GENETIC ASSESSMENT OF COLUMBIA RIVER STOCKS

BPA Project # 2008-907-00
Report covers work performed and completed under BPA contract #(s) 73354 REL 87 (4/1/23 – 3/31/2024) and 73354 REL 72 (4/1/22 – 3/31/23)
1/1/2023 – 12/31/2023

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This report was funded by the Bonneville Power Administration (BPA), U.S. Department of Energy, as part of BPA's program to protect, mitigate, and enhance fish and wildlife affected by the development and operation of hydroelectric facilities on the Columbia River and its tributaries. The views in this report are those of the authors and do not necessarily represent the views of BPA.

This report should be cited as follows:
Jon E. Hess et al. 2024, GENETIC ASSESSMENT OF COLUMBIA RIVER STOCKS, 1/1/2023 - 12/31/2023 Annual Report, 2008-907-00

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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 genotyping more samples and loci in less time and at significantly cheaper cost than our previous 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 and 17 additional amplicons for species identification); Coho salmon (*O. kisutch* – 248 loci including two sex determination markers and 11 additional markers used for species identifiication), White sturgeon (*Acipenser transmontanus* – 325 loci), Pacific lamprey (*Entosphenus tridentatus* – 294 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 GT-seq markers will be developed for SNPs identified from Pool-seq data in the coming year. Our GT-seq panels were used to genotype 145,937 samples in 2023 (**Figure 1**). The largest portion of samples were Chinook salmon (85,140), then Pacific lamprey (21,419), Steelhead (17,679), Coho (15,181), Sockeye (6,042), and White sturgeon (476).

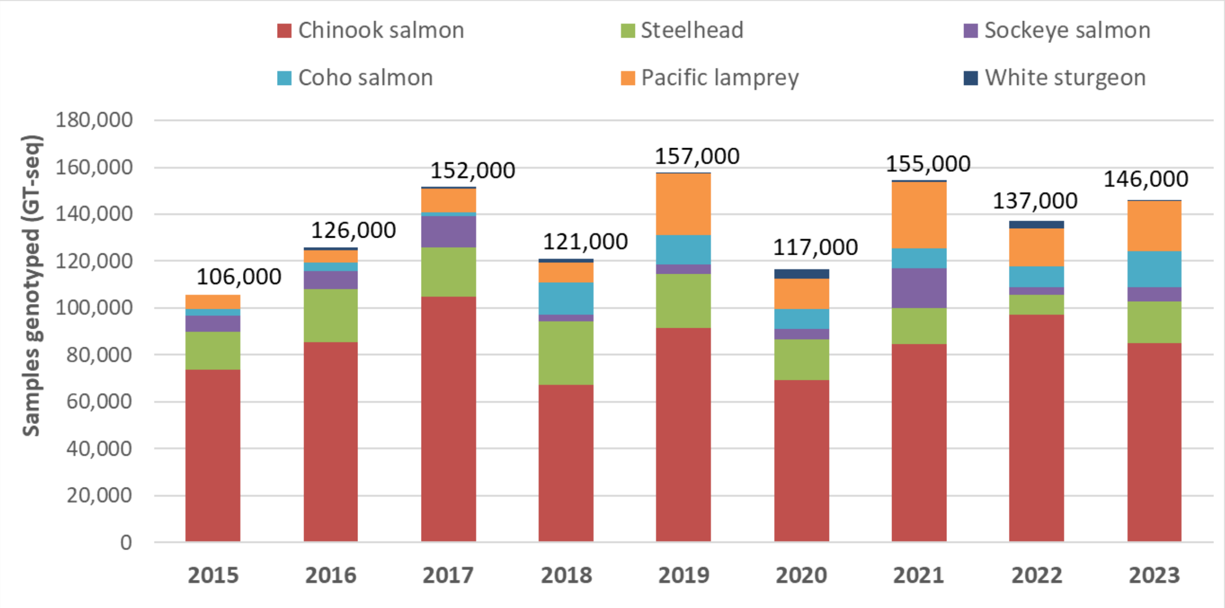

Figure 1. Summary of Columbia River fish samples genotyped using GT-seq (2015 – 2023).

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).

Two of the three projects initiated to characterize reference baselines of millions of SNPs for Chinook Salmon and *O. mykiss* were completed in 2023, with the third, focused on Coho salmon, still ongoing. 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. The publication of millions of allele frequencies across populations within the Columbia River basin can be used to further refine GSI and PBT applications for our study species. In 2023, a study was initiated to select new SNP markers from the Chinook salmon whole genome re-sequencing data to refine GSI reporting groups and increase assignment accuracy. In addition, these projects will be able to utilize SNPs for several other applications that involve elucidation of genetic mechanisms underlying fitness traits of interest.

Objective 3) implement GSI programs for mainstem Chinook salmon, Sockeye salmon, and steelhead fisheries. In this section, we first described a new method for estimating abundance from catch estimates and at Bonneville Dam using functions that minimize bias from expansion of PBT tag rates. This method allowed us to take PBT tag rates into account, and accurately estimate attributes of natural-origin fish without being influenced by the attributes of unmarked hatchery-origin fish that were not assigned with PBT. We have continued implementing this approach in all our harvest estimates for 2021-2023. 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 2022 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 831 coded-wire tags (CWTs) that were identified to hatchery stock and broodyear (BY) among the snouts recovered from the lower river fisheries in 2022, and 630 of these CWTs also were PBT assigned (76%). Of the 630 fish with both CWT and PBT, there were 575 fish (91%) that were concordant across results from these tagging methods according to the hatchery source and the broodyear.

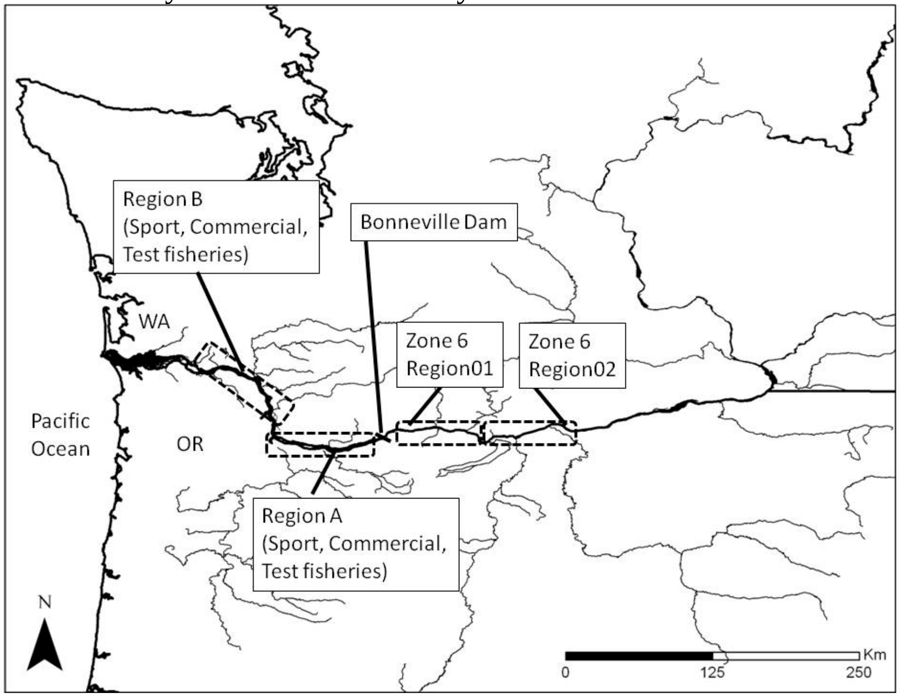

Figure 2. Sources of fishery mixtures in the lower Columbia River mainstem.

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. 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 2 weeks (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.

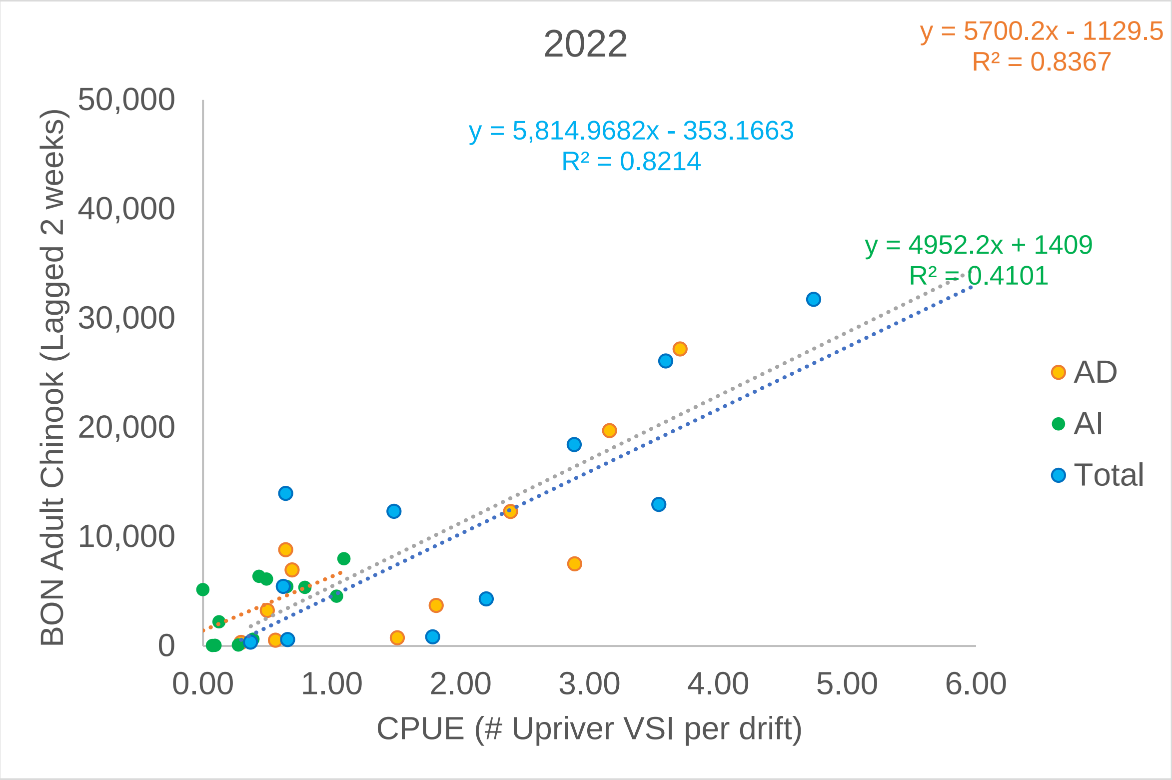

Figure 3. The relationship between the test fishery upriver Chinook Salmon CPUE and weekly fish counts at Bonneville Dam in 2022 with 2 week lag.

As expected, the stock composition varied substantially across the Non-Treaty sport 2022 fisheries that were executed in the spring and summer periods. However, the largest difference in stock compositions across the spring and summer fisheries was the high estimates of of upper Columbia summer-run stock (18_UCOLSF) and lower river stock from the Willamette River (04_WILLAM) captured below Bonneville Dam in the spring and summer periods compared to the spring sport fishery in Zone 6 (Figure 4). This relatively high capture rate of 04_WILLAM stock below Bonneville Dam is generally expected when compared to Zone 6 because the stock does not typically pass upstream of the dam in high numbers. The presence of 18_UCOLSF stock in the sport fishery below Bonneville Dam and absence of this stock in the sport fishery above Bonneville Dam may have been due to timing of the fishing effort weighted more heavily in June in the fishery below Bonneville Dam when the summer Chinook are present in higher numbers.

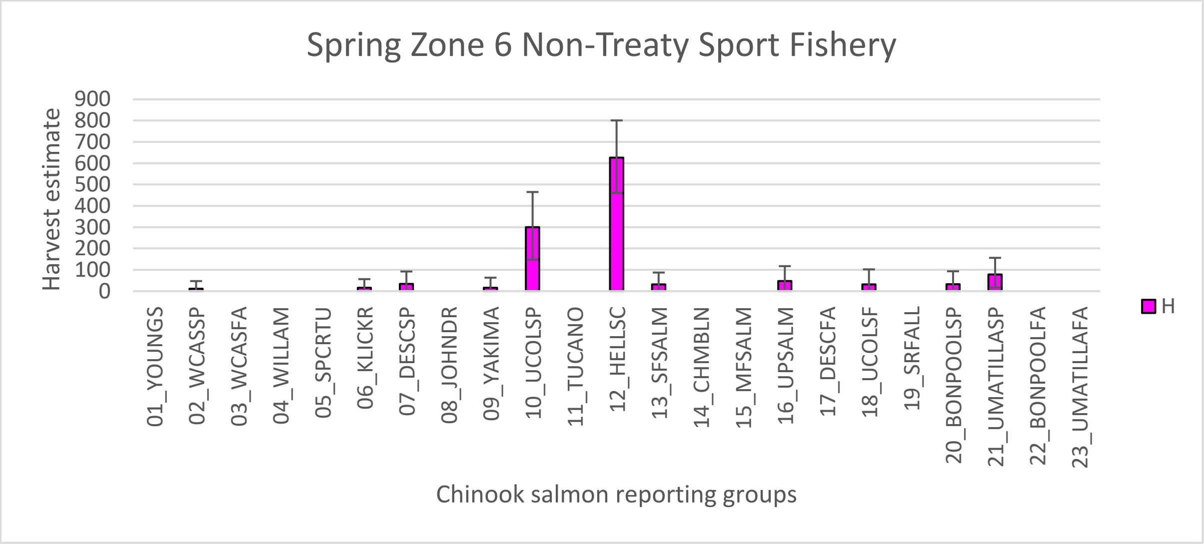

Figure 4. Genetic stock composition of the Non-Treaty Zone 6 Sport Chinook fishery during the spring period analyzed in 2022.

In 2022, we sampled the Non-Treaty Sport fisheries above and below Bonneville Dam and the Non-Treaty Commercial fishery below Bonneville Dam during the Fall Chinook salmon management period. We continue to find that despite both the Non-Treaty sport and commercial fishery being executed at similar times near Bonneville Dam, the sport fishery is comprised of dramatically lower abundance of “tules” (Figure 5). This difference may be largely due to sport fishers preferentially keeping the VSI bright fish over the tule fish.

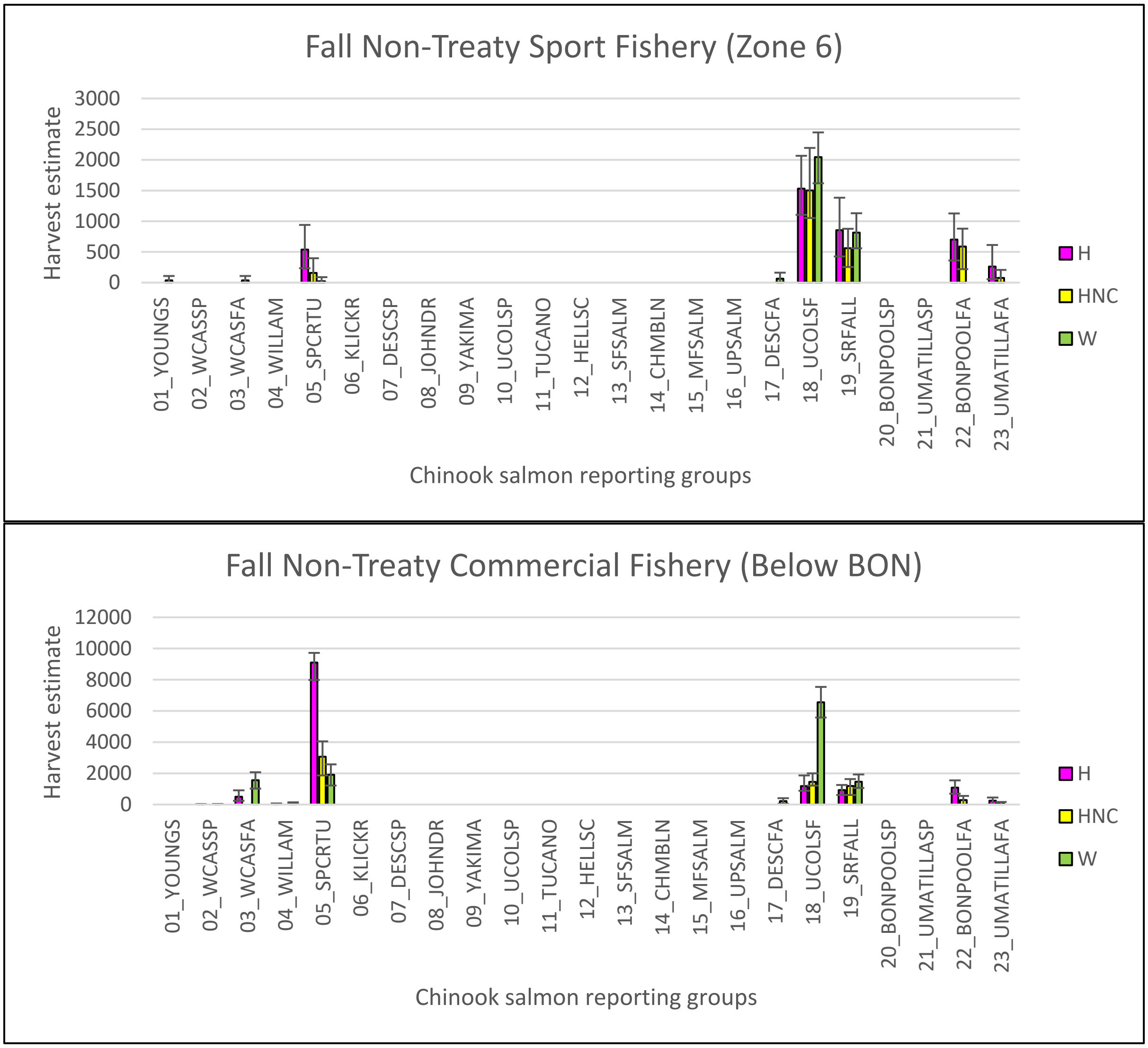

Figure 5. Genetic stock composition of the Fall Non-Treaty Chinook salmon fisheries analyzed in 2022.

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 2022 (post-season analyses). Further, in-season analyses were completed for fish returning throughout 2023 and provided to regional fisheries managers that serve the U.S. v OR Technical Advisory Committee (TAC).

In 2022, there were 11 major (i.e., abundance >1000 fish) Chinook salmon stocks represented in the total estimated relative abundance (N=141,588) of natural-origin (i.e., excluding unclipped hatchery-origin fish) Chinook salmon passing Bonneville Dam in 2022 (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 (71,689), 19_SRFALL (18,817), 05_SPCRTU (14,435), 12_HELLSC (8,773), 10_UCOLSP (7,088), 13_SFSALM (5,506), 17_DESCFA (3,921), 16_UPSALM (3,178), 04_WILLAM (2,279), 15_MFSALM (2,140), and 09_YAKIMA(1,764). These stock abundance estimates were generated using SCOBI DEUX and SPIBETR functions and the estimates of clipped and unclipped adults distributed by TAC.

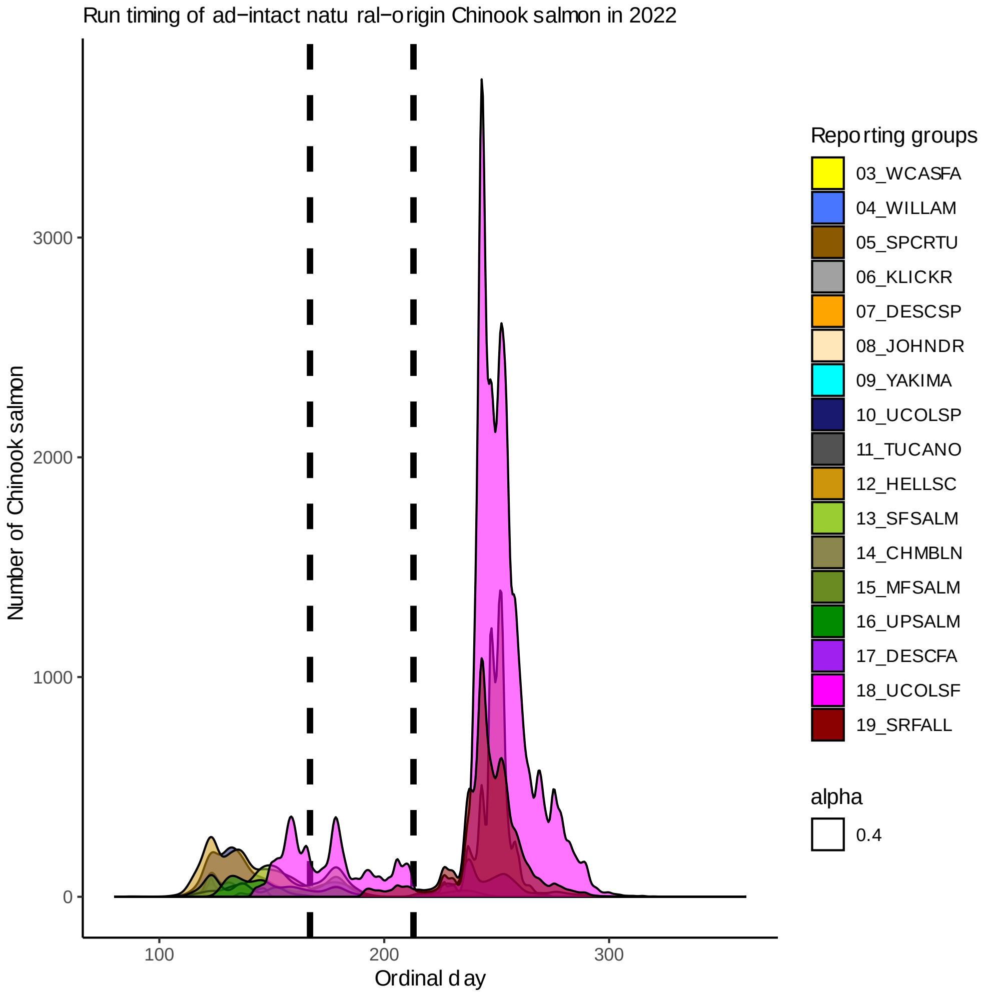

Figure 6. Estimated abundance of natural origin (excluding adipose-intact hatchery-origin fish) adult-sized Chinook salmon reporting groups at Bonneville Dam in 2022.

There were five major stocks (abundance >1000) represented in the total estimated abundance (N=82,033) of clipped hatchery origin steelhead passing Bonneville Dam in 2022. These stocks in order of decreasing magnitude were 07_MGILCS (27,302), 10_SFCLWR (20,174, B-Index; 3,942 A-Index), 14_UPSALM (19,830), 09_UPPCOL (5,701 A-Index; 1,100 B-Index), and 03_SKAMAN (3,008) (Figure 7). There were two major stocks (abundance >1000) represented in the total estimated abundance (N=5,025) of unclipped hatchery origin steelhead passing Bonneville Dam in 2022 (14_UPSALM, A-Index; 10_SFCLWR, B-Index). There were four major stocks (abundance >1000) represented in the total estimated abundance (N=29,911) of natural origin (excluding adipose unclipped hatchery-origin fish) summer A-/B-Index steelhead passing Bonneville Dam in 2022 (Figure 7). These stocks in order of decreasing magnitude were 07_MGILCS (17,835 A-Index; 1,831 B-Index), 14_UPSALM (2,097 A-Index), 11_UPCLWR (1,593, B-Index), and 06_KLICKR (1,308). The results of the SCOBI DEUX 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.

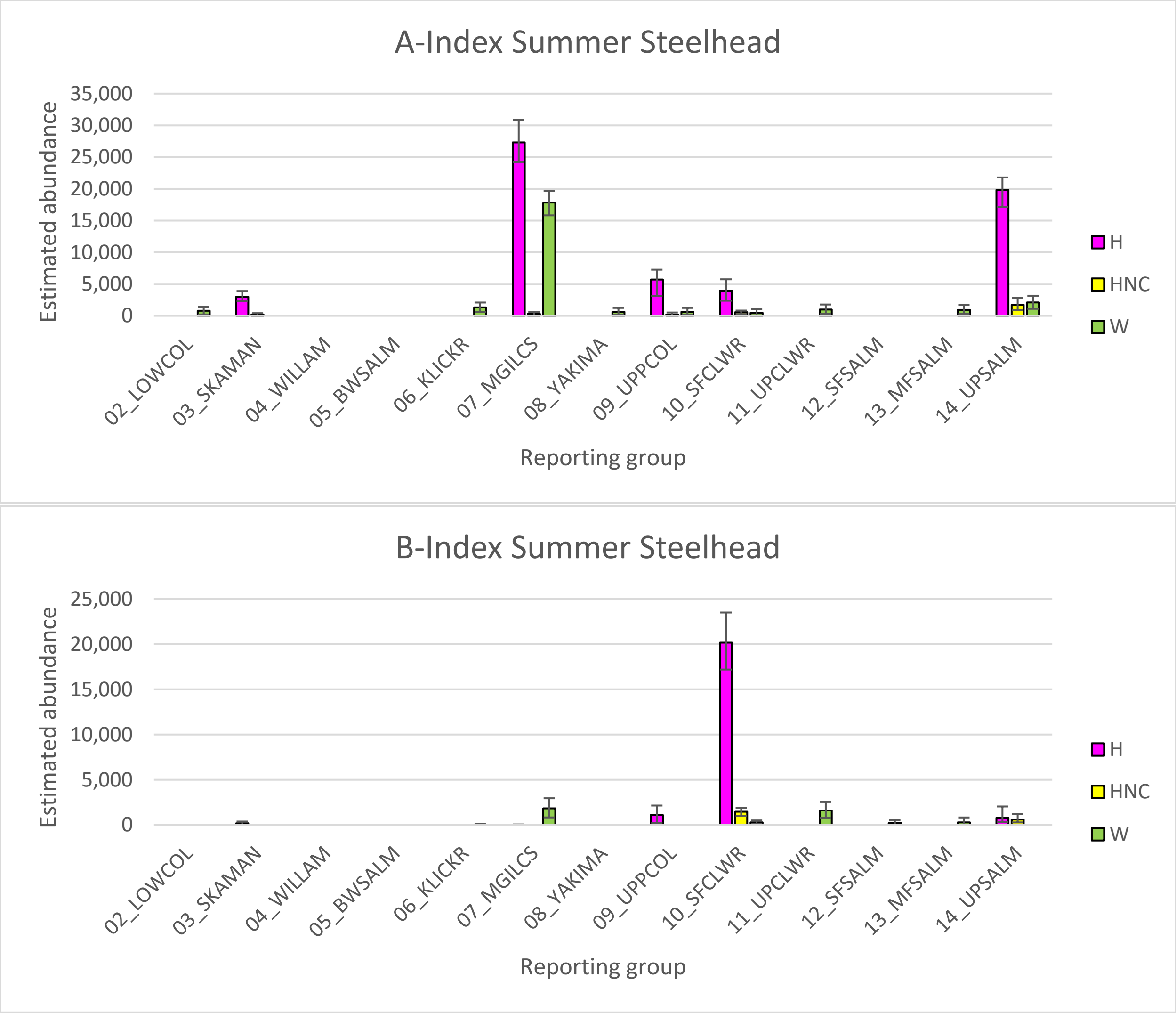

Figure 7. Estimated abundance (± 95% CI) of A-Index (<780mm FL, top) and B-Index (>=780mm FL, bottom) hatchery origin (clipped "H" and unclipped "HNC") and natural-origin ("W") steelhead assigned to genetic stock of origin that were sampled at Bonneville Dam in 2022.

Stock abundance for sockeye salmon was estimated over a course of 18 statistical weeks (i.e. weeks 22 – 39). A total of 1,303 sockeye salmon were sampled at Bonneville Dam in 2022 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 2022, The Okanogan stock had the highest relative abundance (513,367), followed by the Wenatchee (147,430). This year there were a small number of sockeye estimated from Snake River (2,456). The Lake Billy Chinook stock had zero estimated abundance. The reintroduced stock from Yakima River also had zero estimated abundance in 2022 (Figure 8).

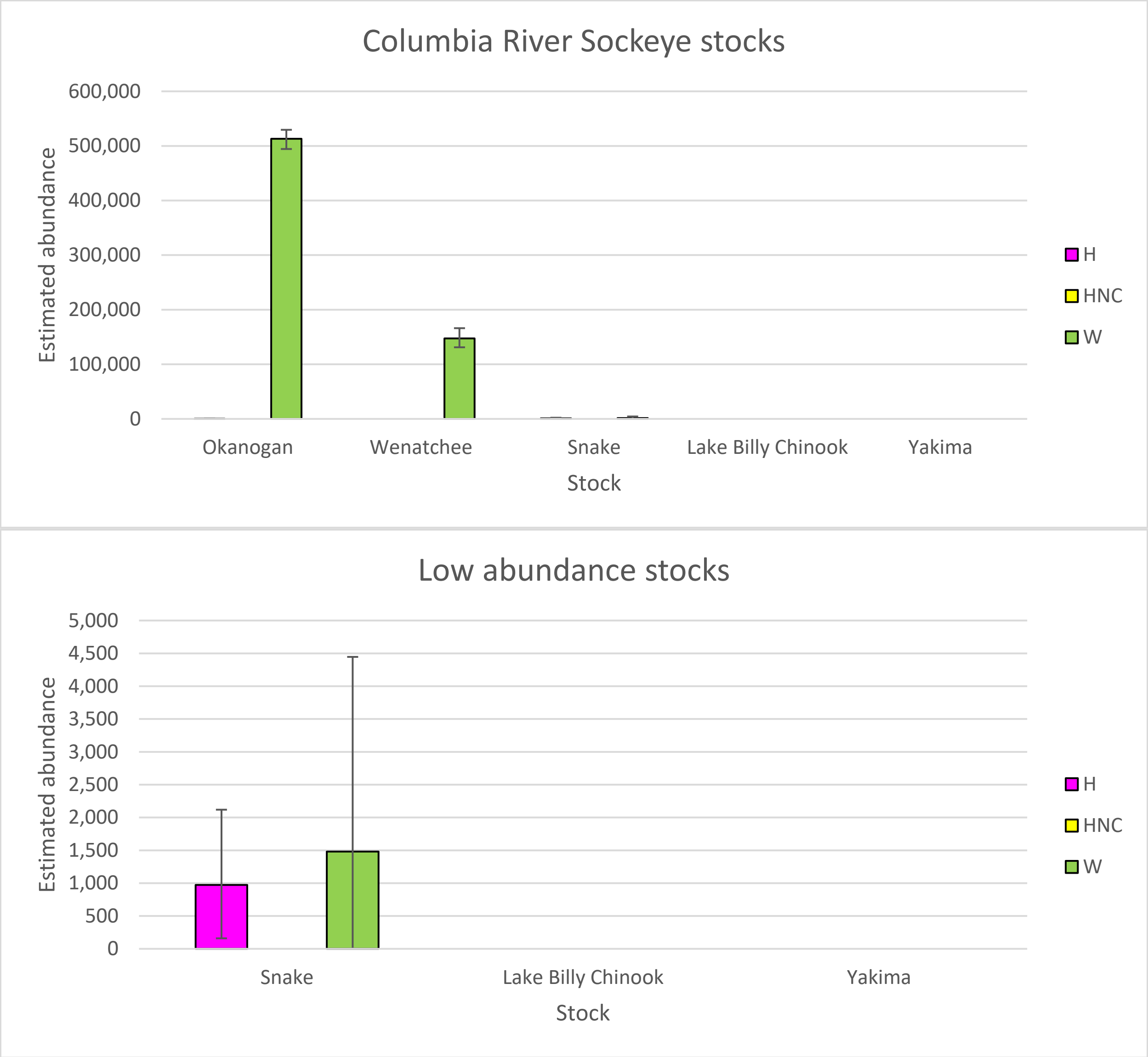

Figure 8. Estimated abundance (± 95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2022.

In 2022, 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 41% (4,591 fish) and 58% (6,459 fish) of the total abundance estimated in those two periods, respectively. For natural-origin 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 one reporting groups (Figure 9). Run timing distributions for sockeye salmon sampled at Bonneville Dam broadly overlapped in 2022. The Wenatchee, Okanogan, Snake, and Yakima stocks had nearly identical run timing distributions each with an average median date on 06/28/22.

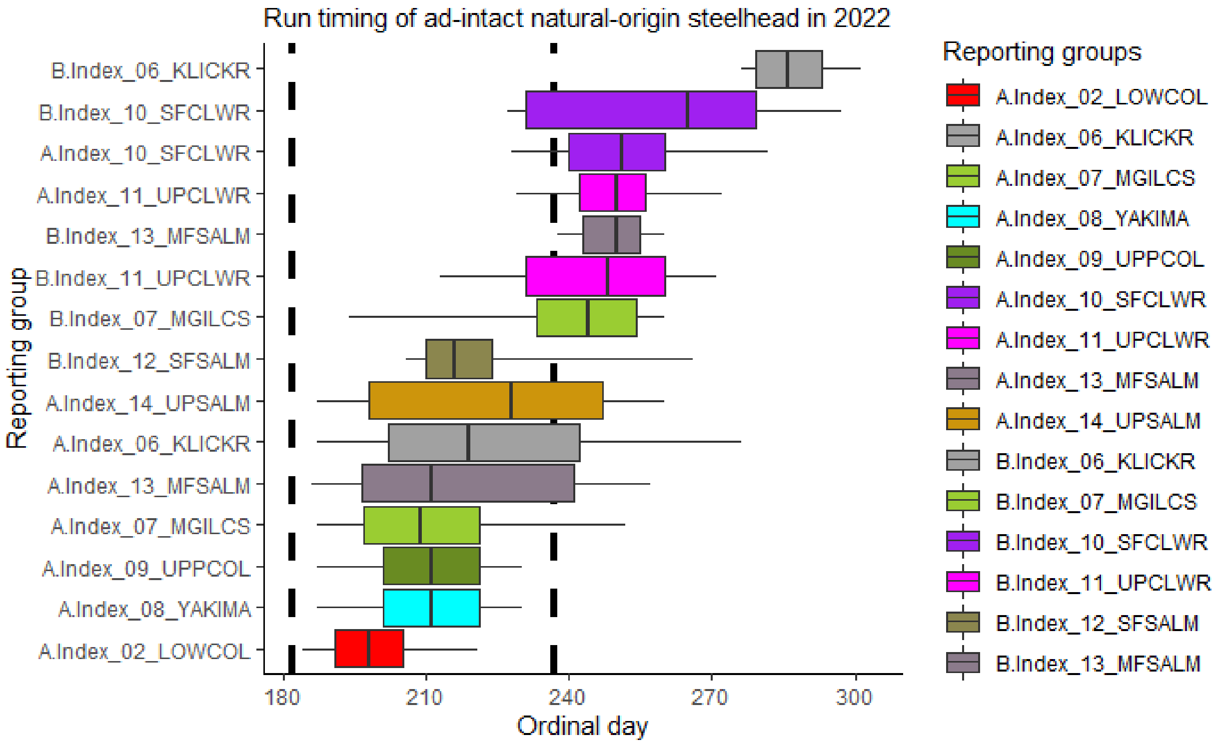

Figure 9. Reporting group level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for natural-origin steelhead (unclipped hatchery-origin fish excluded) that were sampled at Bonneville Dam in 2022 and split by A-Index and B-Index size category. August 25th 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 2023 (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 was non-zero abundance estimated for Sockeye salmon that returned to Bonneville Dam in 2023 originating from the Yakama Nation reintroduction program in the Yakima River basin (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 2023 fish runs for Chinook salmon, steelhead, and Sockeye salmon.

Species	Management Period	Data coverage	Samples Arrive	Analysis begins	Report distributed
Chinook	Spring	01/01/2023 – 04/30/2023	5/1/2023	5/4/2023	5/8/2023
		01/01/2023 – 05/14/2023	5/15/2023	5/18/2023	5/22/2023
		01/01/2023 – 05/28/2023	5/30/2023	6/2/2023	6/5/2023
		01/01/2023 – 06/15/2023	6/16/2023	6/21/2023	6/23/2023
	Summer	06/16/2023 – 07/02/2023	7/5/2023	7/11/2023	7/12/2023
		06/16/2023 – 07/31/2023	8/1/2023	8/4/2023	8/7/2023
	Fall	08/01/2023 – 8/27/2023	8/28/2023	8/31/2023	9/4/2023
		08/01/2023 – 10/29/2023	10/30/2023	11/2/2023	11/6/2023
Steelhead	Skamania	04/01/2023 – 06/30/2023	7/5/2023	7/11/2023	7/12/2023
	Summer A-/B-Index	07/01/2023 – 07/31/2023	8/1/2023	8/4/2023	8/7/2023
		07/01/2023 – 08/27/2023	8/28/2023	8/31/2023	9/4/2023
		07/01/2023 – 10/31/2023	10/30/2023	11/2/2023	11/6/2023
Sockeye	Total	01/01/2023 – 07/31/2023	8/1/2023	8/4/2023	8/7/2023

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 Roger Dick Jr for distribution to TAC members.

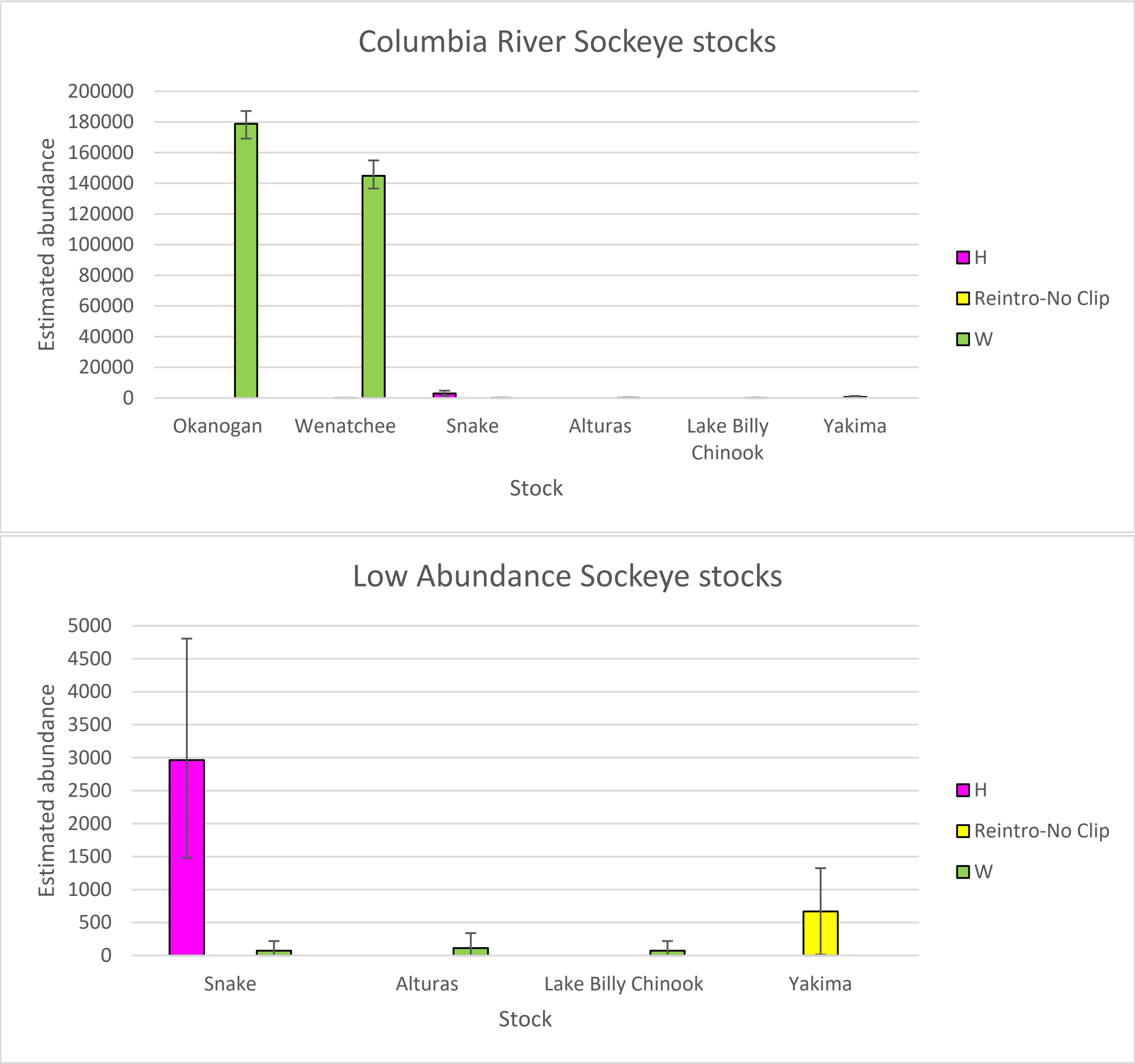

Figure 10. In-season analysis estimated a relatively large return of sockeye salmon overall in 2023 comprised of a mixture of Wenatchee and Osoyoos genetic stocks and non-zero abundance estimated from Snake River and Yakima River.

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 (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; Collins et al. 2022), 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). Run-timing related to maturity in steelhead (Hess et al. 2016; Micheletti et al. 2018c; Collins et al. 2020; Willis et al. 2020; Willis et al. 2023) and Chinook salmon (Hess and Narum 2011; Narum et al. 2018; Koch and Narum 2020; Willis et al. 2021; Horn and Narum 2023) has been shown to be controlled by a genomic region of major effect with the same candidate genes in both species (*GREB1L*, *ROCK1*, intergenic region; Figure 53). The major findings of studies to date were synthesized in a recent publication (Narum et al. 2023). A recent whole genome resequencing study in Chinook salmon demonstrated the breadth of allele frequency differences among early vs. late migrating populations (**Figure 11**) and verified the presence of a duplication in this region (Horn and Narum 2023). 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.

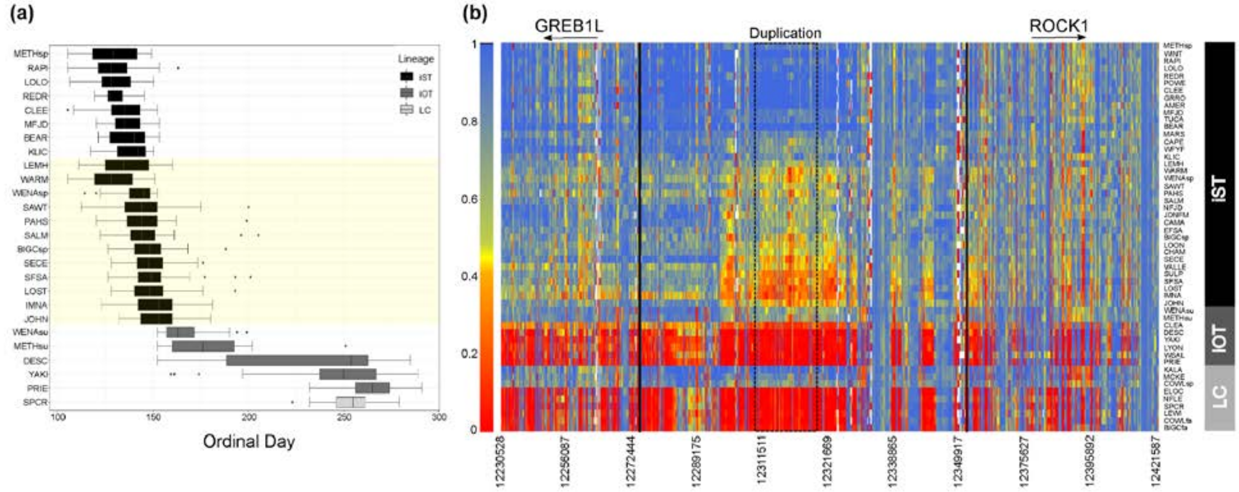

Figure 11. Allele frequencies for hundreds of SNPs spanning GREB1 through ROCK1 for 53 populations of Chinook Salmon based on whole genome sequencing (Horn and Narum 2023).

A) Populations are sorted within each lineage by adult migration timing with early at the top and late at the bottom. Lineages include interior stream-type (iST), interior ocean-type (iOT), and coastal (Lower Columbia/LC). The yellow shaded box corresponds to populations in the iST lineage that exhibited heterozygosity for the duplicated block within the intergenic region as noted by Horn and Narum (2023). B) Allele frequencies for populations within each lineage of Chinook Salmon with early allele frequencies in blue and late allele frequencies in red. The duplicated region found by Thompson et al. (2020) is outlined by a dashed box. For a list of population abbreviations, see Horn and Narum (2023).

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 diversity are likely to aid managers in understanding the impacts of limited habitat in the confines of the mid-Columbia impoundments that may be exacerbated by further anthropogenic influences.

Acknowledgements

The authors thank the following individuals and organizations for providing time and expertise toward this project: The Bonneville Power Administration for providing funding for this research project and to its staff for their assistance. Tissue samples were collected and provided by Ken Keller, Chris Kern, Terra Schultz, Jason Vogel, John Whiteaker, Marc Whitman, Bill Young, and Joe Zendt. Collection of samples from the Non-Treaty commercial, sport, and test fishery were coordinated with Ken Keller, Beth Deacy, and Bonnie Jackman. We are grateful for extensive contributions in the genetics laboratory from Janae Cole, Ben Fredericksen, Travis Jacobson, Lori Maxwell, Megan Moore, Vanessa Morman, and Mike Parks. John Whiteaker, Devayne Lewis, Megan Moore, and Janae Cole coordinated broodstock sample collections for parentage based tagging analyses. John Whiteaker and Jeff Fryer lead the sampling program at the Bonneville Dam AFF, and John Whiteaker coordinates the CRITFC technicians for PBT sampling. Substantial data and statistical guidance was contributed by Idaho Department of Fish and Game, and the following agencies made significant biological tissue and/or DNA sample contributions: Washington Department of Fish and Wildlife, United States Fish and Wildlife Service, Abernathy Fish Technology Center, and NOAA fisheries.

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, Coho salmon. PBT is used to monitor translocations of lamprey throughout the interior of the Columbia River, and reintroductions of Coho salmon in the upper Columbia and Snake River basins, 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 2022. 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 2022. 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 2023. These in-season and post-season 2023 results were provided to fisheries managers that participate on the U.S. v OR 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) and parentage-based tagging (PBT). 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 facilities high-throughput, rapid identification of genetic variation. In the past, we have used methods such as restriction-site associated DNA sequencing (RAD-seq: Method: RAD (Restriction site Associated DNA) sequencing v1.0 (monitoringresources.org)) 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: Method: Whole Genome Resequencing: Poolseq Individual Barcode v1.0 (monitoringresources.org)). Whole genome resequencing methods include individually barcoded samples or pools of samples (Pool-seq, Method: Whole Genome Resequencing: Poolseq Pooled v1.0 (monitoringresources.org); 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: Method: SNP genotyping using Genotyping in Thousands (GT-seq) on Illumina Sequencer platform v1.0 (monitoringresources.org)) 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: Method: SNP genotyping using Genotyping in Thousands (GT-seq) on Illumina

Sequencer platform v1.0 (monitoringresources.org)) Parameters used for primer design are as follows (product size range: 50-120 bases, optimal annealing temperature: 60°C, primer size range: 18-24 bases, optimal GC content: 50%). Primers were then screened for hetero-dimers and specificity using MFEprimer3 (Wang et al., 2019).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 alongside routine genetic monitoring collections. 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. GT-seq 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/zakrobinson/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.

Although rare, non-target species in genetic monitoring collections can increase material and personnel costs due to failed genotyping attempts on the incorrect, species-specific GT-seq panel. To address this issue, we used existing amplicons within four species-specific GT-seq panels for chinook salmon, coho salmon, sockeye salmon, and steelhead to identify novel species diagnostic variant sites. Initial testing identified primer pairs with consistent cross-species amplification by processing GT-seq libraries with samples of all four species on all four species-specific panels. Consensus sequences were then generated for each species and each candidate amplicon in *Geneious Prime* v2022.0.1 (https://www.geneious.com). These consensus sequences were aligned, and species-informative variants were manually identified. The primer pairs that were confirmed to be valuable for species identification were incorporated into each of the four species-specific GT-seq panel. Once incorporated, additional species diagnostic variants were identified for 9 other salmonid species by running test libraries with reference samples.

Results

The GT-seq genotyping method has allowed for genotyping more samples and loci in less time and at significantly cheaper cost than our previous 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 and 17 additional amplicons for species identification); Coho salmon (*O. kisutch* – 248 loci including two sex determination markers and 11 additional markers used for species identification), White sturgeon (*Acipenser transmontanus* – 325 loci), Pacific lamprey (*Entosphenus tridentatus* – 294 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 GT-seq markers will be developed for SNPs identified from Pool-seq data in the coming year. Our GT-seq panels were used to genotype 145,937 samples in 2023 (Figure 12). The largest portion of samples were Chinook salmon (85,140), then Pacific lamprey (21,419), Steelhead (17,679), Coho (15,181), Sockeye (6,042), and White sturgeon (476).

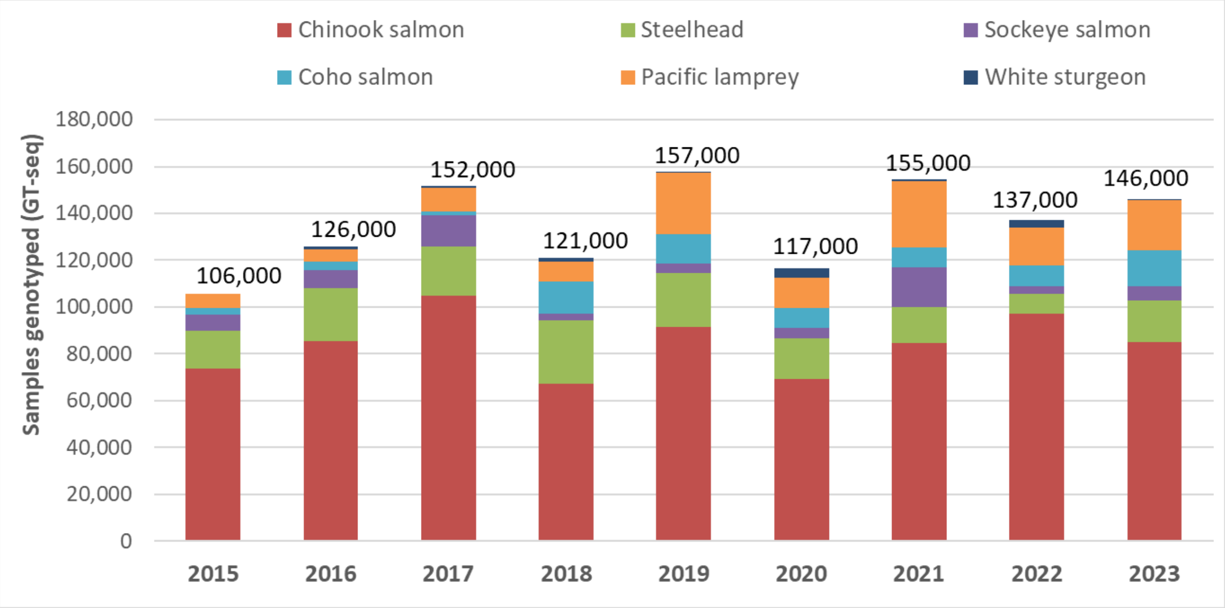

Figure 12. **Summary of Columbia River fish samples genotyped using GT-seq in calendar years 2015 – 2023**.

The species identification marker development and testing concluded in 2023, and nineteen amplicons containing species-informative variants were successfully incorporated into species-specific GT-seq panels for chinook salmon, coho salmon, sockeye salmon, and steelhead. Within the identified amplicons, 51 variant positions were identified that effectively discriminate among 11 species of salmonids and two subspecies of cutthroat trout (Robinson et al. *in review*). A custom script, CallSpecies.py, was developed to automate species identification as part of our routine GT-seq genotyping pipeline (https://github.com/zakrobinson/CallSpecies). These tools were empirically validated using 41,964 reference samples primarily from the Columbia River Basin and found they correctly identified the sample greater than 99.9% of the time, on average (Table 2).

In addition to the marker set currently in peer-review, two additional markers are used to distinguish between steelhead and cutthroat trout ssp. (Ocl_gshpx-357 and Omy_Omyclmk438-96), which are only present on the steelhead GT-seq panel (Appendix 6). Two markers, LampSD_478 and LampSD_700, distinguish between the genera Lampetra and Entosphenus, and are present in the two lamprey GT-seq panels (Appendix 10-11). Additionally, a variant position (Omy_RAD79314-58-25) that appears to distinguish Westslope cutthroat trout from steelhead and other cutthroat subspecies is also now in use. The species and subspecies identified with our current species marker set are available in Table 3. Descriptions of the species marker primer pairs can be found in Appendix 6-12, and the allelic associations for each species can be found in Appendix 13.

In 2023, marker development began for target SNPs associated with male anadromy and female iteroparity behavior (i.e., kelting) in steelhead trout. Primer design was completed for five SNPs identified on chromosome 12 in Collins et al.,(2022) that were significantly associated with male anadromy. After testing with the active steelhead GT-seq panel, it was determined that the primers needed to be redesigned due to heterodimer formation and non-target amplification. Ten primer pairs have been redesigned and will be tested in 2024. Primer design was completed for 29 target SNPs on chromosome 25 identified in Willis et al., (2023) and associated with female iteroparity in steelhead. Primer pairs for both chromosome 12 and 25 regions will be ordered, tested, and incorporated into the active steelhead panel in 2024.

In 2023, marker development began to improve the assignment accuracy for nine Chinook salmon GSI reporting groups. Existing whole genome re-sequencing data of Chinook salmon across the Columbia River basin (Horn and Narum 2023) was leveraged to identify informative markers for refining GSI assignments. A total of 246 GT-seq primer pairs have been ordered and primer testing is ongoing. To date, we have performed three 96 sample test libraries, and 143 candidates were dropped due to heterodimers, non-target amplification, or low genetic variation. Additional testing of the remaining 103 candidate markers, will confirm their value for refining GSI assignments and performance within the active Chinook salmon panel. Pool-seq studies are ongoing to scan the genome for regions associated with age-at-maturity using 2,753 samples of Chinook salmon from multiple populations representing each of the lineages in the Columbia River. Once identified, SNPs associated with age-at-maturity will be targeted for GT-seq marker design.

Table 2. Results of species diagnostic marker validation testing.
The species, tissue sample source and sample size are reported. The percentage of species calls that were correct, included the true species among alternatives, and excluded the true species are provided. The number of samples for which no species call was made is also reported.

			Species Calls			
Species	**Sample Source**	***N***	**Correct**	**True Sp. Included**	**True Sp. Excluded**	**No Call**
O. clarkii clarkii	Coquille River, OR	8	100.000%	0.000%	0.000%	0
	Umpqua River, OR	13	100.000%	0.000%	0.000%	0
O. clarkii bouveri	Henry's Lake, ID	8	100.000%	0.000%	0.000%	0
O. clarkii utah	Grace Fish Hatchery, ID	8	100.000%	0.000%	0.000%	0
O. kisutch	Columbia River Basin	2,205	99.955%	0.045%	0.000%	0
	Nez Perce Tribal Fish Hatchery, ID	8	100.000%	0.000%	0.000%	0
O. mykiss	Columbia River Basin	9,755	99.836%	0.154%	0.010%	0
	Lochsa River, ID	8	100.000%	0.000%	0.000%	0
O. nerka	Columbia River Basin	218	99.541%	0.459%	0.000%	0
	Eagle Fish Hatchery, ID	8	100.000%	0.000%	0.000%	0
O. tshawytscha	Columbia River Basin	29,677	99.997%	0.003%	0.000%	0
	Salmon River, ID	8	100.000%	0.000%	0.000%	0
S. confluentus	Salmon River, ID	16	100.000%	0.000%	0.000%	1
S. fontinalis	Little Lost River, ID	8	100.000%	0.000%	0.000%	0

	Boise River, ID	8	100.000%	0.000%	0.000%	0
S. trutta	CPW Research Hatchery, CO	8	100.000%	0.000%	0.000%	0

Table 3. Species designations for species diagnostic markers

SpeciesID Designation	Species Name(s)
Ocl1a	*O. clarkii clarkii*
Ocl1b	*O. clarkii lewisi*
Ocl2	*O. clarkii utah* or *O. clarkii bouvieri*
Ogo	*O. gorbuscha*
Oke	*O. keta*
Oki	*O. kisutch*
Omy	*O. mykiss*
One	*O. nerka*
Ots	*O. tshawytscha*
Sco	*S. confluentus*
Sfo	*S. fontinalis*
Ssa	*S. salar*
Str	*S. trutta*
Oma	*O. masu*
Lampetra	*Lampetra ssp.*
Entosphenus	*Entosphenus ssp.*

GT-seq Panel Updates

The active Steelhead panel for 2023 was supplemented with 6 amplicons associated with resistance to Bacterial Coldwater Disease in steelhead/rainbow trout (Liu et al., 2022). These marker names begin with the prefix Omy_GTA. Loci information can be seen in Appendix 6. The active Chinook panel underwent no significant changes in 2023. Loci used in the standard panel are shown in Appendix 7. The active Sockeye panel was supplemented with 17 amplicons from the suite of species diagnostic loci. A single age-at-maturity marker (One_Six6-3) identified in Waters et al. 2021 was added to the active panel. Loci information be seen in Appendix 8. The active Coho panel was supplemented with one age-at-maturity marker (Oki_Six6-3) identified in Waters et al. 2021. Loci information can be seen in Appendix 9. The active Pacific lamprey panel underwent no changes in 2023. Loci information can be seen in Appendix 10. The active panel for species complex of lampreys in the genus *Lampetra* underwent no changes in 2023. Loci information can be seen in **Appendix 11**. The active White sturgeon panel underwent no changes in 2023. Loci information can be seen in Appendix 12.

Note that correction factors were removed and are currently not being used for genotyping analysis.

Discussion

The GT-seq genotyping method has allowed for genotyping more samples and loci in less time and at significantly cheaper cost than our previous method (TaqMan genotyping assays; Campbell et al. 2015). 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, 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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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 is 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 & Stepian 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: Method: SNP genotyping using Genotyping in Thousands (GT-seq) on Illumina Sequencer platform v1.0 (monitoringresources.org) (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.

Once new Chinook salmon and steelhead PBT broodstock collections are genotyped and prepared to for adding to the PBT baseline, we perform analyses that identify which fish assigned to broodstock collections from previous spawn years that comprise the existing PBT baseline. For the current analysis period, we analyzed the Chinook salmon and steelhead SY2021 PBT broodstock collections that CRITFC genotyped (primarily outside the Snake River basin). For each SY2021 broodstock collection, we identified any duplicate genotypes, failed samples (missing >10% of the SNP loci used for parentage), PBT assignments, and GSI assignments. Tag rates for the broodstock collections are calculated by the 'squared' method (Method: Estimating genetic tagging rates for PBT applications v1.0 (monitoringresources.org)): (*proportion genotyped samples*)^2. In this case we use the total number of fish that were spawned by the hatchery (based on hatchery records) and use that as the denominator to divide our total number of successful genotypes as the numerator to calculate the "proportion genotyped samples". We calculate this tag rate for every broodstock collection in the PBT baseline. However, for all new PBT collections, we can also calculate an "expected tag rate" which is based on a weighted average tag rate of all broodstocks that assigned to individual fish in the new PBT collection. This expected tag rate allows us to test whether the tag rates we calculated for each broodstock reflect the observed proportion of PBT assignments for a new PBT broodstock collection. For example, if a new hatchery collection ("X") is 50% comprised of fish that assign to hatchery "A" and 25% of fish that assign to hatchery "B", and the remaining fish are PBT "unassigned", then the observed tag rate for collection X is 75%. If hatchery A and B have tag rates that are 100%, then the expected tag rate of collection X would be 100% (weighted average of tag rates for hatchery A and B). Because this expected tag rate is higher than the observed tag rate for hatchery collection X, we can then begin to investigate reasons why that may be. These reasons could include incorporation of natural-origin fish in the broodstock of hatchery collection X, or there may be a missing hatchery broodstock that was not included in the PBT baseline, as well as other explanations.

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 2023 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 4), Coho Salmon (Table 5), and *O. mykiss* (Table 6). Allele frequencies from millions of SNPs have now been generated for Chinook salmon (doi:10.5061/dryad.r4xgxd2ht) and O. mykiss (doi:10.5061/dryad.qfttdz0qg) with those data freely available for download. 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. For the Chinook salmon dataset, the allele frequencies are currently being used to develop new GSI markers that will aid in strengthening the assignments of fish to GSI reporting groups. A total of 13 pairwise test of GSI reporting groups were selected for additional analysis, representing those in which there is occasional mis-assignment. Principal components analysis and neighbor-joining trees were used to detect SNPs that provided the most differentiation between GSI groups. Based on these analyses, 246 SNP primers have been ordered and testing has begun.

Table 4. 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
Imnaha 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 5. Creation of a Coho Salmon SNP baseline by whole genome resequencing of pools of samples

Stock	n	Location	Region (BPA subbasin)	Lineage
Wenatchee	987	Leavenworth NFH	Wenatchee	Oki-Lower Columbia
Bonneville Dam	175	Bonneville Dam	Mixed	Mixed

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

Lineage	Reporting Group	Major Subbasin	Subbasin	Reach	Sites	N	Mapped Reads	*Genome Proportion
Coastal	02_LOWCOL	L. Columbia	Cowlitz	Cowlitz	Cowlitz R, Coweeman R	95	257,455,270	0.61
Coastal	02_LOWCOL	L. Columbia	Lewis	Lewis	EF Lewis R	78	325,463,369	0.65
Coastal	02_LOWCOL	L. Columbia	Columbia Gorge	Columbia Gorge	Mill Cr	96	232,750,154	0.56
Coastal	02_LOWCOL	L. Columbia	Columbia Gorge	Sandy Cr	Sandy Cr	87	291,529,099	0.64
Coastal	02_LOWCOL	L. Columbia	Hood	EF Hood	EF Hood R	48	260,113,702	0.62
Coastal	02_LOWCOL	L. Columbia	Hood	EF Hood	Parkdale Fish Facility	83	219,546,080	0.51
Coastal	02_LOWCOL	L. Columbia	Hood	WF Hood	WF Hood R	79	212,615,249	0.45
Coastal	03_SKAMAN	L. Columbia	Washougal	Washougal	Skamania Hatchery Stock	60	250,089,125	0.58
Coastal	04_WILLAM	L. Columbia	Willamette	Willamette	Eagle Cr	61	254,529,741	0.58
Coastal	04_WILLAM	L. Columbia	Willamette	Willamette	Little Rock, Mad Crks	50	265,050,782	0.55
Coastal	05_BWSALM	L. Columbia	Big White Salmon	Big White Salmon	Big White Salmon R	95	194,626,391	0.48
Inter-mediate	06_KLICKR	L. Columbia	Klickitat	Klickitat	Swale, Brush, Dead Canyon, Synder, White, Tepee, Fish Lake Crks	95	227,020,456	0.52
Inland	07_MGILCS	L. Columbia	Middle Columbia	Middle Columbia	Rock, Squaw Crks	91	216,427,544	0.61

Inland	07_MGILCS	L. Columbia	Middle Columbia	Fifteen Mile Cr	Fifteenmile Cr	92	520,699,926	0.72
Inland	07_MGILCS	L. Columbia	John Day	John Day	MF John Day R, Granite, Rudio, Wall, Trail Crks	95	285,409,446	0.58
Inland	07_MGILCS	L. Columbia	John Day	MF John Day	Upper John Day R, Beech, Belshaw, Canyon Crks	69	246,704,439	0.57
Inland	07_MGILCS	L. Columbia	John Day	SF John Day	Murderers, Deer, Black Canyon Crks	96	224,529,764	0.57
Inland	07_MGILCS	L. Columbia	Deschutes	Deschutes	Deschutes R, Warm Springs R, Trout Cr	95	262,227,329	0.61
Inland	07_MGILCS	L. Columbia	Umatilla	Umatilla	Minthorn Springs	74	222,263,607	0.54
Inland	07_MGILCS	L. Columbia	Umatilla	Umatilla	Umatilla R	70	236,157,293	0.54
Inland	07_MGILCS	L. Columbia	Walla Walla	Walla Walla	Walla Walla R, Touchet R, Yellowhawk Cr	95	380,515,222	0.69
Inland	07_MGILCS	Snake	Tucannon	Tucannon	Tucannon R	42	214,476,660	0.55
Inland	07_MGILCS	Snake	Lower Snake	Lower Snake	Alpowa Cr	53	287,842,645	0.63
Inland	07_MGILCS	Snake	Asotin	Asotin	George Creek	58	321,868,839	0.66
Inland	07_MGILCS	Snake	Asotin	Asotin	Asotin Cr	60	227,071,819	0.57
Inland	07_MGILCS	Snake	Clearwater	L Clearwater	Lapwai, Mission Crks	119	310,700,629	0.73
Inland	07_MGILCS	Snake	Clearwater	L Clearwater	Little Bear Cr	46	267,109,802	0.60
Inland	07_MGILCS	Snake	Clearwater	L Clearwater	Sweetwater Cr	51	224,853,521	0.53
Inland	07_MGILCS	Snake	Clearwater	L Clearwater	Potlatch R	50	217,298,385	0.51
Inland	07_MGILCS	Snake	Clearwater	NF Clearwater	Dworshak Hatchery	68	699,424,228	0.71
Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	Big Canyon Cr	95	251,726,901	0.59
Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	Catherine Cr	91	199,865,574	0.53
Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	Joseph Cr	88	240,989,824	0.52
Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	upper Grande Ronde R	58	190,569,290	0.61
Inland	07_MGILCS	Snake	Imnaha	Imnaha	Gumboot Cr	38	233,911,089	0.54
Inland	07_MGILCS	Snake	Imnaha	Imnaha	Lightning Cr	95	319,903,348	0.66
Inland	07_MGILCS	Snake	Imnaha	Imnaha	Little Sheep Cr	76	235,566,015	0.53
Inland	07_MGILCS	Snake	Salmon	L Salmon	Little Salmon R, Hazard, Boulder Crks	95	248,041,850	0.59
Inland	07_MGILCS	Snake	Salmon	L Salmon	Rapid River	78	337,982,422	0.73
Inland	07_MGILCS	Snake	Salmon	L Salmon	White Bird Cr	50	200,302,136	0.46
Inland	08_YAKIMA	U. Columbia	Yakima	Yakima	Naches R, Nile Cr	38	402,080,355	0.62
Inland	08_YAKIMA	U. Columbia	Yakima	Yakima	Satus R	67	208,951,362	0.49
Inland	08_YAKIMA	U. Columbia	Yakima	Yakima	Toppenish Cr	95	295,948,341	0.63

Inland	08_YAKIMA	U. Columbia	Yakima	Yakima	Teanaway R, Big Cr, Roza Dam	95	384,909,116	0.69
Inland	09_UPPCOL	U. Columbia	Entiat	Entiat	Entiat R	43	336,470,474	0.65
Inland	09_UPPCOL	U. Columbia	Methow	Methow	Winthrop NFH	93	180,992,366	0.46
Inland	09_UPPCOL	U. Columbia	Okanogan	Okanogan	Bonaparte, Salmon, Omak Crks	95	278,354,930	0.58
Inland	09_UPPCOL	U. Columbia	Wenatchee	Wenatchee	Chiwaukum Cr	54	227,418,107	0.56
Inland	10_SFCLWR	Snake	Clearwater	SF Clearwater	Clear Cr	61	243,826,940	0.59
Inland	10_SFCLWR	Snake	Clearwater	SF Clearwater	Crooked R	86	216,426,527	0.51
Inland	10_SFCLWR	Snake	Clearwater	SF Clearwater	Lolo Cr	68	159,912,565	0.59
Inland	10_SFCLWR	Snake	Clearwater	SF Clearwater	Tenmile Cr	60	288,038,275	0.64
Inland	11_UPCLWR	Snake	Clearwater	Lochsa	Canyon, Deadman Crks	68	285,197,311	0.61
Inland	11_UPCLWR	Snake	Clearwater	Lochsa	upper Lochsa R	72	295,662,531	0.72
Inland	11_UPCLWR	Snake	Clearwater	Selway	Hell's Half Acre	55	307,760,209	0.72
Inland	11_UPCLWR	Snake	Clearwater	Selway	Little Clearwater R	65	236,963,840	0.55
Inland	11_UPCLWR	Snake	Clearwater	Selway	upper Selway R	51	246,349,248	0.69
Inland	11_UPCLWR	Snake	Clearwater	Selway	White Cap Cr	72	264,031,261	0.60
Inland	12_SFSALM	Snake	Salmon	SF Salmon	Johnson Cr	95	201,270,498	0.48
Inland	12_SFSALM	Snake	Salmon	SF Salmon	Lick Cr	70	200,066,360	0.56
Inland	12_SFSALM	Snake	Salmon	SF Salmon	Secesh R	30	263,042,376	0.60
Inland	12_SFSALM	Snake	Salmon	SF Salmon	East Fork SF Salmon R	53	363,259,811	0.73
Inland	12_SFSALM	Snake	Salmon	SF Salmon	Stolle Meadows	42	366,401,888	0.68
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Bargamin Cr	60	189,953,336	0.53
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Big, Rush Crks	95	328,230,174	0.67
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Camas Cr	70	268,890,213	0.70
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Loon Cr	51	320,069,394	0.65
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Marsh Cr	60	334,274,383	0.72
Inland	14_UPSALM	Snake	Salmon	NF Salmon	EF Salmon R	51	304,068,477	0.64
Inland	14_UPSALM	Snake	Salmon	NF Salmon	Yankee Fork Salmon R	58	191,268,742	0.52
Inland	14_UPSALM	Snake	Salmon	NFSalmon	Lemhi R, Bear Valley Cr	95	225,800,707	0.51
Inland	14_UPSALM	Snake	Salmon	NF Salmon	Morgan Cr	39	337,843,016	0.73
Inland	14_UPSALM	Snake	Salmon	NF Salmon	Pahsimeroi Hatchery	56	284,569,935	0.70
Inland	14_UPSALM	Snake	Salmon	NF Salmon	Sawtooth Hatchery	47	241,483,030	0.57

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

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

The development of an allele frequency baseline for millions of SNPs across the genome and across the Columbia River basin for Chinook salmon (Horn and Narum 2023) is enabling the development of new GSI SNP markers (see https://doi.org/10.5061/dryad.r4xgxd2ht for the full list of allele frequencies). There are 13 pairwise comparisons among nine of the GSI reporting groups in which a small percentage of false positive assignments occur. In an effort to reduce the number of false positives, the whole genome resequencing data was used to run pairwise comparisons between reporting groups in the program PPanalyze, part of the PoolParty package. A Fisher's exact test and an FST test were used to generate a list of significant SNPs to differentiate the two reporting groups. A principal components analysis was used to visualize the clustering of populations within reporting groups using all SNPs, compared to those flagged as significant between reporting groups. From this initial list of significant SNPs, the top 10-20 were selected for primer development. A total of 246 primer pairs were ordered and testing began in 2023 and is ongoing.

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, Appendix 3, Appendix 4, and Appendix 5) 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 1).

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).

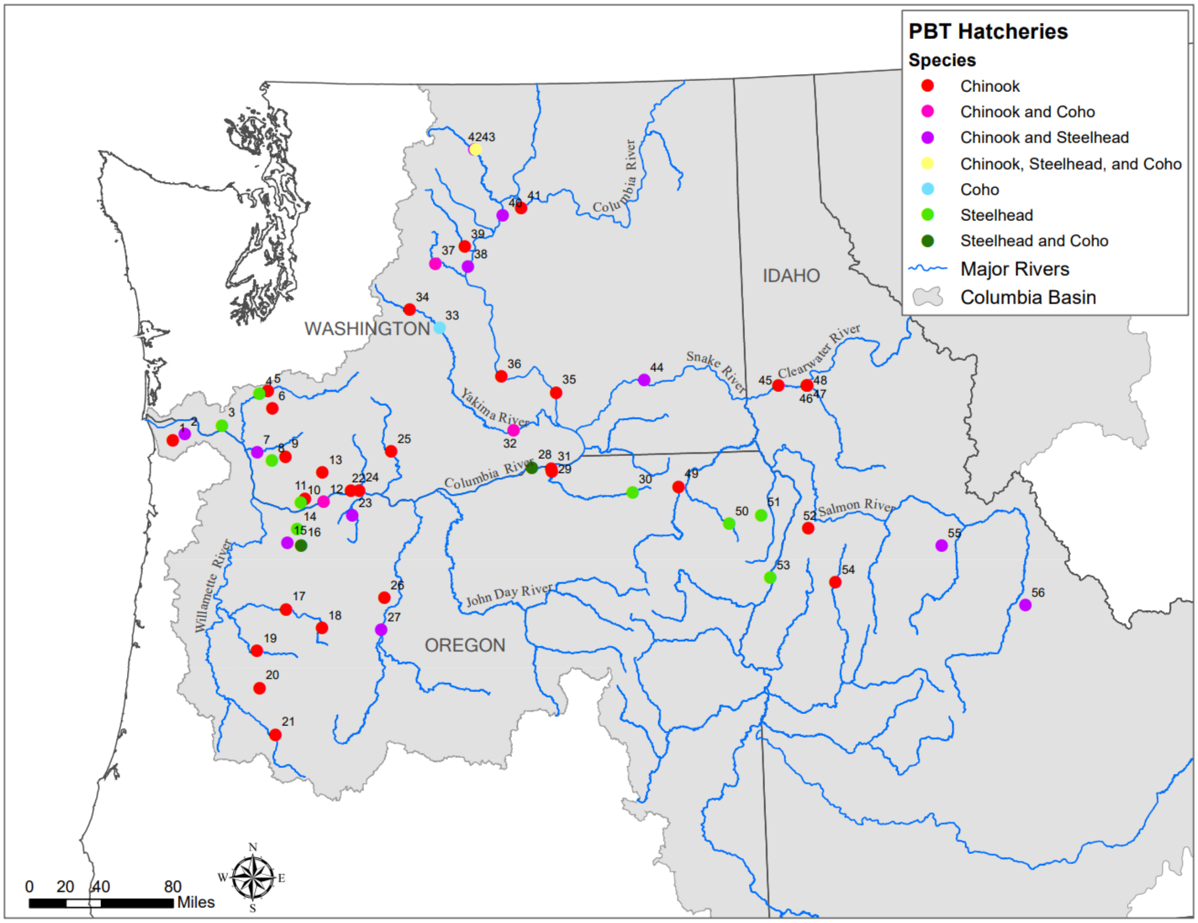

Figure 13. Chinook Salmon, Steelhead, and Coho Salmon PBT hatcheries. Numbers correspond to map ID and hatchery descriptions (Appendix 3, Appendix 4, Appendix 5).

The PBT tagging technology has been implemented through annual hatchery broodstock sampling to create a temporally structured parental genotype baseline. As adult fish return to participating hatcheries in the Columbia River basin, broodstock are sampled by collection of fin tissue during hatchery spawning. Required data for PBT sampling includes a hatchery record of phenotypic sex and spawn date. Additional and optional information was collected at some hatcheries when resources allowed, including fork length, and mated cross records of male and female broodstock individuals. The PBT baseline expansion during the 2023 report period included spawn year 2022 for all hatcheries. The total numbers of fish genotyped for PBT baselines in 2023 included n=16,743 spring Chinook Salmon, n=2,939 upper Columbia summer Chinook Salmon, n=28,644 fall Chinook Salmon (Appendix 1), n=1,191 steelhead trout (Appendix 2), and n=8,557 Coho Salmon (Appendix 2). 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.

The PBT-assignment composition of the SY2021 Chinook salmon broodstock collections that were genotyped by CRITFC primarily outside the Snake River basin and added to the PBT baseline in 2023 is shown in Table 7. Mostly the fish in each broodstock collection assign at high rates back to the hatchery that they returned to, which leads to their expected tag rate being similar to their observed tag rate and these tag rates are usually higher than 90% (Figure 14). Exceptions to high rates of observed and expected tag rates occur in situations in which broodstock programs are integrated such that despite genotyping >90% of broodstock in past spawn years, each broodstock collection is comprised of nearly zero hatchery origin fish (~0% observed PBT assignments; e.g. OtsYRRD_int_sp21 and OtsCHJO_int_sp21, Figure 14). The other type of scenario that leads to low observed tag rates despite relatively high expected tag rates occurs when an entire SY collection is missing from the baseline (e.g. OtsNSAN_seg_sp21 and OtsSSAN_seg_sp21 had low observed rates due to SY2018 missing from the baseline for those broodstock programs, Figure 14).

Table 7. PBT broodstock composition of the SY2021 Columbia River Chinook hatchery collections.

				Method					PBT Rate	
Exp. GSI	Collection	PBT Source	Source Rate	duplicate	failed	GSI	PBT	Total	Exp.	Obs.
02_WCASSP	OtsCOWL_seg_sp21	OtsCOWL_seg_fa17	0.8090				1	1	0.8090	
02_WCASSP	OtsCOWL_seg_sp21	OtsCOWL_seg_sp15	0.8814				1	1	0.8814	
02_WCASSP	OtsCOWL_seg_sp21	OtsCOWL_seg_sp16	0.4054				9	9	3.6486	
02_WCASSP	OtsCOWL_seg_sp21	OtsCOWL_seg_sp17	0.9369				961	961	900.3609	
02_WCASSP	OtsCOWL_seg_sp21	OtsCOWL_seg_sp18	0.8438				44	44	37.1272	
02_WCASSP	OtsCOWL_seg_sp21	OtsKALA_seg_fa17	0.7518				3	3	2.2554	
02_WCASSP	OtsCOWL_seg_sp21	OtsKALA_seg_fa18	0.8585				1	1	0.8585	
02_WCASSP	OtsCOWL_seg_sp21	OtsSPEE_seg_sp17	0.5727				1	1	0.5727	
02_WCASSP	OtsCOWL_seg_sp21	Unassigned	1.0000	8	112	176		296	0.9270	0.8530
02_WCASSP	OtsKALA_seg_sp21	OtsCOWL_seg_sp17	0.9369				4	4	3.7476	
02_WCASSP	OtsKALA_seg_sp21	OtsKALA_seg_fa17	0.7518				40	40	30.0720	
02_WCASSP	OtsKALA_seg_sp21	OtsKALA_seg_fa18	0.8585				3	3	2.5755	
02_WCASSP	OtsKALA_seg_sp21	OtsKALA_seg_sp16	0.7307				250	250	182.6750	
02_WCASSP	OtsKALA_seg_sp21	OtsKALA_seg_sp17	0.9707				273	273	265.0011	
02_WCASSP	OtsKALA_seg_sp21	OtsKALA_seg_sp18	0.5941				6	6	3.5646	
02_WCASSP	OtsKALA_seg_sp21	OtsSPEE_seg_sp16	0.6520				4	4	2.6080	
02_WCASSP	OtsKALA_seg_sp21	OtsSPEE_seg_sp17	0.5727				6	6	3.4362	
02_WCASSP	OtsKALA_seg_sp21	OtsSPEE_seg_sp18	0.8331				7	7	5.8317	
02_WCASSP	OtsKALA_seg_sp21	Unassigned	1.0000	14	45	169		228	0.8417	0.7770
02_WCASSP	OtsPARK_seg_sp21	OtsPARK_seg_sp16	0.9450				11	11	10.3950	
02_WCASSP	OtsPARK_seg_sp21	OtsPARK_seg_sp17	0.9341				142	142	132.6422	
02_WCASSP	OtsPARK_seg_sp21	OtsPARK_seg_sp18	0.7730				3	3	2.3190	
02_WCASSP	OtsPARK_seg_sp21	Unassigned	1.0000			24		24	0.9318	0.8667
02_WCASSP	OtsSPEE_seg_sp21	OtsCARS_seg_sp17	0.9841				1	1	0.9841	
02_WCASSP	OtsSPEE_seg_sp21	OtsKALA_seg_sp17	0.9707				3	3	2.9121	
02_WCASSP	OtsSPEE_seg_sp21	OtsSPEE_seg_sp16	0.6520				54	54	35.2080	
02_WCASSP	OtsSPEE_seg_sp21	OtsSPEE_seg_sp17	0.5727				292	292	167.2284	
02_WCASSP	OtsSPEE_seg_sp21	OtsSPEE_seg_sp18	0.8331				28	28	23.3268	
02_WCASSP	OtsSPEE_seg_sp21	Unassigned	1.0000	14	189	594		797	0.6076	0.3889
03_WCASFA	OtsCOWL_seg_fa21	OtsBIGC_seg_fa18	0.7120				1	1	0.7120	
03_WCASFA	OtsCOWL_seg_fa21	OtsCOWL_seg_fa16	0.7906				30	30	23.7180	
03_WCASFA	OtsCOWL_seg_fa21	OtsCOWL_seg_fa17	0.8090				854	854	690.8860	
03_WCASFA	OtsCOWL_seg_fa21	OtsCOWL_seg_fa18	0.5904				167	167	98.5968	
03_WCASFA	OtsCOWL_seg_fa21	OtsCOWL_seg_fa19	0.9303				14	14	13.0242	
03_WCASFA	OtsCOWL_seg_fa21	OtsCOWL_seg_sp17	0.9369				3	3	2.8107	
03_WCASFA	OtsCOWL_seg_fa21	OtsCOWL_seg_sp18	0.8438				1	1	0.8438	
03_WCASFA	OtsCOWL_seg_fa21	OtsKALA_seg_fa16	0.6348				2	2	1.2696	
03_WCASFA	OtsCOWL_seg_fa21	OtsKALA_seg_fa17	0.7518				59	59	44.3562	
03_WCASFA	OtsCOWL_seg_fa21	OtsKALA_seg_fa18	0.8585				18	18	15.4530	
03_WCASFA	OtsCOWL_seg_fa21	OtsNSAN_seg_sp18	0.6524				1	1	0.6524	

03_WCASFA	OtsCOWL_seg_fa21	Unassigned	1.0000	43	164	618		825	0.7759	0.6505
03_WCASFA	OtsKALA_seg_fa21	OtsBIGC_seg_fa18	0.7120				10	10	7.1200	
03_WCASFA	OtsKALA_seg_fa21	OtsCOWL_seg_fa17	0.8090				3	3	2.4270	
03_WCASFA	OtsKALA_seg_fa21	OtsCOWL_seg_sp17	0.9369				1	1	0.9369	
03_WCASFA	OtsKALA_seg_fa21	OtsKALA_seg_fa16	0.6348				62	62	39.3576	
03_WCASFA	OtsKALA_seg_fa21	OtsKALA_seg_fa17	0.7518				1275	1275	958.5450	
03_WCASFA	OtsKALA_seg_fa21	OtsKALA_seg_fa18	0.8585				609	609	522.8265	
03_WCASFA	OtsKALA_seg_fa21	OtsKALA_seg_fa19	0.7950				4	4	3.1800	
03_WCASFA	OtsKALA_seg_fa21	OtsNSAN_seg_sp18	0.6524				1	1	0.6524	
03_WCASFA	OtsKALA_seg_fa21	OtsNTOU_seg_fa16	0.9110				1	1	0.9110	
03_WCASFA	OtsKALA_seg_fa21	OtsNTOU_seg_fa17	0.7854				1	1	0.7854	
03_WCASFA	OtsKALA_seg_fa21	OtsNTOU_seg_fa18	0.6002				2	2	1.2004	
03_WCASFA	OtsKALA_seg_fa21	OtsWASH_seg_fa17	0.5004				1	1	0.5004	
03_WCASFA	OtsKALA_seg_fa21	Unassigned	1.0000	70	107	635		812	0.7809	0.7562
03_WCASFA	OtsNTOU_seg_fa21	OtsKALA_seg_fa17	0.7518				2	2	1.5036	
03_WCASFA	OtsNTOU_seg_fa21	OtsNTOU_seg_fa16	0.9110				2	2	1.8220	
03_WCASFA	OtsNTOU_seg_fa21	OtsNTOU_seg_fa17	0.7854				13	13	10.2102	
03_WCASFA	OtsNTOU_seg_fa21	OtsNTOU_seg_fa18	0.6002				19	19	11.4038	
03_WCASFA	OtsNTOU_seg_fa21	Unassigned	1.0000	4	9	212		225	0.6928	0.1452
03_WCASFA	OtsWASH_seg_fa21	OtsKALA_seg_fa17	0.7518				3	3	2.2554	
03_WCASFA	OtsWASH_seg_fa21	OtsSPEE_seg_sp16	0.6520				1	1	0.6520	
03_WCASFA	OtsWASH_seg_fa21	OtsWASH_seg_fa16	0.4356				8	8	3.4848	
03_WCASFA	OtsWASH_seg_fa21	OtsWASH_seg_fa17	0.5004				172	172	86.0688	
03_WCASFA	OtsWASH_seg_fa21	OtsWASH_seg_fa18	0.5770				102	102	58.8540	
03_WCASFA	OtsWASH_seg_fa21	OtsWASH_seg_fa19	0.4767				1	1	0.4767	
03_WCASFA	OtsWASH_seg_fa21	Unassigned	1.0000	2	113	344		459	0.5289	0.4548
04_WILLAM	OtsNSAN_seg_sp21	OtsNSAN_seg_sp18	0.6524				5	5	3.2620	
04_WILLAM	OtsNSAN_seg_sp21	OtsSSAN_seg_sp16	0.9410				1	1	0.9410	
04_WILLAM	OtsNSAN_seg_sp21	OtsSSAN_seg_sp18	0.5355				1	1	0.5355	
04_WILLAM	OtsNSAN_seg_sp21	Unassigned	1.0000	25	38	731		794	0.6769	0.0095
04_WILLAM	OtsSSAN_seg_sp21	OtsSSAN_seg_sp16	0.9410				153	153	143.9730	
04_WILLAM	OtsSSAN_seg_sp21	OtsSSAN_seg_sp18	0.5355				2	2	1.0710	
04_WILLAM	OtsSSAN_seg_sp21	Unassigned	1.0000	57	176	413		646	0.9358	0.2729
05_SPCRTU	OtsSPCR_seg_fa21	OtsSPCR_seg_fa16	0.6343				1	1	0.6343	
05_SPCRTU	OtsSPCR_seg_fa21	OtsSPCR_seg_fa17	0.5992				250	250	149.8000	
05_SPCRTU	OtsSPCR_seg_fa21	OtsSPCR_seg_fa18	1.0000				4193	4193	4193.0000	
05_SPCRTU	OtsSPCR_seg_fa21	OtsSPCR_seg_fa19	0.9068				686	686	622.0648	
05_SPCRTU	OtsSPCR_seg_fa21	Unassigned	1.0000	54	472	917		1443	0.9679	0.8484
06_KLICKR	OtsKLIC_seg_sp21	OtsKLIC_seg_sp16	1.0000				63	63	63.0000	
06_KLICKR	OtsKLIC_seg_sp21	OtsKLIC_seg_sp17	0.9757				421	421	410.7697	
06_KLICKR	OtsKLIC_seg_sp21	OtsKLIC_seg_sp18	0.9665				10	10	9.6650	
06_KLICKR	OtsKLIC_seg_sp21	OtsLWSN_seg_sp17	0.9418				1	1	0.9418	
06_KLICKR	OtsKLIC_seg_sp21	OtsRAPH_seg_sp17	0.9939				1	1	0.9939	
06_KLICKR	OtsKLIC_seg_sp21	Unassigned	1.0000	3	12	15		30	0.9786	0.9706
07_DESCSP	OtsRBFH_seg_sp21	OtsCLWH_seg_sp17	0.9897				1	1	0.9897	

07_DESCSP	OtsRBFH_seg_sp21	OtsIMNW_seg_ss17	0.9040				1	1	0.9040	
07_DESCSP	OtsRBFH_seg_sp21	OtsRAPH_seg_sp17	0.9939				1	1	0.9939	
07_DESCSP	OtsRBFH_seg_sp21	OtsRBFH_seg_sp17	0.8889				49	49	43.5561	
07_DESCSP	OtsRBFH_seg_sp21	OtsRBFH_seg_sp18	0.9603				22	22	21.1266	
07_DESCSP	OtsRBFH_seg_sp21	OtsWSNF_seg_sp17	0.7951				104	104	82.6904	
07_DESCSP	OtsRBFH_seg_sp21	OtsWSNF_seg_sp18	0.8985				5	5	4.4925	
07_DESCSP	OtsRBFH_seg_sp21	Unassigned	1.0000	2	13	20		35	0.8456	0.9015
07_DESCSP	OtsWSNF_seg_sp21	OtsRBFH_seg_sp17	0.8889				4	4	3.5556	
07_DESCSP	OtsWSNF_seg_sp21	OtsRBFH_seg_sp18	0.9603				2	2	1.9206	
07_DESCSP	OtsWSNF_seg_sp21	OtsWSNF_seg_sp16	0.9874				1	1	0.9874	
07_DESCSP	OtsWSNF_seg_sp21	OtsWSNF_seg_sp17	0.7951				169	169	134.3719	
07_DESCSP	OtsWSNF_seg_sp21	OtsWSNF_seg_sp18	0.8985				13	13	11.6805	
07_DESCSP	OtsWSNF_seg_sp21	Unassigned	1.0000		93	25		118	0.8070	0.8832
09_YAKIMA	OtsYRRD_int_sp21	OtsYRRD_int_sp16	0.7232				1	1	0.7232	
09_YAKIMA	OtsYRRD_int_sp21	OtsYRRD_int_sp17	0.9943				13	13	12.9259	
09_YAKIMA	OtsYRRD_int_sp21	OtsYRRD_int_sp18	0.9811				1	1	0.9811	
09_YAKIMA	OtsYRRD_int_sp21	OtsYRRD_seg_sp17	0.9807				1	1	0.9807	
09_YAKIMA	OtsYRRD_int_sp21	Unassigned	1.0000	1	2	423		426	0.9757	0.0364
09_YAKIMA	OtsYRRD_seg_sp21	OtsYRRD_int_sp17	0.9943				20	20	19.8860	
09_YAKIMA	OtsYRRD_seg_sp21	OtsYRRD_int_sp18	0.9811				18	18	17.6598	
09_YAKIMA	OtsYRRD_seg_sp21	OtsYRRD_seg_sp17	0.9807				76	76	74.5332	
09_YAKIMA	OtsYRRD_seg_sp21	OtsYRRD_seg_sp18	1.0000				152	152	152.0000	
09_YAKIMA	OtsYRRD_seg_sp21	Unassigned	1.0000	1	1	12		14	0.9928	0.9571
10_UCOLSP	OtsCHJO_seg_sp21	OtsCHJO_seg_sp16	0.9754				27	27	26.3358	
10_UCOLSP	OtsCHJO_seg_sp21	OtsCHJO_seg_sp17	0.9209				157	157	144.5813	
10_UCOLSP	OtsCHJO_seg_sp21	OtsCHJO_seg_su17	0.9032				2	2	1.8064	
10_UCOLSP	OtsCHJO_seg_sp21	OtsDWOR_seg_sp17	0.9924				1	1	0.9924	
10_UCOLSP	OtsCHJO_seg_sp21	OtsLNFH_seg_sp16	1.0000				1	1	1.0000	
10_UCOLSP	OtsCHJO_seg_sp21	OtsLNFH_seg_sp17	0.8606				236	236	203.1016	
10_UCOLSP	OtsCHJO_seg_sp21	OtsLWSN_seg_sp18	0.9392				1	1	0.9392	
10_UCOLSP	OtsCHJO_seg_sp21	OtsRAPH_seg_sp17	0.9939				1	1	0.9939	
10_UCOLSP	OtsCHJO_seg_sp21	OtsWELL_seg_su17	0.8901				1	1	0.8901	
10_UCOLSP	OtsCHJO_seg_sp21	OtsWINT_seg_sp16	1.0000				1	1	1.0000	
10_UCOLSP	OtsCHJO_seg_sp21	OtsWINT_seg_sp17	0.9445				3	3	2.8335	
10_UCOLSP	OtsCHJO_seg_sp21	OtsWINT_seg_sp18	0.7993				2	2	1.5986	
10_UCOLSP	OtsCHJO_seg_sp21	Unassigned	1.0000	4	36	72		112	0.8916	0.8574
10_UCOLSP	OtsEAST_seg_sp21	OtsEAST_seg_sp16	0.9032				1	1	0.9032	
10_UCOLSP	OtsEAST_seg_sp21	OtsEAST_seg_sp17	0.9811				52	52	51.0172	
10_UCOLSP	OtsEAST_seg_sp21	Unassigned	1.0000		8	137		145	0.9796	0.2789
10_UCOLSP	OtsLNFH_seg_sp21	OtsLNFH_seg_sp16	1.0000				15	15	15.0000	
10_UCOLSP	OtsLNFH_seg_sp21	OtsLNFH_seg_sp17	0.8606				714	714	614.4684	
10_UCOLSP	OtsLNFH_seg_sp21	OtsLNFH_seg_sp18	0.5506				18	18	9.9108	
10_UCOLSP	OtsLNFH_seg_sp21	Unassigned	1.0000		64	170		234	0.8559	0.8146
10_UCOLSP	OtsMETH_seg_sp21	OtsCHJO_seg_sp17	0.9209				1	1	0.9209	
10_UCOLSP	OtsMETH_seg_sp21	OtsMETH_seg_sp17	0.9051				11	11	9.9561	

10_UCOLSP	OtsMETH_seg_sp21	OtsWINT_seg_sp17	0.9445				4	4	3.7780	
10_UCOLSP	OtsMETH_seg_sp21	Unassigned	1.0000		2	50		52	0.9159	0.2424
10_UCOLSP	OtsWINT_seg_sp21	OtsMETH_seg_sp17	0.9051				104	104	94.1304	
10_UCOLSP	OtsWINT_seg_sp21	OtsMETH_seg_sp18	0.7778				12	12	9.3336	
10_UCOLSP	OtsWINT_seg_sp21	OtsWINT_seg_sp16	1.0000				13	13	13.0000	
10_UCOLSP	OtsWINT_seg_sp21	OtsWINT_seg_sp17	0.9445				249	249	235.1805	
10_UCOLSP	OtsWINT_seg_sp21	OtsWINT_seg_sp18	0.7993				3	3	2.3979	
10_UCOLSP	OtsWINT_seg_sp21	Unassigned	1.0000	5	11	49		65	0.9292	0.8860
18_UCOLSF	OtsCHJO_int_su21	OtsCHJO_int_su16	0.9896				12	12	11.8752	
18_UCOLSF	OtsCHJO_int_su21	OtsCHJO_int_su17	0.7549				2	2	1.5098	
18_UCOLSF	OtsCHJO_int_su21	OtsCHJO_seg_su16	0.9915				1	1	0.9915	
18_UCOLSF	OtsCHJO_int_su21	OtsCHJO_seg_su17	0.9032				1	1	0.9032	
18_UCOLSF	OtsCHJO_int_su21	OtsENFH_seg_su16	1.0000				1	1	1.0000	
18_UCOLSF	OtsCHJO_int_su21	Unassigned	1.0000	2	92	553		647	0.9576	0.0298
18_UCOLSF	OtsCHJO_seg_su21	OtsCHJO_int_su15	0.8910				2	2	1.7820	
18_UCOLSF	OtsCHJO_seg_su21	OtsCHJO_int_su16	0.9896				241	241	238.4936	
18_UCOLSF	OtsCHJO_seg_su21	OtsCHJO_int_su17	0.7549				62	62	46.8038	
18_UCOLSF	OtsCHJO_seg_su21	OtsCHJO_seg_su15	0.9584				1	1	0.9584	
18_UCOLSF	OtsCHJO_seg_su21	OtsCHJO_seg_su16	0.9915				37	37	36.6855	
18_UCOLSF	OtsCHJO_seg_su21	OtsCHJO_seg_su17	0.9032				10	10	9.0320	
18_UCOLSF	OtsCHJO_seg_su21	OtsEAST_seg_su16	0.9831				37	37	36.3747	
18_UCOLSF	OtsCHJO_seg_su21	OtsEAST_seg_su17	0.9661				13	13	12.5593	
18_UCOLSF	OtsCHJO_seg_su21	OtsENFH_seg_su16	1.0000				5	5	5.0000	
18_UCOLSF	OtsCHJO_seg_su21	OtsENFH_seg_su17	0.8393				3	3	2.5179	
18_UCOLSF	OtsCHJO_seg_su21	OtsWELL_seg_su16	1.0000				26	26	26.0000	
18_UCOLSF	OtsCHJO_seg_su21	OtsWELL_seg_su17	0.8901				5	5	4.4505	
18_UCOLSF	OtsCHJO_seg_su21	Unassigned	1.0000		107	24		131	0.9517	0.9485
18_UCOLSF	OtsEAST_seg_su21	OtsCHJO_seg_su16	0.9915				1	1	0.9915	
18_UCOLSF	OtsEAST_seg_su21	OtsEAST_seg_sp17	0.9811				1	1	0.9811	
18_UCOLSF	OtsEAST_seg_su21	OtsEAST_seg_su15	1.0000				1	1	1.0000	
18_UCOLSF	OtsEAST_seg_su21	OtsEAST_seg_su16	0.9831				191	191	187.7721	
18_UCOLSF	OtsEAST_seg_su21	OtsEAST_seg_su17	0.9661				131	131	126.5591	
18_UCOLSF	OtsEAST_seg_su21	OtsWELL_seg_su16	1.0000				1	1	1.0000	
18_UCOLSF	OtsEAST_seg_su21	OtsWELL_seg_su17	0.8901				1	1	0.8901	
18_UCOLSF	OtsEAST_seg_su21	Unassigned	1.0000	3	11	378		392	0.9761	0.4638
18_UCOLSF	OtsENFH_seg_su21	OtsEAST_seg_su16	0.9831				1	1	0.9831	
18_UCOLSF	OtsENFH_seg_su21	OtsENFH_seg_su15	0.7290				1	1	0.7290	
18_UCOLSF	OtsENFH_seg_su21	OtsENFH_seg_su16	1.0000				214	214	214.0000	
18_UCOLSF	OtsENFH_seg_su21	OtsENFH_seg_su17	0.8393				53	53	44.4829	
18_UCOLSF	OtsENFH_seg_su21	OtsENFH_seg_su18	0.7628				1	1	0.7628	
18_UCOLSF	OtsENFH_seg_su21	Unassigned	1.0000		24	36		60	0.9665	0.8824
18_UCOLSF	OtsPRIE_seg_fa21	OtsLWSN_seg_fa16	1.0000				1	1	1.0000	
18_UCOLSF	OtsPRIE_seg_fa21	OtsLWSN_seg_fa17	0.9595				5	5	4.7975	
18_UCOLSF	OtsPRIE_seg_fa21	OtsLYON_seg_fa17	0.9443				4	4	3.7772	
18_UCOLSF	OtsPRIE_seg_fa21	OtsLYON_seg_fa18	0.8865				1	1	0.8865	

18_UCOLSF	OtsPRIE_seg_fa21	OtsNPFH_seg_fa17	1.0000				2	2	2.0000	
18_UCOLSF	OtsPRIE_seg_fa21	OtsPRIE_seg_fa16	1.0000				90	90	90.0000	
18_UCOLSF	OtsPRIE_seg_fa21	OtsPRIE_seg_fa17	0.9095				3647	3647	3316.9465	
18_UCOLSF	OtsPRIE_seg_fa21	OtsPRIE_seg_fa18	0.8617				373	373	321.4141	
18_UCOLSF	OtsPRIE_seg_fa21	OtsPROS_seg_fa17	0.3964				1	1	0.3964	
18_UCOLSF	OtsPRIE_seg_fa21	OtsRING_seg_fa17	0.9340				6	6	5.6040	
18_UCOLSF	OtsPRIE_seg_fa21	OtsUMAT_seg_fa18	0.9573				3	3	2.8719	
18_UCOLSF	OtsPRIE_seg_fa21	OtsWELL_seg_su17	0.8901				1	1	0.8901	
18_UCOLSF	OtsPRIE_seg_fa21	Unassigned	1.0000	43	436	1071		1550	0.9073	0.7942
18_UCOLSF	OtsPROS_seg_fa21	OtsLWSN_seg_fa16	1.0000				4	4	4.0000	
18_UCOLSF	OtsPROS_seg_fa21	OtsLWSN_seg_fa17	0.9595				39	39	37.4205	
18_UCOLSF	OtsPROS_seg_fa21	OtsLWSN_seg_fa19	1.0000				6	6	6.0000	
18_UCOLSF	OtsPROS_seg_fa21	OtsLYON_seg_fa17	0.9443				3	3	2.8329	
18_UCOLSF	OtsPROS_seg_fa21	OtsLYON_seg_fa18	0.8865				3	3	2.6595	
18_UCOLSF	OtsPROS_seg_fa21	OtsPROS_seg_fa16	1.0000				1	1	1.0000	
18_UCOLSF	OtsPROS_seg_fa21	OtsPROS_seg_fa17	0.3964				2	2	0.7928	
18_UCOLSF	OtsPROS_seg_fa21	OtsPROS_seg_fa18	0.8668				1	1	0.8668	
18_UCOLSF	OtsPROS_seg_fa21	OtsRING_seg_fa17	0.9340				25	25	23.3500	
18_UCOLSF	OtsPROS_seg_fa21	OtsRING_seg_fa19	0.9602				1	1	0.9602	
18_UCOLSF	OtsPROS_seg_fa21	OtsUMAT_seg_fa18	0.9573				8	8	7.6584	
18_UCOLSF	OtsPROS_seg_fa21	OtsUMAT_seg_fa19	1.0000				1	1	1.0000	
18_UCOLSF	OtsPROS_seg_fa21	Unassigned	1.0000	4	5	25		34	0.9419	0.7899
18_UCOLSF	OtsRING_seg_fa21	OtsLWSN_seg_fa17	0.9595				3	3	2.8785	
18_UCOLSF	OtsRING_seg_fa21	OtsLYON_seg_fa18	0.8865				2	2	1.7730	
18_UCOLSF	OtsRING_seg_fa21	OtsPRIE_seg_fa16	1.0000				16	16	16.0000	
18_UCOLSF	OtsRING_seg_fa21	OtsPRIE_seg_fa17	0.9095				429	429	390.1755	
18_UCOLSF	OtsRING_seg_fa21	OtsPRIE_seg_fa18	0.8617				201	201	173.2017	
18_UCOLSF	OtsRING_seg_fa21	OtsPRIE_seg_fa19	0.9615				1	1	0.9615	
18_UCOLSF	OtsRING_seg_fa21	OtsRING_seg_fa17	0.9340				2	2	1.8680	
18_UCOLSF	OtsRING_seg_fa21	OtsUMAT_seg_fa18	0.9573				8	8	7.6584	
18_UCOLSF	OtsRING_seg_fa21	Unassigned	1.0000	3	110	94		207	0.8981	0.8757
18_UCOLSF	OtsWELL_seg_su21	OtsCHJO_int_su16	0.9896				44	44	43.5424	
18_UCOLSF	OtsWELL_seg_su21	OtsCHJO_seg_su16	0.9915				122	122	120.9630	
18_UCOLSF	OtsWELL_seg_su21	OtsCHJO_seg_su17	0.9032				11	11	9.9352	
18_UCOLSF	OtsWELL_seg_su21	OtsEAST_seg_su15	1.0000				1	1	1.0000	
18_UCOLSF	OtsWELL_seg_su21	OtsEAST_seg_su16	0.9831				114	114	112.0734	
18_UCOLSF	OtsWELL_seg_su21	OtsEAST_seg_su17	0.9661				1	1	0.9661	
18_UCOLSF	OtsWELL_seg_su21	OtsENFH_seg_su16	1.0000				11	11	11.0000	
18_UCOLSF	OtsWELL_seg_su21	OtsENFH_seg_su17	0.8393				1	1	0.8393	
18_UCOLSF	OtsWELL_seg_su21	OtsWELL_seg_su15	1.0000				1	1	1.0000	
18_UCOLSF	OtsWELL_seg_su21	OtsWELL_seg_su16	1.0000				452	452	452.0000	
18_UCOLSF	OtsWELL_seg_su21	OtsWELL_seg_su17	0.8901				23	23	20.4723	
18_UCOLSF	OtsWELL_seg_su21	Unassigned	1.0000	3	54	128		185	0.9908	0.8592
19_SRFALL	OtsNPFH_seg_fa21	OtsLWSN_seg_fa16	1.0000				1	1	1.0000	
19_SRFALL	OtsNPFH_seg_fa21	OtsLYON_seg_fa16	0.9435				11	11	10.3785	

19_SRFALL	OtsNPFH_seg_fa21	OtsLYON_seg_fa17	0.9443				229	229	216.2447	
19_SRFALL	OtsNPFH_seg_fa21	OtsLYON_seg_fa18	0.8865				50	50	44.3250	
19_SRFALL	OtsNPFH_seg_fa21	OtsNPFH_seg_fa16	0.9726				7	7	6.8082	
19_SRFALL	OtsNPFH_seg_fa21	OtsNPFH_seg_fa17	1.0000				163	163	163.0000	
19_SRFALL	OtsNPFH_seg_fa21	OtsNPFH_seg_fa18	0.8617				10	10	8.6170	
19_SRFALL	OtsNPFH_seg_fa21	OtsPRIE_seg_fa17	0.9095				2	2	1.8190	
19_SRFALL	OtsNPFH_seg_fa21	Unassigned	1.0000		10	212		222	0.9560	0.6905
20_BONPOOLSP	OtsCARS_seg_sp21	OtsCARS_seg_sp16	1.0000				6	6	6.0000	
20_BONPOOLSP	OtsCARS_seg_sp21	OtsCARS_seg_sp17	0.9841				1263	1263	1242.9183	
20_BONPOOLSP	OtsCARS_seg_sp21	OtsCARS_seg_sp18	1.0000				27	27	27.0000	
20_BONPOOLSP	OtsCARS_seg_sp21	OtsDWOR_seg_sp17	0.9924				1	1	0.9924	
20_BONPOOLSP	OtsCARS_seg_sp21	OtsLWSN_seg_sp17	0.9418				4	4	3.7672	
20_BONPOOLSP	OtsCARS_seg_sp21	Unassigned	1.0000	7	8	30		45	0.9844	0.9775
20_BONPOOLSP	OtsLWSN_seg_sp21	OtsCARS_seg_sp17	0.9841				186	186	183.0426	
20_BONPOOLSP	OtsLWSN_seg_sp21	OtsCARS_seg_sp18	1.0000				10	10	10.0000	
20_BONPOOLSP	OtsLWSN_seg_sp21	OtsLWSN_seg_sp16	0.9349				21	21	19.6329	
20_BONPOOLSP	OtsLWSN_seg_sp21	OtsLWSN_seg_sp17	0.9418				498	498	469.0164	
20_BONPOOLSP	OtsLWSN_seg_sp21	OtsLWSN_seg_sp18	0.9392				8	8	7.5136	
20_BONPOOLSP	OtsLWSN_seg_sp21	Unassigned	1.0000	9	12	366		387	0.9533	0.6639
21_UMATILLASP	OtsUMAT_seg_sp21	OtsCARS_seg_sp18	1.0000				2	2	2.0000	
21_UMATILLASP	OtsUMAT_seg_sp21	OtsUMAT_seg_sp16	1.0000				11	11	11.0000	
21_UMATILLASP	OtsUMAT_seg_sp21	OtsUMAT_seg_sp17	1.0000				437	437	437.0000	
21_UMATILLASP	OtsUMAT_seg_sp21	OtsUMAT_seg_sp18	0.9913				14	14	13.8782	
21_UMATILLASP	OtsUMAT_seg_sp21	Unassigned	1.0000		6	19		25	0.9997	0.9607
22_BONPOOLFA	OtsLWSN_seg_fa21	OtsLWSN_seg_fa15	0.9514				10	10	9.5140	
22_BONPOOLFA	OtsLWSN_seg_fa21	OtsLWSN_seg_fa16	1.0000				1261	1261	1261.0000	
22_BONPOOLFA	OtsLWSN_seg_fa21	OtsLWSN_seg_fa17	0.9595				4570	4570	4384.9150	
22_BONPOOLFA	OtsLWSN_seg_fa21	OtsLWSN_seg_fa18	0.7313				1145	1145	837.3385	
22_BONPOOLFA	OtsLWSN_seg_fa21	OtsLWSN_seg_fa19	1.0000				4	4	4.0000	
22_BONPOOLFA	OtsLWSN_seg_fa21	OtsLYON_seg_fa18	0.8865				3	3	2.6595	
22_BONPOOLFA	OtsLWSN_seg_fa21	OtsNPFH_seg_fa17	1.0000				7	7	7.0000	
22_BONPOOLFA	OtsLWSN_seg_fa21	OtsNPFH_seg_fa18	0.8617				1	1	0.8617	
22_BONPOOLFA	OtsLWSN_seg_fa21	OtsPRIE_seg_fa17	0.9095				2	2	1.8190	
22_BONPOOLFA	OtsLWSN_seg_fa21	OtsPRIE_seg_fa18	0.8617				458	458	394.6586	
22_BONPOOLFA	OtsLWSN_seg_fa21	OtsRING_seg_fa17	0.9340				1	1	0.9340	
22_BONPOOLFA	OtsLWSN_seg_fa21	OtsRING_seg_fa18	0.8320				33	33	27.4560	
22_BONPOOLFA	OtsLWSN_seg_fa21	OtsSPCR_seg_fa18	1.0000				1	1	1.0000	
22_BONPOOLFA	OtsLWSN_seg_fa21	Unassigned	1.0000	10	45	768		823	0.9249	0.9071
23_UMATILLAFA	OtsUMAT_seg_fa21	OtsLWSN_seg_fa16	1.0000				3	3	3.0000	
23_UMATILLAFA	OtsUMAT_seg_fa21	OtsLWSN_seg_fa17	0.9595				67	67	64.2865	
23_UMATILLAFA	OtsUMAT_seg_fa21	OtsLYON_seg_fa16	0.9435				1	1	0.9435	
23_UMATILLAFA	OtsUMAT_seg_fa21	OtsLYON_seg_fa17	0.9443				2	2	1.8886	
23_UMATILLAFA	OtsUMAT_seg_fa21	OtsLYON_seg_fa18	0.8865				9	9	7.9785	
23_UMATILLAFA	OtsUMAT_seg_fa21	OtsNPFH_seg_fa17	1.0000				3	3	3.0000	
23_UMATILLAFA	OtsUMAT_seg_fa21	OtsNPFH_seg_fa18	0.8617				1	1	0.8617	

23_UMATILLAFA	OtsUMAT_seg_fa21	OtsRING_seg_fa17	0.9340				118	118	110.2120	
23_UMATILLAFA	OtsUMAT_seg_fa21	OtsUMAT_seg_fa18	0.9573				188	188	179.9724	
23_UMATILLAFA	OtsUMAT_seg_fa21	Unassigned	1.0000		16	41		57	0.9493	0.9053
			Total	391	2603	9551	31239	43784		

Note: The relatively low observed tag rate given the high expected tag rate could be due to a few reasons including the use of natural-origin fish for broodstock or a gap in the PBT baseline.

The GSI assignments of the Chinook Salmon SY2021 PBT broodstock collections generally show high rates of observed GSI assignments to the reporting group that is expected (Table 8). Most of these rates of “correct” assignment are higher than 70%, but there are two exceptions. The OtsPARK_seg_sp21 collection from Parkdale Hatchery on the Hood River had a correct assignment rate of 0.6% and the OtsNPFH_seg_fa21 collection of Fall Chinook from Nez Perce Tribal Fish Hatchery had a 49.9% correct assignment. For Parkdale, the broodstock were reintroduced from the Deschutes River (07_DESCSP = expected reporting group) and Carson Hatchery (10_UCOLSP = expected reporting group) because the expected reporting group that was present in the Hood River historically (02_WCASSP) was extirpated. The Snake River Fall Chinook generally have high misassignment rates to the upper Columbia River su/fa (18_UCOLSF) GSI group, which explains the low correct assignment of the OtsNPFH_seg_fa21 collection.

Table 8. GSI composition of the SY2021 Columbia River Chinook hatchery collections

		Observed GSI																		
Exp GSI	Collection	01_YOUNGS	02_WCASSP	03_WCASFA	04_WILLAM	05_SPCRTU	06_KLICKR	07_DESCSP	08_JOHNDR	09_YAKIMA	10_UCOLSP	12_HELLSC	13_SFSALM	16_UPSALM	17_DESCFA	18_UCOLSF	19_SRFALL	NA	Total	% Correct
02_WCASSP	OtsCOWL_seg_sp21		1034	132	28	2										2		119	1317	86.3%
	OtsKALA_seg_sp21		590	70	99	1	2											59	821	77.4%
	OtsPARK_seg_sp21		1		6		3	82	2	1	77	8							180	0.6%
	OtsSPEE_seg_sp21		877	16	6		71			1	1							203	1175	90.2%
03_WCASFA	OtsCOWL_seg_fa21		199	1549	11	7										1	1	207	1975	87.6%
	OtsKALA_seg_fa21		54	2385	67	96										2		178	2782	91.6%
	OtsNTOU_seg_fa21		2	240	1	5												13	261	96.8%
	OtsWASH_seg_fa21		8	617		6												115	746	97.8%
04_WILLAM	OtsNSAN_seg_sp21		5		733													63	801	99.3%
	OtsSSAN_seg_sp21		6		562													233	801	98.9%
05_SPCRT	OtsSPCR_seg_fa21			30		6017												526	6573	99.5%
06_KLICK	OtsKLIC_seg_sp21				1		473			18	17	2						15	526	92.6%
07_DESCSP	OtsRBFH_seg_sp21						1	145	2	3	41	11						15	218	71.4%
	OtsWSNF_seg_sp21						1	198	2		11	2						93	307	92.5%
09_YAKIMA	OtsYRRD_int_sp21						4			414	19	1				1		3	442	94.3%
	OtsYRRD_seg_sp21						1		1	241	36	1						2	282	86.1%
10_UCOLSP	OtsCHJO_seg_sp21									3	488	10	1			3		40	545	96.6%
	OtsEAST_seg_sp21									1	187	2						8	198	98.4%
	OtsLNFH_seg_sp21								1	4	895	13	4					64	981	97.6%
	OtsMETH_seg_sp21										64	2						2	68	97.0%
	OtsWINT_seg_sp21						1				423	5	1					16	446	98.4%
18_UCOLSF	OtsCHJO_int_su21															565	5	94	664	99.1%
	OtsCHJO_seg_su21															458	8	107	573	98.3%
	OtsEAST_seg_su21										1					695	8	15	719	98.7%

	OtsENFH_seg_su21															303	3	24	330	99.0%
	OtsPRIE_seg_fa21			2												4942	261	479	5684	94.9%
	OtsPROS_seg_fa21															106	13	9	128	89.1%
	OtsRING_seg_fa21															720	36	113	869	95.2%
	OtsWELL_seg_su21															895	14	57	966	98.5%
19_SRF	OtsNPFH_seg_fa21			1												342	342	10	695	49.9%
20_BON POOLSP	OtsCARS_seg_sp21						2	2	2	2	1283	38	2					15	1346	96.4%
	OtsLWSN_seg_sp21							1		5	1049	28	6					21	1110	96.3%
21_ UM	OtsUMAT_seg_sp21									1	465	16	1					6	489	96.3%
22_ BO	OtsLWSN_seg_fa21		2	43	2	4										7540	673	55	8319	91.2%
23_ UM	OtsUMAT_seg_fa21			1												382	50	16	449	88.2%
Total		0	2778	5086	1516	6138	559	428	10	694	5057	139	15	0	0	16957	1414	2995	43786	

Note: “Collection” is the expected GSI Reporting Group for each PBT Collection given the geographic location of the hatchery and the history of the hatchery stock utilized by the hatchery. “Observed GSI” is the observed GSI reporting group that was assigned for each individual in the hatchery collection using the GSI baseline. “%Correct” is the percent of all the hatchery collection that assigned to the expected GSI reporting group.

The PBT-assignment composition of the SY2021 steelhead broodstock collections that were genotyped by CRITFC primarily outside the Snake River basin and added to the PBT baseline in 2023 is shown in Table 9. Mostly the fish in each broodstock collection assign at high rates back to the hatchery that they returned to, which leads to their expected tag rate being similar to their observed tag rate and these tag rates are usually higher than 90% (Figure 15). Exceptions to high rates of observed and expected tag rates occur in situations in which broodstock programs are integrated such that despite genotyping >90% of broodstock in past spawn years, each broodstock collection is comprised of nearly zero hatchery origin fish (~0% observed PBT assignments; e.g. OmyWINT_su21, Figure 15). The other type of scenario that leads to low observed tag rates despite relatively high expected tag rates occurs when an entire SY collection is missing from the baseline, but this scenario did not apply to steelhead broodstock collections from SY2021.

Table 9. PBT broodstock composition of the SY2021 Columbia River Steelhead hatchery collections

				Method					PBT Rate	
Exp. GSI	**Collection**	**PBT Source**	**Source Rate**	**duplicate**	**failed**	**GSI**	**PBT**	**Total**	**Exp.**	**Obs.**
03_SKAMAN	OmySKAM_su21	OmySKAM_su16	0.2010				2	2	0.4020	
		OmySKAM_su17	0.9400				212	212	199.2800	
		Unassigned	1.0000		2	48	0	50	0.9331	0.8168
	OmySKAM_wi21	OmySKAM_wi17	0.9590				3	3	2.8770	
		OmySKAM_wi18	0.6140				71	71	43.5940	
		Unassigned	1.0000	1	2	9	0	12	0.6280	0.8916
07_MGILCS	OmyMINT_su21	OmyDWOC_su17	0.9824				1	1	0.9824	
		OmyMINT_su17	0.9730				24	24	23.3520	
		OmyMINT_su18	0.9760				1	1	0.9760	
		Unassigned	1.0000			47	0	47	0.9735	0.3562
	OmyROUN_su21	OmyROUN_su16	1.0000				1	1	1.0000	
		OmyROUN_su17	0.9980				406	406	405.1880	
		OmyROUN_su18	0.9850				24	24	23.6400	
		Unassigned	1.0000	1	5	9	0	15	0.9973	0.9795
09_UPPCOL	OmyEAST_su21	OmyEAST_su16	1.0000				2	2	2.0000	
		OmyEAST_su17	1.0000				47	47	47.0000	
		OmyEAST_su18	0.9460				5	5	4.7300	
		Unassigned	1.0000	2	3	50	0	55	0.9950	0.5192
	OmyWELL_su21	OmyPAHH_su17	0.9800				1	1	0.9800	
		OmySAWT_su17	0.9939				1	1	0.9939	0.5189
		OmyWELL_su17	0.9550				22	22	21.0100	
		OmyWINT_su16	1.0000				22	22	22.0000	
		OmyWINT_su17	1.0000				16	16	16.0000	
		OmyWMET_su17	1.0000				31	31	31.0000	
		OmyWMET_su18	0.9660				10	10	9.6600	
		OmyWOKA_su17	1.0000				27	27	27.0000	
		OmyWOKA_su18	1.0000				2	2	2.0000	
		OmyWOMA_su18	1.0000				1	1	1.0000	
		Unassigned	1.0000		1	16	0	17	0.9898	0.8926

OmyWINT_su21	OmyWINT_su16	1.0000				1	1	1.0000	
	OmyWINT_su17	1.0000				1	1	1.0000	
	Unassigned	1.0000		1	85	0	86	1.0000	0.0230
		Total	4	14	264	934	1216		

The GSI assignments of the steelhead SY2021 PBT broodstock collections generally show high rates of observed GSI assignments to the reporting group that is expected (Table 10). Most of these rates of “correct” assignment are higher than 70%. The lowest rates were from the broodstocks of the upper Columbia River (e.g., OmyWELL_su21 and OmyWINT_su21) which typically have high rates of misassignment to the middle Columbia reporting group (07_MGILCS).

Table 10. GSI composition of the SY2021 Columbia River Steelhead hatchery collection.

Exp GSI	Collection	02_LOWCOL	03_SKAMAN	04_WILLAM	06_KLICKR	07_MGILCS	08_YAKIMA	09_UPPCOL	10_SFCLWR	11_UPCLWR	12_SFSALM	13_MFSALM	14_UPSALM	NA	Total	% Correct
03_SKAMAN	OmySKAM_su21	1	261											2	264	99.6%
	OmySKAM_wi21	78	2	4										2	86	92.9%
07_MGILCS	OmyMINT_su21				1	61		7	1					3	73	87.1%
	OmyROUN_su21					399	2	27						18	446	93.2%
09_UPPCOL	OmyEAST_su21					9		84						16	109	90.3%
	OmyWELL_su21				1	31		107	2					9	150	75.9%
	OmyWINT_su21					22	1	58						7	88	71.6%
Total		79	263	4	2	522	3	283	3	0	0	0	0	57	1216	

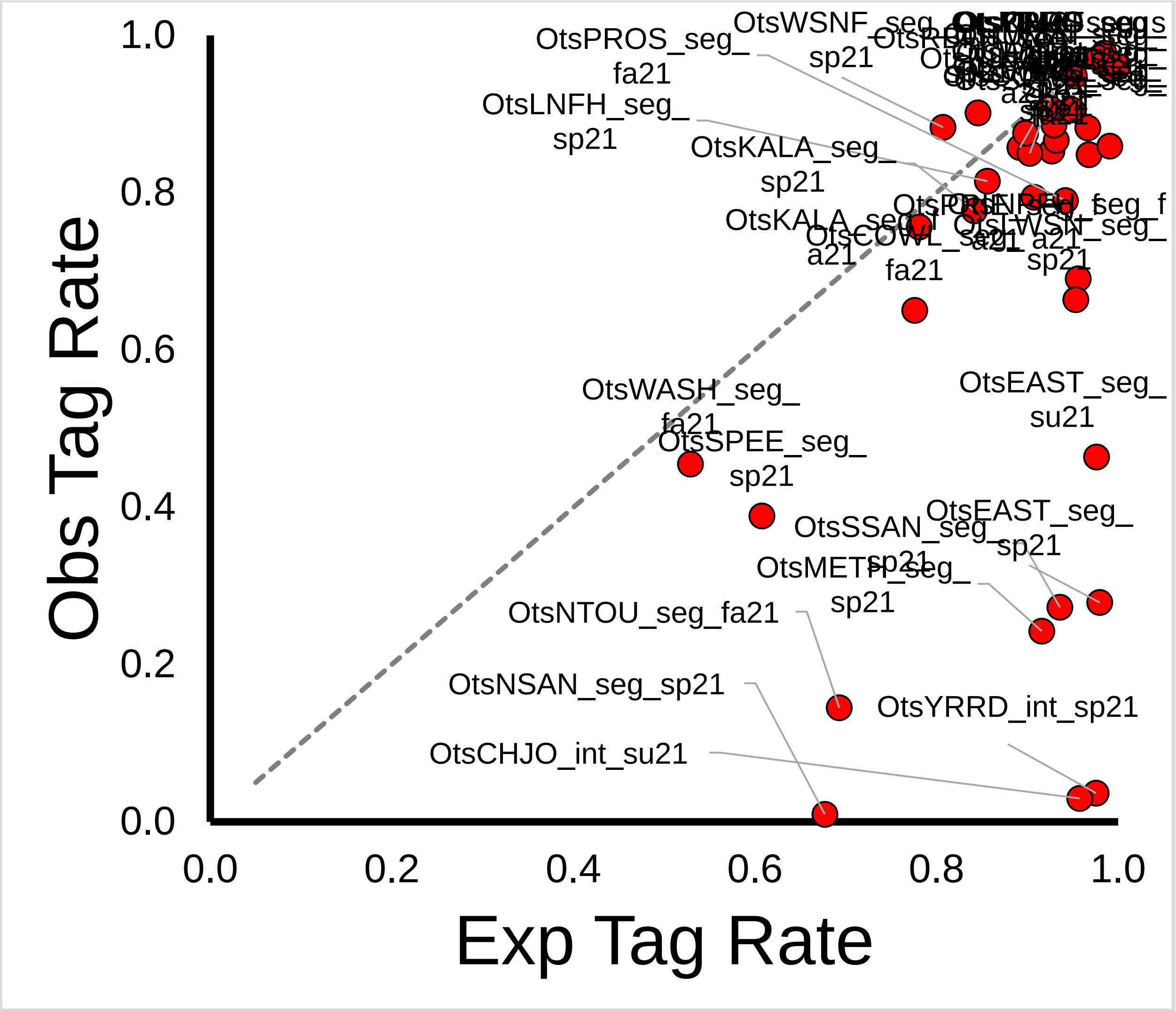

Figure 14. Observed versus expected PBT rates for SY2021 Columbia River Chinook hatchery broodstock collections.

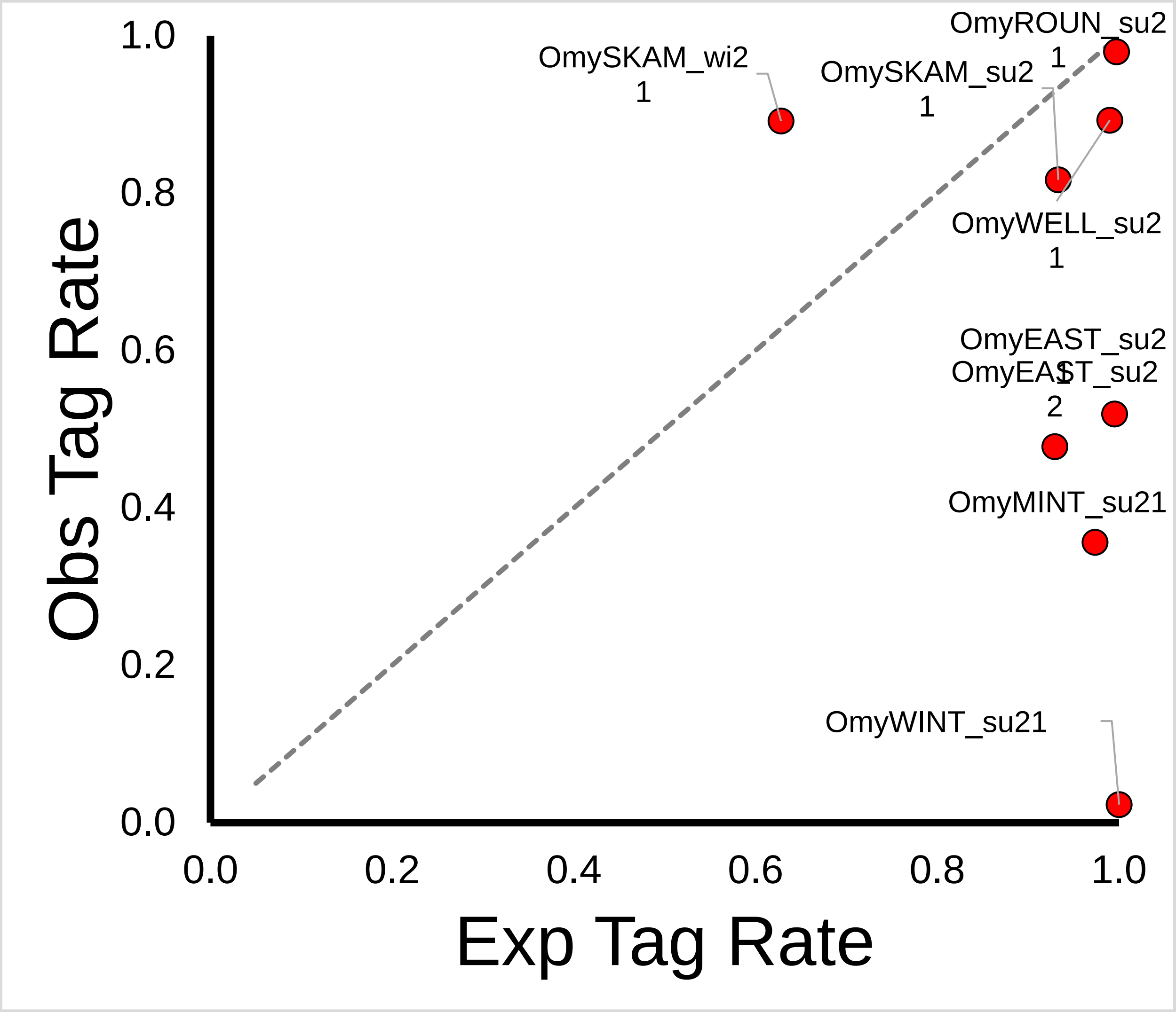

Figure 15. Observed versus expected PBT rates for SY2021 Columbia River Steelhead hatchery broodstock collections.

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 using allele frequencies for millions of SNPs from whole genome resequencing that can be drawn from at any time should the need for more markers be necessary. An example of such need is basin-wide coverage to account for stock transfers or reintroductions throughout the basin.

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Appendix 1. Chinook Salmon hatchery broodstock sampled for PBT baselines.

									2023 genotyping	
Map ID	Spawning hatchery	Broodstock Code	Run type	Lineage	Region	Latitude	Longitude	1st SY	Current SY	Completed
1	Klaskanine (NF brood)	OtsKLNF_seg_fa	fall (tule)	LC	Col.	46.09000	-123.71800	na	na	na
1	Klaskanine (SF brood)	OtsKLSF_seg_fa	fall (tule)	LC	Col.	46.09000	-123.71800	na	na	na
2	Big Creek	OtsBIGC_seg_fa	fall (tule)	LC	Col.	46.14616	-123.58102	2015	na	na
5	Cowlitz Salmon	OtsCOWL_seg_fa	fall (tule)	LC	Col.	46.51145	-122.62935	2015	2022	715
5	Cowlitz Salmon	OtsCOWL_seg_sp	spring	LC	Col.	46.51145	-122.62935	2015	2022	1320
6	North Toutle	OtsNTOU_seg_fa	fall (tule)	LC	Col.	46.37464	-122.57200	2015	2022	210
7	Kalama Falls	OtsKALA_seg_fa	fall (tule)	LC	Col.	46.01624	-122.73284	2016	2022	1397
7	Kalama Falls	OtsKALA_seg_sp	spring	LC	Col.	46.01624	-122.73284	2015	2022	650
9	Speelyai (Lewis R)	OtsSPEE_seg_sp	spring	LC	Col.	45.98849	-122.40618	2015	2022	1135
15	Clackamas	OtsCLAC_seg_sp	spring	LC	Col.	45.29600	-122.36200	na	na	na
18	Marion Forks	OtsMARF_seg_sp	spring	LC	Col.	44.61200	-121.94800	na	na	na
17	North Santiam	OtsNSAN_seg_sp	spring	LC	Col.	44.75790	-122.35980	2020	2022	1557
19	South Santiam	OtsSSAN_seg_sp	spring	LC	Col.	44.41600	-122.67500	2020	2022	651
20	McKenzie	OtsMCKE_seg_sp	spring	LC	Col.	44.11800	-122.63700	2020	2022	607
21	Willamette	Ots_WILL_seg_sp	spring	LC	Col.	43.74500	-122.44400	na	na	na
11	Washougal	OtsWASH_seg_fa	fall (tule)	LC	Col.	45.65344	-122.16910	2015	2022	946
12	Bonneville, Tanner Cr.	OtsBONN_seg_fa	fall (tule)	LC	Col.	45.63300	-121.95700	na	2022	2664
24	Spring Creek NFH	OtsSPRCR_seg_fa	fall (tule)	LC	Col.	45.72779	-121.54529	2015	2022	6741
22	Little White Salmon NFH	OtsLWSN_seg_fa	fall	IOT	Col.	45.72226	-121.64010	2013	2022	6871
29	Three Mile Dam	OtsUMAT_seg_fa	fall	IOT	Col.	45.88172	-119.32256	2012	2022	69
32	Prosser	OtsPROS_seg_fa	fall	IOT	Col.	46.21512	-119.75962	2012	2022	119
35	Ringold Springs	OtsRING_seg_fa	fall	IOT	Col.	46.51401	-119.25926	2016	2022	161
36	Priest Rapids	OtsPRIE_seg_fa	fall	IOT	Col.	46.64728	-119.89895	2012	2022	8039
44	Lyons Ferry	OtsLYON_seg_fa	fall	IOT	Snake	46.59725	-118.22823	2011	2022	WDFW
45	Nez Perce Tribal	OtsNPFH_seg_fa	fall	IOT	Snake	46.51954	-116.66010	2011	2022	712
38	Eastbank	OtsEAST_seg_su	summer	IOT	Col.	47.53367	-120.28911	2012	2022	698
39	Entiat NFH	OtsENFH_seg_su	summer	IOT	Col.	47.69806	-120.32310	2013	2022	333
40	Wells	OtsWELL_seg_su	summer	IOT	Col.	47.94582	-119.87115	2012	2022	971
41	Chief Joseph	OtsCHJO_SIN_su	summer	IOT	Col.	48.00060	-119.64510	2013	2022	937
22	Little White Salmon NFH	OtsLWSN_seg_sp	spring	IST	Col.	45.72226	-121.64010	2013	2022	1036
31	South Fork Walla Walla	OtsUMAT_seg_sp	spring	IST	Col.	45.90200	-119.32700	2012	2022	672
44	Lyons Ferry	OtsLYON_seg_sp	spring	IST	Snake	46.59725	-118.22823	2008	2022, 2023	152, 69
45	Nez Perce Tribal	OtsNPFH_seg_sp	spring	IST	Snake	46.51954	-116.66010	2008	2022	278
38	Eastbank	OtsEAST_seg_sp	spring	IST	Col.	47.53367	-120.28911	2012	2022	198
41	Chief Joseph	OtsCHJO_seg_sp	spring	IST	Col.	48.00060	-119.64510	2014	2022	603
13	Carson NFH	OtsCARS_seg_sp	spring	IST	Col.	45.86826	-121.97417	2012	2022	1268
23	Parkdale	OtsPARK_seg_sp	spring	IST	Col.	45.52439	-121.62157	2012	2022	283
25	Klickitat	OtsKLIC_seg_sp	spring	IST	Col.	46.04236	-121.18232	2008	2022	615
26	Warm Springs NFH	OtsWSNF_seg_sp	spring	IST	Col.	44.86201	-121.24503	2012	2021	229
27	Round Butte	OtsRBFH_seg_sp	spring	IST	Col.	44.60503	-121.27784	2012	2021	206
34	Cle Elum SRF	OtsYRRD_SIN_sp	spring	IST	Col.	47.18679	-120.97618	2012	2022	833
37	Leavenworth NFH	OtsLNFH_seg_sp	spring	IST	Col.	47.55842	-120.67383	2013	2022	907
42	Methow	OtsMETH_seg_sp	spring	IST	Col.	48.47703	-120.20513	2012	2022	127
43	Winthrop NFH	OtsWINT_seg_sp	spring	IST	Col.	48.47366	-120.18910	2013	2022	380
49	Lookingglass	OtsLOOK_seg_sp	spring	IST	Snake	45.73136	-117.86397	2008	2022	604
47	Powell	OtsPOWP_seg_sp	spring	IST	Snake	46.50429	-116.32773	2008	2022	450
46	Dworshak NFH	OtsDWOR_seg_sp	spring	IST	Snake	46.50206	-116.32324	2008	2022	1568
48	Kooskia	Ots_KOOS_seg_sp	spring	IST	Snake	46.50206	-116.32324	2008	2022	476
47	Clearwater	OtsCLWH_seg_sp	spring	IST	Snake	46.50429	-116.32773	2008	2022, 2023	2051, 2145
52	Rapid River	OtsRAPH_seg_ss	spring/summer	IST	Snake	45.35411	-116.39381	2008	2022, 2023	2317, 2745
54	SF Salmon, McCall	OtsMCCA_seg_ss	spring/summer	IST	Snake	44.90777	-116.11649	2008	2022	IDFG
54	Johnson Creek	OtsJHNW_int_ss	spring/summer	IST	Snake	44.90777	-116.11649	2008	2022	90
56	Pahsimeroi	OtsPAHH_seg_ss	spring/summer	IST	Snake	44.62284	-113.98627	2008	2022	IDFG
55	Sawtooth	OtsSAWT_seg_ss	spring/summer	IST	Snake	44.15174	-114.88429	2008	2022	IDFG

Note: The Map ID indicates the sites of the hatcheries corresponding to Figure 13. 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).

Appendix **2.** Steelhead and Coho Salmon hatchery broodstock sampled for PBT baselines.

