

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* – 363 loci including a sex determination marker and 14 additional amplicons used for species identification), Steelhead trout (*O. mykiss* – 402 loci including a sex determination marker and 16 additional amplicons for species identification); Sockeye salmon (*O. nerka* – 364 loci including a sex determination marker); Coho salmon (*O. kisutch* – 236 loci including two sex determination markers), White sturgeon (*Acipenser transmontanus* – 325 loci), Pacific lamprey (*Entosphenus tridentatus* – 290 loci including 4 for species identification), and a species complex of lampreys in the genus *Lampetra* (*L. richardsoni*, *L. ayresii*, and *L. pacifica* – 365 loci including 4 for species identification). 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 137,184 samples in 2022 (Figure 1). The largest portion of samples were Chinook salmon (97,253), then Pacific lamprey (16,200), Coho (8,863), Steelhead (8,438), White sturgeon (3,232), and Sockeye (3,198).

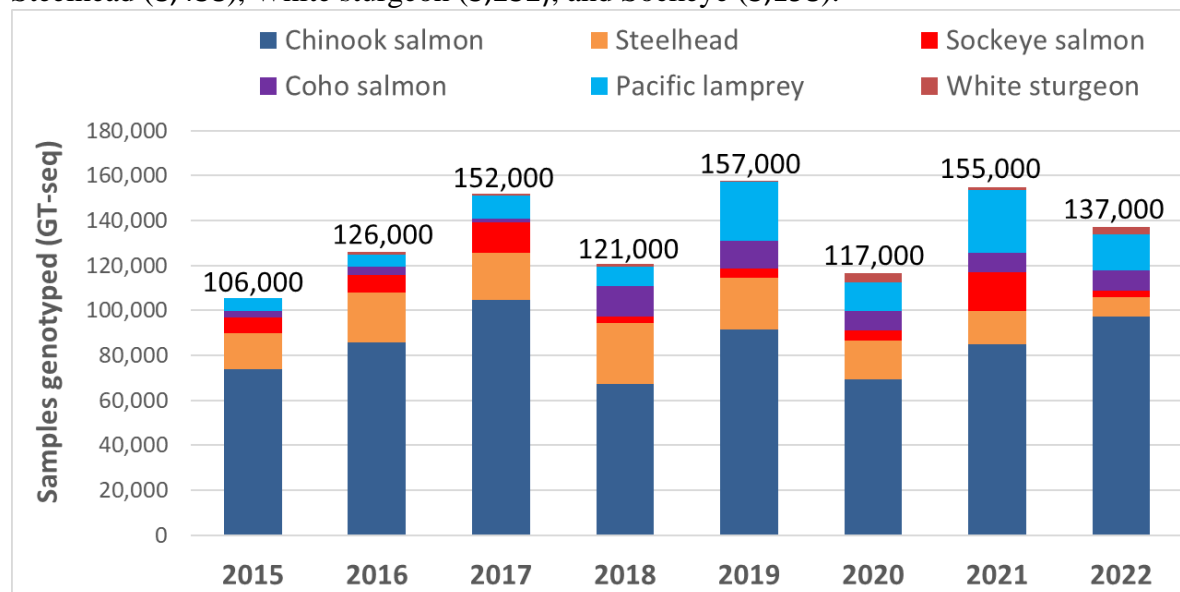


Figure 1. Summary of Columbia River fish samples genotyped using GT-seq (2015 – 2022).

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).

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 re-sequencing methods that barcode individual samples, sequenced as a pool, to represent different collections and 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. Major accomplishments in 2022 include refining the SNP marker set associated with adult migration timing (GREB1L/ROCK1) for Chinook salmon with the use of whole genome re-sequencing data from 53 populations located throughout the Columbia River Basin. The phenotype of migration timing in the three major genetic lineages of Chinook salmon was compared to the allele frequencies at each SNP position in GREB1L/ROCK1 to assess the SNP markers accuracy in determining migration timing.

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 2021-2022. For Chinook salmon, we employ 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 2021 in Non-Treaty sport and commercial fisheries in the mainstem Columbia River during the spring, summer, and fall management periods (Figure 2). PBT is also applied to Sockeye salmon and can identify fish that are part of the Yakima River reintroduction using a baseline of translocated adults.

There were 495 coded-wire tags (CWTs) that were identified to hatchery stock and broodyear (BY) among the snouts recovered from the lower river fisheries in 2021, and 298 of these CWTs also were PBT assigned (60%). Of the 298 fish with both CWT and PBT, there were 278 fish (93%) that were concordant across results from these tagging methods according to the hatchery source and the broodyear.

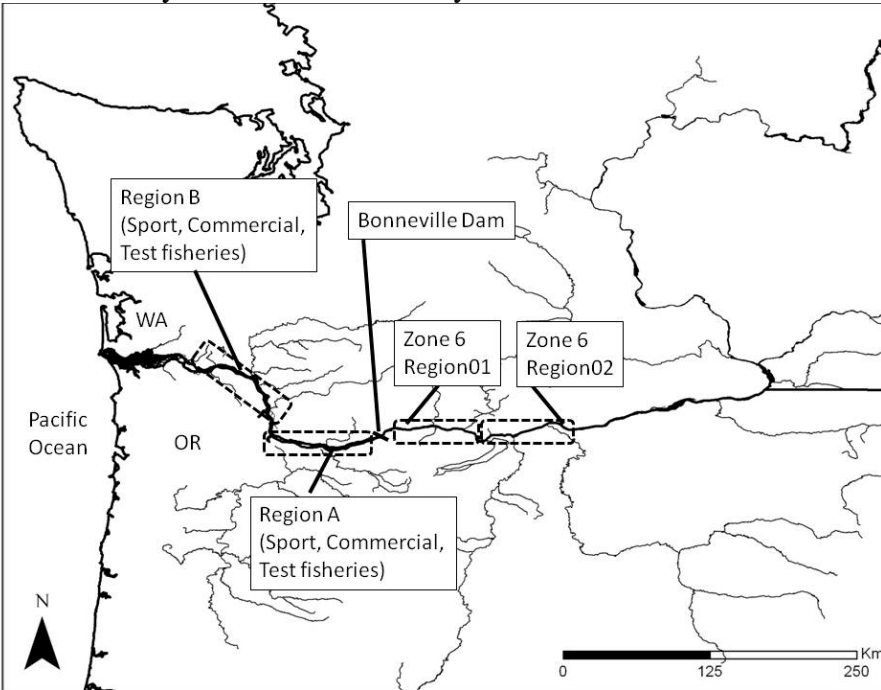


Figure 2. Sources of fishery mixtures in the lower Columbia River mainstem.

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). We analyzed the 2022 test fishery as part of our in season reporting. Consistent with our previous analyses of 2018 – 2021 test fishery data, the 2022 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.

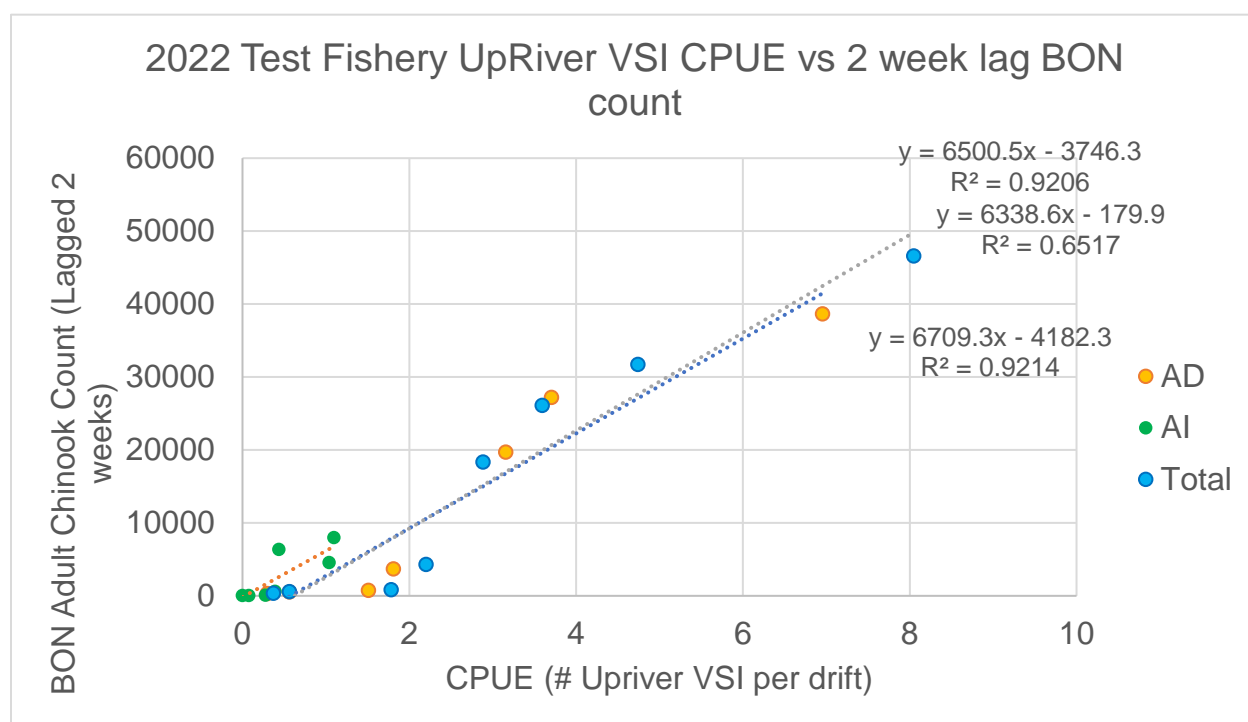
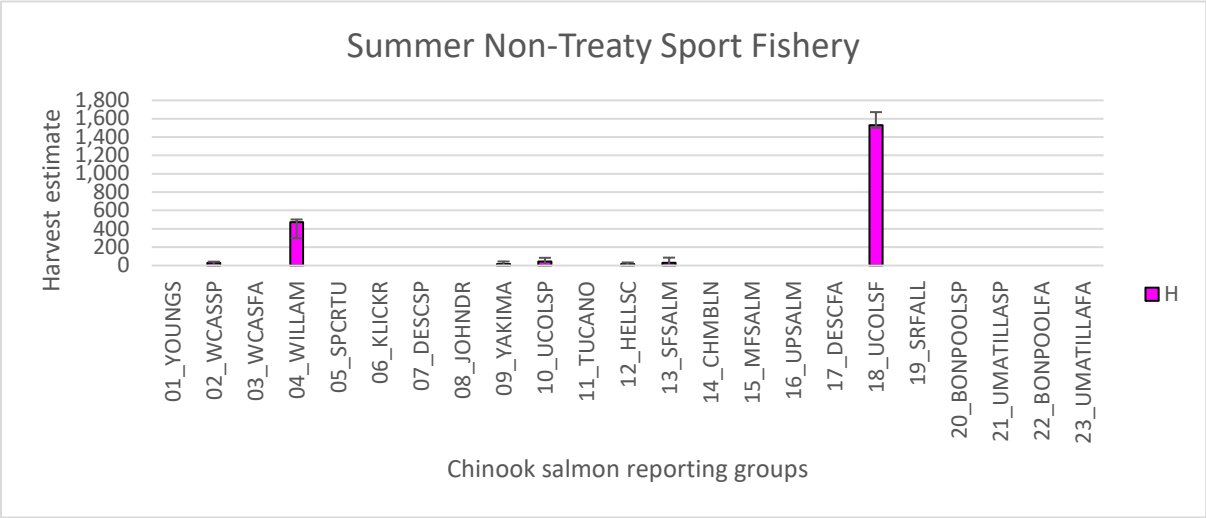


Figure 3. The relationship between the test fishery upriver Chinook Salmon CPUE and weekly fish counts at Bonneville Dam in 2022 with 2 week lag.

As expected, the stock composition varied substantially across the Non-Treaty sport 2021 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

568 capture rate may have been due to fishing effort in region B but is unexpected due to the summer
569 timing of the fishery since Willamette River stock is spring-run.

570



571

572 **Figure 4. Genetic stock composition of the Non-Treaty Sport Chinook fishery**
573 **during the summer period analyzed in 2021.**

574

575 In 2021, we sampled the Non-Treaty Sport fisheries above and below Bonneville Dam
576 and the Non-Treaty Commercial fishery below Bonneville Dam during the Fall Chinook salmon
577 management period. We continue to find that despite both the Non-Treaty sport and commercial
578 fishery being executed at similar times near Bonneville Dam, the sport fishery is comprised of
579 dramatically lower abundance of “tules” (Figure 5). This difference may be largely due to sport
580 fishers preferentially keeping the VSI bright fish over the tule fish.

581

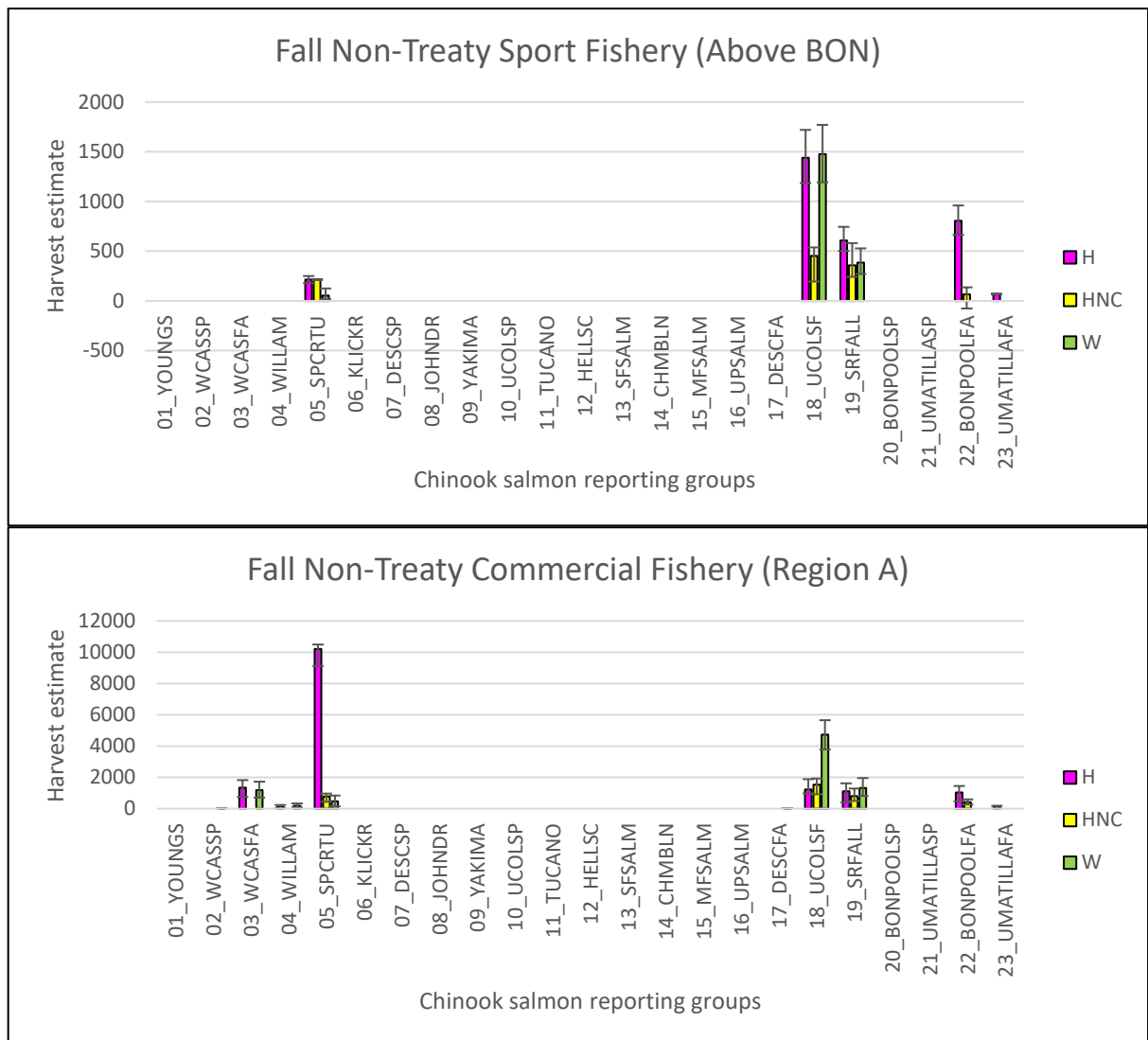


Figure 5. Genetic stock composition of the Non-Treaty sport fishery above BON and lower river Non-Treaty commercial Chinook salmon fishery analyzed in 2021.

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 2021 (post-season analyses). Further, in-season analyses were completed for fish returning throughout 2022 and provided to regional fisheries managers that serve the U.S. v OR Technical Advisory Committee (TAC).

In 2021, there were 9 major (i.e., abundance >1000 fish) Chinook salmon stocks represented in the total estimated relative abundance (N=116,212) of natural-origin (i.e., excluding unclipped hatchery-origin fish) Chinook salmon passing Bonneville Dam in 2021 (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 (82,079), 19_SRFALL (18,726), 17_DESCFA (3,050), 12_HELLSC (2,476), 10_UCOLSP (2,134), 16_UPSALM (1,588), 09_YAKIMA(1,544), 05_SPCRTU (1,109), and 13_SFSALM (1,064). These stock abundance estimates were generated using SCOBIDEUX and SPIBETR functions and the estimates of clipped and unclipped adults distributed by TAC.

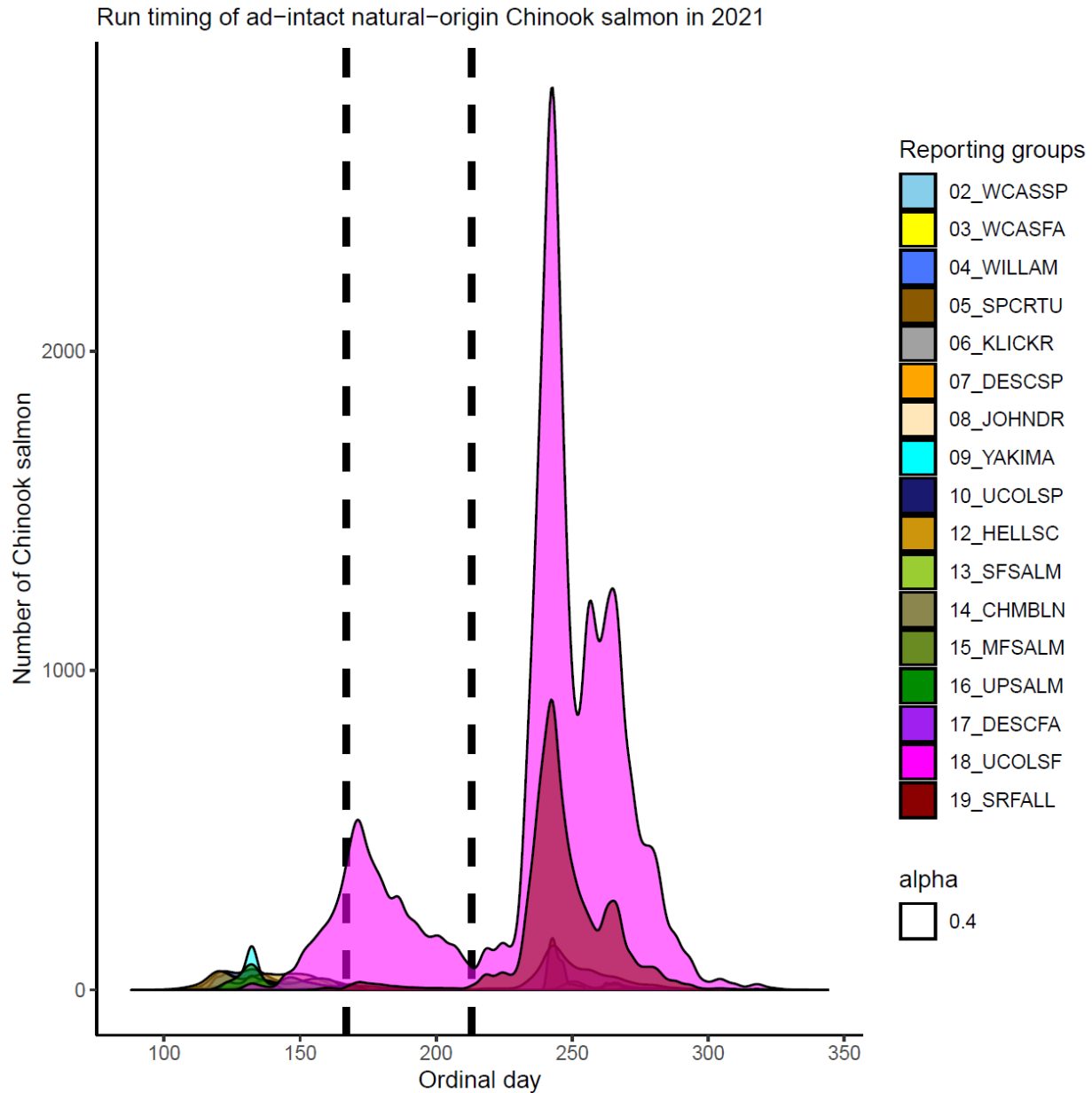


Figure 6. Estimated abundance of natural origin (excluding adipose-intact hatchery-origin fish) adult-sized Chinook salmon sampled at Bonneville Dam in 2021 assigned to genetic stock of origin.

There were five major stocks (abundance >1000) represented in the total estimated abundance (N=44,227) of clipped hatchery origin steelhead passing Bonneville Dam in 2021. These stocks in order of decreasing magnitude were 14_UPSALM (15,325), 07_MGILCS (12,139), 10_SFCLWR (8,504, B-Index), 10_SFCLWR (4,823, A-Index), and 09_UPPCOL (3,059) (Figure 7). There was a single major stock (14_UPSALM, abundance >1000) represented in the total estimated abundance (N=2,866) of unclipped hatchery origin steelhead passing Bonneville Dam in 2021. There were two major stocks (abundance >1000) represented

in the total estimated abundance (N=20,659) of natural origin (excluding adipose unclipped hatchery-origin fish) summer A-/B-Index steelhead passing Bonneville Dam in 2021 (Figure 7). These stocks in order of decreasing magnitude were 07_MGILCS (12,610 A-Index; 480 B-Index), and 14_UPSALM (3,724 A-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.

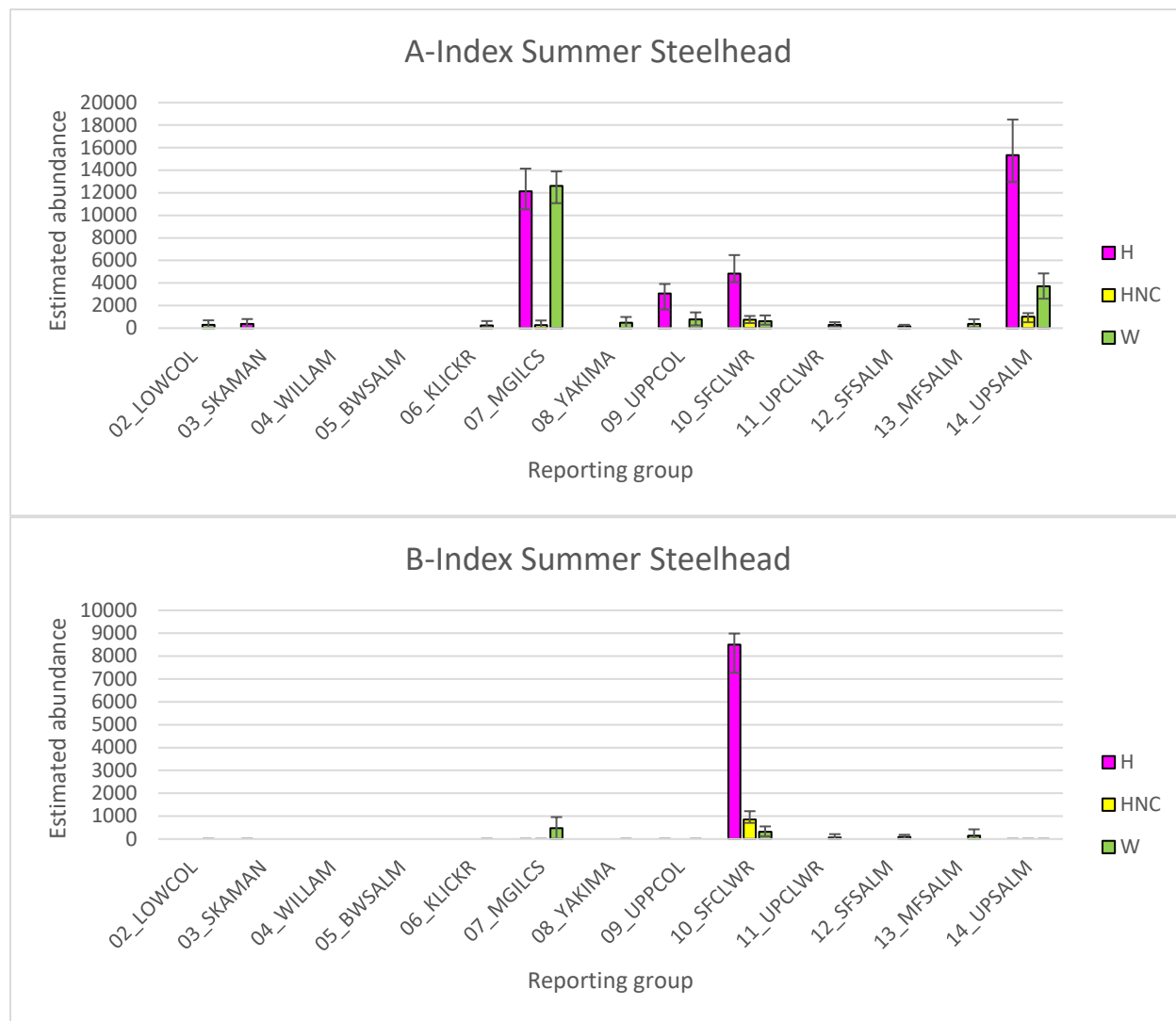


Figure 7. Estimated abundance (± 95% CI) of A-Index (<780mm FL, top) and B-Index (≥780mm FL, bottom) hatchery origin (clipped “H” and unclipped “HNC”) and natural-origin (“W”) steelhead assigned to genetic stock of origin that were sampled at Bonneville Dam in 2021.

Stock abundance for sockeye salmon was estimated over a course of 21 statistical weeks (i.e. weeks 18 – 39). A total of 1,451 sockeye salmon were sampled at Bonneville Dam in 2021 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 2021, The

Okanogan stock had the highest relative abundance (105,650), followed by the Wenatchee (41,269). This year there were a small number of sockeye estimated from Snake River (1,311). The Lake Billy Chinook stock had zero estimated abundance. The reintroduced stock from Yakima River had a non-zero abundance and was estimated at 3,535 fish in 2021 (Figure 8).

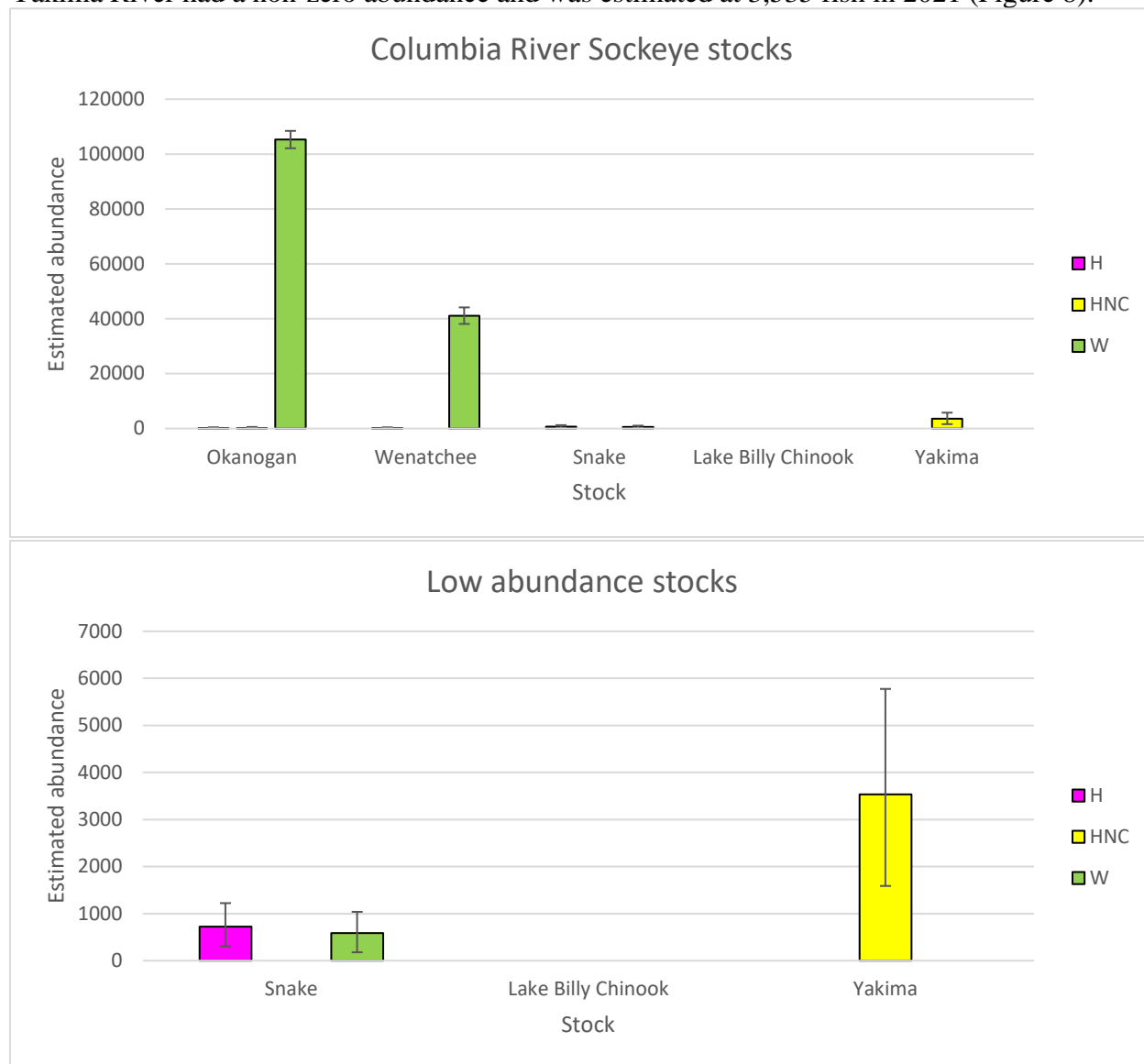


Figure 8. Estimated abundance (\pm 95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2021.

In 2021, 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% (3,933 fish) and 76% (12,562 fish) of the total abundance estimated in those two periods, respectively. For steelhead, the patterns generally are consistent with past years. The late arriving stocks with median dates on or after August 25th were 13_MFSALM (B-Index), 10_SFCLWR (both A-Index

and B-Index), 11_UPCLWR (both A-Index and B-Index), and 12_SFSALM (both A-Index and B-Index). For the five 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 2021. The Wenatchee, Okanogan, Snake, and Yakima stocks had nearly identical run timing distributions each with an average median date on 06/29/21.

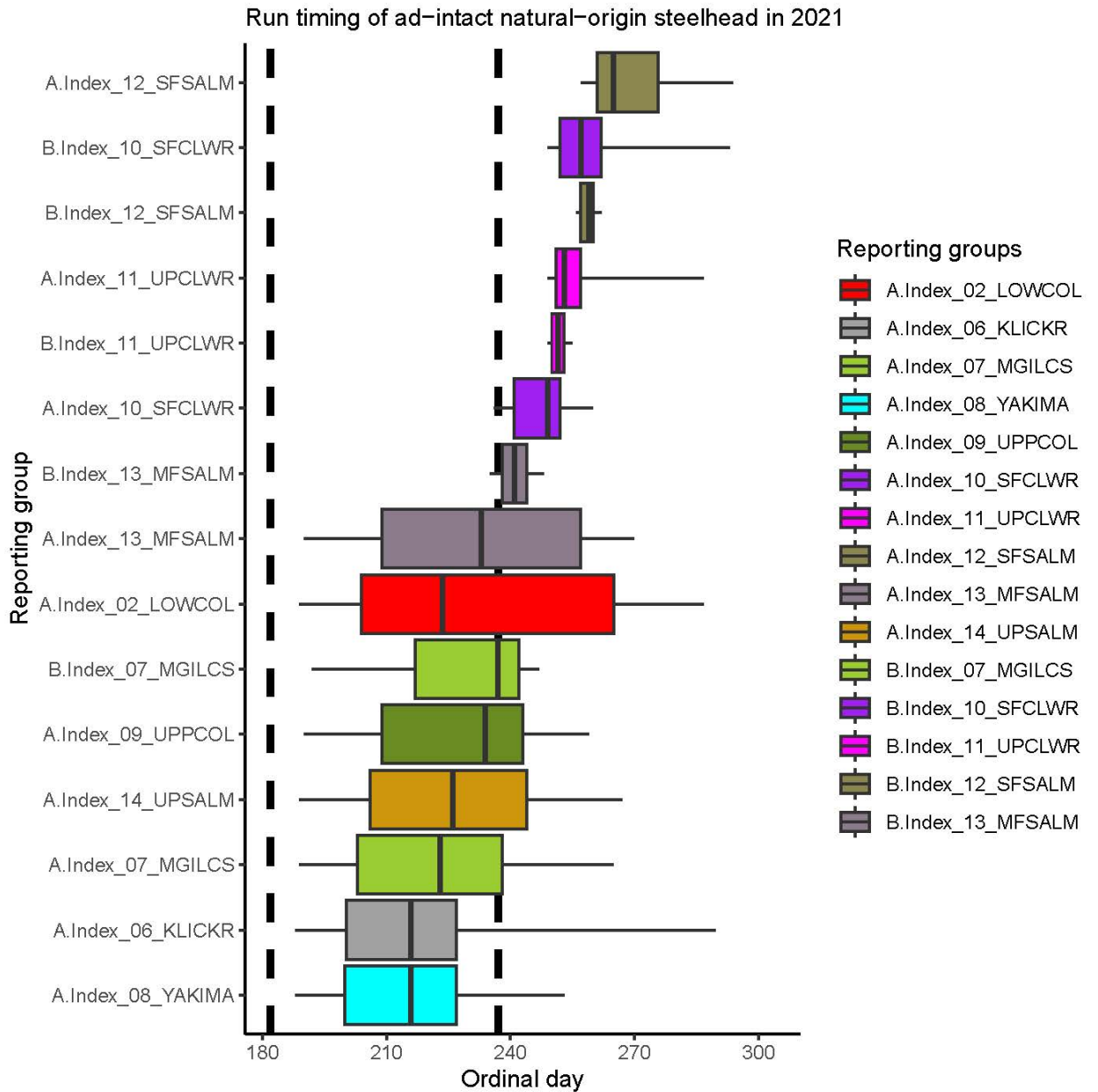


Figure 9. Reporting group level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for natural-origin steelhead (unclipped hatchery-origin fish excluded) that were sampled at Bonneville Dam in 2021 and split by A-Index and B-Index size category. August 25th 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 2022 (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 there were zero estimated Sockeye salmon returned to Bonneville Dam in 2022 originating from the Yakama Nation reintroduction program in the Yakima River basin despite there being a relatively large return of Sockeye salmon overall (Figure 10). Mostly the Sockeye salmon run was comprised of Okanagan and Wenatchee genetic stocks.

Table 1. The in-season and post-season report timing and scope of the 2022 fish runs for Chinook salmon, steelhead, and Sockeye salmon.

Species	Management Period	Data coverage	Samples Arrive	Analysis begins	Report distributed
Chinook	Spring	01/01/2022 – 04/30/2022	5/2/2022	5/5/2022	5/9/2022
		01/01/2022 – 05/14/2022	5/16/2022	5/19/2022	5/23/2022
		01/01/2022 – 05/28/2022	5/30/2022	6/2/2022	6/6/2022
		01/01/2022 – 06/15/2022	6/16/2022	6/21/2022	6/24/2022
	Summer	06/16/2022 – 06/30/2022	7/1/2022	7/7/2022	7/11/2022
		06/16/2022 – 07/31/2022	8/1/2022	8/4/2022	8/8/2022
	Fall	08/01/2022 – 8/27/2022	8/29/2022	9/1/2022	9/5/2022
		08/01/2022 – 10/29/2022	10/31/2022	11/3/2022	11/7/2022
	Skamania	04/01/2022 – 06/30/2022	7/1/2021	7/7/2022	7/11/2022
Steelhead	Summer A-/B-Index	07/01/2022 – 07/31/2022	8/1/2022	8/4/2022	8/8/2022
		07/01/2022 – 08/27/2022	8/29/2022	9/1/2022	9/5/2022
		07/01/2022 – 10/31/2022	10/31/2022	11/3/2022	11/7/2022
Sockeye	Total	01/01/2022 – 07/31/2022	8/1/2022	8/4/2022	8/8/2022

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.

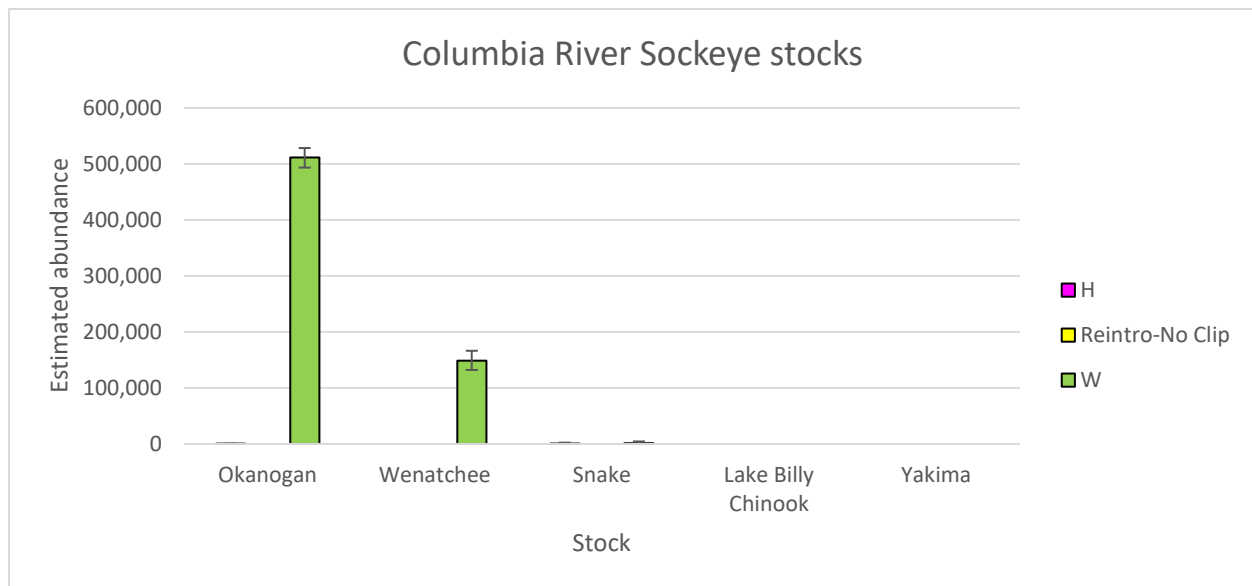


Figure 10. In-season analysis estimated a relatively large return of sockeye salmon overall in 2022 comprised of a mixture of Wenatchee and Osoyoos genetic stocks and zero abundance estimated from Yakima River.

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. Recent study of resident vs. anadromous *O. mykiss* revealed a significant region on Chr. 12 that may represent a minor effect gene for male anadromy and will be developed for further validation in GT-seq panels (**Figure 11**).

Figure 11. Manhattan plot of differences in allele frequencies between resident and anadromous collections across the genome based on sliding window FST (sFST). The minimum coverage threshold was 15 reads and the minor allele frequency was ≥ 0.05 . (from Collins et al. 2022)

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 upper Columbia and 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 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 that historical gene flow was moderated by distance from the upper Snake River down to the Lower Columbia River below Bonneville Dam. 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 estimate parentage and relatedness in focal populations. 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

756 diversity are likely to aid managers in understanding the impacts of limited habitat in the
757 confines of the mid-Columbia impoundments that may be exacerbated by further anthropogenic
758 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 estimate stock specific abundance and run timing and incorporate life history traits of salmon and steelhead. GSI provides the ability to perform stock composition of the different runs of salmonid species as they pass Bonneville Dam and this information can be compared to other tagging methodologies like PIT and CWT. 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), and these genetic data can also be generated quicker than ever before. Therefore, we plan to estimate stock composition of multiple species passing Bonneville Dam and provide this information on a timely basis to fisheries managers using in-season reports as well as post-season 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 2021. 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 2021. 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 2022. These in-season and post-season 2022 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 adaptors for 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 markers for species diagnostic analysis were first 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, Atlantic salmon, 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 vgl13) with age of maturity variation in Chinook, coho, sockeye, and steelhead. To avoid nearby polymorphic sites that could interfere with primer annealing, the Waters et al. reference sequences flanking each marker were (1) aligned against reference genomes when available and (2) their genomic coordinates were searched against an internal database of pool-seq SNPs when available. Our standard Chinook panel includes three markers developed from the two genes in association. Our steelhead panel includes four markers across three amplicons from the two genes. Preliminary testing was completed for the sockeye and coho panels. A single marker is planned for each panel initially with additional work needed to design additional primers.

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* – 363 loci including a sex determination marker and 14 additional amplicons used for species identification), Steelhead trout (*O. mykiss* – 402 loci including a sex determination marker and 16 additional amplicons for species identification); Sockeye salmon (*O. nerka* – 364 loci including a sex determination marker); Coho salmon (*O. kisutch* – 236 loci including two sex determination markers), White sturgeon (*Acipenser transmontanus* – 325 loci), Pacific lamprey (*Entosphenus tridentatus* – 290

loci including 4 for species identification), and a species complex of lampreys in the genus *Lampetra* (*L. richardsoni*, *L. ayresii*, and *L. pacifica* – 365 loci including 4 for species identification. 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 137,184 samples in 2022 (**Figure 12**). The largest portion of samples were Chinook salmon (97,253), then Pacific lamprey (16,200), Coho (8,863), Steelhead (8,438), White sturgeon (3,232), and Sockeye (3,198).

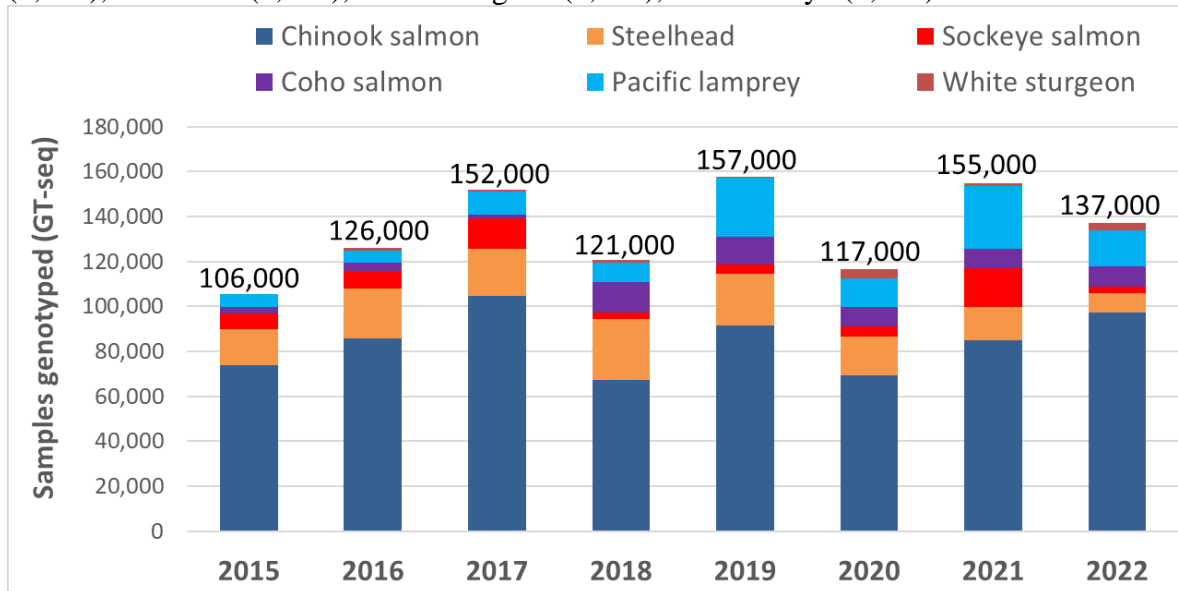


Figure 12. Summary of Columbia River fish samples genotyped using GT-seq in calendar years 2015 – 2022.

The Chinook panel underwent no significant changes for 2022. We continued to utilize species diagnostic loci in this panel with fourteen loci from other panels and 5 loci already included. Loci used in the standard panel are shown in Appendix 2. 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. Sequencing for 2,753 individuals across the population and age groups was completed in 2022 using both Illumina NextSeq 2000 NovaSeq platforms. Bioinformatics and statistical analyses are ongoing. Additional loci from this effort and a secondary effort to develop additional GSI loci are expected to be designed and tested in 2023.

The active Steelhead panel for 2022 added 16 amplicons from the suite of species diagnostic loci, and 4 age at maturity markers that were designed from Waters et al. 2021 data. Loci information can be seen in Appendix 1.

The Sockeye panel remained the same for 2022. We plan to add a single age at maturity marker early in 2023 with additional markers considered for the future. Loci information can be seen in Appendix 3.

The Coho panel underwent no significant changes in 2022. Markers for age at maturity were tested with a single marker chosen to be added to the panel in 2023. Loci information can be seen in Appendix 4.

The Pacific lamprey panel underwent no changes in 2022. Work was completed to design sex diagnostic markers based on whole genome sequencing data. Markers were designed and tested but were not found to be useful for determining sex. Loci information can be seen in Appendix 5.

The panel for species complex of lampreys in the genus *Lampetra* had 19 underperforming loci removed for 2022. Reasons included low genotyping percentage, low minor allele frequency, low on target percentage, and excessive read usage. Loci information can be seen in Appendix 6.

The White sturgeon panel underwent no changes in 2022. Sex identifying loci were tested (See sturgeon section) but no useful markers were found. Additional testing is currently delayed until additional genome work is completed. Loci information can be seen in Appendix 7. Note that correction factors were removed and are currently not being used for genotyping analysis.

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. Additional testing is needed to confirm application across the Columbia River Basin. The species markers are currently incorporated in the Chinook and steelhead panels and will soon be incorporated into coho and sockeye panels. SNP information for the loci used 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, Collins et al. 2020; Willis et al. 2020).

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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1196 *Appendix 1. GT-seq SNP panel for steelhead trout.*
 1197

Assay	A 1	A 2	A1-Probe	A2-Probe	FWD Primer	Corr ectio n	Rev Primer
M09AAC. 055	C	T	ACCTCCACGCTGT CC	ACCTCCACACTG TCC	GTCTCCGACGTGTGGCT	0,0	TGGAACGAACCTGAGAACAT AAGG
M09AAD. 076	T	C	CACCAACCACTG GTGAA	CCAACCGCTGGT GAA	ACTGTTACCACTCTCTCATCAACCT	0,0	GGGTCCAGGAGGTTTTTAAA CAACAT
M09AAE. 082	T	G	AGGTTGTTTTACA AATTTAA	AGGTTGTTTTAC ACATTTAA	CTATGTGCAGTGCCCTTCTCA	0,0	GGCTTACAAGTATGCATGAC TAGCT
M09AAJ. 163	G	A	AACAAAGTGAAA GTGTCCT	CAAAGTGAAAGT GTCTT	TCCCATGGCCCTTACTCTATCAA	0,0	TTGAGGTGTATGTTGAAAAG TAAACTT
Ocl_gshp x-357	T	G	ATCCGTCCAGGA AATG	TCCGTCCCGGAA ATG	GAGATCCTGAGGTCCCTGAAGTAT	0,0	AAGTGGAATTTGGGCTCAA AGC
OMGH1P ROM1- SNP1	A	T	TAGTGTTCACTGA CTTCA	TAGTGTAACACTG ACTTCA	TCAAACCTGCATTTGATGGAAACAA ACAT	0,0	AGGACAATTCTAAGTGACCT CAAACCTG
OMS0000 2	A	C	TGTTTTGCAGCGC TC	TGTTTGGCAGCG CT	TTTGATTTGATTTGTATCTGCTTCT T	0,0	CCAACATGCCTCACACAAAA
OMS0000 3	T	G	CTTTACTGTGCGAC ATTTTA	TACTGTGCGCCAT TTTA	GTGCCACTGATGAGGATGAGATCA	0,0	GTAATAAAGCCCTTTTGTGA GGAAAAACTAAT
OMS0000 6	T	C	CACTTACAAATA CAAAATT	CTTACAAATGCA AAATT	TCCACGTAGGACATAGTTTGAGCT A	0,0	TGTGGTGTGATGTTTGCCCTA C
OMS0000 8	A	T	CTTCAAATATCCA TAATTATATC	TCAAATATCCAT AATAATATC	CCCTTTAAGGAGGATTTTAAATAT GTGAGATAGAA	0,0	GGATACAGCGTTTTGGAATG AAACT
OMS0001 3	A	G	CTTCTTTTCCCTT GCTACTC	CTTTTCCCTCGCT ACTC	GCCTTTGTTCTCCTTGGTGGTTA	0,0	AGAAAAGTGTGGACTGAGGT TGAG
OMS0001 4	T	C	TGATTTGATGAAT TAAACTTC	TTGATGAATTGA ACTTC	CTTACACACAAGGGCTTCATTCTG	0,0	GATGTCTCTGGGTGGTTGTCA
OMS0001 5	A	T	CAAGTCACACTTT TAATGAA	CAAGTCACACTT ATAATGAA	TCAGACCCTATTTTTGGCACAAGT	0,0	GTCTAACTGATCCCACTTCTG CAT
OMS0001 7	A	G	TAGACCTCGGTG CTGTAG	CCTCGGCGCTGT AG	ATTAAGTTCATACAAAAGTTCATC ATAAATATTTTCCTTT	0,0	GGAGAACAAAGGGAAAGAG AAGACA
OMS0001 8	T	G	AACCACATAATT AATAATTC	CCACATAATTCA TAATTC	AGAGTACATGTGTGGCTGCAA	0,0	GTCATAAATCAACACAATTA TCTTCTTCACAGAA

OMS0002 4	T	G	AA[AC]CCCAAAT TTTAC	AA[CA]CCCAATT TTAC	CACATACAACCATCACCCCTTCCTA A	0,0	AGCATTGAGCGAAATTACCA AGAGT
OMS0003 0	T	G	ATGAGGGTCCCT ATACAGG	ATGAGGGTCCCT CTACAGG	CCTCGTGACTACAGAGCTATACAA C	0,0	GATCTGATCGGTCTGGGAGAG A
OMS0003 9	A	G	GTACGTGTCTCTG ACC	GTGCGTGTCTCT GACC	GTCAGTACTGTGTGTGTCTGTGT	0,0	CCATCTACATTGTCAGCAGTG TGA
OMS0004 1	G	C	CCACTCTATGCCT GCCCT	CACTCTATGCGT GCCCT	GATTCTGTTCCATCCTCTTTCTGTC A	0,0	AAACATAAAAAAGGGCATGA AGGTGTC
OMS0004 8	T	C	CAGCTAAACTCA GCAAAA	AGCTAAACTCGG CAAAA	GGAAGAGCTGGAGAACAACGT	0,0	TGCAGTTGACAGAGGCTTTCT TT
OMS0005 2	T	G	CTTCCTTTTGAGA ATAAT	CCTTTTGCGAAT AAT	TGCGTTTTTCATCCCAATCATTAC	0,0	GGCATCAGGCTCTTCTTCCT
OMS0005 3	T	C	ATTTATATGTATC AATCA	ATTTATACGTAT CAATCA	GGAGCCAGGTCAAGGTGATC	0,0	GGATGTCTGGTGTGGCTGTA AA
OMS0005 6	T	C	TAGCTTGACCAA ATAGCA	CTTGACCGAATA GCA	TCAGGAAGTAAACTGAAAATTCCA ATGTATGA	0,0	CCCCAACCATGCTTGTTATTG AAC
OMS0005 7	T	G	CTCCACAGAACC TTG	CTCCACAGCACC TTG	GAGAAAGGGAGCATGAGACAGA	0,0	GTTGGGCTCCGGTACGAT
OMS0005 8	A	G	CAACACTTTGTAC CCCTC	CACCTTGCACCC CTC	GTGACATTTGGAGCCACTGC	0,0	GCTAGGAGACAGAGGGTGAA AG
OMS0006 1	T	C	CATTGCCATTTAC AGACTT	TGCCATTTGCAG ACTT	AAGTGGAGGCTGACCTGTTG	0,0	GCTGATGGCACCTGACAGTT AATT
OMS0006 2	T	C	TTGACCAGCAGA TGGTGTA	ACCAGCAGGTGG TGTA	ACCCTGGGAAGGCTACTGTAC	0,0	TGAACAGAGATCTGGAGAGT TGGAT
OMS0006 4	T	G	CAGGCAACATTTT ATATAACTA	CAGGCAACATTT TATCTAACTA	GTGGATATGTAGTTCGATGGAACA GT	0,0	TTTACAACAATCTTCTTTTAA TAAAAATATAGCCACTTAT
OMS0006 8	A	G	AATATGCCTCCTT CGTCTC	TATGCCTCCTCC GTCTC	GCACTAACTGGACAACATTTTTTAA GAATGA	0,0	GGCAGTTGAGCATTTTGGGA TATT
OMS0007 0	T	C	CAAAATACGGAA ATGCAG	AAATACGGGAAT GCAG	CGTTCCTGCGGGACAGT	0,0	GTTTCTCTCACGTCCACAGAT CT
OMS0007 1	A	G	CTTGTTTGAGCTT TTTCT	TTGTTTGAGCCT TTTCT	CCGGAGTGACCTCACATTTGG	0,0	GCATCGTACAGTTCACCTACC T
OMS0007 2	A	G	TAGAAGGTCCAT GTATCTC	AAGGTCCATGCA TCTC	GTGGGAGAGCTCGTCTATGG	0,0	ACAACAGGTCATTGGATGTG ATCAG
OMS0007 4	T	G	TGAAACAAAACA AATGTTCC	AAACAAAACAC ATGTTCC	CCTGTTTATTCATCTAAACCAGTTC TTTAAAAT	0,0	AACTTAATTTAGCAAACAAA TGTCTGAACAGAA

OMS0007 7	C	G	TTCCGGTGGTGA AGTT	CCGGTGCTGAAG TT	AATACCATCTTGAGCTCATTAGTA ATTATTCAA	0,0	CCAGACTTTACACACTCTTGA CTGA
OMS0007 8	T	C	TTCACATGCATAA GAGTG	TCACATGCATGA GAGTG	GAGGGAAGCAGCCATAAACAGAA TA	0,0	GTCTCACTATGGTCCATATCT GTGTAGA
OMS0007 9	T	C	CTACTTTTTCACAG TAACACAG	CTACTTTTTCACA GTGACACAG	GTAACATTATGAATCTATCAGTTTC CCTAGCT	0,0	ACCTGCAACGTTAGAGCTGT TTATT
OMS0008 7	A	G	GTTA[CA]AACTG ACAAAGTGTG	GTTA[CA]AGCTG ACAAAGTGT	GCAAATTTTACCCTTAACGTGGTTT	0,0	GATTTGATGTGTGTGTATTAC CTCCTCTA
OMS0008 9	A	G	ATGAATCCCAAA TAAGAAC	AATCCCAAACAA GAAC	GCACCATTTGAATAAAAAATCTGC TTTGT	0,0	GCAACCCAATTCAATATTAA GCACATGAT
OMS0009 0	T	C	ACAACCACACAA GATT	AACCACGCAAG ATT	AGGGCACAACACCACTCTAAATT	0,0	TCGAAAAGCAACATCTGTCT CAGT
OMS0009 2	A	C	CAGCTGAGAATA GGTTC	AGCTGAGAAGA GGTTC	TCTCCAGGTGTATCTTGAGAAGGT	0,0	AGGGTTCACACAGGGAAGAT ATCAT
OMS0009 5	A	T	AGGCAACTATAT ATTTTTTT	AGGCAACTATAT ATATTTTT	CTCCAATGGCTGTCAACAATTA TATAAGAC	0,7,0	GTGTGCTGGTCTCTTCTTTTA TTCTCA
OMS0009 6	T	G	AAAGAGGAAGAG TCTCG	AAAGAGGAAGC GTCTCG	CATGAGAATGGATCAGTCTCCACA A	0,0	GATGAAATCTGAATGTGTTG ACACTACAG
OMS0010 1	A	G	CTCTAGTAGCCTT ATAGAAAG	CTAGTAGCCTTA CAGAAAG	GCGTGTCTGTTGGGTCAGTTAAATA	0,0	GTGCAATCCAACCTATTAGT AGATATGCT
OMS0010 3	A	T	CTCCACAGTAATT TTTTTTT	CCACAGTAATTA TTTTTT	GAGATCACTGTAGGATTGGCTGTT T	0,0	CCTCAGAGCAGCTCACAATG GCATC
OMS0010 5	T	G	CTGCTATTCAAAT TGCT	CTGCTATTACAA TTGCT	ACATTTGAAGTCAGTATGGGTGTT GAG	0,0	GAACCTCACCACAGTACTAA ATGCA
OMS0010 6	T	G	TCTGATGGAAAC TTTC	TGATGGCAACTT TC	CGTGTAGCATTCTTGAGGAAGCTT	0,0	TTTCCAACAGATGCCAGAAT CCT
OMS0011 1	T	C	CAACCAGACTAC CATTC	AACCAGACTGCC ATTC	CATGCGGACCTGCATAGCT	0,0	GCTTAGCCATTGACAGAGCA TATCA
OMS0011 2	A	T	CCGGTTTCAAGTT TACTTGT	CGGTTTCAAGTA TACTTGT	TGGCAGCAAAAAGGGATGCA	0,0	TCCTGAGCAACCAGTCAACA TT
OMS0011 4	T	G	AAACGTTTTCACAT GCACC	AAACGTTTTCACC TGCACC	GGATGATGCTGTGAGTCGAGAAG	0,0	ACCTTCGCCACCCATGTTTTTA TT
OMS0011 6	T	A	CTTTTACATTTTC AATATTCTG	TTTACATTTTCA ATTTTCTG	GCCTTTCTCCCATATCACATTCTGA	0,0	AAACGCATCTTACACTGTGTT GTG
OMS0011 8	T	G	GCGGGGTGTGC[A G]CATT	GCGGGGGGTGC[AG]CATT	GCTTATTTAGAGTGCATGCCAGAT G	0,0	TGGAACCAATGGGACAGTCC TA

OMS0011 9	A	T	CCACACAGCTGC CTGT	CACACAGCAGCC TGT	AGCGGCAGTTGTGTTAATGAGA	0,0	CTTCCTAAAGCCTGACAGTCT GT
OMS0012 0	A	G	C[GA]CCCCTAA AAC	C[GA]CCCACCAA AAC	GGCAGAAGAGGAGAGAGATATGA TTG	0,0	CCTCAAATACCTCTGACATTG AAGGTT
OMS0012 1	T	C	ACAGCGTGATAA ATT	CAGCGTGGTAAA TT	GGAAGGAGGTCCAGTGTGAGT	0,0	AAAATATGCAACACCACTAA AACTGGAAAA
OMS0012 7	T	G	CACACACCCAAA TGTA	ACACACCCCAAT GTA	CACCTTTCTCTCTCTCTCCATCTCA	0,0	AGTGTGCTACACAACCTTAA AAAATATATATCTATT
OMS0012 8	T	G	ACTCTCAGAATTA ATTATG	CACTCTCAGAAT TCATTATG	ATGAAAGAACTCCCAGACACGTAT TTT	0,0	ACATTTTAAACACAGTAACAC TAATACACACCA
OMS0012 9	C	G	TTGAACAACAAG AAAAA	TTGAACAACAAC AAAAA	GGAGATGATGAAATAAAAAATTGA GGAAAAGATGA	0,0	TGTCTGGTGAATTATCGCAA ATAACCA
OMS0013 2	A	T	CAGCAGTCCTCTG TGTGG	AGCAGTCCTCAG TGTGG	GTTTATGACTCCATTGCCGAAATG ATT	0,0	ACGCGACCTGCAATTCATCA ATA
OMS0013 3	A	G	CGCCTCCATCTTT GTGGT	CGCCTCCATCTC TGTGGT	GACCACTTCACTCATTCCCTCCTTTT	0,0	TCCGGTTTACACACTTCATGC A
OMS0013 4	A	G	TCTATAGCTGCAG TATATTA	TAGCTGCAGCAT ATTA	GAAACTGAAATGATCCCATCGTGT T	0,0	GCTAGCATAACAGCATTGCC ATAT
OMS0013 8	T	G	CTAACAATAACC AAAGACTG	CTAACAATAACC ACAGACTG	TCGGACCACATGAGCAGTTC	0,0	GTTCAACAGGTGCCCACAC
OMS0014 3	T	C	CCTGATCCAGAA TCTAGA	CCTGATCCAGAG TCTAGA	GGAGGCACGCCCCAAA	0,0	TTTGTTAATAATAGAGCCCTTA GTGGGTTT
OMS0014 9	T	G	GCTAAATGCACA G	GCTAAAGGCACA G	GGCATCATTGTTCTTGCTCTGTTTA	0,0	CCTGGGAGGGTTTATATCGG AGTAT
OMS0015 1	A	G	TCATGACCTTGAT AATC	ATGACCTCGATA ATC	CTAACGTCTTCCCAATGATATTTCA CAAGATA	0,0	ACCGTGGAATACAATTTTTTT ATGCCAAT
OMS0015 3	T	G	ACAAAATGTAAT TTTCC	CAAAATGTCATT TTCC	ACTTTGCACCATAGGCTTGACAT	0,0	TGATAAGGATGATCAAAAAG CTGAAGTATGTA
OMS0015 4	A	T	ACAGGGCTTCTG ATTGA	AGGGCTTCAGAT TGA	GATGTTGGCTGGAGGTGTAGT	0,0	TGGGAACACTTTGCCTACCC
OMS0015 6	A	T	TGTGTGTCCTGCT GTAACA	TGTGTCTGCGAG TAACA	GAGCAGAACACATAGAGGAAAGA CT	0,0	GTAATCACCTCTTAGCCTGT ATGG
OMS0016 4	T	G	CCAGATTCAATTA AATTTA	CAGATTCAATTC AATTTA	CAGAGGAGAGGAGAGCAAAATAC TT	0,0	ACAACCTACTCATTGAAACT CATTGGA
OMS0016 9	A	G	CAAAAAGCATTG ATATCAAT	AAAAGCATTGAC ATCAAT	AGCACTTGACTCAAACCTCACATAA ATCA	0,0	CTGAGACAGGAAGAACAATG TTAACAAAA

OMS0017 3	T	C	CATTAGCTTGTGT ATGAACT	ATTAGCTTGTGT GTGAACT	TGGAAGTAGCTACTTAACAGGAAA TGG	0,0	AACACGTGTGCTTGTTTTGTG CA
OMS0017 4	A	C	CAAGAACAGG[A C]TAAATGT	CAAGAACAGG[A C]GAAATGT	TGACTAACTATGCAGCCTGAAAGG	0,0	GGGATACTCTTGTAATAAAC TGTTGGTTAGTA
OMS0017 5	T	C	ATCACTAGTTCAA ATACAA	ATCACTAGTTCA GATACAA	TTGCGATATGGGACTGTATACATT TATTCC	0,0	ACTACCTCCAGTTAAAATAG TGTGGGAAA
OMS0017 6	T	G	TTCCAGCACTGCT GTC	CCAGCCCTGCTG TC	GTTGGAAGTTCCGGTGGTAGAG	0,0	CTGGGTCTCTGAAGGAGCTT
OMS0017 9	A	C	TGCCTCTTCTCTT TTCTCAT	CCTCTTCTCTTGT CTCAT	GTCATAACAAAATCAGGGCTTTCC AA	0,0	TGGGAGATTTGGGCTGCTTTA AA
OMS0018 0	T	G	CTAAAAGTGCAT TAAGCC	CTAAAAGTGCCT TAAGCC	GCGCCGAATGGCATTAGG	0,0	CACATTGCTGTCGTTTAGTTT GACT
Omy_100 4	A	T	CATGTGATGTTTT TTTGC	ATGTGATGATTT TTGC	GAGAATCGGAGCTAATCTTAGTTA TTGTGA	0,0	CACTTTATTGAGCTACATGGC AAATCTG
Omy_101 554-306	T	C	TGCTTCTCACATT TTTA	TGCTTCTCACGT TTTTA	GCCTGTATTTCTCCTGTATGTGCAT	0,0	TCAACTTTTGCAAACCTTTTTT ATTCTTTGTCAATT
Omy_101 832-195	A	C	TGTAGTCTTTCAG AGTAGTATG	TAGTCTTTCAGA GGAGTATG	TGGCTCTGGACCTGTTGAGA	0,0	CGTCACAGCTATTTTAGGCGT AGT
Omy_101 993-189	A	T	CTTGATTTGCAGC TTGTCAA	TGATTTGCAGCA TGTCAA	ACAAAACACAGTGGAATTACAATT AACGTT	0,0	GGAAGTTAAATTTGCTTCGT CAGAA
Omy_102 505-102	A	G	AACAGGATGTTTT TGC	CAGGATGCTTTTT GC	CTGCAAACCTGACATGGTAGCAAAA	0,0	TGCTTGCTTTTTTAAAAACAAT CTCCCA
Omy_102 867-443	T	G	TTTGGGTACATAA TTTTT	TGGGTACATCAT TTTT	CATTTGTTTAATTTGATTTGGCACA ACTTCA	0,0	CCCTAGTTCTGTAACACAAG ACGTAA
Omy_103 705-558	T	C	AGACTTACCCAG AGTGAGAG	ACTTACCCAGGG TGAGAG	CTCCAATCGCAAATACCCAGACT	0,0	CGCAGGAGACGGATGCC
Omy_104 519-624	T	C	CAGCAGGATACA TCCGACT	AGCAGGATACGT CCGACT	CGTGTGAGTTTGCGGTAAAGAC	0,0	TGACGAGTCCGTCTTATCATC CT
Omy_104 569-114	A	C	CGCCACTCCGAC GCC	CCACGCCGACGC C	CCGAGGCCGACGTGATC	0,5,0	GCGCCTCGCTCATCATCA
Omy_105 075-162	T	G	CTTTCTCTCCTAC TTTCC	CTTTCTCTCCTCC TTTCC	GGAGAAGGACAAGGACATTGGTA AT	0,0	AAAGCAGACCACACCATACT TCTC
Omy_105 105-448	C	T	AAGGAGAATGCA TAATC	TGAAAGGAGAA TACATAATC	CAATTTGCAAGCAGGGAAAGGTTA T	0,0	GTGATGGGCTGCAATTGCTT
Omy_105 385-406	T	C	CTTGGAACCATTG CTAC	TTGGAACCGTTG CTAC	GTAACCTACCCTCACCTGAACTTC A	0,0	GTCGCTCTTCTGGGCGTATCG

Omy_105 714-265	C	T	CTGTTGTTTGAGG TTCAG	TGTTGTTTGAGA TTCAG	CCACTCAGTGCAAGCATGGA	0,0	GCTTTCAATCCTTGGCTCCAA TATC
Omy_107 031-704	C	T	TGGACATGATTG CATAGAC	CTGGACATGATT ACATAGAC	GGCTTTCGGATACTGAGCAACAA	0,0	TGAACTCACTGTTGGTATGG ACTAGA
Omy_107 285-69	C	G	ATACGTTACTTTT GACCTTGT	ACGTTACTTTTC ACCTTGT	GCCCTTGTGACAATGCACTGTTAT A	0,0	AGGTCTAGACAGTGTGCCAT TTG
Omy_107 336-170	C	G	CACTCCTGGGTGC AGAA	ACTCCTGCGTGC AGAA	GCCCTCTCACTCATGACATCAAC	0,0	GCTCCAGCCACTCGCA
Omy_107 806-34	C	T	ATTGGATGTCAGT GTCATT	ATTGGATGTCAA TGTCATT	TCTTTGTCCATGCACATTGATATT	0,0	AGCACATTTAGTTAGCAGTG ATGGA
Omy_108 007-193	A	G	ATGTTTTCTCCCT ACTTAAC	TTTTCTCCCCACT TAAC	GTGAATACCACCCAGGCTTGT	0,0	GTCCCTTCCCCAGTTTCACTT AATT
Omy_109 243-222	A	C	TGTTTCATTAAATT GACTTTTT	TTCATTAAATGG ACTTTTT	ATGTGCACCTCTTAAATTGTAAGT AAAATGT	0,0	ACCCTATATTCAGTGGCAAG ATTGC
Omy_109 525-403	A	G	CCTACACCTCTTT TTCCACA	CCTACACCTCTT TTCTCCACA	CCTCATTCTCATTGGTGAGTTGTCT	0,0	TGTAAGATCTGACCACATGA GTATAACCA
Omy_109 894-185	T	C	CTCCCTGATCCCC C	CTCCCTGGTCCC CC	GGGAGGAATTGGAATGACAGATTA AC	0,0.5	CGGTGTCAATTATGGTTGTCAT TGTG
Omy_110 064-419	T	G	ACGTTAGCTTTTA ATTTT	AACGTTAGCTTT TCATTTT	GTGCAAGGGACCTAGCTAATCC	0,0	TCTGAACTGACACTGAAGAA CAAAGAA
Omy_110 201-359	T	G	TTTGGCTATTGAA ATTATACATT	TTGGCTATTGAA ATTCTACATT	GGTAAGGCCTGTCTGACTATTTTG A	0,0	AGAGGTCAATGGATGCCAGT TT
Omy_110 362-585	G	A	CACCGCCCTGCCC GT	CACCGCCTTGCC CGT	GCAGCCAAGATGAACGAAAACCTC	0,0	CCGGCCTGGGTCTCAATG
Omy_110 689-148	A	C	CAAATGAACACA TTATTTATC	ATGAACACATGA TTTATC	GTGTGTGGCAGAGAACTAACTGAT	0,0	GGTTAAGACATTAACATAAC ACTGGACTCT
Omy_111 084-526	A	C	CCAGTGAAATTT ATTTTT	CAGTGAAATGTA TTTTT	CACCACACCAAGCAACTATTTTCAT T	0,0	ACCCAATACTGTCCCATTTT TCAT
Omy_111 383-51	C	T	AGCAAGCGCACT[AG]GGT	AGCAAGTGCAC[AG]GGT	CACGCGCAATCTCTCGTTTTTAC	0,0	TCTTTAGGCAACAAGCGTGT CA
Omy_111 666-301	T	A	AGTATAACACAG TAAGACAAT	AGTATAACACAG TTAGACAAT	GGGTGAAAAGAGTGGGACATTTTAC A	0,0	GTCAATTTCAAGGCACCAGA CAAT
Omy_112 301-202	T	G	AATGCGAAGACA AACT	AATGCGAAGCCA AACT	GTAAACCCTGCCCACATAATTAGG T	0,0	CTGAGACACTGCTCCAAGGT
Omy_112 820-82	G	A	CGCCGCCAAGTT A	CGCCGCTAAGTT A	CCTTTCCTTTTGCATTTCTCTACTT ATTTATTT	0,0	AAATGAACTCACGTTGACCT CTGA

Omy_113 490-159	C	T	CATCTGTTTTGGT TTAGC	CATCTGTTTTAG TTTAGC	CATAGTACATTTACAGATAATGTT TTAAAGTGCATGT	0,0	CGAGATACCAAAAATGCCACA GTTACAT
Omy_114 315-438	T	G	TTATGGGCTTAAG GGTC	TTATGGGCTTAC GGGTC	CCTCACCGATCTAGTCAACTTCATC	0,0	AGGAGGCTGAGGGAGATTCT AG
Omy_114 587-480	T	G	CCTGTCCAAAATT GT	CCTGTCCACAAT TGT	CAGATTACGTTATTACGTTTGGGA AATTTTAAAGT	0,0	GTGAAAGAGTGGGAAATATA ATTATAAGGTCAGA
Omy_114 976-223	T	G	ACCGATGGAACA ATC	CCGATGGCACAA TC	GACAAACAGCACTTCATTGCAGTA A	0,0	GTTGCTCCAGCACCAGGT
Omy_116 733-349	C	T	AGAGAATCTGAT AGTATTTTC	AGAGAATCTGAT AATATTTTC	GAAATGGACATGCCTACAAATTGC T	0,0	GATGTGATCAGTTTAGGCAA GGC
Omy_116 938-264	A	G	CCTTGTCTCAATT TTTCCTCT	CTTGTCTCAATT TCTCCTCT	GTTTCATTCATGTTGAAGTGCGACA T	0,0	CTCTGCATGCTCCCATCCT
Omy_117 286-374	A	T	CTTTCCTCATCAT ACTCTATGG	TCCTCATCATAC ACTATGG	TGATGTGTTGTTTCCTCATGGCTTA	0,0	CTGTGCATTTATTCTTGTGAT GCTAGG
Omy_117 370-400	A	G	CAACTCCAATGA ATTAA	AACTCCAACGAA TTAA	TGCAAACACAGAGGAAAGGGATTT	0,0	GGCTTATTTGTTCCGTACTTG CATT
Omy_117 540-259	T	G	TGTCACCTCAAAG TTTG	TGTCACCTCAAC GTTTG	GGCAGGTTAACACAGTCATCTACT ATAAA	0,0	CAGCATGTTGCTTTAATCCTT CACA
Omy_117 815-81	C	T	CTATACGGGAGAC CAGC	CTATACGGAAAC CAGC	CTGCTTTATGCACACCACATTGT	0,0	GCTCTTTCTGGAGAACAAGG TACTG
Omy_118 175-396	T	A	CTCTTGACAGACAT ACCCGTA	CTCTTGACAGACA TTCCCGTA	AGGCTTCACACACACATGCA	0,0	GACGCGCAACCTCTAGATTA TACTT
Omy_118 205-116	A	G	CTACTGAGGCTG AGTGCT	TACTGAGGCCGA GTGCT	CTGCGGTGGGCTACACA	0,0	CGCAGCTGCGGATGAG
Omy_118 654-91	A	G	TCAGCTTGTCTTG CCGC	CAGCTTGTCTTG CCGC	CAGCGTAGACCGTTTCCTCATTAT	0,0	GCGCCGATGAGCAGCTT
Omy_120 255-332	A	T	ACTATGCCATGA AGTTA	ACTATGCCAAGA AGTTA	GCTAGCTAACATTGAAGGGTGGAA T	0,0	GGCTACAGGGACTTTACAAT GGG
Omy_128 693-455	T	C	CACTCAACTGAT ACCC	CTCAGCTGATAC CC	GCCTGCAGGAGAAGGTAGAGTTA	0,0.8	GAAATGGAATGGACCCCAAT CCT
Omy_128 923-433	T	C	CTTCATTTTCATT CACTGTTTT	CATTTTCATTCTG CTGTTTT	CTATGTCCTTGGCAGAAGTCTACA	0,0	ACGTTTCTTTGGGCTGAGACT TATT
Omy_128 996-481	T	G	CAAACCTCAACC AC	CAAACCGCAACC AC	CTCATCCACACTGTACAGTACAAG T	0,0	CATGCCTTCGTCTCATCAATA ACAC
Omy_129 870-756	C	T	ACAGGTATTTTCGT GAAATG	CAGGTATTTTCAT GAAATG	TCGTTATTTTGCCTCGCGGTA	0,0	TCCCATGAAGATGTATACAT GTTTTGTGA

Omy_130 524-160	C	G	ATGGCTTGATCCT CA	ATGGCTTCATCC TCA	CGAAGGTAGCGATTGGTCGTT	0,0	TGTCTGTTCTGCTGTGTGCTT
Omy_131 460-646	C	T	AATAAAGCAGAA TTTGTTACTG	AAAGCAGAATTT ATTACTG	GTGAAAAGGAATGGAGGAGTACA GT	0,0	TGCTAGGACAGGAAGATCAT TTGTG
Omy_187 760-385	A	T	TCCTTATCCAAAA TTATTGTGC	CTTATCCAAAAT AATTGTGC	CGGCTATTCTCGCGTAAAAGCT	0,0	AAATGCAACCAGAAACGGAA TGTC
Omy_962 22-125	T	C	AACTACAACGT AGCTAATT	CAACTGTGGCTA ATT	GTAAGGAACTAATTGGCGCAACAT T	0,0	CAGTTTGTCTAACACCCAGG CATAT
Omy_970 77-73	T	A	TGGTGCAATAGA AATA	CATGGTGCAATA GTAATA	GTGTAAACAAAATGACTCTGGGAT TCAG	0,0	AGAAGTGGCAATGGTGTGAA GTAT
Omy_976 60-230	C	G	ACGTAACTTGTA GCGTTTT	ACGTAACTTGTA CCGTTTT	TCAGTTATGTGTAATCTCATTACCT CTCCAA	0,0	AACAGAAAAGGTCTCAATGT ATTTTTTGCA
Omy_978 65-196	A	G	ATTAATTAACAA GCTC	ATTAATTGACAA GCT	TCCAGACTTCTGGTTTGTTCATT	0,0	CCAGCCCCATATTCACAATT AAGTGT
Omy_979 54-618	C	T	CAACGCTTACCG GTGTGT	CAACGCTTACCA GTGTGT	GCTCTGCTTCCTCGGCAAATA	0,0	CACAATTGGTTTTTGCACAAA AGTAAAGTATT
Omy_986 83-165	A	C	AGCCAGATACAT ATTTGT	CCAGATACAGAT TTGT	GCCATTGCCAGAGAATTTGGTTAA	0,0	AACACACGCACCATCTTAAA GC
Omy_993 00-202	T	A	TCAGGCATGAGA GAAA	ATCAGGCATGTG AGAAA	CAGTTTGACCCGATGGTGTGA	0,0	GATTATGGCGTGGCCTTTTGG
Omy_ada 10-71	C	T	CTTCCTGCGTCCA A	CTTCCTGCATCC AA	TCTTTGAGCGACAAAGTCCTTGT	0,0	ACCCACACATGAACGCAAAA G
Omy_anp- 17	C	A	CTCTCATTGGTAT AGTAACC	CTCATTGGTATA TTAACC	GGTAATGCCACATGCGGTAAATT	0,0	GGCGAAATCTGAAAATGTGC TGTTA
Omy_aro mat-280	T	C	TCTTGCAAACCTCC	TCTTGCGAACTC C	CTCCATTGATTCATGCCGAACATT	1,0	GGAGAGGTCAAACATAGCCT GGTA
Omy_arp- 630	G	A	CCGCTCCGTCTGC T	CCGCTCTGTCTG CT	CTGCACAACTTGTTTCCTGCTATT	0,0	ACCAAGTGTCCCTGTAAGCC
Omy_asp AT-123	T	C	CCTTCCTAGGCAG TCAG	TTCCTGGGCAGT CAG	GCCCATTTCACTGATGCTGTGA	0,0	AGGAGACCACTCCAAAGAGA ACT
Omy_b1- 266	G	T	TCTATAAACAAAC ATTTTTTC	TCTATAAACAAA ATTTTTTC	TCATGTGAACTTTAATTGACTAGG AAGTCG	0,0	GATATGAAAATATCTGAAGA GTTATATTTGGGAAATTGAC
Omy_b9- 164	T	-	CCTACAACCTTGAT CTAACGTG	CCTACAACCTTGA TCTACGTG	GCACAGAACACAGCCAATATTAAC A	0,0	GCCTTGACTCTCCCTTCATGA C
Omy_BA C-B4-324	G	T	CATTGCCAAATA CG	TACATTGACAAA TACG	CGTACTTTTCTTTTACAAAATTAAG TGGAGGAT	0,0	GCCTAATATTGGCCTAATGTC CTTCA

Omy_BA C-F5.284	C	T	CAGTAGGGCGGC AAG	ACAGTAGGACG GCAAG	CCTCATTTACTGTAGGACCATGCA	0,0	ACAACGCCAACAACCTTTCTCT TG
Omy_BA MBI2.312	G	T	CCGAAAAGTTCAA CTTT	CCGAAAAGTTAAA CTTT	CGAGCTCATGTCCGAAACTCAT	2.1,0	TTTGACAGCCTCAACTTCTAG GG
Omy_BA MBI4.238	T	C	CACCGCAATCAC CG	ACCGCGATCACC G	CATGATGAGGAGGACCAAGATGA G	0,0	AGGTGTGGTTCAGGGCAG
Omy_bcA Kala- 380rd	G	A	CATACCCATCCTA TGTCAG	CATACTCATCCT ATGTCAG	TTGCTCTCTTCTGGTTGCCTTA	0,0	CTTCAGGAGAAAGCGCTACT GT
Omy_ca0 50-64	T	G	CAGTTTGAAGAA TATACTC	CAGTTTGAAGAC TATACTC	GTCATACAGAACTGTTTTGTTGTGT CAA	0,0	ACCTTGAATTGGTTCCTAATG CTATTGT
Omy_carb an1-264	G	A	CATTAATATTGCT AATAACACCAAG	ATTAATATTGCT AATAACACTAAG	GCAAAGCCTCATCTTCAATCATTT GT	0,0	GCAAAACACAAGTCAGGAAT CACTTA
Omy_cd2 8-130	T	C	CCTGTTCATTCAC CC	CTGTTCGTTCAC CC	CACAACCTCCACAGAGACAGTGA	0,2.7	GAGGACAAAACCTGACCGTAT GGT
Omy_cd5 9-206	C	T	CAACAATCGAAG GTAAAT	CAACAATCAAAG GTAAAT	CGATTGGCCCAGATGTTTCCAT	0,0	GCTCCGTTGCATAGGTGACT
Omy_cd5 9b-112	C	T	CTAAAAGCCTAT AGCAAACCT	CTAAAAGCCTAT AACAAACCT	TTTGGATAAGATTGTCTTATATGAC TAAAATGTCATGT	0,0.6	GCCAACGTCCTAGATATGGT GTAAT
Omy_cin- 172	C	T	CGCTCACCGTGGT TAC	CGCTCACCATGG TTAC	CGCATGGGACAGGTGTGT	0,0	GAGAAAGCCTGTAGAACCAT GTCT
Omy_cox 1-221	T	A	CGGTAAGACCAT TAAAA	CGGTAAGACCAT TTAAA	CACTGAACTGTAAGCCATTGTGAT T	0,0	GCAACATGGGAATGATTCAT AAATGCA
Omy_cox 2-335	T	G	CTTTAAAGACAA AGACTTTAT	TTTAAAGACAAA GCCTTTAT	AGCTGGGCTGTATTTGTCAATACTT	0,0	CAGCCCGCCACTGTCT
Omy_crb- 106	G	T	TTGCAATGCGTCT TT	TTGCAATGAGTC TTT	GCTCAAAAAGATTCTGCCAAATTC ACA	0,0	ATTACAATGAAAGTACTTGA GTGTTTATGCAAA
Omy_cyp 17-153	C	T	ATACCTGAGTGTC ATCG	ATACCTGAGTAT CATCG	GCCCTCCAAGTTCCAAGTGAAAA	0,0	CAGGTCATTGATGAAACGTC AGAAC
Omy_e1- 147	G	T	CCATCCTGAATCT GATTAA	CCATCCTGAATA TGATTAA	GCACTGACTGTTACCAGGAAAGAG	0,0	GTACTGCAGTGTTGAGGCTA TATCA
Omy_ftzf 1-217	A	T	TCATGACGAGTTC TGATTT	TGACGAGTTCAG ATTT	ACAGGGATGGGCAACTTTGTT	0,0	GGATGACCCACGTGACACT
Omy_g1- 103	T	C	CCTTTTACAATGA AGATC	CTTTTACAGTGA AGATC	AGTCGTGACAAATGAGAAACAGTGT T	0,0	CTCAGCAAAAAAGAAACGTC CCTTT
Omy_g12 -82	T	C	CAAACCTCTCAGG ATTAG	AAACTCTCGGGA TTAG	GATCAATTCGATCGCTCATGAAAC TT	0,0	CTTCTCTCGTTCTCATTGTGT CTCA

Omy_G3P D_2.246	C	T	AGTAAAGCCCAT TGTTGAGT	AGTAAAGCCCAT TATTGAGT	TCATGTATCAATTAAGGCATTGTCT TGTCT	0,0	GTTAGACACAGTGACCACCT CTTT
Omy_G3P D_2-371	C	A	AGACATGTGGAT TGGCA	CAGACATGTGTA TTGGCA	GCAGGTAAGGTACACCATAGAGAC A	0,0	CTCCCCCTGCCTTACCAAAC
Omy_gad d45-332	T	C	TTGCTCCAAAATG G	TTGCTCCGAAAT GG	AGAGAAGACTCACTGCTGTTTGC	0,0	AAATCAGTTCCCACGCTATG CT
Omy_gdh -271	C	T	TCACCCTGAAGT GTAGAC	TCACCCTGAAAT GTAGAC	AGGTCAGTCTACTTACAGTATAAA GCAGT	0,0	GTCATGTCAACAGAGTAACA TAATAAATCTGC
Omy_GH IP1_2	C	T	AAACTGTTGAAC GGTAGTG	AAACTGTTGAAC AGTAGTG	TGCATTTGATGGAAACAAACATAT- TTATAATGTGT	0,0	CAAAAACAAGGACAATTCTA AGTGACCTC
Omy_gh- 475	C	T	CTGAAACTCATG GTATACA	CTGAAACTCATG ATATACA	AAGTTACCAGAATTTTGCAAACCTC AACT	0,0	CCATATTTTGAGGTGTAGCTT TACCCT
Omy_GH SR-121	T	C	CCTAATAACCAT GATAACAGC	AATAACCATGGT AACAGC	CTGTGTATAAGTTTATACAGTCAG CACAGT	0,0	TTCAGAGAGAGAAATGGCAG AAAGG
Omy_glu R-79	C	T	CAAGTATTTTGCG TAGGAAT	CAAGTATTTTGC ATAGGAAT	GACTGTCTATAGCTATTCTTCTCAA ACTGT	0,0	AGAAACTACCATTGTGATTA ACAGATAGAAAATACAT
Omy_GR EB1_05	T	G	CGGTGGCTCTC	CGGTGGCTCGC	TGGGCAGATATGGAAGAACGG	0,0	ACCTTCTAAATGGCCTCTGTG T
Omy_GR EB1_09	T	G	TCAATGGAGA	TCAAGGGAGA	CCAGTGGCAACCTCAGGTAG	0,0	GACTCCAGTCACCCAAGTCA
Omy_hsc 715-80	C	A	AACTGTATTTGGG AAAAT	ATAAACTGTATT TGTGAAAAT	CCGGTCTACCCTATAGCTGTTG	0,0	AGTCAGTCAATTAGTGGTTTG AAATACTATCA
Omy_hsf1 b-241	A	-	CAGTGTTTTGTTT TTTGTGATT	AGTGTTTTGTTTT TGTCATT	AGCCCGAACTATCCTAAAGCATTT T	0,0	AAATCAATAGCTCAGAGAAT AATGAACACCA
Omy_hsf2 -146	A	-	ATAATCTACTA	ATAATCTAACA	CCAACAATTGCAGCCTCATCTTAA T	0,0	GGAGCAGAAAAAGGATTGGA CCTT
Omy_hsp 47-86	T	A	CAGGAGTGTA TGTTT	ACAGGAGTGAT ATGTTT	CACATTAAGCACTCCCAGGGA	0,0	TTGCAAAGGCCAAACAGCAT T
Omy_hsp 70aPro- 329	A	G	ACATTCCAATATT CAACTAT	CATTCCAATATC CAACTAT	TGCGTATTATTGTTTTTCAAGGACT TTCAAA	0,0	TGAATATTTTCAAATACATGC CAATTCTTTCCAA
Omy_hsp 90BA-193	C	T	CCTCCGCGCCTGC	CCTCCGCACCTG C	GGAATCGATGACGACGAAGTGATC	0,5,0	TTCCTCCATGCGTGATGCA
Omy_hus 1-52	G	A	CCCATCCCTCCTC CTGG	CCCATCCCTTCT CCTGG	CTTGCCGGAGGGTAGCT	0,0,5	CCACAACCTTCTCAAATGAAT GGAATGT
Omy_IL1 7-185	G	A	AAGAATCTCACC TGCCCAT	AAGAATCTCACT TGCCCAT	CCACCACACTCTGCAGCTT	0,0	TTGACGGGAATCCGAGACTT C

Omy_IL-1b_028	T	C	CTGAGGCAACTTT TGT	TGAGGCAGCTTT TGT	ACTGTCTGGCTAGAGCACATTG	0,0	ATCTTCTACCACCGCACTGTT TTAA
Omy_IL1b-163	T	G	CTGAGGTCATAA AAATA	CTGAGGTCATAC AAATA	GGAACAACAGGATTAAGCCTACTC T	0,0	CCTAAAGGCCTAGGAAACTA AACTTCA
Omy_IL6-320	C	T	CTATAGGAGAGA GGACAACA	ATAGGAGAGAA GACAACA	CGACTGATCTCCTGCAGACATG	0,0	CTTGTTCTCGTTGTCTTCCTT CTA
Omy_impal-55	C	T	CGAGATGATGCG TCTACA	CGAGATGATGCA TCTACA	CGCTGAGAGGATTGTCAA	0,0	TTTTCTTTGTTTCAGTCTTCTGT CTCTG
Omy_inos-97	C	A	CCTTTCTTGATGG TATCC	TCCTTTCTTGATT GTATCC	GATGGACAGGGTCTCTTCAC	0,0	CCTGTAGATAAAACATGGTA CCAGGTC
Omy_LDHB-1_i2	C	T	ATGGGCAGTCAT TCA	TGGGCAATCATT CA	ACGCACACTTATCCTTGACAATGT T	0,0	ACTGTGACAACAAATTCGGT GACA
Omy_LDHB-2_e5	T	C	TTTACCTGTCAAC	CCTGTGCGAC	TGCTAGGTGAGTCAGAGGTACATA TT	0,0	GACTGGAAGGCCACCCATAA G
Omy_LDHB-2_i6	G	T	CTGTGTTTTGCTT CCCCA	CTGTGTTTTGAT TCCCCA	TCCTCGCCAATACCATAACATGTC	0,0.5	AGAGTGAAGCTAACACACAC ATTTCT
Omy_lpl-220	C	G	AGTGACAGTCA	AGTCACAGTCA	TGACAATCACTGAGCAACTGAAC T	0,0	GTCCAGTCTTGCTTCAACTCA TTCT
Omy_mapK3-103	A	T	AATTATTAAGCCT ATTTTTTT	ATTATTAAGCCT AATTTTTT	GAAGTCATTACTGGTCAGTGGTCA A	0,0	GCACAAAACATGAGGAAAGT TGAGA
Omy_mcsf-268	T	C	AAATAATAGATA AA[CT]CCT	AAATAACAGATA AA[CT]CCT	CCAGCATTTCGTTCCCATTTCC	0,0	CTTTTAATGTAGATTATATTC TTCTGTAGCCACTATGG
Omy_metA-161	T	G	CAAGTAAGTGGT TATATTCT	CAAGTAAGTGGT TCTATTCT	CGCATGCACCAGTTGTAAGAAAG	0,0	AGTGCCACCAGCGATAAGAA AA
Omy_metB-138	T	A	TTCGCCAAAGAG AAAT	TTCGCCAAAGTG AAAT	TCTGTCCCTGACGCTATAAAAAACG	0,0	GAAGTATTTTCAGCTTAATTTTC ACTGTTGAGTT
Omy_MYC_2	T	C	CATAGACTTTTTG ACCTTAT	CATAGACTTTTT GGCCTTAT	CGGTTGCAGAACTCTCATGTTTG	0,0	CACGCCATGTCTTAACTTGCA TTA
Omy_myclarp404-111	T	G	CAAAGCCATACG TGGCC	AAGCCATCCGTG GCC	GCTGTGGTGCTCATGGGTAAA	0,0	CCAGGGCAGGGTTGTTCTC
Omy_myoD-178	A	C	TTTTATGAGATAT AATTTCC	TTTTATGAGATA TCATTTCC	GGTCAAATATTTTCAATTTACGATTAC ACTTAGGC	0,0	TGGCAAAGCTGTCAATTCCTTC TAAT
Omy_nach-200	A	T	AACTGACAGAGT CACAAC	CTGACAGAGACA CAAC	CTCATGAAAAACGGGAGAGCAAAA G	0,0	CAGCGGCTCTTCAGTAGTCT

Omy_Na KATPa3- 50	A	C	CACTCTGTTTCCT TTCTTT	TCTGTTTCCGTTT TTT	GTTGAGCGTGTTATGGGAAAAGAG	0,0	TTGCATCGGCTTTCTGAAAAC C
Omy_ndk -152	A	G	ACCCACTTTCAAA AC	ACCCACTCTCAA AAC	AAGAATTGAGGGATAAAAACAAA ATAATATATAAACATGA	0,0	CAAACCTACATTCATTAAAG TCCAGTTTTGT
Omy_nips -299	T	-	CTGGATTTTACAT GTAATAC	CTGGATTTTACG TAATAC	GACAGGATAGGAACGGTTTCTCAA T	0,0	ATCAGAAAGTTTAATTCAATAT GTACACGATCCT
Omy_nkef -241	C	A	CTTCTGTATCATT TTTG	TCTTCTGTATAA TTTTTG	AGTGTCATTGATGTCGGCCTATTTT	0,0	AAACGAATGTCCACCTCAGA TGTT
Omy_ntl- 27	G	A	CAGACAAGAGTA CCCCAAGAC	CAGACAAGAGT ACTCCAAGAC	GGTGTGTTACTGTAGTTGTGTCCTT	0,0	TGTGTAGCTAGTGATCCTGAT TGTCT
Omy_nxt2 -273	C	T	AAGGCAC	AAGGCAT	CTTTAGAAAAGCCAAGGTATATTT TAACATACTTCT	0,0	CTGCTGCCCTCTAATGGTAAG ATAG
Omy_Ogo 4-212	T	C	CATTTGATGAGA CATCTT	ATTTGATGAGGC ATCTT	TGAAAGGTTTTATGCAGGTATTTT CT	0,0	GTGTGTGTTAAATAAGCATTT GATGA
Omy_Om yclmk438 -96	A	C	TACGCAAATTAG GTTTAAA	CGCAAATTAGGG TTAAA	CCCGACTCTACTTCACTACTTTCTT	0,0	GGCCTAGGACAATAGGACTG AAC
Omy_Om yP9-180	C	G	CTGTAGTAGTCCC CATTGT	CTGTAGTAGTCC GCATTGT	CTGGATGTGTAGTATCGGTGGAAA A	0,0	CACTGGGCACCTCTGATCTC
Omy_Ots 249-227	C	T	CCCTCTGAGAACT AC	CCTCTGAAAAC TAC	CTATCTATCTATCTATCTATCTATC TATCTATCTATCTACTTACTGAGA	0,0	CCCCTAGATTAAACCTGTCCA GTCT
Omy_oxct -85	A	T	CATCGCTTATTTA TGC	CATCGCTAATTT ATGC	CGTCACTGAAACATTACTGTAACA TCCA	0,0	CATCATCACGCTGTTGGTTTC TTAA
Omy_p53 -262	T	A	CAAGTAGTATGG AGCTCTAT	AAGTAGTATGGT GCTCTAT	CCCCAACATCCAGTATACAGTTTC A	0,0	CCCAAATTGGCAATTTTAATA GGATTGAGA
Omy_pad- 196	C	T	AAGACAAAGGTG TAATACC	AAGACAAAGGT ATAATACC	CAAACAACCACAGTAGTCCTCCAA T	0,0	GCTTTTACCCTTTTGTAAT TAAGCCAAA
Omy_ppie -232	C	T	AAATAGCGGAGA AAAT	AAAATAGCAGA GAAAAT	CTGTTTTAGATTAGAATGTTTTTGG TCAGGT	0,0	CTGAACATAGGCTTTTCATTTT AGACAT
Omy_RA D103359- 45	C	T	CCTGTAACGCAC AG	CCTGTAATGCAC AG	GGAGAAGGATGTGCTCCCTG	0.4,0	ATTTGGAGGTGGAGGGTCCA
Omy_RA D10733- 10	A	G	AGGGTGAAGAAC TG	AGGGTGAGGAA CTG	TATAGACCCCCTGCCAGTCA	0,0	ACAGAGAAACCCCGTCATT
Omy_RA D116-59	T	C	CCACAATGTCAA C	CCACAACGTCAA C	GGAAGAAGTGAGAGCCCTGG	0,0	CTGTAGTCCACGATCCGCTC

