

# **GENETIC ASSESSMENT OF COLUMBIA RIVER STOCKS**

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## Executive Summary

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

### Objective 1) discover and evaluate SNP markers in salmon and steelhead and other anadromous fishes.

The GT-seq genotyping method has allowed for 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* – 377 loci including a sex determination marker and 14 additional amplicons used for species identification), Steelhead trout (*O. mykiss* – 383 loci including a sex determination marker, 16 additional amplicons for species identification, and 31 test markers); Sockeye salmon (*O. nerka* – 365 loci including a sex determination marker and 17 additional amplicons for species identification); Coho salmon (*O. kisutch* – 236 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 158,120 samples in 2024 (Figure 1). The largest portion of samples were Chinook salmon (97,909), then Steelhead (22,486), Pacific lamprey (15,443), Coho (12,249), Sockeye (9,060), and White sturgeon (973).

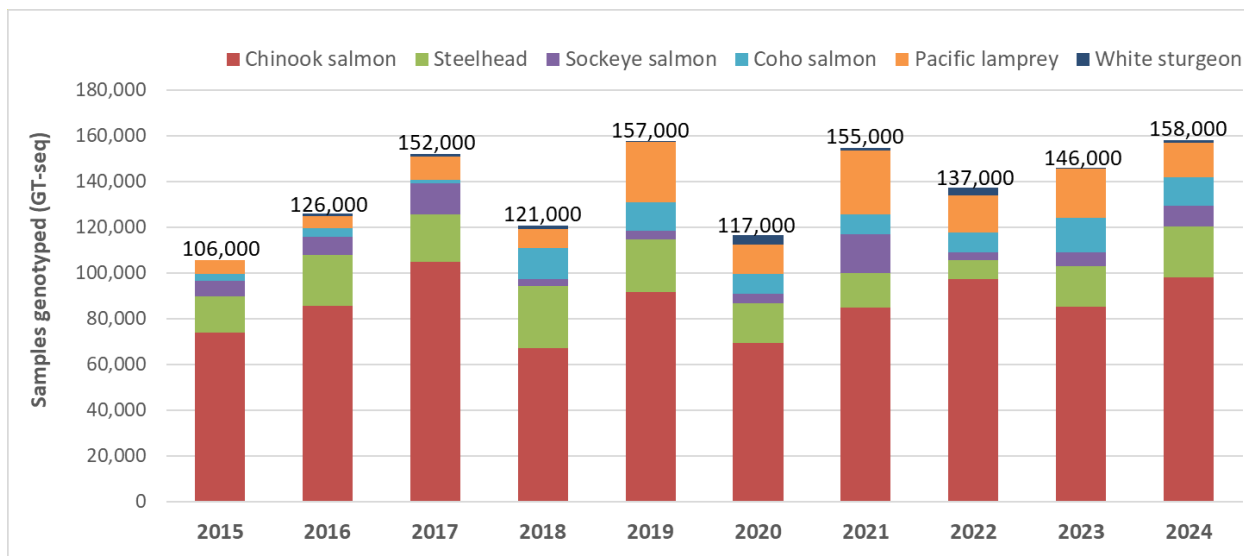


Figure 1. Summary of Columbia River fish samples genotyped using GT-seq (2015 – 2024).

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

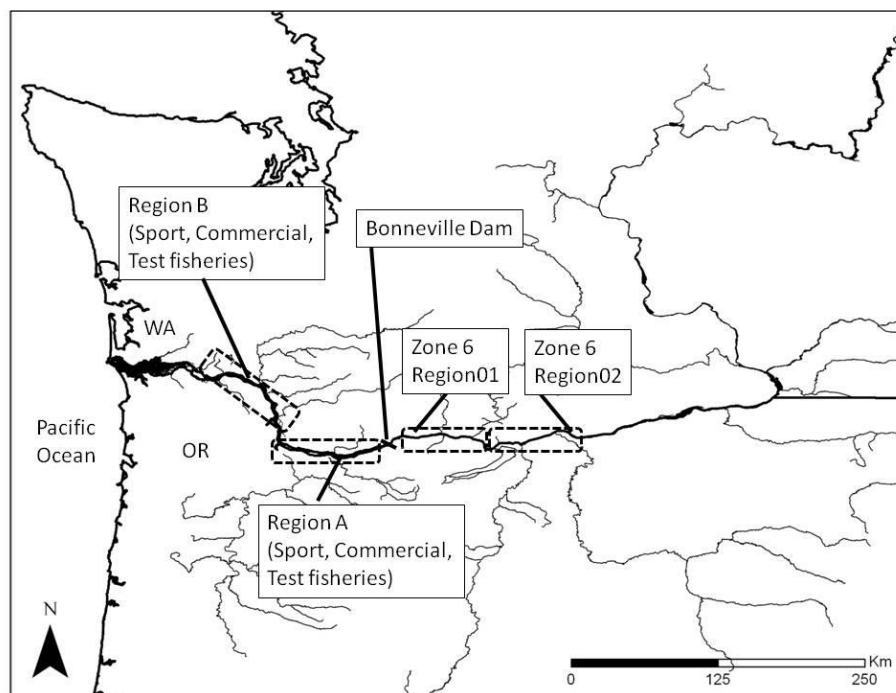
efforts to evaluate genetic diversity among populations that will inform managers in the areas of harvest monitoring, and conservation monitoring. Our approach involves the collection, analysis, interpretation, and distribution of genotypic data. These data are being compiled as species-specific reference 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*, *O. nerka*), 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).

The three projects initiated to characterize reference baselines of millions of SNPs for Chinook and Coho salmon and *O. mykiss* were completed in 2024. 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 2024, a study was completed 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 2021-2024. 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.

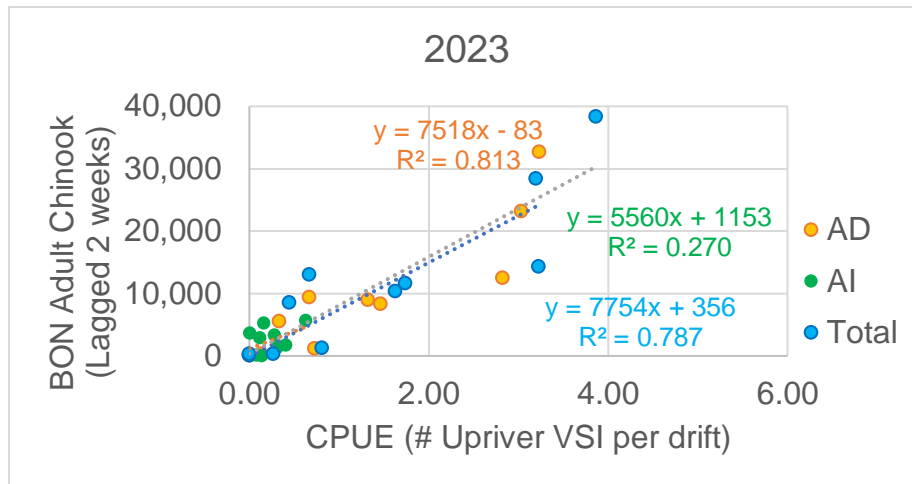
We used a combination of PBT and GSI analyses to determine stock composition of Chinook salmon harvested in 2023 in Non-Treaty sport and commercial fisheries in the mainstem Columbia River during the spring, summer, and fall management periods (Figure 2). PBT is also applied to Sockeye salmon and can identify fish that are part of the Yakima River reintroduction using a baseline of translocated adults.

There were 285 coded-wire tags (CWTs) that were identified to hatchery stock and broodyear (BY) among the snouts recovered from the lower river fisheries in 2023, and 226 of these CWTs also were PBT assigned. Of the 226 fish with both CWT and PBT, there were 211 fish (93%) that were concordant across results from these tagging methods according to the hatchery source and the broodyear.