		Broodstock							2023 genotyping	
Map ID	Spawning hatchery	Code	Run type	Lineage	Region	Latitude	Longitude	1st SY	Current SY	Completed
	Steelhead									
2	Big Creek	OmyBIGC_wi	winter	coastal	Col.	46.14620	-123.58100	na	na	na
3	Abernathy FTC	OmyABER_wi	winter	coastal	Col.	46.22600	-123.15300	2012	na	na
4	Cowlitz Trout	OmyCOWL_wi	winter	coastal	Col.	46.48770	-122.72700	na	na	na
7	Kalama Falls	OmyKALA_wi	winter	coastal	Col.	46.01620	-122.73280	na	na	na
8	Merwin	OmyMERW_wi	winter	coastal	Col.	45.95400	-122.56400	na	na	na
15	Clackamas	OmyCLAC_wi	winter	coastal	Col.	45.29600	-122.36200	na	na	na
16	Eagle Creek NFH	OmyECFH_wi	winter	coastal	Col.	45.27600	-122.20200	na	na	na
14	Sandy	OmySAND_wi	winter	coastal	Col.	45.40700	-122.25400	na	na	na
10	Skamania	OmySKAM_sw	summer/winter	coastal	Col.	45.62180	-122.21730	2013	2022	223
23	Parkdale	OmyPARK_wi	winter	coastal	Col.	45.52440	-121.62160	2012	2021	na
27	Round Butte	OmyROUN_su	summer	inland	Col.	44.60500	-121.27784	2013	2022	469
28	Umatilla	OmyUMAT_su	summer	inland	Col.	45.91300	-119.55200	2012	2021	na
38	Eastbank	OmyEAST_su	summer	inland	Col.	47.53370	-120.28910	2012	2022	92
40	Wells	OmyWELL_su	summer	inland	Col.	47.94580	-119.87120	2013	2022	221
42	Methow (Twisp)	OmyMETH_su	summer	inland	Col.	48.47700	-120.20510	2013	2021	na
43	Winthrop NFH	OmyWINT_su	summer	inland	Col.	48.47370	-120.20510	2013	2022	109
44	Lyons Ferry	OmyLYON_su	summer	inland	Snake	46.59730	-118.22820	2009	2022	IDFG
50	Wallowa	OmyWALL_su	summer	inland	Snake	45.41780	-117.30040	2009	2022	IDFG
53	Oxbow	OmyOXBO_su	summer	inland	Snake	44.97270	-116.85480	2008	2022	IDFG
46	Dworshak NFH	OmyDWOR_su	summer	inland	Snake	46.50210	-116.32320	2008	2022	IDFG
56	Pahsimeroi	OmyPAHH_su	summer	inland	Snake	44.62280	-113.98630	2008	2022	IDFG
55	Sawtooth	OmySAWT_su	summer	inland	Snake	45.15170	-114.88430	2008	2022	IDFG
51	Little Sheep Creek	OmyLSCR_su	summer	inland	Snake	45.47770	-116.93060	2008	2022	IDFG
30	Minthorn Springs	OmyMINT_su	summer	inland	Col.	45.69938	-118.39647	2012	2022	77
	Coho									
28	Umatilla	OkiUMA_seg_fa	fall	lower Col.	Col.	45.91300	-119.55200	2015	2022	666
32	Prosser	OkiPRO_seg_fa	fall	lower Col.	Col.	46.21510	-119.75960	2016	2022	638
37	Leavenworth NFH	OkiLNFH_seg_fa	fall	lower Col.	Col.	47.55840	-120.67380	2012	2022, 2023	1111, 1110
43	Winthrop NFH	OkiWTP_seg_fa	fall	lower Col.	Col.	48.47370	-120.18910	2012	2022, 2023	1006, 626
46	Dworshak NFH	OkiNPT_seg_fa	fall	lower Col.	Snake	46.50210	-116.32320	2015	2022	1537
16	Eagle Creek NFH	OkiEGLC_seg_fa	fall	lower Col.	Col.	45.27600	-122.20200	2019	2022	1444
12	Bonneville	OkiBONN_seg_fa	fall	lower Col.	Col.	45.63300	-121.95700	2019	2022	930
33	Mel R Sampson	OkiMRS_SIN_fa	fall	lower Col.	Col.	47.04200	-120.62600	2022	2022	793

* Steelhead Methow Hatchery Twisp stock spawned at Winthrop NFH starting in 2017; not distiguished from Winthrop stock.
Note: The map ID indicates site locations corresponding with Figure 13. Genetic lineage is coastal or inland. Year refers to the first year of PBT sampling for each hatchery: na – not currently a PBT hatchery. Some 2017 PBT samples have been archived awaiting shipment to the Hagerman Genetics Laboratory as of the

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

Appendix 3. Checklist of PBT broodstock collections that comprise the PBT baselines for Chinook salmon from 2008 through 2022.

Code	Run type	Map ID	Hatchery	Species	Lineage	Year														
						2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
OtsCLWH_seg_sp	01Spring	47	Clearwater Fish Hatchery	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsPOWP_seg_sp	01Spring	47	Clearwater Fish Hatchery - Powell Facility	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsDWOR_seg_sp	01Spring	46	Dworshak National Fish Hatchery	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsKOOS_seg_sp	01Spring	48	Dworshak National Fish Hatchery	Chinook	Interior stream type															X
OtsLOOK_seg_sp	01Spring	49	Lookingglass Fish Hatchery - Catherine Creek	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsLOOK_seg_sp	01Spring	49	Lookingglass Fish Hatchery - Grande Ronde	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsIMNW_seg_ss	02Spring/Summer	49	Lookingglass Fish Hatchery - Imnaha River	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsLOOK_seg_sp	01Spring	49	Lookingglass Fish Hatchery - Lookingglass Creek	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsLOOK_seg_sp	01Spring	49	Lookingglass Fish Hatchery - Lostine River	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsLYON_seg_sp	01Spring	44	Lyons Ferry Fish Hatchery	Chinook	Interior stream type	*	*	*	*	X	X	X	X	X	X	X	X	X	X	X
OtsLYON_seg_sp	01Spring	44	Lyons Ferry Fish Hatchery - Tucannon River	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsLYON_seg_fa	04Fall	44	Lyons Ferry Fish Hatchery	Chinook	Interior ocean type	*	*	*	X	X	X	X	X	X	X	X	X	X	X	X
OtsJHNW_int_ss	02Spring/Summer	54	McCall Fish Hatchery - Johnson Creek	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsMCCA_seg_ss	02Spring/Summer	54	McCall Fish Hatchery - South Fork Salmon	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsNPFH_seg_fa	04Fall	45	Nez Perce Tribal Fish Hatchery	Chinook	Interior ocean type	*	*	*	X	X	X	X	X	X	X	X	X	X	X	X
OtsNPFH_seg_sp	01Spring	45	Nez Perce Tribal Fish Hatchery	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsPAHH_seg_ss	02Spring/Summer	56	Pahsimeroi Fish Hatchery	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsRAPH_seg_sp	01Spring	52	Rapid River Fish Hatchery	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsSAWT_seg_ss	02Spring/Summer	55	Sawtooth Fish Hatchery	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsBIGC_seg_fa	04Fall	2	Big Creek Hatchery	Chinook	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	X	X	*	*
OtsCARS_seg_sp	01Spring	13	Carson National Fish Hatchery	Chinook	Interior stream type	*	*	*	*	X	X	X	X	X	X	X	X	X	X	X
OtsCHJO_seg_sp	01Spring	41	Chief Joseph Hatchery	Chinook	Interior stream type	*	*	*	*	*	*	X	X	X	X	X	X	X	X	X
OtsCHJO_int_su	03Summer	41	Chief Joseph Hatchery - Integrated	Chinook	Interior ocean type	*	*	*	*	*	X	X	X	X	X	X	X	X	X	X
OtsCHJO_seg_su	03Summer	41	Chief Joseph Hatchery - Segregated	Chinook	Interior ocean type	*	*	*	*	*	X	X	X	X	X	X	X	X	X	X
OtsCOWL_seg_sp	01Spring	5	Cowlitz Salmon	Chinook	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	X	X	X	X
OtsCOWL_seg_fa	04Fall	5	Cowlitz Salmon	Chinook	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	X	X	X	X
OtsEAST_seg_sp	01Spring	38	Eastbank Fish Hatchery	Chinook	Interior stream type	*	*	*	*	*	X	X	X	X	X	X	X	X	X	X
OtsEAST_seg_su	03Summer	38	Eastbank Fish Hatchery	Chinook	Interior ocean type	*	*	*	*	X	X	X	X	X	X	X	X	X	X	X
OtsENFH_seg_su	03Summer	39	Entiat National Fish Hatchery	Chinook	Interior ocean type	*	*	*	*	*	X	X	X	X	X	X	X	X	X	X
OtsKALA_seg_sp	01Spring	7	Kalama Falls	Chinook	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	X	X	X	X
OtsKALA_seg_fa	04Fall	7	Kalama Falls	Chinook	Lower Columbia	*	*	*	*	*	*	*	*	X	X	X	X	X	X	X
OtsKLIC_seg_sp	01Spring	25	Klickitat State Fish Hatchery	Chinook	Interior stream type	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
OtsKLIC_seg_fa	04Fall	25	Klickitat State Fish Hatchery	Chinook	Interior ocean type	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	X	X	X	†	†
OtsLNFH_seg_sp	01Spring	37	Leavenworth National Fish Hatchery	Chinook	Interior stream type	*	*	*	*	*	X	X	X	X	X	X	X	X	X	X
OtsSPEE_seg_sp	01Spring	9	Speelyai Hatchery	Chinook	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	**	**	X	X
OtsLWSN_seg_fa	04Fall	22	Little White Salmon National Fish Hatchery	Chinook	Interior ocean type	*	*	*	*	*	X	X	X	X	X	X	X	X	X	X
OtsLWSN_seg_sp	01Spring	22	Little White Salmon National Fish Hatchery	Chinook	Interior stream type	*	*	*	*	*	X	X	X	X	X	X	X	X	X	X
OtsTOUC_seg_sp	01Spring	22	Little White Salmon National Fish Hatchery - Touchet River	Chinook	Interior stream type	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	X	*	*	†	†
OtsNSAN_seg_sp	01Spring	18	Marion Forks Hatchery	Chinook	Willamette	*	*	*	*	*	*	*	*	*	*	X	X	*	X	X
OtsMETH_seg_sp	01Spring	42	Methow State Fish Hatchery	Chinook	Interior stream type	*	*	*	*	X	X	X	X	X	X	X	X	X	X	X
OtsPARK_seg_sp	01Spring	23	Parkdale Fish Facility	Chinook	Lower Columbia	*	*	*	*	X	X	X	X	X	X	X	X	X	X	X
OtsPRIE_seg_fa	04Fall	36	Priest Rapids Hatchery	Chinook	Interior ocean type	*	*	*	*	X	X	X	X	X	X	X	X	X	X	X
OtsRBFH_seg_sp	01Spring	27	Round Butte Fish Hatchery	Chinook	Interior stream type	*	*	*	*	X	X	X	X	X	X	X	X	X	X	X
OtsRING_seg_fa	04Fall	35	Ringold Springs State Hatchery	Chinook	Interior ocean type	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	X	X	X	X	X	X	X
OtsSSAN_seg_sp	01Spring	19	South Santiam Hatchery	Chinook	Willamette	*	*	*	*	*	*	*	X	X	*	X	X	X	X	X
OtsSPCR_seg_fa	04Fall	24	Spring Creek National Fish Hatchery	Chinook	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	X	X	X	X
OtsNTOU_seg_fa	04Fall	6	North Toutle Hatchery	Chinook	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	**	X	X	X
OtsUMAT_seg_fa	04Fall	29	Three mile dam, Umatilla River	Chinook	Interior ocean type	*	*	*	*	X	X	X	~	~	~	X	X	X	X	X
OtsUMAT_seg_sp	01Spring	31	South Fork Walla Walla facility	Chinook	Interior stream type	*	*	*	*	X	X	X	X	X	X	X	X	X	X	X
OtsWASH_seg_fa	04Fall	11	Washougal	Chinook	Lower Columbia	*	*	*	*	*	*	*	X	X	X	X	X	X	X	X
OtsWSNF_seg_sp	01Spring	26	Warm Springs National Fish Hatchery	Chinook	Interior stream type	*	*	*	*	X	X	X	~	~	~	X	X	X	X	X
OtsWELL_seg_su	03Summer	40	Wells Fish Hatchery	Chinook	Interior ocean type	*	*	*	*	X	X	X	X	X	X	X	X	X	X	X
OtsWINT_seg_sp	01Spring	43	Winthrop National Fish Hatchery	Chinook	Interior stream type	*	*	*	*	*	X	X	X	X	X	X	X	X	X	X
OtsPROS_seg_fa	04Fall	32	Yakima Nation Prosser Hatchery	Chinook	Interior ocean type	*	*	*	*	X	X	*	X	X	X	X	X	X	X	X
OtsYRRD_int_sp	01Spring	34	Levi George/Cle Elum (Integrated)	Chinook	Interior stream type	*	*	*	*	X	X	X	X	X	X	X	X	X	X	X
OtsYRRD_seg_sp	01Spring	34	Levi George/Cle Elum (Segregated)	Chinook	Interior stream type	*	*	*	*	X	X	X	X	X	X	X	X	X	X	X
OtsBONN_seg_fa	04Fall	12	Bonneville Dam Hatchery	Chinook	Lower Columbia	*	*	*	*	*	*	*	*	*	*	*	*	*	*	X
OtsMCKE_seg_sp	01Spring	20	McKenzie Hatchery	Chinook	Willamette	*	*	*	*	*	*	*	*	*	*	*	*	*	*	X

Note: Species-specific collections code along with run type and genetic lineage are provided for both species. Map numbers correspond with Figure 13.

X	Chinook tissues genotyped using 351 SNPs
X	Chinook tissues genotyped using 343 SNPs
X	Chinook tissues genotyped using 298 SNPs
X	Chinook tissues genotyped using 96 SNPs
~	Chinook broodstock sampled, spawned at another hatchery and genotyped using 298 SNPs
a	Chinook Lyons Ferry stock consolidated under 'OtsLYON' starting in 2012
b	Chinook Umatilla fall stock spawned at Little White Salmon Hatchery in 2015 & 2016; not distinguished from LWS stock. Broodstock collected/spawned at Ringold Springs in 2017; not distiguished from Ringold stock.
c	Chinook typically spawned at Little White Salmon NFH, but due to low returns in 2018 they were spawned at Klickitat Hatchery.
h	Chinook Warm Springs NFH spring stock spawned at Little White Salmon Hatchery starting in 2015-2017.
N/A	Stock discontinued/non-existent
*	Broodstock not sampled
**	Broodstock sampled, tissues archived until funding identified for processing

† Chinook broodstock sampled, spawned at another hatchery and genotyped using 351 SNPs

Appendix 4. Checklist of PBT broodstock collections that comprise the PBT baselines for steelhead from 2008 through 2022.

Map ID	Hatchery	Species	Code	Run type	Lineage	Year														
						2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
46	Dworshak National Fish Hatchery	Steelhead	OmyDWOR_su	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
51	Little Sheep Creek Hatchery	Steelhead	OmyLSCR_su	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
44	Lyons Ferry Fish Hatchery- Touchet	Steelhead	OmyTOUW_su	Summer	Interior	*	X	X	X	X	X	X	X	X	X	X	X	X	X	X
44	Lyons Ferry Fish Hatchery	Steelhead	OmyLYON_su	Summer	Interior	*	X	X	X	X	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
44	Lyons Ferry Fish Hatchery - Grande Ronde	Steelhead	OmyCGRW_su	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
44	Lyons Ferry Fish Hatchery - Tucannon	Steelhead	OmyTUCW_su	Summer	Interior	*	X	X	X	X	X	X	X	X	X	X	X	X	X	X
44	Lyons Ferry Fish Hatchery - Wallowa	Steelhead	OmyWALW_su	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	N/A
53	Oxbow	Steelhead	OmyOXBO_su	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
55	Sawtooth Fish Hatchery	Steelhead	OmySAWT_su	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
55	Sawtooth Fish Hatchery - East Fork Salmon	Steelhead	OmyEFSW_su	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
55	Sawtooth Fish Hatchery - Squaw Creek	Steelhead	OmySQUW_su	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
56	Pahsimeroi Fish Hatchery	Steelhead	OmyPAHH_su	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
50	Wallowa Fish Hatchery	Steelhead	OmyWALL_su	Summer	Interior	*	X	X	X	X	X	X	X	X	X	X	X	X	X	X
38	Eastbank Hatchery	Steelhead	OmyEAST_su	Summer	Interior	*	*	*	*	X	X	X	X	X	X	X	X	X	X	X
42	Methow Hatchery (Twisp)	Steelhead	OmyMETH _su	Summer	Interior	*	*	*	*	*	X	X	X	X	~	~	~	~	~	~
23	Parkdale Fish Facility	Steelhead	OmyPARK_wi	Winter	Coastal	*	*	*	*	X	X	X	X	X	X	X	X	X	*	*
27	Round Butte Fish Hatchery	Steelhead	OmyROUN_su	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X	X	X	X	X
10	Skamania Hatchery (Summer)	Steelhead	OmySKAM_su	Summer	Coastal	*	*	*	*	*	X	X	X	X	X	X	X	X	X	X
10	Skamania Hatchery (Winter)	Steelhead	OmySKAM_wi	Winter	Coastal	*	*	*	*	*	X	X	X	X	X	X	X	X	X	X
30	Minthorn Springs	Steelhead	OmyMINT _su	Summer	Interior	*	*	*	*	X	X	X	X	X	X	X	*	X	X	X
40	Wells Hatchery - On Station	Steelhead	OmyWELL_su	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X	X	X	X	X
40	Wells Hatchery - Okanogan stock	Steelhead	OmyWOKA _su	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X	*	*	*	*
40	Wells Hatchery - Omak stock	Steelhead	OmyWOMA _su	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X	*	*	*	*
40	Wells Hatchery - Methow stock	Steelhead	OmyWMET _su	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X	*	*	*	*
43	Winthrop National Fish Hatchery	Steelhead	OmyWINT_su	Summer	Interior	*	*	*	*	X	X	X	X	X	X	X	X	X	X	X

Note map numbers correspond to sites in Figure 13.

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

Appendix 5. Checklist of PBT broodstock collections that comprise the PBT baselines for Coho Salmon from 2011 through 2022.

Map num.	Hatchery	Species	Code	Run type	Lineage	Year											
						2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
29	Three Mile Dam, Umatilla River	Coho	OkiUMA_seg_fa22	Fall	Lower Columbia					X	X	X	X	X	X	X	X
37	Leavenworth National Fish Hatchery	Coho	OkiLNFH_seg_fa22	Fall	Lower Columbia	X	X	X	X	X	X	X	X	X	X	X	X
46	Dworshak National Fish Hatchery	Coho	OkiNPT_seg_fa22	Fall	Lower Columbia			*	*	X	X	X	X	X	X	*	X
32	Yakima Nation Prosser Hatchery	Coho	OkiPRO_seg_fa22	Fall	Lower Columbia						X	X	X	X	X	*	X
33	Mel R Sampson Hatchery	Coho	OkiMRS_int_fa22	Fall	Lower Columbia											*	X
43	Winthrop National Fish Hatchery	Coho	OkiWTP_seg_fa22	Fall	Lower Columbia		X	X	X	X	X	X	X	X	X	X	X
16	Eagle Creek National Fish Hatchery	Coho	OkiEGLC_seg_fa22	Fall	Lower Columbia									X			X
12	Bonneville Hatchery	Coho	OkiBONN_seg_fa22	Fall	Lower Columbia									X			X

Note: map numbers correspond to sites in Figure 12.
X	Coho tissues genotyped at 235 loci
*	Samples received, but not genotyped.

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 2022 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 3).

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 11th year of analysis of Sockeye salmon fisheries in the Columbia River mainstem, which consists of fish harvested in 2022 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 2022 from a total of five different mixture sources: the spring period harvest of the 1) sport fishery (above and below Bonneville Dam); 2) test fishery; the summer period harvest of the 3) lower river sport fishery; and the fall period harvest of the 4) sport (above and below Bonneville Dam), and 5) lower river commercial. 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 17; Table 9). 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 17): Region A corresponds to our grouping of pre-existing Oregon and Washington state sport fishing sections 1-4 (or commercial zones 4-5), Region B corresponds to our grouping of sport sections 5-10 (or commercial zones 1-3). In the Zone 6, we typically distinguish Region 01 (Bonneville Pool) from Region 02 (Dalles and John Day Pools) because of the stock composition differences that can occur between the two regions particularly in the fall period when tules are observed in high proportions in Region 01. These sets of groupings were established for this study in order to achieve balanced sampling for analysis of these fishery datasets, as well as to best match the stratification of the reported catch.

Non-Treaty fisheries during the spring management period for Chinook salmon are mark-selective based on absence or presence of the adipose fin to distinguish hatchery fish from natural origin fish, respectively. These adipose markings make it possible to have a mark-selective sport and commercial fishery in which only fish with missing adipose fins (hatchery-origin) are legally retained. Fish with intact adipose fins that are caught in these fisheries are released, but mortality rates are unknown from these releases. In addition to sampling clipped hatchery-origin fish from the spring and summer period mark selective 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 2022 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 2022 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 fourth 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 and so the 2023 Bonneville Dam run year was the fourth 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.

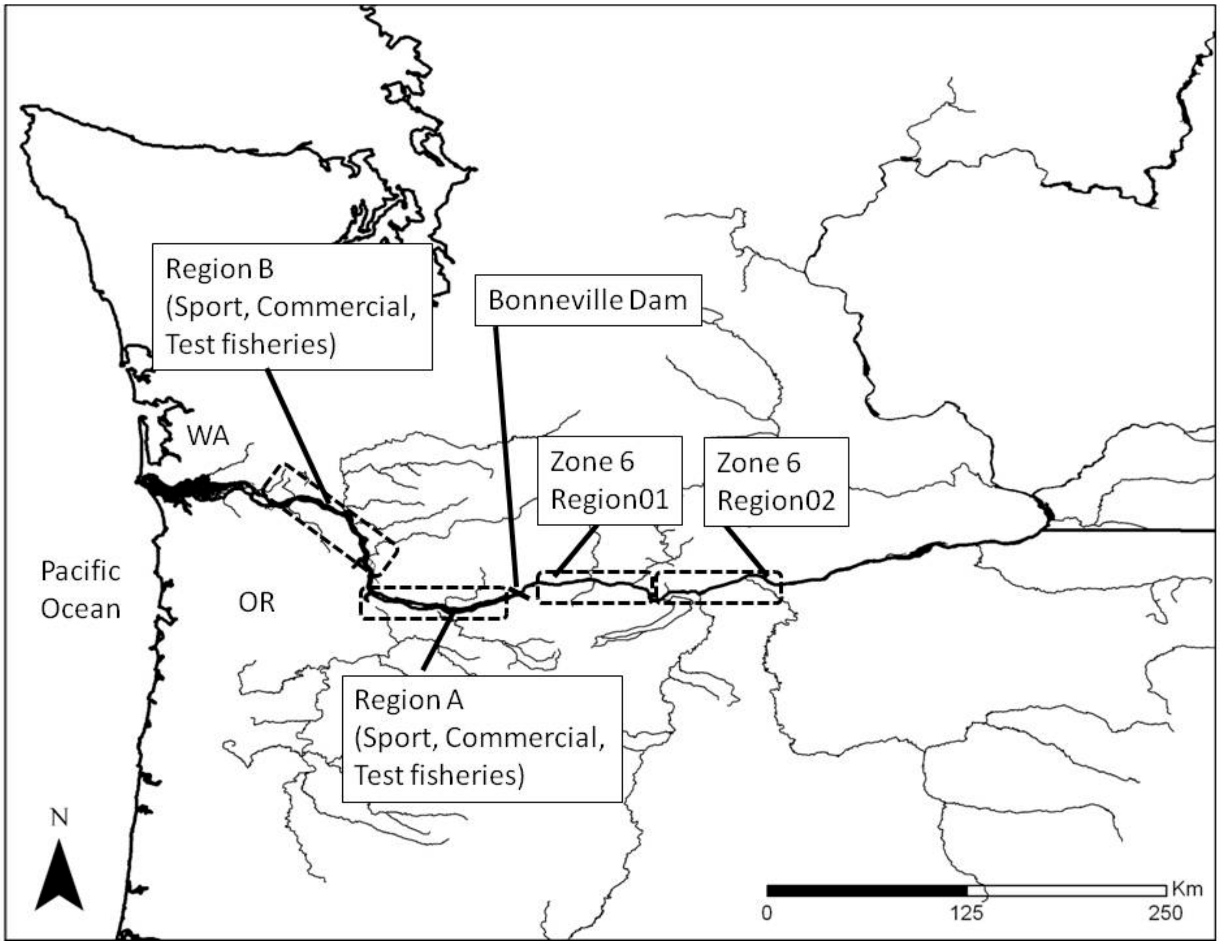


Figure 16. Project scope showing sources of Chinook salmon and Sockeye salmon harvest mixtures that were analyzed using PBT/GSI.

Table 11. Characteristics of Chinook and Sockeye harvest samples by fishery, region, and adipose-clip status by weekly strata in 2022.

						Statistical weeks																																
						Spring															Summer								Fall									
Chinook Period	Fishery	Region	Clip	Sampled	Genotyped	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	25	26	27	28	29	30	31	32	32	33	34	35	36	37	38	39	40	41
Spring	Sport	A	AD	720	649		3	46	67	44					105	186	71	53	62	12																		
		B	AD	973	874	4	1	27	247	206					39	59	47	110	105	29																		
		01 (Zone 6)	AD	13	12								9				3																					
		02 (Zone 6)	AD	77	67								34	20			13																					
	Test	B	AD	353	325		8	7	15	23	31	44	45	54	70	28																						
			AI	71	70		1		1	4	7	17	4	11	11	14																						
Summer	Sport	A	AD	88	82																3	7	12	20	20	6	10	4										
		B	AD	352	330																73	93	61	66	26	4	7											
Fall	Sport	A	AD	136	126																								1	2	3	11	3		19	62	23	2
			AI	473	433																								1	8	7	16	10		115	186	73	17
		B	AD	143	126																								1	21	6	47	46				3	2
			AI	211	197																								13	31	17	64	57				11	4
		01 (Zone 6)	AD	65	60																									1		3	2	12	3	21	13	5
			AI	104	100																											2	4	16	2	37	33	6
		02 (Zone 6)	AD	61	58																												26	6	2	10	12	2
			AI	103	97																												15	8	5	20	48	1
	Commercial	A	AD	433	411																									16	69	155	137			31	3	
			AI	368	348																									28	55	81	84			65	35	
		B	AD	1	1																																	1
			AI	5	5																																	5
	Chinook fishery total			4750	4371	4	13	80	330	277	38	61	92	85	225	287	134	163	167	41	76	100	73	86	46	10	17	4	16	107	157	379	384	42	146	432	254	45
Summer	Sport	A&B	AD	2	2																		60	56	33	4	5	1										
			AI	167	159																				2													
	Sockeye fishery total			169	161	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60	56	35	4	5	1	0	0	0	0	0	0	0	0	0	0

PBT Rate Expansion using SCOBI DEUX 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:

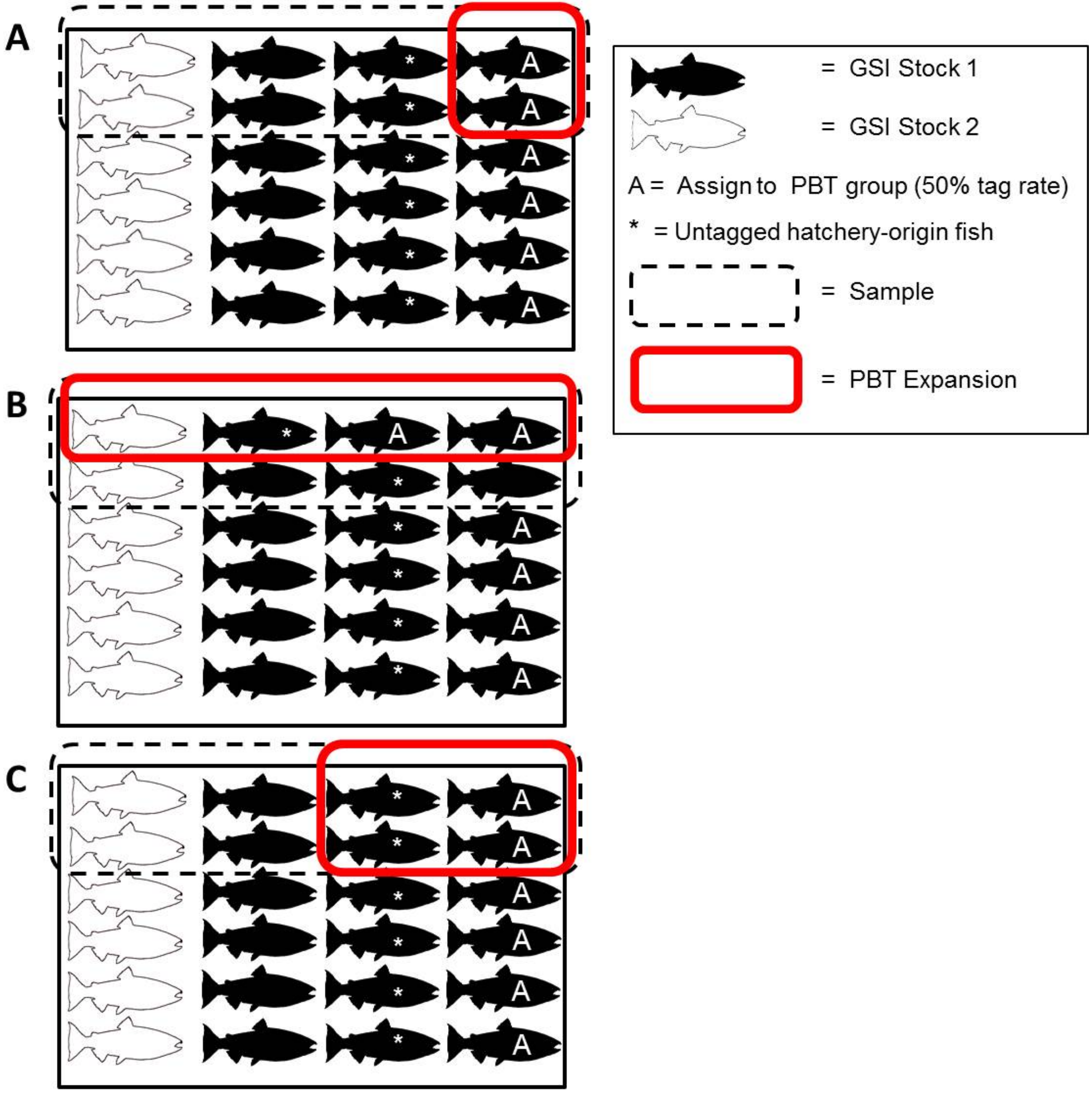


Figure 17. Conceptual illustration of the bias correction the SCOBI DEUX method provides.

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 SCOBI DEUX 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 a 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 10; 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 (Quinault River), 02_LOWCOL (lower Columbia River), 03_SKAMAN (Skamania hatchery releases at three sites in lower Columbia River, Willamette River, and Klickitat River), 04_ WILLAM (Willamette River), 05_BWSALM (Big White Salmon River), 06_KLICKR (Klickitat River), 07_MGILCS (middle Columbia River, Grande Ronde River, Imnaha River, lower Snake River, lower Clearwater River, and lower Salmon River), 08_YAKIMA (Yakima River), 09_UPPCOL (upper Columbia River), 10_SFCLWR (South Fork Clearwater River), 11_UPCLWR (upper Clearwater River), 12_SFSALM (South Fork Salmon River), 13_MFSALM (Middle Fork Salmon River), and 14_UPSALM (upper Salmon River) (Figure 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 (Quinault River). This 335 SNP baseline was determined to be less accurate than the existing version 3.3. baseline for GSI applications (Hess et al. 2020), however, we have observed the panel can improve accuracy for PBT applications.

Table 12. Sample sizes and reporting groups of Chinook salmon baseline populations. Lineages: ST (stream type), OT (ocean type), LC (Lower Columbia).

ID	Collection	(n)	Lineage	Reporting Groups	Reporting Group description
OTS01	Youngs Bay fall-run	91	Rogue	01_YOUNGS	Youngs Bay- Columbia Rogue stock
OTS02	Cowlitz R spring-run	90	LC	02_WCASSP	West Cascade spring-run
OTS03	Kalama R spring-run	83	LC	02_WCASSP	West Cascade spring-run
OTS04	Cowlitz R fall-run	82	LC	03_WCASFA	West Cascade fall-run
OTS05	Elochoman R fall-run	86	LC	03_WCASFA	West Cascade fall-run
OTS06	Lewis R fall-run	93	LC	03_WCASFA	West Cascade fall-run
OTS07	NF Lewis fall-run	178	LC	03_WCASFA	West Cascade fall-run
OTS08	Sandy R fall-run	83	LC	03_WCASFA	West Cascade fall-run
OTS09	McKenzie R spring-run	78	LC	04_WILLAM	Willamette River spring-run
OTS10	N Santiam R spring-run	79	LC	04_WILLAM	Willamette River spring-run
OTS11	Sandy R spring-run	48	LC	04_WILLAM	Willamette River spring-run
OTS12	White Salmon fall-run	77	LC	05_SPCRTU	Spring Creek tule fall-run
OTS13	Spring Creek NFH tule fall-run	49	LC	05_SPCRTU	Spring Creek tule fall-run
OTS14	Klickitat R spring-run	84	ST	06_KLICKR	Klickitat River spring-run
OTS15	Shitike R spring-run	93	ST	07_DESCSP	Deschutes River spring-run
OTS16	Warm Springs R spring-run	90	ST	07_DESCSP	Deschutes River spring-run
OTS17	John Day R spring-run	78	ST	08_JOHNDR	John Day River spring-run
OTS18	Middle Fork John Day R spring-run	47	ST	08_JOHNDR	John Day River spring-run
OTS19	North Fork John Day R spring-run	42	ST	08_JOHNDR	John Day River spring-run
OTS20	American R spring-run	76	ST	09_YAKIMA	Yakima River spring-run
OTS21	Cle-Elum spring-run	88	ST	09_YAKIMA	Yakima River spring-run
OTS22	Winthrop NFH spring-run	82	ST	10_UCOLSP	upper Columbia River spring-run/ Carson Hatchery spring-run
OTS23	little White Salmon R spring-run	93	ST	10_UCOLSP	upper Columbia River spring-run/ Carson Hatchery spring-run
OTS24	Wenatchee R spring-run	109	ST	10_UCOLSP	upper Columbia River spring-run/ Carson Hatchery spring-run
OTS25	Entiat R spring-run	98	ST	10_UCOLSP	upper Columbia River spring-run/ Carson Hatchery spring-run
OTS26	Tucannon R spring-run	81	ST	11_TUCANO	Tucannon River spring-run
OTS27	Wenaha R spring-run	179	ST	12_HELLSC	Hells Canyon spring-run
OTS28	Lostine R spring-run	212	ST	12_HELLSC	Hells Canyon spring-run
OTS29	Grande Ronde R spring-run	314	ST	12_HELLSC	Hells Canyon spring-run
OTS30	Imnaha R spring-run	96	ST	12_HELLSC	Hells Canyon spring-run
OTS31	Lolo Cr spring-run	89	ST	12_HELLSC	Hells Canyon spring-run
OTS32	Red R spring-run	221	ST	12_HELLSC	Hells Canyon spring-run
OTS33	Powell R spring-run	56	ST	12_HELLSC	Hells Canyon spring-run
OTS34	Red R weir spring-run	91	ST	12_HELLSC	Hells Canyon spring-run
OTS35	South Forth Salmon R spring-run	139	ST	13_SFSALM	South Fork Salmon River spring/summer-run
OTS36	Johnson Cr spring-run	137	ST	13_SFSALM	South Fork Salmon River spring/summer-run
OTS37	Secesh R spring-run	252	ST	13_SFSALM	South Fork Salmon River spring/summer-run
OTS38	Chamberlain Cr spring-run	219	ST	14_CHMBLN	Chamberlain Creek spring/summer-run
OTS39	Big Cr spring-run	139	ST	15_MFSALM	Middle Fork Salmon River spring/summer-run
OTS40	Camas Cr spring-run	55	ST	15_MFSALM	Middle Fork Salmon River spring/summer-run
OTS41	Loon Cr spring-run	107	ST	15_MFSALM	Middle Fork Salmon River spring/summer-run
OTS42	Sulphur Cr spring-run	94	ST	15_MFSALM	Middle Fork Salmon River spring/summer-run
OTS43	Bear Valley Cr spring-run	135	ST	15_MFSALM	Middle Fork Salmon River spring/summer-run
OTS44	Capehorn Cr spring-run	214	ST	15_MFSALM	Middle Fork Salmon River spring/summer-run
OTS45	Marsh Cr spring-run	228	ST	15_MFSALM	Middle Fork Salmon River spring/summer-run
OTS46	North Fork Salmon R spring-run	55	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS47	Lemhi R spring-run	96	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS48	Pahsimeroi R spring-run	92	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS49	East Fork Salmon R spring-run	286	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS50	Salmon R spring-run	83	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS51	West Fork Yankee Fork spring-run	75	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS52	Valley Cr spring-run	100	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS53	Sawtooth Hatchery weir spring-run	186	ST	16_UPSALM	upper Salmon River spring/summer-run
OTS54	upper Deschutes R fall-run	252	OT	17_DESCFA	Deschutes River fall-run
OTS55	lower Yakima R fall-run	62	OT	18_UCOLSF	upper Columbia River summer/fall-run
OTS56	Hanford Reach fall-run	93	OT	18_UCOLSF	upper Columbia River summer/fall-run
OTS57	Wenatchee R summer-run	92	OT	18_UCOLSF	upper Columbia River summer/fall-run
OTS58	Entiat R summer-run	51	OT	18_UCOLSF	upper Columbia River summer/fall-run
OTS59	Methow R summer-run	87	OT	18_UCOLSF	upper Columbia River summer/fall-run
OTS60	Lyons Ferry weir fall-run	90	OT	19_SRFALL	Snake River fall-run
OTS61	Clearwater R fall-run	228	OT	19_SRFALL	Snake River fall-run

Combined application of PBT and GSI

We combined PBT and GSI results together by first accepting all confident PBT assignments to hatchery broodstock (i.e., LOD≥14 & FDR≤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 SCOBI DEUX 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 wanded 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 final 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 (**Table 13**). However, we also repeated this analysis using the VSI-lower river chinook salmon to ensure that we were fully estimating an index of abundance of all genetically identified upriver fish, even those that had been originally incorrectly identified as lower river fish via VSI (**Table 14**). Weeks were pooled to obtain sample sizes >10 fish for most strata. We applied these stratified samples to the weekly CPUE estimates of adipose clipped and unclipped VSI-upriver test fish.

Table 13. The sample rate and stratification for genetic analysis of the VSI-upriver adipose clipped and unclipped adult Chinook salmon from the spring test fishery in 2022.

		Estimated # VSI-Upriver			CPUE of VSI-Upriver			Sample of VSI-Upriver			Sample Rate of VSI-Upriver		
Week	Drifts	AD	AI	Total	AD	AI	Total	AD	AI	Total	AD	AI	Total
12	13	7.33	1.22	8.56	0.56	0.09	0.66	6	1	7	45.3%	60.9%	47.9%
13	15	4.44	1.11	5.56	0.30	0.07	0.37	3	0	3			
14	15	22.65	4.12	26.76	1.51	0.27	1.78	11	1	12			
15	11	19.92	4.27	24.19	1.81	0.39	2.20	14	3	17			
16	15	55.56	15.56	71.11	3.70	1.04	4.74	25	7	32			
17	15	104.32	16.41	120.73	6.95	1.09	8.05	38	14	52			
18	14	44.19	6.10	50.29	3.16	0.44	3.59	30	4	34	73.2%	86.4%	75.3%
19	15	35.82	7.41	43.24	2.39	0.49	2.88	28	8	36			
20	13	37.53	8.47	46.00	2.89	0.65	3.54	28	7	35			
21	11	7.62	8.71	16.32	0.69	0.79	1.48	7	8	15	86.9%	92.7%	89.1%
22	7	4.50	0.00	4.50	0.64	0.00	0.64	3	0	3			
23	8	4.00	1.00	5.00	0.50	0.13	0.63	4	1	5			
24	3	0.00	0.00	0.00	0.00	0.00	0.00	0	0	0			

Table 14. The sample rate and stratification for genetic analysis of the VSI-lower river adipose clipped and unclipped adult Chinook salmon from the spring test fishery in 2022

		Estimated # VSI-Lower			CPUE of VSI-Lower			Sample of VSI-Lower			Sample Rate of VSI-Lower		
Week	Drifts	AD	AI	Total	AD	AI	Total	AD	AI	Total	AD	AI	Total
12	13	2.44	0.00	2.44	0.19	0.00	0.19	2	0	2	51.7%	81.0%	54.2%
13	15	4.44	0.00	4.44	0.30	0.00	0.30	4	0	4			
14	15	8.24	0.00	8.24	0.55	0.00	0.55	4	0	4			
15	11	11.38	1.42	12.81	1.03	0.13	1.16	8	1	9			
16	15	8.89	0.00	8.89	0.59	0.00	0.59	4	0	4			
17	15	18.75	3.52	22.27	1.25	0.23	1.48	6	3	9			
18	14	13.71	0.00	13.71	0.98	0.00	0.98	8	0	8	71.7%	81.8%	72.6%
19	15	17.29	2.47	19.76	1.15	0.16	1.32	14	2	16			

20	13	20.58	2.42	23.00	1.58	0.19	1.77	15	2	17			
21	11	18.50	2.18	20.68	1.68	0.20	1.88	17	2	19	94.4%	91.9%	94.3%
22	7	1.50	0.00	1.50	0.21	0.00	0.21	1	0	1			
23	8	9.00	0.00	9.00	1.13	0.00	1.13	9	0	9			
24	3	7.00	0.00	7.00	2.33	0.00	2.33	7	0	7			

<u>*The Spring Chinook salmon sport fishery*</u>:

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 2022 sport fishery was executed in both regions (Table 15), which could introduce bias from geographic differences across regions.

The sport fishery was executed above Bonneville Dam in Zone 6 in 2022 and samples were included in our analysis. We were able to obtain a single tally of all the kept fish from this fishery despite samples coming from regions 01 and 02; this lack of geographic stratification could lead to bias unless the sampling was completely random and representative of the entire catch (**Table 16**).

Table 15. The sample rate and stratification for genetic analysis of the kept adipose clipped adult Chinook salmon from the lower river spring sport fishery in 2022.

	Total Adult Chinook			Sample of Total Adult Chinook Kept			
	Kept	Rel.	Rel. Mortality	regionA	regionB	total	rate
Jan-Feb Total	4	3	0				
March Total	1991	316	32	105	169	274	0.14
April Total	3321	401	40	54	310	364	0.11
May Total	4306	1920	192	263	144	407	0.09
June 1-15 Total	3053	1463	146	101	194	295	0.10
Season Total	12,675	4,103	410	523	817	1340	0.11

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 2022. 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.

Table 16. The sample rate and stratification for genetic analysis of the total kept adipose clipped Chinook salmon from the spring sport fishery above Bonneville Dam in 2022.

Total Chinook			Sample of Total Chinook Kept			
Kept	Rel.	Rel. Mortality	region01	region02	total	rate
1223	485	49	12	67	79	0.06

Note: The season included openings between April 1 and Jun 15 and included the area from Bonneville Dam to the Oregon/Washington border. Both jack- and adult-sized Chinook were included in the sample.

<u>*The spring chinook salmon platform hook and line permit fishery*</u>:

Yakama Nation typically executes this fishery below Bonneville Dam. However, sampling has not occurred since 2020. 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.

<u>*The Summer Chinook salmon sport fishery*</u>:

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 2022, we obtained samples from both regions A and B (Table 17).

Table 17. The sample rate and stratification for genetic analysis of the kept adipose clipped adult Chinook salmon from the summer sport fishery in 2022.

	Total Adult Chinook			Sample of Total Adult Chinook Kept			
	Kept	Rel.	Rel. Mortality	regionA	regionB	total	rate
June 16-30	1306	951	95	10	156	166	0.13
July 1-31	1,938	1081	108	70	154	224	0.12
Season Total	3,244	2,032	203	80	310	390	0.12

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 separated fish harvested in June from those harvested in July as indicated by the outlines in the table.

<u>*The fall Non-Treaty commercial fishery:*</u>

This fishery occurred in two periods in the fall (early period = weeks 33 – 36; late period = weeks 39 – 44) 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 18). 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. All late period samples were pooled into a single stratum regardless of which region they were sampled in. We utilized the same geographic and temporal stratification of the reported catch in our analysis of the genetic sample.

Table 18. The sample rate and stratification for genetic analysis of the adult and jack Chinook salmon from fall Non-Treaty commercial fishery in 2022.

	Harvest estimate		Sample N			
Region	Week	adult+jack	AD	AI	total	rate
A	33	161	16	28	136	0.09

A	34	1328	37	55		
A	35	6666	77	80	157	0.02
A	36	16064	83	83	166	0.01
A	39	4818	20	65	128	0.02
A	40	1112	2	35		
A	41	578				
A	42	0				
B	40	126				
B	41	81	1	5		
B	42	10				
B	43	2				
B	44	2				

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 Regions A and B separately for the late fall weeks (39 – 44).

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 19). The catch estimate for this fishery below Bonneville Dam is reported by month for the adult fish and 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 2022, the sport fishery was also sampled in zone 6 from Bonneville Dam to McNary Dam (Table 20). We obtained samples of clipped and unclipped kept adults on a monthly basis and pooled this sample into a single stratum.

Table 19. 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 2022.

Catch Estimate				Sample of kept			
Month	kept Adult	Released	Release mortality(21%)	AD	AI	Total	rate
Aug	4,643	723	152	116	213	329	0.07
Sep	4,471	382	80	101	293	394	0.08
Oct	749	220	46	5	25	30	
Total	9,863	1325	278	222	531	753	0.08

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 20. 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 2022.

	Catch Estimate			Sample of kept			
Month	kept Adult	Released	Release mortality 21%	AD	AI	total	rate
August				13	4		
September				85	135		
October				10	26		
Total	9,781	1,474	310	108	165	273	0.03

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 2022 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 in 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 2022. Only the sport fishery occurred in 2022, and samples were pooled across months and treated as a single stratum (Table 21).

Table 21. The sample rate and stratification for genetic analysis of the harvested Sockeye salmon from the sport fishery in 2022.

	Catch	Sample						
Month	estimate	LBC	Osoyoos	Redfish	Wenatchee	Yakima	total	rate
June	0						0	0.00
July	1077		117	2	42		161	0.15
total	1,077	0	117	2	42	0	161	0.15

The Sockeye Treaty commercial fishery:

This 2022 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 comprised of sets of SNP markers (~200) that have greater than 10% observed heterozygosity in each of the major lineages of Chinook Salmon (Hess et al. 2020).

Application of the 254 SNP panel to the Chinook Salmon passing Bonneville Dam in 2018 revealed that the use of this expanded panel fully resolved the crashing issue with SNPPIT. This result confirmed that the source of the crashing issue was likely related to the lack of sufficient numbers of SNPs with high information content that is primarily affecting ocean-type broodstocks. Further, the higher number of SNP loci requires decreased computational time to run the parentage analyses, which is extremely helpful for the relatively short time available to process in-season samples. We have continued to use the 254 SNP panel exclusively for the 2023 run year of Chinook salmon.

Comparison of Coded-wire tags and PBT assignments

There were 831 coded-wire tags (CWTs) recovered and identified to hatchery stock and broodyear (BY) among the snouts obtained from the lower river fisheries (Table 22), and 630 of these CWTs also were PBT assigned (76%). Of the 630 fish with both CWT and PBT, there were 575 fish (91%) that appeared concordant with the PBT assignments according to both the hatchery source and the broodyear. There were 55 of the 630 fish with both CWT and PBT that were discordant for either just broodyear (N=17) or just hatchery source (N=25) or both hatchery source and broodyear (N=13). However, in some cases it may be that the CWT readings were swapped; e.g., a pair of Spring Creek National Fish Hatchery and Little White Salmon Nation Fish Hatchery fish were matched for two pairs of fish ("Discordant" rows, Table 22). Resolving these swapping errors would increase the concordance rate even higher than 91%.

Table 22. Comparison of coded-wire tags with parentage-based tags that were identified in the lower river fisheries in 2022.

	Coded-wire tag		Parentage-based tagging assignment			
Period	**Hatchery**	**BY**	**Hatchery**	**BY**	**Status**	**N**
Spring	Carson National Fish Hatchery	2018	Carson National Fish Hatchery	2018	Concordant	2
Spring	Chief Joseph Hatchery	2017	Chief Joseph Hatchery	2017	Concordant	11
Spring	Chief Joseph Hatchery	2017	Entiat National Fish Hatchery	2017	Concordant	1
Spring	Chief Joseph Hatchery	2018	Eastbank Fish Hatchery	2018	Concordant	1
Spring	Chief Joseph Hatchery	2019	Chief Joseph Hatchery	2019	Concordant	1
Spring	Clearwater Fish Hatchery	2018	Clearwater Fish Hatchery	2018	Concordant	5
Spring	Clearwater Fish Hatchery	2019	Clearwater Fish Hatchery	2019	Concordant	5
Spring	Dworshak National Fish Hatchery	2018	Dworshak National Fish Hatchery	2018	Concordant	2
Spring	Eastbank Fish Hatchery	2016	Eastbank Fish Hatchery	2016	Concordant	1
Spring	Eastbank Fish Hatchery	2017	Eastbank Fish Hatchery	2017	Concordant	14
Spring	Eastbank Fish Hatchery	2017	Wells Fish Hatchery	2017	Concordant	1
Spring	Eastbank Fish Hatchery	2018	Eastbank Fish Hatchery	2018	Concordant	21
Spring	Eastbank Fish Hatchery	2018	Entiat National Fish Hatchery	2018	Concordant	1
Spring	Entiat National Fish Hatchery	2017	Entiat National Fish Hatchery	2017	Concordant	6
Spring	Entiat National Fish Hatchery	2017	Wells Fish Hatchery	2017	Concordant	1
Spring	Entiat National Fish Hatchery	2018	Entiat National Fish Hatchery	2018	Concordant	6
Spring	Kalama Falls Hatchery	2017	Kalama Falls Hatchery	2017	Concordant	3
Spring	Kalama Falls Hatchery	2018	Kalama Falls Hatchery	2018	Concordant	1

Spring	Kalama Falls Hatchery	2019	Kalama Falls Hatchery	2019	Concordant	1
Spring	Klickitat Hatchery	2018	Klickitat Hatchery	2018	Concordant	1
Spring	Kooskia National Fish Hatchery	2018	Dworshak National Fish Hatchery	2018	Concordant	2
Spring	Leavenworth National Fish Hatchery	2017	Leavenworth National Fish Hatchery	2017	Concordant	1
Spring	Leavenworth National Fish Hatchery	2018	Leavenworth National Fish Hatchery	2018	Concordant	2
Spring	Lookingglass Fish Hatchery	2018	Lookingglass Fish Hatchery	2018	Concordant	22
Spring	Lookingglass Fish Hatchery	2019	Lookingglass Fish Hatchery	2019	Concordant	9
Spring	McCall Fish Hatchery	2018	McCall Fish Hatchery	2018	Concordant	3
Spring	McCall Fish Hatchery	2019	McCall Fish Hatchery	2019	Concordant	5
Spring	Nez Perce Tribal Fish Hatchery	2018	Dworshak National Fish Hatchery	2018	Concordant	3
Spring	Rapid River Fish Hatchery	2017	Rapid River Fish Hatchery	2017	Concordant	1
Spring	Rapid River Fish Hatchery	2018	Rapid River Fish Hatchery	2018	Concordant	8
Spring	Rapid River Fish Hatchery	2019	Rapid River Fish Hatchery	2019	Concordant	1
Spring	Round Butte Fish Hatchery	2018	Round Butte Fish Hatchery	2018	Concordant	8
Spring	Round Butte Fish Hatchery	2019	Round Butte Fish Hatchery	2019	Concordant	5
Spring	Sawtooth Hatchery	2018	Sawtooth Fish Hatchery	2018	Concordant	2
Spring	Umatilla Fish Hatchery	2018	Umatilla Fish Hatchery	2018	Concordant	2
Spring	Warm Springs National Fish Hatchery	2018	Round Butte Fish Hatchery	2018	Concordant	3
Spring	Warm Springs National Fish Hatchery	2018	Warm Springs National Fish Hatchery	2018	Concordant	8
Spring	Warm Springs National Fish Hatchery	2019	Warm Springs National Fish Hatchery	2019	Concordant	4
Spring	Wells Fish Hatchery	2017	Eastbank Fish Hatchery	2017	Concordant	2
Spring	Wells Fish Hatchery	2017	Entiat National Fish Hatchery	2017	Concordant	1
Spring	Wells Fish Hatchery	2017	Wells Fish Hatchery	2017	Concordant	7
Spring	Wells Fish Hatchery	2018	Wells Fish Hatchery	2018	Concordant	4
Spring	Winthrop National Fish Hatchery	2018	Winthrop National Fish Hatchery	2018	Concordant	1
Spring	Winthrop National Fish Hatchery	2019	Winthrop National Fish Hatchery	2019	Concordant	9
Spring	Yakima River Roza Dam	2018	Yakima River Roza Dam	2018	Concordant	7
Spring	Yakima River Roza Dam	2019	Yakima River Roza Dam	2019	Concordant	4
Summer	Chief Joseph Hatchery	2017	Chief Joseph Hatchery	2017	Concordant	21
Summer	Chief Joseph Hatchery	2018	Eastbank Fish Hatchery	2018	Concordant	1
Summer	Chief Joseph Hatchery	2019	Chief Joseph Hatchery	2019	Concordant	2
Summer	Eastbank Fish Hatchery	2016	Eastbank Fish Hatchery	2016	Concordant	2

Summer	Eastbank Fish Hatchery	2017	Eastbank Fish Hatchery	2017	Concordant	13
Summer	Eastbank Fish Hatchery	2018	Eastbank Fish Hatchery	2018	Concordant	55
Summer	Eastbank Fish Hatchery	2019	Eastbank Fish Hatchery	2019	Concordant	2
Summer	Entiat National Fish Hatchery	2017	Entiat National Fish Hatchery	2017	Concordant	2
Summer	Entiat National Fish Hatchery	2018	Entiat National Fish Hatchery	2018	Concordant	7
Summer	Lyons Ferry Fish Hatchery	2018	Lyons Ferry Fish Hatchery	2018	Concordant	1
Summer	Lyons Ferry Fish Hatchery	2019	Lyons Ferry Fish Hatchery	2019	Concordant	1
Summer	McCall Fish Hatchery	2019	McCall Fish Hatchery	2019	Concordant	1
Summer	Nez Perce Tribal Fish Hatchery	2018	Nez Perce Tribal Fish Hatchery	2018	Concordant	1
Summer	Round Butte Fish Hatchery	2019	Round Butte Fish Hatchery	2019	Concordant	3
Summer	Wells Fish Hatchery	2017	Wells Fish Hatchery	2017	Concordant	10
Summer	Wells Fish Hatchery	2018	Eastbank Fish Hatchery	2018	Concordant	5
Summer	Wells Fish Hatchery	2018	Entiat National Fish Hatchery	2018	Concordant	1
Summer	Wells Fish Hatchery	2018	Wells Fish Hatchery	2018	Concordant	5
Summer	Wells Fish Hatchery	2019	Wells Fish Hatchery	2019	Concordant	1
Fall	Bonneville Hatchery	2017	Ringold Springs State Hatchery	2017	Concordant	2
Fall	Bonneville Hatchery	2018	Umatilla Fish Hatchery	2018	Concordant	3
Fall	Bonneville Hatchery	2019	Bonneville Dam Hatchery	2019	Concordant	10
Fall	Bonneville Hatchery	2020	Bonneville Dam Hatchery	2020	Concordant	1
Fall	Kalama Falls Hatchery	2018	Kalama Falls Hatchery	2018	Concordant	1
Fall	Klickitat Fall	2017	Little White Salmon National Fish Hatchery	2017	Concordant	1
Fall	Klickitat Fall	2017	Ringold Springs State Hatchery	2017	Concordant	4
Fall	Klickitat Fall	2018	Priest Rapids Hatchery	2018	Concordant	4
Fall	Klickitat Fall	2018	Ringold Springs State Hatchery	2018	Concordant	1
Fall	Little White Salmon National Fish Hatchery	2017	Little White Salmon National Fish Hatchery	2017	Concordant	3
Fall	Little White Salmon National Fish Hatchery	2018	Little White Salmon National Fish Hatchery	2018	Concordant	1
Fall	Little White Salmon National Fish Hatchery	2019	Little White Salmon National Fish Hatchery	2019	Concordant	1
Fall	Lyons Ferry Fish Hatchery	2017	Lyons Ferry Fish Hatchery	2017	Concordant	1
Fall	Lyons Ferry Fish Hatchery	2018	Lyons Ferry Fish Hatchery	2018	Concordant	77
Fall	Lyons Ferry Fish Hatchery	2019	Lyons Ferry Fish Hatchery	2019	Concordant	37
Fall	Lyons Ferry Fish Hatchery	2020	Lyons Ferry Fish Hatchery	2020	Concordant	4
Fall	Nez Perce Tribal Fish Hatchery	2017	Nez Perce Tribal Fish Hatchery	2017	Concordant	4

Fall	Nez Perce Tribal Fish Hatchery	2018	Nez Perce Tribal Fish Hatchery	2018	Concordant	14
Fall	Priest Rapids Hatchery	2017	Priest Rapids Hatchery	2017	Concordant	4
Fall	Priest Rapids Hatchery	2018	Priest Rapids Hatchery	2018	Concordant	14
Fall	Priest Rapids Hatchery	2019	Priest Rapids Hatchery	2019	Concordant	5
Fall	Ringold Springs State Hatchery	2017	Priest Rapids Hatchery	2017	Concordant	3
Fall	Ringold Springs State Hatchery	2018	Priest Rapids Hatchery	2018	Concordant	1
Fall	Ringold Springs State Hatchery	2019	Priest Rapids Hatchery	2019	Concordant	3
Fall	Spring Creek National Fish Hatchery	2019	Spring Creek National Fish Hatchery	2019	Concordant	20
Fall	Spring Creek National Fish Hatchery	2020	Spring Creek National Fish Hatchery	2020	Concordant	7
Fall	Umatilla Fish Hatchery	2017	Little White Salmon National Fish Hatchery	2017	Concordant	1
Fall	Umatilla Fish Hatchery	2019	Ringold Springs State Hatchery	2019	Concordant	2
Fall	Umatilla Fish Hatchery	2019	Umatilla Fish Hatchery	2019	Concordant	2
Fall	Washougal Fish Hatchery	2018	Washougal Fish Hatchery	2018	Concordant	1
Spring	Eastbank Fish Hatchery	2017	Eastbank Fish Hatchery	2018	Hatchery	1
Spring	Eastbank Fish Hatchery	2018	Eastbank Fish Hatchery	2017	Hatchery	1
Spring	Eastbank Fish Hatchery	2019	Wells Fish Hatchery	2017	Hatchery	1
Spring	Wells Fish Hatchery	2017	Eastbank Fish Hatchery	2019	Hatchery	1
Spring	Wells Fish Hatchery	2017	Winthrop National Fish Hatchery	2018	Hatchery	1
Spring	Wells Fish Hatchery	2018	Entiat National Fish Hatchery	2017	Hatchery	1
Spring	Winthrop National Fish Hatchery	2018	Wells Fish Hatchery	2017	Hatchery	1
Summer	Chief Joseph Hatchery	2017	Eastbank Fish Hatchery	2018	Hatchery	1
Summer	Eastbank Fish Hatchery	2018	Chief Joseph Hatchery	2017	Hatchery	1
Summer	Wells Fish Hatchery	2018	Chief Joseph Hatchery	2017	Hatchery	1
Fall	Bonneville Hatchery	2018	Priest Rapids Hatchery	2017	Hatchery	1
Fall	Bonneville Hatchery	2020	Little White Salmon National Fish Hatchery	2019	Hatchery	1
Fall	Bonneville Hatchery	2020	Priest Rapids Hatchery	2019	Hatchery	1
Fall	Lyons Ferry Fish Hatchery	2018	Lyons Ferry Fish Hatchery	2019	Hatchery	2
Fall	Lyons Ferry Fish Hatchery	2019	Lyons Ferry Fish Hatchery	2018	Hatchery	1
Fall	Priest Rapids Hatchery	2020	Priest Rapids Hatchery	2019	Hatchery	1
Spring	Clearwater Fish Hatchery	2018	Carson National Fish Hatchery	2018	BY	1
Spring	Clearwater Fish Hatchery	2018	Dworshak National Fish Hatchery	2018	BY	5
Spring	Clearwater Fish Hatchery	2018	Winthrop National Fish Hatchery	2018	BY	1

Spring	Kooskia National Fish Hatchery	2018	Rapid River Fish Hatchery	2018	BY	1
Spring	Lewis River Hatchery	2018	Speelyai Fish Hatchery	2018	BY	1
Spring	Lookingglass Fish Hatchery	2018	Dworshak National Fish Hatchery	2018	BY	1
Spring	Lookingglass Fish Hatchery	2018	Klickitat Hatchery	2018	BY	1
Spring	Lookingglass Fish Hatchery	2018	McCall Fish Hatchery	2018	BY	1
Spring	Lyons Ferry Fish Hatchery	2018	Little White Salmon National Fish Hatchery	2018	BY	1
Spring	Rapid River Fish Hatchery	2018	Dworshak National Fish Hatchery	2018	BY	1
Spring	Round Butte Fish Hatchery	2018	South Santiam Hatchery	2018	BY	1
Spring	Warm Springs National Fish Hatchery	2018	Little White Salmon National Fish Hatchery	2018	BY	1
Spring	Willamette	2018	Dworshak National Fish Hatchery	2018	BY	1
Spring	Winthrop National Fish Hatchery	2018	Carson National Fish Hatchery	2018	BY	1
Spring	Winthrop National Fish Hatchery	2018	Methow Fish Hatchery	2018	BY	1
Spring	Winthrop National Fish Hatchery	2018	Sawtooth Fish Hatchery	2018	BY	1
Summer	Clearwater Fish Hatchery	2019	McCall Fish Hatchery	2019	BY	3
Summer	Round Butte Fish Hatchery	2019	McCall Fish Hatchery	2019	BY	1
Fall	Lyons Ferry Fish Hatchery	2018	Nez Perce Tribal Fish Hatchery	2018	BY	1
Spring	Eastbank Fish Hatchery	2017	McCall Fish Hatchery	2018	Discordant	1
Spring	Entiat National Fish Hatchery	2017	Lookingglass Fish Hatchery	2018	Discordant	1
Spring	Entiat National Fish Hatchery	2017	Round Butte Fish Hatchery	2019	Discordant	1
Spring	Pahsimeroi Fish Hatchery	2018	Eastbank Fish Hatchery	2017	Discordant	1
Spring	Rapid River Fish Hatchery	2017	McCall Fish Hatchery	2018	Discordant	1
Spring	Round Butte Fish Hatchery	2019	Rapid River Fish Hatchery	2018	Discordant	1
Spring	Yakima River Roza Dam	2016	Round Butte Fish Hatchery	2019	Discordant	1
Summer	Eastbank Fish Hatchery	2017	North Santiam Hatchery	2018	Discordant	1
Summer	Wells Fish Hatchery	2018	McCall Fish Hatchery	2019	Discordant	1
Fall	Little White Salmon National Fish Hatchery	2018	Spring Creek National Fish Hatchery	2019	Discordant	1
Fall	Lyons Ferry Fish Hatchery	2018	Little White Salmon National Fish Hatchery	2017	Discordant	1
Fall	Lyons Ferry Fish Hatchery	2018	Ringold Springs State Hatchery	2017	Discordant	1
Fall	Spring Creek National Fish Hatchery	2019	Little White Salmon National Fish Hatchery	2018	Discordant	1
				Total	100.00%	831
				Concordant	69.19%	575
				Hatchery_Concordant	2.05%	17

BY_Concordant	3.01%	25
Discordant	1.56%	13
Failed	8.90%	74
PBT_Unassigned	15.28%	127
PBT only		2260

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”.

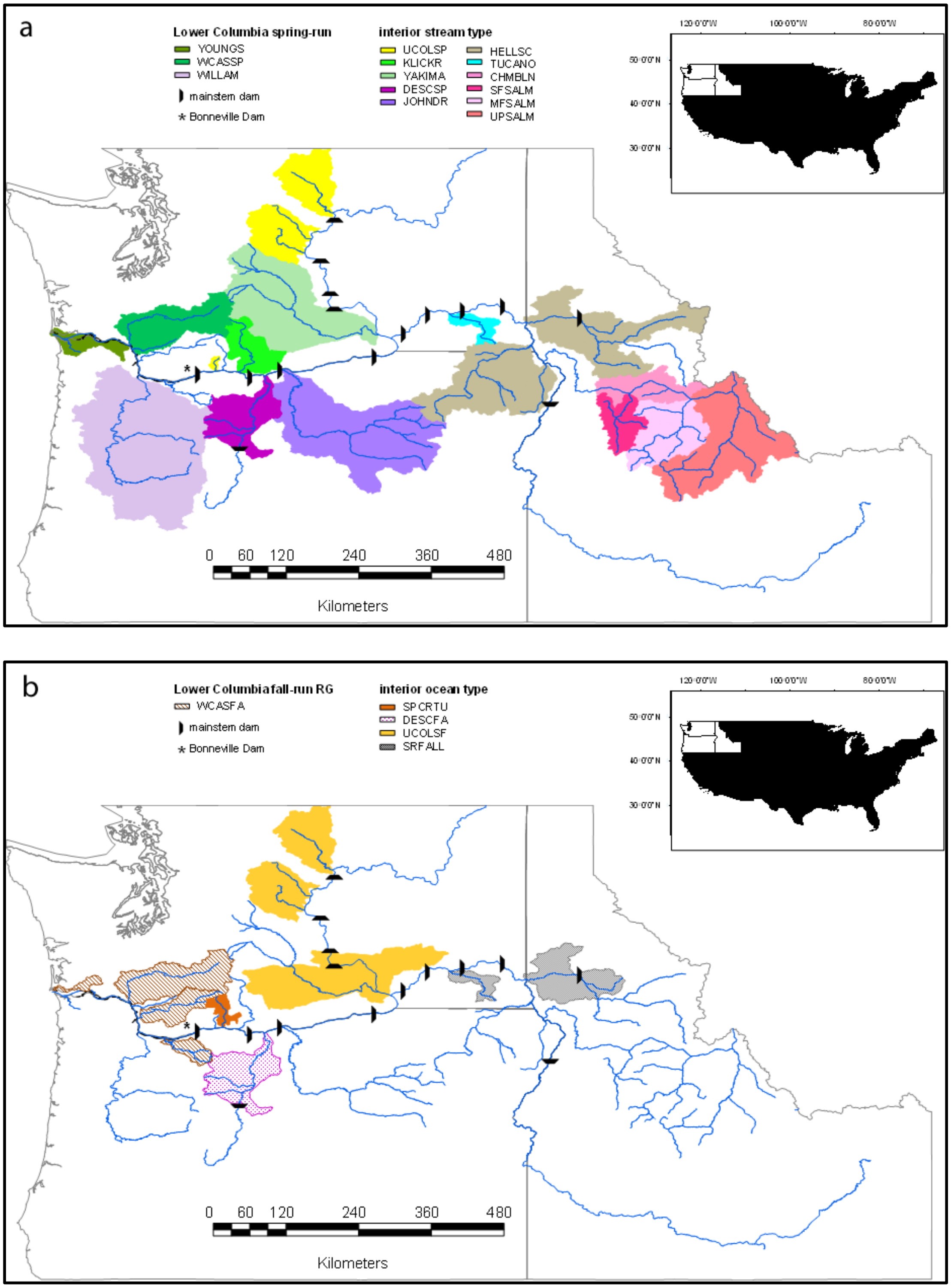


Figure 18. Map of Chinook salmon GSI reporting groups for a) Lower Columbia (LC) and interior stream type (ST) lineage, and b) interior ocean type (OT) lineage.

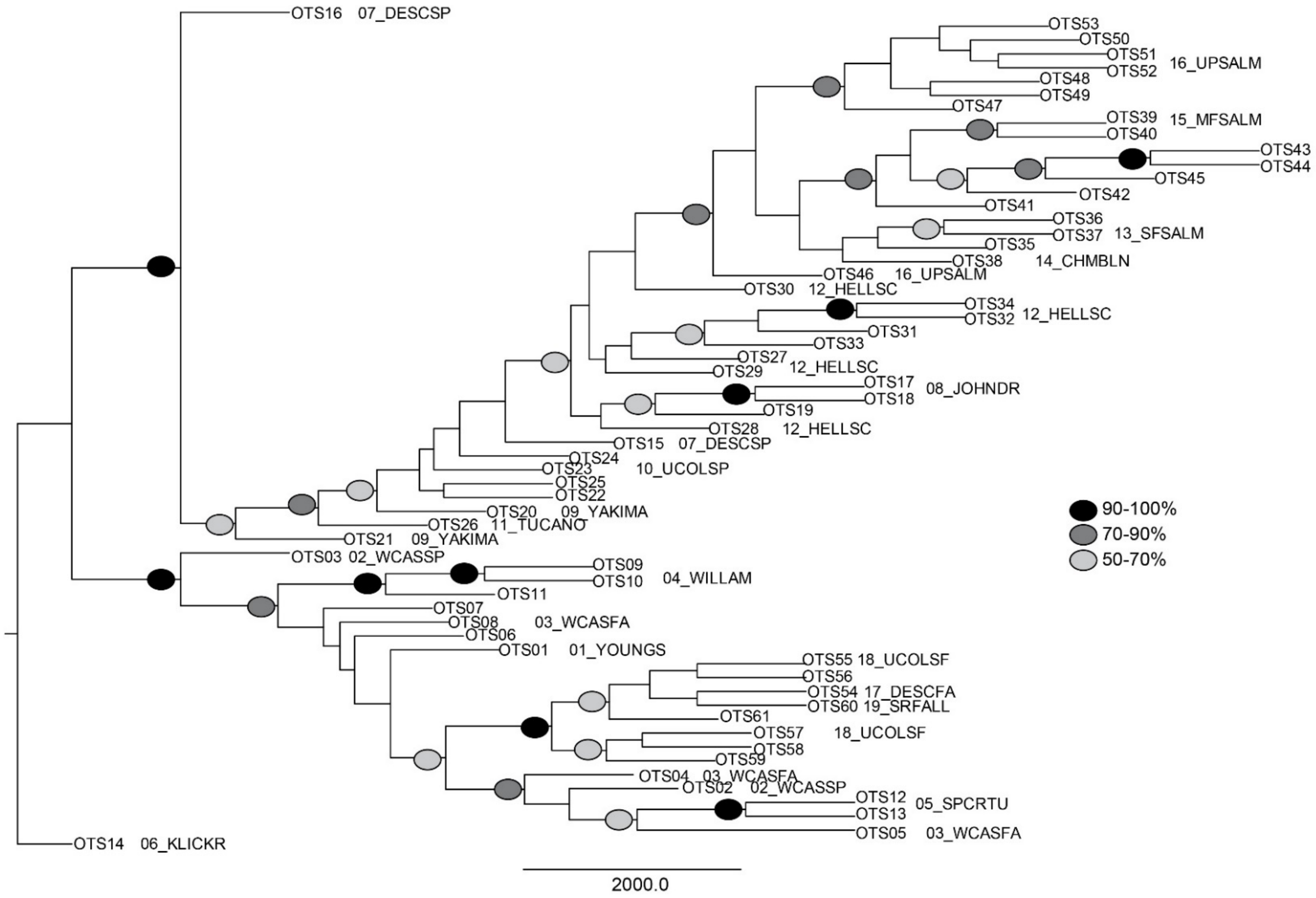


Figure 19. Neighbor-joining tree of Chinook salmon baseline populations using Nei's 1972 genetic distance of 179 SNP loci.

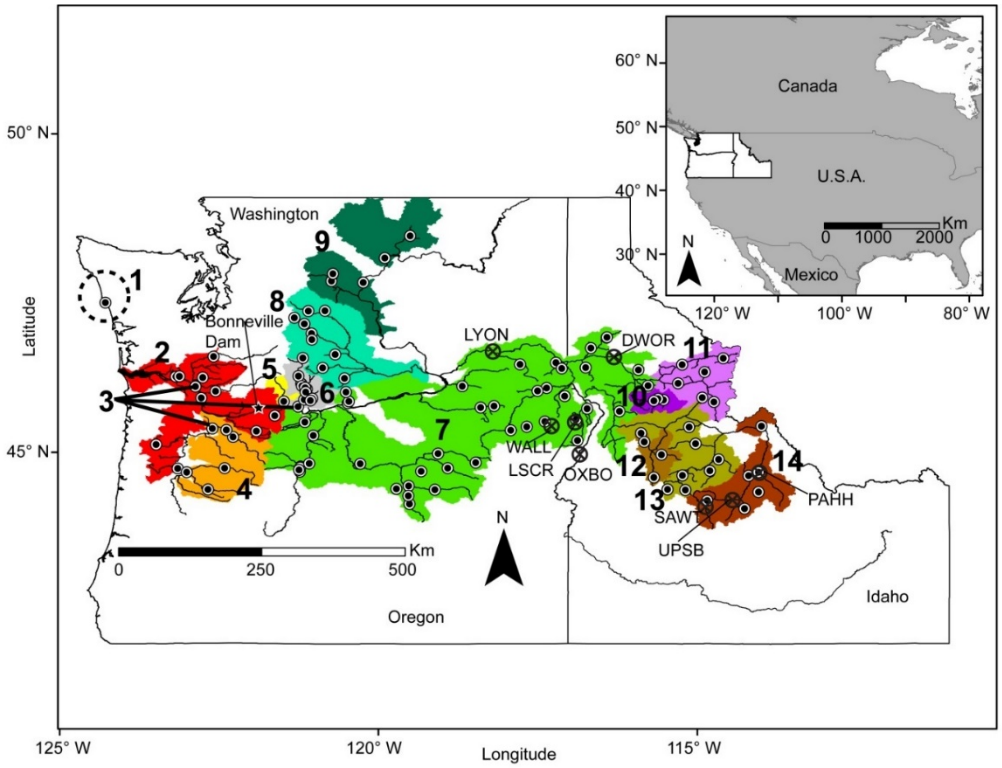


Figure 20. Geographic distribution of collections represented in the Columbia River steelhead GSI and PBT genetic baselines.

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 20). In Figure 20, 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 20) categorized into reporting groups. The PBT baseline is indicated as 8 stocks (crossed circles, Figure 20) corresponding to the following sites where fish are collected and spawned for broodstock: Lyons Ferry Hatchery (LYON), Wallowa (WALL), Little Sheep Creek (LSCR), Oxbow Hatchery (OXBO), Dworshak Hatchery (DWOR), upper Salmon River B-run (UPSB), Sawtooth Hatchery (SAWT), and Pahsimeroi Hatchery (PAHH). Bonneville Dam (star, Figure 20) 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 6), 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 2022 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 (74%, Table 23).

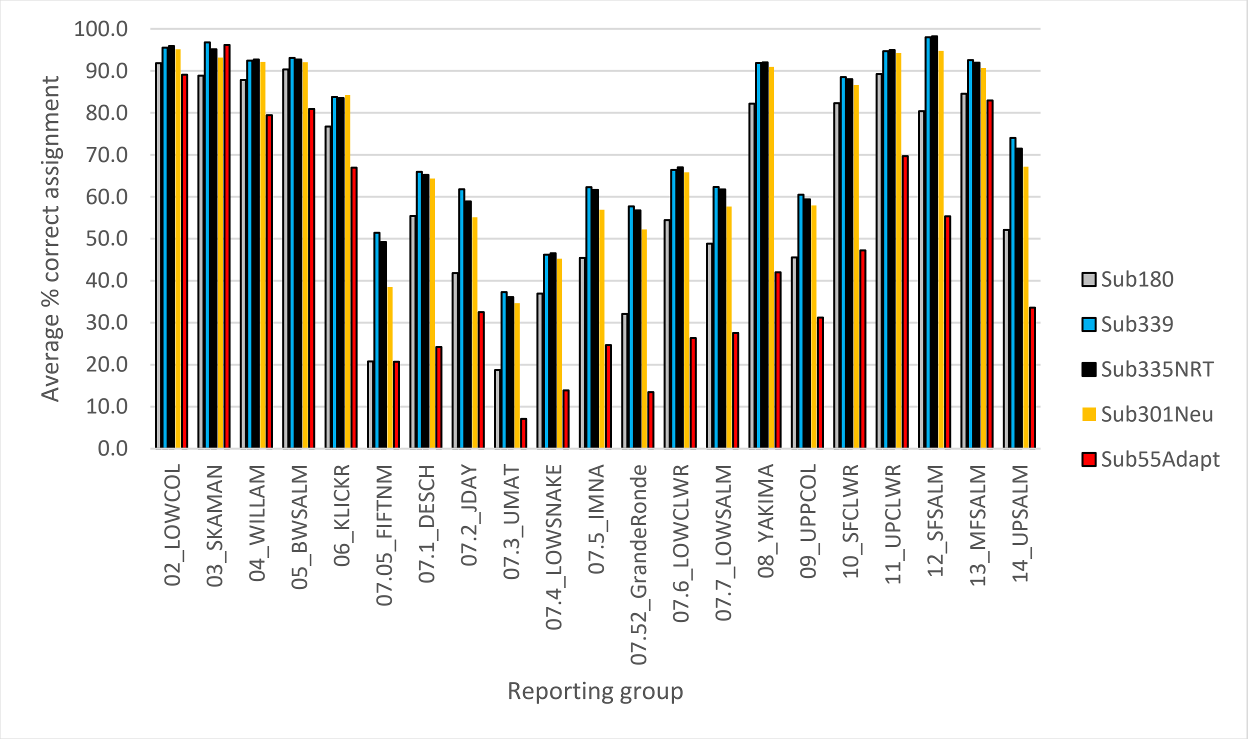


Figure 21. Proportion of steelhead in leave-one-out tests that assigned correctly for each reporting group by lineage using the following subsets of SNPs: 180 SNPs from baseline v3.3 ("Sub180"), 339 SNPs that include putatively neutral and adaptive loci ("Sub339"), 335 SNPs that exclude the run timing candidate SNPs ("Sub335NRT"), 301 SNPs that were putatively neutral ("Sub301Neu"), and 55 SNPs that were putatively adaptive ("Sub55Adapt").

Table 23. Comparison of PBT expected reporting groups versus the observed reporting groups using 177 SNPs (baseline 3.3) based on the assignments from the Bonneville 2022 mixture.

	Observed GSI								
PBT Expected GSI	**03_SKAMAN**	**07_MGILCS**	**09_UPPCOL**	**10_SFCLWR**	**11_UPCLWR**	**14_UPSALM**	**Total**	**%Correct**	
03_SKAMAN	17						17	100.0%	
07_MGILCS		132		1		7	140	94.3%	
09_UPPCOL		23	4	1		3	31	12.9%	
10_SFCLWR				265	3		268	98.9%	
14_UPSALM		31		*29	*1	88	149	59.1%	†73.9%
Grand Total	17	186	4	296	4	98	605		

Note: *There were novel release groups included in this year's analysis from the hatcheries that are expected to assign to UPSALM, but are derived from broodstock that have ancestry with the SFCLWR and UPCLWR groups. This release group is "OmyUSAL_su19" and was spawned at the Pahsimeroi Hatchery. Removing these 30 fish recovers the "% Correct" assignment of this group to 73.9% which is closer to expected assignment rates.

Steelhead 335 SNP panel for PBT applications

Despite having limited utility for GSI applications on a Columbia River Basin wide scale, the expanded set of SNP markers available for steelhead analysis can be extremely useful for increasing the power and accuracy of PBT. We examined a dataset of steelhead passing Bonneville Dam in 2020 and compared assignments based on the original panel of 92 SNPs to assignments based on the new expanded panel of 335 SNPs (Table 24). There were a total of 800 PBT assignments that were perfectly concordant between 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 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 we use to accept a PBT assignment, but the 335 SNP panel LOD score was much higher. The False Discovery Rate was also much lower for these 800 assignments based on the 335 SNP panel (FDR = 6.6X10-6) compared to the 92 SNP panel (FDR = 0.01). We set 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 for failing to meet these thresholds using the smaller panel. In fact, there were 20 fish that were only assigned using the 335 SNP panel and would have escaped detection with the 92 SNP panel. Further, there were 32 assignments that were concordant to the PBT broodstock, however, either the mother or father or both parents were discordant across the assignments generated by these two panels. The 335 PBT panel will be more likely to avoid errors that occur when hatchery broodstock have a high level of relatedness which is the case with steelhead hatcheries. In conclusion, we feel encouraged by these results and have adopted the larger number of SNP markers for PBT applications in steelhead.

Table 24. Comparison of PBT assignments using the new panel of 335 SNPs versus the 92 SNP panel for steelhead passing Bonneville Dam in 2020.

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

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

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

This is the fourth year we have been able to utilize candidate parents that were genotyped from tissues collected from carcass spawning surveys and directly from the fish translocated from Priest Rapids Dam and released into the Yakima River (Table 25). A combination of parent-pair assignments (trio assignment) and single parent assignments were performed to obtain as large of a sample of offspring as possible. Tag rates assumed the ability to perform single parent assignments. We had funding to genotype some of our older candidate parents from the translocation year 2012 and updated the PBT baseline with these older samples as well as new samples from 2020 and 2021. The tag rates increased as a result of the additional genotypes and filtering step changes and are noted in green in Table 25. Specifically, the largest "Change" in tag rates occurred in Spawn Year 2012 in which we now have 18.5% of the candidate parents genotyped and have at least a chance to detect offspring that returned from this first large (10,000+ adults translocated in 2012) translocation event in the Yakima River. This expansion of the parent baseline may be useful when we re-analyze previous years.

Table 25. The numbers of candidate parents genotyped relative to the number of returning and translocated adult sockeye to the Yakima River each year.

						Genotypes			Tag rate		Change
Year	Outplants	Prosser	Roza	O+P	O+R	363	88	Max YR	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%

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

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

Parentage based tagging assignments of Chinook salmon in harvest mixtures

A summary of the Chinook harvest samples that were genotyped (derived from Table 11) is presented in Table 26. Of the 4,750 harvested Chinook analyzed, there were 2,857 hatchery-origin individuals that could be confidently PBT assigned to 126 hatchery broodstock sources (i.e., 18 Lower Columbia, 3 Willamette, 36 Snake River, and 69 Columbia River hatchery broodstocks) spawned in 2016-2020. The majority of PBT assigned individuals (N=1629) were from the 2018 brood year (i.e., 4-years-old).

Table 26. Summary of the Chinook salmon harvest samples by fishery, region, and fin clip in 2022.

			Period			Analysis					
Fishery	**Region**	**AdClip**	**Spring**	**Summer**	**Fall**	**GSI**	**PBT**	**duplicate**	**failed**	**Total**	**%PBT**
Bon22	BONAFF	AD	938	152	582	179	1484		9	1672	89.2%
		AI	476	90	1014	939	627	2	12	1580	40.0%
Sport	A	AD	649			58	578	13	71	720	90.9%
	B	AD	874			235	632	7	99	973	72.9%
	01 (Zone 6)	AD	12			2	10		1	13	83.3%
	02 (Zone 6)	AD	67			12	55		10	77	82.1%
Test	B	AD	325			79	244	2	28	353	75.5%
		AI	70			49	21		1	71	30.0%
Sport	A	AD		82		25	57		6	88	69.5%
	B	AD		330		93	237		22	352	71.8%
Sport	A	AD			126	24	102		10	136	81.0%
		AI			433	304	126	3	40	473	29.3%
	B	AD			126	26	99	1	17	143	79.2%
		AI			197	136	59	2	14	211	30.3%
	01 (Zone 6)	AD			60	4	56		5	65	93.3%
		AI			100	55	44	1	4	104	44.4%
	02 (Zone 6)	AD			58	9	49		3	61	84.5%
		AI			97	57	40		6	103	41.2%
Commercial	A	AD			411	65	346		22	433	84.2%
		AI			348	248	98	2	20	368	28.3%
	B	AD			1		1			1	100.0%
		AI			5	4	1			5	20.0%
Grand Total			3411	654	3558	2603	4966	33	400	8002	65.6%

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 82% (range = 70% – 100%, Table 26). The fishery(s) with the minimum and maximum assigned adipose-clipped Chinook salmon was the Non-Treaty summer sport fishery in region A and the Non-Treaty Fall Commercial fishery in region B, respectively. Among the adipose-intact fish, the average assignment via PBT was expectedly lower (average = 32%, range = 20% – 44%; Table 26). Among the fisheries with adipose-intact fish, the minimum and maximum PBT-assigned Chinook salmon was observed in the Non-Treaty Fall Commercial fishery in (region B) and the Fall Sport fishery in Zone 6 (region 02), 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 2 weeks the peak in CPUE appears to correspond with a peak in Bonneville weekly counts (Figure 23). Further, the correlation of CPUE for upriver stocks can sometimes 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 U.S. v OR managers.

Here we show how the CPUE in the test fishery can be further resolved into finer stock units using genetic analysis and the reporting group level for the fish that had previously been only visually identified into two coarse level stocks, lower river and upriver (**Table 27**). The CPUE can be even resolved into finer units of hatchery broodstocks which could allow a high resolution of abundance prediction if this test fishery data were used in-season (**Figure 24**).

Table 27. Summary of the stock composition at the reporting group level of the VSI-identified lower river and upriver spring Chinook salmon in the test fishery of 2022 in units of catch-per-unit-effort (CPUE, # of fish per # of drifts).

		Lower (VSI)			Upriver (VSI)			
	GenStock	H	HNC	W	H	HNC	W	Total
Lower	01_YOUNGS							0.0000
	02_WCASSP	2.1397			1.3720			3.5117
	03_WCASFA							0.0000
	04_WILLAM	8.0320		0.7339	0.7185		0.1971	9.6816

	Subtotal Lower GenStock	10.1717	0.0000	0.7339	2.0905	0.0000	0.1971	13.1932
Upriver	05_SPCRTU							0.0000
	06_KLICKR	0.0000			0.4651			0.4651
	07_DESCSP	0.0000			0.7613			0.7613
	08_JOHNDR							0.0000
	09_YAKIMA	0.1605		0.0909	0.6830		0.2990	1.2334
	10_UCOLSP	0.2537	0.0000	0.0000	3.4216	0.4199	1.2001	5.2953
	11_TUCANO							0.0000
	12_HELLSC	0.8713	0.0000	0.0877	11.1729	0.8569	1.2528	14.2416
	13_SFSALM	0.0000	0.0000	0.0000	1.2408	0.1873	0.2955	1.7236
	14_CHMBLN							0.0000
	15_MFSALM			0.0000			0.2278	0.2278
	16_UPSALM	0.0000	0.0000	0.0000	1.1406	0.0832	0.2037	1.4275
	17_DESCFA							0.0000
	18_UCOLSF	0.9381			0.0000			0.9381
	19_SRFALL							0.0000
	20_BONPOOLSP	0.5859	0.0000		3.9764	0.1213		4.6836
	21_UMATILLASP	0.0000	0.0000		0.1543	0.1149		0.2692
	Subtotal Upriver GenStock	2.8094	0.0000	0.1787	23.0160	1.7835	3.4788	31.2665

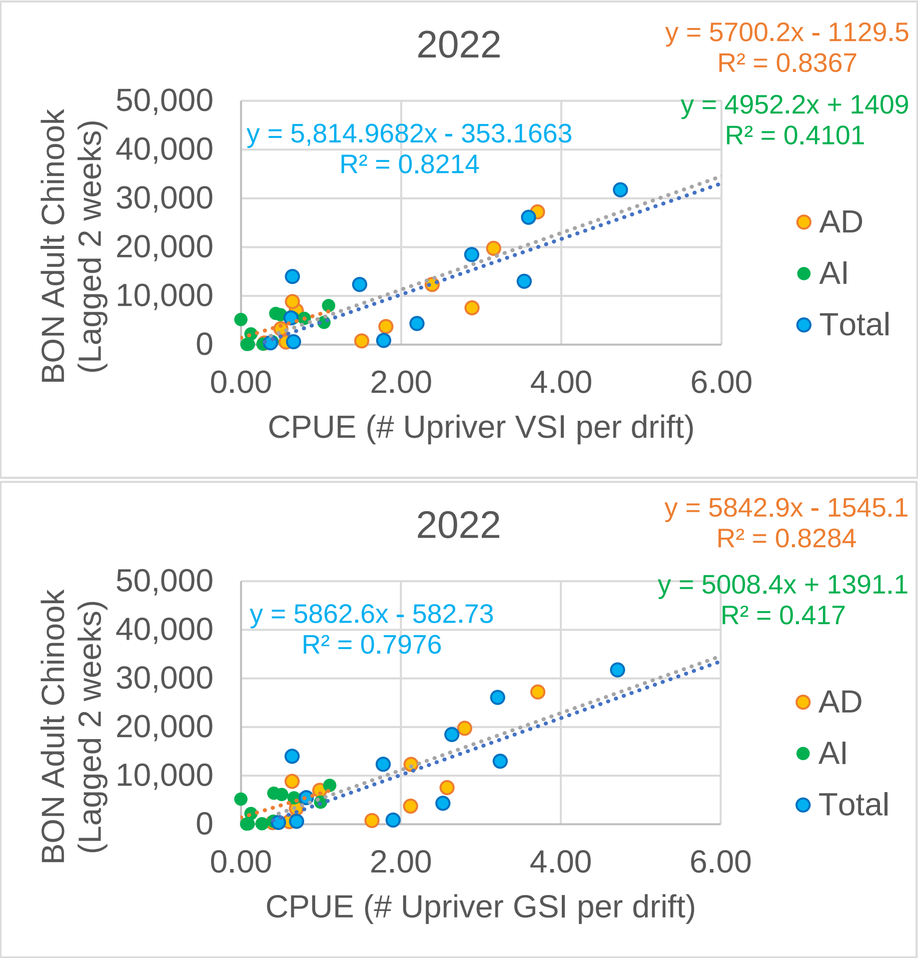


Figure 22. The relationship between the test fishery upriver Chinook Salmon CPUE and weekly fish counts at Bonneville Dam in 2022 with 2 week lag using VSI (top) and GSI (bottom) data.

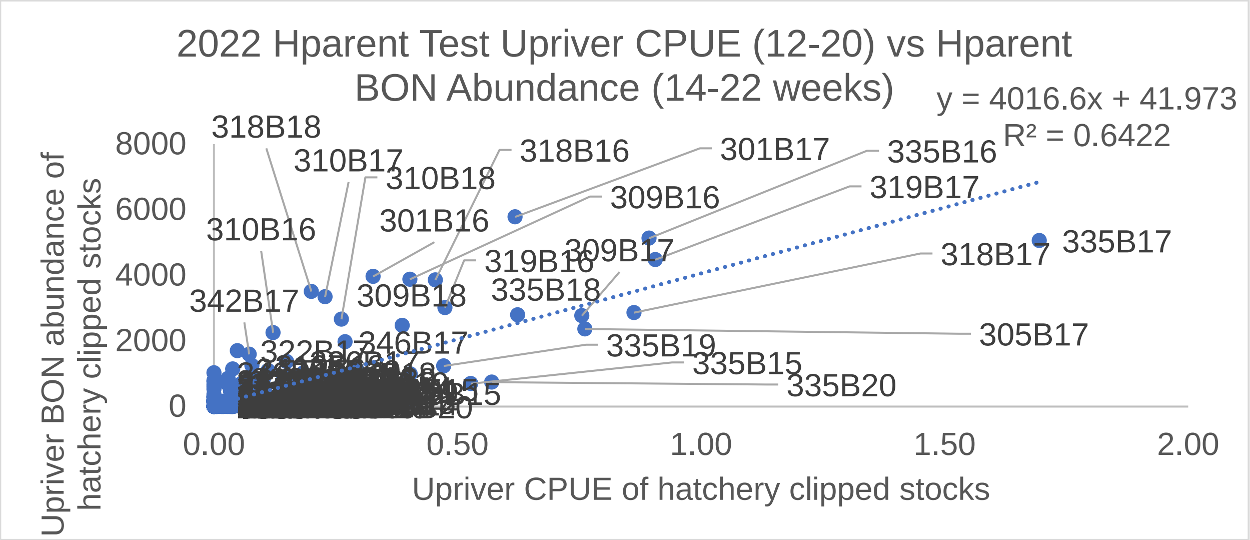


Figure 23. Correlation of the test fishery CPUE with the estimated abundance passing Bonneville Dam of hatchery clipped broodstocks identified by PBT analysis in 2022

The Non-Treaty sport fishery in the Chinook Salmon Spring Management Period of 2022

We reported spring sport fishery results in the lower river below Bonneville Dam for reporting group level stock composition (Table 28) and the hatchery broodstock composition (Table 29) of the kept fish (clipped hatchery-origin fish). We also reported the spring sport fishery executed in zone 6 above Bonneville Dam in units of reporting groups (**Table 30**) and broodstock units (**Table 31**) for the kept fish.

Table 28. Summary of the stock composition at the reporting group level of the kept spring Chinook salmon in the Non-Treaty sport fishery of 2022 in units of reported catch.

		Hatchery origin-Clipped	
Run type	**Reporting Group Code**	**Estimated abundance**	
		Mean	**95% CI**
Spring	01_YOUNGS		
Spring	02_WCASSP	891	755 – 967
Fall	03_WCASFA	6	0 – 24
Spring	04_WILLAM	1,594	1365 – 1763
Fall	05_SPCRTU		
Spring	06_KLICKR	99	54 – 122
Spring	07_DESCSP	539	466 – 779
Spring	08_JOHNDR		
Spring	09_YAKIMA	205	116 – 233
Spring	10_UCOLSP	1,040	920 – 1100
Spring	11_TUCANO	27	10 – 48
Spring/Summer	12_HELLSC	3,593	3372 – 3862
Spring/Summer	13_SFSALM	982	869 – 1139
Spring/Summer	14_CHMBLN		
Spring/Summer	15_MFSALM		
Spring/Summer	16_UPSALM	529	451 – 610
Fall	17_DESCFA		
Summer/Fall	18_UCOLSF	2,001	1771 – 2181
Fall	19_SRFALL		
Spring	20_BONPOOLSP	1,072	918 – 1238
Spring	21_UMATILLASP	96	55 – 137
Fall	22_BONPOOLFA		
Fall	23_UMATILLAFA		
	Total	**12,675**	

Table 29. Summary of the stock composition at the broodstock level of the kept adult spring Chinook salmon in the Non-Treaty sport fishery of 2022 in units of reported catch.

Spring Sport Fishery 2022				**Kept Adult Chinook AD**			
Expected Run Time	**Hatchery**	**Broodstock**	**Broodyear**	**MLE**	**95% CI**	**Percent**	**GSI RepGrp**
01Spring	Cowlitz Salmon Hatchery	OtsCOWL_seg_sp17	2017	62	25 – 105	0.5%	02_WCASSP
01Spring	Cowlitz Salmon Hatchery	OtsCOWL_seg_sp18	2018	103	49 – 161	0.8%	02_WCASSP
01Spring	Kalama Falls Hatchery	OtsKALA_seg_sp17	2017	147	86 – 212	1.2%	02_WCASSP
01Spring	Kalama Falls Hatchery	OtsKALA_seg_sp18	2018	72	18 – 143	0.6%	02_WCASSP
01Spring	Kalama Falls Hatchery	OtsKALA_seg_sp19	2019	13	0 – 38	0.1%	02_WCASSP
01Spring	Parkdale Fish Facility	OtsPARK_seg_sp18	2018	307	211 – 410	2.4%	02_WCASSP
01Spring	Speelyai Fish Hatchery	OtsSPEE_seg_sp17	2017	26	0 – 51	0.2%	02_WCASSP
01Spring	Speelyai Fish Hatchery	OtsSPEE_seg_sp18	2018	149	88 – 217	1.2%	02_WCASSP
01Spring	North Santiam Hatchery	OtsNSAN_seg_sp18	2018	206	119 – 299	1.6%	04_WILLAM
01Spring	South Santiam Hatchery	OtsSSAN_seg_sp18	2018	360	232 – 493	2.8%	04_WILLAM
01Spring	South Santiam Hatchery	OtsSSAN_seg_sp19	2019	15	0 – 44	0.1%	04_WILLAM
01Spring	Klickitat Hatchery	OtsKLIC_seg_sp18	2018	99	45 – 154	0.8%	06_KLICKR
01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp18	2018	305	219 – 409	2.4%	07_DESCSP
01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp19	2019	70	23 – 118	0.6%	07_DESCSP
01Spring	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp18	2018	154	89 – 234	1.2%	07_DESCSP
01Spring	Yakima River Roza Dam	OtsYRRD_int_sp18	2018	140	78 – 206	1.1%	09_YAKIMA
01Spring	Yakima River Roza Dam	OtsYRRD_int_sp19	2019	11	0 – 32	0.1%	09_YAKIMA
01Spring	Yakima River Roza Dam	OtsYRRD_seg_sp18	2018	49	18 – 87	0.4%	09_YAKIMA
01Spring	Chief Joseph Hatchery	OtsCHJO_seg_sp18	2018	16	0 – 48	0.1%	10_UCOLSP
01Spring	Eastbank Fish Hatchery	OtsEAST_seg_sp18	2018	130	76 – 195	1.0%	10_UCOLSP
01Spring	Eastbank Fish Hatchery	OtsEAST_seg_sp19	2019	24	0 – 61	0.2%	10_UCOLSP
01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp17	2017	21	0 – 53	0.2%	10_UCOLSP
01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp18	2018	470	331 – 606	3.7%	10_UCOLSP
01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp19	2019	11	0 – 33	0.1%	10_UCOLSP

01Spring	Methow Fish Hatchery	OtsMETH_seg_sp18	2018	26	0 – 61	0.2%	10_UCOLSP
01Spring	Winthrop National Fish Hatchery	OtsWINT_seg_sp18	2018	89	39 – 146	0.7%	10_UCOLSP
01Spring	Winthrop National Fish Hatchery	OtsWINT_seg_sp19	2019	22	0 – 44	0.2%	10_UCOLSP
01Spring	Little White Salmon National Fish Hatchery	OtsTOUC_seg_sp18	2018	27	0 – 54	0.2%	11_TUCANO
01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp18	2018	254	175 – 329	2.0%	12_HELLSC
01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp19	2019	22	0 – 55	0.2%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp17	2017	7	0 – 22	0.1%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp18	2018	441	334 – 553	3.5%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp19	2019	11	0 – 32	0.1%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsKOOS_seg_sp18	2018	496	392 – 613	3.9%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsLOOK_seg_sp18	2018	276	194 – 366	2.2%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsLOOK_seg_sp19	2019	11	0 – 34	0.1%	12_HELLSC
01Spring	Clearwater Fish Hatchery	OtsPOWP_seg_sp18	2018	86	43 – 140	0.7%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp17	2017	51	18 – 88	0.4%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp18	2018	1,748	1549 – 1943	13.8%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp19	2019	34	11 – 69	0.3%	12_HELLSC
01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp17	2017	7	0 – 22	0.1%	20_BONPOOLSP
01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp18	2018	529	427 – 645	4.2%	20_BONPOOLSP
01Spring	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp17	2017	16	0 – 31	0.1%	20_BONPOOLSP
01Spring	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp18	2018	519	414 – 628	4.1%	20_BONPOOLSP
01Spring	Umatilla Fish Hatchery	OtsUMAT_seg_sp17	2017	7	0 – 22	0.1%	21_UMATILLASP
01Spring	Umatilla Fish Hatchery	OtsUMAT_seg_sp18	2018	88	42 – 136	0.7%	21_UMATILLASP
02Spring/Summer	Lookingglass Fish Hatchery	OtsIMNW_seg_ss18	2018	144	79 – 210	1.1%	12_HELLSC
02Spring/Summer	Lookingglass Fish Hatchery	OtsIMNW_seg_ss19	2019	11	0 – 33	0.1%	12_HELLSC
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss17	2017	44	11 – 88	0.3%	13_SFSALM
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss18	2018	890	749 – 1042	7.0%	13_SFSALM
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss19	2019	33	0 – 66	0.3%	13_SFSALM
02Spring/Summer	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss18	2018	195	119 – 271	1.5%	16_UPSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss17	2017	11	0 – 32	0.1%	16_UPSALM

02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss18	2018	313	217 – 411	2.5%	16_UPSALM
03Summer	Chief Joseph Hatchery	OtsCHJO_int_su17	2017	212	127 – 297	1.7%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su17	2017	82	35 – 128	0.6%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su16	2016	21	0 – 54	0.2%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su17	2017	439	330 – 551	3.5%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su18	2018	321	226 – 417	2.5%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su17	2017	379	266 – 479	3.0%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su18	2018	251	154 – 349	2.0%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su17	2017	190	118 – 272	1.5%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su18	2018	90	38 – 142	0.7%	18_UCOLSF
#N/A	#N/A	Unassigned	#N/A	1,321	1068 – 1583	10.4%	#N/A
		TOTAL		12,675		100.0%	

Table 30. Summary of the stock composition at the reporting group level of the kept spring Chinook salmon in the Zone 6 Non-Treaty sport fishery of 2022 in units of reported catch.

Run type	Reporting Group Code	Hatchery origin-Clipped	
		Estimated abundance	
		Mean	**95% CI**
Spring	01_YOUNGS		
Spring	02_WCASSP	11	0 – 47
Fall	03_WCASFA		
Spring	04_WILLAM		
Fall	05_SPCRTU		
Spring	06_KLICKR	16	0 – 56
Spring	07_DESCSP	33	0 – 92
Spring	08_JOHNDR		
Spring	09_YAKIMA	16	0 – 63
Spring	10_UCOLSP	300	147 – 465

Spring	11_TUCANO		
Spring/Summer	12_HELLSC	626	460 – 801
Spring/Summer	13_SFSALM	32	0 – 87
Spring/Summer	14_CHMBLN		
Spring/Summer	15_MFSALM		
Spring/Summer	16_UPSALM	47	0 – 117
Fall	17_DESCFA		
Summer/Fall	18_UCOLSF	32	0 – 102
Fall	19_SRFALL		
Spring	20_BONPOOLSP	32	0 – 93
Spring	21_UMATILLASP	78	16 – 156
Fall	22_BONPOOLFA		
Fall	23_UMATILLAFA		
	Total	**1,223**	

Table 31. Summary of the stock composition at the broodstock level of the kept adult spring Chinook salmon in the Zone 6 Non-Treaty sport fishery of 2022 in units of reported catch

Spring Zone 6 Sport Fishery 2022				**Kept Adult Chinook AD**			
Expected Run Time	**Hatchery**	**Broodstock**	**Broodyear**	**MLE**	**95% CI**	**Percent**	**GSI RepGrp**
01Spring	Klickitat Hatchery	OtsKLIC_seg_sp18	2018	16	0 – 48	1.3%	06_KLICKR
01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp18	2018	16	0 – 48	1.3%	07_DESCSP
01Spring	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp18	2018	17	0 – 52	1.4%	07_DESCSP
01Spring	Yakima River Roza Dam	OtsYRRD_int_sp18	2018	16	0 – 47	1.3%	09_YAKIMA
01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp17	2017	18	0 – 54	1.5%	10_UCOLSP
01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp18	2018	169	56 – 281	13.8%	10_UCOLSP
01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp19	2019	31	0 – 63	2.5%	10_UCOLSP
01Spring	Winthrop National Fish Hatchery	OtsWINT_seg_sp19	2019	16	0 – 47	1.3%	10_UCOLSP
01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp18	2018	46	0 – 93	3.8%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp18	2018	147	82 – 228	12.0%	12_HELLSC

01Spring	Dworshak National Fish Hatchery	OtsKOOS_seg_sp18	2018	49	16 – 99	4.0%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsKOOS_seg_sp19	2019	17	0 – 50	1.4%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsLOOK_seg_sp18	2018	100	50 – 167	8.2%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp18	2018	245	158 – 351	20.1%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp19	2019	16	0 – 49	1.3%	12_HELLSC
01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp18	2018	15	0 – 46	1.3%	20_BONPOOLSP
01Spring	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp18	2018	16	0 – 49	1.3%	20_BONPOOLSP
01Spring	Umatilla Fish Hatchery	OtsUMAT_seg_sp18	2018	62	16 – 109	5.1%	21_UMATILLASP
01Spring	Umatilla Fish Hatchery	OtsUMAT_seg_sp19	2019	15	0 – 46	1.3%	21_UMATILLASP
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss17	2017	16	0 – 48	1.3%	13_SFSALM
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss18	2018	16	0 – 47	1.3%	13_SFSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss18	2018	31	0 – 77	2.5%	16_UPSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss19	2019	16	0 – 48	1.3%	16_UPSALM
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su17	2017	16	0 – 48	1.3%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su18	2018	16	0 – 47	1.3%	18_UCOLSF
#N/A	#N/A	Unassigned	#N/A	84	0 – 197	6.8%	#N/A
		TOTAL		1,223		100.0%	

The Non-Treaty sport fishery in the Chinook Salmon Summer Management Period of 2022

In 2022, there was a summer Non-Treaty sport fishery that was executed but no summer Non-Treaty commercial fishery. We reported summer sport fishery results for reporting group level stock composition (Table 32) and the hatchery broodstock composition (Table 33) of the kept fish (clipped hatchery-origin fish).

Table 32. Summary of the stock composition at the reporting group level of the kept summer Chinook salmon in the Non-Treaty sport fishery of 2022 in units of reported catch.

		Hatchery origin-Clipped	
Run type	**Reporting Group Code**	**Estimated abundance**	
		Mean	**95% CI**
Spring	01_YOUNGS		
Spring	02_WCASSP	25	16 – 48
Fall	03_WCASFA	40	10 – 60
Spring	04_WILLAM	766	666 – 854
Fall	05_SPCRTU		
Spring	06_KLICKR	8	0 – 24
Spring	07_DESCSP	35	27 – 62
Spring	08_JOHNDR		
Spring	09_YAKIMA	8	0 – 24
Spring	10_UCOLSP	28	10 – 64
Spring	11_TUCANO		
Spring/Summer	12_HELLSC	8	0 – 15
Spring/Summer	13_SFSALM	167	116 – 201
Spring/Summer	14_CHMBLN		
Spring/Summer	15_MFSALM		
Spring/Summer	16_UPSALM	49	16 – 73
Fall	17_DESCFA		
Summer/Fall	18_UCOLSF	2,077	1954 – 2266

Fall	19_SRFALL	33	12 – 60
Spring	20_BONPOOLSP		
Spring	21_UMATILLASP		
Fall	22_BONPOOLFA		
Fall	23_UMATILLAFA		
	Total	**3,244**	

Table 33. Summary of the stock composition at the broodstock level of the kept adult summer Chinook salmon in the Non-Treaty sport fishery of 2022 in units of reported catch.

Summer Sport Fishery 2022				**Kept Adult Chinook AD**			
Expected Run Time	**Hatchery**	**Broodstock**	**Broodyear**	**MLE**	**95% CI**	**Percent**	**GSI RepGrp**
01Spring	Kalama Falls Hatchery	OtsKALA_seg_sp17	2017	8	0 – 24	0.2%	02_WCASSP
01Spring	Parkdale Fish Facility	OtsPARK_seg_sp19	2019	8	0 – 24	0.2%	02_WCASSP
01Spring	North Santiam Hatchery	OtsNSAN_seg_sp18	2018	164	88 – 244	5.1%	04_WILLAM
01Spring	South Santiam Hatchery	OtsSSAN_seg_sp18	2018	76	29 – 137	2.4%	04_WILLAM
01Spring	Klickitat Hatchery	OtsKLIC_seg_sp18	2018	8	0 – 24	0.3%	06_KLICKR
01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp18	2018	9	0 – 27	0.3%	07_DESCSP
01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp19	2019	26	9 – 52	0.8%	07_DESCSP
01Spring	Yakima River Roza Dam	OtsYRRD_int_sp18	2018	8	0 – 24	0.2%	09_YAKIMA
01Spring	Eastbank Fish Hatchery	OtsEAST_seg_sp19	2019	28	0 – 57	0.9%	10_UCOLSP
01Spring	Clearwater Fish Hatchery	OtsPOWP_seg_sp18	2018	8	0 – 24	0.2%	12_HELLSC
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss18	2018	66	32 – 107	2.0%	13_SFSALM
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss19	2019	101	58 – 151	3.1%	13_SFSALM
02Spring/Summer	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss18	2018	9	0 – 26	0.3%	16_UPSALM
02Spring/Summer	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss19	2019	16	0 – 39	0.5%	16_UPSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss19	2019	24	8 – 49	0.8%	16_UPSALM
03Summer	Chief Joseph Hatchery	OtsCHJO_int_su16	2016	9	0 – 26	0.3%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCHJO_int_su17	2017	255	176 – 341	7.9%	18_UCOLSF

03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su16	2016	9	0 – 26	0.3%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su17	2017	119	71 – 175	3.7%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su19	2019	8	0 – 25	0.3%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su16	2016	18	0 – 44	0.5%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su17	2017	217	156 – 288	6.7%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su18	2018	744	625 – 848	22.9%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su17	2017	123	75 – 180	3.8%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su18	2018	189	125 – 253	5.8%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su16	2016	9	0 – 26	0.3%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su17	2017	133	77 – 190	4.1%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su18	2018	79	38 – 127	2.4%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su19	2019	33	8 – 59	1.0%	18_UCOLSF
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa18	2018	40	10 – 71	1.2%	03_WCASFA
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	2018	21	0 – 43	0.7%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	2018	11	0 – 32	0.3%	19_SRFALL
#N/A	#N/A	Unassigned	#N/A	669	529 – 822	20.6%	#N/A
		TOTAL		3,244		100.0%	

The Non-Treaty sport fishery in the Chinook Salmon Fall Management Period of 2022

The 2022 fall Non-Treaty sport fishery executed below Bonneville Dam was not mark-selective and could be characterized by reporting group composition of clipped and unclipped hatchery-origin and natural-origin stocks (Table 34). We also reported the broodstock composition of the hatchery-origin Chinook salmon (Table 35). In 2022, we were also able to report on reporting group and broodstock composition of the stocks in the fall Non-Treaty sport fishery executed above Bonneville Dam (Table 36,Table 37).

Table 34. Summary of the stock composition at the reporting group level of the kept adult Chinook salmon of the fall Non-Treaty sport fishery below Bonneville Dam in 2022 in units of reported catch.

			Hatchery origin- Clipped		Hatchery origin- No Clip		Natural origin- No Clip	
Reporting Group name	**Run type**	**Reporting Group Code**	H		HNC		W	
			Est.	**95% CI**	**Est.**	**95% CI**	**Est.**	**95% CI**
Youngs Bay	Spring	01_YOUNGS	11	0 – 25			27	0 – 57
West Cascade Spring	Spring	02_WCASSP						
West Cascade Fall	Fall	03_WCASFA	269	210 – 341	76	17 – 132	458	331 – 593
Willamette	Spring	04_WILLAM	83	44 – 153			169	96 – 242
Spring Creek Tule	Fall	05_SPCRTU	286	214 – 337	129	29 – 258	12	0 – 53
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					76	27 – 133
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	1224	1021 – 1355	1219	1050 – 1370	3068	2789 – 3341
Snake River fall	Fall	19_SRFALL	615	393 – 780	697	486 – 955	755	591 – 923
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	329	199 – 388	187	122 – 244		
Umatilla fall	Fall	23_UMATILLAFA	133	41 – 205	41	13 – 57		
		Total	**2,949**		**2,349**		**4,565**	

Table 35. 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 2022 in units of reported catch.

Fall Sport Fishery 2022				Adult Chinook AD			Adult Chinook AI			
Expected Run Time	**Hatchery**	**Broodstock**	**Broodyear**	**MLE**	**95% CI**	**Percent**	**MLE**	**95% CI**	**Percent**	**GSI RepGrp**
01Spring	South Santiam Hatchery	OtsSSAN_seg_sp18	2018	27	0 – 80	0.9%			0.0%	04_WILLAM
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su17	2017	15	0 – 44	0.5%			0.0%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su18	2018	14	0 – 43	0.5%			0.0%	18_UCOLSF
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa17	2017	19	0 – 57	0.6%	19	0 – 57	0.8%	03_WCASFA
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa18	2018	149	66 – 233	5.1%	33	0 – 66	1.4%	03_WCASFA
04Fall	North Toutle Hatchery	OtsNTOU_seg_fa18	2018	24	0 – 71	0.8%	24	0 – 71	1.0%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa18	2018	21	0 – 64	0.7%			0.0%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa19	2019	30	0 – 90	1.0%			0.0%	03_WCASFA
04Fall	Bonneville Dam Hatchery	OtsBONN_seg_fa19	2019	69	22 – 153	2.3%	25	0 – 75	1.1%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa18	2018	14	0 – 43	0.5%			0.0%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	2019	176	102 – 270	6.0%	104	43 – 176	4.4%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa20	2020	27	0 – 57	0.9%			0.0%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa17	2017	195	117 – 279	6.6%	229	137 – 323	9.7%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa18	2018	368	255 – 490	12.5%	288	181 – 404	12.3%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa19	2019	465	347 – 598	15.8%	627	491 – 769	26.7%	18_UCOLSF
04Fall	Yakima Nation Prosser Hatchery	OtsPROS_seg_fa19	2019			0.0%	60	0 – 149	2.5%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa17	2017	28	0 – 61	1.0%	15	0 – 46	0.6%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa18	2018	15	0 – 45	0.5%			0.0%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa19	2019	13	0 – 39	0.4%			0.0%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	2017	19	0 – 56	0.6%			0.0%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	2018	331	210 – 458	11.2%	318	194 – 442	13.6%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa19	2019	200	115 – 291	6.8%	300	185 – 400	12.8%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa17	2017			0.0%	29	0 – 74	1.3%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	2018	18	0 – 53	0.6%	35	0 – 70	1.5%	19_SRFALL

04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa19	2019			0.0%	15	0 – 44	0.6%	19_SRFALL
04Fall	Klickitat Hatchery	OtsKLIC_seg_fa18	2018	23	0 – 68	0.8%			0.0%	22_BONPOOLFA
04Fall	Klickitat Hatchery	OtsKLIC_seg_fa19	2019			0.0%	44	0 – 89	1.9%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	2017	87	30 – 146	3.0%	15	0 – 45	0.6%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	2018	207	112 – 321	7.0%	17	0 – 51	0.7%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa19	2019	12	0 – 37	0.4%	111	49 – 173	4.7%	22_BONPOOLFA
04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	2018	120	54 – 189	4.1%	41	13 – 81	1.7%	23_UMATILLAFA
04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa19	2019	12	0 – 37	0.4%			0.0%	23_UMATILLAFA
#N/A	#N/A	Unassigned	#N/A	250	91 – 412	8.5%			0.0%	#N/A
		TOTAL		2,949		100.0%	2,349		100.0%	

Table 36. 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 2022 in units of reported catch.

			Hatchery origin- Clipped		Hatchery origin- No Clip		Natural origin- No Clip	
Reporting Group name	**Run type**	**Reporting Group Code**	H		HNC		W	
			Est.	**95% CI**	**Est.**	**95% CI**	**Est.**	**95% CI**
Youngs Bay	Spring	01_YOUNGS					36	0 – 108
West Cascade Spring	Spring	02_WCASSP						
West Cascade Fall	Fall	03_WCASFA					36	0 – 108
Willamette	Spring	04_WILLAM						
Spring Creek Tule	Fall	05_SPCRTU	539	234 – 940	159	0 – 397	21	0 – 89
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					64	0 – 162
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	1530	1104 – 2066	1502	1052 – 2194	2045	1618 – 2447
Snake River fall	Fall	19_SRFALL	853	426 – 1383	560	254 – 877	813	559 – 1130
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	701	361 – 1127	587	219 – 879		
Umatilla fall	Fall	23_UMATILLAFA	261	56 – 613	75	0 – 207		
		Total	**3,884**		**2,883**		**3,015**	

Table 37. 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 2022 in units of reported catch.

Fall Sport BON Fishery 2022				Adult Chinook AD			Adult Chinook AI			
Expected Run Time	**Hatchery**	**Broodstock**	**Broodyear**	**MLE**	**95% CI**	**Percent**	**MLE**	**95% CI**	**Percent**	**GSI RepGrp**
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	2019	431	232 – 634	11.1%	159	40 – 280	5.6%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa20	2020	108	0 – 216	2.8%			0.0%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa17	2017	234	79 – 390	6.0%	158	40 – 277	5.6%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa18	2018	614	371 – 876	15.8%	334	167 – 543	11.8%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa19	2019	484	262 – 711	12.5%	972	711 – 1272	34.3%	18_UCOLSF

04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa17	2017	38	0 – 114	1.0%			0.0%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa18	2018	85	0 – 203	2.2%			0.0%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa19	2019	75	0 – 185	1.9%	37	0 – 112	1.3%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	2017	46	0 – 132	1.2%			0.0%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	2018	435	212 – 670	11.2%	179	45 – 357	6.3%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa19	2019	373	187 – 562	9.6%	337	150 – 525	11.9%	19_SRFALL
04Fall	Klickitat Hatchery	OtsKLIC_seg_fa18	2018	125	0 – 274	3.2%			0.0%	22_BONPOOLFA
04Fall	Klickitat Hatchery	OtsKLIC_seg_fa19	2019	60	0 – 171	1.5%	64	0 – 191	2.2%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	2017	75	0 – 183	1.9%	75	0 – 150	2.6%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	2018	190	49 – 344	4.9%	197	49 – 393	6.9%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa19	2019	252	108 – 396	6.5%	252	108 – 396	8.9%	22_BONPOOLFA
04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	2018	261	112 – 413	6.7%	75	0 – 150	2.6%	23_UMATILLAFA
#N/A	#N/A	Unassigned	#N/A	0	0 – 150	0.0%			0.0%	#N/A
		TOTAL		3,884		100.00%	2,838		100.00%	

The Non-Treaty commercial fishery in the Chinook Salmon Fall Management Period of 2022

The fall Non-Treaty commercial fishery is shown by the composition of the combined adult and jack harvest using reporting group level (Table 38) and broodstock level (Table 39) resolution. The early and late season fishery was executed in two different regions, however, we reported the stock compositions for both regions as a single stratum. These genetic composition results represent the combined reported catch from Region A and B. When results are available for both regions separately, 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.

Table 38. Summary of the stock composition at the reporting group level of the adult and jack Chinook salmon of the fall Non-Treaty commercial fishery below Bonneville Dam in 2022 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	16	0 – 26			11	0 – 33
West Cascade Fall	Fall	03_WCASFA	500	242 – 910			1558	1021 – 2070
Willamette	Spring	04_WILLAM	53	10 – 68			87	44 – 142
Spring Creek Tule	Fall	05_SPCRTU	9103	7983 – 9721	3062	1866 – 4051	1905	1218 – 2575
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					214	44 – 407
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	1181	883 – 1867	1454	1210 – 1999	6556	5579 – 7540
Snake River fall	Fall	19_SRFALL	926	611 – 1253	1194	609 – 1632	1462	1062 – 1928
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	1079	694 – 1548	284	5 – 553		
Umatilla fall	Fall	23_UMATILLAFA	247	8 – 449	55	2 – 164		
		Total	**13,105**		**6,049**		**11,794**	

Note: Hatchery clipped (H), Hatchery unclipped (HNC), and natural-origin (W) estimated abundances (Est.) are indicated for the combined Region A and B to estimate genetic stocks.

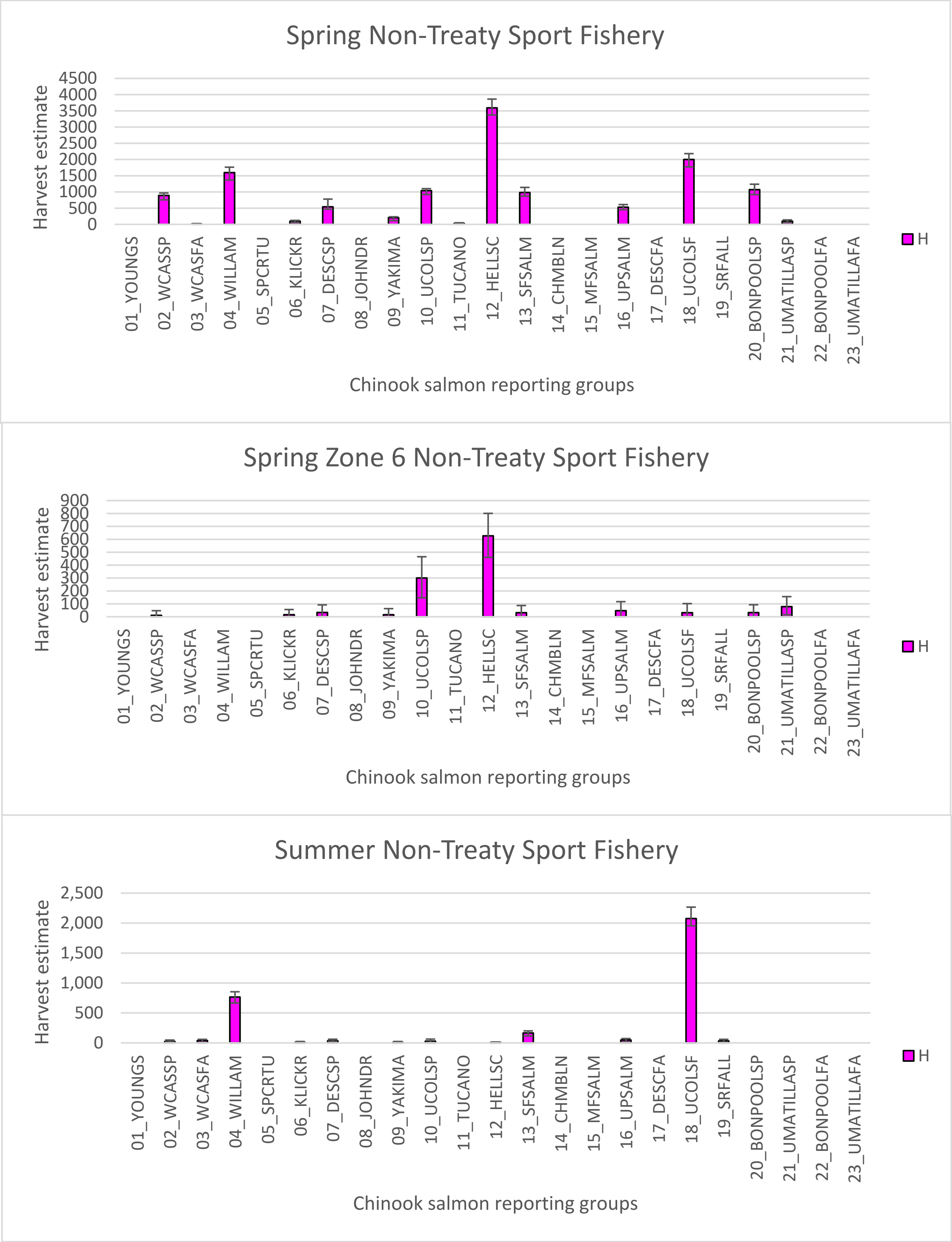
Table 39. Summary of the stock composition at the broodstock level of the adult and jack Chinook salmon of the fall Non-Treaty commercial fishery below Bonneville Dam in 2022 in units of reported catch.

Fall Commercial Fishery 2022				**Adult/jack Chinook AD**			**Adult/jack Chinook AI**			
Run	**Hatchery**	**Broodstock**	**Broodyear**	**MLE**	**95% CI**	**Percent**	**MLE**	**95% CI**	**Percent**	**GSI RepGrp**
01Spring	North Santiam Hatchery	OtsNSAN_seg_sp18	2018	17	0 – 51	0.1%			0.0%	04_WILLAM
04Fall	Big Creek Hatchery	OtsBIGC_seg_fa18	2018	49	0 – 146	0.4%			0.0%	03_WCASFA
04Fall	Big Creek Hatchery	OtsBIGC_seg_fa19	2019	111	0 – 331	0.8%			0.0%	03_WCASFA
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa18	2018	71	0 – 158	0.5%			0.0%	03_WCASFA
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa19	2019	67	0 – 193	0.5%			0.0%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa18	2018	111	0 – 275	0.8%			0.0%	03_WCASFA
04Fall	Bonneville Dam Hatchery	OtsBONN_seg_fa19	2019	2762	1810 – 3558	21.1%	93	0 – 280	1.5%	05_SPCRTU
04Fall	Bonneville Dam Hatchery	OtsBONN_seg_fa20	2020	43	0 – 128	0.3%			0.0%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa18	2018	280	55 – 548	2.1%			0.0%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	2019	5243	4225 – 6216	40.0%	2969	2198 – 3809	49.1%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa20	2020	773	396 – 1211	5.9%			0.0%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa17	2017	243	61 – 469	1.9%	340	166 – 572	5.6%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa18	2018	454	158 – 786	3.5%	568	271 – 927	9.4%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa19	2019	165	53 – 331	1.3%	475	211 – 777	7.9%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa20	2020			0.0%	71	0 – 213	1.2%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa18	2018	162	0 – 393	1.2%			0.0%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa19	2019	55	0 – 166	0.4%			0.0%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa16	2016			0.0%	56	0 – 168	0.9%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	2017	84	0 – 212	0.6%			0.0%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	2018	474	236 – 749	3.6%	974	533 – 1456	16.1%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa19	2019	155	11 – 368	1.2%	123	23 – 246	2.0%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa17	2017	54	0 – 141	0.4%			0.0%	19_SRFALL

04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	2018	133	27 – 254	1.0%	41	14 – 82	0.7%	19_SRFALL
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	2017	530	233 – 872	4.0%	55	0 – 166	0.9%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	2018	496	155 – 865	3.8%	132	0 – 397	2.2%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa19	2019	53	0 – 159	0.4%	97	0 – 290	1.6%	22_BONPOOLFA
04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	2018	187	0 – 390	1.4%	55	0 – 166	0.9%	23_UMATILLAFA
04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa20	2020	59	0 – 178	0.5%			0.0%	23_UMATILLAFA
#N/A	#N/A	Unassigned	#N/A	274	50 – 1149	2.1%			0.0%	#N/A
		TOTAL		13,105		100.0%	6,049		100.0%	

Comparison of stock composition of the clipped Chinook salmon stocks among spring-and summer-management period Chinook salmon sport fisheries in 2022

The stock composition varied in expected ways across the Non-Treaty sport fisheries that were executed in the spring versus summer period (Figure **25**). The largest difference in stock compositions across the spring and summer fisheries was the high estimates of upper Columbia summer-run stock (18_UCOLSF) and lower river stock from the Willamette River (04_WILLAM) captured below Bonneville Dam in the spring and summer periods compared to the spring sport fishery in Zone 6 (Figure **25**). This relatively high capture rate of 04_WILLAM stock below Bonneville Dam is generally expected when compared to Zone 6 because the stock does not typically pass upstream of the dam in high numbers. The presence of 18_UCOLSF stock in the sport fishery below Bonneville Dam and absence of this stock in the sport fishery above Bonneville Dam may have been due to timing of the fishing effort weighted more heavily in June in the fishery below Bonneville Dam when the summer Chinook are present in higher numbers (Table 11).



Spring Non-Treaty Sport Fishery

Spring Zone 6 Non-Treaty Sport Fishery

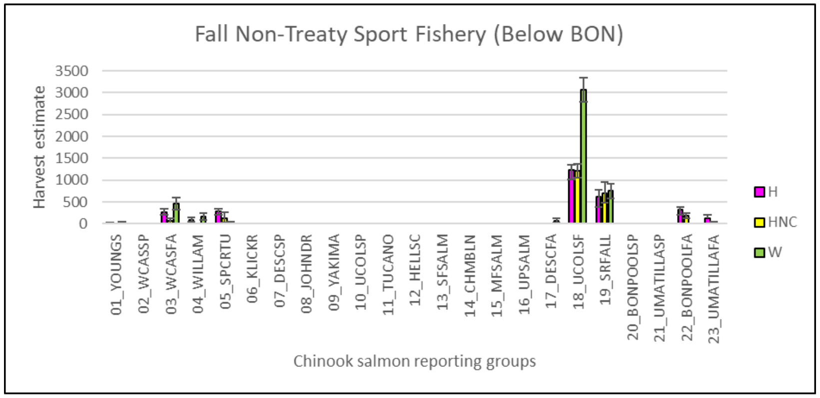
Summer Non-Treaty Sport Fishery

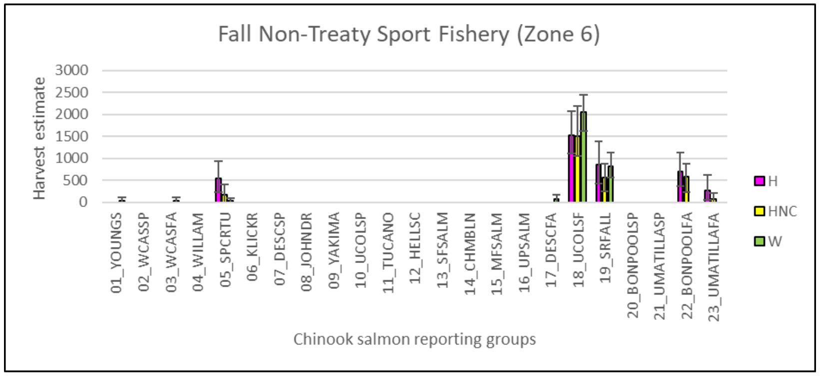
Figure 24. Stock composition of spring and summer management period Chinook salmon harvest mixtures in 2022.

Comparison of stock composition of the clipped and unclipped Chinook salmon stocks among the Non-Treaty fall-management period fisheries in 2022

The primary stock that distinguished the composition of the various Non-Treaty fall fisheries was the “tule” (05_SPCRTU) stock (Figure 26). 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 similar among the sport fisheries from below Bonneville Dam and in the Bonneville Pool and the commercial fishery, except for the higher numbers of 22-BONPOOLFA stock present in the fall sport fishery executed in Zone 6 above Bonneville Dam (Figure 26). Most notably, the Non-Treaty commercial harvest executed primarily in region A below Bonneville Dam 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 26) and commercial fishery (region A, Figure 26) being executed at similar times near Bonneville Dam, the sport fishery is comprised of dramatically lower abundance of “tules”. This difference may be largely due to sport fishers preferentially keeping the VSI bright fish over the tule fish.


Fall Non-Treaty Sport Fishery (Below BON)


Fall Non-Treaty Sport Fishery (Zone 6)

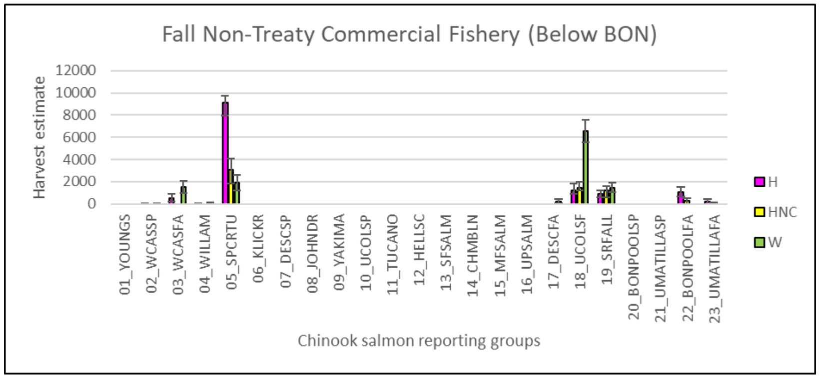

Fall Non-Treaty Commercial Fishery (Below BON)

Figure 25. Genetic stock composition of the Fall Non-Treaty Chinook salmon fisheries analyzed in 2022.

Comparison of stock composition among sockeye salmon fisheries from 2022

Sockeye salmon were sampled from the lower Columbia River below Bonneville Dam in the Non-Treaty sport fishery and were assigned to five major Columbia River sockeye genetic stocks (Table 40). Low sample numbers of *O. nerka* make it difficult to estimate narrow confidence intervals for estimates of the low abundance stocks: Yakima River, Snake River, and Lake Billy Chinook stocks (Table 40).

The timing of the sockeye salmon fisheries may influence the harvested proportion of each stock. The Wenatchee stock has an early shifted run in some years like 2019. This difference in run timing may explain differences in proportions of each stock when compared to Bonneville Dam (Table 40). In 2022, however, the stock proportions in the fishery were very similar to those estimated at Bonneville Dam. For example, Okanogan stock was 77% at Bonneville Dam compared to 73% in the fishery; Wenatchee stock was 22% at Bonneville Dam compared to 26% in the fishery; the Snake River stock was 0.4% at Bonneville Dam compared to 1.2% in the fishery; and the Yakima reintroduced stock was 0% at Bonneville Dam compared to 0% in the fishery (Table 38). The 95% confidence intervals for all stock abundances in the Non-Treaty sport fishery were also estimated (Table 39). Despite small sample size for this fishery, our estimates captured a stock that typically has low abundance, Snake River stock.

Table 40. Comparison of stock-specific abundance and percent composition among sockeye salmon fisheries. The mean stock abundance estimate is provided for each fishery harvest in 2022.

Mixture source	Mean						Stock proportion					
	Okanogan	Wenatchee	Snake	LBC	Yakima	other	Okanogan	Wenatchee	Snake	LBC	Yakima	other
Sport	783	281	13	0	0	0	72.67%	26.09%	1.24%	0.00%	0.00%	0.00%
Total Harvest	783	281	13	0	0	0	72.67%	26.09%	1.24%	0.00%	0.00%	0.00%
Bonneville Dam	513,367	147,430	2,456	0	0	0	77.40%	22.23%	0.37%	0.00%	0.00%	0.00%

Table 41. The reporting group composition of the Non-Treaty Sport Sockeye salmon fishery in 2022.

	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					783	722 – 843
Wenatchee	7	0 – 20			274	214 – 334
Snake	7	0 – 20			7	0 – 20
Lake Billy Chinook						
Yakima						
Odell						
Total	13		0		1064	

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 tenth year in which we were able to assign all three major age classes of spring Chinook from Snake River hatcheries and the sixth 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 was 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 tenth 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. We recently added 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 2022 run year is the fourth 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 four 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 (SCOBI DEUX 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:

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

The in-river estimates of stock composition, stock-specific abundance, escapement, catch, and age distribution were addressed for the spring-management test fishery, the non-treaty spring-management sport fishery, the non-treaty summer-management sport fishery, and the non-treaty mainstem fall-management sport and commercial fisheries. For the spring management period of Chinook salmon in 2022, we observed typical differences in the composition of hatchery stocks represented in spring vs. summer management period harvest of Chinook salmon. Run-timing plays an important role in this difference (i.e., late-running stocks appear more abundant among the upriver spring-type lineage that are caught in the summer management period). This pattern is consistent when compared to known origin PIT tagged adult and jack fish tagged as juveniles. Known origin adult-aged upriver spring and Snake River spring Chinook salmon typically have passed Bonneville by June 15 in most years. The fall management period fisheries were also found to show typical distinctions for the Non-Treaty sport versus Non-treaty commercial fisheries: namely, the Spring Creek tule stock is largely absent in the sport fishery but in high abundance in the commercial fishery. The reason for this is likely a preference exhibited by Non-treaty sport fishers for “bright” Chinook salmon stocks which cause them to catch and release more of the visually darker fish that are from the Spring Creek tule stock.

The sockeye salmon tribal fishery is managed in a way that attempts to harvest as many harvestable sockeye salmon as possible under the allowed harvest rate schedule in the U.S. v. Oregon Management Agreement. We covered the 2022 year of analysis of the sockeye salmon harvest in this current report. The 2022 Non-treaty sport fishery harvested a surprisingly representative composition of stocks compared to Bonneville Dam, which is unlike more typical years where we have found that there may be some over representation of the Wenatchee sockeye stocks in the Zone 6 harvest as compared to the stock proportions that are present at Bonneville Dam. The results for Snake River sockeye salmon are dependent upon representative sampling at Bonneville Dam, but low sample rate and the rarity of this stock leads to uncertainty and high variation around estimates of Snake River sockeye salmon from Bonneville Dam. Despite this rarity, the fishery mixture evaluated in 2022 estimated non-zero abundance of Snake River stock.

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

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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 2022. 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 (e.g., 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 conventional 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 2023 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 2023, 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 42 for the number and timing of reports for each species and run that were delivered in-season and post-season in 2023). One new addition to these reports is the inclusion of post-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 provided a demonstration of the analysis of Coho Salmon in this current 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 10th 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 8th year in which these can be assigned to some Columbia River hatcheries. This is the fifth year that Sockeye salmon from the Yakima River reintroduction can be assigned to candidate parents, allowing this stock to be identified in fisheries and at Bonneville Dam. This study integrates PBT and GSI results to provide the greatest amount of stock-specific information available for hatchery- and natural-origin steelhead, Sockeye and Chinook salmon passing Bonneville Dam.

Time line for completion of objectives

Objectives will be ongoing and GSI results updated each year for analyses of salmon and steelhead throughout the accords-funding. This report that is written in February 2024 features the final analyses of 2022, as well as the preliminary in-season and post-season analyses of 2023. 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 42. The in-season and post-season report timing and scope of the 2023 fish runs.

Species	Management Period	Data coverage	Samples Arrive	Analysis begins	Report distributed
Chinook	Spring	01/01/2023 – 04/30/2023	5/1/2023	5/4/2023	5/8/2023
		01/01/2023 – 05/14/2023	5/15/2023	5/18/2023	5/22/2023
		01/01/2023 – 05/28/2023	5/30/2023	6/2/2023	6/5/2023
		01/01/2023 – 06/15/2023	6/16/2023	6/21/2023	6/23/2023
	Summer	06/16/2023 – 07/02/2023	7/5/2023	7/11/2023	7/12/2023
		06/16/2023 – 07/31/2023	8/1/2023	8/4/2023	8/7/2023
	Fall	08/01/2023 – 8/27/2023	8/28/2023	8/31/2023	9/4/2023
		08/01/2023 – 10/29/2023	10/30/2023	11/2/2023	11/6/2023
Steelhead	Skamania	04/01/2023 – 06/30/2023	7/5/2023	7/11/2023	7/12/2023
	Summer A-/B-Index	07/01/2023 – 07/31/2023	8/1/2023	8/4/2023	8/7/2023
		07/01/2023 – 08/27/2023	8/28/2023	8/31/2023	9/4/2023
		07/01/2023 – 10/31/2023	10/30/2023	11/2/2023	11/6/2023
Sockeye	Total	01/01/2023 – 07/31/2023	8/1/2023	8/4/2023	8/7/2023

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 Roger Dick Jr. for distribution to TAC members.

Methods

Sample Collection

Tissue samples were obtained from adult steelhead (n=864), Chinook (n=2,838), sockeye salmon (n=1,303), and Coho salmon (n=150) adults in 2022 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 (04/17/22) and was completed on 10/15/22 (statistical week 42). Sampling occurred at the Adult Fish Facility (AFF) located on the northern end of Bonneville Dam. Fish were sampled 4–5 d per statistical week (except when reduced due to restrictions on trap use or low run size at the beginning and end of the run) and for 4–6 h per day. A picket weir was used to divert migrating fish ascending the Washington shore fish ladder into the AFF collection pool. An attraction flow was used to draw fish through a false weir where they were selected for sampling. After sampling was completed and fish recovered from the anesthetic, they were returned to the Washington shore fish ladder above the picket weir. A small portion of the adult Chinook salmon run was missed prior to the statistical week in which sampling was initiated by April 17 (week 17). There was 0.4% of the clipped adults and 0.1% of the unclipped adults estimated to have passed in weeks prior to the start of sampling in 2022. 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 2022 (Figure 27), 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 2022 for the spring and summer management periods was 0.7%, whereas the average sample rate for adult fall Chinook was 0.6% (Table 43).