Omy_RA D1186-59	A	G	CCAGGACATCCA GG	CCAGGACGTCCA GG	CACAGCCTGGATGTGGTTCT	0,0	ACAAGTTCCGGGAGTTTCCT
Omy_RA D12439- 64	G	A	CTTCTCCGATGTC A	CTTCTCCAATGT CA	GGAAC TTTTCACATCATGTTGACT G	0,0	GCACAGAGAACTCCAGGCAA
Omy_RA D12566- 14	C	T	ATGTAAACAAAT TG	ATGTAAATAAAT TG	GTGGACATTCTGCAGGGAT	0,0	TCCCACAAATATTTTCATACGC ACA
Omy_RA D13034- 67	A	C	ATAAATCACAA	CTAAATCACAA	GAGTGATTCCCAGCCCTCC	0,0	TCTCTCCGTTGGCCAGAAAC
Omy_RA D13034- 67-21	C	T	CTCCCCGAACC	CTCCCTGAACC	GAGTGATTCCCAGCCCTCC	0,0	
Omy_RA D13034- 67-35	A	T	CTGAGTGGACA	CTGTGTGGACA	GAGTGATTCCCAGCCCTCC	0,0	
Omy_RA D13073- 16	G	A	AAAGGGGACATT ACG	AAAAGGGACATT ACG	GTGAGGGATCACACCTGCAG	0,0	GCACCCATTCGTAATGTCCC
Omy_RA D13499- 13	T	C	CGCCCTGTCCGCC A	CGCCCTGCCCGC CA	GTTACCTGACGACCAAGGT	0,0	GCTGGGGGAGCTTTACATGA
Omy_RA D14033- 46	A	G	ATAGAGGAATAG AC	ATAGAGGGATA GAC	GCAGGAGATTTATTTGGCCCC	0,0	ACCCTTGTGATCACATACTGT CT
Omy_RA D15709- 53	G	A	ATGCAAGGCTTA AA	ATGCAAGACTTA AA	TGCAGGACTTGGATAACACAGA	0,0	TGGTTATATCTACAGTACAGT TCGT
Omy_RA D16104- 20	A	G	AGGGCAAAG[AT] CAAAGG	AGGGCAAAGG[AT]]CAAAGG	ATTCCAAAACCTGCAGGGGT	0,0	TCAGGATTTGGTAAGGTGGC C
Omy_RA D17632- 23	C	T	CATGTGAGACCTT TGCA	CATGTGAGATCT TTGCA	AAGCTCCTGCAGGTCATCTC	0,0	TCTGTGAACTGTCTTCTGCAA GT
Omy_RA D17849- 16	G	C	AGACGGACTCCC C	AGACCGACTCCC C	GACTCCACAGCCTACATGGG	1.1,0	CCGTTAATGCCAGGGGAGTC

Omy_RA D18903-48	A	G	AGGAGACACCA	AGGAGGCACCA	GGGGATGAGTTCTTCGGTGG	0,0	CCACCAAATCCCCGAAGAA
Omy_RA D1919-22	A	G	CAGGGAGGAGG	CAGGGGGGAGG	CAGGTCACAGACACACAGGG	0,0	CTACACCACCCACGTTCTG
Omy_RA D19340-24	A	G	CATGGAAATACA TA	CATGGAGATACA TA	GCAGGGAGCAGCATATACATG	0,0	TGGGGTGATTTGAGTGACAC
Omy_RA D19578-59	A	G	GGTTAAGAGTAT TC	GGTTAAGGGTAT TC	GGTTGGACACCTCCTGGTTA	0,1,2	TCAACCAAGCAACAGATTAT AGCT
Omy_RA D20917-11	T	C	AGGTTGCGAGGT C	AGGTCGCGAGGT C	CGTTGTCGTCTCCAATCAGGA	0,0	ACCAGCTCGATGCCATTGC
Omy_RA D22123-69	T	C	CCAAAGATGTCA GA	CCAAAGACGTCA GA	TGGGAAAGCATAGGAGGGGA	0,0	TGTGTGCCTGTCTTATAGCCC
Omy_RA D23577-43	T	C	TCTGGCTCTGTCTG GTCT	TCTGGCTCCGTC GGTCT	AATAGGAACCAAGCCCCAGC	0,0	CAGAGCCTGAACCCATGGAG
Omy_RA D23894-58	A	T	GTGGATTAGGGG	GTGGATTTGGGG	TGCAGAAAGGCTGTGTGGAT	0,0	TCTTAACACAGTCCTCATGGA ACA
Omy_RA D24287-74	A	G	GGTCACTACCTCC C	GGTCACTGCCTC CC	ATTGTCTGTCTGCCGAGGTG	0,0	TGGCGACCTGTCTACTAATGC
Omy_RA D25042-68	G	T	AATTTCTGCCCAA A	AATTTCTTCCCA AA	GCTGCTGAAACTGGTTTGCA	0,0	TCATGCAGATGAGCTTCCCTG
Omy_RA D2567-8	A	T	GCAATGGGCTAT TT	GCATTGGGCTAT TT	CTGTCTGGATAGCCTTGCCC	0,0	TCTATCTCTGGGGAAAATAG CCC
Omy_RA D26080-69	G	A	ATTAGTAGCATC ATCGAG	ATTAGTAACATC ATCGAG	TGTGGGACAGCACATACTCC	0,0	CCAGGACACCAGTGGAGAAG
Omy_RA D26691-36	A	G	TCTCCTAACAGA AC	TCTCCTAGCAGA AC	TGCAGGAAACCGTCAATCTACA	0,0	CAGGAATTAATTGTATGGCC GGA
Omy_RA D27740-55	A	T	TAACTTTAAAAA AA	TAACTTTAAAAA AA	TCGGCCTGTACTAGTCTCACT	0,0	GCCTAAAAATGGCCACTTTCAT CA

Omy_RA D28236-38	T	C	ATCTGTCTTCGTG C	ATCTGTCCTCGT GC	GGCACACATCTGTCCCGTAG	0,0	GCACTAAGGTCTAGGAGCAC G
Omy_RA D29700-18	C	A	ACAATTCAAATG ATTTA	ACAATTAATAATG ATTTA	AATGGAATTGGCCCCAACCC	0,0	TCTCCATTGTGTGTAATCATG GT
Omy_RA D2976-26	G	A	CAGCTGGGTTGA GA	CAGCTGGATTGA GA	AGGACTGTGATCCTCTCAGCT	0,0	AGCTCTGCTGAAACATCAGT CT
Omy_RA D30392-17	T	C	CTGAGACTGTGT GT	CTGAGACCGTGT GT	CCACTACTCACAGACCTGCA	0,0	GCTCAAGGACCAACAAAAAG CT
Omy_RA D30619-61	T	A	CACTGTAAAA	CACTGTAAAA	CTGCAGGTCAATGGGTGCTA	0,0	ACACTGATCACATTTTTGTCA CACT
Omy_RA D31408-67	T	C	ACAGAATGCAGA AA	ACAGAACGCAG AAA	CAACCCTGCAGGCTACAGAA	0,0	TGGAGTGCCAACAAAAGAAG C
Omy_RA D3209-10	A	G	CGGTATCCCTGGC	CGGTGTCCCTGG C	CGGAGGAGTTTGAGCAGTCT	0,0	CTTCTACCACCACCTCGCTG
Omy_RA D32139-58	G	A	TCGACATGACCT GA	TCGACATAACCT GA	GCAGGAAACAGGTACAAAGGA	0,0,4	TGGCTTCTTCCTTGCTGAGC
Omy_RA D33122-47	G	C	CCACAGGGTGGT GC	CCACAGGCTGGT GC	CAGGCTTTGTGGACATGTGC	0,0,6	GTGCTCTATCTTGCTCTTGGC
Omy_RA D33798-24	T	C	GAGTCTATCAAG AT	GAGTCTACCAAG AT	CAGGAGGGTCAAGTGGAGTC	1,4,0	TTGGGCCCTCTCTTTTTGGG
Omy_RA D35005-13	C	T	CCAACTCCCGAC GG	CCAACTCTCGAC GG	TGGTCAAAGTTGAGGGTGGT	0,0	CAGGGCCCTGATTAACCACT
Omy_RA D35149-9	G	A	GCGCGCTTATGTC	GCGCACTTATGT C	GAGTCAATAGAGCCCCCTGC	0,0	TGGTTAGCAGGAGCAATCTC A
Omy_RA D35417-9	G	A	TGCAGGACGTGC TTTGT	TGCAGGACATGC TTTGT	GCACTTGACCACATAGCTGG	0,0	ACTCCACACTCCACAAAGCA
Omy_RA D3651-48	G	T	GTTGGGAGAACT TT	GTTGGGATAACT TT	GAGTACAGTGCAGTGTGGGG	0,0	CCTTCCTCTTGCCACCATCA
Omy_RA D366-7	C	A	CAGGACTTGCTTT T	CAGGAATTGCTT TT	ACCAAATTAGAGCCTGCAGGA	0,0,5	GGAGAGGCCTTTCCGTGATC

Omy_RA D36848-7	G	A	TGCAGGGACACC ACCCT	TGCAGGAACACC ACCCT	CGAGGACGTTTCATAGGGAGC	0,5,0	TCGATAAGTCCACCAGCTGG
Omy_RA D36952- 53	C	A	AGGACATCTTCAT C	AGGACATATTCA TC	TGTACGTCATTGGGGCTGAG	0,0	CCTACCAGACCACACGATGA
Omy_RA D37816- 68	A	T	GCGGCGTAAAAA TG	GCGGCGTTAAAA TG	CTCATTCCTGGCCGTCTG	0,0	CCACTCACACTGGCTTATGC
Omy_RA D38406- 19	T	A	AGGCTTTATATGG CC	AGGCATTATATG GCC	CTGCAGGGGTATTAGGAGGC	0,0	AATGAGTTGTGGCGGTGAGT
Omy_RA D39156- 33	T	C	ACCGTAATGGAG AG	ACCGTAACGGAG AG	GGGTGTGACATGTGTGCAGA	0,0	ACTGCTTGTCCCCACCAAG
Omy_RA D3926-22	T	C	TTCACTTTTCCCT G	TTCACTTCTCCCT G	CGTTCCTGCAGGCTTTTCAC	0,0	TTGGCACAGAGAGTACGCAG
Omy_RA D40132- 55	A	C	TCTGTGCAGTCCT C	TCTGTGCCGTCC TC	TGCAGGGCCTGTATATTGCT	0,0	TCAAAGGACTGGGGAGAGGA
Omy_RA D40520- 48	T	G	GTCAGATTGCGCT G	GTCAGATGGCGC TG	TGTTTCATCTGATCAGCTGTCAG	0,0	ACACGTCGGTCTTCTTCTCC
Omy_RA D40641- 58	T	C	AGTGATATCAAG TG	AGTGATACCAAG TG	GGCAAACCTGGCTTGTGAGTG	0,0	AAGGCTCTGCTTCTGCTTGA
Omy_RA D41594- 34	A	G	CAGAGATACGTT CC	CAGAGATGCGTT CC	TGCAGGGTTATAATGTGTCTTTGT	0,0	AAATCTCGGGCTGAGGAACG
Omy_RA D42465- 32	G	T	CCAGGCTGGAAG AA	CCAGGCTTGAAG AA	GTGGATCTTGGACTCCAGGC	0,0	TAGACATCGGCCCTCACAGA
Omy_RA D42793- 59	T	C	CAGAGAATGCCA ACAGA	CAGAGAACGCC AACAGA	CACGGCTAGTGGCATGTACC	0,0	CCACACCTGCATCAGTCTGT
Omy_RA D43573- 37	A	G	GAAAGAGAGAGT TT	GAAAGAGGGAG TTT	TGCAGGGAACGATGAAACCA	0,0	ACAGACACAGCATTGGCCAA
Omy_RA D43612- 42	T	C	AAATGTGTATTTG TGTA	AAATGTGCATTT GTGTA	GTGGAGAGGGATTTTGGGGG	0,0	TGACAGGACAAACACAAGCC A

Omy_RA D43694- 41	A	C	AGGGAAGAGCGG AG	AGGGAAGCGCG GAG	CCCCTCTCCCTGGCTAGAAT	0,1.1	TCAGGGGGTGTGCTTTTCC
Omy_RA D45104- 18	A	G	CAAGACACCGCA CACAG	CAAGACGCCGCA CACAG	TGGTGCTTCAGTGCTGTCAA	0,0	AGAGTGAAAACCTGTGTGCGG
Omy_RA D46314- 35	A	G	TAGCAATGGT	TAGCGATGGT	ACTGCATCTTTTCCCCTGCA	0,0	TGAAGATACCCAGAGACACC A
Omy_RA D46452- 51	A	G	TGAAGTCAGAAG TT	TGAAGTCGGAAG TT	TGCAGGTAAGACTTGATCTGGA	0,0	TGACTCCAACCTAAGTGCAT GT
Omy_RA D46672- 27	C	G	GTGGTAGCCCAT CA	GTGGTAGGCCAT CA	TGCAGGAGGTCTTTTTCCTTGT	0,0	AACACATTCTTATTTGCAATG ATGG
Omy_RA D47080- 54	A	G	TGCAAGACTTAA AACGA	TGCAAGGCTTAA AACGA	TCAAAACCTGCAGGACTTGGA	0,0	TGGTTATATCTACAGTACAGT TCGT
Omy_RA D47444- 53	C	T	GGCGAGCTTGGC CCAAA	GGCGAGTTTGGC CCAAA	GTCGTCTGGAGGAGCTGAAG	0,0	GGGTGACGTTTTCTTCAGC
Omy_RA D47955- 51	G	T	TTGGAATAGAAT CTATA	TTGGAATATAAT CTATA	AGTGTGCTAGAATGGGCCTG	0,0	ACCATGGGCAGTTCATTTC
Omy_RA D4848-14	G	T	GAGACAAGGACA GA	GAGACAATGAC AGA	TGTCCCTCTTCTGCACGATG	0,0	AGTTGGTAGCTCACTCTCTGT
Omy_RA D48799- 69	A	G	CATCCTAGAATA GAAGT	CATCCTGGAATA GAAGT	GCTGAGCCACCTACACACAG	0,0	GTCTAACACTCGCAGCAGGT
Omy_RA D49111- 35	T	C	TTTCTTATATTTG A	TTTCTTACATTTG A	GCAGGCTTAGCATTGCTGAC	0,0	GGAACCTGGGTGGGAGAATG
Omy_RA D50632- 21	C	T	TCAGCACCTCCA GCC	TCAGTACCTCCA GCC	CCTGCAGGCTGGGTCATTAT	0,0	GAGCCAGCTGTACCTTCTCC
Omy_RA D52458- 17	C	A	ATGGCCCC[CT]A AGAACCC	ATGGCCCCA[CT]A AGAACCC	ACGTGTCCCTGAGGATGGTA	0,0	AGCTCTAGGTCTGGGTCCTG

Omy_RA D52812- 28	C	G	CAACCTC[TC]ATT CCACAT	CAACCTG[TC]AT TCCACAT	AGGAGTCCTGTCCCATGTCA	0,0	GCTTAAGGCTGTGGTATGTG G
Omy_RA D5374-56	A	C	AGAGGGAAAGAG AG	AGAGGGACAGA GAG	GCTGTTACCGTGTGATGTTGA	0,0	AGAGTTCTGGCCTCTCCCTC
Omy_RA D55404- 54	C	T	ATTGTTTCTGAAG G	ATTGTTTTTTGAA GG	GCAGGGTGTCCACTACAGAC	0,0	AGGAGTCCTGAGAGTTGGGC
Omy_RA D55997- 10	A	C	AGGCTGCAATGT TT	AGGCTGCCATGT TT	CATTTTCTACCTGCAGGCTGC	0,9,0	AGCCTACATACATAAAGCCA ACA
Omy_RA D57916- 29	A	C	CAGGGGCAAAAC GG	CAGGGGCCAAA CGG	GCAGGGCCTTAGAAACAGACT	0,0	TACACGCCTCACTGTTCTGC
Omy_RA D58213- 70	A	T	TTTTTT[TA]AAAA TATACT	TTTTTT[AT]TAA ATATACT	CCTGATGGGTGCTCTTCTCTC	0,0	AAACAGCATCATTATCCATA GTGTT
Omy_RA D58835- 15	G	T	ATAGCTGCTGGG ACCCA	ATAGCTTCTGGG ACCCA	GTCTGCTAAGGTCCTGCAGG	0,0,2	GCCGACCATGAGAGACCTG
Omy_RA D59758- 41	T	C	TGATTGCTACTGA C	TGATTGCCACTG AC	GGCCCCCTTCTTTCAGGAAT	0,0	CACACACTCAACGGGTCAGT
Omy_RA D59950- 44	G	A	GGAGGGGAAGGG	GAAGGGGAAGG G	GGAGCTCATATCGCCGATGG	0,0	GAACTCTGTCACCCTGCCC
Omy_RA D60135- 12	C	G	GAACATACCGGA AC	GAACATAGCGG AAC	AGCATACACACCTGCAGGAA	0,0	TGGTAGGAGGAGATGCTCTG T
Omy_RA D619-59	T	C	TGCTGGATCCCC A	TGCTGGACCCCC CA	CATGGAGAAACAGACCCGCT	0,0	TGCTGTGTGTGTATCTGGGG
Omy_RA D62596- 38	A	T	TTAAAAAATATA TATTA	TTAAAATATATA TATTA	GCAGGACACTGGTTCCCAAA	0,5,0	CCTGAGATTTGAGATCACTG GCT
Omy_RA D65808- 68	T	G	ATCGGGATTCACT T	ATCGGGAGTCAC TT	TCCTTCACTCTCGATCGGGA	0,0	TCAAACCTGGGCCACTACTGT
Omy_RA D65959- 69	G	A	TTTTGTCGTTCTT T	TTTTGTCATTCTT T	ACATTTTGGTGTAAACAACCCTGT	0,0	GCTAGCGAAGACCCTGAAGG

Omy_RA D66402-36	T	C	AACCACTTCTCTG	AACCACCTCTCTG	GGTGTGATACCTCAGAGCTCTG	0,1.7	CGTCTCCGGATCGTTCAGAG
Omy_RA D66834-17	C	T	TCTGGCTGACACCTTTA	TCTGGTTGACACCTTTA	CTCCTGCAGGTCATCTCTGG	0,0	CTGTCTTGTGCTCAATGCCTG
Omy_RA D68634-40	A	C	CCTCTAAACTGAAT	CCTCTAACCTGAAT	TGCAGGACTCCTTTGAAACGT	0,0	TAACGCCAGCTGCATGATGA
Omy_RA D7016-31	C	A	ATAATTTTCATTTAA	ATAATTTAATTTAA	GCAGGAATATTCAGTGTGCCA	0,0	TCTAAAATGTCGTTGGCGGC
Omy_RA D7210-8	C	A	TGCAGGACTTGCTTTGT	TGCAGGAATTGCTTTGT	ACACCACACTCCACAAAGCA	0,0	GCGCCTTGGTCTCCTTCATA
Omy_RA D72528-44	A	T	TTGGAACAACTGT	TTGGAACCTAAGTGT	TGATGATCCGGACCCTCTCT	0,0	CCCGGATTCCCTCCACAGTT
Omy_RA D73204-63	G	C	GTGCCCCGCTCTCCACCG	GTGCCCCCTCTCCACCG	CCTGGGCAATGACCTCCAC	0,0	AGCTCCCTTCTCTCTCCCTC
Omy_RA D7384-50	T	C	GCCTCTGGCAG	GCCTCCGGCAG	GACACGCCCTCAGCCAG	0,0	CTGGTACCTTCCTGCTGTGG
Omy_RA D739-59	C	G	GAGTTGGCTATTTT	GAGTTGGGTATT	ACGAGGCTTGTAATGCAGT	0,0	TGCCTTTATACCAATGTCTGCTG
Omy_RA D73963-73	T	A	TTTCTTTTGGA	TTTCTATTGGA	CCCTCTCAGGAAAGTGACCAC	0,0	GGATCATGTCAATCTGATGAGTTGG
Omy_RA D76060-20	C	T	GGGCGCTGTAGGCAA	GGGTGCTGTAGGCAA	TGCAGGGTGTGAGTATTGGG	0,0	TCCCATGCAAATTCCAAATGCT
Omy_RA D76570-62	T	G	AGAGGTGTTCTGT	AGAGGTGGTCTGT	GCAGGTAGGTAGGAAGGAAAGC	0,0	TCTGACTGGTATTGAAAGGACCA
Omy_RA D77789-54	T	C	TAAATTATATTTGACAG	TAAATTACATTTGACAG	AGACAAAACCTGCAGGGGAC	0,0	AGCACGTAAAAACCAAAGTCTCA
Omy_RA D78147-27	C	T	CAAAGTCCCAGAGA	CAAAGTCTCAGAGA	GCATTTTAGCCCTCCCAAAGTC	0,2.6	CCTTCTTCCAGTTGTTAAAACCCA

Omy_RA D78502- 57	T	G	GGAAATATCACACA	GGAAATAGCACACA	GAGAGGCATCCTGTCTAGGG	0,0	ACCATGCTCTTTCTGTAGGTG T
Omy_RA D78776- 10	T	C	GGGTAATCCTGGCT	GGGTAACCCCTGGCT	CACAGCTTCCTGCAGGGTAA	0,0	GCTTGCATGGTCTCGCTAGT
Omy_RA D79314- 58	C	T	AGACCTTGTC	AGACTTTGTC	CACACTGACTCATCCCTCGC	0,0	GAGTGTCTTACCGAGCTGCC
Omy_RA D79314- 58-25	C	T	CTCGCCCTGCG	CTCGCCCTGTG	CACACTGACTCATCCCTCGC	0,0	
Omy_RA D79314- 58-27	T	C	GTCACRCCTGC	GCCACRCCTGC	CACACTGACTCATCCCTCGC	0,0	
Omy_RA D79314- 58-31	G	A	ACGCCTGCCCT	ACACCTGCCCT	CACACTGACTCATCCCTCGC	0,0	
Omy_RA D79314- 58-66	C	A	CAGTGTC AACC	CAGTGTC A AAC	CACACTGACTCATCCCTCGC	0,0	
Omy_RA D85131- 35	T	C	GATGGTATGGTGAG	GATGGTACGGTGAG	TTCAATAACTACAGGCAGATGGT	0,0	AGTTCCCAAATGCACTGTAC A
Omy_RA D86706- 72	C	T	TACGTTTCATTTCT	TACGTTTTATTTCT	TTCCCTGTAACTGTCACGCC	0,0	CCACATCACACCCTGACCTC
Omy_RA D88028-7	G	A	TGCAGGGGCTGG	TGCAGGAGCTGG	TAGCCCAGTTCGGTTCCAAC	0,0	AGTGTCTTTGGTGCGTCCTC
Omy_RA D88122- 32	G	A	GCTGTGGAGATCAT[CT]CG	GCTGTGGAAATCAT[CT]CG	TCAGTGGATGGAGTGTCCCT	0,0	GGTCTTTGGCCTTGTTGCTG
Omy_RA D9004-13	G	A	TCATCTGAAGGGGG	TCATCTAAAGGGGG	TATACCACGCCTTCCCTGGA	0,0	CAGAGAGAAATCCCCCACCC
Omy_RA D92485- 64	T	A	GTGTAGATATACAT	GTGTAGAAATACAT	CCAGTCAGTCTTGCCTCAGG	0,0	GGTCACCACAGGATTGGAGG
Omy_RA D93580- 37	T	G	AGTCACCTGGGATT	AGTCACCGGGGATT	AGGCAGAGGAGGGTTGTTTG	0,0	TGCAGAAGTCAAATCACGAA CA

Omy_RA D98715- 53	T	G	CAGGACTTCTCCC C	CAGGACTGCTCC CC	CGTAACGGGGAGCTGATCTG	0,1,9	GCTGGTAAAATGCTGAGGGG
Omy_rapd -167	G	T	AAACAATCCCC CCAAA	AAACAATCCCAC CCAAA	CCCAACATGCTCTATTGCAGCTA	0,0	AGTTGCATAAGATGAATCAA TAAATTA AAAACACAGAT
Omy_rbm 4b-203	-	T	CACGTTATTATGA AAAGGATGT	ACGTTATTATGA AAAAGGATGT	CTGAAATTTGATGAATGGAAGCTG CA	0,0	CGTATTCAAGTCGATATACA GTCACGAT
Omy_redd 1-410	C	T	AAAATATCCTGC AAGGAAT	AATATCCTGCAA GAAAT	GTACTCCCACTAACATACAGTAGA CTCA	0,0	GGCACCATTGTGTTTTAGGAT GTAG
Omy_sast -264	G	A	CTAGCCAATGCG TCTAA	ATCTAGCCAATG TGTCTAA	GAAGTAGGGTTTGTTGACCATGTG A	0,0	TGGATTCCATTTTAGGCTGTA ATACATCTT
Omy_SE CC22b-88	T	C	CTGTCTGTCCATA TATC	CTGTCTGTCCGT ATATC	GGATCCCTCCTTTTAACACAAGAC T	0,0	CTACAGGATGACTACCTAAT TGCTAATAAAACA
Omy_srp0 9-37	C	T	TTGTGCTATTGAC GCCACAG	TTGTGCTATTGA CACCACAG	TAGTTGTATTAACCTCTCTTTGAGT CTAGA	0,0	TCATTCCAGCTCCGTTCTCTT C
Omy_sSO D-1	T	G	CCACAACAAGAC CC	CCACAACCAGAC CC	GCCGGACCCCACTTCAA	0,0	CAGACTAACCGAACAGCATC AGTGG
Omy_star- 206	A	G	TCTTTGGCACTAT ATCT	TTTGGCACCATA TCT	CGTGTGCCAGCCCTTCT	0,0	GACCACTGAGATCATTGCTG TGA
Omy_stat 3-273	G	-	CCAGTTTG	TCAGTTTG	CAGACCTCCTCTATCTCCCTATGAG	0,0	ACCTCCTTTAAATTGTGCCCA AGAA
Omy_sys1 -188	C	A	AAACATGTACGA CCTGTC	TGTAAACATGTA CTACCTGTC	CTTAAATGGTGCTGGTTGCTGTATT	0,0	AGTGATATCTTAGTGGGTCG AGGAAA
Omy_tlr3- 377	C	T	CGTGATTAGGTTC TTC	CGTGATTAGATT CTTC	GTCGCTCCGGGTGCTT	0,0	GGCCCAAACACTTCCTTCCT
Omy_tlr5- 205	T	A	CAGTAATATTTCA GTGCCCCG	CAGTAATATTTT TGTGCCCCG	GAGCGTATCTGGTATGGTAACAAC A	0,0	CTCCAGCAGCTTTAGAGAGT TTACA
Omy_txni p-343	T	C	AACTGAAGAGAT CTG	AACTGAAGGGAT CTG	CCTTCAAACCTAACGCATCATAGAC ATG	0,0	GGTCACTTGGCTAATCCCCTT AT
Omy_u07 -79-166	G	T	ACTTGGAATAC CCCAGCC	CTTGGAATAAC CCAGCC	CCCGCTATATTATTTGATCACCCCTT GA	0,0	ATTTAAATCCATTTCTAAAAA TAAGCAAACCTAACCA
Omy_u09 -53.469	T	C	TTGCAGCCCTTAT TGTG	TTGCAGCCCTTG TTGTG	ACAGCCTGAGCGTTTGCA	0,0	GGAAACTGGGAGAGATCAAA GGA
Omy_u09 -54-311	C	T	TGGTAATTATTCA ACAGATCAGT	TGGTAATTATTC AACAAATCAGT	GTGGCTCCCCAGGAACAAG	0,0	AAGTTTCATGTCACATTCCAG TTACCT
Omy_u09 -56.119	T	C	AGTGAGCTGAAA CAGAGCA	TGAGCTGAAGCA GAGCA	CCAAGGTGGACCCACCAG	0,0	GCTGAGTTTATAGGTCAGTC ATTATACATATTGA

Omy_u09-61.043	A	T	CACTTGGTCCTTTTCA	CTTGGTCCATTTTCA	TAGTCACATCCATAGTAATACTTCC	0,0.4	TGTTTCAGAAGCAGAAAAACCAATCTCT
Omy_U11_2b-154	T	C	AATGATACTTTTTCAGATTGTAAC	TGATACTTTTTCAGGTTGTAAC	GGGAAGCAGAAAAACTGGAAGTT	0,0	CCCTCTGTGGGCTTGATATTCA
Omy_UBA3b	A	T	TGGAGATAACGCTAACTATT	AGATAACGCAAACTATT	GCCACTCAATGCATGTGTTTTCTAG	0,0	CAGCTAGCTTAAGTGGGATGCAA
Omy_UT16_2-173	C	T	ACAGTCAACAAGGGACTTAA	ACAGTCAATAAGGGACTTAA	ATTGACTCATTATCACCTTAGTTGTAGCTTCA	0,0	GCAGCTACTTGCTGTATCACATGTTTGT
Omy_vamp5-303	A	-	TGGCCGTAGTAGTTGGTCA	TGGCCGTAGTTGTCA	CTGCTTCCCAATTCAGTATCGTCTT	0,0	AGGCTGAAGCATTTCTGAGTATGAA
Omy_vatf-406	T	C	ATGACTATCCACA	ATGACTGTCCACA	TTGCTTCATTTTGTGCATAACCTTGGG	0,0	TGCATGCTCTGACAAATGTTACACT
Omy_VGLL3-1_AT	A	T	ATAGTAATGGC	ATTGTAATGGC	GGTGTCCAGACTAGACGAA	0,0	CGTGCGTAAAAGCGCCAAT
Omy_VGLL3-1_GT	G	T	TGTGTTCTGAAT	TGTGTTCTAAT	GGTGTCCAGACTAGACGAA	0,0	CGTGCGTAAAAGCGCCAAT
Omy_VGLL3-6_AT	A	T	ATATTATTGTTCA	ATATTTTGTTC	TGAAATTGTTGCATGTTGCGT	0,0	TGTAGGTCAGCCTTGAACCTTT
Omy_VGLL3-6_CT	C	T	TACACACCAATA	TACACATCAATA	AGATGTAGGGCATGATTGCCA	0,0	GCCTAGTGTTCTGTATGTGTGGA
Omy_zg57-91	C	A	CACAGACTGCACAGCC	CCACAGACTTCA	CACTCATACACTCACTCACAAAGGA	0,0	AGCAGATAAGCCTTGTGAGTGAATCTT
OMY1011SNP	C	A	CTTTACCTCGAAGACAAT	ACTTTACCTCTAAGACAAT	AGGCTGGTTTGGGATTCACTG	0,0.6	CGCCAAACACTAACTCTCTGTCT
Omy25_61284413	A	C	CATTAGAAACA	CATTAGAACCA	CAGTGCTGGCGTCATTAGAA	0,0	TGTTTTGGTTTATGGGCTGA
Omy25_61285646	C	A	AGAATGTCTATT	AGAATGTATATT	TTGACACTGGTCCTGAGAATG	0,0	AAGCAGAGGGGTGCACTG
Omy25_61286316	T	G	ATGCTAACCTT	ATGCTAACCTG	GGCCTCCTGAAGAGGAAAAA	0,0	AGGGACTTGTGCCCAGATTA
Omy25_61287415	T	C	TACCCATTCCCTG	TACCCATTCCCG	TGTCTGGTGATGTTGCTCCT	0,0	ACCTGACGTGGCCTTCTGTA
Omy25_61294400	A	G	GCTGGTCAGCACATGCTTTGA	GCTGGTCAGCGCATGCTTTGA	GACAGATTATCTTGGCGTTTTG	0,0	AAACGGATTACCAGGACACG

Omy25_6 1316270	G	T	AGGCCCTATAGTT	AGTCCCTATAGT T	ATCGACTGTGCCCTATCTGG	0,0	ATCAATGGGTTCCTTTTCGTT
Omy25_6 1317685	A	G	TCTGCATTAACCA C	TCTGCATTAGCC AC	TGGGCTAGATTTTCAGTCTGC	0,0	ATGCATCCTCTTGAATGGTG
Omy25_6 1317777	A	G	AATTTAAAAAAC GGTATGCTT	AATTTAAAAAGC GGTATGCTT	TTCGTTCTCTGTTGTTTTTATTCG	0,0	CAAGCAGCAGGCATGACA
Omy25_6 1318852	A	G	AAAAAAAGGGAG CTCG	AAAAAGAGGGA GCTCG	TACGCGAATGGTACTTGCAG	0,0	TTCCGACTTGTGTGGGAGT
Omy25_6 1322413	C	G	CTAGGGGACACA	CTAGGGGACAG A	ATCAGGGCAACTAGGGGACA	0,0	CCGCATCATTAGTGCTGATT
Omy28_1 1607954	G	A	TGTGGGCTGCGA ACATACTCA	TGTGGGCTGCAA ACATACTCA	TGACACTGATCACAATGGTGAAAT	0,0	TAAACTGGAAGGAGAGAGCA AAAT
Omy28_1 1625241	A	G	CCTCCTCCCTATG GTTGTCTC	CCTCCTCCCTGT GGTTGTCTC	CAACATTTAGGGAGAGGTTGCTAT	0,0	ATCATCAAGTTTGCCTACGAC AC
Omy28_1 1632591	G	A	TGAGAAGAACAC AGAGG	TGAGAAAAACA CAGAGG	GTAGAGGCCAAAGGCTTGAG	0,0	TGCTCTTATTACCTTCCAGAC TCC
Omy28_1 1658853	A	C	TGGTACAGACAC GCACTAGCA	TGGTACAGACCC GCACTAGCA	CAACATATGACCACTCGAAAACCTC	0,0	ATTAATCACACCGTGAGACT CCTC
Omy28_1 1667578	T	C	GTATTGATCCTGT GGGAGACA	GTATTGATCCCG TGGGAGACA	ACAGTAAACCCATTTCAGGCATAGT	0,0	TTATCCTCTCAATCCACATCA AGA
Omy28_1 1671116	C	T	CTGGTGAGAACA GGAATTACC	CTGGTGAGAATA GGAATTACC	AATTTCCCCAAATTTGAAACTCTT	0,0	GTGTACATTGTCAGGCAGAA ACAT
Omy28_1 1676622	T	G	ACATGTCATTTAT TGTTATCT	ACATGTCATTGA TTGTTATCT	CGAATGCACTGTAGCTCATTCTAA	0,0	GCAGTAGAATGTCTCGCAAA TACA
Omy28_1 1683204	G	T	ATGTAAAAAAGG GCAGAAAA	ATGTAAAAAATG GCAGAAAA	CAAGAAAGAAACAGATGTTGTCCA	0,0	TTGTGACTCAAATCTGCAACC TAT
Omy28_1 1773194	A	T	GCAATTTTTTAAA ATTACCGC	GCAATTTTTTTA AATTACCGC	AGTTTGACACCCCTGTACTAGAGC	0,0	GTCTAACAAGCTCTGGGTGA TTTA
Omy4_82 60712	G	C	GAGGTACCATGA TCAACCAAT	GAGGTACCATCA TCAACCAAT	AGATCCCGAATTTCCCACTT	0,0	GAAACCTGGCGCCTTAAATT AG
Omy4_82 61223	A	G	ATATATGGTCCA	ATGTATGGTCCA	CACATGGGATGTTGGTTAATGT	0,0	GTTTGCATACGCCTATTCATG G
Omy4_82 69484	A	C	CAATGTAT	CCATGTAT	GCCCAACTCCCTATTAAAGGTC	0,0	AAGGTACTTCATTCTTACCCA GAAA
Omy4_82 72302	T	C	ATGTTGAAAGTC ACTGA	ATGTTGAAAGCC ACTGA	GTTGGAAAAGTGGCATCCTATT	0,0	AACATTGGCCTTACTGAAGA GC

Omy4_83 25040	G	A	CTGCAGCTACGG AATGCTTAC	CTGCAGCTACAG AATGCTTAC	AGCCAAGTTTGGCGATTTACT	0,0	TGGATCAGCCAATGAATTAC AC
Omy4_83 27140	G	A	TCATCTAGTCGGT GCAGG	TCATCTAGTCAG TGCAGG	ATTGGAGTTAAATGCCTTGCTC	0,0	CAAAAGGTTGCTGGTTCAAA TC
Omy4_83 43709	C	A	GGTGAATTAATC ACC	GGTGAATTAATA ACC	TTTGGCATTGTGTTTTAGGGTA	0,0	AGTCTGCTTTCCACCAGACAC T
Omy4_83 45868	A	C	ATTGTTTAAATGT CTAAC	ATTGTTTCAATG TCTAAC	TCAAACCTATTCCTTTGGCTACAA	0,0	AAGCATTTTCCATAAAGAAG TCTG
OmyR145 89Pearse	T	A	ATCCCTGTTATCT AATCATT	ATCCCTGTAATC TAATCATT	GTAACCATGACATCCACCAATC	0,0	CCTATGCACAAAGCCTTCAC
OmyR191 98Pearse	G	A	ATTTAGCAGGAG GCCTCTCCA	ATTTAGCAGAAG GCCTCTCCA	TCATTACCTACGCAGTGGAG	0,0	ATCTCTGGGCCTGAACAAT
OmyR243 70Pearse	G	A	TAAGACTTGGCA TAAGCATG	TAAGACTTAGCA TAAGCATG	CAGGAGTAATGCATCCCAATG	0,0	CAAGTTGATAACGAGACATA AGGG
OmyR335 62Pearse	A	G	GTGGTTACAAAG GGTCTGCA	GTGGTTACAAGG GGTCTGCA	GGTGACTGAGCTGGATGT	0,0	TTTAGAGAATTTGGCAGTAC GTC
OmyR402 52Pearse	T	A	AATGCTATATTGA ACCTTAA	AATGCTAAATTG AACCTTAA	ACTCTGAATTCCTCAGGCTT	0,0	TCGAACCAGCTGTCTTTCT
OmyR403 19Pearse	C	T	TGCAAGTGC[TA] GCCCTTTTAT	TGCAAGTGC[TA] GCCTTTTTAT	AAAGATTGCTGCGATGTCTAAT	0,0	CGCAGAGAACAGAGGATGA

1199 **Appendix 2. *GT-seq* SNP panel for Chinook salmon.**
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Assay	A 1	A 2	A1-Probe	A2-Probe	FWD Primer	Corr ectio n	Rev Primer
Ots_100884-287	T	C	ATAGAACTACAA TTCACATATAT	AACTACAATTCG CATATAT	CGGAAGACCAGATTCTCCAAGA GTA	0,0	CGACCAAGTAGCGGCACTT
Ots_101119-381	T	C	TGCCACATGATA ATTGA	CCACATGGTAAT TGA	TTTTCTAGGACAGGTTGCTTGCA	0,0	CCAGGTTTCTTTAGCCTACT TATTCTTTACA
Ots_101554-407	C	G	ATGGAGGATTGT GGTTGT	ATGGAGGATTCT GGTTGT	TGAAAGATATCAATTGTAGTAGT GGTGGTG	0,0	ACACGCCAGTCCACAAGT
Ots_101704-143	T	G	CTTAGACGTCAG AGGTC	CTTAGACGTCCG AGGTC	ACTTCTTGAGCCAATCGGATGAT G	0,0	CCAGAGATAAACTAGTGGA GGAGATCA
Ots_102213-210	A	G	CTGTATACAGTA AGAGTATTAAT	ACAGTAAGAGC ATTAAT	CATTCCATGACAATGATTGAAAT CTAAAAACAC	0,0	GAGTATCTCAATTGCAACAC TATGGTATGT
Ots_102414-395	A	G	CACATAGTGTAG CTTTACTAC	CACATAGTGTAG CTCTACTAC	GCCTACTGATAAATGTATGACAG TAATGGA	0,0	CAATAACAAACAAGCTAGG AACAAAAGTGT
Ots_102457-132	A	G	TGGGGCAACGCA CAATTGGCT	TGGGGCGACGCA CAATTGGCT	CCAGCAGAGACTGGGTTCAC	0,0	TTCCCTACCGGCGAAACC
Ots_102801-308	C	A	AGGGACAGTTTC GCAGACG	AAGGGACAGTTT CTCAGACG	TGGGACAGAGGTGGGAATTGA	0,0	CCCAAAGATGCTTAACTGA AGATGTG
Ots_102867-609	A	G	ACAGAGAGAAGT CCCAGGTG	AGAGAGAAGCC CCAGGTG	CTCTGCCATTCATTTGGGCTTTG	0,0	GTCTAAAGTGGTCCCCTTGG AT
Ots_103041-52	G	A	CATCCTGCTGGAC CC	CATCCTGTTGGA CCC	ACCACCCACCTCCTCAGA	0,0	AGACAGAGAAAGTCGGGAC ACT
Ots_103122-180	T	C	CATCAACACAAT CTGC	CATCAACACGAT CTGC	CAAACGCGCACTCACACACA	0,0	TCACAATGGTACGATTTTAC GACTCAA
Ots_104063-132	C	T	CTTTCGTCCTTAG CACATAG	CTTTCGTCCTTA ACACATAG	GCGTTACTGGTGTATAAACGTT AGC	0.5,0	GTTTATTTAATTATGAAGGA CGATGTTGAAGTCA
Ots_104415-88	C	T	TCCTGAAAAACG ACATCC	CTGAAAAACAAC ATCC	CCTGAGCATCCCAGTTGAACT	0,0	TGTTTTCAATACACTGCAAT TTAGTTTTGGT
Ots_105105-613	C	G	CCGAGCTTGAGTT AGGA	CCGAGCTTGACT TAGGA	AGTACAAGTGCAGAGAATGACA TCATG	0,0	GGTGTTTTATTTTCCCATAT ATCTTTTAACCTTTAAGCT
Ots_105132-200	G	T	CAAGAGTGGCAT AAAA	CAAGAGTGGAAAT AAAA	CGATGTACTGAGGGCAGTGT	0,0	GAGTGGAGTTCCCTTAATAAT CATTGACCTT
Ots_105385-421	A	G	CCTCCTGGGTATA TCG	CTCCTGGGCATA TCG	GACTGTCTTGGAACCGTTGCTA	0,0	TCCCGGAACACACCAATGTC
Ots_105401-325	G	T	CCCGGACAAGAT GAGACAG	CCCGGACAAGAT GAGACCG	GAACTGAGCGGCTGCTG	0,0	CGCCTCCTGGTGTCTATCCT

Ots_105407-117	T	A	CAGGTTAGGAAT GGTTG	CAGGTTAGGATT GGTTG	TGTGTACATCCGCGTAAATATTG AAGATAA	0,0,2	CTGTGAGCTGCTGCAAACC
Ots_106313-729	A	G	AAGAGTCCAGCG TTACTT	AAGAGTCCAGTG TTACTT	TTGTTCAATGGGCATTAATGCAT GTT	0,0	TGCTTATGTGCAGATACTTG AGACAAA
Ots_106419b-618	G	T	CAATGATTAATG ATTAATCCTTC	TGATTAATGATT CATCCTTC	CAAGGGCACATTGGCAGATTTT	0,0	ACCGGACCAAAGCACACA
Ots_106499-70	C	G	CATTTTTCAGAAT TGTATTC	CATTTTTCAGAA TTCTATTC	ACTCTATCATCGGCAGGACCAT	0,0	ACCGTAAGTGTGGTTGTGTT CATT
Ots_106747-239	C	A	CCCGCGGTGAGT AT	CCCGCTGTGAGT AT	ATCGAGGATGCCTCAAAGACAT C	0,0	GTTAGACCCACCACCAGTCA TC
Ots_107074-284	A	T	ACCGTAGCTGCA CCTG	CGTAGCAGCACC TG	CCCACCTCCAGAGCCTGAA	0,0	TTTTCCATGGCTGTGTGTAC TGT
Ots_107285-93	T	A	AAGTAACGTATC AAATGGC	AAAGTAACGTAT CATATGGC	GCCCTTGTGACAATGCACTGTTA TA	0,0	AACATACACCAATACTTAG GTCTAGACAGT
Ots_107607-315	A	C	ATGGGAGACAGA TAACT	ATGGGAGACATA TAACT	GTGATGAGAGGTTTCCGGAAAA TCT	0,0	GTGTTCTGGATTCCATTGTG CAAA
Ots_107806-821	T	A	CAAAGAAAATCA AAATTT	CAAAGAAAATCT AAATTT	TGCAGTGCTGAATTAGAGATTAA TTTTTGTG	0,0	CTCCCTTGCTTTTGGTCATT GG
Ots_108007-208	A	T	CAGTTTCACTTAA TTTTAAAATG	TTTCACTTAATTT AAAAATG	CAGGCTTGTGTAAAGTAGGGAG AAA	0,0	CATTGGACAAGACCGGGTA GTC
Ots_108390-329	G	C	CTACTTATGTAGC ATTTTAA	CTACTTATGTAG GATTTTAA	GAGGTTTGTACTGTACCCATA GA	0,0	CCTGCTGTAGCAAACGTCT CAAA
Ots_108735-302	C	T	AAACAAACAACG CCTCATG	AACAAACAACA CCTCATG	CCTTTTCTTATTAGTTTACTTC CCCAGAGA	0,0	CAATTCCATTCTTGATTCTG TTTAACGGT
Ots_108820-336	G	A	ATTGCCCATCTCA GAATA	AATTGCCCATCT TAGAATA	TGAAATAAATTGTTCTGTTGATA TGTGAATTTTGA	0,0	CAACGACACACCAACAACG T
Ots_109525-816	C	T	CATGAGGCGTTC GGC	ATGAGGCATTTCG GC	GCCAGATAGTAGCGTACATCATG AG	0,0	CTCCCCATGTCCCTGAGTCT
Ots_109693-392	T	G	TCCGTTAGTTCAT CCTGG	TCCGTTAGTTCC TCCTGG	TCTCCCTCATTCCCATGTCATATC A	0,0	GGGAACGTATCAGGTGAGT GT
Ots_110064-383	C	T	CTACGTAATGAA CGTTAGCT	ACGTAATGAACA TTAGCT	AACAAAGAATGTTAAACACCAA ACAGGAA	0,0	GTGCAAGGGACCTAGCTAA TCC
Ots_110201-363	A	T	TTTTAAAA+CTGG CATCCA	TTTTTAAACTGG CATCCA	GTTTGGCTATTGAAATTATACAT TAAAACATGTAGCT	0,0	CCATGGCATCCTGTAAAGA ACAACA
Ots_110381-164	A	G	ATTTGCGTCTTCT CCC	TTGCGTCCTCTC CC	CTCTTGTTTGCTATGGGAGATGT AGT	0,0	CCGTATCCTAAACCCTTCAC TGTT
Ots_110495-380	G	C	CATAGAC[AG]GG GGCCAT	CATACAC[AG]GG GGCCAT	GCCTAGGTATGTACGAACTTCA CA	1,9,0	AGGCTTTTTTCAGATGGTCGT ATGA
Ots_110551-64	C	A	ACGCTCGGAACA TT	ACGCTCTGAACA TT	GAGTGGTCAAGGTTTCAGTTTCT G	0,0	GAAATGGACAGACACAAGG TCAAAC

Ots_110689-218	T	G	CACCAATCAATT AATTATT	ACCAATCAATTC ATTATT	GTATAAACTAGAGTCCAGTGTTA TGTTAATGTCTT	0,0	CATGGCAGACAACAGTAGA GAATATGA
Ots_111084b-619	C	A	TCCATGG[AT]AA CGGACAAT	TCCATGG[AT]AA CTGACAAT	TTGTGGAATTACACCTTCAGAGT TCAAT	0,0	GCCTGTTTGGCTTTCTTAAA CTGAT
Ots_111681-657	G	T	TAGCGCAAACCC CGAACC	CGCAAACACCGA ACC	CTGAGCTTTTTCAACTTACTTGTT GGA	0,0	GGCGCAGCAGCAACTG
Ots_112208-722	C	A	TGTGAGGGCGGT CTT	ATGTGAGGTCGG TCTT	CTGCATGAACGTTAACTCAAATA AAAGGT	0,0	AATGAGTTCTACTGACATTG TATACTAGAATAAGTATCA
Ots_112301-43	T	C	CGTCGCATTTCAGC	CGTCGCGTTCAG C	GCATGGCTGCCCTAGAACA	0,0	TCAGAACATTTTCCTTCAGCT TCGT
Ots_112419-131	A	T	AAGCGACTTGAT TATC	AGCGACATGATT ATC	GTGGGTAATCGATGCCAAAGAG AT	0,0	TGGCAGTGTTTTCAACTAGC TTTG
Ots_112820-284	C	T	ACTCACACTCGA GTGACT	ACTCACACTCAA GTGACT	CATAGATGTTTATATGAAAAACC TCCCCTGT	0,0	GCATCCAAAAAGACGTGTG TGTTT
Ots_112876-371	C	A	CATCACAACGAT GTGTG	CACATCACAAC ATGTGTG	GCCTACAGCAAATTCAGCTACAC AT	0,0	TGGACCTTCAATCATCACAG CTT
Ots_113242-216	C	T	ATTACCAACGGA GAACC	TTACCAACAGAG AACC	GAGGCCTAATGTCTCTTGAGT	0,0	GACATCTTCAACAAGTGTTT ATTCACC
Ots_113457-40R	C	T	CCCT[AG]TTCTCC AATCCATAT	CCCT[AG]TTCTC TAATCCATATG	CCCAAGTGAGTGAGTGTCAGT	0,0	ACTACAACAGGTGTTGATA ATAGAATCATTCTC
Ots_115987-325	T	G	ATGCATAAAAGG TAATTGTG	ATGCATAAAAGG TCATTGTG	GGAGGTGTAGTGAAATGGGAAG AT	0,0	GCATTCAAGTGAACCAGTAGT GCTAT
Ots_117242-136	A	G	CAGCACATAACT TGACCTC	AGCACATAACCT GACCTC	GTGACAGGAGACAGAAAGAGAC ATT	0,0	TGGTCCTCCCTGTCTCTATC TACTA
Ots_117259-271	T	G	CTCTCCTGATCAC TCTGT	CTCTCCTGATCC CTCTGT	ACACCCACTTCAACCTCCATAAC	0,0	GCCTCAGAGCTTAGCTTGGA
Ots_117370-471	G	T	ACGGAACAAATA AGACATTT	CGGAACAAATA AGCCATTT	GTTGGCTCCTTCAATTCAATTTG GA	0,0	TGCAAACACAGAGGAAAGG GATTT
Ots_117432-409	A	G	TTTAGACTTTGCT CTATAACAG	ACTTTGCTCCAT AACAG	TCATCAAAACATGCCTCTTCTGT GT	0,0	TGTTGAACCTGTCACCTCTGT CTTC
Ots_118175-479	C	T	AGAATGAAGTGA AAAGAA	AGAATGAAGTA AAAAGAA	TGCGCGTCTCATTCAACCAT	0,0	ACCTTACGTCCTAGGTAGGA AACA
Ots_118205-61	T	C	TAGTAGCCCCTAC ACCTC	TAGCCCCTGCAC CTC	CCATACAGCCAGTCCAGGTG	0,0,4	ACTGGACAGGGCTGGGT
Ots_118938-325	C	T	AGAGATGCAAAG TGGAGTT	AGAGATGCAAA ATGGAGTT	ATTTTCAAACAGGCATTTATCAT TGGTGAA	0,0	GGTCTGTCCCTCATTCTTTG CA
Ots_120950-417	A	T	CTGGACCAGAAC TCTGA	CTGGACCAGATC TCTGA	CAGACAGGTCACCATCACACT	0,0	TGGTGAAGCTGTAGGAGAA GGA
Ots_122414-56	C	T	TGTATGACCTCTG ACCTGT	TGTATGACCTCT AACCTGT	GCACCGTATCAACGAGCTCAT	0,0	TGCATGGATTTCTTTGTGT TGTTG

Ots_123048-521	A	C	TCACATCCAACTC AGTACT	CATCCAACGCAG TACT	CTCAACAGTGCACCTCCCTTAAT T	0,0	CCAAACACACCCTTCCATAA TCTCT
Ots_123921-111	A	G	TGCTAAATGGCA TATATTAT	CTAAATGGCACA TATTAT	TCGCTAGGCAGAAATATAGGGTT CT	0,0	GAGCATGGCGCTTGCA
Ots_124774-477	T	C	CCACCGCCATCTG ATA	CACCGCCGTCTG ATA	AGTTGTTCTTTTTATATTGTGTTT TTATTCCATTCCA	0,0	GCCAAATAAAAAACAAAGCA TGAACACA
Ots_126619-400	C	T	AGAAAGTTCTAG AAATAATT	AAAGTTCTAGGA ATAATT	GGATGGTTGTCATTTCTCTGCAA A	2,0	CCGGGATACAATAATAATA TTTGGTTAAGAGTTTTTT
Ots_127236-62	T	A	TCTCTTATCTGAG TTCTGC	CTCTTATCTGTG TTCTGC	TGGAGAACTTGCACTGAATGTGA AA	0,0	GCTGTTGGACCTTGACTTTA ACAAATT
Ots_127760-569	C	T	CCGGTTTACCGAT TTG	CGGTTTACCAAT TTG	CTGCTGGCGCAGACATG	0,0	CGTTATAGAGGATAGTTTGG AGGAAGGA
Ots_128302-57	C	T	CCTGCAATACGA CCAAC	CTGCAATACAAC CAAC	GGTTGCAGGGCAGAACTGT	0,0	ACCCATCCAATAACCCATTT TCCTT
Ots_128693-461	C	T	CTGGTACCCA	CTGATACCCA	TCAATGTTTCATCAATGCACTTCC TGTA	0,0	GCCTGCAGGAGAAGGTAGA GTTA
Ots_128757-61R	A	-	TTGTGCATTTTCC CC	TGTGCATTTCCC CC	CGTGTCCGGCTTCTTTTATTTTCAT T	0,0	GATGGGTATGTTAATCATAT TACCAGCGTAA
Ots_129144-472	C	A	TGGGTCTCGAGC CTGTA	TGGGTCTCGATC CTGTA	CTGTTAGTGCAGAAGACGTAGCT	0,0	GCAGAGCTATTGAGCCAAG TTACAA
Ots_129170-683	C	A	ATTAGAACTCGT AGAACTAT	ATATTAGAACTC GTATAACTAT	AACCCTATGGGAACTCGTAGAA CT	0,6,0	GCTAGGAGTTCTCAAAAGG GTTCT
Ots_129458-451	T	C	CATCTGGCAATG CCTT	CATCTGGCAGTG CCTT	TGGGACCCACATAAAGCAACTG	0,0	GACATAAGACCCATTTAGCC CCTTTT
Ots_129870-55	A	T	ATGCATTACCTG TATTAT	TGCATTACCCAG TATTAT	GCATGTAACACATTATTTGGCAT ATGTACT	0,0	CAGTACACTGGAGATTGCA ATGTT
Ots_130720-99	A	G	CCTGTCTCATTCC C	CTGTCCCATTCC C	CGGTCATTGTAAATGTCAACGGT TT	0,0	TGCTTGCATGTTCTTGGTGT AGTAA
Ots_131460-584	T	C	CTATCAAAGCAA TACATTG	CTATCAAAGCAG TACATTG	CCTATTTTTGATAGGTCATAGTG AATGGGATAG	0,0	CTGTACTCCTCCATTTCCTTTT CACT
Ots_131802-393	C	T	TGTTGAGAAATG AAGATGAGTAA	TCGAGAATGAAG GTGAGTAA	TGATTGTCTCATGGCCAATTGTC A	0,0	TGTAAATTCCACTTGGCAAT CTTTGG
Ots_131906-141	A	T	CACGGTTTACACT CCTATTA	ACGGTTTACACT CCAATTA	GGCTCGAACCACCCAGTTTA	0,0	TGCCCAACTGGTTTGCAATC
Ots_94857-232R	T	C	CAGGATAATAAC AAACAAG	CAGGATAATAAC GAACAAG	GGCACTCTCCCTGGCTAGA	0,0	CCCCATCACTTCTCTGGCTT TAAAT
Ots_94903-99R	G	T	CAAACCAGCAAA CAT	ACAAACCAGAA AACAT	CCGTCTGAGTAGGAGGATCAAT ACA	0,0	TTTGGATCCAGCTCTCCGTA TAGA
Ots_95442b-204	A	T	TGGTTCCCCAAAT TT	TGATGGTTCCCC TAATTT	GTCTCTCTCTTTGCATCATTAC ACT	0,0	GGACTCTTGAGCTGTCTGGC TATAT

Ots_96222-525	C	T	TGTAGCTAATTTT AAGTTCTC	AGCTAATTTTAA ATTCTC	GCTCTTGCCCATCTGTAGGAT	0,0	GGCGCAACATATGTATTAA GCAACT
Ots_96500-180	G	T	AAAACAAATCAT TTTTCG	AAAAACAAATA ATTTTTTCG	CAGGTCTGGTCTACATCGAACAC	0,0	GATCATGTCAGATAGGATG CTGAAAGT
Ots_96899-357R	T	A	CTGAATGTTTTT TTAATCTTT	CTGAATGTTTT TTTTATCTTT	TCTCCTGAACATAATTTAGACCTC TGAATGT	0,0	CCTCATATTGCTTTCATCTG AAGAGAGA
Ots_97077-179R	G	T	TCACAAATGTATC CTAAAGC	CACAAATGTATA CTAAAGC	CCTGAACAAATACTTAACGCTCC AGTT	0,0	GTAATAATACTTCACACCAT TGCCACTTC
Ots_97660-56	A	T	ACGAGACAGATA TTC	ACGAGACTGATA TTC	TTCCCTAATCTGACGTACTACCA ACT	0,0	CGCCACTGACGTTTCATTCCA
Ots_99550-204	C	T	AAGGCTTTGGTTG TTTG	AAGGCTTTGATT GTTTG	TGACAGATTTTCACCTTTAACTAG CTAAGC	0,0	GCAACCTCTTTTCACACTTCA GTAAC
Ots_afmid-196	G	C	CAAAGTCAAAGA TCCTATTA	AAGTCAAAGATC GTATTA	CGTGGAGTAGGTGGTTACAGTTT AT	1.9,0	CTCGTAACAAGCTACTGTAG TGTA
Ots_AldB1-122	C	T	TGTTGGCGAAGT G[GT]GT	TGTTGGTGAAGT G[GT]GT	GCCATGGAGGACTGGATGA	0,0	GCCACCACTACTTGCTGAGA AAATA
Ots_AldoB4-183	T	A	CTGTGTGTCTAAG ACAAT	CTGTGTGTCTAT GACAAT	TTTGTGCGTAAAGTCAGGTAGTG T	0,0	GTGCATGCCATGAGAACTTT GTTT
Ots_ARNT	G	T	TACAGATGTCATT TTAC	CTACAGATGTAA TTTTAC	CCACTGGCTGTGGAGCTT	2.2,0	GGGTTCAGTGATAGTTGGGC AAAT
Ots_arp-436	A	T	CTAGGTGAAACT TTTTTTAA	CTAGGTGAAACT TTTTAAAA	GCCCTGGAGAAGTACGTTTTTAA CTAA	0,0	GCAACCATGTCAACATTGCA CATAA
Ots_AsnRS-60	T	C	TGAGTCCCTGACC AGC	AGTCCCCGACCA GC	CCGACGCCTCACTGAGT	0,0	TGGTTTTTCAGGTCATGGTT TCCA
Ots_aspat-196	G	C	CACTCTTTATATC CACACC[GA]	CAGTCTTTATAT CCACACC[GA]	CCTGAACAGGTACACACAAACG A	0,0	TCCAACCTGATGAATATGACC AACATGAAT
Ots_BMP2-SNP1	C	T	CCCACTTCGCTGA AGT	CCCACTTCACTG AAGT	ACTGCCACAGACACGAACTC	0,0	GCCACTATCCACTCGTTCCA
Ots_brp16-64	T	C	AAGTCAGCATCTT TCA	AGTCAGCGTCTT TCA	ACTCTGGGTCCAGGAGGTTTT	0,0	CTGACGAGACCATGCACCA A
Ots_Cath_D141	T	C	TGGGAAGCAATC AA	AATTGGGAAGCA GTCAA	CACTTGTTCTGCACACTACTTGT C	0,2	CACACATGGATTTTGCCTGT CTAAA
Ots_CCR7	C	T	CCACGTAGCGAT CG	ACCACATAGCGA TCG	CTGCTCACCTGCATCAGTGT	0,0	CCATGGTGGTCTGGACGAT
Ots_CD59-2	G	A	CTAAAATGTCAT GTAAATAT	ACTAAAATGTCA TATAAATAT	CATGTTACCCAGCTAAAAGTCTA TAGCA	0.5,0	TGTTTATCTCTGAGTGAAAA AGGTGTGT
Ots_CD63	A	C	AGATCATGGGAA TCATAT	ATCATGGGCATC ATAT	TGCATGTTTTCTAACTGTGTTTTT GTGT	0,0	TGAATGCCCCCATCAACA
Ots_cgo24-22	T	C	CCAGATGAACAA CTTCAC	CCAGATGAGCAA CTTCAC	AGGTCCTCTGTGCGACCTA	0,0	GGAGGCGAGGTCTGGTG

Ots_CHI0602 7687_143477	G	A	GGAGATAGTCAG GG	GGAAATAGTCAG GG	GCGAGTGTTAAAAGGGTCAAA	0,0	TCTCAAGCCATAAGACGGG TA
Ots_CHI0603 5945_4547	C	T	CCGCAACAGATC	CTGCAACAGATC	AGCGAGGCTTGCGTTTTACT	0,0	GTGCAGTCTGGGCTTGTCTT
Ots_CHI0604 8618_5222	T	G	ATTGTGCTTATCA CA	ATTGTGCTTAGC ACA	GCAATTACCCATGACTCTGTGA	0,0	GCCAAAAAGAGACCGAATC A
Ots_CHI0610 5101_16717	C	T	CCTCACATACTCC CTT	CCTCATATACTC CCTT	AAGGCCGTGAACATCTGTG	1,8,0	ATCGCAGGCTAGCTTTTCAA
Ots_CHI0610 5101_18523	A	G	GGCGGCTCGGAA AATTATTTT	GGCGGCTCGGGA AATTATTTT	GCGGTGGGATACCTCCTCTA	0,0	GCGAGAAAAGCACTGAATG A
Ots_CirpA	C	T	CAGTTCGTGAATG CATT	CAGTTTTGTAAT GCATT	GCTGTGATTGTGCTCTAAAGACA TG	0,0	CTCCCACTTAGCATTTCCTAC CTT
Ots_cox1-241	C	T	CACTACGGTAAG ACCAT	CACTACAGTAAG ACCAT	CACTGAACTGTAAGCCATTGTGA TT	0,0	GTAAATGTAGTATACAGTAT AGGCATCGTAGGT
Ots_CRB211	A	C	CTACCGTACTGA ACTC	CCGTACGGAACT C	CAACGCGGGAATGGCTTTTAA	0,0	GCCAGAGTCGCCAAAATAG TAGAAT
Ots_crRAD1 0447-25	C	T	AGCTAGCGCTCCT C	AGCTAGTGCTCC TC	CCGTTGCAGGACTCATCAGT	0,0	GCGTGTTCAACAGCAGTG
Ots_crRAD1 1620-55	C	T	AGAAGCCCAGCT CC	AGAAGCTCAGCT CC	TGGGATAGAACAGGAGCTTAAA CA	0,0	TGTCTTGGTCGCGCAGTT
Ots_crRAD1 2037-39	A	G	CATTCAAAAAGT AT	CATTCAAAAAGT AT	TGCAGGAACTTGCTATGCT	0,0	TGTGAAAAAAGTCAAGGGG TCT
Ots_crRAD1 3725-51	C	A	GAGGCCCCAGAT TC	GAGGCCACAGAT TC	TGCAGGAGGAGGAAGGCA	0,0	AGAGCTGCCAGGTGGAGT
Ots_crRAD1 6540-50	C	T	ATTAAACGT[CA]T GGA	ATTAAATGT[CA] TGGA	TGTGTATTTCGTCGACCGGA	0,0	TCACCTGACCAAAGCACTG G
Ots_crRAD1 7527-58	C	T	TAGCTCCGAGCT AA	TAGCTCTGAGCT AA	TGCCGCTGGATTTATTGACA	0,0	GCGTCAGATCAGCTGGTCT
Ots_crRAD1 8289-33	T	C	GAATGGTGTTAA AT	GAATGGCGTTAA AT	GCAGGGAAAACCTGGTCAGGA	0,0	AGGTGAACCTCCGTCCCA
Ots_crRAD1 8492-65	C	T	TTATGGCTATTAT T	TTATGGTTATTA TT	GCAGGGCGCAAAGTTCTT	0,0	CAGTGAGCGACTGTAATCTG A
Ots_crRAD1 8937-60	G	A	CTCCTCAGGTGG GC	CTCCTCAAGTGG GC	GGCACAGCGACAGGAGTT	0,0	TGAGCTGGTGCGTCTGAG
Ots_crRAD2 0262-46	A	G	GGTTACA[TC]CCC AAA	GGTTACG[TC]CC CAAA	CCTCTGCTGAGTTTGAGGGG	0,0	TGAGCAGAGCCTATGAGGA CT
Ots_crRAD2 0376-66	G	A	GGGA[TA]GGAGT ATTT	GGGA[TA]GAAGT ATTT	GGGAGGCAGGCAAAAGGT	0,0	GGTTCACCACCAGCCTTCT
Ots_crRAD2 0887-70	G	A	GAACCTCGTCGTTG G	GAACCTCATCGTT GG	CTGCTTGTAGCCGTTTACG	0,0	AGAACACATCTGGCCAGGT

Ots_crRAD2 1115-24	C	T	CACACACATGCA CG	CACACATATGCA CG	TGCAGGTGGGACTTAAACACA	0,0	ACCTGTGGCAACGGTTGA
Ots_crRAD2 2960-32	C	T	CGACACCACTTA CA	CGACACTACTTA CA	ATCAGGTCTGGGGCGACA	0,0	TTCACCTCTGCCATCGCC
Ots_crRAD2 3631-48	G	A	GGGCTTGGGGGC AT	GGGCTTAGGGGC AT	GCCATATCCCGGGGCTTG	0,0	TGCCTCTGAGCACTGACTG
Ots_crRAD2 4807-74	A	T	ATGATAAT	ATGATATT	TGCAGGAGAGCAGGGTAGA	0.8,0	CGTGCCTAACATCATGTGCA
Ots_crRAD2 5367-50	T	G	GTATATTTAGAAT G	GTATATGTAGAA TG	ACTGCAGGCGTCATGCTT	0,0	TGGACAAAAGACCACAGGC T
Ots_crRAD2 55-59	T	C	AACTGTTCAAAC CC	AACTGTCCAAAC CC	TGCAGGAGCTGTGATGGG	0,0	GTACGGAGCGTCACTGCT
Ots_crRAD2 6081-28	T	G	TGGAGGTGGAGG AG	TGGAGGGGGAG GAG	GGGAGAGGGAGACGTGGA	0,0	TCACCAGCTCCTCCTCCTC
Ots_crRAD2 6165-69	C	T	CTCT[GA]CCCCTG GAC	CTCT[GA]CTCCT GGAC	GGGCCACGGGGTTGTAAA	0,0	TCCCAGGATGCAATGGGA
Ots_crRAD2 7164-55	A	T	AATTTGAATGAC CA	AATTTGTATGAC CA	GGAGGCTCTACGTAGGCCT	0,0	ACAATATCTGACACTGACTT GGTCA
Ots_crRAD2 7515-69	T	A	GCATTTTAAAAAT C	GCATTTAAAAAA TC	CAGATGGTGCAGGCCGAA	0,0	ACTCGTTGTGATTCCAGCCA
Ots_crRAD2 806-42	C	A	GTTTGGCATAAA GT	GTTTGGGAATAAA GT	GCAGGGGCAGACTGAAGG	0,0	ACTTCATGCCAATCTCACTA AACA
Ots_crRAD3 3491-71	C	T	GAGAGCCGAGCT TT	GAGAGCTGAGCT TT	CAGTTCGCTTCTCCAGGGA	0,0	TGTGGGTAGCAGACTGACG
Ots_crRAD3 4397-33	C	G	AA[GA]GTGCCTT CCCC	AA[GA]GTGGCTT CCCC	TGCCTAAACACTCCCAAGGT	0.4,0	GTTCCGTTTTTTGTTCCGCGA
Ots_crRAD3 5313-66	A	G	TTTAAGATGTAGT T	TTTAAGGTGTAG TT	TGCAGGAAGAGTTCAGAGAAAT CT	0,0	GCTCGTTGCAGGTAGAAAT GT
Ots_crRAD3 6072-29	T	C	AACCTGTGTGATT T	AACCTGCGTGAT TT	TGCAGGACCAACTTTCTCAT	0,0	GGCTGACTGGTGAAGGGG
Ots_crRAD3 6152-44	C	T	CTGCCACCCTTTG A	CTGCCATCCTTT GA	CAAAGTGCAGGTGCTGGC	0,0	CCAGCCAGGTGTTGAGCA
Ots_crRAD4 4588-67	C	T	GTGA[AG]CCAAT CAAT	GTGA[AG]CTAAT CAAT	CGCAAGTCAGCAGGGTGA	0,0	TGGGGTTTTAGGCTGGGT
Ots_crRAD4 6081-56	C	T	GCACCACTGGAC CC	GCACCATTTGGAC CC	GCAGGGTCTGTGTGGGTT	0,0	ATGAGGACACTCCGCCCA
Ots_crRAD4 6751-42	C	T	TTTCTACTTAGTA A	TTTCTATTTAGT AA	CAGGAACCTGCTTTAATGCTCT	0,0	GCTTCTGCAGGGGGACAA
Ots_crRAD4 7297-55	T	C	TAGCCGTCACCG AT	TAGCCGCCACCG AT	CTCCCTGTTGCTAGCCG	0,0	GGACGACCAAAGGTAGAAC CC

Ots_crRAD5 5400-59	C	T	CTAACCCGGA[CA][GA]AC	CTAACCTGGA[C A][GA]AC	CGCAATGAGCCAACCCCT	0,0	CTGGTTTGTTCGCCGGGCT
Ots_crRAD5 5475-26	T	G	CCATTTTAATTCC A	CCATTTGAATTC CA	TGCAGGGTTGGGGACAATT	0,0	AGTCTATTTCCCGATTTGAC TGGA
Ots_crRAD5 7376-68	T	C	ATAAAGTGTGTT AT	ATAAAGCGTGTT AT	TGCAGGCATCATGCTTAATAACT	0,0	ACGTGACACAGGTCTGGG
Ots_crRAD5 7520-66	T	G	TTTTTGTTCAAAA G	TTTTTGGTCAAA AG	ACAGAGCTGTGTCTACCAGA	0,0	ACCCTCTCTTGGCCTTGC
Ots_crRAD5 7687-34	T	G	ACAAATTAATTA AA	ACAAATGAATTA AA	TGCAGGGACGGGGCT	0,0.7	TGCTGTTGTCTTGGGTCTCT C
Ots_crRAD6 0614-46	G	T	AAGATGGTATGT AT	AAGATGTTATGT AT	TGCCGTGAGAACTGGTCA	0,0	TTTCCTCCTCTCTGCCTCA
Ots_crRAD6 0620-51	A	G	GTACGGAAAAAA CA	GTACGGGAAAA ACA	CAGGCAGTCACTGAGTCCG	0,0	TTTGAGCACCGTTTCCGA
Ots_crRAD6 1523-71	A	G	CAGAGCATGTGC TG	CAGAGCGTGTGC TG	GCCAAGTGATCAAGTGCTTGT	0.2,0	CCAGCAGTTCAGTTGCGG
Ots_crRAD6 6330-60	G	T	AGAGAGGGGTCA AA	AGAGAGTGGTCA AA	ACTCTCCCAGAAGGATTCAGAG A	0,0	TCCCAAAGCATCCTGCCA
Ots_crRAD6 9327-53	G	T	ATAGGAGAATTG GA	ATAGGATAATTG GA	GCCATTTGACCAACGGAGC	0,0	ACTCATACAGTATTTCCGCC TGT
Ots_crRAD7 3823-60	T	A	GCACGATG[CT]A GAAC	GCACGAAG[CT]A GAAC	GCAGGAAGCAAAGTTCGGTG	0,0	AGCAACTCATCGCGTGGT
Ots_crRAD7 4766-28	G	A	AGACTGGTAAAA G[AT]	AGACTGATAAAA G[AT]	GCTGACCACCGACCACAG	0,0	AGCTCTGCAGTAACAATGG GA
Ots_crRAD7 5581-70	A	G	GAACTTAAAACA CT	GAACTTGAAACA CT	ACACATGGCTCGTCTGCA	0,0	GGAGCTCAGGGTGCAGGA
Ots_crRAD7 6512-28	A	T	TAAAAAAATATA AA	TAAAAATATATA AA	GCAGGGACAGGGCCCT	0.3,0	TGGTGCTGGGTGCTGTAC
Ots_crRAD7 8968-46	C	T	AG[CA]AATC[CA] CACAGC	AG[CA]AATT[CA] CACAGC	CCTGCTCTGTGTCTGGGC	0,0	GTGAAGACGACCCCGGTG
Ots_crRAD9 2420-25	G	T	CAATCGGAAGTC GG	CAATCGTAAGTC GG	AGTGCAGGTCTCCAGATTTACA	0,0	ACCGAAGTGTATGTAAACTT CCGA
Ots_crRAD9 615-69	T	C	TATTGGTCAGGG AA	TATTGGCCAGGG AA	GAATGCAGGGCCAGGGAG	0,0	ACTCCCAGACCATCCAGCT
Ots_DDX5- 171	C	T	TTCATAATTGAAC GATTCA	CATAATTGAACA ATTTCA	ATGACCAATTGAAGAGTTCTTCC GT	0,0	CAAAGCCAAACGTCACATTT ACACT
Ots_E2-275	A	G	CCCCCATATTGCT G	CCCCACATTGCT G	GGTGCCACTTTAGTATAGCTGCT TA	0,0	CCCTACCCCTGTGTTCCA
Ots_EndoRB 1-486	G	A	TCCTTCTCACGCT TCT	CTCCTTCTCATG CTTCT	CCTTTGGGTCTGCTTGAGGTT	0,0	GGAGCCAAATCCTAATGCT GAAGTA

Ots_EP-529	A	G	CAGTGTCAATTTTC GGC	ATCAGTGTCAATC TTCGGC	GCCCTGCCTGCAACTTC	0,0	GAAACCAACGTCTTGATGTA GACCTA
Ots_Est1363	A	T	CCATCCTGTCTTG TCTG	CATCCTGTCAATG TCTG	GGTGATTTTGCCACAGAGTAGAG AT	0,0	AGTGTTAAATGTAACCTTGCA TATACAGGCAAT
Ots_Est740	T	C	TCTGGATGGAAC CGTTAG	CTGGATGGAGCC GTTAG	GGACTCGTGCTTGAGGAAGATG	0,0	TGCATGGCTCCAACCTCCTT
Ots_ETIF1A	A	C	CAACTGAAGAAA ATAATATG	CTGAAGAAAAG AATATG	TCTGAACCTACCAAAGGAACACT TG	0,0	GAGAGAAAAGGAGAAATGA TTGCCATT
Ots_FARSLA-220	G	A	CCTTGGATGGGA	CCTTGGATAGGA	GTTCGTGGGATTGTTCAATGTTC AT	0,0	CTTGGACAGGCTCACATTAC CATA
Ots_FGF6B_1	A	C	CCTGTTATCAGAC CCAAAT	CTGTTATCAGCC CCAAAT	GAGACAAAGGTTTGCAGGTTTCAT G	0,0	GGGAGCCATGCACTAATAT ATTGGA
Ots_GCSH	C	T	TATCTGGGCGGG CTG	CTATCTGGACGG GCTG	GTTCTTTTTTAATGATGACTACAG GTCTTTTCAC	0,0	GCTACTTTACATAATACCAT TTGAGCTGAGA
Ots_GDH-81x	C	-	TGTTACGGGACA TACT	TCTGTTACGGAC ATACT	CTTTTCTGAATTAGTGCTGTGCTT GT	0,0	CCAACTTCTTCAACTCTGTC AGTGA
Ots_GH2	A	T	TGACTCTCAGCA[TA]CTG	TGACTCTCTGCA[TA]CTG	GCGTACTGAGCCTGGATGACA	1.8,0	CCCCCAGGTTCTGGTAGTAG TTC
Ots_GnRH-271	C	T	CAATGAATACAA TATCTAACCTAAT	AATGAATACAAT ATCTAATCTAAT	CAGATGAAAAATAAATAATTGG GCCATTAGGAA	0,0	CAGAGAGACTGAGACCATA TGATGTAGT
Ots_GPDH-338	G	A	CCACTACTTAACG TGCTTT	CCACTACTTAAC ATGCTTT	CACTAAATATTCCTTATCATTTC ATACTAAGTCTGAAGAA	1,0	AGCTGATACACAATCAAAA CACAAAACAT
Ots_GPH-318	C	T	ATCAAGCTGACG AACCA	CAAGCTGACAAA CCA	GGTGATAACAGGTGTTGCACCA A	0,0	TCAGGTGGTGGTGGACAAC
Ots_GST-207	G	A	ATGAGAGAGTCT TTCTCTGTT	ATGAGAGAGTCT TTTTCTGTT	GGAGAACATGCATCACCATTCA AG	0,0	TCAGCAAACGAAGGCTATG TAGAAT
Ots_GST-375	C	T	TTTCTTGTAGGCG TCAGAG	TCTTGTAGGCAT CAGAG	CAGCCCGTCCCAAAATCAAG	0,0	CAGGAATATCACTGTTTGCC ATTGC
Ots_GTH2B-550	C	G	ATAACATCTGCA GCATTAA	ATAACATGTGCA GCATTAA	CACAGGAAGGACGTGTTTTGATG	0,0	TGACTACCCGTTGTACCAAT GAAC
Ots_HFABP-34	C	T	TCGAACTCCGCTC CTAG	TCGAACTCCACT CCTAG	CAAGAACACCGAGATCTCCTTCA	0,0	TCGGCGGTGGTCTCG
Ots_HMGB1-73	G	T	ACTGTATATGTTA CGTTTTTC	ACTGTATATGTT AAGTTTTTC	TGCTTCAGTGAAAATAAGCGTGA GA	0,0	GTCGAGCGGTATGAATACTT TCTGA
Ots_hnRNPL-533	A	T	CATTTACCAGTTC TCACACAC	TTTACCAGTTCA CACACAC	TCTTTGATATTGAGCTCATAAAA GCAAGGT	0,0	TCCTTGTTTCATCCATCAGGC ATAAAA
Ots_hsc71-3'-488	C	T	TTTCCAATGGTAT AGATATGA	TTTCCAATGATA TAGATATGA	TGCATCCATTTCATACCTGACCAA TT	0,0	TTTGGTTAGGCACACGATAA TTTGC
Ots_hsp27b-150	G	A	[CT]GATCTGGACC AGGCT	[CT]GATTTGGAC CAGGCT	TAGGAGTTGGAAAGACTGCACA	0,0	CCCATTGGTTCTTTGGTGTT

Ots_Hsp90a	G	C	ATTTGACTTGTCT TTTT	ATTTGACTTGTG TTTTT	GTCGTTTTTTCATAGAAAATAGCT CACAGTT	0,0	ACAGTATACCGGCTGCCTAT TCATA
Ots_HSP90B-100	C	T	TCTATGGTGTGAT TCATT	TTCTATGGTGTA ATTCATT	CACCTTAGTTCCACGCAACATG	0,0	CTGCGTGTATTGTAGTGGTG ACA
Ots_IGF-I.1-76	A	T	CTGCCTAGTTAAA TAAAATA	CTGCCTAGTTAA ATTAAATA	GGTAGGCCGTGAGTGTAATAAATA AGT	0,0	GATGGAGGCCACTGTGTTCT TA
Ots_Ikaros-250	G	A	ACAGAAGATTTT CGGCTGC	ACAGAAGATTTT CGACTGC	GAGGCTGACTTGGACTTTGC	0,0	GGCCTGTCAGCCAAGGA
Ots_IL11	T	C	AGCTCCATGCGG ACT	AGCTCCACGCGG ACT	CCTCCAGATGAGACCCACTCT	0,0	CAAAATGGTGTCTCAAACGA CTTCA
Ots_IL8R_C8	C	T	CTGGACGCCGTT ACA	TGGACGCCATTA CA	CGTGGTGTTTCGCCTTCCT	0.5,0	TGTCGGCCATCACTGTCATG
Ots_IsoT	T	C	AACCAGTAGAAT AACC	CAGTGGAATAAC C	GACTCAGGTAAGGAAACATCAA TGTC	0.5,0	GAAAGCAAAGCATTTTATCC ACCACTA
Ots_LWSop-638	T	C	TTTAACAAGAAA ATTATACATTTT	CAAGAAAGTTAT ACATTTT	CAATTACTCTTTCTCAGCCCTGT GT	0,0	GCGGTAAGATGCAGTTTTAC ATGGA
Ots_mapK-3'-309	T	G	ATGCTATTAAATG AATATTC	ATGCTATTAAAT GACTATTC	GGCCACTGTCATAGAATTAGGCA TT	0,0	CGTGACCCTTGTAAGTGA AGC
Ots_mapKpr-151	A	T	CGTATGTGCAAT GCATG	CGTATGTGCATT GCATG	TGTTGTCTCGGACTGCATGAC	0,0	GAAGGCACAGAGATGAAGG ACAT
Ots_MetA	T	A	CCTTAAGCATATT TCT	CCTTAAGCGTAT TTCT	GATCATTTATCAAGACTATAGGC TATGGATACG	1.8,0	AGTTGAGTTAAGTAATTGGT AATTAGCCTGTT
Ots_MHC2	T	G	CTGGAGCGTTTCT GTA	CTGGAGCGTGTC TGTA	GTCCTCAGCTGGGTCAAGAG	0.5,0	GTAGTGGAGAGCAGCGTTA GG
Ots_mybp-85	C	T	AGAGCATGTAGT TTTG	AGCATGTAATTT TG	CAAGGGATGTGACAAATTAATC AAACACATAA	0,0	AAGAGGTCTAATAAATCTCC AATGTAAAAACGT
Ots_Myc-366	T	C	TCTCTGCTCATCT GTC	CTCTGCTCGTCT GTC	CCTTAGCTGCTCTTTGAAGTTGA CT	0,0	GGCTATAGAGTGTATTTACA GCATGCA
Ots_myol1a-384	A	C	ACAGATCCATCC ACCACT	AGATCCAGCCAC CACT	CTCCCCCCTGGACTTTGG	0,0	GCTCTATTGCACCGTGTCT G
Ots_myod-364	T	G	TCATCTTTTGTTA TTTCCTTG	ATCTTTTGTTCTT TCCTTG	GTGTGTGTGTGTGTGTGTCATCG T	0.9,0	TTTACACATATACAAAAATG GTCCTCTATTGTCAT
Ots_NAML1-2-SNP1	A	G	AAACCATTTTCAT TCTTTTG	CCATTTTCACTC TTTTG	TGCCACCTCAGTTTTAGTGTAT ATCC	0,0	AGCGCCAACCTGTCACT
Ots_nelfd-163	A	G	ACCCACCAGTGT CATT	CCACCAGCGTCA TT	CTCACTGCAAATCCAACCTTCATC AT	0,0	CCACTACATCCTCATCCAAG GTT
Ots_NFYB-147	C	T	TGTTCCAATGTAA AATGTATGC	TTCCAATGTAAA ATATATGC	CAGATGATAGCTTCAGTAAGTGG TTCA	0,0	CCGTCCACAGCACAAGACT ATAATA
Ots_nkef-192	C	T	AATAGGCCGACA TCAA	AAATAGGCCAAC ATCAA	CATTTAGCAGACACTCTTATCTT AGTGTCA	0,0	CGAATGTCCACCTCAGATGT TACAA

Ots_NOD1	C	G	CCAACGGCGACT TG	CCAACGCCGACT TG	GTGCTGCAGGAACCATGTG	0,0	CTGTGTGGACTGCTGTCTAA GG
Ots_nramp- 321	G	A	AAC[GT]GGCATG AACGACTT	AAC[GT]GGCATG AATGACTT	GGCCATCTTTCAGGACGTACAG	0,0	GCATGCTCTGCAATACGTTG AG
Ots_ntl-255	T	A	ATTCTTCCTC[TC] ACAATTG	ATACTTCCTC[TC]]ACAATTG	TGCAGTTACAAGCCTAAGACAAT CT	0,0	CAACTAAAGTAACACACCA GCAACTG
Ots_Ostm1	C	G	CCGTGGTATTGTT TCAA	CCGTGGTATTCT TTCAA	CCAGCCCCGTAACACACAT	0,0	GAGAGGAAGCAGAAAGGTC GTTTAA
Ots_OTALD BINT1-SNP1	T	C	CTACTGTTGTATT TTCTC	CTGTTGTGTTTTTC TC	CGCTGGGCATGGATGAGT	0,0	GGCCAACACTGCTACTTCCT
Ots_OTDES MIN19-SNP1	C	A	CCAGTCATGGGT CATT	TCCAGTCATTGG TCATT	GGTCTGTCTGTCTGTCTATCTGTC AATG	0,0	TGTGTGTCTTTGTTTCATTCCCT ACCA
Ots_Ots311- 101x	A	-	CTGAGATCACTTT GAGCAC	ACTGAGATCACT GAGCAC	AAATGAGGCCGTCTTTTACACT	0,0	GCAATACAAGCCCTTGATA ATGAAGT
Ots_OTSMT A-SNP1	C	T	AATTGCCTCATTG GGTG	AATTGCCTCATT AGGTG	GCCGAAAAATAAGCGATTAGTG ATGA	0,0	GCCCCATGGTAAACCTAATT AACCT
Ots_OTSTF1 -SNP1	G	T	CCGCCACCTTGGC T	CGCCACATTGGC T	CGGACAAAGAGCTACAGAAATG C	0,0	CGTCCCTCTTCACGCATGA
Ots_P450	T	A	CCCCGAAGTACTT TT	CCCCGAAGAACTT TT	TGAGCGAGATTTATCAAACCTGTC AAAGA	0,0	CCCAAGCGGGAGAACTTAC AG
Ots_P450- 288	A	G	CTATAAAGTTGG ACAGTTGG	AAAGTTGGGCAG TTGG	ATGTCAATATATTTCACTATAAT GATTGGAAGCCA	0,0	CACTGAACTCGAAGCTGTTA GGA
Ots_P53	G	A	CTGGGTCGGCGC T	TGGGTCGACGCT C	GGAACCTCCTCTCCCGTTCTG	0,0	GCACACACACGCACCTCAA
Ots_parp3- 286	A	G	AGTTACAAGTGG TGTTTCA	ACAAGTGCGGTT TCA	AGTCAGTGTGGTGTAGTGAAGA GA	0,0	CATTTGTGGAGTGTTTATTG AACAGTAACA
Ots_PEMT	C	T	TGC[AT]TTGCTAA GACTTG	TGC[AT]TTGTTA AGACTTG	AGAGCATTCAATTTAAAAGCTGA AAACGA	0,0	CTTTGATCCCTGCTTGCAGT ATTTT
Ots_PGK-54	T	A	CCACCATCAAGC ACTG	CCACCATCATGC ACTG	CTCATACTTTGTACCTGTGTGTTC CA	0,0	CGACCCAAGTGGCTCATCA G
Ots_pigh-105	A	-	TGACCTGAAAAT A[TC]ATATTTTT	ACCTGAAAATA[TC]ATTTTTTT	GCATTACTAAAAACTGGTGTGTG GAA	0,0	GTTTGGAATGTTTCTCTGAT TGTGTTAACAA
Ots_pop5-96	T	C	TTCTGTTACTGGA C	CTGTTACTGGGC	CTCTTGCTACTTGCAGTGTATCT CA	0,0	AGTTTGAGGGCTCTATTCTG TCATG
Ots_ppie-245	C	A	ATGTCTGAAATG AAAGCC	AATGTCTGAAAT TAAAGCC	TGTTTTTGGTCATGTATTTTCTCT GCTATTTTT	0,0	GGACTGGAGCTGCTGAACA TA
Ots_Prl2	A	G	ATGTATTGTTTCAT TTAATG	TGTATTGTTTCGT TTAATG	CCTGGTCTGTTTGTGATCAAGAT G	0,0	GGTTAACTCAAATAGAACA TACTCTGACACA
Ots_RAD454 3-52	T	C	TACATATGACTA ATGAAA	TACATACGACTA ATGAAA	TCTTTGGACTGTGTATACCAGGT GTA	0,0	GCCAGATGCTGTGTGTGTTT

Ots_RAG3	C	T	CTCTACAGTATG	CTCTACAATATG	CATTTCCACGAAAAGCCAGATG AC	0,0	ACAGAATAAAGTATCTTCCT CTTACATCACTACTAAT
Ots_RAS1	C	T	CAATCTATCATCG ACCAGC	CAATCTATCATC AACCAGC	TCATAAACATGGTGTCTTTCAGT CAGTT	0,0	CTGACATGTGAACTACTAA AGCATTTAATCAC
Ots_redd1- 187	A	G	ATTCTGACAGCTG TTTTG	CTGACAGCCGTT TTG	TTCTGGGTTGCCATACTCTTTCA AT	0,0	AGTTGAGACCTTCAGTTCTT AGGGTAT
Ots_RFC2- 558	A	-	TGCATGTAACAA ATAACAT	TGCATGTAACAT AACAT	AAGGTCTACTCCGGTTGTATTCTG GT	0,0	CAATACGACAGTACCGGTG TTAAACT
Ots_S7-1	T	C	TACAGGAGATAA GGTCGCA	CAGGAGATAGG GTCGCA	TGCCATCATAAACCAACCTAACAA GTAAC	0,0	CCTGGTTTAAAAACGGCCA ACTG
Ots_SClkF2R 2-135	A	T	ATTCAAAGTCAA ATTTT	ATTCAAAGTCTA ATTTT	CCAAATACAGACCAGCTACTTGT GT	0,0	CTTCAAGTCCCTGAATAATG GTACGT
Ots_sept9-78	G	A	CTCTTCGATGTCT AGACA	CTCTTCAATGTC TAGACA	GTCGATTACCGTTAGCTTCATCC T	0,0	ATTTCTCCTGTGTCTCTCTCT GTCT
Ots_SEXY3- 1	X	Y	NA	TCAGCGAAGTGG AGAT	GGTCTTGCAGTCAGGAGAGG	#N/A	CCAGGTGGTGAAGGTAGGA A
Ots_Six6- 3_AG	A	G	AGTAAATGTAT GA	AGTAAAGTGTAT GA	GACACCATAAACGCTGTAGCC	0,0	TCAACTTTGCAATGAAAATG ACAAG
Ots_Six6- 3_AT	A	T	GAGTAAACATTG AA	GAGTAAACTTTG AA	GCGAGCAATTATTTCGGGCAA	0,0	AAGGTAACTGAACTATAGG GTAGC
Ots_SL	A	G	TCAAAGATATGA TTCAATTAA	AAGATATGGTTC AATTAA	AATATTGGCTTTCTGAGAATGCA TTTGG	0,0	CCAAGATACTTCCTTTAACT TCTCTGTCA
Ots_slc7a2- 71	G	T	GTCTCTGACGGTG TGCTTTC	GTCTCTGACTGT GTGCTTTC	CCATTCCCATCGGCATCGT	0,0	GCAGCAGACACACCGAAGT A
Ots_stk6-516	C	A	AACATAACGGAC TCCC	TAGAACATAACT GACTCCC	TGTGTTTAGGATTGAACTGACCA TGTT	0,0	GTAAACTCCACCTGCAAGA AGGA
Ots_SWS1op -182	T	A	ATGTACTTTAACG ATTCATTT	ATGTACTTTAAC GTTTCATTT	TCAAAGACATCGAACACAAGAA CGA	0,0	GCAGGTAAATTCAAACGTC ATCATAAGAA
Ots_TAPBP	C	T	CAGCTGTCCAGTT CTG	CAGTTGTCCAGT TCTG	TTTCTCATCCTTCTCTTCCAGT CT	0,0	GGACAAACCAGCACTCCAG AA
Ots_TCTA- 58	C	T	CTGCCATGAAGT GCTAG	TGCCATGAAATG CTAG	ACCAGTACCTAAACGTTAGAAA GCAA	0,0	CGTTAGTTAGCTATGTCTGA AAGGCA
Ots_TGFB	C	T	AGCCTAGCTCTCG GAAG	AGCCTAGTTCTC GGAAG	GCCTCACATTTTACTGATGTCAC TTC	0,0	GAGCAGATCTCTTCAGTAGT GGTTT
Ots_Thio	T	C	CAGTGTATTAGTC ATTCTTA	CAGTGTATTAGT CGTTCTTA	TTTTAAAAATGGAGATAAACTCC TGACCTGAA	0,0	AATACCAAACCATGCCACT AATACCT
Ots_TLR3	C	T	CTGTGGTTTGTGG CGTG	CTGTGGTTTGTG GCGTG	TGCACCTGCGAGAGCAT	0,0	CTGGCGTTTGTTCGGTTCAG
Ots_TNF	C	T	CTGGCTGTAAAC GAAGA	TGGCTGTAAACA AAGA	CCAAATCCTCATCCCACACACT	2,0	CCGTTGCACTTGACCCTAAA C

