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 since 2012 has been 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 (Steele et al. 2019). 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 no longer rely solely on GSI to determine stock of origin because PBT can be used to identify reintroduced fish to the Yakima River starting with the spawn year of 2012. For the 2019 Chinook harvest, multiple age classes (3-, 4-, 5-, and 6-year old fish) can be identified from Lower Columbia, Middle Columbia, and Snake River stocks using PBT (Appendix 5).

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 and Sockeye 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. Importantly, we can now estimate abundance of all genetic stocks using the reported catch estimates of each fishery.

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 and Sockeye salmon harvested in sport, commercial, and tribal fisheries in the mainstem Columbia River, 2) estimate abundance of all stocks based on catch estimates for each fishery. 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 has not been sampled since 2017 and could not be included in analyses. However, there is a new research gear (pound net) being tested by the joint states in the fall fisheries below Bonneville Dam. We have included analysis of the 2019 pound net fishery that was in operation during the spring, summer, and fall management periods. We estimated stock abundance of spring, summer, and fall Chinook salmon among the clipped fish that were retained (kept) and the unclipped fish that were released. This report would have represented the 7th year of analysis of Sockeye salmon fisheries in the Columbia River mainstem, but 2019 fishery data will not be available until next year’s report. In general, 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. Similar to 2018 analysis, we can now identify a stock of reintroduced Sockeye salmon to the Yakima River using PBT and can estimate the contribution of this reintroduced stock to each harvest of Sockeye salmon and the run at large.

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 2019 from a total of 10 different mixture sources: the spring-run seasons of the following fisheries: 1) lower river test, 2) lower river sport, 3) Zone 6 Treaty permit, and 4) the pound net, the summer management period harvests of the following fisheries: 5) Zone 6 tribal summer and 6) the pound net, and the fall-run harvest from 7) pound net, 8) lower river commercial, 9) sport (above and below Bonneville Dam), and 10) 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). 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. Therefore, we split the AFF sample of Chinook salmon into adults and jacks and analyze them separately. 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, test fishery, and in the Treaty permit fishery (Figure 17; Table 5). The summer management period fisheries were sampled below Bonneville Dam in the pound net, and above Bonneville Dam in the Zone 6 Treaty commercial fishery. In most cases, we analyzed all the random samples obtained from the various fisheries sampled above and below Bonneville Dam and included some non-random samples that were positive for a CWT to compare to our PBT assignments. For any fisheries in which we had to subsample the harvest, we selected fish randomly and with a balanced design

across spatial regions. However, each subsample should be tailored to the way the catch is reported for each fishery to accurately represent the geographic and temporal stratification of the CREEL.

Stock proportions were estimated and expanded by the catch reported for each fishery source, such that stock abundance could be compared across fisheries. We use the following four main geographic regions (Figure 17): Region A corresponds to our grouping of pre-existing Oregon and Washington state sport fishing sections 1-4 (or commercial zones 4-5), Region B corresponds to our grouping of sport sections 5-10 (or commercial zones 1-3). In the Zone 6, we typically distinguish Region 01 (Bonneville Pool) from Region 02 (Dalles and John Day Pools) because of the stock composition differences that can occur between the two regions particularly in the fall period when tules are observed in high proportions in Region 01. 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 best match the stratification of the reported catch.

Non-Treaty 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 clipped hatchery-origin fish from the mark selective commercial and sport fisheries, we were able to obtain samples from unclipped hatchery and natural origin fish from Bonneville Dam, the test fishery, the pound net, fall Non-Treaty commercial fishery, and the Treaty Zone 6 fishery above Bonneville Dam.

Tissues were sampled from sockeye salmon in 2019 from four fishery mixture sources: 1) pound net, 2) Bonneville Dam (see Section 4), and 3) the Treaty fishery in Zone 6. All samples obtained from these fisheries were genotyped but analysis will be presented in a future report.

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 (Hess et al. 2019), and further reduced from 179 SNPs to 177 SNPs because we were unable to transition the full set of 186 SNPs to GT-seq protocols and subsequent iterations of our active GT-seq panels. These 177 SNP markers were used for GSI, and for PBT analyses, we used 93 of the SNPs (legacy panel) as well as an expanded panel of 254 SNPs. We used 363 SNP markers for GSI and PBT of sockeye mixtures. For steelhead, this was the first year we could utilize a larger set of 335 SNP markers for PBT. The 335 SNP was genotyped for all PBT steelhead collections of the Columbia River basin since SY2017 to SY2018 and so the 2020 Bonneville Dam run year was the first year in which both 1-ocean and 2-ocean age steelhead could be assigned using the expanded panel of SNPs. We use a set of 92 SNPs to perform PBT analysis on collections of steelhead representing older spawn years before SY2017.

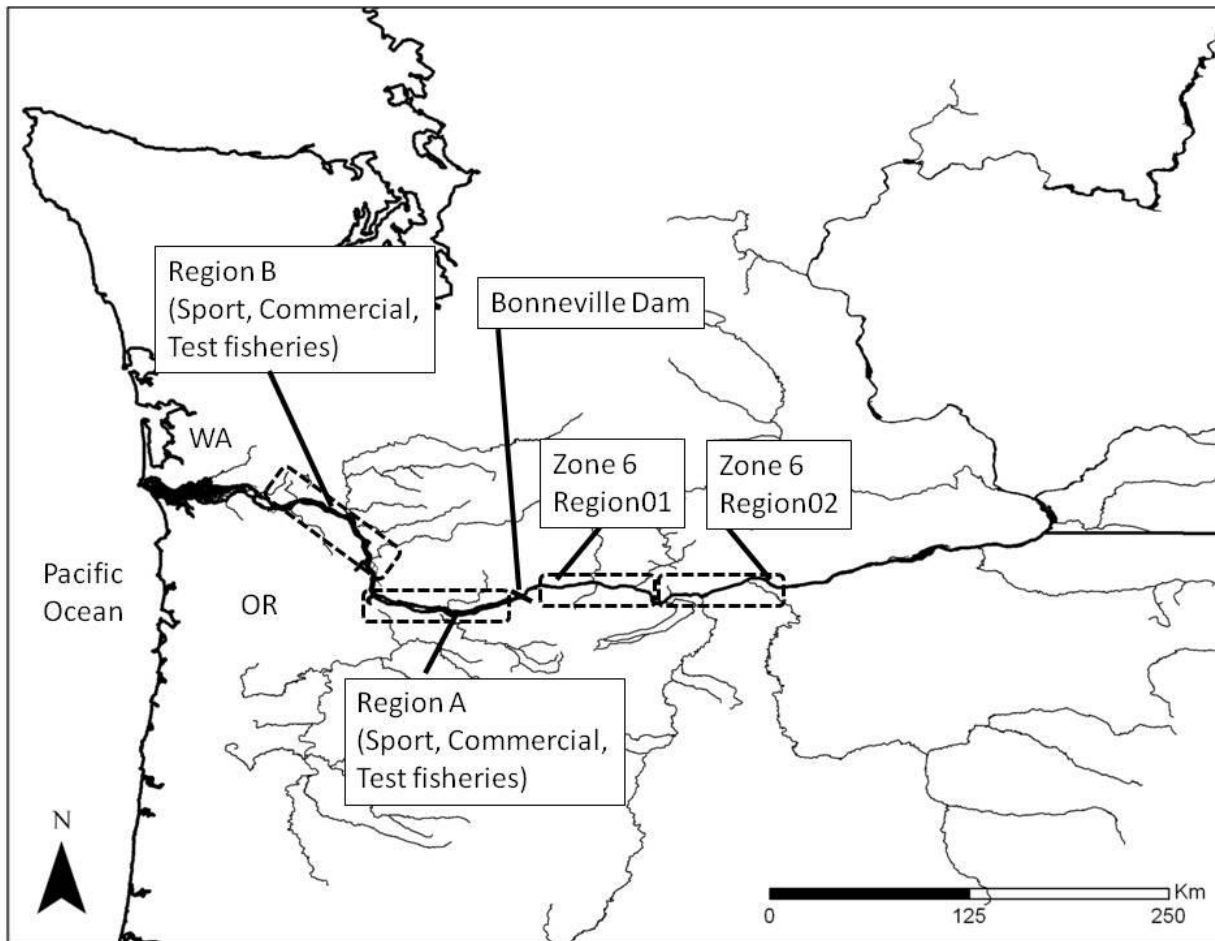


Figure 17. Project scope showing sources of Chinook salmon and Sockeye salmon harvest mixtures that were analyzed using PBT/GSI.

555 **Table 5. Characteristics of Chinook and Sockeye harvest samples by fishery, region, and adipose-clip status by weekly strata in 2019.**

					Spring														Summer			Fall													
					Statistical weeks																														
Period	Fishery	Region	Clip	Genotyped	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	31	32	33	34	35	36	37	38	39	40	41	42	43	
Spring	Permit	01_BON	AD	17									11		6																				
			AI	9									5		4																				
		02_TDA	AD	130								46	84																						
			AI	43								18	25																						
		BELOW_BON	AD	3									3																						
			Sport	B	AD	258	1	2	40	147	51	4	8	5																					
	Test	Zone 2	AD	166			1	8	7	2	52	31	49	16																					
			AI	45			3	4	2	3	18	2	6	7																					
	WFC Pound	Zone83	AD	58										1	1	4	11	17	24																
			AI	19												1	4	4	10																
Summer	Treaty	01_BON	AD	10																	10														
		02_TDA	AD	111																	38	73													
			AI	37																	18	19													
	WFC Pound	Zone83	AD	41																26	14	1													
			AI	24																11	12	1													
Fall	Treaty	01_BON	AD	25																							3	7		2	13				
			AI	27																							16	7		2	2				
		02_JDA	AD	7																							1	5		1					
			AI	31																							8	10	3	8	2				
	Commercial	02_TDA	AD	79																						1	16	8	15	17	11	10	1		
			AI	433																						7	78	64	55	79	76	73	1		
		A	AD	122																													4		
			AI	193																													78		
		B	AD	126																												36	5	1	1
			AI	186																												96	8	6	
	Sport	01_BON	AD	69																							12	15	20	21	1				
			AI	80																															
		A	AD	61																							1	1	12	15	31	20			
			AI	222																															
		B	AD	66																															
			AI	123																															
	WDFW Pound	Zone83	AD	194																							24	91	54	16	9				
			AI	179																							53	71	36	12	7				
	WFC Pound	Zone83	AD	54																															
			AI	73																															
Sockeye	Treaty	Zone6	-	98																75	23														

556

WDFW Pound	Zone83	-	844																														
			4263	1	6	52	156	56	74	41	127	149	1	15	16	36	127	346	496	214	1	2	147	447	450	441	240	168	117	232	97	7	1

PBT Rate Expansion using SCOBIDEUX and SPIBETR functions

The use of PBT adds complexity to analyses when each hatchery broodstock is genotyped at rates less than 100%. Expansion of hatchery-origin adipose-intact fish can lead to bias when we characterize natural-origin stocks by attributes (Figure 18). We have developed and implemented a fully automated method which minimizes the bias that PBT rate expansion can impose (Delomas and Hess, 2020). The correction implemented by this method (SPIBETR, Salmonid Prior Information to Balance Expansion from Tag Rates) is illustrated below:

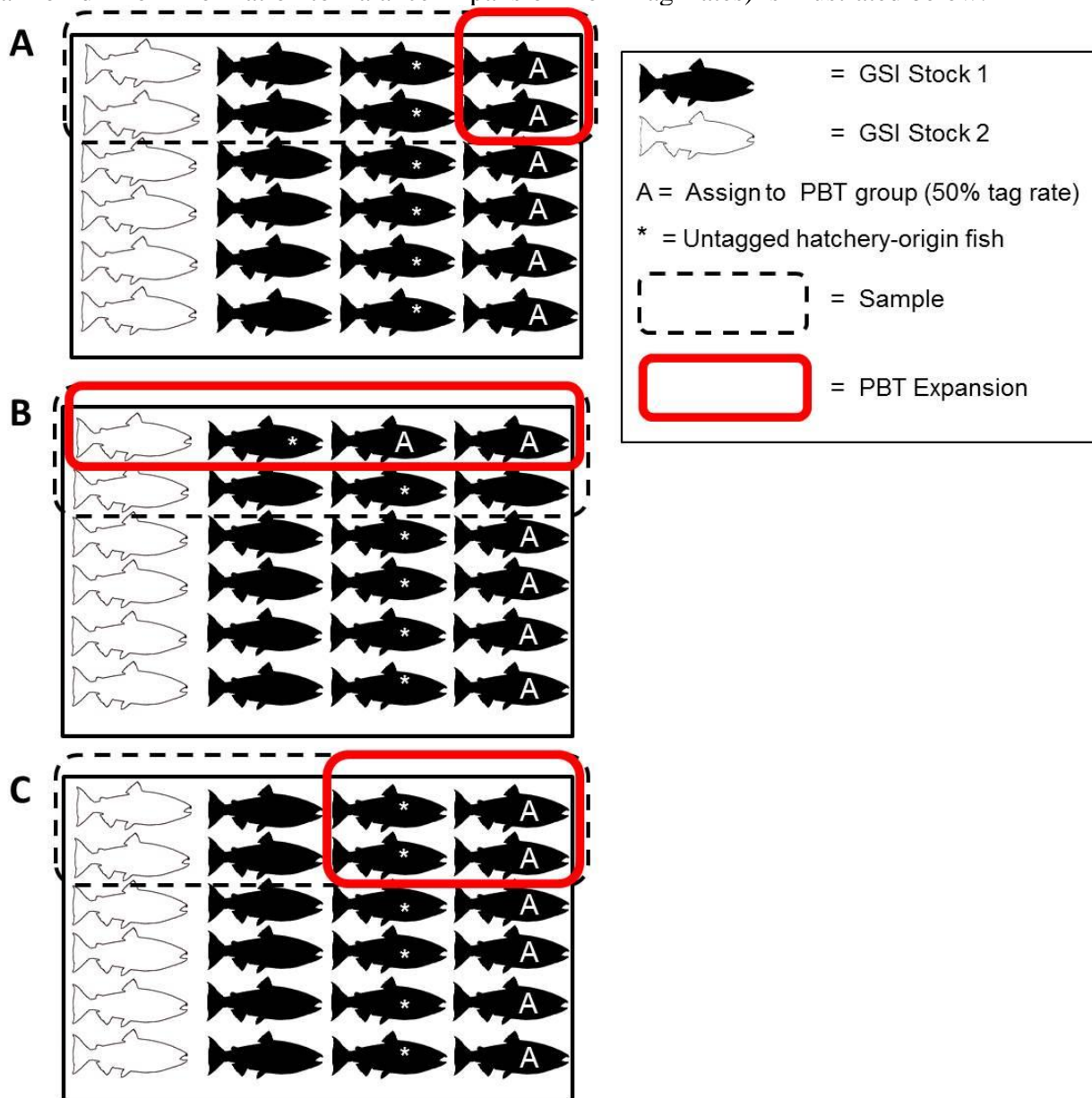


Figure 18. Conceptual illustration of the bias correction the SCOBIDEUX method provides.

In Figure 18, each panel shows a mixture of fish consisting of two natural-origin stocks (GSI Stock 1 and 2) and one PBT group with a 50% tag rate. The true proportions are 50% hatchery origin, 25% natural-origin GSI stock 1, and 25% natural-origin GSI stock 2. When PBT rates

are ignored, we would estimate the mixture to be 25% hatchery origin, 50% natural-origin GSI stock 1, and 25% natural-origin GSI stock 2 (Figure 18, A); this estimate is biased low toward the hatchery-origin fish. However, if we were to take PBT rates into account but did not adjust for the GSI information in the mixture, we could end up with estimates that accurately reflect the true proportion of hatchery-origin fish but do not accurately reflect the true stock composition of the natural-origin fish: e.g., Figure 18, B: yields an estimate of 50% hatchery origin, 37.5% natural-origin GSI stock 1, and 12.5% natural-origin GSI stock 2. Finally, using the corrections implemented by the SCOBIDEUX and SPIBETR functions, we are able to expand GSI stock 1 by PBT rates and correct this expansion by proportionally decreasing the GSI stock 1 in the remaining sample mixture, which yields scenario C (Figure 18): the mixture would be estimated to be 50% hatchery origin, 25% natural-origin GSI stock 1, and 25% natural-origin GSI stock 2.

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>). However, we made on slight modification and decreased the number of SNP markers to 177 that were included in the latest iteration of the GT-seq panel. 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 6; 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 363 SNPs was used for these analyses.

For steelhead, we have the following two GSI baselines available: 1) GSI baseline version 3.3 with 177 SNPs and 2) a new GSI baseline with 335 SNPs. The GSI version 3.3 comprises 116 collections from throughout the Columbia River basin that are partitioned into the following 14 reporting groups: 01_WCOAST (Quinalt 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) (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/>) (Hess et al. 2019). The GSI baseline with 335 SNPs comprises 128 collections throughout the Columbia River that are partitioned into 13 reporting groups (Hess et al. 2019), which are all the reporting groups listed in version 3.3 except 01_WCOAST (Quinalt River). This 335 SNP baseline was determined to be less accurate than the existing version 3.3. baseline for GSI applications (Hess et al. 2020), however, in this study we have observed the panel can deliver improvements to PBT applications.

658 **Table 6. 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

Combined application of PBT and GSI

We combined PBT and GSI results together by first accepting all confident PBT assignments to hatchery broodstock (i.e., $\text{LOD} \geq 14$ & $\text{FDR} \leq 0.1$) (See methods for [Parentage assignments using SNPPIT software v1.0](#), ID: 1341). For the remaining individuals, we used the best estimate of GSI assignments (regardless of the probability of assignment) 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. We also have a baseline of candidate parents used in the reintroduction of Sockeye salmon which requires both SNPPIT and a program to perform single parentage assignments (SEQUOIA). 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.

Use of SCOBIDEUX and SPIBETR functions to expand PBT and GSI for abundance in harvest samples

After combining PBT and GSI assignments, we examined the stratification of the harvest samples for the way in which harvest managers stratify the data to perform CREEL estimates of total harvested fish. In some cases, fisheries are mark selective and so only adipose clipped fish are necessary to sample to estimate the stock-specific abundances in the harvest. We also pooled our sample into the same temporal and spatial stratification in which harvest managers report CREEL estimates. For example, if the total harvested fish is only estimated for the entire catch without further breakdown into weeks or months, we had to treat our harvest sample as a single stratum. Ideally, fish are sampled randomly to acquire the DNA tissue samples in the same stratification units that harvest managers report. However, there are several ways in which the selection of the harvest samples has been non-random in the past. For example, the harvest monitors that work for the joint states (ODFW and WDFW) classify their samples into 3 “sample categories” in which samples can either be random without a CWT, random with a CWT, or non-random with a CWT. The current management of the Chinook salmon fisheries rely on CWT data, and fish that are not part of the normal random sample for the CREEL estimates will be wanded for the presence of CWTs and those fish that have a positive CWT detection will be sampled with biodata and genetic tissue collection. For genetic analysis, the non-random CWT fish should be excluded to obtain a random sample, but could be used for purposes of comparing CWT and PBT stock ID results. In past years, we may have inadvertently subsampled both random and non-random samples and used both types in our analyses.

We made every effort to match representative DNA sampling of these harvest management strata, which is the approach we began implementing since the 2018 harvest analysis, however, in prior years this was not the case. Specifically, we describe our stratification for each fishery sample in the following section:

The spring test fishery:

This fishery is conducted in the early portion of the spring Chinook salmon management period and occurs in the commercial zones 2 and 3 (a portion of “Region B”). Chinook salmon are visually stock-identified (VSI) to lower river and upriver stock classifications. A fleet of boats conduct drift fishing each week and catch per unit effort (CPUE) is estimated using the number of fish caught per number of drifts for each week. Tissue samples are obtained from both the clipped and unclipped fish caught in the test fishery at a high rate (>50%). Similar to

2018 (Hess et al. 2020), the CPUE estimated in the 2019 test fishery appears to be a good predictor for the timing and strength of the first peak of the run of spring chinook at Bonneville Dam. In this report we refined a strategy for analysis of this sample to obtain stock-specific CPUE for both the clipped and unclipped upriver chinook salmon. For our sample, we first used only the VSI-upriver chinook salmon that were caught in sections 2 and 3 of the test fishery, and stratified by weekly drifts (as indicated in Table 7). However, we also repeated this analysis using the VSI-lower river chinook salmon in order to ensure that we were fully estimating an index of abundance of all genetically identified upriver fish, even those that had been originally incorrectly identified as lower river fish via VSI (Table 8). Weeks were pooled to obtain sample sizes >10 fish for most strata. We applied these stratified samples to the weekly CPUE estimates of adipose clipped and unclipped VSI-upriver test fish.

Table 7. The sample rate and stratification for genetic analysis of the VSI-upriver adipose clipped and unclipped adult Chinook salmon from the spring test fishery in 2019.

			Estimated # VSI-Upriver			CPUE of VSI-Upriver			Sample of VSI-Upriver			Sample Rate of VSI-Upriver		
Week	Drifts		AD	AI	Total	AD	AI	Total	AD	AI	Total	AD	AI	Total
12	15		0.00	1.00	1.00	0.00	0.07	0.07		1	1	93.0%	75.0%	88.7%
13	15		4.00	0.00	4.00	0.27	0.00	0.27	4		4			
14	15		5.63	2.00	7.63	0.38	0.13	0.51	5		5			
15	15		2.00	0.00	2.00	0.13	0.00	0.13			0			
16	15		26.00	9.00	35.00	1.73	0.60	2.33	26	8	34			
17	12		24.00	9.00	33.00	2.00	0.75	2.75	22	1	23	93.9%	52.9%	83.3%
18	14		19.00	3.00	22.00	1.36	0.21	1.57	19	3	22			
19	14		6.00	5.00	11.00	0.43	0.36	0.79	5	5	10			
			86.63	29.00	115.63	6.29	2.12	8.42	81	18	99	93.5%	62.1%	85.6%

Note: These are the visual stock identified (VSI) upriver Chinook salmon that were analyzed from the spring test fishery. The Catch per Unit Effort (CPUE) was calculated from the number of fish observed / the number of “Drifts” made total for the fleet of boats used in the test fishery. DNA “Samples” of the test fishery were pooled across weeks to obtain 9 or more samples for each stratum of adipose clipped (AD), adipose intact (AI), and Total samples.

Table 8. The sample rate and stratification for genetic analysis of the VSI-lower river adipose clipped and unclipped adult Chinook salmon from the spring test fishery in 2019.

			Estimated # VSI-Lower river			CPUE of VSI-Lower river			Sample of VSI-Lower river			Sample Rate of VSI-Lower river		
Week	Drifts		AD	AI	Total	AD	AI	Total	AD	AI	Total	AD	AI	Total
12	15		1.00	2.00	3.00	0.07	0.13	0.20	1	2	3	91.0%	90.9%	90.9%
13	15		4.00	3.00	7.00	0.27	0.20	0.47	4	3	7			
14	15		3.38	2.00	5.38	0.23	0.13	0.36	2	2	4			
15	15		2.00	3.00	5.00	0.13	0.20	0.33	2	3	5			
16	15		27.00	12.00	39.00	1.80	0.80	2.60	25	10	35			
17	12		7.00	2.00	9.00	0.58	0.17	0.75	8	1	9	100.0%	50.0%	93.6%
18	14		25.00	5.00	30.00	1.79	0.36	2.14	25	2	27			

19	14	7.00	1.00	8.00	0.50	0.07	0.57	7	1	8			
76.38	30.00	106.38	5.36	2.06	7.42	74	24	98	96.9%	80.0%	92.1%		

Note: These are the visual stock identified (VSI) lower river Chinook salmon that were analyzed from the spring test fishery. The Catch per Unit Effort (CPUE) was calculated from the number of fish observed / the number of “Drifts” made total for the fleet of boats used in the test fishery. DNA “Samples” of the test fishery were pooled across weeks to obtain 4 or more samples for each stratum of adipose clipped (AD), adipose intact (AI), and Total samples.

The Spring Chinook salmon sport fishery:

This fishery is mark-selective, which means only the adipose-clipped fish are retained (“kept” fish). All the adipose-intact fish are released, and none of these released fish are tissue sampled, however, a portion of them are counted as mortalities. It may be possible in the future to use the sport test fishery unclipped chinook salmon stock composition to characterize the release mortalities from the spring sport fishery because the test fishery overlaps in timing and region with the spring sport fishery. Harvest is estimated and reported for the total lower Columbia mainstem instead of being geographically stratified into regions A and B. This lack of geographic stratification could be problematic and lead to bias in the genetic analysis unless all sampling is random and occurs at the same rate across regions. We have shown in the past that there are different compositions of stocks across regions (Hess et al. 2019). Sampling conducted by the joint states is typically random and sampling rates are even across the fishing zones, which may help minimize this bias.

Table 9. The sample rate and stratification for genetic analysis of the kept adipose clipped adult Chinook salmon from the spring sport fishery in 2019.

	Total Adult Chinook			Sample of Total Adult Chinook Kept			
	Kept	Rel.	Rel. Mortality	regionA	regionB	total	rate
Jan-Feb Total	4	1	0				
March Total	317	76	8	0	63	63	0.20
April Total	1,356	240	24	0	195	195	0.14
May Total	0	61	6	0	0	0	0.00
June 1-15 Total	0	102	10	0	0	0	0.00
Season Total	1,677	480	48	0	258	258	0.15

Note: The released fish (“Rel.”) were not sampled for genetic analysis and so only the “kept” fish could be analyzed. The samples of kept fish usually come from both the regions A and B but in 2019 only region B was fished. Monthly strata were used and the first stratum was pooled to include all fish harvested from January through March as indicated by the outlines in the table.

The spring chinook salmon platform hook and line permit fishery:

Yakama Nation executed this fishery in 2019 below Bonneville Dam. We did not utilize total catch information because we only obtained 3 samples and assumed this sample rate would be inadequate. All samples were adipose clipped.

The spring chinook salmon zone 6 ceremonial permit fishery was also not analyzed due to the non-representative manner in which samples were obtained. Samples are difficult to obtain

in general due to the use of these fish for ceremonies. Ideally, samples would be collected from the harvest of all four member tribes and temporal stratification would be applied; however, samples were gathered from the Yakama Nation harvest exclusively in 2019 (N=199, Table 5) and the harvested fish are not possible to report on a weekly basis or by reservoir.

The summer chinook salmon sport fishery is mark-selective similar to the spring sport fishery however it was not executed in 2019. The summer chinook salmon Treaty commercial fishery in zone 6 is estimated by adipose clipped and unclipped adults by statistical week (Table 10). We split our sample by adipose clip and pooled samples across weeks to obtain a minimum of 10 fish per stratum to analyze the stock composition of this harvest.

Table 10. The sample rate and stratification for genetic analysis of the adipose clipped and unclipped adult Chinook salmon from the zone 6 summer Treaty fishery in 2019.

Week	Harvest Estimate		Sample N		Sample rate	
	AD	AI	AD	AI	AD	AI
25	182	61	-	-		
26	1,712	494	38	18	0.04	0.06
27	1,466	110	83	19		
28	237	67	-	-		
29	203	57	-	-		
30	151	43	-	-		
31	77	22	-	-		

Note: The adipose clipped (AD) and unclipped/intact (AI) fish shown by harvest estimate and sample size. Samples were pooled across weeks as indicated by the boxed samples in the table. Sampling was conducted on only weeks 26 and 27 when the commercial fishery was open; all other weeks harvest was restricted to platform/hook and line fishing only and could not be analyzed.

The fall Non-Treaty commercial fishery:

This fishery occurred in two periods in the fall (early period = weeks 33 and 34) and was reported by total adults and jacks. We obtained random samples of both adipose clipped and unclipped chinook salmon (both adults and jacks) and stratified by weeks to analyze the genetic stock composition of this harvest (Table 11). Funds allowed us to use all random samples which helped to avoid subsampling and any associated bias by differing proportions of clipped and unclipped fish in a subsample as compared to the total random sample.

Table 11. The sample rate and stratification for genetic analysis of the adult and jack Chinook salmon from fall Non-Treaty commercial fishery in 2019.

Region	Week	Harvest estimate adult+jack	Sample N			
			AD	AI	total	rate
A	33	3351	55	78	133	0.04
A	34	4969	106	113	219	0.04
A	41	1686	3	78	81	0.05
B	40	481	36	97	133	0.28

B	41	122	5	8	13	0.11
B	42	57	1	6	7	
B	43	16	1	0	1	

Note: The harvest estimate combines both adults and jacks and does not distinguish clipped (AD) and unclipped (AI) fish. The total sample was a random sample of the harvest which excludes any fish that were non-randomly sampled due to presence of a CWT.

The fall Non-Treaty sport fishery:

This fishery is not mark-selective and the stock composition of the released fish is assumed to be similar to the kept fish (although this assumption has been likely violated with past observations that the kept fish have lower proportions of tules as compared to other clipped samples in the lower river, Hess et al. 2020). We stratified the samples of kept fish by month and estimated the stock composition of the clipped and unclipped fish using the sample data (Table 12). The catch estimate for this fishery below Bonneville Dam is reported by month for the adult fish and further is not stratified geographically into regions. We recorded geographic region in the sample data and so this geographic stratification could be applied if the harvest estimates were stratified similarly. This geographic stratification should only be necessary if the sample were not obtained randomly with respect to time and region, therefore we avoided this extra step by only using the random samples obtained from this fishery. In 2019, the sport fishery was also sampled in zone 6 in the Bonneville Pool (Table 13). We obtained samples of clipped and unclipped kept adults on a weekly basis and stratified this sample into two groups of weeks.

Table 12. The sample rate and stratification for genetic analysis of the kept adult Chinook salmon from the fall Non-Treaty sport fishery from Tongue Point to Bonneville Dam in 2019.

Catch Estimate				Sample of kept		
Month	kept Adult	Released	Release mortality	AD	AI	rate
Aug	4616	198	42	97	240	0.07
Sep	2549	5975	1255	24	98	0.05
Oct	0	564	118	0	0	0.00
	7165			121	338	0.06

Note: The sample numbers of the kept Chinook salmon were stratified by month and adipose clip data was used to estimate the stock composition of both adipose clipped (AD) and adiposed intact (AI) stocks.

Table 13. The sample rate and stratification for genetic analysis of the kept adult Chinook salmon from the fall Non-Treaty sport fishery from the Bonneville Pool in 2019.

Catch Estimate				Sample of kept		
Week	kept Adult	Released	Release mortality	AD	AI	rate
31	7	0	0	0	0	0.0
32	0	0	0	0	0	-
33	5	0	0	0	1	0.2

34	0	0	0	0	1	-
35	155	12	3	12	12	0.2
36	123	0	0	15	15	0.2
37	629	47	10	20	31	0.1
38	607	70	15	21	20	0.1
39	342	67	14	1	0	0.0
40	0	0	0	0	0	-
41	0	0	0	0	0	-
42	0	108	23	0	0	-
43	3	65	14	0	0	0.0
44	0	10	2	0	0	-
	1871	379	80	69	80	0.1

Note: The sample numbers of the kept Chinook salmon were pooled into two strata across weeks 31-36 and 37-44 and adipose clip data was used to estimate the stock composition of both adipose clipped (AD) and adiposed intact (AI) stocks.

The fall Treaty commercial fishery:

This fishery was executed in zone 6 across several weeks of the fall management period. This fishery is monitored by visually identifying tules versus bright stocks and estimating each separately (Table 14). Tissue collection is mostly obtained from the fish identified as bright stocks, and very few tule stocks are sampled. Therefore, genetic analysis was constrained to estimating stock composition within the visually-identified bright harvest.

Table 14. The sample rate and stratification for genetic analysis of the adult bright Chinook salmon from the Fall Treaty Zone 6 Commercial Fishery in 2019.

Week	Harvest estimate		Sample of Brights		
	Brights	Tules	AD	AI	rate
34	754	460	1	7	0.02
35	5,425	536	16	78	
36	7,714	1,160	12	87	0.01
37	12,360	1,538	27	71	0.01
38	17,284	2,404	17	81	0.01
39	10,526	1,414	13	86	0.01
40	3,588	1,020	23	77	0.03
total	57,651	8,531	109	487	0.01

The pound net fishery:

The pound net is a relatively recent gear type that is being developed by the joint states. Similar to 2018, the 2019 fall pound net fishery was conducted in the Cathlamet Channel (zone 83 in region B) and the numbers and genetic samples of the kept (Table 15) and released (Table 16) adult and jack-sized Chinook salmon were stratified by week. In 2019, the pound net was

operated in the spring, summer, and fall periods for testing what compositions of fish it could access in these different times of year and for purposes of this testing all fish that were sampled were released only (Table 16).

Table 15. The sample rate and stratification for genetic analysis of the kept adipose clipped Chinook salmon from the fall pound net fishery in 2019.

2019 Pound Net Trap Kept Catch Summary (all adipose-clipped)						
Week	Sample			Sample		
	Chin Adults	Chin Adults	Rate	Chin Jacks	Chin Jacks	Rate
35	23	19	0.83	3	3	1.00
36	86	82	0.95	5	5	1.00
37	43	42	0.98	1	0	0.00
38	16	14	0.88		0	-
39	9	9	1.00		0	-
	177	166	0.94	9	8	0.89

Note: The "Sample" indicates numbers of successfully genotyped fish in each stratum. The weekly strata were pooled into a single stratum. The "Rate" is the sample rate attained for each week and rates were high across all weeks.

Table 16. The sample rate and stratification for genetic analysis of the released adult and jack Chinook salmon from the fall pound net fishery in 2019.

2019 Pound Net Trap Released Catch Summary												
Week	Released Chin Adults		Sample Chin Adults				Released Chin Jacks		Sample Chin Jacks			
	AD	AI	AD	AI	AD_rate	AI_rate	AD	AI	AD	AI	AD_rate	AI_rate
19			0	0	-	-	1		1	0	1.00	-
20	1		1	0	1.00	-			0	0	-	-
21	4	1	4	1	1.00	1.00			0	0	-	-
22	11	4	11	4	1.00	1.00			0	0	-	-
23	16	4	16	4	1.00	1.00	1		1	0	1.00	-
24	22	9	22	9	1.00	1.00	2	1	2	1	1.00	1.00
Spring	54	18	54	18	1.00	1.00	4	1	4	1	1.00	1.00
25	22	9	22	9	1.00	1.00	4	2	4	2	1.00	1.00
26	14	10	14	10	1.00	1.00		2	0	2	-	1.00
27	1	1	1	1	1.00	1.00			0	0	-	-
Summer	37	20	37	20	1.00	1.00	4	4	4	4	1.00	1.00
31		1	0	1	-	1.00			0	0	-	-
34	19	29	19	29	1.00	1.00	8	8	8	8	1.00	1.00
35	21	58	21	58	1.00	1.00	4	11	4	11	1.00	1.00
36	3	77	3	75	1.00	0.97	13	18	13	15	1.00	0.83
37	0	16	0	16	-	1.00	6	21	6	20	1.00	0.95
38	0	8	0	8	-	1.00	3	5	2	4	0.67	0.80

39	0	5	0	5	-	1.00	0	2	0	2	-	1.00
Fall	43	193	43	191	1.00	0.99	34	65	33	60	0.97	0.92

Note: The “Sample” indicates numbers of successfully genotyped fish in each stratum. The weekly strata were pooled into a single stratum for each management period. The “Rate” is the sample rate attained for each week and pooled strata.

The Sockeye Non-Treaty sport and commercial fishery:

This fishery did not occur in 2019. There were 4 sockeye caught in the Non-Treaty commercial fishery.

The Sockeye Treaty commercial fishery:

This fishery occurred in zone 6 and catch estimates were reported by week in the summer and additional estimates of sockeye were reported in zone 6 during the spring and fall periods as well as below Bonneville Dam. All Sockeye salmon catch estimates were combined for the total harvest of 1,078.

The Sockeye pound net fishery:

The pound net sampled approximately 900 sockeye salmon in 2019. These genotypes were not available for this report but will be analyzed and presented in a future report.

Results

Use of the expanded panel of 254 SNPs for Chinook salmon 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 had been problematic (Hess et al. 2019) is that there are individual genotypes that have been causing the software SNPPIT to crash. We resolved this issue by selecting a set of 254 SNPs that was comprised of sets of SNP markers (~200) that have greater than 10% observed heterozygosity in each of the major lineages of Chinook Salmon (Hess et al. 2020).

Application of the 254 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. 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. Further, the higher number of SNP loci requires decreased computational time to run the parentage analyses, which is extremely helpful for the relatively short time available to process in-season samples. We have continued to use the 254 SNP panel exclusively for the 2020 run year of Chinook salmon.

Comparison of Coded-wire tags and PBT assignments

There were 162 coded-wire tags (CWTs) recovered and identified to hatchery stock and broodyear (BY) among the snouts recovered from the lower river fisheries (Table 17), and 113 of these CWTs also were PBT assigned (70%). Of the 113 fish with both CWT and PBT, there were 107 fish (95%) that appeared concordant with the PBT assignments according to both the hatchery source and the broodyear. There were 6 of the 113 fish with both CWT and PBT that were discordant for either hatchery source (N=2) or both hatchery source and broodyear (N=4). However, in some cases it may be that the CWT readings were swapped; e.g., a pair of Warm Springs and Lewis River hatchery fish had the same broodyear but had opposing hatchery origins for the same pair of fish (“BY_Concordant” rows, Table 17). Resolving these swapping errors would increase the concordance rate even higher than 95%.

Table 17. Comparison of coded-wire tags with parentage-based tags that were identified in the lower river fisheries in 2019.

Period	Coded-wire tag		Parentage-based tagging assignment			N
	Hatchery	BY	Hatchery	BY	Status	
Spring	Carson National Fish Hatchery	2015	Carson National Fish Hatchery	2015	Concordant	1
Spring	Chief Joseph Hatchery	2015	Chief Joseph Hatchery	2015	Concordant	4
Spring	Clearwater Fish Hatchery	2014	Clearwater Fish Hatchery	2014	Concordant	1
Spring	Clearwater Fish Hatchery	2015	Clearwater Fish Hatchery	2015	Concordant	6
Spring	Little White Salmon National Fish Hatchery	2015	Little White Salmon National Fish Hatchery	2015	Concordant	2
Spring	Rapid River Fish Hatchery	2015	Rapid River Fish Hatchery	2015	Concordant	1
Spring	Round Butte Fish Hatchery	2015	Round Butte Fish Hatchery	2015	Concordant	2
Spring	Speelyai Fish Hatchery	2015	Speelyai Fish Hatchery	2015	Concordant	1
Spring	Winthrop National Fish Hatchery	2015	Winthrop National Fish Hatchery	2015	Concordant	10
Spring	Yakima River Roza Dam	2015	Yakima River Roza Dam	2015	Concordant	1
Fall	Big Creek Hatchery	2016	Big Creek Hatchery	2016	Concordant	3
Fall	Chief Joseph Hatchery	2015	Chief Joseph Hatchery	2015	Concordant	4
Fall	Chief Joseph Hatchery	2016	Chief Joseph Hatchery	2016	Concordant	1

Fall	Little White Salmon National Fish Hatchery	2015	Little White Salmon National Fish Hatchery	2015	Concordant	5
Fall	Lyons Ferry Fish Hatchery	2014	Lyons Ferry Fish Hatchery	2014	Concordant	5
Fall	Lyons Ferry Fish Hatchery	2015	Lyons Ferry Fish Hatchery	2015	Concordant	9
Fall	Lyons Ferry Fish Hatchery	2016	Lyons Ferry Fish Hatchery	2016	Concordant	6
Fall	Nez Perce Tribal Fish Hatchery	2015	Nez Perce Tribal Fish Hatchery	2015	Concordant	6
Fall	Nez Perce Tribal Fish Hatchery	2016	Nez Perce Tribal Fish Hatchery	2016	Concordant	5
Fall	North Toutle Hatchery	2015	North Toutle Hatchery	2015	Concordant	1
Fall	North Toutle Hatchery	2016	North Toutle Hatchery	2016	Concordant	1
Fall	Priest Rapids Hatchery	2015	Priest Rapids Hatchery	2015	Concordant	4
Fall	Priest Rapids Hatchery	2016	Priest Rapids Hatchery	2016	Concordant	4
Fall	Priest Rapids Hatchery	2017	Priest Rapids Hatchery	2017	Concordant	1
Fall	Spring Creek National Fish Hatchery	2016	Spring Creek National Fish Hatchery	2016	Concordant	2
Fall	Spring Creek National Fish Hatchery	2017	Spring Creek National Fish Hatchery	2017	Concordant	3
Fall	Washougal Fish Hatchery	2016	Washougal Fish Hatchery	2016	Concordant	2
Spring	Nez Perce Tribal Fish Hatchery	2015	Dworshak National Fish Hatchery	2015	Concordant	1
Fall	Bonneville Hatchery	2014	Little White Salmon National Fish Hatchery	2014	Concordant	2
Fall	Klickitat Hatchery	2015	Little White Salmon National Fish Hatchery	2015	Concordant	10
Fall	Klickitat Hatchery	2016	Little White Salmon National Fish Hatchery	2016	Concordant	2
Fall	Umatilla Fish Hatchery	2015	Little White Salmon National Fish Hatchery	2015	Concordant	1
Spring	Lewis River Hatchery	2015	Warm Springs National Fish Hatchery	2015	BY	1
Spring	Warm Springs National Fish Hatchery	2015	Speelyai Fish Hatchery	2015	BY	1
Fall	Bonneville Hatchery	2014	Little White Salmon National Fish Hatchery	2015	Discordant	1
Fall	Nez Perce Tribal Fish Hatchery	2016	Spring Creek National Fish Hatchery	2017	Discordant	1
Fall	Similkameen Hatchery	2015	Spring Creek National Fish Hatchery	2017	Discordant	1
Fall	Washougal Fish Hatchery	2015	Little White Salmon National Fish Hatchery	2016	Discordant	1
Spring	Chief Joseph Hatchery	2015	NA	NA	Failed	1
Spring	Willamette Hatchery	2015	NA	NA	Failed	1
Spring	Winthrop National Fish Hatchery	2015	NA	NA	Failed	2
Fall	Big Creek Hatchery	2016	NA	NA	Failed	2

Fall	Chief Joseph Hatchery	2015	NA	NA	Failed	1
Fall	Cowlitz Salmon Hatchery	2016	NA	NA	Failed	1
Fall	Klickitat Hatchery	2015	NA	NA	Failed	1
Fall	Nez Perce Tribal Fish Hatchery	2015	NA	NA	Failed	1
Fall	Nez Perce Tribal Fish Hatchery	2016	NA	NA	Failed	1
Fall	Priest Rapids Hatchery	2015	NA	NA	Failed	1
Fall	South Santiam	2017	NA	NA	Failed	1
Fall	Washougal Fish Hatchery	2015	NA	NA	Failed	1
Spring	McKenzie River Hatchery	2014	NA	NA	Unassigned	2
Spring	Sandy Hatchery	2014	NA	NA	Unassigned	1
Spring	Warm Springs National Fish Hatchery	2015	NA	NA	Unassigned	1
Spring	Willamette Hatchery	2014	NA	NA	Unassigned	1
Spring	Willamette Hatchery	2015	NA	NA	Unassigned	1
Spring	Winthrop National Fish Hatchery	2015	NA	NA	Unassigned	1
Spring	Yakima River Roza Dam	2015	NA	NA	Unassigned	1
Fall	Big Creek Hatchery	2016	NA	NA	Unassigned	6
Fall	Big Creek Hatchery	2017	NA	NA	Unassigned	1
Fall	Bonneville Hatchery	2017	NA	NA	Unassigned	2
Fall	Chief Joseph Hatchery	2015	NA	NA	Unassigned	2
Fall	Cowlitz Salmon Hatchery	2016	NA	NA	Unassigned	1
Fall	Hanford Reach	2014	NA	NA	Unassigned	1
Fall	Kalama Falls Hatchery	2015	NA	NA	Unassigned	2
Fall	Klickitat Hatchery	2015	NA	NA	Unassigned	1
Fall	Lyons Ferry Fish Hatchery	2015	NA	NA	Unassigned	1
Fall	Lyons Ferry Fish Hatchery	2016	NA	NA	Unassigned	1
Fall	Priest Rapids Hatchery	2015	NA	NA	Unassigned	1
Fall	Spring Creek National Fish Hatchery	2016	NA	NA	Unassigned	4
Fall	Spring Creek National Fish Hatchery	2017	NA	NA	Unassigned	1
Fall	Washougal Fish Hatchery	2015	NA	NA	Unassigned	3
				Total	100.0%	162

900

Concordant	66.0%	107
BY_Concordant	1.2%	2
Discordant	2.5%	4
Failed	8.6%	14
PBT_Unassigned	21.6%	35

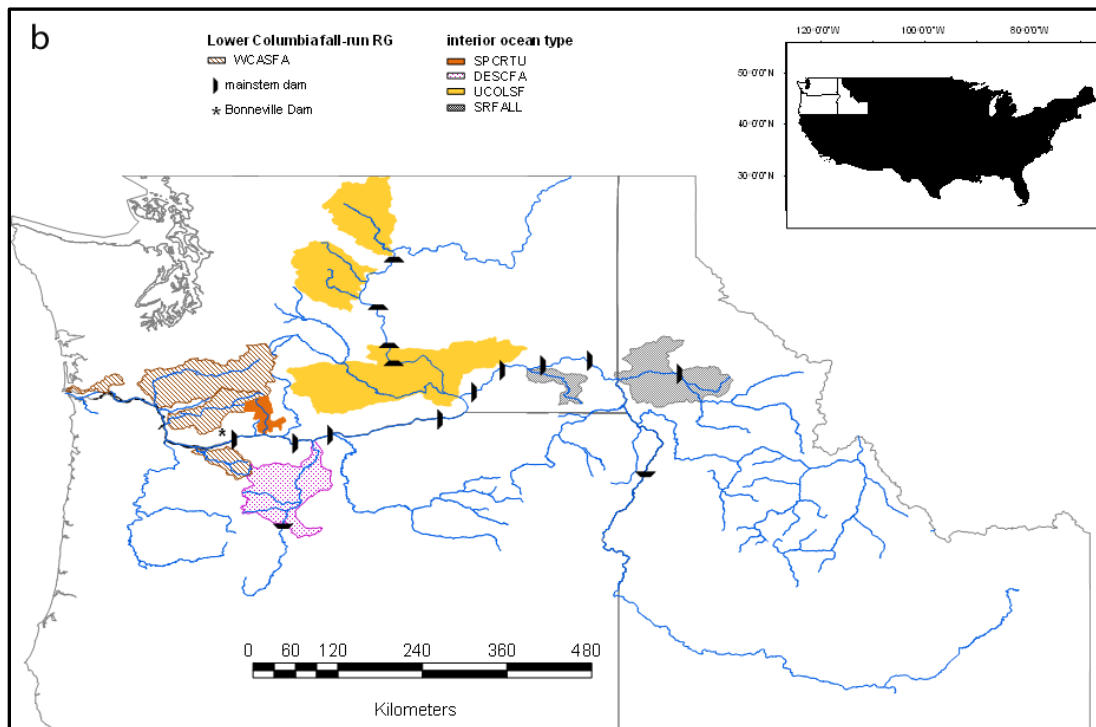
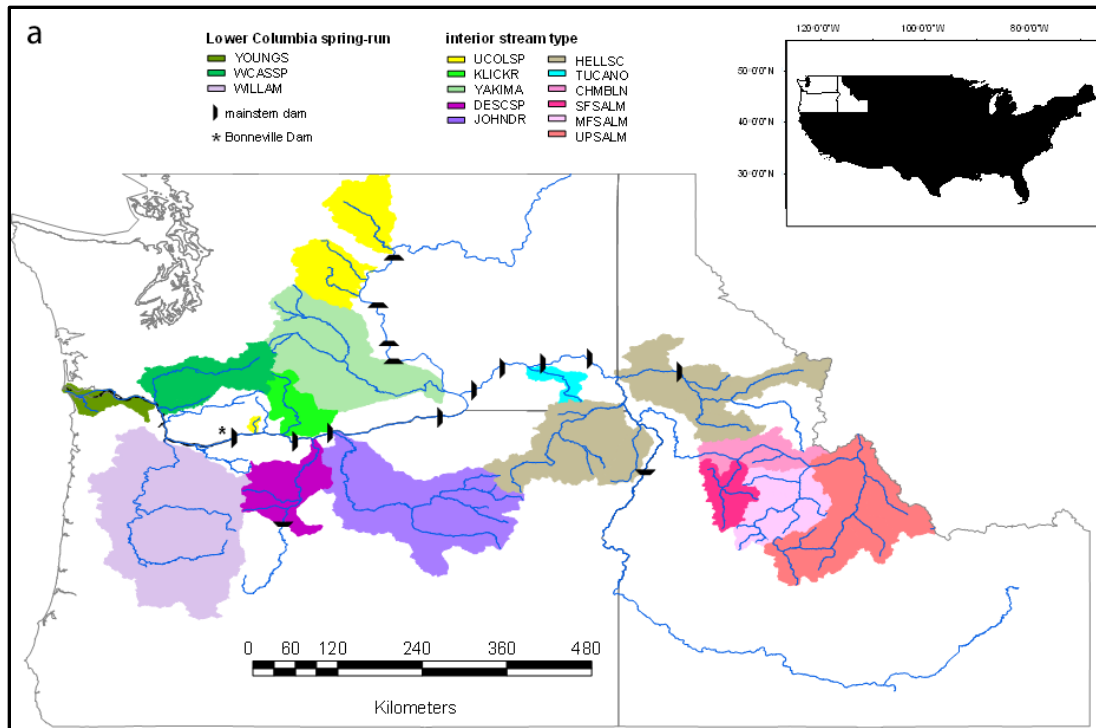
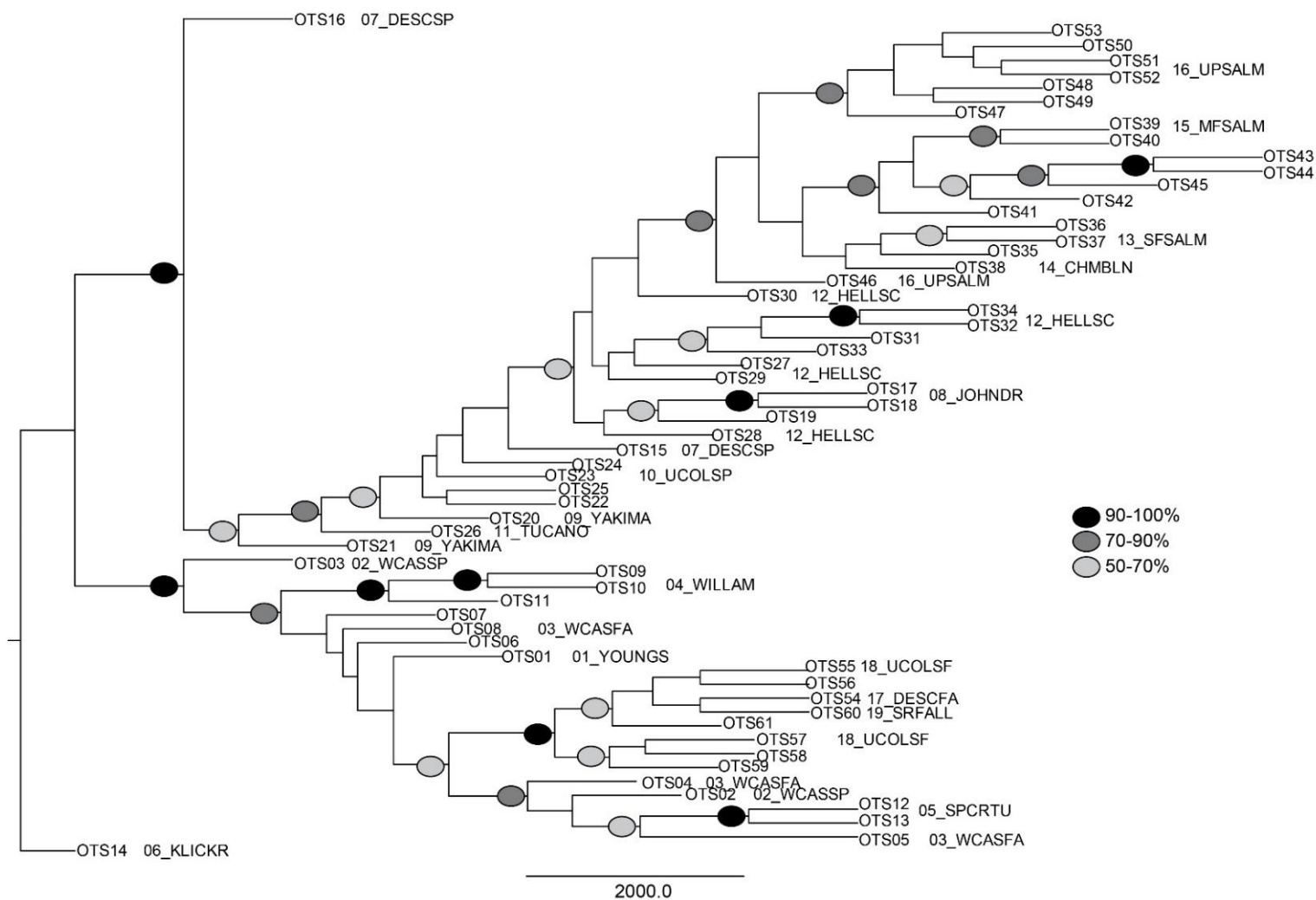


Figure 19. Map of Chinook salmon GSI reporting groups for a) Lower Columbia (LC) and interior stream type (ST) lineage, and b) interior ocean type (OT) lineage.



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

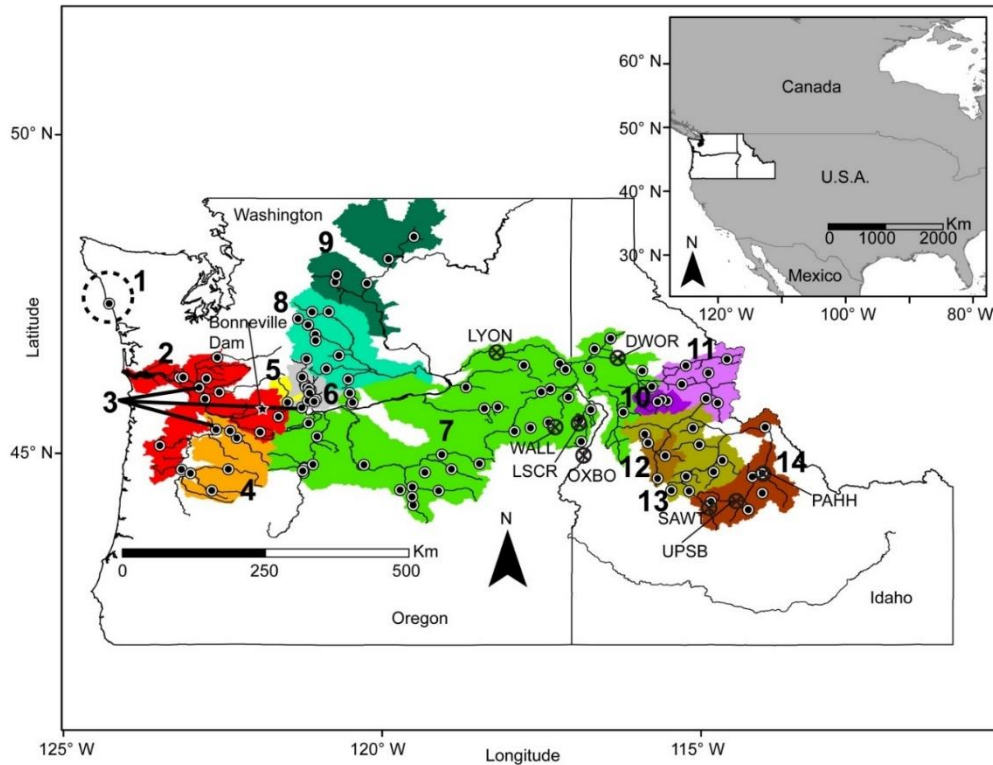


Figure 21. Geographic distribution of collections represented in the Columbia River steelhead GSI and PBT genetic baselines.

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.

Steelhead 177 SNP and 335 SNP baselines

For steelhead, we have 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). However, a set of 335 SNP loci is now available for a similar set of collections representing 13 of the 14 reporting groups (N=7422 individuals). We tested the accuracy of this new panel of 335 SNP loci by performing leave-1-out tests (Hess et al. 2020). Specifically, we generated the following different subsets of loci (Figure 22): 180 SNPs from baseline v3.3 (“Sub180”), 339 SNPs that include putatively neutral and adaptive loci (“Sub339”), 335 SNPs that exclude the run timing candidate SNPs (“Sub335NRT”), 301 SNPs that were putatively neutral (“Sub301Neu”), and 55 SNPs that were putatively adaptive (“Sub55Adapt”). We found that the 335 and 339 SNPs both performed best, but we felt it would be better to exclude the run timing candidate SNPs to avoid any unintended bias for stocks containing within population variation in run timing. Therefore, we propose testing of the 335 SNP baseline to determine whether it can replace the original 177 SNP v3.3. baseline.

However, recent testing using comparisons of PBT and GSI assignments have highlighted some potential accuracy issues with the new 335 SNP baseline. First, this new baseline is not able to accurately assign smaller subgroups within the MCGILCS reporting group (Hess et al. 2020 Table 4. Creation of *O. mykiss* SNP baseline by whole genome resequencing of pools of samples), which is one of the primary reasons it was developed. Second, the original set of reporting groups may not have improved with this new panel of SNPs. The PBT broodstocks can be categorized into “expected” reporting groups according to where they are located and which genetic stock they use for broodstock. We found that the original 177 SNP baseline was more accurate for one stock in particular, Upper Salmon River, and assigned a greater number of PBT assignments (82%) to this Upper Salmon River stock compared to the new SNP baseline of 335 SNPs (35% assigned correctly, Hess et al. 2020). Although assignment accuracies to the other reporting groups we could analyze in this way were similar between SNP panels, the poor accuracy of the Upper Salmon River stock prevents us from using this baseline to replace the version 3.3 baseline until more testing can be conducted. Therefore, we continue to use the panel of 177 SNPs (version 3.3) for the GSI applications in this report. Similar to our previous results, we show that the fish passing Bonneville Dam in 2020 that were from PBT hatcheries in the Upper Salmon River correctly assign using GSI by a high percentage to the Upper Salmon River genetic stock (84%, Table 18).