Based on numbers of fish collected, samples were pooled into a combination of weekly strata and multi-week strata for Chinook (Table 43), steelhead (Table 44), and sockeye salmon (Table 45) 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).

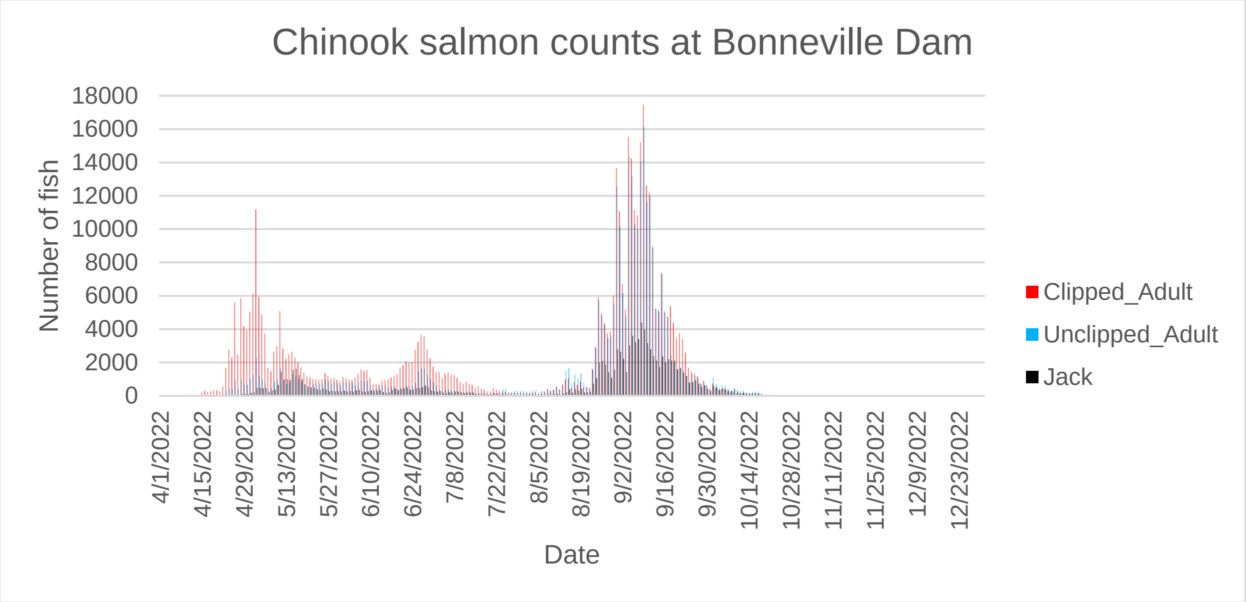

Figure 26. Daily passage of Chinook salmon (Clipped adults=red, Unclipped adult=blue, and jacks=black) at Bonneville Dam in 2022 (source: https://www.fpc.org; US v OR TAC).

Table 43. Sample numbers by weekly strata for adult-sized Chinook salmon that were DNA sampled or tallied for abundance at Bonneville Dam in 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	3,254	1,604	1	14	6	3	15	9	0.46%	0.56%
		26	13,740	3,939		7	4	1	7	5	0.05%	0.13%
		27	18,723	8,489		6	1	1	6	2	0.03%	0.02%
		28	8,800	2,355	3	15	5	4	18	9	0.20%	0.38%
		29	4,865	1,463	4	47	13	4	51	17	1.05%	1.16%
		30	2,475	1,109	1	24	8	6	25	14	1.01%	1.26%
		31	1,572	2,422	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%
		42-53	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%

Note: Statistical weeks 1–16 are 1/1/22 – 4/16/22 and 42–53 is 10/9/22–12/31/22. ‘TAC count’ is based on the estimates of clip and unclipped adult Chinook salmon provided by US v OR Technical Advisory Committee using data from the Fish Passage Center (http://www.fpc.org) observed by the 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 sample rate. The management periods approximate the date ranges from January 1st to June 15th (Spring management period), June 16th to July 31st (Summer management period), and August 1st to December 31 (Fall management period) which are used to categorize spring-, summer-, and fall-run Chinook salmon, respectively. The number of sampled fish that were assigned via PBT or GSI are shown.

Table 44. Sample numbers by monthly strata for steelhead that were DNA sampled or tallied for abundance at Bonneville Dam in 2022.

				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	3,923	2,979	1	12	9	0	0	0	0	0	13	9	0.33%	0.30%
A-/B-Index	27-30	16,576	10,978	6	80	49	4	0	2	1	0	88	54	0.53%	0.49%
	31-33	16,485	9,911	5	81	52	2	0	2	3	0	88	57	0.53%	0.58%
	34	9,105	3,214	5	62	26	4	0	18	5	2	85	37	0.93%	1.15%
	35-38	29,585	7,708	6	35	14	3	1	29	9	2	71	28	0.24%	0.36%
	39	5,073	1,308	3	31	8	7	3	65	10	10	102	35	2.01%	2.68%
	40	2,849	855	2	21	6	5	7	56	4	10	86	25	3.02%	2.92%
	41-45	2,360	962	0	19	5	3	0	40	4	15	59	27	2.50%	2.81%
Summer A-/B-Index subtotal		82,033	34,936	27	329	160	28	11	212	36	39	579	263	0.71%	0.75%
Total		85,956	37,915	28	341	169	28	11	212	36	39	592	272	0.69%	0.72%

Note: Statistical week 14-27 is 4/1/22–6/30/22 (Skamania Management Period) and 27-29 begins the A-/B-Index Period that runs from 7/1/2022-10/31/2022. ‘Fish count’ is based on tallies of adipose-clipped and unclipped adult steelhead provided by the Fish Passage Center (http://www.fpc.org) observed by the Corps of Engineers at their fish counting window. The total sum of all samples for each clipped and unclipped category obtained in a given stratum was used to calculate sample rate. The clipped and unclipped sample numbers were grouped by size (A-Index < 780 mm fork length; B-Index >=780 mm fork length) and further split according to the number of samples that were either assigned via PBT or GSI.

Table 45. Sample numbers for genetic stock assignments of sockeye salmon that passed Bonneville Dam in 2022.

Statistical week grouping	Bonneville dam fish window count	Genetic stock						Total	Sample rate (%)
						Yakima			
		OKA	WEN	RED	LBC	OKA	WEN		
1-24	7963	67	3	0	0	0	0	70	0.88%
25	28150	146	13	0	0	0	0	159	0.56%
26	169056	217	39	1	0	0	0	257	0.15%
27	286050	135	56	1	0	0	0	192	0.07%
28	98371	208	56	0	0	0	0	264	0.27%
29	42150	104	27	0	0	0	0	131	0.31%
30	21644	101	26	2	0	0	0	129	0.60%
31-39	9869	69	32	0	0	0	0	101	1.02%
40-52	0	0	0	0	0	0	0	0	0.00%
Total	663253	1047	252	4	0	0	0	1303	0.20%

Note: Statistical week 22 begins on 5/22/22 and 39 ends 9/24/22; there were no sockeye counted before or after those dates. 'Fish count' is based on tallies of sockeye salmon adults provided by the Fish Passage Center (http://www.fpc.org) observed by the Corps of Engineers at their fish counting window. GSI stocks are Okanagan (OKA), Wenatchee (WEN), Snake River (RED), and Lake Billy Chinook (LBC) and PBT can identify fish from the Yakima reintroduction which consist of two genetic stocks (OKA and WEN). The number of samples for a given statistical week or pooled stratum was used to calculate sample rate. Relatively few sockeye salmon were sampled from the RED, LBC, and Yakima stocks, and limits inference regarding run-timing and abundance of these stocks.

Results

Estimated relative abundance of Chinook salmon stocks in 2022

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

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There were 15 major (i.e., abundance >1000 fish) clipped hatchery origin Chinook salmon stocks represented in the total estimated abundance (N=445,285) of clipped hatchery Chinook salmon passing Bonneville Dam in 2022 (Table 46; Figure 28). These stocks in order of decreasing magnitude were 18_UCOLSF (122,494), 05_SPCRTU (115,071), 12_HELLSC (51,927), 19_SRFALL (37,362), 22_BONPOOLFA (31,349), 20_BONPOOLSP (22,423), 10_UCOLSP (19,691), 23_UMATILLAFA (14,257), 16_UPSALM (6,825), 07_DESCSP (6,806), 13_SFSALM (4,433), 21_UMATILLASP (4,126), 02_WCASSP (3,797), 09_YAKIMA (2,055), and 06_KLICKR (1,772) (Table 46).

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 46). Further, using PBT assignments we can now provide abundance and run-timing estimates for particular hatchery broodstocks (Table 47) which will allow for improved abundance estimates (Figure 28). In 2022, there were 66 different broodstocks of clipped hatchery-origin fish with abundances greater than 0 and 45 of them had abundance estimates >1000 fish (Table 47). The top five major clipped hatchery broodstocks were from Spring Creek, Priest Rapids, Little White Salmon, and Eastbank hatcheries which were fall and summer run. The largest spring run clipped broodstock was represented by Rapid River Hatchery (SY2018; 16,301 fish), which is typically one of the largest spring run hatchery stocks**.**

Table 46. Stock-specific abundance and run-timing of clipped hatchery origin adult Chinook salmon passing Bonneville Dam in 2022.

Reporting Group	Estimated abundance					Run-timing distribution						
	Mean	Sample N	Management Period			Ordinal day						
			Spring	Summer	Fall		1st	3rd	5th	95th	Median	Interquartile
			Jan. 1-Jun. 15	Jun. 16-Jul. 31	Aug. 1-Dec. 31	Median	quartile	quartile	percentile	percentile	date	range (days)
01_YOUNGS	0	1	0	0	0	-	-	-	-	-	-	
02_WCASSP	3,797	16	2,615	1,182	0	143	135	173	122	185	5/23/2022	38
03_WCASFA	0		0	0	0	-	-	-	-	-	-	
04_WILLAM	888	6	9	67	812	236	227	238	198	239	8/24/2022	11
05_SPCRTU	115,071	169	0	0	115,071	250	245	253	236	261	9/7/2022	8
06_KLICKR	1,772	13	1,772	0	0	145	131	157	123	164	5/25/2022	26
07_DESCSP	6,806	38	5,761	1,045	0	135	123	144	116	180	5/15/2022	21
08_JOHNDR	0		0	0	0	-	-	-	-	-	-	
09_YAKIMA	2,055	15	2,055	0	0	135	124	139	121	148	5/15/2022	15
10_UCOLSP	19,691	103	18,126	1,564	0	124	119	131	113	176	5/4/2022	12
11_TUCANO	0		0	0	0	-	-	-	-	-	-	
12_HELLSC	51,927	283	49,901	2,026	0	124	119	132	113	159	5/4/2022	13
13_SFSALM	4,433	31	3,390	1,043	0	155	142	166	135	185	6/4/2022	24
14_CHMBLN	9	1	9	0	0	146	143.8	146.3	142.35	147.65	44707	
15_MFSALM	0	1	0	0	0	-	-	-	-	-	-	
16_UPSALM	6,825	49	5,857	968	0	144	133	156	123	180	5/24/2022	23
17_DESCFA	0		0	0	0	-	-	-	-	-	-	
18_UCOLSF	122,494	422	13,724	44,978	63,792	236	178	254	156	268	8/24/2022	76
19_SRFALL	37,362	66	0	555	36,807	244	239	251	226	263	9/1/2022	12
20_BONPOOLSP	22,423	111	22,423	0	0	122	118	125	113	136	5/2/2022	7
21_UMATILLASP	4,126	21	4,126	0	0	123	119	129	113	134	5/3/2022	10
22_BONPOOLFA	31,349	50	0	0	31,349	250	244	255	237	271	9/7/2022	11
23_UMATILLAFA	14,257	32	0	0	14,257	254	250	259	247	268	9/11/2022	9
Total	445,285	1,428	129,769	53,429	262,087							

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

Table 47. Hatchery broodstock-specific abundance and run-timing distributions of clipped adult Chinook salmon passing Bonneville Dam in 2022.

Run	GSI RepGrp	Hatchery	Brood stock	Sample N	Estimated abundance				Run-timing distribution						
					Total	Management Period			Ordinal day						Inter
						Spring	Summer	Fall		1st	3rd	5th	95th	Median	quartile
						Jan. 1 - Jun. 15	Jun. 16 - Jul. 31	Aug. 1 - Dec. 1	Median	quartile	quartile	%	%	date	range
01Spring	02_WCASSP	Parkdale Fish Facility	OtsPARK_seg_sp18	16	3,797	2,615	1,182	0	143	135	173	122	185	5/23/2022	38
	04_WILLAM	North Santiam Hatchery	OtsNSAN_seg_sp18	1	812	0	0	812	237	230	238	220	239	8/25/2022	8
	06_KLICKR	Klickitat Hatchery	OtsKLIC_seg_sp18	13	1,772	1,772	0	0	145	131	157	123	164	5/25/2022	26
	07_DESCSP	Round Butte Fish Hatchery	OtsRBFH_seg_sp18	20	3,409	3,409	0	0	127	123	138	116	149	5/7/2022	15
	07_DESCSP	Round Butte Fish Hatchery	OtsRBFH_seg_sp19	1	1,045	0	1,045	0	178	174	182	169	189	6/27/2022	8
	07_DESCSP	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp17	1	214	214	0	0	117	115	119	108	120	4/27/2022	4
	07_DESCSP	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp18	12	2,042	2,042	0	0	134	123	138	115	158	5/14/2022	15
	09_YAKIMA	Yakima River Roza Dam	OtsYRRD_int_sp18	10	1,689	1,689	0	0	135	123	138	121	149	5/15/2022	15
	09_YAKIMA	Yakima River Roza Dam	OtsYRRD_seg_sp18	3	358	358	0	0	142	131	145	129	148	5/22/2022	14
	10_UCOLSP	Eastbank Fish Hatchery	OtsEAST_seg_sp18	9	1,381	1,381	0	0	126	123	148	121	159	5/6/2022	25
	10_UCOLSP	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp17	1	305	305	0	0	123	122	125	121	126	5/3/2022	3
	10_UCOLSP	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp18	38	13,230	11,665	1,564	0	124	118	132	113	179	5/4/2022	14
	10_UCOLSP	Methow Fish Hatchery	OtsMETH_seg_sp18	1	219	219	0	0	117	115	119	109	120	4/27/2022	4
	10_UCOLSP	Winthrop National Fish Hatchery	OtsWINT_seg_sp18	14	3,638	3,638	0	0	123	119	125	114	132	5/3/2022	6
	12_HELLSC	Clearwater Fish Hatchery	OtsCLWH_seg_sp18	35	6,093	6,093	0	0	125	122	135	115	147	5/5/2022	13
	12_HELLSC	Clearwater Fish Hatchery	OtsPOWP_seg_sp18	2	266	266	0	0	141	137	160	135	165	5/21/2022	23
	12_HELLSC	Clearwater Fish Hatchery	OtsCLWH_seg_sp19	1	137	137	0	0	137	136	139	135	141	5/17/2022	3
	12_HELLSC	Dworshak National Fish Hatchery	OtsKOOS_seg_sp18	48	10,444	9,432	1,012	0	125	120	132	114	178	5/5/2022	12
	12_HELLSC	Dworshak National Fish Hatchery	OtsDWOR_seg_sp18	66	11,826	11,826	0	0	123	118	131	113	145	5/3/2022	13
	12_HELLSC	Dworshak National Fish Hatchery	OtsKOOS_seg_sp19	1	98	98	0	0	152	150	154	149	155	6/1/2022	4
	12_HELLSC	Lookingglass Fish Hatchery	OtsLOOK_seg_sp18	20	3,917	3,917	0	0	124	121	131	114	153	5/4/2022	10
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH_seg_sp17	3	700	700	0	0	123	121	124	114	126	5/3/2022	3
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH_seg_sp18	82	16,301	16,301	0	0	123	118	131	113	144	5/3/2022	13
	20_BONPOOLSP	Carson National Fish Hatchery	OtsCARS_seg_sp17	1	173	173	0	0	117	115	119	109	120	4/27/2022	4
	20_BONPOOLSP	Carson National Fish Hatchery	OtsCARS_seg_sp18	60	12,073	12,073	0	0	122	118	125	113	135	5/2/2022	7
	20_BONPOOLSP	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp18	50	10,177	10,177	0	0	123	118	126	113	139	5/3/2022	8
	21_UMATILLASP	Umatilla Fish Hatchery	OtsUMAT_seg_sp18	21	4,126	4,126	0	0	123	119	129	113	134	5/3/2022	10
02Spring/Summer	12_HELLSC	Lookingglass Fish Hatchery	OtsIMNW_seg_ss17	2	325	325	0	0	134	131	159	129	165	5/14/2022	28
	12_HELLSC	Lookingglass Fish Hatchery	OtsIMNW_seg_ss18	5	1,521	508	1,013	0	174	156	180	131	188	6/23/2022	24
	12_HELLSC	Lookingglass Fish Hatchery	OtsIMNW_seg_ss19	1	133	133	0	0	160	158	163	156	166	6/9/2022	5

	13_SFSALM	McCall Fish Hatchery	OtsMCCA_seg_ss18	29	4,199	3,222	977	0	156	143	166	136	183	6/5/2022	23
	16_UPSALM	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss18	21	2,368	2,368	0	0	146	138	153	132	162	5/26/2022	15
	16_UPSALM	Sawtooth Fish Hatchery	OtsSAWT_seg_ss18	25	4,276	3,309	968	0	142	131	163	123	183	5/22/2022	32
03Summer	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_su16	2	1,066	92	974	0	177	172	181	153	188	6/26/2022	9
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_su17	20	5,602	1,565	3,328	709	178	164	193	147	237	6/27/2022	29
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_su17	13	2,602	1,337	1,265	0	166	159	179	153	195	6/15/2022	20
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_su18	1	99	0	99	0	197	193	203	191	210	7/16/2022	10
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_su19	1	996	0	996	0	178	174	182	169	189	6/27/2022	8
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_su19	1	101	0	101	0	197	193	203	191	210	7/16/2022	10
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su16	1	101	0	101	0	197	193	203	191	210	7/16/2022	10
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su17	31	7,516	2,772	4,179	566	174	160	181	149	234	6/23/2022	21
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su18	73	20,227	1,815	16,754	1,658	180	174	192	158	235	6/29/2022	18
	18_UCOLSF	Entiat National Fish Hatchery	OtsENFH_seg_su17	19	2,447	2,447	0	0	153	146	159	139	165	6/2/2022	13
	18_UCOLSF	Entiat National Fish Hatchery	OtsENFH_seg_su18	20	9,225	1,665	7,560	0	177	170	182	153	190	6/26/2022	12
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su16	1	91	91	0	0	152	150	154	149	155	6/1/2022	4
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su17	19	5,472	910	3,953	609	179	172	191	149	237	6/28/2022	19
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su18	14	4,844	738	4,106	0	178	171	185	158	200	6/27/2022	14
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su19	9	1,818	256	1,562	0	180	173	193	159	205	6/29/2022	20
04Fall	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa18	6	3,987	0	0	3,987	247	243	251	235	269	9/4/2022	8
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	119	85,988	0	0	85,988	250	246	254	236	262	9/7/2022	8
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa20	13	11,610	0	0	11,610	247	242	250	231	253	9/4/2022	8
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa17	15	7,526	0	0	7,526	244	242	260	233	268	9/1/2022	18
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa18	61	26,066	0	0	26,066	254	248	261	242	275	9/11/2022	13
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa19	64	22,130	0	0	22,130	256	251	263	247	274	9/13/2022	12
	18_UCOLSF	Ringold Springs State Hatchery	OtsRING_seg_fa17	3	906	0	0	906	259	256	265	254	272	9/16/2022	9
	18_UCOLSF	Ringold Springs State Hatchery	OtsRING_seg_fa19	7	2,219	0	0	2,219	258	255	262	254	274	9/15/2022	7
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	5	3,003	0	0	3,003	248	244	253	241	265	9/5/2022	9
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	22	14,479	0	223	14,256	245	238	252	224	260	9/2/2022	14
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa19	24	16,407	0	103	16,304	244	241	248	230	262	9/1/2022	7
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	2	743	0	115	628	236	225	238	194	239	8/24/2022	13
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa19	1	556	0	0	556	237	230	238	220	239	8/25/2022	8
	22_BONPOOLFA	Klickitat Hatchery	OtsKLIC_seg_fa18	1	230	0	0	230	270	269	272	268	274	9/27/2022	3
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	11	6,886	0	0	6,886	251	246	254	237	266	9/8/2022	8
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	32	21,293	0	0	21,293	248	243	254	236	275	9/5/2022	11
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa19	6	2,941	0	0	2,941	252	249	257	247	270	9/9/2022	8

	23_UMATILLAFA	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	32	14,257	0	0	14,257	254	250	259	247	268	9/11/2022	9
	#N/A	#N/A	Unassigned	174	18,790	1,593	247	16,950	251	245	255	125	261	9/8/2022	10
			Total	1,436	445,285	129,769	53,429	262,087							

There were 7 major (i.e., abundance >1000 fish) ***unclipped*** hatchery origin Chinook salmon stocks represented in the total estimated abundance (N=165,764) of unclipped hatchery Chinook salmon passing Bonneville Dam in 2021 (Table 48; Figure 28). These stocks in order of decreasing magnitude were 05_SPCRTU (52,233), 18_UCOLSF (47,347), 19_SRFALL (40,222), 22_BONPOOLFA (13,901), 12_HELLSC (4,253), 10_UCOLSP (3,666), and 20_BONPOOLSP (1,238) (Table 48).

In 2022, there were 52 different broodstocks of unclipped hatchery-origin fish with abundances greater than 0 and 14 of them had abundance estimates >1000 fish (Table 49). The top five major unclipped hatchery broodstocks were from Spring Creek, Priest Rapids Hatchery, and Lyons Ferry hatcheries which were all fall run. The largest spring run unclipped broodstock was represented by Eastbank Hatchery (SY2018, 2,002 fish).

Table 48. Stock-specific abundance and run-timing of unclipped hatchery origin adult Chinook salmon passing Bonneville Dam in 2022.

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	0		0	0	0	-	-	-	-	-	-	-
02_WCASSP	235	1	235	0	0	123	122	125	121	126	5/3/2022	3
03_WCASFA	0		0	0	0	-	-	-	-	-	-	-
04_WILLAM	0		0	0	0	-	-	-	-	-	-	-
05_SPCRTU	52,233	123	0	0	52,233	252	248	255	237	260	9/9/2022	7
06_KLICKR	123	1	123	0	0	160	158	163	156	166	6/9/2022	5
07_DESCSP	0		0	0	0	-	-	-	-	-	-	-
08_JOHNDR	0		0	0	0	-	-	-	-	-	-	-
09_YAKIMA	121	1	121	0	0	160	158	163	156	166	6/9/2022	5
10_UCOLSP	3,666	32	3,666	0	0	132	123	144	116	158	5/12/2022	21
11_TUCANO	0		0	0	0	-	-	-	-	-	-	-
12_HELLSC	4,253	35	4,253	0	0	123	118	136	113	157	5/3/2022	18
13_SFSALM	854	11	743	111	0	148	142	157	136	206	5/28/2022	15
14_CHMBLN	0		0	0	0	-	-	-	-	-	-	-
15_MFSALM	0		0	0	0	-	-	-	-	-	-	-
16_UPSALM	538	7	538	0	0	138	134	144	129	147.1	5/18/2022	10
17_DESCFA	0		0	0	0	-	-	-	-	-	-	-
18_UCOLSF	47,347	202	1,630	7,580	38,137	250	242	256	170	269	9/7/2022	14
19_SRFALL	40,222	89	0	508	39,714	242	236	248	222	254	8/30/2022	12
20_BONPOOLSP	1,238	9	1,238	0	0	118	116	122	110	125	4/28/2022	6
21_UMATILLASP	630	5	630	0	0	128	122	136	115	153	5/8/2022	14
22_BONPOOLFA	13,901	38	0	0	13,901	251	248	253	246	263	9/8/2022	5
23_UMATILLAFA	404	2	0	0	404	257	255	259	254	264	9/14/2022	4
Total	165,764	556	13,177	8,199	144,389							

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

Table 49. Hatchery broodstock-specific abundance and run-timing distributions of unclipped adult Chinook salmon passing Bonneville Dam in 2022.

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	235	235	0	0	123	122	125	121	126	5/3/2022	3
	06_KLICKR	Klickitat Hatchery	OtsKLIC_seg_sp18	1	123	123	0	0	160	158	163	156	166	6/9/2022	5
	09_YAKIMA	Yakima River Roza Dam	OtsYRRD_int_sp18	1	121	121	0	0	160	158	163	156	166	6/9/2022	5
	10_UCOLSP	Eastbank Fish Hatchery	OtsEAST_seg_sp18	21	2,002	2,002	0	0	134	131	146	123	157	5/14/2022	15
	10_UCOLSP	Eastbank Fish Hatchery	OtsEAST_seg_sp19	1	133	133	0	0	160	158	163	156	166	6/9/2022	5
	10_UCOLSP	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp18	3	534	534	0	0	118	116	120	111	147	4/28/2022	5
	10_UCOLSP	Methow Fish Hatchery	OtsMETH_seg_sp18	6	934	934	0	0	124	122	136	116	144	5/4/2022	14
	10_UCOLSP	Winthrop National Fish Hatchery	OtsWINT_seg_sp18	1	64	64	0	0	145	144	147	142	148	5/25/2022	4
	12_HELLSC	Clearwater Fish Hatchery	OtsCLWH_seg_sp18	3	365	365	0	0	117	115	119	110	120	4/27/2022	4
	12_HELLSC	Clearwater Fish Hatchery	OtsPOWP_seg_sp18	6	613	613	0	0	150	135	159	130	165	5/30/2022	24
	12_HELLSC	Dworshak National Fish Hatchery	OtsDWOR_seg_sp17	1	51	51	0	0	145	143	147	142	148	5/25/2022	4
	12_HELLSC	Dworshak National Fish Hatchery	OtsDWOR_seg_sp18	8	953	953	0	0	129	120	134	114	146	5/9/2022	14
	12_HELLSC	Dworshak National Fish Hatchery	OtsKOOS_seg_sp18	7	836	836	0	0	122	117	136	113	143	5/2/2022	19
	12_HELLSC	Lookingglass Fish Hatchery	OtsLOOK_seg_sp18	3	479	479	0	0	123	120	130	114	133	5/3/2022	10
	12_HELLSC	Nez Perce	OtsNPFH_seg_sp18	2	296	296	0	0	125	123	136	121	140	5/5/2022	13
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH_seg_sp18	5	659	659	0	0	118	115	120	110	138	4/28/2022	5
	20_BONPOOLSP	Carson National Fish Hatchery	OtsCARS_seg_sp18	6	849	849	0	0	120	116	123	112	126	4/30/2022	7
	20_BONPOOLSP	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp18	3	389	389	0	0	117	115	119	110	120	4/27/2022	4
	21_UMATILLASP	Umatilla Fish Hatchery	OtsUMAT_seg_sp18	4	534	534	0	0	125	121	132	115	153	5/5/2022	11
	21_UMATILLASP	Umatilla Fish Hatchery	OtsUMAT_seg_sp19	1	96	96	0	0	137	136	139	135	141	5/17/2022	3
02Spring/Summer	13_SFSALM	McCall Fish Hatchery	OtsMCCA_seg_ss18	7	485	485	0	0	143	138	147	135	153	5/23/2022	9
	13_SFSALM	McCall Fish Hatchery	OtsJHNW_int_ss18	2	136	136	0	0	150	146	153	143	155	5/30/2022	7
	13_SFSALM	McCall Fish Hatchery	OtsMCCA_seg_ss19	1	122	122	0	0	160	158	163	156	166	6/9/2022	5
	13_SFSALM	McCall Fish Hatchery	OtsJHNW_int_ss19	1	111	0	111	0	204	196	208	192	211	7/23/2022	12
	16_UPSALM	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss18	4	250	250	0	0	143	138	146	135	148	5/23/2022	8
	16_UPSALM	Sawtooth Fish Hatchery	OtsSAWT_seg_ss18	3	288	288	0	0	135	131	139	129	147	5/15/2022	8
03Summer	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_su17	3	382	382	0	0	154	152	159	149	165	6/3/2022	7
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_su17	3	951	225	726	0	177	167	180	152	187	6/26/2022	13
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su17	1	679	0	679	0	178	174	181	168	188	6/27/2022	7
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su18	9	3,185	205	2,980	0	178	174	183	161	205	6/27/2022	9

	18_UCOLSF	Entiat National Fish Hatchery	OtsENFH_seg_su18	4	2,724	0	2,724	0	178	175	182	168	192	6/27/2022	7
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su17	3	362	362	0	0	159	155	162	150	166	6/8/2022	7
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su18	5	590	454	135	0	160	154	166	145	209	6/9/2022	12
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su19	2	222	0	222	0	204	196	208	192	212	7/23/2022	12
04Fall	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	122	51,643	0	0	51,643	252	248	255	238	260	9/9/2022	7
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa20	1	590	0	0	590	236	228	238	218	239	8/24/2022	10
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa17	13	3,092	0	0	3,092	250	246	254	242	268	9/7/2022	8
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa18	47	10,926	0	0	10,926	251	245	257	242	271	9/8/2022	12
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa19	109	23,238	0	115	23,123	253	249	258	238	271	9/10/2022	9
	18_UCOLSF	Ringold Springs State Hatchery	OtsRING_seg_fa18	2	849	0	0	849	250	248	252	247	268	9/7/2022	4
	18_UCOLSF	Ringold Springs State Hatchery	OtsRING_seg_fa19	1	75	0	0	75	280	277	285	275	291	10/7/2022	8
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	4	1,687	0	0	1,687	237	231	240	220	245	8/25/2022	9
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	24	12,047	0	250	11,797	237	231	243	218	252	8/25/2022	12
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa19	51	22,157	0	0	22,157	246	240	251	227	257	9/3/2022	11
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa17	2	966	0	0	966	238	234	243	222	245	8/26/2022	9
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	6	2,996	0	258	2,739	235	227	238	206	239	8/23/2022	11
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa19	2	369	0	0	369	257	255	259	254	270	9/14/2022	4
	22_BONPOOLFA	Klickitat Hatchery	OtsKLIC_seg_fa19	2	1,759	0	0	1,759	252	249	254	247	259	9/9/2022	5
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	3	118	0	0	118	270	269	272	268	274	9/27/2022	3
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	4	2,026	0	0	2,026	251	248	252	247	280	9/8/2022	4
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa19	29	9,998	0	0	9,998	251	248	254	244	261	9/8/2022	6
	23_UMATILLAFA	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	2	404	0	0	404	257	255	259	254	264	9/14/2022	4
	#N/A	#N/A	Unassigned	0	72	0	0	72	##	##	##	##	##	10/7/2022	8
			Total	556	165,693	13,177	8,199	144,317							

Table 50. Stock-specific abundance and run-timing of natural origin adult Chinook salmon passing Bonneville Dam in 2022.

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	0	0	0	0	0	-	-	-	-	-	-	-
02_WCASSP	0	0	0	0	0	-	-	-	-	-	-	-
03_WCASFA	38	1	0	0	38	270	269	272	268	273.2	9/27/2022	3
04_WILLAM	2,279	6	378	1,311	590	179	171	216	133	238	6/28/2022	45
05_SPCRTU	14,435	47	0	0	14,435	250	246	252	236	259	9/7/2022	6
06_KLICKR	237	2	237	0	0	133	131	136	129	140	5/13/2022	5
07_DESCSP	771	6	771	0	0	125	122	136	116	140	5/5/2022	14
08_JOHNDR	484	3	484	0	0	123	121	124	114	126	5/3/2022	3
09_YAKIMA	1,764	16	1,764	0	0	131	124	140	121	152	5/11/2022	16
10_UCOLSP	7,088	60	5,777	1,311	0	135	126	151	121	181	5/15/2022	25
11_TUCANO	122	1	121.669	0	0	117	115	119	110.85	120	4/27/2022	4
12_HELLSC	8,773	79	8,118	656	0	135	124	150	116	176	5/15/2022	26
13_SFSALM	5,506	47	3,539	1,967	0	154	145	176	126	184	6/3/2022	31
14_CHMBLN	350	6	350	0	0	144	140.25	146	135	148	5/24/2022	6
15_MFSALM	2,140	19	2,140	0	0	133	123	143	116	156.4	5/13/2022	20
16_UPSALM	3,178	30	2,522	656	0	146	135	163	130	181	5/26/2022	28
17_DESCFA	3,921	16	0	0	3,921	243	237	254	224	278	8/31/2022	17
18_UCOLSF	71,689	429	4,591	6,459	60,639	248	242	256	162	277	9/5/2022	14
19_SRFALL	18,817	85	0	824	17,993	245	240	253	216	269	9/2/2022	13
20_BONPOOLSP	-	-	-	-	-	-	-	-	-	-	-	-
21_UMATILLASP	-	-	-	-	-	-	-	-	-	-	-	-
22_BONPOOLFA	-	-	-	-	-	-	-	-	-	-	-	-
23_UMATILLAFA	-	-	-	-	-	-	-	-	-	-	-	-
Total	141,588	853	30,791	13,182	97,615							

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.

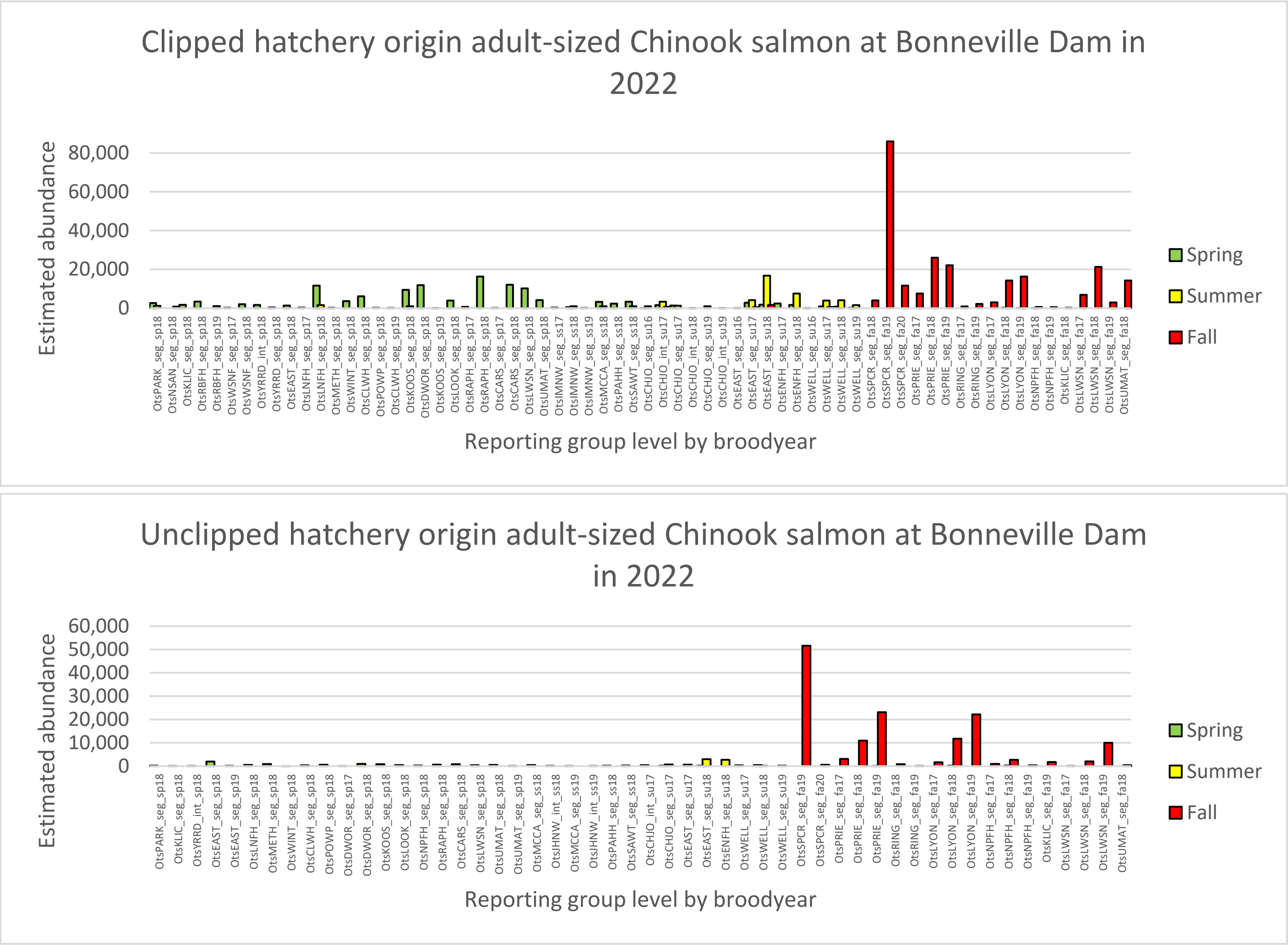
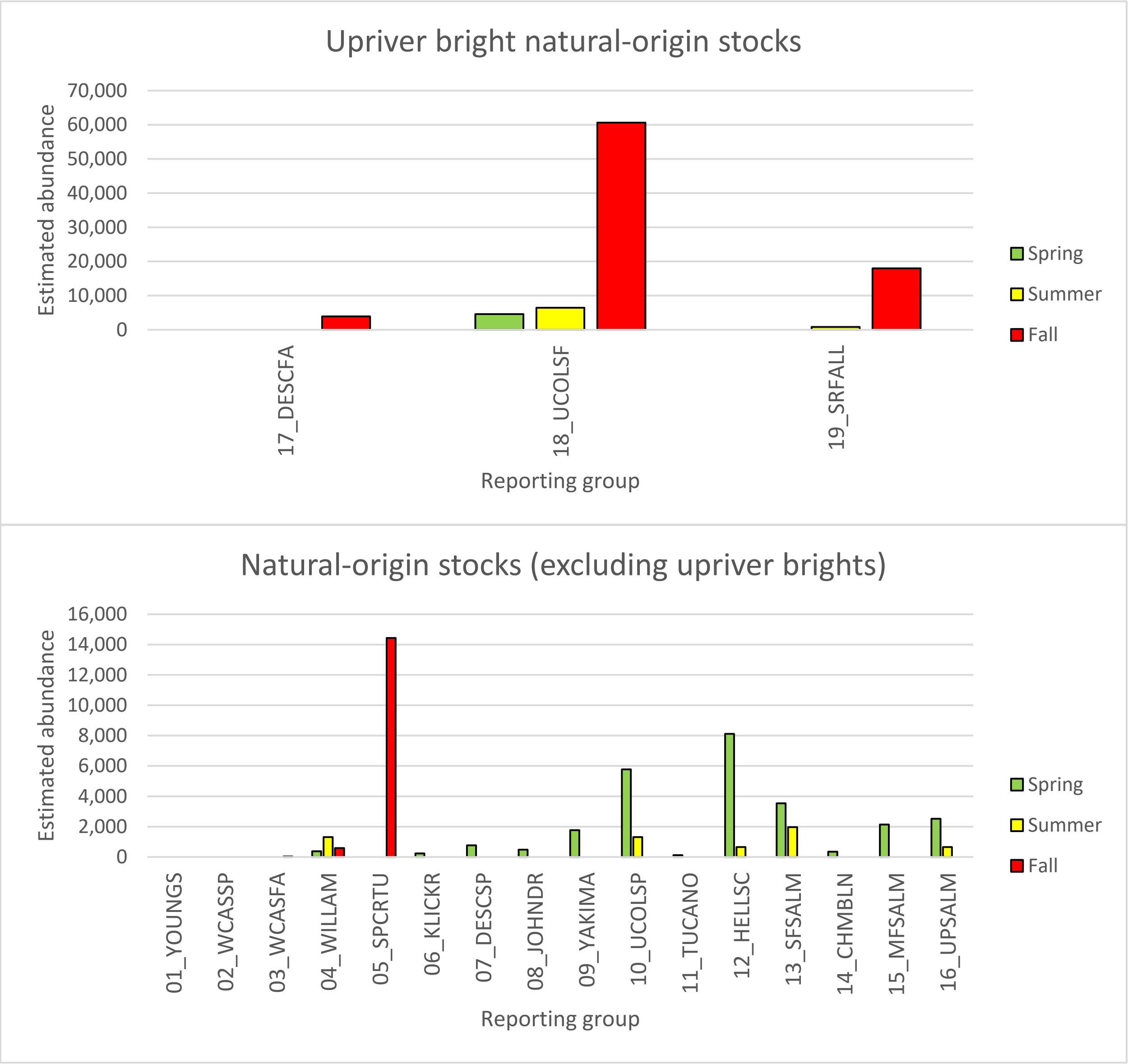


Figure 27. Estimated abundance of clipped (top) and unclipped (bottom) hatchery origin adult-sized Chinook salmon assigned to PBT broodstock groups that were sampled at Bonneville Dam in 2022 during spring (green), summer (yellow) and fall (red) management periods.

There were 11 major (i.e., abundance >1000 fish) Chinook salmon stocks represented in the total estimated relative abundance (N=141,588) of natural-origin (i.e., excluding unclipped hatchery-origin fish) Chinook salmon passing Bonneville Dam in 2022 (Table 50;Figure 29). These natural-origin stocks in order of decreasing magnitude were 18_UCOLSF (71,689), 19_SRFALL (18,817), 05_SPCRTU (14,435), 12_HELLSC (8,773), 10_UCOLSP (7,088), 13_SFSALM (5,506), 17_DESCFA (3,921), 16_UPSALM (3,178), 04_WILLAM (2,279), 15_MFSALM (2,140), and 09_YAKIMA(1,764). These stock abundance estimates were generated using SCOBI DEUX and SPIBETR functions and the estimates of clipped and unclipped adults distributed by TAC (Table 43).



Upriver bright natural-origin stocks

Natural-origin stocks (excluding upriver brights)

Figure 28. Estimated abundance of natural origin reporting groups (excluding unclipped hatchery-origin fish) of adult-sized Chinook salmon sampled at Bonneville Dam in 2022 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 2022

We plotted the run-timing distributions of the clipped and unclipped hatchery-origin Chinook salmon reporting group stocks (Figure 30) and provided the subtotals of reporting group abundance for each management period (clipped Table 46, unclipped Table 48). 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 10_UPCOLSP, 07_DESCSP, 16_UPSALM, 02_WCASSP, and 13_SFSALM was found to extend beyond the spring management period (total abundance in the summer period was 6,757 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 46, Table 48). 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 23% (15,353 fish) and 77% (52,558 fish) of the total abundance estimated in those two periods, respectively.

We also plotted run-timing distributions for each broodstock of clipped (Figure 32) and unclipped (Figure 33) hatchery origins and provided the subtotals of these broodstock abundance estimates for each management period (clipped Table 47, unclipped Table 49). Although most stocks with sample sizes ≥ 5 had median dates that fit within their expected management period, there was one summer run Upper Columbia clipped broodstock from Entiat that had a median date in the spring (Figure 32); there was one spring/summer run hatchery clipped broodstock with sample size ≥ 5 that had median dates in the summer (OtsIMNW_seg_ss18).

We plotted the run-timing distributions of the natural-origin (excluding adipose unclipped hatchery-origin fish, Figure 31) Chinook salmon stocks and provide subtotals of abundance for each management period (Table 50). 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 4,589 fish). We also estimated that 85% (25,822 fish) of the natural origin spring stocks passed Bonneville Dam in the spring period and 15% (4,589 fish) of the spring stock abundance passed in the summer period (Table 50). 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 42% (4,591 fish) and 58% (6,459 fish) of the total abundance estimated in those two periods, respectively.

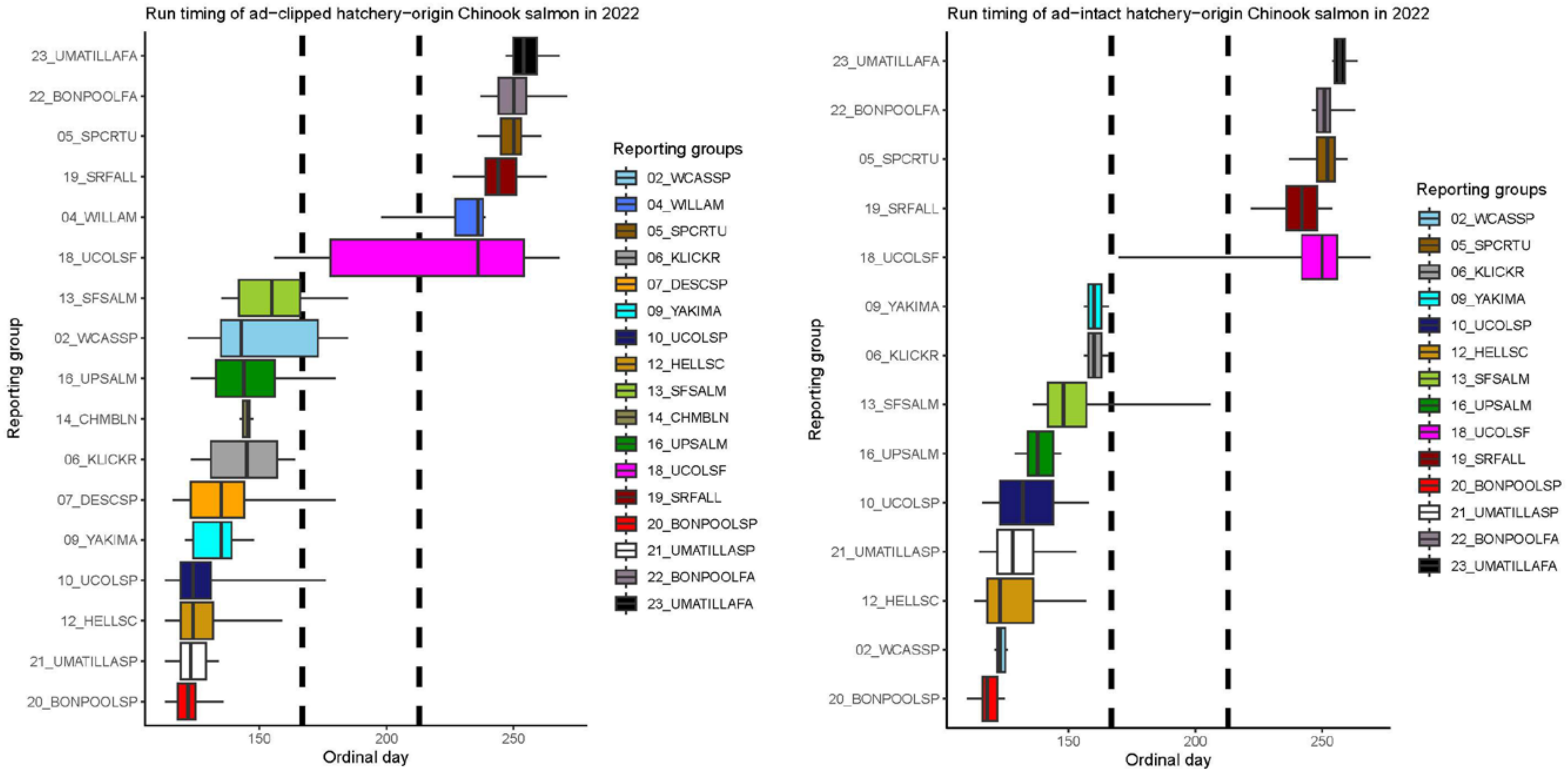


Figure 29. Reporting group-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for clipped and unclipped hatchery-origin adult-sized Chinook salmon that were sampled at Bonneville Dam in 2022 during the spring, summer, and fall management periods (separated by dashed lines).

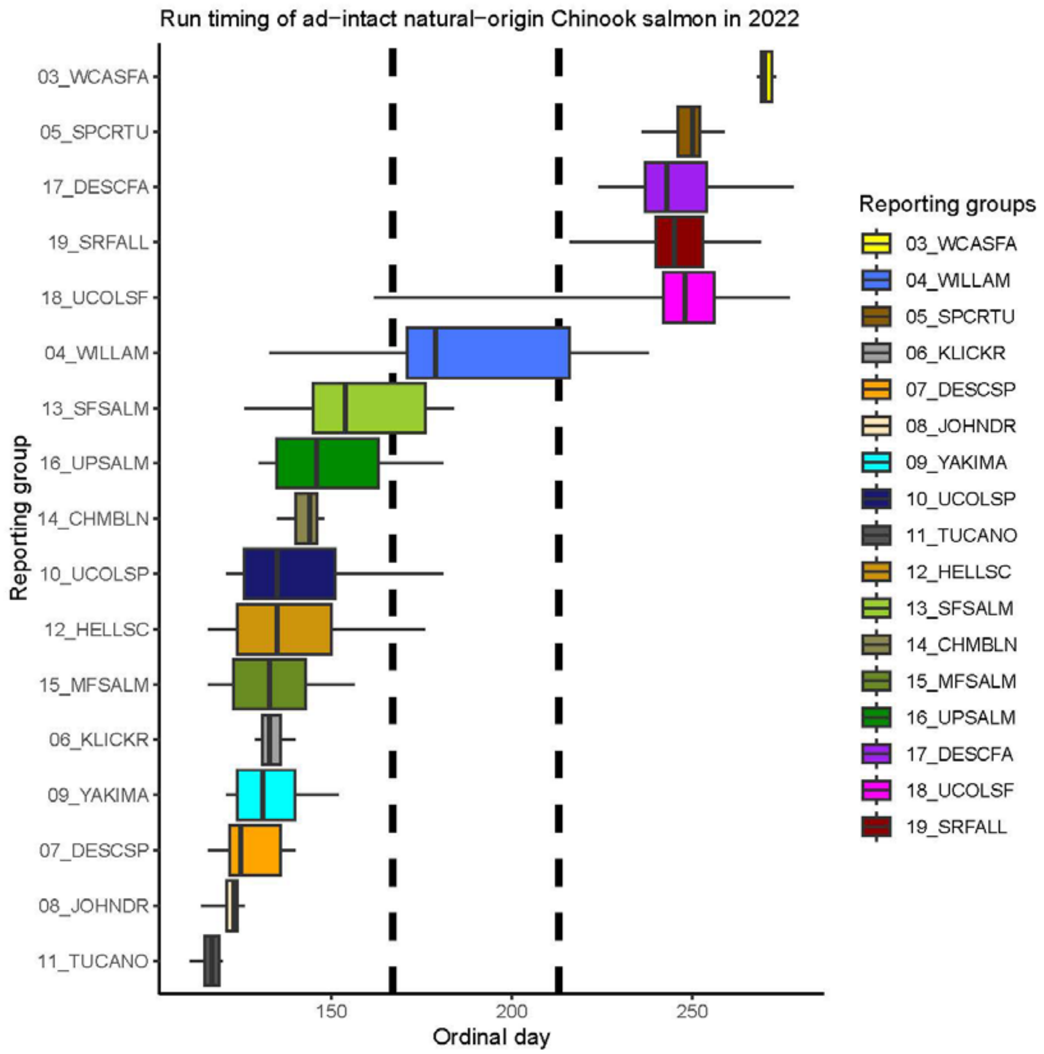


Figure 30. Reporting group-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for natural-origin adult-sized Chinook salmon that were sampled at Bonneville Dam in 2022 during the spring, summer, and fall management periods (separated by dashed lines).

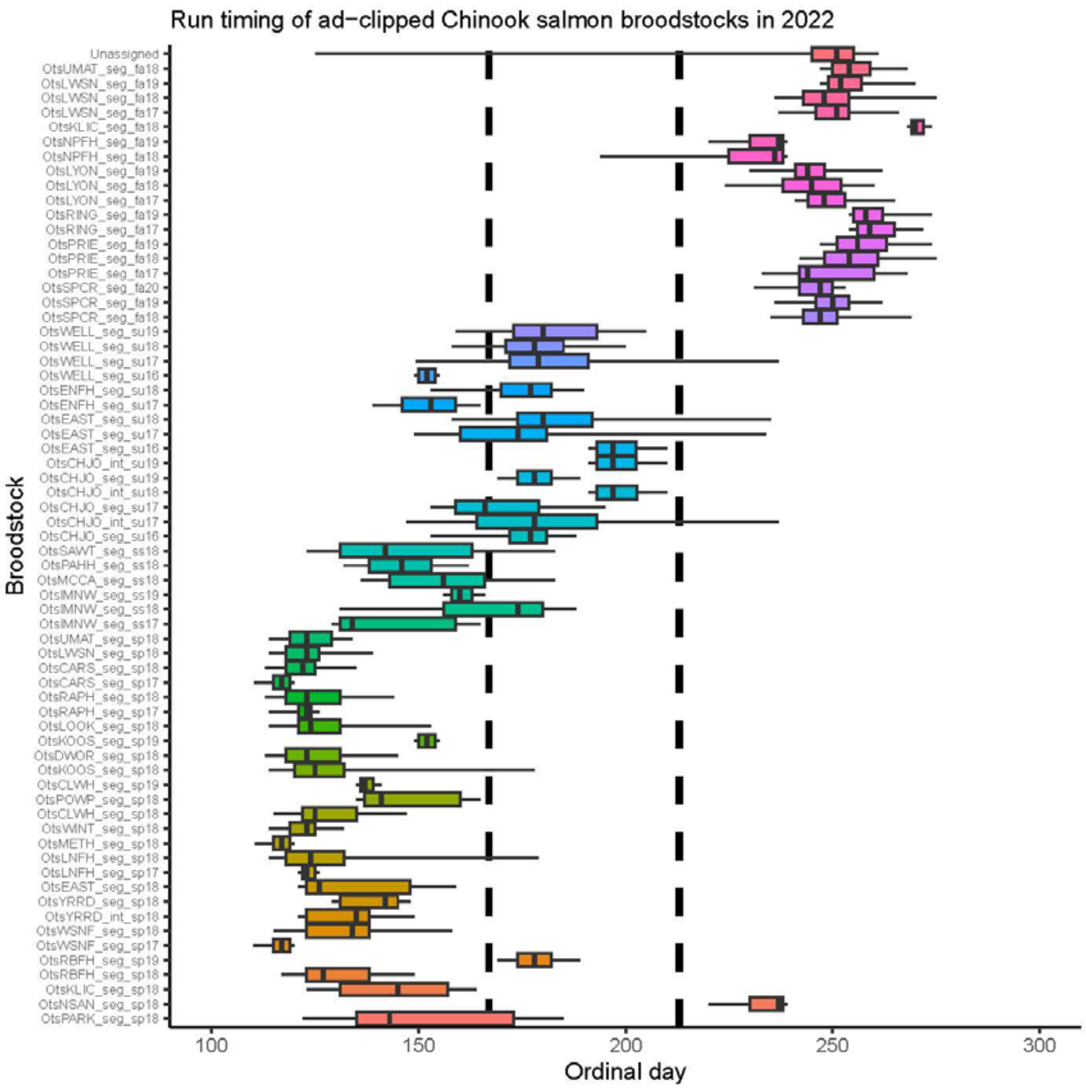


Figure 31. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for clipped adult-sized Chinook salmon that were sampled at Bonneville Dam in 2022 during the spring, summer, and fall management periods (separated by dashed lines).

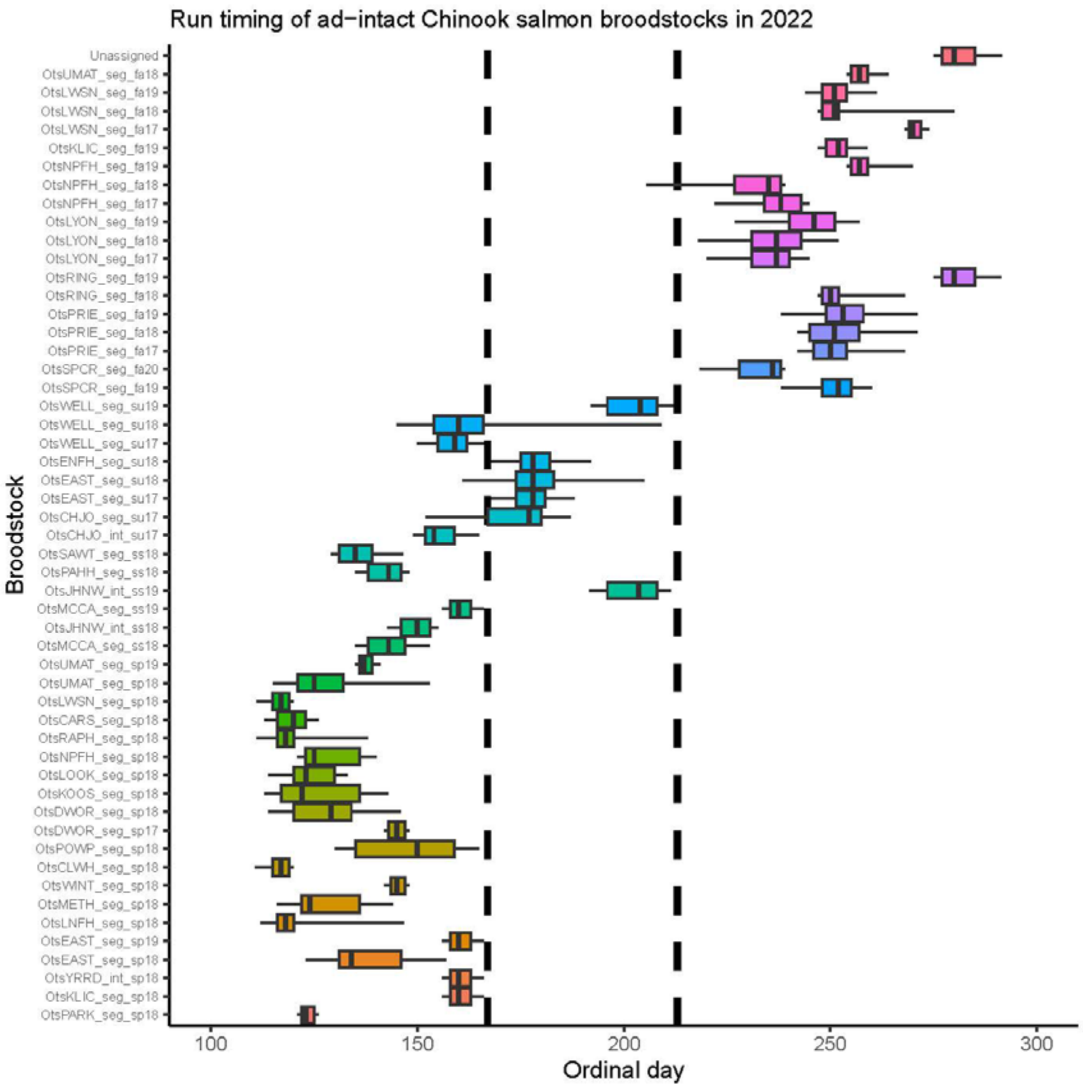


Figure 32. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for unclipped adult-sized Chinook salmon that were sampled at Bonneville Dam in 2022 during the spring, summer, and fall management periods (separated by dashed lines).

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 2021 – 2022

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 2018 (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 SY2018 broodstocks that returned to Bonneville Dam as adults in 2021 and 2022 (i.e., 3- and 4-year-olds, respectively). Inclusion of the abundance estimates from 2021 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 (0.34) of the linear trend (Figure 34). 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 R2 (0.44) 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 second analysis where we summed abundance of a single broodyear of adult return across age-classes (i.e., ages 3 and 4) that passed Bonneville Dam in consecutive years. 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 323 Spring Chinook salmon smolts released converted to 1 adult-sized 4-year-old Spring Chinook salmon returned to Bonneville Dam in 2022. In addition, we observed a trend of 333 Fall Chinook salmon smolts converted to 1 adult-sized 3- or 4-year-old Summer/Fall Chinook salmon returned to Bonneville Dam combined across 2021 and 2022.

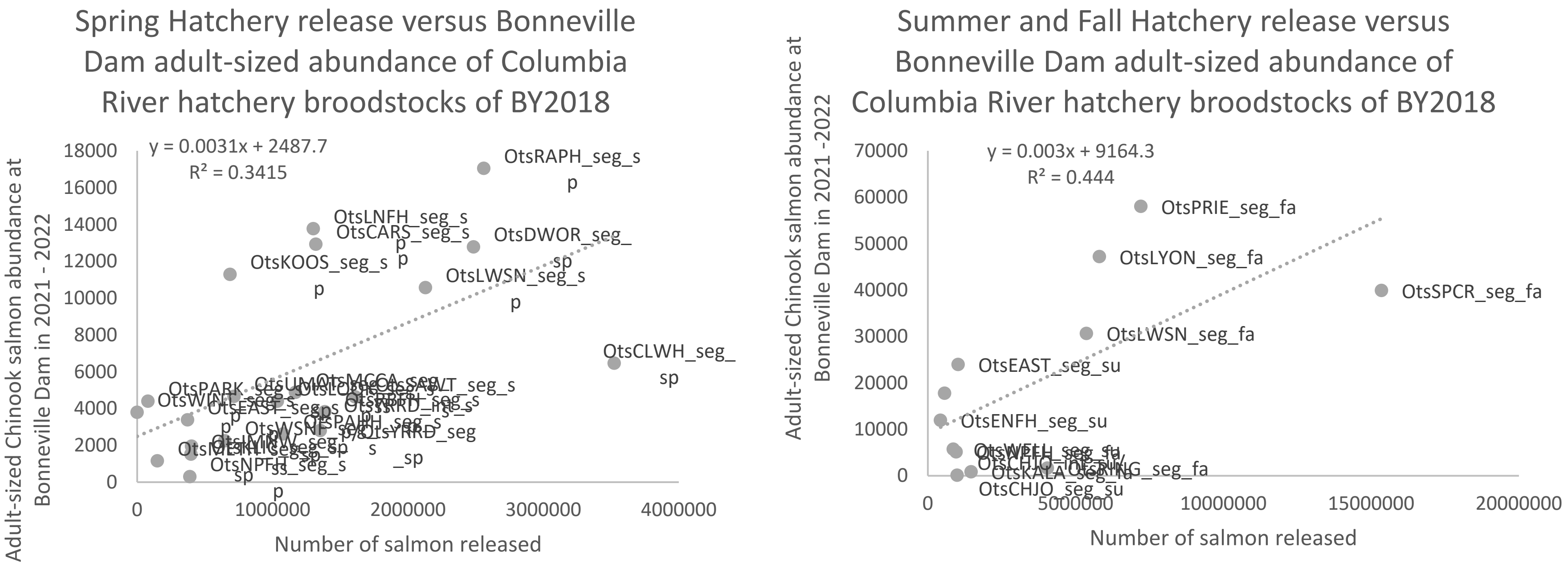


Figure 33. Smolt release numbers of hatchery-origin Spring Chinook salmon (left) and Summer/Fall Chinook (right) of BY2018 from Columbia River hatcheries above Bonneville Dam versus the estimated abundance of BY2018 adult-sized fish that passed Bonneville Dam in 2021 – 2022.

Estimated relative abundance of steelhead stocks in 2022

Daily passage of summer A-/B-Index steelhead at Bonneville Dam in 2022 is provided in Figure 35. Among clipped hatchery-origin summer A-/B-Index steelhead, there were five major stocks (abundance >1000) represented in the total estimated abundance (N=82,033) of clipped hatchery origin steelhead passing Bonneville Dam in 2022 (Table 51). These stocks in order of decreasing magnitude were 07_MGILCS (27,302), 10_SFCLWR (20,174, B-Index; 3,942, A-Index), 14_UPSALM (19,830), 09_UPPCOL (5,701, A-Index; 1,100, B-Index), and 03_SKAMAN (3,008) (Table 51; Figure 36). All of these major clipped stocks were A-Index size fish except for 10_SFCLWR and 09_UPPCOL which had a combination of both A-Index and B-Index fish.

Among the unclipped hatchery-origin summer A-/B-Index steelhead, there were two major stocks (abundance >1000) represented in the total estimated abundance (N=5,025) of unclipped hatchery origin steelhead passing Bonneville Dam in 2022 (Table 52; Figure 36). These stocks in order of decreasing magnitude were 14_UPSALM (1,736, A-Index) and 10_SFCLWR (1,471, B-Index).

Using PBT assignments we can now provide abundance (Table 54; Figure 37) and run-timing estimates for each of the clipped and unclipped hatchery broodstocks (Table 54). There were 15 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 2022 (Table 54). These stocks in order of decreasing magnitude were OmyDWOC_su19 (21114 total; A-Index = 2401 and B-Index = 18714), OmyWALL_su19 (8532 total; A-Index = 8532 and B-Index = 0), OmyCGRW_su19 (7002 total; A-Index = 7002 and B-Index = 0), OmyPAHH_su19 (6997 total; A-Index = 6908 and B-Index = 89), OmyWELL_su19 (5994 total; A-Index = 4894 and B-Index = 1100), OmyOXBO_su19 (5477 total; A-Index = 5442 and B-Index = 36), OmySFCR_su19 (3218 total; A-Index = 571 and B-Index = 2646), OmyUSAL_su19 (3184 total; A-Index = 1921 and B-Index = 1262), OmySKAM_su19 (3020 total; A-Index = 3020 and B-Index = 0), OmySAWT_su19 (2847 total; A-Index = 2847 and B-Index = 0), OmyCGRW_su20 (2011 total; A-Index = 2011 and B-Index = 0), OmyWALL_su20 (1888 total; A-Index = 1888 and B-Index = 0), OmyROUN_su19 (1764 total; A-Index = 1764 and B-Index = 0), OmyLSCR_su19 (1463 total; A-Index = 1463 and B-Index = 0), and OmySAWT_su20 (1259 total; A-Index = 1259 and B-Index = 0). Almost all of these abundances were dominated by A-Index fish except for four major B-Index stocks (OmyDWOC_su19, OmyWELL_su19, OmySFCR_su19, and OmyUSAL_su19).

There were four major stocks (abundance >1000) represented in the total estimated abundance (N=29,911) of natural origin (excluding adipose unclipped hatchery-origin fish) summer A-/B-Index steelhead passing Bonneville Dam in 2022 (Table 53). These stocks in order of decreasing magnitude were 07_MGILCS (17,835 A-Index; 1,831 B-Index), 14_UPSALM (2,097 A-Index), 11_UPCLWR (1,593 B-Index), and 06_KLICKR (1,308 A-Index). This year the 07_MGILCS was the stock observed to have the greatest abundance of natural-origin B-Index.

Table 51. Stock-specific abundance and run-timing by A-/B-Index categories of clipped hatchery-origin summer A-/B-Index steelhead passing Bonneville Dam in 2022.

						Run-timing distribution						
	Hatchery origin- Clipped					Ordinal day						
Size	**Reporting Group name**	**Reporting Group Code**	Sample N	**Estimated abundance**			1st	3rd	5th	95th	Median	Interquartile
				Mean	**95% CI**	Median	quartile	quartile	percentile	percentile	date	range (days)
A-INDEX	Lower Columbia	02_LOWCOL	0			-	-	-	-	-	-	-
	Skamania	03_SKAMAN	15	3,008	2288 – 3891	203	194	220	186	254	7/22/2022	26
	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	154	27,302	24233 – 30831	221	202	243	188	260	8/9/2022	41
	Yakima	08_YAKIMA	0			-	-	-	-	-	-	-
	upper Columbia	09_UPPCOL	25	5,701	3113 – 7266	215	202	240	188	258	8/3/2022	38
	SF Clearwater	10_SFCLWR	34	3,942	2372 – 5744	254	244	263	232	277	9/11/2022	19
	upper Clearwater	11_UPCLWR	0			-	-	-	-	-	-	-
	SF Salmon	12_SFSALM				-	-	-	-	-	-	-
	MF Salmon	13_MFSALM	0			-	-	-	-	-	-	-
	upper Salmon	14_UPSALM	128	19,830	17112 – 21789	224	206	243	189	264	8/12/2022	37
		A-INDEX Subtotal	**356**	**59,784**								
B-INDEX	Lower Columbia	02_LOWCOL				-	-	-	-	-	-	-
	Skamania	03_SKAMAN	1	174	0 – 376	195	190	200	184	204.2	7/14/2022	10
	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	1	0	0 – 53	-	-	-	-	-	-	-
	Yakima	08_YAKIMA				-	-	-	-	-	-	-
	upper Columbia	09_UPPCOL	6	1,100	206 – 2145	233	228	252	191	262	8/21/2022	24
	SF Clearwater	10_SFCLWR	205	20,174	17195 – 23507	255	244	264	229	279	9/12/2022	20
	upper Clearwater	11_UPCLWR	0			-	-	-	-	-	-	-
	SF Salmon	12_SFSALM	0			-	-	-	-	-	-	-
	MF Salmon	13_MFSALM	0			-	-	-	-	-	-	-
	upper Salmon	14_UPSALM	10	801	305 – 2042	261	251	268	241	281	9/18/2022	17
		B-INDEX Subtotal	**223**	**22,249**								

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.

Table 52. Stock-specific abundance and run-timing by A-/B-Index categories of unclipped hatchery-origin summer A-/B-Index steelhead passing Bonneville Dam in 2022.

						Run-timing distribution						
	Hatchery origin-Unclipped					Ordinal day						
Size	**Reporting Group name**	**Reporting Group Code**	Sample N	**Estimated abundance**			1st	3rd	5th	95th	Median	Interquartile
				Mean	**95% CI**	Median	quartile	quartile	percentile	percentile	date	range (days)
A-INDEX	Lower Columbia	02_LOWCOL	0									
	Skamania	03_SKAMAN	1	203	0 – 407	195	190	200	184	204	7/14/2022	10
	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	2	290	0 – 601	199	192	227	185	231	7/18/2022	35
	Yakima	08_YAKIMA	0									
	upper Columbia	09_UPPCOL	1	174	0 – 514	213	209	220	206	225	8/1/2022	
	SF Clearwater	10_SFCLWR	12	549	258 – 822	265	263	271	228	290	9/22/2022	8
	upper Clearwater	11_UPCLWR	0									
	SF Salmon	12_SFSALM										
	MF Salmon	13_MFSALM	0									
	upper Salmon	14_UPSALM	12	1,736	936 – 2807	240	208	253	189	270	8/28/2022	45
		A-INDEX Subtotal	**28**	**2,953**								
B-INDEX	Lower Columbia	02_LOWCOL										
	Skamania	03_SKAMAN	0	0	0 – 0							
	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	0	0	0 – 0							
	Yakima	08_YAKIMA										
	upper Columbia	09_UPPCOL	0	0	0 – 0							
	SF Clearwater	10_SFCLWR	31	1,471	1020 – 1909	272	261	281	231	298	9/29/2022	20
	upper Clearwater	11_UPCLWR	0									
	SF Salmon	12_SFSALM	0									
	MF Salmon	13_MFSALM	0									
	upper Salmon	14_UPSALM	8	601	279 – 1205	256	243	264	228	267	9/13/2022	21
		B-INDEX Subtotal	**39**	**2,073**								

Table 53. Stock-specific abundance and run-timing by A-/B-Index categories of unclipped natural-origin summer A-/B-Index steelhead passing Bonneville Dam in 2022.

	Natural origin- No Clip					Run-timing distribution						
						Ordinal day						
Size	**Reporting Group name**	**Reporting Group Code**	Sample N	**Estimated abundance**		Median	1st quartile	3rd quartile	5th percentile	95th percentile	Median date	Interquartile range (days)
				Mean	**95% CI**							
A-INDEX	Lower Columbia	02_LOWCOL	4	784	203 – 1394	198	191	205	184	220.95	7/17/2022	14
	Skamania	03_SKAMAN	0			-	-	-	-	-	-	-
	Willamette	04_WILLAM				-	-	-	-	-	-	-
	Big White Salmon	05_BWSALM				-	-	-	-	-	-	-
	Klickitat	06_KLICKR	10	1,308	622 – 2088	219	202	242	187	276	8/7/2022	40
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	108	17,835	15824 – 19652	209	197	221	187	252	7/28/2022	24
	Yakima	08_YAKIMA	4	638	174 – 1248	211	201	221	187	230	7/30/2022	20
	upper Columbia	09_UPPCOL	4	638	174 – 1248	211	201	221	187	230	7/30/2022	20
	SF Clearwater	10_SFCLWR	7	466	71 – 1012	251	240	260	228	282	9/8/2022	20
	upper Clearwater	11_UPCLWR	6	981	307 – 1775	250	242	256	229	272	9/7/2022	14
	SF Salmon	12_SFSALM		0	0 – 0	-	-	-	-	-	-	-
	MF Salmon	13_MFSALM	5	943	275 – 1724	211	197	241	186	257	7/30/2022	45
	upper Salmon	14_UPSALM	12	2,097	1101 – 3163	228	198	247	187	260	8/16/2022	49
		A-INDEX Subtotal	**160**	**25,689**								
B-INDEX	Lower Columbia	02_LOWCOL		0	0 – 0	-	-	-	-	-	-	-
	Skamania	03_SKAMAN	0			-	-	-	-	-	-	-
	Willamette	04_WILLAM				-	-	-	-	-	-	-
	Big White Salmon	05_BWSALM				-	-	-	-	-	-	-
	Klickitat	06_KLICKR	1	36	0 – 107	286	279	293	276	301	10/13/2022	14
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	8	1,831	830 – 2948	244	233	254	194	260	9/1/2022	21

	Yakima	08_YAKIMA		0	0 – 0	-	-	-	-	-	-	-
	upper Columbia	09_UPPCOL	0	0	0 – 0	-	-	-	-	-	-	-
	SF Clearwater	10_SFCLWR	7	278	115 – 495	265	231	279	227	297	9/22/2022	48
	upper Clearwater	11_UPCLWR	17	1,593	777 – 2541	248	231	260	213	271	9/5/2022	29
	SF Salmon	12_SFSALM	2	210	0 – 558	216	210	224	206	266	8/4/2022	14
	MF Salmon	13_MFSALM	1	274	0 – 826	250	243	255	238	260	9/7/2022	12
	upper Salmon	14_UPSALM	0	0	0 – 0	-	-	-	-	-	-	-
		B-INDEX Subtotal	**36**	**4,222**								

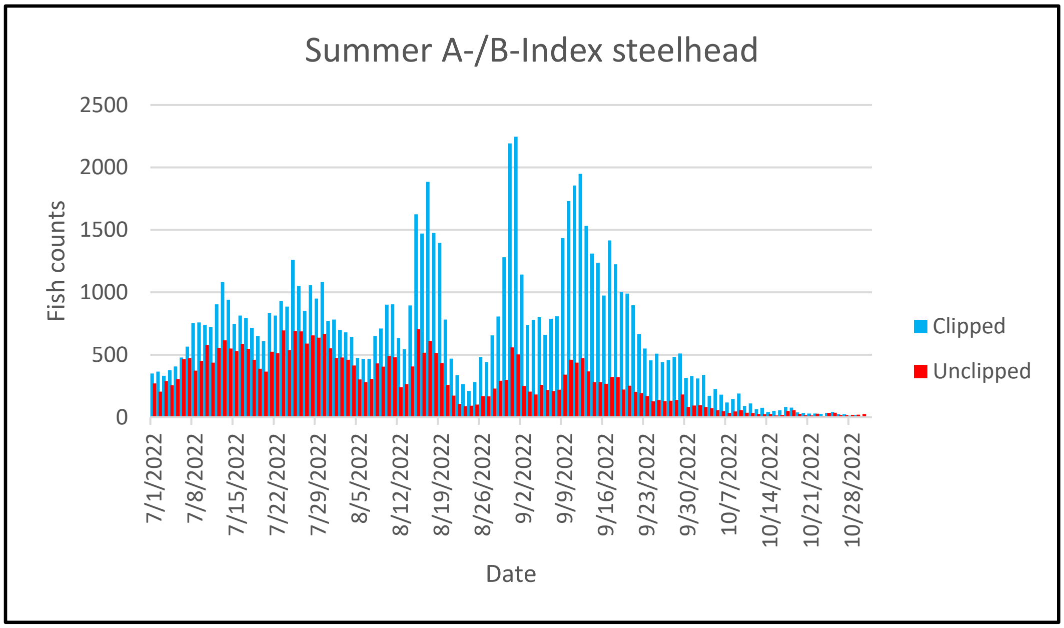


Figure 34. Daily passage of clipped (blue) and unclipped (red) steelhead at Bonneville Dam in 2022 during the summer A-/B-Index management period (source: https://www.fpc.org).

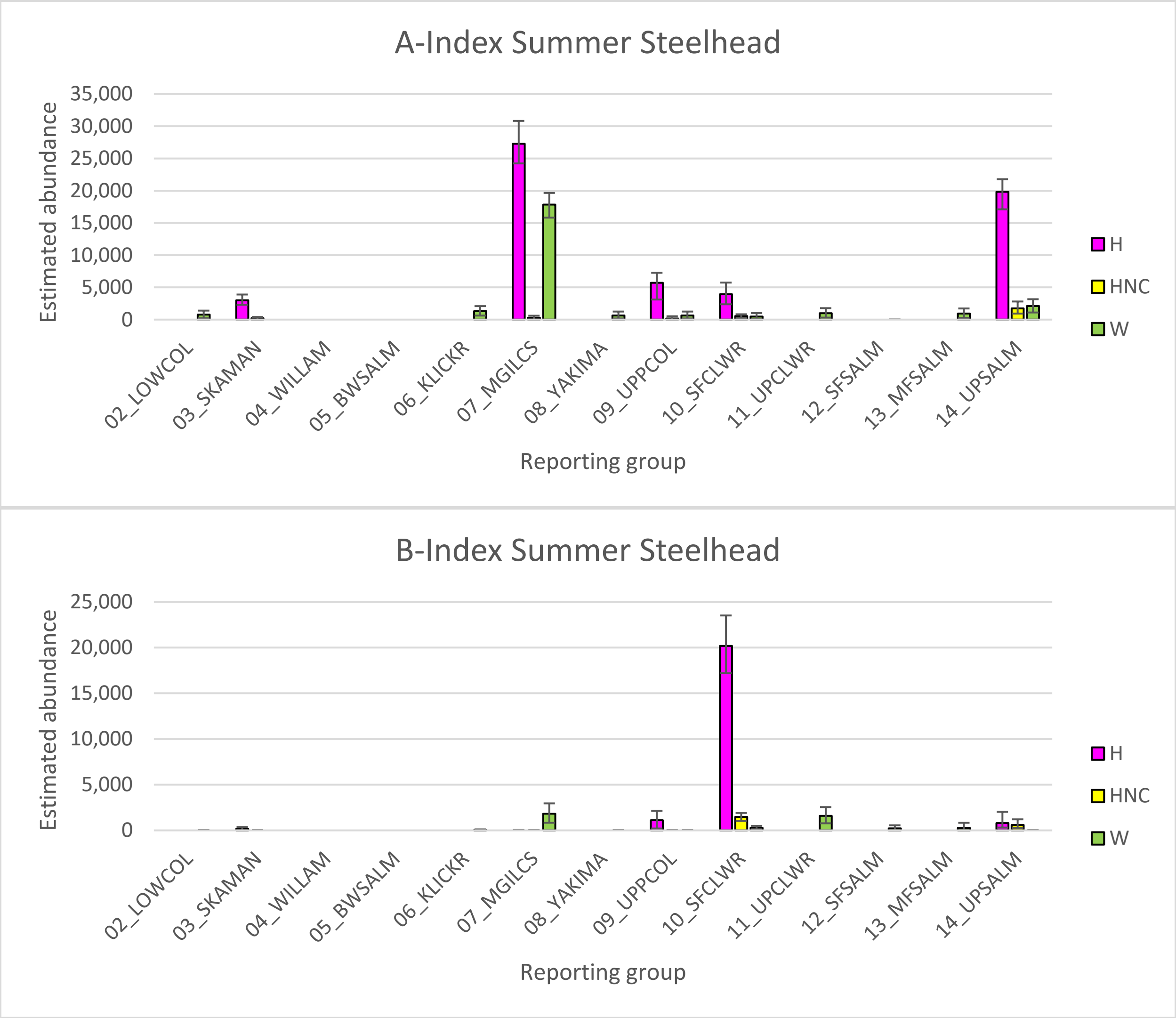


Figure 35. Estimated abundance (± 95% CI) of A-Index (<780mm FL, top) and B-Index (>=780mm FL, bottom) hatchery origin (clipped "H" and unclipped "HNC") and natural-origin ("W") steelhead assigned to genetic stock of origin that were sampled at Bonneville Dam in 2022.

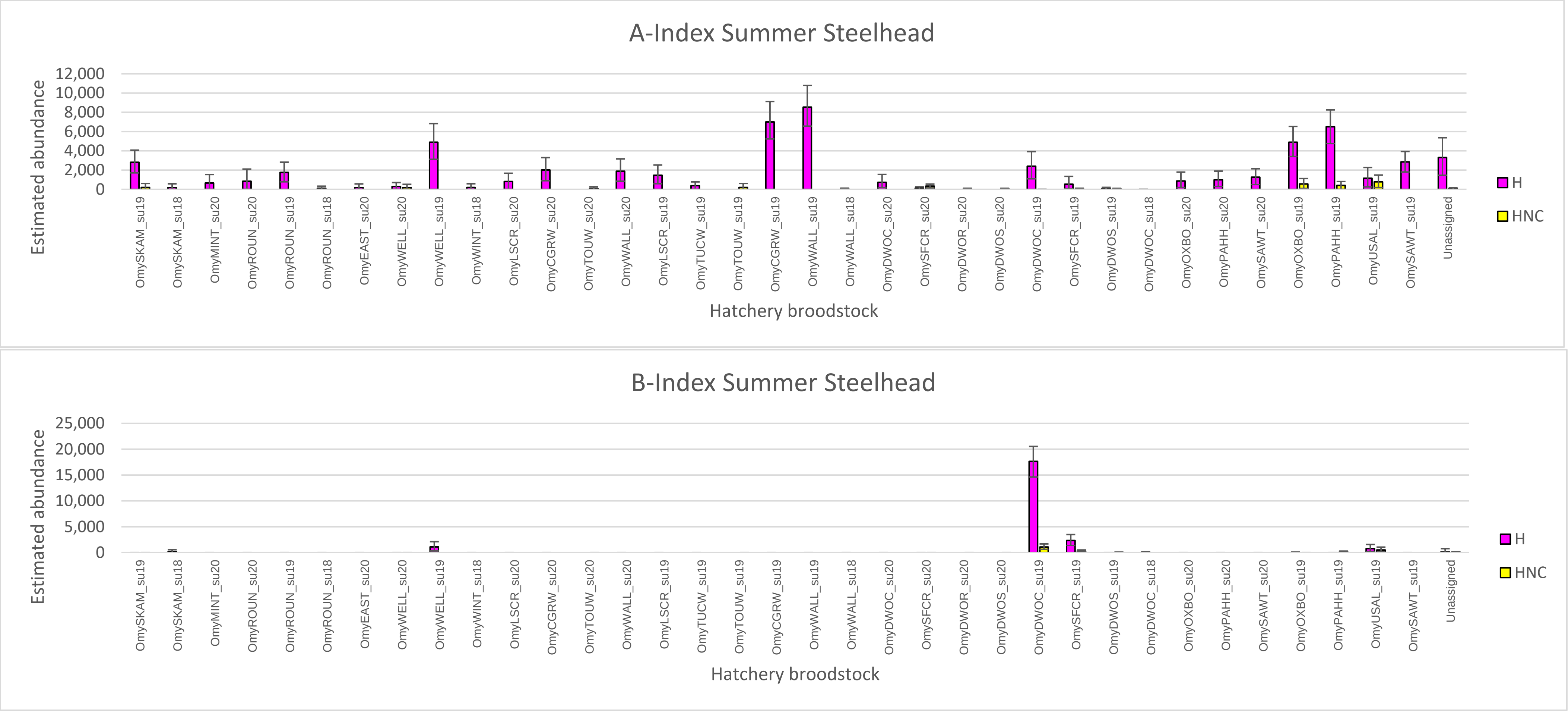


Figure 36. Estimated abundance (± 95% CI) of A-Index (<780mm FL, top) and B-Index (>=780mm FL, bottom) hatchery origin steelhead (adipose clipped and unclipped) assigned to broodstock of origin that were sampled at Bonneville Dam in 2022.

Key to broodstock collection is presented in Appendix 4.

Table 54. Hatchery broodstock-specific estimated abundance of clipped and unclipped A-Index and B-Index PBT-assigned steelhead passing Bonneville Dam in 2022.

					Hatchery clipped				Hatchery Unclipped			
					A-INDEX		B-INDEX		A-INDEX		B-INDEX	
Hatchery	**Stock**	**GSI RepGrp**	**Broodstock**	**Broodyear**	**Est.**	**95% CI**	**MLE**	**95% CI**	**MLE**	**95% CI**	**MLE**	**95% CI**
Skamania Hatchery	Summer	03_SKAMAN	OmySKAM_su19	2019	2,817	1710 – 4069	0	0 – 0	203	0 – 610	0	0 – 0
Skamania Hatchery	Summer	03_SKAMAN	OmySKAM_su18	2018	191	0 – 574	174	0 – 543				
Minthorn Springs Satellite	Minthorn Springs	07_MGILCS	OmyMINT_su20	2020	654	0 – 1537	0	0 – 0				
Round Butte	Deschutes River	07_MGILCS	OmyROUN_su20	2020	841	0 – 2102	0	0 – 0				
Round Butte	Deschutes River	07_MGILCS	OmyROUN_su19	2019	1,764	782 – 2819	0	0 – 0				
Round Butte	Deschutes River	07_MGILCS	OmyROUN_su18	2018	109	0 – 326	0	0 – 0				
Eastbank	Wenatchee	09_UPPCOL	OmyEAST_su20	2020	187	0 – 562	0	0 – 0				
Wells Fish Hatchery	WMET/WOKA/WOMA/WELLS	09_UPPCOL	OmyWELL_su20	2020	299	0 – 706	0	0 – 0	174	0 – 522	0	0 – 0
Wells Fish Hatchery	WMET/WOKA/WOMA/WELLS	09_UPPCOL	OmyWELL_su19	2019	4,894	3115 – 6828	1,100	296 – 2104				
Winthrop NFH	Methow River	09_UPPCOL	OmyWINT_su18	2018	193	0 – 579	0	0 – 0				
Little Sheep Satellite	Imnaha	07_MGILCS	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_MGILCS	OmyCGRW_su20	2020	2,011	895 – 3296	0	0 – 0				
Lyons Ferry Hatchery	Touchet (in Walla Walla River basin)	07_MGILCS	OmyTOUW_su20	2020					87	0 – 261	0	0 – 0
Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGILCS	OmyWALL_su20	2020	1,888	841 – 3161	0	0 – 0				
Little Sheep Satellite	Imnaha	07_MGILCS	OmyLSCR_su19	2019	1,463	584 – 2526	0	0 – 0				
Lyons Ferry Hatchery	Tucannon	07_MGILCS	OmyTUCW_su19	2019	387	0 – 775	0	0 – 0				
Lyons Ferry Hatchery	Touchet (in Walla Walla River basin)	07_MGILCS	OmyTOUW_su19	2019					203	0 – 610	0	0 – 0
Wallowa Fish Hatchery	Wallowa stock -released at Cottonwood and other Washington sites	07_MGILCS	OmyCGRW_su19	2019	7,002	5235 – 9120	0	0 – 0				
Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGILCS	OmyWALL_su19	2019	8,532	6558 – 10791	0	0 – 0				
Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGILCS	OmyWALL_su18	2018	40	0 – 120	0	0 – 0				
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su20	2020	734	175 – 1549	0	0 – 0				
Dworshak NFH	SF Clearwater	10_SFCLWR	OmySFCR_su20	2020	130	0 – 260	0	0 – 0	332	142 – 544	0	0 – 0
Dworshak NFH	All Dworshak stocks	10_SFCLWR	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_SFCLWR	OmyDWOS_su20	2020					36	0 – 107	0	0 – 0
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su19	2019	2,401	1097 – 3920	17,643	14624 – 20548	0	0 – 0	1,071	609 – 1669
Dworshak NFH	SF Clearwater	10_SFCLWR	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_SFCLWR	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_SFCLWR	OmyDWOC_su18	2018	0	0 – 0	53	0 – 160				
Oxbow (IDFG)	Oxbow	14_UPSALM	OmyOXBO_su20	2020	869	194 – 1789	0	0 – 0				
Pahsimeroi	Pashsimeroi	14_UPSALM	OmyPAHH_su20	2020	988	296 – 1892	0	0 – 0				
Sawtooth	Sawtooth	14_UPSALM	OmySAWT_su20	2020	1,259	495 – 2137	0	0 – 0				
Oxbow (IDFG)	Oxbow	14_UPSALM	OmyOXBO_su19	2019	4,887	3406 – 6529	36	0 – 107	555	93 – 1123	0	0 – 0
Pahsimeroi	Pashsimeroi	14_UPSALM	OmyPAHH_su19	2019	6,502	4752 – 8248	0	0 – 0	407	0 – 813	89	0 – 266
Pahsimeroi	Upper Salmon	14_UPSALM	OmyUSAL_su19	2019	1,147	250 – 2268	766	225 – 1566	775	191 – 1481	497	148 – 1045
Sawtooth	Sawtooth	14_UPSALM	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	

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 passed the Bonneville Dam at the fish counting window. Key to broodstock collection is presented in Appendix 4.

Run-timing of steelhead stocks in 2022

We were able to characterize the run-timing distributions at the broodstock level for the clipped (Figure 38) and unclipped (Figure 39) hatchery steelhead stocks arriving during the summer A-/B-Index management period. Very few winter-run steelhead stocks exist above Bonneville Dam and our sampling program at Bonneville AFF does not trap or collect fish between December and March when winter-run steelhead would be most likely to occur. The Skamania summer steelhead period is 4/1/2022 – 6/30/ 2022, and the summer A-/B-Index period begins on 7/1/2022 and lasts until 10/31/2022. For the clipped stocks arriving in the A-/B-Index period, the broodstock that typically has late run-timing is the Dworshak stock, which often arrives after August 25th (Ordinal day 237) at Bonneville Dam (Figure 38). There were a total of 31 different clipped hatchery broodstocks and of these 31, there were 14 broodstocks (OmyDWOC_su18, OmyDWOC_su19, OmyDWOC_su20, OmyDWOS_su19, OmyLSCR_su20, OmyMINT_su20, OmyOXBO_su19, OmyOXBO_su20, OmyROUN_su20, OmySAWT_su20, OmySFCR_su19, OmySFCR_su20, OmyUSAL_su19, and OmyWALL_su18) that had median dates that were observed after August 25th in 2022. For three broodstocks in which both A-Index and B-Index were represented, the B-Index stock had a later median date in all cases. For the unclipped stocks arriving in the A-/B-Index period, there were 13 unique broodstocks and 7 of them had a median run date after August 25th (Figure 39).

We characterized the run-timing distributions for natural-origin steelhead stocks (Figure 40); the patterns generally are consistent with past years. The late arriving stocks with median dates on or after August 25th were 07_MGILCS (A-Index), 11_UPCLWR (both A-Index and B-Index), 13_MFSALM (B-Index), 10_SFCLWR (both A-Index and B-Index), and 06_KLICKR (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 one reporting group (11_UPCLWR).

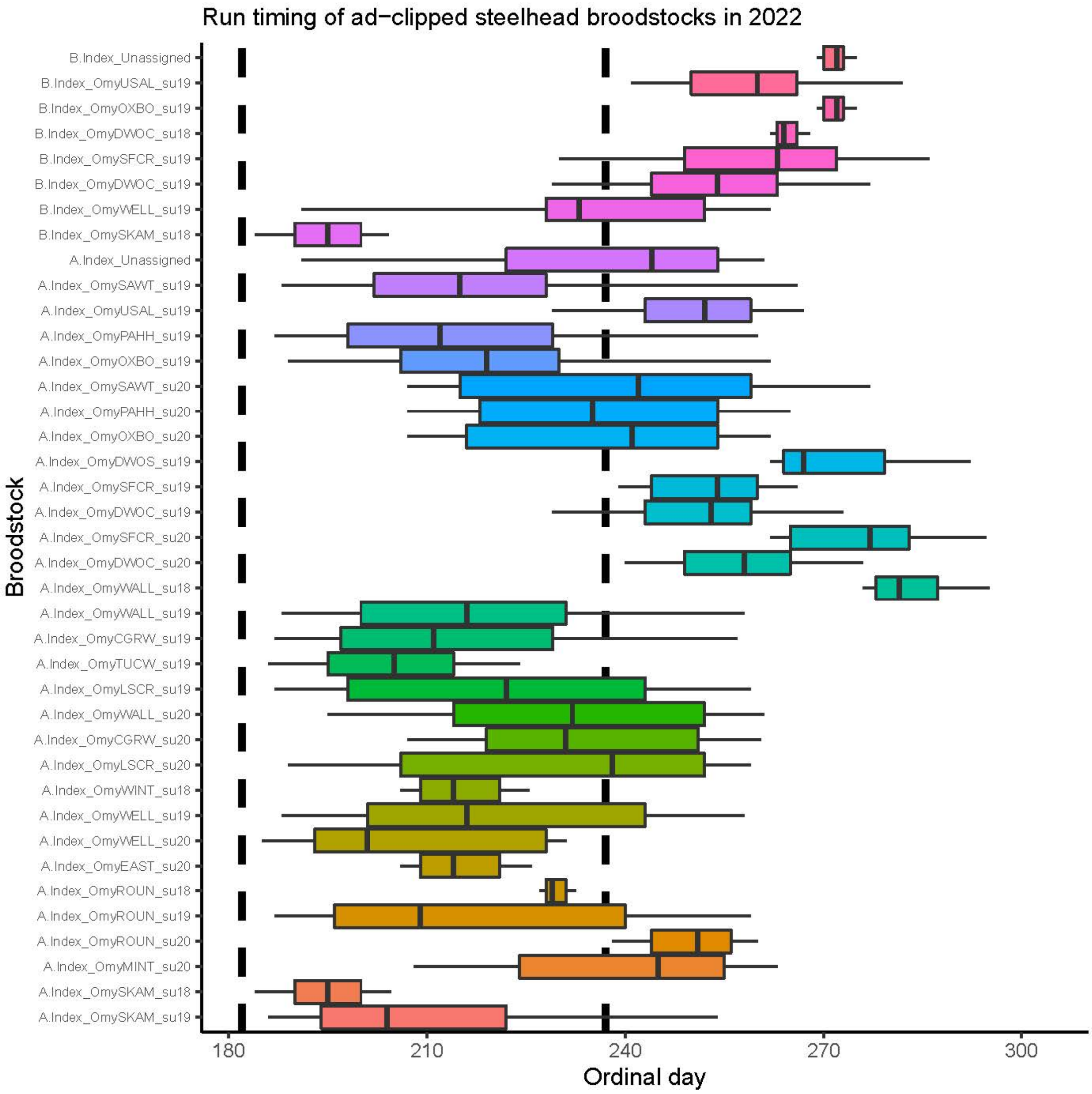


Figure 37. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for clipped hatchery-origin steelhead that were sampled at Bonneville Dam in 2022 and reported by A-Index and B-Index size category.

Key to broodstock collection is presented in Appendix 12.

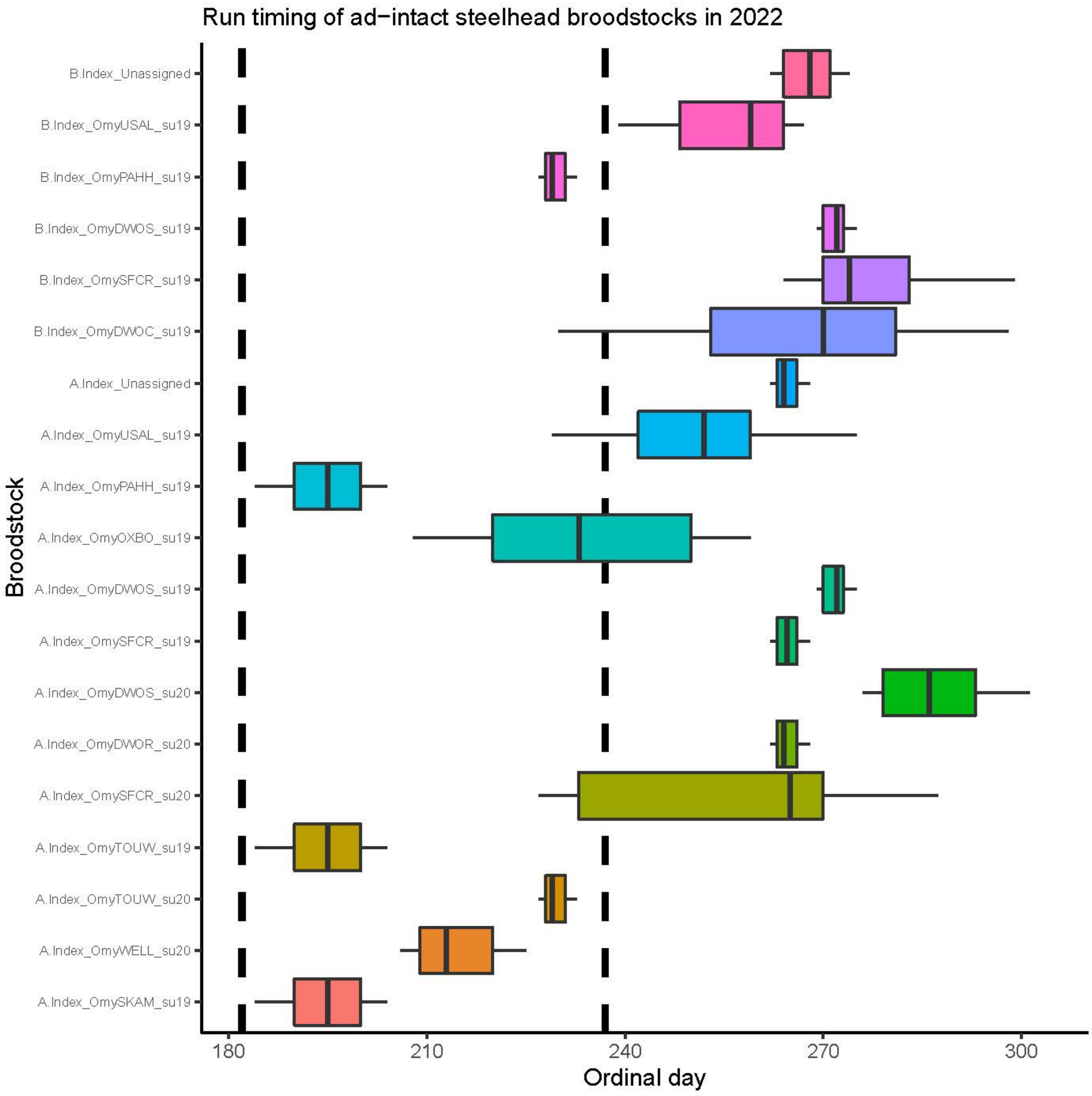


Figure 38. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for unclipped hatchery-origin steelhead that were sampled at Bonneville Dam in 2022 and reported by A-Index and B-Index size category.
Key to broodstock collection is presented in Appendix 12.

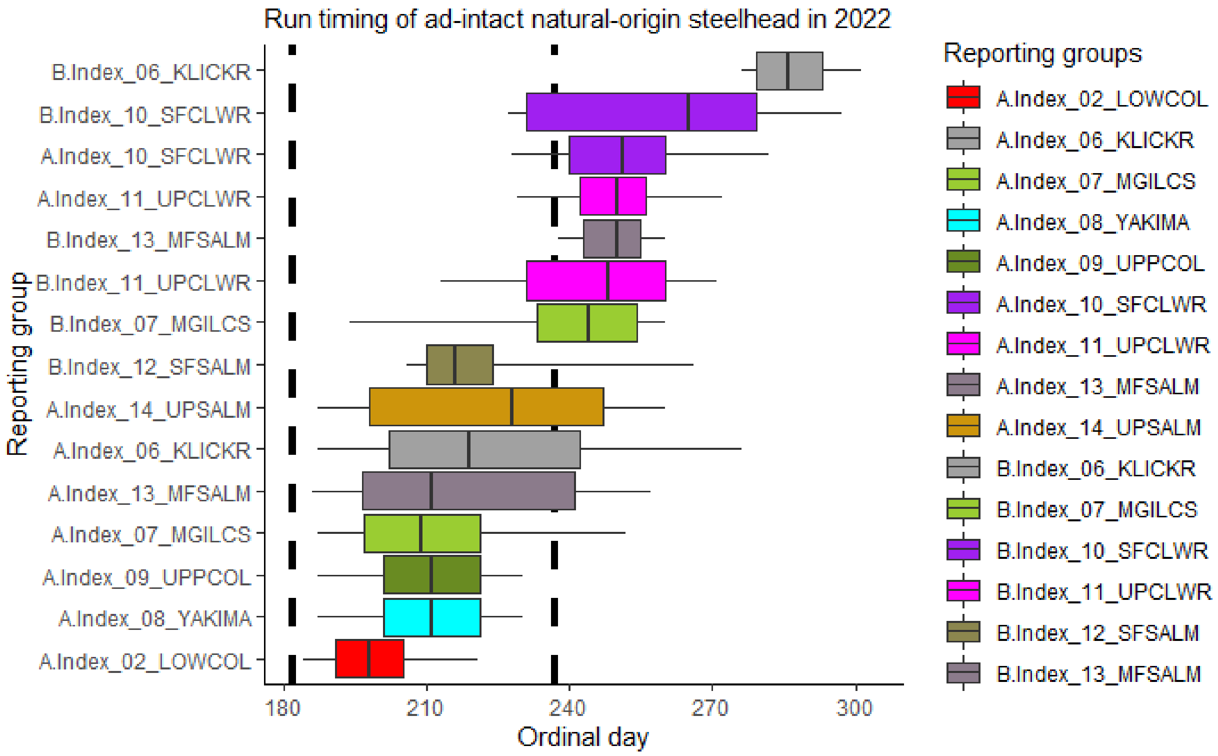


Figure 39. Reporting group level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for natural-origin steelhead (unclipped hatchery-origin fish excluded) that were sampled at Bonneville Dam in 2022 and split by A-Index and B-Index size category.

Estimated abundance and run-timing of Sockeye salmon stocks in 2022
Daily passage of Sockeye salmon at Bonneville Dam in 2022 is provided in Figure 41. Stock abundance for sockeye salmon was estimated over a course of 17 statistical weeks (i.e. weeks 22 – 39). A total of 1,303 sockeye salmon were sampled at Bonneville Dam in 2022 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 45). The Okanogan stock had the highest relative abundance (513,367), followed by the Wenatchee (147,430) (Table 55). This year there were a small number of sockeye estimated from Snake River (2,456). The Lake Billy Chinook and the reintroduced stock from Yakima River had zero estimated abundance (Table 55, Figure 42).

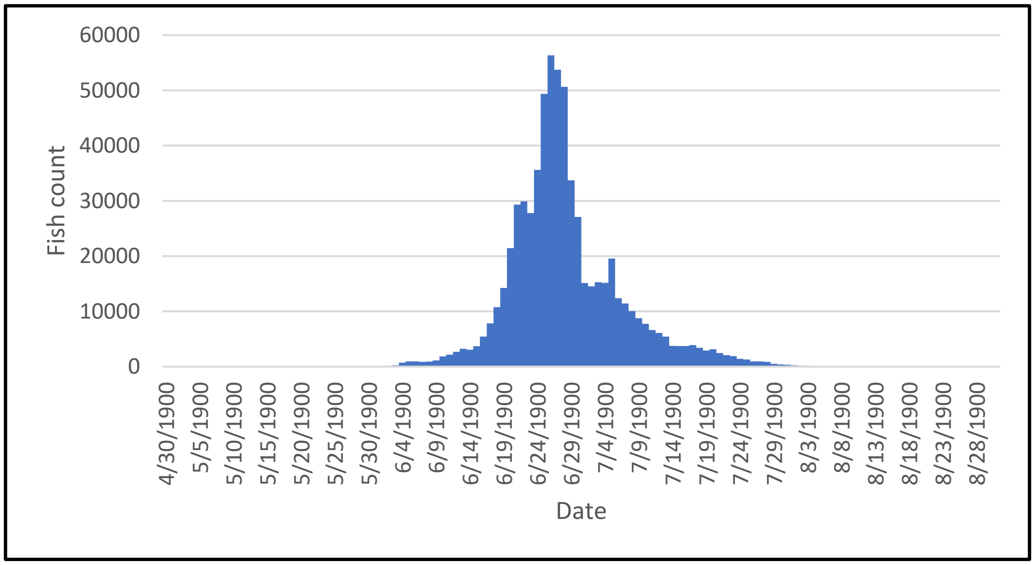


Figure 40. Daily passage of sockeye at Bonneville Dam in 2022 (source: https://www.fpc.org).

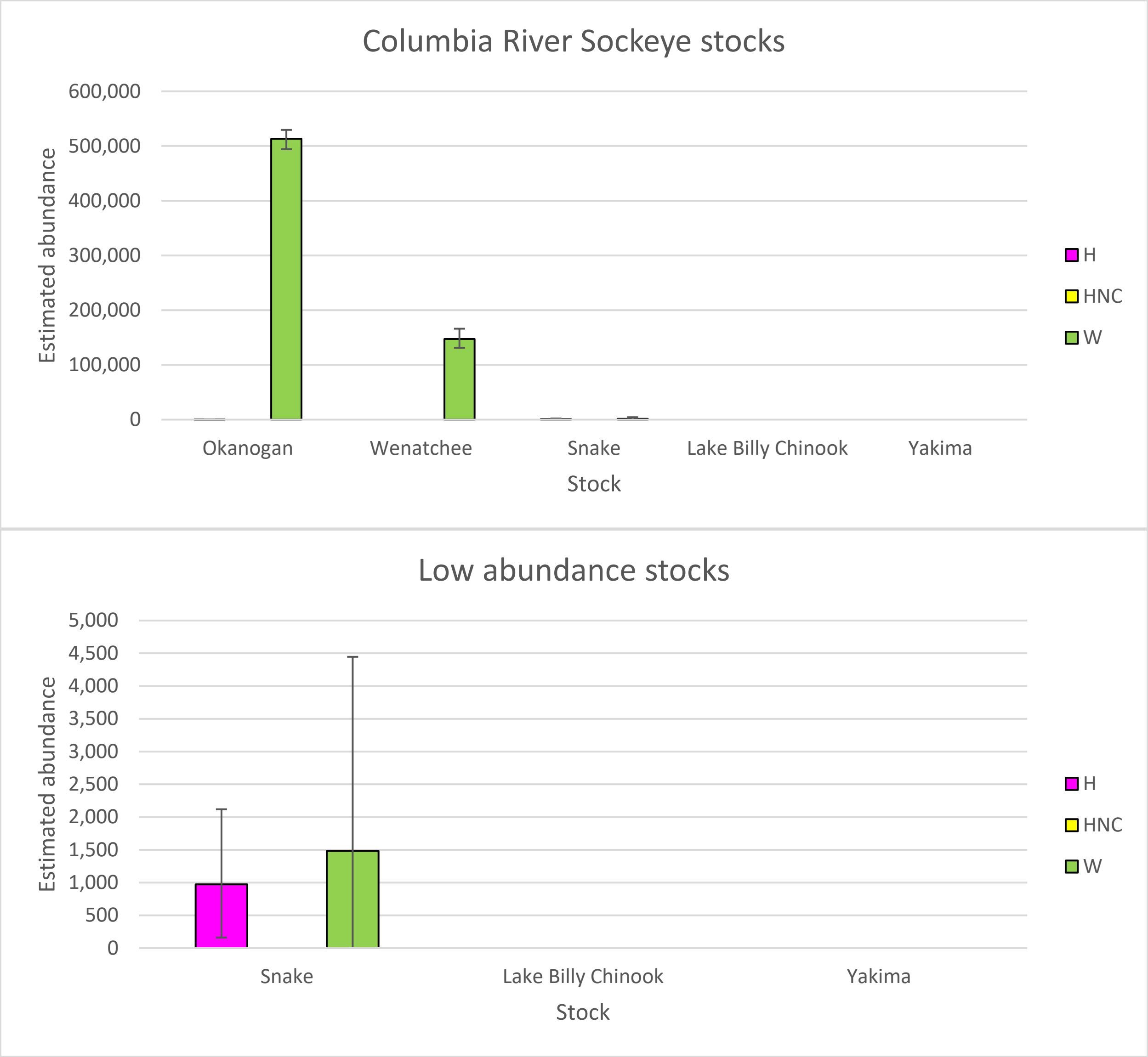


Figure 41. Estimated abundance (± 95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2022.

We characterized the run-timing distributions for all detected sockeye salmon stocks (Figure 43). The Wenatchee, Okanogan, and Snake stocks had nearly identical run timing distributions each with an average median date on 06/28/22 (Figure 43).

Table 55. Estimated abundance of sockeye salmon stocks passing Bonneville Dam in 2022.

	Estimated abundance					
	H		HNC		W	
Reporting Group name	**Est.**	**95% CI**	**Est.**	**95% CI**	**Est.**	**95% CI**
Okanogan	160	0 – 481			513,207	494338 – 529503
Wenatchee					147,430	131154 – 166182
Snake	973	160 – 2119			1,482	0 – 4446
Lake Billy Chinook						
Yakima						
Total	1,134		0		662,119	

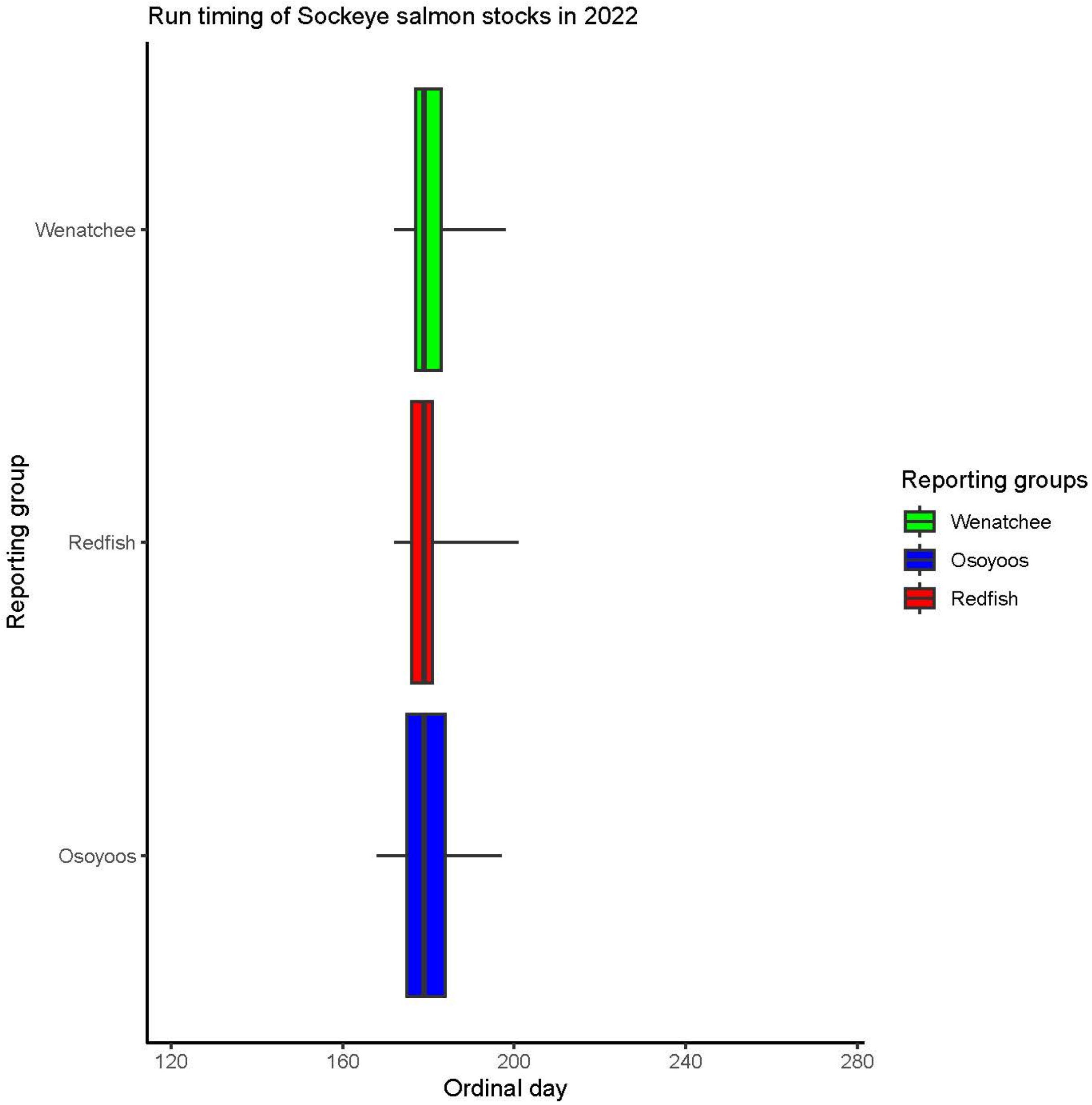


Figure 42. Run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for the major stocks of sockeye salmon that were sampled at Bonneville Dam in 2022 and assigned to stock of origin.

Estimated abundance and run-timing of Coho salmon stocks in 2022
Daily passage of Coho salmon at Bonneville Dam in 2022 is provided in Figure 43. A total of 150 Coho salmon were sampled at Bonneville Dam in 2022 from October 12 - October 14, 2022 and six were assigned to one of three hatcheries (i.e., Bonneville Hatchery, n=1; Eagle Creek NFH, n=3; Three Mile Dam Hatchery, n=2) using PBT; the remaining 144 samples did not assign to a hatchery. The relative abundance for Bonneville Hatchery, Eagle Creek NFH, and Three Mile Dam fish ranged from 49-147 (Figure 44).

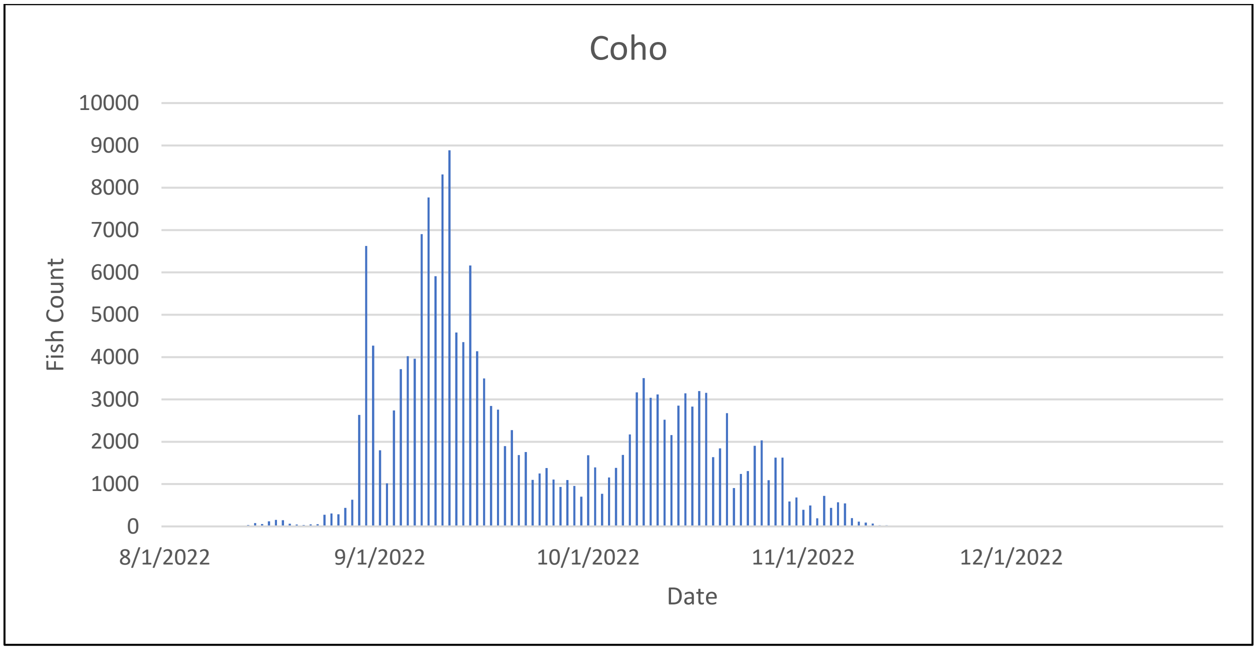


Figure 43. Number of Coho salmon returning over Bonneville Dam in 2022.

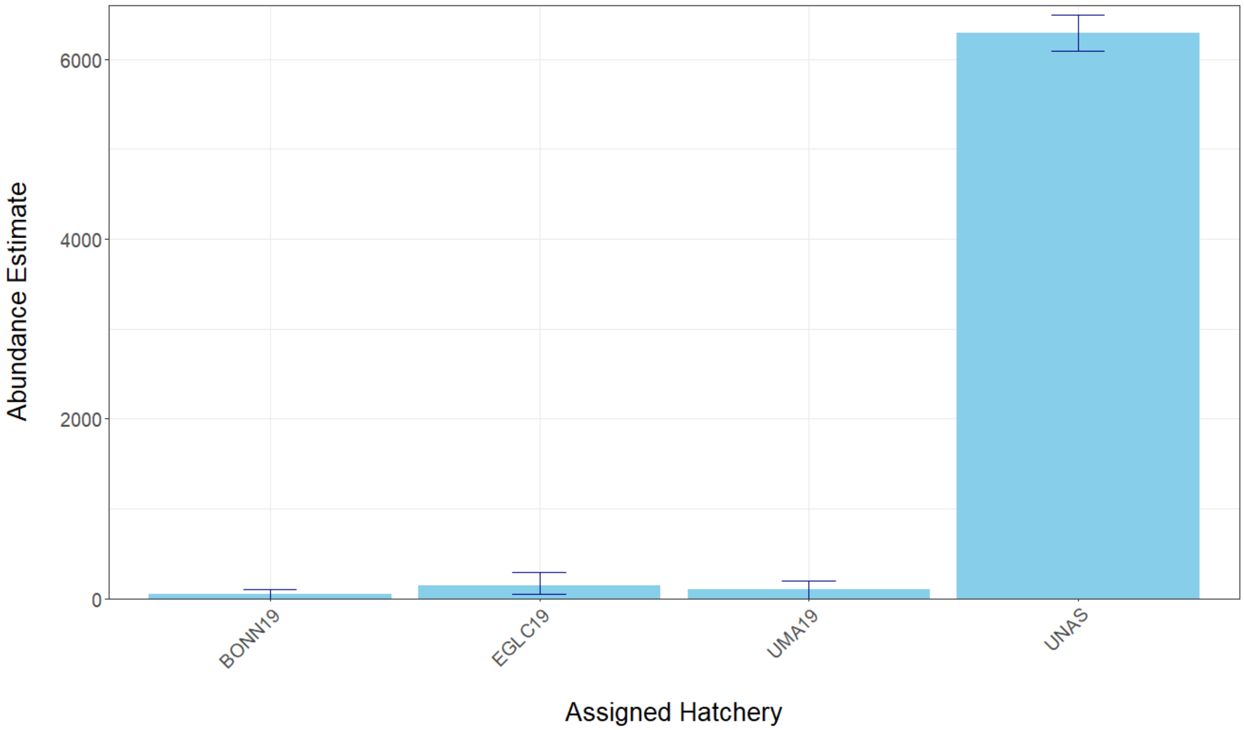


Figure 44. Abundance estimates of Coho salmon sampled at Bonneville in 2022.

In-season analysis of Chinook salmon passing Bonneville Dam in 2023

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 42). The first report was distributed to members of the U.S. v OR TAC on May 8, 2023. 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 2022. We use window counts of the adult-sized fish in order to estimate stock-specific abundances of adult-size Chinook Salmon. In the past, our BPA reports included stock-specific abundance and run-timing estimates of all Chinook Salmon, including jack-sized fish. Management of Chinook Salmon fisheries in the Columbia River is based solely on adult-sized Chinook Salmon (>560 mm fork length), and so we restrict our sample to this fork length threshold for our in-season analysis. Further, we used TAC estimates of the clipped and unclipped adult Chinook salmon and expanded genetic stock proportions with those estimates.

A total of 3,288 adult-sized Chinook Salmon were collected and analyzed for the 2023 in-season reports (Table 56). 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 6, 2023 provided sub-totals for each stock that were broken out by management period (clipped hatchery-origin stocks, Table 57; unclipped hatchery-origin stocks, Table 58; natural-origin stocks, Table 59). 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 59) and upper Columbia River spring Chinook Salmon stocks (Reporting group 10_UCOLSP, Table 59). 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 90 unique hatchery broodstocks in 2023 (Table 60). The total estimated abundances of these clipped and unclipped broodstocks were comprised of <0.1% Lower Columbia, 0.2% Willamette, 24.7% Snake River, and 72.7% of hatcheries from the rest of the Columbia River above Bonneville Dam (Figure 45). Similar to the natural- and hatchery-origin abundance estimates, the subtotals of these hatchery broodstock abundances were provided to U.S. v OR

TAC for each management period and bi-weekly strata for the in-season reporting in 2023. 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 61). In fact, in 2023, the percentage of adipose-clipped fish abundance that were estimated to be PBT broodstock ranged from 92 – 100%, 86 – 100%, and 93 – 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). Unlike in past years, all three management periods demonstrated high tag rates which is a result of the PBT baseline having increased in coverage with time (Appendix 3).

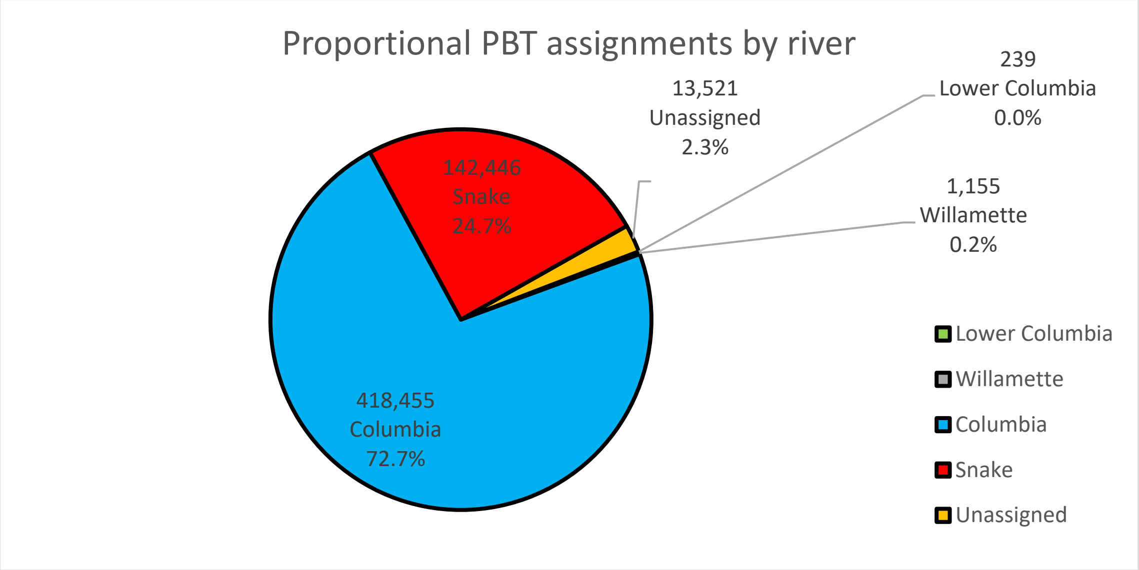


Figure 45. Proportion of hatchery broodstocks from the Snake River versus the rest of the Columbia River above Bonneville Dam in 2023.

Table 56. The sample sizes of Chinook salmon at the Bonneville Dam AFF during the spring, summer, and fall management periods of 2023.

		Statistical	TAC		Sample (N)							
		week	clip	unclip	Clipped		Non-clipped		Subtotal		Rate	
			count	count	GSI	PBT	GSI	PBT	clip	unclip	clip	unclip
Management period	Spring	1-16	1,813	263	0	0	0	0	0	0	0.00%	0.00%
		17	8,992	1,374	12	97	9	9	109	18	1.21%	1.31%
		18	12,529	1,795	8	156	16	18	164	34	1.31%	1.89%
		19	32,641	5,677	4	146	28	12	150	40	0.46%	0.70%
		20	23,140	5,318	9	162	35	14	171	49	0.74%	0.92%
		21	8,335	3,336	6	125	45	22	131	67	1.57%	2.01%
		22	5,564	2,972	12	100	46	22	112	68	2.01%	2.29%
		23	9,401	3,662	11	148	53	24	159	77	1.69%	2.10%
		24	7,700	2,274	7	58	10	9	65	19	0.84%	0.84%
	Summer	24	4,083	1,133	1	11	7	5	12	12	0.29%	1.06%
		25	10,230	2,533	11	54	14	10	65	24	0.64%	0.95%
		26	9,950	2,931	10	54	10	15	64	25	0.64%	0.85%
		27	6,511	1,615	4	36	10	6	40	16	0.61%	0.99%
		28	3,896	1,436	3	25	12	10	28	22	0.72%	1.53%
		29	2,602	1,643	4	20	15	11	24	26	0.92%	1.58%
		30	1,448	1,448		8	9	1	8	10	0.55%	0.69%
		31	492	492		3	3		3	3	0.61%	0.61%
	Fall	31	1,513	2,150	2	16	6	6	18	12	1.19%	0.56%
		32	2,181	4,084		8	13	8	8	21	0.37%	0.51%
		33	4,278	6,785					0	0	0.00%	0.00%
		34	26,787	16,667	4	44	35	59	48	94	0.18%	0.56%
		35	85,959	60,792	3	41	33	51	44	84	0.05%	0.14%
		36	50,764	60,613	2	41	49	43	43	92	0.08%	0.15%
		37	60,734	44,364	9	68	93	73	77	166	0.13%	0.37%
		38	26,765	21,071	10	73	118	74	83	192	0.31%	0.91%
		39	8,204	20,088	6	50	89	34	56	123	0.68%	0.61%
		40	5,806	7,636	8	43	94	47	51	141	0.88%	1.85%
		41	3,624	6,180	2	23	67	28	25	95	0.69%	1.54%
		42-44	1,428	4,302					0	0	0.00%	0.00%
		Total	**427,371**	**294,632**	**148**	**1,610**	**919**	**611**	**1,758**	**1,530**	0.41%	0.52%

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

Table 57. Preliminary in-season reporting of clipped hatchery-origin stock-specific abundance estimates of adult-sized Chinook Salmon passing Bonneville Dam across all management periods in 2023.

		H	Spring		Summer		Fall		Cumulative total date Nov. 1
Reporting Group name	**Run type**	**Reporting Group Code**	**Est. abund.**		**Est. abund.**		**Est. abund.**		**Est. abund.**
			Mean	**95% CI**	**Mean**	**95% CI**	**Mean**	**95% CI**	**Mean**
Youngs Bay	Spring	01_YOUNGS							0
West Cascade Spring	Spring	02_WCASSP	1,008	797 – 1599	325	0 – 1138			1,333
West Cascade Fall	Fall	03_WCASFA					239	0 – 478	239
Willamette	Spring	04_WILLAM	192	39 – 292	613	0 – 1677	731	0 – 1457	1,536
Spring Creek Tule	Fall	05_SPCRTU					81,413	70639 – 91870	81,413
Klickitat	Spring	06_KLICKR	454	366 – 816					454
Deschutes spring	Spring	07_DESCSP	3,942	3158 – 4575	190	0 – 857			4,132
John Day	Spring	08_JOHNDR	88	0 – 85					88
Yakima	Spring	09_YAKIMA	926	592 – 1173					926
Upper Columbia spring	Spring	10_UCOLSP	14,251	13412 – 15904					14,251
Tucannon	Spring	11_TUCANO	294	0 – 509					294
Hells Canyon	Spring/Summer	12_HELLSC	37,963	35458 – 38785	530	0 – 1239			38,493
South Fork Salmon	Spring/Summer	13_SFSALM	4,680	3559 – 5676	834	75 – 1683			5,514
Chamberlain Creek	Spring/Summer	14_CHMBLN							0
Middle Fork Salmon	Spring/Summer	15_MFSALM							0
Upper Salmon	Spring/Summer	16_UPSALM	5,874	5336 – 7292	328	0 – 834			6,202
Deschutes fall	Fall	17_DESCFA							0
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	14,141	13586 – 14658	35,769	33586 – 37273	107,299	89978 – 121023	157,209
Snake River fall	Fall	19_SRFALL			622	75 – 1362	58,445	51126 – 64339	59,067

Bonneville Pool spring	Spring	20_BONPOOLSP	23,295	21923 – 25069					23,295
Umatilla spring	Spring	21_UMATILLASP	3,010	3021 – 3634					3,010
Bonneville Pool fall	Fall	22_BONPOOLFA					25,595	21964 – 31795	25,595
Umatilla fall	Fall	23_UMATILLAFA					4,320	2037 – 7706	4,320
		Total	**110,116**		**39,212**		**278,042**		**427,371**

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 7, 2023 are provided. Bonneville 2023 spring, summer, and fall management period Chinook PBT/GSI analyses that corresponds with statistical weeks 1 – 25 (01/01/23-06/15/23: spring), 25 – 31 (6/16/23-7/31/23:summer) and 31 – 44 (8/1/2023-11/7/2023:fall).

Table 58. Preliminary in-season reporting of unclipped hatchery-origin stock-specific abundance estimates of adult-sized Chinook Salmon passing Bonneville Dam across all management periods in 2023.

		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	63	0 – 189					63
West Cascade Fall	Fall	03_WCASFA							0
Willamette	Spring	04_WILLAM							0
Spring Creek Tule	Fall	05_SPCRTU					12,810	6910 – 16706	12,810
Klickitat	Spring	06_KLICKR							0
Deschutes spring	Spring	07_DESCSP	157	5 – 363					157
John Day	Spring	08_JOHNDR							0
Yakima	Spring	09_YAKIMA	109	0 – 218					109

Upper Columbia spring	Spring	10_UCOLSP	2,126	1433 – 2920	90	0 – 359			2,216
Tucannon	Spring	11_TUCANO							0
Hells Canyon	Spring/Summer	12_HELLSC	2,762	2250 – 3835					2,762
South Fork Salmon	Spring/Summer	13_SFSALM	1,212	1003 – 1803	111	0 – 389			1,323
Chamberlain Creek	Spring/Summer	14_CHMBLN							0
Middle Fork Salmon	Spring/Summer	15_MFSALM							0
Upper Salmon	Spring/Summer	16_UPSALM	521	111 – 1011	293	0 – 834			814
Deschutes fall	Fall	17_DESCFA							0
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	1,504	1382 – 2439	4,767	3348 – 6188	68,407	59024 – 77331	74,678
Snake River fall	Fall	19_SRFALL			740	278 – 1391	31,731	21335 – 33624	32,471
Bonneville Pool spring	Spring	20_BONPOOLSP	444	91 – 763					444
Umatilla spring	Spring	21_UMATILLASP	482	284 – 662					482
Bonneville Pool fall	Fall	22_BONPOOLFA					19,942	16915 – 24359	19,942
Umatilla fall	Fall	23_UMATILLAFA					174	3 – 397	174
		Total	**9,380**		**6,000**		**133,064**		**148,445**

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 07, 2023 are provided.

Table 59. Preliminary in-season reporting of natural-origin stock-specific abundance estimates of adult-sized Chinook Salmon passing Bonneville Dam across all management periods in 2023.

		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	62	0 – 185			234	0 – 701	296
West Cascade Spring	Spring	02_WCASSP	124	0 – 309					124
West Cascade Fall	Fall	03_WCASFA			90	0 – 269	850	270 – 1552	940
Willamette	Spring	04_WILLAM					234	0 – 701	234
Spring Creek Tule	Fall	05_SPCRTU					2,827	984 – 5629	2,827
Klickitat	Spring	06_KLICKR			216	0 – 433			216
Deschutes spring	Spring	07_DESCSP	144	0 – 325					144
John Day	Spring	08_JOHNDR	863	460 – 1266					863
Yakima	Spring	09_YAKIMA	1,692	1026 – 2398					1,692
Upper Columbia spring	Spring	10_UCOLSP	3,202	2429 – 4089	108	0 – 324			3,310
Tucannon	Spring	11_TUCANO							0
Hells Canyon	Spring/Summer	12_HELLSC	4,750	3709 – 5701	108	0 – 324			4,858
South Fork Salmon	Spring/Summer	13_SFSALM	2,082	1500 – 2698	411	105 – 736			2,493
Chamberlain Creek	Spring/Summer	14_CHMBLN	250	50 – 482					250
Middle Fork Salmon	Spring/Summer	15_MFSALM	698	324 – 1141					698
Upper Salmon	Spring/Summer	16_UPSALM	1,473	938 – 2054					1,473
Deschutes fall	Fall	17_DESCFA					2,259	976 – 3904	2,259
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	1,950	1447 – 2455	5,370	4434 – 6330	94,578	85200 – 102678	101,898
Snake River fall	Fall	19_SRFALL			927	475 – 1399	20,687	15798 – 26008	21,614
		Total	**17,289**		**7,230**		**121,668**		**146,187**

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 07, 2023 are provided.

Table 60. The estimated abundances of the clipped and unclipped adult-sized Chinook salmon assigned to PBT hatchery broodstock that passed Bonneville Dam in 2023 (1/01/2023 – 11/07/2023).