Ots_tpx2-125	C	T	CAGGCGGTTCTCC	CAGGCAGTTCTC C	TGTTGTAATCTTTCTGAATATTTG CTTGCTT	0,0	TCTTCCAAATTGAGCACAAA AGCAT
Ots_trnau1ap- 86	G	T	AATCCCTCCTTTT TCC	TCCCTCATTTTTC C	GGACAAGTTGAAACAGATCAGG AAGT	0,0	GCCACTGGATACCATCACTT CAAA
Ots_txnlp- 321	T	C	TCTGGCGGATTTA CA	CTGGCGGGTTTA CA	CCTTCAAACATAACACATCATAGA CATGCTT	0,0	TTATCAAACGAAGGCGGA TTTACTGA
Ots_u07- 07.161	C	T	ATCAGTGACATA AGTTGTCCA	TCAGTGACATAA ATTGTCCA	GTCAACAAATGCAGGTAACATA AATGGT	0,0	GATGCAAACACCTGTGAAA TTGTGA
Ots_u07- 17.135	A	G	AAAATGTACCAC ATACTTGT	AAATGTACCACA TACTCGT	CTCGCCTCTGTCATTGTATTACCT T	0,0	TGACACACGAGCCATTTTGA TGAT
Ots_u07- 18.378	A	T	ATATGGTATGTA GAGGCTAGTTA	TATGTAGAGGCA AGTTA	GGAAACCAGCTAGGATTCAGGA A	0,0	CGTTATATGGTTTGCTTGTT TGCGATA
Ots_u07- 20.332	A	C	ACCATTTGATATA ACTGCGTTAG	CATTTGATATAA CGGCGTTAG	CGCGAGTTAGCTCGAATATTATG ATTTT	0,0	TCAAGCTAGCATAGCAACTT CATCAA
Ots_u07- 25.325	T	C	CCGCTTGAAAGTT TGA	CGCTTGAAGGTT TGA	AGACAATCATGGTGTTTTGAGTC TTTCT	0,0	GCCTAGGCTTGATGGAGTCA
Ots_u07- 49.290	G	A	CTTTCCCCGTGTT GGT	ACTTTCCCTGTG TTGGT	GCTGAGGAAGGATTCTGTATTTG CT	0,0	TCGGACAGAGCGCATCC
Ots_u07- 53.133	C	T	TAACACATGTTG GAGGTC	AACACATGTTAG AGGTC	AGCTAGGCTGTAAATGCAAGGA T	0,0	CAGTGCTTTCAATTCATGCT GTCAA
Ots_u07- 57.120	A	T	GTGACAAGGTAG GGGTTG	GTGACATGGTAG GGGTTG	GGTTTGAGCCAATCAGTTGTGTT	0,0	CGGTCTAATGTCCATTGCTC ATGTT
Ots_u07- 64.221	G	C	ATCGACCCTGTCA TTAG	CGACCCTGTGAT TAG	GAGGATGACACTGTCCGTTTGT	0,0	CACAGTCCTTCGTATTCACC TTGAT
Ots_u1002-75	T	C	ATGGCCCTTACAC TATC	TGGCCCTTACGC TATC	CCGCCTTTCCACCTTCTC	0,0	TCAAACGAGAACACACTAA GGTTGT
Ots_u1007- 124	A	G	TGTCCTGTCCTCA GATCA	TCCTGTCCCCAG ATCA	CGAAATAAGGGCCTGGTGTTTAA AA	0,0	TGTACCAGGTGGAAGCTTTG G
Ots_u1008- 108	T	A	TTGGTAAACCTGT TTATTGGTA	TGGTAAACCTGT TTTTTGGTA	GGATGACTCCTACTAATAGACGG ATGT	0,0	AGGACAGGAAAGAAGCAGC AAATA
Ots_u202-161	T	A	AGCTAGTGCTTA GCAGCTA[AC]	AGCTAGTGCATA GCAGCTA[AC]	CACTTTTGACTTTTACATGGAAC TAACATCAT	1,4,0	GGGACTTCACTTTCTACAAA CATGTCA
Ots_u211-85	C	T	TCCCAAAGTCGA GTGTG	CCCAAAGTCAAG TGTG	TGGTGAGAGCAGCTTTAAATGTC TT	0,0	ACCCATTCTTCTGTCTGGTT TAAGC
Ots_U212- 158	G	A	CTGGAAGAAGGC CTC	CTGGAAAAAGG CCTC	CCCCATATGAGACGCTACAGTAA TG	1,5,0	CAAATGCCCTCTAAGCAGA CCTT
Ots_U2305- 63	T	-	AATGTCATATAG AAATCTAC	AATGTCATAGAA ATCTACTG	TGTCATCTCTATTGCAATCTCAG TAGATTTCTAT	2,0	CCAGGTCTGCTTTATTGCAG ATTATCA
Ots_U2362- 227	A	T	AAGAAGCATTTTT T[GT][GT]	AAGAAGCATTTA TTTT	TCGTGGATTGTGGCTTACGT	0,0	GGGTGTTTAACAAGTAGTCC CTTCA

Ots_U2362-330	A	G	ACTGGGAAGATT GTTTG	CTGGGAAGACTG TTTG	AATGGGTAACAAAGAAATAGCT AGCTACTT	0,0	GACAGACCACAGTGAAGGT GAAA
Ots_U2446-123	C	A	CTGCAACTCGAC GCAAG	ACTGCAACTCTA CGCAAG	CTGGTCTGTGACGTCAAAATGAT G	0,0	AGCTAGACCAGGCCATTTG AG
Ots_U2567-104	G	A	GAGACTGTTGAG AC	GAGACTATTGAG AC	CATAGTATAGTGATTTCGAGTCTG GAGTCT	0,0	CGGGCTTTCTTAGGATATTT TCCTGA
Ots_u4-92	T	C	CTGTGTTGAATTT AACATAAT	TCTGTGTTGAAT TTAACGTAAT	ATCCAAGGAGCCCCATTAAAGA TTT	0,0	CGTACCAGAGTTGTAGAAG CATCT
Ots_U5049-250	G	T	TGGAATGGGTAA GGTGTA	TGGAATGTGTAA GGTGTA	CAATGTCTAAAGTAATGGTGGTA TTCTTGC	0,0	TCTTTGACACACCATCTGCC AATT
Ots_U5121-34	A	G	AGGGTCTCATGCT CCCT	AGGGTCTCGTGC TCCCT	CCAGAGGTTAGATGGCCCTTT	0,0	CTGAGCCAGAACCACAAAT TGAATT
Ots_u6-75	C	T	TTAGTCAACTGTT GTTTTT	TTAGTCAACTGT TATTTTT	GAAAAAGTAAAGTAAAAGTAAA GTATTATACCACTAAAGACAAT	0,0	GATCCACACTGTTGGTCTAC TACAA
Ots_unk1104-38	C	T	CCACTAAGGATT ACGTTACG	CACTAAGGATTA CATTACG	TAACCATGACTTCTATCAATCAC CCC	0,0	CCTCCATACATCGTCAAAGC TGTA
Ots_unk1832-39	C	T	CACCACTAGAAC TCTC	CACCACTAAAAC TCTC	GAAACGTCTATGCTGTCCCCTTT AA	0,0	CTGCAGTATTAGCTCTAGTT GAATCCA
Ots_unk3513-49	C	T	AGTGCGAAGAAC C	AGTGCAAAGAA CC	TTTGAGTGAGTCACTGCACCAA	0,0	CAGCTCCACAGTGTCACCAT
Ots_unk526	A	G	CAACATTCCAGTC TGAAAC	CATTCCAGCCTG AAAC	TCAAGACTGTGCTGTAGTTGTCT AC	0,0	CCTCCCCCTTTTCCACATCA G
Ots_unk7936-50	C	G	AGACATGTAGCT ATGTAGGTAA	AGACATGTAGCT ATCTAGGTAA	ATGGGTTGGGATTATGGTTCATT GT	0,0	CAAAATGGTTACTTGCATAG TCTTTTGT
Ots_unk9480-51	G	C	CTCCCACAAACC C	TCCCAGAAACCC	CAAATCAGAACAAAACCTCCCA CAA	0,0	GGAAGTCTGTCTGAATGGTT GTCTT
Ots_vatf-251	G	-	AGACCACAAGAT ACAGTACC	AGACCACAAGAT AGTACC	CTTTTCGGGTTATTCATGCTGTTG T	0,0	GCAAGCATTTGAAAAACAG ACTGGAT
Ots_VGLL3-1	C	A	ACCTGCTCTAACT A	ACCTGATCTAAC TA	AGGAGTCCGAGTCATTCT	0,0	AGATGTGGGTGTACAGAA CTC
Ots_wenYhap_25067_92	A	G	GCATAGTTTGG	GCATGGTTTGG	ATAATGTTTCCTGACATGTTGGT G	0,0	AAGTGAAGGTCAAGCCATG AGT
Ots_wenYhap_71572	C	T	GCCACACTGTT	GCCATACTGTT	CTAGTCCTGACATGTAGGCTCAT C	0,0	GAAATCATGCACAGAATGA ACAGT
Ots_zn593-346	A	T	TCTTGCAATCATT TTTAAC	CTTGCAATCATA TTTAAC	CTACGCGAGAAATAACACTTTTC AAAAC	0,0	GGCGAGTTTATTACGGTGTT ATGAC
Ots_ZR-575	G	A	CC[GA]ACACAAT TTTGT	CC[GA]ACATAAT TTTGT	GCCTACCAGAAAGTACCAATTGT GA	0,0	ACTTTTCACTGTCCTATTAC AATTAGTATTTGTGATAT
Ots1_72858599	A	G	GGTGGAGGGAAA AAGCAGTG	GGTGGAGGGGA AAAGCAGTG	AACCATTGTTCTTGTATTCTGCT	0,0	CCATCCTTTTCATTCGTCTTTT TAC

Ots10_21244 146	A	C	CCATTATCATTAT	CCCTTATCATTA T	CTTCCAGGAGGTATTGTTGGTTA T	0,0	CTGTATATGGCAAACCTACG TTCA
Ots11_11925 999	G	T	CATTTAAAATGGT AAAAATCA	CATTTAAAATTG TAAAAATCA	TTTATATTCAGACATTCGCCAAA A	0,0	AAACCATTTCTATGTTACTG TGACAA
Ots11_32418 659	A	T	AGCCAATTGTAG CCTTAGTGC	AGCCAATTGTTG CCTTAGTGC	CAATTGTAGCCCTCTAACTTTTC C	0,0	TACAATTGGCTTTGTGTGTC GTAT
Ots11_32468 959	G	C	GTGATAGTTTGAT AGTTTTAT	GTGATAGTTTCA TAGTTTTAT	AACACAGATCAAATGTTTTCACA C	0,0	TCAACATTCTGTTTTTCCTGT GTT
Ots12_23066 874	A	G	TCCCCACCAAAA TTAAGCAAA	TCCCCACCAAGA TTAAGCAAA	CTCTTTCAGTTGTCTTTGCTCTTG	0,0	ACCCTGTTTCATGCCTTTTCA TAAT
Ots14_54530 33	G	A	TCTCTAAAAAAGG TACAGTATA	TCTCTAAAAAAG TACAGTATA	ATTATTCAAACAGAGATGGCGA AA	0,0	ATCATGTTCTATGCAAACCT CCTC
Ots15_18157 381	C	T	CCCTGGAGATCT	CTCTGGAGATCT	TCTCAATGTGATTGAAATGGATG T	0,0	CACCGTACACACAAACTAC AGACA
Ots17_14864 79_C6	G	A	CTGTAGTGACGC CGCAACAC	CTGTAGTGACAC CGCAACAC	GTCACGATCAGCAATGAGACAG	0,0	TTCAATGCAGTGCCTTAGTC C
Ots17_22360 456	T	G	AGTCTGTCTGTTGT	AGGCTGTCTGTTG T	ATGGTTAAATTGACTCCTCCCTA T	0,0	GCAGATGACAGAACAGTAG TAGGC
Ots17_88536 4	C	A	TAGCCTTAAGCG CTTCCTGCC	TAGCCTTAAGAG CTTCCTGCC	GTAAAGAAACATGACCTTTTCTG AG	0,0	TTTAACTATGATGGCCATAA CCTG
Ots18_29943 476	A	G	GCCTGACTGGAC AACCATTG	GCCTGACTGGGC AACCATTG	GTTCATTTTGAAATAACTGCATC G	0,0	CTAATGTGCATGGACCTTGT AGAG
Ots18_30099 101	C	T	ATTGCATACTCGA GTCATCCA	ATTGCATACTTG AGTCATCCA	CAAATGTAAGGATACGCTTGAAT G	0,0	AATACATGTAATCGCTTGCA ACTC
Ots18_32088 284	T	C	ATGTTACATGTA	ACGTTACATGTA	CATGAGACACCCTGGAGAAAA	0,0	GCCCCAAGAAGGTACTATC AAAAT
Ots18_34171 74	A	C	CTGAATCCTGTAA G	CTGCATCCTGTA AG	TGAGGTATTACTTGCTGAGTTTG C	0,0	TGGGAATTAGTTCACATCTT CTTG
Ots18_34262 99	T	A	AATGCCATTTTGT	AAAGCCATTTTG T	TTATTTTGGGCTTCATATGGTTCT	0,0	TCCAAAAATATCAACATCAT GACC
Ots18_35418 13	T	C	CTACCTACCTTAG TGCTC	CTACCTACCTCA GTGCTC	CCCCAAAAACATCAAGAAGTCT AA	0,0	TTAGTCTACCTTTTCCTCAC CATGT
Ots18_35500 47	A	G	TCATTTTTGCAGA GAGAGAAT	TCATTTTTGCGG AGAGAGAAT	ATCATCTCTGCTCAGAGGCTATT C	0,0	AGTGTAAGACGTTCTCTCCA CTCT
Ots19_46172 133	C	T	GCAAATCTCCGA TGTAAGT	GCAAATCTCTGA TGTAAGT	CACATGGCTCTTTGCTCAAAAT	1,0	AACATTCAACACATAATGGT AGGC
Ots19_46172 427	G	A	TATTCAAAAGGA GCAGTTCAT	TATTCAAAAGAA GCAGTTCAT	CAGTTCCTGACATTCACCAAAAT A	0,8,0	CTGTATTAGTGATGGGTTGT TTGC
Ots2_382642 69	A	C	TCCCTTGTCTATG GTATATCT	TCCCTTGTCTCT GGTATATCT	GTATGAGTTGTGTGGTTGCAATG T	0,0	GGACATTGTGCAATAGGCT AGAG

Ots2_424056 43	G	T	CAGGTTGTTGGTT GTT	CAGGTTGTTGGTT TGTT	GAGAGAGTGCATTCTTCATCAAG TT	0,0	ATTGGGAAAAACCCTGTACT GA
Ots22_32650 802	G	A	GGGAGAGGAGGC CTGTCTTTA	GGGAGAGGAGA CCTGTCTTTA	AAGGAGCAGGAGATGTTATTGA AG	0,0	CAGTGGACCAGTGAAGTAC CTAGT
Ots28_11023 212	A	G	AACGTGACACAA T	AACGTGACACGA T	AGAAAGCCATCATCATGAGACC	0,0	TTCTGACCATTTTTGTTTGGT TGT
Ots28_11025 336	A	C	CAATGAAGTTAA TTTAATTGG	CAATGAAGTTCA TTTAATTGG	TGCAATATAGAACAAATCCGAA AA	0,0	ATGTATGTGAAGCCAAGGG TTATT
Ots28_11033 282	G	A	TAAAAATGGTTG ATATGTA	TAAAAATGATTG ATATGTA	GGCTTTCTGATGATCTTGAACCTT T	0,0	TAGGGACTTCCTCTCTCTCA CACT
Ots28_11062 192	C	G	TTCTCAAGTCCTA CTCAACTG	TTCTCAAGTCGT ACTCAACTG	AGATGATATGGATTTGCTGTGTG T	0,0	TCTTTCTCTGATCGTTATGTT CAA
Ots28_11070 757	A	G	ACCCATGAATAA GGACGAGAG	ACCCATGAATGA GGACGAGAG	TTTTGGAACCCTTTTACTACGA G	0,0	CCCTCTCCTCTGCTATACTG ATGT
Ots28_11071 377	T	C	CATCTTAGCCTCT CTGACCCC	CATCTTAGCCCC TCTGACCCC	ATTTGCTGTGTGTGGAGTGAAT	0,0	CCTCCAAGAGCATCTGTCAC TAC
Ots28_11072 994	C	T	CCATATGTCGCTT GT	CCATATGTCGTT TGT	GGGAGACTTAAAACAACCTCAA AA	0,0	ACTGTTGAATAGAAGGTTGC AGGT
Ots28_11073 102	T	A	ACATTACTTTTCA AAAATATT	ACATTACTTTAC AAAATATT	GGTGAGCCATTCATAACAATCTT	0,0	TCTCTTGAATGATCCAGGAT AACA
Ots28_11073 668	T	A	TACAGTTTCCTGT CTGA	TACAGTTTCCAG TCTGA	CCTAAGAGGAGACGAGCATTAC AG	0,0	CGAGTGGTCATATGTTGATT TACC
Ots28_11075 348	G	A	GTGTGAAAGGGG AGAAGGGCT	GTGTGAAAGGA GAGAAGGGCT	CATTTCAAATAGGAGGTTAGG G	0,0	ACAGGCCACAGCTCTCATCT
Ots28_11075 712	C	T	GAAAACTCTGCC CTG	GAAAACTCTGTC CTG	GCTTAAACAGCTGCTATTAGGAC A	0,0	ATTAGAGCTGGCAACAAAT CCTTA
Ots28_11077 016	C	T	GTCAAACCAACT TTGCCAAGG	GTCAAACCAATT TTGCCAAGG	AAAATATGTGCAACATCCAATGT C	0,0	ATTAGCTTCAGCCAGCTTGT GT
Ots28_11077 172	G	A	ACACACACAAGA GACACCCAC	ACACACACAAA AGACACCCAC	GTTTTGCCAGAGAGAATGTACAA A	0,0.4	GCTAGTCCAATGCTCTAACC ACTA
Ots28_11077 576	A	G	GAAGGCCAAATA AAATTG	GAAGGCCGAAT AAATTG	TGTGCGGAATTACTGATAATTGA C	0,0	AGCAGTGTGTAAAATGCA GAGC
Ots28_11095 755	A	T	AGAGTTGAATGG C	AGTGTGAATGG C	CCAATGGTGATTTTAGAACCATT AC	0,0	TGCTGTTGATCCATACTCTG TTTT
Ots28_11143 508	G	A	TTCACGTACGGCC CAT	TTCACATACGGC CCAT	ACCTTTTAGCCAGTGACAACATT T	0,0	CTATCGTCGAGAGTTTCTTG CAT
Ots28_11160 599	G	T	CTCTCTGCTTGCG TT	CTCTCTGCTTTC GTT	GTGCATATTTTACGTGGTTGAAG T	0,0	AAATTCATATGGGTGAAAT GGAAT
Ots28_11164 637	C	A	CTGGCGGGGTCT GGG	CTGGCGGGGTAT GGG	TGATTTGACTTTTTGTGGTGTTTT	0,0	AAGAGAGCAAAAACAGATT GGAAC

Ots28_11186 543	A	T	AAAGCTGATTAA AAA	AAAGCTGATTTA AAA	GGCTTGCCTTTAGATAGAATCTT G	0,0	TTTGTTTTTGGACTTGTGAG ATTT
Ots28_11201 129	T	G	ACTGAAGGAATT TAAC	ACTGAAGGAAGT TAAC	TGCGAGATTTATCTACTTGTCCA G	0,0	TTAGCAATTGCGTACAAAAC TACC
Ots28_11202 190	T	C	CAAAAGTCTGTA TTTTCAAAA	CAAAAGTCTGCA TTTTCAAAA	GCTAAATGTAAATCGAGTGGCTG T	0,0	TAGAACACTGAGAGGACCC ATGTA
Ots28_11202 400	C	T	GACACACTCACG A	GACACACTCATG A	CCCTCCAAAAAGAAAACATTTG AT	0,0	AACCAGTGTTTGATTAGCCA ATTT
Ots28_11202 863	C	A	ATAAAAAATTCT GCGTGAATG	ATAAAAAATTAT GCGTGAATG	GAGGATGGATGAGACTTTTCAG AT	0,0	CTTCATATAAACCCGGTAAA GAGC
Ots28_11205 423	A	G	CCTGCACACATGT CAAACCG	CCTGCACACGTG TCAAACCG	TTAAATCACCCAGAGCTTGTTAG A	0,0	TTGTGGTTGTTATCTAGGTC AGGT
Ots28_11205 993	C	T	GCTATTAAAAGG	GTTATTAAAAGG	GCTGCTATTTCCGACCTTACAAT A	0,0	TTCTGGTGAGTGTTTTGTCT TGAT
Ots28_11206 740	T	C	CCTTCCCTCCTAG GGCAACGT	CCTTCCCTCCCA GGGCAACGT	ACTTTGAGGACTTACTCCTGTCC T	0,0	GATCATCATCTTGTCTTTCT CCAG
Ots28_11207 428	T	G	GTTGGGAGCGTC CCAAAATGG	GTTGGGAGCGGC CCAAAATGG	TATACCTTTGTAGCATCCCTCTC C	0,5,0	GTCAAACGCTGTCCACTTTA TATG
Ots28_11210 919	C	T	GACCTCAAGCAG TCAG	GACCTTAAGCAG TCAG	AGTGCTCCATGCTGGAGTTT	0,0	AGCCTCTCCTTCTGCTTCAT C
Ots29_18791 740	T	G	CCTATGAAGTT	CCGATGAAGTT	GTTTTGGTGTGGTCTCAAATCC	0,0	CGGCACCTGGAACAGTC
Ots29_23344 676	T	C	TGCAAGTCCTTCA AAGGCTCA	TGCAAGTCCTCC AAAGGCTCA	GAACTATCCTGACTCCCATTGAA A	0,0	CATAACAACCAGGAGGAAC TCAG
Ots3_348942 54	T	C	TAACCTACAGTC	TAACCTACAGCC	TGATATATTTTGCTGCAATGATC TG	0,0	AACATTGTCCACCTTCCCTC T
Ots3_570555 18	T	C	TGATCATATCTCG TTCAGT	TGATCATACCTC GTTTCAGT	TTAGCAGGCGATCTAATTCTGAT T	0,0	CAGAGAATACAGCAGTTAG CGTGT
Ots30_17330 452	G	C	CATGTCAGTGC	CATGTCACTGC	CACAAATGTGACCGTTTTTCATC	0,0	TTGAACCAGGGTGTCTGTAG TG
Ots30_17330 688	T	C	TGTGTCTGAGA	TGTGTCCGAGA	CTGACAAAAGTGATCTGCCTGA	0,0	TGCTTGGTTACACAGTTTGA CA
Ots33_19359 879	T	C	AAATAAACGCTG GGTCTAATT	AAATAAACGCCG GGTCTAATT	AGCGCCTGTTTTACATAAAACACT T	0,0	TTGCTCAGTCTTTACGGTAC TCAC
Ots4_409422 76	G	A	GGAGTCAGATAC	GAAGTCAGATAC	ATTAGTGCATATGAATCGGGCTA T	0,0	CAATATGTACGTTCAACCTT TTGG
Ots4_416387 10	G	A	CCTGAGATTAGG	CCTGAGATTAAG	CAGCAGCTGTTTATGACTGACTT C	0,0	CATTTCACATCGGTTACACG AG
Ots4_423787 41	C	T	AGATGAACACCA ACTGGCCGG	AGATGAACACTA ACTGGCCGG	CAGTTTAAGTGTTACCACCACGA G	0,0	CGTTAACGCTCACCTGCAC

Ots4_649788 18	C	A	TCAAGTGTTCCT TTATTTTG	TCAAGTGTTCCT TTTATTTTG	AGAACCCATGCTTTCAGTACACT T	0,0	GAGCGATACATTTCTGTCCA TTTT
Ots5_447950 73	C	T	TTTTTGTGTCCGC CATGAATT	TTTTTGTGTCTGC CATGAATT	GCACTGTATACAAAATCGTGTGG T	0,0	TATTGGGCATTGTCTGTCTT AATG
Ots5_709086 26	T	C	AGCCTCTTCCTCT CTG	AGCCTCTTCCCC TCTG	TACGGTAGGAAGACTGAATGAG TG	0,0	TACAAGCTATCTGGAGAGG TAGGG
Ots6_109049 49	C	T	CCTTTGTACACCGC TCATCAGC	CCTTTGTCACTG CTCATCAGC	AAATCACCCCATTCTTTTGTG	0,0	TGCTTATGCACATCACCTTT CTAC
Ots6_335051 44	T	A	AACATATGAGTT GTAATGCCC	AACATATGAGAT GTAATGCCC	CCCACCATAACAATAAAGGCATGT	0,0	TGGGTATTTGTTTATGGGAG AGAT
Ots7_509971 24	G	T	GGGCCTTCGGGG TGCCTGTCC	GGGCCTTCGGTG TGCCTGTCC	AGATCAAGCTTGCTGACTTCG	0,0	CAGCAAAATACAGTGTGGT GTATG
Ots7_514094 15	T	C	TGGTCTACTTTGT GC	TGGTCTACTTCG TGC	ACAACTAGTCATCGTGGAATCTG A	0,0	CCTCATTCCTTTCTTTTAGCA TGT
Ots7_532910 35	G	A	GCTAGCAAACGT CGCCA	GCTAGCAAACAT CGCCA	TCAAATTGAATGTAGACAGATG GAA	0,0	TAATGTTAGCTTTGCGAGCT ATTT
Ots7_536315 22	A	G	TGAGTTTTCAAGG GGTT	TGAGTTTTCAGG GGGT	CTTATCTCAAAGGAATGGGAATG A	0,0	CAAAGCTGCATCCAAATACT GTAG
Ots7_542129 44	T	A	AATATATTTTTTA TAGGC	AATATATATTTT ATAGGC	AAACCACGGTATCCTTTATTCAT C	0,0	TTTAGACATATTTTGGGGTT AGGAA
Ots9_161150 48	G	A	CCAGTGAGATGC TGTGTTGCA	CCAGTGAGATAC TGTGTTGCA	ATAGAGCTTTTGGTGTTCATTC C	0,0	AGGCCAGTACACAGTACAC ACACT
Ots9_289752 21	A	T	TTTGCCAAAGAG TTCAGATAC	TTTGCCAAAGTG TTCAGATAC	GCCTGCCCTACTTATCTCTTATC A	0,0	CAGCAAATTTTACAGTGAA GAGGT

1201
1202

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	ACATTCAGAAAGGGGAAGGT 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	TGCATTAATGTAAAAACCG 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	CCCCAGCTAAATAACAAT 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	AAGCATGACGAGTGTTCCGT	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	TGTTTCGCCCCCCT	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	ACACACACACACTCCAAGC 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 TTTGATTAA	GAAC TTTGATTAA	AGGGTTGCAACATTTTGGGA	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	TTGTGGTCGCCTGA	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	GAATGTATTAAAA 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	TGTTCTTAAGCCCG	TGTTCTTGAGCCCG	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	CTTGGCGGTGATAGAGACG 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	CCCTTCAGGTTCAT	CCCTTCATGTTCAT	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	CCCCACATGTATA	CCCCACTTGTATA	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	AGGTGTTTCCTAATGTTTTG 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	ACATTTCCCTGAAGCCATTA 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	TATGAATTCCTCCCGCAGCC	0,0	TTATGGATGAGCTGGGAGG C
One_2.715 12-50	C	T	TTTGATTCAATTCCA	TTTGATTTATTCCA	ACCTTTCTCATTGTGGATTT 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	GTTCTGTTCATGTCCCACCC 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	TGTGTTTTTCCCCACAAAA 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	AGAACTATTCTGGGTGCT 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	GTAACCTCATTAC	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	AAACAATGTAACTCGAGG 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	ACCTTTCTATTTCAAGTGTG 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	TTTTAATAATACTG	TTTTAATCATACTG	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	TGGCAGAATTTAACCACTG 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	TTGCCCCTCAACATTTCC 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	CTCCACATTGATCTGGACGTA	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	AGGTTAAGCTGTGTATAAGT	TTAAGCTGTGAATAAGT	TGTAACAATACAAGGATAATGCAAATAATGTAGGT	0,0	GGTTATTAGGTTACTGTGCTGACTGT
One_GPDH-201	T	C	CTTCACCCCTGGAGCC	CACCCCGGAGCC	GAAGCTGATCCTAGACCTGTACCTA	0,0	TGGTATGATGGTGCTACTGGAAGT
One_GTHa	A	G	CAAGAACTAGAAATGAAACAGA	AAGAACTAGAAATGAAACAGA	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	TTATTGACTATGGCAATTG	TTGACTATGGCGCAATTG	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	TGGTCAGGGTATCGCCATA	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 CCAACCT
One_pax7- 248	C	A	AATTCAAAACGAAAT GTG	TGAATTCAAAACTA AATGTG	AGTAAAGGTAGTGATGCAAT GATGCA	0,0	AACCGCATAGGACGTAAA GCA
One_PIP_3	C	T	AACACACATTTCTCA ACACA	ACACACATTTTTCA 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	GATTCTGAGATCATACAGTG 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	AGCAGGTGTAAGCATGTGTA CTT	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	CAGCCCCTCGAGGTAAGT	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	CTATGACATGTTTATTTAAT 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	CAAACCTTTTCATCT ACATTTA	ACTTTTTCATCCAC 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	CCATTCATGTTCTATTTCAGAT 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	TCATTCAGACAGTTGGGAG 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	TCCAGCCAGTCCATTTCAGAC	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	AGTCTACCATTCTACAAGTT CCTT
Oki_106479-278	A	G	ACTACACAGATG CA	ACTACACGGATG CA	CCCTCTAGGTCTTTAGCAAA CACT	0,0	TCAGTCATTTGTTTACGTGC TGT
Oki_107031-314	A	T	TTTTTGTATTTAC 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	GGCTGTTGTATATCATCCC 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.TAGTTCCTT T	CGA.TAGGTCTTT T	GGCGATTTCAGAGCAGGTCA T	0,0	TGGGAAATGTGTTGAATGTC CT
Oki_114448-101	C	T	CACTGCACCCGT CA	CACTGCATCCGTC A	ATGTTTCGATCAACCACTGCA	0,0	CCTCCTGCTGGACTAGGCTA
Oki_114587-309	T	G	TTACTATTCATTT T	TTACTATGCATTT T	GTCACAAATGATCTGCAAA ACACA	0,0	ACCAGGTGAGGGGTTAACC 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	ACCATAATTTACAAACGA 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	TCTCACCAGTCTT T	TCTGGGTAAAGTGTGCCTTT T	0,0	TCGATTCCAGGGTCTCAAAA GA
Oki_123044-68	C	A	TT.AAAACGTTTT T	TT.AAAAAGTTTT T	ACTGCCATATCAGTATTGGG GG	0,0	TGCTATGTTAATAAACC GG 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	GAAGTCCAGGTGTCAGGT 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	CCACCTCGATCTCCTTTTCGG	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	TGAAAGCTTGTCTGGGCTCTT
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	TCACCTTGTCCGGTTCCTGG
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	GGAAGTCTGGAGAAGGTAA 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	TGTCTAGTTCCAGCTTGTT 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	GTCACCTCTGAAGTAGCTGC 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	GGTCCTCCTGTCTCTTCCT	0,0	AGAGGGCAAGCAGTCAGTT C
Oki_RAD372 78-54	T	C	TTTTGGTGATTTG G	TTTTGGCGATTTG G	AGCGTGGTGTAACCTCAGA 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	GGCACCGTGGA 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	AGTGGCCTAACTTTAATTG 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	CCTACTGTTTGTGTC 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	GCAGCCCCTACCTACCATTC	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	TAAAATTA ACTC AA	TGCAGGCTAAAACCA GTAC TT	0,0	TGACCAGAAGACCCCTCTGT

Oki_RAD640 84-65	C	A	AATATACGTTTTA G	AATATAAGTTTTA G	AGGCAATTTTTTACATAGATG 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	AAGCTGATTTCCCTTGGCAAA 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	GGCTGTGCGGTGTTTCACAAT	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	CCCCATTAAGTCTCCCACG
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	GCAACAACCTGGT 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	GCTTGACACAGAG 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	TGGGGGGTTCGTA 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	AGCTCATTTCCTT T	AGCTCACTTCCTT 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	AGGTCACCTGCTG 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	GCAACCAGCACCATTTTCACT
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	GTCACCTTCAATGCCCCGCTT
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	GCAGGAGACCCCTTGCTTG 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	TAGTTGC GTTGAAAGCGAGC
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	CATGCAGCCGACAAACTG 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	TCGTCGTCATCGTCGTCATC
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	ACGTGTAAACCGAGCCACT
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	TGTTCATGAAGGGCACTGAGA
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	GAACCTTGATGGTTT GGG	GAACCTTGATAGTTT 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	CGTATCCTTTCATG 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	GACAATTGTACGT GCC	GACAATTGTTACGT 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	TGAGTGTTCTCGGGGAG 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	TCACAAAATTAACT 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	TTCACGTTCTTAATGCTGTCTGA
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	AATGAATCGTGGCCCCCTCTC
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	CGTACGTCCGACACCACTG
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	AACAACTTTAATTC GGC	AACAACTTTCATTC 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	CCGCGTGTTCAGC	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	TGGAGGGAATGCCTTGTCAG
Etr_5581	G	A	ACCTAATCCGTCT	ACCTAATCCATCT	CCCCACCTACCTGCTGAT GA	0,0	TGATAGGCGCGAAACCCATT
Etr_5600	G	T	CCAATGTCACCTTG 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	GTCTGAATTTTCCTTGTCCTCA
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	TTTGGTGCAAAC TT ACC	TTTGGTG CAGACTT ACC	CCCCCAAACATTGCTTTG GT	0,0	ATGCTGGTTGGGCTCTTACC
Etr_6318- 70	C	T	TGCCCCGACGCGACT C	GTGCCCCGATGCGAC TC	GACTTGTTCCGGCACTAC 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	GCTGCCAGGCACTTG TG
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	AGCACAATTCGTCTGTAAAGGG
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	GTGTCGGCAAGGGTGAG 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	GCTTGTTGCTCACGACA CT	0,0	ACCTCGAACTCGCTTGCT
Etr_824	C	G	ACCGATGTTGTTGG CCG	ACCGATGTTGGTGG CCG	TGCAGATGTTGTCACCG 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	GACCCATACCGGTTTCACCAT

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 CTTATTAAA
LampSD_327	A	G	AAGTAGGTGTCTCA GTAAAA	AGGTGTCTCGG TAAAA	GCCTAAACCACTCGGATG CA	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
Lri100P121189	A	G	CACAGGCTCCGG	CGCAGGCTCCG G	GGGGAGGGAGAACACCAC T	0,0	GCCGATGAGCTGTATCTGCT T
Lri101P139377 1	C	T	GGTACGGGGCGGT	GGTACGGGGTG GT	CTGCAGGAACCCATGTAA ATC	0,0	CGGTGGCATATTTTGTTTGA C
Lri102P190027 7	G	T	AAATCCTTGCGGC	AAATCCTTGCT GC	CTAGTGTGGGGGTACAGC AGAC	0,0	AGCTCTCCTGCCTGGGTATA G
Lri1046P6449	C	T	GCTCCAGACGGCG	GCTTCAGACGG CG	CAAAGCGGGGTGTTTTGT	0,0	GTACACGCACCGCACCAG
Lri104P686936	G	A	AGGACTTCTCGGA	AGGACTTCTCA GA	CAGCAGGCGTTTGAGCAC	0,0	CAGGCGATGATCTGGAGGT
Lri105P123191 4	G	A	TCACGGCCCTGGA	TCACGGCCCTA GA	GACAACCAGCTGGAGAGT CTG	0,0	CTCACCTTAAGGCGGTTTCC
Lri106P125261 8	C	T	AGCGTGAACGCAT	AGCGTGAACGT AT	AAGCTACAGTCGTGCACA TTT	0,0	CAGGGTTGGCTAGGTGAATG
Lri106P179066 8	A	G	AATTGGGGTTC	AGTTGGGGTTC	AGACATGGTGCGGAATTA TACA	0,0	GCTCAGATCGGTTTTAATTT GTG
Lri107P679417	A	G	GCCTGCAGGAT	GCCTGCAGGGT	CTTGATATCGCTGCCGAGT	0,0	AGTCGCGTGCAGTTGGAAT
Lri108P658763	C	A	GGGCGCCGGCATG	GGGCGCAGGCA TG	CTGAGACCATGCGATCGA G	0,0	CAGCAACCCACTTGCTGTAC T

Lri109P766527	A	G	CATTAATAATAGA	CATTAATAGTA GA	GAGAAGCACTGTCTAGGC CATAA	0,0	CCAGAATCATCATTGTCAGT GG
Lri10P1667154	C	T	TCCGTCCGGCCGG	TCCGTCTGGCC GG	CTGCAGGAGCAGCTCGAC	0,0	CGAAAGAAGTTCAACACACG TA
Lri10P6216903	C	T	CAGGGCGTGCTCG	CAGGGTGTGCT CG	TGGAAGAGTAGGCCAAAA ACAC	0,0	CAACAACATCCTCACAGACA CC
Lri10P8084542	G	A	CTTAAACCAAGAC	CTTAAACCAAA AC	CTGCAGGTGCTGGTTAATA TAGG	0,0	GTGCCTGGGAAAATGAGAG AC
Lri10P8119699	G	A	CAATGACACGGGGA	CAATGACACGA GGA	GTTCTCCGCGAGCTCCAC	0,0	CAGCTCTTGTAGCAGGGTTG AC
Lri10P9580222	T	C	CAGAGTACCACCC	CAGAGCACCAC CC	CTCCTTGCCAGCTTTCGTA AC	0,0	CACCAAAGCACCAGCAGAT
Lri112P152406 2	G	A	CCAACGAGCCGCG	CCAACGAGCCA CG	ATAGATGAGCACCGGGAC GA	0,0	ATGAAGGCGTCGATGTAGTC
Lri113P109152	C	T	TTGACATGACCTC	TTGACATGACT TC	TCCACTCAGAAGAACTTG ACTCC	0,0	GGATGAGTGGCTGCTGCT
Lri11433P5520 TD58	A	G	CGTCTATTTCA	CGTCTGTTTCA	CTGCACTCACTACACGCAG GT	0,0	AGTTGATGCTGCCGGATG
Lri11465P555	C	T	CTGCAGGGCTC	CTGCAGGGCTT	CCACTGAAGGTTGTGAAA GGTT	0,0	TGCATCAATAATTAACGTGT TGG
Lri117P110714 7	A	G	GGCGCTCGGTACCT	GGCGCTCGGTG CCT	ATGATGAAGCCATGTCTG ACC	0,0	CTGCAGGAGAGCGATAGTGA C
Lri118P147752 1	G	T	AATGCCTGCAGGAA	AATTCCTGCAG GAA	ACGGCATCTATTAGTCCAC CTC	0,0	CGAGCGAGGTAGTTTGATGT TT
Lri118P434131	A	G	CAAGTGTTGGGCA	CAGGTGTTGGG CA	CCCAGGATGGACACGTTG	0,0	GAGTCGGCTGGGATTTTCT
Lri119P143678 5	A	T	TTTGACAGCACAC	TTTGACTGCAC AC	CCTGCAGGGAAAAAGTGA GTT	0,0	TTTGTTTGAGAGTGCACGTT GT
Lri11P1153619 0	A	G	CGCTCAGACCGCTG	CGCTCGGACCG CTG	ACCCCTTCAAAGCAGTGG AT	0,0	TTAGTGGCGGGTTTTAAAAG TG
Lri11P1170496 5	A	G	GTAACGTTCAAAT	GTGACGTTCAA AT	ACAGTCGTTCCGGCTCAATG	0,0	TCAGTCCCAACCAAACAAGT
Lri11P2066282	T	C	TTATAAACCACAA	TTACAAACCAC AA	TAATGGGAAGACAGACGA CGAT	0,0	CCAAACTTCCACAAGTTCAC CT

Lri11P311028	A	G	GCGGCTCCTCACG	GCGGCTCCTCG CG	TACTTCCCAGCGAAGAAA GTCT	0,0	ACGGCGTCACCAACAAC
Lri11P3590370	T	G	GCGGGACGCGTAA	GCGGGACGCGG AA	CAGGAGCTGCACAAACAC C	0,0	ACGGGGAGTCGTAATGCTCT
Lri11P8775214	A	G	TCCGCACGCGACA	TCCGCACGCGG CA	GATCTCGTCGCCGTGGTT	0,0	AGCAGAGTGGCGTTGCTC
Lri125P779292	G	C	TTCTAACGGA	TTCTAACCGA	TCGCGTCGAGGTCAAAAG	0,0	GATGATCCCTTCCCACAGG
Lri12696P1650	C	A	CTTGGGACTG	CTTGGGAATG	ACCAATATCAAACTGGG GTTG	0,0	GTTCAATTGTCCTGCAGGTTGT
Lri128P486601	C	T	CTGTGGTGGAC	CTGTGGTGGAT	ACGTCTGCACACGAGGTC AT	0,0	GGACCCTGCAGGAGAGGAC
Lri12P1146007 5	G	A	CCCTCGCCGCTCG	CCCTCGCCACT CG	GCACCTGCAGGAGATTCA TTTA	0,0	AGTATCGGTGCGGTGTGATT
Lri12P1774736	C	G	GACTGTCGTTACAGC	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
Lri12P1838366	G	A	GTGCCGAAGCGTT	GTGCCGAAGCA TT	CAAGGCGGTACCTTTACCC T	0,0	GACGATGGGATGGCGAAG
Lri12P279478	G	A	TCCAAACAAGGAG	TCCAAACAAAG AG	GCATTTTTATCATGCGCCT ATT	0,0	GTGTCATGCAGTGCTGAAAA A
Lri12P3082762	G	A	GGTGGCTAACGAC	GGTGGCTAACA AC	AAATGAATTGCGTGCAAG AGA	0,0	GGCAAACAAAACAAAGGAG AG
Lri12P5470970	A	G	TCCCACGCTGACG	TCCCACGCTGG CG	AAAATGTGCGTTTAGATTA TTTGG	0,0	AGCTCTTTTTCAATGGTGAC CT
Lri12P6060911	T	C	CAGTCGCCCTTCAG	CAGTCGCCCTC CAG	TCAAGATCGACCTTTGTAG AGGA	0,0	TCTTTCCCCTCCTACTTTGTT G
Lri12P7199624	G	A	GGTGTACAAAA	AGTGTACAAAA	TTATTGTGAGGGCGATGTT AT	0,0	GGGCTAACTCTCCTTGAAC TG
Lri12P8386432	C	G	TCTTTAGCAACGT	TCTTTAGCAAG GT	AAAGACCTGCAGGCTCAT AAAG	0,0	AACAGCTCCCGGTATTTCTC TT

Lri12P9648016	G	A	GCAGGCAGCAGAG	GCAGGCAGCAA AG	TCGCTGCACACAACATCC	0,0	CTCTGTCTGCGTGGAAGGTA G
Lri131P901089	C	A	GAGAAAACAGCAAT	GAGAAAACAGA AAT	TATTTACCCACAATTGTCA GCA	0,0	GTTACGGTCAGTAGAGGGCA GT
Lri134P444626	G	A	ATCGAGCCGAGTC	ATCGAGCCGAA TC	GCAGGGTCCTGTTTATTAT TGG	0,0	AGACATCGTCCACCATTGTA C
Lri137P957664	A	C	TCAACCACAAATA	TCAACCACAAC TA	GTAGCAAACCAGAGGGGA AAAT	0,0	TCGTAGTAGTTATTGTTACA GGTGTGT
Lri139P639349	G	A	GACCGGAGGGCTG	GACCGGAAGGC TG	ATTTTCGAGCCAGTGTGACA AAT	0,0	GCTCCAGTACGCACTGCTTG T
Lri13P1083889 5	C	T	GTGTCAGGTCCCG	GTGTCAGGTCT CG	CCCTATTATAAGCGCCTAG TGG	0,0	AGGGAGTGACATCACCAATA CC
Lri13P1111612 5	C	T	TGCTCCATGGC	TGTTCCATGGC	AGCTGCTGTTGCTGGTGAG	0,0	ATGCGAAGGCCAAGAAATA C
Lri13P4766961	T	G	GTTATGATATTT	GTTATGATATG T	CAAGAGGATGCAGGTGGT GT	0,0	GTTGAGGAGCACTGGGCTAT C
Lri13P6132767	A	C	GTGTACAGACCGT	GTGTACAGCCC GT	CTGACACTGCTCCAGCACCT T	0,0	TGCCCTCGACATGTTTGTG
Lri13P6221318	C	T	ACGCTGCTGCACG	ACGCTGCTGTA CG	CTCCTCGCAGCTCTCCAA	0,0	CAGAGGACCAGGATGAGAC TG
Lri13P6230623	T	G	AAATAGAGACTCG	AAATAGAGACG CG	TTGTCCTCCACTGCTAGGC TAT	0,0	CCTGCAGGCCGTATGTGT
Lri13P7256497	G	A	TTATGCCTTTGAC	TTATGCCTTTAA C	AACCATCGGTCATTATCCA GTC	0,0	CCACCCTGCAGGTTTTAGAA TA
Lri140P591452	C	T	GGGCCGATGACAG	GGGCCGATGAT AG	GCCTGTAGCACGGCACCT	0,0	GTGTCATGTGTCACGTGTGT G
Lri1432P16471	A	G	TGCCATCAGAATC	TGCCATCAGAG TC	GGAACAACACTTTGCCTTT GAT	0,0	GAAGGCCAATTTAAAGAGGT GA
Lri144P657672	C	T	TCAGTCACCCTGTG	TCAGTCACCTT GTG	CCTGCAGGTTCCACTGACT C	0,0	AGAGACTGATGCCCCCTTG
Lri148P462863	G	C	TTACGCACTCAAT	TTACCCACTCA AT	TAGGCAAGTGGTAAAGGG TGAT	0,0	GGTGAGTGGGTGAAGTCTGT G
Lri149P787096	T	G	GGATGGCATGTCT	GGATGGCATGG CT	TTGTCTCGATGTGAGCAAG ACT	0,0	GCGCCTATAGAGACACACTC G

Lri14P11709110	A	G	CACTCCACCAAGT	CACTCCACCAGGT	CACACTCAGCTCCGTCTTC A	0,0	CTCCAGCCTTGACCCATGT
Lri14P2900879	G	A	CCTCCTGGGCGAG	CCTCCTGGGCAAG	ATCGAAGGCACCTTGGTA GTT	0,0	GACTACCTGGTGGTAGCCAG TC
Lri14P3595836	C	G	TGCAGGTGCTC	TGCAGGTGCTG	GTGAATGCCGCCAGTAAG AC	0,0	CGCCTGCAGGAATTGTAAAT A
Lri14P3895562	T	G	CTTATTTTATTT	CGTATTTTATTT	TGGTTGTGTTGCTGTACAT TTG	0,0	CGCTGTTTTATTGCAGATTTC A
Lri14P3943878	G	T	AGGAAACATTGT	ATGAAACATTG T	GCCAAGGTACGTTCGATCA T	0,0	TTCACGGTGGAGTCTGAGAT TA
Lri14P4079387	C	A	AAAAGTAATGCTA	AAAAGTAATGA TA	AAATCCCAGGTATAAGCC TTTG	0,0	TTACAGTTGGCACCATTGAA AC
Lri14P4102727	G	A	GAGCCATTCCGGC	GAGCCATTCCA GC	AATAGCCTATCTTTCCTGC CATC	0,0	GGGCGTACAATAAATGGTTT G
Lri14P4106054	G	A	GACGAGATCTGGC	GACGAGATCTA GC	AACACGACATGTCTGCAG AGTC	0,0	TCTAACACCATTGCATGAAC AA
Lri14P4985173	A	C	AAGGACAGGGAAC	AAGGACAGGGC AC	TCAACAAACTTAAACTCAC CGTAT	0,0	CCTGCAGGTTATCATCAAGA AG
Lri151P237159	A	C	CGTCACATCACCA	CGTCACATCCC CA	GGCCCAAACCATTGAACA GT	0,0	AGCCCCATGACAAGACTCC
Lri159P658357	T	C	AGCGCGGCCGTAC	AGCGCGGCCGC AC	GTTTGTAGCCCCTTGCCAA C	0,0	CGGTGACAAAAGAGTTTCAG AG
Lri15P1409554	T	A	GAGTTTGAATCCG	GAGTTTGA AAC CG	GCAGGTTGAAATTGGAGG TTAC	0,0	AACCCTTCTTGCTGGGATG
Lri15P2172074	A	G	AAATTGTAATTA	AGATTGTAATT A	CGCACTGGGAAAGTTGAG TAA	0,0	TCAAGACAAGTGTTCAACAA TG
Lri15P6598748	G	A	GTAATGTGCAC	ATAATGTGCAC	ATGTGTCCGTGTGTTCTAT GGT	0,0	GCAGGGAGAAATCCTTTCAA TA
Lri16103P3900	T	C	AGCAGACCTATGC	AGCAGACCTAC GC	TTCAGCCACTTCAAGGAG AACT	0,0	CTGGTAAATGGCCTTCCTGT AG
Lri162P690722	C	T	CTCCAAATCAG	TTCCAAATCAG	ATTGCGTGCTGTGCTGTCT	0,0	GGAATTATGGGCTGAGTTGA TG
Lri1725P9022	G	A	ACGGGGGGACGCA	ACGGGGGAACG CA	ACGCTGGCCCTGAGAGAC	0,0.4	CGTCCCCGTGTCTCTGTC

Lri172P144187	T	C	CATGCAGAGTCG	CACGCAGAGTC G	AAATAGCCGAGGCATGGA C	0,0	GACACAGCAGAGGGTCAGC
Lri17742P215	G	A	ACTTATAGATGTA	ACTTATAGATA TA	CTCGCGGACAGGAGGTCT	0,0	TCAGGACTGTTAGAGTGTTG GA
Lri177P26697	A	C	ACCAGCATGGA	ACCAGCATGGC	ACGGACAGCTCGTCGTTG	0,0	CCGCAGGACCTTAACCTGAT
Lri178P237573	A	C	ATTGGTGAGATCTA	ATTGGTGAGCT CTA	GTTCCGTTTATTTCCGACT TCC	0,0	GTCAAGTGGCGCATTTTCAT
Lri178P423530	G	A	TGGAGCCGTGTGA	TGAAGCCGTGT GA	AGTGGATAAAATTGACGCC GTAT	0,0	CGTAGATCGCACCACCAAC
Lri17P2957024	G	A	TCTCGATGATCAG	TCTCGATAATC AG	CATCACCCCTCCAGAGTCA G	0,0	GGAAACCCTTCATCCAACAG T
Lri17P3232763	A	G	TCGCACACCGACT	TCGCACACCGG CT	CTGTGCTGCATCCAAACAA G	0,0	AAATGCCCCGAGGGATAAT
Lri17P385674	T	C	ATGACGTGATACG	ATGACGTGACA CG	GGGATCGCAGTGCCTAT	0,0	CTCGCTCTCCGTCCAGGT
Lri17P5047059	T	G	CGACCAAGGGTTT	CGACCAAGGGG TT	CAAGGTATATCGGCAGTG TGC	0,0	GTAATGCTGGTTTGAATGTT CG
Lri17P6620172	T	C	AATTGTCGTG	AATTGTCGCG	CCCGGTGATGAAAATTGC	0,0	AACTTTGTGGAAAGTCAGGT TTTT
Lri17P7594234 TD43	A	C	ATGTAA[AG]TTA[TG]	ATGTAC[AG]TT A[TG]	CAACCAGCAATCATGTGA AACT	0,0	AACATTGGCTCATGTGAGTG AC
Lri17P7943131	C	A	CCTACCTTATTAC	CCTACATTATT AC	TACATTCCCGTCAACCCCT TAT	0,0	GTCGTCTTTCTCCCTCGTGAT
Lri17P8218359	T	C	TCGGGCCACGTTC	TCGGGCCACGC TC	CCTGGGCTTTCTCTGTGTT C	0,0	ACTCACTTGTGGTGGTGAAC G
Lri17P8999134	T	G	GATGAATTCCACAT	GATGAATGCCA CAT	CAGCCATGATCTATCAACT TGTG	0,0	CAGGGGCTAGATGGATTGTT AC
Lri17P9471416	G	A	GCAGGTGTGCCCC	GCAGGTATGCC CC	TGAATGGTCTCTGCACGAT CT	0,0	GCCTGGCGAGAGACACTTTT AT
Lri18P1201819	A	G	GGCCAGCCACTTC	GGCCGGCCACT TC	AAGCGCACGTCGAGGTCT	0,0	AGTCGCACACCTGTGAGAAG TC
Lri18P163972	G	A	ACTTGTTGGCGTGC	ACTTGTTGGCA TGC	GTCGAAGGGCTGCACGTT	0,0	GAGAGGTCTACTGGTCCGAC TG

Lri18P3516203	A	C	CATTTATCAAT	CATTTATCACT	GCTGGTGTATGCCTGTAAA CAA	0,0	CAGCCCTGCAGGTTTGAG
Lri18P4745725	A	G	ATTGTGCTGTATC	ATTGTGCTGTG TC	TGGGACCGAATTCTGAGT GTAT	0,0	AAAACCGACGTCTCCTTTAG C
Lri18P5626860	T	C	ACTGTACAAATGT	ACCGTACAAAT GT	TGCATGATCTTAGAGTTCA CGTT	0,0	ACTCAAAGCGATGTTGCTGA G
Lri18P5985385	G	A	TGCAAGCATGGCG	TGCAAGCATGA CG	GCTCGGGTCTCCCGTACA	0,0	CAGGTGAACCCACAGTTGC
Lri18P6463787	A	C	TCATCCAGAGA	TCATCCAGAGC	TTGTATTTCTCTTGCTAAT AATGTCCA	0,0	TCTGGCAAGCGTGAAAAATA
Lri18P654758	T	C	CCGCGTGCAGAGG	CCGCGCGCAGA GG	GCGGTCTGCGTTGTCTTG	0,0	GATGCGGGTCATCTTGCT
Lri18P7974729	C	T	TTGCTCGGGTTCTG	TTGTTCTGGGTTCTG	AGTGCCTGCAGGACGTGT	0,0	GCAGAAGGAGAGATGGACA GAC
Lri18P8805776	A	G	AGCTCCCTGCA	GGCTCCCTGCA	GCCAGATCACGGAGAGAA ATAA	0,0	CTCCGGCCGTGTGAAATC
Lri18P9016369	A	G	CATTTGGTGCA	CATTTGGTGCG	TGTACATACCCAACCGTGC TAA	0,0	CTCGCCACAAACATCACCT
Lri19P6892352	C	G	GCGTCTCGGCCAC	GCGTCTCGGCG AC	GAGCTGCCCCATCGTCTC	0,0	GGCTGCTCAGACGTCACCT
Lri19P7387400	T	C	TGTGCACAGCT	CGTGCACAGCT	CAGCGTGAGCGAGTCCTG	0,0	ACTAGGATGACATGGACCTG GA
Lri19P9473436	C	T	TCCCTGGTGTCCA	TCTCTGGTGTCC A	GGTTAGTACAGATTGGTG AAAGTGG	0,0	GGTGCTGGTCCTGGAAGG
Lri19P9852768 TD53	A	T	GATA[GT]ATTCAT	GATA[GT]TTTC AT	ATTGCCTGCAGGTTGGAAT	0,0	ACATTTCAACAATGACCACG TT
Lri1P11647852	C	A	TTGTCACACACT	TTGTCACACAA T	GTGCTCTCCAAGCTCTAAC CTG	0,0	GTGACCACCACCCCATCAC
Lri1P16171976	G	A	AGTAAAAGGA	AGTAAAAGGA	GTTTGCACAGCGTTTTGAG AT	0,0	CAAGACCCTTTGCTTCTTCTG T
Lri1P17366484	T	A	GCTGATCTCCTCA	GCTGATCTCCA CA	CCTCCGGAAGAAAACAA G	0,0	CTGCAGGTCCACAGTTCATT G
Lri1P17392168	T	A	GAACGTCTGCTGC	GAACGTCTGCA GC	TTTATGAACACCAGTGCAA CCT	0,0	CAGGTGAGTGGCGCTGTAT

Lri1P17477528	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
Lri20P3277044	C	T	ATCTTCCTCCAGG	ATCTTCTTCCAG G	CGGAGTCCTCGACGAACT CTAT	0,0	GCTTCCCCAACCCCTCTT
Lri21P4463586	T	G	AAAAGCATTGAGA	AAAAGCATGGA GA	GAAATGGAACAGAAGCTG AAAA	0,0	AGCATTGTGTACGTAATCCTT GT
Lri21P5493330	T	C	GCAATCCTGTTGT	GCAATCCTGTC GT	GGAGGTGACCGATATTGT GAGT	0,0	CTCACTATGGCCAAATGATG CT
Lri21P6647296	G	A	GGTCCGGCTGGAA	GGTCCGGCTGA AA	TTCTAACTGTTCTCTTGT GACG	0,0	GAGGCAGGGAGACTTAAGT GAG
Lri21P702243	G	A	GGGTGAGCGCGGT	GGGTGAGCGCA GT	TCCCTGCAGGAGCTCGAC	0,0	CTCGACGCACTTGGACATAA T
Lri21P9294857	G	A	TGTTGTTGTTGCA	TGTTGTTGTTAC A	ACACAAACCCCACTGCAA AG	0,0	AATGTCCTGCAGGTGACTGA G
Lri222P307512	C	T	AGCCTTTGCGCAA	AGCCTTTGCGT AA	ATTAGGGCTTAATCACCTG GAG	0,0	CGGCGAGTGGTTTTAATTTT AC
Lri22434P974	G	C	GCTCTTCCTCT	CCTCTTCCTCT	CTGCAAGGTGGTGGTGAC	0,0	CGACGAGGATCCAGTAGTAG TTG
Lri22P1323692	C	T	ATCATCATCCCGT	ATCATCATCCT GT	TCGTCATTAGCAGCAATAG CAT	0,0	TGTGTGTTGTCTGAGTAGTA TTTGTGA
Lri22P3313925	G	C	GCTTGACGCGTG	GCTTGACGCC TG	GTCGACAATAACCTGGGG AAAC	0,0	GCAATATCACCCACCAAAC GT
Lri22P7082523	A	C	CGCTGCAGGACAA	CGCTGCAGGCC AA	AGCAGGGGGAACACACAG	0,0	ACCGCCTGCACACTCGATA
Lri22P7625675	T	C	TTGGAAGGTTC	CTGGAAGGTTC	CATGGCAAAAGGATTTCA CTTC	0,0	CACAGTGGTACTCATTGTAT CAGC
Lri22P8175926	G	A	CCCCTGCAGGGTG	CCCCTGCAGGA TG	ACTAGGGCAAGTCATCAC ATCA	0,0	CCTGGAATCTAGGAGTGATT CG
Lri23P3389463	G	A	GGCTCGTGCAACG	GGCTCATGCAA CG	CAGGCTTGCCACTTTTTGA C	0,0	GACAGGCGTAGTAGCACCAG TT

Lri23P8725518	A	C	CGACATCACAATG	CGACATCACCA TG	GTTGAACCGTAGCGATGA ACTC	0,0	GGCTATGCGTGTGACGTTT
Lri23P9526641	T	C	GAAGTTTGCGCGT	GAAGCTTGCGC GT	CATCTCCACCCCCAGGAT	0,0	CGACTGTGCCAGGACCTT
Lri24296P1937	C	T	GAATTGGTTTCAC	GAATTGGTTTT AC	GGGGAGCACACGATTCAC	0,0	CAGCCTGTTGTATTGCCAGA
Lri2481P8393	G	A	GTGAGAGCACGGCA	GTGAGAGCAC GCA	CAGGATGGACCACTGGAG AC	0,0	CTGAGGGGACTCTTCCTCAT CT
Lri24P3183281	A	C	GTTCCCAACTAA	GTTCCCAACTC A	CCGACAATCCTATTTGAAC CTC	0,0	AGCCAACCGTGCTAATAAGA AG
Lri24P3549440	A	C	CCCACTGAATA	CCCACTGAATC	CAGCTAAGTTCCGCATTGT AG	0,0	ATTTGCAACCCCGATACAAT CT
Lri24P3934915	A	C	TCCACCACCAACT	TCCACCACCAC CT	AGGTAGCCTTCACCGTACT GC	0,0	TTGAGAGGTACATCCAGGAT CA
Lri24P4354883	T	A	AATTTTACTATTT	AATATTACTAT TT	CAAAGCCCACTGGCAATT ACT	0,0	GCAACCACCCATTTATTTTC AA
Lri24P4954513	G	A	AGAGACAAGGCCAC	AGAAACAAGGC CAC	GGGCTGTGGCACTGTAAT AAT	0,0	ACATTGTAGCCATTATGAAG CA
Lri24P6514737	G	A	CATTAAGAAATAA	CATTAAAAAAT AA	TAAAATGCATGTGAGCCA TTTC	0,0	GATTTTCCCACTTGTGGTTT T
Lri24P6808546	T	A	GCACTTTTAATT	GCACTTTTAAA T	GAAATAGACCGTGTACAC GTATTGA	0,0	CGGTGGAAGGACAACAAAC TA
Lri24P7481704	A	G	CTACGTTTTTACG	CTACGTTTTTGC G	AAGCAGGTAAAGAGGGTT CACA	0,0	TGAAAACAATACAAGTTCAC AACAA
Lri24P7765916	T	G	CATCACCTCTTCT	CATCACCGCTT CT	CTTCCTTAGCTGCCATTTC ATT	0,0	TAAATGGACTTGGGTAGGGA CA
Lri25061P2542	C	T	TTTGCCACGGCCA	TTTGCCATGGC CA	GTCCTGCAGGGTTCGTAGA GT	0,0	TTGTAGCTCCTTCGCGTTAG AT
Lri25P2230291	G	A	GTCTGTAGGCGGA	GTCTGTAGGCA GA	TTCTTGTGTGAGATTCCCA CCT	0,0	TTGTCAATAACACTGCCTTT GG
Lri25P7373093	C	T	GGCTATACAT	GGTTATACAT	TTTCAAGCACGGTGAAAT ACTG	0,0	TTCTCGAAGCTTTCATTAGTT GG
Lri25P8275961	A	G	GCATGGTTCCTGG	GCGTGGTTCCT GG	GACAACCACAAGGCAGAC ATC	0,0	ATGATGGCTCACCGATGAAG T

Lri25P8435093	T	A	TTTTTTTATTT	TTTTTTAATTT	CAGGCTGTGGGTGCAGTA	0,0	CTTGCTCACAGAACTGTAC GA
Lri25P8849487	A	T	GTCAGTCAGCACCT	GTCAGTCAGCT CCT	GCAATGTTCAATTCCACCT G	0,0	CTTGTCGTGATGTACATTCTG C
Lri26245P408	A	C	CAACAGGAAAAAG	CAACAGGAAAC AG	TTAAATTAAATTGGGCCTT AGCC	0,0	GACTTCGCCTGTGACTCG
Lri262P62290	T	C	ATTTACAGCATGC	ATTTACAGCAC GC	CGTTATAAACACACGCGTT CC	0,0	TATAGCGCCACGTGTTGTAT TC
Lri26500P1136	T	C	AATATGCGTCTGA	AATATGCGTCC GA	GATCAATTTGCTTGCACCT G	0,0	AAGCAGTATCCATCACTTTG CAT
Lri26P4406096	A	G	GGAAAGTGGCGTT	GGAAGGTGGCG TT	CTGCAGGTGATGCTTGAG AC	0,0	TACAACCTGACGGTGCACAT
Lri26P6719186	C	T	GCAACAGCTTCAG	GCAACAGCTTT AG	ATCCTGAACCACCCGATGT	0,0	AGGCTGGTGTGAACTGATA CA
Lri2718P13929	C	T	AGTAGCCCGCTGA	AGTAGTCCGCT GA	TTTTGGCTTTTATAAGACA GTACATTA	0,0	AAACTGAAAGGCATGCAGA AAC
Lri27P6150884	T	C	TTACTCAAGATTC	TTACTCAAGAC TC	CATCGAGGTTGTGTTTTGA GAT	0,0	CCACACACAAGACATTCATC AAC
Lri28P383709	G	C	CGAGCAGGACC	CGACCAGGACC	GAACAACGACAGGTCCAT GA	0,0	GTCAGAGGACCTCGTACCTG AG
Lri28P4794703	A	G	CCTGCAGGTTATT	CCTGCAGGTTG TT	CATGTGCTTATATTGCCTT CCT	0,0	CCCAGTGGCTCGATTAAAGT AG
Lri28P5155821	C	T	TCACCATCCACG	TCACCATCCAT G	AAATTCCTGTGCCCCATT	0,0	TGCTGCGTCTGGTAGTTGTCT A
Lri28P628762	C	T	GTGAGTTACCTTC	GTGAGTTATCT TC	ACGTCTCCGGCTTCGTTAG	0,0	CCAAAGACAAGGGTCCCAAC
Lri29P1902704	C	T	CGGGGTAGGCCGG	CGGGGTAGGCT GG	GGAGAGCGTGCCTTCTGG	0,0	CCATTCCTTCACCTTCATCT C
Lri29P2715537	C	T	ACCCACCGGTTGGC	ACCTACCGGTT GGC	TATCCGACATGCCAAACTA CAC	0,0	ACACCCGAGACGGCTTTT
Lri29P3853819	T	C	TGGGGTACACTGT	TGGGGTACACC GT	GTCCGATAGCATTTTGCTC ACT	0,0	ATCCATGGAAAATACACGAT CC
Lri2P10660681	A	T	GGAGGAGGGAACG	GGAGGAGGGAT CG	GTTGACATCATCTCGGCTG TAA	0,0	GAGCGAGGTGTCTCGTCTG

Lri2P10747040	C	T	TCAGTTAGTTCCT	TCAGTTAGTTTC T	ATACAAAAGGGACCTTGC GTTG	0,0	AGATGGAGCGGCTGGTAAT
Lri2P10948512	T	C	GGTAGAGTGGTCG	GGTAGAGTGGC CG	GACGTGATCTGCACCTCCT C	0,0	GTCAACCCCATCATCTACTC C
Lri2P11971110	A	C	GGCCTCTTATA	GGCCTCTTATC	GACAGATTCAAAATGGAT GTGG	0,0	GCAGGAGACACGCCAACT
Lri2P12835756 TD51	A	G	AGACCACTGTG	AGACCGCTGTG	AGCAGTATTTGTCCGATTC TGT	0,0	TTCTCTGCCACCTTGGCTAC
Lri2P14986968	T	C	TACCACGGTCT	CACCACGGTCT	CTCCCGAGGGGCTCATACT	0,0	GCAGAGCTGCTGCTTGTTCT
Lri2P16247548	A	T	TCCACGAACAATG	TCCACGTACAA TG	GCACCGTATTTGGACAAC G	0,0	ATCGTTCAGATCCGGCAAG
Lri2P16250399	T	C	AAATCATAGATAA	AAATCACAGAT AA	ACTCATCACTTTGCCACTA CCC	0,0	GGTATGCAACTCGCAAAAGT TA
Lri2P16333005	T	A	TCCTACATCCT	TCCTACATCCA	CAACGTAATGGACAAATG ATGG	0,0	CGCTTTACAGAAGGATGATG TG
Lri2P16367064	A	G	ACAATCTGTCATG	ACAATCTGTCG TG	AAGCAAGAAATGTAAATC TGCTCTC	0,0	AACCAGAGAGAAGTGCATGT GA
Lri2P2907377	C	A	GACATCCCCTCGG	GACATCCCCTA GG	CTGCAGGTCTCGTCTCATG TAA	0,0	GTCAGCCGTAGGAGAGAAC G
Lri2P3548449	G	A	TTCCGTTACGGCA	TTCCGTTACGA CA	AGGAGATGGCTGGCAATG	0,0	GCCTGATGAAGAGCAGAGAT TG
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
Lri30P2608358	G	A	GAGACCGTGTTTT	GAGACCGTAGT TT	GGCCTCCCACTTCGAATC	0,0	TGTTGTTGCCAAGTCGAAAA TA

Lri30P2645807	C	T	AAGTGCCCTCCTG	AAGTGCCCTCT TG	GCTACATCATTGTCGTTGT GGT	0,0	GAGAGCGTGCAACAGATCCT
Lri31P1720639	T	C	CCTTGACTGCCTGC	CCTCGACTGCC TGC	GTGGTAGTAAAACATCGC GACA	0,0	GTGCTGTTGGTGAGTGAATG AT
Lri31P2117932	A	G	CCATCCGTTT	CCGTCCGTTT	ATGAATTGTACGATACGT GGT	0,0	GCAAACGAAACAGAAGGGA ATA
Lri31P2211794	T	C	GGGCCCTTCCACA	GGGCCCTCCCA CA	TGTGTGTGCATGTTTCAGAC CT	0,0	GATGAAATGCAGCCAGATCA C
Lri32744P2002	T	C	TGATGCAGGGTGG	TGATGCAGGGC GG	CAGGTATGGTGTCCGGTGCT	0,0	CATGTTGTAGAGCTCGTGGA AG
Lri32P2538291	T	C	ATTTAGTTGCTGA	ATTTAGTTGCC GA	CATACGTGTGCATATGTTT GTCA	0,0	TCCTTGGGTTTACAGAAGCA CT
Lri32P3507996	A	G	CTGCAGGTGCATA	CTGCAGGTGCG TA	GCTAGATTGTGTGCTCGAT TGC	0,0	CATGCTAGCAATACAAGTGG AAA
Lri32P517584	A	G	CCCCACGGTGACA	CCCCACGGTG CA	GAATGACACAAGGCATCA TCC	0,0	AAATACGCGCTGTGGGTTT
Lri33P2602672	C	T	GACGAGAACGGTT	GATGAGAACGG TT	CTTCCTGCAGGTCGTGTGT	0,0	CTCAAAGTGAACGAAGCCGT AG
Lri34P1263783	T	A	TCCGTAGCTCGGC	TCCGAAGCTCG GC	GCAAAGCACTCTCCCTTAC ACT	0,0	GTCTTTGTGTTGCAGGCACT C
Lri34P1457601	G	T	TGCCGGACTCGCG	TGCCGGACTCT CG	GGCGGTGCCCTTGTAGAC	0,0	CCCATGGACTGCGTCAAG
Lri35P1746600	G	T	CTGTTGTGGGAA	CTGTTGTTGGA A	GTCGATCACATTACTCGTA CCG	0,0	CTCCTCGCTCAAATGAGCAC T
Lri35P3483061	G	A	CTACACCGATGTA	CTACACCAATG TA	TATTGGTTCTGTCGCTACA TCG	0,0	CCGGATAGCCTGTAACAAAC TG
Lri3691P10383	A	C	AGGGTCTGTTA	AGGGTCTGTTC	CCTGCAAGTCATCTCAATC AGT	0,0.3	ACTGCTGTGCCAGGCTAGGT
Lri36P402209	A	G	GAACATCACAGAG	GAACATCGCAG AG	AGTCCTTAGAAGAAGGCG ATCC	0,0	AGGAACCGATCCATCTTCAT AC
Lri37P1167580	G	T	CACCTGGCCAGAT	CACCTGTCCAG AT	GGCAACAGTTTGCTTACGA TTC	0,0	CCTCCAGGCACTGTGATTTT AT
Lri37P1334668	A	T	AATATTCTCATA	AATATTCTCTTA	GGACCCTGAGTCTGTGCTT G	0,0	GTTCAATTCCTGGTTACCCTC A

Lri37P1937714	T	C	AGGAAATATTCCA	AGGAAATATCC CA	AGTCACACGAACAATGGC TTCT	0,0	ACCAGCGTATCCTTTGGAAA AT
Lri37P4230445	C	T	TGGTAACGCTCC	TGGTAACGCTT C	AGTTTGTGAAAGTTGGCA GGAT	0,0	GAAATAAAAGGCCAAGAAC ATACA
Lri37P4502867	A	C	ACTACCAGATATA	ACTACCAGATC TA	AAATGAGCAACGAGAAGT ACGA	0,0	AGTTCTCCCGCAGTGGAGT
Lri37P731186	T	C	CTACTTTCTCTACT	CTACTTTCTCCA CT	TGAAACCATCATGTGAGG AAAG	0,0	CACCAACAGGGAACATAGC AC
Lri38430P1343	G	C	CCTGCAGGTTGAG	CCTGCAGGTTC AG	GAGTGGTGAGGATACGGT TGTT	0,0	GGAGGCTGACAACAATGAG ATT
Lri39P2374814	G	C	GCAGCGAGCTG	GCAGCGAGCTC	GTACGAACCTGAATCCCG ACT	0,0	GGGTTTTTGGTCGGCTTG
Lri39P3784671	C	G	ATTCAAGGCACAG	ATTCAAGGCAG AG	GAACACCAAGCCCCATTG T	0,0	CGTGCGAGGATGAGGTCT
Lri39P4974575	C	T	TTTCTTTTATTACA	TTTTTTTTATTA CA	GACACTGCCAGCCCCAAA TA	0,0	GGCTTTTCTGGGTAAATAAG AAAT
Lri39P5026600	T	C	CCGACGGGCATGG	CCGACGGGCAC GG	GAGTGGGGCTTCCAGCAG	0,0	CACGCGAAGTTGTGGAGAGT
Lri3P10860799	A	G	ACACAGCGTAGTG	ACACAGCGTGG TG	CGGGTTTTCTGTCACATAT CCT	0,0	GAGTTTAAACATACACGTGG CATT
Lri3P11837289	G	C	AGGGGCATCTTT	AGGCGCATCTT T	CTGGCCAGTGTGCAAGAA C	0,0	GAAGGCTTTCCACCAAGAGA G
Lri3P13239723	T	G	TGCCTCCTGCA	GGCCTCCTGCA	TGAGCTCATCCTTTTCACA GAG	0,0	AAGGCGAGTGGTGCAGTG
Lri3P15907151	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	ATGTGGTTCAACTAAGCA ATGG	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

Lri40P5376191	C	A	GCTCCTCGGCCGA	GTCCTCGGCA GA	AAGACACGGCGTTCATCA TC	0,0	GTTGAAGGGTACCAGGACAG AG
Lri40P897424T D38	A	G	TATACACCATA	TATACGCCATA	AAGCTATTGCAGTTGAGC AGTG	0,0	TCAACCTTTAGCGAATGTAT GG
Lri4109P7946	A	T	CAGGTCACTCATC	CAGGTCACTCT TC	AGGGAGAAAGGGTGACAC AGAT	0,0	ATGGAGGCAGCGTGACAATA
Lri41P393985	C	T	CCTGGCCCCGTCCT	CCTGGCTCGTC CT	AGTCCCGTGCCAATTTACA G	0,0	GCTTCAAAGTGACCTAGTA TGG
Lri41P476134	C	T	GGCCGGGCGCGGT	GGCCGGGCGGT GGT	CGTACTGGAAGAGGCTCA GG	0,0	CCTACATGGTGGACGGTTTG
Lri4294P2756	T	C	GGCTCTGCTGTGT	GGCTCTGCTGC GT	GGTTGCGAACTTAAGGAC CTC	0,0	TATTTAACTCAATGTCATTA ACAAACC
Lri43P1676686	A	C	ATGTGTCACCACG	ATGTGTCACCC CG	GATGGGCGCAAACATCAC	0,0	TTTGCACTAACTTTCTGCCTT TC
Lri44P106745	G	C	CTGCAGGGAGGC	CTGCAGGGAGC C	GATGGCATAGAGCAAATC GAC	0,0	TTCGAGTGCGTCGTCAAA
Lri44P3432223	T	C	TTATTTTAGCT	TTATTTTAGCC	CTGCAGGTTGCGTCTTCTT	0,0	CCTGGCGACCTCTTCGTAT
Lri44P3836279	A	T	AGACGCCTCCA	AGACGCCTCCT	CCCTTATTTAAATTCCCCG AGA	0,0	GTGCAGTGTTCGTATTTGCG TA
Lri44P527021	A	G	GATCAGACCTGC	GGTCAGACCTG C	GACACCCTGGGGTTTGTG	0,0	CTCCTGCAGGCACCAAAT
Lri45P1246569	C	G	GACGGACAGGCA	GACGGACAGGG A	CACCGCCTCCACAAACTG	0,0	GTGACAGGTGAGGGTGAGA GT
Lri4631P8667T D39	G	T	TGGCTGGGACC	TGGCTTGGACC	AAGAGCAACCCCAAACAT TAC	0,0	CTATAGCACGGACGACTTAC CC
Lri46P2660109	C	T	CGCGGAACGCAGA	CGTGGAACGCA GA	GTTGCGCATGGAGGAAGT	0,0	GATGATGGCGAAGCTGTAGA C
Lri46P2937100	T	C	CGTCGTGGAGTGG	CGTCGTGGAGC GG	AGGAAATGGTGAAGGTCA TCC	0,0	GCATCTCTTCGTTTCGCATCT
Lri46P4260004	T	C	TGCAGGGCTCCT	TGCAGGGCCCC T	CTCAATCAAGTGCAATTTT GTC	0,0	ATGCATATTCACACGCACAC AC
Lri47P1274188	A	G	CACGCACGGCAA	CACGCACGGCG A	CACCAAAGCGTATATCTGC CTA	0,0	CCACTGACGGATCACATTAG C

Lri47P4802446	A	G	CGCCGTGTTTATG	CGCCGTGTTTG TG	CTGCAGGTGTTGCCGTCT	0,0	GGATAAAATTAAATAGTCCC AACTCG
Lri47P580971	G	T	GCAGGTCAAAGCG	GCAGGTCAAAT CG	GACACTCCGACTTTTGTTC CTC	0,0	CTTGTGGTGGTGGTGGTTTT
Lri48P66561	T	C	GGGCAAACCTACCGC	GGGCAAACCAC CGC	CCTGCCTGCAGGATTGAT	0,0	CTTTGGAGCGCAAACATTG
Lri48P1014973	T	C	CCGACCATGAT	CCGACCATGAC	TGCAGTTTTACTCTGGCTT TGA	0,0	GGTCGTAGTGCATGTTGGTC AT
Lri4P11912704	C	T	GGGTATCCGCGTC	GGGTATCTGCG TC	ATCTTAATCCGGCCCTGCA T	0,0	GAAGCTGCCACGGCTCAT
Lri4P12290187	T	C	GGATGGACTGTAC	GGATGGACTGC AC	CTCCCAGGCTGAACTCCTG	0,0	ATAACCCATTGACACATTGC AG
Lri4P14283823	A	C	TGCAGGGCCCAAGT	TGCAGGGCCCC AGT	CTCGAGCTTCCAGAGACTT CC	0,0	CCTCCTCCTCAAACCTCAACT C
Lri4P1741698	C	G	AGGCCTTGTGCAC	AGGCCTTGTGG AC	GGGGATCACTATGCTGGT ATTG	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	CTGCAGGGCATGAGAATAGA T
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
Lri50P1221681	G	C	TTGCCACGTA	TTCCCCACGTA G	AAGATCTGGCCACACCAA ACT	0,0	GCATCTGTTCGTCCAGCTCT A
Lri50P1657665	T	C	TTTCTCCAAC	TTTCCCCAACT	GCGTAACAAGGTCTCATTA TTGC	0,0	CTGAAAGCTGTCCCAGTAGG TT

Lri51P900701	A	G	TGCTCAATGAAGA	TGCTCAATGAG GA	AGGATGAGAAGCACCAGC TCT	0,0	CCCTCACTTCTGTTCTTGAT CT
Lri5215P4376	C	G	CATGCCGCTCTCA	CATGCCGCTGT CA	AGTCCTCTTGCCACCCATC	0,0	TCCGTCTTCGACACGTCAG
Lri5229P1229	A	C	TCCCCACACCAAC	TCCCCACACCC AC	AAGGCAACAAAAACACCC TTC	0,0	AATGAAGGCCTACCCATGTT C
Lri5244P5218	T	A	GTAGTAATAATA	GTAGTAATAAAA A	CGTGTTAGACCACAGAAC GAAC	0,0	GCAGGCACGAAAGTTTCAA
Lri5270P9970	A	T	ACGATATAACAAC	ACGATTTAACA AC	AATGTCCACGTTTCATATG TGC	0,0	ATTACCAAGAGCATTGACCA AC
Lri5345P10185	T	A	GAACGGTGTAGTC	GAACGGTGAAG TC	TGCAGGTATAAACTAACC CTCGT	0,0	CTGTGGTCCTACATTGGGAT G
Lri53P1124643	G	C	GGCATTTTGAGTG	GGCATTTTGAC TG	TGCAGGTTAGGGGAAATG AGTA	0,0	GGAGAAGTGCTGCTCGAAAG
Lri53P2383812	A	G	TGCAAAATACACCC	TGCGAAATACA CCC	ACTGCCTCCAGGAATTCAT CAT	0,0	GCAGCTTAAGTTAACACAAA TTGTAA
Lri53P2456049	A	G	TTGCAAAGTTAAA	TTGCAAGGTTA AA	TTAACGGTCTCCCTCTTCC AG	0,0	GATGTAAGCCGCCTTGTTAC AG
Lri53P338003	G	C	CTGACCGTCTGCTG	CTGACCGTCTC CTG	AAGCCGTACGGTGTTTC	0,0	GTCAGTGGCACCCCTGCTC
Lri54P1001845	A	G	CGGGCGCAAGAGA	CGGGCGCAAGG GA	TTCTGCGGGTCCTTGAAGT	0,0	GATCATCTGGCTGGGTCTGT A
Lri55P2165401	G	A	CTGCAGGCGAGTC	CTGCAGGCGAA TC	CCGTCTTGTTCTGATCCTT CTT	0,0	ACGCTTTCCCCAAAGTTAAG
Lri55P3190566	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
Lri5P12934722	G	C	CCTGGAGCTGGAGC	CCTCGAGCTGG AGC	GTACCTTCCCAGTACCGCA AAT	0,0	TTTAGAACAAGGGGATTTGT CA

Lri5P13075196	G	C	ATTCCGATGCTAT	ATTCCGATCCT AT	GCAATAAAAGGCCACGAA ATTA	0,0	ACCTCTGGTACCTCAGGGTC A
Lri5P13191816	T	G	TGGCTCTGCATCT	TGGCTCTGCAG CT	GCAATAATTGTGTCCATCA TGC	0,0	CTGCAGGGGTGCTTGTCTA
Lri5P14389115	C	T	GCACGGGCACAC	GTACGGGCACA C	GTGCCCCGGTTACTGATG	0,0	GTGGGCAGCGTTGTGAGA
Lri5P14629399	G	T	TGCGACCTTGGCT	TGCGACCTTGT CT	AGCTCTGTCCTGCCCTCCT	0,0	TGTTACCATTAAAATACACA AATCTCG
Lri5P2456252	T	C	TTTTTGTCTAGAA	TTTTTGTCCAGA A	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	TGAAAATAATGGGTCCCT AACA	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	AAACCTTAACATTTACAGCA CTCG	0,0	GACCTGGAAGGAGTGTCAC TT
Lri5P9366468	T	A	GAAAAAGTTACGT	GAAAAAGTAAC GT	GCAGGCAGAATAGTGGAA 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	CAGTAGGACGCCCACAGC
Lri61P3097033	T	C	CGCTCTCATCTGC	CGCTCTCATCC GC	GTTTCGTGGACACGTAGTG AGA	0,0	CTTGCCCGTGTGGTTGTAG

Lri61P414412	G	A	ATGGAGTAACTAA	ATGGAATAACTAA	CTGCAGGCCAGTATACAA CATT	0,0	AGTTTAATTTTCGGGCATTGG AT
Lri63P1075345	T	C	CCTGCAGGCATACA	CCTGCAGGCAC ACA	ACAAATGAGTTCGTGCCAT AAG	0,0	CAATTGCAAGATGATTTCCA GA
Lri64P1877052	C	T	ACACTAATTCATA	ACACTAATTTA TA	AATATGTGGTCTCTGGGTT TGC	0,0	CATGCCTGCAGGGGAAAT
Lri64P3699994	C	G	ACCGGTGGGGGGG	ACGGGTGGGGG GG	CTGCAGGATTGTGAAGGC TAC	0,0	GCGATCTCCTCCTGAGACAC
Lri65P1192162	T	C	TCTCAGAGCTC	CCTCAGAGCTC	GAGGGCCACATCAACCAC	0,0	TGCTCATTGGCGTTGTAGAC
Lri65P2520673	A	G	AATTGATAGGT	GATTGATAGGT	GAGGGAATTCCGAAGTTG AGTA	0,0	CGTATGGTGCAAAAGAAGTT CA
Lri65P2642230	T	C	TGCACAGCAAG	CGCACAGCAAG	AACCTCTACGTGACCTCGA TCT	0,0	GTGAAGTGCTCCACGATGTT T
Lri66P303856	C	A	AAACACACCCCGG	AAACACACCCA GG	AGAATGTCTGGGACATCAT GC	0,0	TTCATCAGGCAAACAACACG
Lri67P441125	A	G	GGTGCAATGGA	GGTGCAATGGG	AGCGAGGACAAGAAGACC TG	0,0	AGAGGGTCGTGCTTACTTCT C
Lri69P3566988	C	T	TAAAACATGTCCT	TAAAACATGTT CT	GCTGGCTATCATCCCTTCT AAA	0,0	TGTCTGAAGTAAAGTGGGCT TG
Lri6P10286942	T	A	AAGTAATGTATCT	AAGTAATGTAA CT	GTGTGCATTGATTTGACAG GTT	0,0	CTAATGGGGAGCCAAATAAA C
Lri6P10328882	T	A	GGAAACCTTTTTTC	GGAAACCATTT TC	AGTTGGGTGGCCTCAATGT	0,0	GAAGCTCCGTCTCTAGAAGT GC
Lri6P10383294	C	G	GCATGCATCCCGT	GCATGCATCCG GT	TGTTTAATGTGAGCAGTTA ATCGTG	0,0	TTTCACTCGATTACCCCTCTG T
Lri6P10474030	C	T	AATCCCTCCCATGA	AATTCCTCCCA TGA	CCGAATCGTCACCGATCAT A	0,0	TCAAATGCAATGCCACTAGA AC
Lri6P10581411	T	C	TTTCTCACAGTAT	TTTCTCACAGC AT	AGATAGGGACAAATTTGG GTCA	0,0	ACTCCAGGCAATGCAGTCAC
Lri6P11041437	A	G	ACAACACTGTGCT	ACGACACTGTG CT	ATGTAACCAAGCAGACCA CAGT	0,0	AGGGATTGCAGAAACAAAG AAC
Lri6P13329068	C	A	CCACGTTGTGATGG	CCAAGTTGTGA TGG	AGACGAAGCTGCATCGAG AC	0.1,0	ACTTTACCGAAAGGACCAAG A

Lri6P2036382	G	A	TCCAAGCCACGGC	TCCAAGCCACA GC	GTGGTGGTGTGCATTAATT GGT	0,0	GATTGCCTGCAGGATTGTG
Lri6P5039589	C	T	TTGTGGCGGTCCA	TTGTGGCGGTT CA	TCACGAATTCACTCGCTGT ACT	0,0	GGCAAGGGTTGGTGGATT
Lri6P5524704	T	C	GGCATTCGAGTCC	GGCATCCGAGT CC	ATGGAGGGAGACCTCTGG AT	0,0	AGGAATCCGATGAGCTATGA AG
Lri6P6080845	G	A	CGCCTTCATGAAG	CGCCTTCATAA AG	GTGGTTAACGCACCGACT G	0,0	GTTTGAGATGGACGAGGTGA GT
Lri6P6130428	T	C	GAGTATATTC	GAGTACATTC	CTTCCCTTCGATCATCCAG TC	0,0	GAACATAGGGGACATTTGAA GC
Lri6P7202854	G	T	CAAGCGCTGTCTGA	CAAGCGCTTTC GA	ACAAAACGTGGCCTCGT G	0,0	GATGATGGTGGTGGTATGA T
Lri6P8338530	T	C	GCTCTGAAGAG	GCTCCGAAGAG	GCAACAACACCAGGACCA AC	0,0	CGCCTATCTCCCAACCAAAT
Lri7079P1000	T	A	ATCACATATCTT	ATCACATATCA T	GTCTTGATGGTGGAACCTT ACC	0,0	AGAGCCGTCGCCTAACCT
Lri70P1263023	G	A	TTCACCGTTC	TTCACCATTC	TGCAAAAGTAATTTATTAT GGAAATG	0,0	AGAACTACACCTGCAGGCAC AT
Lri71P1277485	C	G	ACGCTGCATGCCC	ACGCTGCATGG CC	CTTCCAGAGCTGGCGGTA	0,0	GTCGTGGAGCTGTTTCAGG
Lri73P2199950	C	T	AGGTTGTGTGCC	AGGTTGTGTGT C	GAATATCCCTTGCAAAAC ATGG	0,0	ATGTCACCACAAGCCTACGT CT
Lri7435P3947	C	T	GGGGTCAAGCTGA	GGGGTCAAGTT GA	AGTGGGCTGGATGCTCTG	0,0	ATGGTTCTGCTGCTCTTCGT
Lri74P1110420	A	G	GCACCGTCACATA	GCACCGTCACG TA	CTGTCTCTCCCGCAGTGG	0,0	CTTGTCGCTGTAGCTGAAGG
Lri75P276391	C	T	TTTAAATAGGCGA	TTTAAATAGGT GA	AGTGGCCAGAACTAGGGG GTA	0,0	AATTGAGGAGGTAATGGTTC GAT
Lri76P1581919	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	GGATTGATCACGGCTGAT G	0,0	TCGACTCTGAGCGAGTACAA G
Lri78P1108359	G	C	GTTTATACACGC	GTTTATACACC C	TGCAC TTCTCTATATGCGG TGT	0,0	AGGTGATCTGCTTCCCTCCT
Lri78P1274279	G	A	AGCGCGAGACGTG	AGCGCGAGACA TG	GAAGCCCTGCCAAACGAC	0,0	ATTGTCGGAGCGCGTTGT
Lri78P1520535	A	G	AGTAAGCAAGATG	AGTAAGCAAGG TG	TGGTAGGGTTAAGGCGAT TAAA	0,0	CCTTAACCACTGGCTTCTTCA C
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
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	ATTTTCATAAATGAGGGG GATG	0,0	AGACGCTCCACACTCACCAC
Lri84P876835	T	A	CGCAAGCGGGTAA	CGCAAGCGGGA AA	TACCTGTTTTAGGCCCTTT CAG	0,0	CGCCAAGCTTTTGTCTGCTA
Lri84P876852	G	T	TGCAGGAGAGAT	TGCAGGATAGA T	AGCAGAAACCGCTGAAAG TG	0,0	CTAATTCTGCGCCAAGCTTTT
Lri85P2050795	G	A	GAAGCAGTTTT	AAAGCAGTTTT	CGAGTGGCCCAGGGAGTA	0,0	GTTGAAAAACAGCCTGAAAG AT
Lri85P2095420	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	TGGTGCAGTGTTACGTC	0,0	TTTTACCTGCTGGTAGATCTC G
Lri86P103182	T	G	AAGCGTAGCGTGA	AAGCGTAGCGG GA	TTAGGTCTGCACCCAAAA ATAA	0,0	CAATTAGGCATGAAAGCATT TG
Lri88P1164318	T	C	GCCCATTTAGTCC	GCCCATTTAGC CC	TCTTCTCCAGCCCATCTCA C	0,0	CTGGGTCCAATGAACTTCTG TT
Lri89P2322061	A	G	TTTTCCGACAAGC	TTTTCCGACAG GC	TTTTTGTCTCCACATTGC AC	0,0	GCTCTTACAACGTTTGGAGC AT
Lri8P1441255	A	T	GTGTCTGGACA	GTGTCTGGACT	GGTGAAGATGCTGTGTC AGAG	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	CGATTGTTCTGTCAGGTGT

Lri91P204352	T	A	AAGAGTATTCTG	AAGAGTATTCA G	TCACGCAGGTAAC TCATTT CAT	0,0	GATGTCACAGTGGTTCACAG GT
Lri91P2342186	T	C	GTGTCCAGGGG	GTGCCCAGGGG	CTGAAATTAATCCCTGCTC CAG	0,0	GGCACACCTGGACACATCT
Lri91P730506	C	A	GACGCATTTTCTA	GACGCATTTTA TA	GCTACCGAACCGGTGACTT	0,0	TTAATAACACGCATCAAAGA TACATT
Lri93P1340289	A	G	AGAAGCAGAAAC	AGAAGCAGAAG C	GAGCGATTCTCTCCGTACC AT	0,0	CAGGAACAGCTCCTTGTTGA A
Lri96P1067926 TD50	T	C	AA[CT]GTTGGGTT	AA[CT]GTCGGG TT	GCTAGCTGAACCCGTTACA CAT	0,0	GCATATTTGCGGAATACACC AC
Lri98P763276	A	C	AGGGTCGCGCAGC	AGGGTCGCGCC GC	GCGTCTTCAAAC TCATCGA GAC	0,0	GCGTACGGATGTCAGTGCTT AG
Lri99P330522	A	G	GCAGGTTGCAAG	GCAGGTTGCAG G	TTAGTAACCCTTTCCCGAG ATG	0,0	CCTGAATAAAATGAACGCTG A
Lri9P10378057	C	T	GATCGGGTCTC	GATCGGGTCTT	ACAAAGGTGGCCAGACAT GA	0,0	GGCTACTTATAACCCACGTT GC
Lri9P1124057	G	T	AAAACACGGTGCA	AAAACACGGTT CA	TGTGAACCTCGGGGGAAG	0,0	ATGAAATGCGGTAGTGTCTT G
Lri9P12500977	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	Rev Primer
Atr_1030 4-61	G	A	TGGCTTGGCAGTGG	TGGCTTGACAGTGG	GCCTTTGTTCTCCAGCTTGC	TCTAAACAGACCAATCCCCTG
Atr_1032 2-43	G	A	GCAGCGAAACAAAG A	GCAGCAAAACAAAG A	TGCAGGGGCTATCAGAGACT	AATCAGTGTGGGAGCTCAGC
Atr_1042 8-71	T	A	AGAGAGCTAGCA	AGAGAGCAAGCA	CGCACACACACAAAGAGAGC	GGATCCAGAGCCACAGTGTC
Atr_1043 7-26	T	G	TTTTTTGGCAACTGT	TTTTTGGGCAACTGT	TGCAGGTGGGTATGGGTG	TGAATTAAACAGGTACAGTTGC AGA
Atr_1067 2-61	C	T	GACCACACTGGGCA G	GACCATACTGGGCA G	GCAAAATTGGCAGGGATGGT	GCAGGTGTTTGCTTGAGCTC
Atr_1086 7-69	C	T	TGGTATACAATGAA	TGGTATATAATGAA	AGGACTGGGTAGGGAGCATT	ACCGAGCTGGATGACTTGAA
Atr_1099 8-72	T	C	AGTAATGTGTT	AGTAATGCGTT	CAAAGCGCCCATGATTGTCA	TTAGCAGGCACAACCTGACAA
Atr_1104 6-75	T	A	GGCCCAAT	GGCCCAAA	GGAGGGCCTGGGAATCCT	TTCAGGGGGAACAAGGTGAG
Atr_1110 4-35	T	C	TGCACTGTCGTGTCT	TGCACCGTCGTGTCT	CGCTAGTAGTGAAGTGAAGTG C	CCCTCTCAGGTGCTGTTCAC
Atr_1158 5-33	C	T	TAAAGCCAAGTTTGT	TAAAGTCAAGTTTGT	GGTTGGTAGTTTGCGGCATT	AGTGGAGTTCTCCGATCCCA
Atr_1178 7-73	G	A	CTAACCCGCG	CTAACCCACG	ACAGTCCCTACAGGCATTGC	GATTCCAGAGGGAGTGTTCG
Atr_1186 4-68	T	C	ATATCGCTGACCAC	ATATCGCCGACCAC	GGTACCACCGCCAATATCGC	CAGAGCTGCTGGTTGTTTCG
Atr_1221 9-56	A	C	ATAGTATATGCGGG	ATAGTATCTGCGGG	GCAGGGAAGTCTAAACCCCA	AATTGTGTTCTTTGCCCCGC
Atr_1261 6-36	G	A	GCCGTTCGTGAAGC	GCCGTTCATGAAGC	TCCTGCCATGCTAGCAAGAG	TCCACCGGCTATTCTCTTT
Atr_1267 7-44	A	G	ATGTACTATTTAGC	ATGTACTGTTTAGC	TGCAGGAGAGGATGTATACGT C	ACTTCAAACAACAAAAGGCTGC T

