

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.

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). In the current year of this project, we have continued our use of GT-seq protocols and SNP discovery. Our laboratory has designed and currently uses seven SNP panels for the following species: Chinook salmon (*Oncorhynchus tshawytscha* – 365 loci including a sex determination marker and 14 amplicons used for species identification), Steelhead trout (*O. mykiss* – 376 loci including a sex determination marker); Sockeye salmon (*O. nerka* – 363 loci including a sex determination marker); 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 were used to genotype 154,739 samples in 2021 (Figure 1). The largest portion of samples were Chinook salmon (84,766), then Pacific lamprey (28,154), Sockeye (17,062), Steelhead (15,134), Coho (8,485), and White sturgeon (1,138).

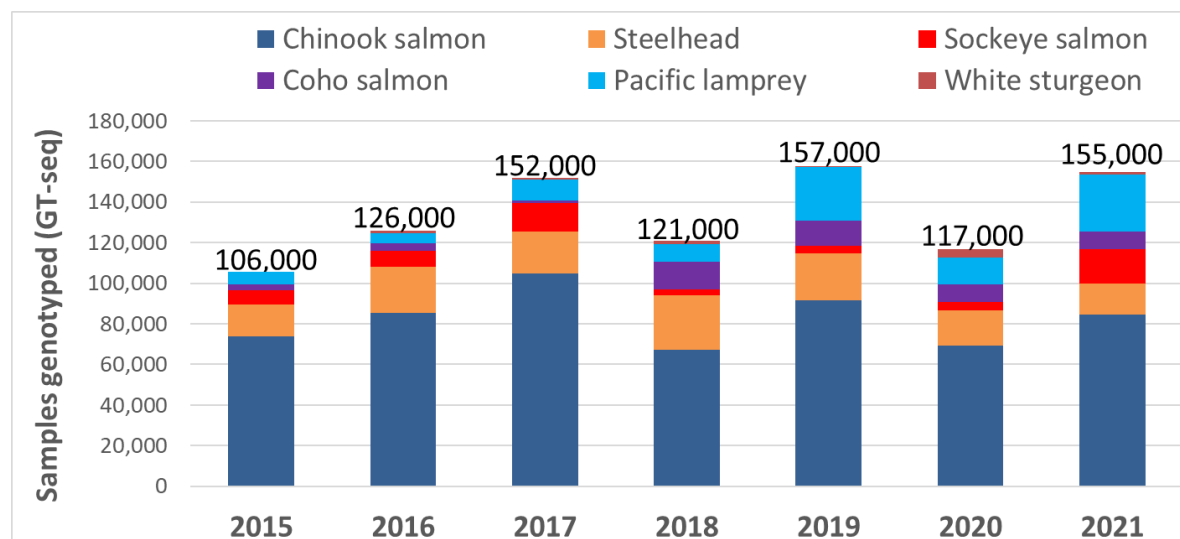


Figure 1. Summary of Columbia River fish samples genotyped using GT-seq (2015 – 2021).

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 2021 include genotyping additional markers from genes associated with adult migration timing (GREB1L/ROCK1) for Chinook salmon and steelhead and age at maturity (SIX6) in steelhead to examine allele frequencies in hatchery programs and fish passage locations.

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 several 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 2020-2021. For Chinook salmon, we have switched to a 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 2020 in Non-Treaty sport, commercial, and pound net 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 463 coded-wire tags (CWTs) that were identified to hatchery stock and broodyear (BY) among the snouts recovered from the lower river fisheries, and 287 of these CWTs also were PBT assigned (62%). Of the 287 fish with both CWT and PBT, there were 277 fish (97%) that were concordant across results from these tagging methods according to the hatchery source and the broodyear.

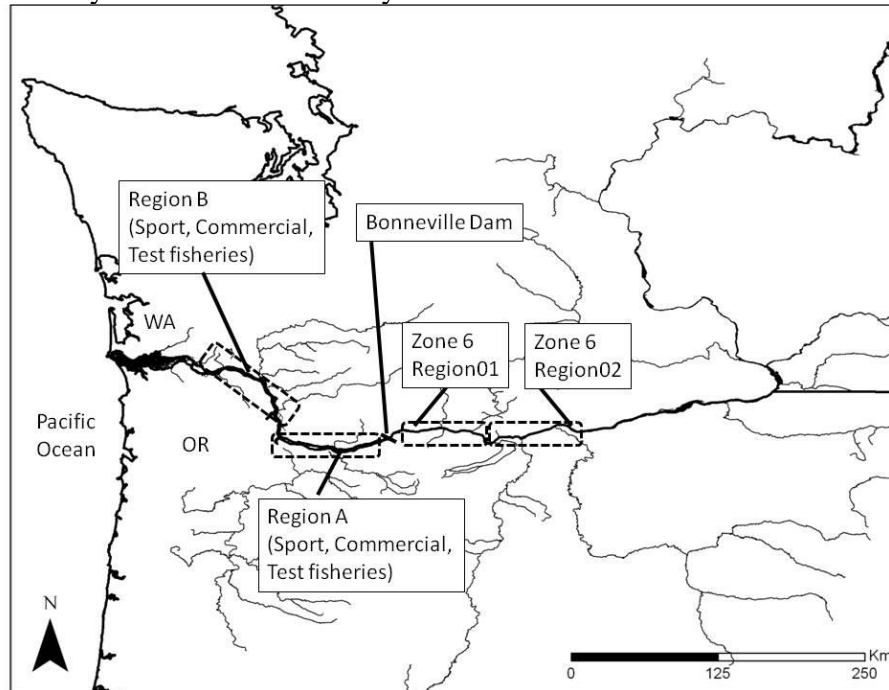


Figure 2. Sources of fishery mixtures in the lower Columbia River mainstem.

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). The test fishery was not conducted in 2020 due to COVID, however, we were able to analyze the 2021 test fishery as part of our in season reporting. Consistent with our previous analyses of 2018 and 2019 test fishery data, the 2021 test fishery CPUE was correlated with the Bonneville weekly counts with a lag of 13 days difference (Figure 3). 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.

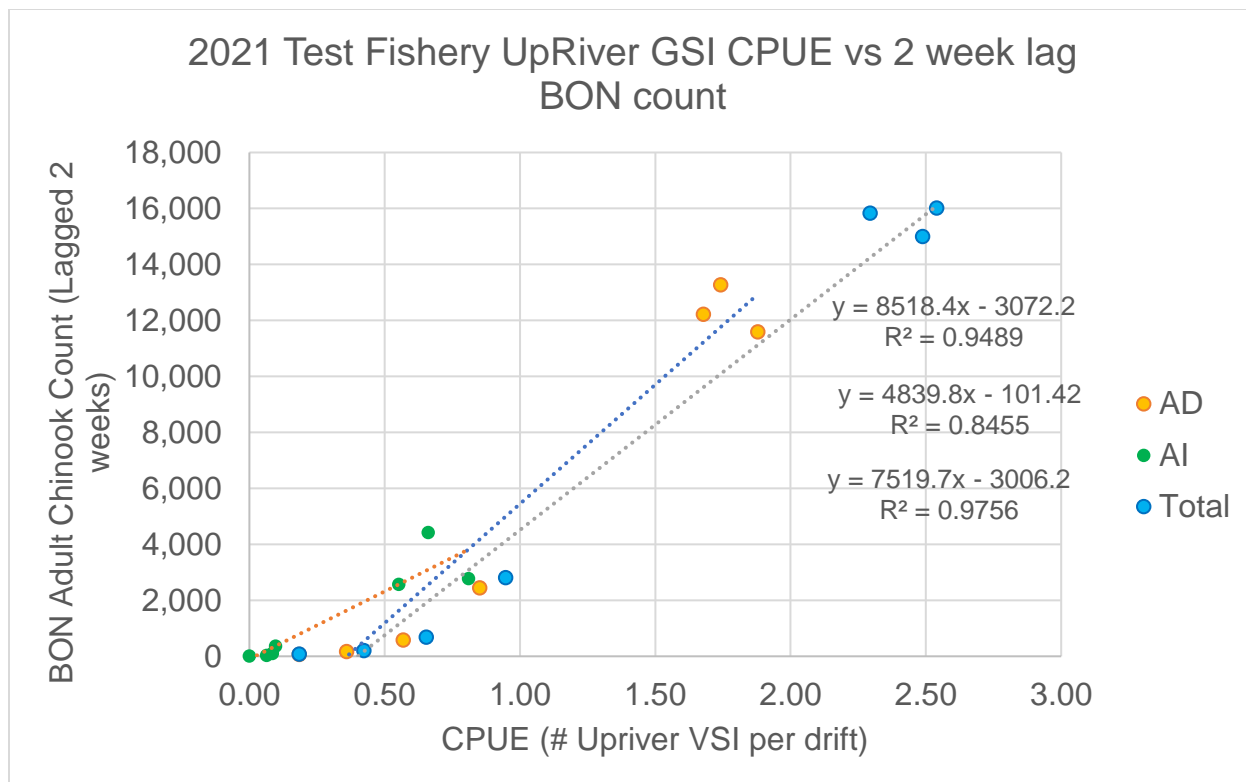


Figure 3. The relationship between the test fishery upriver Chinook Salmon CPUE and weekly fish counts at Bonneville Dam in 2021 with 2 week lag.

As expected, the stock composition varied substantially across the Non-Treaty sport 2020 fisheries that were executed in the spring versus summer period. The largest difference in stock compositions across the spring and summer fisheries was the high estimate of Hells Canyon stock during the spring period compared to the summer, and the high estimate of upper Columbia summer-run stock (18_UCOLSF) captured during the summer period compared to the spring (Figure 4). However, it was unexpected to observe such a high estimate of lower river stock from the Willamette River (04_WILLAM) during the summer period sport fishery. This high capture rate may have been due to fishing effort in region B but is unexpected due to the summer timing of the fishery since Willamette River stock is spring-run.

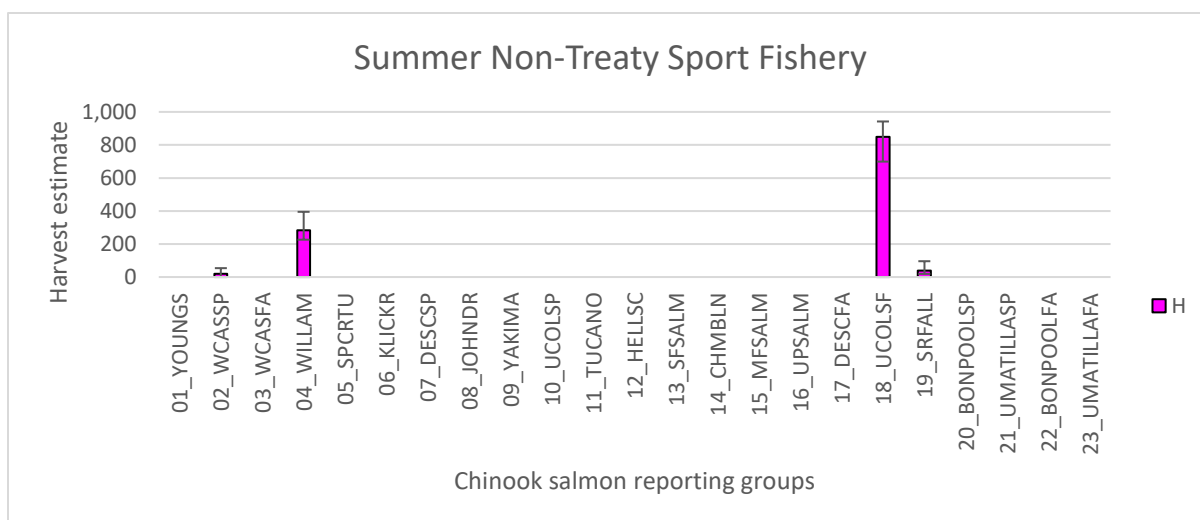


Figure 4. Genetic stock composition of the Non-Treaty Sport Chinook fishery during the summer period analyzed in 2020.

In 2020, the pound net was operated in the Cathlamet Channel (Region B) during the Fall Chinook salmon management period. The composition of the stocks in the pound net fishery was used to compare to other fall fisheries in the lower river. The compositions of the pound net fishery and the Non-Treaty sport harvest below Bonneville Dam were similar, likely due to close geographic proximity (Figure 5).

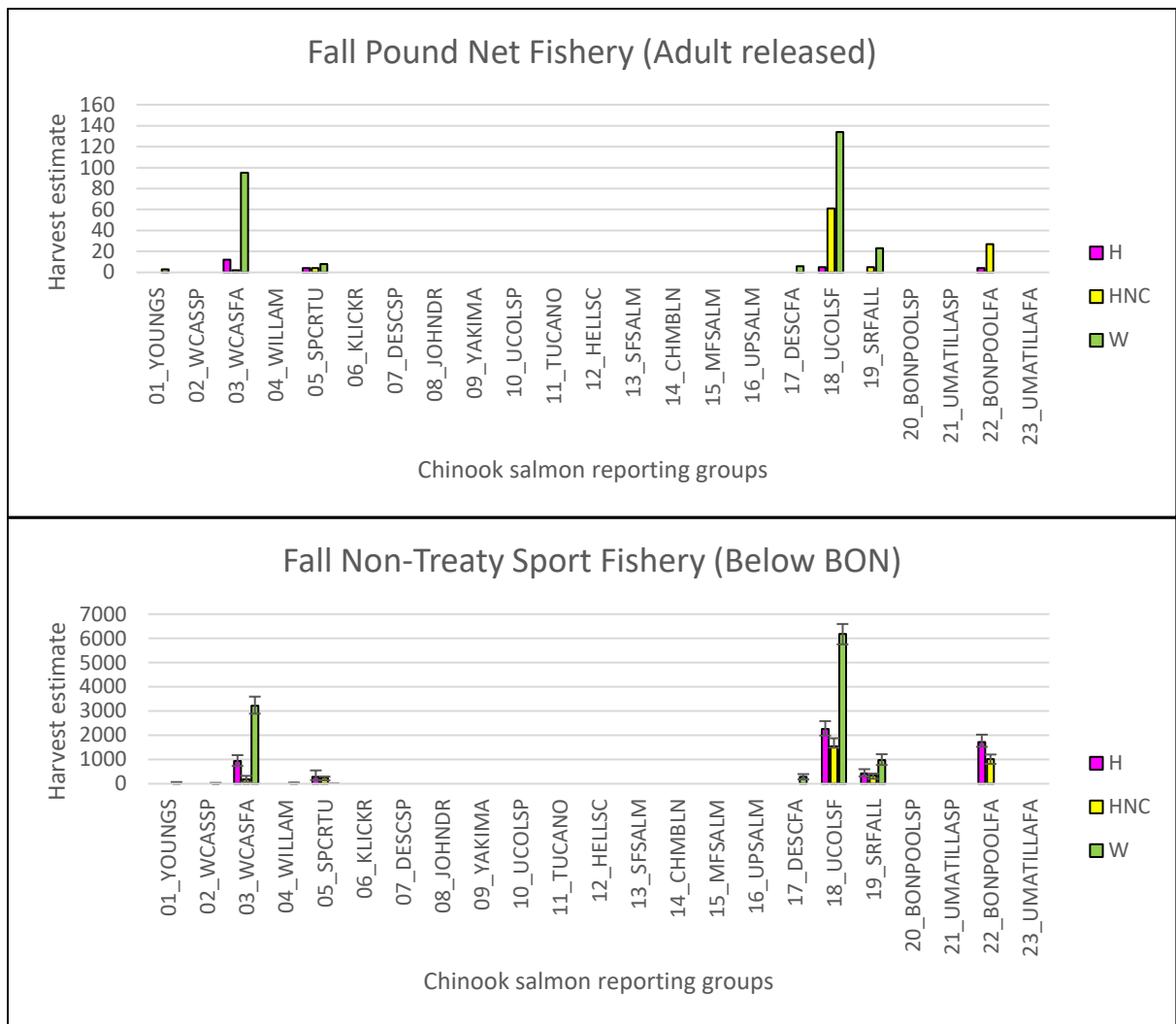


Figure 5. Genetic stock composition of the Non-Treaty fall pound net (released adults) and lower river sport Chinook salmon fisheries analyzed in 2020.

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 2020 (post-season analyses). Further, in-season analyses were completed for fish returning throughout 2021 and provided to regional fisheries managers that serve the U.S. v OR Technical Advisory Committee (TAC).

In 2020, there were 9 major (i.e., abundance >1000 fish) Chinook salmon stocks represented in the total estimated relative abundance (N=160,350) of natural-origin (i.e., excluding unclipped hatchery-origin fish) Chinook salmon passing Bonneville Dam in 2020 (Figure 6). The dotted lines in Figure 6 mark the beginning of the summer and fall management periods (June 16 = Ordinal day 167; Aug 1 = Ordinal day 213, respectively). These natural-origin stocks in order of decreasing magnitude were 18_UCOLSF (119,478), 19_SRFALL (18,652), 17_DESCFA (4,494), 12_HELLSC (4,227), 16_UPSALM (3,195), 13_SFSALM (2,784), 10_UCOLSP (2,692), 15_MFSALM (1,316), and 03_WCASFA (1,358). These stock abundance estimates were generated using SCOBIDEUX and SPIBETR functions and the estimates of clipped and unclipped adults distributed by TAC.

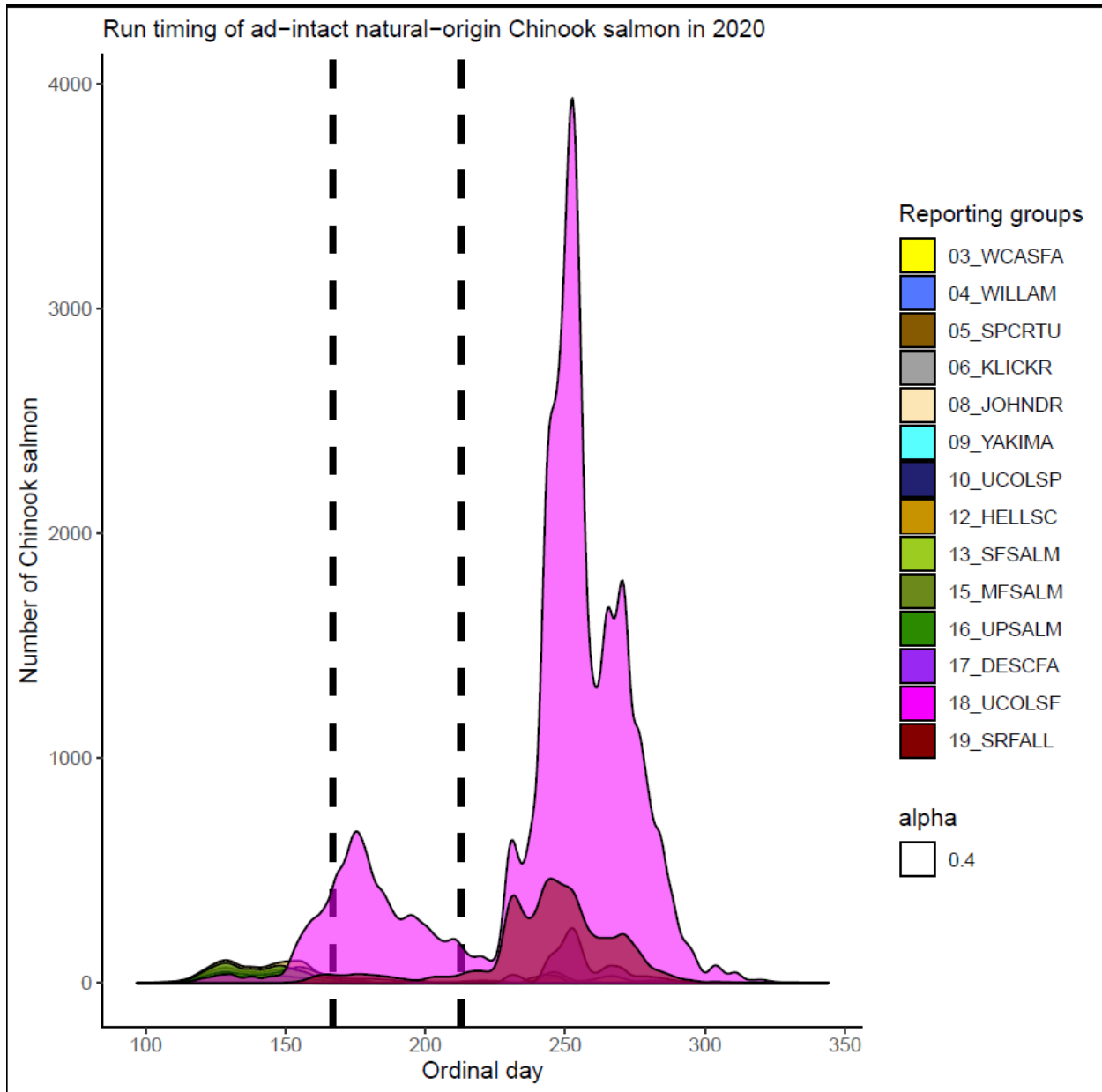


Figure 6. Estimated abundance of natural origin (excluding adipose-intact hatchery-origin fish) adult-sized Chinook salmon sampled at Bonneville Dam in 2020 assigned to genetic stock of origin.

There were five major stocks (abundance >1000) represented in the total estimated abundance (N=65,543) of clipped hatchery origin steelhead passing Bonneville Dam in 2020. These stocks in order of decreasing magnitude were 10_SFCLWR (22,091, B-Index), 14_UPSALM (20,619), 07_MGILCS (14,576), 03_SKAMAN (3,174), 09_UPPCOL (2,303), and 10_SFCLWR (1,811, A-Index) (Figure 7). There were three major stocks (abundance >1000) represented in the total estimated abundance (N=8,805) of unclipped hatchery origin

steelhead passing Bonneville Dam in 2020. These stocks in order of decreasing magnitude were 10_SFCLWR (3,994, B-Index), 10_SFCLWR (1,812, A-Index), 07_MGILCS (1,238), and 14_UPSALM (1,116). There were five major stocks (abundance >1000) represented in the total estimated abundance (N=16,621) of natural origin (excluding adipose unclipped hatchery-origin fish) steelhead passing Bonneville Dam in 2020 (Figure 7). These stocks in order of decreasing magnitude were 07_MGILCS (20,053 A-Index; 1,576 B-Index), 14_UPSALM (3,093), 08_YAKIMA (2,209 A-Index; 70 B-Index), 11_UPCLWR (707 A-Index; 1,503 B-Index) and 10_SFCLWR (289 A-Index; 1,123 B-Index). 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.

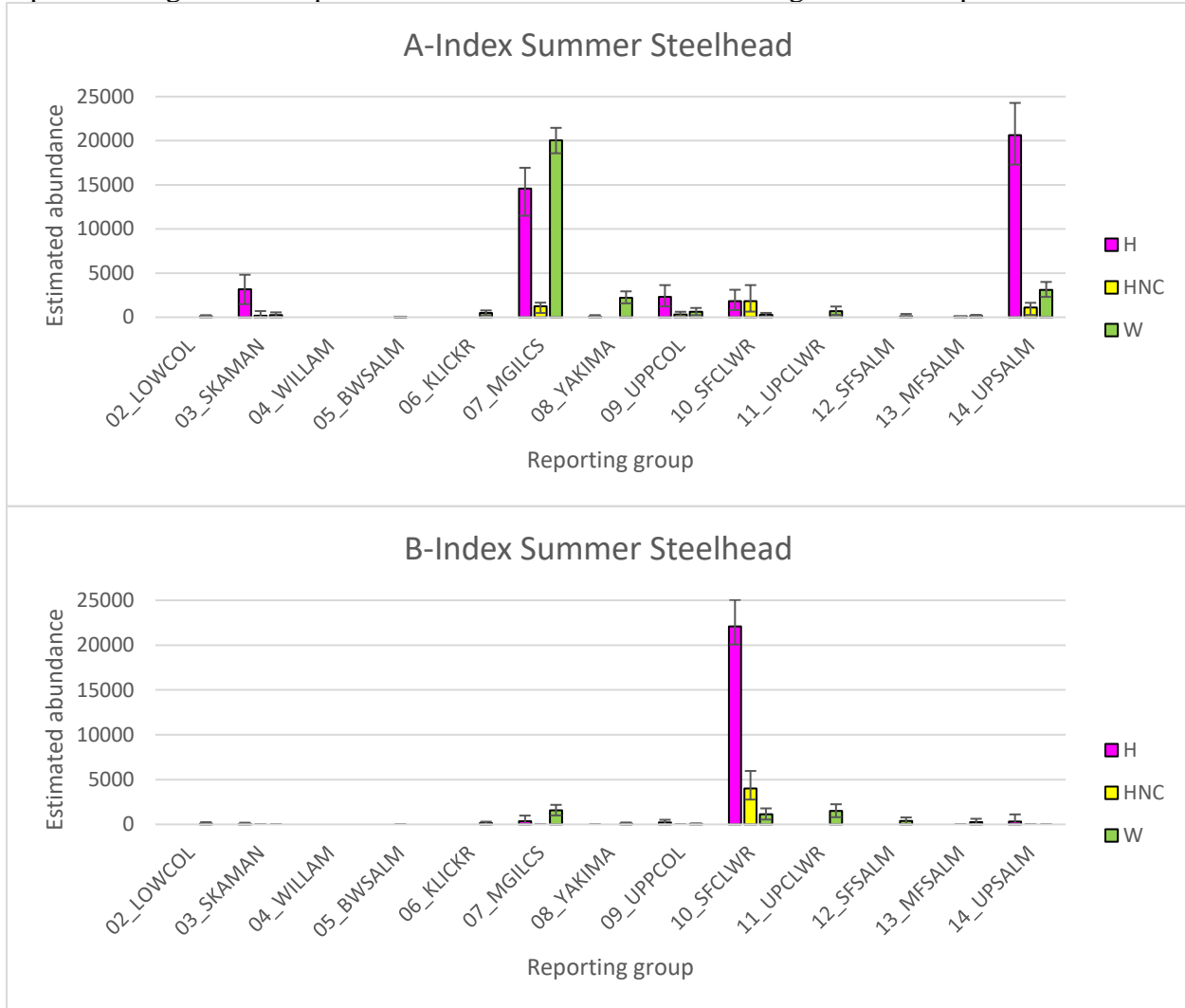


Figure 7. Estimated abundance (\pm 95% CI) of A-Index (<780mm FL, top) and B-Index (\geq 780mm FL, bottom) hatchery origin (clipped “H” and unclipped “HNC”) and natural-origin (“W”) steelhead assigned to genetic stock of origin that were sampled at Bonneville Dam in 2020.

Stock abundance for sockeye salmon was estimated over a course of 15 statistical weeks (i.e. weeks 23-37). A total of 1,729 sockeye salmon were sampled at Bonneville Dam in 2020 and were assigned to one of four genetic stocks (i.e., Okanogan, Wenatchee, Snake, and Lake Billy Chinook) using GSI and one reintroduced stock (Yakima) using PBT. In 2020, the Okanogan stock had the highest relative abundance (274,008), followed by the Wenatchee (55,890). This year there were a small number of sockeye salmon estimated from Snake River (122). The Lake Billy Chinook stock had zero estimated abundance. The reintroduced stock from Yakima River had a record high sample size and was estimated at 11,719 fish in 2020 (Figure 8).

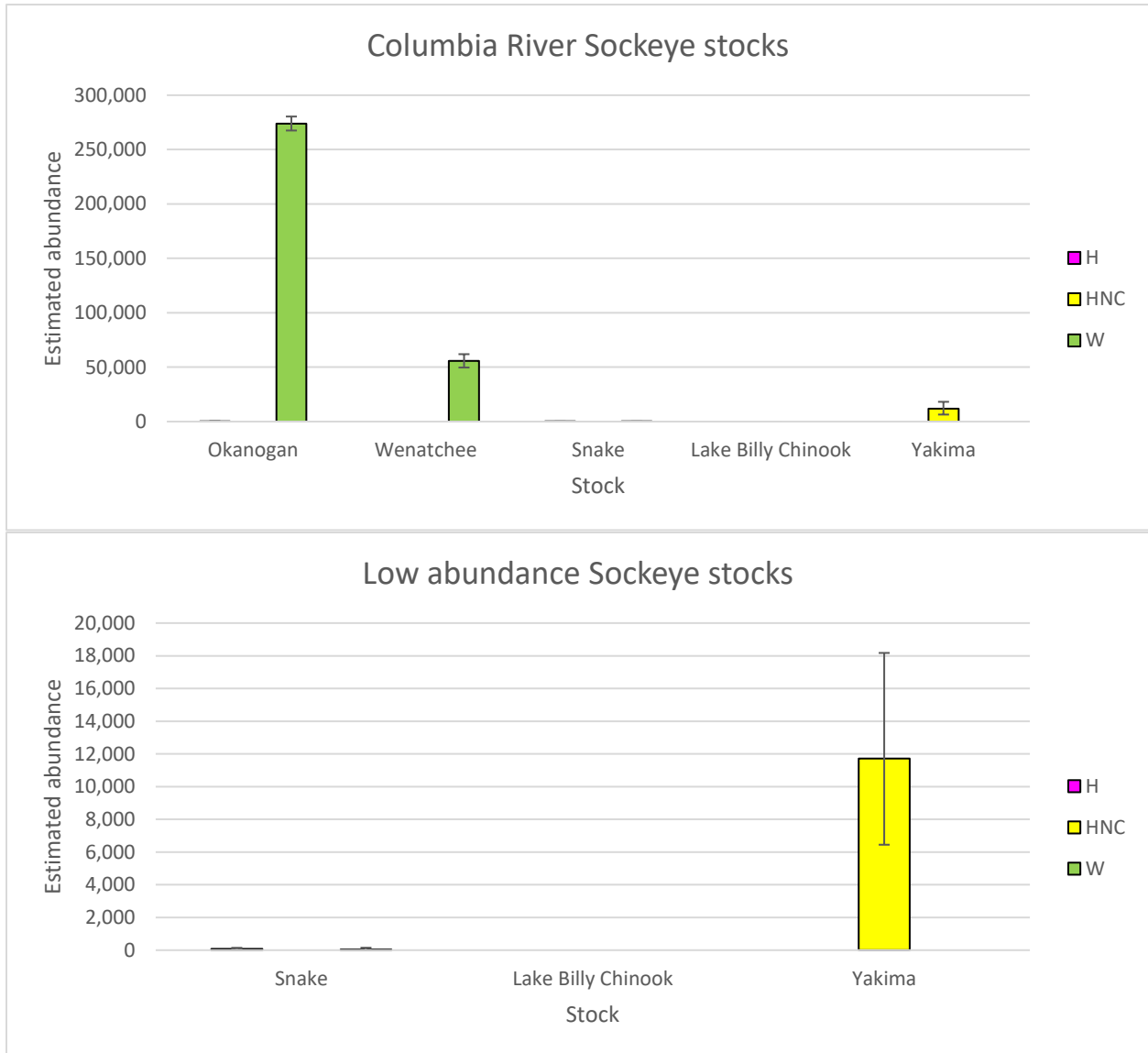


Figure 8. Estimated abundance (\pm 95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2020.

In 2020, 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 was estimated to pass in both spring and summer periods at 24% (5,312 fish) and 76% (17,042 fish) of the total abundance estimated in those two periods, respectively. 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 12_SFSA LM (both A-Index and B-Index), 11_UPCLWR (both A-Index and B-Index), 13_MFSALM (B-Index), and 10_SFCLWR (B-Index). For the nine reporting groups in which both A-Index and B-Index were represented, the B-Index stock had a later median date in all but two reporting groups (Figure 9). Run timing distributions for sockeye salmon sampled at Bonneville Dam broadly overlapped in 2020. The Wenatchee, Okanogan, and Yakima stocks had nearly identical run timing distributions each with a median date on 06/29/20, and the Snake River stock was timed slightly later (07/20/20).

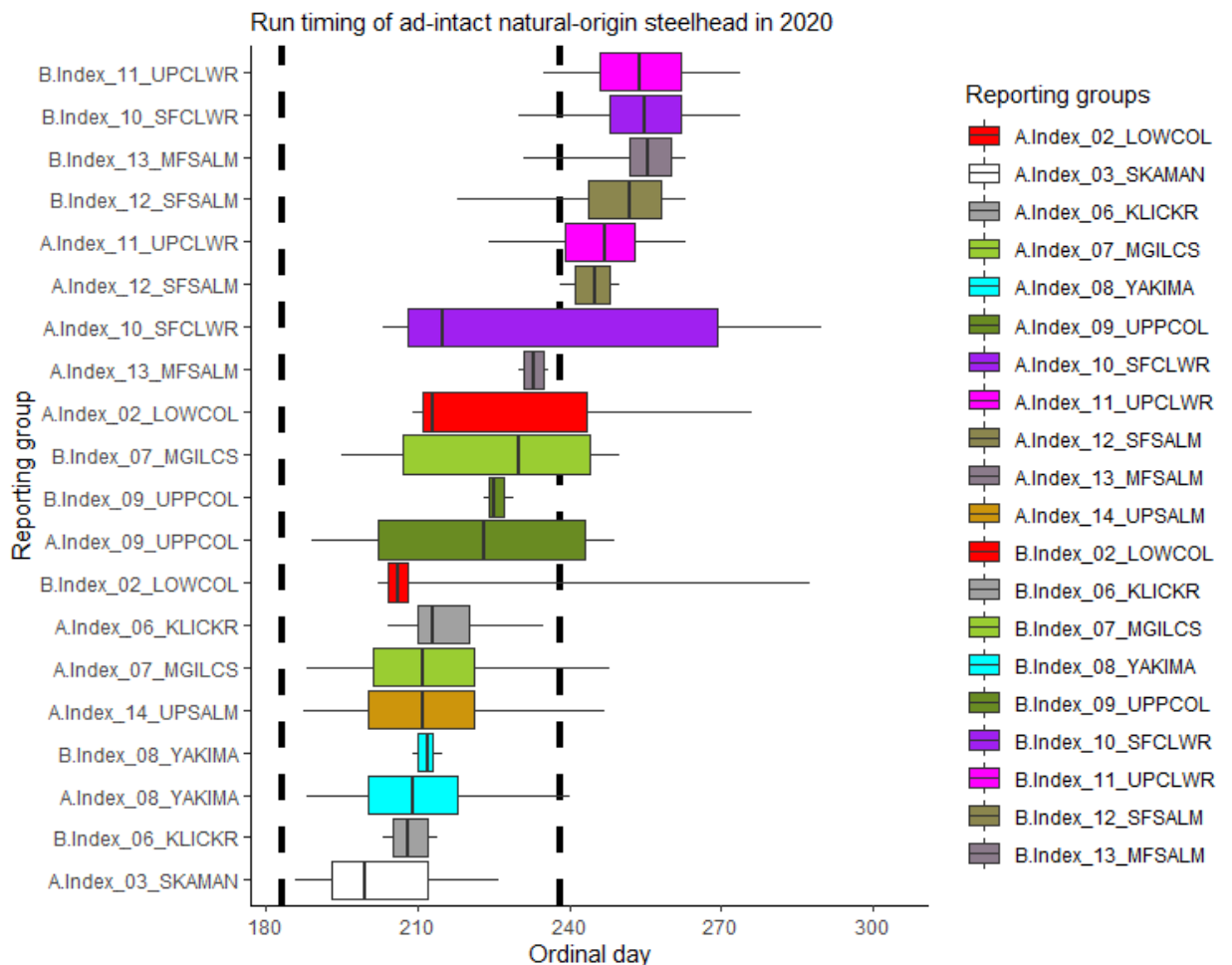


Figure 9. Reporting group level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for natural-origin steelhead (unclipped hatchery-origin fish excluded) that were sampled at Bonneville Dam in 2020 and split by A-Index and B-Index size category. August 25th 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 2021 (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 around 3,500 Sockeye salmon returned to Bonneville Dam in 2021 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 93% 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 2021 fish runs for Chinook salmon, steelhead, and Sockeye salmon.

Species	Management Period	Data coverage	Samples Arrive	Analysis begins	Report distributed
Chinook	Spring	01/01/2021 – 04/30/2021	5/3/2021	5/6/2021	5/10/2020
		01/01/2021 – 05/14/2021	5/17/2021	5/20/2021	5/24/2021
		01/01/2021 – 05/28/2021	5/31/2021	6/3/2021	6/7/2021
		01/01/2021 – 06/15/2021	6/16/2021	6/21/2021	6/25/2021
	Summer	06/16/2021 – 06/30/2021	7/1/2021	7/7/2021	7/12/2021
		06/16/2021 – 07/31/2021	8/2/2021	8/5/2021	8/9/2021
		08/01/2021 – 8/27/2021	8/30/2021	9/2/2021	9/6/2021
	Fall	08/01/2021 – 10/29/2021	11/1/2021	11/4/2021	11/8/2021
Steelhead	Skamania	04/01/2021 – 06/30/2021	7/1/2021	7/7/2021	7/12/2021
	Summer A-/B-Index	07/01/2021 – 07/31/2021	8/2/2021	8/5/2021	8/9/2021
		07/01/2021 – 08/27/2021	8/30/2021	9/2/2021	9/6/2021
		07/01/2020 – 10/31/2020	11/1/2021	11/4/2021	11/8/2021
Sockeye	Total	01/01/2021 – 07/31/2021	8/2/2021	8/5/2021	8/9/2021

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.

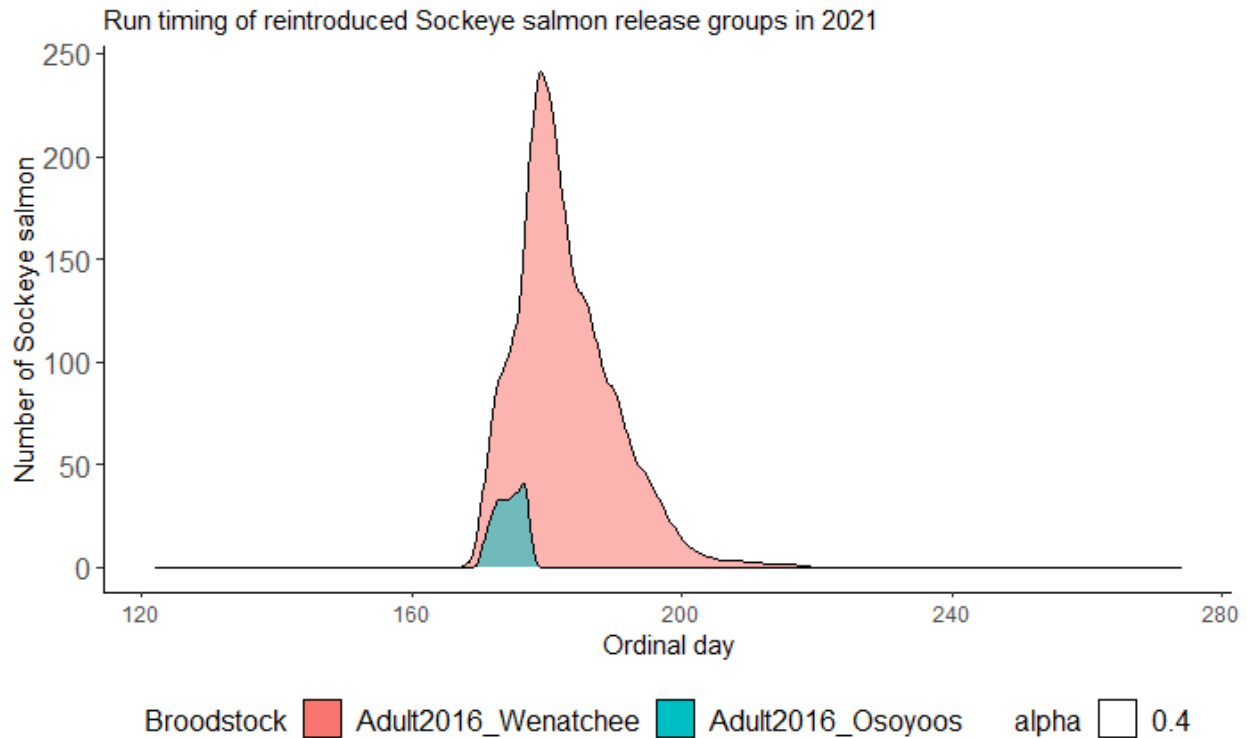


Figure 10. In-season analysis estimated a relatively large return of reintroduced Yakima River sockeye salmon in 2021 comprised of a mixture of Wenatchee and Osoyoos genetic stocks.

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; Alshwairikh et al. 2021). 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 and summer/fall Chinook salmon in the Columbia River Basin (Micheletti et al. 2018a; Alshwairikh et al. 2021).

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; Willis et al. 2021), 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 fish from 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 or locks at hydropower dams 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 population viability. The contemporary status and temporal trends in genetic diversity are likely to aid managers in

789 understanding the impacts of limited habitat in the confines of the mid-Columbia impoundments
790 that may be exacerbated by 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 technology facilitates high-throughput, rapid identification of genetic variation. 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. Publicly available reference genome assemblies for Chinook, coho, sockeye and steelhead, have enabled whole genome resequencing for investigating adaptive variation across large portions 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 of pooled samples 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 instruments.

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. Testing was done

by combining the newly designed primers with the existing GTseq primers for the target species. These new primer pools were then used to create test libraries containing 96 samples using the GT-seq protocol (Campbell et al. 2015). 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. To evaluate the new primers, sequencing reads that started with the designed forward primer sequence were collected and sorted by abundance. Primer success was determined if the read variation was dominated by one type of sequence with a single variable SNP site. GTseq probes were designed based on the dominate read sequence. Following this step, 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.

Candidate species diagnostic markers were chosen by testing a mixed sample plate including Chinook, steelhead coho, sockeye, and Yellowstone cutthroat against GT-seq SNP panels for Chinook, steelhead, coho and sockeye. Loci amplifying across all species with evidence of sequence divergence between at least two species were identified for further testing. We also modified one marker identified by Beacham et al. (2020) as having diagnostic data. Sections of this sequence region were previously included in the coho and steelhead panels but did not amplify for all species of interest. Additional testing was then done by spiking the test markers into the Chinook panel and testing against additional samples that included representative sample/s for mykiss and cutthroat subspecies, chum salmon, pink salmon, brown trout, bull trout, and brook trout. Probe locations were then isolated and used to generate SNP type data.

Waters et al. (2020) identified an association of two genes (six6 and vgll3) with age of maturity variation in Chinook, coho, sockeye, and steelhead. Using the provided reference sequences and markers, we designed GTseq primers and probe sequences. Testing on Chinook has been completed where primers were tested against samples from three lineages. To avoid nearby polymorphic sites that could interfere with primer annealing, the Waters et al. reference sequences flanking each marker were (1) aligned against the Chinook reference genome and (2) their genomic coordinates were searched against an internal database of Chinook pool-seq SNPs. Finally, the GTseqsix6 and vgll3 markers were integrated with the Chinook marker panel.

Results

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). In the current year of this project, we have continued our use of GT-seq protocols and SNP discovery. Our laboratory has designed and currently uses seven SNP panels for the following species: Chinook salmon (*Oncorhynchus tshawytscha* – 365 loci including a sex determination marker and 14 amplicons used for species identification), Steelhead trout (*O. mykiss* – 376 loci including a sex determination marker; Sockeye salmon (*O. nerka* – 363 loci including a sex determination marker); 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 were used to genotype 154,739 samples in 2021 (Figure 11). The largest portion of samples were Chinook salmon (84,766), then Pacific lamprey (28,154), Sockeye (17,062), Steelhead (15,134), Coho (8,485), and White sturgeon (1,138).

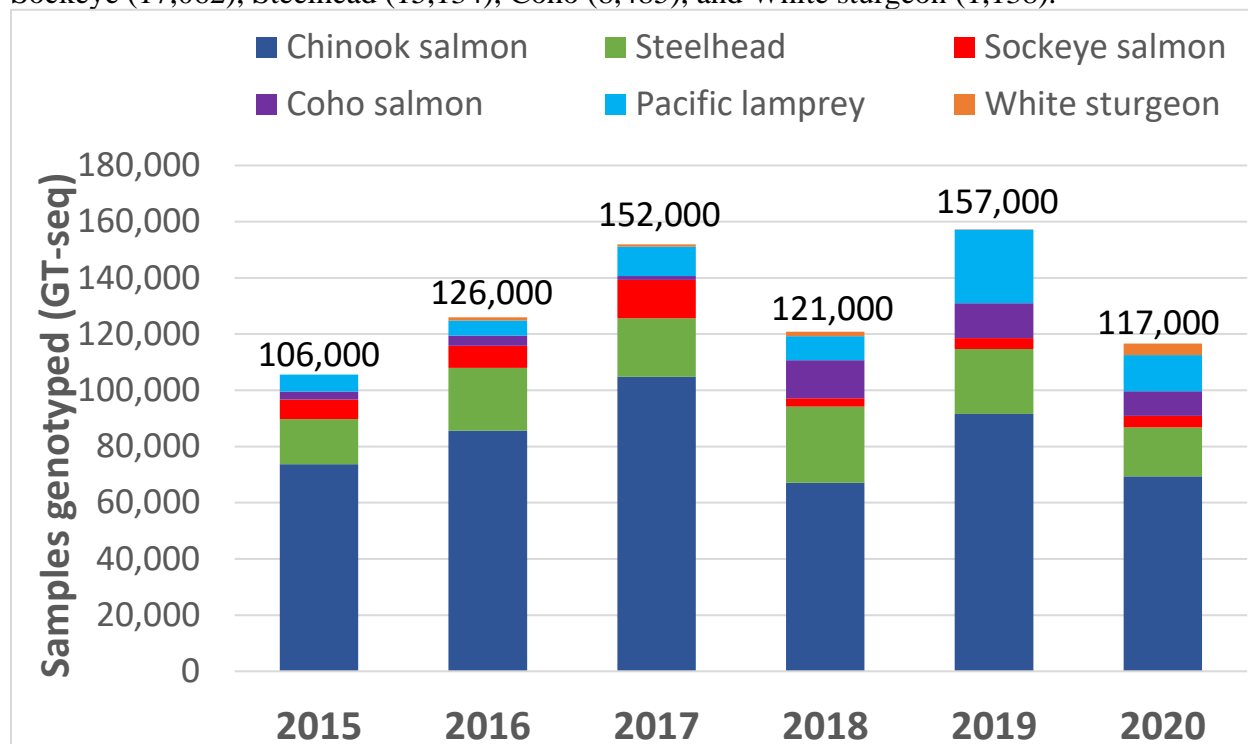


Figure 11. Summary of Columbia River fish samples genotyped using GT-seq in calendar year 2020.

The Chinook panel underwent three changes in 2020. Three markers were dropped due to sequencing issues (Ots17_1345774_C6, Ots17_1488679_C6, Ots17_1066109_C6). We added three markers modified from Waters et al. (2021 Ots_Six6-3_AT, Ots_Six6-3_AG, Ots_VGLL3-1) to be tested for use in analyzing age at maturity status. Fourteen loci from other panels were also incorporated along with 5 loci already included to be used as species diagnostic markers. Loci used in the standard panel are shown in Appendix 2.

The active Steelhead panel underwent no changes in 2021. Markers for age at maturity were designed and ordered and will be tested in 2022. This panel includes three loci diagnostic for cutthroat trout. Loci information can be seen in Appendix 1.

The Sockeye panel had a single marker added (One_SEXsdY-F19R20) from Royle et al. 2018. Preliminary testing showed 97.8% (180/184 fish) concordance with phenotypic gender. Age at maturity markers were designed and ordered and will be tested in 2022. Loci information can be seen in Appendix 3.

The Coho panel underwent no changes in 2021. Markers for age at maturity were designed and ordered and will be tested in 2022. The coho panel includes 2 loci that are diagnostic for sex. Loci information can be seen in Appendix 4.

The Pacific lamprey panels underwent no changes in 2021. Preliminary work was completed to design sex diagnostic markers based on whole genome sequencing data. Both panels include four loci used to identify lamprey species. Loci information can be seen in Appendix 5 and Appendix 6.

The White sturgeon panel underwent no changes in 2021. Sex identifying loci were tested (See sturgeon section) and additional testing including additional loci will be completed in 2022. Loci information can be seen in Appendix 7.

SNP analysis identified 19 amplicons and 54 SNPs sites that showed diversity or expected diversity between species. Two of the positions have three alleles. Initial analysis suggests that the combination of markers will be able to differentiate between the primary species of interest. Testing in 2022 will be designed to include samples that represent a larger portion of each species within the Columbia River Basin. The 19 amplicons will also be added to the other salmonid panels. SNP information can be seen in Appendix 8.

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 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. NextSeq500,1000,2000) 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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1210 *Appendix 1. GT-seq SNP panel for steelhead trout.*

Assay	A 1	A 2	Forward	Reverse	A1-Probe	A2-Probe	Allele Corr ectio ns	GCF_0 021634 95.1 chromo some	GCF_0 021634 95.1 SNP Coordi nate
OmyY1 _2SEX Y	X	Y	GCGCATTTGTATGGTGAAAA	GCCTGGCATATGAGTGT TGA	NA	ATGTGTTTCAT ATGCCAG	NA		
Omy_R AD7252 8-44	A	T	TGATGATCCGGACCCTCTCT	CCCGGATTCCCTCCACA GTT	TTGGAACAAA CTGT	TTGGAACATA CTGT	0,0	omy01	735451 3
OMS00 078	T	C	GAGGGAAGCAGCCATAAAC AGAATA	GTCTCACTATGGTCCAT ATCTGTGTAGA	TTCACATGCA TAAGAGTG	TCACATGCAT GAGAGTG	0,0	omy01	104993 33
Omy_R AD6580 8-68	T	G	TCCTTCACTCTCGATCGGGA	TCAAACCTGGGCCACTAC TGT	ATCGGGATTTC ACTT	ATCGGGAGTC ACTT	0,0	omy01	121876 98
Omy_ga dd45- 332	T	C	AGAGAAGACTCACTGCTGTT TGC	AAATCAGTTCCCACGCT ATGCT	TTGCTCCAAA ATGG	TTGCTCCGAA ATGG	0,0	omy01	122400 53
Omy_10 7031- 704	C	T	GGCTTTTCGGATACTGAGCAA CAA	TGAACTCACTGTTGGTA TGGACTAGA	TGGACATGAT TGCATAGAC	CTGGACATGA TTACATAGAC	0,0	omy01	181317 99
Omy_R AD7396 3-73	T	A	CCCTCTCAGGAAAGTGACC AC	GGATCATGTCAATCTGA TGAGTTGG	TTTCTTTTGGA	TTTCTATTGG A	0,0	omy01	237295 39
Omy_m etA-161	T	G	CGCATGCACCAGTTGTAAG AAAG	AGTGCCACCAGCGATA AGAAAA	CAAGTAAGTG GTTATATTCT	CAAGTAAGT GGTTCTATTCT	0,0	omy01	242573 40
Omy_R AD5063 2-21	C	T	CCTGCAGGCTGGGTCATTAT	GAGCCAGCTGTACCTTC TCC	TCAGCACCTC CAGCC	TCAGTACCTC CAGCC	0,0	omy01	389865 33
Omy_R AD5791 6-29	A	C	GCAGGGCCTTAGAAACAGA CT	TACACGCCTCACTGTTC TGC	CAGGGGCAAA ACGG	CAGGGGCCA AACGG	0,0	omy01	444299 31
OMS00 070	T	C	CGTTCCTGCGGGACAGT	GTTTCTCTCACGTCCAC AGATCT	CAAAATACGG AAATGCAG	AAATACGGG AATGCAG	0,0	omy01	552792 96

OMS00 003	T	G	GTGCCACTGATGAGGATGA GATCA	GTAATAAAGCCCTTTTG TGAGGAAAACTAAT	CTTTACTGTGCG ACATTTTA	TACTGTGCGCC ATTTTA	0,0	omy01	594643 48
Omy_gd h-271	C	T	AGGTCAGTCTACTTACAGTA TAAAGCAGT	GTCATGTCAACAGAGT AACATAATAAATCTGC	TCACCCTGAA GTGTAGAC	TCACCCTGAA ATGTAGAC	0,0	omy01	637384 13
Omy_cy p17-153	C	T	GCCCTCCAAGTTCCAAGTGA AAA	CAGGTCATTGATGAAA CGTCAGAAC	ATACCTGAGT GTCATCG	ATACCTGAGT ATCATCG	0,0	omy01	645098 89
OMGH 1PROM 1-SNP1	A	T	TCAAACCTGCATTTGATGGAA ACAAACAT	AGGACAATTCTAAGTG ACCTCAAACCTG	TAGTGTTTAC TGACTTCA	TAGTGTTTAC TGACTTCA	0,0	omy01	704664 74
Omy_G H1P1_2	C	T	TGCATTTGATGGAAACAAA CATAT-TTATAATGTGT	CAAAAACAAGGACAAT TCTAAGTGACCTC	AAACTGTTGA ACGGTAGTG	AAACTGTTGA ACAGTAGTG	0,0	omy01	704664 83
OMS00 008	A	T	CCCTTTAAGGAGGATTTTAA ATATGTGAGATAGAA	GGATACAGCGTTTTGGA ATGAAACT	CTTCAAATAT CCATAATTAT ATC	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	-	CAGACCTCCTCTATCTCCCT ATGAG	ACCTCCTTTAAATTGTG CCCAAGAA	CCAGTTTG	TCAGTTTG	0,0	omy01	79XXX XXX
Omy_G 3PD_2- 371	C	A	GCAGGTAAGGTACACCATA GAGACA	CTCCCCCTGCCTTACCA AAC	AGACATGTGG ATTGGCA	CAGACATGTG TATTGGCA	0,0	omy02	608394 6
Omy_G 3PD_2.2 46	C	T	TCATGTATCAATTAAGGCAT TGTCTTGTCT	GTTAGACACAGTGACC ACCTCTTT	AGTAAAGCCC ATTGTTGAGT	AGTAAAGCC CATTATTGAG T	0,0	omy02	608407 1
Omy_98 683-165	A	C	GCCATTGCCAGAGAATTTGG TTAA	AACACACGCACCATCTT AAAGC	AGCCAGATAC ATATTTGT	CCAGATACA GATTTGT	0,0	omy02	855514 0
OMS00 156	A	T	GAGCAGAACACATAGAGGA AAGACT	GTAATCACCCCTCTTAGC CTGTATGG	TGTGTGTCCT GCTGTAACA	TGTGTGTCCTGC AGTAACA	0,0	omy02	123971 97
Omy_11 4587- 480	T	G	CAGATTACGTTATTACGTTT GGGAAATTTTAAAGT	GTGAAAGAGTGGGAAA TATAATTATAAGGTCAG A	CCTGTCCAAA ATTGT	CCTGTCCACA ATTGT	0,0	omy02	162045 63
OMS00 138	T	G	TCGGACCACATGAGCAGTTC	GTTCAACAGGTGCCCAC AC	CTAACAATAA CCAAAGACTG	CTAACAATAA CCACAGACTG	0,0	omy02	223184 48
Omy_N aKATPa 3-50	A	C	GTTGAGCGTGTTATGGGAA AAGAG	TTGCATCGGCTTTCTGA AAACC	CACTCTGTTTC CTTCTTT	TCTGTTTCCG TTCTTT	0,0	omy02	238931 57

Omy_R AD2504 2-68	G	T	GCTGCTGAAACTGGTTTGCA	TCATGCAGATGAGCTTC CCTG	AATTTCTGCC CAAA	AATTTCTTCC CAAA	0,0	omy02	327931 23
Omy_cd 59b-112	C	T	TTTGGATAAGATTGTCTTAT ATGACTAAAATGTCATGT	GCCAACGTCCTAGATAT GGTGTAAT	CTAAAAGCCT ATAGCAAACCT	CTAAAAGCCT ATAACAAACCT	0,0.6	omy02	389226 11
Omy_R AD2774 0-55	A	T	TCGGCCTGTACTAGTCTCAC T	GCCTAAAATGGCCACTT TCATCA	TAACTTTAAA AAAA	TAACTTTTAA AAAA	0,0	omy02	427459 63
Omy_u0 9- 53.469	T	C	ACAGCCTGAGCGTTTGCA	GGAAACTGGGAGAGAT CAAAGGA	TTGCAGCCCT TATTGTG	TTGCAGCCCT TGTTGTG	0,0	omy02	488598 83
Omy_R AD2091 7-11	T	C	CGTTGTCGTCTCCAATCAGG A	ACCAGCTCGATGCCATT GC	AGGTTGCGAG GTC	AGGTCGCGA GGTC	0,0	omy02	523844 97
Omy_m etB-138	T	A	TCTGTCCCTGACGCTATAAA AACG	GAAGTATTTTCTCAGCTTAA TTTCACTGTTGAGTT	TTCGCCAAAG AGAAAT	TTCGCCAAAG TGAAAT	0,0	omy02	537920 50
Omy_R AD9004 -13	G	A	TATACCACGCCTTCCCTGGA	CAGAGAGAAATCCCCC ACCC	TCATCTGAAG GGGG	TCATCTAAAG GGGG	0,0	omy02	540448 36
Omy_lp 1-220	C	G	TGACAATCACTGAGCAACT GAACTC	GTCCAGTCTTGCTTCAA CTCATTCT	AGTGACAGTC A	AGTCACAGTC A	0,0	omy02	600228 13
Omy_R AD1610 4-20	A	G	ATTCCAAAACCTGCAGGGG T	TCAGGATTTGGTAAGGT GGCC	AGGGCAAAG[AT]CAAAGG	AGGGCAAGG[AT]CAAAGG	0,0	omy02	671193 13
Omy_R AD3781 6-68	A	T	CTCATTCCCTGGCCGTCTG	CCACTCACACTGGCTTA TGC	GCGGCGTAAA AATG	GCGGCGTTAA AATG	0,0	omy02	735000 31
Omy_R AD4631 4-35	A	G	ACTGCATCTTTTCCCCTGCA	TGAAGATACCCAGAGA CACCA	TAGCAATGGT	TAGCGATGGT	0,0	omy02	784801 58
Omy_R AD7320 4-63	G	C	CCTGGGCAATGACCTCCAC	AGCTCCCTTCTCTCTCC CTC	GTGCCCCGCTC TCCACCG	GTGCCCCCTC TCCACCG	0,0	omy03	246702 64
OMS00 096	T	G	CATGAGAATGGATCAGTCTC CACAA	GATGAAAATCTGAATGT GTTGACACTACAG	AAAGAGGAAG AGTCTCG	AAAGAGGAA GCGTCTCG	0,0	omy03	291093 94
Omy_11 2301- 202	T	G	GTAAACCCTGCCCACATAAT TAGGT	CTGAGACACTGCTCCAA GGT	AATGCGAAGA CAAACCT	AATGCGAAG CCAAACCT	0,0	omy03	375905 54

Omy_R AD3379 8-24	T	C	CAGGAGGGTCAAGTGGAGT C	TTGGGGCCCTCTCTTTTT GGG	GAGTCTATCA AGAT	GAGTCTACCA AGAT	1,4,0	omy03	383366 51
Omy_R AD1349 9-13	T	C	GTTCACCTGACGACCAAGGT	GCTGGGGGAGCTTTAC ATGA	CGCCCTGTCC GCCA	CGCCCTGCCC GCCA	0,0	omy03	384089 41
Omy_u0 9-54- 311	C	T	GTGGCTCCCCAGGAACAAG	AAGTTTCATGTCACATT CCAGTTACCT	TGGTAATTAT TCAACAGATC AGT	TGGTAATTAT TCAACAAATC AGT	0,0	omy03	429205 02
Omy_R AD5883 5-15	G	T	GTCTGCTAAGGTCCTGCAGG	GCCGACCATGAGAGAC CTG	ATAGCTGCTG GGACCCA	ATAGCTTCTG GGACCCA	0,0,2	omy03	537353 38
Omy_u0 7-79- 166	G	T	CCCGCTATATTATTTGATCA CCCTTGA	ATTTAAATCCATTTCTA AAAATAAGCAAACCTA ACCA	ACTTGGAAT ACCCAGCC	CTTGGAATA ACCCAGCC	0,0	omy03	575236 76
Omy_11 7815-81	C	T	CTGCTTTATGCACACCACAT TGT	GCTCTTTCTGGAGAACA AGGTACTG	CTATACGGAG ACCAGC	CTATACGGAA ACCAGC	0,0	omy03	678942 57
Omy_11 8654-91	A	G	CAGCGTAGACCGTTTCCTCA TTAT	GCGCCGATGAGCAGCT T	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	AAAGCAGACCACACCA TACTTCTC	CTTTCTCTCCT ACTTTCC	CTTTCTCTCC TCCTTTCC	0,0	omy04	763533 4
Omy_m yoD- 178	A	C	GGTCAAATATTTTCATTTACG ATTACACTTAGGC	TGGCAAAGCTGTCATTC CTTCTAAT	TTTTATGAGA TATAATTTCC	TTTTATGAGA TATCATTTCC	0,0	omy04	105207 93
Omy_12 8923- 433	T	C	CTATGTCCTTGGCAGAAAGTC TACA	ACGTTTCTTTGGGCTGA GACTTATT	CTTCATTTTCA TTCAGTGT	CATTTTCATT CGCTGTTTT	0,0	omy04	164362 34
Omy_13 0524- 160	C	G	CGAAGGTAGCGATTGGTCG TT	TGTCTGTTCTGCTGTGT GCTT	ATGGCTTGAT CCTCA	ATGGCTTCAT CCTCA	0,0	omy04	288890 24
Omy_R AD7778 9-54	T	C	AGACAAAACCTGCAGGGGA C	AGCACGTAAAAACCAA ACTGTCA	TAAATTATAT TTGACAG	TAAATTACAT TTGACAG	0,0	omy04	309761 38
OMS00 079	T	C	GTAACATTATGAATCTATCA GTTTCCCTAGCT	ACCTGCAACGTTAGAG CTGTTTATT	CTACTTTTCAC AGTAACACAG	CTACTTTTCA CAGTGACAC AG	0,0	omy04	352504 73

Omy_11 7286- 374	A	T	TGATGTGTTGTTTCCTCATGG CTTA	CTGTGCATTTATTCTTG TGATGCTAGG	CTTTCCTCATC ATACTCTATG G	TCCTCATCAT ACACTATGG	0,0	omy04	523101 65
OMS00 087	A	G	GCAAATTTACCCCTTAACGT GGTTT	GATTTGATGTGTGTGTA TTACCTCCTCTA	GTTA[CA]AAC TGACAAAGTG TG	GTTA[CA]AGC TGACAAAGT GT	0,0	omy04	525119 64
OMS00 111	T	C	CATGCGGACCTGCATAGCT	GCTTAGCCATTGACAGA GCATATCA	CAACCAGACT ACCATTTC	AACCAGACT GCCATTTC	0,0	omy04	630315 81
Omy_R AD9248 5-64	T	A	CCAGTCAGTCTTGCCTCAGG	GGTCACCACAGGATTG GAGG	GTGTAGATAT ACAT	GTGTAGAAAT ACAT	0,0	omy04	683184 64
OMS00 116	T	A	GCCTTTCTCCCATATCACAT TCGA	AAACGCATCTTACACTG TGTTGTG	CTTTTACATTT TCAATATTCT G	TTTACATTTT CAATTTTCTG	0,0	omy05	113417 54
Omy_R AD1307 3-16	G	A	GTGAGGGATCACACCTGCA G	GCACCCATTCGTAATGT 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	AATGCTATAT TGAACCTTAA	AATGCTAAAT TGAACCTTAA	0,0	omy05	316752 78
OmyR1 9198	T	A	GTAACCATGACATCCACCA ATC	CCTATGCACAAAGCCTT CAC	ATCCCTGTTAT CTAATCATT	ATCCCTGTAA TCTAATCATT	0,0	omy05	349734 85
Omy_R AD2389 4-58	A	T	TGCAGAAAGGCTGTGTGGA T	TCTTAACACAGTCCTCA TGGAACA	GTGGATTAGG GG	GTGGATTTGG GG	0,0	omy05	409271 21
OmyR3 3562	G	A	CAGGAGTAATGCATCCCAA TG	CAAGTTGATAACGAGA CATAAGGG	TAAGACTTGG CATAAGCATG	TAAGACTTAG CATAAGCATG	0,0	omy05	473375 40
Omy_bc AKala- 380rd	G	A	TTGCTCTCTTCTGGTTGCCTT A	CTTCAGGAGAAAGCGC TACTGT	CATACCCATC CTATGTCAG	CATACTCATC CTATGTCAG	0,0	omy05	534692 95
OmyR1 4589	A	G	GGTGA CTGAGCTGGATGT	TTTAGAGAATTTGGCAG TACGTC	GTGGTTACAA AGGGTCTGCA	GTGGTTACAA GGGGTCTGCA	0,0	omy05	561627 85

Omy_u0 9- 61.043	A	T	TAGTCACATCCATAGTAATA CTTCC	TGTTTCAGAAAGCAGAAA ACCAATCTCT	CACTTGGTCC TTTTTCA	CTTGGTCCAT TTTCA	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	CTGTCTGTCC ATATATC	CTGTCTGTCC GTATATC	0,0	omy05	618289 03
OmyR4 0319	C	T	AAAGATTGCTGCGATGTCTA AT	CGCAGAGAACAGAGGA TGA	TGCAAGTGC[T A]GCCCTTTTA T	TGCAAGTGC[TA]GCCCTTTT AT	0,0	omy05	631589 19
OMS00 169	A	G	AGCACTTGACTCAAACCTCAC ATAAATCA	CTGAGACAGGAAGAAC AATGTTAACAAAA	CAAAAAGCAT TGATATCAAT	AAAAGCATT GACATCAAT	0,0	omy05	675681 74
Omy_R AD8513 1-35	T	C	TTCAATAACTACAGGCAGAT GGT	AGTTCCCAAATGCACTG TACA	GATGGTATGG TGAG	GATGGTACG GTGAG	0,0	omy05	755346 97
Omy_10 9525- 403	A	G	CCTCATTCTCATTGGTGAGT TGTCT	TGTAAGATCTGACCACA TGAGTATAACCA	CCTACACCTC TTTTTCCACA	CCTACACCTC TTTTCTCCAC A	0,0	omy05	842248 92
Omy_R AD4357 3-37	A	G	TGCAGGGAACGATGAAACC A	ACAGACACAGCATTGG CCAA	GAAAGAGAGA GTTT	GAAAGAGGG AGTTT	0,0	omy06	174595 4
Omy_10 5714- 265	C	T	CCACTCAGTGCAAGCATGG A	GCTTTCAATCCTTGGCT CCAATATC	CTGTTGTTTGA GGTTCAG	TGTTGTTTGA GATTCAG	0,0	omy06	759484 7
Omy_10 7285-69	C	G	GCCCTTGTGACAATGCACTG TTATA	AGGTCTAGACAGTGTG CCATTTG	ATACGTTACT TTTGACCTTGT	ACGTTACTTT TCACCTTGT	0,0	omy06	980915 6
OMS00 013	A	G	GCCTTTGTTCTCCTTGGTGG TTA	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	-	GCACAGAACACAGCCAATA TTAACA	GCCTTGACTCTCCCTTC ATGAC	CCTACAACTT GATCTAACGT G	CCTACAACTT GATCTACGTG	0,0	omy06	175997 31
Omy_R AD4795 5-51	G	T	AGTGTGCTAGAATGGGCCT G	ACCATGGGCAGTTCATT TCA	TTGGAATAGA ATCTATA	TTGGAATATA ATCTATA	0,0	omy06	231917 48

Omy_va mp5- 303	A	-	CTGCTTCCCAATTCAGTATC GTCTT	AGGCTGAAGCATTCTG 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	TAACGCCAGCTGCATG ATGA	CCTCTAAACT GAAT	CCTCTAACCT GAAT	0,0	omy06	402608 00
Omy_R AD3695 2-53	C	A	TGTACGTCATTGGGGCTGAG	CCTACCAGACCACACG ATGA	AGGACATCTT CATC	AGGACATATT CATC	0,0	omy06	402609 70
Omy_IL 1b-163	T	G	GGAACAACAGGATTAAGCC TACTCT	CCTAAAGGCCTAGGAA ACTAAACTTCA	CTGAGGTCAT AAAAATA	CTGAGGTCAT ACAAATA	0,0	omy06	423131 29
Omy_R AD7016 -31	C	A	GCAGGAATATTCAGTGTGC CA	TCTAAAATGTCGTTGGC GGC	ATAATTTTCAAT TAA	ATAATTTAAT TTAA	0,0	omy06	514907 60
Omy_R AD6013 5-12	C	G	AGCATACACACCTGCAGGA A	TGGTAGGAGGAGATGC TCTGT	GAACATACCG GAAC	GAACATAGC GGAAC	0,0	omy06	561100 72
Omy_R AD3514 9-9	G	A	GAGTCAATAGAGCCCCCTG C	TGGTTAGCAGGAGCAA TCTCA	GCGCGCTTAT GTC	GCGCACTTAT GTC	0,0	omy06	601825 01
Omy_R AD3915 6-33	T	C	GGGTGTGACATGTGTGCAG A	ACTGCTTGTCCCCACCA AG	ACCGTAATGG AGAG	ACCGTAACG GAGAG	0,0	omy06	468XX XXX
Omy_R AD366- 7	C	A	ACCAAATTAGAGCCTGCAG GA	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	CCCGACTCTACTTCACTACT TTCCT	GGCCTAGGACAATAGG ACTGAAC	TACGCAAATT AGGTTTAAA	CGCAAATTAG GGTTAAA	0,0	omy07	109760 28
OMS00 176	T	G	GTTGGAAGTTCCGGTGGTAG AG	CTGGGTCCTGAAGGAG CTT	TTCCAGCACT GCTGTC	CCAGCCCTGC TGTC	0,0	omy07	110291 67
Omy_13 1460- 646	C	T	GTGAAAAGGAATGGAGGAG TACAGT	TGCTAGGACAGGAAGA TCATTTGTG	AATAAAGCAG AATTTGTTACT G	AAAGCAGAA TTTATTACTG	0,0	omy07	366000 38

Omy_R AD3061 9-61	T	A	CTGCAGGTCAATGGGTGCTA	ACACTGATCACATTTTT GTCACACT	CACTGTATAAA	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_pa d-196	C	T	CAAACAACCACAGTAGTCC TCCAAT	GCTTTTCACCTTTTGT AAATTAAGCCAAA	AAGACAAAGG TGTAATACC	AAGACAAAG GTATAATACC	0,0	omy07	444706 19
Omy_R AD1243 9-64	G	A	GGAACTTTTACATCATGTT GACTG	GCACAGAGAACTCCAG GCAA	CTTCTCCGAT GTCA	CTTCTCCAAT GTCA	0,0	omy07	445378 93
OMS00 064	T	G	GTGGATATGTAGTTCGATGG AACAGT	TTTACAACAATCTTCTT TTAATAAAAAATATAGCC ACTTAT	CAGGCAACAT TTTATATAACT A	CAGGCAACA TTTTATCTAA CTA	0,0	omy07	452277 50
Omy_R AD6259 6-38	A	T	GCAGGACACTGGTTCCCAA A	CCTGAGATTTGAGATCA CTGGCT	TTAAAAAATA TATATTA	TTAAAAATATA TATATTA	0,5,0	omy07	499777 94
OMS00 154	A	T	GATGTTGGCTGGAGGTGTA GT	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	CTGCACAACCTGTTTCCTGC TATT	ACCAAGTGTCCCTGTAA GCC	CCGCTCCGTC TGCT	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	GTGTAAACAAAATGACTCT GGGATTGAG	AGAAGTGGCAATGGTG TGAAGTAT	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	CAATTTGCAAGCAGGGAAA GGTTAT	GTGATGGGCTGCAATTG CTT	AAGGAGAATG CATAATC	TGAAAGGAG AATACATAAT C	0,0	omy07	683035 84
Omy_cd 28-130	T	C	CACAACTCCACAGAGACAG TGA	GAGGACAAAAGTACC GTATGGT	CCTGTTCATTG ACCC	CTGTTCGTTC 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	GGAATCGATGACGACGAAG TGATC	TTCCTCCATGCGTGATG CA	CCTCCGCGCC TGC	CCTCCGCACC TGC	0.5,0	omy08	106673 61
OMS00 153	T	G	ACTTTGCACCATAGGCTTGA CAT	TGATAAGGATGATCAA AAAGCTGAAGTATGTA	ACAAAATGTA ATTTTCC	CAAAATGTCA TTTTCC	0,0	omy08	163033 16
Omy_hs f2-146	A	-	CCAACAATTGCAGCCTCATC TTAAT	GGAGCAGAAAAAGGAT 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	TCATTCCAGCTCCGTTT TCTTC	TTGTGCTATTG ACGCCACAG	TTGTGCTATT GACACCACA G	0,0	omy08	214268 23
OMS00 151	A	G	CTAACGTCTTCCCAATGATA TTTCACAAGATA	ACCGTGGAATAACAAT TTTTTATGCCAAT	TCATGACCTT GATAATC	ATGACCTCGA TAATC	0,0	omy08	239492 30
OMS00 179	A	C	GTCATAACAAAATCAGGGC TTTCCAA	TGGGAGATTTGGGCTGC TTTAAA	TGCCTCTTCTC TTTTCTCAT	CCTCTTCTCT TGTCTCAT	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	GCTAGCTAACATTGAAGGG TGGAAT	GGCTACAGGGACTTTAC AATGGG	ACTATGCCAT GAAGTTA	ACTATGCCAA GAAGTTA	0,0	omy08	291028 20
Omy_R AD2823 6-38	T	C	GGCACACATCTGTCCCGTAG	GCACTAAGGTCTAGGA GCACG	ATCTGTCTTCG TGC	ATCTGTCTCTC 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	AGCAGGATA CGTCCGACT	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	CCACCAAATCCCCGA AGAA	AGGAGACACC A	AGGAGGCAC CA	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	TCCAGACTTCTGGTTTGTTT CATT	CCAGCCCCTATATTCAC AATTAAGTG	ATTAATTAAC AAGCTC	ATTAATTGAC AAGCT	0,0	omy08	825133 44
Omy_rb m4b- 203	-	T	CTGAAATTTGATGAATGGA AGCTGCA	CGTATTCAAGTCGATAT ACAGTCACGAT	CACGTTATTA TGAAAAGGAT GT	ACGTTATTAT GAAAAAGGA TGT	0,0	omy09	124851 17
Omy_11 2820-82	G	A	CCTTTCCTTTTGCATTTCTC TACTTATTTATTT	AAATGAACTCACGTTG ACCTCTGA	CGCCGCCAAG TTA	CGCCGCTAAG TTA	0,0	omy09	218612 64
Omy_R AD6595 9-69	G	A	ACATTTTGGTGTTAACAACC CTGT	GCTAGCGAAGACCCTG AAGG	TTTTGTCTGTT CTT	TTTTGTCTATT CCTT	0,0	omy09	363384 72
OMS00 103	A	T	GAGATCACTGTAGGATTGG CTGTTT	CCTCAGAGCAGCTCAC AATGGCATC	CTCCACAGTA ATTTTTTTTT	CCACAGTAAT TATTTTTT	0,0	omy09	383356 92
OMS00 056	T	C	TCAGGAAGTAAACTGAAAA TTCCAATGTATGA	CCCCAACCATGCTTGTT ATTGAAC	TAGCTTGACC AAATAGCA	CTTGACCGAA TAGCA	0,0	omy09	437713 25
OMS00 175	T	C	TTGCGATATGGGACTGTATA CATTTATTCC	ACTACCTCCAGTTAAAA TAGTGTGGGAAA	ATCACTAGTT CAAATACAA	ATCACTAGTT CAGATACAA	0,0	omy09	503817 07
Omy_tlr 5-205	T	A	GAGCGTATCTGGTATGGTAA CAACA	CTCCAGCAGCTTTAGAG AGTTTACA	CAGTAATATT TCAGTGCCCCG	CAGTAATATT TCTGTGCCCCG	0,0	omy09	605104 83
Omy_11 4315- 438	T	G	CCTCACCGATCTAGTCAACT TCATC	AGGAGGCTGAGGGAGA TTCTAG	TTATGGGCTT AAGGGTC	TTATGGGCTT ACGGGTC	0,0	omy09	645645 08
Omy_gl uR-79	C	T	GACTGTCTATAGCTATTCTT CTCAAACGT	AGAAACTACCATTGTG ATTAACAGATAGAAAA TACAT	CAAGTATTTT GCGTAGGAAT	CAAGTATTTT GCATAGGAA T	0,0	omy10	750822 1
Omy_R AD3213 9-58	G	A	GCAGGAAACAGGTACAAAG GA	TGGCTTCTTCCTTGCTG AGC	TCGACATGAC CTGA	TCGACATAAC CTGA	0,1	omy10	107738 03

Omy_10 9894- 185	T	C	GGGAGGAATTGGAATGACA GATTAAC	CGGTGTCATTATGGTTG TCATTGTG	CTCCCTGATC CCCC	CTCCCTGGTC CCCC	0,0,5	omy10	108522 82
Omy_R AD6640 2-36	T	C	GGTGTGATACCTCAGAGCTC TG	CGTCTCCGGATCGTTCA GAG	AACCACTTCT CTG	AACCACCTCT CTG	0,2	omy10	303720 84
M09AA E.082	T	G	CTATGTGCAGTGCCCTTCTC A	GGCTTACAAGTATGCAT GACTAGCT	AGGTTGTTTT ACAAATTTAA	AGGTTGTTTT ACACATTTAA	0,0	omy10	328727 04
OMS00 095	A	T	CTCCAATGGCTGTCAACAAT TAAATATAAGAC	GTGTGCTGGTCTCTTCT TTTATTCTCA	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	ACAGAGAAACCCCCGT CATT	AGGGTGAAGA ACTG	AGGGTGAGG AACTG	0,0	omy10	414117 54
Omy_ft zf1-217	A	T	ACAGGGATGGGCAACTTTG TT	GGATGACCCACGTGAC ACT	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	GATCTGATCGGTCTGGG AGAGA	ATGAGGGTCC CTATACAGG	ATGAGGGTCC CTCTACAGG	0,0	omy10	604014 05
Omy_U T16_2- 173	C	T	ATTGACTCATTATCACCTTA GTTGTAGCTTCA	GCAGCTACTTGCTGTAT CACATGTTTGT	ACAGTCAACA AGGGACTTAA	ACAGTCAATA AGGGACTTA A	0,0	omy10	614962 64
Omy_R AD3684 8-7	G	A	CGAGGACGTTTCATAGGGAG C	TCGATAAGTCCACCAGC TGG	TGCAGGGACA CCACCCT	TGCAGGAAC ACCACCCT	0,5,0	omy10	636507 47
Omy_R AD5374 -56	A	C	GCTGTTACCGTGTGATGTTG A	AGAGTTCTGGCCTCTCC CTC	AGAGGGAAAG AGAG	AGAGGGACA GAGAG	0,0	omy11	618693 7
Omy_g1 2-82	T	C	GATCAATTCGATCGCTCATG AAACTT	CTTCTCTCGTTCTCATT GTGTCTCA	CAAACCTCTCA GGATTAG	AAACTCTCGG GATTAG	0,0	omy11	147648 07

Omy_B AMBI4. 238	T	C	CATGATGAGGAGGACCAAG ATGAG	AGGTGTGGTTCAGGGC AG	CACCGCAATC ACCG	ACCGCGATCA CCG	0,0	omy11	244110 85
Omy_M YC_2	T	C	CGGTTGCAGAACTCTCATGT TTG	CACGCCATGTCTTAACT TGCATTA	CATAGACTTT TTGACCTTAT	CATAGACTTT TTGGCCTTAT	0,0	omy11	338412 60
Omy_R AD7850 2-57	T	G	GAGAGGCATCCTGTCTAGG G	ACCATGCTCTTTCTGTGA GGTGT	GGAAATATCA CACA	GGAAATAGC ACACA	0,0	omy11	370317 57
Omy_B AC- F5.284	C	T	CCTCATTTACTGTAGGACCA TGCA	ACAACGCCAACAACTTT CTCTTG	CAGTAGGGCG GCAAG	ACAGTAGGA CGGCAAG	0,0	omy11	427893 02
Omy_co x1-221	T	A	CACTGAACTGTAAGCCATTG TGATT	GCAACATGGGAATGAT TCATAAATGCA	CGGTAAGACC ATTAAAA	CGGTAAGAC CATTTAAA	0,0	omy11	470523 10
OMS00 120	A	G	GGCAGAAGAGGAGAGAGAT ATGATTG	CCTCAAATACCTCTGAC ATTGAAGGTT	C[GA]CCCACCT AAAAC	C[GA]CCCACC AAAAC	0,0	omy11	510131 77
Omy_R AD4279 3-59	T	C	CACGGCTAGTGGCATGTACC	CCACACCTGCATCAGTC TGT	CAGAGAATGC CAACAGA	CAGAGAACG CCAACAGA	0,0	omy11	514085 22
Omy_10 2867- 443	T	G	CATTTGTTTAATTTGATTTG GCACAACTTCA	CCCTAGTTCTGTAACAC AAGACGTAA	TTTGGGTACA TAATTTTT	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	GGCAGGTTAACACAGTCAT CTACTATAAA	CAGCATGTTGCTTTAAT CCTTCACA	TGTCACCTTCA AAGTTTG	TGTCACCTTCA ACGTTTG	0,0	omy12	507937 1
Omy_11 0201- 359	T	G	GGTAAGGCCTGTCTGACTAT TTTGA	AGAGGTCAATGGATGC CAGTTT	TTTGGCTATTG AAATTATACA TT	TTGGCTATTG AAATTCTACA TT	0,0	omy12	287279 52
OMS00 074	T	G	CCTGTTTATTCATCTAAACC AGTTCTTTAAAAT	AACTTAATTTAGCAAAC AAATGTCTGAACAGAA	TGAAACAAAA CAAATGTTCC	AAACAAAAC ACATGTTCC	0,0	omy12	311047 27
Omy_hs c715-80	C	A	CCGGTCTACCCTATAGCTGT TG	AGTCAGTCAATTAGTGG TTTGAAATACTATCA	AACTGTATTT GGGAAAAT	ATAAACTGTA TTTGTGAAAA T	0,0	omy12	401363 09
Omy_R AD2669 1-36	A	G	TGCAGGAAACCGTCAATCT ACA	CAGGAATTAATTGTATG GCCGGA	TCTCCTAACA GAAC	TCTCCTAGCA GAAC	0,0	omy12	472849 87

Omy_R AD3840 6-19	T	A	CTGCAGGGGTATTAGGAGG C	AATGAGTTGTGGCGGT GAGT	AGGCTTTATA TGGCC	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	CAGGTCACAGACACACAGG G	CTACACCACCCACGTT CTG	CAGGGAGGAG G	CAGGGGGGA GG	0,0	omy12	533837 57
Omy_nd k-152	A	G	AAGAATTGAGGGATAAAAA CAAAATAATATATAAACAT GA	CAAACCTACATTCATTA AAGTCCAGTTTTGT	ACCCACTTTC AAAAC	ACCCACTCTC AAAAC	0,0	omy12	562779 59
Omy_R AD7657 0-62	T	G	GCAGGTAGGTAGGAAGGAA AGC	TCTGACTGGTATTGAAA GGACCA	AGAGGTGTTC TGGT	AGAGGTGGT CTGGT	0,0	omy12	562977 52
Omy_gh -475	C	T	AAGTTACCAGAATTTTGCAA ACTCAACT	CCATATTTTGAGGTGTA GCTTTACCT	CTGAAACTCA TGGTATACA	CTGAAACTCA TGATATACA	0,0	omy12	623081 22
Omy_R AD3312 2-47	G	C	CAGGCTTTGTGGACATGTGC	GTGCTCTATCTTGCTCT TGCC	CCACAGGGTG GTGC	CCACAGGCTG GTGC	0,0.6	omy12	660787 52
Omy_hs p70aPro -329	A	G	TGCGTATTATTGTTTTTCAA GGACTTTCAA	TGAATATTTTCAAATAC ATGCCAATTCTTTCAA	ACATTCCAAT ATTCAACTAT	CATTCCAATA TCCAATAT	0,0	omy12	668288 36
OMS00 053	T	C	GGAGCCAGGTCAAGGTGAT C	GGATGTCTGGTGTGGCT GTAAA	ATTTATATGT ATCAATCA	ATTTATACGT ATCAATCA	0,0	omy12	669178 68
OMS00 112	A	T	TGGCAGCAAAAGGGATGCA	TCCTGAGCAACCAGTCA ACATT	CCGGTTTCAA GTTTACTTGT	CGGTTTCAAG TATACTTGT	0,0	omy12	683820 81
Omy_11 1666- 301	T	A	GGGTGAAAAGAGTGGGACA TTTACA	GTCAATTTCAAGGCACC AGACAAT	AGTATAACAC AGTAAGACAA T	AGTATAACAC AGTTAGACA AT	0,0	omy12	709908 44
OMS00 149	T	G	GGCATCATTGTTCTTGCTCT GTTTA	CCTGGGAGGGTTTATAT CGGAGTAT	GCTAAATGCA CAG	GCTAAAGGC ACAG	0,0	omy12	6589X XXX
Omy_R AD6683 4-17	C	T	CTCCTGCAGGTCATCTCTGG	CTGTCTTGCTCAATG CCTG	TCTGGCTGAC ACCTTTA	TCTGGTTGAC ACCTTTA	0,0	omy13	101126 20
Omy_11 8175- 396	T	A	AGGCTTCACACACACATGC A	GACGCGCAACCTCTAG ATTATACTT	CTCTTGCAGA CATACCCGTA	CTCTTGCAGA CATTCCCGTA	0,0	omy13	202824 78

Omy_12 9870- 756	C	T	TCGTTATTTTGCCTCGCGGT A	TCCCATGAAGATGTATA CATGTTTTGTGA	ACAGGTATTT CGTGAAATG	CAGGTATTTT ATGAAATG	0,0	omy13	229151 61
Omy_11 3490- 159	C	T	CATAGTACATTTACAGATAA TGTTTTAAAGTGCATGT	CGAGATACCAAATGC CACAGTTACAT	CATCTGTTTTG GTTTAGC	CATCTGTTTT AGTTTAGC	0,0	omy13	264948 31
Omy_na ch-200	A	T	CTCATGAAAAACGGGAGAG CAAAG	CAGCGGCTCTTCAGTAG TCT	AACTGACAGA GTCACAAC	CTGACAGAG ACACAAC	0,0	omy13	300017 96
OMS00 180	T	G	GCGCCGAATGGCATTAGG	CACATTGCTGTCGTTTA GTTTGACT	CTAAAAGTGC ATTAAGCC	CTAAAAGTGC CTTAAGCC	0,0	omy13	324627 75
Omy_11 0064- 419	T	G	GTGCAAGGGACCTAGCTAA TCC	TCTGAACTGACACTGAA GAACAAAGAA	ACGTTAGCTT TTAATTTT	AACGTTAGCT TTTCATTT	0,0	omy13	362728 50
Omy_g1 -103	T	C	AGTCGTGACAATGAGAAAC AGTGTT	CTCAGCAAAAAAGAAA CGTCCCTTT	CCTTTTACAAT GAAGATC	CTTTTACAGT GAAGATC	0,0	omy13	392872 32
Omy_IL 6-320	C	T	CGACTGATCTCCTGCAGACA TG	CTTGTTCCCTCGTTGTCTT CCTTCTA	CTATAGGAGA GAGGACAACA	ATAGGAGAG AAGACAACA	0,0	omy14	710240 7
OMS00 089	A	G	GCACCATTTGAATAAAAAA TCTGCTTTGT	GCAACCCAATTCAATAT TAAGCACATGAT	ATGAATCCCA AATAAGAAC	AATCCCAAAC AAGAAC	0,0	omy14	131505 34
Omy_hs flb-241	A	-	AGCCCGAACTATCCTAAAG CATTTT	AAATCAATAGCTCAGA GAATAATGAACACCA	CAGTGTTTTGT TTTTTGTCATT	AGTGTTTTGT TTTTTGTCATT	0,0	omy14	145167 42
Omy_11 6733- 349	C	T	GAAATGGACATGCCTACAA ATTGCT	GATGTGATCAGTTTAGG CAAGGC	AGAGAATCTG ATAGTATTTT	AGAGAATCT GATAATATTT C	0,0	omy14	184980 42
Omy_nt l-27	G	A	GGTGTGTTACTGTAGTTGTG TCCTT	TGTGTAGCTAGTGATCC TGATTGTCT	CAGACAAGAG TACCCCAAGA C	CAGACAAGA GTACTCCAAG AC	0,0	omy14	220710 34
Omy_tx nip-343	T	C	CCTTCAAACCTAACGCATCAT AGACATG	GGTCACTTGGCTAATCC CCTTAT	AACTGAAGAG ATCTG	AACTGAAGG GATCTG	0,0	omy14	244358 25
Omy_U BA3b	A	T	GCCACTCAATGCATGTGTTT TCTAG	CAGCTAGCTTAAGTGG GATGCAA	TGGAGATAAC GCTAACTATT	AGATAACGC AACTATT	0,0	omy14	285526 49
Omy_R AD5540 4-54	C	T	GCAGGGTGTCCACTACAGA C	AGGAGTCCTGAGAGTT GGGC	ATTGTTTCTGA AGG	ATTGTTTTTG AAGG	0,0	omy14	438768 69
Omy_R AD1256 6-14	C	T	GTGGACATTCTGCAGGGAT	TCCCACAAATATTTTCAT ACGCACA	ATGTAAACAA ATTG	ATGTAAATAA ATTG	0,0	omy14	441253 36

Omy_R AD3926 -22	T	C	CGTTCCTGCAGGCTTTTCAC	TTGGCACAGAGAGTAC GCAG	TTCAC TTTTCC CTG	TTCAC TTTCTC CCTG	0,0	omy14	453455 47
Omy_m csf-268	T	C	CCAGCATTCGTTCCCATTTTC C	CTTTTAATGTAGATTAT ATTCTTCTGTAGCCACT ATGG	AAATAATAGA TAAA[CT]CCT	AAATAACAG ATAAA[CT]CC T	0,0	omy14	487584 70
Omy_10 1554- 306	T	C	GCCTGTATTTCTCCTGTATG TGCAT	TCAACTTTTGCAAAC TT TTTTATTCTTTGTCATTT	TGCTTCTCAC ATTTT TA	TGCTTCTCAC GTTTT TA	0,0	omy14	536601 17
Omy_R AD4744 4-53	C	T	GTCGTCTGGAGGAGCTGAA G	GGGTGACGTTTTCTTC AGC	GGCGAGCTTG GCCCAA	GGCGAGTTTG GCCCAA	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	GTGGGAGAGCTCGTCTATG G	ACAACAGGTCATTGGA TGTGATCAG	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	CTTTAGAAAAGCCAAGGTA TATTTTAACATACTTCT	CTGCTGCCCTCTAATGG TAAGATAG	AAGGCAC	AAGGCAT	0,0	omy14	719697 84
Omy_11 0689- 148	A	C	GTGTGTGGCAGAGAACTAA CTGAT	GGTTAAGACATTAACAT AACACTGGACTCT	CAAATGAACA CATTATTTATC	ATGAACACAT GATTTATC	0,0	omy14	7235X XXX
Omy_R AD8802 8-7	G	A	TAGCCCAGTTCGGTCCAAC	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	CCACAAC TCTCAAATG AATGGAATGT	CCCATCCCTC CTCCTGG	CCCATCCCTT CTCCTGG	0,0.5	omy15	130422 22
Omy_11 1084- 526	A	C	CACCACACCAAGCAACTATT TCATT	ACCCAAC TACTGTCCCA TTTTTCAT	CCAGTGAAAT TTATTTTT	CAGTGAAAT GTATTTTT	0,0	omy15	173008 50
Omy_11 1383-51	C	T	CACGCGCAATCTCTCGTTTT AC	TCTTTAGGCAACAAGCG TGTC A	AGCAAGCGCA CT[AG]GGT	AGCAAGTGC ACT[AG]GGT	0,0	omy15	212397 68
Omy_ca rbal1- 264	G	A	GCAAAGCCTCATCTTCAATC ATTTGT	GCAAAACACAAGTCAG GAATCACTTA	CATTAATATT GCTAATAACA CCAAG	ATTAATATTG CTAATAACAC TAAG	0,0	omy15	214540 64

Omy_96 222-125	T	C	GTAAGGAACTAATTGGCGC AACATT	CAGTTTGTCTAACACCC AGGCATAT	AACTACAACCT GTAGCTAATT	CAACTGTGGC TAATT	0,0	omy15	240411 11
Omy_R AD2357 7-43	T	C	AATAGGAACCAAGCCCCAG C	CAGAGCCTGAACCCAT GGAG	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	AAGTGGAGGCTGACCTGTT G	GCTGATGGCACCTGAC AGTTAATT	CATTGCCATTT ACAGACTT	TGCCATTTGC AGACTT	0,0	omy15	312319 75
Omy_ni ps-299	T	-	GACAGGATAGGAACGGTTT CTCAAT	ATCAGAAAGTTTAATTCA ATATGTACACGATCCT	CTGGATTTCA CATGTAATAC	CTGGATTTCA 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	TTTGTTAAAAATAGAGCC 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 CTTGCATT	CAACTCCAAT GAATTAA	AACTCCAACG AATTAA	0,0	omy16	148539 62
OMS00 062	T	C	ACCCTGGGAAGGCTACTGT AC	TGAACAGAGATCTGGA GAGTTGGAT	TTGACCAGCA GATGGTGTA	ACCAGCAGG TGGTGTA	0,0	omy16	148580 81
Omy_R AD8812 2-32	G	A	TCAGTGGATGGAGTGTCCCT	GGTCTTTGGCCTTGTTG CTG	GCTGTGGAGA TCAT[CT]CG	GCTGTGGAA ATCAT[CT]CG	0,0	omy16	163340 74
Omy_R AD4064 1-58	T	C	GGCAAACCTGGCTTGTGAGT G	AAGGCTCTGCTTCTGCT TGA	AGTGATATCA AGTG	AGTGATACCA AGTG	0,0	omy16	178582 78
OMS00 041	G	C	GATTCTGTTCCATCCTCTTTC TGTCA	AAACATAAAAAAGGGC ATGAAGGTGTC	CCACTCTATG CCTGCCCT	CACTCTATGC GTGCCCT	0,0	omy16	182791 74
OMS00 119	A	T	AGCGGCAGTTGTGTTAATGA GA	CTTCCTAAAGCCTGACA GTCTGT	CCACACAGCT GCCTGT	CACACAGCA GCCTGT	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	GACTCCACAGCCTACATGG G	CCGTTAATGCCAGGGG AGTC	AGACGGACTC CCC	AGACCGACTC CCC	1.1,0	omy16	441164 56
M09AA J.163	G	A	TCCCATGGCCCTTACTCTAT CAA	TTGAGGTGTATGTTGAA AAGTAACTT	AACAAAGTGA AAGTGTCTT	CAAAGTGAA AGTGTCTT	0,0	omy16	448434 40
OMS00 018	T	G	AGAGTACATGTGTGGCTGC AA	GTCATAAATCAACACA ATTATCTTCTTCACAGA A	AACCACATAA TTAATAATTC	CCACATAATT CATAATTC	0,0	omy16	464324 62
OMS00 134	A	G	GAAACTGAAATGATCCCAT CGTGTT	GCTAGCATAACAGCATT GCCATAT	TCTATAGCTG CAGTATATTA	TAGCTGCAGC ATATTA	0,0	omy16	477436 37
Omy_R AD3140 8-67	T	C	CAACCCTGCAGGCTACAGA A	TGGAGTGCCAACAAAA GAAGC	ACAGAATGCA GAAA	ACAGAACGC AGAAA	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	TCTGTGCAGT CCTC	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	GGTAATGCCACATGCGGTA AATT	GGCGAAAATCTGAAAAT GTGCTGTTA	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	CCTTGTCTCA ATTTTCTCTCT	CTTGTCTCAA TTTCTCCTCT	0,0	omy17	715446 3
OMS00 128	T	G	ATGAAAGAACTCCCAGACA CGTATTTT	ACATTTTAAACACAGTAA CACTAATACACACCA	ACTCTCAGAA TTAATTATG	CACTCTCAGA ATTCATTATG	0,0	omy17	144885 87
Omy_10 1832- 195	A	C	TGGCTCTGGACCTGTTGAGA	CGTCACAGCTATTTTAG GCGTAGT	TGTAGTCTTTC AGAGTAGTAT G	TAGTCTTTCA GAGGAGTAT G	0,0	omy17	170156 58
Omy_R AD4510 4-18	A	G	TGGTGCTTCAGTGCTGTCAA	AGAGTGAAAACGTGTG GCGG	CAAGACACCG CACACAG	CAAGACGCC GCACACAG	0,0	omy17	206937 54

Omy_10 1993- 189	A	T	ACAAAACACAGTGGGAATTA CAATTAACGTT	GGAAGTTAAATTTTCGCT TCGTCAGAA	CTTGATTTGC AGCTTGTCAA	TGATTTGCAG CATGTCAA	0,0	omy17	214912 90
Omy_R AD2212 3-69	T	C	TGGGAAAGCATAGGAGGGG A	TGTGTGCCTGTCTTATA GCCC	CCAAAGATGT CAGA	CCAAAGACG TCAGA	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	TGAGCTGAA GCAGAGCA	0,0	omy17	416909 56
Omy_ca 050-64	T	G	GTCATACAGAACTGTTTTGT TGTGTCAA	ACCTTGAATTGGTTCCT AATGCTATTGT	CAGTTTGAAG AATATACTC	CAGTTTGAAG ACTATACTC	0,0	omy17	486517 93
Omy_R AD4369 4-41	A	C	CCCCTCTCCCTGGCTAGAAT	TCAGGGGGTGTGCTTTT CC	AGGGAAGAGC GGAG	AGGGAAGCG CGGAG	0,1.1	omy17	577285 49
Omy_R AD4667 2-27	C	G	TGCAGGAGGTCTTTTTCCTT GT	AACACATTCTTATTTGC AATGATGG	GTGGTAGCCC ATCA	GTGGTAGGCC ATCA	0,0	omy17	582563 53
Omy_R AD5821 3-70	A	T	CCTGATGGGTGCTCTTCTCT C	AAACAGCATCATTATCC ATAGTGTT	TTTTTT[TA]AA AATATACT	TTTTTT[AT]T AAATATACT	0,0	omy17	582662 27
Omy_U 11_2b- 154	T	C	GGGAAGCAGAAAAACTGGA AGTT	CCCTCTGTGGGCTTGAT ATTCA	AATGATACTT TTCAGATTGT AAC	TGATACTTTT CAGGTTGTAA C	0,0	omy17	594666 96
Ocl_gsh px-357	T	G	GAGATCCTGAGGTCCCTGA AGTAT	AAGTGGAATTTGGGC TCAAAGC	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	GGAGCTCATATCGCCGATG G	GA ACTCTGTCACCCTGC CC	GGAGGGGAAG GG	GAAGGGGAA GGG	0,0	omy18	172929 64
Omy_R AD4246 5-32	G	T	GTGGATCTTGGACTCCAGGC	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	GTGGAGAGGGATTTTGGGG G	TGACAGGACAAACACA AGCCA	AAATGTGTAT TTGTGTA	AAATGTGCAT TTGTGTA	0,0	omy18	291187 77
Omy_12 8996- 481	T	G	CTCATCCACACTGTACAGTA CAAGT	CATGCCTTCGTCTCATC AATAACAC	CAAACCTCAA CCAC	CAAACCGCA ACCAC	0,0	omy18	308021 01
OMS00 121	T	C	GGAAGGAGGTCCAGTGTGA GT	AAAATATGCAACACCA CTAAAACTGGAAAA	ACAGCGTGAT AAATT	CAGCGTGGTA AATT	0,0	omy18	342329 91
OMS00 127	T	G	CACCTTTCTCTCTCTCCAT 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	GCGGGGGGT GC[AG]CATT	0,0	omy18	422122 99
Omy_R AD7210 -8	C	A	ACACCACACTCCACAAAGC A	GCGCCTTGGTCTCCTTC ATA	TGCAGGACTT GCTTTGT	TGCAGGAATT GCTTTGT	0,0	omy18	425586 54
Omy_R AD1934 0-24	A	G	GCAGGGAGCAGCATATACA TG	TGGGGTGATTTGAGTGA CAC	CATGGAAATA CATA	CATGGAGAT ACATA	0,0	omy18	427018 41
Omy_R AD3209 -10	A	G	CGGAGGAGTTTGAGCAGTC T	CTTCTACCACCACCTCG CTG	CGGTATCCCT GGC	CGGTGTCCCT GGC	0,0	omy18	509849 53
M09AA D.076	T	C	ACTGTTACCACTCTCTCATC AACCT	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	AGCTGAGAA GAGGTTC	0,0	omy19	125185 51
OMS00 017	A	G	ATTAAGTTCATACAAAAGTT CATCATAAATATTTTCCTT	GGAGAACAAAGGGAAA GAGAAGACA	TAGACCTCGG TGCTGTAG	CCTCGGCGCT GTAG	0,0	omy19	191115 91
OMS00 105	T	G	ACATTTGAAGTCAGTATGGG TGTTGAG	GAACCTCACCACAGTA CTAAATGCA	CTGCTATTCA AATTGCT	CTGCTATTCA CATTGCT	0,0	omy19	202649 68

OMS00 133	A	G	GACCACTTCACTCATTCCTC CTTTT	TCCGGTTTACACACTTC ATGCA	CGCCTCCATC TTTGTGGT	CGCCTCCATC TCTGTGGT	0,0	omy19	237020 93
Omy_ra pd-167	G	T	CCCAACATGCTCTATTGCAG CTA	AGTTGCATAAGATGAA TCAATAAATTAAAAAC ACAGAT	AAACAATCCC CCCCAAA	AAACAATCCC ACCCAAA	0,0	omy19	273624 24
Omy_12 8693- 455	T	C	GCCTGCAGGAGAAGGTAGA GTTA	GAAATGGAATGGACCC CAATCCT	CACTCAACTG ATACCC	CTCAGCTGAT ACCC	0,1,4	omy19	328900 59
Omy_R AD4911 1-35	T	C	GCAGGCTTAGCATTGCTGAC	GGAACCTGGGTGGGAG AATG	TTTCTTATATT TGA	TTTCTTACAT TTGA	0,0	omy19	400501 11
Omy_R AD739- 59	C	G	ACGAGGCTTGTAATGCAG T	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	AGGCTGGTTTGGGATTCAC T	CGCCAAACACTAACTCT CTGTCT	CTTTACCTCG AAGACAAT	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	AATGGAATTGGCCCCAACC C	TCTCCATTGTGTGTAAT CATGGT	ACAATTCAAA TGATTTA	ACAATTAAA ATGATTTA	0,0	omy20	167319 6
OMS00 039	A	G	GTCAGTACTGTGTGTGTCTG TGT	CCATCTACATTGTCAGC AGTGTGA	GTACGTGTCT CTGACC	GTGCGTGTCT CTGACC	0,0	omy20	480049 5
OMS00 114	T	G	GGATGATGCTGTGAGTCGA GAAG	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	TTGCTTCATTTTGTGATAAC CTTGGG	TGCATGCTCTGACAAAT GTTACACT	ATGACTATCC ACA	ATGACTGTCC ACA	0,0	omy21	238062 20
Omy_L DHB- 2_e5	T	C	TGCTAGGTGAGTCAGAGGT ACATATT	GACTGGAAGGCCACCC ATAAG	TTTACCTGTCA AC	CCTGTGCGAC	0,0	omy21	241299 07

Omy_L DHB- 2_i6	G	T	TCCTCGCCAATACCATACAT GTC	AGAGTGAAGCTAACAC ACACATTTCT	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	AGCAGATAAGCCTTGT GAGTGAATCTT	CACAGACTGC ACAGCC	CCACAGACTT CACAGCC	0,0	omy21	327667 40
Omy_R AD3500 5-13	C	T	TGGTCAAAGTTGAGGGTGG T	CAGGGCCCTGATTAACC ACT	CCAACTCCCG ACGG	CCAACTCTCG ACGG	0,0	omy21	371884 35
Omy_b1 -266	G	T	TCATGTGAACTTTAATTGAC TAGGAAGTCG	GATATGAAAATATCTG AAGAGTTATATTTGGGA AATTGAC	TCTATAAACA ACATTTTTC	TCTATAAACA AAATTTTTC	0,0	omy21	412557 73
Omy_10 04	A	T	GAGAATCGGAGCTAATCTT AGTTATTGTGA	CACTTTATTGAGCTACA TGGCAAATCTG	CATGTGATGT TTTTTTGC	ATGTGATGAT TTTTGC	0,0	omy21	419442 18
Omy_10 2505- 102	A	G	CTGCAAACCTGACATGGTAG CAAAA	TGCTTGCTTTTTTAAAAA CAATCTCCCA	AACAGGATGT TTTTGC	CAGGATGCTT TTGC	0,0	omy22	775932 8
OMS00 173	T	C	TGGAAGTAGCTACTTAACA GGAAATGG	AACACGTGTGCTTGTTT TGTCAA	CATTAGCTTG TGTATGAACT	ATTAGCTTGT GTGTGAACT	0,0	omy22	910589 1
Omy_Ot s249- 227	C	T	CTATCTATCTATCTATCTAT CTATCTATCTATCTATCTAC TTACTGAGA	CCCCTAGATTAAACCTG TCCAGTCT	CCCTCTGAGA ACTAC	CCTCTGAAAA CTAC	0,0	omy22	189174 30
OMS00 058	A	G	GTGACATTTGGAGCCACTGC	GCTAGGAGACAGAGGG TGAAAG	CAACACTTTG TACCCCTC	CACTTTGCAC CCCTC	0,0	omy22	199221 39
Omy_R AD9358 0-37	T	G	AGGCAGAGGAGGGTTGTTT G	TGCAGAAGTCAAATCA CGAACA	AGTCACCTGG GATT	AGTCACCGG GGATT	0,0	omy22	242478 65
Omy_IL 17-185	G	A	CCACCACACTCTGCAGCTT	TTGACGGGAATCCGAG ACTTC	AAGAATCTCA CCTGCCCCAT	AAGAATCTCA CTTGCCCCAT	0,0	omy22	272260 63
Omy_R AD1033 59-45	C	T	GGAGAAGGATGTGCTCCCT G	ATTTGGAGGTGGAGGG TCCA	CCTGTAACGC ACAG	CCTGTAATGC ACAG	0,4,0	omy22	405024 75
Omy_R AD4848 -14	G	T	TGTCCCTCTTCTGCACGATG	AGTTGGTAGCTCACTCT CTGT	GAGACAAGGA CAGA	GAGACAATG ACAGA	0,0	omy23	549364 8

Omy_10 7806-34	C	T	TCTTTGTCCATGCACATTGA TATT	AGCACATTTAGTTAGCA GTGATGGA	ATTGGATGTC AGTGTCAATT	ATTGGATGTC AATGTCAATT	0,0	omy23	100954 18
Omy_R AD4879 9-69	A	G	GCTGAGCCACCTACACACA G	GTCTAACACTCGCAGCA GGT	CATCCTAGAA TAGAAGT	CATCCTGGAA TAGAAGT	0,0	omy23	215810 80
Omy_18 7760- 385	A	T	CGGCTATTCTCGCGTAAAAG CT	AAATGCAACCAGAAAAC GGAATGTC	TCCTTATCCA AAATTATTGT GC	CTTATCCAAA ATAATTGTGC	0,0	omy23	236597 37
OMS00 024	T	G	CACATACAACCATCACCTT CCTAA	AGCATTGAGCGAAATT ACCAAGAGT	AA[AC]CCCAA ATTTTAC	AA[CA]CCCA ATTTTAC	0,0	omy23	314183 39
Omy_R AD3651 -48	G	T	GAGTACAGTGCAGTGTGGG G	CCTTCCTCTTGCCACCA TCA	GTTGGGAGAA CTTT	GTTGGGATAA CTTT	0,0	omy23	320298 60
OMS00 048	T	C	GGAAGAGCTGGAGAACAAC GT	TGCAGTTGACAGAGGC TTTCTTT	CAGCTAAACT CAGCAAAA	AGCTAAACTC GGCAAAA	0,0	omy23	371256 68
Omy_e1 -147	G	T	GCACTGACTGTTACCAGGA AAGAG	GTACTGCAGTGTTGAGG CTATATCA	CCATCCTGAA TCTGATTAA	CCATCCTGAA TATGATTAA	0,0	omy23	383133 38
Omy_10 9243- 222	A	C	ATGTGCACCTCTTAAATTGT AAGTAAAATGT	ACCCTATATTCAAGTGGC AAGATTGC	TGTTTCATTAA ATTGACTTTTT	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	GATGGACAGGGTCCTCTTCA C	CCTGTAGATAAAACAT GGTACCAGGTC	CCTTTCTTGAT GGTATCC	TCCTTTCTTG ATTGTATCC	0,0	omy24	245476 87
Omy_R AD5599 7-10	A	C	CATTTTCTACCTGCAGGCTG C	AGCCTACATACATAAA GCCAACA	AGGCTGCAAT GTTT	AGGCTGCCAT GTTT	1,5,0	omy24	274058 86
OMS00 052	T	G	TGCGTTTTTCATCCCAATCA TTCAC	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	GGCCCCCTTCTTTCAGGAAT	CACACACTCAACGGGT CAGT	TGATTGCTAC TGAC	TGATTGCCAC TGAC	0,0	omy25	402193 56

OMS00174	A	C	TGACTAACTATGCAGCCTGA AAGG	GGGATACTCTTGTAATA AACTGTTGGTTAGTA	CAAGAACAGG [AC]TAAATGT	CAAGAACAG G[AC]GAAAT GT	0,0	omy25	473253 93
OMS00071	A	G	CCGGAGTGACCTCACATTTG G	GCATCGTACAGTTCACC TACCT	CTTGTTTGAG CTTTTTCT	TTGTTTGAGC CTTTTCT	0,0	omy25	482484 74
Omy_ppie-232	C	T	CTGTTTTAGATTAGAATGTT TTTGGTCAGGT	CTGAACATAGGCTTTCA TTTCAGACAT	AAATAGCGGA GAAAAT	AAAATAGCA GAGAAAAT	0,0	omy25	549909 25
Omy_RAD14033-46	A	G	GCAGGAGATTTATTTGGCCC C	ACCCTTGTGATCACATA CTGTCT	ATAGAGGAAT AGAC	ATAGAGGGA TAGAC	0,0	omy25	600640 21
Omy_RAD1186-59	A	G	CACAGCCTGGATGTGGTTCT	ACAAGTTCCGGGAGTTT CCT	CCAGGACATC CAGG	CCAGGACGTC CAGG	0,0	omy25	702523 14
OMS00002	A	C	TTTGATTTGATTTGTATCTGC TTCTT	CCAACATGCCTCACACA AAA	TGTTTTGCAG CGCTC	TGTTTGGCAG CGCT	0,0	omy25	823663 95
Omy_RAD41594-34	A	G	TGCAGGGTTATAATGTGTCT TTGT	AAATCTCGGGCTGAGG AACG	CAGAGATACG TTCC	CAGAGATGC GTTCC	0,0	omy26	560047 5
Omy_cd59-206	C	T	CGATTGGCCCAGATGTTTCC AT	GCTCCGTTGCATAGGTG ACT	CAACAATCGA AGGTAAAT	CAACAATCA AAGGTAAAT	0,0	omy26	802832 2
Omy_RAD13034-67	A	C	GAGTGATTCCCAGCCCTCC	TCTCTCCGTTGGCCAGA AAC	ATAAATCACA A	CTAAATCACA A	0,0	omy26	125370 39
Omy_adal10-71	C	T	TCTTTGAGCGACAAAGTCCT TGT	ACCCACACATGAACGC AAAAG	CTTCCTGCGTC CAA	CTTCCTGCAT CCAA	0,0	omy26	183154 20
Omy_aspAT-123	T	C	GCCCATTTCACTGATGCTGT GA	AGGAGACCACTCCAAA GAGAACT	CCTTCCTAGG CAGTCAG	TTCCTGGGCA GTCAG	0,0	omy26	192895 82
OMS00014	T	C	CTTACACACAAGGGCTTCAT TCTG	GATGTCTCTGGGTGGTT GTCA	TGATTTGATG AATTAACTT C	TTGATGAATT GAACTTC	0,0	omy27	629752 6
OMS00015	A	T	TCAGACCCTATTTTTGGCAC AAGT	GTCTAACTGATCCCACT TCTGCAT	CAAGTCACAC TTTTAATGAA	CAAGTCACAC TTATAATGAA	0,0	omy27	237309 45
Omy_hsp47-86	T	A	CACATTAAGCACTCCCAGG GA	TTGCAAAGGCCAAACA GCATT	CAGGAGTGTA AATGTTT	ACAGGAGTG TATATGTTT	0,0	omy27	279444 94
OMS00090	T	C	AGGGCACAACACCACTCTA AATT	TCGAAAAGCAACATCT GTCTCAGT	ACAACCACAC AAGATT	AACCACGCA AGATT	0,0	omy28	424599 7

Omy28_11607954	G	A	TGACACTGATCACAATGGTGAAAT	TAAACTGGAAGGAGAGAGCAAAAT	TGTGGGCTGCGAACATACTCA	TGTGGGCTGCGAACATACTCA	0,0	omy28	11607954
Omy_RAD52458-17	C	A	ACGTGTCCCTGAGGATGGTA	AGCTCTAGGTCTGGGTCCTG	ATGGCCCC[CT]AAGAACCC	ATGGCCCA[CT]AAGAACCC	0,0	omy28	11609794
Omy_GREB1_05	T	G	TGGGCAGATATGGAAGAACGG	ACCTTCTAAATGGCCTCTGTGT	CGGTGGCTCTC	CGGTGGCTCGC	0,0	omy28	11618027
Omy28_11625241	A	G	CAACATTTAGGGAGAGGTTGCTAT	ATCATCAAGTTTGCCTACGACAC	CCTCCTCCCTATGGTTGTCTC	CCTCCTCCCTGTGGTTGTCTC	0,0	omy28	11625241
Omy28_11632591	G	A	GTAGAGGCCAAAGGCTTGA	TGCTCTTATTACCTTCCAGACTCC	TGAGAAGAACACAGAGG	TGAGAAAAACACAGAGG	0,0	omy28	11632591
Omy_GREB1_09	T	G	CCAGTGGCAACCTCAGGTA	GACTCCAGTCACCCAA	TCAATGGAGA	TCAAGGGAG	0,0	omy28	11641623
Omy28_11658853	A	C	CAACATATGACCACTCGAA	ATTAATCACACCGTGAG	TGGTACAGACACGCACTAGCA	TGGTACAGACCCGCACTAGCA	0,0	omy28	11658853
Omy28_11667578	T	C	ACAGTAAACCCATTTCAGGC	TTATCCTCTCAATCCAC	GTATTGATCC	GTATTGATCC	0,0	omy28	11667578
Omy_RAD47080-54	A	G	TCAAAACCTGCAGGACTTG	TGGTTATATCTACAGTACAGTTCGT	TGCAAGACTTAAAACGA	TGCAAGGCTTAAAACGA	0,0	omy28	11667915
Omy_RAD15709-53	G	A	TGCAGGACTTGGATAACAC	TGGTTATATCTACAGTACAGTTCGT	ATGCAAGGCTTAAA	ATGCAAGACTTAAA	0,0	omy28	11667915
Omy28_11671116	C	T	AATTTCCCCAAATTTGAAAC	GTGTACATTGTCAGGCA	CTGGTGAGAACAGGAATTACC	CTGGTGAGATAGGAATTACC	0,0	omy28	11671116
Omy28_11676622	T	G	CGAATGCACTGTAGCTCATTCTAA	GCAGTAGAATGTCTCGCAAATACA	ACATGTCATT	ACATGTCATT	0,0	omy28	11676622
Omy28_11683204	G	T	CAAGAAAGAAACAGATGTTGTCCA	TTGTGACTCAAATCTGCAACCTAT	ATGTAAAAAAGGCAGAAAA	ATGTAAAAAATGGCAGAAAA	0,0	omy28	11683204

Omy28_11773194	A	T	AGTTTGACACCCCTGTACTA GAGC	GTCTAACAAGCTCTGGG TGATTTA	GCAATTTTTTA AAATTACCGC	GCAATTTTTT TAAATTACCG C	0,0	omy28	11773194
Omy_R AD76060-20	C	T	TGCAGGGTGTCTAGTATTGGG	TCCCATGCAAATTCCAA ATGCT	GGGCGCTGTA GGCAA	GGGTGCTGTA GGCAA	0,0	omy28	21561303
OMS00129	C	G	GGAGATGATGAAATAAAAA TTGAGGAAAAGATGA	TGTCTGGTGAATTATCG CAAATAACCA	TTGAACAACA AGAAAAA	TTGAACAACA ACAAAAA	0,0	omy28	22531125
Omy_R AD46452-51	A	G	TGCAGGTAAGACTTGATCTG GA	TGACTCCAACCTAAGTG CATGT	TGAAGTCAGA AGTT	TGAAGTCGG AAGTT	0,0	omy28	27516610
Omy_97660-230	C	G	TCAGTTATGTGTAATCTCAT TACCTCTCCAA	AACAGAAAAGGTCTCA ATGTATTTTTTGCA	ACGTAACTTG TAGCGTTTT	ACGTAACTTG TACCGTTTT	0,0	omy28	35742946
Omy_i mpal-55	C	T	CGCTGAGAGGATTGTCAA	TTTTCTTTGTTCAGTCTT CTGTCTCTG	CGAGATGATG CGTCTACA	CGAGATGAT GCATCTACA	0,0	omy28	36390509
Omy_B AC-B4-324	G	T	CGTACTTTTCTTTTACAAAA TTAAGTGGAGGAT	GCCTAATATTGGCCTAA TGTCCTTCA	CATTGCCAAA TACG	TACATTGACA AATACG	0,0	omy29	14528635
Omy_O myP9-180	C	G	CTGGATGTGTAGTATCGGTG GAAAA	CACTGGGCACCTCTGAT CTC	CTGTAGTAGT CCCCATTGT	CTGTAGTAGT CCGCATTGT	0,0	omy29	15673414
OMS00164	T	G	CAGAGGAGAGGAGAGCAAA ATACTT	ACAACCTACTCATTGAA ACTCATTGGA	CCAGATTCAA TTAAATTTA	CAGATTCAAT TCAATTTA	0,0	omy29	17249654
Omy_cr b-106	G	T	GCTCAAAAAGATTCTGCCA AATTCACA	ATTACAATGAAAGTACT TGAGTGTTTATGCAAA	TTGCAATGCG TCTTT	TTGCAATGAG TCTTT	0,0	omy29	30701374
Omy_118205-116	A	G	CTGCGGTGGGCTACACA	CGCAGCTGCGGATGAG	CTACTGAGGC TGAGTGCT	TACTGAGGCC GAGTGCT	0,0	omy29	33267127
Omy_sS OD-1	T	G	GCCGGACCCCACTTCAA	CAGACTAACCGAACAG CATCAGTGG	CCACAACAAG ACCC	CCACAACCA GACCC	0,0	omy29	39802221
Omy_R AD19578-59	A	G	GGTTGGACACCTCCTGGTTA	TCAACCAAGCAACAGA TTATAGCT	GGTTAAGAGT ATTC	GGTTAAGGGT ATTC	0,1.8	NA	NA
Omy_R AD40520-48	T	G	TGTTTCATCTGATCAGCTGTC AG	ACACGTCGGTCTTCTTC TCC	GTCAGATTGC GCTG	GTCAGATGGC GCTG	0,0	NA	NA

Omy_R AD7814 7-27	C	T	GCATTTTAGCCCTCCCAAAG TC	CCTTCTTCCAGTTGTTA AAACCCA	CAAAGTCCCA GAGA	CAAAGTCTCA GAGA	0,2.6	NA	NA
Omy_R AD619- 59	T	C	CATGGAGAAACAGACCCGC T	TGCTGTGTGTGTATCTG GGG	TGCTGGATCC CCCA	TGCTGGACCC CCCA	0,0	NA	NA
Omy_R AD9871 5-53	T	G	CGTAACGGGGAGCTGATCT G	GCTGGTAAAATGCTGA GGGG	CAGGACTTCT CCCC	CAGGACTGCT CCCC	0,1.9	NA	NA

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Appendix 2. *GT-seq SNP panel for Chinook salmon.*

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 CGTTTAAAT G	0,0	Ots01	46840 237	Ots01	40924 770
Ots_Ikaros-250	G	A	GAGGCTGACTTGGACT TTGC	GGCCTGTCAGCCAA GGA	ACAGAAGA TTTTCGGCT GC	ACAGAAGA TTTTCGACT GC	0,0	Ots01	50283 457	Ots01	45385 098
Ots_107806-821	T	A	TGCAGTGCTGAATTAG AGATTAATTTTTGTG	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	GAACTTAAA ACACT	GAACTTGA 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	GCATTTAA 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 ACAACTTCA 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	CTCCCTGTTCTGCTAGC 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 ATTTTCATT	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 AGTGTTCA 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	TTCCTAACCCCAA 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	CAGGCTTGTGTTAAGT 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 GGTGTATGAC	TCTTGCAAT CATTTTAA 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	CTCTTTCAGTTGTCTTT 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	ACTTTCCTT 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	GTTCTTTTTAATGATGA CTACAGGTCTTTCAC	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 TTTTTTTTA 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	CCGCCTTTCCACCTTC 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	CCC GCGGTG AGTAT	CCC GCTGT GAGTAT	0,0	Ots24	95681 30	Ots24	17321 046
Ots_PEMT	C	T	AGAGCATTCAATTTAA 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	GGGAGACTTAAAACAA 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	AAATCTCACAAGTC 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	CAGTGTGAT 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 CTTGTTCGATA	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	TGGGTGCA 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_txnlp -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	ATTCTCTCTGTGTCT 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 AATCTC	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 GGAACCTAACTCAT	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 GTTCAATTGT	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	AACAAAGAATGTAAAA 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

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Appendix 3. GT-seq SNP panel for Sockeye salmon.