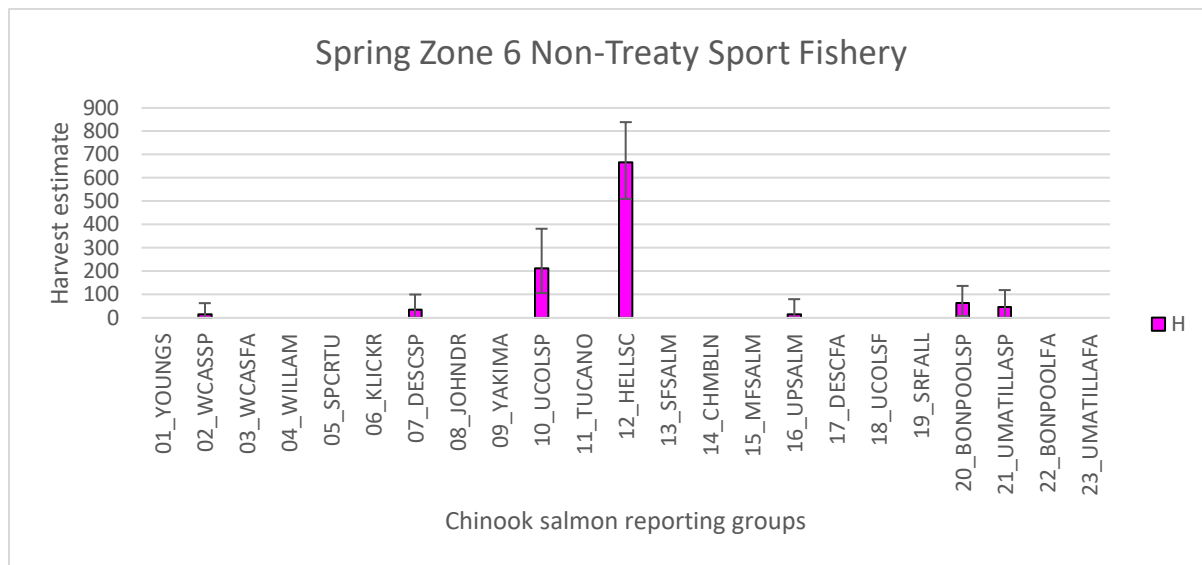
**Figure 2. Sources of fishery mixtures in the lower Columbia River mainstem.**

We examined one source of information that could potentially be useful to managers particularly on years when the spring Chinook Salmon run is delayed, and passage data is not available from Bonneville Dam. There is a test fishery in the lower Columbia River that is typically conducted by WDFW on Sundays each week in the early spring (February – May). We analyzed the 2023 test fishery. Consistent with our previous analyses of 2018 – 2022 test fishery data, the 2023 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.



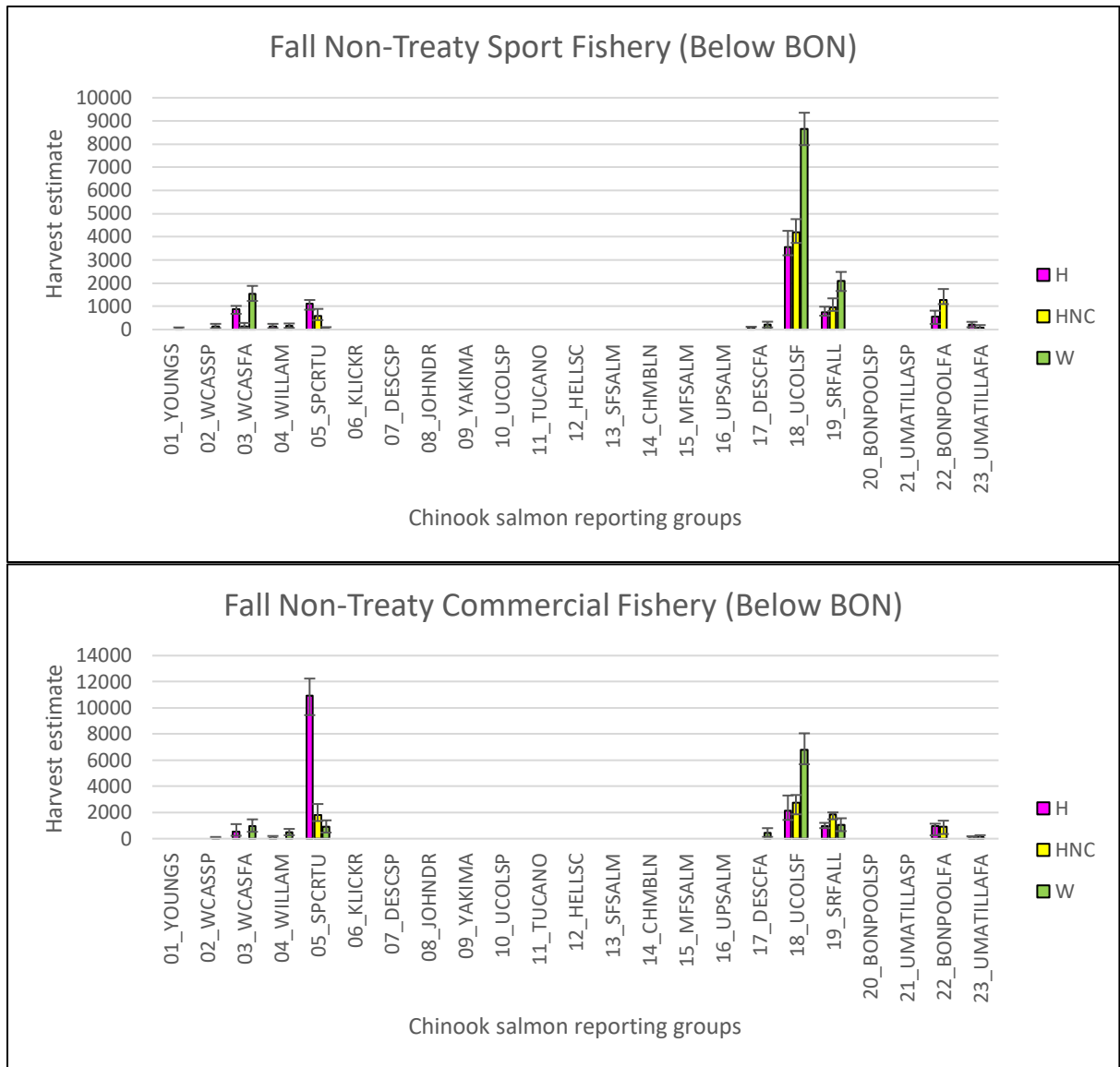
**Figure 3. The relationship between the test fishery upriver Chinook Salmon CPUE and weekly fish counts at Bonneville Dam in 2023 with 2 week lag.**

As expected, the stock composition varied substantially across the Non-Treaty sport 2023 fisheries that were executed in the spring and summer periods. The largest difference in stock compositions across the spring and summer fisheries was the estimate of upper Columbia summer-run stock (18\_UCOLSF) which tends to be higher in the summer period compared to the spring period for the sport fishery (Figure 4). There can also be differences in the capture of Willamette River stock (04\_WILLAM) below Bonneville Dam compared to Zone 6 because the stock does not typically pass upstream of the dam in high numbers in the spring period. The 2023 harvest year showed both of these typical patterns. Deviations in these patterns sometimes occurs 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 2023.**

In 2023, 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.