Atr_1307 3-61	T	A	TTTTAATTTGCATT	TTTTAATATGCATT	GCTGCAGCTTACAGTCTTCA	TGCAGAGCTCAATCCAAACCT
Atr_1313 2-45	G	A	GCCACGAAGAACAT G	GCCACAAAGAACAT G	GTGACCAGCATGACCACCAT	TATCACAGGGAGCTGGGGAT
Atr_1347 6-65	A	T	TTATCAGTATGCAGC	TTATCTGTATGCAGC	CGTTTTCCAGCACCACAGGT	CTGACCTTTGGCTTGTGTGC
Atr_1370 6-54	A	T	GTGAGAGAAGACTA	GTGAGAGTAGACTA	AGGCTACTTGCATCTGCCAG	TCATAAGAGCTGTCTGAACTG A
Atr_1372 9-47	T	C	GCACAAGTTTTTTT	GCACAAGCTTTTTT	CCATAGCTTTTGTGCAGCACA	TGCCTTTATGTTGACAGGGTCA
Atr_1391 7-71	C	A	AACTACTCATCA	AACTACTAATCA	CCTTCCCAGGGAGCTTGATG	CAGAATGCAAGGTACACTGTTG A
Atr_1393 0-72	A	T	GTTTTATAAGC	GTTTTATTAGC	TGTTTTAGTGGGACCAGTGCT	TGCAAAATAAAACACTGTGGAA AAA
Atr_1399 6-43	T	C	TATTCTGTAATGTTT	TATTCCGTAATGTTT	CAGGTCTGCTGTGTGTGACA	TCAAGTTCACCTCGACAGCA
Atr_1441 0-52	T	A	GAAGCAATCCCCAG	GAAGCAAACCCCAG	ACAGGTGGTTCATCTGCAAAC	TGGCATTGTTTCCACTGGGG
Atr_1463 5-67	C	A	GGAGCACCAAAAAC	GGAGCACAAAAAAC	ATCCCCAGCTGATTTGCCTC	ACCACTTTAATGCATCTCCTGG
Atr_1482 4-32	A	G	TTAACATGAAAGTCA	TTAACGTGAAAGTC A	TGCAGGGATCCACAGAAATGT	AAGCAGCTGAACACAATGGG
Atr_1486 2-38	T	C	TTGACTCCCTTTAAG	TTGACCCCCTTTAAG	CGCCTCCCCAGGACTATTTT	TTTCCTGTGGCCATTTTTATTGT
Atr_1491 7-56	C	T	AACACATCTTAACA	AACACATTTTAACA	TGCGCCACCTAGAAACACAT	TGCACAAAGAAAGGTCCTGGT
Atr_1517 9-54	G	T	TTCAAATGACCCCA	TTCAAATTACCCCA	GCAGGGTAAGTTAGTTTAAGC GC	GGTGCAGCTTGTATGGGGT
Atr_1520 1-45	A	C	TTACTGAAACACAT	TTACTGACACACAT	GGGTACAGTGCAAGAAATGGC	TAGTCAGGTTGGCTGTGAGC
Atr_1527 3-44	T	G	ATAGATCCTGTCCTA	ATAGAGCCTGTCCTA	GGGAATGTTTCTCTGTTTGG T	ACTCCAGTCTGGACATAAACTC A
Atr_1529 4-66	T	A	TGGGATAGAATTTTC	TGGGAAAGAATTTTC	TGTATTGTTCGGATGAATTGGG A	TCTGATGTAGAACTTCTGTGTA GTT

Atr_1529 8-72	G	A	TCTCACTGTAT	TCTCACTATAT	TCTCAGCATCTTTCACTACCCA	TGATAAAGCAACCTTGAGCCCT
Atr_1587 5-62	C	T	CCTGCCCCGTGGAA	CCTGCCCTGTGGAA	TCCATCAGAGCTCACCAGGA	AGTGTTGCATTGGCTCTGGA
Atr_1680 3-66	C	T	GGCAGCACGCCTCT	GGCAGCATGCCTCT	CATGTTGTGTGTCCGGTGC	TCCCTGGAATTGGTGCAAAA
Atr_1720 -33	C	A	GGGGGCTTTGAGAG C	GGGGGATTTGAGAG C	GGCAAAGCAGAAGGGGG	TGTGTGTATCTGTCTGTGTGGT
Atr_1771 0-71	T	C	CAGGATGCCC	CAGGACGCCC	GCTCTCCCATCTTTTGCAGC	AACTGACGGCAGCTATTCC
Atr_1813 3-56	G	A	TGGGTTTGTGTAT	TGGGTTTATTGTAT	AGTCAAGTGTGTGTGTGGGT	AGCAGGGAAGATACTGGTTGC
Atr_1829 5-67	T	C	ACCTGCATGGCAAA	ACCTGCACGGCAAA	CTCGTCTTGAGGCACCTGC	TGAAAACCTGGCAGCTTTGTGA
Atr_1833 4-74	A	G	ATGGTGGAC	ATGGTGGGC	GGAAGTTGGTCTCAGAGGC	AATGAGTGCCATCAGCCACT
Atr_1840 3-29	C	G	AGATCCATGAAGCTC	AGATCGATGAAGCT C	TGCAGGTAATGAATGTTGCCT	TGCGTTCTGTTTCATCCCTCT
Atr_1949 6-44	A	G	GAGTGAGGCTATTGG	GAGTGGGGCTATTG G	CACACCTAGGGGCACATTGA	TCAACAGCGAGAAGGGTTGT
Atr_1966 6-61	G	T	ACATTCAGGGCATA	ACATTCATGGCATA	CAGGCCTCAAGCTCTTCTGT	TGTAGTGAGGTTACCTTATTAT GCC
Atr_1978 3-57	C	A	TCTAACATGGACATC	TCTAAAATGGACATC	TCTTCTTCTGGAATGATTACAT CCA	GACAGTGAAGCAAGAGAAATC CA
Atr_2001 3-55	C	T	GCCTGCTCCCCTCG	GCCTGCTTCCCTCG	GATGCTAACCTGGCTCTGGG	CCGAATATCCGCGGGAAGAA
Atr_2003 7-39	G	A	AGAACGTGTTCTCTGC	AGAACATGTTCTCTGC	GCAGGCGTAGAGTTACAGCA	ACAGTAGACGTCAACGGGAT
Atr_2011 7-55	A	G	GCTTCACCCCAGGCA	GCTTCGCCCCAGGCA	CCTGCTCCCAAACAGGACAA	TCAGATGGGCCTGGTGAAAC
Atr_2021 9-65	A	G	ATGCCAGGCTTTCTA	ATGCCGGGCTTTCTA	TGGACCTTATTAGAAGCTTAAT GCC	GCACCTCTATGGCACTTTTTGG
Atr_2025 2-35	T	C	ATGGGGGTTGTAAT	ATGGGGGCTGTAAT	ACTTGGACGAGGCATCATGG	GCCAAATTCAACTGCTGGGA

Atr_2033 2-60	T	A	GTATAACTAGAACAA	GTATAACAAGAACA	ACATTGCCTACACCTCACCC	TTTGA CTGCCACAAGCTCCT
Atr_2048 2-41	C	T	CGGGAGCCGAGCTT	CGGGAGCTGAGCTT	CTCATTGCAATTGGGCTCGG	GCAGCCTAGCAGGATCTCAT
Atr_2052 9-52	A	G	GCACAAC TTTT TACA	GCACAGCTTTT TACA	ATCGCAGCTTGACAGTGAGT	AGTAATTCCAAAAAGCCCACTG G
Atr_2074 0-65	T	C	ATTGCTCTCTGCCCT	ATTGCCCTCTGCCCT	AACATCATCCCCCTTCCTGCG	GAGTTCAGAGCCAGCACAGA
Atr_2084 -45	A	G	GGTTTGAAAATGTT	GGTTTGAGAATGTT	TGAGGTAGCCAGCAGGTTTG	AATGATGCCAGAGCGCTGAT
Atr_2095 2-49	T	C	ACACTACTCTGCCC	ACACTACCCTGCCC	TCCCCAGCTGACATGAACAC	CACAATTGGCCAAGTGCTGC
Atr_2168 5-29	A	G	GTGCTGAAGGCTCC	GTGCTGAGGGCTCC	TGCAGGTTTGGTTCTCTGTTTG	CCACCAGCCAAAGAGACAGT
Atr_2200 8-56	C	T	TACTGAACAGTGAT	TACTGAATAGTGAT	GGGCAAGAAAAGACCCAAACC	GCCTTCTGGTCCTAATATAAAG TGC
Atr_2272 7-31	C	T	TTTGCCAGATTTT CAG	TTTGCTAGATTTT CAG	GCAGGAAACCATGATGCACC	TGACTTACTAGACATCTGCAAC TGA
Atr_2307 0-31	C	A	CAGTCTCCGCATTT	CAGTCTCAGCATTT	GCCTTTGCCCTCCAGTCTC	TCCTCTGATCCCACGACCTT
Atr_2414 6-56	A	C	ACATGTTAATCTTG	ACATGTTCATCTTG	TGGCTAAAGATCTAGAACACA TGT	TCAACCGAGCTCTGTTGCTT
Atr_2515 9-57	T	C	TATTTTAGTGGAAGC	TATTT CAGTGGAAGC	CCTGAGTGTGTGAACCAGCT	ACATGTTAGCCAAGAGTTGCA
Atr_2540 -75	A	C	TCTGGTAA	TCTGGTAC	TCAAGCATGCTAAGTGTCTGGT	TGTTCCCGGGTGCCAAAAA
Atr_2554 0-60	C	T	AATTCCCAGCTATGC	AATTCTCAGCTATGC	AGCAGACCACTGGCATGAAT	TCTATCATGGGCATCTGCAAA
Atr_2556 2-47	A	G	CGGCAAGCAATAAA A	CGGCAGGCAATAAA A	CGGTTATAGGATTAGTATGCGG C	GCAGAGTGCAGTGAAATAGCC
Atr_2588 4-65	T	G	AAAATTTTCCCGAA	AAAATGTTTCCCGAA	GCAGGGAGATTGGGAAGTCA	AACAGCAAAATTTAAATTCGGG AAA
Atr_2590 5-72	G	A	AAACCACGGAA	AAACCACAGAA	TGAGGGGAAGTTGAGGTGTT	TTCCTCTTGACCTTTCAATTGAT C

Atr_2631 0-63	A	C	GAACGAAGCTTAGTT	GAACGCAGCTTAGTT	CAAAATGCCCGATCACCCAC	TTTGCCTGTTTGACCTCTG
Atr_2684 -39	A	T	ACTGGACAGAGATC	ACTGGACTGAGATC	CAGGAGACGCAGGGAGAAAG	GCCCACACTGTCATTGAGCT
Atr_2707 2-33	T	A	TTTATGATAGTGAT	TTTATGAAAGTGAT	GCAGGTGATTGGTGGAAATAG C	TGGACTCGCATCACCTTCAC
Atr_2736 7-69	T	C	AAATAAATACACAG	AAATAAACACACAG	CGTTTCCACAGTGGCAATCA	TGTGTGAATTTGGATTTCTCTGT GT
Atr_2739 5-73	C	T	CAGG[GA]CGC	CAGG[GA]TGC	TGCGACTCTGCTGTGTATGA	GACATTTTGCTGTCCAGAAGGG
Atr_2743 0-71	A	G	ATTGCCCATGCC	ATTGCCCCTGCC	CTGGTCTGGTCAGCAATTGC	AGTGCCCCAACACAGTATGG
Atr_2768 -35	C	T	CGCCTGGCCAGTTG	CGCCTGGTCAGTTG	TGCAGGTGTTTCAGTTGAGCA	AGACAATACAGCAGACCCAACT
Atr_2817 5-70	T	G	TTTAGTTTTGC	TTTAGGTTTGC	AGGTAGGCTAGAAATCGGTTC A	TGGTCTTGATTAAGGGGTGCA
Atr_2828 0-63	A	G	TGATCAGAAACCTT	TGATCAGGAACCTT	TCCACTTTGAACTCACCGGG	ACTGTACACTTTGCTTGTCTTCA CA
Atr_2841 1-65	A	G	GTGCCCAACAGGAC	GTGCCCAGCAGGAC	AAACCAAGCAGCGTCTGGAA	GCAGCTCTGTCAGTCTCAGG
Atr_2858 -58	C	G	ACCAGCTGTGCCGGG	ACCAGGTGTGCCGG G	TGCAGGCATTTTGTGGACC	CACAGTACCATGGGAGTCCC
Atr_2860 9-62	A	T	CAAACATATCATTG	CAAACATTTTCATTG	GCAGCAGGGTAAGGATGACA	AAGCAGGGAAATACAAATACA ATGA
Atr_2874 6-28	T	A	AGGTTCTTCACTTT	AGGTTCTTCACTTT	AGGGGTGTTGGGCATAAGG	AGTAAGCACAGGATATAACAA AGTG
Atr_2883 4-39	T	A	ATGTAGGTGACAGT	ATGTAGGAGACAGT	TGCAGGAGTGATCACAAAGAT GT	TGTGAATACCCCGACTGCTG
Atr_2886 1-59	T	A	GACCCTGGTGCAGAT	GACCCAGGTGCAGAT T	ACCCAGGACCAAAGGGAGAT	GTGTGACTCACATCTGCACC
Atr_2902 4-55	A	G	CTCTCAAGTCCTTGA	CTCTCGAGTCCTTGA	TCCAAAGGCCGGTAACTCAC	AAGGCCAGTGAACCCACAAT
Atr_2908 6-33	C	T	TTGTCAACGGGTTT	TTGTCAATGGGTTT	GGTTTGGTTCAACCGCACAG	AGAGAGCGCCTGTAGACAGT

Atr_2927 7-35	C	G	TGAAACAGCAGTAT G	TGAAAGAGCAGTAT G	GGATCGCTCTCTGCTTGTGA	TGCCAAGCCCTAACTGCTAG
Atr_2930 2-34	C	T	CTGCTC[GA]TCTACA GT	CTGCTT[GA]TCTACA GT	GCAGGCTGTATAGTGAACTG G	TTACTACTCACCTCACCTGAAA AA
Atr_2941 4-61	C	T	TTCCAACCGGGGAT	TTCCAACCTGGGGAT	CAGGGCTGGGGTCTGGA	GGCGCACTCTGTCTCCAAAT
Atr_3014 5-46	T	C	AAGGAAATACTTGC	AAGGAAACACTTGC	TGCAGGTTGCCCATTTGTATCA	TATTCCTACTGCGCTCTGGC
Atr_3027 1-58	G	A	AGGAGTCGTATTTT	AGGAGTCATATTTT	ATGCAGAATCCACAGGAGTC	AAGGAGCTTAGACACTGCCA
Atr_3037 6-68	C	T	CAGGAAACGACTCA	CAGGAAATGACTCA	CCGCCAGCAGTCAGGAAA	TTGGTCCACAATCCCCCATC
Atr_3091 6-62	G	A	GACTGGGGCTATTT	GACTGGGACTATTT	AGGTCGTGCTGTATTGGTCA	CAGGTGTGATGAGGGGAAAT
Atr_3099 2-26	C	T	TAATGGTCGTTAAT	TAATGGTTGTTAAT	GCAGGTCTGAAATGAGGTAAT GG	GCTCCCTTTTTATTGTGTGTGAC T
Atr_3191 7-28	T	C	AAAACCTGGTCGCTCA	AAAACCGGTCGCTC A	TGCAGGACCAAGTGGGATTA	TTACAGAGGAAGGTGAGCGAC
Atr_3223 4-71	C	T	CACGCCACGGGG	CACGCCATGGGG	CTCAGGAGGATGGCCATTCT	TGTTACAAAAGGTCTCATCCCC
Atr_3238 2-60	G	A	TATACTCGGAAACA	TATACTCAGAAACA	CAAACCCTGGTCCCTTGGTC	GGGACTGCAGTGCACCTAG
Atr_3254 5-55	A	G	ACTCAACACGCCCT	ACTCAACGCGCCCT	TCCACTTGGGATGATCTAATCT CC	TTGAGAACCAGTTGGGCACT
Atr_3255 1-51	G	A	AGGTCGAAGTAGTG G	AGGTCAAAGTAGTG G	GCTCTCCAGGTTGTCGTTGA	AGAGTCCAGCGGGCCTAC
Atr_3284 0-74	T	A	TTCATTA	TTCATAA	TGGCACAGCTTTACCGGTTT	GTCCACAGAGTTGTTTGTGAAA
Atr_3294 5-42	G	T	AAAAGAAGAGTTCC	AAAAGAATAGTTCC	TGCTCTTTCAAATCCTATGACT CA	AGCAGAAATCGTTTTACAAGGA AC
Atr_3312 3-54	T	C	AAAGCAATGATTAA	AAAGCAACGATTAA	ACTGTGTTCAAGAGACCATTGG A	AGAGTTTTTACAACATTATTGC CCT
Atr_3364 5-66	G	C	TCGCTCTGTGAGGT	TCGCTCTCTGAGGT	TGCGTGTCTGCATCTCCAAT	GGCAGCACAGACCATACAGT

Atr_3379 8-72	G	T	GTGCCGCTG	GTGCCTCTG	ATTTTGGTTTGTGGCGGTGC	GGTTTCCCATTTTCCTCCAGC
Atr_3380 3-28	G	T	AGCTGCAGGGATGG	AGCTGCATGGATGG	GGAATGTAATGTGACCAGCTG C	ACCAGGAATGGATCAAACCTGCT
Atr_34- 41	G	C	GTCCTGCAATGCTGT	GTCCTCCAATGCTGT	CCTGCCTGTGTGCAATTCAG	CCGTGAAGCCACTACAGCAT
Atr_3445 4-29	G	A	GACCAGGGTTGCCT	GACCAGGATTGCCT	GATTGTGGCACTCCAGGACC	ACCCGAAAACCTAGAAGCCCT
Atr_3449 7-36	C	T	GATAGTTCGCTCTT	GATAGTTTGCTCTT	GGAGGTGCTGCTGGTGATAG	GCTTGGTGGTTGTAGGTGCT
Atr_3451 -52	T	G	GTGCTTTACCAACAT	GTGCTGTACCAACAT	GGTTTGGAGGAAGTTTGTGCT	CTCTGTCCCTTCAATTGGAGGA
Atr_3541 5-62	C	A	CAGAACGTTAAAATT	CAGAAAGTTAAAAT T	GGAAGTTGGTCTTATGATTAGT GTT	AAACAAGATGTTGGAGTACAA AAGT
Atr_3544 0-36	A	T	ATACCATACATACA	ATACCATTCATACA	CAGGTCCTACCACTGCTGAC	TGCAAAGTGTTGTTCCCTGTATG
Atr_3581 -53	T	A	TTTTATTTTTCATA	TTTTATTATTCATA	AGCTCCAGTTCACAAAGCCT	TGCAGCTTCTTTGGGGATCA
Atr_3619 4-59	T	C	CTTTCTGTTCTCAGA	CTTTCCGTTCTCAGA	CCATCTGCAGTGTGGAATCCT	GCCGCTTCTTCTCCTCTGAG
Atr_3627 -31	A	T	GTCTATTAGTGTTT	GTCTATTTGTGTTT	GTTCAAACCACACAACTGTCTA T	ACTGCAATGAGACACAGATGT
Atr_3633 1-53	C	T	TGTGGCTCGAGGGC	TGTGGCTTGAGGGC	CGGAAGGCCTCAGATTGTGG	AGTCCGCTGCCTTGAACCTAC
Atr_3648 5-28	C	T	CCTCATCCTAGCCC	CCTCATCTTAGCCC	GGTGCTAGCAGCCCTCATC	CACAGACCCAATCATGCCCT
Atr_3674 0-33	G	A	TAGAAGTGTAGATG A	TAGAAATGTAGATG A	TGCAGGCTAATATAAAGTAGA AAGC	ACAAGTTCCTGGTTAAAAACAG CT
Atr_3696 0-37	A	G	CCATGCCAGTCCGT	CCATGCCGGTCCGT	CTTGACGCCAGCTGCAGAA	TGAGGGTGAGGAGCCATACT
Atr_3706 8-70	C	T	TTTGTCTTTTCG	TTTGTTTTTTCG	ATAAAGCATGAACACCACATG G	GGCTGTTTTGTTCTCAGTGTGT
Atr_3773 9-28	T	C	ATAGCTGGTACAGGT	ATAGCCGGTACAGG T	GCAGGATCATGCATGCGC	TGAACCCAGACAAGAAGGACA

Atr_3789 8-35	C	A	GCTGGCTTGGTCGTG	GCTGGATTGGTCGTG	CAGGCTGGCCTTTGTCCATA	TTAAGG TTCAGTGGGCGTCC
Atr_3827 8-50	C	A	GTGCATGCAA ACTA	GTGCATGAAA ACTA	TCCTCCAA ACCACAGTGTGC	TACAGTGCATGCCTTCCTGG
Atr_3859 1-73	A	T	CCGTCATT	CCGTCTTT	GCTGAAGTATAAAACAACATCA CCGT	AATTGGGAGAACTTTACAGTCC T
Atr_3901 8-58	C	A	AAAAGACCATTTC A	AAAAGACAATTTC A	GGTTCAGACCCACTGTGTATCA	AGCCAGCCTAAGGTTTTGAA
Atr_3902 3-56	C	T	AGTGACACGGAGAG	AGTGACATGGAGAG	GGTCCACCTGTCAATAATGGC	TCGAGAGAGAGAGCCCTCAC
Atr_3903 -41	G	A	AGCTGGTGAATCGG A	AGCTGATGAATCGG A	TGCAGGTTGAGTTCAGATTGT	GATAGGGCTGTCTGCATCCG
Atr_3907 1-73	G	A	CTTCACAGAC	CTTCACAAAA	ATAGCCCAGGTGGATGCATG	TGGATAAGCGGTTCTGCAGA
Atr_3908 1-73	C	T	TTTAGATCAG	TTTAGATTAG	TGGATGGAGGTTTAATAGGAC CA	GGGCCCTTCCAGTTGAGATT
Atr_3912 5-48	T	C	ATAGTGTTGAAACT	ATAGTGTCGAAACT	GCAACATCGTGAAAACGCCA	TGATTCAAAAGGAATGCTTGGC A
Atr_4011 0-57	G	A	TAGGGCCGCATGCA	TAGGGCCACATGCA	GCACTGTGCCACTGACATAT	CAATCGCTATTGATTGCTGCA
Atr_4016 9-65	C	T	AGACCCAGTTGTGGC	AGACCTAGTTGTGGC	GGGTGGTTCCTACATGACGT	TGCCCTGTA ACTACCCCTGT
Atr_4031 6-51	A	T	ATTAAAGAAAAATA	ATTAAAGTAAAATA	TGCAGGTTTGT TTTCTGTGAATG G	CTCTGTCACAAGGCCACAGA
Atr_4034 3-66	G	A	CTGCTTCGTTAGGG	CTGCTTCATTAGGG	CAGCAACGCTTACAGCACAG	AACAAGCATCGTCTCTCCCT
Atr_4077 4-37	A	G	ACTCAACTCTGACCC	ACTCAGCTCTGACCC	TGCAGGCAAACAGTCTTTAGAC	CCTGGACTGGATTGGATCTCG
Atr_4095 4-66	G	T	ATTGGGGGTAAAAT	ATTGGGGTTAAAAT	TTGGACATTGCAAATTGGGG	TGCATGACTATGGGCGTGTT
Atr_4097 4-63	G	A	GAGATGTGATCTGT	GAGATGTAATCTGT	GGACCACAGAGTGAGATCCG	GCAAAGCATGCGAAACAGAT
Atr_4182 8-27	A	C	TAAAGGGAAACAGT	TAAAGGGCAACAGT	GCAGGAGTCCTACAAAGTTAA AGG	TGTTTTTACATGCTTTACGGTC A

Atr_4194 8-31	A	G	GAATTGAAGAAGTA	GAATTGAGGAAGTA	TGCAGGGAGGGACATCTCTT	TCATGTTTCGAGTCAAGGAGCT
Atr_4198 6-71	G	T	AGTGGCAGAATG	AGTGGCATAATG	ATTGTATGGCGCTTCCTGCT	AGAAGGGTTGAGCATGTCCC
Atr_4203 9-63	T	C	AGGCCAGTGGCGAG	AGGCCAGCGGCGAG	ACCAATCCAATCAGCCTCGG	TCTGTCCGTGCTGGTTTGAG
Atr_4240 5-55	C	A	CCCCAGTCCCTTAA	CCCCAGTACCTTAA	CAACACTGACAGACCCCCAG	TGCAGCACAGCGTGATCTAT
Atr_4274 1-51	T	A	CGTCATTTTGAAATT	CGTCAATTTGAAATT	TGTGCAGACTAAAAGCATGCG	ACTCAGGAGTCTAACTGAAGCC
Atr_4310 7-50	G	A	ATCTGCTGTAGCAC	ATCTGCTATAGCAC	GGTGTCTGCCTGAGCTCAAT	GAGGCCAAAAGTGGCAATGACT
Atr_4340 2-63	A	T	AGATCACTCAACAA A	AGATCTCTCAACAA A	GCAGGTTTGACTTGCTTGGG	GTCAGGCCCAATGTCCACTT
Atr_4341 4-51	C	T	TATGAGCCGAGTCT	TATGAGCTGAGTCT	AGTCTTCCCGAGGGACAGTT	CCCTTTCGTAAATGAGGCCCT
Atr_4353 1-74	G	A	GTGCGCCGC	GTGCGCCAC	AACTGTTCAGTGAAGTGCGC	CCAACCTGAGCCCCAACATA
Atr_4357 1-39	C	A	TACATCTATCTGGTT	TACATATATCTGGTT	TGCAGGGATATAGTATGTCACT TT	TGCACCCCCTATTCTGAAGTG
Atr_4380 9-42	A	T	AAAATA[AT]AAAAA ATA	AAAATT[AT]AAAAA ATA	GCAGGGCGTATCGACAGATT	GCCAACCTGCTCACCCTTA
Atr_4447 3-38	T	C	ACATTGATATCTCA	ACATTGACATCTCA	GCAGGTGGTGGAGCTCATAG	CTCCTTCTGCAGCATCACCA
Atr_4451 3-72	T	C	GTGGCTCTAGA	GTGGCTCCAGA	CAAACGATATGAAAGCTGTGG C	GGTCCATTTCTAGTCAGCTCGT
Atr_4487 3-44	C	T	GCTGACATCTGTCAT	GCTGATATCTGTCAT	ATGGTCTTTTCCCCCTGGG	AGCTCAGCCAATCAGCACAA
Atr_4507 4-45	T	G	GTGCATTTTCAGCAG	GTGCATTGCAGCAG	GGAGAAACACACACCAAGCG	AGTCTGCTTCTACTCCCAGT
Atr_4549 4-35	G	T	CATTTTCAGTCGAGG	CATTTTCATTCGAGG	GCAGGACATACACGGTGGA	TCCAGAGCTACACACCTCGA
Atr_457- 66	G	A	TCAACTGGGACCAT	TCAACTGAGACCAT	GAAGGGCTGAAGTGATGGCT	ACCCTCATGTCACAAATGTAAA AGA

Atr_4589 0-59	G	T	GTGAGGAGACCTGT	GTGAGGATACCTGT	TAAGGGCTGCAGTGGTGAAG	CCACGGTACCTGTGCTGATT
Atr_4600 6-31	C	A	TGCTGCATGCTTCAC	TGCTGAATGCTTCAC	TGCAGGATATAATAGTAAAGG GGTC	CCCCCTTCATGTGAAAAAGTGT
Atr_4608 8-36	T	C	TCATCTGTAATATG	TCATCTGCAATATG	GGCAGTCATGATATAAAGCGG G	TCTAGTGACCTCTGGTGGCT
Atr_4613 4-46	T	C	TCCCTGCTGATTTT	TCCCTGCCGATTTT	TGCTTGACCTAGCCAGTAGTG	TGGGGGCTAGGGAGACAAAA
Atr_4622 9-66	G	A	TTGCTCCGTACAAA	TTGCTCCATACAAA	AGTGACAGGGAATTGTATGCCT	ATGTCACACTTCCCAGGGAC
Atr_4624 7-56	C	T	TAAACCGGGGCTCTG	TAAACTGGGGCTCTG	GTCAGGGACTCGTGGACTTC	AAGGGAGCTGGAGGAAGAGT
Atr_4643 -39	A	G	TATGTATACCTGAG	TATGTATGCCTGAG	GGCAAGAGAGAGCATCAGCA	TCATTCAAGCCCACCACCTC
Atr_4661 -28	C	T	GTTAGTCCGGGGCA	GTTAGTCTGGGGCA	GCAGGTAGATCTCCAGCTGG	CTTTGCCAGTGCGGTTGAAA
Atr_4663 7-57	C	G	AGCGTCACAGGCTA	AGCGTCAGAGGCTA	CATAAGCGCTGGGATAGGGG	TGCAGGAGCTGACCTTTGAG
Atr_4669 0-29	A	C	CTGCCAAAGGATCT	CTGCCAACGGATCT	GGCTCTCAGAGTAATTACTGCC A	TTCCCTCACTCCAAAGAGCA
Atr_4672 0-39	G	A	GTAGAGCTGTATTAT	GTAGAACTGTATTAT	TGTTTTACAGCTTGCTCCTAGT	ACATTGCTGCATGGCATATGA
Atr_4674 -42	C	A	TTCCTCCTCCTTATC	TTCCTACTCCTTATC	GGTGTCTGCTTTGAGCTTGG	CTTCCAGAAGGAGCACTGCA
Atr_4677 -47	C	G	TCCCGGACCGGGCC	TCCCGGAGCGGGCC	CCTGACACTGGCACTCAACA	CACCAGGCTGGAGAGGTTTG
Atr_4698 3-45	T	A	GTTCGTTTCTACAG	GTTCGTTACTACAG	CCTGGTAGCATGTGGGTGTT	TGCCTCATTGTAATCATATCAG GAC
Atr_4716 3-58	C	T	TGCAGCGGCACATG G	TGCAGTGGCACATG G	ATCCATCTGTCCCTCCAGCT	GCACTTCACCATCCGGAAG
Atr_4719 5-73	T	C	AAGCCGTAA	AAGCCGTCAA	GAAACGCTCAGGAGTGGAAC	CAGTGGGCGTGTTACGTAAG
Atr_4735 2-72	A	G	GCCGAGCACTC	GCCGAGCGCTC	CTCATGCCGCTCTCCTTCAC	TTGTGTTCTGGTCCCAGCG

Atr_4748 4-45	T	C	GTAGGGGTTGCTCT	GTAGGGGCTGCTCT	GCAGGGGTCTGTTAGAGCTC	AATCAGCAGTCACCTCACCG
Atr_4752 9-73	C	A	TAAGCAACTT	TAAGCAAATT	GCTGCCATTAATGATCTTGTCC T	CGCAGGACCAAGAAGATGTT
Atr_4797 9-72	T	A	GCCTTTATATC	GCCTTTAAATC	AGGCAGAACTAAATACAGCAC TG	AGGGAACGAAGGGAACATTT
Atr_4875 4-60	G	A	CTGCAACGACGTGT	CTGCAACAACGTGT	GCTTTCTCCTTTCAGTGGCC	TCCACGACACACATACACGT
Atr_4938 8-52	G	A	CATGTGTGTCTGTC	CATGTGTATCTGTC	GGGACCCATGTATAAGATGGC C	AGTTTGGTGAAGATTGGCAGT
Atr_4953 2-44	T	G	AAACTTTAT[CA]GTC TG	AAACTGTAT[CA]GTC TG	GCAGGAACTTTGCAACTACTGT	AGCATTACTGTGTAGGCTTTAC AGA
Atr_4962 9-71	G	A	CATGCCTGGGGA	CATGCCTAGGGA	CCAGCAGAGCCATGGGAATC	CGGAGGCAGGTCGAACAG
Atr_4979 0-61	C	A	TGCACTACTCTTCT	TGCACTAATCTTCT	GCTACAGTACCACCTGCACT	CCCCTCCAGAAATCAGGAGTC
Atr_5017 9-30	T	C	GCCAATGGGTTGAA G	GCCAACGGGTTGAA G	TGCAGGCCTCTTAGCTGTTG	AGCATCTTGCCACATCCACA
Atr_5019 -45	C	T	TCCTGCAGC[TA]TTC CT	TCCTGTAGC[TA]TTC CT	GCACCGCTGAATGCTACATC	TTTCGTGCAGGCTGAGACAT
Atr_5021 2-69	C	A	AGAGACTATGGC	AGAGAATATGGC	TCACTACAGAATGTGTTTCAGCT CA	TGCAATTATGATGTTCTCAGCC A
Atr_5064 2-59	C	G	CCCTACTTAATGACA	CCCTAGTTAATGACA	CAGGATCGTGGTGCTCCAG	GCAGTAGGCCATCACTGTCA
Atr_5117 6-35	G	T	AAAAGTTGCACAAC	AAAAGTTTCACAAC	TGCAGGTGAGATGAGGTTACT G	ACTCCAGCACATAAGAGCAGT
Atr_5145 8-37	T	A	CTCGCACTGTTGGC	CTCGCACAGTTGGC	TCAATCTGATGCTGGGCCTC	GACTGAGGAGCCGCCAAAT
Atr_5183 2-58	A	C	CAGTCAATGC[TC]GA TT	CAGTCCATGC[TC]GA TT	GCTGTAGGGTCCACGGTAGA	TGGGGATTCCAGAGTGAGTA
Atr_5199 9-44	A	G	AATATAATGGGTAA G	AATATGATGGGTAA G	TAGGGTCCCAGGGCAGTTTA	GGTGTGCAACCCAATGAATACA
Atr_5202 1-40	C	T	AGATGCACTGCATTA	AGATGTACTGCATTA	TGCAGGTGTACATTCAGTGT	ACTGACCACAACCTCAAAGTGT

Atr_5216 4-31	A	T	TTTTTTTAAAGAGC	TTTTTTTAAAGAGC	TGCAGGGATAAGCCAAAGC	AGCTTGGTGGAATCCAGGTG
Atr_525- 66	G	C	AACAAGAAGCAAAG A	AACAACAAGCAAAG A	TCCAGCATGACCATCTCTGC	GGGTCACTGTGTCTCTTTGCT
Atr_5265 0-66	A	G	AGACAGTATGTTTG	AGACAGTGTGTTTG	CCCTTGCTGTGGCTCTTCAA	AGCCCCCTATAGTCTCCACCA
Atr_5266 6-51	A	G	AAAGGGTAGTTATT	AAAGGGTGGTTATT	GCAGGCCTTCTGTATGTAAACC	TGCTTTCTTAGAATTTAAGGCT GCA
Atr_5267 5-47	C	T	TGAACCGCGACCTC	TGAACCGTGACCTC	CAGTTTGTGAGCCGGTGTG	CTCCACCAAGAGAGTGCCTG
Atr_5271 5-59	C	T	AGTATACCCCTTGT	AGTATACTCCTTGT	ACTGTAGTGTGGTTATGTGGTT	TGAAGATTGTATGTTGTTGGCA CA
Atr_5286 8-38	C	T	TTGCAAACGGAGCA	TTGCAAATGGAGCA	CAGGGTCCCAGCTGAAGAG	CGCAAGAAGCTGATGTGCTC
Atr_5315 7-67	G	C	GACAAGAGAGACAG	GACAAGACAGACAG	CCAGCCTAGCCATGGACAAG	TCACATCCAACCTCTTGCCAGT
Atr_5321 0-55	C	T	AGAAGCCAATAGGT G	AGAAGTCAATAGGT G	TCTTGCATCATGCCTACCAGT	ACGCTTCATGGCATTTTGTGT
Atr_5336 -58	A	T	AAACCACAGCATTC	AAACCACTGCATTC	CTCACCTCACAGGCTACACC	CTTTCAGTGCAGTCAGAATGC
Atr_5352 1-30	C	T	ATCCCTTCCTACCG	ATCCCTTTCTACCG	TGCAGGTCATCATCTGAACAAG A	ACCAATCCTTCCTGACAGTTTG T
Atr_5368 6-72	A	C	AATACAAAT	AATACCAAT	CCCGTGGTTTGTAAGCAGGA	CTGGGGACTACTTGAGCTGC
Atr_5390 4-44	A	G	AGTCAATTAGTCAAG	AGTCAGTTAGTCAA G	TGCAGGAGACCGTGAAATGT	GGTATCCTCCCTGGCTTGAC
Atr_5403 8-48	A	G	CCGGGGAAAGGATG	CTGGGGAGAGGATG	CACAGGTATGCCACAGGACA	AGGAAGCTAAACACAATCTACC A
Atr_5404 1-38	C	T	TTTGAATCTTAAGA	TTTGAATTTTAAGA	ACTGTCTTGGGTGGCAAAC	ACCTAACTCGGAAATGTGATTT GT
Atr_5416 0-70	T	C	TCATTTTGGGTC	TCATTTTCGGGTC	TTTGCGGTTGAGATGTGGGT	AGAGCACACAAAACATTTTCGG T
Atr_5426 6-27	G	A	GTTACTTGTATTGG	GTTACTTATATTGG	TGCAGGCTTCACTACATAGGT	ACATCCACCCTCAACAAGCT

Atr_5476 4-45	G	A	AGCACTCGCTCCCA	AGCACTCACTCCCA	TGGGGAGCCAAGTAATGAGC	AACCAGAGAGGCCCCGAGTAT
Atr_5479 5-72	G	A	CATTTGTAT	CATTTATAT	TGCACTGATGATGAAGGTGT	GCAATTTTAAAGGTGTGGAGAC A
Atr_5558 3-67	G	A	TTACCGGGATTGAC	TTACCAGGATTGAC	ACGAGGCATTGATTAAGTCCA GT	AACGCTACTGACTTGAGGCC
Atr_5589 2-54	G	A	ATCTCGTAGACCTCA	ATCTCATAGACCTCA	AGCCTGTCACTTCCAATGAGG	TGAACACCCCTCTGAGGTCT
Atr_5602 4-45	C	A	CAAGTAGCGATCAG	CAAGTAGAGATCAG	AGGTCAGCCCGTCCCTATAA	TGGTCTTCTTCTCAAGATGTGCT
Atr_5603 3-37	C	T	GCTACAGCTTTATT	GCTACAGTTTTATT	TCTAGTCCCTCCCGCTACAG	ATGGCCCGATAGTTTTGGCA
Atr_5610 -27	A	G	GTGACACAAGATTA	GTGACACGAGATTA	TGCAGGTACAAGCAGAGCAG	GCCACTTGCAACTGGGAAAA
Atr_5610 9-40	C	T	CAGAACTCGCCCTG	CAGAACTTGCCCTG	CGCATGCGTCCGATAGCC	ATAGAGAACTGCAGCAGGGC
Atr_5685 4-26	A	C	GGAAAGTAGGGGTA	GGAAAGTCGGGGTA	GACGTGCACGGGTGGAAA	CACAGCCTCAGTGCTTCAGA
Atr_5701 8-28	C	T	GCGTTGTCCTCCGA	GCGTTGTTCTCCGA	CTTGCCTGTAAGCTGCGTTG	TTTACACACTGCAGGCCCTT
Atr_5754 2-29	A	T	CCAGAAAATGGCTC	CCAGAAATTGGCTC	CTGGCCTTTGTCCTCCAGAA	CAGTGTGTGTCCTCCGATCC
Atr_5775 6-67	C	T	CAATCAACGAGCAG	CAATCAATGAGCAG	TGCAGGTAAGGGCAGATGAC	TTTTCCATGGGTCTGCTGCT
Atr_5779 -55	T	G	TTTTTCTTTTCCCT	TTTTTCTGTTCCCT	TGCAGGTATTGAAGACATTCTC TGA	GACGTGAATGGAGGGGTCAG
Atr_5783 2-69	C	A	GAACACGCTGACAC	GAACACGATGACAC	ACCAGTTCCAGAGATATGGGT G	GGGCCGCTTTATCACAAGGA
Atr_5787 0-70	A	C	ACTACCTAACCAG	ACTACCTCACCAG	TTACCTTACATATGTGTCACTA CCT	CTCACGTGAGAGTTGCTCTGT
Atr_5830 5-70	G	A	CCACTGTGGTG	CCACTATGGTG	TGTCTACAGTTGTTACATGTCC A	GCCATGTCCAGCTTTTACACC
Atr_5834 2-71	T	C	TCCTTCTTTCTG	TCCTTCTCTCTG	GGGTGTGTTGTCTCTCCTTCT	GACTGAGGAAATAGCAAAGCG T

Atr_5843 4-42	G	A	CCAGTCCGTTTTCC	CCAGTCCATTTTCC	GCAGAACCACGCCAGTCC	GAGGGCGAGGAACCAGC
Atr_5856 2-59	G	T	TATAATTGACCTCT	TATAATTTACCTCT	GACAGGATCCACCACACACT	AAAGAGGACCGGTCAAGAGG
Atr_5872 0-60	A	G	TTCCTATAGTTTAG	TTCCTATGGTTTAG	CCAGTCAAGTGCAAGGGTGA	TGAACTTGAAACTCATTTTGAC CA
Atr_5883 1-60	G	A	GTAAAATGTACGGC	GTAAAATATACGGC	TGCGTGTTTATCTTGAGAAACC G	TCTTTTTATGAGCACTGCCGT
Atr_5890 -29	T	C	CTTCGTATGAGATG	CTTCGTACGAGATG	CAGGTGTAAACCCCCGAGTC	TCGTTCCGAGCAACAGGAC
Atr_5892 -46	A	C	TCATTCCAGAATCC	TCATTCCCGAATCC	CAATAGCATGGCCGCACTTC	TGGACACAGCACAAAGAAGAG T
Atr_5920 1-47	G	A	CAGCAGGGTCCACT	CAGCAGGATCCACC	GCTTGATTTCACTGGGTGCC	ACCAGGCACTCACAATGACA
Atr_5928 4-42	G	T	CAGAGATGAATTTT	CAGAGATTAATTTT	AACCTCGTCACCCTCTCTCA	GCTCAAGCAGAGGTTTGTGG
Atr_5931 0-44	A	C	CTCAGCGAGCACTC	CTCAGCGCGCACTC	GCAGTTTGGTGAAGCTCAGC	GAAGCCTCAGGAAGCACCAG
Atr_5948 7-73	C	T	ATAAACGT	ATAAATGT	ACTTGAGCAAAAGGAATGCAG A	TGAACCTCTACTCTTATTTTGCA CA
Atr_5980 0-43	C	G	ACAGTCCCTAACTAT	ACAGTGCCTAACTAT	CACTGTAGCAGGGTGACGAG	TCTGCGGTTTACAGAGGCAA
Atr_5984 2-43	G	A	GGCGGTGAACCAG	GGCGGTAAACCAG	CATCTCTCTTGTGAGGGCGG	TCCAGCTACATTGCCTGTGG
Atr_6016 2-29	T	A	TTTTTTTTTAATTTG	TTTTTTTAAATTTG	TGCAGGCAGGACTGTTTC	GAACAGTCCCACACGCTAGG
Atr_6026 5-55	C	A	GGCTTCCCAGTGTC	GGCTTCCAAGTGTC	AGGGGTCGGATTAGCCACTA	AGGTGGACATTCTAGGTGAGGA
Atr_6036 8-72	A	T	AGGAACCAGCA	AGGAACCTGCA	CGATGGCCTCCAAGGAACC	CCCTATCATTCCTGTCACTCGT
Atr_6068 8-70	C	T	GAACCAGCGGTTG	GAACCAGTGGTTG	CCTCCAATGACCTACTGAACCA	GGTGCTGGTGGCTAACTGAT
Atr_6085 9-44	T	C	AATTCAATTGACCC	AATTCAACTGACCC	AGGGGTCAGAATCTGCATGC	AAGTGTCCATCGCTTGTGGG

Atr_6106 2-75	C	A	ATCTGGGC	ATCTGGGA	TGCCCTGAAAGAGGTCAGTT	TGACTGTATGAAAGAAGGCAGT
Atr_6117 1-66	C	T	GATGTGACTGCACG	GATGTGATTGCACG	CCGACGCTGTAAGTTCTGGA	TGTCCTCCGAAACGACTGC
Atr_6191 1-75	C	G	ATTGCC	ATTGCG	AGTGGCAGCTCCTTCACTTC	GCGCCGGTACACTTTTCAGTA
Atr_6233 0-56	A	C	AGGGTGAAGTCCCA	AGGGTGACGTCCCA	GGGCCAGGAAGGAAAAGCAT	ACTACCAGGAGCTTTTGGGAC
Atr_6241 9-71	G	A	CTGCAACGACAC	CTGCAACAACAC	CCTGCAGAGAGACACAGACG	GGCCAGACAAAGGAAGGACA
Atr_6246 3-34	C	T	TGCAGAGCGTTCAC	TGCAGAGTGTTAC	GCAGGGATAGAAATAAGACTC TGGT	GCTTGTTACGTATACACTGGCA
Atr_6251 -29	G	T	TCAGGGGGAGATGC A	TCAGGTGGAGATGC A	TGCAGGGACACAAGAGCTTC	GCTTTCTTGACTTGCCTGCC
Atr_6295 2-34	T	C	TTCTCCTTGTGGTG	TTCTCCTCGTGGTG	GGATTGGAAGCAACGTTTCTCC	AGGACCAGGAATGAAATGGCA
Atr_6304 2-40	T	C	ACTCATTGACCTCTG	ACTCACTGACCTCTG	GTCTTTGCCCTCCATGAGCT	TCCAGGTACTCCACAGCAGA
Atr_6307 6-27	T	A	ACAAATTTCAATTCA	ACAAATTACATTCA	GCAGGCAACAACAACCTCAC	ACAGTATCATAGTGGAGGTGAA TG
Atr_6310 1-44	A	G	ACCAGGCAAATTTTC	ACCAGGCGAATTTTC	CCATTGTTACAGGGTTTGGGG	TGTCTGGACATAACCTGGAAAC T
Atr_6324 6-38	A	G	GTGTATTATGTATC	GTGTATTGTGTATC	CAGTCAGCTGCATTGTGTGT	AACTCACTATGCTGCCTGGG
Atr_6388 5-66	C	T	GCTGCCGTCGGTCAG	GCTGCTGTCGGTCAG	TGTTACCCAAGCTGTGTTTCAG	TGCTAATTTTCTTTCTTCTGACC GA
Atr_6400 6-52	C	T	GGTTTACCCTGAAG	GGTTTACTCTGAAG	CTGGATGGGGAGCGGTTTAC	CAGCTCCCACCCACTGTAAG
Atr_6421 7-68	A	G	CCTTAAATTCGAG	CCTTAGATTCGAG	TGTTAACAAGGGAAACGCCG	TTTTTAGTTACCCTCACCAGG
Atr_6456 -50	G	A	GTTCACTGTCAGGT	GTTCAAACGTCAGGT	GCATTGCTGCCAGGTTAACA	GGAAAACACAACCCTGTTCG
Atr_6470 6-45	T	A	CACTGACTGCTGTA	CACTGACAGCTGTA	TGCAGGGATGGTCCTTGTTG	ATGACCAAGCCAACCTGCCTT

Atr_6509 4-30	A	G	AGAGCAGACGCCAG T	AGAGCGGACGCCAG T	GCAGGGCTGTCTTCGAGAG	GACCAAGCTGCCTCTTTCCA
Atr_6535 9-46	T	C	CATCTTCAATCAG[CT]T	CATCTCCAATCAG[C T]T	GTAGTTCCCCTGCCTTGCAT	ATCGCTCTGTGTTTGGACCC
Atr_6537 7-56	G	A	TAACAGGATAATAG G	TAACAAGATAATAG G	CTGGTGATCCCTGCTGTAGG	CTGCAGAACCCAGAGACCTG
Atr_6572 9-42	T	G	GTTACCATCTCTAC	GTTACCAGCTCTAC	TTAATTCAACAATGTAGCAGTTA CCA	GCGCACCACTCTATTTCAAACCT
Atr_6584 3-52	G	T	GCGTCAGGTGGGAA	GCGTCAGTTGGGAA	AATGTGAGTAAGGGGGCGTC	CACTTTCAAAGCAAATGTTGGT CA
Atr_6612 -39	A	C	TGCCCATATACATGG	TGCCCCATATACATGG	TGCAGGGATGCCTATTGTACA	GGGATCCCAGGTCATTTCCA
Atr_6656 3-34	A	G	AACCTCTATACAGT	AACCTCTGTACAGT	TGCAGGTAAATGTCCACATCA	GGCTCCCAACCACATCGTTA
Atr_6666 4-59	C	T	CTCAGAGCTCCCTG	CTCAGAGTTCCTG	AGGTACCCCTTGCCAAATGG	TGCAAAGTAGAAGGCAGGGA
Atr_6680 6-52	T	C	TTACCTGTTTGAGA	TTACCTGCTTGAGA	AGCCCTGCTTTAACAGTGGT	TAACCCTCCATCCCCTCAGG
Atr_6753 4-27	C	T	CATAACTACAAATAT	CATAATTACAAATAT	GCAGGCAAGTGCAACATCAA	GCTGTGGCAGAGTGTAGGAG
Atr_6775 9-28	G	A	GGCACGGCACAAAA C	GGCACAGCACAAAA C	AGGGGAAGAGCCAGTGAGAG	AATTGCTGTGCTTGCCATGG
Atr_6818 6-72	C	T	ACAGTCCCTGC	ACAGTCCTTGC	TACCAGTCGCCTGACCAGTA	TCTGCCTCTCCCACAGGTTA
Atr_6868 0-72	T	C	CATGATCAG	CATGACCAG	TTACCAAGGAAACCAGGGGC	ACATGCTAAAGTGGCTGCTG
Atr_6876 2-59	A	T	CTCAGATAGTGAGA	CTCAGATTGTGAGA	GGGTGCAGCAAGGATGGTAT	CCTGCACCAAGGTAAGCTCT
Atr_6880 8-31	A	T	GTATTAAAGCTGGC	GTATTAATGCTGGC	GGTAATGCCTCCCCACTTGT	GGAGGAGTTTATTGAAAGCAGG C
Atr_6904 7-33	A	G	TAATTATATGAAAG	TAATTATGTGAAAG	GCAGGCTGCTACTGTAGTCT	GTGAAAACAGTCCTTTCCCCT
Atr_6921 7-58	A	G	TCAAAGCACCCGAG	TCAAAGCGCCCGAG	AAGCCCCCTTTCTGCTTCTC	ACTGCTTCGTCAGTAGAAAAGT

Atr_6988-51	T	C	TTAACTTTAGATCA	TTAACTTCAGATCA	TGGTTCTGGCAGGAACTCAC	TGCTTGATGTTTACCTGATTGTGA T
Atr_7001-57	T	C	CACATTATTTCTGT	CACATTACTTCTGT	CCAGAGTGATGTGCATAAAGC C	TGCTGTGTCTTCTGGTTCTGT
Atr_70139-39	G	A	ATTACGATCCCCCA	ATTACAATCCCCCA	GGAGTCCTACAAAGTTAAAGG GC	CACGTTTAATGAACTGTGGGGG
Atr_70167-40	C	T	CAGACCTCGTCCTG	CAGACCTTGTCTG	GCATGCATCAGATAGCCAGC	ACTATATTGCACTGTAGCAGGA C
Atr_7026-63	C	A	AATTCACCAAGTTT	AATTCACAAAGTTT	GGGGTGCCCAAATATATTGCA	AGAGTTGCTGCTTGTTTAAACT T
Atr_70459-55	C	T	TCTGTTTCACATTG	TCTGTTTTACATTG	GGAAGATTCCGATGACAGAAC T	GCAGAGAAAAGAGCCGCAAT
Atr_70467-53	A	G	TAAGCACTTCAGAAT	TAAGCGCTTCAGAAT	TGACACACCTGAAAAACACCA C	TTAGCTGTGGGATCATGCCA
Atr_70479-48	T	A	CATAGATTGCTTCA	CATAGATAGCTTCA	GTCTGGGAAATGTCTGGGCA	CAGCCTAGGTCTCTGTTTGCA
Atr_70609-65	A	T	TCTGGACAGATTAA	TCTGGACTGATTAA	GCAATGGCTAAACATCTGGAA CA	TCATTTCCACCGAGTTCTCTCT
Atr_7072-61	C	T	AAGGACGTTGCTCGC	AAGGATGTTGCTCGC	ACGCACCTCAAACCAGTTGA	GCTGGGGCTGGATAAAATGG
Atr_70880-74	T	C	CCCTCACTT	CCCTCACCT	GCTTTTCTTTGGCCCAAGGG	GCATGCAGCGGGAACATTTT
Atr_71195-60	A	T	CAGAAAGATGGGGT G	CAGAATGATGGGGT G	TGATGTTGAAGCCTCTACACCA	ACGATACTTCATCCACCCCA
Atr_72165-47	C	A	GGTCTCGGGGTTTCC	GGTCTAGGGGTTTCC	GGGTTGCCTACCTCTGGTCT	GTGGCTGATCACATCCCCTT
Atr_72251-33	A	C	TTAGGAGATGCTGA	TTAGGAGCTGCTGA	AGAAGCTGGGAGTGGTTAGGA	TGGGGTTTTAAAGCTATACACC A
Atr_72558-41	C	T	TCCATGTCGTCTAA	TCCATGTTGTCTAA	GCAGGGCTAGTGACTCTTCA	TCTGTCTTATCTGTAGTGTGATC AC
Atr_72693-61	A	G	TTAAGGCATACATA	TTAAGGCGTACATA	CGGTGTGCTGCTATTTAAGGC	TCCTGAAGACATTGACTAGAGG A
Atr_7298-56	C	T	GTCCCGACCAGGCG	GTCCCGATCAGGCG	CGGTCAGTATGGCTCCTGTC	GCAGTGCCCCCTGATGTATT

Atr_7343 8-69	T	C	TGAAATAAACAA	TGAAACAAACAA	AGCTGCACCCCTTTTAACT	CCCTGCATGAAGTCCAAGGT
Atr_7350 5-52	A	T	CATTCAAAACACAC	CATTCAATACACAC	GCAGGAAAAACAAGCCAGGG	AGAACGAATGGTCATTGTGTGT
Atr_7360 8-61	C	T	CGACCCGGGTCTATT	CGACCTGGGTCTATT	TGCATTTTGCTTCGCTCGAC	CTGCTTAACCCAGGTCCCAG
Atr_7374 0-69	T	C	ACATTTCTGTGC	ACATTCCTGTGC	CCTTTCGTAGGCACACTAGACA	AGTCATTCAACCTTTCATGGCA C
Atr_7390 5-66	A	T	AAGTTTTAAAACTG	AAGTTTTTAAACTG	AGGTTCCCTCCTGTTTACAAGTT	GGTACAGGCTCGCTCGTAAT
Atr_7398 7-49	G	A	GCATGGCCAGTTATA	GCATGACCAGTTATA	CTTACCCTCCACTGCTAGCTG	CCGGCAAACACCTACACCA
Atr_7399 4-27	C	T	CAAGACTATGAAGA G	CAAGATTATGAAGA G	TGCAGGTCTATTTTCTAACAGC A	ACCAGTGGACATGCTTACGG
Atr_7409 4-36	G	A	TGCCCGTCATTATGC	TGCCCATCATTATGC	GGATGTGCAAGCATGGAACC	GCACATGCGATACTCCAGCA
Atr_7432 2-45	A	G	GGTTTATACACATG	GGTTTATGCACATG	CAGAGGGCAGGTCCAAGAAA	AGCCACCCTGAATCATCATGT
Atr_7466 2-68	T	C	AAAAGTTTCCCCCT	AAAAGTTCCCCCCT	AGGGGAGTGCTGTGTTTGTG	ATGGTGGCTCAGTCCCAAAG
Atr_7473 0-29	G	A	AAGCCGCAGAAAGA C	AAGCCACAGAAAGA C	GCAGGTCAGAGGGAGTTTGA	TGCTGCTGTGTTTCAAGAGAGG
Atr_7474 7-45	C	T	CAATTTGCTATCAG	CAATTTGTTATCAG	TGCAGGCAAAACAAGACAGAC	GCCTGGAAGTACTGAACTGGA
Atr_7484 4-59	T	A	CCTTTTGTTGTTACA	CCTTTAGTTGTTACA	GTGAACCACACTTGTCTTTCTG T	TGACTGTTTTGTTCCACGTTGT
Atr_7498 7-50	T	C	TTTACTTCAAACACTAC	TTTACCTCAAACACTAC	GCAGGGCGAATTCTCAATATG G	AGGTATGGTGTCTCTTGTAGTT GA
Atr_7514 0-58	C	T	GAGTATGCTTTCAT	GAGAATGTTTTTCAT	CACCAGAGTGCTTTAAGGTTTA TAA	CTGTTGTTTCATGAGCCGTATAA T
Atr_7540 7-53	G	T	ACAGACAGGGTCTC	ACAGACATGGTCTC	GGAAAGGTACAGTACAGGGCA	AAGCCCTGAAGCAATCGGAA
Atr_756- 60	T	A	ATCTAACTACTGAC	ATCTAACAACTGAC	TGCAGGCATTCTATAAACCACG	AGAGGGCTTTGAGATGAAGGA

Atr_7598 2-70	G	T	ATGAAGAAGAT	ATGAATAAGAT	CAGGAAGATCCGGCAAAAGA	TGCTGCCTCTTGCTCATCTT
Atr_7625 3-44	G	A	CTGTCTCGCCTCTC	CTGTCTCACCTCTC	AGGTTCTTATTACATGCCTCTG TCT	GGGTCTGGTGCTGTGATTA
Atr_7640 9-55	G	A	CAGCCGCAGGAGAG C	CAGCCACAGGAGAG C	TCAGCGAGTGAGTGGACAAC	TGATCATAAATGTAAACTGCTC TCC
Atr_7641 8-65	A	T	CCGGCTTATCTGAA	CCGGCTTTTCTGAA	GGTAATGCGTGGGTGGTGTT	ACCAGCAATAACGTCTTCCTGT
Atr_7657 1-26	C	A	CGATGTTACGTGC	CGATGCTAACGTGC	GAGGGTCCGCTAGCGATG	GCACTGCTCTCTATCTGGGG
Atr_7679 1-46	G	A	TATCCGCTGTAGCAC	TATCCACTGTAGCAC	GTCCCCTGAGCTCACCAAG	ATTGAGGCAAAACCAGCAGG
Atr_7688 8-43	C	T	TGTCAAGCGATTGA	TGTCAAGTGATTGA	ACAACAGAATCAGGGCTGTCA	TGTGAATGAGACGGATGCAGT
Atr_7689 0-36	G	A	TTCTCGATCTCGCTT	TTCTCAATCTCGCTT	CAGTCGCCGAATCCTGTTCT	GATACGTGCTAGGACCCTGC
Atr_769- 65	C	T	CCTCTCAAACATAAAA	CCTCTTAAACATAAAA	GTCCACACAGTACTTGGCCT	TCATGCTAAGGACCTTGATTAC GA
Atr_7777 8-67	C	T	AGTAGATCACCAGA	AGTAGATTACCAGA	TTGCCTACCCCTGCTTTAGC	AAACTGTGCAAGTGGACACA
Atr_7793 -68	C	A	CGGTACTCAAATAA	CGGTACTAAAATAA	TAGGGAAAGGGAGTCAGCCA	ACTTCCATTCCACAGCTAATGA
Atr_7817 3-42	T	C	GGCATTGGAAC[CG] GTC	GGCATCGGAAC[CG] GTC	CTCAGGTCACCCAGCAGAG	GTTGAGCCGCTTGCAATCTC
Atr_7817 -58	G	A	ACAC[CT]GTTTCATCA GC	ACAC[CT]ATTCATCA GC	GCCTCAGCTGAAAACACAAGA	CCGTGTGAGTTTGTCTGCTG
Atr_7841 3-36	G	T	TACCCGAGTCTAAA	TACCCGATTCTAAA	TGCAGGTGTGTATTGCTGACA	AGCAGATATGAGTAAAACATTG CCT
Atr_7857 1-74	A	C	AAGTGAGAC	AAGTGAGCC	GACTTGCAGGTGTTTCGGAGT	AGTTCGGCTTGCTTGTTTTT
Atr_7860 0-73	C	A	CCCAGCTCAG	CCCAGCTAAG	AATAAGGAGCAAGCCCAGCT	GTCGACTTTGGGGAGCAAGG
Atr_7885 8-41	A	G	CATGAACCATTTTTT	CATGAGCCATTTTTT	AGCTGACAACGACATCATGA	TCCGCATGAGTCAAAATCATAC T

Atr_7928 -34	C	A	GTCATAACTGCTCA	GTCATAAATGCTCA	GGGGTTGCAGTACCTTGAGG	TCAAAGGCATCAACAGGAGT
Atr_7944 -51	C	A	GGCAGCTCGCGGCC	GGCAGCTAGCGGCC	GTGACCAGTACGTGACCCAG	GTCTTCTTCTCGTCCTCGGC
Atr_8314 -34	T	A	GATATTGTATGTGGC	GATATAGTATGTGGC	TGCAGGATTCCTTTACAGAAGA	TGAACAGCTCTGGATGCACG
Atr_9723 -56	C	T	ATGCGCAGTCTGTAG	ATGCGTAGTCTGTAG	TGATGGGCCATCTTTCACGG	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	GCCTTGTCAT
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	GTAAGYTTTCWTG	GTAAYTTTCWTG
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	GATTCGCCAGT	GATTCTCCAGT
Oki_aspAT-273-37	C	T	CTGGACACAAT	CTGGATACAAT
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	TTKG TAGAGCA	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_myo1a-384-36	C	T	CACCACTACCA	CACCATTACCA
Ots_myo1a-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	TCCCASAAACT	TCCCASAAACC
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 and Campbell 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.

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 2022 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 individually barcoded samples (Pool-seq; Schlotterer et al. 2014; Horn et al. 2020) 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

Population	Samples	OTS-Pop	Reporting Grp	Lineage	Latitude	Longitude	Num Reads
Big Creek Tule	71	OTS01	01_YOUNGS	LC	46.1461	-123.581	876,322,470
Cowlitz River spring-run	96	OTS02	02_WCASSP	LC	46.51331	-122.635	1,020,300,000
Kalama R spring-run	93	OTS03	02_WCASSP	LC	46.01714	-122.733	406,152,284
Cowlitz River fall-run	100	OTS04	03_WCASFA	LC	46.51	-122.615	499,200,000
Elochoman R fall-run	86	OTS05	03_WCASFA	LC	46.26122	-123.298	407,799,958
Lewis R fall-run	68	OTS06	03_WCASFA	LC	45.86683	-122.724	483,726,426
North Fork Lewis fall-run	48	OTS07	03_WCASFA	LC	45.86683	-122.724	959,700,000
McKenzie River spring-run	45	OTS09	04_WILLAM	LC	44.07051	-122.381	956,400,000
White Salmon fall-run	78	OTS12	18_UCOLSF	OT	46.54443	-119.309	428,842,398
Spring Creek NFH tule fall-run	94	OTS13	05_SPCRTU	LC	45.72813	-121.543	1,502,731,956
Klickitat River spring-run	96	OTS14	06_KLICKR	ST	45.71669	-121.259	1,134,700,000
Warm Springs R spring-run	93	OTS16	07_DESCSP	ST	44.8609	-121.244	496,062,406
John Day North Fork-Main Stem	52	OTS17	08_JOHNDR	ST	45.01371	-118.882	296,858,980
Middle Fork John Day R spring-run	36	OTS18	08_JOHNDR	ST	44.65934	-118.672	959,759,282
North Fork John Day R spring-run	39	OTS19	08_JOHNDR	ST	44.93192	-118.447	278,388,350
American R spring-run	62	OTS20	09_YAKIMA	ST	46.97637	-121.158	392,336,046
Cle-Elum spring-run	48	OTS21	09_YAKIMA	ST	46.7487	-120.466	998,400,000
Winthrop NFH spring-run	83	OTS22	10_UCOLSP	ST	48.4733	-120.189	680,014,854
Wenatchee R spring-run	51	OTS24	10_UCOLSP	ST	47.61622	-120.723	555,478,648
Tucannon River spring-run	52	OTS26	11_TUCANO	ST	46.256	-118.142	443,568,542
Lostine R spring-run	41	OTS28	12_HELLSC	ST	45.30799	-117.391	411,211,362
Grande Ronde R spring-run	30	OTS29	12_HELLSC	ST	45.307	-117.866	558,325,266
Innaha River spring-run	76	OTS30	12_HELLSC	ST	45.8173	-116.765	424,031,248
Lolo Creek spring-run	48	OTS31	12_HELLSC	ST	46.27909	-115.775	401,823,090
Red River spring-run	45	OTS32	12_HELLSC	ST	45.71117	-115.347	391,919,308
Powell R spring-run	94	OTS33	12_HELLSC	ST	46.508	-114.68	937,476,242
Rapid River Hatchery	96	OTS34	12_HELLSC	ST	45.35468	-116.392	389,030,348
South Fork Salmon R spring-run	45	OTS35	13_SFSALM	ST	44.88272	-115.706	434,963,404
Johnson Creek spring-run	48	OTS36	13_SFSALM	ST	44.899	-115.492	1,040,800,000
Secesh R spring-run	90	OTS37	13_SFSALM	ST	45.21183	-115.809	497,472,052

Chamberlain Creek spring-run	78	OTS38	14_CHMBLN	ST	45.45244	-114.933	1,140,726,086
Big Creek spring-run	48	OTS39	15_MFSALM	ST	45.138	-115.038	476,534,340
Camas Creek spring-run	60	OTS40	15_MFSALM	ST	45.09217	-114.732	415,383,358
Loon Creek spring-run	42	OTS41	15_MFSALM	ST	44.68436	-114.748	497,627,426
Sulphur Creek spring-run	35	OTS42	15_MFSALM	ST	44.54552	-115.397	1,216,270,604
Bear Valley Creek spring-run	33	OTS43	15_MFSALM	ST	44.54779	-115.305	378,559,250
Capehorn Creek spring-run	60	OTS44	15_MFSALM	ST	44.44673	-115.233	421,140,028
Marsh Creek spring-run	44	OTS45	15_MFSALM	ST	44.39292	-115.171	437,375,204
Lemhi R spring-run	95	OTS47	16_UPSALM	ST	45.15964	-113.833	376,783,802
Pahsimeroi R spring-run	92	OTS48	16_UPSALM	ST	44.68448	-114.04	282,773,700
East Fork Salmon R spring-run	96	OTS49	16_UPSALM	ST	44.11543	-114.43	407,770,412
Salmon River spring-run	61	OTS50	16_UPSALM	ST	44.15056	-114.885	486,564,624
West Fork Yankee Fork spring-run	93	OTS51	16_UPSALM	ST	44.34893	-114.726	479,445,090
Valley Creek spring-run	42	OTS52	16_UPSALM	ST	44.21806	-114.939	416,699,376
Sawtooth Hatchery weir spring-run	91	OTS53	16_UPSALM	ST	44.1507	-114.884	553,402,070
upper Deschutes River fall-run	48	OTS54	17_DESCFA	OT	45.25075	-121.043	908,200,000
lower Yakima R fall-run	46	OTS55	18_UCOLSF	OT	46.31219	-119.473	1,006,674,880
Wenatchee R summer-run	61	OTS57	18_UCOLSF	OT	47.61643	-120.722	952,590,894
Methow R summer-run	68	OTS59	18_UCOLSF	OT	48.296	-120.084	965,303,560
Lyons Ferry weir fall-run	92	OTS60	19_SRFALL	OT	45.59	-118.22	430,956,778
Clearwater River fall-run	96	OTS61	19_SRFALL	OT	46.42603	-116.918	713,200,000
Methow R spring-run	87	U	10_UCOLSP	ST	48.296	-120.084	416,082,474
Priest Rapids fall-run	46	U	18_UCOLSF	OT	46.64	-119.93	912,400,000

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	791	Leavenworth NFH	Wenatchee	Oki-Lower Columbia
Bonneville Dam	175	Bonneville Dam	Mixed	Mixed

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

Lineage	Reporting Group	Major Subbasin	Subbasin	Reach	Sites	N	Mapped Reads	*Genome Proportion
Coastal	02_LOWCOL	L. Columbia	Cowlitz	Cowlitz	Cowlitz R, Coweeman R	95	257,455,270	0.61
Coastal	02_LOWCOL	L. Columbia	Lewis	Lewis	EF Lewis R	78	325,463,369	0.65
Coastal	02_LOWCOL	L. Columbia	Columbia Gorge	Columbia Gorge	Mill Cr	96	232,750,154	0.56

Coastal	02_LOWCOL	L. Columbia	Columbia Gorge	Sandy Cr	Sandy Cr	87	291,529,099	0.64
Coastal	02_LOWCOL	L. Columbia	Hood	EF Hood	EF Hood R	48	260,113,702	0.62
Coastal	02_LOWCOL	L. Columbia	Hood	EF Hood	Parkdale Fish Facility	83	219,546,080	0.51
Coastal	02_LOWCOL	L. Columbia	Hood	WF Hood	WF Hood R	79	212,615,249	0.45
Coastal	03_SKAMAN	L. Columbia	Washougal	Washougal	Skamania Hatchery Stock	60	250,089,125	0.58
Coastal	04_WILLAM	L. Columbia	Willamette	Willamette	Eagle Cr	61	254,529,741	0.58
Coastal	04_WILLAM	L. Columbia	Willamette	Willamette	Little Rock, Mad Crks	50	265,050,782	0.55
Coastal	05_BWSALM	L. Columbia	Big White Salmon	Big White Salmon	Big White Salmon R	95	194,626,391	0.48
Inter-mediate	06_KLICKR	L. Columbia	Klickitat	Klickitat	Swale, Brush, Dead Canyon, Synder, White, Tepee, Fish Lake Crks	95	227,020,456	0.52
Inland	07_MGILCS	L. Columbia	Middle Columbia	Middle Columbia	Rock, Squaw Crks	91	216,427,544	0.61
Inland	07_MGILCS	L. Columbia	Middle Columbia	Fifteen Mile Cr	Fifteenmile Cr	92	520,699,926	0.72
Inland	07_MGILCS	L. Columbia	John Day	John Day	MF John Day R, Granite, Rudio, Wall, Trail Crks	95	285,409,446	0.58
Inland	07_MGILCS	L. Columbia	John Day	MF John Day	Upper John Day R, Beech, Belshaw, Canyon Crks	69	246,704,439	0.57
Inland	07_MGILCS	L. Columbia	John Day	SF John Day	Murderers, Deer, Black Canyon Crks	96	224,529,764	0.57
Inland	07_MGILCS	L. Columbia	Deschutes	Deschutes	Deschutes R, Warm Springs R, Trout Cr	95	262,227,329	0.61
Inland	07_MGILCS	L. Columbia	Umatilla	Umatilla	Minthorn Springs	74	222,263,607	0.54
Inland	07_MGILCS	L. Columbia	Umatilla	Umatilla	Umatilla R	70	236,157,293	0.54
Inland	07_MGILCS	L. Columbia	Walla Walla	Walla Walla	Walla Walla R, Touchet R, Yellowhawk Cr	95	380,515,222	0.69
Inland	07_MGILCS	Snake	Tucannon	Tucannon	Tucannon R	42	214,476,660	0.55
Inland	07_MGILCS	Snake	Lower Snake	Lower Snake	Alpowa Cr	53	287,842,645	0.63
Inland	07_MGILCS	Snake	Asotin	Asotin	George Creek	58	321,868,839	0.66
Inland	07_MGILCS	Snake	Asotin	Asotin	Asotin Cr	60	227,071,819	0.57
Inland	07_MGILCS	Snake	Clearwater	L Clearwater	Lapwai, Mission Crks	119	310,700,629	0.73
Inland	07_MGILCS	Snake	Clearwater	L Clearwater	Little Bear Cr	46	267,109,802	0.60
Inland	07_MGILCS	Snake	Clearwater	L Clearwater	Sweetwater Cr	51	224,853,521	0.53
Inland	07_MGILCS	Snake	Clearwater	L Clearwater	Potlatch R	50	217,298,385	0.51
Inland	07_MGILCS	Snake	Clearwater	NF Clearwater	Dworshak Hatchery	68	699,424,228	0.71

Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	Big Canyon Cr	95	251,726,901	0.59
Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	Catherine Cr	91	199,865,574	0.53
Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	Joseph Cr	88	240,989,824	0.52
Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	upper Grande Ronde R	58	190,569,290	0.61
Inland	07_MGILCS	Snake	Imnaha	Imnaha	Gumboot Cr	38	233,911,089	0.54
Inland	07_MGILCS	Snake	Imnaha	Imnaha	Lightning Cr	95	319,903,348	0.66
Inland	07_MGILCS	Snake	Imnaha	Imnaha	Little Sheep Cr	76	235,566,015	0.53
Inland	07_MGILCS	Snake	Salmon	L Salmon	Little Salmon R, Hazard, Boulder Crks	95	248,041,850	0.59
Inland	07_MGILCS	Snake	Salmon	L Salmon	Rapid River	78	337,982,422	0.73
Inland	07_MGILCS	Snake	Salmon	L Salmon	White Bird Cr	50	200,302,136	0.46
Inland	08_YAKIMA	U. Columbia	Yakima	Yakima	Naches R, Nile Cr	38	402,080,355	0.62
Inland	08_YAKIMA	U. Columbia	Yakima	Yakima	Satus R	67	208,951,362	0.49
Inland	08_YAKIMA	U. Columbia	Yakima	Yakima	Toppenish Cr	95	295,948,341	0.63
Inland	08_YAKIMA	U. Columbia	Yakima	Yakima	Teanaway R, Big Cr, Roza Dam	95	384,909,116	0.69
Inland	09_UPPCOL	U. Columbia	Entiat	Entiat	Entiat R	43	336,470,474	0.65
Inland	09_UPPCOL	U. Columbia	Methow	Methow	Winthrop NFH	93	180,992,366	0.46
Inland	09_UPPCOL	U. Columbia	Okanogan	Okanogan	Bonaparte, Salmon, Omak Crks	95	278,354,930	0.58
Inland	09_UPPCOL	U. Columbia	Wenatchee	Wenatchee	Chiwaukum Cr	54	227,418,107	0.56
Inland	10_SFCLWR	Snake	Clearwater	SF Clearwater	Clear Cr	61	243,826,940	0.59
Inland	10_SFCLWR	Snake	Clearwater	SF Clearwater	Crooked R	86	216,426,527	0.51
Inland	10_SFCLWR	Snake	Clearwater	SF Clearwater	Lolo Cr	68	159,912,565	0.59
Inland	10_SFCLWR	Snake	Clearwater	SF Clearwater	Tenmile Cr	60	288,038,275	0.64
Inland	11_UPCLWR	Snake	Clearwater	Lochsa	Canyon, Deadman Crks	68	285,197,311	0.61
Inland	11_UPCLWR	Snake	Clearwater	Lochsa	upper Lochsa R	72	295,662,531	0.72
Inland	11_UPCLWR	Snake	Clearwater	Selway	Hell's Half Acre	55	307,760,209	0.72
Inland	11_UPCLWR	Snake	Clearwater	Selway	Little Clearwater R	65	236,963,840	0.55
Inland	11_UPCLWR	Snake	Clearwater	Selway	upper Selway R	51	246,349,248	0.69
Inland	11_UPCLWR	Snake	Clearwater	Selway	White Cap Cr	72	264,031,261	0.60
Inland	12_SFSALM	Snake	Salmon	SF Salmon	Johnson Cr	95	201,270,498	0.48
Inland	12_SFSALM	Snake	Salmon	SF Salmon	Lick Cr	70	200,066,360	0.56
Inland	12_SFSALM	Snake	Salmon	SF Salmon	Secesh R	30	263,042,376	0.60
Inland	12_SFSALM	Snake	Salmon	SF Salmon	East Fork SF Salmon R	53	363,259,811	0.73
Inland	12_SFSALM	Snake	Salmon	SF Salmon	Stolle Meadows	42	366,401,888	0.68
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Bargamin Cr	60	189,953,336	0.53
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Big, Rush Crks	95	328,230,174	0.67
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Camas Cr	70	268,890,213	0.70

Inland	13_MFSALM	Snake	Salmon	MF Salmon	Loon Cr	51	320,069,394	0.65
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Marsh Cr	60	334,274,383	0.72
Inland	14_UPSALM	Snake	Salmon	NF Salmon	EF Salmon R	51	304,068,477	0.64
Inland	14_UPSALM	Snake	Salmon	NF Salmon	Yankee Fork Salmon R	58	191,268,742	0.52
Inland	14_UPSALM	Snake	Salmon	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:

SNP marker refinement and development with O. tshawytscha whole genome re-sequencing data:

There are 28 SNP markers within the genomic region associated with migration timing in Chinook salmon that have been incorporated into the PBT baseline (Koch and Narum 2020; Willis et al. 2021). Their efficiency in discriminating early versus late run-timing has been investigated (Koch and Narum 2020; Willis et al. 2021), but in a small number of populations spanning the three genetic lineages of Chinook salmon (interior ocean-type lineage, iOT; interior stream-type lineage, iST; lower Columbia lineage, LC). With the whole genome re-sequencing data for Chinook salmon (Table 2) that encompasses populations from all genetic lineages and migration timing within those lineages, the migration timing SNP markers were assessed. To do this, the allele frequencies of all SNP positions encompassing this region on chromosome 28 (Chr28) were extracted from all populations. The allele frequency data was directly compared to the phenotype of run-timing, extrapolated from PIT tag data collected for a subset of populations and reported in Willis et al. (2021). Correlation between migration timing (mean and median) and the minimum allele frequency (MAF) for SNP positions within the migration timing region was assessed using linear regression in R v4.0.2 using the *lm* function.

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 13, Figure 14, 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 235 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).

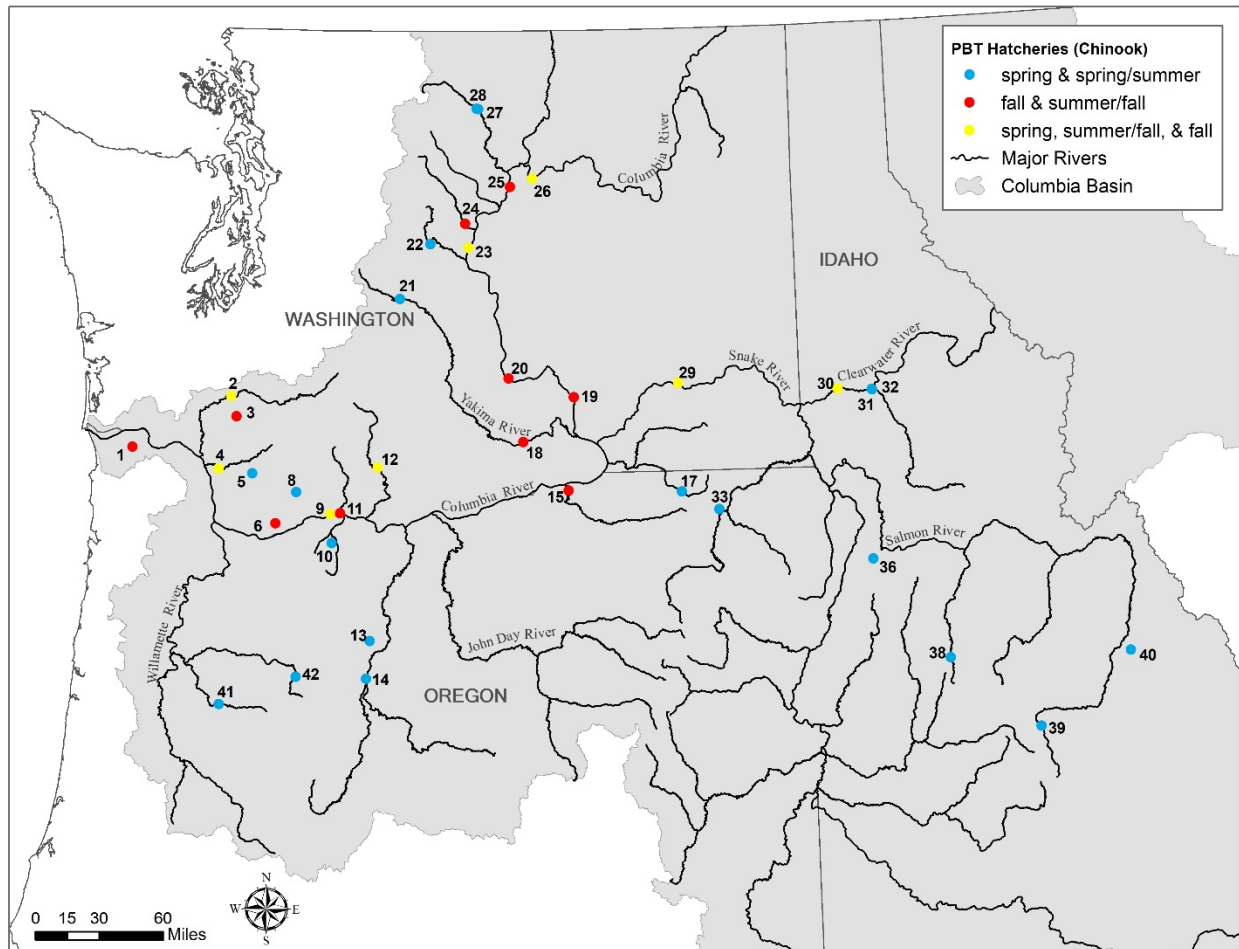


Figure 13. Chinook Salmon, PBT hatcheries. Numbers correspond to map ID and hatchery descriptions (Appendix 11).

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 2022 report period included spawn year 2020 for one hatchery, but primarily spawn year 2021 was genotyped for most hatcheries. The total numbers of fish genotyped for PBT baselines in 2022 included n=20,395 spring Chinook Salmon, n=3,252 upper Columbia summer Chinook Salmon, n=29,229 fall Chinook Salmon (Appendix 9), n=1,308 steelhead trout (Appendix 10), and n=4,098 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 235 SNP loci for Coho Salmon using a GTseq protocol: (<https://www.monitoringresources.org/Document/Method/Details/5446>). Hatchery offspring that are subsequently sampled either as juveniles or adults (e.g., in a fishery) are then PBT assigned

back to spawned parents which provides the individual age and specific hatchery of origin for each offspring.

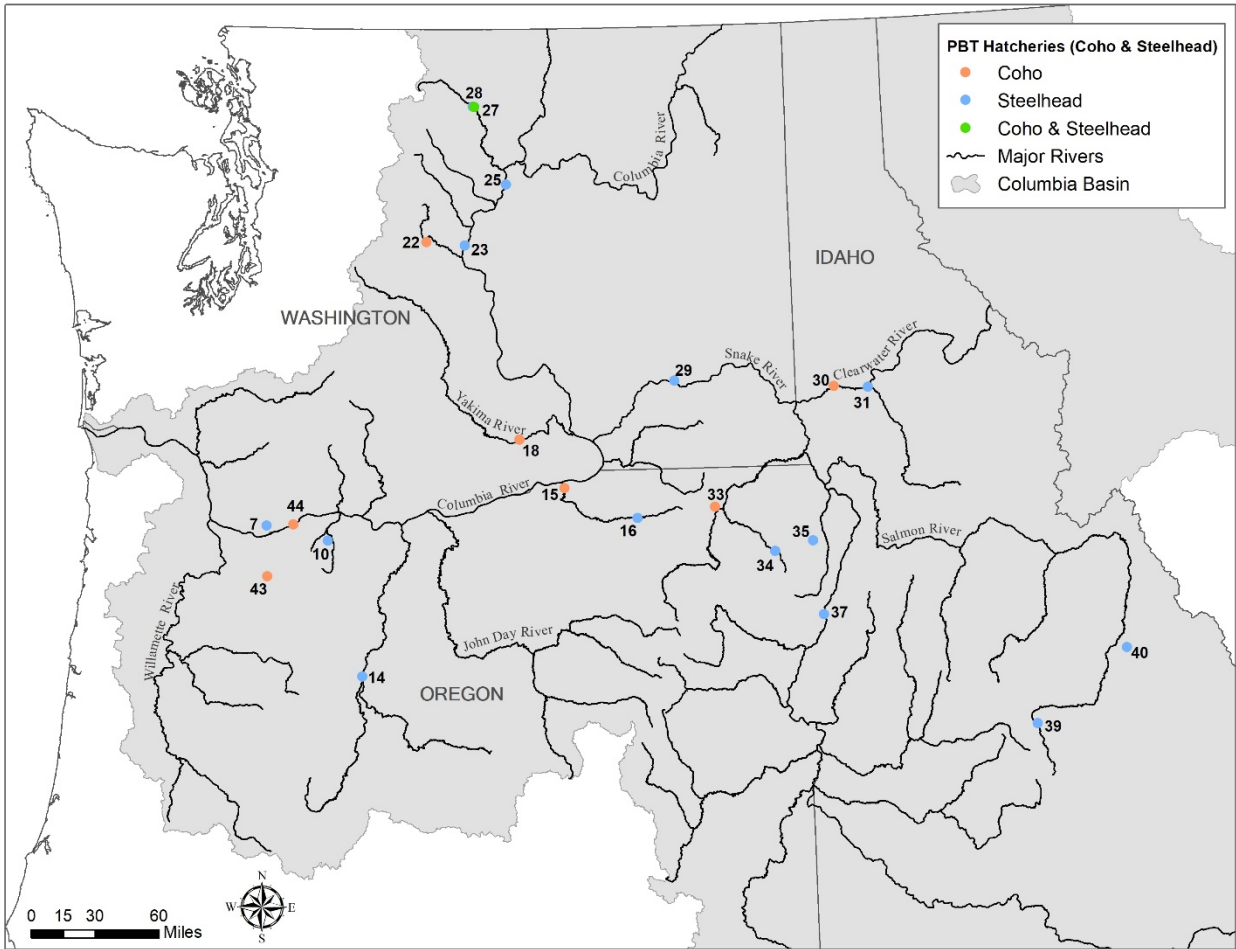


Figure 14. Steelhead and Coho Salmon, PBT hatcheries. Numbers correspond to map ID and hatchery descriptions (Appendix 12, Appendix 13).

SNP marker refinement with O. tshawytscha whole genome re-sequencing data:

Of the 28 markers developed for the migration timing region on Chr28, 22 were present in the whole genome re-sequencing data and allele frequencies were extracted. Several of the markers, Ots28_11202190, Ots28_11205423, Ots28_11205993, Ots28_11206740 (at SNP positions 12,401,520, 12,404,734, 12,405,298, 12,406,045 on Chr28) do not distinguish between early and late run populations with the LC lineage (Figure 15). Similarly, the SNP Ots28_11210919 (at position 12,410,152 on Chr28) does not distinguish early versus late run populations in the iST lineage (Figure 15). A linear regression analysis of the allele frequencies at each SNP position within lineages, indicated that the SNPs Ots28_11075348 and Ots28_11095755 (at positions 12,279,292 and 12,299,996 on Chr28) were most effective in differentiating run-timing (Figure 15) with Ots28_11095755 especially effective at

differentiating run-timing in iST lineages (Figure 16). The combination of several SNPs from this region to provide haplotypes for individual fish are expected to be more diagnostic for migration timing than any single SNP marker. Thus, we recommend multiple markers to provide the highest accuracy in conservation applications in Chinook salmon.

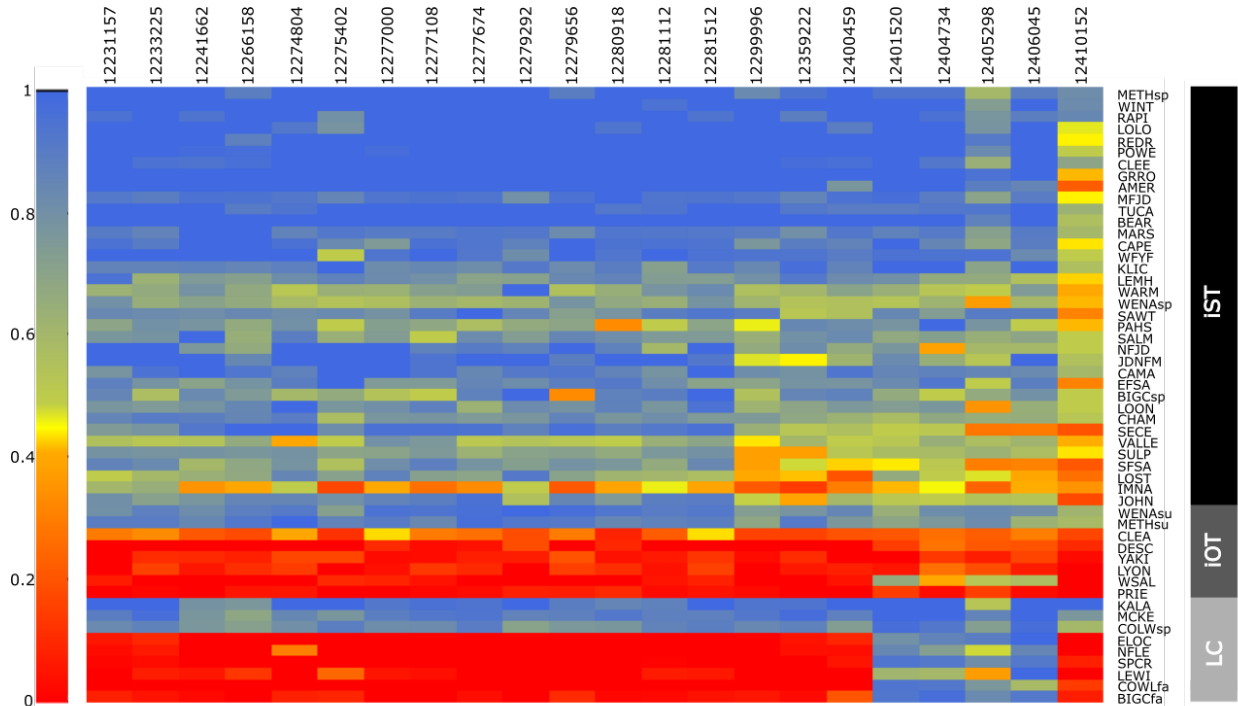


Figure 15. Allele frequencies of the SNP positions in which GT-seq markers have been developed for genotyping for all populations (rows) in the whole genome re-sequencing dataset. Blue represents an allele frequency of 1 and is more common in early run populations and red represents an allele frequency of 0 and is more common in late run populations. The populations are grouped by lineage: iST, interior stream-type; iOT, interior ocean-type; LC, Lower Columbia.

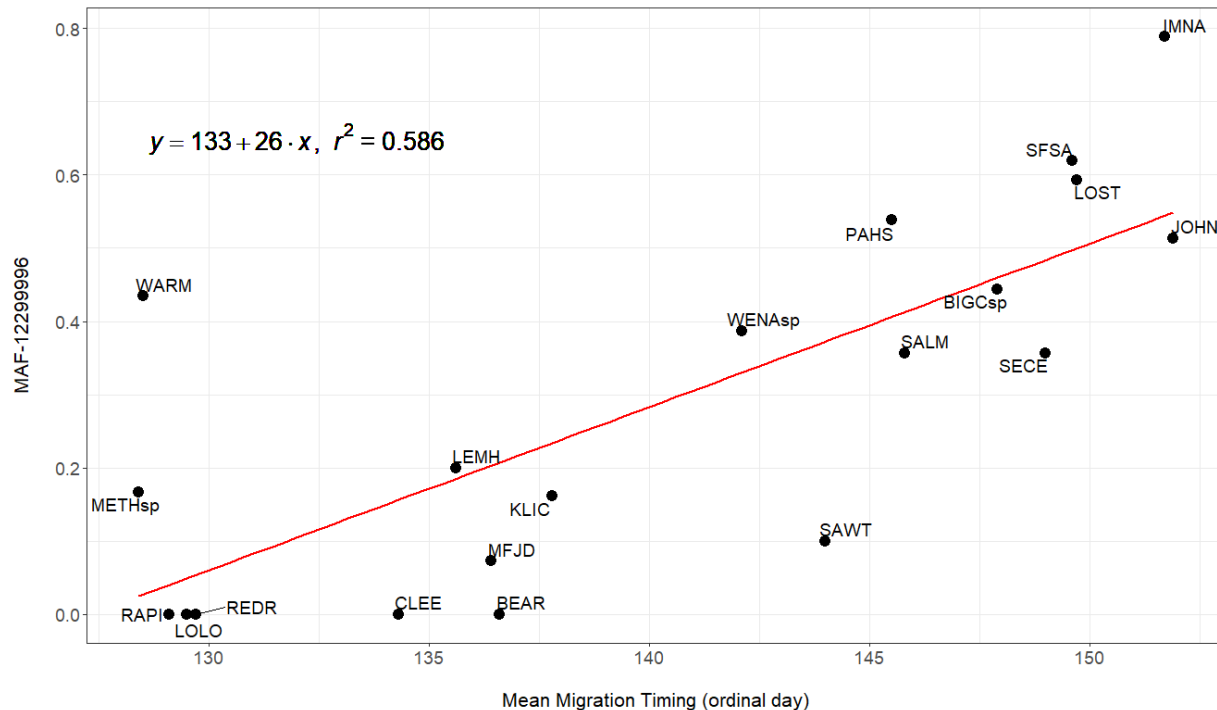


Figure 16. The minimum allele frequency (MAF, y-axis) plotted against the mean migration timing date (x-axis) at Ots28_11095755 (SNP position 12299996) for the interior stream-type populations.

Discussion

Over the course of the Genetic Assessment project we have compiled extensive data sets of SNP genotypes for Chinook salmon, steelhead trout and *O. nerka*, and continue to improve resources for Coho Salmon and Pacific Lamprey. The populations we have evaluated span diverse regions in the Columbia River Basin (including the Snake River Basin). We continue to update and maintain SNP reference baselines for evaluation of these species in future generations. This long-term strategy informs harvest management and assures the greatest likelihood of discerning temporal variation among reproductively distinct species aggregates (Waples 1991), while monitoring population viability related to demographic trends that occur locally and/or regionally. Philopatry (Quinn et al. 1991, Hendry et al. 2003) and hatchery supplementation activities (Ford et al. 2006; Hard & Heard 1999) play a major role in how genetic divergence and differentiation is distributed geographically. For managing sustainable fisheries, it is necessary to understand the magnitude of influence that these and other factors have on our ability to differentiate populations, both qualitatively (phenotypes; landscapes) and quantitatively (e.g., genetic stock identification). This becomes particularly important where mixed stock fisheries may consist of both ESA listed and unlisted populations, and where differential harvest may have the greatest impact on specific populations. Our current efforts have largely focused on expanding numbers of markers and non-neutral markers associated with maturation. However, loci for adaptive divergence (landscape genetics) remains as one of our primary objectives for strengthening our understanding of non-neutral genetic variation among populations. Data collected through whole genome re-sequencing and GT-seq techniques has yielded large numbers of potential SNPs, and demonstrated their utility for characterizing

adaptive variation, and identifying environmental and life history related variables that are likely to have significant influence on allele frequencies (e.g., precipitation, temperature, run-timing.; Hecht et al. 2015, Hess et al. 2016b; Micheletti et al. 2017; Narum et al. 2018; Micheletti et al. 2018; Collins et al. 2020). The expansion efforts reported here also provided improved ability to differentiate stocks on regional and local scales through application of GSI and PBT methods.