Assay	A 1	A 2	A1-Probe	A2-Probe	FWD Primer	Corre ction	Rev Primer
One_1a.11 217-58	C	T	ACCTAACCCTAACC	ACCTAACTCTAACC	AGCTGACAGCCACAAAGTCA	0,0	AGGTTAGCAGTGCTTTTAA GGT
One_1a.11 387-56	C	T	TGGCTTCCGGATGT	TGGCTTCTGGATGT	CAGTCACCAGTGTTTCCTCC A	0,0	TGACCATGCTCCTTAACAT CC
One_1a.12 158-56	G	T	CTAAAATGAACTTA	CTAAAATTAACCTTA	TCTGACCCACGACGTCCTAT	0,0	TTCCAGACGCACACAGTTC A
One_1a.12 851-49	C	T	AATCTGCCCTGCTA	AATCTGCTCTGCTA	CCAGACCGTACAGAATCTGC	0,0	ACCAATCACAGGCTGTCTT TG
One_1a.13 961-31	A	T	ATTACAAAGAATAT	ATTACACTGAATAT	TGCAGGTTAGTGAAGATAAA TGGGA	0,0	TGTCACAGAAACCACAGTC TGA
One_1a.14 403-38	C	T	TAGAGCGCGATGAG	TAGAGCGTGATGA G	CACCCAGCCTGCCACAAG	0,0	ACCAGGCTGTGTCATAACC G
One_1a.14 866-33	C	G	AGGAGGACTTTTGT	AGGAGGAGTTTGT	TTGTGTGTGGGTGTCAGGAG	0,0	CCGAGCTATGAGGTCAAG AGT
One_1a.15 933-53	A	G	GCCCTGCACTGCCC	GCCCTGCGCTGCCC	ATTGGTGACACGGGCAC	0,0	GCAAAGGATCTGACAATG GC
One_1a.17 043-35	A	C	GTAGTGTATGGTAG	GTAGTGTCTGGTAG	GCAGGTGGAGTTATAGTGCT CA	0,0	ACAACCACTACTGAGCTAC CA
One_1a.20 787-45	A	C	AAAAGATAATGTGC	AAAAGATCATGTG C	TGCAGGGTATGTCATGTTTT GT	0,0	GCACAACGTAGCCAAATTG C
One_1a.20 814-68	A	G	AAGGTCCATTACAA	AAGGTCCGTTACAA	ACATTTCAGAAAGGGGAAGGT CC	0,0	CTACTTCCCCTTCCCATGC C
One_1a.22 268-41	C	T	GGCATCACGAGGGA	GGCATCATGAGGG A	GAGGGACTGGTGCACTTCAC	1,5,0	TCCCTCATTTTCCCTCCCTC
One_1a.22 351-67	C	T	CAGACATCGCTCAG	CAGACATTGCTCAG	GGAGGCTATCAGCTTCTGCA	0,0	TCCAGTAGTATGTCTTGGA GCT
One_1a.23 491-46	A	G	TTGGCCCAACAGTC	TTGGCCCGACAGTC	GCAGGTTTTCACTCCAACCC	0,0	AGTTATGTTACGGGTCTCA TTACCA

One_1a.23 626-48	A	C	TGAAAAAACCCCTTC	TGAAAAACCCCTTC	ATGCAAGGGAAGGGAAGTG A	0,0	CATCTCTCTCTGTTGTAAA GAAGGG
One_1a.24 137-66	G	T	AGAGAGAGATGTTG	AGAGAGATATGTT G	ACTCTCTCTCCCACTCTGCA	0,0	TCTTGGATGTCACTGTACT ACAACA
One_1a.25 746-65	C	T	TGGCCTGCCTGCAA	TGGCCTGTCTGCAA	ATGAATCACATTGGCCATGC A	0,0	AACGTTTCAAGTTCGTTGC AG
One_1a.25 904-44	A	C	ATAAAAAAATTTCA	ATAAAAAACATTTCA	GCAGGTGCATCTTAAGGGTG	0,0	TCACTCAAGAGGTAGAGCT GC
One_1a.27 200-35	A	C	TGAGAGTATTTGTA	TGAGAGTCTTTGTA	TGCAGGCCCAAGTTATAGATC A	0,0	TCTTCATCATCTTTATGCTT TCGTT
One_1a.27 760-67	C	T	TGGTGCTCAACGAG	TGGTGCTTAACGAG	GACCTGCAGTTCCACATCCC	0,0	ACCCTCTGCGTAATTGGCT C
One_1a.28 530-58	C	T	GCTGGCACACTAGC	GCTGGCATACTAGC	GGCCAGGTGTATGGACCCTA	0,0	TCCAACAGAGCAGTGTGTG T
One_1a.29 135-58	A	G	ATCTGCAATCGTTT	ATCTGCAGTCGTTT	GCCCCGGGTCTCTTTAATC	0,0	TGCAGGATGAAGAGGAGG AA
One_1a.30 563-32	C	T	TGAACTGCGTTTCC	TGAACTGTGTTTCC	TGCAGGCTTATTTCTGGGTTT	0,0	GCTTAACACGGAAGCCAA GC
One_1a.32 514-40	C	G	ACCTTCCCCTCCAC	ACCTTCCGCTCCAC	CAGCCACACCCACCAGAC	0,0	CCTGAGCAGCTATGGAGTG G
One_1a.35 102-40	C	T	CTTTTACCGTACGA	CTTTTACTGTACGA	GGTTCATGCTTTACAACAGG GG	0,0	TAGCACCTCCCACCAGAAC A
One_1a.36 888-37	A	G	TTTTTGGATATTGA	TTTTTGGGTATTGA	TGCAGGTTCACGGGAAGAAA	0,0	AGTCATTGACTCTCGCTGA TCA
One_1a.37 709-28	G	T	ACGAGAGGCTCGGC	ACGAGAGTCTCGG C	GCAGGAGAGACGGTGGTTTA	0,0	CCCGAGGGATGTGAGTACT G
One_1a.39 597-30	G	T	TCTTGATGATTGAC	TCTTGATTATTGAC	TGCAGGCTCTGGGTTTTATCT	0,0	ACTAGGTCCTTCTTTGCGG C
One_1a.39 667-45	A	C	TGTAACAAAGATGA	TGTAACACAGATG A	ACCACATGGGAGGAGGATGT	0,0	AACAAAGATGCCAGGGT CC
One_1a.40 490-31	A	G	TGGATTTAAATGGA	TGGATTTGAATGGA	TGCAGGCACCATAAGCACTA	0,0	AGCCTACTTGCATAGCCTT CTC
One_1a.40 540-34	A	G	AGTAGCAATAGCAG	AGTAGCAGTAGCA G	TGCAGGACTCCTAATTCATT CAGA	0,0	AACGGCAGACTGGGTACA TG

One_1a.40 596-58	A	C	AACCCAAAACCCTG	AACCCAACACCCTG	ATGAGTACTGTACGTGCGGC	0,0	TCGGTCAGTTGGTTGGACA C
One_1a.41 039-32	A	T	AAATAAAAAAATAA	AAATAAATAAATA A	AGGGAAGGGAGCTGGGATTT	0,0	CTCTCTTGTTCGGGATGTGT GT
One_1a.41 570-62	C	G	GGTCACGCCAAGGT	GGTCACGGCAAGG T	TTTGCAGAGAACGACAGGCT	1,1,0	CCTGCATCCTACCAGAGTG C
One_1a.41 669-43	C	T	TAATGCACAGCGTT	TAATGCATAGCGTT	GGAGGTTTTCCCTGTAATGC A	0,0	GACTGCCTGCAATGACAAG C
One_1a.42 159-31	C	T	AGTTCTCCTCTACG	AGTTCTCTTCTACG	AAGCATGCAGAGCTCCAGTT	1,5,0	ATGGGGGTGTATCCTGGGT G
One_1a.42 211-64	A	T	ATCTAAGAGGATGT	ATCTAAGTGGATGT	CCAACCACGTCAACTGAGCA	0,0	TGCATTAATGTTAAAACCG TTAGCT
One_1a.44 788-39	A	G	CACTGAGATGGATG	CACTGAGGTGGAT G	TGCAGGTTGGAGATGTGGTG	0,0	GCACAAACAGACTGGAAC TGTG
One_1a.45 935-29	A	C	TGGAAGGAGAAGCT	TGGAAGGCGAAGC T	GCTATATGAGCGACCGGTGG	0,0	CCCCCAGCTAAATAACAAT GAGG
One_1a.48 100-30	C	G	CACAATACAAATGG	CACAATAGAAATG G	AGGATCCTGCAGTTTGTACA CA	0,0	CCCTCGCTGTATCATGTGC T
One_1a.49 00-40	A	G	TTTTGCTACCCCAT	TTTTGCTGCCCAT	TGCAGGATATTAACTTTAAA GCTGT	0,0	TCCATGCTAATTTCTTGCA ATTCT
One_1a.51 402-35	A	G	TGTTATCATGATAG	TGTTATCGTGATAG	TGCAGGGGAGAGAACAGAA TG	0,0	TGGTACACTGTAGGGCTAC A
One_1a.53 13-43	A	G	GGGAAGGACCAGGA	GGGAAGGGCCAGG A	TGGCCATGAGGGTTTACTGG	0,0	AGGGTGCCATTTGGGATAC A
One_1a.53 797-66	A	T	CAACTTTAAAAAAA	CAACTTTTAAAAAAA	TGTTACAGACGGTGCCAACT	0,0	AGGCATTTTTTCCTGAAGAC GT
One_1a.54 07-55	A	T	GCAAGAGATTATTG	GCAAGAGTTTATTG	GCAGGAGGGGATAGTTGCC	0,0	ACAGAAACACAGCTAGCC CA
One_1a.54 542-52	A	G	TTGACCAAAAGGGG	TTGACCAGAAGGG G	GCAGGTTGTGATCGTGACCA	0,2	TGAAGAGACTACGCCCCCT T
One_1a.55 218-55	C	T	GGCCCAACTTCAAC	GGCCCAATTTCAAC	CAGGCCCATACTGAACCGAG	0,0	CCTTGGGGTGCGGTTGAA
One_1b.56 018-52	C	T	GAAGAAACGTGTGT	GAAGAAATGTGTG T	AAGCATGACGAGTGTTCCTG	0,0	GCACTCCCTGCCCCTATAC A

One_1b.56 276-30	A	G	CTAGAGCATGATAA	CTAGAGCGTGATA A	CTGGCCCTGAGTCGCTAGAG	0,0	AATAGGCCGAGTGTGTCC G
One_1b.56 339-60	C	T	GTGGCATCTCATT	GTGGCATTTCATT	CCGAAACTTTGGAGCGAACC	0,0	TCCTTTAACCTGTGAGACA CCT
One_1b.56 528-40	G	T	TAGAAATGATGAGG	TAGAAATTATGAG G	GCAGGGTTGTGGCTGTTCTA	0,0	CCAAAGATGAAACCAGTTC CTGT
One_1b.56 760-39	G	T	TGTAAATGAATATA	TGTAAATTAATATA	TGCAGGTCTGAGAAGAAATC AA	0,0	ACTTCATCAACCCAACCCA T
One_1b.57 80-62	C	G	TGTTTCGCCCCCT	TGTTTCGGCCCCCT	TTGTGTCTGGCAGTGTTCG	0,0	CAGTGGCAGGCACAATGA TG
One_1b.58 33-45	A	G	CATCACTAAGACCA	CATCACTGAGACCA	CGGCCTTATCGTCAGTCTCC	0,0	TGAAGTTGCATGGAAGTCA TCA
One_1b.58 946-27	C	G	TCTGCTGCCTTAGG	TCTGCTGGCTTAGG	TGCAGGCCAAACAAGTTATT TCT	0,0	ACACACACACTCCAAGC T
One_1b.58 981-44	A	G	AGAACTCATTAATC	AGAACTCGTTAATC	CAGCCGATTCTGCTTTTTGA	0,0	CCTCTGGACGGCATCAATC T
One_1b.59 232-51	A	G	TGCAGTGATGCCAT	TGCAGTGGTGCCAT	ATTCTGCGTCCATCAGACC	0,0	TCCGGGATAGCCAGAACTC A
One_1b.60 577-60	A	G	TGGACGAAGACTGA	TGGACGAGGACTG A	ATCGCACACAGGCCTTCAG	0,0	ACATTGAGGTGCGTGTCA T
One_1b.60 684-45	G	T	GACGTTTGAGTTAA	GACGTTTTAGTTAA	CGGGAGGAGCAAACACAGT A	0,0	CATTGACTGACCCCCTGCT T
One_1b.61 920-50	C	T	TTTTTTTCAAACCG	TTTTTTTAAACCG	GCAGGAAAGGTGAATTATTT TCTGG	0,0	TCTGTTCAAGACGTCATTT ACCA
One_1b.61 967-31	A	G	GGCGTTCACGCAAT	GGCGTTCGCGCAAT	AACCTAGGACCTTGCGGTT	0,0	GACGGAGGGAAAGCATGG AG
One_1b.63 191-29	A	G	TATTCCAATGTATA	TATTCCAGTGTATA	GCAGGAAAGTAGCATCTTCG C	0,0	GCAAGATAGCCTATCCAGT ATACA
One_1b.63 942-34	G	T	AGAGGGGGAGTTGC	AGAGGGGTAGTTG C	CAGGATCAGTGGCTGTGTGA	0,0	AGTAGCATTGGTTCTGGCC C
One_1b.64 367-65	A	C	GTGGACTAATACTT	GTGGACTCATACTT	ATGAGGCTCTGGGATGTGGA	0,0	CCTGCAATCTCATTCATAA CGCA
One_1b.64 886-42	C	T	ACCTACGCCTCACG	ACCTACGTCTCACG	CGCATGGCAGTGACATACCT	0,0	TGCATCTTAAGCCAGGGGA A

One_1b.67 122-29	A	G	CCTCCGGATCATCT	CCTCCGGGTCATCT	AGGTCAGTCTAGGTCCTCCG	0,0	TAGGGTGTGTCTGCACTGA G
One_1b.68 250-26	A	G	TGGAGGAAGAAGAG	TGGAGGAGGAAGA G	TTGCCCTCGTGCTTGGAG	0,0	TTAACGGTGATGGAGCTGG C
One_1b.69 39-43	C	T	GTGATGGCGGGGGT	GTGATGGTGGGGG T	GGCCTCAGAACCCTGTTTGA	0,0	TCTGCATTTCTGGTGATGG CT
One_1b.70 246-46	C	T	GCTATGGCGACTCC	GCTATGGTGACTCC	TTTGTGGAGAGCCTGCGTAG	0,0	GTACGAGAAGGCTGGCAG G
One_1b.70 297-45	C	G	GGGCCGGCAACTGG	GGGCCGGGAAC TG G	CAGTGGGCTGTAACAGAGGG	0,0	GCAGAGGAAGGGGGTTCT TC
One_1b.70 694-28	C	T	CAACAAGCTGCTTA	CAACAAGTTGCTTA	TGCAGGCTTGACTGGAAAGG	0,0	ACTCCGGTATCTCCTGTGC T
One_1b.70 768-40	A	G	GTCTACTACTGGAG	GTCTACTGCTGGAG	GGGCCAAGTTTACCCGTCTA	0,0	CCGTAATCGTCCTGGCAGT T
One_1b.72 136-33	C	T	CCTAAACCTCTACT	CCTAAACTTCTACT	TGCAGGATGATGTCATGGTG T	0,0	ACAGTACAGGTTTAGGCTG TAAGA
One_1b.72 637-54	A	T	AGCGAGAACAAACA	AGCGAGATCAAAC A	TCCACACTGAACTGGTTGCC	0,0	AGTGCACAGAAAAC TTTGG GC
One_1b.72 787-38	G	T	TTCTGGGGTTTTGT	TTCTGGGTTTTTGT	CGTGAGCAGTCTACAGTATC AAC	0,0	TGTGTACCATGGGGCATTG T
One_1b.72 992-37	A	G	CAGAAGTACATGAC	CAGAAGTGCATGA C	TGCAGGTTTTAGCAAAGCCA	0,0	TCCCATATTTGAGTCGAAT TG GT
One_1b.73 420-52	C	T	GAAC TTTCGATTAA	GAAC TTTTGATTAA	AGGGTTGCAACATTTTG GGA	0,0	AGGGAATCTGGAATCCTCC GA
One_1b.73 656-45	C	T	TACAGTACGTATAT	TACAGTATGTATAT	ACTTCCAGGGGGATCTCTGT	0,0	TGCATTCTCAAAAGACGGC T
One_1b.74 472-27	C	T	CACTGCCCCTGTGT	CACTGCCTCTGTGT	TGCAGGTTTCAAAGCTAGAC CA	0,0	CAGACCAGACAGAGGGCA TG
One_1b.74 818-26	C	G	AAAACACCAGACGA	AAAACACGAGACG A	TGCAGGAAAACAAGAGGAC A	0,0	TGTAAATCTACTGCCCCAT CGT
One_1b.75 116-33	G	T	CGAAAAGCTTCAT	CGAAAATCTTCAT	TGCAGGGCTGAAATTCAATT CA	0,0	TGTGTTGCATGTGAGCCTC A
One_1b.76 686-31	A	C	ATAGTTTAATATTC	ATAGTTTCATATTC	TGCAGGTGATGTATGTGTGT	0,0	CATGGCCTTTGTCAGGGAG T

One_1b.76 828-42	A	C	AGTCACCACCATAG	AGTCACCCCCATAG	CAGGAGGGAAGGGTGGAGG	0,0	AGTTTACTCACCACACCCC G
One_1b.77 679-43	A	C	GAGATCCAACGACC	GAGATCCCACGAC C	CCAAGCTGAGCTTCGGAGAT	0,0	GAAACCCAGGTAGCCAGT CC
One_1b.78 278-49	C	T	TACATCACCTAGTA	TACATCATCTAGTA	AGCATTCACCAAAGATAGCA TGG	0,0	CAAAAGCCAAAACGTGCA GC
One_1b.78 365-62	A	C	GGCATCCATGTCAA	GGCATCCCTGTCAA	CGTCACGTGATGTCCCCATA	0,0	CTTCAGGTGGCCATCTTGG A
One_1b.79 240-40	A	G	TTCTTGCACTCTAG	TTCTTGCGCTCTAG	TTGCCCAATGAGGAAAGGCC	0,0	CAGCTGGAGAGGGCCATG
One_1b.79 575-35	C	T	TTGTGGTTCGCCTGA	TTGTGGTTGCCTGA	TTGGCTACACAAAGGACGGT	0,0	GACGGGTTGCTAAGGTCAG G
One_1b.80 431-46	C	T	GAAACCACAATGAC	GAAACCATAATGA C	TACTGGCCCCCTAGCTACAG	0,0	TGTCTGTTCTGTTCTTGCTT GT
One_1b.80 929-65	A	G	AGACATGAGATTAC	AGACATGGGATTA C	CCAAAGGGGACAGACAGCTT	0,0	ATGAGCGGGAGAATGTAG CT
One_1b.83 667-61	A	C	CCAAGTCATCCTGC	CCAAGTCCTCCTGC	GCAGGATGTCACGACACAGA	0,0	CGCAGGAGTCCCTAGAGG A
One_1b.85 587-38	C	G	AGAGTGTCTTTTTG	AGAGTGTGTTTTTG	GCAGGCAGTCAGGATGTCTC	0,0	AGGCAGTTCTAATGACAAG TCCT
One_1b.88 442-61	A	G	CGTTCAAATACCCA	CGTTCAAGTACCCA	AGTAACCAAAAAGTCTCTCG TTCA	0,0	GGCTTGCTCAAGTGTGAC A
One_1b.88 59-52	A	G	TGGGAGAAGGAGGG	TGGGAGAGGGAGG G	AGGGACTTGGCTTTCAGCTG	0,0	CTCTCTCCCCCTTCTCCCTC
One_1b.89 789-50	A	C	CTGTGCCAATTTGA	CTGTGCCCATTTGA	CCAGACGGTCACTGTGCC	0,0	GGACAGGCAGCATGTGTG A
One_1b.90 162-56	A	C	CGCAAGCATGCTAA	CGCAAGCCTGCTAA	TCAAGCGACCACCAGATCAC	0,0	CCGTGGCTCTTCCCCTTTTA
One_1b.90 239-52	A	G	CCATCGCACAAACA	CCATCGCGCAAAC A	CAACCTCTACCACGACCCAC	0,0	AGTTGTAAAAGAGGAGAG AAGTGT
One_1b.91 34-28	C	T	CTCATTACGCATGG	CTCATTATGCATGG	TGCAGGACGTTGCCTTATCA	0,0	AATGGCAAGGTCCCAGTTG G
One_1b.93 62-41	C	T	AAGGTAGCGTGCAT	AAGGTAGTGTGCAT	GCAGGCTCTGGTAGTATTCA CA	0,0	CGGGGTGCTATTCTCCACT C

One_1c.34 041-34	C	G	GATGAACCAGACTG	GATGAACGAGACT G	GCGTTTGGAATTGCTCCCA	0,0	ACAAGACCTCAGAGTGCTG T
One_1c.51 810-33	C	G	CAGAGGACGAGCCG	CAGAGGAGGAGCC G	TGCAGGAGGAACCGCCC	1.1,0	GCAAAATGGAGTGTACG GC
One_1c.57 65-39	G	T	GTACGCCGCCAGCG	GTACGCCTCCAGCG	CACAGAGGCTGCTCCAGTAC	0,0	TCCTACCTTGACCAACTCC GA
One_1c.70 294-64	A	T	GAATGTAATAAAAA	GAATGTATTA AAA A	AACAAAAGGAACCTTGAACA ACT	0,0	CTTTCGTTGCGCCACAGTG
One_1c.85 338-32	C	T	ACAAAAGCTACTAC	ACAAAAGTTACTAC	TGCAGGCCTATTGTTGATGT CT	0,0	TCCTCCTCTTGCACTCCTCT
One_1c.87 896-59	C	T	AGGTAGTCGCATTA	AGGTAGTTGCATTA	GAGGGAGAAGCATCAGAGG T	0,0	CCTGGCCCTTTACACCAAG T
One_1d.80 954-64	A	T	CACTCACACACACA	CACTCACTCACACA	CTGCGGGGACTGATGTCTAC	0,0	GGGAGTTACCACACACTGC A
One_2.106 23-54	G	T	GATTCTTGTGGGC	GATTCTTTTTGGGC	GCTAATGTGAAAACGTGCCT GA	0,0	TAGCCTGTTGCACAAACCC T
One_2.130 49-68	A	C	GGAAGTTAATTTTA	GGAAGTTCATTTTA	ACATCGTTGGCAATGGAAGT	0,0	TCTCAATCATCGGCATGTG GT
One_2.137 57-55	C	T	ACCCTCCCCTAACC	ACCCTCCTCTAACC	ACAAGGAGTCGCTTGAGCC	0,0	GGGAGTCCCATAGAGTTGC G
One_2.140 18-56	A	G	GGTGGTGACCGACA	GGTGGTGGCCGAC A	ACCAGCTGTCAGAGATGCAC	0,0	GGCATCCTTCTCTCTGTCTG G
One_2.156 28-38	A	C	CGGATACAGCAGCC	CGGATACCGCAGC C	CAACTTCCTGTCCAGCGGAT	0,0	CAATCTCCAGCTCCCACAG G
One_2.167 66-45	A	G	CTCCCCGATGCTTA	CTCCCCGGTGCTTA	GCCTCGATAAAGCCTGGGTC	0,0	TCCGGCAGTTCTCGATTTA CA
One_2.200 11-31	A	G	TTTCGGAAGACGCA	TTTCGGAGGACGCA	TCACGCCGGTCACGTTTC	0,0	GGGAGAGGCAAAGGTCAA GT
One_2.201 30-27	A	T	TGTGCTAAATACAA	TGTGCTATATACAA	TGCAGGCTTTACTCTCTTGGT	0,0	GGCATTAAAGAGAGGCGAG GT
One_2.213 62-59	A	C	ATAGATTACAAAAA	ATAGATTCCAAAA A	GCAGGGACACACACACACTA	0,0	TCTTCCCTTGTGTACTCTTC TTT
One_2.214 98-40	A	C	AACATTTAAGCAAG	AACATTTTCAGCAAG	TCAGAGGTATGGCCAGCCTA	0,0	AGCGCACAGATCTGGGAA TT

One_2.217 35-50	C	T	GGAGGCTCGTGTTA	GGAGGCTTGTGTTA	TGCAGGAGAGAGGGTCTTTA	0,0	TCCTCTGAATCAGTATCTC TCCT
One_2.219 90-53	A	T	TACTCTTACCAACA	TACTCTTTCCAACA	GAAGTCGATGTGTTGCAGCA	0,0	TGCAAATTTTCGCATGAATT GATTT
One_2.232 30-33	G	T	GTTCTCAGGTGCAT	GTTCTCATGTGCAT	GGTGTAATCCAAAAACAGCC CT	0,0	TCAGAGATGTGTCCTGATA TACAGT
One_2.244 34-33	A	C	TATAGAGAGAGAGA	TATAGAGCGAGAG A	AGACTCTCTCCCTTCTGCAGT	0,0	TCAGTTCTTAAGTTCTGTG AGGT
One_2.247 95-33	C	T	CAGCTAACTGGGTC	CAGCTAATTGGGTC	ACAGTCAATCAAGCTGCAGC	0,0	GCTCTGGTAAGATGGGGCA G
One_2.274 13-63	G	T	TTAATATGGAGAAA	TTAATATTGAGAAA	TCCTTTGAACATCACTTAATT GACA	0,0	TCCCTAAAGCAAAGTGACT ATGC
One_2.279 4-52	A	G	AAGTGGCACAGTTA	AAGTGGCGCAGTT A	ACGACCTTTCCTCAAGTGGC	0,0	GGCCAGCCAACAGAGAGT T
One_2.283 76-51	G	T	TGTGCATGGGCAGT	TGTGCATTGGCAGT	CTGTGATACCCGATACCCGC	0,0	AGAGAAACAAGAGAGAAA CTGCC
One_2.289 55-38	C	T	CCGCTCTCGGGCAC	CCGCTCTTGGGCAC	ATCAGCACTCGCCGCTC	0,0	CCCATGTATTTGGTTTGAC GGA
One_2.290 37-65	A	G	TGTTCCCTAAGCCCG	TGTTCCCTGAGCCCG	TCTCCTCCTGCAGAGTGTGA	0,0	GTCCGGGGAGACACATGA AT
One_2.307 61-49	G	T	ATTGTGGGTTTTTCC	ATTGTGGTTTTTTCC	ACCTTGGACAGCTGCTGAAA	0,0	CCTGGTGAGGACAACAAG CA
One_2.328 04-64	A	T	GGATATAATAAACA	GGATATATTAAACA	TCGGATTTGGGAGTGTGTGG	0,0	GGATGGATCGGATGGCAT GT
One_2.343 98-57	C	G	ACCATCTCGGTCAG	ACCATCTGGGTCAG	GCTCCTTAATCTTGACCCCCA	0,0	CTTGCGGGTGATAGAGACG G
One_2.349 43-66	A	C	TTTACATATTTTAA	TTTACATCTTTTAA	TGGTTAGATCCTAGGATAAT GCAAC	0,0	TGTCTTAAACCTGGACCCC A
One_2.353 96-68	A	G	TCATGGAATCACAC	TCATGGAGTCACAC	GTGAGAGTGGAGCTGTAGGC	0,0	GGGGAAGTGTGTCTGTGTG A
One_2.380 70-37	A	G	ATATTCCAATAGTT	ATATTCCGATAGTT	GCAGGGAATGTTGTAGAAAC ACA	0,0	CTGCGAGACTGCTCACAAC T
One_2.388 69-26	A	G	TGTTAAGACAAAGG	TGTTAAGGCAAAG G	GGACAGTCCTGAGGGTGTTA	0,0	TCTCCTCTCCAGAGCAGA C

One_2.392 54-69	A	T	AGAACACACTCTCT	AGAACACTCTCTCT	GGTTCCTGGAGCTACATCG	0,0	TGACAAAGAGGAGGTGGC TC
One_2.397 27-26	C	T	CGGGGAACATGGTG	CGGGGAATATGGT G	AGGTAGTGTGAATAGACGGG GA	0,0	CACCACCCATGATCCCAGT G
One_2.409 76-37	A	G	GCCATGTACACTTC	GCCATGTGCACTTC	CATGTTGTTGTCAGCACGGG	0,0	CCCCACTTCTCTGCCAGTT G
One_2.411 28-67	C	T	TGAATAGCGTCTCT	TGAATAGTGTCTCT	AGTGGCTGCCTTTGTTCCCTT	0,0	TCAGTCAGCTGCACAGAGA C
One_2.412 31-65	C	T	CAAGCTACTGAGGC	CAAGCTATTGAGGC	TCAACCTGAGTTTCCTGAGG C	0,0	GGATGCGGATGGTATAGCC C
One_2.413 71-35	G	T	CCCTTCAGGTTTCAT	CCCTTCATGTTTCAT	GGATGTTATCCTTAGAGTAT CCCTT	0,0	ATCATTTTCCTGCTGGGCC A
One_2.441 03-35	A	G	GAGAGTAAACATG	GAGAGTAGAAAAT G	GGAGGAAGGAGAGGATGGG A	0,0	GGGCTTCTTTCCCTTGATGTT GA
One_2.453 96-65	A	T	CCCCCACATGTATA	CCCCCACTTGTATA	AGTTCAAGGAGAAAACCCCC	0,0	AGTGTTTGAGGACTTCACT GT
One_2.454 75-58	A	C	GCAGGGTAACGCCA	GCAGGGTCACGCC A	ACAAGGTGTTGTGCAGGGT	0,0	AGACCTCTGCATCACGGTT G
One_2.457 76-68	A	G	CGGAGACATCCTAG	CGGAGACGTCCTA G	ATTGTGCAGGTAGACGCCTC	0,0	AGAGAATAGGCCTCTCCGC T
One_2.458 77-55	A	G	AGTATTTATATGTC	AGTATTTGTATGTC	TCCCAATAATCGCCAACCGT	0,0	GAGTGGAGCCCAGCAACA AT
One_2.459 57-54	C	T	GGTATATCGC	GGTATATTGC	CGTTGTGTCGGAATCTTCTTC T	0,0	TTTCCATCCCGCACAGTAG G
One_2.460 12-53	C	G	CCTACTTCGAACAG	CCTACTTGGAACAG	GTCTCCAGAGGGTTGTGCAT	0,0	GCTCAGCTGACAGACAGG AG
One_2.461 52-39	G	T	GTGCCCTGGTTCCC	GTGCCCTTGTTC	TTTTGTGCTGAGCAAGGTGC	0,0	GACCCATGCATCCATCTGC T
One_2.486 09-47	A	G	GGTCCTCATGTGAG	GGTCCTCGTGTGAG	AGTTAGGCAAACCACACCGG	0,0	AAGGTGGCCAATAGCAAG AC
One_2.486 37-56	A	C	TTGATTAAGGACAG	TTGATTACGGACAG	GCTTTTTGCAGTGCGATGTC	0,0	TTGTCAAGATGGGGAGAG GC
One_2.489 52-59	A	C	GACTGTGAGGCCGT	GACTGTGCTGCCGT	AAGAGCACCAGACAAGCCTG	0,0	CTACAGCCCTAGCATAACGG C

One_2.511 43-68	G	T	AGGGCTGGATTCAA	AGGGCTGTATTCAA	TGCAGAAGGACTTAGGGCTG	0,0	GCTCAATCGAAAATCACCT TCA
One_2.511 90-49	A	G	TTCTATCACCTCAA	TTCTATCGCCTCAA	AGCACCTAACCTGTAAATAC CT	0,0	AGGTGTTTCTAATGTTTTG TACACT
One_2.522 03-44	G	T	CCAATTTGGTTGTT	CCAATTTTGTGTT	GCAGGTACAGTGAGCTCCAG	0,0	TGTCCTTGTATCATTACAG AGCCA
One_2.523 94-28	C	G	TCCCATACAGCACC	TCCCATAGAGCACC	GAGACAGGCTGCGTCCCATA	0,0	CCCTGGTCAGAAGATGTGC A
One_2.533 8-43	G	T	GAAGTTAGTGCAGT	GAAGTTATTGCAGT	ACCACAGTACGTAGCTATGA AGT	0,0	ACATTTCTGAAGCCATTA CTGC
One_2.537 15-43	G	T	AGCTGGTGGCCAAA	AGCTGGTTGCCAAA	AGCTTCTTTCACAGGCAGCT	0,0	TGGTCCATCTCTTAACCCC T
One_2.543 44-58	A	G	TGGACGAATGTATG	TGGACGAGTGTATG	CTCCCACCAATGGCGTGAT	0,2	AAACAAACTGCATGGCGCT C
One_2.565 4-67	C	G	GCACTTACTCAAAA	GCACTTAGTCAAAA	GGATGTGCCTGAGACCTACC	0,0	AGGGATTGATGATTCATTG ATTTGT
One_2.574 4-26	A	C	ATCATAAAAAAAAAA	ATCATAACAAAAA A	GGACGGAGGCTGGGATCATA	0,0	GTCCCTCATGTCGTGATGT GT
One_2.582 00-50	A	T	TCAAAAAACATGTT	TCAAAAATCATGTT	TCTGTGGGGTATAGAGATAC GGT	0,0	TAACCCCCGCTGTACCAAA C
One_2.588 80-45	G	T	TTGAGACGCTCATC	TTGAGACTCTCATC	GGACAGCCTGGTGTTTGAGA	0,0	AGCAGGCTGATGTAGTGCT G
One_2.598 97-41	C	T	CCACCGTCAGGGTG	CCACCGTTAGGGTG	CGGAGTTTTCCCTGGCACA	0,0	GCACCACCCTAGACTGAAC A
One_2.622 40-45	C	G	TGTTTGCCTCTTTT	TGTTTGCCTCTTTT	TGGAGAGGTATTGGTTTCAA GGT	0,0	GCTACTAAATAACTCTCCA TCAGTG
One_2.624 8-65	A	T	TCTCATTAGAAGGG	TCTCATTTGAAGGG	GGGAAAGAGGGAGGAGCCT A	0,0	ACTCAACCATGCCTCCTTG C
One_2.634 02-51	C	G	CCATTAGCAGTTTG	CCATTAGGAGTTTG	CCAGAGCCAAAGCCAGGTAG	0,0	GATCCCAGACCTGTCAGTG C
One_2.637 62-51	A	G	TCATTTAATGGACT	TCATTTAGTGGACT	TGTGCCTGTTGCTGCTGATA	0,0	GGAATATTCCCCCTATGCT TTTGT
One_2.639 84-53	A	G	AGCTCACAGATCCA	AGCTCACGGATCCA	GTCACAGACATACAGGAGCT CA	0,0	TCCACGTAACAACAGGCCT G

One_2.641 50-27	A	G	AATAAAAAACAGTCA	AATAAAAGCAGTC A	TGCAGGAGAGAGGAGGAAT GA	0,0	CCACAGGTCCTGGAGGTGT A
One_2.652 9-40	C	G	TCACCGTCTGTGAC	TCACCGTGTGTGAC	CAGGGTGGCCTCCACAAC	0,0	CCACCCTGGAGCAGTCAC
One_2.653 69-59	A	G	AATAACAA.GAGCA	AATAACAG.GAGCA	GCAGGGGACACAACAACAA C	0,0	AGCTTTGCTTGTTGTTGCTC
One_2.659 98-48	G	T	CAGAGCCGCTGCGC	CAGAGCCTCTGCGC	CAGGCTCTCACACTCCTTGG	0,0	GCATGCACTTTTCACGCTG A
One_2.664 68-68	A	G	TGTATCCAAACATG	TGTATCCGAACATG	TGCTTGTGCCTCGCATCAA	0,0	TGAGGACACTTTATGGATT CTCC
One_2.707 11-39	C	T	AGGTGCTCGTGCGT	AGGTGCTTGTGCGT	TGCCCTGTTGTGATGAGCAT	0,0	GGCTGTGTAGAACGACCCC
One_2.710 25-65	A	C	ATTACCCAGTGTGT	ATTACCCCGTGTGT	TATGAATTCCCTCCCGCAGCC	0,0	TTATGGATGAGCTGGGAGG C
One_2.715 12-50	C	T	TTTGATTCAATCCA	TTTGATTTATTCCA	ACCTTTCTCATTTGTGGATTT GAT	0,0	CTGCCAAGTCGATGTTCAA ACA
One_2.721 82-45	G	T	GCCATGTGGTGAAG	GCCATGTTGTGAAG	TCTTGATTAGTGTCCAGCCAT GT	0,0	TGTGTCGCTCTGTTCTGGA C
One_2.732 81-30	A	G	TCTGTCCACATTCTG	TCTGTCCGCATTCTG	GCAGGTGACAAAGTCTCTAC A	0,0	CCACTGTACATAAACCATG CAGA
One_2.734 87-56	A	G	AGCGCACATACTGC	AGCGCACGTACTGC	CTGTTCCACACCCCTCCATC	0,0	GTTCTGTGTCATGTCCCACCC C
One_2.749 98-68	A	G	ATTGTTGAGGTGCT	ATTGTTGGGGTGCT	TGCAGGGACACAAGGAGAG A	0,0	CCTGCAGTGTTCAAAGCAC C
One_2.755 86-34	A	G	AAATTAAACTGAGG	AAATTAAGCTGAG G	TCGTCTAAGACCTGTCACCC A	0,0	TGTGTTTTTTCCCCACAAAA GTGA
One_2.756 17-47	C	T	ACCTGCTCATGGTC	ACCTGCTTATGGTC	GAGAGTACCGGGCAGACAA G	0,0	TGGTGGTGCTCTTCCCATA C
One_2.758 47-69	A	C	TTCCCTAAAACACT	TTCCCTACAACACT	GCCCCCAGGATCATGTTGTA	0,0	AGAAACTATTCTGGGTGCT GCA
One_2.763 28-30	C	T	GCTGAGCCCTGTGA	GCTGAGCTCTGTGA	TGCACACCATACTCCTGCTG	0,0	AAGAACGTCCAGAACACG CT
One_2.765 32-58	C	G	GGAAATGCTTTTAC	GGAAATGGTTTAC	TGCAGAATACCAATTCATAC ATTCA	0,0	CTCTCGCCCCCTTTACTGT G

One_2.771 64-35	A	C	AGGCATCAGCCCTG	AGGCATCCGCCCTG	AGGGGGACCATTCCAGACTA	0,0	AATGAGGAGAAGCTTGGC CC
One_2.781 98-36	C	T	CTGTCAGCGTTGAT	CTGTCAGTGTTGAT	TGTACTACACATTCCCTGTCA G	0,0	CGCTCCCAGAACAAACCTC T
One_2.801 77-55	C	T	CGATTGACCAAACG	CGATTGATCAAACG	CTTACGGGATCGGTGACCC	0,0	ACTTACAACCTCATGCTAA TCACA
One_2.805 25-35	A	G	TGTTAGAACGCAAT	TGTTAGAGCGCAAT	CCTGCCACAAGGGGTTGTTA	0,0	GTTTGGCCCCGCCTTTACTT G
One_2.815 73-50	C	G	AGAAGAGCAAAGAG	AGAAGAGGAAAGA G	CCTGCACACCTGAGGAGAAG	0,0	AATAGTTCCAGTCCTTACA TTCTCT
One_2.840 41-67	C	T	CCTGGGCCGACCAC	CCTGGGCTGACCAC	CCTGGCCTACTCTGTGTACG	0,0	GCTCTGCTGGTCCTCGTG
One_2.852 2-64	A	G	ATGTAAGATAATCT	ATGTAAGGTAATCT	ACCAGACCTTCCCGAGATCA	0,0	TGAGCTGTGTGACATTATC CACA
One_2.853 40-30	A	G	GCTTCACAAGGGAC	GCTTCACGAGGGA C	GCTGAAGGAGCCGTCGG	0,0	CTGGCTGACCCCATGACAT T
One_2.868 89-62	A	T	CCAACATATGTGTT	CCAACATTTGTGTT	AACACAAGTCCATCTCCAAC A	0,0	AGACAACACAGGAAGCAG CC
One_2.868 98-35	A	C	AAAGGAGATCCTTC	AAAGGAGCTCCTTC	GGCGGTCACTGAGTCTAAGG	0,0	TGGTTTTTGGGGTTCATGT TGA
One_2.872 40-34	A	C	TCCTGGGATTCTGT	TCCTGGGCTTCTGT	TGCAGGACAGGGAGCATG	0,0	CATCACGTACAGGTCCCCA C
One_2.903 71-33	A	C	GTAACCTAATTTAC	GTAACCTCATTTAC	GCAGGTGCAGAATCATTTAA CCT	0,0	GGAAGGAGTACAGAAGGT GTCG
One_2.905 29-63	A	G	AATCAACAATGCTA	AATCAACGATGCTA	CAGGATCAGAAGGGGAGCA A	0,0	GTGAGCACACGGTAATTAG CA
One_2.984 0-29	A	T	CGTATCAATATCAA	CGTATCATTATCAA	GGGCTAAGAACAGATTTGCG T	0,0	AAACAATGTTAACCTCGAGG TTTGA
One_3RFP. 12866-45	A	C	GCTTCTCATGCTGC	GCTTCTCCTGCTGC	GAGCTTTGTGATTGGGGGAG A	1,8,0	TCTGACCAATCGCAGAGCA G
One_3RFP. 18602-33	A	G	CTATCACAAGCAGC	CTATCACGAGCAGC	TCATCTGTGCATGTGCTATCA C	0,0	TTACTCGTGCCAAAGAGCG A

One_3RFP. 19596-43	A	T	CACTATGACTAGCT	CACTATGTCTAGCT	AGGCCTTCGACTGCTCTCTA	0,0	GATGTTGCTGCTGTGCTTC G
One_3RFP. 22492-53	A	C	AATAACTAATCTAC	AATAACTCATCTAC	GCAGGAGCCCAAGGTGAG	0,0	TCTGTTTTGAGGACATTCA GTTGT
One_3RFP. 22594-56	A	G	GCCGAGCATGAAAT	GCCGAGCGTGAAA T	ATAGAGACCCGACGTTGGCT	0,0	CTTGCCCTAAGCAGAGAG C
One_3RFP. 22665-32	A	G	AGTTAGAACCCTCT	AGTTAGAGCCCTCT	TGCAGGAGGTTTTAGGAGAG G	0,2	GAGTTGGAGTGGTTCCCAG T
One_3RFP. 25184-65	A	G	CATCGCCACTTTGT	CATCGCCGCTTTGT	GCAGGTCGACGCTTTTTAAA G	0,0	TCCCTCAGCTGTTTACCAA AC
One_3RFP. 25749-53	A	G	GCACAGCATTGAGA	GCACAGCGTTGAG A	GCCACCACATTAGGGAGGAG	0,0	GCCCCATTGCAGGTAATCT C
One_3RFP. 26492-46	A	C	ATAACTAAATAATG	ATAACTACATAATG	GCAGGACAAGGTACGAGAC A	0,0	ACCATGTTTTGACATGCTG AGA
One_3RFP. 27065-48	A	T	ACTGAGGAGTATGT	ACTGAGGTGTATGT	GTCACCTGGACAGTTGATGG A	0,0	GCCAATCAGAATGTTTTTC CCCA
One_3RFP. 28357-29	C	T	GCTCCAAGTGTCTT	GCTCCAATTGTCTT	CAGGCCTGGGTAGCTCCA	0,0	GAGAGAGAGGGGAGGCGA TA
One_3RFP. 36741-50	A	T	ATAGCCAAGATCCT	ATAGCCATGATCCT	TGTGTACACAGATATGCATG AGA	0,0	AAACAATCTGCCAGTCGCC T
One_3RFP. 38229-53	A	G	TAAACACACTCGTG	TAAACACGCTCGTG	GCAGGCCAACCACATCAAAG	0,0	GCGGTGTGCGTGTGTAC

One_3RFP. 39193-43	C	T	GAGGATGCTCCTCC	GAGGATGTTCTCC	AGAGTCTGTTTCCCTGAGGG	0,0	ACCTTTCTATTTCAGTGTG GAGGA
One_3RFP. 40708-40	A	C	AACTCCAGTGGCT	AACTCCCGTGGCT	TGTTAACACACTTCTTCACAC TCC	0,0	CCTTCCATCCTTGCTGCAG A
One_3RFP. 43935-63	C	T	AACACATCGGTTAC	AACACATTGGTTAC	CACACCTCCTCCTTAGCCAC	0,0	ATGCAATGGCCCAGTGTGA T
One_3RFP. 46202-49	A	C	CGTTAGTAGTTTTT	CGTTAGTCGTTTTT	GGGACGGGTGAGTAAGGTG A	0,0	CAGGCAGGAATGTACAAG CG
One_3RFP. 46608-58	G	T	CCTTCATGAACTGT	CCTTCATTAAGTGT	TGGTGCATGAACACTGAGCT	0,0	TTCCGGATTGCTCTCACAC C
One_3RFP. 47148-54	A	G	CATGAATAGAAGGG	CATGAATGGAAGG G	GCCTTCCTCAGCGATGACTC	0,1.1	ACCGGTAGCTACACAATTC CC
One_3RFP. 50303-37	C	T	TCTCTGGCCTGCAA	TCTCTGGTCTGCAA	GCTTCAGCTCTCCCACAACA	0,0	GGCACCTGCAAAGATCTCC A
One_3RFP. 52579-51	A	G	ATTATTAAC.TAAC	ATTATTAGC.TAAC	CACCTTGCTCTCTGCCTGTA	0,2.1	TCTGCTCCTCCATGGTAGC T
One_3RFP. 53804-31	A	G	ACGGATAAGGGGCA	ACGGATAGGGGGC A	GGTACTTCTTCTCCTGGACG G	0,0	GACCTTGGTGTGCGTCTCA A
One_3RFP. 53932-47	C	T	AACTAACCCATCAT	AACTAACTCATCAT	TGTTGCCAAGTTGACTAAAG AACT	0,0	ACAGTGGATTATCTACCAA CAGTAC
One_3RFP. 56125-30	C	T	CAATTGTCTTATAT	CAATTGTTTTATAT	TGCAGGAGTTAACAGGAAGT CA	0,0	AGCCAATGTGTACTAGTGC CA

One_3RFP. 60219-36	C	T	ATTGTTTCTCCGA	ATTGTTTCTCCGA	TGACCTTGGTTGTCAGGTGA	0,0	CTTAAGCCGGAAGCCAGCT
One_3RFP. 60536-30	C	G	GTGGTTTCATTTGG	GTGGTTTGATTTGG	CTGAATTTGGCCTGGGGGT	0,0	TGTTTTTGCTCAAACCTGG GGG
One_3RFP. 62278-33	C	G	CCTCAATCCCATGG	CCTCAATGCCATGG	CACCACCGCTGTCCTCAAT	0,0	TTCTCCTCCCTGTTTCCCCC
One_3RFP. 6937-57	A	G	TTGCAAAATCCAAC	TTGCAAAGTCCAAC	TGGTTTACAGATGCATTGCA AA	0,0	ATGGTTTTAAGAGCTGGTT TGG
One_3RFP. 70374-61	A	T	GCTCATGATTGGCT	GCTCATGTTTGGCT	GGGACTGATCATCACGGCTC	0,0	TCTTCAGCTTGTGGTGGAC C
One_3RFP. 70898-49	C	G	CTTATATCGTTTTT	CTTATATGGTTTTT	GCACCTTCGGCAATGTGAC	0,0	ACCTGGAGAACCTGACCAT TC
One_3RFP. 70952-46	A	G	TACATGGATGTAA	TACATGGGTGTAA	GTAAGCTTTGCAGGCCTTCA	0,0	TGCGAACCTGGAACATTTG T
One_3RFP. 71744-45	C	T	TGT.TGGCCGGCAG	TGT.TGGTCGGCAG	AGGCAACCAGAGTTCAGCTC	0,0	CACGGCCTGCTCTTCCTC
One_3RFP. 72056-60	A	C	TTTAAATAATACTG	TTTAAATCATACTG	TCAGCCAACGCCTTGATCTT	0,0	ACCCAAAGGACATCTAACC AGA
One_3RFP. 72689-27	A	C	ACAGTGGAGACTAC	ACAGTGGCGACTA C	GCCACCCGAAGAAGAACAGT	1.75,0	CCTGTGAATCGTGGGTGAG T
One_3RFP. 74551-60	A	C	AACAACAAAACAC	AACAACACAAACA C	ACGGTCCTCTCAGTTCCTCT	0,0	GCCAAGATATCCAGTTCCA GT
One_3RFP. 7464-69	A	G	CCACAGGATTTCTC	CCACAGGGTTTCTC	TGCTGAGTACACACGTCACT	0,0	TGGCAGAATTTAACCCTG TTTT

One_3RFP. 76568-44	A	T	CCCTAGTACTTCTC	CCCTAGTTCTTCTC	GAACCTTCGCCCAGAGCTC	0,0	TTGGGGGCTGGAACAAAC AG
One_3RFP. 77278-58	A	T	CAACAAAAATGGAA	CAACAAATATGGA A	TTTCCAGCCCCAGAGTTGAG	0,0	CCATCACATCGGCACAAAG C
One_3RFP. 80015-44	A	C	TAAAAATATAGGAT	TAAAAATCTAGGAT	TGCAGGGACAGGGGATTAAA	0,0	GTGGTGTCTCTCTGGTCGT G
One_3RFP. 80215-59	A	C	TTTCCGGAGTCCAT	TTTCCGGCGTCCAT	ACTATGCAGCTAAACGCCCT	0,0	ACAGCCTGGATGGGATTTTC C
One_3RFP. 81817-50	G	T	TGCTTTGGGCACCT	TGCTTTGTGCACCT	ATCCGGCCCAAGATGCTTTG	0,0	CAACAAGGACAGGTGCCT CT
One_3RFP. 83488-50	A	C	CTCACTTAATTTTG	CTCACTTCATTTTG	AGGATTTTAGGGCTTGACCA G	0,0	GTGTTCTTTTCTTCTCAGGA AGGC
One_3RFP. 89355-44	C	G	TCTGGGACGCGGTC	TCTGGGAGGCGGTC	TCTATCTTCTCCATGTTCTGG GA	0,2	AGTCAGGGAGCATGCAGA AC
One_4a.12 382-55	A	T	CTACGCCAGAGCAG	CTACGCCTGAGCAG	GGTGCAAAGGGAGTCAAATG T	0,0	AGTGCACCCACACAACCAT A
One_4a.13 104-68	C	G	CTCCCCTCTGACAT	CTCCCCTGTGACAT	AACCGAAAAGTGTCTCTCCCC	0,0	ATCCACTTTCCACAGCTGG A
One_4a.14 909-37	A	T	TTATAACACTTCCT	TTATAACTCTTCCT	GCAGGACTGTCACAGCTTCT	0,0	AATGCAGTCCCAGGTGCG
One_4a.19 795-33	G	T	CACGCGGGAATCTG	CACGCGGTAATCTG	TGAATGGTTTGTACACGCG G	0,0	TGCAACAGAGGTGGTTTGG T
One_4a.21 799-29	A	G	GGTGGGGAAGCTCT	GGTGGGGGAGCTC T	GTGTGCGTCGCCTGGAG	0,0	GCTGTGAAGTAAACCAGC GC
One_4a.22 514-58	A	G	TTGTGTTATCCTCG	TTGTGTTGTCCTCG	CCACTGTAGTGTCTGTGT	0,0	GGTGACGCCTCCACATACA A
One_4a.24 016-53	C	T	GTTCTTCAAGATG	GTTCTTTAAGATG	AGCAGCACACTAGCATGAGC	0,0	TTGCAACCAGGAAATGACC A

One_4a.25 035-26	G	T	GGCTACAGATGTAC	GGCTACATATGTAC	TGCAGGAGCCCATAGGAATG	0,0	AGTTCTCCTGCAACATGGT GA
One_4a.25 174-68	C	T	AAGGGGGCGGCAGG	AAGGGGGTGGCAG G	GCACCTCCCGTGAACTTGAT	0,0	CACCGCTCTAACCACTAGG C
One_4a.28 062-27	A	G	CTTACTGATCAACT	CTTACTGGTCAACT	GCAGGAGGAGATCTCTGACC	0,0	GCTTTTCCCTCCCTCACCA A
One_4a.32 159-43	A	G	CACCCACAGGCCAA	CACCCACGGGCCA A	TGCAGGACTTTTTGCCACAT	0,0	GACCACTGCATCACTCAGG A
One_4a.32 895-28	A	G	ATAGCTTATGGGAC	ATAGCTTGTGGGAC	TGCAGGAAAAGCTAGACTAG AAT	0,0	AGCTTGCGTCCCTTGGAAT A
One_4a.32 932-27	A	C	GACTGATAGACCTG	GACTGATCGACCTG	TGCAGGTTAGTCACTTGATA GACT	0,0	TCTGTCAAGAGACTAACCT ACAGG
One_4a.40 410-31	A	C	ATTCATTAATATTT	ATTCATTCATATTT	TGCAGGACAACAGAGGATG G	0,0	AGCCTTCACACTGCACCTT T
One_4a.41 625-38	C	G	CACTTAACACACAA	CACTTAAGACACA A	TGCAGGCATCAAAGGGGAC	0,0	CCCTGATCACTGTGTCTGT GA
One_4a.43 537-65	A	T	TTAAAAGACTTAAC	TTAAAAGTCTTAAC	ACGCAGCACACAGATGGTTA	0,0	TGTGTAACCATCTCCTTGC TGT
One_4a.44 564-40	G	T	GCTGAGAGGGCAGT	GCTGAGATGGCAG T	TGCAGGAGTGAAAATAGATT CGT	0,0	TCTAGGTAGCCTATGTGTT CAACA
One_4a.46 542-38	C	T	ACATATCCCTCTAC	ACATATCTCTCTAC	GCAGGTGGCAGATAATTGTA GT	0,0	CCTATTACCCCTGGTTGGC A
One_4a.47 407-42	C	T	CCAACAACGCACAC	CCAACAATGCACA C	AGGAACATGGTGCATCCTGG	0,0	ACTGTGTGTGTGTGCGTAC A
One_4a.47 733-44	A	C	ACCTCCAAACTCCT	ACCTCCACACTCCT	CTGACCACCCTCCTCAAACC	0,0	GGTATGTTCAGGGCCCTGT C
One_4a.50 42-49	C	T	GAAGCATCGGGGAT	GAAGCATTGGGGA T	GGGGCAAGGGAAAAAGAGG A	1,3,0	TTGCCCCTCAACATTTC T
One_4a.51 425-41	C	T	GAACGAGCTGCGTG	GAACGAGTTGCGT G	GATGAACACGGCGCTGAAC	0,0	AGGGTGTCCAGCACAAACAT C
One_4a.52 596-64	A	G	C.TTCAGACTTCGG	C.TTCAGGCTTCGG	TGCAGGGAACAAAGGTGTGA	0,0	GCCTTACTCGGCCCCGAAG
One_4a.53 531-43	A	G	CCGTGACACTTATT	CCGTGACGCTTATT	TGCACTGCAGAGGAGGGG	0,0	AGAGACGATAGCAGCAAC ATT

One_4a.58 187-48	A	T	AGGTCAAATTCCTG	AGGTCAATTTCTG	TATCTGGGCCTGGAGGAGAG	0,0	AGATGGCTCAGCTGAAGC AA
One_4a.59 326-51	A	C	CAATACAATGGGTA	CAATACACTGGGTA	GCAGGACATAAACTGGGCCT	0,0	GCCTGTGTATGCCCTACCC
One_4a.63 494-55	C	G	TGTCCAGCGTCACA	TGTCCAGGGTCACA	GCGTCACTGCTTTGCTGTTT	0,0	TCCCTCTCCCAGAATGCAG A
One_4a.63 914-64	G	T	GGCTACTGATAAAG	GGCTACTTATAAAG	CACTGTTGAGAGCCGTCCT	0,0	TGGGACTAAGTTAAGAGA GTGTGT
One_4a.65 66-43	G	T	TGTAACAGGACAAA	TGTAACATGACAA A	TGCAGGTGTCTCAGAGGGAT	0,0	CCATACCCCTACCCCTTA TCA
One_4a.67 550-44	C	T	AGATAGACCTGCAA	AGATAGATCTGCA A	GTGAAGAGCTCTGCCTCCAG	0,0	GCCTGAGGTCTCGTACGAT G
One_4a.71 19-57	A	C	TCAGAAAAAGTGAC	TCAGAAACAGTGA C	TGCAGGGTAAGTTTGAATCA AAA	0,0	CCCCCAGACCATAAAGCCA C
One_4a.84 616-28	A	T	AGTATCAAGTCCTC	AGTATCATGTCCTC	TGCAGGACGGAATACAGAGT	0,1.3	AGGCAGGAGGACATGATA CT
One_4a.94 96-33	A	C	GATTGTCAGAGCTA	GATTGTCCGAGCTA	TGCAGGAGAAGCTTAGCAGG	0,0	GCTGAAGAACATGCTTGGC C
One_ACBP -79	G	A	CAGAGGTCATGGTTC TA	CAGAGGTCATAGTT CTA	GAGGTGTGGGCTGACCA	0,0	TCGACCGCTGGCAGTG
One_agt- 132	A	C	ACAGGAAAATCACG AGCCT	CAGGAAAATCCCG AGCCT	GACCCAGATCAACAACCTTCA TCCA	0,0	TGGTTGAGCTAAGGTCCTT GAAC
One_aldB- 152	A	G	CTCAGGCATTACCTT C	CAGGCATCACCTTC	CGATCAGGTGACGCTAAAAT TAACTC	0,0	GTGGCTTCCTCTTCACTCT GA
One_apoe- 83	C	T	TTTAGACGGCGGTCT C	ATTTAGACAGCGGT CTC	CGCCATGGACAAGGTCAAG	0,0	GGCACAGTGCTTCCAAACC
One_CD9- 269	C	T	TGGAATGGAGAAATC	ATGGAATGAAGAA ATC	ACGCTCTGAGGTGATATGAA ACAC	0,0	CATCCGACGTCAACATCCA AAC
One_cetn1- 167	A	C	TTGACGAAGCAGACC GA	TTGACGAAGCCGA CCGA	CAGAAATCCTGACTGTAAAA ACAATGCA	0,0	CTGCTCGTTGATCTCTCCA TCTC
One_CFP1	C	T	TGCAGTTCAACATCA A	CTGCAGTTCAATAT CAA	CGCAGGTCAAAGTAGTACTT AGCAT	0,0	GAGCGTCACTTCCTGGAAC TT
One_cin- 177	C	T	TCACGCACGGGACAG	CACGCACGGAACA G	CCTCAGACTAGTGACCGTAC CTA	0,0	CGCTCACCGTGGTTACGT

One_dds-529	A	G	AGCAATCCCATCTCTC	AGCAACCCCATCTCTC	CATAATGCTCCCCATCTTGAATTGG	0,0	CACTCAGCCCTTTAGGGAA GA
One_DDX5-86	C	T	AGGACTTCCTGAAGGAC	AGGACTTCCTAAAGGAC	CTCCCACATTGATCTGGACGTA	0,0	TGCCACTTGGCCCAAAGAG
One_E2-65	C	T	CATTGTCCCTAGGAAAG	ATTGTCCCTAGAAAAG	GTGGCACCCCTTTCTCT	0,0	TGCAAACCTCAGTGGAGAAC
One_gdh-212	C	A	ATCTGTTACCAGAATGTTT	ATCTGTTACCATAATGTTT	CCTGTGTTGAAGTGGAGTAGGTTAA	0,0	GCTTTATACTGTAAGTGGA CTGACCTT
One_GHII-2165	T	A	CACAAATGGAAATTGA	CACAAATGGTAATTGA	GGCATCAACCTGCTCATCGA	0,0	TGCACAAAGTGCGGCAC
One_ghsR-66	A	T	AGGTTAAGCTGTGTA TAAGT	TTAAGCTGTGAATAAGT	TGTAACAATACAAGGATAATGCAAATAATGTAGGT	0,0	GGTTATTAGGTTACTGTGCTGACTGT
One_GPDH-201	T	C	CTTCACCCCTGGAGCC	CACCCCGGAGCC	GAAGCTGATCCTAGACCTGTACCTA	0,0	TGGTATGATGGTGCTACTGGAAGT
One_GTHa	A	G	CAAGAACTAGAAATGAAACAGA	AAGAACTAGAAATGGAACAGA	CAAGAAGAATCAAGAGAAA GAGAGATGGT	0,0	CCTAGTGTCATGCACATAACGTGTA
One_HGF A-49	A	T	CTAAAGCACCATGTTGC	ACTAAAGCACCTTGTGTC	ACTTGCTACTTCAGGGTTTTTGTGA	0,0	TGGCAGAACAATTCTCTCAATGCATA
One_HpaI-99	C	T	AACGGAAGAAACCCCTCAA	AACGGAAGAAACTCCTCAA	CCTGAGTTGTGTTCAATGGGCATAA	0,0	TGGGTCATGTTCAATTAGAGCACAAA
One_hsc71-220	C	A	ATTGGCCACAGCGC	ATTGGCAACAGCGC	ACAGCGAAACTATTGATTTAAGGCTCAT	2,0	CGCAGGTAAATCACTGATCATGTTT
One_Hsp47	A	G	TTATTGACTATGGCA CATTG	TTGACTATGGCGCA TTG	CGTTCAAATAAATGCTGTTTGGCCTTT	0,0	GTGGTGTTCCGATTTTTTCC TGAAA
One_IL8r-362	C	T	CAGCCAAAGAAGAGTC	AGCCAAAAAAGAGTC	TTGCTAGAAGCGTTGGTTATGATGA	0,0	CAGCAAAATTGAGAAGTC ACTAGGAAAA
One_ins-107	C	T	TACAGTAGTCCATAC AACATA	ATACAGTAGTTCATACAACATAT	TTGAAATGAATGTGAAGGCA	0,0	GAACCCTGCAAGAGGAGAA
One_KCT1-453	G	T	TGGTCAGGGTATCGC CATA	TGGTCAGGGTATCTCCATA	GGGAAAGTATGCTGTGGGATCAG	0,0	GGTTCCTCAGTGAGTGTTCTCTATG

One_KPN A-422	A	G	CTGGTATGAGAAGGC ACA	TGGTATGAGGAGG CACA	TGGGCCCTGGGAAACATC	0,0	CCATAGCCACTTTTCGATAC AGGTAA
One_LEI- 87	A	G	ACTCGCCACCTCTGT	TCGCCGCCTCTGT	ACAGCGCATCCCCATAATGG	0,0	GCCTTTGTGGAGGTCAACG A
One_lpp1- 44	C	T	TTGTGCTTTCCTGAC CTAT	TTGTGCTTTCCTAA CCTAT	GGTCCAATAGGGAGCTCAGA CA	0,0	GGGAATGAACCAGACATG TGAATG
One_LRRC 9_68810	T	G	CTTGGATGAAAAATA TCA	CTTGGATGAAACAT ATCA	TGCAGGGAAATTACTTATGT GATCAT	0,0	AAGACAGATCAGTCCGCA GAAAA
One_MAR CKS-241	T	A	TTGCTTAAAAGGTCT TCC	TTGCTTAAAAGGTC ATCC	CCTATCACAGCTTGGTTGAG TTCAA	0,0	TCCACCCGCTCATTTTTGT AAGAT
One_metA- 253	C	G	AGGCAATTGAGGTTA AT	AGGCAATTGACGTT AAT	TTCTTATCGCTGGTGGCACTT T	0,0	GACCAAAGACTATTTAGTT GCCACCTA
One_Mkpr o-129	A	G	ATGCATATACATGTA ATATAT	TGCATATACATGTA ACATAT	TGACGTATGTGCAATGCATG TCTAT	0,0	AGATGAAGGACATGGCTG AAAACAT
One_ODC1 -196	C	T	CCACCTCCGATGTCC	CACCTCCAATGTCC	CCGAGGTGGGATTCAACATG AC	0,0	TGTCCTCAGACCCAGGGAA A
One_Ots20 8-234	-	A	CACACGTTACATCAG ATAACT	CACACAATGTTACA TCAGATAAC	CAGCCGACATGCATCAGTTA	0,0	TGACCCCATGTTTCATGCT
One_Ots21 3-181	T	A	CTTTGAATTAAAAAC ATTTTT	CTTTGAATTAAAAA CTTTTTT	CCATAGTGTATCACACAATA CTCATGTCT	0,0	TCTATCATCTGCAAATCTG TGTACTIONACT
One_p53- 534	C	A	TCCAAAGATCTGG	TCCAAATATCTGG	GACAATCTTAAAGCGGTGGT CTTG	0,0	AACCTTTATCAGCCATCAT CCAACT
One_pax7- 248	C	A	AATTCAAAACGAAAT GTG	TGAATTCAAAACTA AATGTG	AGTAAAGGTAGTGATGCAAT GATGCA	0,0	AACCGCATAGGACGTAAA GCA
One_PIP_3	C	T	AACACACATTTCTCA ACACA	ACACACATTTTTC ACACA	ACAGAGTCAGGACTTGATAT GTACAGA	0,0	CCTGACGAGGGTCTACTAC ACT
One_Prl2	G	T	ACCAATGGGACGAGT G	CCACCAATTGGACG AG	ACCTCTCTCTCTCAGGACT CTCA	0,0	GAGGAGGTGTGACACATA GATGGA
One_psme2 -354	A	G	TGATGCAGTAGCTAA AG	ATGCAGTGGCTAA AG	TGGTCCTTCAGGTACTTTTCA GAGA	0,1.8	CAAATGCCAATTCTCACCA CATGA
One_rab1a- 76	G	T	TGTGGAGCAAGGTAA CT	TGTGGAGCAATGTA ACT	TCGCCATATTCTCTCTCCCTA TCC	0,0	ATCCACTCAGACCCATATC TACCAA

One_RAG3-93	C	T	CATTTTGGACTTCGG GACC	CATTTTGGACTTTG GGACC	AGATAAAGATGGTTTCAAAG TCACCCA	0,0	GGGCTGCCATCTAAAAAAT ATTGCT
One_redd1-414rd	A	G	CCTAAGTCAGTCACT GTAG	CCCAAGTCAGTCAC TGTA	GTTGGCTACATCCTAAAACA CAATGG	0,0	CAGCCCTGGAGTACTGAAT CAG
One_RFC2-102	A	G	ATCACGTTGTATTTT TTT	CACGTTGTGTTTCT TT	TCCAGGAGCTGCATTTTGAG TTAAA	0,0	AAGGTGGATGACAATGTGT TAGTGT
One_RFC2-285	A	T	CACGACATCTAAGCT GAA	CACGACATCTATGC TGAA	GGATGAGGCTGACAGGTAAG TC	0,0	ACAGTCGTTATAGGTACAG GTACACT
One_RH2o p-395	G	T	TGGGAACATCATTTT TTAA	TTGGGAACATAATT TTTTAA	GCTGCTAGGTCAAACCTCGAA GAG	0,0	CAGCCTTGTTCAACCCCAT TATCTA
One_rpo2j-261	G	T	CACATGTTTTACTCA TTTGA	CACATGTTTTACTA ATTTGA	GATTCTGAGATCATAAGTG GATTGGT	0,0	GCTTGTCATCTTTCAGCAC ATACCTA
One_sast-211	G	T	CATCATTTGCATTAT TG	CATCATTTGAATTA TTG	TGTACTTAGTCCAATAAGCA TTTCAACAGT	0,0	TGGCTAGATTCACATGGTC AACAAA
One_SEXs dY-F19R20	X	Y	NA	CTCCAACCTGTTGT	CCCAACACCCTTCCTATCTCC		CCTTCCTCCCTAGAGCTTA AAAC
One_spf30-207	G	T	AGGGACATCTTACCT CAAAA	AGGGACATCTTACC TAAAAA	AGCATTTTCAGTTTTGTACATT TACAGTAAAACA	0,0	ACCTACTCGTAATTTTCAGG GCAAAA
One_srp09-127	T	A	CAGCGAAGGATATGC T	CAGCGAAGGTTAT GCT	CGGAGCTGGAATGACGACAT	0,0	AGGTTTCAGCAAATCCCTCT TTAGAG
One_ssrd-135	-	T	CTGCGGCTTTGTCTT G	TGCGGCTTTTGTCT TG	TGGAAACTCCTAGTGTACTT CATTCTCA	0,0	CGTTCACGCTCCCTAGAA TAGA
One_STR07	G	C	ACGCACACTGTCCTT	ACGCACACTCTCCT T	CACACCTGAGGCACAAGCT	0,0	GTATGTCTACCAGAGAGGT CAAGGA
One_SUM O1-6	C	A	CAAGAT[AT]GAAATT GGTTTGC	CAAGATTGAAATTT GTTTGC	GCACAAGCCAAAAAGTTTTC TCCAT	0,0	GGACATAGTTGGAGGCAG ACAAAA
One_sys1-230	T	G	CAAAGCAAGTGATAT ATTAGTG	AAAGCAAGTGATA TCTTAGTG	CTACCTGTCTAACAGTGAAT GCTAACTT	0,0	TGAAACCATTAAGCTCTTT GTAGGACAA

One_taf12-248	G	T	CCAGACAAAATCAA ATTA	CCAGACAAAATAA AATTA	ACCTTCAATATGGTGGTGGT TACC	0,0	ACTAAACGCACAACAGCA AACG
One_Tf_ex11-750	G	A	CAGGGTCGCTGCAC	CCAGGGTCACTGCAC	AGCAGGTGTAAGCATGTGTACTT	0,0	CCTGCTCTGCCTCAACAAT GTAA
One_txnlp-401	C	T	TGACTGCACTAGTTT AGAC	TGACTGCACTAATT TAGAC	GCCAGATCCCTTCAGTTGGA	0,0	GGCCATTTCAAAAGGCTGC AT
One_U1003-75	C	T	AGAGACTACTTCCTT TTTG	AGAGACTACTTCTT TTTTG	TCACGAGCCCCAGTCAGA	0,0	CGGGTTTCGGTGGTTTAGT ATTCTA
One_U1004-183	A	G	AAGTTCCCTGTATTT CTT	TCCCTGCATTTCTT	GGTGTGACTGCTGTGTTTAA TTGC	0,0	ACCATCATTACACAGCAAT TCTGAGT
One_U1009-91	A	G	CATGTTCTGTATGGA CCC	TGTTCTGTGTGGAC CC	CTCTGTCCCTGAACTGTTGTC TGTT	0,0	GCCGCTGCTACTCTTCCT
One_U1010-81	A	G	CACACCAACGTTATG TAGAG	CACCAACGTTGTGT AGAG	CAGCCCCCTCGAGGTAAGT	0,0	GTTGAGACAACAAAACGT CTACTGT
One_U1012-68	C	T	TGACGGGTGTTTCTG ATAA	TGACGGGTGTTCTT GATAA	TCTATTACCATACAGGCCCA GTACA	0,0	CCTTTTGTGTCTTCCAGTCA TGTGA
One_U1013-108	G	T	ACGGAATTCCTGTTG CCCT	ACGGAATTCCTTTT GCCCT	TCTGTGCTCTCCTCCAGGAT	0,0	CGAAACTGAGGAGTGCTCT GA
One_U1014-74	C	T	TTGACCTGCGCCAGT AT	TTTTGACCTGCACC AGTAT	TCCCCTGCAGCAACTGTTTT	0,0	GGCAGAGACGGCATCCT
One_U1024-197	G	T	ACCTGACCCAACAAA	ACCTGACACAACA AA	CTGAACTGATCTACCGCTCT GT	0,1.1	GGAACAGATACTCCAGGA GAGATGA
One_U1101	C	A	TGGACGTATGTCATA TTT	TGGACGTATGTAAT ATTT	CTATGACATGTTTATTTTAAT TAGCCACCAACT	0,0	AGTATAGCTAGGGAACCTT TCGATCTT
One_U1105	T	A	CCTGTTTTTTTTAAAA GAC	TCCTGTTTTTTTTTA AAGAC	GCCTTAATAGTGTCTTCTGAT CCCTTT	0,0	CCCTCTGTTGTCCAGACTC TTAG
One_U1201-492	A	G	AAGACTTCCTCCAGG CTC	ACTTCCCCCAGGCT C	GCTTATGACGGAGAAGAGAT GCA	0,0	AGGATACTGAAGCCCAGA GACA
One_U1202-1052	T	C	CAAACTTTTTCATCT ACATTTA	ACTTTTTTCATCCAC ATTTA	CGATTTGAGTCTCCAATGGT CTCT	0,0	ATTCCTATGGTTAACATCA ATTCTATAAAGTCAT
One_U1203-175	G	A	CCATAGTTGCTGGGC TT	CTCCATAGTTACTG GGCTT	CCCGGAGACATACTTGATGC A	0,0	GGAGGACCTGCAGGATCA C

One_U120 4-53	C	T	ATGCATACACGCTGA TGC	ATGCATACACACTG ATGC	GTAAAACCCCTTCATGTTGGC CATT	0,0	CTCCATGTCTGAATGTCCC ATCA
One_U120 5-57	A	G	AGTTATCATGGTCAT CTCT	AGTTATCATGGTCG TCTCT	AGTAAATGGTTATTCACGTA ACGGATAAG	0,0.8	CAGGACAGTTCCACATTCT AACAGA
One_U120 6-108	G	T	AACATTGAGCTTCCC	ATAACATTGATCTT CCC	CTGAGATGGTGCTTTCTGAG GATA	0,0	TGGATGAAAGGGAAATTCT GTCAACA
One_U120 7-231	C	T	ACATTCCTTGGCATT GC	CATTCCTTGACATT GC	GGCCAAACTGACAGGGATCT ATTAA	0,0	GGGTCCAGTCTGTACACCA TCTAT
One_U120 8-67	A	C	CCCAATGTGATTGTC AC	CCAATGTGCTTGTC AC	ACTTGAATGTCTGTTTCGTAG GTGAT	0,0	ACACAGTTGACAGTGGAG CAA
One_U120 9-111	C	T	CTCACATCGAGATGA TC	TCACATCGAAATGA TC	GTCACGTAATCACGAGAAAG ATACTAAATGT	0,0	TCTGCGTCTCCAGAGAGGT T
One_U121 2-106	A	G	TTTTGACATACAAAA AATA	TTTGACATACAGAA AATA	CGTAATGACCTACCACCATA TCAGT	0,0	TGGCATGACTTTAACAATT CCCCAAAAA
One_U121 4-107	A	C	TAGTGACCTATTAAA TTGC	TGACCTATTCAATT GC	CCAAATGTACTCCATGTTGG TTAGC	0,0	TGCCTGAGTATTAAGCTAT ATCATTGAAGTTTT
One_U121 5-82	A	C	AATGAGACAAAGTAT TTGGT	AATGAGACAAAGT CTTTGGT	GTTGCTTGGTTTCGTTTGGAG TAG	0,1.9	CTCCAGAAGAGGAATACC ACAGTTC
One_U121 6-230	A	T	CCTGGCTACTAAGTA AC	CTGGCTACAAAGTA AC	TGGGATCGGACGTCAATAGA TTTC	0,0	GTAATACAGAGTGAGCGT GATACATTGT
One_U301- 92	T	G	CCATGGATTAAAATA TTT	CCATGGATTAAACT ATTT	AGCCAGTAGCCGATAATGTT TGTC	0,0	CCCCTCCCAAATTGCTAGC T
One_U401- 224	C	A	CACCTGGAAAGGACT GA	ACACCTGGAAATG ACTGA	GGGTGGAGACGAACGGATTC	0,0	GTACGATTTTTTTGTAGCC CCAAGT
One_U502- 167	A	G	CTTCTTGATCAATAA CG	CTTCTTGATCGATA ACG	GCTTTTTGTGCAATAGCTATGT TGCTTA	0,0	GCAAAGGTAGGCAGCAGA TTG
One_U503- 170	T	G	AAGTACTAAAATC[A T]GTTTTACATTG	TACTAAAATCAGTT GTACATTG	GATTCAGAATTGCCACGACA AAGAA	0,0	GTGATTGGTACATGTCTGT CGAGTT
One_U504- 141	C	A	TCAAGGACACAAAC AA	TCAAGGACAAAAA CAA	GCTATAGCTCACAGAGGATC CCA	0,0	TATTGGCGGGTGAGGGATG

One_UCA-24	C	T	CGAACAGGGCTGGATG	CGAACAGGACTGGATG	AACTCTGCGTCTGTCTGCTT	0,0	TCAGATGGTTCATTATGACAGCAACAGC
One_vamp5-255	C	T	TAGGCTCCGTGCTCAGT	TAGGCTCCGTACTCAGT	GGTTGACTTTTCTTAACTTTT TAATCTGTGATATTGT	0,0	GCTGAGCTAGTGATGGTACCATT
One_vatf-214	C	A	TGGTATTACTGTGCA TTGAC	ATG[CG]TATTA[AC] TGTTCAATTGAC	TCATTCTTTTGCCTGGAGCAT T	0,0	GGCATACAGCAAAACAATTCAACCA
One_VIM-569	G	A	AAGTGTTTCCATACT CACTATA	AAGTGTTTCCATAT TCACTATA	TTCTGGGTGGACTCATTGAT CAC	0,0	ATGCGTTATACCTGTAATCTGCAAGT
One_ZNF-61	C	A	CTATGGACATGATCT TT	TTCTATGGACATTA TCTTT	CCATTCATGTTCTATTCAGAT ATATTTTGTGCA	0,0	CCTAGCTAGAGCTCAACAA TATGCA
One_Zp3b-49	C	A	AGGCCCAATCCTT	AGGCCAAATCCTT	TCCTCGTGGTTATAGTTATAA AGATGTCAGT	0,0	TTGGCTCTGCACTCGGTTT A

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Appendix 4. GT-seq SNP panel for Coho salmon.

Assay	A 1	A 2	A1-Probe	A2-Probe	FWD Primer	Correcti on	Rev Primer
Oki_101419-103	C	A	CTACTTGCCTGTC T	CTACTTGACTGTC T	CCCAATTGGAGACCAGGGT T	0,0	TCATTGAGACAGTTGGGAG ACA
Oki_101770-525	C	A	ATTAAGTCATGT GT	ATTAAGTAATGT GT	GCACTCCTCTGCACTCTGTT	0,0	ACAGGGCCCTCTTCCTTAGT
Oki_102195-92	A	G	AAACATGAGGAA AA	AAACATGGGGAA AA	ACACTTGATTACCACTGCGT	0,0	TGCACTGTTGACAATGTGCA
Oki_102213-604	C	T	AGGAAAGCATTT TC	AGGAAAGTATTT TC	CTGTGTCGTAACAGGTAAG GA	0,0	ACACAGCAGGTAAGGAGAA GT
Oki_102267-166	A	T	ATGTGGAAGCCG CT	ATGTGGATGCCG CT	GACAGCCACGCAACAAGTT T	0,0	AAGTAACTTGTGCTAGCGG C
Oki_102457-67	C	A	AAAGGTTCAAGT AA	AAAGGTTAAAGT AA	TTCAAAGTGGCCAATGCTTG	0,0	GGAGGGCCCTACCAAGACAT T
Oki_103271-161	A	G	AGTTATGACAGA TT	AGTTATGGCAGA TT	AGACAACTAAGCAACCTCT GAGA	0,0	TCATCCAGCGCTTGCAAATG
Oki_103577-70	A	T	ATGTGAAATGTG GA	ATGTGAATTGTG GA	AGCGAGAGGGCCTACAGTT A	0,0	CACATGAAGAATTTCCCTCC ACA
Oki_103713-182	A	G	TGAAATGAAGAT AC	TGAAATGGAGAT AC	CACCAAGGCAGAGAGCTCT C	0,0	TTGTGGCACCAATCTACTGT
Oki_104515-99	T	G	CAGACTTTGGGC TG	CAGACTTGGGGC TG	TCCAGCCAGTCCATTGAGAC	0,0	AGCTGAAAGTGAACGAATT ACGC
Oki_104519-45	C	T	TTGATGACGCCG CT	TTGATGATGCCG CT	TGAGAAAGAGGTGTGAGCG A	0,0	CCCAAATAGGAGGGGCTGT G
Oki_105105-245	T	G	ATGTAACCTCTCA AA	ATGTAACGCTCA AA	GCGTATCAAGCATCAACGC C	0,0	TCTTTCAGCAAGGTTGGGCA
Oki_105115-49	T	G	CTTTAAGTTATTT C	CTTTAAGGTATTT C	TCGGGTAACACTTTCGTAGC T	0,0	GCGTTGAGGTGACATGTAG C
Oki_105132-169	C	T	CACGATGCACTG AG	CACGATGTACTG AG	TGCCCTGAACCACATGTCA A	0,0	TGGAATAAAAACCTGCAGA CACTG
Oki_105407-161	C	T	CAGCCTTCGTTTG T	CAGCCTTTGTTTG T	GCAGCAGCTCACAGCCTT	0,2	TGTCCTGACAGCCTATAGGA T

Oki_106172-60	C	T	AACCCTCCATCGT G	AACCCTCTATCGT G	ACTACTTGGCGTGTGTGTGG G	0,0	TCCACTGAGAGGATGAGGC A
Oki_106313-353	A	G	ACTTACCAACTGT T	ACTTACCGACTGT T	TCCCCATTACAATATGTCCC TGAC	0,0	TGAGTTTTTCCAAACCCTGTG TG
Oki_106419-292	T	G	CTAAAACTGAAA GG	CTAAACGGAAA GG	TGCATCTGTAAGTAGCTCTG GA	0,0	AGTCTACCATCTACAAGTT CCTT
Oki_106479-278	A	G	ACTACACAGATG CA	ACTACACGGATG CA	CCCTCTAGGTCTTTAGCAAA CACT	0,0	TCAGTCATTTGTTTACGTGC TGT
Oki_107031-314	A	T	TTTTTGATTTAC T	TTTTTGTTTTTAC T	AAAAACAGCCAGCGAAGGG A	0,1	TGTCCTCAGCTACACACGAG
Oki_107607-213	A	G	CTACATCACTGG AG	CTACATCGCTGG AG	TGCGTTGCACCTGATCTAGA	0,0	AGGTAAACCGCGTTCCATGT
Oki_107974-46	A	G	CTGCGCCACTGG TG	CTGCGCCGCTGG TG	AACTGGCAGACCTCGAACT G	0,0	TCATTGACATCTACGGCGCG
Oki_109525-359	A	G	CATTGGTAAGTT GT	CATTGGTGAGTT GT	CTTCCAGACATCACGCCTCA	0,0	TGAGCAGCAAGTCCTACAC C
Oki_109651-152	A	T	TTTTTTTAAAGCT A	TTTTTTTAAAGCT A	GGCTGTTGTCATATCATCCC G	0,0	GTCTACACACAGCCCAGGTT
Oki_109894-418	C	A	CTGGTTGCTTGAA C	CTGGTTGATTGA AC	GGAGGTACCAGGTGAGCTC A	0,0	GACCAGACCATAGACATTG CCT
Oki_110078-191	T	G	TACACTCTAATGT C	TACACTCGAATG TC	ACACACACACTCGCTCTAG C	0,0	ACAGTGTTCTGAAAGGGCC A
Oki_110381-77	A	G	GGGTTTAAGATA CG	GGGTTTAGGATA CG	TGAAACGTCCCCAACTTCCC	0,2	ACCTCATGGACGATGCCATC
Oki_111312-141	C	A	AAAAAATCATAA AA	AAAAAATAATAA AA	GGGAGGGCTAAAAATACAG ACCA	0,0	CTGGGGTCCTATTGCTACTG T
Oki_113457-324	A	G	CTCTGTGACTCGT T	CTCTGTGGCTCGT T	TTACTGAGGTGGTCCAGGCT	0,0	ACCAGCAACTCTTTCCTCCC
Oki_114250-187	T	G	CGA.TAGTTCTTT T	CGA.TAGGTCTTT T	GGCGATTGAGAGCAGGTCA T	0,0	TGGGAAATGTGTTGAATGTC CT
Oki_114448-101	C	T	CACTGCACCCGT CA	CACTGCATCCGTC A	ATGTTGATCAACCACTGCA	0,0	CCTCCTGCTGGACTAGGCTA
Oki_114587-309	T	G	TTACTATTCATTT T	TTACTATGCATTT T	GTCACAAATGATCTGCAAA ACACA	0,0	ACCAGGTGAGGGGTAAACC A

Oki_116362-411	A	T	TTACACAAAACA TT	TTACACATAACA TT	GGATGCAGGTGAGGGTTGA A	0,0	AATTCCCACCTTGCCTGCTA
Oki_117043-374	C	T	AGGACACCGATA AC	AGGACACTGATA AC	TTCCTCTTAACCACCGCAGC	0,0	ACCAAGACTATGCAAGGCC C
Oki_117742-259	C	T	GTCTGCACGTGG AC	GTCTGCATGTGG AC	GAGACTTCTGGTGGCGTCTG	0,3,0	TGCAGAACTCCACTGAGAC G
Oki_118152-314	A	G	TTTAGCTATCTAC T	TTTAGCTGTCTAC T	ACGGTACAAACAGGCTCAC A	0,0	CTCCAGAACCTGTTGTTGGG A
Oki_118654-330	C	T	ACACCTCCGACC AG	ACACCTCTGACC AG	TCCTTAACACTGTCCGACGC	0,0	TTGCTGACCTGGTTGAGGAC
Oki_120024-226	T	G	TTGATTATAGTTT C	TTGATTAGAGTTT C	ACCATAATTTACAAAACGA GGCC	0,0	AGCAGAGGTCTGAATGAACG G
Oki_121006-412	C	A	CAAAAACCTCAA CC	CAAAAACATCAA CC	AGGCAGAGGACAGTGACTC T	0,0	TGCAGTACTCCAAGGGTTG A
Oki_122593-430	A	G	TCTCACCAGTCTT T	TCTCACCGGTCTT T	TCTGGGTAAAGTGTGCCTTT T	0,0	TCGATTCCAGGGTCTCAAAA GA
Oki_123044-68	C	A	TT.AAAACGTTTT T	TT.AAAAAGTTTT T	ACTGCCATATCAGTATTGGG GG	0,0	TGCTATGTAACTAAACCGG AATCA
Oki_123921-90	A	G	ATTGTAAATTATC T	ATTGTAAGTTATC T	GGCGACGGAGATGAAGGTA T	0,0	CCAAGCCCTGAACCTTAGG G
Oki_124162-62	A	T	AGCAAAAATATA AA	AGCAAAAATTATA AA	GAACTGCCAGGTGTCAGGT G	0,0	ACCTTTTTGTGCACTTTACA TGT
Oki_125998-340	T	G	AACATACTGAGG GC	AACATACGGAGG GC	CGCAGGTCTTCTTCTAAGCA G	0,0	TCACTTTTATTTCGTACAGGC CCT
Oki_126160-142	C	T	TTTGATCCTAAAT	TTTGATCTGAAAT	TGCTCACCAACACCTGTTTG	0,0	TCCGGTCACTCCCTTGTACA
Oki_126619-265	T	G	CGGATTGTGCAC AC	CGGATTGGGCAC AC	TGCGTAGTTAATTTTCACCT CGG	0,2	TACGCAGCACTGAAGACTG G
Oki_127645-235	C	A	GTGGCCTAAAAA	GTGGCATAAAAA	TTGGTTGGATCTGGTGCCTC	0,0	GCTACTTGTATGAACTTTGA TCGCT
Oki_128302-547	A	G	AACAAATAGGGA TG	AACAAATGGGGA TG	AGCTGGAGGGGATTCACTG A	0,0	GGGATAAGAGGGTTTACAG TAAAGT
Oki_128693-70	C	A	AGAATTACATTTT C	AGAATTAAATTTT C	AGAGGTCAGGGGTCAAGAG G	0,0	CATGTCCCCACCAAAGTGG A

Oki_128757-232	A	T	TTTGGGAAAGCT TT	TTTGGGATAGCTT T	TCAAAAACGTTATTGTACGAT GACCT	0,0	GACCGGGTGCAACACAAAA A
Oki_128851-185	A	G	TAACCAGACTCC CT	TAACCAGGCTCC CT	CTCCAGTCTCCCAGTTTACA CA	0,0	GGCCCTCTCCTGGAGAAAA C
Oki_129870-552	A	G	TGCTATTATGTTT T	TGCTATTGTGTTT T	AGGGAGACAGGCTGACATC A	0,0	AGGAACAGAAATGTTGCGT CA
Oki_130113-304	T	G	TACAAATTTATCG T	TACAAATGTATC GT	GGGAGAGTGTTGGAATCCC C	0,0	CTTGTTTCAGGGGCAGAACG A
Oki_130295-48	A	G	AAGCAATAAACA GT	AAGCAATGAACA GT	TGAGCACAAATATAAATGT GGCTGT	0,0	AGAAAAATATTCTGTGGTCC CCT
Oki_130524-184	C	T	CAGGAAGCTGAC TC	CAGGAAGTTGAC TC	CGATTGGTCGTTGGCATGAC	0,0	TGCTCTGCTGTGTGCTTACA
Oki_131147-353	T	G	AAAA.ATTTTTGG G	AAAA.ATGTTTGG G	GGCCTTTGTCAAAAGTAGT GCA	0,0	CCAGTCTCTTTGCGTCCCAA
Oki_131460-243	C	A	TTTCCTTCTACAT C	TTTCCTTATACAT C	GGAACAATCGAGCAAGGAG C	0,0	GCTTGGCCATGATAACCTCA
Oki_94903-192	A	T	AATTTAAAGTCA AT	AATTTAATGTCA AT	TCCAAACCGCATCGTAAAA GT	0,0	CCGACATATGTGAATGCGA GA
Oki_95318-100	C	T	TTGAAGGCTGTT AA	TTGAAGGTTGTTA A	CGCCTGCACTAAATATGTA GACA	0,0	GGGTGAAGTGCCCCCTTAAC
Oki_96158-278	A	G	CTATTGTAGGGTC G	CTATTGTGGGGTC G	CCACCTCGATCTCCTTTCGG	0,0	ACTGTCCAGTTTGTGACGGG
Oki_96376-63	A	T	GAGAGTTAAAAA AA	GAGAGTTTAAAA AA	CTGCTACGTGTTTGACAGTG A	0,0	TGTGGAACATGAACTCAAA ACGT
Oki_97660-149	T	G	GGTTACATACAG GG	GGTTACAGACAG GG	CACTGGTCCGGTCCAAATG A	0,0	CTGTTACTCCCCAACCTGT
Oki_99550-284	T	G	TGTTTCTTTT.TTT	TGTTTCTGTT.TTT	AGAGGTTGCAATTGTAAGT CTTGT	0,0	CTCACAGTGAGGGATCTCTT CT
Oki_afp4-10	T	C	ACAGCTCTATGG GC	ACAGCTCCATGG GC	ACCTTATCACCTCGGACCGA	0,0	TGAAAGCTTGTCGGGCTCTT
Oki_arp-105	C	T	GCTTGTGCAGTA CT	GCTTGTGTAGTAC T	TGGCCATTGACAAAGCAGG T	0,0	TTGCAGGGGAAACAAGAGC A
Oki_aspAT-273	C	T	AGTGGGGCACGG TG	AGTGGGGTACGG TG	ATGCTGGGAGAAACAGTGG G	0,0	CTCCTCTGTAAGGGGTGGGT

Oki_bcAKal-274	T	A	AGTTCCTTACTA C	AGTTCCTTACTA C	ACGGACACCACAAGTCCC	0,0	GCAATCAAACCTAAGGCCAC ACA
Oki_gdh-189	T	A	.ATTTTTTCTGTGTA	.ATTTTTATCTGTGTA	CCTGTGTTGAAGTGGAGTA GGT	0,0	GCTTTATACTGTAAGTGGAC TGACC
Oki_gh-183	A	G	CATCAATACAAT TT	CATCAATGCAAT TT	ATGTGGTACTGGCTCAAAA CT	0,0	TGCAGTAGAGCATGCTTGGT
Oki_gshpx-152	A	C	TTGCAACATTGTGTA G	TTGCAACCTTGTGTA G	TGTAGTTTTGTGCGCAGTTGT TG	0,0	GTTTCAATGATGAGTCCCAA AAGT
Oki_hsc71b-56	C	T	TGAGTCTCGTGA CT	TGAGTCTTGTGAC T	TGTGTTCTACCCTCTTGTGT CTG	0,0	TCAAATTTCACTCCTTGACA AGTCA
Oki_hsc71p-313	T	G	TGGTTATTAACCTA C	TGGTTATGAACCT AC	TGAACTGTGCCATGTAGTA GGT	0,0	GGGGCAGGCATAAAAGTAG A
Oki_itpa-85	G	T	TAAATAAGTTGTT T	TAAATAATTTGTT T	ACCACACTCCGTCCTCCATA	0,0	AGCGACTTGACTCTGAACA GA
Oki_nips-159	G	T	TCAAAATGACAT GC	TCAAAATTACAT GC	TCTTTCCTGTGTCGGCATCA A	0,0	TCCAAGTCTGGTTAGAGCCC T
Oki_parp3-19	-	T	CCAATTTAAAGC C	CCAATTTTAAAG CC	AGCTTTGCCTCTAGACTTGT GT	0,0	ACCTTGAAGATCCATCCTGG C
Oki_pigh-33	T	A	GTAAACATTTCCC A	GTAAACAATTTCCC A	ACCGCATACCAAGTCATGC A	0,0	TCATCAGTTTTTCTTTCCATT GGGA
Oki_pop5-265	G	T	TACTCCTGGAAT AG	TACTCCTTGAATA G	AGAAAACCATGAGGCTCCG G	0,0	CAGCTGCATTGAAGCACCA G
Oki_RAD100-310-36	T	C	TAAAAATGCCGA GC	TAAAAACGCCGA GC	TGCAGGACTTGTTTGGTTTA CTG	0,0	TGGGAGAGAAAGGTATGTC TGT
Oki_RAD100-331-48	G	A	CAGACCGCGTCT CA	CAGACCACGTCT CA	CGCCACCCAAATAACCCAG A	0,0	TTCCCAGGCAGTTCTGAGAC
Oki_RAD100-388-66	A	G	AAACAGATAGTA CC	AAACAGGTAGTA CC	CGATTTGTTGAGGGGCCCTA	0,0	AATATTCCCTCCAGGCACGC
Oki_RAD100-479-50	G	A	ATGGACGTGTTTT T	ATGGACATGTTTT T	GGTCTTTTCCACACTGCTGC	0,0	TCCAGAGAAAGGGCTCATC C
Oki_RAD100-507-58	T	G	TTCTCTTACAAGC T	TTCTCTGACAAGC T	TGCAGGCGTGTATAGTGGA G	0,0	CAGCTGGTCCACTGTCTATC A
Oki_RAD101-032-66	C	T	TATGCGCTGATTT A	TATGCGTTGATTT A	TTGCACCATCTGGAGACTG G	0,0	CCCCACTACACCAATCGAA GA

Oki_RAD101 136-60	A	G	ACTGACAGTCTA AA	ACTGACGGTCTA AA	TGCAGGCCTCAATGCTCAA A	0,0	TGGTCACTTGTAACCTGTAG CTGT
Oki_RAD101 478-57	C	T	AACCACCATTA CC	AACCACTATTAA CC	AGAGCATATGGCCACGTCT G	0,0	GCTCTCTCTCGCCCACAAC
Oki_RAD101 607-49	C	T	GAGATGCGTCCG TG	GAGATGTGTCCG TG	CCGGGGCTTTCAGAGAGAT G	0,0	TGTTTTCCCCCTTTTGCCT
Oki_RAD104 180-61	G	T	AAAATGGCAGGA TG	AAAATGTCAGGA TG	ATATAGGCTGGGAGGGGAG GAG	1,1,0	ACAGCTGTGACTTGAACCA CA
Oki_RAD104 335-44	T	C	CCGCTGTGAGGG GA	CCGCTGCGAGGG GA	GTAGTGCAAAGCTGAACGC C	0,0	TCACTTTGTCCGGTTCCTGG
Oki_RAD104 946-41	C	T	GAGGGGCGCCCT GG	GAGGGGTGCCCT GG	CATGTGGCTGTAGTGGAGG GG	0,0	GCCCCTGAATGACAGCTCA G
Oki_RAD106 191-62	T	C	GAGAAGTGATCA CC	GAGAAGCGATCA CC	TGAGATCGAGCTTGCTGTG G	0,0	CCCTCCCGAGCCTCAAAATA
Oki_RAD106 666-44	T	C	CGGCTATACACA GG	CGGCTACACACA GG	ACGCCAGTCTGATTGGAGT C	0,0	CGGTTTTGATTACCTGGCC G
Oki_RAD109 528-59	T	A	ATTATGTTATTTT C	ATTATGATATTTT C	GGCCTCAAAGAGAAAGAGC A	0,0	GGAActCTGGAGAAGGTAA AGAA
Oki_RAD111 744-32	A	T	GGGTCGAAGGTC CG	GGGTCGTAGGTC CG	CTTTGACAGACAGGGTGGG GT	0,0	CCATGCTCCAGAGTCTCGAC
Oki_RAD115 799-69	C	G	ATCCTGCTCCGGC A	ATCCTGGTCCGG CA	CTGCATCGGTAGTGGTCGAT G	0,0	CCAGGAGTTTGCCCTGGAAT
Oki_RAD118 44-57	T	G	AAACACTGACAT AA	AAACACGGACAT AA	TGCAGGTATTTCCGCTACAC T	0,0	TCGCAGAAGGCCATTTTATG T
Oki_RAD121 24-45	A	C	TCGAAAACCTGTA AT	TCGAAACCTGTA AT	TGCAGGAACTTGATGATCT GA	0,0	CCAGGATTTGGTTCATTGCT T
Oki_RAD161 67-62	C	T	GCGTGTCCAACA AA	GCGTGTTCACA AA	GGAGTCGGCTGTCTTTGACT T	0,0	GCAAACAGCATTTTCGTTCGA
Oki_RAD237 88-32	C	A	TATTATCCTAAAC A	TATTATACTAAAC A	AGGGGGCTTAAACACAGCA T	0,0	TCTTTGAAATTGTTGCATGT TGC
Oki_RAD252 12-35	G	C	TTCTGGGACATCC C	TTCTGGCACATCC C	TGTCTAGTTCCCAGCTTGTT CT	0,0	TGGAGAACCATCGAGCAAC G
Oki_RAD278 01-45	T	A	CACAGCTAACCG CA	CACAGCAAACCG CA	GCAGGTAGCGATGTGGAAG T	0,0	CCTCTTTGGTATTCTGTGCG G