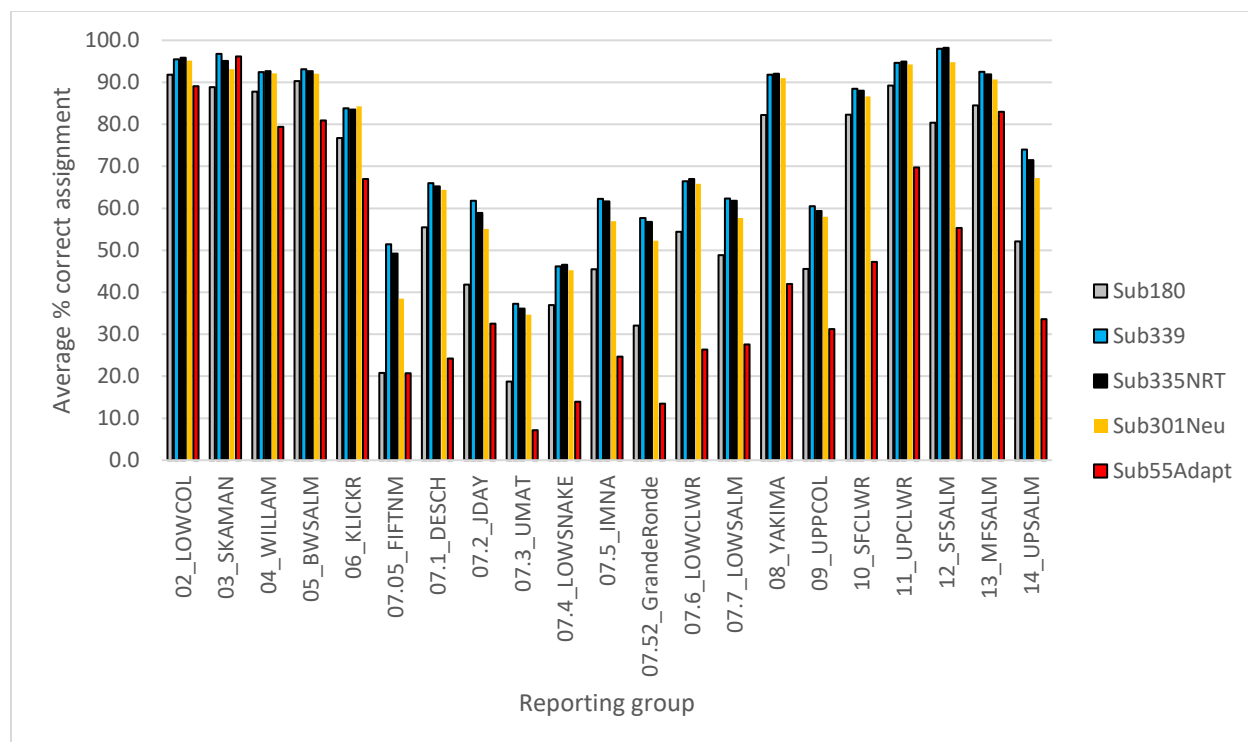


Figure 22. Proportion of steelhead in leave-one-out tests that assigned correctly for each reporting group by lineage using the following subsets of SNPs: 180 SNPs from baseline v3.3 (“Sub180”), 339 SNPs that include putatively neutral and adaptive loci (“Sub339”), 335 SNPs that exclude the run timing candidate SNPs (“Sub335NRT”), 301 SNPs that were putatively neutral (“Sub301Neu”), and 55 SNPs that were putatively adaptive (“Sub55Adapt”).

967 **Table 18. Comparison of PBT expected reporting groups versus the observed reporting groups using 177 SNPs (baseline 3.3)**
 968 **based on the assignments from the Bonneville 2020 mixture.**

PBT Expected GSI	Observed GSI									Total	Correct%
	02_LOWCOL	03_SKAMAN	07_MGILCS	08_YAKIMA	09_UPPCOL	10_SFCLWR	11_UPCLWR	13_MFSALM	14_UPSALM		
03_SKAMAN	1	29	0	0	0	0	0	0	0	30	96.7%
07_MGILCS	0	0	159	1	3	0	0	1	23	187	85.0%
09_UPPCOL	0	0	11	0	9	2	0	0	10	32	28.1%
10_SFCLWR	0	0	5	0	0	377	1	0	1	384	98.2%
14_UPSALM	0	0	32	0	0	0	0	1	177	210	84.3%

969
 970
 971 *Steelhead 335 SNP panel for PBT applications*

972 Despite having limited utility for GSI applications on a Columbia River Basin wide scale, the expanded set of SNP markers
 973 available for steelhead analysis can be extremely useful for increasing the power and accuracy of PBT. We examined a dataset of
 974 steelhead passing Bonneville Dam in 2020 and compared assignments based on the original panel of 92 SNPs to assignments based on
 975 the new expanded panel of 335 SNPs (**Table 19**). There were a total of 800 PBT assignments that were perfectly concordant between
 976 panels of markers (both the mother and father IDs were the same), however, even for these cases the LOD score for the 335 SNP panel
 977 averaged 30 versus the 92 SNP panel LOD score average of 20.6. Both averages were well above the threshold LOD score of 14 that
 978 we use to accept a PBT assignment, but the 335 SNP panel LOD score was much higher. The False Discovery Rate was also much
 979 lower for these 800 assignments based on the 335 SNP panel ($FDR = 6.6 \times 10^{-6}$) compared to the 92 SNP panel ($FDR = 0.01$). We set
 980 an FDR threshold at 0.1 and so the 335 SNP panel will likely make it possible to accept assignments that would have been borderline
 981 for failing to meet these thresholds using the smaller panel. In fact, there were 20 fish that were only assigned using the 335 SNP
 982 panel and would have escaped detection with the 92 SNP panel. Further, there were 32 assignments that were concordant to the PBT
 983 broodstock, however, either the mother or father or both parents were discordant across the assignments generated by these two
 984 panels. The 335 PBT panel will be more likely to avoid errors that occur when hatchery broodstock have a high level of relatedness
 985 which is the case with steelhead hatcheries. In conclusion, we feel encouraged by these results and will be adopting the larger number
 986 of SNP markers for PBT applications in steelhead from now on.

987

988 **Table 19.** Comparison of PBT assignments using the new panel of 335 SNPs versus the 92 SNP panel for steelhead passing
 989 Bonneville Dam in 2020.

PBT335								
Method	PopName	PopName-fin	PA- Ma_Same	Ma_Diff	Pa_Diff	Pa- Ma_Diff	Unassigned	Total
duplicate	NA	Unassigned					5	5
failed177	NA	Unassigned					25	25
GSI	NA	OmyDWOR17S				1		1
		OmyDWOR18S				2		2
		OmyEASTBK17				1		1
		OmyEFSW17S				1		1
		OmyLSCR18S				1		1
		OmyOXBO17S				3		3
		OmyPAHH17S				5		5
		OmyPAHH18S				1		1
		OmyRB17				1		1
		OmySAWT17S				1		1
		OmySAWT18S				1		1
		OmyUMA17				1		1
		OmyWTP16				1		1
		Unassigned					591	591
PBT	OmyCGRW17S	OmyLYON17S	61					61
		Unassigned					3	3
	OmyCGRW18S	OmyLYON18S	11					11
		Unassigned					1	1
	OmyDWOC16S	Unassigned					2	2
	OmyDWOC17S	OmyDWOR17S	250					250
		Unassigned					1	1
	OmyDWOC18S	OmyDWOR18S	3					3
	OmyEASTBK16	OmyEASTBK16	1					1

OmyLSCR17S	OmyLSCR17S	12					12
OmyLSCR18S	OmyLSCR18S	2					2
OmyOXBO17S	OmyOXBO17S	37					37
Unassigned						1	1
OmyOXBO18S	OmyOXBO18S	24					24
OmyPAHH17S	OmyPAHH17S	54					54
OmyPAHH18S	OmyPAHH18S	16					16
OmyRB17	OmyRB17	27		1			28
Unassigned						3	3
OmySAWT17S	OmySAWT17S	70					70
OmySAWT18S	OmySAWT18S	9					9
OmySFCW17S	OmyDWOR17S	83	5	3	23		114
OmySKH16_su	OmySKH16_su	2					2
OmySKH17_su	OmySKH17_su	26					26
Unassigned						2	2
OmyTOUW17S	OmyLYON17S	3					3
OmyTUCW17S	OmyLYON17S	3					3
OmyTUCW18S	OmyLYON18S	1					1
OmyUSAL17S	OmyPAHH17S	15					15
OmyWALW17S	OmyWALL17S	51					51
OmyWALW18S	OmyWALL18S	8					8
OmyWEL_MET17	OmyWEL_MET17	4					4
OmyWEL_OKA17	OmyWEL_OKA17	4					4
OmyWEL17	OmyWEL17	15					15
OmyWEL18	OmyWEL_MET18	1					1
	OmyWEL18	2					2
OmyWTP17	OmyWTP17	5					5
		800	5	4	43	634	1486

Sockeye (363 SNPs) parent baseline for identifying reintroduced stocks from Yakima River

This is the second year we have been able to utilize candidate parents that were genotyped from tissues collected from carcass spawning surveys and directly from the fish translocated from Priest Rapids Dam and released into the Yakima River (Table 20). A combination of parent-pair assignments (trio assignment) and single parent assignments were performed to obtain as large of a sample of offspring as possible. Tag rates assumed the ability to perform single parent assignments. We had funding to genotype some of our older candidate parents from the translocation year 2012 and updated the PBT baseline. The tag rates that increased as a result of the additional genotypes are noted in green in Table 20. Specifically the largest “Change” in tag rates occurred in Spawn Year 2012 in which we now have 13% of the candidate parents genotyped and have at least a chance to detect offspring that returned from this first large (10,000+ adults translocated in 2012) translocation event in the Yakima River. This will be useful when we re-analyze previous years with the PBT baseline.

Table 20. The numbers of candidate parents genotyped relative to the number of returning and translocated adult sockeye to the Yakima River each year.

Year	Outplants	Prosser	Roza	O+P	O+R	Genotypes		Max YR	Tag rate		Change
						383	88		383	88	383
2009	1000	12	17	1012	1017	0	0	1017	0.0%	0.0%	0.0%
2010	2500	11	40	2511	2540	0	0	2540	0.0%	0.0%	0.0%
2011	4000	0	13	4000	4013	0	29	4013	0.0%	1.4%	0.0%
2012	10000	47	154	10047	10154	689	985	10154	13.1%	18.5%	13.1%
2013	4500	696	691	5196	5191	1166	1244	5196	39.8%	42.2%	0.0%
2014	10000	2678	2576	12678	12576	2906	3146	12678	40.6%	43.5%	0.0%
2015	10000	342	95	10342	10095	698	1182	10342	13.0%	21.6%	0.0%
2016	10000	3742	3949	13742	13949	4435	4245	13949	53.5%	51.6%	1.9%
2017	1000	372	137	1372	1137	426	422	1372	52.5%	52.1%	0.4%
2018	4700	456	201	5156	4901	1378	1368	5156	46.3%	46.0%	0.3%
2019	0	110	201	110	201	203	199	201	100.0%	100.0%	0.0%

Note: “Outplants” indicate the number of sockeye translocated into the Yakima River, and “Prosser” and “Roza” dam counts were summed (“O+P” or “O+R”) with the outplants to provide an estimate of the total escapement of spawners in the Yakima River each year. We used whichever number was greatest (“O+P” or “O+R”) to provide the maximum escapement of the Yakima River (“Max YR”). A portion of these spawners were successfully genotyped either using 383 or 88 (the legacy panel) SNPs and tag rates were

1008 *calculated using the Max YR as the denominator. When cross information and the gender of the broodstock samples is unknown, then*
1009 *the tag rate for single parentage is : $1-(f_t)^2$, where f_t is the fraction of the total broodstock not genotyped.*

1010 *Parentage based tagging assignments of Chinook salmon in harvest mixtures*
1011 A summary of the Chinook harvest samples that were genotyped (derived from Table 5)
1012 is presented in Table 21. Of the 5,434 harvest Chinook analyzed, there were 1,446 hatchery-
1013 origin individuals that could be confidently PBT assigned to 93 hatchery broodstock sources
1014 (i.e., 13 Lower Columbia, 2 Willamette, 26 Snake River, and 52 Columbia River hatchery
1015 broodstocks) spawned in 2013-2017. The majority of PBT assigned individuals were from the
1016 2015 brood year (i.e., 4-years-old).

1017 **Table 21. Summary of the Chinook salmon harvest samples by fishery, region, and fin clip**
1018 **in 2019.**

Fishery	Region	Clip	Period			Analysis					
			Spring	Summer	Fall	GSI	PBT	Dup.	failed	Total	%PBT
Bon19	BONAFF	AD	1086	396	488	229	1713	1	27	1970	88.2%
		AI	414	184	1104	1303	377	4	18	1702	22.4%
Permit	01_BON	AD	17				17			17	100.0%
		AI	9			5	4			9	44.4%
	02_TDA	AD	132			8	122		2	132	93.8%
		AI	44			30	13		1	44	30.2%
	BELOW_BON	AD	3				3			3	100.0%
		AD		10	89	7	28		64	99	80.0%
Treaty	01_BON	AI			142	20	7		115	142	25.9%
		AD			40	1	6		33	40	85.7%
	02_JDA	AI			152	27	4		121	152	12.9%
		AD		112	330	21	169		252	442	88.9%
	02_TDA	AI		39	1774	382	88		1343	1813	18.7%
		AD	168			70	96	1	1	168	57.8%
Test	Zone 2	AI	47			39	6	1	1	47	13.3%
		AD			209	88	108		13	209	55.1%
Pound	Zone83	AI			183	150	29	1	3	183	16.2%
		AD	61	42	57	76	77	1	6	160	50.3%
	WFC	AI	19	24	80	95	21	1	6	123	18.1%
		AD	275		82	73	252	2	30	357	77.5%
Sport	B	AI			148	103	20		25	148	16.3%
		AD			65	14	47		4	65	77.0%
	A	AI			237	181	42		14	237	18.8%
		AD			75	14	55		6	75	79.7%
	01_BON	AI			87	61	20		6	87	24.7%
		AD			46	9	34		3	46	79.1%
Commercial	B	AI			133	99	12		22	133	10.8%
		AD			209	67	138		4	209	67.3%
	A	AI			294	241	28		25	294	10.4%
			2275	807	6024	3413	3536	12	2145	9106	50.9%

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Comparison of proportion of PBT assignments among Chinook salmon fisheries

The average of adipose-clipped Chinook salmon from fishery mixtures across all periods was that were assigned via PBT was 78% (range = 50% – 100%, Table 21). The fishery(s) with the minimum and maximum assigned adipose-clipped Chinook salmon was the pound net fishery in region B and the Treaty ceremonial permit fishery, respectively. Among the adipose-intact fish, the average assignment via PBT was expectedly lower (average = 20%, range = 10% – 44%; Table 21). Among the fisheries with adipose-intact fish, the minimum and maximum PBT-assigned Chinook salmon was observed in the Non-treaty commercial fishery in region A and the spring Treaty ceremonial permit fishery in Bonneville Pool, respectively. For the clipped fish, the collections with the minimum PBT-assigned fish were due to areas that receive higher proportions of lower river hatchery fish that are not as well covered in the PBT baseline (e.g. the pound net in Cathlamet Channel). However, for the predominant SY2015 that was expected in these harvest mixtures, the broodstock with the lowest tag rate was OtsWSNFH15_sp (tag rate = 18%). These Warm Springs National Fish Hatchery spring run Chinook salmon would likely show up in the ceremonial permit fishery and may have been the primary reason for the low PBT recoveries for this collection clipped fish.

The test fishery in the Chinook Salmon Spring Management Period of 2019

We examined one source of information that could potentially be useful to managers particularly for 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. For example, we characterized reporting groups among the hatchery clipped, hatchery unclipped, and natural-origin VSI-upriver and VSI-lower river fish caught in the test fishery (Table 22). 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 23). 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 (Table 23) and Bonneville Dam showed that these samples from these two sources have very similar compositions of stocks (Figure 24). Further, there is high correlation ($R^2=0.7$) 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 25).

Table 22. Summary of the stock composition at the reporting group level of the VSI-identified lower river and upriver spring Chinook salmon in the test fishery of 2019 in units of catch-per-unit-effort (CPUE, # of fish per # of drifts).

Run type	Reporting Group Code	H		HNC		W	
		VSI		VSI		VSI	
		Lower	Upper	Lower	Upper	Lower	Upper
Spring	01_YOUNGS	0.00	0.03				
Spring	02_WCASSP	0.65	0.17				
Fall	03_WCASFA						
Spring	04_WILLAM	3.45	0.51			1.62	0.24
Fall	05_SPCRTU						
Spring	06_Klickr	0.07	0.00				
Spring	07_Descsp	0.00	0.61				
Spring	08_JohnDR						
Spring	09_YAKIMA	0.15	0.69			0.00	0.47
Spring	10_UCOLSP	0.36	0.47	0.07	0.00	0.07	0.55
Spring	11_TUCANO					0.15	0.00
Spring/Summer	12_HELLSC	0.31	2.22	0.00	0.33	0.15	0.38
Spring/Summer	13_SFSALM	0.00	0.08				
Spring/Summer	14_CHMBLN						
Spring/Summer	15_MFSALM					0.00	0.15
Spring/Summer	16_UPSALM	0.00	0.17				
Fall	17_DescFA						
Summer/Fall	18_UCOLSF						
Fall	19_SRFALL						
Spring	20_BONPOOLSP	0.37	1.27				
Spring	21_UMATILLASP	0.00	0.07				
Fall	22_BONPOOLFA						
Fall	23_UMATILLAFA						
	Lower River Rep. Gr.	4.10	0.71	0.00	0.00	1.62	0.24
	Upriver Rep. Gr.	1.27	5.59	0.07	0.33	0.37	1.55
	Total	5.37	6.30	0.07	0.33	1.99	1.79

Note: Genetic stocks are broken down by hatchery clipped (H), hatchery unclipped (HNC), and natural-origin (W) stocks from samples of fish from the test fishery that were initially visually determined as belonging to lower river (Lower) or upriver (Upper) stocks. Genetic reporting groups were also split into lower river versus upriver (shaded cells) and the subtotals for the CPUE estimated for each of these groups is listed at the bottom of the Table.

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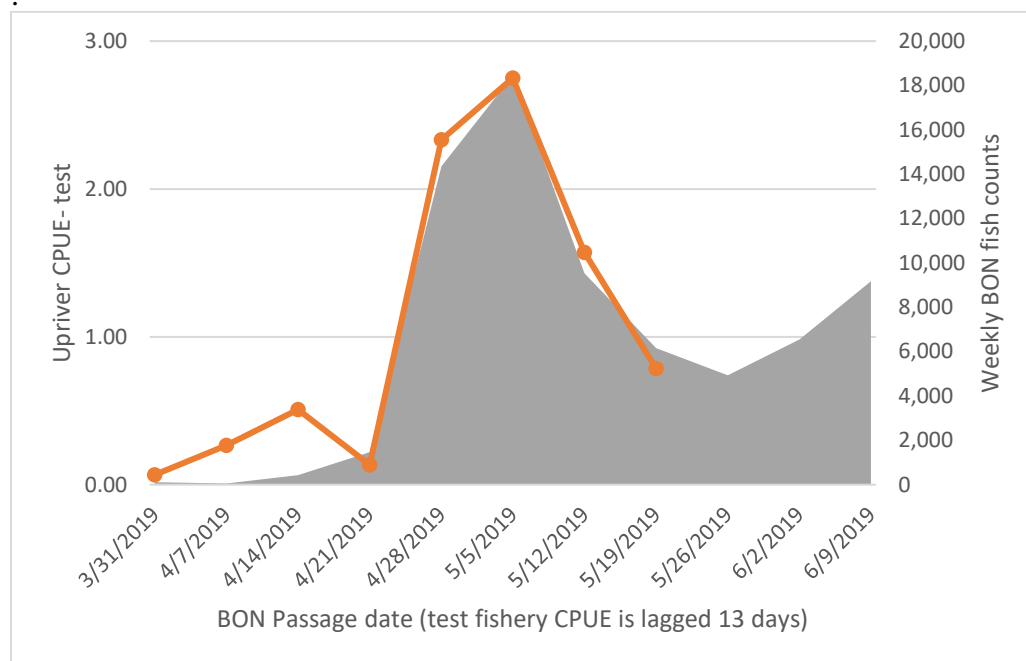
Table 23. Summary of the stock composition at the broodstock level of the hatchery-origin VSI-identified lower river and upriver spring Chinook salmon in the test fishery of 2019 in units of catch-per-unit-effort (CPUE, # of fish per # of drifts).

Spring Test Fishery 2019				Adult Chinook AD			Adult Chinook AI		
Expected Run Time	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	MLE	95% CI	Percent
01Spring	Cowlitz Salmon Hatchery	OtsCOW15_sp	2015	0.1	0 – 0.3	0.71%			0.00%
01Spring	Kalama Falls Hatchery	OtsKAL15_sp	2015	0.2	0 – 0.3	1.34%			0.00%
01Spring	Parkdale Fish Facility	OtsPFF15_sp	2015	0.2	0 – 0.5	2.12%			0.00%
01Spring	South Santiam Hatchery	OtsSSANT15_sp	2015	0.2	0 – 0.4	1.58%			0.00%
01Spring	Klickitat Hatchery	OtsKH14_sp	2014	0.1	0 – 0.2	0.63%			0.00%
01Spring	Round Butte Fish Hatchery	OtsRB15_sp	2015	0.2	0 – 0.4	1.32%			0.00%
01Spring	Warm Springs National Fish Hatchery	OtsWSNFH15_sp	2015	0.5	0 – 0.9	3.89%			0.00%
01Spring	Yakima River Roza Dam	OtsYR14int_sp	2014	0.1	0 – 0.2	0.61%			0.00%
01Spring	Yakima River Roza Dam	OtsYR15int_sp	2015	0.8	0.4 – 1.2	6.60%			0.00%
01Spring	Chief Joseph Hatchery	OtsCJH15_sp	2015	0.2	0.1 – 0.4	1.85%			0.00%
01Spring	Leavenworth National Fish Hatchery	OtsLNFH15_sp	2015	0.2	0 – 0.5	1.67%			0.00%
01Spring	Winthrop National Fish Hatchery	OtsWTP15_sp	2015	0.2	0 – 0.4	1.87%	0.1	0 – 0.2	18.00%
01Spring	Clearwater Fish Hatchery	OtsPOWP15S_sp	2015	0.4	0.1 – 0.7	3.35%	0.2	0 – 0.5	59.81%
01Spring	Clearwater Fish Hatchery	OtsCLWH15S_sp	2015	0.3	0.1 – 0.6	2.66%			0.00%
01Spring	Dworshak National Fish Hatchery	OtsDWOR15S_sp	2015	0.4	0.2 – 0.7	3.39%	0.1	0 – 0.3	22.19%
01Spring	Lookingglass Fish Hatchery	OtsLOOK15S_sp	2015	0.1	0 – 0.3	0.77%			0.00%
01Spring	Rapid River Fish Hatchery	OtsRAPH14S_sp	2014	0.1	0 – 0.2	0.62%			0.00%
01Spring	Rapid River Fish Hatchery	OtsRAPH15S_sp	2015	1.2	0.7 – 1.7	10.00%			0.00%
01Spring	Carson National Fish Hatchery	OtsCAR14_sp	2014	0.2	0 – 0.4	1.49%			0.00%

01Spring	Carson National Fish Hatchery	OtsCAR15_sp	2015	0.6	0.2 – 0.9	4.74%			0.00%
01Spring	Little White Salmon National Fish Hatchery	OtsLWS14_sp	2014	0.2	0 – 0.3	1.32%			0.00%
01Spring	Little White Salmon National Fish Hatchery	OtsLWS15_sp	2015	0.8	0.4 – 1.2	6.54%			0.00%
01Spring	Umatilla Fish Hatchery	OtsUMA14_sp	2014	0.1	0 – 0.2	0.61%			0.00%
02Spring/Summer	Lookingglass Fish Hatchery	OtsIMNW15S_spsu	2015	0.1	0 – 0.2	0.66%			0.00%
02Spring/Summer	McCall Fish Hatchery	OtsMCCA15S_spsu	2015	0.1	0 – 0.3	0.72%			0.00%
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT14S_spsu	2014	0.1	0 – 0.2	0.71%			0.00%
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT15S_spsu	2015	0.1	0 – 0.2	0.71%			0.00%
#N/A	#N/A	Unassigned	#N/A	4.4	3.8 – 5.3	37.49%			0.00%
		TOTAL		11.7		100.0%	0.4		100.0%

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Figure 23. The relationship between the test fishery upriver Chinook Salmon CPUE (line) and weekly fish counts at Bonneville Dam (solid gray) in 2019.

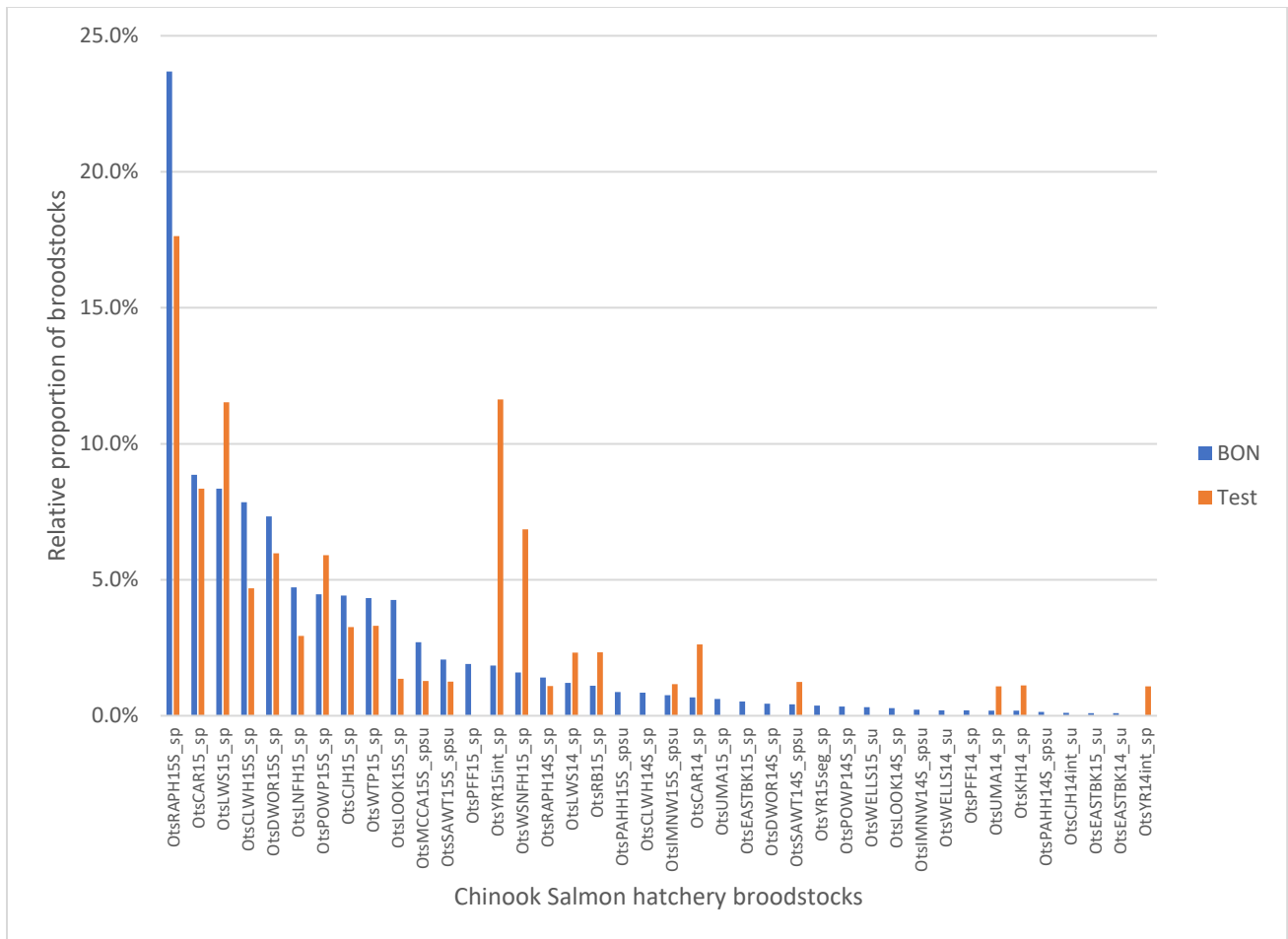


Figure 24. Relative proportions of hatchery clipped broodstocks of upriver Chinook Salmon caught in the test fishery (March 18 – May 5) compared to Chinook Salmon that passed Bonneville Dam in corresponding weeks lagged 13 days from the test fishery (March 31 – May 25) in 2019.

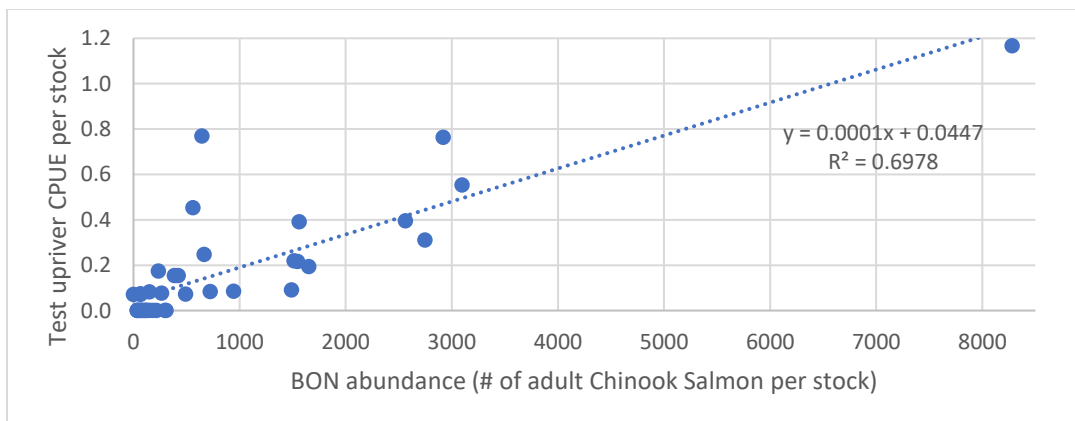


Figure 25. Correlation of the test fishery CPUE with the estimated abundance passing Bonneville Dam of hatchery clipped broodstocks identified by PBT analysis in 2019.

We reported spring sport fishery results for reporting group level stock composition (Table 24) and the hatchery broodstock composition (Table 25) of the kept fish (clipped hatchery-origin fish).

Table 24. Summary of the stock composition at the reporting group level of the kept spring Chinook salmon in the Non-Treaty sport fishery of 2019 in units of reported catch.

Run type	Reporting Group Code	Hatchery origin- Clipped	
		Estimated abundance	
		Mean	95% CI
Spring	01_YOUNGS		
Spring	02_WCASSP	47	
Fall	03_WCASFA	3	
Spring	04_WILLAM	119	
Fall	05_SPCRTU		
Spring	06_KLICKR	5	
Spring	07_DESCSP	79	
Spring	08_JOHNDR		
Spring	09_YAKIMA	11	
Spring	10_UCOLSP	328	
Spring	11_TUCANO		
Spring/Summer	12_HELLSC	575	
Spring/Summer	13_SFSALM		
Spring/Summer	14_CHMBLN		
Spring/Summer	15_MFSALM		
Spring/Summer	16_UPSALM	7	
Fall	17_DESCFA		
Summer/Fall	18_UCOLSF		
Fall	19_SRFALL		
Spring	20_BONPOOLSP	495	
Spring	21_UMATILLASP	7	
Fall	22_BONPOOLFA		
Fall	23_UMATILLAFA		
	Total	1,677	

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Table 25. Summary of the stock composition at the broodstock level of the kept adult spring Chinook salmon in the Non-Treaty sport fishery of 2019 in units of reported catch.

Spring Sport Fishery 2019				Kept Adult Chinook AD			
Expected Run Time	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	GSI RepGrp
01Spring	Parkdale Fish Facility	OtsPFF15_sp	2015	7	0 – 22	0.4%	02_WCASSP
01Spring	Speelyai Fish Hatchery	OtsLEW15_sp	2015	28	0 – 56	1.7%	02_WCASSP
01Spring	Klickitat Hatchery	OtsKH14_sp	2014	5	0 – 15	0.3%	06_KLICKR
01Spring	Round Butte Fish Hatchery	OtsRB15_sp	2015	13	0 – 29	0.8%	07_DESCSP
01Spring	Warm Springs National Fish Hatchery	OtsWSNFH15_sp	2015	66	0 – 143	4.0%	07_DESCSP
01Spring	Yakima River Roza Dam	OtsYR15int_sp	2015	5	0 – 16	0.3%	09_YAKIMA
01Spring	Chief Joseph Hatchery	OtsCJH14_sp	2014	16	0 – 39	0.9%	10_UCOLSP
01Spring	Chief Joseph Hatchery	OtsCJH15_sp	2015	80	45 – 122	4.8%	10_UCOLSP
01Spring	Leavenworth National Fish Hatchery	OtsLNFH14_sp	2014	7	0 – 21	0.4%	10_UCOLSP
01Spring	Leavenworth National Fish Hatchery	OtsLNFH15_sp	2015	76	39 – 116	4.5%	10_UCOLSP
01Spring	Winthrop National Fish Hatchery	OtsWTP15_sp	2015	101	59 – 144	6.0%	10_UCOLSP
01Spring	Clearwater Fish Hatchery	OtsCLWH14S_sp	2014	23	5 – 42	1.4%	12_HELLSC
01Spring	Clearwater Fish Hatchery	OtsPOWP14S_sp	2014	14	0 – 35	0.8%	12_HELLSC
01Spring	Clearwater Fish Hatchery	OtsPOWP15S_sp	2015	68	34 – 103	4.0%	12_HELLSC
01Spring	Clearwater Fish Hatchery	OtsCLWH15S_sp	2015	59	28 – 96	3.5%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsDWOR15S_sp	2015	65	33 – 98	3.9%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsLOOK14S_sp	2014	6	0 – 18	0.3%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsLOOK15S_sp	2015	8	0 – 23	0.5%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH14S_sp	2014	38	14 – 64	2.3%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH15S_sp	2015	285	216 – 355	17.0%	12_HELLSC
01Spring	Carson National Fish Hatchery	OtsCAR15_sp	2015	144	94 – 195	8.6%	20_BONPOOLSP
01Spring	Little White Salmon National Fish Hatchery	OtsLWS14_sp	2014	55	26 – 88	3.3%	20_BONPOOLSP

01Spring	Little White Salmon National Fish Hatchery	OtsLWS15_sp	2015	296	230 – 364	17.6%	20_BONPOOLSP
01Spring	Umatilla Fish Hatchery	OtsUMA14_sp	2014	7	0 – 21	0.4%	21_UMATILLASP
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT14S_spsu	2014	7	0 – 21	0.4%	16_UPSALM
#N/A	#N/A	Unassigned	#N/A	199	103 – 292	11.9%	#N/A
TOTAL				1677		100.0%	

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Our analyses of the spring Treaty permit fishery that was executed above and below Bonneville Dam, allowed us to estimate the portion of assignments that were natural-origin (17.3%, “W”) compared to the total catch that included clipped and unclipped hatchery-origin Chinook salmon (Table 26). We could further estimate abundances of hatchery broodstocks among the hatchery-origin fish (Table 27).

Table 26. Summary of the genetic assignments at the reporting group level of the Yakama Nation permit fishery below Bonneville Dam and Zone 6 in 2019.

Reporting Group name	Run type	Reporting Group Code	BELOW BON	01_BON				02_TDA				Grand Total										
			H	total	H	HNC	W	total	H	HNC	W		total									
Youngs Bay	Spring	01_YOUNGS	3	3	8		2	10	98	4	14	116	129									
West Cascade Spring	Spring	02_WCASSP																				
West Cascade Fall	Fall	03_WCASFA																				
Willamette	Spring	04_WILLAM																				
Spring Creek Tule	Fall	05_SPCRTU																				
Klickitat	Spring	06_KLICKR																				
Deschutes spring	Spring	07_DESCSP												1	1	2	1		1	3		
John Day	Spring	08_JOHNDR																4	4	4		
Yakima	Spring	09_YAKIMA															2		4	6	6	
Upper Columbia spring	Spring	10_UCOLSP												3	2	2	7	25	8	5	38	45
Tucannon	Spring	11_TUCANO													1		1				1	
Hells Canyon	Spring/Summer	12_HELLSC														2	10					
South Fork Salmon	Spring/Summer	13_SFSALM																	1	1	2	2
Chamberlain Creek	Spring/Summer	14_CHMBLN																				
Middle Fork Salmon	Spring/Summer	15_MFSALM																				
Upper Salmon	Spring/Summer	16_UPSALM																2		2	4	4
Deschutes fall	Fall	17_DESCFA																				

Upper Columbia summer/fall	Summer/Fall	18_UCOLSF		1	1	2	2	1					
Snake River fall	Fall	19_SRFALL											
Bonneville Pool spring	Spring	20_BONPOOLSP		4	4			6					
Umatilla spring	Spring	21_UMATILLASP		1	1			1					
Bonneville Pool fall	Fall	22_BONPOOLFA											
Umatilla fall	Fall	23_UMATILLAFA											
Total			3	3	17	4	5	26	130	13	30	173	202

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1117 **Table 27. Summary of the genetic assignments at the broodstock level of the Yakama Nation permit fishery below**
1118 **Bonneville Dam and in Zone 6 for 2019.**

				BELOW BON	01_BON		02_TDA		Total	GSI RepGrp		
Expected Run Time	Hatchery	Broodstock	Broodyear	H	H	HNC	H	HNC				
01Spring	Round Butte Fish Hatchery	OtsRB15_sp	2015			1			1	07_DESCSP		
#N/A	#N/A	Unassigned	#N/A					1		1	07_DESCSP	
01Spring	Yakima River Roza Dam	OtsYR15int_sp	2015					1		1	09_YAKIMA	
#N/A	#N/A	Unassigned	#N/A					1		1	09_YAKIMA	
01Spring	Chief Joseph Hatchery	OtsCJH15_sp	2015			1		9		10	10_UCOLSP	
01Spring	Eastbank Fish Hatchery	OtsEASTBK15_sp	2015						1	1	10_UCOLSP	
01Spring	Leavenworth National Fish Hatchery	OtsLNFH15_sp	2015						11	1	12	10_UCOLSP
01Spring	Methow Fish Hatchery	OtsMETH14_sp	2014							1	1	10_UCOLSP
01Spring	Methow Fish Hatchery	OtsMETH15_sp	2015					1		2	3	10_UCOLSP
01Spring	Winthrop National Fish Hatchery	OtsWTP14_sp	2014							1	1	10_UCOLSP
01Spring	Winthrop National Fish Hatchery	OtsWTP15_sp	2015				2	1	4	2	9	10_UCOLSP
#N/A	#N/A	Unassigned	#N/A						1		1	10_UCOLSP
01Spring	Lyons Ferry Fish Hatchery	OtsLYON15S_sp	2015					1			1	11_TUCANO
01Spring	Clearwater Fish Hatchery	OtsCLWH14S_sp	2014				1				1	12_HELLSC
01Spring	Clearwater Fish Hatchery	OtsCLWH15S_sp	2015				2		15	1	18	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsDWOR15S_sp	2015		3		18		21	12_HELLSC		
01Spring	Lookingglass Fish Hatchery	OtsLOOK15S_sp	2015				6		6	12_HELLSC		
01Spring	Clearwater Fish Hatchery	OtsPOWP15S_sp	2015		1		12	2	15	12_HELLSC		
01Spring	Rapid River Fish Hatchery	OtsRAPH14S_sp	2014				2		2	12_HELLSC		
01Spring	Rapid River Fish Hatchery	OtsRAPH15S_sp	2015	3	1		39	1	44	12_HELLSC		

01Spring	Rapid River Fish Hatchery	OtsRAPH16S_sp	2016				2		2	12_HELLSC
#N/A	#N/A	Unassigned	#N/A				4		4	12_HELLSC
02Spring/Summer	McCall Fish Hatchery	OtsMCCA15S_spsu	2015					1	1	13_SFSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT15S_spsu	2015				1		1	16_UPSALM
#N/A	#N/A	Unassigned	#N/A				1		1	16_UPSALM
03Summer	Wells Fish Hatchery	OtsWELLS14_su	2014		1				1	18_UCOLSF
01Spring	Carson National Fish Hatchery	OtsCAR15_sp	2015		1				1	20_BONPOOLSP
01Spring	Carson National Fish Hatchery	OtsCAR16_sp	2016				1		1	20_BONPOOLSP
01Spring	Little White Salmon National Fish Hatchery	OtsLWS15_sp	2015		3		1		4	20_BONPOOLSP
01Spring	Umatilla Fish Hatchery	OtsUMA15_sp	2015		1				1	21_UMATILLASP
TOTAL				3	17	4	130	13	167	

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1122 In 2019, there were no summer Non-Treaty sport or commercial fisheries that were
1123 executed.

1124 The stock composition of the 2019 summer Treaty zone 6 commercial fishery was
1125 characterized by reporting group level of the clipped and unclipped hatchery-origin and the
1126 natural-origin Chinook salmon (**Error! Reference source not found.**). We further categorized h
1127 atchery-origin stocks by broodstock (Table 29).
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Table 28. Summary of the stock composition at the reporting group level of the summer Treaty Zone 6 commercial fishery in 2019 in units of reported catch.

Run type	Reporting Group Code	H		HNC		W	
		Est.	95% CI	Est.	95% CI	Est.	95% CI
Spring	01_YOUNGS						
Spring	02_WCASSP						
Fall	03_WCASFA						
Spring	04_WILLAM						
Fall	05_SPCRTU						
Spring	06_KLICKR						
Spring	07_DESCSP						
Spring	08_JOHNDR						
Spring	09_YAKIMA					34	0 – 86
Spring	10_UCOLSP			52	0 – 121	17	0 – 52
Spring	11_TUCANO						
Spring/Summer	12_HELLSC	28					
Spring/Summer	13_SFSALM	54		18	0 – 71		
Spring/Summer	14_CHMBLN						
Spring/Summer	15_MFSALM						
Spring/Summer	16_UPSALM	54				17	0 – 52
Fall	17_DESCFA						
Summer/Fall	18_UCOLSF	3,042		170	65 – 306	278	192 – 367
Fall	19_SRFALL					17	0 – 52
Spring	20_BONPOOLSP						
Spring	21_UMATILLASP						
Fall	22_BONPOOLFA						

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Fall	23_UMATILLAFA						
Total		3,178		240		364	

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Table 29. Summary of the stock composition at the broodstock level of the summer Treaty Zone 6 commercial fishery of 2019 in units of reported catch.

Summer Treaty Fishery 2019				Adult Chinook AD			Adult Chinook AI			GSI RepGrp
Expected Run Time	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	MLE	95% CI	Percent	
01Spring	Eastbank Fish Hatchery	OtsEASTBK15_sp	2015			0.0%	52	17 – 104	21.6%	10_UCOLSP
01Spring	Rapid River Fish Hatchery	OtsRAPH15S_sp	2015	28	0 – 83	0.9%			0.0%	12_HELLSC
02Spring/Summer	McCall Fish Hatchery	OtsMCCA15S_spsu	2015	54	0 – 110	1.7%	18	0 – 53	7.4%	13_SFSALM
02Spring/Summer	Pahsimeroi Fish Hatchery	OtsPAHH15S_spsu	2015	27	0 – 82	0.9%			0.0%	16_UPSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT14S_spsu	2014	27	0 – 80	0.8%			0.0%	16_UPSALM
03Summer	Chief Joseph Hatchery	OtsCJH13int_su	2013	34	0 – 100	1.1%			0.0%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCJH13seg_su	2013	29	0 – 87	0.9%			0.0%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCJH14seg_su	2014	484	293 – 684	15.2%			0.0%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCJH14int_su	2014	230	111 – 369	7.2%			0.0%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCJH15seg_su	2015	275	138 – 411	8.6%			0.0%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCJH15int_su	2015	173	58 – 289	5.4%	19	0 – 58	8.1%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCJH16int_su	2016	27	0 – 81	0.8%			0.0%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEASTBK14_su	2014	481	294 – 668	15.1%	35	0 – 86	14.4%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEASTBK15_su	2015	214	107 – 347	6.7%	17	0 – 52	7.2%	18_UCOLSF

03Summer	Entiat National Fish Hatchery	OtsENFH14_su	2014	264	126 – 421	8.3%			0.0%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH15_su	2015	298	154 – 455	9.4%	47	0 – 118	19.7%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELLS14_su	2014	294	160 – 427	9.2%	35	0 – 69	14.4%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELLS15_su	2015	240	107 – 374	7.6%	17	0 – 52	7.2%	18_UCOLSF
#N/A	#N/A	Unassigned	#N/A	0	0 – 41	0.0%			0.0%	#N/A
		TOTAL		3,178		100.00%	240		100.00%	

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1139 For the 2019 fall period, the pound net fishery reported a total of 177 kept Chinook salmon (all clipped hatchery-origin, Table
 1140 15), which were comprised of 42% lower river stocks (03_WCASFA), and 58% upriver stocks (40% Spring Creek tules and the
 1141 remaining were upriver brights). Among the natural-origin released stocks, 21% were lower river and the rest were upriver stocks
 1142 (Table 30). The hatchery-origin fish were identified by broodstock (Table 31), and the lower river stocks were found to be comprised
 1143 of Big Creek, Cowlitz Salmon Hatchery, Kalama Falls Hatchery, North Toutle Hatchery, and Washougal Fish Hatchery.

1144 The pound net fishery was also operating in the spring and summer periods but all fish that were sampled were released and
 1145 used to compare to the compositions of harvested fish from the various fisheries that were sampled in those periods.

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 1147 **Table 30. Summary of the genetic stock assignments at the reporting group level of the pound net fishery in 2019 for all**
 1148 **sampled fish that were kept and released.**

Period	Reporting Group Code	KEPT		RELEASED					
		Adult	Jack	Adult			Jack		
		H	H	H	HNC	W	H	HNC	W
		Est.	Est.	Est.	Est.	Est.	Est.	Est.	Est.
Spring	01_YOUNGS			1					
	02_WCASSP			1		2			
	04_WILLAM			15		2			
	06_KLICKR						1		
	12_HELLSC						1		1
	18_UCOLSF			37	4	10	2		
Summer	04_WILLAM			11		3			
	13_SFSALM								1
	16_UPSALM								1
	18_UCOLSF			26	3	14	4		2
Fall	01_YOUNGS					1			1
	02_WCASSP		1	1		1			1
	03_WCASFA	69	1	16	1	32	5		10
	04_WILLAM						1		2
	05_SPCRTU	65	6	16	4	13	6	3	1

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	17_DESCFA			1		1	1		4
	18_UCOLSF	13		3	14	98	13	7	22
	19_SRFALL	4		3	5	16	5	3	6
	22_BONPOOLFA	15		3	6		2		
	Total	166	8	134	37	193	41	13	52

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Table 31. Summary of the genetic assignments for kept and released Chinook salmon at the broodstock level of the pound net fishery of 2019.

Period	Expected Run Time	Hatchery	Broodstock	Broodyear	GSI RepGrp	KEPT		RELEASED		Total
						Adult	Jack	Adult	Jack	
						H	H	H	HNC	
Spring	01Spring	#N/A	Unassigned	#N/A	01_YOUNGS			1		1
	01Spring	Cowlitz Salmon Hatchery	OtsCOW15_sp	2015	02_WCASSP			1		1
	01Spring	South Santiam Hatchery	OtsSSANT15_sp	2015	04_WILLAM			1		1
	01Spring	#N/A	Unassigned	#N/A	04_WILLAM			14		14
	01Spring	Klickitat Hatchery	OtsKH16_sp	2016	06_KLICKR				1	1
	01Spring	Rapid River Fish Hatchery	OtsRAPH16S_sp	2016	12_HELLSC				1	1
	03Summer	Chief Joseph Hatchery	OtsCJH14int_su	2014	18_UCOLSF			6	2	8
	03Summer	Chief Joseph Hatchery	OtsCJH14seg_su	2014	18_UCOLSF			4		4
	03Summer	Chief Joseph Hatchery	OtsCJH15int_su	2015	18_UCOLSF			1		1
	03Summer	Eastbank Fish Hatchery	OtsEASTBK14_su	2014	18_UCOLSF			7	1	8
	03Summer	Eastbank Fish Hatchery	OtsEASTBK15_su	2015	18_UCOLSF				1	1
	03Summer	Entiat National Fish Hatchery	OtsENFH14_su	2014	18_UCOLSF			4		4
	03Summer	Entiat National Fish Hatchery	OtsENFH15_su	2015	18_UCOLSF			1	1	2
	03Summer	Wells Fish Hatchery	OtsWELLS14_su	2014	18_UCOLSF			7		7

	03Summer	Wells Fish Hatchery	OtsWELLS16_su	2016	18_UCOLSF				1		1
	03Summer	#N/A	Unassigned	#N/A	18_UCOLSF	7					7
Summer	01Spring	#N/A	Unassigned	#N/A	04_WILLAM	11					11
	03Summer	Chief Joseph Hatchery	OtsCJH14int_su	2014	18_UCOLSF	2					2
	03Summer	Chief Joseph Hatchery	OtsCJH14seg_su	2014	18_UCOLSF	6					6
	03Summer	Chief Joseph Hatchery	OtsCJH15int_su	2015	18_UCOLSF	1					1
	03Summer	Chief Joseph Hatchery	OtsCJH15seg_su	2015	18_UCOLSF				1		1
	03Summer	Eastbank Fish Hatchery	OtsEASTBK14_su	2014	18_UCOLSF	4	3				7
	03Summer	Eastbank Fish Hatchery	OtsEASTBK15_su	2015	18_UCOLSF	3					3
	03Summer	Eastbank Fish Hatchery	OtsEASTBK16_su	2016	18_UCOLSF				1		1
	03Summer	Entiat National Fish Hatchery	OtsENFH14_su	2014	18_UCOLSF	1					1
	03Summer	Wells Fish Hatchery	OtsWELLS14_su	2014	18_UCOLSF	1					1
	03Summer	Wells Fish Hatchery	OtsWELLS15_su	2015	18_UCOLSF	3					3
	03Summer	#N/A	Unassigned	#N/A	18_UCOLSF	5			2		7
Fall	01Spring	#N/A	Unassigned	#N/A	02_WCASSP	1	1				2
	04Fall	Big Creek Hatchery	OtsBIG15_fa	2015	03_WCASFA	2					2
	04Fall	Big Creek Hatchery	OtsBIG16_fa	2016	03_WCASFA	8		1			9
	04Fall	Big Creek Hatchery	OtsBIG17_fa	2017	03_WCASFA	6	1				7
	04Fall	Cowlitz Salmon Hatchery	OtsCOW17_fa	2017	03_WCASFA				1		1

04Fall	Kalama Falls Hatchery	OtsKAL16_fa	2016	03_WCASFA	5	4				9
04Fall	Kalama Falls Hatchery	OtsKAL17_fa	2017	03_WCASFA				2		2
04Fall	North Toutle Hatchery	OtsTOU15_fa	2015	03_WCASFA	1	1				2
04Fall	North Toutle Hatchery	OtsTOU16_fa	2016	03_WCASFA	2	1				3
04Fall	Washougal Fish Hatchery	OtsWAS16_fa	2016	03_WCASFA	18					18
04Fall	#N/A	Unassigned	#N/A	03_WCASFA	27	10		2		39
#N/A	#N/A	Unassigned	#N/A	04_WILLAM				1		1
04Fall	Spring Creek National Fish Hatchery	OtsSPCR15_fa	2015	05_SPCRTU	1	1				2
04Fall	Spring Creek National Fish Hatchery	OtsSPCR16_fa	2016	05_SPCRTU	10	1	2			13
04Fall	Spring Creek National Fish Hatchery	OtsSPCR17_fa	2017	05_SPCRTU	6	3	2	2	3	18
04Fall	#N/A	Unassigned	#N/A	05_SPCRTU	48	3	12	4		67
04Fall	#N/A	Unassigned	#N/A	17_DESCFA		1		1		2
04Fall	Priest Rapids Hatchery	OtsPRH15_fa	2015	18_UCOLSF	2		7			9
04Fall	Priest Rapids Hatchery	OtsPRH16_fa	2016	18_UCOLSF	9		7		1	17
04Fall	Priest Rapids Hatchery	OtsPRH17_fa	2017	18_UCOLSF				8	6	14
04Fall	#N/A	Unassigned	#N/A	18_UCOLSF	2	3		5		10
04Fall	Lyons Ferry Fish Hatchery	OtsLYON15S_1_fa	2015	19_SRFALL	3	1	1			5
04Fall	Lyons Ferry Fish Hatchery	OtsLYON16S_1_fa	2016	19_SRFALL		1	2			3

	04Fall	Lyons Ferry Fish Hatchery	OtsLYON17S_1_fa	2017	19_SRFALL	1	1	2	4	3	7					
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH15S_1_fa	2015	19_SRFALL							2	2			
	04Fall	#N/A	Unassigned	#N/A	19_SRFALL							1	3			
	04Fall	Little White Salmon National Fish Hatchery	OtsLWS14_fa	2014	22_BONPOOLFA							1	1			
	04Fall	Little White Salmon National Fish Hatchery	OtsLWS15_fa	2015	22_BONPOOLFA							9	2	2	13	
	04Fall	Little White Salmon National Fish Hatchery	OtsLWS16_fa	2016	22_BONPOOLFA							5	1	4	1	11
	04Fall	Little White Salmon National Fish Hatchery	OtsLWS17_fa	2017	22_BONPOOLFA										1	
Total						166	8	134	37	41	13	399				

The 2019 fall Non-Treaty sport fishery executed below Bonneville Dam was not mark-selective and could be characterized by reporting group composition of clipped and unclipped hatchery-origin and natural-origin stocks (Table 32). We also reported the broodstock composition of the hatchery-origin Chinook salmon (Table 33). In 2019, we were also able to report on reporting group and broodstock composition of the stocks in the fall Non-Treaty sport fishery executed above Bonneville Dam (Table 34, Table 35).

Table 32. Summary of the stock composition at the reporting group level of the kept adult Chinook salmon of the fall Non-Treaty sport fishery below Bonneville Dam in 2019 in units of reported catch.

Reporting Group name	Run type	Reporting Group Code	H		HNC		W	
			Est.	95% CI	Est.	95% CI	Est.	95% CI
Youngs Bay	Spring	01_YOUNGS						
West Cascade Spring	Spring	02_WCASSP	43	1 – 85			41	13 – 82
West Cascade Fall	Fall	03_WCASFA	364	142 – 493			397	274 – 522
Willamette	Spring	04_WILLAM						
Spring Creek Tule	Fall	05_SPCRTU	275	152 – 327	91	0 – 229	0	0 – 14
Klickitat	Spring	06_KLICKR						
Deschutes spring	Spring	07_DESCSP						
John Day	Spring	08_JOHNDR						
Yakima	Spring	09_YAKIMA						
Upper Columbia spring	Spring	10_UCOLSP						
Tucannon	Spring	11_TUCANO						
Hells Canyon	Spring/Summer	12_HELLSC						
South Fork Salmon	Spring/Summer	13_SFSALM						
Chamberlain Creek	Spring/Summer	14_CHMBLN						
Middle Fork Salmon	Spring/Summer	15_MFSALM						
Upper Salmon	Spring/Summer	16_UPSALM						
Deschutes fall	Fall	17_DESCFA					42	0 – 104
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	349	217 – 442	435	240 – 670	3470	3183 – 3740

Snake River fall	Fall	19_SRFALL	228	127 – 338	195	71 – 363	447	317 – 582
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	571	446 – 660	218	83 – 386		
Umatilla fall	Fall	23_UMATILLAFA						
Total			1,830		939		4,396	

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Table 33. Summary of the stock composition at the broodstock level of the kept adult Chinook salmon of the fall Non-Treaty sport fishery below Bonneville Dam in 2019 in units of reported catch.

Fall Sport Fishery 2019				Adult Chinook AD			Adult Chinook AI			GSI RepGrp
Expected Run Time	Hatchery	Broodstock	Brood year	MLE	95% CI	Percent	MLE	95% CI	Percent	
03Summer	Chief Joseph Hatchery	OtsCJH15int_su	2015	46	15 – 92	2.5%			0.0%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEASTBK14_su	2014	14	0 – 41	0.7%			0.0%	18_UCOLSF
04Fall	Kalama Falls Hatchery	OtsKAL16_fa	2016	43	0 – 86	2.4%			0.0%	03_WCASFA
04Fall	North Toutle Hatchery	OtsTOU15_fa	2015	16	0 – 47	0.9%			0.0%	03_WCASFA
04Fall	North Toutle Hatchery	OtsTOU16_fa	2016	15	0 – 45	0.8%			0.0%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWAS15_fa	2015	62	0 – 187	3.4%			0.0%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWAS16_fa	2016	96	0 – 192	5.2%			0.0%	03_WCASFA
04Fall	Spring Creek National Fish Hatchery	OtsSPCR15_fa	2015	14	0 – 42	0.8%			0.0%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR16_fa	2016	98	22 – 184	5.3%			0.0%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR17_fa	2017	161	58 – 266	8.8%	91	23 – 160	9.7%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRH14_fa	2014	14	0 – 41	0.7%	35	0 – 84	3.7%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRH15_fa	2015	145	69 – 227	7.9%	324	207 – 449	34.5%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRH16_fa	2016	41	14 – 82	2.2%	76	27 – 131	8.1%	18_UCOLSF

04Fall	Lyons Ferry Fish Hatchery	OtsLYON14S_1_fa	2014	14	0 – 42	0.8%	22	0 – 65	2.3%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON15S_1_fa	2015	44	15 – 88	2.4%	44	0 – 88	4.7%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON16S_1_fa	2016	87	29 – 145	4.8%	59	0 – 125	6.3%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH15S_1_fa	2015	43	14 – 85	2.3%	43	13 – 85	4.5%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH16S_1_fa	2016	21	0 – 64	1.2%	28	0 – 70	3.0%	19_SRFALL
04Fall	Little White Salmon National Fish Hatchery	OtsLWS14_fa	2014			0.0%	14	0 – 41	1.5%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWS15_fa	2015	419	289 – 557	22.9%	80	29 – 137	8.5%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWS16_fa	2016	152	76 – 243	8.3%	125	55 – 208	13.3%	22_BONPOOLFA
#N/A	#N/A	Unassigned	#N/A	285	128 – 482	15.6%			0.0%	#N/A
		TOTAL		1,830		100.00%	939		100.00%	

Table 34. Summary of the stock composition at the reporting group level of the kept adult Chinook salmon of the fall Non-Treaty sport fishery above Bonneville Dam in 2019 in units of reported catch.