						Abundance estimate				
						Clipped		Unclipped		
Period	Expected Run Time	Hatchery	Broodstock	Broodyear	GSI RepGrp	Est.	95% C.I.	Est.	95% C.I.	Total
Spring	01Spring	Parkdale Fish Facility	OtsPARK_seg_sp19	2019	02_WCASSP	1,008	514 – 1546	63	0 – 189	1,071
	01Spring	North Santiam Hatchery	OtsNSAN_seg_sp19	2019	04_WILLAM	147	0 – 441			147
	01Spring	Klickitat Hatchery	OtsKLIC_seg_sp19	2019	06_KLICKR	317	0 – 752			317
	01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp19	2019	07_DESCSP	1,898	1109 – 2745	101	0 – 302	1,999
	01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp20	2020	07_DESCSP	78	0 – 233			78
	01Spring	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp19	2019	07_DESCSP	1,965	1193 – 2827	56	0 – 169	2,022
	01Spring	Yakima River Roza Dam	OtsYRRD_int_sp19	2019	09_YAKIMA	813	341 – 1326	109	0 – 328	922
	01Spring	Yakima River Roza Dam	OtsYRRD_seg_sp19	2019	09_YAKIMA	113	0 – 276			113
	01Spring	Chief Joseph Hatchery	OtsCHJO_seg_sp19	2019	10_UCOLSP	1,108	478 – 1834			1,108
	01Spring	Eastbank Fish Hatchery	OtsEAST_seg_sp18	2018	10_UCOLSP	64	0 – 191	152	0 – 369	216
	01Spring	Eastbank Fish Hatchery	OtsEAST_seg_sp19	2019	10_UCOLSP	1,142	481 – 1966	602	233 – 1022	1,743
	01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp18	2018	10_UCOLSP	488	0 – 1068			488
	01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp19	2019	10_UCOLSP	7,550	5855 – 9188	53	0 – 158	7,602
	01Spring	Methow Fish Hatchery	OtsMETH_seg_sp19	2019	10_UCOLSP			1,112	630 – 1640	1,112
	01Spring	Winthrop National Fish Hatchery	OtsWINT_seg_sp19	2019	10_UCOLSP	3,139	2041 – 4413	208	0 – 416	3,347
	01Spring	Little White Salmon National Fish Hatchery	OtsTOUC_seg_sp19	2019	11_TUCANO	294	0 – 664			294
	01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp18	2018	12_HELLSC	267	64 – 509			267
	01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp19	2019	12_HELLSC	6,508	4977 – 8078	470	162 – 849	6,978
	01Spring	Clearwater Fish Hatchery	OtsPOWP_seg_sp19	2019	12_HELLSC			149	0 – 317	149
	01Spring	Clearwater Fish Hatchery	OtsPOWP_seg_sp20	2020	12_HELLSC			62	0 – 185	62
	01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp18	2018	12_HELLSC	171	0 – 410	96	0 – 287	267
	01Spring	Dworshak National Fish Hatchery	OtsKOOS_seg_sp18	2018	12_HELLSC	144	0 – 431			144
	01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp19	2019	12_HELLSC	4,751	3504 – 6135	565	206 – 974	5,316
	01Spring	Dworshak National Fish Hatchery	OtsKOOS_seg_sp19	2019	12_HELLSC	4,115	2896 – 5512			4,115
	01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp20	2020	12_HELLSC	70	0 – 209			70

	01Spring	Lookingglass Fish Hatchery	OtsLOOK_seg_sp18	2018	12_HELLSC	230	0 – 678			230
	01Spring	Lookingglass Fish Hatchery	OtsLOOK_seg_sp19	2019	12_HELLSC	2,167	1352 – 3047	146	0 – 438	2,313
	01Spring	Nez Perce	OtsNPFH_seg_sp19	2019	12_HELLSC	2,086	1098 – 3136	951	502 – 1480	3,037
	01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp18	2018	12_HELLSC	591	153 – 1124			591
	01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp19	2019	12_HELLSC	16,020	13694 – 18248	260	0 – 559	16,280
	01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp20	2020	12_HELLSC			63	0 – 189	63
	01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp18	2018	20_BONPOOLSP	149	0 – 347			149
	01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp19	2019	20_BONPOOLSP	9,823	8068 – 11900	233	0 – 517	10,056
	01Spring	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp18	2018	20_BONPOOLSP	914	389 – 1537	97	0 – 290	1,011
	01Spring	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp19	2019	20_BONPOOLSP	12,408	10334 – 14483	114	0 – 342	12,522
	01Spring	Umatilla Fish Hatchery	OtsUMAT_seg_sp19	2019	21_UMATILLASP	3,010	2155 – 4020	482	190 – 861	3,492
	02Spring/Summer	Lookingglass Fish Hatchery	OtsIMNW_seg_ss19	2019	12_HELLSC	534	234 – 903			534
	02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss18	2018	13_SFSALM	50	0 – 151			50
	02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss19	2019	13_SFSALM	4,545	3710 – 5425	937	606 – 1301	5,482
	02Spring/Summer	McCall Fish Hatchery	OtsJHNW_int_ss19	2019	13_SFSALM			274	93 – 461	274
	02Spring/Summer	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss18	2018	16_UPSALM	127	0 – 281			127
	02Spring/Summer	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss19	2019	16_UPSALM	889	481 – 1324			889
	02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss19	2019	16_UPSALM	4,534	3482 – 5678	521	238 – 883	5,055
	02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss20	2020	16_UPSALM	77	0 – 231			77
	03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su17	2017	18_UCOLSF	85	0 – 254			85
	03Summer	Chief Joseph Hatchery	OtsCHJO_int_su17	2017	18_UCOLSF			82	0 – 246	82
	03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su19	2019	18_UCOLSF	448	159 – 766			448
	03Summer	Chief Joseph Hatchery	OtsCHJO_int_su19	2019	18_UCOLSF	362	129 – 647			362
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su17	2017	18_UCOLSF	145	0 – 317			145
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su18	2018	18_UCOLSF	4,574	3750 – 5390	356	125 – 605	4,930
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su19	2019	18_UCOLSF	584	251 – 917	62	0 – 185	646
	03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su17	2017	18_UCOLSF	332	91 – 605			332
	03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su18	2018	18_UCOLSF	1,945	1331 – 2665	81	0 – 243	2,026
	03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su19	2019	18_UCOLSF	811	432 – 1219	66	0 – 198	877

	03Summer	Wells Fish Hatchery	OtsWELL_seg_su18	2018	18_UCOLSF	1,144	635 – 1702	226	75 – 452	1,370
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su19	2019	18_UCOLSF	2,968	2295 – 3735	632	335 – 935	3,600
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su20	2020	18_UCOLSF	79	0 – 236			79
	#N/A	#N/A	Unassigned	#N/A	#N/A	2,335	1409 – 3621			2,335
			Spring Subtotal			110,116		9,380		119,497
Summer	01Spring	Parkdale Fish Facility	OtsPARK_seg_sp19	2019	02_WCASSP	176	0 – 527			176
	01Spring	Parkdale Fish Facility	OtsPARK_seg_sp20	2020	02_WCASSP	149	0 – 448			149
	01Spring	North Santiam Hatchery	OtsNSAN_seg_sp19	2019	04_WILLAM	288	0 – 864			288
	01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp19	2019	07_DESCSP	190	0 – 571			190
	01Spring	Eastbank Fish Hatchery	OtsEAST_seg_sp20	2020	10_UCOLSP			90	0 – 269	90
	01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp19	2019	12_HELLSC	172	0 – 517			172
	02Spring/Summer	Lookingglass Fish Hatchery	OtsIMNW_seg_ss19	2019	12_HELLSC	358	0 – 715			358
	02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss19	2019	13_SFSALM	683	177 – 1236	111	0 – 333	794
	02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss20	2020	13_SFSALM	151	0 – 454			151
	02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss19	2019	16_UPSALM	177	0 – 532	112	0 – 335	289
	02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss20	2020	16_UPSALM	151	0 – 453	181	0 – 452	332
	03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su17	2017	18_UCOLSF			99	0 – 298	99
	03Summer	Chief Joseph Hatchery	OtsCHJO_int_su18	2018	18_UCOLSF	149	0 – 448			149
	03Summer	Chief Joseph Hatchery	OtsCHJO_int_su19	2019	18_UCOLSF	3,036	2052 – 4219	514	183 – 899	3,550
	03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su19	2019	18_UCOLSF	1,539	847 – 2433			1,539
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su17	2017	18_UCOLSF	155	0 – 464	112	0 – 336	267
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su18	2018	18_UCOLSF	13,084	11162 – 15008	1,652	1087 – 2325	14,736
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su19	2019	18_UCOLSF	1,825	987 – 2686	396	90 – 739	2,221
	03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su17	2017	18_UCOLSF	205	0 – 615			205
	03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su18	2018	18_UCOLSF	2,030	902 – 3158	401	117 – 827	2,431
	03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su19	2019	18_UCOLSF	3,386	2172 – 4648	96	0 – 287	3,481
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su17	2017	18_UCOLSF			122	0 – 365	122
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su18	2018	18_UCOLSF	2,852	1804 – 4110	350	109 – 678	3,202
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su19	2019	18_UCOLSF	4,099	2939 – 5408	1,026	485 – 1512	5,125

	03Summer	Wells Fish Hatchery	OtsWELL_seg_su20	2020	18_UCOLSF	154	0 – 462			154
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa19	2019	19_SRFALL	467	156 – 935	467	187 – 841	934
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa20	2020	19_SRFALL			181	0 – 453	181
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa19	2019	19_SRFALL			92	0 – 277	92
	#N/A	#N/A	Unassigned	#N/A	#N/A	3,734	2271 – 5323			3,734
			Summer Subtotal			39,212		6,000		45,212
Fall	01Spring	North Santiam Hatchery	OtsNSAN_seg_sp18	2018	04_WILLAM	720	0 – 2111			720
	03Summer	Chief Joseph Hatchery	OtsCHJO_int_su19	2019	18_UCOLSF	1,438	473 – 2875			1,438
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su18	2018	18_UCOLSF	2,368	945 – 4252			2,368
	04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa19	2019	03_WCASFA	239	0 – 716			239
	04Fall	Bonneville Dam Hatchery	OtsBONN_seg_fa19	2019	05_SPCRTU	828	0 – 2261			828
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	2019	05_SPCRTU	18,965	11507 – 27148	6,712	3914 – 10044	25,678
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa20	2020	05_SPCRTU	56,705	45601 – 67493	5,726	3357 – 8372	62,432
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa21	2021	05_SPCRTU	1,791	0 – 4336	4,513	2262 – 7001	6,303
	04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa17	2017	18_UCOLSF	158	0 – 472			158
	04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa18	2018	18_UCOLSF	4,518	748 – 9148	436	63 – 1056	4,954
	04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa19	2019	18_UCOLSF	66,956	55607 – 78667	44,858	38007 – 51657	111,814
	04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa20	2020	18_UCOLSF	24,046	16578 – 31513	17,055	12551 – 21919	41,101
	04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa19	2019	18_UCOLSF	4,177	1531 – 7213			4,177
	04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa20	2020	18_UCOLSF	1,261	124 – 2943			1,261
	04Fall	Yakima Nation Prosser Hatchery	OtsPROS_seg_fa19	2019	18_UCOLSF			4,054	564 – 8672	4,054
	04Fall	Yakima Nation Prosser Hatchery	OtsPROS_seg_fa20	2020	18_UCOLSF			116	0 – 348	116
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	2017	19_SRFALL	615	0 – 1844			615
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	2018	19_SRFALL	6,620	1931 – 11577	332	0 – 995	6,951
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa19	2019	19_SRFALL	33,985	23953 – 44113	21,874	17141 – 26680	55,859
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa20	2020	19_SRFALL	7,133	3190 – 12107	5,991	3410 – 9187	13,124
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	2018	19_SRFALL	579	0 – 1736			579
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa19	2019	19_SRFALL	6,158	2077 – 11457	963	241 – 1697	7,121

	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa20	2020	19_SRFALL	1,560	0 – 3677	961	0 – 2329	2,522
	04Fall	Klickitat Hatchery	OtsKLIC_seg_fa19	2019	22_BONPOOLFA			3,055	414 – 6177	3,055
	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	2017	22_BONPOOLFA	119	0 – 356			119
	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	2018	22_BONPOOLFA	2,980	966 – 5487	150	0 – 450	3,130
	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa19	2019	22_BONPOOLFA	17,366	9586 – 26137	15,987	11605 – 20535	33,352
	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa20	2020	22_BONPOOLFA	5,020	2224 – 8225	110	0 – 331	5,130
	04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	2018	23_UMATILLAFA	3,296	958 – 6042	171	0 – 400	3,467
	04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa20	2020	23_UMATILLAFA	993	330 – 1782			993
	#N/A	#N/A	Unassigned	#N/A	#N/A	7,451	3267 – 17183			7,451
			Fall Subtotal			278,042		133,064		411,107

Table 61. Expanded abundance of PBT-assigned Chinook Salmon stocks across management periods in 2023.

		Statistical week	Sample (Tag-rate-Corrected abundance)				**Total GSI**	**Total PBT**	% PBT of Clipped fish
			Clipped		Non-clipped				
			GSI	PBT	GSI	PBT			
Management period	Spring	1-16	-	-	-	-	-	-	-
		17	687	8,305	666	708	**1,353**	**9,013**	92.4%
		18	190	12,339	825	971	**1,014**	**13,310**	98.5%
		19	0	32,641	3,929	1,749	**3,929**	**34,389**	100.0%
		20	465	22,675	3,769	1,549	**4,234**	**24,224**	98.0%
		21	129	8,207	2,199	1,137	**2,328**	**9,343**	98.5%
		22	397	5,167	1,990	982	**2,387**	**6,149**	92.9%
		23	196	9,205	2,475	1,187	**2,672**	**10,391**	97.9%
		24	514	7,186	1,141	1,133	**1,655**	**8,319**	93.3%
	Summer	24	0	4,083	657	476	**657**	**4,559**	100.0%
		25	1,270	8,960	1,421	1,112	**2,691**	**10,072**	87.6%
		26	1,230	8,720	1,117	1,814	**2,348**	**10,533**	87.6%
		27	539	5,972	971	644	**1,510**	**6,616**	91.7%
		28	243	3,653	760	675	**1,003**	**4,329**	93.8%
		29	362	2,240	924	719	**1,285**	**2,960**	86.1%
		30	0	1,448	1,297	151	**1,297**	**1,598**	100.0%
		31	0	492	492	0	**492**	**492**	100.0%
	Fall	31	87	1,425	1,042	1,109	**1,129**	**2,534**	94.2%
		32	0	2,181	2,478	1,606	**2,478**	**3,787**	100.0%
		33	-	-	-	-	-	-	-
		34	751	26,036	5,569	11,098	**6,320**	**37,134**	97.2%
		35	2,130	83,829	20,763	40,029	**22,893**	**123,858**	97.5%
		36	191	50,573	30,425	30,187	**30,617**	**80,760**	99.6%
		37	3,943	56,791	23,616	20,748	**27,559**	**77,539**	93.5%
		38	1,824	24,942	12,228	8,842	**14,052**	**33,784**	93.2%
		39	0	8,204	13,735	6,353	**13,735**	**14,557**	100.0%
		40	325	5,481	4,768	2,868	**5,094**	**8,348**	94.4%
		41	0	3,624	4,149	2,031	**4,149**	**5,655**	100.0%
		42-44	-	-	-	-	-	-	-
		Total	15,476	404,377	143,404	139,877	**158,880**	**544,254**	

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

In-season analysis of steelhead passing Bonneville Dam in 2023

There were three reports provided to U.S. v OR TAC during the summer A-/B-Index Management Period (7/1/2023 – 10/31/2023, Table 42). The Skamania Management Period (4/1/2023 – 6/30/2023) had a single report that covered the entire Skamania period. There was a total of 353 clipped and 208 unclipped steelhead that were sampled at the Bonneville Dam AFF and genotyped in 2023 (Table 62). 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 62). 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 63, Table 64, Table 65). 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 is issue is now resolved through our implementation of SCOBI DEUX and SPIBETR methodologies described previously (Section 3). Finally, as we have demonstrated in our post-season analyses, the preliminary analysis reports for 2023 include a breakdown of all the A- and B-Index steelhead abundance by broodstock for both clipped and unclipped hatchery-origin groups (Table 64).

Table 62. The sample sizes of Summer Steelhead at the Bonneville Dam AFF during the Skamania and A-/B-Index management periods of 2023.

						Sample (N)											
						A-Index				B-Index						Clipped	Non-clipped
		Statistical		Clipped	Non-Clipped	Clipped		Non-clipped		Clipped		Non-clipped		Clipped	Non-clipped	Sample	Sample
		week	Strata	count	count	GSI	PBT	GSI	PBT	GSI	PBT	GSI	PBT	Total	Total	rate	rate
Management period	Skamania	14	1	19	21									0	0	0.00%	0.00%
		15	1	68	90									0	0	0.00%	0.00%
		16	1	54	37									0	0	0.00%	0.00%
		17	1	23	24									0	0	0.00%	0.00%
		18	1	21	26									0	0	0.00%	0.00%
		19	1	43	12									0	0	0.00%	0.00%
		20	1	23	11									0	0	0.00%	0.00%
		21	1	46	16		1							1	0	2.17%	0.00%
		22	1	45	20		1	3			1			2	3	4.44%	15.00%
		23	1	94	33		3	3						3	3	3.19%	9.09%
		24	1	88	74			2						0	2	0.00%	2.70%
		25	1	210	168		2							2	0	0.95%	0.00%
		26	1	428	392		3	4						3	4	0.70%	1.02%
		27	1	544	574		5	2						5	2	0.92%	0.35%
		Subtotal Skamania		1706	1498	0	15	14	0	0	1	0	0	16	14	0.94%	0.93%
	A-/B-Index	27	1	390	404									0	0	0.00%	0.00%
		28	1	1875	2,224		10	5						10	5	0.53%	0.22%
		29	1	3481	3,707		11	8	1					11	9	0.32%	0.24%
		30	1	3570	3,611	1	18	25	1		1			20	26	0.56%	0.72%
		31	1	2526	2,990	1	2	3				1		3	4	0.12%	0.13%
		32	2	6603	5,125	3	26	44	1					29	45	0.44%	0.88%
		33	2	8085	4,942	5	33	26	1		5			43	27	0.53%	0.55%
		34	3	6447	2,964									0	0	0.00%	0.00%
		35	3	6,313	2,329	4	23	6		1	7	1	2	35	9	0.55%	0.39%

	36	3	11,000	3,435		6	3			3			9	3	0.08%	0.09%
	37	3	7,561	2,403	1	22	3	1		13	1	2	36	7	0.48%	0.29%
	38	4	6,202	1,887	1	24	6	2		14	3	4	39	15	0.63%	0.79%
	39	4	2,853	902	3	12	2	3		7		1	22	6	0.77%	0.67%
	40	5	2,607	867	2	31	6	7		8		2	41	15	1.57%	1.73%
	41	5	1,395	558	3	13	4	3		5	1		21	8	1.51%	1.43%
	42	5	568	383	2	15	7	6		1		2	18	15	3.17%	3.92%
	43	5	164	105									0	0	0.00%	0.00%
	44	5	110	72												
	45	5	11	18									0	0	0.00%	0.00%
	Summer A-/B-Index subtotal		**71,761**	**38,926**	**26**	**246**	**148**	**26**	**1**	**64**	**7**	**13**	**337**	**194**	0.47%	0.50%
	Total		**75,173**	**41,922**	**26**	**261**	**162**	**26**	**1**	**65**	**7**	**13**	**353**	**208**	0.47%	0.50%

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 63. Estimated abundance of clipped hatchery-origin stocks of Summer Steelhead that passed Bonneville Dam in 2023 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	1,066	533 – 1599	107	0 – 427	1,016	476 – 1900	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	213	0 – 640	0	0 – 0	20,050	16310 – 22069	257	0 – 1045
Yakima	08_YAKIMA								
upper Columbia	09_UPPCOL	107	0 – 427	0	0 – 0	6,513	4760 – 8248	0	0 – 0
SF Clearwater	10_SFCLWR					6,244	4300 – 7283	14,274	12848 – 16979
upper Clearwater	11_UPCLWR								
SF Salmon	12_SFSALM								
MF Salmon	13_MFSALM								
upper Salmon	14_UPSALM	213	0 – 640	0	0 – 0	23,286	21495 – 27601	122	3 – 299
	Total	**1,599**		**107**		**57,109**		**14,652**	

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 64. Estimated abundance of unclipped hatchery-origin stocks of Summer Steelhead that passed Bonneville Dam in 2023 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								
Willamette	04_WILLAM								
Big White Salmon	05_BWSALM								
Klickitat	06_KLICKR					52	0 – 102	0	0 – 0
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	107				684	55 – 1390	294	0 – 869
Yakima	08_YAKIMA								
upper Columbia	09_UPPCOL					639	7 – 1327	0	0 – 0
SF Clearwater	10_SFCLWR					1,061	740 – 1275	3,225	1724 – 4437
upper Clearwater	11_UPCLWR								

SF Salmon	12_SFSALM								
MF Salmon	13_MFSALM								
upper Salmon	14_UPSALM					762	355 – 1292	0	0 – 0
	Total	**107**		**0**		**3,198**		**3,519**	

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 65. Estimated abundance of natural-origin stocks (excluding unclipped hatchery-origin) of Summer Steelhead that passed Bonneville Dam in 2023 during the Skamania and A-/B-Index Management Periods.

	W	Subtotal for Skamania Period (Apr 1 - Jun 30)		Subtotal for Skamania Period (Apr 1 - Jun 30)		Subtotal for A-/B-Index Period (Jul 01 - Oct 31)		Subtotal for A-/B-Index Period (Jul 01 - Oct 31)	
		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	428	107 – 749			294	0 – 882	0	0 – 0
Skamania	03_SKAMAN	214	0 – 428			140	0 – 419	0	0 – 0
Willamette	04_WILLAM								
Big White Salmon	05_BWSALM								
Klickitat	06_KLICKR	428	107 – 749			294	0 – 882	0	0 – 0
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	321	107 – 642			20,213	17417 – 22744	719	0 – 1890
Yakima	08_YAKIMA					1,159	140 – 2471	0	0 – 0
upper Columbia	09_UPPCOL					2,783	1370 – 4340	51	0 – 155
SF Clearwater	10_SFCLWR					1,423	422 – 2722	714	0 – 1883
upper Clearwater	11_UPCLWR					273	0 – 552	133	0 – 398
SF Salmon	12_SFSALM								
MF Salmon	13_MFSALM					294	0 – 882	0	0 – 0
upper Salmon	14_UPSALM					3,720	2273 – 5353	0	0 – 0
	Total	**1,391**		**0**		**30,593**		**1,616**	

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 66. Estimated abundance of clipped and unclipped hatchery-origin A-/B-Index Summer Steelhead that passed Bonneville Dam in 2023 (July 1 – Oct 31) and were assigned to PBT broodstocks.

					Hatchery clipped				Hatchery unclipped			
					A-INDEX		B-INDEX		A-INDEX		B-INDEX	
Hatchery	**Stock**	**GSI RepGrp**	**Broodstock**	**Brood year**	**Est.**	**95% CI**	**MLE**	**95% CI**	**MLE**	**95% CI**	**MLE**	**95% CI**
Skamania Hatchery	Summer	03_SKAMAN	OmySKAM_su21	2021	273	0 – 820	0	0 – 0				
Skamania Hatchery	Summer	03_SKAMAN	OmySKAM_su20	2020	742	0 – 1485	0	0 – 0				
Minthorn Springs Satellite	Minthorn Springs	07_MGILCS	OmyMINT_su21	2021	1,520	634 – 2711	0	0 – 0				
Round Butte	Deschutes River	07_MGILCS	OmyROUN_su21	2021					296	0 – 902	0	0 – 0
Minthorn Springs Satellite	Minthorn Springs	07_MGILCS	OmyMINT_su20	2020	61	0 – 182	0	0 – 0				
Round Butte	Deschutes River	07_MGILCS	OmyROUN_su20	2020	477	0 – 1160	0	0 – 0				
Eastbank	Wenatchee	09_UPPCOL	OmyEAST_su21	2021					586	0 – 1758	0	0 – 0
Wells Fish Hatchery	WMET/WOKA/WOMA /WELLS	09_UPPCOL	OmyWELL_su21	2021	4,200	2504 – 5866	0	0 – 0	53	0 – 160	0	0 – 0
Wells Fish Hatchery	WMET/WOKA/WOMA /WELLS	09_UPPCOL	OmyWELL_su20	2020	1,503	686 – 2461	0	0 – 0				
Winthrop NFH	Methow River	09_UPPCOL	OmyWINT_su20	2020	406	0 – 1217	0	0 – 0				
Little Sheep Satellite	Imnaha	07_MGILCS	OmyLSCR_su21	2021	2,562	1390 – 3820	0	0 – 0				
Lyons Ferry Hatchery	Wallowa stock - trapped/spawned at Cottonwood, released at Cottonwood and other Washington sites	07_MGILCS	OmyCGRW_su21	2021	2,362	1076 – 3902	0	0 – 0				
Lyons Ferry Hatchery	Tucannon	07_MGILCS	OmyTUCA_su21	2021					336	0 – 783	0	0 – 0
Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGILCS	OmyWALL_su21	2021	3,805	2228 – 5522	0	0 – 0				
Little Sheep Satellite	Imnaha	07_MGILCS	OmyLSCR_su20	2020	834	269 – 1668	0	0 – 0				
Lyons Ferry Hatchery	Wallowa stock - trapped/spawned at Cottonwood, released at Cottonwood and other Washington sites	07_MGILCS	OmyCGRW_su20	2020	3,092	1886 – 4485	0	0 – 0				
Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGILCS	OmyWALL_su20	2020	2,928	1468 – 4372	0	0 – 0	53	0 – 158	0	0 – 0

Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGILCS	OmyWALL_su19	2019	149	0 – 447	0	0 – 0				
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su21	2021	1,418	698 – 2329	0	0 – 0	53	0 – 159	0	0 – 0
Dworshak NFH	SF Clearwater	10_SFCLWR	OmySFCR_su21	2021	1,113	633 – 1673	0	0 – 0	529	211 – 900	0	0 – 0
Dworshak NFH	Dworshak stock-trapped and spawned at Dworshak, reared at Magic Valley FH, released in Salmon basin	10_SFCLWR	OmyDWOS_su21	2021	61	0 – 182	0	0 – 0	211	53 – 422	0	0 – 0
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su20	2020	1,958	763 – 3519	11,736	9019 – 14460	268	0 – 538	1,682	429 – 3124
Dworshak NFH	SF Clearwater	10_SFCLWR	OmySFCR_su20	2020	513	61 – 1296	2,538	1222 – 4009	0	0 – 0	1,490	318 – 2958
Dworshak NFH	Dworshak stock-trapped and spawned at Dworshak, reared at Magic Valley FH, released in Salmon basin	10_SFCLWR	OmyDWOS_su20	2020	148	0 – 445	0	0 – 0	0	0 – 0	53	0 – 158
Oxbow (IDFG)	Oxbow	14_UPSALM	OmyOXBO_su21	2021	4,198	2450 – 6032	0	0 – 0				
Pahsimeroi	Pashsimeroi	14_UPSALM	OmyPAHH_su21	2021	3,351	1816 – 5125	62	0 – 184				
Pahsimeroi	Upper Salmon	14_UPSALM	OmyUSAL_su21	2021	210	0 – 509	0	0 – 0	239	53 – 504	0	0 – 0
Sawtooth	Sawtooth	14_UPSALM	OmySAWT_su21	2021	7,796	5690 – 10112	0	0 – 0	53	0 – 158	0	0 – 0
Sawtooth	EF Salmon	14_UPSALM	OmyEFSW_su21	2021					171	0 – 514	0	0 – 0
Oxbow (IDFG)	Oxbow	14_UPSALM	OmyOXBO_su20	2020	1,980	973 – 3117	0	0 – 0	299	0 – 882	0	0 – 0
Pahsimeroi	Pashsimeroi	14_UPSALM	OmyPAHH_su20	2020	3,950	2279 – 5842	0	0 – 0				
Pahsimeroi	Upper Salmon	14_UPSALM	OmyUSAL_su20	2020	0	0 – 0	60	0 – 181				
Sawtooth	Sawtooth	14_UPSALM	OmySAWT_su20	2020	944	269 – 2012	0	0 – 0				
#N/A	#N/A	#N/A	Unassigned	#N/A	4,552	2759 – 6526	257	0 – 1061	52	0 – 158	294	0 – 882
			TOTAL		57,109		14,652		3,198		3,519	

Post-season analysis of Sockeye Salmon passing Bonneville Dam in 2023

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 7, 2023 (Table 42). 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 2023, there were 1,107 Sockeye Salmon that were sampled at the AFF and genotyped for this analysis (Table 67). This year we estimated low but non-zero abundance for the ESA listed stock (Redfish Lake Sockeye Salmon from the Snake River, abundance=3,036) (Table 67, Figure 46). The genetic analyses provide additional information that cannot be obtained by conventional tagging methods. For example, PIT-tags placed in adults at the Bonneville Dam AFF can identify the stock-of-origin only for fish that survive and are detected at upstream dams. However, the genetic analysis can provide stock-of-origin on most fish regardless of whether they survive further upstream of Bonneville Dam. This ability has allowed greater numbers of fish to be detected from the relatively rare ESA listed Snake River stock, which improves accuracy and precision of abundance estimates. In addition, the Lake Billy Chinook stock from the Deschutes River is rare and difficult to detect with PIT-tags because of limited arrays in the Deschutes River. Therefore, the ability for the genetic baseline to identify individuals from this stock provides the only way to effectively monitor this stock‘s abundance in the mainstem Columbia River. In 2023, we were able to estimate a small but non-zero abundance of the Lake Billy Chinook stock (abundance = 73 fish). Importantly, we have the ability to estimate the reintroduced stock from the Yakima River using our PBT baseline and the stock abundance estimate for 2023 was 669 fish (identified as BY2020). Although run years 2020 and 2021 had produced abundance estimates of the Yakima stock that were greater than 3,000 fish, recent years have shown a decline. However, 2020 – 2021 run 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.

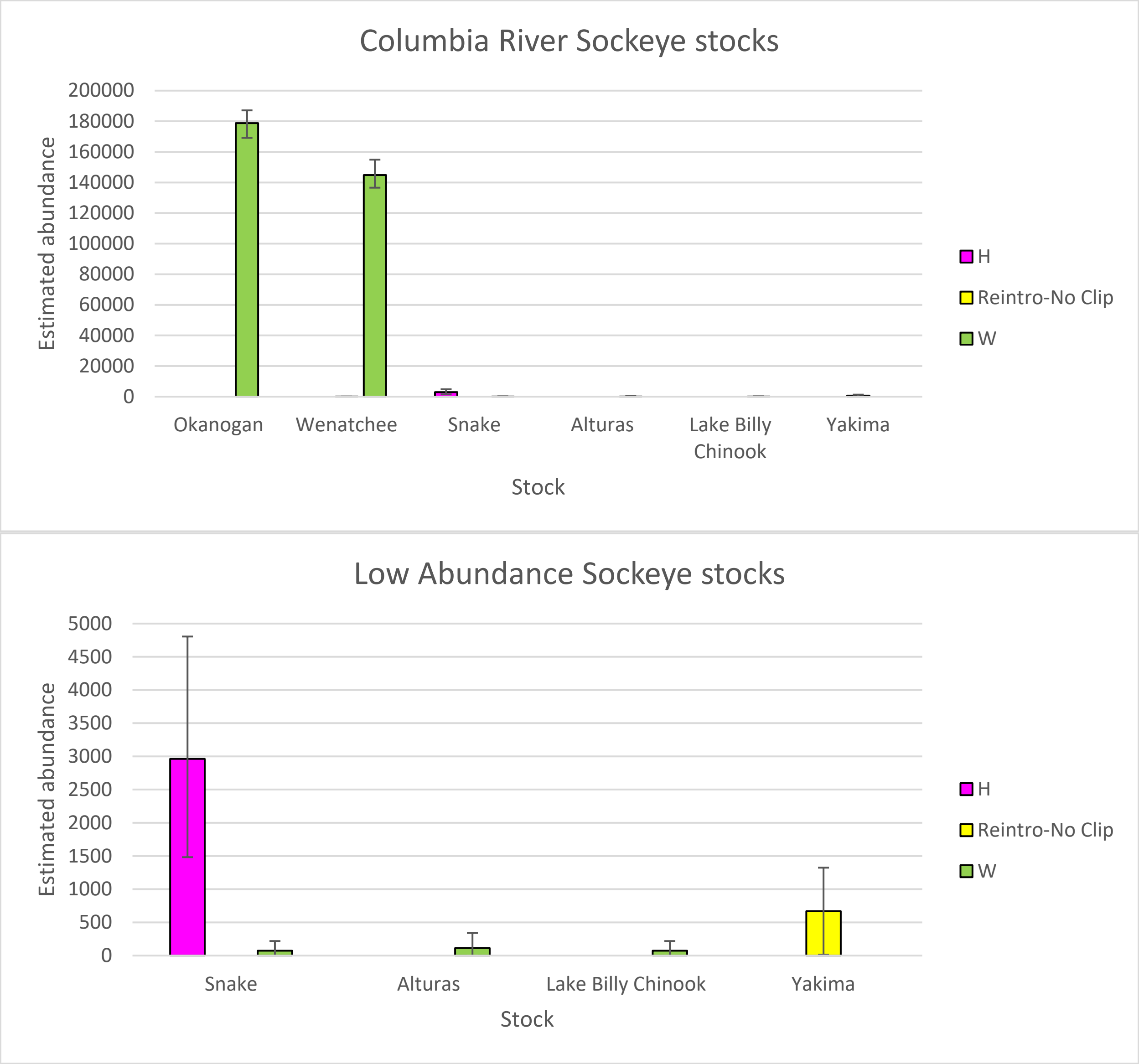


Figure 46. Estimated abundance (± 95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2023.

Table 67. Estimated abundance of Sockeye Salmon genetic stocks that passed Bonneville Dam in 2023.

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					178,796	169131 – 187099			648	648
Wenatchee			73	0 – 73	144,840	136573 – 154893			442	442
Snake	2,963	1482 – 4805			73	0 – 219	14		1	15
Alturas					113	0 – 340			1	
Lake Billy Chinook					73	0 – 219			1	1
Yakima			669	13 – 1324				1		1
Total	2,963		742		323,896		14	1	1,093	1,107

Note: The abundance is estimated from the total fish counts at the fish ladder windows at Bonneville Dam. Most stocks are identified 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 96% of fish that were clipped hatchery-origin summer A-/B-Index steelhead at Bonneville Dam in 2022 to 35 broodstock sources. This percentage of PBT assigned abundance is consistently high over recent years and demonstrates our baseline has complete coverage of hatcheries above Bonneville Dam and our tag rates reflect true values (mostly >90%). We observed that this high rate of PBT assignments of clipped steelhead appears to be maintained based on the in-season analyses of steelhead at Bonneville Dam in 2023 (93%).

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 2023. Namely, the percentage of adipose-clipped fish abundance that were estimated to be PBT broodstock ranged from 92 – 100%, 86 – 100%, and 93 – 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 all three management periods attained high percentages gives us confidence that the PBT baseline coverage is nearly complete for Chinook Salmon above Bonneville Dam. Even the summer management period showed a high average of 93% across all weeks.

This is the fourth 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 (2018). The trend suggested 322 smolts were needed to be released to equal 1 adult-sized 4-year-old Spring Chinook at Bonneville Dam in 2022. Further, we estimated that 333 smolts of summer- and fall-run Chinook salmon were needed to equal 1 adult-sized 3- or 4-year-old at Bonneville Dam in 2021 and 2022. Future work could sum all abundance of the SY2018 adult return across age-classes (i.e., age 3, 4, and 5 in run years 2021, 2022, and 2023, 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 several 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 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 15 major clipped Chinook salmon hatchery-origin stocks (66 clipped hatchery broodstock sources), 7 major unclipped hatchery-origin stocks (52 unclipped hatchery broodstock sources) and 11 natural-origin stocks estimated to have relative abundances ≥1,000 fish passing Bonneville Dam in 2022. The Spring Chinook stocks of 2022 were observed to spillover into the summer period by 5% for hatchery-origin stocks and 15% for natural-origin stocks out of the total estimated abundance of these stocks across spring and summer periods. This overlap of run distributions of natural-origin Spring stocks in the summer period was not as extreme as the overlap of upper Columbia River summer-run stocks that spill into the spring period. In fact, the summer-run stocks from the upper Columbia River showed more than a quarter (23 – 42%) 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, two major unclipped hatchery-origin stock (15 major hatchery broodstock sources), and four major natural-origin stocks estimated to have relative abundances ≥1,000 fish passing Bonneville Dam in 2022. 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 2022, the relatively large (≥78 cm) steelhead were found primarily to originate from Dworshak hatchery broodstock (OmyDWOC_su19, OmySFCR_su19). 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. However in addition to Dworshak, there were fish from Wells Hatchery in the upper Columbia (OmyWELL_su19) and some fish released to the upper Salmon River (OmyUSAL_su19) that were major B-sized sources of abundance. 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 eleventh 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 2022 and found that the Okanogan stock has the greatest relative abundance followed by the Wenatchee stock. We found 2,456 fish from the Snake River stock, estimated 0 fish from Lake Billy Chinook and the reintroduced stock in Yakima River (based on PBT). We also found that the migratory run timing for all the Sockeye salmon stocks overlaps broadly at Bonneville Dam.

This year (2023) 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.

References

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

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

Section 5: Local adaptation in salmonids

Introduction

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

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

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

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

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

Fish Population RM&E

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

Uncertainty Research

See Appendix A for table of critical uncertainties research.

Project Map:
http://www.cbfish.org/Project.mvc/Map/2009-005-00
Contract Map(s):
http://www.cbfish.org/Contract.mvc/Map/61839
http://www.cbfish.org/Contract.mvc/Map/65575

Methods: Protocols, Study Designs, and Study Area

Method Title: Whole Genome Resequencing

- **Method Link:**
- Whole Genome Resequencing: Poolseq Individual Barcode v1.0 (ID: 6754) Published
- Whole Genome Resequencing: Poolseq Pooled v1.0 (ID: 6775) Published

Method Summary:

With reference genome assemblies now publicly available for both Chinook salmon and steelhead, this enables whole genome resequencing for investigating adaptive variation across a large portion of the genome (50-80%) in these species. Whole genome resequencing methods include individually barcoded samples, or pools of samples (Pool-seq; Schlotterer et al. 2014) depending on the study design. For both methods, sequence data is aligned to the reference genome assembly, and allele frequencies from millions of SNPs are analyzed to detect statistically significant regions of the genome associated with specific traits or adaptation to environmental factors. Putatively neutral regions of the genome are also useful for standard phylogeny and demographic analyses of populations. In most studies, allele frequencies are available for collections but sequencing depth is typically not high enough to provide individual genotypes. However, candidate SNPs may be developed into standard panels with GTseq or other approaches to genotype many individuals to validate trait association, determine inheritance, and estimate linkage disequilibrium.

Method Title: RAD sequencing v1.0
Method Link: http://www.monitoringmethods.org/Method/Details/4144
Method Summary:
RAD sequencing is a technique for tagging DNA at restriction enzyme cut sites with adapters used in massively parallel sequencing. This method allows thousands of SNPs to be discovered and genotyped in several individuals. Through the use of sample specific DNA barcodes included in the adapters, information for specific samples can be separated in silico following sequencing. This method effectively reduces sequence complexity by targeting only sequence surrounding restriction enzyme cut sites making alignments among sequencing reads far less computationally intense. The sequence alignments among samples can then be analyzed for both identification and genotyping of SNPs (Single Nucleotide Polymorphisms). This method was first described by Baird et al. (2008).

Method Title: Obtain gene expression data via RNAseq v1.0
Method Link: http://www.monitoringmethods.org/Method/Details/607
Method Summary:
Compare gene expression between fish of different genetic backgrounds but raised in the same environment. Molecular techniques such as RNAseq provide the opportunity to investigate transcriptional response and further identify mechanisms for thermal adaptation. Patterns of gene expression are important to determining evolutionary adaptation among conspecific populations that occupy various environments.

Results

Objective 1) Environment & Landscape Genetics

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

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

Activities implemented:
Multiple studies have been initiated to investigate local adaptation with a landscape genetics/genomics approach to address the two hypotheses above. Our work has focused on steelhead and Chinook salmon throughout the Columbia River Basin. Studies continue to progress as more markers become available throughout the genome of each species.
For steelhead, landscape genetics work has been done at both fine and broad scales. Fine scale landscape genetics approaches were used to identify ecological patterns of residence vs anadromy and found consistent evidence that certain landscape features have led to prevalence of certain life history types in *O. mykiss* (Narum et al. 2008a) but also *O. nerka* (Nichols et al. 2016). Broad scale studies were initially done with panel of 188 SNP markers to investigate patterns of landscape genetics across 145 populations in the Columbia River Basin (Matala et al. 2014). Results indicated that precipitation and temperature were the primary environmental drivers of local adaptation and neutral genetic structure largely reflected isolation by distance. These results were shown to be robust due to replication of multiple populations representing each distinct genetic unit (Hand et al. 2016). A follow-up study (Micheletti et al. 2018a) was done with a much larger number of genetic markers (~20K SNPs) at broad scale and found evidence that the mainstem Columbia River migratory corridor exhibits greater selective pressure on steelhead than natal tributaries (Figure 47). 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 **68**). 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 48a). Annual precipitation had the greatest effect when all collections were analyzed together (Figure 48a). Environmental variables retained in the coastal lineage RDA were average temperature of the coldest quarter and precipitation of the wettest month (Figure 48b). Environmental variables retained in the interior lineage RDA were 20-year average

August water temperature and minimum temperature of the warmest month (Figure 48c). 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.

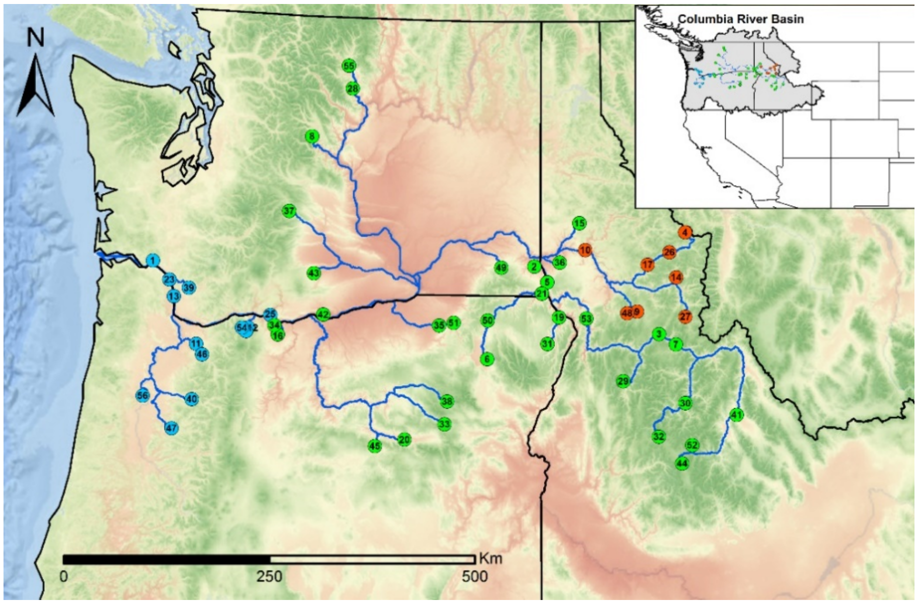


Figure 47. **Steelhead collection localities colored by genetic cluster (from Micheletti et al. 2018a). blue = coastal, green = inland, red = inland-Clearwater. Blue lines indicate each population's migration path to the ocean. Map layer shows mean annual temperature for the warmest quarter with transition from colder (green) to warmer (red).**

Table 68. **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_meantrange	Mean Diurnal Range	°C	1000	Temperature	WorldClim	N
B3_isotherm	Isothermality	°C	1000	Temperature	WorldClim	Y
B4_tseason	Temp Seasonality	°C	1000	Temperature	WorldClim	N
B5_maxtwarmmon	Max Temp Warmest Month	°C	1000	Temperature	WorldClim	Y
B6_mintcoldmon	Min Temp Coldest Month	°C	1000	Temperature	WorldClim	N
B7_trange	Temp Annual Range	°C	1000	Temperature	WorldClim	N
B8_meantwetq	Mean Temp Wettest Quarter	°C	1000	Temperature	WorldClim	N
B9_meantdryq	Mean Temp Driest Quarter	°C	1000	Temperature	WorldClim	N
B10_meantwarmq	Mean Temp Warmest Quarter	°C	1000	Temperature	WorldClim	N
B11_meantcoldq	Mean Temp Coldest Quarter	°C	1000	Temperature	WorldClim	Y
B12_Prec	Annual Precip	mm	1000	Precipitation	WorldClim	Y
B13_precwetmon	Precip Wettest Month	mm	1000	Precipitation	WorldClim	Y
B14_precdrymon	Precip Driest Month	mm	1000	Precipitation	WorldClim	N
B15_precseason	Precip Seasonality	mm	1000	Precipitation	WorldClim	N
B16_precwetq	Precip Wettest Quarter	mm	1000	Precipitation	WorldClim	N
B17_precdryq	Precip Driest Quarter	mm	1000	Precipitation	WorldClim	N
B18_precwarmq	Precip Warmest Quarter	mm	1000	Precipitation	WorldClim	N
B19_preccoldq	Precip Coldest Quarter	mm	1000	Precipitation	WorldClim	N

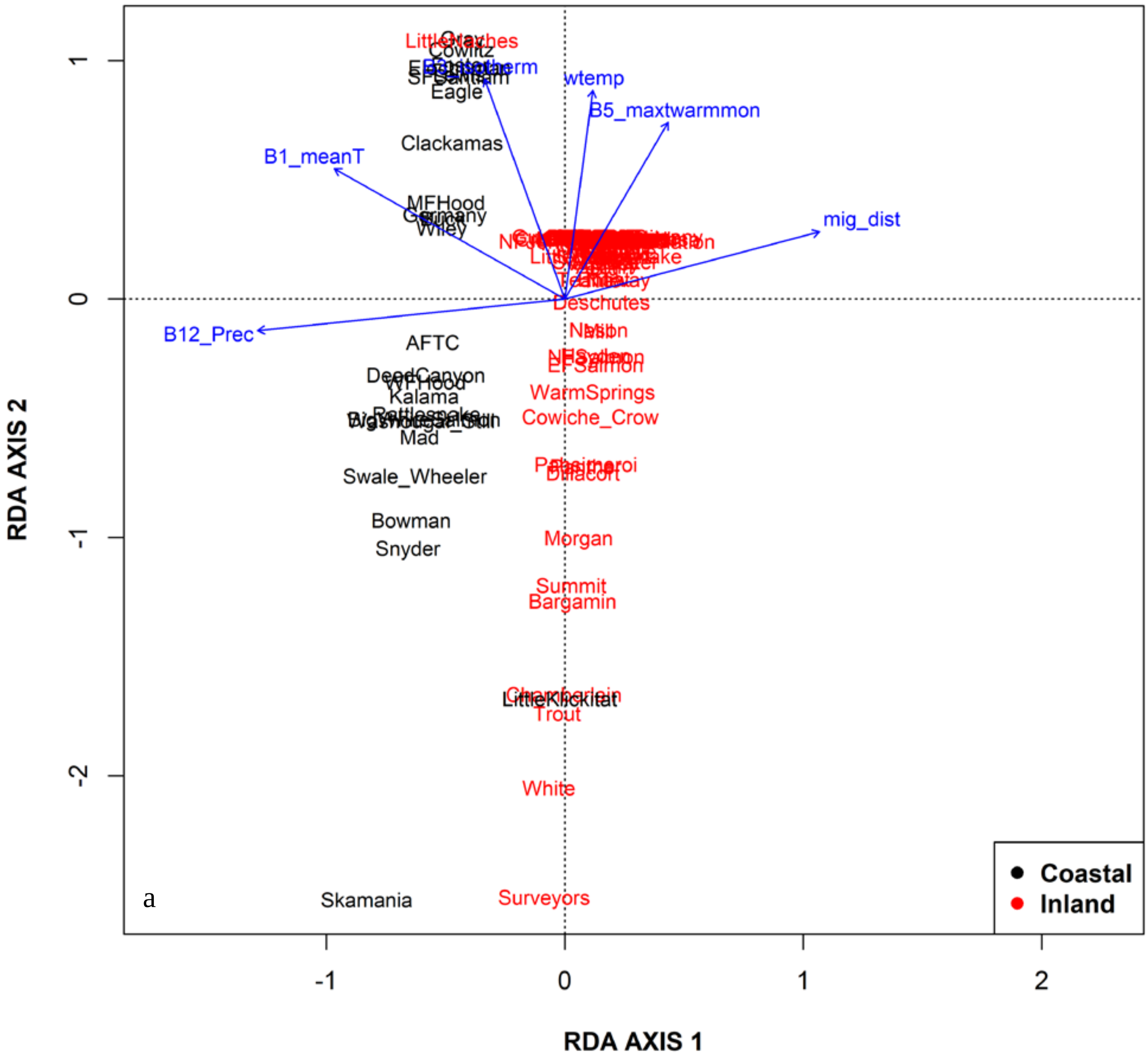
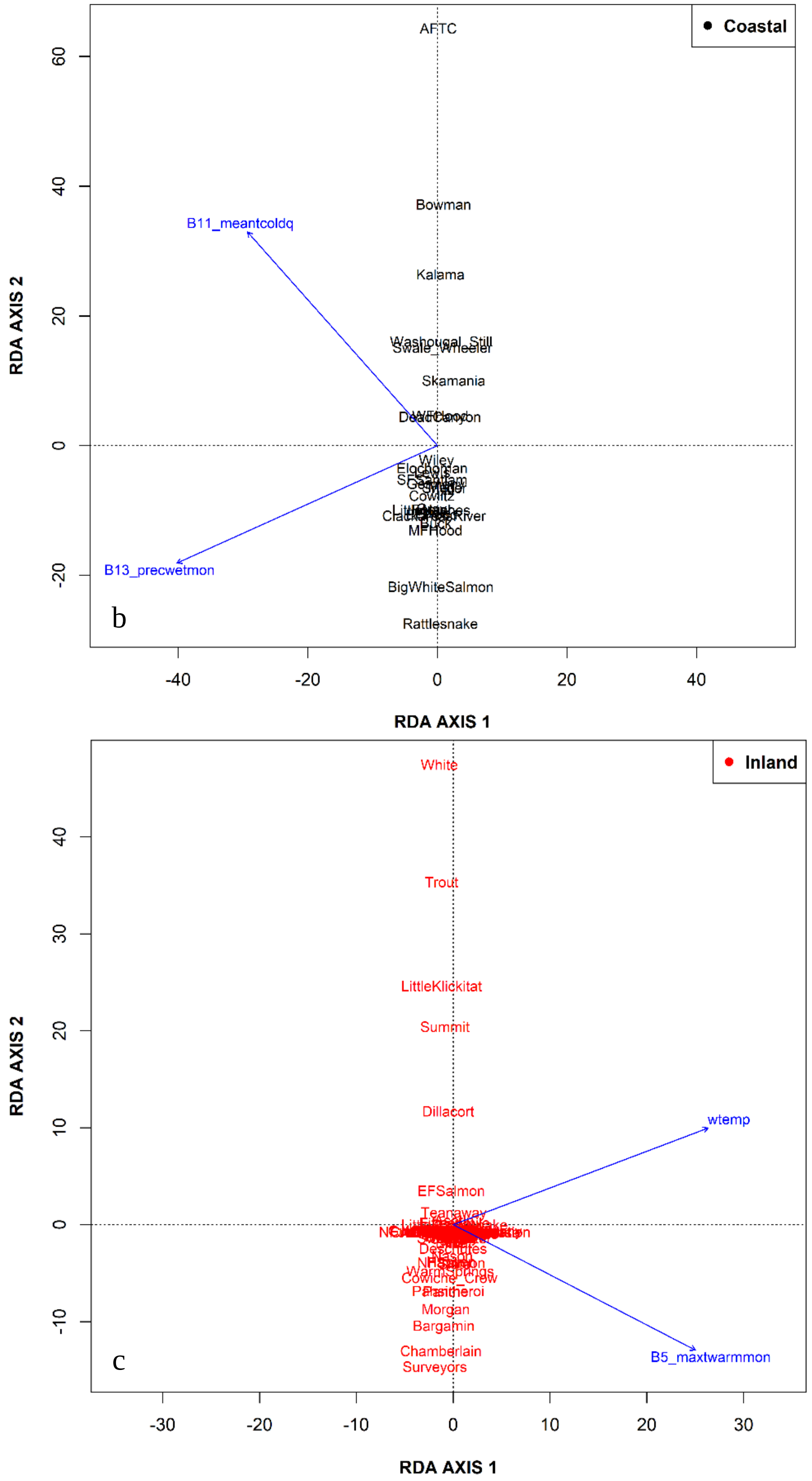


Figure 48 a-c. RDA of all steelhead collections in Columbia River basin to model the degree to which the variation in environmental variables explains the variation in allele frequencies for candidate markers for all collections in the *greb1L* haplotype block (2,3,6). Coastal populations (b) and inland populations (c) were analyzed separately.


● Coastal
AFTC
Bowman
B11_meantcoldq
Kalama
Washougal_Still
Swale_Wheeler
Skamania
DeadCanyon
WFHood
Wiley
Elochoman
Cowlitz
ClackamasRiver
MFHood
B13_precwetmon
BigWhiteSalmon
Rattlesnake
b
RDA AXIS 2
RDA AXIS 1
60
40
20
0
-20
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-20
0
20
40
● Inland
White
Trout
LittleKlickitat
Summit
Dillacort
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EFSalmon
Tearaway
Deschutes
WarmSprings
Cowiche_Crew
Panther
Morgan
Bargamin
Chamberlain
Surveyors
B5_maxtwarmmon
c
RDA AXIS 2
RDA AXIS 1
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Figure 48 **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 **49**a). Several candidate markers were associated with local adaptation within and among lineages (Figure **49**b; 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.

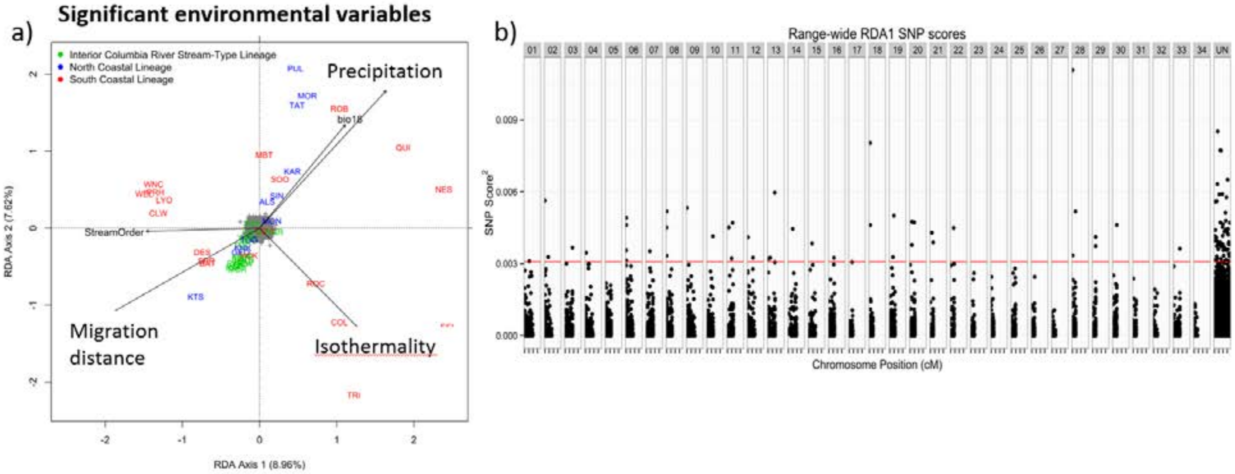


Figure 49. **a) Environmental drivers of selection and b) candidate markers for local adaptation in Chinook salmon (from Hecht et al. 2015). a) Population scores for canonical RDA axis 1 and 2 are represented by the three-letter abbreviation for each population, coloured to represent the lineage assignment 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 4 & Table 6) 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:
<u>Hypothesis 1</u>: 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.
<u>Hypothesis 2</u>: 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).

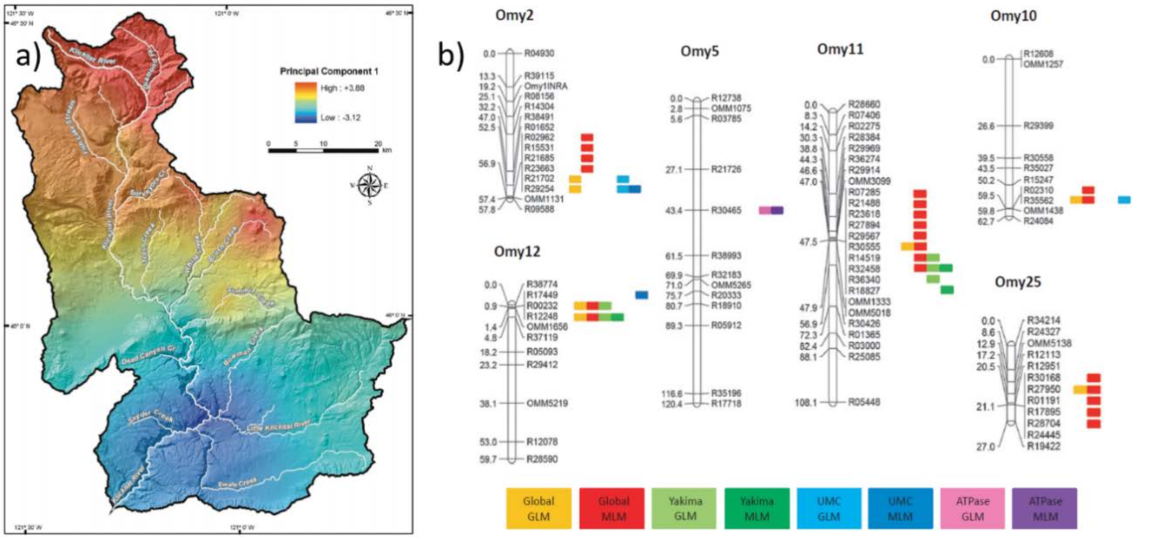


Figure 50. **a) Synthesis map illustrating interpolation principal component (PC1) that accounts for 59% of variation in resident (red) vs anadromous (red) life history (from Narum et al. 2008a). b) Significant loci detected from eight individual association tests, where each test is represented by a 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 51; Collins et al. 2022). Results indicate that the significant regionon 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. Primer design is complicated in this region by structural variation but testing is ongoing to develop markers.

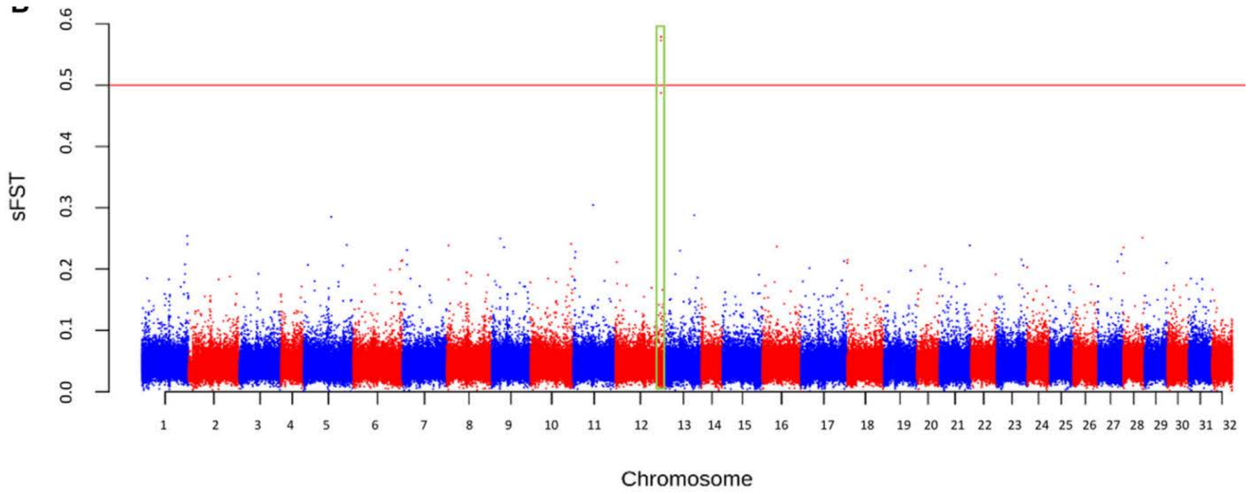


Figure 51. Manhattan plot of differences in allele frequencies between resident and anadromous collections across the genome based on sliding window FST (sFST). The minimum coverage threshold was 15 reads and the minor allele frequency was > = 0.05. (from Collins et al. 2022)

Run-timing related to maturity in steelhead (Hess et al. 2016; Micheletti et al. 2018c; Collins et al. 2020; Willis et al. 2020; Willis et al. 2023) and Chinook salmon (Hess and Narum 2011; Narum et al. 2018; Koch and Narum 2020; Willis et al. 2021; Horn and Narum 2023) 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 52). The major findings of studies to date were synthesized in a recent publication (Narum et al. 2023).

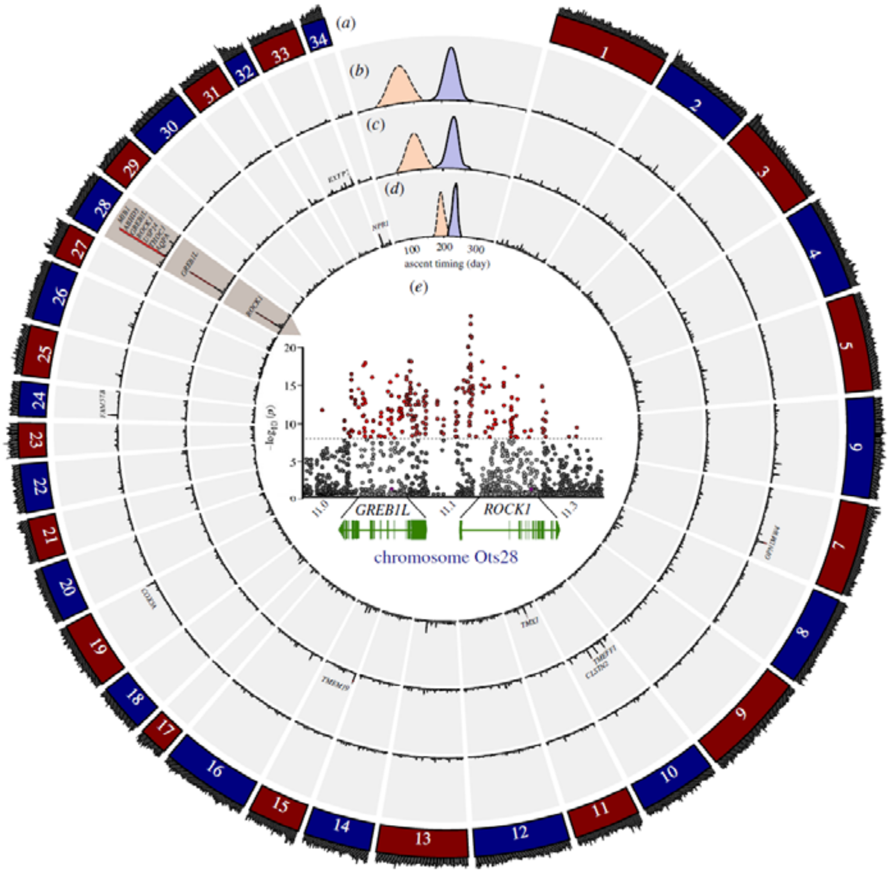


Figure 52. Manhattan plot for premature and mature collections of Chinook salmon (from Narum et al. 2018). (a) Sequence coverage (black outer ring) for each chromosome. (b) Significant divergence between premature and mature migrating coastal lineage Chinook salmon. (c) Significant divergence between 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 GREB1 L, 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 **69**). 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 migration timing from the whole genome resequencing conducted by Micheletti et al. (2018c). Premature, mature, and heterozygote genotypes for adult migration timing were established based on genotype association from previous studies (Hess et al. 2016; Micheletti et al. 2018c), as well as using a reference collection of Skamania Hatchery steelhead, which is a hatchery-strain intensively selected for early adult migration and cultured since 1956 with steelhead from the Washougal and Klickitat Rivers (Crawford et al. 1979; Chilcote et al. 1986). Premature, mature, and heterozygote adult migration timing genotype proportions were assessed across all collection locations. A total of 9,471 individuals from 113 populations met inclusion criteria (>90% loci successfully genotyped and had an estimated <0.5% genotyping error based on replicate genotyping) and were included in this study. Further validation of assocation with run-timing phenotypes and genotypes from Chr28 was demonstrated in Willis et al. (2020).

Table 69. 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	*greb1L*	TGACACTGATCACAATGGTGAAAT	TAAACTGGAAGGAGAGAGCAAAAT	TGTGGGCTGC**[A/G]**AACATACTCA	+
2	Omy_RAD52458-17	28	11609794	*greb1L*	ACGTGTCCCTGAGGATGGTA	AGCTCTAGGTCTGGGTCCTG	ATGGCCC**[C/A][**CT]AAGAACCC	-
3	Omy_GREB1_05	28	11618027	*greb1L*	TGGGCAGATATGGAAGAACGG	ACCTTCTAAATGGCCTCTGTGT	CGGTGGCTC**[T/G]**C	+
4	Omy28_11625241	28	11625241	*greb1L*	CAACATTTAGGGAGAGGTTGCTAT	ATCATCAAGTTTGCCTACGACAC	CCTCCTCCCT**[A/G]**TGGTTGTCTC	+
5	Omy28_11632591	28	11632591	*greb1L*	GTAGAGGCCAAAGGCTTGAG	TGCTCTTATTACCTTCCAGACTCC	TGAGAA**[G/A]**AACACAGAGG	+
6	Omy_GREB1_09	28	11641623	*greb1L*	CCAGTGGCAACCTCAGGTAG	GACTCCAGTCACCCAAGTCA	TCAA**[T/G]**GGAGA	+
7	Omy28_11658853	28	11658853	intergenic	CAACATATGACCACTCGAAAACTC	ATTAATCACACCGTGAGACTCCTC	TGGTACAGAC**[A/C]**CGCACTAGCA	+
8	Omy28_11667578	28	11667578	intergenic	ACAGTAAACCCATTCAGGCATAGT	TTATCCTCTCAATCCACATCAAGA	GTATTGATCC**[T/C]**GTGGGAGACA	+
9	Omy_RAD47080-54	28	11667915	intergenic	TCAAAACCTGCAGGACTTGGA	TGGTTATATCTACAGTACAGTTCGT	TGCAAG**[A/G]**CTTAAAACGA	+
10	Omy28_11671116	28	11671116	intergenic	AATTTCCCCAAATTTGAAACTCTT	GTGTACATTGTCAGGCAGAAACAT	CTGGTGAGAA**[C/T]**AGGAATTACC	+
11	Omy28_11676622	28	11676622	intergenic	CGAATGCACTGTAGCTCATTCTAA	GCAGTAGAATGTCTCGCAAATACA	ACATGTCATT**[T/G]**ATTGTTATCT	+
12	Omy28_11683204	28	11683204	intergenic	CAAGAAAGAAACAGATGTTGTCCA	TTGTGACTCAAATCTGCAACCTAT	ATGTAAAAAA**[G/T]**GGCAGAAAA	+
13	Omy28_11773194	28	11773194	*rock1*	AGTTTGACACCCCTGTACTAGAGC	GTCTAACAAGCTCTGGGTGATTTA	GCAATTTTTT**[T/A]**AAATTACCGC	+

We assessed linkage disequilibrium (LD) within the 13 candidate markers to identify haplotype blocks that would be informative for estimating frequencies of adult migration types. Candidate markers were analyzed for all sampling locations in Haploview with solid spine and this resulted in two haploblocks, one with markers 1-7 and another with markers 8-13 (Figure 53). 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.

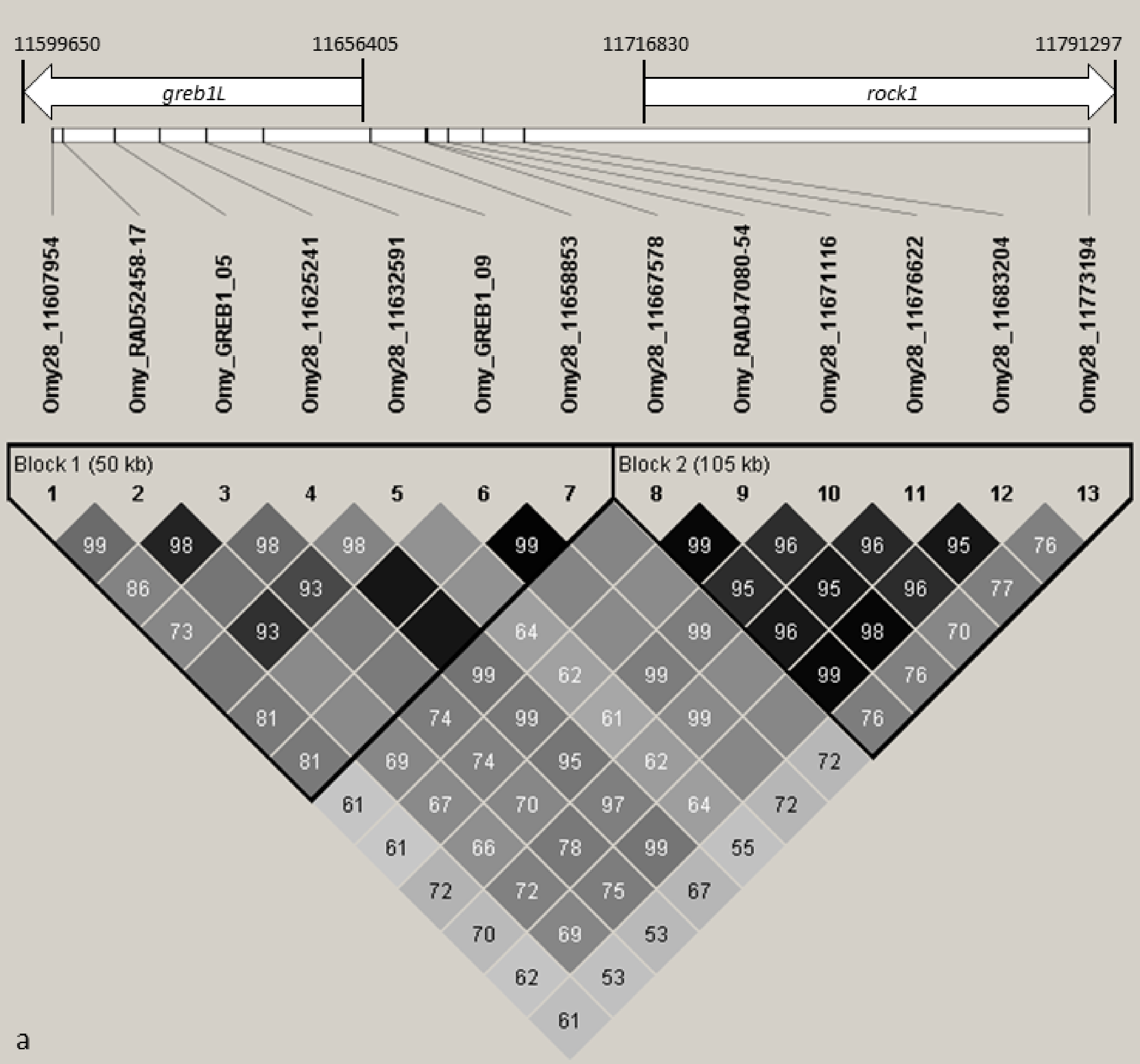
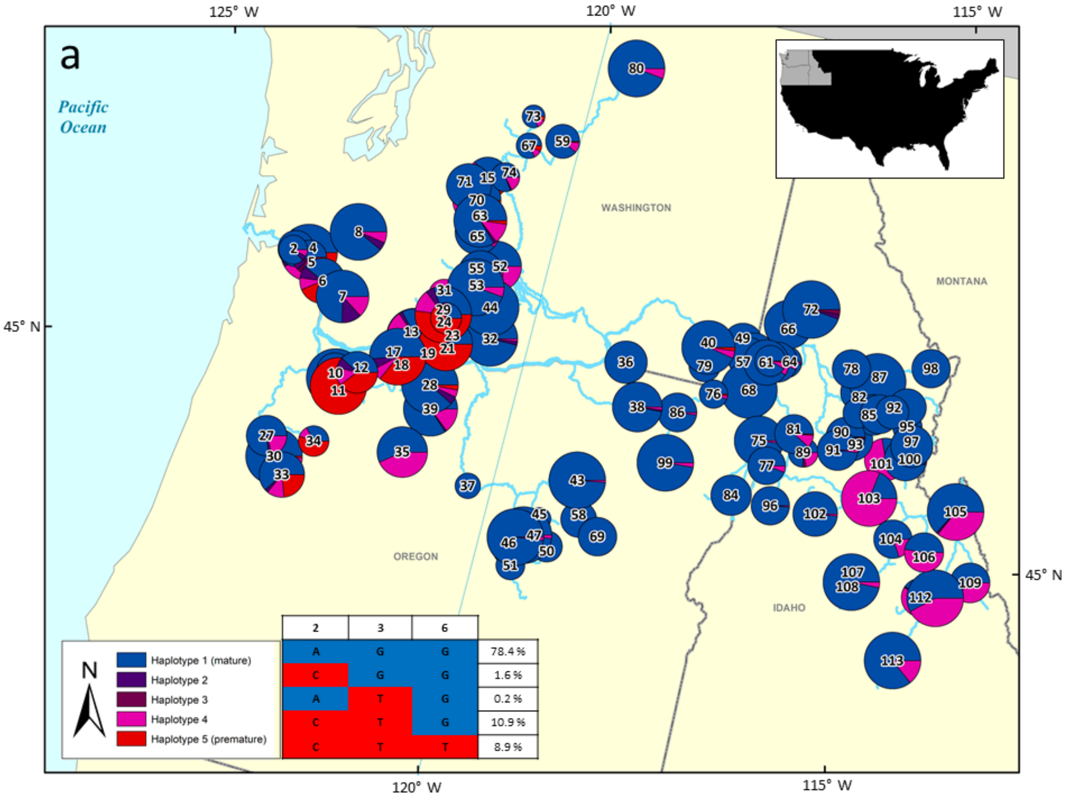


Figure 53. **Linkage relationships for 13 candidate markers in Haploview for all steelhead populations.**

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 54a. 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 54a). The haplotypes with a mixture of blue and red represent the different possible heterozygote genotypes (Figure 54a). 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 54a-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 54a). Haplotype frequencies for collections (Figure 54a) showed similar patterns of geographic distribution as the genotype frequencies (Figure 54b), but with improved resolution for heterozygous haplotypes that were within a single haplotype block underlying *greb1L*. According to results of overall haplotype frequency (Figure 54a), 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 54a).



2	3	6	
A	G	G	78.4 %
C	G	G	1.6 %
A	T	G	0.2 %
C	T	G	10.9 %
C	T	T	8.9 %

Figure 54a. **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.**

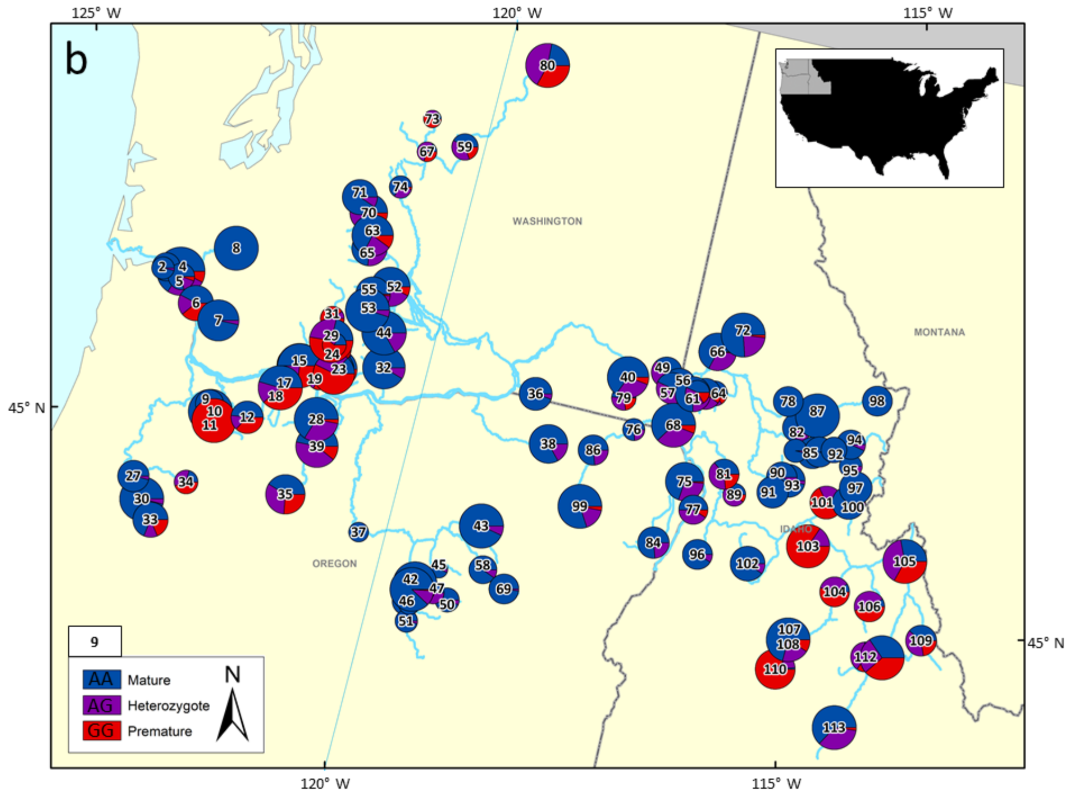


Figure 54**b.**

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 55; 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 56). 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.

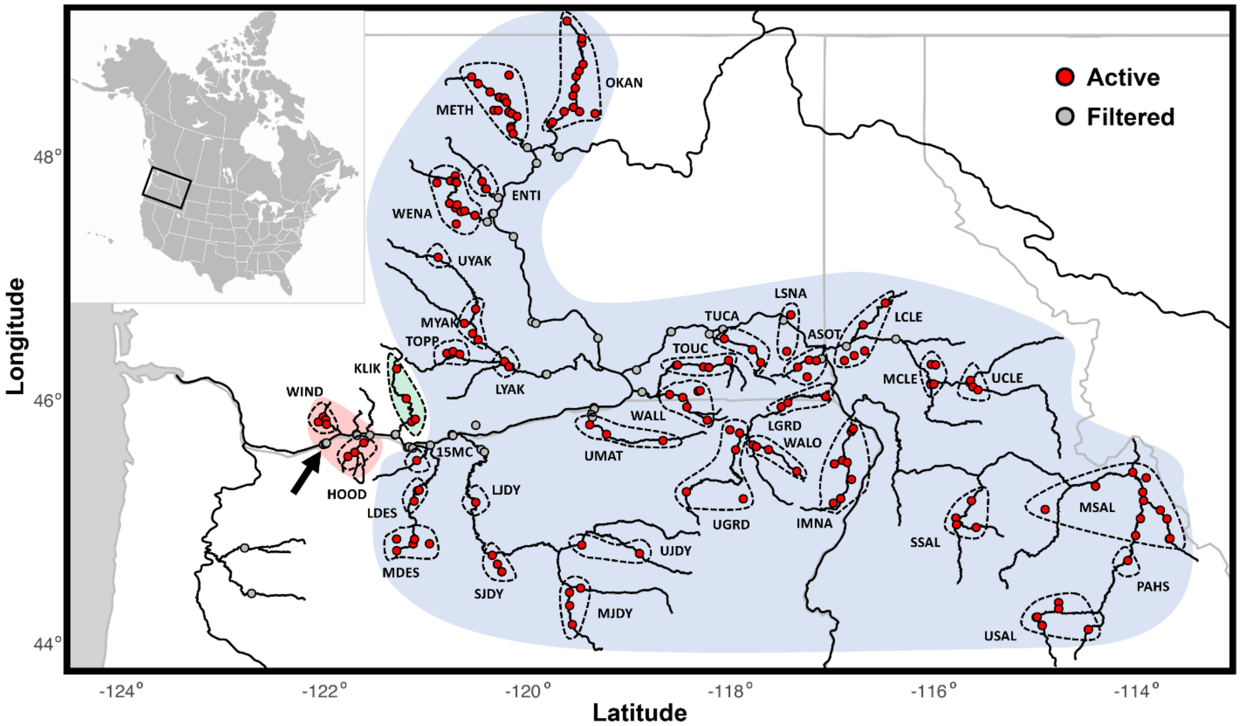


Figure 55. Columbia River Basin with active and filtered passive integrated transponder arrays. River courses in black; borders and coast in gray. Hydrological unit groupings, identified by dashed lines, are organized into lineages and sub-basins as follows: coastal lineage in Red, intermediate lineage affiliation in Green, inland lineage in Blue; Bonneville Dam is identified by an arrow.

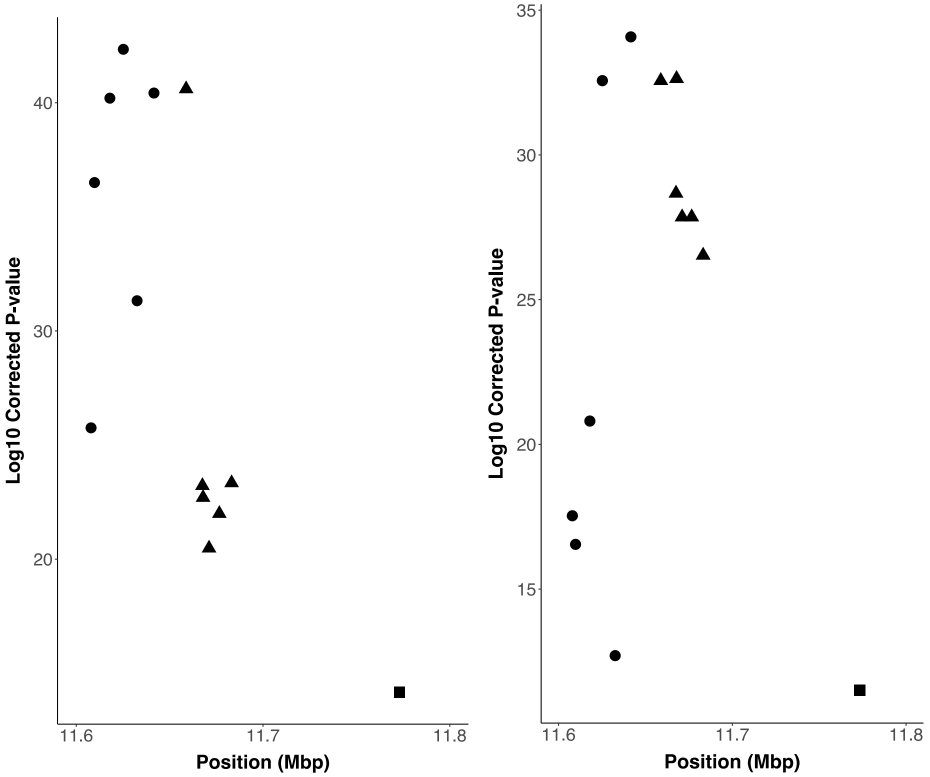


Figure 56. Significance of association of chromosome 28 markers with run timing in BONAFF (left) and Hood River (right) steelhead. Position refers to SNP locus position on chromosome 28. Circle: GREB1L, triangle: intergenic; square: ROCK1.

Given the complexity of genotype-phenotype associations for lineages of Steelhead within the Columbia River basin, more extensive whole genome resequencing was determined necessary to further examine variation from all SNPs in the GREB1L through ROCK1 region (Willis et al. 2023). A total of 74 populations of Steelhead (n=4,873) were individually barcoded and sequenced at low depth to estimate allele frequencies within each population to test for differences among groups. The coastal lineage included populations that represented summer vs. winter migration timing, and also included the Skamania strain that exhibits extreme early summer migration and acts as an effective reference collection for alleles associated with early migration. A heat map of allele frequencies (**Figure 57**) illustrated the differences in allele frequency across populations with a range of adult migration timing. Differences in allele frequency between early and late collections of coastal lineage Steelhead indicated the breadth of association for this phenotype spanned approximately 112Kb from the GREB1L region through the intergenic region and into the 5’ end of ROCK1. In contrast, the inland lineage was represented by Steelhead that had a gradient of passage timing over Bonneville Dam, with the earliest returning fish from Middle Fork Salmon and the latest returning fish from populations in the Clearwater River (Hess et al. 2016a). This lineage generally had low variation in the GREB1L gene region compared to high variation through the intergenic region, and the breadth of association in the inland lineage was estimated to be only ~26Kb of the intergenic region of Omy28 (with exceptions in a few populations).

Examination of allele frequencies across populations suggested that SNPs in the intergenic region were the most informative for migration timing of inland lineage Steelhead of the Columbia River , and early alleles in this intergenic region were more common in regional populations such as the upper Columbia, Klickitat, lower Salmon, Middle Fork Salmon, and upper Salmon rivers (Willis et al. 2023). The loss of variation in the GREB1L region may be directly related to the constricted return timing of inland lineage steelhead, especially if this gene directly effects freshwater entry timing.

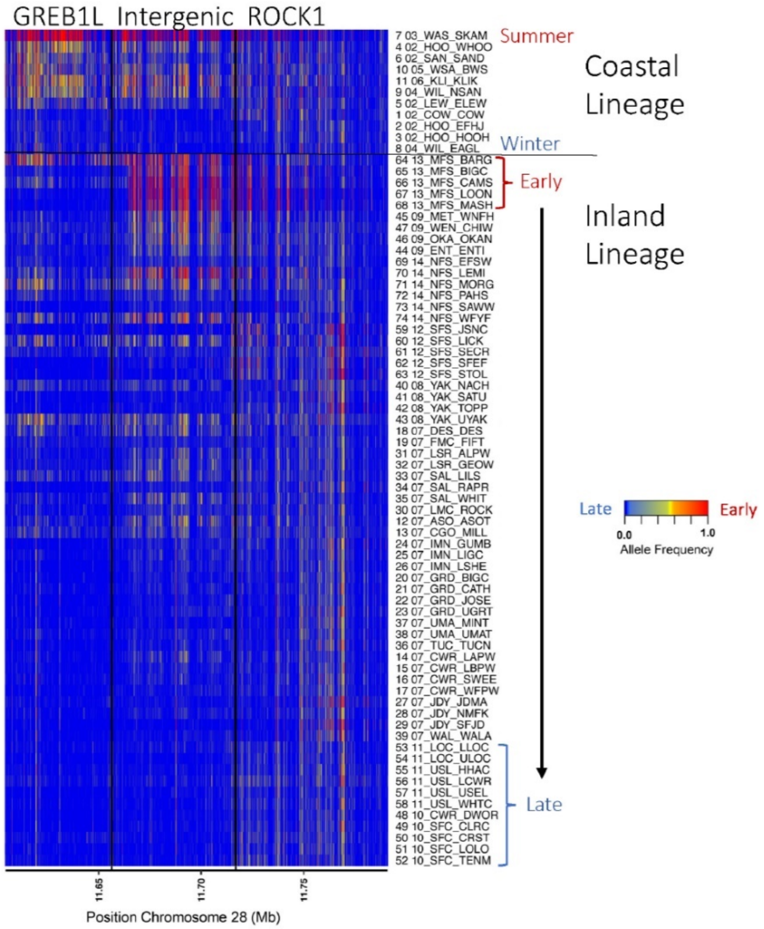


Figure 57. Allele frequencies for hundreds of SNPs spanning GREB1 through ROCK1 for 74 populations of Steelhead based on wholegenome sequencing (Willis et al., 2023). Populations are sorted within each lineage by early at the top and late at the bottom. The coastal lineage includes the Skamania stock at the top that is nearly fixed for early alleles due to artificial selection. The legend shows the scale of frequency for populations ranging from early (red) to late (blue).

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

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

Association tests validated that the majority of markers were significantly associated with migration timing for all three lineages (Figure 59). The strongest association was consistently observed for markers within or upstream of the rock1 gene, closely followed by markers located within or upstream of greb1L. Out of the 33 candidate SNPs, 13 SNPs were significantly associated with fitness (Figure 60).

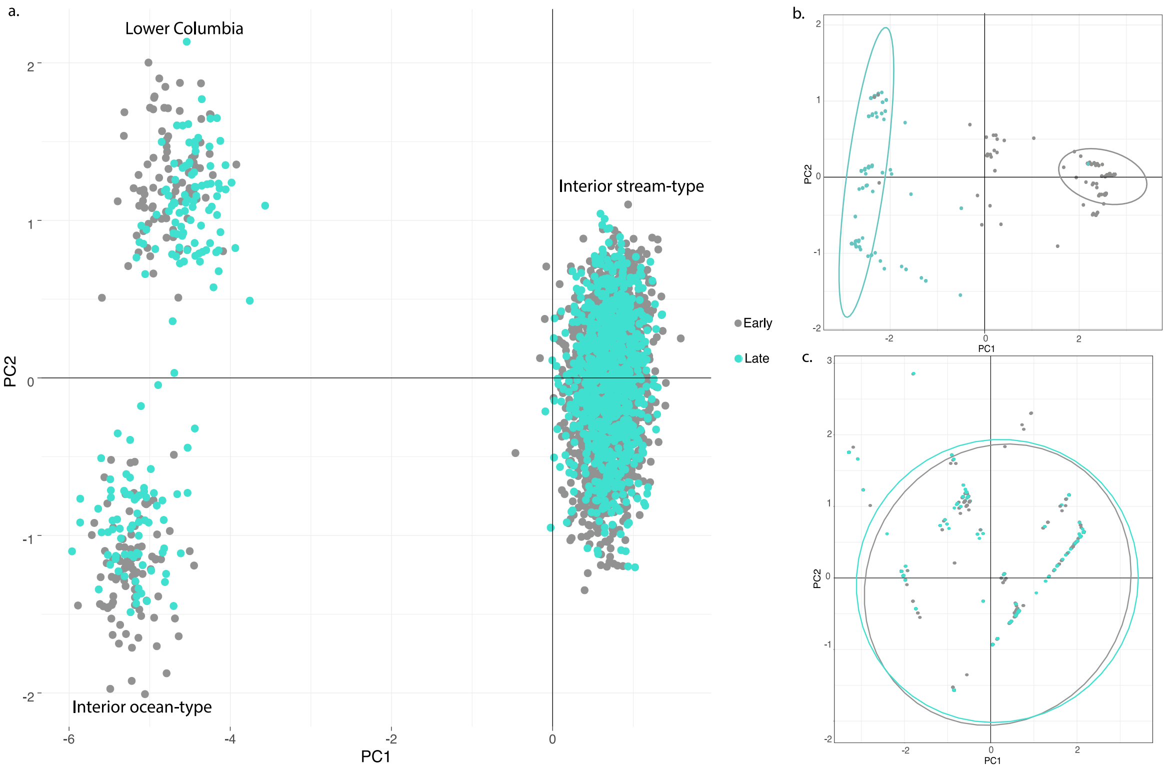


Figure 58. PCA of genetic variation in Chinook Salmon (from Koch and Narum 2020). Results presented represent A) 185 neutral SNP markers, B) 33 chromosome 28 markers for the Lower Columbia and Interior ocean-type populations combined, and C) 33 chromosome 28 markers for the Interior stream-type population.

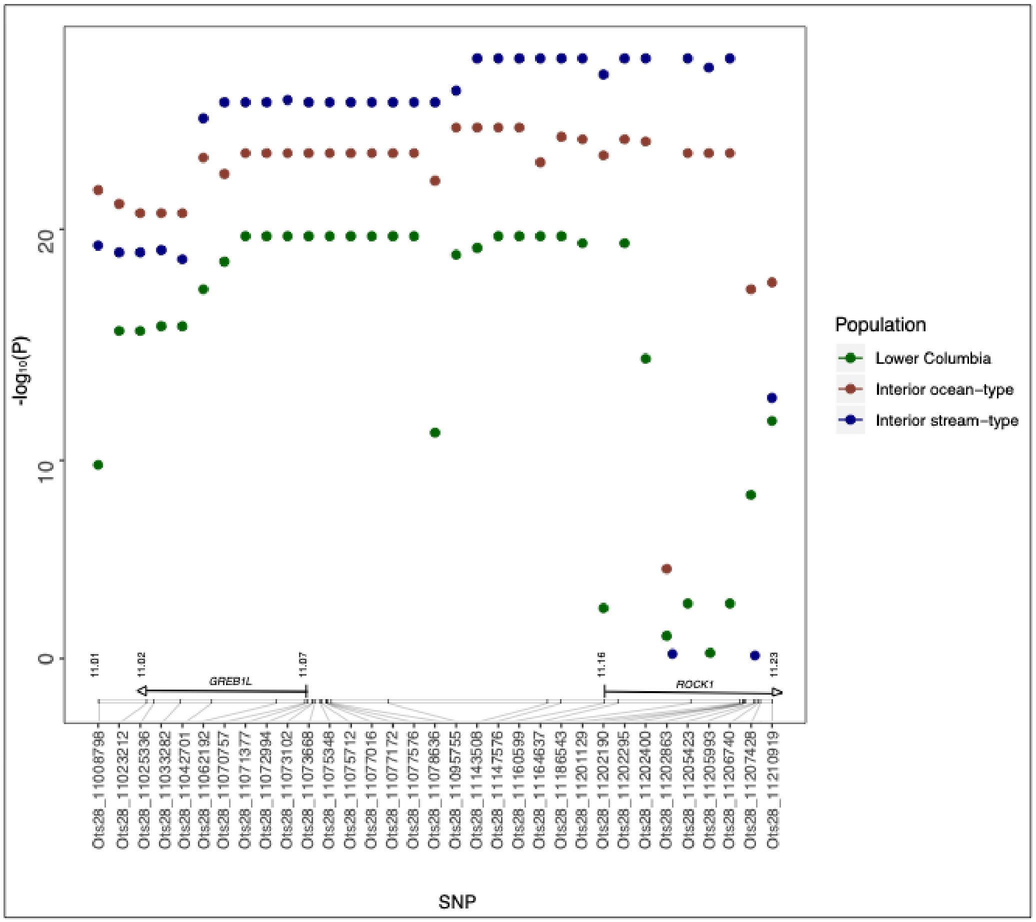


Figure 59. Association of each candidate SNP marker with migration timing within three lineages of Chinook Salmon (from Koch and Narum 2020). The colored dots for each lineage represent sliding windows for consecutive pairs of SNPs along the candidate genomic region. SNP number on the x-axis corresponds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

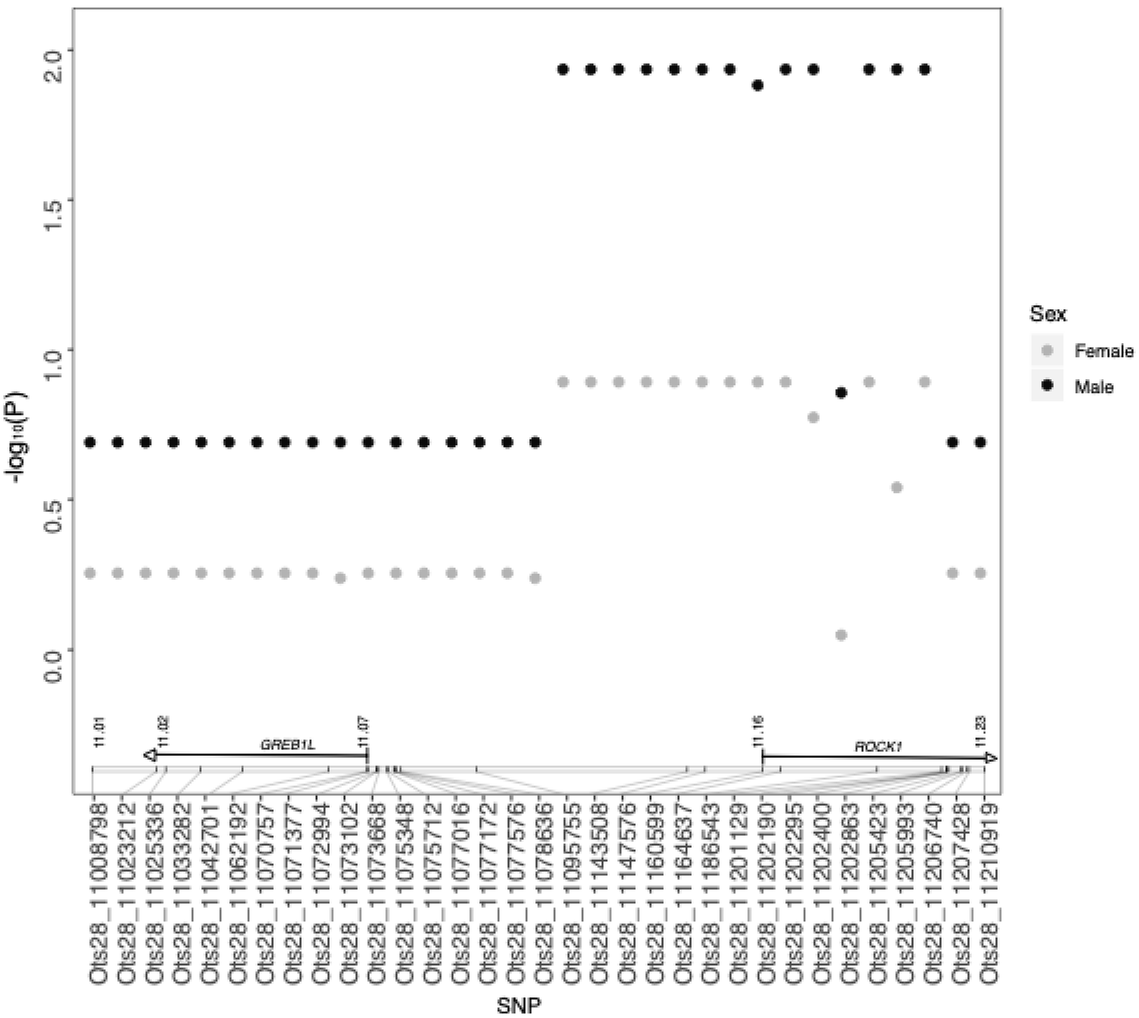


Figure 60. Association of each candidate SNP marker with fitness within the Interior stream-type population. The dots represent sliding windows for consecutive pairs of SNPs along the candidate genomic region with sexes presented separately. SNP number on the x-axis corresponds to the 33 candidate markers, while the genome position of markers on chromosome 28 (NCBI accession GCA_002831465.1) is depicted in the gene diagrams above the x-axis. Y-axis represents −log$_{10}$(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 61). 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.

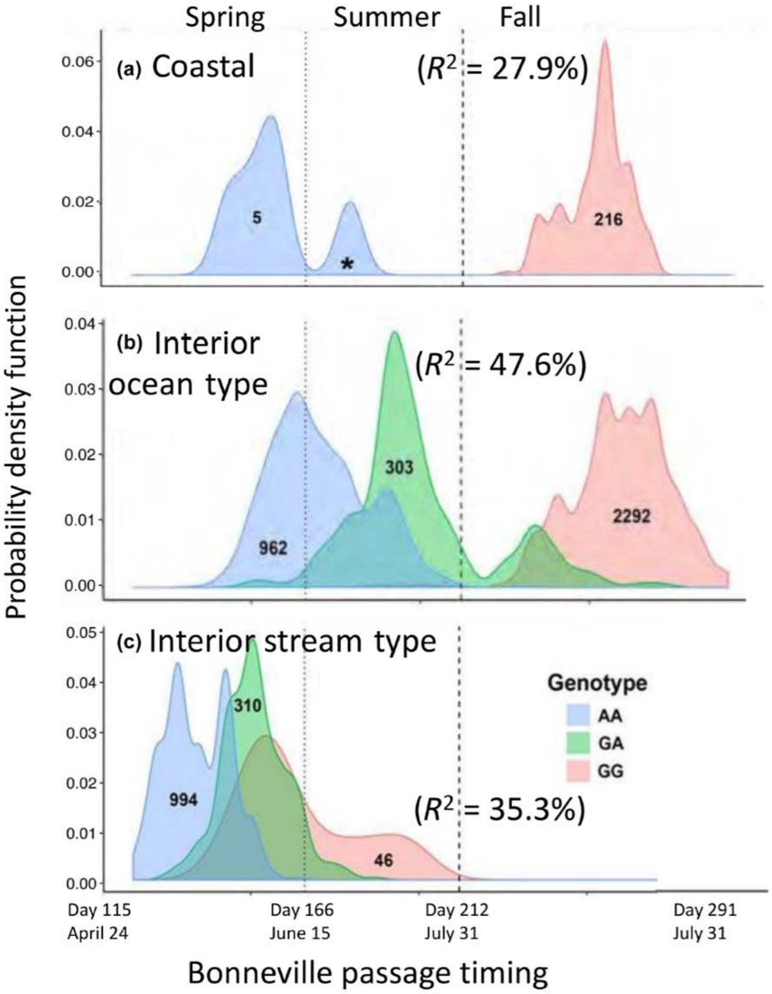


Figure 61. Run-timing phenotypes and genotypes at Bonneville Dam for each lineage of Chinook salmon (coastal, interior-stream type, and interior ocean-type) show a strong association (results from Narum et al. 2018; Willis et al. 2021; Narum

et al. 2023). Early and late returning fish are found in all three lineages with heterozygotes observed with intermediate timing.

Despite several intriguing results from validation studies, more thorough characterization of genomic variation in the GREB1L/ROCK1 region of Ots28 was necessary at the population level for Chinook Salmon. This was further apparent after a duplication was noted in this region of Ots28 in a study of coastal lineage Chinook Salmon from populations in California and Oregon (Thompson et al. 2020) that indicated structural variation may reduce recombination in this region and copy number may be related with early vs. late migration timing. A large whole genome resequencing study (Horn and Narum 2023) of Chinook Salmon populations from the Columbia River enabled population level allele frequencies across the entire GREB1L/ROCK1 region (Figure 63) and the ability to test for copy number effects on migration timing. A total of 53 populations were individually barcoded (n = 3,566) and sequenced at low depth to estimate allele frequencies for ~13 million SNPs (Horn and Narum 2023). The coastal lineage included populations that represented spring (early) vs. fall (late) run-timing, the interior ocean-type lineage included populations of summer (early) and fall (late) run-timing, while the interior stream-type lineage included populations with a gradient of passage timing at Bonneville Dam ranging from spring (early) through summer (late). Differences in allele frequency between early and late collections indicated the breadth of association spanned approximately 200Kb from the GREB1L region through intergenic and into the 5’ end of ROCK1 for both the coastal and interior ocean-type lineages. In contrast, the interior stream-type lineage was represented by Chinook Salmon populations that had a gradient of passage timing over Bonneville Dam, with the earliest returning fish from the upper Columbia River and Rapid River, and the latest returning fish from populations in the Salmon River (Hess et al. 2014). The interior stream-type lineage generally had weaker differences in allele frequency within the GREB1L gene region compared to high differences in allele frequency in SNPs through the intergenic region, and the breadth of association in the interior stream-type lineage was estimated to be only ~26Kb of the intergenic region of Ots28 (Horn and Narum 2023). Examination of allele frequencies across populations suggested that SNPs within the intergenic region were the most informative for adult migration timing in Chinook Salmon lineages of the Columbia River. Across all populations, one of the most diagnostic SNPs in this intergenic region (position 12,299,996 on Ots28) provided an indication of the frequency of early alleles throughout the Columbia River basin. Each lineage had a frequency of early alleles that ranged from modest in the coastal lineage (34%) and the interior ocean-type lineage (31%), to high (85%) in the interior stream-type lineage (based on allele frequencies from Willis et al. 2021 and Horn et al. 2023). Further, the duplication noted by Thompson et al. (2020) was found to exhibit higher copy numbers in late returning fish from each lineage relative to early returning fish (Horn and Narum 2023), suggesting that structural variation in the form of this duplication within the intergenic region between GREB1L and ROCK1 may be a driver of phenotypic differences (Horn and Narum 2023). These results validate that GREB1L/intergenic region of Ots28 has phenotypic effects on adult migration timing phenotypes for all lineages of Chinook Salmon in the Columbia River, but the mechanisms of expression on any specific migration phenotypes remain unknown.

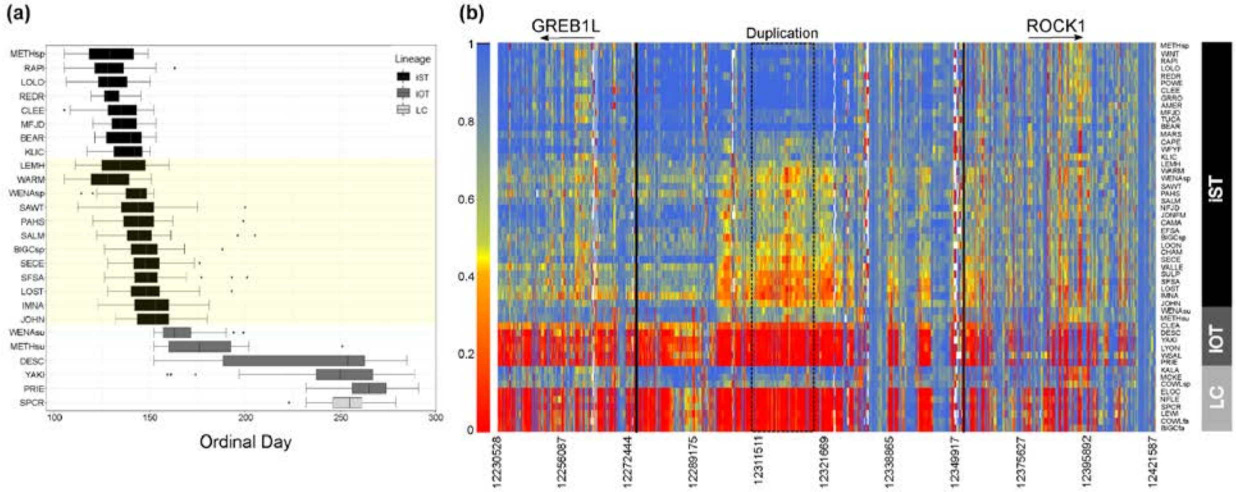


Figure 62. Allele frequencies for hundreds of SNPs spanning GREB1 through ROCK1 for 53 populations of Chinook Salmon based on whole genome sequencing (Horn and Narum 2023). A) Populations are sorted within each lineage by adult migration timing with early at the top and late at the bottom. Lineages include interior stream-type (iST), interior ocean-type (iOT), and coastal (Lower Columbia/LC). The yellow shaded box corresponds to populations in the iST lineage that exhibited heterozygosity for the duplicated block within the intergenic region as noted by Horn and Narum (2023). B) Allele frequencies for populations within each lineage of Chinook Salmon with early allele frequencies in blue and late allele frequencies in red. The duplicated region found by Thompson et al. (2020) is outlined by a dashed box. For a list of population abbreviations, see Horn and Narum (2023).

Age at maturity in Chinook salmon appears to be a polygenic trait but genes of greatest effect differ between sexes (Figure 63; females = OPN4, males = TMEM19; Micheletti and Narum 2018b). Recent studies by other labs have identified Y-linked haplotypes on Chromsome 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 assocation 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 64). 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 65).

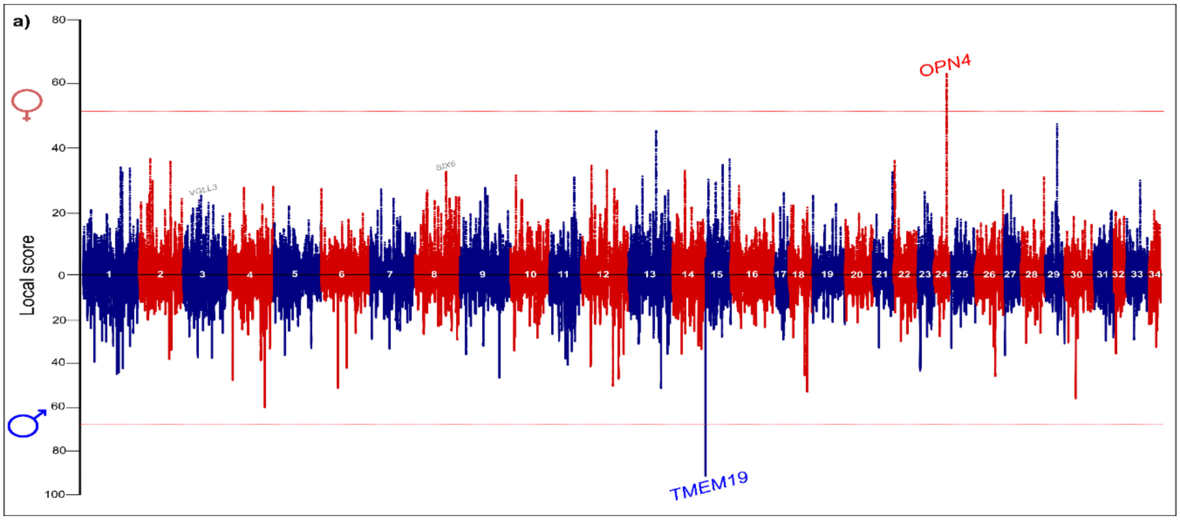


Figure 63. Manhattan plot (from Micheletti and Narum 2018b) illustrating differentiated regions within age classes of females (top; 4- vs. 5-year-olds) and males (bottom; 3- vs. 4- vs. 5-year-olds). Red dashed lines indicate α = 0.01 significance threshold for the local score test with Bonferroni correction. 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.

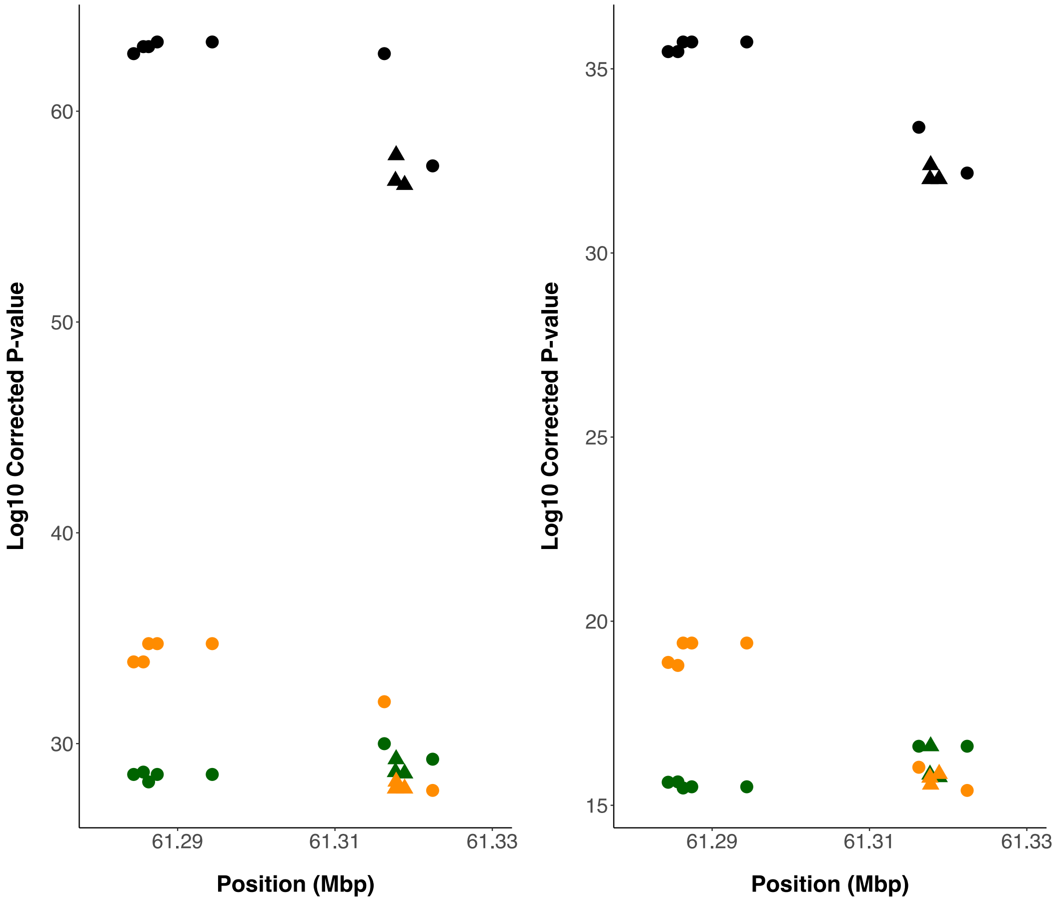


Figure 64. Significance of association of chromosome 25 markers with fork length (left) and ocean age (right) in BONAFF steelhead. Position refers to SNP locus position on chromosome 25. Circle: Intergenic, triangle: SIX6; orange: female; green: male; black: combined male and female.

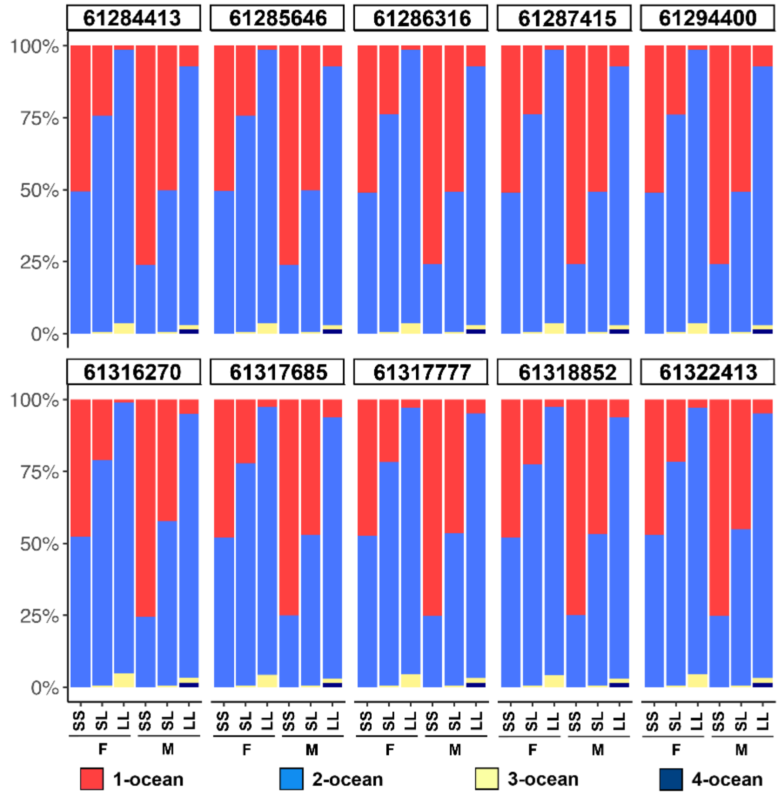


Figure 65. Frequency of ocean-age individuals for genotype and sex for each of the chromosome 25 SNP markers (identified by genomic position).

Further analyses of steelhead whole genome data indicated that age-at-maturity and phenology of iteroparity are determined by overlapping physiological processes and genetic pathways. Steelhead trout are distinct from other forms of Pacific salmon in exhibiting iteroparity, that is, multiple rounds of reproduction, and this life history variation is important not only for maintaining population stability and cross-generation connectivity, but simply for increasing the total reproduction of the population per season. Using genome wide association scanning using genomic resequencing data from individuals with distinct spawning phenology (consecutive or skip spawning) from two stocks in the Columbia Basin (Yakima and Clearwater), we identified a number of genomic regions that may be important for mediating iteroparity. One in particular was nearby, and transcriptionally upstream of, a gene coding for an estrogen receptor (ERβ) that has been suggested to mediate metabolic processes involved in gonadal recrudescence and maturation. Moreover, this iteroparity-associated region sits adjacent to the region associated with age-at-maturity (ocean age and size at first reproduction) in steelhead, and these two regions occupy a joint or overlapping island of linkage disequilibrium in the examined stocks (Figure 67), indicating that they may jointly or interactively influence spawning phenology in steelhead. This work was recently published in *Evolutionary Applications* as a part of the special issue on salmonid genetics (Willis et al. 2023).

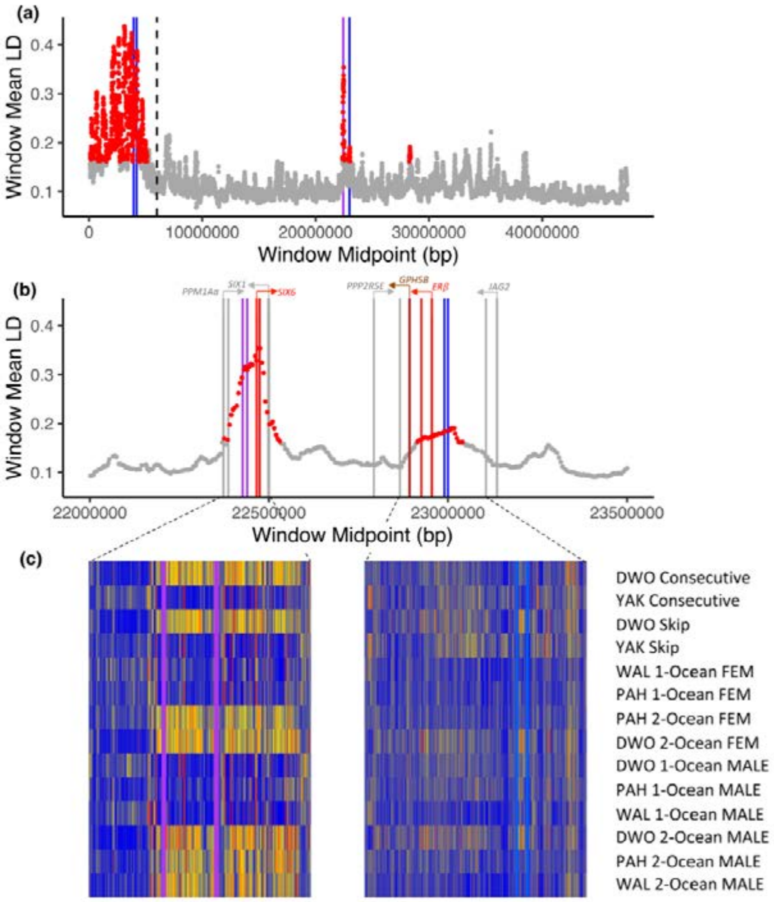


Figure 66. **Mean linkage disequilibrium among sites on Omy25 q-arm in sliding windows of 100Kbp and steps of 5Kbp, with LD outlier windows (red) identified as ≥2xIQR after excluding the centromeric region (bounds indicated by dashed line) in consecutive and skip spawning female steelhead (Dataset 1). Regions significant in local score analyses of consecutive and skip spawning female steelhead are indicated with blue lines, and the region significant in variable ocean age female steelhead is indicated with purple lines. (a) Full extent of Omy25 (b) 22–23.5 Mbp, the area containing the *SIX6* and *ERß/GPHB5* outlier regions. Genes overlapping or transcriptionally downstream of the outlier regions are indicated with red or brown lines, and other adjacent genes are identified with grey lines. The annotated direction of transcription is indicated with arrows above each gene; for full annotation, see Willis et al. (2023). (c) Heat maps indicating differences in allele frequency for the outlier regions of Omy25 among consecutive and skip spawning and variable age-at-maturity female steelhead. The y-axis lists the collection based on location, sex, and phenotype (Willis et al. 2023).**

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 67; 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 68), and markers were developed from this candidate gene for further validation. As these candidate genes for traits have begun to be identified (Figure 67; Chen et al. 2018a; Chen and Narum 2020; Andrews et al. 2022), 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 in test populations of anadromous steelhead and Chinook salmon following similar measurements of phenotypes as used for redband trout.

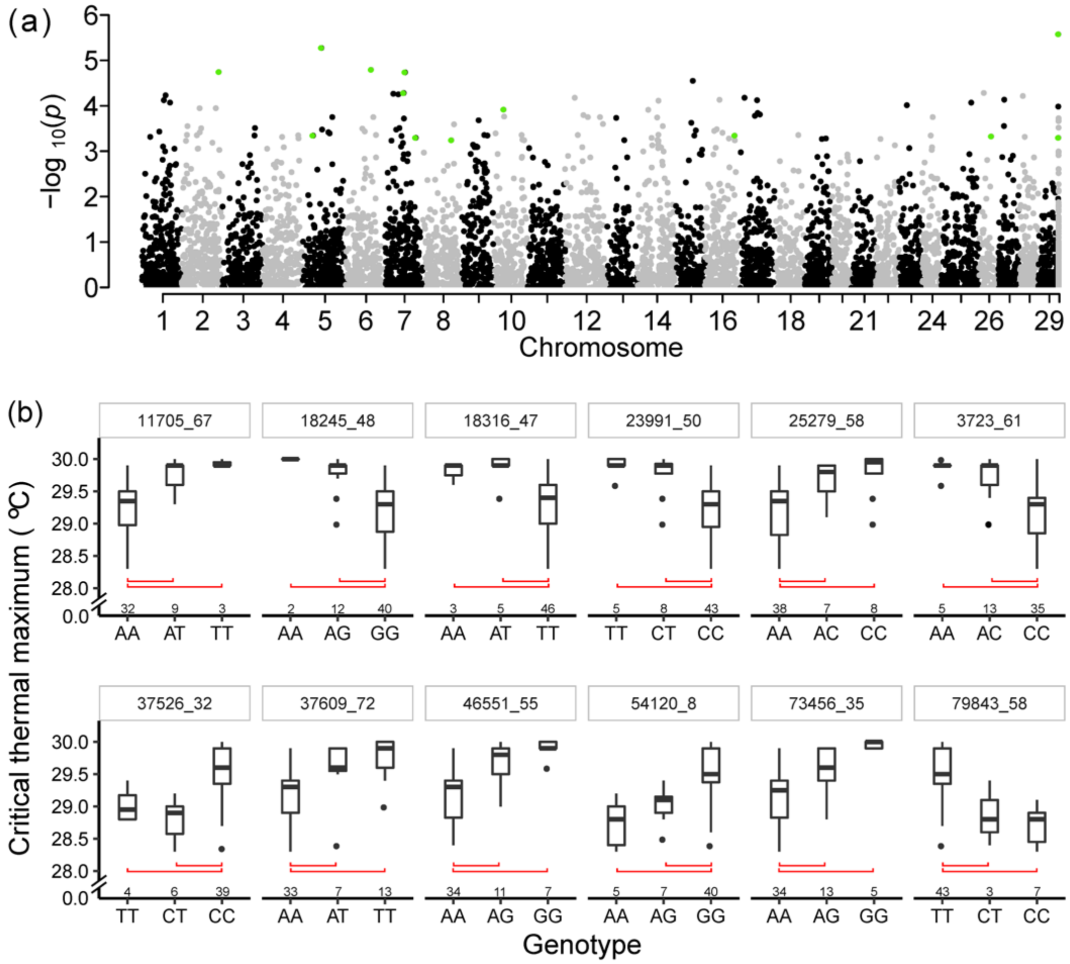


Figure 67. Results from Chen et al. (2018a) that demonstrate association of loci with thermal tolerance in natural populations of redband trout from desert, cool montane, and cold montane environments. Outlier loci and the association with critical thermal maximum (CTMAX). (a) Manhattan plot of calibrated 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 α=0.05 in one-way ANOVA on ranks with subsequent Dunn's post−hoc test. Numbers above genotypes represent the sample size.

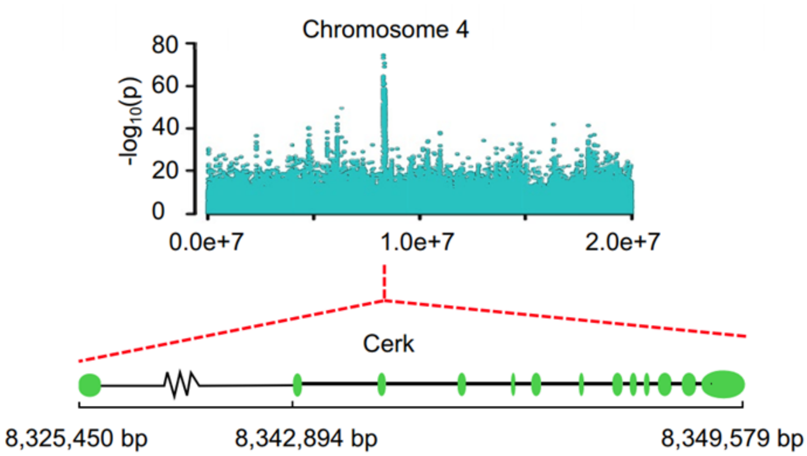


Figure 68. **Results from Chen and Narum (2020) that identified a highly significant peak on Chromosome 4 in the *cerk* gene associated with thermal tolerance (survival/mortality) and cardiac performance under heat stress.**

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 70). 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 69) if warranted, as described in a recent review (Chen et al. 2021).

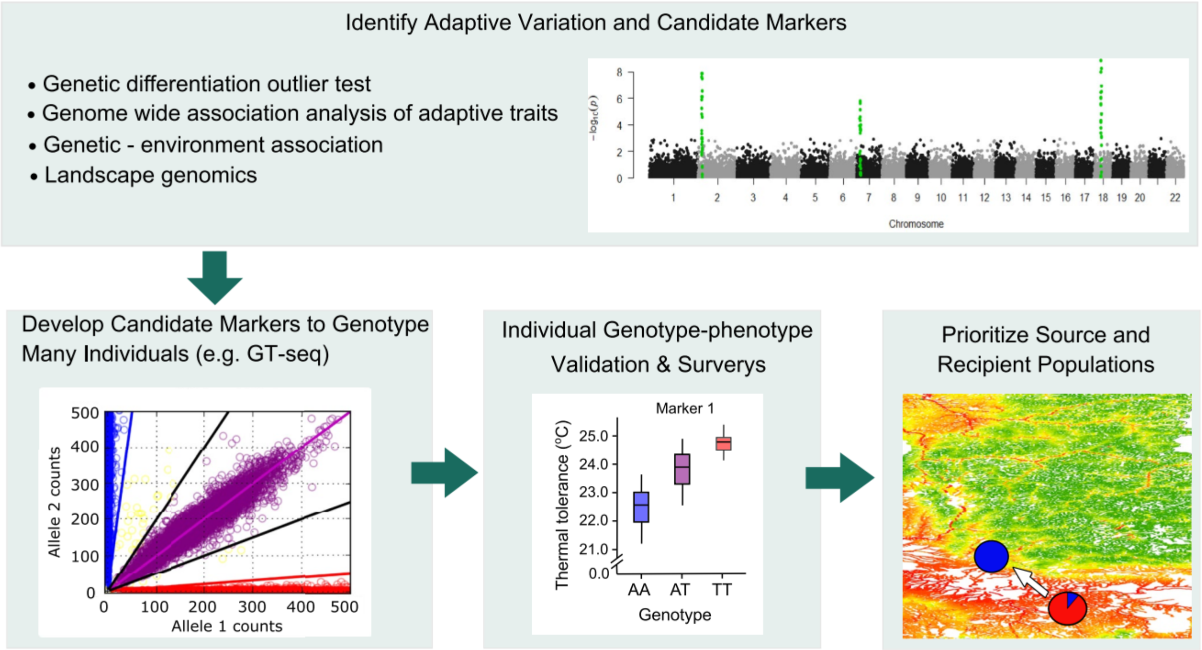


Figure 69. Schematic showing genomic approaches for applying assisted migration with adaptive alleles. The top panel illustrates a Manhattan plot with significant peaks for candidate loci from genome scan approaches, leading to development of specific candidate markers (e.g., genotyping-thousands by 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.

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.

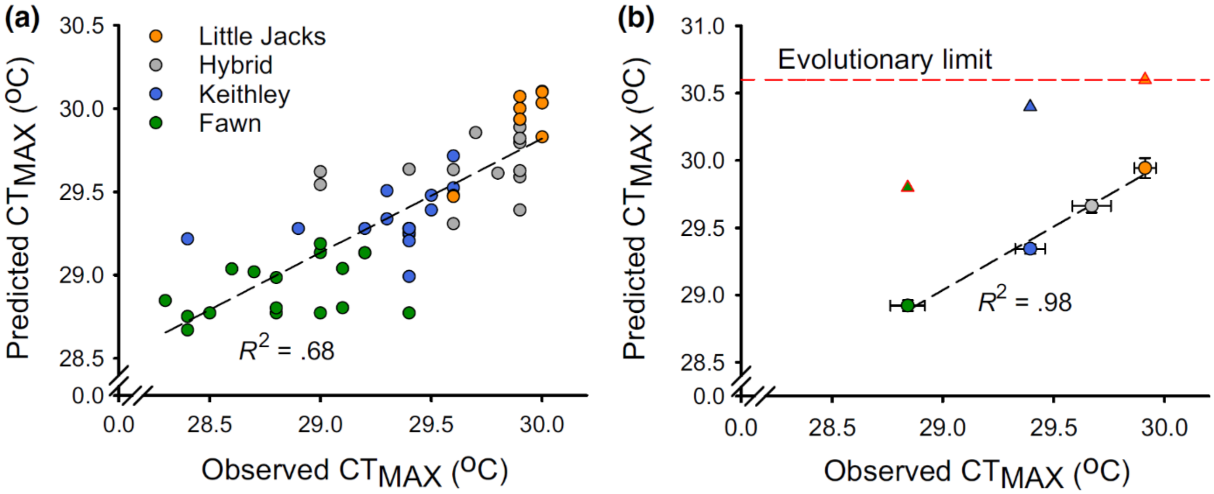


Figure 70. **Critical thermal maximum (CTMAX) prediction (from Chen et al. 2018a). (a) Correlation between observed and predicted individual CTMAX values. (b) Prediction of population mean CTMAX (SEM) and evolutionary limits for populations (triangle) and species (dash line).**

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. Our bioinformatic pipeline is designed to produce ploidy-accurate genotypes (Delomas et al. 2021), and we have utilized the data collected with our ploidysensitive 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 2023, we genotyped broodstock candidates collected for use at the Yakama Nation (YN) sturgeon hatchery as well as sturgeon from population surveys in the mid-upper Columbia (Priest Rapids and Rocky Reach segments), most of which consist of progeny of previous YN broodstock outplanted in adjacent segments. 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 **71**).

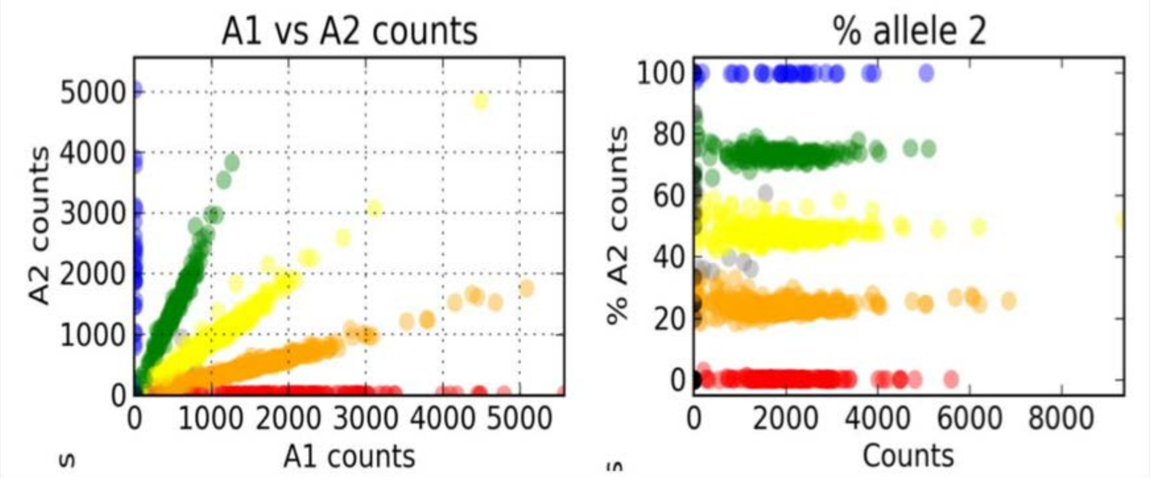


Figure 71. Example of a locus GT-seq plot from octoploid (functionally tetraploid) white sturgeon.

However, individuals that are greater ploidy (5N, 6N) exhibit some distinct and exclusive read ratios (e.g. AAABB, ABBBBB), 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 **72**).

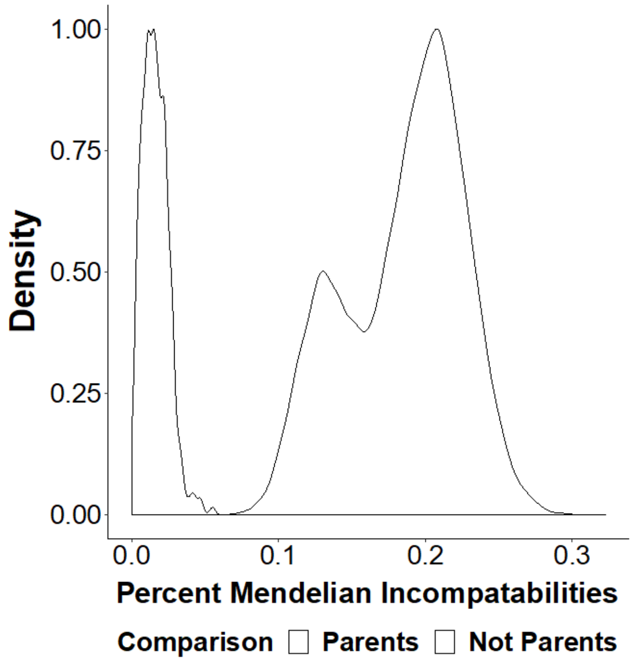


Figure 72. Distribution of Mendelian incompatibilities (parents and offspring with mismatched alleles) observed among all offspring in six reciprocal crosses of white sturgeon.

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 **73**). 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 **70**). 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).

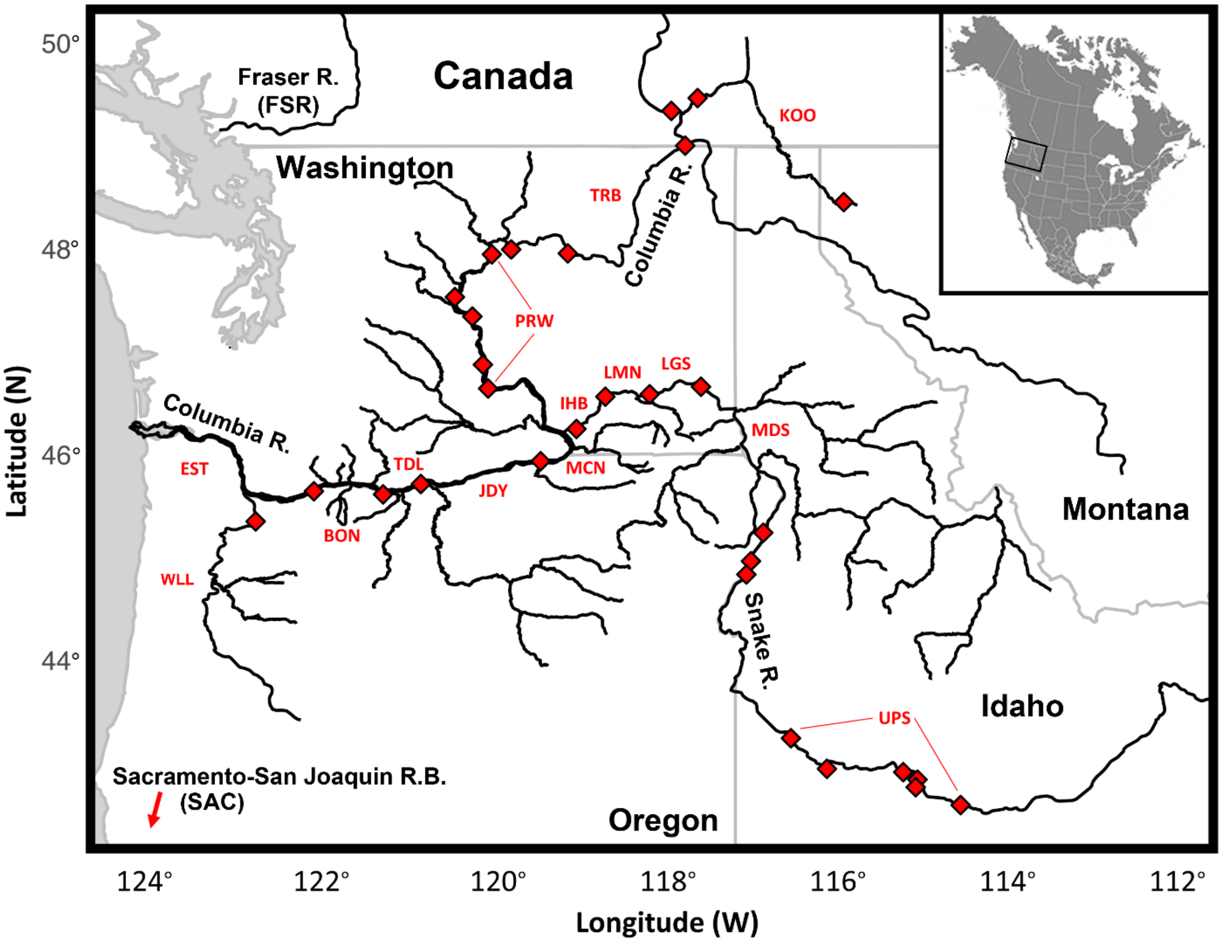


Figure 73. Reaches from which white sturgeon were collected for the study of population structure. Diamonds represent hydroelectric dams or water falls delineating reaches inhabited by white sturgeon analyzed (labeled). Lines indicated reaches from which fish were pooled for group-wise analysis.

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 70. 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.

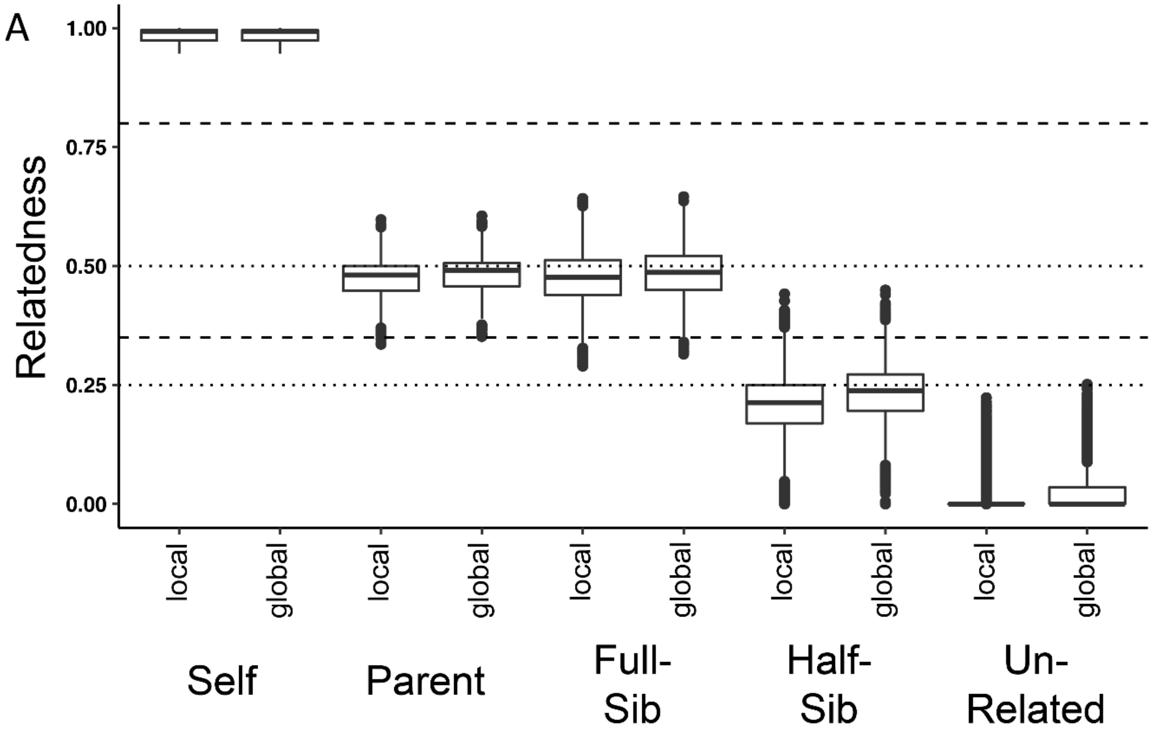


Figure 74. Maximum likelihood estimation of relatedness in known full- and half-sib families from broodstock collected in John Day reach. Estimates were made with local (left) and global (right) allele frequencies. Dotted lines represented the expected relatedness values for first degree and second degree 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 75**). 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 71**), 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 **72**). 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 73**). 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.