Oki_RAD290 28-42	A	T	ACTTCCAGGAAT TA	ACTTCCTGGAATT A	GTCACTCTGAAGTAGCTGC ACT	0,0	AGCCACAGGAATAGAAAGC AA
Oki_RAD291 36-50	T	G	GTAAGGTTTCCTC A	GTAAGGGTTCCT CA	CCTTCACAAAGACAACATG ACTGT	0,0	AGCAACGGAAATAGGCAAG GA
Oki_RAD344 32-38	T	G	TGTGAATAGATG GC	TGTGAAGAGATG GC	TGCAGGATTTTGTGGAGAG GA	0,0	TCATCGGTCTACCTGACGGT
Oki_RAD345 -59	G	A	CAGAGGGGCTTC CT	CAGAGGAGCTTC CT	GACACTTCTCACTAGCGGCC	0,0	TGACTCACTACCGCTGAGG A
Oki_RAD352 19-62	T	C	AGGATATGGCTC AT	AGGATACGGCTC AT	ACCGAACGGAGGTGAGGAT A	0,0	TCAGCCACAGTCTTGGTGTG
Oki_RAD359 90-63	A	C	CTCAAGAGGGGT AA	CTCAAGCGGGGT AA	TCAAGACATACAACAAAAA GTGGT	0,0	CACAGTTAAAGACCCATTG CGG
Oki_RAD366 69-48	A	G	CTTCCTATCAGTG T	CTTCCTGTCAGTG T	GGTCCTCCTGTCCTCTTCCT	0,0	AGAGGGCAAGCAGTCAGTT C
Oki_RAD372 78-54	T	C	TTTTGGTGATTTG G	TTTTGGCGATTTG G	AGCGTGGTGTAAC TTCAGA GG	0,0	CTCAAGTTAGGATTCAGCCC CA
Oki_RAD374 93-51	G	A	CCAGCCGGGAAC AC	CCAGCCAGGAAC AC	ACGCATCACAGTGAGACCA G	0,0	AAAGTAACCGCCTCACCGA G
Oki_RAD375 37-45	T	C	ATGTACTCACAG TA	ATGTACCCACAG TA	AGTCCACTTGTAACACCATG T	0,0	TCCACCCATTACCACGAACC
Oki_RAD376 98-60	T	G	A[GA]TTTTTGGG AGTA	A[GA]TTTTTGGGG AGTA	TGCTGAGGTCTTTTCTGTTG C	0,0	TCTCTCTTGGATAAGGTGAG TTTT
Oki_RAD379 79-59	G	T	TATGAAGACATT CC	TATGAATACATTC C	GGGGTCTCTGTCATTCAAAG GA	0,0.5	TCACTGTGTTTTCCCAAGGA A
Oki_RAD401 79-68	T	C	CTGAAGTTGACT AC	CTGAAGCTGACT AC	AATGCCACCCATCTACAGC A	0,0	AGAGCAGCACATAGGGTTT GT
Oki_RAD410 30-31	T	C	GGGGCCTAGGGG CT	GGGGCCCAGGGG CT	GCTGAGCCTGGTCTGGG	0,0	TGGATACCCCAACTCCTCCA
Oki_RAD416 03-39	T	C	GCACACTAGAGG TT	GCACACCAGAGG TT	GCAGGATGCACAGATAACA CAG	0,0	CGACCATTCCGATTAATTGG GC
Oki_RAD422 04-39	C	T	ATTCAGCACATT A[GA]	ATTCAGTACATTA [GA]	TGCAGGGAGAGGAGAAGGA A	0,0	AGGTTGTGCGTAAGGTACA GT
Oki_RAD430 51-33	G	A	CAGCCGGCTGAG CA	CAGCCGACTGAG CA	AGGACGTTGGTAAAGCCCT G	1.2,0	ACCAGTTTCGGCTACATGCT

Oki_RAD436 27-30	T	A	CATTTTAAAAATT A	CATTTTAAAAAATT A	GCAGGCAGCATGTGGTTAA A	0,0	AGGACACACAGATAAGAGA CAGA
Oki_RAD442 68-51	T	C	TGAGTTTACAAA AC	TGAGTTCACAAA AC	ACAGACAATGACCTACACT GAGT	0,0	AGTGCCTTTGAACAGGGTGT
Oki_RAD444 44-52	G	A	TTACATGTAGGTC A	TTACATATAGGTC A	TGCCAGTAGGTAGCTCAGG T	0,0	AGGCCTCAAAGTGTAGCAC A
Oki_RAD456 91-45	T	G	GAGTACTGCATG[TA]C	GAGTACGGCATG[TA]C	GGGCCCCGCGTTATCTGATTA	0,0	CTGATTTCGGTCTGGCCTGAA
Oki_RAD458 78-53	G	T	ACAGGGGTTCGA GA	ACAGGGTTTCGA GA	AGGACAGATCGAGTTTCGC C	0,0	TTTCTCTCTCGCCCTCTCGA
Oki_RAD461 60-48	C	G	GTGCTACTGAAT GA	GTGCTAGTGAAT GA	TGCAGGTGTCTGTAGCTTGG	0,0	ATTCTTGTTAGCTCGCGCAC
Oki_RAD467 44-47	T	C	TCGCTCTTCATAC A	TCGCTCCTCATAC A	GCAGGCCCGATGGTATTGTT	0,0	GTTTCATGCCTTCCTGCCAG
Oki_RAD469 74-68	T	G	CATTTTAAATGTT A	CATTTTGAATGTT A	TGGAACGGTTCACCCATTTT	0,0.4	CACATGAATTAACCCAGGG AATCG
Oki_RAD473 13-50	G	A	GGCACCGTGGTA AG	GGCACCATGGTA AG	TGCAGGACTCTGAGGTTAC AG	0,0	ACCCAAGACAAGAGATAAA CTTACC
Oki_RAD491 11-64	C	A	GGGATGCTCTGG GA	GGGATGATCTGG GA	TTACTGAACAGCCACCTCCG	0,0	TATGCATGCACAGCTGGTTG
Oki_RAD493 48-51	G	A	CAAAGCGGAGCG AT	CAAAGCAGAGCG AT	AGCCCTCTCTACGTGTCTCA	0,0	AACAAACGCACAACATCGC T
Oki_RAD514 28-47	A	G	GTTATAACAGCA GT	GTTATAGCAGCA GT	CTGCAGCCAGGGAGGTTAT A	0,0	CCAGAGGAAACCCAGCAGA G
Oki_RAD515 85-47	G	T	TCACTTGGTAGA GC	TCACTTTGTAGAG C	ACTTTCTAGTAGGCGTGTGG C	0,0	CAAAACCCTGGCGTTGCAA G
Oki_RAD520 40-63	G	T	AAAAA[CT]GATT GTAA	AAAAA[CT]TATT GTAA	CGCCCAACCAAACACTAAC CCT	0,0	AGTGGCCTAACTTTAATTTG ACACA
Oki_RAD527 85-52	C	A	GCAAC[AT]CGGC CACT	GCAAC[AT]AGGC CACT	CTAAAACACAAGCCCTGGC A	0,0	TTTAATTATCTACCTGTTCA GTGGC
Oki_RAD531 21-66	C	T	CATTCCCTCATTC C	CATTCCCTCATTC C	CTCTAAATACCCGGGTGCCC	0,0	CACATTCTTGAGACAAGCA AGGG
Oki_RAD536 55-42	T	C	GGGGATTTGAGA AA	GGGGATCTGAGA AA	GGTGAAGGTTTCAGAGGGG G	0,0	GCGCTCTCCGTGATCTCATT

Oki_RAD537 03-50	C	T	GCCTCACGAGTG GT	GCCTCATGAGTG GT	TGCAGGAGGACACAAACAC A	0,0	CACAGCCTTAGACCACTGC A
Oki_RAD537 50-45	A	G	CGTGACAGTAGA AA	CGTGACGGTAGA AA	CAGAGGAGGGGCCGTGA	0,0	CCCTGTATCAACACGGTGCT
Oki_RAD549 18-40	T	C	TCATCCTGAGGC CA	TCATCCCGAGGC CA	CAGGCCCAGCTGTGAGTAA A	0,0	ATAGGGTGCCATCTTGGAC G
Oki_RAD550 90-49	C	A	GAGAGCCGGACG GG	GAGAGCAGGACG GG	ATCGCAGCACGGCTCTATG	0,0	CTCCATCTCCTTTGGGCTGG
Oki_RAD556 90-46	A	C	GTAAAGACCCCT AA	GTAAAGCCCCCT AA	CCACAAGGGCACAATGAGT C	0,0	GACCAGTAGTCGCATAGGG C
Oki_RAD560 94-43	G	T	CGCACCGTTCCTT C	CGCACCTTTCCTT C	AAGAGGTATGCCACGATCC C	0,0	AAACGAACCTCCAACCTCC A
Oki_RAD573 07-33	A	G	CTCAAGATTTTAA A	CTCAAGGTTTAA A	TGCAGGGCTTGAGTTGAGA A	0,0	ACGGGCATTGATCCAGTCA G
Oki_RAD578 26-44	T	C	TTGGCATCAGATT G	TTGGCACCAGAT TG	TGCAGGTGACGCTTTAGAG T	0,0	GTGCAACACCAGAGTTCGA A
Oki_RAD579 56-47	C	G	CCTACTCTTTGTC A	CCTACTGTTTGTG A	AGGTCATGGATGAGGCATG CA	0,0	CCTTTTAGCATGGCGCATCC
Oki_RAD583 10-55	A	G	ATCACTACTATCC C	ATCACTGCTATCC C	CGGCCCTCTGTTGAGTATGG	0,0	GGATATGGATTAGGGGATA GGGGA
Oki_RAD590 54-54	A	T	TTTTGTAAAAAA AA	TTTTGTAAAAAA A	TGATTGAATACCTAGTCTCC CTATG	0,0	CGCCACTCAGAAGCCCAAT A
Oki_RAD595 56-32	T	C	CATTAGTGTAAT AA	CATTAGCGTAAT AA	GGCCATAGCAGCTGCCTGC	0,0	ACCATGTCTCATAGTAGACA TGCA
Oki_RAD599 20-68	G	A	ACACAGGACAT[T A]AG	ACACAGAACAT[T A]AG	GGCTGAATCCCCCTAGAAC AC	0,0	GCCATGGTTAAAGGTTTCAA GC
Oki_RAD599 45-45	T	C	GCTCTCTTTGTTC C	GCTCTCCTTGTTC C	CAGGTGGATGAGAGGCTTG G	0,0	CCAAGACCAGCCCTGAGC
Oki_RAD602 46-68	A	C	ATTCTCACGAAG TG	ATTCTCCCGAAGT G	GCAGCCCCTACCTACCATTG	0,0	GAACATCGCCAGGCATTGA A
Oki_RAD617 46-62	C	T	GCTATTCGGAAA GA	GCTATTTGGAAA GA	TTGGGGAGAACTGTGTGTG G	0,0	CGCCCATTGCACTGTTGATC
Oki_RAD618 21-61	A	T	TAAAATAAACTC AA	TAAAATTAATC AA	TGCAGGCTAAAACCACTAC TT	0,0	TGACCAGAAGACCCCTCTGT

Oki_RAD640 84-65	C	A	AATATACGTTTTA G	AATATAAGTTTTA G	AGGCAATTTTTACATAGATG GCAA	0,0	TCGCAAGATCATTATCCAGT GGT
Oki_RAD646 27-67	T	A	AATAAATAGGCT CC	AATAAAAAGGCT CC	GGTCCTCCTTGGTGATTGGT	0,0	GGTTACATCCTCAATGGGTC CA
Oki_RAD652 34-35	T	G	CCAGATTTTTTGT T	CCAGATGTTTTGT T	TGCAGGAAGAGGTTAGAAA ATAGA	0,0	ATGTATGGACTTGACAACA ACAAA
Oki_RAD653 88-37	C	A	AAAAAACCATGT GG	AAAAAAACATGT GG	GTGGTGGTGGTCAGAGACA G	0,0	AAGCTGATTCCTTGGCAAA AT
Oki_RAD656 10-58	A	T	GTTATTACCTGTG C	GTTATTTCTGTG C	TGCAGGCCAGTTCAGTGTTT	0,0	GGCAGTTAATCACGTGCAC A
Oki_RAD659 02-30	C	T	CTTTGCCGGAAA AA	CTTTGCTGGAAA AA	CCTTGTTCAACCAGGCTTTGC	0,0	ACCGTTGACTCTGAGCTGTG
Oki_RAD662 65-54	C	T	AGGTTCCGTCAG AT	AGGTTCTGTCAG AT	TGTTGTGATTGAGTTTGGGG GA	0,0	TTTCCACCACCAAGACACCC
Oki_RAD666 63-68	G	A	ACCACCGTAACA AT	ACCACCATAACA AT	GCCCACTGCTAAGGCCTAT A	0,0	CGCCATTAGTCCAGTTTGCA
Oki_RAD669 94-58	G	A	GGACTAGTCTGC TC	GGACTAATCTGC TC	AAAAAGTGGGAGCAGCATC G	0,0	AAGCCTCCTCCTCACAGCTA
Oki_RAD670 81-48	G	A	TGATGCGGTGAC AT	TGATGCAGTGAC AT	GGCTGTCGGTGTTTCACAAT	0,0	AGCAATTTGATGACCATA GCT
Oki_RAD671 14-64	T	A	ATGATATGTACA GA	ATGATAAGTACA GA	AGTCAGGTGAGACTCAAAT CCT	0,0	GACAGGAGTCTACCGTGGT T
Oki_RAD676 74-60	C	T	ATCTTCCATTTAG G	ATCTTCTATTTAG G	TGCAGGAGTAAACAACACC A	0,0	AGCACCGACTGTTGCTCAAT
Oki_RAD680 33-63	A	G	TATCACAATGTA GG	TATCACGATGTA GG	CCTGAACAAAACACATTAG GAATCA	0,0	TCTCTCCAATTCATACTGAC CACT
Oki_RAD681 90-55	G	A	GCTAGGGACGTG GG	GCTAGGAACGTG GG	TGAGGGGGTTGGGAGGGG	0,0	CCCCATTAAGTCTCCACG
Oki_RAD691 61-64	G	T	TTGTGAGAATGA TG	TTGTGATAATGAT G	CCAGTATGAATGCATCGGTT GT	0,0	AGGAGAAGATGAAGCATCG TCA
Oki_RAD693 55-42	G	A	CACCCTGGACTC AG	CACCCTAGACTC AG	GCCCTTCAGCAACATGGTTG	0,0	GGAGAAAGGTGCTGGCATC T
Oki_RAD702 62-64	C	A	CTTAACCCTTATC C	CTTAACACTTATC C	GCAGGATAAGGCACCCTAC G	0,0	CAGCACTGAATCATGCGCA G

Oki_RAD706 00-60	G	A	AAAAAGGGACAT CG	AAAAAGAGACAT CG	CTGCACCTACCACCAACAG T	0,0	ACGATAAAGTCTTGCACTCC GA
Oki_RAD708 12-52	A	T	AGTATGATAAAC TA	AGTATGTAAAC TA	TGCAGGGGTTGTTGATGTTA	0,0	AGACGACCCAGAGATTCTC A
Oki_RAD708 20-47	A	T	ATACGGAGGTGA TT	ATACGGTGGTGA TT	TACCGACAACCTTGCTCTC	0,0	CAGACCCCATCCCCAATCAC
Oki_RAD709 63-47	A	G	GCAACAACTGGT TA	GCAACAGCTGGT TA	GGTCAGACCTGCCTTTATCT GA	0,0	CAGATCAGATGAGGCCGAC A
Oki_RAD713 46-63	T	C	AGAGGATGTTGG GC	AGAGGACGTTGG GC	ATGGGACTGGATTTGTCGCT	0,0	CGACTCATTTGCAACCTTGG T
Oki_RAD714 42-69	G	A	TGAATGGAAGTT TA	TGAATGAAAGTT TA	AGGGTGTGCTTCAGTATGA CA	0,0	AGACAGTGCACCAACGTTG T
Oki_RAD719 48-56	A	G	TTATTGAAATCTA C	TTATTGGAATCTA C	AGGACCAGCTTAGCCTCTCC	0,0	CATCAGGTCGCAGGTAGGA G
Oki_RAD720 95-45	A	C	AAAATAAATGGA GC	AAAATACATGGA GC	GGACACACAAATCACAGGG GA	0,0	GCAGCATTGCCCCTGAAGT A
Oki_RAD721 01-67	A	G	GCTTGACAGAG CA	GCTTGCGCAGAG CA	TGCAGGTGCGAGAAACAAG A	0,0	GCAGGAGTGGTTGGAATTG C
Oki_RAD727 59-48	A	G	CATGAGACTGTA AC	CATGAGGCTGTA AC	CCAGGTTCAATGGTAGCTA GCT	0,0	AGGGGGTGAATACTTTCGC A
Oki_RAD729 79-40	G	A	GAGAATGATGAA GT	GAGAATAATGAA GT	TGCAGGCTGTGTAAGGACT C	0,0	TCGGGTGATTCTGGAGGCTA
Oki_RAD730 94-68	A	G	AAACACATACGC AC	AAACACGTACGC AC	AGCGCCACCAGAACTAAAC A	0,0	TGCATGTACGTATGTGTGCG
Oki_RAD731 30-59	T	C	AATACCTCCTAA CG	AATACCCCCTAA CG	TCAGCCTGGTGAGCAAACA A	0,0	TAGCAACAACCAGGAGGCA G
Oki_RAD732 34-42	T	C	TCTCGCTTCGCAT T	TCTCGCCTCGCAT T	TTGGGCCCAGTTATCCCTCT	0,0	TAACAGGGCTGCAACCACA A
Oki_RAD759 09-38	T	C	GGTGGATGTTCT GC	GGTGGACGTTCT GC	CCAGTCTACTTCCAGCTGGT GG	0,0	AGTCCTGCTCTGAGGGGAA G
Oki_RAD759 11-69	G	T	GACCTTGAAGGC AA	GACCTTTAAGGC AA	ACTAATCAGCGGCTCACCA C	0,0	TACCCTGTTGTAGCACCCCT
Oki_RAD762 18-42	T	G	ACCATTTCCCCAG G	ACCATTGCCCA GG	CCACAACCAGATCAGCACC A	0,0	AGCCTGTTGGAGTTGAGGT G

Oki_RAD772 07-61	A	G	GGAACCATTTAG GA	GGAACCGTTTAG GA	GACGGTTCTGACTGTGAGG G	0,0	CCTGGGGCTTGGCATTAGAT
Oki_RAD772 10-64	A	T	GTGCAAAGA[TC] ATTA	GTGCAATGA[TC] ATTA	TGAACAGCCCTGCTCAAGA A	0,0	TGTTTTGCCATTGTGTTTCC CT
Oki_RAD778 03-60	G	A	TCATATGTTGTTA T	TCATATATTGTTA T	TGAATGTGTCTGCTAAGTGT CA	0,0	TCTTCTGTAGCGTCCGTTGG
Oki_RAD778 83-62	C	G	TGGGGGCTCGTA CA	TGGGGGGTCGTA CA	CACCAGCGCCTCAAAATTG T	0,0	TGCATCGGCTGTGAGATTAA
Oki_RAD781 12-64	T	G	AATAAATGCACG AG	AATAAAGGCACG AG	ACCCGCATCATACTTATGCA	0,0	CTGTGTCCAGGCATGTGGTA
Oki_RAD785 43-33	A	G	CTCATCAGCATTC A	CTCATCGGCATTC A	CAGGGCACATCCTCTGGC	2,0	CTTTGGGAAGGAGCTGAGC A
Oki_RAD797 61-66	A	G	TATTAGATTTGTA T	TATTAGGTTTGTA T	TGTGTTGGCTTTATGTAGGC T	0,0	GTCTCTCAAAATCATTGTCT GTGGT
Oki_RAD804 60-54	C	T	AACACTCTGGCTT C	AACACTTTGGCTT C	GCAGGGTAAGCTCTACTGT CA	0,0	TTTAGCAGCCCTAGTGCCAG
Oki_RAD806 45-70	G	C	GCACAGGTGACG	GCACAGCTGACG	TGCAGGGAGGATAGACAAC C	0,0	TGCTGTTATTACCCCTCGT
Oki_RAD809 82-68	T	C	GCCGGGTATCGT CG	GCCGGGCATCGT CG	CAGCCTAGTGGACACCTGC	0,0	GTCCCCACCGTCTCCATAAC
Oki_RAD813 87-37	G	A	CTATCTGACTAGT T	CTATCTAACTAGT T	GCAGGAGTCCATGTCTACTC AG	0,0	AGTCCAATGGCTCCTGCAAT
Oki_RAD828 56-48	C	T	CGCCTACCAGTC GA	CGCCTATCAGTC GA	TGCACATGACCAGTACTCG C	0,0	GATCCACTGCATGCTCCAGT
Oki_RAD837 66-63	T	A	AAAGACTGAGGA AA	AAAGACAGAGGA AA	AGCAACATGACCACGTCAC T	0,0	TTGTTTTGTCCGGCTCCTGT
Oki_RAD838 75-36	G	A	TGTGATGTAGCT GC	TGTGATATAGCT GC	AGCTTGGCAAGGAAGTCTG T	0,0	GAAGTGGGCTAAACGCTCC T
Oki_RAD845 77-58	T	G	ACCTACTTCTGCC A	ACCTACGTCTGCC A	CAGAGAGAAGCACAGCACC TA	0,0	TGCTCTGCTTCCCTGTGTTT
Oki_RAD854 48-48	A	T	ATGGAGATATCT AC	ATGGAGTTATCT AC	AGGCAAAGCAATGGAGTGG A	0,1,0	GGAGGCATCTCTTGAAATG CTG
Oki_RAD859 49-47	G	A	TAACACGCGTTCT A	TAACACACGTTCT A	TCAGTTAGTGGGTCTCCTCT CT	0,0	TCGTCAACAGTGCAGTAGG C

Oki_RAD866 27-60	A	T	AGCATTATCACTT T	AGCATTTTCACTT T	TCCTCCAAACACCTGCTTCG	0,0	CTTGGGTAGCAAATCAGCC A
Oki_RAD871 41-55	T	C	AGCTCATTTCTTT T	AGCTCACTTCTTT T	ACCACCCAGTAAGGCTCCT A	0,0	TCTGTCCTCCAGACTCCTGT
Oki_RAD874 46-62	G	A	GTGTATGCAATC CC	GTGTATAACAATC CC	TGTGTGAGAGAGTGTGCGT G	0,0	GGGGAGCCCTGCATTAAGG
Oki_RAD876 21-67	T	G	C[CT]GCATTGCTG CTA	C[CT]GCATGGCT GCTA	TGCCCAAGGAATGACTCAC C	0,0	CAGCCCTGGTTGCATCCTTA
Oki_RAD877 77-48	A	T	GCCAACAAAGAC TT	GCCAACTAAGAC TT	TCGTAAATAAAGCGCGCCA A	0,0	AGGCTCTAGTCTATCTTGGG T
Oki_RAD885 51-51	A	G	GAAAGCATTTGC AT	GAAAGCGTTTGC AT	GGCTAAGGGCTACGCTAAC C	0,0	TGGCTCCCGAGATTCTGAGA
Oki_RAD892 59-51	T	G	TATTACTGAACA AT	TATTACGGAACA AT	GCAGGGTATCTGAGGCACA T	0,0	GGCAAAGAACAGCTATTAT GACCA
Oki_RAD893 74-40	T	G	GTACTTTCCAAG AT	GTACTTGCCAAG AT	TGCAGGCAAGGGAAGTTTA AC	0,0	CTGGTACTTAAGCCAGCAG GT
Oki_RAD913 62-68	C	A	ATGGCACATATTT T	ATGGCAAATATT TT	GCAGCAGAAGAGGCACAAG A	0,0	ACTGTAGAATTGCTAAAATC CCACA
Oki_RAD914 30-44	A	G	GCTGCTACAAAT GG	GCTGCTGCAAAT GG	TGCGAGGCCCTTCAATGTTA	0,0	AGTCTCACAACCCCTCTCT
Oki_RAD914 70-66	C	A	AGGTCACTGCTG AG	AGGTCAATGCTG AG	GGACCTGAACAAGTGGAGC T	0,0	TGCAATGCATGGAACCTCCTC A
Oki_RAD914 78-52	T	C	CGGCTATAGCTG TG	CGGCTACAGCTG TG	TGTAGCAGTCTAATGACCG GC	0,0	GCCTAGTTGCCTGACAATGC
Oki_RAD919 07-38	T	G	ACTGGTTGTGAG AC	ACTGGTGGTGAG AC	ACAGAGGAGCACATACTGG T	0,0	GGGCAGAAGGTAAGATATC AGACT
Oki_RAD928 75-31	C	T	ACACCACGCCGC TC	ACACCATGCCGC TC	CCAAGAGGGTGTCCATCGA C	0,0	TCGCCAACCCATCTCAACAT
Oki_RAD930 28-59	A	G	GCTCACAGAACT CA	GCTCACGGAAC CA	GGTGTGTAACCTGTCTGGAC A	0,0	GCCAAGCCAATTAGCTGTG C
Oki_RAD942 15-66	A	G	GAGGATAAGGCG GA	GAGGATGAGGCG GA	AAGGAGACACGATGGGGAG A	0,0	CTGCAGCTCCAGATGATCG A
Oki_RAD942 41-30	C	G	CAGTAGCCTCTTA T	CAGTAGGCTCTT AT	TGCAGGTGGGCAACAAGAT T	0,0	CTGTATCTCTGGACCATGCA GT

Oki_RAD960 72-42	A	G	TGAAGGATAAGC AC	TGAAGGGTAAGC AC	AGGGCACAGGAGGAGTCAT T	0,0	GCAGTGGGAGTTTGTGTGTC
Oki_RAD964 98-69	C	A	GCCAAACGCATC CT	GCCAAAAGCATC CT	CCACAAGGAGTTGCAAGAG CAT	0,0	CATAGGGCGCCGCATAATT G
Oki_RAD973 25-35	T	A	TCTTGGTCAGCTC C	TCTTGGACAGCTC C	TGCAGGGAGCTACAATGGT A	0,0	GCTCACCTCTCTAGCCCTCT
Oki_RAD979 93-40	C	T	TGGTTCCGTAATA C	TGGTTCTGTAATA C	GCTGCCCTGAGAACAGAGT T	0,0	CCTGTCTGTGTGATGAGGTG G
Oki_RAD982 80-45	G	C	TTTACAGTTGGTT T	TTTACACTTGGTT T	GGTCACGAGTCCTCTTGAGC	0,0	GGTGTGATGTGGCTGAAAC C
Oki_RAD984 85-66	A	G	TATTCTAATTGGC A	TATTCTGATTGGC A	GGGACCTTGACTGTTTAAAT TCAA	0,0	AGCACATGTGAAAGCCGAG A
Oki_RAD999 31-47	T	C	TTACCATCAATAT G	TTACCACCAATAT G	GCTCCAGAGGCTCCCTTTTC	0,0	CGCTCACTCCCTCCATCAAT
Oki_sast-230	A	G	AAGTAGTATTTGT T	AAGTAGTGTTTGT T	ACAGTAGTATCTATGCCTTT GAGCA	0,0	CGCATTGGCTAGATTACAT GG
Oki_SECC22- 67	T	G	TCCCAACTGTCTG T	TCCCAACGGTCT GT	ACTGTTGAAGACTTGTTTTT CCCA	0,0	ACCACTACAGGATGACTAC CT
Oki_srp09- 107	A	G	TGAGAGGAGAAA TC	TGAGAGGGGAAA TC	AACGGAAGAGAACGGAGCT G	0,0	GCAGCGAAGGTTATGCTCTC
Oki_sys1-141	T	G	TGGAAATTAAC GA	TGGAAATGAAC GA	TGGAACATTGCACACCTCTC A	0,0	GCAACCAGCACCATTTCAGT
Oki_taf12-40	-	T	CCTTTTAAATGCT	CCTTTTTTAATGC T	GTGTGTGATTTGTCAGCTCC AC	0,0	GAGTGTGTGATTTTGGCCAG T
Oki_thyK-100	T	G	ATTACCATTAGA CT	ATTACCAGTAGA CT	CCACCCTGCAACTCTGATCA	2.2,0	CCAATCCAAGTCAACTTCCC C
Oki_txnip-35	C	G	AGCTCTCCTCTGT G	AGCTCTCGTCTGT G	GGCAGGACCAAGGTCTTCC	0.5,0	GATGGTCTTTCCTGCCAGG
Oki30_54734 92	C	T	TCCTTTGTACAGC	TCTTTTGTACAGC	TCTGGAAGCACACCAATGA A	0,0	TCAGTTTTGCGCATAGAATT TG
Oki30_55514 09	T	C	TTTAACAGCTTG	TTTAACAGCTCG	CAGGGAAGAGGACAGTGTG A	0,0	CTGAACAAGGAGGTACCAG GA

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Appendix 5. GT-seq SNP panel for Pacific lamprey.

Assay	A 1	A 2	A1-Probe	A2-Probe	FWD Primer	Correc tion	Rev Primer
Etr_1004	A	T	TGCGATTAACGGTT CC	TGCGATTATCGGTT CC	GCGGTCTGCGTT	0,0	CGACCGCTTTCTCTCTGCAAA
Etr_1007	C	T	CACTCATCAGCGAG CCT	CACTCATCAACGAG CCT	ACACGAACACCCAAAAG TGATGT	0,0	ATGACTACTGACGATTCCCATTG AC
Etr_1022	C	T	TTTGGTCTGGTGAT CTG	ATTTTGGTCTAGT GATCTG	GCACGAAAGCACTGAAG CT	0,0	TCAGGAAGGTTTTGCATTGATA CCA
Etr_1034	T	G	CCGAATCCTTGAGC TG	CCGAATCCTGGAGC TG	CAGCAGCAGAACCGAAT CCT	0,0	ACCTTTGATGGTCCATGGGG
Etr_1060	A	G	ACTCGCCACATTGC	CTCGCCGCATTGC	TCGCACGCACTCACGTTA	0,0	GTGAAGTCCGTCGTCTTACCTTT T
Etr_1068	G	A	CCTCAACAGACTCT TGG	CCTCAACAGATTCT TGG	GGGCCCTGGAGGGTCA	0,0	GCACACGCAATACAAAGATTCC T
Etr_1104	A	G	GGGAATGACAACA CAA	GGGAATGACGACA CAA	AGCAGAGGGGGAAGAGG AAA	0,0	CCACTTGAGCTGCAATGTTGA
Etr_1106	T	C	GAAACCCAGTAGA ATTA	GAAACCCAGCAGA ATTA	TCCCTAGTTCTGAGAAAC CCAG	0,0	AAGGTCGCATCGTCAGTGTT
Etr_1131	C	T	GAGCTATCTCTGCA GA	GAGCTATCTTTGCA GA	TTAACGGCGTGTCATGCAT G	0,0	AAACTGGTGGAAAAATGTGGG
Etr_1163	A	T	TGCAACCGTGTTTA TAGAG	CAACCGTGTTTTTA GAG	TGCAGGAACGCGTAAAC	0,0	TCTGACGCTTGTATGGAATCTGT TC
Etr_1181	G	A	CACTCCACAGAAAC GGG	CACTCCACAAAAA CGGG	AGTCGACCACCTTGCTGA AG	0,0	GGGCAGCTGTCCCGTTT
Etr_1184	A	G	CCAGGCGACATGA GCTC	CCAGGCGACGTGA GCTC	CTTGCAGACCCAGGCGAC	0,0	GCTGTCTTTGTTTTTCGGGGT
Etr_1187	C	G	GCTGCAAATCT	GCTGCAAATGT	ACAAAAGCTGTCTGGCCT GA	0,0	CAAAGGACCGGGCTCTGTC
Etr_1193	T	G	GCGTTTTATTGACT G	GCGTTTTATGGACT G	AGCTACACTACTTTGGTG CGT	0,0	CTCCATCCAGCAGTGGGATT
Etr_1210	G	A	AGGCCGGCTCCTG	AGGCCAGCTCCTG	GAAGGAGCTCGAGTCGA GAG	0,0	GACACCGTAGAACTACCATGCA

Etr_1238	A	G	CATAACGGTGAAG CGAC	CATAACGGTGGAG CGAC	GATCTGGCAGAAGGCAA ACAG	0,0	AGATCTGGACGCTTGCAAGAC
Etr_1257	C	T	TGCGAAGTGATGCT GATAT	TTGCGAAGTGATAC TGATAT	GGCAAACGACCGCATCA AC	0,0	CACGAGCGGGTCCCT
Etr_1321	G	A	AGCCTGCGCAGACC	AGCCTGCACAGAC C	GTGGCGGACGCATTCAAG	0,0	GCGTCGTGCGAGGATGA
Etr_1341	C	T	CCAACCGGCGATAT G	TCCAACCGGTGATA TG	TGCAGGAATAACATTCTGA ATTCTACTC	0,0	GACATGACAGTCGCTAGATTCC T
Etr_1349	G	C	CCTGGGTTCAACCC	CCTGGCTTCAACCC	CGGTGAGCAGCCTCTGG	0,0	GGTGAAACCCCTTCATTGTGTG A
Etr_1359	T	A	TCGCAGACTTGCG	TCGCAGACTAGCG	CTGTATTGGTTGCTGTGCG CA	0,0	GTCACTTTCAATGCCCCGCTT
Etr_1376	C	A	CTGCATGTTCTGAC ACTG	CCTGCATGTTCTTA CACTG	GCAACTCAGGTGGGAAA CG	0,0	GCGGTCCAGATGAGATTCCA
Etr_1378	G	C	TCGAGATGTGGAA AGCC	TCGAGATGTGCGAA AGCC	ACACAAAGACTGGAGCA AATGG	0,0	CTCCCATAGGCTTGCTCGAG
Etr_1383	G	A	TCAAGCCGAACGTT G	TCAAGCCAAACGTT G	GGAGAGGACAGGTCCAA GGT	0,0	CGTAGAGCCTGCGAAAGTGTT
Etr_140	A	C	AACACAGTTGTCAC TGCT	ACAGTTGGCACTGC T	TGCGGTGGTATCTATACG ACGAT	0,0	ACACACACCAAGTACCACT
Etr_1428	T	C	TTGCGGTCATGATG C	TTGCGGTCGTGATG C	CAGCAGGGATATCATCAC CTTCTT	0,0	ATGGCACGGGCAGAGAA
Etr_1507	C	T	ACGGCAGCGCGCG GGGC	ACGGCAGCGTGCG GGGC	AAGGGACAATCTGAGAG CGC	0,0	CAAACCCGGACAGTGGCAA
Etr_1509	A	C	TATATGTATATCTC CAC	TATATGTATCTCTC CAC	CCACGGGTGGGTATGCAT AT	0,0	CCGAGGCCTAATTCACACCA
Etr_1522	T	C	CGCGATCCTCACCG C	CGCGATCCCCACCG C	TTTGCCGTGCTCATGTAT CTACA	0,0	GACCCTGCGGTGATCACA
Etr_1548	T	C	ATATTGCACTGACT	ATATTGCACCGACT	GCCCTAGCTATTAATGCC GGT	0,0	CTGGCACACAACGGCCTA
Etr_1551	C	G	CTACAAACCCCCGG CAA	CTACAAACCGCCG GCAA	GCGTAGAACAACAGGCC CTA	0,0	ACCCGGCTGTACCTGAGATA
Etr_1556	A	G	TGGCTGGAGACGCT GCC	TGGCTGGAGGCGCT GCC	AGCGCACATGGCTGGAG	0,0	GGTGCTCTGGATCAGGAACC

Etr_1561	A	G	GCCAAAGTCACGCT GTT	GCCAAAGTCGCGCT GTT	GTCGAAGAAGACGCCAA AGTC	0,0	TCGCCTTTTCTTAATGCGCG
Etr_1567	T	A	ACAGTTCGAAAGCC AG	ACAGTTCGTAAGCC AG	TTGCACCACCTCCTTGCT	0,0	GTAATGGTGGGACAATGCAAAG G
Etr_1569	A	T	TTGTTGCTGATTTT ATT	TTGTTGCTGTTTTT ATT	CGGGGTGAAGCAGTTTC CA	0,0	AAGTCACAACCTCTCTGGGT
Etr_1589	G	A	AACCGCAGGACAC ACA	AACCGCAGAACAC ACA	TGTGACCGCGTGAGCAG	0,0	CTTTGACTCCGTGCGTCTCT
Etr_1613	C	G	CCCCTGCCACCGTC C	CCCCTGCCAGCGTC C	CGCTTACGACCCAGTGCA TA	0,0	TTTACTGGTAGCACGCTCGT
Etr_162	T	C	CTGACCCCAACGAC C	TCTGACCCCGACGA CC	CGAGGCCTTCGCTGAGAA	0,0	CTGCGGTGACATGAAGTTGAAT
Etr_1667	A	C	GTTATTGCCACAAA TT	GTTATTGCCCCAAA TT	CGACACGGCACATCATT TAAGG	0,0	AGGTCAGCAAGGTATTGTGGT
Etr_1684	T	C	TGAGAGCCTTTCCA TCGC	AGAGCCTTCCCATC GC	GAGGAACCTGCGGGAGA AG	0,0	TGTGTTTGCGTGGAGGAGATG
Etr_1696	G	A	CCCGCGGCCGCC	CCCGCAGCCGCC	CCGTGTAGAGGTGGACAT AGG	0,0	TGGCCATCTGCATGTTGGT
Etr_172	T	C	TGTCCCCTATAAGG AGG	TGTCCCCTACAAGG AGG	CTCACGCTGCCCCCAGG	0,0	TACACGAGCAGCTCCTCCTT
Etr_1762	A	C	CCCCCTCTCATCTG GGG	CCCCCTCTCCTCTG GGG	TGTCACCAGAACCCCCTC TC	0,0	CACCCTCCCTGAGAAATGCC
Etr_1765	C	T	TTGGAGTCCCAAGC ACG	TTGGAGTCCTAAGC ACG	CGCACCGATAACTAGAGC GA	0,0	ACCAAAAAGAGGGGGCTCAA
Etr_1773	A	G	TTCAGTGAACACGT GGT	TTCAGTGAAGACGT GGT	GGTCTGGCTGAACGACAA TT	0,0	CAAACACATGGTGCCACACA
Etr_1795	C	T	GCGAGATCCCAAAT GGG	GCGAGATCCTAAAT GGG	CAGCGGGTGAACGTAGCT AC	0,0	ATTCAACACCTCGCCACCAT
Etr_1806	A	G	AACACTGACAATAT CTAAAG	CACTGACAATGTCT AAAG	GTAATGGCGCTGTCCGTT TG	0,0	CGAGTACTACTCTGGCCATGTA G
Etr_181	C	A	TCTCATCTCTCGCC TGCT	CTCTCATCTCTCTC TGCT	GAGCGGATGGGCGACTT	0,0	GCGCGCAGCACACA
Etr_1843	C	G	GTGCGACCCCAACG AAA	GTGCGACCCGAAC GAAA	TTACGGCAGCAAAAACA GCC	0,0	GCCCTGCTGAGTTTCAATGC

Etr_1848	G	A	TCTACATATGCATG TGG	TCTACATATACATG TGG	ACCGAATAAAGTGTGTCT AGCA	0,0	TAACTGACACCCACACTC
Etr_1857	G	T	GGTCTCCGTGGCTG TGT	GGTCTCCGTTGCTG TGT	CTGCTGTTCCGCGTGTGT	0,0	GGAGATGATCTGCATGCAGC
Etr_1875	C	A	CACCGAAGCCCAAT ATC	CACCGAAGCACAA TATC	CGACTTCCACATTAGCAC CG	0,0	GTGCATTATTCCAGCATTGCCT
Etr_1882	G	T	GGCGCGTTAGGATC TAC	GGCGCGTTATGATC TAC	TGCTCTGCTTTCCACAGA CG	0,0	GGGTTTGGCCACGTAATGATG
Etr_190	A	G	CTGACATTACAATG TTTTAT	TGACATTACAGTGT TTTTAT	GCAGGAGACCCTTGCTTG TC	0,0	AGGTGGCACACGAAAGTATCAA AT
Etr_1944	C	T	AAGGCTATCCGTGC	AAGGCTATCTGTGC	TGAAGTAGGTCTCCCAA GGC	0,0	CCCACAGGTACGCAAAGGTA
Etr_1975	C	A	GCAGCCCTGCAACT GCT	GCAGCCCTGAAACT GCT	TGTTAGATGTGTAAAGGC GCAG	0,0	AGAGGTCACAAACAGCCCTC
Etr_2013	C	T	TCAAGAATCACAG GCAGAG	TCAAGAATCACAA GCAGAG	CGTGGCGTCGCTTTCC	0,0	CCGACGCTCCGAGTGAAA
Etr_2015	C	T	GCTCGATGACGAG ACCG	GCTCGATGATGAG ACCG	GGGCTTCGGCTGCGTTAT AA	0,0	AGCTCCTTCTTCTGCTGCG
Etr_2016- 70	C	T	TCGACTTCCCGACA ATTT	TCGACTTCCTGACA ATTT	TTTCATTATTTTCTTGACG CTTGTG	0,0	GGATAGACGCCTCTGCTGAG
Etr_2050	T	C	GCTGTGCAGTGGAG GAG	GCTGTGCAGCGGA GGAG	CCCATGCTAAACGACCAG CT	0,0	GCACCTCACACATCTGCTCT
Etr_2066	G	A	CGCCTGCTCGCGCT CCT	CGCCTGCTCACGCT CCT	GAACCTGTGCGCCCTCACT C	0,0	GCGCAGGATGAAATTGCAGA
Etr_2068	C	T	GTGCGCACGCGGA ATGT	GTGCGCACGTGGA ATGT	CAGCACTGCATCGACGTG	0,0	CAGCTCTACTCGTACCTGGC
Etr_2071	A	C	GGCACAGGCACGA CACA	GGCACAGGCCCGA CACA	CACAGGTTCACTCTGGGT GG	0,0	AGAGCTGCTCATTGGTTTTCA
Etr_2097	C	T	CAGGTCTGGGAGCC GA	CAGGTCTGAGAGC CGA	GGGCGTGCGGACATACT	0,0	GCGAACATGGTCAACGAATGC
Etr_2099	G	A	ACCCGCGCGGACA CGTG	ACCCGCGCGAACA CGTG	AAGACCCACGGCGATTCA TC	0,0	CCCTCAACAGCCTTGCCATA
Etr_2107	C	T	CGAACGGCGCGAG AAGC	CGAACGGCGTGAG AAGC	TGACCACACGGCGTCTTC	0,0	AAGCACGAGAGCGCGTT

Etr_211B	T	G	GCGTAACCTTGAGC ACT	GCGTAACCTGGAG CACT	GGGTGGAGGAGCGTAAC CT	0,0	GTGCACGTAGTTGCGGTTG
Etr_212	A	G	TGCTTCTCTACTTTT GC	TGCTTCTCTGCTTTT GC	TCTTTCCCCGTGTGCTTCT C	0,0	GCGACACGAGGGTATTCGAT
Etr_2126	A	G	CCGTCCCAATTTCGC GCA	CGTCCCAACTCGCG CA	GAGACCGTGGGCGACT	0,0	GACGCGGCGATGTAGGT
Etr_2193	C	G	TGCGGCTGGAGAC G	TGCGGCTGCAGAC G	GGTTCATCTGGGAGCTTT TGC	0,0	AAGCCCACAGAGAAGTGACATC
Etr_2226	T	C	TTTGC GTTCTCGAC GCT	TTTGC GTTCCCGAC GCT	GCAAAACGCCGTACACCT TT	0,0	TAGTTGCGTTGAAAGCGAGC
Etr_223	A	G	CTATTGGTTATGAG GTT	CTATTGGTTGTGAG GTT	GTAAGGCGTGGGCTATTG GT	0,0	AGTTACTGAGATGACCGAGGA
Etr_225	C	G	CACTGGCATTGTCTG	CACTGCCATTGTCTG	TGGTTGAATCCAGTGCGG ATAAA	0,0	GTGCAAACCCGGTCTCTAATG
Etr_2272	A	C	GAGAGAAGGAAT	GAGAGAAGGCAT	AAGGGGCAGGGAGAGAA GG	0,0	ACAACAAGAACTGCAGCAGTG
Etr_2287	T	G	CTGCTTGTATCTCC CCT	CTGCTTGTAGCTCC CCT	TTCATGTGACACCTGCTG CT	0,0	GAGGCGGGTGTGCATACAGAG
Etr_2304	G	A	CGTGCTGTAGAGAG A	CGTGCTGTAAAGA GA	ATCGGCACATTTCTTCCC GT	0,0	GCTAAAGAAGCGCGATGGAC
Etr_231	G	A	ACGATGCCGTCCGC C	CGATGCCATCCGCC	CCAGGAATAAGGACACG GTTTGG	0,0	CGTCCCCTCCCTCCTTGT
Etr_2334	C	T	TTCGCTCAGCTCCC CG	TCGCTCAACTCCCC G	CCAGCCACCACGTTCAAG T	0,0	GTGCGGTTGGCAGAGATG
Etr_234	T	C	CCCCAGTGTGACAC C	CCCAGTGCAGACACC	CTCCTCCACGGCGATGTT	0,0	TGCACTACGAGAACAACCTCTCC
Etr_2409	G	T	CCGCACGGGGAGG TCCA	CCGCACGGGTAGG TCCA	CCAGGTGCTGAAGGGCC	0,0	GCTCTCGGCCTGGACAAC
Etr_2414	A	G	GCCAAGCGGACCC CTCT	GCCAAGCGGGCCC CTCT	AGACCATTCCTCTGCCAA GC	0,0	CCCCAGGGTGCTCTTAAACA
Etr_2416	C	T	TGGTGCGGTGCACG C	TGGTGCGGTACACG C	TCATTACACGAAGCCTCG TTCAG	0,0	CGGAGCCCTCCCTGTGT
Etr_2418	C	T	TAATCTTACCAAGT TTC	TAATCTTACTAAGT TTC	TCGGCCTATTAACCTCCGT GC	0,0	TGGGTACTGGCAGGAGAGAA

Etr_2451	C	A	TATACCTGTCGCCC CCA	TATACCTGTAGCCC CCA	GTGAGGGAGAGAGGGAA GAGT	0,0	CGAGAACACATACTGGGGGC
Etr_2460	T	C	CTGGCGGCTTCGCA CGG	CTGGCGGCTCCGCA CGG	CATGCAGCCGACAACTG G	0,0	CAACCTGCCCCGAGGAGTTC
Etr_2499	G	A	CAGAGAGACGGTG CTCT	CAGAGAGACAGTG CTCT	CCCGAGGGAGTCATCAGA GA	0,0	CCGTGCCGTTGGGTGAA
Etr_2512	A	G	TTTCCCGTGGACTC AC	CCGCGGACTCAC	AGCACGAGGAGCGAGAG A	0,0	TGCACTTTGAACATGGGTACAC
Etr_2517	G	A	AACCACTGCGACAC CGC	AACCACTGCAACA CCGC	GGCAGGCTGTGTAAACCA CT	0,0	ACGGAATGAGCGATCGATGT
Etr_2603	A	G	GTGCACATTATGGA CAG	GTGCACATTGTGGA CAG	GCTTTGTGCACCCTAACA ACA	0,0	AACCCAAGTGGCAAAACCTG
Etr_2642	T	C	GCTCCAAACTGGCA T	GCTCCAAACCGGC AT	AGAGATCCCTGTGGCTCC AA	0,0	TCGTGTCATCGTCGTCATC
Etr_2675	G	A	AAGACGACGATTCC CT	AAGACGACAATTC CCT	GCTGGATAATTGGCATCT CACACA	0,0	CTCAATCGTCTGTTCGCCAAAC
Etr_2730	G	A	GTTGAACCCGTAGC GCG	GTTGAACCCATAGC GCG	CAGCCACCTCGAGAGCTG	0,0	ATGGGAGGGCATTGAGGTG
Etr_2765	C	T	TTAATCATGCCAAT GCC	TTAATCATGTCAAT GCC	ATCTGCACAAGCTTCAGG TT	0,0	ACGTGTTAAACCGAGCCACT
Etr_2776	A	C	GGAGCACCCAAAC	GGAGCACCCCAAC	GTACCTGGACGTCAAGCA CA	0,0	CGACAGCTGCATTGACATCG
Etr_2791	A	G	CCCAGAGAAACAG CAGA	CCCAGAGAAGCAG CAGA	AGGTGGTACTGCAATGGA CC	0,0	GCTCCGTCCATACCATCATATGT
Etr_2823	C	T	CGCACGCGCCGAG CAGT	CGCACGCGCTGAG CAGT	ATGTGCGCCATGCCGAT	0,0	CACACGGGGGATCTTTGTCT
Etr_2841	G	A	CGCATCTTTGTCCC TGC	CGCATCTTTATCCC TGC	ACAGGTAGTACTGCAACG CA	0,0	GCTGGATGCTTGGAGACCAT
Etr_2858	T	G	GAAAAGAAATGGT TTGA	GAAAAGAAAGGGT TTGA	GGCAGAGATCCTTGAGAG CA	0,0	CTCCACTATTCCGCATCGTGA
Etr_2878	C	T	CTTGTCAATCTCCA CGA	CTTGTCAATTTCCA CGA	AGCTTGCATCCGTGACTT CA	0,0	GGTTGTCAAGGTTCTCGTGGA
Etr_2915	C	G	ACAGCCTCCCTTCC AC	AGCCTCCGTTCCAC	GCCCTTCAAGTTCCAGTT CAC	0,0	GTTACAGTAGATCTTGACCCTT CA

Etr_292	A	G	CAAATAAACACCA CACA	CAAATAAACGCCA CACA	ACATGCAGAATAGGGAC AGAACA	0,0	CGTGTGCCTCACAGTGAGAA
Etr_2937	T	C	GGCCACGTTTTTCC GCG	GGCCACGTTCTTCC GCG	CTTCGTGCTGGTGATCGG TC	0,0	CACCACCTCCACGTAGCAG
Etr_2971	T	A	CATTGAGGGTGCA	CATTGAGGGAGCA	AAGCTTTACGTGCAGGCT CA	0,0	CAGCACCACCTTTTTCCGTG
Etr_2974	G	A	CGCCTGCCCCGCACA CCT	CGCCTGCCCCACACA CCT	TGAGACCAGCGCACCTG	0,0	TGAGTGTGCATGGTGAGTGT
Etr_2990	A	G	CTCAGAGACATCCT CGG	CTCAGAGACGTCCT CGG	GAGCCTCTGGGTGATCTC CT	0,0	GGAGAACCCGTTTGCGTTTC
Etr_3007	G	A	GGTTGTAAGGGTTG GGA	GGTTGTAAGAGTTG GGA	CGGTGTGAAAATCAGACG GG	0,0	CCGGTTGGCCTCACATAACT
Etr_3037- 68	A	G	TCTGCAAAAGACAC AGA	TCTGCAAAAGACA CGGA	CACCTTCAGGAAGCACAC GA	0,0	GGGTACGCACAACTCTTGGG
Etr_3038	G	A	TTTCTACTCGGCTC TAC	TTTCTACTCAGCTC TAC	AGTCGACCCCTCAACCAC AA	0,0	ACGTAGTGCAACAGTAGAGC
Etr_3069	C	T	TTAAGGCGCAACAC AC	TTTAAGGCACAACA CAC	GGCAATCACATCTGTTTC ATGCA	0,0	CCAGACGCAGCCATGTATACTG
Etr_3081	T	G	TCACAATCATCTCC TGG	TCACAATCAGCTCC TGG	TCCCTCCCTGTTTCAAAG CC	0,0	CTCGGCTTGTCTTCCAGGAG
Etr_3107	C	T	AAAGGACACCACA GATT	AAAGGACACTACA GATT	GGCAAATCCTTTCTAATT ACCATCC	0,0	GCATCTCTGGCTGGCTAACA
Etr_3128	C	A	ACCAGTCACCAATG ACT	ACCAGTCACAAAT GACT	GGGACACTTGGAAGGAC ACC	0,0	AGGATTCCGACCACTTCACA
Etr_3145	C	T	GGTGCCCATCGGAG GA	GGTGCCCATTTGGAG GA	TGGTGATGACGATCGTGG TG	0,0	TTCATCATCTTCCGCACGGT
Etr_3169	C	T	AAGCCGGTGCCACC GAG	AAGCCGGTGTACC GAG	ATAATGGTTCGCGACAGG CA	0,0	ATAACACCGCAGCATCTCGG
Etr_3189	C	T	CACGCGCGCACGC	CACGCGCACACGC	CAGGTGCAGTACGCACTC A	0,0	GCGCCAACCGCTACAC
Etr_3234	T	C	TGATTTCTTTAGCT CCT	TGATTTCTTCAGCT CCT	CCAAGTGCTAAGTACTCA CTCTGT	0,0	TGTTTCATGAAGGGCACTGAGA
Etr_3240	T	C	AAACCTGGGTGTGG GCC	AAACCTGGGCGTG GGCC	ACCTGCGTCAGCTGAAAA AC	0,0	AAAACCATTTTCGTTGAGGGCC

Etr_3253	A	G	CGAGTTCACACGCG AA	CGAGTTCACGCGCG AA	CAGGAGCAAGAGCAGTC TCA	0,0	CCACTTGAGCTTAAGTTCGCG
Etr_3255	C	T	GTGGGGGTCCCCGA TGG	GTGGGGGTCTCCGA TGG	CAGCCACTCCACCACCAT G	0,0	TTCGAGTGCCAGATGACGC
Etr_3262	C	A	CCAAGAATGCT	CCAAGAATGAT	AGGTGCCTCCTTCCAAAA GT	0,0	ACTGTACCAGCTTAAGTGGAAA
Etr_3292	G	A	TGCTCTCAAACGTG TTCCA	TGCTCTCAAACATG TTCCA	GCAGGTGAACTGATTTCA TGTATCCA	0,0	GAGCGGCAGCCTAGGAA
Etr_3330	G	A	GAAGTTGATGGTTT GGG	GAAGTTGATAGTTT GGG	ACTGGGGAAATGTGAACT TGA	0,0	ACAACCCCTTGTGTCTGTC
Etr_3350	G	T	AGCAGGCCGTCTGT C	AGCAGGCCTTCTGT C	GGCAGGCAATAGATCCTC ATTCAG	0,0	TGATTTTGGGCGAAGATTAACG T
Etr_3356	T	G	GCATACACGTACAA CAG	GCATACACGGACA ACAG	GTCATTGCTCCACACACG TG	0,0	CGGTGCTCGCAAAAAGAGAG
Etr_337	T	C	AGGTGAGTCTTTGT	AGGTGAGTCCTTGT	ATCGTCAGGAGGAGCCCA G	0,0	CTGGGTGGCAGGTTTCACAA
Etr_3383	T	G	CACCCGTTATAGAA AC	CACCCGTTCTAGAA AC	GGTCGTCTCGAGGTGTTT GG	0,0	GCACGCACGCGTCAA
Etr_3403	T	C	CGTATCCTTTTCATG GGG	CGTATCCTTCCATG GGG	GCAAACCCAAATACGCAT CGT	0,0	TTCCAGACAGCAAGGGCAG
Etr_3411	G	C	GCCGACCCCGCAGC CCG	GCCGACCCCGCAGC CCG	ATGTCGCACCTCCACATG AG	0,0	CGGGATAACTCACGGGCTG
Etr_346	G	A	TGAATTTTCGGCCA TAC	TGAATTTTCAGCCA TAC	TGGCGTGATCGGTAGAAA CT	0,0	TGCAGCAATATAGACCTTACCT GT
Etr_3466	G	T	AATGGACACGATTC CAC	AATGGACACTATTC CAC	TGCCCCGAACATTGTAAT GGA	0,0	ACGTAGCCATTCGACCACTT
Etr_3502	A	T	AACCCAAAAAAAT GCTT	AACCCAAAATAAT GCTT	TACAGCGCTACACATGCA CA	0,0	GTCTTTAACGTGAAAGAACCTC CA
Etr_3549	A	G	CCCGTACATGGTCA CC	CCGTACACGGTCAC C	CAACCGCCATGCTTGCA	0,0	CTGCCGCTCGGGTCT
Etr_3555	C	T	CACCAACCGTGGCA AT	CACCAACCATGGC AAT	GCCCATCGCTCGTTTCAC	0,0	GCAGTGCGCCAACCATAA
Etr_360	G	T	TGGTGCGTTGGTGG TGC	TGGTGCGTTTGTGG TGC	TGCTTTCCATGAGTGGTG GT	0,0	AAGTGTGCGCATTTTCATCCG

Etr_3601	T	A	CCCAAATAATAAAC TTT	CCCAAATAAAAAA CTTT	TGGCTCTCCACTATCCCA AA	0,0	GCCTTTGTTTTGATTACAAGAGC A
Etr_3638	C	T	ATTGTAGACCGAGC TGC	ATTGTAGACTGAGC TGC	TGTGCACGTTCTTAGGTC AGA	0,0	ATTAGTTGTGCACGCAGCTC
Etr_3725	T	C	TAGGTATCCTAGCT CCA	TAGGTATCCCAGCT CCA	ACACTGCTCCAGTAGGTA TCC	0,0	AGATAGGGCCCAGACAGCA
Etr_378	G	T	AGTCAAAATGTATT TTA	AGTCAAAATTTATT TTA	CTGAGAGGCTGTCTGCAG AG	0,0	GCCCTACATTTGGGGAGTCA
Etr_3837	C	T	GACAATTGTACGTC GCC	GACAATTGTTACGTC GCC	TGCCCTAAAGTTGACATC CGT	0,0	CCAGAAAGAATAAGCGCGGG
Etr_384	G	T	CCAAGATTTGTAAT CTC	CCAAGATTTTAAAT CTC	GCCACCCATTCTGGAATT CCT	0,0	ACGCATGTCCCATGATGCT
Etr_3885	T	A	AACATTATTTACAG TTA	AACATTATTAACAG TTA	GCACTTTGCTCGTACTGA ACA	0,0	GCCAGTGATCCTGAGGTTTCT
Etr_3939	C	A	GGAGACCAACATA TATC	GGAGACCAAAATA TATC	TGAGTGTTCCCTCGGGGAG AC	0,0	TTCGCTGAGGGAAGGAGAGT
Etr_3960	T	C	CATCGCCATTGATC G	ATCGCCATCGATCG	TGCAGGGGATTACTGGTGT CAAAAT	0,0	CCCCTGGCCGCTTAGAAA
Etr_3963	C	A	TGTTGTGTGCGATG A	TGTTGTGTGAGATG A	CCCAGAAGGATGTTTGT GTGT	0,0	GCATTGCGGTTAGAGCACTG
Etr_4000	T	C	TTGCACGTCTAAC	TTGCACGTCCAAC	CAGCGCTCTGGATTGCAC	0,0	TAGGCCCAGGAGGAAGCC
Etr_4015	G	A	TCTCGTCTCGGGGA CTG	TCTCGTCTCAGGGA CTG	ACTGTCTGATTTCCCTTCT CGT	0,0	CGGTAAATCGTGCATTGGGC
Etr_4028	T	C	ATAAATCAATGTCG CCC	ATAAATCAACGTCG CCC	TGCCTTGGAATCCGACA CC	0,0	TGTTGTTCCGTGGGCGAC
Etr_4037	G	T	TCACAAAATGAACT TGA	TCACAAAATTAAC TGA	TCCTGGTCTCTTTATTTCT CACAA	0,0	GCTTTCTCACAGCACTTGCC
Etr_4079	G	A	CTACATTCAGTTTA ATG	CTACATTCAATTTA ATG	TCTATGGGTGATTGCCAT GTT	0,0	TGCACCAATCTTACCACGGA
Etr_412	G	A	CCTCGAAGCAGCTT T	CCTCGAAACAGCTT T	GGTAGCTTCTCCCCCTAA TGCT	0,0	TGGTGAGAAAGAAGTTCAACAT GCA
Etr_4130	A	G	ACGATGGCAACGA CG	ACGATGGCGACGA CG	CAGGCCGTTCTGCG	0,0	GCTCCCCTCGGAAGCC

Etr_4142	T	C	TGTGCAAGCTGCCT TCA	TGTGCAAGCCGCCT TCA	CATCCTGTGGTCTGCACC TG	0,0	GAGACGATGTTGCTGAAGGC
Etr_4156	A	G	TAGCAGCTCAGGGT GCA	TAGCAGCTCGGGGT GCA	GTAGCGGTTGGTGTCTAG CA	0,0	GACGTCATCCTCAACGGCC
Etr_4165	C	A	GCCAATATTCTC	GCCAATATTATC	ACTTTCCTCTATCTTGCGC CA	0,0	GGAGACCGAACAGAGAATGGG
Etr_4173	A	G	CCAATGCATAAGTA ATC	CAATGCATGAGTA ATC	GCACAACAATGTTATAAC GGCACAA	0,0	GACGCCATGTCAGAGAGACT
Etr_4194	A	C	TGCGAATCAAACCTT CAA	TGCGAATCACACTT CAA	ACTTTCCTCAATGTGCCATG CG	0,0	ACTCCATCGTAACTGCAGTGA
Etr_4214	C	T	TGCGTTCACGTTCA TAG	TGCGTTCACATTCA TAG	TGGGTTCCCTCGCACTGTT AG	0,1	TTCACGTTCCCTAATGCTGTCTGA
Etr_4215	A	G	GATGTAGCGATACG TGA	GATGTAGCGGTAC GTGA	TCCTCGTGGATGATGTAG CG	0,0	GGGCTGCACCAATACCTCTT
Etr_4254	G	A	CTTTCCCATGTGTG CCT	CTTTCCCATATGTG CCT	ATTCTGCTTGTGCACGC TT	0,0	CGAGAGCCTTCACGCCTAAT
Etr_4281	A	T	ACGTGGCAGTCTAT G	ACGTGGCTGTCTAT G	TGCAGGAGGACTACACCA ACT	0,0	GCACGGTTAGTCATTGGGTCAA
Etr_4288	A	T	AAGGATGATAG	AAGGATGATTG	AGCCACATTGCTCCTCAT GT	0,0	TGGTGATCGACTGAACCAGC
Etr_4390	T	C	CGGTGGTCATGGGT CAT	CGGTGGTCACGGGT CAT	ACGTAATAGTTGGCGGTG GT	0,0	GGGCCTCACCTGGTTTTTCAA
Etr_4414	G	C	AGGAGGCCGCCCCG AG	AGGAGCCCGCCCCG AG	CTCCGCATTAACCCCTTT GTC	0,0	GCGCGTGTGTCCAAAATTG
Etr_4455	T	C	GTCTGAGCTTGCGG GGG	GTCTGAGCTCGCGG GGG	TCGTTCCGGGGGTCTGAG	0,0	GCCGTAGCTATTTGAGTCACG
Etr_4479	C	T	CATGATGCCCTTCT TGC	CATGATGCCTTTCT TGC	AATGATGTGCGCGCTGTA CT	0,0	CTTGCGTGGGAGTACCGC
Etr_4498	T	C	GCAAGGGGTTGGT	GCAAGGGGTCGGT	TGGCAAGTGGCGGTAATT CT	0,0	AATGAATCGTGGCCCCTCTC
Etr_4504	C	T	CTGATTGTCCACAC CAA	CTGATTGTCTACAC CAA	TCAGACACTCCTGAGATC CCA	0,0	TTCATGGGTGGGAGTGGGAT
Etr_4521	C	A	GGTTGCACGCAAA GTCC	GGTTGCACGAAAA GTCC	GTAGCACAGCGGGATCTC C	0,0	CCTCGTCTCGCTGGACTTT

Etr_4531	G	A	CCGCACGCGCTCG	CCGCACACGCTCG	GTTTGAGTTTGCGAAAGG TACGA	0,0	GTACGTAGCGAGCGTGTGT
Etr_4544	G	C	TGTGATTCAGCAAC CCT	TGTGATTCACCAAC CCT	GGCACACTGGTTCCATCT CT	0,0	GAATTCGGGGTGTGGAGGTT
Etr_4574	G	T	CTTCCAAAGGCCCT GGT	CTTCCAAAGTCCCT GGT	CGGCGCACATCTTCCAAA G	0,0	GAGTGAAGACGACGTCTCG
Etr_4596 B	G	C	TTCTGGTAGGCCGG AGG	TTCTGGTAGCCCGG AGG	GTGTGGGTGAGATGAACC GT	0,0.7	TTCCACATTAAGGCCTCCGG
Etr_4633	G	A	CTGGGCAACGAAA GCA	CTGGGCAACAAAA GCA	GAAGGGACGAGGAGGAG AGG	0,0	CATGTCCAAGTCGCTGCTTT
Etr_464	C	A	TAGCGCTTCACCCC GTCCA	CGCTTCACACCGTC CA	TGCAGGGACCGCGTTAC	0,0	GTGCCCCACCGGTCT
Etr_4670	G	A	CCGTAACACTGTCC CCGG	CGTAACACTGTTCC CGG	AGGATCCGAGCCCATAAT GAGA	0,0	GTTTGGTTCGACATCGGAAAAGG
Etr_4686	T	C	GGTCTGCTATTCGG TG	GGTCTGCTACTCGG TG	CTAGGATAGCAGCACCGA CG	0,0	CCAAGGCCCTATGCGTAAA
Etr_4694	A	C	ATCACATACATAAA	ATCACATACCTAAA	GCACCATGACGCCTTCAT TC	0,0	TCTGTTGAGTGGTGTGATATGCA
Etr_4716	G	A	CATCAGAACGATA GCCC	CATCAGAACAATA GCCC	GCCGACACGAGCATCAG AA	0,0	CCTGACTGTCTTGCCACGTA
Etr_4750	T	G	AGCTCGTTTTTC	AGCTCGTTTGC	CAAGGTAAGCGGCAGTC AGA	0,0	ACTGCAATATACACCTGTCCTT
Etr_477	C	T	AGCTGCAGATCACC A	AGCTGCAAATCACC A	AAGTGGGTGCTGGACTGG	0,0	TCGCTGGTCCAGTAGATGGT
Etr_4800	G	A	ACCTGGTGCGAGA ACGG	ACCTGGTGCAAGA ACGG	GCGCTTGGGTTTCTTGTT GA	0,0	CTGCTGCTGCTGATTGAGTG
Etr_480- 67	C	T	TTACGAACACTCG	TTACGAACATTCG	CGCACGTGCCTTGTTTAT GT	0,0	TCCGACAATTCGCAAGTCGA
Etr_4845	G	T	AGATGTCCAGTCGG GGC	AGATGTCCATTCGG GGC	AGGAATCCGATGAGCTAC GA	0,0	CGTACGTCGGACACCACTG
Etr_485	A	G	CACCAATTAAGCAT TGTATTT	CCAATTAAGCGTTG TATTT	CAGCCACCGTCGACACA	0,0	AACTGCTGAAGTTACTGATGTTC ACA
Etr_4853	C	T	CGTCGAAGGCCTCC AGC	CGTCGAAGGTCTCC AGC	CCTCGCACGGGGGTCTAT A	2.4,0	GTGCAGGTTCACTCTCCCC

Etr_4859	C	G	CACAGGGATCGAT GGCA	CACAGGGATGGAT GGCA	CCCTGACCACCCACTCAC	0,0	AGCTTATATTAACGCAAGCGGC
Etr_4889	T	C	AGGTTATGTTATGA AGG	AGGTTATGTCATGA AGG	TGTTGGGAACAGGGCACA AA	0,0	CTTTGTTTCGCGCCTTCGTTC
Etr_49	A	T	TTGTGATGCAACTT CGT	TTGTGATGCATCTT CGT	TGGGTGAGCGAGGATGGT	0,0	CGTCCACACTGCGTTCAAC
Etr_4965	T	C	CCACCGAGTTGGCT AC	CACCGAGTCGGCTA C	GCGCCAGGTGAGGAGA	0,0	CTCCTCTTCCTCGTTGCAACTT
Etr_5020	A	C	TGCAACGAAATAAT TTAC	TGCAACGAAATCAT TTAC	CCCCCACGTGACGCA	0,0	GCTGCAATGTGGGAGACCTTT
Etr_5043	A	C	AACAACCTTTAATTC GGC	AACAACCTTTCATTC GGC	TGCAGGGTTTATATTTGC CAAATCA	0,0	GGCGAATGGCGGTTGTTATT
Etr_5112	C	T	TTGGGGGTGCCCTT AGA	TTGGGGGTGTCCTT AGA	AGAACAGCTTGCATTGGG GG	0,0	GGCGTCTCGGAGCAAGTTAT
Etr_518	C	G	TCAGCGGTGCCAGG TCG	TCAGCGGTGGCAG GTCG	CCGGGATTCTGAATTCTGG GT	0,0	CCTGAGCAGCCCGATGG
Etr_5193	T	G	TGGTTAATTCACCA GAAGTA	TGGTTAATTCACCC GAAGTA	ATTGGCCGCCCTCATGAA	0,0	ATACACTGTGAAGCAGATGGAA CTT
Etr_5197	C	T	ATATATTTACGCGA TCTAAC	ATATTTACGCAATC TAAC	GCAGGTGATTTGTCCATA AGAGGTT	0,0	GTGGTGGGTTTAACGACACATT T
Etr_5267	G	T	GAGACGCGCGGGC ATGC	GAGACGCGCTGGC ATGC	GGAAAGAGGCTCCGGCT G	0,0	AGTTGTCCATCATGCGCTCA
Etr_527	A	C	CAGCAGAAAAAGC A	AGCAGCAAAAGCA	GGTTACTCGGTTGGTATC ACACA	0,0	GGCAATGCTGCTGCTTCTG
Etr_5272	C	T	GCGCGCAAACGAT GCTC	GCGCGCAAATGAT GCTC	CACCGTGTCCGAGTCGTG	0,0	GAGGACAGAGCGTGAAGGAG
Etr_5317	A	C	CACGAAATTTTGAA CTTTT	ACGAAATTTTGCAC TTTT	CGGATTTTCACCTTTTCTG CGTTTC	0,0	CAGTTCACGAGCCAGACTACAG
Etr_534	T	C	CCGTGCTCGTACAA	CCGTGCTCGCACAA	CTCCACGGTCTGCGTGAA C	0,0	CGGGTTAGCCTTCAAGGGAG
Etr_5346	T	C	AAGGCTCAATAATG C	AAGGCTCAGTAAT GC	TGTGTGGGAAATGACAAC ATCCAT	0,0	GACATACGGTGCTGGTACTACA AT
Etr_5352	A	G	AGAATCTGGACAAT GGC	AGAATCTGGGCAA TGGC	ACAGGATCTATGGTCTGC AGAG	0,0	ACCCGTGAGACTCGTGAAAA

Etr_5465	A	G	CCGCGTGTTCACAGC	CGCGTGCTCCAGC	CGACTGCCCTTCGATGCA	0,0	TTGACCTTGACGGATTGGATCTC
Etr_5510	A	G	TCGTGTTGACCTCT TCAGTA	CGTGTTGACCTCCT CAGTA	TGCAGGAAGTAACTGTGT AATTAAACG	0,0	GCGACGTAAATATGTCTGCAAG TTT
Etr_5540	A	G	CTTTATGCCAACTG ACA	CTTTATGCCGACTG ACA	AGGCTGGAGTGGCGAATT TA	0,0	TGGAGGGAATGCCTTGTTCAG
Etr_5581	G	A	ACCTAATCCGTCT	ACCTAATCCATCT	CCCCACCTACCTGCTGAT GA	0,0	TGATAGGCGCGAAACCCATT
Etr_5600	G	T	CCAATGTCACCTTGC ACCGA	ACCAATGTCACCTTT CACCGA	CAGGAGACGTAGCCCCTC TA	0,0	GAGTAGACAAGAGAAGACGAA TTCACA
Etr_5603	G	A	GATACTCCAGCTCC TTG	GATACTCCAACCTCC TTG	CGCTCCACATTGTTGAGA GC	0,0	GTTGTTGTGAGCTGTGCTGC
Etr_5626	T	C	TGTGTGATGTATTG GGC	TGTGTGATGCATTG GGC	ACGTTTTTGATAAAGGTC CCGC	0,0	GTCTGAATTTTCCTTGTGCCCA
Etr_5654	T	G	TGAGGAATGTAAA ACTG	TGAGGAATGGAAA ACTG	AGGAGATCGAGAGGCTC ACA	0,0	TGAGACAAGGGTTCACGTGG
Etr_57	A	G	ATTAGCACAACGTG CCG	ATTAGCACAGCGTG CCG	GCGCCAATTGTGTTTTGT TGA	0,0	CCCCTCGGAGGTTTATTGCA
Etr_5711	C	G	CTCCTCTGCCGCGC GCA	CTCCTCTGCGGCGC GCA	CTCAGGCTGGATCGATGT CG	0,0	TTAACGCACGGACATCACCA
Etr_5757	A	G	GGTGCCAGGAAAG G	GGTGCCAGGGAAG G	TAACCAGCATCGCTTCGG AC	0,0	ATGTCCACATCGTCCTGCAG
Etr_5762	C	G	GCGCGACACCAAC GACG	GCGCGACACGAAC GACG	GGTAAACGTGGAAAGAG CGC	0,0	AAAGTCCCCGTCTCTTCGTC
Etr_5780	T	G	TTGTGATCTTCAGT ATT	TTGTGATCTGCAGT ATT	AGCTGGGTGGTTGAGTTG AG	0,0	ACAATGCGTGTGTTCAACCG
Etr_5831	A	G	GCAATGCGCATGCG CGC	GCAATGCGCGTGC GCGC	GCGCTCTCGATCCCTTGT TA	0,0	ATAAACTTCGGGTGGCCCAG
Etr_5960	C	A	ACTCGTCCACCAAA CAT	ACTCGTCCAACAAA CAT	TGAAGCCAAACACTCGTC CA	0,0	ACATGGAGGGCATGCAAATG
Etr_5993	T	A	TGGAGTCGATTGGA AAC	TGGAGTCGAATGG AAAC	GACACGTCCACCACAGGG	0,0	TGTCAGTGTTTTCGCAACGAC
Etr_6026	C	T	TCCACCCAGCCCTA CC	TCCACCCAGTCCTA CC	TCGGGAGGCACGTTCTTC	0,0	GCATAAAATCGGCAGAAATGAG AGA

Etr_603	G	A	AGGTGTTCCAAGTT TGTT	AGGTGTTCCAAATT TGTT	CAGGAGGAGAAGCCGTG G	0,0	GGGCAGGGAAGAAGTGAGT
Etr_6076	T	C	AGGAGAAATTCCTC AGC	AGGAGAAATCCCT CAGC	GCTGAGCATTCTCCGAG GT	0,0	TCAGCCAGCCACTTATAGGC
Etr_615	A	G	CACGGCACGGTCG	ACGGCGCGGTCG	GCGGCTTGGGATGTTATC TTCAATA	1,0	GCCTGGGCGGCCTATC
Etr_6179	T	C	AGCTCGCAGTGAC	AGCTCGCAGCGAC	ATGCCAGGACACAAGTTC GT	0,0	CTGCTCATGCTCCACAGGTC
Etr_6229	A	G	TTTGGTGCAAACCTT ACC	TTTGGTGCAAGACTT ACC	CCCCCAAACATTGCTTTG GT	0,0	ATGCTGGTTGGGCTCTTACC
Etr_6318- 70	C	T	TGCCCCGACGCGACT C	GTGCCCCGATGCGAC TC	GACTTGTTCGGCACTAC CC	0,0	GCCGTGAAAGAGAGCGTGAG
Etr_6363	A	G	CTAAAGTATAATTA AAG	CTAAAGTATGATTA AAG	CACGATGCCACAAACATG TCA	0,0	GCGTTTCATTTTTTCATTGGATCC C
Etr_6369	C	T	GCTGGTGCACAAGC AGA	GCTGGTGCATAAGC AGA	GAGCAGGACAAAGGCAG GAG	0,0	CTCCGCTCCAGCTGATTCA
Etr_6389	G	A	AATGGTAAACAGA GCATTG	ATGGTAAACAAAG CATTG	ACATTACCTGTAGGTGGT TGTTAAAGG	0,0	CCACGATTATAATCGGCAAGAT CAC
Etr_64	A	C	CCTGTACTGAAAGT AACTC	CTGTACTGAACGTA ACTC	GGAGGCGCTGTAGCTTCA T	0,0	AGGACTTTCTTTTAGGTTTGTA GCCAAT
Etr_640	G	A	AAGTAGGATGGTG GCCT	AAGTAGGATAGTG GCCT	AGGTAGCACAGCAAGTA GGA	0,0	AATGCCCCAAAAATCCGTGG
Etr_642	G	T	TGCAAGGTTGGAA	TGCAAGGTTTGAA	GACGCTCACTGCATGCAA G	0,0	ACCATTTTCATGCCACCCCA
Etr_6436	G	A	GTCAACAATGTGCG ACA	GTCAACAATATGCG ACA	CAGGGAGCACTCGTCAAC AA	0,0	GATGTGGCCAGTGACAGACT
Etr_6440	G	A	ACAGCGGTTGTCCT CAG	ACAGCGGTTATCCT CAG	AGTCAGTACATTGAGTTC CAACT	0,0	ATCCCTCATCCCCATGGTCA
Etr_668	A	G	CGCAACCAATGCCG C	CGCAACCAGTGCC GC	GTCCCGTGGACAAGAGTC A	0,0	GCTGCCAGGCACTTGTG
Etr_673	C	T	CGGCCGCTTCTCT	CGGCCACTTCTCT	GCCGACAGCTGCTTCTCT	0,0.5	CCACGTTGCTGTTGTTTTGTCA
Etr_678	G	T	GGTAGGTCAGGTCC GCT	GGTAGGTCATGTCC GCT	AAACTGGGCTTGGTAGGT CA	0,0	ATTCTTGACCGTCGGCTGTC

Etr_681	C	T	AGCACGAGACGAG CGG	CACGAGACAAGCG G	CGCGTCGCCATAGGTGTT	0,0	CAAGCACATGCTCAGCAACAG
Etr_687	C	T	TCGCCACTTCATTC ACC	TCGCCACTTTATTC ACC	AAGAAGCTCCATCGCCAC TT	0,0	CGTGGTTTCAGTTGCGAAGG
Etr_705	G	A	CCGCTATCTCCGGC TGG	CCGCTATCTCCAGC TGG	AGCAGAGACACGCAACG TAAATA	0,0	GGTTGTGCTGGACATTGTTATTT GA
Etr_7081	T	C	ACATTGTTCTATTC TCA	ACATTGTTCCATTC TCA	GGAAGAAAGAGGGAGGC CTG	0,0	AGCACAATTCGTCGTAAAGGG
Etr_7142	G	A	GGTCTTGGCGCCAC GGT	GGTCTTGGCACCAC GGT	ACCGGTGTTCTCTTAGGG GT	0,0	GGCATAGTCAGGGTCGAACC
Etr_7166- 73	G	A	TTCAAAAGTTGTCTG A	TTCAAAAGTTGTCA A	CAAGCAGCAGTGAGAGG ACA	0,0	TGCCAGTTTAAAGCTAAGCGA
Etr_717	T	G	CAAGACAAAGATC CACACGTG	CAAGACAAAGATC CCCACGTG	CCCCAAAGAGTACGAAC GGTTA	0,0	CGATCGCTCGTCAGATTCTCA
Etr_7292	T	G	TGGTAAAATTTACT	TGGTAAAATGTACT	CAGAAGTGATTTGGAATC GGCA	0,0	GGCCTTCTCTGCATATATACCAG T
Etr_73	T	C	CGCTGTCATGTTCC	CGCTGTCGTGTTCC	TGGCAGGTGTGGAAAGC A	0,0	CTCGCGCTGTAAACCTCTTG
Etr_7358	T	C	GCCAGTGAATGTGA ACG	GCCAGTGAACGTG AACG	GAAACACAACCGCAGCC G	0,0	TGGCGTTCACGTGTTTTGTC
Etr_7382	C	G	CAGTGGAGGCAGTT AGA	CAGTGGAGGGAGT TAGA	AGGTGGTAGGGTTAAGGC GA	0,0	TCCTCAAACACCCCGATTGC
Etr_7387	G	T	AAGGAGTGGCGGT GTAA	TGAAGGAGTGGCT GTGTAA	CGGTGGTCGAGGCGAA	0,0	CGTCTCCGCGGAAGGT
Etr_7416	T	C	CTCCTGTGACATCC AG	TCCTGTGGCATCCA G	GTGTGGCAAGGGTGAG ATAT	0,0	AGGAGCTTGACAAAACAAAAAC AGATTTATTATC
Etr_7443	T	G	TCCTAGGTTTG	TCCTAGGTTGG	GCCTCGATCAGGTCCTAG GT	0,0	CCTCTTCACCCTCCCCTCTT
Etr_752	A	G	GTGCGTGATAAA	GTGCGTGATGAA	TGGGTGGGTGAGTTTGTG AG	0,0	GCTGTTAGCGAGCACAAACAC
Etr_754	T	C	CTCGTTTCCGTTCT GCCT	TCGTTTCCGCTCTG CCT	CAATTATAGCCGAGGAGC CCAT	0,0	AAGATCGGTGAGGCAGAGAGA

Etr_7649	G	A	ACGAGTGGGAGCC TG	CGAGTGAGAGCCT G	CCTTCCCAGACAGAGGTT GGA	0,0	GGCAAACACGCACCTGTAG
Etr_766	T	C	ACGATCTGTTCTCT TAGTAGC	CGATCTGTTCTCCT AGTAGC	GGAAGCTGACAGCCAAC ATTG	0,0	GGCCTGCGAGACATTGAGT
Etr_7781	T	C	GGGGGAGTGTGGC TGTC	GGGGGAGTGCGGC TGTC	CTCCCTGCAACCACCTGA C	0,0	CACGTACTCAGCTCACAGCC
Etr_781	C	A	CTGGAAGAAATGA TTCTC	ACTGGAAGAAATT ATTCTC	GCCACTCTTGTCGTTAAC CTTGA	0,0	CGGGCTTGGGTAGGATATGTC
Etr_785	C	T	TTGGTGCAGGAAGT GA	TTGGTGCAGAAAGT GA	GGACGCGTGCCAATTGAG	0,0	GCCCGATTGGCCACCAT
Etr_786	A	T	TGCTTCCCCAGCAA TTT	TGCTTCCCCTGCAA TTT	TCCTCTTTCTGTTGCTTCC CC	0,0	AACGAGCTCGGGAAAAGAGG
Etr_7872	T	C	GGAATTCTATGGAG GCT	GGAATTCTACGGA GGCT	GCACAATGCAAACAAGG CTG	0,0	GCACTGGAAGCCCTTACACT
Etr_7918	T	C	CCGACGGGATATCC GAG	CCGACGGGACATC CGAG	TACGGACCCAAAGCAGGT TG	0,0	AGCTCCACTCCTCACTCCTC
Etr_7974- 70	C	T	TTCGTGTCGACACC	TTCGTGTCGATACC	CTTCAGCGCCACGTTCTC AG	0,0	AATTCAGCAGGAGAGGCCTC
Etr_8064	A	G	GATCTGTCCACCAT TGG	GATCTGTCCGCCAT TGG	GTGTGATGCTTCTGATCT GTCC	0,0	GCGCAAAGTGTGAAAATCTGG
Etr_810	A	G	CCAAAGGCACCCTC C	CAAAGGCGCCCTCC	CAGGTAGTTGATGGTGAC CCA	0,0	GCAGCGCTCGCATCCT
Etr_814	C	T	TTTCTGCCCCAACA CC	TTTTCTGTCCCAAC ACC	GGTCCACGGTCCGATGTG	0,0	ATGAGATGACTTAACAAACAAA GATTGCA
Etr_8196	A	C	AGAAGGACCTCAA ATAGAT	AAGGACCTCCAAT AGAT	GCTTGTTTCGCTCACGACA CT	0,0	ACCTCGAACTCGCTTGCT
Etr_824	C	G	ACCGATGTTTCGTGG CCG	ACCGATGTTGGTGG CCG	TGCAGATGTTTCGTACCG AT	0,0	CGACCCAGCCTCAAATGAGT
Etr_8281	G	A	CCTTCTGCAGCCTT CGC	CCTTCTGCAACCTT CGC	GGAGAGTATTCCTCGTGC CG	0,0	ACAGACTGGTGAGGCAAGTG
Etr_8298	G	A	GAACGAGCAGAGC TGGT	GAACGAGCAAAGC TGGT	TCTGCTGAAGTGAAATCC GGT	0,0	AGCAATTAAGCAGGACCCCT

Etr_832	C	T	ACGAGTTCTCGACG TTCA	ACGAGTTCTCAACG TTCA	GCAGGTCAAAGTAGACA GTCTTGTG	0,0	GCACCTACGAGATCTGCTTCAG
Etr_833	G	T	GCAGCATGTGGGG GCAG	GCAGCATGTTGGG GCAG	CTTCGGGAGGCAGCATGT	0,0	AGCTGTTTTCGTGGGCCATTA
Etr_836	A	G	ACGTGATCACTGCC GTC	CGTGATCACCGCCG TC	ACGCAGCTGCTCTCTGAT TG	0,0	GTGCCGCTCAACAGCAT
Etr_84	A	G	CTGAAGTCTCGTAG TTACG	AAGTCTCGTGGTTA CG	TGCAGGTAAATAGAGGTG TGATCCA	0,0	CCCTGTGCTGATGTGTGTAGAA
Etr_8649	G	A	AAGGCACCGGGAG CAAC	AAGGCACCGAGAG CAAC	TCTCAGGAGGCTGGGTAA GG	0,0	GCCAAGGCAAGTAAACAGTGT
Etr_8681	T	C	GACGCAGGCTGGTT GGC	GACGCAGGCCGGT TGGC	CTTACACGGACCCACGCT G	0,1.4	CGACCGTGTGATTTGCATCG
Etr_874	C	T	GAGTGGCGTCGAC GCAT	GAGTGGCGTTGAC GCAT	AGGGAGAGCCTCAAGAG CAT	0,0	TGAGAGTGATGGTTCTCAGGA
Etr_875	C	T	AGCGCGCCTCGTC	CAGCGCACCTCGTC	TGCAGGCAACGGTTGTAG AG	0,0	CCCAACGGGACGAGGTTTT
Etr_8780	T	C	GCATAAACTTCAA ATC	GCATAAAACCTCA AATC	TCGTTGTTGAAACATTGG CAT	0,0	ACATCTCGGCGTAAGTGATTTG
Etr_8960	G	A	CAATGCCCCGAATG GTG	CAATGCCCCAAATG GTG	TTCAAAACGCCTCGCCAA TG	0,0	AGTGGCAGTGTTCCGGAAAA
Etr_899	A	G	CATTCGCCACTTGC T	ATTGCGCGCTTGCT	ACGGTGACATAGTCTCCT GGTA	0,0	GGCACTGGATTACACCATGA
Etr_905	C	T	GTGCGTGTCTCCC GCA	GTGCGTGTCTCCC GCA	GCTTCTGCAGGGAGTCTT GT	0,0	TGAAGTTCCTGCGGTACCAC
Etr_906	G	A	CACCGTCTTGATGC T	CACCGTCTTAATGC T	AGCCAGAGTTTGCTTCAC CA	0,0	GCATGCGAAGGCCAAGAAAT
Etr_9113	C	A	ATATGCGTCCGATA GTT	ATATGCGTCAGATA GTT	CTGCAACACGGCTCGAAA TA	0,0	ATCACTTTGCATGCCCCGAA
Etr_917	G	A	TGAGGAAATCTGG ACACTC	TGAGGAAATCTAG ACACTC	CAGGTGGCACCGTTGGAT	0,0.3	CCACAAATATTGAACACAATA AGACACAT
Etr_9189	G	A	AGGACACACGTAA CATC	AGGACACACATAA CATC	GACACGTGTCACCCTGTC TG	0,0	TGTAAAATGTTTTACGCAAGA TGT

Etr_930-35	G	C	TGACGGGGAGCGG TAAGG	TGACGGGGAGCCG TAAGG	GAAGCATCAGGGAGGGT GAC	0,0	TGCACACGTCTGATTGATCAC
Etr_951	G	A	TCATTTGCTGGTTG G	TCATTTGCTAGTTG G	TCCCTCAAAACGAATGTT CAATT	0,0	GCGTGTCACTGCTGAAACAT
Etr_963	T	G	TGCGTCTATGTGTT ATTAT	CGTCTATGTGGTAT TAT	GCTCCCACCACTGATGGA T	0,0	CGGATTGACCATATCTGGTGAA GAT
Etr_965	C	T	TGTAGGCAACGGA GCCC	TGTAGGCAATGGA GCCC	GGTGTCTCTGCACTATGA GGT	0,0	TCCTCTCTGGTCATCGTGGG
Etr_97	T	G	AGTCGCATGCCCC	AGTCGCCTGCCCC	GGTAGCGCTCCGGTCAG	0,0	GACCTCCATGGCTCTTTGCT
Etr_972	C	T	ACGTGACACCTGAG TGC	ACGTGACACTTGAG TGC	TCGCACTGAATCACGTGA CA	0,0	AGTGGCATTGGCTGGAGAAA
Etr_98	T	C	TTCACACTGTAGGT C	TTCACACTGCAGGT C	CCGTTTTTAAGCCACGTG ATG	0,0	CTCAAGCAGCCAGTGGACC
LampSD_1589	G	T	AGGGAGCCGATATT G	CAGGGAGCCTATAT TG	CGACGTTGGGCAAATCGT T	0,0	TCACTGTTTCCATCGCAGTACTT ATTAAA
LampSD_327	A	G	AAGTAGGTGTCTCA GTAAAA	AGGTGTCTCGGTAA AA	GCCTAAACCACTCGGATG CA	0,0	ATGTCAACAAACACAATCCACA CAATT
LampSD_478	G	A	CCCAGGGCGTGCCG	CCCAGGGTGTGCCG	CAGGAGTAGGCCGCAGT AG	0,0	CGCTGTGCCTGTGTCAGAT
LampSD_700	G	T	ACGACGCAAAGCG	CGACGAAAAGCG	TGCGATCGCTGATGCTGT AG	0,0	GACCCATAACCGGTTTCACCAT

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Appendix 6. GT-seq SNP panel for lamprey species complex.

Assay	A 1	A 2	A1-Probe	A2-Probe	FWD Primer	Correct ion	Rev Primer
LampSD_1589	G	T	AGGGAGCCGATATT G	CAGGGAGCCTA TATTG	CGACGTTGGGCAAATCGTT	0,0	TCACTGTTTCCATCGCAGTA CTTATTA
LampSD_327	A	G	AAGTAGGTGTCTCA GTAAAA	AGGTGTCTCGG TAAAA	GCCTAAACCACTCGGATGC A	0,0	ATGTCAACAAACACAATCCA CACAATT
LampSD_478	G	A	CCCAGGGCGTGCCG	CCCAGGGTGTG CCG	CAGGAGTAGGCCGCAGTA G	0,0	CGCTGTGCCTGTGTCAGAT
LampSD_700	G	T	ACGACGCAAAGCG	CGACGAAAAGC G	TGCGATCGCTGATGCTGTA G	0,0	GACCCATACCGGTTTCACCA T
Lri100P12118 9	A	G	CACAGGCTCCGG	CGCAGGCTCCG G	GGGGAGGGAGAACACCAC T	0,0	GCCGATGAGCTGTATCTGCT T
Lri101P13937 71	C	T	GGTACGGGGCGGT	GGTACGGGGTG GT	CTGCAGGAACCCATGTAA ATC	0,0	CGGTGGCATATTTTGTGTTGA C
Lri102P19002 77	G	T	AAATCCTTGCGGC	AAATCCTTGCT GC	CTAGTGTGGGGGTACAGC AGAC	0,0	AGCTCTCCTGCCTGGGTATA G
Lri1046P6449	C	T	GCTCCAGACGGCG	GCTTCAGACGG CG	CAAAGCGGGGTGTTTTGT	0,0	GTACACGCACCGCACCAG
Lri104P68693 6	G	A	AGGACTTCTCGGA	AGGACTTCTCA GA	CAGCAGGCGTTTGAGCAC	0,0	CAGGCGATGATCTGGAGGT
Lri105P12319 14	G	A	TCACGGCCCTGGA	TCACGGCCCTA GA	GACAACCAGCTGGAGAGT CTG	0,0	CTCACCTTAAGGCGGTTTCC
Lri105P88144 2	A	C	TCACACACTTATT	TCACACACTTC TT	TATGGGGATGTCTGAATTT TCC	0,0	TGCAGGGTTACGTTTTTGAT AA
Lri106P12526 18	C	T	AGCGTGAACGCAT	AGCGTGAACGT AT	AAGCTACAGTCGTGCACAT TT	0,0	CAGGGTTGGCTAGGTGAATG
Lri106P17906 68	A	G	AATTGGGGTC	AGTTGGGGTC	AGACATGGTGCGGAATTA TACA	0,0	GCTCAGATCGGTTTTAATTT GTG
Lri107P67941 7	A	G	GCCTGCAGGAT	GCCTGCAGGGT	CTTGATATCGCTGCCGAGT	0,0	AGTCGCGTGCAGTTGGAAT
Lri108P65876 3	C	A	GGGCGCCGGCATG	GGGCGCAGGCA TG	CTGAGACCATGCGATCGA G	0,0	CAGCAACCCACTTGCTGTAC T

Lri109P76652 7	A	G	CATTAATAATAGA	CATTAATAGTA GA	GAGAAGCACTGTCTAGGC CATAA	0,0	CCAGAATCATCATTGTCAGT GG
Lri10P166715 4	C	T	TCCGTCCGGCCCGG	TCCGTCTGGCC GG	CTGCAGGAGCAGCTCGAC	0,0	CGAAAGAAGTTCAACACAC GTA
Lri10P621690 3	C	T	CAGGGCGTGCTCG	CAGGGTGTGCT CG	TGGAAGAGTAGGCCAAAA ACAC	0,0	CAACAACATCCTCACAGACA CC
Lri10P808454 2	G	A	CTTAAACCAAGAC	CTTAAACCAAA AC	CTGCAGGTGCTGGTTAATA TAGG	0,0	GTGCCTGGGAAAATGAGAG AC
Lri10P811969 9	G	A	CAATGACACGGGGA	CAATGACACGA GGA	GTTCTCCGCGAGCTCCAC	0,0	CAGCTCTTGTAGCAGGGTTG AC
Lri10P958022 2	T	C	CAGAGTACCACCC	CAGAGCACCAC CC	CTCCTTGCCAGCTTTCGTA AC	0,0	CACCAAAGCACCAGCAGAT
Lri110P97104 0	G	A	CACTCACAGCGC	CACTCACAGCA C	GACCTCTCCGACCTGGTG	0,0	GATTATAAAAGCCACGCCAG AG
Lri112P15240 62	G	A	CCAACGAGCCGCG	CCAACGAGCCA CG	ATAGATGAGCACCGGGAC GA	0,0	ATGAAGGCGTCGATGTAGTC
Lri113P10915 2	C	T	TTGACATGACCTC	TTGACATGACT TC	TCCACTCAGAAGAACTTGA CTCC	0,0	GGATGAGTGGCTGCTGCT
Lri11433P552 0TD58	A	G	CGTCTATTTCA	CGTCTGTTTCA	CTGCACTCACTACACGCAG GT	0,0	AGTTGATGCTGCCGGATG
Lri11465P555	C	T	CTGCAGGGCTC	CTGCAGGGCTT	CCACTGAAGGTTGTGAAA GGTT	0,0	TGCATCAATAATTAACGTGT TGG
Lri116P66671	T	C	TCTTCATTGTGCT	TCTTCATTGCGC T	AGGTACAAATGGCCAAAA ACC	0,0	TACAGCCTGCGGATAGGTCA C
Lri117P11071 47	A	G	GGCGCTCGGTACCT	GGCGCTCGGTG CCT	ATGATGAAGCCATGTCTGA CC	0,0	CTGCAGGAGAGCGATAGTG AC
Lri118P14775 21	G	T	AATGCCTGCAGGAA	AATTCCTGCAG GAA	ACGGCATCTATTAGTCCAC CTC	0,0	CGAGCGAGGTAGTTTGATGT TT
Lri118P43413 1	A	G	CAAGTGTTGGGCA	CAGGTGTTGGG CA	CCCAGGATGGACACGTTG	0,0	GAGTCGGCTGGGATTTTCT
Lri119P14367 85	A	T	TTTGACAGCACAC	TTTGACTGCAC AC	CCTGCAGGGAAAAAGTGA GTT	0,0	TTTGTTTGAGAGTGCACGTT GT
Lri11P115361 90	A	G	CGCTCAGACCGCTG	CGCTCGGACCG CTG	ACCCCTTCAAAGCAGTGG AT	0,0	TTAGTGGCGGGTTTTAAAAG TG

Lri11P117049 65	A	G	GTAACGTTCAAAT	GTGACGTTCAA AT	ACAGTCGTTTCGGCTCAATG	0,0	TCAGTCCCAACCAAACAAGT
Lri11P206628 2	T	C	TTATAAACCACAA	TTACAAACCAC AA	TAATGGGAAGACAGACGA CGAT	0,0	CCAAACTTCCACAAGTTCAC CT
Lri11P311028	A	G	GCGGCTCCTCACG	GCGGCTCCTCG CG	TACTTCCCAGCGAAGAAA GTCT	0,0	ACGGCGTCACCAACAAC
Lri11P359037 0	T	G	GCGGGACGCGTAA	GCGGGACGCGG AA	CAGGAGCTGCACAAACAC C	0,0	ACGGGGAGTCGTAATGCTCT
Lri11P877521 4	A	G	TCCGCACGCGACA	TCCGCACGCGG CA	GATCTCGTCGCCGTGGTT	0,0	AGCAGAGTGGCGTTGCTC
Lri125P77929 2	G	C	TTCTAACGGA	TTCTAACCGA	TCGCGTCGAGGTCAAAAG	0,0	GATGATCCCTTCCCACAGG
Lri12696P165 0	C	A	CTTGGGACTG	CTTGGGAATG	ACCAATATCAAAACTGGG GTTG	0,0	GTTCAATTGTCCTGCAGGTTG T
Lri128P48660 1	C	T	CTGTGGTGGAC	CTGTGGTGGAT	ACGTCTGCACACGAGGTC AT	0,0	GGACCCTGCAGGAGAGGAC
Lri12P114600 75	G	A	CCCTCGCCGCTCG	CCCTCGCCACT CG	GCACCTGCAGGAGATTTCAT TTA	0,0	AGTATCGGTGCGGTGTGATT
Lri12P177473 6	C	G	GACTGTCGTTTCAGC	GACTGTCGTTG AGC	CACCTCCACTCAGCCTTGT T	0,0	AATTTCCCTGCACAAGAACA C
Lri12P182981	A	C	CTAACGAAACATG	CTCACGAAACA TG	GCGGCATACGACTATTAG GG	0,0	CAATTTGCATGCACAAATAC AA
Lri12P183087	A	G	TGTGGCGAATACA	TGTGGCGAATG CA	ATTGTACGCAAAAACAAT GTGC	0,0	GTGTCTCGTCTGCATAGTTTC C
Lri12P183836 6	G	A	GTGCCGAAGCGTT	GTGCCGAAGCA TT	CAAGGCGGTACCTTTCACC T	0,0	GACGATGGGATGGCGAAG
Lri12P279478	G	A	TCCAAACAAGGAG	TCCAAACAAAG AG	GCATTTTTATCATGCGCCT ATT	0,0	GTGTCATGCAGTGCTGAAAA A
Lri12P308276 2	G	A	GGTGGCTAACGAC	GGTGGCTAACA AC	AAATGAATTGCGTGCAAG AGA	0,0	GGCAAACAAAACAAAGGAG AG
Lri12P547097 0	A	G	TCCCACGCTGACG	TCCCACGCTGG CG	AAAATGTGCGTTTAGATTA TTTGG	0,0	AGCTCTTTTTCAATGGTGAC CT
Lri12P606091 1	T	C	CAGTCGCCCTTCAG	CAGTCGCCCTC CAG	TCAAGATCGACCTTTGTAG AGGA	0,0	TCTTTCCCCTCCTACTTTGTT G

Lri12P719962 4	G	A	GGTGTACAAAA	AGTGTACAAAA	TTATTGTGAGGGCGATGTT AT	0,0	GGGCTAACTCTCCTTGAAC TG
Lri12P838643 2	C	G	TCTTTAGCAACGT	TCTTTAGCAAG GT	AAAGACCTGCAGGCTCAT AAAG	0,0	AACAGCTCCCGGTATTTCTC TT
Lri12P964801 6	G	A	GCAGGCAGCAGAG	GCAGGCAGCAA AG	TCGCTGCACACAACATCC	0,0	CTCTGTCTGCGTGGAAGGTA G
Lri131P90108 9	C	A	GAGAAAACAGCAAT	GAGAAAACAGA AAT	TATTTACCACAATTGTCA GCA	0,0	GTTACGGTCAGTAGAGGGCA GT
Lri134P44462 6	G	A	ATCGAGCCGAGTC	ATCGAGCCGAA TC	GCAGGGTCCTGTTTATTAT TGG	0,0	AGACATCGTCCACCATTGTA C
Lri137P95766 4	A	C	TCAACCACAAATA	TCAACCACAAC TA	GTAGCAAACCAGAGGGGA AAAT	0,0	TCGTAGTAGTTATTGTTACA GGTGTGT
Lri139P63934 9	G	A	GACCGGAGGGCTG	GACCGGAAGGC TG	ATTTTCGAGCCAGTGTGACA AAT	0,0	GCTCCAGTACGCACTGCTTG T
Lri13P108388 95	C	T	GTGTCAGGTCCCG	GTGTCAGGTCT CG	CCCTATTATAAGCGCCTAG TGG	0,0	AGGGAGTGACATCACCAATA CC
Lri13P111161 25	C	T	TGCTCCATGGC	TGTTCCATGGC	AGCTGCTGTTGCTGGTGAG	0,0	ATGCGAAGGCCAAGAAATA C
Lri13P476696 1	T	G	GTTATGATATTT	GTTATGATATG T	CAAGAGGATGCAGGTGGT GT	0,0	GTTGAGGAGCACTGGGCTAT C
Lri13P613276 7	A	C	GTGTACAGACCGT	GTGTACAGCCC GT	CTGACACTGCTCCAGCACCC T	0,0	TGCCCTCGACATGTTTGTG
Lri13P622131 8	C	T	ACGCTGCTGCACG	ACGCTGCTGTA CG	CTCCTCGCAGCTCTCCAA	0,0	CAGAGGACCAGGATGAGAC TG
Lri13P623062 3	T	G	AAATAGAGACTCG	AAATAGAGACG CG	TTGTCCTCCACTGCTAGGC TAT	0,0	CCTGCAGGCCGTATGTGT
Lri13P725649 7	G	A	TTATGCCTTTGAC	TTATGCCTTTAA C	AACCATCGGTCATTATCCA GTC	0,0	CCACCCTGCAGGTTTTAGAA TA
Lri140P42965 1	G	A	GAGTATTTGTGCG	GAGTATTTGTA CG	GGGATCTTTGACGTCCACT GT	0,0	CGCAGAAATTCCCGGTAG
Lri140P59145 2	C	T	GGGCCGATGACAG	GGGCCGATGAT AG	GCCTGTAGCACGGCACCT	0,0	GTGTCATGTGTACGTGTGT G
Lri1419P1548 6	T	C	CTGAGTCCTGTA	CCGAGTCCTGT A	ACCTCCTGCAGGGCACTAT T	0,0	TGAGGTGGTAGCCAGATAGG AT

Lri1432P1647 1	A	G	TGCCATCAGAATC	TGCCATCAGAG TC	GGAACAACACTTTGCCTTT GAT	0,0	GAAGGCCAATTTAAAGAGGT GA
Lri144P65767 2	C	T	TCAGTCACCCTGTG	TCAGTCACCTT GTG	CCTGCAGGTTCCACTGACT C	0,0	AGAGACTGATGCCCCCTTG
Lri145P41302 1	T	C	CGTATGAACAAGA	CGCATGAACAA GA	AAGAAGGAAAACGAGGAG CTG	0,0	GCAGCCGTACCTGTGAAGAT
Lri148P46286 3	G	C	TTACGCACTCAAT	TTACCCACTCA AT	TAGGCAAGTGGTAAAGGG TGAT	0,0	GGTGAGTGGGTGAAGTCTGT G
Lri149P78709 6	T	G	GGATGGCATGTCT	GGATGGCATGG CT	TTGTCTCGATGTGAGCAAG ACT	0,0	GCGCCTATAGAGACACACTC G
Lri14P117091 10	A	G	CACTCCACCAAGT	CACTCCACCAG GT	CACACTCAGCTCCGTCTTC A	0,0	CTCCAGCCTTGACCCATGT
Lri14P290087 9	G	A	CCTCCTGGGCGAG	CCTCCTGGGCA AG	ATCGAAGGCACCTTGGTA GTT	0,0	GACTACCTGGTGGTAGCCAG TC
Lri14P359583 6	C	G	TGCAGGTGCTC	TGCAGGTGCTG	GTGAATGCCGCCAGTAAG AC	0,0	CGCCTGCAGGAATTGTAAAT A
Lri14P389556 2	T	G	CTTATTTTATTT	CGTATTTTATTT	TGGTTGTGTTGCTGTACAT TTG	0,0	CGCTGTTTTATTGCAGATTTC A
Lri14P394387 8	G	T	AGGAAACATTGT	ATGAAACATTG T	GCCAAGGTACGTCGATCAT	0,0	TTCACGGTGGAGTCTGAGAT TA
Lri14P407938 7	C	A	AAAAGTAATGCTA	AAAAGTAATGA TA	AAATCCCAGGTATAAGCCT TTG	0,0	TTACAGTTGGCACCATTGAA AC
Lri14P410272 7	G	A	GAGCCATTCCGGC	GAGCCATTCCA GC	AATAGCCTATCTTTCCTGC CATC	0,0	GGGCGTACAATAAATGGTTT G
Lri14P410605 4	G	A	GACGAGATCTGGC	GACGAGATCTA GC	AACACGACATGTCTGCAG AGTC	0,0	TCTAACACCATTGCATGAAC AA
Lri14P498517 3	A	C	AAGGACAGGGAAC	AAGGACAGGGC AC	TCAACAAACTTAACTCAC CGTAT	0,0	CCTGCAGGTTATCATCAAGA AG
Lri151P23715 9	A	C	CGTCACATCACCA	CGTCACATCCC CA	GGCCCCAAACCATTGAACA GT	0,0	AGCCCCATGACAAGACTCC
Lri159P65835 7	T	C	AGCGCGGCCGTAC	AGCGCGGCCGC AC	GTTTGTAGCCCCTTGCCAA C	0,0	CGGTGACAAAAGAGTTTCAG AG
Lri15P140955 4	T	A	GAGTTTGAATCCG	GAGTTTGA AAC CG	GCAGGTTGAAATTGGAGG TTAC	0,0	AACCCTTCTTGCTGGGATG