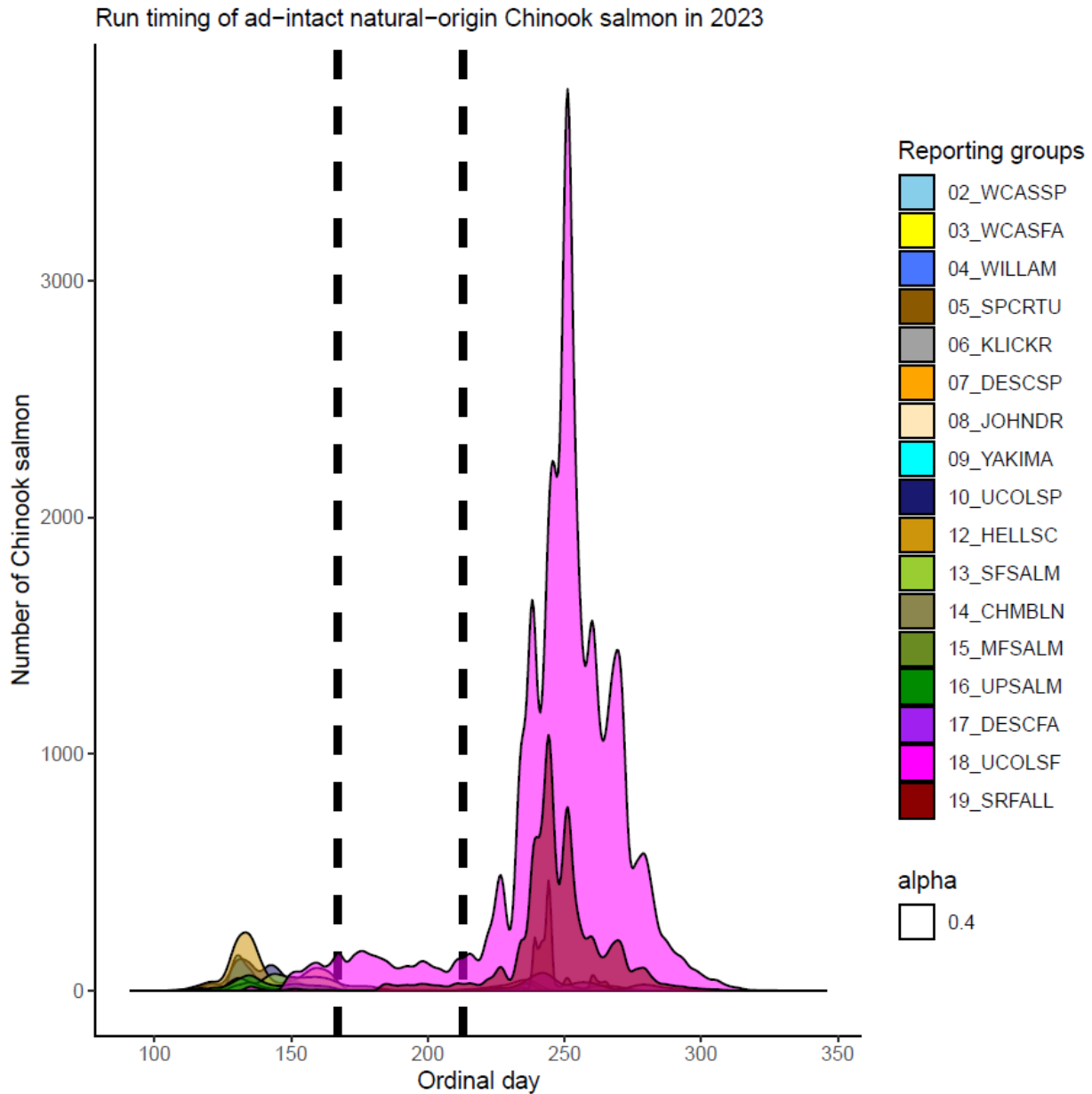


**Figure 5. Genetic stock composition of the Fall Non-Treaty Chinook salmon fisheries analyzed in 2023.**

**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 2023 (post-season analyses). Further, in-season analyses were completed for fish returning throughout 2024 and provided to regional fisheries managers that serve the U.S. v OR Technical Advisory Committee (TAC).

In 2023, there were 10 major (i.e., abundance >1000 fish) Chinook salmon stocks represented in the total estimated relative abundance (N=132,417) of natural-origin (i.e., excluding unclipped hatchery-origin fish) Chinook salmon passing Bonneville Dam (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 (90,098), 19\_SRFALL (19,639), 12\_HELLSC (5,006), 10\_UCOLSP (3,106), 05\_SPCRTU (2,733), 13\_SFSALM (2,601), 17\_DESCFA (2,044), 09\_YAKIMA(1,692), 16\_UPSALM (1,420), and 03\_WCASFA (1,055). These stock abundance estimates were generated using SCOBIDEUX and SPIBETR functions and the estimates of clipped and unclipped adults distributed by TAC.

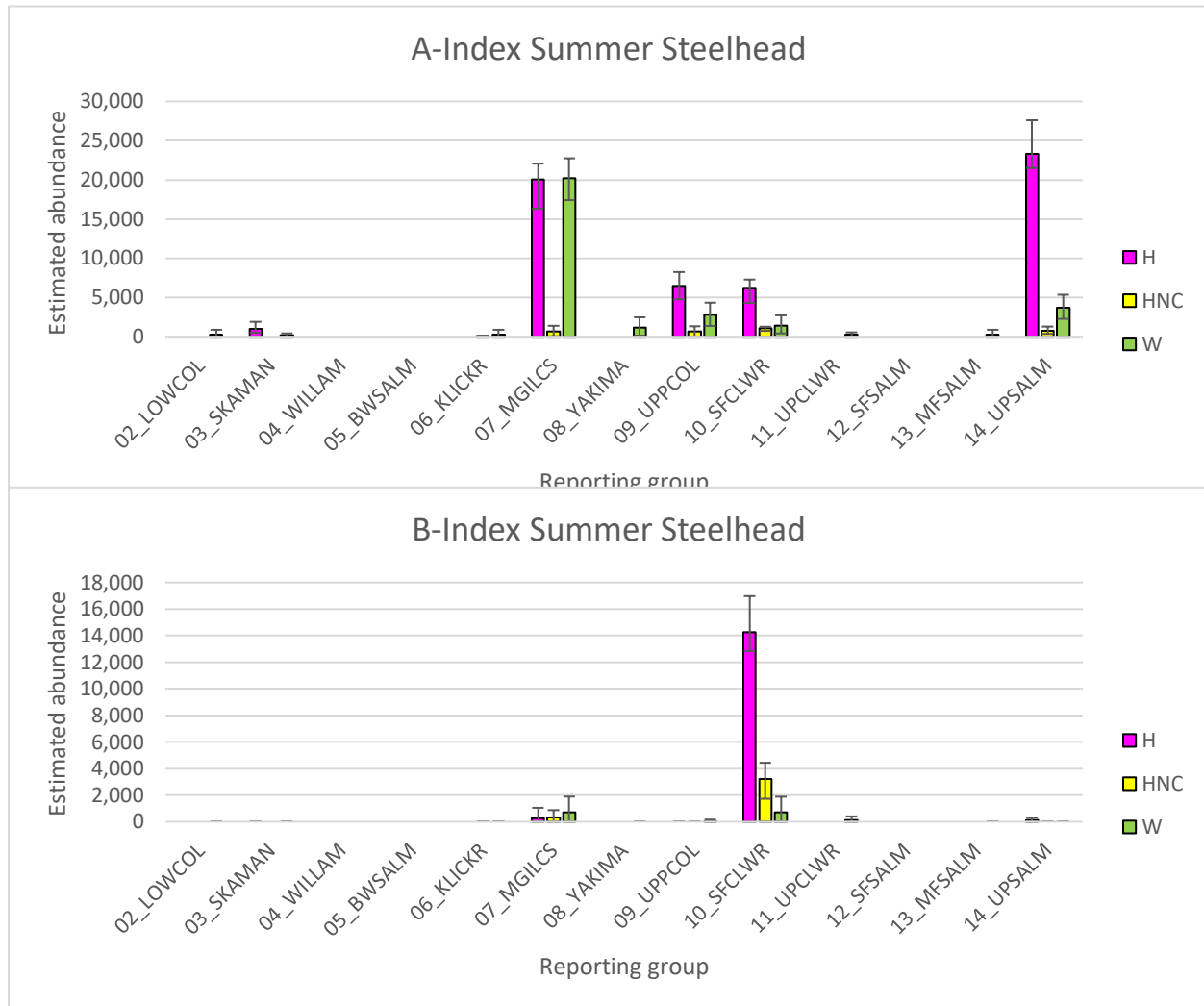




**Figure 6. Estimated abundance of natural origin (excluding adipose-intact hatchery-origin fish) adult-sized Chinook salmon reporting groups at Bonneville Dam in 2023.**

There were five major stocks (abundance >1000) represented in the total estimated abundance (N=71,761) of clipped hatchery origin steelhead passing Bonneville Dam in 2023. These stocks in order of decreasing magnitude were 07\_MGILCS (20,050), 10\_SFCLWR (14,274, B-Index; 6,244, A-Index), 14\_UPSALM (23,286), 09\_UPPCOL (6,513), and 03\_SKAMAN (1,016) (Figure 7). There was one major stock (abundance >1000) represented in the total estimated abundance (N=6,717) of unclipped hatchery origin steelhead passing Bonneville Dam in 2023 (10\_SFCLWR 3,225, B-Index; 1,061, A-Index). There were five major stocks (abundance >1000) represented in the total estimated abundance (N=32,209) of natural origin (excluding adipose unclipped hatchery-origin fish) summer A-/B-Index steelhead passing Bonneville Dam in 2023 (Figure 7). These stocks in order of decreasing magnitude were

07\_MGILCS (20,213 A-Index), 14\_UPSALM (3,720 A-Index), 09\_UPPCOL (2,783 A-Index), 10\_SFCLWR (1,423 A-Index), and 08\_YAKIMA (1,159 A-Index). This year there were no major stocks of natural-origin B-Index. The results of the SCOBIDEUX SPIBETR function minimized bias from tag rate expansion of the unclipped hatchery-origin fish and represent a significant improvement for accuracies of natural-origin stock composition.