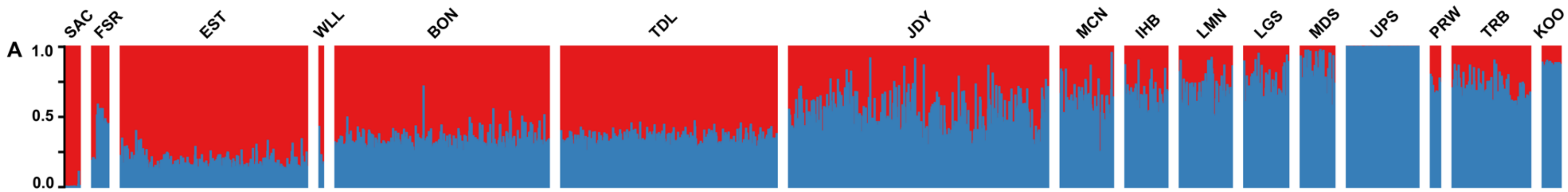
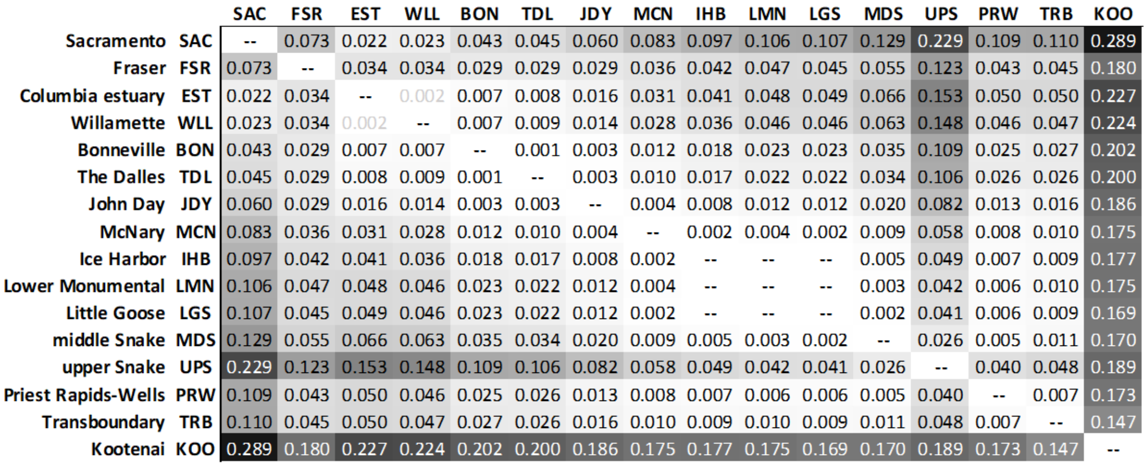
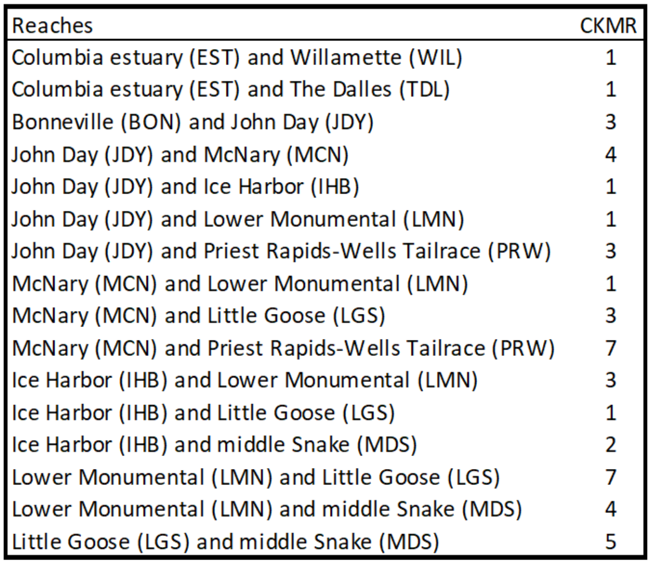


Figure 75. Bar blots of admixture proportion of individual white sturgeon to an optimized k*=2 populations made with Structure.



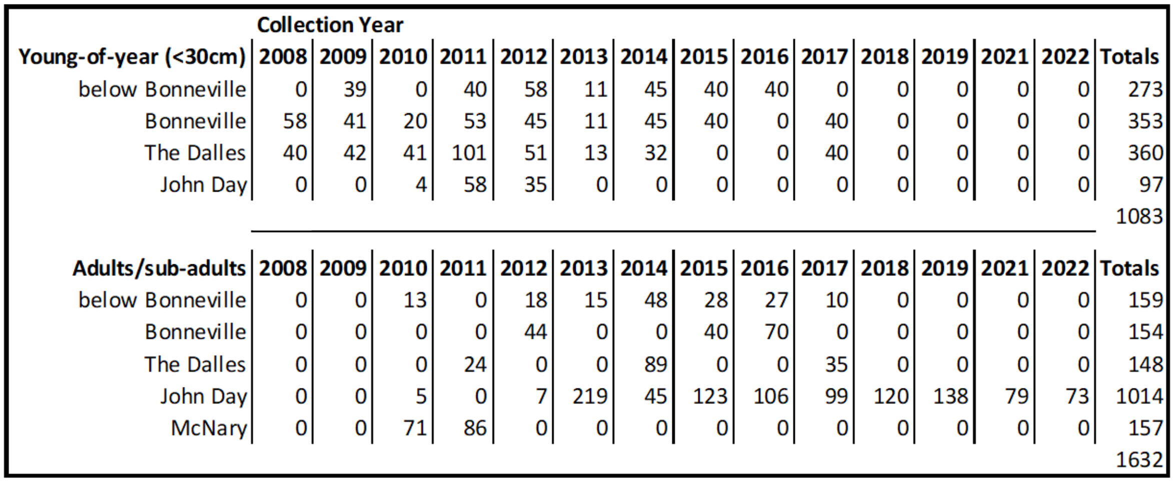
		SAC	FSR	EST	WLL	BON	TDL	JDY	MCN	IHB	LMN	LGS	MDS	UPS	PRW	TRB	KOO
Sacramento	SAC	--	0.073	0.022	0.023	0.043	0.045	0.060	0.083	0.097	0.106	0.107	0.129	0.229	0.109	0.110	0.289
Fraser	FSR	0.073	--	0.034	0.034	0.029	0.029	0.029	0.036	0.042	0.047	0.045	0.055	0.123	0.043	0.045	0.180
Columbia estuary	EST	0.022	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	--

Table 71. 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



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

Table 72. 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														
Young-of-year (<30cm)	**2008**	**2009**	**2010**	**2011**	**2012**	**2013**	**2014**	**2015**	**2016**	**2017**	**2018**	**2019**	**2021**	**2022**	**Totals**
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	**2008**	**2009**	**2010**	**2011**	**2012**	**2013**	**2014**	**2015**	**2016**	**2017**	**2018**	**2019**	**2021**	**2022**	**Totals**
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

Table 73. 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 71). 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 **72**), 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 etal. 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 highly repetitive (ancestrally octoploid, functionally tetraploid) 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. Since 2021, we have been working to improve our genome assembly using linkage map data from hatchery crosses. Using an RNA-seq-derived linkage map, our current assembly incorporates 3,819 of the scaffolds from our phased (approximately ‘ploidy proportional’, i.e. not haploid) assembly into 431 linkage groups (approximating chromosomes or chromosome arms; relative to a karyology derived estimate of ~360 chromosomes), reflecting 1.775 billion base pairs (Gbp), or approximately 28% of the 6.26Gbp phased assembly. Attempts to utilize additional SNP markers and extend the map are ongoing. 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 2022. 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 2022, 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 as we showed for 2023. 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 U.S. v OR Technical Advisory Committee (TAC).

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

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

Appendices

Appendix 6. GT-seq SNP panel for Steelhead trout.

Assay	A1	A2	A1-Probe	A2-Probe	FWD Primer	Corr	Flag	Rev Primer
OmyY1_2SEXY	X	Y		ATGTGTTCATATGCCAG	GCGCATTTGTATGGTGAAAA	NA	0	GCCTGGCATATGAGTGTTGA
M09AAC.055	C	T	ACCTCCACGCTGTCC	ACCTCCACACTGTCC	GTCTCCGACGTGTGGCT	(0,0)	1	TGGAACGAACCTGAGAACATAAGG
M09AAD.076	T	C	CACCAACCACTGGTGAA	CCAACCGCTGGTGAA	ACTGTTACCACTCTCTCATCAACCT	(0,0)	1	GGGTCCAGGAGGTTTTTAAACAACAT
M09AAE.082	T	G	AGGTTGTTTTACAAATTTAA	AGGTTGTTTTACACATTTAA	CTATGTGCAGTGCCCTTCTCA	(0,0)	1	GGCTTACAAGTATGCATGACTAGCT
M09AAJ.163	G	A	AACAAAGTGAAAGTGTCCT	CAAAGTGAAAGTGTCTT	TCCCATGGCCCTTACTCTATCAA	(0,0)	1	TTGAGGTGTATGTTGAAAAGTAAACTT
Ocl_gshpx-357	T	G	ATCCGTCCAGGAAATG	TCCGTCCCGGAAATG	GAGATCCTGAGGTCCCTGAAGTAT	(0,0)	3	AAGTGGAAATTTGGGCTCAAAGC
Oki_101419-103-27	A	C	AATCCACTTCC	AATCCCCTTCC	CCCAATTGGAGACCAGGGTT	(0,0)	3	TCATTCAGACAGTTGGGAGACA
Oki_101419-103-44	T	C	GTTCTCCTACT	GTTCTCCCACT	CCCAATTGGAGACCAGGGTT	(0,0)	4	
Oki_105105-245-23	T	G	GCCTTTTCCAT	GCCTTGTCCAT	GCGTATCAAGCATCAACGCC	(0,0)	3	TCTTTCAGCAAGGTTGGGCA
Oki_105105-245-56	G	A	CTCATGCCCAA	CTCATACCCAA	GCGTATCAAGCATCAACGCC	(0,0)	4	
Oki_106172-60-38	C	T	GTGCGCATCAA	GTGCGTATCAA	ACTACTTGGCGTGTGTGTGGG	(0,0)	3	TCCACTGAGAGGATGAGGCA
Oki_106172-60-47	G	A	AACGCGCTGAC	AACGCACTGAC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_106172-60-47c	A	C	AACGCACTGAC	AACGCCCTGAC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_106172-60-53	C	T	CTGACCGCYGC	CTGACTGCYGC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_111681-407-38	C	T	AGAAACTGCAA	AGAAACTGTAA	TTCATCCCATTGGAAGCCCC	(0,0)	3	ACAGCCTATATCTGTGCGCT
Oki_120255mod-99	A	C	GACTAAAACGT	GACTACAACGT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	3	CATTGAAGGGTGGAATTGAAG
Oki_120255mod-105	C	T	AACGTCAGTTA	AACGTTAGTTA	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-113	G	A	AGTTACTGG	AGTTACTAG	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-115	G	T	TTACTRGGGTA	TTACTRGTGTA	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-119	G	A	GTAGYTTCWTG	GTAAYTTCWTG	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-120	C	T	CTTCWTGGCAT	TTTCWTGGCAT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-133	T	C	TGGCATAGTC	TGGCATAGCC	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-135	A	C	GGCATAGYCAT	GGCATAGYCCT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-137	A	T	ATAGYCMTAGAT	ATAGYCMTTGAT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-141	A	G	ATAGYCMTWGATA	ATAGYCMTWGATG	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_126619-265-31	A	C	GGATTGKGCAC	GGATTGKGCCC	TGCGTAGTTAATTTTCACCTCGG	(0,0)	3	TACGCAGCACTGAAGACTGG
Oki_126619-265-35	A	G	CAGCACAGCTG	CGGCACAGCTG	TGCGTAGTTAATTTTCACCTCGG	(0,0)	4	
Oki_126619-265-50	G	T	GATTCGCCAGT	GATTCTCCAGT	TGCGTAGTTAATTTTCACCTCGG	(0,0)	4	
Oki_aspAT-273-37	C	T	CTGGACACAAT	CTGGATACAAT	ATGCTGGGAGAAACAGTGGG	(0,0)	3	CTCCTCTGTAAGGGGTGGGT
Oki_aspAT-273-45	T	A	AATCCTTAACA	AATCCATAACA	ATGCTGGGAGAAACAGTGGG	(0,0)	4	
Oki_RAD41030-31-36	C	T	GAAGGYCRGGG	GAAGGYTRGGG	GCTGAGCCTGGTCTGGG	(0,0)	3	TGGATACCCCAACTCCTCCA
Oki_RAD41030-31-37	G	A	GGGGSTCTGTG	AGGGSTCTGTG	GCTGAGCCTGGTCTGGG	(0,0)	4	
Oki_RAD41030-31-41	G	C	GGGGTCTGTGG	GGGCTCTGTGG	GCTGAGCCTGGTCTGGG	(0,0)	4	
Oki_RAD41030-31-55	G	T	AGCTCGGGCTG	AGCTCTGGCTG	GCTGAGCCTGGTCTGGG	(0,0)	4	
Oki_RAD51585-47-25	C	G	GTGGCTCACTT	GTGGCTCAGTT	ACTTTCTAGTAGGCGTGTGGC	(0,0)	3	CAAAACCCTGGCGTTGCAAG
Oki_RAD51585-47-28	G	A	TCACTTGGTAGAGC	TCACTTAGTAGAGC	ACTTTCTAGTAGGCGTGTGGC	(0,0)	4	
Oki_RAD51585-47-31	A	C	TTKGTAGAGCA	TTKGTCGAGCA	ACTTTCTAGTAGGCGTGTGGC	(0,0)	4	
OMGH1PROM1-SNP1	A	T	TAGTGTTCACTGACTTCA	TAGTGTACACTGACTTCA	TCAAACTGCATTTGATGGAAACAAACAT	(0,0)	1	AGGACAATTCTAAGTGACCTCAAACTG
OMS00002	A	C	TGTTTTGCAGCGCTC	TGTTTGGCAGCGCT	TTTGATTTGATTTGTATCTGCTTCTT	(0,0)	1	CCAACATGCCTCACACAAAA
OMS00003	T	G	CTTTACTGTCGACATTTTA	TACTGTCGCCATTTTA	GTGCCACTGATGAGGATGAGATCA	(0,0)	1	GTAATAAAGCCCTTTTGTGAGGAAAAACTAAT
OMS00006	T	C	CACTTACAAATACAAAATT	CTTACAAATGCAAAATT	TCCACGTAGGACATAGTTTGAGCTA	(0,0)	1	TGTGGTGTCATGTTTGCCCTAC
OMS00008	A	T	CTTCAAATATCCATAATTATATC	TCAAATATCCATAATAATATC	CCCTTTAAGGAGGATTTTAAATATGTGAGATAGAA	(0,0)	1	GGATACAGCGTTTTGGAATGAAACT
OMS00013	A	G	CTTCTTTTCCCTTGCTACTC	CTTTTCCCTCGCTACTC	GCCTTTGTTCTCCTTGGTGGTTA	(0,0)	1	AGAAAAGTGTGGACTGAGGTTGAG
OMS00014	T	C	TGATTTGATGAATTAAACTTC	TTGATGAATTGAACTTC	CTTACACACAAGGGCTTCATTCTG	(0,0)	1	GATGTCTCTGGGTGGTTGTCA
OMS00015	A	T	CAAGTCACACTTTTAATGAA	CAAGTCACACTTATAATGAA	TCAGACCCTATTTTTGGCACAAGT	(0,0)	1	GTCTAACTGATCCCACTTCTGCAT
OMS00017	A	G	TAGACCTCGGTGCTGTAG	CCTCGGCGCTGTAG	ATTAAGTTCATACAAAAGTTCATCATAAATATTTTCCTTT	(0,0)	1	GGAGAACAAAGGGAAAGAGAAGACA
OMS00018	T	G	AACCACATAATTAATAATTC	CCACATAATTCATAATTC	AGAGTACATGTGTGGCTGCAA	(0,0)	1	GTCATAAATCAACACAATTATCTTCTTCACAGAA
OMS00024	T	G	AA[AC]CCCAAATTTTAC	AA[CA]CCCAATTTTAC	CACATACAACCATCACCCTTCCTAA	(0,0)	1	AGCATTGAGCGAAATTACCAAGAGT
OMS00030	T	G	ATGAGGGTCCCTATACAGG	ATGAGGGTCCCTCTACAGG	CCTCGTGACTACAGAGCTATACAAC	(0,0)	1	GATCTGATCGGTCGGGAGAGA
OMS00039	A	G	GTACGTGTCTCTGACC	GTGCGTGTCTCTGACC	GTCAGTACTGTGTGTGTCTGTGT	(0,0)	1	CCATCTACATTGTCAGCAGTGTGA
OMS00041	G	C	CCACTCTATGCCTGCCCT	CACTCTATGCGTGCCCT	GATTCTGTTCCATCCTCTTTCTGTCA	(0,0)	1	AAACATAAAAAAGGGCATGAAGGTGTC
OMS00048	T	C	CAGCTAAACTCAGCAAAA	AGCTAAACTCGGCAAAA	GGAAGAGCTGGAGAACAACGT	(0,0)	1	TGCAGTTGACAGAGGCTTTCTTT

OMS00052	T	G	CTTCCTTTTGAGAATAAT	CCTTTTGCGAATAAT	TGCGTTTTTCATCCCAATCATTCAC	(0,0)	1	GGCATCAGGCTCTTCTTCCT
OMS00053	T	C	ATTTATATGTATCAATCA	ATTTATACGTATCAATCA	GGAGCCAGGTCAAGGTGATC	(0,0)	1	GGATGTCTGGTGTGGCTGTAAA
OMS00056	T	C	TAGCTTGACCAAATAGCA	CTTGACCGAATAGCA	TCAGGAAGTAAACTGAAAATTCCAATGTATGA	(0,0)	1	CCCCAACCATGCTTGTTATTGAAC
OMS00057	T	G	CTCCACAGAACCTTG	CTCCACAGCACCTTG	GAGAAAGGGAGCATGAGACAGA	(0,0)	1	GTTGGGCTCCGGTACGAT
OMS00058	A	G	CAACACTTTGTACCCCTC	CACTTTGCACCCCTC	GTGACATTTGGAGCCACTGC	(0,0)	1	GCTAGGAGACAGAGGGTGAAAG
OMS00061	T	C	CATTGCCATTTACAGACTT	TGCCATTTGCAGACTT	AAGTGGAGGCTGACCTGTTG	(0,0)	1	GCTGATGGCACCTGACAGTTAATT
OMS00062	T	C	TTGACCAGCAGATGGTGTA	ACCAGCAGGTGGTGTA	ACCCTGGGAAGGCTACTGTAC	(0,0)	1	TGAACAGAGATCTGGAGAGTTGGAT
OMS00064	T	G	CAGGCAACATTTTATATAACTA	CAGGCAACATTTTATCTAACTA	GTGGATATGTAGTTCGATGGAACAGT	(0,0)	1	TTTACAACAATCTTCTTTTAATAAAAATATAGCCACTTAT
OMS00068	A	G	AATATGCCTCCTTCGTCTC	TATGCCTCCTCCGTCTC	GCACTAACTGGACAACATTTTTAAGAATGA	(0,0)	1	GGCAGTTGAGCATTTTGGGATATT
OMS00070	T	C	CAAAATACGGAAATGCAG	AAATACGGGAATGCAG	CGTTCCTGCGGGACAGT	(0,0)	1	GTTTCTCTCACGTCCACAGATCT
OMS00071	A	G	CTTGTTTGAGCTTTTTCT	TTGTTTGAGCCTTTTCT	CCGGAGTGACCTCACATTTGG	(0,0)	1	GCATCGTACAGTTCACCTACCT
OMS00072	A	G	TAGAAGGTCCATGTATCTC	AAGGTCCATGCATCTC	GTGGGAGAGCTCGTCTATGG	(0,0)	1	ACAACAGGTCATTGGATGTGATCAG
OMS00074	T	G	TGAAACAAAACAAATGTTCC	AAACAAAACACATGTTCC	CCTGTTTATTCATCTAAACCAGTTCTTTAAAAT	(0,0)	1	AACTTAATTTAGCAAACAAATGTCTGAACAGAA
OMS00077	C	G	TTCCGGTGGTGAAGTT	CCGGTGCTGAAGTT	AATACCATCTTGAGCTCATTAGTAATTATTCAA	(0,0)	1	CCAGACTTTACACACTCTTGACTGA
OMS00078	T	C	TTCACATGCATAAGAGTG	TCACATGCATGAGAGTG	GAGGGAAGCAGCCATAAACAGAATA	(0,0)	1	GTCTCACTATGGTCCATATCTGTGTAGA
OMS00079	T	C	CTACTTTTCACAGTAACACAG	CTACTTTTCACAGTGACACAG	GTAACATTATGAATCTATCAGTTTCCCTAGCT	(0,0)	1	ACCTGCAACGTTAGAGCTGTTTATT
OMS00087	A	G	GTTA[CA]AACTGACAAAGTGTG	GTTA[CA]AGCTGACAAAGTGT	GCAAATTTCACCCTTAACGTGGTTT	(0,0)	1	GATTTGATGTGTGTGTATTACCTCCTCTA
OMS00089	A	G	ATGAATCCCAAATAAGAAC	AATCCCAAACAAGAAC	GCACCATTTGAATAAAAAATCTGCTTTGT	(0,0)	1	GCAACCCAATTCAATATTAAGCACATGAT
OMS00090	T	C	ACAACCACACAAGATT	AACCACGCAAGATT	AGGGCACAACACCACTCTAAATT	(0,0)	1	TCGAAAAGCAACATCTGTCTCAGT
OMS00092	A	C	CAGCTGAGAATAGGTTC	AGCTGAGAAGAGGTTC	TCTCCAGGTGTATCTTGAGAAGGT	(0,0)	1	AGGGTTCACACAGGGAAGATATCAT
OMS00095	A	T	AGGCAACTATATATTTTTTT	AGGCAACTATATATATTTTT	CTCCAATGGCTGTCAACAATTAAATATAAGAC	(0.7,0)	1	GTGTGCTGGTCTCTTCTTTTATTCTCA
OMS00096	T	G	AAAGAGGAAGAGTCTCG	AAAGAGGAAGCGTCTCG	CATGAGAATGGATCAGTCTCCACAA	(0,0)	1	GATGAAATCTGAATGTGTTGACACTACAG
OMS00101	A	G	CTCTAGTAGCCTTATAGAAAG	CTAGTAGCCTTACAGAAAG	GCGTGTCGTGGGTCAGTTAAATA	(0,0)	1	GTGCAATCCAACCTATTAGTAGATATGCT
OMS00103	A	T	CTCCACAGTAATTTTTTTTT	CCACAGTAATTATTTTTT	GAGATCACTGTAGGATTGGCTGTTT	(0,0)	1	CCTCAGAGCAGCTCACAATGGCATC
OMS00105	T	G	CTGCTATTCAAATTGCT	CTGCTATTCACATTGCT	ACATTTGAAGTCAGTATGGGTGTTGAG	(0,0)	1	GAACCTCACCACAGTACTAAATGCA
OMS00106	T	G	TCTGATGGAAACTTTC	TGATGGCAACTTTC	CGTGTAGCATTCTTGAGGAAGCTT	(0,0)	1	TTTCCAACAGATGCCAGAATCCT
OMS00111	T	C	CAACCAGACTACCATTC	AACCAGACTGCCATTC	CATGCGGACCTGCATAGCT	(0,0)	1	GCTTAGCCATTGACAGAGCATATCA
OMS00112	A	T	CCGGTTTCAAGTTTACTTGT	CGGTTTCAAGTATACTTGT	TGGCAGCAAAAGGGATGCA	(0,0)	1	TCCTGAGCAACCAGTCAACATT
OMS00114	T	G	AAACGTTTCACATGCACC	AAACGTTTCACCTGCACC	GGATGATGCTGTGAGTCGAGAAG	(0,0)	1	ACCTTCGCCACCCATGTTTTATT
OMS00116	T	A	CTTTTACATTTTCAATATTCTG	TTTACATTTTCAATTTTCTG	GCCTTTCTCCCATATCACATTCGA	(0,0)	1	AAACGCATCTTACACTGTGTTGTG
OMS00118	T	G	GCGGGGTGTGC[AG]CATT	GCGGGGGGTGC[AG]CATT	GCTTATTTAGAGTGCATGCCAGATG	(0,0)	1	TGGAACCAATGGGACAGTCCTA
OMS00119	A	T	CCACACAGCTGCCTGT	CACACAGCAGCCTGT	AGCGGCAGTTGTGTTAATGAGA	(0,0)	1	CTTCCTAAAGCCTGACAGTCTGT
OMS00120	A	G	C[GA]CCCACTAAAAC	C[GA]CCCACCAAAAC	GGCAGAAGAGGAGAGAGATATGATTG	(0,0)	1	CCTCAAATACCTCTGACATTGAAGGTT
OMS00121	T	C	ACAGCGTGATAAATT	CAGCGTGGTAAATT	GGAAGGAGGTCCAGTGTGAGT	(0,0)	1	AAAATATGCAACACCACTAAAACTGGAAAA
OMS00127	T	G	CACACACCCAAATGTA	ACACACCCCAATGTA	CACCTTTCTCTCTCTCTCCATCTCA	(0,0)	1	AGTGTGCTACACAACCTTAAAAAATATATATCTATT
OMS00128	T	G	ACTCTCAGAATTAATTATG	CACTCTCAGAATTCATTATG	ATGAAAGAACTCCCAGACACGTATTTT	(0,0)	1	ACATTTTAACACAGTAACACTAATACACACCA
OMS00129	C	G	TTGAACAACAAGAAAAA	TTGAACAACAACAAAAA	GGAGATGATGAAATAAAAATTGAGGAAAAGATGA	(0,0)	1	TGTCTGGTGAATTATCGCAAATAACCA
OMS00132	A	T	CAGCAGTCCTCTGTGTGG	AGCAGTCCTCAGTGTGG	GTTTATGACTCCATTGCCGAAATGATT	(0,0)	1	ACGCGACCTGCAATTCATCAATA
OMS00133	A	G	CGCCTCCATCTTTGTGGT	CGCCTCCATCTCTGTGGT	GACCACTTCACTCATTCCTCCTTTT	(0,0)	1	TCCGGTTTACACACTTCATGCA
OMS00134	A	G	TCTATAGCTGCAGTATATTA	TAGCTGCAGCATATTA	GAAACTGAAATGATCCCATCGTGTT	(0,0)	1	GCTAGCATAACAGCATTGCCATAT
OMS00138	T	G	CTAACAATAACCAAAGACTG	CTAACAATAACCACAGACTG	TCGGACCACATGAGCAGTTC	(0,0)	1	GTTCAACAGGTGCCCACAC
OMS00143	T	C	CCTGATCCAGAATCTAGA	CCTGATCCAGAGTCTAGA	GGAGGCACGCCCCAAA	(0,0)	1	TTTGTTAAAATAGAGCCCTTAGTGGGTTT
OMS00149	T	G	GCTAAATGCACAG	GCTAAAGGCACAG	GGCATCATTGTTCTTGCTCTGTTTA	(0,0)	1	CCTGGGAGGGTTTATATCGGAGTAT
OMS00151	A	G	TCATGACCTTGATAATC	ATGACCTCGATAATC	CTAACGTCTTCCCAATGATATTTCACAAGATA	(0,0)	1	ACCGTGGAAATACAATTTTTTATGCCAAT
OMS00153	T	G	ACAAAATGTAATTTTCC	CAAAATGTCATTTTCC	ACTTTGCACCATAGGCTTGACAT	(0,0)	1	TGATAAGGATGATCAAAAAGCTGAAGTATGTA
OMS00154	A	T	ACAGGGCTTCTGATTGA	AGGGCTTCAGATTGA	GATGTTGGCTGGAGGTGTAGT	(0,0)	1	TGGGAACACTTTGCCTACCC
OMS00156	A	T	TGTGTGTCCTGCTGTAACA	TGTGTCCTGCAGTAACA	GAGCAGAACACATAGAGGAAAGACT	(0,0)	1	GTAATCACCCTCTTAGCCTGTATGG
OMS00164	T	G	CCAGATTCAATTAAATTTA	CAGATTCAATTCAATTTA	CAGAGGAGAGGAGAGCAAAATACTT	(0,0)	1	ACAACCTACTCATTGAAACTCATTGGA
OMS00169	A	G	CAAAAAGCATTGATATCAAT	AAAAGCATTGACATCAAT	AGCACTTGACTCAAACTCACATAAATCA	(0,0)	1	CTGAGACAGGAAGAACAATGTTAACAAAA
OMS00173	T	C	CATTAGCTTGTGTATGAACT	ATTAGCTTGTGTGTGAACT	TGGAAGTAGCTACTTAACAGGAAATGG	(0,0)	1	AACACGTGTGCTTGTTTTGTCAA
OMS00174	A	C	CAAGAACAGG[AC]TAAATGT	CAAGAACAGG[AC]GAAATGT	TGACTAACTATGCAGCCTGAAAGG	(0,0)	1	GGGATACTCTTGTAATAAACTGTTGGTTAGTA
OMS00175	T	C	ATCACTAGTTCAAATACAA	ATCACTAGTTCAGATACAA	TTGCGATATGGGACTGTATACATTTATTCC	(0,0)	1	ACTACCTCCAGTTAAAATAGTGTGGGAAA
OMS00176	T	G	TTCCAGCACTGCTGTC	CCAGCCCTGCTGTC	GTTGGAAGTTCCGGTGGTAGAG	(0,0)	1	CTGGGTCCTGAAGGAGCTT
OMS00179	A	C	TGCCTCTTCTCTTTTCTCAT	CCTCTTCTCTTGTCTCAT	GTCATAACAAAATCAGGGCTTTCCAA	(0,0)	1	TGGGAGATTTGGGCTGCTTTAAA
OMS00180	T	G	CTAAAAGTGCATTAAGCC	CTAAAAGTGCCTTAAGCC	GCGCCGAATGGCATTAGG	(0,0)	1	CACATTGCTGTCGTTTAGTTTGACT
Omy_1004	A	T	CATGTGATGTTTTTTTGC	ATGTGATGATTTTTGC	GAGAATCGGAGCTAATCTTAGTTATTGTGA	(0,0)	1	CACTTTATTGAGCTACATGGCAAATCTG
Omy_101554-306	T	C	TGCTTCTCACATTTTTA	TGCTTCTCACGTTTTTA	GCCTGTATTTCTCCTGTATGTGCAT	(0,0)	1	TCAACTTTTGCAAACTTTTTTATTCTTTGTCATTT
Omy_101832-195	A	C	TGTAGTCTTTCAGAGTAGTATG	TAGTCTTTCAGAGGAGTATG	TGGCTCTGGACCTGTTGAGA	(0,0)	1	CGTCACAGCTATTTTAGGCGTAGT
Omy_101993-189	A	T	CTTGATTTGCAGCTTGTCAA	TGATTTGCAGCATGTCAA	ACAAAACACAGTGGAATTACAATTAACGTT	(0,0)	1	GGAAGTTAAATTTCGCTTCGTCAGAA
Omy_102505-102	A	G	AACAGGATGTTTTTGC	CAGGATGCTTTTGC	CTGCAAACTGACATGGTAGCAAAA	(0,0)	1	TGCTTGCTTTTTAAAAACAATCTCCCA
Omy_102867-443	T	G	TTTGGGTACATAATTTTT	TGGGTACATCATTTTT	CATTTGTTTAATTTGATTTGGCACAACTTCA	(0,0)	1	CCCTAGTTCTGTAACACAAGACGTAA

Omy_103705-558	T	C	AGACTTACCCAGAGTGAGAG	ACTTACCCAGGGTGAGAG	CTCCAATCGCAAATACCCAGACT	(0,0)	1	CGCAGGAGACGGATGCC
Omy_104519-624	T	C	CAGCAGGATACATCCGACT	AGCAGGATACGTCCGACT	CGTGTGAGTTTGCGGTAAAGAC	(0,0)	1	TGACGAGTCCGTCTTATCATCCT
Omy_104569-114	A	C	CGCCACTCCGACGCC	CCACGCCGACGCC	CCGAGGCCGACGTGATC	(0.5,0)	1	GCGCCTCGCTCATCATCA
Omy_105075-162	T	G	CTTTCTCTCCTACTTTCC	CTTTCTCTCCTCCTTTCC	GGAGAAGGACAAGGACATTGGTAAT	(0,0)	1	AAAGCAGACCACACCATACTTCTC
Omy_105105-448	C	T	AAGGAGAATGCATAATC	TGAAAGGAGAATACATAATC	CAATTTGCAAGCAGGGAAAGGTTAT	(0,0)	1	GTGATGGGCTGCAATTGCTT
Omy_105385-406	T	C	CTTGGAACCATTGCTAC	TTGGAACCGTTGCTAC	GTAACCTACCCTCACCTGAACTTCA	(0,0)	1	GTCGCTCTTCTGGGCGTATCG
Omy_105714-265	C	T	CTGTTGTTTGAGGTTCAG	TGTTGTTTGAGATTCAG	CCACTCAGTGCAAGCATGGA	(0,0)	1	GCTTTCAATCCTTGGCTCCAATATC
Omy_107031-704	C	T	TGGACATGATTGCATAGAC	CTGGACATGATTACATAGAC	GGCTTTCGGATACTGAGCAACAA	(0,0)	1	TGAACTCACTGTTGGTATGGACTAGA
Omy_107285-69	C	G	ATACGTTACTTTTGACCTTGT	ACGTTACTTTTCACCTTGT	GCCCTTGTGACAATGCACTGTTATA	(0,0)	1	AGGTCTAGACAGTGTGCCATTTG
Omy_107336-170	C	G	CACTCCTGGGTGCAGAA	ACTCCTGCGTGCAGAA	GCCCTCTCACTCATGACATCAAC	(0,0)	1	GCTCCAGCCACTCGCA
Omy_107806-34	C	T	ATTGGATGTCAGTGTCATT	ATTGGATGTCAATGTCATT	TCTTTGTCCATGCACATTGATATT	(0,0)	1	AGCACATTTAGTTAGCAGTGATGGA
Omy_108007-193	A	G	ATGTTTTCTCCCTACTTAAC	TTTTCTCCCCACTTAAC	GTGAATACCACCCAGGCTTGT	(0,0)	1	GTCCCTTCCCCAGTTTCACTTAATT
Omy_109243-222	A	C	TGTTCATTAAATTGACTTTTT	TTCATTAAATGGACTTTTT	ATGTGCACCTCTTAAATTGTAAGTAAAATGT	(0,0)	1	ACCCTATATTCAGTGGCAAGATTGC
Omy_109525-403	A	G	CCTACACCTCTTTTTTCCACA	CCTACACCTCTTTTCTCCACA	CCTCATTCTCATTGGTGAGTTGTCT	(0,0)	1	TGTAAGATCTGACCACATGAGTATAACCA
Omy_109894-185	T	C	CTCCCTGATCCCCC	CTCCCTGGTCCCCC	GGGAGGAATTGGAATGACAGATTAAC	(0,0.5)	1	CGGTGTCATTATGGTTGTCATTGTG
Omy_110064-419	T	G	ACGTTAGCTTTTAATTTC	AACGTTAGCTTTTCATTTC	GTGCAAGGGACCTAGCTAATCC	(0,0)	1	TCTGAACTGACACTGAAGAACAAAGAA
Omy_110201-359	T	G	TTTGGCTATTGAAATTATACATT	TTGGCTATTGAAATTCTACATT	GGTAAGGCCTGTCTGACTATTTTGA	(0,0)	1	AGAGGTCAATGGATGCCAGTTT
Omy_110362-585	G	A	CACCGCCCTGCCCGT	CACCGCCTTGCCCGT	GCAGCCAAGATGAACGAAAACTTC	(0,0)	1	CCGGCCTGGGTCTCAATG
Omy_110689-148	A	C	CAAATGAACACATTATTTATC	ATGAACACATGATTTATC	GTGTGTGGCAGAGAACTAACTGAT	(0,0)	1	GGTTAAGACATTAACATAACACTGGACTCT
Omy_111084-526	A	C	CCAGTGAAATTTATTTTT	CAGTGAAATGTATTTTT	CACCACACCAAGCAACTATTTCATT	(0,0)	1	ACCCAACTACTGTCCCATTTTTCAT
Omy_111383-51	C	T	AGCAAGCGCACT[AG]GGT	AGCAAGTGCACT[AG]GGT	CACGCGCAATCTCTCGTTTTAC	(0,0)	1	TCTTTAGGCAACAAGCGTGTCA
Omy_111666-301	T	A	AGTATAACACAGTAAGACAAT	AGTATAACACAGTTAGACAAT	GGGTGAAAAGAGTGGGACATTTACA	(0,0)	1	GTCAATTTCAAGGCACCAGACAAT
Omy_112301-202	T	G	AATGCGAAGACAAACT	AATGCGAAGCCAAACT	GTAAACCCTGCCCACATAATTAGGT	(0,0)	1	CTGAGACACTGCTCCAAGGT
Omy_112820-82	G	A	CGCCGCCAAGTTA	CGCCGCTAAGTTA	CCTTTCCTTTTGCATTTCCTCTACTTATTTATTT	(0,0)	1	AAATGAACTCACGTTGACCTCTGA
Omy_113490-159	C	T	CATCTGTTTTGGTTTAGC	CATCTGTTTTAGTTTAGC	CATAGTACATTTACAGATAATGTTTTAAAGTGCATGT	(0,0)	1	CGAGATACCAAAATGCCACAGTTACAT
Omy_114315-438	T	G	TTATGGGCTTAAGGGTC	TTATGGGCTTACGGGTC	CCTCACCGATCTAGTCAACTTCATC	(0,0)	1	AGGAGGCTGAGGGAGATTCTAG
Omy_114587-480	T	G	CCTGTCCAAAATTGT	CCTGTCCACAATTGT	CAGATTACGTTATTACGTTTGGGAAATTTTTAAGT	(0,0)	1	GTGAAAGAGTGGGAAATATAATTATAAGGTCAGA
Omy_114976-223	T	G	ACCGATGGAACAATC	CCGATGGCACAATC	GACAAACAGCACTTCATTGCAGTAA	(0,0)	1	GTTGCTCCAGCACCAGGT
Omy_116733-349	C	T	AGAGAATCTGATAGTATTTC	AGAGAATCTGATAATATTTC	GAAATGGACATGCCTACAAATTGCT	(0,0)	1	GATGTGATCAGTTTAGGCAAGGC
Omy_116938-264	A	G	CCTTGTCTCAATTTTTCCTCT	CTTGTCTCAATTTCTCCTCT	GTTCATTCATGTTGAAGTGCGACAT	(0,0)	1	CTCTGCATGCTCCCATCCT
Omy_117286-374	A	T	CTTTCCTCATCATACTCTATGG	TCCTCATCATACACTATGG	TGATGTGTTGTTCCTCATGGCTTA	(0,0)	1	CTGTGCATTTATTCTTGTGATGCTAGG
Omy_117370-400	A	G	CAACTCCAATGAATTAA	AACTCCAACGAATTAA	TGCAAACACAGAGGAAAGGGATTT	(0,0)	1	GGCTTATTTGTTCCGTACTTGCATT
Omy_117540-259	T	G	TGTCACTTCAAAGTTTG	TGTCACTTCAACGTTTG	GGCAGGTTAACACAGTCATCTACTATAAA	(0,0)	1	CAGCATGTTGCTTTAATCCTTCACA
Omy_117815-81	C	T	CTATACGGAGACCAGC	CTATACGGAAACCAGC	CTGCTTTATGCACACCACATTGT	(0,0)	1	GCTCTTTCTGGAGAACAAGGTACTG
Omy_118175-396	T	A	CTCTTGCAGACATACCCGTA	CTCTTGCAGACATTCCCGTA	AGGCTTCACACACACATGCA	(0,0)	1	GACGCGCAACCTCTAGATTATACTT
Omy_118205-116	A	G	CTACTGAGGCTGAGTGCT	TACTGAGGCCGAGTGCT	CTGCGGTGGGCTACACA	(0,0)	1	CGCAGCTGCGGATGAG
Omy_118654-91	A	G	TCAGCTTGTCTTGCCGC	CAGCTTGTCCTGCCGC	CAGCGTAGACCGTTTCCTCATTAT	(0,0)	1	GCGCCGATGAGCAGCTT
Omy_120255-332	A	T	ACTATGCCATGAAGTTA	ACTATGCCAAGAAGTTA	GCTAGCTAACATTGAAGGGTGGAAT	(0,0)	1	GGCTACAGGGACTTTACAATGGG
Omy_128693-455	T	C	CACTCAACTGATACCC	CTCAGCTGATACCC	GCCTGCAGGAGAAGGTAGAGTTA	(0,0.8)	1	GAAATGGAATGGACCCCAATCCT
Omy_128923-433	T	C	CTTCATTTTCATTCACTGTTTT	CATTTTCATTCGCTGTTTT	CTATGTCCTTGGCAGAAGTCTACA	(0,0)	1	ACGTTTCTTTGGGCTGAGACTTATT
Omy_128996-481	T	G	CAAACCTCAACCAC	CAAACCGCAACCAC	CTCATCCACACTGTACAGTACAAGT	(0,0)	1	CATGCCTTCGTCTCATCAATAACAC
Omy_129870-756	C	T	ACAGGTATTTCGTGAAATG	CAGGTATTTCATGAAATG	TCGTTATTTTGCCTCGCGGTA	(0,0)	1	TCCCATGAAGATGTATACATGTTTTGTGA
Omy_130524-160	C	G	ATGGCTTGATCCTCA	ATGGCTTCATCCTCA	CGAAGGTAGCGATTGGTCGTT	(0,0)	1	TGTCTGTTCTGCTGTGTGCTT
Omy_131460-646	C	T	AATAAAGCAGAATTTGTTACTG	AAAGCAGAATTTATTACTG	GTGAAAAGGAATGGAGGAGTACAGT	(0,0)	1	TGCTAGGACAGGAAGATCATTTGTG
Omy_187760-385	A	T	TCCTTATCCAAAATTATTGTGC	CTTATCCAAAATAATTGTGC	CGGCTATTCTCGCGTAAAAGCT	(0,0)	1	AAATGCAACCAGAAACGGAATGTC
Omy_96222-125	T	C	AACTACAACTGTAGCTAATT	CAACTGTGGCTAATT	GTAAGGAACTAATTGGCGCAACATT	(0,0)	1	CAGTTTGTCTAACACCCAGGCATAT
Omy_97077-73	T	A	TGGTGCAATAGAAATA	CATGGTGCAATAGTAATA	GTGTAAACAAAATGACTCTGGGATTCAG	(0,0)	1	AGAAGTGGCAATGGTGTGAAGTAT
Omy_97660-230	C	G	ACGTAACTTGTAGCGTTTT	ACGTAACTTGTACCGTTTT	TCAGTTATGTGTAATCTCATTACCTCTCCAA	(0,0)	1	AACAGAAAAGGTCTCAATGTATTTTTTGCA
Omy_97865-196	A	G	ATTAATTAACAAGCTC	ATTAATTGACAAGCT	TCCAGACTTCTGGTTTGTTCCATT	(0,0)	1	CCAGCCCCTATATTCACAATTAAGTGT
Omy_97954-618	C	T	CAACGCTTACCGGTGTGT	CAACGCTTACCAGTGTGT	GCTCTGCTTCCTCGGCAAATA	(0,0)	1	CACAATTGGTTTTTGCACAAAAGTAAAGTATT
Omy_98683-165	A	C	AGCCAGATACATATTTGT	CCAGATACAGATTTGT	GCCATTGCCAGAGAATTTGGTTAA	(0,0)	1	AACACACGCACCATCTTAAAGC
Omy_99300-202	T	A	TCAGGCATGAGAGAAA	ATCAGGCATGTGAGAAA	CAGTTTGACCCGATGGTGTGA	(0,0)	1	GATTATGGCGTGGCCTTTTGG
Omy_ada10-71	C	T	CTTCCTGCGTCCAA	CTTCCTGCATCCAA	TCTTTGAGCGACAAAGTCCTTGT	(0,0)	1	ACCCACACATGAACGCAAAAG
Omy_anp-17	C	A	CTCTCATTGGTATAGTAACC	CTCATTGGTATATTAACC	GGTAATGCCACATGCGGTAAATT	(0,0)	1	GGCGAAATCTGAAAATGTGCTGTTA
Omy_aromat-280	T	C	TCTTGCAAACTCC	TCTTGCGAACTCC	CTCCATTGATTCATGCCGAACATT	(1,0)	1	GGAGAGGTCAAACATAGCCTGGTA
Omy_arp-630	G	A	CCGCTCCGTCTGCT	CCGCTCTGTCTGCT	CTGCACAACTTGTTTCCTGCTATT	(0,0)	1	ACCAAGTGTCCCTGTAAGCC
Omy_aspAT-123	T	C	CCTTCCTAGGCAGTCAG	TTCCTGGGCAGTCAG	GCCCATTTCACTGATGCTGTGA	(0,0)	1	AGGAGACCACTCCAAAGAGAACT
Omy_b1-266	G	T	TCTATAAACAACATTTTTC	TCTATAAACAAAATTTTTC	TCATGTGAACTTTAATTGACTAGGAAGTCG	(0,0)	1	GATATGAAAATATCTGAAGAGTTATATTTGGGAAATTGAC
Omy_b9-164	T	-	CCTACAACTTGATCTAACGTG	CCTACAACTTGATCTACGTG	GCACAGAACACAGCCAATATTAACA	(0,0)	1	GCCTTGACTCTCCCTTCATGAC
Omy_BAC-B4-324	G	T	CATTGCCAAATACG	TACATTGACAAATACG	CGTACTTTTCTTTTACAAAATTAAGTGGAGGAT	(0,0)	1	GCCTAATATTGGCCTAATGTCCTTCA
Omy_BAC-F5.284	C	T	CAGTAGGGCGGCAAG	ACAGTAGGACGGCAAG	CCTCATTTACTGTAGGACCATGCA	(0,0)	1	ACAACGCCAACAACTTTCTCTTG

Omy_BAMBI2.312	G	T	CCGAAAGTTCAACTTT	CCGAAAGTTAAACTTT	CGAGCTCATGTCCGAAACTCAT	(2.1,0)	1	TTTGACAGCCTCAACTTCTAGGG
Omy_BAMBI4.238	T	C	CACCGCAATCACCG	ACCGCGATCACCG	CATGATGAGGAGGACCAAGATGAG	(0,0)	1	AGGTGTGGTTCAGGGCAG
Omy_bcAKala-380rd	G	A	CATACCCATCCTATGTCAG	CATACTCATCCTATGTCAG	TTGCTCTCTTCTGGTTGCCTTA	(0,0)	1	CTTCAGGAGAAAGCGCTACTGT
Omy_ca050-64	T	G	CAGTTTGAAGAATATACTC	CAGTTTGAAGACTATACTC	GTCATACAGAACTGTTTTGTTGTGTCAA	(0,0)	1	ACCTTGAATTGGTTCCTAATGCTATTGT
Omy_carban1-264	G	A	CATTAATATTGCTAATAACACCAAG	ATTAATATTGCTAATAACACTAAG	GCAAAGCCTCATCTTCAATCATTTGT	(0,0)	1	GCAAAACACAAGTCAGGAATCACTTA
Omy_cd28-130	T	C	CCTGTTCATTCACCC	CTGTTCGTTCACCC	CACAACTCCACAGAGACAGTGA	(0,2.7)	1	GAGGACAAAACTGACCGTATGGT
Omy_cd59-206	C	T	CAACAATCGAAGGTAAAT	CAACAATCAAAGGTAAAT	CGATTGGCCCAGATGTTTCCAT	(0,0)	1	GCTCCGTTGCATAGGTGACT
Omy_cd59b-112	C	T	CTAAAAGCCTATAGCAAACT	CTAAAAGCCTATAACAAACT	TTTGGATAAGATTGTCTTATATGACTAAAATGTCATGT	(0,0.6)	1	GCCAACGTCCTAGATATGGTGTAAT
Omy_cin-172	C	T	CGCTCACCGTGGTTAC	CGCTCACCATGGTTAC	CGCATGGGACAGGTGTGT	(0,0)	1	GAGAAAGCCTGTAGAACCATGTCT
Omy_cox1-221	T	A	CGGTAAGACCATTAAAA	CGGTAAGACCATTTAAA	CACTGAACTGTAAGCCATTGTGATT	(0,0)	1	GCAACATGGGAATGATTCATAAATGCA
Omy_cox2-335	T	G	CTTTAAAGACAAAGACTTTAT	TTTAAAGACAAAGCCTTTAT	AGCTGGGCTGTATTTGTCAATACTT	(0,0)	1	CAGCCCGCCACTGTCT
Omy_crb-106	G	T	TTGCAATGCGTCTTT	TTGCAATGAGTCTTT	GCTCAAAAAGATTCTGCCAAATTCACA	(0,0)	1	ATTACAATGAAAGTACTTGAGTGTTTATGCAAA
Omy_cyp17-153	C	T	ATACCTGAGTGTCATCG	ATACCTGAGTATCATCG	GCCCTCCAAGTTCCAAGTGAAAA	(0,0)	1	CAGGTCATTGATGAAACGTCAGAAC
Omy_e1-147	G	T	CCATCCTGAATCTGATTAA	CCATCCTGAATATGATTAA	GCACTGACTGTTACCAGGAAAGAG	(0,0)	1	GTACTGCAGTGTTGAGGCTATATCA
Omy_ftzf1-217	A	T	TCATGACGAGTTCTGATTT	TGACGAGTTCAGATTT	ACAGGGATGGGCAACTTTGTT	(0,0)	1	GGATGACCCACGTGACACT
Omy_g1-103	T	C	CCTTTTACAATGAAGATC	CTTTTACAGTGAAGATC	AGTCGTGACAATGAGAAACAGTGTT	(0,0)	1	CTCAGCAAAAAAGAAACGTCCCTTT
Omy_g12-82	T	C	CAAACTCTCAGGATTAG	AAACTCTCGGGATTAG	GATCAATTCGATCGCTCATGAAACTT	(0,0)	1	CTTCTCTCGTTCTCATTGTGTCTCA
Omy_G3PD_2.246	C	T	AGTAAAGCCCATTGTTGAGT	AGTAAAGCCCATTATTGAGT	TCATGTATCAATTAAGGCATTGTCTTGTCT	(0,0)	1	GTTAGACACAGTGACCACCTCTTT
Omy_G3PD_2-371	C	A	AGACATGTGGATTGGCA	CAGACATGTGTATTGGCA	GCAGGTAAGGTACACCATAGAGACA	(0,0)	1	CTCCCCCTGCCTTACCAAAC
Omy_gadd45-332	T	C	TTGCTCCAAAATGG	TTGCTCCGAAATGG	AGAGAAGACTCACTGCTGTTTGC	(0,0)	1	AAATCAGTTCCCACGCTATGCT
Omy_gdh-271	C	T	TCACCCTGAAGTGTAGAC	TCACCCTGAAATGTAGAC	AGGTCAGTCTACTTACAGTATAAAGCAGT	(0,0)	1	GTCATGTCAACAGAGTAACATAATAAATCTGC
Omy_GH1P1_2	C	T	AAACTGTTGAACGGTAGTG	AAACTGTTGAACAGTAGTG	TGCATTTGATGGAAACAAACATATTTATAATGTGT	(0,0)	1	CAAAAACAAGGACAATTCTAAGTGACCTC
Omy_gh-475	C	T	CTGAAACTCATGGTATACA	CTGAAACTCATGATATACA	AAGTTACCAGAATTTTGCAAACTCAACT	(0,0)	1	CCATATTTTGAGGTGTAGCTTTACCCT
Omy_GHSR-121	T	C	CCTAATAACCATGATAACAGC	AATAACCATGGTAACAGC	CTGTGTATAAGTTTATACAGTCAGCACAGT	(0,0)	1	TTCAGAGAGAGAAATGGCAGAAAGG
Omy_gluR-79	C	T	CAAGTATTTTGCGTAGGAAT	CAAGTATTTTGCATAGGAAT	GACTGTCTATAGCTATTCTTCTCAAACTGT	(0,0)	1	AGAAACTACCATTGTGATTAACAGATAGAAAATACAT
Omy_GREB1_05	T	G	CGGTGGCTCTC	CGGTGGCTCGC	TGGGCAGATATGGAAGAACGG	(0,0)	1	ACCTTCTAAATGGCCTCTGTGT
Omy_GREB1_09	T	G	TCAATGGAGA	TCAAGGGAGA	CCAGTGGCAACCTCAGGTAG	(0,0)	1	GACTCCAGTCACCCAAGTCA
Omy_GTA0162575	G	T	CTGATAACATCTGCC	CTGATAACATCTGCA	TGCTTTGATAACGCGTCTTCATG	(0,0)	1	GTGGCGCCACGTGCA
Omy_GTA0162621	A	G	TGTCTAAACTGGACA	TGTCTAAACTGGACG	CGCATAAGGCTTGGACTGTT	(0,0)	1	CTGGACTAGTGTCATGCACCCA
Omy_GTA0246634	A	G	GAATCTGTTACTAGA	GAATCTGTTACTAGG	TCGTCACGTAGCCCAGC	(0,0)	1	AGGGTACTACCAGCATCCACAATG
Omy_GTA0262322	A	G	GCTAGCACTGCAGTA	GCTAGCACTGCAGTG	AATGAATCTACTACTGAAAACATAAGCTAC	(0,0)	1	CCCTCTCTTTGAGTGAACTACTGACA
Omy_GTA0262327	G	T	TAGCACAGGCTCTAC	TAGCACAGGCTCTAA	TGCCCTTTTATTACTGACAACATCA	(0,0)	1	CAGGGATTTAGGGATTTGATGCATCT
Omy_GTA0266143	C	A	AAGTAGTGCACTATC	AAGTAGTGCACTATA	GCCCATAGTGTTCTGGTCAAA	(0,0)	1	GGGCCTGCATCTCAAGTGG
Omy_hsc715-80	C	A	AACTGTATTTGGGAAAAT	ATAAACTGTATTTGTGAAAAT	CCGGTCTACCCTATAGCTGTTG	(0,0)	1	AGTCAGTCAATTAGTGGTTTGAAATACTATCA
Omy_hsf1b-241	A	-	CAGTGTTTTGTTTTTTGTCATT	AGTGTTTTGTTTTTGTCATT	AGCCCGAACTATCCTAAAGCATTTT	(0,0)	1	AAATCAATAGCTCAGAGAATAATGAACACCA
Omy_hsf2-146	A	-	ATAATCTACTA	ATAATCTAACA	CCAACAATTGCAGCCTCATCTTAAT	(0,0)	1	GGAGCAGAAAAAGGATTGGACCTT
Omy_hsp47-86	T	A	CAGGAGTGTAAATGTTT	ACAGGAGTGTATATGTTT	CACATTAAGCACTCCCAGGGA	(0,0)	1	TTGCAAAGGCCAAACAGCATT
Omy_hsp70aPro-329	A	G	ACATTCCAATATTCAACTAT	CATTCCAATATCCAACTAT	TGCGTATTATTGTTTTTCAAGGACTTTCAAA	(0,0)	1	TGAATATTTTCAAATACATGCCAATTCTTTCCAA
Omy_hsp90BA-193	C	T	CCTCCGCGCCTGC	CCTCCGCACCTGC	GGAATCGATGACGACGAAGTGATC	(0.5,0)	1	TTCCTCCATGCGTGATGCA
Omy_hus1-52	G	A	CCCATCCCTCCTCCTGG	CCCATCCCTTCTCCTGG	CTTGCCGGAGGGTAGCT	(0,0.5)	1	CCACAACTTCTCAAATGAATGGAATGT
Omy_IL17-185	G	A	AAGAATCTCACCTGCCCAT	AAGAATCTCACTTGCCCAT	CCACCACACTCTGCAGCTT	(0,0)	1	TTGACGGGAATCCGAGACTTC
Omy_Il-1b_.028	T	C	CTGAGGCAACTTTTGT	TGAGGCAGCTTTTGT	ACTGTCTGGCTAGAGCACATTG	(0,0)	1	ATCTTCTACCACCGCACTGTTTTAA
Omy_IL1b-163	T	G	CTGAGGTCATAAAAATA	CTGAGGTCATACAAATA	GGAACAACAGGATTAAGCCTACTCT	(0,0)	1	CCTAAAGGCCTAGGAAACTAAACTTCA
Omy_IL6-320	C	T	CTATAGGAGAGAGGACAACA	ATAGGAGAGAAGACAACA	CGACTGATCTCCTGCAGACATG	(0,0)	1	CTTGTTCCTCGTTGTCTTCCTTCTA
Omy_impa1-55	C	T	CGAGATGATGCGTCTACA	CGAGATGATGCATCTACA	CGCTGAGAGGATTGTCAA	(0,0)	1	TTTTCTTTGTTCAGTCTTCTGTCTCTG
Omy_inos-97	C	A	CCTTTCTTGATGGTATCC	TCCTTTCTTGATTGTATCC	GATGGACAGGGTCCTCTTCAC	(0,0)	1	CCTGTAGATAAAACATGGTACCAGGTC
Omy_LDHB-1_i2	C	T	ATGGGCAGTCATTCA	TGGGCAATCATTCA	ACGCACACTTATCCTTGACAATGTT	(0,0)	1	ACTGTGACAACAAATTCGGTGACA
Omy_LDHB-2_e5	T	C	TTTACCTGTCAAC	CCTGTCGAC	TGCTAGGTGAGTCAGAGGTACATATT	(0,0)	1	GACTGGAAGGCCACCCATAAG
Omy_LDHB-2_i6	G	T	CTGTGTTTTGCTTCCCCA	CTGTGTTTTGATTCCCCA	TCCTCGCCAATACCATACATGTC	(0,0.5)	1	AGAGTGAAGCTAACACACACATTTCT
Omy_lpl-220	C	G	AGTGACAGTCA	AGTCACAGTCA	TGACAATCACTGAGCAACTGAACTC	(0,0)	1	GTCCAGTCTTGCTTCAACTCATTCT
Omy_mapK3-103	A	T	AATTATTAAGCCTATTTTTTT	ATTATTAAGCCTAATTTTTT	GAAGTCATTACTGGTCAGTGGTCAA	(0,0)	1	GCACAAAACATGAGGAAAGTTGAGA
Omy_mcsf-268	T	C	AAATAATAGATAAA[CT]CCT	AAATAACAGATAAA[CT]CCT	CCAGCATTCGTTCCCATTTCC	(0,0)	1	CTTTTAATGTAGATTATATTCTTCTGTAGCCACTATGG
Omy_metA-161	T	G	CAAGTAAGTGGTTATATTCT	CAAGTAAGTGGTTCTATTCT	CGCATGCACCAGTTGTAAGAAAG	(0,0)	1	AGTGCCACCAGCGATAAGAAAA
Omy_metB-138	T	A	TTCGCCAAAGAGAAAT	TTCGCCAAAGTGAAAT	TCTGTCCCTGACGCTATAAAAACG	(0,0)	1	GAAGTATTTCAGCTTAATTTCACTGTTGAGTT
Omy_MYC_2	T	C	CATAGACTTTTTGACCTTAT	CATAGACTTTTTGGCCTTAT	CGGTTGCAGAACTCTCATGTTTG	(0,0)	1	CACGCCATGTCTTAACTTGCATTA
Omy_myclarp404-111	T	G	CAAAGCCATACGTGGCC	AAGCCATCCGTGGCC	GCTGTGGTGCTCATGGGTAAA	(0,0)	3	CCAGGGCAGGGTTGTTCTC
Omy_myoD-178	A	C	TTTTATGAGATATAATTTCC	TTTTATGAGATATCATTTCC	GGTCAAATATTTCATTTACGATTACACTTAGGC	(0,0)	1	TGGCAAAGCTGTCATTCCTTCTAAT
Omy_nach-200	A	T	AACTGACAGAGTCACAAC	CTGACAGAGACACAAC	CTCATGAAAAACGGGAGAGCAAAG	(0,0)	1	CAGCGGCTCTTCAGTAGTCT
Omy_NaKATPa3-50	A	C	CACTCTGTTTCCTTTCTTT	TCTGTTTCCGTTCTTT	GTTGAGCGTGTTATGGGAAAAGAG	(0,0)	1	TTGCATCGGCTTTCTGAAAACC
Omy_ndk-152	A	G	ACCCACTTTCAAAAC	ACCCACTCTCAAAAC	AAGAATTGAGGGATAAAAACAAAATAATATATAAACATGA	(0,0)	1	CAAACCTACATTCATTAAAGTCCAGTTTTGT
Omy_nips-299	T	-	CTGGATTTCACATGTAATAC	CTGGATTTCACGTAATAC	GACAGGATAGGAACGGTTTCTCAAT	(0,0)	1	ATCAGAAGTTTAATTCAATATGTACACGATCCT

Omy_nkef-241	C	A	CTTCTGTATCATTTTTG	TCTTCTGTATAATTTTTG	AGTGTCATTGATGTCGGCCTATTTT	(0,0)	1	AAACGAATGTCCACCTCAGATGTT
Omy_ntl-27	G	A	CAGACAAGAGTACCCCAAGAC	CAGACAAGAGTACTCCAAGAC	GGTGTGTTACTGTAGTTGTGTCCTT	(0,0)	1	TGTGTAGCTAGTGATCCTGATTGTCT
Omy_nxt2-273	C	T	AAGGCAC	AAGGCAT	CTTTAGAAAAGCCAAGGTATATTTTAACATACTTCT	(0,0)	1	CTGCTGCCCTCTAATGGTAAGATAG
Omy_Ogo4-212	T	C	CATTTGATGAGACATCTT	ATTTGATGAGGCATCTT	TGAAAGGTTTTATGCAGGTTATTTTCT	(0,0)	1	GTGTGTGTTAAATAAGCATTTGATGA
Omy_Omyclmk438-96	A	C	TACGCAAATTAGGTTTAAA	CGCAAATTAGGGTTAAA	CCCGACTCTACTTCACTACTTTCCT	(0,0)	3	GGCCTAGGACAATAGGACTGAAC
Omy_OmyP9-180	C	G	CTGTAGTAGTCCCCATTGT	CTGTAGTAGTCCGCATTGT	CTGGATGTGTAGTATCGGTGGAAAA	(0,0)	1	CACTGGGCACCTCTGATCTC
Omy_Ots249-227	C	T	CCCTCTGAGAACTAC	CCTCTGAAAACTAC	CTATCTATCTATCTATCTATCTATCTATCTATCTATCTACTTACTGAGA	(0,0)	1	CCCCTAGATTAAACCTGTCCAGTCT
Omy_oxct-85	A	T	CATCGCTTATTTATGC	CATCGCTAATTTATGC	CGTCACTGAAACATTACTGTAACATCCA	(0,0)	1	CATCATCACGCTGTTGGTTTCTTAA
Omy_p53-262	T	A	CAAGTAGTATGGAGCTCTAT	AAGTAGTATGGTGCTCTAT	CCCCAACATCCAGTATACAGTTTCA	(0,0)	1	CCCAAATTGGCAATTTTAATAGGATTCAGA
Omy_pad-196	C	T	AAGACAAAGGTGTAATACC	AAGACAAAGGTATAATACC	CAAACAACCACAGTAGTCCTCCAAT	(0,0)	1	GCTTTTCACCCTTTTGTAAATTAAGCCAAA
Omy_ppie-232	C	T	AAATAGCGGAGAAAAT	AAAATAGCAGAGAAAAT	CTGTTTTAGATTAGAATGTTTTTGGTCAGGT	(0,0)	1	CTGAACATAGGCTTTCATTTCAGACAT
Omy_RAD103359-45	C	T	CCTGTAACGCACAG	CCTGTAATGCACAG	GGAGAAGGATGTGCTCCCTG	(0.4,0)	1	ATTTGGAGGTGGAGGGTCCA
Omy_RAD10733-10	A	G	AGGGTGAAGAACTG	AGGGTGAGGAACTG	TATAGACCCCCTGCCAGTCA	(0,0)	1	ACAGAGAAACCCCCGTCATT
Omy_RAD116-59	T	C	CCACAATGTCAAC	CCACAACGTCAAC	GGAAGAAGTGAGAGCCCTGG	(0,0)	1	CTGTAGTCCACGATCCGCTC
Omy_RAD1186-59	A	G	CCAGGACATCCAGG	CCAGGACGTCCAGG	CACAGCCTGGATGTGGTTCT	(0,0)	1	ACAAGTTCCGGGAGTTTCCT
Omy_RAD12439-64	G	A	CTTCTCCGATGTCA	CTTCTCCAATGTCA	GGAACTTTTCACATCATGTTGACTG	(0,0)	1	GCACAGAGAACTCCAGGCAA
Omy_RAD12566-14	C	T	ATGTAAACAAATTG	ATGTAAATAAATTG	GTGGACATTCCTGCAGGGAT	(0,0)	1	TCCCACAAATATTTCATACGCACA
Omy_RAD13034-67	A	C	ATAAATCACAA	CTAAATCACAA	GAGTGATTCCCAGCCCTCC	(0,0)	1	TCTCTCCGTTGGCCAGAAAC
Omy_RAD13034-67-21	C	T	CTCCCCGAACC	CTCCCTGAACC	GAGTGATTCCCAGCCCTCC	(0,0)	4	
Omy_RAD13034-67-35	A	T	CTGAGTGGACA	CTGTGTGGACA	GAGTGATTCCCAGCCCTCC	(0,0)	4	
Omy_RAD13073-16	G	A	AAAGGGGACATTACG	AAAAGGGACATTACG	GTGAGGGATCACACCTGCAG	(0,0)	1	GCACCCATTCGTAATGTCCC
Omy_RAD13499-13	T	C	CGCCCTGTCCGCCA	CGCCCTGCCCGCCA	GTTCACCTGACGACCAAGGT	(0,0)	1	GCTGGGGGAGCTTTACATGA
Omy_RAD14033-46	A	G	ATAGAGGAATAGAC	ATAGAGGGATAGAC	GCAGGAGATTTATTTGGCCCC	(0,0)	1	ACCCTTGTGATCACATACTGTCT
Omy_RAD15709-53	G	A	ATGCAAGGCTTAAA	ATGCAAGACTTAAA	TGCAGGACTTGGATAACACAGA	(0,0)	1	TGGTTATATCTACAGTACAGTTCGT
Omy_RAD16104-20	A	G	AGGGCAAAG[AT]CAAAGG	AGGGCAAGG[AT]CAAAGG	ATTCCAAAACCTGCAGGGGT	(0,0)	1	TCAGGATTTGGTAAGGTGGCC
Omy_RAD17632-23	C	T	CATGTGAGACCTTTGCA	CATGTGAGATCTTTGCA	AAGCTCCTGCAGGTCATCTC	(0,0)	1	TCTGTGAACTGTCTTCTGCAAGT
Omy_RAD17849-16	G	C	AGACGGACTCCCC	AGACCGACTCCCC	GACTCCACAGCCTACATGGG	(1.1,0)	1	CCGTTAATGCCAGGGGAGTC
Omy_RAD18903-48	A	G	AGGAGACACCA	AGGAGGCACCA	GGGGATGAGTTCTTCGGTGG	(0,0)	1	CCACCAAATCCCCCGAAGAA
Omy_RAD1919-22	A	G	CAGGGAGGAGG	CAGGGGGGAGG	CAGGTCACAGACACACAGGG	(0,0)	1	CTACACCACCCCACGTTCTG
Omy_RAD19340-24	A	G	CATGGAAATACATA	CATGGAGATACATA	GCAGGGAGCAGCATATACATG	(0,0)	1	TGGGGTGATTTGAGTGACAC
Omy_RAD19578-59	A	G	GGTTAAGAGTATTC	GGTTAAGGGTATTC	GGTTGGACACCTCCTGGTTA	(0,1.2)	1	TCAACCAAGCAACAGATTATAGCT
Omy_RAD20917-11	T	C	AGGTTGCGAGGTC	AGGTCGCGAGGTC	CGTTGTCGTCTCCAATCAGGA	(0,0)	1	ACCAGCTCGATGCCATTGC
Omy_RAD22123-69	T	C	CCAAAGATGTCAGA	CCAAAGACGTCAGA	TGGGAAAGCATAGGAGGGGA	(0,0)	1	TGTGTGCCTGTCTTATAGCCC
Omy_RAD23577-43	T	C	TCTGGCTCTGTCGGTCT	TCTGGCTCCGTCGGTCT	AATAGGAACCAAGCCCCAGC	(0,0)	1	CAGAGCCTGAACCCATGGAG
Omy_RAD23894-58	A	T	GTGGATTAGGGG	GTGGATTTGGGG	TGCAGAAAGGCTGTGTGGAT	(0,0)	1	TCTTAACACAGTCCTCATGGAACA
Omy_RAD24287-74	A	G	GGTCACTACCTCCC	GGTCACTGCCTCCC	ATTGTCTGTCTGCCGAGGTG	(0,0)	1	TGGCGACCTGTCACTAATGC
Omy_RAD25042-68	G	T	AATTTCTGCCCAAA	AATTTCTTCCCAAA	GCTGCTGAAACTGGTTTGCA	(0,0)	1	TCATGCAGATGAGCTTCCCTG
Omy_RAD2567-8	A	T	GCAATGGGCTATTT	GCATTGGGCTATTT	CTGTCTGGATAGCCTTGCCC	(0,0)	1	TCTATCTCTGGGGAAAATAGCCC
Omy_RAD26080-69	G	A	ATTAGTAGCATCATCGAG	ATTAGTAACATCATCGAG	TGTGGGACAGCACATACTCC	(0,0)	1	CCAGGACACCAGTGGAGAAG
Omy_RAD26691-36	A	G	TCTCCTAACAGAAC	TCTCCTAGCAGAAC	TGCAGGAAACCGTCAATCTACA	(0,0)	1	CAGGAATTAATTGTATGGCCGGA
Omy_RAD27740-55	A	T	TAACTTTAAAAAAA	TAACTTTTAAAAAA	TCGGCCTGTACTAGTCTCACT	(0,0)	1	GCCTAAAATGGCCACTTTCATCA
Omy_RAD28236-38	T	C	ATCTGTCTTCGTGC	ATCTGTCCTCGTGC	GGCACACATCTGTCCCGTAG	(0,0)	1	GCACTAAGGTCTAGGAGCACG
Omy_RAD29700-18	C	A	ACAATTCAAATGATTTA	ACAATTAAAATGATTTA	AATGGAATTGGCCCCAACCC	(0,0)	1	TCTCCATTGTGTGTAATCATGGT
Omy_RAD2976-26	G	A	CAGCTGGGTTGAGA	CAGCTGGATTGAGA	AGGACTGTGATCCTCTCAGCT	(0,0)	1	AGCTCTGCTGAAACATCAGTCT
Omy_RAD30392-17	T	C	CTGAGACTGTGTGT	CTGAGACCGTGTGT	CCACTACTCACAGACCTGCA	(0,0)	1	GCTCAAGGACCAACAAAAAGCT
Omy_RAD30619-61	T	A	CACTGTTAAA	CACTGTAAAA	CTGCAGGTCAATGGGTGCTA	(0,0)	1	ACACTGATCACATTTTTGTCACACT
Omy_RAD31408-67	T	C	ACAGAATGCAGAAA	ACAGAACGCAGAAA	CAACCCTGCAGGCTACAGAA	(0,0)	1	TGGAGTGCCAACAAAAGAAGC
Omy_RAD3209-10	A	G	CGGTATCCCTGGC	CGGTGTCCCTGGC	CGGAGGAGTTTGAGCAGTCT	(0,0)	1	CTTCTACCACCACCTCGCTG
Omy_RAD32139-58	G	A	TCGACATGACCTGA	TCGACATAACCTGA	GCAGGAAACAGGTACAAAGGA	(0,0.4)	1	TGGCTTCTTCCTTGCTGAGC
Omy_RAD33122-47	G	C	CCACAGGGTGGTGC	CCACAGGCTGGTGC	CAGGCTTTGTGGACATGTGC	(0,0.6)	1	GTGCTCTATCTTGCTCTTGGC
Omy_RAD33798-24	T	C	GAGTCTATCAAGAT	GAGTCTACCAAGAT	CAGGAGGGTCAAGTGGAGTC	(1,0)	1	TTGGGCCCTCTCTTTTTGGG
Omy_RAD35005-13	C	T	CCAACTCCCGACGG	CCAACTCTCGACGG	TGGTCAAAGTTGAGGGTGGT	(0,0)	1	CAGGGCCCTGATTAACCACT
Omy_RAD35149-9	G	A	GCGCGCTTATGTC	GCGCACTTATGTC	GAGTCAATAGAGCCCCCTGC	(0,0)	1	TGGTTAGCAGGAGCAATCTCA
Omy_RAD35417-9	G	A	TGCAGGACGTGCTTTGT	TGCAGGACATGCTTTGT	GCACTTGACCACATAGCTGG	(0,0)	1	ACTCCACACTCCACAAAGCA
Omy_RAD3651-48	G	T	GTTGGGAGAACTTT	GTTGGGATAACTTT	GAGTACAGTGCAGTGTGGGG	(0,0)	1	CCTTCCTCTTGCCACCATCA
Omy_RAD366-7	C	A	CAGGACTTGCTTTT	CAGGAATTGCTTTT	ACCAAATTAGAGCCTGCAGGA	(0,0.2)	1	GGAGAGGCCTTTCCGTGATC
Omy_RAD36848-7	G	A	TGCAGGGACACCACCCT	TGCAGGAACACCACCCT	CGAGGACGTTCATAGGGAGC	(0.5,0)	1	TCGATAAGTCCACCAGCTGG
Omy_RAD36952-53	C	A	AGGACATCTTCATC	AGGACATATTCATC	TGTACGTCATTGGGGCTGAG	(0,0)	1	CCTACCAGACCACACGATGA
Omy_RAD37816-68	A	T	GCGGCGTAAAAATG	GCGGCGTTAAAATG	CTCATTCCCTGGCCGTCTG	(0,0)	1	CCACTCACACTGGCTTATGC
Omy_RAD38406-19	T	A	AGGCTTTATATGGCC	AGGCATTATATGGCC	CTGCAGGGGTATTAGGAGGC	(0,0)	1	AATGAGTTGTGGCGGTGAGT
Omy_RAD39156-33	T	C	ACCGTAATGGAGAG	ACCGTAACGGAGAG	GGGTGTGACATGTGTGCAGA	(0,0)	1	ACTGCTTGTCCCCACCAAG

Omy_RAD3926-22	T	C	TTCACTTTTCCCTG	TTCACTTCTCCCTG	CGTTCCTGCAGGCTTTTCAC	(0,0)	1	TTGGCACAGAGAGTACGCAG
Omy_RAD40132-55	A	C	TCTGTGCAGTCCTC	TCTGTGCCGTCCTC	TGCAGGGCCTGTATATTGCT	(0,0)	1	TCAAAGGACTGGGGAGAGGA
Omy_RAD40520-48	T	G	GTCAGATTGCGCTG	GTCAGATGGCGCTG	TGTTCATCTGATCAGCTGTCAG	(0,0)	1	ACACGTCGGTCTTCTTCTCC
Omy_RAD40641-58	T	C	AGTGATATCAAGTG	AGTGATACCAAGTG	GGCAAACTGGCTTGTGAGTG	(0,0)	1	AAGGCTCTGCTTCTGCTTGA
Omy_RAD41594-34	A	G	CAGAGATACGTTCC	CAGAGATGCGTTCC	TGCAGGGTTATAATGTGTCTTTGT	(0,0)	1	AAATCTCGGGCTGAGGAACG
Omy_RAD42465-32	G	T	CCAGGCTGGAAGAA	CCAGGCTTGAAGAA	GTGGATCTTGGACTCCAGGC	(0,0)	1	TAGACATCGGCCCTCACAGA
Omy_RAD42793-59	T	C	CAGAGAATGCCAACAGA	CAGAGAACGCCAACAGA	CACGGCTAGTGGCATGTACC	(0,0)	1	CCACACCTGCATCAGTCTGT
Omy_RAD43573-37	A	G	GAAAGAGAGAGTTT	GAAAGAGGGAGTTT	TGCAGGGAACGATGAAACCA	(0,0)	1	ACAGACACAGCATTGGCCAA
Omy_RAD43612-42	T	C	AAATGTGTATTTGTGTA	AAATGTGCATTTGTGTA	GTGGAGAGGGATTTTGGGGG	(0,0)	1	TGACAGGACAAACACAAGCCA
Omy_RAD43694-41	A	C	AGGGAAGAGCGGAG	AGGGAAGCGCGGAG	CCCCTCTCCCTGGCTAGAAT	(0,1.1)	1	TCAGGGGGTGTGCTTTTCC
Omy_RAD45104-18	A	G	CAAGACACCGCACACAG	CAAGACGCCGCACACAG	TGGTGCTTCAGTGCTGTCAA	(0,0)	1	AGAGTGAAAACTGTGTGCGG
Omy_RAD46314-35	A	G	TAGCAATGGT	TAGCGATGGT	ACTGCATCTTTTCCCCTGCA	(0,0)	1	TGAAGATACCCAGAGACACCA
Omy_RAD46452-51	A	G	TGAAGTCAGAAGTT	TGAAGTCGGAAGTT	TGCAGGTAAGACTTGATCTGGA	(0,0)	1	TGACTCCAACCTAAGTGCATGT
Omy_RAD46672-27	C	G	GTGGTAGCCCATCA	GTGGTAGGCCATCA	TGCAGGAGGTCTTTTTCCTTGT	(0,0)	1	AACACATTCTTATTTGCAATGATGG
Omy_RAD47080-54	A	G	TGCAAGACTTAAAACGA	TGCAAGGCTTAAAACGA	TCAAAACCTGCAGGACTTGGA	(0,0)	1	TGGTTATATCTACAGTACAGTTCGT
Omy_RAD47444-53	C	T	GGCGAGCTTGGCCCAAA	GGCGAGTTTGGCCCAAA	GTCGTCTGGAGGAGCTGAAG	(0,0)	1	GGGTGACGTTTTCCTTCAGC
Omy_RAD47955-51	G	T	TTGGAATAGAATCTATA	TTGGAATATAATCTATA	AGTGTGCTAGAATGGGCCTG	(0,0)	1	ACCATGGGCAGTTCATTTCA
Omy_RAD4848-14	G	T	GAGACAAGGACAGA	GAGACAATGACAGA	TGTCCCTCTTCTGCACGATG	(0,0)	1	AGTTGGTAGCTCACTCTCTGT
Omy_RAD48799-69	A	G	CATCCTAGAATAGAAGT	CATCCTGGAATAGAAGT	GCTGAGCCACCTACACACAG	(0,0)	1	GTCTAACACTCGCAGCAGGT
Omy_RAD49111-35	T	C	TTTCTTATATTTGA	TTTCTTACATTTGA	GCAGGCTTAGCATTGCTGAC	(0,0)	1	GGAACCTGGGTGGGAGAATG
Omy_RAD50632-21	C	T	TCAGCACCTCCAGCC	TCAGTACCTCCAGCC	CCTGCAGGCTGGGTCATTAT	(0,0)	1	GAGCCAGCTGTACCTTCTCC
Omy_RAD52458-17	C	A	ATGGCCCC[CT]AAGAACCC	ATGGCCCA[CT]AAGAACCC	ACGTGTCCCTGAGGATGGTA	(0,0)	1	AGCTCTAGGTCTGGGTCCTG
Omy_RAD52812-28	C	G	CAACCTC[TC]ATTCCACAT	CAACCTG[TC]ATTCCACAT	AGGAGTCCTGTCCCATGTCA	(0,0)	1	GCTTAAGGCTGTGGTATGTGG
Omy_RAD5374-56	A	C	AGAGGGAAAGAGAG	AGAGGGACAGAGAG	GCTGTTACCGTGTGATGTTGA	(0,0)	1	AGAGTTCTGGCCTCTCCCTC
Omy_RAD55404-54	C	T	ATTGTTTCTGAAGG	ATTGTTTTTGAAGG	GCAGGGTGTCCACTACAGAC	(0,0)	1	AGGAGTCCTGAGAGTTGGGC
Omy_RAD55997-10	A	C	AGGCTGCAATGTTT	AGGCTGCCATGTTT	CATTTTCTACCTGCAGGCTGC	(0.9,0)	1	AGCCTACATACATAAAGCCAACA
Omy_RAD57916-29	A	C	CAGGGGCAAAACGG	CAGGGGCCAAACGG	GCAGGGCCTTAGAAACAGACT	(0,0)	1	TACACGCCTCACTGTTCTGC
Omy_RAD58213-70	A	T	TTTTTT[TA]AAAATATACT	TTTTTT[AT]TAAATATACT	CCTGATGGGTGCTCTTCTCTC	(0,0)	1	AAACAGCATCATTATCCATAGTGTT
Omy_RAD58835-15	G	T	ATAGCTGCTGGGACCCA	ATAGCTTCTGGGACCCA	GTCTGCTAAGGTCCTGCAGG	(0,0.2)	1	GCCGACCATGAGAGACCTG
Omy_RAD59758-41	T	C	TGATTGCTACTGAC	TGATTGCCACTGAC	GGCCCCCTTCTTTCAGGAAT	(0,0)	1	CACACACTCAACGGGTCAGT
Omy_RAD59950-44	G	A	GGAGGGGAAGGG	GAAGGGGAAGGG	GGAGCTCATATCGCCGATGG	(0,0)	1	GAACTCTGTCACCCTGCCC
Omy_RAD60135-12	C	G	GAACATACCGGAAC	GAACATAGCGGAAC	AGCATACACACCTGCAGGAA	(0,0)	1	TGGTAGGAGGAGATGCTCTGT
Omy_RAD619-59	T	C	TGCTGGATCCCCCA	TGCTGGACCCCCCA	CATGGAGAAACAGACCCGCT	(0,0)	1	TGCTGTGTGTGTATCTGGGG
Omy_RAD62596-38	A	T	TTAAAAAATATATATTA	TTAAAATATATATATTA	GCAGGACACTGGTTCCCAAA	(0.5,0)	1	CCTGAGATTTGAGATCACTGGCT
Omy_RAD65808-68	T	G	ATCGGGATTCACTT	ATCGGGAGTCACTT	TCCTTCACTCTCGATCGGGA	(0,0)	1	TCAAACTGGGCCACTACTGT
Omy_RAD65959-69	G	A	TTTTGTCGTTCCTT	TTTTGTCATTCCTT	ACATTTTGGTGTTAACAACCCTGT	(0,0)	1	GCTAGCGAAGACCCTGAAGG
Omy_RAD66402-36	T	C	AACCACTTCTCTG	AACCACCTCTCTG	GGTGTGATACCTCAGAGCTCTG	(0,1.7)	1	CGTCTCCGGATCGTTCAGAG
Omy_RAD66834-17	C	T	TCTGGCTGACACCTTTA	TCTGGTTGACACCTTTA	CTCCTGCAGGTCATCTCTGG	(0,0)	1	CTGTCTTGTGCTCAATGCCTG
Omy_RAD68634-40	A	C	CCTCTAAACTGAAT	CCTCTAACCTGAAT	TGCAGGACTCCTTTGAAACGT	(0,0)	1	TAACGCCAGCTGCATGATGA
Omy_RAD7016-31	C	A	ATAATTTCATTTAA	ATAATTTAATTTAA	GCAGGAATATTCACTGTTGCCA	(0,0)	1	TCTAAAATGTCGTTGGCGGC
Omy_RAD7210-8	C	A	TGCAGGACTTGCTTTGT	TGCAGGAATTGCTTTGT	ACACCACACTCCACAAAGCA	(0,0)	1	GCGCCTTGGTCTCCTTCATA
Omy_RAD72528-44	A	T	TTGGAACAAACTGT	TTGGAACTAACTGT	TGATGATCCGGACCCTCTCT	(0,0)	1	CCCGGATTCCCTCCACAGTT
Omy_RAD73204-63	G	C	GTGCCCGCTCTCCACCG	GTGCCCCCTCTCCACCG	CCTGGGCAATGACCTCCAC	(0,0)	1	AGCTCCCTTCTCTCTCCCTC
Omy_RAD7384-50	T	C	GCCTCTGGCAG	GCCTCCGGCAG	GACACGCCCTCAGCCAG	(0,0)	1	CTGGTACCTTCCTGCTGTGG
Omy_RAD739-59	C	G	GAGTTGGCTATTTT	GAGTTGGGTATTTT	ACGAGGCTTGTAAATGCAGT	(0,0)	1	TGCCTTTATACCAATGTCTGCTG
Omy_RAD73963-73	T	A	TTTCTTTTGGA	TTTCTATTGGA	CCCTCTCAGGAAAGTGACCAC	(0,0)	1	GGATCATGTCAATCTGATGAGTTGG
Omy_RAD76060-20	C	T	GGGCGCTGTAGGCAA	GGGTGCTGTAGGCAA	TGCAGGGTGTCAGTATTGGG	(0,0)	1	TCCCATGCAAATTCCAAATGCT
Omy_RAD76570-62	T	G	AGAGGTGTTCTGGT	AGAGGTGGTCTGGT	GCAGGTAGGTAGGAAGGAAAGC	(0,0)	1	TCTGACTGGTATTGAAAGGACCA
Omy_RAD77789-54	T	C	TAAATTATATTTGACAG	TAAATTACATTTGACAG	AGACAAAACCTGCAGGGGAC	(0,0)	1	AGCACGTTAAAACCAAACTGTCA
Omy_RAD78147-27	C	T	CAAAGTCCCAGAGA	CAAAGTCTCAGAGA	GCATTTTAGCCCTCCCAAAGTC	(0,2.6)	1	CCTTCTTCCAGTTGTTAAAACCCA
Omy_RAD78502-57	T	G	GGAAATATCACACA	GGAAATAGCACACA	GAGAGGCATCCTGTCTAGGG	(0,0)	1	ACCATGCTCTTTCTGTAGGTGT
Omy_RAD78776-10	T	C	GGGTAATCCTGGCT	GGGTAACCCTGGCT	CACAGCTTCCTGCAGGGTAA	(0,0)	1	GCTTGCATGGTCTCGCTAGT
Omy_RAD79314-58	C	T	AGACCTTGTC	AGACTTTGTC	CACACTGACTCATCCCTCGC	(0,0)	1	GAGTGTCTTACCGAGCTGCC
Omy_RAD79314-58-25	C	T	CTCGCCCTGCG	CTCGCCCTGTG	CACACTGACTCATCCCTCGC	(0,0)	4	
Omy_RAD79314-58-27	T	C	GTCACRCCTGC	GCCACRCCTGC	CACACTGACTCATCCCTCGC	(0,0)	4	
Omy_RAD79314-58-31	G	A	ACGCCTGCCCT	ACACCTGCCCT	CACACTGACTCATCCCTCGC	(0,0)	4	
Omy_RAD79314-58-66	C	A	CAGTGTCAACC	CAGTGTCAAAC	CACACTGACTCATCCCTCGC	(0,0)	4	
Omy_RAD85131-35	T	C	GATGGTATGGTGAG	GATGGTACGGTGAG	TTCAATAACTACAGGCAGATGGT	(0,0)	1	AGTTCCCAAATGCACTGTACA
Omy_RAD86706-72	C	T	TACGTTTCATTTCT	TACGTTTTATTTCT	TTCCCTGTAACTGTCACGCC	(0,0)	1	CCACATCACACCCTGACCTC
Omy_RAD88028-7	G	A	TGCAGGGGCTGG	TGCAGGAGCTGG	TAGCCCAGTTCGGTTCCAAC	(0,0)	1	AGTGTCTTTGGTGCGTCCTC
Omy_RAD88122-32	G	A	GCTGTGGAGATCAT[CT]CG	GCTGTGGAAATCAT[CT]CG	TCAGTGGATGGAGTGTCCCT	(0,0)	1	GGTCTTTGGCCTTGTTGCTG

Omy_RAD9004-13	G	A	TCATCTGAAGGGGG	TCATCTAAAGGGGG	TATACCACGCCTTCCCTGGA	(0,0)	1	CAGAGAGAAATCCCCCACCC
Omy_RAD92485-64	T	A	GTGTAGATATACAT	GTGTAGAAATACAT	CCAGTCAGTCTTGCCTCAGG	(0,0)	1	GGTCACCACAGGATTGGAGG
Omy_RAD93580-37	T	G	AGTCACCTGGGATT	AGTCACCGGGGATT	AGGCAGAGGAGGGTTGTTTG	(0,0)	1	TGCAGAAGTCAAATCACGAACA
Omy_RAD98715-53	T	G	CAGGACTTCTCCCC	CAGGACTGCTCCCC	CGTAACGGGGAGCTGATCTG	(0,1.9)	1	GCTGGTAAAATGCTGAGGGG
Omy_rapd-167	G	T	AAACAATCCCCCCCAAA	AAACAATCCCACCCAAA	CCCAACATGCTCTATTGCAGCTA	(0,0)	1	AGTTGCATAAGATGAATCAATAAATTAAAAACACAGAT
Omy_rbm4b-203	-	T	CACGTTATTATGAAAAGGATGT	ACGTTATTATGAAAAAGGATGT	CTGAAATTTGATGAATGGAAGCTGCA	(0,0)	1	CGTATTCAAGTCGATATACAGTCACGAT
Omy_redd1-410	C	T	AAAATATCCTGCAAGGAAT	AATATCCTGCAAGAAAT	GTACTCCCACTAACATACAGTAGACTCA	(0,0)	1	GGCACCATTGTGTTTTAGGATGTAG
Omy_sast-264	G	A	CTAGCCAATGCGTCTAA	ATCTAGCCAATGTGTCTAA	GAAGTAGGGTTTGTTGACCATGTGA	(0,0)	1	TGGATTCCATTTTAGGCTGTAATACATCTT
Omy_SECC22b-88	T	C	CTGTCTGTCCATATATC	CTGTCTGTCCGTATATC	GGATCCCTCCTTTTAACACAAGACT	(0,0)	1	CTACAGGATGACTACCTAATTGCTAATAAAACA
Omy_srp09-37	C	T	TTGTGCTATTGACGCCACAG	TTGTGCTATTGACACCACAG	TAGTTGTATTAACTCTTCTTTGAGTCTAGA	(0,0)	1	TCATTCCAGCTCCGTTCTCTTC
Omy_sSOD-1	T	G	CCACAACAAGACCC	CCACAACCAGACCC	GCCGGACCCCACTTCAA	(0,0)	1	CAGACTAACCGAACAGCATCAGTGG
Omy_star-206	A	G	TCTTTGGCACTATATCT	TTTGGCACCATATCT	CGTGTGCCAGCCCTTCT	(0,0)	1	GACCACTGAGATCATTGCTGTGA
Omy_stat3-273	G	-	CCAGTTTG	TCAGTTTG	CAGACCTCCTCTATCTCCCTATGAG	(0,0)	1	ACCTCCTTTAAATTGTGCCCAAGAA
Omy_sys1-188	C	A	AAACATGTACGACCTGTC	TGTAAACATGTACTACCTGTC	CTTAAATGGTGCTGGTTGCTGTATT	(0,0)	1	AGTGATATCTTAGTGGGTCGAGGAAA
Omy_tlr3-377	C	T	CGTGATTAGGTTCTTC	CGTGATTAGATTCTTC	GTCGCTCCGGGTGCTT	(0,0)	1	GGCCCAAACACTTCCTTCCT
Omy_tlr5-205	T	A	CAGTAATATTTCAGTGCCCG	CAGTAATATTTCTGTGCCCG	GAGCGTATCTGGTATGGTAACAACA	(0,0)	1	CTCCAGCAGCTTTAGAGAGTTTACA
Omy_txnip-343	T	C	AACTGAAGAGATCTG	AACTGAAGGGATCTG	CCTTCAAACTAACGCATCATAGACATG	(0,0)	1	GGTCACTTGGCTAATCCCCTTAT
Omy_u07-79-166	G	T	ACTTGGGAATACCCCAGCC	CTTGGGAATAACCCAGCC	CCCGCTATATTATTTGATCACCCTTGA	(0,0)	1	ATTTAAATCCATTTCTAAAAATAAGCAAACCTAACCA
Omy_u09-53.469	T	C	TTGCAGCCCTTATTGTG	TTGCAGCCCTTGTTGTG	ACAGCCTGAGCGTTTGCA	(0,0)	1	GGAAACTGGGAGAGATCAAAGGA
Omy_u09-54-311	C	T	TGGTAATTATTCAACAGATCAGT	TGGTAATTATTCAACAAATCAGT	GTGGCTCCCCAGGAACAAG	(0,0)	1	AAGTTTCATGTCACATTCCAGTTACCT
Omy_u09-56.119	T	C	AGTGAGCTGAAACAGAGCA	TGAGCTGAAGCAGAGCA	CCAAGGTGGACCCACCAG	(0,0)	1	GCTGAGTTTATAGGTCAGTCATTATACATATTGA
Omy_u09-61.043	A	T	CACTTGGTCCTTTTTCA	CTTGGTCCATTTTCA	TAGTCACATCCATAGTAATACTTCC	(0,0.4)	1	TGTTCAGAAGCAGAAAACCAATCTCT
Omy_U11_2b-154	T	C	AATGATACTTTTCAGATTGTAAC	TGATACTTTTCAGGTTGTAAC	GGGAAGCAGAAAAACTGGAAGTT	(0,0)	1	CCCTCTGTGGGCTTGATATTCA
Omy_UBA3b	A	T	TGGAGATAACGCTAACTATT	AGATAACGCAAACTATT	GCCACTCAATGCATGTGTTTTCTAG	(0,0)	1	CAGCTAGCTTAAGTGGGATGCAA
Omy_UT16_2-173	C	T	ACAGTCAACAAGGGACTTAA	ACAGTCAATAAGGGACTTAA	ATTGACTCATTATCACCTTAGTTGTAGCTTCA	(0,0)	1	GCAGCTACTTGCTGTATCACATGTTTGT
Omy_vamp5-303	A	-	TGGCCGTAGTAGTTGGTCA	TGGCCGTAGTTGGTCA	CTGCTTCCCAATTCAGTATCGTCTT	(0,0)	1	AGGCTGAAGCATTTCTGAGTATGAA
Omy_vatf-406	T	C	ATGACTATCCACA	ATGACTGTCCACA	TTGCTTCATTTTGTCATAACCTTGGG	(0,0)	1	TGCATGCTCTGACAAATGTTACACT
Omy_VGLL3-1_AT	A	T	ATAGTAATGGC	ATTGTAATGGC	GGTGTCCAGACTAGACGAA	(0,0)	1	CGTGCGTAAAAGCGCCAAT
Omy_VGLL3-1_GT	G	T	TGTGTTCGAAT	TGTGTTCTAAT	GGTGTCCAGACTAGACGAA	(0,0)	2	CGTGCGTAAAAGCGCCAAT
Omy_VGLL3-6_AT	A	T	ATATTATTGTTCAA	ATATTTTTGTTCAA	TGAAATTGTTGCATGTTGCGT	(0,0)	1	TGTAGGTCAGCCTTGAACTTT
Omy_VGLL3-6_CT	C	T	TACACACCAATA	TACACATCAATA	AGATGTAGGGCATGATTGCCA	(0,0)	1	GCCTAGTGTTCTGTATGTGTGGA
Omy_zg57-91	C	A	CACAGACTGCACAGCC	CCACAGACTTCACAGCC	CACTCATACACTCACTCACAAAGGA	(0,0)	1	AGCAGATAAGCCTTGTGAGTGAATCTT
OMY1011SNP	C	A	CTTTACCTCGAAGACAAT	ACTTTACCTCTAAGACAAT	AGGCTGGTTTGGGATTCACTG	(0,0.6)	1	CGCCAAACACTAACTCTCTGTCT
Omy25_61284413	A	C	CATTAGAAACA	CATTAGAACCA	CAGTGCTGGCGTCATTAGAA	(0,0)	1	TGTTTTGGTTTATGGGCTGA
Omy25_61285646	C	A	AGAATGTCTATT	AGAATGTATATT	TTGACACTGGTCCTGAGAATG	(0,0)	1	AAGCAGAGGGGTGCACTG
Omy25_61286316	T	G	ATGCTAACCTT	ATGCTAACCTG	GGCCTCCTGAAGAGGAAAAA	(0,0)	1	AGGGACTTGTGCCCAGATTA
Omy25_61287415	T	C	TACCCATTCCTG	TACCCATTCCCG	TGTCTGGTGATGTTGCTCCT	(0,0)	1	ACCTGACGTGGCCTTCTGTA
Omy25_61294400	A	G	GCTGGTCAGCACATGCTTTGA	GCTGGTCAGCGCATGCTTTGA	GACAGATTATCTTGGCGTTTTG	(0,0)	1	AAACGGATTACCAGGACACG
Omy25_61316270	G	T	AGGCCCTATAGTT	AGTCCCTATAGTT	ATCGACTGTGCCCTATCTGG	(0,0)	1	ATCAATGGGTTCCTTTCGTT
Omy25_61317685	A	G	TCTGCATTAACCAC	TCTGCATTAGCCAC	TGGGCTAGATTTTCAGTCTGC	(0,0)	1	ATGCATCCTCTTGAATGGTG
Omy25_61317777	A	G	AATTTAAAAAACGGTATGCTT	AATTTAAAAAGCGGTATGCTT	TTCGTTCTCTGTTGTTTTTATTCG	(0,0)	1	CAAGCAGCAGGCATGACA
Omy25_61318852	A	G	AAAAAAAGGGAGCTCG	AAAAAGAGGGAGCTCG	TACGCGAATGGTACTTGCAG	(0,0)	1	TTTCCGACTTGTGTGGGAGT
Omy25_61322413	C	G	CTAGGGGACACA	CTAGGGGACAGA	ATCAGGGCAACTAGGGGACA	(0,0)	1	CCGCATCATTAGTGCTGATT
Omy28_11607954	G	A	TGTGGGCTGCGAACATACTCA	TGTGGGCTGCAAACATACTCA	TGACACTGATCACAATGGTGAAAT	(0,0)	1	TAAACTGGAAGGAGAGAGCAAAAT
Omy28_11625241	A	G	CCTCCTCCCTATGGTTGTCTC	CCTCCTCCCTGTGGTTGTCTC	CAACATTTAGGGAGAGGTTGCTAT	(0,0)	1	ATCATCAAGTTTGCCTACGACAC
Omy28_11632591	G	A	TGAGAAGAACACAGAGG	TGAGAAAAACACAGAGG	GTAGAGGCCAAAGGCTTGAG	(0,0)	1	TGCTCTTATTACCTTCCAGACTCC
Omy28_11658853	A	C	TGGTACAGACACGCACTAGCA	TGGTACAGACCCGCACTAGCA	CAACATATGACCACTCGAAAACTC	(0,0)	1	ATTAATCACACCGTGAGACTCCTC
Omy28_11667578	T	C	GTATTGATCCTGTGGGAGACA	GTATTGATCCCGTGGGAGACA	ACAGTAAACCCATTCAGGCATAGT	(0,0)	1	TTATCCTCTCAATCCACATCAAGA
Omy28_11671116	C	T	CTGGTGAGAACAGGAATTACC	CTGGTGAGAATAGGAATTACC	AATTTCCCCAAATTTGAAACTCTT	(0,0)	1	GTGTACATTGTCAGGCAGAAACAT
Omy28_11676622	T	G	ACATGTCATTTATTGTTATCT	ACATGTCATTGATTGTTATCT	CGAATGCACTGTAGCTCATTCTAA	(0,0)	1	GCAGTAGAATGTCTCGCAAATACA
Omy28_11683204	G	T	ATGTAAAAAAGGGCAGAAAA	ATGTAAAAAATGGCAGAAAA	CAAGAAAGAAACAGATGTTGTCCA	(0,0)	1	TTGTGACTCAAATCTGCAACCTAT
Omy28_11773194	A	T	GCAATTTTTTAAAATTACCGC	GCAATTTTTTTAAATTACCGC	AGTTTGACACCCCTGTACTAGAGC	(0,0)	1	GTCTAACAAGCTCTGGGTGATTTA
Omy4_8260712	G	C	GAGGTACCATGATCAACCAAT	GAGGTACCATCATCAACCAAT	AGATCCCGAATTTCCCACTT	(0,0)	1	GAAACCTGGCGCCTTAAATTAG
Omy4_8261223	A	G	ATATATGGTCCA	ATGTATGGTCCA	CACATGGGATGTTGGTTAATGT	(0,0)	1	GTTTGCATACGCCTATTCATGG
Omy4_8269484	A	C	CAATGTAT	CCATGTAT	GCCCAACTCCCTATTAAAGGTC	(0,0)	1	AAGGTACTTCATTCTTACCCAGAAA
Omy4_8272302	T	C	ATGTTGAAAGTCACTGA	ATGTTGAAAGCCACTGA	GTTGGAAAAGTGGCATCCTATT	(0,0)	1	AACATTGGCCTTACTGAAGAGC
Omy4_8325040	G	A	CTGCAGCTACGGAATGCTTAC	CTGCAGCTACAGAATGCTTAC	AGCCAAGTTTGGCGATTTACT	(0,0)	1	TGGATCAGCCAATGAATTACAC
Omy4_8327140	G	A	TCATCTAGTCGGTGCAGG	TCATCTAGTCAGTGCAGG	ATTGGAGTTAAATGCCTTGCTC	(0,0)	1	CAAAAGGTTGCTGGTTCAAATC
Omy4_8343709	C	A	GGTGAATTAATCACC	GGTGAATTAATAACC	TTTGGCATTGTGTTTTAGGGTA	(0,0)	1	AGTCTGCTTTCCACCAGACACT
Omy4_8345868	A	C	ATTGTTTAAATGTCTAAC	ATTGTTTCAATGTCTAAC	TCAAACTATTCCTTTGGCTACAA	(0,0)	1	AAGCATTTTCCATAAAGAAGTCTG
OmyR14589Pearse	T	A	ATCCCTGTTATCTAATCATT	ATCCCTGTAATCTAATCATT	GTAACCATGACATCCACCAATC	(0,0)	1	CCTATGCACAAAGCCTTCAC

OmyR19198Pearse	G	A	ATTTAGCAGGAGGCCTCTCCA	ATTTAGCAGAAGGCCTCTCCA	TCATTACCTACGCAGTGGAG	(0,0)	1	ATCTCTGGGCCTGAACAAT
OmyR24370Pearse	G	A	TAAGACTTGGCATAAGCATG	TAAGACTTAGCATAAGCATG	CAGGAGTAATGCATCCCAATG	(0,0)	1	CAAGTTGATAACGAGACATAAGGG
OmyR33562Pearse	A	G	GTGGTTACAAAGGGTCTGCA	GTGGTTACAAGGGGTCTGCA	GGTGACTGAGCTGGATGT	(0,0)	1	TTTAGAGAATTTGGCAGTACGTC
OmyR40252Pearse	T	A	AATGCTATATTGAACCTTAA	AATGCTAAATTGAACCTTAA	ACTCTGAATTCCTCAGGCTT	(0,0)	1	TCGAACCAGCTGTCTTTCT
OmyR40319Pearse	C	T	TGCAAGTGC[TA]GCCCTTTTAT	TGCAAGTGC[TA]GCCTTTTTAT	AAAGATTGCTGCGATGTCTAAT	(0,0)	1	CGCAGAGAACAGAGGATGA
One_1a.54542-52-44	C	T	GCCTTGTGCTT	GCCTTGTGTTT	GCAGGTTGTGATCGTGACCA	(0,0)	3	TGAAGAGACTACGCCCCCTT
One_1a.54542-52-47	G	C	TTGACCAGAAG	TTCACCAGAAG	GCAGGTTGTGATCGTGACCA	(0,0)	4	
One_2.70711-39-28	G	T	AGGYGCTYGTRC	ATGYGCTYGTRC	TGCCCTGTTGTGATGAGCAT	(0,0)	3	GGCTGTGTAGAACGACCCC
One_2.70711-39-30	T	C	GTGCTYGTRCG	GCGCTYGTRCG	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-43	G	A	CGTCCGCGGGC	CGTCCACGGGC	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-56	C	G	GGCTAAGGATC	GGCTAAGGATG	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-57	G	A	GCTAAGGATSG	GCTAAGGATSA	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-64	T	G	TTCCCTAGGGG	TTCCCGAGGGG	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
Ots_ARNT-29	A	G	GTGCTAGCTAC	GTGCTGGCTAC	CCACTGGCTGTGGAGCTT	(0,0)	3	GGGTTCAGTGATAGTTGGGCAAAT
Ots_ARNT-29c	A	C	GTGCTAGCTAC	GTGCTCGCTAC	CCACTGGCTGTGGAGCTT	(0,0)	4	
Ots_crRAD9615-69-19	T	A	GGGAGTGGGAG	GGGAGAGGGAG	GAATGCAGGGCCAGGGAG	(0,0)	3	ACTCCCAGACCATCCAGCT
Ots_crRAD9615-69-50	A	T	CTGGGAGGAGA	CTGGGTGGAGA	GAATGCAGGGCCAGGGAG	(0,0)	4	
Ots_myo1a-384-36	C	T	CACCACTACCA	CACCATTACCA	CTCCCCCCTGGACTTTGG	(0,0)	3	GCTCTATTGCACCGTGTTCTG
Ots_myo1a-384-57	C	T	CTGCAGAACAC	CTGCAGAATAC	CTCCCCCCTGGACTTTGG	(0,0)	4	
Ots_P53-25	G	T	TTCTGCAGGGG	TTCTGCAGTGG	GGAACTTCCTCTCCCGTTCTG	(0,0)	3	GCACACACACGCACCTCAA
Ots_P53-28	G	C	GGGCAGCTCCT	GGCCAGCTCCT	GGAACTTCCTCTCCCGTTCTG	(0,0)	4	
Ots_P53-40	T	C	CTCCTGGGTCG	CTCCTGGGCCG	GGAACTTCCTCTCCCGTTCTG	(0,0)	4	
Ots_unk9480-51-38	T	C	TCCCASAAACT	TCCCASAAACC	CAAATCAGAACAAAACCTCCCACAA	(0,0)	3	GGAAGTCTGTCTGAATGGTTGTCTT
Ots_unk9480-51-39	C	A	CTAAGGAGACC	ATAAGGAGACC	CAAATCAGAACAAAACCTCCCACAA	(0,0)	4	

Appendix 7. GT-seq SNP panel for Chinook salmon.

Assay	A1	A2	A1-Probe	A2-Probe	FWD Primer	Corr	Flag	Rev Primer
Ots_SEXY3-1	X	Y	NA	TCAGCGAAGTGGAGAT	GGTCTTGCAGTCAGGAGAGG	NA	0	CCAGGTGGTGAAGGTAGGAA
Oki_101419-103-27	A	C	AATCCACTTCC	AATCCCCTTCC	CCCAATTGGAGACCAGGGTT	(0,0)	3	TCATTCAGACAGTTGGGAGACA
Oki_101419-103-44	T	C	GTTCTCCTACT	GTTCTCCCACT	CCCAATTGGAGACCAGGGTT	(0,0)	4	
Oki_105105-245-23	T	G	GCCTTTTCCAT	GCCTTGTCCAT	GCGTATCAAGCATCAACGCC	(0,0)	3	TCTTTCAGCAAGGTTGGGCA
Oki_105105-245-56	G	A	CTCATGCCCAA	CTCATACCCAA	GCGTATCAAGCATCAACGCC	(0,0)	4	
Oki_106172-60-38	C	T	GTGCGCATCAA	GTGCGTATCAA	ACTACTTGGCGTGTGTGTGGG	(0,0)	3	TCCACTGAGAGGATGAGGCA
Oki_106172-60-47	G	A	AACGCGCTGAC	AACGCACTGAC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_106172-60-47c	A	C	AACGCACTGAC	AACGCCCTGAC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_106172-60-53	C	T	CTGACCGCYGC	CTGACTGCYGC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_111681-407-38	C	T	AGAAACTGCAA	AGAAACTGTAA	TTCATCCCATTGGAAGCCCC	(0,0)	3	ACAGCCTATATCTGTGCGCT
Oki_120255mod-105	C	T	AACGTCAGTTA	AACGTTAGTTA	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-99	A	C	GACTAAAACGT	GACTACAACGT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	3	CATTGAAGGGTGGAATTGAAG
Oki_120255mod-113	G	A	AGTTACTGG	AGTTACTAG	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-115	G	T	TTACTRGGGTA	TTACTRGTGTA	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-119	G	A	GTAGYTTCWTG	GTAAYTTCWTG	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-120	C	T	CTTCWTGGCAT	TTTCWTGGCAT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-133	T	C	TGGCATAGTC	TGGCATAGCC	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-135	A	C	GGCATAGYCAT	GGCATAGYCCT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-137	A	T	ATAGYCMTAGAT	ATAGYCMTTGAT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-141	A	G	ATAGYCMTWGATA	ATAGYCMTWGATG	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_126619-265-31	A	C	GGATTGKGCAC	GGATTGKGCCC	TGCGTAGTTAATTTTCACCTCGG	(0,0)	3	TACGCAGCACTGAAGACTGG
Oki_126619-265-35	A	G	CAGCACAGCTG	CGGCACAGCTG	TGCGTAGTTAATTTTCACCTCGG	(0,0)	4	
Oki_126619-265-50	G	T	GATTCGCCAGT	GATTCTCCAGT	TGCGTAGTTAATTTTCACCTCGG	(0,0)	4	
Oki_aspAT-273-37	C	T	CTGGACACAAT	CTGGATACAAT	ATGCTGGGAGAAACAGTGGG	(0,0)	3	CTCCTCTGTAAGGGGTGGGT
Oki_aspAT-273-45	T	A	AATCCTTAACA	AATCCATAACA	ATGCTGGGAGAAACAGTGGG	(0,0)	4	
Oki_RAD41030-31-36	C	T	GAAGGYCRGGG	GAAGGYTRGGG	GCTGAGCCTGGTCTGGG	(0,0)	3	TGGATACCCCAACTCCTCCA
Oki_RAD41030-31-37	G	A	GGGGSTCTGTG	AGGGSTCTGTG	GCTGAGCCTGGTCTGGG	(0,0)	4	
Oki_RAD41030-31-41	G	C	GGGGTCTGTGG	GGGCTCTGTGG	GCTGAGCCTGGTCTGGG	(0,0)	4	
Oki_RAD41030-31-55	G	T	AGCTCGGGCTG	AGCTCTGGCTG	GCTGAGCCTGGTCTGGG	(0,0)	4	
Oki_RAD51585-47-25	C	G	GTGGCTCACTT	GTGGCTCAGTT	ACTTTCTAGTAGGCGTGTGGC	(0,0)	3	CAAAACCCTGGCGTTGCAAG
Oki_RAD51585-47-28	G	A	TCACTTGGTAGAGC	TCACTTAGTAGAGC	ACTTTCTAGTAGGCGTGTGGC	(0,0)	4	
Oki_RAD51585-47-31	A	C	TTKGTAGAGCA	TTKGTCGAGCA	ACTTTCTAGTAGGCGTGTGGC	(0,0)	4	
Omy_myclarp404-111	T	G	CAAAGCCATACGTGGCC	AAGCCATCCGTGGCC	GCTGTGGTGCTCATGGGTAAA	(0,0)	3	CCAGGGCAGGGTTGTTCTC
Omy_RAD13034-67-21	C	T	CTCCCCGAACC	CTCCCTGAACC	GAGTGATTCCCAGCCCTCC	(0,0)	3	TCTCTCCGTTGGCCAGAAAC
Omy_RAD13034-67-35	A	T	CTGAGTGGACA	CTGTGTGGACA	GAGTGATTCCCAGCCCTCC	(0,0)	4	
Omy_RAD79314-58-25	C	T	CTCGCCCTGCG	CTCGCCCTGTG	CACACTGACTCATCCCTCGC	(0,0)	3	GAGTGTCTTACCGAGCTGCC
Omy_RAD79314-58-27	T	C	GTCACRCCTGC	GCCACRCCTGC	CACACTGACTCATCCCTCGC	(0,0)	4	
Omy_RAD79314-58-31	G	A	ACGCCTGCCCT	ACACCTGCCCT	CACACTGACTCATCCCTCGC	(0,0)	4	
Omy_RAD79314-58-66	C	A	CAGTGTCAACC	CAGTGTCAAAC	CACACTGACTCATCCCTCGC	(0,0)	4	
One_1a.54542-52-44	C	T	GCCTTGTGCTT	GCCTTGTGTTT	GCAGGTTGTGATCGTGACCA	(0,0)	3	TGAAGAGACTACGCCCCCTT
One_1a.54542-52-47	G	C	TTGACCAGAAG	TTCACCAGAAG	GCAGGTTGTGATCGTGACCA	(0,0)	4	
One_2.70711-39-28	G	T	AGGYGCTYGTRC	ATGYGCTYGTRC	TGCCCTGTTGTGATGAGCAT	(0,0)	3	GGCTGTGTAGAACGACCCC
One_2.70711-39-30	T	C	GTGCTYGTRCG	GCGCTYGTRCG	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-43	G	A	CGTCCGCGGGC	CGTCCACGGGC	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-56	C	G	GGCTAAGGATC	GGCTAAGGATG	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-57	G	A	GCTAAGGATSG	GCTAAGGATSA	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-64	T	G	TTCCCTAGGGG	TTCCCGAGGGG	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
Ots_100884-287	T	C	ATAGAACTACAATTCACATATAT	AACTACAATTCGCATATAT	CGGAAGACCAGATTCTCCAAGAGTA	(0,0)	1	CGACCAAGTAGCGGCACTT
Ots_101119-381	T	C	TGCCACATGATAATTGA	CCACATGGTAATTGA	TTTTCTAGGACAGGTTGCTTGCA	(0,0)	1	CCAGGTTTCTTTAGCCTACTTATTCTTTACA
Ots_101554-407	C	G	ATGGAGGATTGTGGTTGT	ATGGAGGATTCTGGTTGT	TGAAAGATATCAATTGTAGTAGTGGTGGTG	(0,0)	1	ACACGCCAGTCCACAAGT
Ots_101704-143	T	G	CTTAGACGTCAGAGGTC	CTTAGACGTCCGAGGTC	ACTTCTTGAGCCAATCGGATGATG	(0,0)	1	CCAGAGATAAACTAGTGGAGGAGATCA
Ots_102213-210	A	G	CTGTATACAGTAAGAGTATTAAT	ACAGTAAGAGCATTAAT	CATTCCATGACAATGATTGAAATCTAAAAACAC	(0,0)	1	GAGTATCTCAATTGCAACACTATGGTATGT
Ots_102414-395	A	G	CACATAGTGTAGCTTTACTAC	CACATAGTGTAGCTCTACTAC	GCCTACTGATAAATGTATGACAGTAATGGA	(0,0)	1	CAATAACAAACAAGCTAGGAACAAAAGTGT
Ots_102457-132	A	G	TGGGGCAACGCACAATTGGCT	TGGGGCGACGCACAATTGGCT	CCAGCAGAGACTGGGTTCAC	(0,0)	1	TTCCCTACCGGCGAAACC
Ots_102801-308	C	A	AGGGACAGTTTCGCAGACG	AAGGGACAGTTTCTCAGACG	TGGGACAGAGGTGGGAATTGA	(0,0)	1	CCCAAAGATGCTTAACTGAAGATGTG
Ots_102867-609	A	G	ACAGAGAGAAGTCCCAGGTG	AGAGAGAAGCCCCAGGTG	CTCTGCCATTCATTTGGGCTTTG	(0,0)	1	GTCTAAAGTGGTCCCCTTGGAT

Ots_103041-52	G	A	CATCCTGCTGGACCC	CATCCTGTTGGACCC	ACCACCCACCTCCTCAGA	(0,0)	1	AGACAGAGAAAGTCGGGACACT
Ots_103122-180	T	C	CATCAACACAATCTGC	CATCAACACGATCTGC	CAAACGCGCACTCACACACA	(0,0)	1	TCACAATGGTACGATTTTACGACTCAA
Ots_104063-132	C	T	CTTTCGTCCTTAGCACATAG	CTTTCGTCCTTAACACATAG	GCGTTACTGGTGTTATAAACGTTAGC	(0.5,0)	1	GTTTATTTAATTATGAAGGACGATGTTGAAGTCA
Ots_104415-88	C	T	TCCTGAAAAACGACATCC	CTGAAAAACAACATCC	CCTGAGCATCCCAGTTGAACT	(0,0)	1	TGTTTTCAATACACTGCAATTTAGTTTTGGT
Ots_105105-613	C	G	CCGAGCTTGAGTTAGGA	CCGAGCTTGACTTAGGA	AGTACAAGTGCAGAGAATGACATCATG	(0,0)	1	GGTGTTTTATTTTCCCATATATCTTTTAACTTTAAGCT
Ots_105132-200	G	T	CAAGAGTGGCATAAAA	CAAGAGTGGAATAAAA	CGATGTACTGAGGGCAGTGT	(0,0)	1	GAGTGGAGTTCCTTAATAATCATTGACCTT
Ots_105385-421	A	G	CCTCCTGGGTATATCG	CTCCTGGGCATATCG	GACTGTCTTGGAACCGTTGCTA	(0,0)	1	TCCCGGAACACACCAATGTC
Ots_105401-325	G	T	CCCGGACAAGATGAGACAG	CCCGGACAAGATGAGACCG	GAACTGAGCGGCTGCTG	(0,0)	1	CGCCTCCTGGTGTCTATCCT
Ots_105407-117	T	A	CAGGTTAGGAATGGTTG	CAGGTTAGGATTGGTTG	TGTGTACATCCGCGTAAATATTGAAGATAA	(0,0.2)	1	CTGTGAGCTGCTGCAAACC
Ots_106313-729	A	G	AAGAGTCCAGCGTTACTT	AAGAGTCCAGTGTTACTT	TTGTTCAATGGGCATTAATGCATGTT	(0,0)	1	TGCTTATGTGCAGATACTTGAGACAAA
Ots_106419b-618	G	T	CAATGATTAATGATTAATCCTTC	TGATTAATGATTCATCCTTC	CAAGGGCACATTGGCAGATTTT	(0,0)	1	ACCGGACCAAAGCACACA
Ots_106499-70	C	G	CATTTTTCAGAATTGTATTC	CATTTTTCAGAATTCTATTC	ACTCTATCATCGGCAGGACCAT	(0,0)	1	ACCGTAAGTGTGGTTGTGTTCATTA
Ots_106747-239	C	A	CCCGCGGTGAGTAT	CCCGCTGTGAGTAT	ATCGAGGATGCCTCAAAGACATC	(0,0)	1	GTTAGACCCACCACCAGTCATC
Ots_107074-284	A	T	ACCGTAGCTGCACCTG	CGTAGCAGCACCTG	CCCACTTCCAGAGCCTGAA	(0,0)	1	TTTTCCATGGCTGTGTGTACTGT
Ots_107285-93	T	A	AAGTAACGTATCAAATGGC	AAAGTAACGTATCATATGGC	GCCCTTGTGACAATGCACTGTTATA	(0,0)	1	AACATACACCAATACTTAGGTCTAGACAGT
Ots_107607-315	A	C	ATGGGAGACAGATAACT	ATGGGAGACATATAACT	GTGATGAGAGGTTTCCGGAAAATCT	(0,0)	1	GTGTTCTGGATTCCATTGTGCAAA
Ots_107806-821	T	A	CAAAGAAAATCAAAATTT	CAAAGAAAATCTAAATTT	TGCAGTGCTGAATTAGAGATTAATTTTTGTG	(0,0)	1	CTCCCTTGCTTTTGGTCATTGG
Ots_108007-208	A	T	CAGTTTCACTTAATTTTAAAATG	TTTCACTTAATTTAAAAATG	CAGGCTTGTGTTAAGTAGGGAGAAA	(0,0)	1	CATTGGACAAGACCGGGTAGTC
Ots_108390-329	G	C	CTACTTATGTAGCATTTTAA	CTACTTATGTAGGATTTTAA	GAGGTTTGTTACTGTCACCCATAGA	(0,0)	1	CCTGCTGTAGCAAACTGTCTCAAA
Ots_108735-302	C	T	AAACAAACAACGCCTCATG	AACAAACAACACCTCATG	CCTTTTTCTTATTAGTTTTACTTCCCCAGAGA	(0,0)	1	CAATTCCATTCTTGATTCTGTTTAACGGT
Ots_108820-336	G	A	ATTGCCCATCTCAGAATA	AATTGCCCATCTTAGAATA	TGAAATAAATTGTTCTGTTGATATGTGAATTTTGGA	(0,0)	1	CAACGACACACCAACAACGT
Ots_109525-816	C	T	CATGAGGCGTTCGGC	ATGAGGCATTCGGC	GCCAGATAGTAGCGTACATCATGAG	(0,0)	1	CTCCCCATGTCCCTGAGTCT
Ots_109693-392	T	G	TCCGTTAGTTCATCCTGG	TCCGTTAGTTCCTCCTGG	TCTCCCTCATTCCCATGTCATATCA	(0,0)	1	GGGAACGTATCAGGTGAGTGT
Ots_110064-383	C	T	CTACGTAATGAACGTTAGCT	ACGTAATGAACATTAGCT	AACAAAGAATGTTAAACACCAAACAGGAA	(0,0)	1	GTGCAAGGGACCTAGCTAATCC
Ots_110201-363	A	T	TTTTAAAA+CTGGCATCCA	TTTTTAAACTGGCATCCA	GTTTGGCTATTGAAATTATACATTAAAACATGTAGCT	(0,0)	1	CCATGGCATCCTGTAAAGAACAACA
Ots_110381-164	A	G	ATTTGCGTCTTCTCCC	TTGCGTCCTCTCCC	CTCTTGTTTGCTATGGGAGATGTAGT	(0,0)	1	CCGTATCCTAAACCCTTCACTGTT
Ots_110495-380	G	C	CATAGAC[AG]GGGGCCAT	CATACAC[AG]GGGGCCAT	GCCTAGGTATGTACGAAACTTCACA	(1.9,0)	1	AGGCTTTTTCAGATGGTCGTATGA
Ots_110551-64	C	A	ACGCTCGGAACATT	ACGCTCTGAACATT	GAGTGGTCAAGGTTTCAGTTTCTG	(0,0)	1	GAAATGGACAGACACAAGGTCAAAC
Ots_110689-218	T	G	CACCAATCAATTAATTATT	ACCAATCAATTCATTATT	GTATAAACTAGAGTCCAGTGTTATGTTAATGTCTT	(0,0)	1	CATGGCAGACAACAGTAGAGAATATGA
Ots_111084b-619	C	A	TCCATGG[AT]AACGGACAAT	TCCATGG[AT]AACTGACAAT	TTGTGGAATTACACCTTCAGAGTTCAAT	(0,0)	1	GCCTGTTTGGCTTTCTTAAACTGAT
Ots_111681-657	G	T	TAGCGCAAACCCCGAACC	CGCAAACACCGAACC	CTGAGCTTTTTCAACTTACTTGTTGGA	(0,0)	1	GGCGCAGCAGCAACTG
Ots_112208-722	C	A	TGTGAGGGCGGTCTT	ATGTGAGGTCGGTCTT	CTGCATGAACGTTAACTCAAATAAAAGGT	(0,0)	1	AATGAGTTCTACTGACATTGTATACTAGAATAAGTATCA
Ots_112301-43	T	C	CGTCGCATTCAGC	CGTCGCGTTCAGC	GCATGGCTGCCCTAGAACA	(0,0)	1	TCAGAACATTTCCTTCAGCTTCGT
Ots_112419-131	A	T	AAGCGACTTGATTATC	AGCGACATGATTATC	GTGGGTAATCGATGCCAAAGAGAT	(0,0)	1	TGGCAGTGTTTTCAACTAGCTTTG
Ots_112820-284	C	T	ACTCACACTCGAGTGACT	ACTCACACTCAAGTGACT	CATAGATGTTTATATGAAAAACCTCCCACTGT	(0,0)	1	GCATCCAAAAAGACGTGTGTGTTT
Ots_112876-371	C	A	CATCACAACGATGTGTG	CACATCACAACTATGTGTG	GCCTACAGCAAATTCAGCTACACAT	(0,0)	1	TGGACCTTCAATCATCACAGCTT
Ots_113242-216	C	T	ATTACCAACGGAGAACC	TTACCAACAGAGAACC	GAGGCCTAATGTCTCTTGTGACT	(0,0)	1	GACATCTTCAACAAGTGTTCATTCACC
Ots_113457-40R	C	T	CCCT[AG]TTCTCCAATCCATAT	CCCT[AG]TTCTCTAATCCATATG	CCCAAGTGGTGAGTGTCAGT	(0,0)	1	ACTACAACAGGTGTTGATAATAGAATCATTCTC
Ots_115987-325	T	G	ATGCATAAAAGGTAATTGTG	ATGCATAAAAGGTCATTGTG	GGAGGTGTAGTGAAATGGGAAGAT	(0,0)	1	GCATTCAGTGAACCAGTAGTGCTAT
Ots_117242-136	A	G	CAGCACATAACTTGACCTC	AGCACATAACCTGACCTC	GTGACAGGAGACAGAAAGAGACATT	(0,0)	1	TGGTCCTCCCTGTCTCTATCTACTA
Ots_117259-271	T	G	CTCTCCTGATCACTCTGT	CTCTCCTGATCCCTCTGT	ACACCCACTTCAACCTCCATAAC	(0,0)	1	GCCTCAGAGCTTAGCTTGGA
Ots_117370-471	G	T	ACGGAACAAATAAGACATTT	CGGAACAAATAAGCCATTT	GTTGGCTCCTTCAATTCAATTTGGA	(0,0)	1	TGCAAACACAGAGGAAAGGGATTT
Ots_117432-409	A	G	TTTAGACTTTGCTCTATAACAG	ACTTTGCTCCATAACAG	TCATCAAAACATGCCTCTTCTGTGT	(0,0)	1	TGTTGAACCTGTCACTCTGTCTTC
Ots_118175-479	C	T	AGAATGAAGTGAAAAGAA	AGAATGAAGTAAAAAGAA	TGCGCGTCTCATTCAACCAT	(0,0)	1	ACCTTACGTCCTAGGTAGGAAACA
Ots_118205-61	T	C	TAGTAGCCCCTACACCTC	TAGCCCCTGCACCTC	CCATACAGCCAGTCCAGGTG	(0,0.4)	1	ACTGGACAGGGCTGGGT
Ots_118938-325	C	T	AGAGATGCAAAGTGGAGTT	AGAGATGCAAAATGGAGTT	ATTTTCAAACAGGCATTTATCATTGGTGAA	(0,0)	1	GGTCTGTCCCTCATTCTTTGCA
Ots_120950-417	A	T	CTGGACCAGAACTCTGA	CTGGACCAGATCTCTGA	CAGACAGGTCACCATCACACT	(0,0)	1	TGGTGAAGCTGTAGGAGAAGGA
Ots_122414-56	C	T	TGTATGACCTCTGACCTGT	TGTATGACCTCTAACCTGT	GCACCGTATCAACGAGCTCAT	(0,0)	1	TGCATGGATTTCCTTTGTGTTGTTG
Ots_123048-521	A	C	TCACATCCAACTCAGTACT	CATCCAACGCAGTACT	CTCAACAGTGCACCTCCCTTAATT	(0,0)	1	CCAAACACACCCTTCCATAATCTCT
Ots_123921-111	A	G	TGCTAAATGGCATATATTAT	CTAAATGGCACATATTAT	TCGCTAGGCAGAAATATAGGGTTCT	(0,0)	1	GAGCATGGCGCTTGCA
Ots_124774-477	T	C	CCACCGCCATCTGATA	CACCGCCGTCTGATA	AGTTGTTCTTTTTATATTGTGTTTTTATTCCATTCCA	(0,0)	1	GCCAAATAAAAACAAAGCATGAACACA
Ots_126619-400	C	T	AGAAAGTTCTAGAAATAATT	AAAGTTCTAGGAATAATT	GGATGGTTGTCATTTCTCTGCAAA	(2,0)	1	CCGGGATACAATAATAATATTTGGTTAAGAGTTTTTT
Ots_127236-62	T	A	TCTCTTATCTGAGTTCTGC	CTCTTATCTGTGTTCTGC	TGGAGAACTTGCACTGAATGTGAAA	(0,0)	1	GCTGTTGGACCTTGACTTTAACAAATT
Ots_127760-569	C	T	CCGGTTTACCGATTTG	CGGTTTACCAATTTG	CTGCTGGCGCAGACATG	(0,0)	1	CGTTATAGAGGATAGTTTGGAGGAAGGA
Ots_128302-57	C	T	CCTGCAATACGACCAAC	CTGCAATACAACCAAC	GGTTGCAGGGCAGAACTGT	(0,0)	1	ACCCATCCAATAACCCATTTTCCTT
Ots_128693-461	C	T	CTGGTACCCA	CTGATACCCA	TCAATGTTCATCAATGCACTTCCTGTA	(0,0)	1	GCCTGCAGGAGAAGGTAGAGTTA
Ots_128757-61R	A	-	TTGTGCATTTTCCCC	TGTGCATTTCCCCC	CGTGTCCGGCTTCTTTTATTTCATT	(0,0)	1	GATGGGTATGTTAATCATATTACCAGCGTAA
Ots_129144-472	C	A	TGGGTCTCGAGCCTGTA	TGGGTCTCGATCCTGTA	CTGTTAGTGCAGAAGACGTAGCT	(0,0)	1	GCAGAGCTATTGAGCCAAGTTACAA
Ots_129170-683	C	A	ATTAGAACTCGTAGAACTAT	ATATTAGAACTCGTATAACTAT	AACCCTATGGGAACTCGTAGAACT	(0.6,0)	1	GCTAGGAGTTCTCAAAAGGGTTCT
Ots_129458-451	T	C	CATCTGGCAATGCCTT	CATCTGGCAGTGCCTT	TGGGACCCACATAAAGCAACTG	(0,0)	1	GACATAAGACCCATTTAGCCCCTTTT

Ots_129870-55	A	T	ATGCATTCACCTGTATTAT	TGCATTCACCAGTATTAT	GCATGTAACACATTATTTGGCATATGTACT	(0,0)	1	CAGTACACTGGAGATTTGCAATGTT
Ots_130720-99	A	G	CCTGTCTCATTCCC	CTGTCCCATTCCC	CGGTCATTGTAAATGTCAACGGTTT	(0,0)	1	TGCTTGCATGTTCTTGGTGTAGTAA
Ots_131460-584	T	C	CTATCAAAGCAATACATTG	CTATCAAAGCAGTACATTG	CCTATTTTTGATAGGTCATAGTGAATGGGATAG	(0,0)	1	CTGTACTCCTCCATTCCTTTTCACT
Ots_131802-393	C	T	TGTTCGAGAATGAAGATGAGTAA	TCGAGAATGAAGGTGAGTAA	TGATTGTCTCATGGCCAATTGTCA	(0,0)	1	TGTAAATTCCACTTGGCAATCTTTGG
Ots_131906-141	A	T	CACGGTTTACACTCCTATTA	ACGGTTTACACTCCAATTA	GGCTCGAACCACCCAGTTTA	(0,0)	1	TGCCCAACTGGTTTGCAATC
Ots_94857-232R	T	C	CAGGATAATAACAAACAAG	CAGGATAATAACGAACAAG	GGCACTCTCCCTGGCTAGA	(0,0)	1	CCCCATCACTTCTCTGGCTTTAAAT
Ots_94903-99R	G	T	CAAACCAGCAAACAT	ACAAACCAGAAAACAT	CCGTCTGAGTAGGAGGATCAATACA	(0,0)	1	TTTGGATCCAGCTCTCCGTATAGA
Ots_95442b-204	A	T	TGGTTCCCCAAATTT	TGATGGTTCCCCTAATTT	GTCTCTCTCTCTTTGCATCATTACACT	(0,0)	1	GGACTCTTGAGCTGTCTGGCTATAT
Ots_96222-525	C	T	TGTAGCTAATTTTAAGTTCTC	AGCTAATTTTAAATTCTC	GCTCTTGCCCATCTGTAGGAT	(0,0)	1	GGCGCAACATATGTATTAAGCAACT
Ots_96500-180	G	T	AAAACAAATCATTTTTCG	AAAAACAAATAATTTTTCG	CAGGTCTGGTCTACATCGAACAC	(0,0)	1	GATCATGTCAGATAGGATGCTGAAAGT
Ots_96899-357R	T	A	CTGAATGTTTTTTTTAATCTTT	CTGAATGTTTTTTTTTATCTTT	TCTCCTGAACTAATTTAGACCTCTGAATGT	(0,0)	1	CCTCATATTGCTTTCATCTGAAGAGAGA
Ots_97077-179R	G	T	TCACAAATGTATCCTAAAGC	CACAAATGTATACTAAAGC	CCTGAACAAATACTTAACGCTCCAGTT	(0,0)	1	GTAATAATACTTCACACCATTGCCACTTC
Ots_97660-56	A	T	ACGAGACAGATATTC	ACGAGACTGATATTC	TTCCCTAATCTGACGTACTACCAACT	(0,0)	1	CGCCACTGACGTTCATTCCA
Ots_99550-204	C	T	AAGGCTTTGGTTGTTTG	AAGGCTTTGATTGTTTG	TGACAGATTTCACCTTTAACTAGCTAAGC	(0,0)	1	GCAACCTCTTTCACACTTCAGTAAC
Ots_afmid-196	G	C	CAAAGTCAAAGATCCTATTAAA	AAGTCAAAGATCGTATTAAA	CGTGGAGTAGGTGGTTACAGTTTAT	(1.9,0)	1	CTCGTAACAAGCTACTGTAGTGTACT
Ots_AldB1-122	C	T	TGTTGGCGAAGTG[GT]GT	TGTTGGTGAAGTG[GT]GT	GCCATGGAGGACTGGATGA	(0,0)	1	GCCACCACTACTTGCTGAGAAAATA
Ots_AldoB4-183	T	A	CTGTGTGTCTAAGACAAT	CTGTGTGTCTATGACAAT	TTTGTGCGTAAAGTCAGGTAGTGT	(0,0)	1	GTGCATGCCATGAGAACTTTGTTT
Ots_ARNT	G	T	TACAGATGTCATTTTAC	CTACAGATGTAATTTTAC	CCACTGGCTGTGGAGCTT	(2.2,0)	1	GGGTTCAGTGATAGTTGGGCAAAT
Ots_ARNT-29	A	G	GTGCTAGCTAC	GTGCTGGCTAC	CCACTGGCTGTGGAGCTT	(0,0)	4	
Ots_ARNT-29c	A	C	GTGCTAGCTAC	GTGCTCGCTAC	CCACTGGCTGTGGAGCTT	(0,0)	4	
Ots_arp-436	A	T	CTAGGTGAAACTTTTTTTAAA	CTAGGTGAAACTTTTTAAAAA	GCCCTGGAGAAGTACGTTTTAAACTAA	(0,0)	1	GCAACCATGTCAACATTGCACATAA
Ots_AsnRS-60	T	C	TGAGTCCCTGACCAGC	AGTCCCCGACCAGC	CCGACGCCTCACTGAGT	(0,0)	1	TGGTTTTTCAGGTCATGGTTTCCA
Ots_aspat-196	G	C	CACTCTTTATATCCACACC[GA]	CAGTCTTTATATCCACACC[GA]	CCTGAACAGGTACACACAAACGA	(0,0)	1	TCCAACTGATGAATATGACCAACATGAAT
Ots_BMP2-SNP1	C	T	CCCACTTCGCTGAAGT	CCCACTTCACTGAAGT	ACTGCCACAGACACGAACTC	(0,0)	1	GCCACTATCCACTCGTTCCA
Ots_brp16-64	T	C	AAGTCAGCATCTTTCA	AGTCAGCGTCTTTCA	ACTCTGGGTCCAGGAGGTTTT	(0,0)	1	CTGACGAGACCATGCACCAA
Ots_Cath_D141	T	C	TGGGAAGCAATCAA	AATTGGGAAGCAGTCAA	CACTTGTTCTGCACACTACTTGTC	(0,2)	1	CACACATGGATTTTGCCTGTCTAAA
Ots_CCR7	C	T	CCACGTAGCGATCG	ACCACATAGCGATCG	CTGCTCACCTGCATCAGTGT	(0,0)	1	CCATGGTGGTCTGGACGAT
Ots_CD59-2	G	A	CTAAAATGTCATGTAAATAT	ACTAAAATGTCATATAAATAT	CATGTTACCCAGCTAAAAGTCTATAGCA	(0.5,0)	1	TGTTTATCTCTGAGTGAAAAAGGTGTGT
Ots_CD63	A	C	AGATCATGGGAATCATAT	ATCATGGGCATCATAT	TGCATGTTTTCTAACTGTGTTTTTGTGT	(0,0)	1	TGAATGCCCCCCATCAACA
Ots_cgo24-22	T	C	CCAGATGAACAACTTCAC	CCAGATGAGCAACTTCAC	AGGTCCTCTGTCGCACCTA	(0,0)	1	GGAGGCGAGGTCTGGTG
Ots_CHI06027687_143477	G	A	GGAGATAGTCAGGG	GGAAATAGTCAGGG	GCGAGTGTTAAAAGGGTCAAA	(0,0)	1	TCTCAAGCCATAAGACGGGTA
Ots_CHI06035945_4547	C	T	CCGCAACAGATC	CTGCAACAGATC	AGCGAGGCTTGCGTTTTACT	(0,0)	1	GTGCAGTCTGGGCTTGTCTT
Ots_CHI06048618_5222	T	G	ATTGTGCTTATCACA	ATTGTGCTTAGCACA	GCAATTACCCATGACTCTGTGA	(0,0)	1	GCCAAAAAGAGACCGAATCA
Ots_CHI06105101_16717	C	T	CCTCACATACTCCCTT	CCTCATATACTCCCTT	AAGGCCGTGAACATCTGTG	(1.8,0)	1	ATCGCAGGCTAGCTTTTCAA
Ots_CHI06105101_18523	A	G	GGCGGCTCGGAAAATTATTTT	GGCGGCTCGGGAAATTATTTT	GCGGTGGGATACCTCCTCTA	(0,0)	1	GCGAGAAAAGCACTGAATGA
Ots_CirpA	C	T	CAGTTCTGTAATGCATT	CAGTTTTGTAATGCATT	GCTGTGATTGTGCTCTAAAGACATG	(0,0)	1	CTCCCACTTAGCATTCCTACCTT
Ots_cox1-241	C	T	CACTACGGTAAGACCAT	CACTACAGTAAGACCAT	CACTGAACTGTAAGCCATTGTGATT	(0,0)	1	GTAAATGTAGTATACAGTATAGGCATCGTAGGT
Ots_CRB211	A	C	CTACCGTACTGAACTC	CCGTACGGAACTC	CAACGCGGGAATGGCTTTTAA	(0,0)	1	GCCAGAGTCGCCAAAATAGTAGAAT
Ots_crRAD10447-25	C	T	AGCTAGCGCTCCTC	AGCTAGTGCTCCTC	CCGTTGCAGGACTCATCAGT	(0,0)	1	GCGTGGTTCAACAGCAGTG
Ots_crRAD11620-55	C	T	AGAAGCCCAGCTCC	AGAAGCTCAGCTCC	TGGGATAGAACAGGAGCTTAAACA	(0,0)	1	TGTCTTGGTCGCGCAGTT
Ots_crRAD12037-39	A	G	CATTCAAAAAGTAT	CATTCAGAAAGTAT	TGCAGGAACTTGCTATGCT	(0,0)	1	TGTGGAAAAAGTCAAGGGGTCT
Ots_crRAD13725-51	C	A	GAGGCCCCAGATTC	GAGGCCACAGATTC	TGCAGGAGGAGGAAGGCA	(0,0)	1	AGAGCTGCCAGGTGGAGT
Ots_crRAD16540-50	C	T	ATTAAACGT[CA]TGGA	ATTAAATGT[CA]TGGA	TGTGTATTCGTCGACCGGA	(0,0)	1	TCACCTGACCAAAGCACTGG
Ots_crRAD17527-58	C	T	TAGCTCCGAGCTAA	TAGCTCTGAGCTAA	TGCCGCTGGATTTATTGACA	(0,0)	1	GCGTCAGATCAGCTGGTCT
Ots_crRAD18289-33	T	C	GAATGGTGTTAAAT	GAATGGCGTTAAAT	GCAGGGAAAACTGGTCAGGA	(0,0)	1	AGGTGAACCTCCGTCCCA
Ots_crRAD18492-65	C	T	TTATGGCTATTATT	TTATGGTTATTATT	GCAGGGCGCAAAGTTCTT	(0,0)	1	CAGTGAGCGACTGTAATCTGA
Ots_crRAD18937-60	G	A	CTCCTCAGGTGGGC	CTCCTCAAGTGGGC	GGCACAGCGACAGGAGTT	(0,0)	1	TGAGCTGGTGCGTCTGAG
Ots_crRAD20262-46	A	G	GGTTACA[TC]CCCAAA	GGTTACG[TC]CCCAAA	CCTCTGCTGAGTTTGAGGGG	(0,0)	1	TGAGCAGAGCCTATGAGGACT
Ots_crRAD20376-66	G	A	GGGA[TA]GGAGTATTT	GGGA[TA]GAAGTATTT	GGGAGGCAGGCAAAAGGT	(0,0)	1	GGTTCACCACCAGCCTTCT
Ots_crRAD20887-70	G	A	GAACTCGTCGTTGG	GAACTCATCGTTGG	CTGCTTGTAGCCGTTCAGC	(0,0)	1	AGAACACATCTGGCCAGGT
Ots_crRAD21115-24	C	T	CACACACATGCACG	CACACATATGCACG	TGCAGGTGGGACTTAAACACA	(0,0)	1	ACCTGTGGCAACGGTTGA
Ots_crRAD22960-32	C	T	CGACACCACTTACA	CGACACTACTTACA	ATCAGGTCTGGGGCGACA	(0,0)	1	TTCACCTCTGCCATCGCC
Ots_crRAD23631-48	G	A	GGGCTTGGGGGCAT	GGGCTTAGGGGCAT	GCCATATCCCGGGGCTTG	(0,0)	1	TGCCTCTGAGCACTGACTG
Ots_crRAD24807-74	A	T	ATGATAAT	ATGATATT	TGCAGGAGAGCAGGGTAGA	(0.8,0)	1	CGTGCCTAACATCATGTGCA
Ots_crRAD25367-50	T	G	GTATATTTAGAATG	GTATATGTAGAATG	ACTGCAGGCGTCATGCTT	(0,0)	1	TGGACAAAAGACCACAGGCT
Ots_crRAD255-59	T	C	AACTGTTCAAACCC	AACTGTCCAAACCC	TGCAGGAGCTGTGATGGG	(0,0)	1	GTACGGAGCGTCACTGCT
Ots_crRAD26081-28	T	G	TGGAGGTGGAGGAG	TGGAGGGGGAGGAG	GGGAGAGGGAGACGTGGA	(0,0)	1	TCACCAGCTCCTCCTCCTC
Ots_crRAD26165-69	C	T	CTCT[GA]CCCCTGGAC	CTCT[GA]CTCCTGGAC	GGGCCACGGGGTTGTAAA	(0,0)	1	TCCCAGGATGCAATGGGA
Ots_crRAD27164-55	A	T	AATTTGAATGACCA	AATTTGTATGACCA	GGAGGCTCTACGTAGGCCT	(0,0)	1	ACAATATCTGACACTGACTTGGTCA
Ots_crRAD27515-69	T	A	GCATTTTAAAAATC	GCATTTAAAAAATC	CAGATGGTGCAGGCCGAA	(0,0)	1	ACTCGTTGTGATTCCAGCCA