Lri15P217207 4	A	G	AAATTGTAATTA	AGATTGTAATT A	CGCACTGGGAAAGTTGAG TAA	0,0	TCAAGACAAGTGTTCACCAA TG
Lri15P659874 8	G	A	GTAATGTGCAC	ATAATGTGCAC	ATGTGTCCGTGTGTTCTAT GGT	0,0	GCAGGGAGAAATCCTTTCAA TA
Lri16103P390 0	T	C	AGCAGACCTATGC	AGCAGACCTAC GC	TTCAGCCACTTCAAGGAGA ACT	0,0	CTGGTAAATGGCCTTCCTGT AG
Lri162P69072 2	C	T	CTCCAAATCAG	TTCCAAATCAG	ATTGCGTGCTGTGCTGTCT	0,0	GGAATTATGGGCTGAGTTGA TG
Lri170P51161 9	G	A	ACGCGGGTGATGG	ACACGGGTGAT GG	GTGAACATGGGTAGCTTCT TGG	0,0	AGTCGTGATGGAGACAAGGT C
Lri1725P9022	G	A	ACGGGGGGACGCA	ACGGGGGAACG CA	ACGCTGGCCCTGAGAGAC	0,0.4	CGTCCCCGTGTCTCTGTC
Lri172P14418 7	T	C	CATGCAGAGTCG	CACGCAGAGTC G	AAATAGCCGAGGCATGGA C	0,0	GACACAGCAGAGGGTCAGC
Lri17742P215	G	A	ACTTATAGATGTA	ACTTATAGATA TA	CTCGCGGACAGGAGGTCT	0,0	TCAGGACTGTTAGAGTGTG GA
Lri177P26697	A	C	ACCAGCATGGA	ACCAGCATGGC	ACGGACAGCTCGTCGTTG	0,0	CCGCAGGACCTTAACCTGAT
Lri178P23757 3	A	C	ATTGGTGAGATCTA	ATTGGTGAGCT CTA	GTTCCGTTTATTTCCGACT TCC	0,0	GTCAAGTGGCGCATTTTCAT
Lri178P42353 0	G	A	TGGAGCCGTGTGA	TGAAGCCGTGT GA	AGTGGATAAATTGACGCC GTAT	0,0	CGTAGATCGCACCACCAAC
Lri17P270428 5	C	A	TCATTTAAAGGG	TAATTTAAAGG G	TGTTGTTGCTGTTGTTGCT GTA	0,0	GAAACTTGACCGCAGGTGAC
Lri17P295702 4	G	A	TCTCGATGATCAG	TCTCGATAATC AG	CATCACCCCTCCAGAGTCA G	0,0	GGAAACCCTTCATCCAACAG T
Lri17P323276 3	A	G	TCGCACACCGACT	TCGCACACCGG CT	CTGTGCTGCATCCAAACAA G	0,0	AAATGCCCCGAGGGATAAT
Lri17P385674	T	C	ATGACGTGATACG	ATGACGTGACA CG	GGGATCGCAGTGCGCTAT	0,0	CTCGCTCTCCGTCCAGGT
Lri17P504705 9	T	G	CGACCAAGGGTTT	CGACCAAGGGG TT	CAAGGTATATCGGCAGTGT GC	0,0	GTAATGCTGGTTTGAATGTT CG
Lri17P662017 2	T	C	AATTGTCGTG	AATTGTCGCG	CCCGGTGATGAAAATTGC	0,0	AACTTTGTGGAAAGTCAGGT TTTT

Lri17P759423 4TD43	A	C	ATGTAA[AG]TTA[TG]	ATGTAC[AG]TT A[TG]	CAACCAGCAATCATGTGA AACT	0,0	AACATTGGCTCATGTGAGTG AC
Lri17P794313 1	C	A	CCTACCTTATTAC	CCTACATTATT AC	TACATTCCCGTCAACCCCT TAT	0,0	GTCGTCTTTCTCCCTCGTGAT
Lri17P821835 9	T	C	TCGGGCCACGTTC	TCGGGCCACGC TC	CCTGGGCTTTCTCTGTGTT C	0,0	ACTCACTTGTGGTGGTGAAC G
Lri17P899913 4	T	G	GATGAATTCCACAT	GATGAATGCCA CAT	CAGCCATGATCTATCAACT TGTG	0,0	CAGGGGCTAGATGGATTGTT AC
Lri17P947141 6	G	A	GCAGGTGTGCCCC	GCAGGTATGCC CC	TGAATGGTCTCTGCACGAT CT	0,0	GCCTGGCGAGAGACACTTTT AT
Lri18P120181 9	A	G	GGCCAGCCACTTC	GGCCGGCCACT TC	AAGCGCACGTCGAGGTCT	0,0	AGTCGCACACCTGTGAGAAG TC
Lri18P163972	G	A	ACTTGTTGGCGTGC	ACTTGTTGGCA TGC	GTCGAAGGGCTGCACGTT	0,0	GAGAGGTCTACTGGTCCGAC TG
Lri18P351620 3	A	C	CATTTATCAAT	CATTTATCACT	GCTGGTGTATGCCTGTAAA CAA	0,0	CAGCCCTGCAGGTTTGAG
Lri18P474572 5	A	G	ATTGTGCTGTATC	ATTGTGCTGTG TC	TGGGACCGAATTCTGAGTG TAT	0,0	AAAACCGACGTCTCCTTTAG C
Lri18P505534 0	G	T	AATAACAAAGCTG	AATAACAAATC TG	CTTCCCCCGCACCTCTTAT	0,0	AGGTGGTCAGTAGAGGGCA GTA
Lri18P562686 0	T	C	ACTGTACAAATGT	ACCGTACAAAT GT	TGCATGATCTTAGAGTTCA CGTT	0,0	ACTCAAAGCGATGTTGCTGA G
Lri18P598538 5	G	A	TGCAAGCATGGCG	TGCAAGCATGA CG	GCTCGGGTCTCCCGTACA	0,0	CAGGTGAACCCACAGTTGC
Lri18P646378 7	A	C	TCATCCAGAGA	TCATCCAGAGC	TTGTATTTCTCTTGCTAAT AATGTCCA	0,0	TCTGGCAAGCGTGAAAAATA
Lri18P654758	T	C	CCGCGTGCAGAGG	CCGCGCGCAGA GG	GCGGTCTGCGTTGTCTTG	0,0	GATGCGGGTCATCTTGCT
Lri18P797472 9	C	T	TTGCTCGGGTTCTG	TTGTTCCGGTTCTG	AGTGCCTGCAGGACGTGT	0,0	GCAGAAGGAGAGATGGACA GAC
Lri18P880577 6	A	G	AGCTCCCTGCA	GGCTCCCTGCA	GCCAGATCACGGAGAGAA ATAA	0,0	CTCCGGCCGTGTGAAATC
Lri18P901636 9	A	G	CATTTGGTGCA	CATTTGGTGCG	TGTACATACCCAACCGTGC TAA	0,0	CTCGCCACAAACATCACCT

Lri19P689235 2	C	G	GCGTCTCGGCCAC	GCGTCTCGGCG AC	GAGCTGCCCCATCGTCTC	0,0	GGCTGCTCAGACGTCACTT
Lri19P738740 0	T	C	TGTGCACAGCT	CGTGCACAGCT	CAGCGTGAGCGAGTCCTG	0,0	ACTAGGATGACATGGACCTG GA
Lri19P947343 6	C	T	TCCCTGGTGTCCA	TCTCTGGTGTCC A	GGTTAGTACAGATTGGTGA AAGTGG	0,0	GGTGCTGGTCTCTGGAAGG
Lri19P985276 8TD53	A	T	GATA[GT]ATTCAT	GATA[GT]TTTC AT	ATTGCCTGCAGGTTGGAAT	0,0	ACATTTCAACAATGACCACG TT
Lri1P1164785 2	C	A	TTGTCACACACT	TTGTCACACAA T	GTGCTCTCCAAGCTCTAAC CTG	0,0	GTGACCACCACCCCATCAC
Lri1P1617197 6	G	A	AGTAAAAGGA	AGTAAAAAGA	GTTTGCACAGCGTTTTGAG AT	0,0	CAAGACCCTTTGCTTCTTCTG T
Lri1P1736648 4	T	A	GCTGATCTCCTCA	GCTGATCTCCA CA	CCTCCGGCAAGAAAACAA G	0,0	CTGCAGGTCCACAGTTCATT G
Lri1P1739216 8	T	A	GAACGTCTGCTGC	GAACGTCTGCA GC	TTTATGAACACCAGTGCAA CCT	0,0	CAGGTGAGTGGCGCTGTAT
Lri1P1747752 8	G	A	CCAACGCAGCGGC	CCAACGCAGCA GC	GGCAATTGCAAAGATCGT G	0,0	CCACCTCCTCCTCGAACAC
Lri1P6957846	G	T	GGGGGCCACTGCG	GGGGGCCACTT CG	ACACCCTGCAGGATCAGC	0,0	AGCAGCATCGGAATGAAATC
Lri1P8709918	T	C	GCTTTTCCTAGCT	GCTTTCCCTAG CT	GCACAACACTCTGGTGCT TTG	0,0	TGCAACCTCATCTTCTCTACC A
Lri20P327704 4	C	T	ATCTTCCTCCAGG	ATCTTCTTCCAG G	CGGAGTCCTCGACGAACTC TAT	0,0	GCTTCCCCAACCCCTCTT
Lri20P498001 3	G	A	CTGGTTCTGAGC	CTGGTTCTGAA C	CGGTCAGATGTCGTTTGAA AAA	0,0	AGTCACTGTTCTGGCCTCTG TG
Lri21P446358 6	T	G	AAAAGCATTGAGA	AAAAGCATGGA GA	GAAATGGAACAGAAGCTG AAAA	0,0	AGCATTTGTTACGTAATCCT TGT
Lri21P549333 0	T	C	GCAATCCTGTTGT	GCAATCCTGTC GT	GGAGGTGACCGATATTGT GAGT	0,0	CTCACTATGGCCAAATGATG CT
Lri21P664729 6	G	A	GGTCCGGCTGGAA	GGTCCGGCTGA AA	TTCTAACTGTTCTCTTGT GACG	0,0	GAGGCAGGGAGACTTAAGT GAG
Lri21P702243	G	A	GGGTGAGCGCGGT	GGGTGAGCGCA GT	TCCCTGCAGGAGCTCGAC	0,0	CTCGACGCACTTGGACATAA T

Lri21P929485 7	G	A	TGTTGTTGTTGCA	TGTTGTTGTTAC A	ACACAAACCCCACTGCAA AG	0,0	AATGTCCTGCAGGTGACTGA G
Lri222P30751 2	C	T	AGCCTTTGCGCAA	AGCCTTTGCGT AA	ATTAGGGCTTAATCACCTG GAG	0,0	CGGCGAGTGGTTTTAATTTT AC
Lri22434P974	G	C	GCTCTTCCTCT	CCTCTTCCTCT	CTGCAAGGTGGTGGTGAC	0,0	CGACGAGGATCCAGTAGTAG TTG
Lri22P132369 2	C	T	ATCATCATCCCGT	ATCATCATCCT GT	TCGTCATTAGCAGCAATAG CAT	0,0	TGTGTGTTGTCTGAGTAGTA TTTGTGA
Lri22P331392 5	G	C	GCTTGACGCGTG	GCTTGACGCC TG	GTCGACAATAACCTGGGG AAAC	0,0	GCAATATCACCCACCAAAC GT
Lri22P708252 3	A	C	CGCTGCAGGACAA	CGCTGCAGGCC AA	AGCAGGGGGAACACACAG	0,0	ACCGCCTGCACACTCGATA
Lri22P762567 5	T	C	TTGGAAGGTTC	CTGGAAGGTTC	CATGGCAAAAGGATTTCA CTTC	0,0	CACAGTGGTACTCATTGTAT CAGC
Lri22P762578 6	C	T	GAGGTACTGGCCT	GAGGTACTGGT CT	ACTGTGTGGAAAATAAGC AGCA	0,0	CAAGCTCAGAAAATGGTGA ACA
Lri22P817592 6	G	A	CCCCTGCAGGGTG	CCCCTGCAGGA TG	ACTAGGGCAAGTCATCAC ATCA	0,0	CCTGGAATCTAGGAGTGATT CG
Lri23P338946 3	G	A	GGCTCGTGCAACG	GGCTCATGCAA CG	CAGGCTTGCCACTTTTTGA C	0,0	GACAGGCGTAGTAGCACCA GTT
Lri23P872551 8	A	C	CGACATCACAATG	CGACATCACCA TG	GTTGAACCGTAGCGATGA ACTC	0,0	GGCTATGCGTGTGACGTTT
Lri23P952664 1	T	C	GAAGTTTGCGCGT	GAAGCTTGCGC GT	CATCTCCACCCCAGGAT	0,0	CGACTGTGCCAGGACCTT
Lri24296P193 7	C	T	GAATTGGTTTTCAC	GAATTGGTTTT AC	GGGGAGCACACGATTCAC	0,0	CAGCCTGTTGTATTGCCAGA
Lri2481P8393	G	A	GTGAGAGCACGGCA	GTGAGAGCACA GCA	CAGGATGGACCACTGGAG AC	0,0	CTGAGGGGACTCTTCCTCAT CT
Lri24P318328 1	A	C	GTTCCCAACTAA	GTTCCCAACTC A	CCGACAATCCTATTTGAAC CTC	0,0	AGCCAACCGTGCTAATAAGA AG
Lri24P354944 0	A	C	CCCACTGAATA	CCCACTGAATC	CAGCTAAGTTCCGCATTGT AG	0,0	ATTTGCAACCCCGATACAAT CT
Lri24P393491 5	A	C	TCCACCACCAACT	TCCACCACCAC CT	AGGTAGCCTTCACCGTACT GC	0,0	TTGAGAGGTACATCCAGGAT CA

Lri24P435488 3	T	A	AATTTTACTATTT	AATATTACTAT TT	CAAAGCCCACTGGCAATT ACT	0,0	GCAACCACCCATTTATTTTC AA
Lri24P445107 5	T	G	CGAAGGATGTTGG	CGAAGGAGGTT GG	GGACGCACCGTGTGGTAG	0,0	CATCATTGAGACCATGGACA AC
Lri24P495451 3	G	A	AGAGACAAGGCCAC	AGAAACAAGGC CAC	GGGCTGTGGCACTGTAATA AT	0,0	ACATTGTAGCCATTATGAAG CA
Lri24P651473 7	G	A	CATTAAGAAATAA	CATTAAAAAAT AA	TAAAATGCATGTGAGCCAT TTC	0,0	GATTTTCCCACCTTGTGGTTT T
Lri24P680854 6	T	A	GCACTTTTAATT	GCACTTTTAAA T	GAAATAGACCGTGTACACA GTATTGA	0,0	CGGTGGAAGGACAACAAAC TA
Lri24P748170 4	A	G	CTACGTTTTTACG	CTACGTTTTTGC G	AAGCAGGTAAAGAGGGTT CACA	0,0	TGAAAACAATACAAGTTCAC AACAA
Lri24P776591 6	T	G	CATCACCTCTTCT	CATCACCGCTT CT	CTTCCTTAGCTGCCATTTT ATT	0,0	TAAATGGACTTGGGTAGGGA CA
Lri25061P254 2	C	T	TTTGCCACGGCCA	TTTGCCATGGC CA	GTCTGCAGGGTTCGTAGA GT	0,0	TTGTAGCTCCTTCGCGTTAG AT
Lri25P223029 1	G	A	GTCTGTAGGCGGA	GTCTGTAGGCA GA	TTCTTGTGTGAGATTCCCA CCT	0,0	TTGTCAATAACACTGCCTTT GG
Lri25P737309 3	C	T	GGCTATACAT	GGTTATACAT	TTTCAAGCACGGTGAAATA CTG	0,0	TTCTCGAAGCTTTCATTAGTT GG
Lri25P827596 1	A	G	GCATGGTTCCTGG	GCGTGGTTCCT GG	GACAACCACAAGGCAGAC ATC	0,0	ATGATGGCTCACCGATGAAG T
Lri25P843509 3	T	A	TTTTTTTATTT	TTTTTTAATTT	CAGGCTGTGGGTGCAGTA	0,0	CTTGCTCACAGAACTGTAC GA
Lri25P884948 7	A	T	GTCAGTCAGCACCT	GTCAGTCAGCT CCT	GCAATGTTCAATTCCACCT G	0,0	CTTGTCGTGATGTACATTCT GC
Lri26245P408	A	C	CAACAGGAAAAAG	CAACAGGAAAC AG	TTAAATTAAATTGGGCCTT AGCC	0,0	GACTTCGCCTGTGACTCG
Lri262P62290	T	C	ATTTACAGCATGC	ATTTACAGCAC GC	CGTTATAAACACACGCGTT CC	0,0	TATAGCGCCACGTGTTGTAT TC
Lri26500P113 6	T	C	AATATGCGTCTGA	AATATGCGTCC GA	GATCAATTTGCTTGACCT G	0,0	AAGCAGTATCCATCACTTTG CAT
Lri26P440609 6	A	G	GGAAAGTGGCGTT	GGAAGGTGGCG TT	CTGCAGGTGATGCTTGAGA C	0,0	TACAACCTGACGGTGCACAT

Lri26P671918 6	C	T	GCAACAGCTTCAG	GCAACAGCTTT AG	ATCCTGAACCACCCGATGT	0,0	AGGCTGGTGTGAACTGATA CA
Lri2718P1392 9	C	T	AGTAGCCCGCTGA	AGTAGTCCGCT GA	TTTTGGCTTTTATAAGACA GTACATTA	0,0	AAACTGAAAGGCATGCAGA AAC
Lri27P615088 4	T	C	TTACTCAAGATTC	TTACTCAAGAC TC	CATCGAGGTTGTGTTTTGA GAT	0,0	CCACACACAAGACATTCATC AAC
Lri28P383709	G	C	CGAGCAGGACC	CGACCAGGACC	GAACAACGACAGGTCCAT GA	0,0	GTCAGAGGACCTCGTACCTG AG
Lri28P479470 3	A	G	CCTGCAGGTTATT	CCTGCAGGTTG TT	CATGTGCTTATATTGCCTT CCT	0,0	CCCAGTGGCTCGATTAAAGT AG
Lri28P515582 1	C	T	TCACCATCCACG	TCACCATCCAT G	AAATTTCCCTGTGCCCCATT	0,0	TGCTGCGTCTGGTAGTTGTC TA
Lri28P628762	C	T	GTGAGTTACCTTC	GTGAGTTATCT TC	ACGTCTCCGGCTTCGTTAG	0,0	CCAAAGACAAGGGTCCCAA C
Lri29P190270 4	C	T	CGGGGTAGGCCGG	CGGGGTAGGCT GG	GGAGAGCGTGCCTTCTGG	0,0	CCATTTCCCTCACCTTCATCT C
Lri29P192843 7	G	T	TTCCTGTTGTGCC	TTCCTGTTTTGC C	CCACAAAAGCCTCTTGACG AC	0,0	GCGTTTGTTCGATCTTGTTTA TC
Lri29P271553 7	C	T	ACCCACCGGTTGGC	ACCTACCGGTT GGC	TATCCGACATGCCAAACTA CAC	0,0	ACACCCGAGACGGCTTTT
Lri29P385381 9	T	C	TGGGGTACACTGT	TGGGGTACACC GT	GTCCGATAGCATTTTGCTC ACT	0,0	ATCCATGGAAAATACACGAT CC
Lri2P1066068 1	A	T	GGAGGAGGGAACG	GGAGGAGGGAT CG	GTTGACATCATCTCGGCTG TAA	0,0	GAGCGAGGTGTCTCGTCTG
Lri2P1074704 0	C	T	TCAGTTAGTTCCT	TCAGTTAGTTTC T	ATACAAAAGGGACCTTGC GTTG	0,0	AGATGGAGCGGCTGGTAAT
Lri2P1094851 2	T	C	GGTAGAGTGGTCG	GGTAGAGTGGC CG	GACGTGATCTGCACCTCCT C	0,0	GTCAACCCCATCATCTACTC C
Lri2P1190046 7	A	G	AGAAAGCGGCAAGT	AGAAAGCGGCG AGT	GCTCCTGTTGACCTCTCTT GAT	0,0	TTTCATTTATTTTCTTGCTC TTG
Lri2P1197111 0	A	C	GGCCTCTTATA	GGCCTCTTATC	GACAGATTCAAAATGGAT GTGG	0,0	GCAGGAGACACGCCAACT
Lri2P1283575 6TD51	A	G	AGACCACTGTG	AGACCGCTGTG	AGCAGTATTTGTCCGATTC TGT	0,0	TTCTCTGCCACCTTGGCTAC

Lri2P1498696 8	T	C	TACCACGGTCT	CACCACGGTCT	CTCCCGAGGGGCTCATACT	0,0	GCAGAGCTGCTGCTTGTTT
Lri2P1624754 8	A	T	TCCACGAACAATG	TCCACGTACAA TG	GCACCGTATTTGGACAACG	0,0	ATCGTTCAGATCCGGCAAG
Lri2P1625039 9	T	C	AAATCATAGATAA	AAATCACAGAT AA	ACTCATCACTTTGCCACTA CCC	0,0	GGTATGCAACTCGCAAAAAGT TA
Lri2P1633300 5	T	A	TCCTACATCCT	TCCTACATCCA	CAACGTAATGGACAAATG ATGG	0,0	CGCTTTACAGAAGGATGATG TG
Lri2P1636706 4	A	G	ACAATCTGTCTATG	ACAATCTGTCTG TG	AAGCAAGAAATGTAAATC TGCTCTC	0,0	AACCAGAGAGAAGTGCATG TGA
Lri2P2907377	C	A	GACATCCCCTCGG	GACATCCCCTA GG	CTGCAGGTCTCGTCTCATG TAA	0,0	GTCAGCCGTAGGAGAGAAC G
Lri2P3548449	G	A	TTCCGTTACGGCA	TTCCGTTACGA CA	AGGAGATGGCTGGCAATG	0,0	GCCTGATGAAGAGCAGAGA TTG
Lri2P5451779	G	T	TGTGGTACTCGTA	TGTGGTACTCTT A	TTCCGGAGCATGCTATAAC C	0,0	GAGTGAATTACTCTACCTGA CATGAA
Lri2P697855	C	G	TTGCTCATGTGGG	TTGCTGATGTG GG	CCAGATCAGTATTGTTTGT GTGA	0,0	TTTATTGAGGTAACGAGCAT GG
Lri2P7179941	A	G	GGTGCTTGGAATA	GGTGCTTGGA TA	AGGTTCTGCAGGACATCA AAGT	0,0	CACTTGCCCCAAAAGTTCAT
Lri2P7418446	T	G	TATATGCTCTT	GATATGCTCTT	AGGGCATGTGCAAACCAT	0,0	AGTCTTAACCCAGGGGAATC AA
Lri2P9432908	T	C	CATAAGACACCAA	CACAAGACACC AA	CAATTGTGTTTCATGTGGG ATT	0,0	GCCTACTGACCACCTCTTAG CC
Lri30P260835 8	G	A	GAGACCGTGGTTT	GAGACCGTAGT TT	GGCCTCCCACTTCGAATC	0,0	TGTTGTTGCCAAGTCGAAAA TA
Lri30P264580 7	C	T	AAGTGCCCTCCTG	AAGTGCCCTCT TG	GCTACATCATTGTCGTTGT GGT	0,0	GAGAGCGTGCAACAGATCCT
Lri31P172063 9	T	C	CCTTGACTGCCTGC	CCTCGACTGCC TGC	GTGGTAGTAAAACATCGC GACA	0,0	GTGCTGTTGGTGAGTGAATG AT
Lri31P211793 2	A	G	CCATCCGTTT	CCGTCCGTTT	ATGAATTGTACGATACGT GGT	0,0	GCAAACGAAACAGAAGGGA ATA
Lri31P221179 4	T	C	GGGCCCTTCCACA	GGGCCCTCCCA CA	TGTGTGTGCATGTTTACAGAC CT	0,0	GATGAAATGCAGCCAGATCA C

Lri32744P200 2	T	C	TGATGCAGGGTGG	TGATGCAGGGC GG	CAGGTATGGTGTTCGGTGCT	0,0	CATGTTGTAGAGCTCGTGGA AG
Lri32P253829 1	T	C	ATTTAGTTGCTGA	ATTTAGTTGCC GA	CATACGTGTGCATATGTTT GTCA	0,0	TCCTTGGGTTTACAGAAGCA CT
Lri32P350799 6	A	G	CTGCAGGTGCATA	CTGCAGGTGCG TA	GCTAGATTGTGTGCTCGAT TGC	0,0	CATGCTAGCAATACAAGTGG AAA
Lri32P517584	A	G	CCCCACGGTGACA	CCCCACGGTG CA	GAATGACACAAGGCATCA TCC	0,0	AAATACGCGCTGTGGGTTT
Lri33P260267 2	C	T	GACGAGAACGGTT	GATGAGAACGG TT	CTTCCTGCAGGTCGTGTGT	0,0	CTCAAAGTGAACGAAGCCGT AG
Lri34301P369	A	C	GAGCCTGCAGGA	GCGCCTGCAGG A	ATCAGATCGAGATGCTGA CCTC	0,0	CTCACCTTCCCCGACCTT
Lri34P126378 3	T	A	TCCGTAGCTCGGC	TCCGAAGCTCG GC	GCAAAGCACTCTCCCTTAC ACT	0,0	GTCTTTGTGTTGCAGGCACT C
Lri34P145760 1	G	T	TGCCGGACTCGCG	TGCCGGACTCT CG	GGCGGTGCCCTTGTAGAC	0,0	CCCATGGACTGCGTCAAG
Lri35P174660 0	G	T	CTGTTGTGGGAA	CTGTTGTGGAA A	GTCGATCACATTACTCGTA CCG	0,0	CTCCTCGCTCAAATGAGCAC T
Lri35P348306 1	G	A	CTACACCGATGTA	CTACACCAATG TA	TATTGGTTCTGTGCTACAA TCG	0,0	CCGGATAGCCTGTAACAAAC TG
Lri3691P1038 3	A	C	AGGGTCTGTTA	AGGGTCTGTTC	CCTGCAAGTCATCTCAATC AGT	0,0.3	ACTGCTGTGCCAGGCTAGGT
Lri36P402209	A	G	GAACATCACAGAG	GAACATCGCAG AG	AGTCCTTAGAAGAAGGCG ATCC	0,0	AGGAACCGATCCATCTTCAT AC
Lri37P116758 0	G	T	CACCTGGCCAGAT	CACCTGTCCAG AT	GGCAACAGTTTGCTTACGA TTC	0,0	CCTCCAGGCACTGTGATTTT AT
Lri37P133466 8	A	T	AATATTCTCATA	AATATTCTCTTA	GGACCCTGAGTCTGTGCTT G	0,0	GTTCAATTCCTGGTTACCCTC A
Lri37P193771 4	T	C	AGGAAATATTCCA	AGGAAATATCC CA	AGTCACACGAACAATGGC TTCT	0,0	ACCAGCGTATCCTTTGGAAA AT
Lri37P423044 5	C	T	TGGTAACGCTCC	TGGTAACGCTT C	AGTTTGTGAAAGTTGGCAG GAT	0,0	GAAATAAAAGGCCAAGAAC ATACA
Lri37P450286 7	A	C	ACTACCAGATATA	ACTACCAGATC TA	AAATGAGCAACGAGAAGT ACGA	0,0	AGTTCTCCCGCAGTGGAGT

Lri37P731186	T	C	CTACTTTCTCTACT	CTACTTTCTCCA CT	TGAAACCATCATGTGAGG AAAG	0,0	CACCAACAGGGAACATAGC AC
Lri38430P134 3	G	C	CCTGCAGGTTGAG	CCTGCAGGTTT AG	GAGTGGTGAGGATACGGT TGTT	0,0	GGAGGCTGACAACAATGAG ATT
Lri39P237481 4	G	C	GCAGCGAGCTG	GCAGCGAGCTC	GTACGAACCTGAATCCCG ACT	0,0	GGGTTTTTGGTCGGCTTG
Lri39P378467 1	C	G	ATTCAAGGCACAG	ATTCAAGGCAG AG	GAACACCAAGCCCCATTGT	0,0	CGTGCGAGGATGAGGTCT
Lri39P497457 5	C	T	TTTCTTTTATTACA	TTTTTTTTTATTA CA	GACACTGCCAGCCCCAAAA TA	0,0	GGCTTTTCTGGGTAAATAAG AAAT
Lri39P502660 0	T	C	CCGACGGGCATGG	CCGACGGGCAC GG	GAGTGGGGCTTCCAGCAG	0,0	CACGCGAAGTTGTGGAGAGT
Lri3P1086079 9	A	G	ACACAGCGTAGTG	ACACAGCGTGG TG	CGGGTTTTCTGTACATAT CCT	0,0	GAGTTTAAACATACACGTGG CATT
Lri3P1183728 9	G	C	AGGGGCATCTTT	AGGCGCATCTT T	CTGGCCAGTGTGCAAGAA C	0,0	GAAGGCTTTCCACCAAGAGA G
Lri3P1323972 3	T	G	TGCCTCCTGCA	GGCCTCCTGCA	TGAGCTCATCCTTTTCACA GAG	0,0	AAGGCGAGTGGTGCAGTG
Lri3P1590715 1	T	C	TGAGAAGGCATGC	TGAGAAGGCAC GC	GTCCCAAGATTACCACAG GAGA	0,0	CATCCACGGTTAACAAAAAT CC
Lri3P169003	T	A	AGGGTTGTTGTGT	AGGGTAGTTGT GT	GCAAGCAGGACTTGAATC AAAC	0,0	CCTGCAGCGTAAATATGACC TT
Lri3P5546698	T	G	TGGCTTTGTTTG	TGGCTTTGTTG G	ATGTGGTTCAACTAAGCAA TGG	0,0	GAAGGCAGATAAACCAACG AC
Lri3P9055258	C	T	AAACCCAGGCCCA	AAACTCAGGCC CA	GTGCCTGGACTCGGGAAA C	0,0	CGGTGATGACACTCGTGACT
Lri3P9532051	G	T	TGCTTCCCACGT	TGCTTCCCACCT	CAGGCTGAGGACGACAAT G	0,0	TTCTGCCAGCAATGACACC
Lri40P537619 1	C	A	GCTCCTCGGCCGA	GCTCCTCGGCA GA	AAGACACGGCGTTCATCAT C	0,0	GTTGAAGGGTACCAGGACA GAG
Lri40P897424 TD38	A	G	TATACACCATA	TATACGCCATA	AAGCTATTGCAGTTGAGCA GTG	0,0	TCAACCTTTAGCGAATGTAT GG
Lri4109P7946	A	T	CAGGTCACTCATC	CAGGTCACTCT TC	AGGGAGAAAGGGTGACAC AGAT	0,0	ATGGAGGCAGCGTGACAAT A

Lri41P393985	C	T	CCTGGCCCGTCCT	CCTGGCTCGTC CT	AGTCCCGTGCCAATTTACA G	0,0	GCTTCAAAGTGCACCTAGTA TGG
Lri41P476134	C	T	GGCCGGGCGCGGT	GGCCGGGCGGT GGT	CGTACTGGAAGAGGCTCA GG	0,0	CCTACATGGTGGACGGTTTG
Lri4294P2756	T	C	GGCTCTGCTGTGT	GGCTCTGCTGC GT	GGTTGCGAACTTAAGGAC CTC	0,0	TATTTAACTCAATGTCATTA ACAAACC
Lri43P167668 6	A	C	ATGTGTCACCACG	ATGTGTCACCC CG	GATGGGCGCAAACATCAC	0,0	TTTGCACTAACTTTCTGCCTT TC
Lri44P106745	G	C	CTGCAGGGAGGC	CTGCAGGGAGC C	GATGGCATAGAGCAAATC GAC	0,0	TTCGAGTGCCTCGTCAAA
Lri44P343222 3	T	C	TTATTTTAGCT	TTATTTTAGCC	CTGCAGGTTGCGTCTTCTT	0,0	CCTGGCGACCTCTTCGTAT
Lri44P383627 9	A	T	AGACGCCTCCA	AGACGCCTCCT	CCCTTATTTAAATTCCCCG AGA	0,0	GTGCAGTGTTTCGTATTTGCG TA
Lri44P527021	A	G	GATCAGACCTGC	GGTCAGACCTG C	GACACCCTGGGGTTTGTG	0,0	CTCCTGCAGGCACCAAAT
Lri45P124656 9	C	G	GACGGACAGGCA	GACGGACAGGG A	CACCGCCTCCACAAACTG	0,0	GTGACAGGTGAGGGTGAGA GT
Lri4631P8667 TD39	G	T	TGGCTGGGACC	TGGCTTGGACC	AAGAGCAACCCCAAACAT TAC	0,0	CTATAGCACGGACGACTTAC CC
Lri46P266010 9	C	T	CGCGGAACGCAGA	CGTGGAACGCA GA	GTTGCGCATGGAGGAAGT	0,0	GATGATGGCGAAGCTGTAGA C
Lri46P293710 0	T	C	CGTCGTGGAGTGG	CGTCGTGGAGC GG	AGGAAATGGTGAAGGTCA TCC	0,0	GCATCTCTTCGTTTCGCATCT
Lri46P426000 4	T	C	TGCAGGGCTCCT	TGCAGGGCCCC T	CTCAATCAAGTGCAATTTC GTC	0,0	ATGCATATTCACACGCACAC AC
Lri47P127418 8	A	G	CACGCACGGCAA	CACGCACGGCG A	CACCAAAGCGTATATCTGC CTA	0,0	CCACTGACGGATCACATTAG C
Lri47P480244 6	A	G	CGCCGTGTTTATG	CGCCGTGTTTG TG	CTGCAGGTGTTGCCGTCT	0,0	GGATAAAATTAAATAGTCCC AACTCG
Lri47P580971	G	T	GCAGGTCAAAGCG	GCAGGTCAAAT CG	GACACTCCGACTTTTGTTT CTC	0,0	CTTGTGGTGGTGGTGGTTTT
Lri487P66561	T	C	GGGCAAACACCGC	GGGCAAACAC CGC	CCTGCCTGCAGGATTGAT	0,0	CTTTGGAGCGCAAACATTG

Lri48P101497 3	T	C	CCGACCATGAT	CCGACCATGAC	TGCAGTTTTACTCTGGCTT TGA	0,0	GGTCGTAGTGCATGTTGGTC AT
Lri4P1191270 4	C	T	GGGTATCCGCGTC	GGGTATCTGCG TC	ATCTTAATCCGGCCCTGCA T	0,0	GAAGCTGCCACGGCTCAT
Lri4P1229018 7	T	C	GGATGGACTGTAC	GGATGGACTGC AC	CTCCCAGGCTGAACTCCTG	0,0	ATAACCCATTGACACATTGC AG
Lri4P1428382 3	A	C	TGCAGGGCCCAAGT	TGCAGGGCCCC AGT	CTCGAGCTTCCAGAGACTT CC	0,0	CCTCCTCCTCAAACCTCAAC TC
Lri4P1741698	C	G	AGGCCTTGTGCAC	AGGCCTTGTGG AC	GGGGATCACTATGCTGGTA TTG	0,0	CCTTTGGTGACCTATGCAGT G
Lri4P2731292	G	A	TGTGACATGTCC	TATGACATGTC C	CCATTACCTGCTGCAAGTT GAC	0,0	GGCTTGCGTTCTCTGCTACTT A
Lri4P3128860	T	C	AGTTGGAAGCTAG	AGTTGGAAGCC AG	AAGCCCCTTTCTTTAAATG TCA	0,0	CCTGCCTGCAGGGTACTACT AA
Lri4P5424460	T	C	GGTAATTGTAT	GGTAATTGTAC	AGCATCCTTGGACGACATT ACT	0,0	GCGAAATTGTCCCACAGC
Lri4P8684156	C	T	CACACACAACCCCC	CACACACAAC CCC	CCGAATGATAAAGGCGAC AA	0,0	CTGCAGGGCATGAGAATAG AT
Lri4P8958596	C	T	TGCAGGCAAGCCA	TGCAGGCAAGT CA	ACGCTATACGTGACATTTG TGG	0,0	ACCCTGTGTTAAGGCCAACT C
Lri4P9222922	T	C	TGGCCTTAAGTCC	TGGCCTTAAGC CC	TTCCACATCATGGTCAAGT ACC	0,0	GGGATACATGAACTCCATAC CC
Lri4P9982449	T	A	CACAGCCACAT	CACAGCCACAA	AACTGTAGGTGGAAAGGT CACA	0,0	CACATTTTCAGGCAGCTGAT
Lri50P122168 1	G	C	TTGCCCACGTAG	TTCCCCACGTA G	AAGATCTGGCCACACCAA ACT	0,0	GCATCTGTTCGTCCAGCTCT A
Lri50P165766 5	T	C	TTTCTCCAAC	TTTCCCCAACT	GCGTAACAAGGTCTCATT TTGC	0,0	CTGAAAGCTGTCCCAGTAGG TT
Lri51P900701	A	G	TGCTCAATGAAGA	TGCTCAATGAG GA	AGGATGAGAAGCACCAGC TCT	0,0	CCCTCACTTCTGTTTCCTTGAT CT
Lri5215P4376	C	G	CATGCCGCTCTCA	CATGCCGCTGT CA	AGTCCTCTTGCCACCCATC	0,0	TCCGTCTTCGACACGTCAG
Lri5229P1229	A	C	TTCCCACACCAAC	TTCCCACACCC AC	AAGGCAACAAAAACACCC TTC	0,0	AATGAAGGCCTACCCATGTT C

Lri5244P5218	T	A	GTAGTAATAATA	GTAGTAATAAA A	CGTGTTAGACCACAGAAC GAAC	0,0	GCAGGCACGAAAGTTTCAA
Lri5270P9970	A	T	ACGATATAACAAC	ACGATTTAACA AC	AATGTCCACGTTTCATATG TGC	0,0	ATTACCAAGAGCATTGACCA AC
Lri5345P1018 5	T	A	GAACGGTGTAGTC	GAACGGTGAAG TC	TGCAGGTATAAACTAACCC TCGT	0,0	CTGTGGTCCTACATTGGGAT G
Lri53P112464 3	G	C	GGCATTTTGAGTG	GGCATTTTGAC TG	TGCAGGTTAGGGGAAATG AGTA	0,0	GGAGAAGTGCTGCTCGAAA G
Lri53P238381 2	A	G	TGCAAAATACACCC	TGCGAAATACA CCC	ACTGCCTCCAGGAATTCAT CAT	0,0	GCAGCTTAAGTTAACACAAA TTGTAA
Lri53P245604 9	A	G	TTGCAAAGTTAAA	TTGCAAGGTTA AA	TTAACGGTCTCCCTCTTCC AG	0,0	GATGTAAGCCGCCTTGTTAC AG
Lri53P338003	G	C	CTGACCGTCTGCTG	CTGACCGTCTC CTG	AAGCCGTACGGTGTTTC	0,0	GTCAGTGGCACCCCTGCTC
Lri54P100184 5	A	G	CGGGCGCAAGAGA	CGGGCGCAAGG GA	TTCTGCGGGTCCTTGAAGT	0,0	GATCATCTGGCTGGGTCTGT A
Lri55P216540 1	G	A	CTGCAGGCGAGTC	CTGCAGGCGAA TC	CCGTCTTGTTCTGATCCTT CTT	0,0	ACGCTTTCCCCAAAGTTAAG
Lri55P319056 6	C	T	ATCTTAAAAACTC	ATCTTAAAAAT TC	ACTCACTCGCTGTGGTCAT AGA	0,0	CGTTTTGGAGAACAGGAGGA T
Lri563P38486	G	A	AGAACTCTGCGCC	AGAACTCTGCA CC	TTTGGGAGTGAATGTTTGT CAG	0,0	TAAGACGTGGACGTCAAAAC C
Lri5898P7578	C	A	CAGGCGGCGGAT	CAGGAGGCGGA T	GATTAGCTTTCCGTCAACG TCT	0,0	ATCGTCTAACCGGTTACCT C
Lri5P1244864	G	C	CGGCAATTCCAG	CCGCAATTCCA G	TTTGATGTCGTTTCGTCATA AGG	0,0	CTGTCATACACGTGCACCCT AC
Lri5P1293472 2	G	C	CCTGGAGCTGGAGC	CCTCGAGCTGG AGC	GTACCTTCCCAGTACCGCA AAT	0,0	TTTAGAACAAGGGGATTTGT CA
Lri5P1307519 6	G	C	ATTCCGATGCTAT	ATTCCGATCCT AT	GCAATAAAAGGCCACGAA ATTA	0,0	ACCTCTGGTACCTCAGGGTC A
Lri5P1319181 6	T	G	TGGCTCTGCATCT	TGGCTCTGCAG CT	GCAATAATTGTGTCCATCA TGC	0,0	CTGCAGGGGTGCTTGTCTA
Lri5P1438911 5	C	T	GCACGGGCACAC	GTACGGGCACA C	GTGCCCCGGTTACTGATG	0,0	GTGGGCAGCGTTGTGAGA

Lri5P1462939	G	T	TGCGACCTTGGCT	TGCGACCTTGTCT	AGCTCTGTCCTGCCCTCCT	0,0	TGTTACCATTAAAATACACA AATCTCG
Lri5P2456252	T	C	TTTTTGTCTAGAA	TTTTTGTCCAGAA	ATCTGCCTGCAGGAATTTG AT	0,0	TAGTCGTTTCACTGGACACC TG
Lri5P3706885	G	A	TTTGGACTTGGCA	TTTGGACTTGA CA	TTTTTCTCATGTTTGCAAG GAG	0,0	ACAGGTACAAGCAGGCTCTG G
Lri5P4043379	C	G	TTAAGGCTGACT	TTAAGGCTGAG T	CACGTAGACACTCATCTCT TTGC	0,0	ACAGTATAAAACAAATGCCT CCA
Lri5P4269100	A	G	TCCTCATCCTC	TCCTCGTCCTC	CTGGTCGTCCTCCTGCTC	0,0	TCCTCGCCGTGGATTTTC
Lri5P4640927	A	T	TCTTCATTCCAGC	TCTTCTTTCCAG C	TGAAAATAATGGGTCCCTA ACA	0,0	TCCCTCAGGGTACAAACATA CA
Lri5P5071040	T	A	ATTATTCTCTCA	ATTATTCTCAC A	GTCACAAGGCTTATGCAA ATGT	0,0	AGACTTCACGAATATGGCAA CC
Lri5P7155011	T	C	GTGAATGTGTTGG	GTGAATGTGTC GG	AATTCGCATCAGGGTCTCA G	0,0	ATTGTTGTCGTTGCATTCATC T
Lri5P9200047	G	T	GAGAGAATCTGCG	GAGAGAATCTT CG	AAACCTTAACATTTTCAGCA CTCG	0,0	GACCTGGAAGGAGTGTCACT TT
Lri5P9366468	T	A	GAAAAAGTTACGT	GAAAAAGTAAC GT	GCAGGCAGAATAGTGGA TGTT	0,0	TTGCTTCAATCAGAAGCTGA AG
Lri5P9979583	C	T	TGCAGGTAATCGTG	TGCAGGTAATT GTG	TTGATCAAACCTACATACA ACCAA	0,0	CTGTCACCAGAGCCAACTCA T
Lri60P1197606	C	T	AGGTACAACGTGT	AGGTACAATGT GT	TGCAAGGCTTGTTAAGTCA GTG	0,0	CAGCTGCCACGGTTTCAA
Lri60P2434871	G	A	CGGTGGTCACGGC	CGGTGGTCACA GC	TGCAGAGTGAGCAGAGCA AG	0,0	CAGTAGGACGCCCCACAGC
Lri61P3097033	T	C	CGCTCTCATCTGC	CGCTCTCATCC GC	GTTTCGTGGACACGTAGTG AGA	0,0	CTTGCCCGTGTGGTTGTAG
Lri61P414412	G	A	ATGGAGTAACTAA	ATGGAATAACT AA	CTGCAGGCCAGTATACAA CATT	0,0	AGTTTAATTTTCGGGCATTGG AT
Lri63P1075345	T	C	CCTGCAGGCATACA	CCTGCAGGCAC ACA	ACAAATGAGTTCGTGCCAT AAG	0,0	CAATTGCAAGATGATTTCCA GA
Lri64P1877052	C	T	ACACTAATTCATA	ACACTAATT TA	AATATGTGGTCTCTGGGTT TGC	0,0	CATGCCTGCAGGGGAAAT

Lri64P3699994	C	G	ACCGGTGGGGGGG	ACGGGTGGGGGG	CTGCAGGATTGTGAAGGCTAC	0,0	GCGATCTCCTCCTGAGACAC
Lri65P1192162	T	C	TCTCAGAGCTC	CCTCAGAGCTC	GAGGGCCACATCAACCAC	0,0	TGCTCATTGGCGTTGTAGAC
Lri65P2520673	A	G	AATTGATAGGT	GATTGATAGGT	GAGGGAATTCCGAAGTTGAGTA	0,0	CGTATGGTGCAAAAGAAGTTCA
Lri65P2642230	T	C	TGCACAGCAAG	CGCACAGCAAG	AACCTCTACGTGACCTCGATCT	0,0	GTGAAGTGCTCCACGATGTTT
Lri66P303856	C	A	AAACACACCCCGG	AAACACACCCAGG	AGAATGTCTGGGACATCATGC	0,0	TTCATCAGGCAAACAACACG
Lri67P441125	A	G	GGTGCAATGGA	GGTGCAATGGG	AGCGAGGACAAGAAGACCTG	0,0	AGAGGGTCGTGCTTACTTCTC
Lri69P3566988	C	T	TAAAACATGTCCT	TAAAACATGTCT	GCTGGCTATCATCCCTTCTAAA	0,0	TGTCTGAAGTAAAGTGGGCTTG
Lri6P10286942	T	A	AAGTAATGTATCT	AAGTAATGTAACT	GTGTGCATTGATTTGACAGGTT	0,0	CTAATGGGGAGCCAAATAAAC
Lri6P10328882	T	A	GGAAACCTTTTTTC	GGAAACCATTTTC	AGTTGGGTGGCCTCAATGT	0,0	GAAGCTCCGTCTCTAGAAGTGC
Lri6P10383294	C	G	GCATGCATCCCGT	GCATGCATCCGGT	TGTTTAATGTGAGCAGTTAATCGTG	0,0	TTTCACTCGATTACCCCTCTGT
Lri6P10395996	G	T	AAAGTTTCGATGGC	AAATTTTCGATGGC	AATGATTTCAGTGTAATAGTGTTTCCT	0,0	GCATGCACATGTTTGAAAATAC
Lri6P10474030	C	T	AATCCCTCCCATGA	AATTCCTCCCATGA	CCGAATCGTCACCGATCATAC	0,0	TCAAATGCAATGCCACTAGAAC
Lri6P10581411	T	C	TTTCTCACAGTAT	TTTCTCACAGCAT	AGATAGGGACAAATTTGGGTCA	0,0	ACTCCAGGCAATGCAGTCAC
Lri6P11041437	A	G	ACAACACTGTGCT	ACGACACTGTGCT	ATGTAACCAAGCAGACCAACAGT	0,0	AGGGATTGCAGAAACAAAGAAC
Lri6P13329068	C	A	CCACGTTGTGATGG	CCAAGTTGTGATGG	AGACGAAGCTGCATCGAGAC	0,1,0	ACTTTACCGAAAGGACCAAGAA
Lri6P2036382	G	A	TCCAAGCCACGGC	TCCAAGCCACAGC	GTGGTGGTGTGCATTAATTGGT	0,0	GATTGCCTGCAGGATTGTG
Lri6P5039589	C	T	TTGTGGCGGTCCA	TTGTGGCGGTTCA	TCACGAATTCACTCGCTGTACT	0,0	GGCAAGGGTTGGTGGATT

Lri6P5524704	T	C	GGCATTTCGAGTCC	GGCATCCGAGT CC	ATGGAGGGAGACCTCTGG AT	0,0	AGGAATCCGATGAGCTATGA AG
Lri6P6080845	G	A	CGCCTTCATGAAG	CGCCTTCATAA AG	GTGGTTAACGCACCGACTG	0,0	GTTTGAGATGGACGAGGTGA GT
Lri6P6130428	T	C	GAGTATATTC	GAGTACATTC	CTTCCCTTCGATCATCCAG TC	0,0	GAACATAGGGGACATTTGAA GC
Lri6P6693459	C	T	G TTCAGCACCGTG	G TTCAGCACTG TG	TGTGACGGTTTGATGAATC G	0,0	GCCATGAGATGCTGCTAATT T
Lri6P7202854	G	T	CAAGCGCTGTCTGA	CAAGCGCTTTC GA	ACAAAACGTGGCCTCGTG	0,0	GATGATGGTGGTGGTGATGA T
Lri6P8338530	T	C	GCTCTGAAGAG	GCTCCGAAGAG	GCAACAACACCAGGACCA AC	0,0	CGCCTATCTCCCAACCAAAT
Lri7079P1000	T	A	ATCACATATCTT	ATCACATATCA T	GTCTTGATGGTGGAACCTT ACC	0,0	AGAGCCGTCGCCTAACCT
Lri70P126302 3	G	A	TTCACCGTTC	TTCACCATTC	TGCAAAAAGTAATTTATTAT GGAAATG	0,0	AGAACTACACCTGCAGGCAC AT
Lri71P127748 5	C	G	ACGCTGCATGCCC	ACGCTGCATGG CC	CTTCCAGAGCTGGCGGTA	0,0	GTCGTGGAGCTGTTTCAGG
Lri73P219995 0	C	T	AGGTTGTGTGCC	AGGTTGTGTGT C	GAATATCCCTTGCAAAACA TGG	0,0	ATGTCACCACAAGCCTACGT CT
Lri7435P3947	C	T	GGGGTCAAGCTGA	GGGGTCAAGTT GA	AGTGGGCTGGATGCTCTG	0,0	ATGGTTCTGCTGCTCTTCGT
Lri74P111042 0	A	G	GCACCGTCACATA	GCACCGTCACG TA	CTGTCTCTCCCGCAGTGG	0,0	CTTGTCGCTGTAGCTGAAGG
Lri75P276391	C	T	TTTAAATAGGCGA	TTTAAATAGGT GA	AGTGGCCAGAACTAGGGG GTA	0,0	AATTGAGGAGGTAATGGTTC GAT
Lri76P158191 9	C	T	GTCAGCGGGATA	GTCAGTGGGAT A	GATTGGTGAATGACGCAA AAC	0,0	CTCCCTCCTGCAGGTAATTC AT
Lri76P839426	T	C	CACAACTCCATGG	CACAACTCCAC GG	CCTGCAGGTACCTTATTGA TGG	0,0	AGGTAGGGGTGGTGGAGAG A
Lri76P849517	T	G	TAAGGCACCTTAT	TAAGGCACCTG AT	CTGCAGGAAACATGCAGA ATAG	0,0	ATATCTGGGGAAAATGGCAA G
Lri77P239810	T	C	CTTGTGCTGGTTC	CTTGTGCTGGC TC	GGATTGATCACGGCTGATG	0,0	TCGACTCTGAGCGAGTACAA G

Lri78P1108359	G	C	GTTTATACACGC	GTTTATACACC C	TGCACTTCTCTATATGCGG TGT	0,0	AGGTGATCTGCTTCCCTCCT
Lri78P1274279	G	A	AGCGCGAGACGTG	AGCGCGAGACA TG	GAAGCCCTGCCAAACGAC	0,0	ATTGTCGGAGCGCGTTGT
Lri78P1520535	A	G	AGTAAGCAAGATG	AGTAAGCAAGG TG	TGGTAGGGTTAAGGCGATT AAA	0,0	CCTTAACCACTGGCTTCTTC AC
Lri78P2370671	G	T	ACCTGCAGGCGGC	ACCTGCAGGCT GC	TAACCACACTTTAACCCAC CAT	0,0	ACCCTGGTTAAATAATAGAC ATCG
Lri78P482602	T	C	CCACCATGCACTT	CCACCACGCAC TT	CACTCTCCGTACCTGCTTC TG	0,0	CTGCCCTGCTGGATGTACC
Lri79P2948990	A	G	ACTGTCCGTAACA	ACTGTCCGTAG CA	AGTAGATCACTGCAACGA CACG	0,0	GAGCTCAATTCCCAACGTTA TT
Lri7P12869891	T	C	GCCATGTTTCCCC	GCCATGCTTCC CC	AGGAATGAACCCCTTTCTG TGT	0,0	AAAAGTTTAGTTTAAAGACC ACGATG
Lri7P1684065	G	C	AAGAACCCAGGGG	AAGAACCCAGC GG	TGCAGGGAGAGACTGATT AAAA	0,0	GTGGTTCAGGTATTGGGTGA TT
Lri7P2921566	C	T	GCACTGCCCCGCT	GCACTGCCCTG CT	TTCTCTTTCTGGTTCATTCC TC	0,0	CTTGATGGCTCTGGGAAG
Lri7P474819	A	T	TAAAAATACCCT	TTAAAAATACCC T	AGATGCCGATAAGCAAAC AAAG	0,0	CAGCGGCAGAAACAAATAA ATA
Lri7P4842789	A	G	AGCGCCATTTCCC	AGCGCCGTTTC CC	CCTGCAGGGAGGTTAGAC AAC	0,0	GTCGTCCTGACGCCTGAC
Lri80P1637884	G	T	TGGCTGACGGTG	TTGCTGACGGT G	CATGCTTCTTTGTGAGCTT TC	0,0	CACTAATCTGCTCGCCCACT
Lri82P53126	G	T	CGAGCAGCTGGTT	CGAGCAGCTGT TT	CAGGAAGGAGAGTGGGTC CT	0,0	ATCCAGGCGGCCATAACT
Lri83P1195764	T	C	TATTTCCGAGTGG	TATTTCCGAGC GG	AGCTGCCCTCTGCACAGTT	0,0	GAAAAAGGGTGGCTGACTTT TA
Lri83P1335304	G	A	ACAGGGGGGCGGA G	ACAGGGGGGCA GAG	CCTGCAGGCTCTTGATCGT	0,0	AAGACGGAGGGCAAGACC
Lri83P2068917	C	A	TCCGTGGCTACGAC	TCCGTGGCTAA GAC	ACTCCCCTTTGTAGAGCGT GTA	0,0	GAGTACTTTGGGAACGTCCT TG
Lri83P564737	G	A	GAAATGAGAAT	AAAATGAGAAT	GCACAACCGTGAAAACCT	0,0	CCTGCAGGACATTTCCAAAT TA

Lri84P170406	A	G	CTTTGTTATGCTA	CTTTGTTGTGCT A	ATTTTCATAAATGAGGGGG ATG	0,0	AGACGCTCCACACTCACCAC
Lri84P876835	T	A	CGCAAGCGGGTAA	CGCAAGCGGGA AA	TACCTGTTTTAGGCCCTTT CAG	0,0	CGCCAAGCTTTTGTCTGCTA
Lri84P876852	G	T	TGCAGGAGAGAT	TGCAGGATAGA T	AGCAGAAACCGCTGAAAG TG	0,0	CTAATTCTGCGCCAAGCTTT T
Lri85P205079 5	G	A	GAAGCAGTTTT	AAAGCAGTTTT	CGAGTGGCCCAGGGAGTA	0,0	GTTGGAAAACAGCCTGAAA GAT
Lri85P209542 0	T	C	CTCAACGACGTCC	CTCAACGACGC CC	GCGTCGATACCAATGGAT G	0,0	GAAAGATTTGCACGGTCCTA AG
Lri85P213759	C	G	AGGCCAGGGGCGT	AGGCCAGGGGG GT	GACCGTGGTCTGTATGCAT CT	0,0	GGTCATGTGACCGTCATGG
Lri85P891582	C	T	GGCCCCGGCGTTC	GGTCCCGGCGT TC	GCGATGACATCTACCAGC AATA	0,0	GTTACCGGCACGGTGATG
Lri85P956410	G	A	TCCGCCGCCTGGA	TCCGCCGCCTA GA	TGGTGCAGTGTTACAGTC	0,0	TTTTACCTGCTGGTAGATCTC G
Lri86P103182	T	G	AAGCGTAGCGTGA	AAGCGTAGCGG GA	TTAGGTCTGCACCCAAAAA TAA	0,0	CAATTAGGCATGAAAGCATT TG
Lri88P116431 8	T	C	GCCCATTTAGTCC	GCCCATTTAGC CC	TCTTCTCCAGCCCATCTCA C	0,0	CTGGGTCCAATGAACTTCTG TT
Lri89P232206 1	A	G	TTTTCCGACAAGC	TTTTCCGACAG GC	TTTTTGTTCTCCACATTGC AC	0,0	GCTCTTACAACGTTTGGAGC AT
Lri8P1288030 7	C	G	CTGCTGAACTCTT	CTGCTGAACTG TT	TGAATTATCCACCAATGCT GAG	0,0	AGGATTGTGGTTGAACAGTG TG
Lri8P1441255	A	T	GTGTCTGGACA	GTGTCTGGACT	GGTGAAGATGCTGTCGTCA GAG	0,0	CACAGCCTGGGCTGAAGT
Lri8P4138772	A	T	GTATGTATTTA	GTATGTATTTT	ACAGCTCCACCCAGCTTCA TA	0,0	ATGCGACTCAAACCACTACT CA
Lri8P4295266	T	G	CATCATGCAATA	CATCATGCAAG A	TAATTTTCCATGAGGTGTT TGA	0,0	GATTGTGATCACCAGAACA GA
Lri8P9543505	A	G	CTCCACAGCTAAT	CTCCACAGCTG AT	CGATGCAGTAGTGCGGTCT	0,0	ACAGCATGGCGAGCATGA
Lri90P257157	A	C	AGCATTTTCATC	CGCATTTTCATC	TGATTATGATGTCCATCGG TAAAG	0,0	TGCAGGTTATGTTTGTCTCCT G

Lri90P618248	A	G	ACATCACCGCC	GCATCACCGCC	ACGACGCGATAGAGCAGG T	0,3,0	CGATTGTTTCCTGCAGGTGT
Lri91P204352	T	A	AAGAGTATTCTG	AAGAGTATTCA G	TCACGCAGGTAACCTCATTT CAT	0,0	GATGTCACAGTGGTTCACAG GT
Lri91P234218 6	T	C	GTGTCCAGGGG	GTGCCCAGGGG	CTGAAATTAATCCCTGCTC CAG	0,0	GGCACACCTGGACACATCT
Lri91P730506	C	A	GACGCATTTTCTA	GACGCATTTTA TA	GCTACCGAACCGGTGACTT	0,0	TTAATAACACGCATCAAAGA TACATT
Lri93P134028 9	A	G	AGAAGCAGAAAC	AGAAGCAGAAG C	GAGCGATTCTCTCCGTACC AT	0,0	CAGGAACAGCTCCTTGTTGA A
Lri96P106792 6TD50	T	C	AA[CT]GTTGGGTT	AA[CT]GTCGGG TT	GCTAGCTGAACCCGTTACA CAT	0,0	GCATATTTGCGGAATACACC AC
Lri98P763276	A	C	AGGGTCGCGCAGC	AGGGTCGCGCC GC	GCGTCTTCAAACCTCATCGA GAC	0,0	GCGTACGGATGTCAGTGCTT AG
Lri99P330522	A	G	GCAGGTTGCAAG	GCAGGTTGCAG G	TTAGTAACCCTTTCCCGAG ATG	0,0	CCTGAATAAAATGAACGCTG A
Lri9P1037805 7	C	T	GATCGGGTCTC	GATCGGGTCTT	ACAAAGGTGGCCAGACAT GA	0,0	GGCTACTTATAACCCACGTT GC
Lri9P1124057	G	T	AAAACACGGTGCA	AAAACACGGTT CA	TGTGAACCTCGGGGGAAG	0,0	ATGAAATGCGGTAGTGTCTT G
Lri9P1250097 7	T	G	AGTGAGGTGGTCG	AGTGAGGTGGG CG	GTGAGGTGGGCCAGCAGT	0,0	CCTCCATCTCCAGCTCGTC
Lri9P4476882	A	G	GTCAGCACGCA	GTCAGCACGCG	GGTTTCCACTATCCTGGTG TGT	0,0	GCATACCAGCGTTCAATAAA CA

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Appendix 7. GT-seq SNP panel for White Sturgeon.

Assay	A 1	A 2	A1-Probe	A2-Probe	FWD Primer	Correcti on	Rev Primer
Atr_103 04-61	G	A	TGGCTTGGCAGTG G	TGGCTTGACAGTG G	GCCTTTGTTCTCCAGCTTGC	0,0	TCTAAACAGACCAATCCCAC TG
Atr_103 22-43	G	A	GCAGCGAAACAAA GA	GCAGCAAAACAAA GA	TGCAGGGGCTATCAGAGACT	0,0,3	AATCAGTGTGGGAGCTCAGC
Atr_104 28-71	T	A	AGAGAGCTAGCA	AGAGAGCAAGCA	CGCACACACACAAAGAGAG C	0,2	GGATCCAGAGCCACAGTGTC
Atr_104 37-26	T	G	TTTTTTGGCAACTG T	TTTTTGGGCAACTG T	TGCAGGTGGGTTATGGGTTG	0,0	TGAATTAAACAGGTACAGTT GCAGA
Atr_106 72-61	C	T	GACCACACTGGGC AG	GACCATACTGGGC AG	GCAAAATTGGCAGGGATGG T	0,0	GCAGGTGTTTGCTTGAGCTC
Atr_108 67-69	C	T	TGGTATACAATGA A	TGGTATATAATGA A	AGGACTGGGTAGGGAGCAT T	0,0	ACCGAGCTGGATGACTTGAA
Atr_109 98-72	T	C	AGTAATGTGTT	AGTAATGCGTT	CAAAGCGCCCATGATTGTCA	0,0	TTAGCAGGCACAACACTGACAA
Atr_110 46-75	T	A	GGCCCAAT	GGCCCAAA	GGAGGGCCTGGGAATCCT	0,0	TTCAGGGGGAACAAGGTGAG
Atr_111 04-35	T	C	TGCACTGTCGTGTC T	TGCACCGTCGTGTC T	CGCTAGTAGTGAAGTGAAGT GC	0,5,0	CCCTCTCAGGTGCTGTTCAC
Atr_115 85-33	C	T	TAAAGCCAAGTTT GT	TAAAGTCAAGTTT GT	GGTTGGTAGTTTGCGGCATT	0,0	AGTGGAGTTCTCCGATCCCA
Atr_117 87-73	G	A	CTAACCCGCG	CTAACCCACG	ACAGTCCCTACAGGCATTGC	0,0	GATTCCAGAGGGAGTGTCGC
Atr_118 64-68	T	C	ATATCGCTGACCA C	ATATCGCCGACCA C	GGTACCACCGCCAATATCGC	0,0	CAGAGCTGCTGGTTGTTTCG
Atr_122 19-56	A	C	ATAGTATATGCGG G	ATAGTATCTGCGG G	GCAGGGAAGTCTAAACCCC A	0,0	AATTGTGTTCTTTGCCCCGC
Atr_126 16-36	G	A	GCCGTTCGTGAAG C	GCCGTTCATGAAG C	TCCTGCCATGCTAGCAAGAG	0,0	TCCACCGGCTATTCTCTTT
Atr_126 77-44	A	G	ATGTACTATTTAGC	ATGTACTGTTTAGC	TGCAGGAGAGGATGTATAC GTC	0,0	ACTTCAAACAACAAAAGGCT GCT

Atr_130 73-61	T	A	TTTTAATTTGCATT	TTTTAATATGCATT	GCTGCAGCTTACAGTCTTCA	0,0	TGCAGAGCTCAATCCAAACC T
Atr_131 32-45	G	A	GCCACGAAGAACA TG	GCCACAAAGAACA TG	GTGACCAGCATGACCACCAT	1,8,0	TATCACAGGGAGCTGGGGAT
Atr_134 76-65	A	T	TTATCAGTATGCAG C	TTATCTGTATGCAG C	CGTTTTCCAGCACCACAGGT	0,3,0	CTGACCTTTGGCTTGTGTGC
Atr_137 06-54	A	T	GTGAGAGAAGACT A	GTGAGAGTAGACT A	AGGCTACTTGCATCTGCCAG	0,0	TCATAAGAGCTGTCTGAAAC TGA
Atr_137 29-47	T	C	GCACAAGTTTTTTT	GCACAAGCTTTTTT	CCATAGCTTTTGTGCAGCAC A	0,0	TGCCTTTATGTTGACAGGGT CA
Atr_139 17-71	C	A	AACTACTCATCA	AACTACTAATCA	CCTTCCCAGGGAGCTTGATG	0,0	CAGAATGCAAGGTACACTGT TGA
Atr_139 30-72	A	T	GTTTTATAAGC	GTTTTATTAGC	TGTTTTAGTGGGACCAGTGC T	0,0	TGCAAAATAAAACACTGTGG AAAAA
Atr_139 96-43	T	C	TATTCTGTAATGTT T	TATTCCGTAATGTT T	CAGGTCTGCTGTGTGTGACA	0,0	TCAAGTTCACCTCGACAGCA
Atr_144 10-52	T	A	GAAGCAATCCCCA G	GAAGCAAACCCCCA G	ACAGGTGGTTCATCTGCAAA C	0,0,3	TGGCATTGTTTCCACTGGGG
Atr_146 35-67	C	A	GGAGCACCAAAAAA C	GGAGCACAAAAAA C	ATCCCCAGCTGATTTGCCTC	0,0,3	ACCACTTTAATGCATCTCCTG G
Atr_148 24-32	A	G	TTAACATGAAAGT CA	TTAACGTGAAAGT CA	TGCAGGGATCCACAGAAAT GT	0,0	AAGCAGCTGAACACAATGGG
Atr_148 62-38	T	C	TTGACTCCCTTTAA G	TTGACCCCCTTTAA G	CGCCTCCCCAGGACTATTTT	0,0	TTTCCTGTGGCCATTTTTATT GT
Atr_149 17-56	C	T	AACACATCTTAAC A	AACACATTTTAAC A	TGCGCCACCTAGAAACACAT	0,0	TGCACAAAGAAAGGTCCTGG T
Atr_151 79-54	G	T	TTCAAATGACCCC A	TTCAAATTACCCCCA	GCAGGGTAAGTTAGTTTAAG CGC	0,0	GGTGCAGCTTGTATGGGGT
Atr_152 01-45	A	C	TTACTGAAACACA T	TTACTGACACACA T	GGGTACAGTGCAAGAAATG GC	0,0	TAGTCAGGTTGGCTGTGAGC
Atr_152 73-44	T	G	ATAGATCCTGTCCT A	ATAGAGCCTGTCC TA	GGGAATGTTTCTCTGTTTTG GAT	0,0	ACTCCAGTCTGGACATAAAC TCA
Atr_152 94-66	T	A	TGGGATAGAATTTT C	TGGGAAAGAATTT TC	TGTATTGTTCCGGATGAATTG GGA	0,0	TCTGATGTAGAACTTCTGTGT AGTT

Atr_152 98-72	G	A	TCTCACTGTAT	TCTCACTATAT	TCTCAGCATCTTTCACTACC CA	0,0	TGATAAAGCAACCTTGAGCC CT
Atr_158 75-62	C	T	CCTGCCCCGTGGA A	CCTGCCCTGTGGA A	TCCATCAGAGCTCACCAGGA	0,0	AGTGTTGCATTGGCTCTGGA
Atr_168 03-66	C	T	GGCAGCACGCCTC T	GGCAGCATGCCTC T	CATGTTGTGTGTCCGGTGC	0,0	TCCCTGGAATTGGTGCAAAA
Atr_172 0-33	C	A	GGGGGCTTTGAGA GC	GGGGGATTTGAGA GC	GGCAAAGCAGAAGGGGG	0,0.7	TGTGTGTATCTGTCTGTGTGG T
Atr_177 10-71	T	C	CAGGATGCCC	CAGGACGCCC	GCTCTCCCATCTTTTGACGC	0.6,0	ACACTGACGGCAGCTATTCC
Atr_181 33-56	G	A	TGGGTTTGTGTAT	TGGGTTTATTGTAT	AGTCAAGTGTGTGTGTTGGG T	0,0	AGCAGGGAAGATACTGGTTG C
Atr_182 95-67	T	C	ACCTGCATGGCAA A	ACCTGCACGGCAA A	CTCGTCTTGAGGCACCTGC	0,0	TGAAAACCTGGCAGCTTTGTG A
Atr_183 34-74	A	G	ATGGTGGAC	ATGGTGGGC	GGAAGTTGGTCCTCAGAGGC	0,0	AATGAGTGCCATCAGCCACT
Atr_184 03-29	C	G	AGATCCATGAAGC TC	AGATCGATGAAGC TC	TGCAGGTAATGAATGTTGCC T	0,0	TGCGTTCTGTTCATCCCTCT
Atr_194 96-44	A	G	GAGTGAGGCTATT GG	GAGTGGGGCTATT GG	CACACCTAGGGGCACATTGA	0.6,0	TCAACAGCGAGAAGGGTTGT
Atr_196 66-61	G	T	ACATTCAGGGCAT A	ACATTCATGGCAT A	CAGGCCTCAAGCTCTTCTGT	0,0	TGTAGTGAGGTTACCTTATT ATGCC
Atr_197 83-57	C	A	TCTAACATGGACA TC	TCTAAAATGGACA TC	TCTTCTTCTGGAATGATTAC ATCCA	0,0	GACAGTGAAGCAAGAGAAA TCCA
Atr_200 13-55	C	T	GCCTGCTCCCCTCG	GCCTGCTTCCCTCG	GATGCTAACCTGGCTCTGGG	0,0	CCGAATATCCGCGGGAAGAA
Atr_200 37-39	G	A	AGAACGTGTTTCCT GC	AGAACATGTTTCCT GC	GCAGGCGTAGAGTTACAGC A	0,0	ACAGTAGACGTCAACGGGAT
Atr_201 17-55	A	G	GCTTCACCCCAGG CA	GCTTCGCCCCAGG CA	CCTGCTCCCAAACAGGACAA	0,0	TCAGATGGGCCTGGTGAAAC
Atr_202 19-65	A	G	ATGCCAGGCTTTCT A	ATGCCGGGCTTTCT A	TGGACCTTATTAGAAGCTTA ATGCC	0,0	GCACCTCTATGGCACTTTTTG G
Atr_202 52-35	T	C	ATGGGGGTTGTAA T	ATGGGGGCTGTAA T	ACTTGGACGAGGCATCATGG	0,0	GCCAAATTCAACTGCTGGGA

Atr_203 32-60	T	A	GTATAACTAGAAC A	GTATAACAAGAAC A	ACATTGCCTACACCTCACCC	0,0	TTTGACTGCCACAAGCTCCT
Atr_204 82-41	C	T	CGGGAGCCGAGCT T	CGGGAGCTGAGCT T	CTCATTGCAATTGGGCTCGG	0,0,3	GCAGCCTAGCAGGATCTCAT
Atr_205 29-52	A	G	GCACAACTTTTTAC A	GCACAGCTTTTTAC A	ATCGCAGCTTGACAGTGAGT	0,0	AGTAATTCCAAAAAGCCCAC TGG
Atr_207 40-65	T	C	ATTGCTCTCTGCCC T	ATTGCCCTCTGCCC T	AACATCATCCCCCTTCCTGCG	0,6,0	GAGTTCAGAGCCAGCACAGA
Atr_208 4-45	A	G	GGTTTGAAAATGTT	GGTTTGAGAATGT T	TGAGGTAGCCAGCAGGTTTG	0,0	AATGATGCCAGAGCGCTGAT
Atr_209 52-49	T	C	ACACTACTCTGCCC	ACACTACCCTGCC C	TCCCCAGCTGACATGAACAC	0,0	CACAATTGGCCAAGTGCTGC
Atr_216 85-29	A	G	GTGCTGAAGGCTC C	GTGCTGAGGGCTC C	TGCAGGTTTGGTTCTCTGTTT G	0,0	CCACCAGCCAAAGAGACAGT
Atr_220 08-56	C	T	TACTGAACAGTGA T	TACTGAATAGTGA T	GGGCAAGAAAAGACCCAAA CC	0,0	GCCTTCTGGTCCTAATATAA AGTGC
Atr_227 27-31	C	T	TTTGCCAGATTTCA G	TTTGCTAGATTTCA G	GCAGGAAACCATGATGCAC C	0,0	TGACTTACTAGACATCTGCA ACTGA
Atr_230 70-31	C	A	CAGTCTCCGCATTT	CAGTCTCAGCATTT	GCCTTTGCCCTCCAGTCTC	0,0	TCCTCTGATCCCACGACCTT
Atr_241 46-56	A	C	ACATGTTAATCTTG	ACATGTTCATCTTG	TGGCTAAAGATCTAGAACAC ATGT	0,0	TCAACCGAGCTCTGTTGCTT
Atr_251 59-57	T	C	TATTTTAGTGGAAG C	TATTTCAGTGGA GC	CCTGAGTGTGTGAACCAGCT	0,0	ACATGTTAGCCAAGAGTTGC A
Atr_254 0-75	A	C	TCTGGTAA	TCTGGTAC	TCAAGCATGCTAAGTGTCTG GT	0,0	TGTTCCCGGGTGCCAAAAA
Atr_255 40-60	C	T	AATTCCCAGCTATG C	AATTCTCAGCTATG C	AGCAGACCACTGGCATGAAT	0,0	TCTATCATGGGCATCTGCAA A
Atr_255 62-47	A	G	CGGCAAGCAATAA AA	CGGCAGGCAATAA AA	CGGTTATAGGATTAGTATGC GGC	0,0	GCAGAGTGCAGTGAAATAGC C
Atr_258 84-65	T	G	AAAAATTTTCCCGA A	AAAATGTTTCCCG AA	GCAGGGAGATTGGGAAGTC A	0,0	AACAGCAAAATTTAAATTCG GGAAA
Atr_259 05-72	G	A	AAACCACGGAA	AAACCACAGAA	TGAGGGGAAGTTGAGGTGTT	0,0	TTCCTCTTGACCTTTCAATTG ATC

Atr_263 10-63	A	C	GAACGAAGCTTAG TT	GAACGCAGCTTAG TT	CAAAATGCCCCGATCACCCAC	0,0	TTTGCGCTGTTTGACCTCTG
Atr_268 4-39	A	T	ACTGGACAGAGAT C	ACTGGACTGAGAT C	CAGGAGACGCAGGGAGAAA G	0,0	GCCCACACTGTCATTGAGCT
Atr_270 72-33	T	A	TTTATGATAGTGAT	TTTATGAAAGTGA T	GCAGGTGATTGGTGGAAATA GC	0,0	TGGACTCGCATCACCTTCAC
Atr_273 67-69	T	C	AAATAAATACACA G	AAATAAACACACA G	CGTTTCCACAGTGGCAATCA	0,0	TGTGTGAATTTGGATTTCTCT GTGT
Atr_273 95-73	C	T	CAGG[GA]CGC	CAGG[GA]TGC	TGCGACTCTGCTGTGTATGA	0,0	GACATTTTGCTGTCCAGAAG GG
Atr_274 30-71	A	G	ATTGCCCATGCC	ATTGCCCGTGCC	CTGGTCTGGTCAGCAATTGC	0,0	AGTGCCCCAACACAGTATGG
Atr_276 8-35	C	T	CGCCTGGCCAGTT G	CGCCTGGTCAGTT G	TGCAGGTGTTCAAGTTGAGCA	0,0	AGACAATACAGCAGACCCAA CT
Atr_281 75-70	T	G	TTTAGTTTTGC	TTTAGGTTTGC	AGGTAGGCTAGAAATCGGTT CA	0,0	TGGTCTTGATTAAGGGGTGC A
Atr_282 80-63	A	G	TGATCAGAAACCT T	TGATCAGGAACCT T	TCCACTTTGAACTCACCGGG	0,0	ACTGTACACTTTGCTTGTCT TACA
Atr_284 11-65	A	G	GTGCCCAACAGGA C	GTGCCCAGCAGGA C	AAACCAAGCAGCGTCTGGA A	0,0	GCAGCTCTGTCAGTCTCAGG
Atr_285 8-58	C	G	ACCAGCTGTGCCG GG	ACCAGGTGTGCCG GG	TGCAGGCATTTTGTGGACC	0,0	CACAGTACCATGGGAGTCCC
Atr_286 09-62	A	T	CAAACATATCATT G	CAAACATTTTCATTG	GCAGCAGGGTAAGGATGAC A	0,0	AAGCAGGGAAATACAAATA CAATGA
Atr_287 46-28	T	A	AGGTTCTTCACTTT	AGGTTCTACACTTT	AGGGGTTGTTGGGCATAAGG	0,0	AGTAAGCACAGGATATAACA AAGTG
Atr_288 34-39	T	A	ATGTAGGTGACAG T	ATGTAGGAGACAG T	TGCAGGAGTGATCACAAAG ATGT	0,0	TGTGAATACCCCGACTGCTG
Atr_288 61-59	T	A	GACCCTGGTGCAG AT	GACCCAGGTGCAG AT	ACCCAGGACCAAAGGGAGA T	0,0	GTGTGACTCACATCTGCACC
Atr_290 24-55	A	G	CTCTCAAGTCCTTG A	CTCTCGAGTCCTTG A	TCCAAAGGCCGGTAACTCAC	0,0	AAGGCCAGTGAACCCACAAT
Atr_290 86-33	C	T	TTGTCAACGGGTTT	TTGTCAATGGGTTT	GGTTTGGTTCAACCGCACAG	0,0	AGAGAGCGCCTGTAGACAGT

Atr_292 77-35	C	G	TGAAACAGCAGTA TG	TGAAAGAGCAGTA TG	GGATCGCTCTCTGCTTGTGA	0,0	TGCCAAGCCCTAACTGCTAG
Atr_293 02-34	C	T	CTGCTC[GA]TCTAC AGT	CTGCTT[GA]TCTAC AGT	GCAGGCTGTATAGTGAAACT GG	0,0	TTACTACTCACCTCACCTGA AAAA
Atr_294 14-61	C	T	TTCCAACCGGGGA T	TTCCAACCTGGGGA T	CAGGGCTGGGGTCTGGA	0,0	GGCGCACTCTGTCTCCAAAT
Atr_301 45-46	T	C	AAGGAAATACTTG C	AAGGAAACACTTG C	TGCAGGTTGCCCATTGTATC A	0,0	TATTCTACTGCGCTCTGGC
Atr_302 71-58	G	A	AGGAGTCGTATTTT	AGGAGTCATATTT C	ATGCAGAATCCACAGGAGTC	0,0	AAGGAGCTTAGACACTGCCA
Atr_303 76-68	C	T	CAGGAAACGACTC A	CAGGAAATGACTC A	CCGCCAGCAGTCAGGAAA	0,0	TTGGTCCACAATCCCCCATC
Atr_309 16-62	G	A	GACTGGGGCTATTT	GACTGGGACTATT T	AGGTCGTGCTGTATTGGTCA	0,0	CAGGTGTGATGAGGGGAAAT
Atr_309 92-26	C	T	TAATGGTCGTTAAT	TAATGGTTGTTAAT	GCAGGTCTGAAATGAGGTA ATGG	0,0	GCTCCCTTTTTATTGTGTGTG ACT
Atr_319 17-28	T	C	AAAACCTGGTCGCT CA	AAAACCGGTCGCT CA	TGCAGGACCAAGTGGGATTA	0,0	TTACAGAGGAAGGTGAGCGA C
Atr_322 34-71	C	T	CACGCCACGGGG	CACGCCATGGGG	CTCAGGAGGATGGCCATTCT	0,0	TGTTACAAAAGGTCTCATCC CC
Atr_323 82-60	G	A	TATACTCGGAAAC A	TATACTCAGAAAC A	CAAACCCTGGTCCCTTGGTC	1,8,0	GGGACTGCAGTGCACCTAG
Atr_325 45-55	A	G	ACTCAACACGCCC T	ACTCAACGCGCCC T	TCCACTTGGGATGATCTAAT CTCC	0,0	TTGAGAACCAGTTGGGCACT
Atr_325 51-51	G	A	AGGTCGAAGTAGT GG	AGGTCAAAGTAGT GG	GCTCTCCAGGTTGTCGTTGA	0,0	AGAGTCCAGCGGGCCTAC
Atr_328 40-74	T	A	TTCATTA	TTCATAA	TGGCACAGCTTTACCGGTTT	0,0	GTCCACAGAGTTGTTTGTGA AA
Atr_329 45-42	G	T	AAAAGAAGAGTTC C	AAAAGAATAGTTC C	TGCTCTTTCAAATCCTATGA CTCA	0,0	AGCAGAAATCGTTTTACAAG GAAC
Atr_331 23-54	T	C	AAAGCAATGATTA A	AAAGCAACGATTA A	ACTGTGTTCAAGAGACCATT GGA	0,0	AGAGTTTTTACAACATTATT GCCCT
Atr_336 45-66	G	C	TCGCTCTGTGAGGT	TCGCTCTCTGAGGT	TGCGTGTCTGCATCTCCAAT	0,0	GGCAGCACAGACCATAACAGT

Atr_337 98-72	G	T	GTGCCGCTG	GTGCCTCTG	ATTTTGGTTTGTGGCGGTGC	0,0,3	GGTTTCCCATTTTCCTCCAGC
Atr_338 03-28	G	T	AGCTGCAGGGATG G	AGCTGCATGGATG G	GGAATGTAATGTGACCAGCT GC	0,0	ACCAGGAATGGATCAAACCTG CT
Atr_34- 41	G	C	GTCCTGCAATGCTG T	GTCCTCCAATGCTG T	CCTGCCTGTGTGCAATTCAG	0,0	CCGTGAAGCCACTACAGCAT
Atr_344 54-29	G	A	GACCAGGGTTGCC T	GACCAGGATTGCC T	GATTGTGGCACTCCAGGACC	1.5,0	ACCCGAAAACCTAGAAGCCCT
Atr_344 97-36	C	T	GATAGTTCGCTCTT	GATAGTTTGTCTTT	GGAGGTGCTGCTGGTGATAG	0,0	GCTTGGTGGTTGTAGGTGCT
Atr_345 1-52	T	G	GTGCTTTACCAACA T	GTGCTGTACCAAC AT	GGTTTGGAGGAAGTTTGTGC T	0,0	CTCTGTCCCTTCAATTGGAG GA
Atr_354 15-62	C	A	CAGAACGTTAAAA TT	CAGAAAGTTAAAA TT	GGAAGTTGGTCTTATGATTA GTGTT	0,0	AAACAAGATGTTGGAGTACA AAAGT
Atr_354 40-36	A	T	ATACCATACATAC A	ATACCATTACATAC A	CAGGTCCTACCACTGCTGAC	0,0	TGCAAAGTGTTGTTCTCTGTAT G
Atr_358 1-53	T	A	TTTTATTTTTCATA	TTTTATTATTCATA	AGCTCCAGTTCACAAAGCCT	0,0	TGCAGCTTCTTTGGGGATCA
Atr_361 94-59	T	C	CTTTCTGTTCTCAG A	CTTTCCGTTCTCAG A	CCATCTGCAGTGTGGAATCC T	0.9,0	GCCGCTTCTTCTCCTCTGAG
Atr_362 7-31	A	T	GTCTATTAGTGTTT	GTCTATTTGTGTTT	GTTCAAACCCACACAAGTGT TAT	0,0	ACTGCAATGAGACACAGATG T
Atr_363 31-53	C	T	TGTGGCTCGAGGG C	TGTGGCTTGAGGG C	CGGAAGGCCTCAGATTGTGG	1.6,0	AGTCCGCTGCCTTGAACCTAC
Atr_364 85-28	C	T	CCTCATCCTAGCCC	CCTCATCTTAGCCC	GGTGCTAGCAGCCCTCATC	0,0	CACAGACCCAATCATGCCCT
Atr_367 40-33	G	A	TAGAAGTGTAGAT GA	TAGAAATGTAGAT GA	TGCAGGCTAATATAAAGTAG AAAGC	0,0	ACAAGTTCCTGGTTAAAAAC AGCT
Atr_369 60-37	A	G	CCATGCCAGTCCGT	CCATGCCGGTCCG T	CTTGACGCCAGCTGCAGAA	0,0	TGAGGGTGAGGAGCCATACT
Atr_370 68-70	C	T	TTTGTCTTTTCG	TTTGTTTTTTCG	ATAAAGCATGAACACCACAT GG	0,0	GGCTGTTTTTGTCTCAGTGTG T
Atr_377 39-28	T	C	ATAGCTGGTACAG GT	ATAGCCGGTACAG GT	GCAGGATCATGCATGCGC	0.3,0	TGAACCCAGACAAGAAGGA CA

Atr_378 98-35	C	A	GCTGGCTTGGTCGT G	GCTGGATTGGTCG TG	CAGGCTGGCCTTTGTCCATA	0,0	TTAAGGTTTCAGTGGGCGTCC
Atr_382 78-50	C	A	GTGCATGCAAAC A	GTGCATGAAAAC A	TCCTCCAAACCACAGTGTGC	0,0	TACAGTGCATGCCTTCCTGG
Atr_385 91-73	A	T	CCGTCATT	CCGTCTTT	GCTGAAGTATAAACAAACATC ACCGT	0,0	AATTGGGAGAACTTTACAGT CCT
Atr_390 18-58	C	A	AAAAGACCATTTTC A	AAAAGACAATTTTC A	GGTTCAGACCCACTGTGTAT CA	0,0	AGCCAGCCTAAGGTTTTGAA
Atr_390 23-56	C	T	AGTGACACGGAGA G	AGTGACATGGAGA G	GGTCCACCTGTCAATAATGG C	0,0	TCGAGAGAGAGAGCCCTCAC
Atr_390 3-41	G	A	AGCTGGTGAATCG GA	AGCTGATGAATCG GA	TGCAGGTTGAGTTCAGATTG T	0,0	GATAGGGCTGTCTGCATCCG
Atr_390 71-73	G	A	CTTCACAGAC	CTTCACAAAA	ATAGCCCAGGTGGATGCATG	0,0	TGGATAAGCGGTTCTGCAGA
Atr_390 81-73	C	T	TTTAGATCAG	TTTAGATTAG	TGGATGGAGGTTTAATAGGA CCA	0,0	GGGCCCTTCCAGTTGAGATT
Atr_391 25-48	T	C	ATAGTGTTGAAAC T	ATAGTGTCGAAAC T	GCAACATCGTGAAAACGCC A	0,0	TGATTCAAAAGGAATGCTTG GCA
Atr_401 10-57	G	A	TAGGGCCGCATGC A	TAGGGCCACATGC A	GCACTGTGCCACTGACATAT	0,0	CAATCGCTATTGATTGCTGC A
Atr_401 69-65	C	T	AGACCCAGTTGTG GC	AGACCTAGTTGTG GC	GGGTGGTTCCTACATGACGT	0,0	TGCCCTGTAACCTACCCCTGT
Atr_403 16-51	A	T	ATTAAAGAAAAAT A	ATTAAAGTAAAAT A	TGCAGGTTTGTCTGTGAA TGG	0,0	CTCTGTCACAAGGCCACAGA
Atr_403 43-66	G	A	CTGCTTCGTTAGGG	CTGCTTCATTAGGG	CAGCAACGCTTACAGCACAG	0,0	AACAAGCATCGTCTCTCCCT
Atr_407 74-37	A	G	ACTCAACTCTGACC C	ACTCAGCTCTGAC CC	TGCAGGCAAACAGTCTTTAG AC	0,0	CCTGGACTGGATTGGATCTC G
Atr_409 54-66	G	T	ATTGGGGGTAAAA T	ATTGGGGTTAAAA T	TTGGACATTGCAAATTGGGG	0,0	TGCATGACTATGGGCGTGTT
Atr_409 74-63	G	A	GAGATGTGATCTG T	GAGATGTAATCTG T	GGACCACAGAGTGAGATCC G	0,0	GCAAAGCATGCGAAACAGAT
Atr_418 28-27	A	C	TAAAGGGAAACAG T	TAAAGGGCAACAG T	GCAGGAGTCCTACAAAGTTA AAGG	1.5,0	TGTTTTTACATGTCTTTACGG TCA

Atr_419 48-31	A	G	GAATTGAAGAAGT A	GAATTGAGGAAGT A	TGCAGGGAGGGACATCTCTT	0,0	TCATGTTTCGAGTCAAGGAGC T
Atr_419 86-71	G	T	AGTGGCAGAATG	AGTGGCATAATG	ATTGTATGGCGCTTCCTGCT	0,0	AGAAGGGTTGAGCATGTCCC
Atr_420 39-63	T	C	AGGCCAGTGGCGA G	AGGCCAGCGGCGA G	ACCAATCCAATCAGCCTCGG	0,0	TCTGTCCGTGCTGGTTTGAG
Atr_424 05-55	C	A	CCCCAGTCCCTTAA	CCCCAGTACCTTA A	CAACACTGACAGACCCCCAG	0,0	TGCAGCACAGCGTGATCTAT
Atr_427 41-51	T	A	CGTCATTTTGAAAT T	CGTCAATTTGAAA TT	TGTGCAGACTAAAAGCATGC G	0,0	ACTCAGGAGTCTAACTGAAG CC
Atr_431 07-50	G	A	ATCTGCTGTAGCAC	ATCTGCTATAGCA C	GGTGTCTGCCTGAGCTCAAT	0,0	GAGGCAAAACTGGCAATGAC T
Atr_434 02-63	A	T	AGATCACTCAACA AA	AGATCTCTCAACA AA	GCAGGTTTGACTTGCTTGGG	0,0	GTCAGGCCCAATGTCCACTT
Atr_434 14-51	C	T	TATGAGCCGAGTC T	TATGAGCTGAGTC T	AGTCTTCCCGAGGGACAGTT	0,0	CCCTTTCGTAAATGAGGCCC T
Atr_435 31-74	G	A	GTGCGCCGC	GTGCGCCAC	AACTGTTTCAGTGAAGTGCGC	0,6,0	CCAACCTGAGCCCCAACATA
Atr_435 71-39	C	A	TACATCTATCTGGT T	TACATATATCTGGT T	TGCAGGGATATAGTATGTCA CTTT	0,0	TGCACCCCCTATTCTGAAGT G
Atr_438 09-42	A	T	AAAATA[AT]AAAA AATA	AAAATT[AT]AAAA AATA	GCAGGGCGTATCGACAGATT	0,0	GCCAACCTGCTCACCCTTA
Atr_444 73-38	T	C	ACATTGATATCTCA	ACATTGACATCTC A	GCAGGTGGTGGAGCTCATAG	0,2	CTCCTTCTGCAGCATCACCA
Atr_445 13-72	T	C	GTGGCTCTAGA	GTGGCTCCAGA	CAAACGATATGAAAGCTGTG GC	0,0	GGTCCATTTCTAGTCAGCTC GT
Atr_448 73-44	C	T	GCTGACATCTGTCA T	GCTGATATCTGTCA T	ATGGTCTTTTTCCCCCTGGG	0,0	AGCTCAGCCAATCAGCACAA
Atr_450 74-45	T	G	GTGCATTTTCAGCA G	GTGCATTGCAGCA G	GGAGAAACACACACCAAGC G	0,0	AGTCTGCTTCTACTCCCAGT
Atr_454 94-35	G	T	CATTTTCAGTCGAG G	CATTTTCATTGAGG	GCAGGACATACACGGTGGA A	0,0	TCCAGAGCTACACACCTCGA
Atr_457- 66	G	A	TCAACTGGGACCA T	TCAACTGAGACCA T	GAAGGGCTGAAGTGATGGC T	0,0	ACCCTCATGTACAAATGTA AAAGA

Atr_458 90-59	G	T	GTGAGGAGACCTG T	GTGAGGATACCTG T	TAAGGGCTGCAGTGGTGAA G	1,6,0	CCACGGTACCTGTGCTGATT
Atr_460 06-31	C	A	TGCTGCATGCTTCA C	TGCTGAATGCTTCA C	TGCAGGATATAATAGTAAAG GGGTC	0,0	CCCCCTTCATGTGAAAAAGT GT
Atr_460 88-36	T	C	TCATCTGTAATATG	TCATCTGCAATATG	GGCAGTCATGATATAAAGCG GG	0,0	TCTAGTGACCTCTGGTGGCT
Atr_461 34-46	T	C	TCCCTGCTGATTTT	TCCCTGCCGATTTT	TGCTTGACCTAGCCAGTAGT G	0,3,0	TGGGGGCTAGGGAGACAAA A
Atr_462 29-66	G	A	TTGCTCCGTACAAA	TTGCTCCATACAA A	AGTGACAGGGAATTGTATGC CT	0,0	ATGTCACACTTCCCAGGGAC
Atr_462 47-56	C	T	TAAACCGGGGCTC TG	TAAACTGGGGCTC TG	GTCAGGGACTCGTGGACTTC	0,0	AAGGGAGCTGGAGGAAGAG T
Atr_464 3-39	A	G	TATGTATACCTGAG	TATGTATGCCTGA G	GGCAAGAGAGAGCATCAGC A	0,0	TCATTCAAGCCCACCACCTC
Atr_466 1-28	C	T	GTTAGTCCGGGGC A	GTTAGTCTGGGGC A	GCAGGTAGATCTCCAGCTGG	0,0	CTTTGCCAGTGCGGTTGAAA
Atr_466 37-57	C	G	AGCGTCACAGGCT A	AGCGTCAGAGGCT A	CATAAGCGCTGGGATAGGG G	0,0	TGCAGGAGCTGACCTTTGAG
Atr_466 90-29	A	C	CTGCCAAAGGATC T	CTGCCAACGGATC T	GGCTCTCAGAGTAATTACTG CCA	0,0	TTCCCTCACTCCAAAGAGCA
Atr_467 20-39	G	A	GTAGAGCTGTATT AT	GTAGAACTGTATT AT	TGTTTTACAGCTTGCTCCTA GT	0,0	ACATTGCTGCATGGCATATG A
Atr_467 4-42	C	A	TTCCTCCTCCTTAT C	TTCCTACTCCTTAT C	GGTGTCTGCTTTGAGCTTGG	0,0	CTTCCAGAAGGAGCACTGCA
Atr_467 7-47	C	G	TCCCGGACCGGGC C	TCCCGGAGCGGGC C	CCTGACACTGGCACTCAACA	0,0	CACCAGGCTGGAGAGGTTTG
Atr_469 83-45	T	A	GTTCGTTTCTACAG	GTTCGTTACTACAG	CCTGGTAGCATGTGGGTGTT	0,0	TGCCTCATTGTAATCATATCA GGAC
Atr_471 63-58	C	T	TGCAGCGGCACAT GG	TGCAGTGGCACAT GG	ATCCATCTGTCCCTCCAGCT	0,0	GCACTTCACCATCCGGAAG
Atr_471 95-73	T	C	AAGCCGTAA	AAGCCGTCAA	GAAACGCTCAGGAGTGGA C	0,0	CAGTGGGCGTGTTACGTAAG
Atr_473 52-72	A	G	GCCGAGCACTC	GCCGAGCGCTC	CTCATGCCGCTCTCCTTCAC	0,0	TTGTGTTCTGGTCCCAGCG

Atr_474 84-45	T	C	GTAGGGGTTGCTCT	GTAGGGGCTGCTC T	GCAGGGGTCTGTAGAGCTC	0,0	AATCAGCAGTCACCTCACCG
Atr_475 29-73	C	A	TAAGCAACTT	TAAGCAAATT	GCTGCCATTAATGATCTTGT CCT	0,0	CGCAGGACCAAGAAGATGTT
Atr_479 79-72	T	A	GCCTTTATATC	GCCTTTAAATC	AGGCAGAACTAAATACAGC ACTG	0,0	AGGGAACGAAGGGAACATTT
Atr_487 54-60	G	A	CTGCAACGACGTG T	CTGCAACAACGTG T	GCTTTCTCCTTTCAGTGGCC	0,0	TCCACGACACACATACACGT
Atr_493 88-52	G	A	CATGTGTGTCTGTC	CATGTGTATCTGTC	GGGACCCATGTATAAGATGG CC	0,0	AGTTTGGTGAAGATTGGCAG T
Atr_495 32-44	T	G	AAACTTTAT[CA]GT CTG	AAACTGTAT[CA]G TCTG	GCAGGAACTTTGCAACTACT GT	0,0	AGCATTACTGTGTAGGCTTT ACAGA
Atr_496 29-71	G	A	CATGCCTGGGGA	CATGCCTAGGGA	CCAGCAGAGCCATGGGAAT C	0,0	CGGAGGCAGGTCTGAACAG
Atr_497 90-61	C	A	TGCACTACTCTTCT	TGCACTAATCTTCT	GCTACAGTACCACCTGCACT	0,0	CCCCTCCAGAAATCAGGAGT C
Atr_501 79-30	T	C	GCCAATGGGTTGA AG	GCCAACGGGTTGA AG	TGCAGGCCTCTTAGCTGTTG	0,4,0	AGCATCTTGCCACATCCACA
Atr_501 9-45	C	T	TCCTGCAGC[TA]TT CCT	TCCTGTAGC[TA]TT CCT	GCACCGCTGAATGCTACATC	0,0,3	TTTCGTGCAGGCTGAGACAT
Atr_502 12-69	C	A	AGAGACTATGGC	AGAGAATATGGC	TCACTACAGAATGTGTTTCAG CTCA	0,0	TGCAATTATGATGTTCTCAG CCA
Atr_506 42-59	C	G	CCCTACTTAATGAC A	CCCTAGTTAATGA CA	CAGGATCGTGGTGCTCCAG	0,0	GCAGTAGGCCATCACTGTCA
Atr_511 76-35	G	T	AAAAGTTGCACAA C	AAAAGTTTCACAA C	TGCAGGTGAGATGAGGTTAC TG	0,0	ACTCCAGCACATAAGAGCAG T
Atr_514 58-37	T	A	CTCGCACTGTTGGC	CTCGCACAGTTGG C	TCAATCTGATGCTGGGCCTC	0,0	GACTGAGGAGCCGCCAAAT
Atr_518 32-58	A	C	CAGTCAATGC[TC] GATT	CAGTCCATGC[TC] GATT	GCTGTAGGGTCCACGGTAGA	0,0	TGGGGATTCCAGAGTGAGTA
Atr_519 99-44	A	G	AATATAATGGGTA AG	AATATGATGGGTA AG	TAGGGTCCCAGGGCAGTTTA	0,0	GGTGTGCAACCCAATGAATA CA
Atr_520 21-40	C	T	AGATGCACTGCAT TA	AGATGTACTGCAT TA	TGCAGGTGTACATTCACTG T	0,0	ACTGACCACAACCTCAAACCTG T

Atr_521 64-31	A	T	TTTTTTTAAAGAGC	TTTTTTTAAAGAGC	TGCAGGGATAAGCCAAAGC	0,0	AGCTTGGTGGAATCCAGGTG
Atr_525- 66	G	C	AACAAGAAGCAAA GA	AACAACAAGCAAA GA	TCCAGCATGACCATCTCTGC	0,0	GGGTCAGTGTGTCTCTTTGCT
Atr_526 50-66	A	G	AGACAGTATGTTT G	AGACAGTGTGTTT G	CCCTTGCTGTGGCTCTTCAA	0,0	AGCCCCCTATAGTCTCCACCA
Atr_526 66-51	A	G	AAAGGGTAGTTAT T	AAAGGGTGGTTAT T	GCAGGCCTTCTGTATGTAAA CC	0,0	TGCTTTCTTAGAATTTAAGGC TGCA
Atr_526 75-47	C	T	TGAACCGCGACCT C	TGAACCGTGACCT C	CAGTTTGTGAGCCGGTGTTG	0,0	CTCCACCAAGAGAGTGCCTG
Atr_527 15-59	C	T	AGTATACCCCTTGT	AGTATACTCCTTGT	ACTGTAGTGTGGTTATGTGG TT	0,0	TGAAGATTGTATGTTGTTGG CACA
Atr_528 68-38	C	T	TTGCAAACGGAGC A	TTGCAAATGGAGC A	CAGGGTCCCAGCTGAAGAG	0,0	CGCAAGAAGCTGATGTGCTC
Atr_531 57-67	G	C	GACAAGAGAGACA G	GACAAGACAGACA G	CCAGCCTAGCCATGGACAAG	0,0	TCACATCCAACTCTTGCCAG T
Atr_532 10-55	C	T	AGAAGCCAATAGG TG	AGAAGTCAATAGG TG	TCTTGCATCATGCCTACCAG T	0,0	ACGCTTCATGGCATTTTGTGT
Atr_533 6-58	A	T	AAACCACAGCATT C	AAACCACTGCATT C	CTCACCTCACAGGCTACACC	0,0	CTTTCAGTGCAGTCAGAATG C
Atr_535 21-30	C	T	ATCCCTTCCTACCG	ATCCCTTTCTACCG	TGCAGGTCATCATCTGAACA AGA	0,0	ACCAATCCTTCCTGACAGTTT GT
Atr_536 86-72	A	C	AATACAAAT	AATACCAAT	CCCGTGTTTGTAAAGCAGGA	0,0	CTGGGGACTACTTGAGCTGC
Atr_539 04-44	A	G	AGTCAATTAGTCA AG	AGTCAGTTAGTCA AG	TGCAGGAGACCGTGAAATGT	0,2,0	GGTATCCTCCCTGGCTTGAC
Atr_540 38-48	A	G	CCGGGGAAAGGAT G	CTGGGGAGAGGAT G	CACAGGTATGCCACAGGAC A	0,0	AGGAAGCTAAACACAATCTA CCA
Atr_540 41-38	C	T	TTTGAATCTTAAGA	TTTGAATTTTAAGA	ACTGTCTTGGGTGGCAAAC	0,0	ACCTAACTCGGAAATGTGAT TTGT
Atr_541 60-70	T	C	TCATTTTGGGTC	TCATTTTCGGGTC	TTTGCGGTTTCAGATGTGGGT	0,0	AGAGCACACAAAACATTTTC GGT
Atr_542 66-27	G	A	GTTACTTGTATTGG	GTTACTTATATTGG	TGCAGGCTTCACTACATAGG T	1,1,0	ACATCCACCCTCAACAAGCT

Atr_547 64-45	G	A	AGCACTCGCTCCC A	AGCACTCACTCCC A	TGGGGAGCCAAGTAATGAG C	0,0	AACCAGAGAGGCCCGAGTAT
Atr_547 95-72	G	A	CATTTGTAT	CATTTATAT	TGCACTGATGATGAAGGTGT	0,0	GCAATTTTAAAGGTGTGGAG ACA
Atr_555 83-67	G	A	TTACCGGGATTGA C	TTACCAGGATTGA C	ACGAGGCATTGATTAAGTCC AGT	0,0	AACGCTACTGACTTGAGGCC
Atr_558 92-54	G	A	ATCTCGTAGACCTC A	ATCTCATAGACCTC A	AGCCTGTCACTTCCAATGAG G	0,0	TGAACACCCCTCTGAGGTCT
Atr_560 24-45	C	A	CAAGTAGCGATCA G	CAAGTAGAGATCA G	AGGTCAGCCCGTCCCTATAA	0,0	TGGTCTTCTTCTCAAGATGTG CT
Atr_560 33-37	C	T	GCTACAGCTTTATT	GCTACAGTTTATT	TCTAGTCCCTCCCGCTACAG	0,0	ATGGCCCGATAGTTTTGGCA
Atr_561 0-27	A	G	GTGACACAAGATT A	GTGACACGAGATT A	TGCAGGTACAAGCAGAGCA G	0,0	GCCACTTGCAACTGGGAAAA
Atr_561 09-40	C	T	CAGAACTCGCCCT G	CAGAACTTGCCCT G	CGCATGCGTCCGATAGCC	0,0	ATAGAGAACTGCAGCAGGGC
Atr_568 54-26	A	C	GGAAAGTAGGGGT A	GGAAAGTCGGGGT A	GACGTGCACGGGTGGAAA	0,0	CACAGCCTCAGTGCTTCAGA
Atr_570 18-28	C	T	GCGTTGTCCTCCGA	GCGTTGTTCTCCGA	CTTGCCTGTAAGCTGCGTTG	0,0	TTTACACACTGCAGGCCCTT
Atr_575 42-29	A	T	CCAGAAAATGGCT C	CCAGAAATTGGCT C	CTGGCCTTTGTCCTCCAGAA	0,0	CAGTGTGTGTCCTCCGATCC
Atr_577 56-67	C	T	CAATCAACGAGCA G	CAATCAATGAGCA G	TGCAGGTAAGGGCAGATGA C	0,0	TTTTCCATGGGTCTGCTGCT
Atr_577 9-55	T	G	TTTTTCTTTTCCCT	TTTTTCTGTTCCCT	TGCAGGTATTGAAGACATTC TCTGA	0,0	GACGTGAATGGAGGGGTCAG
Atr_578 32-69	C	A	GAACACGCTGACA C	GAACACGATGACA C	ACCAGTTCCAGAGATATGGG TG	0,0	GGGCCGCTTTATCACAAGGA
Atr_578 70-70	A	C	ACTACCTAACCAG	ACTACCTCACCAG	TTACCTTACATATGTGTCAC TACCT	0,0	CTCACGTGAGAGTTGCTCTG T
Atr_583 05-70	G	A	CCACTGTGGTG	CCACTATGGTG	TGTCTACAGTTGTTACATGT CCA	0,0	GCCATGTCCAGCTTTTACAC C
Atr_583 42-71	T	C	TCCTTCTTTCTG	TCCTTCTCTCTG	GGGTGTGTTGTCTCTCCTTCT	0,0,3	GACTGAGGAAATAGCAAAG CGT

Atr_584 34-42	G	A	CCAGTCCGTTTTCC	CCAGTCCATTTTCC	GCAGAACCACGCCAGTCC	0,1.5	GAGGGCGAGGAACCAGC
Atr_585 62-59	G	T	TATAATTGACCTCT	TATAATTTACCTCT	GACAGGATCCACCACACACT	0,0	AAAGAGGACCGGTCAAGAG G
Atr_587 20-60	A	G	TTCCTATAGTTTAG	TTCCTATGGTTTAG	CCAGTCAAGTGCAAGGGTG A	0,0	TGAACTTGAACTCATTTTG ACCA
Atr_588 31-60	G	A	GTAAAATGTACGG C	GTAAAATATACGG C	TGCGTGTTTATCTTGAGAAA CCG	0,0	TCTTTTTATGAGCACTGCCGT
Atr_589 0-29	T	C	CTTCGTATGAGATG	CTTCGTACGAGAT G	CAGGTGTAAACCCCCGAGTC	0,0	TCGTTCCGAGCAACAGGAC
Atr_589 2-46	A	C	TCATTCCAGAATCC	TCATTCCCAGATCC	CAATAGCATGGCCGCACTTC	0,0	TGGACACAGCACAAAGAAG AGT
Atr_592 01-47	G	A	CAGCAGGGTCCAC T	CAGCAGGATCCAC C	GCTTGATTTCACTGGGTGCC	0,0	ACCAGGCACTCACAATGACA
Atr_592 84-42	G	T	CAGAGATGAATTT T	CAGAGATTAATTTT	AACCTCGTCACCCTCTCTCA	0,0	GCTCAAGCAGAGGTTTGTGG
Atr_593 10-44	A	C	CTCAGCGAGCACT C	CTCAGCGCGCACT C	GCAGTTTGGTGAAGCTCAGC	0,0	GAAGCCTCAGGAAGCACCAG
Atr_594 87-73	C	T	ATAAACGT	ATAAATGT	ACTTGAGCAAAAGGAATGC AGA	0,0	TGAACCTCTACTCTTATTTTG CACA
Atr_598 00-43	C	G	ACAGTCCCTAACT AT	ACAGTGCCTAACT AT	CACTGTAGCAGGGTGACGA G	0,0	TCTGCGGTTTACAGAGGCAA
Atr_598 42-43	G	A	GGCGGTTGAACCA G	GGCGGTAAACCA G	CATCTCTCTTGTGAGGGCGG	0,1.2	TCCAGCTACATTGCCTGTGG
Atr_601 62-29	T	A	TTTTTTTTAATTTG	TTTTTTTAAATTTG	TGCAGGCAGGACTGTTTC	0,0	GAACAGTCCCACACGCTAGG
Atr_602 65-55	C	A	GGCTTCCCAGTGTC	GGCTTCCAAGTGT C	AGGGGTCGGATTAGCCACTA	0,0	AGGTGGACATTCTAGGTGAG GA
Atr_603 68-72	A	T	AGGAACCAGCA	AGGAACCTGCA	CGATGGCCTCCAAGGAACC	0,0	CCCTATCATTCCTGTCACTCG T
Atr_606 88-70	C	T	GAACCAGCGGTTG	GAACCAGTGGTTG	CCTCCAATGACCTACTGAAC CA	0,0	GGTGCTGGTGGCTAACTGAT
Atr_608 59-44	T	C	AATTCAATTGACCC	AATTCAACTGACC C	AGGGGTCAGAATCTGCATGC	0,0	AAGTGTCCATCGCTTGTGGG

Atr_610 62-75	C	A	ATCTGGGC	ATCTGGGA	TGCCCTGAAAGAGGTCAGTT	0,0	TGACTGTATGAAAGAAGGCA GT
Atr_611 71-66	C	T	GATGTGACTGCAC G	GATGTGATTGCAC G	CCGACGCTGTAAGTTCTGGA	0,0	TGTCCTCCGAAACGACTGC
Atr_619 11-75	C	G	ATTGCC	ATTGCG	AGTGGCAGCTCCTTCACTTC	0,0	GCGCCGGTACACTTTCAGTA
Atr_623 30-56	A	C	AGGGTGAAGTCCC A	AGGGTGACGTCCC A	GGGCCAGGAAGGAAAAGCA T	0,0	ACTACCAGGAGCTTTTGGGA C
Atr_624 19-71	G	A	CTGCAACGACAC	CTGCAACAACAC	CCTGCAGAGAGACACAGAC G	0,0	GGCCAGACAAAGGAAGGAC A
Atr_624 63-34	C	T	TGCAGAGCGTTCA C	TGCAGAGTGTTCAC C	GCAGGGATAGAAATAAGAC TCTGGT	0,0	GCTTGTTACGTATACACTGG CA
Atr_625 1-29	G	T	TCAGGGGGAGATG CA	TCAGGTGGAGATG CA	TGCAGGGACACAAGAGCTTC	0,0	GCTTTCTTGACTTGCCTGCC
Atr_629 52-34	T	C	TTCTCCTTGTGGTG	TTCTCCTCGTGGTG	GGATTGGAAGCAACGTTTCT CC	0,0	AGGACCAGGAATGAAATGG CA
Atr_630 42-40	T	C	ACTCATTGACCTCT G	ACTCACTGACCTCT G	GTCTTTGCCCTCCATGAGCT	0,1,8	TCCAGGTACTCCACAGCAGA
Atr_630 76-27	T	A	ACAAATTTTCATTCA	ACAAATTACATTCA A	GCAGGCAACAACAACCTCA C	0,1,2	ACAGTATCATAGTGGAGGTG AATG
Atr_631 01-44	A	G	ACCAGGCAAATTT C	ACCAGGCGAATTT C	CCATTGTTACAGGGTTTGGG G	0,0	TGTCTGGACATAACCTGGAA ACT
Atr_632 46-38	A	G	GTGTATTATGTATC	GTGTATTGTGTATC	CAGTCAGCTGCATTGTGTGT	0,0	AACTCACTATGCTGCCTGGG
Atr_638 85-66	C	T	GCTGCCGTCGGTC AG	GCTGCTGTTCGGTC AG	TGTTACCCAAGCTGTGTTCA G	0,0	TGCTAATTTTCTTTCTTCTGA CCGA
Atr_640 06-52	C	T	GGTTTACCCTGAA G	GGTTTACTCTGAA G	CTGGATGGGGAGCGGTTTAC	0,0	CAGCTCCCACCCACTGTAAG
Atr_642 17-68	A	G	CCTTAAATTCGAG	CCTTAGATTTCGAG	TGTTAACAAGGGAAACGCC G	0,0	TTTTTAGTTACCCTCACCCAG G
Atr_645 6-50	G	A	GTTTCACTGCAG GT	GTTCAAACCTGCAG GT	GCATTGCTGCCAGGTTAACA	0,0	GGAAAACACAACCCTGTCGC
Atr_647 06-45	T	A	CACTGACTGCTGTA	CACTGACAGCTGT A	TGCAGGGATGGTCCTTGTTG	1,9,0	ATGACCAAGCCAACCTGCCTT

Atr_650 94-30	A	G	AGAGCAGACGCCA GT	AGAGCGGACGCCA GT	GCAGGGCTGTCTTCGAGAG	0,0	GACCAAGCTGCCTCTTTCCA
Atr_653 59-46	T	C	CATCTTCAATCAG[CT]T	CATCTCCAATCAG[CT]T	GTAGTTCCCCTGCCTTGCAT	0,0	ATCGCTCTGTGTTTGGACCC
Atr_653 77-56	G	A	TAACAGGATAATA GG	TAACAAGATAATA GG	CTGGTGATCCCTGCTGTAGG	0,0	CTGCAGAACCCAGAGACCTG
Atr_657 29-42	T	G	GTTACCATCTCTAC	GTTACCAGCTCTAC	TTAATTCACAATGTAGCAGT TACCA	0,0	GCGCACCCTCTATTTCAAA CT
Atr_658 43-52	G	T	GCGTCAGGTGGGA A	GCGTCAGTTGGGA A	AATGTGAGTAAGGGGGCGT C	0,0	CACTTTCAAAGCAAATGTTG GTCA
Atr_661 2-39	A	C	TGCCCATATACATG G	TGCCCCTATACATG G	TGCAGGGATGCCTATTGTAC A	0,0	GGGATCCCAGGTCATTTCCA
Atr_665 63-34	A	G	AACCTCTATACAGT	AACCTCTGTACAG T	TGCAGGTTAAATGTCCACAT CA	0,0	GGCTCCCAACCACATCGTTA
Atr_666 64-59	C	T	CTCAGAGCTCCCTG	CTCAGAGTTCCCTG	AGGTACCCCTTGCCAAATGG	0,0	TGCAAAGTAGAAGGCAGGG A
Atr_668 06-52	T	C	TTACCTGTTTGAGA	TTACCTGCTTGAGA	AGCCCTGCTTTAACAGTGGT	0,0	TAACCCTCCATCCCCTCAGG
Atr_675 34-27	C	T	CATAACTACAAAT AT	CATAATTACAAAT AT	GCAGGCAAGTGCAACATCA A	0,0	GCTGTGGCAGAGTGTAGGAG
Atr_677 59-28	G	A	GGCACGGCACAAA AC	GGCACAGCACAAA AC	AGGGGAAGAGCCAGTGAGA G	0,0	AATTGCTGTGCTTGCCATGG
Atr_681 86-72	C	T	ACAGTCCCTGC	ACAGTCCTTGC	TACCAGTCGCCTGACCAGTA	0,0	TCTGCCTCTCCCACAGGTTA
Atr_686 80-72	T	C	CATGATCAG	CATGACCAG	TTACCAAGGAAACCAGGGG C	0,0.7	ACATGCTAAAGTGGCTGCTG
Atr_687 62-59	A	T	CTCAGATAGTGAG A	CTCAGATTGTGAG A	GGGTGCAGCAAGGATGGTA T	0,0	CCTGCACCAAGGTAAGCTCT
Atr_688 08-31	A	T	GTATTAAAGCTGG C	GTATTAATGCTGG C	GGTAATGCCTCCCCACTTGT	0,0	GGAGGAGTTTATTGAAAGCA GGC
Atr_690 47-33	A	G	TAATTATATGAAA G	TAATTATGTGAAA G	GCAGGCTGCTACTGTAGTCT	2,0	GTGAAAACAGTCCTTTCCCC T
Atr_692 17-58	A	G	TCAAAGCACCCGA G	TCAAAGCGCCCGA G	AAGCCCCCTTTCTGCTTCTC	0,0	ACTGCTTCGTCAGTAGAAAA GT

Atr_698 8-51	T	C	TTAACTTTAGATCA	TTAACTTCAGATCA	TGGTTCTGGCAGGAACTCAC	0,0	TGCTTGATGTTTACCTGATTT GAT
Atr_700 1-57	T	C	CACATTATTTCTGT	CACATTACTTCTGT	CCAGAGTGATGTGCATAAAG CC	0,0	TGCTGTGTCTTCTGGTTCTGT
Atr_701 39-39	G	A	ATTACGATCCCCC A	ATTACAATCCCCC A	GGAGTCCTACAAAGTTAAAG GGC	0,0	CACGTTTAATGAACTGTGGG GG
Atr_701 67-40	C	T	CAGACCTCGTCCTG	CAGACCTTGTCTG	GCATGCATCAGATAGCCAGC	0,0	ACTATATTGCACTGTAGCAG GAC
Atr_702 6-63	C	A	AATTCACCAAGTTT	AATTCACAAAGTT T	GGGGTGCCCAAATATATTGC A	0,0	AGAGTTGCTGCTTGTTTAAA CTT
Atr_704 59-55	C	T	TCTGTTTCACATTG	TCTGTTTTACATTG	GGAAGATTCCGATGACAGA ACT	0,0	GCAGAGAAAAGAGCCGCAA T
Atr_704 67-53	A	G	TAAGCACTTCAGA AT	TAAGCGCTTCAGA AT	TGACACACCTGAAAAACACC AC	0,0	TTAGCTGTGGGATCATGCCA
Atr_704 79-48	T	A	CATAGATTGCTTCA	CATAGATAGCTTC A	GTCTGGGAAATGTCTGGGCA	1,8,0	CAGCCTAGGTCTCTGTTTGC A
Atr_706 09-65	A	T	TCTGGACAGATTA A	TCTGGACTGATTA A	GCAATGGCTAAACATCTGGA ACA	0,0	TCATTTCCACCGAGTTCTCTC T
Atr_707 2-61	C	T	AAGGACGTTGCTC GC	AAGGATGTTGCTC GC	ACGCACCTCAAACCAGTTGA	0,0	GCTGGGGCTGGATAAAATGG
Atr_708 80-74	T	C	CCCTCACTT	CCCTCACCT	GCTTTTCTTTGGCCCAAGGG	0,0	GCATGCAGCGGGAACATTTT
Atr_711 95-60	A	T	CAGAAAGATGGGG TG	CAGAATGATGGGG TG	TGATGTTGAAGCCTCTACAC CA	0,0	ACGATACTTCATCCACCCCA
Atr_721 65-47	C	A	GGTCTCGGGGTTTC C	GGTCTAGGGGTTT CC	GGGTTGCCTACCTCTGGTCT	0,0,3	GTGGCTGATCACATCCCCTT
Atr_722 51-33	A	C	TTAGGAGATGCTG A	TTAGGAGCTGCTG A	AGAAGCTGGGAGTGGTTAG GA	0,0	TGGGGTTTTAAAGCTATACA CCA
Atr_725 58-41	C	T	TCCATGTCGTCTAA	TCCATGTTGTCTAA	GCAGGGCTAGTGACTCTTCA	0,0	TCTGTCTTATCTGTAGTGTGA TCAC
Atr_726 93-61	A	G	TTAAGGCATACAT A	TTAAGGCGTACAT A	CGGTGTGCTGCTATTTAAGG C	0,0	TCCTGAAGACATTGACTAGA GGA
Atr_729 8-56	C	T	GTCCCGACCAGGC G	GTCCCGATCAGGC G	CGGTCAGTATGGCTCCTGTC	0,0	GCAGTGCCCCCTGATGTATT

Atr_734 38-69	T	C	TGAAATAAACAA	TGAAACAAACAA	AGCTGCACCCCTTTTAACT	0,0	CCCTGCATGAAGTCCAAGGT
Atr_735 05-52	A	T	CATTCAAAACACA C	CATTCAATACACA C	GCAGGAAAAACAAGCCAGG G	0,0	AGAACGAATGGTCATTGTGT GT
Atr_736 08-61	C	T	CGACCCGGGTCTA TT	CGACCTGGGTCTA TT	TGCATTTTGCTTCGCTCGAC	0,0,3	CTGCTTAACCCAGGTCCCAG
Atr_737 40-69	T	C	ACATTTCTGTGC	ACATTCCTGTGC	CCTTTCGTAGGCACACTAGA CA	0,0	AGTCATTCAACCTTTCATGG CAC
Atr_739 05-66	A	T	AAGTTTTTAAACT G	AAGTTTTTAAACTG	AGGTTTCCTCCTGTTTACAAG TT	0,0	GGTACAGGCTCGCTCGTAAT
Atr_739 87-49	G	A	GCATGGCCAGTTA TA	GCATGACCAGTTA TA	CTTACCCTCCACTGCTAGCT G	0,0	CCGGCAAACACCTACACCA
Atr_739 94-27	C	T	CAAGACTATGAAG AG	CAAGATTATGAAG AG	TGCAGGTCTATTTTCTAACA GCA	0,0	ACCAGTGGACATGCTTACGG
Atr_740 94-36	G	A	TGCCCCGTCATTATG C	TGCCCCATCATTATG C	GGATGTGCAAGCATGGAAC C	0,3,0	GCACATGCGATACTCCAGCA
Atr_743 22-45	A	G	GGTTTATACACATG	GGTTTATGCACAT G	CAGAGGGCAGGTCCAAGAA A	0,0	AGCCACCCTGAATCATCATG T
Atr_746 62-68	T	C	AAAAGTTTCCCCCT	AAAAGTTCCCCC T	AGGGGAGTGCTGTGTTTGTG	1,8,0	ATGGTGGCTCAGTCCCAAAG
Atr_747 30-29	G	A	AAGCCGCAGAAAG AC	AAGCCACAGAAAG AC	GCAGGTTTCAGAGGGAGTTTG A	0,0	TGCTGCTGTGTTTCAGAGAGG
Atr_747 47-45	C	T	CAATTTGCTATCAG	CAATTTGTTATCAG	TGCAGGCAAAACAAGACAG AC	0,0	GCCTGGAAGTACTGAACTGG A
Atr_748 44-59	T	A	CCTTTTGTTGTTAC A	CCTTTAGTTGTTAC A	GTGAACCACACTTGTCTTTC TGT	0,0	TGACTGTTTTGTTCCACGTTG T
Atr_749 87-50	T	C	TTTACTTCAAACATA C	TTTACCTCAAACATA C	GCAGGGCGAATTCTCAATAT GG	0,0	AGGTATGGTGTCTCTTGTAG TTGA
Atr_751 40-58	C	T	GAGTATGCTTTTCAT	GAGAATGTTTTTCAT	CACCAGAGTGCTTTAAGGTT TATAA	0,0	CTGTTGTTTCATGAGCCGTAT AAT
Atr_754 07-53	G	T	ACAGACAGGGTCT C	ACAGACATGGTCT C	GGAAAGGTACAGTACAGGG CA	0,0	AAGCCCTGAAGCAATCGGAA
Atr_756- 60	T	A	ATCTAACTACTGAC	ATCTAACAACCTGA C	TGCAGGCATTTCATAAACCAC G	0,0	AGAGGGCTTTGAGATGAAGG A

Atr_759 82-70	G	T	ATGAAGAAGAT	ATGAATAAGAT	CAGGAAGATCCGGCAAAAG A	0,0	TGCTGCCTCTTGCTCATCTT
Atr_762 53-44	G	A	CTGTCTCGCCTCTC	CTGTCTCACCTCTC	AGGTTCTTATTACATGCCTC TGTCT	0,0	GGGTCCTGGTGCTGTGATTA
Atr_764 09-55	G	A	CAGCCGCAGGAGA GC	CAGCCACAGGAGA GC	TCAGCGAGTGAGTGGACAA C	0,0,4	TGATCATAAATGTAACTGC TCTCC
Atr_764 18-65	A	T	CCGGCTTATCTGAA	CCGGCTTTTCTGAA	GGTAATGCGTGGGTGGTGTT	0,0	ACCAGCAATAACGTCTTCCT GT
Atr_765 71-26	C	A	CGATGTTACAGTGC	CGATGCTAACGTG C	GAGGGTCCGCTAGCGATG	0,0	GCACTGCTCTCTATCTGGGG
Atr_767 91-46	G	A	TATCCGCTGTAGCA C	TATCCACTGTAGC AC	GTCCCCTGAGCTCACCAAG	0,0	ATTGAGGCAAAACCAGCAGG
Atr_768 88-43	C	T	TGTCAAGCGATTG A	TGTCAAGTGATTG A	ACAACAGAATCAGGGCTGTC A	0,0	TGTGAATGAGACGGATGCAG T
Atr_768 90-36	G	A	TTCTCGATCTCGCT T	TTCTCAATCTCGCT T	CAGTCGCCGAATCCTGTTCT	0,0	GATACGTGCTAGGACCCTGC
Atr_769- 65	C	T	CCTCTCAAATAA AA	CCTCTTAAATAA AA	GTCCACACAGTACTTGGCCT	0,0	TCATGCTAAGGACCTTGATT ACGA
Atr_777 78-67	C	T	AGTAGATCACCAG A	AGTAGATTACCAG A	TTGCCTACCCCTGCTTTAGC	0,0	AAACTGTGCAAGTGGACACA
Atr_779 3-68	C	A	CGGTACTCAAATA A	CGGTACTAAAATA A	TAGGGAAAGGGAGTCAGCC A	0,0	ACTTCCATTCCACAGCTAAT GA
Atr_781 73-42	T	C	GGCATTGGAAC[CG]GTC	GGCATCGGAAC[CG]GTC	CTCAGGTCACCCAGCAGAG	0,3,0	GTTGAGCCGCTTGCAATCTC
Atr_781 7-58	G	A	ACAC[CT]GTTCATC AGC	ACAC[CT]ATTCATC AGC	GCCTCAGCTGAAAACACAA GA	0,0	CCGTGTGAGTTTGTCTGCTG
Atr_784 13-36	G	T	TACCCGAGTCTAA A	TACCCGATTCTAA A	TGCAGGTGTGTATTGCTGAC A	0,0	AGCAGATATGAGTAAAACAT TGCCT
Atr_785 71-74	A	C	AAGTGAGAC	AAGTGAGCC	GACTTGCAAGGTGTTTCGGAGT	0,0,5	AGTTCGGCTTGCTTGTTTTT
Atr_786 00-73	C	A	CCCAGCTCAG	CCCAGCTAAG	AATAAGGAGCAAGCCCAGC T	0,0	GTCGACTTTGGGGAGCAAGG
Atr_788 58-41	A	G	CATGAACCATTTTT T	CATGAGCCATTTTT T	AGCTGACAACGACATCATGA	0,0	TCCGCATGAGTCAAAATCAT ACT

Atr_792 8-34	C	A	GTCATAACTGCTCA	GTCATAAATGCTC A	GGGGTTGCAGTACCTTGAGG	0,0	TCAAAGGCATCAACAGGAGT
Atr_794 4-51	C	A	GGCAGCTCGCGGC C	GGCAGCTAGCGGC C	GTGACCAGTACGTGACCCAG	0,0	GTCTTCTTCTCGTCCTCGGC
Atr_831 4-34	T	A	GATATTGTATGTGG C	GATATAGTATGTG GC	TGCAGGATTCTTTACAGAA GA	0,0	TGAACAGCTCTGGATGCACG
Atr_972 3-56	C	T	ATGCGCAGTCTGT AG	ATGCGTAGTCTGT AG	TGATGGGCCATCTTTCACGG	0,0	GAGAAGCCTTGGAGTGGACC

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Appendix 8. Assays and SNP sites used for species diagnostic testing.