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

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Map ID	Spawning hatchery	Run type	Lineage	Region	Latitude	Longitude	Year	<u>2022 genotyping</u>	
								Sampled	Completed
1	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
	Big Creek	fall (tule)	LC	Col.	46.14616	-123.581	2015	2021	
	Cowlitz Salmon	fall (tule)	LC	Col.	46.51145	-122.629	2015	2021	1975
	Cowlitz Salmon	spring	LC	Col.	46.51145	-122.629	2015	2021	1317
	Toutle	fall (tule)	LC	Col.	46.37464	-122.572	2015	2021	261
	Kalama Falls	fall (tule)	LC	Col.	46.01624	-122.733	2016	2021	2782
	Kalama Falls	spring	LC	Col.	46.01624	-122.733	2015	2021	819
	Speelyai (Lewis R)	spring	LC	Col.	45.98849	-122.406	2015	2021	1143
	Clackamas	spring	LC	Col.	45.296	-122.362	na		
	Marion Forks	spring	LC	Col.	44.612	-121.948	na		
	North Santiam	spring	LC	Col.			2020	2021	800
	South Santiam	spring	LC	Col.	44.416	-122.675	2020	2021	800
	McKenzie	spring	LC	Col.	44.118	-122.637	2020	2021	na
	Willamette	spring	LC	Col.	43.745	-122.444	na		
6	Washougal	fall (tule)	LC	Col.	45.65344	-122.169	2015	2021	746
	Bonneville, Tanner Cr.	fall (tule)	LC	Col.	45.633	-121.957	na	2021	na
11	Spring Creek NFH	fall (tule)	LC	Col.	45.72779	-121.545	2015	2021	6573
9	Little White Salmon NFH	fall	IOT	Col.	45.72226	-121.64	2013	2021	8319
15	Umatilla	fall	IOT	Col.	45.88172	-119.323	2012	2021	449
18	Prosser	fall	IOT	Col.	46.21512	-119.76	2012	2020,2021	748,128
19	Ringold Springs	fall	IOT	Col.	46.51401	-119.259	2016	2021	869
20	Priest Rapids	fall	IOT	Col.	46.64728	-119.899	2012	2021	5684
29	Lyons Ferry	fall	IOT	Snake	46.59725	-118.228	2011	2021	WDFW
30	Nez Perce Tribal	fall	IOT	Snake	46.51954	-116.66	2011	2021	695
23	Eastbank	summer	IOT	Col.	47.53367	-120.289	2012	2021	719
24	Entiat NFH	summer	IOT	Col.	47.69806	-120.323	2013	2021	330
25	Wells	summer	IOT	Col.	47.94582	-119.871	2012	2021	966
26	Chief Joseph	summer	IOT	Col.	48.0006	-119.645	2013	2021	1237
9	Little White Salmon NFH	spring	IST	Col.	45.72226	-121.64	2013	2021	1107
15	Umatilla	spring	IST	Col.	45.88172	-119.323	2012	2021	489
29	Lyons Ferry	spring	IST	Snake	46.59725	-118.228	2008	2021	93
30	Nez Perce Tribal	spring	IST	Snake	46.51954	-116.66	2008	2021	285
23	Eastbank	spring	IST	Col.	47.53367	-120.289	2012	2021	198
26	Chief Joseph	spring	IST	Col.	48.0006	-119.645	2014	2021	532
8	Carson NFH	spring	IST	Col.	45.86826	-121.974	2012	2021	1346
10	Parkdale	spring	IST	Col.	45.52439	-121.622	2012	2021	180
12	Klickitat	spring	IST	Col.	46.04236	-121.182	2008	2021	526
13	Warm Springs NFH	spring	IST	Col.	44.86201	-121.245	2012	2021	229
14	Round Butte	spring	IST	Col.	44.60503	-121.278	2012	2021	206
21	Cle Elum SRF	spring	IST	Col.	47.18679	-120.976	2012	2021	278
22	Leavenworth NFH	spring	IST	Col.	47.55842	-120.674	2013	2021	981
27	Methow	spring	IST	Col.	48.47703	-120.205	2012	2021	68
28	Winthrop NFH	spring	IST	Col.	48.47366	-120.189	2013	2021	440
33	Lookingglass	spring	IST	Snake	45.73136	-117.864	2008	2021	804
31	Powell	spring	IST	Snake			2008	2021	154
	Dworshak NFH	spring	IST	Snake	46.50206	-116.323	2008	2021	1624
32	Kooskia	spring	IST	Snake			2008	2021	557
	Clearwater	spring	IST	Snake	46.50429	-116.328	2008	2021	2499
36	Rapid River	spring/ summer	IST	Snake	45.35411	-116.394	2008	2021	2820
38	SF Salmon, McCall	spring/ summer	IST	Snake	44.65554	-115.702	2008	2021	IDFG
40	Johnson Creek	spring/ summer	IST	Snake			2008	2021	100
	Pahsimeroi	spring/ summer	IST	Snake	44.62284	-113.986	2008	2021	IDFG

1767	39	Sawtooth	spring/ summer	IST	Snake	44.15174	-114.884	2008	2021	IDFG
1768	Note: The Map ID indicates the sites of the hatcheries corresponding to Figure 12. Genetic lineage is lower Col. (LC), interior ocean-type (IOT), and interior stream-type (IST). Year refers to the first year of PBT sampling for each hatchery: na – not currently a PBT hatchery. For some hatchery PBT samples, genotyping efforts have begun to backdate collections that were initially archived- the “sampled” field indicates which collection years were genotyped in 2022. The project collaborators at Idaho Department of Fish and Game (IDFG) were responsible for genotyping of Snake River hatcheries (see “completed” column).									
1769										
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								2022 genotyping	
Map ID	Spawning hatchery	Run type	Lineage	Region	Latitude	Longitude	Year	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	-122.733	na	na	na
	Merwin	winter	coastal	Col.	45.954	-122.564	na	na	na
	Clackamas	winter	coastal	Col.	45.296	-122.362	na	na	na
	Eagle Creek NFH	winter	coastal	Col.	45.276	-122.202	na	na	na
	Sandy	winter	coastal	Col.	45.407	-122.254	na	na	na
7	Skamania	summer/winter	coastal	Col.	45.6218	-122.217	2013	2021	350
10	Parkdale	winter	coastal	Col.	45.5244	-121.622	2012	2021	na
14	Round Butte	summer	inland	Col.	44.605	-121.622	2013	2021	446
	Umatilla	summer	inland	Col.	45.913	-119.552	2012	2021	73
23	Eastbank	summer	inland	Col.	47.5337	-120.289	2012	2021	201
25	Wells	summer	inland	Col.	47.9458	-119.871	2013	2021	150
27	Methow (Twisp)	summer	inland	Col.	48.477	-120.205	2013	2021	na
28	Winthrop NFH	summer	inland	Col.	48.4737	-120.205	2013	2021	88
29	Lyons Ferry	summer	inland	Snake	46.5973	-118.228	2009	2021	IDFG
34	Wallowa	summer	inland	Snake	45.4178	-117.3	2009	2021	IDFG
37	Oxbow	summer	inland	Snake	44.9727	-116.855	2008	2021	IDFG
31	Dworshak NFH	summer	inland	Snake	46.5021	-116.323	2008	2021	IDFG
40	Pahsimeroi	summer	inland	Snake	44.6228	-113.986	2008	2021	IDFG
39	Sawtooth	summer	inland	Snake	45.1517	-114.884	2008	2021	IDFG
35	Little Sheep Creek	summer	inland	Snake	45.4777	-116.931	2008	2021	IDFG
Coho									
15	Umatilla	fall	lower Col.	Col.	45.913	-119.552	2015	2021	386
18	Prosser	fall	lower Col.	Col.	46.2151	-119.76	2016	2021	612
22	Leavenworth NFH	fall	lower Col.	Col.	47.5584	-120.674	2012	2021	1038
28	Winthrop NFH	fall	lower Col.	Col.	48.4737	-120.189	2012	2021	662
31	Dworshak NFH	fall	lower Col.	Snake	46.5021	-116.323	2015	2021	1400
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
	Mel R Sampson	Fall	Lower Col.	Col.	47.042	-120.626	2021	2021	658

1775
1776
1777 * Steelhead Methow Hatchery Twisp stock spawned at Winthrop NFH starting in 2017; not distiguished from Winthrop stock.
1778 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
1779 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
1780 drafting of this report. The project collaborators at Idaho Department of Fish and Game (IDFG) were responsible for genotyping of Snake River hatcheries (see
1781 “completed” column). All Coho broodstocks sampled for PBT broodstock were designated for release of fish upstream of Bonneville Dam.

Appendix 11. Checklist of PBT broodstock collections that comprise the PBT baselines for Chinook salmon from 2008 through 2021.

Map num.	Hatchery	Species	Code	Run type	Lineage	Year															
						2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021		
32	Clearwater Fish Hatchery	Chinook	OtsCLWH	Spring	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
32	Clearwater Fish Hatchery - Powell Facility	Chinook	OtsPOWP	Spring	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
31	Dworshak National Fish Hatchery	Chinook	OtsDWOR	Spring	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
33	Lookingglass Fish Hatchery - Catherine Creek	Chinook	OtsCTHW	Spring/Summer	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
33	Lookingglass Fish Hatchery - Grande Ronde	Chinook	OtsGRUW	Spring	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
33	Lookingglass Fish Hatchery - Imnaha River	Chinook	OtsIMNW	Spring/Summer	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
33	Lookingglass Fish Hatchery - Lookingglass Creek	Chinook	OtsLOOK	Spring	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
33	Lookingglass Fish Hatchery - Lostine River	Chinook	OtsLSTW	Spring	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
29	Lyons Ferry Fish Hatchery	Chinook	OtsLYON	Spring	IST	*	*	*	*	X	X	X	X	X	X	X	X	X	X		
29	Lyons Ferry Fish Hatchery - Tucannon River	Chinook	OtsTUCW a	Spring	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
29	Lyons Ferry Fish Hatchery	Chinook	OtsLYON_1	Fall	IOT	*	*	*	X	X	X	X	X	X	X	X	X	X	X		
38	McCall Fish Hatchery - Johnson Creek	Chinook	OtsJHNW	Spring/Summer	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
38	McCall Fish Hatchery - South Fork Salmon	Chinook	OtsMCCA	Spring	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
30	Nez Perce Tribal Fish Hatchery	Chinook	OtsNPFH_1	Fall	IOT	*	*	*	X	X	X	X	X	X	X	X	X	X	X		
30	Nez Perce Tribal Fish Hatchery	Chinook	OtsNPFH	Spring	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
40	Pahsimeroi Fish Hatchery	Chinook	OtsPAHH	Spring	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
36	Rapid River Fish Hatchery	Chinook	OtsRAPH	Spring	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
39	Sawtooth Fish Hatchery	Chinook	OtsSAWT	Spring	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
1	Big Creek Hatchery	Chinook	OtsBIG_fa	Fall	LC	*	*	*	*	*	*	*	X	X	X	X	X	X			
8	Carson National Fish Hatchery	Chinook	OtsCAR_sp	Spring	IST	*	*	*	*	X	X	X	X	X	X	X	X	X	X		
26	Chief Joseph Hatchery	Chinook	OtsCJH_sp	Spring	IST	*	*	*	*	*	*	X	X	X	X	X	X	X			
26	Chief Joseph Hatchery - Integrated	Chinook	OtsCJHint_su	Summer	IOT	*	*	*	*	*	X	X	X	X	X	X	X	X	X		
26	Chief Joseph Hatchery - Segregated	Chinook	OtsCJHseg_su	Summer	IOT	*	*	*	*	*	X	X	X	X	X	X	X	X	X		
2	Cowlitz Salmon	Chinook	OtsCOW_sp	Spring	IST	*	*	*	*	*	*	*	X	X	X	X	X	X			
2	Cowlitz Salmon	Chinook	OtsCOW_fa	Fall	IST	*	*	*	*	*	*	*	X	X	X	X	X	X			
23	Eastbank Fish Hatchery	Chinook	OtsEASTBK_sp	Spring	IST	*	*	*	*	*	X	X	X	X	X	X	X	X			
23	Eastbank Fish Hatchery	Chinook	OtsEASTBK_su	Summer	IOT	*	*	*	*	X	X	X	X	X	X	X	X	X			
24	Entiat National Fish Hatchery	Chinook	OtsENFH_su	Summer	IOT	*	*	*	*	*	X	X	X	X	X	X	X	X	X		
4	Kalama Falls	Chinook	OtsKAL_sp	Spring	IST	*	*	*	*	*	*	*	X	X	X	X	X	X			
4	Kalama Falls	Chinook	OtsKAL_fa	Fall	IST	*	*	*	*	*	*	*	X	X	X	X	X	X			
12	Klickitat State Fish Hatchery	Chinook	OtsKH_sp	Spring	IST	X	X	X	X	X	X	X	X	X	X	X	X	X	X		
12	Klickitat State Fish Hatchery	Chinook	OtsKH_fa c	Fall	IOT	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	IST	*	*	*	*	*	X	X	X	X	X	X	X	X	X		
5	Speelyai Hatchery	Chinook	OtsLEW_sp	Spring	IST	*	*	*	*	*	*	*	X	X	X	X	**	**			
9	Little White Salmon National Fish Hatchery	Chinook	OtsLWS_fa	Fall	IOT	*	*	*	*	*	X	X	X	X	X	X	X	X	X		
9	Little White Salmon National Fish Hatchery	Chinook	OtsLWS_sp	Spring	IST	*	*	*	*	*	X	X	X	X	X	X	X	X	X		
9	Little White Salmon National Fish Hatchery - Touchet River	Chinook	OtsTOUCH_sp	Spring	IST	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	IST	*	*	*	*	*	*	*	*	*	*	X	X	*			
27	Methow State Fish Hatchery	Chinook	OtsMETH_sp	Spring	IST	*	*	*	*	X	X	X	X	X	X	X	X	X			
10	Parkdale Fish Facility	Chinook	OtsPFF_sp	Spring	IST	*	*	*	*	X	X	X	X	X	X	X	X	X	X		
20	Priest Rapids Hatchery	Chinook	OtsPRH_fa	Fall	IOT	*	*	*	*	X	X	X	X	X	X	X	X	X	X		
14	Round Butte Fish Hatchery	Chinook	OtsRB_sp	Spring	IST	*	*	*	*	X	X	X	X	X	X	X	X	X			
19	Ringold Springs State Hatchery	Chinook	OtsRG_fa	Fall	IOT	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	X	X	X	X	X	X		
41	South Santiam Hatchery	Chinook	OtsSSANT_sp	Spring	IST	*	*	*	*	*	*	*	X	X	*	X	X	X			
11	Spring Creek National Fish Hatchery	Chinook	OtsSPCR_fa	Fall	LC	*	*	*	*	*	*	*	X	X	X	X	X	X	X		
3	North Toutle Hatchery	Chinook	OtsTOU_fa	Fall	IOT	*	*	*	*	*	*	*	X	X	X	X	**	X			
15	Three mile dam, Umatilla River	Chinook	OtsUMA_fa b	Fall	IOT	*	*	*	*	X	X	X	~	~	~	X	X	X	X		
17	South Fork Walla Walla facility	Chinook	OtsUMA_sp	Spring	IST	*	*	*	*	X	X	X	X	X	X	X	X	X	X		
6	Washougal	Chinook	OtsWAS_fa	Fall	IOT	*	*	*	*	*	*	*	X	X	X	X	X	X			
13	Warm Springs National Fish Hatchery	Chinook	OtsWSNFH_sp h	Spring	IST	*	*	*	*	X	X	X	~	~	~	X	X	X			
25	Wells Fish Hatchery	Chinook	OtsWELLS_su	Summer	IOT	*	*	*	*	X	X	X	X	X	X	X	X	X	X		
28	Winthrop National Fish Hatchery	Chinook	OtsWTP_sp	Spring	IST	*	*	*	*	*	X	X	X	X	X	X	X	X			
18	Yakima Nation Prosser Hatchery	Chinook	OtsPRO_fa	Fall	IOT	*	*	*	*	X	X	*	X	X	X	X	X	X			
21	Levi George/Cle Elum (Integrated)	Chinook	OtsYRint_sp	Spring	IST	*	*	*	*	X	X	X	X	X	X	X	X	X			
21	Levi George/Cle Elum (Segregated)	Chinook	OtsYRseg_sp	Spring	IST	*	*	*	*	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.

█ 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 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	2021		
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			
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	*	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		

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- Note map numbers correspond to sites in Figure 12.
- X Steelhead tissues genotyped using 96 SNPs
- X Steelhead tissues genotyped using 379 SNPs
- X Steelhead tissues genotyped using 269 SNPs
- X Steelhead tissues genotyped using 192 SNPs
- X Steelhead tissues genotyped using 390 SNPs
- X Steelhead tissues genotyped using 368 SNPs
- ~ Steelhead broodstock sampled, spawned at another hatchery and genotyped using 379 SNPs
- Steelhead broodstock sampled, spawned at another hatchery and genotyped using 368 SNPs
- c Steelhead Lyons Ferry stock consolidated under 'OmyLYON' starting in 2012
- d Steelhead Lyons Ferry stock discontinued starting in 2013
- e Steelhead Sawtooth stock consolidated under 'OmySAWT' from 2012-2013
- 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
- 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.
- i Steelhead Methow Hatchery Twisp stock spawned at Winthrop NFH starting in 2017; not distiguished from Withrop stock
- 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										
						2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021
15	Three Mile Dam, Umatilla River	Coho	OkiUMA	Fall	Lower Columbia					X	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	X
30	Dworshak National 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	X	*
	Mel R Sampson Hatchery	Coho	OkiMRS	Fall	Lower Columbia											*
28	Winthrop National Fish Hatchery	Coho	OkiWTP, OkiMET	Fall	Lower Columbia		X	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		

1821
1822 Note: map numbers correspond to sites in Figure 12.
1823 X Coho tissues genotyped at 235 loci
1824 * Samples received, but not genotyped.
1825 ** Samples collected, but not received.
1826

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 CRB, 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?

At times we have tailored 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. We have also included results for new research gear. For example, the pound net was a gear that was tested by the joint states in the fall fisheries below Bonneville Dam. In past reports, we 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.

This report includes the 10th year of analysis of Sockeye salmon fisheries in the Columbia River mainstem, which consists of fish harvested in 2021 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. Since our 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 2021 from a total of five different mixture sources: the spring-run season of the 1) lower river recreational fishery; 2) test fishery; the summer management period harvest of the 3) lower river recreational fishery; and the fall-run harvest from 4) lower river commercial, 5) sport (above and below Bonneville Dam). 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 16; Table 6). Issues related to COVID prevented Treaty fisheries from being sampled since 2020. Typically for the summer management period fisheries, we may obtain samples from below Bonneville Dam in the recreational fishery, and above Bonneville Dam in the Zone 6 recreational fishery and the 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 16): 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, and the fall Non-Treaty sport and commercial fishery.

Tissues were sampled from sockeye salmon in 2021 from two fishery mixture sources: 1) Bonneville Dam (see Section 4), and 2) the recreational fishery below Bonneville Dam. All samples obtained from the recreational (Non-Treaty sport) fishery in 2021 are 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 third 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 SY2020 and so the 2022 Bonneville Dam run year was the third year in which both 1-ocean and 2-ocean age steelhead could be assigned using the expanded panel of SNPs. We use a set of 92 SNPs to perform PBT analysis on collections of steelhead representing older spawn years before SY2017.

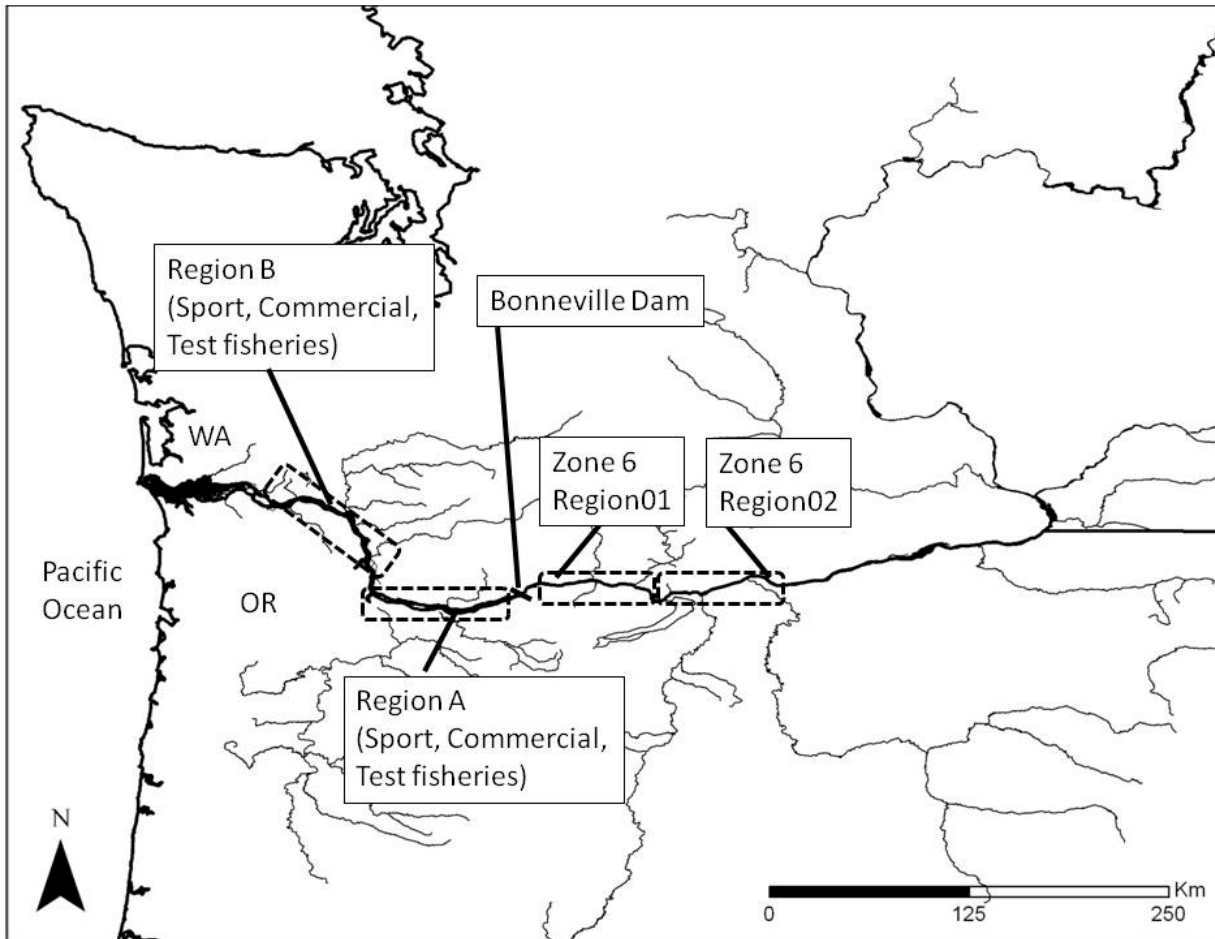


Figure 17. Project scope showing sources of Chinook salmon and Sockeye salmon harvest mixtures that were analyzed using PBT/GSI.

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2002 **Table 5. Characteristics of Chinook and Sockeye harvest samples by fishery, region, and adipose-clip status by weekly strata in 2021.**

						Spring															Summer					Fall														
						Statistical weeks																																		
Chinook Period	Fishery	Region	Clip	Sampled	Genotyped	11	12	13	14	15	16	17	18	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	
Spring	Sport	A	AD	154	128			2	19	8						26	19	17	26	11																				
		B	AD	397	332	3	2	55	107	5							4	12	9	89	46																			
Summer	Test	B	AD	134	131		1	5	6	13	27	22	33	14	10																									
			AI	35	33			1			5	9	10	4	4																									
	Sport	A	AD	37	30														5	7	9	9																		
		B	AD	152	132														31	76	13	11		1																
Fall	Sport	A	AD	239	164																							1	6	15	16	22	69	18	5	5	7			
			AI	670	449																								2	8	43	31	45	204	46	31	26	11	2	
		B	AD	250	182																					4	5	19	99	51								4		
			AI	407	298																								1	31	161	101						3	1	
	01 (Zone 6)	AD	31	31																										3	12	1			12	3				
		AI	27	26																											2	12	1			10	1			
		02 (Zone 6)	AD	20	20																									2	12		1	1	3		1			
			AI	27	26																										2	8	2		3	2	1	6		2
	Commercial	A	AD	423	381																								31	19	177	135			17	2				
			AI	224	199																								58	12	48	49			28	4				
		B	AD	10	1																																1			
			AI	36	2																																1			1
Chinook fishery subtotal				3273	2565	3	3	63	132	26	32	31	43	18	14	30	31	26	115	93	83	22	20	0	1	0	4	98	99	568	409	70	277	136	49	45	19	4	1	
Sockeye harvest			AI	54	50															2	18	14	12	2		2														
Sockeye fishery subtotal				54	50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	18	14	12	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0

2003
2004 Note: In this analysis, a large number of failures for genotypes across Chinook harvest collections was observed and resolved via recent quality control.

PBT Rate Expansion using SCOBIDEUX and SPIBETR functions

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

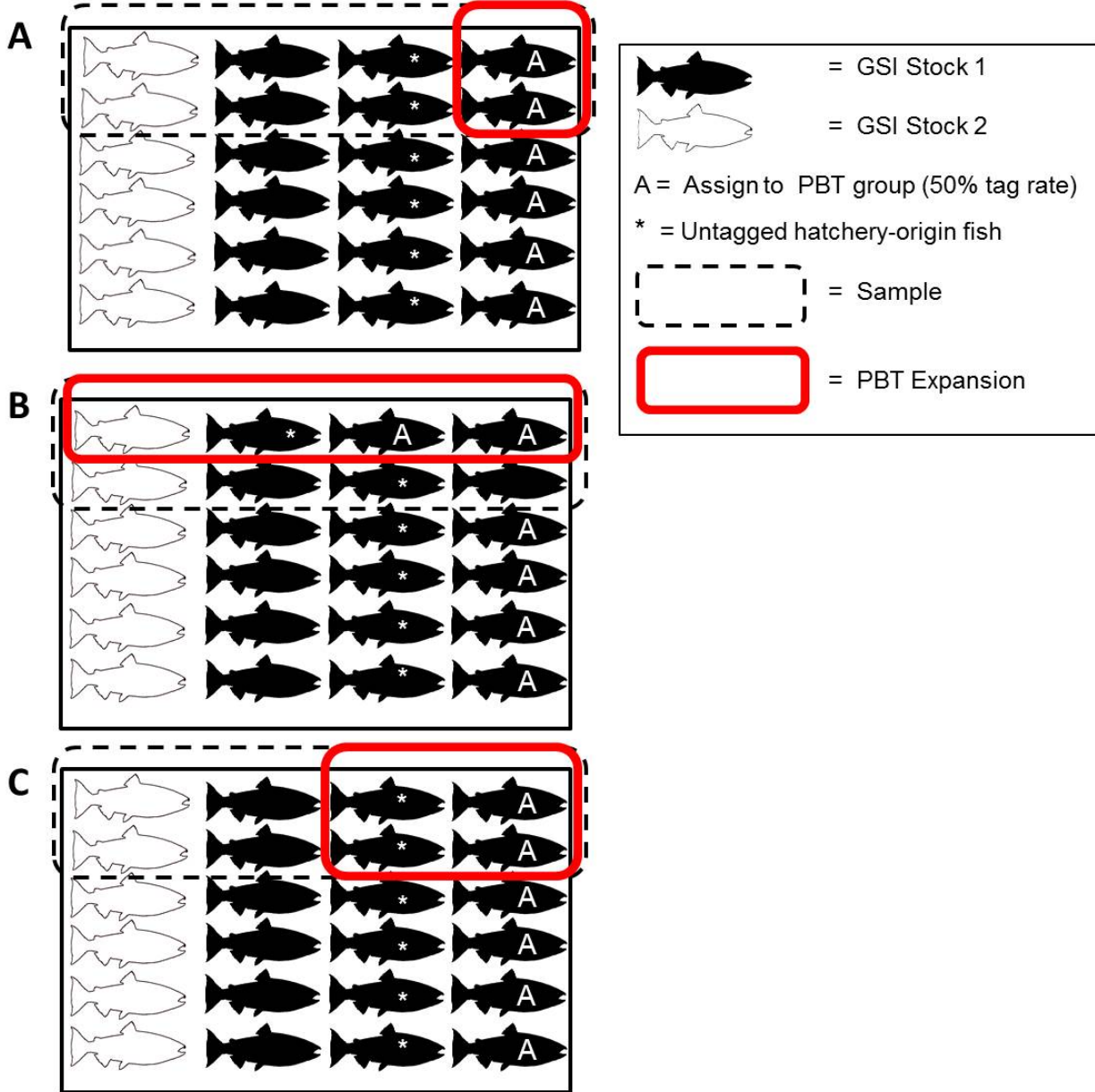


Figure 18. Conceptual illustration of the bias correction the SCOBIDEUX method provides.

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

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

GSI baselines for Chinook salmon, sockeye salmon, and steelhead

Chinook salmon GSI analyses were performed using the updated baseline referred to as “Columbia River Basin Chinook salmon GSI baseline version 3.1” and is available on the FishGen website (<https://www.fishgen.net>). However, we made on slight modification and decreased the number of SNP markers to 177 that were included in the latest iteration of the GT-seq panel. This baseline consists of 61 collections that are delineated into the following 19 reporting groups: Columbia Rogue “01_YOUNGS”, West Cascade spring-run “02_WCASSP”, West Cascade fall-run “03_WCASFA”, Willamette River spring-run “04_WILLAM”, Spring Creek Group Tule fall-run “05_SPCRTU”, Klickitat River spring-run “06_KLICKR”, Deschutes River spring-run “07_DESCSP”, John Day River spring-run “08_JOHNDR”, Yakima River spring-run “09_YAKIMA”, upper Columbia River spring-run “10_UCOLSP”, Tucannon River spring-run “11_TUCANO”, Hells Canyon spring-run “12_HELLSC”, South Fork Salmon River spring-run “13_SFSALM”, Chamberlain Creek spring-run “14_CHMBLN”, Middle Fork Salmon River spring-run “15_MFSALM”, upper Salmon River spring-run “16_UPSALM”, Deschutes River fall-run “17_DESCFA”, upper Columbia River summer/fall-run “18_UCOLSF”, and Snake River fall-run “19_SRFALL” (Table 6; Figure 19). Reporting groups were primarily determined by the relative genetic similarity among populations according to a phylogenetic analysis, and our previous results demonstrate sufficient power to discern three reporting groups (17_DESCFA, 18_UCOLSF, and 19_SRFALL) among the interior ocean-type collections. In one year, we had grouped all interior ocean-type collections into a single reporting group “Interior_Columbia_R_su/fa” (Hess et al. 2013). Genetic distances were computed from allele frequencies based on Nei’s (1972) genetic distance, with the PHYLIP v 3.69 (Felsenstein 1989) and 1000 bootstrap replicates were performed. Distances were clustered using the Neighbor – Joining method (Saitou and Nei, 1987), and a consensus tree was constructed (<http://evolution.genetics.washington.edu/phylip/>) (Figure 20). The clusters are labeled with names of reporting groups used to aggregate the collections based on a combination of factors including genetic similarity, life history, and geographic proximity. Bootstrap support is shown with shaded ovals (Source: Hess et al. 2015).

The 10_UCOLSP reporting group includes the following Bonneville pool hatchery stocks: Carson stock (Ots22), and Little White Salmon R. (Ots23) because they are genetically indistinguishable from Upper Columbia R. spring Chinook salmon (includes Walla Walla and Umatilla River stocks). This composite group is notable because inclusion of these Bonneville

pool stocks explains why a large proportion of fish from the Wind R. sport fishery should assign to this 10_UCOLSP reporting group. However, the PBT baseline is now able to specifically identify fish from Carson Hatchery and Little White Salmon Hatchery allowing them to be distinguished from fish returning to the upper Columbia R. The 01_YOUNGS reporting group represents an out-of-basin genetic stock (originating from the Rogue R., OR) that is reared within the Columbia R. at Youngs Bay. Basic QAQC was performed to remove duplicate individuals and strays from the reference populations in the baseline. The baseline and reporting group data is available on FishGen.

GSI analyses for *O. nerka* utilized a baseline that included sockeye salmon and kokanee populations from throughout the Columbia River basin. This baseline included sockeye populations from the Osoyoos (i.e., Okanogan), Wenatchee, and Redfish Lake (i.e., Snake), and a kokanee population from Lake Whatcom that were included in “Sockeye GSI baseline v1.0, and were shown to accurately discriminate among these major stock (Hess et al 2013). We updated our baseline to included additional kokanee populations from Alturas Lake, Fishhook Creek, Lake Billy Chinook, Meadow Creek, Suttle Creek, Cougar, Gold, North Fork Tieton, Odell, Speylai, Stanley, Warm, Wizard, Wallowa River, and Wallowa Lake, and refer to this as “Sockeye GSI baseline v3.0”. The transition to GT-seq required omission of a few loci due to poor genotyping quality with the new protocols. A total of 363 SNPs was used for these analyses.

For steelhead, we have the following two GSI baselines available: 1) GSI baseline version 3.3 with 177 SNPs and 2) a new GSI baseline with 335 SNPs. The GSI version 3.3 comprises 116 collections from throughout the Columbia River basin that are partitioned into the following 14 reporting groups: 01_WCOAST (Quinalt River), 02_LOWCOL (lower Columbia River), 03_SKAMAN (Skamania hatchery releases at three sites in lower Columbia River, Willamette River, and Klickitat River), 04_WILLAM (Willamette River), 05_BWSALM (Big White Salmon River), 06_KLICKR (Klickitat River), 07_MGILCS (middle Columbia River, Grande Ronde River, Imnaha River, lower Snake River, lower Clearwater River, and lower Salmon River), 08_YAKIMA (Yakima River), 09_UPPCOL (upper Columbia River), 10_SFCLWR (South Fork Clearwater River), 11_UPCLWR (upper Clearwater River), 12_SFSALM (South Fork Salmon River), 13_MFSALM (Middle Fork Salmon River), and 14_UPSALM (upper Salmon River) (Figure 21). Genetic distances were computed from allele frequencies based on Nei’s (1972) genetic distance, with the PHYLIP v 3.69 (Felsenstein 1989) and 1000 bootstrap replicates were performed. Distances were clustered using the Neighbor – Joining method (Saitou and Nei, 1987), and a consensus tree was constructed (<http://evolution.genetics.washington.edu/phylip/>) (Hess et al. 2019). The GSI baseline with 335 SNPs comprises 128 collections throughout the Columbia River that are partitioned into 13 reporting groups (Hess et al. 2019), which are all the reporting groups listed in version 3.3 except 01_WCOAST (Quinalt River). This 335 SNP baseline was determined to be less accurate than the existing version 3.3. baseline for GSI applications (Hess et al. 2020), however, 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 Rubias (Moran and Anderson 2019) to determine likely reporting group of origin (Method: [Assigning individual samples using Individual Assignment \(IA\) genetic methods v1.0](#), ID: 1334). In a previous report (Hess et al. 2022), we showed improvements in accuracy of assignments using Rubias compared to the program ONCOR and this was the first year since having made a switch between those assignment programs. For the assignment of sockeye, GSI via Rubias 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. When possible, we 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%). We performed a preliminary analysis of the 2022 test fishery. Similar to the 2021 test fishery (Hess et al. 2022), the CPUE estimated in the 2022 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.

2170 **Table 7. The sample rate and stratification for genetic analysis of the VSI-upriver adipose clipped and unclipped adult**
 2171 **Chinook salmon from the spring test fishery in 2021.**

Week	Drifts	Estimated # VSI-Upriver			CPUE of VSI-Upriver			Sample of VSI-Upriver			Sample Rate of VSI-Upriver		
		AD	AI	Total	AD	AI	Total	AD	AI	Total	AD	AI	Total
12	15	3.00	0.00	3.00	0.20	0.00	0.20	1		1	56.9%	49.4%	55.5%
13	15	5.83	1.17	7.00	0.39	0.08	0.47	5	1	6			
14	14	7.22	1.44	8.67	0.52	0.10	0.62	3		3			
15	16	9.33	1.87	11.20	0.58	0.12	0.70	3		3			
16	17	29.09	7.66	36.75	1.71	0.45	2.16	19	5	24			
17	16	22.22	11.11	33.33	1.39	0.69	2.08	12	6	18	54.0%	54.0%	54.0%
18	15	21.25	4.25	25.50	1.42	0.28	1.70	15	3	18	70.6%	70.6%	70.6%
19	15	15.91	9.55	25.45	1.06	0.64	1.70	5	3	8	35.6%	35.0%	35.3%
20	15	3.78	1.89	5.67	0.25	0.13	0.38	2	1	3			

2172
 2173
 2174 **Table 8. The sample rate and stratification for genetic analysis of the VSI-lower river adipose clipped and unclipped**
 2175 **adult Chinook salmon from the spring test fishery in 2021**

Week	Drifts	Estimated # VSI-Upriver			CPUE of VSI-Upriver			Sample of VSI-Upriver			Sample Rate of VSI-Upriver		
		AD	AI	Total	AD	AI	Total	AD	AI	Total	AD	AI	Total
12	15	0.00	0.00	0.00	0.00	0.00	0.00				59.4%	65.3%	59.9%
13	15	0.00	0.00	0.00	0.00	0.00	0.00						
14	14	4.33	0.00	4.33	0.31	0.00	0.31	3		3			
15	16	16.80	0.00	16.80	1.05	0.00	1.05	9		9			
16	17	9.19	3.06	12.25	0.54	0.18	0.72	6	2	8			
17	16	14.81	1.85	16.67	0.93	0.12	1.04	8	1	9	54.0%	54.0%	54.0%
18	15	18.42	7.08	25.50	1.23	0.47	1.70	13	5	18	70.6%	70.6%	70.6%
19	15	9.55	0.00	9.55	0.64	0.00	0.64	3		3	40.9%	52.9%	43.1%
20	15	7.56	3.78	11.33	0.50	0.25	0.76	4	2	6			

2176

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. The 2021 sport fishery was executed in both regions (Table 9), which could introduce 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 2021.

	Total Adult Chinook			Sample of Total Adult Chinook Kept			
	Kept	Rel.	Rel. Mortality	regionA	regionB	total	rate
Jan-Feb Total	6	0	0	0	0		
March Total	1,534	203	20	11	96	107	0.07
April Total	1,403	126	13	18	73	91	0.06
May Total	652	309	31	36	14	226	0.09
June 1-15							
Total	1,790	790	79	47	129		
Season Total	5,385	1,428	143	112	312	424	0.08

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 which was the case for 2021. 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 has not occurred since 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 2021, we obtained samples from both 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 2021.

	Total Adult Chinook			Sample of Total Adult Chinook Kept			
	Kept	Rel.	Rel. Mortality	regionA	regionB	total	rate
June 16-30	1797	732	73	14	104		
July 1-31	337	266	27	11	19	148	0.07
Season Total	2,134	998	100	25	123	148	0.07

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 – 36) 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. However, we could only analyze Region A due to insufficient sampling obtained from Region B. We utilized 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 2021.

Region	Harvest estimate		Sample N			
	Week	adult+jack	AD	AI	total	rate
A	33	333	29	58	112	0.11
A	34	703	13	12		
A	35	10722	104	48	152	0.01
A	36	9470	78	49	162	0.01
A	39	2963	2	28		
A	40	1122	1	4		
A	41	735	0			
A	42	529	0			
B	40	387	1	1	2	0.01
B	41	142			0	0.00
B	42	71			0	0.00
B	43	7			0	0.00

B 44 7 1 1 0.14

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. Samples were stratified by pools of weeks indicated by the lines in the table. There were not enough samples to analyze harvest in Region B.

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 2021, the sport fishery was also sampled in zone 6 from Bonneville Dam to McNary Dam (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 2021.

Catch Estimate				Sample of kept			
Month	kept Adult	Released	Release mortality(21%)	AD	AI	Total	rate
Aug	6184	287	60	177	310	487	0.08
Sep	10964	683	143	119	350	469	0.04
Oct	1752	76	16	16	38	54	0.03
Total	18900	1046	220	312	698	1010	0.05

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 in Zone 6 in 2021.

Catch Estimate				Sample of kept			
Month	kept Adult	Released	Release mortality 21%	AD	AI	total	rate
August				22	14		
September				24	24		
October				1	7		
Total	6141	343	72	47	45	92	0.01

Note: The sample numbers of the kept Chinook salmon were pooled from BON, TDA, and JDA reservoirs into a single stratum across months of August to October 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 2021 due to lack of resources, 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 Sockeye Non-Treaty sport and commercial fishery:

There was no Non-Treaty commercial fishery in 2021. Only the sport fishery occurred in 2021, and samples were pooled across months and treated as a single stratum (Table 14).

Table 14. The sample rate and stratification for genetic analysis of the harvested Sockeye salmon from the sport fishery in 2021.

Month	Catch	Sample						
	estimate	LBC	Osoyoos	Redfish	Wenatchee	Yakima	total	rate
June	385		19	1	10		30	0.08
July	149		12		7	1	20	0.13
total	534	0	31	1	17	1	50	0.09

The Sockeye Treaty commercial fishery:

This 2021 fishery occurred in zone 6 and catch estimates are typically 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. There were no samples from this year to analyze.

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

2307 comprised of sets of SNP markers (~200) that have greater than 10% observed heterozygosity in
2308 each of the major lineages of Chinook Salmon (Hess et al. 2020).

2309 Application of the 254 SNP panel to the Chinook Salmon passing Bonneville Dam in
2310 2018 revealed that the use of this expanded panel fully resolved the crashing issue with SNPPIT.
2311 This result confirmed that the source of the crashing issue was likely related to the lack of
2312 sufficient numbers of SNPs with high information content that is primarily affecting ocean-type
2313 broodstocks. Further, the higher number of SNP loci requires decreased computational time to
2314 run the parentage analyses, which is extremely helpful for the relatively short time available to
2315 process in-season samples. We have continued to use the 254 SNP panel exclusively for the 2022
2316 run year of Chinook salmon.

2317 *Comparison of Coded-wire tags and PBT assignments*

2318 There were 495 coded-wire tags (CWTs) recovered and identified to hatchery stock and broodyear (BY) among the snouts
 2319 obtained from the lower river fisheries (Table 15), and 298 of these CWTs also were PBT assigned (60%). Of the 298 fish with both
 2320 CWT and PBT, there were 278 fish (93%) that appeared concordant with the PBT assignments according to both the hatchery source
 2321 and the broodyear. There were 20 of the 298 fish with both CWT and PBT that were discordant for either just broodyear (N=9) or just
 2322 hatchery source (N=6) or both hatchery source and broodyear (N=5). However, in some cases it may be that the CWT readings were
 2323 swapped; e.g., a pair of Entiat National Fish Hatchery and Klickitat hatchery fish were matched for two pairs of fish (“Discordant”
 2324 rows, Table 15). Resolving these swapping errors would increase the concordance rate even higher than 93%.

2325

2326 **Table 15. Comparison of coded-wire tags with parentage-based tags that were identified in the lower river fisheries in**
 2327 **2021.**

Period	Coded-wire tag		Parentage-based tagging assignment			N
	Hatchery	BY	Hatchery	BY	Status	
Spring	Wells Hatchery	2016	Eastbank Fish Hatchery	2016	Concordant	2
Spring	Wells Hatchery	2017	Eastbank Fish Hatchery	2017	Concordant	1
Spring	Carson National Fish Hatchery	2017	Carson National Fish Hatchery	2017	Concordant	1
Spring	Eastbank Fish Hatchery	2016	Eastbank Fish Hatchery	2016	Concordant	6
Spring	Eastbank Fish Hatchery	2016	Chief Joseph Hatchery	2016	Concordant	1
Spring	Eastbank Fish Hatchery	2016	Wells Fish Hatchery	2016	Concordant	1
Spring	Eastbank Fish Hatchery	2017	Eastbank Fish Hatchery	2017	Concordant	7
Spring	Chief Joseph Hatchery	2017	Chief Joseph Hatchery	2017	Concordant	1
Spring	Yakima River Roza Dam	2017	Yakima River Roza Dam	2017	Concordant	4
Spring	Yakima River Roza Dam	2018	Yakima River Roza Dam	2018	Concordant	1
Spring	Clearwater Fish Hatchery	2017	Clearwater Fish Hatchery	2017	Concordant	2
Spring	Clearwater Fish Hatchery	2017	Clearwater Fish Hatchery	2017	Concordant	1
Spring	Clearwater Fish Hatchery	2018	Dworshak National Fish Hatchery	2018	Concordant	1
Spring	Dworshak National Fish Hatchery	2017	Dworshak National Fish Hatchery	2017	Concordant	1
Spring	Entiat National Fish Hatchery	2016	Entiat National Fish Hatchery	2016	Concordant	1

Spring	Kalama Falls Hatchery	2017	Kalama Falls Hatchery	2017	Concordant	1
Spring	Klickitat Hatchery	2017	Klickitat Hatchery	2017	Concordant	1
Spring	Klickitat Hatchery	2018	Klickitat Hatchery	2018	Concordant	1
			Leavenworth National Fish Hatchery			
Spring	Leavenworth National Fish Hatchery	2017	Hatchery	2017	Concordant	2
	Little White Salmon National Fish Hatchery		Little White Salmon National Fish Hatchery			
Spring		2017		2017	Concordant	3
Spring	Lookingglass Fish Hatchery	2017	Lookingglass Fish Hatchery	2017	Concordant	2
Spring	Lookingglass Fish Hatchery	2018	Lookingglass Fish Hatchery	2018	Concordant	1
Spring	McCall Fish Hatchery	2017	McCall Fish Hatchery	2017	Concordant	4
Spring	Rapid River Fish Hatchery	2017	Rapid River Fish Hatchery	2017	Concordant	2
Spring	Rapid River Fish Hatchery	2018	Rapid River Fish Hatchery	2018	Concordant	1
Spring	Round Butte Fish Hatchery	2018	Round Butte Fish Hatchery	2018	Concordant	2
Spring	Chief Joseph Hatchery	2016	Chief Joseph Hatchery	2016	Concordant	1
Spring	Chief Joseph Hatchery	2017	Chief Joseph Hatchery	2017	Concordant	2
			Warm Springs National Fish Hatchery			
Spring	Warm Springs National Fish Hatchery	2017	Hatchery	2017	Concordant	5
Spring	Warm Springs National Fish Hatchery	2017	Round Butte Fish Hatchery	2017	Concordant	2
Spring	Warm Springs National Fish Hatchery	2018	Round Butte Fish Hatchery	2018	Concordant	1
Spring	Wells Fish Hatchery	2016	Wells Fish Hatchery	2016	Concordant	11
Spring	Wells Fish Hatchery	2016	Eastbank Fish Hatchery	2016	Concordant	2
Spring	Wells Fish Hatchery	2017	Wells Fish Hatchery	2017	Concordant	7
Spring	Wells Fish Hatchery	2018	Wells Fish Hatchery	2018	Concordant	1
Summer	Eastbank Fish Hatchery	2015	Eastbank Fish Hatchery	2015	Concordant	1
Summer	Eastbank Fish Hatchery	2016	Eastbank Fish Hatchery	2016	Concordant	1
Summer	Eastbank Fish Hatchery	2016	Eastbank Fish Hatchery	2016	Concordant	7
Summer	Eastbank Fish Hatchery	2017	Eastbank Fish Hatchery	2017	Concordant	6
Summer	Chief Joseph Hatchery	2016	Chief Joseph Hatchery	2016	Concordant	4
Summer	Chief Joseph Hatchery	2016	Methow Fish Hatchery	2016	Concordant	1
Summer	Chief Joseph Hatchery	2017	Chief Joseph Hatchery	2017	Concordant	1
Summer	Eastbank Fish Hatchery	2016	Eastbank Fish Hatchery	2016	Concordant	2
Summer	Eastbank Fish Hatchery	2016	Wells Fish Hatchery	2016	Concordant	1
Summer	Eastbank Fish Hatchery	2017	Eastbank Fish Hatchery	2017	Concordant	1

Summer	Entiat National Fish Hatchery	2016	Entiat National Fish Hatchery	2016	Concordant	2
Summer	Entiat National Fish Hatchery	2017	Entiat National Fish Hatchery	2017	Concordant	2
Summer	Pahsimeroi Fish Hatchery	2018	Pahsimeroi Fish Hatchery	2018	Concordant	1
Summer	Chief Joseph Hatchery	2016	Chief Joseph Hatchery	2016	Concordant	3
Summer	Wells Fish Hatchery	2016	Wells Fish Hatchery	2016	Concordant	7
Summer	Wells Fish Hatchery	2016	Eastbank Fish Hatchery	2016	Concordant	2
Summer	Wells Fish Hatchery	2017	Wells Fish Hatchery	2017	Concordant	3
Fall	Big Creek Hatchery	2018	Big Creek Hatchery	2018	Concordant	1
Fall	Bonneville Hatchery	2017	Ringold Springs State Hatchery	2017	Concordant	2
Fall	Bonneville Hatchery	2019	Bonneville Dam Hatchery	2019	Concordant	3
Fall	Bonneville Hatchery	2017	Ringold Springs State Hatchery	2017	Concordant	1
Fall	Cowlitz Salmon Hatchery	2017	Cowlitz Salmon Hatchery	2017	Concordant	2
Fall	Kalama Falls Hatchery	2016	Kalama Falls Hatchery	2016	Concordant	1
Fall	Lyons Ferry Fish Hatchery	2017	Lyons Ferry Fish Hatchery	2017	Concordant	9
Fall	Lyons Ferry Fish Hatchery	2018	Lyons Ferry Fish Hatchery	2018	Concordant	2
Fall	Kalama Falls Hatchery	2017	Kalama Falls Hatchery	2017	Concordant	1
Fall	Klickitat Fall	2018	Priest Rapids Hatchery	2018	Concordant	1
Fall	Klickitat Fall	2016	Little White Salmon National Fish Hatchery	2016	Concordant	1
Fall	Klickitat Fall	2017	Ringold Springs State Hatchery	2017	Concordant	3
Fall	Little White Salmon National Fish Hatchery	2017	Little White Salmon National Fish Hatchery	2017	Concordant	2
Fall	Little White Salmon National Fish Hatchery	2018	Little White Salmon National Fish Hatchery	2018	Concordant	1
Fall	Little White Salmon National Fish Hatchery	2017	Little White Salmon National Fish Hatchery	2017	Concordant	1
Fall	Little White Salmon National Fish Hatchery	2018	Little White Salmon National Fish Hatchery	2018	Concordant	1
Fall	Little White Salmon National Fish Hatchery	2016	Little White Salmon National Fish Hatchery	2016	Concordant	1
Fall	Lyons Ferry Fish Hatchery	2016	Lyons Ferry Fish Hatchery	2016	Concordant	3
Fall	Lyons Ferry Fish Hatchery	2017	Lyons Ferry Fish Hatchery	2017	Concordant	7
Fall	Lyons Ferry Fish Hatchery	2018	Lyons Ferry Fish Hatchery	2018	Concordant	17

Fall	Lyons Ferry Fish Hatchery	2019	Lyons Ferry Fish Hatchery	2019	Concordant	4
Fall	#N/A	2017	Eastbank Fish Hatchery	2017	Concordant	1
Fall	Nez Perce Tribal Fish Hatchery	2017	Nez Perce Tribal Fish Hatchery	2017	Concordant	17
Fall	Priest Rapids Hatchery	2017	Priest Rapids Hatchery	2017	Concordant	10
Fall	Priest Rapids Hatchery	2017	Priest Rapids Hatchery	2017	Concordant	10
Fall	Priest Rapids Hatchery	2018	Priest Rapids Hatchery	2018	Concordant	2
Fall	Priest Rapids Hatchery	2019	Priest Rapids Hatchery	2019	Concordant	1
Fall	Ringold Springs State Hatchery	2017	Priest Rapids Hatchery	2017	Concordant	2
Fall	Ringold Springs State Hatchery	2017	Priest Rapids Hatchery	2017	Concordant	10
Fall	Spring Creek National Fish Hatchery	2017	Spring Creek National Fish Hatchery	2017	Concordant	3
Fall	Spring Creek National Fish Hatchery	2018	Spring Creek National Fish Hatchery	2018	Concordant	18
Fall	Spring Creek National Fish Hatchery	2019	Spring Creek National Fish Hatchery	2019	Concordant	3
Fall	Spring Creek National Fish Hatchery	2018	Spring Creek National Fish Hatchery	2018	Concordant	1
Fall	Spring Creek National Fish Hatchery	2019	Spring Creek National Fish Hatchery	2019	Concordant	1
Fall	Umatilla Fish Hatchery	2016	Little White Salmon National Fish Hatchery	2016	Concordant	1
Fall	Umatilla Fish Hatchery	2018	Umatilla Fish Hatchery	2018	Concordant	1
Fall	Washougal Fish Hatchery	2018	Washougal Fish Hatchery	2018	Concordant	2
Fall	Little White Salmon National Fish Hatchery	2017	Little White Salmon National Fish Hatchery	2017	Concordant	3
Spring	Yakima River Roza Dam	2017	Yakima River Roza Dam	2018	Hatchery	1
Fall	Lyons Ferry Fish Hatchery	2018	Lyons Ferry Fish Hatchery	2016	Hatchery	1
Fall	Lyons Ferry Fish Hatchery	2017	Lyons Ferry Fish Hatchery	2016	Hatchery	1
Spring	Eastbank Fish Hatchery	2017	Wells Fish Hatchery	2016	Hatchery	1
Spring	Wells Fish Hatchery	2016	Chief Joseph Hatchery	2017	Hatchery	1
Summer	Eastbank Fish Hatchery	2016	Wells Fish Hatchery	2017	Hatchery	1
Summer	Wells Fish Hatchery	2017	Eastbank Fish Hatchery	2016	Hatchery	1
Fall	Bonneville Hatchery	2019	Spring Creek National Fish Hatchery	2017	Hatchery	1

Fall	Spring Creek National Fish Hatchery	2017	Bonneville Dam Hatchery	2019	Hatchery	1
Spring	Yakima River Roza Dam	2017	Entiat National Fish Hatchery	2017	*BY	2
Spring	Cowlitz Salmon Hatchery	2017	Eastbank Fish Hatchery	2017	*BY	1
Spring	Willamette	2017	Speelyai Fish Hatchery	2017	*BY	1
Spring	Entiat National Fish Hatchery	2017	Yakima River Roza Dam	2017	*BY	1
Fall	Lyons Ferry Fish Hatchery	2017	Priest Rapids Hatchery	2017	*BY	1
Spring	Entiat National Fish Hatchery	2016	Klickitat Hatchery	2018	Discordant	1
Spring	Klickitat Hatchery	2018	Entiat National Fish Hatchery	2016	Discordant	1
Summer	Cowlitz Salmon Hatchery	2015	Wells Fish Hatchery	2016	Discordant	1
Fall	Klickitat Fall	2017	Spring Creek National Fish Hatchery	2018	Discordant	1
Fall	Spring Creek National Fish Hatchery	2018	Ringold Springs State Hatchery	2017	Discordant	1
				Total	100.00%	495
				Concordant	56.16%	278
				Hatchery_Concordant	1.82%	9
				BY_Concordant	1.21%	6
				Discordant	1.01%	5
				Failed	18.99%	94
				PBT_Unassigned	20.81%	103

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Note: *Indicates that only the BY was concordant but these two samples in particular appear to have been switched.
 “Hatchery” under status indicates only the hatchery was concordant but not the BY. In some cases spawning hatcheries coordinate releases across multiple hatcheries and so in cases where we determined this likely occurred we allowed mismatching hatchery names to be classified as “concordant”.

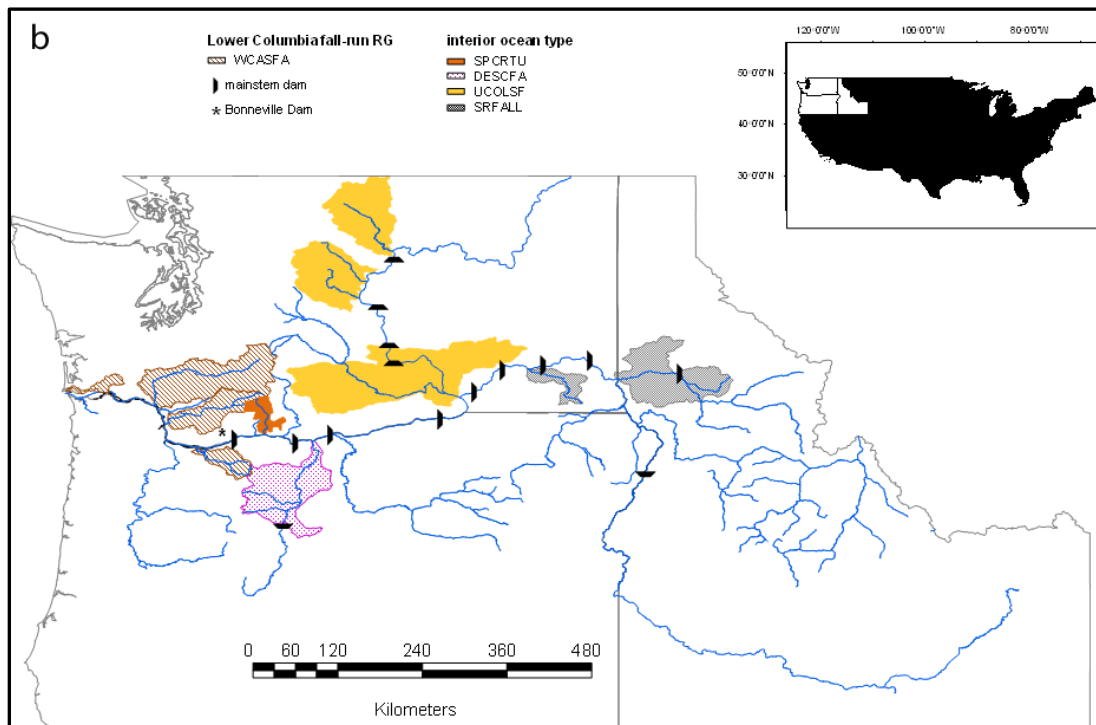
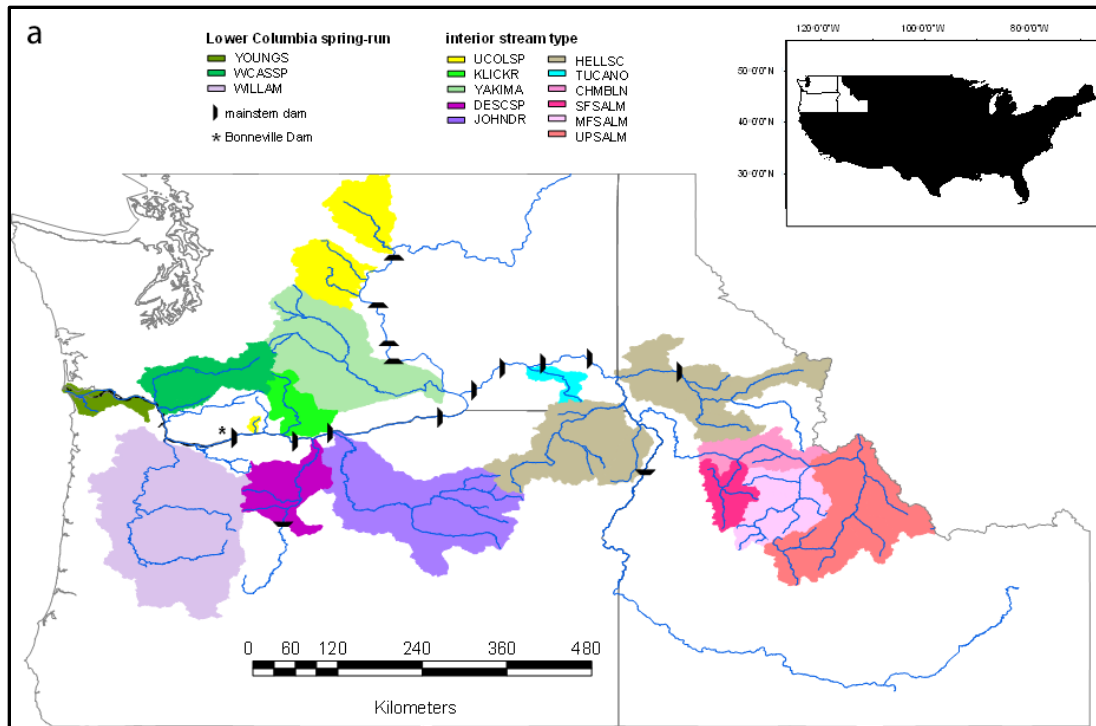
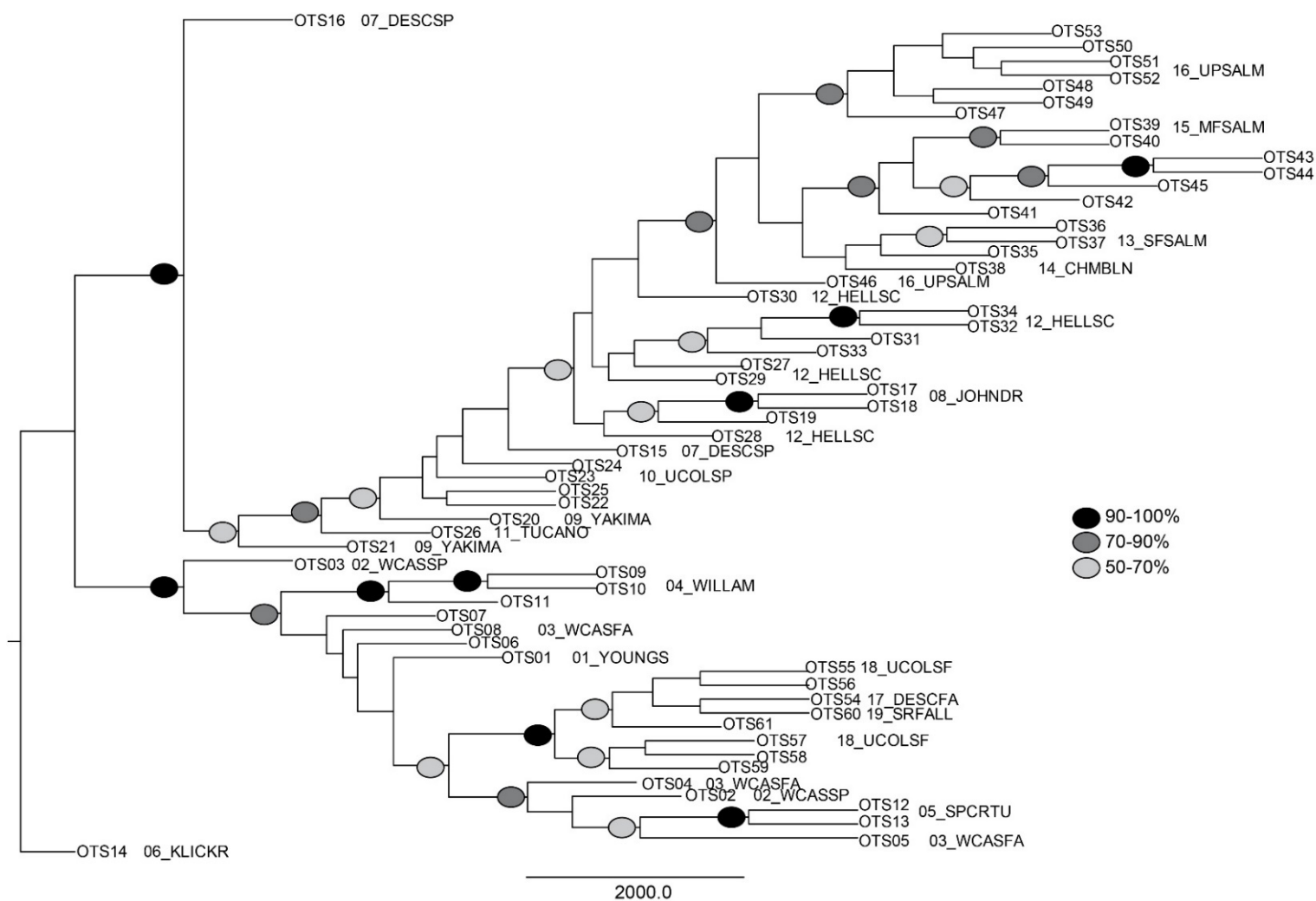


Figure 19. Map of Chinook salmon GSI reporting groups for a) Lower Columbia (LC) and interior stream type (ST) lineage, and b) interior ocean type (OT) lineage.



2338 **Figure 20. Neighbor-joining tree of Chinook salmon baseline populations using Nei's 1972 genetic distance of 179 SNP loci.**

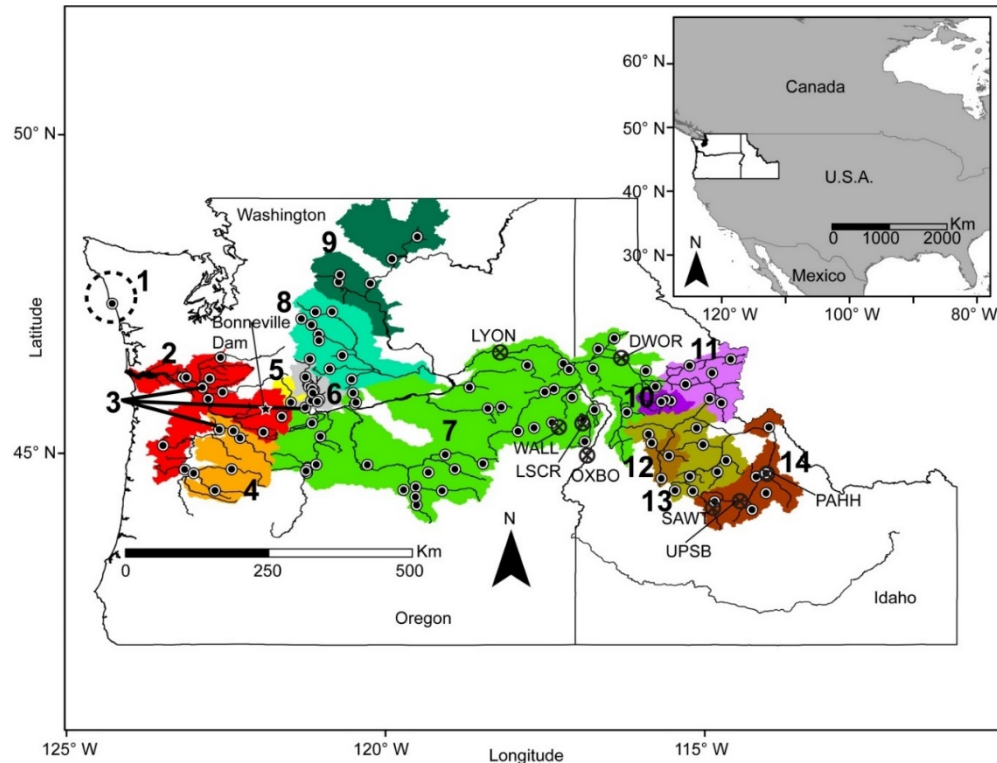


Figure 21. Geographic distribution of collections represented in the Columbia River steelhead GSI and PBT genetic baselines.

Steelhead 177 SNP and 335 SNP baselines

For steelhead, we have used GSI baseline v3.3 that comprises 116 collections from throughout the Columbia River basin that are partitioned into 14 reporting groups (N= 9991) (Figure 21). In Figure 21, the shape overlay represents the geographic extent of the following 14 reporting groups in the GSI baseline: 1) Quinault (WCOAST), 2) lower Columbia River (LOWCOL), 3) Skamania hatchery releases at three sites in lower Columbia River, Willamette River, and Klickitat River (SKAMAN), 4) Willamette River (WILLAM), 5) Big White Salmon River (BWSALM), 6) Klickitat River (KLICKR), 7) middle Columbia River, Grande Ronde River, Imnaha River, lower Snake River, lower Clearwater River, and lower Salmon River (MGILCS), 8) Yakima River (YAKIMA), 9) upper Columbia River (UPPCOL), 10) South Fork Clearwater River (SFCLWR), 11) upper Clearwater River (UPCLWR), 12) South Fork Salmon River (SFSALM), 13) Middle Fork Salmon River (MFSALM), and 14) upper Salmon River (UPSALM). There are 116 collections (filled circles, Figure 21) categorized into reporting groups. The PBT baseline is indicated as 8 stocks (crossed circles, Figure 21) 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 Pahasimeroi Hatchery (PAHH). Bonneville Dam (star, Figure 21) 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 22): 180 SNPs from baseline v3.3 (“Sub180”), 339 SNPs that include putatively neutral and adaptive loci (“Sub339”), 335 SNPs that exclude the run timing candidate SNPs (“Sub335NRT”), 301 SNPs that were putatively neutral (“Sub301Neu”), and 55 SNPs that were putatively adaptive (“Sub55Adapt”). We found that the 335 and 339 SNPs both performed best, but we felt it would be better to exclude the run timing candidate SNPs to avoid any unintended bias for stocks containing within population variation in run timing. Therefore, we proposed 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 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 177SNPs (version 3.3) for the GSI applications in this report. Similar to our previous results, we show that the fish passing Bonneville Dam in 2021 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 (86%, Table 16).

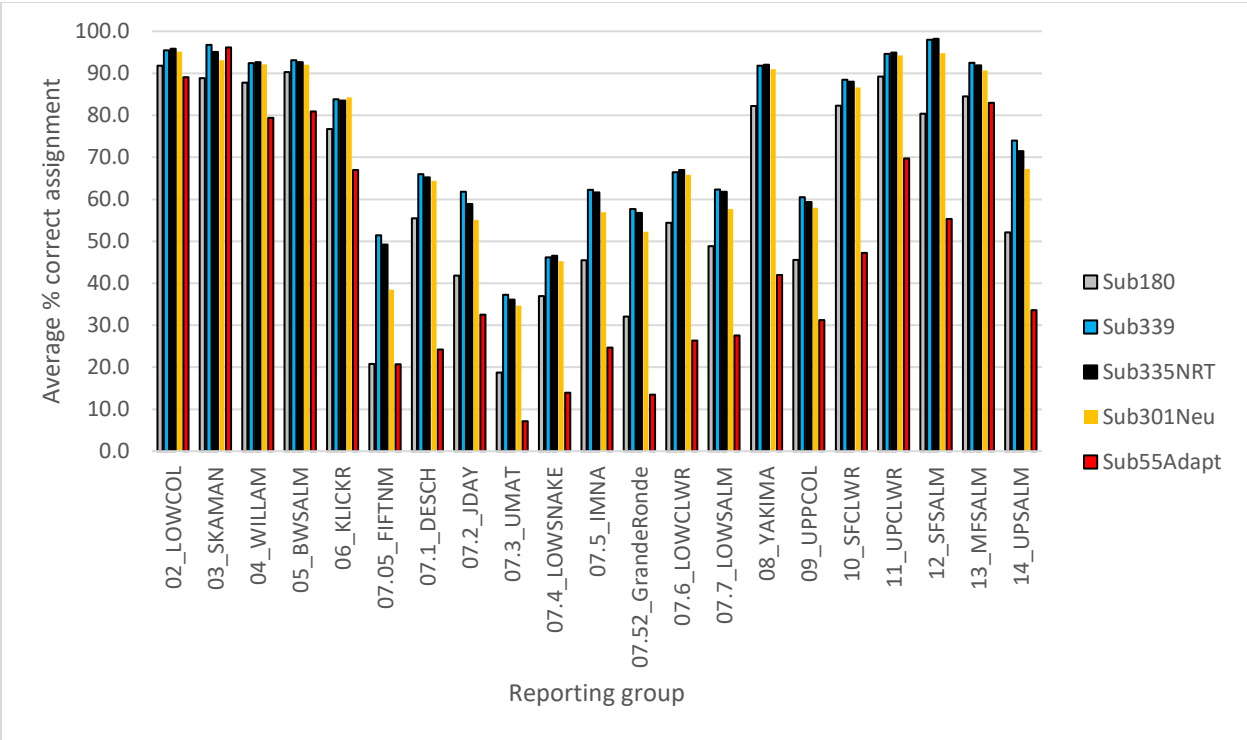


Figure 22. Proportion of steelhead in leave-one-out tests that assigned correctly for each reporting group by lineage using the following subsets of SNPs: 180 SNPs from baseline v3.3 (“Sub180”), 339 SNPs that include putatively neutral and adaptive loci (“Sub339”), 335 SNPs that exclude the run timing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

2398 **Table 16. Comparison of PBT expected reporting groups versus the observed reporting groups using 177 SNPs (baseline 3.3)**
 2399 **based on the assignments from the Bonneville 2021 mixture.**

PBT Expected GSI	Observed GSI							Total	%Correct
	02_LOWCOL	03_SKAMAN	07_MGILCS	09_UPPCOL	10_SFCLWR	11_UPCLWR	12_SFSALM	14_UPSALM	
02_LOWCOL	2							2	100.0%
03_SKAMAN		4						4	100.0%
07_MGILCS			66	1	2			12	81.5%
09_UPPCOL			8	7				3	38.9%
10_SFCLWR			3		185	1	1	190	97.4%
14_UPSALM			12		10			132	85.7%

2400
 2401
 2402 *Steelhead 335 SNP panel for PBT applications*

2403 Despite having limited utility for GSI applications on a Columbia River Basin wide scale, the expanded set of SNP markers
 2404 available for steelhead analysis can be extremely useful for increasing the power and accuracy of PBT. We examined a dataset of
 2405 steelhead passing Bonneville Dam in 2020 and compared assignments based on the original panel of 92 SNPs to assignments based on
 2406 the new expanded panel of 335 SNPs (Table 17). There were a total of 800 PBT assignments that were perfectly concordant between
 2407 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
 2408 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
 2409 we use to accept a PBT assignment, but the 335 SNP panel LOD score was much higher. The False Discovery Rate was also much
 2410 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
 2411 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
 2412 for failing to meet these thresholds using the smaller panel. In fact, there were 20 fish that were only assigned using the 335 SNP
 2413 panel and would have escaped detection with the 92 SNP panel. Further, there were 32 assignments that were concordant to the PBT
 2414 broodstock, however, either the mother or father or both parents were discordant across the assignments generated by these two
 2415 panels. The 335 PBT panel will be more likely to avoid errors that occur when hatchery broodstock have a high level of relatedness
 2416 which is the case with steelhead hatcheries. In conclusion, we feel encouraged by these results and have adopted the larger number of
 2417 SNP markers for PBT applications in steelhead.

2418

2419 **Table 17.** Comparison of PBT assignments using the new panel of 335 SNPs versus the 92 SNP panel for steelhead passing
 2420 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

2421

2422 *Sockeye (363 SNPs) parent baseline for identifying reintroduced stocks from Yakima River*

2423 This is the third year we have been able to utilize candidate parents that were genotyped from tissues collected from carcass
 2424 spawning surveys and directly from the fish translocated from Priest Rapids Dam and released into the Yakima River (Table 18). A
 2425 combination of parent-pair assignments (trio assignment) and single parent assignments were performed to obtain as large of a sample
 2426 of offspring as possible. Tag rates assumed the ability to perform single parent assignments. We had funding to genotype some of our
 2427 older candidate parents from the translocation year 2012 and updated the PBT baseline with these older samples as well as new
 2428 samples from 2020 and 2021. The tag rates increased as a result of the additional genotypes and filtering step changes and are noted
 2429 in green in Table 18. Specifically, the largest “Change” in tag rates occurred in Spawn Year 2012 in which we now have 18.5% of the
 2430 candidate parents genotyped and have at least a chance to detect offspring that returned from this first large (10,000+ adults
 2431 translocated in 2012) translocation event in the Yakima River. This expansion of the parent baseline may be useful when we re-
 2432 analyze previous years.

2433

2434 **Table 18. The numbers of candidate parents genotyped relative to the number of returning and translocated adult sockeye to**
 2435 **the Yakima River each year.**

Year	Outplants	Prosser	Roza	O+P	O+R	Genotypes		Max YR	Tag rate		Change
						363	88		363	88	363
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	985	985	10154	18.5%	18.5%	5.3%
2013	4500	696	691	5196	5191	1168	1244	5196	39.9%	42.2%	-0.1%
2014	10000	2678	2576	12678	12576	2942	3146	12678	41.0%	43.5%	-0.1%
2015	10000	342	95	10342	10095	706	1182	10342	13.2%	21.6%	0.0%
2016	10000	3742	3949	13742	13949	4633	4245	13949	55.4%	51.6%	1.8%
2017	1000	372	137	1372	1137	426	422	1372	52.5%	52.1%	-0.1%
2018	4700	456	201	5156	4901	1377	1368	5156	46.3%	46.0%	-0.1%
2019	0	110	201	110	201	203	199	201	100.0%	100.0%	0.0%
2020	10000	2549	4379	12549	14379	5895		14379	65.2%		65.2%
2021	2700	135	95	2835	2795	525		2835	33.6%		33.6%

2436 *Note: “Outplants” indicate the number of sockeye translocated into the Yakima River, and “Prosser” and “Roza” dam counts were*
 2437 *summed (“O+P” or “O+R”) with the outplants to provide an estimate of the total escapement of spawners in the Yakima River each*
 2438 *year. We used whichever number was greatest (“O+P” or “O+R”) to provide the maximum escapement of the Yakima River (“Max*

2439 *YR*”). A portion of these spawners were successfully genotyped either using 383 or 88 (the legacy panel) SNPs and tag rates were
2440 calculated using the Max *YR* as the denominator. When cross information and the gender of the broodstock samples is unknown, then
2441 the tag rate for single parentage is : $1-(f_t)^2$, where f_t is the fraction of the total broodstock not genotyped.

2442 *Parentage based tagging assignments of Chinook salmon in harvest mixtures*
2443 A summary of the Chinook harvest samples that were genotyped (derived from Table 5)
2444 is presented in Table 19. Of the 3,273 harvested Chinook analyzed, there were 1,455 hatchery-
2445 origin individuals that could be confidently PBT assigned to 100 hatchery broodstock sources
2446 (i.e., 18 Lower Columbia, 1 Willamette, 26 Snake River, and 55 Columbia River hatchery
2447 broodstocks) spawned in 2015-2019. The majority of PBT assigned individuals (N=833) were
2448 from the 2017 brood year (i.e., 4-years-old).

2449 **Table 19. Summary of the Chinook salmon harvest samples by fishery, region, and fin clip**
 2450 **in 2021.**

Fishery	Region	AdClip	Period			Analysis					
			Spring	Summer	Fall	GSI	PBT	duplicate	failed	Total	%PBT
Bon21	BONAFF	AD	1276	336	472	175	1886	3	20	2084	91.5%
		AI	500	167	897	1026	517	5	16	1564	33.5%
Sport	A	AD	128			16	112	1	25	154	87.5%
	B	AD	332			96	236		65	397	71.1%
Test	B	AD	131			41	90	1	2	134	68.7%
		AI	33			18	15	2		35	45.5%
Sport	A	AD		30		5	25		7	37	83.3%
	B	AD		132		43	89		20	152	67.4%
Sport	A	AD			164	42	122	1	74	239	74.4%
		AI			449	320	129	3	218	670	28.7%
	B	AD			182	42	140	1	67	250	76.9%
		AI			298	192	106	1	108	407	35.6%
	Region01	AD			31	5	26			31	83.9%
		AI			26	19	7		1	27	26.9%
	Region02	AD			20	5	15			20	75.0%
		AI			26	17	9		1	27	34.6%
Comm.	A	AD			381	103	278	1	41	423	73.0%
		AI			199	144	55	1	24	224	27.6%
	B	AD			1	1			9	10	0.0%
		AI			2	1	1		34	36	50.0%
Grand Total			2400	665	3148	2311	3858	20	732	6921	62.5%

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 76% (range = 67% – 88%, Table 19). The fishery(s) with the minimum and maximum assigned adipose-clipped Chinook salmon was the Non-Treaty summer sport fishery in region B and the Non-Treaty Spring Sport fishery in region A, respectively. Among the adipose-intact fish, the average assignment via PBT was expectedly lower (average = 33%, range = 27% – 46%; Table 19). Among the fisheries with adipose-intact fish, the minimum and maximum PBT-assigned Chinook salmon was observed in the Non-Treaty fall sport fishery in Zone 6 (region 02) and the spring test fishery, respectively.

The test fishery in the Chinook Salmon Spring Management Period of 2022

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 23). Further, the correlation of CPUE for upriver stocks has been shown to improve when genetic data is used to identify upriver stocks compared to using Visual Stock ID exclusively. 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.

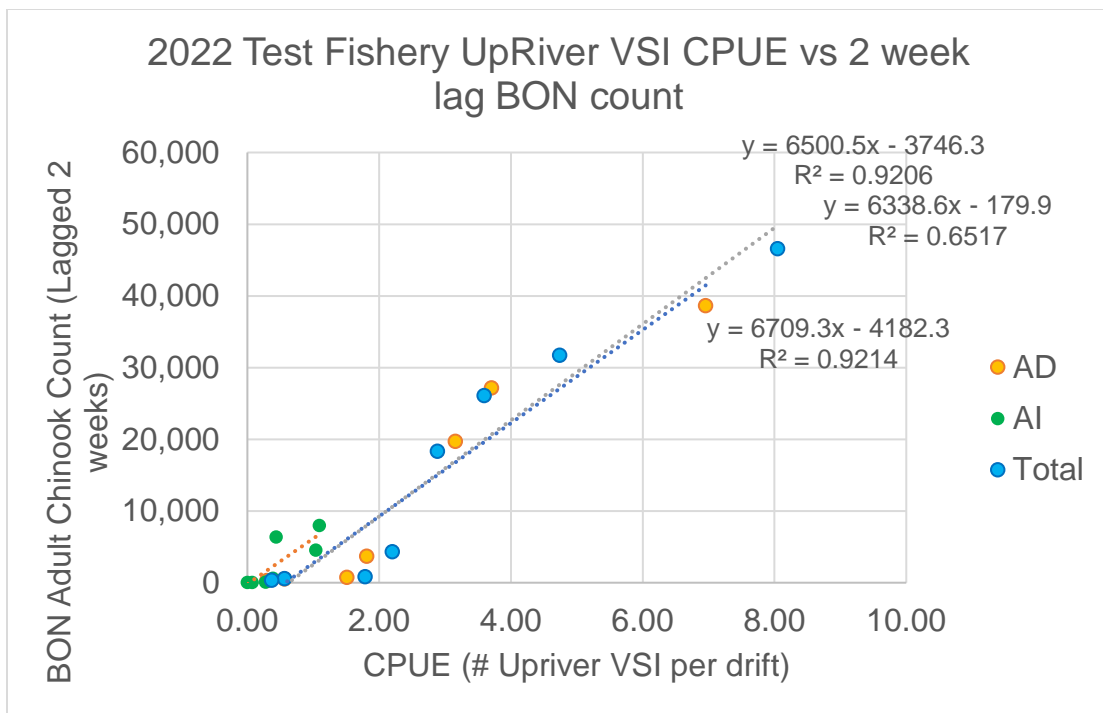


Figure 23. The relationship between the test fishery upriver Chinook Salmon CPUE and weekly fish counts at Bonneville Dam in 2022 with 2 week lag using VSI data.

2485 *The Non-Treaty sport fishery in the Chinook Salmon Spring Management Period of 2021*
 2486 We reported spring sport fishery results for reporting group level stock composition
 2487 (Table 20) and the hatchery broodstock composition (Table 21) of the kept fish (clipped
 2488 hatchery-origin fish).

2489
 2490 **Table 20. Summary of the stock composition at the reporting group level of the kept spring**
 2491 **Chinook salmon in the Non-Treaty sport fishery of 2021 in units of reported catch.**

Run type	Reporting Group Code	Hatchery origin- Clipped	
		Estimated abundance	
		Mean	95% CI
Spring	01_YOUNGS		
Spring	02_WCASSP	402	214 – 567
Fall	03_WCASFA	11	0 – 31
Spring	04_WILLAM	1,075	687 – 1253
Fall	05_SPCRTU		
Spring	06_KLICKR	93	45 – 114
Spring	07_DESCSP	190	127 – 297
Spring	08_JOHNDR		
Spring	09_YAKIMA	108	52 – 126
Spring	10_UCOLSP	255	124 – 489
Spring	11_TUCANO		
Spring/Summer	12_HELLSC	1,404	1211 – 1689
Spring/Summer	13_SFSALM	211	113 – 263
Spring/Summer	14_CHMBLN		
Spring/Summer	15_MFSALM		
Spring/Summer	16_UPSALM	54	12 – 65
Fall	17_DESCFA		
Summer/Fall	18_UCOLSF	1,296	1199 – 1413
Fall	19_SRFALL		
Spring	20_BONPOOLSP	211	150 – 347
Spring	21_UMATILLASP	75	45 – 121
Fall	22_BONPOOLFA		
Fall	23_UMATILLAFA		
	Total	5,385	

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Table 21. Summary of the stock composition at the broodstock level of the kept adult spring Chinook salmon in the Non-Treaty sport fishery of 2021 in units of reported catch.

Spring Sport Fishery 2021				Kept Adult Chinook AD			
Expected Run Time	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	GSI RepGrp
01Spring	Cowlitz Salmon Hatchery	OtsCOWL_seg_sp16	2016	38	0 – 114	0.7%	02_WCASSP
01Spring	Cowlitz Salmon Hatchery	OtsCOWL_seg_sp17	2017	42	0 – 85	0.8%	02_WCASSP
01Spring	Kalama Falls Hatchery	OtsKALA_seg_sp16	2016	59	20 – 118	1.1%	02_WCASSP
01Spring	Kalama Falls Hatchery	OtsKALA_seg_sp17	2017	53	11 – 99	1.0%	02_WCASSP
01Spring	Parkdale Fish Facility	OtsPARK_seg_sp17	2017	28	0 – 61	0.5%	02_WCASSP
01Spring	Speelyai Fish Hatchery	OtsSPEE_seg_sp16	2016	22	0 – 66	0.4%	02_WCASSP
01Spring	Speelyai Fish Hatchery	OtsSPEE_seg_sp17	2017	129	50 – 235	2.4%	02_WCASSP
01Spring	South Santiam Hatchery	OtsSSAN_seg_sp16	2016	88	31 – 149	1.6%	04_WILLAM
01Spring	Klickitat Hatchery	OtsKLIC_seg_sp16	2016	26	0 – 62	0.5%	06_KLICKR
01Spring	Klickitat Hatchery	OtsKLIC_seg_sp17	2017	55	11 – 100	1.0%	06_KLICKR
01Spring	Klickitat Hatchery	OtsKLIC_seg_sp18	2018	11	0 – 34	0.2%	06_KLICKR
01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp17	2017	58	16 – 106	1.1%	07_DESCSP
01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp18	2018	11	0 – 34	0.2%	07_DESCSP
01Spring	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp17	2017	111	47 – 184	2.1%	07_DESCSP
01Spring	Yakima River Roza Dam	OtsYRRD_int_sp17	2017	93	40 – 153	1.7%	09_YAKIMA
01Spring	Yakima River Roza Dam	OtsYRRD_seg_sp17	2017	16	0 – 47	0.3%	09_YAKIMA
01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp17	2017	231	124 – 337	4.3%	10_UCOLSP
01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp17	2017	76	29 – 137	1.4%	12_HELLSC
01Spring	Clearwater Fish Hatchery	OtsPOWP_seg_sp17	2017	22	0 – 55	0.4%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp16	2016	15	0 – 44	0.3%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsKOOS_seg_sp17	2017	61	16 – 121	1.1%	12_HELLSC

01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp17	2017	99	47 – 166	1.8%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsKOOS_seg_sp18	2018	11	0 – 34	0.2%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp18	2018	11	0 – 34	0.2%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsLOOK_seg_sp17	2017	89	36 – 153	1.6%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp16	2016	45	0 – 90	0.8%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp17	2017	868	711 – 1042	16.1%	12_HELLSC
01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp16	2016	14	0 – 43	0.3%	20_BONPOOLSP
01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp17	2017	135	61 – 209	2.5%	20_BONPOOLSP
01Spring	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp17	2017	62	15 – 123	1.2%	20_BONPOOLSP
01Spring	Umatilla Fish Hatchery	OtsUMAT_seg_sp17	2017	75	29 – 135	1.4%	21_UMATILLASP
02Spring/Summer	Lookingglass Fish Hatchery	OtsIMNW_seg_ss17	2017	60	24 – 108	1.1%	12_HELLSC
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss17	2017	193	122 – 259	3.6%	13_SFSALM
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss18	2018	11	0 – 33	0.2%	13_SFSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss17	2017	33	11 – 65	0.6%	16_UPSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss18	2018	22	0 – 54	0.4%	16_UPSALM
03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su16	2016	98	44 – 153	1.8%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCHJO_int_su16	2016	33	11 – 66	0.6%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCHJO_int_su17	2017	57	14 – 115	1.1%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su17	2017	36	11 – 72	0.7%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su16	2016	407	308 – 506	7.6%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su17	2017	112	56 – 168	2.1%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su16	2016	151	86 – 216	2.8%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su17	2017	64	26 – 116	1.2%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su16	2016	184	119 – 259	3.4%	18_UCOLSF

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03Summer	Wells Fish Hatchery	OtsWELL_seg_su17	2017	109	60 – 158	2.0%	18_UCOLSF
#N/A	#N/A	Unassigned	#N/A	1,161	951 – 1388	21.6%	#N/A
		TOTAL		5,385		100.0%	

2500 *The Non-Treaty sport fishery in the Chinook Salmon Summer Management Period of 2021*

2501 In 2021, there was a summer Non-Treaty sport fishery that was executed but no summer Non-Treaty commercial fishery. We
 2502 reported summer sport fishery results for reporting group level stock composition (Table 22) and the hatchery broodstock composition
 2503 (Table 23) of the kept fish (clipped hatchery-origin fish).

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2506 **Table 22. Summary of the stock composition at the reporting group level of the kept summer Chinook salmon in the**
 2507 **Non-Treaty sport fishery of 2021 in units of reported catch.**

Run type	Reporting Group Code	Hatchery origin- Clipped Estimated abundance	
		Mean	95% CI
Spring	01_YOUNGS		
Spring	02_WCASSP	29	0 – 42
Fall	03_WCASFA		
Spring	04_WILLAM	473	298 – 502
Fall	05_SPCRTU		
Spring	06_KLICKR		
Spring	07_DESCSP		
Spring	08_JOHNDR		
Spring	09_YAKIMA	15	0 – 44
Spring	10_UCOLSP	43	1 – 84
Spring	11_TUCANO		
Spring/Summer	12_HELLSC	16	0 – 33
Spring/Summer	13_SFSALM	29	1 – 86
Spring/Summer	14_CHMBLN		
Spring/Summer	15_MFSALM		
Spring/Summer	16_UPSALM		
Fall	17_DESCFA		
Summer/Fall	18_UCOLSF	1,529	1502 – 1672

Fall	19_SRFALL		
Spring	20_BONPOOLSP		
Spring	21_UMATILLASP		
Fall	22_BONPOOLFA		
Fall	23_UMATILLAFA		
Total		2,134	

Table 23. Summary of the stock composition at the broodstock level of the kept adult summer Chinook salmon in the Non-Treaty sport fishery of 2021 in units of reported catch.

Summer Sport Fishery 2021					Kept Adult Chinook AD		
Expected Run Time	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	GSI RepGrp
01Spring	Kalama Falls Hatchery	OtsKALA_seg_sp17	2017	15	0 – 45	0.7%	02_WCASSP
01Spring	South Santiam Hatchery	OtsSSAN_seg_sp16	2016	15	0 – 46	0.7%	04_WILLAM
01Spring	Yakima River Roza Dam	OtsYRRD_int_sp17	2017	15	0 – 44	0.7%	09_YAKIMA
01Spring	Methow Fish Hatchery	OtsMETH_seg_sp16	2016	14	0 – 43	0.7%	10_UCOLSP
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp18	2018	16	0 – 49	0.8%	12_HELLSC
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss17	2017	15	0 – 44	0.7%	13_SFSALM
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss18	2018	15	0 – 44	0.7%	13_SFSALM
03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su16	2016	145	73 – 218	6.8%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCHJO_int_su16	2016	102	44 – 160	4.8%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su17	2017	32	0 – 80	1.5%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCHJO_int_su17	2017	76	19 – 153	3.6%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su15	2015	14	0 – 43	0.7%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su16	2016	337	235 – 455	15.8%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su17	2017	194	119 – 284	9.1%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su16	2016	72	29 – 130	3.4%	18_UCOLSF

03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su17	2017	172	86 – 275	8.1%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su16	2016	231	144 – 332	10.8%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su17	2017	65	16 – 113	3.0%	18_UCOLSF
#N/A	#N/A	Unassigned	#N/A	588	443 – 739	27.6%	#N/A
TOTAL				2,134		100.0%	

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2513 *The Non-Treaty sport fishery in the Chinook Salmon Fall Management Period of 2021*

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2515 The 2021 fall Non-Treaty sport fishery executed below Bonneville Dam was not mark-selective and could be characterized by
 2516 reporting group composition of clipped and unclipped hatchery-origin and natural-origin stocks (Table 24). We also reported the
 2517 broodstock composition of the hatchery-origin Chinook salmon (Table 25). In 2021, we were also able to report on reporting group
 2518 and broodstock composition of the stocks in the fall Non-Treaty sport fishery executed above Bonneville Dam (Table 26, Table 27).

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2520 **Table 24. Summary of the stock composition at the reporting group level of the kept adult Chinook salmon of the fall Non-**
 2521 **Treaty sport fishery below Bonneville Dam in 2021 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					23	0 – 70
West Cascade Spring	Spring	02_WCASSP						
West Cascade Fall	Fall	03_WCASFA	915	868 – 1186	83	18 – 145	1584	1310 – 1868
Willamette	Spring	04_WILLAM	96	58 – 135			13	0 – 38
Spring Creek Tule	Fall	05_SPCRTU	347	227 – 428	156	54 – 224	72	21 – 136
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					306	187 – 447
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	2706	2415 – 2798	3173	2640 – 3895	5737	5230 – 6243
Snake River fall	Fall	19_SRFALL	376	282 – 539	453	350 – 625	1162	913 – 1415
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	1071	894 – 1415	588	292 – 909		
Umatilla fall	Fall	23_UMATILLAFA	38	1 – 86				
Total			5,549		4,454		8,897	

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Table 25. 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 2021 in units of reported catch.