Ots_crRAD2806-42	C	A	GTTTGGCATAAAGT	GTTTGGAATAAAGT	GCAGGGGCAGACTGAAGG	(0,0)	1	ACTTCATGCCAATCTCACTAAACA
Ots_crRAD33491-71	C	T	GAGAGCCGAGCTTT	GAGAGCTGAGCTTT	CAGTTCGCTTCTCCAGGGA	(0,0)	1	TGTGGGTAGCAGACTGACG
Ots_crRAD34397-33	C	G	AA[GA]GTGCCTTCCCC	AA[GA]GTGGCTTCCCC	TGCCTAAACACTCCCAAGGT	(0.4,0)	1	GTTCCGTTTTTGTTCCGCGA
Ots_crRAD35313-66	A	G	TTTAAGATGTAGTT	TTTAAGGTGTAGTT	TGCAGGAAGAGTTCAGAGAAATCT	(0,0)	1	GCTCGTTGCAGGTAGAAATGT
Ots_crRAD36072-29	T	C	AACCTGTGTGATTT	AACCTGCGTGATTT	TGCAGGACCAACTTTCTCAT	(0,0)	1	GGCTGACTGGTGAAGGGG
Ots_crRAD36152-44	C	T	CTGCCACCCTTTGA	CTGCCATCCTTTGA	CAAAGTGCAGGTGCTGGC	(0,0)	1	CCAGCCAGGTGTTGAGCA
Ots_crRAD44588-67	C	T	GTGA[AG]CCAATCAAT	GTGA[AG]CTAATCAAT	CGCAAGTCAGCAGGGTGA	(0,0)	1	TGGGGTTTTAGGCTGGGT
Ots_crRAD46081-56	C	T	GCACCACTGGACCC	GCACCATTGGACCC	GCAGGGTCTGTGTGGGTT	(0,0)	1	ATGAGGACACTCCGCCCA
Ots_crRAD46751-42	C	T	TTTCTACTTAGTAA	TTTCTATTTAGTAA	CAGGAACCTGCTTTAATGCTCT	(0,0)	1	GCTTCTGCAGGGGGACAA
Ots_crRAD47297-55	T	C	TAGCCGTCACCGAT	TAGCCGCCACCGAT	CTCCCTGTTCGCTAGCCG	(0,0)	1	GGACGACCAAAGGTAGAACCC
Ots_crRAD55400-59	C	T	CTAACCCGGA[CA][GA]AC	CTAACCTGGA[CA][GA]AC	CGCAATGAGCCAACCCCT	(0,0)	1	CTGGTTTGTTCCCGGGCT
Ots_crRAD55475-26	T	G	CCATTTTAATTCCA	CCATTTGAATTCCA	TGCAGGGTTGGGGACAATT	(0,0)	1	AGTCTATTTCCCGATTTGACTGGA
Ots_crRAD57376-68	T	C	ATAAAGTGTGTTAT	ATAAAGCGTGTTAT	TGCAGGCATCATGCTTAATAACT	(0,0)	1	ACGTGACACAGGTCTGGG
Ots_crRAD57520-66	T	G	TTTTTGTTCAAAAG	TTTTTGGTCAAAAG	ACAGAGCTGTGTCTACCAGA	(0,0)	1	ACCCTCTCTTGGCCTTGC
Ots_crRAD57687-34	T	G	ACAAATTAATTAAA	ACAAATGAATTAAA	TGCAGGGACGGGGCT	(0,0.7)	1	TGCTGTTGTCTTGGGTCTCTC
Ots_crRAD60614-46	G	T	AAGATGGTATGTAT	AAGATGTTATGTAT	TGCCGTGAGAAACTGGTCA	(0,0)	1	TTTCCTCCTCTCTGCCTCA
Ots_crRAD60620-51	A	G	GTACGGAAAAAACA	GTACGGGAAAAACA	CAGGCAGTCACTGAGTCCG	(0,0)	1	TTTGAGCACCGTTTCCGA
Ots_crRAD61523-71	A	G	CAGAGCATGTGCTG	CAGAGCGTGTGCTG	GCCAAGTGATCAAGTGCTTGT	(0.2,0)	1	CCAGCAGTTCAGTTGCGG
Ots_crRAD66330-60	G	T	AGAGAGGGGTCAAA	AGAGAGTGGTCAAA	ACTCTCCCAGAAGGATTCAGAGA	(0,0)	1	TCCCAAAGCATCCTGCCA
Ots_crRAD69327-53	G	T	ATAGGAGAATTGGA	ATAGGATAATTGGA	GCCATTTGACCAACGGAGC	(0,0)	1	ACTCATACAGTATTTCCGCCTGT
Ots_crRAD73823-60	T	A	GCACGATG[CT]AGAAC	GCACGAAG[CT]AGAAC	GCAGGAAGCAAAGTTCGGTG	(0,0)	1	AGCAACTCATCGCGTGGT
Ots_crRAD74766-28	G	A	AGACTGGTAAAAG[AT]	AGACTGATAAAAG[AT]	GCTGACCACCGACCACAG	(0,0)	1	AGCTCTGCAGTAACAATGGGA
Ots_crRAD75581-70	A	G	GAACTTAAAACACT	GAACTTGAAACACT	ACACATGGCTCGTCTGCA	(0,0)	1	GGAGCTCAGGGTGCAGGA
Ots_crRAD76512-28	A	T	TAAAAAAATATAAA	TAAAAATATATAAA	GCAGGGACAGGGCCCT	(0.3,0)	1	TGGTGCTGGGTGCTGTAC
Ots_crRAD78968-46	C	T	AG[CA]AATC[CA]CACAGC	AG[CA]AATT[CA]CACAGC	CCTGCTCTGTGTCTGGGC	(0,0)	1	GTGAAGACGACCCCGGTG
Ots_crRAD92420-25	G	T	CAATCGGAAGTCGG	CAATCGTAAGTCGG	AGTGCAGGTCTCCAGATTTACA	(0,0)	1	ACCGAAGTGTATGTAAACTTCCGA
Ots_crRAD9615-69	T	C	TATTGGTCAGGGAA	TATTGGCCAGGGAA	GAATGCAGGGCCAGGGAG	(0,0)	1	ACTCCCAGACCATCCAGCT
Ots_crRAD9615-69-19	T	A	GGGAGTGGGAG	GGGAGAGGGAG	GAATGCAGGGCCAGGGAG	(0,0)	4	
Ots_crRAD9615-69-50	A	T	CTGGGAGGAGA	CTGGGTGGAGA	GAATGCAGGGCCAGGGAG	(0,0)	4	
Ots_DDX5-171	C	T	TTCATAATTGAACGATTTCA	CATAATTGAACAATTTCA	ATGACCAATTGAAGAGTTCTTCCGT	(0,0)	1	CAAAGCCAAACGTCACATTTACACT
Ots_E2-275	A	G	CCCCCATATTGCTG	CCCCACATTGCTG	GGTGCCACTTTAGTATAGCTGCTTA	(0,0)	1	CCCTACCCCCTGTGTTCCA
Ots_EndoRB1-486	G	A	TCCTTCTCACGCTTCT	CTCCTTCTCATGCTTCT	CCTTTGGGTCTGCTTGAGGTT	(0,0)	1	GGAGCCAAATCCTAATGCTGAAGTA
Ots_EP-529	A	G	CAGTGTCATTTTCGGC	ATCAGTGTCATCTTCGGC	GCCCTGCCTGCAACTTC	(0,0)	1	GAAACCAACGTCTTGATGTAGACCTA
Ots_Est1363	A	T	CCATCCTGTCTTGTCTG	CATCCTGTCATGTCTG	GGTGATTTTGCCACAGAGTAGAGAT	(0,0)	1	AGTGTTAAATGTAACTTGCATATACAGGCAAT
Ots_Est740	T	C	TCTGGATGGAACCGTTAG	CTGGATGGAGCCGTTAG	GGACTCGTGCTTGAGGAAGATG	(0,0)	1	TGCATGGCTCCAACTCCTT
Ots_ETIF1A	A	C	CAACTGAAGAAAATAATATG	CTGAAGAAAAGAATATG	TCTGAACTCACCAAAGGAACACTTG	(0,0)	1	GAGAGAAAAGGAGAAATGATTGCCATT
Ots_FARSLA-220	G	A	CCTTGGATGGGA	CCTTGGATAGGA	GTTCGTGGGATTGTTCAATGTTCAT	(0,0)	1	CTTGGACAGGCTCACATTACCATA
Ots_FGF6B_1	A	C	CCTGTTATCAGACCCAAAT	CTGTTATCAGCCCCAAAT	GAGACAAAGGTTTGCAGGTTCATG	(0,0)	1	GGGAGCCATGCACTAATATATTGGA
Ots_GCSH	C	T	TATCTGGGCGGGCTG	CTATCTGGACGGGCTG	GTTCTTTTTAATGATGACTACAGGTCTTTCAC	(0,0)	1	GCTACTTTACATAATACCATTTGAGCTGAGA
Ots_GDH-81x	C	-	TGTTACGGGACATACT	TCTGTTACGGACATACT	CTTTTCTGAATTAGTGCTGTGCTTGT	(0,0)	1	CCAACTTCTTCAACTCTGTCAGTGA
Ots_GH2	A	T	TGACTCTCAGCA[TA]CTG	TGACTCTCTGCA[TA]CTG	GCGTACTGAGCCTGGATGACA	(1.8,0)	1	CCCCCAGGTTCTGGTAGTAGTTC
Ots_GnRH-271	C	T	CAATGAATACAATATCTAACCTAAT	AATGAATACAATATCTAATCTAAT	CAGATGAAAAATAAATAATTGGGCCATTAGGAA	(0,0)	1	CAGAGAGACTGAGACCATATGATGTAGT
Ots_GPDH-338	G	A	CCACTACTTAACGTGCTTT	CCACTACTTAACATGCTTT	CACTAAATATTCCTTATCATTTCATACTAAGTCTGAAGAA	(1,0)	1	AGCTGATACACAATCAAAACACAAAACAT
Ots_GPH-318	C	T	ATCAAGCTGACGAACCA	CAAGCTGACAAACCA	GGTGATAACAGGTGTTGCACCAA	(0,0)	1	TCAGGTGGTGGTGGACAAC
Ots_GST-207	G	A	ATGAGAGAGTCTTTCTCTGTT	ATGAGAGAGTCTTTTTCTGTT	GGAGAACATGCATCACCATTCAAG	(0,0)	1	TCAGCAAACGAAGGCTATGTAGAAT
Ots_GST-375	C	T	TTTCTTGTAGGCGTCAGAG	TCTTGTAGGCATCAGAG	CAGCCCGTCCCAAAATCAAG	(0,0)	1	CAGGAATATCACTGTTTGCCATTGC
Ots_GTH2B-550	C	G	ATAACATCTGCAGCATTAA	ATAACATGTGCAGCATTAA	CACAGGAAGGACGTGTTTTGATG	(0,0)	1	TGACTACCCGTTGTACCAATGAAC
Ots_HFABP-34	C	T	TCGAACTCCGCTCCTAG	TCGAACTCCACTCCTAG	CAAGAACACCGAGATCTCCTTCA	(0,0)	1	TCGGCGGTGGTCTCG
Ots_HMGB1-73	G	T	ACTGTATATGTTACGTTTTC	ACTGTATATGTTAAGTTTTC	TGCTTCAGTGAAAATAAGCGTGAGA	(0,0)	1	GTCGAGCGGTATGAATACTTTCTGA
Ots_hnRNPL-533	A	T	CATTTACCAGTTCTCACACAC	TTTACCAGTTCACACACAC	TCTTTGATATTGAGCTCATAAAAGCAAGGT	(0,0)	1	TCCTTGTTCATCCATCAGGCATAAAA
Ots_hsc71-3'-488	C	T	TTTCCAATGGTATAGATATGA	TTTCCAATGATATAGATATGA	TGCATCCATTCATACCTGACCAATT	(0,0)	1	TTTGGTTAGGCACACGATAATTTGC
Ots_hsp27b-150	G	A	[CT]GATCTGGACCAGGCT	[CT]GATTTGGACCAGGCT	TAGGAGTTGGAAAGACTGCACA	(0,0)	1	CCCATTGGTTCTTTGGTGTT
Ots_Hsp90a	G	C	ATTTGACTTGTCTTTTT	ATTTGACTTGTGTTTTT	GTCGTTTTTCATAGAAAATAGCTCACAGTT	(0,0)	1	ACAGTATACCGGCTGCCTATTCATA
Ots_HSP90B-100	C	T	TCTATGGTGTGATTCATT	TTCTATGGTGTAATTCATT	CACCTTAGTTCCACGCAACATG	(0,0)	1	CTGCGTGTATTGTAGTGGTGACA
Ots_IGF-I.1-76	A	T	CTGCCTAGTTAAATAAAATA	CTGCCTAGTTAAATTAAATA	GGTAGGCCGTCAGTGTAAAATAAGT	(0,0)	1	GATGGAGGCCACTGTGTTCTTA
Ots_Ikaros-250	G	A	ACAGAAGATTTTCGGCTGC	ACAGAAGATTTTCGACTGC	GAGGCTGACTTGGACTTTGC	(0,0)	1	GGCCTGTCAGCCAAGGA
Ots_IL11	T	C	AGCTCCATGCGGACT	AGCTCCACGCGGACT	CCTCCAGATGAGACCCACTCT	(0,0)	1	CAAAATGGTGCTCAAACGACTTCA
Ots_IL8R_C8	C	T	CTGGACGCCGTTACA	TGGACGCCATTACA	CGTGGTGTTCGCCTTCCT	(0.5,0)	1	TGTCGGCCATCACTGTCATG
Ots_IsoT	T	C	AACCAGTAGAATAACC	CAGTGGAATAACC	GACTCAGGTAAGGAAACATCAATGTCA	(0.5,0)	1	GAAAGCAAAGCATTTTATCCACCACTA
Ots_LWSop-638	T	C	TTTAACAAGAAAATTATACATTTC	CAAGAAAGTTATACATTTC	CAATTACTCTTTCTCAGCCCTGTGT	(0,0)	1	GCGGTAAGATGCAGTTTTACATGGA

Ots_mapK-3'-309	T	G	ATGCTATTAAATGAATATTC	ATGCTATTAAATGACTATTC	GGCCACTGTCATAGAATTAGGCATT	(0,0)	1	CGTGACCCTTGTAACTGAAAAGC
Ots_mapKpr-151	A	T	CGTATGTGCAATGCATG	CGTATGTGCATTGCATG	TGTTGTCTCGGACTGCATGAC	(0,0)	1	GAAGGCACAGAGATGAAGGACAT
Ots_MetA	T	A	CCTTAAGCATATTTCT	CCTTAAGCGTATTTCT	GATCATTTATCAAGACTATAGGCTATGGATACG	(1.8,0)	1	AGTTGAGTTAAGTAATTGGTAATTAGCCTGTT
Ots_MHC2	T	G	CTGGAGCGTTTCTGTA	CTGGAGCGTGTCTGTA	GTCCTCAGCTGGGTCAAGAG	(0.5,0)	1	GTAGTGGAGAGCAGCGTTAGG
Ots_mybp-85	C	T	AGAGCATGTAGTTTTG	AGCATGTAATTTTG	CAAGGGATGTGACAAATTAATCAAACACATAA	(0,0)	1	AAGAGGTCTAATAAATCTCCAATGTAAAAACGT
Ots_Myc-366	T	C	TCTCTGCTCATCTGTC	CTCTGCTCGTCTGTC	CCTTAGCTGCTCTTTGAAGTTGACT	(0,0)	1	GGCTATAGAGTGTATTTACAGCATGCA
Ots_myo1a-384	A	C	ACAGATCCATCCACCACT	AGATCCAGCCACCACT	CTCCCCCCTGGACTTTGG	(0,0)	1	GCTCTATTGCACCGTGTTCTG
Ots_myo1a-384-36	C	T	CACCACTACCA	CACCATTACCA	CTCCCCCCTGGACTTTGG	(0,0)	4	
Ots_myo1a-384-57	C	T	CTGCAGAACAC	CTGCAGAATAC	CTCCCCCCTGGACTTTGG	(0,0)	4	
Ots_myoD-364	T	G	TCATCTTTTGTTATTTCCTTG	ATCTTTTGTTCTTTCCTTG	GTGTGTGTGTGTGTGTGTCATCGT	(0.9,0)	1	TTTACACATATACAAAAATGGTCCTCTATTGTCAT
Ots_NAML12-SNP1	A	G	AAACCATTTTCATTCTTTTG	CCATTTTCACTCTTTTG	TGCCACCTCAGTTTTAGTGTTATATCC	(0,0)	1	AGCGCCAACCTGTCACT
Ots_nelfd-163	A	G	ACCCACCAGTGTCATT	CCACCAGCGTCATT	CTCACTGCAAATCCAACTTCATCAT	(0,0)	1	CCACTACATCCTCATCCAAGGTT
Ots_NFYB-147	C	T	TGTTCCAATGTAAAATGTATGC	TTCCAATGTAAAATATATGC	CAGATGATAGCTTCAGTAAGTGGTTCA	(0,0)	1	CCGTCCACAGCACAAGACTATAATA
Ots_nkef-192	C	T	AATAGGCCGACATCAA	AAATAGGCCAACATCAA	CATTTAGCAGACACTCTTATCTTAGTGTCA	(0,0)	1	CGAATGTCCACCTCAGATGTTACAA
Ots_NOD1	C	G	CCAACGGCGACTTG	CCAACGCCGACTTG	GTGCTGCAGGAACCATGTG	(0,0)	1	CTGTGTGGACTGCTGTCTAAGG
Ots_nramp-321	G	A	AAC[GT]GGCATGAACGACTT	AAC[GT]GGCATGAATGACTT	GGCCATCTTTCAGGACGTACAG	(0,0)	1	GCATGCTCTGCAATACGTTGAG
Ots_ntl-255	T	A	ATTCTTCCTC[TC]ACAATTG	ATACTTCCTC[TC]ACAATTG	TGCAGTTACAAGCCTAAGACAATCT	(0,0)	1	CAACTAAAGTAACACACCAGCAACTG
Ots_Ostm1	C	G	CCGTGGTATTGTTTCAA	CCGTGGTATTCTTTCAA	CCAGCCCCGTAACACACAT	(0,0)	1	GAGAGGAAGCAGAAAGGTCGTTTAA
Ots_OTALDBINT1-SNP1	T	C	CTACTGTTGTATTTTCTC	CTGTTGTGTTTTCTC	CGCTGGGCATGGATGAGT	(0,0)	1	GGCCAACACTGCTACTTCCT
Ots_OTDESMIN19-SNP1	C	A	CCAGTCATGGGTCATT	TCCAGTCATTGGTCATT	GGTCTGTCTGTCTGTCTATCTGTCAATG	(0,0)	1	TGTGTGTCTTTGTTCATTCCTACCA
Ots_Ots311-101x	A	-	CTGAGATCACTTTGAGCAC	ACTGAGATCACTGAGCAC	AAATGAGGCCGTCCTTTACACT	(0,0)	1	GCAATACAAGCCCTTGATAATGAAGT
Ots_OTSMTA-SNP1	C	T	AATTGCCTCATTGGGTG	AATTGCCTCATTAGGTG	GCCGAAAAATAAGCGATTAGTGATGA	(0,0)	1	GCCCCATGGTAAACCTAATTAACCT
Ots_OTSTF1-SNP1	G	T	CCGCCACCTTGGCT	CGCCACATTGGCT	CGGACAAAGAGCTACAGAAATGC	(0,0)	1	CGTCCCTCTTCACGCATGA
Ots_P450	T	A	CCCCGAAGTACTTTT	CCCGAAGAACTTTT	TGAGCGAGATTTATCAAACTGTCAAAGA	(0,0)	1	CCCAAGCGGGAGAACTTACAG
Ots_P450-288	A	G	CTATAAAGTTGGACAGTTGG	AAAGTTGGGCAGTTGG	ATGTCAATATATTTCACTATAATGATTGGAAGCCA	(0,0)	1	CACTGAACTCGAAGCTGTTAGGA
Ots_P53	G	A	CTGGGTCGGCGCT	TGGGTCGACGCTC	GGAACTTCCTCTCCCGTTCTG	(0,0)	1	GCACACACACGCACCTCAA
Ots_P53-25	G	T	TTCTGCAGGGG	TTCTGCAGTGG	GGAACTTCCTCTCCCGTTCTG	(0,0)	4	
Ots_P53-28	G	C	GGGCAGCTCCT	GGCCAGCTCCT	GGAACTTCCTCTCCCGTTCTG	(0,0)	4	
Ots_P53-40	T	C	CTCCTGGGTCG	CTCCTGGGCCG	GGAACTTCCTCTCCCGTTCTG	(0,0)	4	
Ots_parp3-286	A	G	AGTTACAAGTGGTGTTTCA	ACAAGTGGCGTTTCA	AGTCAGTGTTGGTGTAGTGAAGAGA	(0,0)	1	CATTTGTGGAGTGTTTATTGAACAGTAACA
Ots_PEMT	C	T	TGC[AT]TTGCTAAGACTTG	TGC[AT]TTGTTAAGACTTG	AGAGCATTCAATTTAAAAGCTGAAAACGA	(0,0)	1	CTTTGATCCCTGCTTGCAGTATTTT
Ots_PGK-54	T	A	CCACCATCAAGCACTG	CCACCATCATGCACTG	CTCATACTTTGTACCTGTGTGTTCCA	(0,0)	1	CGACCCAAGTGGCTCATCAG
Ots_pigh-105	A	-	TGACCTGAAAATA[TC]ATATTTTT	ACCTGAAAATA[TC]ATTTTTTT	GCATTACTAAAAACTGGTGTGTGGAA	(0,0)	1	GTTTGGAATGTTTCTCTGATTGTGTTAACAA
Ots_pop5-96	T	C	TTCTGTTACTGGAC	CTGTTACTGGGC	CTCTTGCTACTTGCAGTGTATCTCA	(0,0)	1	AGTTTGAGGGCTCTATTCTGTCATG
Ots_ppie-245	C	A	ATGTCTGAAATGAAAGCC	AATGTCTGAAATTAAAGCC	TGTTTTTGGTCATGTATTTTCTCTGCTATTTTT	(0,0)	1	GGACTGGAGCTGCTGAACATA
Ots_Prl2	A	G	ATGTATTGTTCATTTAATG	TGTATTGTTCGTTTAATG	CCTGGTCTGTTTGTGATCAAGATG	(0,0)	1	GGTTAACTCAAATAGAACATACTCTGACACA
Ots_RAD4543-52	T	C	TACATATGACTAATGAAA	TACATACGACTAATGAAA	TCTTTGGACTGTGTATACCAGGTGTA	(0,0)	1	GCCAGATGCTGTGTGTGTTT
Ots_RAG3	C	T	CTCTACAGTATG	CTCTACAATATG	CATTTCCACGAAAAGCCAGATGAC	(0,0)	1	ACAGAATAAAGTATCTTCCTCTTACATCACTACTAAT
Ots_RAS1	C	T	CAATCTATCATCGACCAGC	CAATCTATCATCAACCAGC	TCATAAACATGGTGTCTTTCAGTCAGTT	(0,0)	1	CTGACATGTGAAACTACTAAAGCATTTAATCAC
Ots_redd1-187	A	G	ATTCTGACAGCTGTTTTG	CTGACAGCCGTTTTG	TTCTGGGTTGCCATACTCTTTCAAT	(0,0)	1	AGTTGAGACCTTCAGTTCTTAGGGTAT
Ots_RFC2-558	A	-	TGCATGTAACAAATAACAT	TGCATGTAACATAACAT	AAGGTCTACTCCGGTTGTATTCGGT	(0,0)	1	CAATACGACAGTACCGGTGTTAAACT
Ots_S7-1	T	C	TACAGGAGATAAGGTCGCA	CAGGAGATAGGGTCGCA	TGCCATCATAAACAACCTAACAAGTAACT	(0,0)	1	CCTGGTTTAAAAACGGCCAACTG
Ots_SClkF2R2-135	A	T	ATTCAAAGTCAAATTTT	ATTCAAAGTCTAATTTT	CCAAATACAGACCAGCTACTTGTGT	(0,0)	1	CTTCAAGTCCCTGAATAATGGTACGT
Ots_sept9-78	G	A	CTCTTCGATGTCTAGACA	CTCTTCAATGTCTAGACA	GTCGATTACCGTTAGCTTCATCCT	(0,0)	1	ATTTCTCCTGTGTCTCTCTCTGTCT
Ots_Six6-3_AG	A	G	AGTAAAATGTATGA	AGTAAAGTGTATGA	GACACCATAAACGCTGTAGCC	(0,0)	1	TCAACTTTGCAATGAAAATGACAAG
Ots_Six6-3_AT	A	T	GAGTAAACATTGAA	GAGTAAACTTTGAA	GCGAGCAATTATTCGGGCAA	(0,0)	1	AAGGTAACTGAACTATAGGGTAGC
Ots_SL	A	G	TCAAAGATATGATTCAATTAA	AAGATATGGTTCAATTAA	AATATTGGCTTTCTGAGAATGCATTTGG	(0,0)	1	CCAAGATACTTCCTTTAACTTCTCTGTCA
Ots_slc7a2-71	G	T	GTCTCTGACGGTGTGCTTTC	GTCTCTGACTGTGTGCTTTC	CCATTCCCATCGGCATCGT	(0,0)	1	GCAGCAGACACACCGAAGTA
Ots_stk6-516	C	A	AACATAACGGACTCCC	TAGAACATAACTGACTCCC	TGTGTTTAGGATTGAACTGACCATGTT	(0,0)	1	GTAAACTCCACCTGCAAGAAGGA
Ots_SWS1op-182	T	A	ATGTACTTTAACGATTCATTT	ATGTACTTTAACGTTTCATTT	TCAAAGACATCGAACACAAGAACGA	(0,0)	1	GCAGGTAAATTCAAACGTCATCATAAGAA
Ots_TAPBP	C	T	CAGCTGTCCAGTTCTG	CAGTTGTCCAGTTCTG	TTTCTCATCCTTCTCTCTTCCAGTCT	(0,0)	1	GGACAAACCAGCACTCCAGAA
Ots_TCTA-58	C	T	CTGCCATGAAGTGCTAG	TGCCATGAAATGCTAG	ACCAGTACCTAAACGTTAGAAAGCAA	(0,0)	1	CGTTAGTTAGCTATGTCTGAAAGGCA
Ots_TGFB	C	T	AGCCTAGCTCTCGGAAG	AGCCTAGTTCTCGGAAG	GCCTCACATTTTACTGATGTCACTTC	(0,0)	1	GAGCAGATCTCTTCAGTAGTGGTTT
Ots_Thio	T	C	CAGTGTATTAGTCATTCTTA	CAGTGTATTAGTCGTTCTTA	TTTTAAAAATGGAGATAAACTCCTGACCTGAA	(0,0)	1	AATACCAAACCATGCCACTAATACCT
Ots_TLR3	C	T	CTGTGGTTTGTGGCGTG	CTGTGGTTTGTAGCGTG	TGCACCTGCGAGAGCAT	(0,0)	1	CTGGCGTTTGTTCCGTTCAG
Ots_TNF	C	T	CTGGCTGTAAACGAAGA	TGGCTGTAAACAAAGA	CCAAATCCTCATCCCACACACT	(2,0)	1	CCGTTGCACTTGACCCTAAAC
Ots_tpx2-125	C	T	CAGGCGGTTCTCC	CAGGCAGTTCTCC	TGTTGTAATCTTTCTGAATATTTGCTTGCTT	(0,0)	1	TCTTCCAAATTGAGCACAAAAGCAT
Ots_trnau1ap-86	G	T	AATCCCTCCTTTTTCC	TCCCTCATTTTTCC	GGACAAGTTGAAACAGATCAGGAAGT	(0,0)	1	GCCACTGGATACCATCACTTCAAA
Ots_txnip-321	T	C	TCTGGCGGATTTACA	CTGGCGGGTTTACA	CCTTCAAACTAACACATCATAGACATGCTT	(0,0)	1	TTATCAAACTGAAGGCGGATTTACTGA
Ots_u07-07.161	C	T	ATCAGTGACATAAGTTGTCCA	TCAGTGACATAAATTGTCCA	GTCAACAAATGCAGGTAACATAAATGGT	(0,0)	1	GATGCAAACACCTGTGAAATTGTGA

Ots_u07-17.135	A	G	AAAATGTACCACATACTTGT	AAATGTACCACATACTCGT	CTCGCCTCTGTCATTGTATTACCTT	(0,0)	1	TGACACACGAGCCATTTTGATGAT
Ots_u07-18.378	A	T	ATATGGTATGTAGAGGCTAGTTA	TATGTAGAGGCAAGTTA	GGAAACCAGCTAGGATTCAGGAA	(0,0)	1	CGTTATATGGTTTGCTTGTTTGCGATA
Ots_u07-20.332	A	C	ACCATTTGATATAACTGCGTTAG	CATTTGATATAACGGCGTTAG	CGCGAGTTAGCTCGAATATTATGATTTC	(0,0)	1	TCAAGCTAGCATAGCAACTTCATCAA
Ots_u07-25.325	T	C	CCGCTTGAAAGTTTGA	CGCTTGAAGGTTTGA	AGACAATCATGGTGTTTTGAGTCTTTCT	(0,0)	1	GCCTAGGCTTGATGGAGTCA
Ots_u07-49.290	G	A	CTTTCCCCGTGTTGGT	ACTTTCCCTGTGTTGGT	GCTGAGGAAGGATTCTGTATTTGCT	(0,0)	1	TCGGACAGAGCGCATCC
Ots_u07-53.133	C	T	TAACACATGTTGGAGGTC	AACACATGTTAGAGGTC	AGCTAGGCTGTAAATGCAAGGAT	(0,0)	1	CAGTGCTTTCAATTCATGCTGTCAA
Ots_u07-57.120	A	T	GTGACAAGGTAGGGGTTG	GTGACATGGTAGGGGTTG	GGTTTGAGCCAATCAGTTGTGTT	(0,0)	1	CGGTCTAATGTCCATTGCTCATGTT
Ots_u07-64.221	G	C	ATCGACCCTGTCATTAG	CGACCCTGTGATTAG	GAGGATGACACTGTCCGTTTGT	(0,0)	1	CACAGTCCTTCGTATTCACCTTGAT
Ots_u1002-75	T	C	ATGGCCCTTACACTATC	TGGCCCTTACGCTATC	CCGCCTTTCCCACCTTCTC	(0,0)	1	TCAAACGAGAACACACTAAGGTTGT
Ots_u1007-124	A	G	TGTCCTGTCCTCAGATCA	TCCTGTCCCCAGATCA	CGAAATAAGGGCCTGGTGTTTAAAA	(0,0)	1	TGTACCAGGTGGAAGCTTTGG
Ots_u1008-108	T	A	TTGGTAAACCTGTTTATTGGTA	TGGTAAACCTGTTTTTTGGTA	GGATGACTCCTACTAATAGACGGATGT	(0,0)	1	AGGACAGGAAAGAAGCAGCAAATA
Ots_u202-161	T	A	AGCTAGTGCTTAGCAGCTA[AC]	AGCTAGTGCATAGCAGCTA[AC]	CACTTTTGACTTTACATGGAACTTAACTCAT	(1.4,0)	1	GGGACTTCACTTTCTACAAACATGTCA
Ots_u211-85	C	T	TCCCAAAGTCGAGTGTG	CCCAAAGTCAAGTGTG	TGGTGAGAGCAGCTTTAAATGTCTT	(0,0)	1	ACCCATTCTTCTGTCTGGTTTAAGC
Ots_U212-158	G	A	CTGGAAGAAGGCCTC	CTGGAAAAAGGCCTC	CCCCATATGAGACGCTACAGTAATG	(1.5,0)	1	CAAATGCCCTCTAAGCAGACCTT
Ots_U2305-63	T	-	AATGTCATATAGAAATCTAC	AATGTCATAGAAATCTACTG	TGTCATCTCTATTGCAATCTCAGTAGATTTCTAT	(2,0)	1	CCAGGTCGTCTTTATTGCAGATTATCA
Ots_U2362-227	A	T	AAGAAGCATTTTTT[GT][GT]	AAGAAGCATTTATTTT	TCGTGGATTGTGGCTTACGT	(0,0)	1	GGGTGTTTAACAAGTAGTCCCTTCA
Ots_U2362-330	A	G	ACTGGGAAGATTGTTTG	CTGGGAAGACTGTTTG	AATGGGTAACAAAGAAATAGCTAGCTACTT	(0,0)	1	GACAGACCACAGTGAAGGTGAAA
Ots_U2446-123	C	A	CTGCAACTCGACGCAAG	ACTGCAACTCTACGCAAG	CTGGTCTGTGACGTCAAAATGATG	(0,0)	1	AGCTAGACCAGGCCATTTGAG
Ots_U2567-104	G	A	GAGACTGTTGAGAC	GAGACTATTGAGAC	CATAGTATAGTGATTCGAGTCTGGAGTCT	(0,0)	1	CGGGCTTTCTTAGGATATTTTCCTGA
Ots_u4-92	T	C	CTGTGTTGAATTTAACATAAT	TCTGTGTTGAATTTAACGTAAT	ATCCAAGGAGCCCCATTAAAGATTT	(0,0)	1	CGTACCAGAGTTGTAGAAGCATCT
Ots_U5049-250	G	T	TGGAATGGGTAAGGTGTA	TGGAATGTGTAAGGTGTA	CAATGTCTAAAGTAATGGTGGTATTCTTGC	(0,0)	1	TCTTTGACACACCATCTGCCAATT
Ots_U5121-34	A	G	AGGGTCTCATGCTCCCT	AGGGTCTCGTGCTCCCT	CCAGAGGTTAGATGGCCCTTT	(0,0)	1	CTGAGCCAGAACCACAAATTGAATT
Ots_u6-75	C	T	TTAGTCAACTGTTGTTTTT	TTAGTCAACTGTTATTTTT	GAAAAAGTAAAGTAAAAGTAAAGTATTATACCACTAAAGACAAT	(0,0)	1	GATCCACACTGTTGGTCTACTACAA
Ots_unk1104-38	C	T	CCACTAAGGATTACGTTACG	CACTAAGGATTACATTACG	TAACCATGACTTCTATCAATCACCCC	(0,0)	1	CCTCCATACATCGTCAAAGCTGTA
Ots_unk1832-39	C	T	CACCACTAGAACTCTC	CACCACTAAAACTCTC	GAAACGTCTATGCTGTCCCCTTTAA	(0,0)	1	CTGCAGTATTAGCTCTAGTTGAATCCA
Ots_unk3513-49	C	T	AGTGCGAAGAACC	AGTGCAAAGAACC	TTTGAGTGAGTCACTGCACCAA	(0,0)	1	CAGCTCCACAGTGTCACCAT
Ots_unk526	A	G	CAACATTCCAGTCTGAAAC	CATTCCAGCCTGAAAC	TCAAGACTGTGCTGTAGTTGTCTAC	(0,0)	1	CCTCCCCCTTTTCCACATCAG
Ots_unk7936-50	C	G	AGACATGTAGCTATGTAGGTAA	AGACATGTAGCTATCTAGGTAA	ATGGGTTGGGATTATGGTTCATTGT	(0,0)	1	CAAAATGGTTACTTGCATAGTCTTTTGT
Ots_unk9480-51	G	C	CTCCCACAAACCC	TCCCAGAAACCC	CAAATCAGAACAAAACCTCCCACAA	(0,0)	1	GGAAGTCTGTCTGAATGGTTGTCTT
Ots_unk9480-51-38	T	C	TCCCASAAACT	TCCCASAAACC	CAAATCAGAACAAAACCTCCCACAA	(0,0)	4	
Ots_unk9480-51-39	C	A	CTAAGGAGACC	ATAAGGAGACC	CAAATCAGAACAAAACCTCCCACAA	(0,0)	4	
Ots_vatf-251	G	-	AGACCACAAGATACAGTACC	AGACCACAAGATAGTACC	CTTTTCGGGTTATTCATGCTGTTGT	(0,0)	1	GCAAGCATTTGAAAAACAGACTGGAT
Ots_VGLL3-1	C	A	ACCTGCTCTAACTA	ACCTGATCTAACTA	AGGAGTCCGAGTCATTCT	(0,0)	1	AGATGTGGGTGTCACAGAACTC
Ots_wenYhap_25067_92	A	G	GCATAGTTTGG	GCATGGTTTGG	ATAATGTTTCCTGACATGTTGGTG	(0,0)	1	AAGTGAAGGTCAAGCCATGAGT
Ots_wenYhap_71572	C	T	GCCACACTGTT	GCCATACTGTT	CTAGTCCTGACATGTAGGCTCATC	(0,0)	1	GAAATCATGCACAGAATGAACAGT
Ots_zn593-346	A	T	TCTTGCAATCATTTTTAAC	CTTGCAATCATATTTAAC	CTACGCGAGAAATAACACTTTTCAAAACT	(0,0)	1	GGCGAGTTTATTACGGTGTTATGAC
Ots_ZR-575	G	A	CC[GA]ACACAATTTTGT	CC[GA]ACATAATTTTGT	GCCTACCAGAAAGTACCAATTGTGA	(0,0)	1	ACTTTTCACTGTCCTATTACAATTAGTATTTGTGATAT
Ots1_72858599	A	G	GGTGGAGGGAAAAAGCAGTG	GGTGGAGGGGAAAAGCAGTG	AACCATTGTTCTTGTATTCCTGCT	(0,0)	1	CCATCCTTTCATTCGTCTTTTTAC
Ots10_21244146	A	C	CCATTATCATTAT	CCCTTATCATTAT	CTTCCAGGAGGTATTGTTGGTTAT	(0,0)	1	CTGTATATGGCAAACCTACGTTCA
Ots11_11925999	G	T	CATTTAAAATGGTAAAAATCA	CATTTAAAATTGTAAAAATCA	TTTATATTCAGACATTCGCCAAAA	(0,0)	1	AAACCATTTCTATGTTACTGTGACAA
Ots11_32418659	A	T	AGCCAATTGTAGCCTTAGTGC	AGCCAATTGTTGCCTTAGTGC	CAATTGTAGCCCTCTAACTTTTCC	(0,0)	1	TACAATTGGCTTTGTGTGTCGTAT
Ots11_32468959	G	C	GTGATAGTTTGATAGTTTTAT	GTGATAGTTTCATAGTTTTAT	AACACAGATCAAATGTTTTCACAC	(0,0)	1	TCAACATTCTGTTTTTCCTGTGTT
Ots12_23066874	A	G	TCCCCACCAAAATTAAGCAAA	TCCCCACCAAGATTAAGCAAA	CTCTTTCAGTTGTCTTTGCTCTTG	(0,0)	1	ACCCTGTTCATGCCTTTTCATAAT
Ots14_5453033	G	A	TCTCTAAAAAGGTACAGTATA	TCTCTAAAAAAGTACAGTATA	ATTATTCAAACAGAGATGGCGAAA	(0,0)	1	ATCATGTTCTATGCAAACCTCCTC
Ots15_18157381	C	T	CCCTGGAGATCT	CTCTGGAGATCT	TCTCAATGTGATTGAAATGGATGT	(0,0)	1	CACCGTACACACAAACTACAGACA
Ots17_1486479_C6	G	A	CTGTAGTGACGCCGCAACAC	CTGTAGTGACACCGCAACAC	GTCACGATCAGCAATGAGACAG	(0,0)	1	TTCAATGCAGTGCCTTAGTCC
Ots17_22360456	T	G	AGTCTGTCGTTGT	AGGCTGTCGTTGT	ATGGTTAAATTGACTCCTCCCTAT	(0,0)	1	GCAGATGACAGAACAGTAGTAGGC
Ots17_885364	C	A	TAGCCTTAAGCGCTTCCTGCC	TAGCCTTAAGAGCTTCCTGCC	GTAAAGAAACATGACCTTTTCTGAG	(0,0)	1	TTTAACTATGATGGCCATAACCTG
Ots18_29943476	A	G	GCCTGACTGGACAACCATTTG	GCCTGACTGGGCAACCATTTG	GTTCATTTTGAAATAACTGCATCG	(0,0)	1	CTAATGTGCATGGACCTTGTAGAG
Ots18_30099101	C	T	ATTGCATACTCGAGTCATCCA	ATTGCATACTTGAGTCATCCA	CAAATGTAAGGATACGCTTGAATG	(0,0)	1	AATACATGTAATCGCTTGCAACTC
Ots18_32088284	T	C	ATGTTACATGTA	ACGTTACATGTA	CATGAGACACCCTGGAGAAAA	(0,0)	1	GCCCCAAGAAGGTACTATCAAAAT
Ots18_3417174	A	C	CTGAATCCTGTAAG	CTGCATCCTGTAAG	TGAGGTATTACTTGCTGAGTTTGC	(0,0)	1	TGGGAATTAGTTCACATCTTCTTG
Ots18_3426299	T	A	AATGCCATTTTGT	AAAGCCATTTTGT	TTATTTTGGGCTTCATATGGTTCT	(0,0)	1	TCCAAAAATATCAACATCATGACC
Ots18_3541813	T	C	CTACCTACCTTAGTGCTC	CTACCTACCTCAGTGCTC	CCCCAAAAACATCAAGAAGTCTAA	(0,0)	1	TTAGTCTACCTTTTCCTCACCATGT
Ots18_3550047	A	G	TCATTTTTGCAGAGAGAGAAT	TCATTTTTGCGGAGAGAGAAT	ATCATCTCTGCTCAGAGGCTATTC	(0,0)	1	AGTGTAAGACGTTCCTTCCACTCT
Ots19_46172133	C	T	GCAAATCTCCGATGTAAAGT	GCAAATCTCTGATGTAAAGT	CACATGGCTCTTTGCTCAAAAT	(1,0)	1	AACATTCAACACATAATGGTAGGC
Ots19_46172427	G	A	TATTCAAAAGGAGCAGTTCAT	TATTCAAAAGAAGCAGTTCAT	CAGTTCCTGACATTCACCAAAATA	(0.8,0)	1	CTGTATTAGTGATGGGTTGTTTGC
Ots2_38264269	A	C	TCCCTTGTCTATGGTATATCT	TCCCTTGTCTCTGGTATATCT	GTATGAGTTGTGTGGTTGCAATGT	(0,0)	1	GGACATTGTGCAATAGGCTAGAG
Ots2_42405643	G	T	CAGGTTGTTGGTTGTT	CAGGTTGTTGTTTGTT	GAGAGAGTGCATTCTTCATCAAGTT	(0,0)	1	ATTGGGAAAAACCCTGTACTGA
Ots22_32650802	G	A	GGGAGAGGAGGCCTGTCTTTA	GGGAGAGGAGACCTGTCTTTA	AAGGAGCAGGAGATGTTATTGAAG	(0,0)	1	CAGTGGACCAGTGAAGTACCTAGT

Ots28_11023212	A	G	AACGTGACACAAT	AACGTGACACGAT	AGAAAGCCATCATCATGAGACC	(0,0)	1	TTCTGACCATTTTTGTTTGTTTGT
Ots28_11025336	A	C	CAATGAAGTTAATTTAATTGG	CAATGAAGTTCATTTAATTGG	TGCAATATAGAACAAATCCGAAAA	(0,0)	1	ATGTATGTGAAGCCAAGGGTTATT
Ots28_11033282	G	A	TAAAAATGGTTGATATGTA	TAAAAATGATTGATATGTA	GGCTTTCTGATGATCTTGAACTTT	(0,0)	1	TAGGGACTTCCTCTCTCTCACACT
Ots28_11062192	C	G	TTCTCAAGTCCTACTCAACTG	TTCTCAAGTCGTACTCAACTG	AGATGATATGGATTTGCTGTGTGT	(0,0)	1	TCTTTCTCTGATCGTTATGTTCAA
Ots28_11070757	A	G	ACCCATGAATAAGGACGAGAG	ACCCATGAATGAGGACGAGAG	TTTTGGAACCCTTTTTACTACGAG	(0,0)	1	CCCTCTCCTCTGCTATACTGATGT
Ots28_11071377	T	C	CATCTTAGCCTCTCTGACCCC	CATCTTAGCCCCTCTGACCCC	ATTTGCTGTGTGTGGAGTGAAT	(0,0)	1	CCTCCAAGAGCATCTGTCACTAC
Ots28_11072994	C	T	CCATATGTCGCTTGT	CCATATGTCGTTTGT	GGGAGACTTAAAACAACCTCAAAA	(0,0)	1	ACTGTTGAATAGAAGGTTGCAGGT
Ots28_11073102	T	A	ACATTACTTTTCAAAAATATT	ACATTACTTTACAAAAATATT	GGTGAGCCATTCATAACAATCTT	(0,0)	1	TCTCTTGAATGATCCAGGATAACA
Ots28_11073668	T	A	TACAGTTTCCTGTCTGA	TACAGTTTCCAGTCTGA	CCTAAGAGGAGACGAGCATTACAG	(0,0)	1	CGAGTGGTCATATGTTGATTTACC
Ots28_11075348	G	A	GTGTGAAAGGGGAGAAGGGCT	GTGTGAAAGGAGAGAAGGGCT	CATTTCAAAATTAGGAGGTTAGGG	(0,0)	1	ACAGGCCACAGCTCTCATCT
Ots28_11075712	C	T	GAAAACTCTGCCCTG	GAAAACTCTGTCCTG	GCTTAAACAGCTGCTATTAGGACA	(0,0)	1	ATTAGAGCTGGCAACAAATCCTTA
Ots28_11077016	C	T	GTCAAACCAACTTTGCCAAGG	GTCAAACCAATTTTGCCAAGG	AAAATATGTGCAACATCCAATGTC	(0,0)	1	ATTAGCTTCAGCCAGCTTGTGT
Ots28_11077172	G	A	ACACACACAAGAGACACCCAC	ACACACACAAAAGACACCCAC	GTTTTGCCAGAGAGAATGTACAAA	(0,0.4)	1	GCTAGTCCAATGCTCTAACCACTA
Ots28_11077576	A	G	GAAGGCCAAATAAAATTG	GAAGGCCGAATAAAATTG	TGTGCGGAATTACTGATAATTGAC	(0,0)	1	AGCAGTGTTGTAAAATGCAGAGC
Ots28_11095755	A	T	AGAGTTGAATGGC	AGTGTTGAATGGC	CCAATGGTGATTTTAGAACCATTAC	(0,0)	1	TGCTGTTGATCCATACTCTGTTTT
Ots28_11143508	G	A	TTCACGTACGGCCCAT	TTCACATACGGCCCAT	ACCTTTTAGCCAGTGACAACATTT	(0,0)	1	CTATCGTCGAGAGTTTCTTGCAT
Ots28_11160599	G	T	CTCTCTGCTTGCGTT	CTCTCTGCTTTCGTT	GTGCATATTTTACGTGGTTGAAGT	(0,0)	1	AAATTCATATGGGTGAAATGGAAT
Ots28_11164637	C	A	CTGGCGGGGTCTGGG	CTGGCGGGGTATGGG	TGATTTGACTTTTTGTGGTGTTTT	(0,0)	1	AAGAGAGCAAAAACAGATTGGAAC
Ots28_11186543	A	T	AAAGCTGATTAAAAA	AAAGCTGATTTAAAA	GGCTTGCCTTTAGATAGAATCTTG	(0,0)	1	TTTGTTTTTGGACTTGTGAGATTT
Ots28_11201129	T	G	ACTGAAGGAATTTAAC	ACTGAAGGAAGTTAAC	TGCGAGATTTATCTACTTGTCCAG	(0,0)	1	TTAGCAATTGCGTACAAAACTACC
Ots28_11202190	T	C	CAAAAGTCTGTATTTTCAAAA	CAAAAGTCTGCATTTTCAAAA	GCTAAATGTAAATCGAGTGGCTGT	(0,0)	1	TAGAACACTGAGAGGACCCATGTA
Ots28_11202400	C	T	GACACACTCACGA	GACACACTCATGA	CCCTCCAAAAAGAAAACATTTGAT	(0,0)	1	AACCAGTGTTTGATTAGCCAATTT
Ots28_11202863	C	A	ATAAAAAATTCTGCGTGAATG	ATAAAAAATTATGCGTGAATG	GAGGATGGATGAGACTTTTCAGAT	(0,0)	1	CTTCATATAAACCCGGTAAAGAGC
Ots28_11205423	A	G	CCTGCACACATGTCAAACCG	CCTGCACACGTGTCAAACCG	TTAAATCACCCAGAGCTTGTTAGA	(0,0)	1	TTGTGGTTGTTATCTAGGTCAGGT
Ots28_11205993	C	T	GCTATTAAAAGG	GTTATTAAAAGG	GCTGCTATTTCCGACCTTACAATA	(0,0)	1	TTCTGGTGAGTGTTTTGTCTTGAT
Ots28_11206740	T	C	CCTTCCCTCCTAGGGCAACGT	CCTTCCCTCCCAGGGCAACGT	ACTTTGAGGACTTACTCCTGTCCT	(0,0)	1	GATCATCATCTTGTCTTTCTCCAG
Ots28_11207428	T	G	GTTGGGAGCGTCCCAAAATGG	GTTGGGAGCGGCCCAAAATGG	TATACCTTTGTAGCATCCCTCTCC	(0.5,0)	1	GTCAAACGCTGTCCACTTTATATG
Ots28_11210919	C	T	GACCTCAAGCAGTCAG	GACCTTAAGCAGTCAG	AGTGCTCCATGCTGGAGTTT	(0,0)	1	AGCCTCTCCTTCTGCTTCATC
Ots29_18791740	T	G	CCTATGAAGTT	CCGATGAAGTT	GTTTTGGTGTGGTCTCAAATCC	(0,0)	1	CGGCACCTGGAAACAGTC
Ots29_23344676	T	C	TGCAAGTCCTTCAAAGGCTCA	TGCAAGTCCTCCAAAGGCTCA	GAACTATCCTGACTCCCATTGAAA	(0,0)	1	CATAACAACCAGGAGGAACTCAG
Ots3_34894254	T	C	TAACTTACAGTC	TAACTTACAGCC	TGATATATTTTGCTGCAATGATCTG	(0,0)	1	AACATTGTCCACCTTCCCTCT
Ots3_57055518	T	C	TGATCATATCTCGTTCAGT	TGATCATACCTCGTTCAGT	TTAGCAGGCGATCTAATTCTGATT	(0,0)	1	CAGAGAATACAGCAGTTAGCGTGT
Ots30_17330452	G	C	CATGTCAGTGC	CATGTCACTGC	CACAAATGTGACCGTTTTCATC	(0,0)	1	TTGAACCAGGGTGTCTGTAGTG
Ots30_17330688	T	C	TGTGTCTGAGA	TGTGTCCGAGA	CTGACAAAAGTGATCTGCCTGA	(0,0)	1	TGCTTGGTTACACAGTTTGACA
Ots33_19359879	T	C	AAATAAACGCTGGGTCTAATT	AAATAAACGCCGGGTCTAATT	AGCGCCTGTTTTACATAAACACTT	(0,0)	1	TTGCTCAGTCTTTACGGTACTCAC
Ots4_40942276	G	A	GGAGTCAGATAC	GAAGTCAGATAC	ATTAGTGCATATGAATCGGGCTAT	(0,0)	1	CAATATGTACGTTCAACCTTTTGG
Ots4_41638710	G	A	CCTGAGATTAGG	CCTGAGATTAAG	CAGCAGCTGTTTATGACTGACTTC	(0,0)	1	CATTTCACATCGGTTACACGAG
Ots4_42378741	C	T	AGATGAACACCAACTGGCCGG	AGATGAACACTAACTGGCCGG	CAGTTTAAGTGTTACCACCACGAG	(0,0)	1	CGTTAACGCTCACCTGCAC
Ots4_64978818	C	A	TCAAGTGTTTCCTTTATTTTG	TCAAGTGTTTACTTTATTTTG	AGAACCCATGCTTTCAGTACACTT	(0,0)	1	GAGCGATACATTTCTGTCCATTTT
Ots5_44795073	C	T	TTTTTGTGTCCGCCATGAATT	TTTTTGTGTCTGCCATGAATT	GCACTGTATACAAAATCGTGTGGT	(0,0)	1	TATTGGGCATTGTCTGTCTTAATG
Ots5_70908626	T	C	AGCCTCTTCCTCTCTG	AGCCTCTTCCCCTCTG	TACGGTAGGAAGACTGAATGAGTG	(0,0)	1	TACAAGCTATCTGGAGAGGTAGGG
Ots6_10904949	C	T	CCTTTGTCACCGCTCATCAGC	CCTTTGTCACTGCTCATCAGC	AAATCACCCCATTTCTTTTGTG	(0,0)	1	TGCTTATGCACATCACCTTTCTAC
Ots6_33505144	T	A	AACATATGAGTTGTAATGCCC	AACATATGAGATGTAATGCCC	CCCACCATACAATAAAGGCATGT	(0,0)	1	TGGGTATTTGTTTATGGGAGAGAT
Ots7_50997124	G	T	GGGCCTTCGGGGTGCCTGTCC	GGGCCTTCGGTGTGCCTGTCC	AGATCAAGCTTGCTGACTTCG	(0,0)	1	CAGCAAAATACAGTGTGGTGTATG
Ots7_51409415	T	C	TGGTCTACTTTGTGC	TGGTCTACTTCGTGC	ACAACTAGTCATCGTGGAATCTGA	(0,0)	1	CCTCATTCCTTTCTTTTAGCATGT
Ots7_53291035	G	A	GCTAGCAAACGTCGCCA	GCTAGCAAACATCGCCA	TCAAATTGAATGTAGACAGATGGAA	(0,0)	1	TAATGTTAGCTTTGCGAGCTATTT
Ots7_53631522	A	G	TGAGTTTTCAAGGGGTT	TGAGTTTTCAGGGGGTT	CTTATCTCAAAGGAATGGGAATGA	(0,0)	1	CAAAGCTGCATCCAAATACTGTAG
Ots7_54212944	T	A	AATATATTTTTTATAGGC	AATATATATTTTATAGGC	AAACCACGGTATCCTTTATTCATC	(0,0)	1	TTTAGACATATTTTGGGGTTAGGAA
Ots9_16115048	G	A	CCAGTGAGATGCTGTGTTGCA	CCAGTGAGATACTGTGTTGCA	ATAGAGCTTTTGGTGTTTCATTCC	(0,0)	1	AGGCCAGTACACAGTACACACACT
Ots9_28975221	A	T	TTTGCCAAAGAGTTCAGATAC	TTTGCCAAAGTGTTCAGATAC	GCCTGCCCTACTTATCTCTTATCA	(0,0)	1	CAGCAAATTTTACAGTGAAGAGGT

Appendix 8. GT-seq SNP panel for Sockeye salmon.

Assay	A1	A2	A1-Probe	A2-Probe	FWD Primer	Corr	Flag	Rev Primer
One_SEXsdY-F19R20	X	Y	NA	CTCCAACCTGTTGT	CCCAACACCCTTCCTATCTCC	NA	0	CCTTCCTCCCTAGAGCTTAAAAC
Oki_101419-103-27	A	C	AATCCACTTCC	AATCCCCTTCC	CCCAATTGGAGACCAGGGTT	(0,0)	3	TCATTCAGACAGTTGGGAGACA
Oki_101419-103-44	T	C	GTTCTCCTACT	GTTCTCCCACT	CCCAATTGGAGACCAGGGTT	(0,0)	4	
Oki_105105-245-23	T	G	GCCTTTTCCAT	GCCTTGTCCAT	GCGTATCAAGCATCAACGCC	(0,0)	3	TCTTTCAGCAAGGTTGGGCA
Oki_105105-245-56	G	A	CTCATGCCCAA	CTCATACCCAA	GCGTATCAAGCATCAACGCC	(0,0)	4	
Oki_106172-60-38	C	T	GTGCGCATCAA	GTGCGTATCAA	ACTACTTGGCGTGTGTGTGGG	(0,0)	3	TCCACTGAGAGGATGAGGCA
Oki_106172-60-47	G	A	AACGCGCTGAC	AACGCACTGAC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_106172-60-47c	A	C	AACGCACTGAC	AACGCCCTGAC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_106172-60-53	C	T	CTGACCGCYGC	CTGACTGCYGC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_111681-407-38	C	T	AGAAACTGCAA	AGAAACTGTAA	TTCATCCCATTGGAAGCCCC	(0,0)	3	ACAGCCTATATCTGTGCGCT
Oki_120255mod-99	A	C	GACTAAAACGT	GACTACAACGT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	3	CATTGAAGGGTGGAATTGAAG
Oki_120255mod-105	C	T	AACGTCAGTTA	AACGTTAGTTA	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-113	G	A	AGTTACTGG	AGTTACTAG	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-115	G	T	TTACTRGGGTA	TTACTRGTGTA	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-119	G	A	GTAGYTTCWTG	GTAAYTTCWTG	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-120	C	T	CTTCWTGGCAT	TTTCWTGGCAT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-133	T	C	TGGCATAGTC	TGGCATAGCC	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-135	A	C	GGCATAGYCAT	GGCATAGYCCT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-137	A	T	ATAGYCMTAGAT	ATAGYCMTTGAT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-141	A	G	ATAGYCMTWGATA	ATAGYCMTWGATG	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_126619-265-31	A	C	GGATTGKGCAC	GGATTGKGCCC	TGCGTAGTTAATTTTCACCTCGG	(0,0)	3	TACGCAGCACTGAAGACTGG
Oki_126619-265-35	A	G	CAGCACAGCTG	CGGCACAGCTG	TGCGTAGTTAATTTTCACCTCGG	(0,0)	4	
Oki_126619-265-50	G	T	GATTCGCCAGT	GATTCTCCAGT	TGCGTAGTTAATTTTCACCTCGG	(0,0)	4	
Oki_aspAT-273-37	C	T	CTGGACACAAT	CTGGATACAAT	ATGCTGGGAGAAACAGTGGG	(0,0)	3	CTCCTCTGTAAGGGGTGGGT
Oki_aspAT-273-45	T	A	AATCCTTAACA	AATCCATAACA	ATGCTGGGAGAAACAGTGGG	(0,0)	4	
Oki_RAD41030-31-36	C	T	GAAGGYCRGGG	GAAGGYTRGGG	GCTGAGCCTGGTCTGGG	(0,0)	3	TGGATACCCCAACTCCTCCA
Oki_RAD41030-31-37	G	A	GGGGSTCTGTG	AGGGSTCTGTG	GCTGAGCCTGGTCTGGG	(0,0)	4	
Oki_RAD41030-31-41	G	C	GGGGTCTGTGG	GGGCTCTGTGG	GCTGAGCCTGGTCTGGG	(0,0)	4	
Oki_RAD41030-31-55	G	T	AGCTCGGGCTG	AGCTCTGGCTG	GCTGAGCCTGGTCTGGG	(0,0)	4	
Oki_RAD51585-47-25	C	G	GTGGCTCACTT	GTGGCTCAGTT	ACTTTCTAGTAGGCGTGTGGC	(0,0)	3	CAAAACCCTGGCGTTGCAAG
Oki_RAD51585-47-28	G	A	TCACTTGGTAGAGC	TCACTTAGTAGAGC	ACTTTCTAGTAGGCGTGTGGC	(0,0)	4	
Oki_RAD51585-47-31	A	C	TTKGTAGAGCA	TTKGTCGAGCA	ACTTTCTAGTAGGCGTGTGGC	(0,0)	4	
Omy_myclarp404-111	T	G	CAAAGCCATACGTGGCC	AAGCCATCCGTGGCC	GCTGTGGTGCTCATGGGTAAA	(0,0)	3	CCAGGGCAGGGTTGTTCTC
Omy_RAD13034-67-21	C	T	CTCCCCGAACC	CTCCCTGAACC	GAGTGATTCCCAGCCCTCC	(0,0)	3	TCTCTCCGTTGGCCAGAAAC
Omy_RAD13034-67-35	A	T	CTGAGTGGACA	CTGTGTGGACA	GAGTGATTCCCAGCCCTCC	(0,0)	4	
Omy_RAD79314-58-25	C	T	CTCGCCCTGCG	CTCGCCCTGTG	CACACTGACTCATCCCTCGC	(0,0)	3	GAGTGTCTTACCGAGCTGCC
Omy_RAD79314-58-27	T	C	GTCACRCCTGC	GCCACRCCTGC	CACACTGACTCATCCCTCGC	(0,0)	4	
Omy_RAD79314-58-31	G	A	ACGCCTGCCCT	ACACCTGCCCT	CACACTGACTCATCCCTCGC	(0,0)	4	
Omy_RAD79314-58-66	C	A	CAGTGTCAACC	CAGTGTCAAAC	CACACTGACTCATCCCTCGC	(0,0)	4	
One_1a.11217-58	C	T	ACCTAACCCTAACC	ACCTAACTCTAACC	AGCTGACAGCCACAAAGTCA	(0,0)	1	AGGTTAGCAGTGCTTTTAAGGT
One_1a.11387-56	C	T	TGGCTTCCGGATGT	TGGCTTCTGGATGT	CAGTCACCAGTGTTTCCTCCA	(0,0)	1	TGACCATGCTCCTTAACATCC
One_1a.12158-56	G	T	CTAAAATGAACTTA	CTAAAATTAACTTA	TCTGACCCACGACGTCCTAT	(0,0)	1	TTCCAGACGCACACAGTTCA
One_1a.12851-49	C	T	AATCTGCCCTGCTA	AATCTGCTCTGCTA	CCAGACCGTACAGAATCTGC	(0,0)	1	ACCAATCACAGGCTGTCTTTG
One_1a.13961-31	A	T	ATTACAAAGAATAT	ATTACACTGAATAT	TGCAGGTTAGTGAAGATAAATGGGA	(0,0)	1	TGTCACAGAAACCACAGTCTGA
One_1a.14403-38	C	T	TAGAGCGCGATGAG	TAGAGCGTGATGAG	CACCCAGCCTGCCACAAG	(1,0)	1	ACCAGGCTGTGTCATAACCG
One_1a.14866-33	C	G	AGGAGGACTTTTGT	AGGAGGAGTTTTGT	TTGTGTGTGGGTGTCAGGAG	(0,0)	1	CCGAGCTATGAGGTCAAGAGT
One_1a.15933-53	A	G	GCCCTGCACTGCCC	GCCCTGCGCTGCCC	ATTGGTGACACGGGCAC	(0,0)	1	GCAAAGGATCTGACAATGGC
One_1a.17043-35	A	C	GTAGTGTATGGTAG	GTAGTGTCTGGTAG	GCAGGTGGAGTTATAGTGCTCA	(0,0)	1	ACAACCACTACTGAGCTACCA
One_1a.20787-45	A	C	AAAAGATAATGTGC	AAAAGATCATGTGC	TGCAGGGTATGTCATGTTTTGT	(0,0)	1	GCACAACGTAGCCAAATTGC
One_1a.20814-68	A	G	AAGGTCCATTACAA	AAGGTCCGTTACAA	ACATTCAGAAAGGGGAAGGTCC	(0,0)	1	CTACTTCCCCTTCCCATGCC
One_1a.22268-41	C	T	GGCATCACGAGGGA	GGCATCATGAGGGA	GAGGGACTGGTGCACTTCAC	(1.5,0)	1	TCCCTCATTTTCCCTCCCTC
One_1a.22351-67	C	T	CAGACATCGCTCAG	CAGACATTGCTCAG	GGAGGCTATCAGCTTCTGCA	(0,0)	1	TCCAGTAGTATGTCTTGGAGCT
One_1a.23491-46	A	G	TTGGCCCAACAGTC	TTGGCCCGACAGTC	GCAGGTTTTCACTCCAACCC	(0,0)	1	AGTTATGTTACGGGTCTCATTACCA
One_1a.23626-48	A	C	TGAAAAAACCCTTC	TGAAAAACCCCTTC	ATGCAAGGGAAGGGAAGTGA	(0,0)	1	CATCTCTCTCTGTTGTAAAGAAGGG
One_1a.24137-66	G	T	AGAGAGAGATGTTG	AGAGAGATATGTTG	ACTCTCTCTCCCACTCTGCA	(0,0)	1	TCTTGGATGTCACTGTACTACAACA
One_1a.25746-65	C	T	TGGCCTGCCTGCAA	TGGCCTGTCTGCAA	ATGAATCACATTGGCCATGCA	(0,0)	1	AACGTTTCAAGTTCGTTGCAG
One_1a.25904-44	A	C	ATAAAAAAATTTCA	ATAAAAACATTTCA	GCAGGTGCATCTTAAGGGTG	(0,0)	1	TCACTCAAGAGGTAGAGCTGC
One_1a.27200-35	A	C	TGAGAGTATTTGTA	TGAGAGTCTTTGTA	TGCAGGCCCAGTTATAGATCA	(0,0)	1	TCTTCATCATCTTTATGCTTTCGTT
One_1a.27760-67	C	T	TGGTGCTCAACGAG	TGGTGCTTAACGAG	GACCTGCAGTTCCACATCCC	(0,0)	1	ACCCTCTGCGTAATTGGCTC
One_1a.28530-58	C	T	GCTGGCACACTAGC	GCTGGCATACTAGC	GGCCAGGTGTATGGACCCTA	(0,0)	1	TCCAACAGAGCAGTGTGTGT
One_1a.29135-58	A	G	ATCTGCAATCGTTT	ATCTGCAGTCGTTT	GCCCGGGGTCCTCTTTAATC	(0,0)	1	TGCAGGATGAAGAGGAGGAA
One_1a.30563-32	C	T	TGAACTGCGTTTCC	TGAACTGTGTTTCC	TGCAGGCTTATTTCGGGTTT	(0,0)	1	GCTTAACACGGAAGCCAAGC
One_1a.32514-40	C	G	ACCTTCCCCTCCAC	ACCTTCCGCTCCAC	CAGCCACACCCACCAGAC	(0,0)	1	CCTGAGCAGCTATGGAGTGG
One_1a.35102-40	C	T	CTTTTACCGTACGA	CTTTTACTGTACGA	GGTTCATGCTTTACAACAGGGG	(0,0)	1	TAGCACCTCCCACCAGAACA
One_1a.36888-37	A	G	TTTTTGGATATTGA	TTTTTGGGTATTGA	TGCAGGTTCACGGGAAGAAA	(0,0)	1	AGTCATTGACTCTCGCTGATCA
One_1a.37709-28	G	T	ACGAGAGGCTCGGC	ACGAGAGTCTCGGC	GCAGGAGAGACGGTGGTTTA	(0,0)	1	CCCGAGGGATGTGAGTACTG
One_1a.39597-30	G	T	TCTTGATGATTGAC	TCTTGATTATTGAC	TGCAGGCTCTGGGTTTTATCT	(0,0)	1	ACTAGGTCCTTCTTTGCGGC
One_1a.39667-45	A	C	TGTAACAAAGATGA	TGTAACACAGATGA	ACCACATGGGAGGAGGATGT	(0,0)	1	AACAAAGATGCCCAGGGTCC
One_1a.40490-31	A	G	TGGATTTAAATGGA	TGGATTTGAATGGA	TGCAGGCACCATAAGCACTA	(0,0)	1	AGCCTACTTGCATAGCCTTCTC

One_1a.40540-34	A	G	AGTAGCAATAGCAG	AGTAGCAGTAGCAG	TGCAGGACTCCTAATTCATTCAGA	(0,0)	1	AACGGCAGACTGGGTACATG
One_1a.40596-58	A	C	AACCCAAAACCCTG	AACCCAACACCCTG	ATGAGTACTGTACGTGCGGC	(0,0)	1	TCGGTCAGTTGGTTGGACAC
One_1a.41039-32	A	T	AAATAAAAAAATAA	AAATAAATAAATAA	AGGGAAGGGAGCTGGGATTT	(0,0)	1	CTCTCTTGTCGGGATGTGTGT
One_1a.41570-62	C	G	GGTCACGCCAAGGT	GGTCACGGCAAGGT	TTTGCAGAGAACGACAGGCT	(0.8,0)	1	CCTGCATCCTACCAGAGTGC
One_1a.41669-43	C	T	TAATGCACAGCGTT	TAATGCATAGCGTT	GGAGGTTTTCCCTGTAATGCA	(0,0)	1	GACTGCCTGCAATGACAAGC
One_1a.42159-31	C	T	AGTTCTCCTCTACG	AGTTCTCTTCTACG	AAGCATGCAGAGCTCCAGTT	(0.9,0)	1	ATGGGGGTGTATCCTGGGTG
One_1a.42211-64	A	T	ATCTAAGAGGATGT	ATCTAAGTGGATGT	CCAACCACGTCAACTGAGCA	(0,0)	1	TGCATTAATGTTAAAACCGTTAGCT
One_1a.44788-39	A	G	CACTGAGATGGATG	CACTGAGGTGGATG	TGCAGGTTGGAGATGTGGTG	(0,0)	1	GCACAAACAGACTGGAACTGTG
One_1a.45935-29	A	C	TGGAAGGAGAAGCT	TGGAAGGCGAAGCT	GCTATATGAGCGACCGGTGG	(0,0)	1	CCCCCAGCTAAATAACAATGAGG
One_1a.48100-30	C	G	CACAATACAAATGG	CACAATAGAAATGG	AGGATCCTGCAGTTTGTACACA	(0,0)	1	CCCTCGCTGTATCATGTGCT
One_1a.4900-40	A	G	TTTTGCTACCCCAT	TTTTGCTGCCCCAT	TGCAGGATATTAACTTTAAAGCTGT	(0,0)	1	TCCATGCTAATTTCTTGCAATTCT
One_1a.51402-35	A	G	TGTTATCATGATAG	TGTTATCGTGATAG	TGCAGGGGAGAGAACAGAATG	(0,0)	1	TGGTACACTGTAGGGCTACA
One_1a.5313-43	A	G	GGGAAGGACCAGGA	GGGAAGGGCCAGGA	TGGCCATGAGGGTTTACTGG	(0,0)	1	AGGGTGCCATTTGGGATACA
One_1a.53797-66	A	T	CAACTTTAAAAAAA	CAACTTTTAAAAAA	TGTTACAGACGGTGCCAACT	(0,0)	1	AGGCATTTTTCCTGAAGACGT
One_1a.5407-55	A	T	GCAAGAGATTATTG	GCAAGAGTTTATTG	GCAGGAGGGGATAGTTGCC	(0,0)	1	ACAGAAACACAGCTAGCCCA
One_1a.54542-52	A	G	TTGACCAAAAGGGG	TTGACCAGAAGGGG	GCAGGTTGTGATCGTGACCA	(0,2)	1	TGAAGAGACTACGCCCCCTT
One_1a.54542-52-44	C	T	GCCTTGTGCTT	GCCTTGTGTTT	GCAGGTTGTGATCGTGACCA	(0,0)	4	
One_1a.54542-52-47	G	C	TTGACCAGAAG	TTCACCAGAAG	GCAGGTTGTGATCGTGACCA	(0,0)	4	
One_1a.55218-55	C	T	GGCCCAACTTCAAC	GGCCCAATTTCAAC	CAGGCCCATACTGAACCGAG	(0,0)	1	CCTTGGGGTGCGGTTGAA
One_1b.56018-52	C	T	GAAGAAACGTGTGT	GAAGAAATGTGTGT	AAGCATGACGAGTGTTCCGT	(0,0)	1	GCACTCCCTGCCCCTATACA
One_1b.56276-30	A	G	CTAGAGCATGATAA	CTAGAGCGTGATAA	CTGGCCCTGAGTCGCTAGAG	(0,0)	1	AATAGGCCGAGTGTTGTCCG
One_1b.56339-60	C	T	GTGGCATCTCATTA	GTGGCATTTCATTA	CCGAAACTTTGGAGCGAACC	(0,0)	1	TCCTTTAACCTGTGAGACACCT
One_1b.56528-40	G	T	TAGAAATGATGAGG	TAGAAATTATGAGG	GCAGGGTTGTGGCTGTTCTA	(0,0)	1	CCAAAGATGAAACCAGTTCCTGT
One_1b.56760-39	G	T	TGTAAATGAATATA	TGTAAATTAATATA	TGCAGGTCTGAGAAGAAATCAA	(0,0)	1	ACTTCATCAACCCAACCCAT
One_1b.5780-62	C	G	TGTTTCGCCCCCCT	TGTTTCGGCCCCCT	TTGTGTCTGGCAGTGTTTCG	(0,0)	1	CAGTGGCAGGCACAATGATG
One_1b.5833-45	A	G	CATCACTAAGACCA	CATCACTGAGACCA	CGGCCTTATCGTCAGTCTCC	(0,0)	1	TGAAGTTGCATGGAAGTCATCA
One_1b.58946-27	C	G	TCTGCTGCCTTAGG	TCTGCTGGCTTAGG	TGCAGGCCAAACAAGTTATTTCT	(0,0)	1	ACACACACACACTCCAAGCT
One_1b.58981-44	A	G	AGAACTCATTAATC	AGAACTCGTTAATC	CAGCCGATTCCTGCTTTTTGA	(0,0)	1	CCTCTGGACGGCATCAATCT
One_1b.59232-51	A	G	TGCAGTGATGCCAT	TGCAGTGGTGCCAT	ATTCCTGCGTCCATCAGACC	(0,0)	1	TCCGGGATAGCCAGAACTCA
One_1b.60577-60	A	G	TGGACGAAGACTGA	TGGACGAGGACTGA	ATCGCACACAGGCCTTCAG	(0,0)	1	ACATTGAGGTGCGTGTCACT
One_1b.60684-45	G	T	GACGTTTGAGTTAA	GACGTTTTAGTTAA	CGGGAGGAGCAAACACAGTA	(0,0)	1	CATTGACTGACCCCCTGCTT
One_1b.61920-50	C	T	TTTTTTTCAAACCG	TTTTTTTTAAACCG	GCAGGAAAGGTGAATTATTTTCTGG	(0,0)	1	TCTGTTCAAGACGTCATTTACCA
One_1b.61967-31	A	G	GGCGTTCACGCAAT	GGCGTTCGCGCAAT	AACCTAGGACCTTGGCGTTC	(0,0)	1	GACGGAGGGAAAGCATGGAG
One_1b.63191-29	A	G	TATTCCAATGTATA	TATTCCAGTGTATA	GCAGGAAAGTAGCATCTTCGC	(0,0)	1	GCAAGATAGCCTATCCAGTATACA
One_1b.63942-34	G	T	AGAGGGGGAGTTGC	AGAGGGGTAGTTGC	CAGGATCAGTGGCTGTGTGA	(0,0)	1	AGTAGCATTGGTTCTGGCCC
One_1b.64367-65	A	C	GTGGACTAATACTT	GTGGACTCATACTT	ATGAGGCTCTGGGATGTGGA	(0,0)	1	CCTGCAATCTCATTCATAACGCA
One_1b.64886-42	C	T	ACCTACGCCTCACG	ACCTACGTCTCACG	CGCATGGCAGTGACATACCT	(0,0)	1	TGCATCTTAAGCCAGGGGAA
One_1b.67122-29	A	G	CCTCCGGATCATCT	CCTCCGGGTCATCT	AGGTCAGTCTAGGTCCTCCG	(0,0)	1	TAGGGTGTGTCTGCACTGAG
One_1b.68250-26	A	G	TGGAGGAAGAAGAG	TGGAGGAGGAAGAG	TTGCCCTCGTGCTTGGAG	(0,0)	1	TTAACGGTGATGGAGCTGGC
One_1b.6939-43	C	T	GTGATGGCGGGGGT	GTGATGGTGGGGGT	GGCCTCAGAACCCTGTTTGA	(0,0)	1	TCTGCATTTCTGGTGATGGCT
One_1b.70246-46	C	T	GCTATGGCGACTCC	GCTATGGTGACTCC	TTTGTGGAGAGCCTGCGTAG	(0,0)	1	GTACGAGAAGGCTGGCAGG
One_1b.70297-45	C	G	GGGCCGGCAACTGG	GGGCCGGGAACTGG	CAGTGGGCTGTAACAGAGGG	(0,0)	1	GCAGAGGAAGGGGGTTCTTC
One_1b.70694-28	C	T	CAACAAGCTGCTTA	CAACAAGTTGCTTA	TGCAGGCTTGACTGGAAAGG	(0,0)	1	ACTCCGGTATCTCCTGTGCT
One_1b.70768-40	A	G	GTCTACTACTGGAG	GTCTACTGCTGGAG	GGGCCAAGTTTACCCGTCTA	(0,0)	1	CCGTAATCGTCCTGGCAGTT
One_1b.72136-33	C	T	CCTAAACCTCTACT	CCTAAACTTCTACT	TGCAGGATGATGTCATGGTGT	(0,0)	1	ACAGTACAGGTTTAGGCTGTAAGA
One_1b.72637-54	A	T	AGCGAGAACAAACA	AGCGAGATCAAACA	TCCACACTGAACTGGTTGCC	(0,0)	1	AGTGCACAGAAAACTTTGGGC
One_1b.72787-38	G	T	TTCTGGGGTTTTGT	TTCTGGGTTTTTGT	CGTGAGCAGTCTACAGTATCAAC	(0,0)	1	TGTGTACCATGGGGCATTGT
One_1b.72992-37	A	G	CAGAAGTACATGAC	CAGAAGTGCATGAC	TGCAGGTTTTAGCAAAGCCA	(0,0)	1	TCCCATATTTGAGTCGAATTGGT
One_1b.73420-52	C	T	GAACTTTCGATTAA	GAACTTTTGATTAA	AGGGTTGCAACATTTTGGGA	(0,0)	1	AGGGAATCTGGAATCCTCCGA
One_1b.73656-45	C	T	TACAGTACGTATAT	TACAGTATGTATAT	ACTTCCAGGGGGATCTCTGT	(0,0)	1	TGCATTCTCAAAAGACGGCT
One_1b.74472-27	C	T	CACTGCCCCTGTGT	CACTGCCTCTGTGT	TGCAGGTTTCAAAGCTAGACCA	(0,0)	1	CAGACCAGACAGAGGGCATG
One_1b.74818-26	C	G	AAAACACCAGACGA	AAAACACGAGACGA	TGCAGGAAAACAAGAGGACA	(0,0)	1	TGTAAATCTACTGCCCCATCGT
One_1b.75116-33	G	T	CGAAAAGCTTCAT	CGAAAATCTTCAT	TGCAGGGCTGAAATTCAATTCA	(0,0)	1	TGTGTTGCATGTGAGCCTCA
One_1b.76686-31	A	C	ATAGTTTAATATTC	ATAGTTTCATATTC	TGCAGGTGATGTATGTGTGT	(0,0)	1	CATGGCCTTTGTCAGGGAGT
One_1b.76828-42	A	C	AGTCACCACCATAG	AGTCACCCCCATAG	CAGGAGGGAAGGGTGGAGG	(0,0.8)	1	AGTTTACTCACCACACCCCG
One_1b.77679-43	A	C	GAGATCCAACGACC	GAGATCCCACGACC	CCAAGCTGAGCTTCGGAGAT	(0,0)	1	GAAACCCAGGTAGCCAGTCC
One_1b.78278-49	C	T	TACATCACCTAGTA	TACATCATCTAGTA	AGCATTCACCAAAGATAGCATGG	(0,0)	1	CAAAAGCCAAAACGTGCAGC
One_1b.78365-62	A	C	GGCATCCATGTCAA	GGCATCCCTGTCAA	CGTCACGTGATGTCCCCATA	(0,0)	1	CTTCAGGTGGCCATCTTGGA
One_1b.79240-40	A	G	TTCTTGCACTCTAG	TTCTTGCGCTCTAG	TTGCCCAATGAGGAAAGGCC	(0,0)	1	CAGCTGGAGAGGGCCATG
One_1b.79575-35	C	T	TTGTGGTCGCCTGA	TTGTGGTTGCCTGA	TTGGCTACACAAAGGACGGT	(0,0)	1	GACGGGTTGCTAAGGTCAGG
One_1b.80431-46	C	T	GAAACCACAATGAC	GAAACCATAATGAC	TACTGGCCCCCTAGCTACAG	(0,0)	1	TGTCTGTTCTGTTCTTGCTTGT
One_1b.80929-65	A	G	AGACATGAGATTAC	AGACATGGGATTAC	CCAAAGGGGACAGACAGCTT	(0,0)	1	ATGAGCGGGAGAATGTAGCT
One_1b.83667-61	A	C	CCAAGTCATCCTGC	CCAAGTCCTCCTGC	GCAGGATGTCACGACACAGA	(0,0)	1	CGCAGGAGTCCCTAGAGGA
One_1b.85587-38	C	G	AGAGTGTCTTTTTG	AGAGTGTGTTTTTG	GCAGGCAGTCAGGATGTCTC	(0,0)	1	AGGCAGTTCTAATGACAAGTCCT
One_1b.88442-61	A	G	CGTTCAAATACCCA	CGTTCAAGTACCCA	AGTAACCAAAAAGTCTCTCGTTCA	(0,0)	1	GGCTTGCTCAAGTGTTGACA
One_1b.8859-52	A	G	TGGGAGAAGGAGGG	TGGGAGAGGGAGGG	AGGGACTTGGCTTTCAGCTG	(0,0)	1	CTCTCTCCCCCTTCTCCCTC
One_1b.89789-50	A	C	CTGTGCCAATTTGA	CTGTGCCCATTTGA	CCAGACGGTCACTGTGCC	(0,0)	1	GGACAGGCAGCATGTGTGA
One_1b.90162-56	A	C	CGCAAGCATGCTAA	CGCAAGCCTGCTAA	TCAAGCGACCACCAGATCAC	(0,0)	1	CCGTGGCTCTTCCCCTTTTA
One_1b.90239-52	A	G	CCATCGCACAAACA	CCATCGCGCAAACA	CAACCTCTACCACGACCCAC	(0,0)	1	AGTTGTAAAAGAGGAGAGAAGTGT
One_1b.9134-28	C	T	CTCATTACGCATGG	CTCATTATGCATGG	TGCAGGACGTTGCCTTATCA	(0,0)	1	AATGGCAAGGTCCCAGTTGG
One_1b.9362-41	C	T	AAGGTAGCGTGCAT	AAGGTAGTGTGCAT	GCAGGCTCTGGTAGTATTCACA	(0,0)	1	CGGGGTGCTATTCTCCACTC
One_1c.34041-34	C	G	GATGAACCAGACTG	GATGAACGAGACTG	GCGTTTGGAAATTGCTCCCA	(0,0)	1	ACAAGACCTCAGAGTGCTGT
One_1c.51810-33	C	G	CAGAGGACGAGCCG	CAGAGGAGGAGCCG	TGCAGGAGGAACCGCCC	(0.5,0)	1	GCAAAATGGAGTGTCACGGC
One_1c.5765-39	G	T	GTACGCCGCCAGCG	GTACGCCTCCAGCG	CACAGAGGCTGCTCCAGTAC	(0,0)	1	TCCTACCTTGACCAACTCCGA

One_1c.70294-64	A	T	GAATGTAATAAAAA	GAATGTATTAAAAA	AACAAAAGGAACCTTGAACAACT	(0,0)	1	CTTTCGTTGCGCCACAGTG
One_1c.85338-32	C	T	ACAAAAGCTACTAC	ACAAAAGTTACTAC	TGCAGGCCTATTGTTGATGTCT	(0,0)	1	TCCTCCTCTTGCACTCCTCT
One_1c.87896-59	C	T	AGGTAGTCGCATTA	AGGTAGTTGCATTA	GAGGGAGAAGCATCAGAGGT	(0,0)	1	CCTGGCCCTTTACACCAAGT
One_1d.80954-64	A	T	CACTCACACACACA	CACTCACTCACACA	CTGCGGGGACTGATGTCTAC	(0,0)	1	GGGAGTTACCACACACTGCA
One_2.10623-54	G	T	GATTCTTGTTGGGC	GATTCTTTTTGGGC	GCTAATGTGAAAACGTGCCTGA	(0,0)	1	TAGCCTGTTGCACAAACCCT
One_2.13049-68	A	C	GGAAGTTAATTTTA	GGAAGTTCATTTTA	ACATCGTTGGCAATGGAAGT	(0,0)	1	TCTCAATCATCGGCATGTGGT
One_2.13757-55	C	T	ACCCTCCCCTAACC	ACCCTCCTCTAACC	ACAAGGAGTCGCTTGAGCC	(0.8,0)	1	GGGAGTCCCATAGAGTTGCG
One_2.14018-56	A	G	GGTGGTGACCGACA	GGTGGTGGCCGACA	ACCAGCTGTCAGAGATGCAC	(0,0)	1	GGCATCCTTCTCTCTGTCGG
One_2.15628-38	A	C	CGGATACAGCAGCC	CGGATACCGCAGCC	CAACTTCCTGTCCAGCGGAT	(0,0)	1	CAATCTCCAGCTCCCACAGG
One_2.16766-45	A	G	CTCCCCGATGCTTA	CTCCCCGGTGCTTA	GCCTCGATAAAGCCTGGGTC	(0,0)	1	TCCGGCAGTTCTCGATTTACA
One_2.20011-31	A	G	TTTCGGAAGACGCA	TTTCGGAGGACGCA	TCACGCCGGTCACGTTTC	(0,0)	1	GGGAGAGGCAAAGGTCAAGT
One_2.20130-27	A	T	TGTGCTAAATACAA	TGTGCTATATACAA	TGCAGGCTTTACTCTCTTGGT	(0,0)	1	GGCATTAAGAGAGGCGAGGT
One_2.21362-59	A	C	ATAGATTACAAAAA	ATAGATTCCAAAAA	GCAGGGACACACACACTA	(0,0)	1	TCTTCCCTTGTGTACTCTTCTTT
One_2.21498-40	A	C	AACATTTAAGCAAG	AACATTTCAGCAAG	TCAGAGGTATGGCCAGCCTA	(0,0)	1	AGCGCACAGATCTGGGAATT
One_2.21735-50	C	T	GGAGGCTCGTGTTA	GGAGGCTTGTGTTA	TGCAGGAGAGAGGGTCTTTA	(0,0)	1	TCCTCTGAATCAGTATCTCTCCT
One_2.21990-53	A	T	TACTCTTACCAACA	TACTCTTTCCAACA	GAAGTCGATGTGTTGCAGCA	(0,0)	1	TGCAAATTTCGCATGAATTGATTT
One_2.23230-33	G	T	GTTCTCAGGTGCAT	GTTCTCATGTGCAT	GGTGTAATCCAAAAACAGCCCT	(0,0)	1	TCAGAGATGTGTCCTGATATACAGT
One_2.24434-33	A	C	TATAGAGAGAGAGA	TATAGAGCGAGAGA	AGACTCTCTCCCTTCTGCAGT	(0,0)	1	TCAGTTCTTAAGTTCTGTGAGGT
One_2.24795-33	C	T	CAGCTAACTGGGTC	CAGCTAATTGGGTC	ACAGTCAATCAAGCTGCAGC	(0,0)	1	GCTCTGGTAAGATGGGGCAG
One_2.27413-63	G	T	TTAATATGGAGAAA	TTAATATTGAGAAA	TCCTTTGAACATCACTTAATTGACA	(0,0)	1	TCCCTAAAGCAAAGTGACTATGC
One_2.2794-52	A	G	AAGTGGCACAGTTA	AAGTGGCGCAGTTA	ACGACCTTTCCTCAAGTGGC	(0,0)	1	GGCCAGCCAACAGAGAGTT
One_2.28376-51	G	T	TGTGCATGGGCAGT	TGTGCATTGGCAGT	CTGTGATACCCGATACCCGC	(0,0)	1	AGAGAAACAAGAGAGAAACTGCC
One_2.28955-38	C	T	CCGCTCTCGGGCAC	CCGCTCTTGGGCAC	ATCAGCACTCGCCGCTC	(0,0)	1	CCCATGTATTTGGTTTGACGGA
One_2.29037-65	A	G	TGTTCCTAAGCCCG	TGTTCCTGAGCCCG	TCTCCTCCTGCAGAGTGTGA	(0,0)	1	GTCCGGGGAGACACATGAAT
One_2.30761-49	G	T	ATTGTGGGTTTTCC	ATTGTGGTTTTTCC	ACCTTGGACAGCTGCTGAAA	(0,0)	1	CCTGGTGAGGACAACAAGCA
One_2.32804-64	A	T	GGATATAATAAACA	GGATATATTAAACA	TCGGATTTGGGAGTGTGTGG	(0,0)	1	GGATGGATCGGATGGCATGT
One_2.34398-57	C	G	ACCATCTCGGTCAG	ACCATCTGGGTCAG	GCTCCTTAATCTTGACCCCCA	(0,0)	1	CTTGGCGGTGATAGAGACGG
One_2.34943-66	A	C	TTTACATATTTTAA	TTTACATCTTTTAA	TGGTTAGATCCTAGGATAATGCAAC	(0,0)	1	TGTCTTAAACCTGGACCCCA
One_2.35396-68	A	G	TCATGGAATCACAC	TCATGGAGTCACAC	GTGAGAGTGGAGCTGTAGGC	(0,0)	1	GGGGAACTGTGTCTGTGTGA
One_2.38070-37	A	G	ATATTCCAATAGTT	ATATTCCGATAGTT	GCAGGGAATGTTGTAGAAACACA	(0,0)	1	CTGCGAGACTGCTCACAACT
One_2.38869-26	A	G	TGTTAAGACAAAGG	TGTTAAGGCAAAGG	GGACAGTCCTGAGGGTGTTA	(0,0)	1	TCTCCTCTCCCAGAGCAGAC
One_2.39254-69	A	T	AGAACACACTCTCT	AGAACACTCTCTCT	GGTTCCCTGGAGCTACATCG	(0,0)	1	TGACAAAGAGGAGGTGGCTC
One_2.39727-26	C	T	CGGGGAACATGGTG	CGGGGAATATGGTG	AGGTAGTGTGAATAGACGGGGA	(0,0)	1	CACCACCCATGATCCCAGTG
One_2.40976-37	A	G	GCCATGTACACTTC	GCCATGTGCACTTC	CATGTTGTTGTCAGCACGGG	(0,0)	1	CCCCACTTCTCTGCCAGTTG
One_2.41128-67	C	T	TGAATAGCGTCTCT	TGAATAGTGTCTCT	AGTGGCTGCCTTTGTTCCTT	(0,0)	1	TCAGTCAGCTGCACAGAGAC
One_2.41231-65	C	T	CAAGCTACTGAGGC	CAAGCTATTGAGGC	TCAACCTGAGTTTCCTGAGGC	(0,0)	1	GGATGCGGATGGTATAGCCC
One_2.41371-35	G	T	CCCTTCAGGTTCAT	CCCTTCATGTTCAT	GGATGTTATCCTTAGAGTATCCCTT	(0,0)	1	ATCATTTTCCTGCTGGGCCA
One_2.44103-35	A	G	GAGAGTAAAACATG	GAGAGTAGAAAATG	GGAGGAAGGAGAGGATGGGA	(0,0)	1	GGGCTTCTTTCCTTGATGTTGA
One_2.45396-65	A	T	CCCCCACATGTATA	CCCCCACTTGTATA	AGTTCAAGGAGAAAACCCCC	(0,0)	1	AGTGTTTGAGGACTTCACTGT
One_2.45475-58	A	C	GCAGGGTAACGCCA	GCAGGGTCACGCCA	ACAAGGTGTTGTGCAGGGT	(0,0)	1	AGACCTCTGCATCACGGTTG
One_2.45776-68	A	G	CGGAGACATCCTAG	CGGAGACGTCCTAG	ATTGTGCAGGTAGACGCCTC	(0,0)	1	AGAGAATAGGCCTCTCCGCT
One_2.45877-55	A	G	AGTATTTATATGTC	AGTATTTGTATGTC	TCCCAATAATCGCCAACCGT	(0,0)	1	GAGTGGAGCCCAGCAACAAT
One_2.45957-54	C	T	GGTATATCGC	GGTATATTGC	CGTTGTGTCGGAATCTTCTTCT	(0,0)	1	TTTCCATCCCGCACAGTAGG
One_2.46012-53	C	G	CCTACTTCGAACAG	CCTACTTGGAACAG	GTCTCCAGAGGGTTGTGCAT	(0,0)	1	GCTCAGCTGACAGACAGGAG
One_2.46152-39	G	T	GTGCCCTGGTTCCC	GTGCCCTTGTTCCC	TTTTGTGCTGAGCAAGGTGC	(0,0)	1	GACCCATGCATCCATCTGCT
One_2.48609-47	A	G	GGTCCTCATGTGAG	GGTCCTCGTGTGAG	AGTTAGGCAAACCACACCGG	(0,0)	1	AAGGTGGCCAATAGCAAGAC
One_2.48637-56	A	C	TTGATTAAGGACAG	TTGATTACGGACAG	GCTTTTTGCAGTGCGATGTC	(0,0)	1	TTGTCAAGATGGGGAGAGGC
One_2.48952-59	A	C	GACTGTGAGGCCGT	GACTGTGCTGCCGT	AAGAGCACCAGACAAGCCTG	(0,0)	1	CTACAGCCCTAGCATACGGC
One_2.51143-68	G	T	AGGGCTGGATTCAA	AGGGCTGTATTCAA	TGCAGAAGGACTTAGGGCTG	(0,0)	1	GCTCAATCGAAAATCACCTTCA
One_2.51190-49	A	G	TTCTATCACCTCAA	TTCTATCGCCTCAA	AGCACCTAACCCTGTAATACCT	(0,0)	1	AGGTGTTCCTAATGTTTTGTACACT
One_2.52203-44	G	T	CCAATTTGGTTGTT	CCAATTTTGTTGTT	GCAGGTACAGTGAGCTCCAG	(0,0)	1	TGTCCTTGTATCATTACAGAGCCA
One_2.52394-28	C	G	TCCCATACAGCACC	TCCCATAGAGCACC	GAGACAGGCTGCGTCCCATA	(0,0)	1	CCCTGGTCAGAAGATGTGCA
One_2.5338-43	G	T	GAAGTTAGTGCAGT	GAAGTTATTGCAGT	ACCACAGTACGTAGCTATGAAGT	(0,0)	1	ACATTTCCTGAAGCCATTACTGC
One_2.53715-43	G	T	AGCTGGTGGCCAAA	AGCTGGTTGCCAAA	AGCTTCTTTCACAGGCAGCT	(0,0)	1	TGGTCCATCTCTTAACCCCT
One_2.54344-58	A	G	TGGACGAATGTATG	TGGACGAGTGTATG	CTCCCACCAATGGCGTGAT	(0,2)	1	AAACAAACTGCATGGCGCTC
One_2.5654-67	C	G	GCACTTACTCAAAA	GCACTTAGTCAAAA	GGATGTGCCTGAGACCTACC	(0,0)	1	AGGGATTGATGATTCATTGATTTGT
One_2.5744-26	A	C	ATCATAAAAAAAAA	ATCATAACAAAAAA	GGACGGAGGCTGGGATCATA	(0,0)	1	GTCCCTCATGTCGTGATGTGT
One_2.58200-50	A	T	TCAAAAAACATGTT	TCAAAAATCATGTT	TCTGTGGGGTATAGAGATACGGT	(0,0)	1	TAACCCCCGCTGTACCAAAC
One_2.58880-45	G	T	TTGAGACGCTCATC	TTGAGACTCTCATC	GGACAGCCTGGTGTTTGAGA	(0,0)	1	AGCAGGCTGATGTAGTGCTG
One_2.59897-41	C	T	CCACCGTCAGGGTG	CCACCGTTAGGGTG	CGGAGTTTTCCCTGGCACA	(0,0)	1	GCACCACCCTAGACTGAACA
One_2.62240-45	C	G	TGTTTGCCTCTTTT	TGTTTGCGTCTTTT	TGGAGAGGTATTGGTTTCAAGGT	(0,0)	1	GCTACTAAATAACTCTCCATCAGTG
One_2.6248-65	A	T	TCTCATTAGAAGGG	TCTCATTTGAAGGG	GGGAAAGAGGGAGGAGCCTA	(0,0)	1	ACTCAACCATGCCTCCTTGC
One_2.63402-51	C	G	CCATTAGCAGTTTG	CCATTAGGAGTTTG	CCAGAGCCAAAGCCAGGTAG	(0,0)	1	GATCCCAGACCTGTCAGTGC
One_2.63762-51	A	G	TCATTTAATGGACT	TCATTTAGTGGACT	TGTGCCTGTTGCTGCTGATA	(0,0)	1	GGAATATTCCCCCTATGCTTTTGT
One_2.63984-53	A	G	AGCTCACAGATCCA	AGCTCACGGATCCA	GTCACAGACATACAGGAGCTCA	(0,0)	1	TCCACGTAACAACAGGCCTG
One_2.64150-27	A	G	AATAAAAACAGTCA	AATAAAAGCAGTCA	TGCAGGAGAGAGGAGGAATGA	(0,0)	1	CCACAGGTCCTGGAGGTGTA
One_2.6529-40	C	G	TCACCGTCTGTGAC	TCACCGTGTGTGAC	CAGGGTGCCCTCCACAAC	(0,0)	1	CCACCCTGGAGCAGTCAC
One_2.65369-59	A	G	AATAACAA.GAGCA	AATAACAG.GAGCA	GCAGGGGACACAACAACAAC	(0,0)	1	AGCTTTGCTTGTTGTTGCTC
One_2.65998-48	G	T	CAGAGCCGCTGCGC	CAGAGCCTCTGCGC	CAGGCTCTCACACTCCTTGG	(0,0)	1	GCATGCACTTTTCACGCTGA
One_2.66468-68	A	G	TGTATCCAAACATG	TGTATCCGAACATG	TGCTTGTGCCTCGCATCAA	(0,0)	1	TGAGGACACTTTATGGATTCTCC
One_2.70711-39	C	T	AGGTGCTCGTGCGT	AGGTGCTTGTGCGT	TGCCCTGTTGTGATGAGCAT	(0,0)	1	GGCTGTGTAGAACGACCCC
One_2.70711-39-28	G	T	AGGYGCTYGTRC	ATGYGCTYGTRC	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-30	T	C	GTGCTYGTRCG	GCGCTYGTRCG	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-43	G	A	CGTCCGCGGGC	CGTCCACGGGC	TGCCCTGTTGTGATGAGCAT	(0,0)	4	

One_2.70711-39-56	C	G	GGCTAAGGATC	GGCTAAGGATG	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-57	G	A	GCTAAGGATSG	GCTAAGGATSA	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-64	T	G	TTCCCTAGGGG	TTCCCGAGGGG	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.71025-65	A	C	ATTACCCAGTGTGT	ATTACCCCGTGTGT	TATGAATTCCTCCCGCAGCC	(0,0)	1	TTATGGATGAGCTGGGAGGC
One_2.71512-50	C	T	TTTGATTCATTCCA	TTTGATTTATTCCA	ACCTTTCTCATTTGTGGATTTGAT	(0,0)	1	CTGCCAAGTCGATGTTCAAACA
One_2.72182-45	G	T	GCCATGTGGTGAAG	GCCATGTTGTGAAG	TCTTGATTAGTGTCCAGCCATGT	(0,0)	1	TGTGTCGCTCTGTTCTGGAC
One_2.73281-30	A	G	TCTGTCCACATTCG	TCTGTCCGCATTCG	GCAGGTGACAAAGTCTCTACA	(0,0)	1	CCACTGTACATAAACCATGCAGA
One_2.73487-56	A	G	AGCGCACATACTGC	AGCGCACGTACTGC	CTGTTCCACACCCCTCCATC	(0,0)	1	GTTCTGTCATGTCCCACCCC
One_2.74998-68	A	G	ATTGTTGAGGTGCT	ATTGTTGGGGTGCT	TGCAGGGACACAAGGAGAGA	(0,0)	1	CCTGCAGTGTTCAAAGCACC
One_2.75586-34	A	G	AAATTAAACTGAGG	AAATTAAGCTGAGG	TCGTCTAAGACCTGTCACCCA	(0,0)	1	TGTGTTTTTCCCCACAAAAGTGA
One_2.75617-47	C	T	ACCTGCTCATGGTC	ACCTGCTTATGGTC	GAGAGTACCGGGCAGACAAG	(0,0)	1	TGGTGGTGCTCTTCCCATAC
One_2.75847-69	A	C	TTCCCTAAAACACT	TTCCCTACAACACT	GCCCCCAGGATCATGTTGTA	(0,0)	1	AGAAACTATTCTGGGTGCTGCA
One_2.76328-30	C	T	GCTGAGCCCTGTGA	GCTGAGCTCTGTGA	TGCACACCATACTCCTGCTG	(0,0)	1	AAGAACGTCCAGAACACGCT
One_2.76532-58	C	G	GGAAATGCTTTCAC	GGAAATGGTTTCAC	TGCAGAATACCAATTCATACATTCA	(0,0)	1	CTCTCGCCCCCTTTACTGTG
One_2.77164-35	A	C	AGGCATCAGCCCTG	AGGCATCCGCCCTG	AGGGGGACCATTCCAGACTA	(0,0)	1	AATGAGGAGAAGCTTGGCCC
One_2.78198-36	C	T	CTGTCAGCGTTGAT	CTGTCAGTGTTGAT	TGTACTACACATTCCCTGTCAG	(0,0)	1	CGCTCCCAGAACAAACCTCT
One_2.80177-55	C	T	CGATTGACCAAACG	CGATTGATCAAACG	CTTACGGGATCGGTGACCC	(0,0)	1	ACTTACAACCTCATGCTAATCACA
One_2.80525-35	A	G	TGTTAGAACGCAAT	TGTTAGAGCGCAAT	CCTGCCACAAGGGGTTGTTA	(0,0)	1	GTTTGGCCCGCCTTTACTTG
One_2.81573-50	C	G	AGAAGAGCAAAGAG	AGAAGAGGAAAGAG	CCTGCACACCTGAGGAGAAG	(0,0)	1	AATAGTTCCAGTCCTTACATTCTCT
One_2.84041-67	C	T	CCTGGGCCGACCAC	CCTGGGCTGACCAC	CCTGGCCTACTCTGTGTACG	(0,0)	1	GCTCTGCTGGTCCTCGTG
One_2.8522-64	A	G	ATGTAAGATAATCT	ATGTAAGGTAATCT	ACCAGACCTTCCCGAGATCA	(0,0)	1	TGAGCTGTGTGACATTATCCACA
One_2.85340-30	A	G	GCTTCACAAGGGAC	GCTTCACGAGGGAC	GCTGAAGGAGCCGTCGG	(0,0)	1	CTGGCTGACCCCATGACATT
One_2.86889-62	A	T	CCAACATATGTGTT	CCAACATTTGTGTT	AACACAAGTCCATCTCCAACA	(0,0)	1	AGACAACACAGGAAGCAGCC
One_2.86898-35	A	C	AAAGGAGATCCTTC	AAAGGAGCTCCTTC	GGCGGTCACTGAGTCTAAGG	(0,0)	1	TGGTTTTTGGGGTTCATGTTGA
One_2.87240-34	A	C	TCCTGGGATTCTGT	TCCTGGGCTTCTGT	TGCAGGACAGGGAGCATG	(0,0)	1	CATCACGTACAGGTCCCCAC
One_2.90371-33	A	C	GTAACCTAATTTAC	GTAACCTCATTTAC	GCAGGTGCAGAATCATTTAACCT	(0,0)	1	GGAAGGAGTACAGAAGGTGTCG
One_2.90529-63	A	G	AATCAACAATGCTA	AATCAACGATGCTA	CAGGATCAGAAGGGGAGCAA	(0,0)	1	GTGAGCACACGGTAATTAGCA
One_2.9840-29	A	T	CGTATCAATATCAA	CGTATCATTATCAA	GGGCTAAGAACAGATTTGCGT	(0,0)	1	AAACAATGTTAACTCGAGGTTTGA
One_3RFP.12866-45	A	C	GCTTCTCATGCTGC	GCTTCTCCTGCTGC	GAGCTTTGTGATTGGGGGAGA	(1.8,0)	1	TCTGACCAATCGCAGAGCAG
One_3RFP.18602-33	A	G	CTATCACAAGCAGC	CTATCACGAGCAGC	TCATCTGTGCATGTGCTATCAC	(0,0)	1	TTACTCGTGCCAAAGAGCGA
One_3RFP.19596-43	A	T	CACTATGACTAGCT	CACTATGTCTAGCT	AGGCCTTCGACTGCTCTCTA	(0,0)	1	GATGTTGCTGCTGTGCTTCG
One_3RFP.22492-53	A	C	AATAACTAATCTAC	AATAACTCATCTAC	GCAGGAGCCCAAGGTGAG	(0,0)	1	TCTGTTTTGAGGACATTCAGTTGT
One_3RFP.22594-56	A	G	GCCGAGCATGAAAT	GCCGAGCGTGAAAT	ATAGAGACCCGACGTTGGCT	(0,0)	1	CTTGGCCCTAAGCAGAGAGC
One_3RFP.22665-32	A	G	AGTTAGAACCCTCT	AGTTAGAGCCCTCT	TGCAGGAGGTTTTAGGAGAGG	(0,2)	1	GAGTTGGAGTGGTTCCCAGT
One_3RFP.25184-65	A	G	CATCGCCACTTTGT	CATCGCCGCTTTGT	GCAGGTCGACGCTTTTTAAAG	(0,0)	1	TCCCTCAGCTGTTTACCAAAC
One_3RFP.25749-53	A	G	GCACAGCATTGAGA	GCACAGCGTTGAGA	GCCACCACATTAGGGAGGAG	(0,0)	1	GCCCCATTGCAGGTAATCTC
One_3RFP.26492-46	A	C	ATAACTAAATAATG	ATAACTACATAATG	GCAGGACAAGGTACGAGACA	(0.6,0)	1	ACCATGTTTTGACATGCTGAGA
One_3RFP.27065-48	A	T	ACTGAGGAGTATGT	ACTGAGGTGTATGT	GTCACCTGGACAGTTGATGGA	(0,0)	1	GCCAATCAGAATGTTTTTCCCCA
One_3RFP.28357-29	C	T	GCTCCAACTGTCTT	GCTCCAATTGTCTT	CAGGCCTGGGTAGCTCCA	(0,0)	1	GAGAGAGAGGGGAGGCGATA
One_3RFP.36741-50	A	T	ATAGCCAAGATCCT	ATAGCCATGATCCT	TGTGTACACAGATATGCATGAGA	(0,0)	1	AAACAATCTGCCAGTCGCCT
One_3RFP.38229-53	A	G	TAAACACACTCGTG	TAAACACGCTCGTG	GCAGGCCAACCACATCAAAG	(0,0)	1	GCGGTGTGCGTGTGTAC
One_3RFP.39193-43	C	T	GAGGATGCTCCTCC	GAGGATGTTCCTCC	AGAGTCTGTTTCCCTGAGGG	(0,0)	1	ACCTTTCTATTTCAGTGTGGAGGA
One_3RFP.40708-40	A	C	ACACTCCAGTGGCT	ACACTCCCGTGGCT	TGTTAACACACTTCTTCACACTCC	(0,0)	1	CCTTCCATCCTTGCTGCAGA
One_3RFP.43935-63	C	T	AACACATCGGTTAC	AACACATTGGTTAC	CACACCTCCTCCTTAGCCAC	(0,0)	1	ATGCAATGGCCCAGTGTGAT
One_3RFP.46202-49	A	C	CGTTAGTAGTTTTT	CGTTAGTCGTTTTT	GGGACGGGTGAGTAAGGTGA	(0,0)	1	CAGGCAGGAATGTACAAGCG
One_3RFP.46608-58	G	T	CCTTCATGAACTGT	CCTTCATTAACTGT	TGGTGCATGAACACTGAGCT	(0,0)	1	TTCCGGATTGCTCTCACACC
One_3RFP.47148-54	A	G	CATGAATAGAAGGG	CATGAATGGAAGGG	GCCTTCCTCAGCGATGACTC	(0,1.1)	1	ACCGGTAGCTACACAATTCCC
One_3RFP.50303-37	C	T	TCTCTGGCCTGCAA	TCTCTGGTCTGCAA	GCTTCAGCTCTCCCACAACA	(0,0)	1	GGCACCTGCAAAGATCTCCA
One_3RFP.52579-51	A	G	ATTATTAAC.TAAC	ATTATTAGC.TAAC	CACCTTGCTCTCTGCCTGTA	(0,2.1)	1	TCTGCTCCTCCATGGTAGCT
One_3RFP.53804-31	A	G	ACGGATAAGGGGCA	ACGGATAGGGGGCA	GGTACTTCTTCTCCTGGACGG	(0,0)	1	GACCTTGGTGTGCGTCTCAA
One_3RFP.53932-47	C	T	AACTAACCCATCAT	AACTAACTCATCAT	TGTTGCCAAGTTGACTAAAGAACT	(0,0)	1	ACAGTGGATTATCTACCAACAGTAC
One_3RFP.56125-30	C	T	CAATTGTCTTATAT	CAATTGTTTTATAT	TGCAGGAGTTAACAGGAAGTCA	(0,0)	1	AGCCAATGTGTACTAGTGCCA
One_3RFP.60219-36	C	T	ATTGTTTCCTCCGA	ATTGTTTTCTCCGA	TGACCTTGGTTGTCAGGTGA	(0,0)	1	CTTAAGCCGGAAGCCAGCT
One_3RFP.60536-30	C	G	GTGGTTTCATTTGG	GTGGTTTGATTTGG	CTGAATTTGGCCTGGGGGT	(0,0)	1	TGTTTTTGCTCAAACTTGGGGG
One_3RFP.62278-33	C	G	CCTCAATCCCATGG	CCTCAATGCCATGG	CACCACCGCTGTCCTCAAT	(0,0)	1	TTCTCCTCCCTGTTTCCCCC
One_3RFP.6937-57	A	G	TTGCAAAATCCAAC	TTGCAAAGTCCAAC	TGGTTTACAGATGCATTGCAAA	(0,0)	1	ATGGTTTTAAGAGCTGGTTTGG
One_3RFP.70374-61	A	T	GCTCATGATTGGCT	GCTCATGTTTGGCT	GGGACTGATCATCACGGCTC	(0,0)	1	TCTTCAGCTTGTGGTGGACC
One_3RFP.70898-49	C	G	CTTATATCGTTTTT	CTTATATGGTTTTT	GCACCTTCGGCAATGTGAC	(0,0)	1	ACCTGGAGAACCTGACCATTC
One_3RFP.70952-46	A	G	TACATGGATGTTAA	TACATGGGTGTTAA	GTAAGCTTTGCAGGCCTTCA	(0,0)	1	TGCGAACCTGGAACATTTGT
One_3RFP.71744-45	C	T	TGT.TGGCCGGCAG	TGT.TGGTCGGCAG	AGGCAACCAGAGTTCAGCTC	(0,0.4)	1	CACGGCCTGCTCTTCCTC
One_3RFP.72056-60	A	C	TTTTAATAATACTG	TTTTAATCATACTG	TCAGCCAACGCCTTGATCTT	(0,0)	1	ACCCAAAGGACATCTAACCAGA
One_3RFP.72689-27	A	C	ACAGTGGAGACTAC	ACAGTGGCGACTAC	GCCACCCCGAAGAAGAACAGT	(1.75,0)	1	CCTGTGAATCGTGGGTGAGT
One_3RFP.74551-60	A	C	AACAACAAAAACAC	AACAACACAAACAC	ACGGTCCTCTCAGTTCCTCT	(0,0)	1	GCCAAGATATCCAGTTCCAGT
One_3RFP.7464-69	A	G	CCACAGGATTTCTC	CCACAGGGTTTCTC	TGCTGAGTACACACGTCACT	(0,0)	1	TGGCAGAATTTAACCACTGTTTT
One_3RFP.76568-44	A	T	CCCTAGTACTTCTC	CCCTAGTTCTTCTC	GAACCTTCGCCCAGAGCTC	(0,0)	1	TTGGGGGCTGGAACAAACAG
One_3RFP.77278-58	A	T	CAACAAAAATGGAA	CAACAAATATGGAA	TTTCCAGCCCCAGAGTTGAG	(0,0)	1	CCATCACATCGGCACAAAGC
One_3RFP.80015-44	A	C	TAAAAATATAGGAT	TAAAAATCTAGGAT	TGCAGGGACAGGGGATTAAA	(0,0)	1	GTGGTGTCTCTCTGGTCGTG
One_3RFP.80215-59	A	C	TTTCCGGAGTCCAT	TTTCCGGCGTCCAT	ACTATGCAGCTAAACGCCCT	(0,0)	1	ACAGCCTGGATGGGATTTCC
One_3RFP.81817-50	G	T	TGCTTTGGGCACCT	TGCTTTGTGCACCT	ATCCGGCCCAAGATGCTTTG	(0,0)	1	CAACAAGGACAGGTGCCTCT
One_3RFP.83488-50	A	C	CTCACTTAATTTTG	CTCACTTCATTTTG	AGGATTTTAGGGCTTGACCAG	(0,0)	1	GTGTTCTTTTCTTCTCAGGAAGGC
One_3RFP.89355-44	C	G	TCTGGGACGCGGTC	TCTGGGAGGCGGTC	TCTATCTTCTCCATGTTCTGGGA	(0,2)	1	AGTCAGGGAGCATGCAGAAC
One_4a.12382-55	A	T	CTACGCCAGAGCAG	CTACGCCTGAGCAG	GGTGCAAAGGGAGTCAAATGT	(0,0)	1	AGTGCACCCACACAACCATA
One_4a.13104-68	C	G	CTCCCCTCTGACAT	CTCCCCTGTGACAT	AACCGAAAAGTGTCCTCCCC	(0,0)	1	ATCCACTTTCCACAGCTGGA
One_4a.14909-37	A	T	TTATAACACTTCCT	TTATAACTCTTCCT	GCAGGACTGTCACAGCTTCT	(0,0)	1	AATGCAGTCCCAGGTGCG

One_4a.19795-33	G	T	CACGCGGGAATCTG	CACGCGGTAATCTG	TGAATGGTTTGTTACACGCGG	(0,0)	1	TGCAACAGAGGTGGTTTGGT
One_4a.21799-29	A	G	GGTGGGGAAGCTCT	GGTGGGGGAGCTCT	GTGTGCGTCGCCTGGAG	(0,0)	1	GCTGTGAAGTAAACCAGCGC
One_4a.22514-58	A	G	TTGTGTTATCCTCG	TTGTGTTGTCCTCG	CCACTGTAGTGTCGTCTGTGT	(0,0)	1	GGTGACGCCTCCACATACAA
One_4a.24016-53	C	T	GTTCCTTCAAGATG	GTTCCTTTAAGATG	AGCAGCACACTAGCATGAGC	(0,0)	1	TTGCAACCAGGAAATGACCA
One_4a.25035-26	G	T	GGCTACAGATGTAC	GGCTACATATGTAC	TGCAGGAGCCCATAGGAATG	(0,0)	1	AGTTCTCCTGCAACATGGTGA
One_4a.25174-68	C	T	AAGGGGGCGGCAGG	AAGGGGGTGGCAGG	GCACCTCCCGTGAACTTGAT	(0,0)	1	CACCGCTCTAACCACTAGGC
One_4a.28062-27	A	G	CTTACTGATCAACT	CTTACTGGTCAACT	GCAGGAGGAGATCTCTGACC	(0,0)	1	GCTTTTCCCTCCCTCACCAA
One_4a.32159-43	A	G	CACCCACAGGCCAA	CACCCACGGGCCAA	TGCAGGACTTTTTGCCACAT	(0,0)	1	GACCACTGCATCACTCAGGA
One_4a.32895-28	A	G	ATAGCTTATGGGAC	ATAGCTTGTGGGAC	TGCAGGAAAAGCTAGACTAGAAT	(0,0)	1	AGCTTGCGTCCCTTGGAATA
One_4a.32932-27	A	C	GACTGATAGACCTG	GACTGATCGACCTG	TGCAGGTTAGTCACTTGATAGACT	(0,0)	1	TCTGTCAAGAGACTAACCTACAGG
One_4a.40410-31	A	C	ATTCATTAATATTT	ATTCATTCATATTT	TGCAGGACAACAGAGGATGG	(0,0)	1	AGCCTTCACACTGCACCTTT
One_4a.41625-38	C	G	CACTTAACACACAA	CACTTAAGACACAA	TGCAGGCATCAAAGGGGAC	(0,0)	1	CCCTGATCACTGTGTCTGTGA
One_4a.43537-65	A	T	TTAAAAGACTTAAC	TTAAAAGTCTTAAC	ACGCAGCACACAGATGGTTA	(0,0)	1	TGTGTAACCATCTCCTTGCTGT
One_4a.44564-40	G	T	GCTGAGAGGGCAGT	GCTGAGATGGCAGT	TGCAGGAGTGAAAATAGATTCGT	(0,0)	1	TCTAGGTAGCCTATGTGTTCAACA
One_4a.46542-38	C	T	ACATATCCCTCTAC	ACATATCTCTCTAC	GCAGGTGGCAGATAATTGTAGT	(0,0)	1	CCTATTACCCCTGGTTGGCA
One_4a.47407-42	C	T	CCAACAACGCACAC	CCAACAATGCACAC	AGGAACATGGTGCATCCTGG	(0,0)	1	ACTGTGTGTGTGTGCGTACA
One_4a.47733-44	A	C	ACCTCCAAACTCCT	ACCTCCACACTCCT	CTGACCACCCTCCTCAAACC	(0,0)	1	GGTATGTTCAGGGCCCTGTC
One_4a.5042-49	C	T	GAAGCATCGGGGAT	GAAGCATTGGGGAT	GGGGCAAGGGAAAAAGAGGA	(1.3,0)	1	TTGCCCGTCCAACATTTCCT
One_4a.51425-41	C	T	GAACGAGCTGCGTG	GAACGAGTTGCGTG	GATGAACACGGCGCTGAAC	(0,0)	1	AGGGTGTCCAGCACAACATC
One_4a.52596-64	A	G	C.TTCAGACTTCGG	C.TTCAGGCTTCGG	TGCAGGGAACAAAGGTGTGA	(0,0)	1	GCCTTACTCGGCCCGAAG
One_4a.53531-43	A	G	CCGTGACACTTATT	CCGTGACGCTTATT	TGCACTGCAGAGGAGGGG	(0,0)	1	AGAGACGATAGCAGCAACATT
One_4a.58187-48	A	T	AGGTCAAATTCCTG	AGGTCAATTTCCTG	TATCTGGGCCTGGAGGAGAG	(0,0)	1	AGATGGCTCAGCTGAAGCAA
One_4a.59326-51	A	C	CAATACAATGGGTA	CAATACACTGGGTA	GCAGGACATAAACTGGGCCT	(0,0)	1	GCCTGTGTATGCCCTACCC
One_4a.63494-55	C	G	TGTCCAGCGTCACA	TGTCCAGGGTCACA	GCGTCACTGCTTTGCTGTTT	(0,0)	1	TCCCTCTCCCAGAATGCAGA
One_4a.63914-64	G	T	GGCTACTGATAAAG	GGCTACTTATAAAG	CACTGTTGAGAGCCGTCACT	(0,0)	1	TGGGACTAAGTTAAGAGAGTGTGT
One_4a.6566-43	G	T	TGTAACAGGACAAA	TGTAACATGACAAA	TGCAGGTGTCTCAGAGGGAT	(0,0)	1	CCATACCCCCTACCCCTTATCA
One_4a.67550-44	C	T	AGATAGACCTGCAA	AGATAGATCTGCAA	GTGAAGAGCTCTGCCTCCAG	(0,0)	1	GCCTGAGGTCTCGTACGATG
One_4a.7119-57	A	C	TCAGAAAAAGTGAC	TCAGAAACAGTGAC	TGCAGGGTAAGTTTGAATCAAAA	(0,0)	1	CCCCCAGACCATAAAGCCAC
One_4a.84616-28	A	T	AGTATCAAGTCCTC	AGTATCATGTCCTC	TGCAGGACGGAATACAGAGT	(0,1.3)	1	AGGCAGGAGGACATGATACT
One_4a.9496-33	A	C	GATTGTCAGAGCTA	GATTGTCCGAGCTA	TGCAGGAGAAGCTTAGCAGG	(0,0)	1	GCTGAAGAACATGCTTGGCC
One_ACBP-79	G	A	CAGAGGTCATGGTTCTA	CAGAGGTCATAGTTCTA	GAGGTGTGGGCTGACCA	(0,0)	1	TCGACCGCTGGCAGTG
One_agt-132	A	C	ACAGGAAAATCACGAGCCT	CAGGAAAATCCCGAGCCT	GACCCAGATCAACAACTTCATCCA	(0,0)	1	TGGTTGAGCTAAGGTCCTTGAAC
One_aldB-152	A	G	CTCAGGCATTACCTTC	CAGGCATCACCTTC	CGATCAGGTGACGCTAAAATTAACTC	(0,0)	1	GTGGCTTCCTCTTCACTCTGA
One_apoe-83	C	T	TTTAGACGGCGGTCTC	ATTTAGACAGCGGTCTC	CGCCATGGACAAGGTCAAG	(0,0)	1	GGCACAGTGCTTCCAAACC
One_CD9-269	C	T	TGGAATGGAGAAATC	ATGGAATGAAGAAATC	ACGCTCTGAGGTGATATGAAACAC	(0,0)	1	CATCCGACGTCAACATCCAAAC
One_cetn1-167	A	C	TTGACGAAGCAGACCGA	TTGACGAAGCCGACCGA	CAGAAATCCTGACTGTTAAAACAATGCA	(0,0)	1	CTGCTCGTTGATCTCTCCATCTC
One_CFP1	C	T	TGCAGTTCAACATCAA	CTGCAGTTCAATATCAA	CGCAGGTCAAAGTAGTACTTAGCAT	(0,0)	1	GAGCGTCACTTCCTGGAACTT
One_cin-177	C	T	TCACGCACGGGACAG	CACGCACGGAACAG	CCTCAGACTAGTGACCGTACCTA	(0,0)	1	CGCTCACCGTGGTTACGT
One_dds-529	A	G	AGCAATCCCATCTCTC	AGCAACCCCATCTCTC	CATAATGCTCCCCATCTTGAATTGG	(0,0)	1	CACTCAGCCCTTTAGGGAAGA
One_DDX5-86	C	T	AGGACTTCCTGAAGGAC	AGGACTTCCTAAAGGAC	CTCCCACATTGATCTGGACGTA	(0,0)	1	TGCCACTTGGCCCAAAGAG
One_E2-65	C	T	CATTGTCCCTAGGAAAG	ATTGTCCCTAGAAAAG	GTGGCACCCCCTTTCTCT	(0,0)	1	TGCAAACCTCAGTGGAGAACC
One_gdh-212	C	A	ATCTGTTACCAGAATGTTT	ATCTGTTACCATAATGTTT	CCTGTGTTGAAGTGGAGTAGGTTAA	(0,0)	1	GCTTTATACTGTAAGTGGACTGACCTT
One_GHII-2165	T	A	CACAAATGGAAATTGA	CACAAATGGTAATTGA	GGCATCAACCTGCTCATCGA	(0,0)	1	TGCACAAAGTGCGGCAC
One_ghsR-66	A	T	AGGTTAAGCTGTGTATAAGT	TTAAGCTGTGAATAAGT	TGTAACAATACAAGGATAATGCAAATAATGTAGGT	(0,0)	1	GGTTATTAGGTTACTGTGCTGACTGT
One_GPDH-201	T	C	CTTCACCCCTGGAGCC	CACCCCCGGAGCC	GAAGCTGATCCTAGACCTGTACCTA	(0,0)	1	TGGTATGATGGTGCTACTGGAAGT
One_GTHa	A	G	CAAGAACTAGAATGAAACAGA	AAGAACTAGAATGGAACAGA	CAAGAAGAATCAAGAGAAAGAGAGATGGT	(0,0)	1	CCTAGTGTCATGCACATAACGTGTA
One_HGFA-49	A	T	CTAAAGCACCATGTTGC	ACTAAAGCACCTTGTTGC	ACTTGCTACTTCAGGGTTTTTGTGA	(0,0)	1	TGGCAGAACAATTCCTCAATGCATA
One_HpaI-99	C	T	AACGGAAGAAACCCCTCAA	AACGGAAGAAACTCCTCAA	CCTGAGTTGTGTTCAATGGGCATAA	(0,0)	1	TGGGTCATGTTCATTAGAGCACAAA
One_hsc71-220	C	A	ATTGGCCACAGCGC	ATTGGCAACAGCGC	ACAGCGAAACTATTGATTTAAGGCTCAT	(2,0)	1	CGCAGGTAAATCACTGATCATGTTT
One_Hsp47	A	G	TTATTGACTATGGCACATTG	TTGACTATGGCGCATTG	CGTTCAAATAAATGCTGTTTGGCCTTT	(0,0)	1	GTGGTGTTCGGATTTTTCCTGAAA
One_IL8r-362	C	T	CAGCCAAAGAAGAGTC	AGCCAAAAAAGAGTC	TTGCTAGAAGCGTTGGTTATGATGA	(0,0)	1	CAGCAAAATTGAGAAGTCACTAGGAAAA
One_ins-107	C	T	TACAGTAGTCCATACAACATA	ATACAGTAGTTCATACAACATAT	TTGAAATGAATGTGAAGGCA	(0,0)	1	GAACCCTGCAAGAGGAGAA
One_KCT1-453	G	T	TGGTCAGGGTATCGCCATA	TGGTCAGGGTATCTCCATA	GGGAAAGTATGCTGTGGGATCAG	(0,0)	1	GGTTCCTCAGTGAGTGTTCTCTATG
One_KPNA-422	A	G	CTGGTATGAGAAGGCACA	TGGTATGAGGAGGCACA	TGGGCCCTGGGAAACATC	(0,0)	1	CCATAGCCACTTTCGATACAGGTAA
One_LEI-87	A	G	ACTCGCCACCTCTGT	TCGCCGCCTCTGT	ACAGCGCATCCCCATAATGG	(0,0)	1	GCCTTTGTGGAGGTCAACGA
One_lpp1-44	C	T	TTGTGCTTTCCTGACCTAT	TTGTGCTTTCCTAACCTAT	GGTCCAATAGGGAGCTCAGACA	(0,0)	1	GGGAATGAACCAGACATGTGAATG
One_LRRC9_68810	T	G	CTTGGATGAAAAATATCA	CTTGGATGAAACATATCA	TGCAGGGAAATTACTTATGTGATCAT	(0,0)	1	AAGACAGATCAGTCCGCAGAAAA
One_MARCKS-241	T	A	TTGCTTAAAAGGTCTTCC	TTGCTTAAAAGGTCATCC	CCTATCACAGCTTGGTTGAGTTCAA	(0,0)	1	TCCACCCGCTCATTTTTGTAAGAT
One_metA-253	C	G	AGGCAATTGAGGTTAAT	AGGCAATTGACGTTAAT	TTCTTATCGCTGGTGGCACTTT	(0,0)	1	GACCAAAGACTATTTAGTTGCCACCTA
One_Mkpro-129	A	G	ATGCATATACATGTAATATAT	TGCATATACATGTAACATAT	TGACGTATGTGCAATGCATGTCTAT	(0,0)	1	AGATGAAGGACATGGCTGAAAACAT
One_ODC1-196	C	T	CCACCTCCGATGTCC	CACCTCCAATGTCC	CCGAGGTGGGATTCAACATGAC	(0,0)	1	TGTCCTCAGACCCAGGGAAA
One_Ots208-234	-	A	CACACGTTACATCAGATAACT	CACACAATGTTACATCAGATAAC	CAGCCGACATGCATCAGTTA	(0,0)	1	TGACCCCATGTTTCATGCT
One_Ots213-181	T	A	CTTTGAATTAAAAACATTTTT	CTTTGAATTAAAAACTTTTTTT	CCATAGTGTATCACACAATACTCATGTCT	(0,0)	1	TCTATCATCTGCAAATCTGTGTACTAGACT
One_p53-534	C	A	TCCAAAGATCTGG	TCCAAATATCTGG	GACAATCTTAAAGCGGTGGTCTTG	(0,0)	1	AACCTTTATCAGCCATCATCCAACT
One_pax7-248	C	A	AATTCAAAACGAAATGTG	TGAATTCAAAACTAAATGTG	AGTAAAGGTAGTGATGCAATGATGCA	(0,0)	1	AACCGCATAGGACGTAAAGCA
One_PIP_3	C	T	AACACACATTTCTCAACACA	ACACACATTTTTCAACACA	ACAGAGTCAGGACTTGATATGTACAGA	(0,0)	1	CCTGACGAGGGTCTACTACACT
One_Prl2	G	T	ACCAATGGGACGAGTG	CCACCAATTGGACGAG	ACCTCTCTCTCTCTCAGGACTCTCA	(0,0)	1	GAGGAGGTGTGACACATAGATGGA
One_psme2-354	A	G	TGATGCAGTAGCTAAAG	ATGCAGTGGCTAAAG	TGGTCCTTCAGGTACTTTTCAGAGA	(0,1.8)	1	CAAATGCCAATTCTCACCACATGA
One_rab1a-76	G	T	TGTGGAGCAAGGTAACT	TGTGGAGCAATGTAACT	TCGCCATATTCTCTCTCCCTATCC	(0,0)	1	ATCCACTCAGACCCATATCTACCAA
One_RAG3-93	C	T	CATTTTGGACTTCGGGACC	CATTTTGGACTTTGGGACC	AGATAAAGATGGTTTCAAAGTCACCCA	(0,0)	1	GGGCTGCCATCTAAAAAATATTGCT
One_redd1-414rd	A	G	CCTAAGTCAGTCACTGTAG	CCCAAGTCAGTCACTGTA	GTTGGCTACATCCTAAAACACAATGG	(0,0)	1	CAGCCCTGGAGTACTGAATCAG
One_RFC2-102	A	G	ATCACGTTGTATTTCTTT	CACGTTGTGTTTCTTT	TCCAGGAGCTGCATTTTGAGTTAAA	(0,0)	1	AAGGTGGATGACAATGTGTTAGTGT
One_RFC2-285	A	T	CACGACATCTAAGCTGAA	CACGACATCTATGCTGAA	GGATGAGGCTGACAGGTAAGTC	(0,0)	1	ACAGTCGTTATAGGTACAGGTACACT
One_RH2op-395	G	T	TGGGAACATCATTTTTTAA	TTGGGAACATAATTTTTTAA	GCTGCTAGGTCAAACTCGAAGAG	(0,0)	1	CAGCCTTGTTCAACCCCATTATCTA