Reporting Group name	Run type	Reporting Group Code	H		HNC		W	
			Est.	95% CI	Est.	95% CI	Est.	95% CI
Youngs Bay	Spring	01_YOUNGS						
West Cascade Spring	Spring	02_WCASSP						
West Cascade Fall	Fall	03_WCASFA						
Willamette	Spring	04_WILLAM						
Spring Creek Tule	Fall	05_SPCRTU	83	35 – 135			23	0 – 57

Klickitat	Spring	06_KLICKR						
Deschutes spring	Spring	07_DESCSP						
John Day	Spring	08_JOHNDR						
Yakima	Spring	09_YAKIMA						
Upper Columbia spring	Spring	10_UCOLSP						
Tucannon	Spring	11_TUCANO						
Hells Canyon	Spring/Summer	12_HELLSC						
South Fork Salmon	Spring/Summer	13_SFSALM						
Chamberlain Creek	Spring/Summer	14_CHMBLN						
Middle Fork Salmon	Spring/Summer	15_MFSALM						
Upper Salmon	Spring/Summer	16_UPSALM						
Deschutes fall	Fall	17_DESCFA					5	0 – 16
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	257	186 – 371	80	5 – 182	631	496 – 769
Snake River fall	Fall	19_SRFALL	80	49 – 132	34	0 – 99	93	41 – 155
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	427	341 – 506	157	52 – 297		
Umatilla fall	Fall	23_UMATILLAFA						
Total			847		271		753	

Table 35. Summary of the stock composition at the broodstock level of the kept adult Chinook salmon of the fall Non-Treaty sport fishery above Bonneville Dam in 2019 in units of reported catch.

Fall Sport BON Fishery 2019				Adult Chinook AD			Adult Chinook AI			GSI RepGrp
Expected Run Time	Hatchery	Broodstock	Brood year	MLE	95% CI	Percent	MLE	95% CI	Percent	
03Summer	Chief Joseph Hatchery	OtsCJH15int_su	2015	6	0 – 17	0.7%			0.0%	18_UCOLSF

04Fall	Spring Creek National Fish Hatchery	OtsSPCR16_fa	2016	27	0 – 82	3.2%			0.0%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR17_fa	2017	9	0 – 25	1.0%			0.0%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRH15_fa	2015	80	28 – 137	9.4%	62	17 – 115	23.0%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRH16_fa	2016	45	5 – 90	5.3%	17	0 – 52	6.4%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON14S_1_fa	2014			0.0%	18	0 – 54	6.6%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON15S_1_fa	2015	30	5 – 67	3.5%	6	0 – 17	2.1%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON16S_1_fa	2016	24	0 – 61	2.8%	5	0 – 16	2.0%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH15S_1_fa	2015			0.0%	5	0 – 16	2.0%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH16S_1_fa	2016	23	0 – 59	2.7%			0.0%	19_SRFALL
04Fall	Little White Salmon National Fish Hatchery	OtsLWS13_fa	2013	17	0 – 52	2.1%			0.0%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWS14_fa	2014			0.0%	17	0 – 52	6.4%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWS15_fa	2015	255	158 – 352	30.1%	18	0 – 55	6.7%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWS16_fa	2016	155	85 – 236	18.2%	122	52 – 208	44.8%	22_BONPOOLFA
#N/A	#N/A	Unassigned	#N/A	176	93 – 271	20.8%			0.0%	#N/A
		TOTAL		847		100.00%	271		100.00%	

The fall Non-Treaty commercial fishery is shown by the composition of the combined adult and jack harvest using reporting group level (**Table 36**) and broodstock level (Table 37) resolution. The early and late season fishery was executed in two different regions and allowed us to report the stock compositions for these regions separately. A primary difference in the compositons between regions was the large abundance of spring creek tules (05_SPCRTU) stock in region A and absence of this stock in region B (**Table 36**).

1181 **Table 36. Summary of the stock composition at the reporting group level of the adult and jack Chinook salmon of the fall Non-**
1182 **Treaty commercial fishery in 2019 in units of reported catch.**

Reporting Group name	Run type	Reporting Group Code	REGION B			REGION A		
			H	HNC	W	H	HNC	W
			Est.	Est.	Est.	Est.	Est.	Est.
Youngs Bay	Spring	01_YOUNGS						
West Cascade Spring	Spring	02_WCASSP			4			96
West Cascade Fall	Fall	03_WCASFA	34		181	528		521
Willamette	Spring	04_WILLAM	9			25		23
Spring Creek Tule	Fall	05_SPCRTU				2,059	80	86
Klickitat	Spring	06_KLICKR						25
Deschutes spring	Spring	07_DESCSP						
John Day	Spring	08_JOHNDR						
Yakima	Spring	09_YAKIMA						
Upper Columbia spring	Spring	10_UCOLSP						
Tucannon	Spring	11_TUCANO						
Hells Canyon	Spring/Summer	12_HELLSC						
South Fork Salmon	Spring/Summer	13_SFSALM						
Chamberlain Creek	Spring/Summer	14_CHMBLN						
Middle Fork Salmon	Spring/Summer	15_MFSALM						
Upper Salmon	Spring/Summer	16_UPSALM						
Deschutes fall	Fall	17_DESCFA			33			48
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	86	33	187	408	141	3,742
SNAKE RIVER fall	Fall	19_SRFALL	10	4	25	278	375	896
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						

Bonneville Pool fall	Fall	22_BONPOOLFA	56	14		556	119	
Umatilla fall	Fall	23_UMATILLAFA						
Total			195	51	430	3,853	715	5,438

Note: Hatchery clipped (H), Hatchery unclipped (HNC), and natural-origin (W) estimated abundances (Est.) are indicated for the portions of this fishery that occurred in Regions B (commercial zones 1-3) and Region A (commercial zones 4 and 5).

Table 37. Summary of the stock composition at the broodstock level of the adult and jack Chinook salmon of the fall Non-Treaty commercial fishery of 2019 in units of reported catch.

Fall Commercial Fishery 2019				Adult/jack Chinook AD			Adult/jack Chinook AI			GSI RepGrp
Run	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	MLE	95% CI	Percent	
03Summer	Chief Joseph Hatchery	OtsCJH15int_su	2015	25	0 – 75	0.6%			0.0%	18_UCOLSE
03Summer	Chief Joseph Hatchery	OtsCJH16int_su	2016	25	0 – 76	0.6%			0.0%	18_UCOLSE
04Fall	Washougal Fish Hatchery	OtsWAS15_fa	2015	401	103 – 620	9.9%			0.0%	03_WCASEF
04Fall	Washougal Fish Hatchery	OtsWAS16_fa	2016	59	0 – 155	1.5%			0.0%	03_WCASEF
04Fall	Spring Creek National Fish Hatchery	OtsSPCR15_fa	2015	221	104 – 340	5.4%			0.0%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR16_fa	2016	221	74 – 364	5.4%			0.0%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR17_fa	2017	1442	1085 – 1775	35.6%	80	0 – 168	10.4%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRH14_fa	2014			0.0%	25	0 – 76	3.3%	18_UCOLSE
04Fall	Priest Rapids Hatchery	OtsPRH15_fa	2015	299	180 – 437	7.4%	97	26 – 184	12.7%	18_UCOLSE

04Fall	Priest Rapids Hatchery	OtsPRH16_fa	2016	29	11 – 43	0.7%	34	4 – 79	4.4%	18_UCOLSE
04Fall	Priest Rapids Hatchery	OtsPRH17_fa	2017	48	22 – 77	1.2%	18	4 – 39	2.4%	18_UCOLSE
04Fall	Lyons Ferry Fish Hatchery	OtsLYON14S_1_fa	2014	47	0 – 116	1.2%	49	0 – 101	6.4%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON15S_1_fa	2015	181	76 – 302	4.5%	129	51 – 222	16.8%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON16S_1_fa	2016	10	0 – 30	0.2%			0.0%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH15S_1_fa	2015	50	0 – 102	1.2%	201	99 – 305	26.2%	19_SRFALL
04Fall	Little White Salmon National Fish Hatchery	OtsLWS14_fa	2014	23	0 – 68	0.6%			0.0%	22_BONPOOL
04Fall	Little White Salmon National Fish Hatchery	OtsLWS15_fa	2015	541	377 – 715	13.4%	98	24 – 193	12.8%	22_BONPOOL
04Fall	Little White Salmon National Fish Hatchery	OtsLWS16_fa	2016	44	11 – 90	1.1%	35	7 – 77	4.6%	22_BONPOOL
04Fall	Little White Salmon National Fish Hatchery	OtsLWS17_fa	2017	4	0 – 11	0.1%			0.0%	22_BONPOOL
#N/A	#N/A	Unassigned	#N/A	379	189 – 779	9.4%			0.0%	#N/A
		TOTAL		4,048		100.0%	766		100.0%	

1189

1190 The fall Treaty Zone 6 commercial fishery is reported by “tule” (i.e. Spring Creek Hatchery tules) and “bright” (upriver bright
 1191 stocks include 17_DESCFA, 18_UCOLSF, and 19_SRFALL) stocks. The YN monitors sample only the bright stock for DNA
 1192 analysis and so we provide estimated abundances of the stocks that comprise this Visual Stock Identification “bright” group of fish. It
 1193 was expected that there would be a small portion of “tule” fish within this group due to some misidentification of the stock using VSI.
 1194 We estimated 409 tules (05_SPCRTU) which comprised 4% of the total clipped hatchery-origin catch (Table 38). The broodstock
 1195 composition estimates identified a number of adult-sized jacks (18%) that were included in this harvest from Spring Creek, Priest
 1196 Rapids, Lyons Ferry, Nez Perce Tribal, and Little White Salmon hatcheries (Broodyear 2016, Table 39).

1197
 1198 **Table 38. Summary of the stock composition at the reporting group level of the adult VSI-bright Chinook salmon of the fall**
 1199 **Treaty zone 6 commercial fishery in 2019 in units of reported catch.**

Reporting Group name	Run type	Reporting Group Code	H		HNC		W	
			Est.	95% CI	Est.	95% CI	Est.	95% CI
Youngs Bay	Spring	01_YOUNGS						
West Cascade Spring	Spring	02_WCASSP						
West Cascade Fall	Fall	03_WCASFA						
Willamette	Spring	04_WILLAM						
Spring Creek Tule	Fall	05_SPCRTU	409	2 – 1090				
Klickitat	Spring	06_KLICKR						
Deschutes spring	Spring	07_DESCSP						
John Day	Spring	08_JOHNDR						
Yakima	Spring	09_YAKIMA						
Upper Columbia spring	Spring	10_UCOLSP						
Tucannon	Spring	11_TUCANO						
Hells Canyon	Spring/Summer	12_HELLSC						
South Fork Salmon	Spring/Summer	13_SFSALM						
Chamberlain Creek	Spring/Summer	14_CHMBLN						
Middle Fork Salmon	Spring/Summer	15_MFSALM						
Upper Salmon	Spring/Summer	16_UPSALM						
Deschutes fall	Fall	17_DESCFA					36	0 – 108

Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	4516	3264 – 5888	3695	2237 – 5768	33340	31157 – 35347
SNAKE RIVER fall	Fall	19_SRFALL	1585	1162 – 2201	3867	2535 – 5513	5488	4248 – 6844
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	4066	2813 – 4746	650	191 – 1424		
Umatilla fall	Fall	23_UMATILLAFA						
Total			10,576		8,212		38,863	

Table 39. Summary of the stock composition at the broodstock level of the adult VSI-bright Chinook salmon of the fall Treaty zone 6 commercial fishery in 2019 in units of reported catch.

Fall Sport BON Fishery 2019				Adult Chinook AD			Adult Chinook AI			
Expected Run Time	Hatchery	Brood stock	Brood year	MLE	95% CI	Percent	MLE	95% CI	Percent	GSI RepGrp
04Fall	Spring Creek National Fish Hatchery	OtsSPCR16_fa	2016	374	0 – 834	3.5%			0.0%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRH14_fa	2014	61	0 – 182	0.6%	138	0 – 294	1.7%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRH15_fa	2015	3078	2100 – 4130	29.1%	2750	1846 – 3715	33.5%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRH16_fa	2016	729	284 – 1260	6.9%	729	304 – 1240	8.9%	18_UCOLSF
04Fall	Yakima Nation Prosser Hatchery	OtsPRO15_fa	2015			0.0%	78	0 – 234	0.9%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON14S_1_fa	2014	447	125 – 832	4.2%	636	205 – 1172	7.8%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON15S_1_fa	2015	409	78 – 835	3.9%	924	427 – 1545	11.3%	19_SRFALL

04Fall	Lyons Ferry Fish Hatchery	OtsLYON16S_1_fa	2016	134	0 – 401	1.3%	262	64 – 588	3.2%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH13S_1_fa	2013			0.0%	127	0 – 382	1.5%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH15S_1_fa	2015	211	0 – 472	2.0%	1774	1093 – 2540	21.6%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH16S_1_fa	2016	192	0 – 441	1.8%	142	0 – 347	1.7%	19_SRFALL
04Fall	Little White Salmon National Fish Hatchery	OtsLWS14_fa	2014	485	126 – 930	4.6%			0.0%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWS15_fa	2015	3116	2222 – 4050	29.5%	346	64 – 692	4.2%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWS16_fa	2016	464	72 – 929	4.4%	304	36 – 627	3.7%	22_BONPOOLFA
#N/A	#N/A	Unassigned	#N/A	876	378 – 1523	8.3%			0.0%	#N/A
		TOTAL		10,576		100.0%	8,212		100.0%	

1205
1206
1207

The Treaty Sockeye salmon fishery could not be analyzed this year but the collections will soon be genotyped and included in a future report.

Reporting Group name	Hatchery origin-Clipped		Reintroduction- No Clip		Natural origin- No Clip	
	Estimated abundance		Estimated abundance		Estimated abundance	
	Mean	95% CI	Mean	95% CI	Mean	95% CI
Okanogan	25	0 – 74			6,052	5654 – 6418
Wenatchee					1,312	932 – 1729
Snake	150	50 – 299				
Lake Billy Chinook					5	0 – 16
Yakima			149	0 – 558		
Odell					34	0 – 103
Total	174		149		7,369	

Table 40. Summary of the stock composition at the broodstock level for the reintroduced sockeye salmon from the Yakima River caught in the Treaty fishery in 2018 in units of reported catch

Reintroduced Yakima sockeye					
Stock	Broodyear	Age	MLE	95% CI	Percent
Wenatchee	2014	4	123	0 – 369	82.4%
Okanogan	2013	5	26	0 – 66	17.6%
TOTAL			149		100.0%

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 five major Columbia River sockeye genetic stocks (Table 41, an additional kokanee stock “Odell” was detected). The lower river commercial harvest did not occur in 2018, and there was no Zone 6 sport fishery in 2018. Low sample numbers of *O. nerka* make it difficult to estimate narrow confidence intervals for abundance estimates of the Yakima River, Snake River, and Lake Billy Chinook stocks (Table 42).

The timing of the sockeye salmon fisheries may influence the harvested proportion of each stock. The Wenatchee stock has an early shifted run in some years like 2018. The Snake River stock (i.e., Redfish Lake) was only represented by 3 fish in the Zone 6 tribal fishery sample (Table 41) making run-timing estimates imprecise for this stock. Of the 3 Snake River fish identified with GSI, all fish were sampled in week 26. Notable difference in stock proportions between Bonneville Dam and the Zone 6 tribal harvest were observed for the Okanogan stock (90% vs. 79%) and for the Wenatchee stock (9% vs. 17%) in the Bonneville Dam vs. harvest mixture samples, respectively (Table 42).

1232 **Table 41. Summary of sample sizes and stock assignments for the 2018 sockeye salmon fisheries by weekly strata.**

Fishery	Stock	Statistical week							
		23	24	25	26	27	28	29	30
Sport	Okanogan					3	3	2	1
Treaty Zone 6	Lake Billy Chinook							1	
	Odell					1			
	Okanogan	3	1	40	33	40	32	25	7
	Snake				3				
	Wenatchee			11	13	4	2	3	1
	Yakima				1			2	

1233

1234 **Table 42. Comparison of stock-specific abundance and percent composition among sockeye salmon fisheries. The mean stock**
1235 **abundance estimate is provided for each fishery harvest in 2018.**

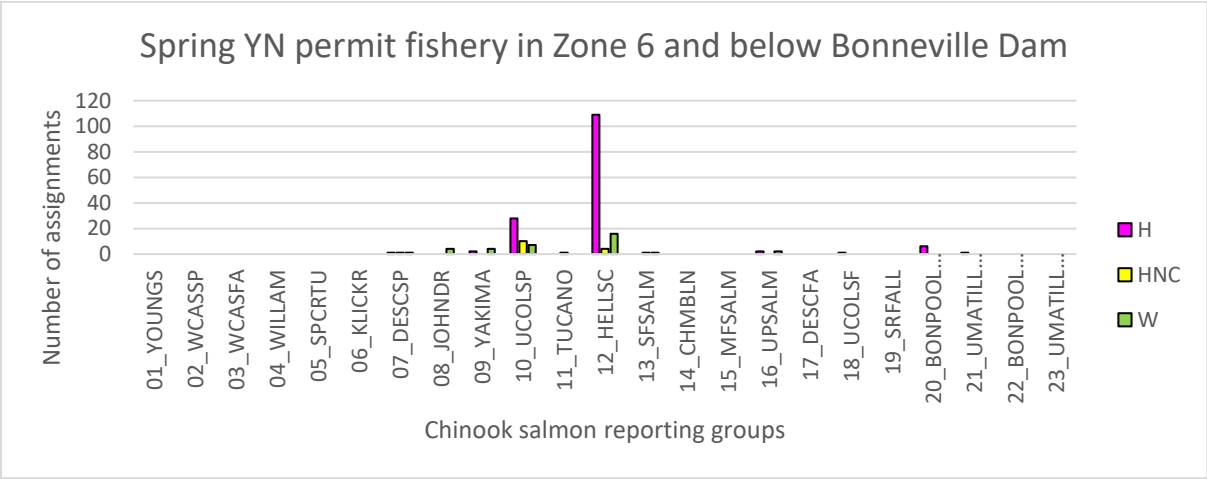
Mixture source	Mean						Stock proportion					
	Okanogan	Wenatchee	Snake	LBC	Yakima	other	Okanogan	Wenatchee	Snake	LBC	Yakima	other
Sport	111	-	-	-	-	-	100.0%	-	-	-	-	-
Treaty Zone 6	6,076	1,312	150	5	149	34	78.6%	17.0%	1.9%	0.1%	1.9%	0.4%
Total Harvest	6,187	1,312	150	5	149	34	78.9%	16.7%	1.9%	0.1%	1.9%	0.4%
Bonneville Dam	174,416	17,675	351	80	1,294	-	90.0%	9.1%	0.2%	0.0%	0.7%	-

1236

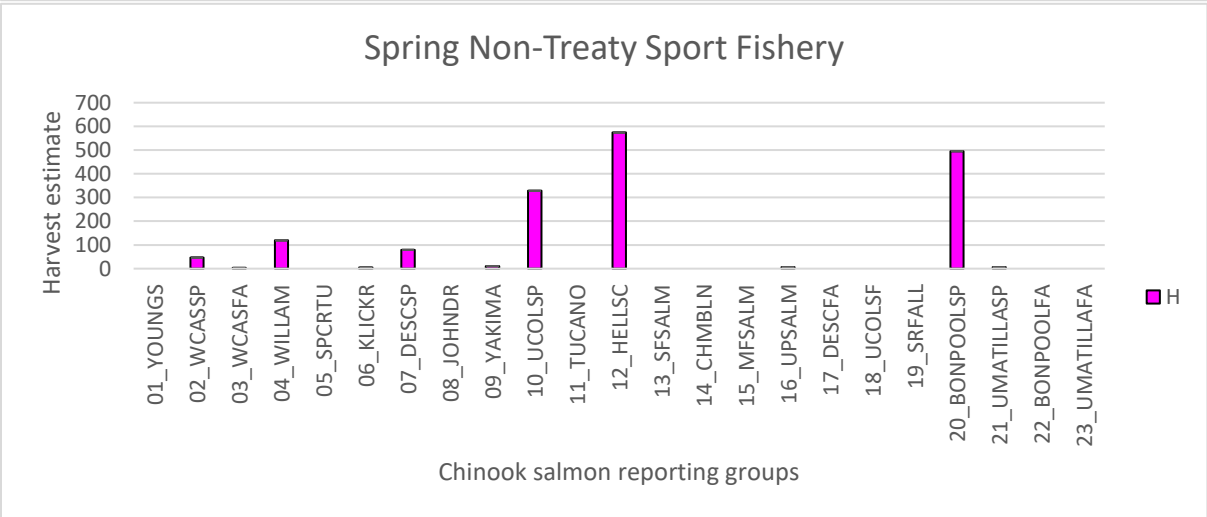
1237 *Comparison of stock composition of the clipped and unclipped Chinook salmon stocks among*
1238 *spring-management period Chinook salmon fisheries*

1239 The stock composition varied substantially across the fisheries that were executed in the
1240 spring period due to a number of factors related to location, timing, and gear type (Figure 26).
1241 For example, the test fishery uses drift nets and captures clipped and unclipped fish early in the
1242 spring period which resulted in high numbers of lower river stocks and low numbers of upper
1243 Columbia summer stocks. However, the pound net fishery operated late in the spring period and
1244 primarily caught upper Columbia summer stocks. The non-Treaty sport fishery was comprised
1245 only of clipped stocks but they were similar in composition to the clipped stocks caught in the
1246 Treaty ceremonial permit fishery. The sport fishery contained more of the lower river stocks
1247 (02_WCASSP and 04_WILLAM) as would be expected given the location of the fishing effort
1248 in region B (Table 5).
1249

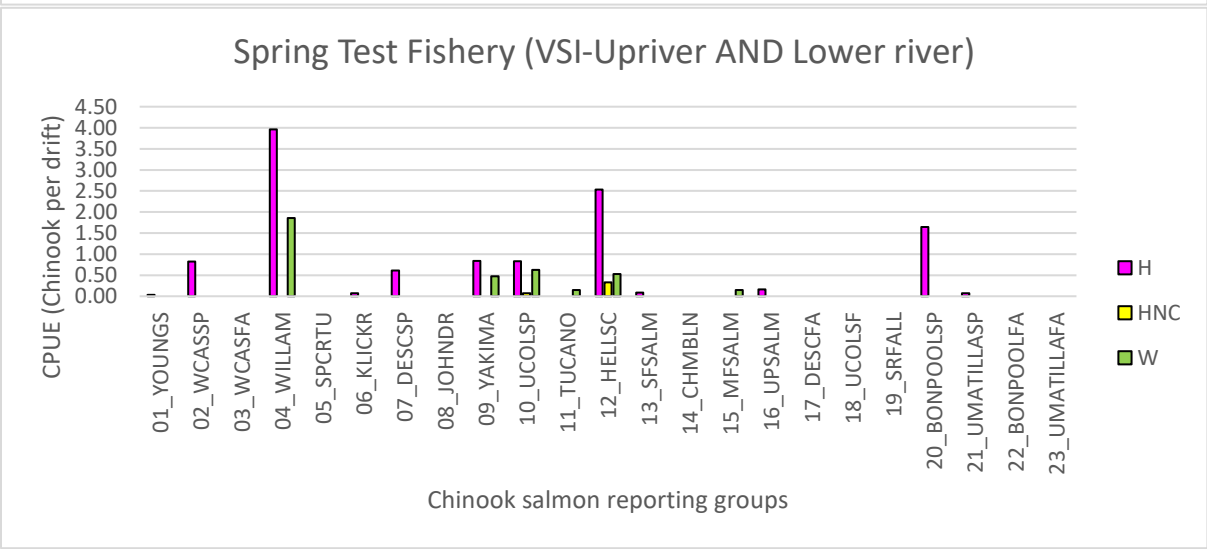
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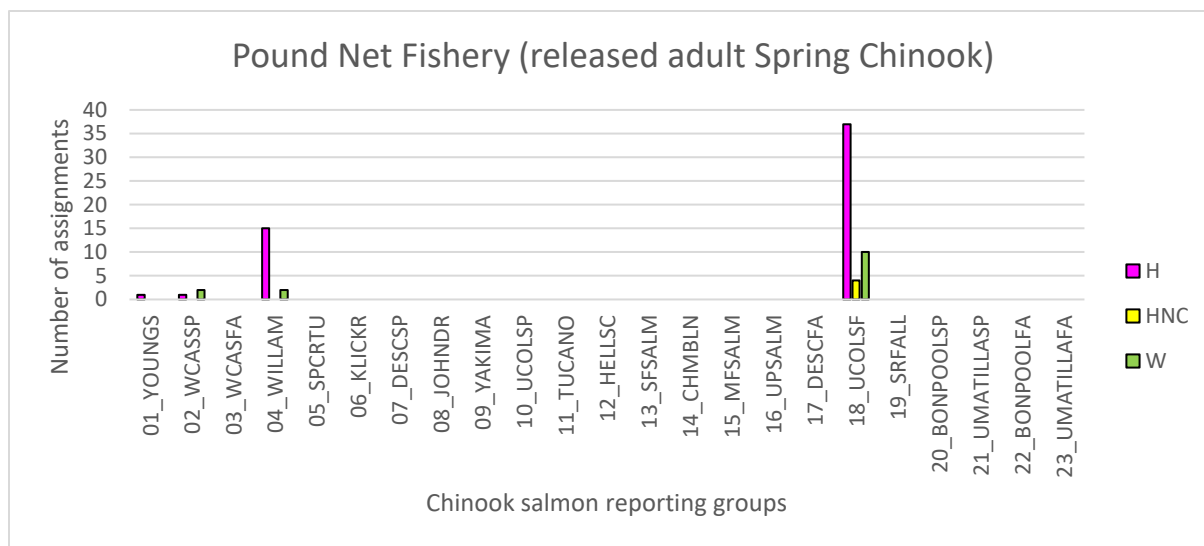


Figure 26. Stock composition of spring management period clipped and unclipped Chinook salmon harvest mixtures in 2019.

Comparison of stock composition of the summer-management period fisheries

Analysis of Chinook salmon fisheries in the summer management period (June 16 – August 1) can typically address 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. However, due to closure of the Non-Treaty sport and commercial fishery during the summer management period in 2019, we could not compare these harvests to the Treaty commercial harvest. We were however able to compare the Treaty commercial harvest (executed during two weekly openings) to the composition of stocks in the pound net fishery. The largest difference in the composition of these two fisheries is the presence of lower river stocks (04_WILLAM) in the pound net compared to the zone 6 fishery (Figure 27). There were small but detectable abundances of Snake River spring stocks Treaty summer fisheries which were likely not detected in the pound net due to low sample size.

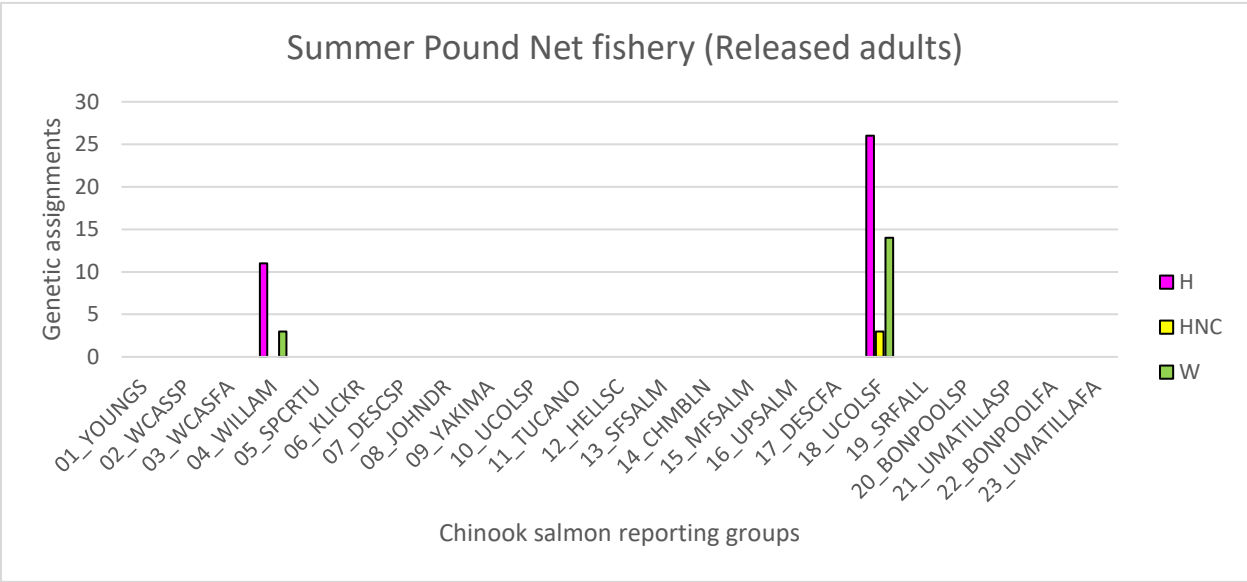
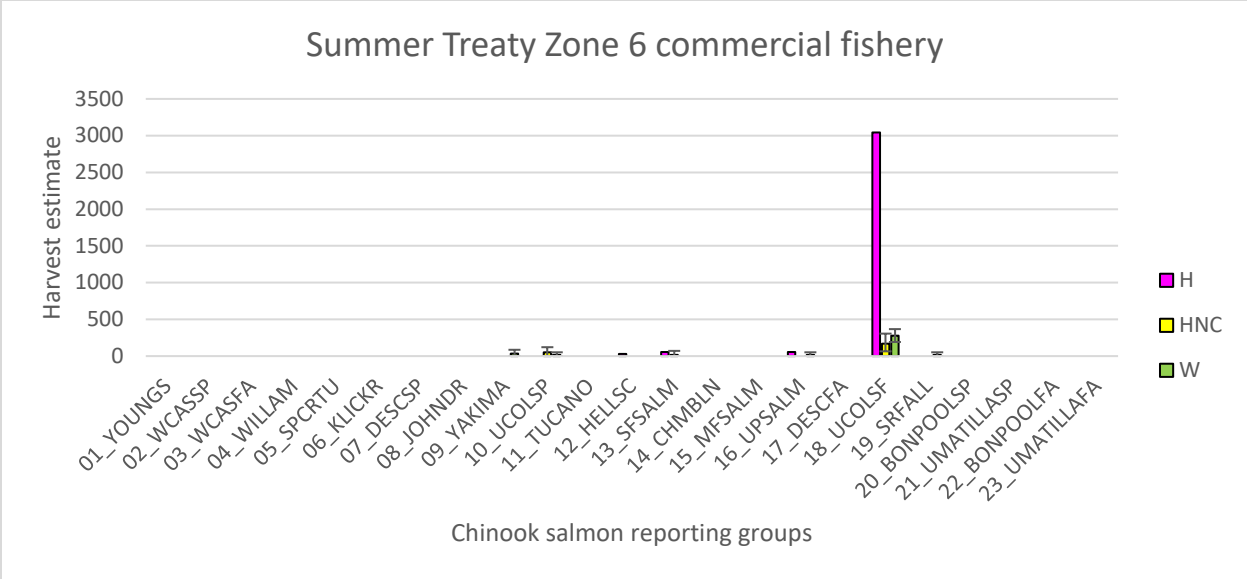


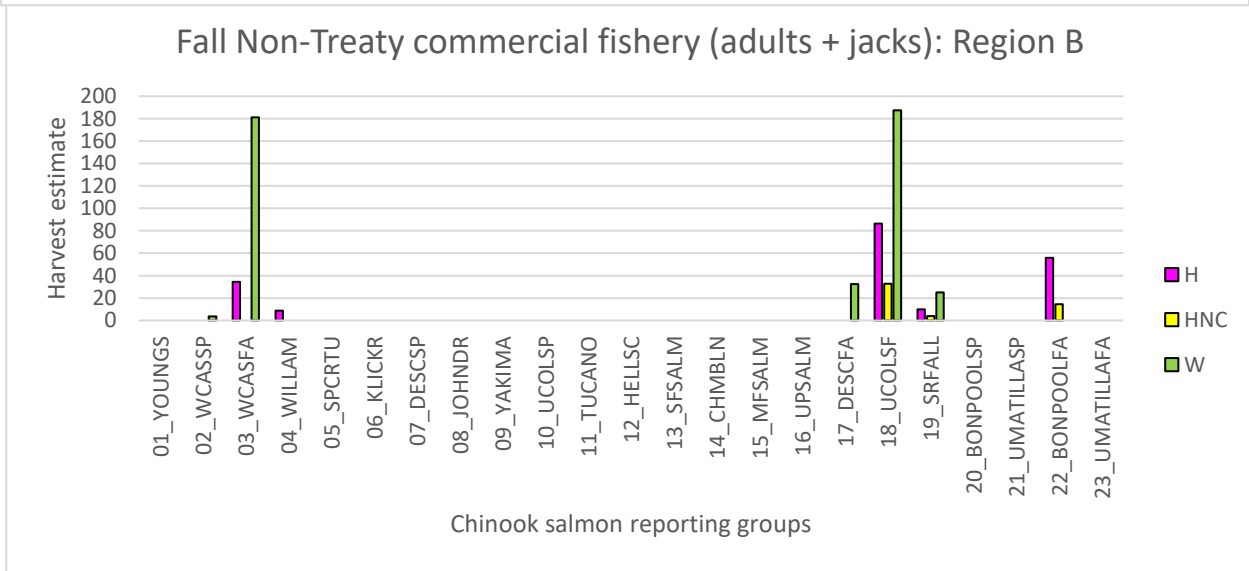
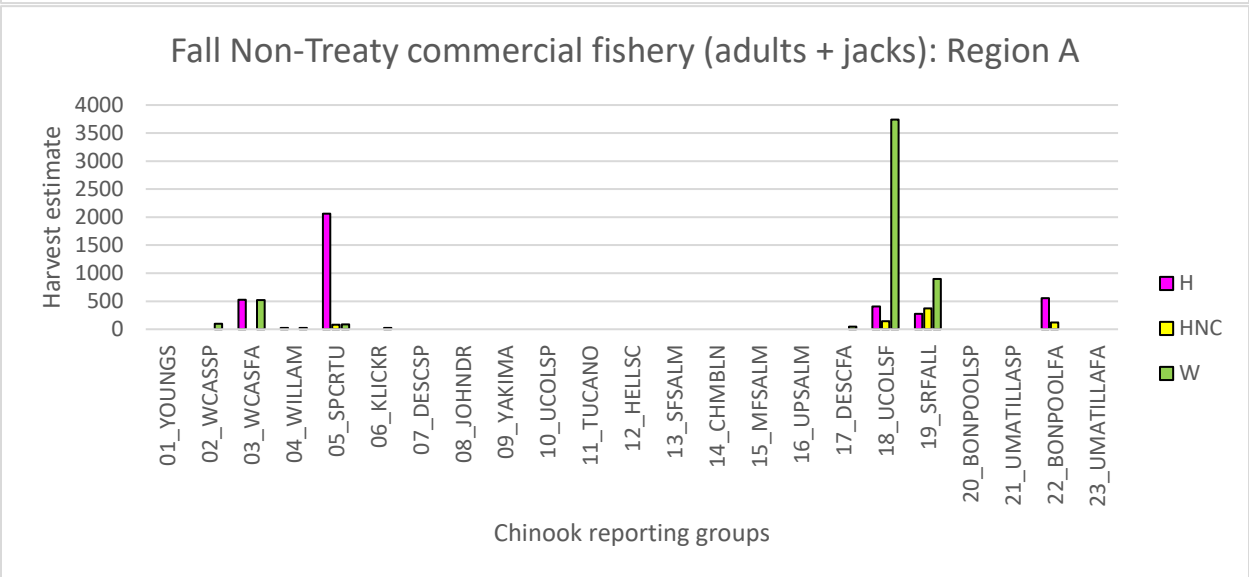
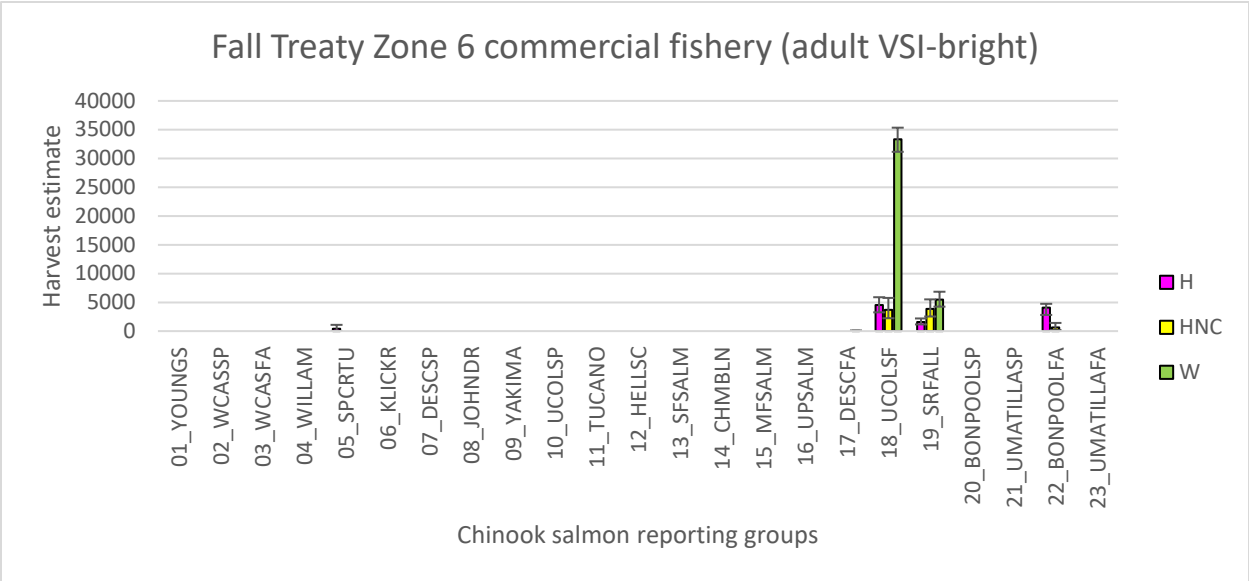
Figure 27. Genetic stock composition of the summer Chinook salmon fisheries analyzed in 2019.

Comparison of stock composition of the clipped and unclipped Chinook salmon stocks among the Treaty and Non-Treaty fall-management period fisheries

The two stocks that distinguished the composition of the Treaty and Non-Treaty commercial fall fisheries were the “tule” (05_SPCRTU) and West Cascade (03_WCASFA) stocks (Figure 28). There were very low numbers of this stock present in the Treaty Zone 6 fishery due to the way that it was sampled; monitors visually assessed fish as belonging to either “tule” or “bright” category and only DNA sampled the “bright” stock. As such, the Treaty harvest composition can only be used to assess the relative abundance of stocks within the VSI-bright group of fish. The “bright” stocks (ignoring abundance of 05_SPCRTU and

03_WCASFA) were nearly identical between the Zone 6 Treaty and Region A Non-Treaty commercial harvests (Figure 28). However, the two Non-Treaty commercial harvests from regions A and B were distinguished most notably by the larger presence of West Cascade (03_WCASFA) stock in the region B harvest.

The pound net fishery was most similar to the region B Non-Treaty commercial fishery because both were executed in similar locations (Figure 29). The two Non-Treaty sport fisheries executed below and above Bonneville Dam were most clearly distinguished by the higher abundance of the 22_BONPOOLFA stock (Little White Salmon Hatchery assigned by PBT) in the harvest above the dam in the Bonneville Pool. We continue to find that despite both the Non-Treaty sport (above Bonneville, Figure 29) and commercial fishery (region A, Figure 28) being executed at similar times near Bonneville Dam, the sport fishery is comprised of dramatically lower abundance of “tules”. This difference may be largely due to sport fishers preferentially keeping the VSI bright fish over the tule fish.



1303 **Figure 28. Genetic stock composition of the fall Treaty and Non-Treaty Chinook salmon**
1304 **commercial fisheries analyzed in 2019.**
1305

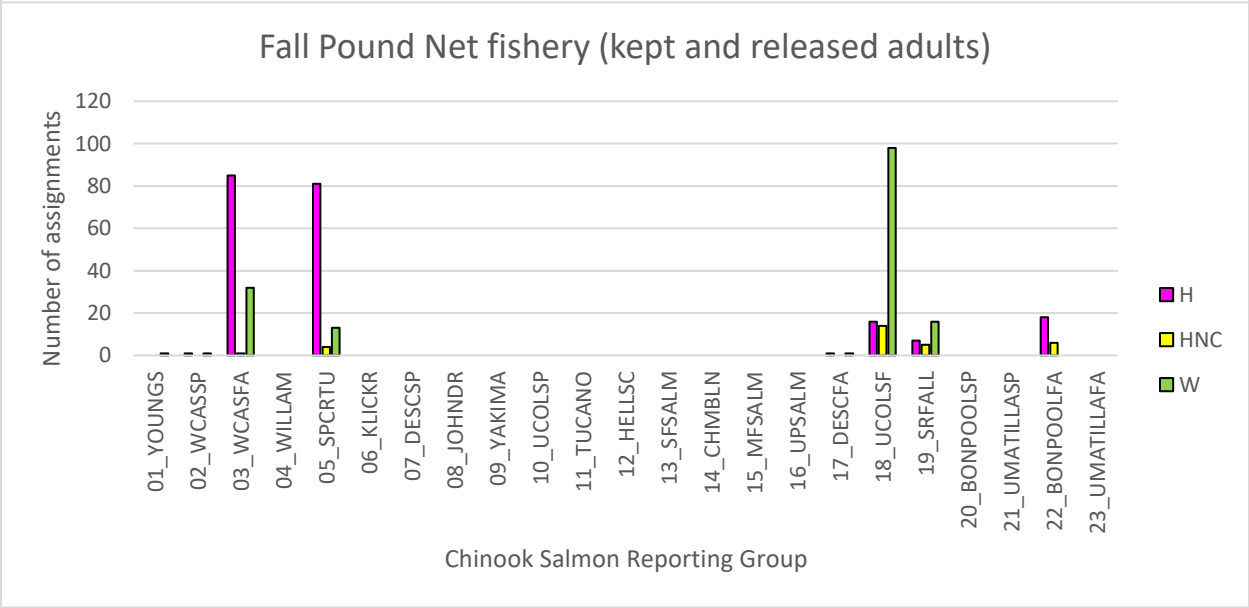
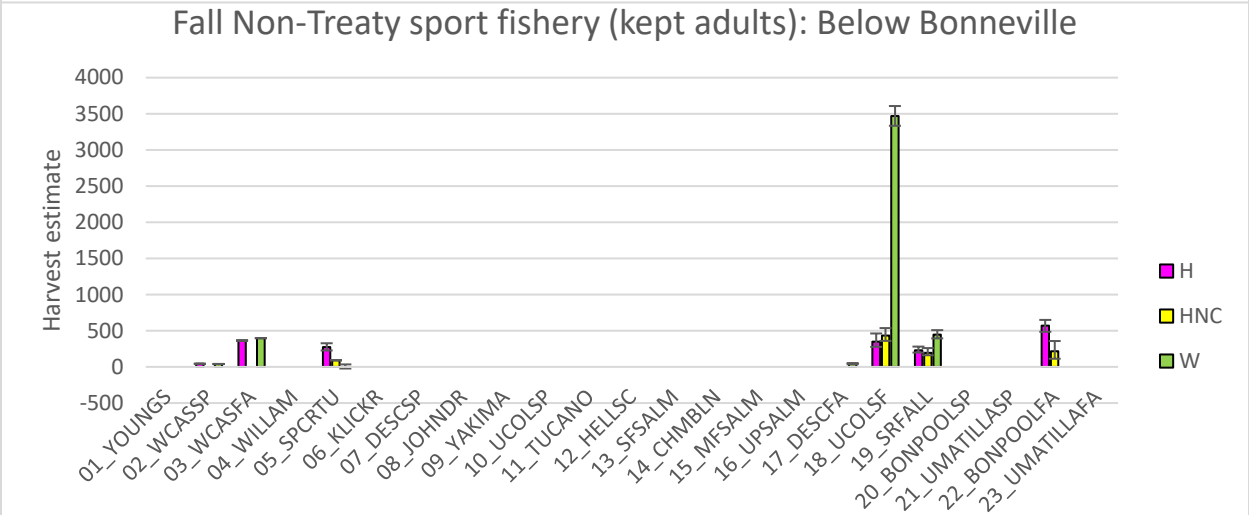
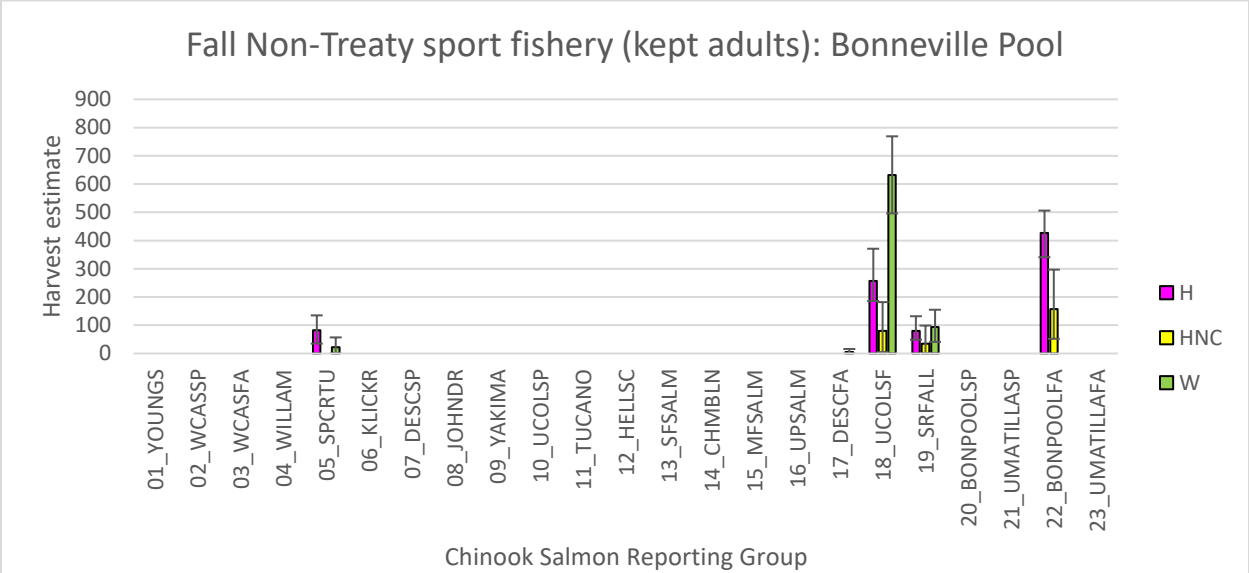


Figure 29. Genetic stock composition of the Non-Treaty Chinook salmon sport fisheries and Pound Net fishery analyzed in 2019.

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 seventh year in which we were able to assign all three major age classes of spring Chinook from Snake River hatcheries and the third 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 has now allowed the ability to assign all yearling hatchery jacks and subyearling 5-year-olds originating above Bonneville Dam (complete spawn years date back to 2015), and so future years of analyses will contain all major year classes. 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 expect there will be benefits 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. An expanded panel of 254 SNP loci was utilized in this report because of its optimal information content across the three major genetic lineages of Chinook Salmon found in the Columbia River Basin and now most broodstocks have complete genotypes. This report is the seventh year of genetic analysis on sockeye salmon harvest. We have been able to utilize a PBT baseline that can identify offspring of parents from the Yakima River reintroduction. Our efforts this year included adding new genotypes of candidate parents to this sockeye PBT baseline such that the baseline now extends back to SY2012 which was the first transfer of 10,000 fish to the Yakima River basin. In the future we can utilize this baseline to analyze prior years to identify the offspring of this reintroduced Yakima River stock. 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 PBT and GSI on sockeye salmon harvest in the future to gain further insight into these patterns. The steelhead PBT baseline also is likely to reap benefits of improved power by expanding the SNP marker panel to 335 SNPs. The 2020 run year will be the first year in which both 1-ocean and 2-ocean steelhead can be assigned using the 335 SNP PBT panel and we will continue to use this panel in the future.

We continued a significant achievement initiated in last year's report which is our ability to expand estimated genetic stock proportions by the reported catch estimates for each fishery. This improvement required tailoring each analysis to the way in which catch is stratified and reported. Our analyses take advantage of new methods (SCOBIDEUX and SPIBETR programs, Delomas and Hess 2020) that are now available to perform tag rate expansions and balance those expansions by proportionally decreasing other stocks in the natural-origin category.

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

1351 **1) Harvest RM&E: F&W Program Management Question: What are your in-river**
1352 **monitoring results and what are your estimates of stock composition and stock-**
1353 **specific abundance, escapement, catch, and age distribution?**
1354

1355 The in-river estimates of stock composition, stock-specific abundance, escapement,
1356 catch, and age distribution were addressed for part of the treaty mainstem spring-management
1357 period fisheries Chinook salmon harvests below Bonneville Dam, the spring-management test
1358 fishery, the non-treaty spring-management sport fishery, the treaty summer-management
1359 fisheries, the non-treaty and treaty mainstem fall-management fisheries, and the pound net
1360 fishery in the Cathlamet Channel. For the spring management period of Chinook salmon, we
1361 continue to observe a spatial pattern for the stock composition of lower Columbia River stocks
1362 which appear more abundant downstream from the Willamette River mouth as compared to
1363 upstream of this point which is consistent with a long history of CWT data. We observed
1364 differences in the composition of hatchery stocks represented in spring vs. summer management
1365 period harvest of Chinook salmon, and run-timing plays an important role in this difference (i.e.,
1366 late-running stocks appear more abundant among the upriver spring-type lineage that are caught
1367 in the summer management period). This pattern is consistent when compared to known origin
1368 PIT tagged adult and jack fish tagged as juveniles. Known origin adult age upriver spring and
1369 Snake River spring Chinook salmon are almost all past Bonneville by June 15 in most years.

1370 The sockeye salmon tribal fishery is managed in a way that attempts to harvest as many
1371 harvestable sockeye salmon as possible under the allowed harvest rate schedule in the U.S. v.
1372 Oregon Management Agreement. This 2019 year of analysis of the sockeye salmon harvest will
1373 be covered in a future report. We have typically found that there may be some over
1374 representation of the Wenatchee sockeye stocks in the Zone 6 harvest as compared to the stock
1375 proportions that are present at Bonneville Dam. The results for Snake River sockeye salmon are
1376 dependent upon representative sampling at Bonneville Dam, but low sample rate and the rarity of
1377 this stock leads to uncertainty and high variation around estimates of Snake River sockeye
1378 salmon from Bonneville Dam. Sampling protocols at Bonneville Dam may have higher
1379 representation of young fish as compared to harvest mixtures. Timing of the fishery may also
1380 influence the proportion of each stock, as has been shown by characterizing run-timing
1381 distributions in previous reports; the Wenatchee stock has relatively early run-timing but the
1382 timing of the Snake River stock is uncertain due to inconsistent results between PIT-tag and GSI
1383 methods. Future analysis will be needed to examine these patterns for consistency and delve into
1384 explanations. Importantly, the Yakima River reintroduction of sockeye can have a measurable
1385 (albeit small) impact on the Treaty fishery in zone 6 and will be possible to evaluate in future
1386 years.
1387

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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 2019. 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 2020 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 2020, 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 43 for the number and timing of reports for each species and run that were delivered in-season and post-season in 2019).

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, Steele et al. 2019), 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 7th 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 5th year in which these can be assigned to some Columbia River hatcheries. This is the second year that Sockeye salmon from the Yakima River reintroduction can be assigned to candidate parents, allowing this stock to be identified in fisheries and at Bonneville Dam. This study integrates PBT and GSI results to provide the greatest amount of stock-specific information available for hatchery- and natural-origin steelhead, Sockeye 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 February 2021 features the final analyses of 2019, as well as the preliminary in-season and post-season analyses of 2020.

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 43. The in-season and post-season report timing and scope of the 2020 fish runs.

Species	Management Period	Data coverage	Samples Arrive	Analysis begins	Report distributed
Chinook	Spring	01/01/2020 – 05/01/2020	5/4/2020	5/7/2020	5/11/2020
		01/01/2020 – 05/15/2020	5/18/2020	5/21/2020	5/26/2020
		01/01/2020 – 05/29/2020	6/1/2020	6/4/2020	6/8/2020
		01/01/2020 – 06/15/2020	6/16/2020	6/22/2020	6/24/2020
	Summer	06/16/2020 – 07/03/2020	7/6/2020	7/9/2020	7/13/2020
		06/16/2020 – 07/31/2020	8/3/2020	8/6/2020	8/10/2020
	Fall	08/01/2020 – 8/28/2020	8/31/2020	9/3/2020	9/8/2020
		08/01/2020 – 10/30/2020	11/2/2020	11/5/2020	11/9/2020
Steelhead	Skamania	04/01/2020 – 06/30/2020	7/6/2020	7/9/2020	7/13/2020
	Summer A-/B-Index	07/01/2020 – 07/31/2020	8/3/2020	8/6/2020	8/10/2020
		07/01/2020 – 08/28/2020	8/31/2020	9/3/2020	9/8/2020
		07/01/2020 – 10/30/2020	11/2/2020	11/5/2020	11/9/2020
Sockeye	Total	01/01/2020 – 07/31/2020	8/3/2020	8/6/2020	8/10/2020

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 U.S. v OR TAC members Stuart Ellis and Kate Self for distribution to TAC members.

Methods

Sample Collection

Tissue samples were obtained from adult steelhead (n=814), Chinook (n=3,622) and sockeye salmon (n=971) adults in 2019 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 17 (04/25/19) and was completed on 10/18/19 (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 0.9% of the total Spring management period (i.e., January 1-June 15) adult Chinook salmon count had passed Bonneville prior to the statistical week in which sampling was initiated by April 21 (week 17). In previous years, 2.0–2.5% of the total Spring management period adult Chinook salmon count has passed Bonneville by this sampling start date. However, the adult migration run was more average timed at Bonneville Dam in the spring of 2019 (Figure 30) and 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 spring Chinook run in 2019 for the spring and summer management periods was 2.2%, whereas the average sample rate for adult fall Chinook was 0.6% (Table 44).

Based on numbers of fish collected, samples were pooled into weekly strata for Chinook (Table 44), multi-week strata for steelhead (Table 45), or a combination thereof for sockeye salmon (Table 46) 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, Sockeye and Chinook salmon are provided in Section 1.

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 Chinook salmon, Sockeye salmon, and steelhead samples. Individuals were assigned using a ‘best estimate’ approach [Assigning individual samples using Individual Assignment \(IA\) genetic methods v1.0](#) (ID: 1334) (Published). ONCOR assignments were used to estimate stock composition of Bonneville Dam mixture strata for all three species. Additional detail regarding the specific application to Bonneville Dam are published in Hess et al. (2013, 2016).

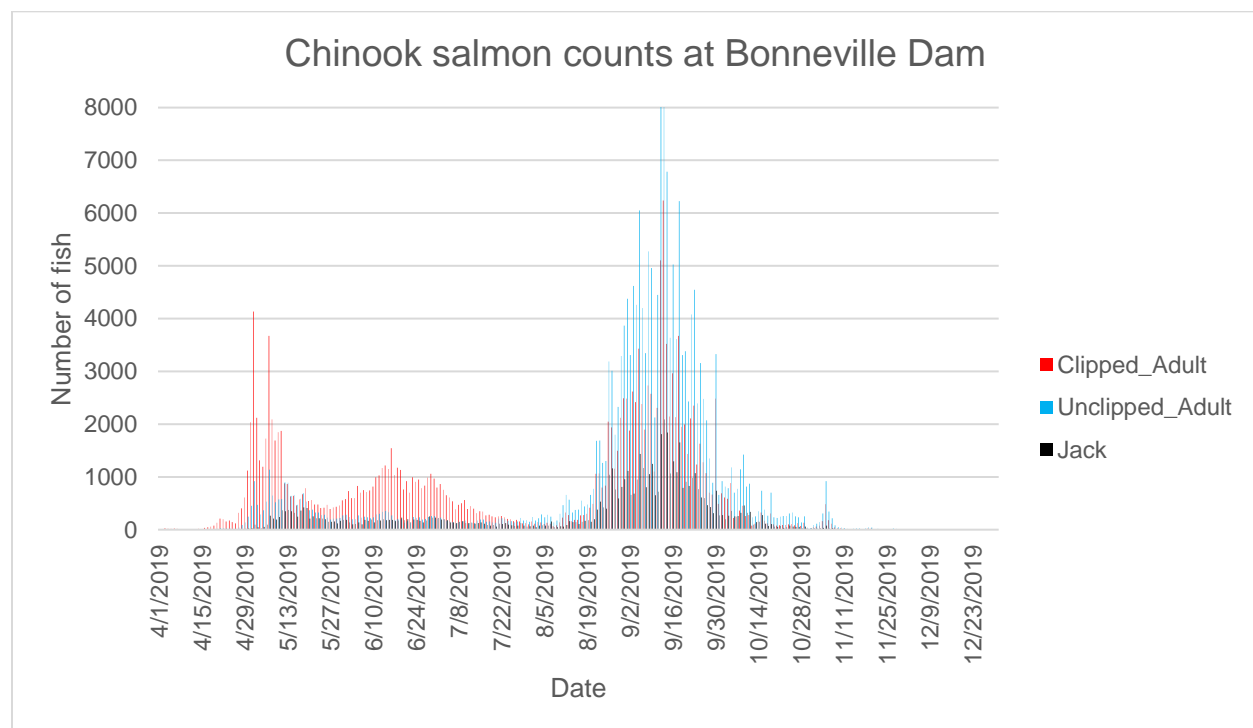


Figure 30. Daily passage of Chinook salmon (Clipped adults=red, Unclipped adult=blue, and jacks=black) at Bonneville Dam in 2019 (source: <https://www.fpc.org>; US v OR TAC).