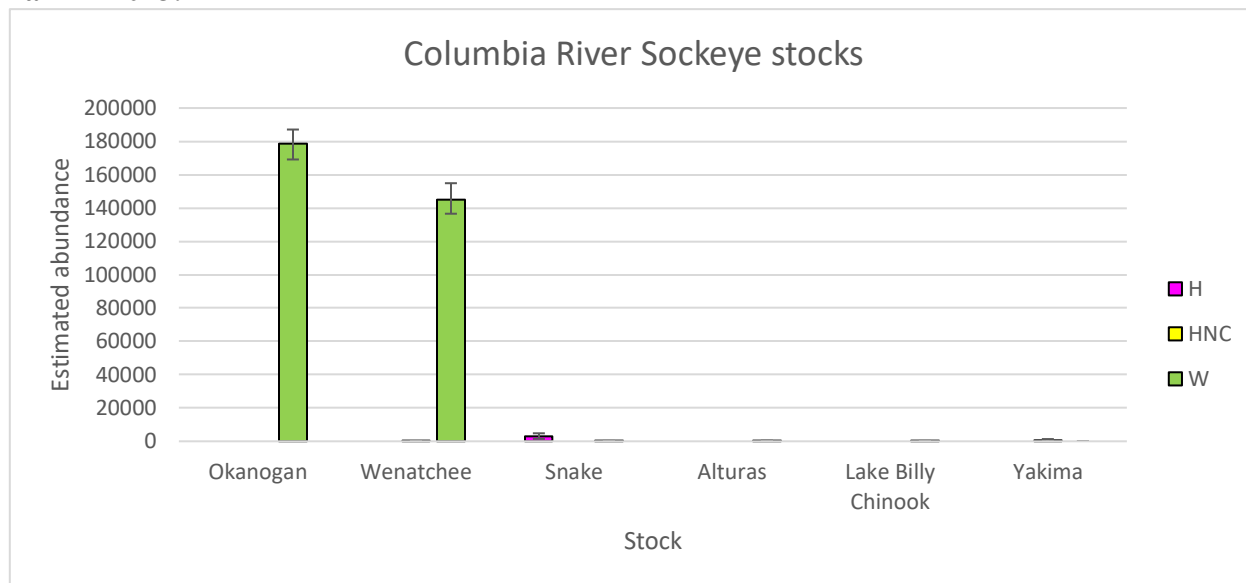


**Figure 7. Estimated abundance ( $\pm$  95% CI) of A-Index (<780mm FL, top) and B-Index ( $\geq$ 780mm FL, bottom) hatchery origin (clipped “H” and unclipped “HNC”) and natural-origin (“W”) steelhead assigned to genetic stock of origin that were sampled at Bonneville Dam in 2023.**

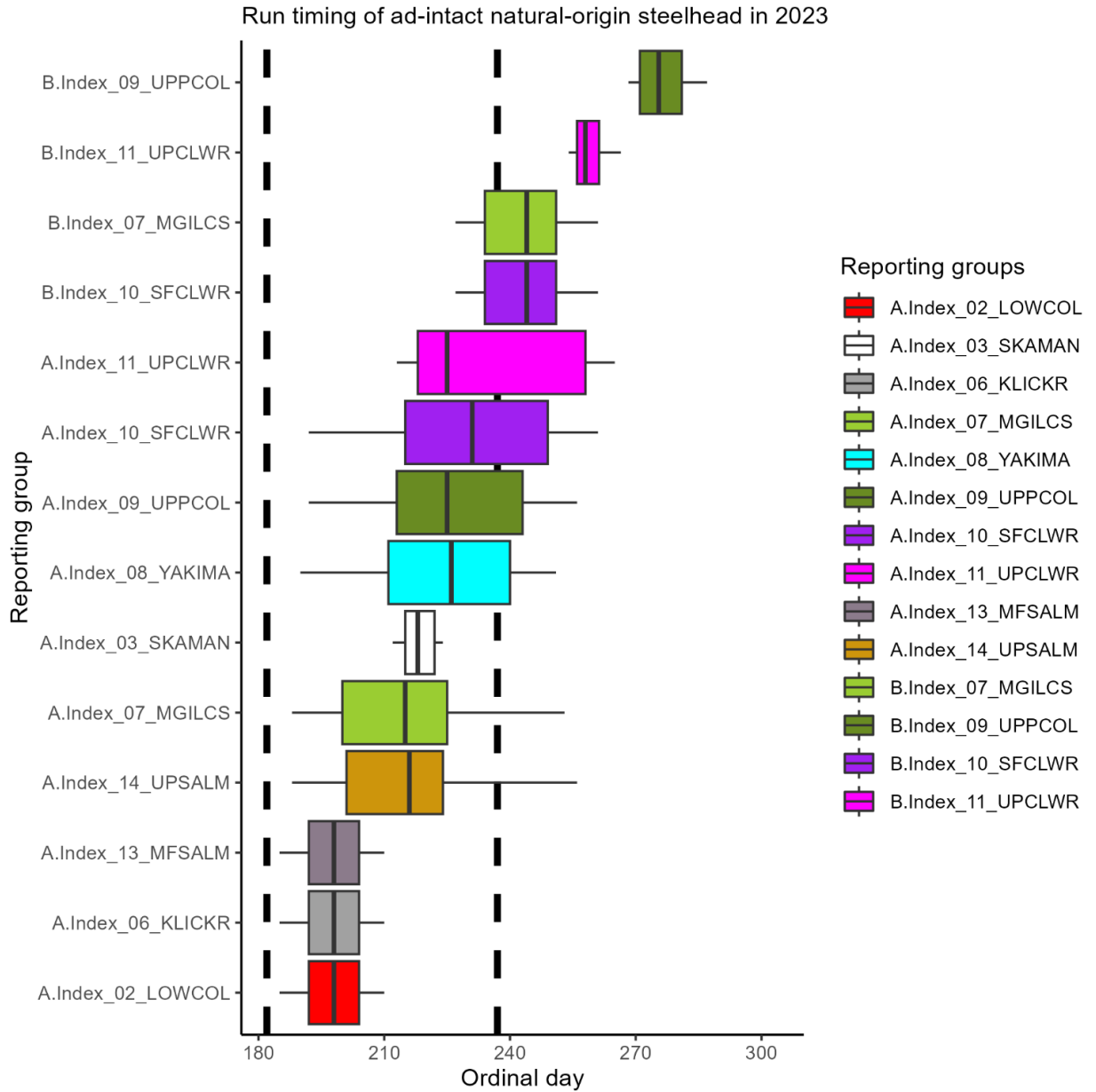
Stock abundance for sockeye salmon was estimated over a course of 18 statistical weeks (i.e. weeks 19 – 37). A total of 1,108 sockeye salmon were sampled at Bonneville Dam in 2023 and were assigned to one of four genetic stocks (i.e., Okanogan, Wenatchee, Snake (and Alturas), and Lake Billy Chinook) using GSI and one reintroduced stock (Yakima) using PBT. In 2023, the Okanogan stock had the highest relative abundance (178,796), followed by the Wenatchee (144,914). This year there were a small number of sockeye estimated from Snake

River (3,036). The Lake Billy Chinook stock had 73 and the reintroduced stock from Yakima River had 669 estimated abundance (Figure 8).

**Figure 8. Estimated abundance ( $\pm$  95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2023.**



In 2023, 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 95<sup>th</sup> percentile of the run passed before the summer period). However, 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 25% (1,926 fish) and 75% (5,723 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 25<sup>th</sup> 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 2023. The Wenatchee and Okanogan stocks had nearly identical run timing distributions with the same median date on 06/29/23. Snake River stock was relatively later timed (median date of 7/5/2023 and Yakima was earlier timed (6/21/2023 median date).