One_rpo2j-261	G	T	CACATGTTTTACTCATTTGA	CACATGTTTTACTAATTTGA	GATTCTGAGATCATACAGTGGATTGGT	(0,0)	1	GCTTGTCATCTTTCAGCACATACCTA
One_sast-211	G	T	CATCATTTGCATTATTG	CATCATTTGAATTATTG	TGTACTTAGTCCAATAAGCATTTCAACAGT	(0,0)	1	TGGCTAGATTCACATGGTCAACAAA
One_Six6-3	A	C	TAATATTTACGGAA	TAATCTTTACGGAA	AGGCTACCCTATAGTTCAGTTACC	(0,0)	1	GGCTACAGCGTTTATGGTGTC
One_spf30-207	G	T	AGGGACATCTTACCTCAAAA	AGGGACATCTTACCTAAAAA	AGCATTTCAGTTTTGTACATTTACAGTAAAACA	(0,0)	1	ACCTACTCGTAATTTCAGGGCAAAA
One_srp09-127	T	A	CAGCGAAGGATATGCT	CAGCGAAGGTTATGCT	CGGAGCTGGAATGACGACAT	(0,0)	1	AGGTTCAGCAAATCCCTCTTTAGAG
One_ssrd-135	-	T	CTGCGGCTTTGTCTTG	TGCGGCTTTTGTCTTG	TGGAAACTCCTAGTGTACTTCATTCTCA	(0,0)	1	CGTTCCACGCTCCCTAGAATAGA
One_STR07	G	C	ACGCACACTGTCCTT	ACGCACACTCTCCTT	CACACCTGAGGCACAAGCT	(0,0)	1	GTATGTCTACCAGAGAGGTCAAGGA
One_SUMO1-6	C	A	CAAGAT[AT]GAAATTGGTTTGC	CAAGATTGAAATTTGTTTGC	GCACAAGCCAAAAAGTTTTCTCCAT	(0,0)	1	GGACATAGTTGGAGGCAGACAAAA
One_sys1-230	T	G	CAAAGCAAGTGATATATTAGTG	AAAGCAAGTGATATCTTAGTG	CTACCTGTCTAACAGTGAATGCTAACTT	(0,0)	1	TGAAACCATTAAGCTCTTTGTAGGACAA
One_taf12-248	G	T	CCAGACAAAATCAAATTA	CCAGACAAAATAAAATTA	ACCTTCAATATGGTGGTGGTTACC	(0,0)	1	ACTAAACGCACAACAGCAAACG
One_Tf_ex11-750	G	A	CAGGGTCGCTGCAC	CCAGGGTCACTGCAC	AGCAGGTGTAAGCATGTGTACTT	(0,0)	1	CCTGCTCTGCCTCAACAATGTTAA
One_txnip-401	C	T	TGACTGCACTAGTTTAGAC	TGACTGCACTAATTTAGAC	GCCAGATCCCTTCAGTTGGA	(0,0)	1	GGCCATTTCAAAAGGCTGCAT
One_U1003-75	C	T	AGAGACTACTTCCTTTTTG	AGAGACTACTTCTTTTTTG	TCACGAGCCCCAGTCAGA	(0,0)	1	CGGGTTTCGGTGGTTTAGTATTCTA
One_U1004-183	A	G	AAGTTCCCTGTATTTCTT	TCCCTGCATTTCTT	GGTGTGACTGCTGTGTTTAATTGC	(0,0)	1	ACCATCATTACACAGCAATTCTGAGT
One_U1009-91	A	G	CATGTTCTGTATGGACCC	TGTTCTGTGTGGACCC	CTCTGTCCTTGAACTGTTGTCTGTT	(0,0)	1	GCCGCTGCTACTCTTCCT
One_U1010-81	A	G	CACACCAACGTTATGTAGAG	CACCAACGTTGTGTAGAG	CAGCCCCTCGAGGTAACTG	(0,0)	1	GTTGAGACAACAAAACGTCTACTGT
One_U1012-68	C	T	TGACGGGTGTTCCTGATAA	TGACGGGTGTTCTTGATAA	TCTATTACCATACAGGCCCAGTACA	(0,0)	1	CCTTTTGTGTCTTCCAGTCATGTGA
One_U1013-108	G	T	ACGGAATTCCTGTTGCCCT	ACGGAATTCCTTTTGCCCT	TCTGTGCTCTCCTCCAGGAT	(0,0)	1	CGAAACTGAGGAGTGCTCTGA
One_U1014-74	C	T	TTGACCTGCGCCAGTAT	TTTTGACCTGCACCAGTAT	TCCCCTGCAGCAACTGTTTT	(0,0)	1	GGCAGAGACGGCATCCT
One_U1024-197	G	T	ACCTGACCCAACAAA	ACCTGACACAACAAA	CTGAACTGATCTACCGCTCTGT	(0,0.5)	1	GGAACAGATACTCCAGGAGAGATGA
One_U1101	C	A	TGGACGTATGTCATATTT	TGGACGTATGTAATATTT	CTATGACATGTTTATTTTAATTAGCCACCAACT	(0,0)	1	AGTATAGCTAGGGAACCTTTCGATCTT
One_U1105	T	A	CCTGTTTTTTTTAAAAGAC	TCCTGTTTTTTTTTAAAGAC	GCCTTAATAGTGTCTTCTGATCCCTTT	(0,0)	1	CCCTCTGTTGTCCAGACTCTTAG
One_U1201-492	A	G	AAGACTTCCTCCAGGCTC	ACTTCCCCCAGGCTC	GCTTATGACGGAGAAGAGATGCA	(0,0)	1	AGGATACTGAAGCCCAGAGACA
One_U1202-1052	T	C	CAAACTTTTTCATCTACATTTA	ACTTTTTCATCCACATTTA	CGATTTGAGTCTCCAATGGTCTCT	(0,0)	1	ATTCCTATGGTTAACATCAATTCTATAAAGTCAT
One_U1203-175	G	A	CCATAGTTGCTGGGCTT	CTCCATAGTTACTGGGCTT	CCCGGAGACATACTTGATGCA	(0,0)	1	GGAGGACCTGCAGGATCAC
One_U1204-53	C	T	ATGCATACACGCTGATGC	ATGCATACACACTGATGC	GTAAAACCCTTCATGTTGGCCATT	(0,0)	1	CTCCATGTCTGAATGTCCCATCA
One_U1205-57	A	G	AGTTATCATGGTCATCTCT	AGTTATCATGGTCGTCTCT	AGTAAATGGTTATTCACGTAACGGATAAG	(0,0.8)	1	CAGGACAGTTCCACATTCTAACAGA
One_U1206-108	G	T	AACATTGAGCTTCCC	ATAACATTGATCTTCCC	CTGAGATGGTGCTTTCTGAGGATA	(0,0)	1	TGGATGAAAGGGAAATTCTGTCAACA
One_U1207-231	C	T	ACATTCCTTGGCATTGC	CATTCCTTGACATTGC	GGCCAAACTGACAGGGATCTATTAA	(0,0)	1	GGGTCCAGTCTGTACACCATCTAT
One_U1208-67	A	C	CCCAATGTGATTGTCAC	CCAATGTGCTTGTCAC	ACTTGAATGTCTGTTTCGTAGGTGAT	(0,0)	1	ACACAGTTGACAGTGGAGCAA
One_U1209-111	C	T	CTCACATCGAGATGATC	TCACATCGAAATGATC	GTCACGTAATCACGAGAAAGATACTAAATGT	(0,0)	1	TCTGCGTCTCCAGAGAGGTT
One_U1212-106	A	G	TTTTGACATACAAAAAATA	TTTGACATACAGAAAATA	CGTAATGACCTACCACCATATCAGT	(0,0)	1	TGGCATGACTTTAACAATTCCCAAAAAA
One_U1214-107	A	C	TAGTGACCTATTAAATTGC	TGACCTATTCAATTGC	CCAAATGTACTCCATGTTGGTTAGC	(0,0)	1	TGCCTGAGTATTAAGCTATATCATTGAAGTTTT
One_U1215-82	A	C	AATGAGACAAAGTATTTGGT	AATGAGACAAAGTCTTTGGT	GTTGCTTGGTTTCGTTTGGAGTAG	(0,1.9)	1	CTCCAGAAGAGGAATACCACAGTTC
One_U1216-230	A	T	CCTGGCTACTAAGTAAC	CTGGCTACAAAGTAAC	TGGGATCGGACGTCAATAGATTTC	(0,0)	1	GTAATACAGAGTGAGCGTGATACATTGT
One_U301-92	T	G	CCATGGATTAAAATATTT	CCATGGATTAAACTATTT	AGCCAGTAGCCGATAATGTTTGTC	(0,0)	1	CCCCTCCCAAATTGCTAGCT
One_U401-224	C	A	CACCTGGAAAGGACTGA	ACACCTGGAAATGACTGA	GGGTGGAGACGAACGGATTC	(0,0)	1	GTACGATTTTTTTGTAGCCCCAAGT
One_U502-167	A	G	CTTCTTGATCAATAACG	CTTCTTGATCGATAACG	GCTTTTGTGCAATAGCTATGTTGCTTA	(0,0)	1	GCAAAGGTAGGCAGCAGATTG
One_U503-170	T	G	AAGTACTAAAATC[AT]GTTTTACATTG	TACTAAAATCAGTTGTACATTG	GATTCAGAATTGCCACGACAAAGAA	(0,0)	1	GTGATTGGTACATGTCTGTCGAGTT
One_U504-141	C	A	TCAAGGACACAAACAA	TCAAGGACAAAAACAA	GCTATAGCTCACAGAGGATCCCA	(0,0)	1	TATTGGCGGGTGAGGGATG
One_UCA-24	C	T	CGAACAGGGCTGGATG	CGAACAGGACTGGATG	AACTCTGCGTCTGTCTGCTT	(0,0)	1	TCAGATGGTTCATTATGACAGCAACAGC
One_vamp5-255	C	T	TAGGCTCCGTGCTCAGT	TAGGCTCCGTACTCAGT	GGTTGACTTTTCTTAACTTTTTAATCTGTGATATTGT	(0,0)	1	GCTGAGCTAGTGATGGTACCATTT
One_vatf-214	C	A	TGGTATTACTGTGCATTGAC	ATG[CG]TATTA[AC]TGTTCATTGAC	TCATTCCTTTGCCTGGAGCATT	(0,0)	1	GGCATACAGCAAAACAATTCAACCA
One_VIM-569	G	A	AAGTGTTTCCATACTCACTATA	AAGTGTTTCCATATTCACTATA	TTCTGGGTGGACTCATTGATCAC	(0,0)	1	ATGCGTTATACCTGTAATCTGCAAGT
One_ZNF-61	C	A	CTATGGACATGATCTTT	TTCTATGGACATTATCTTT	CCATTCATGTTCTATTCAGATATATTTTGTGCA	(0,0)	1	CCTAGCTAGAGCTCAACAATATGCA
One_Zp3b-49	C	A	AGGCCCAATCCTT	AGGCCAAATCCTT	TCCTCGTGGTTATAGTTATAAAGATGTCAGT	(0,0)	1	TTGGCTCTGCACTCGGTTTA
Ots_ARNT-29	A	G	GTGCTAGCTAC	GTGCTGGCTAC	CCACTGGCTGTGGAGCTT	(0,0)	3	GGGTTCAGTGATAGTTGGGCAAAT
Ots_ARNT-29c	A	C	GTGCTAGCTAC	GTGCTCGCTAC	CCACTGGCTGTGGAGCTT	(0,0)	4	
Ots_crRAD9615-69-19	T	A	GGGAGTGGGAG	GGGAGAGGGAG	GAATGCAGGGCCAGGGAG	(0,0)	3	ACTCCCAGACCATCCAGCT
Ots_crRAD9615-69-50	A	T	CTGGGAGGAGA	CTGGGTGGAGA	GAATGCAGGGCCAGGGAG	(0,0)	4	
Ots_myo1a-384-36	C	T	CACCACTACCA	CACCATTACCA	CTCCCCCCTGGACTTTGG	(0,0)	3	GCTCTATTGCACCGTGTTCTG
Ots_myo1a-384-57	C	T	CTGCAGAACAC	CTGCAGAATAC	CTCCCCCCTGGACTTTGG	(0,0)	4	
Ots_P53-25	G	T	TTCTGCAGGGG	TTCTGCAGTGG	GGAACTTCCTCTCCCGTTCTG	(0,0)	3	GCACACACACGCACCTCAA
Ots_P53-28	G	C	GGGCAGCTCCT	GGCCAGCTCCT	GGAACTTCCTCTCCCGTTCTG	(0,0)	4	
Ots_P53-40	T	C	CTCCTGGGTCG	CTCCTGGGCCG	GGAACTTCCTCTCCCGTTCTG	(0,0)	4	
Ots_unk9480-51-38	T	C	TCCCASAAACT	TCCCASAAACC	CAAATCAGAACAAAACCTCCCACAA	(0,0)	3	GGAAGTCTGTCTGAATGGTTGTCTT
Ots_unk9480-51-39	C	A	CTAAGGAGACC	ATAAGGAGACC	CAAATCAGAACAAAACCTCCCACAA	(0,0)	4	

Appendix 9. GT-seq SNP panel for Coho salmon

Assay	A1	A2	A1-Probe	A2-Probe	FWD Primer	Corr	Flag	Rev Primer
Oki_101419-103	C	A	CTACTTGCCTGTCT	CTACTTGACTGTCT	CCCAATTGGAGACCAGGGTT	(0,0)	1	TCATTCAGACAGTTGGGAGACA
Oki_101419-103-27	A	C	AATCCACTTCC	AATCCCCTTCC	CCCAATTGGAGACCAGGGTT	(0,0)	4	
Oki_101419-103-44	T	C	GTTCTCCTACT	GTTCTCCCACT	CCCAATTGGAGACCAGGGTT	(0,0)	4	
Oki_101770-525	C	A	ATTAAGTCATGTGT	ATTAAGTAATGTGT	GCACTCCTCTGCACTCTGTT	(0,0)	1	ACAGGGCCCTCTTCCTTAGT
Oki_102195-92	A	G	AAACATGAGGAAAA	AAACATGGGGAAAA	ACACTTGATTACCACTGCGT	(0,0)	1	TGCACTGTTGACAATGTGCA
Oki_102213-604	C	T	AGGAAAGCATTTTC	AGGAAAGTATTTTC	CTGTGTCGTAACAGGTAAGGA	(0,0)	1	ACACAGCAGGTAAGGAGAAGT
Oki_102267-166	A	T	ATGTGGAAGCCGCT	ATGTGGATGCCGCT	GACAGCCACGCAACAAGTTT	(0,0)	1	AAGTAACTTGTGCTAGCGGC
Oki_102457-67	C	A	AAAGGTTCAAGTAA	AAAGGTTAAAGTAA	TTCAAAGTGGCCAATGCTTG	(0,0)	1	GGAGGCCCTACCAAGACATT
Oki_103271-161	A	G	AGTTATGACAGATT	AGTTATGGCAGATT	AGACAACTAAGCAACCTCTGAGA	(0,0)	1	TCATCCAGCGCTTGCAAATG
Oki_103577-70	A	T	ATGTGAAATGTGGA	ATGTGAATTGTGGA	AGCGAGAGGGCCTACAGTTA	(0,0)	1	CACATGAAGAATTTCCCTCCACA
Oki_103713-182	A	G	TGAAATGAAGATAC	TGAAATGGAGATAC	CACCAAGGCAGAGAGCTCTC	(0,0)	1	TTGTGGCACCAATCTACTGT
Oki_104515-99	T	G	CAGACTTTGGGCTG	CAGACTTGGGGCTG	TCCAGCCAGTCCATTCAGAC	(0,0)	1	AGCTGAAAGTGAACGAATTACGC
Oki_104519-45	C	T	TTGATGACGCCGCT	TTGATGATGCCGCT	TGAGAAAGAGGTGTGAGCGA	(0,0)	1	CCCAAATAGGAGGGGCTGTG
Oki_105105-245	T	G	ATGTAACTCTCAAA	ATGTAACGCTCAAA	GCGTATCAAGCATCAACGCC	(0,0)	1	TCTTTCAGCAAGGTTGGGCA
Oki_105105-245-23	T	G	GCCTTTTCCAT	GCCTTGTCCAT	GCGTATCAAGCATCAACGCC	(0,0)	4	
Oki_105105-245-56	G	A	CTCATGCCCAA	CTCATACCCAA	GCGTATCAAGCATCAACGCC	(0,0)	4	
Oki_105115-49	T	G	CTTTAAGTTATTTC	CTTTAAGGTATTTC	TCGGGTAACACTTTCGTAGCT	(0,0)	1	GCGTTGAGGTGACATGTAGC
Oki_105132-169	C	T	CACGATGCACTGAG	CACGATGTACTGAG	TGCCCTGAACCACATGTCAA	(0,0)	1	TGGAATAAAAACCTGCAGACACTG
Oki_105407-161	C	T	CAGCCTTCGTTTGT	CAGCCTTTGTTTGT	GCAGCAGCTCACAGCCTT	(0,2)	1	TGTCCTGACAGCCTATAGGAT
Oki_106172-60	C	T	AACCCTCCATCGTG	AACCCTCTATCGTG	ACTACTTGGCGTGTGTGTGGG	(0,0)	1	TCCACTGAGAGGATGAGGCA
Oki_106172-60-38	C	T	GTGCGCATCAA	GTGCGTATCAA	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_106172-60-47	G	A	AACGCGCTGAC	AACGCACTGAC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_106172-60-47c	A	C	AACGCACTGAC	AACGCCCTGAC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_106172-60-53	C	T	CTGACCGCYGC	CTGACTGCYGC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_106313-353	A	G	ACTTACCAACTGTT	ACTTACCGACTGTT	TCCCCATTACAATATGTCCCTGAC	(0,0)	1	TGAGTTTTCCAAACCCTGTGTG
Oki_106419-292	T	G	CTAAAACTGAAAGG	CTAAAACGGAAAGG	TGCATCTGTAAGTAGCTCTGGA	(0,0)	1	AGTCTACCATTCTACAAGTTCCTT
Oki_106479-278	A	G	ACTACACAGATGCA	ACTACACGGATGCA	CCCTCTAGGTCTTTAGCAAACACT	(0,0)	1	TCAGTCATTTGTTTACGTGCTGT
Oki_107031-314	A	T	TTTTTGTATTTACT	TTTTTGTTTTTACT	AAAAACAGCCAGCGAAGGGA	(0,0.6)	1	TGTCCTCAGCTACACACGAG
Oki_107607-213	A	G	CTACATCACTGGAG	CTACATCGCTGGAG	TGCGTTGCACCTGATCTAGA	(0,0)	1	AGGTAAACCGCGTTCCATGT
Oki_107974-46	A	G	CTGCGCCACTGGTG	CTGCGCCGCTGGTG	AACTGGCAGACCTCGAACTG	(0,0)	1	TCATTGACATCTACGGCGCG
Oki_109525-359	A	G	CATTGGTAAGTTGT	CATTGGTGAGTTGT	CTTCCAGACATCACGCCTCA	(0,0)	1	TGAGCAGCAAGTCCTACACC
Oki_109651-152	A	T	TTTTTTTAAAGCTA	TTTTTTTTAAGCTA	GGCTGTTGTCATATCATCCCG	(0,0)	1	GTCTACACACAGCCCAGGTT
Oki_109894-418	C	A	CTGGTTGCTTGAAC	CTGGTTGATTGAAC	GGAGGTACCAGGTGAGCTCA	(0,0)	1	GACCAGACCATAGACATTGCCT
Oki_110078-191	T	G	TACACTCTAATGTC	TACACTCGAATGTC	ACACACACACTCGCTCTAGC	(0,0)	1	ACAGTGTTCTGAAAGGGCCA
Oki_110381-77	A	G	GGGTTTAAGATACG	GGGTTTAGGATACG	TGAAACGTCCCCAACTTCCC	(0,2)	1	ACCTCATGGACGATGCCATC
Oki_111312-141	C	A	AAAAAATCATAAAA	AAAAAATAATAAAA	GGGAGGGCTAAAAATACAGACCA	(0.3,0)	1	CTGGGGTCCTATTGCTACTGT
Oki_111681-407-38	C	T	AGAAACTGCAA	AGAAACTGTAA	TTCATCCCATTGGAAGCCCC	(0,0)	3	
Oki_113457-324	A	G	CTCTGTGACTCGTT	CTCTGTGGCTCGTT	TTACTGAGGTGGTCCAGGCT	(0,0)	1	ACCAGCAACTCTTTCCTCCC
Oki_114250-187	T	G	CGA.TAGTTCTTTT	CGA.TAGGTCTTTT	GGCGATTCAGAGCAGGTCAT	(0,0)	1	TGGGAAATGTGTTGAATGTCCT
Oki_114448-101	C	T	CACTGCACCCGTCA	CACTGCATCCGTCA	ATGTTCGATCAACCACTGCA	(0,0)	1	CCTCCTGCTGGACTAGGCTA
Oki_114587-309	T	G	TTACTATTCATTTT	TTACTATGCATTTT	GTCACAAATGATCTGCAAAACACA	(0,0)	1	ACCAGGTGAGGGGTTAACCA
Oki_116362-411	A	T	TTACACAAAACATT	TTACACATAACATT	GGATGCAGGTGAGGGTTGAA	(0,0)	1	AATTCCCACCTTGCCTGCTA
Oki_117043-374	C	T	AGGACACCGATAAC	AGGACACTGATAAC	TTCCTCTTAACCACCGCAGC	(0,0)	1	ACCAAGACTATGCAAGGCCC
Oki_117742-259	C	T	GTCTGCACGTGGAC	GTCTGCATGTGGAC	GAGACTTCTGGTGGCGTCTG	(0.3,0)	1	TGCAGAACTCCACTGAGACG
Oki_118152-314	A	G	TTTAGCTATCTACT	TTTAGCTGTCTACT	ACGGTACAAACAGGCTCACA	(0,0)	1	CTCCAGAACCTGTTGTTGGGA
Oki_118654-330	C	T	ACACCTCCGACCAG	ACACCTCTGACCAG	TCCTTAACACTGTCCGACGC	(0,0)	1	TTGCTGACCTGGTTGAGGAC
Oki_120024-226	T	G	TTGATTATAGTTTC	TTGATTAGAGTTTC	ACCATAATTTCACAAACGAGGCC	(0,0)	1	AGCAGAGGTCGAATGAACGG
Oki_120255mod-99	A	C	GACTAAAACGT	GACTACAACGT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	3	
Oki_120255mod-105	C	T	AACGTCAGTTA	AACGTTAGTTA	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-113	G	A	AGTTACTGG	AGTTACTAG	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-115	G	T	TTACTRGGGTA	TTACTRGTGTA	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-119	G	A	GTAGYTTCWTG	GTAAYTTCWTG	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-120	C	T	CTTCWTGGCAT	TTTCWTGGCAT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-133	T	C	TGGCATAGTC	TGGCATAGCC	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-135	A	C	GGCATAGYCAT	GGCATAGYCCT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_120255mod-137	A	T	ATAGYCMTAGAT	ATAGYCMTTGAT	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	

Oki_120255mod-141	A	G	ATAGYCMTWGATA	ATAGYCMTWGATG	GGGTAGGCTAAAACTAAATTACTCAAA	(0,0)	4	
Oki_121006-412	C	A	CAAAAACCTCAACC	CAAAAACATCAACC	AGGCAGAGGACAGTGACTCT	(0,0)	1	TGCAGTACTCCAAGGGTTGA
Oki_122593-430	A	G	TCTCACCAGTCTTT	TCTCACCGGTCTTT	TCTGGGTAAAGTGTGCCTTTT	(0,0)	1	TCGATTCCAGGGTCTCAAAAGA
Oki_123044-68	C	A	TT.AAAACGTTTTT	TT.AAAAAGTTTTT	ACTGCCATATCAGTATTGGGGG	(0,0)	1	TGCTATGTTAACTAAACCGGAATCA
Oki_123921-90	A	G	ATTGTAAATTATCT	ATTGTAAGTTATCT	GGCGACGGAGATGAAGGTAT	(0,0)	1	CCAAGCCCTGAACCTTAGGG
Oki_124162-62	A	T	AGCAAAAATATAAA	AGCAAAATTATAAA	GAACTGCCAGGTGTCAGGTG	(0,0)	1	ACCTTTTTGTGCACTTTACATGT
Oki_125998-340	T	G	AACATACTGAGGGC	AACATACGGAGGGC	CGCAGGTCTTCTTCTAAGCAG	(0,0)	1	TCACTTTTATTCGTACAGGCCCT
Oki_126160-142	C	T	TTTGATCCTAAAT	TTTGATCTGAAAT	TGCTCACCAACACCTGTTTG	(0,0)	1	TCCGGTCACTCCCTTGTACA
Oki_126619-265	T	G	CGGATTGTGCACAC	CGGATTGGGCACAC	TGCGTAGTTAATTTTCACCTCGG	(0,2)	1	TACGCAGCACTGAAGACTGG
Oki_126619-265-31	A	C	GGATTGKGCAC	GGATTGKGCCC	TGCGTAGTTAATTTTCACCTCGG	(0,0)	4	
Oki_126619-265-35	A	G	CAGCACAGCTG	CGGCACAGCTG	TGCGTAGTTAATTTTCACCTCGG	(0,0)	4	
Oki_126619-265-50	G	T	GATTCGCCAGT	GATTCTCCAGT	TGCGTAGTTAATTTTCACCTCGG	(0,0)	4	
Oki_127645-235	C	A	GTGGCCTAAAAA	GTGGCATAAAAA	TTGGTTGGATCTGGTGCCTC	(0,0)	1	GCTACTTGTATGAACTTTGATCGCT
Oki_128302-547	A	G	AACAAATAGGGATG	AACAAATGGGGATG	AGCTGGAGGGGATTCACTGA	(0,0)	1	GGGATAAGAGGGTTTACAGTAAAGT
Oki_128693-70	C	A	AGAATTACATTTTC	AGAATTAAATTTTC	AGAGGTCAGGGGTCAAGAGG	(0,0)	1	CATGTCCCCACCAAACTGGA
Oki_128757-232	A	T	TTTGGGAAAGCTTT	TTTGGGATAGCTTT	TCAAAACGTTATTGTACGATGACCT	(0,0)	1	GACCGGGTGCAACACAAAAA
Oki_128851-185	A	G	TAACCAGACTCCCT	TAACCAGGCTCCCT	CTCCAGTCTCCCAGTTTACACA	(0,0)	1	GGCCCTCTCCTGGAGAAAAC
Oki_129870-552	A	G	TGCTATTATGTTTT	TGCTATTGTGTTTT	AGGGAGACAGGCTGACATCA	(0,0)	1	AGGAACAGAAATGTTGCGTCA
Oki_130113-304	T	G	TACAAATTTATCGT	TACAAATGTATCGT	GGGAGAGTGTTGGAATCCCC	(0,0)	1	CTTGTTCAGGGGCAGAACGA
Oki_130295-48	A	G	AAGCAATAAACAGT	AAGCAATGAACAGT	TGAGCACAAATATAAATGTGGCTGT	(0,0)	1	AGAAAAATATTCTGTGGTCCCCT
Oki_130524-184	C	T	CAGGAAGCTGACTC	CAGGAAGTTGACTC	CGATTGGTCGTTGGCATGAC	(0,0)	1	TGCTCTGCTGTGTGCTTACA
Oki_131147-353	T	G	AAAA.ATTTTTGGG	AAAA.ATGTTTGGG	GGCCTTTGTCAAAAGTAGTGCA	(0,0)	1	CCAGTCTCTTTGCGTCCCAA
Oki_131460-243	C	A	TTTCCTTCTACATC	TTTCCTTATACATC	GGAACAATCGAGCAAGGAGC	(0,0)	1	GCTTGGCCATGATAACCTCA
Oki_94903-192	A	T	AATTTAAAGTCAAT	AATTTAATGTCAAT	TCCAAACCGCATCGTAAAAGT	(0,0)	1	CCGACATATGTGAATGCGAGA
Oki_95318-100	C	T	TTGAAGGCTGTTAA	TTGAAGGTTGTTAA	CGCCTGCACTAAATATGTAGACA	(0,0)	1	GGGTGAAGTGCCCCTTTAAC
Oki_96158-278	A	G	CTATTGTAGGGTCG	CTATTGTGGGGTCG	CCACCTCGATCTCCTTTCGG	(0,0)	1	ACTGTCCAGTTTGTGACGGG
Oki_96376-63	A	T	GAGAGTTAAAAAAA	GAGAGTTTAAAAAA	CTGCTACGTGTTTGACAGTGA	(0,0)	1	TGTGGAACATGAACTCAAAACGT
Oki_97660-149	T	G	GGTTACATACAGGG	GGTTACAGACAGGG	CACTGGTCCGGTCCAAATGA	(0,0)	1	CTGTTACTCCCCAACCCTGT
Oki_99550-284	T	G	TGTTTCTTTT.TTT	TGTTTCTGTT.TTT	AGAGGTTGCAATTGTAAGTCTTGT	(0,0)	1	CTCACAGTGAGGGATCTCTTCT
Oki_afp4-10	T	C	ACAGCTCTATGGGC	ACAGCTCCATGGGC	ACCTTATCACCTCGGACCGA	(0,0)	1	TGAAAGCTTGTCGGGCTCTT
Oki_arp-105	C	T	GCTTGTGCAGTACT	GCTTGTGTAGTACT	TGGCCATTGACAAAGCAGGT	(0,0)	1	TTGCAGGGGAAACAAGAGCA
Oki_aspAT-273	C	T	AGTGGGGCACGGTG	AGTGGGGTACGGTG	ATGCTGGGAGAAACAGTGGG	(0,0)	1	CTCCTCTGTAAGGGGTGGGT
Oki_aspAT-273-37	C	T	CTGGACACAAT	CTGGATACAAT	ATGCTGGGAGAAACAGTGGG	(0,0)	4	
Oki_aspAT-273-45	T	A	AATCCTTAACA	AATCCATAACA	ATGCTGGGAGAAACAGTGGG	(0,0)	4	
Oki_bcAKal-274	T	A	AGTTCCCTTACTAC	AGTTCCCATACTAC	ACGGACACCACAAGTTCCC	(0,0)	1	GCAATCAAACTAAGGCCACACA
Oki_gdh-189	T	A	.ATTTTTTTCTGTA	.ATTTTTATCTGTA	CCTGTGTTGAAGTGGAGTAGGT	(0,0)	1	GCTTTATACTGTAAGTGGACTGACC
Oki_gh-183	A	G	CATCAATACAATTT	CATCAATGCAATTT	ATGTGGTACTGGCTCAAAACT	(0,0)	1	TGCAGTAGAGCATGCTTGGT
Oki_gshpx-152	A	C	TTGCAACATTGTAG	TTGCAACCTTGTAG	TGTAGTTTTGTCGCAGTTGTTG	(0,0)	1	GTTTCAATGATGAGTCCCAAAAGT
Oki_hsc713-56	C	T	TGAGTCTCGTGACT	TGAGTCTTGTGACT	TGTGTTCTACCCTCTTGTGTCTG	(0,0)	1	TCAAATTTCACTCCTTGACAAGTCA
Oki_hsc71p-313	T	G	TGGTTATTAACTAC	TGGTTATGAACTAC	TGAACTGTGCCATGTAGTAGGT	(0,0)	1	GGGGCAGGCATAAAAGTAGA
Oki_itpa-85	G	T	TAAATAAGTTGTTT	TAAATAATTTGTTT	ACCACACTCCGTCCTCCATA	(0,0)	1	AGCGACTTGACTCTGAACAGA
Oki_nips-159	G	T	TCAAAATGACATGC	TCAAAATTACATGC	TCTTTCCTGTGTCGGCATCAA	(0,0)	1	TCCAAGTCTGGTTAGAGCCCT
Oki_parp3-19	-	T	CCAATTTAAAGCC	CCAATTTTAAAGCC	AGCTTTGCCTCTAGACTTGTGT	(0,0)	1	ACCTTGAAGATCCATCCTGGC
Oki_pigh-33	T	A	GTTAACATTTCCCA	GTTAACAATTCCCA	ACCGCATACCAAGTCATGCA	(0,0)	1	TCATCAGTTTTTCTTTCCATTGGGA
Oki_pop5-265	G	T	TACTCCTGGAATAG	TACTCCTTGAATAG	AGAAAACCATGAGGCTCCGG	(0,0)	1	CAGCTGCATTGAAGCACCAG
Oki_RAD100310-36	T	C	TAAAAATGCCGAGC	TAAAAACGCCGAGC	TGCAGGACTTGTTTGGTTTACTG	(0,0)	1	TGGGAGAGAAAGGTATGTCTGT
Oki_RAD100331-48	G	A	CAGACCGCGTCTCA	CAGACCACGTCTCA	CGCCACCCAAATAACCCAGA	(0,0)	1	TTCCCAGGCAGTTCTGAGAC
Oki_RAD100388-66	A	G	AAACAGATAGTACC	AAACAGGTAGTACC	CGATTTGTTGAGGGGCCCTA	(0,0)	1	AATATTCCCTCCAGGCACGC
Oki_RAD100479-50	G	A	ATGGACGTGTTTTT	ATGGACATGTTTTT	GGTCTTTTCCACACTGCTGC	(0,0)	1	TCCAGAGAAAGGGCTCATCC
Oki_RAD100507-58	T	G	TTCTCTTACAAGCT	TTCTCTGACAAGCT	TGCAGGCGTGTATAGTGGAG	(0,0)	1	CAGCTGGTCCACTGTCTATCA
Oki_RAD101032-66	C	T	TATGCGCTGATTTA	TATGCGTTGATTTA	TTGCACCATCTGGAGACTGG	(0,0)	1	CCCCACTACACCAATCGAAGA
Oki_RAD101136-60	A	G	ACTGACAGTCTAAA	ACTGACGGTCTAAA	TGCAGGCCTCAATGCTCAAA	(0,0)	1	TGGTCACTTGTAACTTGTAGCTGT
Oki_RAD101478-57	C	T	AACCACCATTAACC	AACCACTATTAACC	AGAGCATATGGCCACGTCTG	(0,0)	1	GCTCTCTCTCGCCCACAAC
Oki_RAD101607-49	C	T	GAGATGCGTCCGTG	GAGATGTGTCCGTG	CCGGGGCTTTCAGAGAGATG	(0,0)	1	TGTTTTCCCCCTTTTGCCCT
Oki_RAD104180-61	G	T	AAAATGGCAGGATG	AAAATGTCAGGATG	ATATAGGCTGGGAGGGGAGGAG	(0.7,0)	1	ACAGCTGTGACTTGAACCACA
Oki_RAD104335-44	T	C	CCGCTGTGAGGGGA	CCGCTGCGAGGGGA	GTAGTGCAAAGCTGAACGCC	(0,0)	1	TCACTTTGTCCGGTTCCTGG
Oki_RAD104946-41	C	T	GAGGGGCGCCCTGG	GAGGGGTGCCCTGG	CATGTGGCTGTAGTGGAGGGG	(0,0)	1	GCCCCTGAATGACAGCTCAG
Oki_RAD106191-62	T	C	GAGAAGTGATCACC	GAGAAGCGATCACC	TGAGATCGAGCTTGCTGTGG	(0,0)	1	CCCTCCCGAGCCTCAAAATA
Oki_RAD106666-44	T	C	CGGCTATACACAGG	CGGCTACACACAGG	ACGCCAGTCTGATTGGAGTC	(0,0)	1	CGGTTTTGATTTACCTGGCCG
Oki_RAD109528-59	T	A	ATTATGTTATTTTC	ATTATGATATTTTC	GGCCTCAAAGAGAAAGAGCA	(0,0)	1	GGAACTCTGGAGAAGGTAAAGAA

Oki_RAD111744-32	A	T	GGGTCGAAGGTCCG	GGGTCGTAGGTCCG	CTTTGACAGACAGGGTGGGGT	(0,0)	1	CCATGCTCCAGAGTCTCGAC
Oki_RAD115799-69	C	G	ATCCTGCTCCGGCA	ATCCTGGTCCGGCA	CTGCATCGGTAGTGGTCGATG	(0,0)	1	CCAGGAGTTTGCCCTGGAAT
Oki_RAD11844-57	T	G	AAACACTGACATAA	AAACACGGACATAA	TGCAGGTATTTCCGCTACACT	(0,0)	1	TCGCAGAAGGCCATTTTATGT
Oki_RAD12124-45	A	C	TCGAAAACTGTAAT	TCGAAACCTGTAAT	TGCAGGAACTTGATGATCTGA	(0,0)	1	CCAGGATTTGGTTCATTGCTT
Oki_RAD16167-62	C	T	GCGTGTCCAACAAA	GCGTGTTCAACAAA	GGAGTCGGCTGTCTTTGACT	(0,0)	1	GCAAACAGCATTTCGTTCGA
Oki_RAD23788-32	C	A	TATTATCCTAAACA	TATTATACTAAACA	AGGGGGCTTAAACACAGCAT	(0,0)	1	TCTTTGAAATTGTTGCATGTTGC
Oki_RAD25212-35	G	C	TTCTGGGACATCCC	TTCTGGCACATCCC	TGTCTAGTTCCCAGCTTGTTCT	(0,0)	1	TGGAGAACCATCGAGCAACG
Oki_RAD27801-45	T	A	CACAGCTAACCGCA	CACAGCAAACCGCA	GCAGGTAGCGATGTGGAAGT	(0,0)	1	CCTCTTTGGTATTCTGTGCGG
Oki_RAD29028-42	A	T	ACTTCCAGGAATTA	ACTTCCTGGAATTA	GTCACTCTGAAGTAGCTGCACT	(0,0)	1	AGCCACAGGAATAGAAAGCAA
Oki_RAD29136-50	T	G	GTAAGGTTTCCTCA	GTAAGGGTTCCTCA	CCTTCACAAAGACAACATGACTGT	(0,0)	1	AGCAACGGAAATAGGCAAGGA
Oki_RAD34432-38	T	G	TGTGAATAGATGGC	TGTGAAGAGATGGC	TGCAGGATTTTGTGGAGAGGA	(0,0)	1	TCATCGGTCTACCTGACGGT
Oki_RAD345-59	G	A	CAGAGGGGCTTCCT	CAGAGGAGCTTCCT	GACACTTCTCACTAGCGGCC	(0,0)	1	TGACTCACTACCGCTGAGGA
Oki_RAD35219-62	T	C	AGGATATGGCTCAT	AGGATACGGCTCAT	ACCGAACGGAGGTGAGGATA	(0,0)	1	TCAGCCACAGTCTTGGTGTG
Oki_RAD35990-63	A	C	CTCAAGAGGGGTAA	CTCAAGCGGGGTAA	TCAAGACATACAACAAAAAGTGGT	(0,0)	1	CACAGTTAAAGACCCATTGCGG
Oki_RAD36669-48	A	G	CTTCCTATCAGTGT	CTTCCTGTCAGTGT	GGTCCTCCTGTCCTCTTCCT	(0,0)	1	AGAGGGCAAGCAGTCAGTTC
Oki_RAD37278-54	T	C	TTTTGGTGATTTGG	TTTTGGCGATTTGG	AGCGTGGTGTAACTTCAGAGG	(0,0)	1	CTCAAGTTAGGATTCAGCCCCA
Oki_RAD37493-51	G	A	CCAGCCGGGAACAC	CCAGCCAGGAACAC	ACGCATCACAGTGAGACCAG	(0,0)	1	AAAGTAACCGCCTCACCGAG
Oki_RAD37537-45	T	C	ATGTACTCACAGTA	ATGTACCCACAGTA	AGTCCACTTGTAACACCATGT	(0,0)	1	TCCACCCATTACCACGAACC
Oki_RAD37698-60	T	G	A[GA]TTTTTGGGAGTA	A[GA]TTTTGGGGAGTA	TGCTGAGGTCTTTTCTGTTGC	(0,0)	1	TCTCTCTTGGATAAGGTGAGTTTT
Oki_RAD37979-59	G	T	TATGAAGACATTCC	TATGAATACATTCC	GGGGTCTCTGTCATTCAAAGGA	(0,0.5)	1	TCACTGTGTTTTCCCAAGGAA
Oki_RAD40179-68	T	C	CTGAAGTTGACTAC	CTGAAGCTGACTAC	AATGCCACCCATCTACAGCA	(0,0)	1	AGAGCAGCACATAGGGTTTGT
Oki_RAD41030-31	T	C	GGGGCCTAGGGGCT	GGGGCCCAGGGGCT	GCTGAGCCTGGTCTGGG	(0,0)	1	TGGATACCCCAACTCCTCCA
Oki_RAD41030-31-36	C	T	GAAGGYCRGGG	GAAGGYTRGGG	GCTGAGCCTGGTCTGGG	(0,0)	4	
Oki_RAD41030-31-37	G	A	GGGGSTCTGTG	AGGGSTCTGTG	GCTGAGCCTGGTCTGGG	(0,0)	4	
Oki_RAD41030-31-41	G	C	GGGGTCTGTGG	GGGCTCTGTGG	GCTGAGCCTGGTCTGGG	(0,0)	4	
Oki_RAD41030-31-55	G	T	AGCTCGGGCTG	AGCTCTGGCTG	GCTGAGCCTGGTCTGGG	(0,0)	4	
Oki_RAD41603-39	T	C	GCACACTAGAGGTT	GCACACCAGAGGTT	GCAGGATGCACAGATAACACAG	(0,0)	1	CGACCATTCCGATTAATTGGGC
Oki_RAD42204-39	C	T	ATTCAGCACATTA[GA]	ATTCAGTACATTA[GA]	TGCAGGGAGAGGAGAAGGAA	(0,0)	1	AGGTTGTGCGTAAGGTACAGT
Oki_RAD43051-33	G	A	CAGCCGGCTGAGCA	CAGCCGACTGAGCA	AGGACGTTGGTAAAGCCCTG	(0.6,0)	1	ACCAGTTTCGGCTACATGCT
Oki_RAD43627-30	T	A	CATTTTTAAAATTA	CATTTTAAAAATTA	GCAGGCAGCATGTGGTTAAA	(0,0)	1	AGGACACACAGATAAGAGACAGA
Oki_RAD44268-51	T	C	TGAGTTTACAAAAC	TGAGTTCACAAAAC	ACAGACAATGACCTACACTGAGT	(0,0)	1	AGTGCCTTTGAACAGGGTGT
Oki_RAD44444-52	G	A	TTACATGTAGGTCA	TTACATATAGGTCA	TGCCAGTAGGTAGCTCAGGT	(0,0)	1	AGGCCTCAAAGTGTAGCACA
Oki_RAD45691-45	T	G	GAGTACTGCATG[TA]C	GAGTACGGCATG[TA]C	GGGCCCGCGTTATCTGATTA	(0,0)	1	CTGATTCGGTCTGGCCTGAA
Oki_RAD45878-53	G	T	ACAGGGGTTCGAGA	ACAGGGTTTCGAGA	AGGACAGATCGAGTTTCGCC	(0,0)	1	TTTCTCTCTCGCCCTCTCGA
Oki_RAD46160-48	C	G	GTGCTACTGAATGA	GTGCTAGTGAATGA	TGCAGGTGTCTGTAGCTTGG	(0,0)	1	ATTCTTGTTAGCTCGCGCAC
Oki_RAD46744-47	T	C	TCGCTCTTCATACA	TCGCTCCTCATACA	GCAGGCCCGATGGTATTGTT	(0,0)	1	GTTTCATGCCTTCCTGCCAG
Oki_RAD46974-68	T	G	CATTTTTAATGTTA	CATTTTGAATGTTA	TGGAACGGTTCACCCATTTT	(0,0.4)	1	CACATGAATTAACCCAGGGAATCG
Oki_RAD47313-50	G	A	GGCACCGTGGTAAG	GGCACCATGGTAAG	TGCAGGACTCTGAGGTTACAG	(0,0)	1	ACCCAAGACAAGAGATAAACTTACC
Oki_RAD49111-64	C	A	GGGATGCTCTGGGA	GGGATGATCTGGGA	TTACTGAACAGCCACCTCCG	(0,0)	1	TATGCATGCACAGCTGGTTG
Oki_RAD49348-51	G	A	CAAAGCGGAGCGAT	CAAAGCAGAGCGAT	AGCCCTCTCTACGTGTCTCA	(0,0)	1	AACAAACGCACAACATCGCT
Oki_RAD51428-47	A	G	GTTATAACAGCAGT	GTTATAGCAGCAGT	CTGCAGCCAGGGAGGTTATA	(0,0)	1	CCAGAGGAAACCCAGCAGAG
Oki_RAD51585-47	G	T	TCACTTGGTAGAGC	TCACTTTGTAGAGC	ACTTTCTAGTAGGCGTGTGGC	(0,0)	1	CAAAACCCTGGCGTTGCAAG
Oki_RAD51585-47-25	C	G	GTGGCTCACTT	GTGGCTCAGTT	ACTTTCTAGTAGGCGTGTGGC	(0,0)	4	
Oki_RAD51585-47-28	G	A	TCACTTGGTAGAGC	TCACTTAGTAGAGC	ACTTTCTAGTAGGCGTGTGGC	(0,0)	4	
Oki_RAD51585-47-31	A	C	TTKGTAGAGCA	TTKGTCGAGCA	ACTTTCTAGTAGGCGTGTGGC	(0,0)	4	
Oki_RAD52040-63	G	T	AAAAA[CT]GATTGTAA	AAAAA[CT]TATTGTAA	CGCCCAACCAAACACTAACCCT	(0,0)	1	AGTGGCCTAACTTTAATTTGACACA
Oki_RAD52785-52	C	A	GCAAC[AT]CGGCCACT	GCAAC[AT]AGGCCACT	CTAAAACACAAGCCCTGGCA	(0,0)	1	TTTAATTATCTACCTGTTCAGTGGC
Oki_RAD53121-66	C	T	CATTCCCTCATTCC	CATTCCTTCATTCC	CTCTAAATACCCGGGTGCCC	(0,0)	1	CACATTCTTGAGACAAGCAAGGG
Oki_RAD53655-42	T	C	GGGGATTTGAGAAA	GGGGATCTGAGAAA	GGTGAAGGTTTCAGAGGGGG	(0,0)	1	GCGCTCTCCGTGATCTCATT
Oki_RAD53703-50	C	T	GCCTCACGAGTGGT	GCCTCATGAGTGGT	TGCAGGAGGACACAAACACA	(0,0)	1	CACAGCCTTAGACCACTGCA
Oki_RAD53750-45	A	G	CGTGACAGTAGAAA	CGTGACGGTAGAAA	CAGAGGAGGGGCCGTGA	(0,0)	1	CCCTGTATCAACACGGTGCT
Oki_RAD54918-40	T	C	TCATCCTGAGGCCA	TCATCCCGAGGCCA	CAGGCCCAGCTGTGAGTAAA	(0,0)	1	ATAGGGTGCCATCTTGGACG
Oki_RAD55090-49	C	A	GAGAGCCGGACGGG	GAGAGCAGGACGGG	ATCGCAGCACGGCTCTATG	(0,0)	1	CTCCATCTCCTTTGGGCTGG
Oki_RAD55690-46	A	C	GTAAAGACCCCTAA	GTAAAGCCCCCTAA	CCACAAGGGCACAATGAGTC	(0,0)	1	GACCAGTAGTCGCATAGGGC
Oki_RAD56094-43	G	T	CGCACCGTTCCTTC	CGCACCTTTCCTTC	AAGAGGTATGCCACGATCCC	(0,0)	1	AAACGAACCTCCAACCTCCA
Oki_RAD57307-33	A	G	CTCAAGATTTTAAA	CTCAAGGTTTTAAA	TGCAGGGCTTGAGTTGAGAA	(0,0)	1	ACGGGCATTGATCCAGTCAG
Oki_RAD57826-44	T	C	TTGGCATCAGATTG	TTGGCACCAGATTG	TGCAGGTGACGCTTTAGAGT	(0,0)	1	GTGCAACACCAGAGTTCGAA
Oki_RAD57956-47	C	G	CCTACTCTTTGTCA	CCTACTGTTTGTCA	AGGTCATGGATGAGGCATGCA	(0,0)	1	CCTTTTAGCATGGCGCATCC
Oki_RAD58310-55	A	G	ATCACTACTATCCC	ATCACTGCTATCCC	CGGCCCTCTGTTGAGTATGG	(0,0)	1	GGATATGGATTAGGGGATAGGGGA
Oki_RAD59054-54	A	T	TTTTGTAAAAAAAA	TTTTGTTAAAAAAA	TGATTGAATACCTAGTCTCCCTATG	(0,0)	1	CGCCACTCAGAAGCCCAATA

Oki_RAD59556-32	T	C	CATTAGTGTAATAA	CATTAGCGTAATAA	GGCCATAGCAGCTGCCTGC	(0,0)	1	ACCATGTCTCATAGTAGACATGCA
Oki_RAD59920-68	G	A	ACACAGGACAT[TA]AG	ACACAGAACAT[TA]AG	GGCTGAATCCCCCTAGAACAC	(0,0)	1	GCCATGGTTAAAGGTTTCAAGC
Oki_RAD59945-45	T	C	GCTCTCTTTGTTCC	GCTCTCCTTGTTCC	CAGGTGGATGAGAGGCTTGG	(0,0)	1	CCAAGACCAGCCCTGAGC
Oki_RAD60246-68	A	C	ATTCTCACGAAGTG	ATTCTCCCGAAGTG	GCAGCCCCTACCTACCATTC	(0,0)	1	GAACATCGCCAGGCATTGAA
Oki_RAD61746-62	C	T	GCTATTCGGAAAGA	GCTATTTGGAAAGA	TTGGGGAGAACTGTGTGTGG	(0,0)	1	CGCCCATTGCACTGTTGATC
Oki_RAD61821-61	A	T	TAAAATAAACTCAA	TAAAATTAACTCAA	TGCAGGCTAAAACCAGTACTT	(0,0)	1	TGACCAGAAGACCCCTCTGT
Oki_RAD64084-65	C	A	AATATACGTTTTAG	AATATAAGTTTTAG	AGGCAATTTTTACATAGATGGCAA	(0,0)	1	TCGCAAGATCATTATCCAGTGGT
Oki_RAD64627-67	T	A	AATAAATAGGCTCC	AATAAAAAGGCTCC	GGTCCTCCTTGGTGATTGGT	(0,0)	1	GGTTACATCCTCAATGGGTCCA
Oki_RAD65234-35	T	G	CCAGATTTTTTGTT	CCAGATGTTTTGTT	TGCAGGAAGAGGTTAGAAAATAGA	(0,0)	1	ATGTATGGACTTGACAACAACAAA
Oki_RAD65388-37	C	A	AAAAAACCATGTGG	AAAAAAACATGTGG	GTGGTGGTGGTCAGAGACAG	(0,0)	1	AAGCTGATTTCCTTGGCAAAAT
Oki_RAD65610-58	A	T	GTTATTACCTGTGC	GTTATTTCCTGTGC	TGCAGGCCAGTTCAGTGTTT	(0,0)	1	GGCAGTTAATCACGTGCACA
Oki_RAD65902-30	C	T	CTTTGCCGGAAAAA	CTTTGCTGGAAAAA	CCTTGTTCACCAGGCTTTGC	(0,0)	1	ACCGTTGACTCTGAGCTGTG
Oki_RAD66265-54	C	T	AGGTTCCGTCAGAT	AGGTTCTGTCAGAT	TGTTGTGATTGAGTTTGGGGGA	(0,0)	1	TTTCCACCACCAAGACACCC
Oki_RAD66663-68	G	A	ACCACCGTAACAAT	ACCACCATAACAAT	GCCCACTGCTAAGGCCTATA	(0,0)	1	CGCCATTAGTCCAGTTTGCA
Oki_RAD66994-58	G	A	GGACTAGTCTGCTC	GGACTAATCTGCTC	AAAAAGTGGGAGCAGCATCG	(0,0)	1	AAGCCTCCTCCTCACAGCTA
Oki_RAD67081-48	G	A	TGATGCGGTGACAT	TGATGCAGTGACAT	GGCTGTCGGTGTTTCACAAT	(0,0)	1	AGCAATTTCGATGACCATAGCT
Oki_RAD67114-64	T	A	ATGATATGTACAGA	ATGATAAGTACAGA	AGTCAGGTGAGACTCAAATCCT	(0,0)	1	GACAGGAGTCTACCGTGGTT
Oki_RAD67674-60	C	T	ATCTTCCATTTAGG	ATCTTCTATTTAGG	TGCAGGAGTAAACAACACCA	(0,0)	1	AGCACCGACTGTTGCTCAAT
Oki_RAD68033-63	A	G	TATCACAATGTAGG	TATCACGATGTAGG	CCTGAACAAAACACATTAGGAATCA	(0,0)	1	TCTCTCCAATTCATACTGACCACT
Oki_RAD68190-55	G	A	GCTAGGGACGTGGG	GCTAGGAACGTGGG	TGAGGGGGTTGGGAGGGG	(0,0)	1	CCCCCATTAAGTCTCCCACG
Oki_RAD69161-64	G	T	TTGTGAGAATGATG	TTGTGATAATGATG	CCAGTATGAATGCATCGGTTGT	(0,0)	1	AGGAGAAGATGAAGCATCGTCA
Oki_RAD69355-42	G	A	CACCCTGGACTCAG	CACCCTAGACTCAG	GCCCTTCAGCAACATGGTTG	(0,0)	1	GGAGAAAGGTGCTGGCATCT
Oki_RAD70262-64	C	A	CTTAACCCTTATCC	CTTAACACTTATCC	GCAGGATAAGGCACCCTACG	(0,0)	1	CAGCACTGAATCATGCGCAG
Oki_RAD70600-60	G	A	AAAAAGGGACATCG	AAAAAGAGACATCG	CTGCACCTACCACCAACAGT	(0,0)	1	ACGATAAAGTCTTGCACTCCGA
Oki_RAD70812-52	A	T	AGTATGATAAACTA	AGTATGTTAAACTA	TGCAGGGGTTGTTGATGTTA	(0,0)	1	AGACGACCCAGAGATTCTCA
Oki_RAD70820-47	A	T	ATACGGAGGTGATT	ATACGGTGGTGATT	TACCGACAACCTTGCCTCTC	(0,0)	1	CAGACCCCATCCCCAATCAC
Oki_RAD70963-47	A	G	GCAACAACTGGTTA	GCAACAGCTGGTTA	GGTCAGACCTGCCTTTATCTGA	(0,0)	1	CAGATCAGATGAGGCCGACA
Oki_RAD71346-63	T	C	AGAGGATGTTGGGC	AGAGGACGTTGGGC	ATGGGACTGGATTTGTCGCT	(0,0)	1	CGACTCATTTGCAACCTTGGT
Oki_RAD71442-69	G	A	TGAATGGAAGTTTA	TGAATGAAAGTTTA	AGGGTGTGCTTCAGTATGACA	(0,0)	1	AGACAGTGCACCAACGTTGT
Oki_RAD71948-56	A	G	TTATTGAAATCTAC	TTATTGGAATCTAC	AGGACCAGCTTAGCCTCTCC	(0,0)	1	CATCAGGTCGCAGGTAGGAG
Oki_RAD72095-45	A	C	AAAATAAATGGAGC	AAAATACATGGAGC	GGACACACAAATCACAGGGGA	(0,0)	1	GCAGCATTGCCCCTGAAGTA
Oki_RAD72101-67	A	G	GCTTGCACAGAGCA	GCTTGCGCAGAGCA	TGCAGGTGCGAGAAACAAGA	(0,0)	1	GCAGGAGTGGTTGGAATTGC
Oki_RAD72759-48	A	G	CATGAGACTGTAAC	CATGAGGCTGTAAC	CCAGGTTCAATGGTAGCTAGCT	(0,0)	1	AGGGGGTGAATACTTTCGCA
Oki_RAD72979-40	G	A	GAGAATGATGAAGT	GAGAATAATGAAGT	TGCAGGCTGTGTAAGGACTC	(0,0)	1	TCGGGTGATTCTGGAGGCTA
Oki_RAD73094-68	A	G	AAACACATACGCAC	AAACACGTACGCAC	AGCGCCACCAGAACTAAACA	(0,0)	1	TGCATGTACGTATGTGTGCG
Oki_RAD73130-59	T	C	AATACCTCCTAACG	AATACCCCCTAACG	TCAGCCTGGTGAGCAAACAA	(0,0)	1	TAGCAACAACCAGGAGGCAG
Oki_RAD73234-42	T	C	TCTCGCTTCGCATT	TCTCGCCTCGCATT	TTGGGCCCAGTTATCCCTCT	(0,0)	1	TAACAGGGCTGCAACCACAA
Oki_RAD75909-38	T	C	GGTGGATGTTCTGC	GGTGGACGTTCTGC	CCAGTCTACTTCCAGCTGGTGG	(0,0)	1	AGTCCTGCTCTGAGGGGAAG
Oki_RAD75911-69	G	T	GACCTTGAAGGCAA	GACCTTTAAGGCAA	ACTAATCAGCGGCTCACCAC	(0,0)	1	TACCCTGTTGTAGCACCCCT
Oki_RAD76218-42	T	G	ACCATTTCCCCAGG	ACCATTGCCCCAGG	CCACAACCAGATCAGCACCA	(0,0)	1	AGCCTGTTGGAGTTGAGGTG
Oki_RAD77207-61	A	G	GGAACCATTTAGGA	GGAACCGTTTAGGA	GACGGTTCTGACTGTGAGGG	(0,0)	1	CCTGGGGCTTGGCATTAGAT
Oki_RAD77210-64	A	T	GTGCAAAGA[TC]ATTA	GTGCAATGA[TC]ATTA	TGAACAGCCCTGCTCAAGAA	(0,0)	1	TGTTTTGCCATTGTGTTTCCCT
Oki_RAD77803-60	G	A	TCATATGTTGTTAT	TCATATATTGTTAT	TGAATGTGTCTGCTAAGTGTCA	(0.6,0)	1	TCTTCTGTAGCGTCCGTTGG
Oki_RAD77883-62	C	G	TGGGGGCTCGTACA	TGGGGGGTCGTACA	CACCAGCGCCTCAAAATTGT	(0,0)	1	TGCATCGGCTGTGAGATTAA
Oki_RAD78112-64	T	G	AATAAATGCACGAG	AATAAAGGCACGAG	ACCCGCATCATACTTATGCA	(0,0)	1	CTGTGTCCAGGCATGTGGTA
Oki_RAD78543-33	A	G	CTCATCAGCATTCA	CTCATCGGCATTCA	CAGGGCACATCCTCTGGC	(2,0)	1	CTTTGGGAAGGAGCTGAGCA
Oki_RAD79761-66	A	G	TATTAGATTTGTAT	TATTAGGTTTGTAT	TGTGTTGGCTTTATGTAGGCT	(0,0)	1	GTCTCTCAAAATCATTGTCTGTGGT
Oki_RAD80460-54	C	T	AACACTCTGGCTTC	AACACTTTGGCTTC	GCAGGGTAAGCTCTACTGTCA	(0,0)	1	TTTAGCAGCCCTAGTGCCAG
Oki_RAD80645-70	G	C	GCACAGGTGACG	GCACAGCTGACG	TGCAGGGAGGATAGACAACC	(0,0)	1	TGCTGTTATTCACCCCTCGT
Oki_RAD80982-68	T	C	GCCGGGTATCGTCG	GCCGGGCATCGTCG	CAGCCTAGTGGACACCTGC	(0,0)	1	GTCCCCACCGTCTCCATAAC
Oki_RAD81387-37	G	A	CTATCTGACTAGTT	CTATCTAACTAGTT	GCAGGAGTCCATGTCTACTCAG	(0,0)	1	AGTCCAATGGCTCCTGCAAT
Oki_RAD82856-48	C	T	CGCCTACCAGTCGA	CGCCTATCAGTCGA	TGCACATGACCAGTACTCGC	(0,0)	1	GATCCACTGCATGCTCCAGT
Oki_RAD83766-63	T	A	AAAGACTGAGGAAA	AAAGACAGAGGAAA	AGCAACATGACCACGTCACT	(0,0)	1	TTGTTTTGTCCGGCTCCTGT
Oki_RAD83875-36	G	A	TGTGATGTAGCTGC	TGTGATATAGCTGC	AGCTTGGCAAGGAAGTCTGT	(0,0)	1	GAAGTGGGCTAAACGCTCCT
Oki_RAD84577-58	T	G	ACCTACTTCTGCCA	ACCTACGTCTGCCA	CAGAGAGAAGCACAGCACCTA	(0,0)	1	TGCTCTGCTTCCCTGTGTTT
Oki_RAD85448-48	A	T	ATGGAGATATCTAC	ATGGAGTTATCTAC	AGGCAAAGCAATGGAGTGGA	(0.1,0)	1	GGAGGCATCTCTTGAAATGCTG
Oki_RAD85949-47	G	A	TAACACGCGTTCTA	TAACACACGTTCTA	TCAGTTAGTGGGTCTCCTCTCT	(0,0)	1	TCGTCAACAGTGCAGTAGGC
Oki_RAD86627-60	A	T	AGCATTATCACTTT	AGCATTTTCACTTT	TCCTCCAAACACCTGCTTCG	(0,0)	1	CTTGGGTAGCAAATCAGCCA
Oki_RAD87141-55	T	C	AGCTCATTTCTTTT	AGCTCACTTCTTTT	ACCACCCAGTAAGGCTCCTA	(0,0)	1	TCTGTCCTCCAGACTCCTGT
Oki_RAD87446-62	G	A	GTGTATGCAATCCC	GTGTATACAATCCC	TGTGTGAGAGAGTGTGCGTG	(0,0)	1	GGGGAGCCCTGCATTAAGG

Oki_RAD87621-67	T	G	C[CT]GCATTGCTGCTA	C[CT]GCATGGCTGCTA	TGCCCAAGGAATGACTCACC	(0,0)	1	CAGCCCTGGTTGCATCCTTA
Oki_RAD87777-48	A	T	GCCAACAAAGACTT	GCCAACTAAGACTT	TCGTAAATAAAGCGCGCCAA	(0,0)	1	AGGCTCTAGTCTATCTTGGGT
Oki_RAD88551-51	A	G	GAAAGCATTTGCAT	GAAAGCGTTTGCAT	GGCTAAGGGCTACGCTAACC	(0,0)	1	TGGCTCCCGAGATTCTGAGA
Oki_RAD89259-51	T	G	TATTACTGAACAAT	TATTACGGAACAAT	GCAGGGTATCTGAGGCACAT	(0,0)	1	GGCAAAGAACAGCTATTATGACCA
Oki_RAD89374-40	T	G	GTACTTTCCAAGAT	GTACTTGCCAAGAT	TGCAGGCAAGGGAAGTTTAAC	(0,0)	1	CTGGTACTTAAGCCAGCAGGT
Oki_RAD91362-68	C	A	ATGGCACATATTTT	ATGGCAAATATTTT	GCAGCAGAAGAGGCACAAGA	(0,0)	1	ACTGTAGAATTGCTAAAATCCCACA
Oki_RAD91430-44	A	G	GCTGCTACAAATGG	GCTGCTGCAAATGG	TGCGAGGCCCTTCAATGTTA	(0,0)	1	AGTCTCACAACCCCCTCTCT
Oki_RAD91470-66	C	A	AGGTCACTGCTGAG	AGGTCAATGCTGAG	GGACCTGAACAAGTGGAGCT	(0,0)	1	TGCAATGCATGGAACTCCTCA
Oki_RAD91478-52	T	C	CGGCTATAGCTGTG	CGGCTACAGCTGTG	TGTAGCAGTCTAATGACCGGC	(0,0)	1	GCCTAGTTGCCTGACAATGC
Oki_RAD91907-38	T	G	ACTGGTTGTGAGAC	ACTGGTGGTGAGAC	ACAGAGGAGCACATACTGGT	(0,0)	1	GGGCAGAAGGTAAGATATCAGACT
Oki_RAD92875-31	C	T	ACACCACGCCGCTC	ACACCATGCCGCTC	CCAAGAGGGTGTCCATCGAC	(0,0)	1	TCGCCAACCCATCTCAACAT
Oki_RAD93028-59	A	G	GCTCACAGAACTCA	GCTCACGGAACTCA	GGTGTGTAACCTGTCTGGACA	(0,0)	1	GCCAAGCCAATTAGCTGTGC
Oki_RAD94215-66	A	G	GAGGATAAGGCGGA	GAGGATGAGGCGGA	AAGGAGACACGATGGGGAGA	(0,0)	1	CTGCAGCTCCAGATGATCGA
Oki_RAD94241-30	C	G	CAGTAGCCTCTTAT	CAGTAGGCTCTTAT	TGCAGGTGGGCAACAAGATT	(0,0)	1	CTGTATCTCTGGACCATGCAGT
Oki_RAD96072-42	A	G	TGAAGGATAAGCAC	TGAAGGGTAAGCAC	AGGGCACAGGAGGAGTCATT	(0,0)	1	GCAGTGGGAGTTTGTTGTGC
Oki_RAD96498-69	C	A	GCCAAACGCATCCT	GCCAAAAGCATCCT	CCACAAGGAGTTGCAAGAGCAT	(0,0)	1	CATAGGGCGCCGCATAATTG
Oki_RAD97325-35	T	A	TCTTGGTCAGCTCC	TCTTGGACAGCTCC	TGCAGGGAGCTACAATGGTA	(0,0)	1	GCTCACCTCTCTAGCCCTCT
Oki_RAD97993-40	C	T	TGGTTCCGTAATAC	TGGTTCTGTAATAC	GCTGCCCTGAGAACAGAGTT	(0,0)	1	CCTGTCTGTGTGATGAGGTGG
Oki_RAD98280-45	G	C	TTTACAGTTGGTTT	TTTACACTTGGTTT	GGTCACGAGTCCTCTTGAGC	(0,0)	1	GGTGTGATGTGGCTGAAACC
Oki_RAD98485-66	A	G	TATTCTAATTGGCA	TATTCTGATTGGCA	GGGACCTTGACTGTTTAAATTCAA	(0,0)	1	AGCACATGTGAAAGCCGAGA
Oki_RAD99931-47	T	C	TTACCATCAATATG	TTACCACCAATATG	GCTCCAGAGGCTCCCTTTTC	(0,0)	1	CGCTCACTCCCTCCATCAAT
Oki_sast-230	A	G	AAGTAGTATTTGTT	AAGTAGTGTTTGTT	ACAGTAGTATCTATGCCTTTGAGCA	(0,0)	1	CGCATTGGCTAGATTCACATGG
Oki_SECC22-67	T	G	TCCCAACTGTCTGT	TCCCAACGGTCTGT	ACTGTTGAAGACTTGTTTTTCCCA	(0,0)	1	ACCACTACAGGATGACTACCT
Oki_Six6-3	C	T	ATTAGATTTCAAAT	ATTAGATTTTAAAT	ACAGCTCTATTTCAATGTTTACTCG	(0,0)	1	GCGAGCAATTATTCGGGCAA
Oki_srp09-107	A	G	TGAGAGGAGAAATC	TGAGAGGGGAAATC	AACGGAAGAGAACGGAGCTG	(0,0)	1	GCAGCGAAGGTTATGCTCTC
Oki_sys1-141	T	G	TGGAAATTAACTGA	TGGAAATGAACTGA	TGGAACATTGCACACCTCTCA	(0,0)	1	GCAACCAGCACCATTTCAGT
Oki_taf12-40	-	T	CCTTTTTAATGCT	CCTTTTTTAATGCT	GTGTGTGATTTGTCAGCTCCAC	(0,0)	1	GAGTGTGTGATTTTGGCCAGT
Oki_thyK-100	T	G	ATTACCATTAGACT	ATTACCAGTAGACT	CCACCCTGCAACTCTGATCA	(2,0)	1	CCAATCCAAGTCAACTTCCCC
Oki_txnip-35	C	G	AGCTCTCCTCTGTG	AGCTCTCGTCTGTG	GGCAGGACCAAGGTCTTCC	(0.5,0)	1	GATGGTCTTTCCCTGCCAGG
Oki30_5473492	C	T	TCCTTTGTACAGC	TCTTTTGTACAGC	TCTGGAAGCACACCAATGAA	(0,0)	1	TCAGTTTTGCGCATAGAATTTG
Oki30_5551409	T	C	TTTAACAGCTTG	TTTAACAGCTCG	CAGGGAAGAGGACAGTGTGA	(0,0)	1	CTGAACAAGGAGGTACCAGGA
Omy_myclarp404-111	T	G	CAAAGCCATACGTGGCC	AAGCCATCCGTGGCC	GCTGTGGTGCTCATGGGTAAA	(0,0)	3	CCAGGGCAGGGTTGTTCTC
Omy_RAD13034-67-21	C	T	CTCCCCGAACC	CTCCCTGAACC	GAGTGATTCCCAGCCCTCC	(0,0)	3	TCTCTCCGTTGGCCAGAAAC
Omy_RAD13034-67-35	A	T	CTGAGTGGACA	CTGTGTGGACA	GAGTGATTCCCAGCCCTCC	(0,0)	4	
Omy_RAD79314-58-25	C	T	CTCGCCCTGCG	CTCGCCCTGTG	CACACTGACTCATCCCTCGC	(0,0)	3	GAGTGTCTTACCGAGCTGCC
Omy_RAD79314-58-27	T	C	GTCACRCCTGC	GCCACRCCTGC	CACACTGACTCATCCCTCGC	(0,0)	4	
Omy_RAD79314-58-31	G	A	ACGCCTGCCCT	ACACCTGCCCT	CACACTGACTCATCCCTCGC	(0,0)	4	
Omy_RAD79314-58-66	C	A	CAGTGTCAACC	CAGTGTCAAAC	CACACTGACTCATCCCTCGC	(0,0)	4	
One_1a.54542-52-44	C	T	GCCTTGTGCTT	GCCTTGTGTTT	GCAGGTTGTGATCGTGACCA	(0,0)	3	TGAAGAGACTACGCCCCCTT
One_1a.54542-52-47	G	C	TTGACCAGAAG	TTCACCAGAAG	GCAGGTTGTGATCGTGACCA	(0,0)	4	
One_2.70711-39-28	G	T	AGGYGCTYGTRC	ATGYGCTYGTRC	TGCCCTGTTGTGATGAGCAT	(0,0)	3	GGCTGTGTAGAACGACCCC
One_2.70711-39-30	T	C	GTGCTYGTRCG	GCGCTYGTRCG	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-43	G	A	CGTCCGCGGGC	CGTCCACGGGC	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-56	C	G	GGCTAAGGATC	GGCTAAGGATG	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-57	G	A	GCTAAGGATSG	GCTAAGGATSA	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
One_2.70711-39-64	T	G	TTCCCTAGGGG	TTCCCGAGGGG	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
Ots_ARNT-29	A	G	GTGCTAGCTAC	GTGCTGGCTAC	CCACTGGCTGTGGAGCTT	(0,0)	3	GGGTTCAGTGATAGTTGGGCAAAT
Ots_ARNT-29c	A	C	GTGCTAGCTAC	GTGCTCGCTAC	CCACTGGCTGTGGAGCTT	(0,0)	4	
Ots_crRAD9615-69-19	T	A	GGGAGTGGGAG	GGGAGAGGGAG	GAATGCAGGGCCAGGGAG	(0,0)	3	ACTCCCAGACCATCCAGCT
Ots_crRAD9615-69-50	A	T	CTGGGAGGAGA	CTGGGTGGAGA	GAATGCAGGGCCAGGGAG	(0,0)	4	
Ots_myo1a-384-36	C	T	CACCACTACCA	CACCATTACCA	CTCCCCCCTGGACTTTGG	(0,0)	3	GCTCTATTGCACCGTGTTCTG
Ots_myo1a-384-57	C	T	CTGCAGAACAC	CTGCAGAATAC	CTCCCCCCTGGACTTTGG	(0,0)	4	
Ots_P53-25	G	T	TTCTGCAGGGG	TTCTGCAGTGG	GGAACTTCCTCTCCCGTTCTG	(0,0)	3	GCACACACACGCACCTCAA
Ots_P53-28	G	C	GGGCAGCTCCT	GGCCAGCTCCT	GGAACTTCCTCTCCCGTTCTG	(0,0)	4	
Ots_P53-40	T	C	CTCCTGGGTCG	CTCCTGGGCCG	GGAACTTCCTCTCCCGTTCTG	(0,0)	4	
Ots_unk9480-51-38	T	C	TCCCASAAACT	TCCCASAAACC	CAAATCAGAACAAAACCTCCCACAA	(0,0)	3	GGAAGTCTGTCTGAATGGTTGTCTT
Ots_unk9480-51-39	C	A	CTAAGGAGACC	ATAAGGAGACC	CAAATCAGAACAAAACCTCCCACAA	(0,0)	4	

Appendix 10. GT-seq SNP panel for Pacific lamprey

Assay	A1	A2	A1-Probe	A2-Probe	FWD Primer	Corr	Flag	REV Primer
Etr_1004	A	T	TGCGATTAACGGTTCC	TGCGATTATCGGTTCC	CGCCCAGCGTGTTCAC	(0,0)	1	CGACCGCTTTCTCTCTGCAAA
Etr_1007	C	T	CACTCATCAGCGAGCCT	CACTCATCAACGAGCCT	ACACGAACACCCAAAAGTGATGT	(0,0)	1	ATGACTACTGACGATTCCCATTGAC
Etr_1022	C	T	TTTGGTCTGGTGATCTG	ATTTTTGGTCTAGTGATCTG	GCACGAAAGCACTGAAGCT	(0,0)	1	TCAGGAAGGTTTTGCATTGATACCA
Etr_1034	T	G	CCGAATCCTTGAGCTG	CCGAATCCTGGAGCTG	CAGCAGCAGAACCGAATCCT	(0,0)	1	ACCTTTGATGGTCCATGGGG
Etr_1060	A	G	ACTCGCCACATTGC	CTCGCCGCATTGC	TCGCACGCACTCACGTTA	(0,0)	1	GTGAAGTCCGTCGTCTTACCTTTT
Etr_1068	G	A	CCTCAACAGACTCTTGG	CCTCAACAGATTCTTGG	GGGCCCTGGAGGGTCA	(0,0)	1	GCACACGCAATACAAAGATTCCT
Etr_1104	A	G	GGGAATGACAACACAA	GGGAATGACGACACAA	AGCAGAGGGGGAAGAGGAAA	(0,0)	1	CCACTTGAGCTGCAATGTTGA
Etr_1106	T	C	GAAACCCAGTAGAATTA	GAAACCCAGCAGAATTA	TCCCTAGTTCTGAGAAACCCAG	(0,0)	1	AAGGTCGCATCGTCAGTGTT
Etr_1131	C	T	GAGCTATCTCTGCAGA	GAGCTATCTTTGCAGA	TTAACGGCGTGCATGCATG	(0,0)	1	AAACTGGTGGAAAAATGTGGG
Etr_1163	A	T	TGCAACCGTGTTTATAGAG	CAACCGTGTTTTTAGAG	TGCAGGAACGCGTAAAC	(0,0)	1	TCTGACGCTTGTATGGAATCTGTTC
Etr_1181	G	A	CACTCCACAGAAACGGG	CACTCCACAAAAACGGG	AGTCGACCACCTTGCTGAAG	(0,0)	1	GGGCAGCTGTCCCGTTT
Etr_1184	A	G	CCAGGCGACATGAGCTC	CCAGGCGACGTGAGCTC	CTTGCAGACCCAGGCGAC	(0,0)	1	GCTGTCTTTGTTTTTCGGGGT
Etr_1187	C	G	GCTGCAAATCT	GCTGCAAATGT	ACAAAAGCTGTCTGGCCTGA	(0,0)	1	CAAAGGACCGGGCTCTGTC
Etr_1193	T	G	GCGTTTTATTGACTG	GCGTTTTATGGACTG	AGCTACACTACTTTGGTGCGT	(0,0)	1	CTCCATCCAGCAGTGGGATT
Etr_1210	G	A	AGGCCGGCTCCTG	AGGCCAGCTCCTG	GAAGGAGCTCGAGTCGAGAG	(0,0)	1	GACACCGTAGAACTACCATGCA
Etr_1238	A	G	CATAACGGTGAAGCGAC	CATAACGGTGGAGCGAC	GATCTGGCAGAAGGCAAACAG	(0,0)	1	AGATCTGGACGCTTGCAAGAC
Etr_1257	C	T	TGCGAAGTGATGCTGATAT	TTGCGAAGTGATACTGATAT	GGCAAACGACCGCATCAAC	(0,0)	1	CACGAGCGGGTCCCT
Etr_1321	G	A	AGCCTGCGCAGACC	AGCCTGCACAGACC	GTGGCGGACGCATTCAAG	(0,0)	1	GCGTCGTGCGAGGATGA
Etr_1341	C	T	CCAACCGGCGATATG	TCCAACCGGTGATATG	TGCAGGAATAACATTCGAATTTCTACTC	(0,0)	1	GACATGACAGTCGCTAGATTCCT
Etr_1349	G	C	CCTGGGTTCAACCC	CCTGGCTTCAACCC	CGGTGAGCAGCCTCTGG	(0,0)	1	GGTGAAACCCCTTCATTGTGTGA
Etr_1359	T	A	TCGCAGACTTGCG	TCGCAGACTAGCG	CTGTATTGGTTGCTGTCGCA	(0,0)	1	GTCACTTTCAATGCCCGCTT
Etr_1376	C	A	CTGCATGTTCTGACACTG	CCTGCATGTTCTTACACTG	GCAACTCAGGTGGGAAACG	(0,0)	1	GCGGTCCAGATGAGATTCCA
Etr_1378	G	C	TCGAGATGTGGAAAGCC	TCGAGATGTCGAAAGCC	ACACAAAGACTGGAGCAAATGG	(0,0)	1	CTCCCATAGGCTTGCTCGAG
Etr_1383	G	A	TCAAGCCGAACGTTG	TCAAGCCAAACGTTG	GGAGAGGACAGGTCCAAGGT	(0,0)	1	CGTAGAGCCTGCGAAAGTGTT
Etr_140	A	C	AACACAGTTGTCACTGCT	ACAGTTGGCACTGCT	TGCGGTGGTATCTATACGACGAT	(0,0)	1	ACACACACCAAGTACCACT
Etr_1428	T	C	TTGCGGTCATGATGC	TTGCGGTCGTGATGC	CAGCAGGGATATCATCACCTTCTT	(0,0)	1	ATGGCACGGGCAGAGAA
Etr_1507	C	T	ACGGCAGCGCGCGGGGC	ACGGCAGCGTGCGGGGC	AAGGGACAATCTGAGAGCGC	(0,0)	1	CAAACCCGGACAGTGGCAA
Etr_1509	A	C	TATATGTATATCTCCAC	TATATGTATCTCTCCAC	CCACGGGTGGGTATGCATAT	(0,0)	1	CCGAGGCCTAATTCACACCA
Etr_1522	T	C	CGCGATCCTCACCGC	CGCGATCCCCACCGC	TTTGCCGTGCTCATGTATCTACA	(0,0)	1	GACCCTGCGGTGATCACA
Etr_1548	T	C	ATATTGCACTGACT	ATATTGCACCGACT	GCCCTAGCTATTAATGCCGGT	(0,0)	1	CTGGCACACAACGGCCTA
Etr_1551	C	G	CTACAAACCCCCGGCAA	CTACAAACCGCCGGCAA	GCGTAGAACAACAGGCCCTA	(0,0)	1	ACCCGGCTGTACCTGAGATA
Etr_1556	A	G	TGGCTGGAGACGCTGCC	TGGCTGGAGGCGCTGCC	AGCGCACATGGCTGGAG	(0,0)	1	GGTGCTCTGGATCAGGAACC
Etr_1561	A	G	GCCAAAGTCACGCTGTT	GCCAAAGTCGCGCTGTT	GTCGAAGAAGACGCCAAAGTC	(0,0)	1	TCGCCTTTTCTTAATGCGCG
Etr_1567	T	A	ACAGTTCGAAAGCCAG	ACAGTTCGTAAGCCAG	TTGCACCACCTCCTTGCT	(0,0)	1	GTAATGGTGGGACAATGCAAAGG
Etr_1569	A	T	TTGTTGCTGATTTTATT	TTGTTGCTGTTTTTATT	CGGGGTTGAAGCAGTTTCCA	(0,0)	1	AAGTCACAACTCTCCTGGGT
Etr_1589	G	A	AACCGCAGGACACACA	AACCGCAGAACACACA	TGTGACCGCGTGAGCAG	(0,0)	1	CTTTGACTCCGTGCGTCTCT
Etr_1613	C	G	CCCCTGCCACCGTCC	CCCCTGCCAGCGTCC	CGCTTACGACCCAGTGCATA	(0,0)	1	TTTACTGGTAGCACGCTCGT
Etr_162	T	C	CTGACCCCAACGACC	TCTGACCCCGACGACC	CGAGGCCTTCGCTGAGAA	(0,0)	1	CTGCGGTGACATGAAGTTGAAT
Etr_1667	A	C	GTTATTGCCACAAATT	GTTATTGCCCCAAATT	CGACACGGCACATCATTATAAGG	(0,0)	1	AGGTCAGCAAGGTATTGTGGT
Etr_1684	T	C	TGAGAGCCTTTCCATCGC	AGAGCCTTCCCATCGC	GAGGAACCTGCGGGAGAAG	(0,0)	1	TGTGTTTGCGTGGAGGAGATG
Etr_1696	G	A	CCCGCGGCCGCC	CCCGCAGCCGCC	CCGTGTAGAGGTGGACATAGG	(0,0)	1	TGGCCATCTGCATGTTGGT
Etr_172	T	C	TGTCCCCTATAAGGAGG	TGTCCCCTACAAGGAGG	CTCACGCTGCCCCCAGG	(0,0)	1	TACACGAGCAGCTCCTCCTT
Etr_1762	A	C	CCCCCTCTCATCTGGGG	CCCCCTCTCCTCTGGGG	TGTCACCAGAACCCCCTCTC	(0,0)	1	CACCCTCCCTGAGAAATGCC
Etr_1765	C	T	TTGGAGTCCCAAGCACG	TTGGAGTCCTAAGCACG	CGCACCGATAACTAGAGCGA	(0,0)	1	ACCAAAAAGAGGGGGCTCAA
Etr_1773	A	G	TTCACTGAAAACGTGGT	TTCACTGAAGACGTGGT	GGTCTGGCTGAACGACAATT	(0,0)	1	CAAACACATGGTGCCACACA
Etr_1795	C	T	GCGAGATCCCAAATGGG	GCGAGATCCTAAATGGG	CAGCGGGTGAACGTAGCTAC	(0,0)	1	ATTCAACACCTCGCCACCAT
Etr_1806	A	G	AACACTGACAATATCTAAAG	CACTGACAATGTCTAAAG	GTAATGGCGCTGTCCGTTTG	(0,0)	1	CGAGTACTACTCTGGCCATGTAG
Etr_181	C	A	TCTCATCTCTCGCCTGCT	CTCTCATCTCTCTCCTGCT	GAGCGGATGGGCGACTT	(0,0)	1	GCGCGCAGCACACA
Etr_1843	C	G	GTGCGACCCCAACGAAA	GTGCGACCCGAACGAAA	TTACGGCAGCAAAAACAGCC	(0,0)	1	GCCCTGCTGAGTTTCAATGC
Etr_1848	G	A	TCTACATATGCATGTGG	TCTACATATACATGTGG	ACCGAATAAAGTGTGTCTAGCA	(0,0)	1	TACACTGCACACCCACACTC
Etr_1857	G	T	GGTCTCCGTGGCTGTGT	GGTCTCCGTTGCTGTGT	CTGCTGTTCGCCGTGTGT	(0,0)	1	GGAGATGATCTGCATGCAGC
Etr_1875	C	A	CACCGAAGCCCAATATC	CACCGAAGCACAATATC	CGACTTCCACATTAGCACCG	(0,0)	1	GTGCATTATTCCAGCATTGCCT
Etr_1882	G	T	GGCGCGTTAGGATCTAC	GGCGCGTTATGATCTAC	TGCTCTGCTTTCCACAGACG	(0,0)	1	GGGTTTGGCCACGTAATGATG
Etr_190	A	G	CTGACATTACAATGTTTTAT	TGACATTACAGTGTTTTAT	GCAGGAGACCCTTGCTTGTC	(0,0)	1	AGGTGGCACACGAAAGTATCAAAT
Etr_1944	C	T	AAGGCTATCCGTGC	AAGGCTATCTGTGC	TGAAGTAGGTCTCCCAAAGGC	(0,0)	1	CCCACAGGTACGCAAAGGTA
Etr_1975	C	A	GCAGCCCTGCAACTGCT	GCAGCCCTGAAACTGCT	TGTTAGATGTGTAAAGGCGCAG	(0,0)	1	AGAGGTCACAAACAGCCCTC
Etr_2013	C	T	TCAAGAATCACAGGCAGAG	TCAAGAATCACAAGCAGAG	CGTGGCGTCGCTTTCC	(0,0)	1	CCGACGCTCCGAGTGAAA
Etr_2015	C	T	GCTCGATGACGAGACCG	GCTCGATGATGAGACCG	GGGCTTCGGCTGCGTTATAA	(0,0)	1	AGCTCCTTCTTCTGCTGCG
Etr_2016-70	C	T	TCGACTTCCCGACAATTT	TCGACTTCCTGACAATTT	TTTCATTATTTCTTGACGCTTGTG	(0,0)	1	GGATAGACGCCTCTGCTGAG
Etr_2050	T	C	GCTGTGCAGTGGAGGAG	GCTGTGCAGCGGAGGAG	CCCATGCTAAACGACCAGCT	(0,0)	1	GCACCTCACACATCTGCTCT
Etr_2066	G	A	CGCCTGCTCGCGCTCCT	CGCCTGCTCACGCTCCT	GAACCTGTCGCCCTCACTC	(0,0)	1	GCGCAGGATGAAATTGCAGA
Etr_2068	C	T	GTGCGCACGCGGAATGT	GTGCGCACGTGGAATGT	CAGCACTGCATCGACGTG	(0,0)	1	CAGCTCTACTCGTACCTGGC
Etr_2071	A	C	GGCACAGGCACGACACA	GGCACAGGCCCGACACA	CACAGGTTCACTCTGGGTGG	(0,0)	1	AGAGCTGCTCATTGGTTTTCA
Etr_2097	C	T	CAGGTCTGGGAGCCGA	CAGGTCTGAGAGCCGA	GGGCGTGCGGACATACT	(0,0)	1	GCGAACATGGTCAACGAATGC
Etr_2099	G	A	ACCCGCGCGGACACGTG	ACCCGCGCGAACACGTG	AAGACCCACGGCGATTCATC	(0,0)	1	CCCTCAACAGCCTTGCCATA
Etr_2107	C	T	CGAACGGCGCGAGAAGC	CGAACGGCGTGAGAAGC	TGACCACACGGCGTCTTC	(0,0.6)	1	AAGCACGAGAGCGCGTT
Etr_211B	T	G	GCGTAACCTTGAGCACT	GCGTAACCTGGAGCACT	GGGTGGAGGAGCGTAACCT	(0,0)	1	GTGCACGTAGTTGCGGTTG
Etr_212	A	G	TGCTTCTCTACTTTTGC	TGCTTCTCTGCTTTTGC	TCTTTCCCCGTGTGCTTCTC	(0,0)	1	GCGACACGAGGGTATTCGAT
Etr_2126	A	G	CCGTCCCAATTCGCGCA	CGTCCCAACTCGCGCA	GAGACCGTGGGCGACT	(0,0)	1	GACGCGGCGATGTAGGT

Etr_2193	C	G	TGCGGCTGGAGACG	TGCGGCTGCAGACG	GGTTCATCTGGGAGCTTTTGC	(0,0)	1	AAGCCCACAGAGAAGTGACATC
Etr_2226	T	C	TTTGCGTTCTCGACGCT	TTTGCGTTCCCGACGCT	GCAAAACGCCGTACACCTTT	(0,0)	1	TAGTTGCGTTGAAAGCGAGC
Etr_223	A	G	CTATTGGTTATGAGGTT	CTATTGGTTGTGAGGTT	GTAAGGCGTGGGCTATTGGT	(0,0)	1	AGTTACTGAGATGACCGAGGA
Etr_225	C	G	CACTGGCATTGTCG	CACTGCCATTGTCG	TGGTTGAATCCAGTGCGGATAAA	(0,0)	1	GTGCAAACCCGGTCTCTAATG
Etr_2272	A	C	GAGAGAAGGAAT	GAGAGAAGGCAT	AAGGGGCAGGGAGAGAAGG	(0,0)	1	ACAACAAGAACTGCAGCAGTG
Etr_2287	T	G	CTGCTTGTATCTCCCCT	CTGCTTGTAGCTCCCCT	TTCATGTGACACCTGCTGCT	(0,0)	1	GAGGCGGGTGTCATACAGAG
Etr_2304	G	A	CGTGCTGTAGAGAGA	CGTGCTGTAAAGAGA	ATCGGCACATTTCTTCCCGT	(0,0)	1	GCTAAAGAAGCGCGATGGAC
Etr_231	G	A	ACGATGCCGTCCGCC	CGATGCCATCCGCC	CCAGGAATAAGGACACGGTTTGG	(0,0)	1	CGTCCCCTCCCTCCTTGT
Etr_2334	C	T	TTCGCTCAGCTCCCCG	TCGCTCAACTCCCCG	CCAGCCACCACGTTCAAGT	(0,0)	1	GTGCGGTTGGCAGAGATG
Etr_234	T	C	CCCCAGTGTGACACC	CCCAGTGCGACACC	CTCCTCCACGGCGATGTT	(0,0)	1	TGCACTACGAGAACAACTCTCC
Etr_2409	G	T	CCGCACGGGGAGGTCCA	CCGCACGGGTAGGTCCA	CCAGGTGCTGAAGGGCC	(0,0)	1	GCTCTCGGCCTGGACAAC
Etr_2414	A	G	GCCAAGCGGACCCCTCT	GCCAAGCGGGCCCCTCT	AGACCATTCCTCTGCCAAGC	(0,0)	1	CCCCAGGGTGCTCTTAAACA
Etr_2416	C	T	TGGTGCGGTGCACGC	TGGTGCGGTACACGC	TCATTACACGAAGCCTCGTTCAG	(0,0)	1	CGGAGCCCTCCCTGTGT
Etr_2418	C	T	TAATCTTACCAAGTTTC	TAATCTTACTAAGTTTC	TCGGCCTATTAACTCCGTGC	(0,0)	1	TGGGTACTGGCAGGAGAGAA
Etr_2451	C	A	TATACCTGTCGCCCCCA	TATACCTGTAGCCCCCA	GTGAGGGAGAGAGGGAAGAGT	(0,0)	1	CGAGAACACATACTGGGGGC
Etr_2460	T	C	CTGGCGGCTTCGCACGG	CTGGCGGCTCCGCACGG	CATGCAGCCGACAAACTGG	(0,0)	1	CAACCTGCCCGAGGAGTTC
Etr_2499	G	A	CAGAGAGACGGTGCTCT	CAGAGAGACAGTGCTCT	CCCGAGGGAGTCATCAGAGA	(0,0)	1	CCGTGCCGTTGGGTGAA
Etr_2512	A	G	TTTCCCGTGGACTCAC	CCGCGGACTCAC	AGCACGAGGAGCGAGAGA	(0,0)	1	TGCACTTTGAACATGGGTTACAAC
Etr_2517	G	A	AACCACTGCGACACCGC	AACCACTGCAACACCGC	GGCAGGCTGTGTTAACCACT	(0,0)	1	ACGGAATGAGCGATCGATGT
Etr_2603	A	G	GTGCACATTATGGACAG	GTGCACATTGTGGACAG	GCTTTGTGCACCCTAACAACA	(0,0)	1	AACCCAAGTGGCAAAACCTG
Etr_2642	T	C	GCTCCAAACTGGCAT	GCTCCAAACCGGCAT	AGAGATCCCTGTGGCTCCAA	(0,0)	1	TCGTCGTCATCGTCGTCATC
Etr_2675	G	A	AAGACGACGATTCCCT	AAGACGACAATTCCCT	GCTGGATAATTGGCATCTCACACA	(0,0)	1	CTCAATCGTCTGTTCGCCAAAC
Etr_2730	G	A	GTTGAACCCGTAGCGCG	GTTGAACCCATAGCGCG	CAGCCACCTCGAGAGCTG	(0,0)	1	ATGGGAGGGCATTTGAGGTG
Etr_2765	C	T	TTAATCATGCCAATGCC	TTAATCATGTCAATGCC	ATCTGCACAAGCTTCAGGTT	(0,0)	1	ACGTGTTAAACCGAGCCACT
Etr_2776	A	C	GGAGCACCCAAAC	GGAGCACCCCAAC	GTACCTGGACGTCAAGCACA	(0,0.6)	1	CGACAGCTGCATTGACATCG
Etr_2791	A	G	CCCAGAGAAACAGCAGA	CCCAGAGAAGCAGCAGA	AGGTGGTACTGCAATGGACC	(0,0)	1	GCTCCGTCCATACCATCATATGT
Etr_2823	C	T	CGCACGCGCCGAGCAGT	CGCACGCGCTGAGCAGT	ATGTGCGCCATGCCGAT	(0,0)	1	CACACGGGGGATCTTTGTCT
Etr_2841	G	A	CGCATCTTTGTCCCTGC	CGCATCTTTATCCCTGC	ACAGGTAGTACTGCAACGCA	(0,0)	1	GCTGGATGCTTGGAGACCAT
Etr_2858	T	G	GAAAAGAAATGGTTTGA	GAAAAGAAAGGGTTTGA	GGCAGAGATCCTTGAGAGCA	(0,0)	1	CTCCACTATTCCGCATCGTGA
Etr_2878	C	T	CTTGTCAATCTCCACGA	CTTGTCAATTTCCACGA	AGCTTGCATCCGTGACTTCA	(0,0)	1	GGTTGTCAAGGTTCTCGTGGA
Etr_2915	C	G	ACAGCCTCCCTTCCAC	AGCCTCCGTTCCAC	GCCCTTCAAGTTCCAGTTCAC	(0,0)	1	GTTCACAGTAGATCTTGACCCTTCA
Etr_292	A	G	CAAATAAACACCACACA	CAAATAAACGCCACACA	ACATGCAGAATAGGGACAGAACA	(0,0)	1	CGTGTGCCTCACAGTGAGAA
Etr_2937	T	C	GGCCACGTTTTTCCGCG	GGCCACGTTCTTCCGCG	CTTCGTGCTGGTGATCGGTC	(0,0)	1	CACCACCTCCACGTAGCAG
Etr_2971	T	A	CATTGAGGGTGCA	CATTGAGGGAGCA	AAGCTTTACGTGCAGGCTCA	(0,0)	1	CAGCACCACCTTTTTCCGTG
Etr_2974	G	A	CGCCTGCCCGCACACCT	CGCCTGCCCACACACCT	TGAGACCAGCGCACCTG	(0,0)	1	TGAGTGTGCATGGTGAGTGT
Etr_2990	A	G	CTCAGAGACATCCTCGG	CTCAGAGACGTCCTCGG	GAGCCTCTGGGTGATCTCCT	(0,0)	1	GGAGAACCCGTTTGCGTTTC
Etr_3007	G	A	GGTTGTAAGGGTTGGGA	GGTTGTAAGAGTTGGGA	CGGTGTGAAAATCAGACGGG	(0,0)	1	CCGGTTGGCCTCACATAACT
Etr_3037-68	A	G	TCTGCAAAAGACACAGA	TCTGCAAAAGACACGGA	CACCTTCAGGAAGCACACGA	(0,0)	1	GGGTACGCACAACTCTTGGG
Etr_3038	G	A	TTTCTACTCGGCTCTAC	TTTCTACTCAGCTCTAC	AGTCGACCCCTCAACCACAA	(0,0)	1	ACGTAGTGCAACAGTAGAGC
Etr_3069	C	T	TTAAGGCGCAACACAC	TTTAAGGCACAACACAC	GGCAATCACATCTGTTTCATGCA	(0,0)	1	CCAGACGCAGCCATGTATACTG
Etr_3081	T	G	TCACAATCATCTCCTGG	TCACAATCAGCTCCTGG	TCCCTCCCTGTTTCAAAGCC	(0,0)	1	CTCGGCTTGTCTTCCAGGAG
Etr_3107	C	T	AAAGGACACCACAGATT	AAAGGACACTACAGATT	GGCAAATCCTTTCTAATTACCATCC	(0,0)	1	GCATCTCTGGCTGGCTAACA
Etr_3128	C	A	ACCAGTCACCAATGACT	ACCAGTCACAAATGACT	GGGACACTTGGAAGGACACC	(0,0)	1	AGGATTCCGACCACTTCACA
Etr_3145	C	T	GGTGCCCATCGGAGGA	GGTGCCCATTGGAGGA	TGGTGATGACGATCGTGGTG	(0,0)	1	TTCATCATCTTCCGCACGGT
Etr_3169	C	T	AAGCCGGTGCCACCGAG	AAGCCGGTGTCACCGAG	ATAATGGTTCGCGACAGGCA	(0,0)	1	ATAACACCGCAGCATCTCGG
Etr_3189	C	T	CACGCGCGCACGC	CACGCGCACACGC	CAGGTGCAGTACGCACTCA	(0,0)	1	GCGCCAACCGCTACAC
Etr_3234	T	C	TGATTTCTTTAGCTCCT	TGATTTCTTCAGCTCCT	CCAAGTGCTAAGTACTCACTCTGT	(0,0)	1	TGTTCATGAAGGGCACTGAGA
Etr_3240	T	C	AAACCTGGGTGTGGGCC	AAACCTGGGCGTGGGCC	ACCTGCGTCAGCTGAAAAAC	(0,0)	1	AAAACCATTTCGTTGAGGGCC
Etr_3253	A	G	CGAGTTCACACGCGAA	CGAGTTCACGCGCGAA	CAGGAGCAAGAGCAGTCTCA	(0,0)	1	CCACTTGAGCTTAAGTTCGCG
Etr_3255	C	T	GTGGGGGTCCCCGATGG	GTGGGGGTCTCCGATGG	CAGCCACTCCACCACCATG	(0,0)	1	TTCGAGTGCCAGATGACGC
Etr_3262	C	A	CCAAGAATGCT	CCAAGAATGAT	AGGTGCCTCCTTCCAAAAGT	(0,0)	1	ACTGTACCAGCTTAAGTGGAAA
Etr_3292	G	A	TGCTCTCAAACGTGTTCCA	TGCTCTCAAACATGTTCCA	GCAGGTGAACTGATTTCATGTATCCA	(0,0)	1	GAGCGGCAGCCTAGGAA
Etr_3330	G	A	GAACTTGATGGTTTGGG	GAACTTGATAGTTTGGG	ACTGGGGAAATGTGAACTTGA	(0,0)	1	ACAACCCCTTGTGTCGTCAA
Etr_3350	G	T	AGCAGGCCGTCTGTC	AGCAGGCCTTCTGTC	GGCAGGCAATAGATCCTCATTCAG	(0,0)	1	TGATTTTGGGCGAAGATTAACGT
Etr_3356	T	G	GCATACACGTACAACAG	GCATACACGGACAACAG	GTCATTGCTCCACACACGTG	(0,0)	1	CGGTGCTCGCAAAAAGAGAG
Etr_337	T	C	AGGTGAGTCTTTGT	AGGTGAGTCCTTGT	ATCGTCAGGAGGAGCCCAG	(0,0)	1	CTGGGTGGCAGGTTTCACAA
Etr_3383	T	G	CACCCGTTATAGAAAC	CACCCGTTCTAGAAAC	GGTCGTCTCGAGGTGTTTGG	(0,0)	1	GCACGCACGCGTCAA
Etr_3403	T	C	CGTATCCTTTCATGGGG	CGTATCCTTCCATGGGG	GCAAACCCAAATACGCATCGT	(0,0)	1	TTCCAGACAGCAAGGGCAG
Etr_3411	G	C	GCCGACCCCGCAGCCCG	GCCGACCCCCCAGCCCG	ATGTCGCACCTCCACATGAG	(0,0)	1	CGGGATAACTCACGGGCTG
Etr_346	G	A	TGAATTTTCGGCCATAC	TGAATTTTCAGCCATAC	TGGCGTGATCGGTAGAAACT	(0,0)	1	TGCAGCAATATAGACCTTACCTGT
Etr_3466	G	T	AATGGACACGATTCCAC	AATGGACACTATTCCAC	TGCCCCGAACATTGTAATGGA	(0,0)	1	ACGTAGCCATTCGACCACTT
Etr_3502	A	T	AACCCAAAAAAATGCTT	AACCCAAAATAATGCTT	TACAGCGCTACACATGCACA	(0,0)	1	GTCTTTAACGTGAAAGAACCTCCA
Etr_3549	A	G	CCCGTACATGGTCACC	CCGTACACGGTCACC	CAACCGCCATGCTTGCA	(0,0)	1	CTGCCGCTCGGGTCT
Etr_3555	C	T	CACCAACCGTGGCAAT	CACCAACCATGGCAAT	GCCCATCGCTCGTTTCAC	(0,0)	1	GCAGTGCGCCAACCATAA
Etr_360	G	T	TGGTGCGTTGGTGGTGC	TGGTGCGTTTGTGGTGC	TGCTTTCCATGAGTGGTGGT	(0,0)	1	AAGTGTGCGCATTTCATCCG
Etr_3601	T	A	CCCAAATAATAAACTTT	CCCAAATAAAAAACTTT	TGGCTCTCCACTATCCCAAA	(0,0)	1	GCCTTTGTTTTGATTACAAGAGCA
Etr_3638	C	T	ATTGTAGACCGAGCTGC	ATTGTAGACTGAGCTGC	TGTGCACGTTCTTAGGTCAGA	(0,0)	1	ATTAGTTGTGCACGCAGCTC
Etr_3725	T	C	TAGGTATCCTAGCTCCA	TAGGTATCCCAGCTCCA	ACACTGCTCCAGTAGGTATCC	(0,0)	1	AGATAGGGCCCAGACAGCA
Etr_378	G	T	AGTCAAAATGTATTTTA	AGTCAAAATTTATTTTA	CTGAGAGGCTGTCTGCAGAG	(0,0)	1	GCCCTACATTTGGGGAGTCA
Etr_3837	C	T	GACAATTGTCACGTGCC	GACAATTGTTACGTGCC	TGCCCTAAAGTTGACATCCGT	(0,0)	1	CCAGAAAGAATAAGCGCGGG
Etr_384	G	T	CCAAGATTTGTAATCTC	CCAAGATTTTTAATCTC	GCCACCCATTCTGGAATTCCT	(0,0)	1	ACGCATGTCCCATGATGCT
Etr_3885	T	A	AACATTATTTACAGTTA	AACATTATTAACAGTTA	GCACTTTGCTCGTACTGAACA	(0,0)	1	GCCAGTGATCCTGAGGTTTCT
Etr_3939	C	A	GGAGACCAACATATATC	GGAGACCAAAATATATC	TGAGTGTTCCTCGGGGAGAC	(0,0)	1	TTCGCTGAGGGAAGGAGAGT
Etr_3960	T	C	CATCGCCATTGATCG	ATCGCCATCGATCG	TGCAGGGATTACTGGTGTCAAAAT	(0,0)	1	CCCCTGGCCGCTTAGAAA

Etr_3963	C	A	TGTTGTGTGCGATGA	TGTTGTGTGAGATGA	CCCAGAAGGATGTTTGTTGTGT	(0,0)	1	GCATTGCGGTTAGAGCACTG
Etr_4000	T	C	TTGCACGTCTAAC	TTGCACGTCCAAC	CAGCGCTCTGGATTGCAC	(0,0)	1	TAGGCCCAGGAGGAAGCC
Etr_4015	G	A	TCTCGTCTCGGGGACTG	TCTCGTCTCAGGGACTG	ACTGTCGTATTTCCCTTCTCGT	(0,0)	1	CGGTAAATCGTGCATTGGGC
Etr_4028	T	C	ATAAATCAATGTCGCCC	ATAAATCAACGTCGCCC	TGCCTTGGAAATCCGACACC	(0,0)	1	TGTTGTTCCGTGGGCGAC
Etr_4037	G	T	TCACAAAATGAACTTGA	TCACAAAATTAACTTGA	TCCTGGTCTCTTTATTTCTCACAA	(0,0)	1	GCTTTCTCACAGCACTTGCC
Etr_4079	G	A	CTACATTCAGTTTAATG	CTACATTCAATTTAATG	TCTATGGGTGATTGCCATGTT	(0,0)	1	TGCACCAATCTTACCACGGA
Etr_412	G	A	CCTCGAAGCAGCTTT	CCTCGAAACAGCTTT	GGTAGCTTCTCCCCCTAATGCT	(0,0)	1	TGGTGAGAAAGAAGTTCAACATGCA
Etr_4130	A	G	ACGATGGCAACGACG	ACGATGGCGACGACG	CAGGCCGTTCCTGCG	(0,0)	1	GCTCCCCTCGGAAGCC
Etr_4142	T	C	TGTGCAAGCTGCCTTCA	TGTGCAAGCCGCCTTCA	CATCCTGTGGTCTGCACCTG	(0,0)	1	GAGACGATGTTGCTGAAGGC
Etr_4156	A	G	TAGCAGCTCAGGGTGCA	TAGCAGCTCGGGGTGCA	GTAGCGGTTGGTGTCTAGCA	(0,0)	1	GACGTCATCCTCAACGGCC
Etr_4165	C	A	GCCAATATTCTC	GCCAATATTATC	ACTTTCCTCTATCTTGCGCCA	(0,0)	1	GGAGACCGAACAGAGAATGGG
Etr_4173	A	G	CCAATGCATAAGTAATC	CAATGCATGAGTAATC	GCACAACAATGTTATAACGGCACAA	(0,0)	1	GACGCCATGTCAGAGAGACT
Etr_4194	A	C	TGCGAATCAAACTTCAA	TGCGAATCACACTTCAA	ACTTTCCAATGTGCCATGCG	(0,0)	1	ACTCCATCGTAACTGCAGTGA
Etr_4214	C	T	TGCGTTCACGTTCATAG	TGCGTTCACATTCATAG	TGGGTTCCTCGCACTGTTAG	(0,0.4)	1	TTCACGTTCCTAATGCTGTCTGA
Etr_4215	A	G	GATGTAGCGATACGTGA	GATGTAGCGGTACGTGA	TCCTCGTGGATGATGTAGCG	(0,0)	1	GGGCTGCACCAATACCTCTT
Etr_4254	G	A	CTTTCCCATGTGTGCCT	CTTTCCCATATGTGCCT	ATTCCTGCTTGTGCACGCTT	(0,0)	1	CGAGAGCCTTCACGCCTAAT
Etr_4281	A	T	ACGTGGCAGTCTATG	ACGTGGCTGTCTATG	TGCAGGAGGACTACACCAACT	(0,0)	1	GCACGGTTAGTCATTGGGTCAA
Etr_4288	A	T	AAGGATGATAG	AAGGATGATTG	AGCCACATTGCTCCTCATGT	(0,0)	1	TGGTGATCGACTGAACCAGC
Etr_4390	T	C	CGGTGGTCATGGGTCAT	CGGTGGTCACGGGTCAT	ACGTAATAGTTGGCGGTGGT	(0,0)	1	GGGCCTCACCTGGTTTTCAA
Etr_4414	G	C	AGGAGGCCGCCCGAG	AGGAGCCCGCCCGAG	CTCCGCATTAACCCCTTTGTC	(0,0)	1	GCGCGTGTTGTCCAAAATTG
Etr_4455	T	C	GTCTGAGCTTGCGGGGG	GTCTGAGCTCGCGGGGG	TCGTTCCGGGGGTCTGAG	(0,0)	1	GCCGTAGCTATTTGAGTCACG
Etr_4479	C	T	CATGATGCCCTTCTTGC	CATGATGCCTTTCTTGC	AATGATGTCGGCGCTGTACT	(0,0)	1	CTTGCGTGGGAGTACCGC
Etr_4498	T	C	GCAAGGGGTTGGT	GCAAGGGGTCGGT	TGGCAAGTGGCGGTAATTCT	(0,0)	1	AATGAATCGTGGCCCCTCTC
Etr_4504	C	T	CTGATTGTCCACACCAA	CTGATTGTCTACACCAA	TCAGACACTCCTGAGATCCCA	(0,0)	1	TTCATGGGTGGGAGTGGGAT
Etr_4521	C	A	GGTTGCACGCAAAGTCC	GGTTGCACGAAAAGTCC	GTAGCACAGCGGGATCTCC	(0,0)	1	CCTCGTCTCGCTGGACTTT
Etr_4531	G	A	CCGCACGCGCTCG	CCGCACACGCTCG	GTTTGAGTTTGCGAAAGGTACGA	(0,0)	1	GTACGTAGCGAGCGTGTGT
Etr_4544	G	C	TGTGATTCAGCAACCCT	TGTGATTCACCAACCCT	GGCACACTGGTTCCATCTCT	(0,0)	1	GAATTCGGGGTGTGGAGGTT
Etr_4574	G	T	CTTCCAAAGGCCCTGGT	CTTCCAAAGTCCCTGGT	CGGCGCACATCTTCCAAAG	(0,0)	1	GAGTGGAAGACGACGTCTCG
Etr_4633	G	A	CTGGGCAACGAAAGCA	CTGGGCAACAAAAGCA	GAAGGGACGAGGAGGAGAGG	(0,0)	1	CATGTCCAAGTCGCTGCTTT
Etr_464	C	A	TAGCGCTTCACCCCGTCCA	CGCTTCACACCGTCCA	TGCAGGGACCGCGTTAC	(0,0)	1	GTGCCCCACCGGTCT
Etr_4670	G	A	CCGTAACACTGTCCCCGG	CGTAACACTGTTCCCGG	AGGATCCGAGCCCATAATGAGA	(0,0)	1	GTTTGGTCGACATCGGAAAAGG
Etr_4686	T	C	GGTCTGCTATTCGGTG	GGTCTGCTACTCGGTG	CTAGGATAGCAGCACCGACG	(0,0)	1	CCAAGGCCCCTATGCGTAAA
Etr_4694	A	C	ATCACATACATAAA	ATCACATACCTAAA	GCACCATGACGCCTTCATTC	(0,0)	1	TCTGTTGAGTGGTGTGATATGCA
Etr_4716	G	A	CATCAGAACGATAGCCC	CATCAGAACAATAGCCC	GCCGACACGAGCATCAGAA	(0,0)	1	CCTGACTGTCTTGCCACGTA
Etr_4750	T	G	AGCTCGTTTTC	AGCTCGTTTGC	CAAGGTAAGCGGCAGTCAGA	(0,0)	1	ACTGCAATATACACCTGTCCTT
Etr_477	C	T	AGCTGCAGATCACCA	AGCTGCAAATCACCA	AAGTGGGTGCTGGACTGG	(0,0)	1	TCGCTGGTCCAGTAGATGGT
Etr_4800	G	A	ACCTGGTGCGAGAACGG	ACCTGGTGCAAGAACGG	GCGCTTGGGTTTCTTGTTGA	(0,0)	1	CTGCTGCTGCTGATTGAGTG
Etr_480-67	C	T	TTACGAACACTCG	TTACGAACATTCG	CGCACGTGCCTTGTTTATGT	(0,0)	1	TCCGACAATTCGCAAGTCGA
Etr_4845	G	T	AGATGTCCAGTCGGGGC	AGATGTCCATTCGGGGC	AGGAATCCGATGAGCTACGA	(0,0)	1	CGTACGTCGGACACCACTG
Etr_485	A	G	CACCAATTAAGCATTGTATTT	CCAATTAAGCGTTGTATTT	CAGCCACCGTCGACACA	(0,0)	1	AACTGCTGAAGTTACTGATGTTCACA
Etr_4853	C	T	CGTCGAAGGCCTCCAGC	CGTCGAAGGTCTCCAGC	CCTCGCACGGGGGTCTATA	(2.2,0)	1	GTGCAGGTTCACTCTCCCC
Etr_4859	C	G	CACAGGGATCGATGGCA	CACAGGGATGGATGGCA	CCCTGACCACCCACTCAC	(0,0)	1	AGCTTATATTAACGCAAGCGGC
Etr_4889	T	C	AGGTTATGTTATGAAGG	AGGTTATGTCATGAAGG	TGTTGGGAACAGGGCACAAA	(0,0)	1	CTTTGTTCGCGCCTTCGTTC
Etr_49	A	T	TTGTGATGCAACTTCGT	TTGTGATGCATCTTCGT	TGGGTGAGCGAGGATGGT	(0,0)	1	CGTCCACACTGCGTTCAAC
Etr_4965	T	C	CCACCGAGTTGGCTAC	CACCGAGTCGGCTAC	GCGCCAGGTGAGGAGA	(0,0)	1	CTCCTCTTCCTCGTTGCAACTT
Etr_5020	A	C	TGCAACGAAATAATTTAC	TGCAACGAAATCATTTAC	CCCCCACGTGACGCA	(0,0)	1	GCTGCAATGTGGGAGACCTTT
Etr_5043	A	C	AACAACTTTAATTCGGC	AACAACTTTCATTCGGC	TGCAGGGTTTATATTTGCCAAATCA	(0,0)	1	GGCGAATGGCGGTTGTTATT
Etr_5112	C	T	TTGGGGGTGCCCTTAGA	TTGGGGGTGTCCTTAGA	AGAACAGCTTGCATTGGGGG	(0,0)	1	GGCGTCTCGGAGCAAGTTAT
Etr_518	C	G	TCAGCGGTGCCAGGTCG	TCAGCGGTGGCAGGTCG	CCGGGATTCGAATTCTGGGT	(0,0)	1	CCTGAGCAGCCCGATGG
Etr_5193	T	G	TGGTTAATTCACCAGAAGTA	TGGTTAATTCACCCGAAGTA	ATTGGCCGCCCTCATGAA	(0,0)	1	ATACACTGTGAAGCAGATGGAACTT
Etr_5197	C	T	ATATATTTACGCGATCTAAC	ATATTTACGCAATCTAAC	GCAGGTGATTTGTCCATAAGAGGTT	(0,0)	1	GTGGTGGGTTTAACGACACATTT
Etr_5267	G	T	GAGACGCGCGGGCATGC	GAGACGCGCTGGCATGC	GGAAAGAGGCTCCGGCTG	(0,0)	1	AGTTGTCCATCATGCGCTCA
Etr_527	A	C	CAGCAGAAAAAGCA	AGCAGCAAAAGCA	GGTTACTCGGTTGGTATCACACA	(0,0)	1	GGCAATGCTGCTGCTTCTG
Etr_5272	C	T	GCGCGCAAACGATGCTC	GCGCGCAAATGATGCTC	CACCGTGTCCGAGTCGTG	(0,0)	1	GAGGACAGAGCGTGAAGGAG
Etr_5317	A	C	CACGAAATTTTGAACTTTT	ACGAAATTTTGCACTTTT	CGGATTTTCACCTTTTCTGCGTTTC	(0,0)	1	CAGTTCACGAGCCAGACTACAG
Etr_534	T	C	CCGTGCTCGTACAA	CCGTGCTCGCACAA	CTCCACGGTCTGCGTGAAC	(0,0)	1	CGGGTTAGCCTTCAAGGGAG
Etr_5346	T	C	AAGGCTCAATAATGC	AAGGCTCAGTAATGC	TGTGTGGGAAATGACAACATCCAT	(0,0)	1	GACATACGGTGCTGGTACTACAAT
Etr_5352	A	G	AGAATCTGGACAATGGC	AGAATCTGGGCAATGGC	ACAGGATCTATGGTCTGCAGAG	(0,0)	1	ACCCGTGAGACTCGTGAAAA
Etr_5465	A	G	CCGCGTGTTCCAGC	CGCGTGCTCCAGC	CGACTGCCCTTCGATGCA	(0,0)	1	TTGACCTTGACGGATTGGATCTC
Etr_5510	A	G	TCGTGTTGACCTCTTCAGTA	CGTGTTGACCTCCTCAGTA	TGCAGGAAGTAACTGTGTAATTAAACG	(0,0)	1	GCGACGTAAATATGTCTGCAAGTTT
Etr_5540	A	G	CTTTATGCCAACTGACA	CTTTATGCCGACTGACA	AGGCTGGAGTGGCGAATTTA	(0,0)	1	TGGAGGGAATGCCTTGTCAG
Etr_5581	G	A	ACCTAATCCGTCT	ACCTAATCCATCT	CCCCACCTACCTGCTGATGA	(0,0)	1	TGATAGGCGCGAAACCCATT
Etr_5600	G	T	CCAATGTCACTTGCACCGA	ACCAATGTCACTTTCACCGA	CAGGAGACGTAGCCCCTCTA	(0,0)	1	GAGTAGACAAGAGAAGACGAATTCACA
Etr_5603	G	A	GATACTCCAGCTCCTTG	GATACTCCAACTCCTTG	CGCTCCACATTGTTGAGAGC	(0,0)	1	GTTGTTGTGAGCTGTGCTGC
Etr_5626	T	C	TGTGTGATGTATTGGGC	TGTGTGATGCATTGGGC	ACGTTTTTGATAAAGGTCCCGC	(0,0)	1	GTCTGAATTTTCCTTGTGCCCA
Etr_5654	T	G	TGAGGAATGTAAAACTG	TGAGGAATGGAAAACTG	AGGAGATCGAGAGGCTCACA	(0,0)	1	TGAGACAAGGGTTCACGTGG
Etr_57	A	G	ATTAGCACAACGTGCCG	ATTAGCACAGCGTGCCG	GCGCCAATTGTGTTTTGTTGA	(0,0)	1	CCCCTCGGAGGTTTATTGCA
Etr_5711	C	G	CTCCTCTGCCGCGCGCA	CTCCTCTGCGGCGCGCA	CTCAGGCTGGATCGATGTCG	(0,0)	1	TTAACGCACGGACATCACCA
Etr_5757	A	G	GGTGCCAGGAAAGG	GGTGCCAGGGAAGG	TAACCAGCATCGCTTCGGAC	(0,0)	1	ATGTCCACATCGTCCTGCAG
Etr_5762	C	G	GCGCGACACCAACGACG	GCGCGACACGAACGACG	GGTAAACGTGGAAAGAGCGC	(0,0)	1	AAAGTCCCCGTCTCTTCGTC
Etr_5780	T	G	TTGTGATCTTCAGTATT	TTGTGATCTGCAGTATT	AGCTGGGTGGTTGAGTTGAG	(0,0)	1	ACAATGCGTGTGTTCAACCG
Etr_5831	A	G	GCAATGCGCATGCGCGC	GCAATGCGCGTGCGCGC	GCGCTCTCGATCCCTTGTTA	(0,0)	1	ATAAACTTCGGGTGGCCCAG
Etr_5960	C	A	ACTCGTCCACCAAACAT	ACTCGTCCAACAAACAT	TGAAGCCAAACACTCGTCCA	(0,0)	1	ACATGGAGGGCATGCAAATG
Etr_5993	T	A	TGGAGTCGATTGGAAAC	TGGAGTCGAATGGAAAC	GACACGTCCACCACAGGG	(0,0)	1	TGTCAGTGTTTTCGCAACGAC

Etr_6026	C	T	TCCACCCAGCCCTACC	TCCACCCAGTCCTACC	TCGGGAGGCACGTTCTTC	(0,0)	1	GCATAAAATCGGCAGAAATGAGAGA
Etr_603	G	A	AGGTGTTCCAAGTTTGTT	AGGTGTTCCAAATTTGTT	CAGGAGGAGAAGCCGTGG	(0,0)	1	GGGCAGGGAAGAAGTGAGT
Etr_6076	T	C	AGGAGAAATTCCTCAGC	AGGAGAAATCCCTCAGC	GCTGAGCATTTCTCCGAGGT	(0,0)	1	TCAGCCAGCCACTTATAGGC
Etr_615	A	G	CACGGCACGGTCG	ACGGCGCGGTCG	GCGGCTTGGGATGTTATCTTCAATA	(0.3,0)	1	GCCTGGGCGGCCTATC
Etr_6179	T	C	AGCTCGCAGTGAC	AGCTCGCAGCGAC	ATGCCAGGACACAAGTTCGT	(0,0)	1	CTGCTCATGCTCCACAGGTC
Etr_6229	A	G	TTTGGTGCAAACTTACC	TTTGGTGCAGACTTACC	CCCCCAAACATTGCTTTGGT	(0,0)	1	ATGCTGGTTGGGCTCTTACC
Etr_6318-70	C	T	TGCCCGACGCGACTC	GTGCCCGATGCGACTC	GACTTGTTCCGGCACTACCC	(0,0)	1	GCCGTGAAAGAGAGCGTGAG
Etr_6363	A	G	CTAAAGTATAATTAAAG	CTAAAGTATGATTAAAG	CACGATGCCACAAACATGTCA	(0,0)	1	GCGTTTCATTTTTCATTGGATCCC
Etr_6369	C	T	GCTGGTGCACAAGCAGA	GCTGGTGCATAAGCAGA	GAGCAGGACAAAGGCAGGAG	(0,0)	1	CTTCCGCTCCAGCTGATTCA
Etr_6389	G	A	AATGGTAAACAGAGCATTG	ATGGTAAACAAAGCATTG	ACATTACCTGTAGGTGGTTGTTAAAGG	(0,0)	1	CCACGATTATAATCGGCAAGATCAC
Etr_64	A	C	CCTGTACTGAAAGTAACTC	CTGTACTGAACGTAACTC	GGAGGCGCTGTAGCTTCAT	(0,0)	1	AGGACTTTCTTTTTAGGTTTGTAGCCAAT
Etr_640	G	A	AAGTAGGATGGTGGCCT	AAGTAGGATAGTGGCCT	AGGTAGCACAGCAAGTAGGA	(0,0)	1	AATGCCCCAAAAATCCGTGG
Etr_642	G	T	TGCAAGGTTGGAA	TGCAAGGTTTGAA	GACGCTCACTGCATGCAAG	(0,0)	1	ACCATTTTCATGCCACCCCA
Etr_6436	G	A	GTCAACAATGTGCGACA	GTCAACAATATGCGACA	CAGGGAGCACTCGTCAACAA	(0,0)	1	GATGTGGCCAGTGACAGACT
Etr_6440	G	A	ACAGCGGTTGTCCTCAG	ACAGCGGTTATCCTCAG	AGTCAGTACATTGAGTTCCAACT	(0,0)	1	ATCCCTCATCCCCATGGTCA
Etr_668	A	G	CGCAACCAATGCCGC	CGCAACCAGTGCCGC	GTCCCGTGGACAAGAGTCA	(0,0)	1	GCTGCCAGGCACTTGTG
Etr_673	C	T	CGGCCGCTTCTCT	CGGCCACTTCTCT	GCCGACAGCTGCTTCTCT	(0,0.5)	1	CCACGTTGCTGTTGTTTTGTCA
Etr_678	G	T	GGTAGGTCAGGTCCGCT	GGTAGGTCATGTCCGCT	AAACTGGGCTTGGTAGGTCA	(0,0)	1	ATTCTTGACCGTCGGCTGTC
Etr_681	C	T	AGCACGAGACGAGCGG	CACGAGACAAGCGG	CGCGTCGCCATAGGTGTT	(0,0)	1	CAAGCACATGCTCAGCAACAG
Etr_687	C	T	TCGCCACTTCATTCACC	TCGCCACTTTATTCACC	AAGAAGCTCCATCGCCACTT	(0,0)	1	CGTGGTTTCAGTTGCGAAGG
Etr_705	G	A	CCGCTATCTCCGGCTGG	CCGCTATCTCCAGCTGG	AGCAGAGACACGCAACGTAAATA	(0,0)	1	GGTTGTGCTGGACATTGTTATTTGA
Etr_7081	T	C	ACATTGTTCTATTCTCA	ACATTGTTCCATTCTCA	GGAAGAAAGAGGGAGGCCTG	(0,0)	1	AGCACAATTCGTCGTAAAGGG
Etr_7142	G	A	GGTCTTGGCGCCACGGT	GGTCTTGGCACCACGGT	ACCGGTGTTCTCTTAGGGGT	(0,0)	1	GGCATAGTCAGGGTCGAACC
Etr_7166-73	G	A	TTCAAAAGTTGTCGA	TTCAAAAGTTGTCAA	CAAGCAGCAGTGAGAGGACA	(0,0)	1	TGCCAGTTTAAAGCTAAGCGA
Etr_717	T	G	CAAGACAAAGATCCACACGTG	CAAGACAAAGATCCCCACGTG	CCCCAAAGAGTACGAACGGTTA	(0,0)	1	CGATCGCTCGTCAGATTCTCA
Etr_7292	T	G	TGGTAAAATTTACT	TGGTAAAATGTACT	CAGAAGTGATTTGGAATCGGCA	(0,0)	1	GGCCTTCTCTGCATATATACCAGT
Etr_73	T	C	CGCTGTCATGTTCC	CGCTGTCGTGTTCC	TGGCAGGTGTGGAAAGCA	(0,0)	1	CTCGCGCTGTTAAACCTCTTG
Etr_7358	T	C	GCCAGTGAATGTGAACG	GCCAGTGAACGTGAACG	GAAACACAACCGCAGCCG	(0,0)	1	TGGCGTTCACGTGTTTTGTC
Etr_7382	C	G	CAGTGGAGGCAGTTAGA	CAGTGGAGGGAGTTAGA	AGGTGGTAGGGTTAAGGCGA	(0,0)	1	TCCTCAAACACCCCGATTGC
Etr_7387	G	T	AAGGAGTGGCGGTGTAA	TGAAGGAGTGGCTGTGTAA	CGGTGGTCGAGGCGAA	(0,0)	1	CGTCTCCGCGGAAGGT
Etr_7416	T	C	CTCCTGTGACATCCAG	TCCTGTGGCATCCAG	GTGTCGGCAAGGGTGAGATAT	(0,0)	1	AGGAGCTTGACAAAACAAAAACAGATTTATTATC
Etr_7443	T	G	TCCTAGGTTTG	TCCTAGGTTGG	GCCTCGATCAGGTCCTAGGT	(0,0)	1	CCTCTTCACCCTCCCCTCTT
Etr_752	A	G	GTGCGTGATAAA	GTGCGTGATGAA	TGGGTGGGTGAGTTTGTGAG	(0,0)	1	GCTGTTAGCGAGCACAACAC
Etr_754	T	C	CTCGTTTCCGTTCTGCCT	TCGTTTCCGCTCTGCCT	CAATTATAGCCGAGGAGCCCAT	(0,0)	1	AAGATCGGTGAGGCAGAGAGA
Etr_7649	G	A	ACGAGTGGGAGCCTG	CGAGTGAGAGCCTG	CCTTCCCAGACAGAGGTTGGA	(0,0)	1	GGCAAACACGCACCTGTAG
Etr_766	T	C	ACGATCTGTTCTCTTAGTAGC	CGATCTGTTCTCCTAGTAGC	GGAAGCTGACAGCCAACATTG	(0,0)	1	GGCCTGCGAGACATTGAGT
Etr_7781	T	C	GGGGGAGTGTGGCTGTC	GGGGGAGTGCGGCTGTC	CTCCCTGCAACCACCTGAC	(0,0)	1	CACGTACTCAGCTCACAGCC
Etr_781	C	A	CTGGAAGAAATGATTCTC	ACTGGAAGAAATTATTCTC	GCCACTCTTGTCGTTAACCTTGA	(0,0)	1	CGGGCTTGGGTAGGATATGTC
Etr_785	C	T	TTGGTGCAGGAAGTGA	TTGGTGCAGAAAGTGA	GGACGCGTGCCAATTGAG	(0,0)	1	GCCCGATTGGCCACCAT
Etr_786	A	T	TGCTTCCCCAGCAATTT	TGCTTCCCCTGCAATTT	TCCTCTTTCTGTTGCTTCCCC	(0,0)	1	AACGAGCTCGGGAAAAGAGG
Etr_7872	T	C	GGAATTCTATGGAGGCT	GGAATTCTACGGAGGCT	GCACAATGCAAACAAGGCTG	(0,0)	1	GCACTGGAAGCCCTTACACT
Etr_7918	T	C	CCGACGGGATATCCGAG	CCGACGGGACATCCGAG	TACGGACCCAAAGCAGGTTG	(0,0)	1	AGCTCCACTCCTCACTCCTC
Etr_7974-70	C	T	TTCGTGTCGACACC	TTCGTGTCGATACC	CTTCAGCGCCACGTTCTCAG	(0,0)	1	AATTCAGCAGGAGAGGCCTC
Etr_8064	A	G	GATCTGTCCACCATTGG	GATCTGTCCGCCATTGG	GTGTGATGCTTCTGATCTGTCC	(0,0)	1	GCGCAAAGTGTGAAAATCTGG
Etr_810	A	G	CCAAAGGCACCCTCC	CAAAGGCGCCCTCC	CAGGTAGTTGATGGTGACCCA	(0,0)	1	GCAGCGCTCGCATCCT
Etr_814	C	T	TTTCTGCCCCAACACC	TTTTCTGTCCCAACACC	GGTCCACGGTCCGATGTG	(0,0)	1	ATGAGATGACTTAACAAACAAAGATTGCA
Etr_8196	A	C	AGAAGGACCTCAAATAGAT	AAGGACCTCCAATAGAT	GCTTGTTCGCTCACGACACT	(0,0)	1	ACCTCGAACTCGCTTGCT
Etr_824	C	G	ACCGATGTTCGTGGCCG	ACCGATGTTGGTGGCCG	TGCAGATGTTCGTCACCGAT	(0,0)	1	CGACCCAGCCTCAAATGAGT
Etr_8281	G	A	CCTTCTGCAGCCTTCGC	CCTTCTGCAACCTTCGC	GGAGAGTATTCCTCGTGCCG	(0,0)	1	ACAGACTGGTGAGGCAAGTG
Etr_8298	G	A	GAACGAGCAGAGCTGGT	GAACGAGCAAAGCTGGT	TCTGCTGAAGTGAAATCCGGT	(0,0)	1	AGCAATTAAGCAGGACCCCT
Etr_832	C	T	ACGAGTTCTCGACGTTCA	ACGAGTTCTCAACGTTCA	GCAGGTCAAAGTAGACAGTCTTGTG	(0,0)	1	GCACCTACGAGATCTGCTTCAG
Etr_833	G	T	GCAGCATGTGGGGGCAG	GCAGCATGTTGGGGCAG	CTTCGGGAGGCAGCATGT	(0,0)	1	AGCTGTTTCGTGGGCCATTA
Etr_836	A	G	ACGTGATCACTGCCGTC	CGTGATCACCGCCGTC	ACGCAGCTGCTCTCTGATTG	(0,0)	1	GTGCCGCTCAACAGCAT
Etr_84	A	G	CTGAAGTCTCGTAGTTACG	AAGTCTCGTGGTTACG	TGCAGGTAAATAGAGGTGTGATCCA	(0,0)	1	CCCTGTGCTGATGTGTGTAGAA
Etr_8649	G	A	AAGGCACCGGGAGCAAC	AAGGCACCGAGAGCAAC	TCTCAGGAGGCTGGGTAAGG	(0,0)	1	GCCAAGGCAAGTAAACAGTGT
Etr_8681	T	C	GACGCAGGCTGGTTGGC	GACGCAGGCCGGTTGGC	CTTACACGGACCCACGCTG	(0,0.5)	1	CGACCGTGTGATTTGCATCG
Etr_874	C	T	GAGTGGCGTCGACGCAT	GAGTGGCGTTGACGCAT	AGGGAGAGCCTCAAGAGCAT	(0,0)	1	TGAGAGTGATGGTTCTCAGGA
Etr_875	C	T	AGCGCGCCTCGTC	CAGCGCACCTCGTC	TGCAGGCAACGGTTGTAGAG	(0,0)	1	CCCAACGGGACGAGGTTTT
Etr_8780	T	C	GCATAAAACTTCAAATC	GCATAAAACCTCAAATC	TCGTTGTTGAAACATTGGCAT	(0,0)	1	ACATCTCGGCGTAAGTGATTTG
Etr_8960	G	A	CAATGCCCCGAATGGTG	CAATGCCCCAAATGGTG	TTCAAAACGCCTCGCCAATG	(0,0)	1	AGTGGCAGTGTTCCGGAAAA
Etr_899	A	G	CATTCGCCACTTGCT	ATTCGCCGCTTGCT	ACGGTGACATAGTCTCCTGGTA	(0,0)	1	GGCACTGGATTCACACCATGA
Etr_905	C	T	GTGCGTGTTCTCCCGCA	GTGCGTGTTTTCCCGCA	GCTTCTGCAGGGAGTCTTGT	(0,0)	1	TGAAGTTCCTGCGGTACCAC
Etr_906	G	A	CACCGTCTTGATGCT	CACCGTCTTAATGCT	AGCCAGAGTTTGCTTCACCA	(0,0)	1	GCATGCGAAGGCCAAGAAAT
Etr_9113	C	A	ATATGCGTCCGATAGTT	ATATGCGTCAGATAGTT	CTGCAACACGGCTCGAAATA	(0,0)	1	ATCACTTTGCATGCCCCGAA
Etr_917	G	A	TGAGGAAATCTGGACACTC	TGAGGAAATCTAGACACTC	CAGGTGGCACCGTTGGAT	(0,0.3)	1	CCACAAATATTGAACACAACTAAGACACAT
Etr_9189	G	A	AGGACACACGTAACATC	AGGACACACATAACATC	GACACGTGTCACCCTGTCTG	(0,0)	1	TGTAAAATGTTTTCACGCAAGATGT
Etr_930-35	G	C	TGACGGGGAGCGGTAAGG	TGACGGGGAGCCGTAAGG	GAAGCATCAGGGAGGGTGAC	(0,0)	1	TGCACACGTCTGATTGATCAC
Etr_951	G	A	TCATTTGCTGGTTGG	TCATTTGCTAGTTGG	TCCCTCAAAACGAATGTTCAATT	(0,0)	1	GCGTGTCACTGCTGAAACAT
Etr_963	T	G	TGCGTCTATGTGTTATTAT	CGTCTATGTGGTATTAT	GCTCCCACCACTGATGGAT	(0,0)	1	CGGATTGACCATATCTGGTGAAGAT
Etr_965	C	T	TGTAGGCAACGGAGCCC	TGTAGGCAATGGAGCCC	GGTGTCTCTGCACTATGAGGT	(0,0)	1	TCCTCTCTGGTCATCGTGGG
Etr_97	T	G	AGTCGCATGCCCC	AGTCGCCTGCCCC	GGTAGCGCTCCGGTCAG	(0,0)	1	GACCTCCATGGCTCTTTGCT
Etr_972	C	T	ACGTGACACCTGAGTGC	ACGTGACACTTGAGTGC	TCGCACTGAATCACGTGACA	(0,0)	1	AGTGGCATTGGCTGGAGAAA
Etr_98	T	C	TTCACACTGTAGGTC	TTCACACTGCAGGTC	CCGTTTTTAAGCCACGTGATG	(0,0)	1	CTCAAGCAGCCAGTGGACC
LampSD_327	A	G	AAGTAGGTGTCTCAGTAAAA	AGGTGTCTCGGTAAAA	GCCTAAACCACTCGGATGCA	(0,0)	3	ATGTCAACAAACACAATCCACACAATT

LampSD_478	G	A	CCCAGGGCGTGCCG	CCCAGGGTGTGCCG	CAGGAGTAGGCCGCAGTAG	(0,0)	3	CGCTGTGCCTGTGTCAGAT
LampSD_700	G	T	ACGACGCAAAGCG	CGACGAAAAGCG	TGCGATCGCTGATGCTGTAG	(0,0)	3	GACCCATACCGGTTTCACCAT
LampSD_1589	G	T	AGGGAGCCGATATTG	CAGGGAGCCTATATTG	CGACGTTGGGCAAATCGTT	(0,0)	3	TCACTGTTTCCATCGCAGTACTTATTAAA