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Table 44. Sample numbers by weekly strata for Chinook salmon that were DNA sampled or tallied for abundance at Bonneville Dam in 2019.

		Statistical week	TAC		Sample (N)							
			clip count	unclip count	Clipped		Non-clipped		Subtotal		Rate	
					GSI	PBT	GSI	PBT	clip	unclip	clip	unclip
Management period	Spring	1-17	1,867	228	1	10	1	4	11	5	0.59%	2.19%
		18	11,741	2,606	21	238	36	23	259	59	2.21%	2.26%
		19	14,090	4,357	11	214	56	19	225	75	1.60%	1.72%
		20	4,715	4,822	16	128	38	23	144	61	3.05%	1.27%
		21	3,671	2,485	16	121	50	22	137	72	3.73%	2.90%
		22	3,316	1,621	10	68	31	13	78	44	2.35%	2.71%
		23	4,922	1,618	19	77	29	9	96	38	1.95%	2.35%
		24	7,111	2,065	8	108	34	9	116	43	1.63%	2.08%
	Summer	25	7,278	1,276	14	71	18	4	85	22	1.17%	1.72%
		26	6,502	1,590	8	75	17	6	83	23	1.28%	1.45%
		27	5,193	1,374	5	42	24	2	47	26	0.91%	1.89%
		28	3,150	972	5	74	34	5	79	39	2.51%	4.01%
		29	2,044	1128	2	47	26	1	49	27	2.40%	2.39%
		30	1,495	1245	2	26	19	3	28	22	1.87%	1.77%
		31	501	724	1	16	22	1	17	23	3.39%	3.18%
	Fall	31-34	7,228	12,609	4	44	84	26	48	110	0.66%	0.87%
		35	12,083	18,788	3	27	62	19	30	81	0.25%	0.43%
		36	17,106	30,167	7	40	62	17	47	79	0.27%	0.26%
		37	23,583	45,451	38	95	109	39	133	148	0.56%	0.33%
		38	16,304	27,628	20	77	182	42	97	224	0.59%	0.81%
		39	10,371	20,080	14	64	176	49	78	225	0.75%	1.12%
		40	6,403	8,569	1	13	32	9	14	41	0.22%	0.48%
		41-53	5,580	14,116	3	38	161	32	41	193	0.73%	1.37%

		Total	176,254	205,519	229	1,713	1,303	377	1,942	1,680	1.10%	0.82%
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1649 Note: Statistical weeks 1–17 are 1/1/19 – 4/27/19 and 41–53 is 10/6/19–12/31/19. ‘TAC count’ is based on the estimates of clip and unclipped adult
1650 Chinook salmon provided by US v OR Technical Advisory Committee using data from the Fish Passage Center (<http://www.fpc.org>) observed by the
1651 Corps of Engineers at their fish counting window. The sum for each of the clipped and unclipped samples in a given week was used to calculate
1652 sample rate. The management periods approximate the date ranges from January 1st to June 15th (Spring management period), June 16th to July 31st
1653 (Summer management period), and August 1st to December 31 (Fall management period) which are used to categorize spring-, summer-, and fall-run
1654 Chinook salmon, respectively. The number of sampled fish that were assigned via PBT or GSI are shown.

1655 **Table 45. Sample numbers by monthly strata for steelhead that were DNA sampled or tallied for abundance at Bonneville**
1656 **Dam in 2019.**

				Sample (N)											
				A-Index				B-Index				Clipped		Non-clipped	
		Clipped	Non-Clipped	Clipped		Non-clipped		Clipped		Non-clipped		Clipped	Non-clipped	Sample	Sample
Strata		count	count	GSI	PBT	GSI	PBT	GSI	PBT	GSI	PBT	Total	Total	rate	rate
Skamania	14-26	1,495	1,639	1	13	13	0	0	0	1	0	14	14	0.94%	0.85%
A-/B-Index	27-29	4,810	7,764	9	32	62	0	0	0	3	0	41	65	0.85%	0.84%
	30-32	9,761	12,785	5	44	62	0	0	0	0	0	112	131	1.15%	1.02%
	33-34	7,063	5,962	9	54	67	1	0	0	1	0	47	32	0.67%	0.54%
	35-37	6,898	4,001	9	55	33	5	0	4	1	2	68	28	0.99%	0.70%
	38-39	4,529	1,961	3	38	16	5	0	27	5	3	64	36	1.41%	1.84%
	40-41	3,074	1,431	2	55	17	14	1	51	6	16				
	42-44	1,586	841	1	32	11	7	0	12	2	4	111	51	7.00%	6.06%
Summer A-/B-Index subtotal		37,721	34,745	38	310	268	32	1	94	18	25	443	343	1.17%	0.99%
Total		39,216	36,384	39	323	281	32	1	94	19	25	457	357	1.17%	0.98%

1657 Note: Statistical week 14-26 is 4/1/19–6/30/19 (Skamania Management Period) and 27-29 begins the A-/B-Index Period that runs
1658 from 7/1/2019-10/31/2019. ‘Fish count’ is based on tallies of adipose-clipped and unclipped adult steelhead provided by the Fish
1659 Passage Center (<http://www.fpc.org>) observed by the Corps of Engineers at their fish counting window. The total sum of all samples
1660 for each clipped and unclipped category obtained in a given stratum was used to calculate sample rate. The clipped and unclipped
1661 sample numbers were grouped by size (A-Index < 780 mm fork length; B-Index ≥780 mm fork length) and further split according to
1662 the number of samples that were either assigned via PBT or GSI.

1663 **Table 46. Sample numbers for genetic stock assignments of sockeye salmon that passed**
 1664 **Bonneville Dam in 2019.**

Statistical week	Bonneville dam fish window count	Genetic stock					Total	Sample	
									rate (%)
		OK A	WE N	RE D	LB C	Yakima			
22	39								1.7%
23	552	14	1					15	
24	4188	61	5					66	
25	14951	116	23					139	0.9%
26	22132	241	43			1		285	1.3%
27	12990	186	22					208	1.6%
28	5141	132	11		2			145	2.8%
29	1932	60	3		1	1		65	3.4%
30	732	19	5		4			28	3.8%
31	223	14	3		3			20	5.1%
32	96								
33	39								
34	11								
35	18								
36	2								
Total	63046	843	116	0	10	2		971	1.5%

1665 Note: Statistical week 22 begins on 5/26/19 and 36 ends 9/7/19; there were no sockeye counted
 1666 before or after these dates. ‘Fish count’ is based on tallies of sockeye salmon adults provided by
 1667 the Fish Passage Center (<http://www.fpc.org>) observed by the Corps of Engineers at their fish
 1668 counting window. GSI stocks are Okanagan (OKA), Wenatchee (WEN), Snake River (RED),
 1669 and Lake Billy Chinook (LBC) and PBT can identify fish from the Yakima reintroduction. The
 1670 number of samples for a given statistical week or pooled stratum was used to calculate sample
 1671 rate. Relatively few sockeye salmon were sampled from the RED, LBC, and Yakima stocks, and
 1672 limits inference regarding run-timing and abundance of these stocks.
 1673

1674 **Results**

1675 *Estimated relative abundance of Chinook salmon stocks in 2019*

1676 In previous years the 10_UCOLSP reporting group included Carson Hatchery for
 1677 estimates of relative abundance due to genetic similarity in GSI assignments, so the abundance
 1678 estimates for this reporting group did not represent actual returns specifically to the upper
 1679 Columbia River. Beginning in 2017, we have categorized several hatcheries as their own
 1680 reporting groups to alleviate this issue and so that a more accurate assessment of the number of
 1681 Chinook returning to the upper Columbia River can be determined. To that end, we have

1682 included the following reporting groups that are comprised of collections from our PBT baseline.
1683 The 20_BONPOOLSP reporting group includes spring Chinook from Caron Hatchery and Little
1684 White Salmon Hatchery. The 21_UMATILLASP reporting group includes spring Chinook from
1685 the Umatilla Hatchery. The 22_BONPOOLFA reporting group includes fall Chinook from the
1686 Little White Salmon Hatchery. The 22_UMATILLAFA reporting group includes fall Chinook
1687 from the Umatilla Hatchery.

There were 10 major (i.e., abundance >1000 fish) clipped hatchery origin Chinook salmon stocks represented in the total estimated abundance (N=176,254) of clipped hatchery Chinook salmon passing Bonneville Dam in 2019 (Table 47; Figure 31). These stocks in order of decreasing magnitude were 18_UCOLSF (58,630), 22_BONPOOLFA (38,513), 05_SPCRTU (28,244), 12_HELLSC (19,212), 19_SRFALL (10,535), 20_BONPOOLSP (6,781), 10_UCOLSP (5,510), 13_SFSALM (2,328), 16_UPSALM (1,815), and 07_DESCSP (1,704) (Table 47).

In Table 48, 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_UMATILLFAFA 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.

With the exception of reporting groups 20_BONPOOLSP, 21_UMATILLASP, 22_BONPOOLFA, and 23_UMATILLFAFA), which only include abundance from PBT assignments, the other reporting group abundance estimates include abundance estimated from 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 47). Further, using PBT assignments we can now provide abundance and run-timing estimates for particular hatchery broodstocks (**Table 48**) which will allow for much improved abundance estimates (**Figure 31**). In 2019, there were 64 different broodstocks of clipped hatchery-origin fish with abundances greater than 0 and 31 of them had abundance estimates >1000 fish (**Table 48**). The top five major clipped hatchery broodstocks were from Little White Salmon, Spring Creek, and Priest Rapids hatcheries which were all fall run. The largest spring run clipped broodstock was represented by Rapid River Hatchery (SY2015, 8,414 fish).

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Table 47. Stock-specific abundance and run-timing of clipped hatchery origin adult Chinook salmon passing Bonneville Dam in 2019.

Reporting Group	Sample N	Estimated abundance				Run-timing distribution						
		Total	Management Period			Ordinal day						
			Spring	Summer	Fall		1st	3rd	5th	95th	Median	
			Jan. 1-Jun. 15	Jun. 16-Jul. 31	Aug. 1-Dec. 1	Median	quartile	quartile	percentile	percentile	date	range (days)
01_YOUNGS						-	-	-	-	-	-	-
02_WCASSP	16	825	825			131	127	137	121	147	5/11/2019	10
03_WCASFA	4	991			991	252	234	256	220	257	9/9/2019	22
04_WILLAM	13	376	312	64		155	142	158	134.7	176	6/4/2019	16
05_SPCRTU	113	28,244			28,244	253	246	257	235	266	9/10/2019	11
06_KLICKR	2	124	124			131	128	156	126	159	5/11/2019	28
07_DESCSP	20	1,314	1,314			124	122	138	115	152	5/4/2019	16
08_JOHNDR						-	-	-	-	-	-	-
09_YAKIMA	15	775	775			130	127	135	121	142	5/10/2019	8
10_UCOLSP	118	5,510	5,510			127	122	134	118	146	5/7/2019	12
11_TUCANO						-	-	-	-	-	-	-
12_HELLSC	360	19,212	19,024	188		127	122	131	117	143	5/7/2019	9
13_SFSALM	46	2,328	2,054	274		148	139	156	127	178	5/28/2019	17
14_CHMBLN						-	-	-	-	-	-	-
15_MFSALM						-	-	-	-	-	-	-
16_UPSALM	36	1,815	1,724	91		139	130	148	124	167	5/19/2019	18
17_DESCFA						-	-	-	-	-	-	-
18_UCOLSF	602	58,630	12,709	25,261	20,660	185	168	247	154	276	7/4/2019	79
19_SRFALL	43	10,535		284	10,251	242	238	257	219.45	273	8/30/2019	19
20_BONPOOLSP	128	6,781	6,781			124	122	130	115	142	5/4/2019	8
21_UMATILLASP	5	281	281			129	127	132	125	137	5/9/2019	5
22_BONPOOLFA	167	38,513			38,513	257	250	267	239	284	9/14/2019	17
23_UMATILLAFA						-	-	-	-	-	-	-
Total	1,688	176,254	51,433	26,163	98,658							

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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.

Table 48. Hatchery broodstock-specific abundance and run-timing distributions of clipped adult Chinook salmon passing Bonneville Dam in 2019.

Run	GSI RepGrp	Hatchery	Brood stock	Sample N	Estimated abundance			Run-timing distribution							
					Total	Management Period			Ordinal day						Inter
						Spring	Summer	Fall		1st	3rd	5th	95th	Median	quartile
						Jan. 1 - Jun. 15	Jun. 16 - Jul. 31	Aug. 1 - Dec. 1	Median	quartile	quartile	%	%	date	range
01Spring	02_WCASSP	Parkdale Fish Facility	OtsPFF14_sp	1	70	70			128	127	130	125	131	5/8/2019	3
	02_WCASSP	Parkdale Fish Facility	OtsPFF15_sp	14	717	717			131	127	138	121	148	5/11/2019	11
	04_WILLAM	South Santiam Hatchery	OtsSSANT15_sp						-	-	-	-	-	-	-
	06_KLICKR	Klickitat Hatchery	OtsKH14_sp	1	66	66			128	127	130	125	131	5/8/2019	3
	07_DESCSP	Round Butte Fish Hatchery	OtsRB15_sp	8	450	450			130	125	136	120	157	5/10/2019	11
	07_DESCSP	Warm Springs National Fish Hatchery	OtsWSNFH15_sp	3	754	754			122	121	146	113	151	5/2/2019	25
	09_YAKIMA	Yakima River Roza Dam	OtsYR15int_sp	13	644	644			131	127	137	122	143	5/11/2019	10
	09_YAKIMA	Yakima River Roza Dam	OtsYR15seg_sp	2	131	131			126	122	128	117	131	5/6/2019	6
	10_UCOLSP	Chief Joseph Hatchery	OtsCJH15_sp	31	1,608	1,608			128	123	133	119	144	5/8/2019	10
	10_UCOLSP	Eastbank Fish Hatchery	OtsEASTBK14_sp						-	-	-	-	-	-	-
	10_UCOLSP	Eastbank Fish Hatchery	OtsEASTBK15_sp	5	243	243			136	131	145	126	158	5/16/2019	14
	10_UCOLSP	Eastbank Fish Hatchery	OtsEASTBK16_sp						-	-	-	-	-	-	-
	10_UCOLSP	Leavenworth National Fish Hatchery	OtsLNFH15_sp	29	1,765	1,765			126	122	131	117	147	5/6/2019	9
	10_UCOLSP	Methow Fish Hatchery	OtsMETH14_sp						-	-	-	-	-	-	-
	10_UCOLSP	Methow Fish Hatchery	OtsMETH15_sp						-	-	-	-	-	-	-
	10_UCOLSP	Winthrop National Fish Hatchery	OtsWTP15_sp	30	1,515	1,515			127	123	132	118	143	5/7/2019	9
	11_TUCANO	Lyons Ferry Fish Hatchery	OtsLYON15S_sp						-	-	-	-	-	-	-
	12_HELLSC	Clearwater Fish Hatchery	OtsCLWH14S_sp	6	297	297			124	122	131	116	144	5/4/2019	9
	12_HELLSC	Clearwater Fish Hatchery	OtsPOWP14S_sp	2	118	118			126	122	128	118	131	5/6/2019	6
	12_HELLSC	Clearwater Fish Hatchery	OtsCLWH15S_sp	51	2,800	2,800			127	123	130	118	141	5/7/2019	7
	12_HELLSC	Clearwater Fish Hatchery	OtsPOWP15S_sp	29	1,563	1,563			124	122	129	115	137	5/4/2019	7
	12_HELLSC	Clearwater Fish Hatchery	OtsPOWP16S_sp						-	-	-	-	-	-	-
	12_HELLSC	Dworshak National Fish Hatchery	OtsDWOR14S_sp	3	153	153			127	123	131	119	143	5/7/2019	8
	12_HELLSC	Dworshak National Fish Hatchery	OtsDWOR15S_sp	48	2,565	2,565			127	122	131	117	138	5/7/2019	9
	12_HELLSC	Lookingglass Fish Hatchery	OtsLOOK14S_sp	2	98	98			123	121	140	115	144	5/3/2019	19

	12_HELLSC	Lookingglass Fish Hatchery	OtsLOOK15S_sp	24	1,590	1,490	99		127	125	130	119	169	5/7/2019	5
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH14S_sp	9	490	490			122	121	126	113	130	5/2/2019	5
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH15S_sp	146	8,413	8,413			126	122	130	117	139	5/6/2019	8
	20_BONPOOLSP	Carson National Fish Hatchery	OtsCAR14_sp	4	236	236			125	122	130	117	137	5/5/2019	8
	20_BONPOOLSP	Carson National Fish Hatchery	OtsCAR15_sp	56	3,151	3,151			125	122	129	116	140	5/5/2019	7
	20_BONPOOLSP	Little White Salmon National Fish Hatchery	OtsLWS14_sp	8	422	422			123	121	128	115	141	5/3/2019	7
	20_BONPOOLSP	Little White Salmon National Fish Hatchery	OtsLWS15_sp	60	2,973	2,973			124	122	131	115	143	5/4/2019	9
	21_UMATILLASP	Umatilla Fish Hatchery	OtsUMA14_sp	1	66	66			128	127	130	125	131	5/8/2019	3
	21_UMATILLASP	Umatilla Fish Hatchery	OtsUMA15_sp	4	215	215			130	127	133	126	138	5/10/2019	6
02Spring/Summer	12_HELLSC	Lookingglass Fish Hatchery	OtsIMNW14S_spsu	2	77	77			138	134	141	132	144	5/18/2019	7
	12_HELLSC	Lookingglass Fish Hatchery	OtsIMNW15S_spsu	8	370	370			141	134	146	127	151	5/21/2019	12
	12_HELLSC	Lookingglass Fish Hatchery	OtsIMNW16S_spsu	2	150	61	89		182	157	187	153	193	7/1/2019	30
	13_SFSALM	McCall Fish Hatchery	OtsMCCA15S_spsu	42	2,099	2,006	93		147	139	154	127	165	5/27/2019	15
	13_SFSALM	McCall Fish Hatchery	OtsMCCA16S_spsu	2	181		181		180	173	186	167	192	6/29/2019	13
	16_UPSALM	Pahsimeroi Fish Hatchery	OtsPAHH14S_spsu	1	51	51			122	120	123	113	124	5/2/2019	3
	16_UPSALM	Pahsimeroi Fish Hatchery	OtsPAHH15S_spsu	12	600	600			145	135	152	127	165	5/25/2019	17
	16_UPSALM	Sawtooth Fish Hatchery	OtsSAWT14S_spsu	3	148	148			132	128	135	126	138	5/12/2019	7
	16_UPSALM	Sawtooth Fish Hatchery	OtsSAWT15S_spsu	20	1,016	925	91		138	128	147	125	172	5/18/2019	19
03Summer	18_UCOLSF	Chief Joseph Hatchery	OtsCJH13seg_su	2	170	68	102		168	157	174	153	179	6/17/2019	17
	18_UCOLSF	Chief Joseph Hatchery	OtsCJH14int_su	64	5,347	1,263	3,690	394	182	167	194	154	227	7/1/2019	27
	18_UCOLSF	Chief Joseph Hatchery	OtsCJH14seg_su	30	4,095	984	3,111		177	167	186	150	200	6/26/2019	19
	18_UCOLSF	Chief Joseph Hatchery	OtsCJH15int_su	33	3,334	501	2,046	788	182	170	206	160	235	7/1/2019	36
	18_UCOLSF	Chief Joseph Hatchery	OtsCJH15seg_su	25	1,890	470	1,421		181	167	195	160	207	6/30/2019	28
	18_UCOLSF	Chief Joseph Hatchery	OtsCJH16int_su	6	556		365	191	202	186	225	170	235	7/21/2019	39
	18_UCOLSF	Chief Joseph Hatchery	OtsCJH16seg_su	1	61		61		202	198	206	195	211	7/21/2019	8
	18_UCOLSF	Eastbank Fish Hatchery	OtsEASTBK13_su	2	156	68	89		181	164	187	161	193	6/30/2019	23
	18_UCOLSF	Eastbank Fish Hatchery	OtsEASTBK14_su	84	6,059	3,145	2,914		166	161	179	153	195	6/15/2019	18
	18_UCOLSF	Eastbank Fish Hatchery	OtsEASTBK15_su	61	5,316	737	3,715	864	179	169	201	161	240	6/28/2019	32
	18_UCOLSF	Entiat National Fish Hatchery	OtsENFH14_su	21	1,944	725	1,218		175	162	186	153	198	6/24/2019	24

	18_UCOLSF	Entiat National Fish Hatchery	OtsENFH15_su	37	3,733	939	2,794		172	166	179	153	198	6/21/2019	13
	18_UCOLSF	Wells Fish Hatchery	OtsWELLS14_su	64	4,483	2,504	1,979		165	158	176	148	189	6/14/2019	18
	18_UCOLSF	Wells Fish Hatchery	OtsWELLS15_su	34	2,536	850	1,685		170	163	178	147	191	6/19/2019	16
04Fall	03_WCASFA	Washougal Fish Hatchery	OtsWAS15_fa	1	386			386	232	225	235	215	236	8/20/2019	10
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR15_fa	4	1,083			1,083	252	248	255	244	257	9/9/2019	7
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR16_fa	31	11,674			11,674	255	249	259	245	270	9/12/2019	10
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR17_fa	30	12,199			12,199	248	241	255	228	263	9/5/2019	14
	18_UCOLSF	Priest Rapids Hatchery	OtsPRH14_fa						-	-	-	-	-	-	-
	18_UCOLSF	Priest Rapids Hatchery	OtsPRH15_fa	27	6,188			6,188	257	247	268	235	289	9/14/2019	21
	18_UCOLSF	Priest Rapids Hatchery	OtsPRH16_fa	39	8,936			8,936	259	247	270	239	302	9/16/2019	23
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON14S_1_fa	1	192			192	232	225	235	215	236	8/20/2019	10
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON15S_1_fa	19	4,433		223	4,210	243	238	257	212	264	8/31/2019	19
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON16S_1_fa	14	4,288			4,288	242	238	249	225	276	8/30/2019	11
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH15S_1_fa	3	574			574	235	229	259	217	263	8/23/2019	30
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH16S_1_fa	3	747		62	685	242	239	258	203	263	8/30/2019	19
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWS14_fa	4	835			835	255	253	256	251	257	9/12/2019	3
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWS15_fa	95	23,644			23,644	256	247	262	238	278	9/13/2019	15
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWS16_fa	68	14,034			14,034	265	255	273	245	295	9/22/2019	18
Unassigned				203	9,557	1,928	134	7,494							
Total				1,688	176,254	51,433	26,163	98,658							

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1729 There were 6 major (i.e., abundance >1000 fish) *unclipped* hatchery origin Chinook salmon stocks represented in the
1730 total estimated abundance (N=47,182) of unclipped hatchery Chinook salmon passing Bonneville Dam in 2019 (Table 49;
1731 Figure 31). These stocks in order of decreasing magnitude were 18_UCOLSF (17,228), 19_SRFALL (10,401),
1732 22_BONPOOLFA (8,284), 05_SPCRTU (5,012), 10_UCOLSP (2,272), and 12_HELLSC (1,672) (Table 49).
1733 In 2019, there were 46 different broodstocks of unclipped hatchery-origin fish with abundances greater than 0 and 11 of
1734 them had abundance estimates >1000 fish (Table 50). The top five major unclipped hatchery broodstocks were from Priest
1735 Rapids Hatchery, Little White Salmon, Lyons Ferry, and Spring Creek hatcheries which were all fall run. The largest spring
1736 run unclipped broodstock was represented by Winthrop Hatchery (SY2015, 952 fish).

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Table 49. Stock-specific abundance and run-timing of unclipped hatchery origin adult Chinook salmon passing Bonneville Dam in 2019.

Reporting Group	Sample N	Estimated abundance				Run-timing distribution						
		Total	Management Period			Ordinal day						
			Spring	Summer	Fall		1st	3rd	5th	95th	Median	Interquartile
			Jan. 1-Jun. 15	Jun. 16-Jul. 31	Aug. 1-Dec. 1	Median	quartile	quartile	percentile	percentile	date	range (days)
01_YOUNGS						-	-	-	-	-	-	-
02_WCASSP	1	43	43			142	140	143	139	145	5/22/2019	3
03_WCASFA						-	-	-	-	-	-	-
04_WILLAM	1	90		90		174	170	177	167	180	6/23/2019	7
05_SPCRTU	15	5,012			5,012	243	239	256	228	263	8/31/2019	17
06_KLICKR						-	-	-	-	-	-	-
07_DESCSP	2	109	109			131	127	156	126	159	5/11/2019	29
08_JOHNDR						-	-	-	-	-	-	-
09_YAKIMA	1	42	42			141	140	143	139	145	5/21/2019	3
10_UCOLSP	40	2,272	2,272			135	128	143	121	163	5/15/2019	15
11_TUCANO	2	268	268			124	122	141	119	145	43589	19
12_HELLSC	27	1,672	1,596	76		128	124	133	120	144	5/8/2019	9
13_SFSALM	14	799	799			141	135	150	129	164	5/21/2019	15
14_CHMBLN						-	-	-	-	-	-	-
15_MFSALM						-	-	-	-	-	-	-
16_UPSALM						-	-	-	-	-	-	-
17_DESCFA						-	-	-	-	-	-	-
18_UCOLSF	116	17,228	483	860	15,886	256	252	266	178	286	9/13/2019	14
19_SRFALL	44	10,401		61	10,340	248	241	255	225	264	9/5/2019	14
20_BONPOOLSP	4	184	184			122	121	123	116	124	5/2/2019	2
21_UMATILLASP	12	779	779			133	128	136	122	142	5/13/2019	8
22_BONPOOLFA	46	8,284			8,284	256	246	265	236	281	9/13/2019	19
23_UMATILLAFA						-	-	-	-	-	-	-
Total	325	47,182	6,573	1,086	39,523							

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Table 50. Hatchery broodstock-specific abundance and run-timing distributions of unclipped adult Chinook salmon passing Bonneville Dam in 2019.

Run	GSI RepGrp	Hatchery	Brood stock	Sample N	Estimated abundance			Run-timing distribution							
					Total	Management Period			Ordinal day						Inter
						Spring	Summer	Fall		1st	3rd	5th	95th	Median	quartile
						Jan. 1 - Jun. 15	Jun. 16 - Jul. 31	Aug. 1 - Dec. 1	Median	quartile	quartile	%	%	date	range
01Spring	02_WCASSP	Parkdale Fish Facility	OtsPFF14_sp						-	-	-	-	-	-	-
	02_WCASSP	Parkdale Fish Facility	OtsPFF15_sp	1	43	43			142	140	143	139	145	5/22/2019	3
	04_WILLAM	South Santiam Hatchery	OtsSSANT15_sp	1	90		90		174	170	177	167	180	6/23/2019	7
	06_KLICKR	Klickitat Hatchery	OtsKH14_sp						-	-	-	-	-	-	-
	07_DESCSP	Round Butte Fish Hatchery	OtsRB15_sp	2	109	109			131	127	156	126	159	5/11/2019	29
	07_DESCSP	Warm Springs National Fish Hatchery	OtsWSNFH15_sp						-	-	-	-	-	-	-
	09_YAKIMA	Yakima River Roza Dam	OtsYR15int_sp	1	42	42			141	140	143	139	145	5/21/2019	3
	09_YAKIMA	Yakima River Roza Dam	OtsYR15seg_sp						-	-	-	-	-	-	-
	10_UCOLSP	Chief Joseph Hatchery	OtsCJH15_sp	1	85	85			134	133	137	132	138	5/14/2019	4
	10_UCOLSP	Eastbank Fish Hatchery	OtsEASTBK14_sp	1	85	85			134	133	137	132	138	5/14/2019	4
	10_UCOLSP	Eastbank Fish Hatchery	OtsEASTBK15_sp	14	708	708			143	137	150	123	163	5/23/2019	13
	10_UCOLSP	Eastbank Fish Hatchery	OtsEASTBK16_sp	1	64	64			163	162	165	160	166	6/12/2019	3
	10_UCOLSP	Leavenworth National Fish Hatchery	OtsLNFH15_sp	1	53	53			122	121	123	118	124	5/2/2019	2
	10_UCOLSP	Methow Fish Hatchery	OtsMETH14_sp	1	46	46			122	121	123	119	124	5/2/2019	2
	10_UCOLSP	Methow Fish Hatchery	OtsMETH15_sp	5	281	281			126	122	132	119	137	5/6/2019	10
	10_UCOLSP	Winthrop National Fish Hatchery	OtsWTP15_sp	16	952	952			134	128	138	121	161	5/14/2019	10
	11_TUCANO	Lyons Ferry Fish Hatchery	OtsLYON15S_sp	2	268	268			124	122	141	119	145	5/4/2019	19
	12_HELLSC	Clearwater Fish Hatchery	OtsCLWH14S_sp						-	-	-	-	-	-	-
	12_HELLSC	Clearwater Fish Hatchery	OtsPOWP14S_sp						-	-	-	-	-	-	-
	12_HELLSC	Clearwater Fish Hatchery	OtsCLWH15S_sp	4	198	198			123	121	126	118	130	5/3/2019	5
	12_HELLSC	Clearwater Fish Hatchery	OtsPOWP15S_sp	10	588	588			127	123	130	120	136	5/7/2019	7
	12_HELLSC	Clearwater Fish Hatchery	OtsPOWP16S_sp	1	76		76		174	170	177	167	180	6/23/2019	7
	12_HELLSC	Dworshak National Fish Hatchery	OtsDWOR14S_sp						-	-	-	-	-	-	-
	12_HELLSC	Dworshak National Fish Hatchery	OtsDWOR15S_sp	3	153	153			123	122	127	118	131	5/3/2019	5
	12_HELLSC	Lookingglass Fish Hatchery	OtsLOOK14S_sp						-	-	-	-	-	-	-
	12_HELLSC	Lookingglass Fish Hatchery	OtsLOOK15S_sp	4	302	302			133	127	135	121	138	5/13/2019	8
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH14S_sp						-	-	-	-	-	-	-

	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH15S_sp	4	311	311			132	128	135	126	138	5/12/2019	7
	20_BONPOOLSP	Carson National Fish Hatchery	OtsCAR14_sp						-	-	-	-	-	-	-
	20_BONPOOLSP	Carson National Fish Hatchery	OtsCAR15_sp	3	139	139			122	121	123	117	124	5/2/2019	2
	20_BONPOOLSP	Little White Salmon National Fish Hatchery	OtsLWS14_sp						-	-	-	-	-	-	-
	20_BONPOOLSP	Little White Salmon National Fish Hatchery	OtsLWS15_sp	1	45	45			122	121	123	119	124	5/2/2019	2
	21_UMATILLASP	Umatilla Fish Hatchery	OtsUMA14_sp						-	-	-	-	-	-	-
	21_UMATILLASP	Umatilla Fish Hatchery	OtsUMA15_sp	12	779	779			133	128	136	122	142	5/13/2019	8
02Spring/Summer	12_HELLSC	Lookingglass Fish Hatchery	OtsIMNW14S_spsu						-	-	-	-	-	-	-
	12_HELLSC	Lookingglass Fish Hatchery	OtsIMNW15S_spsu	1	44	44			142	140	143	139	145	5/22/2019	3
	12_HELLSC	Lookingglass Fish Hatchery	OtsIMNW16S_spsu						-	-	-	-	-	-	-
	13_SFSALM	McCall Fish Hatchery	OtsMCCA15S_spsu	14	799	799			141	135	150	129	164	5/21/2019	15
	13_SFSALM	McCall Fish Hatchery	OtsMCCA16S_spsu						-	-	-	-	-	-	-
	16_UPSALM	Pahsimeroi Fish Hatchery	OtsPAHH14S_spsu						-	-	-	-	-	-	-
	16_UPSALM	Pahsimeroi Fish Hatchery	OtsPAHH15S_spsu						-	-	-	-	-	-	-
	16_UPSALM	Sawtooth Fish Hatchery	OtsSAWT14S_spsu						-	-	-	-	-	-	-
	16_UPSALM	Sawtooth Fish Hatchery	OtsSAWT15S_spsu						-	-	-	-	-	-	-
03Summer	18_UCOLSF	Chief Joseph Hatchery	OtsCJH13seg_su						-	-	-	-	-	-	-
	18_UCOLSF	Chief Joseph Hatchery	OtsCJH14int_su	3	203	64	139		174	165	198	161	209	6/23/2019	33
	18_UCOLSF	Chief Joseph Hatchery	OtsCJH14seg_su						-	-	-	-	-	-	-
	18_UCOLSF	Chief Joseph Hatchery	OtsCJH15int_su	3	188	53	134		174	159	181	154	191	6/23/2019	22
	18_UCOLSF	Chief Joseph Hatchery	OtsCJH15seg_su	3	217	60	157		171	166	176	161	180	6/20/2019	10
	18_UCOLSF	Chief Joseph Hatchery	OtsCJH16int_su	1	76		76		174	170	177	167	180	6/23/2019	7
	18_UCOLSF	Chief Joseph Hatchery	OtsCJH16seg_su						202	-	-	-	-	7/21/2019	-
	18_UCOLSF	Eastbank Fish Hatchery	OtsEASTBK13_su						-	-	-	-	-	-	-
	18_UCOLSF	Eastbank Fish Hatchery	OtsEASTBK14_su	1	57	57			163	162	165	160	166	6/12/2019	3
	18_UCOLSF	Eastbank Fish Hatchery	OtsEASTBK15_su	4	180	48	133		184	159	189	154	193	7/3/2019	30
	18_UCOLSF	Entiat National Fish Hatchery	OtsENFH14_su						-	-	-	-	-	-	-
	18_UCOLSF	Entiat National Fish Hatchery	OtsENFH15_su						-	-	-	-	-	-	-
	18_UCOLSF	Wells Fish Hatchery	OtsWELLS14_su	2	92	48	44		159	156	186	153	192	6/8/2019	30
	18_UCOLSF	Wells Fish Hatchery	OtsWELLS15_su	6	329	153	176		168	158	185	154	207	6/17/2019	27
04Fall	03_WCASFA	Washougal Fish Hatchery	OtsWAS15_fa						-	-	-	-	-	-	-
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR15_fa	1	269			269	241	239	242	237	243	8/29/2019	3

05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR16_fa	6	2,016			2,016	256	251	259	239	268	9/13/2019	8
05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR17_fa	8	2,727			2,727	241	237	252	223	260	8/29/2019	15
18_UCOLSF	Priest Rapids Hatchery	OtsPRH14_fa	1	79			79	288	282	298	280	309	10/15/2019	16
18_UCOLSF	Priest Rapids Hatchery	OtsPRH15_fa	36	6,961			6,961	256	254	261	239	281	9/13/2019	7
18_UCOLSF	Priest Rapids Hatchery	OtsPRH16_fa	52	8,065			8,065	261	255	269	247	291	9/18/2019	14
19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON14S_1_fa	4	1,067			1,067	252	240	256	228	257	9/9/2019	16
19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON15S_1_fa	15	3,114		61	3,053	254	241	257	224	264	9/11/2019	16
19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON16S_1_fa	11	2,607			2,607	247	244	251	224	270	9/4/2019	7
19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH15S_1_fa	9	2,397			2,397	246	244	248	223	250	9/3/2019	4
19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH16S_1_fa	5	1,216			1,216	242	239	254	238	281	8/30/2019	15
22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWS14_fa	2	581			581	251	241	255	238	257	9/8/2019	14
22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWS15_fa	13	2,313			2,313	255	241	266	229	283	9/12/2019	25
22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWS16_fa	31	5,390			5,390	258	248	266	244	281	9/15/2019	18
Unassigned			4	781			781							
Total			325	47,182	6,573	1,086	39,523							

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1742 Table 51. Stock-specific abundance and run-timing of natural origin adult Chinook salmon passing Bonneville Dam in 2019.

Reporting Group	Sample N	Estimated abundance				Run-timing distribution						
		Total	Management Period			Ordinal day						
			Spring	Summer	Fall		1st	3rd	5th	95th	Median	Interquartile
			Jan. 1-Jun. 15	Jun. 16-Jul. 31	Aug. 1-Dec. 1	Median	quartile	quartile	percentile	percentile	date	range (days)
01_YOUNGS						-	-	-	-	-	-	-
02_WCASSP						-	-	-	-	-	-	-
03_WCASFA	8	1,358			1,358	248	242	266	231	274	9/5/2019	24
04_WILLAM	1	134			134	231	224	234	216	236	8/19/2019	10
05_SPCRTU	14	1,445			1,445	247	242	255	232	262	9/4/2019	13
06_KLICKR						-	-	-	-	-	-	-
07_DESCSP	9	477	477			128	126	149	121	158	5/8/2019	23
08_JOHNDR	9	474	474			128	126	131	121	143	5/8/2019	5
09_YAKIMA	19	940	884	56		133	128	140	122	197	5/13/2019	12
10_UCOLSP	47	2,513	2,513			133	127	140	121	155	5/13/2019	13
11_TUCANO	2	91	91			146	122	149	120	152	5/26/2019	27
12_HELLSC	71	4,217	4,142	75		133	127	138	122	156	5/13/2019	11
13_SFSALM	21	1,129	1,054	75		142	132	153	122	169	5/22/2019	21
14_CHMBLN						-	-	-	-	-	-	-
15_MFSALM	6	308	308			130	127	142	125	150.65	5/10/2019	15
16_UPSALM	19	925	880	44		142	130	151	122	159	5/22/2019	21
17_DESCFA	19	3,003			3,003	259	255	266	237	279	9/16/2019	11
18_UCOLSF	830	123,635	2,300	6,608	114,727	255	245	264	195	285	9/12/2019	19
19_SRFALL	112	17,688	105	365	17,219	255	241	262	222	282	9/12/2019	21
20_BONPOOLSP						-	-	-	-	-	-	-
21_UMATILLASP						-	-	-	-	-	-	-
22_BONPOOLFA						-	-	-	-	-	-	-
23_UMATILLAFA						-	-	-	-	-	-	-
Total	1,187	158,337	13,229	7,223	137,885							

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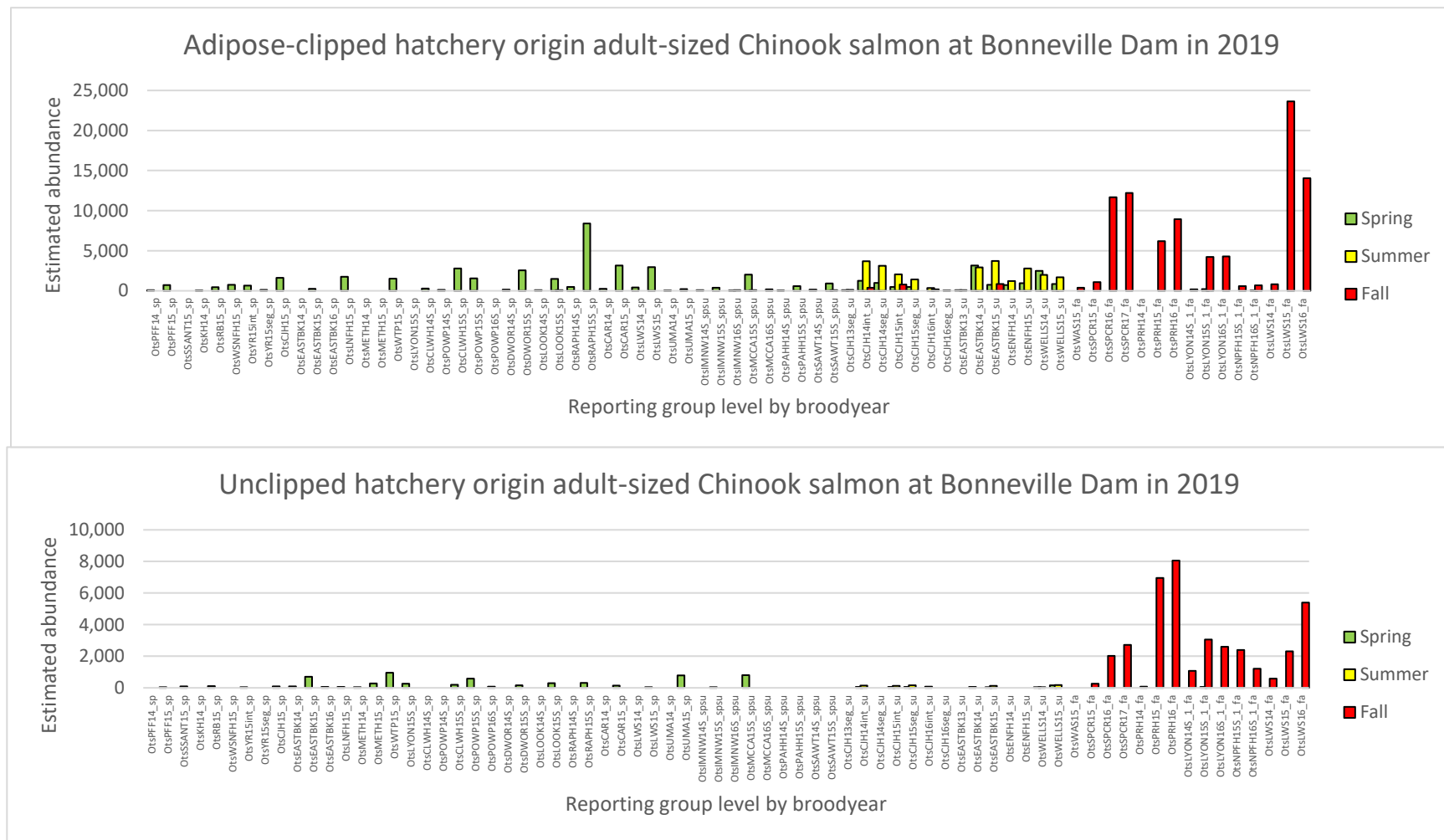


Figure 31. Estimated abundance of clipped (top) and unclipped (bottom) hatchery origin adult-sized Chinook salmon assigned to PBT broodstock groups that were sampled at Bonneville Dam in 2019 during spring (green), summer (yellow) and fall (red) management periods.

1748 There were 8 major (i.e., abundance >1000 fish) Chinook salmon stocks represented in
1749 the total estimated relative abundance (N=158,337) of natural-origin (i.e., excluding unclipped
1750 hatchery-origin fish) Chinook salmon passing Bonneville Dam in 2019 (Table 51; **Error!**
1751 **Reference source not found.**). These natural-origin stocks in order of decreasing magnitude
1752 were 18_UCOLSF (123,635), 19_SRFALL (17,688), 12_HELLSC (4,217), 17_DESCFA
1753 (3,003), 10_UCOLSP (2,513), 05_SPCRTU (1,445), 03_WCASFA (1,358), and 13_SFSALM
1754 (1,129). These stock abundance estimates were generated using SCOBIDEUX and SPIBETR
1755 functions and the estimates of clipped and unclipped adults distributed by TAC (Table 44).

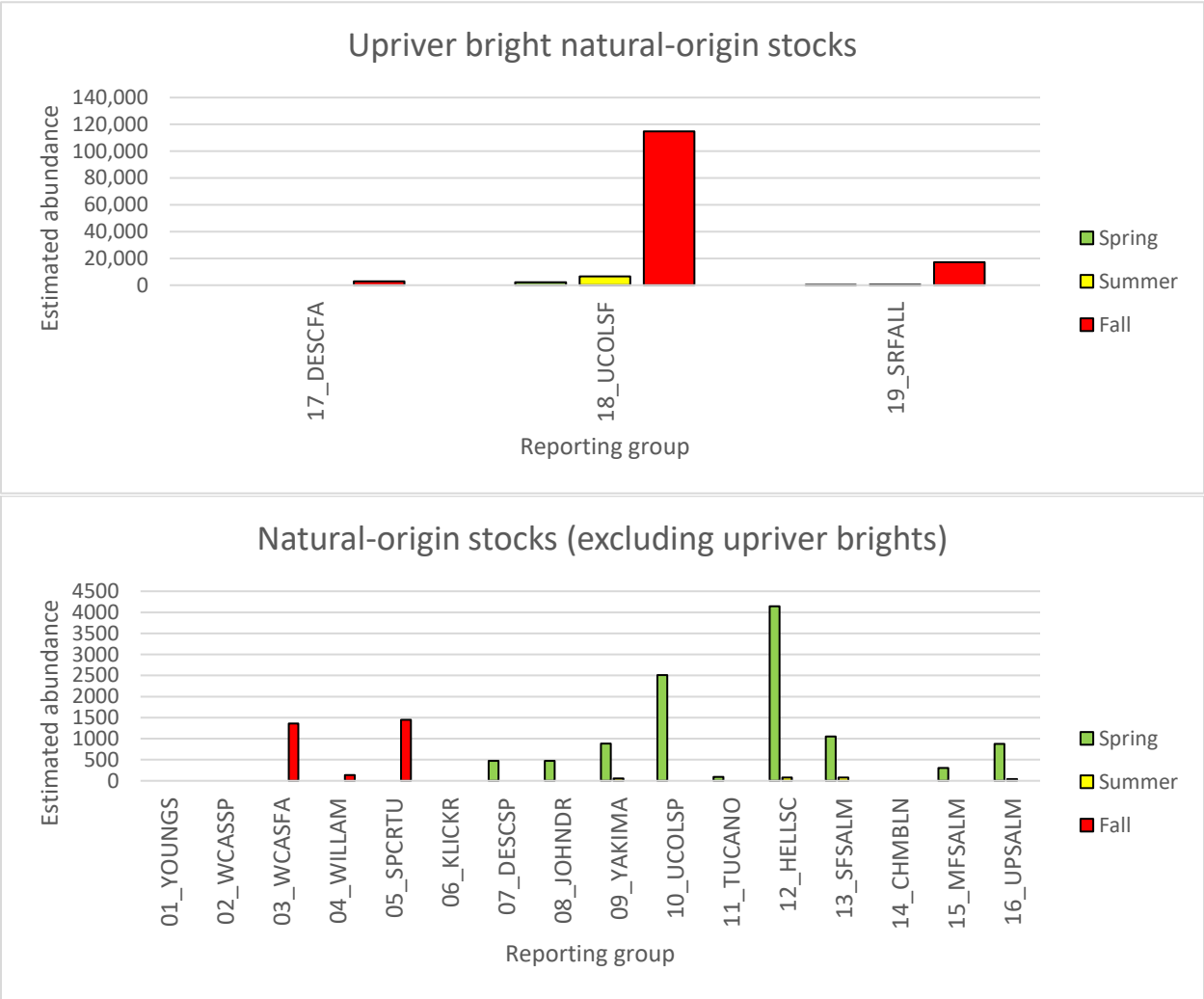


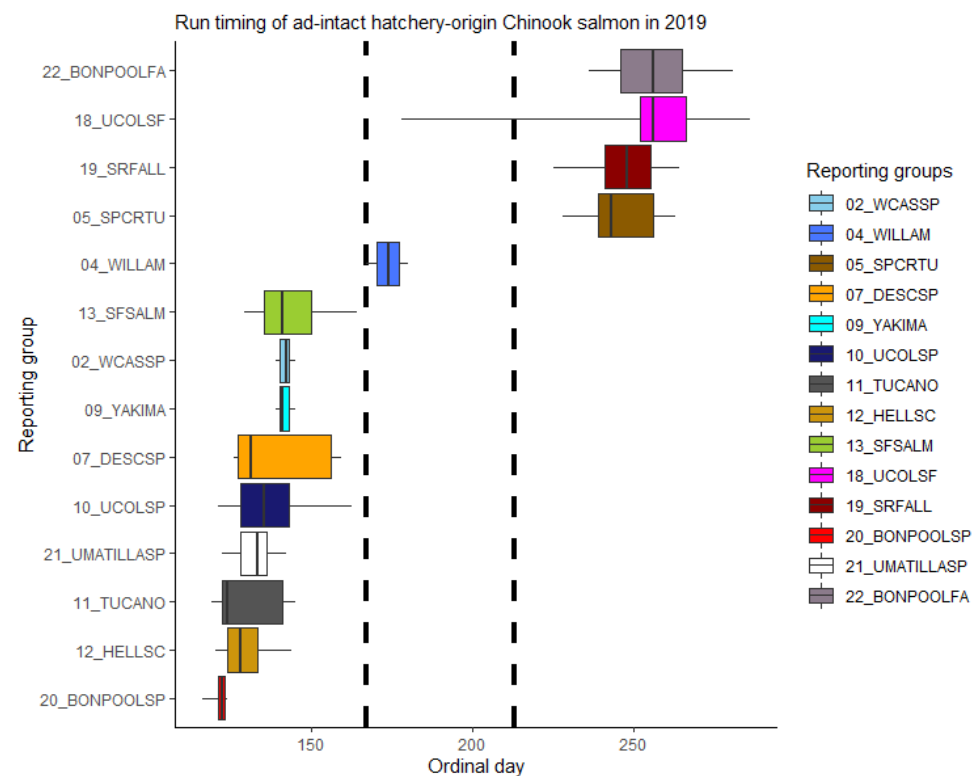
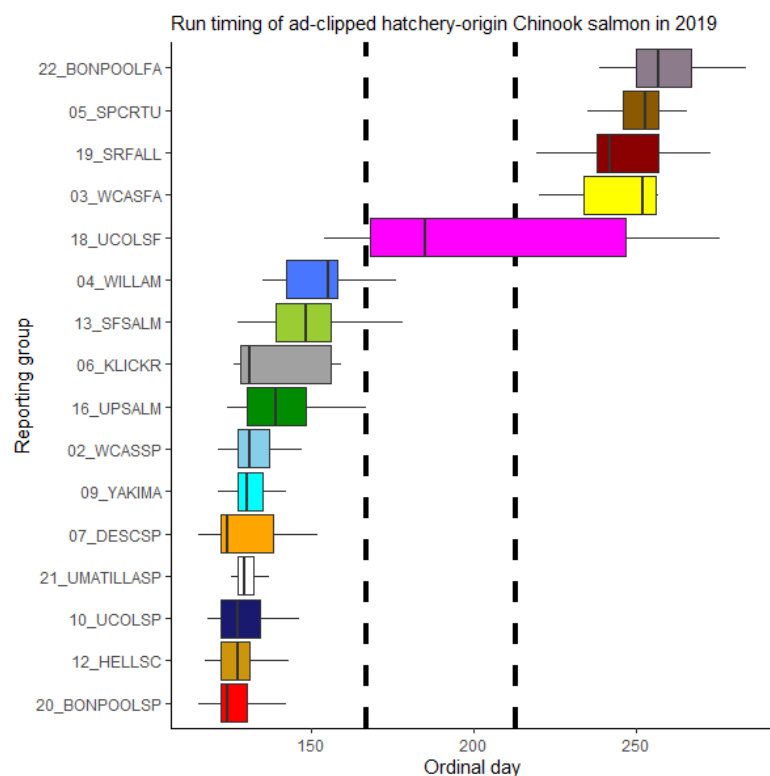
Figure 32. Estimated abundance of natural origin reporting groups (excluding unclipped hatchery-origin fish) of adult-sized Chinook salmon sampled at Bonneville Dam in 2019 during the spring (green), summer (yellow), and fall (red) management periods. Upriver bright Chinook salmon reporting groups (top panel), and all other natural-origin Chinook reporting groups (bottom panel) are shown separately.

Run-timing of Chinook salmon stocks in 2019

We plotted the run-timing distributions of the clipped and unclipped hatchery-origin Chinook salmon reporting group stocks (**Figure 33**) and provided the subtotals of reporting group abundance for each management period (clipped Table 47, unclipped Table 49). While the median date of passage for all hatchery-origin (both clipped and unclipped) spring Chinook stocks occurred well within the spring management period, the run-timing for 12_HELLSC, 13_SFSALM, and 16_UPSALM was found to extend beyond the spring management period (total abundance in the summer period was 630 fish). We estimated that 98% of all hatchery origin spring stocks passed Bonneville Dam in the spring period and 2% of the spring stock abundance passed in the summer period (Table 47, Table 49). The run-timing for the summer run clipped and unclipped hatchery-origin stocks from the upper Columbia River (i.e., 18_UCOLSF) was estimated to pass in both spring and summer periods at 34% (13,192 fish) and 66% (26,121 fish) of the total abundance estimated in those two periods, respectively.

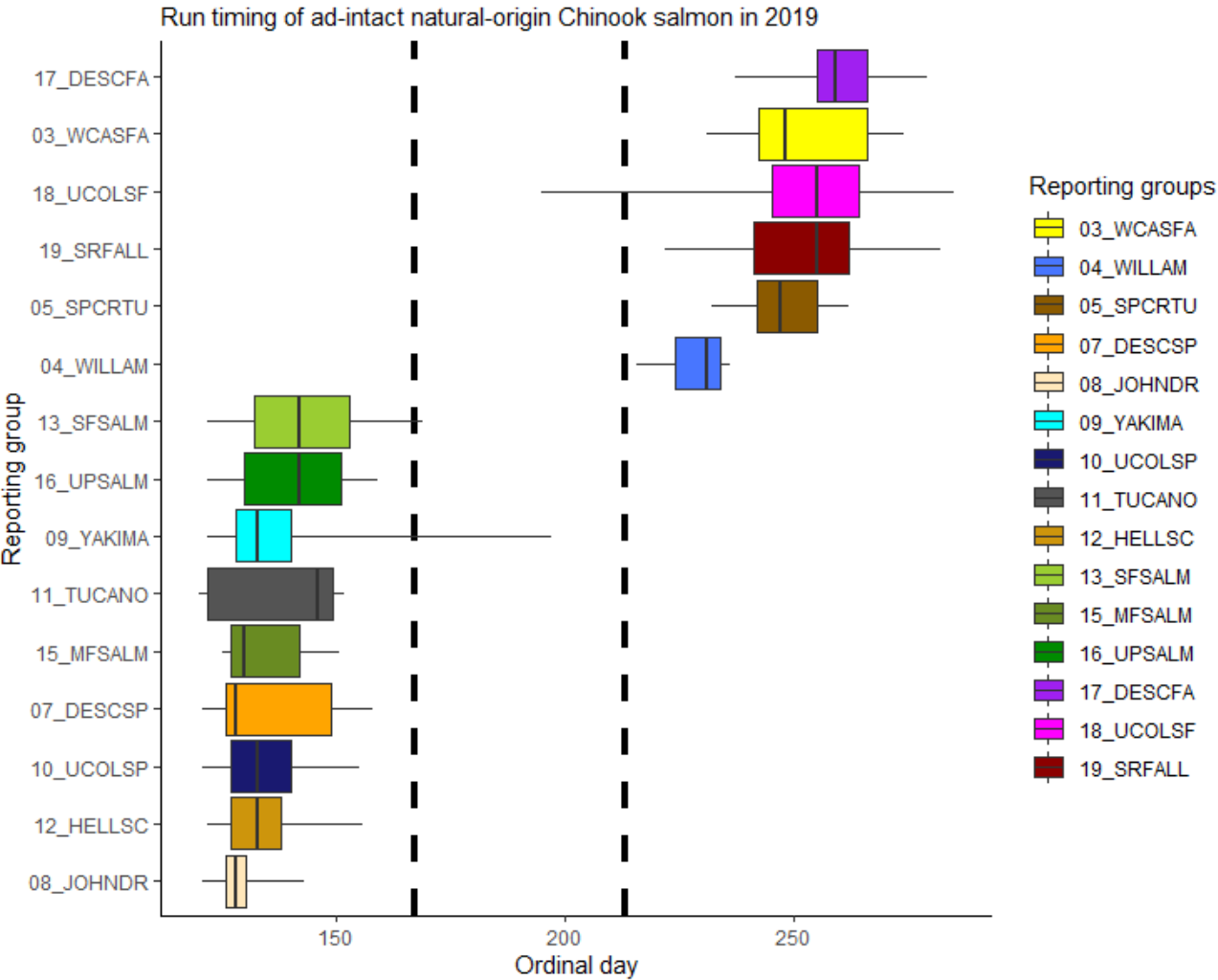
We also plotted run-timing distributions for each broodstock of clipped (**Figure 35**) and unclipped (**Figure 36**) hatchery origins provided the subtotals of these broodstock abundance estimates for each management period (clipped Table 48, unclipped Table 50). Although most stocks had median dates that fit within their expected management period, there were summer run Upper Columbia broodstocks from Wells and Eastbank hatchery that had median dates in the spring; there were also spring/summer run hatchery broodstocks from McCall and Imnaha broodstock that had median dates in the summer. For the spring stocks, only Powell and South Santiam had median dates in the summer period (**Figure 36**).

We plotted the run-timing distributions of the natural-origin (excluding adipose unclipped hatchery-origin fish, **Error! Reference source not found.**) Chinook salmon stocks and provide s ubtotals of abundance for each management period (Table 51). Similar to hatchery-origin stocks, the median date of passage for all natural-origin spring Chinook stocks occurred well within the spring management period, however, the run-timing for 09_YAKIMA, 12_HELLSC, 13_SFSALM, and 16_UPSALM was found to extend beyond the spring management period (total estimated abundance in the summer period for these stocks was 250 fish). We also estimated that 98% of the natural origin spring stocks passed Bonneville Dam in the spring period and 2% of the spring stock abundance passed in the summer period (Table 51). The run-timing for the summer run natural-origin stocks from the upper Columbia River (i.e., 18_UCOLSF) was estimated to pass in both spring and summer periods at 26% (2,300 fish) and 74% (6,608 fish) of the total abundance estimated in those two periods, respectively.



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 1796 **Figure 33. Reporting group-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th**
 1797 **percentile) for clipped and unclipped hatchery-origin adult-sized Chinook salmon that were sampled at Bonneville Dam in**
 1798 **2019 during the spring, summer, and fall management periods (separated by dashed lines).**

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Figure 34. Reporting group-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for natural-origin adult-sized Chinook salmon that were sampled at Bonneville Dam in 2019 during the spring, summer, and fall management periods (separated by dashed lines).