Fall Sport Fishery 2021				Adult Chinook AD			Adult Chinook AI			GSI RepGrp
Expected Run Time	Hatchery	Broodstock	Brood year	MLE	95% CI	Percent	MLE	95% CI	Percent	
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su16	2016	13	0 – 39	0.2%			0.0%	18_UCOLSF
04Fall	Big Creek Hatchery	OtsBIGC_seg_fa17	2017	15	0 – 46	0.3%			0.0%	03_WCASFA
04Fall	Big Creek Hatchery	OtsBIGC_seg_fa18	2018			0.0%	18	0 – 54	0.4%	03_WCASFA
04Fall	Cowlitz Salmon Hatchery	OtsCOWL_seg_fa17	2017	47	0 – 94	0.8%			0.0%	03_WCASFA
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa16	2016	20	0 – 60	0.4%			0.0%	03_WCASFA
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa17	2017	330	200 – 476	5.9%	51	0 – 101	1.1%	03_WCASFA
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa18	2018	44	0 – 89	0.8%	15	0 – 44	0.3%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa17	2017	170	51 – 314	3.1%			0.0%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa18	2018	103	22 – 206	1.9%			0.0%	03_WCASFA
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa18	2018	263	155 – 384	4.7%	49	0 – 98	1.1%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	2019	42	14 – 84	0.8%	108	40 – 185	2.4%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa16	2016	96	25 – 176	1.7%	59	13 – 119	1.3%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa17	2017	1698	1434 – 1986	30.6%	2314	1994 – 2673	52.0%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa18	2018	428	255 – 631	7.7%	737	514 – 969	16.6%	18_UCOLSF

04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa19	2019			0.0%	24	0 – 73	0.5%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa17	2017	125	25 – 225	2.3%	14	0 – 41	0.3%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa18	2018	28	0 – 84	0.5%			0.0%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa19	2019			0.0%	24	0 – 73	0.5%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa16	2016	27	0 – 54	0.5%	13	0 – 40	0.3%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	2017	159	81 – 238	2.9%	40	13 – 81	0.9%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	2018	81	14 – 151	1.5%	210	124 – 308	4.7%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa17	2017	38	0 – 76	0.7%	159	74 – 257	3.6%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	2018			0.0%	29	0 – 59	0.7%	19_SRFALL
04Fall	Klickitat Hatchery	OtsKLIC_seg_fa18	2018	60	0 – 180	1.1%			0.0%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa15	2015			0.0%	13	0 – 40	0.3%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa16	2016	157	74 – 249	2.8%	85	25 – 155	1.9%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	2017	603	417 – 789	10.9%	458	307 – 620	10.3%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	2018	251	106 – 412	4.5%	32	0 – 96	0.7%	22_BONPOOLFA
04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	2018	38	0 – 87	0.7%			0.0%	23_UMATILLAFA
		Unassigned		711	409 – 1019	12.8%			0.0%	
		TOTAL		5,549		100.00%	4,436		100.00%	

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Table 26. Summary of the stock composition at the reporting group level of the kept adult Chinook salmon of the fall Non-Treaty sport fishery above Bonneville Dam in 2021 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						
Willamette	Spring	04_WILLAM						
Spring Creek Tule	Fall	05_SPCRTU	214	3 – 345	214	77 – 434	53	0 – 187
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						
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	1439	850 – 1974	453	224 – 824	1475	1007 – 1979

Snake River fall	Fall	19_SRFALL	609	399 – 868	358	220 – 492	384	165 – 659
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	806	807 – 1559	67	0 – 197		
Umatilla fall	Fall	23_UMATILLAFA	70	0 – 276				
Total			3,137		1,091		1,912	

Table 27. 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 2021 in units of reported catch.

Fall Sport BON Fishery 2021				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_seg_su16	2016	67	0 – 202	2.1%			0.0%	18_UCOLSF
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa18	2018	67	0 – 200	2.1%	67	0 – 200	6.1%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	2019	147	0 – 297	4.7%	147	0 – 294	13.5%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa17	2017	514	220 – 807	16.4%	220	73 – 440	20.2%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa18	2018	542	232 – 852	17.3%	232	77 – 465	21.3%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa16	2016	71	0 – 212	2.3%	71	0 – 212	6.5%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	2017	283	71 – 495	9.0%	212	71 – 424	19.4%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	2018	151	0 – 376	4.8%	75	0 – 226	6.9%	19_SRFALL

04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa17	2017	67	0 – 200	2.1%			0.0%	19_SRFALL
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa16	2016	67	0 – 200	2.1%	67	0 – 200	6.1%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	2017	557	278 – 835	17.7%			0.0%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	2018	183	0 – 365	5.8%			0.0%	22_BONPOOLFA
04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	2018	70	0 – 209	2.2%			0.0%	23_UMATILLAFA
#N/A	#N/A	Unassigned	#N/A	354	34 – 704	11.3%			0.0%	#N/A
		TOTAL		3,137		100.00%	1,091		100.00%	

The Non-Treaty commercial fishery in the Chinook Salmon Fall Management Period of 2021

The fall Non-Treaty commercial fishery is shown by the composition of the combined adult and jack harvest using reporting group level (Table 28) and broodstock level (Table 29) resolution. The early and late season fishery was executed in two different regions however, insufficient sampling of fishing in Region B prevented us from reporting the stock compositions for both regions separately. Therefore, we show only the genetic composition results for Region A reported catch. When results are available for both regions, we have observed the primary difference in the compositions between regions has been a larger abundance of spring creek tules (05_SPCRTU) stock in region A and absence of this stock in region B.

2545 **Table 28. Summary of the stock composition at the reporting group level of the adult and jack Chinook salmon of the fall Non-**
2546 **Treaty commercial fishery in 2021 in units of reported catch for Region A only.**

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					19	0 – 37
West Cascade Fall	Fall	03_WCASFA	1349	752 – 1824			1191	705 – 1726
Willamette	Spring	04_WILLAM	125	39 – 234			182	83 – 332
Spring Creek Tule	Fall	05_SPCRTU	10215	9120 – 10493	778	436 – 962	469	155 – 837
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					9	0 – 28
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	1223	971 – 1882	1538	920 – 1925	4730	3787 – 5654
Snake River fall	Fall	19_SRFALL	1102	409 – 1618	800	492 – 1285	1323	813 – 1955
Bonneville Pool spring	Spring	20_BONPOOLSP						

Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	1024	464 – 1448	405	264 – 592		
Umatilla fall	Fall	23_UMATILLAFA	96	0 – 187				
Total			15,134		3,521		7,922	

Note: Hatchery clipped (H), Hatchery unclipped (HNC), and natural-origin (W) estimated abundances (Est.) are indicated for the portions of this fishery that occurred Region A (commercial zones 4 and 5). Region B was not adequately sampled in order to estimate genetic stocks.

Table 29. Summary of the stock composition at the broodstock level of the adult and jack Chinook salmon of the fall Non-Treaty commercial fishery of 2021 in units of reported catch for Region A only.

Fall Commercial Fishery 2021				Adult/jack Chinook AD			Adult/jack Chinook AI			
Run	Hatchery	Broodstock	Brood year	MLE	95% CI	Percent	MLE	95% CI	Percent	GSI RepGrp
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su17	2017	10	0 – 29	0.1%			0.0%	18_UCOLSF
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa17	2017	386	118 – 779	2.6%			0.0%	03_WCASFA
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa18	2018	107	0 – 320	0.7%			0.0%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa17	2017	765	282 – 1371	5.1%			0.0%	03_WCASFA
04Fall	Bonneville Dam Hatchery	OtsBONN_seg_fa19	2019	513	124 – 994	3.4%			0.0%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa17	2017	1014	438 – 1675	6.7%			0.0%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa18	2018	5615	4610 – 6579	37.1%	141	0 – 282	4.0%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	2019	1206	715 – 1797	8.0%	637	256 – 1063	18.1%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa17	2017	1207	740 – 1758	8.0%	1432	906 – 2012	40.7%	18_UCOLSF

04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa18	2018			0.0%	106	0 – 318	3.0%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa16	2016	150	0 – 299	1.0%	10	0 – 29	0.3%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	2017	532	230 – 897	3.5%	179	29 – 377	5.1%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	2018	296	80 – 596	2.0%	342	80 – 651	9.7%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa16	2016			0.0%	73	0 – 218	2.1%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa17	2017	80	0 – 221	0.5%	197	46 – 365	5.6%	19_SRFALL
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa16	2016	331	98 – 587	2.2%	141	0 – 353	4.0%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	2017	443	157 – 782	2.9%	264	74 – 528	7.5%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	2018	250	0 – 500	1.7%			0.0%	22_BONPOOLFA
04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	2018	96	0 – 287	0.6%			0.0%	23_UMATILLAFA
#N/A	#N/A	Unassigned	#N/A	2134	1174 – 3082	14.1%			0.0%	#N/A
		TOTAL		15,134		100.00%	3,521		100.00%	

2553

Comparison of stock composition of the clipped Chinook salmon stocks among spring-and summer-management period Chinook salmon sport fisheries in 2021

The stock composition varied substantially across the Non-Treaty sport fisheries that were executed in the spring versus summer period as expected (Figure 24). 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 24). 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 5).

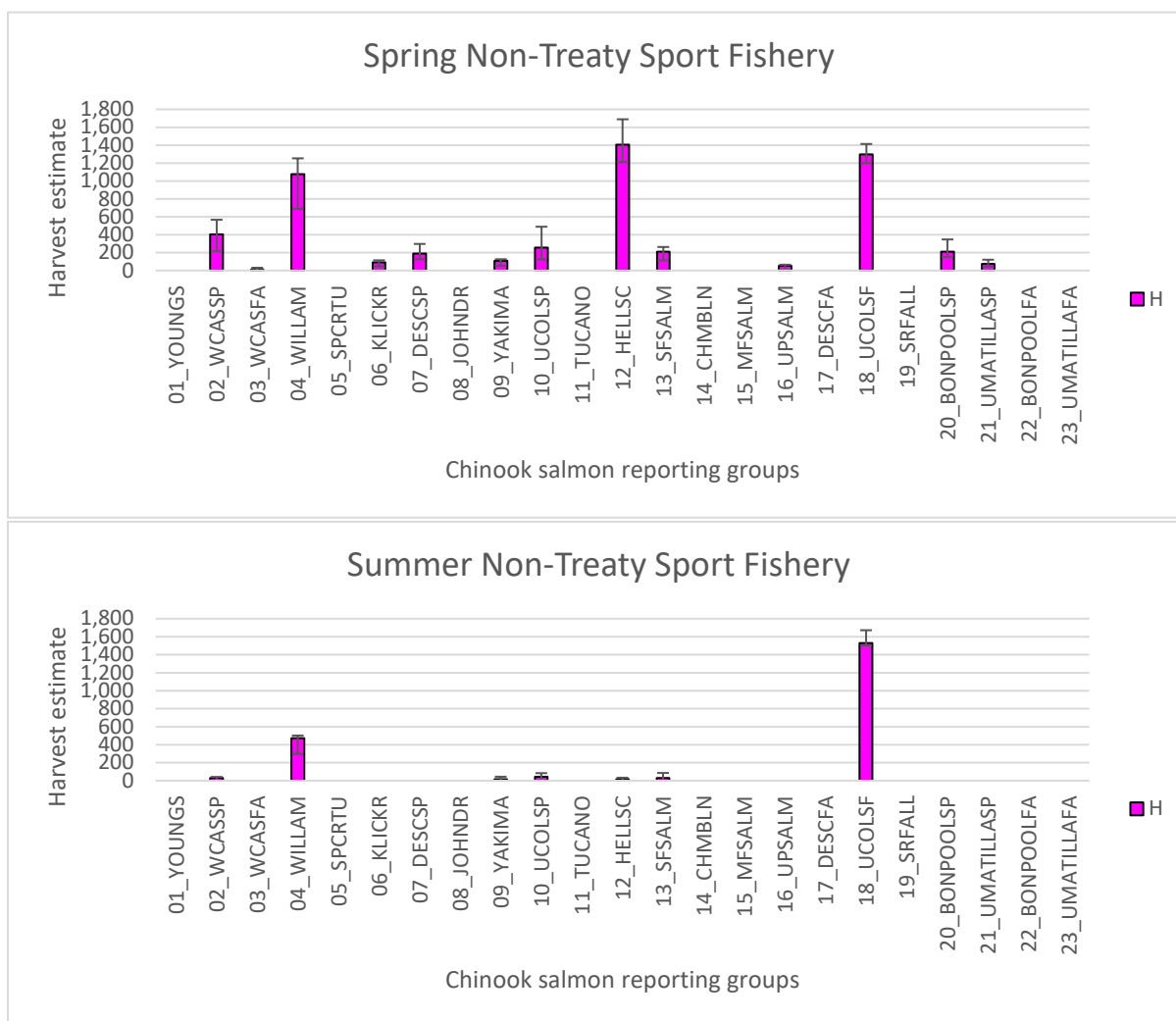


Figure 24. Stock composition of spring and summer management period Chinook salmon harvest mixtures in 2021.

Comparison of stock composition of the clipped and unclipped Chinook salmon stocks among the Non-Treaty fall-management period fisheries in 2021

The two stocks that distinguished the composition of the various Non-Treaty fall fisheries were the “tule” (05_SPCRTU) and Bonneville Pool fall (22_BONPOOLFA) stocks (Figure 25). Most of the 05_SPCRTU 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, except for the higher numbers of 22-BONPOOLFA stock present in the fall sport fishery executed in Zone 6 above Bonneville Dam (Figure 25). Most notably, the Non-Treaty commercial harvest from region A was distinguished from the sport fisheries by the larger proportion of tules (05_SPCRTU).

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 25) and commercial fishery (region A, Figure 25) 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.

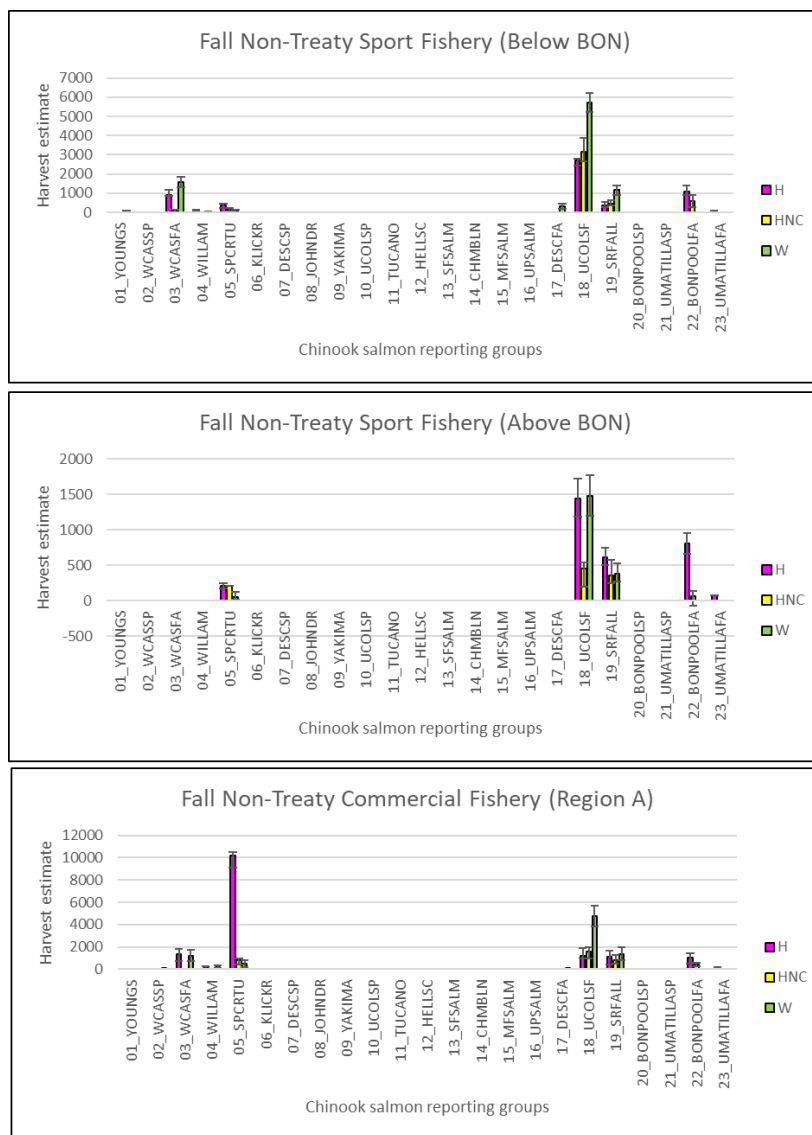


Figure 25. Genetic stock composition of the Fall Non-Treaty Chinook salmon fisheries analyzed in 2021.

2588

2589 *Comparison of stock composition among sockeye salmon fisheries from 2021*

2590 Sockeye salmon were sampled from the lower Columbia River below Bonneville Dam in
2591 the Non-Treaty sport fishery and were assigned to five major Columbia River sockeye genetic
2592 stocks (Table 30). Low sample numbers of *O. nerka* make it difficult to estimate narrow
2593 confidence intervals for estimates of the low abundance stocks: Yakima River, Snake River, and
2594 Lake Billy Chinook stocks (Table 30).

2595 The timing of the sockeye salmon fisheries may influence the harvested proportion of
2596 each stock. The Wenatchee stock has an early shifted run in some years like 2019. This
2597 difference in run timing may explain differences in proportions of each stock when compared to
2598 Bonneville Dam (Table 30). In 2021, however, the stock proportions in the fishery were very
2599 similar to those estimated at Bonneville Dam. For example, Okanogan stock was 70% at
2600 Bonneville Dam compared to 62% in the fishery; Wenatchee stock was 27% at Bonneville Dam
2601 compared to 32% in the fishery; the Snake River stock was 1% at Bonneville Dam compared to
2602 2% in the fishery; and the Yakima reintroduced stock was 2% at Bonneville Dam compared to
2603 4% in the fishery (Table 30). The 95% confidence intervals for all stock abundances in the Non-
2604 Treaty sport fishery were also estimated (Table 31). Despite small sample size for this fishery,
2605 our estimates captured a relatively high diversity of stocks including two stocks that typically
2606 have low abundance, Snake River and Yakima River stocks.

2607

2608 **Table 30. Comparison of stock-specific abundance and percent composition among sockeye salmon fisheries. The mean stock**
 2609 **abundance estimate is provided for each fishery harvest in 2021.**

Mixture source	Mean						Stock proportion					
	Okanogan	Wenatchee	Snake	LBC	Yakima	other	Okanogan	Wenatchee	Snake	LBC	Yakima	other
Sport	331	173	11	0	19	0	62.00%	32.39%	2.00%	0.00%	3.61%	0.00%
Total Harvest	331	173	11	0	19	0	62.00%	32.39%	2.00%	0.00%	3.61%	0.00%
Bonneville Dam	105,650	41,269	1,311	0	3,535	0	69.61%	27.19%	0.86%	0.00%	2.33%	0.00%

2610

2611

2612 **Table 31. The reporting group composition of the Non-Treaty Sport Sockeye salmon fishery in 2021.**

	Hatchery origin- Clipped		Reintroduction- No Clip		Natural origin- No Clip	
Reporting Group name	Estimated abundance		Estimated abundance		Estimated abundance	
	Mean	95% CI	Mean	95% CI	Mean	95% CI
Okanogan	11	0 – 32			320	256 – 384
Wenatchee	11	0 – 32			162	100 – 226
Snake	11	0 – 32				
Lake Billy Chinook						
Yakima			19			
Odell						
Total	32		19		483	

2613 Note: The 19 estimated Yakima fish were comprised entirely of fish from BY2016, 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 ninth year in which we were able to assign all three major age classes of spring Chinook from Snake River hatcheries and the fifth 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 and subyearling hatchery Chinook salmon 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 ninth 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. We have also updated the baseline to be complete through SY2021. 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 continues to benefit from improved power by expanding the SNP marker panel to 335 SNPs. The 2021 run year is the second 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 three 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:

2659 **1) Harvest RM&E: F&W Program Management Question: What are your in-river**
2660 **monitoring results and what are your estimates of stock composition and stock-**
2661 **specific abundance, escapement, catch, and age distribution?**
2662

2663 The in-river estimates of stock composition, stock-specific abundance, escapement,
2664 catch, and age distribution were addressed for the spring-management test fishery, the non-treaty
2665 spring-management sport fishery, the non-treaty summer-management sport fishery, and the non-
2666 treaty mainstem fall-management sport and commercial fisheries. For the spring management
2667 period of Chinook salmon, the 2021 we observed typical differences in the composition of
2668 hatchery stocks represented in spring vs. summer management period harvest of Chinook
2669 salmon. Run-timing plays an important role in this difference (i.e., late-running stocks appear
2670 more abundant among the upriver spring-type lineage that are caught in the summer management
2671 period). This pattern is consistent when compared to known origin PIT tagged adult and jack
2672 fish tagged as juveniles. Known origin adult age upriver spring and Snake River spring Chinook
2673 salmon are almost all past Bonneville by June 15 in most years. The fall management period
2674 fisheries were also found to show typical distinctions for the Non-Treaty sport versus Non-treaty
2675 commercial fisheries: namely, the Spring Creek tule stock is largely absent in the sport fishery
2676 but in high abundance in the commercial fishery. The reason for this is likely a preference
2677 exhibited by Non-treaty sport fishers for “bright” Chinook salmon stocks which cause them to
2678 catch and release more of the visually darker fish that are from the Spring Creek tule stock.

2679 The sockeye salmon tribal fishery is managed in a way that attempts to harvest as many
2680 harvestable sockeye salmon as possible under the allowed harvest rate schedule in the U.S. v.
2681 Oregon Management Agreement. We covered the 2021 year of analysis of the sockeye salmon
2682 harvest in this current report. The 2021 Non-treaty sport fishery harvested a surprisingly
2683 representative composition of stocks compared to Bonneville Dam, which is unlike more typical
2684 years where we have found that there may be some over representation of the Wenatchee
2685 sockeye stocks in the Zone 6 harvest as compared to the stock proportions that are present at
2686 Bonneville Dam. The results for Snake River sockeye salmon are dependent upon representative
2687 sampling at Bonneville Dam, but low sample rate and the rarity of this stock leads to uncertainty
2688 and high variation around estimates of Snake River sockeye salmon from Bonneville Dam.
2689 Despite this rarity, the fishery mixture evaluated in 2021 estimated non-zero abundance of Snake
2690 River and Yakima River stocks.

2691 Explanations for why fishery mixtures may diverge from Bonneville Dam in some years
2692 has been attributed to sampling protocols at Bonneville Dam that may have higher representation
2693 of young fish as compared to harvest mixtures. Timing of the fishery may also influence the
2694 proportion of each stock, as was shown by characterizing run-timing distributions in previous
2695 reports; the Wenatchee stock has relatively early run-timing but the timing of the Snake River
2696 stock is uncertain due to inconsistent results between PIT-tag and GSI methods. Future analysis
2697 will be needed to examine these patterns for consistency and delve into explanations.
2698 Importantly, the Yakima River reintroduction of sockeye can have a measurable (albeit small)
2699 impact on the stock composition of the fisheries. In this report, we estimated 19 Yakima fish
2700 were captured by the sport fishery.
2701

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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, it may be more accurate to use samples from a representative mixture of all hatchery- and natural-origin stocks at a fixed location to 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 2021. 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.

In this report, we continue to provide in-season analysis which was first conducted on Chinook Salmon during the 2017 spring and summer management periods. We have continued in-season reports for Chinook Salmon on an approximately bi-weekly report timing schedule during the 2022 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 2022, 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 32 for the number and timing of reports for each species and run that were delivered in-season and post-season in 2022). One new addition to these reports could be an inclusion of an in-season analysis of Coho Salmon at Bonneville Dam. In 2022, we were able to collect and genotype 150 Coho Salmon near the end of the operations of the Adult Fish Facility at Bonneville Dam. We will provide a demonstration of the analysis of Coho Salmon in a future report.

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 includes Snake River hatcheries as well as most others above Bonneville Dam. PBT baseline maintenance and expansion to other areas of the Columbia River 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. This report is the 9th 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 7th year in which these can be assigned to some Columbia River hatcheries. This is the fourth 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. Next year's report will include PBT analysis of Coho Salmon 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 2023 features the final analyses of 2021, as well as the preliminary in-season and post-season analyses of 2022. 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 32. The in-season and post-season report timing and scope of the 2022 fish runs.

Species	Management Period	Data coverage	Samples Arrive	Analysis begins	Report distributed
Chinook	Spring	01/01/2022 – 04/30/2022	5/2/2022	5/5/2022	5/9/2022
		01/01/2022 – 05/14/2022	5/16/2022	5/19/2022	5/23/2022
		01/01/2022 – 05/28/2022	5/30/2022	6/2/2022	6/6/2022
		01/01/2022 – 06/15/2022	6/16/2022	6/21/2022	6/24/2022
	Summer	06/16/2022 – 06/30/2022	7/1/2022	7/7/2022	7/11/2022
		06/16/2022 – 07/31/2022	8/1/2022	8/4/2022	8/8/2022
	Fall	08/01/2022 – 8/27/2022	8/29/2022	9/1/2022	9/5/2022
		08/01/2022 – 10/29/2022	10/31/2022	11/3/2022	11/7/2022
Steelhead	Skamania	04/01/2022 – 06/30/2022	7/1/2021	7/7/2022	7/11/2022
	Summer A-/B-Index	07/01/2022 – 07/31/2022	8/1/2022	8/4/2022	8/8/2022
		07/01/2022 – 08/27/2022	8/29/2022	9/1/2022	9/5/2022
		07/01/2022 – 10/31/2022	10/31/2022	11/3/2022	11/7/2022
Sockeye	Total	01/01/2022 – 07/31/2022	8/1/2022	8/4/2022	8/8/2022

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=651), Chinook (n=3,136) and sockeye salmon (n=1,451) adults in 2021 during migration runs at Bonneville Dam. This sampling effort is covered under the 2008 – 2017 U.S. vs. Oregon harvest biological opinion for sampling at Bonneville Dam.

Sampling for Chinook salmon at Bonneville Dam began during statistical week 17 (04/20/21) and was completed on 10/12/21 (statistical week 41). 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. A small portion of the adult Chinook salmon run was missed prior to the statistical week in which sampling was initiated by April 20 (week 17). There was 0.3% of the clipped adults and 0.1% of the unclipped adults estimated to have passed in weeks prior to the start of sampling in 2021. This year did not cause significant issues for sampling like the delay that was experienced in 2020 due to restrictions imposed by the Army Corp of Engineers. Typically, 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 earlier timed at Bonneville Dam compared to the timing exhibited by Spring Chinook in 2021 (Figure 26), this can result in a lower proportion of unsampled fish prior to usual initiation of sampling in mid April. In general, 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 2021 for the spring and summer management periods was 1.3%, whereas the average sample rate for adult fall Chinook was 0.4% (Table 33).

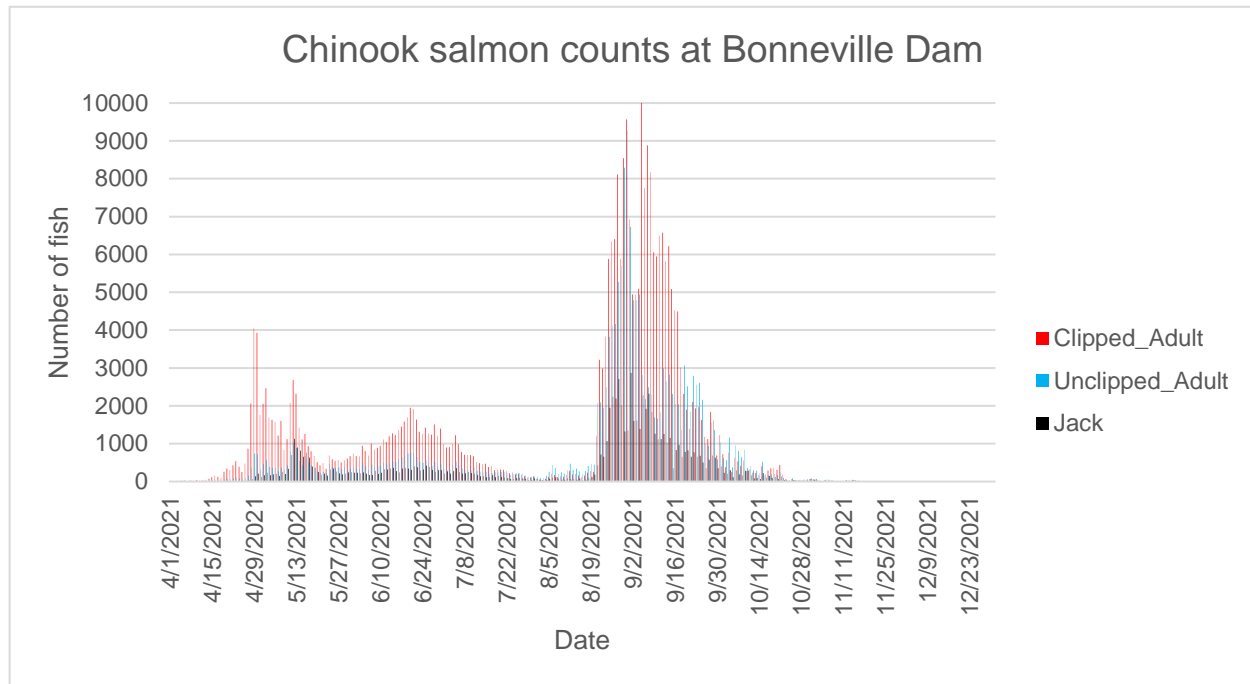
Based on numbers of fish collected, samples were pooled into a combination of weekly strata and multi-week strata for Chinook (Table 33), steelhead (Table 34), and sockeye salmon (Table 35) spanning the majority of the run-year from April to October. We followed a similar protocol as the Monitoring Methods [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 Rubias 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). Rubias 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).



2971 **Figure 26. Daily passage of Chinook salmon (Clipped adults=red, Unclipped adult=blue,**
 2972 **and jacks=black) at Bonneville Dam in 2021 (source: <https://www.fpc.org>; US v OR TAC).**

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Table 33. Sample numbers by weekly strata for adult-sized Chinook salmon that were DNA sampled or tallied for abundance at Bonneville Dam in 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	2359	450	5	95	4	5	100	9	4.24%	2.00%
		18	13396	2439	11	138	12	17	149	29	1.11%	1.19%
		19	12219	2779	19	228	27	23	247	50	2.02%	1.80%
		20	11593	4422	16	155	43	28	171	71	1.48%	1.61%
		21	5093	2728	5	82	29	18	87	47	1.71%	1.72%
		22	3798	2529	4	49	24	16	53	40	1.40%	1.58%
		23	5102	2574	4	96	51	13	100	64	1.96%	2.49%
		24	6527	2937	9	108	53	14	117	67	1.79%	2.28%
		25	3701	1541	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%
		32	739	1540					0	0	0.00%	0.00%
		33	1206	2077			2	1	0	3	0.00%	0.14%
		34	2423	4156		1	4		1	4	0.04%	0.10%
		35	36782	23921	6	44	74	41	50	115	0.14%	0.48%
		36	45885	44529	14	95	82	54	109	136	0.24%	0.31%
		37	53355	14974	8	74	80	42	82	122	0.15%	0.81%
		38	35737	16226	12	78	128	70	90	198	0.25%	1.22%

		39	13234	17555	6	41	82	34	47	116	0.36%	0.66%
		40	8422	7099	7	22	61	21	29	82	0.34%	1.16%
		41	3531	5358	2	19	45	11	21	56	0.59%	1.05%
		42-53	4640	4412		1		1	1	1	0.02%	0.02%
		Total	308175	181348	149	1618	929	440	1767	1369	0.57%	0.75%

2975 Note: Statistical weeks 1–16 are 1/1/21 – 4/17/21 and 42–53 is 10/10/21–12/31/21. ‘TAC count’ is based on the estimates of clip and unclipped adult
 2976 Chinook salmon provided by US v OR Technical Advisory Committee using data from the Fish Passage Center (<http://www.fpc.org>) observed by the
 2977 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
 2978 sample rate. The management periods approximate the date ranges from January 1st to June 15th (Spring management period), June 16th to July 31st
 2979 (Summer management period), and August 1st to December 31 (Fall management period) which are used to categorize spring-, summer-, and fall-run
 2980 Chinook salmon, respectively. The number of sampled fish that were assigned via PBT or GSI are shown.

2981 **Table 34. Sample numbers by monthly strata for steelhead that were DNA sampled or tallied for abundance at Bonneville**
2982 **Dam in 2021.**

				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	798	1,119	1	9	10	0	0	1	0	0	11	10	1.38%	0.89%
A-/B-Index	27-34	11,934	12,461	5	48	0	1	62	0	1	0	115	2	0.96%	0.02%
	35-36	13,328	5,217	6	42	2	9	28	4	4	0	80	15	0.60%	0.29%
	37	5,671	1,905	1	40	0	17	20	3	3	1	64	21	1.13%	1.10%
	38	4,487	1,206	4	63	3	31	13	5	5	3	85	42	1.89%	3.48%
	39-40	6,103	1,910	2	63	2	31	18	5	0	6	88	39	1.44%	2.04%
	41-44	2,704	826	1	41	1	13	13	7	2	1	62	17	2.29%	2.06%
Summer A-/B-Index subtotal		44,227	23,525	19	297	8	102	154	24	15	11	494	136	1.12%	0.58%
Total		45,025	24,644	20	306	18	102	154	25	15	11	505	146	1.12%	0.59%

2983 Note: Statistical week 14-27 is 4/1/21–6/30/21 (Skamania Management Period) and 27-29 begins the A-/B-Index Period that runs
2984 from 7/1/2021-10/31/2021. ‘Fish count’ is based on tallies of adipose-clipped and unclipped adult steelhead provided by the Fish
2985 Passage Center (<http://www.fpc.org>) observed by the Corps of Engineers at their fish counting window. The total sum of all samples
2986 for each clipped and unclipped category obtained in a given stratum was used to calculate sample rate. The clipped and unclipped
2987 sample numbers were grouped by size (A-Index < 780 mm fork length; B-Index >=780 mm fork length) and further split according to
2988 the number of samples that were either assigned via PBT or GSI.

2989 **Table 35. Sample numbers for genetic stock assignments of sockeye salmon that passed**
 2990 **Bonneville Dam in 2021.**

Statistical week grouping	Bonneville dam fish window count	Genetic stock						Total	Sample rate (%)
		OKA	WEN	RED	LBC	Yakima			
		OKA	WEN	RED	LBC	OKA	WEN		
1-24	2970	74	0	0	0	0	0	74	2.49%
25	9882	136	20					156	1.58%
26	50365	308	86	4		1	3	402	0.80%
27	47227	287	124	3			7	421	0.89%
28	26896	107	90	2			3	202	0.75%
29	10385	123	68	2			3	196	1.89%
30-39	4040	51	25	2	0	0	1	79	1.96%
Total	151765	1035	388	11	0	1	16	1451	0.96%

2991 Note: Statistical week 18 begins on 4/25/21 and 39 ends 9/25/21; there were no sockeye counted
 2992 before or after those dates. ‘Fish count’ is based on tallies of sockeye salmon adults provided by
 2993 the Fish Passage Center (<http://www.fpc.org>) observed by the Corps of Engineers at their fish
 2994 counting window. GSI stocks are Okanagan (OKA), Wenatchee (WEN), Snake River (RED),
 2995 and Lake Billy Chinook (LBC) and PBT can identify fish from the Yakima reintroduction which
 2996 consist of two genetic stocks (OKA and WEN). The number of samples for a given statistical
 2997 week or pooled stratum was used to calculate sample rate. Relatively few sockeye salmon were
 2998 sampled from the RED, LBC, and Yakima stocks, and limits inference regarding run-timing and
 2999 abundance of these stocks.

3001 **Results**

3002 *Estimated relative abundance of Chinook salmon stocks in 2021*

3003 In previous years the 10_UCOLSP reporting group included Carson Hatchery for
 3004 estimates of relative abundance due to genetic similarity in GSI assignments, so the abundance
 3005 estimates for this reporting group did not represent actual returns specifically to the upper
 3006 Columbia River. Beginning in 2017, we have categorized several hatcheries as their own
 3007 reporting groups to alleviate this issue and so that a more accurate assessment of the number of
 3008 Chinook returning to the upper Columbia River can be determined. To that end, we have
 3009 included the following reporting groups that are comprised of collections from our PBT baseline.
 3010 The 20_BONPOOLSP reporting group includes spring Chinook from Caron Hatchery and Little
 3011 White Salmon Hatchery. The 21_UMATILLASP reporting group includes spring Chinook from
 3012 the Umatilla Hatchery. The 22_BONPOOLFA reporting group includes fall Chinook from the
 3013 Little White Salmon Hatchery. The 23_UMATILLFA reporting group includes fall Chinook
 3014 from the Umatilla Hatchery. These reporting groups serve the purpose of distinguishing these
 3015 hatchery broodstocks apart from other reporting groups that share genetic affinity with these
 3016 hatcheries but are part of ESA listed groups. For example, 20_BONPOOLSP broodstocks share
 3017 genetic similarity with upper Columbia River spring Chinook Salmon, but only hatchery fish
 3018 from the latter group are ESA listed.

3019 .

There were 14 major (i.e., abundance >1000 fish) clipped hatchery origin Chinook salmon stocks represented in the total estimated abundance (N=308,175) of clipped hatchery Chinook salmon passing Bonneville Dam in 2021 (Table 36; Figure 27). These stocks in order of decreasing magnitude were 18_UCOLSF (131,682), 05_SPCRTU (46,690), 22_BONPOOLFA (40,683), 19_SRFALL (29,428), 12_HELLSC (25,359), 10_UCOLSP (7,291), 20_BONPOOLSP (7,091), 07_DESCSP (4,663), 13_SFSALM (4,004), 23_UMATILLAFA (3,088), 09_YAKIMA (1,891), 21_UMATILLASP (1,553), 16_UPSALM (1,282), and 06_KLICKR (1,230) (Table 36).

With the exception of reporting groups 20_BONPOOLSP, 21_UMATILLASP, 22_BONPOOLFA, and 23_UMATILLAFA), 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 36). Further, using PBT assignments we can now provide abundance and run-timing estimates for particular hatchery broodstocks (Table 37) which will allow for much improved abundance estimates (Figure 27). In 2021, there were 73 different broodstocks of clipped hatchery-origin fish with abundances greater than 0 and 37 of them had abundance estimates >1000 fish (Table 37). The top five major clipped hatchery broodstocks were from Priest Rapids, Spring Creek, Little White Salmon, and Lyons Ferry hatcheries which were all fall run. The largest spring run clipped broodstock was represented by Rapid River Hatchery (SY2017, 10,947 fish), which is typically one of the largest spring run hatchery stocks.

3041 **Table 36. Stock-specific abundance and run-timing of clipped hatchery origin adult Chinook salmon passing Bonneville Dam in 2021.**

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						-	-	-	-	-	-	
02_WCASSP	626	9	530	96		133	124	139	119	169	5/13/2021	15
03_WCASFA	957	2			957	246	243	257	241	260	9/3/2021	14
04_WILLAM	287	3	52	236		175	171	179	159	183	6/24/2021	8
05_SPCRTU	46,690	92			46,690	245	241	251	235	260	9/2/2021	10
06_KLICKR	1,230	22	1,230			144	131	148	123	156	5/24/2021	17
07_DESCSP	4,663	66	4,388	275		132	122	140	112	169	5/12/2021	18
08_JOHNDR	44	1	44			146	144	148	143	149	5/26/2021	4
09_YAKIMA	1,891	24	1,258	632		142	129	173	119	181	5/22/2021	44
10_UCOLSP	7,291	126	7,291			124	119	132	113	145	5/4/2021	13
11_TUCANO						-	-	-	-	-	-	
12_HELLSC	25,359	412	24,204	1,154		126	120	134	114	165	5/6/2021	14
13_SFSALM	4,004	61	3,580	424		144	134	155	130	183	5/24/2021	21
14_CHMBLN						-	-	-	-	-	-	
15_MFSALM		1				-	-	-	-	-	-	
16_UPSALM	1,282	20	1,282			149	134	161	129	166	5/29/2021	27
17_DESCFA	325	1			325	275	271	284	269	295	10/2/2021	13
18_UCOLSF	131,682	641	12,250	34,369	85,063	243	182	255	160	272	8/31/2021	73
19_SRFALL	29,428	53		204	29,224	242	238	251	233	271	8/30/2021	13
20_BONPOOLSP	7,091	115	7,015	75		121	119	127	110	137	5/1/2021	8
21_UMATILLASP	1,553	27	1,553			121	119	125	110	137	5/1/2021	6
22_BONPOOLFA	40,683	85		74	40,609	253	245	259	237	274	9/10/2021	14
23_UMATILLAFA	3,088	6			3,088	252	250	258	248	277	9/9/2021	8
Total	308,175	1,767	64,678	37,541	205,955							

3042 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
3043 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
3044 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
3045 Bonneville Dam fish counting window. This method for estimating run-timing distributions minimizes bias imposed by uneven sampling.

Table 37. Hatchery broodstock-specific abundance and run-timing distributions of clipped adult Chinook salmon passing Bonneville Dam in 2021.

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	
						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	1	52	52	0	0	124	123	126	122	128	5/4/2021	3
	02_WCASSP	Parkdale Fish Facility	OtsPARK_seg_sp17	6	390	390	0	0	128	122	138	118	141	5/8/2021	16
	02_WCASSP	Parkdale Fish Facility	OtsPARK_seg_sp18	2	184	88	96	0	167	132	169	130	170	6/16/2021	37
	06_KLICKR	Klickitat Hatchery	OtsKLIC_seg_sp16	4	238	238	0	0	131	125	144	122	148	5/11/2021	19
	06_KLICKR	Klickitat Hatchery	OtsKLIC_seg_sp17	14	896	896	0	0	144	132	148	123	154	5/24/2021	16
	06_KLICKR	Klickitat Hatchery	OtsKLIC_seg_sp18	1	58	58	0	0	160	158	162	157	163	6/9/2021	4
	07_DESCSP	Round Butte Fish Hatchery	OtsRBFH_seg_sp17	8	586	502	84	0	129	119	138	114	169	5/9/2021	19
	07_DESCSP	Round Butte Fish Hatchery	OtsRBFH_seg_sp18	4	358	166	191	0	185	152	192	137	205	7/4/2021	40
	07_DESCSP	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp17	50	3,668	3,668	0	0	131	122	137	112	154	5/11/2021	15
	09_YAKIMA	Yakima River Roza Dam	OtsYRRD_int_sp17	14	936	936	0	0	132	120	139	118	161	5/12/2021	19
	09_YAKIMA	Yakima River Roza Dam	OtsYRRD_seg_sp17	3	193	193	0	0	133	128	145	123	149	5/13/2021	17
	09_YAKIMA	Yakima River Roza Dam	OtsYRRD_seg_sp18	2	313	0	313	0	176	173	180	171	183	6/25/2021	7
	09_YAKIMA	Yakima River Roza Dam	OtsYRRD_int_sp18	2	319	0	319	0	176	173	180	171	183	6/25/2021	7
	10_UCOLSP	Chief Joseph Hatchery	OtsCHJO_seg_sp17	7	548	548	0	0	121	119	129	117	134	5/1/2021	10
	10_UCOLSP	Eastbank Fish Hatchery	OtsEAST_seg_sp17	11	657	657	0	0	140	136	151	131	155	5/20/2021	15
	10_UCOLSP	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp16	1	32	32	0	0	111	109	113	105	114	4/21/2021	4
	10_UCOLSP	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp17	69	4,903	4,903	0	0	122	119	130	111	135	5/2/2021	11

	10_UCOLSP	Winthrop National Fish Hatchery	OtsWINT_seg_sp17	5	344	344	0	0	132	130	135	123	148	5/12/2021	5
	10_UCOLSP	Winthrop National Fish Hatchery	OtsWINT_seg_sp18	1	90	90	0	0	146	144	148	143	149	5/26/2021	4
	12_HELLSC	Clearwater Fish Hatchery	OtsCLWH_seg_sp16	2	106	106	0	0	145	114	147	108	149	5/25/2021	33
	12_HELLSC	Clearwater Fish Hatchery	OtsCLWH_seg_sp17	40	2,447	2,447	0	0	130	123	133	118	144	5/10/2021	10
	12_HELLSC	Clearwater Fish Hatchery	OtsPOWP_seg_sp17	4	549	73	477	0	175	172	179	145	183	6/24/2021	7
	12_HELLSC	Clearwater Fish Hatchery	OtsPOWP_seg_sp18	1	51	51	0	0	153	152	155	150	156	6/2/2021	4
	12_HELLSC	Dworshak National Fish Hatchery	OtsDWOR_seg_sp17	81	5,107	5,107	0	0	126	120	132	117	140	5/6/2021	12
	12_HELLSC	Dworshak National Fish Hatchery	OtsKOOS_seg_sp17	23	1,500	1,500	0	0	127	120	133	117	142	5/6/2021	13
	12_HELLSC	Lookingglass Fish Hatchery	OtsLOOK_seg_sp17	33	2,164	2,081	83	0	132	124	149	118	166	5/12/2021	25
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH_seg_sp16	1	51	51	0	0	125	123	126	122	128	5/5/2021	3
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH_seg_sp17	184	10,947	10,947	0	0	123	119	129	111	138	5/3/2021	10
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH_seg_sp18	1	84	0	84	0	169	168	170	167	170	6/18/2021	2
	20_BONPOOLSP	Carson National Fish Hatchery	OtsCARS_seg_sp16	1	90	90	0	0	119	118	120	116	121	4/29/2021	2
	20_BONPOOLSP	Carson National Fish Hatchery	OtsCARS_seg_sp17	74	4,574	4,499	75	0	120	119	126	110	137	4/30/2021	7
	20_BONPOOLSP	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp16	1	73	73	0	0	132	131	133	129	135	5/12/2021	2
	20_BONPOOLSP	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp17	39	2,354	2,354	0	0	122	119	127	110	137	5/2/2021	8
	21_UMATILLASP	Umatilla Fish Hatchery	OtsUMAT_seg_sp17	27	1,553	1,553	0	0	121	119	125	110	137	5/1/2021	6
02Spring/Summer	12_HELLSC	Lookingglass Fish Hatchery	OtsIMNW_seg_ss16	2	103	103	0	0	153	151	155	150	156	6/2/2021	4
	12_HELLSC	Lookingglass Fish Hatchery	OtsIMNW_seg_ss17	21	1,648	1,138	511	0	161	149	169	136	180	6/10/2021	20
	13_SFSALM	McCall Fish Hatchery	OtsMCCA_seg_ss17	58	3,724	3,488	236	0	144	135	154	130	169	5/24/2021	19

	13_SFSALM	McCall Fish Hatchery	OtsMCCA_seg_ss18	1	188	0	188	0	192	187	198	185	208	7/11/2021	11
	16_UPSALM	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss17	1	51	51	0	0	153	152	155	150	156	6/2/2021	4
	16_UPSALM	Sawtooth Fish Hatchery	OtsSAWT_seg_ss17	19	1,231	1,231	0	0	148	133	162	129	166	5/28/2021	29
03Summer	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_su15	1	63	63	0	0	160	158	162	157	163	6/9/2021	4
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_su16	33	4,184	710	3,474	0	184	171	192	150	205	7/3/2021	21
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_su16	40	3,682	1,427	2,254	0	171	162	179	152	192	6/20/2021	17
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_su17	29	3,608	726	2,882	0	176	169	186	157	201	6/25/2021	17
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_su17	17	3,093	172	2,921	0	187	176	194	166	206	7/6/2021	18
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su15	1	157	0	157	0	176	173	180	171	183	6/25/2021	7
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su16	100	9,877	3,283	6,594	0	171	165	184	151	200	6/20/2021	19
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su17	56	7,108	1,196	5,077	835	178	170	191	154	238	6/27/2021	21
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su18	3	533	0	533	0	188	181	195	172	206	7/7/2021	14
	18_UCOLSF	Entiat National Fish Hatchery	OtsENFH_seg_su16	29	2,635	862	1,773	0	170	164	176	157	182	6/19/2021	12
	18_UCOLSF	Entiat National Fish Hatchery	OtsENFH_seg_su17	21	2,102	971	1,131	0	169	157	178	140	192	6/17/2021	21
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su16	67	6,732	1,842	4,890	0	173	164	180	152	195	6/22/2021	16
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su17	26	3,079	963	2,116	0	175	165	185	155	201	6/24/2021	20
04Fall	03_WCASFA	Kalama Falls Hatchery	OtsKALA_seg_fa17	1	560	0	0	560	243	242	245	241	247	8/31/2021	3
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa17	4	3,414	0	0	3,414	242	238	246	234	259	8/30/2021	8
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa18	63	32,464	0	0	32,464	246	242	251	235	260	9/3/2021	9
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	13	7,646	0	0	7,646	244	241	248	235	253	9/1/2021	7
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa16	2	1,228	0	0	1,228	239	237	242	233	246	8/27/2021	5

	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa17	113	59,029	0	0	59,029	250	243	258	236	274	9/7/2021	15
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa18	35	16,176	0	0	16,176	257	251	270	243	289	9/14/2021	19
	18_UCOLSF	Ringold Springs State Hatchery	OtsRING_seg_fa17	5	1,904	0	0	1,904	258	255	263	242	267	9/15/2021	8
	18_UCOLSF	Ringold Springs State Hatchery	OtsRING_seg_fa18	1	782	0	0	782	251	249	252	248	254	9/7/2021	3
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa15	1	303	0	0	303	265	263	267	262	268	9/22/2021	4
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	23	13,136	0	0	13,136	248	239	253	234	266	9/5/2021	14
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	20	13,583	0	0	13,583	240	237	246	233	273	8/28/2021	9
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa16	1	335	0	0	335	275	271	284	269	295	10/2/2021	13
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa17	2	1,204	0	0	1,204	239	237	256	233	260	8/27/2021	19
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	1	204	0	204	0	192	187	198	185	208	7/11/2021	11
	22_BONPOOLFA	Klickitat Hatchery	OtsKLIC_seg_fa18	1	600	0	0	600	275	271	284	269	295	10/2/2021	13
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa16	15	6,799	0	74	6,725	250	241	257	234	266	9/7/2021	16
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	58	26,625	0	0	26,625	254	246	259	238	271	9/11/2021	13
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	11	6,659	0	0	6,659	251	247	262	242	284	9/8/2021	15
	23_UMATILLAFA	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	6	3,088	0	0	3,088	252	250	258	248	277	9/9/2021	8
	#N/A	#N/A	Unassigned	165	12,224	1,760	804	9,660	244	236	257	124	273	9/1/2021	21
			Total	1,783	308,175	64,678	37,541	205,955							

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3049 There were 7 major (i.e., abundance >1000 fish) *unclipped* hatchery origin Chinook salmon stocks represented in the
3050 total estimated abundance (N=65,136) of unclipped hatchery Chinook salmon passing Bonneville Dam in 2021 (Table 38;
3051 Figure 27). These stocks in order of decreasing magnitude were 18_UCOLSF (30,750), 19_SRFALL (15,143), 05_SPCRTU
3052 (5,836), 22_BONPOOLFA (4,691), 10_UCOLSP (3,269), 12_HELLSC (2,566), and 13_SFSALM (1,230) (Table 38).

3053 In 2021, there were 55 different broodstocks of unclipped hatchery-origin fish with abundances greater than 0 and 13 of
3054 them had abundance estimates >1000 fish (Table 39). The top five major unclipped hatchery broodstocks were from Priest
3055 Rapids Hatchery, Lyons Ferry, and Spring Creek hatcheries which were all fall run. The largest spring run unclipped
3056 broodstock was represented by Winthrop Hatchery (SY2017, 1,183 fish).

3057 **Table 38. Stock-specific abundance and run-timing of unclipped hatchery origin adult Chinook salmon passing Bonneville Dam in 2021.**

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	178	1		178		176	173	180	171	183	6/25/2021	7
03_WCASFA	-	-	-	-	-	-	-	-	-	-	-	-
04_WILLAM	-	-	-	-	-	-	-	-	-	-	-	-
05_SPCRTU	5,836	24			5,836	243	241	246	233	262	8/31/2021	5
06_KLICKR	-	-	-	-	-	-	-	-	-	-	-	-
07_DESCSP	403	4	201	202		166	137	195	131	207	6/15/2021	58
08_JOHNDR	-	-	-	-	-	-	-	-	-	-	-	-
09_YAKIMA	103	2	103			141	138	160	136	163	5/21/2021	22
10_UCOLSP	3,269	50	3,129	140		132	123	143	116	166	5/12/2021	20
11_TUCANO	-	-	-	-	-	-	-	-	-	-	-	-
12_HELLSC	2,566	37	2,383	182		127	120	136	112	190	5/7/2021	16
13_SFSALM	1,230	21	1,163	67		142	135	149	131	167	5/22/2021	14
14_CHMBLN	-	-	-	-	-	-	-	-	-	-	-	-
15_MFSALM	-	-	-	-	-	-	-	-	-	-	-	-
16_UPSALM	499	8	499			134	126	147	119	160	5/14/2021	21
17_DESCFA	-	-	-	-	-	-	-	-	-	-	-	-
18_UCOLSF	30,750	200	936	2,458	27,356	248	241	260	174	279	9/5/2021	19
19_SRFALL	15,143	62			15,143	243	239	247	230	264	8/31/2021	8
20_BONPOOLSP	301	4	301			120	119	127	117	133	4/30/2021	8
21_UMATILLASP	168	2	168			119	118	120	116.35	121	4/29/2021	2
22_BONPOOLFA	4,691	25			4,691	247	241	266	233	282	9/4/2021	25
23_UMATILLAFA	-	-	-	-	-	-	-	-	-	-	-	-
Total	65,136	440	8,882	3,227	53,026							

3058 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
3059 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
3060 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
3061 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
3062 assignments.

Table 39. Hatchery broodstock-specific abundance and run-timing distributions of unclipped adult Chinook salmon passing Bonneville Dam in 2021.

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	02_WCASSP	Parkdale Fish Facility	OtsPARK_seg_sp18	1	178	0	178	0	176	173	180	171	183	6/25/2021	7
	07_DESCSP	Round Butte Fish Hatchery	OtsRBFH_seg_sp17	1	65	65	0	0	138	137	140	136	142	5/18/2021	3
	07_DESCSP	Round Butte Fish Hatchery	OtsRBFH_seg_sp18	1	57	57	0	0	165	164	166	164	166	6/14/2021	2
	07_DESCSP	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp17	1	78	78	0	0	132	131	133	129	135	5/12/2021	2
	07_DESCSP	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp18	1	202	0	202	0	195	189	202	185	209	7/14/2021	13
	09_YAKIMA	Yakima River Roza Dam	OtsYRRD_int_sp17	1	58	58	0	0	138	137	140	136	142	5/18/2021	3
	09_YAKIMA	Yakima River Roza Dam	OtsYRRD_seg_sp17	1	45	45	0	0	160	158	162	157	163	6/9/2021	4
	10_UCOLSP	Eastbank Fish Hatchery	OtsEAST_seg_sp17	19	1,121	981	140	0	148	136	162	124	177	5/28/2021	26
	10_UCOLSP	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp17	6	484	484	0	0	120	118	132	109	147	4/30/2021	14
	10_UCOLSP	Methow Fish Hatchery	OtsMETH_seg_sp16	1	58	58	0	0	138	137	140	136	142	5/18/2021	3
	10_UCOLSP	Methow Fish Hatchery	OtsMETH_seg_sp17	6	423	423	0	0	128	122	133	118	147	5/8/2021	11
	10_UCOLSP	Winthrop National Fish Hatchery	OtsWINT_seg_sp17	18	1,183	1,183	0	0	128	122	133	113	139	5/8/2021	11
	12_HELLSC	Clearwater Fish Hatchery	OtsCLWH_seg_sp17	7	457	457	0	0	123	120	127	118	133	5/3/2021	7
	12_HELLSC	Clearwater Fish Hatchery	OtsPOWP_seg_sp17	2	109	109	0	0	149	145	159	143	163	5/28/2021	14
	12_HELLSC	Clearwater Fish Hatchery	OtsPOWP_seg_sp18	1	182	0	182	0	195	189	202	185	210	7/14/2021	13
	12_HELLSC	Dworshak National Fish Hatchery	OtsDWOR_seg_sp17	11	705	705	0	0	124	118	133	108	150	5/4/2021	15
	12_HELLSC	Dworshak National Fish Hatchery	OtsKOOS_seg_sp17	2	114	114	0	0	136	125	138	122	141	5/16/2021	13

	12_HELLSC	Lookingglass Fish Hatchery	OtsLOOK_seg_sp17	4	297	297	0	0	128	120	135	118	148	5/8/2021	15
	12_HELLSC	Nez Perce	OtsNPFH_seg_sp17	3	219	219	0	0	132	127	136	122	141	5/12/2021	9
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH_seg_sp17	6	418	418	0	0	120	118	130	109	134	4/30/2021	12
	20_BONPOOLSP	Carson National Fish Hatchery	OtsCARS_seg_sp17	1	85	85	0	0	119	118	120	116	121	4/29/2021	2
	20_BONPOOLSP	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp16	1	90	90	0	0	119	118	120	116	121	4/29/2021	2
	20_BONPOOLSP	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp17	2	125	125	0	0	129	125	132	122	134	5/9/2021	7
	21_UMATILLASP	Umatilla Fish Hatchery	OtsUMAT_seg_sp17	2	168	168	0	0	119	118	120	116	121	4/29/2021	2
02Spring/Summer	12_HELLSC	Lookingglass Fish Hatchery	OtsIMNW_seg_ss17	1	64	64	0	0	138	137	140	136	142	5/18/2021	4
	13_SFSALM	McCall Fish Hatchery	OtsMCCA_seg_ss17	19	1,126	1,060	67	0	141	134	149	131	167	5/21/2021	15
	13_SFSALM	McCall Fish Hatchery	OtsJHNW_int_ss17	2	103	103	0	0	148	145	152	143	156	5/28/2021	7
	16_UPSALM	Sawtooth Fish Hatchery	OtsSAWT_seg_ss17	7	436	436	0	0	133	124	146	118	160	5/13/2021	22
	16_UPSALM	Sawtooth Fish Hatchery	OtsSAWT_seg_ss18	1	63	63	0	0	146	144	148	143	149	5/26/2021	4
03Summer	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_su16	2	85	85	0	0	157	154	160	150	163	6/6/2021	7
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_su16	4	572	0	572	0	188	177	198	168	208	7/7/2021	21
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_su17	5	509	156	353	0	178	165	192	154	207	6/27/2021	27
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_su17	1	241	0	241	0	195	189	202	185	210	7/14/2021	13
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su16	7	793	144	649	0	182	172	194	157	207	7/1/2021	22
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su17	1	59	59	0	0	165	164	166	164	166	6/14/2021	2
	18_UCOLSF	Entiat National Fish Hatchery	OtsENFH_seg_su16	2	195	57	137	0	173	166	178	164	183	6/22/2021	12
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su16	8	397	332	65	0	160	153	165	145	169	6/9/2021	12
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su17	4	269	49	220	0	168	167	169	159	170	6/17/2021	2
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su18	2	275	53	221	0	192	186	201	159	209	7/11/2021	15

04Fall	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa17	1	137	0	0	137	257	256	259	255	261	9/14/2021	3
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa18	15	3,456	0	0	3,456	243	241	247	233	265	8/31/2021	6
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	8	2,243	0	0	2,243	243	240	245	233	253	8/31/2021	5
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa16	5	735	0	0	735	249	244	258	241	281	9/6/2021	14
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa17	119	20,850	0	0	20,850	248	242	259	234	274	9/5/2021	17
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa18	36	4,849	0	0	4,849	262	256	272	244	288	9/19/2021	16
	18_UCOLSF	Ringold Springs State Hatchery	OtsRING_seg_fa17	4	922	0	0	922	244	239	250	232	266	9/1/2021	11
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa16	1	87	0	0	87	257	256	259	255	261	9/14/2021	3
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	20	4,484	0	0	4,484	241	237	246	225	264	8/29/2021	9
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	27	7,090	0	0	7,090	243	239	247	231	265	8/31/2021	8
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa16	1	126	0	0	126	250	249	252	248	254	9/7/2021	3
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa17	8	2,171	0	0	2,171	242	238	244	230	247	8/30/2021	6
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	5	1,186	0	0	1,186	245	243	250	241	278	9/2/2021	7
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa16	8	1,339	0	0	1,339	249	242	263	234	275	9/6/2021	21
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	13	2,702	0	0	2,702	244	239	262	232	280	9/1/2021	23
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	4	651	0	0	651	269	263	277	256	291	9/26/2021	14
Total				440	65,136	8,882	3,227	53,026							

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Table 40. Stock-specific abundance and run-timing of natural origin adult Chinook salmon passing Bonneville Dam in 2021.

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	273	2	0	0	273	268	265	275	262	288	9/25/2021	10
02_WCASSP	181	1	0	181	0	195	189	202.25	185	210	7/14/2021	13
03_WCASFA	518	4	0	0	518	262	251	268	248	283	9/19/2021	17
04_WILLAM	121	1	0	0	121	277	272	282	269	292.25	10/4/2021	10
05_SPCRTU	1,109	5	0	0	1,109	244	243	247	241	266	9/1/2021	4
06_KLICKR	121	2	121	0	0	143	138	146	136	149	5/23/2021	8
07_DESCSP	275	5	275	0	0	137	136	141	107	154	5/17/2021	5
08_JOHNDR	267	4	267	0	0	134	120	142	118	148	5/14/2021	22
09_YAKIMA	1,544	26	1,544	0	0	132	126	134	119	162	5/12/2021	8
10_UCOLSP	2,134	40	2,068	65	0	133	124	148	118	164	5/13/2021	24
11_TUCANO	-	-	-	-	-	-	-	-	-	-	-	-
12_HELLSC	2,476	43	2,277	199	0	138	123	151	114	171	5/18/2021	28
13_SFSALM	1,064	22	1,000	64	0	151	138	158	130	167	5/31/2021	20
14_CHMBLN	98	2	98	0	0	141	137.25	152	136	156	5/21/2021	15
15_MFSALM	588	10	588	0	0	132	128	136	123	141	5/12/2021	8
16_UPSALM	1,588	28	1,457	130	0	135	131	149	123	168	5/15/2021	18
17_DESCFA	3,050	19	0	0	3,050	248	242	259	234.2	279	9/5/2021	17
18_UCOLSF	82,079	605	3,933	12,562	65,585	244	234	260	167	279	9/1/2021	26
19_SRFALL	18,726	110	44	519	18,163	244	239	256	223	275	9/1/2021	17
20_BONPOOLSP	-	-	-	-	-	-	-	-	-	-	-	-
21_UMATILLASP	-	-	-	-	-	-	-	-	-	-	-	-
22_BONPOOLFA	-	-	-	-	-	-	-	-	-	-	-	-
23_UMATILLAFA	-	-	-	-	-	-	-	-	-	-	-	-
Total	116,212	929	13,673	13,720	88,819							

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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.

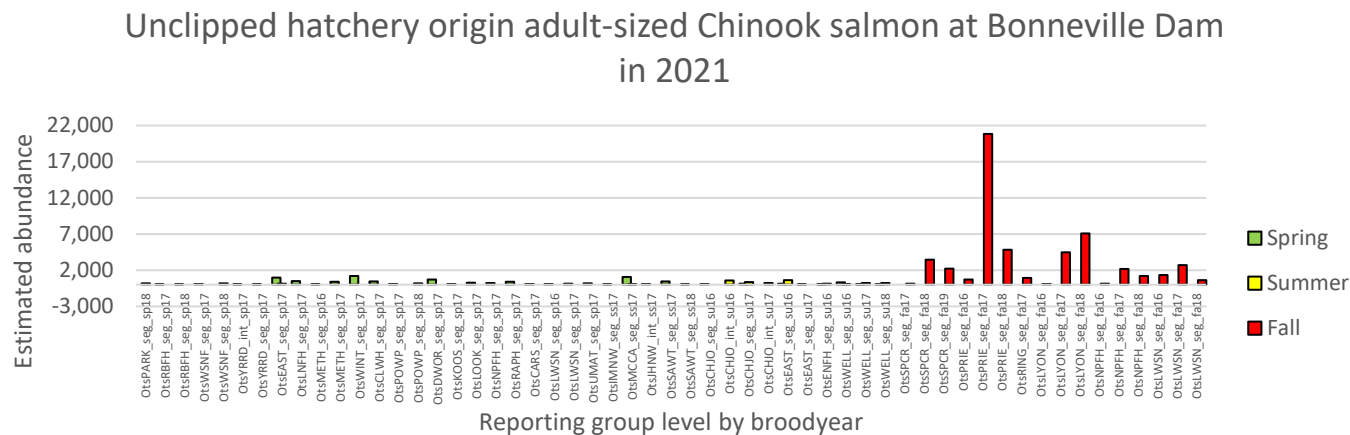
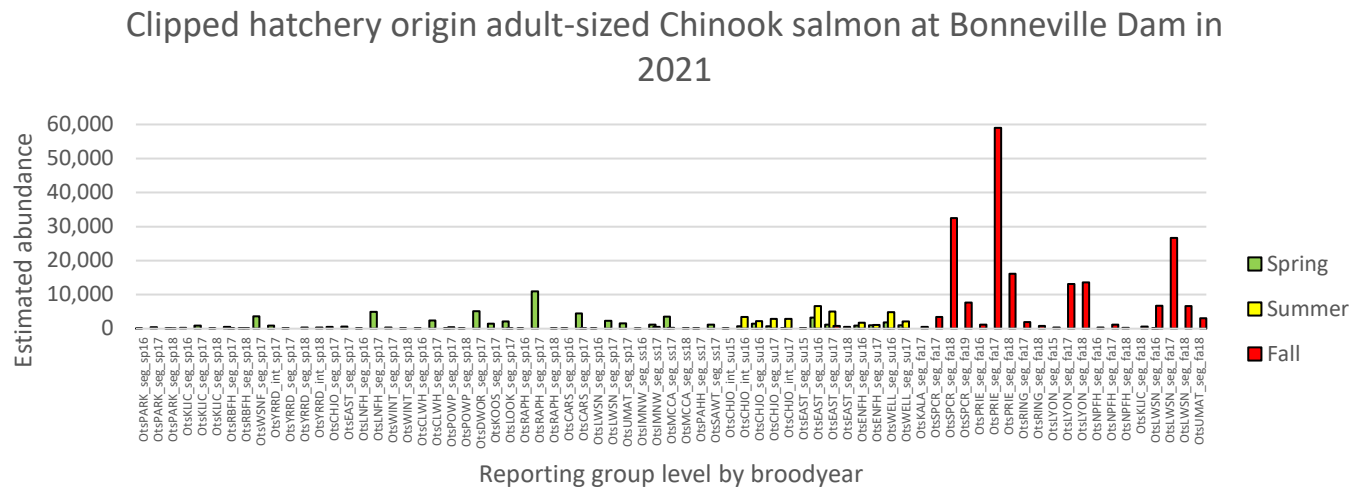


Figure 27. Estimated abundance of clipped (top) and unclipped (bottom) hatchery origin adult-sized Chinook salmon assigned to PBT broodstock groups that were sampled at Bonneville Dam in 2021 during spring (green), summer (yellow) and fall (red) management periods.

3076 There were 9 major (i.e., abundance >1000 fish) Chinook salmon stocks represented in
3077 the total estimated relative abundance (N=116,212) of natural-origin (i.e., excluding unclipped
3078 hatchery-origin fish) Chinook salmon passing Bonneville Dam in 2021 (Table 40;Figure 28).
3079 These natural-origin stocks in order of decreasing magnitude were 18_UCOLSF (82,079),
3080 19_SRFALL (18,726), 17_DESCFA (3,050), 12_HELLSC (2,476), 10_UCOLSP (2,134),
3081 16_UPSALM (1,588), 09_YAKIMA(1,544), 05_SPCRTU (1,109), and 13_SFSALM (1,064).
3082 These stock abundance estimates were generated using SCOBIDEUX and SPIBETR functions
3083 and the estimates of clipped and unclipped adults distributed by TAC (Table 33).

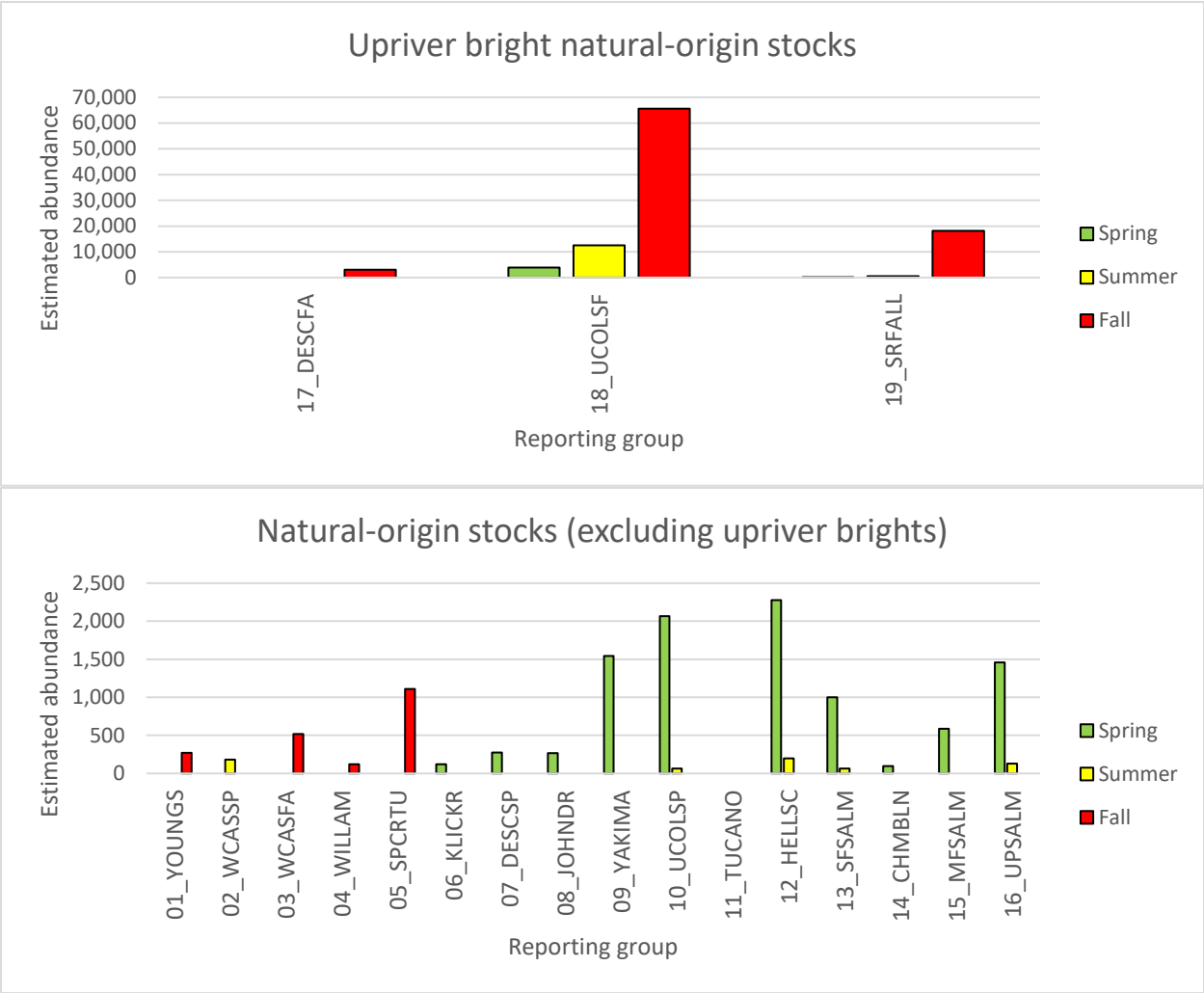


Figure 28. Estimated abundance of natural origin reporting groups (excluding unclipped hatchery-origin fish) of adult-sized Chinook salmon sampled at Bonneville Dam in 2021 during the spring (green), summer (yellow), and fall (red) management periods. Upriver bright Chinook salmon reporting groups (top panel), and all other natural-origin Chinook reporting groups (bottom panel) are shown separately.

Run-timing of Chinook salmon stocks in 2021

We plotted the run-timing distributions of the clipped and unclipped hatchery-origin Chinook salmon reporting group stocks (Figure 29) and provided the subtotals of reporting group abundance for each management period (clipped Table 36, unclipped Table 38). 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, 10_UPCOLSP, 12_HELLSC, and 13_SFSALM was found to extend beyond the spring management period (total abundance in the summer period was 3,153 fish). We estimated that 95% of all hatchery origin spring stocks passed Bonneville Dam in the spring period and 5% of the spring stock abundance passed in the summer period (Table 36, Table 38). 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 26% (13,185 fish) and 74% (36,828 fish) of the total abundance estimated in those two periods, respectively.

We also plotted run-timing distributions for each broodstock of clipped (Figure 31) and unclipped (Figure 32) hatchery origins and provided the subtotals of these broodstock abundance estimates for each management period (clipped Table 37, unclipped Table 39). Although most stocks with sample sizes ≥ 5 had median dates that fit within their expected management period, there was one summer run Upper Columbia unclipped broodstock from Wells that had a median date in the spring (Figure 32); there were no spring run hatchery clipped or unclipped broodstocks with sample sizes ≥ 5 that had median dates in the summer.

We plotted the run-timing distributions of the natural-origin (excluding adipose unclipped hatchery-origin fish, Figure 30) Chinook salmon stocks and provide subtotals of abundance for each management period (Table 40). 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 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 459 fish). We also estimated that 95% (9,696 fish) of the natural origin spring stocks passed Bonneville Dam in the spring period and 5% (459 fish) of the spring stock abundance passed in the summer period (Table 40). 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% (3,933 fish) and 76% (12,562 fish) of the total abundance estimated in those two periods, respectively.

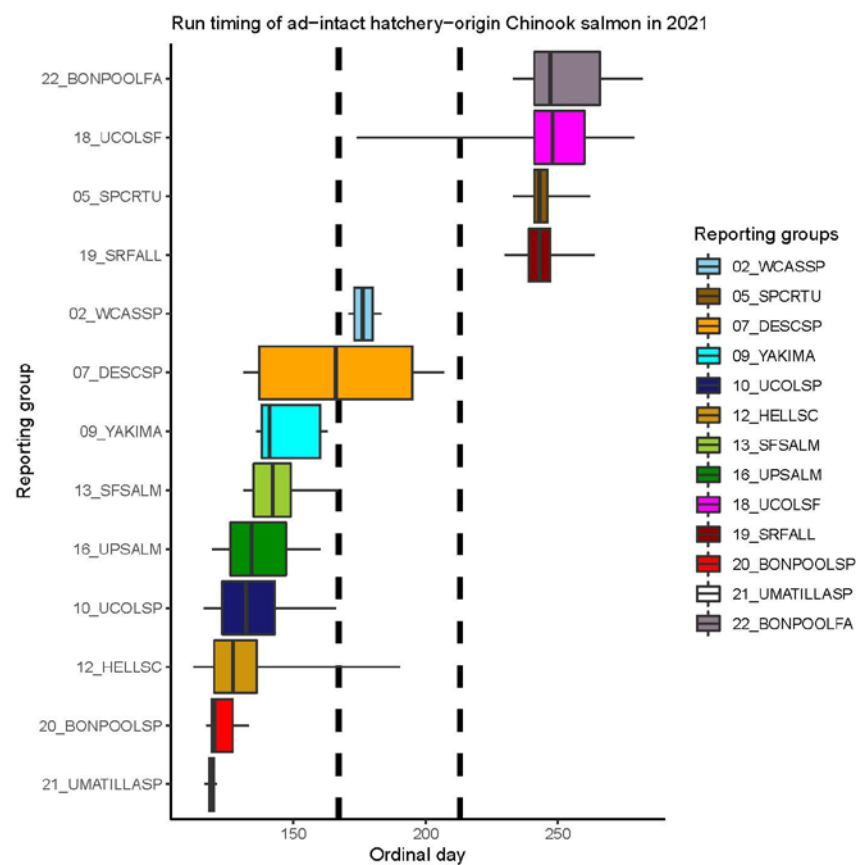
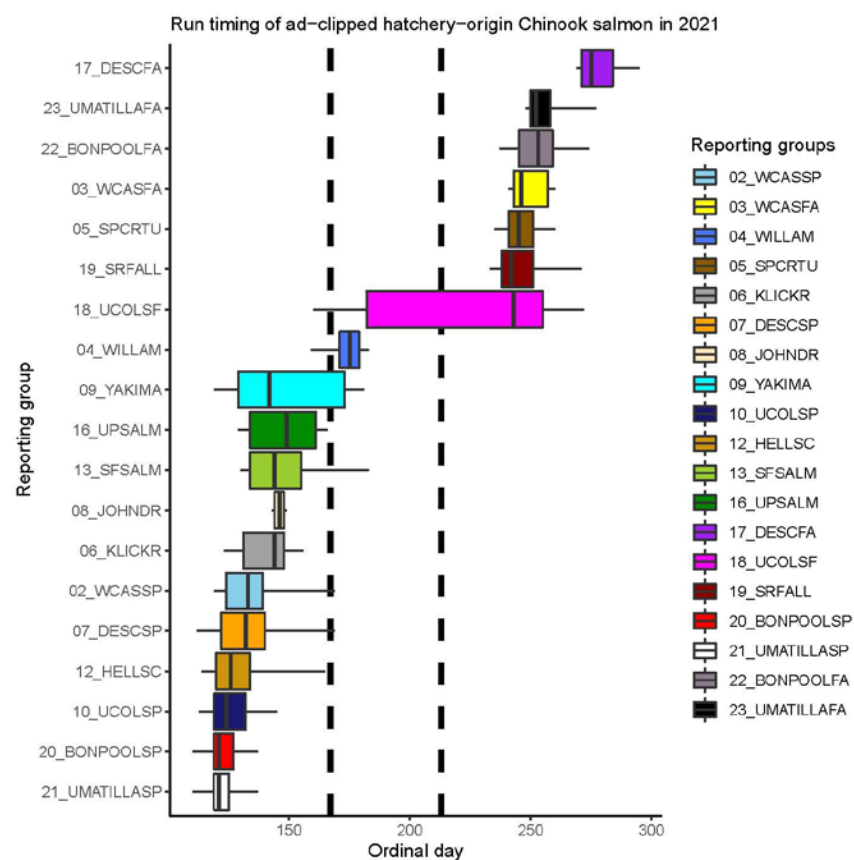


Figure 29. Reporting group-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for clipped and unclipped hatchery-origin adult-sized Chinook salmon that were sampled at Bonneville Dam in 2021 during the spring, summer, and fall management periods (separated by dashed lines).

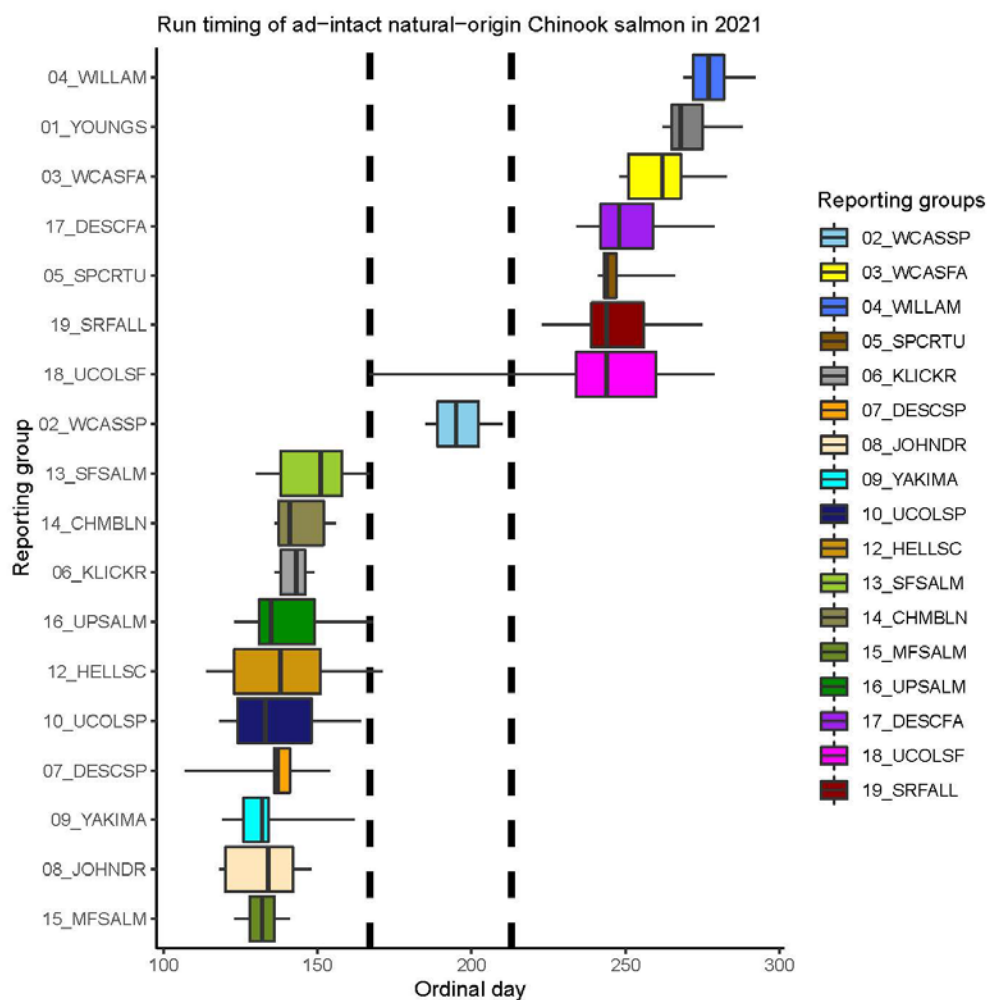


Figure 30. Reporting group-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for natural-origin adult-sized Chinook salmon that were sampled at Bonneville Dam in 2021 during the spring, summer, and fall management periods (separated by dashed lines).

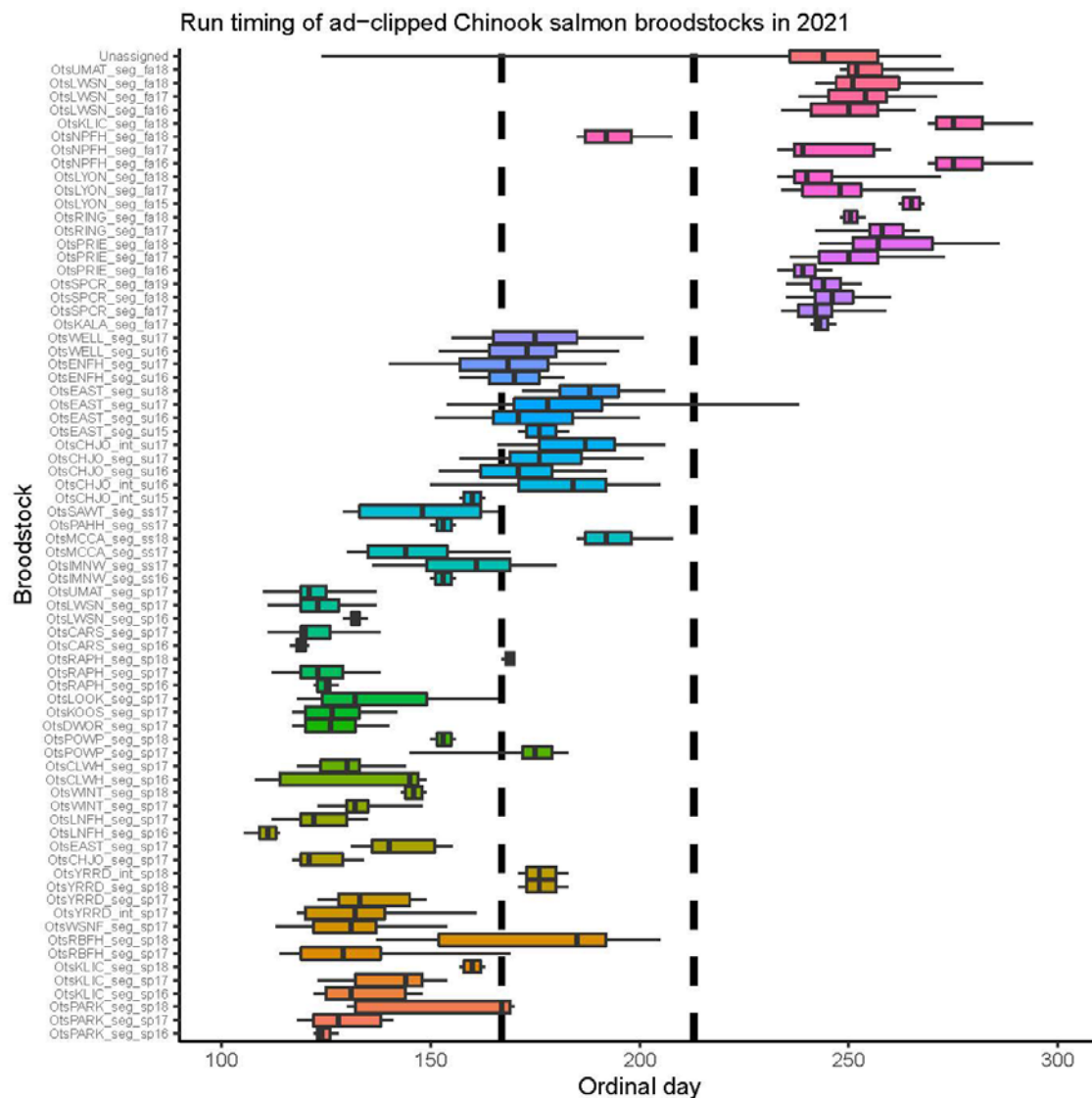


Figure 31. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for clipped adult-sized Chinook salmon that were sampled at Bonneville Dam in 2021 during the spring, summer, and fall management periods (separated by dashed lines).

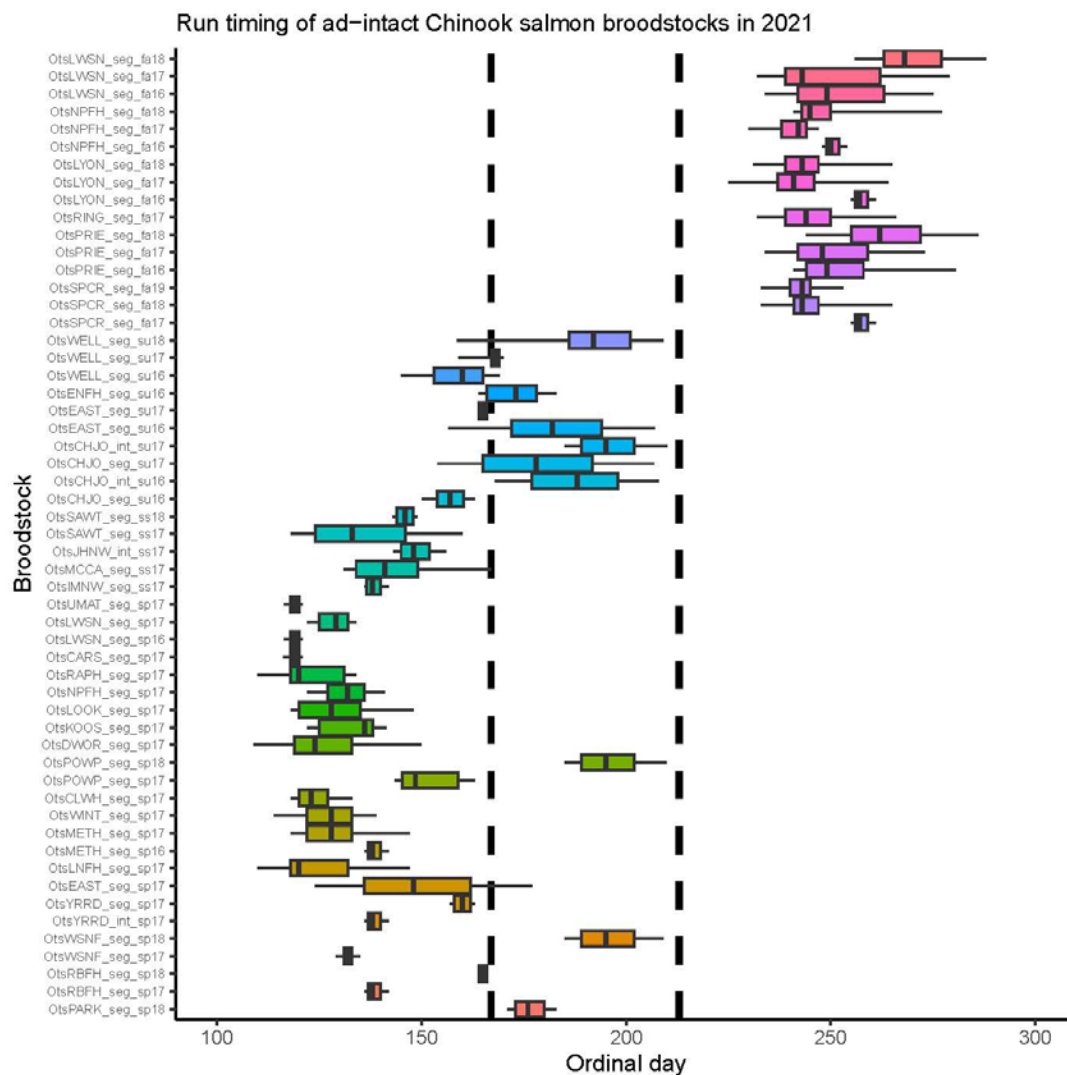


Figure 32. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for unclipped adult-sized Chinook salmon that were sampled at Bonneville Dam in 2021 during the spring, summer, and fall management periods (separated by dashed lines).

Demonstration of PBT to estimate smolt-to-adult survival using the adult Spring- and Summer-/Fall-Run Chinook salmon clipped and unclipped hatchery-origin stocks that passed Bonneville Dam in 2020 – 2021

We obtained the release information for clipped and unclipped hatchery-origin Chinook salmon from Columbia River hatcheries located upstream of Bonneville Dam from Brood Year 2017 (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 “adult-sized” abundance we estimated for the SY2017 broodstocks that returned to Bonneville Dam as adults in 2020 and 2021 (i.e., 3- and 4-year-olds, respectively). Inclusion of the abundance estimates from 2020 was mostly important for the analysis of summer and fall Chinook salmon which can be subyearling 3-year olds when they return at adult sizes (spent 0 years in freshwater and 2 years in saltwater prior to their adult migration as a 3-year-old salmon). There was moderate correspondence of number of clipped and unclipped releases versus Bonneville Dam abundance estimates for Spring-run stocks based on the R^2 (0.49) of the linear trend (Figure 33). There was even higher correspondence of number of clipped and unclipped releases versus Bonneville Dam abundance estimates for Summer and Fall-run stocks based on the R^2 (0.63) of the linear trend.

This smolt-to-adult survival type of analysis may be highly beneficial for management of these hatchery stocks in the future and represents the third attempt at using the hatchery release information and PBT abundance estimates in this kind of analysis. This is the first analysis where we summed abundance of the SY2017 adult return across age-classes (i.e., age 3 and 4 in run years 2020 and 2021, respectively) that passed Bonneville Dam. In future years we could sum abundances from a single broodyear that not only returned to Bonneville Dam but also those that were caught in lower river fisheries below the dam in the same set of years. This would allow a complete run reconstruction of these Chinook salmon broodstock groups to the Columbia River mouth. This current analysis demonstrated a trend of 556 Spring Chinook salmon smolts released converted to 1 adult-sized 4-year-old Spring Chinook salmon returned to Bonneville Dam in 2021. In addition, we observed a trend of 85 Fall Chinook salmon smolts converted to 1 adult-sized 3- or 4-year-old Summer/Fall Chinook salmon returned to Bonneville Dam combined across 2020 and 2021.

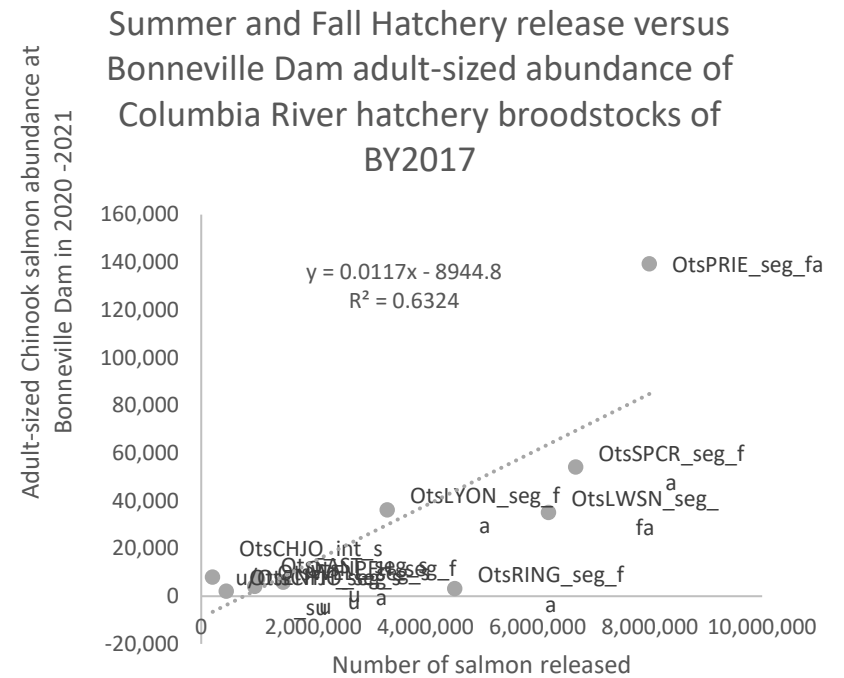
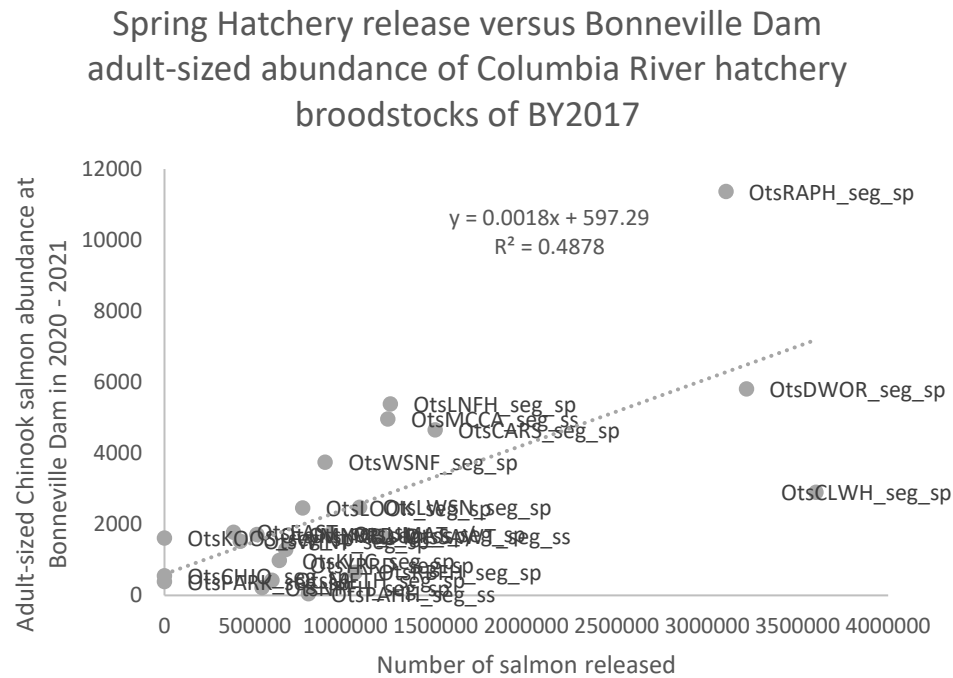


Figure 33. Smolt release numbers of hatchery-origin Spring Chinook salmon (left) and Summer/Fall Chinook (right) of BY2017 from Columbia River hatcheries above Bonneville Dam versus the estimated abundance of BY2017 adult-sized fish that passed Bonneville Dam in 2020 – 2021.

Estimated relative abundance of steelhead stocks in 2021

Daily passage of summer A-/B-Index steelhead at Bonneville Dam in 2021 is provided in Figure 34. Among clipped hatchery-origin summer A-/B-Index steelhead, there were five major stocks (abundance >1000) represented in the total estimated abundance (N=44,227) of clipped hatchery origin steelhead passing Bonneville Dam in 2021 (Table 41). These stocks in order of decreasing magnitude were 14_UPSALM (15,325), 07_MGILCS (12,139), 10_SFCLWR (8,504, B-Index), 10_SFCLWR (4,823, A-Index), and 09_UPPCOL (3,059) (Table 41; Figure 35). 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 summer A-/B-Index steelhead, there was a single major stock (14_UPSALM, abundance >1000) represented in the total estimated abundance (N=2,866) of unclipped hatchery origin steelhead passing Bonneville Dam in 2021 (Table 42; Figure 35).