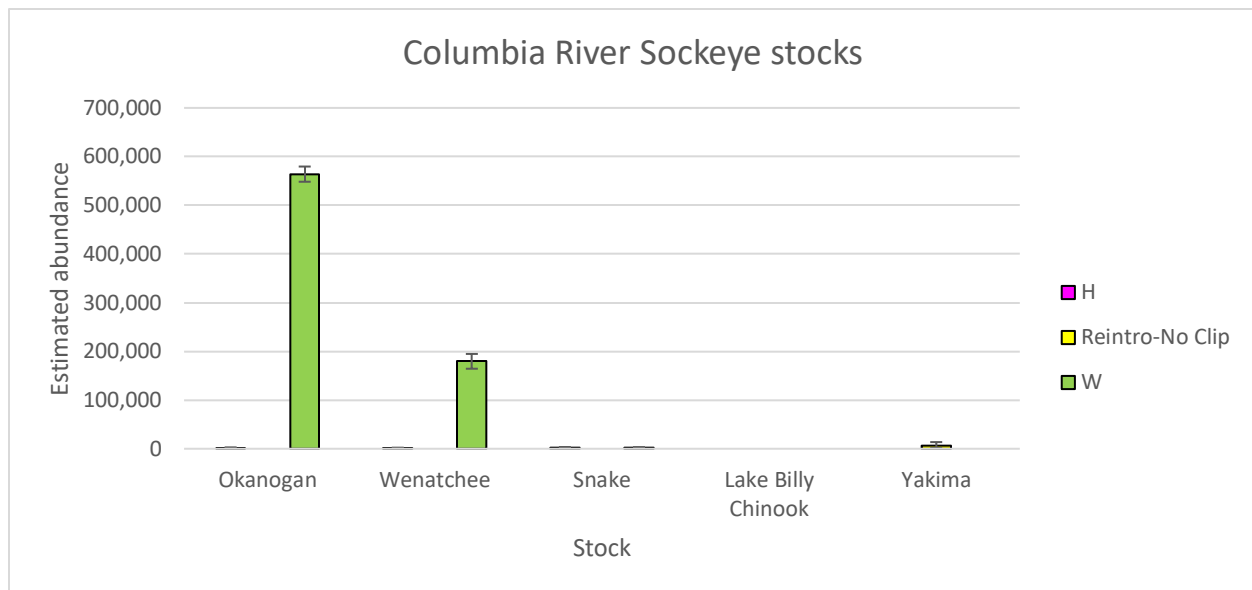
**Figure 9. Reporting group level run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for natural-origin steelhead (unclipped hatchery-origin fish excluded) that were sampled at Bonneville Dam in 2023 and split by A-Index and B-Index size category. August 25<sup>th</sup> 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 2024 (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 6,644 estimated for Sockeye salmon that returned to Bonneville Dam in 2024 originating from the Yakama Nation reintroduction program in the Yakima River basin (Figure 10). Mostly the Sockeye salmon run was comprised of Okanogan and Wenatchee genetic stocks.

**Table 1. The in-season and post-season report timing and scope of the 2024 fish runs for Chinook salmon, steelhead, and Sockeye salmon.**

Species	Management Period	Data coverage	Samples Arrive	Analysis begins	Report distributed
Chinook	Spring	01/01/2024 – 05/04/2024	5/6/2024	5/9/2024	5/13/2024
		01/01/2024 – 05/18/2024	5/20/2024	5/23/2024	5/27/2024
		01/01/2024 – 06/01/2024	6/3/2024	6/6/2024	6/10/2024
		01/01/2024 – 06/15/2024	6/17/2024	6/20/2024	6/24/2024
	Summer	06/16/2024 – 07/06/2024	7/8/2024	7/11/2024	7/12/2024
		06/16/2024 – 07/31/2024	8/5/2024	8/8/2024	8/12/2024
	Fall	08/01/2024 – 8/31/2024	9/2/2024	9/5/2024	9/9/2024
		08/01/2024 – 11/02/2024	11/4/2024	11/7/2024	11/11/2024
Steelhead	Skamania	04/01/2024 – 06/30/2024	7/8/2024	7/11/2024	7/12/2024
	Summer A-/B-Index	07/01/2024 – 08/04/2024	8/5/2024	8/8/2024	8/12/2024
		07/01/2024 – 09/01/2024	9/2/2024	9/5/2024	9/9/2024
		07/01/2024 – 10/31/2024	11/4/2024	11/7/2024	11/11/2024
Sockeye	Total	01/01/2024 – 08/03/2024	8/5/2024	8/8/2024	8/12/2024

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.



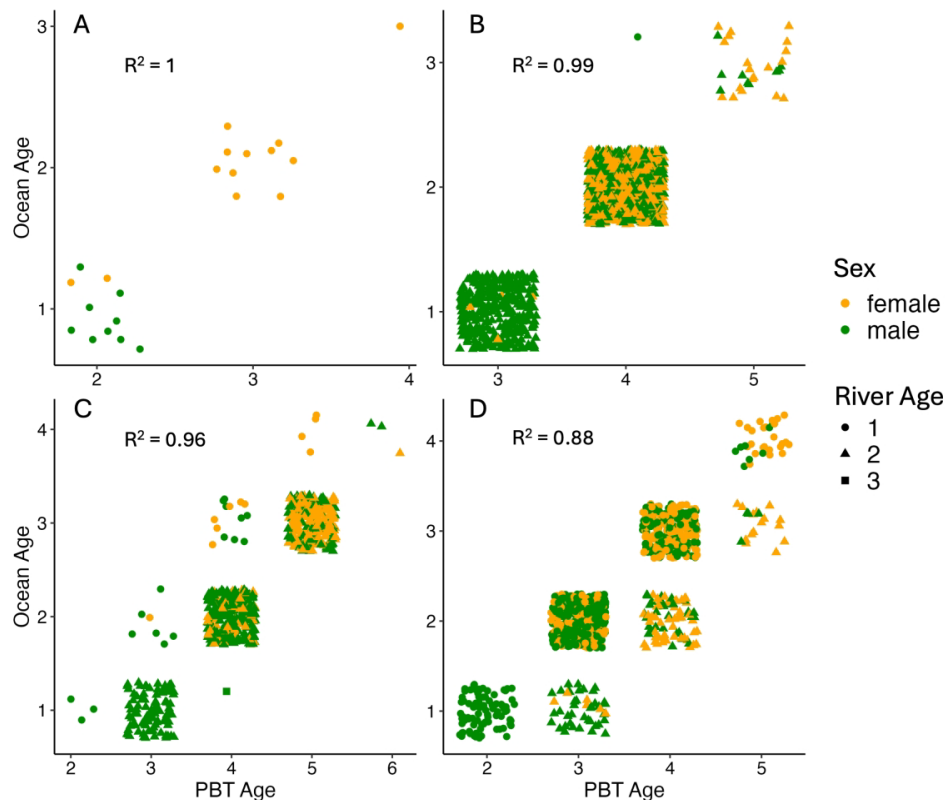
**Figure 10. In-season analysis estimated a relatively large return of sockeye salmon overall in 2024 comprised of a mixture of Wenatchee and Osoyoos genetic stocks and non-zero abundance estimated from Snake River and Yakima River.**

#### **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 52). 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 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 (**Figure 11**), and development of studies to investigate thermal adaptation in anadromous stocks of *O. mykiss* and age/size at maturity and iteroparous phenotypes in steelhead (A vs. B run, Willis et al. 2020; iteroparity phenotypes in females, Willis et al. 2023). 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.** Ocean age from scales (years) versus parentage-based tagging age (years) for hatchery-origin (PBT-assigned) Chinook salmon sampled ( $N = 2,938$ ) at Bonneville Dam from 2014 to 2019 (data from Willis et al. 2021). A) Coastal; B) Interior stream-type; C) Interior ocean-type, summer run; D) Interior ocean-type, fall run.

### 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.

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## **Introduction**

### ***Project overview***

This project combines multiple inter-related studies from the Fish & Wildlife Program Accords that address the following objectives: 1) discover and evaluate genetic variation in salmon, steelhead, white sturgeon, and lamprey; 2) expand and create genetic baselines for multiple species (Chinook, steelhead, sockeye, and coho); 3) implement stock identification (PBT/GSI) sampling programs for mainstem Chinook salmon, sockeye salmon, and steelhead fisheries, 4) stock identification (PBT/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 stock identification. 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, Sockeye salmon, and Coho salmon sampled in mainstem fisheries in 2023. 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 2023. 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 2024. These in-season and post-season 2024 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 facilitates 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