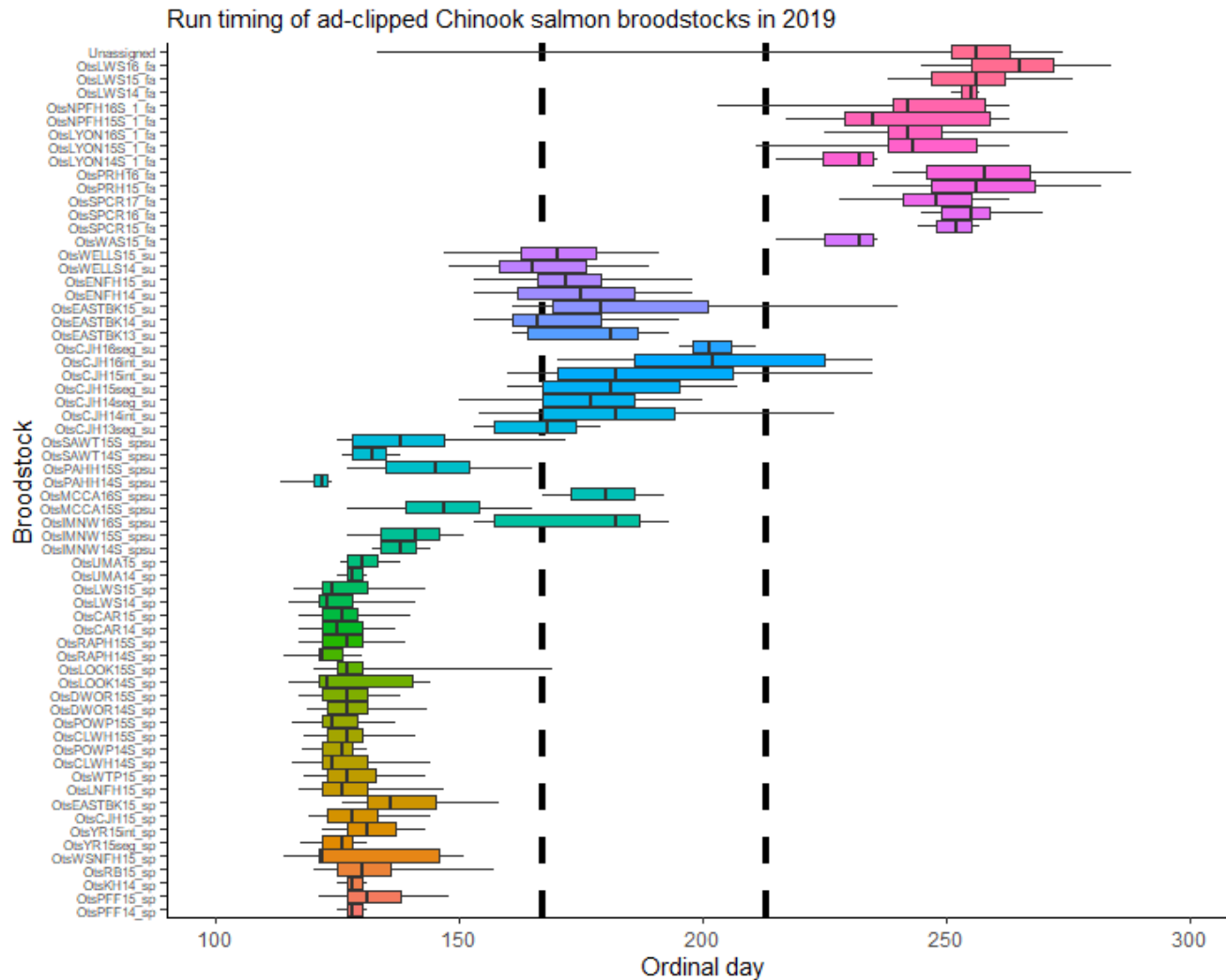


Figure 35. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for clipped adult-sized Chinook salmon that were sampled at Bonneville Dam in 2019 during the spring, summer, and fall management periods (separated by dashed lines).

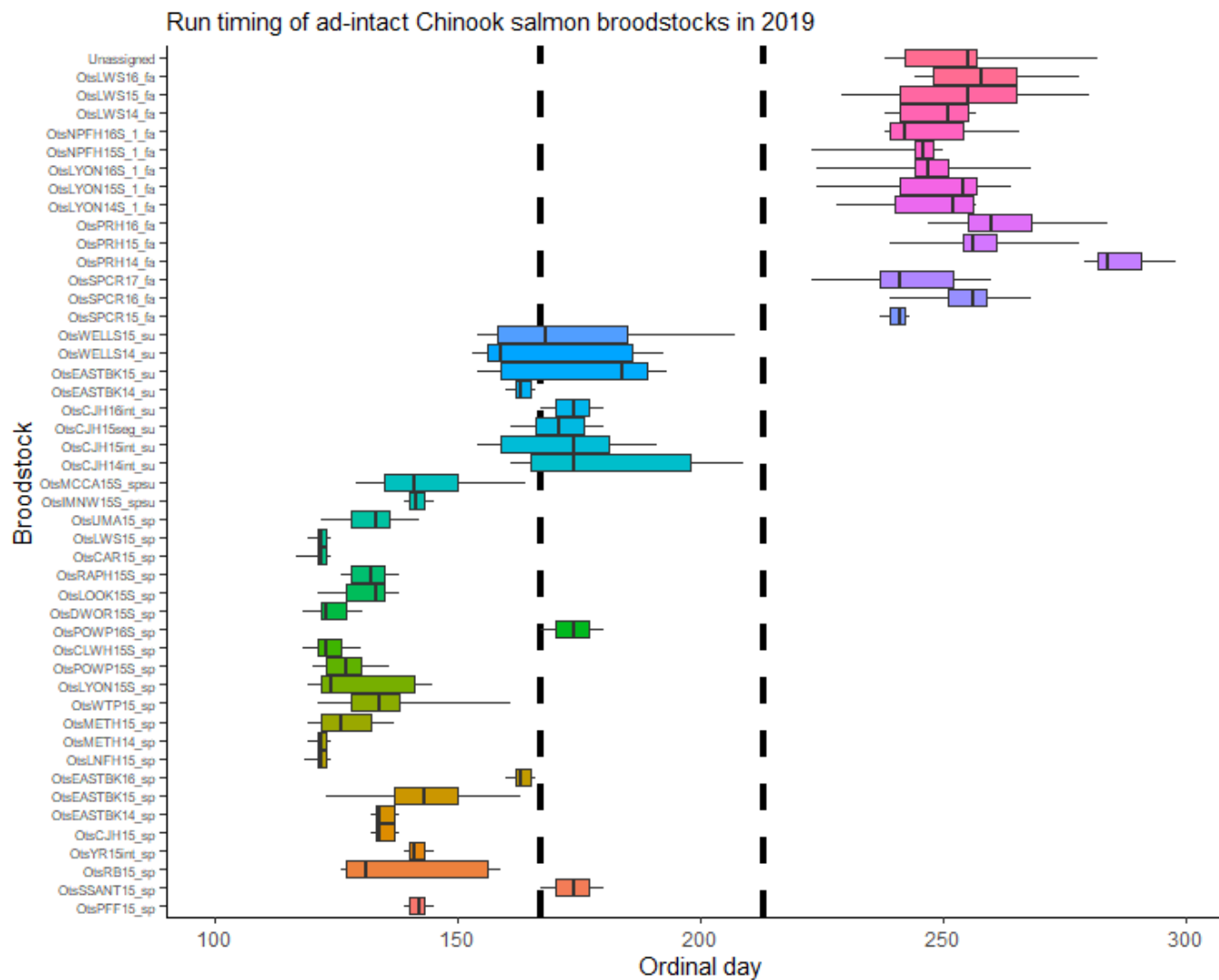
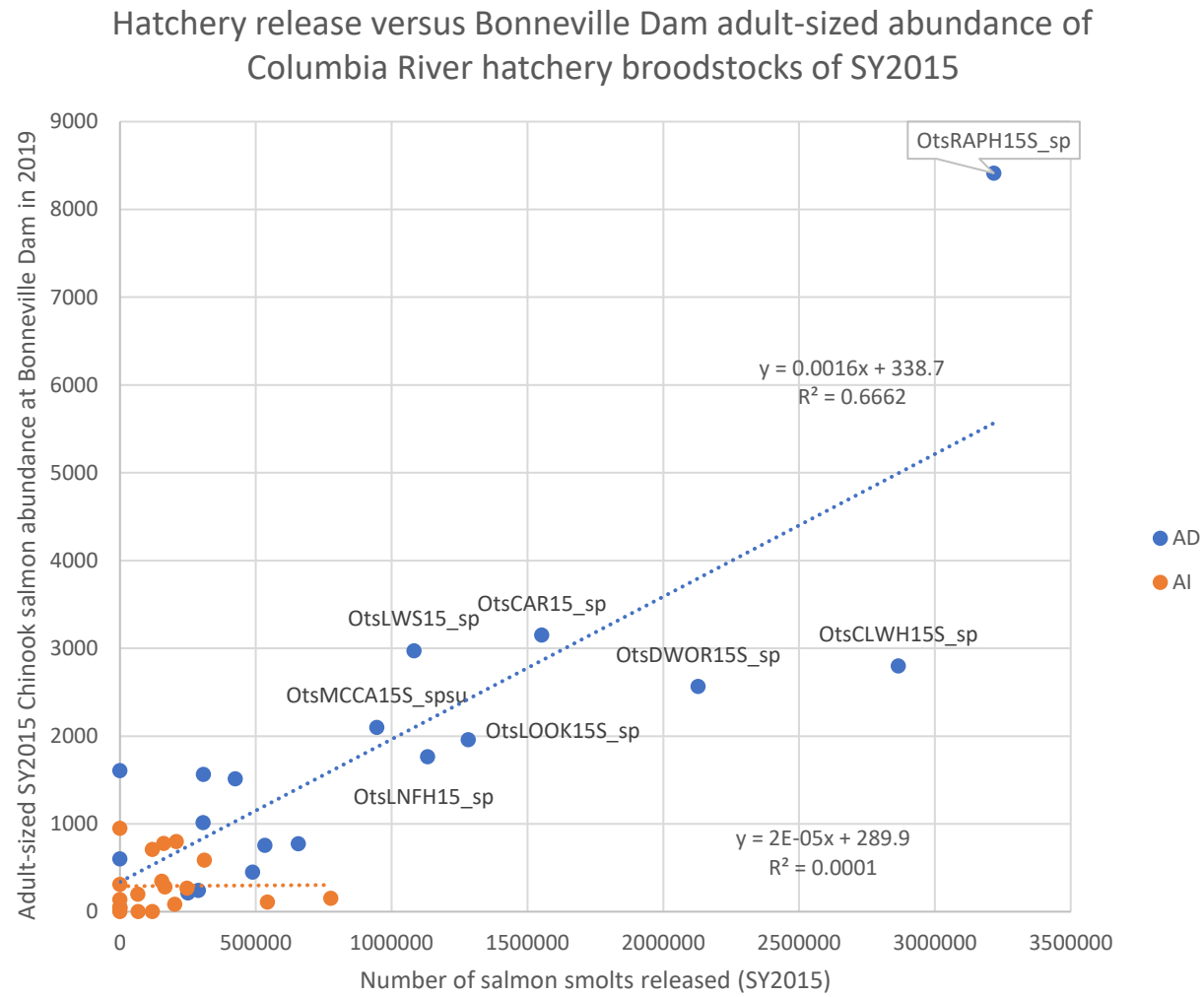


Figure 36. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for unclipped adult-sized Chinook salmon that were sampled at Bonneville Dam in 2019 during the spring, summer, and fall management periods (separated by dashed lines).

Demonstration of PBT to estimate smolt-to-adult survival using the adult Spring Chinook salmon clipped and unclipped hatchery-origin stocks that passed Bonneville Dam in 2019

We obtained the release information for clipped and unclipped hatchery-origin Spring Chinook salmon from Columbia River hatcheries located upstream of Bonneville Dam from Spawn Year 2015 (available at FPC <https://www.fpc.org>). After aligning the hatchery information with the broodstock units used in the PBT baseline, we regressed the numbers of released salmon with the corresponding abundance we estimated for the SY2015 broodstocks that returned to Bonneville Dam as adults in 2019 (i.e., 4-year-olds). There was high correspondence of number of clipped releases versus clipped abundance estimates based on the R^2 (0.67) of the linear trend (**Figure 37**). The unclipped stocks were observed to have low abundance and relative low release numbers which resulted in a lack of a strong linear relationship. This smolt-to-adult survival type of analysis may be highly beneficial for management of these hatchery stocks in the future and represents the first attempt at using the hatchery release information and PBT abundance estimates in this kind of analysis. Future work could sum all abundance of the SY2015 adult return across age-classes (i.e., age 3, 4, and 5 in run years 2018, 2019, and 2020, respectively) that passed Bonneville Dam and were caught in lower river fisheries below the dam in the same set of years. This would allow a complete run reconstruction of these Spring Chinook salmon broodstock groups to the Columbia River mouth. This preliminary analysis demonstrated a trend of 625 Spring Chinook salmon smolts released converted to 1 adult-sized 4-year-old Spring Chinook salmon returned to Bonneville Dam in 2019.



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Figure 37. Smolt release numbers of clipped and unclipped hatchery-origin Spring Chinook salmon of SY2015 from Columbia River hatcheries above Bonneville Dam versus the estimated abundance of SY2015 adult-sized fish that passed Bonneville Dam in 2019.

Estimated relative abundance of steelhead stocks in 2019

Daily passage of steelhead at Bonneville Dam in 2019 is provided in Figure 38.

Among clipped hatchery-origin steelhead, there were four major stocks (abundance >1000) represented in the total estimated abundance (N=37,721) of clipped hatchery origin steelhead passing Bonneville Dam in 2019 (Table 52). These stocks in order of decreasing magnitude were 07_MGILCS (14,240), 14_UPSALM (11,465), 10_SFCLWR (4,029, A-Index), 10_SFCLWR (3,783, B-Index), and 03_SKAMAN (3,082) (Table 52; Figure 39). All of these major clipped stocks were A-Index size fish except for 10_SFCLWR which had a combination of both A-Index and B-Index fish.

Among the unclipped hatchery-origin steelhead, there was a single major stock (abundance >1000) represented in the total estimated abundance (N=2,748) of unclipped hatchery origin steelhead passing Bonneville Dam in 2019 (**Table 53**). This single stock was the A-Index (1,120) and B-Index (1,029) components of 10_SFCLWR (**Table 53**; Figure 39).

Using PBT assignments we can now provide abundance (Table 55; Figure 40) and run-timing estimates for each of the clipped and unclipped hatchery broodstocks (Table 55). There were 16 major hatchery broodstock sources (abundance >1000) represented in the total estimated abundance of clipped and unclipped hatchery-origin steelhead passing Bonneville Dam in 2019 (Table 55). These stocks in order of decreasing magnitude were OmyDWOC16S (7,019 total; A-Index = 2,171 and B-Index = 4,847), OmyCGRW17S (4,823), OmySAWT17S (2,953), OmySKH16_su (2,893), OmyPAHH17S (2,044), OmyOXBO17S (2,032), OmyOXBO16S (1,899), OmyWALW17S (1,830), OmyCGRW16S (1,536), OmyDWOC17S (1,375), OmyLSCR17S (1,346), OmyPAHH16S (1,273; A-Index = 1,209 and B-Index = 64), OmyWALW16S (1,244), OmySAWT16S (1,166), OmyUSAL16S (1,146; A-Index = 935 and B-Index = 211), and OmyLSCR16S (1,097). Unless otherwise noted by details of the split between A-Index and B-Index sized fish, most abundances were all A-Index fish.

There were four major stocks (abundance >1000) represented in the total estimated abundance (N=31,997) of natural origin (excluding adipose unclipped hatchery-origin fish) steelhead passing Bonneville Dam in 2019 (**Table 54**). These stocks in order of decreasing magnitude were 07_MGILCS (19,996 A-Index; 214 B-Index), 14_UPSALM (5,314 A-Index; 68 B-Index), 08_YAKIMA (1,390) and 09_UPPCOL (1,050). Unless specified, these were all A-Index stocks. The largest natural-origin B-Index abundance was estimated for 10_SFCLWR which had nearly equal proportions of both size categories (434 A-Index; 498 B-Index).

1869 **Table 52. Stock-specific abundance and run-timing by A-/B-Index categories of clipped hatchery-origin summer A-/B-Index steelhead passing Bonneville Dam in 2019.**

Size	H		Sample N	Estimated abundance		Run-timing distribution						
						Ordinal day						
	Reporting Group name	Reporting Group Code					1st	3rd	5th	95th	Median	Interquartile
A-INDEX				Mean	95% CI	Median	quartile	quartile	percentile	percentile	date	range (days)
	Lower Columbia	02_LOWCOL		0	0 – 0							
	Skamania	03_SKAMAN	27	3,082	1480 – 4553	198	191	208	184	241	7/17/2019	17
	Willamette	04_WILLAM		0	0 – 0							
	Big White Salmon	05_BWSALM		0	0 – 0							
	Klickitat	06_KLICKR		0	0 – 0							
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	128	14,240	11754 – 17247	222	210	236	192	263	8/10/2019	26
	Yakima	08_YAKIMA	1	0	0 – 0							
	upper Columbia	09_UPPCOL	10	990	219 – 1929	218	198	233	186	254	8/6/2019	35
	SF Clearwater	10_SFCLWR	76	3,783	2655 – 4894	266	256	282	239	296	9/23/2019	26
	upper Clearwater	11_UPCLWR	1	34	0 – 223	264	261	267	259	270	9/21/2019	6
	SF Salmon	12_SFSALM	1	34	0 – 219	264	261	267	259	270	9/21/2019	6
	MF Salmon	13_MFSALM		0	0 – 0							
	upper Salmon	14_UPSALM	118	11,465	8909 – 14418	231	219	249	203	280	8/19/2019	30
		A-INDEX Subtotal	362	33,628								
B-INDEX	Lower Columbia	02_LOWCOL		0	0 – 0							
	Skamania	03_SKAMAN		0	0 – 0							
	Willamette	04_WILLAM		0	0 – 0							
	Big White Salmon	05_BWSALM		0	0 – 0							
	Klickitat	06_KLICKR		0	0 – 0							

mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS		0	0 – 0							
Yakima	08_YAKIMA		0	0 – 0							
upper Columbia	09_UPPCOL		0	0 – 0							
SF Clearwater	10_SFCLWR	94	4,029	3096 – 4977	271	262	282	246	293	9/28/2019	20
upper Clearwater	11_UPCLWR		0	0 – 0							
SF Salmon	12_SFSALM		0	0 – 0							
MF Salmon	13_MFSALM		0	0 – 0							
upper Salmon	14_UPSALM	1	64	0 – 263	264	261	267	259	271	9/21/2019	6
	B-INDEX Subtotal	95	4,093								

Note: These summary statistics of run-timing distributions were calculated using a method to estimate abundance of each stock based on temporally stratified stock proportions and TAC estimates of clipped and unclipped steelhead that passed Bonneville Dam at the fish counting window. This method for estimating abundance minimizes bias imposed by uneven sampling.

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Table 53. Stock-specific abundance and run-timing by A-/B-Index categories of unclipped hatchery-origin summer A-/B-Index steelhead passing Bonneville Dam in 2019.

Size	HNC		Sample N	Estimated abundance		Run-timing distribution						
	Reporting Group name	Reporting Group Code		Ordinal day		Median	1st	3rd	5th	95th	Median	Interquartile
				Mean	95% CI		quartile	quartile	percentile	percentile	date	range (days)
A-INDEX	Lower Columbia	02_LOWCOL										
	Skamania	03_SKAMAN										
	Willamette	04_WILLAM										
	Big White Salmon	05_BWSALM										
	Klickitat	06_KLICKR										
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	4	309	0 – 812	243	235	253	225	279	8/31/2019	18
	Yakima	08_YAKIMA										
	upper Columbia	09_UPPCOL	1	98	0 – 390	246	242	252	238	257	9/3/2019	10
	SF Clearwater	10_SFCLWR	26	1,120	627 – 1686	273	261	284	242	296	9/30/2019	23
	upper Clearwater	11_UPCLWR										
	SF Salmon	12_SFSALM										
	MF Salmon	13_MFSALM										
	upper Salmon	14_UPSALM	1	193	0 – 578	293	289	296	287	302	10/20/2019	7
		A-INDEX Subtotal	32	1,719								
B-INDEX	Lower Columbia	02_LOWCOL										
	Skamania	03_SKAMAN										
	Willamette	04_WILLAM										
	Big White Salmon	05_BWSALM										
	Klickitat	06_KLICKR										

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mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS										
Yakima	08_YAKIMA										
upper Columbia	09_UPPCOL										
SF Clearwater	10_SFCLWR	25	1,029	499 – 1640	276	261	283	242	295	10/3/2019	22
upper Clearwater	11_UPCLWR										
SF Salmon	12_SFSALM										
MF Salmon	13_MFSALM										
upper Salmon	14_UPSALM										
	B-INDEX Subtotal	25	1,029								

1878 **Table 54. Stock-specific abundance and run-timing by A-/B-Index categories of unclipped natural-origin summer A-/B-Index steelhead passing Bonneville Dam in 2019.**

Size					Run-timing distribution							
	Natural origin- No Clip		Sample N	Estimated abundance		Ordinal day						
	Reporting Group name	Reporting Group Code		Mean	95% CI	Median	1st quartile	3rd quartile	5th percentile	95th percentile	Median date	Interquartile range (days)
A-INDEX	Lower Columbia	02_LOWCOL										
	Skamania	03_SKAMAN	6	857	326 – 1476	206	196	217	186	228	7/25/2019	21
	Willamette	04_WILLAM										
	Big White Salmon	05_BWSALM										
	Klickitat	06_KLICKR	10	924	439 – 1538	202	194	224	185	284	7/21/2019	30
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	166	19,996	18209 – 21593	216	203	228	188	258	8/4/2019	25
	Yakima	08_YAKIMA	13	1,390	731 – 2154	215	202	225	188	237	8/3/2019	23
	upper Columbia	09_UPPCOL	9	1,050	465 – 1668	223	210	228	194	234	8/11/2019	18
	SF Clearwater	10_SFCLWR	7	434	168 – 728	259	247	265	239	281	9/16/2019	18
	upper Clearwater	11_UPCLWR	5	206	54 – 418	273	247	281	239	285	9/30/2019	34
	SF Salmon	12_SFSALM	1	68	0 – 203	263	261	267	259	271	9/20/2019	6
	MF Salmon	13_MFSALM	8	704	281 – 1233	225	209	243	190	288	8/13/2019	34
	upper Salmon	14_UPSALM	43	5,314	4010 – 6628	216	205	227	189	254	8/4/2019	22
		A-INDEX Subtotal	268	30,943								
B-INDEX	Lower Columbia	02_LOWCOL	1	119	0 – 358	195	189	199	184	202	7/14/2019	10
	Skamania	03_SKAMAN	1	119	0 – 358	195	189	199	184	202	7/14/2019	10
	Willamette	04_WILLAM										
	Big White Salmon	05_BWSALM										
	Klickitat	06_KLICKR										

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mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	3	214	0 – 478	201	194	265	185	281	7/20/2019	71
Yakima	08_YAKIMA										
upper Columbia	09_UPPCOL										
SF Clearwater	10_SFCLWR	11	498	230 – 817	262	245	274	226	287	9/19/2019	29
upper Clearwater	11_UPCLWR										
SF Salmon	12_SFSALM	1	35	0 – 101	293	289	296	287	301	10/20/2019	7
MF Salmon	13_MFSALM										
upper Salmon	14_UPSALM	1	68	0 – 203	263	261	267	259	271	9/20/2019	6
	B-INDEX Subtotal	18	1,054								

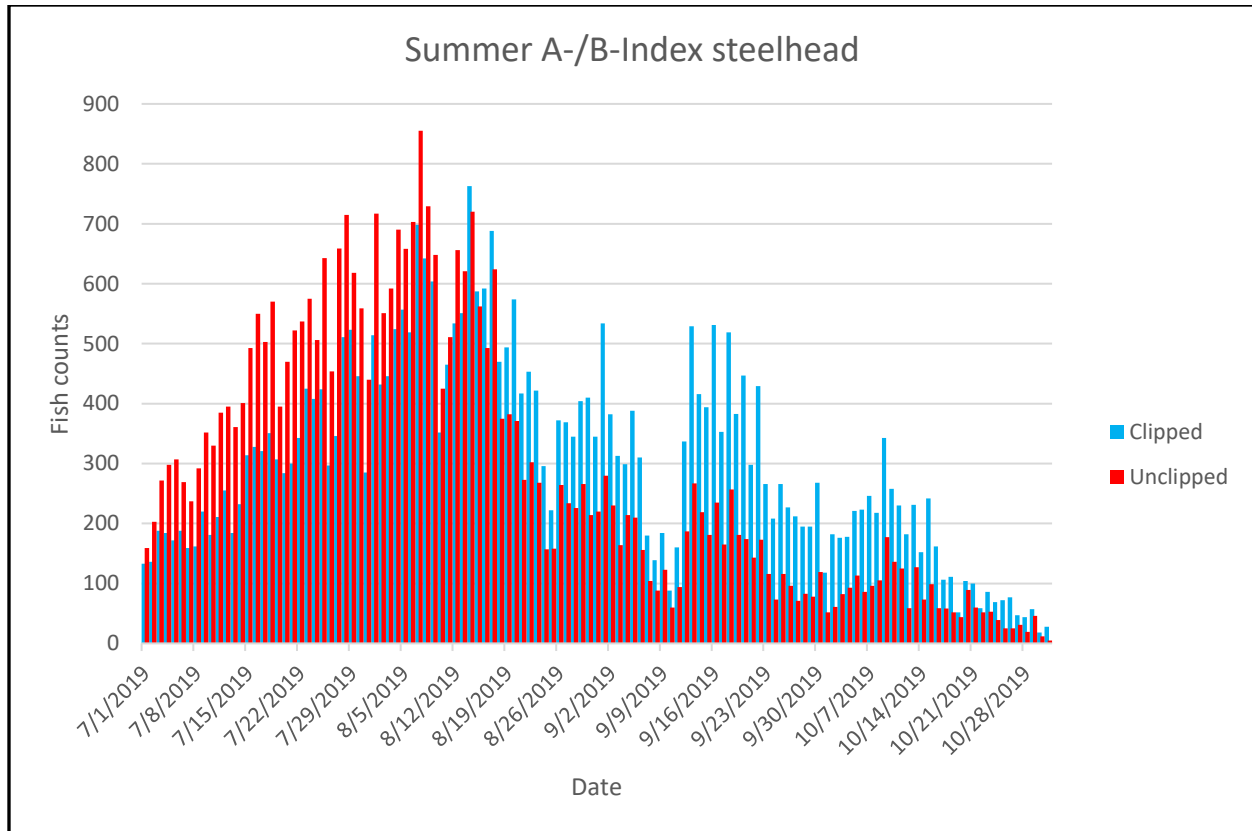


Figure 38. Daily passage of clipped (blue) and unclipped (red) steelhead at Bonneville Dam in 2019 during the summer A-/B-Index management period (source: <https://www.fpc.org>).

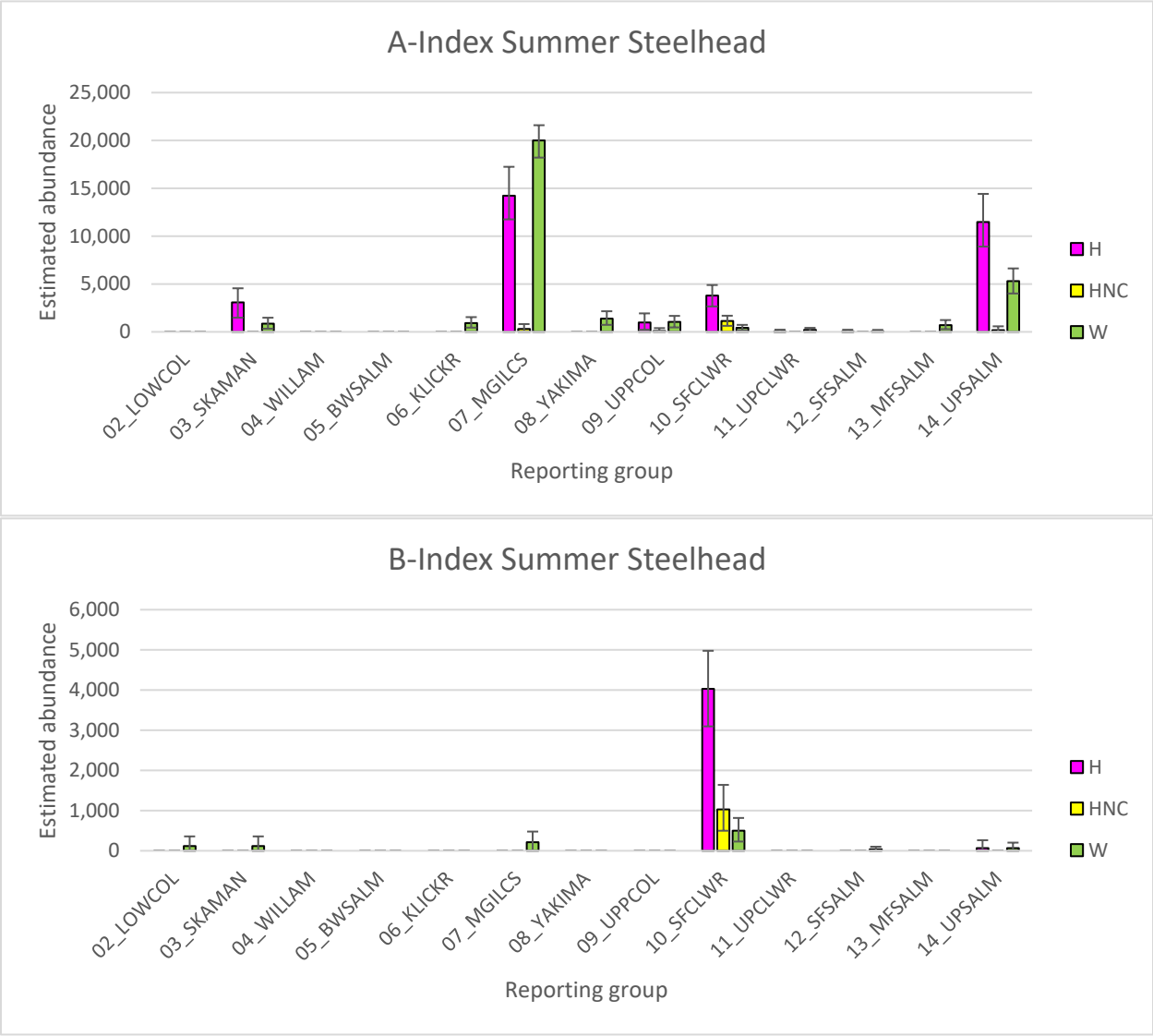


Figure 39. Estimated abundance (\pm 95% CI) of A-Index (<780mm FL, top) and B-Index (\geq 780mm FL, bottom) hatchery origin (clipped “H” and unclipped “HNC”) and natural-origin (“W”) steelhead assigned to genetic stock of origin that were sampled at Bonneville Dam in 2019.

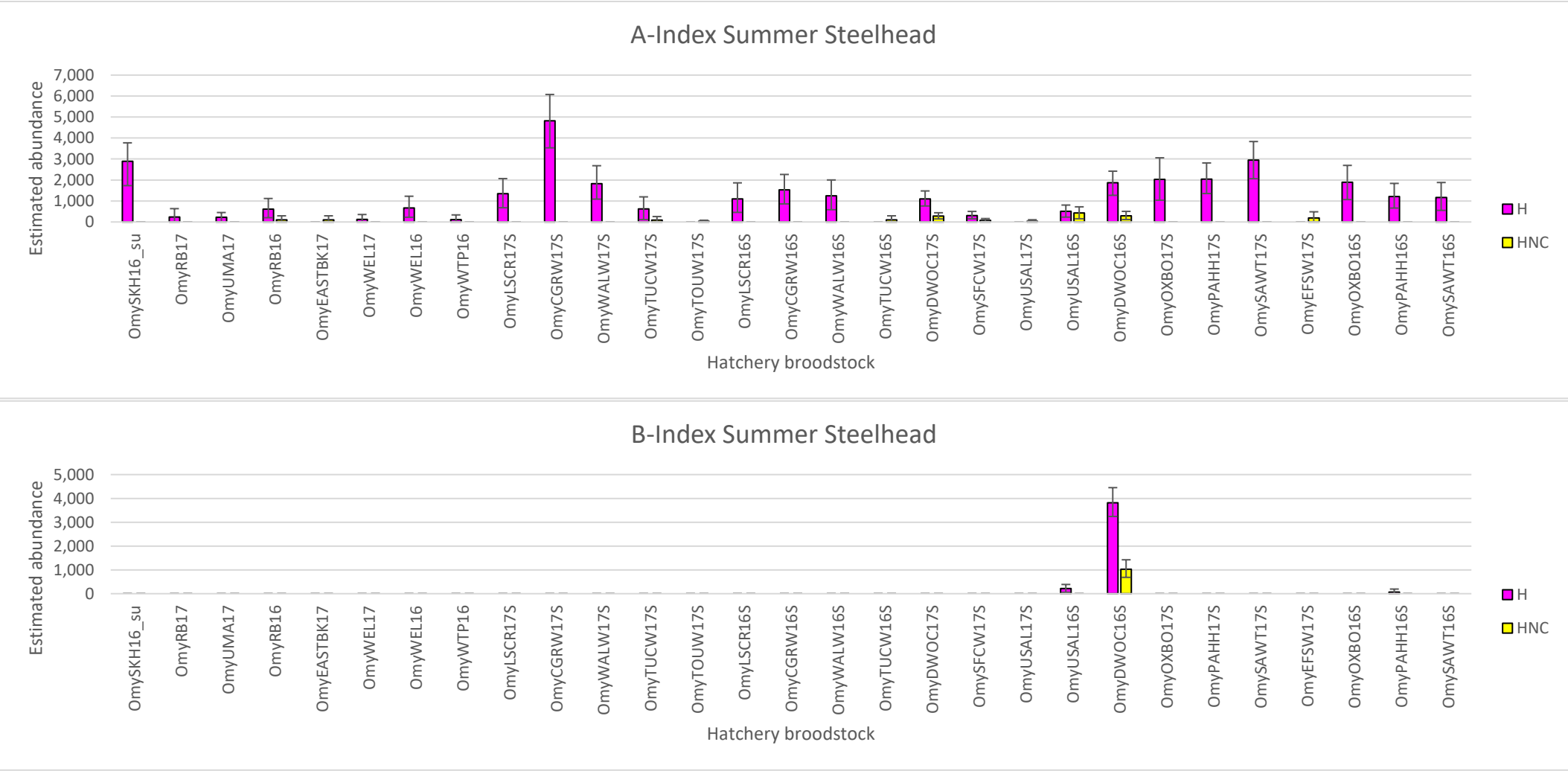


Figure 40. Estimated abundance (\pm 95% CI) of A-Index (<780mm FL, top) and B-Index (\geq 780mm FL, bottom) hatchery origin steelhead (adipose clipped and unclipped) sampled at Bonneville Dam in 2019 that assigned via PBT to 29 hatchery broodstocks of origin. The 2017 age-class (1-ocean fish) and 2016 age-class (2-ocean fish) are shown. Key to broodstock collection is presented in Appendix 6.

Table 55. Hatchery broodstock-specific estimated abundance of clipped and unclipped A-Index and B-Index PBT-assigned steelhead passing Bonneville Dam in 2019.

Hatchery	Stock	GSI RepGrp	Broodstock	Broodyear	Hatchery clipped				Hatchery Unclipped			
					A-INDEX		B-INDEX		A-INDEX		B-INDEX	
					MLE	95% CI	MLE	95% CI	MLE	95% CI	MLE	95% CI
Skamania	Summer	03_SKAMAN	OmySKH16_su	2016	2,893	1732 – 3772	0	0 – 0	0	0 – 0	0	0 – 0
Round Butte	Deschutes River	07_MGILCS	OmyRB17	2017	235	0 – 634	0	0 – 0	0	0 – 0	0	0 – 0
Umatilla	Minthorn Springs	07_MGILCS	OmyUMA17	2017	220	0 – 450	0	0 – 0	0	0 – 0	0	0 – 0
Round Butte	Deschutes River	07_MGILCS	OmyRB16	2016	616	203 – 1119	0	0 – 0	98	0 – 293	0	0 – 0
Eastbank	Chelan/Methow/Okanogan/Wenatchee	09_UPPCOL	OmyEASTBK17	2017	0	0 – 0	0	0 – 0	98	0 – 293	0	0 – 0
Wells	On Station	09_UPPCOL	OmyWEL17	2017	118	0 – 355	0	0 – 0	0	0 – 0	0	0 – 0
Wells	On Station	09_UPPCOL	OmyWEL16	2016	670	225 – 1226	0	0 – 0	0	0 – 0	0	0 – 0
Winthrop NFH	Methow River	09_UPPCOL	OmyWTP16	2016	112	0 – 336	0	0 – 0	0	0 – 0	0	0 – 0
Little Sheep Creek	-	07_MGILCS	OmyLSCR17S	2017	1,346	678 – 2067	0	0 – 0	0	0 – 0	0	0 – 0
Lyons Ferry	Grande Ronde	07_MGILCS	OmyCGRW17S	2017	4,823	3533 – 6077	0	0 – 0	0	0 – 0	0	0 – 0
Lyons Ferry	Wallowa	07_MGILCS	OmyWALW17S	2017	1,830	1087 – 2681	0	0 – 0	0	0 – 0	0	0 – 0
Lyons Ferry	Tucannon	07_MGILCS	OmyTUCW17S	2017	623	112 – 1196	0	0 – 0	86	0 – 259	0	0 – 0
Lyons Ferry	Touchet	07_MGILCS	OmyTOUW17S	2017	0	0 – 0	0	0 – 0	27	0 – 81	0	0 – 0
Little Sheep Creek	-	07_MGILCS	OmyLSCR16S	2016	1,097	456 – 1864	0	0 – 0	0	0 – 0	0	0 – 0
Lyons Ferry	Grande Ronde	07_MGILCS	OmyCGRW16S	2016	1,536	860 – 2264	0	0 – 0	0	0 – 0	0	0 – 0
Lyons Ferry	Wallowa	07_MGILCS	OmyWALW16S	2016	1,244	584 – 2002	0	0 – 0	0	0 – 0	0	0 – 0
Lyons Ferry	Tucannon	07_MGILCS	OmyTUCW16S	2016	0	0 – 0	0	0 – 0	98	0 – 293	0	0 – 0
Dworshak NFH	Clearwater River	10_SFCLWR	OmyDWOC17S	2017	1,095	762 – 1479	0	0 – 0	280	146 – 439	0	0 – 0
Dworshak NFH	SF Clearwater	10_SFCLWR	OmySFCW17S	2017	306	148 – 503	0	0 – 0	81	27 – 162	0	0 – 0
Dworshak NFH	Upper Salmon	10_SFCLWR	OmyUSAL17S	2017	0	0 – 0	0	0 – 0	35	0 – 105	0	0 – 0
Dworshak NFH	Upper Salmon	10_SFCLWR	OmyUSAL16S	2016	506	230 – 806	211	57 – 387	429	153 – 721	0	0 – 0
Dworshak NFH	Clearwater River	10_SFCLWR	OmyDWOC16S	2016	1,876	1269 – 2420	3,818	3242 – 4452	295	115 – 505	1,029	685 – 1423
Oxbow	-	14_UPSALM	OmyOXBO17S	2017	2,032	1035 – 3058	0	0 – 0	0	0 – 0	0	0 – 0
Pahsimeroi	Salmon River	14_UPSALM	OmyPAHH17S	2017	2,044	1355 – 2813	0	0 – 0	0	0 – 0	0	0 – 0
Sawtooth	Salmon River	14_UPSALM	OmySAWT17S	2017	2,953	2062 – 3833	0	0 – 0	0	0 – 0	0	0 – 0
Sawtooth	East Fork Salmon River	14_UPSALM	OmyEFSW17S	2017	0	0 – 0	0	0 – 0	193	0 – 485	0	0 – 0
Oxbow	-	14_UPSALM	OmyOXBO16S	2016	1,899	1067 – 2696	0	0 – 0	0	0 – 0	0	0 – 0
Pahsimeroi	Salmon River	14_UPSALM	OmyPAHH16S	2016	1,209	662 – 1838	64	0 – 193	0	0 – 0	0	0 – 0
Sawtooth	Salmon River	14_UPSALM	OmySAWT16S	2016	1,166	552 – 1881	0	0 – 0	0	0 – 0	0	0 – 0
#N/A	#N/A	#N/A	Unassigned	#N/A	1,180	608 – 2553	0	0 – 23	0	0 – 0	0	0 – 0
TOTAL					33,628		4,093		1,719		1,029	

1894 **Note:** These abundance estimates were calculated using a method to estimate abundance of each stock based on temporally stratified stock proportions and total numbers of clipped and unclipped steelhead that
1895 passed the Bonneville Dam at the fish counting window. Key to broodstock collection is presented in Appendix 6.

Run-timing of steelhead stocks in 2019

We were able to characterize the run-timing distributions at the broodstock level for the clipped (Figure 41) and unclipped (**Figure 42**) hatchery steelhead stocks arriving during the summer A-/B-Index management period. 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. The Skamania summer steelhead period is 4/1/2019 – 6/30/ 2019, and the summer A-/B-Index period begins on 7/1/2019 and lasts until 10/31/2019. For the clipped stocks arriving in the A-/B-Index period, the broodstock that typically has late run-timing is the Dworshak stock, which often arrives after August 25th (Ordinal day 237) at Bonneville Dam (Figure 41). There were seven different clipped hatchery broodstocks with median dates that were observed after August 25th in 2019: OmyDWOC16S (A- and B-Index), OmyDWOC17S, OmyPAHH17S, OmySAWT17S, OmySFCW17S, OmyUSAL16S (A- and B-Index), and OmyPAHH16S (B-Index). Unless otherwise noted these stocks were A-Index size. For the stocks in which both A-Index and B-Index were represented, the B-Index stock had a later median date. For the unclipped stocks arriving in the A-/B-Index period, there were 11 unique broodstocks and ten of them had a median run date after August 25th (**Figure 42**).

We characterized the run-timing distributions for natural-origin steelhead stocks (Figure 43); the patterns generally are consistent with past years. The late arriving stocks with median dates on or after August 25th were 10_SFCLWR (both A-Index and B-Index), 12_SFSALM (both A-Index and B-Index), 14_UPSALM (B-Index), and 11_UPCLWR (A-Index).

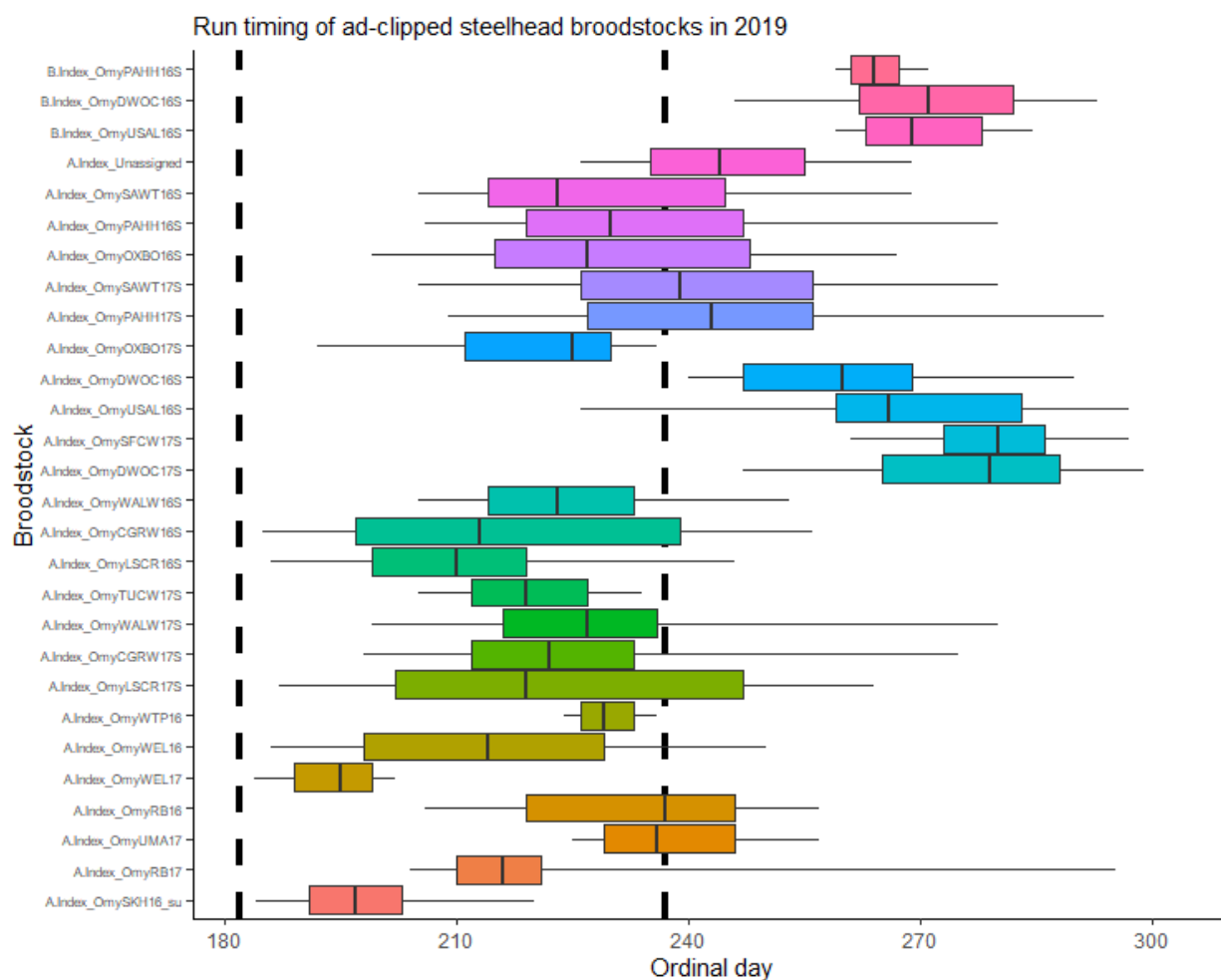


Figure 41. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for clipped hatchery-origin steelhead that were sampled at Bonneville Dam in 2019 and reported by A-Index and B-Index size category. Key to broodstock collection is presented in Appendix 6.

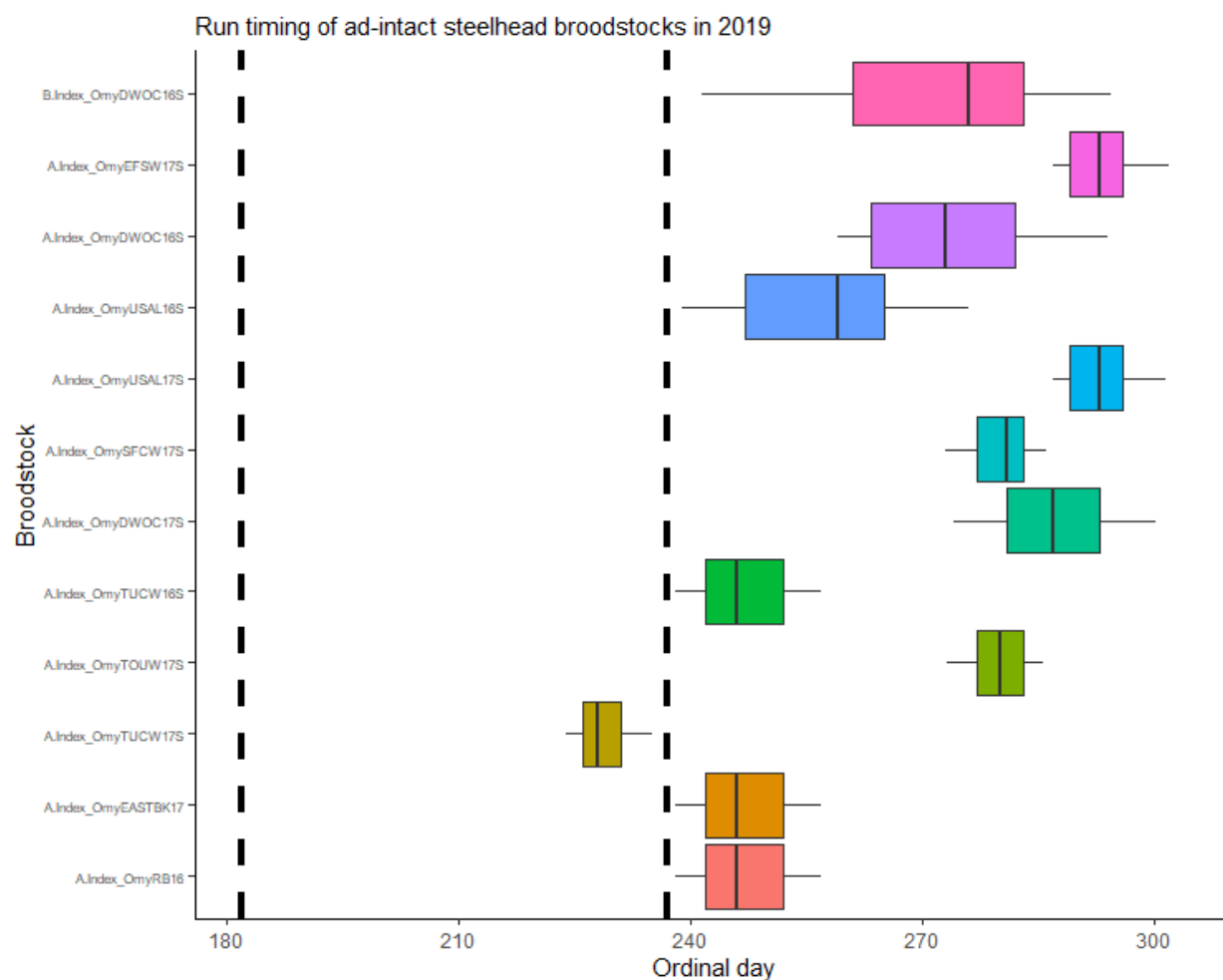


Figure 42. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for unclipped hatchery-origin steelhead that were sampled at Bonneville Dam in 2019 and reported by A-Index and B-Index size category. Key to broodstock collection is presented in Appendix 6.

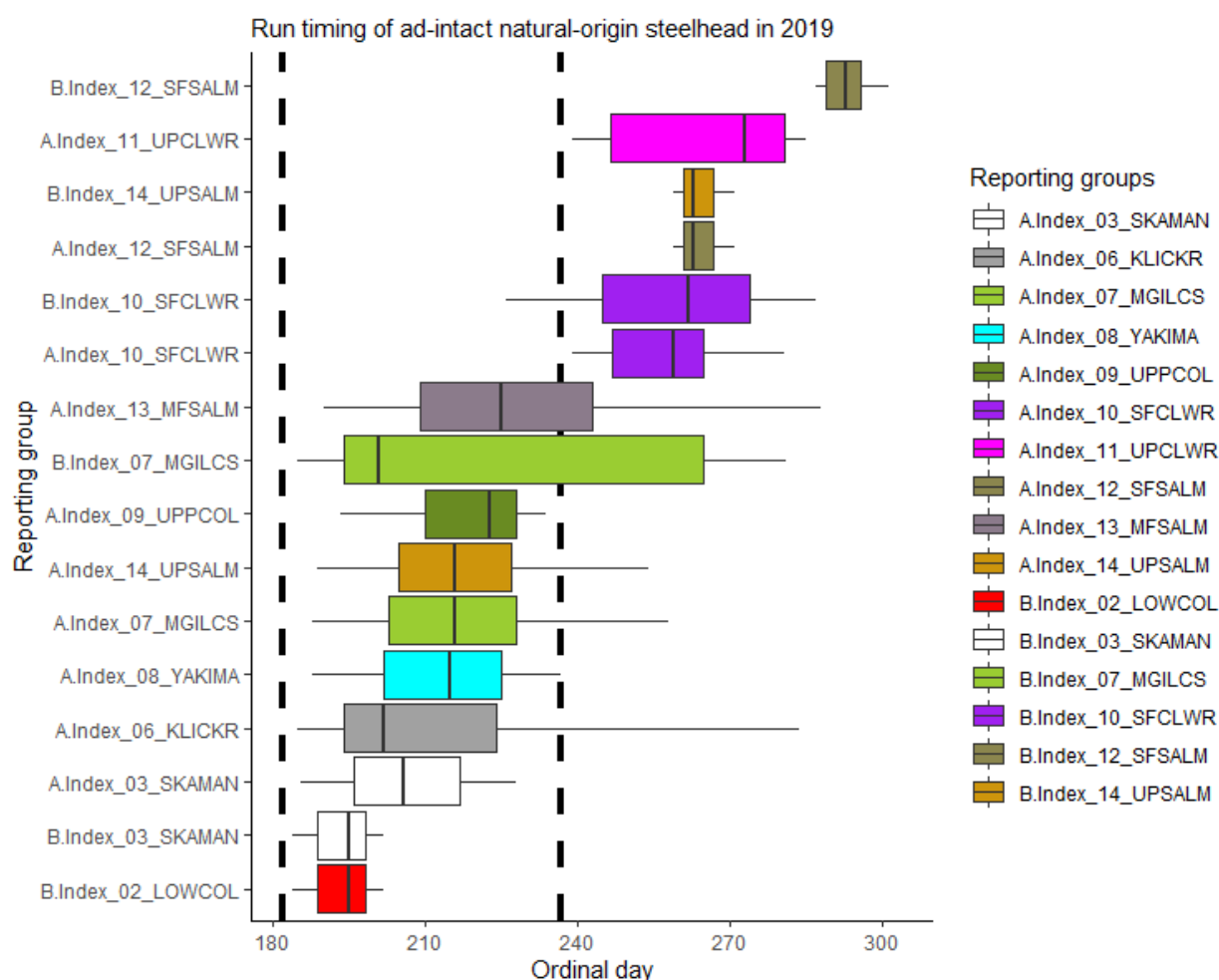


Figure 43. Reporting group level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for natural-origin steelhead (unclipped hatchery-origin fish excluded) that were sampled at Bonneville Dam in 2019 and split by A-Index and B-Index size category.

Estimated abundance and run-timing of Sockeye salmon stocks in 2019

Daily passage of Sockeye salmon at Bonneville Dam in 2019 is provided in Figure 44. Stock abundance for sockeye salmon was estimated over a course of 15 statistical weeks (i.e. weeks 22-36). A total of 971 sockeye salmon were sampled at Bonneville Dam in 2019 and were assigned to one of four genetic stocks (i.e., Okanogan, Wenatchee, Snake, and Lake Billy Chinook) using GSI and one reintroduced stock using PBT (Table 56). The Okanogan stock had the highest relative abundance (54,466), followed by the Wenatchee (8,052) (Table 56). This year was the first year in which we identified zero assignments to the Snake River since 2012 when we initiated genetic monitoring on sockeye salmon at Bonneville Dam. The Lake Billy Chinook stock had estimated abundance < 500, but were based on relatively few genetic assignments (N=10) (Table 56, Figure 45). The reintroduced stock from Yakima River was also low sample size and was estimated at 265 fish in 2019.

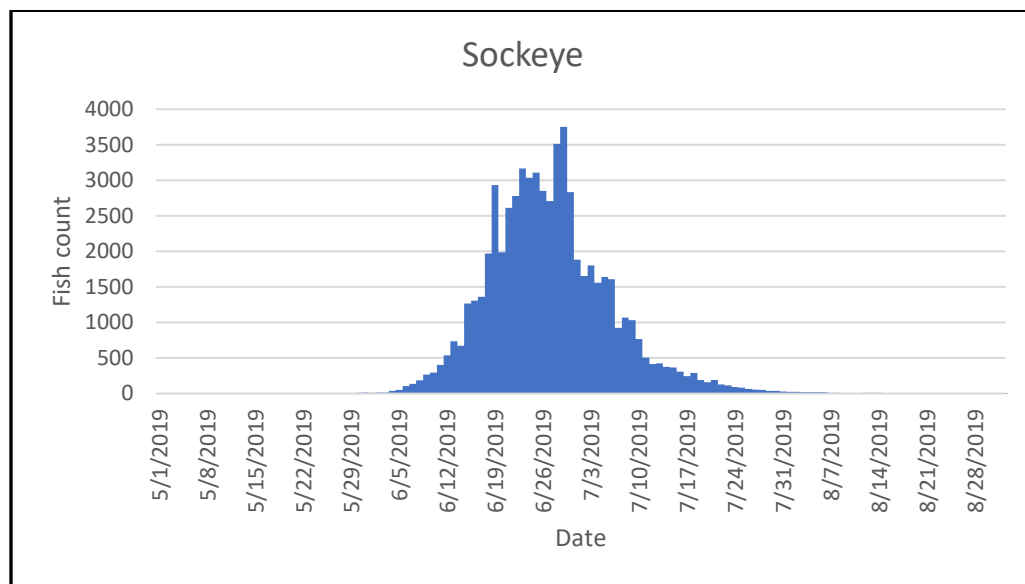
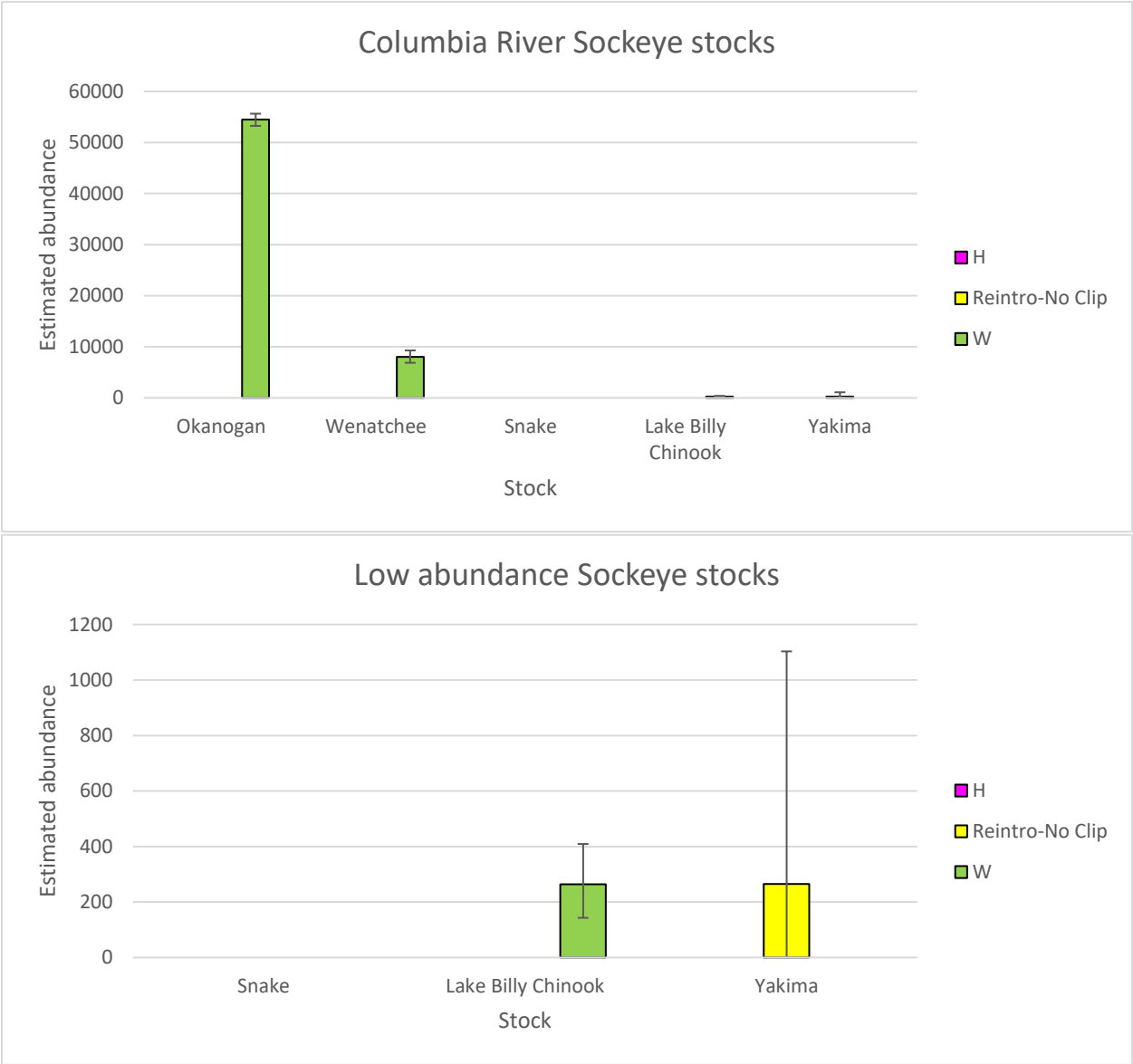


Figure 44. Daily passage of sockeye at Bonneville Dam in 2019 (source: <https://www.fpc.org>).