Using PBT assignments we can now provide abundance (Table 44; Figure 36) and run-timing estimates for each of the clipped and unclipped hatchery broodstocks (Table 44). There were 13 major hatchery broodstock sources (abundance >1000) represented in the total estimated abundance of clipped and unclipped hatchery-origin summer A-/B-Index steelhead passing Bonneville Dam in 2021 (Table 44). These stocks in order of decreasing magnitude were OmyDWOC_su18 (9969 total; A-Index = 2689 and B-Index = 7280), OmySAWT_su19 (5164 total; A-Index = 5164 and B-Index = 0), OmyWALL_su19 (4243 total; A-Index = 4243 and B-Index = 0), OmyPAHH_su19 (3736 total; A-Index = 3736 and B-Index = 0), OmyOXBO_su19 (3448 total; A-Index = 3448 and B-Index = 0), OmySFCR_su18 (2292 total; A-Index = 714 and B-Index = 1578), OmyLSCR_su19 (2070 total; A-Index = 2070 and B-Index = 0), OmyCGRW_su19 (1895 total; A-Index = 1895 and B-Index = 0), OmyWELL_su19 (1882 total; A-Index = 1882 and B-Index = 0), OmyCGRW_su18 (1575 total; A-Index = 1575 and B-Index = 0), OmyDWOC_su19 (1498 total; A-Index = 1498 and B-Index = 0), OmyPAHH_su18 (1198 total; A-Index = 1198 and B-Index = 0), and OmyWALL_su18 (1075 total; A-Index = 1075 and B-Index = 0). Almost all of these abundances were A-Index fish except for two stocks that represented both A- and B-Index (OmyDWOC_su18 and OmySFCR_su18).

There were two major stocks (abundance >1000) represented in the total estimated abundance (N=20,659) of natural origin (excluding adipose unclipped hatchery-origin fish) summer A-/B-Index steelhead passing Bonneville Dam in 2021 (Table 43). These stocks in order of decreasing magnitude were 07_MGILCS (12,610 A-Index; 480 B-Index), and 14_UPSALM (3,724 A-Index). This year the 07_MGILCS (480 B-Index) was observed to have more natural-origin B-Index abundance than was estimated for 10_SFCLWR (322 B-Index).

3208 **Table 41. Stock-specific abundance and run-timing by A-/B-Index categories of clipped hatchery-origin summer A-/B-Index steelhead passing Bonneville Dam in 2021.**

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	0			-	-	-	-	-	-	-
	Skamania	03_SKAMAN	2	377	1 – 806	212	199	224.25	188	233	7/31/2021	25
	Willamette	04_WILLAM				-	-	-	-	-	-	-
	Big White Salmon	05_BWSALM				-	-	-	-	-	-	-
	Klickitat	06_KLICKR	0			-	-	-	-	-	-	-
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	80	12,139	10526 – 14142	236	214	246	192	270	8/24/2021	32
	Yakima	08_YAKIMA	0			-	-	-	-	-	-	-
	upper Columbia	09_UPPCOL	16	3,059	1647 – 3915	225	206	240	190	265	8/13/2021	34
	SF Clearwater	10_SFCLWR	68	4,823	4076 – 6478	259	249	271	238	290	9/16/2021	22
	upper Clearwater	11_UPCLWR	0			-	-	-	-	-	-	-
	SF Salmon	12_SFSALM	0			-	-	-	-	-	-	-
	MF Salmon	13_MFSALM	0			-	-	-	-	-	-	-
	upper Salmon	14_UPSALM	150	15,325	12951 – 18497	246	236	258	197	274	9/3/2021	22
		A-INDEX Subtotal	316	35,723								
B-INDEX	Lower Columbia	02_LOWCOL										
	Skamania	03_SKAMAN		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	0	0	0 – 0	-	-	-	-	-	-	-
Yakima	08_YAKIMA										
upper Columbia	09_UPPCOL		0	0 – 0	-	-	-	-	-	-	-
SF Clearwater	10_SFCLWR	109	8,504	7275 – 8989	255	245	265	236	282	9/12/2021	
upper Clearwater	11_UPCLWR	0									
SF Salmon	12_SFSALM	0									
MF Salmon	13_MFSALM	0									
upper Salmon	14_UPSALM	1	0	0 – 0	-	-	-	-	-	-	-
	B-INDEX Subtotal	110	8,504								

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.

3213 Table 42. Stock-specific abundance and run-timing by A-/B-Index categories of unclipped hatchery-origin summer A-/B-Index steelhead passing Bonneville Dam in
3214 2021.

Size	Hatchery origin- Clipped		Sample N	Estimated abundance		Run-timing distribution							
	Reporting Group name	Reporting Group Code		Ordinal day								Interquartile	
				Mean	95% CI	Median	1st quartile	3rd quartile	5th percentile	95th percentile	Median date		range (days)
A-INDEX	Lower Columbia	02_LOWCOL											
	Skamania	03_SKAMAN											
	Willamette	04_WILLAM											
	Big White Salmon	05_BWSALM											
	Klickitat	06_KLICKR											
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	0	265	6 – 678	241	238	244	235	248	8/29/2021	6	
	Yakima	08_YAKIMA											
	upper Columbia	09_UPPCOL											
	SF Clearwater	10_SFCLWR	12	747	449 – 1079	266	258	279	238	297	9/23/2021	21	
	upper Clearwater	11_UPCLWR											
	SF Salmon	12_SFSALM											
	MF Salmon	13_MFSALM											
	upper Salmon	14_UPSALM	13	1,002	521 – 1330	250	242	260	236	281	9/7/2021	18	
		A-INDEX Subtotal	25	2,013									
B-INDEX	Lower Columbia	02_LOWCOL											
	Skamania	03_SKAMAN											
	Willamette	04_WILLAM											
	Big White Salmon	05_BWSALM											
	Klickitat	06_KLICKR											

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mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	0	0	0 – 0							
Yakima	08_YAKIMA										
upper Columbia	09_UPPCOL										
SF Clearwater	10_SFCLWR	11	853	706 – 1217	264	255	268	238	276	9/21/2021	13
upper Clearwater	11_UPCLWR										
SF Salmon	12_SFSALM										
MF Salmon	13_MFSALM										
upper Salmon	14_UPSALM	0	0	0 – 0							
	B-INDEX Subtotal	11	853								

3217 Table 43. Stock-specific abundance and run-timing by A-/B-Index categories of unclipped natural-origin summer A-/B-Index steelhead passing Bonneville Dam in 2021.

Size	Natural origin- No Clip		Sample N	Estimated abundance		Run-timing distribution						
	Reporting Group name	Reporting Group Code		Mean	95% CI	Ordinal day						Interquartile range (days)
						Median	1st quartile	3rd quartile	5th percentile	95th percentile	Median date	
A-INDEX	Lower Columbia	02_LOWCOL	3	297	0 – 692	223.5	204	265	189	286.7	8/11/2021	61
	Skamania	03_SKAMAN	-	-	-	-	-	-	-	-	-	-
	Willamette	04_WILLAM	-	-	-	-	-	-	-	-	-	-
	Big White Salmon	05_BWSALM	-	-	-	-	-	-	-	-	-	-
	Klickitat	06_KLICKR	2	234	0 – 631	216	200	227	188	290	8/4/2021	27
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	89	12,610	11078 – 13899	223	203	238	189	265	8/11/2021	35
	Yakima	08_YAKIMA	3	466	0 – 989	216	200	227	188	253	8/4/2021	27
	upper Columbia	09_UPPCOL	6	781	244 – 1396	234	209	243	190	259	8/22/2021	34
	SF Clearwater	10_SFCLWR	9	623	305 – 1126	249	241	252	236	260	9/6/2021	11
	upper Clearwater	11_UPCLWR	5	294	106 – 527	253	251	257	249	287	9/10/2021	6
	SF Salmon	12_SFSALM	3	146	0 – 294	265	261	276	257	294	9/22/2021	15
	MF Salmon	13_MFSALM	4	378	70 – 791	233	209	257	190	270	8/21/2021	48
	upper Salmon	14_UPSALM	29	3,724	2609 – 4851	226	206	244	189	267	8/14/2021	38
	A-INDEX Subtotal		153	19,553								
B-INDEX	Lower Columbia	02_LOWCOL	-	-	-	-	-	-	-	-	-	-
	Skamania	03_SKAMAN	-	-	-	-	-	-	-	-	-	-
	Willamette	04_WILLAM	-	-	-	-	-	-	-	-	-	-
	Big White Salmon	05_BWSALM	-	-	-	-	-	-	-	-	-	-
	Klickitat	06_KLICKR	-	-	-	-	-	-	-	-	-	-
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	3	480	0 – 960	237	217	242	192	247	8/25/2021	25

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	Yakima	08_YAKIMA	-	-	-	-	-	-	-	-	-	-
	upper Columbia	09_UPPCOL	-	-	-	-	-	-	-	-	-	-
	SF Clearwater	10_SFCLWR	8	322	121 – 550	257	252	262	249	293	9/14/2021	10
	upper Clearwater	11_UPCLWR	1	71	0 – 212	252	250	253	249	255	9/8/2021	3
	SF Salmon	12_SFSALM	2	93	0 – 186	259	257	260	256	262	9/16/2021	3
	MF Salmon	13_MFSALM	1	141	0 – 423	241	238	244	235	248	8/29/2021	6
	upper Salmon	14_UPSALM	-	-	-	-	-	-	-	-	-	-
		B-INDEX Subtotal	15	1,106								

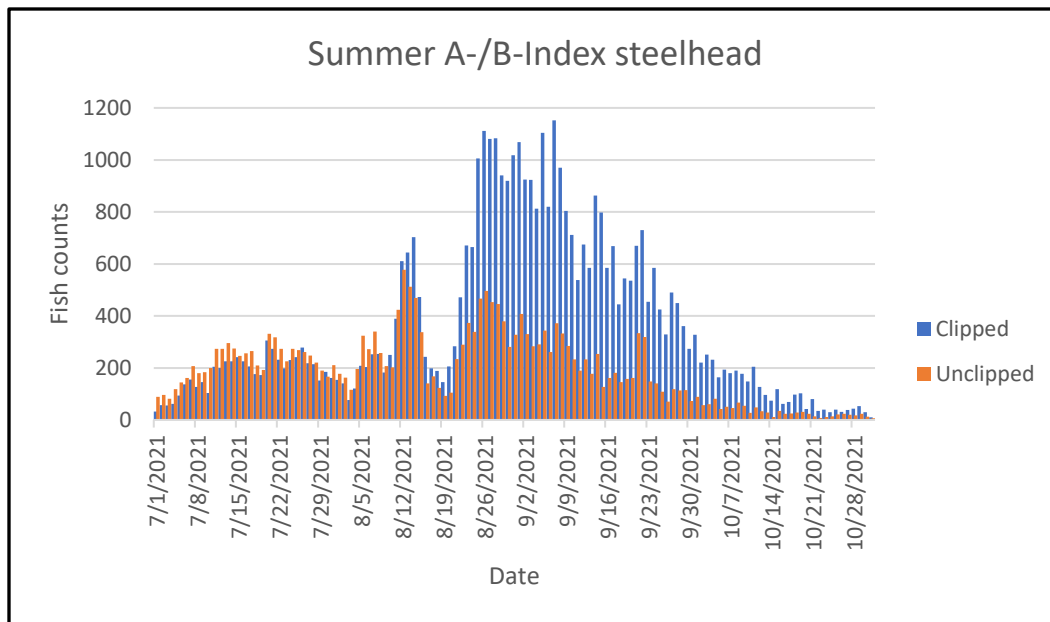


Figure 34. Daily passage of clipped (blue) and unclipped (red) steelhead at Bonneville Dam in 2021 during the summer A-/B-Index management period (source: <https://www.fpc.org>).

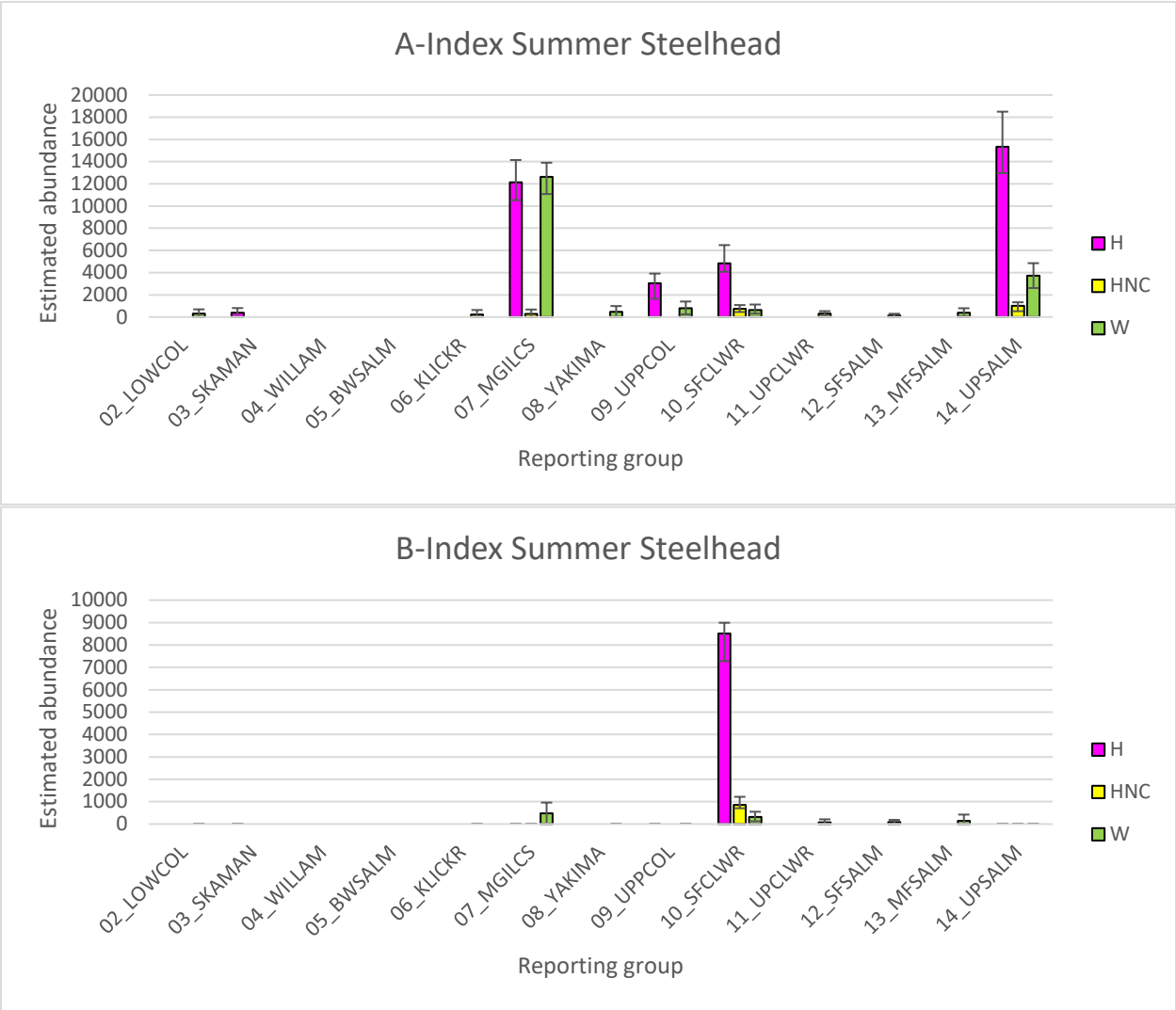


Figure 35. Estimated abundance (± 95% CI) of A-Index (<780mm FL, top) and B-Index (>=780mm FL, bottom) hatchery origin (clipped “H” and unclipped “HNC”) and natural-origin (“W”) steelhead assigned to genetic stock of origin that were sampled at Bonneville Dam in 2021.

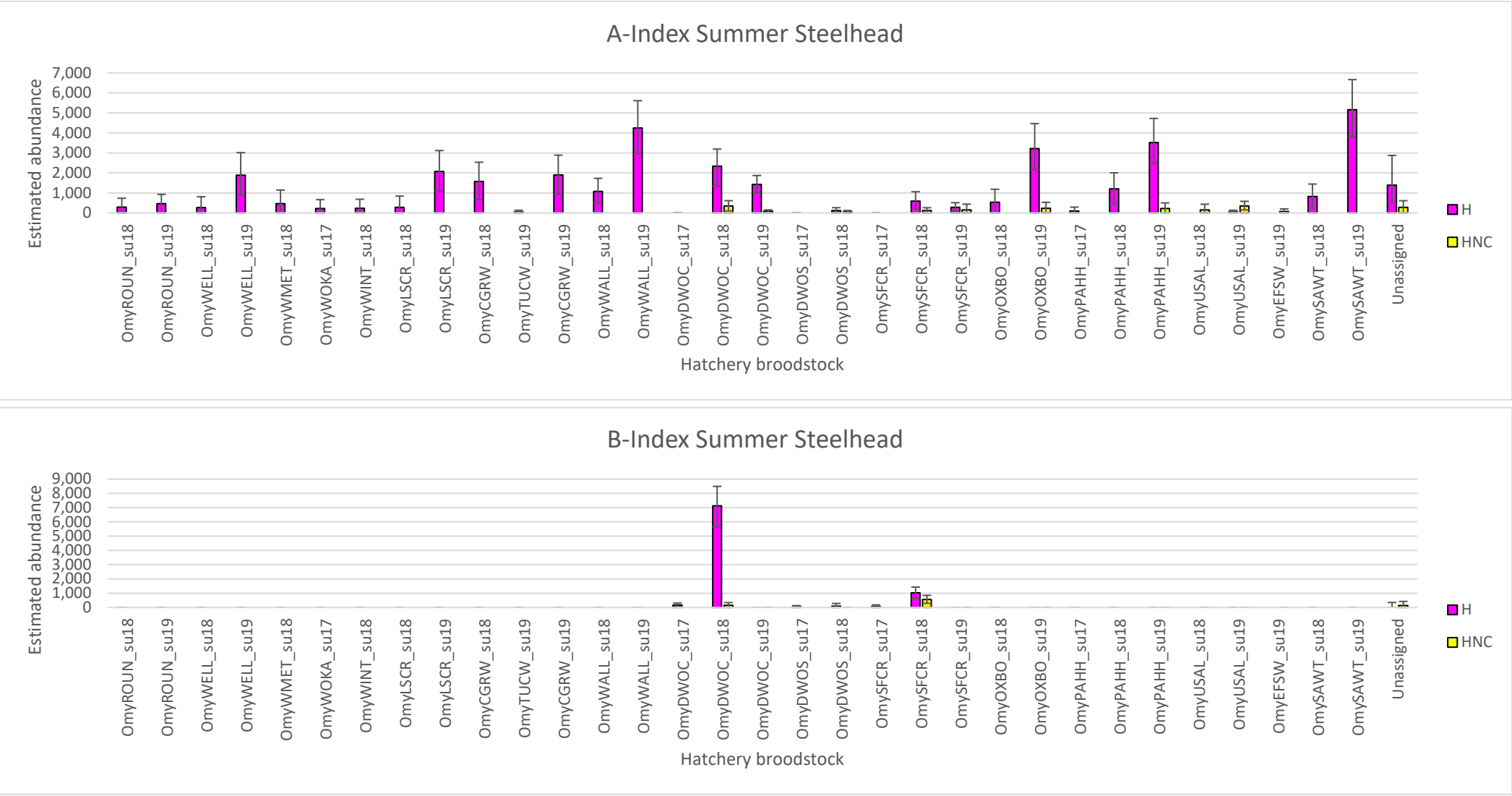


Figure 36. Estimated abundance (\pm 95% CI) of A-Index (<780mm FL, top) and B-Index (\geq 780mm FL, bottom) hatchery origin steelhead (adipose clipped and unclipped) assigned to broodstock of origin that were sampled at Bonneville Dam in 2021.

3232 **Key to broodstock collection is presented in Appendix 12.**

3233 **Table 44. Hatchery broodstock-specific estimated abundance of clipped and unclipped A-Index and B-Index PBT-assigned steelhead passing Bonneville Dam in 2021.**

					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
Round Butte	Deschutes River	07_MGILCS	OmyROUN_su18	2018	286	0 – 733	0	0 – 0				
Round Butte	Deschutes River	07_MGILCS	OmyROUN_su19	2019	462	0 – 927	0	0 – 0				
Wells Fish Hatchery	On Station	09_UPPCOL	OmyWELL_su18	2018	269	0 – 808	0	0 – 0				
Wells Fish Hatchery	WMET/WOKA/WOMA/WELLS	09_UPPCOL	OmyWELL_su19	2019	1,882	905 – 3014	0	0 – 0				
Wells Fish Hatchery	Methow	09_UPPCOL	OmyWMET_su18	2018	458	0 – 1144	0	0 – 0				
Wells Fish Hatchery	Okanogan	09_UPPCOL	OmyWOKA_su17	2017	221	0 – 663	0	0 – 0				
Winthrop NFH	Methow River	09_UPPCOL	OmyWINT_su18	2018	228	0 – 684	0	0 – 0				
Little Sheep Satellite	Imnaha	07_MGILCS	OmyLSCR_su18	2018	280	0 – 841	0	0 – 0				
Little Sheep Satellite	Imnaha	07_MGILCS	OmyLSCR_su19	2019	2,070	1071 – 3119	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	663 – 2534	0	0 – 0				
Lyons Ferry Hatchery	Tucannon	07_MGILCS	OmyTUCW_su19	2019	44	0 – 133	0	0 – 0				
Wallowa Fish Hatchery	Wallowa stock -released at Cottonwood and other Washington sites	07_MGILCS	OmyCGRW_su19	2019	1,895	947 – 2890	0	0 – 0				
Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGILCS	OmyWALL_su18	2018	1,075	468 – 1730	0	0 – 0				
Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGILCS	OmyWALL_su19	2019	4,243	2962 – 5614	0	0 – 0				
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su17	2017	0	0 – 0	162	41 – 307				
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su18	2018	2,337	1343 – 3192	7,122	5637 – 8490	352	101 – 612	158	0 – 344
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su19	2019	1,423	1020 – 1870	0	0 – 0	75	0 – 151	0	0 – 0
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 – 129				
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 – 260	94	0 – 283	41	0 – 120	0	0 – 0
Dworshak NFH	SF Clearwater	10_SFCLWR	OmySFCR_su17	2017	0	0 – 0	60	0 – 178				
Dworshak NFH	SF Clearwater	10_SFCLWR	OmySFCR_su18	2018	595	186 – 1058	1,024	628 – 1429	118	0 – 258	554	286 – 849
Dworshak NFH	SF Clearwater	10_SFCLWR	OmySFCR_su19	2019	280	106 – 511	0	0 – 0	146	0 – 437	0	0 – 0
Oxbow (IDFG)	Oxbow	14_UPSALM	OmyOXBO_su18	2018	536	0 – 1182	0	0 – 0				
Oxbow (IDFG)	Oxbow	14_UPSALM	OmyOXBO_su19	2019	3,221	2163 – 4467	0	0 – 0	227	0 – 529	0	0 – 0
Pahsimeroi	Pahsimeroi	14_UPSALM	OmyPAHH_su17	2017	96	0 – 289	0	0 – 0				
Pahsimeroi	Pahsimeroi	14_UPSALM	OmyPAHH_su18	2018	1,198	428 – 2005	0	0 – 0				
Pahsimeroi	Pahsimeroi	14_UPSALM	OmyPAHH_su19	2019	3,520	2462 – 4725	0	0 – 0	216	0 – 499	0	0 – 0
Pahsimeroi	Upper Salmon	14_UPSALM	OmyUSAL_su18	2018					145	0 – 436	0	0 – 0
Pahsimeroi	Upper Salmon	14_UPSALM	OmyUSAL_su19	2019	44	0 – 132	0	0 – 0	348	148 – 579	0	0 – 0
Sawtooth	EF Salmon	14_UPSALM	OmyEFSW_su19	2019					66	0 – 198	0	0 – 0
Sawtooth	Sawtooth	14_UPSALM	OmySAWT_su18	2018	821	252 – 1443	0	0 – 0				
Sawtooth	Sawtooth	14_UPSALM	OmySAWT_su19	2019	5,164	3825 – 6668	0	0 – 0				
#N/A	#N/A	#N/A	Unassigned	#N/A	1,384	538 – 2873	0	0 – 351	278	0 – 610	141	0 – 423
					TOTAL	35,723	8,504		2,013		853	

3234 **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
3235 passed the Bonneville Dam at the fish counting window. Key to broodstock collection is presented in Appendix 12.

Run-timing of steelhead stocks in 2021

We were able to characterize the run-timing distributions at the broodstock level for the clipped (Figure 37) and unclipped (Figure 38) 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 4/1/2021 – 6/30/ 2021, and the summer A-/B-Index period begins on 7/1/2021 and lasts until 10/31/2021. 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 37). There were a total of 30 different clipped hatchery broodstocks and of these 30, there were 24 broodstocks (OmyWELL_su19, OmyWALL_su19, OmyLSCR_su19, OmyWALL_su18, OmyPAHH_su18, OmySAWT_su18, OmyOXBO_su19, OmyPAHH_su19, OmySAWT_su19, OmyPAHH_su17, OmyDWOS_su18, OmyDWOC_su18, OmySFCR_su18, OmyDWOS_su17, OmyTUCW_su19, OmyUSAL_su19, OmySFCR_su19, OmyDWOC_su17, OmySFCR_su17, and OmyDWOC_su19) that had median dates that were observed after August 25th in 2021. For three broodstocks in which both A-Index and B-Index were represented, the B-Index stock had a later median date in all but one pair. For the unclipped stocks arriving in the A-/B-Index period, there were 11 unique broodstocks and all of them had a median run date after August 25th (Figure 38).

We characterized the run-timing distributions for natural-origin steelhead stocks (Figure 39); the patterns generally are consistent with past years. The late arriving stocks with median dates on or after August 25th were 13_MFSALM (B-Index), 10_SFCLWR (both A-Index and B-Index), 11_UPCLWR (both A-Index and B-Index), and 12_SFSALM (both A-Index and B-Index). For the five 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.

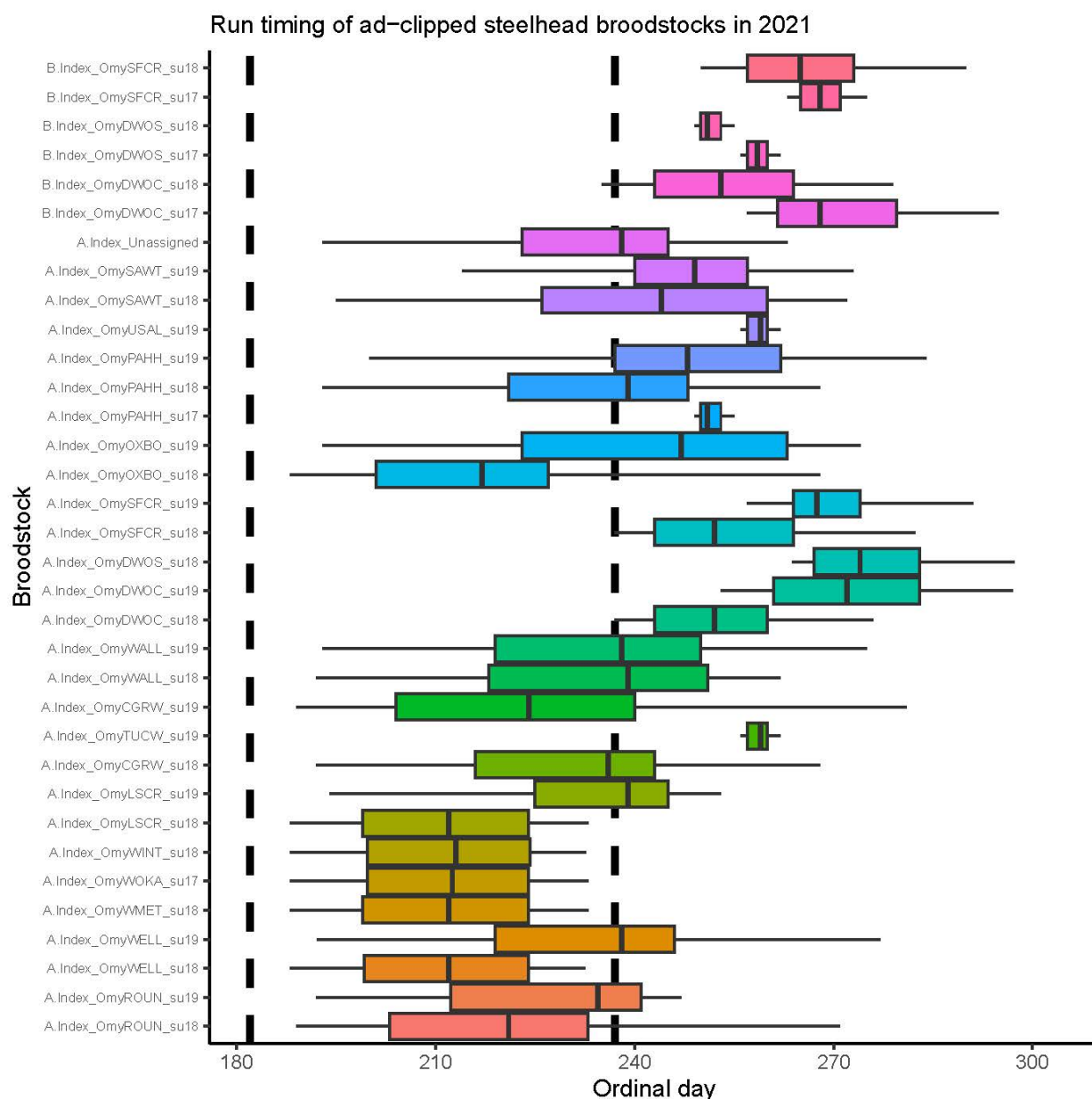


Figure 37. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for clipped hatchery-origin steelhead that were sampled at Bonneville Dam in 2021 and reported by A-Index and B-Index size category.

Key to broodstock collection is presented in Appendix 12.

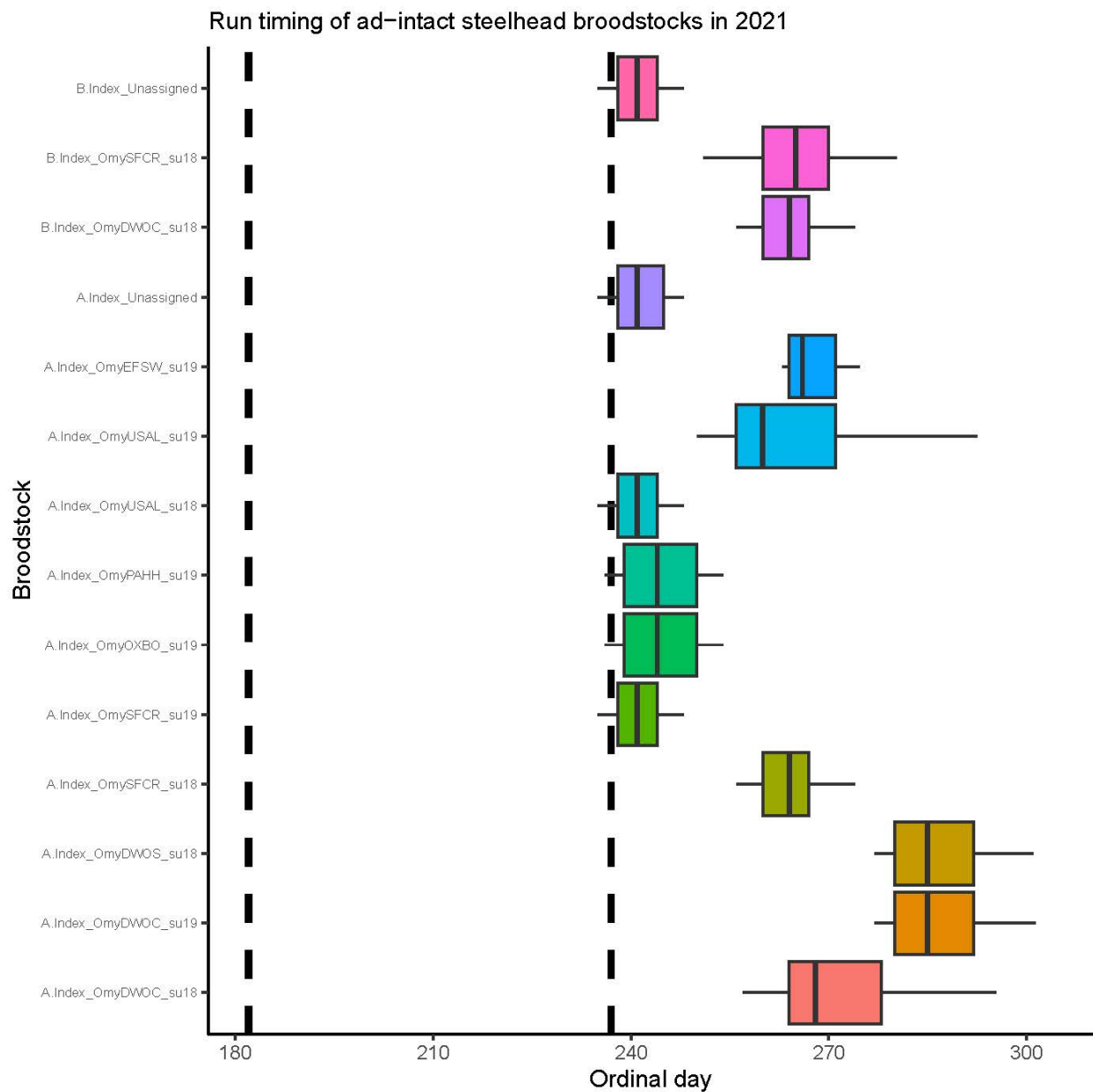


Figure 38. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for unclipped hatchery-origin steelhead that were sampled at Bonneville Dam in 2021 and reported by A-Index and B-Index size category.

Key to broodstock collection is presented in Appendix 12.

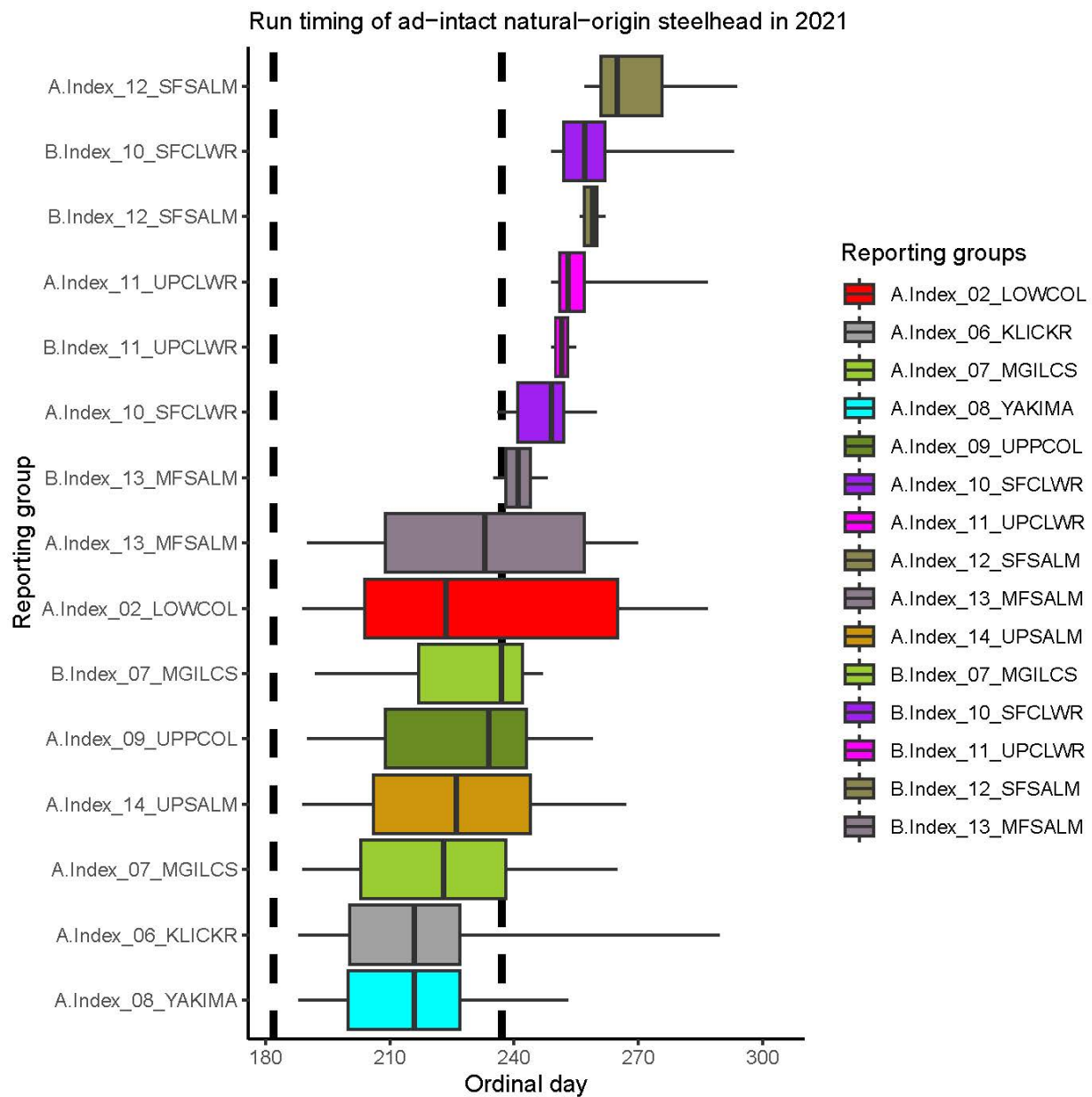


Figure 39. Reporting group level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for natural-origin steelhead (unclipped hatchery-origin fish excluded) that were sampled at Bonneville Dam in 2021 and split by A-Index and B-Index size category.

Estimated abundance and run-timing of Sockeye salmon stocks in 2021

Daily passage of Sockeye salmon at Bonneville Dam in 2021 is provided in Figure 40. Stock abundance for sockeye salmon was estimated over a course of 21 statistical weeks (i.e. weeks 18 – 39). A total of 1,451 sockeye salmon were sampled at Bonneville Dam in 2021 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 35). The Okanogan stock had the highest relative abundance (105,650), followed by the Wenatchee (41,269) (Table 45). This year there were a small number of sockeye estimated from Snake River (1,311). The Lake Billy Chinook stock had zero estimated abundance (Table 45, Figure 41). The reintroduced stock from Yakima River had a non-zero abundance and was estimated at 3,535 fish in 2021.

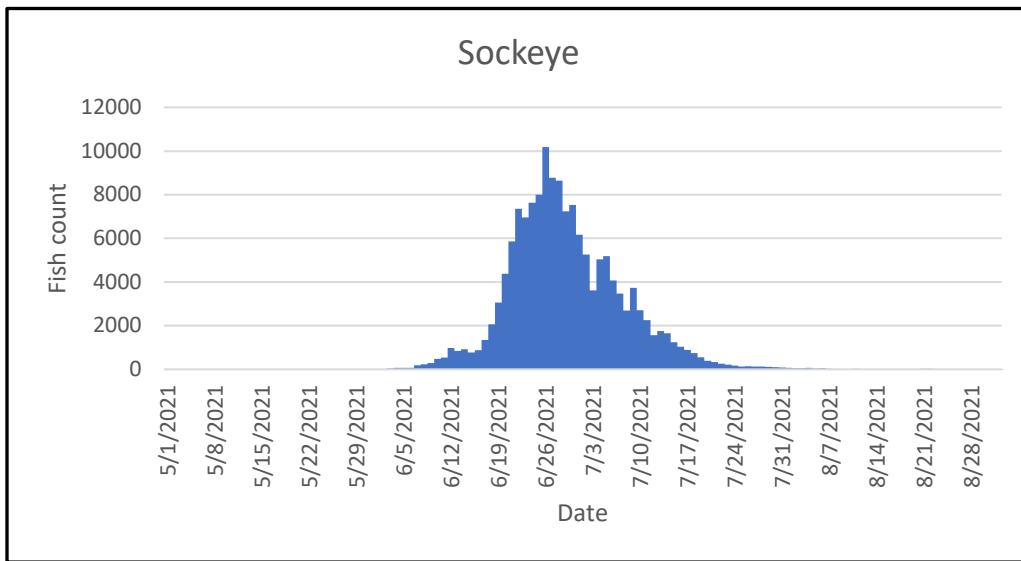
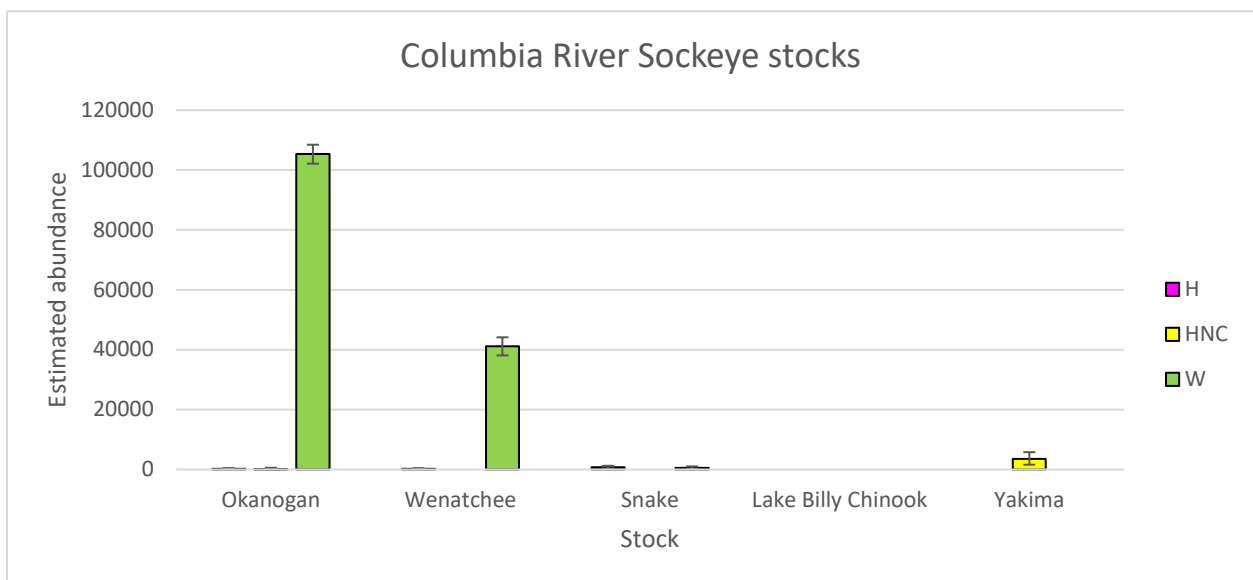


Figure 40. Daily passage of sockeye at Bonneville Dam in 2021 (source: <https://www.fpc.org>).



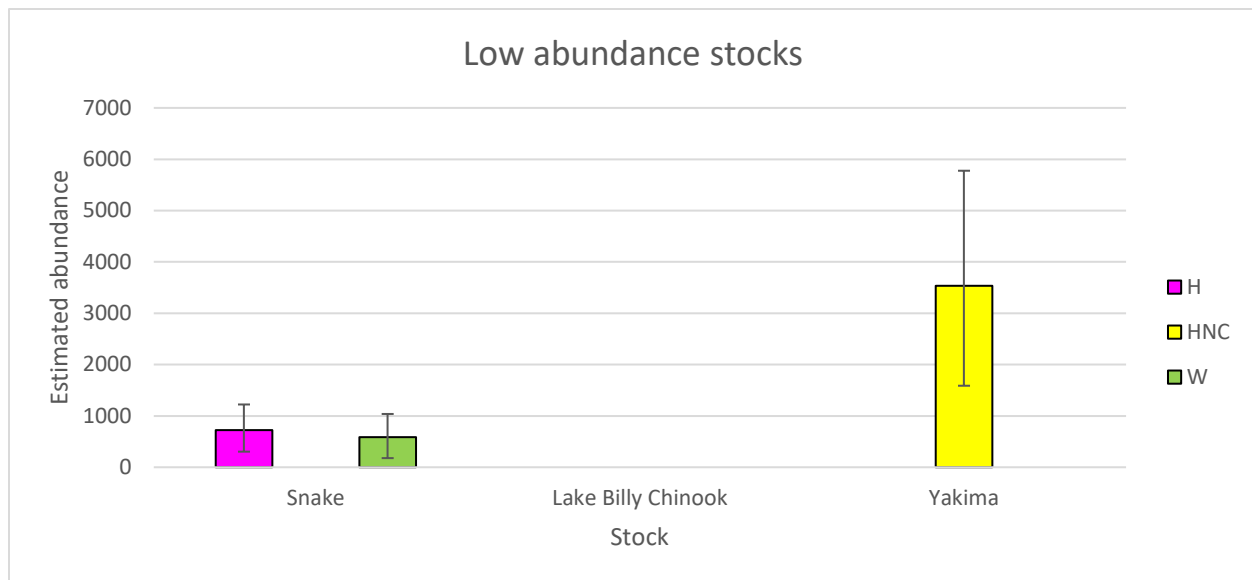


Figure 41. Estimated abundance (\pm 95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2021.

We characterized the run-timing distributions for all detected sockeye salmon stocks (Figure 42). The Wenatchee, Okanogan, Snake, and Yakima stocks had nearly identical run timing distributions each with an average median date on 06/29/21 (Figure 42).

3303 **Table 45. Estimated abundance of sockeye salmon stocks passing Bonneville Dam in 2021.**

Reporting Group name	Estimated abundance					
	H		HNC		W	
	Est.	95% CI	Est.	95% CI	Est.	95% CI
Okanogan	189	0 – 441	112	0 – 561	105,349	102111 – 108455
Wenatchee	178	0 – 429			41,091	38101 – 44134
Snake	725	304 – 1223			586	178 – 1038
Lake Billy Chinook						
Yakima			3,535	1588 – 5776		
Total	1,092		3,647		147,026	

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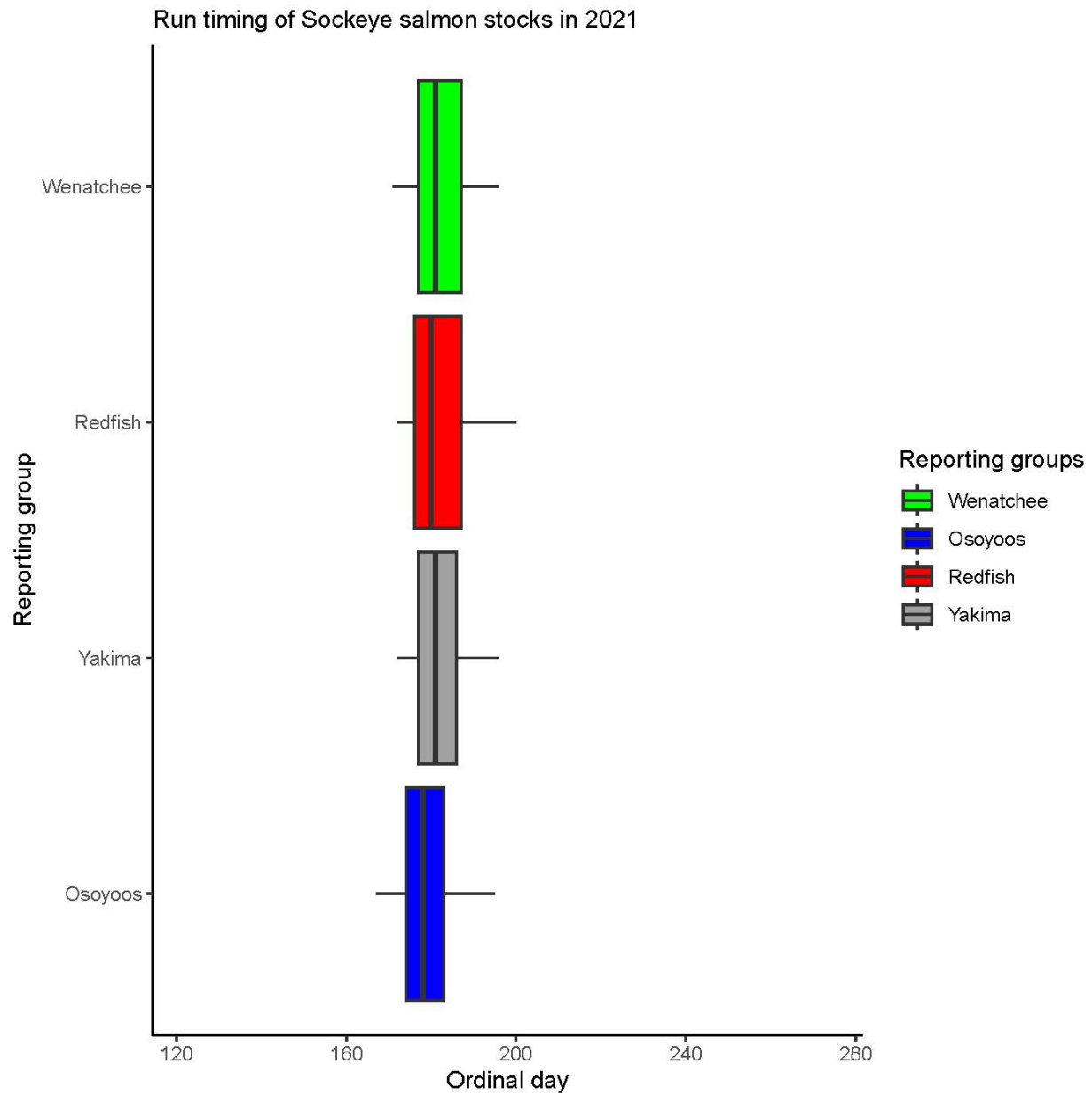


Figure 42. Run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for the major stocks of sockeye salmon that were sampled at Bonneville Dam in 2021 and assigned to stock of origin.

In-season analysis of Chinook salmon passing Bonneville Dam in 2022

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 2022 across all management periods (Table 32). The first report was distributed to members of the U.S. v OR TAC on May 9, 2022. 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 2021. 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 2,838 adult-sized Chinook Salmon were collected and analyzed for the 2022 in-season reports (Table 46). 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 7, 2022 provided sub-totals for each stock that were broken out by management period (clipped hatchery-origin stocks, Table 47; unclipped hatchery-origin stocks, Table 48; natural-origin stocks, Table 49). 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 49) and upper Columbia River spring Chinook Salmon stocks (Reporting group 10_UCOLSP, Table 49). 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 76 unique hatchery broodstocks in 2022 (Table 50). The total estimated abundances of these clipped and unclipped broodstocks were comprised of 23.5% Snake River and 73.2% of hatcheries from the rest of the Columbia River above Bonneville Dam (Figure 43). 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 2022. 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 51). In fact, in 2022, the percentage of adipose-clipped fish abundance that were estimated to be PBT broodstock ranged from 95 – 100%, 75 – 100%, and 88 – 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. However, the PBT baseline has attained higher coverage since then (Appendix 11).

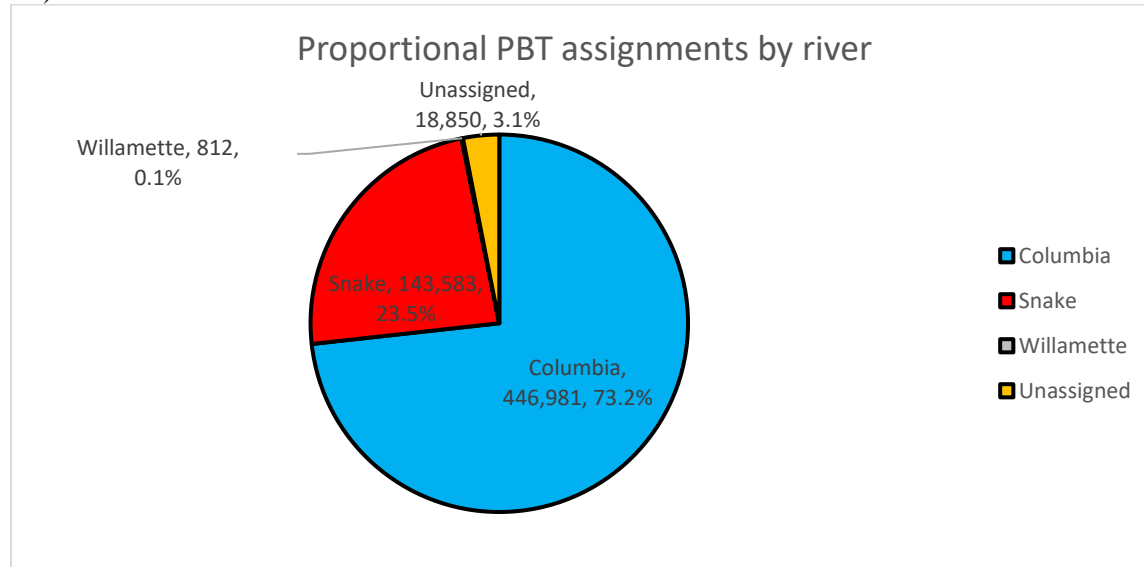


Figure 43. Proportion of hatchery broodstocks from the Snake River versus the rest of the Columbia River above Bonneville Dam in 2022.

3376 **Table 46. The sample sizes of Chinook salmon at the Bonneville Dam AFF during the**
 3377 **spring, summer, and fall management periods of 2022.**

		Statistical week	TAC		Sample (N)							
			clip count	unclip count	Clipped		Non-clipped		Subtotal		Rate	
					GSI	PBT	GSI	PBT	clip	unclip	clip	unclip
Management period	Spring	1-16	1,760	196	0	0	0	0	0	0	0.00%	0.00%
		17	3,690	611		21	1	2	21	3	0.57%	0.49%
		18	27,184	4,546	23	148	19	22	171	41	0.63%	0.90%
		19	38,627	7,978	17	130	33	11	147	44	0.38%	0.55%
		20	19,711	6,370	12	104	33	12	116	45	0.59%	0.71%
		21	12,299	6,123	7	83	49	15	90	64	0.73%	1.05%
		22	7,514	5,432	7	73	81	26	80	107	1.06%	1.97%
		23	6,949	5,360	7	69	50	13	76	63	1.09%	1.18%
		24	8,801	5,151	10	78	45	13	88	58	1.00%	1.13%
		25	3,234	2,201		6	3	1	6	4	0.19%	0.18%
	Summer	25	3254	1604	1	14	6	3	15	9	0.46%	0.56%
		26	13740	3939		7	4	1	7	5	0.05%	0.13%
		27	18723	8489		6	1	1	6	2	0.03%	0.02%
		28	8800	2355	3	15	5	4	18	9	0.20%	0.38%
		29	4865	1463	4	47	13	4	51	17	1.05%	1.16%
		30	2475	1109	1	24	8	6	25	14	1.01%	1.26%
		31	1572	2422	4	10	11	3	14	14	0.89%	0.58%
	Fall	32	994	1,695		7	2	2	7	4	0.70%	0.24%
		33	2,971	2,750	1	9	4	7	10	11	0.34%	0.40%
		34	5,356	8,387	3	13	7	14	16	21	0.30%	0.25%
		35	20,838	20,206	1	21	7	13	22	20	0.11%	0.10%
		36	50,324	46,231	7	35	74	49	42	123	0.08%	0.27%
		37	97,033	89,635	15	85	52	82	100	134	0.10%	0.15%
		38	48,760	48,090	20	82	58	90	102	148	0.21%	0.31%
		39	24,677	11,314	15	96	97	86	111	183	0.45%	1.62%
		40	6,741	6,069	3	42	105	56	45	161	0.67%	2.65%
		41	2,954	4,285	4	31	80	20	35	100	1.18%	2.33%
		42-44	971	2,079	1	6	6		7	6	0.72%	0.29%
		Total	444,819	306,088	166	1,262	854	556	1,428	1,410	0.32%	0.46%

3378 Note: The fish counts indicate the number of adult-sized Chinook Salmon at the fish ladder
 3379 windows at Bonneville Dam and the sample (N) indicates the numbers of adult-sized Chinook
 3380 Salmon (>560 mm fork length) that were collected at the AFF. TAC provides estimates of the
 3381 total clipped an unclipped adult abundance. The AFF sample is broken into adipose-clipped and
 3382 non-clipped categories and then further indicate whether a PBT assignment (PBT) was
 3383 confirmed or if it was not assigned with PBT (GSI). Sample rate relates the total sample for a
 3384 particular stratum to the total fish counted at the window. The boxes around statistical weeks
 3385 indicate the breakpoints in the weekly strata.

3386 **Table 47. Preliminary in-season reporting of clipped hatchery-origin stock-specific abundance estimates of adult-sized**
3387 **Chinook Salmon passing Bonneville Dam across all management periods in 2022.**

		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	–					0
West Cascade Spring	Spring	02_WCASSP	2,611	–	1,182	0 – 2504			3,794
West Cascade Fall	Fall	03_WCASFA							0
Willamette	Spring	04_WILLAM	9	–	67	0 – 189	812	31 – 2599	888
Spring Creek Tule	Fall	05_SPCRTU					115,071	104159 – 125613	115,071
Klickitat	Spring	06_KLICKR	1,771	–					1,771
Deschutes spring	Spring	07_DESCSP	5,767	–	1,045	0 – 2875			6,812
John Day	Spring	08_JOHNDR							0
Yakima	Spring	09_YAKIMA	2,052	–					2,052
Upper Columbia spring	Spring	10_UCOLSP	18,054	–	1,564	0 – 7637			19,619
Tucannon	Spring	11_TUCANO							0
Hells Canyon	Spring/Summer	12_HELLSC	49,879	–	2,026	0 – 3025			51,904
South Fork Salmon	Spring/Summer	13_SFSALM	3,413	–	1,043	0 – 1959			4,456
Chamberlain Creek	Spring/Summer	14_CHMBLN	9	–					9
Middle Fork Salmon	Spring/Summer	15_MFSALM	0	–					0
Upper Salmon	Spring/Summer	16_UPSALM	5,879	–	968	0 – 3871			6,847
Deschutes fall	Fall	17_DESCFA							0
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	13,706	–	44,978	35990 – 49339	63,490	58841 – 68183	122,174
Snake River fall	Fall	19_SRFALL			555	270 – 680	36,796	32876 – 46167	37,351
Bonneville Pool spring	Spring	20_BONPOOLSP	22,418	–					22,418
Umatilla spring	Spring	21_UMATILLASP	4,125	–					4,125
Bonneville Pool fall	Fall	22_BONPOOLFA					31,231	24336 – 36779	31,231
Umatilla fall	Fall	23_UMATILLAFA					14,222	9299 – 16881	14,222
Total			129,694		53,429		261,622		444,745

3388 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
3389 31) management periods and the cumulative total through the window counts on Nov 1, 2022 are provided. Bonneville 2022 spring,
3390 summer, and fall management period Chinook PBT/GSI analyses that corresponds with statistical weeks 1 – 25 (01/01/22-06/15/22:
3391 spring), 25 – 31 (6/16/22-7/31/22:summer) and 31 – 44 (8/1/2022-11/1/2022:fall).
3392
3393

3394 **Table 48. Preliminary in-season reporting of unclipped hatchery-origin stock-specific abundance estimates of adult-sized**
3395 **Chinook Salmon passing Bonneville Dam across all management periods in 2022.**

		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.
			Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean
Youngs Bay	Spring	01_YOUNGS							0
West Cascade Spring	Spring	02_WCASSP	235	–					235
West Cascade Fall	Fall	03_WCASFA							0
Willamette	Spring	04_WILLAM							0
Spring Creek Tule	Fall	05_SPCRTU					52,233	46409 – 59290	52,233
Klickitat	Spring	06_KLICKR	122	–					122
Deschutes spring	Spring	07_DESCSP							0
John Day	Spring	08_JOHNDR							0
Yakima	Spring	09_YAKIMA	121	–					121
Upper Columbia spring	Spring	10_UCOLSP	3,664	–					3,664
Tucannon	Spring	11_TUCANO							0

Hells Canyon	Spring/Summer	12_HELLSC	4,250	–					4,250
South Fork Salmon	Spring/Summer	13_SFSALM	742	–	111	0 – 328			853
Chamberlain Creek	Spring/Summer	14_CHMBLN							0
Middle Fork Salmon	Spring/Summer	15_MFSALM							0
Upper Salmon	Spring/Summer	16_UPSALM	537	–					537
Deschutes fall	Fall	17_DESCFA							0
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	1,628	–	7,580	7531 – 8961	37,921	32594 – 45399	47,129
Snow River fall	Fall	19_SRFALL			508	131 – 769	39,689	35063 – 42188	40,197
Bonneville Pool spring	Spring	20_BONPOOLSP	1,238	–					1,238
Umatilla spring	Spring	21_UMATILLASP	630	–					630
Bonneville Pool fall	Fall	22_BONPOOLFA					13,869	10412 – 20369	13,869
Umatilla fall	Fall	23_UMATILLAFA					404	6 – 741	404
Total			13,167		8,199		144,115		165,481

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 01, 2022 are provided.

Table 49. Preliminary in-season reporting of natural-origin stock-specific abundance estimates of adult-sized Chinook Salmon passing Bonneville Dam across all management periods in 2022.

		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
West Cascade Spring	Spring	02_WCASSP	142	0 – 425					142
West Cascade Fall	Fall	03_WCASFA					38	0 – 113	38
Willamette	Spring	04_WILLAM	236	0 – 473	1,311	0 – 2653	590	0 – 1770	2,137
Spring Creek Tule	Fall	05_SPCRTU					14,435	9011 – 19648	14,435
Klickitat	Spring	06_KLICKR	237	0 – 566					237
Deschutes spring	Spring	07_DESCSP	769	277 – 1345					769
John Day	Spring	08_JOHNDR	579	122 – 1091					579
Yakima	Spring	09_YAKIMA	1,905	1124 – 2713					1,905
Upper Columbia spring	Spring	10_UCOLSP	5,634	4322 – 7008	1,311	0 – 3278			6,945
Tucannon	Spring	11_TUCANO	122	0 – 365					122
Hells Canyon	Spring/Summer	12_HELLSC	8,264	6805 – 9880	656	0 – 1967			8,920
South Fork Salmon	Spring/Summer	13_SFSALM	3,316	2516 – 4218	1,967	656 – 3933			5,283
Chamberlain Creek	Spring/Summer	14_CHMBLN	349	146 – 597					349
Middle Fork Salmon	Spring/Summer	15_MFSALM	2,222	1411 – 3034					2,222
Upper Salmon	Spring/Summer	16_UPSALM	2,401	1666 – 3184	656	0 – 1967			3,056
Deschutes fall	Fall	17_DESCFA					3,873	1942 – 6109	3,873
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	4,586	3586 – 5511	6,459	3876 – 9200	59,802	51973 – 67560	70,847
Snake River fall	Fall	19_SRFALL			824	380 – 1303	17,886	13051 – 22757	18,710
Total			30,762		13,182		96,623		140,568

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 01, 2022 are provided.

3406 **Table 50. The estimated abundances of the clipped and unclipped adult-sized Chinook salmon assigned to PBT hatchery**
3407 **broodstock that passed Bonneville Dam in 2022 (1/01/2021 – 11/01/2022).**

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_sp18	2018	02_WCASSP	2,611	1472 – 3764	235	0 – 704	2,846
	01Spring	Klickitat Hatchery	OtsKLIC_seg_sp18	2018	06_KLICKR	1,771	988 – 2702	122	0 – 367	1,893
	01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp18	2018	07_DESCSP	3,406	2067 – 4753			3,406
	01Spring	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp17	2017	07_DESCSP	214	0 – 627			214
	01Spring	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp18	2018	07_DESCSP	2,039	1099 – 3007			2,039
	01Spring	Yakima River Roza Dam	OtsYRRD_int_sp18	2018	09_YAKIMA	1,686	825 – 2640	121	0 – 362	1,806
	01Spring	Yakima River Roza Dam	OtsYRRD_seg_sp18	2018	09_YAKIMA	358	94 – 792			358
	01Spring	Eastbank Fish Hatchery	OtsEAST_seg_sp18	2018	10_UCOLSP	1,381	636 – 2342	2,001	1300 – 2832	3,382
	01Spring	Eastbank Fish Hatchery	OtsEAST_seg_sp19	2019	10_UCOLSP			133	0 – 398	133
	01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp17	2017	10_UCOLSP	305	0 – 916			305
	01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp18	2018	10_UCOLSP	11,663	8522 – 14181	534	0 – 1161	12,197
	01Spring	Methow Fish Hatchery	OtsMETH_seg_sp18	2018	10_UCOLSP	219	0 – 652	933	310 – 1562	1,151
	01Spring	Winthrop National Fish Hatchery	OtsWINT_seg_sp18	2018	10_UCOLSP	3,638	2029 – 5265	64	0 – 191	3,701
	01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp18	2018	12_HELLSC	6,088	4361 – 7889	365	0 – 730	6,453

01Spring	Clearwater Fish Hatchery	OtsPOWP_se g_sp18	2018	12_HELLSC	265	0 – 650	612	204 – 1089	877
01Spring	Clearwater Fish Hatchery	OtsCLWH_se g_sp19	2019	12_HELLSC	136	0 – 409			136
01Spring	Dworshak National Fish Hatchery	OtsDWOR_se g_sp17	2017	12_HELLSC			51	0 – 153	51
01Spring	Dworshak National Fish Hatchery	OtsKOOS_se g_sp18	2018	12_HELLSC	9,42 9	7346 – 11644	835	321 – 1425	10,2 65
01Spring	Dworshak National Fish Hatchery	OtsDWOR_se g_sp18	2018	12_HELLSC	11,8 21	9390 – 14251	953	405 – 1512	12,7 74
01Spring	Dworshak National Fish Hatchery	OtsKOOS_se g_sp19	2019	12_HELLSC	98	0 – 293			98
01Spring	Lookingglass Fish Hatchery	OtsLOOK_se g_sp18	2018	12_HELLSC	3,91 6	2345 – 5353	479	0 – 980	4,39 6
01Spring	Nez Perce	OtsNPFH_seg _sp18	2018	12_HELLSC			296	0 – 684	296
01Spring	Rapid River Fish Hatchery	OtsRAPH_se g_sp17	2017	12_HELLSC	700	0 – 1399			700
01Spring	Rapid River Fish Hatchery	OtsRAPH_se g_sp18	2018	12_HELLSC	16,2 95	13331 – 18919	659	246 – 1210	16,9 54
01Spring	Carson National Fish Hatchery	OtsCARS_se g_sp17	2017	20_BONPO OLSP	173	0 – 518			173
01Spring	Carson National Fish Hatchery	OtsCARS_se g_sp18	2018	20_BONPO OLSP	12,0 70	9717 – 14668	849	363 – 1396	12,9 19
01Spring	Little White Salmon National Fish Hatchery	OtsLWSN_se g_sp18	2018	20_BONPO OLSP	10,1 75	7881 – 12686	389	130 – 777	10,5 64
01Spring	Umatilla Fish Hatchery	OtsUMAT_se g_sp18	2018	21_UMATI LLASP	4,12 5	2676 – 5727	534	123 – 1043	4,66 0
01Spring	Umatilla Fish Hatchery	OtsUMAT_se g_sp19	2019	21_UMATI LLASP			95	0 – 286	95
01Spring	Lookingglass Fish Hatchery	OtsIMNW_se g_ss17	2017	12_HELLSC	324	0 – 744			324
01Spring	Lookingglass Fish Hatchery	OtsIMNW_se g_ss18	2018	12_HELLSC	508	135 – 972			508

01Spring	Lookingglass Fish Hatchery	OtsIMNW_se g_ss19	2019	12_HELLSC	133	0 – 399			133
01Spring	McCall Fish Hatchery	OtsMCCA_se g_ss18	2018	13_SFSAL M	3,21 6	2315 – 4197	485	199 – 803	3,70 1
01Spring	McCall Fish Hatchery	OtsJHNW_int _ss18	2018	13_SFSAL M			136	0 – 307	136
02Spring/ Summer	McCall Fish Hatchery	OtsMCCA_se g_ss19	2019	13_SFSAL M			121	0 – 364	121
02Spring/ Summer	Pahsimeroi Fish Hatchery	OtsPAHH_se g_ss18	2018	16_UPSAL M	2,36 4	1528 – 3168	250	51 – 493	2,61 4
02Spring/ Summer	Sawtooth Fish Hatchery	OtsSAWT_se g_ss18	2018	16_UPSAL M	3,30 6	2176 – 4588	288	0 – 615	3,59 3
02Spring/ Summer	Chief Joseph Hatchery	OtsCHJO_seg _su16	2016	18_UCOLSF	92	0 – 277			92
02Spring/ Summer	Chief Joseph Hatchery	OtsCHJO_int _su17	2017	18_UCOLSF	1,56 2	798 – 2302	382	0 – 764	1,94 4
02Spring/ Summer	Chief Joseph Hatchery	OtsCHJO_seg _su17	2017	18_UCOLSF	1,33 4	667 – 2040	225	0 – 509	1,56 0
02Spring/ Summer	Eastbank Fish Hatchery	OtsEAST_seg _su17	2017	18_UCOLSF	2,76 8	1988 – 3638			2,76 8
03Summer	Eastbank Fish Hatchery	OtsEAST_seg _su18	2018	18_UCOLSF	1,81 3	1089 – 2595	205	0 – 444	2,01 8
03Summer	Entiat National Fish Hatchery	OtsENFH_se g_su17	2017	18_UCOLSF	2,44 4	1568 – 3368			2,44 4
03Summer	Entiat National Fish Hatchery	OtsENFH_se g_su18	2018	18_UCOLSF	1,66 3	873 – 2414			1,66 3
03Summer	Wells Fish Hatchery	OtsWELL_se g_su16	2016	18_UCOLSF	91	0 – 274			91
03Summer	Wells Fish Hatchery	OtsWELL_se g_su17	2017	18_UCOLSF	909	414 – 1425	362	96 – 723	1,27 1
03Summer	Wells Fish Hatchery	OtsWELL_se g_su18	2018	18_UCOLSF	737	265 – 1302	454	104 – 888	1,19 1
03Summer	Wells Fish Hatchery	OtsWELL_se g_su19	2019	18_UCOLSF	256	0 – 639			256

	#N/A	#N/A	Unassigned	#N/A	#N/A	1,59 2	523 – 4914			1,59 2
			Spring Subtotal			129, 694		13,1 67		142, 861
Summer	01Spring	Parkdale Fish Facility	OtsPARK_se g_sp18	2018	02_WCASS P	1,18 2	0 – 3500			1,18 2
	01Spring	Round Butte Fish Hatchery	OtsRBFH_se g_sp19	2019	07_DESCSP	1,04 5	0 – 3066			1,04 5
	01Spring	Leavenworth National Fish Hatchery	OtsLNFH_se g_sp18	2018	10_UCOLSP	1,56 4	0 – 4089			1,56 4
	01Spring	Dworshak National Fish Hatchery	OtsKOOS_se g_sp18	2018	12_HELLSC	1,01 2	0 – 3029			1,01 2
	02Spring/ Summer	Lookingglass Fish Hatchery	OtsIMNW_se g_ss18	2018	12_HELLSC	1,01 3	0 – 2992			1,01 3
	02Spring/ Summer	McCall Fish Hatchery	OtsMCCA_se g_ss18	2018	13_SFSAL M	977	0 – 2922			977
	02Spring/ Summer	McCall Fish Hatchery	OtsJHNW_int _ss19	2019	13_SFSAL M			111	0 – 333	111
	02Spring/ Summer	Sawtooth Fish Hatchery	OtsSAWT_se g_ss18	2018	16_UPSAL M	968	0 – 2903			968
	03Summer	Chief Joseph Hatchery	OtsCHJO_seg _su16	2016	18_UCOLSF	974	0 – 2922			974
	03Summer	Chief Joseph Hatchery	OtsCHJO_int _su17	2017	18_UCOLSF	3,32 8	787 – 6430			3,32 8
	03Summer	Chief Joseph Hatchery	OtsCHJO_seg _su17	2017	18_UCOLSF	1,26 5	108 – 3272	726	0 – 2177	1,99 1
	03Summer	Chief Joseph Hatchery	OtsCHJO_int _su18	2018	18_UCOLSF	99	0 – 297			99
	03Summer	Chief Joseph Hatchery	OtsCHJO_seg _su19	2019	18_UCOLSF	996	0 – 2981			996
	03Summer	Chief Joseph Hatchery	OtsCHJO_int _su19	2019	18_UCOLSF	101	0 – 303			101
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg _su16	2016	18_UCOLSF	101	0 – 302			101

	03Summer	Eastbank Fish Hatchery	OtsEAST_seg _su17	2017	18_UCOLSF	4,17 9	1194 – 7217	679	0 – 2036	4,85 7
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg _su18	2018	18_UCOLSF	16,7 54	12054 – 21765	2,98 0	997 – 4968	19,7 34
	03Summer	Entiat National Fish Hatchery	OtsENFH_se g_su18	2018	18_UCOLSF	7,56 0	3360 – 11656	2,72 4	859 – 5156	10,2 83
	03Summer	Wells Fish Hatchery	OtsWELL_se g_su17	2017	18_UCOLSF	3,95 3	1392 – 6941			3,95 3
	03Summer	Wells Fish Hatchery	OtsWELL_se g_su18	2018	18_UCOLSF	4,10 6	1414 – 7252	135	0 – 406	4,24 1
	03Summer	Wells Fish Hatchery	OtsWELL_se g_su19	2019	18_UCOLSF	1,56 2	297 – 3497	222	0 – 555	1,78 4
	04Fall	Priest Rapids Hatchery	OtsPRIE_seg _fa19	2019	18_UCOLSF			115	0 – 346	115
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_se g_fa18	2018	19_SRFALL	223	0 – 559	250	0 – 501	474
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_se g_fa19	2019	19_SRFALL	103	0 – 310			103
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg _fa18	2018	19_SRFALL	115	0 – 345	258	0 – 644	372
	#N/A	#N/A	Unassigned	#N/A	#N/A	247	0 – 2818			247
			Summer Subtotal			53,4 29		8,19 9		61,6 28
Fall	01Spring	North Santiam Hatchery	OtsNSAN_se g_sp18	2018	04_WILLAM	812	0 – 2373			812
	03Summer	Chief Joseph Hatchery	OtsCHJO_int _su17	2017	18_UCOLSF	709	0 – 1972			709
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg _su17	2017	18_UCOLSF	566	0 – 1685			566
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg _su18	2018	18_UCOLSF	1,65 8	551 – 3318			1,65 8
	03Summer	Wells Fish Hatchery	OtsWELL_se g_su17	2017	18_UCOLSF	609	0 – 1789			609
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg _fa18	2018	05_SPCRTU	3,98 7	1120 – 7151			3,98 7

04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	2019	05_SPCRTU	85,9 88	73526 – 97102	51,6 43	43962 – 59678	137, 631
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa20	2020	05_SPCRTU	11,6 10	6497 – 17046	590	0 – 1770	12,2 00
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa17	2017	18_UCOLSF	7,50 2	3716 – 12237	3,09 2	1340 – 5444	10,5 95
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa18	2018	18_UCOLSF	25,9 14	18485 – 33128	10,8 71	7477 – 14802	36,7 84
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa19	2019	18_UCOLSF	22,0 15	16895 – 28032	22,9 86	17999 – 28037	45,0 01
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa17	2017	18_UCOLSF	906	0 – 1963			906
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa18	2018	18_UCOLSF			849	0 – 2457	849
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa19	2019	18_UCOLSF	2,20 7	884 – 3908	63	0 – 188	2,27 0
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	2017	19_SRFALL	3,00 3	471 – 6091	1,68 7	398 – 3188	4,69 0
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	2018	19_SRFALL	14,2 56	8338 – 20502	11,7 97	7590 – 16259	26,0 53
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa19	2019	19_SRFALL	16,2 92	10194 – 22429	22,1 32	17169 – 27844	38,4 24
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa17	2017	19_SRFALL			966	0 – 2307	966
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	2018	19_SRFALL	628	0 – 1814	2,73 9	685 – 5477	3,36 6
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa19	2019	19_SRFALL	556	0 – 1669	369	0 – 1029	925
04Fall	Klickitat Hatchery	OtsKLIC_seg_fa18	2018	22_BONPO OLFA	230	0 – 564			230
04Fall	Klickitat Hatchery	OtsKLIC_seg_fa19	2019	22_BONPO OLFA			1,75 9	0 – 4127	1,75 9
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	2017	22_BONPO OLFA	6,88 6	3382 – 10832	118	0 – 236	7,00 4

	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_se g_fa18	2018	22_BONPO OLFA	21,1 75	13518 – 28993	1,99 4	164 – 3905	23,1 69
	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_se g_fa19	2019	22_BONPO OLFA	2,94 1	699 – 5359	9,99 8	6460 – 13724	12,9 39
	04Fall	Umatilla Fish Hatchery	OtsUMAT_se g_fa18	2018	23_UMATI LLAFA	14,2 22	9268 – 19222	404	0 – 1083	14,6 26
	#N/A	#N/A	Unassigned	#N/A	#N/A	16,9 50	9192 – 26818	60	0 – 180	17,0 10
			Fall Subtotal			261, 622		144, 115		405, 737

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3410 **Table 51. Expanded abundance of PBT-assigned Chinook Salmon stocks across**
3411 **management periods in 2022.**

	Statistical	Sample (Tag-rate-Corrected abundance)						% PBT of Clipped fish
		Clipped		Non-clipped		Total GSI	Total PBT	
		GSI	PBT	GSI	PBT			
Spring	1-16							
	17	0	3,690	178	433	178	4,123	100.0%
	18	1,214	25,970	1,862	2,684	3,076	28,654	95.5%
	19	1,763	36,864	5,800	2,178	7,563	39,042	95.4%
	20	0	19,711	4,645	1,726	4,645	21,436	100.0%
	21	142	12,158	4,604	1,519	4,745	13,677	98.8%
	22	123	7,390	4,043	1,389	4,166	8,780	98.4%
	23	182	6,767	4,171	1,189	4,353	7,956	97.4%
	24	359	8,442	3,888	1,263	4,247	9,705	95.9%
	25	0	3,234	1,648	552	1,648	3,787	100.0%
	Summer	25	0	3,254	967	637	967	3,891
26		0	13,740	3,124	815	3,124	14,555	100.0%
27		0	18,723	4,209	4,280	4,209	23,003	100.0%
28		772	8,028	1,208	1,147	1,980	9,175	91.2%
29		94	4,771	1,079	384	1,173	5,155	98.1%
30		0	2,475	1,109	0	1,109	2,475	100.0%
31		393	1,179	1,825	596	2,218	1,776	75.0%
Fall	32	0	994	811	884	811	1,878	100.0%
	33	0	2,971	768	1,982	768	4,953	100.0%
	34	659	4,697	2,337	6,049	2,996	10,747	87.7%
	35	0	20,838	6,004	14,202	6,004	35,040	100.0%
	36	4,016	46,309	26,282	19,948	30,298	66,257	92.0%
	37	6,894	90,138	30,258	59,377	37,152	149,516	92.9%
	38	5,792	42,969	16,360	31,729	22,152	74,698	88.1%
	39	1,305	23,373	5,625	5,689	6,929	29,062	94.7%
	40	0	6,741	3,801	2,268	3,801	9,009	100.0%
	41	0	2,954	3,351	933	3,351	3,888	100.0%
	42-44	53	918	2,079	0	2,132	918	94.6%
Total		23,761	419,299	142,036	163,856	165,797	583,154	

3412 Note: The % PBT of Clipped fish indicates the percentage of adipose clipped fish that are accounted for
3413 by PBT after tag rate expansions. If all hatchery broodstock above Bonneville Dam are included in the
3414 PBT baseline AND our estimated tag rates are accurate for each hatchery broodstock, then this percentage
3415 is expected to be 100% across all strata.

In-season analysis of steelhead passing Bonneville Dam in 2022

There were three reports provided to U.S. v OR TAC during the summer A-/B-Index Management Period (7/1/2022 – 10/31/2022, Table 32). The Skamania Management Period (4/1/2022 – 6/30/2022) had a single report that covered the entire Skamania period. There was a total of 592 clipped and 272 unclipped steelhead that were sampled at the Bonneville Dam AFF and genotyped in 2022 (Table 52). 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 since then and provided a breakdown of those A-/B-Index groups in addition to the adipose clipped and unclipped categories (Table 52). 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 53, Table 54, Table 55). 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 2022 include a breakdown of all the A- and B-Index steelhead abundance by broodstock for both clipped and unclipped hatchery-origin groups (Table 56).

3443 **Table 52. The sample sizes of Summer Steelhead at the Bonneville Dam AFF during the Skamania and A-/B-Index**
3444 **management periods of 2022.**

		Sample (N)														Clipped	Non-clipped
		A-Index				B-Index											
		Clipped		Non-clipped		Clipped		Non-clipped		Clipped	Non-clipped						
		Statistical	Strata	Clipped	Non-Clipped	Clipped	Non-clipped	Clipped	Non-clipped	Clipped	Non-clipped						
		week		count	count	GSI	PBT	GSI	PBT	GSI	PBT	GSI	PBT	Total	Total	Sample rate	Sample rate
Management period	Skamania	14	1	30	46									0	0	0.00%	0.00%
		15	1	40	86									0	0	0.00%	0.00%
		16	1	52	62									0	0	0.00%	0.00%
		17	1	31	48		1							1	0	3.23%	0.00%
		18	1	45	55									0	0	0.00%	0.00%
		19	1	48	84		1	1						1	1	2.08%	1.19%
		20	1	54	58			1						0	1	0.00%	1.72%
		21	1	62	79			2						0	2	0.00%	2.53%
		22	1	124	99		4	1						4	1	3.23%	1.01%
		23	1	140	125		3	1						3	1	2.14%	0.80%
		24	1	365	263		1	2						1	2	0.27%	0.76%
		25	1	505	340		1							1	0	0.20%	0.00%
		26	1	1074	723	1	1	1						2	1	0.19%	0.14%
		27	1	1353	911									0	0	0.00%	0.00%
			Subtotal Skamania	1	3923	2979	1	12	9	0	0	0	0	0	13	9	0.33%
A-/B-Index	27	1	1050	767									0	0	0.00%	0.00%	
	28	1	4080	2,902	1	19	14	1		1	1		21	16	0.51%	0.55%	
	29	1	6005	3,824	1	33	19	2		1			35	21	0.58%	0.55%	
	30	1	5441	3,485	4	28	16	1					32	17	0.59%	0.49%	
	31	2	7029	4,476	1	33	25	1					34	26	0.48%	0.58%	
	32	2	4218	2,718	1	10	11	1			1		11	13	0.26%	0.48%	
	33	2	5238	2,717	3	38	16			2	2		43	18	0.82%	0.66%	

34	3	9105	3,214	5	62	26	4		18	5	2	85	37	0.93%	1.15%
35	4	2,673	956		13	5	1		2	2		15	8	0.56%	0.84%
36	4	9,188	2,292	6	16	7	1		14	6		36	14	0.39%	0.61%
37	4	8,078	2,148		3			1	1			5	0	0.06%	0.00%
38	4	9,646	2,312		3	2	1		12	1	2	15	6	0.16%	0.26%
39	5	5,073	1,308	3	31	8	7	3	65	10	10	102	35	2.01%	2.68%
40	6	2,849	855	2	21	6	5	7	56	4	10	86	25	3.02%	2.92%
41	7	1,373	399		15	3	2		32	3	13	47	21	3.42%	5.26%
42	7	491	179		4	2	1		8	1	2	12	6	2.44%	3.35%
43	7	321	206									0	0	0.00%	0.00%
44	7	167	174												
45	7	8	4									0	0	0.00%	0.00%
Summer A- /B-Index subtotal		82,033	34,936	27	329	160	28	11	212	36	39	579	263	0.71%	0.75%
Total		89,879	40,894	28	341	169	28	11	212	36	39	592	272	0.66%	0.67%

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 32).

Table 53. Estimated abundance of clipped hatchery-origin stocks of Summer Steelhead that passed Bonneville Dam in 2022 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)
		A-Index	B-Index	A-Index	B-Index

Reporting Group name	Reporting Group Code	Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI
Lower Columbia	02_LOWCOL								
Skamania	03_SKAMAN	3,603	1930 – 5247			3,008	2288 – 3891	174	0 – 376
Willamette	04_WILLAM								
Big White Salmon	05_BWSALM								
Klickitat	06_KLICKR								
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	1,211	0 – 2825			27,302	24233 – 30831	0	0 – 53
Yakima	08_YAKIMA								
upper Columbia	09_UPPCOL					5,701	3113 – 7266	1,100	206 – 2145
SF Clearwater	10_SFCLWR					3,942	2372 – 5744	20,174	17195 – 23507
upper Clearwater	11_UPCLWR								
SF Salmon	12_SFSALM								
MF Salmon	13_MFSALM								
upper Salmon	14_UPSALM	433	0 – 1731			19,830	17112 – 21789	801	305 – 2042
Total		5,247		0		59,784		22,249	

Note: Based on the sample data described in Table 52 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 54. Estimated abundance of unclipped hatchery-origin stocks of Summer Steelhead that passed Bonneville Dam in 2022 during the Skamania and A-/B-Index Management Periods.

	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

Reporting Group name	Reporting Group Code	Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI
Lower Columbia	02_LOWCOL								
Skamania	03_SKAMAN	402	0 – 1207			203	0 – 407	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					290	0 – 601	0	0 – 0
Yakima	08_YAKIMA								
upper Columbia	09_UPPCOL					174	0 – 514	0	0 – 0
SF Clearwater	10_SFCLWR					549	258 – 822	1,471	1020 – 1909
upper Clearwater	11_UPCLWR								
SF Salmon	12_SFSALM								
MF Salmon	13_MFSALM								
upper Salmon	14_UPSALM					1,736	936 – 2807	601	279 – 1205
	Total	402		0		2,953		2,073	

Note: Based on the sample data described in Table 52 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 55. Estimated abundance of natural-origin stocks (excluding unclipped hatchery-origin) of Summer Steelhead that passed Bonneville Dam in 2022 during the Skamania and A-/B-Index Management Periods.

Reporting Group name	Reporting Group Code	W		Subtotal for Skamania Period (Apr 1 - Jun 30)		Subtotal for A-/B-Index Period (Jul 01 - Oct 31)		Subtotal for A-/B-Index Period (Jul 01 - Oct 31)	
		A-Index		B-Index		A-Index		B-Index	
		Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI
Lower Columbia	02_LOWCOL					784	203 – 1394	0	0 – 0
Skamania	03_SKAMAN	981	327 – 1635						

Willamette	04_WILLAM								
Big White Salmon	05_BWSALM								
Klickitat	06_KLICKR	981	327 – 1635			1,308	622 – 2088	36	0 – 107
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	327	0 – 981	1,831	830 – 2948	17,835	15824 – 19652	1,831	830 – 2948
Yakima	08_YAKIMA	654	0 – 1308			638	174 – 1248	0	0 – 0
upper Columbia	09_UPPCOL			638	174 – 1248	638	174 – 1248	0	0 – 0
SF Clearwater	10_SFCLWR			466	71 – 1012	466	71 – 1012	278	115 – 495
upper Clearwater	11_UPCLWR			981	307 – 1775	981	307 – 1775	1,593	777 – 2541
SF Salmon	12_SFSALM			0	0 – 0	0	0 – 0	210	0 – 558
MF Salmon	13_MFSALM					943	275 – 1724	274	0 – 826
upper Salmon	14_UPSALM					2,097	1101 – 3163	0	0 – 0
Total		2,943		3,916		25,689		4,222	

Note: Based on the sample data described in Table 52 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.

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Table 56. Estimated abundance of clipped and unclipped hatchery-origin A-/B-Index Summer Steelhead that passed Bonneville Dam in 2022 (July 1 – Oct 31) and were assigned to PBT broodstocks.

Hatchery	Stock	GSI RepGrp	Broodstock	BY	Hatchery clipped				Hatchery unclipped			
					A-INDEX		B-INDEX		A-INDEX		B-INDEX	
					Est.	95% CI	MLE	95% CI	MLE	95% CI	MLE	95% CI
Skamania Hatchery	Summer	03_SKA MAN	OmySKAM_ su19	2019	2,817	1710 – 4069	0	0 – 0	203	0 – 610	0	0 – 0
Skamania Hatchery	Summer	03_SKA MAN	OmySKAM_ su18	2018	191	0 – 574	174	0 – 543				
Minthorn Springs Satellite	Minthorn Springs	07_MGI LCS	OmyMINT_ su20	2020	654	0 – 1537	0	0 – 0				
Round Butte	Deschutes River	07_MGI LCS	OmyROUN_ su20	2020	841	0 – 2102	0	0 – 0				
Round Butte	Deschutes River	07_MGI LCS	OmyROUN_ su19	2019	1,764	782 – 2819	0	0 – 0				
Round Butte	Deschutes River	07_MGI LCS	OmyROUN_ su18	2018	109	0 – 326	0	0 – 0				
Eastbank	Wenatchee	09_UPP COL	OmyEAST_ su20	2020	187	0 – 562	0	0 – 0				
Wells Fish Hatchery	WMET/ WOKA/ WOMA/ WELLS	09_UPP COL	OmyWELL_ su20	2020	299	0 – 706	0	0 – 0	174	0 – 522	0	0 – 0
Wells Fish Hatchery	WMET/ WOKA/ WOMA/ WELLS	09_UPP COL	OmyWELL_ su19	2019	4,894	3115 – 6828	1,100	296 – 2104				
Winthrop NFH	Methow River	09_UPP COL	OmyWINT_ su18	2018	193	0 – 579	0	0 – 0				
Little Sheep Satellite	Imnaha	07_MGI LCS	OmyLSCR_ su20	2020	819	0 – 1670	0	0 – 0				

Lyons Ferry Hatchery	Wallowa stock - trapped/spawned at Cottonwood, released at Cottonwood and other Washington sites	07_MGI LCS	OmyCGRW_su20	2020	2,011	895 – 3296	0	0 – 0				
Lyons Ferry Hatchery	Touchet (in Walla Walla River basin)	07_MGI LCS	OmyTOUW_su20	2020					87	0 – 261	0	0 – 0
Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGI LCS	OmyWALL_su20	2020	1,888	841 – 3161	0	0 – 0				
Little Sheep Satellite	Imnaha	07_MGI LCS	OmyLSCR_su19	2019	1,463	584 – 2526	0	0 – 0				
Lyons Ferry Hatchery	Tucannon	07_MGI LCS	OmyTUCW_su19	2019	387	0 – 775	0	0 – 0				
Lyons Ferry Hatchery	Touchet (in Walla Walla River basin)	07_MGI LCS	OmyTOUW_su19	2019					203	0 – 610	0	0 – 0
Wallowa Fish Hatchery	Wallowa stock - released at Cottonwood and other Washington sites	07_MGI LCS	OmyCGRW_su19	2019	7,002	5235 – 9120	0	0 – 0				
Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGI LCS	OmyWALL_su19	2019	8,532	6558 – 10791	0	0 – 0				

Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGI LCS	OmyWALL_su18	2018	40	0 – 120	0	0 – 0				
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFC LWR	OmyDWOC_su20	2020	734	175 – 1549	0	0 – 0				
Dworshak NFH	SF Clearwater	10_SFC LWR	OmySFCR_su20	2020	130	0 – 260	0	0 – 0	332	142 – 544	0	0 – 0
Dworshak NFH	All Dworshak stocks	10_SFC LWR	OmyDWOR_su20	2020					37	0 – 111	0	0 – 0
Dworshak NFH	Dworshak stock-trapped and spawned at Dworshak, reared at Magic Valley FH, released in Salmon basin	10_SFC LWR	OmyDWOS_su20	2020					36	0 – 107	0	0 – 0
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFC LWR	OmyDWOC_su19	2019	2,401	1097 – 3920	17,643	14624 – 20548	0	0 – 0	1,071	609 – 1669
Dworshak NFH	SF Clearwater	10_SFC LWR	OmySFCR_su19	2019	534	51 – 1344	2,329	1370 – 3484	38	0 – 113	317	174 – 487

Dworshak NFH	Dworshak stock-trapped and spawned at Dworshak, reared at Magic Valley FH, released in Salmon basin	10_SFC LWR	OmyDWOS_su19	2019	95	0 – 205	0	0 – 0	36	0 – 101	37	0 – 99
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFC LWR	OmyDWOC_su18	2018	0	0 – 0	53	0 – 160				
Oxbow (IDFG)	Oxbow	14_UPS ALM	OmyOXBO_su20	2020	869	194 – 1789	0	0 – 0				
Pahsimeroi	Pashsimeroi	14_UPS ALM	OmyPAHH_su20	2020	988	296 – 1892	0	0 – 0				
Sawtooth	Sawtooth	14_UPS ALM	OmySAWT_su20	2020	1,259	495 – 2137	0	0 – 0				
Oxbow (IDFG)	Oxbow	14_UPS ALM	OmyOXBO_su19	2019	4,887	3406 – 6529	36	0 – 107	555	93 – 1123	0	0 – 0
Pahsimeroi	Pashsimeroi	14_UPS ALM	OmyPAHH_su19	2019	6,502	4752 – 8248	0	0 – 0	407	0 – 813	89	0 – 266
Pahsimeroi	Upper Salmon	14_UPS ALM	OmyUSAL_su19	2019	1,147	250 – 2268	766	225 – 1566	775	191 – 1481	497	148 – 1045
Sawtooth	Sawtooth	14_UPS ALM	OmySAWT_su19	2019	2,847	1797 – 3930	0	0 – 0				
#N/A	#N/A	#N/A	Unassigned	#N/A	3,303	1459 – 5356	148	46 – 753	71	0 – 178	63	0 – 165
			TOTAL		59,784		22,249		2,953		2,073	

Post-season analysis of Sockeye Salmon passing Bonneville Dam in 2022

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 8, 2022 (Table 32). 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 2022, there were 1,372 Sockeye Salmon that were sampled at the AFF and genotyped for this analysis (Table 57). This year we estimated low but non-zero abundance for the ESA listed stock (Redfish Lake Sockeye Salmon from the Snake River, abundance=2,483) (Table 57, Figure 44). 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 2022, we were not able to detect any of the Lake Billy Chinook stock. Importantly, we have the ability to estimate the reintroduced stock from the Yakima River using our PBT baseline but the stock abundance estimate for 2022 was zero. This year marks the end of a consecutive two year streak in which the Yakima stock was greater than 3,000 fish. Those past two years demonstrated the potential for long term success of the Yakama Nation Sockeye salmon reintroduction program and there is still critical need for PBT applications to monitor the effectiveness of this program.