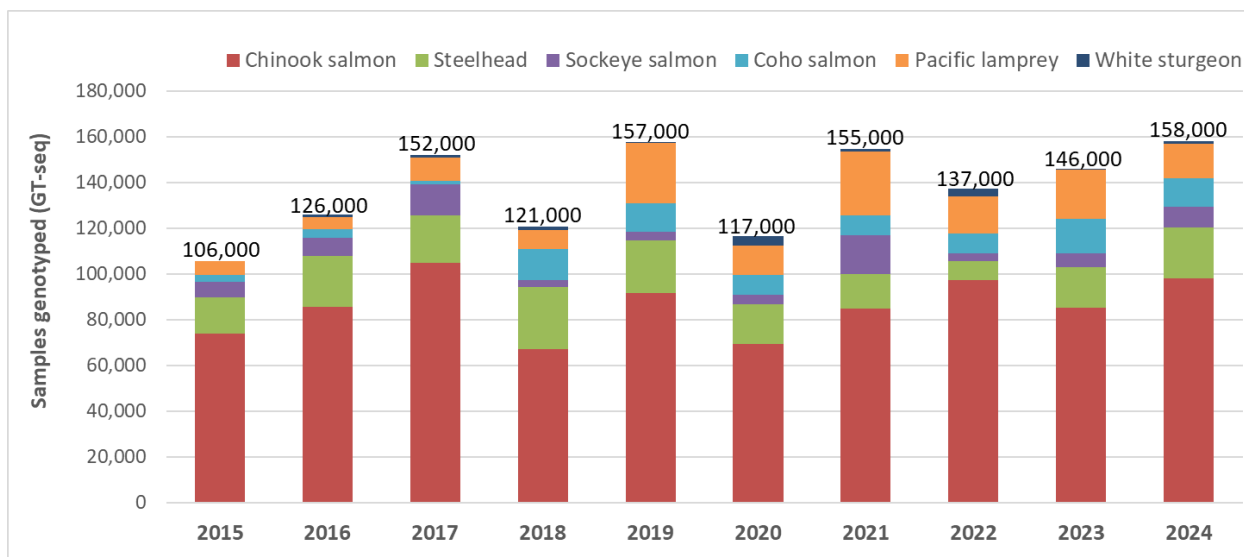
range: 18-24 bases, optimal GC content: 50%). Primers were then screened for hetero-dimers and specificity using MFEprimer3 (Wang et al., 2019). The designed primers were then modified by including adaptors for the Illumina sequencing primer sites. Testing was done by combining the newly designed primers 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* – 377 loci including a sex determination marker and 14 additional amplicons used for species identification), Steelhead trout (*O. mykiss* – 383 loci including a sex determination marker, 16 additional amplicons for species identification, and 31 test markers); Sockeye salmon (*O. nerka* – 365 loci including a sex determination marker and 17 additional amplicons for species identification); Coho salmon (*O. kisutch* – 236 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 158,120 samples in 2024 (**Figure 12**). The largest portion of samples were Chinook salmon (97,909), then Steelhead (22,486), Pacific lamprey (15,443), Coho (12,249), Sockeye (9,060), and White sturgeon (973).

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 158,120 samples in 2024 (Figure 12). The largest portion of samples were Chinook salmon (97,909), then Steelhead (22,486), Pacific lamprey (15,443), Coho (12,249), Sockeye (9,060), and White sturgeon (973).



**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 2024, marker development completed and will improve assignment accuracy for seven 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 were tested with 25 kept and deemed useful in refining GSI assignments. 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	Sample Source	N	Species Calls			
			Correct	True Sp. Included	True Sp. Excluded	No Call
<i>O. clarkii clarkii</i>	Coquille River, OR	8	100.000%	0.000%	0.000%	0
	Umpqua River, OR	13	100.000%	0.000%	0.000%	0
<i>O. clarkii bouveri</i>	Henry's Lake, ID	8	100.000%	0.000%	0.000%	0
<i>O. clarkii utah</i>	Grace Fish Hatchery, ID	8	100.000%	0.000%	0.000%	0
<i>O. kisutch</i>	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
<i>O. mykiss</i>	Columbia River Basin	9,755	99.836%	0.154%	0.010%	0
	Lochsa River, ID	8	100.000%	0.000%	0.000%	0
<i>O. nerka</i>	Columbia River Basin	218	99.541%	0.459%	0.000%	0
	Eagle Fish Hatchery, ID	8	100.000%	0.000%	0.000%	0
<i>O. tshawytscha</i>	Columbia River Basin	29,677	99.997%	0.003%	0.000%	0
	Salmon River, ID	8	100.000%	0.000%	0.000%	0
<i>S. confluentus</i>	Salmon River, ID	16	100.000%	0.000%	0.000%	1
<i>S. fontinalis</i>	Little Lost River, ID	8	100.000%	0.000%	0.000%	0
	Boise River, ID	8	100.000%	0.000%	0.000%	0
<i>S. trutta</i>	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	<i>O. clarkii clarkii</i>
Ocl1b	<i>O. clarkii lewisi</i>
Ocl2	<i>O. clarkii utah</i> or <i>O. clarkii bouvieri</i>
Ogo	<i>O. gorbuscha</i>
Oke	<i>O. keta</i>
Oki	<i>O. kisutch</i>
Omy	<i>O. mykiss</i>
One	<i>O. nerka</i>
Ots	<i>O. tshawytscha</i>
Sco	<i>S. confluentus</i>
Sfo	<i>S. fontinalis</i>
Ssa	<i>S. salar</i>
Str	<i>S. trutta</i>
Oma	<i>O. masu</i>
Lampetra	<i>Lampetra</i> ssp.
Entosphenus	<i>Entosphenus</i> ssp.

### *GT-seq Panel Updates*

The active Steelhead panel for 2024 dropped two markers (Omy4\_8261223 and Omy4\_8325040) due to issues with excessive read counts. These markers were tightly linked with other markers and did not provide additional data. Loci information can be seen in Appendix 6. The steelhead panel for 2024 also included 21 test markers for chromosome 25 and 10 chromosome 12 markers that are not listed in the appendix. The active Chinook panel had 28 markers added in 2024. This includes the 25 previously found to be useful for GSI analysis plus 3 that were discovered at the same time but not found to be useful. Loci used in the standard panel are shown in Appendix 7. Loci included in the panels for Sockeye (Appendix 8), Coho (Appendix 9), Pacific lamprey (Appendix 10), species complex of lamprey (Appendix 11), and White sturgeon (Appendix 12) were not changed in 2024. Note that correction factors are no longer included for White sturgeon as they are not currently 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 in fish passage protocols, transport through the hydro system, artificial rearing practices, or inadequate acclimation (imprinting to natal waters by juvenile salmon). An elevated rate of immigration between populations may erode local adaptations, and lead to changes in spatial and temporal variability within and/or among populations (Hess and Matala 2013; Hess *et al.* 2016a; Matala *et al.* 2017).

In the Columbia River Basin, Chinook Salmon have been studied extensively (e.g., Waples *et al.* 2004; Beacham *et al.* 2006; Narum *et al.* 2008b; Matala *et al.* 2011; Hecht *et al.* 2015), as have steelhead trout (Winans *et al.* 2004; Currens *et al.* 2009; Blankenship *et al.* 2011; Narum *et al.* 2011; Matala *et al.* 2016). The scope of Sockeye Salmon and Coho Salmon genetic monitoring has been comparatively limited but has received greater attention in recent years (Gustafson *et al.* 1997; Kozfkay *et al.* 2008; Iwamoto *et al.* 2012; Galbreath *et al.* 2014). Continued monitoring and evaluation of the genetic structure among salmon populations in the Columbia River Basin has guided managers in establishing and maintaining primary conservation units to protect fisheries resources. The delineation of such conservation units, including distinct population segment (DPS), evolutionarily significant unit (ESU), major population group (MPG), and viable salmonid population (VSP) is guided by a core set of criteria, including population ecology and viability, ancestry and descent, reproductive isolation, and genetic structure and local adaptation (Fraser and Bernatchez 2001; Fraser *et al.* 2011). Although an understanding of adaptive variation is critical to proper salmon management, the majority of genetic information available to managers is based on neutral genetic variation. Landscape genetics is an approach aimed at describing population differentiation relative to features in an organism's environment (Segelbacher 2010; Latch *et al.* 2011; Sepulveda-villet & Stepien 2012; Matala *et al.* 2014). Landscape genetics explores population differentiation relative to features in the environment such as migratory barriers (e.g., dams), or heterogeneous habitats such as variation in local climates or temperatures (Dionne *et al.* 2008; Narum *et al.* 2008a; Micheletti *et al.* 2017). Although local adaptation may be inferred from landscape

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

*Project objectives, timeline and harvest management questions:*

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



## **Methods**

### *Baseline sampling and protocols:*

Our previously established baselines, comprised of putatively neutral SNPs (e.g. 180 loci for *O. mykiss*), have been well characterized and have been used extensively for genetic stock identification (GSI) as described in Hess et al. (2015) and Hasselman et al. (2016). Our most recent efforts focus on expanding genetic characterizations throughout the basin that will provide information about adaptive potentials and natural selective forces contributing to stock structure. Next generation sequencing technologies continue to be employed by the CRITFC genetics lab in order to expand SNP panels for Chinook Salmon, Coho Salmon, Sockeye Salmon, steelhead trout and Pacific lamprey (Hess et al. 2016c). Methods for genotyping by sequencing (GT-seq) are described in Campbell et al. (2015), and protocols for whole genome resequencing are shown below. Detailed laboratory methods are available in Monitoring Methods: [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 SY2023 PBT broodstock collections that CRITFC genotyped (primarily outside the Snake River basin). For each SY2023 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 \(monitoringresources.org\)](#)):  $(\text{proportion genotyped samples})^2$ . 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 PBT assignment rate for collection X is 75%. If hatchery A and B have tag rates that are 100%, then the expected PBT assignment rate of collection X would be 100% (weighted average of tag rates for hatchery A and B). Because this expected PBT assignment 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 2024 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 have been used to develop 25 new GSI markers that strengthen the assignments of fish to seven GSI reporting groups. Self-assignment rates of individuals in the GSI baseline for Chinook salmon increased up to 20% with the addition of the 25 new GSI markers, indicating higher assignment accuracies for those seven GSI reporting groups tested.