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Figure 45. Estimated abundance (\pm 95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2019.

We characterized the run-timing distributions for the two major sockeye salmon stocks (Figure 46). The Wenatchee and Okanogan stocks had nearly identical run timing distributions each with a median date near 06/26/19, and the Yakima and Lake Billy Chinook stocks were timed slightly later (Figure 46).

1960 **Table 56. Estimated abundance of sockeye salmon stocks passing Bonneville Dam in 2019.**

Reporting Group name	Estimated abundance					
	H		Reintro-No Clip		W	
	Est.	95% CI	Est.	95% CI	Est.	95% CI
Okanogan					54,466	53254 – 55645
Wenatchee					8,052	6878 – 9299
Snake						
Lake Billy Chinook					264	143 – 409
Yakima			265	0 – 1103		
Total	0		265		62,781	

1961

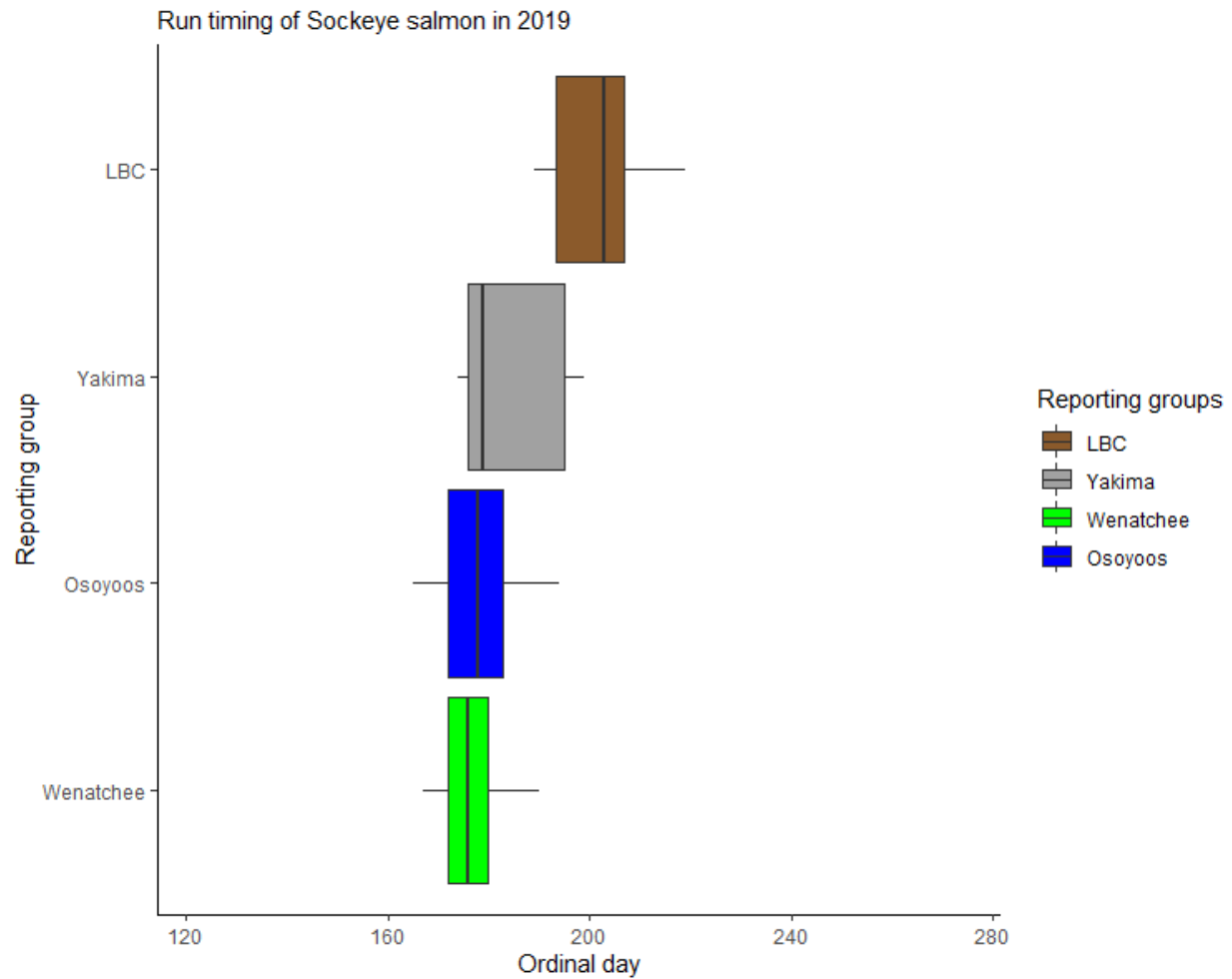


Figure 46. Run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for the major stocks of sockeye salmon that were sampled at Bonneville Dam in 2019 and assigned to stock of origin.

In-season analysis of Chinook salmon passing Bonneville Dam in 2020

There were no in-season reports covering data on Chinook Salmon that passed Bonneville Dam during the Spring Management Period, but we delivered four out of a total planned seven in-season reports for Chinook Salmon in 2020 across all management periods (Table 43). The first report was planned for distribution to members of the U.S. v OR TAC on May 11, 2020, however, the ACOE did not allow operation of the AFF until a permitting issue was resolved. Sampling resumed on May 17, 2019 but a large portion of the spring period could not be sampled. This was the first major interruption in sampling of the spring period since multiple decades of monitoring at the AFF has been conducted by CRITFC. 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 a new analysis similar to the reporting for the Bonneville Dam post-season report for run year 2019. Similar to last year, 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. Further, we used TAC estimates of the clipped and unclipped adult Chinook salmon and expanded genetic stock proportions with those estimates.

A total of 3,101 adult-sized Chinook Salmon were collected and analyzed for the 2020 in-season reports (Table 57). 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 November 9, 2020 provided sub-totals for each stock that were broken out by management period (clipped hatchery-origin stocks, Table 58; unclipped hatchery-origin stocks, Table 59; natural-origin stocks, Table 60). Two stocks that are of particular interest for timely estimation of abundance are the natural-origin Snake River spring/summer run (Reporting groups 11_TUCANO, 12_HELLSC, 13_SFSALM, 14_CHMBLN, 15_MFSALM, and 16_UPSALM; Table 60) and upper Columbia River spring Chinook Salmon stocks (Reporting group 10_UCOLSP, Table 60). 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 U.S. v OR Management Agreement. This year due to sampling limitations, our ability to accurately estimate the spring period stock abundances was severely diminished.

PBT assignments during the Chinook Salmon management periods allowed classification of 58 unique hatchery broodstocks in 2020 (Table 61). The total estimated abundances of these clipped and unclipped broodstocks were comprised of 13% Snake River and 82% of hatcheries from the rest of the Columbia River above Bonneville Dam (Figure 47). Similar to the natural- and hatchery-origin abundance estimates, the subtotals of these hatchery broodstock abundances were provided to U.S. v OR TAC for each management period and bi-weekly strata for the in-season reporting in 2020. 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 62). In fact, in 2020, the percentage of adipose-clipped fish abundance that were estimated to be PBT broodstock ranged from 83 – 97%, 84 – 100%, and 78 – 100% 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 in the past years 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 were covered (Appendix 5). We have observed relatively high coverage in 2020.

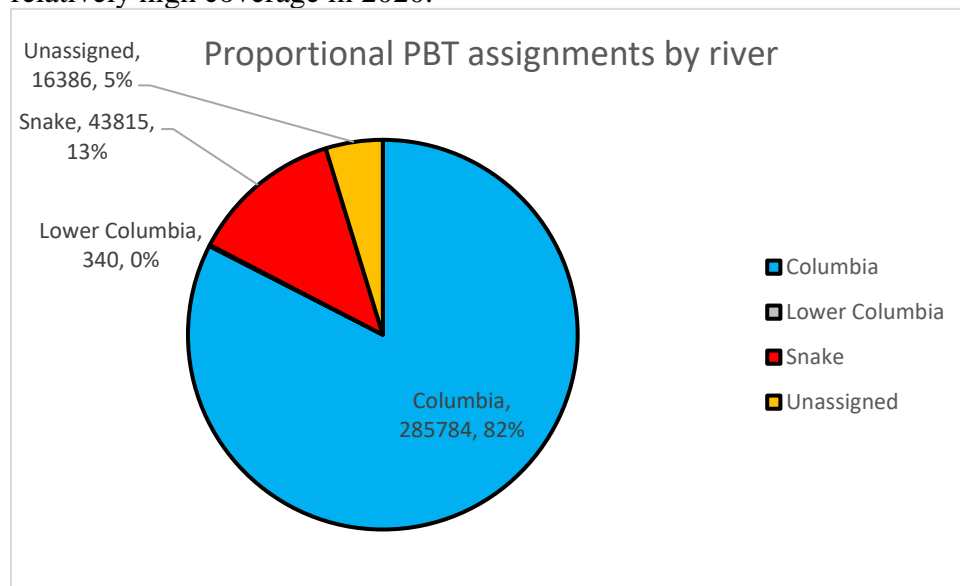


Figure 47. Proportion of hatchery broodstocks from the Snake River versus the rest of the Columbia River above Bonneville Dam in 2020.

2036 **Table 57. The sample sizes of Chinook salmon at the Bonneville Dam AFF during the**
2037 **spring, summer, and fall management periods of 2020.**

		Statistical week	TAC		Sample (N)							
			clip count	unclip count	Clipped		Non-clipped		Subtotal		Rate	
					GSI	PBT	GSI	PBT	clip	unclip	clip	unclip
Management period	Spring	1-16	1,014	158	-	-	-	-	0	0	0.00%	0.00%
		17	2,255	406	-	-	-	-	0	0	0.00%	0.00%
		18	8,641	1,962	-	-	-	-	0	0	0.00%	0.00%
		19	12,019	3,787	-	-	-	-	0	0	0.00%	0.00%
		20	6,272	2,941	-	-	-	-	0	0	0.00%	0.00%
		21	3,785	2,705	2	13	8	2	15	10	0.40%	0.37%
		22	4,706	3,816	7	75	50	16	82	66	1.74%	1.73%
		23	5,750	4,468	12	99	97	12	111	109	1.93%	2.44%
		24	6,644	4,538	4	47	36	9	51	45	0.77%	0.99%
		25	2,467	1,380	3	13	5	2	16	7	0.65%	0.51%
	Summer	25	7407	3361	9	66	32	1	75	33	1.01%	0.98%
		26	11433	5855	13	58	45	7	71	52	0.62%	0.89%
		27	8850	4295		42	19	5	42	24	0.47%	0.56%
		28	5383	2959	1	22	9	2	23	11	0.43%	0.37%
		29	4200	2427	6	43	36	4	49	40	1.17%	1.65%
		30	2504	2090	6	47	52	12	53	64	2.12%	3.06%
		31	1606	1694	1	22	47	7	23	54	1.43%	3.19%
	Fall	31	199	246					0	0	0.00%	0.00%
		32	1,337	1,720	1	25	20	6	26	26	1.94%	1.51%
		33	1,111	1,575	2	4	14	2	6	16	0.54%	1.02%
		34	10,471	12,364	7	51	58	32	58	90	0.55%	0.73%
		35	30,487	12,596	20	81	62	33	101	95	0.33%	0.75%
		36	61,595	41,078	26	114	101	66	140	167	0.23%	0.41%
		37	31,692	43,461	11	56	56	21	67	77	0.21%	0.18%
		38	42,457	16,761	6	72	122	64	78	186	0.18%	1.11%
		39	18,923	19,820	6	75	151	45	81	196	0.43%	0.99%
		40	6,494	14,366	8	64	139	43	72	182	1.11%	1.27%
		41	6,065	7,978	5	38	157	40	43	197	0.71%	2.47%
		42-48	2,147	6,451	2	21	36	12	23	48	1.07%	0.74%
		Total	307,914	227,258	158	1,148	1,352	443	1,306	1,795	0.42%	0.79%

2038 Note: The fish counts indicate the number of adult-sized Chinook Salmon at the fish ladder
2039 windows at Bonneville Dam and the sample (N) indicates the numbers of adult-sized Chinook
2040 Salmon (>560 mm fork length) that were collected at the AFF. TAC provides estimates of the
2041 total clipped an unclipped adult abundance. The AFF sample is broken into adipose-clipped and

2042 non-clipped categories and then further indicate whether a PBT assignment (PBT) was
2043 confirmed or if it was not assigned with PBT (GSI). Sample rate relates the total sample for a
2044 particular stratum to the total fish counted at the window. The alternating gray and clear rows
2045 indicate the breakpoints in the weekly strata at which time one of the seven total in-season
2046 analyses was performed (Table 43). This year the spring period stock abundances could only be
2047 estimated from weeks 21-25 (5/17/20-6/15/20).

2048 **Table 58. Preliminary in-season reporting of clipped hatchery-origin stock-specific abundance estimates of adult-sized**
2049 **Chinook Salmon passing Bonneville Dam across all management periods in 2020.**

		H	Spring		Summer		Fall		Cumulative total date Nov. 1
Reporting Group name	Run type	Reporting Group Code	Est. abund.		Est. abund.		Est. abund.		Est. abund.
			Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean
Youngs Bay	Spring	01_YOUNGS							0
West Cascade Spring	Spring	02_WCASSP	247	0 – 655					247
West Cascade Fall*	Fall	03_WCASFA					340	0 – 1485	340
Willamette	Spring	04_WILLAM			107	0 – 378			107
Spring Creek Tule	Fall	05_SPCRTU			54	0 – 219	58,204	46229 – 69263	58,257
Klickitat	Spring	06_KLICKR	1,582	523 – 3589	406	0 – 1161			1,987
Deschutes spring	Spring	07_DESCSP	299	0 – 679	258	0 – 842			557
John Day	Spring	08_JOHNDR							0
Yakima	Spring	09_YAKIMA	1,274	537 – 2143	216	0 – 699			1,490
Upper Columbia spring	Spring	10_UCOLSP	1,466	457 – 3431					1,466
Tucannon	Spring	11_TUCANO							0
Hells Canyon	Spring/Summer	12_HELLSC	4,628	3075 – 6625	331	0 – 1206			4,959
South Fork Salmon	Spring/Summer	13_SFSALM	1,264	315 – 3027					1,264
Chamberlain Creek	Spring/Summer	14_CHMBLN	536	0 – 2144					536
Middle Fork Salmon	Spring/Summer	15_MFSALM	536	0 – 2678					536
Upper Salmon	Spring/Summer	16_UPSALM	1,892	949 – 2813					1,892
Deschutes fall	Fall	17_DESCFA							0
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	8,879	5938 – 11528	39,304	37770 – 40360	73,553	63417 – 85696	121,735
Snake River fall	Fall	19_SRFALL			651	173 – 1291	23,932	16610 – 31543	24,582
Bonneville Pool spring	Spring	20_BONPOOLSP	750	183 – 1386					750

Umatilla spring	Spring	21_UMATILLASP							0
Bonneville Pool fall	Fall	22_BONPOOLFA			58	0 – 230	56,950	47587 – 67174	57,008
Umatilla fall	Fall	23_UMATILLAFA							0
Total			23,352		41,383		212,978		277,713

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 – dec 31) management periods and the cumulative total through the window counts on Nov 1, 2020 are provided. Bonneville 2020 spring, summer, and fall management period Chinook PBT/GSI analyses that corresponds with statistical weeks 1-25 (01/01/20-06/15/20: spring)***, 25-30 (6/16/20-7/31/20:summer) and 31-48 (8/1/2020-11/1/2020:fall). This year the spring period stock abundances could only be estimated from weeks 21-25 (5/17/20-6/15/20).

Table 59. Preliminary in-season reporting of unclipped hatchery-origin stock-specific abundance estimates of adult-sized Chinook Salmon passing Bonneville Dam across all management periods in 2020.

			HNC		Spring		Summer		Fall		Cumulative total date Nov. 1
Reporting Group name	Run type	Reporting Group Code	Est. abund.		Est. abund.		Est. abund.		Est. abund.		Est. abund.
			Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean
Youngs Bay	Spring	01_YOUNGS									0
West Cascade Spring	Spring	02_WCASSP	167	0 – 834							167
West Cascade Fall*	Fall	03_WCASFA									0
Willamette	Spring	04_WILLAM									0
Spring Creek Tule	Fall	05_SPCRTU					5,761	2068 – 10309			5,761
Klickitat	Spring	06_KLICKR	88	0 – 352							88
Deschutes spring	Spring	07_DESCSP	89	0 – 357							89
John Day	Spring	08_JOHNDR									0
Yakima	Spring	09_YAKIMA	337	0 – 1105							337
Upper Columbia spring	Spring	10_UCOLSP	840	281 – 1538							840

Tucannon	Spring	11_TUCANO							0
Hells Canyon	Spring/Summer	12_HELLSC	1,007	290 – 1855					1,007
South Fork Salmon	Spring/Summer	13_SFSALM	449	0 – 1246	115	0 – 461			565
Chamberlain Creek	Spring/Summer	14_CHMBLN							0
Middle Fork Salmon	Spring/Summer	15_MFSALM							0
Upper Salmon	Spring/Summer	16_UPSALM	352	0 – 835					352
Deschutes fall	Fall	17_DESCFA							0
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	3,078	1820 – 4335	2,566	1248 – 3975	27,843	21996 – 34351	33,488
Snake River fall	Fall	19_SRFALL			517	99 – 1243	10,481	7171 – 14957	10,999
Bonneville Pool spring	Spring	20_BONPOOLSP	381	0 – 963					381
Umatilla spring	Spring	21_UMATILLASP	88	0 – 352					88
Bonneville Pool fall	Fall	22_BONPOOLFA					14,451	10399 – 18757	14,451
Umatilla fall	Fall	23_UMATILLFA							0
Total			6,877		3,199		58,536		68,612

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 – dec 31) management periods and the cumulative total through the window counts on Dec 31, 2020 are provided.

Table 60. Preliminary in-season reporting of natural-origin stock-specific abundance estimates of adult-sized Chinook Salmon passing Bonneville Dam across all management periods in 2020.

			W	Spring	Summer	Fall	Cumulative total date Nov. 1		
Reporting Group name	Run type	Reporting Group Code	Est. abund.		Est. abund.		Est. abund.		Est. abund.
			Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean
Youngs Bay	Spring	01_YOUNGS			31	0 – 94	415	84 – 907	446
West Cascade Spring	Spring	02_WCASSP							0
West Cascade Fall	Fall	03_WCASFA					1,099	511 – 1828	1,099

Willamette	Spring	04_WILLAM	43	0 – 129	63	0 – 125			106
Spring Creek Tule	Fall	05_SPCRTU					546	163 – 2167	546
Klickitat	Spring	06_KLICKR	86	0 – 215					86
Deschutes spring	Spring	07_DESCSP							0
John Day	Spring	08_JOHNDR	219	43 – 438					219
Yakima	Spring	09_YAKIMA	359	107 – 633	31	0 – 94			391
Upper Columbia spring	Spring	10_UCOLSP	1,355	875 – 1904	113	0 – 338			1,468
Tucannon	Spring	11_TUCANO							0
Hells Canyon	Spring/Summer	12_HELLSC	2,178	1544 – 2826	264	61 – 529			2,443
South Fork Salmon	Spring/Summer	13_SFSALM	865	516 – 1257	419	0 – 842			1,285
Chamberlain Creek	Spring/Summer	14_CHMBLN	88	0 – 264					88
Middle Fork Salmon	Spring/Summer	15_MFSALM	612	305 – 963					612
Upper Salmon	Spring/Summer	16_UPSALM	1,328	829 – 1880	113	0 – 338			1,440
Deschutes fall	Fall	17_DESCFA			92	0 – 213	4,281	2362 – 6326	4,373
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	2,895	2098 – 3783	17,416	16229 – 18657	96,296	90330 – 101571	116,606
Snake River fall	Fall	19_SRFALL			941	542 – 1444	17,243	14293 – 20419	18,183
Total			10,030		19,482		119,880		149,392

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 – dec 31) management periods and the cumulative total through the window counts on Dec 31, 2020 are provided.

2073 **Table 61. The estimated abundances of the clipped and unclipped adult-sized Chinook salmon assigned to PBT hatchery**
2074 **broodstock that passed Bonneville Dam in 2020 (5/17/2020 – 12/31/2020).**

Period	Expected Run Time	Hatchery	Broodstock	Brood year	GSI Rep Grp	Clipped		Unclipped		Total
						Est.	95% C.I.	Est.	95% C.I.	
Spring	01Spring	Parkdale Fish Facility	OtsPFF16_sp	2016	02_WCASSP	247	57 – 494			247
	01Spring	Parkdale Fish Facility	OtsPFF17_sp	2017	02_WCASSP			167	0 – 500	167
	01Spring	Klickitat Hatchery	OtsKH16_sp	2016	06_KLICKR	1,493	659 – 2493	88	0 – 264	1,581
	01Spring	Round Butte Fish Hatchery	OtsRB16_sp	2016	07_DESCSP	258	56 – 491			258
	01Spring	Warm Springs National Fish Hatchery	OtsWSNFH16_sp	2016	07_DESCSP			89	0 – 268	89
	01Spring	Yakima River Roza Dam	OtsYR16int_sp	2016	09_YAKIMA	923	477 – 1413	337	0 – 796	1,261
	01Spring	Eastbank Fish Hatchery	OtsEASTBK16_sp	2016	10_UCOLSP	454	160 – 783	533	240 – 921	987
	01Spring	Leavenworth National Fish Hatchery	OtsLNFH16_sp	2016	10_UCOLSP			88	0 – 264	88
	01Spring	Methow Fish Hatchery	OtsMETH16_sp	2016	10_UCOLSP			131	0 – 307	131
	01Spring	Winthrop National Fish Hatchery	OtsWTP16_sp	2016	10_UCOLSP	354	88 – 619	88	0 – 264	442
	01Spring	Clearwater Fish Hatchery	OtsCLWH16S_sp	2016	12_HELLSC	653	326 – 1045	89	0 – 268	742
	01Spring	Clearwater Fish Hatchery	OtsPOWP16S_sp	2016	12_HELLSC			332	43 – 646	332
	01Spring	Dworshak National Fish Hatchery	OtsDWOR16S_sp	2016	12_HELLSC	416	147 – 718			416
	01Spring	Lookingglass Fish Hatchery	OtsLOOK16S_sp	2016	12_HELLSC	748	352 – 1199	273	0 – 622	1,022

01Spring	Rapid River Fish Hatchery	OtsRAPH16S_sp	2016	12_HELLSC	1,102	650 – 1579	134	0 – 314	1,236
01Spring	Rapid River Fish Hatchery	OtsRAPH17S_sp	2017	12_HELLSC	628	0 – 1618			628
01Spring	Carson National Fish Hatchery	OtsCAR16_sp	2016	20_BONPOO LSP	467	200 – 789	287	43 – 624	753
01Spring	Little White Salmon National Fish Hatchery	OtsLWS16_sp	2016	20_BONPOO LSP	284	0 – 568	94	0 – 283	378
01Spring	Umatilla Fish Hatchery	OtsUMA16_sp	2016	21_UMATILL ASP			88	0 – 264	88
02Spring/ Summer	Lookingglass Fish Hatchery	OtsIMNW16S_spsu	2016	12_HELLSC	1,015	584 – 1430	178	0 – 445	1,193
02Spring/ Summer	McCall Fish Hatchery	OtsMCCA15S_spsu	2015	13_SFSALM	239	58 – 479			239
02Spring/ Summer	McCall Fish Hatchery	OtsMCCA16S_spsu	2016	13_SFSALM	407	146 – 700	290	43 – 651	697
02Spring/ Summer	McCall Fish Hatchery	OtsMCCA17S_spsu	2017	13_SFSALM			159	0 – 478	159
02Spring/ Summer	Pahsimeroi Fish Hatchery	OtsPAHH16S_spsu	2016	16_UPSALM	613	258 – 993	88	0 – 265	701
02Spring/ Summer	Sawtooth Fish Hatchery	OtsSAWT16S_spsu	2016	16_UPSALM	1,074	638 – 1550	263	43 – 485	1,337
03Summer	Chief Joseph Hatchery	OtsCJH15int_su	2015	18_UCOLSF	163	0 – 397	524	175 – 1049	687
03Summer	Chief Joseph Hatchery	OtsCJH15seg_su	2015	18_UCOLSF	853	176 – 1971			853
03Summer	Chief Joseph Hatchery	OtsCJH17seg_su	2017	18_UCOLSF	656	0 – 1843			656
03Summer	Eastbank Fish Hatchery	OtsEASTBK14_su	2014	18_UCOLSF			156	0 – 467	156
03Summer	Eastbank Fish Hatchery	OtsEASTBK15_su	2015	18_UCOLSF	906	225 – 1834	199	0 – 467	1,105
03Summer	Eastbank Fish Hatchery	OtsEASTBK16_su	2016	18_UCOLSF	889	229 – 1922	950	475 – 1584	1,840

	03Summer	Entiat National Fish Hatchery	OtsENFH15_su	2015	18_UCOLSF	1,243	274 – 2515	427	0 – 854	1,670
	03Summer	Entiat National Fish Hatchery	OtsENFH16_su	2016	18_UCOLSF	56	0 – 169	156	0 – 467	212
	03Summer	Wells Fish Hatchery	OtsWELLS15_su	2015	18_UCOLSF	684	370 – 1022	199	0 – 510	883
	03Summer	Wells Fish Hatchery	OtsWELLS16_su	2016	18_UCOLSF	169	56 – 338	467	156 – 934	636
	#N/A	#N/A	Unassigned	#N/A	#N/A	6,356	4352 – 8546			6,356
			Spring Subtotal			23,352		6,877		30,229
Summer	01Spring	Klickitat Hatchery	OtsKH16_sp	2016	06_KLICKR	318	0 – 756			318
	01Spring	Klickitat Hatchery	OtsKH17_sp	2017	06_KLICKR	88	0 – 264			88
	01Spring	Round Butte Fish Hatchery	OtsRB16_sp	2016	07_DESCSP	161	0 – 483			161
	01Spring	Yakima River Roza Dam	OtsYR17int_sp	2017	09_YAKIMA	55	0 – 165			55
	01Spring	Lookingglass Fish Hatchery	OtsLOOK16S_sp	2016	12_HELLSC	111	0 – 332			111
	02Spring/ Summer	Lookingglass Fish Hatchery	OtsIMNW16S_spsu	2016	12_HELLSC	220	0 – 661			220
	02Spring/ Summer	McCall Fish Hatchery	OtsMCCA17S_spsu	2017	13_SFSALM			115	0 – 346	115
	03Summer	Chief Joseph Hatchery	OtsCJH15seg_su	2015	18_UCOLSF	1,030	432 – 1640			1,030
	03Summer	Chief Joseph Hatchery	OtsCJH15int_su	2015	18_UCOLSF	1,307	636 – 2072	70	0 – 140	1,377
	03Summer	Chief Joseph Hatchery	OtsCJH16seg_su	2016	18_UCOLSF	5,000	3784 – 6367	241	0 – 627	5,241
	03Summer	Chief Joseph Hatchery	OtsCJH16int_su	2016	18_UCOLSF	4,991	3633 – 6401	729	251 – 1241	5,720
	03Summer	Chief Joseph Hatchery	OtsCJH17seg_su	2017	18_UCOLSF	300	56 – 656	67	0 – 202	367
	03Summer	Eastbank Fish Hatchery	OtsEASTBK15_su	2015	18_UCOLSF	2,721	1713 – 3752	207	0 – 622	2,928

	03Summer	Eastbank Fish Hatchery	OtsEASTBK16_su	2016	18_UCOLSF	11,798	9927 – 13706	722	263 – 1258	12,519
	03Summer	Entiat National Fish Hatchery	OtsENFH15_su	2015	18_UCOLSF	1,738	915 – 2720			1,738
	03Summer	Entiat National Fish Hatchery	OtsENFH16_su	2016	18_UCOLSF	1,733	923 – 2651	225	0 – 450	1,959
	03Summer	Wells Fish Hatchery	OtsWELLS15_su	2015	18_UCOLSF	1,778	1039 – 2605			1,778
	03Summer	Wells Fish Hatchery	OtsWELLS16_su	2016	18_UCOLSF	4,078	2849 – 5328	270	31 – 684	4,348
	03Summer	Wells Fish Hatchery	OtsWELLS17_su	2017	18_UCOLSF	479	0 – 1095	35	0 – 105	514
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON15S_1_fa	2015	19_SRFALL			34	0 – 101	34
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON16S_1_fa	2016	19_SRFALL	232	58 – 407	286	33 – 725	518
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON17S_1_fa	2017	19_SRFALL	58	0 – 174	166	66 – 298	224
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH16S_1_fa	2016	19_SRFALL	201	0 – 402	32	0 – 96	233
	04Fall	Little White Salmon National Fish Hatchery	OtsLWS15_fa	2015	22_BONPOO LFA	58	0 – 173			58
	#N/A	#N/A	Unassigned	#N/A	#N/A	2,930	1950 – 4145			2,930
			Summer Subtotal			41,383		3,199		44,582
Fall	03Summer	Chief Joseph Hatchery	OtsCJH15int_su	2015	18_UCOLSF	617	93 – 1236			617
	03Summer	Chief Joseph Hatchery	OtsCJH16int_su	2016	18_UCOLSF	349	83 – 700			349
	03Summer	Chief Joseph Hatchery	OtsCJH16seg_su	2016	18_UCOLSF	388	0 – 996			388
	03Summer	Eastbank Fish Hatchery	OtsEASTBK15_su	2015	18_UCOLSF	263	0 – 624			263
	03Summer	Eastbank Fish Hatchery	OtsEASTBK16_su	2016	18_UCOLSF	337	84 – 589	86	0 – 257	422

	03Summer	Wells Fish Hatchery	OtsWELLS16_su	2016	18_UCOLSF	331	83 – 579			331
	03Summer	Wells Fish Hatchery	OtsWELLS17_su	2017	18_UCOLSF	289	0 – 690			289
	04Fall	Washougal Fish Hatchery	OtsWAS16_fa	2016	03_WCASFA	340	0 – 925			340
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR16_fa	2016	05_SPCRTU	945	0 – 2351	209	0 – 627	1,154
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR17_fa	2017	05_SPCRTU	45,670	37202 – 52219	4,918	2346 – 7748	50,588
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR18_fa	2018	05_SPCRTU	9,517	6579 – 12741	606	133 – 1127	10,123
	04Fall	Priest Rapids Hatchery	OtsPRH15_fa	2015	18_UCOLSF	978	282 – 1822			978
	04Fall	Priest Rapids Hatchery	OtsPRH16_fa	2016	18_UCOLSF	22,996	18038 – 27893	12,419	9523 – 15371	35,415
	04Fall	Priest Rapids Hatchery	OtsPRH17_fa	2017	18_UCOLSF	44,216	37473 – 50663	15,311	12531 – 18422	59,527
	04Fall	Priest Rapids Hatchery	OtsPRH18_fa	2018	18_UCOLSF	105	0 – 314			105
	04Fall	Ringold Springs State Hatchery	OtsRG17_fa	2017	18_UCOLSF	348	93 – 702			348
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON15S_1_fa	2015	19_SRFALL			295	0 – 739	295
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON16S_1_fa	2016	19_SRFALL	5,205	2917 – 7588	1,690	826 – 2680	6,895
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON17S_1_fa	2017	19_SRFALL	14,757	10842 – 18725	3,640	2222 – 5393	18,397
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH15S_1_fa	2015	19_SRFALL			231	0 – 549	231
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH16S_1_fa	2016	19_SRFALL	2,123	896 – 3581	3,137	1814 – 4589	5,259

	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH17S_1_fa	2017	19_SRFALL	1,134	302 – 2246	1,444	513 – 2650	2,578
	04Fall	Little White Salmon National Fish Hatchery	OtsLWS15_fa	2015	22_BONPOO LFA	6,906	4480 – 9596	201	0 – 414	7,107
	04Fall	Little White Salmon National Fish Hatchery	OtsLWS16_fa	2016	22_BONPOO LFA	44,171	38045 – 50542	12,546	9634 – 15394	56,718
	04Fall	Little White Salmon National Fish Hatchery	OtsLWS17_fa	2017	22_BONPOO LFA	4,027	2448 – 5957	1,670	659 – 2902	5,697
	#N/A	#N/A	Unassigned	#N/A	#N/A	6,968	3325 – 13328	133	0 – 398	7,101
			Fall SubTotal			212,978		58,536	271,514	

2075
2076

2077 **Table 62. Expanded abundance of PBT-assigned Chinook Salmon stocks across**
2078 **management periods in 2020.**

	Statistical week	Sample (Tag-rate-Corrected abundance)				Total GSI	Total PBT	% PBT of Clipped fish	
		Clipped		Non-clipped					
		GSI	PBT	GSI	PBT				
Management period	Spring	1-16							
		17							
		18							
		19							
		20							
		21	417	3,368	2,074	631	2,491	3,999	89.0%
		22	206	4,499	2,846	970	3,052	5,470	95.6%
		23	380	5,370	3,962	506	4,342	5,876	93.4%
		24	215	6,430	3,589	948	3,804	7,378	96.8%
		25	432	2,035	959	421	1,391	2,456	82.5%
	Summer	25	660	6,746	3,258	104	3,918	6,850	91.1%
		26	1,784	9,650	5,058	796	6,842	10,446	84.4%
		27	0	8,850	3,394	901	3,394	9,751	100.0%
		28	190	5,193	2,402	557	2,593	5,749	96.5%
		29	451	3,749	2,176	251	2,627	4,000	89.3%
		30	238	2,266	1,687	403	1,925	2,669	90.5%
		31	34	1,572	1,458	236	1,492	1,808	97.9%
	Fall	31							
		32	0	1,337	1,309	411	1,309	1,748	100.0%
		33	244	867	1,375	200	1,619	1,067	78.0%
		34	0	10,471	7,652	4,712	7,652	15,183	100.0%
		35	2,533	27,954	7,875	4,721	10,408	32,675	91.7%
		36	5,264	56,331	24,116	16,962	29,380	73,293	91.5%
		37	2,512	29,180	30,776	12,685	33,287	41,866	92.1%
		38	0	42,457	10,707	6,054	10,707	48,511	100.0%
		39	312	18,611	15,029	4,791	15,341	23,402	98.4%
		40	434	6,060	10,748	3,618	11,183	9,677	93.3%
		41	505	5,560	6,277	1,701	6,782	7,261	91.7%
		42-48	131	2,016	4,775	1,676	4,906	3,692	93.9%
		Total		16,942	260,572	153,503	64,255	170,445	324,827

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.

In-season analysis of steelhead passing Bonneville Dam in 2020

There were three reports provided to U.S. v OR TAC during the summer A-/B-Index Management Period (7/1/2020 – 10/31/2020, Table 43). The Skamania Management Period (4/1/2020 – 6/30/2020) had been planned to have a report but the previously mentioned sampling limitations described for the Chinook salmon spring management period also prevented our ability from obtaining adequate sample sizes of the Skamania period. There were a total of 839 clipped and 590 unclipped steelhead that were sampled at the Bonneville Dam AFF and genotyped in 2020 (Table 63). 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 U.S. v OR 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 63). 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 64, Table 65, Table 66). 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, Sockeye 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 issue is now resolved through our implementation of SCOBIDEUX and SPIBETR methodologies described previously (Section 3). Finally, as we have demonstrated in our post-season analyses, the preliminary analysis reports for 2020 include a breakdown of all the A- and B-Index steelhead abundance by broodstock for both clipped and unclipped hatchery-origin groups (Table 67).

2112 **Table 63. The sample sizes of Summer Steelhead at the Bonneville Dam AFF during the Skamania and A-/B-Index**
2113 **management periods of 2020.**

					Sample (N)													
	Statistical week	Strata	Clipped count	Unclipped count	A-Index				B-Index				Clipped Total	Unclipped Total	Clipped Sample rate	Unclipped Sample rate		
					Clipped		Unclipped		Clipped		Unclipped							
					GSI	PBT	GSI	PBT	GSI	PBT	GSI	PBT						
Skamania	14	1	76	46									0	0	0.00%	0.00%		
	15	1	151	131									0	0	0.00%	0.00%		
	16	1	92	65									0	0	0.00%	0.00%		
	17	1	44	58									0	0	0.00%	0.00%		
	18	1	39	39									0	0	0.00%	0.00%		
	19	1	23	36									0	0	0.00%	0.00%		
	20	1	18	23									0	0	0.00%	0.00%		
	21	1	28	31									0	0	0.00%	0.00%		
	22	1	39	56	1			1				1	1	2.56%	1.79%			
	23	1	84	133	1	1						2	0	2.38%	0.00%			
	24	1	125	213			3					0	3	0.00%	1.41%			
	25	1	283	445		1	2	1				2	3	0.71%	0.67%			
	26	1	400	896	1	2	3					3	3	0.75%	0.33%			
	27	1	189	338		1	1					1	1	0.53%	0.30%			
		Subtotal Skamania	1	1591	2510	3	5	9	2	0	0	0	0	8	11	0.50%	0.44%	
A-/B-Index	27	1	843	1,299		5	3						5	3	0.59%	0.23%		
	28	1	2233	2,671	1	3	7						4	7	0.18%	0.26%		
	29	1	2970	3,664	8	21	37	2			1		29	40	0.98%	1.09%		
	30	2	5106	5,578	10	50	61	6			6		60	73	1.18%	1.31%		
	31	3	7015	6,188	17	59	81	4		1	3		77	88	1.10%	1.42%		
	32	4	5484	4,028	22	66	75	6		3	5		91	86	1.66%	2.14%		
	33	5	3225	1,932	21	70	44	5	3	3	4		97	53	3.01%	2.74%		
	34	6	4792	2,562	10	50	41	6	1	6	7	2	67	56	1.40%	2.19%		

35	7	5223	2,175	8	36	20	4		22	9	2	66	35	1.26%	1.61%
36	8	7835	3,444	5	13	6		1	27	3	1	46	10	0.59%	0.29%
37	8	6636	2,854		5	1	1		16		5	21	7	0.32%	0.25%
38	8	7167	2,685	4	5	5	3	2	39	8	4	50	20	0.70%	0.74%
39	9	3801	1,448	2	19	2	4		62	6	19	83	31	2.18%	2.14%
40	10	1602	693		15	4	2	1	61	6	18	77	30	4.81%	4.33%
41	11	950	405	5	3	5	3	2	28	3	21	38	32	4.00%	7.90%
42	11	441	253	3	15	11	3		10	3	2	28	19	6.35%	7.51%
43	11	171	127									0	0	0.00%	0.00%
44	11	49	42									0	0	0.00%	0.00%
Summer A-/B- Index subtotal		65,543	42,048	116	435	403	49	10	278	64	74	839	590	1.28%	1.40%
Total		68,725	47,068	122	445	421	53	10	278	64	74	856	612	1.24%	1.30%

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 43).

Table 64. Estimated abundance of clipped hatchery-origin stocks of Summer Steelhead that passed Bonneville Dam in 2020 during the Skamania and A-/B-Index Management Periods.

Reporting Group name	Reporting Group Code	H		Subtotal for Skamania Period (Apr 1 - Jun 30)		Subtotal for A-/B- Index Period (Jul 01 - Oct 31)		Subtotal for A-/B-Index Period (Jul 01 - Oct 31)	
		All size		A-Index		B-Index			
		Est.	95% CI	Est.	95% CI	Est.	95% CI		

Lower Columbia	02_LOWCOL						
Skamania	03_SKAMAN	700	149 – 1120	3,174	1487 – 4819	38	0 – 185
Willamette	04_WILLAM						
Big White Salmon	05_BWSALM						
Klickitat	06_KLICKR						
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	420	0 – 971	14,576	11501 – 16935	349	0 – 980
Yakima	08_YAKIMA			59	0 – 241	0	0 – 0
upper Columbia	09_UPPCOL			2,303	1227 – 3640	219	0 – 515
SF Clearwater	10_SFCLWR			1,811	815 – 3118	22,091	20067 – 25054
upper Clearwater	11_UPCLWR						
SF Salmon	12_SFSALM						
MF Salmon	13_MFSALM						
upper Salmon	14_UPSALM			20,619	17296 – 24283	305	25 – 1115
Total		1,120		42,542		23,001	

Note: Based on the sample data described in Table 63 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.

Table 65. Estimated abundance of unclipped hatchery-origin stocks of Summer Steelhead that passed Bonneville Dam in 2020 during the Skamania and A-/B-Index Management Periods.

	HNC	Subtotal for Skamania Period (Apr 1 - Jun 30)		Subtotal for A-/B- Index Period (Jul 01 - Oct 31)		Subtotal for A-/B- Index Period (Jul 01 - Oct 31)	
Reporting Group name	Reporting Group Code	All size		A-Index		B-Index	
		Est.	95% CI	Est.	95% CI	Est.	95% CI

Lower Columbia	02_LOWCOL						
Skamania	03_SKAMAN	402	0 – 1207	188	0 – 702	0	0 – 0
Willamette	04_WILLAM						
Big White Salmon	05_BWSALM			15	0 – 65	0	0 – 0
Klickitat	06_KLICKR						
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS			1,238	480 – 1659	0	0 – 0
Yakima	08_YAKIMA						
upper Columbia	09_UPPCOL			318	88 – 623	0	0 – 0
SF Clearwater	10_SFCLWR			1,812	641 – 3644	3,994	2769 – 5962
upper Clearwater	11_UPCLWR						
SF Salmon	12_SFSALM						
MF Salmon	13_MFSALM			125		0	
upper Salmon	14_UPSALM			1,116	264 – 1638	0	0 – 0
	Total	402		4,812		3,994	

Note: Based on the sample data described in Table 63 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.

Table 66. Estimated abundance of natural-origin stocks (excluding unclipped hatchery-origin) of Summer Steelhead that passed Bonneville Dam in 2020 during the Skamania and A-/B-Index Management Periods.

	W	Subtotal for Skamania Period (Apr 1 - Jun 30)		Subtotal for A-/B-Index Period (Jul 01 - Oct 31)		Subtotal for A-/B- Index Period (Jul 01 - Oct 31)	
Reporting Group name	Reporting Group Code	All size		A-Index		B-Index	
		Est.	95% CI	Est.	95% CI	Est.	95% CI
Lower Columbia	02_LOWCOL	189	0 – 564	94	0 – 234	93	0 – 245

Skamania	03_SKAMAN	165	0 – 544	257	31 – 555	0	0 – 0
Willamette	04_WILLAM						
Big White Salmon	05_BWSALM						
Klickitat	06_KLICKR	189	0 – 564	475	221 – 777	147	0 – 301
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	757	189 – 1316	20,053	18579 – 21460	1,576	998 – 2181
Yakima	08_YAKIMA	189	0 – 560	2,209	1573 – 2935	70	0 – 211
upper Columbia	09_UPPCOL			622	238 – 1058	37	0 – 109
SF Clearwater	10_SFCLWR			289	95 – 495	1,123	542 – 1786
upper Clearwater	11_UPCLWR			707	271 – 1216	1,503	803 – 2244
SF Salmon	12_SFSALM			125	0 – 375	380	45 – 775
MF Salmon	13_MFSALM			138	45 – 270	254	0 – 626
upper Salmon	14_UPSALM	189	0 – 564	3,093	2307 – 4001	0	0 – 0
Total		1,679		28,061		5,182	

Note: Based on the sample data described in Table 63 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.

*A small number (N=117) were estimated to be B-Index size.

Table 67. Estimated abundance of clipped and unclipped hatchery-origin A-/B-Index Summer Steelhead that passed Bonneville Dam in 2020 (July 1 – Oct 31) and were assigned to PBT broodstocks.

				Hatchery clipped				Hatchery unclipped			
				A-INDEX		B-INDEX		A-INDEX		B-INDEX	
Hatchery	Stock	GSI RepGrp	Broodstock	Est.	95% CI	Est.	95% CI	Est.	95% CI	Est.	95% CI
Skamania	Summer	03_SKAMANA	OmySKH16_su	876	0 – 1674						

Skamania	Summer	03_SKAMANA N	OmySKH17_su	2,009	1292 – 2775			188	0 – 484		
Little Sheep Creek	-	07_MGILCS	OmyLSCR17S	816	403 – 1268			121	0 – 271		
Little Sheep Creek	-	07_MGILCS	OmyLSCR18S	192	0 – 428						
Lyons Ferry	Grande Ronde	07_MGILCS	OmyCGRW17S	4,824	3899 – 5874	157	0 – 382	37	0 – 110		
Lyons Ferry	Touchet	07_MGILCS	OmyTOUW17S					237	36 – 515		
Lyons Ferry	Tucannon	07_MGILCS	OmyTUCW17S	112	0 – 293			69	0 – 206		
Lyons Ferry	-	07_MGILCS	OmyWALW17S	3,394	2482 – 4313			288	46 – 574		
Lyons Ferry	Grande Ronde	07_MGILCS	OmyCGRW18S	889	416 – 1421			49	0 – 148		
Lyons Ferry	Tucannon	07_MGILCS	OmyTUCW18S					51	0 – 151		
Lyons Ferry	Wallowa	07_MGILCS	OmyWALW18S	442	184 – 762						
Round Butte	Deschutes River	07_MGILCS	OmyRB17	2,081	1446 – 2774			125	0 – 375		
Eastbank	Chelan/Met how/Okano gan/Wenatc hee	09_UPPCOL	OmyEASTBK1 6					46	0 – 139		
Wells	Methow Stock	09_UPPCOL	OmyWEL_MET 17	468	117 – 894						
Wells	Okanogan Stock	09_UPPCOL	OmyWEL_OK A17	279	72 – 579	38	0 – 108				
Wells	On Station	09_UPPCOL	OmyWEL17	936	480 – 1405	181	60 – 362				
Wells	On Station	09_UPPCOL	OmyWEL18	246	0 – 493						

Winthrop NFH	Methow River	09_UPPCOL	OmyWTP17					228	90 – 407		
Dworshak NFH	Clearwater River	10_SFCLWR	OmyDWOC16S			124	0 – 371			24	0 – 73
Dworshak NFH	Clearwater River	10_SFCLWR	OmyDWOC17S	1,034	560 – 1615	16,396	14561 – 18212	207	0 – 621	1,344	714 – 2034
Dworshak NFH	Dwor-S	10_SFCLWR	OmyDWOS17S	164	49 – 281	719	274 – 1271	16	0 – 49	302	49 – 717
Dworshak NFH	SF Clearwater	10_SFCLWR	OmySFCW17S	162	0 – 396	4,714	3436 – 5887	298	56 – 699	2,177	1443 – 2960
Dworshak NFH	Upper Salmon	10_SFCLWR	OmyUSAL17S	46	0 – 137			640	203 – 1175	147	62 – 233
Dworshak NFH	Clearwater River	10_SFCLWR	OmyDWOC18S	48	0 – 141			17	0 – 49		
Dworshak NFH	Dwor-S	10_SFCLWR	OmyDWOS18S	28	0 – 85						
Oxbow	-	14_UPSALM	OmyOXBO17S	5,616	3953 – 7058	224	0 – 497	276	0 – 483		
Oxbow	-	14_UPSALM	OmyOXBO18S	2,305	1445 – 3229						
Pahsimeroi	Salmon River	14_UPSALM	OmyPAHH17S	3,856	2942 – 4744			348	71 – 688		
Pahsimeroi	Salmon River	14_UPSALM	OmyPAHH18S	670	335 – 1015			94	0 – 233		
Sawtooth	Salmon River	14_UPSALM	OmySAWT17S	5,641	4457 – 6790	25	0 – 74	203	0 – 454		
Sawtooth	Salmon River	14_UPSALM	OmySAWT18S	556	211 – 943			40	0 – 118		
#N/A	#N/A	#N/A	Unassigned	4,851	3559 – 6836	424	146 – 1043	1,234	683 – 2019		
TOTAL				42,542		23,001		4,812		3,994	

Post-season analysis of Sockeye Salmon passing Bonneville Dam in 2020

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 U.S. v OR TAC on August 10, 2020 (Table 43). 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 2020, there were 1,722 Sockeye Salmon that were sampled at the AFF and genotyped for this analysis (Table 68). This year we estimated low but non-zero abundance for the ESA listed stock (Redfish Lake Sockeye Salmon from the Snake River, N=122) (Table 68, Figure 48). 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. However, in 2020, we were not able to detect any of the Lake Billy Chinook stock. Importantly, we were able to estimate the reintroduced stock from the Yakima River using our PBT baseline and the stock abundance was a record high of 11,719 (95% C.I.: 6,448 – 18,174). This is an exciting result as it clearly demonstrates the success of the Yakama Nation Sockeye salmon reintroduction program and the critical need for PBT applications to monitor this success.

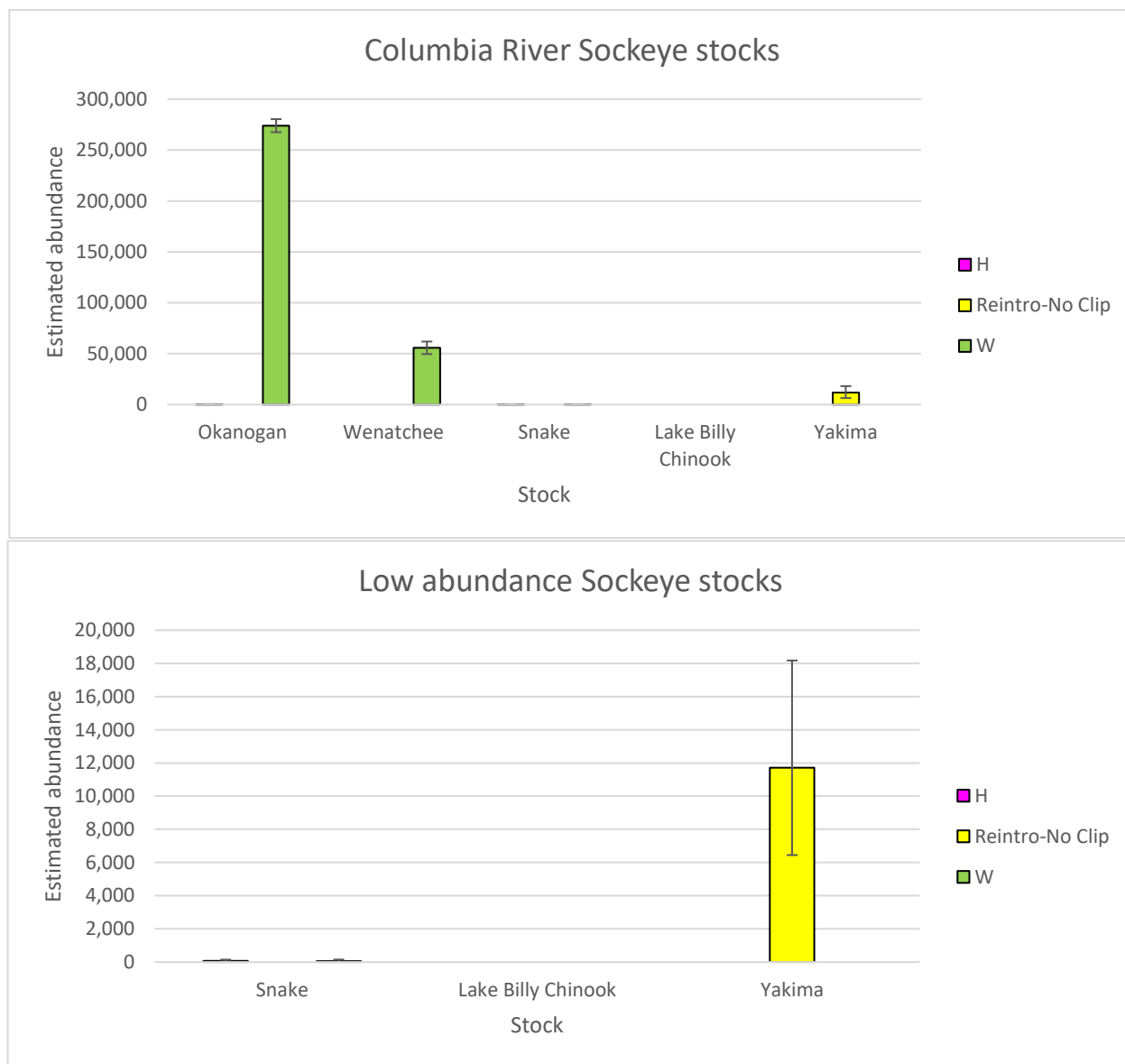


Figure 48. Estimated abundance (\pm 95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2020.

2176 **Table 68. Estimated abundance of Sockeye Salmon genetic stocks that passed Bonneville Dam in 2020.**

Reporting Group name	H		Reintro-No Clip		W		Sample Size			
	Est.	95% CI	Est.	95% CI	Est.	95% CI	H	Reintro-No Clip	W	Total
Okanogan	133	0 – 398			273,876	267546 – 280388	37		1,377	1,414
Wenatchee					55,890	49699 – 61963	4		270	274
Snake	72	19 – 145			50	0 – 150	2		1	3
Lake Billy Chinook										
Yakima			11,719	6448 – 18174				31		31
Total	204		11,719		329,815		43	31	1,648	1,722

2177 Note: The abundance is estimated from the total fish counts at the fish ladder windows at Bonneville Dam. Most stocks are identified
 2178 by GSI assignment, however we are now able to use PBT to identify Yakima fish that were reintroduced.

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 the 91% of fish that were clipped hatchery-origin summer A-/B-Index steelhead at Bonneville Dam in 2019 to 29 broodstock sources. This high percentage of PBT assignments is similar to what we would expect given our known tag rates and provides high confidence that we have the ability to assign most hatchery origin fish to their PBT 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 2020. Namely, the percentage of adipose-clipped fish abundance that were estimated to be PBT broodstock ranged from 83 – 97%, 84 – 100%, and 78 – 100% 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.

This is the first year we examined smolt-to-adult survival estimates using PBT data. We found that PBT abundance estimates of Spring Chinook Adults at Bonneville Dam had strong correspondence with hatchery smolt release data from one broodyear (2015). The trend suggested 625 smolts were needed to be released to equal 1 adult-sized 4-year-old Spring Chinook at Bonneville Dam in 2019. Future work could sum all abundance of the SY2015 adult return across age-classes (i.e., age 3, 4, and 5 in run years 2018, 2019, and 2020, respectively) that passed Bonneville Dam and were caught in lower river fisheries below the dam in the same set of years. This would allow a complete run reconstruction of these Spring Chinook salmon broodstock groups to the Columbia River mouth.

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 10 major clipped Chinook salmon hatchery-origin stocks (64 clipped hatchery broodstock sources), 6 major unclipped hatchery-origin stocks (46 unclipped hatchery broodstock sources) and 8 natural-origin stocks estimated to have relative abundances $\geq 1,000$ fish passing Bonneville Dam in 2019. The Spring Chinook stocks of 2019 were observed to spillover into the summer period by 2% of the total estimated abundance of these stocks across spring and summer periods for both natural-origin and hatchery-origin stocks. This overlap of run distributions of Spring stocks in the summer period was not as extreme as has been observed in some years. In contrast, the summer-run stocks from the upper Columbia River showed a quarter to a third of all combined spring and summer period abundance was observed to occur in the spring period for natural-origin and hatchery-origin stocks respectively.

We identified four clipped steelhead hatchery-origin stocks, a single unclipped hatchery-origin stock (29 total hatchery broodstock sources), and four natural-origin stocks estimated to have relative abundances $\geq 1,000$ fish passing Bonneville Dam in 2019. We found that genetic stocks seemed to fit well into the historical management categories, particularly the hatchery-origin stocks. Some B-Index fish appeared to have later run-timing compared to A-Index fish from the same stock.

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 eighth year (since 2012) that we were able to analyze sockeye salmon using GSI, and similar to that past two analyses, 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 2019, and found that the Okanogan stock has the greatest relative abundance followed by the Wenatchee stock. We found zero fish from the Snake River stock which is the record low for all previous years, and identified fish from Lake Billy Chinook and even from the reintroduced stock in Yakima River using a PBT baseline. We also found that the migratory run timing for the Okanogan and Wenatchee stocks overlaps broadly at Bonneville Dam.

This year (2020) we continued the increased frequency of in-season reporting as we performed in the past two years 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. Delays in these reports were out of our control due to sampling limitations imposed by ACOE during the spring period at the AFF. 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.