Assay	A1	A2	A1-Probe	A2-Probe
Oki_101419-103-27	A	C	AATCCACTTCC	AATCCCCTTCC
Oki_101419-103-44	T	C	GTTCTCCTACT	GTTCTCCCACT
Oki_105105-245-23	T	G	GCCTTTTCCAT	GCCTTGTCCAT
Oki_105105-245-56	G	A	CTCATGCCCAA	CTCATACCCAA
Oki_106172-60-38	C	T	GTGCGCATCAA	GTGCGTATCAA
Oki_106172-60-47	G	A	AACGCGCTGAC	AACGCACTGAC
Oki_106172-60-47c	A	C	AACGCACTGAC	AACGCCCTGAC
Oki_106172-60-53	C	T	CTGACCGCYGC	CTGACTGCGYGC
Oki_111681-407-38	C	T	AGAAACTGCAA	AGAAACTGTAA
Oki_120255mod-105	C	T	AACGTCAGTTA	AACGTTAGTTA
Oki_120255mod-113	G	A	AGTTACTGG	AGTTACTAG
Oki_120255mod-115	G	T	TTACTRGGGTA	TTACTRGTGTA
Oki_120255mod-119	G	A	GTAGYTTCWTG	GTAAYTTCWTG
Oki_120255mod-120	C	T	CTTCWTGGCAT	TTTCWTGGCAT
Oki_120255mod-133	T	C	TGGCATAGTC	TGGCATAGCC
Oki_120255mod-135	A	C	GGCATAGYCAT	GGCATAGYCCT
Oki_120255mod-137	A	T	ATAGYCMTAGAT	ATAGYCMTTGAT
Oki_120255mod-141	A	A	ATAGYCMTWGATA	ATAGYCMTWGATG
Oki_120255mod-99	A	C	GACTAAAACGT	GACTACAACGT
Oki_126619-265-31	A	C	GGATTGKGCAC	GGATTGKGCCC
Oki_126619-265-35	A	G	CAGCACAGCTG	CGGCACAGCTG
Oki_126619-265-50	G	T	GATTGCGCCAGT	GATTCTCCAGT
Oki_aspAT-273-37	C	T	CTGGACACAAT	CTGGATAACAAT
Oki_aspAT-273-45	T	A	AATCCTTAACA	AATCCATAACA
Oki_RAD41030-31-36	C	T	GAAGGYCRGGG	GAAGGYTRGGG
Oki_RAD41030-31-37	G	A	GGGGSTCTGTG	AGGGSTCTGTG
Oki_RAD41030-31-41	G	C	GGGGTCTGTGG	GGGCTCTGTGG
Oki_RAD51585-47-25	C	G	GTGGCTCACTT	GTGGCTCAGTT
Oki_RAD51585-47-28	G	A	TCACTTGGTAGAGC	TCACTTAGTAGAGC
Oki_RAD51585-47-31	A	C	TTKGTTAGAGCA	TTKGTCGAGCA

Omy_myclarp404-111	T	G	CAAAGCCATACGTGGCC	AAGCCATCCGTGGCC
Omy_RAD13034-67-21	C	T	CTCCCCGAACC	CTCCCTGAACC
Omy_RAD13034-67-35	A	T	CTGAGTGGACA	CTGTGTGGACA
Omy_RAD79314-58-25	C	T	CTCGCCCTGCG	CTCGCCCTGTG
Omy_RAD79314-58-27	T	C	GTCACRCCTGC	GCCACRCCTGC
Omy_RAD79314-58-31	G	A	ACGCCTGCCCT	ACACCTGCCCT
Omy_RAD79314-58-66	C	A	CAGTGTCAACC	CAGTGTCAAAC
One_1a.54542-52-44	C	T	GCCTTGTGCTT	GCCTTGTGTTT
One_1a.54542-52-47	G	C	TTGACCAGAAG	TTCACCAGAAG
One_2.70711-39-28	G	T	AGGYGCTYGTGC	ATGYGCTYGTGC
One_2.70711-39-30	T	C	GTGCTYGTGCG	GCGCTYGTGCG
One_2.70711-39-43	G	A	CGTCCGCGGGC	CGTCCACGGGC
One_2.70711-39-56	C	G	GGCTAAGGATC	GGCTAAGGATG
One_2.70711-39-57	G	A	GCTAAGGATSG	GCTAAGGATSA
One_2.70711-39-64	T	G	TTCCCTAGGGG	TTCCCGAGGGG
Ots_ARNT-29	A	G	GTGCTAGCTAC	GTGCTGGCTAC
Ots_ARNT-29c	A	C	GTGCTAGCTAC	GTGCTCGCTAC
Ots_crRAD9615-69-19	T	A	GGGAGTGGGAG	GGGAGAGGGAG
Ots_crRAD9615-69-50	A	T	CTGGGAGGAGA	CTGGGTGGAGA
Ots_myol1a-384-36	C	T	CACCACTACCA	CACCATTACCA
Ots_myol1a-384-57	C	T	CTGCAGAACAC	CTGCAGAATAC
Ots_P53-25	G	T	TTCTGCAGGGG	TTCTGCAGTGG
Ots_P53-28	G	C	GGGCAGCTCCT	GGCCAGCTCCT
Ots_P53-40	T	C	CTCCTGGGTCG	CTCCTGGGCCG
Ots_unk9480-51-38	T	C	TCCASAAACT	TCCASAAACC
Ots_unk9480-51-39	C	A	CTAAGGAGACC	ATAAGGAGACC

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

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 ‘adegetnet’ package in R (Jombart & Ahmed 2011) or in GenAlEx v6.5 (Peakall and Smouse 2006).

Expansion and status of reference baselines for GSI:

Our three primary goals for expanding, maintaining, and evaluating each species-specific baseline are threefold. First, we used genetic stock identification (GSI) analyses for monitoring of fishery returns through the migratory corridor of the Columbia River, including harvest GSI in the lower Columbia River, and fish passage GSI at Bonneville and Lower Granite dams (see sections 3 & 4 of this report). Second, PBT broodstock sampling and genotyping of Columbia River Basin hatcheries has been updated to include 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_T est/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	467	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	Alpowai 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	NF Salmon	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:

Comparison of GSI assignment methods with known parents:

The dataset included 48,835 total *O. tshawytscha* individuals that were exported from the PROGENY database and were genotyped within the current fiscal period (FY April 2021 – March 2022). There were 33,384 *O. tshawytscha* that passed 10% failure and duplicate genotype filters and were included in parentage analyses. There were 22,901 SNPPIT assignments (68.6% of the filtered dataset; LOD>14, FDR<0.1) and of these assignments there were 22,532 *O. tshawytscha* that were assigned to opposite sex parents (based on genetic sex markers). The final mixture dataset consisted of 8,466 *O. tshawytscha* that had known opposite parents and a part of full sibling families with 4 or more members (this requisite was helpful for future testing of sibship relationships). Known mixture samples were assigned to reporting groups with two differing GSI methods. The software used in previous years, ONCOR (Kalinowski et al. 2004), was compared to Rubias software (Anderson 2021) by the proportion of correct assignments of mixture individuals with known parents. We are interested in comparing the two GSI analysis software options because Rubias has been more recently developed, is more compatible with updates to the R software, and completes analyses quicker. To test single parent analysis using SingleSequoia we utilized a subset of the PBT baseline that included only SY2016 and 2017 and removed all known fathers (N=1612). The *O. tshawytscha* within the known mixture that were from SY215 and SY2018 were treated as negative controls for testing.

Table 5. PBT broodstock collections from 2019-2020 with *O. tshawytscha* of known parentage and siblings.

PBT broodstock collection	CRITFC population	N
Cowlitz Salmon Hatchery fall 2019	OtsCOWL_seg_fa19	1059
Cowlitz Salmon Hatchery spring 2019	OtsCOWL_seg_sp19	962
Kalama Falls Hatchery fall 2019	OtsKALA_seg_fa19	2744
Kalama Falls Hatchery spring 2019	OtsKALA_seg_sp19	533
Speelyai Fish Hatchery spring 2019	OtsLEWI_seg_sp19	777
Round Butte Fish Hatchery spring 2019	OtsRBFH_seg_sp19	310
Washougal Fish Hatchery fall 2019	OtsWASH_seg_fa19	1047
Warm Springs National Fish Hatchery spring 2019	OtsWSNF_seg_sp19	238
Big Creek Hatchery fall 2020	OtsBIGC_seg_fa20	218
Bonneville Dam Hatchery fall 2020	OtsBONN_seg_fa20	1777
Carson National Fish Hatchery spring 2020	OtsCARS_seg_sp20	682
Chief Joseph Hatchery summer 2020 – integrated	OtsCHJO_int_su20	419
Chief Joseph Hatchery spring 2020	OtsCHJO_seg_sp20	523
Chief Joseph Hatchery summer 2020	OtsCHJO_seg_su20	454
Clearwater Fish Hatchery spring 2020	OtsCLWH_seg_sp20	1259
Dworshak National Fish Hatchery spring 2020	OtsDWOR_seg_sp20	1464
Entiat National Fish Hatchery summer 2020	OtsENFH_seg_su20	286
Lookingglass Fish Hatchery spring/summer 2020	OtsIMNW_seg_ss20.	786
McCall Fish Hatchery spring/summer 2020 – integrated	OtsJHNV_int_ss20	90
Klickitat Hatchery spring 2020	OtsKLIC_seg_sp20	457
Dworshak National Fish Hatchery spring 2020	OtsKOOS_seg_sp20	570
Leavenworth National Fish Hatchery spring 2020	OtsLNFH_seg_sp20	974
Little White Salmon National Fish Hatchery fall 2020	OtsLWSN_seg_fa20	4310
Little White Salmon National Fish Hatchery spring 2020	OtsLWSN_seg_sp20	1442
Lyons Ferry Fish Hatchery spring 2020	OtsLYON_seg_sp20	43
Nez Perce Tribal Fish Hatchery fall 2020	OtsNPFH_seg_fa20	707
Nez Perce Tribal Fish Hatchery spring 2020	OtsNPFH_seg_sp20	278
Parkdale Fish Facility spring 2020	OtsPARK_seg_sp20	257
Clearwater Fish Hatchery spring 2020	OtsPOWP_seg_sp20	147
Round Butte Fish Hatchery spring 2020	OtsRBFH_seg_sp20	196
Ringold Springs State Hatchery spring 2020	OtsRING_seg_fa20	888
Spring Creek National Fish Hatchery fall 2020	OtsSPCR_seg_fa20	5451
Umatilla Fish Hatchery fall 2020	OtsUMAT_seg_fa20	655
Umatilla Fish Hatchery spring 2020	OtsUMAT_seg_sp20	417
Wells Fish Hatchery summer 2020	OtsWELL_seg_su20	964
	Positive_control	50

Results

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 12, Figure 13, Appendix 11, Appendix 12, and Appendix 13) 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 9).

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).

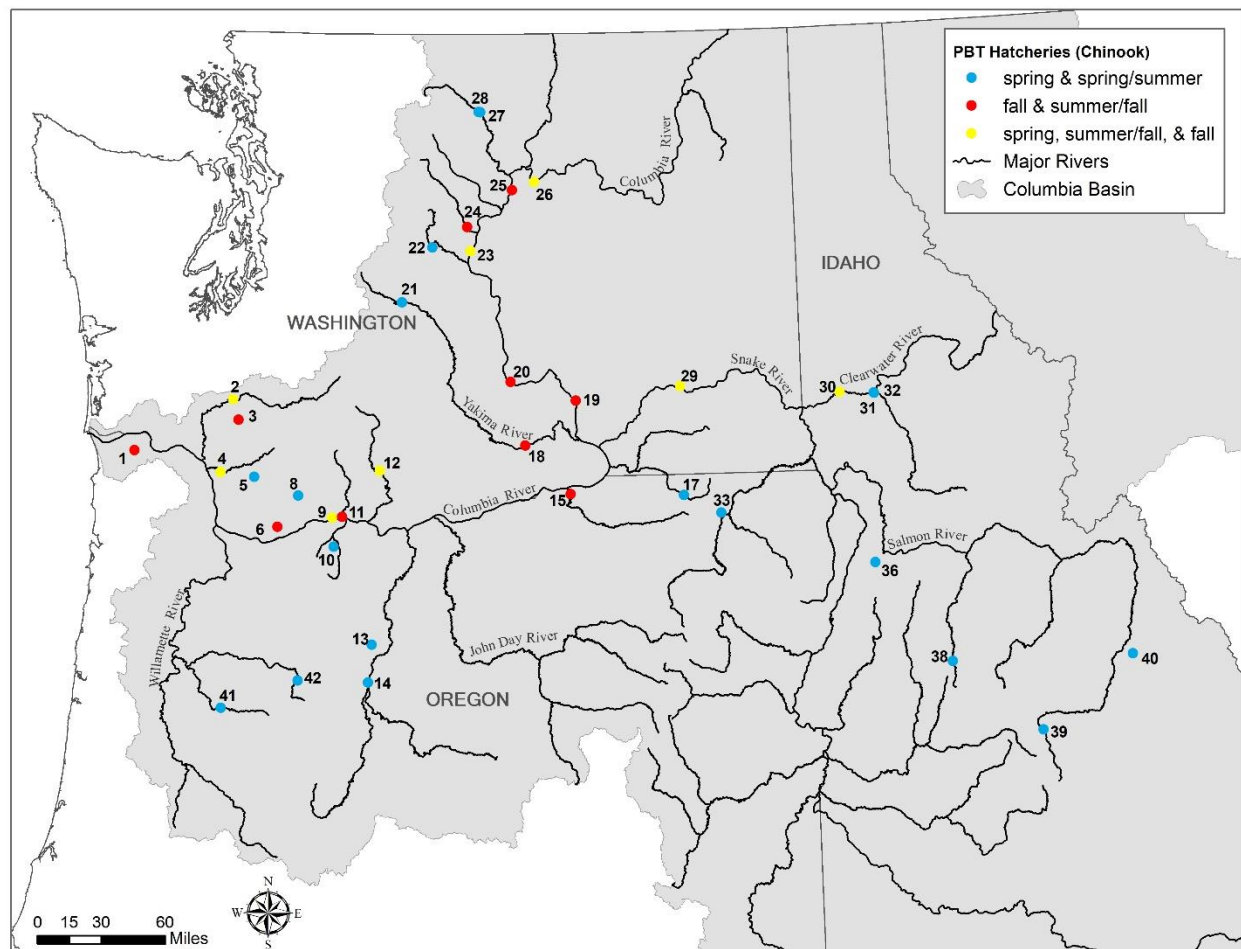


Figure 12. Chinook Salmon, PBT hatcheries. Numbers correspond to map ID and hatchery descriptions (Appendix 11).

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 9), n=2,278 steelhead trout (Appendix 10), and n=6,732 Coho Salmon (Appendix 10). 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>).

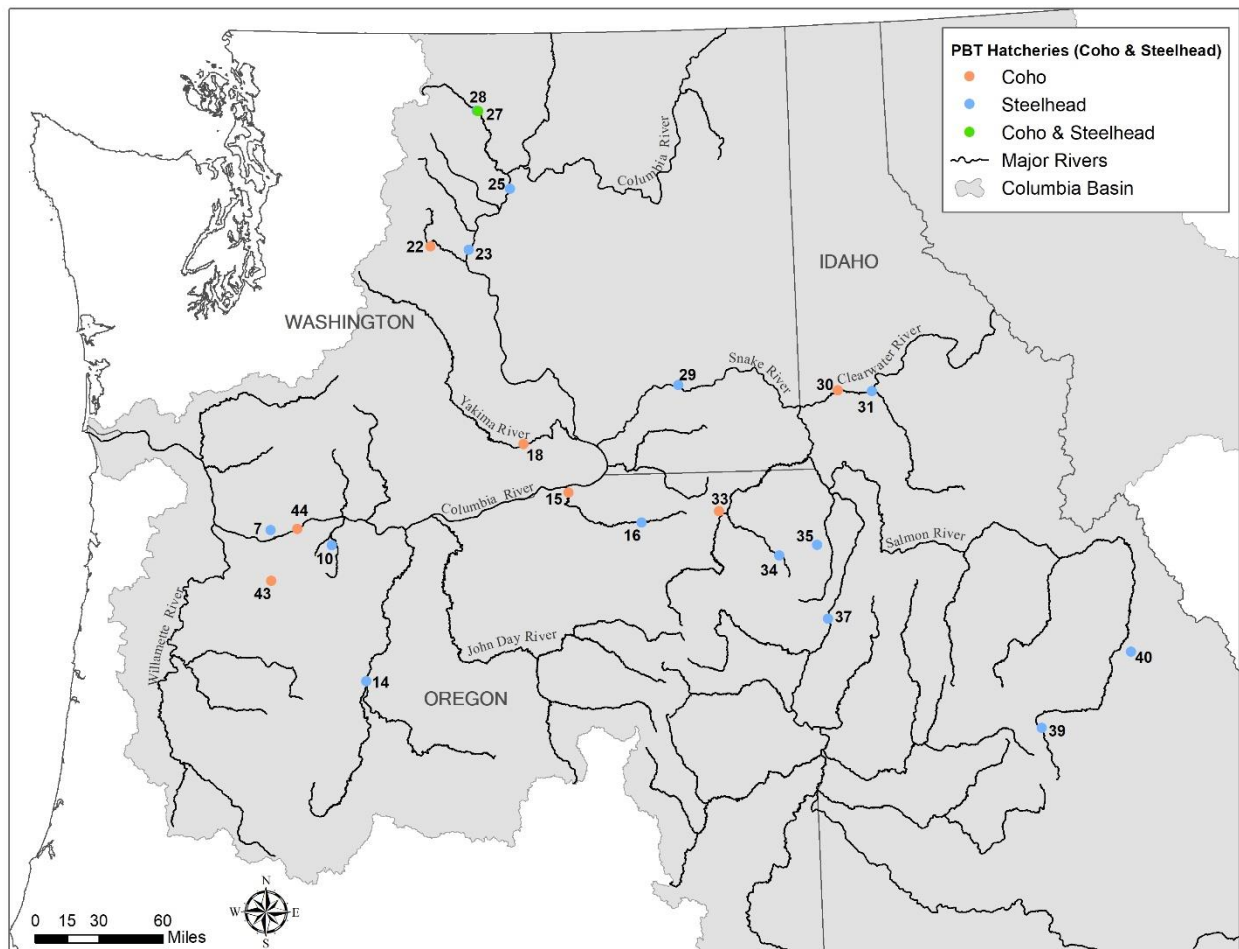


Figure 13. Steelhead and Coho Salmon, PBT hatcheries. Numbers correspond to map ID and hatchery descriptions (Appendix 12, Appendix 13).

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.

Comparison of GSI assignment methods with known parents:

GSI analyses were conducted with Oncor (Figure 14) and Rubias (Figure 15) and the resulting percentages of correct assignments were compared (Figure 16). The significant differences between GSI assignments with Oncor and Rubias were all *O. tshawytscha* PBT broodstock collections that had improved correct assignment percentages with the use of Rubias over Oncor. The *O. tshawytscha* PBT broodstock collections with significant improved correct assignment percentages when analyzed with Rubias software were Cowlitz Salmon Hatchery spring and fall 2019, Kalama Falls Hatchery spring 2019, Big Creek Hatchery fall 2020, Carson National Fish Hatchery spring 2020, Little White Salmon National Fish Hatchery spring 2020, Clearwater Fish Hatchery spring 2020, Dworshak National Fish Hatchery spring 2020, McCall Fish Hatchery spring/summer 2020, and Nez Perce Tribal Fish Hatchery fall 2020. All other collections did not have a significant difference in percentage of correct assignments between the two GSI assignment methods.

The single parent analysis was conducted with SingleSequoia for sample years 2016 through 2017 and samples from 2015 and 2018 were utilized as controls. All true positives and negatives were successfully assigned for the Wells Fish Hatchery summer 2014, Kalama Falls Hatchery spring 2015 and fall 2016, Speelyai Fish Hatchery spring 2015, Parkdale Fish Facility spring 2015, Warm Springs National Fish Hatchery spring 2015, and Spring Creek National Fish Hatchery fall 2018 PBT broodstock collections (Table 6; Figure 17). The only PBT broodstock collection that did not have any successful true positives or true negatives was the McCall Fish Hatchery spring/summer 2016 in the reporting group 13_SFSALM (Table 6; Figure 17). All remaining PBT broodstock collections and reporting groups contain a mixed result of true and false positives and negatives (Table 6; Figure 17).

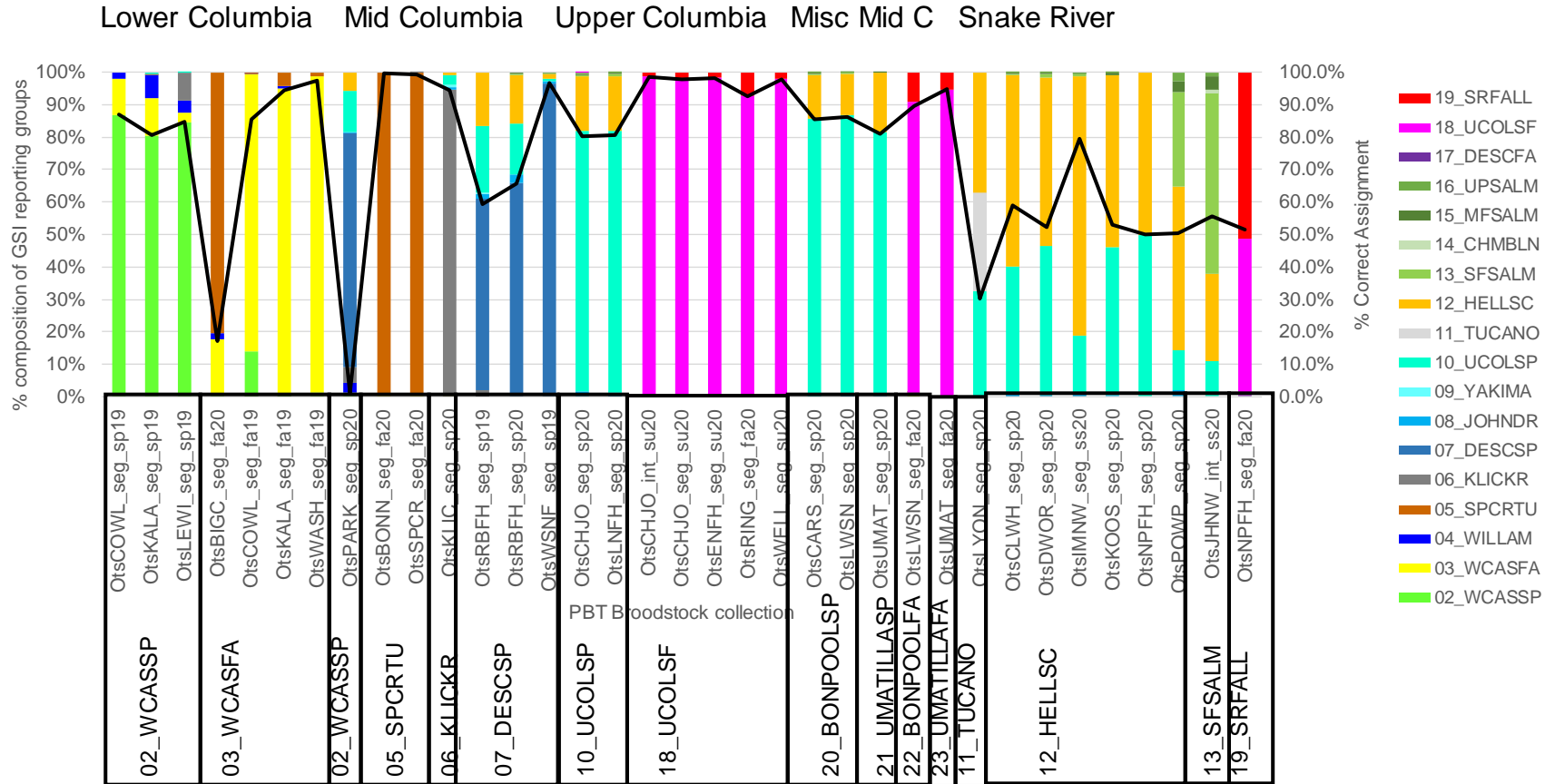


Figure 14. GSI assignments with Oncor software. The PBT broodstock collections are grouped by GSI reporting groups and the assignments are coded by the colors in the legend on the right. The black line represents the percent correctly assigned for each PBT broodstock collection assessed.

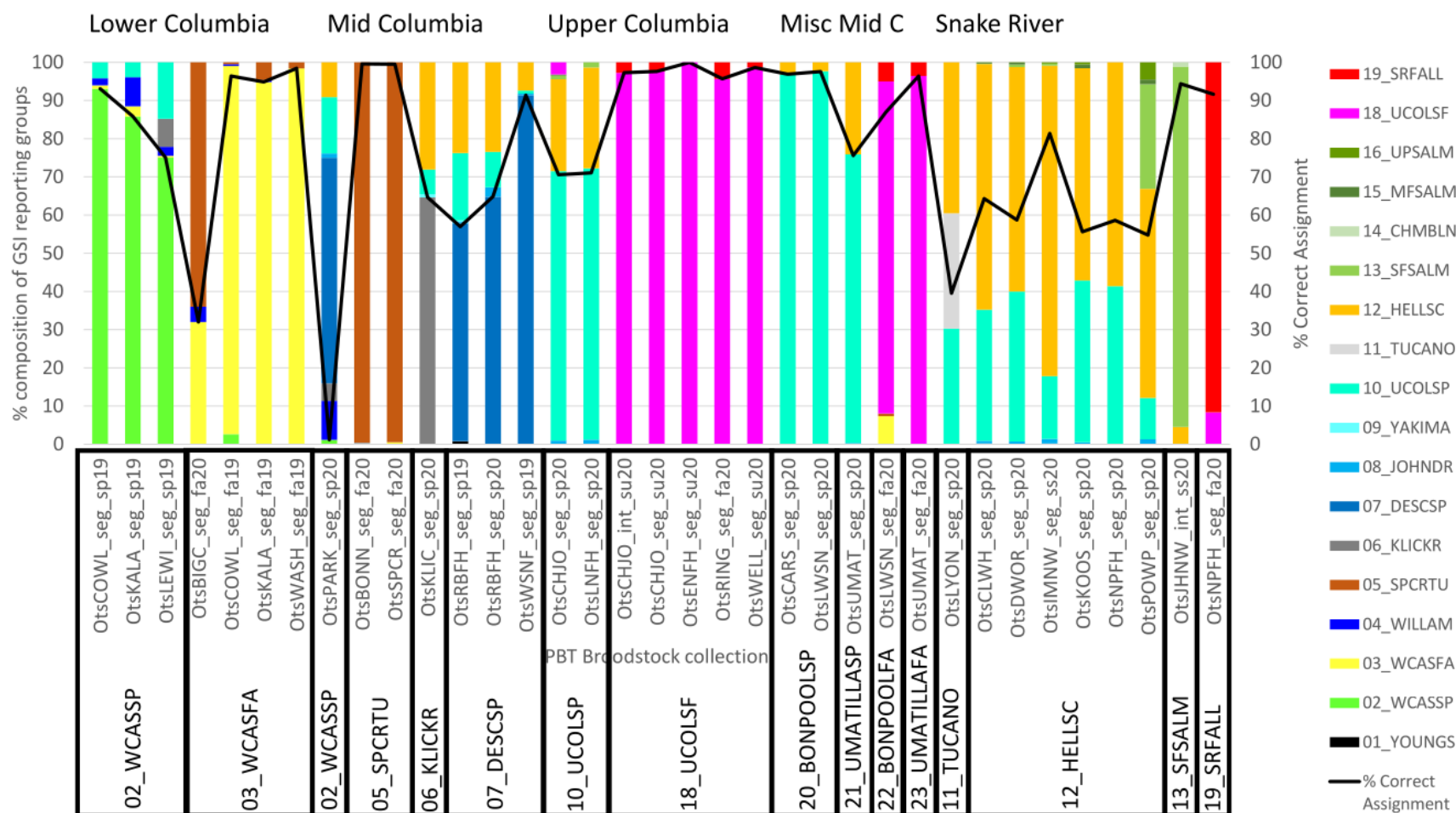


Figure 15. GSI assignments with Rubias software. The PBT broodstock collections are grouped by GSI reporting groups and the assignments are coded by the colors in the legend on the right. The black line represents the percent correctly assigned for each PBT broodstock collection assessed.

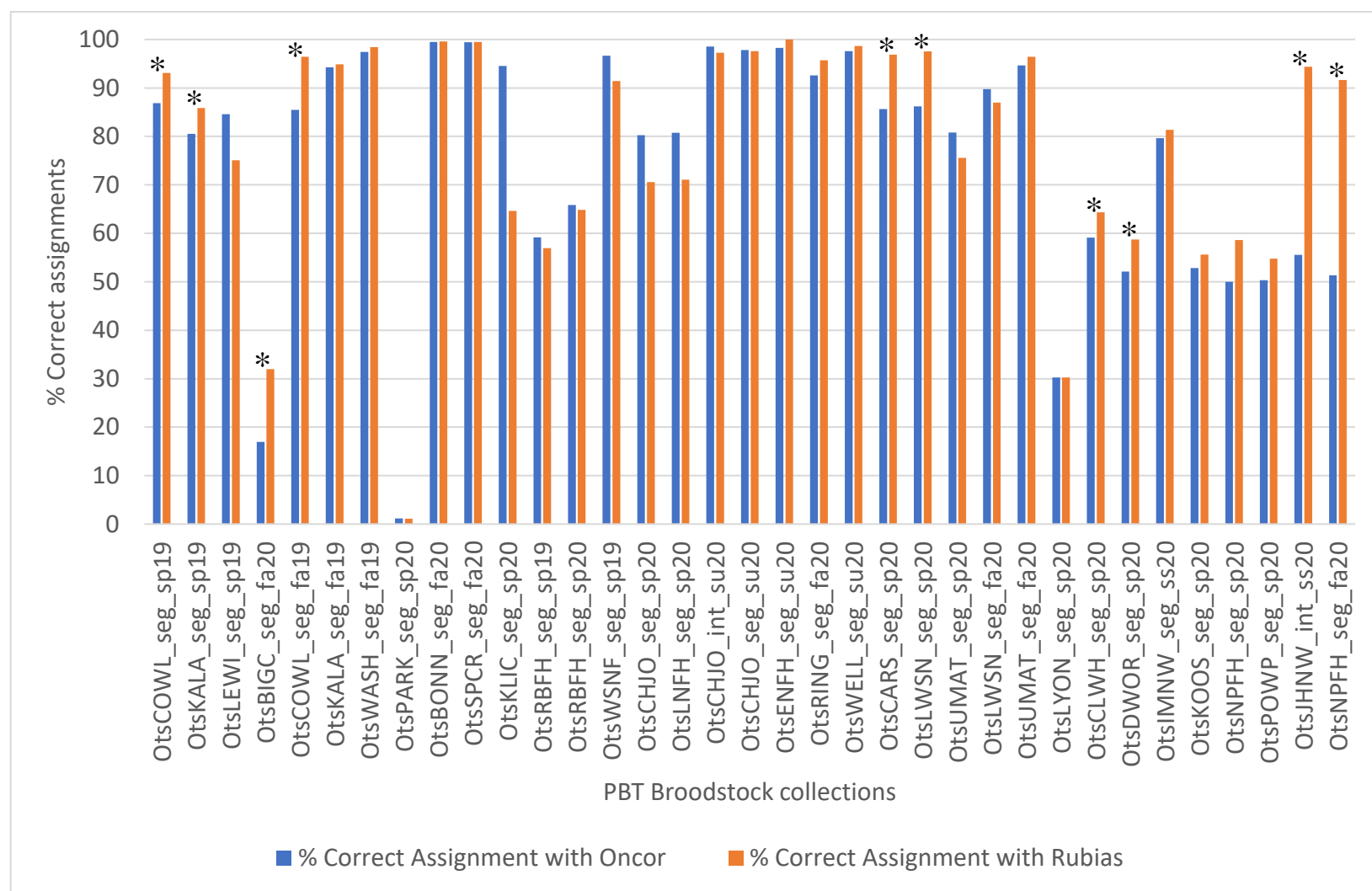


Figure 16. The percent correct assignments with Oncor software compared to percent correct assignment with Rubias software. The asterisk represents significant difference between percent correct assignments with Oncor software compared to percent correct assignment with Rubias software.

Table 6. Accuracy of single parent assignments compared to known parent assignments.

Count of Individual name		TruMa			Grand Total				
			0	1		False positive	False negative	True positive	True negative
2014	18_UCOLSF	OtsWELL_seg_su14			4	4	0.0%		100.0%
2015	02_WCASSP	OtsCOWL_seg_sp15	3		30	33	9.1%		90.9%
		OtsKALA_seg_sp15			8	8	0.0%		100.0%
		OtsLEWI_seg_sp15			31	31	0.0%		100.0%
		OtsPARK_seg_sp15			24	24	0.0%		100.0%
	03_WCASFA	OtsCOWL_seg_fa15	2		23	25	8.0%		92.0%
		OtsWASH_seg_fa15	2		16	18	11.1%		88.9%
	07_DESCSP	OtsRBFH_seg_sp15	1		58	59	1.7%		98.3%
		OtsWSNF_seg_sp15			8	8	0.0%		100.0%
	18_UCOLSF	OtsCHJO_int_su15	6		52	58	10.3%		89.7%
		OtsCHJO_seg_su15	1		3	4	25.0%		75.0%
		OtsENFH_seg_su15	8		65	73	11.0%		89.0%
		OtsWELL_seg_su15	36		286	322	11.2%		88.8%
	22_BONPOOLFA	OtsLWSN_seg_fa15	2		27	29	6.9%		93.1%
2016	02_WCASSP	OtsLEWI_seg_sp16		46	7	53	0.0%	13.2%	86.8%
		OtsPARK_seg_sp16	1	80	90	171	0.6%	52.6%	46.8%
	03_WCASFA	OtsCOWL_seg_fa16	1	45	1	47	2.1%	2.1%	95.7%
		OtsKALA_seg_fa16		19		19	0.0%	0.0%	100.0%
		OtsWASH_seg_fa16		13	1	14	0.0%	7.1%	92.9%
	06_KLICKR	OtsKLIC_seg_sp16		186	35	221	0.0%	15.8%	84.2%
	07_DESCSP	OtsRBFH_seg_sp16		19	20	39	0.0%	51.3%	48.7%
	10_UCOLSP	OtsCHJO_seg_sp16	7	108	93	208	3.4%	44.7%	51.9%

		OtsLNFH_seg_sp16	13	117	312	442	2.9%	70.6%	26.5%
	12_HELLSC	OtsCLWH_seg_sp16	25	285	354	664	3.8%	53.3%	42.9%
		OtsDWOR_seg_sp16	24	345	632	1001	2.4%	63.1%	34.5%
		OtsIMNW_seg_ss16	2	70	17	89	2.2%	19.1%	78.7%
		OtsLOOK_seg_sp16	1	112	19	132	0.8%	14.4%	84.8%
		OtsNPFH_seg_sp16	3	53	71	127	2.4%	55.9%	41.7%
		OtsPOWP_seg_sp16		4	13	17	0.0%	76.5%	23.5%
	13_SFSALM	OtsMCCA_seg_ss16			4	4	0.0%	100.0%	0.0%
	18_UCOLSF	OtsCHJO_int_su16	1	56		57	1.8%	0.0%	98.2%
		OtsENFH_seg_su16	2	9	5	16	12.5%	31.3%	56.3%
		OtsPRIE_seg_fa16		11	1	12	0.0%	8.3%	91.7%
		OtsWELL_seg_su16		143	23	166	0.0%	13.9%	86.1%
	19_SRFALL	OtsNPFH_seg_fa16		9	1	10	0.0%	10.0%	90.0%
	20_BONPOOLSP	OtsCARS_seg_sp16	3	169	162	334	0.9%	48.5%	50.6%
		OtsLWSN_seg_sp16	8	338	326	672	1.2%	48.5%	50.3%
	21_UMATILLASP	OtsUMAT_seg_sp16		76	42	118	0.0%	35.6%	64.4%
	22_BONPOOLFA	OtsLWSN_seg_fa16	31	1229	408	1668	1.9%	24.5%	73.7%
2017	05_SPCRTU	OtsSPCR_seg_fa17	46	792	382	1220	3.8%	31.3%	64.9%
	10_UCOLSP	OtsLNFH_seg_sp17		1	4	5	0.0%	80.0%	20.0%
	18_UCOLSF	OtsPRIE_seg_fa17	8	170	53	231	3.5%	22.9%	73.6%
2018	05_SPCRTU	OtsSPCR_seg_fa18			13	13	0.0%		100.0%
Grand Total			237	4505	3724	8466			

Under “TruMa” a “0” is a false positive (the father parent does not match the SNPPIT assignment), a “1” is a true positive (the father is an exact match with the SNPPIT assignment), and “NA” indicates the individual was not assigned to any parent in the baseline.

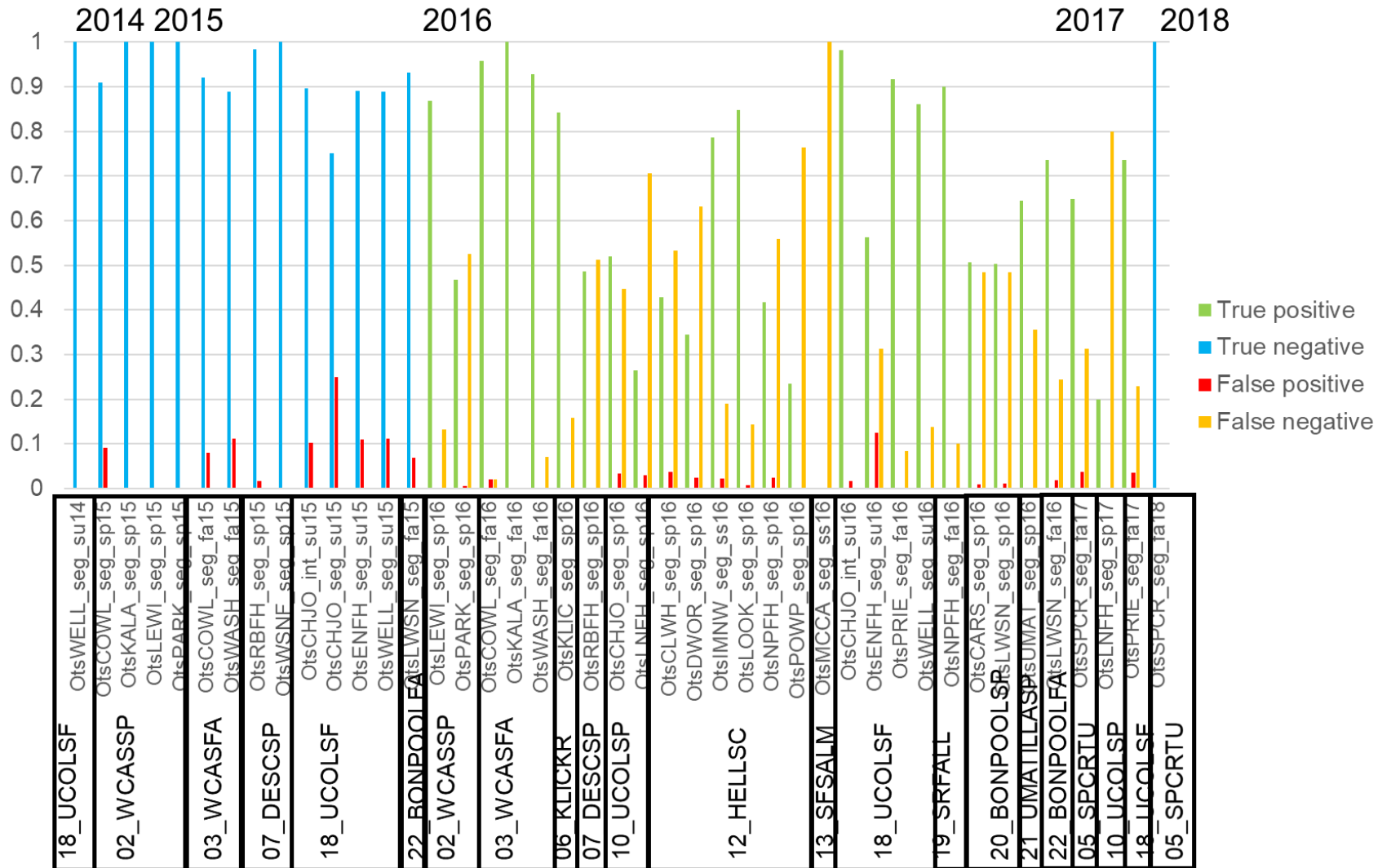


Figure 17. Type I and Type II errors for single parent assignment to the known mixture sample.

1 **Discussion**

2 Over the course of the Genetic Assessment project we have compiled extensive data sets
3 of SNP genotypes for Chinook salmon, steelhead trout and *O. nerka*, and continue to improve
4 resources for Coho Salmon and Pacific Lamprey. The populations we have evaluated span
5 diverse regions in the Columbia River Basin (including the Snake River Basin). We continue to
6 update and maintain SNP reference baselines for evaluation of these species in future
7 generations. This long-term strategy informs harvest management and assures the greatest
8 likelihood of discerning temporal variation among reproductively distinct species aggregates
9 (Waples 1991), while monitoring population viability related to demographic trends that occur
10 locally and/or regionally. Philopatry (Quinn et al. 1991, Hendry et al. 2003) and hatchery
11 supplementation activities (Ford et al. 2006; Hard & Heard 1999) play a major role in how
12 genetic divergence and differentiation is distributed geographically. For managing sustainable
13 fisheries, it is necessary to understand the magnitude of influence that these and other factors
14 have on our ability to differentiate populations, both qualitatively (phenotypes; landscapes) and
15 quantitatively (e.g., genetic stock identification). This becomes particularly important where
16 mixed stock fisheries may consist of both ESA listed and unlisted populations, and where
17 differential harvest may have the greatest impact on specific populations. Our current efforts
18 have largely focused on expanding numbers of markers and non-neutral markers associated with
19 maturation. However, loci for adaptive divergence (landscape genetics) remains as one of our
20 primary objectives for strengthening our understanding of non-neutral genetic variation among
21 populations. Data collected through whole genome resequencing and GT-seq techniques has
22 yielded large numbers of potential SNPs, and demonstrated their utility for characterizing
23 adaptive variation, and identifying environmental and life history related variables that are likely
24 to have significant influence on allele frequencies (e.g., precipitation, temperature, run-timing.;
25 Hecht et al. 2015, Hess et al. 2016b; Micheletti et al. 2017; Narum et al. 2018; Micheletti et al.
26 2018; Collins et al. 2020). The expansion efforts reported here also provided improved ability to
27 differentiate stocks on regional and local scales through application of GSI and PBT methods.

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

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315 **Appendix 9. Chinook Salmon hatchery broodstock sampled for PBT baselines.**

Map ID	Spawning hatchery	Run type	Lineage	Region	Latitude	Longitude	Year	2021 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	2020	221
2	Cowlitz Salmon	fall (tule)	LC	Col.	46.51145	-122.6294	2015	2019-2020	3201
2	Cowlitz Salmon	spring	LC	Col.	46.51145	-122.6294	2015	2019-2020	1398
3	Toutle	fall (tule)	LC	Col.	46.37464	-122.572	2015	2020	na
4	Kalama Falls	fall (tule)	LC	Col.	46.01624	-122.7328	2016	2019-2020	6703
4	Kalama Falls	spring	LC	Col.	46.01624	-122.7328	2015	2019-2020	1346
5	Lewis River	spring	LC	Col.	45.98849	-122.4062	2015	2019-2020	2070
	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	2020	2020	799
	McKenzie	spring	LC	Col.	44.118	-122.637	2020	2020	500
	Willamette	spring	LC	Col.	43.745	-122.444	na	na	na
6	Washougal	fall (tule)	LC	Col.	45.65344	-122.1691	2015	2019-2020	2675
	Bonneville, Tanner Cr.	fall (tule)	LC	Col.	45.633	-121.957	na	na	na
11	Spring Creek NFH	fall (tule)	LC	Col.	45.72779	-121.5453	2015	2020	5569
9	Little White Salmon NFH	fall	IOT	Col.	45.72226	-121.6401	2013	2020	4326
15	Umatilla	fall	IOT	Col.	45.88172	-119.3226	2012	2020	669
18	Prosser	fall	IOT	Col.	46.21512	-119.7596	2012	2020	na
19	Ringold Springs	fall	IOT	Col.	46.51401	-119.2593	2016	2020	923
20	Priest Rapids	fall	IOT	Col.	46.64728	-119.899	2012	2020	5626
29	Lyons Ferry	fall	IOT	Snake	46.59725	-118.2282	2011	2020	na
30	Nez Perce Tribal	fall	IOT	Snake	46.51954	-116.6601	2011	2020	711
23	Eastbank	summer	IOT	Col.	47.53367	-120.2891	2012	2020	745
24	Entiat NFH	summer	IOT	Col.	47.69806	-120.3231	2013	2020	296
25	Wells	summer	IOT	Col.	47.94582	-119.8712	2012	2020	978
26	Chief Joseph	summer	IOT	Col.	48.0006	-119.6451	2013	2020	1042
9	Little White Salmon NFH	spring	IST	Col.	45.72226	-121.6401	2013	2020	1489
15	Umatilla	spring	IST	Col.	45.88172	-119.3226	2012	2020	426
29	Lyons Ferry	spring	IST	Snake	46.59725	-118.2282	2008	2020	43
30	Nez Perce Tribal	spring	IST	Snake	46.51954	-116.6601	2008	2020	279
23	Eastbank	spring	IST	Col.	47.53367	-120.2891	2012	2020	214
26	Chief Joseph	spring	IST	Col.	48.0006	-119.6451	2014	2020	549
8	Carson NFH	spring	IST	Col.	45.86826	-121.9742	2012	2020	700
10	Parkdale	spring	IST	Col.	45.52439	-121.6216	2012	2020	259
12	Klickitat	spring	IST	Col.	46.04236	-121.1823	2008	2020	469
13	Warm Springs NFH	spring	IST	Col.	44.86201	-121.245	2012	2019-2020	601
14	Round Butte	spring	IST	Col.	44.60503	-121.2778	2012	2019-2020	525
21	Cle Elum SRF	spring	IST	Col.	47.18679	-120.9762	2012	2020	2250
22	Leavenworth NFH	spring	IST	Col.	47.55842	-120.6738	2013	2020	1004
27	Methow	spring	IST	Col.	48.47703	-120.2051	2012	2020	78
28	Winthrop NFH	spring	IST	Col.	48.47366	-120.1891	2013	2020	381
33	Lookingglass	spring	IST	Snake	45.73136	-117.864	2008	2020	798
31	Dworshak NFH	spring	IST	Snake	46.50206	-116.3232	2008	2020	1480
32	Clearwater	spring	IST	Snake	46.50429	-116.3277	2008	2020	1515
36	Rapid River	spring/sumr	IST	Snake	45.35411	-116.3938	2008	2020	IDFG
38	SF Salmon, McCall	spring/sumr	IST	Snake	44.65554	-115.7025	2008	2020	IDFG
40	Pahsimeroi	spring/sumr	IST	Snake	44.62284	-113.9863	2008	2020	IDFG
39	Sawtooth	spring/sumr	IST	Snake	44.15174	-114.8843	2008	2020	IDFG

316 Note: The Map ID indicates the sites of the hatcheries corresponding to Figure 12. Genetic lineage is lower Col.
317 (LC), interior ocean-type (IOT), and interior stream-type (IST). Year refers to the first year of PBT sampling for
318 each hatchery: na – not currently a PBT hatchery. For some hatchery PBT samples, genotyping efforts have begun
319 to backdate collections that were initially archived- the “sampled” field indicates which collection years were
320 genotyped in 2018. The project collaborators at Idaho Department of Fish and Game (IDFG) were responsible for
321 genotyping of Snake River hatcheries (see “completed” column).
322

323 **Appendix 10.** Steelhead and Coho Salmon hatchery broodstock sampled for PBT baselines.

Map ID	Spawning hatchery	Run type	Lineage	Region	Latitude	Longitude	Year	2021 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/wi	coastal	Col.	45.6218	-122.2173	2013	2020	314
10	Parkdale	winter	coastal	Col.	45.5244	-121.6216	2012	2020	53
14	Round Butte	summer	inland	Col.	44.605	-121.6216	2013	2020	452
	Umatilla	summer	inland	Col.	45.913	-119.552	2012	2020	0
23	Eastbank	summer	inland	Col.	47.5337	-120.2891	2012	2020	126
25	Wells	summer	inland	Col.	47.9458	-119.8712	2013	2020	161
27	Methow (Twisp)	summer	inland	Col.	48.477	-120.2051	2013	2020	0
28	Winthrop NFH	summer	inland	Col.	48.4737	-120.2051	2013	2020	115
29	Lyons Ferry	summer	inland	Snake	46.5973	-118.2282	2009	2020	IDFG
34	Wallowa	summer	inland	Snake	45.4178	-117.3004	2009	2020	IDFG
37	Oxbow	summer	inland	Snake	44.9727	-116.8548	2008	2020	IDFG
31	Dworshak NFH	summer	inland	Snake	46.5021	-116.3232	2008	2020	IDFG
40	Pahsimeroi	summer	inland	Snake	44.6228	-113.9863	2008	2020	IDFG
39	Sawtooth	summer	inland	Snake	45.1517	-114.8843	2008	2020	IDFG
35	Little Sheep Creek	summer	inland	Snake	45.4777	-116.9306	2008	2020	IDFG
	Coho								
15	Umatilla	fall	lower Col.	Col.	45.913	-119.552	2015	2020	482
18	Prosser	fall	lower Col.	Col.	46.2151	-119.7596	2016	2020	na
22	Leavenworth NFH	fall	lower Col.	Col.	47.5584	-120.6738	2012	2020	982
28	Winthrop NFH	fall	lower Col.	Col.	48.4737	-120.1891	2012	2020	748
31	Dworshak NFH	fall	lower Col.	Snake	46.5021	-116.3232	2015	2019-2020	2417
43	Eagle Creek NFH	fall	lower Col.	Col.	45.276	-122.202	2019	na	na
44	Bonneville	fall	lower Col.	Col.	45.633	-121.957	2019	na	na

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

325 Note: The map ID indicates site locations corresponding with Figure 12. Genetic lineage is coastal or inland. Year refers to the first year of PBT sampling for

326 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

327 drafting of this report. The project collaborators at Idaho Department of Fish and Game (IDFG) were responsible for genotyping of Snake River hatcheries (see

328 “completed” column). All Coho broodstocks sampled for PBT broodstock were designated for release of fish upstream of Bonneville Dam.

329

330

Map num.	Hatchery	Species	Code	Run type	Lineage	Year													
						2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	
32	Clearwater Fish Hatchery	Chinook	OtsCLWH	Spring	Interior stream type	X	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	X	
31	Dworshak National Fish Hatchery	Chinook	OtsDWOR	Spring	Interior stream type	X	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	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	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	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	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	X	
29	Lyons Ferry Fish Hatchery	Chinook	OtsLYON	Spring	Interior stream type	*	*	*	*	X	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	X	
29	Lyons Ferry Fish Hatchery	Chinook	OtsLYON_1	Fall	Interior ocean type	*	*	*	X	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	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	X	
30	Nez Perce Tribal Fish Hatchery	Chinook	OtsNPFH_1	Fall	Interior ocean type	*	*	*	X	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	X	
40	Pahsimeroi Fish Hatchery	Chinook	OtsPAHH	Spring	Interior stream type	X	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	X	
39	Sawtooth Fish Hatchery	Chinook	OtsSAWT	Spring	Interior stream type	X	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	X	
8	Carson National Fish Hatchery	Chinook	OtsCAR_sp	Spring	Interior stream type	*	*	*	*	X	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	X	
26	Chief Joseph Hatchery - Integrated	Chinook	OtsCJHint_su	Summer	Interior ocean type	*	*	*	*	*	X	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	X	
2	Cowlitz Salmon	Chinook	OtsCOW_sp	Spring	Interior stream type	*	*	*	*	*	*	*	X	X	X	X	X	X	
2	Cowlitz Salmon	Chinook	OtsCOW_fa	Fall	Interior stream type	*	*	*	*	*	*	*	X	X	X	X	X	X	
23	Eastbank Fish Hatchery	Chinook	OtsEASTBK_sp	Spring	Interior stream type	*	*	*	*	*	X	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	X	
24	Entiat National Fish Hatchery	Chinook	OtsENFH_su	Summer	Interior ocean type	*	*	*	*	*	X	X	X	X	X	X	X	X	
4	Kalama Falls	Chinook	OtsKAL_sp	Spring	Interior stream type	*	*	*	*	*	*	*	X	X	X	X	X	X	
4	Kalama Falls	Chinook	OtsKAL_fa	Fall	Interior stream type	*	*	*	*	*	*	*	*	X	X	X	X	X	
12	Klickitat State Fish Hatchery	Chinook	OtsKH_sp	Spring	Interior stream type	X	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	X	
22	Leavenworth National Fish Hatchery	Chinook	OtsLNFH_sp	Spring	Interior stream type	*	*	*	*	*	X	X	X	X	X	X	X	X	
5	Speelyai Hatchery	Chinook	OtsLEW_sp	Spring	Interior stream type	*	*	*	*	*	*	*	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	X	
9	Little White Salmon National Fish Hatchery	Chinook	OtsLWS_sp	Spring	Interior stream type	*	*	*	*	*	X	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	Interior stream type	*	*	*	*	*	*	*	*	*	*	X	X	*	
27	Methow State Fish Hatchery	Chinook	OtsMETH_sp	Spring	Interior stream type	*	*	*	*	X	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	X	
20	Priest Rapids Hatchery	Chinook	OtsPRH_fa	Fall	Interior ocean type	*	*	*	*	X	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	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	X	
41	South Santiam Hatchery	Chinook	OtsSSANT_sp	Spring	Interior stream type	*	*	*	*	*	*	*	X	X	*	X	X	X	
11	Spring Creek National Fish Hatchery	Chinook	OtsSPCR_fa	Fall	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	X	X	
3	North Toutle Hatchery	Chinook	OtsTOU_fa	Fall	Interior ocean type	*	*	*	*	*	*	*	X	X	X	X	**	X	
15	Three mile dam, Umatilla River	Chinook	OtsUMA_fa b	Fall	Interior ocean type	*	*	*	*	X	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	X	
6	Washougal	Chinook	OtsWAS_fa	Fall	Interior ocean type	*	*	*	*	*	*	*	X	X	X	X	X	X	
13	Warm Springs National Fish Hatchery	Chinook	OtsWSNFH_sp h	Spring	Interior stream type	*	*	*	*	X	X	X	~	~	~	X	X	X	
25	Wells Fish Hatchery	Chinook	OtsWELLS_su	Summer	Interior ocean type	*	*	*	*	X	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	X	
18	Yakima Nation Prosser Hatchery	Chinook	OtsPRO_fa	Fall	Interior ocean type	*	*	*	*	X	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	X	
21	Levi George/Cle Elum (Segregated)	Chinook	OtsYRseg_sp	Spring	Interior stream type	*	*	*	*	X	X	X	X	X	X	X	X	X	

Note: Species-specific collections code along with run type and genetic lineage are provided for both species. Map numbers correspond with Figure 12.

X Chinook tissues genotyped using 351 SNPs

X Chinook tissues genotyped using 343 SNPs

X Chinook tissues genotyped using 298 SNPs

X Chinook tissues genotyped using 96 SNPs

Chinook broodstock sampled, spawned at another hatchery and genotyped using 298 SNPs

a Chinook Lyons Ferry stock consolidated under 'OtsLYON' starting in 2012

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

c Chinook typically spawned at Little White Salmon NFH, but due to low returns in 2018 they were spawned at Klickitat Hatchery.

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

N/A Stock discontinued/non-existent

* Broodstock not sampled

** Broodstock sampled, tissues archived until funding identified for processing

Map num.	Hatchery	Species	Code	Run type	Lineage	Year														
						2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020		
31	Dworshak National Fish Hatchery	Steelhead	OmyDWOR	Unknown	Interior	X	X	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	X	X	
29	Lyons Ferry Fish Hatchery- Touchet	Steelhead	OmyTOUW c	Summer	Interior	*	X	X	X	X	X	X	X	X	X	X	X	X	X	
29	Lyons Ferry Fish Hatchery	Steelhead	OmyLYON d	Unknown	Interior	*	X	X	X	X	N/A	N/A	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	X	X	
29	Lyons Ferry Fish Hatchery - Tucannon	Steelhead	OmyTUCW c	Summer	Interior	*	X	X	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	N/A	N/A	
37	Oxbow	Steelhead	OmyOXBO	Summer	Interior	X	X	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	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	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	X	X	
40	Pahsimeroi Fish Hatchery	Steelhead	OmyPAHH	Unknown	Interior	X	X	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	X	X	
23	Eastbank Hatchery	Steelhead	OmyEASTBK	Summer	Interior	*	*	*	*	X	X	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	X	X	
14	Round Butte Fish Hatchery	Steelhead	OmyRB	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X	X	X	X	
7	Skamania Hatchery (Summer)	Steelhead	OmySKH_su g	Summer	Coastal	*	*	*	*	*	X	X	X	X	X	X	X	X	X	
7	Skamania Hatchery (Winter)	Steelhead	OmySKH_wi g	Winter	Coastal	*	*	*	*	*	X	X	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	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	X	X	

348 Note map numbers correspond to sites in Figure 12.
349 X Steelhead tissues genotyped using 96 SNPs
350 X Steelhead tissues genotyped using 379 SNPs
351 X Steelhead tissues genotyped using 269 SNPs
352 X Steelhead tissues genotyped using 192 SNPs
353 X Steelhead tissues genotyped using 390 SNPs
354 X Steelhead tissues genotyped using 368 SNPs
355 X Steelhead broodstock sampled, spawned at another hatchery and genotyped using 379 SNPs
356 X Steelhead broodstock sampled, spawned at another hatchery and genotyped using 368 SNPs
357 c Steelhead Lyons Ferry stock consolidated under 'OmyLYON' starting in 2012
358 d Steelhead Lyons Ferry stock discontinued starting in 2013
360 e Steelhead Sawtooth stock consolidated under 'OmySAWT' from 2012-2013
361 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 Shoshone-Bannock tribe beginning in 2017
362 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 Chambers Creek stock to Big Creek stock starting with SY2018.
364 i Steelhead Methow Hatchery Twisp stock spawned at Winthrop NFH starting in 2017; not distiguished from Withrop stock
365 N/A Stock discontinued/non-existent
366 * Broodstock not sampled
367 ** Broodstock sampled, tissues archived until funding identified for processing
368

Map num.	Hatchery	Species	Code	Run type	Lineage	Year									
						2011	2012	2013	2014	2015	2016	2017	2018	2019	2020
15	Three mile dam, Umatilla River	Coho	OkiUMA	Fall	Lower Columbia					X	X	X	X	X	X
22	Leavenworth National Fish Hatchery	Coho	OkiLNFH	Fall	Lower Columbia	X	X	X	X	X	X	X	X	X	X
30	Nez Perce Tribal Fish Hatchery	Coho	OkiNPT	Fall	Lower Columbia			*	*	X	X	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	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	

370
371 Note: map numbers correspond to sites in Figure 12.
372 X Coho tissues genotyped at 257 loci
373 * Samples received, but not genotyped.
374 ** Samples collected, but not received.
375

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 2020 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 11).

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 2020 pound net fishery that was in operation during the fall chinook management period and during the sockeye runs of 2019 and 2020. We estimated stock abundance of fall Chinook salmon among the clipped fish that were retained (kept) and the unclipped fish that were released. This report includes the 7th and 8th years of analysis of Sockeye salmon fisheries in the Columbia River mainstem, because 2019 fishery data were not available in time for last year’s report and were combined with 2020 analysis in this 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?

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 2020 from a total of five different mixture sources: the spring-run season of the 1) lower river recreational fishery; the summer management period harvest of the 2) lower river recreational fishery; and the fall-run harvest from 3) lower river commercial, 4) sport (above and below Bonneville Dam), and 5) pound net fishery (both the kept and released catch). 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 are generally sampled below Bonneville Dam in the sport, test fishery, and in the Treaty permit fishery (Figure 18; Table 7). Issues related to COVID prevented Treaty fisheries from being sampled in 2020, and the spring test fishery was not conducted in 2020. Typically for the summer management period fisheries, we may obtain samples from below Bonneville Dam in the recreational fishery and 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 18): 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 spring and summer period 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, and the fall Non-Treaty sport and commercial fishery.

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 in 2020 and analysis presented in the current report. In 2020, additional tissues from sockeye salmon were collected from a single fishery, the Non-Treaty sport fishery, and analysis of this mixture is also presented in the current 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 a panel of 254 SNPs. We used 363 SNP markers for GSI and PBT of sockeye mixtures. For steelhead, this was the second 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 SY2019 and so the 2021 Bonneville Dam run year was the second 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.

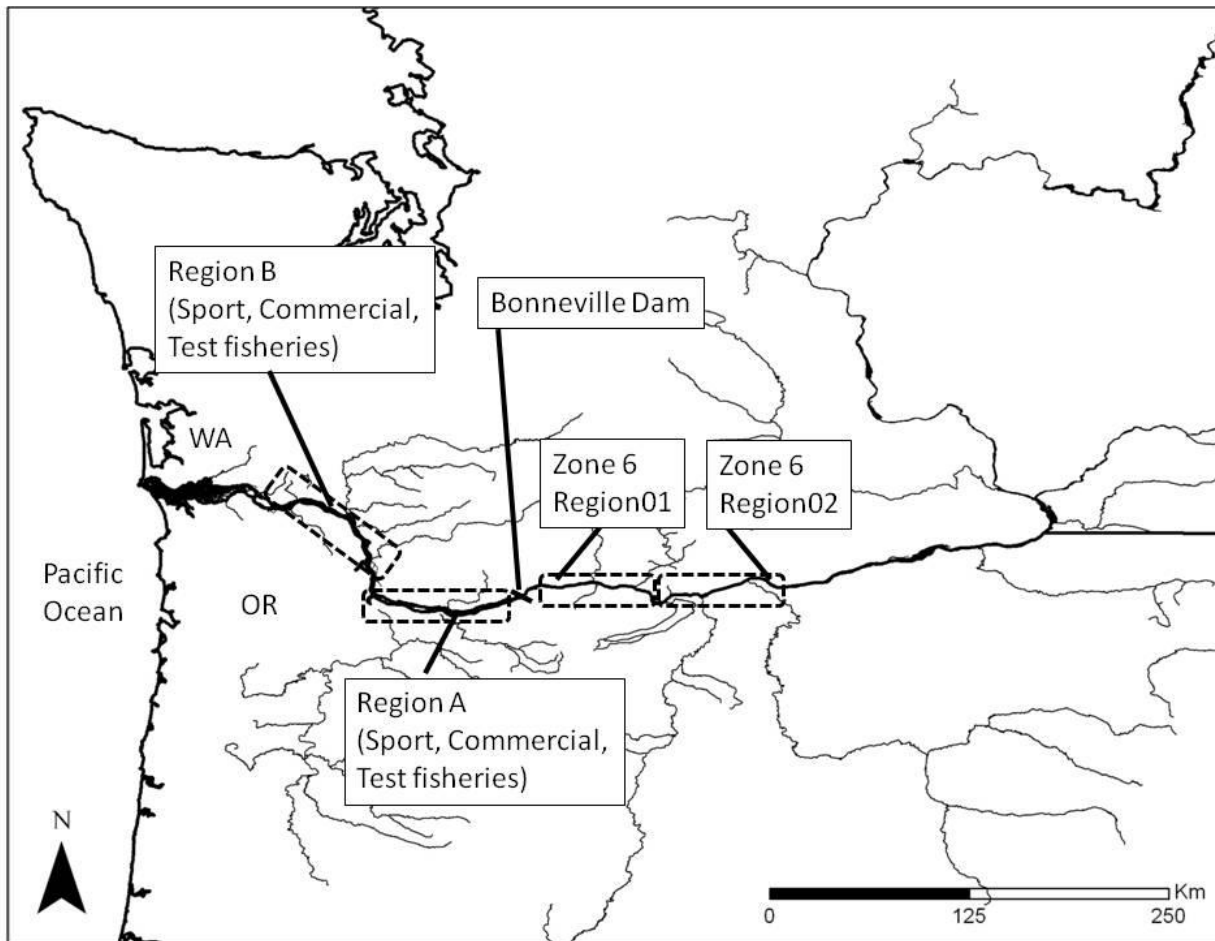


Figure 18. Project scope showing sources of Chinook salmon and Sockeye salmon harvest mixtures that were analyzed using PBT/GSI.

557 **Table 7. Characteristics of Chinook and Sockeye harvest samples by fishery, region, and adipose-clip status by weekly strata in 2020.**

						Spring										Summer						Fall														
						Statistical weeks																														
Chinook Period	Fishery	Region	Clip	Sampled	Genotyped	12	13	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45		
Spring	Sport	A	AD	273	251	7	1	152	53	37		1																								
		B	AD	7	5					1	1	1	1	1																						
Summer	Summer_sport	A	AD	39	36											10	13	9	3	1																
		B	AD	36	31													19	8	3	1															
Fall	Fall_sport	A	AD	195	173																	2	4	7	36	39	35	22	12	8	4	1	3			
			AI	504	468																		2	5	23	121	85	52	59	45	38	12	17	9		
			AD	40	39																		1	2	2	12	20					1		1		
			AI	77	76																		4	2	2	19	36		5		2	2	1	2	1	
	B	AD	264	234																													2			
		AI	560	488																													1	1		
		Fall_Commercial	A	AD	703	664																	71	274	257			32	28			2				
				AI	431	405																		56	106	92			55	77	16		3			
	B	AD	22	20																												7	12	1		
		AI	59	59																											18	27	14			
		Fall_PoundNet (kept)	B	AD	379	350																			33	209	62	19	26	1						
				AI	3	1																				1										
	PoundNet(Released)	B	AD	72	71																				3	36	17	5	9			1				
			AI	465	458																				7	223	115	35	73	5						
Chinook fishery subtotal				4129	3829	7	1	152	53	38	1	2	1	1		10	32	17	6	3	7	145	502	565	824	444	355	368	128	50	64	37	15	1		
Sockeye harvest	Treaty 2019	Zone6	-	98	96										74	22																				
	Pound Net 2019	B	-	844	828						1	15	88	305	333	86																				
	Summer_sport 2020	A&B		330	326							3	77	168	78																					
Sockeye fishery subtotal				1272	1250	0	0	0	0	0	1	18	165	473	485	108	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		

558
559 Note: In this current fiscal year of analysis, we included sockeye fishery collections from 2019 and 2020 because 2019 genotypes were not available in time for last years’ report.

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 19). 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:

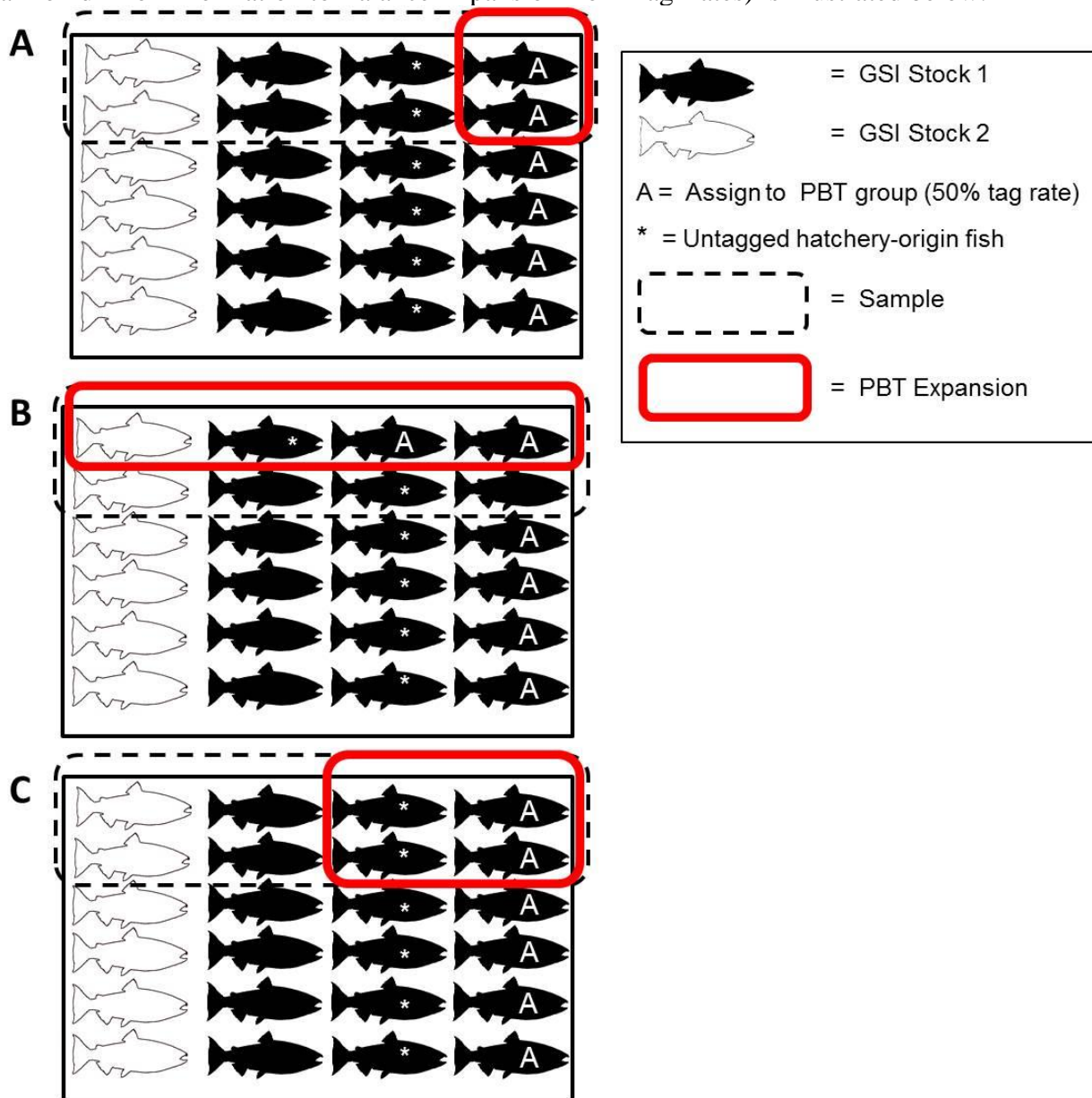


Figure 19. Conceptual illustration of the bias correction the SCOBIDEUX method provides.

In Figure 19, 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 19, 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 19, 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 19): 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 8; Figure 20). 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 21). 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 (Quinault River), 02_LOWCOL (lower Columbia River), 03_SKAMAN (Skamania hatchery releases at three sites in lower Columbia River, Willamette River, and Klickitat River), 04_WILLAM (Willamette River), 05_BWSALM (Big White Salmon River), 06_KLICKR (Klickitat River), 07_MGILCS (middle Columbia River, Grande Ronde River, Imnaha River, lower Snake River, lower Clearwater River, and lower Salmon River), 08_YAKIMA (Yakima River), 09_UPPCOL (upper Columbia River), 10_SFCLWR (South Fork Clearwater River), 11_UPCLWR (upper Clearwater River), 12_SFSALM (South Fork Salmon River), 13_MFSALM (Middle Fork Salmon River), and 14_UPSALM (upper Salmon River) (Figure 22). 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 (Quinault 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, we have observed the panel can improve accuracy for PBT applications.

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 stratified the harvest samples to maximize compatibility with 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 often 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 would be 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 still be wanted for the presence of CWTs. Any “non-random” 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. Specifically, we describe our stratification for each fishery sample in the following section:

The spring test fishery:

This fishery is typically 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%). Due to COVID, the spring test fishery did not occur in 2020, however, we did perform a preliminary analysis of the 2021 test fishery and included them with Bonneville Dam in-season analysis. Similar to the 2019 test fishery (Hess et al. 2021), the CPUE estimated in the 2021 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 continued developing 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. 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. 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.

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. Further, the 2020 sport fishery was almost entirely executed in a single region (Region A, Table 9), which eliminates potential bias from geographic differences across regions.

Table 9. The sample rate and stratification for genetic analysis of the kept adipose clipped adult Chinook salmon from the spring sport fishery in 2020.

	Total Adult Chinook			Sample of Total Adult Chinook Kept			
	Kept	Rel.	Rel. Mortality	regionA	regionB	total	rate
Jan-Feb Total	4	0	0	0	0		
March Total	85	36	4	8	0	8	0.09
April Total	0	0	0	0	0		
May Total	1,373	707	71	218	0	218	0.16
June 1-15							
Total	0	475	48	0	0		
Season Total	1,462	1,218	123	226	0	226	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 2020 only region A 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 typically executes this fishery below Bonneville Dam. However, sampling did not occur in 2020 due to COVID. 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 usually are only possible to obtain from the Yakama Nation harvest and the harvested fish are not possible to report on a weekly basis or by reservoir.

The Summer Chinook salmon sport fishery:

This fishery is similar to the spring sport fishery as it is also mark-selective, and the harvest is estimated and reported for the total lower Columbia mainstem instead of being geographically stratified into regions A and B. In 2020, we obtained nearly equal numbers of samples from regions A and B (Table 10).

Table 10. The sample rate and stratification for genetic analysis of the kept adipose clipped adult Chinook salmon from the summer sport fishery in 2020.

	Total Adult Chinook			Sample of Total Adult Chinook Kept			
	Kept	Rel.	Rel. Mortality	regionA	regionB	total	rate
June 16-21	0	509	51	0	0		
July 1-31	1,191	995	100	35	27	62	0.05
Season Total	1,191	1,504	151	35	27	62	0.05

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 came from both the regions A and B but the reported catch treats these regions as a single area. Monthly strata were pooled to include all fish harvested from June 16 through July 31 as indicated by the outlines in the table.

The fall Non-Treaty commercial fishery:

This fishery occurred in two periods in the fall (early period = weeks 33 – 35) 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). We had sufficient funds to genotype 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. We were also able to utilize the same geographic and temporal stratification of the reported catch in our analysis of the genetic 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 2020.

Harvest estimate	Sample N
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Region	Week	adult+jack	AD	AI	total	rate
A	33	655	64	56	120	0.18
A	34	6094	167	106	273	0.04
A	35	9863	157	92	249	0.03
A	36	0	0	0	0	
A	38	6906	20	55	75	0.01
A	39	6,959	11	77	88	0.01
A	40	706	0	16	16	0.01
A	41	516	0	0	0	
A	42	781	2	3	5	
A	43	234	0	0	0	
B	40	404	4	18	22	0.05
B	41	318	0	0	0	0.11
B	42	125	12	27	39	
B	43	58	1	14	15	
B	44	6	0	0	0	
Total		33625	438	464	902	0.03

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 2020, 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 pooled this sample into a single group 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 2020.

Catch Estimate				Sample of kept			
Month	kept Adult	Released	Release mortality(21%)	AD	AI	Total	rate
Aug	5512	212	45	174	308	482	0.09

Sep	11775	487	102	185	495	680	0.06
Oct	2390	53	11	22	100	122	0.05
Total	19677	752	158	381	903	1284	0.07

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 2020.

Catch Estimate				Sample of kept			
Week	kept Adult	Released	Release mortality 21%	AD	AI	total	rate
33				1	4		
34				2	2		
35				2	1		
36				12	17		
37				19	36		
38							
39					5		
40							
41					2		
42				1	2		
43					1		
44				1	2		
45					1		
Total	3984	274	58	38	73	111	0.03

Note: The sample numbers of the kept Chinook salmon were pooled into a single stratum across weeks 33-45 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 not sampled in 2020 due to COVID, but is typically 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. Tissue collection is typically obtained from the fish identified as bright stocks, and very few tule stocks are sampled. Therefore, genetic analysis is constrained to estimating stock composition within the visually-identified bright harvest. However, in the future it may be possible to utilize genetic analysis as a way to estimate both tule and bright stocks as long as representative sampling of these morphologically distinct stocks can be carried out.

The pound net fishery:

The pound net is a relatively recent gear type that is being developed by the joint states. Similar to 2018 and 2019, the 2020 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 14) and released (Table 15) adult and jack-sized Chinook salmon were stratified by week. In 2020, the pound net samples could be used to test what compositions of fish it were in encountered for both the kept (mark selective) catch as well as a group of released fish that were more representative of the run (Table 15).

Table 14. The sample rate and stratification for genetic analysis of the kept adipose clipped Chinook salmon from the fall pound net fishery in 2020.

2020 Pound Net Trap Kept Catch Summary (all adipose-clipped)						
Week	Chin Adults	Sample		Chin Jacks	Sample	
		Chin Adults	Rate		Chin Jacks	Rate
35	32	32	1.00	1	1	1.00
36	207	207	1.00	2	2	1.00
37	62	62	1.00	0	0	-
38	19	19	1.00	0	0	-
39	26	26				
40	1	1	1.00	0	0	-
	347	347	1.00	3	3	1.00

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. We had to assume in 2020 that all kept fish were sampled in this fishery.

Table 15. The sample rate and stratification for genetic analysis of the released adult and jack Chinook salmon from the fall pound net fishery in 2020.

2020 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
35	-	-	1	6	-	-	-	-	2	1	-	-
36	-	-	13	190	-	-	-	-	23	33	-	-
37	-	-	5	80	-	-	-	-	12	35	-	-
38	-	-	4	27	-	-	-	-	1	8	-	-
39	-	-	1	62	-	-	-	-	8	11	-	-
40	-	-		4	-	-	-	-		1	-	-
41	-	-	1		-	-	-	-			-	-
Fall			25	369					46	89		

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. We had to assume in 2020 that all released fish were sampled in this fishery.

The Sockeye Non-Treaty sport and commercial fishery:

The sport fishery did not occur in 2019. There were 4 sockeye caught in 2019 in the Non-Treaty commercial fishery. In 2020, only the sport fishery occurred, and samples were pooled across months and treated as a single stratum (Table 16).

Table 16. The sample rate and stratification for genetic analysis of the harvested Sockeye salmon from the sport fishery in 2020.

Month	Catch	Sample						total	rate
	estimate	LBC	Osoyoos	Redfish	Wenatchee	Yakima			
May	29		1	0				1	0.03
June	1090		93	2	20	2		117	0.11
June-July	2,069		158	2	40	4		204	0.10
total	3,188	0	252	4	60	6		322	0.10

The Sockeye Treaty commercial fishery:

This 2019 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 into a single stratum representing a total harvest of 1,078 (Table 17).

Table 17. The sample rate and stratification for genetic analysis of the harvested Sockeye salmon from the Treaty fishery in 2019.

Week	Harvest	Sample						total	rate
	estimate	LBC	Osoyoos	Redfish	Wenatchee	Yakima			
25	110							0	0.00
26	445		43		31			74	0.17
27	458		10		12			22	0.05
28	55							0	0.00
29	11							0	0.00
30	0							0	0.00
31	0							0	0.00
total	1,078	0	53		43	0		96	0.09

The Sockeye pound net fishery:

The pound net caught approximately 900 sockeye salmon in 2019 and sampled each week at a high (~90%) rate. These genotypes were not available for our previous report and so were reported here. Stratification of the samples included pooling the first three weeks and treating the subsequent three weeks as separate weekly strata (Table 18).

Table 18. The sample rate and stratification for genetic analysis of the harvested Sockeye salmon from the pound net fishery in 2019.

Week	Catch	Sample						
	estimate	LBC	Osoyoos	Redfish	Wenatchee	Yakima	total	rate
22	1		1				1	1.00
23	16		12		3		15	0.94
24	103		80		8		88	0.85
25	331		262		42	1	305	0.92
26	355		263		67	3	333	0.94
27	90	1	65		19	1	86	0.96
total	896	1	683	0	139	5	828	0.92

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 2021 run year of Chinook salmon.

Comparison of Coded-wire tags and PBT assignments

There were 463 coded-wire tags (CWTs) recovered and identified to hatchery stock and broodyear (BY) among the snouts obtained from the lower river fisheries (Table 19), and 287 of these CWTs also were PBT assigned (62%). Of the 287 fish with both CWT and PBT, there were 277 fish (97%) that appeared concordant with the PBT assignments according to both the hatchery source and the broodyear. There were 10 of the 287 fish with both CWT and PBT that were discordant for either hatchery source (N=2) or both hatchery source and broodyear (N=8). However, in some cases it may be that the CWT readings were swapped; e.g., a pair of Nez Perce and Wells hatchery fish had the same broodyear but had opposing hatchery origins for the same pair of fish ("BY" rows, Table 19). Resolving these swapping errors would increase the concordance rate even higher than 97%.

Table 19. Comparison of coded-wire tags with parentage-based tags that were identified in the lower river fisheries in 2020.

Period	Coded-wire tag		Parentage-based tagging assignment			N
	Hatchery	BY	Hatchery	BY	Status	
Spring	Chief Joseph Hatchery	2016	Chief Joseph Hatchery	2016	Concordant	3
Spring	Clearwater Fish Hatchery	2016	Clearwater Fish Hatchery	2016	Concordant	3
Spring	Dworshak National Fish Hatchery	2016	Dworshak National Fish Hatchery	2016	Concordant	2
Spring	Eastbank Fish Hatchery	2015	Eastbank Fish Hatchery	2015	Concordant	1
Spring	Entiat National Fish Hatchery	2015	Entiat National Fish Hatchery	2015	Concordant	1
Spring	Klickitat Hatchery	2016	Klickitat Hatchery	2016	Concordant	1
Spring	Klickitat Hatchery	2017	Klickitat Hatchery	2017	Concordant	1
Spring	Little White Salmon National Fish Hatchery	2016	Little White Salmon National Fish Hatchery	2016	Concordant	1
Spring	Lookingglass Fish Hatchery	2016	Lookingglass Fish Hatchery	2016	Concordant	4
Spring	Lookingglass Fish Hatchery	2017	Lookingglass Fish Hatchery	2017	Concordant	1
Spring	Warm Springs National Fish Hatchery	2016	Warm Springs National Fish Hatchery	2016	Concordant	1
Spring	Wells Fish Hatchery	2015	Wells Fish Hatchery	2015	Concordant	1
Spring	Winthrop National Fish Hatchery	2016	Winthrop National Fish Hatchery	2016	Concordant	1
Spring	Winthrop National Fish Hatchery	2017	Winthrop National Fish Hatchery	2017	Concordant	1
Spring	Yakima River Roza Dam	2016	Yakima River Roza Dam	2016	Concordant	1
Spring	Yakima River Roza Dam	2017	Yakima River Roza Dam	2017	Concordant	2
Summer	Chief Joseph Hatchery	2016	Chief Joseph Hatchery	2016	Concordant	3
Summer	Chief Joseph Hatchery	2017	Chief Joseph Hatchery	2017	Concordant	1

Summer	Eastbank Fish Hatchery	2015	Eastbank Fish Hatchery	2015	Concordant	1
Summer	Eastbank Fish Hatchery	2016	Eastbank Fish Hatchery	2016	Concordant	7
Summer	Nez Perce Tribal Fish Hatchery	2016	Nez Perce Tribal Fish Hatchery	2016	Concordant	1
Summer	Wells Fish Hatchery	2016	Wells Fish Hatchery	2016	Concordant	10
Fall	Big Creek Hatchery	2016	Big Creek Hatchery	2016	Concordant	1
Fall	Big Creek Hatchery	2017	Big Creek Hatchery	2017	Concordant	8
Fall	Big Creek Hatchery	2018	Big Creek Hatchery	2018	Concordant	1
Fall	Chief Joseph Hatchery	2015	Chief Joseph Hatchery	2015	Concordant	1
Fall	Chief Joseph Hatchery	2016	Chief Joseph Hatchery	2016	Concordant	1
Fall	Cowlitz Salmon Hatchery	2017	Cowlitz Salmon Hatchery	2017	Concordant	1
Fall	Cowlitz Salmon Hatchery	2016	Cowlitz Salmon Hatchery	2016	Concordant	1
Fall	Eastbank Fish Hatchery	2016	Eastbank Fish Hatchery	2016	Concordant	1
Fall	Eastbank Fish Hatchery	2016	Eastbank Fish Hatchery	2016	Concordant	2
Fall	Kalama Falls Hatchery	2017	Kalama Falls Hatchery	2017	Concordant	1
Fall	Kalama Falls Hatchery	2016	Kalama Falls Hatchery	2016	Concordant	3
Fall	Little White Salmon National Fish Hatchery	2016	Little White Salmon National Fish Hatchery	2016	Concordant	5
Fall	Little White Salmon National Fish Hatchery	2017	Little White Salmon National Fish Hatchery	2017	Concordant	2
Fall	Little White Salmon National Fish Hatchery	2015	Little White Salmon National Fish Hatchery	2015	Concordant	3
Fall	Little White Salmon National Fish Hatchery	2016	Little White Salmon National Fish Hatchery	2016	Concordant	10
Fall	Lyons Ferry Fish Hatchery	2015	Lyons Ferry Fish Hatchery	2015	Concordant	2
Fall	Lyons Ferry Fish Hatchery	2016	Lyons Ferry Fish Hatchery	2016	Concordant	7
Fall	Lyons Ferry Fish Hatchery	2017	Lyons Ferry Fish Hatchery	2017	Concordant	6
Fall	Lyons Ferry Fish Hatchery	2018	Lyons Ferry Fish Hatchery	2018	Concordant	1
Fall	Lyons Ferry Fish Hatchery	2015	Lyons Ferry Fish Hatchery	2015	Concordant	2
Fall	Lyons Ferry Fish Hatchery	2016	Lyons Ferry Fish Hatchery	2016	Concordant	18
Fall	Lyons Ferry Fish Hatchery	2017	Lyons Ferry Fish Hatchery	2017	Concordant	8
Fall	Lyons Ferry Fish Hatchery	2018	Lyons Ferry Fish Hatchery	2018	Concordant	1
Fall	Nez Perce Tribal Fish Hatchery	2017	Nez Perce Tribal Fish Hatchery	2017	Concordant	4
Fall	Nez Perce Tribal Fish Hatchery	2016	Nez Perce Tribal Fish Hatchery	2016	Concordant	24

Fall	Nez Perce Tribal Fish Hatchery	2017	Nez Perce Tribal Fish Hatchery	2017	Concordant	3
Fall	Priest Rapids Hatchery	2015	Priest Rapids Hatchery	2015	Concordant	1
Fall	Priest Rapids Hatchery	2016	Priest Rapids Hatchery	2016	Concordant	11
Fall	Priest Rapids Hatchery	2017	Priest Rapids Hatchery	2017	Concordant	6
Fall	Priest Rapids Hatchery	2018	Priest Rapids Hatchery	2018	Concordant	2
Fall	Priest Rapids Hatchery	2016	Priest Rapids Hatchery	2016	Concordant	11
Fall	Priest Rapids Hatchery	2017	Priest Rapids Hatchery	2017	Concordant	3
Fall	Spring Creek National Fish Hatchery	2017	Spring Creek National Fish Hatchery	2017	Concordant	3
Fall	Spring Creek National Fish Hatchery	2017	Spring Creek National Fish Hatchery	2017	Concordant	26
Fall	Spring Creek National Fish Hatchery	2018	Spring Creek National Fish Hatchery	2018	Concordant	3
Fall	Washougal Fish Hatchery	2016	Washougal Fish Hatchery	2016	Concordant	3
Fall	Washougal Fish Hatchery	2016	Washougal Fish Hatchery	2016	Concordant	1
Spring	Clearwater Fish Hatchery	2016	Dworshak National Fish Hatchery	2016	Concordant	2
Spring	Nez Perce Tribal Fish Hatchery	2016	Nez Perce	2016	Concordant	1
Summer	Entiat National Fish Hatchery	2016	Wells Fish Hatchery	2016	Concordant	1
Fall	Bonneville Hatchery	2017	Ringold Springs State Hatchery	2017	Concordant	1
Fall	Bonneville Hatchery	2018	Priest Rapids Hatchery	2018	Concordant	1
Fall	Bonneville Hatchery	2015	Little White Salmon National Fish Hatchery	2015	Concordant	1
Fall	Klickitat Fall	2016	Little White Salmon National Fish Hatchery	2016	Concordant	5
Fall	Klickitat Fall	2015	Little White Salmon National Fish Hatchery	2015	Concordant	4
Fall	Klickitat Fall	2016	Little White Salmon National Fish Hatchery	2016	Concordant	11
Fall	Klickitat Fall	2017	Little White Salmon National Fish Hatchery	2017	Concordant	1
Fall	Ringold Springs State Hatchery	2016	Priest Rapids Hatchery	2016	Concordant	2
Fall	Ringold Springs State Hatchery	2017	Priest Rapids Hatchery	2017	Concordant	2
Fall	Ringold Springs State Hatchery	2016	Priest Rapids Hatchery	2016	Concordant	4
Fall	Ringold Springs State Hatchery	2017	Priest Rapids Hatchery	2017	Concordant	1
Fall	Umatilla Fish Hatchery	2017	Little White Salmon National Fish Hatchery	2017	Concordant	3

Fall	Umatilla Fish Hatchery	2016	Little White Salmon National Fish Hatchery	2016	Concordant	1
Fall	Umatilla Fish Hatchery	2016	Ringold Springs State Hatchery	2016	Concordant	1
Summer	Nez Perce Tribal Fish Hatchery	2016	Wells Fish Hatchery	2016	BY*	1
Summer	Wells Fish Hatchery	2016	Nez Perce Tribal Fish Hatchery	2016	BY*	1
Spring	Rapid River Fish Hatchery	2017	Carson National Fish Hatchery	2016	Discordant	1
Fall	Big Creek Hatchery	2017	Little White Salmon National Fish Hatchery	2016	Discordant	1
Fall	Bonneville Hatchery	2017	Little White Salmon National Fish Hatchery	2016	Discordant	1
Fall	Klickitat Fall	2016	Priest Rapids Hatchery	2017	Discordant	1
Fall	Little White Salmon National Fish Hatchery	2016	Priest Rapids Hatchery	2017	Discordant	1
Fall	Nez Perce Tribal Fish Hatchery	2015	Priest Rapids Hatchery	2016	Discordant	1
Fall	Priest Rapids Hatchery	2017	Little White Salmon National Fish Hatchery	2016	Discordant	1
Fall	Priest Rapids Hatchery	2017	Lyons Ferry Fish Hatchery	2016	Discordant	1
Spring	Chief Joseph Hatchery	2017	#N/A	NA	failed	1
Spring	Leavenworth National Fish Hatchery	2015	#N/A	NA	failed	1
Spring	McCall Fish Hatchery	2015	#N/A	NA	failed	1
Spring	Winthrop National Fish Hatchery	2016	#N/A	NA	failed	1
Spring	Yakima River Roza Dam	2015	#N/A	NA	failed	1
Summer	Chief Joseph Hatchery	2016	#N/A	NA	failed	1
Summer	Eastbank Fish Hatchery	2016	#N/A	NA	failed	1
Summer	Wells Fish Hatchery	2016	#N/A	NA	failed	2
Fall	Chief Joseph Hatchery	2015	#N/A	NA	failed	1
Fall	Chief Joseph Hatchery	2017	#N/A	NA	failed	1
Fall	Eastbank Fish Hatchery	2017	#N/A	NA	failed	1
Fall	Klickitat Fall	2016	#N/A	NA	failed	1
Fall	Klickitat Fall	2018	#N/A	NA	failed	1
Fall	Lyons Ferry Fish Hatchery	2016	#N/A	NA	failed	8
Fall	Lyons Ferry Fish Hatchery	2017	#N/A	NA	failed	8
Fall	Lyons Ferry Fish Hatchery	2018	#N/A	NA	failed	2
Fall	Nez Perce Tribal Fish Hatchery	2016	#N/A	NA	failed	3

Fall	Nez Perce Tribal Fish Hatchery	2018	#N/A	NA	failed	3
Fall	Priest Rapids Hatchery	2016	#N/A	NA	failed	2
Fall	Priest Rapids Hatchery	2017	#N/A	NA	failed	5
Fall	Ringold Springs State Hatchery	2017	#N/A	NA	failed	2
Fall	Sandy Hatchery	2016	#N/A	NA	duplicate	1
Spring	Leavenworth National Fish Hatchery	2017	#N/A	NA	Unassigned	1
Spring	McKenzie River Hatchery	2016	#N/A	NA	Unassigned	1
Spring	Willamette	2016	#N/A	NA	Unassigned	1
Spring	Winthrop National Fish Hatchery	2016	#N/A	NA	Unassigned	4
Spring	Winthrop National Fish Hatchery	2017	#N/A	NA	Unassigned	1
Spring	Yakima River Roza Dam	2016	#N/A	NA	Unassigned	1
Summer	Sandy Hatchery	2016	#N/A	NA	Unassigned	6
Summer	Wells Hatchery	2015	#N/A	NA	Unassigned	1
Fall	Big Creek Hatchery	2016	#N/A	NA	Unassigned	1
Fall	Big Creek Hatchery	2017	#N/A	NA	Unassigned	2
Fall	Big Creek Hatchery	2018	#N/A	NA	Unassigned	1
Fall	Bonneville Hatchery	2017	#N/A	NA	Unassigned	38
Fall	Bonneville Hatchery	2018	#N/A	NA	Unassigned	1
Fall	Chief Joseph Hatchery	2015	#N/A	NA	Unassigned	1
Fall	Hanford Reach	2015	#N/A	NA	Unassigned	1
Fall	Hanford Reach	2016	#N/A	NA	Unassigned	1
Fall	Klickitat Fall	2016	#N/A	NA	Unassigned	2
Fall	Lewis River Hatchery	2016	#N/A	NA	Unassigned	3
Fall	Little White Salmon National Fish Hatchery	2017	#N/A	NA	Unassigned	1
Fall	Lyons Ferry Fish Hatchery	2016	#N/A	NA	Unassigned	6
Fall	Lyons Ferry Fish Hatchery	2017	#N/A	NA	Unassigned	4
Fall	Lyons Ferry Fish Hatchery	2018	#N/A	NA	Unassigned	2
Fall	Nez Perce Tribal Fish Hatchery	2017	#N/A	NA	Unassigned	3
Fall	North Toutle Hatchery	2017	#N/A	NA	Unassigned	1
Fall	Priest Rapids Hatchery	2016	#N/A	NA	Unassigned	1
Fall	Priest Rapids Hatchery	2017	#N/A	NA	Unassigned	2
Fall	Ringold Springs State Hatchery	2017	#N/A	NA	Unassigned	1

Fall	Sandy Hatchery	2016	#N/A	NA	Unassigned	13
Fall	Sandy Hatchery	2017	#N/A	NA	Unassigned	1
Fall	Spring Creek National Fish Hatchery	2016	#N/A	NA	Unassigned	1
Fall	Spring Creek National Fish Hatchery	2017	#N/A	NA	Unassigned	19
Fall	Spring Creek National Fish Hatchery	2018	#N/A	NA	Unassigned	1
Fall	Umatilla Fish Hatchery	2016	#N/A	NA	Unassigned	1
Fall	Washougal Fish Hatchery	2016	#N/A	NA	Unassigned	3
Fall	Washougal Fish Hatchery	2017	#N/A	NA	Unassigned	1
				Total	100.0%	463
				Concordant	59.8%	277
				BY_Concordant	0.4%	2
				Discordant	1.7%	8
				Failed	10.4%	48
				PBT_Unassigned	27.6%	128

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Note: *Indicates that only the BY was concordant but these two samples in particular appear to have been switched.