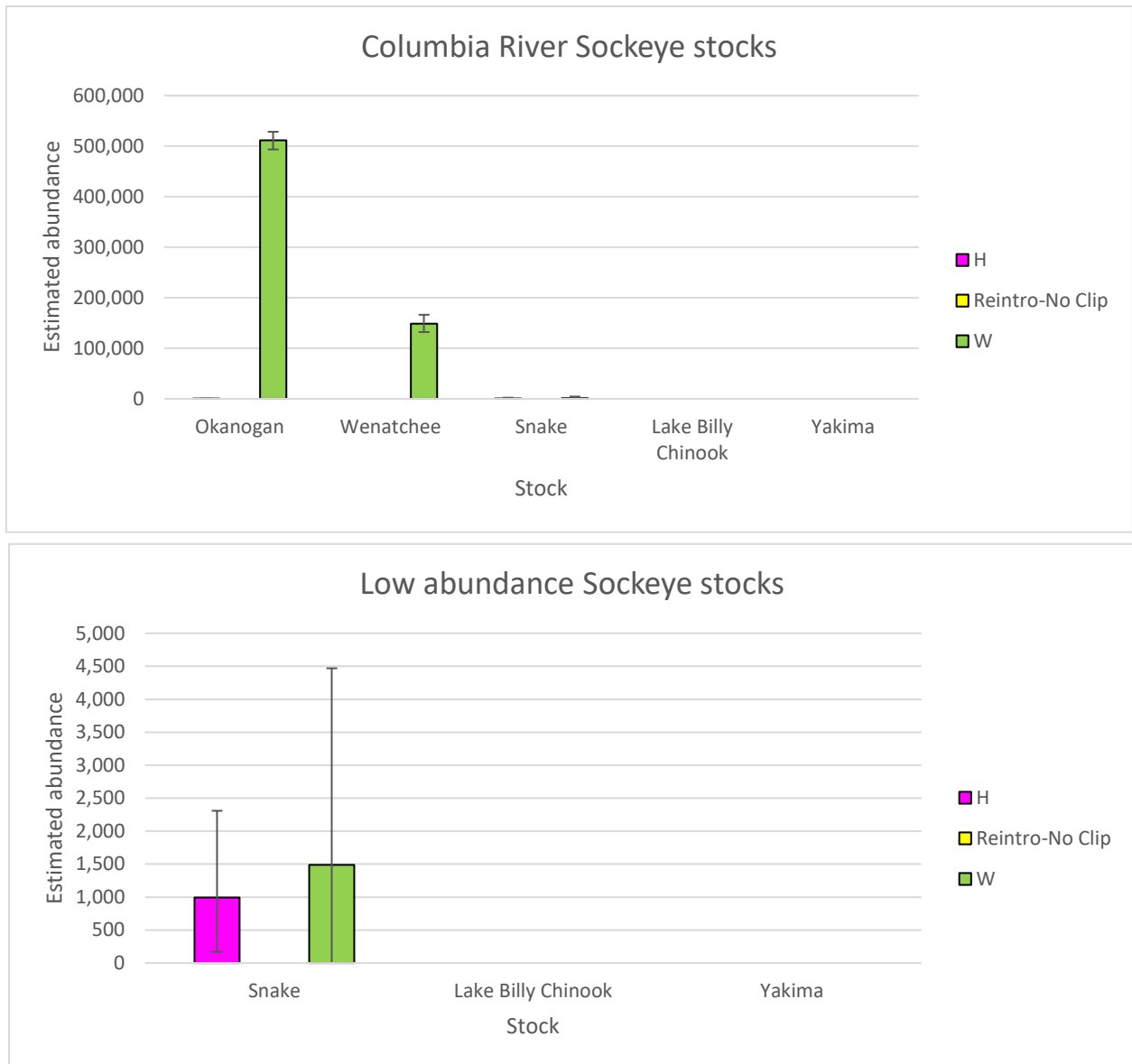


Figure 44. Estimated abundance (\pm 95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2022.

3507 **Table 57. Estimated abundance of Sockeye Salmon genetic stocks that passed Bonneville Dam in 2022.**

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	168	0 – 503			511,493	493404 – 528340	1		1,100	1,101
Wenatchee					148,615	132109 – 166364			267	267
Snake	993	168 – 2309			1,490	0 – 4470	3		1	4
Lake Billy										
Chinook										0
Yakima										0
Total	1,161		0		661,598		4	0	1,368	1,372

3508 Note: The abundance is estimated from the total fish counts at the fish ladder windows at Bonneville Dam. Most stocks are identified
 3509 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 65% of fish that were clipped hatchery-origin summer A-/B-Index steelhead at Bonneville Dam in 2021 to 32 broodstock sources. This percentage of PBT assignments is somewhat lower than what we would expect given our known tag rates (i.e., mostly >90%). Generally, we have high confidence that we have the ability to assign most hatchery origin fish to their PBT broodstock source and slight adjustments may be needed to improve our methodology for assigning steelhead. We observed that this percentage of PBT assignments (93% of all clipped steelhead were assigned with PBT) appears to have recovered based on the more recent in-season analyses of steelhead at Bonneville Dam in 2022.

We continue to see evidence of improved PBT coverage of Chinook salmon based upon our in-season analyses of Chinook Salmon that passed Bonneville Dam in 2022. Namely, the percentage of adipose-clipped fish abundance that were estimated to be PBT broodstock ranged from 95 – 100%, 75 – 100%, and 88 – 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. The 75% minimum value in the range of these percentages for the summer management period only occurred at the very last week of the run but on average the percentage across weeks in the summer period was 95%.

This is the third 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 (2017). The trend suggested 556 smolts were needed to be released to equal 1 adult-sized 4-year-old Spring Chinook at Bonneville Dam in 2021. Further, we estimated that 85 smolts of summer- and fall-run Chinook salmon were needed to equal 1 adult-sized 3- or 4-year-old at Bonneville Dam in 2020 and 2021. Future work could sum all abundance of the SY2017 adult return across age-classes (i.e., age 3, 4, and 5 in run years 2020, 2021, and 2022, 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 14 major clipped Chinook salmon hatchery-origin stocks (73 clipped hatchery broodstock sources), 7 major unclipped hatchery-origin stocks (55 unclipped hatchery broodstock sources) and 9 natural-origin stocks estimated to have relative abundances $\geq 1,000$ fish passing Bonneville Dam in 2021. The Spring Chinook stocks of 2021 were observed to spillover into the summer period by 5% 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 (24 – 26%) 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, one major unclipped hatchery-origin stock (13 major hatchery broodstock sources), and two major natural-origin stocks estimated to have relative abundances $\geq 1,000$ fish passing Bonneville Dam in 2021. 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. At Bonneville Dam in 2021, the relatively large (≥ 78 cm) steelhead were found primarily to originate from Dworshak hatchery broodstock (OmyDWOC_su18, OmySFCR_su18). 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. The MGILCS reporting group produced more natural-origin B-Index steelhead than the SFCLWR reporting group. 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 tenth 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 2021 and found that the Okanogan stock has the greatest relative abundance followed by the Wenatchee stock. We found 1,311 fish from the Snake River stock, estimated 0 fish from Lake Billy Chinook, and estimated 3,535 fish from the reintroduced stock in Yakima River using a PBT baseline. We also found that the migratory run timing for all the Sockeye salmon stocks overlaps broadly at Bonneville Dam.

This year (2022) we continued an increased frequency of in-season reporting as we planned in the past three 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.

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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 45). 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 58). 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 46a). Annual precipitation had the greatest effect when all collections were analyzed together (Figure 46a). Environmental variables retained in the coastal lineage RDA were average temperature of the coldest quarter and precipitation of the wettest month (Figure 46b). Environmental variables retained in the interior lineage RDA were 20-year average

August water temperature and minimum temperature of the warmest month (Figure 46c). 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.

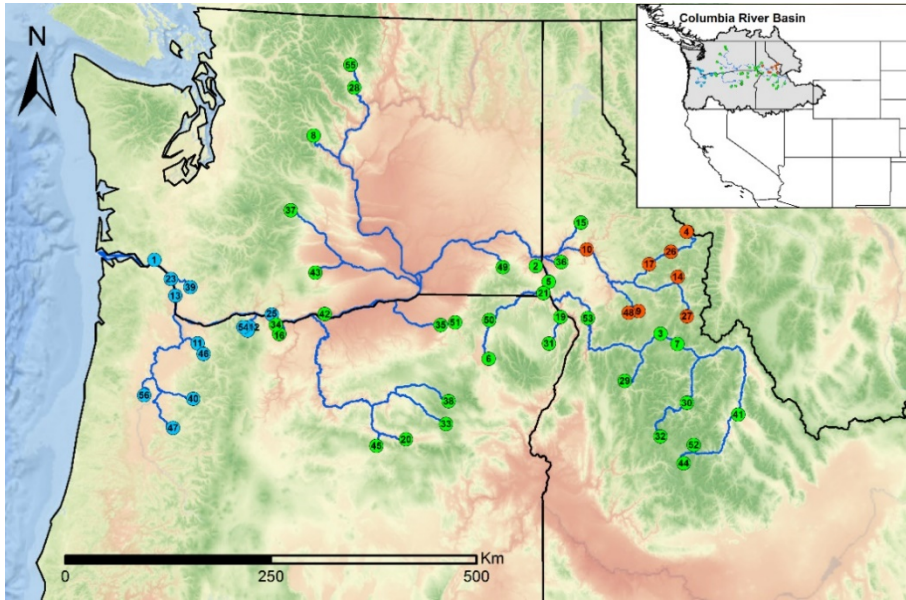


Figure 45. Steelhead collection localities colored by genetic cluster (from Micheletti et al. 2018a). blue = coastal, green = inland, red = inland-Clearwater. Blue lines indicate each population's migration path to the ocean. Map layer shows mean annual temperature for the warmest quarter with transition from colder (green) to warmer (red).

Table 58. Notation, descriptions, units, resolution, variable class, source, and whether the variable was retained in the model are listed for all environmental variables assessed with the RDA models.

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

1

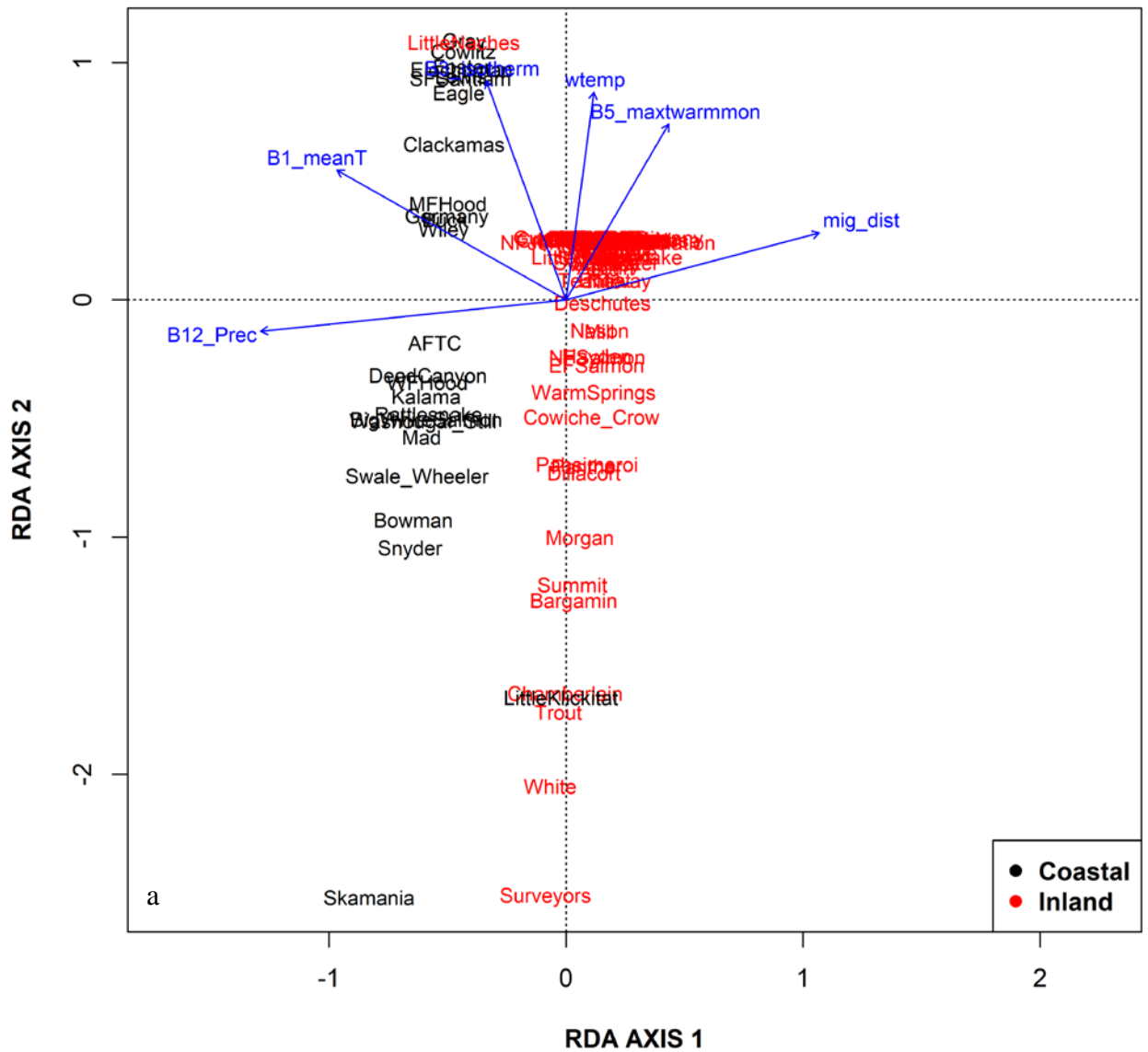


Figure 46 a-c. RDA of all steelhead collections in Columbia River basin to model the degree to which the variation in environmental variables explains the variation in allele frequencies for candidate markers for all collections in the *greb1L* haplotype block (2,3,6). Coastal populations (b) and inland populations (c) were analyzed separately.

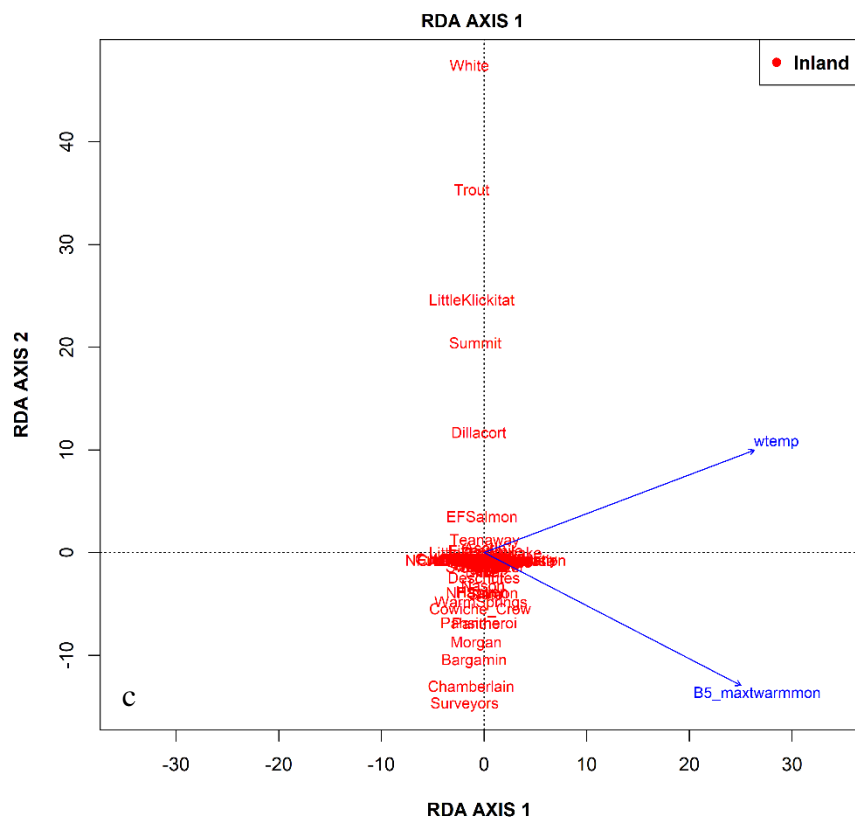
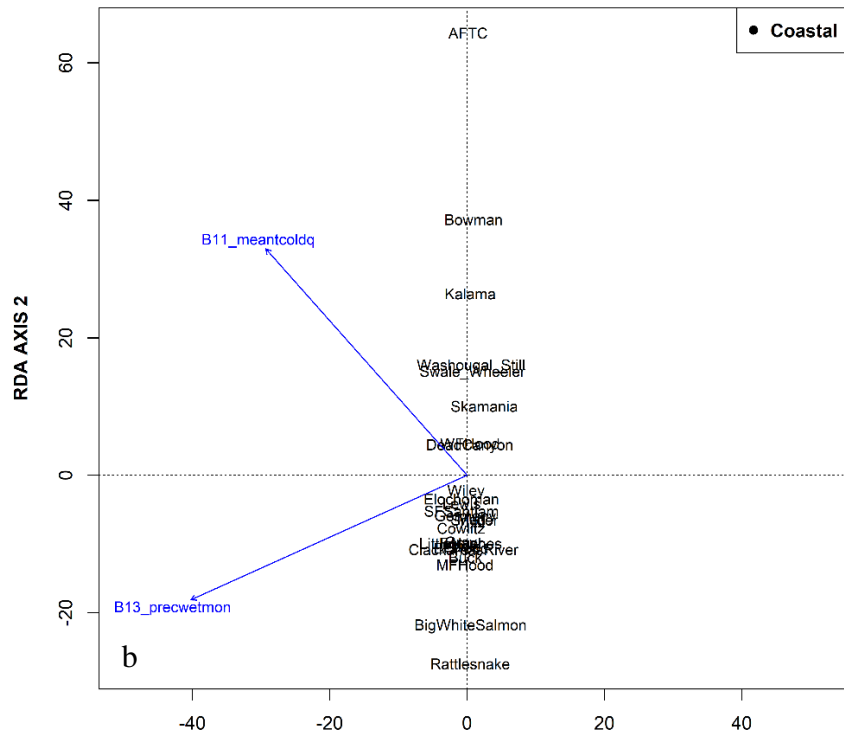


Figure 46 b-c.

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 47a). Several candidate markers were associated with local adaptation within and among lineages (Figure 47b; 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.

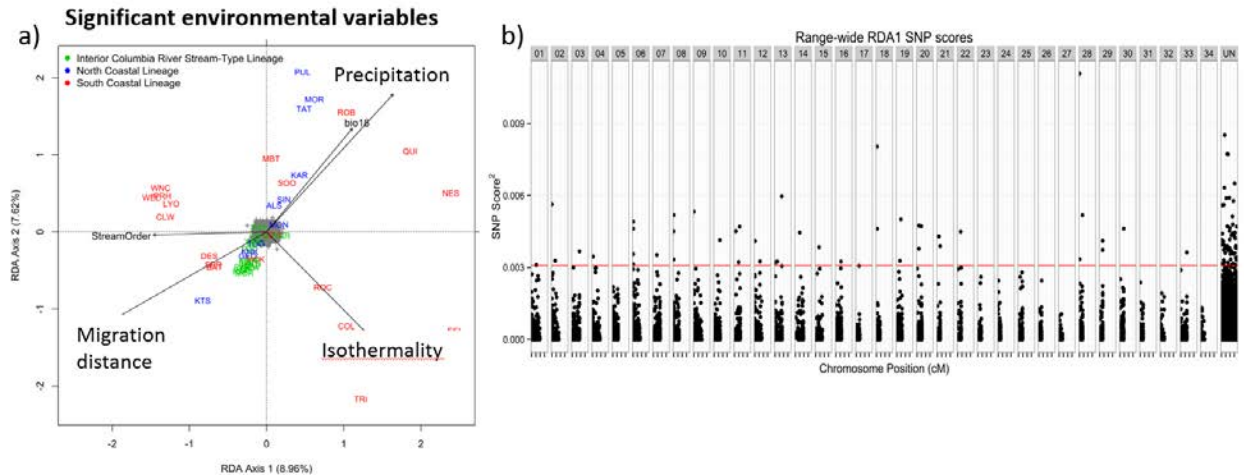


Figure 47. a) Environmental drivers of selection and b) candidate markers for local adaptation in Chinook salmon (from Hecht et al. 2015). a) Population scores for canonical RDA axis 1 and 2 are represented by the three-letter abbreviation for each population, coloured to represent the lineage assignment 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).

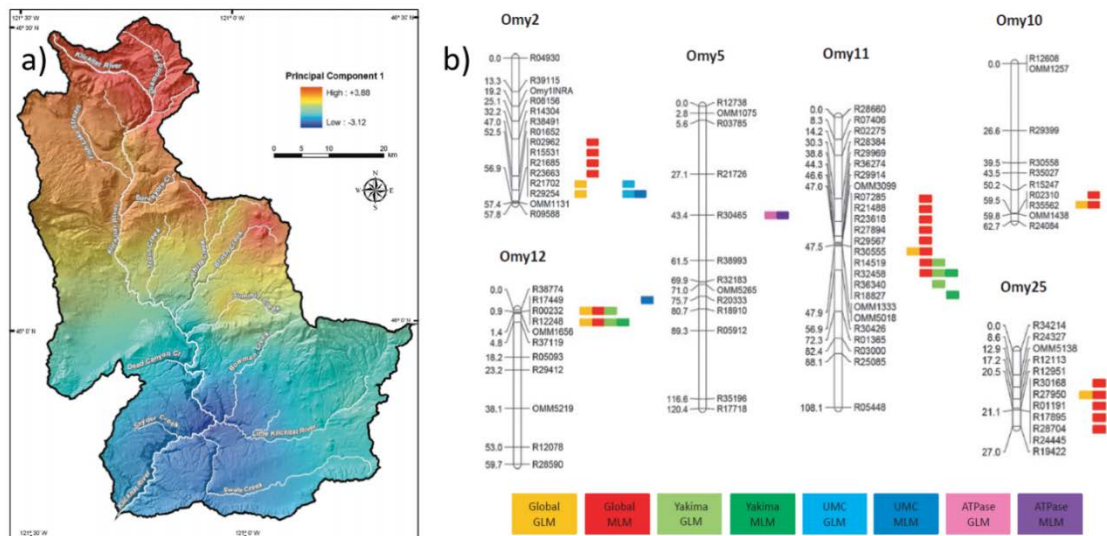


Figure 48. a) Synthesis map illustrating interpolation principal component (PC1) that accounts for 59% of variation in resident (red) vs anadromous (red) life history (from Narum et al. 2008a). b) Significant loci detected from eight individual association tests, where each test is represented by a different colored pill and placed to the right of the linkage group. GLM, general linear model; MLM, mixed linear model (from Hecht et al. 2013).

Further study of resident vs. anadromous *O. mykiss* in the Klickitat River has identified candidate SNP markers on Chromosome 12 that were associated with migration phenotypes in males (Figure 49; Collins et al. 2022). Results indicate that the significant region on Chr. 12 may represent a minor effect gene for male anadromy and suggests that this life history variation is more strongly driven by other mechanisms related to environmental rearing such as epigenetic modification, gene expression, and phenotypic plasticity. However, the candidate SNPs from Chr. 12 will be developed for further validation in GTseq panels.

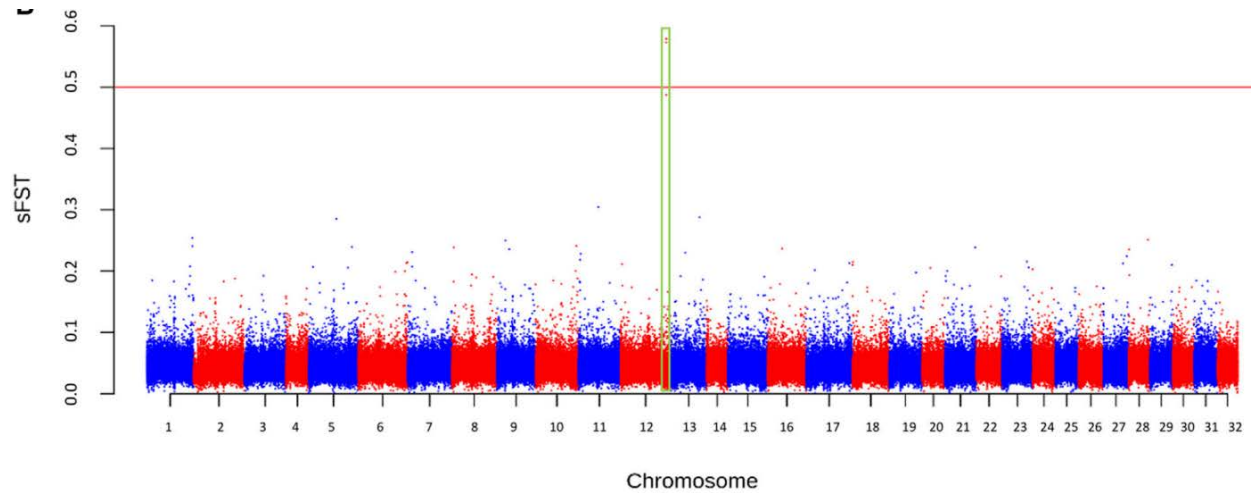


Figure 49. Manhattan plot of differences in allele frequencies between resident and anadromous collections across the genome based on sliding window FST (sFST). The minimum coverage threshold was 15 reads and the minor allele frequency was ≥ 0.05 . (from Collins et al. 2022)

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).

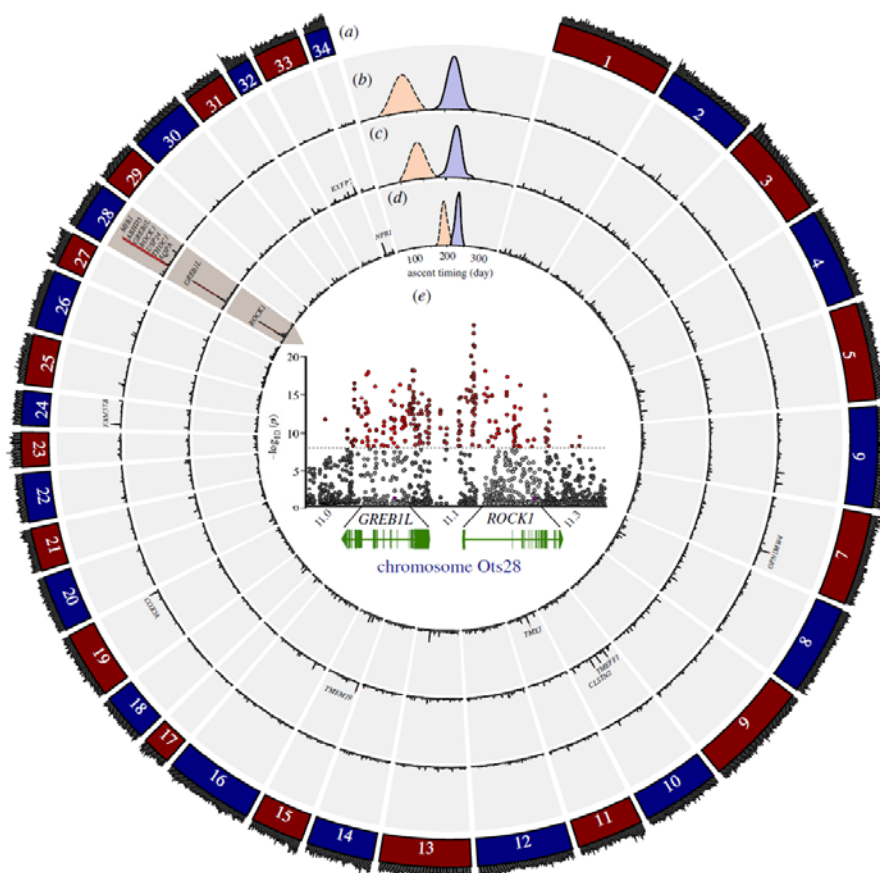


Figure 50. Manhattan plot for premature and mature collections of Chinook salmon (from Narum et al. 2018). (a) Sequence coverage (black outer ring) for each chromosome. (b) Significant divergence between premature and mature migrating coastal lineage Chinook salmon. (c) Significant divergence between 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 59). 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

138 migration timing from the whole genome resequencing conducted by Micheletti et al.
139 (2018c). Premature, mature, and heterozygote genotypes for adult migration timing were
140 established based on genotype association from previous studies (Hess et al. 2016;
141 Micheletti et al. 2018c), as well as using a reference collection of Skamania Hatchery
142 steelhead, which is a hatchery-strain intensively selected for early adult migration and
143 cultured since 1956 with steelhead from the Washougal and Klickitat Rivers (Crawford et
144 al. 1979; Chilcote et al. 1986). Premature, mature, and heterozygote adult migration
145 timing genotype proportions were assessed across all collection locations. A total of
146 9,471 individuals from 113 populations met inclusion criteria (>90% loci successfully
147 genotyped and had an estimated <0.5% genotyping error based on replicate genotyping)
148 and were included in this study. Further validation of association with run-timing
149 phenotypes and genotypes from Chr28 was demonstrated in Willis et al. (2020).

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Table 59. 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>	ACGTGTCCTTGAGGATGGTA	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	CAACATATGACCACTCGAAAACCTC	ATTAATCACACCGTGAGACTCCTC	TGGTACAGAC[A/C]CGCACTAGCA	+
8	Omy28_11667578	28	11667578	intergenic	ACAGTAAACCCATTGAGGCATAGT	TTATCCTCTCAATCCACATCAAGA	GTATTGATCC[T/C]GTGGGAGACA	+
9	Omy_RAD47080-54	28	11667915	intergenic	TCAAAACCTGCAGGACTTGGA	TGTTATATCTACAGTACAGTTCGT	TGCAAG[A/G]CTTAAACGA	+
10	Omy28_11671116	28	11671116	intergenic	AATTTCCCAAATTTGAACTCTT	GTGTACATTGTGAGGCAGAAACAT	CTGGTGAGAA[C/T]AGGAATTACC	+
11	Omy28_11676622	28	11676622	intergenic	CGAATGCACTGTAGCTATTCTAA	GCAGTAGAATGTCTCGCAAATACA	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	GTCTACAAGCTCTGGGTGATTTA	GCAATTTTTT[T/A]AAATTACCGC	+

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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.

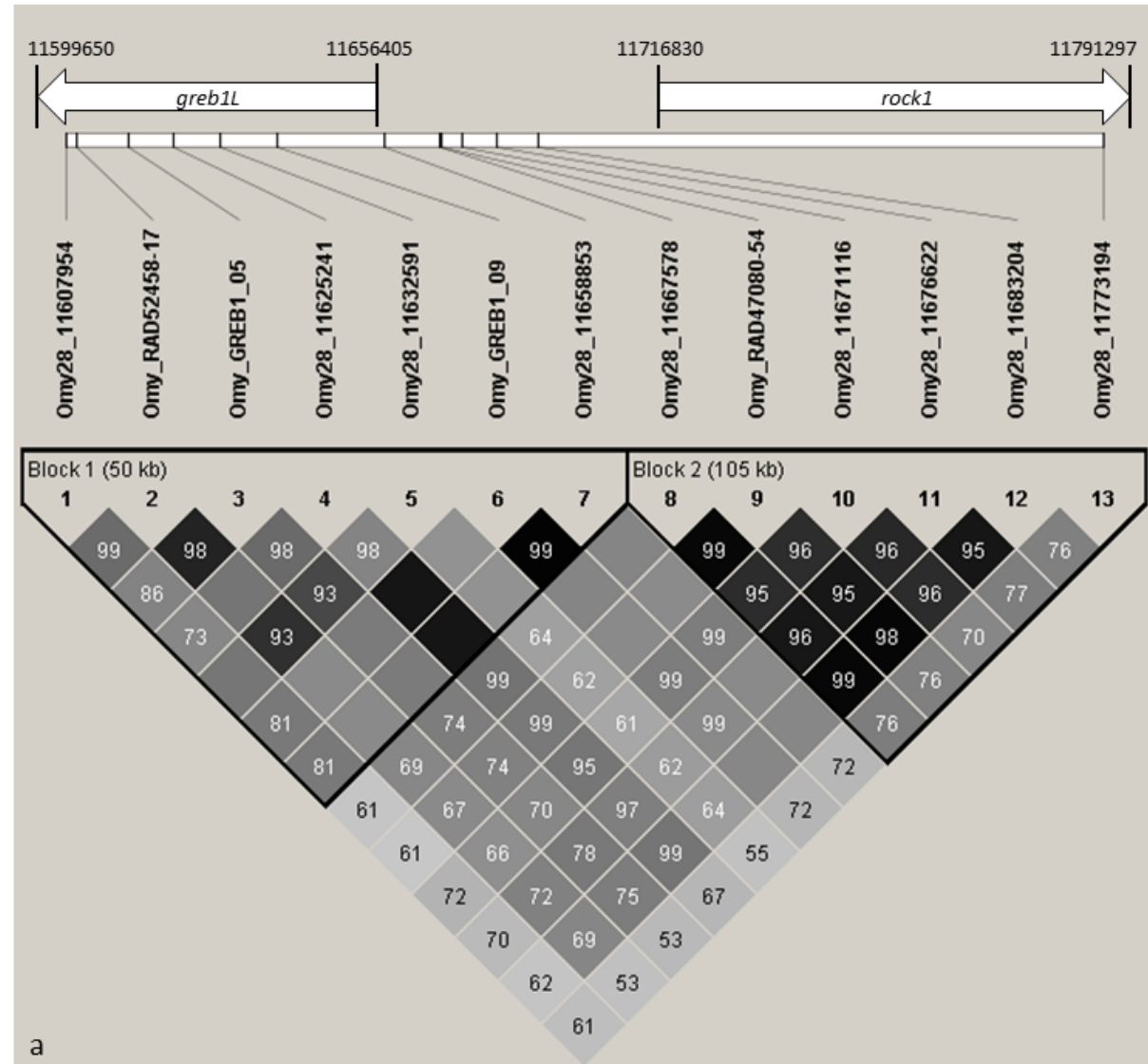


Figure 51. Linkage relationships for 13 candidate markers in Haploview for all steelhead populations.

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).

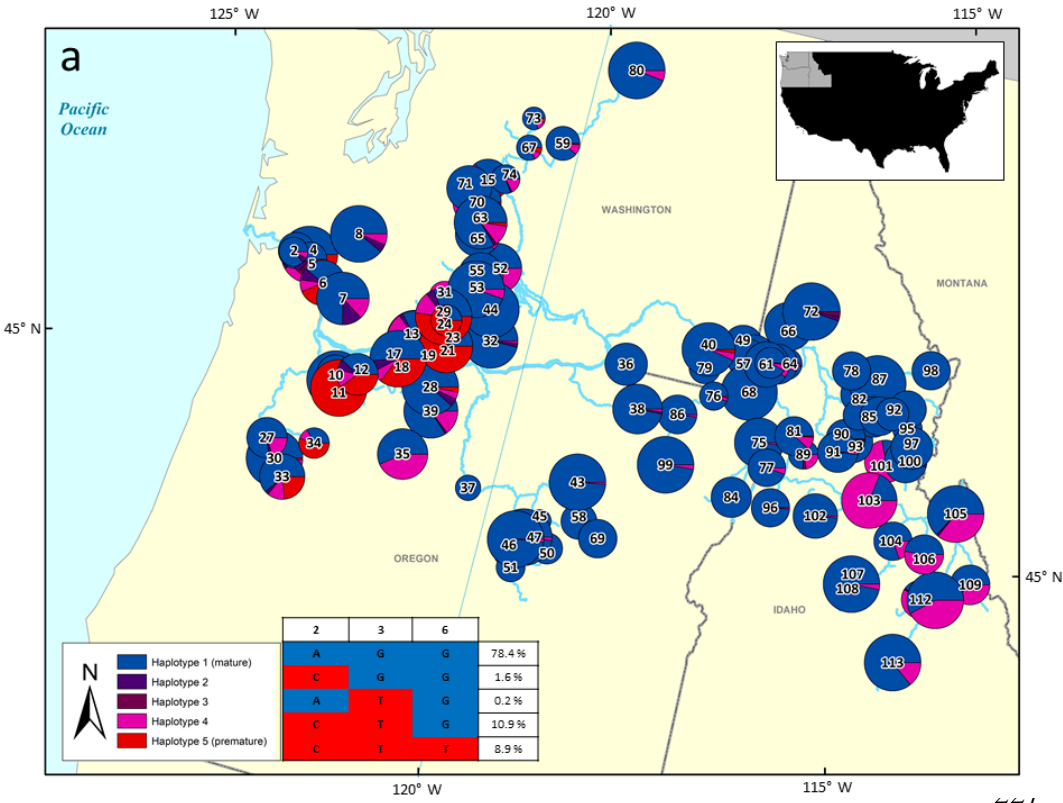


Figure 52a. Maps of haplotype and genotype proportions for all steelhead collection locations. Pie chart size corresponds to population size. The first map (a) demonstrates the proportions of individuals at each collection location with the five unique haplotypes from markers 2, 3, and 6. The second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

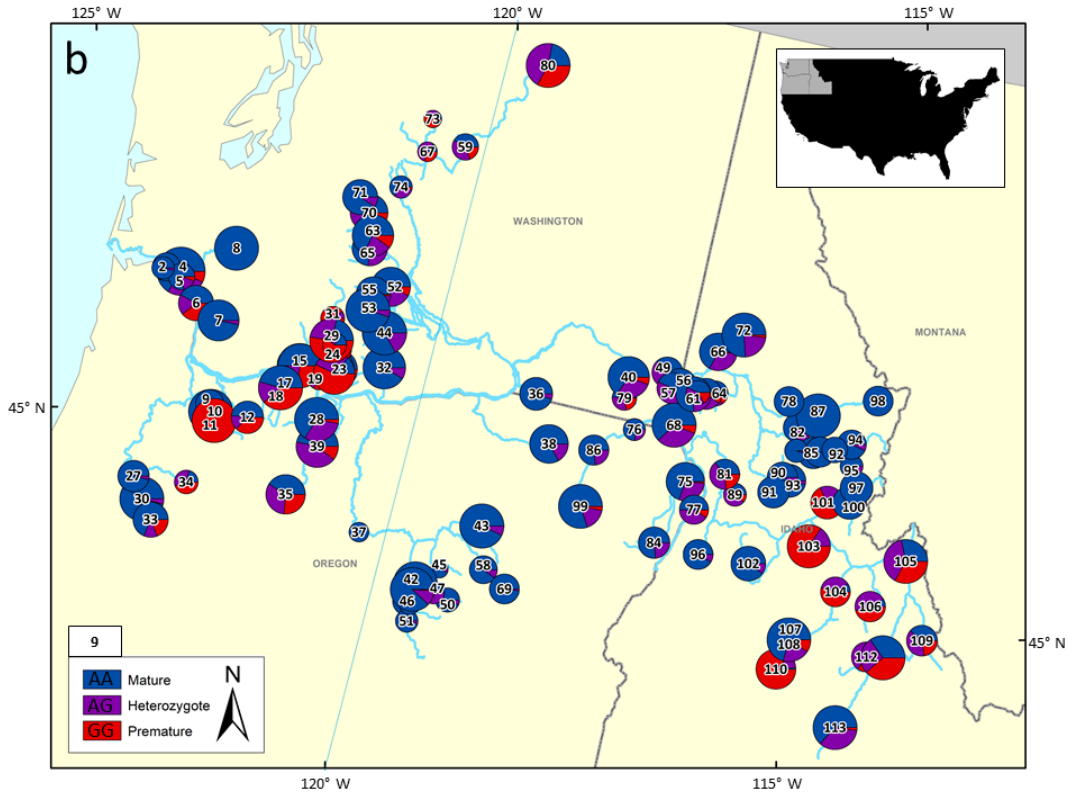


Figure 52b.

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.

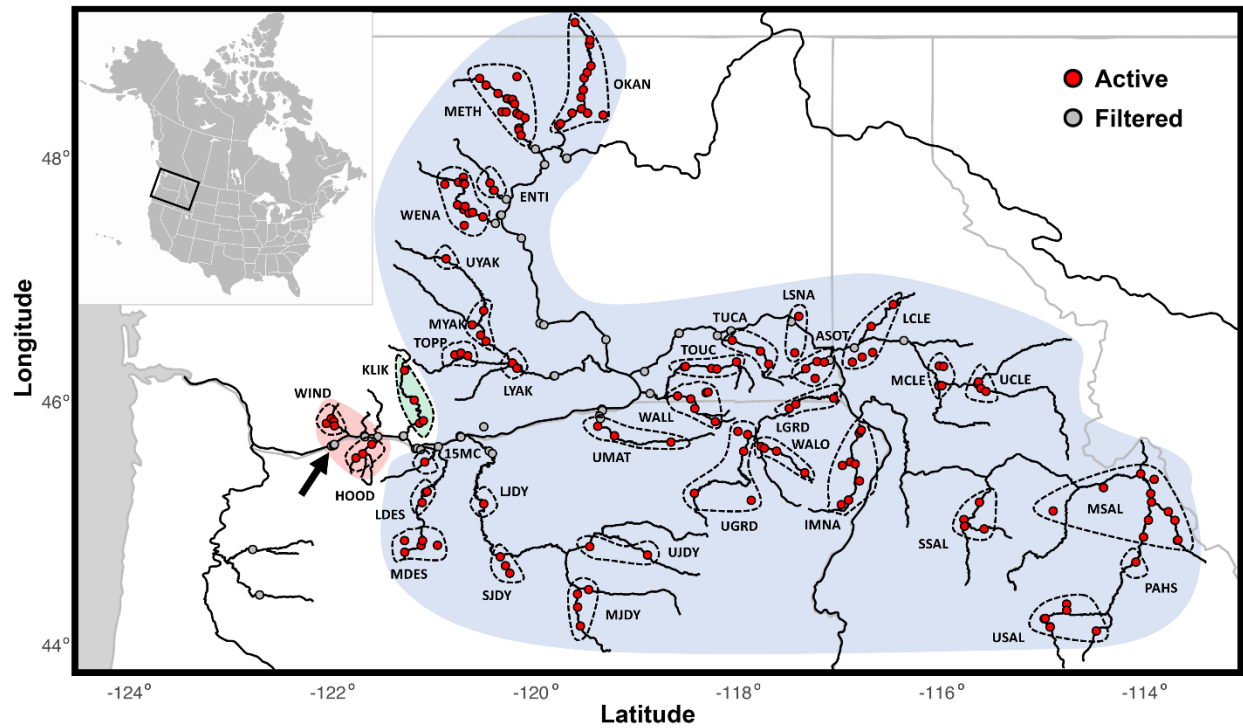


Figure 53. Columbia River Basin with active and filtered passive integrated transponder arrays. River courses in black; borders and coast in gray. Hydrological unit groupings, identified by dashed lines, are organized into lineages and sub-basins as follows: coastal lineage in Red, intermediate lineage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

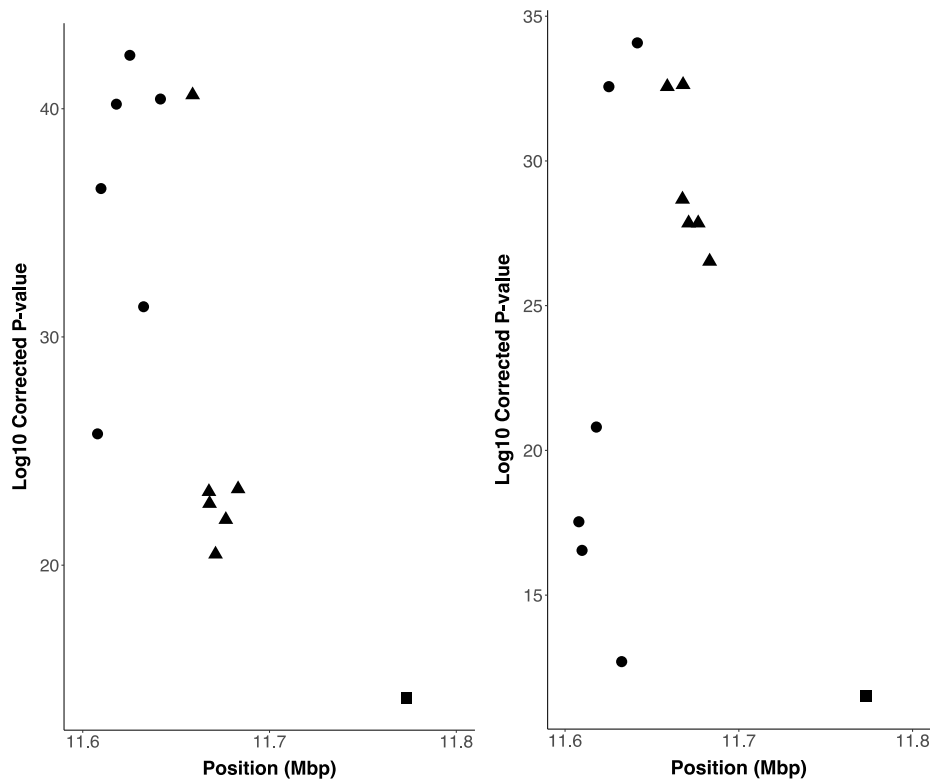


Figure 54. Significance of association of chromosome 28 markers with run timing in BONAFF (left) and Hood River (right) steelhead. Position refers to SNP locus position on chromosome 28. Circle: GREB1L, triangle: intergenic; square: ROCK1.

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).

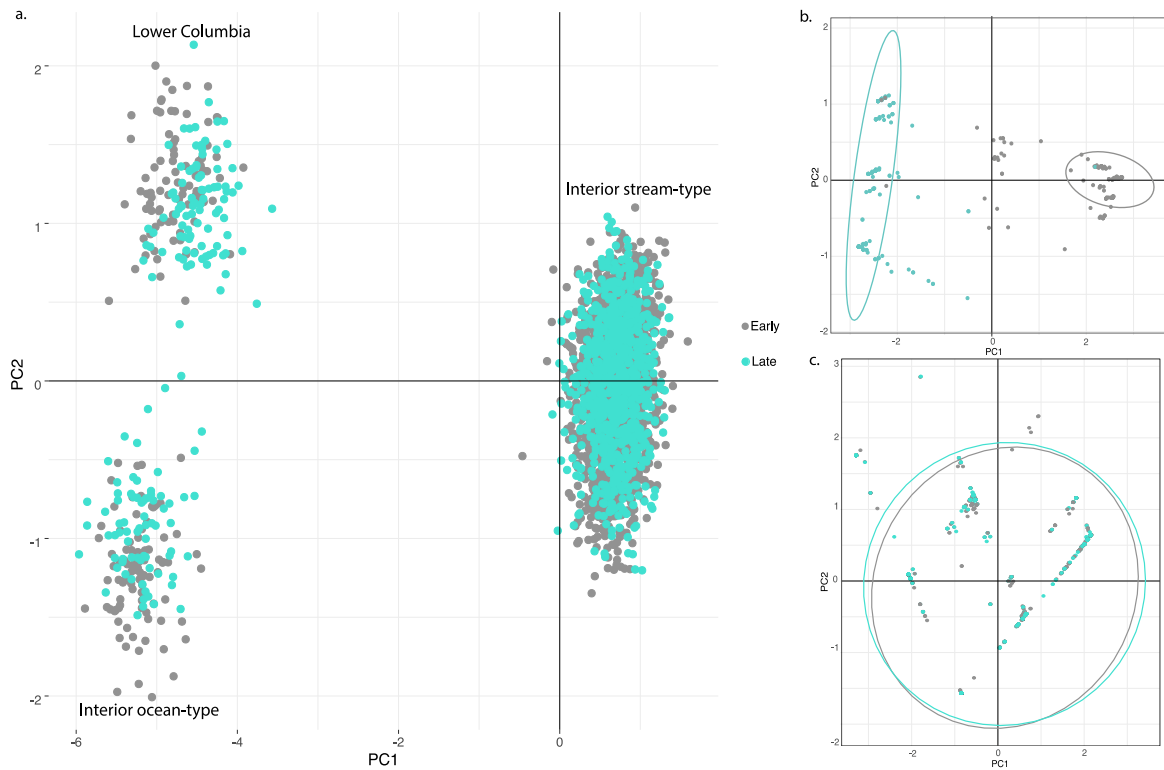


Figure 55. PCA of genetic variation in Chinook Salmon (from Koch and Narum 2020). Results presented represent A) 185 neutral SNP markers, B) 33 chromosome 28 markers for the Lower Columbia and Interior ocean-type populations combined, and C) 33 chromosome 28 markers for the Interior stream-type population.

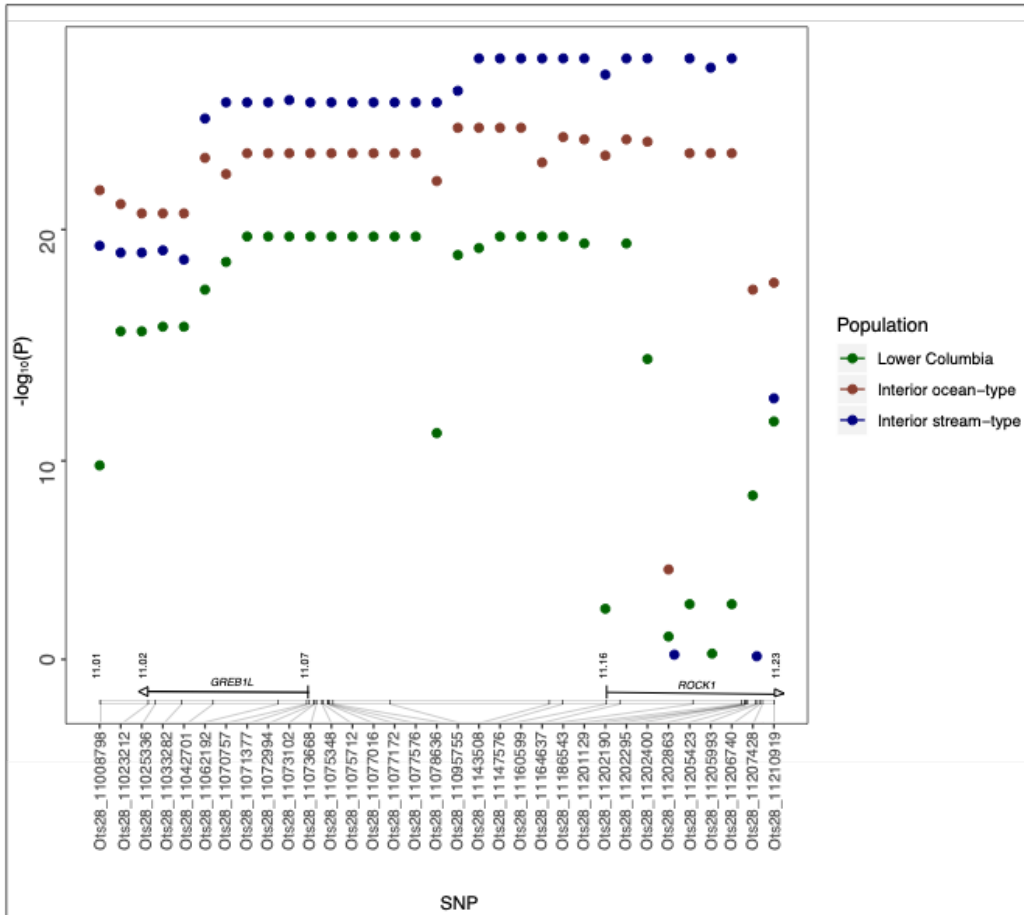


Figure 56. Association of each candidate SNP marker with migration timing within three lineages of Chinook Salmon (from Koch and Narum 2020). The colored dots for each lineage represent sliding windows for consecutive pairs of SNPs along the candidate genomic region. SNP number on the x-axis corresponds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

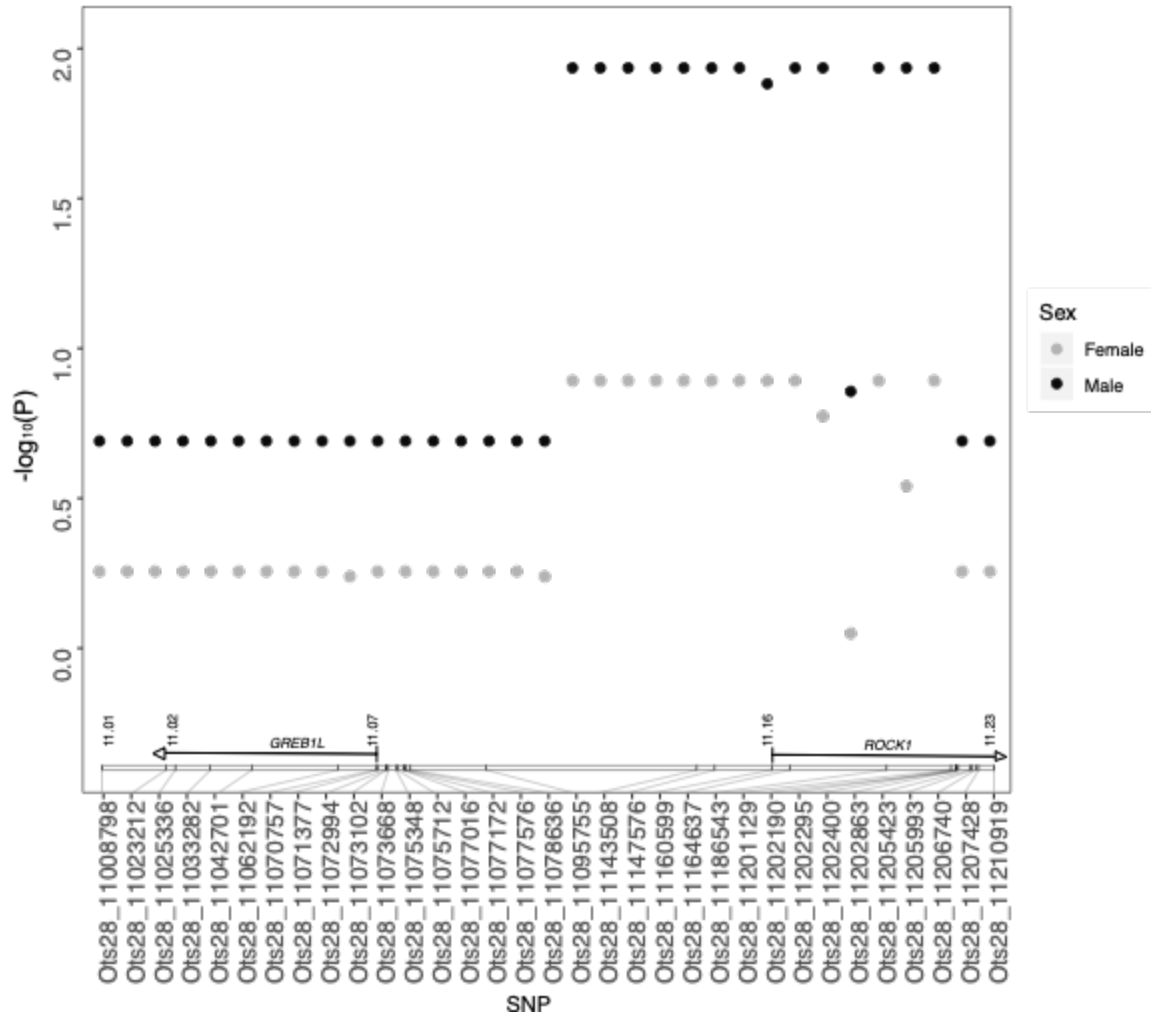


Figure 57. Association of each candidate SNP marker with fitness within the Interior stream-type population. The dots represent sliding windows for consecutive pairs of SNPs along the candidate genomic region with sexes presented separately. SNP number on the x-axis corresponds to the 33 candidate markers, 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.

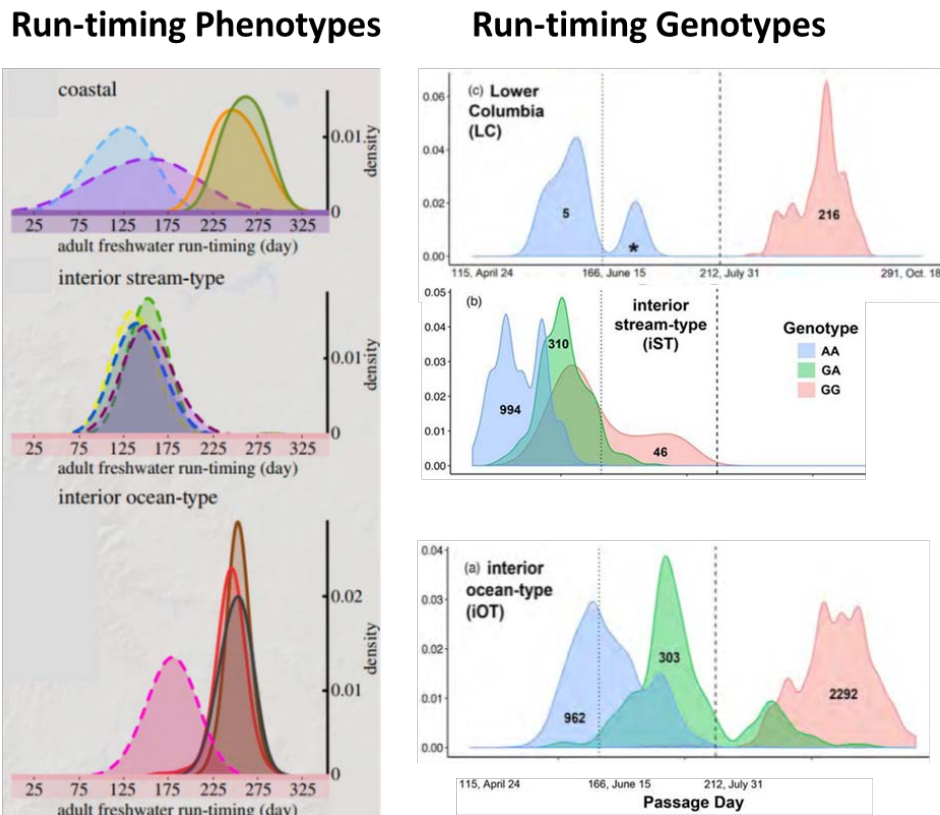


Figure 58. Run-timing phenotypes and genotypes at Bonneville Dam for each lineage of Chinook salmon (coastal, interior-stream type, and interior ocean-type) show a strong association (results from Narum et al. 2018; Willis et al. 2021). Early and late returning fish are found in all three lineages with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

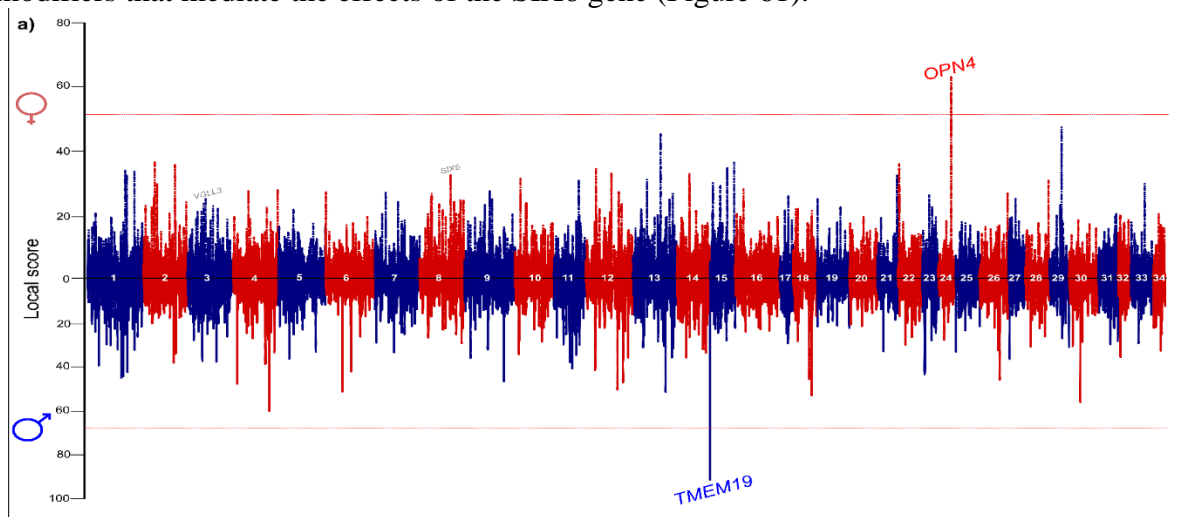


Figure 59. Manhattan plot (from Micheletti and Narum 2018b) illustrating differentiated regions within age classes of females (top; 4- vs. 5-year-olds) and males (bottom; 3- vs. 4- vs. 5-year-olds). Red dashed lines indicate $\alpha = 0.01$ significance threshold for the local score test with Bonferroni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

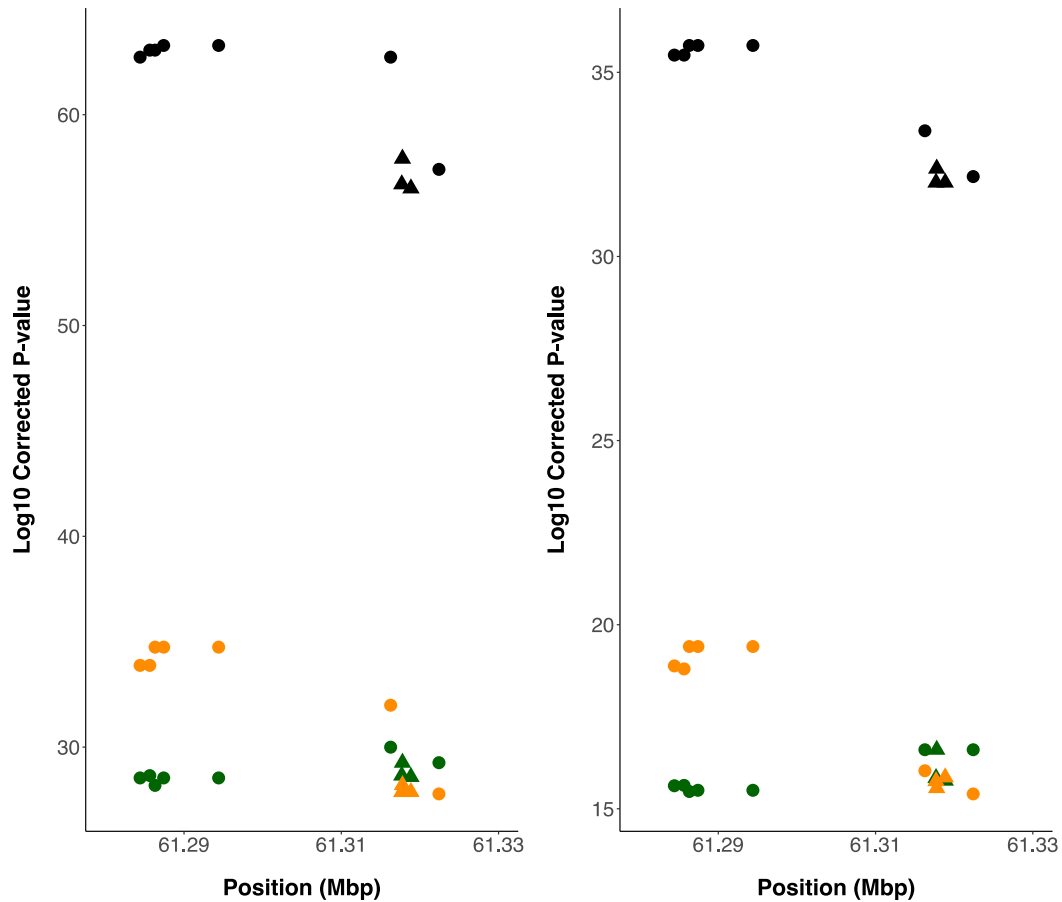


Figure 60. Significance of association of chromosome 25 markers with fork length (left) and ocean age (right) in BONAFF steelhead. Position refers to SNP locus position on chromosome 25. Circle: Intergenic, triangle: SIX6; orange: female; green: male; black: combined male and female.

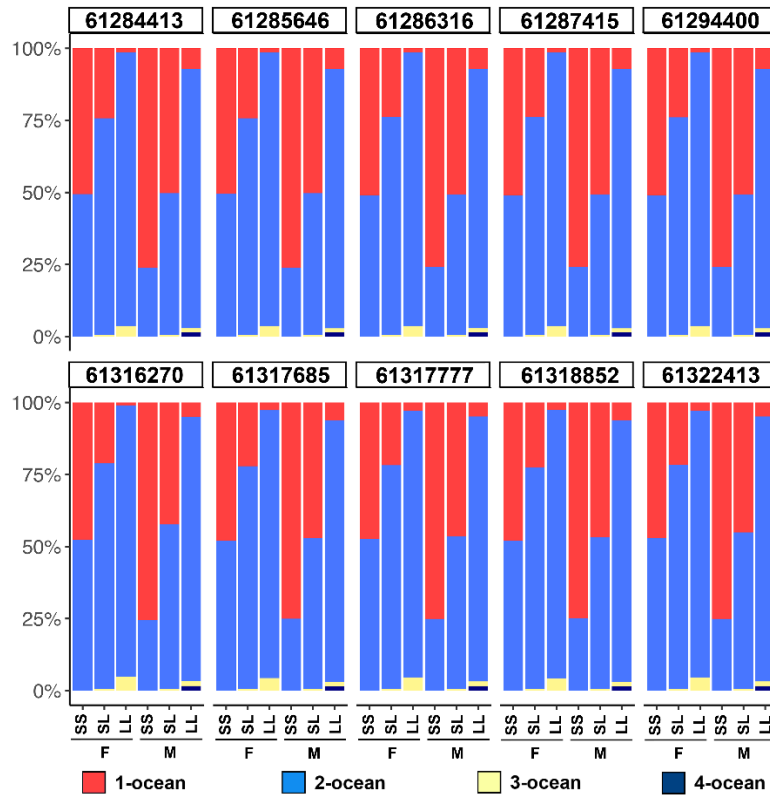


Figure 61. Frequency of ocean-age individuals for genotype and sex for each of the chromosome 25 SNP markers (identified by genomic position).

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

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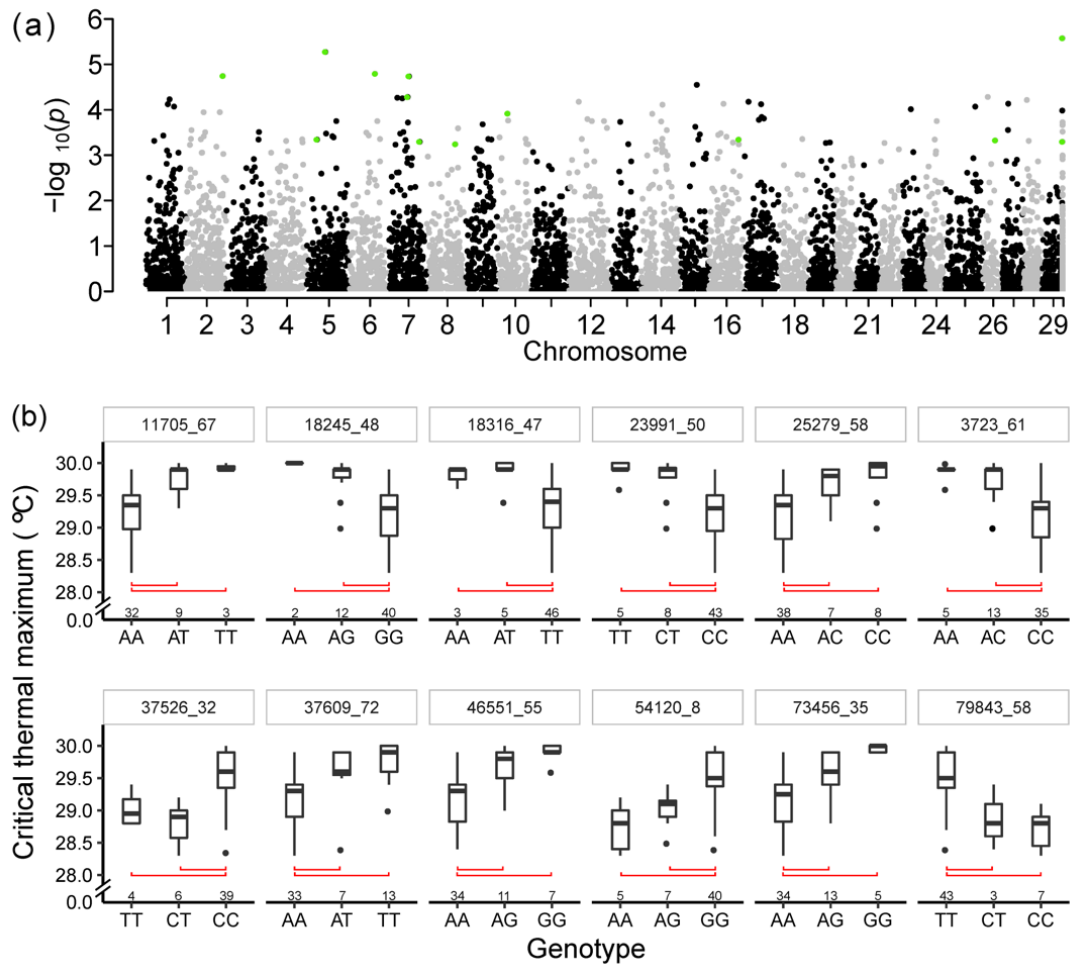


Figure 62. Results from Chen et al. (2018a) that demonstrate association of loci with thermal tolerance in natural populations of redband trout from desert, cool montane, and cold montane environments. Outlier loci and the association with critical thermal maximum (CTMAX). (a) Manhattan plot of calibrated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

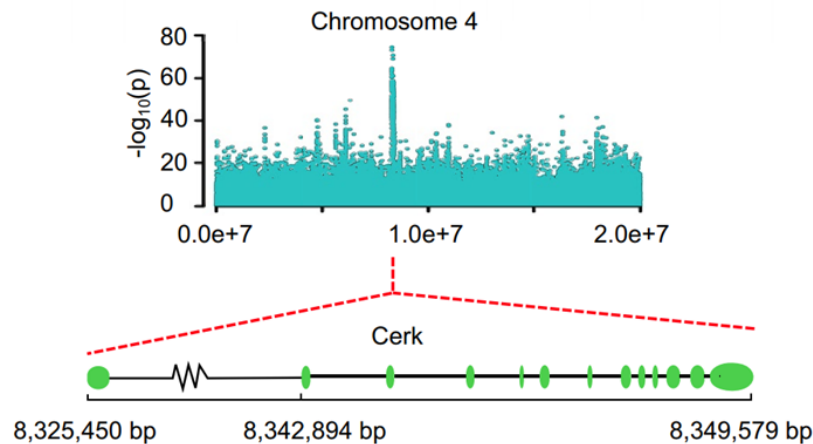


Figure 63. Results from Chen and Narum (2020) that identified a highly significant peak on Chromosome 4 in the *cerk* gene associated with thermal tolerance (survival/mortality) and cardiac performance under heat stress.

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).

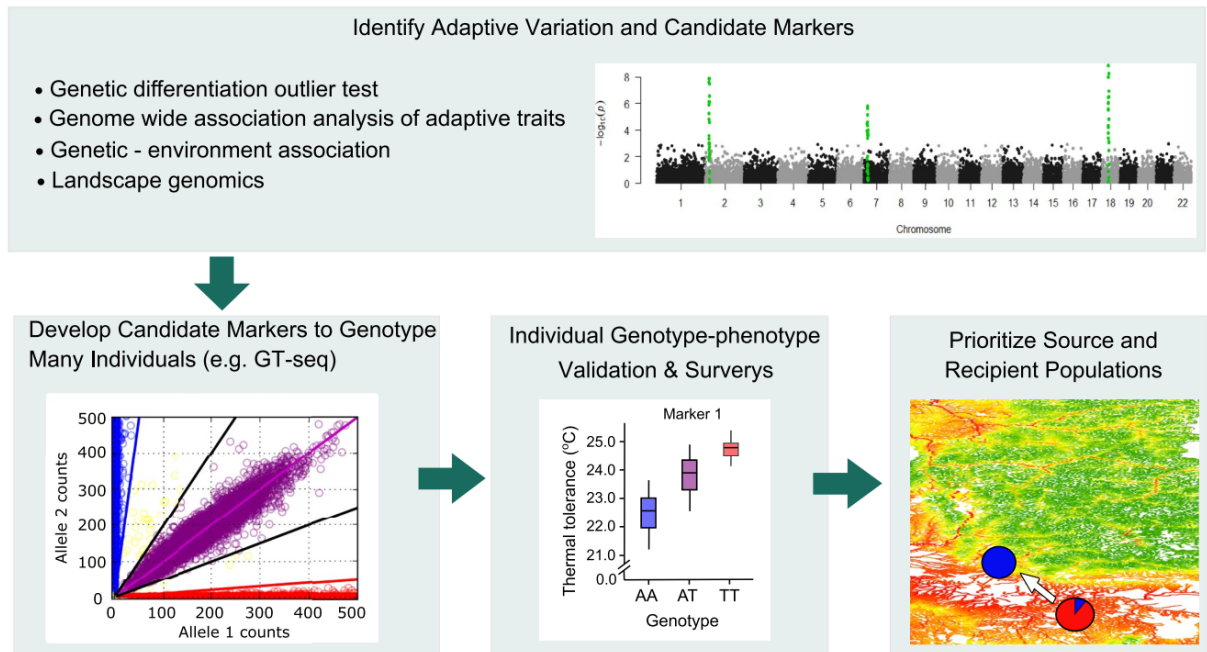


Figure 64. Schematic showing genomic approaches for applying assisted migration with adaptive alleles. The top panel illustrates a Manhattan plot with significant peaks for candidate loci from genome scan approaches, leading to development of specific candidate markers (e.g., genotyping-thousands by 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.

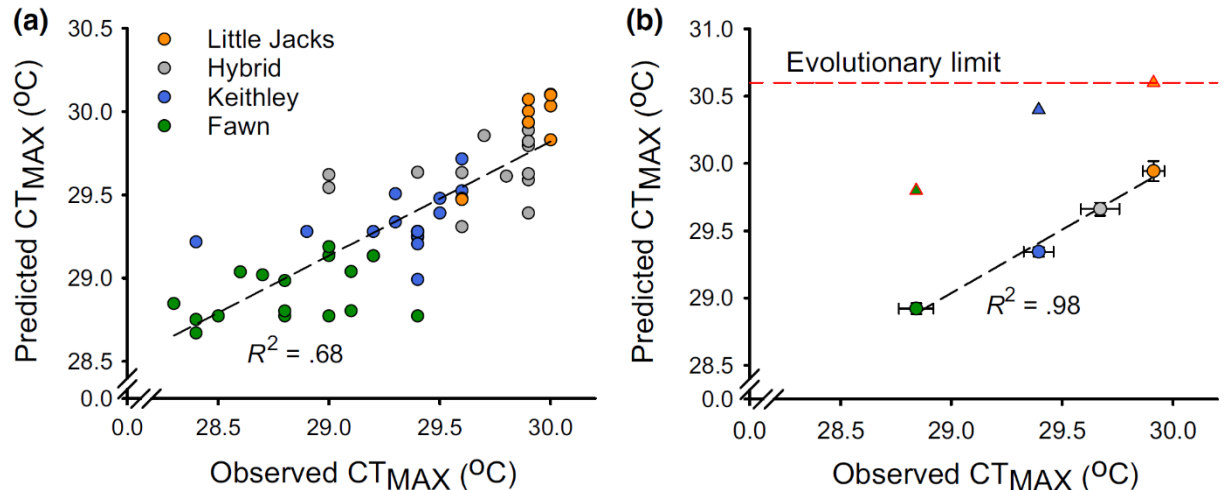


Figure 65. Critical thermal maximum (CTMAX) prediction (from Chen et al. 2018a). (a) Correlation between observed and predicted individual CTMAX values. (b) Prediction of population mean CTMAX (SEM) and evolutionary limits for populations (triangle) and species (dash line).

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 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 we have been using this updated pipeline

to genotype sturgeon samples since. In 2022, we utilized the data collected with our ploidy-sensitive pipeline to conduct and publish analyses of population structure of white sturgeon in the Columbia and other stronghold river basins (Willis et al. 2022). In 2022, we also genotyped targeted collections of adult and young-of-year sampled from the lower/mid-Columbia reaches for a study to understand variation in recruit genetic diversity and ploidy variation and make comparisons to hatchery supplementation cohorts. Analysis of these data is ongoing.

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).

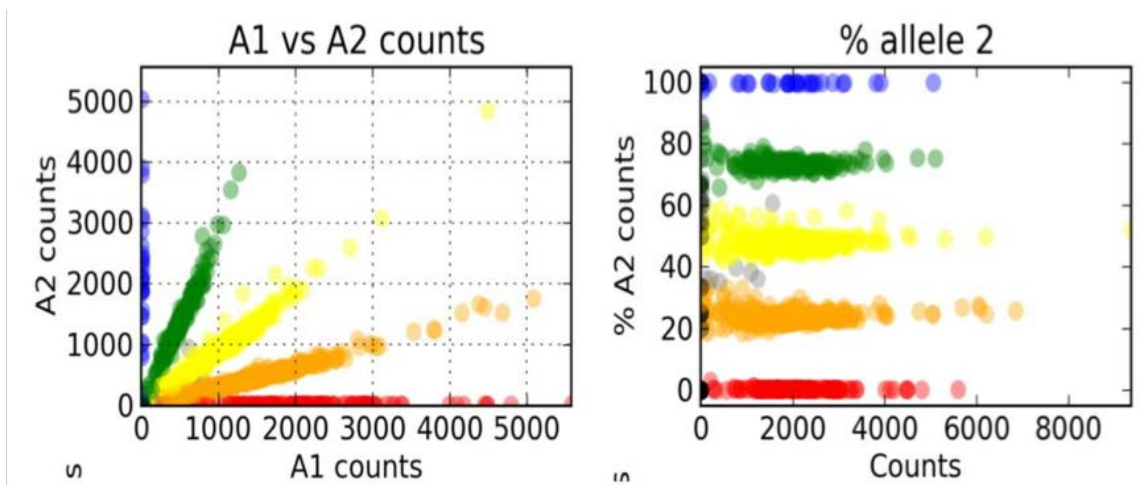


Figure 66. Example of a locus GT-seq plot from octoploid (functionally tetraploid) white sturgeon.

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).

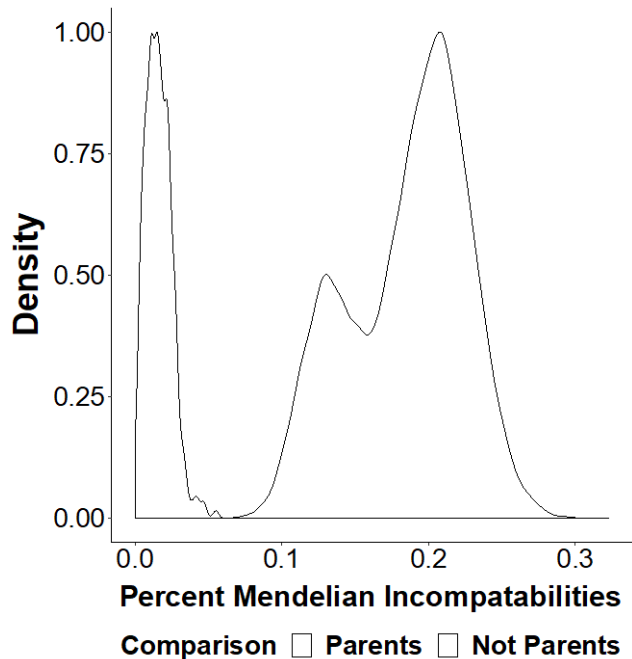


Figure 67. Distribution of Mendelian incompatibilities (parents and offspring with mismatched alleles) observed among all offspring in six reciprocal crosses of white sturgeon.

Given the success in developing this genotyping panel (described in more detail in our 2018 report) and updating our genotyping pipeline (described in more detail in our 2020 report), in 2022, we completed and published our analyses to further resolve population structure of white sturgeon on the US Pacific Coast. Our analyses utilized traditional population genetic methods that are flexible to the ploidy of the samples, rather than being hard coded for diploid, which included population assignment methods such as Structure (Hubisz et al. 2009) as well as parametric methods such as F_{ST} with formulas adapted for higher ploidy.

Results:

Our tissue holdings include over twelve 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 68). 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 the nearby stronghold drainages of Sacramento and Fraser. 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 60). These samples were not discarded, but analyzed separately to evaluate trans-generation dispersal between reaches (a.k.a. close-kin mark recapture). 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).

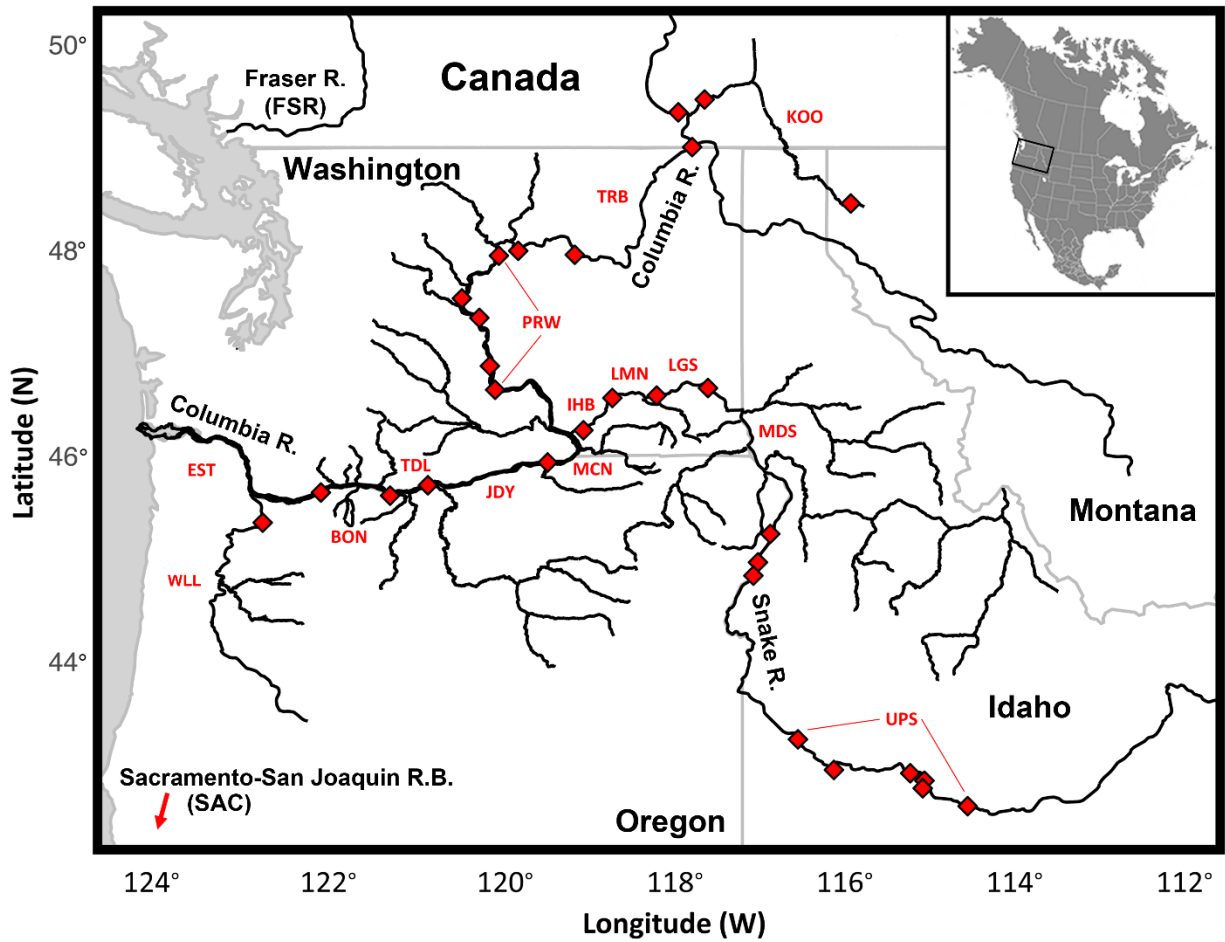


Figure 68. Reaches from which white sturgeon were collected for the study of population structure. Diamonds represent hydroelectric dams or water falls delineating reaches inhabited by white sturgeon analyzed (labeled). Lines indicated reaches from which fish were pooled for group-wise analysis.

Reach	Code	N	r
Sacramento-San Joaquin	SAC	37	37
Fraser River	FSR	44	42
Columbia estuary*	EST	490	432
Willamette	WLL	13	13
Bonneville	BON	504	494
The Dalles	TDL	505	499
John Day	JDY	669	599
McNary	MCN	178	125
Ice Harbor	IHB	108	101
Lower Monumental	LMN	132	124
Little Goose	LGS	112	106
middle Snake	MDS	90	82
upper Snake	UPS	264	169
Priest Rapids-Wells Tailrace	PRW	48	26
Transboundary	TRB	225	183
Kootenai River	KOO	49	46

Table 60. White sturgeon from the Columbia and adjacent basins genotyped for analysis of population structure (N), and filtered by relatedness (r) to exclude first-degree relatives.

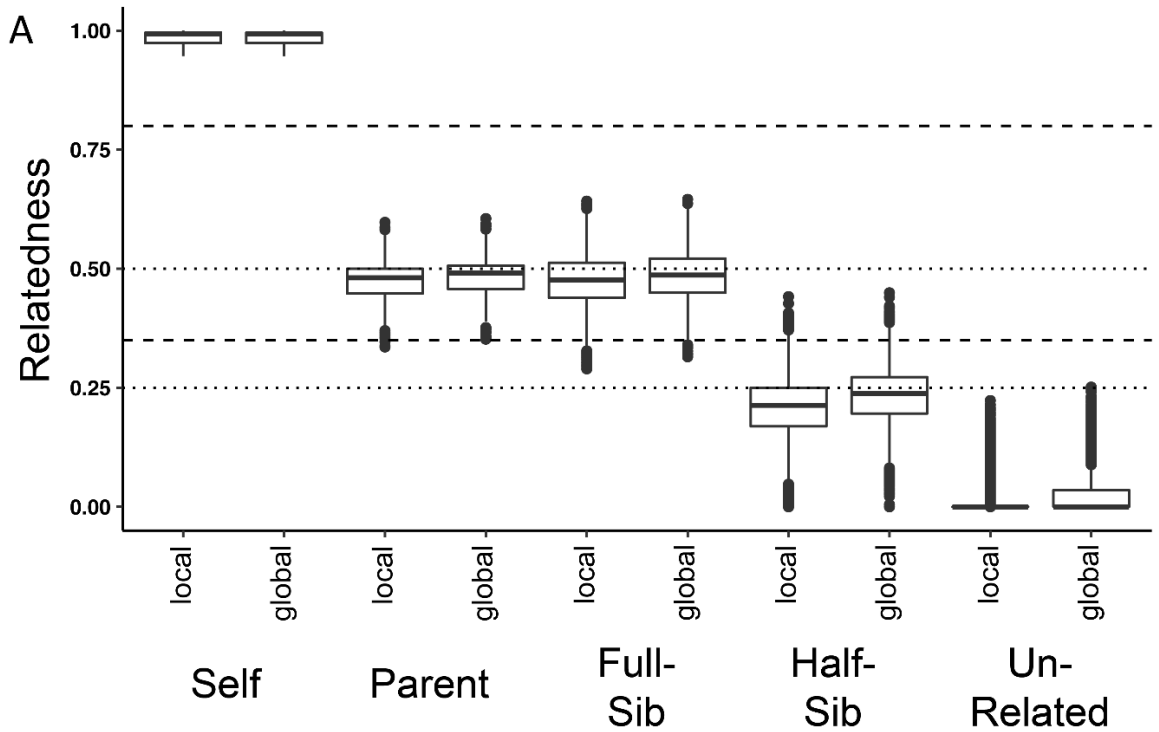
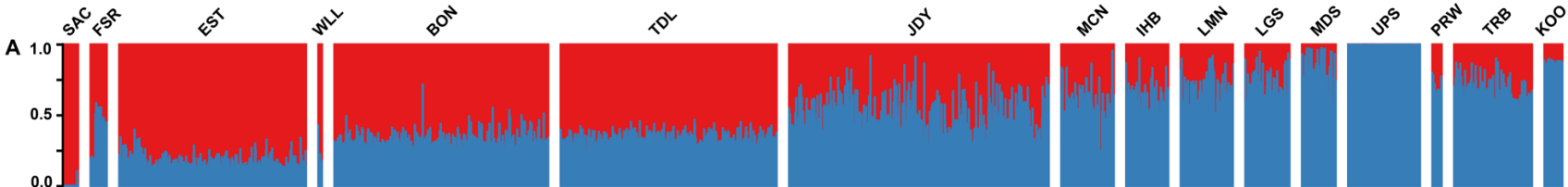


Figure 69. Maximum likelihood estimation of relatedness in known full- and half-sib families from broodstock collected in John Day reach. Estimates were made with local (left) and global (right) allele frequencies. Dotted lines represented the expected relatedness values for first degree and second degree relatives, and the dashed lines represent cutoffs used for identifying repeat captures and filtering first degree relatives.

Results reinforced the observations in previous studies that white sturgeon in the Columbia basin exhibit a gradient of distinctness from the upper reaches to the estuary (Matala et al. 2017) (**Figure 70**). Notably, while the reaches at opposite ends of the basin were significantly if not strongly distinct based on measure of genetic divergence (F_{ST} -analog > 0.1), many adjacent reaches were only marginally or non-significantly divergent (**Table 61**), indicating significant historical connectivity between adjacent sections of the basin but which was constrained by distance. Consistent with this, we also observed several examples of trans-generational (close-kin mark-recapture, CKMR) dispersal events, indicating dispersal across 1-3 hydroelectric facilities and a few hundred kilometers (Table). We were not able to ascertain from meta-data whether the inferred relationships represented parent-offspring, full sibling, or above average 2nd degree relationships, which makes the direction of dispersal difficult to ascertain, but these relationships are consistent with primarily downstream dispersal.

Genotyping efforts in 2022 focused on providing a robust sample of young-of-year fish from multiple years in each lower Columbia River reach, which reflect the genetic diversity of the breeders that contribute to each cohort, and a robust sample of the adult population in each reach (as well as McNary, from which recruits could disperse downstream) (**Table**). These adult samples include the broodstock utilized for hatchery-based supplementation in the John Day reach, which across years is not characterized by appreciable recruitment. Through empirical and simulated genotypes of hatchery offspring using these broodstock samples, we will compare the magnitude and dynamics of genetic diversity in recruits across time, among reaches, and between natural and hatchery cohorts.

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Figure 70. Bar blots of admixture proportion of individual white sturgeon to an optimized $k^*=2$ populations made with Structure.

	SAC	FSR	EST	WLL	BON	TDL	JDY	MCN	IHB	LMN	LGS	MDS	UPS	PRW	TRB	KOO
Sacramento SAC	--	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 FSR	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
Columbia estuary EST	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 WLL	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 BON	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 TDL	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 JDY	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 MCN	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 IHB	0.097	0.042	0.041	0.036	0.018	0.017	0.008	0.002	--	--	--	0.005	0.049	0.007	0.009	0.177
Lower Monumental LMN	0.106	0.047	0.048	0.046	0.023	0.022	0.012	0.004	--	--	--	0.003	0.042	0.006	0.010	0.175
Little Goose LGS	0.107	0.045	0.049	0.046	0.023	0.022	0.012	0.002	--	--	--	0.002	0.041	0.006	0.009	0.169
middle Snake MDS	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 UPS	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 Rapids-Wells PRW	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
Transboundary TRB	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 KOO	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	--

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Table 61. Genetic distinctness (G_{ST}) by reach for white sturgeon sampled in the Columbia River and adjacent basins. Values not significant after correction for multiple tests were omitted. Color indicates magnitude of divergence

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Reaches	CKMR
Columbia estuary (EST) and Willamette (WIL)	1
Columbia estuary (EST) and The Dalles (TDL)	1
Bonneville (BON) and John Day (JDY)	3
John Day (JDY) and McNary (MCN)	4
John Day (JDY) and Ice Harbor (IHB)	1
John Day (JDY) and Lower Monumental (LMN)	1
John Day (JDY) and Priest Rapids-Wells Tailrace (PRW)	3
McNary (MCN) and Lower Monumental (LMN)	1
McNary (MCN) and Little Goose (LGS)	3
McNary (MCN) and Priest Rapids-Wells Tailrace (PRW)	7
Ice Harbor (IHB) and Lower Monumental (LMN)	3
Ice Harbor (IHB) and Little Goose (LGS)	1
Ice Harbor (IHB) and middle Snake (MDS)	2
Lower Monumental (LMN) and Little Goose (LGS)	7
Lower Monumental (LMN) and middle Snake (MDS)	4
Little Goose (LGS) and middle Snake (MDS)	5

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Table 62. Inferred trans-generational dispersals among reaches through close-kin mark-recapture (CKMR), or related pairs among reaches, inferred as the intersection of high relatedness and high probability of sibship.

	Collection Year														Totals
	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2021	2022	
Young-of-year (<30cm)															
below Bonneville	0	39	0	40	58	11	45	40	40	0	0	0	0	0	273
Bonneville	58	41	20	53	45	11	45	40	0	40	0	0	0	0	353
The Dalles	40	42	41	101	51	13	32	0	0	40	0	0	0	0	360
John Day	0	0	4	58	35	0	0	0	0	0	0	0	0	0	97
															1083
Adults/sub-adults															
below Bonneville	0	0	13	0	18	15	48	28	27	10	0	0	0	0	159
Bonneville	0	0	0	0	44	0	0	40	70	0	0	0	0	0	154
The Dalles	0	0	0	24	0	0	89	0	0	35	0	0	0	0	148
John Day	0	0	5	0	7	219	45	123	106	99	120	138	79	73	1014
McNary	0	0	71	86	0	0	0	0	0	0	0	0	0	0	157
															1632

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Table 63. Sample sizes of individuals genotyped at 80% completeness and ploidy confidence of 10LLR across year and life stage for the lower Columbia River reaches.

Discussion:

One of the ongoing challenges with our objectives for white sturgeon is the nature of white sturgeon themselves: functional tetraploid status, as indicated by the mendelian segregation of four alleles at most SNP loci (Figure 66). However, the majority of genetic 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 (Figure 67), we continue to explore more robust methods to fully utilize the information content of tetraploid genotypes.

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 published results with SNP data are consistent with 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 reach, 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 to assist in ordering and orienting (anchor) smaller scaffolds into chromosomes. In 2021, we utilized data from a reduced representation (restriction enzyme associated DNA, or RAD) genomic libraries of a reduced-ploidy Fraser River family 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), in 2022 sequenced these RNA libraries from head/brain tissue as input for another linkage map. 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).

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 and Sockeye 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 2021. 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).

1103 For Objective 5 on local adaptation, candidate genes for several traits have been
1104 identified in both steelhead and Chinook salmon. As these candidate genes for traits have begun
1105 to be identified, SNP markers from these regions are being incorporated in standard genotyping
1106 panels with GTseq to validate and monitor genetic variation for these traits in large numbers of
1107 individuals. Inclusion of candidate markers associated with specific traits allows more detailed
1108 genetic monitoring of stocks in the Columbia Basin. Extensive programs are in place that enable
1109 genetic identification of the origin of individual fish, but candidate markers from this study also
1110 provide the ability to monitor genetic variation for specific traits that are expected to be
1111 necessary to maintain life history variation for long term persistence of populations.

1112 For Objective 6 on white sturgeon genetics, the accumulation of genetic monitoring
1113 results since 2008 for White Sturgeon in the Middle Columbia River and Snake River are similar
1114 to evaluations of population structure reported for other large systems like the Fraser River in
1115 British Columbia Canada. Current demographic trends and genetic variation may be a
1116 consequence of diminished rearing and/or spawning habitat coincident with stream
1117 fragmentation and limited connectivity. Ongoing efforts for this project are designed to utilize
1118 SNP markers that were developed for this species to further resolve regional population structure
1119 and parentage analyses to support tribal efforts to supplement white sturgeon in the Columbia
1120 Basin.