References

Hess, J.E., N.R. Campbell, A.P. Matala, S.R. Narum. 2012. 2011 Annual Report: Genetic Assessment of Columbia River Stocks. U.S. Dept. of Energy Bonneville Power Administration Report Project #2008-907-00.

Hess, J.E., N.R. Campbell, A.P. Matala, S.R. Narum. 2013. 2012 Annual Report: Genetic Assessment of Columbia River Stocks. U.S. Dept. of Energy Bonneville Power Administration Report Project #2008-907-00.

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Steele CA, Campbell MR, Ackerman M, McCane J, Hess MA, Campbell N, Narum SR. 2011. Parentage Based Tagging of Snake River hatchery steelhead and Chinook salmon. Bonneville Power Administration. Annual Progress Report, Project number 2010-031-00.
<https://research.idfg.idaho.gov/Fisheries%20Research%20Reports/Res11-111Steele2010%20Parentage%20Based%20Tagging%20Snake%20River%20Steelhead%20Salmon.pdf>

Section 5: Local adaptation in salmonids

Introduction

Environmental and landscape features can greatly contribute to the population structure, life history diversification, and local adaptation of organisms in aquatic habitats (reviewed in Storfer et al. 2006). Geographic barriers to dispersal include recent events that may have been human induced (e.g., dams) as well as ancient events such as glaciations and formation of mountain chains (e.g., Castric et al. 2001). However, other environmental characteristics such as elevation, temperature, forest cover, and precipitation may influence distribution, adaptation, and gene flow of species (Dionne et al. 2008; Narum et al. 2008). For example, the geographic distributions of species ranges are often determined by thermal tolerance (Brannon et al. 2004) and may necessitate adaptations for survival in extreme environments (Rodnick et al. 2004).

Screening with many genetic markers provides the opportunity to investigate local adaptation in natural populations and identify candidate genes under selection (Beaumont and Nichols 1996; Beaumont and Balding 2004; Excoffier et al. 2009). This has become a commonly employed approach in ecological and population genetics studies to detect outlier loci that are putatively under selection (e.g., Vasemagi and Primmer 2005; Nosil et al. 2008). Additionally, correlation methods can be highly informative to identify markers in coding and cis-regulatory regions of known functional genes that are associated with specific selective pressures or phenotypes (Lyman and Mackay 1998; Chase et al. 2009; Torgerson et al. 2009). With increasing genomic information available for non-model organisms, single nucleotide polymorphisms (SNPs) have begun to see increased use as genetic markers for population genetic studies (e.g., Morin et al. 2004). These sequence polymorphisms are densely scattered throughout the genome of most organisms and are commonly observed in both coding and non-coding regions of functional genes making them ideal markers to study adaptive molecular variation (e.g., Akey et al. 2002). In a large suite of SNPs that are distributed across the genome (e.g., Narum et al. 2018), it is possible to utilize both functionally neutral and adaptive markers within a single study. This combination of information provides a powerful approach to study questions in ecological genetics since both demographic processes (i.e., gene flow and genetic drift) and local adaptation (i.e., selection) may be inferred.

Molecular techniques such as RNA-seq (Wolf 2013) also provide the opportunity to investigate transcriptional response to thermal stress and further identify mechanisms for thermal adaptation. Patterns of gene expression under heat stress are important to determining evolutionary adaptation among conspecific populations that occupy various environments. Multiple genes have been shown to be involved in heat tolerance across many species, including highly conserved heat shock proteins (hsps) that are upregulated under stressful conditions such as exposure to heat (Morimoto et al. 1992; Sorensen et al. 2003). An adaptive heat shock response has additionally been shown to occur among conspecific populations that occupy variable environments (e.g., Dahlhoff and Rank 2000; Sorensen et al. 2001). However, many genes are known to have a role in regulating the effects of temperature and are likely to be involved in thermal adaptation

(Sorensen et al. 2005; Kassahn et al. 2007). Thus, RNA-seq provides the opportunity to investigate differential expression across the transcriptome and identify biological pathways involved in evolutionary response to thermal stress.

Thus, genome scans with large numbers of SNP markers (e.g., RAD sequencing, Baird et al. 2008; Pool-seq, Schlotterer et al. 2014) and gene expression (e.g., RNA-seq) approaches may be effective tools for identifying the genetic architecture underlying specific traits such as thermal tolerance, run-timing/maturation, disease resistance, anadromy, and age-at-maturity. Once these underlying genomic regions are identified, they can be broadly screened in populations throughout the Columbia River Basin to facilitate management for long term conservation and recovery of salmonids.

Fish Population RM&E

F&W Program Strategy: Assess the status and trend of diversity of natural and hatchery origin fish populations.

F&W Program Management Question: What are the status and trend of diversity of natural and hatchery origin fish populations?

Uncertainty Research

See Appendix A for table of critical uncertainties research.

Project Map:

<http://www.cbfish.org/Project.mvc/Map/2009-005-00>

Contract Map(s):

<http://www.cbfish.org/Contract.mvc/Map/61839>

<http://www.cbfish.org/Contract.mvc/Map/65575>

Methods: Protocols, Study Designs, and Study Area

Method Title: Whole Genome Resequencing

- **Method Link:**

- [Whole Genome Resequencing: Poolseq Individual Barcode v1.0](#) (ID: 6754) Published
- [Whole Genome Resequencing: Poolseq Pooled v1.0](#) (ID: 6775) Published

Method Summary:

With reference genome assemblies now publicly available for both Chinook salmon and steelhead, this enables whole genome resequencing for investigating adaptive variation across a large portion of the genome (50-80%) in these species. Whole genome resequencing methods include individually barcoded samples, or pools of samples (Pool-seq; 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 GTseq or other approaches to genotype many individuals to validate trait association, determine inheritance, and estimate linkage disequilibrium.

Method Title: RAD sequencing v1.0

Method Link: <http://www.monitoringmethods.org/Method/Details/4144>

Method Summary:

RAD sequencing is a technique for tagging DNA at restriction enzyme cut sites with adapters used in massively parallel sequencing. This method allows thousands of SNPs to be discovered and genotyped in several individuals. Through the use of sample specific DNA barcodes included in the adapters, information for specific samples can be separated in silico following sequencing. This method effectively reduces sequence complexity by targeting only sequence surrounding restriction enzyme cut sites making alignments among sequencing reads far less computationally intense. The sequence alignments among samples can then be analyzed for both identification and genotyping of SNPs (Single Nucleotide Polymorphisms). This method was first described by Baird et al. (2008).

Method Title: Obtain gene expression data via RNAseq v1.0

Method Link: <http://www.monitoringmethods.org/Method/Details/607>

Method Summary:

Compare gene expression between fish of different genetic backgrounds but raised in the same environment. Molecular techniques such as RNAseq provide the opportunity to investigate transcriptional response and further identify mechanisms for thermal adaptation. Patterns of gene expression are important to determining evolutionary adaptation among conspecific populations that occupy various environments.

Results

Objective 1) Environment & Landscape Genetics

Hypotheses:

Hypothesis 1: Environmental and landscape features act as drivers of selection leading to local adaptation of fish populations. Testing many variables can identify the key environmental drivers of selection.

Hypothesis 2: Environmental drivers of selection act on specific genes resulting in different allelic and genotypic frequencies among adapted populations. Genome scans can identify candidate genes involved in local adaptation of fish populations across heterogeneous landscapes.

Activities implemented:

Multiple studies have been initiated to investigate local adaptation with a landscape genetics/genomics approach to address the two hypotheses above. Our work has focused on steelhead and Chinook salmon throughout the Columbia River Basin. Studies continue to progress as more markers become available throughout the genome of each species.

For steelhead, landscape genetics work has been done at both fine and broad scales. Fine scale landscape genetics approaches were used to identify ecological patterns of residence vs anadromy and found consistent evidence that certain landscape features have led to prevalence of certain life history types in *O. mykiss* (Narum et al. 2008a) but also *O. nerka* (Nichols et al. 2016). Broad scale studies were initially done with panel of 188 SNP markers to investigate patterns of landscape genetics across 145 populations in the Columbia River Basin (Matala et al. 2014). Results indicated that precipitation and temperature were the primary environmental drivers of local adaptation and neutral genetic structure largely reflected isolation by distance. These results were shown to be robust due to replication of multiple populations representing each distinct genetic unit (Hand et al. 2016). A follow-up study (Micheletti et al. 2018a) was done with a much larger number of genetic markers (~20K SNPs) at broad scale and found evidence that the mainstem Columbia River migratory corridor exhibits greater selective pressure on steelhead than natal tributaries (Figure 49). Populations that must migrate long distances through the migratory corridor were under the most intense selection and multiple candidate genes were identified (Micheletti et al. 2018a). Redundancy analyses (RDA) were conducted for all Columbia River basin collections to model the degree to which the variation in environmental variables explained the variation in allele frequencies of migration-timing candidate markers (Collins et al. 2020). Redundancy analysis was performed on two sets of collections, all populations and each lineage (coastal vs. inland). We selected environmental variables for RDAs at collection sites in this study based on the variables significantly associated with adaptive genetic variation in a previous study (Micheletti et al. 2018a; Table 69). The populations are represented by text and colored black or red in accordance with their lineage determined by DAPC in adegenet. The arrows spatially denote a significant influence of environmental variables and the length of the arrow indicates the extent of the effect. Significant environmental variables retained in the RDA for all collections were adult migration distance, minimum temperature of the warmest month, 20-year average August water temperature, annual mean temperature, isothermality, and annual precipitation (Figure 50a). Annual precipitation had the greatest effect when all collections were analyzed together (Figure 50a). Environmental variables retained in the coastal lineage RDA were average temperature of the coldest quarter and precipitation of the wettest month (Figure 50b). Environmental variables retained in the interior lineage RDA were 20-year average

August water temperature and minimum temperature of the warmest month (Figure 50c). The relationships between genotypes and significant environmental variables were not robust for these data, but were significant for maximum temperature of the warmest month, annual precipitation, and migration distance. Additional studies are underway to further pinpoint candidate genes through whole genome resequencing.

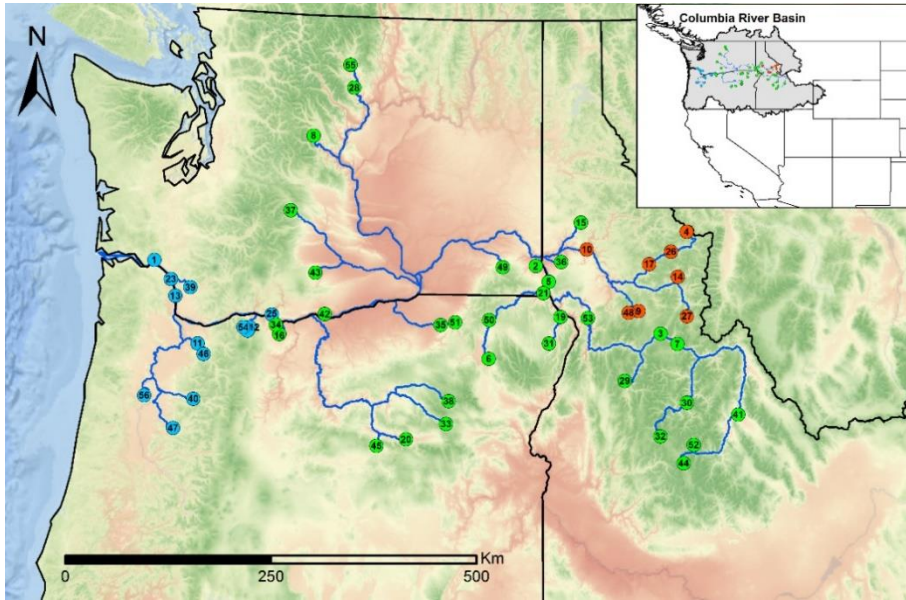


Figure 49. Steelhead collection localities colored by genetic cluster (from Micheletti et al. 2018a). blue = coastal, green = inland, red = inland-Clearwater. Blue lines indicate each population's migration path to the ocean. Map layer shows mean annual temperature for the warmest quarter with transition from colder (green) to warmer (red).

Table 69. Notation, descriptions, units, resolution, variable class, source, and whether the variable was retained in the model are listed for all environmental variables assessed with the RDA models.

Notation	Description	Unit	Res. (m)	Class	Source	Retained in model
mig_dist	Migration Distance	km	30	Topography	USGS	Y
elev_mean	Elevation	m	30	Topography	USGS	N
wtemp	Water Temp	°C	30	Temperature	NorWeST	Y
hli	Heat Load Index	hli	30	Temperature	ESRI	N
B1_meanT	Annual Mean Temp	°C	1000	Temperature	WorldClim	Y
B2_meanrange	Mean Diurnal Range	°C	1000	Temperature	WorldClim	N
B3_isotherm	Isothermality	°C	1000	Temperature	WorldClim	Y
B4_tseason	Temp Seasonality	°C	1000	Temperature	WorldClim	N
B5_maxtwarmon	Max Temp Warmest Month	°C	1000	Temperature	WorldClim	Y
B6_mintcoldmon	Min Temp Coldest Month	°C	1000	Temperature	WorldClim	N
B7_trange	Temp Annual Range	°C	1000	Temperature	WorldClim	N
B8_meantwetq	Mean Temp Wettest Quarter	°C	1000	Temperature	WorldClim	N
B9_meantdryq	Mean Temp Driest Quarter	°C	1000	Temperature	WorldClim	N
B10_meantwarmq	Mean Temp Warmest Quarter	°C	1000	Temperature	WorldClim	N
B11_meantcoldq	Mean Temp Coldest Quarter	°C	1000	Temperature	WorldClim	Y
B12_Prec	Annual Precip	mm	1000	Precipitation	WorldClim	Y
B13_precwetmon	Precip Wettest Month	mm	1000	Precipitation	WorldClim	Y
B14_precdrymon	Precip Driest Month	mm	1000	Precipitation	WorldClim	N
B15_precseason	Precip Seasonality	mm	1000	Precipitation	WorldClim	N
B16_precwetq	Precip Wettest Quarter	mm	1000	Precipitation	WorldClim	N
B17_precdryq	Precip Driest Quarter	mm	1000	Precipitation	WorldClim	N
B18_precwarmq	Precip Warmest Quarter	mm	1000	Precipitation	WorldClim	N
B19_preccoldq	Precip Coldest Quarter	mm	1000	Precipitation	WorldClim	N

1

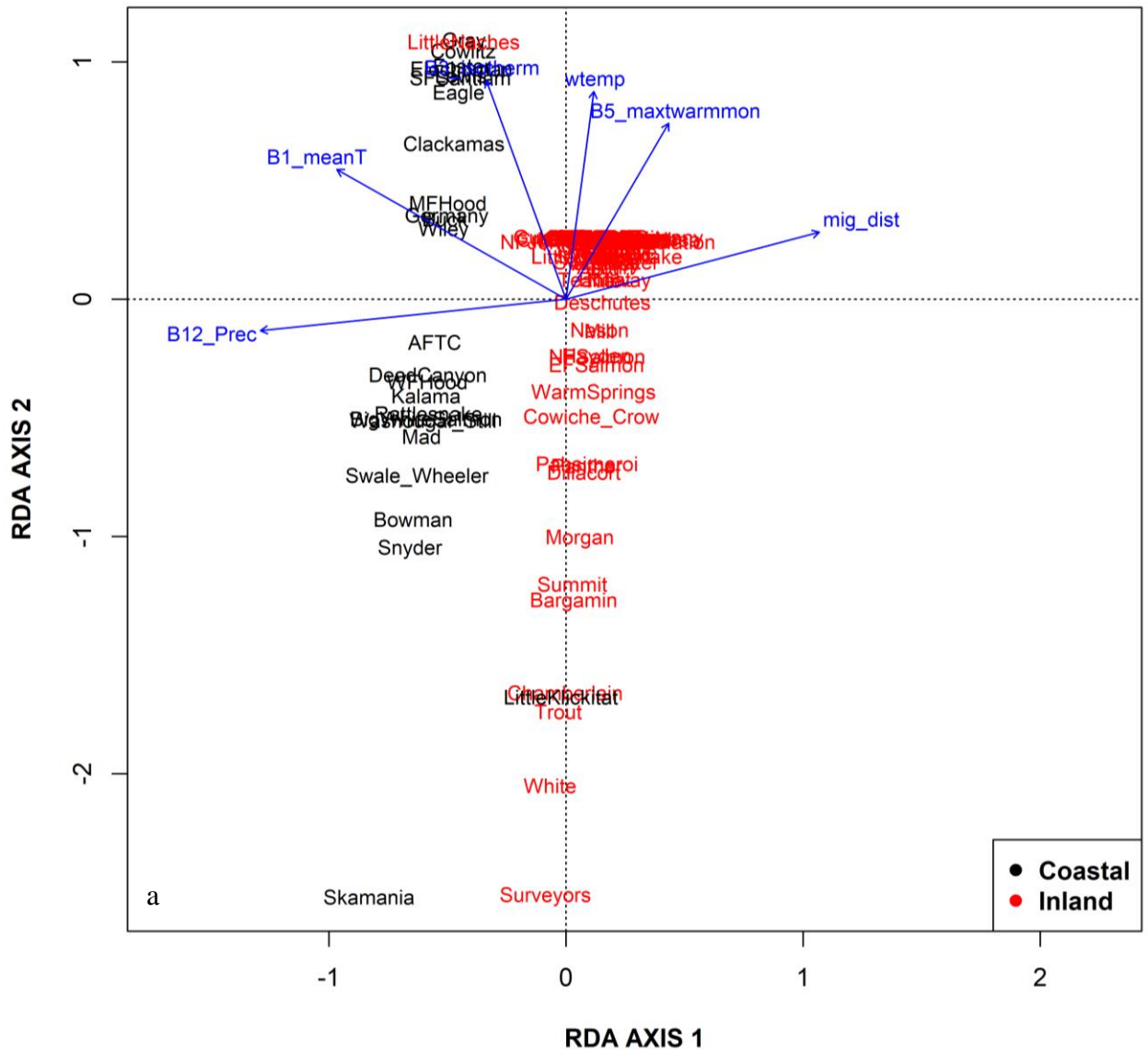
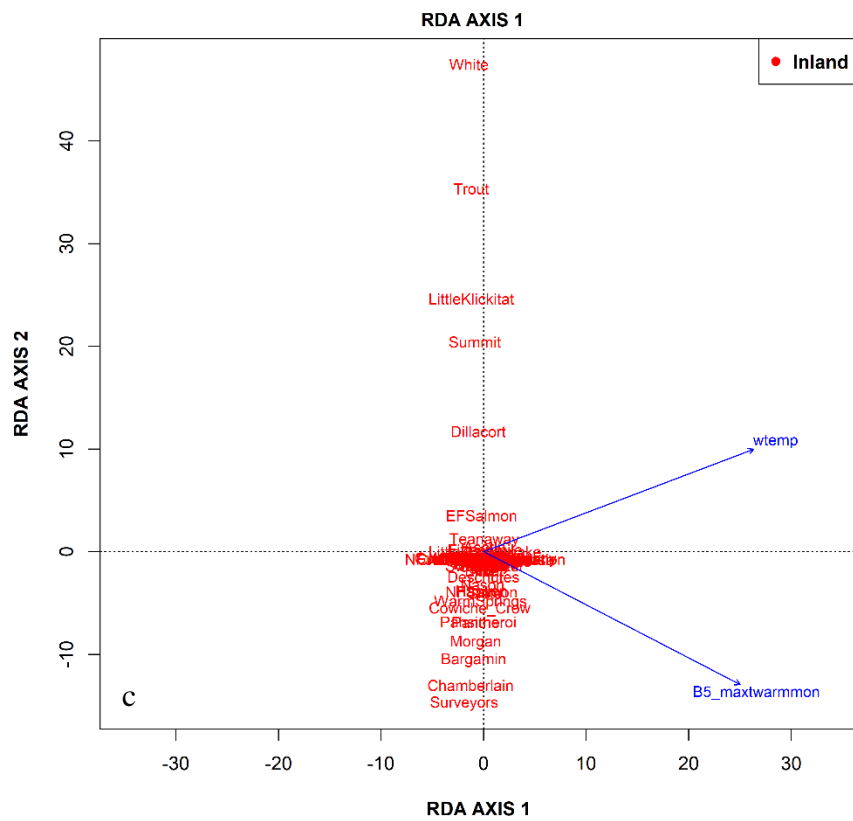
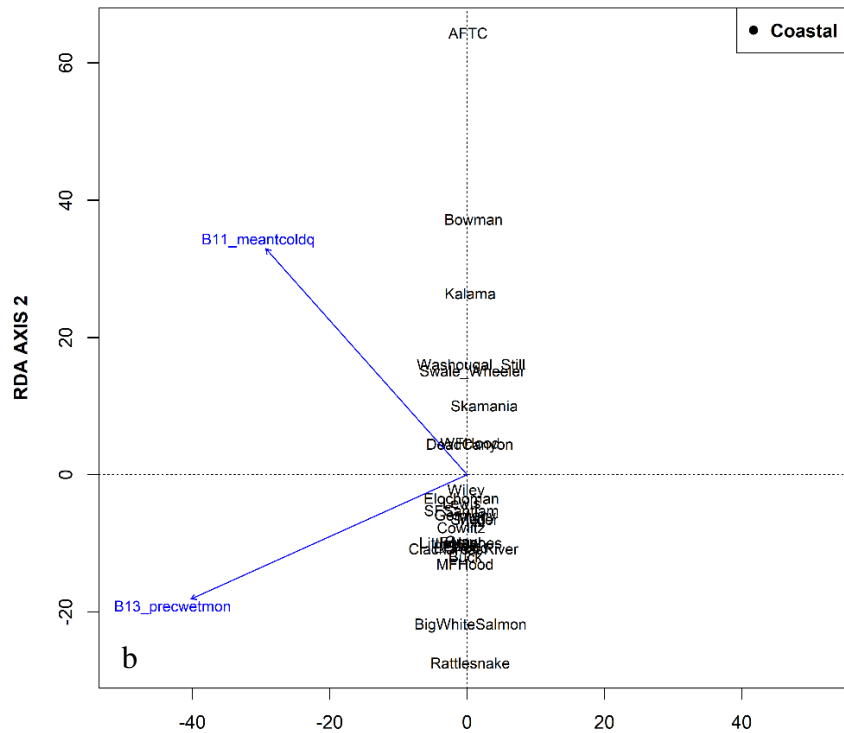


Figure 50 a-c. RDA of all steelhead collections in Columbia River basin to model the degree to which the variation in environmental variables explains the variation in allele frequencies for candidate markers for all collections in the *greb1L* haplotype block (2,3,6). Coastal populations (b) and inland populations (c) were analyzed separately.



For Chinook salmon, landscape genetics work has also been done at both fine and broad scales. Initial studies evaluated the utility of certain marker types for landscape genetics and found consistency in signals among marker types (Narum et al. 2008b; Hess et al. 2011), but that SNPs provided greater potential for identifying candidate genes involved in local adaptation and should be used in subsequent studies (Narum et al. 2013a). Broad scale studies were initially done with panel of 96 SNP markers to investigate patterns of connectivity related to landscape features across 54 populations in the Columbia River Basin (Matala et al. 2011). Results indicated that precipitation, elevation, and temperature were the primary environmental drivers of local adaptation depending on genetic lineage, and neutral genetic structure largely reflected isolation by distance within each lineage (Matala et al 2011). A follow-up study (Hecht et al. 2015) was done with a much larger number of genetic markers (~20K SNPs) at broad scale and found that between 6-22% of genetic variation could be accounted for by environmental features such as precipitation, temperature, and migration distance (Figure 51a). Several candidate markers were associated with local adaptation within and among lineages (Figure 51b; Hecht et al. 2015). A follow-up study to investigate local adaptation through whole genome resequencing has demonstrated that a broad portfolio of diversity persists in Chinook salmon and candidate genes for local adaptation are widespread throughout the genome within and among lineages (Narum et al. 2018). Additional studies are underway to represent genome wide variation for a more thorough set of populations throughout the Columbia River Basin.

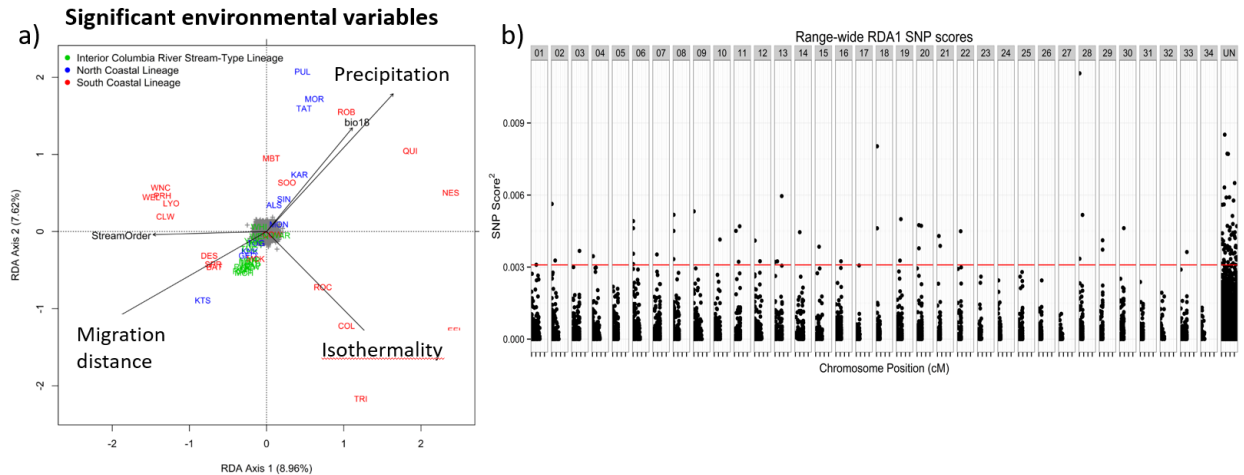


Figure 51. a) Environmental drivers of selection and b) candidate markers for local adaptation in Chinook salmon (from Hecht et al. 2015). a) Population scores for canonical RDA axis 1 and 2 are represented by the three-letter abbreviation for each population, coloured to represent the lineage assignment of that population.

Summary of accomplishments & lessons learned:

Steady progress has been made to better understand landscape genomics and neutral vs. adaptive patterns of genomic variation for steelhead and Chinook salmon as reflected in 12 publications (Narum et al. 2008a; Narum et al. 2008b; Matala et al. 2011; Hess et al. 2011; Narum et al. 2013a; Matala et al. 2014; Hecht et al. 2015; Hand et al. 2016; Nichols et al. 2016; Micheletti et al. 2018a; Narum et al. 2018; Collins et al. 2020). Results consistently show specific environmental variables are drivers of selection in both steelhead and Chinook including precipitation, temperature, and migration distance through the mainstem Columbia River. Neutral variation across studies consistently accounts for highly distinct lineages of each species, and genetic structure within each lineage that is related to geographic location by sub-basins. While adaptive genetic variation can be evident with modest numbers of SNP markers, specific candidate genes are best pinpointed by genome resequencing.

Recent work has focused on collecting genome resequencing data for several populations of Chinook salmon and steelhead to enable landscape genomics analyses with high density markers throughout the genome. This data overlaps with collections that were sequenced under Section 2 (Table 2 & Table 4) that will also be used for baseline allele frequencies. Landscape genomics analyses for both Chinook salmon and steelhead are ongoing.

Objective 2) Genetic Basis for Phenotypic Expression of Traits

Hypotheses:

Hypothesis 1: Many phenotypic traits include a heritable component that must have a genetic basis, which can be detected with association mapping and gene expression to identify candidate genes associated with specific traits.

Hypothesis 2: Markers from candidate genes can be developed into cost efficient assays for genotyping large numbers of individuals to monitor genetic variation for phenotypic

traits at broad scales, with the potential to predict resiliency of populations to environmental changes.

Activities implemented:

Multiple studies have been initiated to investigate the genetic basis for multiple phenotypic traits using association mapping or gene expression approaches. Work has focused on genomic regions associated with several different traits. Work on resident vs. anadromous *O. mykiss* (Narum et al. 2008a; Hecht et al. 2013) has revealed that a combination of environmental and genetic factors contribute to determination of these life history types (Figure 52).

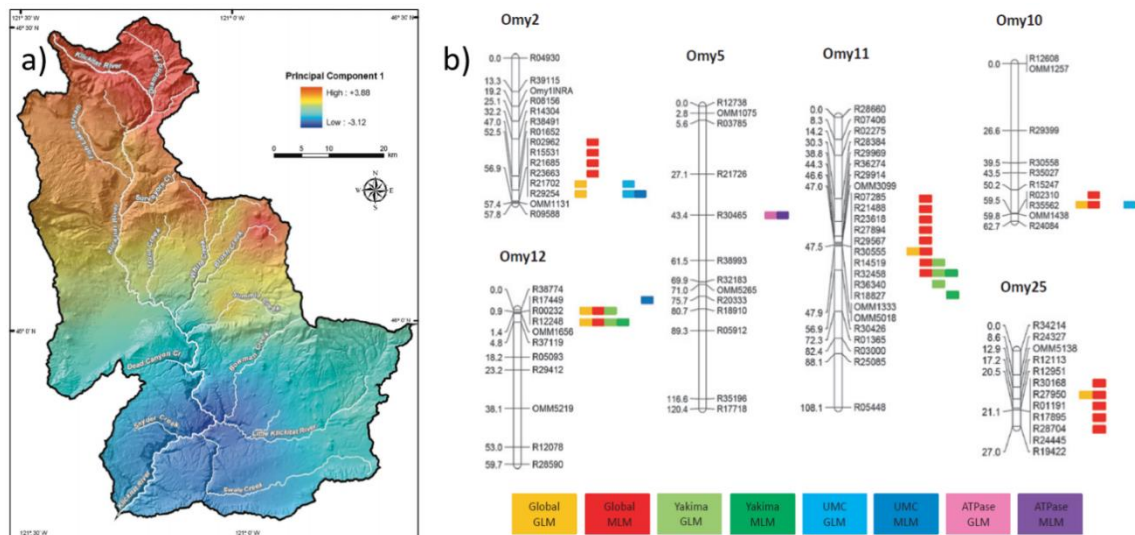


Figure 52. a) Synthesis map illustrating interpolation principal component (PC1) that accounts for 59% of variation in resident (red) vs anadromous (red) life history (from Narum et al. 2008a). b) Significant loci detected from eight individual association tests, where each test is represented by a different colored pill and placed to the right of the linkage group. GLM, general linear model; MLM, mixed linear model (from Hecht et al. 2013).

Run-timing related to maturity in steelhead (Hess et al. 2016; Micheletti et al. 2018c; Collins et al. 2020) and Chinook salmon (Hess and Narum 2011; Narum et al. 2018; Koch and Narum 2020) has been shown to be controlled by a genomic region of major effect with the same candidate genes in both species (*GREB1L*, *ROCK1*, intergenic region; Figure 53).

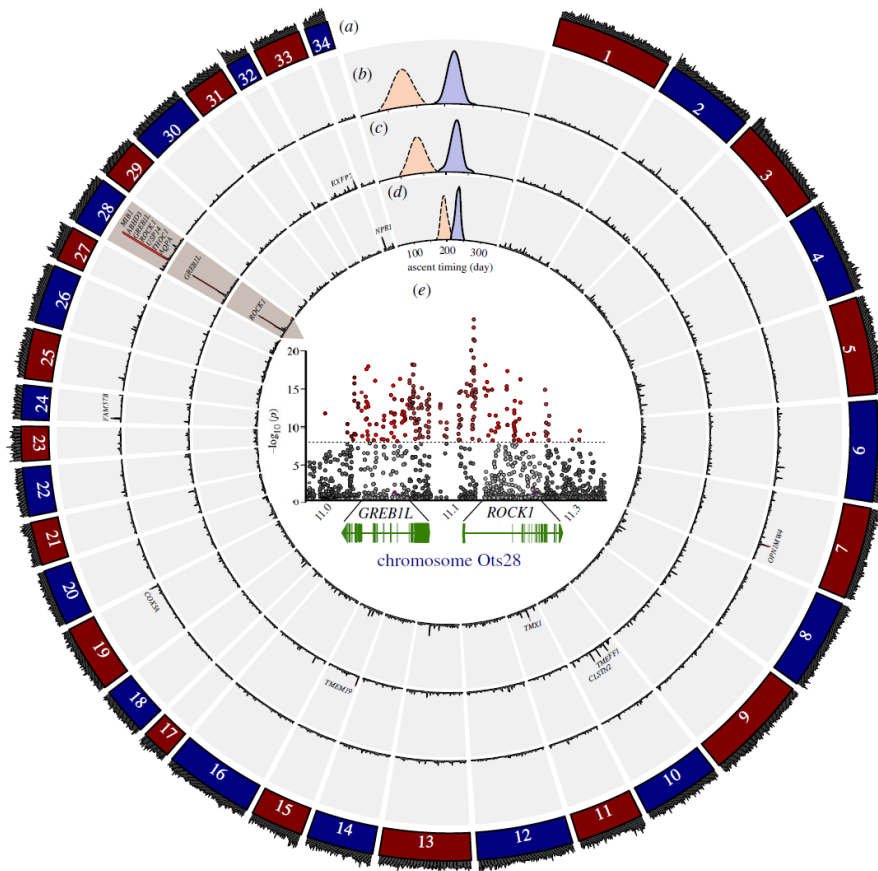


Figure 53. Manhattan plot for premature and mature collections of Chinook salmon (from Narum et al. 2018). (a) Sequence coverage (black outer ring) for each chromosome. (b) Significant divergence between premature and mature migrating coastal lineage Chinook salmon. (c) Significant divergence between premature and mature migrating Chinook salmon within the interior ocean-type lineage. (d) Significant divergence for interior stream-type Chinook salmon on return migrations that enter freshwater premature, but the final ascent to spawning grounds is bimodal with early premature and late mature females. (e) Annotation of the 203 Kb region on Ots28 between *GREB1L*, *ROCK1*, and intergenic regions with significance based on CMH tests.

Pooled-sequencing and a Cochran-Mantel-Haenszel (CMH; Mantel 1963) test executed by Micheletti et al. (2018c) detected steelhead markers associated with migration-timing on chromosome 28 within *GREB1L* and *ROCK1* genes and intergenic region between the two genes. With these markers identified, we can evaluate haplotype variation associated with migration-timing among steelhead populations collected across the Columbia River basin.

The distribution of genetic variation underlying adult migration timing in steelhead across the landscape was described by genotype frequencies (Collins et al. 2020). We examined 13 markers occurring on chromosome 28 within the *greb1l*, *rock1*, and intergenic region between *greb1l* and *rock1* that were previously shown to be strongly associated with adult migration timing (Hess et al. 2016; Micheletti et al. 2018c; Table 70). Initially the two most significant SNPs were retained from a previous RAD study (Hess et al. 2016), and the remaining 11 SNPs with the strongest association with adult

123 migration timing from the whole genome resequencing conducted by Micheletti et al.
124 (2018c). Premature, mature, and heterozygote genotypes for adult migration timing were
125 established based on genotype association from previous studies (Hess et al. 2016;
126 Micheletti et al. 2018c), as well as using a reference collection of Skamania Hatchery
127 steelhead, which is a hatchery-strain intensively selected for early adult migration and
128 cultured since 1956 with steelhead from the Washougal and Klickitat Rivers (Crawford et
129 al. 1979; Chilcote et al. 1986). Premature, mature, and heterozygote adult migration
130 timing genotype proportions were assessed across all collection locations. A total of
131 9,471 individuals from 113 populations met inclusion criteria (>90% loci successfully
132 genotyped and had an estimated <0.5% genotyping error based on replicate genotyping)
133 and were included in this study.

Table 70. Adult steelhead migration timing associated candidate marker information. The ‘Order ID’ column corresponds to the SNP order, according to the physical position within the genome assembly. SNP names, chromosome number, position, gene, primers, probes, and orientation are also listed and are based on the genome assembly NCBI accession GCF_002163495.1. The premature allele is indicated in the probe column with an underline.

Order ID	SNP	Chr	Position	Gene	Forward primer	Reverse primer	Probe	Orientation
1	Omy28_11607954	28	11607954	<i>greb1L</i>	TGACACTGATCACAATGGTGAAT	TAAACTGGAAGGAGAGAGCAAAAT	TGTGGGCTGC[A/G]AACATACTCA	+
2	Omy_RAD52458-17	28	11609794	<i>greb1L</i>	ACGTGTCCTGAGGATGGTA	AGCTCTAGGTCTGGGTCTCTG	ATGGCCC[C/A][CT]AAGAACCC	-
3	Omy_GREB1_05	28	11618027	<i>greb1L</i>	TGGGCAGATATGGAAGAACGG	ACCTTCTAAATGGCCTCTGTGT	CGGTGGCTC[T/G]C	+
4	Omy28_11625241	28	11625241	<i>greb1L</i>	CAACATTTAGGGAGAGGTTGCTAT	ATCATCAAGTTTGCCTACGACAC	CCTCCTCCT[A/G]TGTTGTCTC	+
5	Omy28_11632591	28	11632591	<i>greb1L</i>	GTAGAGGCCAAAGGCTTGAG	TGCTCTTATTACCTCCAGACTCC	TGAGAA[G/A]AACACAGAGG	+
6	Omy_GREB1_09	28	11641623	<i>greb1L</i>	CCAGTGGCAACCTCAGGTAG	GACTCCAGTCACCAAGTCA	TCAA[T/G]GGAGA	+
7	Omy28_11658853	28	11658853	intergenic	CAACATATGACCACTCGAAACTC	ATTAATCACACCGTGAGACTCCTC	TGGTACAGAC[A/C]CGCACTAGCA	+
8	Omy28_11667578	28	11667578	intergenic	ACAGTAAACCCATTCAGGCATAGT	TTATCTCTCAATCCACATCAAGA	GTATTGATCC[T/C]GTGGGAGACA	+
9	Omy_RAD47080-54	28	11667915	intergenic	TCAAAACCTGCAGGACTTGGA	TGGTTATATCTACAGTACAGTTCGT	TGCAAG[A/G]CTTAAACGA	+
10	Omy28_11671116	28	11671116	intergenic	AATTTCCCAAATTTGAACTCTT	GTGTACATTGTCAGGCAGAAACAT	CTGGTGAGAA[C/T]AGGAATTACC	+
11	Omy28_11676622	28	11676622	intergenic	CGAATGCACTGTAGCTCATTCTAA	GCAGTAGAATGTCTCGAAATACA	ACATGTCATT[T/G]ATTGTTATCT	+
12	Omy28_11683204	28	11683204	intergenic	CAAGAAAGAAACAGATGTTGTCCA	TTGTGACTCAAATCTGCAACCTAT	ATGTAAAAAA[G/T]GGCAGAAAA	+
13	Omy28_11773194	28	11773194	<i>rock1</i>	AGTTTGACACCCCTGTACTAGAGC	GTCTAACAAGCTCTGGGTGATTTA	GCAATTTTTT[T/A]AAATTACCGC	+

We assessed linkage disequilibrium (LD) within the 13 candidate markers to identify haplotype blocks that would be informative for estimating frequencies of adult migration types. Candidate markers were analyzed for all sampling locations in Haploview with solid spine and this resulted in two haploblocks, one with markers 1-7 and another with markers 8-13 (Figure 54). One haplotype block contained all markers within *greb1L* and another included all or the majority of markers located within the intergenic region upstream of *greb1L* and *rock1*. There was one marker located within *rock1*, but it did not demonstrate as strong of LD as other markers included in the second haplotype block. The intergenic haplotype block, containing markers 8-12, maintained high LD in both inland and coastal collections.

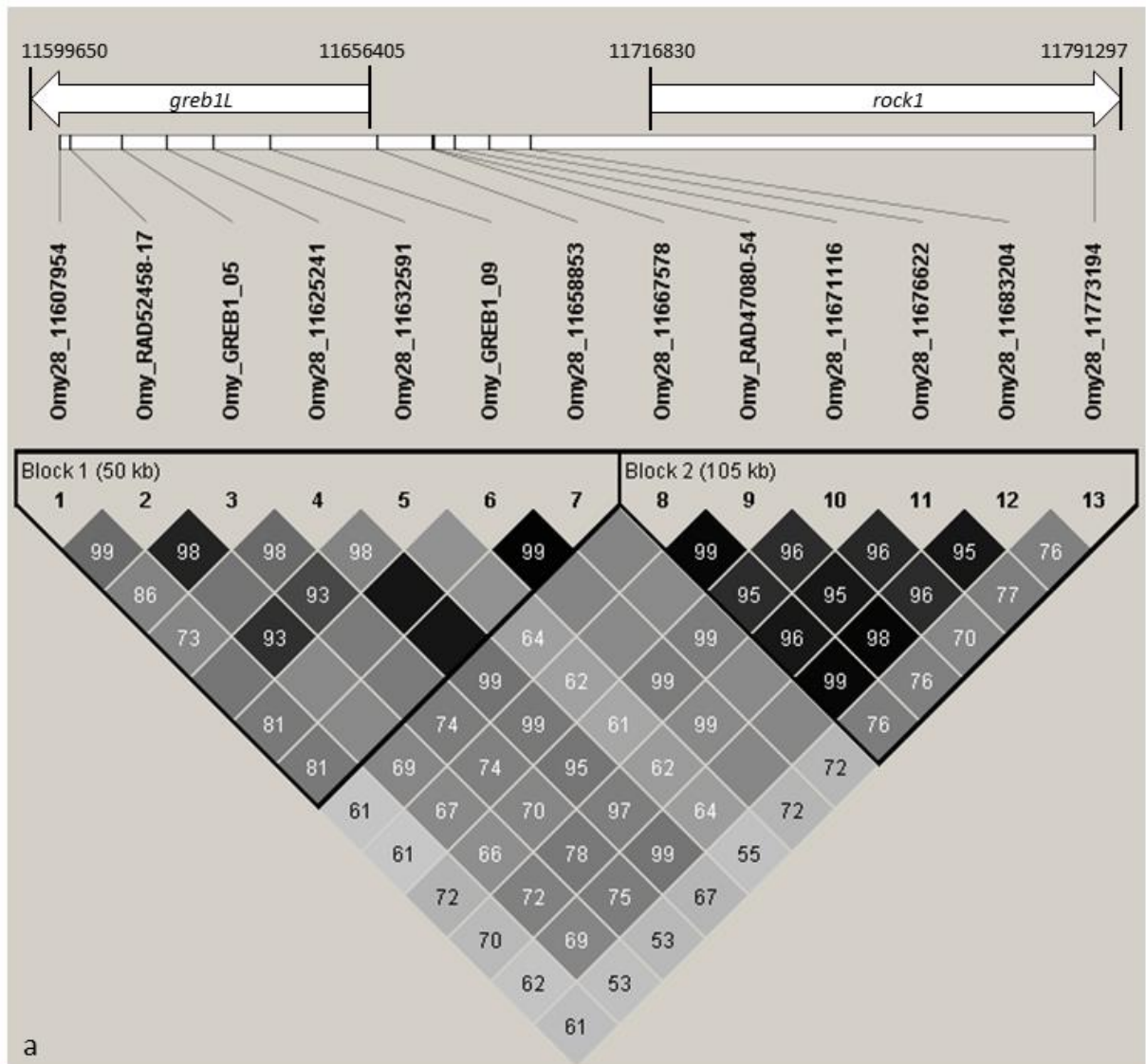


Figure 54. Linkage relationships for 13 candidate markers in Haploview for all steelhead populations.

Genotypes were assessed across the Columbia River basin with the migration timing associated markers. The haplotypes representative of the heterozygote genotype are depicted as a gradient corresponding to the number of markers that match either fixed genotype and the percentage of individuals with each haplotype is reported in Figure 55a. The completely blue haplotype matches the mature genotype and is the most frequent, while the completely red haplotype matches the premature genotype and is the third most frequent (Figure 55a). The haplotypes with a mixture of blue and red represent the different possible heterozygote genotypes (Figure 55a). The mature genotype was predominant throughout much of the range in the Columbia River, however many populations west of the Cascade Mountains and in the Salmon River have greater proportions of the premature genotype than other collections (Figure 55a-b). However, only 9 of the 113 populations had a higher frequency of premature alleles for early adult migration. To evaluate haplotype frequencies for a single haplotype block in as many locations as possible, we further scrutinized haplotypes for markers 2, 3, 6 across the landscape and found five unique haplotypes (Figure 55a). Haplotype frequencies for collections (Figure 55a) showed similar patterns of geographic distribution as the genotype frequencies (Figure 55b), but with improved resolution for heterozygous haplotypes that were within a single haplotype block underlying *greb1L*. According to results of overall haplotype frequency (Figure 55a), the recombinant haplotype 4 is present more frequently than the premature haplotype 5. Additionally, there is a distinct separation of recombinant haplotypes between coastal (haplotypes 2 and 3) and inland (haplotype 4) collections (Figure 55a).

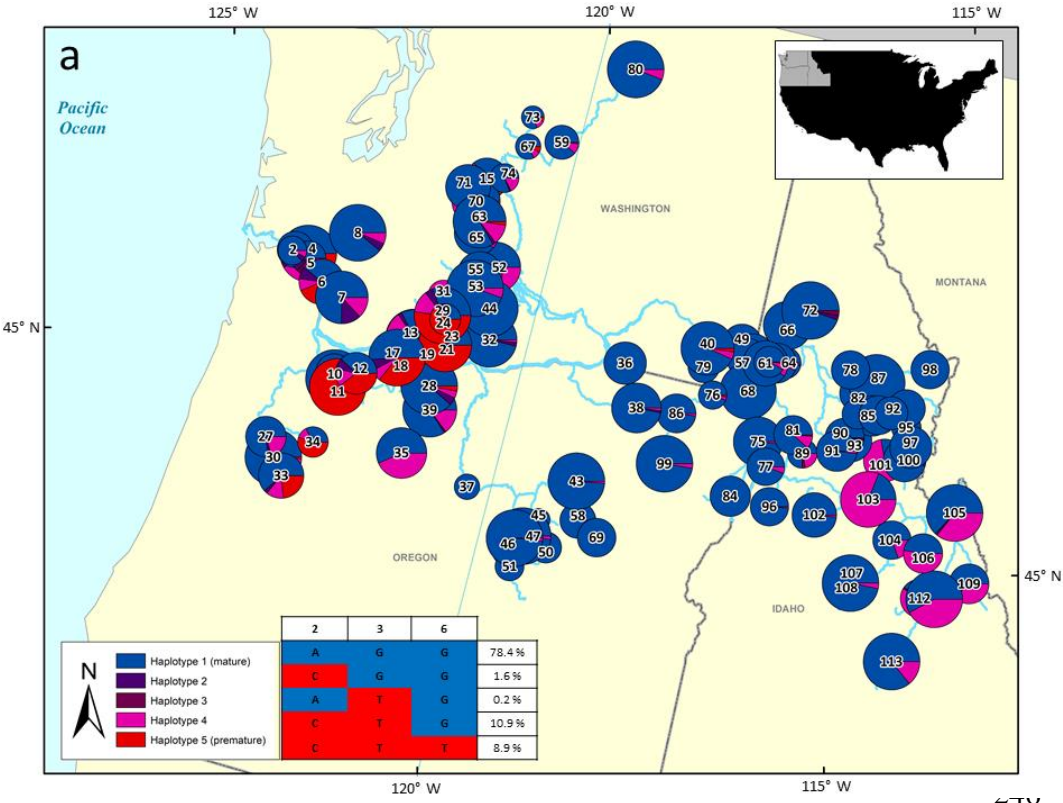


Figure 55a. Maps of haplotype and genotype proportions for all steelhead collection locations. Pie chart size corresponds to population size. The first map (a) demonstrates the proportions of individuals at each collection location with the five unique haplotypes from markers 2, 3, and 6. The second map (b) incorporates only candidate marker 9 (Omy_RAD47080-54), as it was in a different linkage block than the other three markers.

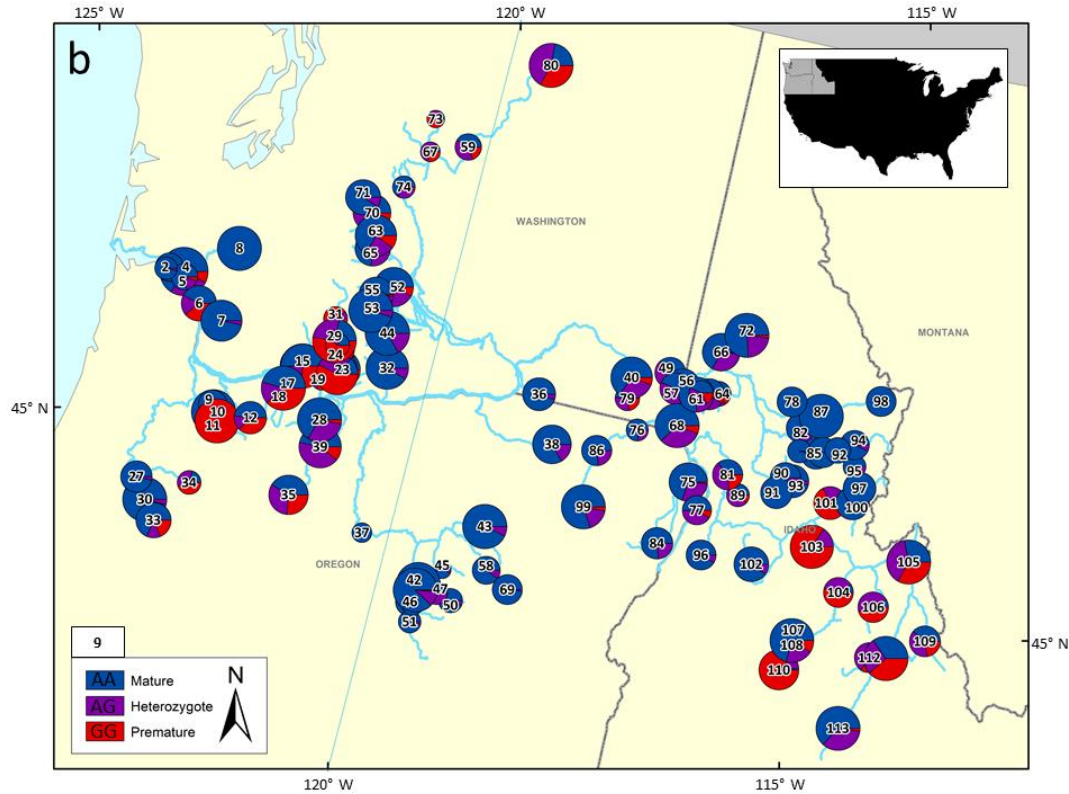


Figure 55b.

We (Willis et al. 2020) also analyzed steelhead collected at Bonneville Adult Fish Facility (N=1,538) and in the Hood River (N=354) for patterns of association of the 13 chromosome 28 (GREB1/ROCK1) markers with two attributes of run-timing: the day each fish passed Bonneville dam and the day each fish was recorded at their most upstream passive integrated transponder (PIT) array (Figure 56). We observed similar patterns of linkage and haplotype frequencies as in basin-wide studies (Collins et al. 2020), and found that chromosome 28 markers explained significant variance in migration timing in both coastal and inland steelhead. In both cases, markers in the same sub-region showed the strongest association indicating that markers in the upstream portion of the GREB1L gene (closer to the transcription start site) and intergenic region immediately adjacent were most predictive of adult migration timing (Figure 57). Similarly, haplotypes containing most or all of the “premature” or “mature” alleles showed the same pattern of association, although haplotype frequencies provided power to predict phenotypes for only the most common haplotypes. However, the degree of association with aspects of adult migration timing differed greatly between coastal lineage, e.g. Hood River fish, and inland lineage fish, which constitute the majority of BONAFF samples. While candidate markers from the chromosome 28 region explained roughly 50% of the variance in migration timing of coastal lineage steelhead, with heterozygotes exhibiting an intermediate to late timing for both Bonneville passage and tributary arrival day, these same genotypes explained less than 10% of phenotypic variation for either trait in inland steelhead.

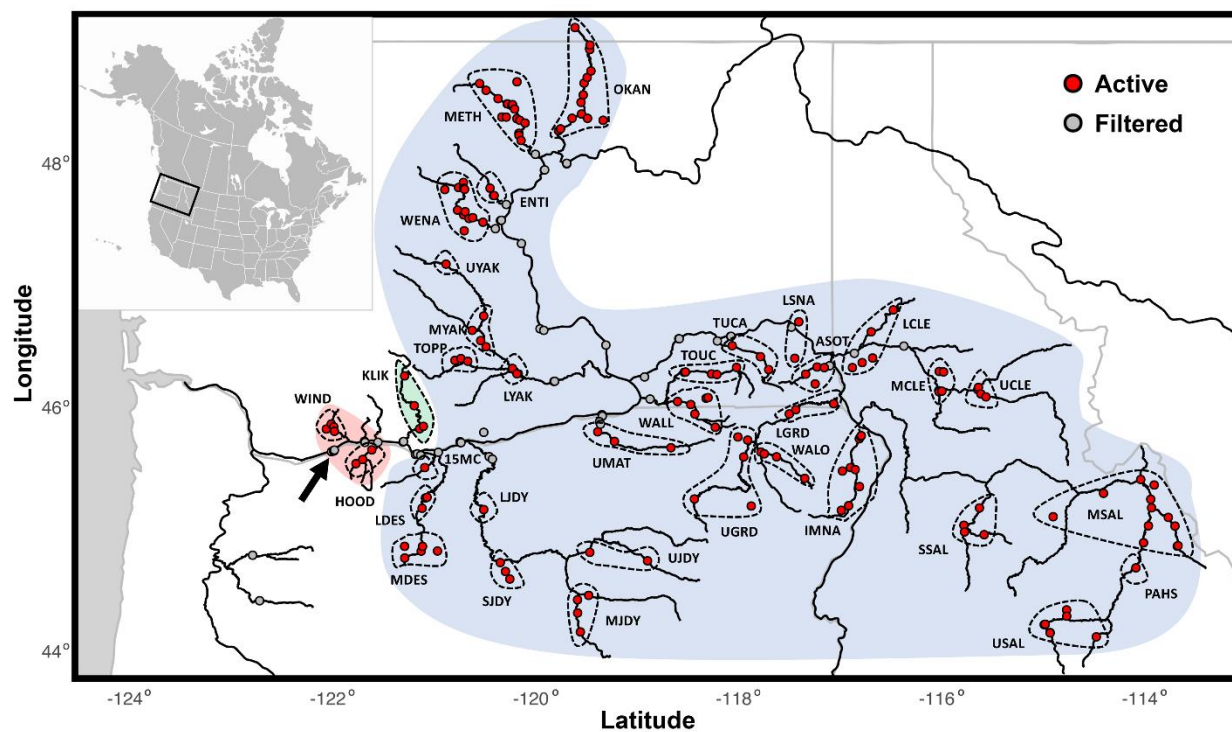


Figure 56. Columbia River Basin with active and filtered passive integrated transponder arrays. River courses in black; borders and coast in gray. Hydrological unit groupings, identified by dashed lines, are organized into lineages and sub-basins as follows: coastal lineage in Red, intermediate lineage affiliation in Green, inland lineage in Blue; Bonneville Dam is identified by an arrow.

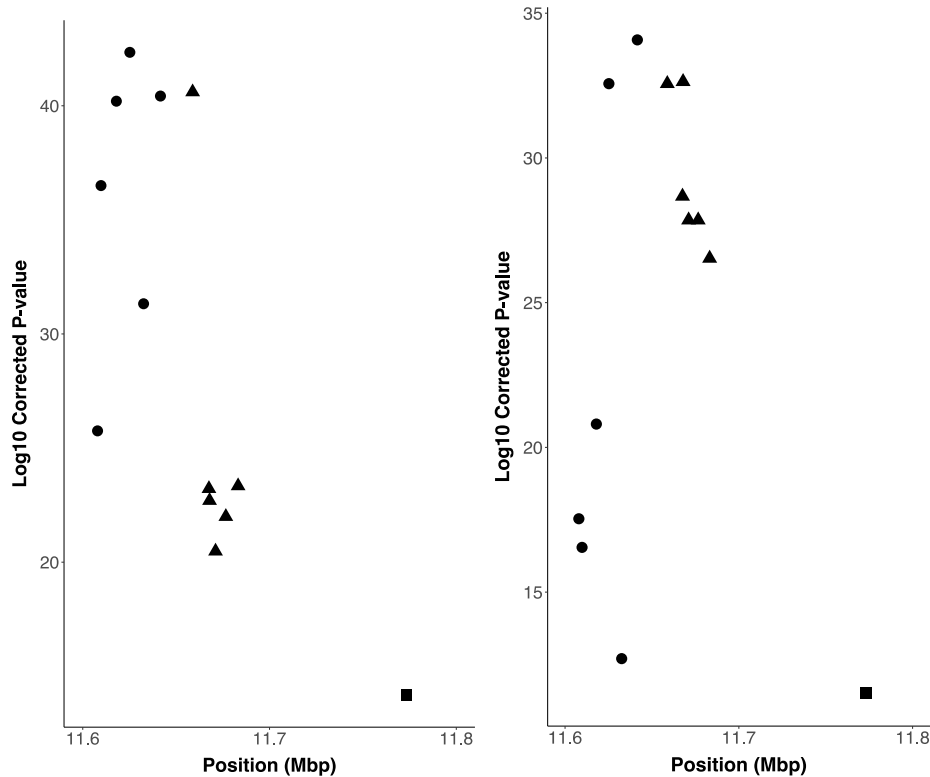


Figure 57. Significance of association of chromosome 28 markers with run timing in BONAFF (left) and Hood River (right) steelhead. Position refers to SNP locus position on chromosome 28. Circle: GREB1L, triangle: intergenic; square: ROCK1.

For Chinook salmon, 33 candidate markers were developed that span 220kb on chromosome 28 including candidate genes *greb1L* and *rock1* for adult migration timing (Koch and Narum 2020). Using individual-level genotypes from these candidate markers, we tested for an association with migration phenotypes across three distinct lineages that demonstrate both an early and late migration phenotype. We then used pedigree data from one of the populations, which enabled association tests between the candidate markers and fitness. Estimates of fitness were based on previous estimates of reproductive success from Janowitz-Koch et al. (2019).

A series of PCA results demonstrated clear differences in clustering between putatively neutral markers and those associated with adult migration timing in both the Lower Columbia and Interior ocean-type lineages (Figure 58). The pattern was investigated separately for the larger set of individual samples from the Interior stream-type lineage that had continuous data for adult migration timing including those fish that were intermediate between early and late migration timing peaks. There was substantial overlap between early and late migrating samples for the Interior stream-type lineage (Figure 58).