**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
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**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

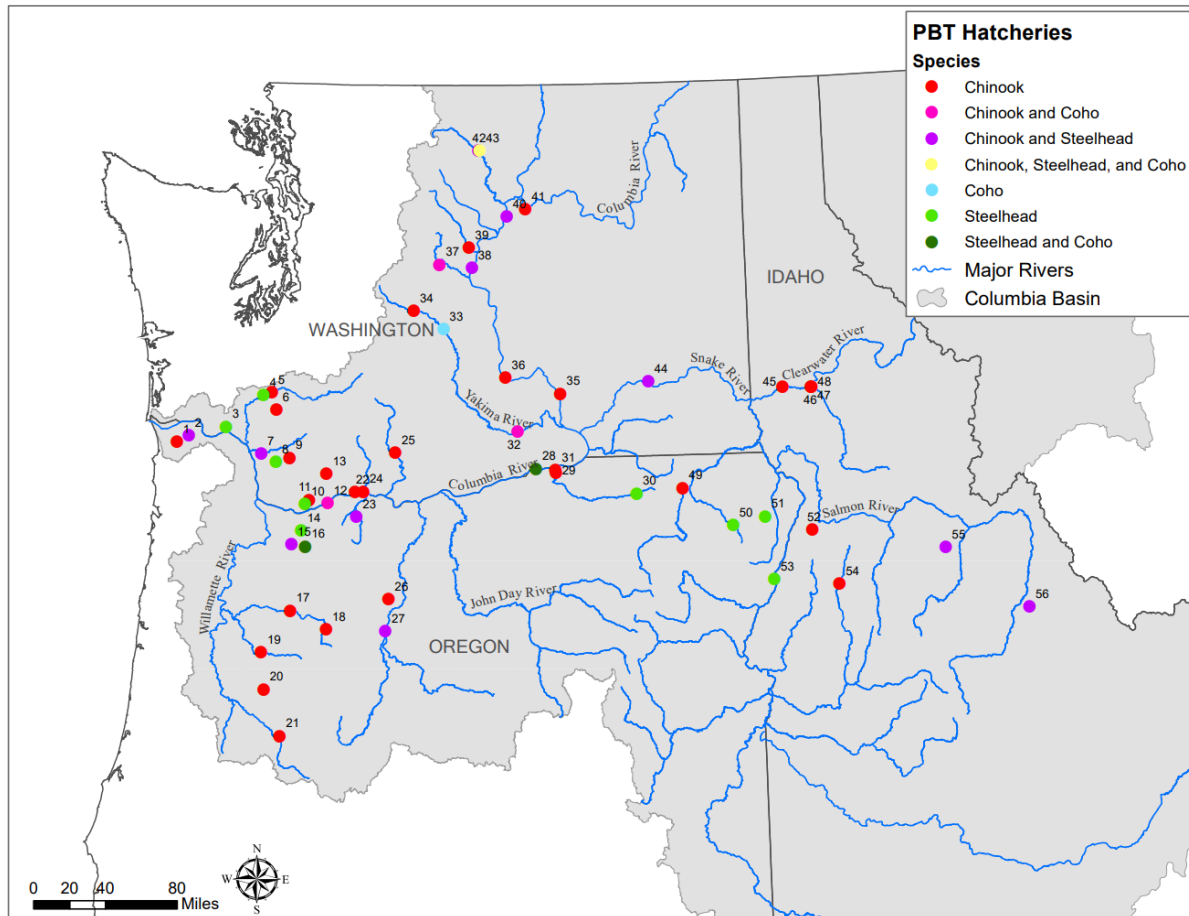
significant between reporting groups. From this initial list of significant SNPs, the top 10-20 were selected for primer development. A total of 246 primer pairs were ordered and after several rounds of testing, a total of 25 SNPs were retained. These additional 25 SNPs produced an up to 20% increase in the assignment rate of seven GSI reporting groups (10\_UCOLSP, 12\_HELLSC, 13\_SFSALM, 15\_MFSALM, 16\_UPSALM, 18\_UCOLSF, 19\_SRFALL).

## ***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 all hatcheries above Bonneville Dam for Chinook Salmon and steelhead. For Coho Salmon, most hatcheries that are releasing Coho Salmon in the interior Columbia River (upstream of Bonneville Dam) are included in the PBT baseline and one hatchery has been added for Sockeye Salmon. Broodstock samples are genotyped with SNP panels of 343 loci for Chinook Salmon, 368 loci for steelhead trout, 235 loci for Coho Salmon, and 365 for Sockeye 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 2024 report period included spawn year 2023 for all hatcheries. The total numbers of fish genotyped for PBT baselines in 2024 included  $n=26,166$  spring Chinook Salmon,  $n=3,080$  upper Columbia summer Chinook Salmon,  $n=34,387$  fall Chinook Salmon (Appendix 1),  $n=1,191$  steelhead trout (Appendix 2),  $n=7,223$  Coho Salmon (Appendix 2), and  $N=2712$  Sockeye 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, 235 SNP loci for Coho Salmon, and 365 loci for Sockeye 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 SY2023 Chinook salmon broodstock collections that were genotyped by CRITFC primarily outside the Snake River basin and added to the PBT baseline in 2024 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\_sp23 and OtsCHJO\_int\_sp23, Figure 14).

Table 7. PBT broodstock composition of the SY2022 Columbia River Chinook hatchery collections.

Exp. GSI	Collection	PBT Source	Source Rate	Method		
				Culled	Duplicate	Failed
02_WCASSP	OtsCOWL_seg_sp22	OtsCOWL_seg_fa18	0.5904	-	-	-
02_WCASSP	OtsCOWL_seg_sp22	OtsCOWL_seg_sp17	0.9369	-	-	-
02_WCASSP	OtsCOWL_seg_sp22	OtsCOWL_seg_sp18	0.8438	-	-	-
02_WCASSP	OtsCOWL_seg_sp22	OtsCOWL_seg_sp19	0.8965	-	-	-
02_WCASSP	OtsCOWL_seg_sp22	OtsKALA_seg_fa17	0.7518	-	-	-
02_WCASSP	OtsCOWL_seg_sp22	OtsKALA_seg_fa18	0.8585	-	-	-
02_WCASSP	OtsCOWL_seg_sp22	OtsNSAN_seg_sp18	0.6524	-	-	-
02_WCASSP	OtsCOWL_seg_sp22	OtsNTOU_seg_fa18	0.6002	-	-	-
02_WCASSP	OtsCOWL_seg_sp22	OtsSPEE_seg_sp18	0.8331	-	-	-
02_WCASSP	OtsCOWL_seg_sp22	Unassigned	1	-	-	-
02_WCASSP	OtsCOWL_seg_sp22	(blank)	(blank)	0	5	571
02_WCASSP	OtsKALA_seg_sp22	OtsCOWL_seg_sp18	0.8438	-	-	-
02_WCASSP	OtsKALA_seg_sp22	OtsKALA_seg_fa18	0.8585	-	-	-
02_WCASSP	OtsKALA_seg_sp22	OtsKALA_seg_sp16	0.7307	-	-	-
02_WCASSP	OtsKALA_seg_sp22	OtsKALA_seg_sp17	0.9707	-	-	-
02_WCASSP	OtsKALA_seg_sp22	OtsKALA_seg_sp18	0.5941	-	-	-
02_WCASSP	OtsKALA_seg_sp22	OtsKALA_seg_sp19	0.8563	-	-	-
02_WCASSP	OtsKALA_seg_sp22	OtsNSAN_seg_sp18	0.6524	-	-	-
02_WCASSP	OtsKALA_seg_sp22	OtsSPEE_seg_sp18	0.8331	-	-	-
02_WCASSP	OtsKALA_seg_sp22	OtsSSAN_seg_sp18	0.5355	-	-	-
02_WCASSP	OtsKALA_seg_sp22	Unassigned	1	-	-	-
02_WCASSP	OtsKALA_seg_sp22	(blank)	(blank)	0	18	21
02_WCASSP	OtsPARK_seg_sp22	OtsCARS_seg_sp18	1	-	-	-
02_WCASSP	OtsPARK_seg_sp22	OtsPARK_seg_sp17	0.9341	-	-	-
02_WCASSP	OtsPARK_seg_sp22	OtsPARK_seg_sp18	0.773	-	-	-
02_WCASSP	OtsPARK_seg_sp22	OtsPARK_seg_sp19	0.9797	-	-	-
02_WCASSP	OtsPARK_seg_sp22	Unassigned	1	-	-	-
02_WCASSP	OtsPARK_seg_sp22	(blank)	(blank)	0	1	3
02_WCASSP	OtsSPEE_seg_sp22	OtsSPEE_seg_sp17	0.5727	-	-	-
02_WCASSP	OtsSPEE_seg_sp22	OtsSPEE_seg_sp18	0.8331	-	-	-
02_WCASSP	OtsSPEE_seg_sp22	OtsSPEE_seg_sp19	0.6836	-	-	-
02_WCASSP	OtsSPEE_seg_sp22	Unassigned	1	-	-	-
02_WCASSP	OtsSPEE_seg_sp22	(blank)	(blank)	0	10	20
03_WCASFA	OtsCOWL_seg_fa22	OtsCOWL_seg_fa16	0.7906	-	-	-
03_WCASFA	OtsCOWL_seg_fa22	OtsCOWL_seg_fa17	0.809	-	-	-
03_WCASFA	OtsCOWL_seg_fa22	OtsCOWL_seg_fa18	0.5904	-	-	-
03_WCASFA	OtsCOWL_seg_fa22	OtsCOWL_seg_fa19	0.9303	-	-	-
03_WCASFA	OtsCOWL_seg_fa22	OtsCOWL_seg_fa20	0.7067	-	-	-