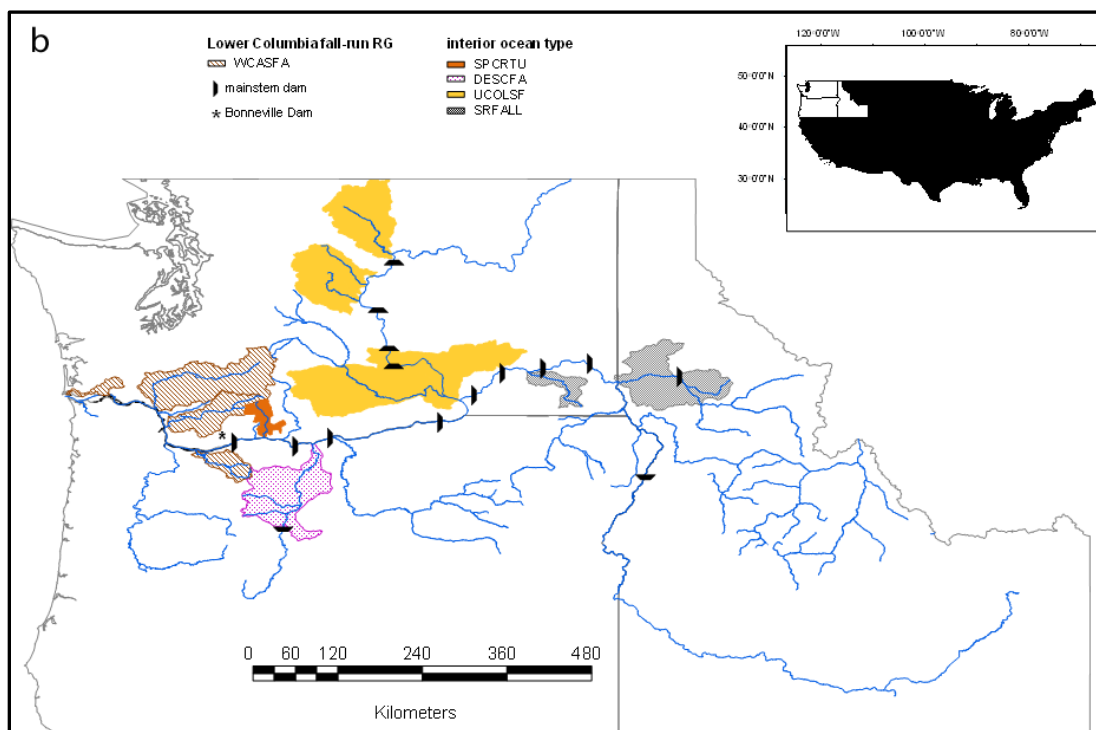
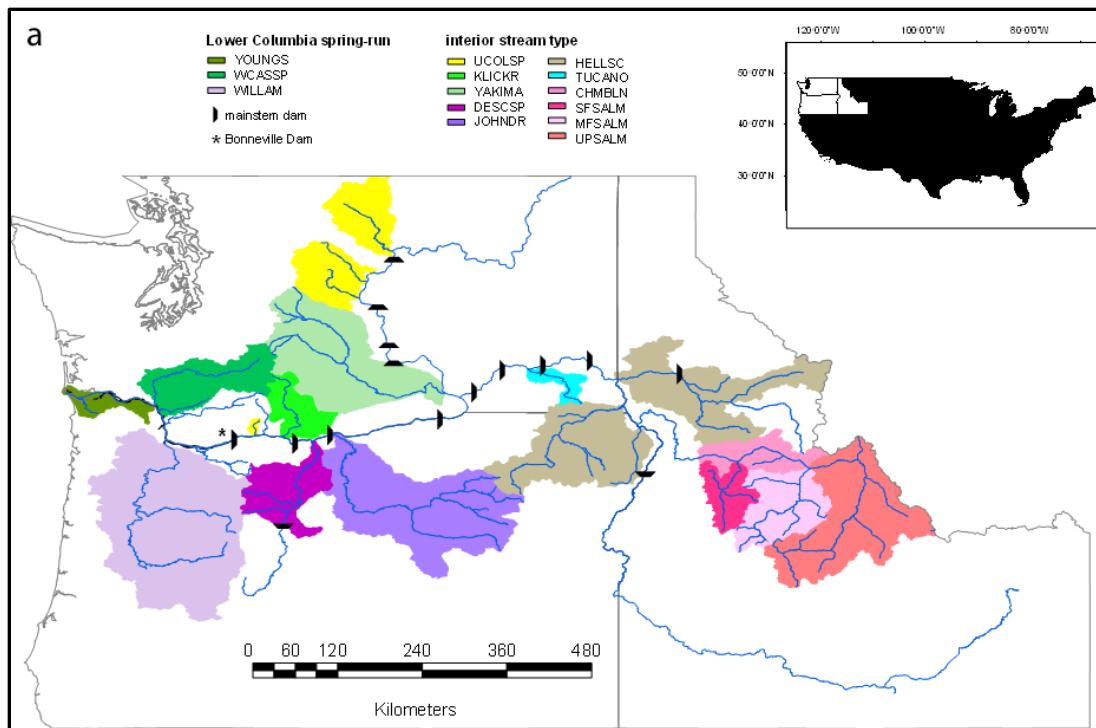
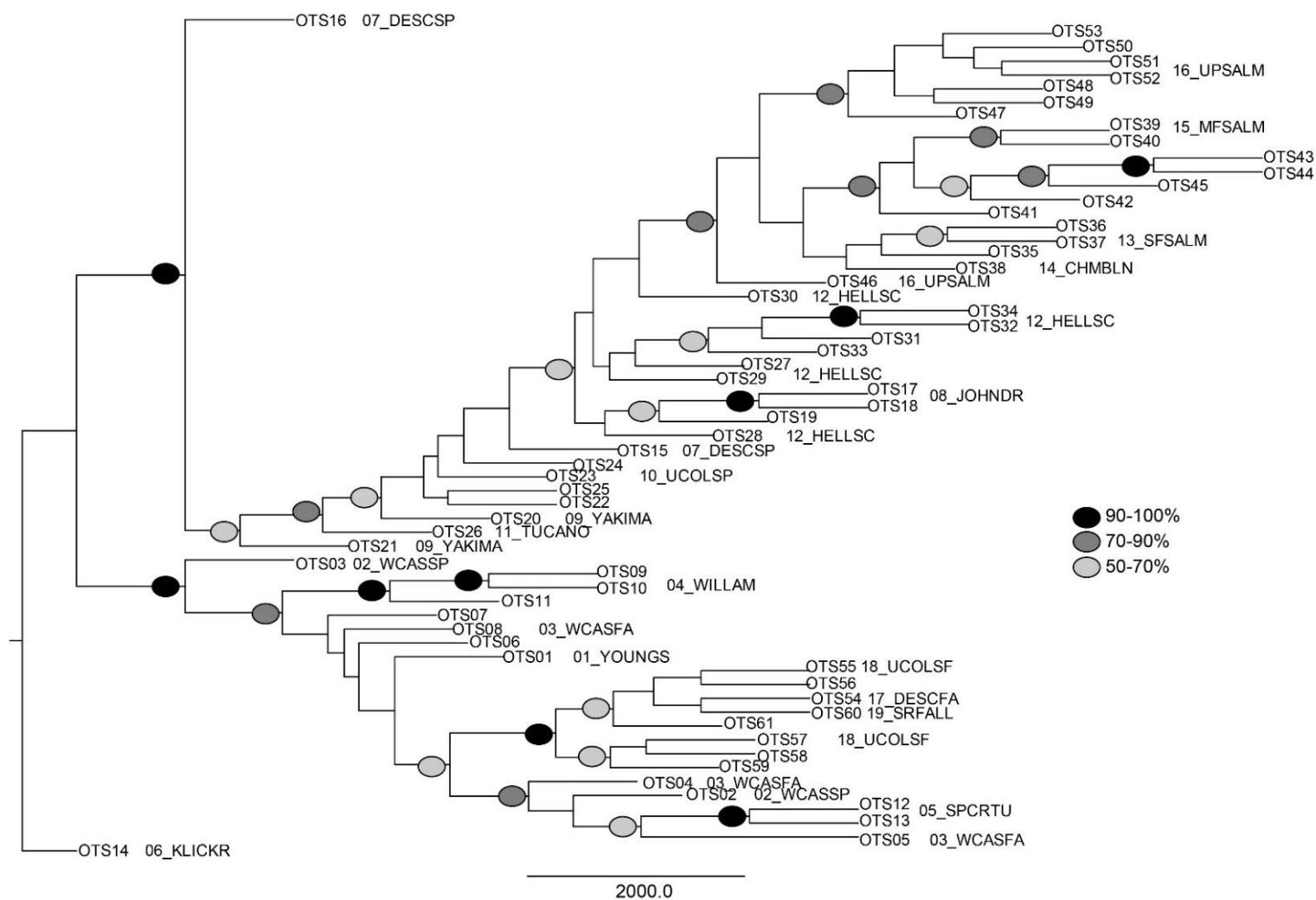


Figure 20. Map of Chinook salmon GSI reporting groups for a) Lower Columbia (LC) and interior stream type (ST) lineage, and b) interior ocean type (OT) lineage.



915 **Figure 21. Neighbor-joining tree of Chinook salmon baseline populations using Nei's 1972 genetic distance of 179 SNP loci.**

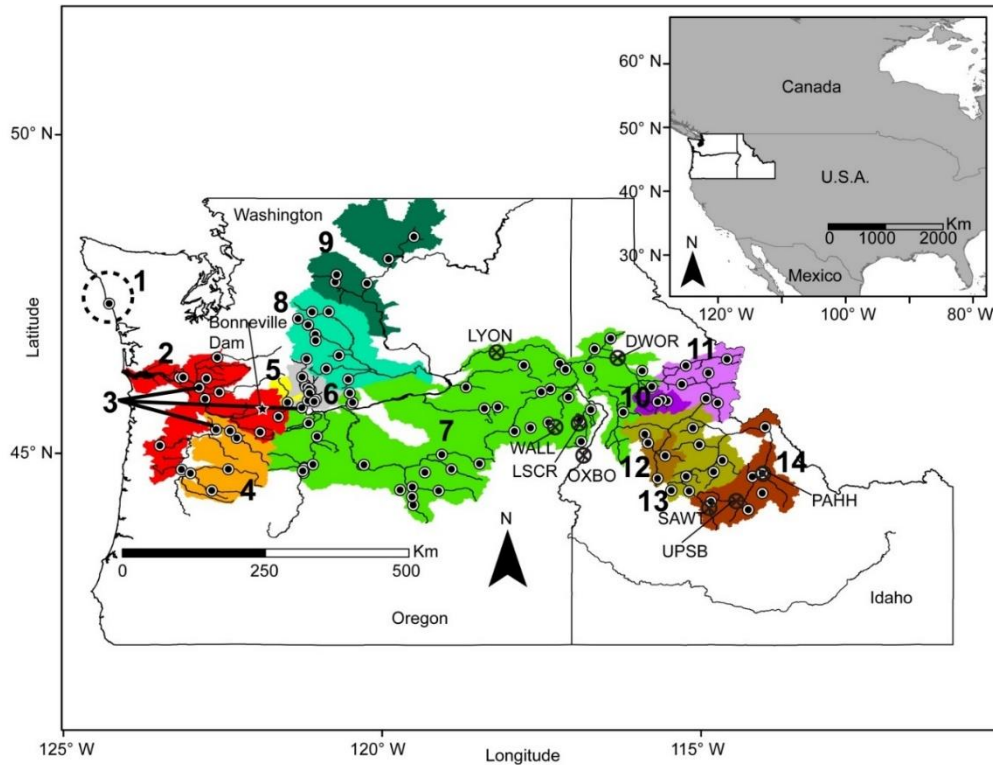


Figure 22. Geographic distribution of collections represented in the Columbia River steelhead GSI and PBT genetic baselines.

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 22). In Figure 22, 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, Figure 22) categorized into reporting groups. The PBT baseline is indicated as 8 stocks (crossed circles, Figure 22) 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, Figure 22) is the site where fish were non-lethally sampled for the mixed-stock analysis.

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 23): 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), 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 20).

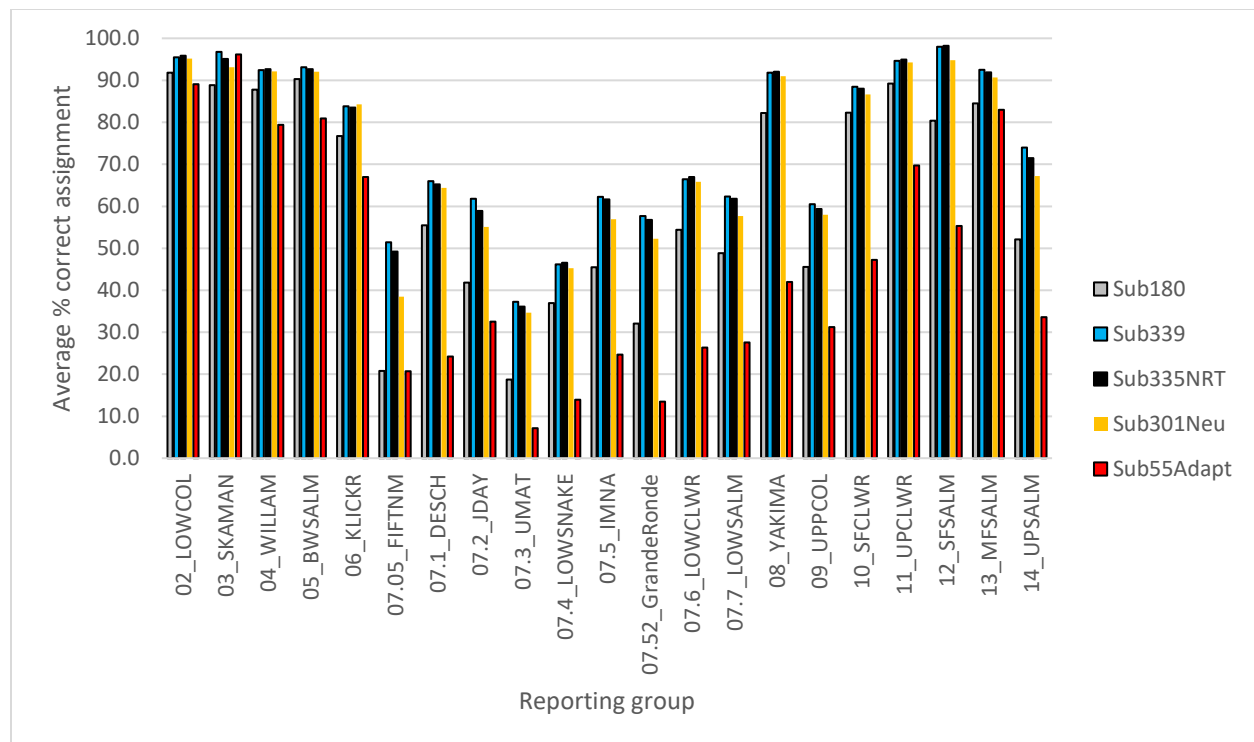


Figure 23. Proportion of steelhead in leave-one-out tests that assigned correctly for each reporting group by lineage using the following subsets of SNPs: 180 SNPs from baseline v3.3 (“Sub180”), 339 SNPs that include putatively neutral and adaptive loci (“Sub339”), 335 SNPs that exclude the run timing candidate SNPs (“Sub335NRT”), 301 SNPs that were putatively neutral (“Sub301Neu”), and 55 SNPs that were putatively adaptive (“Sub55Adapt”).

975 **Table 20. Comparison of PBT expected reporting groups versus the observed reporting groups using 177 SNPs (baseline 3.3)**
 976 **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%

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 979 *Steelhead 335 SNP panel for PBT applications*

980 Despite having limited utility for GSI applications on a Columbia River Basin wide scale, the expanded set of SNP markers
 981 available for steelhead analysis can be extremely useful for increasing the power and accuracy of PBT. We examined a dataset of
 982 steelhead passing Bonneville Dam in 2020 and compared assignments based on the original panel of 92 SNPs to assignments based on
 983 the new expanded panel of 335 SNPs (Table 21). There were a total of 800 PBT assignments that were perfectly concordant between
 984 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
 985 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
 986 we use to accept a PBT assignment, but the 335 SNP panel LOD score was much higher. The False Discovery Rate was also much
 987 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
 988 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
 989 for failing to meet these thresholds using the smaller panel. In fact, there were 20 fish that were only assigned using the 335 SNP
 990 panel and would have escaped detection with the 92 SNP panel. Further, there were 32 assignments that were concordant to the PBT
 991 broodstock, however, either the mother or father or both parents were discordant across the assignments generated by these two
 992 panels. The 335 PBT panel will be more likely to avoid errors that occur when hatchery broodstock have a high level of relatedness
 993 which is the case with steelhead hatcheries. In conclusion, we feel encouraged by these results and will be adopting the larger number
 994 of SNP markers for PBT applications in steelhead from now on.

995

996 **Table 21.** Comparison of PBT assignments using the new panel of 335 SNPs versus the 92 SNP panel for steelhead passing
 997 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 22). 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 increased as a result of the additional genotypes and filtering step changes and are noted in green in Table 22. 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 expansion of the parent baseline may be useful when we re-analyze previous years.

Table 22. 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	1171	1244	5196	40.0%	42.2%	0.2%
2014	10000	2678	2576	12678	12576	2948	3146	12678	41.1%	43.5%	0.5%
2015	10000	342	95	10342	10095	706	1182	10342	13.2%	21.6%	0.2%
2016	10000	3742	3949	13742	13949	4449	4245	13949	53.6%	51.6%	2.0%
2017	1000	372	137	1372	1137	427	422	1372	52.6%	52.1%	0.5%
2018	4700	456	201	5156	4901	1379	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 calculated using the Max YR as the denominator. When cross information and the gender of the broodstock samples is unknown, then the tag rate for single parentage is : $1-(f_t)^2$, where f_t is the fraction of the total broodstock not genotyped.

1018 *Parentage based tagging assignments of Chinook salmon in harvest mixtures*

1019 A summary of the Chinook harvest samples that were genotyped (derived from Table 7)
1020 is presented in Table 23. Of the 4,129 harvest Chinook analyzed, there were 1,789 hatchery-
1021 origin individuals that could be confidently PBT assigned to 95 hatchery broodstock sources
1022 (i.e., 18 Lower Columbia, 1 Willamette, 30 Snake River, and 46 Columbia River hatchery
1023 broodstocks) spawned in 2015-2018. The majority of PBT assigned individuals were from the
1024 2016 brood year (i.e., 4-years-old).

1025 **Table 23. Summary of the Chinook salmon harvest samples by fishery, region, and fin clip**
1026 **in 2020.**

Fishery	Region	Ad Clip	Period			Analysis					
			Spring	Summer	Fall	GSI	PBT	Dup.	failed	Total	%PBT
Bon20	BONAFF	AD	309	421	733	165	1264	2	18	1970	88.5%
		AI	258	342	1372	1446	493	4	21	1702	25.4%
Sport	A	AD	273			26	223	2	22	273	89.6%
	B	AD	7				5		2	7	100.0%
Sport	A	AD		39		6	30		3	39	83.3%
	B	AD		36		11	20		5	36	64.5%
Sport	A	AD			195	48	125		22	195	72.3%
		AI			504	368	99	2	35	504	21.2%
Commercial	Above Bonneville	AD			40	8	31		1	40	79.5%
		AI			77	47	29		1	77	38.2%
	B	AD			264	58	176		30	264	75.2%
		AI			560	376	112	1	71	560	23.0%
	A	AD			703	237	427	3	36	703	64.3%
		AI			431	330	76		25	431	18.7%
	B	AD			22	4	16		2	22	80.0%
		AI			59	55	4			59	6.8%
Pound	B	AD			379	114	235	3	27	379	67.3%
		AI			3	1			2	3	0.0%
Research	B	AD			72	13	58		1	72	81.7%
		AI			465	334	123	1	7	465	26.9%
Grand Total			847	838	5879	3647	3546	18	331	7801	49.3%

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 = 64% – 100%, Table 23). The fishery(s) with the minimum and maximum assigned adipose-clipped Chinook salmon was the Non-Treaty fall commercial fishery in region A and the Non-Treaty Spring Sport fishery in region B, respectively. Among the adipose-intact fish, the average assignment via PBT was expectedly lower (average = 19%, range = 0% – 38%; Table 23). Among the fisheries with adipose-intact fish, the minimum and maximum PBT-assigned Chinook salmon was observed in the pound net fishery in region B and the Non-Treaty fall sport fishery in Bonneville Pool, respectively.

The test fishery in the Chinook Salmon Spring Management Period of 2021

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. 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 24**Error! Reference source not found.**). Further, the correlation of CPUE for upriver stocks appeared to improve when genetic data was used to identify upriver stocks compared to using Visual Stock ID exclusively (Figure 24). 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.

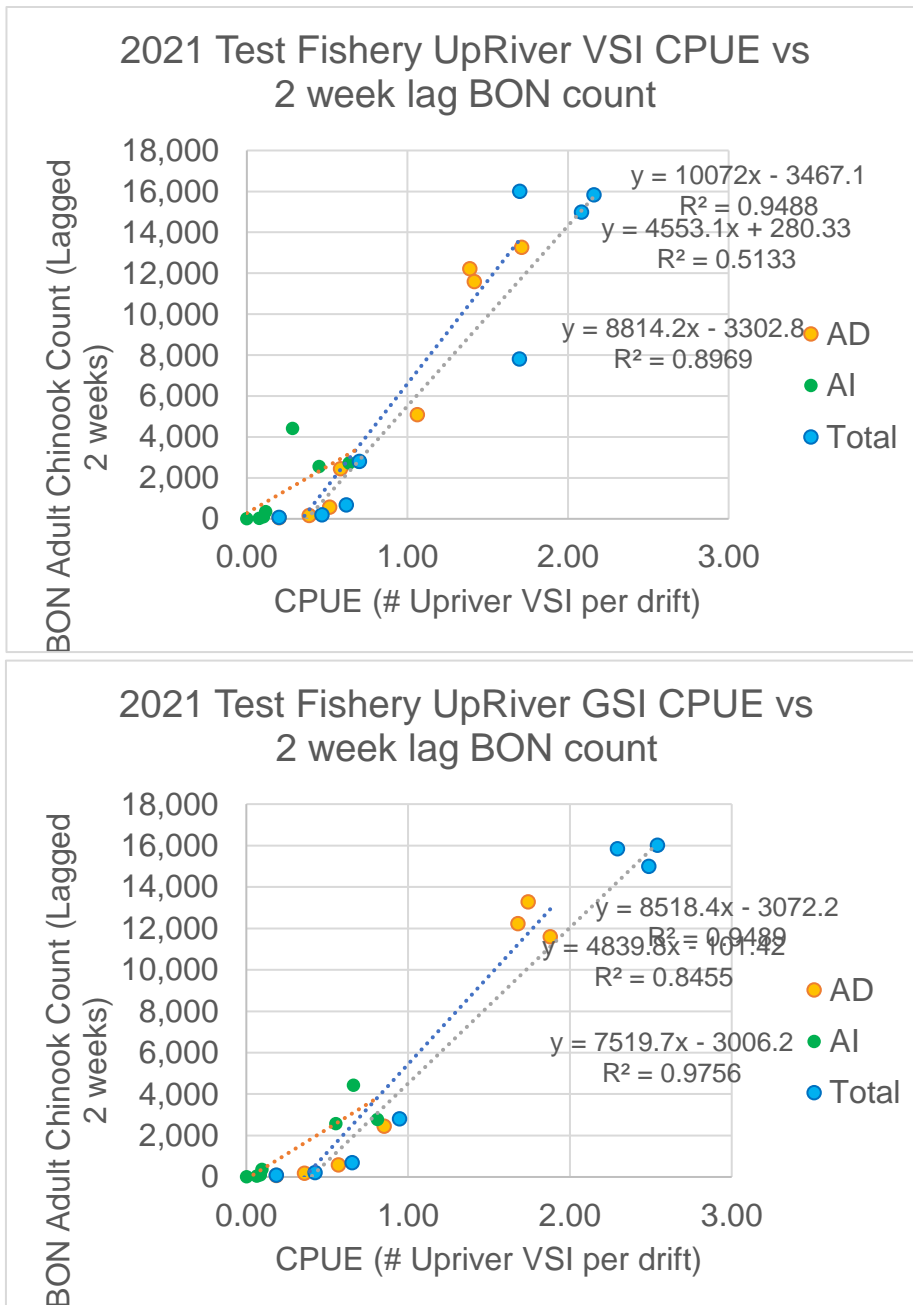


Figure 24. The relationship between the test fishery upriver Chinook Salmon CPUE and weekly fish counts at Bonneville Dam in 2021 with 2 week lag using VSI (top) and GSI (bottom) data.

The Non-Treaty sport fishery in the Chinook Salmon Spring Management Period of 2020
 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 2020 in units of reported catch.

Run type	Reporting Group Code	Hatchery origin- Clipped	
		Estimated abundance	
		Mean	95% CI
Spring	01_YOUNGS		
Spring	02_WCASSP	63	34 – 97
Fall	03_WCASFA		
Spring	04_WILLAM	27	10 – 38
Fall	05_SPCRTU		
Spring	06_KLICKR	38	13 – 87
Spring	07_DESCSP	34	13 – 51
Spring	08_JOHNDR		
Spring	09_YAKIMA	30	12 – 55
Spring	10_UCOLSP	161	112 – 248
Spring	11_TUCANO		
Spring/Summer	12_HELLSC	761	638 – 828
Spring/Summer	13_SFSALM	42	11 – 65
Spring/Summer	14_CHMBLN		
Spring/Summer	15_MFSALM		
Spring/Summer	16_UPSALM	121	84 – 159
Fall	17_DESCFA		
Summer/Fall	18_UCOLSF	34	25 – 47
Fall	19_SRFALL		
Spring	20_BONPOOLSP	144	104 – 184
Spring	21_UMATILLASP	6	0 – 12
Fall	22_BONPOOLFA		
Fall	23_UMATILLAFA		
	Total	1,462	

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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 2020 in units of reported catch.

Spring Sport Fishery 2020

Kept Adult Chinook AD

Expected Run Time	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	GSI RepGrp
01Spring	Kalama Falls Hatchery	OtsKALA_seg_sp16	2016	9	0 – 26	0.6%	02_WCASSP
01Spring	Parkdale Fish Facility	OtsPARK_seg_sp16	2016	54	27 – 87	3.7%	02_WCASSP
01Spring	Klickitat Hatchery	OtsKLIC_seg_sp16	2016	32	13 – 57	2.2%	06_KLICKR
01Spring	Klickitat Hatchery	OtsKLIC_seg_sp17	2017	7	0 – 20	0.4%	06_KLICKR
01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp16	2016	19	6 – 38	1.3%	07_DESCSP
01Spring	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp16	2016	6	0 – 19	0.4%	07_DESCSP
01Spring	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp17	2017	8	0 – 24	0.5%	07_DESCSP
01Spring	Yakima River Roza Dam	OtsYRRD_int_sp16	2016	18	0 – 44	1.2%	09_YAKIMA
01Spring	Chief Joseph Hatchery	OtsCHJO_seg_sp16	2016	33	13 – 59	2.2%	10_UCOLSP
01Spring	Eastbank Fish Hatchery	OtsEAST_seg_sp16	2016	14	0 – 28	1.0%	10_UCOLSP
01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp16	2016	57	32 – 89	3.9%	10_UCOLSP
01Spring	Winthrop National Fish Hatchery	OtsWINT_seg_sp16	2016	19	0 – 38	1.3%	10_UCOLSP
01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp16	2016	123	77 – 168	8.4%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp16	2016	161	116 – 213	11.0%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsLOOK_seg_sp15	2015	26	7 – 54	1.8%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsLOOK_seg_sp16	2016	64	28 – 100	4.4%	12_HELLSC
01Spring	Nez Perce	OtsNPFH_seg_sp16	2016	6	0 – 19	0.4%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp15	2015	24	0 – 47	1.6%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp16	2016	301	237 – 368	20.6%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp17	2017	13	0 – 32	0.9%	12_HELLSC
01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp16	2016	76	44 – 114	5.2%	20_BONPOOLSE
01Spring	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp16	2016	68	34 – 102	4.7%	20_BONPOOLSE
01Spring	Umatilla Fish Hatchery	OtsUMAT_seg_sp16	2016	6	0 – 19	0.4%	21_UMATILLAS
02Spring/Summer	Lookingglass Fish Hatchery	OtsIMNW_seg_ss16	2016	26	6 – 51	1.8%	12_HELLSC

02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss15	2015	26	7 – 46	1.8%	13_SFSALM
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss16	2016	6	0 – 19	0.4%	13_SFSALM
02Spring/Summer	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss15	2015	7	0 – 20	0.5%	16_UPSALM
02Spring/Summer	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss16	2016	19	0 – 38	1.3%	16_UPSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss15	2015	6	0 – 19	0.4%	16_UPSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss16	2016	83	51 – 121	5.7%	16_UPSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss17	2017	6	0 – 19	0.4%	16_UPSALM
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su15	2015	6	0 – 19	0.4%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su16	2016	6	0 – 19	0.4%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su15	2015	9	0 – 26	0.6%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su15	2015	13	0 – 32	0.9%	18_UCOLSF
#N/A	#N/A	Unassigned	#N/A	105	55 – 159	7.2%	#N/A
		TOTAL		1,462		100.0%	

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1081 *The Non-Treaty sport fishery in the Chinook Salmon Summer Management Period of 2020*

1082 In 2020, there was a summer Non-Treaty sport fishery that was executed but no summer Non-Treaty commercial fishery. We
 1083 reported summer sport fishery results for reporting group level stock composition (Table 26) and the hatchery broodstock composition
 1084 (Table 27) of the kept fish (clipped hatchery-origin fish).

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1087 **Table 26. Summary of the stock composition at the reporting group level of the kept summer Chinook salmon in the**
 1088 **Non-Treaty sport fishery of 2020 in units of reported catch.**

Run type	Reporting Group Code	Hatchery origin- Clipped	
		Estimated abundance	
		Mean	95% CI
Spring	01_YOUNGS		
Spring	02_WCASSP	19	0 – 54
Fall	03_WCASFA		
Spring	04_WILLAM	284	226 – 395
Fall	05_SPCRTU		
Spring	06_KLICKR		
Spring	07_DESCSP		
Spring	08_JOHNDR		
Spring	09_YAKIMA		
Spring	10_UCOLSP		
Spring	11_TUCANO		
Spring/Summer	12_HELLSC		
Spring/Summer	13_SFSALM		
Spring/Summer	14_CHMBLN		
Spring/Summer	15_MFSALM		
Spring/Summer	16_UPSALM		
Fall	17_DESCFA		
Summer/Fall	18_UCOLSF	850	699 – 942

Fall	19_SRFALL	39	19 – 96
Spring	20_BONPOOLSP		
Spring	21_UMATILLASP		
Fall	22_BONPOOLFA		
Fall	23_UMATILLAFA		
	Total	1,191	

Table 27. Summary of the stock composition at the broodstock level of the kept adult summer Chinook salmon in the Non-Treaty sport fishery of 2020 in units of reported catch.

Summer Sport Fishery 2020				Kept Adult Chinook AD			
Expected Run Time	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	GSI RepGrp
01Spring	South Santiam Hatchery	OtsSSAN_seg_sp16	2016	20	0 – 60	1.7%	04_WILLAM
03Summer	Chief Joseph Hatchery	OtsCHJO_int_su15	2015	21	0 – 64	1.8%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su15	2015	20	0 – 59	1.7%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su16	2016	95	38 – 172	8.0%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCHJO_int_su16	2016	96	38 – 172	8.0%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCHJO_int_su17	2017	25	0 – 75	2.1%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su17	2017	21	0 – 63	1.8%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su15	2015	38	0 – 76	3.2%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su16	2016	231	135 – 346	19.4%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su15	2015	26	0 – 78	2.2%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su16	2016	38	0 – 76	3.2%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su16	2016	227	132 – 321	19.0%	18_UCOLSF
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa16	2016	39	0 – 97	3.3%	19_SRFALL
#N/A	#N/A	Unassigned	#N/A	295	187 – 412	24.8%	#N/A
TOTAL				1,191		100.0%	

1095 *The Non-Treaty pound net fishery in the Chinook Salmon Fall Management Period of 2020*

1096 For the 2020 fall period, the pound net fishery sampled a total of 382 kept Chinook salmon (all but 3 were clipped hatchery-
 1097 origin, Table 7), which were comprised of 46% lower river stocks (03_WCASFA), and 54% upriver stocks (24% Spring Creek tules
 1098 and the remaining were upriver brights). Among the natural-origin released stocks, 35% were lower river and the rest were upriver
 1099 stocks (Table 28). The hatchery-origin fish were identified by broodstock (Table 29), and the lower river stocks were found to be
 1100 comprised of Big Creek, Cowlitz Salmon Hatchery, Kalama Falls Hatchery, North Toutle Hatchery, and Washougal Fish Hatchery.

1101
 1102 **Table 28. Summary of the genetic stock assignments at the reporting group level of the fall pound net fishery in 2020 for all**
 1103 **sampled fish that were kept and released.**
 1104

Period	Reporting Group Code	KEPT			RELEASED					
		Adult		Jack	Adult			Jack		
		H	W	H	H	HNC	W	H	HNC	W
		Est.	Est.	Est.	Est.	Est.	Est.	Est.	Est.	Est.
Fall	01_YOUNGS						3			5
	03_WCASFA	159	1		12	2	95	16	3	15
	05_SPCRTU	82		3	4	4	8	5		2
	17_DESCFA						6	1		9
	18_UCOLSF	48			5	61	134	17	14	30
	19_SRFALL	11				5	23	4	4	4
	22_BONPOOLFA	46			4	27		1	3	
	23_UMATILLFA							2		
	Total	346	1	3	25	99	269	46	24	65

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Table 29. Summary of the genetic assignments for kept and released Chinook salmon at the broodstock level of the fall pound net fishery of 2020.

						KEPT		RELEASED				
						Adult	Jack	Adult		Jack		
Period	Run	Hatchery	Broodstock	Broodyear	GSI RepGrp	H	H	H	HNC	H	HNC	Total
Fall	04Fall	Big Creek Hatchery	OtsBIGC_seg_fa16	2016	03_WCASFA	3						3
	04Fall	Big Creek Hatchery	OtsBIGC_seg_fa17	2017	03_WCASFA	44		2				46
	04Fall	Big Creek Hatchery	OtsBIGC_seg_fa18	2018	03_WCASFA			5	1	11	3	20
	04Fall	Cowlitz Salmon Hatchery	OtsCOWL_seg_fa16	2016	03_WCASFA	1						1
	04Fall	Cowlitz Salmon Hatchery	OtsCOWL_seg_fa17	2017	03_WCASFA	2		1				3
	04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa16	2016	03_WCASFA	17						17
	04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa17	2017	03_WCASFA	12				2		14
	04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa18	2018	03_WCASFA					1		1
	04Fall	North Toutle Hatchery	OtsNTOU_seg_fa16	2016	03_WCASFA	6						6
	04Fall	North Toutle Hatchery	OtsNTOU_seg_fa17	2017	03_WCASFA			1				1
	04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa16	2016	03_WCASFA	25			1			26
	04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa17	2017	03_WCASFA	1		2				3
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa16	2016	05_SPCRTU	4						4
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa17	2017	05_SPCRTU	26		1	4			31

	04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa18	2018	05_SPCRTU		1	1		3		5
	04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa15	2015	18_UCOLSF	1						1
	04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa16	2016	18_UCOLSF	12			22			34
	04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa17	2017	18_UCOLSF	24		5	38	4	1	72
	04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa18	2018	18_UCOLSF					10	13	23
	04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa17	2017	18_UCOLSF	1						1
	04Fall	Yakima Nation Prosser Hatchery	OtsPROS_seg_fa17	2017	18_UCOLSF				1			1
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa15	2015	19_SRFALL	1						1
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa16	2016	19_SRFALL	2			1		1	4
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	2017	19_SRFALL	6			1		1	8
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	2018	19_SRFALL					2	2	4
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa16	2016	19_SRFALL				2			2
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa17	2017	19_SRFALL				1			1
	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa15	2015	22_BONPOOLFA	4						4
	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa16	2016	22_BONPOOLFA	32		1	21		1	55

	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	2017	22_BONPOOLFA	10		3	6	1	1	21
	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	2018	22_BONPOOLFA						1	1
	04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	2018	23_UMATILLAFA					2		2
	#N/A	#N/A	Unassigned	#N/A	#N/A	112	2	3		10		127
Total						346	3	25	99	46	24	543

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1110 *The Non-Treaty sport fishery in the Chinook Salmon Fall Management Period of 2020*

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1112 The 2020 fall Non-Treaty sport fishery executed below Bonneville Dam was not mark-selective and could be characterized by
 1113 reporting group composition of clipped and unclipped hatchery-origin and natural-origin stocks (Table 30). We also reported the
 1114 broodstock composition of the hatchery-origin Chinook salmon (Table 31). In 2020, we were also able to report on reporting group
 1115 and broodstock composition of the stocks in the fall Non-Treaty sport fishery executed above Bonneville Dam (Table 32, Table 33).

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1117 **Table 30. Summary of the stock composition at the reporting group level of the kept adult Chinook salmon of the fall Non-**
 1118 **Treaty sport fishery below Bonneville Dam in 2020 in units of reported catch.**

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Reporting Group name	Run type	Reporting Group Code	Hatchery origin- Clipped		Hatchery origin- No Clip		Natural origin- No Clip	
			H		HNC		W	
			Est.	95% CI	Est.	95% CI	Est.	95% CI
Youngs Bay	Spring	01_YOUNGS					29	0 – 68
West Cascade Spring	Spring	02_WCASSP					11	0 – 34
West Cascade Fall	Fall	03_WCASFA	939	733 – 1179	185	68 – 326	3,220	2891 – 3595
Willamette	Spring	04_WILLAM					23	0 – 46
Spring Creek Tule	Fall	05_SPCRTU	284	153 – 550	242	136 – 296	0	0 – 19
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					285	180 – 397
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	2,261	1986 – 2584	1,542	1486 – 1878	6,179	5751 – 6592
Snake River fall	Fall	19_SRFALL	425	302 – 600	331	205 – 418	979	776 – 1218
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	1,724	1523 – 2025	1,019	817 – 1206		
Umatilla fall	Fall	23_UMATILLFA						
Total			5,632		3,319		10,726	

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Table 31. 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 2020 in units of reported catch.

Fall Sport Fishery 2020				Adult Chinook AD			Adult Chinook AI			
Expected Run Time	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	MLE	95% CI	Percent	GSI RepGrp
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su15	2015	11	0 – 34	0.2%			0.0%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su16	2016	12	0 – 35	0.2%			0.0%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su16	2016	11	0 – 34	0.2%			0.0%	18_UCOLSF
04Fall	Big Creek Hatchery	OtsBIGC_seg_fa17	2017	41	0 – 83	0.7%			0.0%	03_WCASFA
04Fall	Big Creek Hatchery	OtsBIGC_seg_fa18	2018	16	0 – 48	0.3%			0.0%	03_WCASFA
04Fall	Cowlitz Salmon Hatchery	OtsCOWL_seg_fa17	2017	21	0 – 64	0.4%			0.0%	03_WCASFA
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa16	2016	280	171 – 398	5.0%	27	0 – 82	0.8%	03_WCASFA
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa17	2017	84	30 – 145	1.5%	38	0 – 84	1.2%	03_WCASFA
04Fall	North Toutle Hatchery	OtsNTOU_seg_fa16	2016	13	0 – 38	0.2%			0.0%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa16	2016	145	53 – 264	2.6%	119	40 – 239	3.6%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa17	2017	92	0 – 184	1.6%			0.0%	03_WCASFA
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa17	2017	220	115 – 335	3.9%	230	115 – 356	6.9%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa18	2018			0.0%	11	0 – 34	0.3%	05_SPCRTU

04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa15	2015	17	0 – 52	0.3%	86	29 – 150	2.6%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa16	2016	653	486 – 814	11.6%	642	475 – 812	19.3%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa17	2017	1037	800 – 1274	18.4%	814	620 – 1004	24.5%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa17	2017	19	0 – 56	0.3%			0.0%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa15	2015			0.0%	12	0 – 37	0.4%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa16	2016	134	67 – 213	2.4%	134	67 – 207	4.0%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	2017	116	54 – 189	2.1%	91	30 – 159	2.8%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa16	2016	12	0 – 35	0.2%	59	24 – 106	1.8%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa17	2017	75	23 – 133	1.3%	34	11 – 69	1.0%	19_SRFALL
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa15	2015	166	85 – 254	2.9%	60	12 – 115	1.8%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa16	2016	1129	942 – 1342	20.1%	824	637 – 1022	24.8%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	2017	429	291 – 579	7.6%	111	39 – 188	3.3%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	2018			0.0%	24	0 – 71	0.7%	22_BONPOOLFA
#N/A	#N/A	Unassigned	#N/A	899	653 – 1159	16.0%			0.0%	#N/A
		TOTAL		5,632		100.0%	3,319		100.0%	

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1125

1126 **Table 32. Summary of the stock composition at the reporting group level of the kept adult Chinook salmon of the fall Non-**
1127 **Treaty sport fishery above Bonneville Dam in 2020 in units of reported catch.**

Reporting Group name	Run type	Reporting Group Code	Hatchery origin- Clipped		Hatchery origin- No Clip		Natural origin- No Clip	
			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					36	0 – 108
Willamette	Spring	04_WILLAM						
Spring Creek Tule	Fall	05_SPCRTU	36	0 – 72			36	0 – 108
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	758	504 – 1039	492	233 – 577	1,341	1059 – 1637
Snake River fall	Fall	19_SRFALL	170	65 – 307	266	149 – 489	163	49 – 307
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	400	258 – 554	251	108 – 321		
Umatilla fall	Fall	23_UMATILLAFA						

Total	1,364		1,008		1,612	
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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 above Bonneville Dam in 2020 in units of reported catch.

Fall Sport BON Fishery 2020				Adult Chinook AD			Adult Chinook AI			
Expected Run Time	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	MLE	95% CI	Percent	GSI RepGrp
03Summer	Chief Joseph Hatchery	OtsCHJO_int_su16	2016	36	0 – 109	2.7%			0.0%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa15	2015	36	0 – 108	2.6%			0.0%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa16	2016	215	72 – 359	15.8%	215	72 – 359	21.4%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa17	2017	316	158 – 513	23.1%	276	118 – 434	27.4%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa15	2015			0.0%	39	0 – 116	3.8%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa16	2016	38	0 – 114	2.8%	76	0 – 152	7.5%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	2017			0.0%	114	0 – 228	11.3%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa16	2016			0.0%	37	0 – 111	3.7%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa17	2017	72	0 – 144	5.3%			0.0%	19_SRFALL
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa15	2015	75	0 – 189	5.5%			0.0%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa16	2016	287	144 – 467	21.1%	251	108 – 395	24.9%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	2017	37	0 – 112	2.7%			0.0%	22_BONPOOLFA

#N/A	#N/A	Unassigned	#N/A	251	98 – 418	18.4%			0.0%	#N/A
		TOTAL		1,364		100.0%	1,008		100.0%	

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1134

1135 *The Non-Treaty commercial fishery in the Chinook Salmon Fall Management Period of 2020*

1136 The fall Non-Treaty commercial fishery is shown by the composition of the combined adult and jack harvest using reporting
1137 group level (Table 34) and broodstock level (Table 35) resolution. The early and late season fishery was executed in two different
1138 regions and allowed us to report the stock compositions for these regions separately. A primary difference in the compositions
1139 between regions was the large abundance of spring creek tules (05_SPCRTU) stock in region A and absence of this stock in region B
1140 (Table 34).

1141 **Table 34. Summary of the stock composition at the reporting group level of the adult and jack Chinook salmon of the fall Non-**
1142 **Treaty commercial fishery in 2020 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			0			22
West Cascade Spring	Spring	02_WCASSP						
West Cascade Fall	Fall	03_WCASFA	13		308	493		5,022
Willamette	Spring	04_WILLAM	0		0	12		124
Spring Creek Tule	Fall	05_SPCRTU	0	0	0	8,246	675	254
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	0		9	39		308
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	133	39	286	1,548	1,384	9,043
Snake River fall	Fall	19_SRFALL	21	0	37	511	424	1,794
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	29	37		2,378	436	
Umatilla fall	Fall	23_UMATILLAFA						

Total	196	75	640	13,228	2,919	16,568
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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 35. Summary of the stock composition at the broodstock level of the adult and jack Chinook salmon of the fall Non-Treaty commercial fishery of 2020 in units of reported catch.

Fall Commercial Fishery 2020				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	OtsCHJO_seg_su15	2015	6	0 – 17	0.0%			0.0%	18_UCOLSF
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa16	2016	168	9 – 351	1.3%			0.0%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa16	2016	51	0 – 153	0.4%			0.0%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa17	2017	89	0 – 177	0.7%			0.0%	03_WCASFA
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa16	2016	71	0 – 195	0.5%			0.0%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa17	2017	7139	6080 – 7962	53.2%	675	355 – 1049	22.5%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa18	2018	471	286 – 690	3.5%			0.0%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa15	2015	6	0 – 17	0.0%	11	0 – 22	0.4%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa16	2016	543	253 – 866	4.0%	834	461 – 1270	27.8%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa17	2017	807	399 – 1254	6.0%	538	204 – 939	18.0%	18_UCOLSF
04Fall	Yakima Nation Prosser Hatchery	OtsPROS_seg_fa16	2016			0.0%	39	0 – 118	1.3%	18_UCOLSF

04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa15	2015	6	0 – 18	0.0%	24	0 – 71	0.8%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa16	2016	123	47 – 211	0.9%	65	12 – 149	2.2%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	2017	223	52 – 442	1.7%	166	53 – 285	5.5%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	2018	36	0 – 86	0.3%			0.0%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa16	2016	143	51 – 246	1.1%	142	63 – 239	4.7%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa17	2017			0.0%	28	0 – 66	0.9%	19_SRFALL
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa15	2015	230	94 – 390	1.7%	83	0 – 249	2.8%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa16	2016	2068	1530 – 2631	15.4%	390	209 – 577	13.0%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	2017	110	10 – 271	0.8%			0.0%	22_BONPOOLFA
#N/A	#N/A	Unassigned	#N/A	1135	537 – 1966	8.5%			0.0%	#N/A
		TOTAL		13,423		100.00%	2,994		100.00%	

1149

Comparison of stock composition of the clipped Chinook salmon stocks among spring-and summer-management period Chinook salmon sport fisheries in 2020

The stock composition varied substantially across the Non-Treaty sport fisheries that were executed in the spring versus summer period as expected (Figure 25). The largest difference in stock compositions was the high estimate of Hells Canyon stock during the spring period compared to the summer, and the high estimate of upper Columbia summer-run stock (18_UCOLSF) captured during the summer period compared to the spring (Figure 25). However, it was unexpected to observe the high estimate of lower river stock from the Willamette River (04_WILLAM) during the summer period sport fishery. This high capture rate may have been due to fishing effort in region B, but is unexpected due to the summer timing of the fishery since Willamette River stock is spring-run (Table 7).

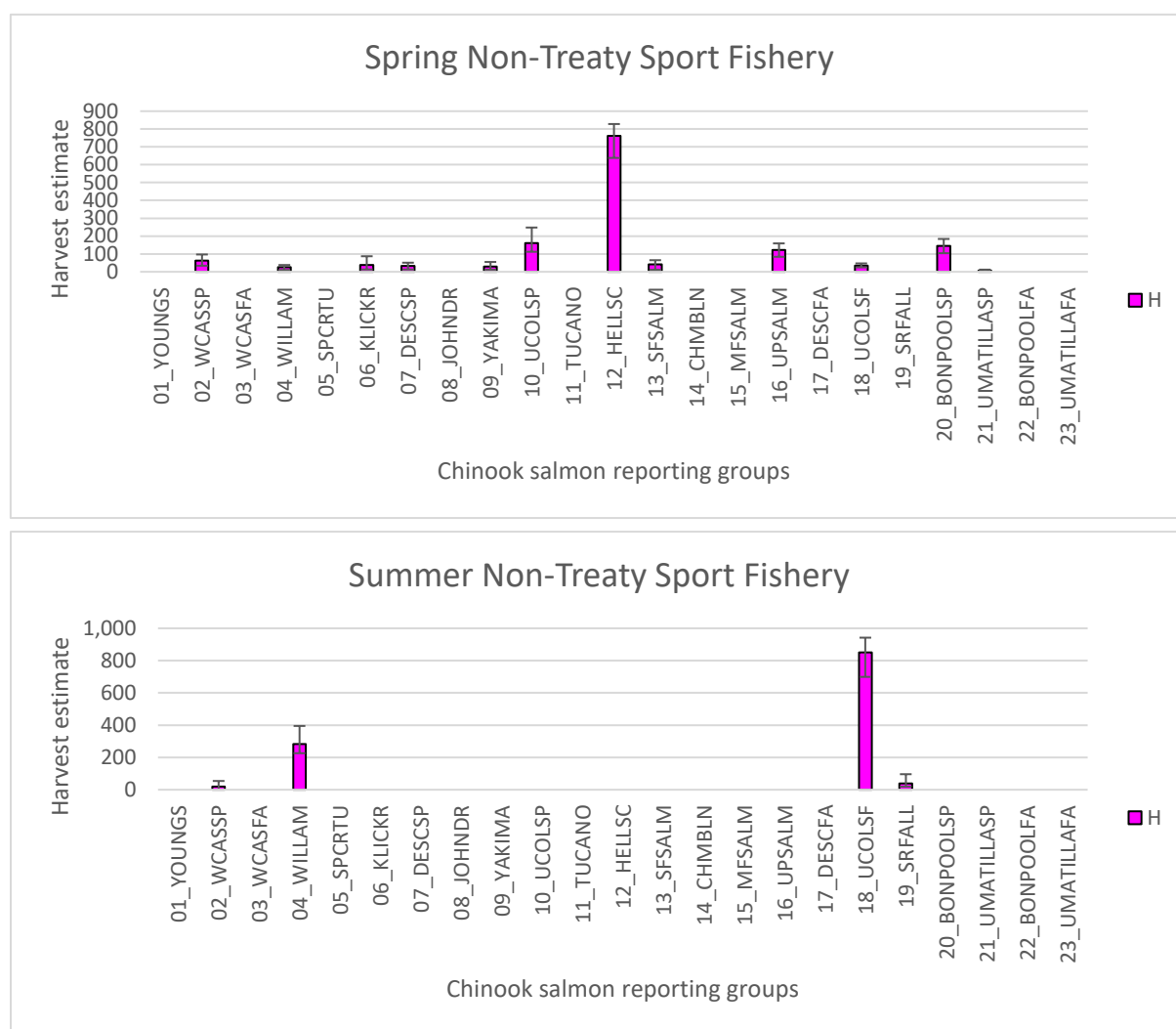


Figure 25. Stock composition of spring and summer management period Chinook salmon harvest mixtures in 2020.

Comparison of stock composition of the clipped and unclipped Chinook salmon stocks among the Non-Treaty fall-management period fisheries in 2020

The two stocks that distinguished the composition of the various Non-Treaty fall fisheries were the “tule” (05_SPCRTU) and West Cascade (03_WCASFA) stocks (Figure 26). There were very low numbers of this stock present among the released adults in the Fall Pound Net fishery because most of these fish originate from Spring Creek Hatchery and are adipose clipped. The “bright” stocks (ignoring abundance of 05_SPCRTU and 03_WCASFA) were nearly identical among the sport fisheries from below Bonneville Dam and in the Bonneville Pool and the commercial fisheries in regions A and B (Figure 26). 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 and the larger proportion of tules (05_SPCRTU) in the region A harvest.

The composition of the pound net fishery was most similar to the region B Non-Treaty commercial fishery because both were executed in similar locations (Figure 26). The two Non-Treaty sport fisheries executed below and above Bonneville Dam were most clearly distinguished by the higher abundance of the 03_WCASFA stock in the harvest below the dam. We continue to find that despite both the Non-Treaty sport (above Bonneville, Figure 26) and commercial fishery (region A, Figure 26) 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.

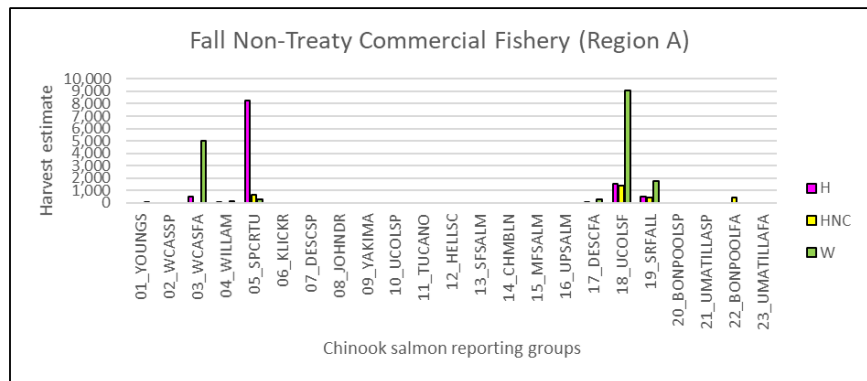
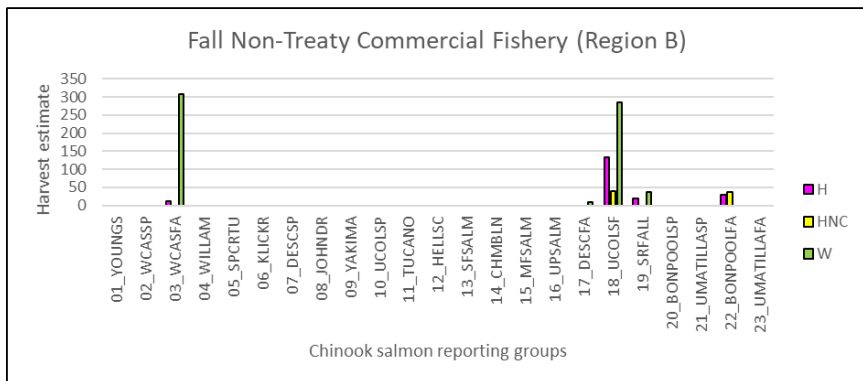
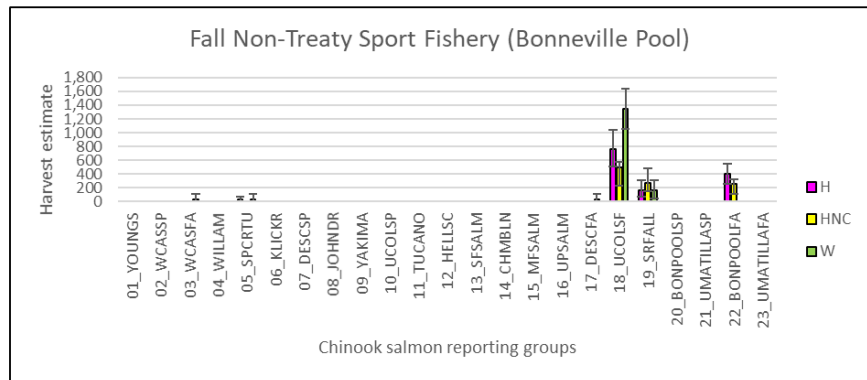
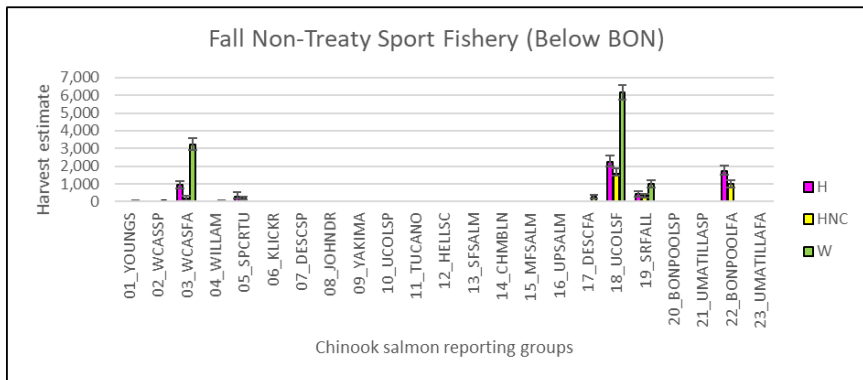
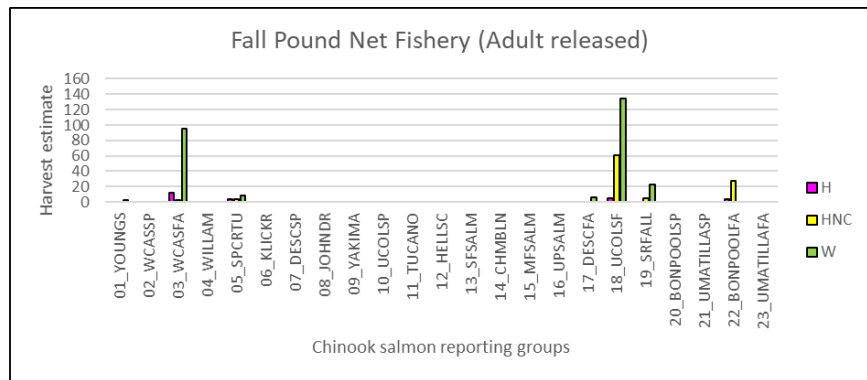
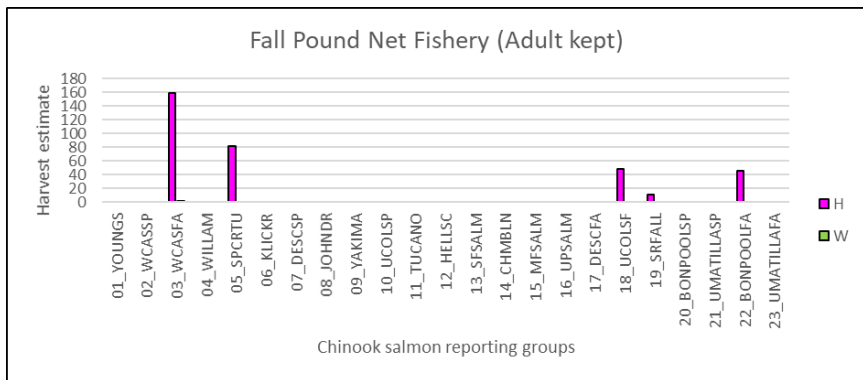


Figure 26. Genetic stock composition of the Fall Non-Treaty Chinook salmon fisheries analyzed in 2020.

The Treaty commercial sockeye fishery of 2019

The Treaty Sockeye salmon fishery could not be analyzed last year and so we included the results in this current report. The reporting group composition of the zone 6 Treaty sockeye salmon fishery showed nearly equal proportions of Wenatchee and Okanogan stock (Table 36).

The Non-Treaty pound net sockeye fishery of 2019

Similar to the Treaty Sockeye salmon fishery, we present the results of the 2019 pound net fishery in this current report (Table 37). The pound net fishery had a large enough sample to detect typically low abundant stocks (e.g. Lake Billy Chinook and Yakima River sockeye).

Table 36. The reporting group composition of the Treaty Sockeye salmon fishery in 2019.

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	22	0 – 45			573	472 – 663
Wenatchee	11	0 – 34			472	382 – 562
Snake						
Lake Billy Chinook						
Yakima						
Odell						
Total	34		0		1,045	

Table 37. The reporting group composition of the Pound Net Sockeye salmon fishery in 2019.

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					737	718 – 756
Wenatchee					147	127 – 166
Snake						
Lake Billy Chinook					1	0 – 3
Yakima			11	2 – 26		
Odell						
Total	0		11		885	

Note: The 11 estimated Yakima fish were comprised of an estimated 6 fish (BY2016, Okanogan genetic stock) and 5 fish (BY2014, Wenatchee genetic stock).

Comparison of stock composition among sockeye salmon fisheries from 2019

Sockeye salmon were sampled from the lower Columbia River below Bonneville Dam in the pound net fishery and above Bonneville Dam in the Zone 6 tribal fishery, and were assigned to five major Columbia River sockeye genetic stocks (Table 38). Low sample numbers of *O. nerka* make it difficult to estimate narrow confidence intervals for estimates of the low abundance stocks: Yakima River, Snake River, and Lake Billy Chinook stocks (Table 38).

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 2019. This difference in run timing may explain why the Treaty fishery had a much larger proportion of the Wenatchee stock compared to the pound net fishery, which had a composition similar to Bonneville Dam (Table 38). The Okanogan stock was higher (>80%) for both the Pound Net and Bonneville Dam, and the Wenatchee stock was lower (<20%) for both the Bonneville Dam and the Pound Net fishery compared to the Treaty fishery (Table 38). The Snake River stock (i.e., Redfish Lake) was not represented at all in any of the fishery mixture samples in 2019 (Table 38).

The Non-Treaty sport sockeye salmon fishery of 2020

We analyzed a single fishery of sockeye salmon in 2020, which was the Non-Treaty sport fishery (Table 39). This fishery captured a relatively high diversity of stocks including two stocks that typically have low abundance, Snake River and Yakima River stocks.

1226

1227 **Table 38. Comparison of stock-specific abundance and percent composition among sockeye salmon fisheries. The mean stock**
 1228 **abundance estimate is provided for each fishery harvest in 2019.**

Mixture source	Mean						Stock proportion					
	Okanogan	Wenatchee	Snake	LBC	Yakima	other	Okanogan	Wenatchee	Snake	LBC	Yakima	other
Pound Net	737	147	0	1	11	0	82.28%	16.36%	0.00%	0.12%	1.24%	0.00%
Treaty Zone 6	595	483	0	0	0	0	55.21%	44.79%	0.00%	0.00%	0.00%	0.00%
Total Harvest	1,333	630	0	1	11	0	67.50%	31.89%	0.00%	0.05%	0.56%	0.00%
Bonneville Dam	54,466	8,052	0	264	265	0	86.39%	12.77%	0.00%	0.42%	0.42%	0.00%

1229

1230

1231 **Table 39. The reporting group composition of the Non-Treaty Sport Sockeye salmon fishery in 2020.**

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	30	0 – 59			2,422	2281 – 2551
Wenatchee					585	467 – 703
Snake	20	0 – 50			20	0 – 50
Lake Billy Chinook						
Yakima			111	18 – 240		
Odell						
Total	50		111		3,028	

1232 Note: The 111 estimated Yakima fish were comprised of an estimated 92 fish (BY2016, Okanogan genetic stock) and 19 fish (BY2016,
 1233 Wenatchee genetic stock).

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 eighth year in which we were able to assign all three major age classes of spring Chinook from Snake River hatcheries and the fourth 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 allowed the ability to assign all yearling hatchery 4-year-olds and subyearling 6-year-olds originating above Bonneville Dam (complete spawn years date back to 2015), and so our analyses now 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 could be utilized exclusively in this report and we no longer depend on the “legacy” panel of smaller numbers of loci to assign mixtures of Chinook salmon. The 254 SNP panel has optimal information content across the three major genetic lineages of Chinook Salmon found in the Columbia River Basin and a complete baseline extends far enough back to encompass all age classes. This report is the eighth 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 a small number of new genotypes of candidate parents to this sockeye PBT baseline such that the baseline has slightly higher tag rates that extend 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 is now benefiting from improved power by expanding the SNP marker panel to 335 SNPs. The 2020 run year is 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 two years ago (Hess et al. 2020) 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:

1278 **1) Harvest RM&E: F&W Program Management Question: What are your in-river**
1279 **monitoring results and what are your estimates of stock composition and stock-**
1280 **specific abundance, escapement, catch, and age distribution?**
1281

1282 The in-river estimates of stock composition, stock-specific abundance, escapement,
1283 catch, and age distribution were addressed for the spring-management test fishery, the non-treaty
1284 spring-management sport fishery, the non-treaty summer-management sport fishery, the non-
1285 treaty mainstem fall-management fisheries, and the pound net fishery in the Cathlamet Channel.
1286 For the spring management period of Chinook salmon, the 2020 year was likely influenced by
1287 COVID restrictions in terms of timing and geographic areas that were fished. We did not
1288 observe typical spatial patterns for the stock composition of lower Columbia River stocks.
1289 Specifically, lower Columbia River stocks were not as apparent in region B because of lower
1290 fishing effort there. We did observe typical differences in the composition of hatchery stocks
1291 represented in spring vs. summer management period harvest of Chinook salmon. Run-timing
1292 plays an important role in this difference (i.e., late-running stocks appear more abundant among
1293 the upriver spring-type lineage that are caught in the summer management period). This pattern
1294 is consistent when compared to known origin PIT tagged adult and jack fish tagged as juveniles.
1295 Known origin adult age upriver spring and Snake River spring Chinook salmon are almost all
1296 past Bonneville by June 15 in most years.

1297 The sockeye salmon tribal fishery is managed in a way that attempts to harvest as many
1298 harvestable sockeye salmon as possible under the allowed harvest rate schedule in the U.S. v.
1299 Oregon Management Agreement. We covered the 2019 year of analysis of the sockeye salmon
1300 harvest in this current report. We have typically found that there may be some over
1301 representation of the Wenatchee sockeye stocks in the Zone 6 harvest as compared to the stock
1302 proportions that are present at Bonneville Dam. The results for Snake River sockeye salmon are
1303 dependent upon representative sampling at Bonneville Dam, but low sample rate and the rarity of
1304 this stock leads to uncertainty and high variation around estimates of Snake River sockeye
1305 salmon from Bonneville Dam. In fact, all of the fishery mixtures evaluated in 2019 estimated
1306 zero abundance of Snake River stock. Sampling protocols at Bonneville Dam may have higher
1307 representation of young fish as compared to harvest mixtures. Timing of the fishery may also
1308 influence the proportion of each stock, as was shown by characterizing run-timing distributions
1309 in previous reports; the Wenatchee stock has relatively early run-timing but the timing of the
1310 Snake River stock is uncertain due to inconsistent results between PIT-tag and GSI methods.
1311 Future analysis will be needed to examine these patterns for consistency and delve into
1312 explanations. Importantly, the Yakima River reintroduction of sockeye can have a measurable
1313 (albeit small) impact on the stock composition of the fisheries. In this report, we estimated 11
1314 Yakima fish were captured by the pound net.
1315

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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, and hydropower. 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 400 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 for each species in 2020. 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. 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 2021 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 2021, 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 40 for the number and timing of reports for each species and run that were delivered in-season and post-season in 2021).

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 adipose-intact 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 8th 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 6th year in which these can be assigned to some Columbia River hatcheries. This is the third 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 2022 features the final analyses of 2020, as well as the preliminary in-season and post-season analyses of 2021.

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 40. The in-season and post-season report timing and scope of the 2021 fish runs.

Species	Management Period	Data coverage	Samples Arrive	Analysis begins	Report distributed
Chinook	Spring	01/01/2021 – 04/30/2021	5/3/2021	5/6/2021	5/10/2020
		01/01/2021 – 05/14/2021	5/17/2021	5/20/2021	5/24/2021
		01/01/2021 – 05/28/2021	5/31/2021	6/3/2021	6/7/2021
	Summer	01/01/2021 – 06/15/2021	6/16/2021	6/21/2021	6/25/2021
		06/16/2021 – 06/30/2021	7/1/2021	7/7/2021	7/12/2021
		06/16/2021 – 07/31/2021	8/2/2021	8/5/2021	8/9/2021
	Fall	08/01/2021 – 8/27/2021	8/30/2021	9/2/2021	9/6/2021
		08/01/2021 – 10/29/2021	11/1/2021	11/4/2021	11/8/2021
Steelhead	Skamania	04/01/2021 – 06/30/2021	7/1/2021	7/7/2021	7/12/2021
	Summer A-/B-Index	07/01/2021 – 07/31/2021	8/2/2021	8/5/2021	8/9/2021
		07/01/2021 – 08/27/2021	8/30/2021	9/2/2021	9/6/2021
		07/01/2020 – 10/31/2020	11/1/2021	11/4/2021	11/8/2021
Sockeye	Total	01/01/2021 – 07/31/2021	8/2/2021	8/5/2021	8/9/2021

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=1,448), Chinook (n=3,101) and sockeye salmon (n=1,729) adults in 2020 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 21 (05/17/20) and was completed on 10/17/20 (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. An unprecedented portion of the adult Chinook salmon run was missed prior to the statistical week in which sampling was initiated by May 17 (week 21). In fact, there was 9.8% of the clipped adults and 4.1% of the unclipped adults estimated to have passed prior to the start of sampling in 2020. This delay was due to restrictions imposed by the Army Corp of Engineers but were resolved for 2021 and hopefully will not continue to pose issues for future years. More often, there is at most 2.5% of the total Spring management period adult Chinook salmon count that passes Bonneville prior to the usual sampling start date (mid April). However, when the adult migration run is average timed at

Bonneville Dam as it was in the spring of 2020 (Figure 27), this can result in a lower proportion of unsampled fish prior to usual initiation of sampling in mid April. Given the delay in sampling in 2020, some early timed stocks are likely 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 2020 for the spring and summer management periods was 0.9%, whereas the average sample rate for adult fall Chinook was 0.7% (Table 41).

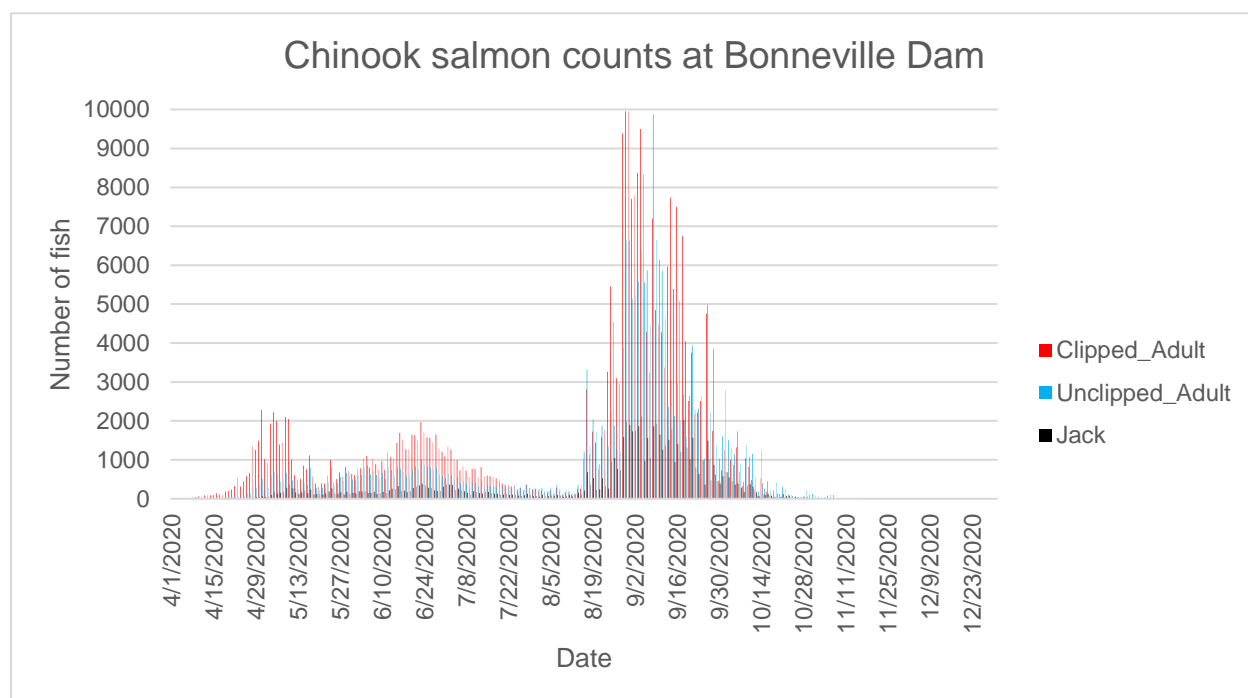
Based on numbers of fish collected, samples were pooled into weekly strata for Chinook (Table 41), multi-week strata for steelhead (Table 42), or a combination thereof for sockeye salmon (Table 43) spanning the majority of the run-year from April to October. We followed a similar protocol as the Monitoring 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).



1582 **Figure 27. Daily passage of Chinook salmon (Clipped adults=red, Unclipped adult=blue,**
1583 **and jacks=black) at Bonneville Dam in 2020 (source: <https://www.fpc.org>; US v OR TAC).**

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Table 41. Sample numbers by weekly strata for adult-sized Chinook salmon that were DNA sampled or tallied for abundance at Bonneville Dam in 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	1014	158	-	-	-	-	0	0	0.00%	0.00%
		17	2255	406	-	-	-	-	0	0	0.00%	0.00%
		18	8641	1962	-	-	-	-	0	0	0.00%	0.00%
		19	12019	3787	-	-	-	-	0	0	0.00%	0.00%
		20	6272	2941	-	-	-	-	0	0	0.00%	0.00%
		21	3785	2705	2	13	8	2	15	10	0.40%	0.37%
		22	4706	3816	7	75	50	16	82	66	1.74%	1.73%
		23	5750	4468	12	99	97	12	111	109	1.93%	2.44%
		24	6644	4538	4	47	36	9	51	45	0.77%	0.99%
		25	2467	1380	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	1337	1720	1	25	20	6	26	26	1.94%	1.51%
		33	1111	1575	2	4	14	2	6	16	0.54%	1.02%
		34	10471	12364	7	51	58	32	58	90	0.55%	0.73%
		35	30487	12596	20	81	62	33	101	95	0.33%	0.75%

	36	61595	41078	26	114	101	66	140	167	0.23%	0.41%
	37	31692	43461	11	56	56	21	67	77	0.21%	0.18%
	38	42457	16761	6	72	122	64	78	186	0.18%	1.11%
	39	18923	19820	6	75	151	45	81	196	0.43%	0.99%
	40	6494	14366	8	64	139	43	72	182	1.11%	1.27%
	41	6065	7978	5	38	157	40	43	197	0.71%	2.47%
	42	1712	4085	2	21	36	12	23	48	1.34%	1.17%
	43-53	500	2875	-	-	-	-	0	0	0.00%	0.00%
Total		307976	227770	158	1,148	1,352	443	1,306	1,795	0.42%	0.79%

1586 Note: Statistical weeks 1–16 are 1/1/20 – 4/18/20 and 43–53 is 10/18/20–12/31/20. ‘TAC count’ is based on the estimates of clip and unclipped adult
 1587 Chinook salmon provided by US v OR Technical Advisory Committee using data from the Fish Passage Center (<http://www.fpc.org>) observed by the
 1588 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
 1589 sample rate. The management periods approximate the date ranges from January 1st to June 15th (Spring management period), June 16th to July 31st
 1590 (Summer management period), and August 1st to December 31 (Fall management period) which are used to categorize spring-, summer-, and fall-run
 1591 Chinook salmon, respectively. The number of sampled fish that were assigned via PBT or GSI are shown. An unprecedented closure of the AFF at
 1592 the start of the spring period lasted until 5/16/20 during which time no fish could be sampled.

1593 **Table 42. Sample numbers by monthly strata for steelhead that were DNA sampled or tallied for abundance at Bonneville**
1594 **Dam in 2020.**

				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	14-27	1,591	2,510	3	5	9	2	0	0	0	0	8	11	0.50%	0.44%
A-/B-Index	27-29	6046	7634	9	29	47	2	0	0	1	0	38	50	0.63%	0.65%
	30	5106	5578	10	50	61	6	0	0	6	0	60	73	1.18%	1.31%
	31	7015	6188	17	59	81	4	0	1	3	0	77	88	1.10%	1.42%
	32	5484	4028	22	66	75	6	0	3	5	0	91	86	1.66%	2.14%
	33	3225	1932	21	70	44	5	3	3	4	0	97	53	3.01%	2.74%
	34	4792	2562	10	50	41	6	1	6	7	2	67	56	1.40%	2.19%
	35-36	13058	5619	13	49	26	4	1	49	12	3	112	45	0.86%	0.80%
	37-38	13803	5539	4	10	6	4	2	55	8	9	71	27	0.51%	0.49%
	39	3801	1448	2	19	2	4	0	62	6	19	83	31	2.18%	2.14%
	40	1602	693	0	15	4	2	1	61	6	18	77	30	4.81%	4.33%
	41-44	1611	827	8	18	16	6	2	38	6	23	66	51	4.10%	6.17%
Summer A-/B- Index subtotal		65,543	42,048	116	435	403	49	10	278	64	74	839	590	0.90%	0.80%
Total		67,134	44,558	119	440	412	51	10	278	64	74	847	601	0.80%	0.80%

1595 Note: Statistical week 14-27 is 4/1/20–6/30/20 (Skamania Management Period) and 27-29 begins the A-/B-Index Period that runs
1596 from 7/1/2020-10/31/2020. ‘Fish count’ is based on tallies of adipose-clipped and unclipped adult steelhead provided by the Fish
1597 Passage Center (<http://www.fpc.org>) observed by the Corps of Engineers at their fish counting window. The total sum of all samples
1598 for each clipped and unclipped category obtained in a given stratum was used to calculate sample rate. The clipped and unclipped
1599 sample numbers were grouped by size (A-Index < 780 mm fork length; B-Index >=780 mm fork length) and further split according to

1600 the number of samples that were either assigned via PBT or GSI. An unprecedented closure of the AFF at the start of the Skamania
1601 period lasted until 5/16/20 during which time no fish could be sampled.

Table 43. Sample numbers for genetic stock assignments of sockeye salmon that passed Bonneville Dam in 2020.

Statistical week grouping	Bonneville dam fish window count	Genetic stock					Total	Sample rate (%)
		OKA	WEN	RED	LBC	Yakima		
1-23	1600	20					20	1.25%
24	10509	106	4				110	1.05%
25	38315	253	27			8	288	0.75%
26	94754	268	77			5	350	0.37%
27	121370	305	74			9	388	0.32%
28	56444	103	17			1	121	0.21%
29	13200	205	52	1		6	264	2.00%
30	4340	120	18	1		1	140	3.23%
31-37	1207	41	5	1		1	48	3.98%
Total	341739	1421	274	3	0	31	1729	0.51%

Note: Statistical week 23 begins on 5/31/20 and 37 ends 9/12/20; there were no sockeye counted before 5/21 (week 21) or after 9/12. ‘Fish count’ is based on tallies of sockeye salmon adults provided by the Fish Passage Center (<http://www.fpc.org>) observed by the Corps of Engineers at their fish counting window. GSI stocks are Okanagan (OKA), Wenatchee (WEN), Snake River (RED), and Lake Billy Chinook (LBC) and PBT can identify fish from the Yakima reintroduction. The number of samples for a given statistical week or pooled stratum was used to calculate sample rate. Relatively few sockeye salmon were sampled from the RED, LBC, and Yakima stocks, and limits inference regarding run-timing and abundance of these stocks.

Results

Estimated relative abundance of Chinook salmon stocks in 2020

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

There were 12 major (i.e., abundance >1000 fish) clipped hatchery origin Chinook salmon stocks represented in the total estimated abundance (N=307,976) of clipped hatchery Chinook salmon passing Bonneville Dam in 2020 (Table 44; Figure 28). These stocks in order of decreasing magnitude were 18_UCOLSF (126,916), 05_SPCRTU (58,619), 22_BONPOOLFA (55,234), 19_SRFALL (24,822), 12_HELLSC (14,741), 16_UPSALM (6,900), 09_YAKIMA (4,654), 20_BONPOOLSP (3,941), 06_KLICKR (3,727), 10_UCOLSP (3,573), 13_SFSALM (2,026), and 07_DESCSP (1,124) (Table 44).

In Table 45, 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_UMATILLFA 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_UMATILLFA), which only include abundance from PBT assignments, the other reporting group abundance estimates include abundance estimated from PBT-assigned fish (adipose clipped and unclipped) 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 44). Further, using PBT assignments we can now provide abundance and run-timing estimates for particular hatchery broodstocks (Table 45) which will allow for much improved abundance estimates (Figure 28). In 2020, there were 49 different broodstocks of clipped hatchery-origin fish with abundances greater than 0 and 35 of them had abundance estimates >1000 fish (Table 45). The top five major clipped hatchery broodstocks were from Spring Creek, Little White Salmon, Priest Rapids, and Lyons Ferry hatcheries which were all fall run. The largest spring run clipped broodstock was represented by Rapid River Hatchery (SY2016, 4,042 fish), however the delay of the initiation of sampling in 2020 likely resulted in an underestimate of these early timed spring stocks.

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Table 44. Stock-specific abundance and run-timing of clipped hatchery origin adult Chinook salmon passing Bonneville Dam in 2020.

Reporting Group	Estimated abundance					Run-timing distribution						
	Mean	Sample N	Management Period			Ordinal day						
			Spring	Summer	Fall		1st	3rd	5th	95th	Median	Interquartile
			Jan. 1-Jun. 15	Jun. 16-Jul. 31	Aug. 1-Dec. 31	Median	quartile	quartile	percentile	percentile	date	range (days)
01_YOUNGS	0					-	-	-	-	-	-	-
02_WCASSP	899	3	899	0	0	129	122	138	114	153	5/8/2020	16
03_WCASFA	485	2	0	0	485	233	230	243.8	229	248	8/20/2020	13.75
04_WILLAM	107	3	0	104	3	206	203	210	201	212.9	7/24/2020	7
05_SPCRTU	58,619	160	0	52	58,567	246	242	252	232	262	9/2/2020	10
06_KLICKR	3,727	18	3,291	436	0	131	125	152	115	186	5/10/2020	27
07_DESCSP	1,124	7	996	128	0	133	125	153	115	174.9	5/12/2020	28
08_JOHNDR	0					-	-	-	-	-	-	-
09_YAKIMA	4,654	18	4,472	183	0	130	123	144	114	166	5/9/2020	21
10_UCOLSP	3,573	11	3,573	0	0	129	122	138	114	156	5/8/2020	16
11_TUCANO	0					-	-	-	-	-	-	-
12_HELLSC	14,741	65	14,375	365	0	130	123	145	114	160	5/9/2020	22
13_SFSALM	2,026	10	2,026	0	0	131	124	148	114	161	5/10/2020	24
14_CHMBLN	0					-	-	-	-	-	-	-
15_MFSALM	0					-	-	-	-	-	-	-
16_UPSALM	6,900	29	6,900	0	0	130	123	143	114	158	5/9/2020	20
17_DESCFA	209	1	0	0	209	240	238	242	236	242	8/27/2020	-
18_UCOLSF	126,916	684	13,080	39,447	74,390	243	180	258	160	272	8/30/2020	78
19_SRFALL	24,822	92	0	611	24,211	247	242	258	228	270	9/3/2020	16
20_BONPOOLSP	3,941	12	3,941	0	0	129	122	138	114	155	5/8/2020	16
21_UMATILLASP	0					-	-	-	-	-	-	-
22_BONPOOLFA	55,234	191	0	57	55,177	254	245	263	235	280	9/10/2020	18
23_UMATILLAFA	0	0				-	-	-	-	-	-	-
Total	307,976	1,306	53,553	41,382	213,042							

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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 45. Hatchery broodstock-specific abundance and run-timing distributions of clipped adult Chinook salmon passing Bonneville Dam in 2020.

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	OtsPARK_seg_sp16	3	899	899	0	0	129	122	138	114	153	5/8/2020	16
	06_KLICKR	Klickitat Hatchery	OtsKLIC_seg_sp16	17	3,639	3,291	348	0	131	124	150	115	181	5/10/2020	26
	06_KLICKR	Klickitat Hatchery	OtsKLIC_seg_sp17	1	88	0	88	0	197	195	199	194	200	7/15/2020	4
	07_DESCSP	Round Butte Fish Hatchery	OtsRBFH_seg_sp16	4	554	554	0	0	132	125	153	116	157	5/11/2020	28
	07_DESCSP	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp16	1	404	404	0	0	128	122	136	114	149	5/7/2020	14
	09_YAKIMA	Yakima River Roza Dam	OtsYRRD_int_sp16	10	3,232	3,232	0	0	130	123	145	114	160	5/9/2020	22
	09_YAKIMA	Yakima River Roza Dam	OtsYRRD_int_sp17	1	54	0	54	0	206	203	210	201	212	7/24/2020	7
	10_UCOLSP	Eastbank Fish Hatchery	OtsEAST_seg_sp16	5	1,533	1,533	0	0	130	123	144	114	164	5/9/2020	21
	10_UCOLSP	Winthrop National Fish Hatchery	OtsWINT_seg_sp16	4	1,596	1,596	0	0	128	122	136	114	149	5/7/2020	14
	12_HELLSC	Clearwater Fish Hatchery	OtsCLWH_seg_sp16	8	2,534	2,534	0	0	128	122	138	114	151	5/7/2020	16
	12_HELLSC	Dworshak National Fish Hatchery	OtsDWOR_seg_sp16	4	1,268	1,268	0	0	128	122	138	114	151	5/7/2020	16
	12_HELLSC	Lookingglass Fish Hatchery	OtsLOOK_seg_sp16	14	3,422	3,277	145	0	131	124	149	115	167	5/10/2020	25
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH_seg_sp16	16	4,042	4,042	0	0	129	122	140	114	155	5/8/2020	18
	20_BONPOOLSP	Carson National Fish Hatchery	OtsCARS_seg_sp16	8	2,234	2,234	0	0	129	122	141	114	160	5/8/2020	19
	20_BONPOOLSP	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp16	4	1,707	1,707	0	0	128	122	136	114	149	5/7/2020	14
02Spring/Summer	12_HELLSC	Lookingglass Fish Hatchery	OtsIMNW_seg_ss16	19	3,348	3,128	220	0	132	125	153	115	182	5/11/2020	28
	13_SFSALM	McCall Fish Hatchery	OtsMCCA_seg_ss15	3	872	872	0	0	129	122	138	114	153	5/8/2020	16

	13_SFSALM	McCall Fish Hatchery	OtsMCCA_seg_ss16	7	1,154	1,154	0	0	134	125	154	11 6	16 4	5/13/20 20	29
	16_UPSALM	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss16	10	2,692	2,692	0	0	129	122	141	11 4	15 9	5/8/202 0	19
	16_UPSALM	Sawtooth Fish Hatchery	OtsSAWT_seg_ss16	19	4,209	4,209	0	0	130	123	144	11 4	15 7	5/9/202 0	21
03Summer	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_s u15	21	3,174	1,327	1,229	617	171	162	189	12 5	24 0	6/19/20 20	27
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_s u15	16	1,754	696	1,058	0	173	162	185	15 4	20 3	6/21/20 20	23
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_s u16	48	5,727	412	4,966	349	187	180	199	16 5	21 9	7/5/202 0	19
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_s u16	44	5,445	137	4,920	388	187	180	198	16 9	23 7	7/5/202 0	18
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_s u17	5	471	208	263	0	170	163	196	15 5	21 0	6/18/20 20	33
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_s u14	3	671	671	0	0	142	126	162	11 7	16 7	5/21/20 20	36
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_s u15	35	4,538	1,474	2,801	263	173	164	182	13 0	22 0	6/21/20 20	18
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_s u16	114	14,12 0	1,976	11,808	337	177	171	187	16 1	20 7	6/25/20 20	16
	18_UCOLSF	Entiat National Fish Hatchery	OtsENFH_seg_s u15	20	3,347	1,533	1,814	0	169	157	176	12 4	19 0	6/17/20 20	19
	18_UCOLSF	Entiat National Fish Hatchery	OtsENFH_seg_s u16	16	2,250	460	1,790	0	178	169	185	16 0	19 6	6/26/20 20	16
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_ su15	27	3,702	1,935	1,767	0	165	137	174	12 0	18 1	6/13/20 20	37
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_ su16	48	5,869	1,379	4,159	331	180	168	192	16 0	21 5	6/28/20 20	24
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_ su17	4	767	0	479	289	189	184	229	18 0	23 4	7/7/202 0	45
	03_WCASFA	Washougal Fish Hatchery	OtsWASH_seg_ fa16	1	340	0	0	340	232	230	233	22 9	23 5	8/19/20 20	3
04Fall	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_f a16	2	945	0	0	945	244	235	247	23 0	24 9	8/31/20 20	12
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_f a17	79	45,66 7	0	0	45,667	246	242	253	23 3	26 2	9/2/202 0	11
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_f a18	28	9,517	0	0	9,517	244	239	249	23 1	26 0	8/31/20 20	10
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa 15	4	963	0	0	963	242	239	267	23 7	28 3	8/29/20 20	28

18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa16	69	23,046	0	0	23,046	253	245	261	239	277	9/9/2020	16
18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa17	132	44,149	0	0	44,149	257	249	263	242	277	9/13/2020	14
18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa18	1	105	0	0	105	273	272	276	271	277	9/29/2020	4
18_UCOLSF	Ringold Springs State Hatchery	OtsRING_seg_fa17	3	365	0	0	365	280	277	284	272	290	10/6/2020	7
19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa16	18	5,434	0	229	5,205	251	242	255	229	267	9/7/2020	13
19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	44	14,798	0	57	14,740	247	243	259	230	268	9/3/2020	16
19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa16	13	2,355	0	199	2,156	242	230	258	203	278	8/29/2020	28
19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa17	4	1,134	0	0	1,134	242	239	246	237	272	8/29/2020	7
22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa15	21	6,997	0	57	6,940	247	243	255	234	270	9/3/2020	12
22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa16	149	44,208	0	0	44,208	254	245	262	235	279	9/10/2020	17
22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	21	4,029	0	0	4,029	267	259	275	241	285	9/23/2020	16
Unassigned			158	12,612	2,721	2,930	6,961	240	170	249	125	277	8/27/2020	79
Total			1,306	307,976	53,553	41,382	213,042							

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1669 There were 6 major (i.e., abundance >1000 fish) *unclipped* hatchery origin Chinook salmon stocks represented in the
1670 total estimated abundance (N=67,420) of unclipped hatchery Chinook salmon passing Bonneville Dam in 2020 (Table 46;
1671 Figure 28). These stocks in order of decreasing magnitude were 18_UCOLSF (31,003), 22_BONPOOLFA (14,533),
1672 19_SRFALL (11,057), 05_SPCRTU (5,714), 10_UCOLSP (2,431), and 12_HELLSC (1,428) (Table 46).
1673 In 2020, there were 41 different broodstocks of unclipped hatchery-origin fish with abundances greater than 0 and 11 of
1674 them had abundance estimates >1000 fish (Table 47). The top five major unclipped hatchery broodstocks were from Priest
1675 Rapids Hatchery, Little White Salmon, Spring Creek, and Lyons Ferry hatcheries which were all fall run. The largest spring
1676 run unclipped broodstock was represented by Eastbank Hatchery (SY2016, 1,767 fish).

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Table 46. Stock-specific abundance and run-timing of unclipped hatchery origin adult Chinook salmon passing Bonneville Dam in 2020.

Reporting Group	Estimated abundance					Run-timing distribution						
	Mean	Sample N	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						-	-	-	-	-	-	-
04_WILLAM						-	-	-	-	-	-	-
05_SPCRTU	5,714	19	0	0	5,714	247	241	253	230	264	9/3/2020	12
06_KLICKR	208	1	208	0	0	133	126.5	144	119	150	5/12/2020	17.5
07_DESCSP	108	1	0	108	0	174	171	177	168	179	6/22/2020	6
08_JOHNDR						-	-	-	-	-	-	-
09_YAKIMA	287	1	287	0	0	133	126	144	119	150	5/12/2020	18
10_UCOLSP	2,431	15	2,431	0	0	138	128	149	119	164	5/17/2020	21
11_TUCANO						-	-	-	-	-	-	-
12_HELLSC	1,428	10	1,428	0	0	140	129	151	119	165	5/19/2020	22
13_SFSALM	362	3	251	111	0	148	131	170	121	178	5/27/2020	39
14_CHMBLN						-	-	-	-	-	-	-
15_MFSALM						-	-	-	-	-	-	-
16_UPSALM	41	1	41	0	0	156	154	157	152	158	6/4/2020	3
17_DESCFA						-	-	-	-	-	-	-
18_UCOLSF	31,003	225	916	2,526	27,560	252	244	265	179	283	9/8/2020	21
19_SRFALL	11,057	73	0	489	10,568	244	233	251	215	266	8/31/2020	18
20_BONPOOLSP	41	1	41	0	0	156	154	157	152	158	6/4/2020	3
21_UMATILLASP	208	1	208	0	0	133	126.5	144	119	150	5/12/2020	17.5
22_BONPOOLFA	14,533	93	0	0	14,533	249	244	259	235	277	9/5/2020	15
23_UMATILLAFA						-	-	-	-	-	-	-
Total	67,420	444	5,810	3,234	58,375							

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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. Run-timing distributions for hatchery-origin fish include stock abundance estimated from PBT and GSI assignments.

Table 47. Hatchery broodstock-specific abundance and run-timing distributions of unclipped adult Chinook salmon passing Bonneville Dam in 2020.

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. 31	Median	quartile	quartile	%	%	date	range
01Spring	06_KLICKR	Klickitat Hatchery	OtsKLIC_seg_sp16	1	208	208	0	0	133	127	144	119	150	5/12/2020	18
	07_DESCSP	Round Butte Fish Hatchery	OtsRBFH_seg_sp16	1	108	0	108	0	174	171	177	168	179	6/22/2020	6
	09_YAKIMA	Yakima River Roza Dam	OtsYRRD_int_sp16	1	287	287	0	0	133	126	144	119	150	5/12/2020	18
	10_UCOLSP	Eastbank Fish Hatchery	OtsEAST_seg_sp16	11	1,767	1,767	0	0	139	128	150	119	165	5/18/2020	22
	10_UCOLSP	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp16	1	208	208	0	0	133	127	144	119	150	5/12/2020	18
	10_UCOLSP	Methow Fish Hatchery	OtsMETH_seg_sp16	2	249	249	0	0	138	128	149	119	157	5/17/2020	21
	10_UCOLSP	Winthrop National Fish Hatchery	OtsWINT_seg_sp16	1	208	208	0	0	133	127	144	119	150	5/12/2020	18
	12_HELLSC	Clearwater Fish Hatchery	OtsCLWH_seg_sp16	1	211	211	0	0	133	126	144	119	150	5/12/2020	18
	12_HELLSC	Clearwater Fish Hatchery	OtsPOWP_seg_sp16	5	521	521	0	0	156	138	163	122	167	6/4/2020	25
	12_HELLSC	Lookingglass Fish Hatchery	OtsLOOK_seg_sp16	1	233	233	0	0	133	126	144	119	150	5/12/2020	18
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH_seg_sp16	1	212	212	0	0	134	127	144	119	150	5/13/2020	17
	20_BONPOOLSP	Carson National Fish Hatchery	OtsCARS_seg_sp16	1	41	41	0	0	156	154	157	152	158	6/4/2020	3
	21_UMATILLASP	Umatilla Fish Hatchery	OtsUMAT_seg_sp16	1	208	208	0	0	133	127	144	119	150	5/12/2020	18
	02Spring/Summer	12_HELLSC	Lookingglass Fish Hatchery	OtsIMNW_seg_ss16	2	251	251	0	0	138	128	149	119	157	5/17/2020
13_SFSALM		McCall Fish Hatchery	OtsMCCA_seg_ss16	2	251	251	0	0	138	128	149	119	157	5/17/2020	21
13_SFSALM		McCall Fish Hatchery	OtsMCCA_seg_ss17	1	111	0	111	0	174	171	177	168	179	6/22/2020	6
16_UPSALM		Sawtooth Fish Hatchery	OtsSAWT_seg_ss16	1	41	41	0	0	156	154	157	152	158	6/4/2020	3
03Summer	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_u15	4	327	255	71	0	165	162	167	159	210	6/13/2020	5
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_u16	8	699	0	699	0	190	184	197	180	208	7/8/2020	13

	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_s u16	2	241	0	241	0	186	183	191	18 0	208	7/4/202 0	8
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_s u17	1	67	0	67	0	197	195	199	19 4	200	7/15/20 20	4
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_s u15	2	248	41	207	0	184	180	188	15 4	192	7/2/202 0	8
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_s u16	13	1,38 1	579	717	86	171	164	180	16 0	217	6/19/20 20	16
	18_UCOLSF	Entiat National Fish Hatchery	OtsENFH_seg_s u16	2	217	0	217	0	174	171	177	16 8	179	6/22/20 20	6
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_ su15	1	41	41	0	0	156	154	157	15 2	158	6/4/202 0	3
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_ su16	3	271	0	271	0	187	183	193	18 0	210	7/5/202 0	10
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_ su17	1	36	0	36	0	206	203	210	20 1	212	7/24/20 20	7
04Fall	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_f a16	1	207	0	0	207	240	238	242	23 6	242	8/27/20 20	4
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_f a17	14	4,90 4	0	0	4,904	249	242	253	23 0	265	9/5/202 0	11
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_f a18	4	603	0	0	603	243	237	248	23 0	261	8/30/20 20	11
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa 16	76	12,1 75	0	0	12,175	252	246	262	23 8	283	9/8/202 0	16
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa 17	112	15,3 00	0	0	15,300	257	248	270	23 9	284	9/13/20 20	22
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_ fa15	3	326	0	34	292	231	230	233	20 6	235	8/18/20 20	3
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_ fa16	13	1,96 9	0	287	1,682	238	230	246	18 5	249	8/25/20 20	16
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_ fa17	27	3,80 7	0	135	3,672	247	239	256	22 3	270	9/3/202 0	17
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_f a15	2	229	0	0	229	242	239	259	23 7	262	8/29/20 20	20
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_f a16	19	3,15 8	0	33	3,125	243	235	249	21 9	255	8/30/20 20	14
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_f a17	8	1,43 7	0	0	1,437	250	235	254	23 0	268	9/6/202 0	19
	22_BONPOO LFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_ fa15	2	201	0	0	201	264	260	267	25 7	270	9/20/20 20	7
	22_BONPOO LFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_ fa16	78	12,5 76	0	0	12,576	248	244	257	23 4	275	9/4/202 0	13
	22_BONPOO LFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_ fa17	13	1,75 6	0	0	1,756	257	252	270	24 5	286	9/13/20 20	18
Unassigned				1	131	0	0	131	240	238	242	23 6	242	8/27/20 20	4

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Total	444	67,4 20	5,810	3,234	58,375
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Table 48. Stock-specific abundance and run-timing of natural origin adult Chinook salmon passing Bonneville Dam in 2020.

Reporting Group	Estimated abundance					Run-timing distribution						
	Mean	Sample N	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	446	4	0	32	415	243	220.25	246	210	249	8/30/2020	25.75
02_WCASSP	0	0				-	-	-	-	-	-	-
03_WCASFA	1,067	9	0	0	1,067	259	246	269	243	288	9/15/2020	23
04_WILLAM	105	3	41	64	0	202	156	208	153	212	7/20/2020	52
05_SPCRTU	544	11	0	0	544	243	238	246	218	257	8/30/2020	8
06_KLICKR	82	2	82	0	0	156	154	157	152	158	6/4/2020	3
07_DESCSP	0	0				-	-	-	-	-	-	-
08_JOHNDR	456	3	456	0	0	136	127	146	119	155	5/15/2020	19
09_YAKIMA	812	8	780	32	0	144	130	156	120	167	5/23/2020	26
10_UCOLSP	2,692	24	2,583	108	0	141	129	153	119	167	5/20/2020	24
11_TUCANO	0					-	-	-	-	-	-	-
12_HELLSC	4,227	38	3,950	278	0	144	130	155	120	172	5/23/2020	25
13_SFSALM	2,784	27	2,363	422	0	150	132	160	121	183	5/29/2020	28
14_CHMBLN	0					-	-	-	-	-	-	-
15_MFSALM	1,316	10	1,316	0	0	138	128	150	119	162.3	5/17/2020	22
16_UPSALM	3,195	24	3,087	108	0	139	128	150	119	166	5/18/2020	22
17_DESCFA	4,494	29	0	92	4,402	253	248	264	232	283	9/9/2020	16
18_UCOLSF	119,478	1009	5,312	17,042	97,124	252	238	265	169	283	9/8/2020	27
19_SRFALL	18,652	153	382	1,270	17,000	246	233	258	183	277	9/2/2020	25
20_BONPOOLSP	0	0				-	-	-	-	-	-	-
21_UMATILLASP	0	0				-	-	-	-	-	-	-
22_BONPOOLFA	0	0				-	-	-	-	-	-	-
23_UMATILLAFA	0					-	-	-	-	-	-	-
Total	160350	1354	20,351	19,448	120,551							

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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. Run-timing distributions for hatchery-origin fish include stock abundance estimated from PBT and GSI assignments.

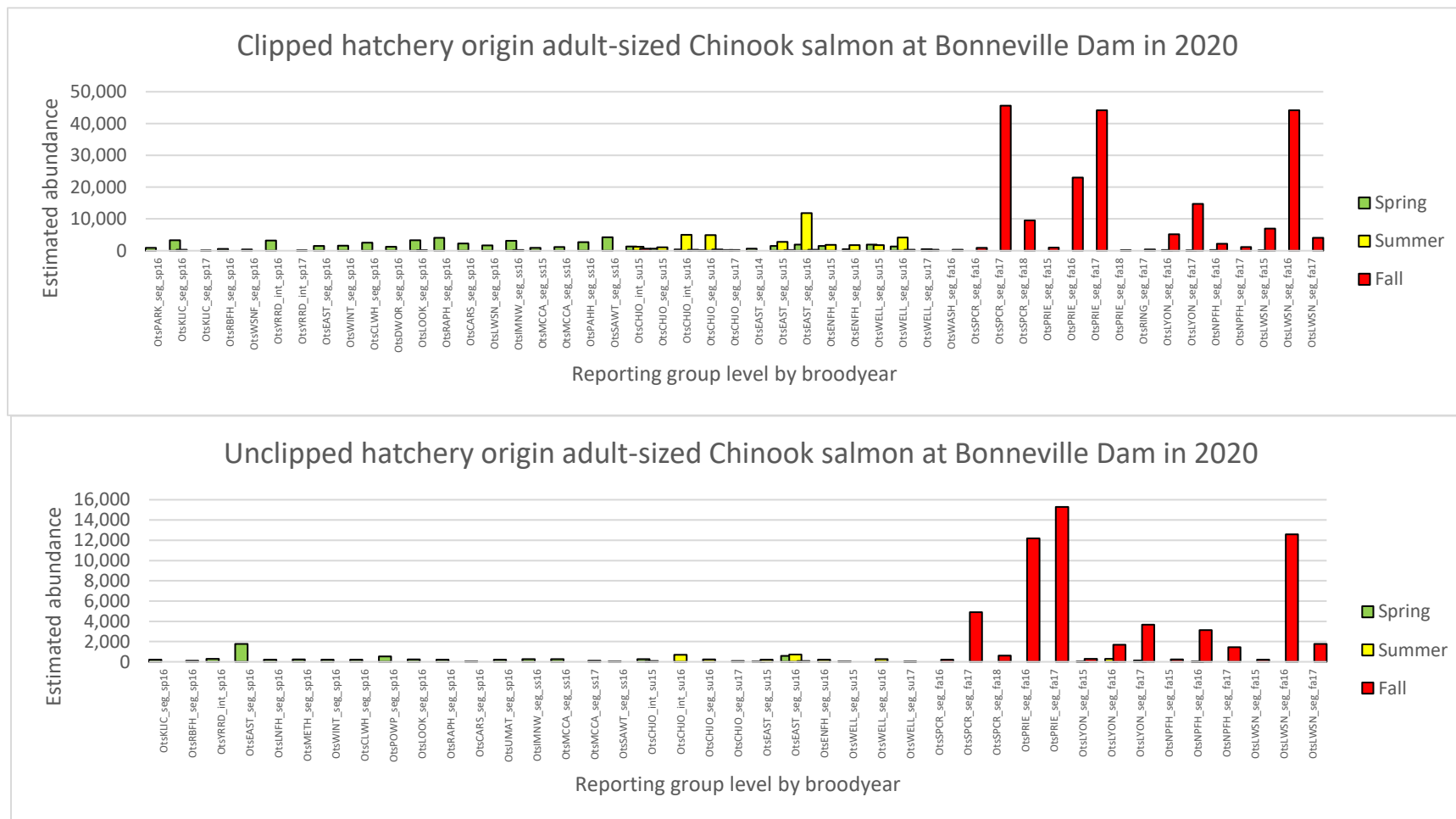


Figure 28. Estimated abundance of clipped (top) and unclipped (bottom) hatchery origin adult-sized Chinook salmon assigned to PBT broodstock groups that were sampled at Bonneville Dam in 2020 during spring (green), summer (yellow) and fall (red) management periods.

1696 There were 9 major (i.e., abundance >1000 fish) Chinook salmon stocks represented in
1697 the total estimated relative abundance (N=160,350) of natural-origin (i.e., excluding unclipped
1698 hatchery-origin fish) Chinook salmon passing Bonneville Dam in 2020 (Table 48;Figure 29).
1699 These natural-origin stocks in order of decreasing magnitude were 18_UCOLSF (119,478),
1700 19_SRFALL (18,652), 17_DESCFA (4,494), 12_HELLSC (4,227), 16_UPSALM (3,195),
1701 13_SFSALM (2,784), 10_UCOLSP (2,692), 15_MFSALM (1,316), and 03_WCASFA (1,358).
1702 These stock abundance estimates were generated using SCOBIDEUX and SPIBETR functions
1703 and the estimates of clipped and unclipped adults distributed by TAC (Table 41).