Appendix 11. GT-seq SNP panel for lamprey species complex

Assay	A1	A2	A1-Probe	A2-Probe	FWD Primer	Corr.	Flag	REV Primer
LampSD_1589	G	T	AGGGAGCCGATATTG	CAGGGAGCCTATATTG	CGACGTTGGGCAAATCGTT	(0,0)	3	TCACTGTTTCCATCGCAGTACTTATTAAA
LampSD_327	A	G	AAGTAGGTGTCTCAGTAAAA	AGGTGTCTCGGTAAAA	GCCTAAACCACTCGGATGCA	(0,0)	3	ATGTCAACAAACACAATCCACACAATT
LampSD_478	G	A	CCCAGGGCGTGCCG	CCCAGGGTGTGCCG	CAGGAGTAGGCCGCAGTAG	(0,0)	3	CGCTGTGCCTGTGTCAGAT
LampSD_700	G	T	ACGACGCAAAGCG	CGACGAAAAGCG	TGCGATCGCTGATGCTGTAG	(0,0)	3	GACCCATACCGGTTTCACCAT
Lri100P121189	A	G	CACAGGCTCCGG	CGCAGGCTCCGG	GGGGAGGGAGAACACCACT	(0,0)	1	GCCGATGAGCTGTATCTGCTT
Lri101P1393771	C	T	GGTACGGGGCGGT	GGTACGGGGTGGT	CTGCAGGAACCCATGTAAATC	(0,0)	1	CGGTGGCATATTTTGTTTGAC
Lri102P1900277	G	T	AAATCCTTGCGGC	AAATCCTTGCTGC	CTAGTGTGGGGGTACAGCAGAC	(0,0)	1	AGCTCTCCTGCCTGGGTATAG
Lri1046P6449	C	T	GCTCCAGACGGCG	GCTTCAGACGGCG	CAAAGCGGGGTGTTTTGT	(0,0)	1	GTACACGCACCGCACCAG
Lri104P686936	G	A	AGGACTTCTCGGA	AGGACTTCTCAGA	CAGCAGGCGTTTGAGCAC	(0,0)	1	CAGGCGATGATCTGGAGGT
Lri105P1231914	G	A	TCACGGCCCTGGA	TCACGGCCCTAGA	GACAACCAGCTGGAGAGTCTG	(0,0)	1	CTCACCTTAAGGCGGTTTCC
Lri106P1252618	C	T	AGCGTGAACGCAT	AGCGTGAACGTAT	AAGCTACAGTCGTGCACATTT	(0,0)	1	CAGGGTTGGCTAGGTGAATG
Lri106P1790668	A	G	AATTGGGGTC	AGTTGGGGTC	AGACATGGTGCGGAATTATACA	(0,0)	1	GCTCAGATCGGTTTTAATTTGTG
Lri107P679417	A	G	GCCTGCAGGAT	GCCTGCAGGGT	CTTGATATCGCTGCCGAGT	(0,0)	1	AGTCGCGTGCAGTTGGAAT
Lri108P658763	C	A	GGGCGCCGGCATG	GGGCGCAGGCATG	CTGAGACCATGCGATCGAG	(0,0)	1	CAGCAACCCACTTGCTGTACT
Lri109P766527	A	G	CATTAATAATAGA	CATTAATAGTAGA	GAGAAGCACTGTCTAGGCCATAA	(0,0)	1	CCAGAATCATCATTGTCAGTGG
Lri10P1667154	C	T	TCCGTCCGGCCGG	TCCGTCTGGCCGG	CTGCAGGAGCAGCTCGAC	(0,0)	1	CGAAAGAAGTTCAACACACGTA
Lri10P6216903	C	T	CAGGGCGTGCTCG	CAGGGTGTGCTCG	TGGAAGAGTAGGCCAAAAACAC	(0,0)	1	CAACAACATCCTCACAGACACC
Lri10P8084542	G	A	CTTAAACCAAGAC	CTTAAACCAAAAC	CTGCAGGTGCTGGTTAATATAGG	(0,0)	1	GTGCCTGGGAAAATGAGAGAC
Lri10P8119699	G	A	CAATGACACGGGGA	CAATGACACGAGGA	GTTCTCCGCGAGCTCCAC	(0,0)	1	CAGCTCTTGTAGCAGGGTTGAC
Lri10P9580222	T	C	CAGAGTACCACCC	CAGAGCACCACCC	CTCCTTGCCAGCTTTCGTAAC	(0,0)	1	CACCAAAGCACCAGCAGAT
Lri112P1524062	G	A	CCAACGAGCCGCG	CCAACGAGCCACG	ATAGATGAGCACCGGGACGA	(0,0)	1	ATGAAGGCGTCGATGTAGTC
Lri113P109152	C	T	TTGACATGACCTC	TTGACATGACTTC	TCCACTCAGAAGAACTTGACTCC	(0,0)	1	GGATGAGTGGCTGCTGCT
Lri11433P5520TD58	A	G	CGTCTATTTCA	CGTCTGTTTCA	CTGCACTCACTACACGCAGGT	(0,0)	1	AGTTGATGCTGCCGGATG
Lri11465P555	C	T	CTGCAGGGCTC	CTGCAGGGCTT	CCACTGAAGGTTGTGAAAGGTT	(0,0)	1	TGCATCAATAATTAACGTGTTGG
Lri117P1107147	A	G	GGCGCTCGGTACCT	GGCGCTCGGTGCCT	ATGATGAAGCCATGTCTGACC	(0,0)	1	CTGCAGGAGAGCGATAGTGAC
Lri118P1477521	G	T	AATGCCTGCAGGAA	AATTCCTGCAGGAA	ACGGCATCTATTAGTCCACCTC	(0,0)	1	CGAGCGAGGTAGTTTGATGTTT
Lri118P434131	A	G	CAAGTGTTGGGCA	CAGGTGTTGGGCA	CCCAGGATGGACACGTTG	(0,0)	1	GAGTCGGCTGGGATTTTCT
Lri119P1436785	A	T	TTTGACAGCACAC	TTTGACTGCACAC	CCTGCAGGGAAAAAGTGAGTT	(0,0)	1	TTTGTTTGAGAGTGCACGTTGT
Lri11P11536190	A	G	CGCTCAGACCGCTG	CGCTCGGACCGCTG	ACCCCTTCAAAGCAGTGGAT	(0,0)	1	TTAGTGGCGGGTTTTAAAAGTG
Lri11P11704965	A	G	GTAACGTTCAAAT	GTGACGTTCAAAT	ACAGTCGTTCGGCTCAATG	(0,0)	1	TCAGTCCCAACCAAACAAGT
Lri11P2066282	T	C	TTATAAACCACAA	TTACAAACCACAA	TAATGGGAAGACAGACGACGAT	(0,0)	1	CCAAACTTCCACAAGTTCACCT
Lri11P311028	A	G	GCGGCTCCTCACG	GCGGCTCCTCGCG	TACTTCCCAGCGAAGAAAGTCT	(0,0)	1	ACGGCGTCACCAACAACT
Lri11P3590370	T	G	GCGGGACGCGTAA	GCGGGACGCGGAA	CAGGAGCTGCACAAACACC	(0,0)	1	ACGGGGAGTCGTAATGCTCT
Lri11P8775214	A	G	TCCGCACGCGACA	TCCGCACGCGGCA	GATCTCGTCGCCGTGGTT	(0,0)	1	AGCAGAGTGGCGTTGCTC
Lri125P779292	G	C	TTCTAACGGA	TTCTAACCGA	TCGCGTCGAGGTCAAAAG	(0,0)	1	GATGATCCCTTCCCACAGG
Lri12696P1650	C	A	CTTGGGACTG	CTTGGGAATG	ACCAATATCAAAACTGGGGTTG	(0,0)	1	GTTCATTGTCCTGCAGGTTGT
Lri128P486601	C	T	CTGTGGTGGAC	CTGTGGTGGAT	ACGTCTGCACACGAGGTCAT	(0,0)	1	GGACCCTGCAGGAGAGGAC
Lri12P11460075	G	A	CCCTCGCCGCTCG	CCCTCGCCACTCG	GCACCTGCAGGAGATTCATTTA	(0,0)	1	AGTATCGGTGCGGTGTGATT
Lri12P1774736	C	G	GACTGTCGTTCAGC	GACTGTCGTTGAGC	CACCTCCACTCAGCCTTGTT	(0,0)	1	AATTTCCCTGCACAAGAACAC
Lri12P182981	A	C	CTAACGAAACATG	CTCACGAAACATG	GCGGCATACGACTATTAGGG	(0,0)	1	CAATTTGCATGCACAAATACAA
Lri12P183087	A	G	TGTGGCGAATACA	TGTGGCGAATGCA	ATTGTACGCAAAAACAATGTGC	(0,0)	1	GTGTCTCGTCTGCATAGTTTCC
Lri12P1838366	G	A	GTGCCGAAGCGTT	GTGCCGAAGCATT	CAAGGCGGTACCTTTCACCT	(0,0)	1	GACGATGGGATGGCGAAG
Lri12P279478	G	A	TCCAAACAAGGAG	TCCAAACAAAGAG	GCATTTTTATCATGCGCCTATT	(0,0)	1	GTGTCATGCAGTGCTGAAAAA
Lri12P3082762	G	A	GGTGGCTAACGAC	GGTGGCTAACAAC	AAATGAATTGCGTGCAAGAGA	(0,0)	1	GGCAAACAAAACAAAGGAGAG
Lri12P5470970	A	G	TCCCACGCTGACG	TCCCACGCTGGCG	AAAATGTGCGTTTAGATTATTTGG	(0,0)	1	AGCTCTTTTTCAATGGTGACCT
Lri12P6060911	T	C	CAGTCGCCCTTCAG	CAGTCGCCCTCCAG	TCAAGATCGACCTTTGTAGAGGA	(0,0)	1	TCTTTCCCCTCCTACTTTGTTG
Lri12P7199624	G	A	GGTGTACAAAA	AGTGTACAAAA	TTATTGTGAGGGCGATGTTAT	(0,0)	1	GGGCTAACTCTCCTTGAACTTG
Lri12P8386432	C	G	TCTTTAGCAACGT	TCTTTAGCAAGGT	AAAGACCTGCAGGCTCATAAAG	(0,0)	1	AACAGCTCCCGGTATTTCTCTT
Lri12P9648016	G	A	GCAGGCAGCAGAG	GCAGGCAGCAAAG	TCGCTGCACACAACATCC	(0,0)	1	CTCTGTCTGCGTGGAAGGTAG
Lri131P901089	C	A	GAGAAAACAGCAAT	GAGAAAACAGAAAT	TATTTCACCACAATTGTCAGCA	(0,0)	1	GTTACGGTCAGTAGAGGGCAGT
Lri134P444626	G	A	ATCGAGCCGAGTC	ATCGAGCCGAATC	GCAGGGTCCTGTTTATTATTGG	(0,0)	1	AGACATCGTCCACCATTTGAC
Lri137P957664	A	C	TCAACCACAAATA	TCAACCACAACTA	GTAGCAAACCAGAGGGGAAAAT	(0,0)	1	TCGTAGTAGTTATTGTTACAGGTGTGT
Lri139P639349	G	A	GACCGGAGGGCTG	GACCGGAAGGCTG	ATTTCGAGCCAGTGTGACAAAT	(0,0)	1	GCTCCAGTACGCACTGCTTGT
Lri13P10838895	C	T	GTGTCAGGTCCCG	GTGTCAGGTCTCG	CCCTATTATAAGCGCCTAGTGG	(0,0)	1	AGGGAGTGACATCACCAATACC

Lri13P11116125	C	T	TGCTCCATGGC	TGTTCCATGGC	AGCTGCTGTTGCTGGTGAG	(0,0)	1	ATGCGAAGGCCAAGAAATAC
Lri13P4766961	T	G	GTTATGATATTT	GTTATGATATGT	CAAGAGGATGCAGGTGGTGT	(0,0)	1	GTTGAGGAGCACTGGGCTATC
Lri13P6132767	A	C	GTGTACAGACCGT	GTGTACAGCCCGT	CTGACACTGCTCCAGCACCT	(0,0)	1	TGCCCTCGACATGTTTGTG
Lri13P6221318	C	T	ACGCTGCTGCACG	ACGCTGCTGTACG	CTCCTCGCAGCTCTCCAA	(0,0)	1	CAGAGGACCAGGATGAGACTG
Lri13P6230623	T	G	AAATAGAGACTCG	AAATAGAGACGCG	TTGTCCTCCACTGCTAGGCTAT	(0,0)	1	CCTGCAGGCCGTATGTGT
Lri13P7256497	G	A	TTATGCCTTTGAC	TTATGCCTTTAAC	AACCATCGGTCATTATCCAGTC	(0,0)	1	CCACCCTGCAGGTTTTAGAATA
Lri140P591452	C	T	GGGCCGATGACAG	GGGCCGATGATAG	GCCTGTAGCACGGCACCT	(0,0)	1	GTGTCATGTGTCACGTGTGTG
Lri1432P16471	A	G	TGCCATCAGAATC	TGCCATCAGAGTC	GGAACAACACTTTGCCTTTGAT	(0,0)	1	GAAGGCCAATTTAAAGAGGTGA
Lri144P657672	C	T	TCAGTCACCCTGTG	TCAGTCACCTTGTG	CCTGCAGGTTCCACTGACTC	(0,0)	1	AGAGACTGATGCCCCCTTG
Lri148P462863	G	C	TTACGCACTCAAT	TTACCCACTCAAT	TAGGCAAGTGGTAAAGGGTGAT	(0,0)	1	GGTGAGTGGGTGAAGTCTGTG
Lri149P787096	T	G	GGATGGCATGTCT	GGATGGCATGGCT	TTGTCTCGATGTGAGCAAGACT	(0,0)	1	GCGCCTATAGAGACACACTCG
Lri14P11709110	A	G	CACTCCACCAAGT	CACTCCACCAGGT	CACACTCAGCTCCGTCTTCA	(0,0)	1	CTCCAGCCTTGACCCATGT
Lri14P2900879	G	A	CCTCCTGGGCGAG	CCTCCTGGGCAAG	ATCGAAGGCACCTTGGTAGTT	(0,0)	1	GACTACCTGGTGGTAGCCAGTC
Lri14P3595836	C	G	TGCAGGTGCTC	TGCAGGTGCTG	GTGAATGCCGCCAGTAAGAC	(0,0)	1	CGCCTGCAGGAATTGTAAATA
Lri14P3895562	T	G	CTTATTTTATTT	CGTATTTTATTT	TGGTTGTGTTGCTGTACATTTG	(0,0)	1	CGCTGTTTTATTGCAGATTTCA
Lri14P3943878	G	T	AGGAAACATTGT	ATGAAACATTGT	GCCAAGGTACGTCGATCAT	(0,0)	1	TTCACGGTGGAGTCTGAGATTA
Lri14P4079387	C	A	AAAAGTAATGCTA	AAAAGTAATGATA	AAATCCCAGGTATAAGCCTTTG	(0,0)	1	TTACAGTTGGCACCATTGAAAC
Lri14P4102727	G	A	GAGCCATTCCGGC	GAGCCATTCCAGC	AATAGCCTATCTTTCCTGCCATC	(0,0)	1	GGGCGTACAATAAATGGTTTG
Lri14P4106054	G	A	GACGAGATCTGGC	GACGAGATCTAGC	AACACGACATGTCTGCAGAGTC	(0,0)	1	TCTAACACCATTGCATGAACAA
Lri14P4985173	A	C	AAGGACAGGGAAC	AAGGACAGGGCAC	TCAACAAACTTAAACTCACCGTAT	(0,0)	1	CCTGCAGGTTATCATCAAGAAG
Lri151P237159	A	C	CGTCACATCACCA	CGTCACATCCCCA	GGCCCAAACCATTGAACAGT	(0,0)	1	AGCCCCATGACAAGACTCC
Lri159P658357	T	C	AGCGCGGCCGTAC	AGCGCGGCCGCAC	GTTTGTAGCCCCTTGCCAAC	(0,0)	1	CGGTGACAAAAGAGTTTCAGAG
Lri15P1409554	T	A	GAGTTTGAATCCG	GAGTTTGAAACCG	GCAGGTTGAAATTGGAGGTTAC	(0,0)	1	AACCCTTCTTGCTGGGATG
Lri15P2172074	A	G	AAATTGTAATTA	AGATTGTAATTA	CGCACTGGGAAAGTTGAGTAA	(0,0)	1	TCAAGACAAGTGTTCACCAATG
Lri15P6598748	G	A	GTAATGTGCAC	ATAATGTGCAC	ATGTGTCCGTGTGTTCTATGGT	(0,0)	1	GCAGGGAGAAATCCTTTCAATA
Lri16103P3900	T	C	AGCAGACCTATGC	AGCAGACCTACGC	TTCAGCCACTTCAAGGAGAACT	(0,0)	1	CTGGTAAATGGCCTTCCTGTAG
Lri162P690722	C	T	CTCCAAATCAG	TTCCAAATCAG	ATTGCGTGCTGTGCTGTCT	(0,0)	1	GGAATTATGGGCTGAGTTGATG
Lri1725P9022	G	A	ACGGGGGGACGCA	ACGGGGGAACGCA	ACGCTGGCCCTGAGAGAC	(0,0.4)	1	CGTCCCCGTGTCTCTGTC
Lri172P144187	T	C	CATGCAGAGTCG	CACGCAGAGTCG	AAATAGCCGAGGCATGGAC	(0,0)	1	GACACAGCAGAGGGTCAGC
Lri17742P215	G	A	ACTTATAGATGTA	ACTTATAGATATA	CTCGCGGACAGGAGGTCT	(0,0)	1	TCAGGACTGTTAGAGTGTTGGA
Lri177P26697	A	C	ACCAGCATGGA	ACCAGCATGGC	ACGGACAGCTCGTCGTTG	(0,0)	1	CCGCAGGACCTTAACCTGAT
Lri178P237573	A	C	ATTGGTGAGATCTA	ATTGGTGAGCTCTA	GTTCCGTTTATTTCCGACTTCC	(0,0)	1	GTCAAGTGGCGCATTTCAT
Lri178P423530	G	A	TGGAGCCGTGTGA	TGAAGCCGTGTGA	AGTGGATAAATTGACGCCGTAT	(0,0)	1	CGTAGATCGCACCACCAAC
Lri17P2957024	G	A	TCTCGATGATCAG	TCTCGATAATCAG	CATCACCCCTCCAGAGTCAG	(0,0)	1	GGAAACCCTTCATCCAACAGT
Lri17P3232763	A	G	TCGCACACCGACT	TCGCACACCGGCT	CTGTGCTGCATCCAAACAAG	(0,0)	1	AAATGCCCCGAGGGATAAT
Lri17P385674	T	C	ATGACGTGATACG	ATGACGTGACACG	GGGATCGCAGTGCGCTAT	(0,0)	1	CTCGCTCTCCGTCCAGGT
Lri17P5047059	T	G	CGACCAAGGGTTT	CGACCAAGGGGTT	CAAGGTATATCGGCAGTGTGC	(0,0)	1	GTAATGCTGGTTTGAATGTTCG
Lri17P6620172	T	C	AATTGTCGTG	AATTGTCGCG	CCCGGTGATGAAAATTGC	(0,0)	1	AACTTTGTGGAAAGTCAGGTTTTT
Lri17P7594234TD43	A	C	ATGTAA[AG]TTA[TG]	ATGTAC[AG]TTA[TG]	CAACCAGCAATCATGTGAAACT	(0,0)	1	AACATTGGCTCATGTGAGTGAC
Lri17P7943131	C	A	CCTACCTTATTAC	CCTACATTATTAC	TACATTCCCGTCAACCCCTTAT	(0,0)	1	GTCGTCTTTCTCCCTCGTGAT
Lri17P8218359	T	C	TCGGGCCACGTTC	TCGGGCCACGCTC	CCTGGGCTTTCTCTGTGTTC	(0,0)	1	ACTCACTTGTGGTGGTGAACG
Lri17P8999134	T	G	GATGAATTCCACAT	GATGAATGCCACAT	CAGCCATGATCTATCAACTTGTG	(0,0)	1	CAGGGGCTAGATGGATTGTTAC
Lri17P9471416	G	A	GCAGGTGTGCCCC	GCAGGTATGCCCC	TGAATGGTCTCTGCACGATCT	(0,0)	1	GCCTGGCGAGAGACACTTTTAT
Lri18P1201819	A	G	GGCCAGCCACTTC	GGCCGGCCACTTC	AAGCGCACGTCGAGGTCT	(0,0)	1	AGTCGCACACCTGTGAGAAGTC
Lri18P163972	G	A	ACTTGTTGGCGTGC	ACTTGTTGGCATGC	GTCGAAGGGCTGCACGTT	(0,0)	1	GAGAGGTCTACTGGTCCGACTG
Lri18P3516203	A	C	CATTTATCAAT	CATTTATCACT	GCTGGTGTATGCCTGTAAACAA	(0,0)	1	CAGCCCTGCAGGTTTGAG
Lri18P4745725	A	G	ATTGTGCTGTATC	ATTGTGCTGTGTC	TGGGACCGAATTCTGAGTGTAT	(0,0)	1	AAAACCGACGTCTCCTTTAGC
Lri18P5626860	T	C	ACTGTACAAATGT	ACCGTACAAATGT	TGCATGATCTTAGAGTTCACGTT	(0,0)	1	ACTCAAAGCGATGTTGCTGAG
Lri18P5985385	G	A	TGCAAGCATGGCG	TGCAAGCATGACG	GCTCGGGTCTCCCGTACA	(0,0)	1	CAGGTGAACCCACAGTTGC
Lri18P6463787	A	C	TCATCCAGAGA	TCATCCAGAGC	TTGTATTTCTCTTGCTAATAATGTCCA	(0,0)	1	TCTGGCAAGCGTGAAAAATA
Lri18P654758	T	C	CCGCGTGCAGAGG	CCGCGCGCAGAGG	GCGGTCTGCGTTGTCTTG	(0,0)	1	GATGCGGGTCATCTTGCT
Lri18P7974729	C	T	TTGCTCGGGTTCTG	TTGTTCGGGTTCTG	AGTGCCTGCAGGACGTGT	(0,0)	1	GCAGAAGGAGAGATGGACAGAC
Lri18P8805776	A	G	AGCTCCCTGCA	GGCTCCCTGCA	GCCAGATCACGGAGAGAAATAA	(0,0)	1	CTCCGGCCGTGTGAAATC
Lri18P9016369	A	G	CATTTGGTGCA	CATTTGGTGCG	TGTACATACCCAACCGTGCTAA	(0,0)	1	CTCGCCACAAACATCACCT
Lri19P6892352	C	G	GCGTCTCGGCCAC	GCGTCTCGGCGAC	GAGCTGCCCCATCGTCTC	(0,0)	1	GGCTGCTCAGACGTCACTT
Lri19P7387400	T	C	TGTGCACAGCT	CGTGCACAGCT	CAGCGTGAGCGAGTCCTG	(0,0)	1	ACTAGGATGACATGGACCTGGA
Lri19P9473436	C	T	TCCCTGGTGTCCA	TCTCTGGTGTCCA	GGTTAGTACAGATTGGTGAAAGTGG	(0,0)	1	GGTGCTGGTCCTGGAAGG
Lri19P9852768TD53	A	T	GATA[GT]ATTCAT	GATA[GT]TTTCAT	ATTGCCTGCAGGTTGGAAT	(0,0)	1	ACATTTCAACAATGACCACGTT
Lri1P11647852	C	A	TTGTCACACACT	TTGTCACACAAT	GTGCTCTCCAAGCTCTAACCTG	(0,0)	1	GTGACCACCACCCCATCAC
Lri1P16171976	G	A	AGTAAAAGGA	AGTAAAAAGA	GTTTGCACAGCGTTTTGAGAT	(0,0)	1	CAAGACCCTTTGCTTCTTCTGT

Lri1P17366484	T	A	GCTGATCTCCTCA	GCTGATCTCCACA	CCTCCGGCAAGAAAACAAG	(0,0)	1	CTGCAGGTCCACAGTTCATTG
Lri1P17392168	T	A	GAACGTCTGCTGC	GAACGTCTGCAGC	TTTATGAACACCAGTGCAACCT	(0,0)	1	CAGGTGAGTGGCGCTGTAT
Lri1P17477528	G	A	CCAACGCAGCGGC	CCAACGCAGCAGC	GGCAATTGCAAAGATCGTG	(0,0)	1	CCACCTCCTCCTCGAACAC
Lri1P6957846	G	T	GGGGGCCACTGCG	GGGGGCCACTTCG	ACACCCTGCAGGATCAGC	(0,0)	1	AGCAGCATCGGAATGAAATC
Lri1P8709918	T	C	GCTTTTCCTAGCT	GCTTTCCCTAGCT	GCACAACTACTCTGGTGCTTTG	(0,0)	1	TGCAACCTCATCTTCTCTACCA
Lri20P3277044	C	T	ATCTTCCTCCAGG	ATCTTCTTCCAGG	CGGAGTCCTCGACGAACTCTAT	(0,0)	1	GCTTCCCCAACCCCTCTT
Lri21P4463586	T	G	AAAAGCATTGAGA	AAAAGCATGGAGA	GAAATGGAACAGAAGCTGAAAA	(0,0)	1	AGCATTTGTTACGTAATCCTTGT
Lri21P5493330	T	C	GCAATCCTGTTGT	GCAATCCTGTCGT	GGAGGTGACCGATATTGTGAGT	(0,0)	1	CTCACTATGGCCAAATGATGCT
Lri21P6647296	G	A	GGTCCGGCTGGAA	GGTCCGGCTGAAA	TTCTAACTGTTCCTCTTGTGACG	(0,0)	1	GAGGCAGGGAGACTTAAGTGAG
Lri21P702243	G	A	GGGTGAGCGCGGT	GGGTGAGCGCAGT	TCCCTGCAGGAGCTCGAC	(0,0)	1	CTCGACGCACTTGGACATAAT
Lri21P9294857	G	A	TGTTGTTGTTGCA	TGTTGTTGTTACA	ACACAAACCCCACTGCAAAG	(0,0)	1	AATGTCCTGCAGGTGACTGAG
Lri222P307512	C	T	AGCCTTTGCGCAA	AGCCTTTGCGTAA	ATTAGGGCTTAATCACCTGGAG	(0,0)	1	CGGCGAGTGGTTTTAATTTTAC
Lri22434P974	G	C	GCTCTTCCTCT	CCTCTTCCTCT	CTGCAAGGTGGTGGTGAC	(0,0)	1	CGACGAGGATCCAGTAGTAGTTG
Lri22P1323692	C	T	ATCATCATCCCGT	ATCATCATCCTGT	TCGTCATTAGCAGCAATAGCAT	(0,0)	1	TGTGTGTTGTCTGAGTAGTATTTGTGA
Lri22P3313925	G	C	GCTTGCACGCGTG	GCTTGCACGCCTG	GTCGACAATAACCTGGGGAAAC	(0,0)	1	GCAATATCACCCACCAAACTGT
Lri22P7082523	A	C	CGCTGCAGGACAA	CGCTGCAGGCCAA	AGCAGGGGGAACACACAG	(0,0)	1	ACCGCCTGCACACTCGATA
Lri22P7625675	T	C	TTGGAAGGTTC	CTGGAAGGTTC	CATGGCAAAAGGATTTCACTTC	(0,0)	1	CACAGTGGTACTCATTGTATCAGC
Lri22P8175926	G	A	CCCCTGCAGGGTG	CCCCTGCAGGATG	ACTAGGGCAAGTCATCACATCA	(0,0)	1	CCTGGAATCTAGGAGTGATTCG
Lri23P3389463	G	A	GGCTCGTGCAACG	GGCTCATGCAACG	CAGGCTTGCCACTTTTTGAC	(0,0)	1	GACAGGCGTAGTAGCACCAGTT
Lri23P8725518	A	C	CGACATCACAATG	CGACATCACCATG	GTTGAACCGTAGCGATGAACTC	(0,0)	1	GGCTATGCGTGTGACGTTT
Lri23P9526641	T	C	GAAGTTTGCGCGT	GAAGCTTGCGCGT	CATCTCCACCCCCAGGAT	(0,0)	1	CGACTGTGCCAGGACCTT
Lri24296P1937	C	T	GAATTGGTTTCAC	GAATTGGTTTTAC	GGGGAGCACACGATTCAC	(0,0)	1	CAGCCTGTTGTATTGCCAGA
Lri2481P8393	G	A	GTGAGAGCACGGCA	GTGAGAGCACAGCA	CAGGATGGACCACTGGAGAC	(0,0)	1	CTGAGGGGACTCTTCCTCATCT
Lri24P3183281	A	C	GTTCCCAACTAA	GTTCCCAACTCA	CCGACAATCCTATTTGAACCTC	(0,0)	1	AGCCAACCGTGCTAATAAGAAG
Lri24P3549440	A	C	CCCACTGAATA	CCCACTGAATC	CAGCTAAGTTCCGCATTGTAG	(0,0)	1	ATTTGCAACCCCGATACAATCT
Lri24P3934915	A	C	TCCACCACCAACT	TCCACCACCACCT	AGGTAGCCTTCACCGTACTGC	(0,0)	1	TTGAGAGGTACATCCAGGATCA
Lri24P4354883	T	A	AATTTTACTATTT	AATATTACTATTT	CAAAGCCCACTGGCAATTACT	(0,0)	1	GCAACCACCCATTTATTTTCAA
Lri24P4954513	G	A	AGAGACAAGGCCAC	AGAAACAAGGCCAC	GGGCTGTGGCACTGTAATAAT	(0,0)	1	ACATTGTAGCCATTATGAAGCA
Lri24P6514737	G	A	CATTAAGAAATAA	CATTAAAAAATAA	TAAAATGCATGTGAGCCATTTC	(0,0)	1	GATTTTTCCCACTTGTGGTTTT
Lri24P6808546	T	A	GCACTTTTAATT	GCACTTTTAAAT	GAAATAGACCGTGTCACAGTATTGA	(0,0)	1	CGGTGGAAGGACAACAAACTA
Lri24P7481704	A	G	CTACGTTTTTACG	CTACGTTTTTGCG	AAGCAGGTAAAGAGGGTTCACA	(0,0)	1	TGAAAACAATACAAGTTCACAACAA
Lri24P7765916	T	G	CATCACCTCTTCT	CATCACCGCTTCT	CTTCCTTAGCTGCCATTTCATT	(0,0)	1	TAAATGGACTTGGGTAGGGACA
Lri25061P2542	C	T	TTTGCCACGGCCA	TTTGCCATGGCCA	GTCCTGCAGGGTTCGTAGAGT	(0,0)	1	TTGTAGCTCCTTCGCGTTAGAT
Lri25P2230291	G	A	GTCTGTAGGCGGA	GTCTGTAGGCAGA	TTCTTGTGTGAGATTCCCACCT	(0,0)	1	TTGTCAATAACACTGCCTTTGG
Lri25P7373093	C	T	GGCTATACAT	GGTTATACAT	TTTCAAGCACGGTGAAATACTG	(0,0)	1	TTCTCGAAGCTTTCATTAGTTGG
Lri25P8275961	A	G	GCATGGTTCCTGG	GCGTGGTTCCTGG	GACAACCACAAGGCAGACATC	(0,0)	1	ATGATGGCTCACCGATGAAGT
Lri25P8435093	T	A	TTTTTTTATTT	TTTTTTAATTT	CAGGCTGTGGGTGCAGTA	(0,0)	1	CTTGCTCACAGAAACTGTACGA
Lri25P8849487	A	T	GTCAGTCAGCACCT	GTCAGTCAGCTCCT	GCAATGTTCAATTCCACCTG	(0,0)	1	CTTGTCGTGATGTACATTCTGC
Lri26245P408	A	C	CAACAGGAAAAAG	CAACAGGAAACAG	TTAAATTAAATTGGGCCTTAGCC	(0,0)	1	GACTTCGCCTGTGACTCG
Lri262P62290	T	C	ATTTACAGCATGC	ATTTACAGCACGC	CGTTATAAACACACGCGTTCC	(0,0)	1	TATAGCGCCACGTGTTGTATTC
Lri26500P1136	T	C	AATATGCGTCTGA	AATATGCGTCCGA	GATCAATTTGCTTGCACCTG	(0,0)	1	AAGCAGTATCCATCACTTTGCAT
Lri26P4406096	A	G	GGAAAGTGGCGTT	GGAAGGTGGCGTT	CTGCAGGTGATGCTTGAGAC	(0,0)	1	TACAACCTGACGGTGCACAT
Lri26P6719186	C	T	GCAACAGCTTCAG	GCAACAGCTTTAG	ATCCTGAACCACCCGATGT	(0,0)	1	AGGCTGGTGTTGAACTGATACA
Lri2718P13929	C	T	AGTAGCCCGCTGA	AGTAGTCCGCTGA	TTTTGGCTTTTATAAGACAGTACATTA	(0,0)	1	AAACTGAAAGGCATGCAGAAAC
Lri27P6150884	T	C	TTACTCAAGATTC	TTACTCAAGACTC	CATCGAGGTTGTGTTTTGAGAT	(0,0)	1	CCACACACAAGACATTCATCAAC
Lri28P383709	G	C	CGAGCAGGACC	CGACCAGGACC	GAACAACGACAGGTCCATGA	(0,0)	1	GTCAGAGGACCTCGTACCTGAG
Lri28P4794703	A	G	CCTGCAGGTTATT	CCTGCAGGTTGTT	CATGTGCTTATATTGCCTTCCT	(0,0)	1	CCCAGTGGCTCGATTAAAGTAG
Lri28P5155821	C	T	TCACCATCCACG	TCACCATCCATG	AAATTTCCTGTGCCCCATT	(0,0)	1	TGCTGCGTCTGGTAGTTGTCTA
Lri28P628762	C	T	GTGAGTTACCTTC	GTGAGTTATCTTC	ACGTCTCCGGCTTCGTTAG	(0,0)	1	CCAAAGACAAGGGTCCCAAC
Lri29P1902704	C	T	CGGGGTAGGCCGG	CGGGGTAGGCTGG	GGAGAGCGTGCCTTCTGG	(0,0)	1	CCATTTCCTTCACCTTCATCTC
Lri29P2715537	C	T	ACCCACCGGTTGGC	ACCTACCGGTTGGC	TATCCGACATGCCAAACTACAC	(0,0)	1	ACACCCGAGACGGCTTTT
Lri29P3853819	T	C	TGGGGTACACTGT	TGGGGTACACCGT	GTCCGATAGCATTTTGCTCACT	(0,0)	1	ATCCATGGAAAATACACGATCC
Lri2P10660681	A	T	GGAGGAGGGAACG	GGAGGAGGGATCG	GTTGACATCATCTCGGCTGTAA	(0,0)	1	GAGCGAGGTGTCTCGTCTG
Lri2P10747040	C	T	TCAGTTAGTTCCT	TCAGTTAGTTTCT	ATACAAAAGGGACCTTGCGTTG	(0,0)	1	AGATGGAGCGGCTGGTAAT
Lri2P10948512	T	C	GGTAGAGTGGTCG	GGTAGAGTGGCCG	GACGTGATCTGCACCTCCTC	(0,0)	1	GTCAACCCCATCATCTACTCC
Lri2P11971110	A	C	GGCCTCTTATA	GGCCTCTTATC	GACAGATTCAAAATGGATGTGG	(0,0)	1	GCAGGAGACACGCCAACT
Lri2P12835756TD51	A	G	AGACCACTGTG	AGACCGCTGTG	AGCAGTATTTGTCCGATTCTGT	(0,0)	1	TTCTCTGCCACCTTGGCTAC
Lri2P14986968	T	C	TACCACGGTCT	CACCACGGTCT	CTCCCGAGGGGCTCATAC	(0,0)	1	GCAGAGCTGCTGCTTGTTC
Lri2P16247548	A	T	TCCACGAACAATG	TCCACGTACAATG	GCACCGTATTTGGACAACG	(0,0)	1	ATCGTTCAGATCCGGCAAG
Lri2P16250399	T	C	AAATCATAGATAA	AAATCACAGATAA	ACTCATCACTTTGCCACTACCC	(0,0)	1	GGTATGCAACTCGCAAAAGTTA

Lri2P16333005	T	A	TCCTACATCCT	TCCTACATCCA	CAACGTAATGGACAAATGATGG	(0,0)	1	CGCTTTACAGAAGGATGATGTG
Lri2P16367064	A	G	ACAATCTGTCATG	ACAATCTGTCGTG	AAGCAAGAAATGTAAATCTGCTCTC	(0,0)	1	AACCAGAGAGAAGTGCATGTGA
Lri2P2907377	C	A	GACATCCCCTCGG	GACATCCCCTAGG	CTGCAGGTCTCGTCTCATGTAA	(0,0)	1	GTCAGCCGTAGGAGAGAACG
Lri2P3548449	G	A	TTCCGTTACGGCA	TTCCGTTACGACA	AGGAGATGGCTGGCAATG	(0,0)	1	GCCTGATGAAGAGCAGAGATTG
Lri2P5451779	G	T	TGTGGTACTCGTA	TGTGGTACTCTTA	TTCCGGAGCATGCTATAACC	(0,0)	1	GAGTGAATTACTCTACCTGACATGAA
Lri2P697855	C	G	TTGCTCATGTGGG	TTGCTGATGTGGG	CCAGATCAGTATTGTTTGTGTGA	(0,0)	1	TTTATTGAGGTAACGAGCATGG
Lri2P7179941	A	G	GGTGCTTGGAATA	GGTGCTTGGAGTA	AGGTTCTGCAGGACATCAAAGT	(0,0)	1	CACTTGCCCCAAAAGTTCAT
Lri2P7418446	T	G	TATATGCTCTT	GATATGCTCTT	AGGGCATGTGCAAACCAT	(0,0)	1	AGTCTTAACCCAGGGGAATCAA
Lri2P9432908	T	C	CATAAGACACCAA	CACAAGACACCAA	CAATTGTGTTTCATGTGGGATT	(0,0)	1	GCCTACTGACCACCTCTTAGCC
Lri30P2608358	G	A	GAGACCGTGGTTT	GAGACCGTAGTTT	GGCCTCCCACTTCGAATC	(0,0)	1	TGTTGTTGCCAAGTCGAAAATA
Lri30P2645807	C	T	AAGTGCCCTCCTG	AAGTGCCCTCTTG	GCTACATCATTGTCGTTGTGGT	(0,0)	1	GAGAGCGTGCAACAGATCCT
Lri31P1720639	T	C	CCTTGACTGCCTGC	CCTCGACTGCCTGC	GTGGTAGTAAAACATCGCGACA	(0,0)	1	GTGCTGTTGGTGAGTGAATGAT
Lri31P2117932	A	G	CCATCCGTTT	CCGTCCGTTT	ATGAATTGTCACGATACGTGGT	(0,0)	1	GCAAACGAAACAGAAGGGAATA
Lri31P2211794	T	C	GGGCCCTTCCACA	GGGCCCTCCCACA	TGTGTGTGCATGTTCAGACCT	(0,0)	1	GATGAAATGCAGCCAGATCAC
Lri32744P2002	T	C	TGATGCAGGGTGG	TGATGCAGGGCGG	CAGGTATGGTGTCGGTGCT	(0,0)	1	CATGTTGTAGAGCTCGTGGAAG
Lri32P2538291	T	C	ATTTAGTTGCTGA	ATTTAGTTGCCGA	CATACGTGTGCATATGTTTGTCA	(0,0)	1	TCCTTGGGTTTACAGAAGCACT
Lri32P3507996	A	G	CTGCAGGTGCATA	CTGCAGGTGCGTA	GCTAGATTGTGTGCTCGATTGC	(0,0)	1	CATGCTAGCAATACAAGTGGAAA
Lri32P517584	A	G	CCCCACGGTGACA	CCCCACGGTGGCA	GAATGACACAAGGCATCATCC	(0,0)	1	AAATACGCGCTGTGGGTTT
Lri33P2602672	C	T	GACGAGAACGGTT	GATGAGAACGGTT	CTTCCTGCAGGTCGTGTGT	(0,0)	1	CTCAAAGTGAACGAAGCCGTAG
Lri34P1263783	T	A	TCCGTAGCTCGGC	TCCGAAGCTCGGC	GCAAAGCACTCTCCCTTACACT	(0,0)	1	GTCTTTGTGTTGCAGGCACTC
Lri34P1457601	G	T	TGCCGGACTCGCG	TGCCGGACTCTCG	GGCGGTGCCCTTGTAGAC	(0,0)	1	CCCATGGACTGCGTCAAG
Lri35P1746600	G	T	CTGTTGTGGGAA	CTGTTGTTGGAA	GTCGATCACATTACTCGTACCG	(0,0)	1	CTCCTCGCTCAAATGAGCACT
Lri35P3483061	G	A	CTACACCGATGTA	CTACACCAATGTA	TATTGGTTCTGTCGCTACATCG	(0,0)	1	CCGGATAGCCTGTAACAAACTG
Lri3691P10383	A	C	AGGGTCTGTTA	AGGGTCTGTTC	CCTGCAAGTCATCTCAATCAGT	(0,0.3)	1	ACTGCTGTGCCAGGCTAGGT
Lri36P402209	A	G	GAACATCACAGAG	GAACATCGCAGAG	AGTCCTTAGAAGAAGGCGATCC	(0,0)	1	AGGAACCGATCCATCTTCATAC
Lri37P1167580	G	T	CACCTGGCCAGAT	CACCTGTCCAGAT	GGCAACAGTTTGCTTACGATTC	(0,0)	1	CCTCCAGGCACTGTGATTTTAT
Lri37P1334668	A	T	AATATTCTCATA	AATATTCTCTTA	GGACCCTGAGTCTGTGCTTG	(0,0)	1	GTTCAATTCCTGGTTACCCTCA
Lri37P1937714	T	C	AGGAAATATTCCA	AGGAAATATCCCA	AGTCACACGAACAATGGCTTCT	(0,0)	1	ACCAGCGTATCCTTTGGAAAAT
Lri37P4230445	C	T	TGGTAACGCTCC	TGGTAACGCTTC	AGTTTGTGAAAGTTGGCAGGAT	(0,0)	1	GAAATAAAAGGCCAAGAACATACA
Lri37P4502867	A	C	ACTACCAGATATA	ACTACCAGATCTA	AAATGAGCAACGAGAAGTACGA	(0,0)	1	AGTTCTCCCGCAGTGGAGT
Lri37P731186	T	C	CTACTTTCTCTACT	CTACTTTCTCCACT	TGAAACCATCATGTGAGGAAAG	(0,0)	1	CACCAACAGGGAACATAGCAC
Lri38430P1343	G	C	CCTGCAGGTTGAG	CCTGCAGGTTCAG	GAGTGGTGAGGATACGGTTGTT	(0,0)	1	GGAGGCTGACAACAATGAGATT
Lri39P2374814	G	C	GCAGCGAGCTG	GCAGCGAGCTC	GTACGAACCTGAATCCCGACT	(0,0)	1	GGGTTTTTGGTCGGCTTG
Lri39P3784671	C	G	ATTCAAGGCACAG	ATTCAAGGCAGAG	GAACACCAAGCCCCATTGT	(0,0)	1	CGTGCGAGGATGAGGTCT
Lri39P4974575	C	T	TTTCTTTTATTACA	TTTTTTTTATTACA	GACACTGCCAGCCCAAAATA	(0,0)	1	GGCTTTTCTGGGTAAATAAGAAAT
Lri39P5026600	T	C	CCGACGGGCATGG	CCGACGGGCACGG	GAGTGGGGCTTCCAGCAG	(0,0)	1	CACGCGAAGTTGTGGAGAGT
Lri3P10860799	A	G	ACACAGCGTAGTG	ACACAGCGTGGTG	CGGGTTTTCTGTCACATATCCT	(0,0)	1	GAGTTTAAACATACACGTGGCATT
Lri3P11837289	G	C	AGGGGCATCTTT	AGGCGCATCTTT	CTGGCCAGTGTGCAAGAAC	(0,0)	1	GAAGGCTTTCCACCAAGAGAG
Lri3P13239723	T	G	TGCCTCCTGCA	GGCCTCCTGCA	TGAGCTCATCCTTTTCACAGAG	(0,0)	1	AAGGCGAGTGGTGCAGTG
Lri3P15907151	T	C	TGAGAAGGCATGC	TGAGAAGGCACGC	GTCCCAAGATTACCACAGGAGA	(0,0)	1	CATCCACGGTTAACAAAAATCC
Lri3P169003	T	A	AGGGTTGTTGTGT	AGGGTAGTTGTGT	GCAAGCAGGACTTGAATCAAAC	(0,0)	1	CCTGCAGCGTAAATATGACCTT
Lri3P5546698	T	G	TGGCTTTGTTTG	TGGCTTTGTTGG	ATGTGGTTCAACTAAGCAATGG	(0,0)	1	GAAGGCAGATAAACCAACGAC
Lri3P9055258	C	T	AAACCCAGGCCCA	AAACTCAGGCCCA	GTGCCTGGACTCGGGAAAC	(0,0)	1	CGGTGATGACACTCGTGACT
Lri3P9532051	G	T	TGCTTCCCACGT	TGCTTCCCACTT	CAGGCTGAGGACGACAATG	(0,0)	1	TTCTGCCAGCAATGACACC
Lri40P5376191	C	A	GCTCCTCGGCCGA	GCTCCTCGGCAGA	AAGACACGGCGTTCATCATC	(0,0)	1	GTTGAAGGGTACCAGGACAGAG
Lri40P897424TD38	A	G	TATACACCATA	TATACGCCATA	AAGCTATTGCAGTTGAGCAGTG	(0,0)	1	TCAACCTTTAGCGAATGTATGG
Lri4109P7946	A	T	CAGGTCACTCATC	CAGGTCACTCTTC	AGGGAGAAAGGGTGACACAGAT	(0,0)	1	ATGGAGGCAGCGTGACAATA
Lri41P393985	C	T	CCTGGCCCGTCCT	CCTGGCTCGTCCT	AGTCCCGTGCCAATTTACAG	(0,0)	1	GCTTCAAAGTGCACCTAGTATGG
Lri41P476134	C	T	GGCCGGGCCGCGGT	GGCCGGGCCGTGGT	CGTACTGGAAGAGGCTCAGG	(0,0)	1	CCTACATGGTGGACGGTTTG
Lri4294P2756	T	C	GGCTCTGCTGTGT	GGCTCTGCTGCGT	GGTTGCGAACTTAAGGACCTC	(0,0)	1	TATTTAACTCAATGTCATTAACAAACC
Lri43P1676686	A	C	ATGTGTCACCACG	ATGTGTCACCCCG	GATGGGCGCAAACATCAC	(0,0)	1	TTTGCACTAACTTTCTGCCTTTC
Lri44P106745	G	C	CTGCAGGGAGGC	CTGCAGGGAGCC	GATGGCATAGAGCAAATCGAC	(0,0)	1	TTCGAGTGCGTCGTCAAA
Lri44P3432223	T	C	TTATTTTAGCT	TTATTTTAGCC	CTGCAGGTTGCGTCTTCTT	(0,0)	1	CCTGGCGACCTCTTCGTAT
Lri44P3836279	A	T	AGACGCCTCCA	AGACGCCTCCT	CCCTTATTTAAATTCCCCGAGA	(0,0)	1	GTGCAGTGTTCGTATTTGCGTA
Lri44P527021	A	G	GATCAGACCTGC	GGTCAGACCTGC	GACACCCTGGGGTTTGTG	(0,0)	1	CTCCTGCAGGCACCAAAT
Lri45P1246569	C	G	GACGGACAGGCA	GACGGACAGGGA	CACCGCCTCCACAAACTG	(0,0)	1	GTGACAGGTGAGGGTGAGAGT
Lri4631P8667TD39	G	T	TGGCTGGGACC	TGGCTTGGACC	AAGAGCAACCCCAAACATTAC	(0,0)	1	CTATAGCACGGACGACTTACCC
Lri46P2660109	C	T	CGCGGAACGCAGA	CGTGGAACGCAGA	GTTGCGCATGGAGGAAGT	(0,0)	1	GATGATGGCGAAGCTGTAGAC
Lri46P2937100	T	C	CGTCGTGGAGTGG	CGTCGTGGAGCGG	AGGAAATGGTGAAGGTCATCC	(0,0)	1	GCATCTCTTCGTTCGCATCT
Lri46P4260004	T	C	TGCAGGGCTCCT	TGCAGGGCCCCT	CTCAATCAAGTGCAATTTCGTC	(0,0)	1	ATGCATATTCACACGCACACAC

Lri47P1274188	A	G	CACGCACGGCAA	CACGCACGGCGA	CACCAAAGCGTATATCTGCCTA	(0,0)	1	CCACTGACGGATCACATTAGC
Lri47P4802446	A	G	CGCCGTGTTTATG	CGCCGTGTTTGTG	CTGCAGGTGTTGCCGTCT	(0,0)	1	GGATAAAATTAAATAGTCCCAACTCG
Lri47P580971	G	T	GCAGGTCAAAGCG	GCAGGTCAAATCG	GACACTCCGACTTTTGTTCCTC	(0,0)	1	CTTGTGGTGGTGGTGGTTTT
Lri487P66561	T	C	GGGCAAACTACCGC	GGGCAAACCACCGC	CCTGCCTGCAGGATTGAT	(0,0)	1	CTTTGGAGCGCAAACATTG
Lri48P1014973	T	C	CCGACCATGAT	CCGACCATGAC	TGCAGTTTTACTCTGGCTTTGA	(0,0)	1	GGTCGTAGTGCATGTTGGTCAT
Lri4P11912704	C	T	GGGTATCCGCGTC	GGGTATCTGCGTC	ATCTTAATCCGGCCCTGCAT	(0,0)	1	GAAGCTGCCACGGCTCAT
Lri4P12290187	T	C	GGATGGACTGTAC	GGATGGACTGCAC	CTCCCAGGCTGAACTCCTG	(0,0)	1	ATAACCCATTGACACATTGCAG
Lri4P14283823	A	C	TGCAGGGCCCAAGT	TGCAGGGCCCCAGT	CTCGAGCTTCCAGAGACTTCC	(0,0)	1	CCTCCTCCTCAAACTTCAACTC
Lri4P1741698	C	G	AGGCCTTGTGCAC	AGGCCTTGTGGAC	GGGGATCACTATGCTGGTATTG	(0,0)	1	CCTTTGGTGACCTATGCAGTG
Lri4P2731292	G	A	TGTGACATGTCC	TATGACATGTCC	CCATTACCTGCTGCAAGTTGAC	(0,0)	1	GGCTTGCGTTCTCTGCTACTTA
Lri4P3128860	T	C	AGTTGGAAGCTAG	AGTTGGAAGCCAG	AAGCCCCTTTCTTTAAATGTCA	(0,0)	1	CCTGCCTGCAGGGTACTACTAA
Lri4P5424460	T	C	GGTAATTGTAT	GGTAATTGTAC	AGCATCCTTGGACGACATTACT	(0,0)	1	GCGAAATTGTCCCACAGC
Lri4P8684156	C	T	CACACACAACCCCC	CACACACAACTCCC	CCGAATGATAAAGGCGACAA	(0,0)	1	CTGCAGGGCATGAGAATAGAT
Lri4P8958596	C	T	TGCAGGCAAGCCA	TGCAGGCAAGTCA	ACGCTATACGTGACATTTGTGG	(0,0)	1	ACCCTGTGTTAAGGCCAACTC
Lri4P9222922	T	C	TGGCCTTAAGTCC	TGGCCTTAAGCCC	TTCCACATCATGGTCAAGTACC	(0,0)	1	GGGATACATGAACTCCATACCC
Lri4P9982449	T	A	CACAGCCACAT	CACAGCCACAA	AACTGTAGGTGGAAAGGTCACA	(0,0)	1	CACATTTTCAGGCAGCTGAT
Lri50P1221681	G	C	TTGCCCACGTAG	TTCCCCACGTAG	AAGATCTGGCCACACCAAACT	(0,0)	1	GCATCTGTTCGTCCAGCTCTA
Lri50P1657665	T	C	TTTCTCCAACT	TTTCCCCAACT	GCGTAACAAGGTCTCATTATTGC	(0,0)	1	CTGAAAGCTGTCCCAGTAGGTT
Lri51P900701	A	G	TGCTCAATGAAGA	TGCTCAATGAGGA	AGGATGAGAAGCACCAGCTCT	(0,0)	1	CCCTCACTTCTGTTCCTTGATCT
Lri5215P4376	C	G	CATGCCGCTCTCA	CATGCCGCTGTCA	AGTCCTCTTGCCACCCATC	(0,0)	1	TCCGTCTTCGACACGTCAG
Lri5229P1229	A	C	TTCCCACACCAAC	TTCCCACACCCAC	AAGGCAACAAAAACACCCTTC	(0,0)	1	AATGAAGGCCTACCCATGTTC
Lri5244P5218	T	A	GTAGTAATAATA	GTAGTAATAAAA	CGTGTTAGACCACAGAACGAAC	(0,0)	1	GCAGGCACGAAAGTTTCAA
Lri5270P9970	A	T	ACGATATAACAAC	ACGATTTAACAAC	AATGTCCACGTTTCATATGTGC	(0,0)	1	ATTACCAAGAGCATTGACCAAC
Lri5345P10185	T	A	GAACGGTGTAGTC	GAACGGTGAAGTC	TGCAGGTATAAACTAACCCTCGT	(0,0)	1	CTGTGGTCCTACATTGGGATG
Lri53P1124643	G	C	GGCATTTTGAGTG	GGCATTTTGACTG	TGCAGGTTAGGGGAAATGAGTA	(0,0)	1	GGAGAAGTGCTGCTCGAAAG
Lri53P2383812	A	G	TGCAAAATACACCC	TGCGAAATACACCC	ACTGCCTCCAGGAATTCATCAT	(0,0)	1	GCAGCTTAAGTTAACACAAATTGTAA
Lri53P2456049	A	G	TTGCAAAGTTAAA	TTGCAAGGTTAAA	TTAACGGTCTCCCTCTTCCAG	(0,0)	1	GATGTAAGCCGCCTTGTTACAG
Lri53P338003	G	C	CTGACCGTCTGCTG	CTGACCGTCTCCTG	AAGCCGTCACGGTGTTTC	(0,0)	1	GTCAGTGGCACCCTGCTC
Lri54P1001845	A	G	CGGGCGCAAGAGA	CGGGCGCAAGGGA	TTCTGCGGGTCCTTGAAGT	(0,0)	1	GATCATCTGGCTGGGTCTGTA
Lri55P2165401	G	A	CTGCAGGCGAGTC	CTGCAGGCGAATC	CCGTCTTGTTCTGATCCTTCTT	(0,0)	1	ACGCTTTCCCCAAAGTTAAG
Lri55P3190566	C	T	ATCTTAAAAACTC	ATCTTAAAAATTC	ACTCACTCGCTGTGGTCATAGA	(0,0)	1	CGTTTTGGAGAACAGGAGGAT
Lri563P38486	G	A	AGAACTCTGCGCC	AGAACTCTGCACC	TTTGGGAGTGAATGTTTGTCAG	(0,0)	1	TAAGACGTGGACGTCAAAACC
Lri5898P7578	C	A	CAGGCGGCGGAT	CAGGAGGCGGAT	GATTAGCTTTCCGTCAACGTCT	(0,0)	1	ATCGTCTAACCGGTTCACCTC
Lri5P1244864	G	C	CGGCAATTCCAG	CCGCAATTCCAG	TTTGATGTCGTTCGTCATAAGG	(0,0)	1	CTGTCATACACGTGCACCCTAC
Lri5P12934722	G	C	CCTGGAGCTGGAGC	CCTCGAGCTGGAGC	GTACCTTCCCAGTACCGCAAAT	(0,0)	1	TTTAGAACAAGGGGATTTGTCA
Lri5P13075196	G	C	ATTCCGATGCTAT	ATTCCGATCCTAT	GCAATAAAAGGCCACGAAATTA	(0,0)	1	ACCTCTGGTACCTCAGGGTCA
Lri5P13191816	T	G	TGGCTCTGCATCT	TGGCTCTGCAGCT	GCAATAATTGTGTCCATCATGC	(0,0)	1	CTGCAGGGGTGCTTGTCTA
Lri5P14389115	C	T	GCACGGGCACAC	GTACGGGCACAC	GTGCCCCGGTTACTGATG	(0,0)	1	GTGGGCAGCGTTGTGAGA
Lri5P14629399	G	T	TGCGACCTTGGCT	TGCGACCTTGTCT	AGCTCTGTCCTGCCCTCCT	(0,0)	1	TGTTACCATTAAAATACACAAATCTCG
Lri5P2456252	T	C	TTTTTGTCTAGAA	TTTTTGTCCAGAA	ATCTGCCTGCAGGAATTTGAT	(0,0)	1	TAGTCGTTTCACTGGACACCTG
Lri5P3706885	G	A	TTTGGACTTGGCA	TTTGGACTTGACA	TTTTTCTCATGTTTGCAAGGAG	(0,0)	1	ACAGGTACAAGCAGGCTCTGG
Lri5P4043379	C	G	TTAAGGCTGACT	TTAAGGCTGAGT	CACGTAGACACTCATCTCTTTGC	(0,0)	1	ACAGTATAAAACAAATGCCTCCA
Lri5P4269100	A	G	TCCTCATCCTC	TCCTCGTCCTC	CTGGTCGTCCTCCTGCTC	(0,0)	1	TCCTCGCCGTGGATTTTC
Lri5P4640927	A	T	TCTTCATTCCAGC	TCTTCTTTCCAGC	TGAAAATAATGGGTCCCTAACA	(0,0)	1	TCCCTCAGGGTACAAACATACA
Lri5P5071040	T	A	ATTATTCTCTCA	ATTATTCTCACA	GTCACAAGGCTTATGCAAATGT	(0,0)	1	AGACTTCACGAATATGGCAACC
Lri5P7155011	T	C	GTGAATGTGTTGG	GTGAATGTGTCGG	AATTCGCATCAGGGTCTCAG	(0,0)	1	ATTGTTGTCGTTGCATTCATCT
Lri5P9200047	G	T	GAGAGAATCTGCG	GAGAGAATCTTCG	AAACCTTAACATTTCAGCACTCG	(0,0)	1	GACCTGGAAGGAGTGTCACTTT
Lri5P9366468	T	A	GAAAAAGTTACGT	GAAAAAGTAACGT	GCAGGCAGAATAGTGGAATGTT	(0,0)	1	TTGCTTCAATCAGAAGCTGAAG
Lri5P9979583	C	T	TGCAGGTAATCGTG	TGCAGGTAATTGTG	TTGATCAAACCTACATACAACCAA	(0,0)	1	CTGTCACCAGAGCCAACTCAT
Lri60P1197606	C	T	AGGTACAACGTGT	AGGTACAATGTGT	TGCAAGGCTTGTTAAGTCAGTG	(0,0)	1	CAGCTGCCACGGTTTCAA
Lri60P2434871	G	A	CGGTGGTCACGGC	CGGTGGTCACAGC	TGCAGAGTGAGCAGAGCAAG	(0,0)	1	CAGTAGGACGCCCACAGC
Lri61P3097033	T	C	CGCTCTCATCTGC	CGCTCTCATCCGC	GTTTCGTGGACACGTAGTGAGA	(0,0)	1	CTTGCCCGTGTGGTTGTAG
Lri61P414412	G	A	ATGGAGTAACTAA	ATGGAATAACTAA	CTGCAGGCCAGTATACAACATT	(0,0)	1	AGTTTAATTTCGGGCATTGGAT
Lri63P1075345	T	C	CCTGCAGGCATACA	CCTGCAGGCACACA	ACAAATGAGTTCGTGCCATAAG	(0,0)	1	CAATTGCAAGATGATTTCCAGA
Lri64P1877052	C	T	ACACTAATTCATA	ACACTAATTTATA	AATATGTGGTCTCTGGGTTTGC	(0,0)	1	CATGCCTGCAGGGGAAAT
Lri64P3699994	C	G	ACCGGTGGGGGGG	ACGGGTGGGGGGG	CTGCAGGATTGTGAAGGCTAC	(0,0)	1	GCGATCTCCTCCTGAGACAC
Lri65P1192162	T	C	TCTCAGAGCTC	CCTCAGAGCTC	GAGGGCCACATCAACCAC	(0,0)	1	TGCTCATTGGCGTTGTAGAC
Lri65P2520673	A	G	AATTGATAGGT	GATTGATAGGT	GAGGGAATTCCGAAGTTGAGTA	(0,0)	1	CGTATGGTGCAAAAGAAGTTCA
Lri65P2642230	T	C	TGCACAGCAAG	CGCACAGCAAG	AACCTCTACGTGACCTCGATCT	(0.5,0)	1	GTGAAGTGCTCCACGATGTTT
Lri66P303856	C	A	AAACACACCCCGG	AAACACACCCAGG	AGAATGTCGGGACATCATGC	(0,0)	1	TTCATCAGGCAAACAACACG

Lri67P441125	A	G	GGTGCAATGGA	GGTGCAATGGG	AGCGAGGACAAGAAGACCTG	(0,0)	1	AGAGGGTCGTGCTTACTTCTC
Lri69P3566988	C	T	TAAAACATGTCCT	TAAAACATGTTCT	GCTGGCTATCATCCCTTCTAAA	(0,0)	1	TGTCTGAAGTAAAGTGGGCTTG
Lri6P10286942	T	A	AAGTAATGTATCT	AAGTAATGTAACT	GTGTGCATTGATTTGACAGGTT	(0,0)	1	CTAATGGGGAGCCAAATAAAC
Lri6P10328882	T	A	GGAAACCTTTTTC	GGAAACCATTTTC	AGTTGGGTGGCCTCAATGT	(0,0)	1	GAAGCTCCGTCTCTAGAAGTGC
Lri6P10383294	C	G	GCATGCATCCCGT	GCATGCATCCGGT	TGTTTAATGTGAGCAGTTAATCGTG	(0,0)	1	TTTCACTCGATTCACCCTCTGT
Lri6P10474030	C	T	AATCCCTCCCATGA	AATTCCTCCCATGA	CCGAATCGTCACCGATCATA	(0,0)	1	TCAAATGCAATGCCACTAGAAC
Lri6P10581411	T	C	TTTCTCACAGTAT	TTTCTCACAGCAT	AGATAGGGACAAATTTGGGTCA	(0,0)	1	ACTCCAGGCAATGCAGTCAC
Lri6P11041437	A	G	ACAACACTGTGCT	ACGACACTGTGCT	ATGTAACCAAGCAGACCACAGT	(0,0)	1	AGGGATTGCAGAAACAAAGAAC
Lri6P13329068	C	A	CCACGTTGTGATGG	CCAAGTTGTGATGG	AGACGAAGCTGCATCGAGAC	(0.1,0)	1	ACTTTACCGAAAGGACCAAGA
Lri6P2036382	G	A	TCCAAGCCACGGC	TCCAAGCCACAGC	GTGGTGGTGTGCATTAATTGGT	(0,0)	1	GATTGCCTGCAGGATTGTG
Lri6P5039589	C	T	TTGTGGCGGTCCA	TTGTGGCGGTTCA	TCACGAATTCACTCGCTGTACT	(0,0)	1	GGCAAGGGTTGGTGGATT
Lri6P5524704	T	C	GGCATTCGAGTCC	GGCATCCGAGTCC	ATGGAGGGAGACCTCTGGAT	(0,0)	1	AGGAATCCGATGAGCTATGAAG
Lri6P6080845	G	A	CGCCTTCATGAAG	CGCCTTCATAAAG	GTGGTTAACGCACCGACTG	(0,0)	1	GTTTGAGATGGACGAGGTGAGT
Lri6P6130428	T	C	GAGTATATTC	GAGTACATTC	CTTCCCTTCGATCATCCAGTC	(0,0)	1	GAACATAGGGGACATTTGAAGC
Lri6P7202854	G	T	CAAGCGCTGTCGA	CAAGCGCTTTCGA	ACAAAACTGTGGCCTCGTG	(0,0)	1	GATGATGGTGGTGGTGATGAT
Lri6P8338530	T	C	GCTCTGAAGAG	GCTCCGAAGAG	GCAACAACACCAGGACCAAC	(0,0)	1	CGCCTATCTCCCAACCAAAT
Lri7079P1000	T	A	ATCACATATCTT	ATCACATATCAT	GTCTTGATGGTGGAACCTTACC	(0,0)	1	AGAGCCGTCGCCTAACCT
Lri70P1263023	G	A	TTCACCGTTC	TTCACCATTC	TGCAAAAGTAATTTATTATGGAAATG	(0,0)	1	AGAACTACACCTGCAGGCACAT
Lri71P1277485	C	G	ACGCTGCATGCCC	ACGCTGCATGGCC	CTTCCAGAGCTGGCGGTA	(0,0)	1	GTCGTGGAGCTGTTTCAGG
Lri73P2199950	C	T	AGGTTGTGTGCC	AGGTTGTGTGTC	GAATATCCCTTGCAAAACATGG	(0,0)	1	ATGTCACCACAAGCCTACGTCT
Lri7435P3947	C	T	GGGGTCAAGCTGA	GGGGTCAAGTTGA	AGTGGGCTGGATGCTCTG	(0,0)	1	ATGGTTCTGCTGCTCTTCGT
Lri74P1110420	A	G	GCACCGTCACATA	GCACCGTCACGTA	CTGTCTCTCCCGCAGTGG	(0,0)	1	CTTGTCGCTGTAGCTGAAGG
Lri75P276391	C	T	TTTAAATAGGCGA	TTTAAATAGGTGA	AGTGGCCAGAACTAGGGGGTA	(0,0)	1	AATTGAGGAGGTAATGGTTCGAT
Lri76P1581919	C	T	GTCAGCGGGATA	GTCAGTGGGATA	GATTGGTGAATGACGCAAAAC	(0,0)	1	CTCCCTCCTGCAGGTAATTCAT
Lri76P839426	T	C	CACAACTCCATGG	CACAACTCCACGG	CCTGCAGGTACCTTATTGATGG	(0,0)	1	AGGTAGGGGTGGTGGAGAGA
Lri76P849517	T	G	TAAGGCACCTTAT	TAAGGCACCTGAT	CTGCAGGAAACATGCAGAATAG	(0,0)	1	ATATCTGGGGAAAATGGCAAG
Lri77P239810	T	C	CTTGTGCTGGTTC	CTTGTGCTGGCTC	GGATTGATCACGGCTGATG	(0,0)	1	TCGACTCTGAGCGAGTACAAG
Lri78P1108359	G	C	GTTTATACACGC	GTTTATACACCC	TGCACTTCTCTATATGCGGTGT	(0,0)	1	AGGTGATCTGCTTCCCTCCT
Lri78P1274279	G	A	AGCGCGAGACGTG	AGCGCGAGACATG	GAAGCCCTGCCAAACGAC	(0,0)	1	ATTGTCGGAGCGCGTTGT
Lri78P1520535	A	G	AGTAAGCAAGATG	AGTAAGCAAGGTG	TGGTAGGGTTAAGGCGATTAAA	(0,0)	1	CCTTAACCACTGGCTTCTTCAC
Lri78P2370671	G	T	ACCTGCAGGCGGC	ACCTGCAGGCTGC	TAACCACACTTTAACCCACCAT	(0,0)	1	ACCCTGGTTAAATAATAGACATCG
Lri78P482602	T	C	CCACCATGCACTT	CCACCACGCACTT	CACTCTCCGTACCTGCTTCTG	(0,0)	1	CTGCCCTGCTGGATGTACC
Lri79P2948990	A	G	ACTGTCCGTAACA	ACTGTCCGTAGCA	AGTAGATCACTGCAACGACACG	(0,0)	1	GAGCTCAATTCCCAACGTTATT
Lri7P12869891	T	C	GCCATGTTTCCCC	GCCATGCTTCCCC	AGGAATGAACCCCTTTCTGTGT	(0,0)	1	AAAAGTTTAGTTTAAAGACCACGATG
Lri7P1684065	G	C	AAGAACCCAGGGG	AAGAACCCAGCGG	TGCAGGGAGAGACTGATTAAAA	(0,0)	1	GTGGTTCAGGTATTGGGTGATT
Lri7P2921566	C	T	GCACTGCCCCGCT	GCACTGCCCTGCT	TTCTCTTTCTGGTTCATTCCTC	(0,0)	1	CTTGGATGGCTCTGGGAAG
Lri7P474819	A	T	TAAAAATACCCT	TTAAAATACCCT	AGATGCCGATAAGCAAACAAAG	(0,0)	1	CAGCGGCAGAAACAAATAAATA
Lri80P1637884	G	T	TGGCTGACGGTG	TTGCTGACGGTG	CATGCTTCTTTGTGAGCTTTC	(0,0)	1	CACTAATCTGCTCGCCCACT
Lri82P53126	G	T	CGAGCAGCTGGTT	CGAGCAGCTGTTT	CAGGAAGGAGAGTGGGTCCT	(0,0)	1	ATCCAGGCGGCCATAACT
Lri83P1195764	T	C	TATTTCCGAGTGG	TATTTCCGAGCGG	AGCTGCCCTCTGCACAGTT	(0,0)	1	GAAAAAGGGTGGCTGACTTTTA
Lri83P1335304	G	A	ACAGGGGGGCGGAG	ACAGGGGGGCAGAG	CCTGCAGGCTCTTGATCGT	(0,0)	1	AAGACGGAGGGCAAGACC
Lri83P2068917	C	A	TCCGTGGCTACGAC	TCCGTGGCTAAGAC	ACTCCCCTTTGTAGAGCGTGTA	(0,0)	1	GAGTACTTTGGGAACGTCCTTG
Lri83P564737	G	A	GAAATGAGAAT	AAAATGAGAAT	GCACAACCGTGAAAACCT	(0,0)	1	CCTGCAGGACATTTCCAAATTA
Lri84P170406	A	G	CTTTGTTATGCTA	CTTTGTTGTGCTA	ATTTTCATAAATGAGGGGGATG	(0,0)	1	AGACGCTCCACACTCACCAC
Lri84P876835	T	A	CGCAAGCGGGTAA	CGCAAGCGGGAAA	TACCTGTTTTAGGCCCTTTCAG	(0,0)	1	CGCCAAGCTTTTGTCGTCTA
Lri84P876852	G	T	TGCAGGAGAGAT	TGCAGGATAGAT	AGCAGAAACCGCTGAAAGTG	(0,0)	1	CTAATTCTGCGCCAAGCTTTT
Lri85P2050795	G	A	GAAGCAGTTTT	AAAGCAGTTTT	CGAGTGGCCCAGGGAGTA	(0,0)	1	GTTGGAAAACAGCCTGAAAGAT
Lri85P2095420	T	C	CTCAACGACGTCC	CTCAACGACGCCC	GCGTCGATACCAATGGATG	(0,0)	1	GAAAGATTTGCACGGTCCTAAG
Lri85P213759	C	G	AGGCCAGGGGCGT	AGGCCAGGGGGGT	GACCGTGGTCTGTATGCATCT	(0,0)	1	GGTCATGTGACCGTCATGG
Lri85P891582	C	T	GGCCCCGGCGTTC	GGTCCCGGCGTTC	GCGATGACATCTACCAGCAATA	(0,0)	1	GTTACCGGCACGGTGATG
Lri85P956410	G	A	TCCGCCGCCTGGA	TCCGCCGCCTAGA	TGGTGCAGTGTTCACGTC	(0,0)	1	TTTTACCTGCTGGTAGATCTCG
Lri86P103182	T	G	AAGCGTAGCGTGA	AAGCGTAGCGGGA	TTAGGTCTGCACCCAAAAATAA	(0,0)	1	CAATTAGGCATGAAAGCATTTG
Lri88P1164318	T	C	GCCCATTTAGTCC	GCCCATTTAGCCC	TCTTCTCCAGCCCATCTCAC	(0,0)	1	CTGGGTCCAATGAACTTCTGTT
Lri89P2322061	A	G	TTTTCCGACAAGC	TTTTCCGACAGGC	TTTTTGTTCTCCACATTGCAC	(0,0)	1	GCTCTTACAACGTTTGGAGCAT
Lri8P1441255	A	T	GTGTCTGGACA	GTGTCTGGACT	GGTGAAGATGCTGTCGTCAGAG	(0,0)	1	CACAGCCTGGGCTGAAGT
Lri8P4138772	A	T	GTATGTATTTA	GTATGTATTTT	ACAGCTCCACCCAGCTTCATA	(0,0)	1	ATGCGACTCAAACCACTACTCA
Lri8P4295266	T	G	CATCATGCAATA	CATCATGCAAGA	TAATTTTCCATGAGGTGTTTGA	(0,0)	1	GATTGTGATCACCCAGAACAGA
Lri8P9543505	A	G	CTCCACAGCTAAT	CTCCACAGCTGAT	CGATGCAGTAGTGCGGTCT	(0,0)	1	ACAGCATGGCGAGCATGA
Lri90P257157	A	C	AGCATTTCATC	CGCATTTCATC	TGATTATGATGTCCATCGGTAAAG	(0,0)	1	TGCAGGTTATGTTTGTCTCCTG
Lri90P618248	A	G	ACATCACCGCC	GCATCACCGCC	ACGACGCGATAGAGCAGGT	(0.3,0)	1	CGATTGTTCCTGCAGGTGT

Lri91P204352	T	A	AAGAGTATTCTG	AAGAGTATTCAG	TCACGCAGGTAACTCATTTCAT	(0,0)	1	GATGTCACAGTGGTTCACAGGT
Lri91P2342186	T	C	GTGTCCAGGGG	GTGCCCAGGGG	CTGAAATTAATCCCTGCTCCAG	(0,0)	1	GGCACACCTGGACACATCT
Lri91P730506	C	A	GACGCATTTTCTA	GACGCATTTTATA	GCTACCGAACCGGTGACTT	(0,0)	1	TTAATAACACGCATCAAAGATACATT
Lri93P1340289	A	G	AGAAGCAGAAAC	AGAAGCAGAAGC	GAGCGATTCTCTCCGTACCAT	(0,0)	1	CAGGAACAGCTCCTTGTTGAA
Lri96P1067926TD50	T	C	AA[CT]GTTGGGTT	AA[CT]GTCGGGTT	GCTAGCTGAACCCGTTACACAT	(0,0)	1	GCATATTTGCGGAATACACCAC
Lri98P763276	A	C	AGGGTCGCGCAGC	AGGGTCGCGCCGC	GCGTCTTCAAACTCATCGAGAC	(0,0)	1	GCGTACGGATGTCAGTGCTTAG
Lri99P330522	A	G	GCAGGTTGCAAG	GCAGGTTGCAGG	TTAGTAACCCTTTCCCGAGATG	(0,0)	1	CCTGAATAAAATGAACGCTGA
Lri9P10378057	C	T	GATCGGGTCTC	GATCGGGTCTT	ACAAAGGTGGCCAGACATGA	(0,0)	1	GGCTACTTATAACCCACGTTGC
Lri9P1124057	G	T	AAAACACGGTGCA	AAAACACGGTTCA	TGTGAACCTCGGGGGAAG	(0.5,0)	1	ATGAAATGCGGTAGTGTCCTG
Lri9P12500977	T	G	AGTGAGGTGGTCG	AGTGAGGTGGGCG	GTGAGGTGGGCCAGCAGT	(0,0)	1	CCTCCATCTCCAGCTCGTC
Lri9P4476882	A	G	GTCAGCACGCA	GTCAGCACGCG	GGTTTCCACTATCCTGGTGTGT	(0,0)	1	GCATACCAGCGTTCAATAAACA

Appendix 12. GT-seq SNP panel for White Sturgeon.

Assay	A1	A2	A1-Probe	A2-Probe	FWD Primer	Rev Primer
Atr_10304-61	G	A	TGGCTTGGCAGTGG	TGGCTTGACAGTGG	GCCTTTGTTCTCCAGCTTGC	TCTAAACAGACCAATCCCACTG
Atr_10322-43	G	A	GCAGCGAAACAAAGA	GCAGCAAAACAAAGA	TGCAGGGGCTATCAGAGACT	AATCAGTGTGGGAGCTCAGC
Atr_10428-71	T	A	AGAGAGCTAGCA	AGAGAGCAAGCA	CGCACACACACAAAGAGAGC	GGATCCAGAGCCACAGTGTC
Atr_10437-26	T	G	TTTTTTGGCAACTGT	TTTTTGGGCAACTGT	TGCAGGTGGGTTATGGGTTG	TGAATTAAACAGGTACAGTTGCAGA
Atr_10672-61	C	T	GACCACACTGGGCAG	GACCATACTGGGCAG	GCAAAATTGGCAGGGATGGT	GCAGGTGTTTGCTTGAGCTC
Atr_10867-69	C	T	TGGTATACAATGAA	TGGTATATAATGAA	AGGACTGGGTAGGGAGCATT	ACCGAGCTGGATGACTTGAA
Atr_10998-72	T	C	AGTAATGTGTT	AGTAATGCGTT	CAAAGCGCCCATGATTGTCA	TTAGCAGGCACAACTGACAA
Atr_11046-75	T	A	GGCCCAAT	GGCCCAAA	GGAGGGCCTGGGAATCCT	TTCAGGGGGAACAAGGTGAG
Atr_11104-35	T	C	TGCACTGTCGTGTCT	TGCACCGTCGTGTCT	CGCTAGTAGTGAAGTGAAGTGC	CCCTCTCAGGTGCTGTTCAC
Atr_11585-33	C	T	TAAAGCCAAGTTTGT	TAAAGTCAAGTTTGT	GGTTGGTAGTTTGCGGCATT	AGTGGAGTTCTCCGATCCCA
Atr_11787-73	G	A	CTAACCCGCG	CTAACCCACG	ACAGTCCCTACAGGCATTGC	GATTCCAGAGGGAGTGTCGC
Atr_11864-68	T	C	ATATCGCTGACCAC	ATATCGCCGACCAC	GGTACCACCGCCAATATCGC	CAGAGCTGCTGGTTGTTTCG
Atr_12219-56	A	C	ATAGTATATGCGGG	ATAGTATCTGCGGG	GCAGGGAAGTCTAAACCCCA	AATTGTGTTCTTTGCCCCGC
Atr_12616-36	G	A	GCCGTTCGTGAAGC	GCCGTTCATGAAGC	TCCTGCCATGCTAGCAAGAG	TCCACCGGCTATTCCTCTTT
Atr_12677-44	A	G	ATGTACTATTTAGC	ATGTACTGTTTAGC	TGCAGGAGAGGATGTATACGTC	ACTTCAAACAACAAAAGGCTGCT
Atr_13073-61	T	A	TTTTAATTTGCATT	TTTTAATATGCATT	GCTGCAGCTTACAGTCTTCA	TGCAGAGCTCAATCCAAACCT
Atr_13132-45	G	A	GCCACGAAGAACATG	GCCACAAAGAACATG	GTGACCAGCATGACCACCAT	TATCACAGGGAGCTGGGGAT
Atr_13476-65	A	T	TTATCAGTATGCAGC	TTATCTGTATGCAGC	CGTTTTCCAGCACCACAGGT	CTGACCTTTGGCTTGTGTGC
Atr_13706-54	A	T	GTGAGAGAAGACTA	GTGAGAGTAGACTA	AGGCTACTTGCATCTGCCAG	TCATAAGAGCTGTCTGAAACTGA
Atr_13729-47	T	C	GCACAAGTTTTTTT	GCACAAGCTTTTTT	CCATAGCTTTTGTGCAGCACA	TGCCTTTATGTTGACAGGGTCA
Atr_13917-71	C	A	AACTACTCATCA	AACTACTAATCA	CCTTCCCAGGGAGCTTGATG	CAGAATGCAAGGTACACTGTTGA
Atr_13930-72	A	T	GTTTTATAAGC	GTTTTATTAGC	TGTTTTAGTGGGACCAGTGCT	TGCAAAATAAAACACTGTGGAAAAA
Atr_13996-43	T	C	TATTCTGTAATGTTT	TATTCCGTAATGTTT	CAGGTCTGCTGTGTGTGACA	TCAAGTTCACCTCGACAGCA
Atr_14410-52	T	A	GAAGCAATCCCCAG	GAAGCAAACCCCAG	ACAGGTGGTTCATCTGCAAAC	TGGCATTGTTTCCACTGGGG
Atr_14635-67	C	A	GGAGCACCAAAAAC	GGAGCACAAAAAAC	ATCCCCAGCTGATTTGCCTC	ACCACTTTAATGCATCTCCTGG
Atr_14824-32	A	G	TTAACATGAAAGTCA	TTAACGTGAAAGTCA	TGCAGGGATCCACAGAAATGT	AAGCAGCTGAACACAATGGG
Atr_14862-38	T	C	TTGACTCCCTTTAAG	TTGACCCCCTTTAAG	CGCCTCCCCAGGACTATTTT	TTTCCTGTGGCCATTTTTATTGT
Atr_14917-56	C	T	AACACATCTTAACA	AACACATTTTAACA	TGCGCCACCTAGAAACACAT	TGCACAAAGAAAGGTCCTGGT
Atr_15179-54	G	T	TTCAAATGACCCCA	TTCAAATTACCCCA	GCAGGGTAAGTTAGTTTAAGCGC	GGTGCAGCTTGTATGGGGT
Atr_15201-45	A	C	TTACTGAAACACAT	TTACTGACACACAT	GGGTACAGTGCAAGAAATGGC	TAGTCAGGTTGGCTGTGAGC
Atr_15273-44	T	G	ATAGATCCTGTCCTA	ATAGAGCCTGTCCTA	GGGAATGTTTCTCTGTTTTGGAT	ACTCCAGTCTGGACATAAACTCA
Atr_15294-66	T	A	TGGGATAGAATTTTC	TGGGAAAGAATTTTC	TGTATTGTTCGGATGAATTGGGA	TCTGATGTAGAACTTCTGTGTAGTT
Atr_15298-72	G	A	TCTCACTGTAT	TCTCACTATAT	TCTCAGCATCTTTCACTACCCA	TGATAAAGCAACCTTGAGCCCT
Atr_15875-62	C	T	CCTGCCCCGTGGAA	CCTGCCCTGTGGAA	TCCATCAGAGCTCACCAGGA	AGTGTTGCATTGGCTCTGGA
Atr_16803-66	C	T	GGCAGCACGCCTCT	GGCAGCATGCCTCT	CATGTTGTGTGTCCGGTGC	TCCCTGGAATTGGTGCAAAA
Atr_1720-33	C	A	GGGGGCTTTGAGAGC	GGGGGATTTGAGAGC	GGCAAAGCAGAAGGGGG	TGTGTGTATCTGTCTGTGTGGT
Atr_17710-71	T	C	CAGGATGCCC	CAGGACGCCC	GCTCTCCCATCTTTTGCAGC	ACACTGACGGCAGCTATTCC
Atr_18133-56	G	A	TGGGTTTGTTGTAT	TGGGTTTATTGTAT	AGTCAAGTGTGTGTGTTGGGT	AGCAGGGAAGATACTGGTTGC
Atr_18295-67	T	C	ACCTGCATGGCAAA	ACCTGCACGGCAAA	CTCGTCTTGAGGCACCTGC	TGAAAACTGGCAGCTTTGTGA
Atr_18334-74	A	G	ATGGTGGAC	ATGGTGGGC	GGAAGTTGGTCCTCAGAGGC	AATGAGTGCCATCAGCCACT
Atr_18403-29	C	G	AGATCCATGAAGCTC	AGATCGATGAAGCTC	TGCAGGTAATGAATGTTGCCT	TGCGTTCTGTTCATCCCTCT
Atr_19496-44	A	G	GAGTGAGGCTATTGG	GAGTGGGGCTATTGG	CACACCTAGGGGCACATTGA	TCAACAGCGAGAAGGGTTGT
Atr_19666-61	G	T	ACATTCAGGGCATA	ACATTCATGGCATA	CAGGCCTCAAGCTCTTCTGT	TGTAGTGAGGTTACCTTATTATGCC
Atr_19783-57	C	A	TCTAACATGGACATC	TCTAAAATGGACATC	TCTTCTTCTGGAATGATTACATCCA	GACAGTGAAGCAAGAGAAATCCA
Atr_20013-55	C	T	GCCTGCTCCCCTCG	GCCTGCTTCCCTCG	GATGCTAACCTGGCTCTGGG	CCGAATATCCGCGGGAAGAA
Atr_20037-39	G	A	AGAACGTGTTCCTGC	AGAACATGTTCCTGC	GCAGGCGTAGAGTTACAGCA	ACAGTAGACGTCAACGGGAT
Atr_20117-55	A	G	GCTTCACCCCAGGCA	GCTTCGCCCCAGGCA	CCTGCTCCCAAACAGGACAA	TCAGATGGGCCTGGTGAAAC
Atr_20219-65	A	G	ATGCCAGGCTTTCTA	ATGCCGGGCTTTCTA	TGGACCTTATTAGAAGCTTAATGCC	GCACCTCTATGGCACTTTTTGG
Atr_20252-35	T	C	ATGGGGGTTGTAAT	ATGGGGGCTGTAAT	ACTTGGACGAGGCATCATGG	GCCAAATTCAACTGCTGGGA
Atr_20332-60	T	A	GTATAACTAGAACA	GTATAACAAGAACA	ACATTGCCTACACCTCACCC	TTTGACTGCCACAAGCTCCT
Atr_20482-41	C	T	CGGGAGCCGAGCTT	CGGGAGCTGAGCTT	CTCATTGCAATTGGGCTCGG	GCAGCCTAGCAGGATCTCAT
Atr_20529-52	A	G	GCACAACTTTTTACA	GCACAGCTTTTTACA	ATCGCAGCTTGACAGTGAGT	AGTAATTCCAAAAAGCCCACTGG
Atr_20740-65	T	C	ATTGCTCTCTGCCCT	ATTGCCCTCTGCCCT	AACATCATCCCCTTCCTGCG	GAGTTCAGAGCCAGCACAGA
Atr_2084-45	A	G	GGTTTGAAAATGTT	GGTTTGAGAATGTT	TGAGGTAGCCAGCAGGTTTG	AATGATGCCAGAGCGCTGAT
Atr_20952-49	T	C	ACACTACTCTGCCC	ACACTACCCTGCCC	TCCCCAGCTGACATGAACAC	CACAATTGGCCAAGTGCTGC
Atr_21685-29	A	G	GTGCTGAAGGCTCC	GTGCTGAGGGCTCC	TGCAGGTTTGGTTCTCTGTTTG	CCACCAGCCAAAGAGACAGT

Atr_22008-56	C	T	TACTGAACAGTGAT	TACTGAATAGTGAT	GGGCAAGAAAAGACCCAAACC	GCCTTCTGGTCCTAATATAAAGTGC
Atr_22727-31	C	T	TTTGCCAGATTTCAG	TTTGCTAGATTTCAG	GCAGGAAACCATGATGCACC	TGACTTACTAGACATCTGCAACTGA
Atr_23070-31	C	A	CAGTCTCCGCATTT	CAGTCTCAGCATTT	GCCTTTGCCCTCCAGTCTC	TCCTCTGATCCCACGACCTT
Atr_24146-56	A	C	ACATGTTAATCTTG	ACATGTTCATCTTG	TGGCTAAAGATCTAGAACACATGT	TCAACCGAGCTCTGTTGCTT
Atr_25159-57	T	C	TATTTTAGTGGAAGC	TATTTCAGTGGAAGC	CCTGAGTGTGTGAACCAGCT	ACATGTTAGCCAAGAGTTGCA
Atr_2540-75	A	C	TCTGGTAA	TCTGGTAC	TCAAGCATGCTAAGTGTCTGGT	TGTTCCCGGGTGCCAAAAA
Atr_25540-60	C	T	AATTCCCAGCTATGC	AATTCTCAGCTATGC	AGCAGACCACTGGCATGAAT	TCTATCATGGGCATCTGCAAA
Atr_25562-47	A	G	CGGCAAGCAATAAAA	CGGCAGGCAATAAAA	CGGTTATAGGATTAGTATGCGGC	GCAGAGTGCAGTGAAATAGCC
Atr_25884-65	T	G	AAAATTTTTCCCGAA	AAAATGTTTCCCGAA	GCAGGGAGATTGGGAAGTCA	AACAGCAAAATTTAAATTCGGGAAA
Atr_25905-72	G	A	AAACCACGGAA	AAACCACAGAA	TGAGGGGAAGTTGAGGTGTT	TTCCTCTTGACCTTTCAATTGATC
Atr_26310-63	A	C	GAACGAAGCTTAGTT	GAACGCAGCTTAGTT	CAAAATGCCCGATCACCCAC	TTTGCGCTGTTTGACCTCTG
Atr_2684-39	A	T	ACTGGACAGAGATC	ACTGGACTGAGATC	CAGGAGACGCAGGGAGAAAG	GCCCACACTGTCATTGAGCT
Atr_27072-33	T	A	TTTATGATAGTGAT	TTTATGAAAGTGAT	GCAGGTGATTGGTGGAAATAGC	TGGACTCGCATCACCTTCAC
Atr_27367-69	T	C	AAATAAATACACAG	AAATAAACACACAG	CGTTTCCACAGTGGCAATCA	TGTGTGAATTTGGATTTCTCTGTGT
Atr_27395-73	C	T	CAGG[GA]CGC	CAGG[GA]TGC	TGCGACTCTGCTGTGTATGA	GACATTTTGCTGTCCAGAAGGG
Atr_27430-71	A	G	ATTGCCCATGCC	ATTGCCCGTGCC	CTGGTCTGGTCAGCAATTGC	AGTGCCCCAACACAGTATGG
Atr_2768-35	C	T	CGCCTGGCCAGTTG	CGCCTGGTCAGTTG	TGCAGGTGTTCAGTTGAGCA	AGACAATACAGCAGACCCAACT
Atr_28175-70	T	G	TTTAGTTTTGC	TTTAGGTTTGC	AGGTAGGCTAGAAATCGGTTCA	TGGTCTTGATTAAGGGGTGCA
Atr_28280-63	A	G	TGATCAGAAACCTT	TGATCAGGAACCTT	TCCACTTTGAACTCACCGGG	ACTGTACACTTTGCTTGTTCTTACA
Atr_28411-65	A	G	GTGCCCAACAGGAC	GTGCCCAGCAGGAC	AAACCAAGCAGCGTCTGGAA	GCAGCTCTGTCAGTCTCAGG
Atr_2858-58	C	G	ACCAGCTGTGCCGGG	ACCAGGTGTGCCGGG	TGCAGGCATTTTGTTGGACC	CACAGTACCATGGGAGTCCC
Atr_28609-62	A	T	CAAACATATCATTG	CAAACATTTCATTG	GCAGCAGGGTAAGGATGACA	AAGCAGGGAAATACAAATACAATGA
Atr_28746-28	T	A	AGGTTCTTCACTTT	AGGTTCTACACTTT	AGGGGTTGTTGGGCATAAGG	AGTAAGCACAGGATATAACAAAGTG
Atr_28834-39	T	A	ATGTAGGTGACAGT	ATGTAGGAGACAGT	TGCAGGAGTGATCACAAAGATGT	TGTGAATACCCCGACTGCTG
Atr_28861-59	T	A	GACCCTGGTGCAGAT	GACCCAGGTGCAGAT	ACCCAGGACCAAAGGGAGAT	GTGTGACTCACATCTGCACC
Atr_29024-55	A	G	CTCTCAAGTCCTTGA	CTCTCGAGTCCTTGA	TCCAAAGGCCGGTAACTCAC	AAGGCCAGTGAACCCACAAT
Atr_29086-33	C	T	TTGTCAACGGGTTT	TTGTCAATGGGTTT	GGTTTGGTTCAACCGCACAG	AGAGAGCGCCTGTAGACAGT
Atr_29277-35	C	G	TGAAACAGCAGTATG	TGAAAGAGCAGTATG	GGATCGCTCTCTGCTTGTGA	TGCCAAGCCCTAACTGCTAG
Atr_29302-34	C	T	CTGCTC[GA]TCTACAGT	CTGCTT[GA]TCTACAGT	GCAGGCTGTATAGTGAAACTGG	TTACTACTCACCTCACCTGAAAAA
Atr_29414-61	C	T	TTCCAACCGGGGAT	TTCCAACTGGGGAT	CAGGGCTGGGGTCTGGA	GGCGCACTCTGTCTCCAAAT
Atr_30145-46	T	C	AAGGAAATACTTGC	AAGGAAACACTTGC	TGCAGGTTGCCCATTGTATCA	TATTCCTACTGCGCTCTGGC
Atr_30271-58	G	A	AGGAGTCGTATTTC	AGGAGTCATATTTC	ATGCAGAATCCACAGGAGTC	AAGGAGCTTAGACACTGCCA
Atr_30376-68	C	T	CAGGAAACGACTCA	CAGGAAATGACTCA	CCGCCAGCAGTCAGGAAA	TTGGTCCACAATCCCCCATC
Atr_30916-62	G	A	GACTGGGGCTATTT	GACTGGGACTATTT	AGGTCGTGCTGTATTGGTCA	CAGGTGTGATGAGGGGAAAT
Atr_30992-26	C	T	TAATGGTCGTTAAT	TAATGGTTGTTAAT	GCAGGTCTGAAATGAGGTAATGG	GCTCCCTTTTTATTGTGTGTGACT
Atr_31917-28	T	C	AAAACTGGTCGCTCA	AAAACCGGTCGCTCA	TGCAGGACCAAGTGGGATTA	TTACAGAGGAAGGTGAGCGAC
Atr_32234-71	C	T	CACGCCACGGGG	CACGCCATGGGG	CTCAGGAGGATGGCCATTCT	TGTTACAAAAGGTCTCATCCCC
Atr_32382-60	G	A	TATACTCGGAAACA	TATACTCAGAAACA	CAAACCCTGGTCCCTTGGTC	GGGACTGCAGTGCACCTAG
Atr_32545-55	A	G	ACTCAACACGCCCT	ACTCAACGCGCCCT	TCCACTTGGGATGATCTAATCTCC	TTGAGAACCAGTTGGGCACT
Atr_32551-51	G	A	AGGTCGAAGTAGTGG	AGGTCAAAGTAGTGG	GCTCTCCAGGTTGTCGTTGA	AGAGTCCAGCGGGCCTAC
Atr_32840-74	T	A	TTCATTA	TTCATAA	TGGCACAGCTTTACCGGTTT	GTCCACAGAGTTGTTTGTGAAA
Atr_32945-42	G	T	AAAAGAAGAGTTCC	AAAAGAATAGTTCC	TGCTCTTTCAAATCCTATGACTCA	AGCAGAAATCGTTTTACAAGGAAC
Atr_33123-54	T	C	AAAGCAATGATTAA	AAAGCAACGATTAA	ACTGTGTTCAAGAGACCATTGGA	AGAGTTTTTACAACATTATTGCCCT
Atr_33645-66	G	C	TCGCTCTGTGAGGT	TCGCTCTCTGAGGT	TGCGTGTCTGCATCTCCAAT	GGCAGCACAGACCATACAGT
Atr_33798-72	G	T	GTGCCGCTG	GTGCCTCTG	ATTTTGGTTTGTGGCGGTGC	GGTTTCCCATTTCCTCCAGC
Atr_33803-28	G	T	AGCTGCAGGGATGG	AGCTGCATGGATGG	GGAATGTAATGTGACCAGCTGC	ACCAGGAATGGATCAAACTGCT
Atr_34-41	G	C	GTCCTGCAATGCTGT	GTCCTCCAATGCTGT	CCTGCCTGTGTGCAATTCAG	CCGTGAAGCCACTACAGCAT
Atr_34454-29	G	A	GACCAGGGTTGCCT	GACCAGGATTGCCT	GATTGTGGCACTCCAGGACC	ACCCGAAAACTAGAAGCCCT
Atr_34497-36	C	T	GATAGTTCGCTCTT	GATAGTTTGCTCTT	GGAGGTGCTGCTGGTGATAG	GCTTGGTGGTTGTAGGTGCT
Atr_3451-52	T	G	GTGCTTTACCAACAT	GTGCTGTACCAACAT	GGTTTGGAGGAAGTTTGTGCT	CTCTGTCCCTTCAATTGGAGGA
Atr_35415-62	C	A	CAGAACGTTAAAATT	CAGAAAGTTAAAATT	GGAAGTTGGTCTTATGATTAGTGTT	AAACAAGATGTTGGAGTACAAAAGT
Atr_35440-36	A	T	ATACCATACATACA	ATACCATTCATACA	CAGGTCCTACCACTGCTGAC	TGCAAAGTGTTGTTCCTGTATG
Atr_3581-53	T	A	TTTTATTTTTCATA	TTTTATTATTCATA	AGCTCCAGTTCACAAAGCCT	TGCAGCTTCTTTGGGGATCA
Atr_36194-59	T	C	CTTTCTGTTCTCAGA	CTTTCCGTTCTCAGA	CCATCTGCAGTGTGGAATCCT	GCCGCTTCTTCTCCTCTGAG
Atr_3627-31	A	T	GTCTATTAGTGTTT	GTCTATTTGTGTTT	GTTCAAACCACACAACTGTCTAT	ACTGCAATGAGACACAGATGT
Atr_36331-53	C	T	TGTGGCTCGAGGGC	TGTGGCTTGAGGGC	CGGAAGGCCTCAGATTGTGG	AGTCCGCTGCCTTGAACTAC
Atr_36485-28	C	T	CCTCATCCTAGCCC	CCTCATCTTAGCCC	GGTGCTAGCAGCCCTCATC	CACAGACCCAATCATGCCCT
Atr_36740-33	G	A	TAGAAGTGTAGATGA	TAGAAATGTAGATGA	TGCAGGCTAATATAAAGTAGAAAGC	ACAAGTTCCTGGTTAAAAACAGCT
Atr_36960-37	A	G	CCATGCCAGTCCGT	CCATGCCGGTCCGT	CTTGACGCCAGCTGCAGAA	TGAGGGTGAGGAGCCATACT
Atr_37068-70	C	T	TTTGTCTTTCG	TTTGTTTTTCG	ATAAAGCATGAACACCACATGG	GGCTGTTTTGTTCTCAGTGTGT

Atr_37739-28	T	C	ATAGCTGGTACAGGT	ATAGCCGGTACAGGT	GCAGGATCATGCATGCGC	TGAACCCAGACAAGAAGGACA
Atr_37898-35	C	A	GCTGGCTTGGTCGTG	GCTGGATTGGTCGTG	CAGGCTGGCCTTTGTCCATA	TTAAGGTTCAGTGGGCGTCC
Atr_38278-50	C	A	GTGCATGCAAACTA	GTGCATGAAAACTA	TCCTCCAAACCACAGTGTGC	TACAGTGCATGCCTTCCTGG
Atr_38591-73	A	T	CCGTCATT	CCGTCTTT	GCTGAAGTATAAACAACATCACCGT	AATTGGGAGAACTTTACAGTCCT
Atr_39018-58	C	A	AAAAGACCATTTCA	AAAAGACAATTTCA	GGTTCAGACCCACTGTGTATCA	AGCCAGCCTAAGGTTTTGAA
Atr_39023-56	C	T	AGTGACACGGAGAG	AGTGACATGGAGAG	GGTCCACCTGTCAATAATGGC	TCGAGAGAGAGAGCCCTCAC
Atr_3903-41	G	A	AGCTGGTGAATCGGA	AGCTGATGAATCGGA	TGCAGGTTGAGTTCAGATTGT	GATAGGGCTGTCTGCATCCG
Atr_39071-73	G	A	CTTCACAGAC	CTTCACAAAA	ATAGCCCAGGTGGATGCATG	TGGATAAGCGGTTCTGCAGA
Atr_39081-73	C	T	TTTAGATCAG	TTTAGATTAG	TGGATGGAGGTTTAATAGGACCA	GGGCCCTTCCAGTTGAGATT
Atr_39125-48	T	C	ATAGTGTTGAAACT	ATAGTGTCGAAACT	GCAACATCGTGAAAACGCCA	TGATTCAAAAGGAATGCTTGGCA
Atr_40110-57	G	A	TAGGGCCGCATGCA	TAGGGCCACATGCA	GCACTGTGCCACTGACATAT	CAATCGCTATTGATTGCTGCA
Atr_40169-65	C	T	AGACCCAGTTGTGGC	AGACCTAGTTGTGGC	GGGTGGTTCCTACATGACGT	TGCCCTGTAACTACCCCTGT
Atr_40316-51	A	T	ATTAAAGAAAAATA	ATTAAAGTAAAATA	TGCAGGTTTGTTTCTGTGAATGG	CTCTGTCACAAGGCCACAGA
Atr_40343-66	G	A	CTGCTTCGTTAGGG	CTGCTTCATTAGGG	CAGCAACGCTTACAGCACAG	AACAAGCATCGTCTCTCCCT
Atr_40774-37	A	G	ACTCAACTCTGACCC	ACTCAGCTCTGACCC	TGCAGGCAAACAGTCTTTAGAC	CCTGGACTGGATTGGATCTCG
Atr_40954-66	G	T	ATTGGGGGTAAAAT	ATTGGGGTTAAAAT	TTGGACATTGCAAATTGGGG	TGCATGACTATGGGCGTGTT
Atr_40974-63	G	A	GAGATGTGATCTGT	GAGATGTAATCTGT	GGACCACAGAGTGAGATCCG	GCAAAGCATGCGAAACAGAT
Atr_41828-27	A	C	TAAAGGGAAACAGT	TAAAGGGCAACAGT	GCAGGAGTCCTACAAAGTTAAAGG	TGTTTTTACATGTCTTTACGGTCA
Atr_41948-31	A	G	GAATTGAAGAAGTA	GAATTGAGGAAGTA	TGCAGGGAGGGACATCTCTT	TCATGTTCGAGTCAAGGAGCT
Atr_41986-71	G	T	AGTGGCAGAATG	AGTGGCATAATG	ATTGTATGGCGCTTCCTGCT	AGAAGGGTTGAGCATGTCCC
Atr_42039-63	T	C	AGGCCAGTGGCGAG	AGGCCAGCGGCGAG	ACCAATCCAATCAGCCTCGG	TCTGTCCGTGCTGGTTTGAG
Atr_42405-55	C	A	CCCCAGTCCCTTAA	CCCCAGTACCTTAA	CAACACTGACAGACCCCCAG	TGCAGCACAGCGTGATCTAT
Atr_42741-51	T	A	CGTCATTTTGAAATT	CGTCAATTTGAAATT	TGTGCAGACTAAAAGCATGCG	ACTCAGGAGTCTAACTGAAGCC
Atr_43107-50	G	A	ATCTGCTGTAGCAC	ATCTGCTATAGCAC	GGTGTCTGCCTGAGCTCAAT	GAGGCAAAACTGGCAATGACT
Atr_43402-63	A	T	AGATCACTCAACAAA	AGATCTCTCAACAAA	GCAGGTTTGACTTGCTTGGG	GTCAGGCCCAATGTCCACTT
Atr_43414-51	C	T	TATGAGCCGAGTCT	TATGAGCTGAGTCT	AGTCTTCCCGAGGGACAGTT	CCCTTTCGTAAATGAGGCCCT
Atr_43531-74	G	A	GTGCGCCGC	GTGCGCCAC	AACTGTTCAGTGAAGTGCGC	CCAACCTGAGCCCCAACATA
Atr_43571-39	C	A	TACATCTATCTGGTT	TACATATATCTGGTT	TGCAGGGATATAGTATGTCACTTT	TGCACCCCCTATTCTGAAGTG
Atr_43809-42	A	T	AAAATA[AT]AAAAAATA	AAAATT[AT]AAAAAATA	GCAGGGCGTATCGACAGATT	GCCAACCTGCTCACCACTTA
Atr_44473-38	T	C	ACATTGATATCTCA	ACATTGACATCTCA	GCAGGTGGTGGAGCTCATAG	CTCCTTCTGCAGCATCACCA
Atr_44513-72	T	C	GTGGCTCTAGA	GTGGCTCCAGA	CAAACGATATGAAAGCTGTGGC	GGTCCATTTCTAGTCAGCTCGT
Atr_44873-44	C	T	GCTGACATCTGTCAT	GCTGATATCTGTCAT	ATGGTCTTTTTCCCCCTGGG	AGCTCAGCCAATCAGCACAA
Atr_45074-45	T	G	GTGCATTTCAGCAG	GTGCATTGCAGCAG	GGAGAAACACACACCAAGCG	AGTCTGCTTCTACTCCCAGT
Atr_45494-35	G	T	CATTTCAGTCGAGG	CATTTCATTCGAGG	GCAGGACATACACGGTGGAA	TCCAGAGCTACACACCTCGA
Atr_457-66	G	A	TCAACTGGGACCAT	TCAACTGAGACCAT	GAAGGGCTGAAGTGATGGCT	ACCCTCATGTCACAAATGTAAAAGA
Atr_45890-59	G	T	GTGAGGAGACCTGT	GTGAGGATACCTGT	TAAGGGCTGCAGTGGTGAAG	CCACGGTACCTGTGCTGATT
Atr_46006-31	C	A	TGCTGCATGCTTCAC	TGCTGAATGCTTCAC	TGCAGGATATAATAGTAAAGGGGTC	CCCCCTTCATGTGAAAAAGTGT
Atr_46088-36	T	C	TCATCTGTAATATG	TCATCTGCAATATG	GGCAGTCATGATATAAAGCGGG	TCTAGTGACCTCTGGTGGCT
Atr_46134-46	T	C	TCCCTGCTGATTTT	TCCCTGCCGATTTT	TGCTTGACCTAGCCAGTAGTG	TGGGGGCTAGGGAGACAAAA
Atr_46229-66	G	A	TTGCTCCGTACAAA	TTGCTCCATACAAA	AGTGACAGGGAATTGTATGCCT	ATGTCACACTTCCCAGGGAC
Atr_46247-56	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_46637-57	C	G	AGCGTCACAGGCTA	AGCGTCAGAGGCTA	CATAAGCGCTGGGATAGGGG	TGCAGGAGCTGACCTTTGAG
Atr_46690-29	A	C	CTGCCAAAGGATCT	CTGCCAACGGATCT	GGCTCTCAGAGTAATTACTGCCA	TTCCCTCACTCCAAAGAGCA
Atr_46720-39	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_46983-45	T	A	GTTCGTTTCTACAG	GTTCGTTACTACAG	CCTGGTAGCATGTGGGTGTT	TGCCTCATTGTAATCATATCAGGAC
Atr_47163-58	C	T	TGCAGCGGCACATGG	TGCAGTGGCACATGG	ATCCATCTGTCCCTCCAGCT	GCACTTCACCATCCGGAAG
Atr_47195-73	T	C	AAGCCGTTAA	AAGCCGTCAA	GAAACGCTCAGGAGTGGAAC	CAGTGGGCGTGTTACGTAAG
Atr_47352-72	A	G	GCCGAGCACTC	GCCGAGCGCTC	CTCATGCCGCTCTCCTTCAC	TTGTGTTCTGGTCCCAGCG
Atr_47484-45	T	C	GTAGGGGTTGCTCT	GTAGGGGCTGCTCT	GCAGGGGTCTGTTAGAGCTC	AATCAGCAGTCACCTCACCG
Atr_47529-73	C	A	TAAGCAACTT	TAAGCAAATT	GCTGCCATTAATGATCTTGTCCT	CGCAGGACCAAGAAGATGTT
Atr_47979-72	T	A	GCCTTTATATC	GCCTTTAAATC	AGGCAGAACTAAATACAGCACTG	AGGGAACGAAGGGAACATTT
Atr_48754-60	G	A	CTGCAACGACGTGT	CTGCAACAACGTGT	GCTTTCTCCTTTCAGTGGCC	TCCACGACACACATACACGT
Atr_49388-52	G	A	CATGTGTGTCTGTC	CATGTGTATCTGTC	GGGACCCATGTATAAGATGGCC	AGTTTGGTGAAGATTGGCAGT
Atr_49532-44	T	G	AAACTTTAT[CA]GTCTG	AAACTGTAT[CA]GTCTG	GCAGGAACTTTGCAACTACTGT	AGCATTACTGTGTAGGCTTTACAGA
Atr_49629-71	G	A	CATGCCTGGGGA	CATGCCTAGGGA	CCAGCAGAGCCATGGGAATC	CGGAGGCAGGTCGAACAG
Atr_49790-61	C	A	TGCACTACTCTTCT	TGCACTAATCTTCT	GCTACAGTACCACCTGCACT	CCCCTCCAGAAATCAGGAGTC

Atr_50179-30	T	C	GCCAATGGGTTGAAG	GCCAACGGGTTGAAG	TGCAGGCCTCTTAGCTGTTG	AGCATCTTGCCACATCCACA
Atr_5019-45	C	T	TCCTGCAGC[TA]TTCCT	TCCTGTAGC[TA]TTCCT	GCACCGCTGAATGCTACATC	TTTCGTGCAGGCTGAGACAT
Atr_50212-69	C	A	AGAGACTATGGC	AGAGAATATGGC	TCACTACAGAATGTGTTCAGCTCA	TGCAATTATGATGTTCTCAGCCA
Atr_50642-59	C	G	CCCTACTTAATGACA	CCCTAGTTAATGACA	CAGGATCGTGGTGCTCCAG	GCAGTAGGCCATCACTGTCA
Atr_51176-35	G	T	AAAAGTTGCACAAC	AAAAGTTTCACAAC	TGCAGGTGAGATGAGGTTACTG	ACTCCAGCACATAAGAGCAGT
Atr_51458-37	T	A	CTCGCACTGTTGGC	CTCGCACAGTTGGC	TCAATCTGATGCTGGGCCTC	GACTGAGGAGCCGCCAAAT
Atr_51832-58	A	C	CAGTCAATGC[TC]GATT	CAGTCCATGC[TC]GATT	GCTGTAGGGTCCACGGTAGA	TGGGGATTCCAGAGTGAGTA
Atr_51999-44	A	G	AATATAATGGGTAAG	AATATGATGGGTAAG	TAGGGTCCCAGGGCAGTTTA	GGTGTGCAACCCAATGAATACA
Atr_52021-40	C	T	AGATGCACTGCATTA	AGATGTACTGCATTA	TGCAGGTGTCACATTCACTGT	ACTGACCACAACTCAAACTGT
Atr_52164-31	A	T	TTTTTTTAAAGAGC	TTTTTTTTAAGAGC	TGCAGGGATAAGCCAAAGC	AGCTTGGTGGAATCCAGGTG
Atr_525-66	G	C	AACAAGAAGCAAAGA	AACAACAAGCAAAGA	TCCAGCATGACCATCTCTGC	GGGTCACTGTGTCTCTTTGCT
Atr_52650-66	A	G	AGACAGTATGTTTG	AGACAGTGTGTTTG	CCCTTGCTGTGGCTCTTCAA	AGCCCCTATAGTCTCCACCA
Atr_52666-51	A	G	AAAGGGTAGTTATT	AAAGGGTGGTTATT	GCAGGCCTTCTGTATGTAAACC	TGCTTTCTTAGAATTTAAGGCTGCA
Atr_52675-47	C	T	TGAACCGCGACCTC	TGAACCGTGACCTC	CAGTTTGTCAGCCGGTGTTG	CTCCACCAAGAGAGTGCCTG
Atr_52715-59	C	T	AGTATACCCCTTGT	AGTATACTCCTTGT	ACTGTAGTGTGGTTATGTGGTT	TGAAGATTGTATGTTGTTGGCACA
Atr_52868-38	C	T	TTGCAAACGGAGCA	TTGCAAATGGAGCA	CAGGGTCCCAGCTGAAGAG	CGCAAGAAGCTGATGTGCTC
Atr_53157-67	G	C	GACAAGAGAGACAG	GACAAGACAGACAG	CCAGCCTAGCCATGGACAAG	TCACATCCAACTCTTGCCAGT
Atr_53210-55	C	T	AGAAGCCAATAGGTG	AGAAGTCAATAGGTG	TCTTGCATCATGCCTACCAGT	ACGCTTCATGGCATTTTGTGT
Atr_5336-58	A	T	AAACCACAGCATTC	AAACCACTGCATTC	CTCACCTCACAGGCTACACC	CTTTCAGTGCAGTCAGAATGC
Atr_53521-30	C	T	ATCCCTTCCTACCG	ATCCCTTTCTACCG	TGCAGGTCATCATCTGAACAAGA	ACCAATCCTTCCTGACAGTTTGT
Atr_53686-72	A	C	AATACAAAT	AATACCAAT	CCCGTGGTTTGTAAGCAGGA	CTGGGGACTACTTGAGCTGC
Atr_53904-44	A	G	AGTCAATTAGTCAAG	AGTCAGTTAGTCAAG	TGCAGGAGACCGTGAAATGT	GGTATCCTCCCTGGCTTGAC
Atr_54038-48	A	G	CCGGGGAAAGGATG	CTGGGGAGAGGATG	CACAGGTATGCCACAGGACA	AGGAAGCTAAACACAATCTACCA
Atr_54041-38	C	T	TTTGAATCTTAAGA	TTTGAATTTTAAGA	ACTGTCTTGGGTGGCAAACT	ACCTAACTCGGAAATGTGATTTGT
Atr_54160-70	T	C	TCATTTTTGGGTC	TCATTTTCGGGTC	TTTGCGGTTCAGATGTGGGT	AGAGCACACAAAACATTTTCGGT
Atr_54266-27	G	A	GTTACTTGTATTGG	GTTACTTATATTGG	TGCAGGCTTCACTACATAGGT	ACATCCACCCTCAACAAGCT
Atr_54764-45	G	A	AGCACTCGCTCCCA	AGCACTCACTCCCA	TGGGGAGCCAAGTAATGAGC	AACCAGAGAGGCCCGAGTAT
Atr_54795-72	G	A	CATTTGTAT	CATTTATAT	TGCACTGATGATGAAGGTGT	GCAATTTTAAAGGTGTGGAGACA
Atr_55583-67	G	A	TTACCGGGATTGAC	TTACCAGGATTGAC	ACGAGGCATTGATTAAGTCCAGT	AACGCTACTGACTTGAGGCC
Atr_55892-54	G	A	ATCTCGTAGACCTCA	ATCTCATAGACCTCA	AGCCTGTCACTTCCAATGAGG	TGAACACCCCTCTGAGGTCT
Atr_56024-45	C	A	CAAGTAGCGATCAG	CAAGTAGAGATCAG	AGGTCAGCCCGTCCCTATAA	TGGTCTTCTTCTCAAGATGTGCT
Atr_56033-37	C	T	GCTACAGCTTTATT	GCTACAGTTTTATT	TCTAGTCCCTCCCGCTACAG	ATGGCCCGATAGTTTTGGCA
Atr_5610-27	A	G	GTGACACAAGATTA	GTGACACGAGATTA	TGCAGGTACAAGCAGAGCAG	GCCACTTGCAACTGGGAAAA
Atr_56109-40	C	T	CAGAACTCGCCCTG	CAGAACTTGCCCTG	CGCATGCGTCCGATAGCC	ATAGAGAACTGCAGCAGGGC
Atr_56854-26	A	C	GGAAAGTAGGGGTA	GGAAAGTCGGGGTA	GACGTGCACGGGTGGAAA	CACAGCCTCAGTGCTTCAGA
Atr_57018-28	C	T	GCGTTGTCCTCCGA	GCGTTGTTCTCCGA	CTTGCCTGTAAGCTGCGTTG	TTTACACACTGCAGGCCCTT
Atr_57542-29	A	T	CCAGAAAATGGCTC	CCAGAAATTGGCTC	CTGGCCTTTGTCCTCCAGAA	CAGTGTGTGTCCTCCGATCC
Atr_57756-67	C	T	CAATCAACGAGCAG	CAATCAATGAGCAG	TGCAGGTAAGGGCAGATGAC	TTTTCCATGGGTCTGCTGCT
Atr_5779-55	T	G	TTTTTCTTTTCCCT	TTTTTCTGTTCCCT	TGCAGGTATTGAAGACATTCTCTGA	GACGTGAATGGAGGGGTCAG
Atr_57832-69	C	A	GAACACGCTGACAC	GAACACGATGACAC	ACCAGTTCCAGAGATATGGGTG	GGGCCGCTTTATCACAAGGA
Atr_57870-70	A	C	ACTACCTAACCAG	ACTACCTCACCAG	TTACCTTACATATGTGTCACTACCT	CTCACGTGAGAGTTGCTCTGT
Atr_58305-70	G	A	CCACTGTGGTG	CCACTATGGTG	TGTCTACAGTTGTTACATGTCCA	GCCATGTCCAGCTTTTACACC
Atr_58342-71	T	C	TCCTTCTTTCTG	TCCTTCTCTCTG	GGGTGTGTTGTCTCTCCTTCT	GACTGAGGAAATAGCAAAGCGT
Atr_58434-42	G	A	CCAGTCCGTTTTCC	CCAGTCCATTTTCC	GCAGAACCACGCCAGTCC	GAGGGCGAGGAACCAGC
Atr_58562-59	G	T	TATAATTGACCTCT	TATAATTTACCTCT	GACAGGATCCACCACACACT	AAAGAGGACCGGTCAAGAGG
Atr_58720-60	A	G	TTCCTATAGTTTAG	TTCCTATGGTTTAG	CCAGTCAAGTGCAAGGGTGA	TGAACTTGAAACTCATTTTGACCA
Atr_58831-60	G	A	GTAAAATGTACGGC	GTAAAATATACGGC	TGCGTGTTTATCTTGAGAAACCG	TCTTTTTATGAGCACTGCCGT
Atr_5890-29	T	C	CTTCGTATGAGATG	CTTCGTACGAGATG	CAGGTGTAAACCCCCGAGTC	TCGTTCCGAGCAACAGGAC
Atr_5892-46	A	C	TCATTCCAGAATCC	TCATTCCCGAATCC	CAATAGCATGGCCGCACTTC	TGGACACAGCACAAAGAAGAGT
Atr_59201-47	G	A	CAGCAGGGTCCACT	CAGCAGGATCCACC	GCTTGATTTCACTGGGTGCC	ACCAGGCACTCACAATGACA
Atr_59284-42	G	T	CAGAGATGAATTTT	CAGAGATTAATTTT	AACCTCGTCACCCTCTCTCA	GCTCAAGCAGAGGTTTGTGG
Atr_59310-44	A	C	CTCAGCGAGCACTC	CTCAGCGCGCACTC	GCAGTTTGGTGAAGCTCAGC	GAAGCCTCAGGAAGCACCAG
Atr_59487-73	C	T	ATAAACGT	ATAAATGT	ACTTGAGCAAAAGGAATGCAGA	TGAACCTCTACTCTTATTTTGCACA
Atr_59800-43	C	G	ACAGTCCCTAACTAT	ACAGTGCCTAACTAT	CACTGTAGCAGGGTGACGAG	TCTGCGGTTTACAGAGGCAA
Atr_59842-43	G	A	GGCGGTTGAACCAG	GGCGGTTAAACCAG	CATCTCTCTTGTGAGGGCGG	TCCAGCTACATTGCCTGTGG
Atr_60162-29	T	A	TTTTTTTTAATTTG	TTTTTTTAAATTTG	TGCAGGCAGGACTGTTTC	GAACAGTCCCACACGCTAGG
Atr_60265-55	C	A	GGCTTCCCAGTGTC	GGCTTCCAAGTGTC	AGGGGTCGGATTAGCCACTA	AGGTGGACATTCTAGGTGAGGA
Atr_60368-72	A	T	AGGAACCAGCA	AGGAACCTGCA	CGATGGCCTCCAAGGAACC	CCCTATCATTCCTGTCACTCGT
Atr_60688-70	C	T	GAACCAGCGGTTG	GAACCAGTGGTTG	CCTCCAATGACCTACTGAACCA	GGTGCTGGTGGCTAACTGAT
Atr_60859-44	T	C	AATTCAATTGACCC	AATTCAACTGACCC	AGGGGTCAGAATCTGCATGC	AAGTGTCCATCGCTTGTGGG

Atr_61062-75	C	A	ATCTGGGC	ATCTGGGA	TGCCCTGAAAGAGGTCAGTT	TGACTGTATGAAAGAAGGCAGT
Atr_61171-66	C	T	GATGTGACTGCACG	GATGTGATTGCACG	CCGACGCTGTAAGTTCTGGA	TGTCCTCCGAAACGACTGC
Atr_61911-75	C	G	ATTGCC	ATTGCG	AGTGGCAGCTCCTTCACTTC	GCGCCGGTACACTTTCAGTA
Atr_62330-56	A	C	AGGGTGAAGTCCCA	AGGGTGACGTCCCA	GGGCCAGGAAGGAAAAGCAT	ACTACCAGGAGCTTTTGGGAC
Atr_62419-71	G	A	CTGCAACGACAC	CTGCAACAACAC	CCTGCAGAGAGACACAGACG	GGCCAGACAAAGGAAGGACA
Atr_62463-34	C	T	TGCAGAGCGTTCAC	TGCAGAGTGTTCAC	GCAGGGATAGAAATAAGACTCTGGT	GCTTGTTACGTATACACTGGCA
Atr_6251-29	G	T	TCAGGGGGAGATGCA	TCAGGTGGAGATGCA	TGCAGGGACACAAGAGCTTC	GCTTTCTTGACTTGCCTGCC
Atr_62952-34	T	C	TTCTCCTTGTGGTG	TTCTCCTCGTGGTG	GGATTGGAAGCAACGTTTCTCC	AGGACCAGGAATGAAATGGCA
Atr_63042-40	T	C	ACTCATTGACCTCTG	ACTCACTGACCTCTG	GTCTTTGCCCTCCATGAGCT	TCCAGGTACTCCACAGCAGA
Atr_63076-27	T	A	ACAAATTTCATTCA	ACAAATTACATTCA	GCAGGCAACAACAACCTCAC	ACAGTATCATAGTGGAGGTGAATG
Atr_63101-44	A	G	ACCAGGCAAATTTC	ACCAGGCGAATTTC	CCATTGTTACAGGGTTTGGGG	TGTCTGGACATAACCTGGAAACT
Atr_63246-38	A	G	GTGTATTATGTATC	GTGTATTGTGTATC	CAGTCAGCTGCATTGTGTGT	AACTCACTATGCTGCCTGGG
Atr_63885-66	C	T	GCTGCCGTCGGTCAG	GCTGCTGTCGGTCAG	TGTTACCCAAGCTGTGTTCAG	TGCTAATTTTCTTTCTTCTGACCGA
Atr_64006-52	C	T	GGTTTACCCTGAAG	GGTTTACTCTGAAG	CTGGATGGGGAGCGGTTTAC	CAGCTCCCACCCACTGTAAG
Atr_64217-68	A	G	CCTTAAATTCGAG	CCTTAGATTCGAG	TGTTAACAAGGGAAACGCCG	TTTTTAGTTACCCTCACCCAGG
Atr_6456-50	G	A	GTTCAGACTGCAGGT	GTTCAAACTGCAGGT	GCATTGCTGCCAGGTTAACA	GGAAAACACAACCCTGTCGC
Atr_64706-45	T	A	CACTGACTGCTGTA	CACTGACAGCTGTA	TGCAGGGATGGTCCTTGTTG	ATGACCAAGCCAACTGCCTT
Atr_65094-30	A	G	AGAGCAGACGCCAGT	AGAGCGGACGCCAGT	GCAGGGCTGTCTTCGAGAG	GACCAAGCTGCCTCTTTCCA
Atr_65359-46	T	C	CATCTTCAATCAG[CT]T	CATCTCCAATCAG[CT]T	GTAGTTCCCCTGCCTTGCAT	ATCGCTCTGTGTTTGGACCC
Atr_65377-56	G	A	TAACAGGATAATAGG	TAACAAGATAATAGG	CTGGTGATCCCTGCTGTAGG	CTGCAGAACCCAGAGACCTG
Atr_65729-42	T	G	GTTACCATCTCTAC	GTTACCAGCTCTAC	TTAATTCACAATGTAGCAGTTACCA	GCGCACCACTCTATTTCAAACT
Atr_65843-52	G	T	GCGTCAGGTGGGAA	GCGTCAGTTGGGAA	AATGTGAGTAAGGGGGCGTC	CACTTTCAAAGCAAATGTTGGTCA
Atr_6612-39	A	C	TGCCCATATACATGG	TGCCCCTATACATGG	TGCAGGGATGCCTATTGTACA	GGGATCCCAGGTCATTTCCA
Atr_66563-34	A	G	AACCTCTATACAGT	AACCTCTGTACAGT	TGCAGGTTAAATGTCCACATCA	GGCTCCCAACCACATCGTTA
Atr_66664-59	C	T	CTCAGAGCTCCCTG	CTCAGAGTTCCCTG	AGGTACCCCTTGCCAAATGG	TGCAAAGTAGAAGGCAGGGA
Atr_66806-52	T	C	TTACCTGTTTGAGA	TTACCTGCTTGAGA	AGCCCTGCTTTAACAGTGGT	TAACCCTCCATCCCCTCAGG
Atr_67534-27	C	T	CATAACTACAAATAT	CATAATTACAAATAT	GCAGGCAAGTGCAACATCAA	GCTGTGGCAGAGTGTAGGAG
Atr_67759-28	G	A	GGCACGGCACAAAAC	GGCACAGCACAAAAC	AGGGGAAGAGCCAGTGAGAG	AATTGCTGTGCTTGCCATGG
Atr_68186-72	C	T	ACAGTCCCTGC	ACAGTCCTTGC	TACCAGTCGCCTGACCAGTA	TCTGCCTCTCCCACAGGTTA
Atr_68680-72	T	C	CATGATCAG	CATGACCAG	TTACCAAGGAAACCAGGGGC	ACATGCTAAAGTGGCTGCTG
Atr_68762-59	A	T	CTCAGATAGTGAGA	CTCAGATTGTGAGA	GGGTGCAGCAAGGATGGTAT	CCTGCACCAAGGTAAGCTCT
Atr_68808-31	A	T	GTATTAAAGCTGGC	GTATTAATGCTGGC	GGTAATGCCTCCCCACTTGT	GGAGGAGTTTATTGAAAGCAGGC
Atr_69047-33	A	G	TAATTATATGAAAG	TAATTATGTGAAAG	GCAGGCTGCTACTGTAGTCT	GTGAAAACAGTCCTTTCCCCT
Atr_69217-58	A	G	TCAAAGCACCCGAG	TCAAAGCGCCCGAG	AAGCCCCCTTTCTGCTTCTC	ACTGCTTCGTCAGTAGAAAAGT
Atr_6988-51	T	C	TTAACTTTAGATCA	TTAACTTCAGATCA	TGGTTCTGGCAGGAACTCAC	TGCTTGATGTTTACCTGATTTGAT
Atr_7001-57	T	C	CACATTATTTCTGT	CACATTACTTCTGT	CCAGAGTGATGTGCATAAAGCC	TGCTGTGTCTTCTGGTTCTGT
Atr_70139-39	G	A	ATTACGATCCCCCCA	ATTACAATCCCCCCA	GGAGTCCTACAAAGTTAAAGGGC	CACGTTTAATGAACTGTGGGGG
Atr_70167-40	C	T	CAGACCTCGTCCTG	CAGACCTTGTCCTG	GCATGCATCAGATAGCCAGC	ACTATATTGCACTGTAGCAGGAC
Atr_7026-63	C	A	AATTCACCAAGTTT	AATTCACAAAGTTT	GGGGTGCCCAAATATATTGCA	AGAGTTGCTGCTTGTTTAAACTT
Atr_70459-55	C	T	TCTGTTTCACATTG	TCTGTTTTACATTG	GGAAGATTCCGATGACAGAACT	GCAGAGAAAAGAGCCGCAAT
Atr_70467-53	A	G	TAAGCACTTCAGAAT	TAAGCGCTTCAGAAT	TGACACACCTGAAAAACACCAC	TTAGCTGTGGGATCATGCCA
Atr_70479-48	T	A	CATAGATTGCTTCA	CATAGATAGCTTCA	GTCTGGGAAATGTCTGGGCA	CAGCCTAGGTCTCTGTTTGCA
Atr_70609-65	A	T	TCTGGACAGATTAA	TCTGGACTGATTAA	GCAATGGCTAAACATCTGGAACA	TCATTTCCACCGAGTTCTCTCT
Atr_7072-61	C	T	AAGGACGTTGCTCGC	AAGGATGTTGCTCGC	ACGCACCTCAAACCAGTTGA	GCTGGGGCTGGATAAAATGG
Atr_70880-74	T	C	CCCTCACTT	CCCTCACCT	GCTTTTCTTTGGCCCAAGGG	GCATGCAGCGGGAACATTTT
Atr_71195-60	A	T	CAGAAAGATGGGGTG	CAGAATGATGGGGTG	TGATGTTGAAGCCTCTACACCA	ACGATACTTCATCCACCCCA
Atr_72165-47	C	A	GGTCTCGGGGTTTCC	GGTCTAGGGGTTTCC	GGGTTGCCTACCTCTGGTCT	GTGGCTGATCACATCCCCTT
Atr_72251-33	A	C	TTAGGAGATGCTGA	TTAGGAGCTGCTGA	AGAAGCTGGGAGTGGTTAGGA	TGGGGTTTTAAAGCTATACACCA
Atr_72558-41	C	T	TCCATGTCGTCTAA	TCCATGTTGTCTAA	GCAGGGCTAGTGACTCTTCA	TCTGTCTTATCTGTAGTGTGATCAC
Atr_72693-61	A	G	TTAAGGCATACATA	TTAAGGCGTACATA	CGGTGTGCTGCTATTTAAGGC	TCCTGAAGACATTGACTAGAGGA
Atr_7298-56	C	T	GTCCCGACCAGGCG	GTCCCGATCAGGCG	CGGTCAGTATGGCTCCTGTC	GCAGTGCCCCCTGATGTATT
Atr_73438-69	T	C	TGAAATAAACAA	TGAAACAAACAA	AGCTGCACCCCTTTTTAACT	CCCTGCATGAAGTCCAAGGT
Atr_73505-52	A	T	CATTCAAAACACAC	CATTCAATACACAC	GCAGGAAAAACAAGCCAGGG	AGAACGAATGGTCATTGTGTGT
Atr_73608-61	C	T	CGACCCGGGTCTATT	CGACCTGGGTCTATT	TGCATTTTGCTTCGCTCGAC	CTGCTTAACCCAGGTCCCAG
Atr_73740-69	T	C	ACATTTCTGTGC	ACATTCCTGTGC	CCTTTCGTAGGCACACTAGACA	AGTCATTCAACCTTTCATGGCAC
Atr_73905-66	A	T	AAGTTTTAAAACTG	AAGTTTTTAAACTG	AGGTTCCTCCTGTTTACAAGTT	GGTACAGGCTCGCTCGTAAT
Atr_73987-49	G	A	GCATGGCCAGTTATA	GCATGACCAGTTATA	CTTACCCTCCACTGCTAGCTG	CCGGCAAACACCTACACCA
Atr_73994-27	C	T	CAAGACTATGAAGAG	CAAGATTATGAAGAG	TGCAGGTCTATTTTCTAACAGCA	ACCAGTGGACATGCTTACGG
Atr_74094-36	G	A	TGCCCGTCATTATGC	TGCCCATCATTATGC	GGATGTGCAAGCATGGAACC	GCACATGCGATACTCCAGCA
Atr_74322-45	A	G	GGTTTATACACATG	GGTTTATGCACATG	CAGAGGGCAGGTCCAAGAAA	AGCCACCCTGAATCATCATGT

Atr_74662-68	T	C	AAAAGTTTCCCCCT	AAAAGTTCCCCCCT	AGGGGAGTGCTGTGTTTGTG	ATGGTGGCTCAGTCCCAAAG
Atr_74730-29	G	A	AAGCCGCAGAAAGAC	AAGCCACAGAAAGAC	GCAGGTTCAGAGGGAGTTTGA	TGCTGCTGTGTTCAGAGAGG
Atr_74747-45	C	T	CAATTTGCTATCAG	CAATTTGTTATCAG	TGCAGGCAAAACAAGACAGAC	GCCTGGAAGTACTGAACTGGA
Atr_74844-59	T	A	CCTTTTGTTGTTACA	CCTTTAGTTGTTACA	GTGAACCACACTTGTCTTTCTGT	TGACTGTTTTGTTCCACGTTGT
Atr_74987-50	T	C	TTTACTTCAAACTAC	TTTACCTCAAACTAC	GCAGGGCGAATTCTCAATATGG	AGGTATGGTGTCTCTTGTAGTTTGA
Atr_75140-58	C	T	GAGTATGCTTTCAT	GAGAATGTTTTCAT	CACCAGAGTGCTTTAAGGTTTATAA	CTGTTGTTCATGAGCCGTATAAT
Atr_75407-53	G	T	ACAGACAGGGTCTC	ACAGACATGGTCTC	GGAAAGGTACAGTACAGGGCA	AAGCCCTGAAGCAATCGGAA
Atr_756-60	T	A	ATCTAACTACTGAC	ATCTAACAACTGAC	TGCAGGCATTCATAAACCACG	AGAGGGCTTTGAGATGAAGGA
Atr_75982-70	G	T	ATGAAGAAGAT	ATGAATAAGAT	CAGGAAGATCCGGCAAAAGA	TGCTGCCTCTTGCTCATCTT
Atr_76253-44	G	A	CTGTCTCGCCTCTC	CTGTCTCACCTCTC	AGGTTCTTATTACATGCCTCTGTCT	GGGTCCTGGTGCTGTGATTA
Atr_76409-55	G	A	CAGCCGCAGGAGAGC	CAGCCACAGGAGAGC	TCAGCGAGTGAGTGGACAAC	TGATCATAAATGTAAACTGCTCTCC
Atr_76418-65	A	T	CCGGCTTATCTGAA	CCGGCTTTTCTGAA	GGTAATGCGTGGGTGGTGTT	ACCAGCAATAACGTCTTCCTGT
Atr_76571-26	C	A	CGATGTTCACGTGC	CGATGCTAACGTGC	GAGGGTCCGCTAGCGATG	GCACTGCTCTCTATCTGGGG
Atr_76791-46	G	A	TATCCGCTGTAGCAC	TATCCACTGTAGCAC	GTCCCCTGAGCTCACCAAG	ATTGAGGCAAAACCAGCAGG
Atr_76888-43	C	T	TGTCAAGCGATTGA	TGTCAAGTGATTGA	ACAACAGAATCAGGGCTGTCA	TGTGAATGAGACGGATGCAGT
Atr_76890-36	G	A	TTCTCGATCTCGCTT	TTCTCAATCTCGCTT	CAGTCGCCGAATCCTGTTCT	GATACGTGCTAGGACCCTGC
Atr_769-65	C	T	CCTCTCAAACTAAAA	CCTCTTAAACTAAAA	GTCCACACAGTACTTGGCCT	TCATGCTAAGGACCTTGATTACGA
Atr_77778-67	C	T	AGTAGATCACCAGA	AGTAGATTACCAGA	TTGCCTACCCCTGCTTTAGC	AAACTGTGCAAGTGGACACA
Atr_7793-68	C	A	CGGTACTCAAATAA	CGGTACTAAAATAA	TAGGGAAAGGGAGTCAGCCA	ACTTCCATTCCACAGCTAATGA
Atr_78173-42	T	C	GGCATTGGAAC[CG]GTC	GGCATCGGAAC[CG]GTC	CTCAGGTCACCCAGCAGAG	GTTGAGCCGCTTGCAATCTC
Atr_7817-58	G	A	ACAC[CT]GTTCATCAGC	ACAC[CT]ATTCATCAGC	GCCTCAGCTGAAAACACAAGA	CCGTGTGAGTTTGTCTGCTG
Atr_78413-36	G	T	TACCCGAGTCTAAA	TACCCGATTCTAAA	TGCAGGTGTGTATTGCTGACA	AGCAGATATGAGTAAAACATTGCCT
Atr_78571-74	A	C	AAGTGAGAC	AAGTGAGCC	GACTTGCAGGTGTTCGGAGT	AGTTCGGCTTGCTTGTTTTT
Atr_78600-73	C	A	CCCAGCTCAG	CCCAGCTAAG	AATAAGGAGCAAGCCCAGCT	GTCGACTTTGGGGAGCAAGG
Atr_78858-41	A	G	CATGAACCATTTTTT	CATGAGCCATTTTTT	AGCTGACAACGACATCATGA	TCCGCATGAGTCAAAATCATACT
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

Appendix 13. Species Associations for Species Diagnostic Markers

Locus	A1	A2	Species-A1	Species-A2	Weight
Oki_101419-103-27	A	C	Ots;Oki;Omy;Ocl1a;Ocl1b;Ocl2	One;Ogo;Oke;Sfo;Ssa;Str	1
Oki_101419-103-44	T	C	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke	Sfo;Ssa;Str	1
Oki_105105-245-23	T	G	Ots;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco;Ssa;Str	One	2
Oki_106172-60-38	C	T	Omy;Ocl1a;Ocl1b;Ocl2	Ots;One;Oki;Ogo;Oke;Sfo;Sco;Ssa;Str	1
Oki_106172-60-47	G	A	Omy;Ocl1a;Ocl1b	Ots;One;Oki;Ocl2;Ogo;Oke	1
Oki_106172-60-47c	A	C	Ots;One;Oki;Ocl2;Ogo;Oke	Sfo;Sco;Ssa;Str	1
Oki_106172-60-53	C	T	Ogo	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Oke;Sfo;Sco;Ssa;Str	2
Oki_111681-407-38	C	T	One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco;Ssa;Str	Ots	2
Oki_120255mod-105	C	T	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco;Ssa;Str	Oma	2
Oki_120255mod-113	G	A	One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco;Ssa;Str	Ots	2
Oki_120255mod-115	G	T	Ots;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco;Ssa;Str	One	2
Oki_120255mod-119	G	A	Ots;One;Oki;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco;Ssa;Str	Omy	2
Oki_120255mod-120	C	T	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sco;Ssa;Str	Sfo	2
Oki_120255mod-133	T	C	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco;Ssa;Str	Oma	2
Oki_120255mod-135	A	C	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Oke;Sfo;Sco;Ssa;Str	Ogo	2
Oki_120255mod-137	A	T	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco;Str	Ssa	2
Oki_120255mod-141	A	G	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Oke;Sfo;Sco;Ssa;Str	Ogo	2
Oki_120255mod-99	A	C	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Sfo;Sco;Ssa;Str	Oke	2
Oki_126619-265-31	A	C	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sco	Sfo	2
Oki_126619-265-35	A	G	Ots;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Oke;Sfo;Sco	One;Ogo	1
Oki_126619-265-50	G	T	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Sfo;Sco	Oke	2
Oki_RAD41030-31-36	C	T	Ots;One;Oki;Ocl1a;Ocl1b;Ogo;Oke;Sfo;Sco;Ssa;Str	Ocl2	2
Oki_RAD41030-31-37	G	A	Ots;One;Oki;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Ssa;Str	Sfo;Sco	1
Oki_RAD41030-31-41	G	C	Ots;Oma;One;Ocl1a;Ocl1b;Ocl2;Oke;Sfo;Sco;Ssa;Str	Oki	2
Oki_RAD41030-31-55	G	T	Ots;One;Oki;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco;Str	Ssa	2
Oki_RAD51585-47-25	C	G	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke	Sfo;Sco;Ssa;Str	1
Oki_RAD51585-47-28	G	A	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Oke;Str	Ogo	2
Oki_RAD51585-47-31	A	C	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ogo;Oke;Sfo;Sco;Ssa;Str	Ocl2	2
Oki_aspAT-273-37	C	T	Ots;One;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco;Ssa;Str	Oki	2
Oki_aspAT-273-45	T	A	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke	Sfo;Sco	1
Omy_RAD13034-67-21	C	T	One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Ssa	Ots	1
Omy_RAD13034-67-35	A	T	Ots;One;Oki;Omy;Ogo;Oke;Ssa	Ocl1a;Ocl1b;Ocl2	2
Omy_RAD79314-58-25	C	T	Ots;Oki;Omy;Ocl1a;Ocl2;Ogo;Oke;Sfo;Sco	One;Ssa;Str;Ocl1b	1
Omy_RAD79314-58-27	T	C	One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke	Ots;Sfo;Sco;Ssa;Str	1
Omy_RAD79314-58-31	G	A	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Oke;Sfo;Sco;Ssa;Str	Ogo	2
Omy_RAD79314-58-66	C	A	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco	Ssa;Str	1
Omy_myclarp404-111	T	G	Omy	Ots;One;Oki;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco;Ssa;Str	2

One_1a.54542-52-44	C	T	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke	Sfo;Sco;Ssa;Str	1
One_1a.54542-52-47	G	C	Ots;One;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco;Ssa;Str	Oki	2
One_2.70711-39-28	G	T	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Sfo;Sco;Ssa;Str	Oke	2
One_2.70711-39-30	T	C	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke	Sfo;Sco;Ssa	1
One_2.70711-39-43	G	A	Ots;One;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco	Ssa	1
One_2.70711-39-57	G	A	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Oke;Sfo;Sco;Ssa;Str	Ogo	2
One_2.70711-39-64	T	G	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Sfo;Sco;Ssa;Str	Oke	2
Ots_ARNT-29	A	G	One;Omy;Ocl1a;Ocl1b;Ocl2;Ogo	Ots;Oki;Sfo;Sco	1
Ots_ARNT-29c	A	C	One;Omy;Ocl1a;Ocl1b;Ocl2;Ogo	Oke	2
Ots_P53-25	G	T	Ots;One;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco;Ssa;Str	Oki	2
Ots_P53-28	G	C	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Ssa;Str	Sco	2
Ots_P53-40	T	C	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke	Sfo;Sco;Ssa;Str	1
Ots_crRAD9615-69-19	T	A	Ots;Oki;Omy;Ocl1a;Ocl1b;Ocl2;Ogo;Oke;Sfo;Sco;Ssa;Str	One	2
Ots_crRAD9615-69-50	A	T	Omy;Ocl1a;Ocl1b;Ocl2;Sfo;Sco;Ssa;Str	Ots;One;Oki;Ogo;Oke	1
Ots_myo1a-384-36	C	T	Ots;One;Oki;Omy;Ocl1a;Ocl1b;Ogo;Oke	Ocl2	2
Ots_unk9480-51-38	T	C	Omy;Ocl1a;Ocl1b;Ocl2	Ots;One;Oki;Oke	1
LampSD_478	G	A	Entosphenus	Lampetra	2
LampSD_700	G	T	Entosphenus	Lampetra	2
Ocl_gshpx-357	T	G	Ocl1a;Ocl1b;Ocl2	Omy	1
Omy_Omyclmk438-96	A	C	Omy	Ocl1a;Ocl1b;Ocl2	1