Association tests validated that the majority of markers were significantly associated with migration timing for all three lineages (Figure 59). The strongest association was consistently observed for markers within or upstream of the *rock1* gene, closely followed

by markers located within or upstream of *greb1L*. Out of the 33 candidate SNPs, 13 SNPs were significantly associated with fitness (Figure 60).

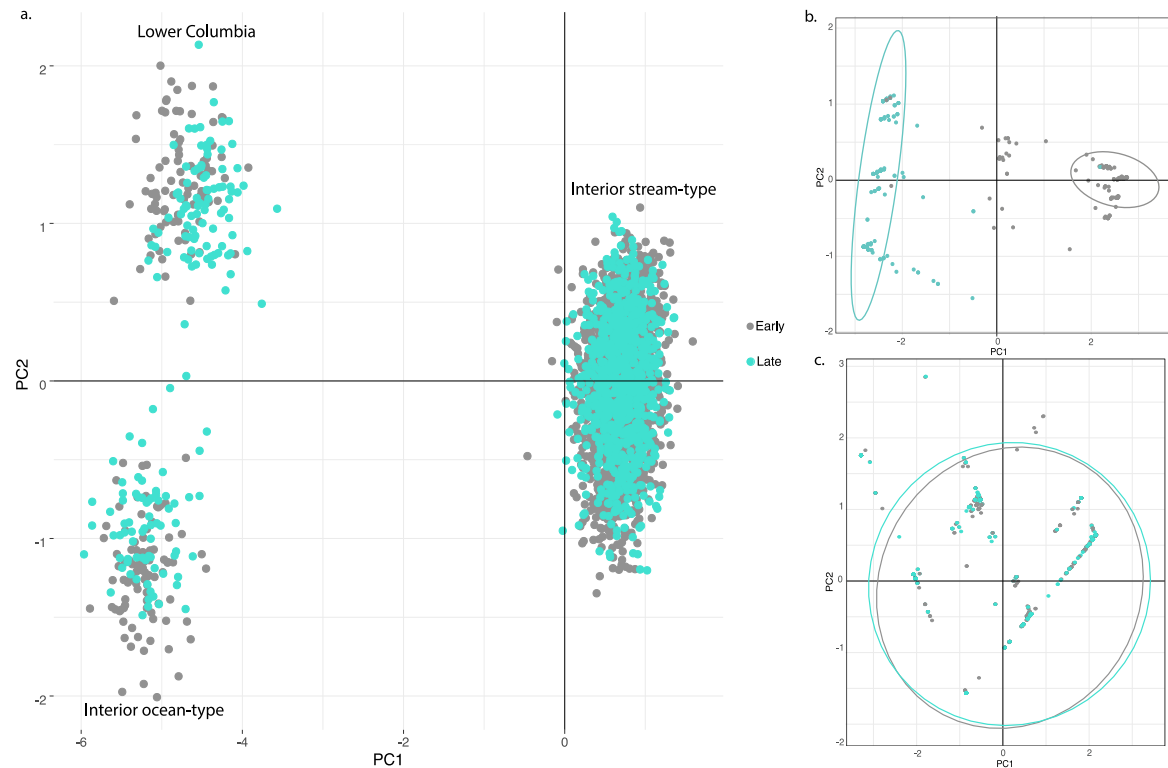


Figure 58. PCA of genetic variation in Chinook Salmon (from Koch and Narum 2020). Results presented represent A) 185 neutral SNP markers, B) 33 chromosome 28 markers for the Lower Columbia and Interior ocean-type populations combined, and C) 33 chromosome 28 markers for the Interior stream-type population.

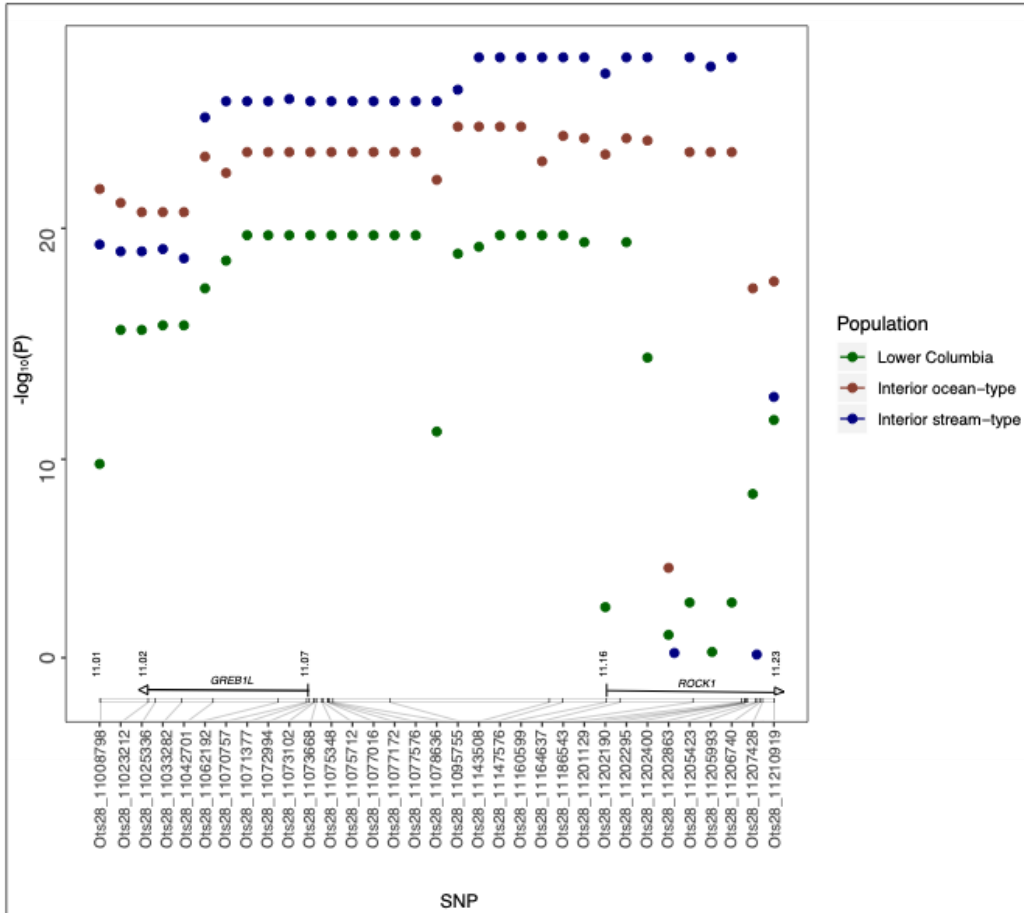


Figure 59. Association of each candidate SNP marker with migration timing within three lineages of Chinook Salmon (from Koch and Narum 2020). The colored dots for each lineage represent sliding windows for consecutive pairs of SNPs along the candidate genomic region. SNP number on the x-axis corresponds to the 33 candidate markers, while the genome position of markers on chromosome 28 (NCBI accession GCA_002831465.1) is depicted in the gene diagrams above the x-axis. Y-axis represents $-\log_{10}(\text{FDR-corrected p-value})$.

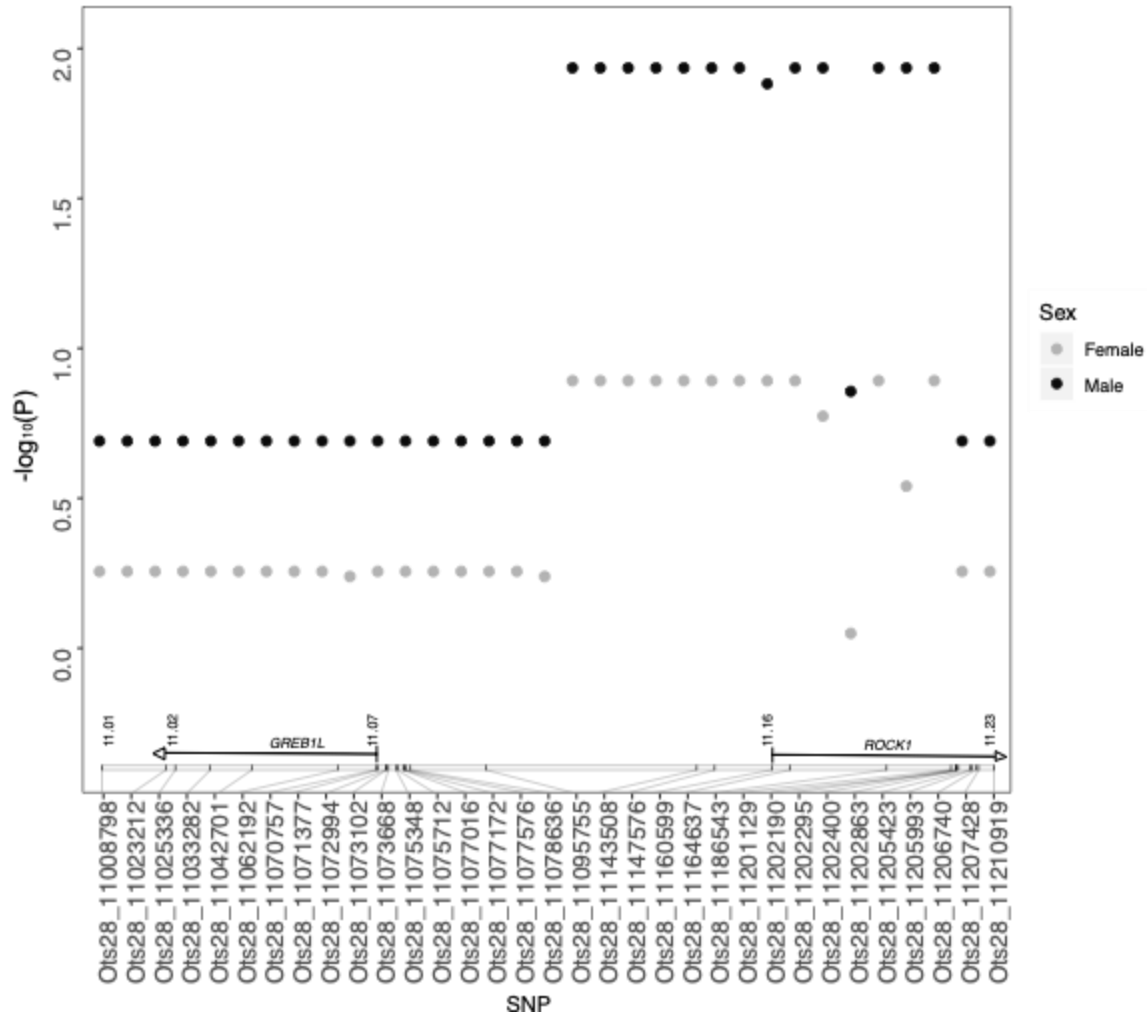


Figure 60. Association of each candidate SNP marker with fitness within the Interior stream-type population. The dots represent sliding windows for consecutive pairs of SNPs along the candidate genomic region with sexes presented separately. SNP number on the x-axis corresponds to the 33 candidate markers, while the genome position of markers on chromosome 28 (NCBI accession GCA_002831465.1) is depicted in the gene diagrams above the x-axis. Y-axis represents $-\log_{10}(\text{FDR-corrected p-value})$.

Age at maturity in Chinook salmon appears to be a polygenic trait but genes of greatest effect differ between sexes (Figure 61; females = OPN4, males = TMEM19; Micheletti and Narum 2018b). Recent studies by other labs have identified Y-linked haplotypes on Chromosome 17 associated with age-at-maturity in Chinook salmon (e.g., McKinney et al. 2020) and markers have been developed to genotype large numbers of individuals to test whether this pattern of association can be verified for the three major lineages of Chinook salmon in the Columbia River. Initial genotyping of these Y-linked markers in approximately 1200 samples from each lineage indicated that SNPs and haplotypes based on these markers are nearly fixed in all Chinook salmon from the Columbia River. With minor allele frequencies $< 0.1\%$ across all populations, these Y-linked markers were not effective and the pattern of association reported by McKinney et al. (2020) was not validated. Further studies are being developed to

scan the genome for regions associated with age-at-maturity in Chinook salmon from multiple populations representing each of the lineages in the Columbia River.

In steelhead, we confirmed the association of markers on chromosome 25 recently identified by a paper in publication (Waters et al. in review), which pointed to a region containing the SIX6 gene (Willis et al. 2020). In the same Bonneville Adult Fish Facility steelhead described above, we found that variation in markers on chromosome 25 in or near the SIX6 gene was significantly associated with both ocean-age and fork length, explaining up to 17% of phenotypic variation (Figure 62). We also identified a sex-dependent pattern of association with ocean age in male versus female steelhead: males showed stronger association of the chromosome 25 markers than females, perhaps implying that there may be sex-linked genes or modifiers that mediate the effects of the SIX6 gene (Figure 63).

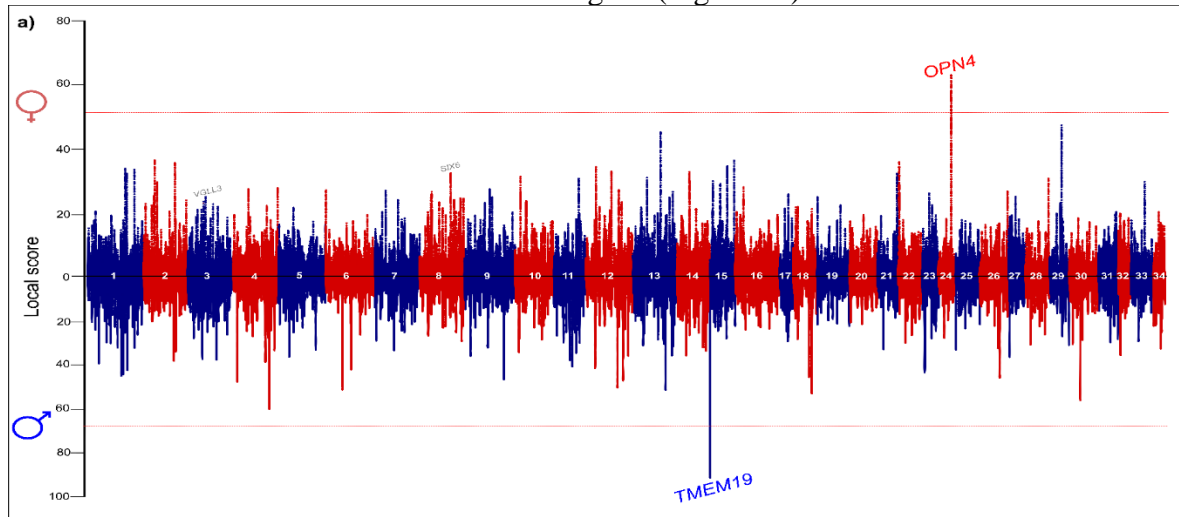


Figure 61. Manhattan plot (from Micheletti and Narum 2018b) illustrating differentiated regions within age classes of females (top; 4- vs. 5-year-olds) and males (bottom; 3- vs. 4- vs. 5-year-olds). Red dashed lines indicate $\alpha = 0.01$ significance threshold for the local score test with Bonferroni correction. Only the opsin 4 (OPN4) gene in females and transmembrane protein 19 (TMEM19) in males were significant using Bonferroni corrected thresholds. Relative locations of the VGLL3 (Ch3) and SIX6 (Chr8) genes which correspond to age at maturity in Atlantic salmon, are displayed in grey and were not significant.

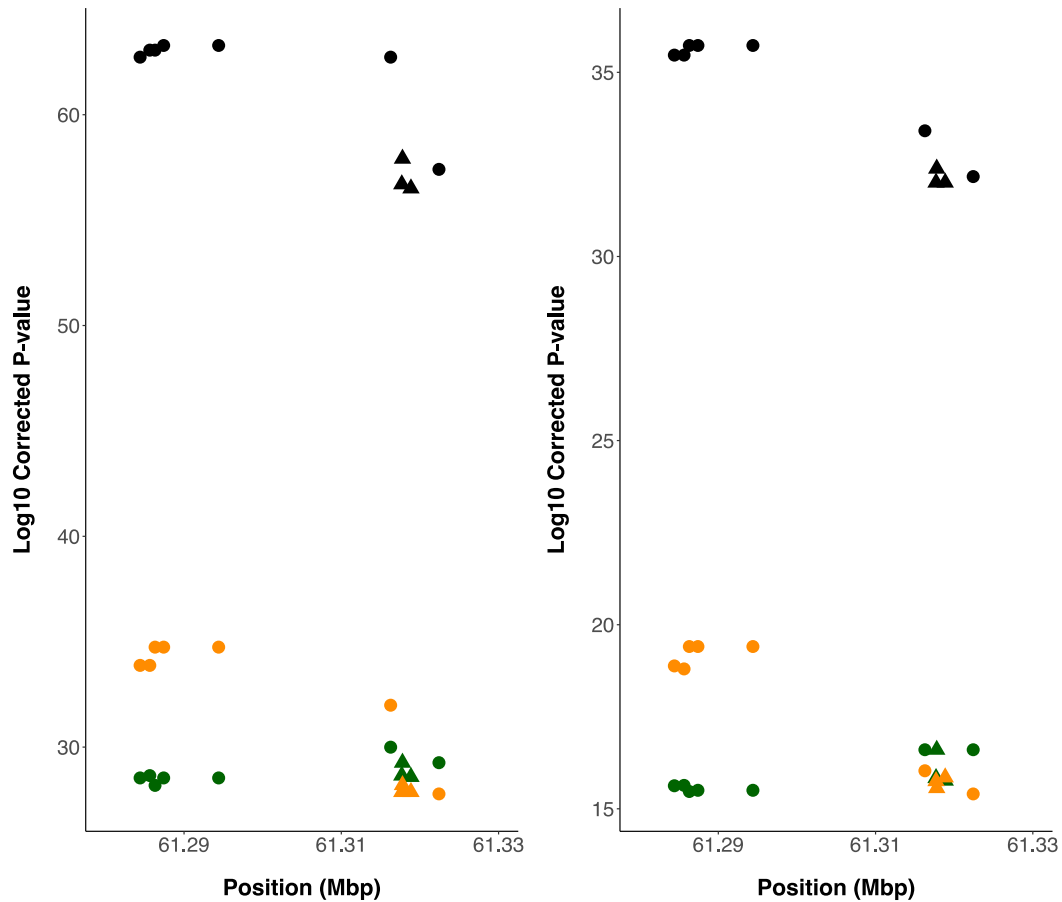


Figure 62. Significance of association of chromosome 25 markers with fork length (left) and ocean age (right) in BONAFF steelhead. Position refers to SNP locus position on chromosome 25. Circle: Intergenic, triangle: SIX6; orange: female; green: male; black: combined male and female.

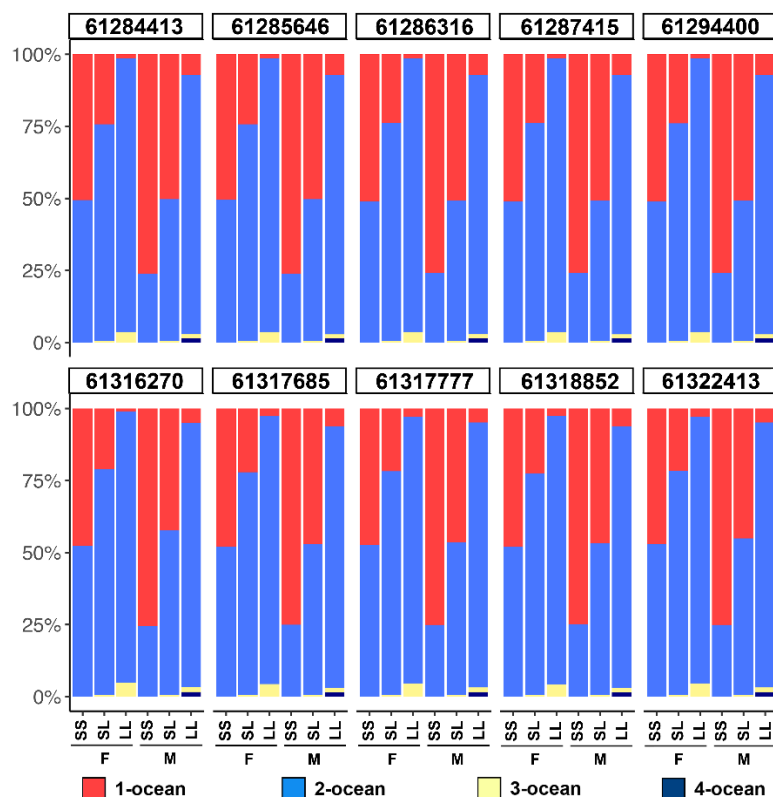


Figure 63. Frequency of ocean-age individuals for genotype and sex for each of the chromosome 25 SNP markers (identified by genomic position).

Disease resistance in *O. mykiss* appears to be highly complex with several genes involved (Campbell and Narum 2015). However, these regions have not been validated and further investigation has been discontinued since other labs are studying genetic basis of disease resistance. Once strong candidate regions are identified by other labs, we will attempt to incorporate markers into genotyping panels for genotyping.

Finally, thermal adaptation has evolved in desert strains of *O. mykiss* (Narum et al. 2010) so that fish have higher thermal tolerance and increased capacity to deliver oxygen to tissues by achieving higher maximum heart rate than montane fish (Chen et al. 2018a; Chen et al. 2018b). The genetic basis for thermal adaptation includes response of heat shock proteins (Narum et al. 2013; Narum et al. 2015; Chen et al. 2018a; Chen et al. 2018b) but also other genes involved in efficient uptake oxygen (Garvin et al. 2015; Narum et al. 2015; Chen et al. 2018a; Figure 64; Chen et al. 2018b). Most recently, a candidate gene known as *cerk* was consistently associated with thermal tolerance and cardiac performance under heat stress (Chen and Narum 2020; Figure 65), and markers were developed from this candidate gene for further validation. As these candidate genes for traits have begun to be identified (Figure 64; Chen et al. 2018a; Chen and Narum 2020), SNP markers from these regions are being incorporated in standard genotyping panels with GTseq in order to validate and monitor genetic variation for these traits in large numbers of individuals. Additionally, thermal tolerance has begun to be evaluated

409 in test populations of anadromous steelhead and Chinook salmon following similar
410 measurements of phenotypes as used for redband trout.
411

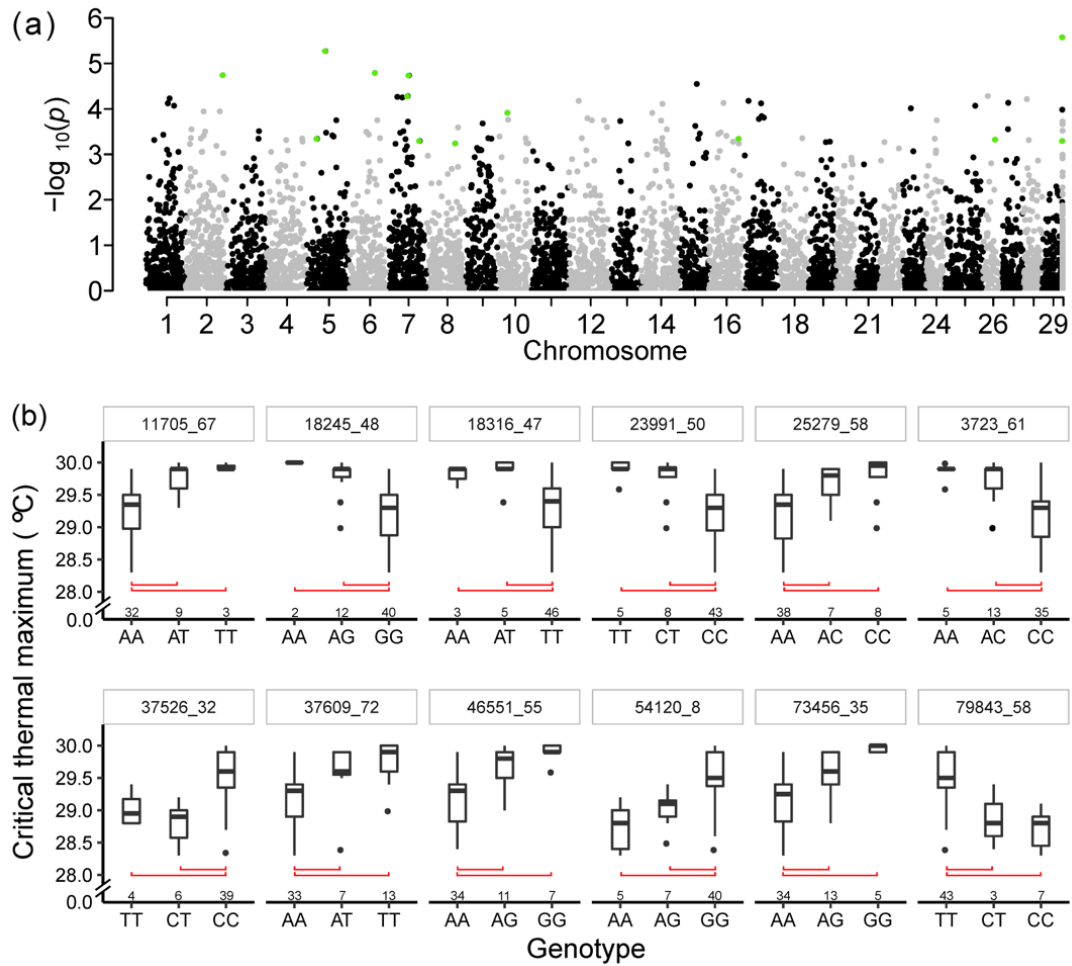


Figure 64. Results from Chen et al. (2018a) that demonstrate association of loci with thermal tolerance in natural populations of redband trout from desert, cool montane, and cold montane environments. Outlier loci and the association with critical thermal maximum (CTMAX). (a) Manhattan plot of calibrated p values, which were derived from the median z-score of results. Outliers identified by at least two analyses are in green. (b) significant associations between CTMAX and genotypes of candidate outlier loci (locus name above each panel). Red brackets indicate significant differences at the level of $\alpha=0.05$ in one-way ANOVA on ranks with subsequent Dunn's post-hoc test. Numbers above genotypes represent the sample size.

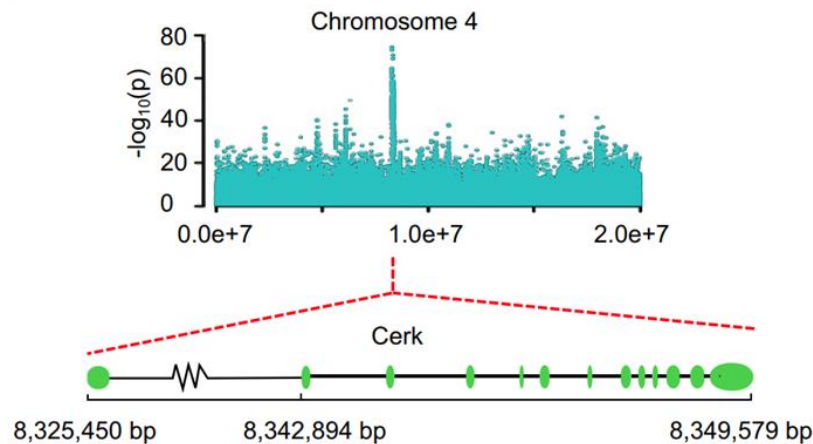


Figure 65. Results from Chen and Narum (2020) that identified a highly significant peak on Chromosome 4 in the *cerk* gene associated with thermal tolerance (survival/mortality) and cardiac performance under heat stress.

Summary of accomplishments & lessons learned:

Steady progress has been made to identify adaptive genomic variation and genetic basis for phenotypic traits in steelhead and Chinook salmon as reflected in 17 publications: Narum et al. 2008a; Narum et al. 2010; Narum and Campbell 2010; Narum et al. 2011; Hess and Narum 2011; Hecht et al. 2013; Narum et al. 2013; Campbell and Narum 2015; Garvin et al. 2015; Narum et al. 2015; Hess et al. 2016; Chen et al. 2018a; Chen et al. 2018b; Micheletti and Narum 2018; Micheletti et al. 2018b; Micheletti et al. 2018c; Narum et al. 2018).

Candidate genes for several traits have been identified in both steelhead and Chinook salmon. As these candidate genes for traits have begun to be identified, SNP markers from these regions are being incorporated in standard genotyping panels with GTseq to validate and monitor genetic variation for these traits in large numbers of individuals.

Synthesis of Findings: Discussion/Conclusions

Fish Population RM&E

Management questions/decisions and anticipated outcomes

Application of research results:

Inclusion of candidate markers associated with specific traits allows more detailed genetic monitoring of stocks in the Columbia Basin. Extensive programs are in place that enable genetic identification of the origin of individual fish, but candidate markers from this study also provide the ability to monitor genetic variation for specific traits that are expected to be necessary to maintain life history variation for long term persistence of populations.

Water temperatures are predicted to increase in this century, e.g. approximately 0.27°C per decade for streams where salmonids are distributed. Thus, it is questionable whether

species and populations will be able to adapt to future environmental changes, especially for freshwater ectotherms with limited migratory opportunities. Local extirpation events might occur if populations experience extreme temperatures above their maximum adaptive capacity from existing genomic variation. According to our predictions based on standing genetic variation at adaptive loci, natural populations appear to have some capacity to evolve a higher mean CT_{MAX} to meet challenges of warmer conditions (Figure 66). However, populations that currently live in warm environments may have a narrow safety margin, and therefore are more vulnerable and may need conservation attention. Thus, phenotypic plasticity and behavioral thermoregulation, such as seeking thermal refugia (e.g. deep pools, cool springs and upwelling groundwater), will become critically important for them to temporarily survive or avoid extreme temperatures in the future. To predict the rate and limits of evolutionary adaptation more acutely in the future, more advanced niche models need to incorporate additional factors such as the intensity of selection, effective population size, heritability and phenotypic plasticity. This information can be incorporated into robust adaptive networks that include a broad portfolio of adaptive diversity, connectivity, and meta-population scale management for long-term persistence.

Markers that are associated with specific phenotypic traits will also enable monitoring of genetic variation for traits that are considered important to managers. In particular, markers have been developed for premature vs. mature arrival to spawning grounds (e.g., migration/maturation timing) in both Chinook salmon and steelhead, and markers for age/size-at-maturity in steelhead that will enable monitoring of genetic variation for these traits for stocks throughout the Columbia Basin.

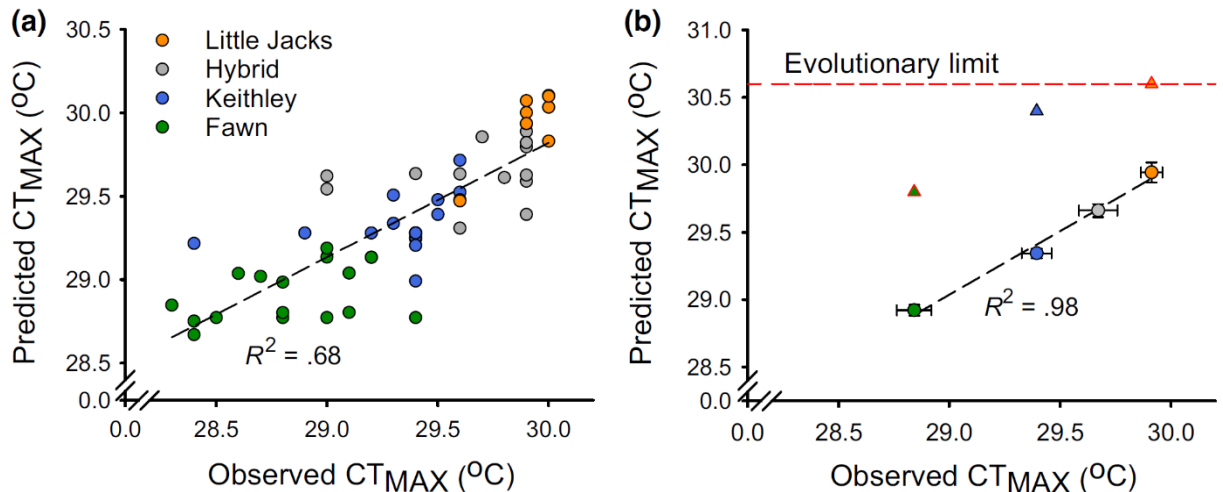


Figure 66. Critical thermal maximum (CTMAX) prediction (from Chen et al. 2018a). (a) Correlation between observed and predicted individual CTMAX values. (b) Prediction of population mean CTMAX (SEM) and evolutionary limits for populations (triangle) and species (dash line).

Project timeline

This project began in 2009 with studies that utilized genetic data available at the time. As genomic methods have advanced over the last decade, more intensive genomic tools have enabled discovery of adaptive genetic variation and the genetic basis for specific phenotypic traits. Work is ongoing to discover adaptive variation and validate the genetic basis for phenotypic variation that is necessary for long-term persistence of salmonids. Thus, the project does not have a clear end date as more work is necessary into the future.

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Section 6: Sturgeon genetics

Introduction

White sturgeon are a long-lived amphidromous species that historically ranged throughout the Columbia River Basin, occurring as broadly distributed, overlapping meta-populations (Parsley 2007; Beamesderfer et al. 2012). Overfishing is believed to have contributed heavily to decreased productivity and declining population abundances as early as the late 1880's (Mallette 2008). Moreover, impacts on white sturgeon populations and trending declines in abundances have been linked to factors associated with the construction of dams (e.g., the hydropower system) in the mainstem Columbia River and its tributaries. Impounding of the Columbia River has significantly fragmented populations (see Nelson et al. 2013). Regional flow regimes and hydrology have been altered and diminished from their natural states (Barton et al. 2010), affecting availability and quality of preferred spawning and rearing habitat for white sturgeon over a large geographic range (Parsley et al. 1993; Rien et al. 2005; Parsley 2007). Most notably, dams have greatly restricted migration through the Columbia River corridor, and fish passage has not provided the same benefit for sturgeon that has been afforded to salmon species (Beamesderfer et al. 2011; Beamesderfer et al. 2012). By some estimates, as many as 24 functionally discrete white sturgeon populations have arisen as a result (Parsley 2007). It is also important to recognize that altered habitat has severely impacted recruitment, predator and prey interactions, and population genetic variability throughout much of the Columbia River Basin (Nelson et al 2012). Considerable monitoring and evaluation efforts have been initiated in the Columbia (KTOI 2007; Drauch-Schreier et al 2012; Drauch-Schreier et al. 2013), and Snake River region (IPC 2005), where sturgeon populations have experienced some of the greatest declines, and where little to no recruitment has been observed in recent years. There have been similar and concerted attempts to characterize white sturgeon population status where relatively larger numbers of sturgeon still persist (e.g. Bonneville Reservoir and the lower Columbia River) but where long-term impacts to habitat and productivity remain a concern for long-term viability and genetic diversity (Mallette 2008; Chapman and Jones 2010).

Since 2008, Tribal managers and CRITFC scientists have been monitoring the genetic population structure of white sturgeon residing in reservoirs impounded by Bonneville Dam, The Dalles Dam, John Day Dam and McNary Dam in the Middle Columbia River. A long-term monitoring effort was initiated in order to assess previously described risks to contemporary population status, including concerns for limited migration potential, declining or low genetic diversity, small effective population sizes, and poor productivity. This report provides a summary of ongoing efforts through 2020 to understand local demographics and resolve population structure. Previously, we reported on our success in overcoming the octoploid nature of the white sturgeon genome, which created difficulties in scoring traditional microsatellite markers, by developing a panel of single nucleotide markers (SNPs) that we are able to genotype as functionally-tetraploid markers. Because the inheritance pattern of these markers is more interpretable than data from microsatellite markers, these data are more amenable to a wider variety of genetic analyses. However, we discovered that ploidy variability in white sturgeon, including not only tetraploidy (4N), but also hexaploidy (6N), which may occur spontaneously due to retention of the second polar body during meiosis (Schreier et al. 2013), and the pentaploids (5N) that result from tetraploid-hexaploid crosses, means that individuals cannot be accurately genotype by assuming a universal ploidy of 4N. In 2020 we worked to modify our bioinformatic pipeline to produce ploidy-accurate genotypes, and have been using this updated pipeline to genotype those samples targeted for sequencing in 2020.

Methods

Our SNP panel consists of 325 loci that met or exceeded quality control criteria, including minor allele frequencies above 5%, and at least 80% genotyping success among samples (Matala et al. 2017). The SNPs were designed using extensive genomic sequence data, and the panel was designed to be genotyped using the GT-seq high throughput sequencing method (Campbell et al. 2015; <https://www.monitoringresources.org/Document/Method/Details/5446>). Genotypes of octoploid white sturgeon segregate into five distinct clusters indicative of four alleles at each locus, indicating functional tetraploidy (i.e. AAAA, AAAB, AABB, ABBB, BBBB) (Figure 67).

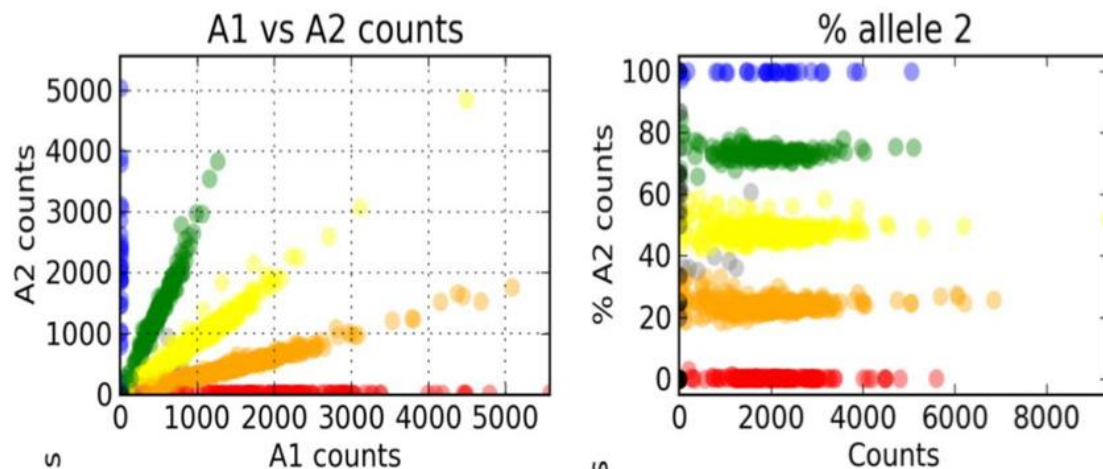
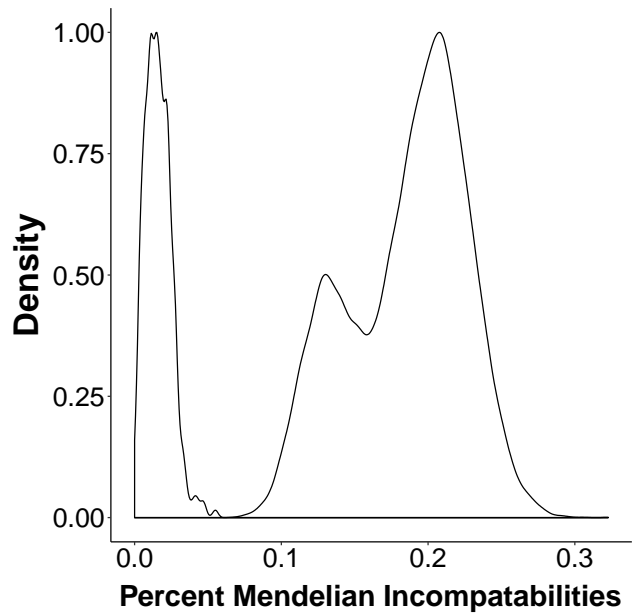


Figure 67. Example of a locus GT-seq plot from octoploid (functionally tetraploid) white sturgeon.

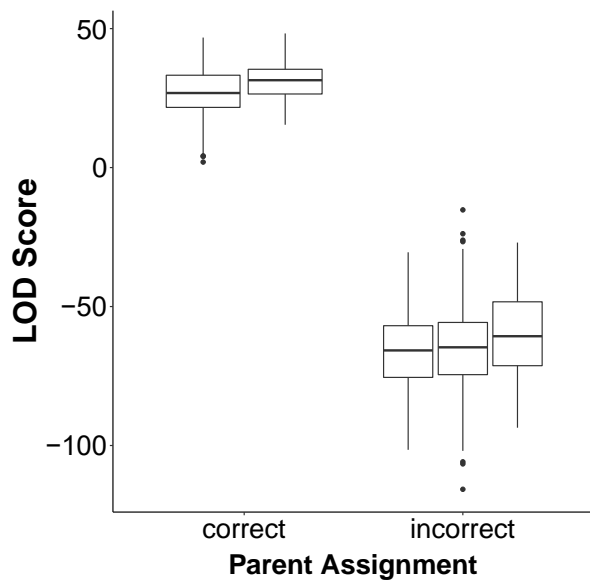
However, individuals that are greater ploidy (5N, 6N) exhibit some distinct and exclusive read ratios (e.g. AAABB, AB BBBB), providing information about the ploidy of each individual. Thus, we modified our genotyping pipeline to use the allele ratios produced by sequencing to first infer the ploidy of each animal by incorporating an algorithm distributed as a package for the R computing environment (TripsAndDipsR; <https://github.com/delomast/tripsAndDipR>). The pipeline subsequently genotypes using ploidies inferred beyond a confidence threshold, and the result of the updated pipeline is genotypes that are accurate for the ploidy of each animal.

The genotyping panel was previously tested using a set of known parent-offspring pairs from 6 reciprocal pairings (6 males x 6 females) of white sturgeon created by the Yakama Nation (D. Miller). Using these known relationships, we were able to establish that the majority of loci exhibited the expected mendelian inheritance patterns (Figure 68). We have also demonstrated success in using statistical parentage assignment techniques, such as single parent assignment in Polygene (Huang et al. 2020) (Figure 69) or in sibling group assignment with Colony (Jones & Wang 2010) (Figure 70).



Comparison ☐ Parents ☐ Not Parents

Figure 68. Distribution of Mendelian incompatibilities (parents and offspring with mismatched alleles) observed among all offspring in six reciprocal crosses of white sturgeon.



Parents Included ☐ both ☐ one ☐ neither

Figure 69. Log-odds scores for parent assignment of known offspring to correct or incorrect parent from known crosses of white sturgeon.



Figure 70. Proportion of half-sibling group assignment completeness in known crosses of white sturgeon.

Given the success in developing this genotyping panel (described in more detail in our 2018 report), in 2019, in collaboration with sturgeon experts at Cramer Fish Sciences (P. Anders), we undertook to organize and expand our tissue holdings for white sturgeon. We were specifically interested to identify representation in our holdings sufficient to meet our continuing objectives, including understanding the relationship of genetic diversity to local adaptation and evolutionary potential in the context of regional and local population structure within the Columbia Basin and relative to other sturgeon strongholds in the Fraser and Sacramento-San Joaquin Basins, as well as local demographic trends in recruitment and spawning success in targeted reaches of the Columbia, their relationship to recent environmental conditions, and their amenability to stock supplementation. In 2020, following the update of our genotyping pipeline to include ploidy inference, we undertook genotyping of these samples for the respective objectives of 1) population structure and 2) variability in ploidy and genetic diversity of recruiting white sturgeon.

Results:

Our tissue holdings include over 11 thousand unique samples from white sturgeon from the Columbia Basin, which we categorized based on the Columbia River reach from which they were collected (Figure 71). From these we identified 3,105 samples that would give a robust examination of population structure and genetic diversity among reaches within the Columbia Basin and outside, and genotyped them in 2020 to 90% genotype completeness using our 325 SNP panel (Table 71). Analysis of these data is ongoing, but preliminary analysis of minor allele frequency suggests that they contain significant signal of population structure and variation in genetic diversity, as indicated by differences among reaches (orange) and comparison with other Pacific versants (green).



Figure 71. Locations in the Columbia Basin where white sturgeon are present.

Reach	N@90
Columbia below Bonneville	445
Willamette	12
Bonneville	440
The Dalles	429
John Day	631
McNary	162
Rocky Reach	36
Lake Roosevelt	220
Ice Harbor	101
Lower Monumental	127
Little Goose	106
middle Snake	78
upper Snake	216
Fraser River	46
Sacramento-San Joaquin	56

Table 71. White sturgeon from the Columbia and adjacent basins genotyped through calendar year 2020 at 90% completeness.

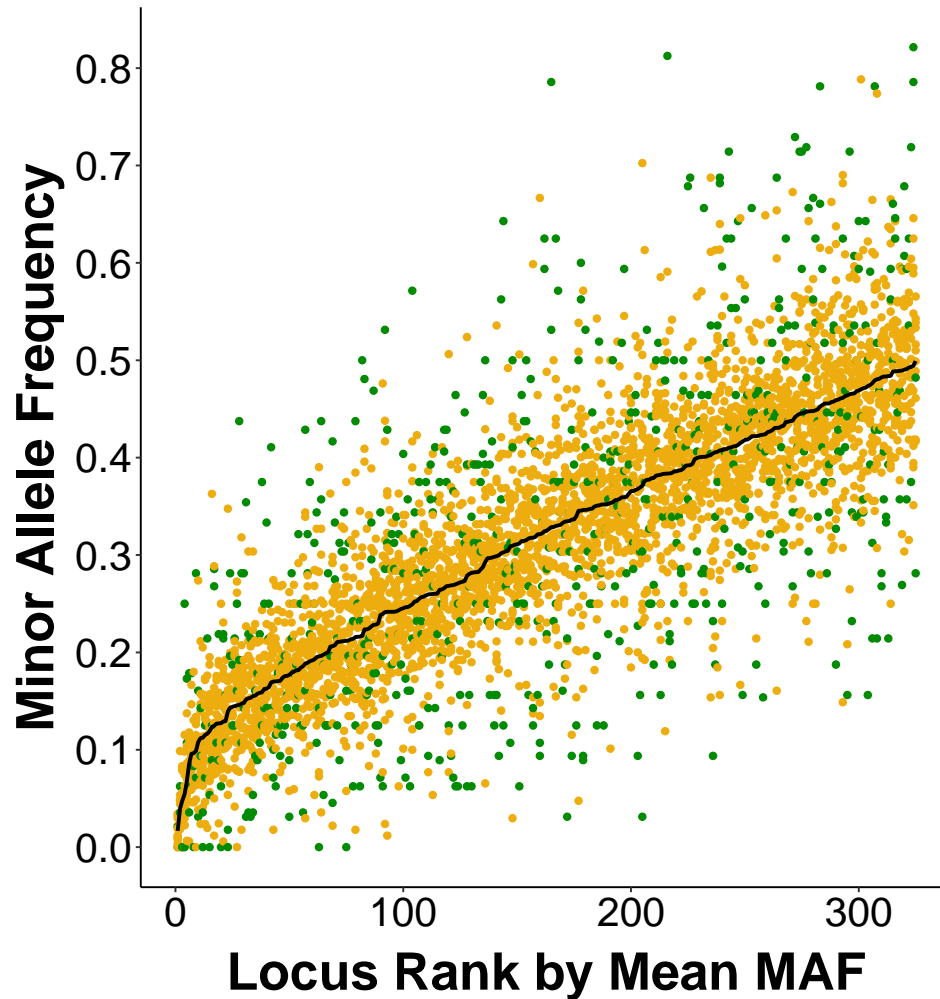


Figure 72. Minor allele frequency of white sturgeon samples from reaches in the Columbia Basin (orange) and Sacramento-San Joaquin or Fraser River Basins (green). Black line represents mean minor allele frequency of the locus.

In addition, we identified 1,948 samples that allow us to examine variations in genetic diversity across life stages in reaches of the Columbia that contrast in their estimated rates of spawning and recruitment, and which were genotyped to 90% genotype completeness (Table 72). Several of these reaches have been targeted for supplementation, because of identification of mismatch between putative adult carrying capacity and rates of *in situ* recruitment. Thus, we utilized samples that represented different year cohorts, allowing us to identify natural rates of genetic distinctness between recruits and the adult population over time (Figure 73). Analysis of this data is ongoing.

	>1000mm	300-1000mm	<300mm
Columbia below Bonneville	80	97	201
Bonneville	77	156	207
The Dalles	10	150	267
John Day	273	206	62
McNary	118	33	11

Table 72. White sturgeon from targeted reaches of the Columbia River genotyped through calendar year 2020 at 90% completeness identified by lengths reflecting different life stages.

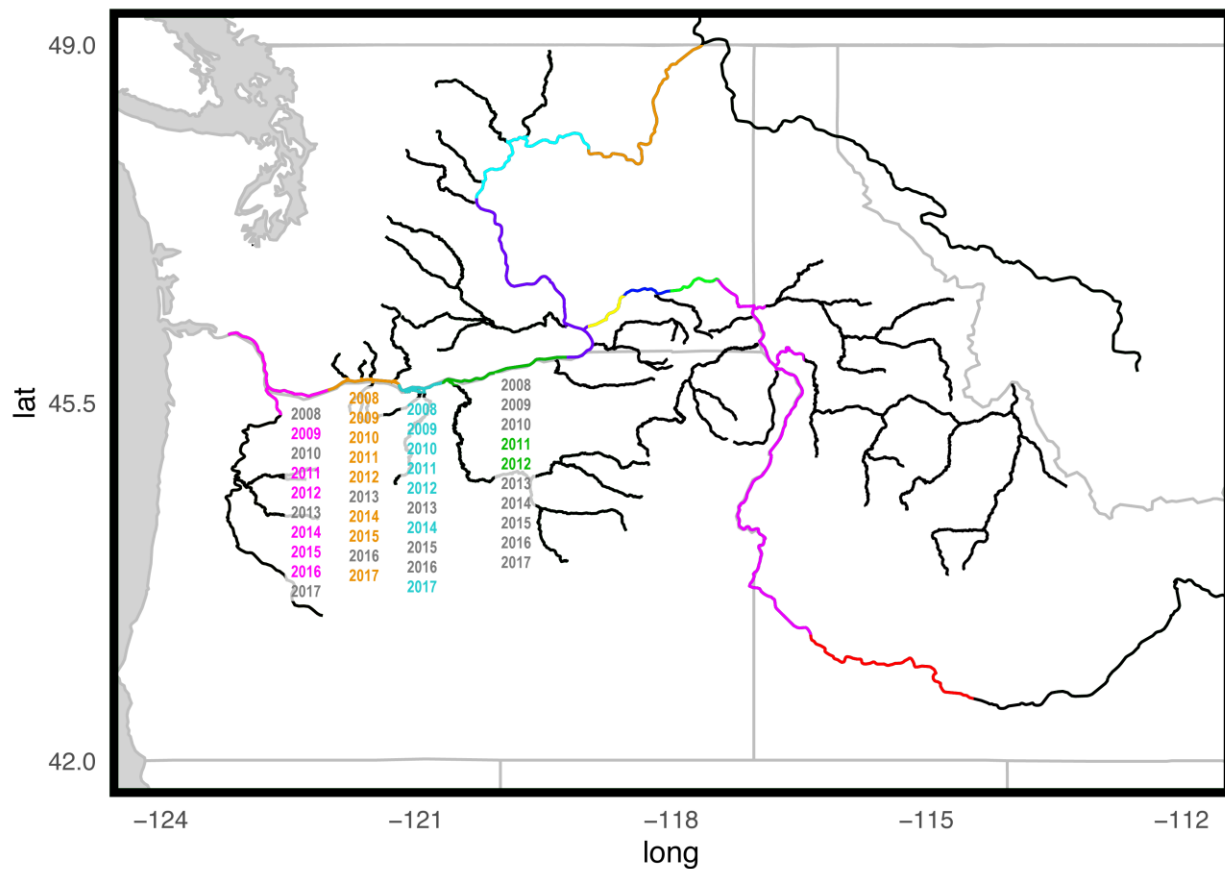


Figure 73. Years included in the sampling of young-of-year (<300mm) white sturgeon in targeted reaches of the lower Columbia River (Table 72).

Discussion:

One of the ongoing challenges with our objectives for white sturgeon is the nature of white sturgeon themselves. Although technically octoploid (8 copies of each chromosome), following

an evolutionarily recent genome duplication from a putatively tetraploid ancestral state (4 copies of each chromosome), the white sturgeon appears to have regained a functional tetraploid status, as indicated by the mendelian segregation of four alleles at the majority of SNP loci (Figure 67). Nonetheless, while the optimization of markers accurately rendering genotypes of the functional tetraploid chromosomal segments empowers our ability to glean information about population genetic structure and diversity, the majority of statistical parentage programs remain designed to process only diploid data (two copies of each chromosome, like humans). While we have garnered some success in identifying likely parent candidates using ad hoc (e.g. mismatch distribution) methods (Figure 68), we continue to explore more robust methods to fully utilize the information content of tetraploid genotypes (e.g. Figure 69, Figure 70).

Our research is guided by previous results which indicate that white sturgeon in the Middle Columbia River have experienced a significant genetic bottleneck and decreased diversity as a result of dramatically restricted migration, altered flow regimes, and loss of spawning and rearing habitat. In addition, little to no genetic differentiation between impoundments in the Middle Columbia River has been observed, although a regional distinction between Snake River and Columbia River populations is evident (Matala et al. 2017). Current demographic trends and genetic variation may be a consequence of diminished rearing and/or spawning habitat coincident with stream fragmentation and limited connectivity. Ongoing efforts for this project are designed to further resolve the dynamics of recruitment and population demographic trends in the context of regional population structure and local adaptation and evolutionary potential, particularly in the John Day and Grand Coulee Reservoirs, where Tribal efforts are underway to identify efficient stock supplementation techniques. While supplementation is a natural proposal for reaches where adult carrying capacity appears to exceed *in situ* recruitment rates, the effects of different rates and types of supplementation remain unclear (e.g. hatchery spawning vs. repatriation). In addition to the traditional questions about the preservation of native genetic diversity, the incidence of spontaneous autopolyploidy (increases to 6N from 4N) may well be greater in hatchery spawned fish (Van Eenennaam et al. 2019), and as the fertility of 6N and backcross (5N) fish has yet to be clarified, there remains a chance that supplementation could have counterintuitive consequences for populations with already diminished recruitment. To this end, our examination of genetic diversity and rates of ploidy variation in these different reaches across life stages is intended to help clarify natural rates of spontaneous autopolyploidy and of variation in genetic diversity between cohorts, as well as between recruits and the adult population (Table 72).

In addition, our continuing efforts with white sturgeon include the development of a draft genome assembly. While extensive whole genome data has provided draft contig sequences, the majority of the genome remains insufficiently anchored for publication due to the challenges of scaffolding a high repetitive (octoploid) genome. To overcome this, we are working closely with collaborators to generate a linkage map from a reduced ploidy line of white sturgeon, which will assist to order or orient (anchor) smaller scaffolds into chromosomes. In 2020, we completed the creation of reduced representation (restriction enzyme associated DNA, or RAD) genomic libraries using these tissue samples and initiated sequencing of these libraries, with analysis of these data to infer genomic linkage to begin soon. The draft genome, once complete, will allow us to use genome-level sequencing data to survey genetic variants underlying phenotypic traits and local adaptation, a type of analysis that the lab has had extensive success completing for

other Columbia Basin species (e.g. Micheletti et al. 2018). However, even without full resolution, some uses of the draft assembly have already proven fruitful. Recently, Kuhl et al. (in review) described the identification of sex-associated regions in genome assemblies of a male and female sterlet sturgeon (*Acipenser ruthenus*). We are pursuing homologous regions in our (female) white sturgeon assembly, thus providing potentially sex-associated regions for white sturgeon (sturgeon females are hypothesized to be the heterogametic sex, ZW, in contrast to most mammals including humans, where males are heterogametic, XY). As a tool to identify potential spawners without having to phenotypically screen individuals in close temporal proximity to spawning, sex markers would be a boon to supplementation efforts in white sturgeon that generally rely on even sex ratios in spawned fish.

Since white sturgeon are long lived and require many years to reach sexual maturity, the value of data generated by this project are largely defined by the project's long-term implementation. It began in 2008 and continues through the present, with samples collected and archived on an annual basis. Among other things, this affords the opportunity to monitor cohorts through various age-classes or life history stages. It also provides more robust analysis as data accumulates. For example, fish that were sampled as subadults in 2008 are reaching (or have reached) sexual maturity and are available to screen as potential parents of juvenile fish sampled subsequently. We anticipate long-term applicability of the data produced, particularly with continued collaborations and data sharing with co-managers in the basin.

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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 (>100,000 fish genotyped in Hagerman Genetics Lab each year since 2015). This 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 developed with whole genome resequencing to provide allele frequency estimates for millions of SNPs in Chinook salmon and steelhead. SNPs identified through 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.

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 2019. 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 continued performing timely post-season reporting of genetic analysis of Chinook, steelhead and Sockeye Salmon at Bonneville Dam in 2020, and also plan to continue to provide in-season results at bi-weekly intervals during the spring and summer management periods of Chinook Salmon, and approximately monthly for the summer and fall runs of steelhead and Chinook Salmon. The timely updates of the genetic analyses for these runs and species of Columbia River fishes improves their utility for fisheries managers such as the Technical Advisory Committee (TAC).

For Objective 5 on local adaptation, candidate genes for several traits have been identified in both steelhead and Chinook salmon. As these candidate genes for traits have begun to be identified, SNP markers from these regions are being incorporated in standard genotyping panels with GTseq to validate and monitor genetic variation for these traits in large numbers of individuals. Inclusion of candidate markers associated with specific traits allows more detailed genetic monitoring of stocks in the Columbia Basin. Extensive programs are in place that enable genetic identification of the origin of individual fish, but candidate markers from this study also provide the ability to monitor genetic variation for specific traits that are expected to be necessary to maintain life history variation for long term persistence of populations.

For Objective 6 on white sturgeon genetics, the accumulation of genetic monitoring results (2008-2018) for White Surgeon in the Middle Columbia River and Snake River are similar to evaluations of population structure reported for similar large systems like the Fraser River in British Columbia Canada. Current demographic trends and genetic variation may be a consequence of diminished rearing and/or spawning habitat coincident with stream fragmentation and limited connectivity. Ongoing efforts for this project are designed to utilize SNP markers that were developed for this species to further resolve regional population structure and parentage analyses to support tribal efforts to supplement white sturgeon in the Columbia Basin.