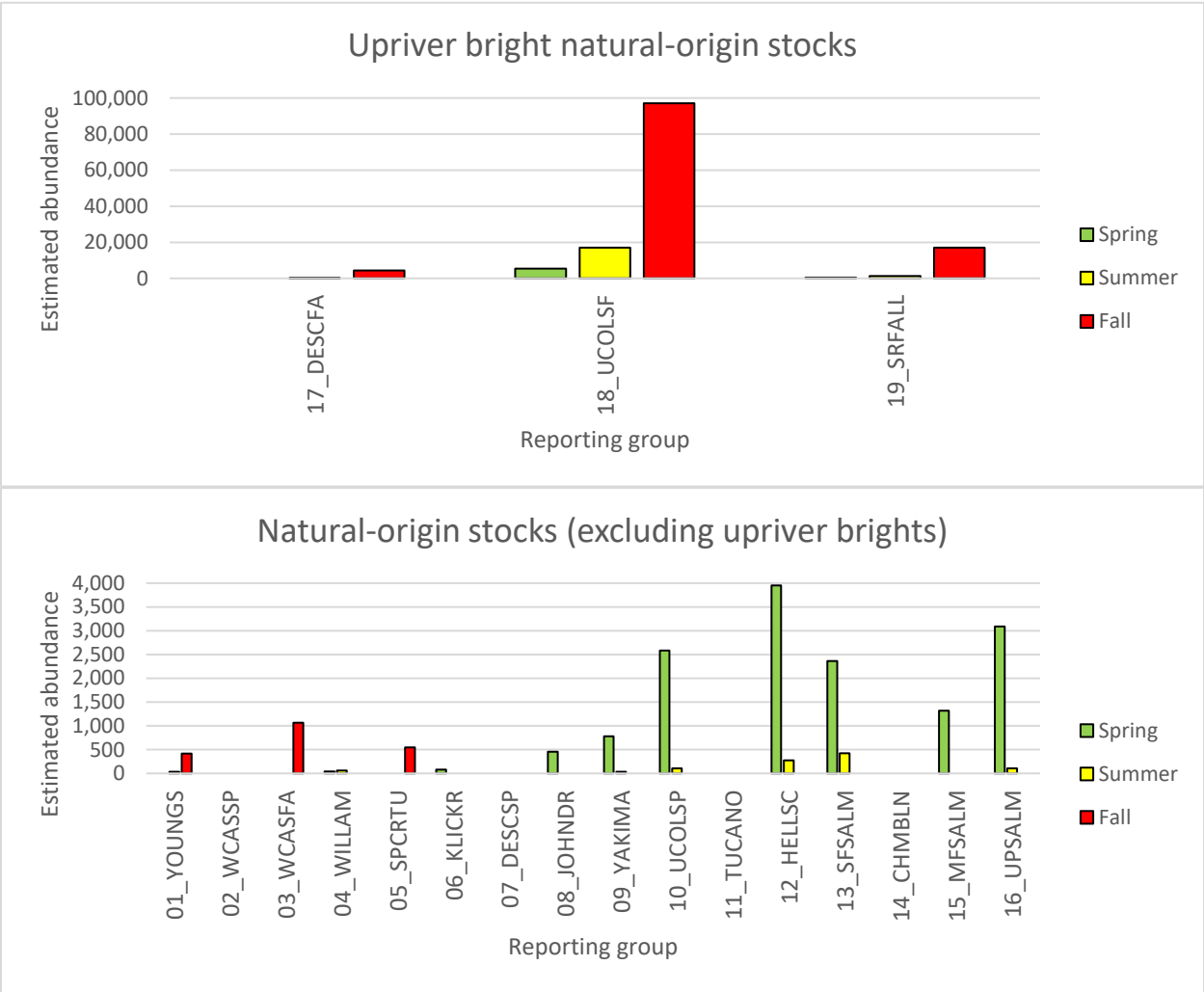


Figure 29. Estimated abundance of natural origin reporting groups (excluding unclipped hatchery-origin fish) of adult-sized Chinook salmon sampled at Bonneville Dam in 2020 during the spring (green), summer (yellow), and fall (red) management periods. Upriver bright Chinook salmon reporting groups (top panel), and all other natural-origin Chinook reporting groups (bottom panel) are shown separately.

Run-timing of Chinook salmon stocks in 2020

We plotted the run-timing distributions of the clipped and unclipped hatchery-origin Chinook salmon reporting group stocks (Figure 30) and provided the subtotals of reporting group abundance for each management period (clipped Table 44, unclipped Table 46). While the median date of passage for most hatchery-origin (both clipped and unclipped) spring Chinook stocks occurred well within the spring management period, the run-timing for 06_KLICKR, 07_DESCSP, 09_YAKIMA, 12_HELLSC, and 13_SFSALM was found to extend beyond the spring management period (total abundance in the summer period was 1,331 fish). We estimated that 97% of all hatchery origin spring stocks passed Bonneville Dam in the spring period and 3% of the spring stock abundance passed in the summer period (Table 44, Table 46). 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 25% (13,996 fish) and 75% (41,973 fish) of the total abundance estimated in those two periods, respectively.

We also plotted run-timing distributions for each broodstock of clipped (Figure 32) and unclipped (Figure 33) hatchery origins and provided the subtotals of these broodstock abundance estimates for each management period (clipped Table 45, unclipped Table 47). 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 run hatchery broodstocks from Klickitat and Yakima broodstock that had median dates in the summer. For the unclipped hatchery spring stocks, only Round Butte and McCall hatcheries had median dates in the summer period (Figure 33).

We plotted the run-timing distributions of the natural-origin (excluding adipose unclipped hatchery-origin fish, Figure 31) Chinook salmon stocks and provide subtotals of abundance for each management period (Table 48). 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, 10_UCOLSP, 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 948 fish). We also estimated that 94% of the natural origin spring stocks passed Bonneville Dam in the spring period and 6% of the spring stock abundance passed in the summer period (Table 48). 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 24% (5,312 fish) and 76% (17,042 fish) of the total abundance estimated in those two periods, respectively.

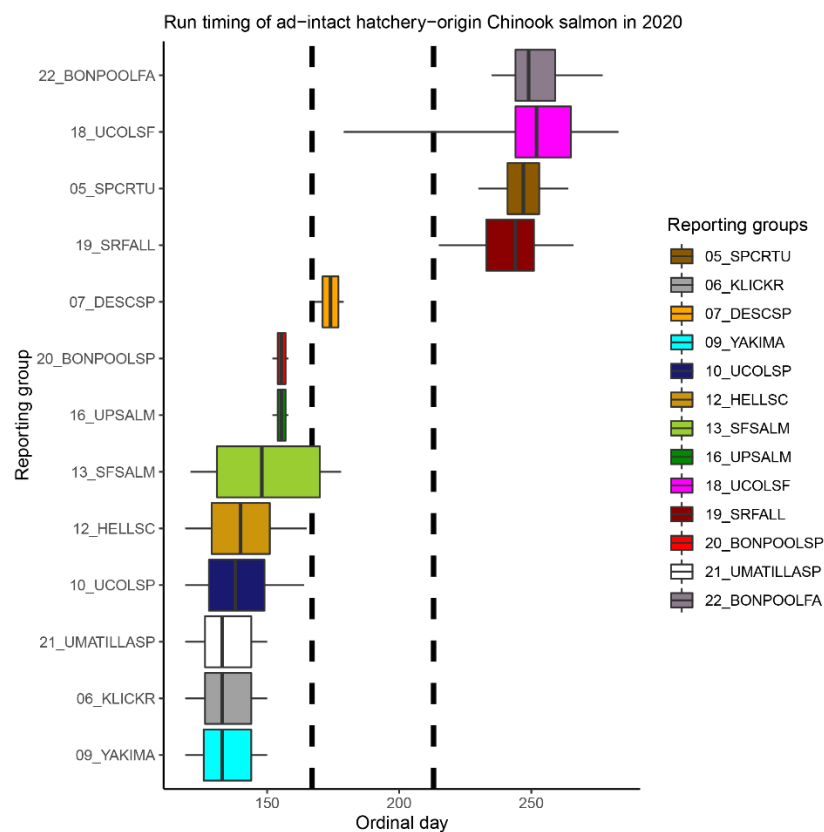
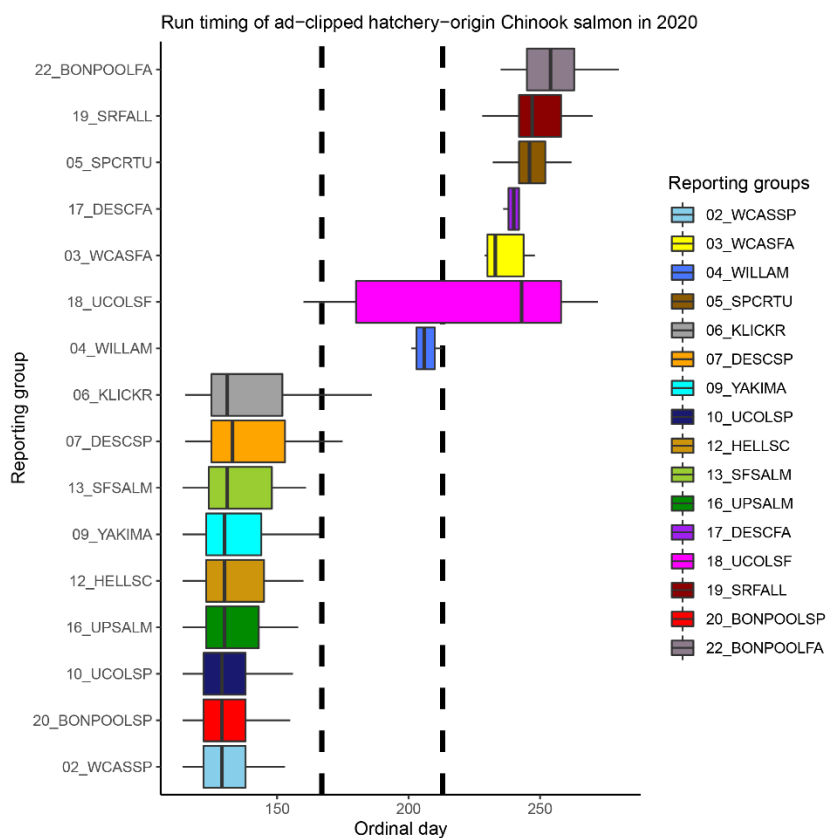


Figure 30. Reporting group-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for clipped and unclipped hatchery-origin adult-sized Chinook salmon that were sampled at Bonneville Dam in 2020 during the spring, summer, and fall management periods (separated by dashed lines).

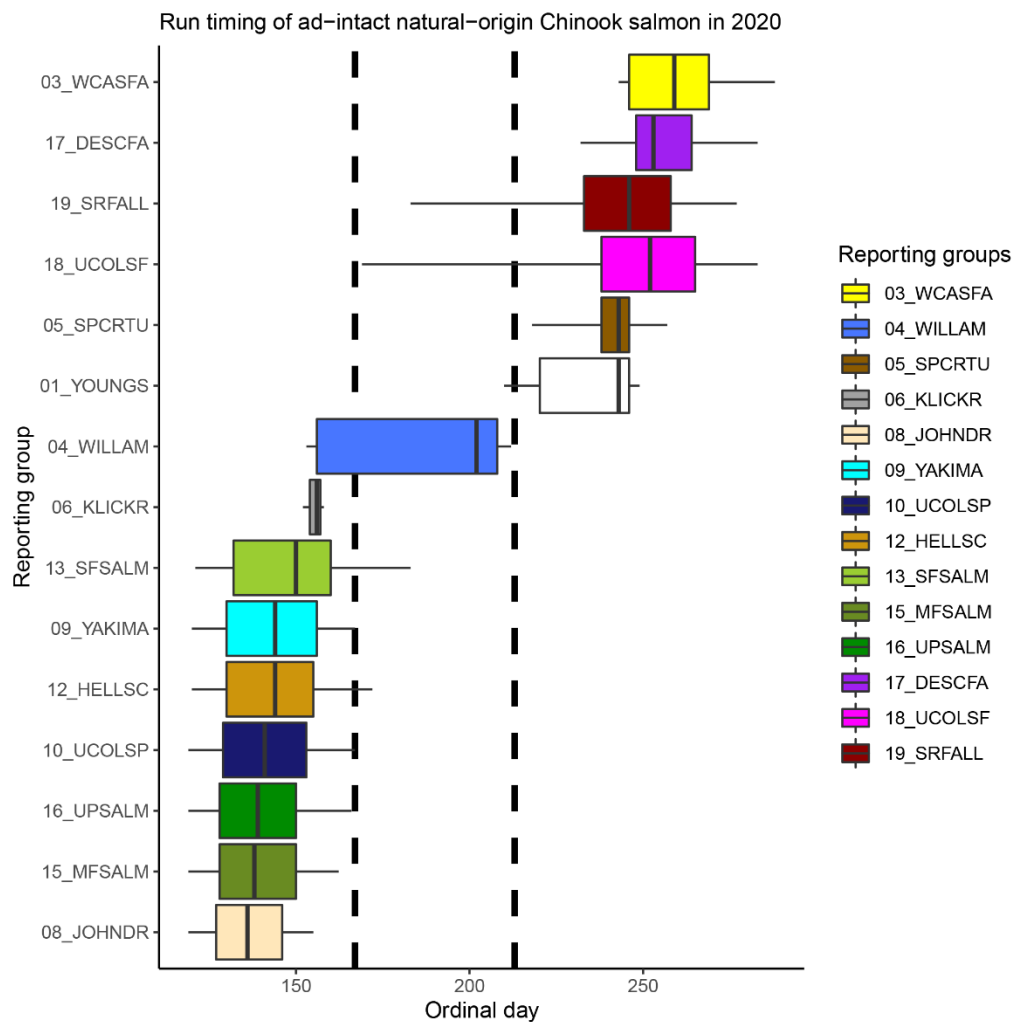


Figure 31. Reporting group-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for natural-origin adult-sized Chinook salmon that were sampled at Bonneville Dam in 2020 during the spring, summer, and fall management periods (separated by dashed lines).

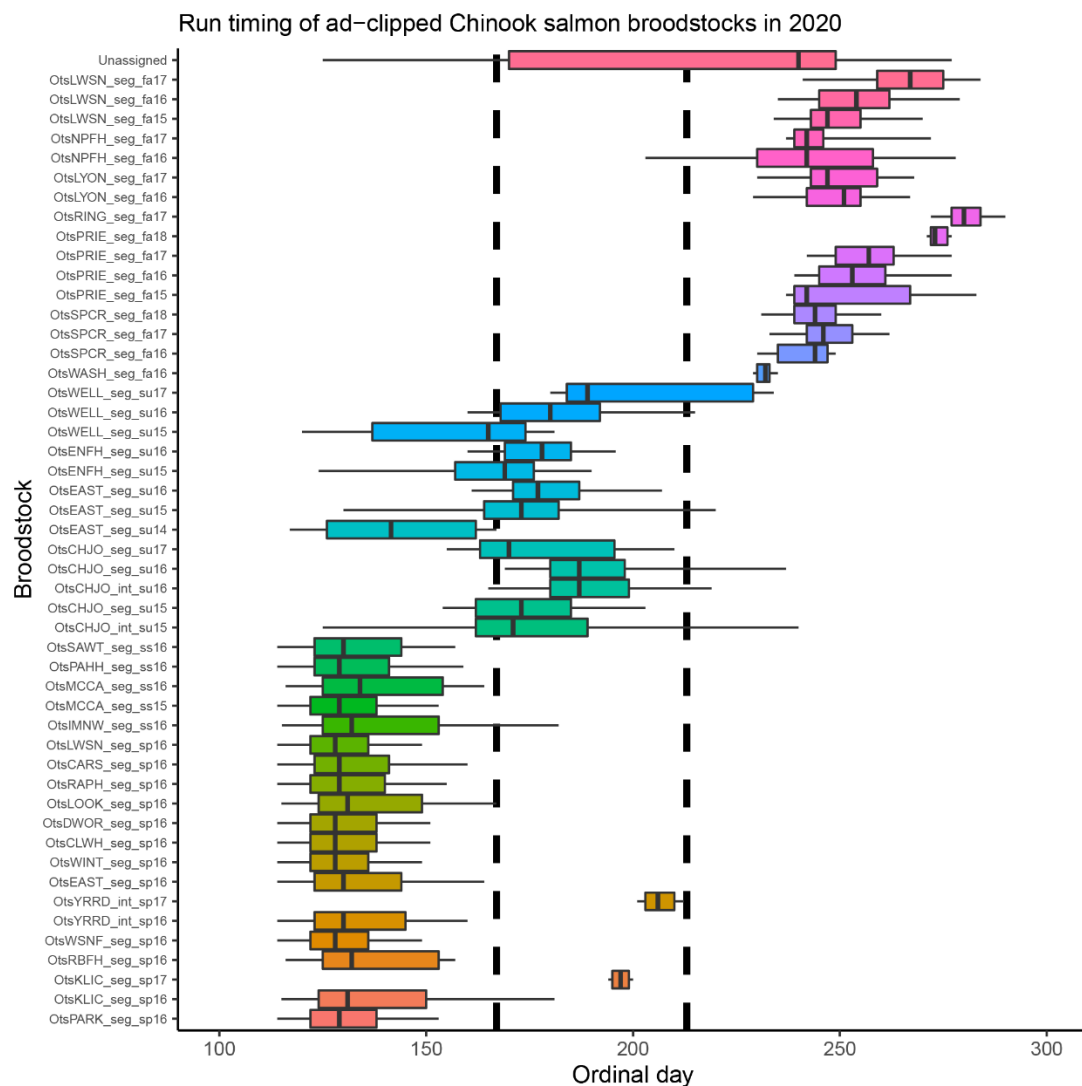


Figure 32. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for clipped adult-sized Chinook salmon that were sampled at Bonneville Dam in 2020 during the spring, summer, and fall management periods (separated by dashed lines).

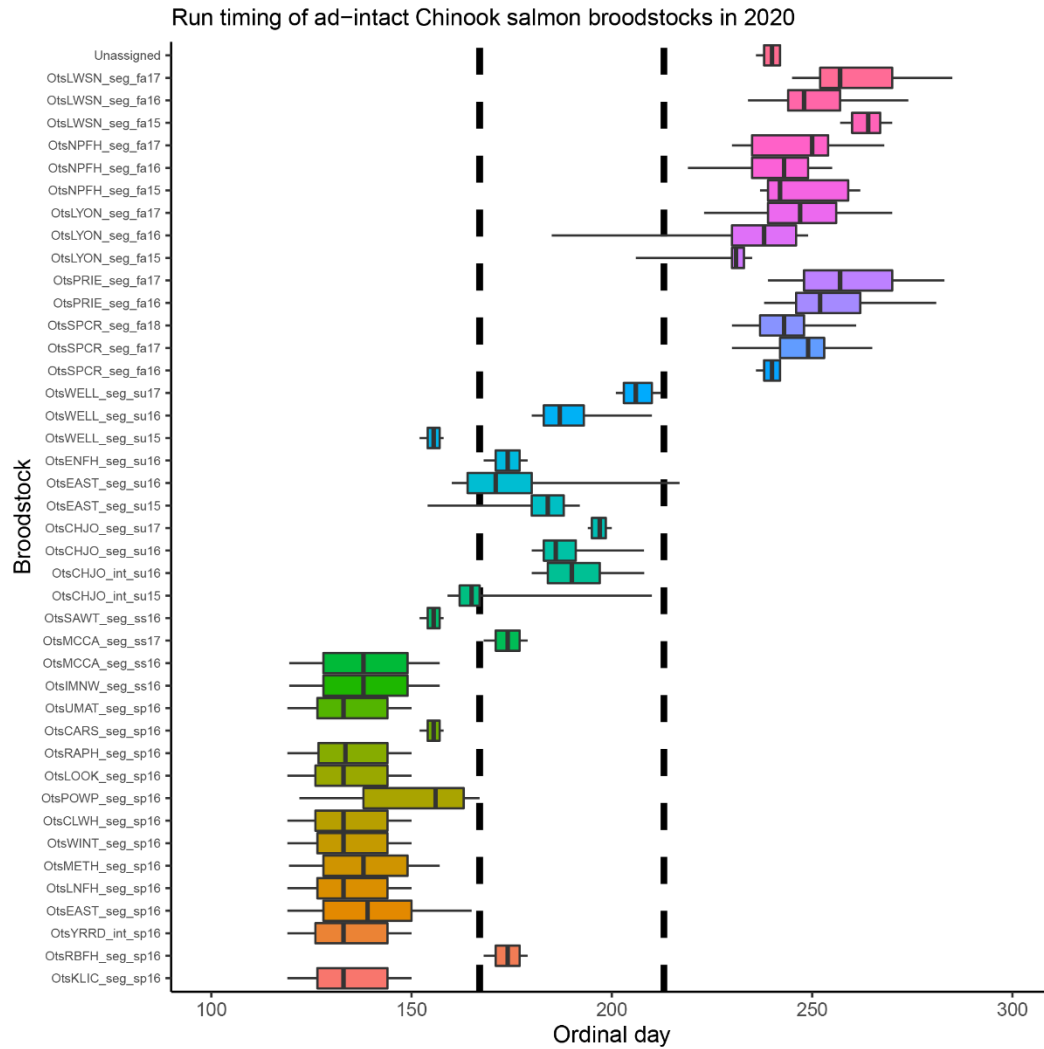
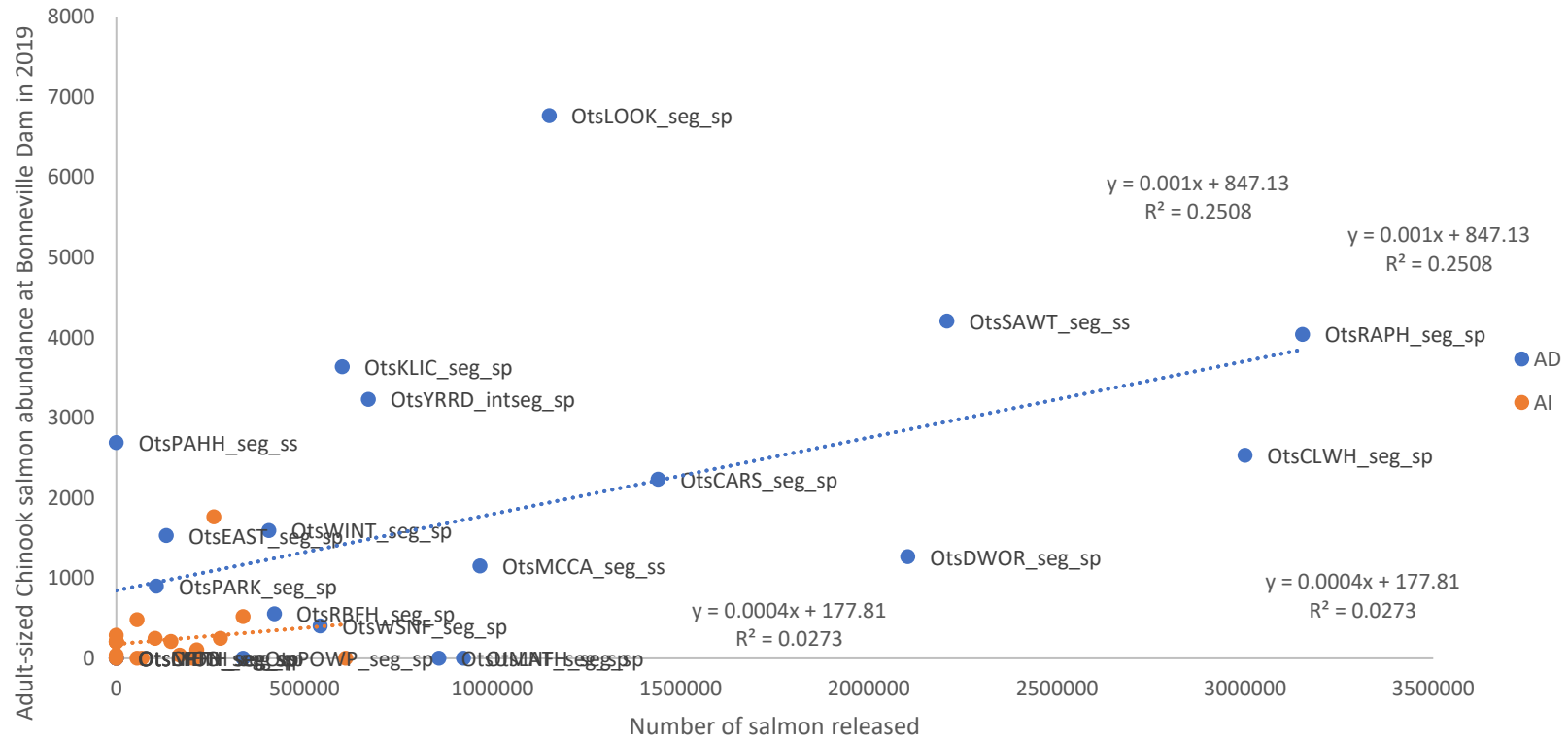


Figure 33. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for unclipped adult-sized Chinook salmon that were sampled at Bonneville Dam in 2020 during the spring, summer, and fall management periods (separated by dashed lines).

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 2020

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 2016 (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 SY2016 broodstocks that returned to Bonneville Dam as adults in 2020 (i.e., 4-year-olds). There was moderate correspondence of number of clipped releases versus clipped abundance estimates based on the R^2 (0.25) of the linear trend (Figure 34). The unclipped stocks were observed to have low abundance and relative low release numbers which resulted in a lack of a strong linear relationship ($R^2=0.03$). This smolt-to-adult survival type of analysis may be highly beneficial for management of these hatchery stocks in the future and represents the second attempt at using the hatchery release information and PBT abundance estimates in this kind of analysis. Future work could sum all abundance of the SY2016 adult return across age-classes (i.e., age 3, 4, and 5 in run years 2019, 2020, and 2021, 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 1,000 Spring Chinook salmon smolts released converted to 1 adult-sized 4-year-old Spring Chinook salmon returned to Bonneville Dam in 2020.

Hatchery release versus Bonneville Dam adult-sized abundance of Columbia River hatchery broodstocks of SY2016



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 1781 **Figure 34. Smolt release numbers of clipped and unclipped hatchery-origin Spring Chinook salmon of SY2016 from Columbia**
 1782 **River hatcheries above Bonneville Dam versus the estimated abundance of SY2016 adult-sized fish that passed Bonneville**
 1783 **Dam in 2020.**

Estimated relative abundance of steelhead stocks in 2020

Daily passage of steelhead at Bonneville Dam in 2020 is provided in Figure 35. Among clipped hatchery-origin steelhead, there were five major stocks (abundance >1000) represented in the total estimated abundance (N=65,543) of clipped hatchery origin steelhead passing Bonneville Dam in 2020 (Table 49). These stocks in order of decreasing magnitude were 10_SFCLWR (22,091, B-Index), 14_UPSALM (20,619), 07_MGILCS (14,576), 03_SKAMAN (3,174), 09_UPPCOL (2,303), and 10_SFCLWR (1,811, A-Index) (Table 49; Figure 36). 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 were three major stocks (abundance >1000) represented in the total estimated abundance (N=8,805) of unclipped hatchery origin steelhead passing Bonneville Dam in 2020 (Table 50). These stocks in order of decreasing magnitude were 10_SFCLWR (3,994, B-Index), 10_SFCLWR (1,812, A-Index), 07_MGILCS (1,238), and 14_UPSALM (1,116) (Table 50; Figure 36).

Using PBT assignments we can now provide abundance (Table 52; Figure 37) and run-timing estimates for each of the clipped and unclipped hatchery broodstocks (Table 52). There were 12 major hatchery broodstock sources (abundance >1000) represented in the total estimated abundance of clipped and unclipped hatchery-origin steelhead passing Bonneville Dam in 2020 (Table 52). These stocks in order of decreasing magnitude were OmyDWOC_su17 (18,980 total; A-Index = 1,241 and B-Index = 17,739), OmySFCR_su17 (7,351 total; A-Index = 461 and B-Index = 6,890), OmyOXBO_su17 (6,116 total; A-Index = 5,892 and B-Index = 224), OmySAWT_su17 (5,868 total; A-Index = 5,843 and B-Index = 25), OmyCGRW_su17 (5,018 total; A-Index = 4,861 and B-Index = 157), OmyPAHH_su17 (4,204), OmyWALL_su17 (3,683), OmyOXBO_su18 (2,305), OmyROUN_su17 (2,206), OmySKAM_su17 (2,197), OmyDWOS_su17 (1,201 total; A-Index = 180 and B-Index = 1,021), and OmyWELL_su17 (1,116 total; A-Index = 936 and B-Index = 181). 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 five major stocks (abundance >1000) represented in the total estimated abundance (N=16,621) of natural origin (excluding adipose unclipped hatchery-origin fish) steelhead passing Bonneville Dam in 2020 (Table 51). These stocks in order of decreasing magnitude were 07_MGILCS (20,053 A-Index; 1,576 B-Index), 14_UPSALM (3,093), 08_YAKIMA (2,209 A-Index; 70 B-Index), 11_UPCLWR (707 A-Index; 1,503 B-Index) and 10_SFCLWR (289 A-Index; 1,123 B-Index). Unless specified, these were all A-Index stocks. The largest natural-origin B-Index abundance was estimated for 11_UPCLWR which had more than 2X more B-Index compared to A-Index fish.

1819 **Table 49. Stock-specific abundance and run-timing by A-/B-Index categories of clipped hatchery-origin summer A-/B-Index steelhead passing Bonneville Dam in 2020.**

Size	Hatchery origin- Clipped		Sample N	Estimated abundance		Run-timing distribution						
						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	26	3,174	1487 – 4819	208	198	213	188	223	7/26/2020	15
	Willamette	04_WILLAM										
	Big White Salmon	05_BWSALM										
	Klickitat	06_KLICKR										
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	213	14,576	11501 – 16935	220	208	235	193	259	8/7/2020	27
	Yakima	08_YAKIMA	1	59	0 – 241	219	218	221	216	222	8/6/2020	3
	upper Columbia	09_UPPCOL	28	2,303	1227 – 3640	211	198	222	188	245	7/29/2020	24
	SF Clearwater	10_SFCLWR	29	1,811	815 – 3118	252	244	266	223	283	9/8/2020	22
	upper Clearwater	11_UPCLWR										
	SF Salmon	12_SFSALM										
	MF Salmon	13_MFSALM										
	upper Salmon	14_UPSALM	254	20,619	17296 – 24283	222	210	244	193	263	8/9/2020	34
		A-INDEX Subtotal	551	42,542								
B-INDEX	Lower Columbia	02_LOWCOL										
	Skamania	03_SKAMAN	1	38	0 – 185	225	224	227	223	229	8/12/2020	3
	Willamette	04_WILLAM										
	Big White Salmon	05_BWSALM										
	Klickitat	06_KLICKR										

mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	3	349	0 – 980	252	244	258	225	263	9/8/2020	14
Yakima	08_YAKIMA		0	0 – 0							
upper Columbia	09_UPPCOL	4	219	0 – 515	220	218	221	216	227	8/7/2020	3
SF Clearwater	10_SFCLWR	275	22,091	20067 – 25054	257	249	264	238	277	9/13/2020	15
upper Clearwater	11_UPCLWR										
SF Salmon	12_SFSALM										
MF Salmon	13_MFSALM										
upper Salmon	14_UPSALM	5	305	25 – 1115	230	214	235	210	283	8/17/2020	21
	B-INDEX Subtotal	288	23,001								

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 50. Stock-specific abundance and run-timing by A-/B-Index categories of unclipped hatchery-origin summer A-/B-Index steelhead passing Bonneville Dam in 2020.

Size					Run-timing distribution							
	Hatchery origin- Clipped		Sample N			Ordinal day						
	Reporting Group name	Reporting Group Code		Estimated abundance			1st	3rd	5th	95th	Median	Interquartile
				Mean	95% CI	Median	quartile	quartile	percentile	percentile	date	range (days)
A-INDEX	Lower Columbia	02_LOWCOL										
	Skamania	03_SKAMAN	2	188	0 – 702	196	191	201	185	227	7/14/2020	10
	Willamette	04_WILLAM										
	Big White Salmon	05_BWSALM	1	15	0 – 65	285	282	288	280	292	10/11/2020	7
	Klickitat	06_KLICKR										
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	19	1,238	480 – 1659	232	216	243	205	249	8/19/2020	27
	Yakima	08_YAKIMA										
	upper Columbia	09_UPPCOL										
			7	318	88 – 623	221	218	232	216	235	8/8/2020	14
	SF Clearwater	10_SFCLWR	20	1,812	641 – 3644	258	254	263	251	280	9/14/2020	9
upper Clearwater	11_UPCLWR											

	SF Salmon	12_SFSALM										
	MF Salmon	13_MFSALM		125		245	241	248	238	250	9/1/2020	7
	upper Salmon	14_UPSALM	13	1,116	264 – 1638	212	205	238	192	250	7/30/2020	33
		A-INDEX Subtotal	62	4,812								
B-INDEX	Lower Columbia	02_LOWCOL										
	Skamania	03_SKAMAN		0	0 – 0							
	Willamette	04_WILLAM										
	Big White Salmon	05_BWSALM		0	0 – 0							
	Klickitat	06_KLICKR										
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS		0	0 – 0							
	Yakima	08_YAKIMA										
	upper Columbia	09_UPPCOL		0	0 – 0							
	SF Clearwater	10_SFCLWR	74	3,994	2769 – 5962	262	254	270	241	285	9/18/2020	16
	upper Clearwater	11_UPCLWR										
	SF Salmon	12_SFSALM										
	MF Salmon	13_MFSALM		0								
	upper Salmon	14_UPSALM		0	0 – 0							
		B-INDEX Subtotal	74	3,994								

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1828 **Table 51. Stock-specific abundance and run-timing by A-/B-Index categories of unclipped natural-origin summer A-/B-Index steelhead passing Bonneville Dam in 2020.**

Size	Natural origin- No Clip		Sample N	Estimated abundance		Run-timing distribution						
	Reporting Group name	Reporting Group Code		Estimated abundance		Ordinal day						Interquartile range (days)
				Mean	95% CI	Median	1st quartile	3rd quartile	5th percentile	95th percentile	Median date	
A-INDEX	Lower Columbia	02_LOWCOL	2	94	0 – 234	213	211	243.5	209	276.3	7/31/2020	33
	Skamania	03_SKAMAN	3	257	31 – 555	200	193	212	186	226	7/18/2020	19
	Willamette	04_WILLAM										
	Big White Salmon	05_BWSALM										
	Klickitat	06_KLICKR	8	475	221 – 777	213	210	220	204	235	7/31/2020	10
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	277	20,053	18579 – 21460	211	201	221	188	248	7/29/2020	20
	Yakima	08_YAKIMA	31	2,209	1573 – 2935	209	200	218	188	240	7/27/2020	18
	upper Columbia	09_UPPCOL	7	622	238 – 1058	223	202	243	189	249	8/10/2020	41
	SF Clearwater	10_SFCLWR	7	289	95 – 495	215	208	269	203	290	8/2/2020	61
	upper Clearwater	11_UPCLWR	8	707	271 – 1216	247	239	253	224	263	9/3/2020	14

B-INDEX	SF Salmon	12_SFSALM	1	125	0 – 375	245	241	248	238	250	9/1/2020	7
	MF Salmon	13_MFSALM	4	138	45 – 270	233	231	235	230	236	8/20/2020	4
	upper Salmon	14_UPSALM	42	3,093	2307 – 4001	211	200	221	187	247	7/29/2020	21
	A-INDEX Subtotal		390	28,061								
B-INDEX	Lower Columbia	02_LOWCOL	2	93	0 – 245	206	204	208	202	288	7/24/2020	4
	Skamania	03_SKAMAN		0	0 – 0							
	Willamette	04_WILLAM										
	Big White Salmon	05_BWSALM										
	Klickitat	06_KLICKR	2	147	0 – 301	208	205	212	203	214	7/26/2020	7
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	22	1,576	998 – 2181	230	207	244	195	250	8/17/2020	37
	Yakima	08_YAKIMA	1	70	0 – 211	212	210	213	209	215	7/30/2020	3
	upper Columbia	09_UPPCOL	1	37	0 – 109	225	224	227	223	229	8/12/2020	3
	SF Clearwater	10_SFCLWR	13	1,123	542 – 1786	255	248	262	230	274	9/11/2020	14
	upper Clearwater	11_UPCLWR	18	1,503	803 – 2244	254	246	262	235	274	9/10/2020	16
	SF Salmon	12_SFSALM	3	380	45 – 775	252	244	258	218	263	9/8/2020	14
	MF Salmon	13_MFSALM	2	254	0 – 626	256	252	260	231	263	9/12/2020	8
	upper Salmon	14_UPSALM		0	0 – 0							
	B-INDEX Subtotal		64	5,182								

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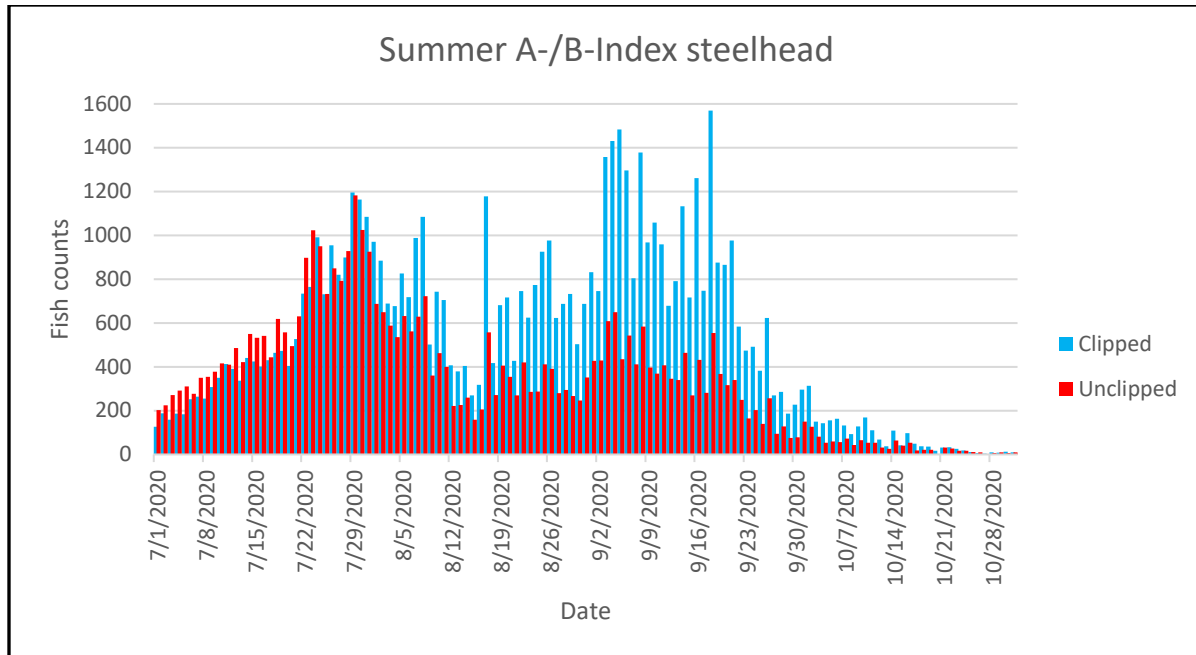


Figure 35. Daily passage of clipped (blue) and unclipped (red) steelhead at Bonneville Dam in 2020 during the summer A-/B-Index management period (source: <https://www.fpc.org>).

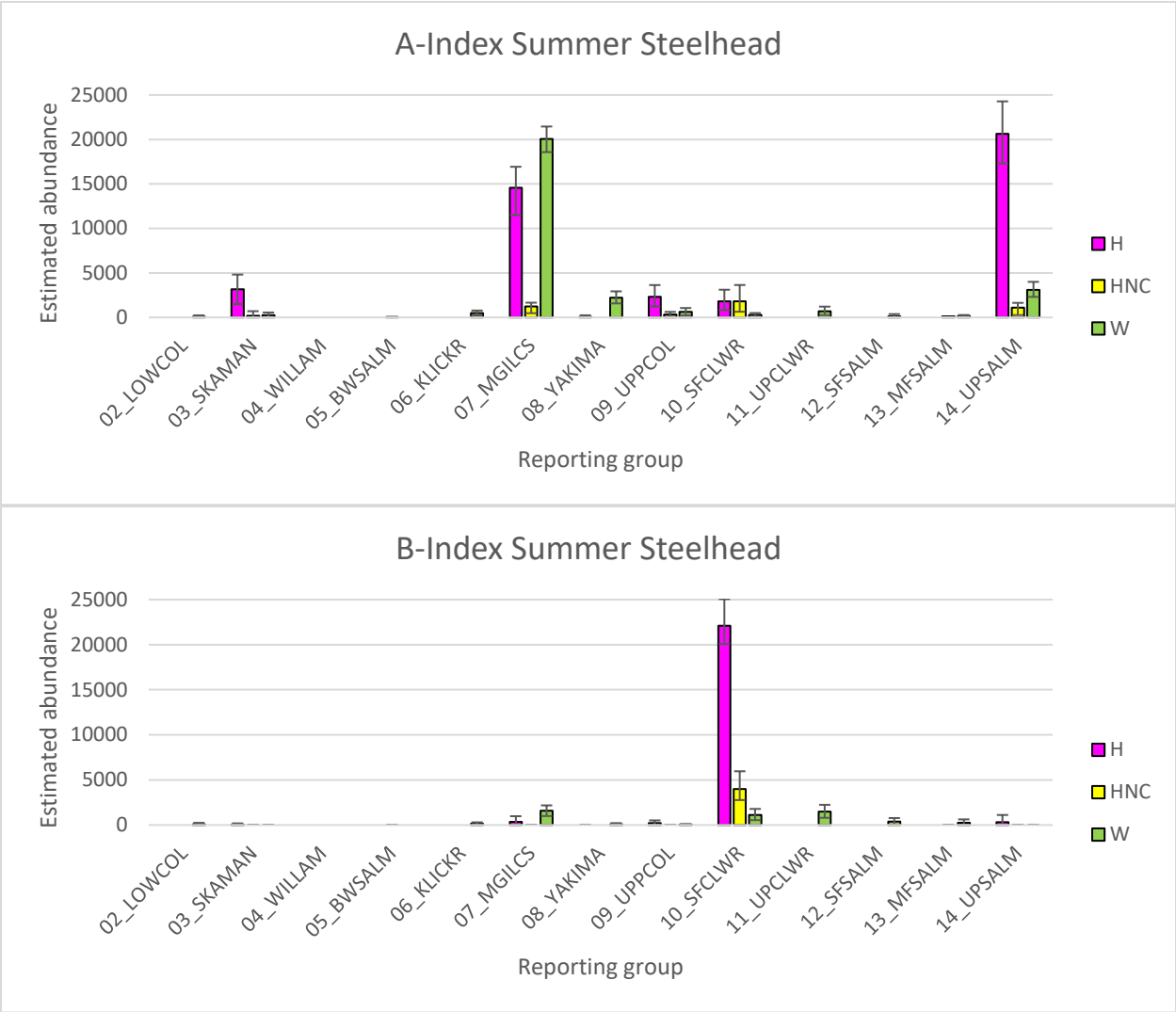
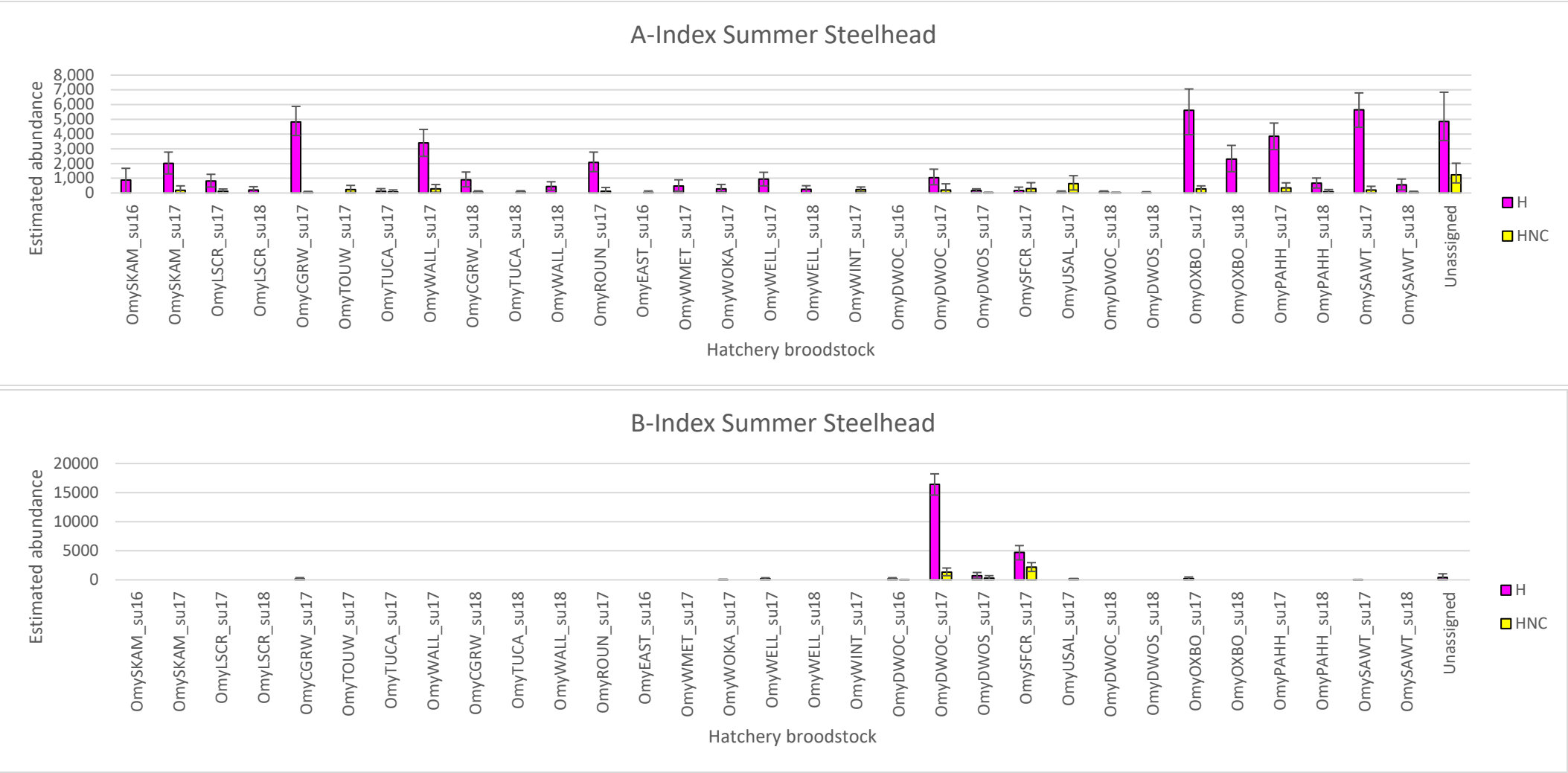


Figure 36. Estimated abundance (± 95% CI) of A-Index (<780mm FL, top) and B-Index (>=780mm FL, bottom) hatchery origin (clipped “H” and unclipped “HNC”) and natural-origin (“W”) steelhead assigned to genetic stock of origin that were sampled at Bonneville Dam in 2020.



1839
1840 **Figure 37. Estimated abundance (\pm 95% CI) of A-Index (<780 mm FL, top) and B-Index (≥ 780 mm FL, bottom) hatchery origin steelhead (adipose clipped**
1841 **and unclipped) assigned to broodstock of origin that were sampled at Bonneville Dam in 2020.**
1842
1843 **Key to broodstock collection is presented in Appendix 12.**

1844 **Table 52. Hatchery broodstock-specific estimated abundance of clipped and unclipped A-Index and B-Index PBT-assigned steelhead passing Bonneville Dam in 2020.**

					Hatchery clipped				Hatchery Unclipped			
					A-INDEX		B-INDEX		A-INDEX		B-INDEX	
Hatchery	Stock	GSI RepGrp	Broodstock	Broodyear	Est.	95% CI	MLE	95% CI	MLE	95% CI	MLE	95% CI
Skamania Hatchery	Summer	03_SKAMAN	OmySKAM_su16	2016	876	0 – 1674						
Skamania Hatchery	Summer	03_SKAMAN	OmySKAM_su17	2017	2,009	1292 – 2775			188	0 – 484		
Little Sheep Satellite	Imnaha	07_MGILCS	OmyLSCR_su17	2017	816	403 – 1268			121	0 – 271		
Little Sheep Satellite	Imnaha	07_MGILCS	OmyLSCR_su18	2018	192	0 – 428						
Lyons Ferry Hatchery	Wallowa stock -trapped/spawned at Cottonwood, released at Cottonwood and other Washington sites	07_MGILCS	OmyCGRW_su17	2017	4,824	3899 – 5874	157	0 – 382	37	0 – 110		
Lyons Ferry Hatchery	Touchet (in Walla Walla River basin)	07_MGILCS	OmyTOUW_su17	2017					237	36 – 515		
Lyons Ferry Hatchery	Tucannon	07_MGILCS	OmyTUCA_su17	2017	112	0 – 293			69	0 – 206		
Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGILCS	OmyWALL_su17	2017	3,394	2482 – 4313			288	46 – 574		
Lyons Ferry Hatchery	Wallowa stock -trapped/spawned at Cottonwood, released at Cottonwood and other Washington sites	07_MGILCS	OmyCGRW_su18	2018	889	416 – 1421			49	0 – 148		
Lyons Ferry Hatchery	Tucannon	07_MGILCS	OmyTUCA_su18	2018					51	0 – 151		
Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGILCS	OmyWALL_su18	2018	442	184 – 762						
Round Butte	Deschutes River	07_MGILCS	OmyROUN_su17	2017	2,081	1446 – 2774			125	0 – 375		
Eastbank	Wenatchee	09_UPPCOL	OmyEAST_su16	2016					46	0 – 139		
Wells Fish Hatchery	Methow	09_UPPCOL	OmyWMET_su17	2017	468	117 – 894						
Wells Fish Hatchery	Okanogan	09_UPPCOL	OmyWOKA_su17	2017	279	72 – 579	38	0 – 108				
Wells Fish Hatchery	On Station	09_UPPCOL	OmyWELL_su17	2017	936	480 – 1405	181	60 – 362				
Wells Fish Hatchery	On Station	09_UPPCOL	OmyWELL_su18	2018	246	0 – 493						
Winthrop NFH	Methow River	09_UPPCOL	OmyWINT_su17	2017					228	90 – 407		
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su16	2016			124	0 – 371			24	0 – 73
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su17	2017	1,034	560 – 1615	16,396	14561 – 18212	207	0 – 621	1,344	714 – 2034
Dworshak NFH	Dworshak stock-trapped and spawned at Dworshak, reared at Magic Valley FH, released in Salmon basin	10_SFCLWR	OmyDWOS_su17	2017	164	49 – 281	719	274 – 1271	16	0 – 49	302	49 – 717
Dworshak NFH	SF Clearwater	10_SFCLWR	OmySFCR_su17	2017	162	0 – 396	4,714	3436 – 5887	298	56 – 699	2,177	1443 – 2960
Pahsimeroi	Upper Salmon	10_SFCLWR	OmyUSAL_su17	2017	46	0 – 137			640	203 – 1175	147	62 – 233
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su18	2018	48	0 – 141			17	0 – 49		
Dworshak NFH	Dworshak stock-trapped and spawned at Dworshak, reared at Magic Valley FH, released in Salmon basin	10_SFCLWR	OmyDWOS_su18	2018	28	0 – 85						
Oxbow (IDFG)	Oxbow	14_UPSALM	OmyOXBO_su17	2017	5,616	3953 – 7058	224	0 – 497	276	0 – 483		
Oxbow (IDFG)	Oxbow	14_UPSALM	OmyOXBO_su18	2018	2,305	1445 – 3229						
Pahsimeroi	Pashsimeroi	14_UPSALM	OmyPAHH_su17	2017	3,856	2942 – 4744			348	71 – 688		
Pahsimeroi	Pashsimeroi	14_UPSALM	OmyPAHH_su18	2018	670	335 – 1015			94	0 – 233		
Sawtooth	Sawtooth	14_UPSALM	OmySAWT_su17	2017	5,641	4457 – 6790	25	0 – 74	203	0 – 454		
Sawtooth	Sawtooth	14_UPSALM	OmySAWT_su18	2018	556	211 – 943			40	0 – 118		
#N/A	#N/A	#N/A	Unassigned	#N/A	4,851	3559 – 6836	424	146 – 1043	1,234	683 – 2019		
TOTAL					42,542		23,001		4,812		3,994	

1845 **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
1846 passed the Bonneville Dam at the fish counting window. Key to broodstock collection is presented in Appendix 12.

Run-timing of steelhead stocks in 2020

We were able to characterize the run-timing distributions at the broodstock level for the clipped (Figure 38) and unclipped (Figure 39) 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 4/1/2020 – 6/30/ 2020, and the summer A-/B-Index period begins on 7/1/2020 and lasts until 10/31/2020. 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 38). There were 27 different clipped hatchery broodstocks and ten broodstocks (OmyCGRW_su17, OmyDWOC_su16, OmyDWOC_su17, OmyDWOC_su18, OmyDWOS_su17, OmyDWOS_su18, OmyOXBO_su18, OmySAWT_su17, OmySFCR_su17, and OmyUSAL_su17) had median dates that were observed after August 25th in 2020. For eight broodstocks in which both A-Index and B-Index were represented, the B-Index stock had a later median date in all but two pairs. For the unclipped stocks arriving in the A-/B-Index period, there were 22 unique broodstocks and eight of them (OmyDWOC_su16, OmyDWOC_su17, OmyDWOC_su18, OmyDWOS_su17, OmyROUN_su17, OmySAWT_su17, OmySFCR_su17, and OmyUSAL_su17) had a median run date after August 25th (Figure 39).

We characterized the run-timing distributions for natural-origin steelhead stocks (Figure 40); the patterns generally are consistent with past years. The late arriving stocks with median dates on or after August 25th were 12_SFSALM (both A-Index and B-Index), 11_UPCLWR (both A-Index and B-Index), 13_MFSALM (B-Index), and 10_SFCLWR (B-Index). For the nine reporting groups in which both A-Index and B-Index were represented, the B-Index stock had a later median date in all but two reporting groups.

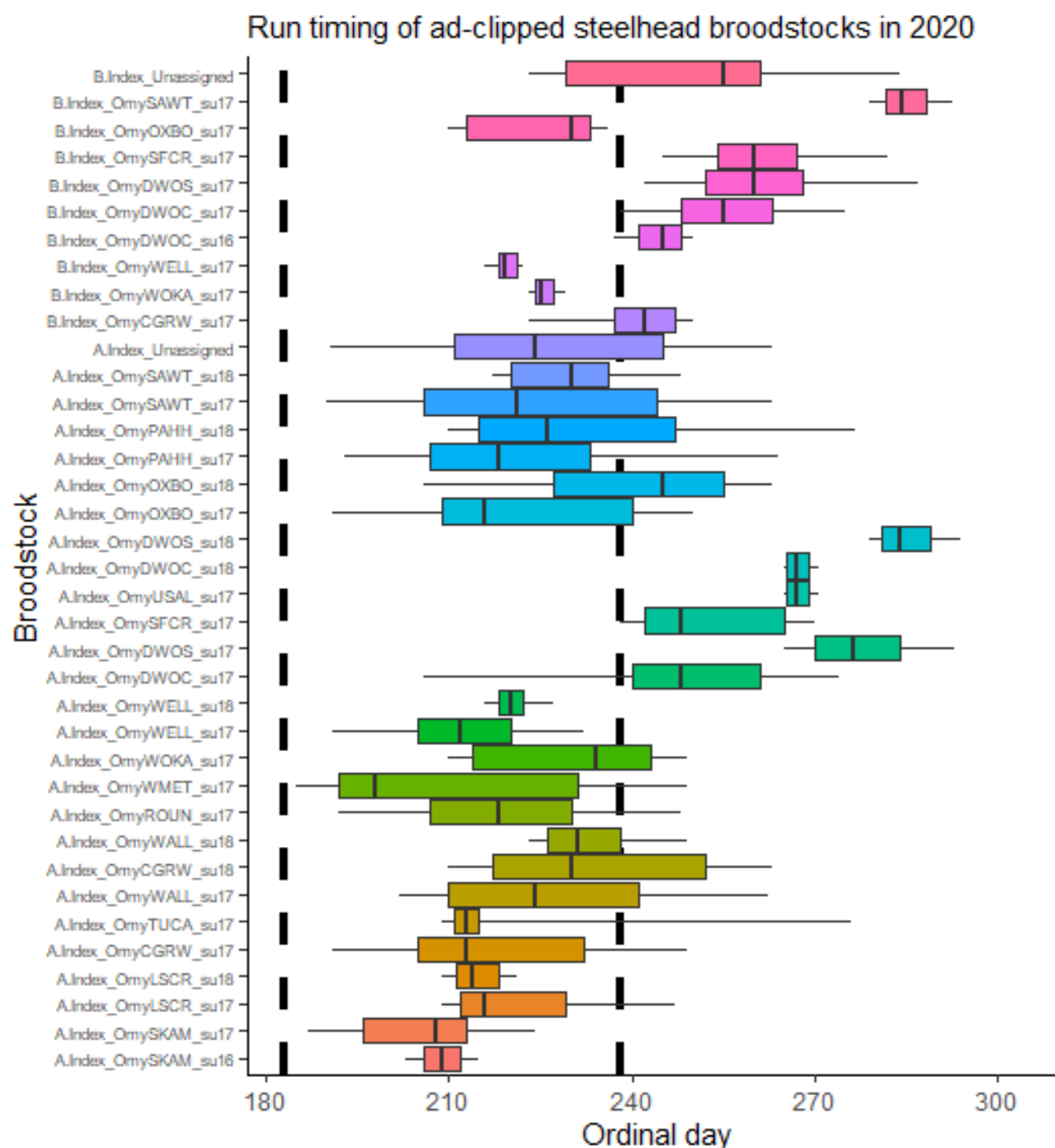


Figure 38. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for clipped hatchery-origin steelhead that were sampled at Bonneville Dam in 2020 and reported by A-Index and B-Index size category.

Key to broodstock collection is presented in Appendix 12.

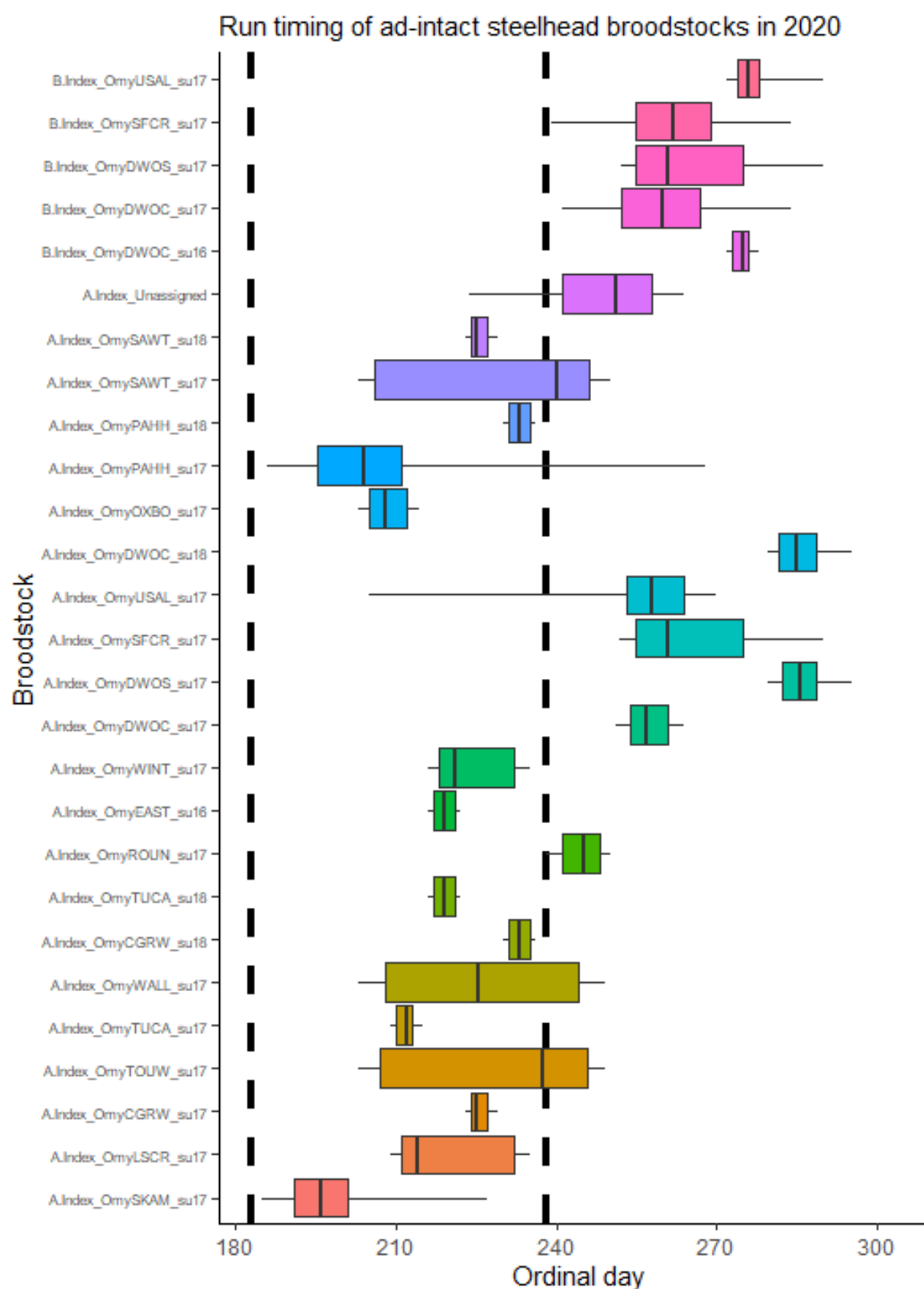


Figure 39. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for unclipped hatchery-origin steelhead that were sampled at Bonneville Dam in 2020 and reported by A-Index and B-Index size category.

1884 **Key to broodstock collection is presented in Appendix 12.**

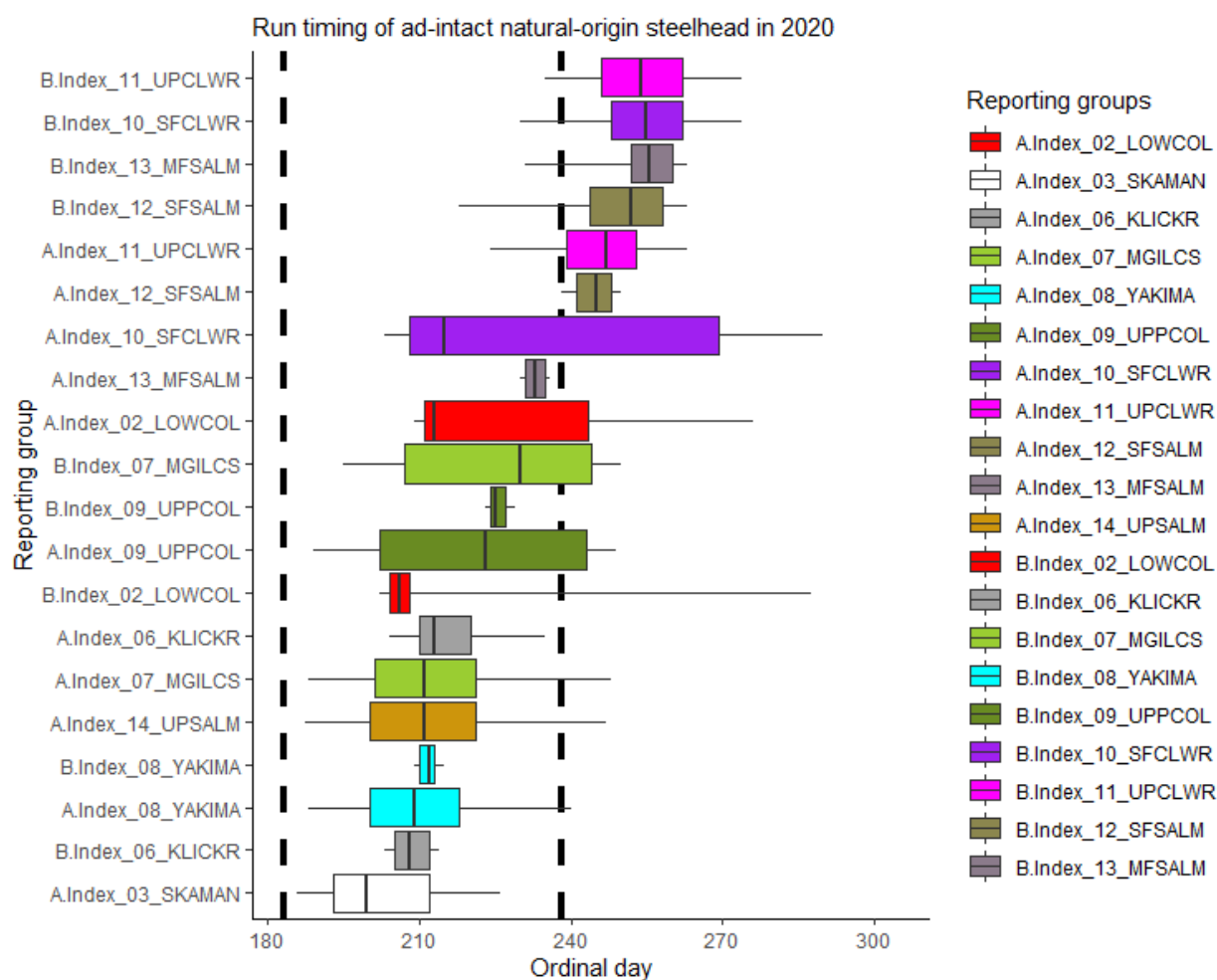


Figure 40. Reporting group level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for natural-origin steelhead (unclipped hatchery-origin fish excluded) that were sampled at Bonneville Dam in 2020 and split by A-Index and B-Index size category.

Estimated abundance and run-timing of Sockeye salmon stocks in 2020

Daily passage of Sockeye salmon at Bonneville Dam in 2020 is provided in Figure 41. Stock abundance for sockeye salmon was estimated over a course of 15 statistical weeks (i.e. weeks 23-37). A total of 1,729 sockeye salmon were sampled at Bonneville Dam in 2020 and were assigned to one of four genetic stocks (i.e., Okanogan, Wenatchee, Snake, and Lake Billy Chinook) using GSI and one reintroduced stock (Yakima) using PBT (Table 53). The Okanogan stock had the highest relative abundance (274,008), followed by the Wenatchee (55,890) (Table 53). This year there were a small number of sockeye estimated from Snake River (122). The Lake Billy Chinook stock had zero estimated abundance (Table 53, Figure 42). The reintroduced stock from Yakima River had a relatively high sample size and was estimated at 11,719 fish in 2020.

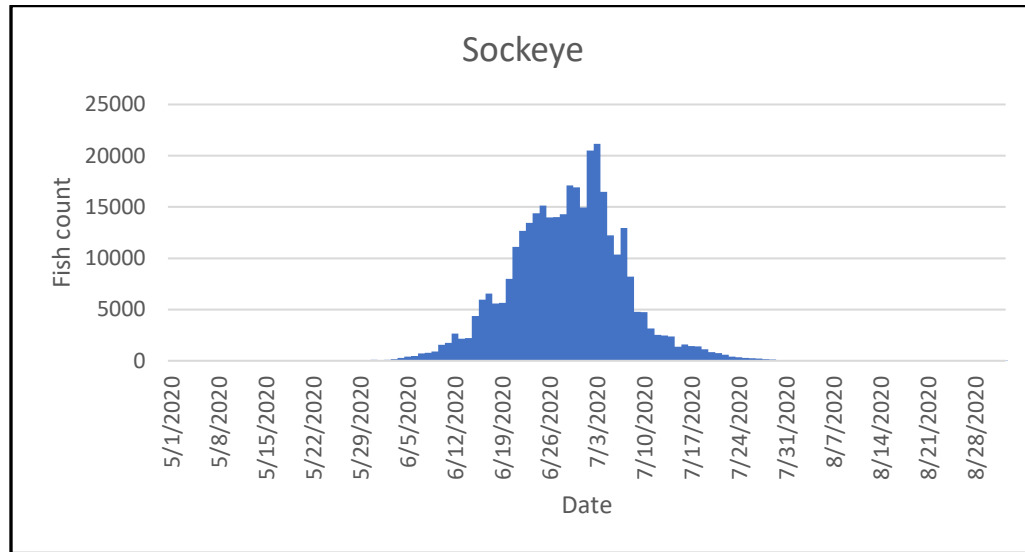


Figure 41. Daily passage of sockeye at Bonneville Dam in 2020 (source: <https://www.fpc.org>).

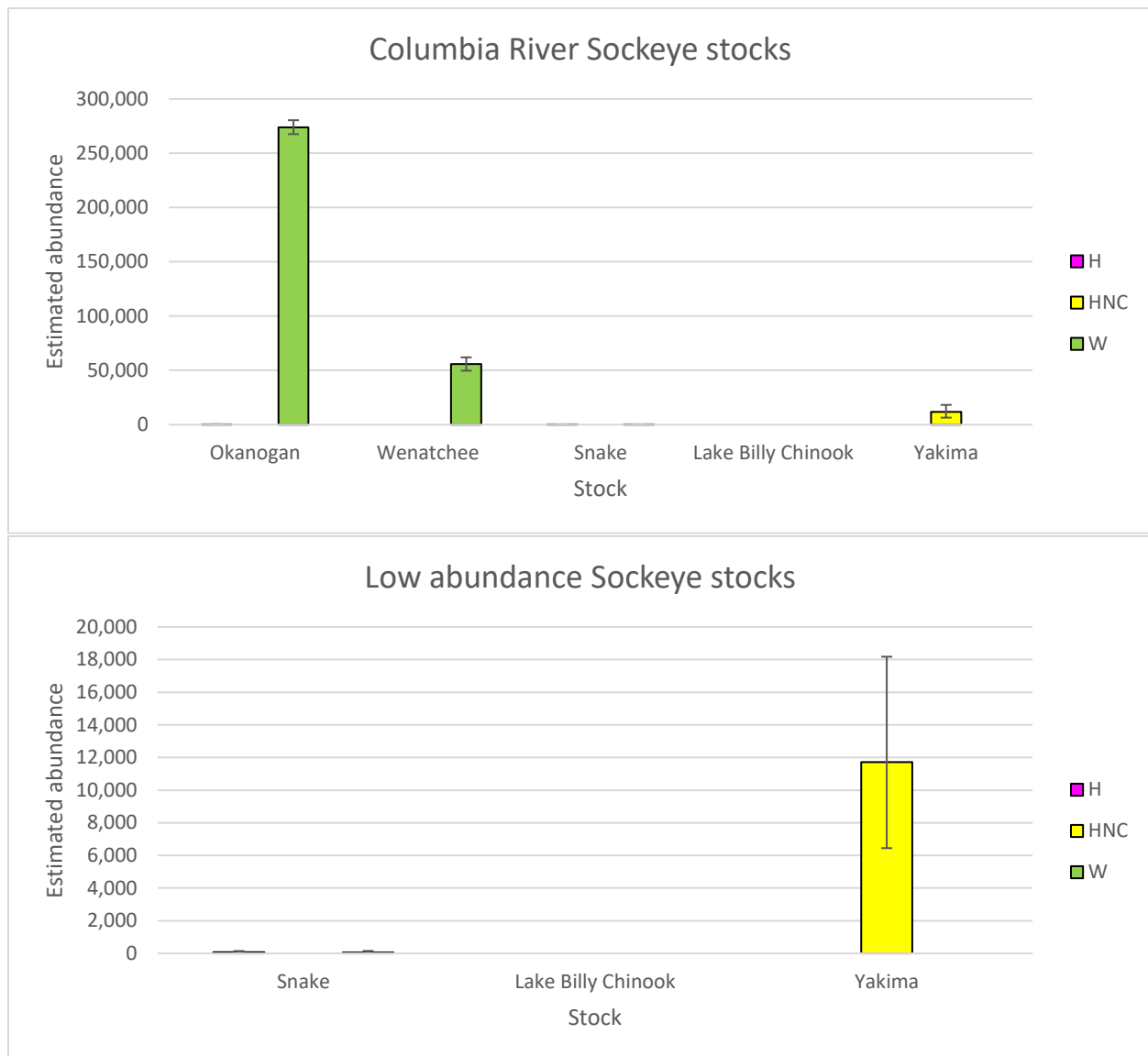


Figure 42. Estimated abundance (\pm 95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2020.

We characterized the run-timing distributions for all detected sockeye salmon stocks (Figure 43). The Wenatchee, Okanogan, and Yakima stocks had nearly identical run timing distributions each with a median date on 06/29/20, and the Snake River stock was timed slightly later (07/20/20; Figure 43).

1917 **Table 53. Estimated abundance of sockeye salmon stocks passing Bonneville Dam in 2020.**

Reporting Group name	Estimated abundance					
	H		HNC		W	
	Est.	95% CI	Est.	95% CI	Est.	95% CI
Okanogan	133	0 – 398			273,876	267546 – 280388
Wenatchee					55,890	49699 – 61963
Snake	72	19 – 145			50	0 – 150
Lake Billy Chinook						
Yakima			11,719	6448 – 18174		
Total	204		11,719		329,815	

1918

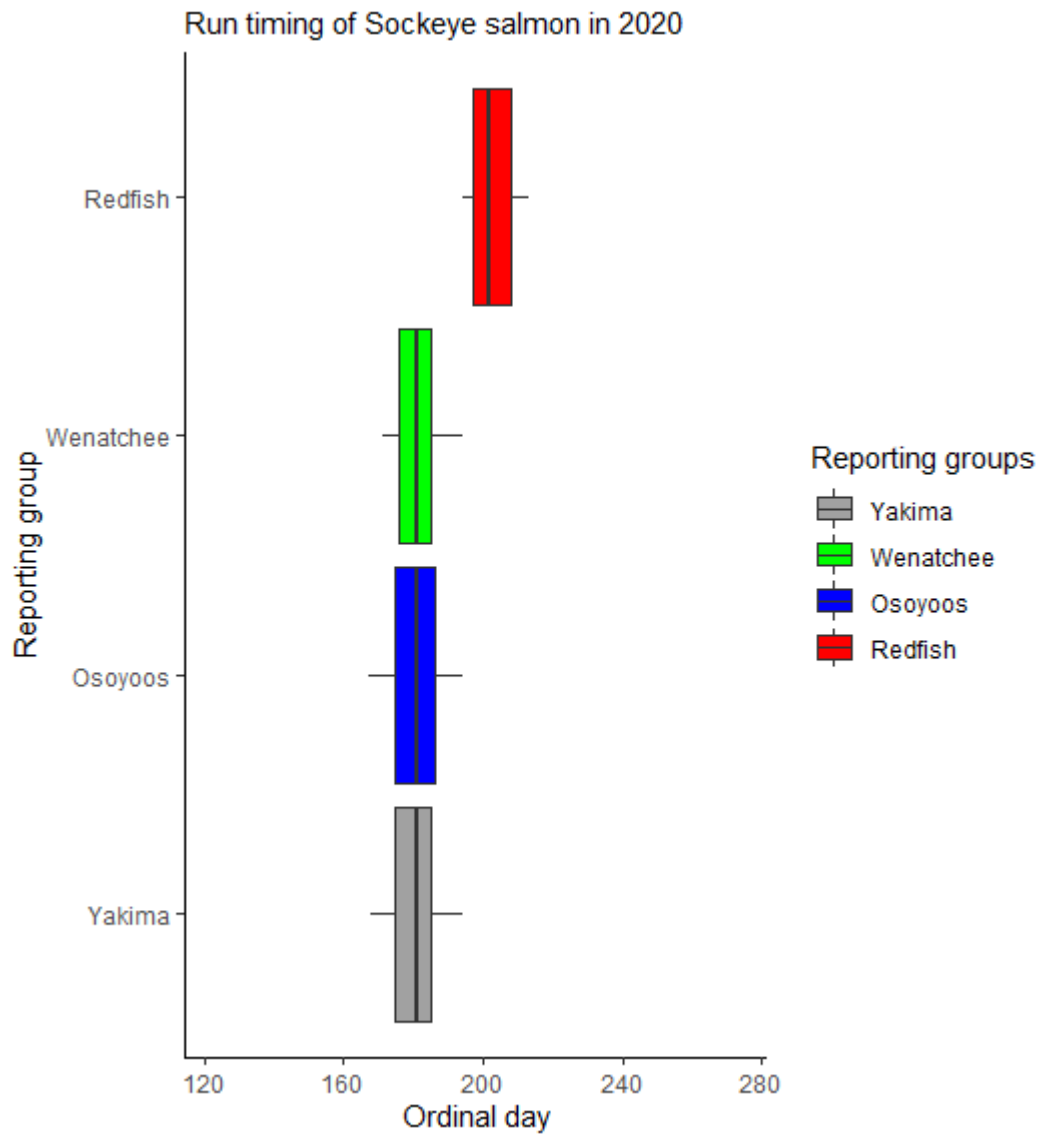


Figure 43. Run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for the major stocks of sockeye salmon that were sampled at Bonneville Dam in 2020 and assigned to stock of origin.

In-season analysis of Chinook salmon passing Bonneville Dam in 2021

There were four in-season reports covering data on Chinook Salmon that passed Bonneville Dam during the Spring Management Period, and we delivered a total of eight planned in-season reports for Chinook Salmon in 2021 across all management periods (Table 40). The first report was distributed to members of the U.S. v OR TAC on May 10, 2021. 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 analysis similar to the reporting for the Bonneville Dam post-season report for run year 2020. We use window counts of only the adult-sized fish in order to estimate stock-specific abundances of adult-size Chinook Salmon. In the more distant 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 restrict 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 3,136 adult-sized Chinook Salmon were collected and analyzed for the 2021 in-season reports (Table 54). 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 8, 2021 provided sub-totals for each stock that were broken out by management period (clipped hatchery-origin stocks, Table 55; unclipped hatchery-origin stocks, Table 56; natural-origin stocks, Table 57). Two groups of 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 57) and upper Columbia River spring Chinook Salmon stocks (Reporting group 10_UCOLSP, Table 57). 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.

PBT assignments during the Chinook Salmon management periods allowed classification of 81 unique hatchery broodstocks in 2021 (Table 58). The total estimated abundances of these clipped and unclipped broodstocks were comprised of 21% Snake River and 76% of hatcheries from the rest of the Columbia River above Bonneville Dam (Figure 44). 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 2021. We observed that this run year of Chinook Salmon at Bonneville Dam represents nearly complete 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 59). In fact, in 2021, the percentage of adipose-clipped fish abundance that were estimated to be PBT broodstock ranged from 95 – 100%, 92 – 100%, and 84 – 100% in the spring, summer, and fall management periods, respectively. These percentages can be estimated higher than 100% due to tag rates being lower than what the true tag rate may be (e.g., by chance, there may be higher rates of return among the sampled parents relative to the unsampled parents). 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 11).

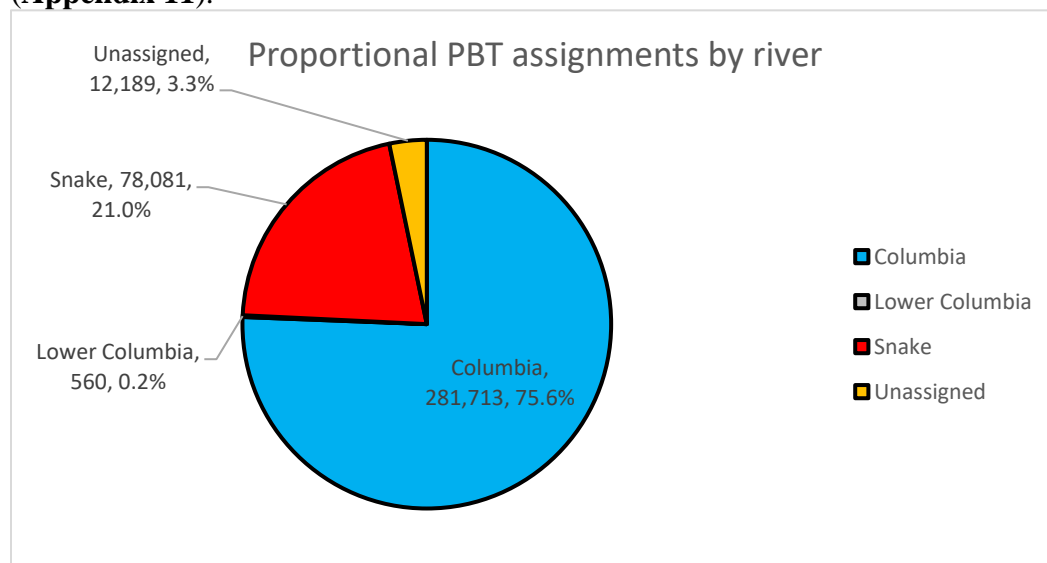


Figure 44. Proportion of hatchery broodstocks from the Snake River versus the rest of the Columbia River above Bonneville Dam in 2021.

1989 **Table 54. The sample sizes of Chinook salmon at the Bonneville Dam AFF during the**
1990 **spring, summer, and fall management periods of 2021.**

		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	889	157	0	0	0	0	0	0	0.00%	0.00%
		17	2,359	450	5	95	4	5	100	9	4.24%	2.00%
		18	13,396	2,439	11	138	12	17	149	29	1.11%	1.19%
		19	12,219	2,779	19	228	27	23	247	50	2.02%	1.80%
		20	11,593	4,422	16	155	43	28	171	71	1.48%	1.61%
		21	5,093	2,728	5	82	29	18	87	47	1.71%	1.72%
		22	3,798	2,529	4	49	24	16	53	40	1.40%	1.58%
		23	5,102	2,574	4	96	51	13	100	64	1.96%	2.49%
		24	6,527	2,937	9	108	53	14	117	67	1.79%	2.28%
		25	3,701	1,541	1	42	18	9	43	27	1.16%	1.75%
	Summer	25	6088	2674	10	72	35	6	82	41	1.35%	1.53%
		26	10782	4254	6	90	32	4	96	36	0.89%	0.85%
		27	8167	2757	1	24	12	3	25	15	0.31%	0.54%
		28	6082	2637	2	28	8	6	30	14	0.49%	0.53%
		29	3402	1849	1	14	10	1	15	11	0.44%	0.59%
		30	1965	1596		15	9		15	9	0.76%	0.56%
		31	1055	1181		7	4	2	7	6	0.66%	0.51%
	Fall	32	739	1,540					0	0	0.00%	0.00%
		33	1,206	2,077			2	1	0	3	0.00%	0.14%
		34	2,423	4,156		1	4		1	4	0.04%	0.10%
		35	36,782	23,921	6	44	74	41	50	115	0.14%	0.48%
		36	45,885	44,529	14	95	82	54	109	136	0.24%	0.31%
		37	53,355	14,974	8	74	80	42	82	122	0.15%	0.81%
		38	35,737	16,226	12	78	128	70	90	198	0.25%	1.22%
		39	13,234	17,555	6	41	82	34	47	116	0.36%	0.66%
		40	8,422	7,099	7	22	61	21	29	82	0.34%	1.16%
		41	3,531	5,358	2	19	45	11	21	56	0.59%	1.05%
		42-44	4,058	3,724		1		1	1	1	0.02%	0.03%
		Total	307,592	180,661	149	1,618	929	440	1,767	1,369	0.57%	0.76%

1991 Note: The fish counts indicate the number of adult-sized Chinook Salmon at the fish ladder
1992 windows at Bonneville Dam and the sample (N) indicates the numbers of adult-sized Chinook
1993 Salmon (>560 mm fork length) that were collected at the AFF. TAC provides estimates of the
1994 total clipped and unclipped adult abundance. The AFF sample is broken into adipose-clipped and
1995 non-clipped categories and then further indicate whether a PBT assignment (PBT) was
1996 confirmed or if it was not assigned with PBT (GSI). Sample rate relates the total sample for a
1997 particular stratum to the total fish counted at the window. The boxes around statistical weeks
1998 indicate the breakpoints in the weekly strata.

1999 **Table 55. Preliminary in-season reporting of clipped hatchery-origin stock-specific abundance estimates of adult-sized**
2000 **Chinook Salmon passing Bonneville Dam across all management periods in 2021.**

		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	530	218 – 799	96				626
West Cascade Fall	Fall	03_WCASFA					957	0 – 1120	957
Willamette	Spring	04_WILLAM	52	0 – 79	236	0 – 378			287
Spring Creek Tule	Fall	05_SPCRTU				0 – 219	46,678	42599 – 51746	46,678
Klickitat	Spring	06_KLICKR	1,230	1055 – 1564	0	0 – 1161			1,230
Deschutes spring	Spring	07_DESCSP	4,388	3600 – 5002	275	0 – 842			4,663
John Day	Spring	08_JOHNDR	44	0 – 182	0				44
Yakima	Spring	09_YAKIMA	1,258	891 – 1476	632	0 – 699			1,891
Upper Columbia spring	Spring	10_UCOLSP	7,291	6101 – 8295	0				7,291
Tucannon	Spring	11_TUCANO							0
Hells Canyon	Spring/Summer	12_HELLSC	24,204	22625 – 25014	1,154	0 – 1206			25,359
South Fork Salmon	Spring/Summer	13_SFSALM	3,580	3134 – 4468	424				4,004
Chamberlain Creek	Spring/Summer	14_CHMBLN							0
Middle Fork Salmon	Spring/Summer	15_MFSALM	0	0 – 18	0				0
Upper Salmon	Spring/Summer	16_UPSALM	1,282	1113 – 1731	0				1,282
Deschutes fall	Fall	17_DESCFA					314	0 – 314	314

Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	12,250	11418 – 13159	34,369	37770 – 40360	84,710	81387 – 92117	131,329
SNAKE RIVER fall	Fall	19_SRFALL			204	173 – 1291	29,156	23417 – 30794	29,361
Bonneville Pool spring	Spring	20_BONPOOLSP	7,015	6411 – 8790	75				7,091
UMATILLA spring	Spring	21_UMATILLASP	1,553	1180 – 1780	0				1,553
Bonneville Pool fall	Fall	22_BONPOOLFA			74	0 – 230	40,481	34601 – 46134	40,556
UMATILLA fall	Fall	23_UMATILLFA					3,076	1360 – 5194	3,076
Total			64,678		37,541		205,372		307,592

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, 2021 are provided. Bonneville 2021 spring, summer, and fall management period Chinook PBT/GSI analyses that corresponds with statistical weeks 1-25 (01/01/21-06/15/21: spring)***, 25-31 (6/16/21-7/31/21:summer) and 31-44 (8/1/2021-11/1/2021:fall).

Table 56. 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 2021.

			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			178						178
West Cascade Fall	Fall	03_WCASFA									0
Willamette	Spring	04_WILLAM									0

Spring Creek Tule	Fall	05_SPCRTU					5,836	4079 – 9159	5,836
Klickitat	Spring	06_KLICKR							0
Deschutes spring	Spring	07_DESCSP	201	66 – 439	202				403
John Day	Spring	08_JOHNDR							0
Yakima	Spring	09_YAKIMA	103	58 – 248	0				103
Upper Columbia spring	Spring	10_UCOLSP	3,129	2468 – 3241	140				3,269
Tucannon	Spring	11_TUCANO							0
Hells Canyon	Spring/Summer	12_HELLSC	2,383	1973 – 2919	182				2,566
South Fork Salmon	Spring/Summer	13_SFSALM	1,163	656 – 1419	67	0 – 461			1,230
Chamberlain Creek	Spring/Summer	14_CHMBLN							0
Middle Fork Salmon	Spring/Summer	15_MFSALM							0
Upper Salmon	Spring/Summer	16_UPSALM	499	371 – 677	0				499
Deschutes fall	Fall	17_DESCFA							0
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	936	806 – 1137	2,458	1248 – 3975	27,217	24180 – 30442	30,611
Snake River fall	Fall	19_SRFALL				99 – 1243	15,132	12956 – 19386	15,132
Bonneville Pool spring	Spring	20_BONPOOLSP	301	88 – 532	0				301
Umatilla spring	Spring	21_UMATILLASP	168	4 – 333	0				168
Bonneville Pool fall	Fall	22_BONPOOLFA					4,657	2697 – 5457	4,657
Umatilla fall	Fall	23_UMATILLAFA							0
Total			8,882		3,227		52,843		64,952

2009

2010

2011

2012

2013

2014

2015

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 57. Preliminary in-season reporting of natural-origin stock-specific abundance estimates of adult-sized Chinook Salmon passing Bonneville Dam across all management periods in 2021.

			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				0 – 94	268	0 – 605	268
West Cascade Spring	Spring	02_WCASSP			181				181
West Cascade Fall	Fall	03_WCASFA					513	123 – 1008	513
Willamette	Spring	04_WILLAM				0 – 125	116	0 – 349	116
Spring Creek Tule	Fall	05_SPCRTU					1,109	244 – 2209	1,109
Klickitat	Spring	06_KLICKR	121	0 – 290	0				121
Deschutes spring	Spring	07_DESCSP	275	91 – 485	0				275
John Day	Spring	08_JOHNDR	267	62 – 495	0				267
Yakima	Spring	09_YAKIMA	1,544	1072 – 2018	0	0 – 94			1,544
Upper Columbia spring	Spring	10_UCOLSP	2,068	1527 – 2671	65	0 – 338			2,134
Tucannon	Spring	11_TUCANO							0
Hells Canyon	Spring/Summer	12_HELLSC	2,277	1690 – 2849	199	61 – 529			2,476
South Fork Salmon	Spring/Summer	13_SFSALM	1,000	663 – 1395	64	0 – 842			1,064

Chamberlain Creek	Spring/Summer	14_CHMBLN	98	0 – 214	0				98
Middle Fork Salmon	Spring/Summer	15_MFSALM	588	298 – 893	0				588
Upper Salmon	Spring/Summer	16_UPSALM	1,457	1003 – 1902	130	0 – 338			1,588
Deschutes fall	Fall	17_DESCFA				0 – 213	3,035	1812 – 4468	3,035
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	3,933	3399 – 4467	12,562	16229 – 18657	65,177	60190 – 69829	81,672
Snake River fall	Fall	19_SRFALL	44	0 – 131	519	542 – 1444	18,097	15027 – 21328	18,660
Total			13,673		13,720		88,316		115,709

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.

2016
2017
2018
2019
2020
2021
2022

2023 **Table 58. The estimated abundances of the clipped and unclipped adult-sized Chinook salmon assigned to PBT hatchery**
2024 **broodstock that passed Bonneville Dam in 2021 (1/01/2021 – 12/31/2021).**

Period	Expected Run Time	Hatchery	Broodstock	Brood year	GSI RepGrp	Abundance estimate				Total
						Clipped		Unclipped		
						Est.	95% C.I.	Est.	95% C.I.	
Spring	01Spring	Parkdale Fish Facility	OtsPARK_seg_sp16	2016	02_WCASSP	52	0 – 157			52
	01Spring	Parkdale Fish Facility	OtsPARK_seg_sp17	2017	02_WCASSP	390	125 – 672			390
	01Spring	Parkdale Fish Facility	OtsPARK_seg_sp18	2018	02_WCASSP	88	0 – 263			88
	01Spring	Klickitat Hatchery	OtsKLIC_seg_sp16	2016	06_KLICKR	238	49 – 473			238
	01Spring	Klickitat Hatchery	OtsKLIC_seg_sp17	2017	06_KLICKR	896	502 – 1284			896
	01Spring	Klickitat Hatchery	OtsKLIC_seg_sp18	2018	06_KLICKR	58	0 – 173			58
	01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp17	2017	07_DESCSP	502	212 – 860	65	0 – 196	568
	01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp18	2018	07_DESCSP	166	52 – 339	57	0 – 171	223
	01Spring	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp17	2017	07_DESCSP	3,668	2783 – 4539	78	0 – 235	3,746
	01Spring	Yakima River Roza Dam	OtsYRRD_int_sp17	2017	09_YAKIMA	936	544 – 1317	58	0 – 174	994
	01Spring	Yakima River Roza Dam	OtsYRRD_seg_sp17	2017	09_YAKIMA	193	0 – 378	45	0 – 134	237

	01Spring	Chief Joseph Hatchery	OtsCHJO_seg_sp17	2017	10_UCOLSP	548	225 – 904			548
	01Spring	Eastbank Fish Hatchery	OtsEAST_seg_sp17	2017	10_UCOLSP	657	352 – 1000	981	604 – 1372	1,638
	01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp16	2016	10_UCOLSP	32	0 – 97			32
	01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp17	2017	10_UCOLSP	4,903	3917 – 5929	484	176 – 837	5,387
	01Spring	Methow Fish Hatchery	OtsMETH_seg_sp16	2016	10_UCOLSP			58	0 – 174	58
	01Spring	Methow Fish Hatchery	OtsMETH_seg_sp17	2017	10_UCOLSP			423	154 – 720	423
	01Spring	Winthrop National Fish Hatchery	OtsWINT_seg_sp17	2017	10_UCOLSP	344	124 – 612	1,183	735 – 1620	1,526
	01Spring	Winthrop National Fish Hatchery	OtsWINT_seg_sp18	2018	10_UCOLSP	90	0 – 269			90
	01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp16	2016	12_HELLSC	106	0 – 251			106
	01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp17	2017	12_HELLSC	2,447	1843 – 3121	457	204 – 745	2,905
	01Spring	Clearwater Fish Hatchery	OtsPOWP_seg_sp17	2017	12_HELLSC	73	0 – 218	109	0 – 242	181

	01Spring	Clearwater Fish Hatchery	OtsPOWP_seg_sp18	2018	12_HELLSC	51	0 – 153			51
	01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp17	2017	12_HELLSC	5,107	4212 – 6090	705	368 – 1054	5,812
	01Spring	Dworshak National Fish Hatchery	OtsKOOS_seg_sp17	2017	12_HELLSC	1,500	952 – 2048	114	0 – 231	1,615
	01Spring	Lookingglass Fish Hatchery	OtsLOOK_seg_sp17	2017	12_HELLSC	2,081	1531 – 2745	297	70 – 549	2,378
	01Spring	Nez Perce	OtsNPFH_seg_sp17	2017	12_HELLSC			219	69 – 446	219
	01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp16	2016	12_HELLSC	51	0 – 152			51
	01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp17	2017	12_HELLSC	10,947	9693 – 12088	418	152 – 713	11,365
	01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp16	2016	20_BONPOOLSP	90	0 – 270			90
	01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp17	2017	20_BONPOOLSP	4,499	3664 – 5350	85	0 – 256	4,585
	01Spring	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp16	2016	20_BONPOOLSP	73	0 – 218	90	0 – 270	162

	01Spring	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp17	2017	20_BONPOOLSP	2,354	1715 – 2977	125	0 – 302	2,479
	01Spring	Umatilla Fish Hatchery	OtsUMAT_seg_sp17	2017	21_UMATILLASP	1,553	1061 – 2115	168	0 – 336	1,721
	02Spring/ Summer	Lookingglass Fish Hatchery	OtsIMNW_seg_ss16	2016	12_HELLSC	103	0 – 255			103
	02Spring/ Summer	Lookingglass Fish Hatchery	OtsIMNW_seg_ss17	2017	12_HELLSC	1,138	698 – 1565	64	0 – 193	1,202
	02Spring/ Summer	McCall Fish Hatchery	OtsMCCA_seg_ss17	2017	13_SFSALM	3,488	2830 – 4239	1,060	668 – 1496	4,548
	02Spring/ Summer	McCall Fish Hatchery	OtsJHNW_int_ss17	2017	13_SFSALM			103	0 – 253	103
	02Spring/ Summer	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss17	2017	16_UPSALM	51	0 – 154			51
	02Spring/ Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss17	2017	16_UPSALM	1,231	778 – 1695	436	183 – 715	1,666
	02Spring/ Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss18	2018	16_UPSALM			63	0 – 190	63
	03Summer	Chief Joseph Hatchery	OtsCHJO_int_su15	2015	18_UCOLSF	63	0 – 188			63
	03Summer	Chief Joseph Hatchery	OtsCHJO_int_su16	2016	18_UCOLSF	710	357 – 1092			710
	03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su16	2016	18_UCOLSF	1,427	1000 – 1876	85	0 – 206	1,512
	03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su17	2017	18_UCOLSF	726	414 – 1079	156	0 – 331	882

	03Summer	Chief Joseph Hatchery	OtsCHJO_int_su17	2017	18_UCOLSF	172	0 – 376			172
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su16	2016	18_UCOLSF	3,283	2641 – 3989	144	39 – 291	3,426
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su17	2017	18_UCOLSF	1,196	777 – 1617	59	0 – 177	1,255
	03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su16	2016	18_UCOLSF	862	513 – 1248	57	0 – 171	919
	03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su17	2017	18_UCOLSF	971	533 – 1377			971
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su16	2016	18_UCOLSF	1,842	1352 – 2374	332	128 – 562	2,174
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su17	2017	18_UCOLSF	963	562 – 1377	49	0 – 148	1,012
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su18	2018	18_UCOLSF			53	0 – 160	53
	#N/A	#N/A	Unassigned	#N/A	#N/A	1,760	1052 – 2783			1,760
			Spring Subtotal			64,678		8,882		73,560
Summer	01Spring	Parkdale Fish Facility	OtsPARK_seg_sp18	2018	02_WCASSP	96		178		274
	01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp17	2017	07_DESCSP	84				84
	01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp18	2018	07_DESCSP	191				191
	01Spring	Warm Springs	OtsWSNF_seg_sp18	2018	07_DESCSP			202		202

		National Fish Hatchery								
01Spring	Yakima River Roza Dam	OtsYRRD_int_sp18	2018	09_YAKIMA	319					319
01Spring	Yakima River Roza Dam	OtsYRRD_seg_sp18	2018	09_YAKIMA	313					313
01Spring	Eastbank Fish Hatchery	OtsEAST_seg_sp17	2017	10_UCOLSP			140			140
01Spring	Clearwater Fish Hatchery	OtsPOWP_seg_sp17	2017	12_HELLSC	477					477
01Spring	Clearwater Fish Hatchery	OtsPOWP_seg_sp18	2018	12_HELLSC			182			182
01Spring	Lookingglass Fish Hatchery	OtsLOOK_seg_sp17	2017	12_HELLSC	83					83
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp18	2018	12_HELLSC	84					84
01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp17	2017	20_BONPOOLSP	75					75
02Spring/ Summer	Lookingglass Fish Hatchery	OtsIMNW_seg_ss17	2017	12_HELLSC	511					511
02Spring/ Summer	McCall Fish Hatchery	OtsMCCA_seg_ss17	2017	13_SFSALM	236		67			303
02Spring/ Summer	McCall Fish Hatchery	OtsMCCA_seg_ss18	2018	13_SFSALM	188					188

	03Summer	Chief Joseph Hatchery	OtsCHJO_int_su16	2016	18_UCOLSF	3,474		572		4,045
	03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su16	2016	18_UCOLSF	2,254				2,254
	03Summer	Chief Joseph Hatchery	OtsCHJO_int_su17	2017	18_UCOLSF	2,921		241		3,162
	03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su17	2017	18_UCOLSF	2,882		353		3,235
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su15	2015	18_UCOLSF	157				157
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su16	2016	18_UCOLSF	6,594		649		7,243
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su17	2017	18_UCOLSF	5,077				5,077
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su18	2018	18_UCOLSF	533				533
	03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su16	2016	18_UCOLSF	1,773		137		1,910
	03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su17	2017	18_UCOLSF	1,131				1,131
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su16	2016	18_UCOLSF	4,890		65		4,955
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su17	2017	18_UCOLSF	2,116		220		2,336
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su18	2018	18_UCOLSF			221		221

	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	2018	19_SRFALL	204				204
	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa16	2016	22_BONPOOLFA	74				74
	#N/A	#N/A	Unassigned	#N/A	#N/A	804				804
			Summer Subtotal			37,541		3,227		40,769
Fall	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su17	2017	18_UCOLSF	835	0 – 2506			835
	04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa17	2017	03_WCASFA	560	0 – 1680			560
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa17	2017	05_SPCRTU	3,414	703 – 6540	137	0 – 410	3,551
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa18	2018	05_SPCRTU	32,453	26425 – 38896	3,456	2048 – 5135	35,909
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	2019	05_SPCRTU	7,646	4182 – 11331	2,243	947 – 3809	9,889
	04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa16	2016	18_UCOLSF	1,228	0 – 2842	730	198 – 1393	1,958
	04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa17	2017	18_UCOLSF	58,853	50347 – 67081	20,784	17417 – 24085	79,637
	04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa18	2018	18_UCOLSF	16,017	11607 – 20468	4,780	3545 – 6221	20,797

	04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa17	2017	18_UCOLSF	1,904	722 – 3412	922	162 – 1812	2,826
	04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa18	2018	18_UCOLSF	782	0 – 2346			782
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa15	2015	19_SRFALL	303	0 – 908			303
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa16	2016	19_SRFALL			87	0 – 261	87
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	2017	19_SRFALL	13,124	8771 – 17601	4,478	2849 – 6288	17,603
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	2018	19_SRFALL	13,544	8821 – 18669	7,090	4956 – 9543	20,634
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa16	2016	19_SRFALL	323	0 – 968	126	0 – 379	449
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa17	2017	19_SRFALL	1,204	0 – 2818	2,171	929 – 3468	3,375
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	2018	19_SRFALL			1,180	285 – 2217	1,180
	04Fall	Klickitat Hatchery	OtsKLIC_seg_fa18	2018	22_BONPOOLFA	579	0 – 1671			579
	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa16	2016	22_BONPOOLFA	6,725	3746 – 9989	1,334	601 – 2248	8,059

	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	2017	22_BONPOOLFA	26,565	21037 – 32090	2,686	1432 – 4107	29,251
	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	2018	22_BONPOOLFA	6,612	3474 – 10196	637	159 – 1180	7,249
	04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	2018	23_UMATILLAFA	3,076	1094 – 5389			3,076
	#N/A	#N/A	Unassigned	#N/A	#N/A	9,626	5093 – 15985			9,626
			Fall SubTotal			205,372		52,843		258,215

2025
2026

2027 **Table 59. Expanded abundance of PBT-assigned Chinook Salmon stocks across**
2028 **management periods in 2021.**

	Statistical	Sample (Tag-rate-Corrected abundance)						% PBT of Clipped fish	
		Clipped		Non-clipped		Total GSI	Total PBT		
		week	GSI	PBT	GSI				PBT
Management period	Spring	1-16							
		17	8	2,351	189	261	197	2,612	99.7%
		18	469	12,928	946	1,493	1,414	14,421	96.5%
		19	469	11,751	1,434	1,344	1,903	13,095	96.2%
		20	570	11,023	2,584	1,838	3,155	12,860	95.1%
		21	28	5,065	1,637	1,091	1,666	6,155	99.4%
		22	142	3,656	1,484	1,045	1,626	4,701	96.3%
		23	-32	5,134	2,041	533	2,009	5,667	100.6%
		24	290	6,237	2,300	637	2,590	6,874	95.6%
		25	-101	3,802	1,013	528	912	4,330	102.7%
	Summer	25	503	5,585	2,258	416	2,761	6,001	91.7%
		26	321	10,461	3,748	506	4,069	10,967	97.0%
		27	-112	8,279	2,182	575	2,070	8,854	101.4%
		28	65	6,017	1,428	1,209	1,493	7,226	98.9%
		29	-8	3,410	1,662	187	1,654	3,597	100.2%
		30	-180	2,145	1,596	0	1,416	2,145	109.2%
		31	-55	1,110	746	435	691	1,545	105.2%
	Fall	32	0	0	0	0	0	0	
		33	0	0	1,344	733	1,344	733	
		34	0	2,423	0	0	0	2,423	100.0%
		35	1,936	34,847	14,756	9,165	16,691	44,012	94.7%
		36	2,891	42,994	25,492	19,038	28,382	62,032	93.7%
		37	1,587	51,768	9,340	5,634	10,927	57,402	97.0%
		38	2,359	33,378	9,880	6,346	12,239	39,724	93.4%
		39	806	12,428	11,900	5,655	12,705	18,084	93.9%
		40	1,291	7,131	5,064	2,035	6,354	9,167	84.7%
		41	-104	3,635	4,168	1,190	4,064	4,825	102.9%
		42-44	-1,491	5,549	-371	4,095	-1,862	9,644	136.7%
		Total		11,652	293,107	108,818	65,990	120,470	359,096

2029 Note: The % PBT of Clipped fish indicates the percentage of adipose clipped fish that are accounted for
2030 by PBT after tag rate expansions. If all hatchery broodstock above Bonneville Dam are included in the
2031 PBT baseline AND our estimated tag rates are accurate for each hatchery broodstock, then this percentage
2032 is expected to be 100% across all strata.

2033
2034
2035 *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 (7/1/2021 – 10/31/2021, Table 40). The Skamania Management Period (4/1/2021 – 6/30/2021) had a single report that covered the entire Skamania period. There were a total of 516 clipped and 156 unclipped steelhead that were sampled at the Bonneville Dam AFF and genotyped in 2021 (Table 60). 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 60). 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 61, Table 62, Table 63). 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 2021 include a breakdown of all the A- and B-Index steelhead abundance by broodstock for both clipped and unclipped hatchery-origin groups (Table 64).

2060 **Table 60. The sample sizes of Summer Steelhead at the Bonneville Dam AFF during the Skamania and A-/B-Index**
2061 **management periods of 2021.**

		Sample (N)														Clipped Sample rate	Unclipped Sample rate
		Statistical week	Strata	Clipped count	Unclipped count	A-Index				B-Index				Clipped Total	Unclipped Total		
						Clipped GSI	Unclipped PBT	Clipped GSI	Unclipped PBT	Clipped GSI	Unclipped PBT	Clipped GSI	Unclipped PBT				
Management period	Skamania	14	1	60	58									0	0	0.00%	0.00%
		15	1	52	57									0	0	0.00%	0.00%
		16	1	44	28									0	0	0.00%	0.00%
		17	1	16	26		1	1		1				2	1	12.50%	3.85%
		18	1	22	21			1						0	1	0.00%	4.76%
		19	1	21	7									0	0	0.00%	0.00%
		20	1	22	12			1						0	1	0.00%	8.33%
		21	1	7	3			1						0	1	0.00%	33.33%
		22	1	28	27		1	1						1	1	3.57%	3.70%
		23	1	33	44									0	0	0.00%	0.00%
		24	1	43	62	1	3	1						4	1	9.30%	1.61%
		25	1	99	119			1						0	1	0.00%	0.84%
		26	1	200	359		1	1						1	1	0.50%	0.28%
		27	1	151	296		3	2						3	2	1.99%	0.68%
			Subtotal Skamania	1	798	1119	1	9	10	0	0	1	0	0	11	10	1.38%
A-/B-Index	27	1	206	385									0	0	0.00%	0.00%	
	28	1	968	1,349		4			6				10	0	1.03%	0.00%	
	29	1	1499	1,821	1	12			17		1		30	1	2.00%	0.05%	
	30	1	1655	1,884	3	12			23				38	0	2.30%	0.00%	
	31	1	1363	1,474		2			2				4	0	0.29%	0.00%	
	32	1	1256	1,668									0	0	0.00%	0.00%	
	33	1	3252	2,729	1	8		1	9				18	1	0.55%	0.04%	
	34	1	1735	1,151		10			5				15	0	0.86%	0.00%	

	35	2	6,558	2,953		8		3	8		2		16	5	0.24%	0.17%
	36	2	6,770	2,264	6	34	2	6	20	4	2		64	10	0.95%	0.44%
	37	3	5,671	1,905	1	40		17	20	3	3	1	64	21	1.13%	1.10%
	38	4	4,487	1,206	4	63	3	31	13	5	5	3	85	42	1.89%	3.48%
	39	5	3,729	1,283		27		21	9	3		4	39	25	1.05%	1.95%
	40	5	2,374	627	2	36	2	10	9	2		2	49	14	2.06%	2.23%
	41	6	1,284	368		29	1	12	8	6	2	1	43	16	3.35%	4.35%
	42	6	750	205	1	12		1	5	1			19	1	2.53%	0.49%
	43	6	425	129									0	0	0.00%	0.00%
	44	6	245	124									0	0	0.00%	0.00%
Summer A-/B- Index subtotal																
			44,227	23,525	19	297	8	102	154	24	15	11	494	136	1.12%	0.58%
	Total		45,823	25,763	21	315	28	102	154	26	15	11	516	156	1.13%	0.61%

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 40).

Table 61. Estimated abundance of clipped hatchery-origin stocks of Summer Steelhead that passed Bonneville Dam in 2021 during the Skamania and A-/B-Index Management Periods.

	H	Subtotal for Skamania Period (Apr 1 - Jun 30)		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	A-Index		B-Index		A-Index		B-Index	
		Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI
Lower Columbia	02_LOWCOL	112	0 – 409	0	0 – 0				
Skamania	03_SKAMAN	147	0 – 435	73	0 – 290	377	67 – 1276	0	0 – 0
Willamette	04_WILLAM								

Big White Salmon	05_BWSALM								
Klickitat	06_KLICKR								
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	313	73 – 619	0	0 – 0	12,13 9	10353 – 13530	0	0 – 0
Yakima	08_YAKIMA								
upper Columbia	09_UPPCOL					3,059	1258 – 5156	0	0 – 0
SF Clearwater	10_SFCLWR					4,823	3554 – 5923	8,504	6964 – 8747
upper Clearwater	11_UPCLWR								
SF Salmon	12_SFSALM								
MF Salmon	13_MFSALM								
upper Salmon	14_UPSALM	152	0 – 381	0	0 – 0	15,32 5	14319 – 17937	0	0 – 218
	Total	725		73		35,72 3		8,504	

Note: Based on the sample data described in Table 60 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 62. Estimated abundance of unclipped hatchery-origin stocks of Summer Steelhead that passed Bonneville Dam in 2021 during the Skamania and A-/B-Index Management Periods.

Reporting Group name	Reporting Group Code	HNC		Subtotal for Skamania Period (Apr 1 - Jun 30)		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)	
		A-Index		B-Index		A-Index		B-Index			
		Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI
Lower Columbia	02_LOWCOL										
Skamania	03_SKAMAN	402	0 – 1207								
Willamette	04_WILLAM										
Big White Salmon	05_BWSALM										
Klickitat	06_KLICKR										

mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS					265	5 – 691	0	0 – 0
Yakima	08_YAKIMA								
upper Columbia	09_UPPCOL								
SF Clearwater	10_SFCLWR					733	382 – 839	857	659 – 1292
upper Clearwater	11_UPCLWR								
SF Salmon	12_SFSALM								
MF Salmon	13_MFSALM								
upper Salmon	14_UPSALM					1,003	660 – 1412	0	0 – 0
Total		402		0		2,001		857	

Note: Based on the sample data described in Table 60 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 63. Estimated abundance of natural-origin stocks (excluding unclipped hatchery-origin) of Summer Steelhead that passed Bonneville Dam in 2021 during the Skamania and A-/B-Index Management Periods.

	W	Subtotal for Skamania Period (Apr 1 - Jun 30)		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	A-Index		B-Index		A-Index		B-Index	
		Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI
Lower Columbia	02_LOWCOL	224	0 – 448			297	34 – 692	0	0 – 0
Skamania	03_SKAMAN								
Willamette	04_WILLAM								
Big White Salmon	05_BWSALM								
Klickitat	06_KLICKR	112	0 – 336			234	0 – 629	0	0 – 0
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	448	112 – 783			12,607	11184 – 14045	480	141 – 960
Yakima	08_YAKIMA					466	71 – 989	0	0 – 0

upper Columbia	09_UPPCOL					781	244 – 1355	0	0 – 0
SF Clearwater	10_SFCLWR					635	321 – 1122	322	122 – 556
upper Clearwater	11_UPCLWR					294	82 – 517	71	0 – 212
SF Salmon	12_SFSALM	112	0 – 336			146	35 – 291	93	0 – 186
MF Salmon	13_MFSALM	112	0 – 336			378	71 – 789	141	0 – 423
upper Salmon	14_UPSALM	112	0 – 336			3,723	2630 – 4857	0	0 – 0
	Total	1,119		0		19,561		1,106	

Note: Based on the sample data described in Table 60 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.

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Table 64. Estimated abundance of clipped and unclipped hatchery-origin A-/B-Index Summer Steelhead that passed Bonneville Dam in 2021 (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	Brood year	Est.	95% CI	MLE	95% CI	MLE	95% CI	MLE	95% CI
Round Butte	Deschutes River	07_MGILCS	OmyROUN_su19	2019	462	0 – 926	0	0 – 0				
Round Butte	Deschutes River	07_MGILCS	OmyROUN_su18	2018	286	0 – 735	0	0 – 0				
Wells Fish Hatchery	WMET/ WOKA/ WOMA/ WELLS	09_UPPCOL	OmyWELL_su19	2019	1,882	915 – 2915	0	0 – 0				
Wells Fish Hatchery	On Station	09_UPPCOL	OmyWELL_su18	2018	269	0 – 791	0	0 – 0				
Wells Fish Hatchery	Methow	09_UPPCOL	OmyWMET_su18	2018	458	0 – 915	0	0 – 0				
Winthrop NFH	Methow River	09_UPPCOL	OmyWINT_su18	2018	228	0 – 684	0	0 – 0				
Wells Fish Hatchery	Okanogan	09_UPPCOL	OmyWOKA_su17	2017	221	0 – 663	0	0 – 0				
Little Sheep Satellite	Imnaha	07_MGILCS	OmyLSCR_su19	2019	2,070	1057 – 3202	0	0 – 0				
Lyons Ferry Hatchery	Tucannon	07_MGILCS	OmyTUCW_su19	2019	44	0 – 133	0	0 – 0				
Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGILCS	OmyWALL_su19	2019	4,243	2944 – 5587	0	0 – 0				
Wallowa Fish Hatchery	Wallowa stock - released at Cottonwood and other Washington sites	07_MGILCS	OmyCGRW_su19	2019	1,895	962 – 2907	0	0 – 0				

Little Sheep Satellite	Imnaha	07_MGILCS	OmyLSCR_su18	2018	280	0 – 841	0	0 – 0				
Lyons Ferry Hatchery	Wallowa stock - trapped/spawned at Cottonwood, released at Cottonwood and other Washington sites	07_MGILCS	OmyCGRW_su18	2018	1,575	648 – 2530	0	0 – 0				
Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGILCS	OmyWALL_su18	2018	1,075	435 – 1794	0	0 – 0				
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su19	2019	1,423	1009 – 1846	0	0 – 0	75	0 – 151	0	0 – 0
Dworshak NFH	SF Clearwater	10_SFCLWR	OmySFCR_su19	2019	280	93 – 496	0	0 – 0	146	0 – 437	0	0 – 0
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su18	2018	2,337	1405 – 3360	7,122	5722 – 8545	352	116 – 616	158	0 – 371
Dworshak NFH	SF Clearwater	10_SFCLWR	OmySFCR_su18	2018	595	192 – 1080	1,024	641 – 1426	118	0 – 257	558	295 – 864
Dworshak NFH	Dworshak stock-trapped and spawned at Dworshak, reared at Magic Valley FH, released in Salmon basin	10_SFCLWR	OmyDWOS_su18	2018	115	0 – 264	94	0 – 278	41	0 – 124	0	0 – 0

Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su17	2017	0	0 – 0	162	44 – 315				
Dworshak NFH	Dworshak stock-trapped and spawned at Dworshak, reared at Magic Valley FH, released in Salmon basin	10_SFCLWR	OmyDWOS_su17	2017	0	0 – 0	43	0 – 132				
Dworshak NFH	SF Clearwater	10_SFCLWR	OmySFCR_su17	2017	0	0 – 0	60	0 – 181				
Oxbow (IDFG)	Oxbow	14_UPSALM	OmyOXBO_su19	2019	3,221	2131 – 4432	0	0 – 0	227	0 – 529	0	0 – 0
Pahsimeroi	Pahsimeroi	14_UPSALM	OmyPAHH_su19	2019	3,520	2385 – 4638	0	0 – 0	216	0 – 504	0	0 – 0
Pahsimeroi	Upper Salmon	14_UPSALM	OmyUSAL_su19	2019	44	0 – 132	0	0 – 0	349	143 – 575	0	0 – 0
Sawtooth	Sawtooth	14_UPSALM	OmySAWT_su19	2019	5,164	3873 – 6537	0	0 – 0				
Sawtooth	EF Salmon	14_UPSALM	OmyEFSW_su19	2019					66	0 – 198	0	0 – 0
Oxbow (IDFG)	Oxbow	14_UPSALM	OmyOXBO_su18	2018	536	62 – 1072	0	0 – 0				
Pahsimeroi	Pahsimeroi	14_UPSALM	OmyPAHH_su18	2018	1,198	490 – 1979	0	0 – 0				
Pahsimeroi	Upper Salmon	14_UPSALM	OmyUSAL_su18	2018					145	0 – 436	0	0 – 0
Sawtooth	Sawtooth	14_UPSALM	OmySAWT_su18	2018	821	282 – 1512	0	0 – 0				
Pahsimeroi	Pahsimeroi	14_UPSALM	OmyPAHH_su17	2017	96	0 – 289	0	0 – 0				
#N/A	#N/A	#N/A	Unassigned	#N/A	1,384	464 – 2828	0	0 – 388	265	0 – 561	141	0 – 423
			TOTAL		35,723		8,504		2,001		857	

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Post-season analysis of Sockeye Salmon passing Bonneville Dam in 2021

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 9, 2021 (Table 40). 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 2021, there were 1,530 Sockeye Salmon that were sampled at the AFF and genotyped for this analysis (Table 65). This year we estimated low but non-zero abundance for the ESA listed stock (Redfish Lake Sockeye Salmon from the Snake River, abundance=1,307) (Table 65, Figure 45). 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 2021, 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 relatively high estimate of 3,531 (95% C.I.: 1,505 – 5,697). This is the second year that the Yakima stock has been greater than 3,000 fish and clearly demonstrates the success of the Yakama Nation Sockeye salmon reintroduction program and the critical need for PBT applications to monitor this success.

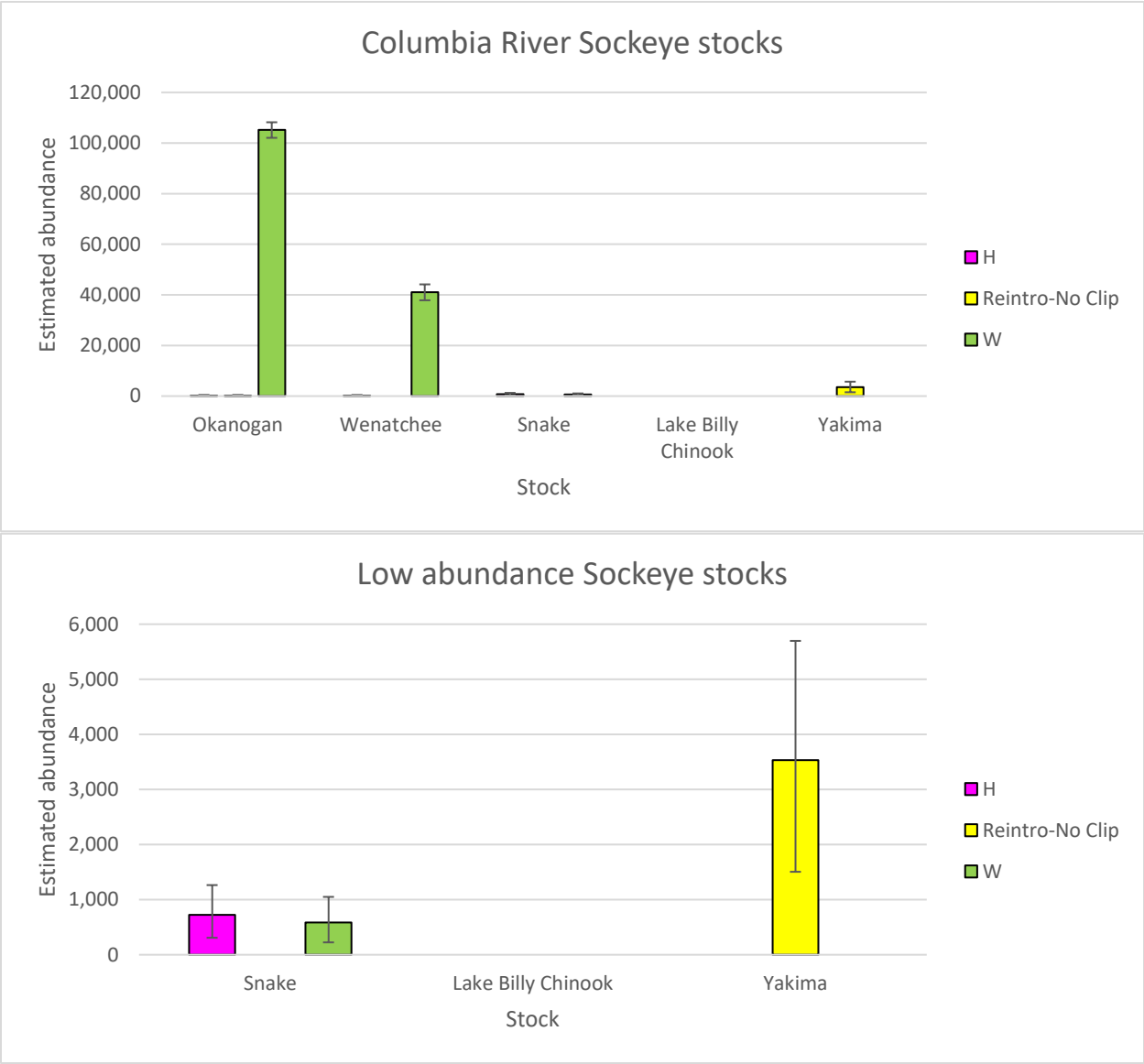


Figure 45. Estimated abundance (\pm 95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2021.

2126 **Table 65. Estimated abundance of Sockeye Salmon genetic stocks that passed Bonneville Dam in 2021.**

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	189	0 – 441	112	0 – 449	105,192	102046 – 108199	2	1	1,083	1,086
Wenatchee	178	0 – 429			41,041	37853 – 44148	2		411	413
Snake	723	307 – 1264			584	224 – 1050	7		6	13
Lake Billy Chinook										0
Yakima			3,531	1505 – 5697				18		18
Total	1,089		3,643		146,817		11	19	1,500	1,530

2127 Note: The abundance is estimated from the total fish counts at the fish ladder windows at Bonneville Dam. Most stocks are identified
 2128 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 85% of fish that were clipped hatchery-origin summer A-/B-Index steelhead at Bonneville Dam in 2020 to 26 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 2021. Namely, the percentage of adipose-clipped fish abundance that were estimated to be PBT broodstock ranged from 95 – 100%, 92 – 100%, and 85 – 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 second 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 moderate correspondence with hatchery smolt release data from one broodyear (2016). The trend suggested 1000 smolts were needed to be released to equal 1 adult-sized 4-year-old Spring Chinook at Bonneville Dam in 2020. Future work could sum all abundance of the SY2016 adult return across age-classes (i.e., age 3, 4, and 5 in run years 2019, 2020, and 2021, 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 12 major clipped Chinook salmon hatchery-origin stocks (49 clipped hatchery broodstock sources), 6 major unclipped hatchery-origin stocks (41 unclipped hatchery broodstock sources) and 9 natural-origin stocks estimated to have relative abundances $\geq 1,000$ fish passing Bonneville Dam in 2020. The Spring Chinook stocks of 2020 were observed to spillover into the summer period by 3%-6% 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 approximately a quarter of all combined spring and summer period abundance was observed to occur in the spring period for both natural-origin and hatchery-origin stocks.

We identified five major clipped steelhead hatchery-origin stocks, three major unclipped hatchery-origin stock (12 major hatchery broodstock sources), and five major natural-origin stocks estimated to have relative abundances $\geq 1,000$ fish passing Bonneville Dam in 2020. 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 ninth year (since 2012) that we were able to analyze sockeye salmon using GSI, and similar to that past three 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 2020 and found that the Okanogan stock has the greatest relative abundance followed by the Wenatchee stock. We found 122 fish from the Snake River stock, estimated 0 fish from Lake Billy Chinook, and estimated a record of 11,719 fish 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 (2021) we continued an increased frequency of in-season reporting as we planned 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. 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.

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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 46). 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 66). 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 47a). Annual precipitation had the greatest effect when all collections were analyzed together (Figure 47a). Environmental variables retained in the coastal lineage RDA were average temperature of the coldest quarter and precipitation of the wettest month (Figure 47b). Environmental variables retained in the interior lineage RDA were 20-year average

August water temperature and minimum temperature of the warmest month (Figure 47c). 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.

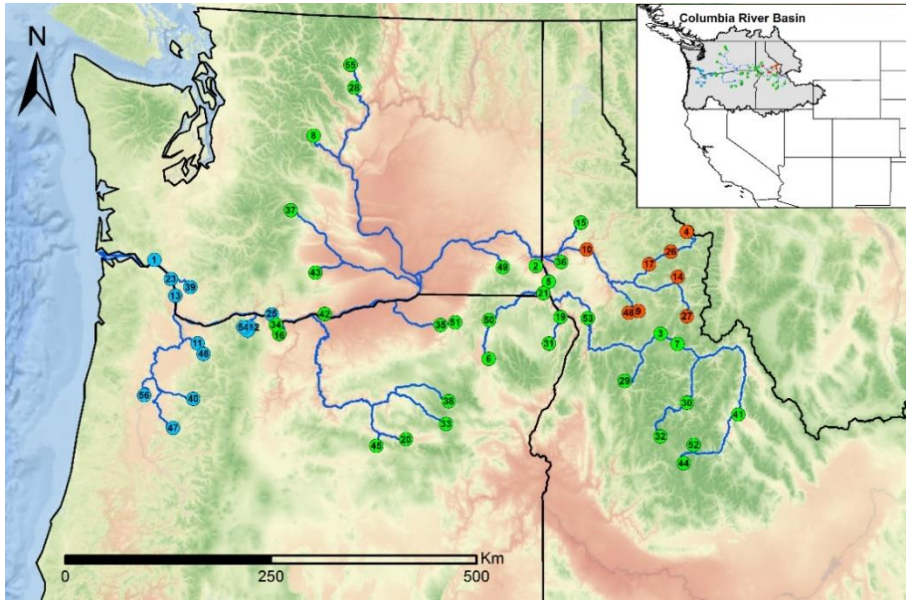


Figure 46. Steelhead collection localities colored by genetic cluster (from Micheletti et al. 2018a). blue = coastal, green = inland, red = inland-Clearwater. Blue lines indicate each population's migration path to the ocean. Map layer shows mean annual temperature for the warmest quarter with transition from colder (green) to warmer (red).

Table 66. 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_maxtwarmmon	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

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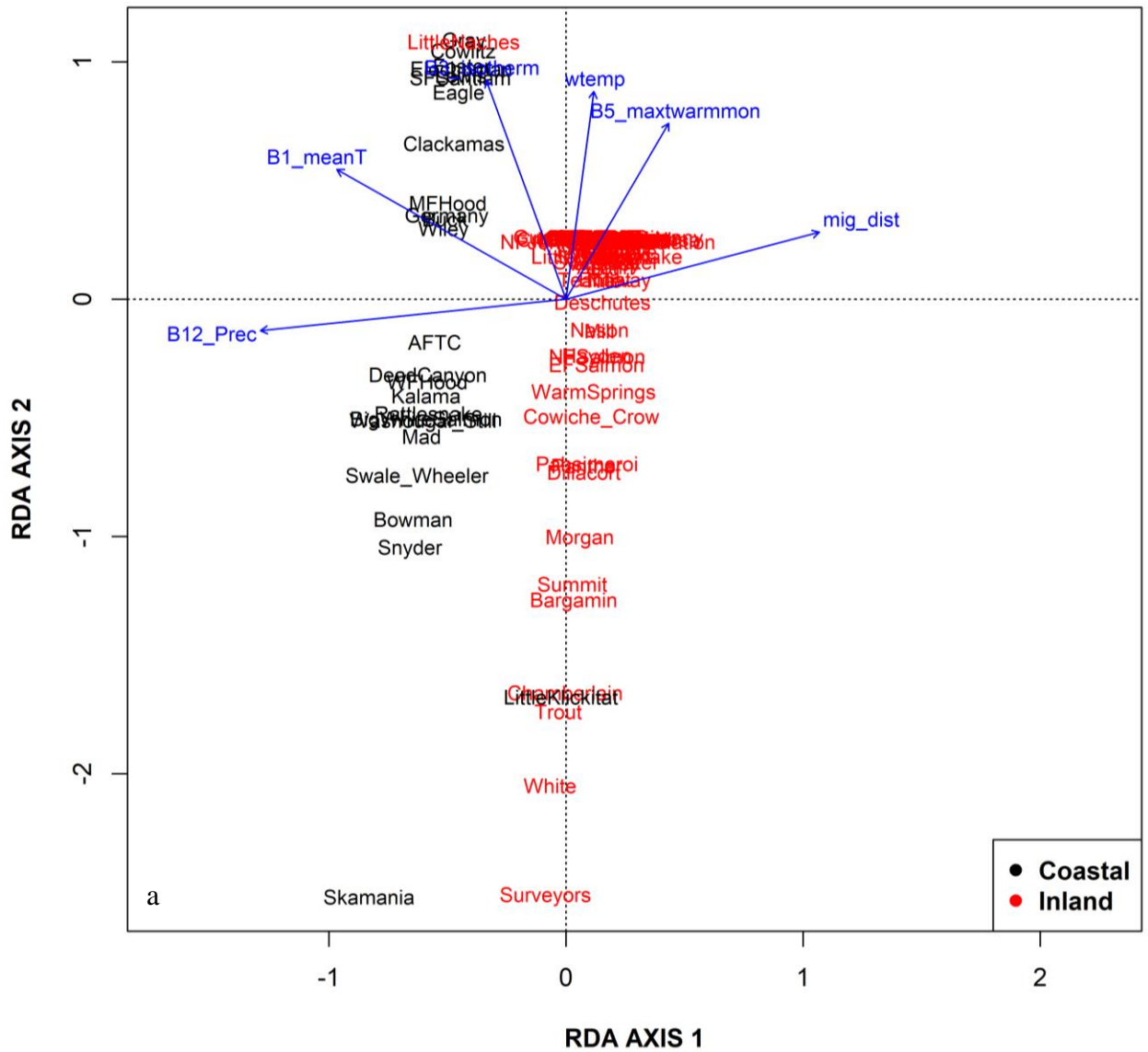
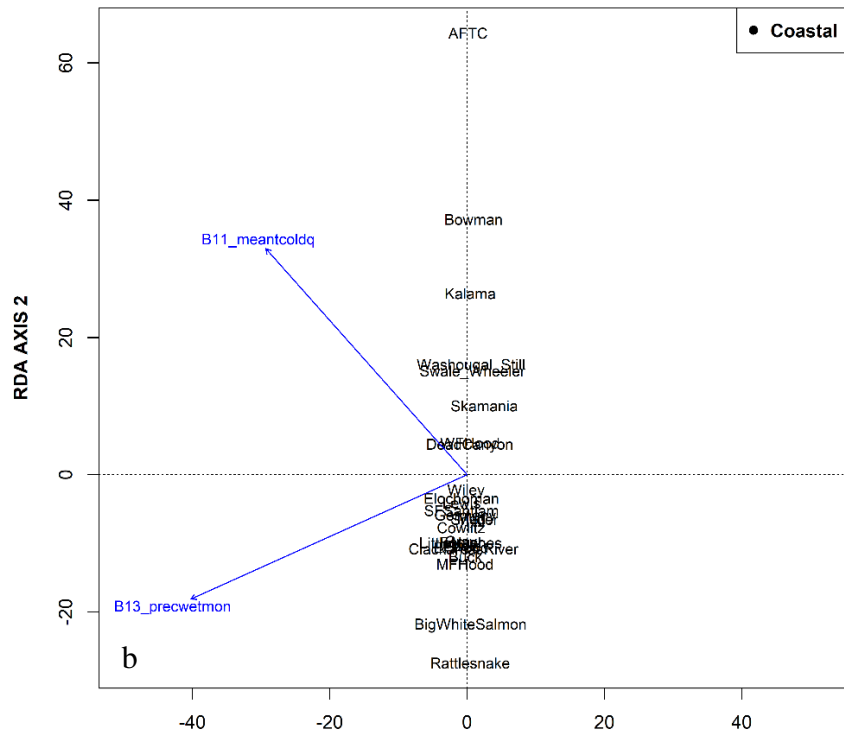
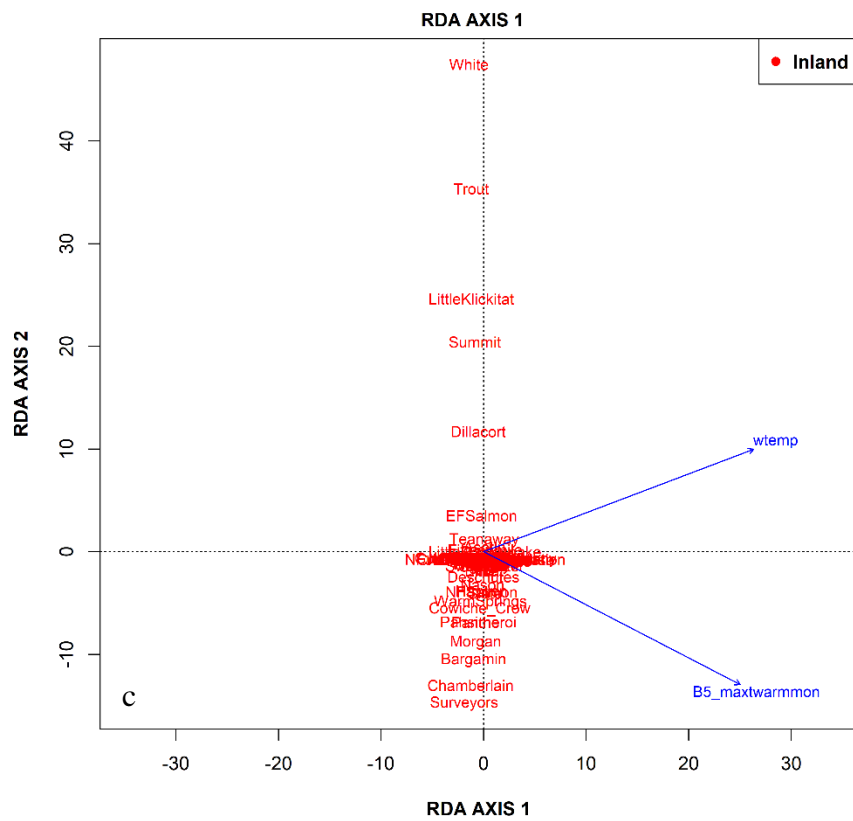


Figure 47 a-c. RDA of all steelhead collections in Columbia River basin to model the degree to which the variation in environmental variables explains the variation in allele frequencies for candidate markers for all collections in the *greb1L* haplotype block (2,3,6). Coastal populations (b) and inland populations (c) were analyzed separately.



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Figure 47 b-c.

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 48a). Several candidate markers were associated with local adaptation within and among lineages (Figure 48b; Hecht et al. 2015). Follow-up studies 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 (Alshwairikh et al. 2021) 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.

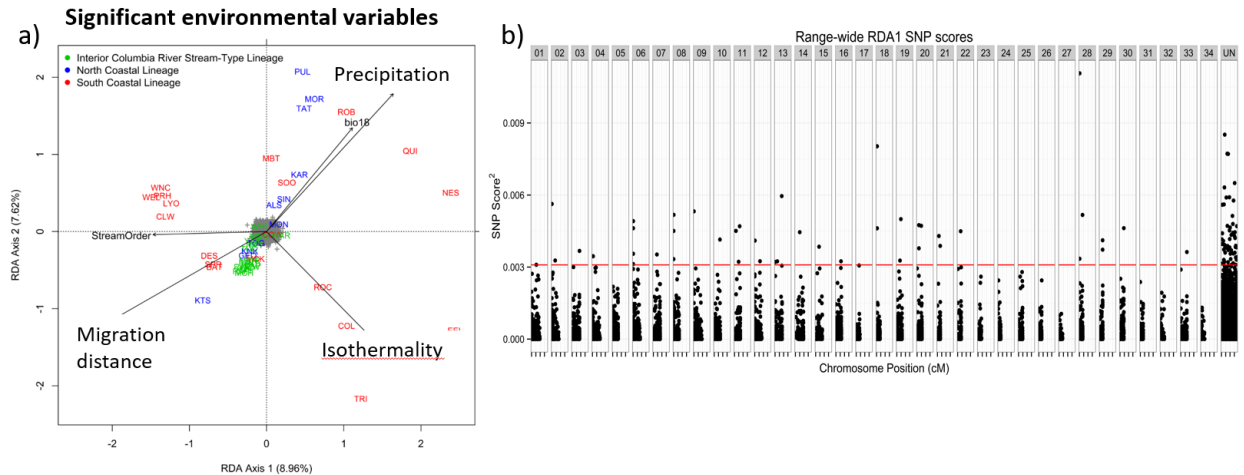


Figure 48. a) Environmental drivers of selection and b) candidate markers for local adaptation in Chinook salmon (from Hecht et al. 2015). a) Population scores for canonical RDA axis 1 and 2 are represented by the three-letter abbreviation for each population, coloured to represent the lineage assignment 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; Alshwairikh et al. 2021). 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 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 49).

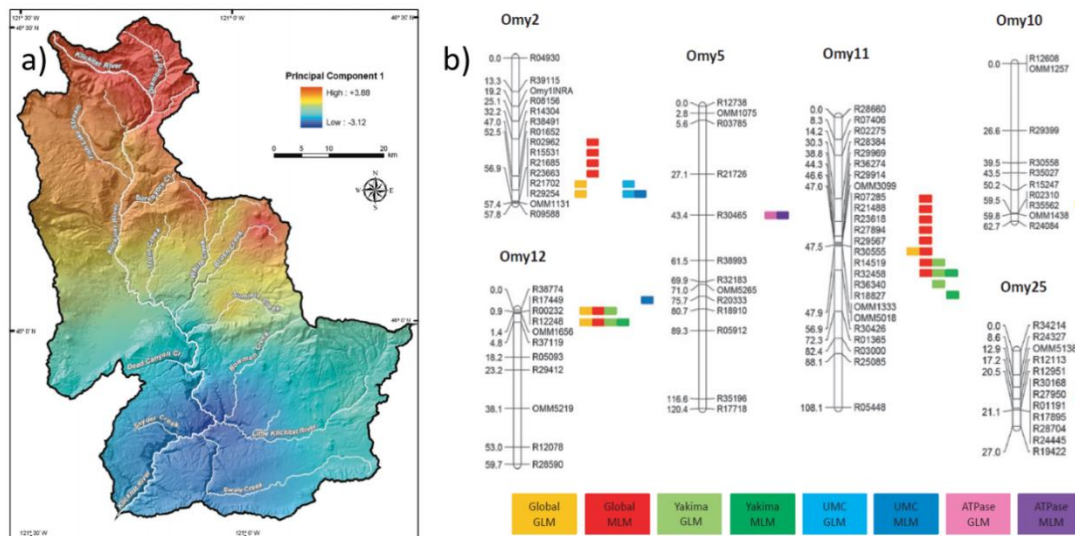


Figure 49. a) Synthesis map illustrating interpolation principal component (PC1) that accounts for 59% of variation in resident (red) vs anadromous (red) life history (from Narum et al. 2008a). b) Significant loci detected from eight individual association tests, where each test is represented by a different 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 50).

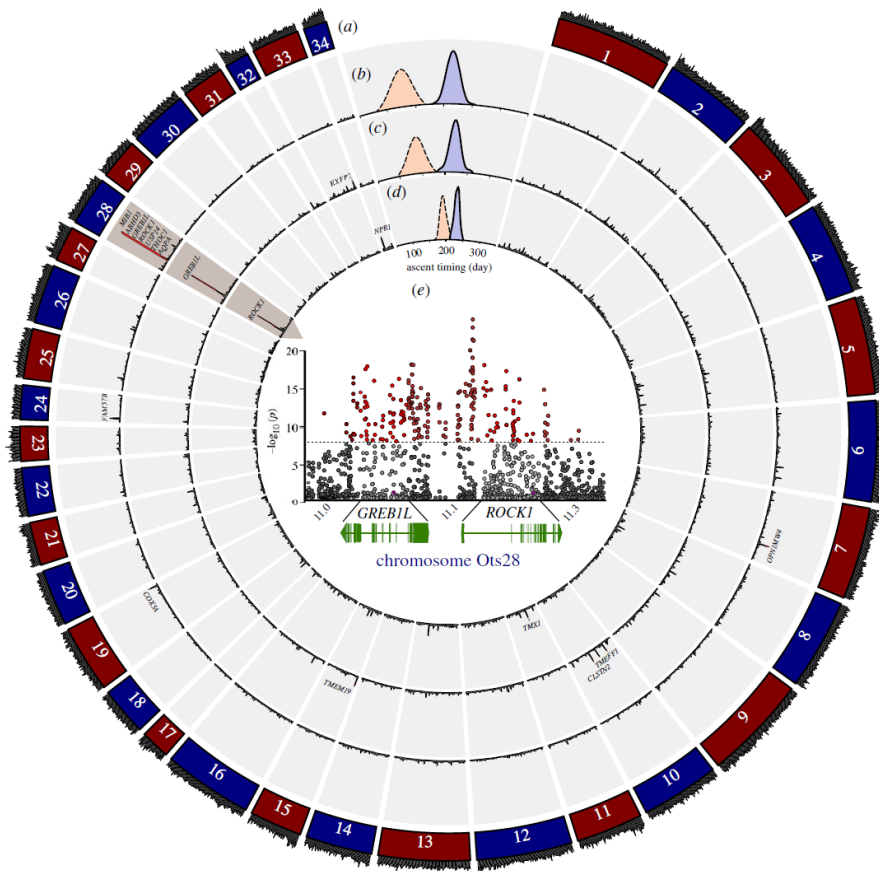


Figure 50. Manhattan plot for premature and mature collections of Chinook salmon (from Narum et al. 2018). (a) Sequence coverage (black outer ring) for each chromosome. (b) Significant divergence between premature and mature migrating coastal lineage Chinook salmon. (c) Significant divergence between 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 67). 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

124 migration timing from the whole genome resequencing conducted by Micheletti et al.
125 (2018c). Premature, mature, and heterozygote genotypes for adult migration timing were
126 established based on genotype association from previous studies (Hess et al. 2016;
127 Micheletti et al. 2018c), as well as using a reference collection of Skamania Hatchery
128 steelhead, which is a hatchery-strain intensively selected for early adult migration and
129 cultured since 1956 with steelhead from the Washougal and Klickitat Rivers (Crawford et
130 al. 1979; Chilcote et al. 1986). Premature, mature, and heterozygote adult migration
131 timing genotype proportions were assessed across all collection locations. A total of
132 9,471 individuals from 113 populations met inclusion criteria (>90% loci successfully
133 genotyped and had an estimated <0.5% genotyping error based on replicate genotyping)
134 and were included in this study. Further validation of association with run-timing
135 phenotypes and genotypes from Chr28 was demonstrated in Willis et al. (2020).
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Table 67. 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>	TGACACTGATCACAATGGTGAAAT	TAAACTGGAAGGAGAGAGCAAAAT	TGTGGGCTGC[A/G]AACATACTCA	+
2	Omy_RAD52458-17	28	11609794	<i>greb1L</i>	ACGTGTCCTGAGGATGGTA	AGCTCTAGGTCTGGGTCCTG	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 51). 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.

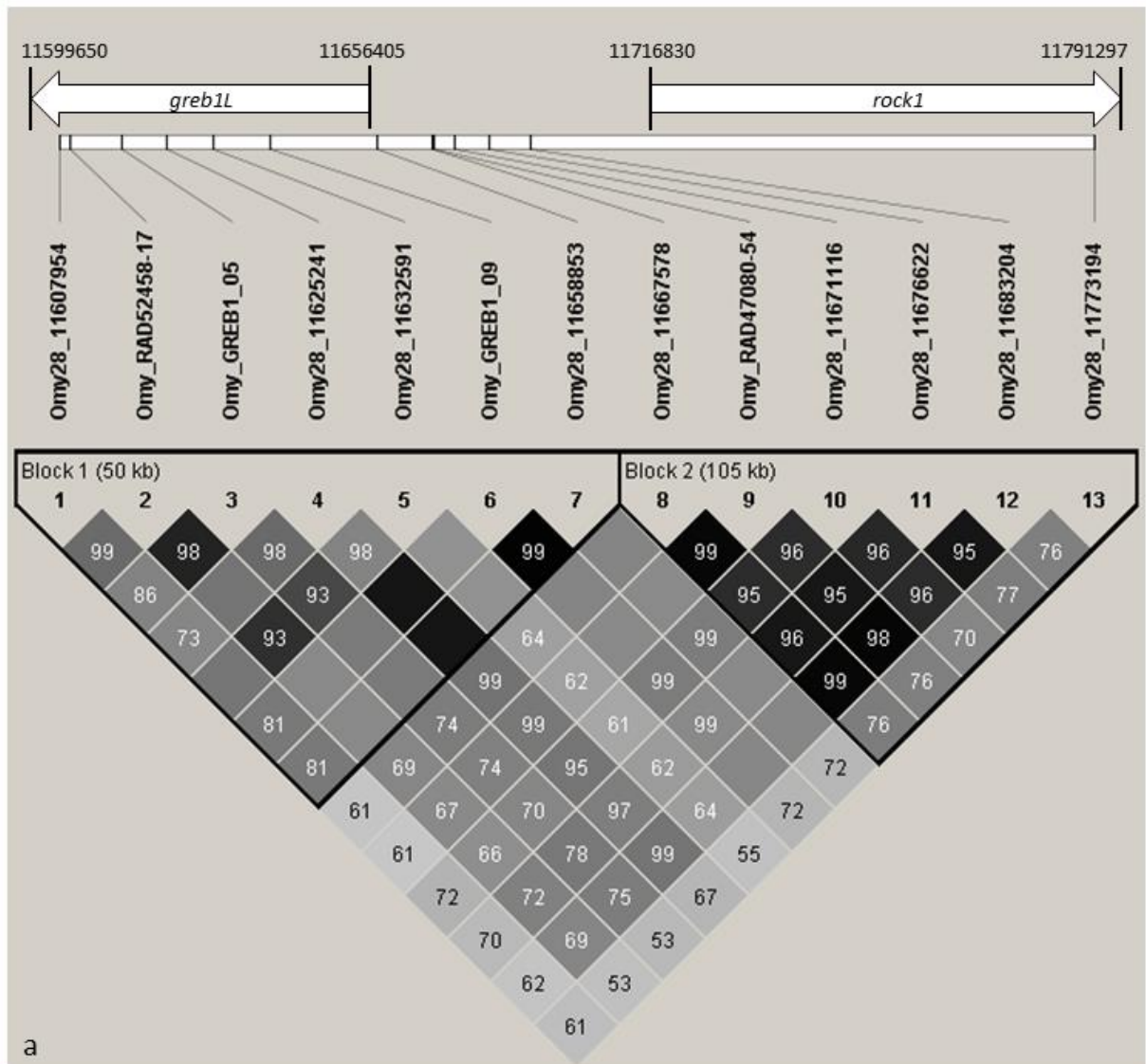


Figure 51. Linkage relationships for 13 candidate markers in Haploview for all steelhead populations.

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 52a. 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 52a). The haplotypes with a mixture of blue and red represent the different possible heterozygote genotypes (Figure 52a). 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 52a-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 52a). Haplotype frequencies for collections (Figure 52a) showed similar patterns of geographic distribution as the genotype frequencies (Figure 52b), but with improved resolution for heterozygous haplotypes that were within a single haplotype block underlying *greb1L*. According to results of overall haplotype frequency (Figure 52a), 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 52a).

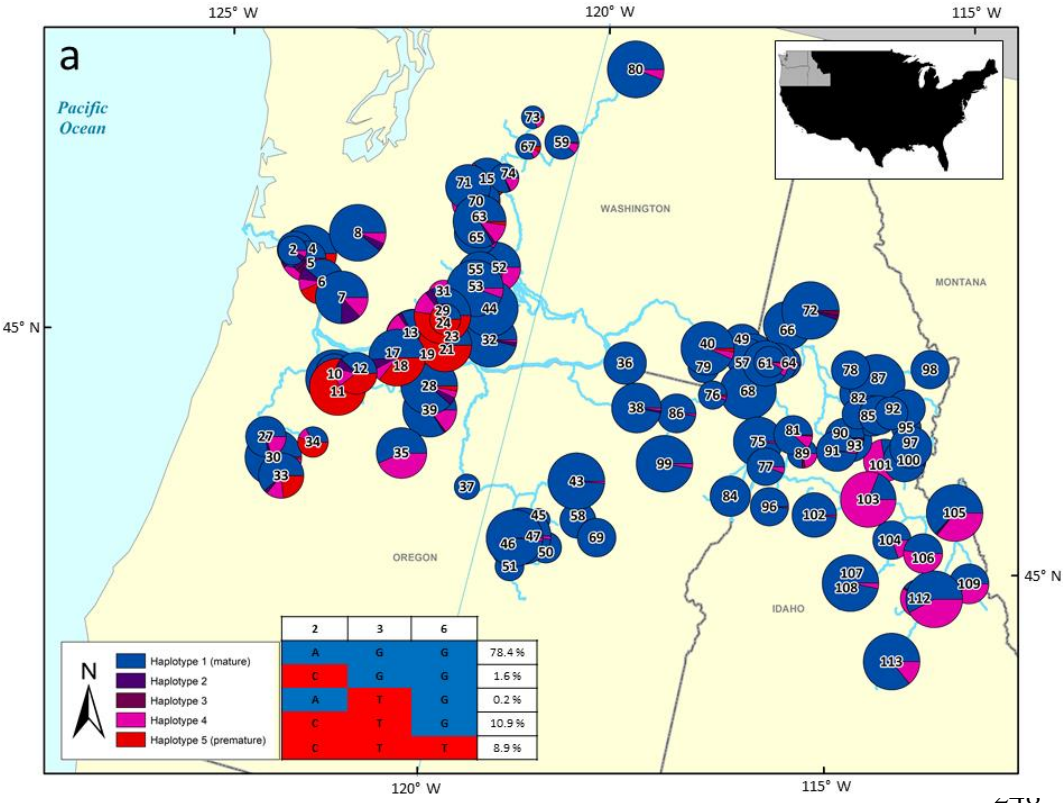


Figure 52a. Maps of haplotype and genotype proportions for all steelhead collection locations. Pie chart size corresponds to population size. The first map (a) demonstrates the proportions of individuals at each collection location with the five unique haplotypes from markers 2, 3, and 6. The second map (b) incorporates only candidate marker 9 (Omy_RAD47080-54), as it was in a different linkage block than the other three markers.

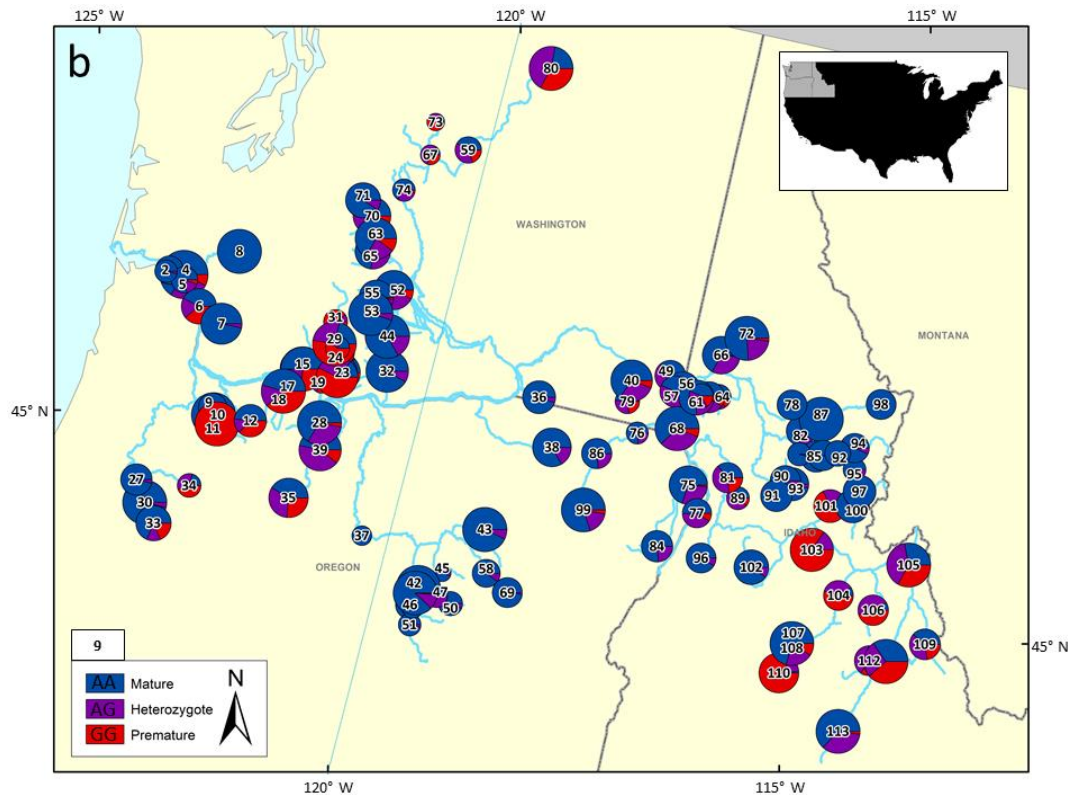


Figure 52b.

We 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 53; Willis et al. 2020). 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 54). 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.

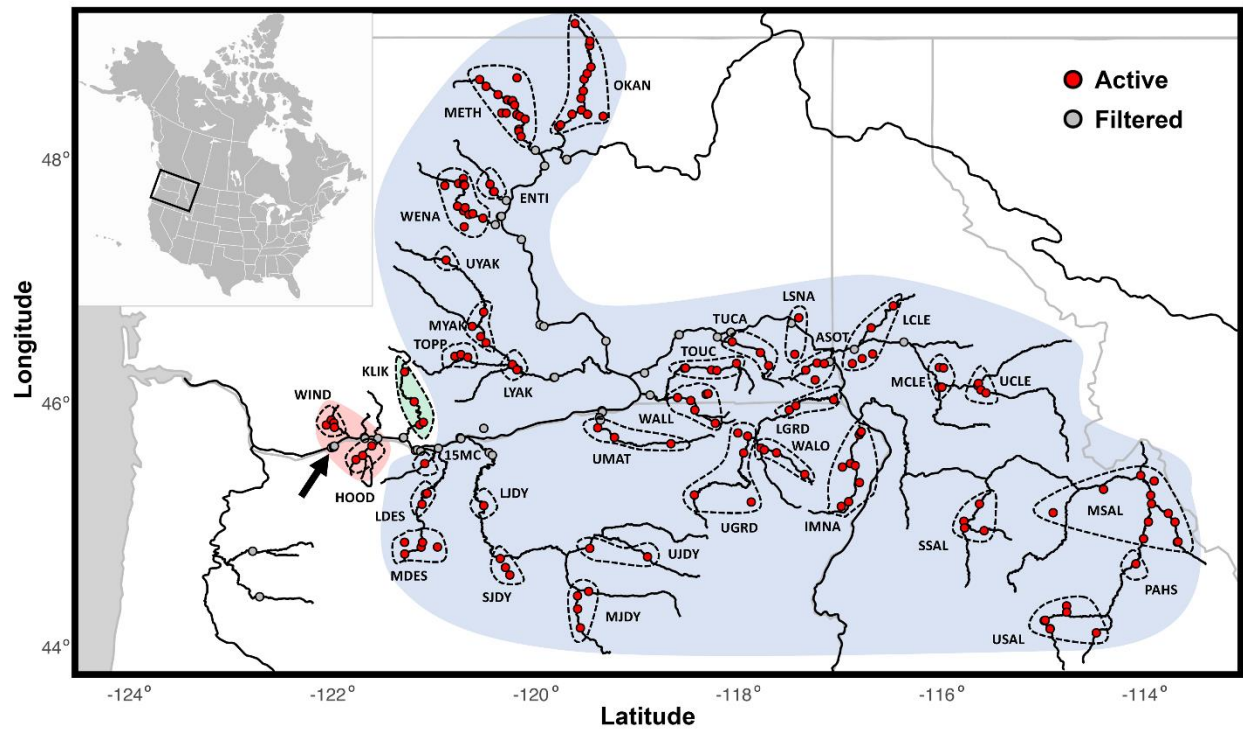


Figure 53. Columbia River Basin with active and filtered passive integrated transponder arrays. River courses in black; borders and coast in gray. Hydrological unit groupings, identified by dashed lines, are organized into lineages and sub-basins as follows: coastal lineage in Red, intermediate lineage affiliation in Green, inland lineage in Blue; Bonneville Dam is identified by an arrow.

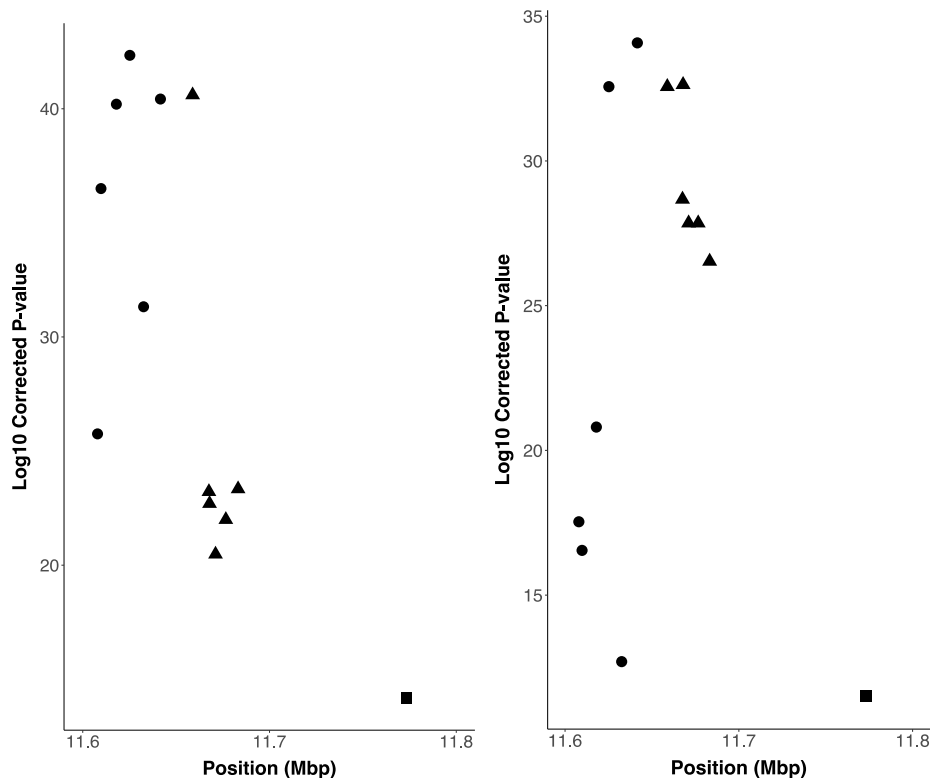


Figure 54. Significance of association of chromosome 28 markers with run timing in BONAFF (left) and Hood River (right) steelhead. Position refers to SNP locus position on chromosome 28. Circle: GREB1L, triangle: intergenic; square: ROCK1.

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 55). 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 55).

Association tests validated that the majority of markers were significantly associated with migration timing for all three lineages (Figure 56). 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 57).

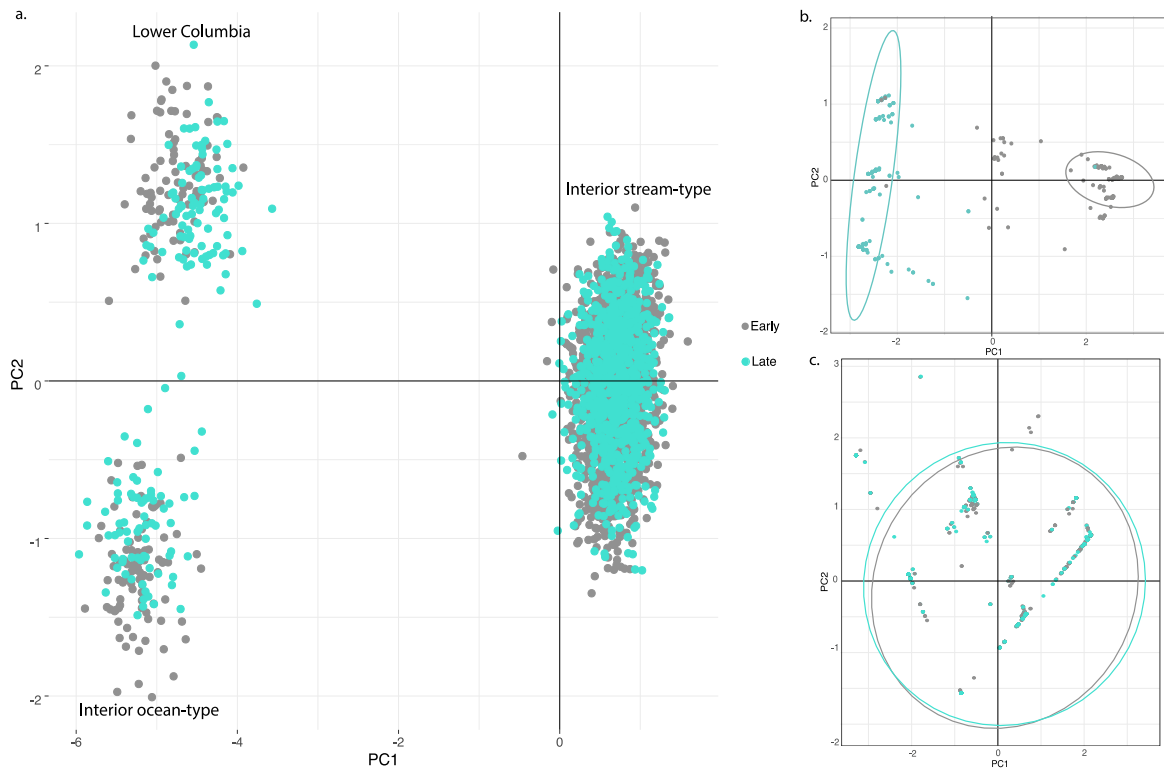


Figure 55. PCA of genetic variation in Chinook Salmon (from Koch and Narum 2020). Results presented represent A) 185 neutral SNP markers, B) 33 chromosome 28 markers for the Lower Columbia and Interior ocean-type populations combined, and C) 33 chromosome 28 markers for the Interior stream-type population.

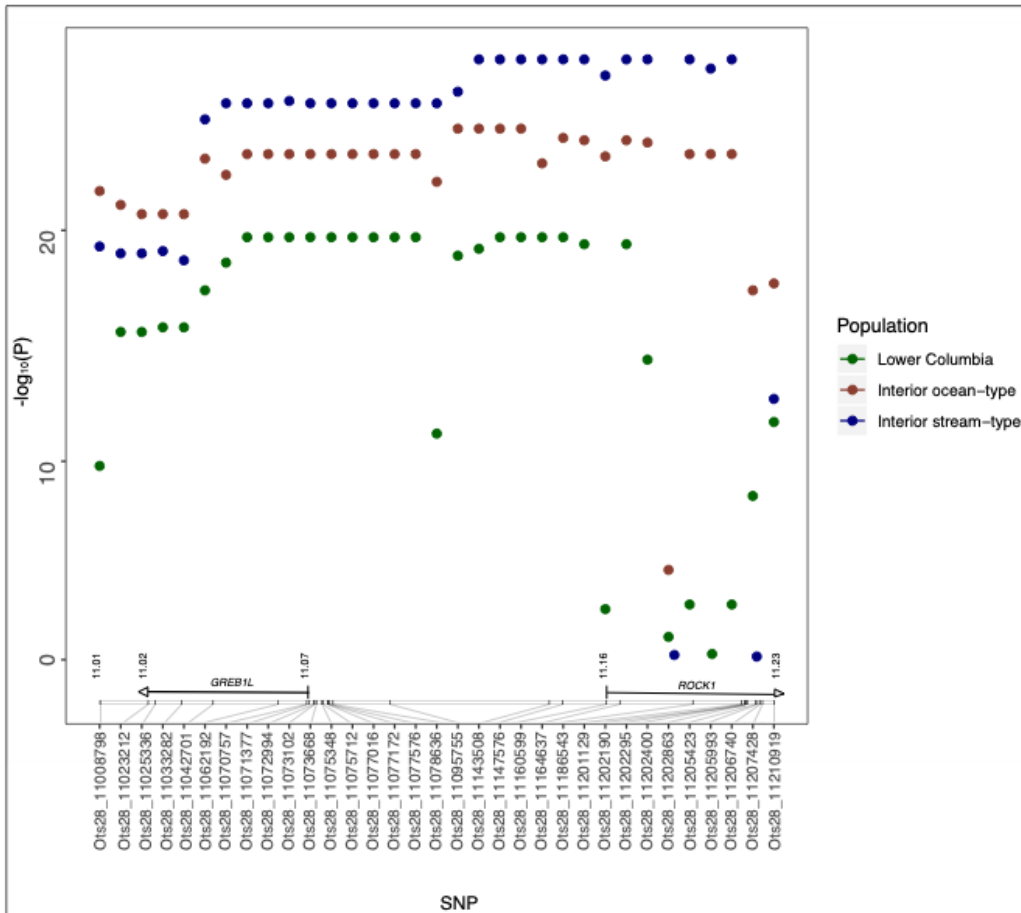


Figure 56. Association of each candidate SNP marker with migration timing within three lineages of Chinook Salmon (from Koch and Narum 2020). The colored dots for each lineage represent sliding windows for consecutive pairs of SNPs along the candidate genomic region. SNP number on the x-axis corresponds 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 $-\log_{10}(\text{FDR-corrected p-value})$.

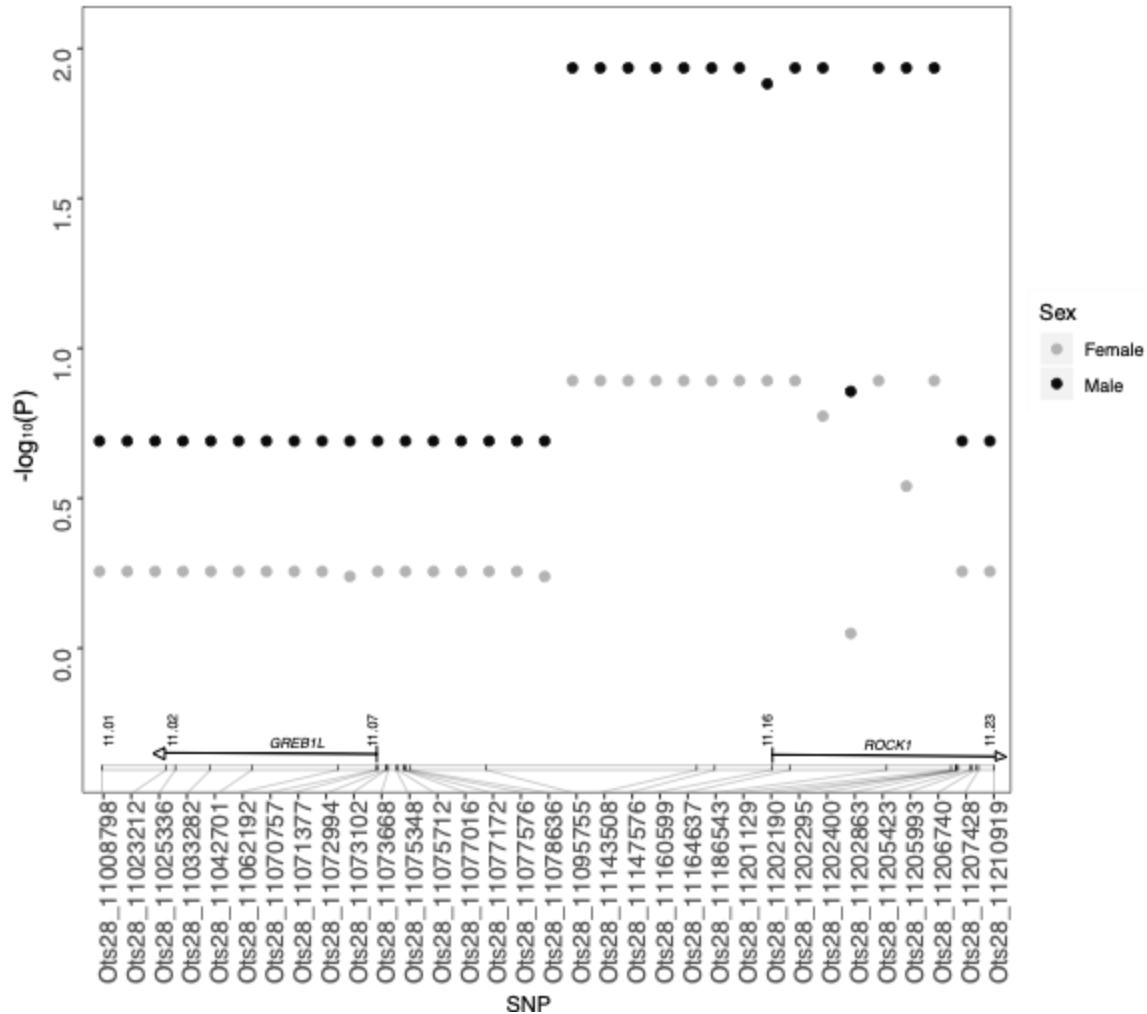


Figure 57. Association of each candidate SNP marker with fitness within the Interior stream-type population. The dots represent sliding windows for consecutive pairs of SNPs along the candidate genomic region with sexes presented separately. SNP number on the x-axis corresponds to the 33 candidate markers, 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 $-\log_{10}(\text{FDR-corrected p-value})$.

Markers from this region on Chr28 were further validated in study (Willis et al. 2021) of all three lineages in the Columbia with two adult migration phenotypes based on data from PIT tags (passage day at Bonneville Dam, and arrival day at spawning grounds). This study by Willis et al. (2021) demonstrated that each of the three lineages is represented by both early and late migrating adults including the interior stream-type lineage (Figure 58). With high-throughput genotyping (GT-seq) and phenotyping methods, we examined the association of genetic variation in 28 markers (spanning GREB1L to ROCK1 of chromosome 28) with individual adult migration timing characteristics gleaned from passive integrated transponder recordings of over 5,000 Chinook salmon from the three major phylogeographic lineages that inhabit the Columbia River Basin. Despite the strong genetic differences among them in putatively neutral genomic regions, each of the three lineages exhibited very similar genetic variants

in the chromosome 28 region that were significantly associated with adult migration timing phenotypes. This is particularly notable for the interior stream-type lineage, which exhibits an earlier and more constrained freshwater entry than the other lineages. In both interior stream-type and interior ocean-type lineages of Chinook salmon, heterozygotes of the most strongly associated linkage groups had largely intermediate migration timing relative to homozygotes, and results indicate codominance or possibly marginal partial dominance of the allele associated with early migration. Our results lend support to utilization of chromosome 28 variation in tracking and predicting run timing in these lineages of Chinook salmon in the Columbia River.

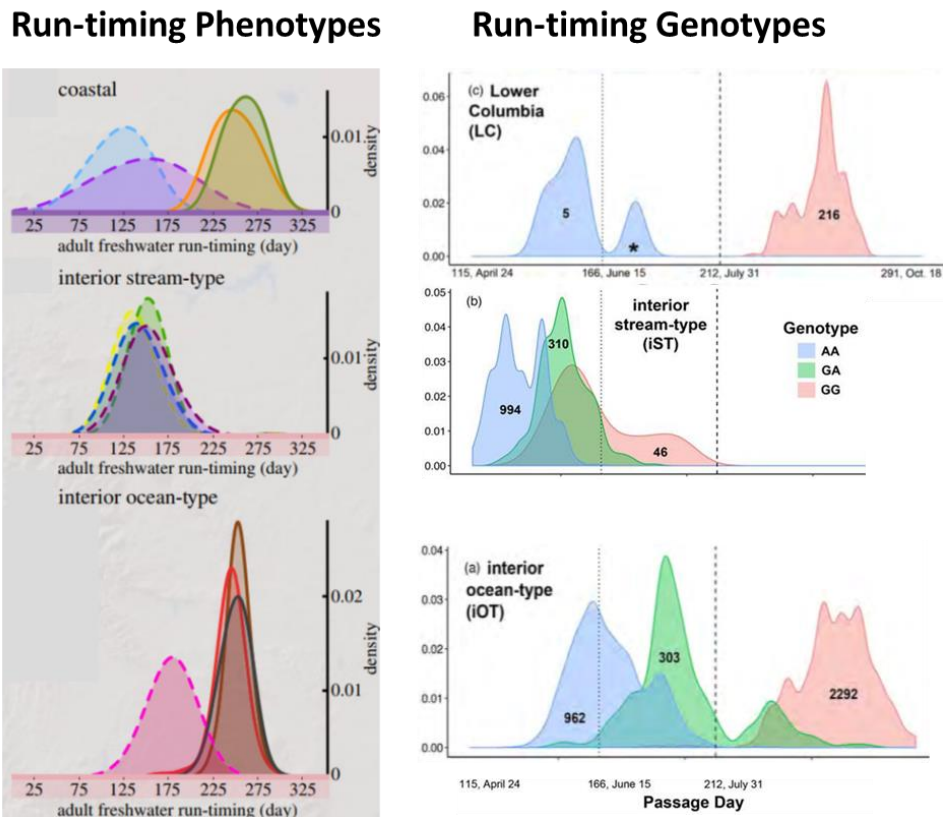


Figure 58. Run-timing phenotypes and genotypes at Bonneville Dam for each lineage of Chinook salmon (coastal, interior-stream type, and interior ocean-type) show a strong association (results from Narum et al. 2018; Willis et al. 2021). Early and late returning fish are found in all three lineages with heterozygotes observed with intermediate timing.

Age at maturity in Chinook salmon appears to be a polygenic trait but genes of greatest effect differ between sexes (Figure 59; 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. 2021), 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 60). 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 61).

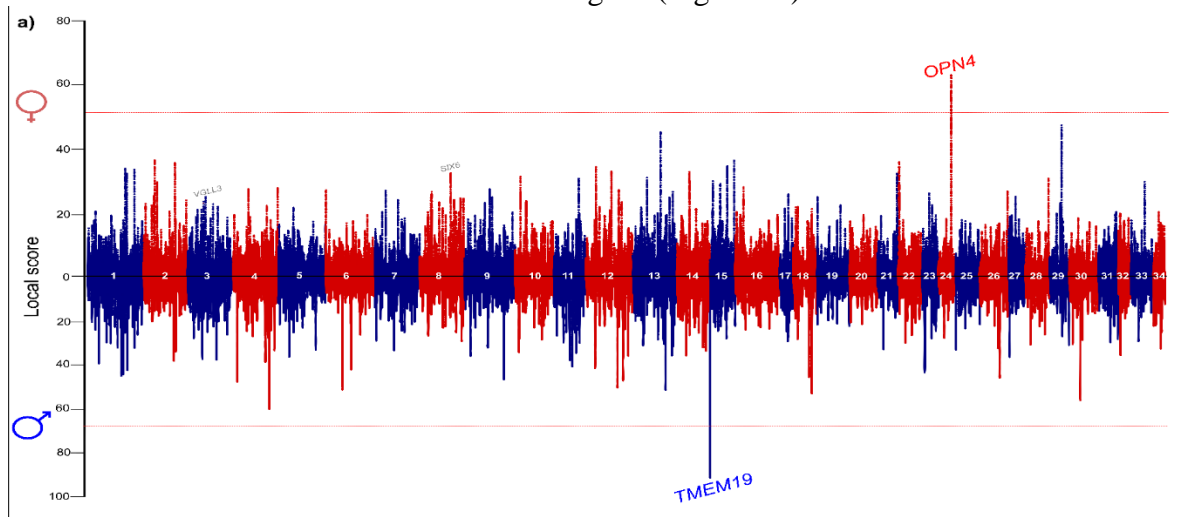


Figure 59. Manhattan plot (from Micheletti and Narum 2018b) illustrating differentiated regions within age classes of females (top; 4- vs. 5-year-olds) and males (bottom; 3- vs. 4- vs. 5-year-olds). Red dashed lines indicate $\alpha = 0.01$ significance threshold for the local score test with Bonferroni 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.

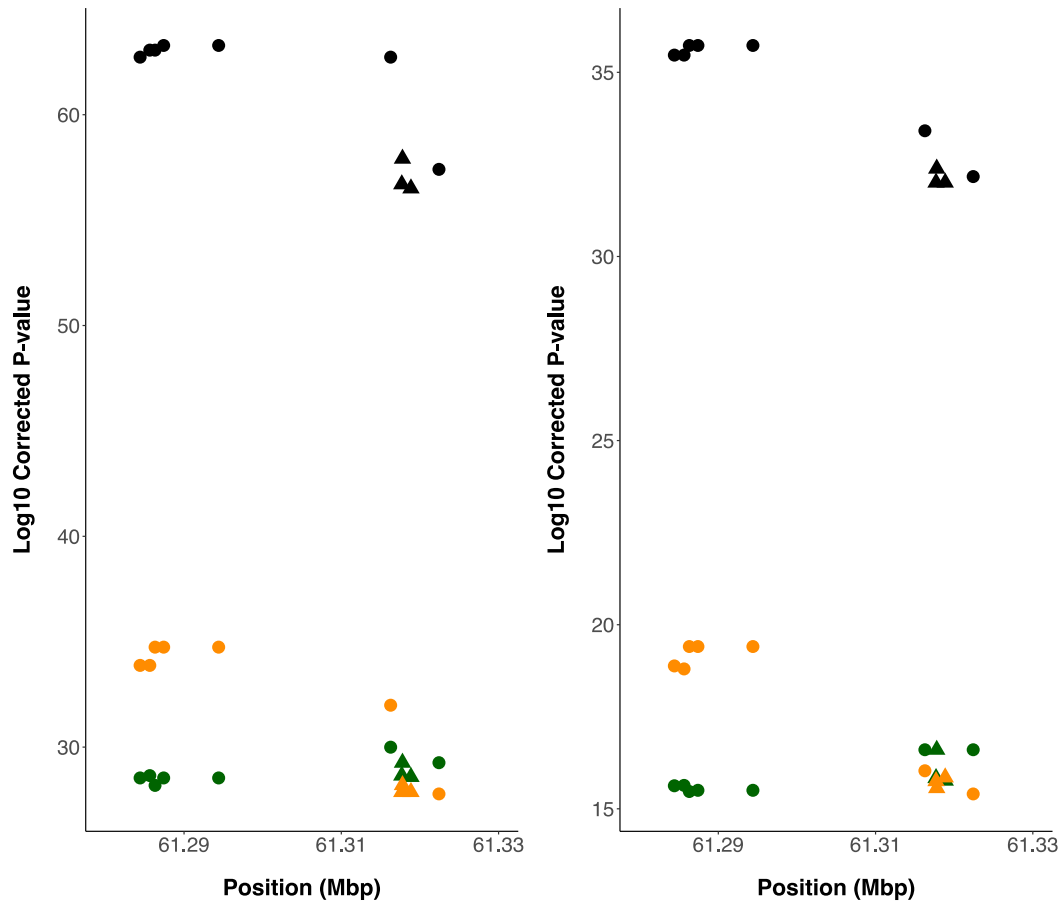


Figure 60. Significance of association of chromosome 25 markers with fork length (left) and ocean age (right) in BONAFF steelhead. Position refers to SNP locus position on chromosome 25. Circle: Intergenic, triangle: SIX6; orange: female; green: male; black: combined male and female.

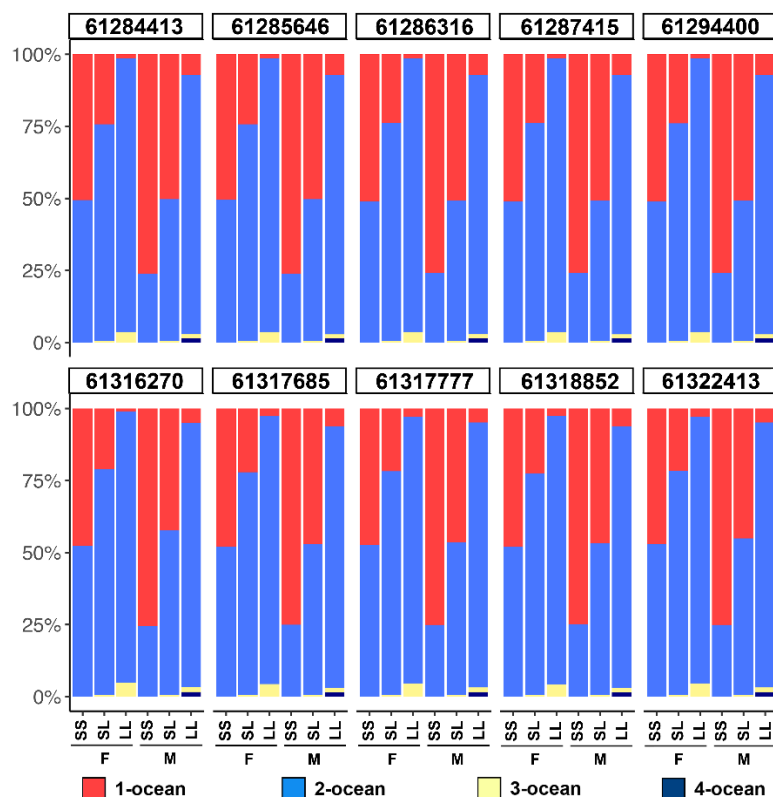


Figure 61. Frequency of ocean-age individuals for genotype and sex for each of the chromosome 25 SNP markers (identified by genomic position).

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 62; 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 63), and markers were developed from this candidate gene for further validation. As these candidate genes for traits have begun to be identified (Figure 62; 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

445 in test populations of anadromous steelhead and Chinook salmon following similar
446 measurements of phenotypes as used for redband trout.
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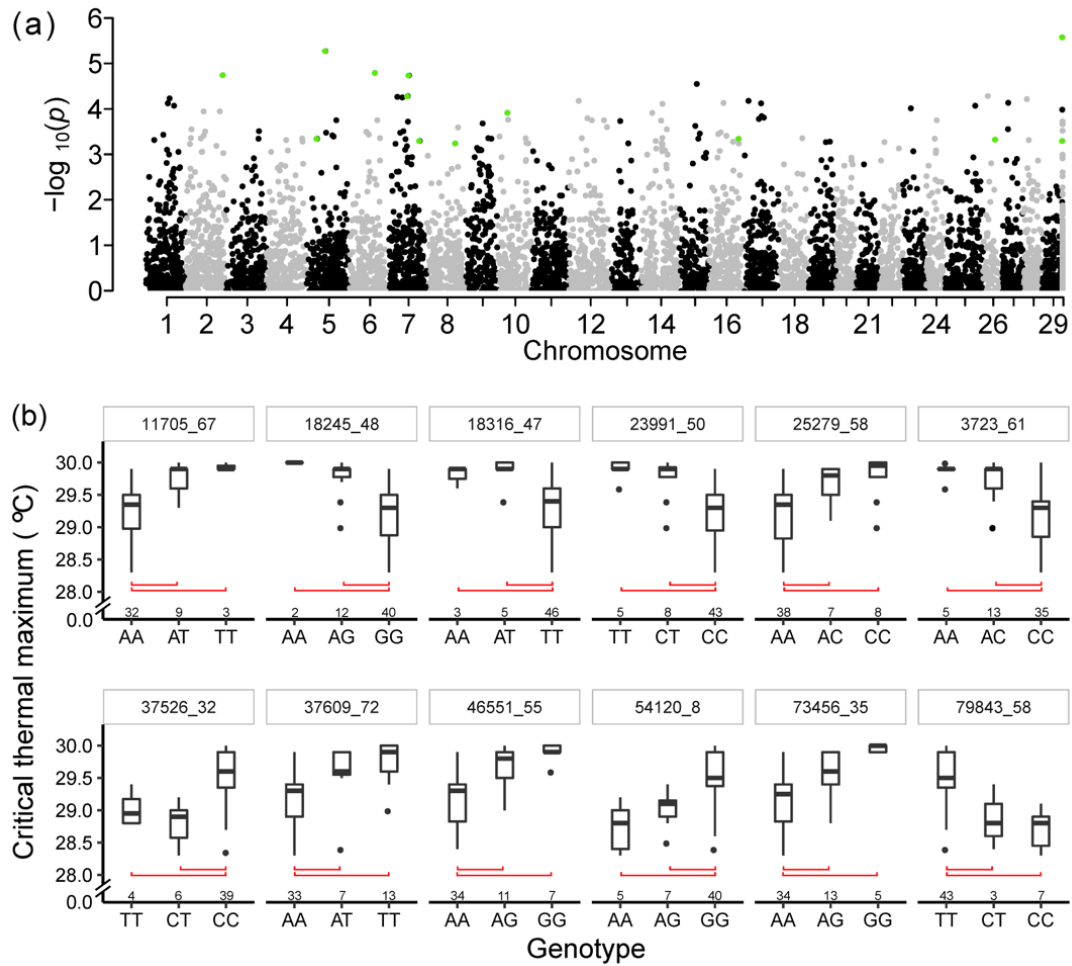


Figure 62. Results from Chen et al. (2018a) that demonstrate association of loci with thermal tolerance in natural populations of redband trout from desert, cool montane, and cold montane environments. Outlier loci and the association with critical thermal maximum (CTMAX). (a) Manhattan plot of calibrated 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.

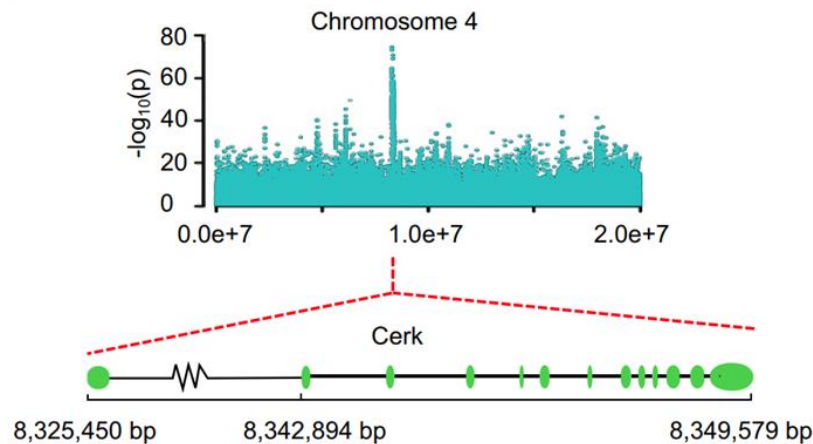


Figure 63. Results from Chen and Narum (2020) that identified a highly significant peak on Chromosome 4 in the *cerk* gene associated with thermal tolerance (survival/mortality) and cardiac performance under heat stress.

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 several 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; Koch and Narum 2020; Willis et al. 2020; Chen et al. 2020; Waters et al. 2021; Willis et al. 2021).

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 65). 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. This may enable conservation actions such as assisted migration (Figure 64) if warranted, as described in a recent review (Chen et al. 2021).

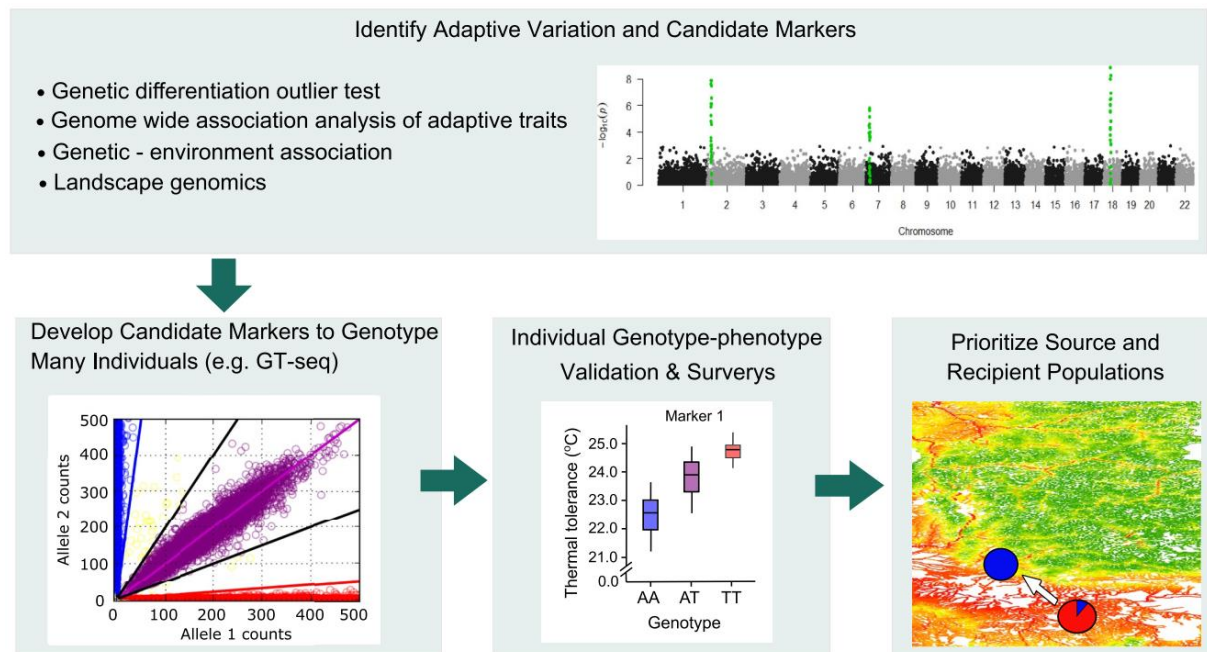


Figure 64. Schematic showing genomic approaches for applying assisted migration with adaptive alleles. The top panel illustrates a Manhattan plot with significant peaks for candidate loci from genome scan approaches, leading to development of specific candidate markers (e.g., genotyping-thousands by sequencing; GT-seq; Campbell et al., 2015) to test for genotype–phenotype validation in many individuals before considering intentional movement of adaptive alleles (red) from source to recipient populations.

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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.

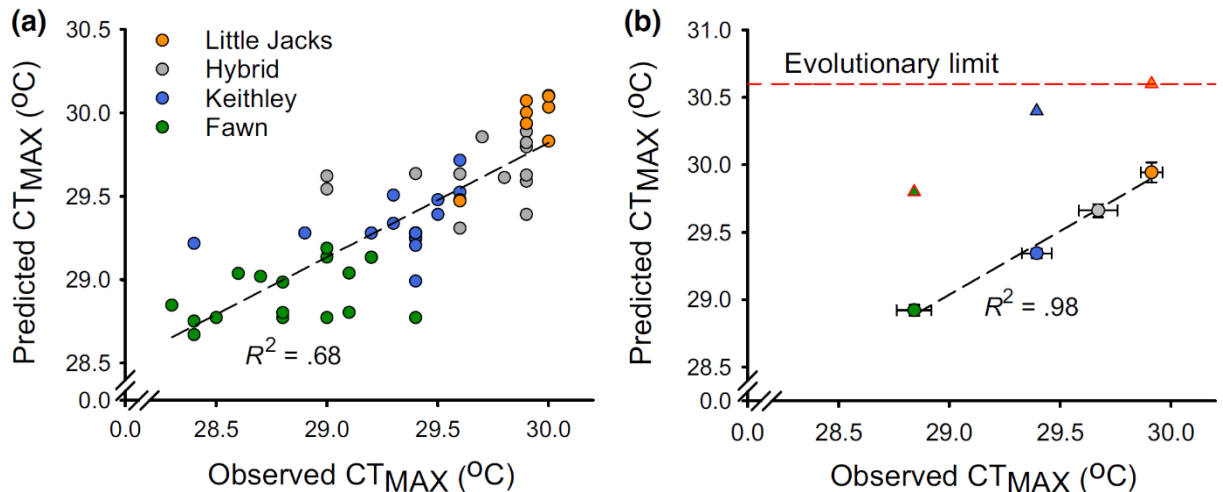


Figure 65. Critical thermal maximum (CTMAX) prediction (from Chen et al. 2018a). (a) Correlation between observed and predicted individual CTMAX values. (b) Prediction of population mean CTMAX (SEM) and evolutionary limits for populations (triangle) and species (dash line).

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 (Delomas et al. 2021), and have been using this updated pipeline to

genotype those samples targeted for sequencing in 2020. In 2021, we genotyped additional sturgeon, and utilized data collected through our updated (ploidy-sensitive) pipeline to conduct preliminary analyses of population structure of white sturgeon in the Columbia and other stronghold river basins.

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 66).

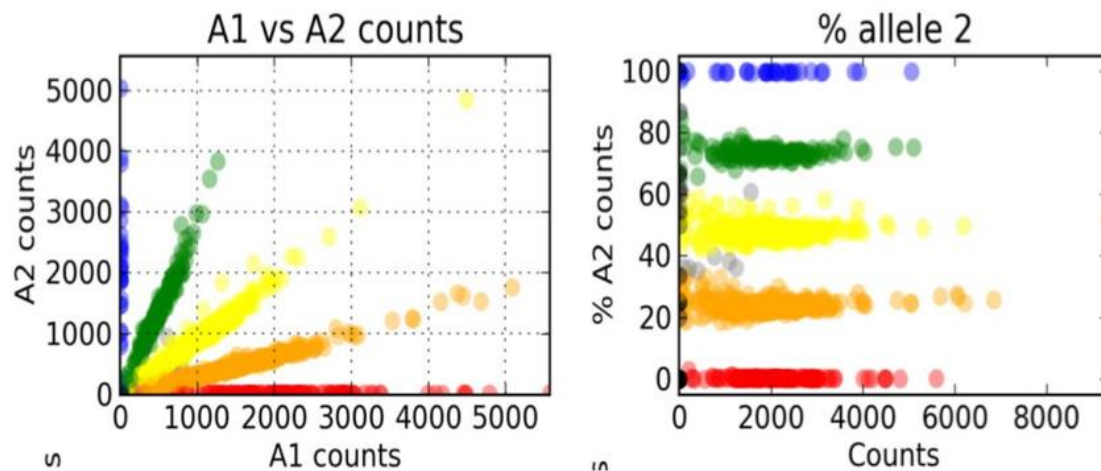
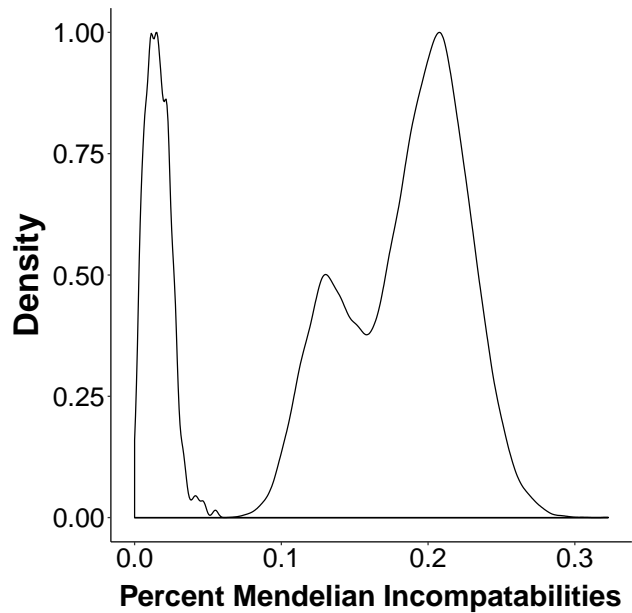


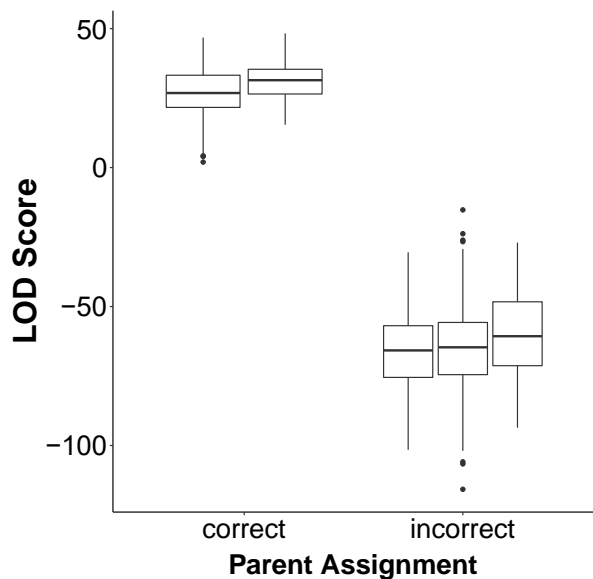
Figure 66. Example of a locus GT-seq plot from octoploid (functionally tetraploid) white sturgeon.

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 67). We have also demonstrated success in using statistical parentage assignment techniques, such as single parent assignment in Polygene (Huang et al. 2020) (Figure 68) or in sibling group assignment with Colony (Jones & Wang 2010) (Figure 69).



812
813 **Figure 67. Distribution of Mendelian incompatibilities (parents and offspring with**
814 **mismatched alleles) observed among all offspring in six reciprocal crosses of white**
815 **sturgeon.**
816



817
818 **Figure 68. Log-odds scores for parent assignment of known offspring to correct or**
819 **incorrect parent from known crosses of white sturgeon.**
820

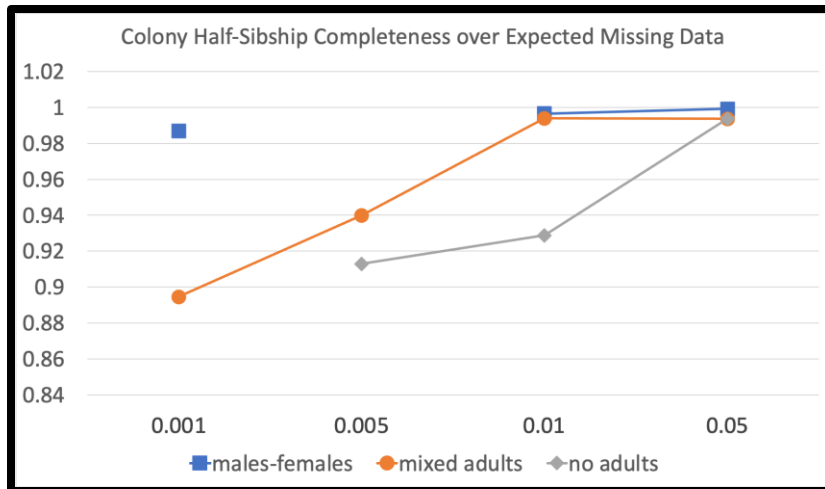


Figure 69. Proportion of half-sibling group assignment completeness in known crosses of white sturgeon.

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.

In 2021, we proceeded with analyzing these data to further resolve population structure of white sturgeon on the US Pacific Coast, concluding that after adding additional samples from putatively distinct sub-populations in the Kootenai, Sacramento, and Fraser Rivers. These samples have been analyzed with traditional population genetic methods that are flexible to the ploidy of the samples, rather than being hard coded for diploid. These included non-parametric methods such as principal components analyses, as well as parametric methods such as F_{ST} with formulas adapted for greater ploidy.

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 70). To analyze population structure, we identified 3,468 putative natural-origin samples with robust ploidy estimates of 4N among reaches within the Columbia Basin and outside (our examinations of ploidy variation in white sturgeon are ongoing, but in these data >4N individuals represented less than 1% of natural origin samples). These were genotyped using our 325 SNP panel, from which estimates of relatedness were made using the maximum

likelihood estimator using local allele frequencies in Polygene (Huang et al. 2020). For those measures that rely on unbiased sampling with respect to family structure in wild origin samples, and hypothesizing that many of our samples come from areas in each reach where sturgeon are known to congregate (e.g. dam tailraces), we implemented filtering using these relatedness measures so as to exclude first degree relatives (parent-offspring, full siblings) (Table 68). These samples were not discarded, but relatedness within and across reaches is currently being analyzed separately through additional methods that make robust estimates of relationship. The value chosen to identify first-degree relatives was estimated from a 5x6 known-cross family set from parents collected at John Day Reservoir and provided by Yakama Nation Fisheries (D. Miller; data not shown).

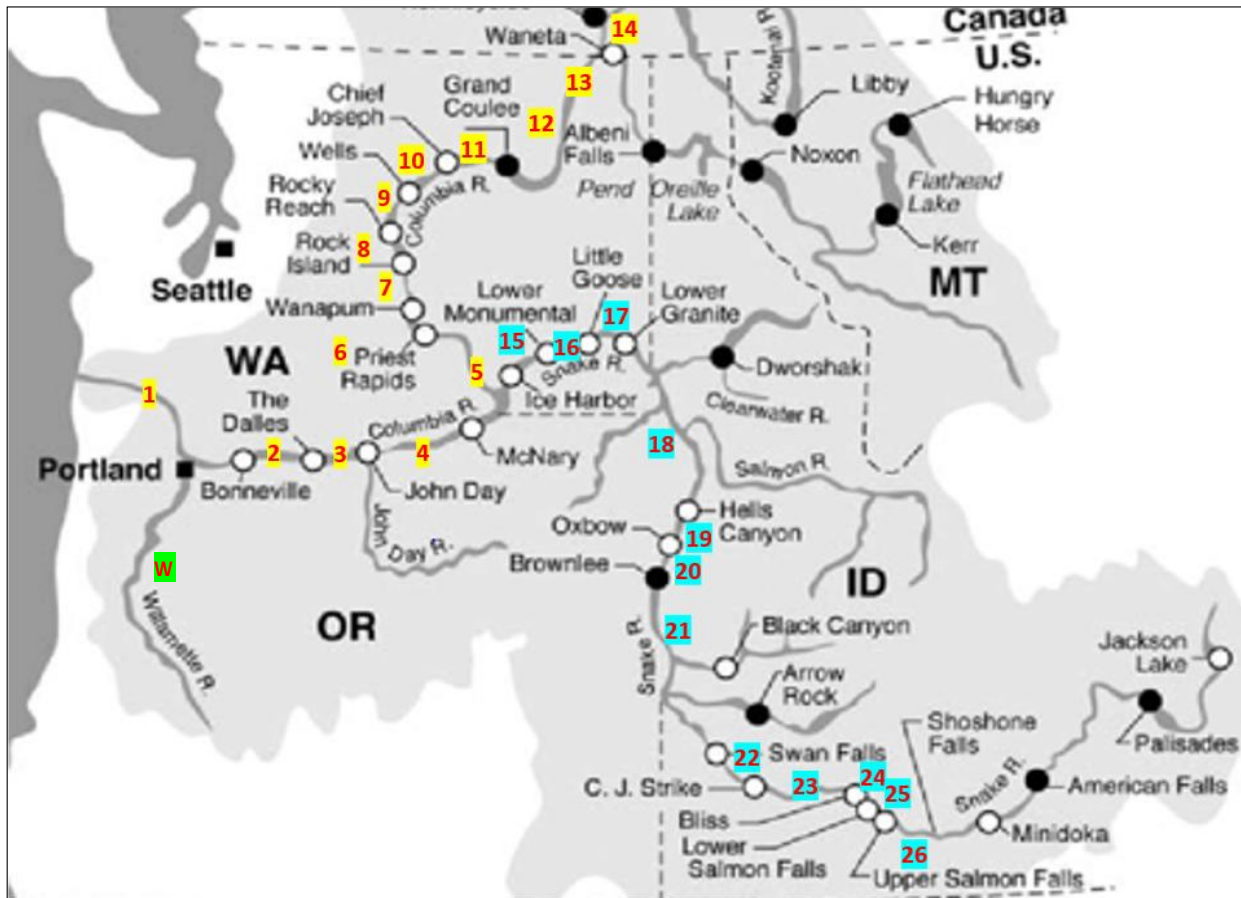


Figure 70. Locations in the Columbia Basin where white sturgeon are present (not numbered: Kootenai River).

	4N	r<0.35
Sacramento_San_Joaquin	37	37
Fraser_River	44	42
Columbia_below_Bonneville	490	432
Willamette	13	13
Bonneville	504	494
The_Dalles	505	499
John_Day	669	599
McNary	178	125
Ice_Harbor	108	101
Lower_Monumental	132	124
Little_Goose	112	106
middle_Snake	90	82
upper_Snake	264	169
Priest_Rapids_Wells_Tailrace	48	26
Lake_Roosevelt	225	183
Kootenai_River	49	46

Table 68. White sturgeon from the Columbia and adjacent basins genotyped for analysis of population structure, and filtered by relatedness (r) to exclude first-degree relatives.

Preliminary results reinforce the observations that white sturgeon in the Columbia basin exhibit a gradient of distinctness from the upper reaches to the reach below Bonneville Dam (Matala et al. 2017) (Figure 71). Most of the sampled reaches exhibit moderate and significant distinctiveness as measured by parametric methods (F_{ST} -analog) (

Gst''	Sacramento-SJ	Fraser	estuary	Willamette	Bonneville	The Dalles	John Day	McNary	Ice Harbor	Lower Monumental	Little Goose	middle Snake	upper Snake	Priest-Wells	Roosevelt	Kootenai
Sacramento-SJ	--	0.073	0.022	0.023	0.043	0.045	0.060	0.083	0.097	0.106	0.107	0.129	0.229	0.109	0.110	0.289
Fraser	0.073	--	0.034	0.034	0.029	0.029	0.029	0.036	0.042	0.047	0.045	0.055	0.123	0.043	0.045	0.180
estuary	0.022	0.034	--	0.002	0.007	0.008	0.016	0.031	0.041	0.048	0.049	0.066	0.153	0.050	0.050	0.227
Willamette	0.023	0.034	0.002	--	0.007	0.009	0.014	0.028	0.036	0.046	0.046	0.063	0.148	0.046	0.047	0.224
Bonneville	0.043	0.029	0.007	0.007	--	0.001	0.003	0.012	0.018	0.023	0.023	0.035	0.109	0.025	0.027	0.202
The Dalles	0.045	0.029	0.008	0.009	0.001	--	0.003	0.010	0.017	0.022	0.022	0.034	0.106	0.026	0.026	0.200
John Day	0.060	0.029	0.016	0.014	0.003	0.003	--	0.004	0.008	0.012	0.012	0.020	0.082	0.013	0.016	0.186
McNary	0.083	0.036	0.031	0.028	0.012	0.010	0.004	--	0.002	0.004	0.002	0.009	0.058	0.008	0.010	0.175
Ice Harbor	0.097	0.042	0.041	0.036	0.018	0.017	0.008	0.002	--	0.001	0.001	0.005	0.049	0.007	0.009	0.177
Lower Monumental	0.106	0.047	0.048	0.046	0.023	0.022	0.012	0.004	0.001	--	0.001	0.003	0.042	0.006	0.010	0.175
Little Goose	0.107	0.045	0.049	0.046	0.023	0.022	0.012	0.002	0.001	0.001	--	0.002	0.041	0.006	0.009	0.169
middle Snake	0.129	0.055	0.066	0.063	0.035	0.034	0.020	0.009	0.005	0.003	0.002	--	0.026	0.005	0.011	0.170
upper Snake	0.229	0.123	0.153	0.148	0.109	0.106	0.082	0.058	0.049	0.042	0.041	0.026	--	0.040	0.048	0.189
Priest-Wells	0.109	0.043	0.050	0.046	0.025	0.026	0.013	0.008	0.007	0.006	0.006	0.005	0.040	--	0.007	0.173
Roosevelt	0.110	0.045	0.050	0.047	0.027	0.026	0.016	0.010	0.009	0.010	0.009	0.011	0.048	0.007	--	0.147
Kootenai	0.289	0.180	0.227	0.224	0.202	0.200	0.186	0.175	0.177	0.175	0.169	0.170	0.189	0.173	0.147	--

Table 69), though both PCA and population assignment results (Figure 72) indicate that individual reaches with the Columbia Basin are not reliably distinguishable, with the exception of the uppermost reaches (Kootenai, upper Snake).

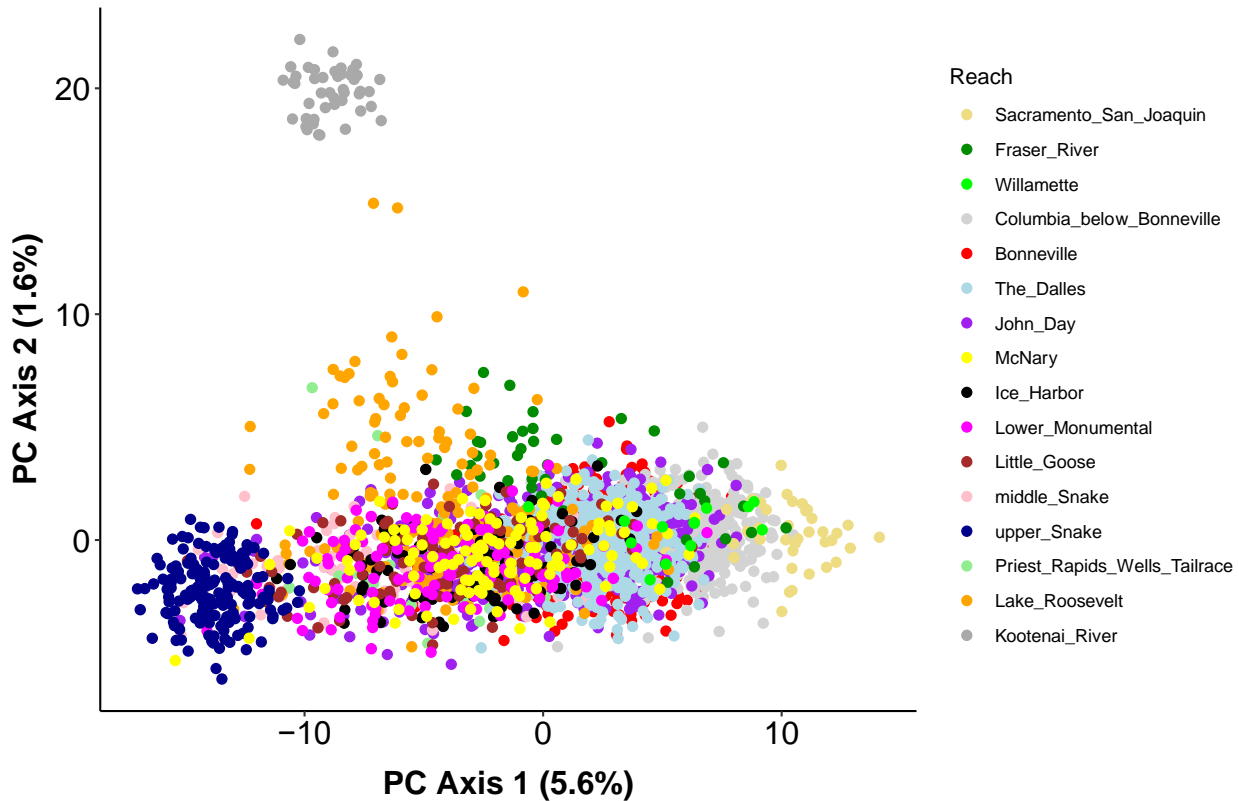


Figure 71. Principal components analysis of 3,468 white sturgeon from the Columbia, Fraser and Sacramento River Basins, based on SNP genotypes.

Gst''	Sacramento - SJ	Fraser	estuary	Willamette	Bonneville	The Dalles	John Day	McNary	Ice Harbor	Lower Monumental	Little Goose	middle Snake	upper Snake	Priest-Wells	Roosevelt	Kootenai
Sacramento-SJ	--	0.073	0.022	0.023	0.043	0.045	0.060	0.083	0.097	0.106	0.107	0.129	0.229	0.109	0.110	0.289
Fraser	0.073	--	0.034	0.034	0.029	0.029	0.029	0.036	0.042	0.047	0.045	0.055	0.123	0.043	0.045	0.180
estuary	0.022	0.034	--	0.002	0.007	0.008	0.016	0.031	0.041	0.048	0.049	0.066	0.153	0.050	0.050	0.227
Willamette	0.023	0.034	0.002	--	0.007	0.009	0.014	0.028	0.036	0.046	0.046	0.063	0.148	0.046	0.047	0.224
Bonneville	0.043	0.029	0.007	0.007	--	0.001	0.003	0.012	0.018	0.023	0.023	0.035	0.109	0.025	0.027	0.202
The Dalles	0.045	0.029	0.008	0.009	0.001	--	0.003	0.010	0.017	0.022	0.022	0.034	0.106	0.026	0.026	0.200
John Day	0.060	0.029	0.016	0.014	0.003	0.003	--	0.004	0.008	0.012	0.012	0.020	0.082	0.013	0.016	0.186
McNary	0.083	0.036	0.031	0.028	0.012	0.010	0.004	--	0.002	0.004	0.002	0.009	0.058	0.008	0.010	0.175
Ice Harbor	0.097	0.042	0.041	0.036	0.018	0.017	0.008	0.002	--	0.001	0.001	0.005	0.049	0.007	0.009	0.177
Lower Monumental	0.106	0.047	0.048	0.046	0.023	0.022	0.012	0.004	0.001	--	0.001	0.003	0.042	0.006	0.010	0.175
Little Goose	0.107	0.045	0.049	0.046	0.023	0.022	0.012	0.002	0.001	0.001	--	0.002	0.041	0.006	0.009	0.169
middle Snake	0.129	0.055	0.066	0.063	0.035	0.034	0.020	0.009	0.005	0.003	0.002	--	0.026	0.005	0.011	0.170
upper Snake	0.229	0.123	0.153	0.148	0.109	0.106	0.082	0.058	0.049	0.042	0.041	0.026	--	0.040	0.048	0.189
Priest-Wells	0.109	0.043	0.050	0.046	0.025	0.026	0.013	0.008	0.007	0.006	0.006	0.005	0.040	--	0.007	0.173
Roosevelt	0.110	0.045	0.050	0.047	0.027	0.026	0.016	0.010	0.009	0.010	0.009	0.011	0.048	0.007	--	0.147
Kootenai	0.289	0.180	0.227	0.224	0.202	0.200	0.186	0.175	0.177	0.175	0.169	0.170	0.189	0.173	0.147	--

Table 69. Genetic distinctness (Gst'') by reach for white sturgeon sampled in the Columbia River and adjacent basins. Significance was tested using 10,000 permutations of individuals, and values below the FDR (Benjamini-Hochberg) are indicated in gray font.

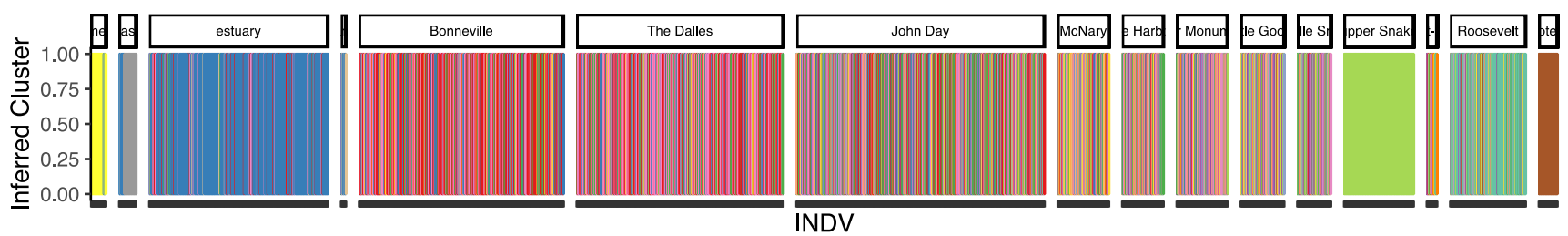


Figure 72. Population assignment (Paetkau et al. 2004) for white sturgeon in the Columbia River and adjacent river basins. Color represents reach to which an individual was assigned, with color-indistinct reaches indicating low assignment to source.

Gst''	Sacramento - SJ	Fraser	estuary	Willamette	Bonneville	The Dalles	John Day	McNary	Ice Harbor	Lower Monumental	Little Goose	middle Snake	upper Snake	Priest-Wells	Roosevelt	Kootenai
Sacramento-SJ	--	0.073	0.022	0.023	0.043	0.045	0.060	0.083	0.097	0.106	0.107	0.129	0.229	0.109	0.110	0.289
Fraser	0.073	--	0.034	0.034	0.029	0.029	0.029	0.036	0.042	0.047	0.045	0.055	0.123	0.043	0.045	0.180
estuary	0.022	0.034	--	0.002	0.007	0.008	0.016	0.031	0.041	0.048	0.049	0.066	0.153	0.050	0.050	0.227
Willamette	0.023	0.034	0.002	--	0.007	0.009	0.014	0.028	0.036	0.046	0.046	0.063	0.148	0.046	0.047	0.224
Bonneville	0.043	0.029	0.007	0.007	--	0.001	0.003	0.012	0.018	0.023	0.023	0.035	0.109	0.025	0.027	0.202
The Dalles	0.045	0.029	0.008	0.009	0.001	--	0.003	0.010	0.017	0.022	0.022	0.034	0.106	0.026	0.026	0.200
John Day	0.060	0.029	0.016	0.014	0.003	0.003	--	0.004	0.008	0.012	0.012	0.020	0.082	0.013	0.016	0.186
McNary	0.083	0.036	0.031	0.028	0.012	0.010	0.004	--	0.002	0.004	0.002	0.009	0.058	0.008	0.010	0.175
Ice Harbor	0.097	0.042	0.041	0.036	0.018	0.017	0.008	0.002	--	0.001	0.001	0.005	0.049	0.007	0.009	0.177
Lower Monumental	0.106	0.047	0.048	0.046	0.023	0.022	0.012	0.004	0.001	--	0.001	0.003	0.042	0.006	0.010	0.175
Little Goose	0.107	0.045	0.049	0.046	0.023	0.022	0.012	0.002	0.001	0.001	--	0.002	0.041	0.006	0.009	0.169
middle Snake	0.129	0.055	0.066	0.063	0.035	0.034	0.020	0.009	0.005	0.003	0.002	--	0.026	0.005	0.011	0.170
upper Snake	0.229	0.123	0.153	0.148	0.109	0.106	0.082	0.058	0.049	0.042	0.041	0.026	--	0.040	0.048	0.189
Priest-Wells	0.109	0.043	0.050	0.046	0.025	0.026	0.013	0.008	0.007	0.006	0.006	0.005	0.040	--	0.007	0.173
Roosevelt	0.110	0.045	0.050	0.047	0.027	0.026	0.016	0.010	0.009	0.010	0.009	0.011	0.048	0.007	--	0.147
Kootenai	0.289	0.180	0.227	0.224	0.202	0.200	0.186	0.175	0.177	0.175	0.169	0.170	0.189	0.173	0.147	--

Population order follows Table 69.

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 66). 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 67), we continue to explore more robust methods to fully utilize the information content of tetraploid genotypes (e.g. Figure 68, Figure 69).

Our research is guided by previous results from microsatellite data which indicate a regional distinction between upper and lower reach Columbia River populations is evident (Matala et al. 2017), and preliminary results from analysis of population structure with SNP data are consistent this while providing additional detail. More broadly, 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 ongoing examination of genetic diversity and rates of ploidy variation in these different reaches across life stages will help clarify natural rates of spontaneous autopolyploidy and of variation in genetic diversity between cohorts, as well as between recruits and the adult population.

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 Fraser River white sturgeon, which will assist to order or orient (anchor) smaller scaffolds into chromosomes. In 2021, we utilized data from a reduced representation (restriction enzyme associated DNA, or RAD) genomic libraries in creation of a linkage map and subsequent anchoring of assembly contigs, with promising results that further anchored ~15% of the assembly. To augment this, in 2021 we also sampled

offspring from a single family of upper Snake River sturgeon (the same reach from which our genome sequenced individual derived), and are currently developing RNA libraries from head/brain tissue from which another linkage map will be inferred. These RNA data will also serve to augment and verify gene annotations of our genome assembly. 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. 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. Recently, Kuhl et al. (2021) described the identification of sex-associated regions in genome assemblies of a male and female sterlet sturgeon (*Acipenser ruthenus*). Our pursuit of homologous regions in our (female/heterogametic) white sturgeon assembly to identify sex-indicative markers for white sturgeon has been productive (3 putatively homologous regions of our assembly were identified). However, while linkage of marker genotypes developed from this region has been as expected for the scaffolds targeted, sex prediction accuracy has thus far only achieved ~96% in females and ~80% in males, indicating some misunderstanding in segregation patterns. Additional marker development and testing to resolve these issues is ongoing, in addition to insight expected from assembly homology resolved by the additional linkage maps.

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. Sample archiving began in 2008 and continues through the present, with samples contributed annually by CRITFC staff and several partner organizations. 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 2020. For sockeye salmon, we used GSI to estimate relative stock abundance and run-timing distributions, and we used PBT to estimate the component of the run that originates from a reintroduction program in the Yakima River. 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 2021, 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.