03_WCASFA	OtsCOWL_seg_fa22	OtsCOWL_seg_sp20	0.7656	-	-	-
03_WCASFA	OtsCOWL_seg_fa22	OtsKALA_seg_fa17	0.7518	-	-	-
03_WCASFA	OtsCOWL_seg_fa22	OtsKALA_seg_fa18	0.8585	-	-	-
03_WCASFA	OtsCOWL_seg_fa22	OtsKALA_seg_fa19	0.795	-	-	-
03_WCASFA	OtsCOWL_seg_fa22	OtsNSAN_seg_sp18	0.6524	-	-	-
03_WCASFA	OtsCOWL_seg_fa22	Unassigned	1	-	-	-
03_WCASFA	OtsCOWL_seg_fa22	(blank)	(blank)	0	2	211
03_WCASFA	OtsKALA_seg_fa22	OtsBIGC_seg_fa19	0.8693	-	-	-
03_WCASFA	OtsKALA_seg_fa22	OtsCOWL_seg_fa17	0.809	-	-	-
03_WCASFA	OtsKALA_seg_fa22	OtsCOWL_seg_fa19	0.9303	-	-	-
03_WCASFA	OtsKALA_seg_fa22	OtsKALA_seg_fa17	0.7518	-	-	-
03_WCASFA	OtsKALA_seg_fa22	OtsKALA_seg_fa18	0.8585	-	-	-
03_WCASFA	OtsKALA_seg_fa22	OtsKALA_seg_fa19	0.795	-	-	-
03_WCASFA	OtsKALA_seg_fa22	OtsKALA_seg_fa20	0.8621	-	-	-
03_WCASFA	OtsKALA_seg_fa22	OtsNSAN_seg_sp18	0.6524	-	-	-
03_WCASFA	OtsKALA_seg_fa22	OtsNTOU_seg_fa18	0.6002	-	-	-
03_WCASFA	OtsKALA_seg_fa22	OtsSPEE_seg_sp18	0.8331	-	-	-
03_WCASFA	OtsKALA_seg_fa22	Unassigned	1	-	-	-
03_WCASFA	OtsKALA_seg_fa22	(blank)	(blank)	0	43	166
03_WCASFA	OtsNTOU_seg_fa22	OtsKALA_seg_fa18	0.8585	-	-	-
03_WCASFA	OtsNTOU_seg_fa22	OtsNTOU_seg_fa17	0.7854	-	-	-
03_WCASFA	OtsNTOU_seg_fa22	OtsNTOU_seg_fa18	0.6002	-	-	-
03_WCASFA	OtsNTOU_seg_fa22	Unassigned	1	-	-	-
03_WCASFA	OtsNTOU_seg_fa22	(blank)	(blank)	0	6	20
03_WCASFA	OtsWASH_seg_fa22	OtsKALA_seg_fa18	0.8585	-	-	-
03_WCASFA	OtsWASH_seg_fa22	OtsWASH_seg_fa17	0.5004	-	-	-
03_WCASFA	OtsWASH_seg_fa22	OtsWASH_seg_fa18	0.577	-	-	-
03_WCASFA	OtsWASH_seg_fa22	OtsWASH_seg_fa19	0.4767	-	-	-
03_WCASFA	OtsWASH_seg_fa22	OtsWASH_seg_fa20	0.7237	-	-	-
03_WCASFA	OtsWASH_seg_fa22	Unassigned	1	-	-	-
03_WCASFA	OtsWASH_seg_fa22	(blank)	(blank)	0	39	144
04_WILLAM	OtsNSAN_seg_sp22	OtsNSAN_seg_sp18	0.6524	-	-	-
04_WILLAM	OtsNSAN_seg_sp22	OtsSSAN_seg_sp18	0.5355	-	-	-
04_WILLAM	OtsNSAN_seg_sp22	Unassigned	1	-	-	-
04_WILLAM	OtsNSAN_seg_sp22	(blank)	(blank)	0	18	109
04_WILLAM	OtsSSAN_seg_sp22	OtsSSAN_seg_sp18	0.5355	-	-	-
04_WILLAM	OtsSSAN_seg_sp22	Unassigned	1	-	-	-
04_WILLAM	OtsSSAN_seg_sp22	(blank)	(blank)	0	19	67
05_SPCRTU	OtsSPCR_seg_fa22	OtsBONN_seg_fa19	0.5676	-	-	-
05_SPCRTU	OtsSPCR_seg_fa22	OtsSPCR_seg_fa18	1	-	-	-
05_SPCRTU	OtsSPCR_seg_fa22	OtsSPCR_seg_fa19	0.9068	-	-	-
05_SPCRTU	OtsSPCR_seg_fa22	OtsSPCR_seg_fa20	1	-	-	-
05_SPCRTU	OtsSPCR_seg_fa22	Unassigned	1	-	-	-
05_SPCRTU	OtsSPCR_seg_fa22	(blank)	(blank)	0	83	135

06_KLICKR	OtsKLIC_seg_sp22	OtsKLIC_seg_sp17	0.9757	-	-	-
06_KLICKR	OtsKLIC_seg_sp22	OtsKLIC_seg_sp18	0.9665	-	-	-
06_KLICKR	OtsKLIC_seg_sp22	OtsKLIC_seg_sp19	1	-	-	-
06_KLICKR	OtsKLIC_seg_sp22	OtsLWSN_seg_sp18	0.9392	-	-	-
06_KLICKR	OtsKLIC_seg_sp22	OtsPARK_seg_sp18	0.773	-	-	-
06_KLICKR	OtsKLIC_seg_sp22	Unassigned	1	-	-	-
06_KLICKR	OtsKLIC_seg_sp22	(blank)	(blank)	0	1	3
07_DESCSP	OtsRBFH_seg_sp22	OtsDWOR_seg_sp18	0.9493	-	-	-
07_DESCSP	OtsRBFH_seg_sp22	OtsLOOK_seg_sp18	0.9276	-	-	-
07_DESCSP	OtsRBFH_seg_sp22	OtsMCCA_seg_ss18	0.9879	-	-	-
07_DESCSP	OtsRBFH_seg_sp22	OtsPARK_seg_sp18	0.773	-	-	-
07_DESCSP	OtsRBFH_seg_sp22	OtsRBFH_seg_sp17	0.8889	-	-	-
07_DESCSP	OtsRBFH_seg_sp22	OtsRBFH_seg_sp18	0.9603	-	-	-
07_DESCSP	OtsRBFH_seg_sp22	OtsRBFH_seg_sp19	0.9042	-	-	-
07_DESCSP	OtsRBFH_seg_sp22	Unassigned	1	-	-	-
07_DESCSP	OtsRBFH_seg_sp22	(blank)	(blank)	0	7	9
07_DESCSP	OtsWSNF_seg_sp22	OtsRBFH_seg_sp18	0.9603	-	-	-
07_DESCSP	OtsWSNF_seg_sp22	OtsWSNF_seg_sp17	0.7951	-	-	-
07_DESCSP	OtsWSNF_seg_sp22	OtsWSNF_seg_sp18	0.8985	-	-	-
07_DESCSP	OtsWSNF_seg_sp22	OtsWSNF_seg_sp19	0.8849	-	-	-
07_DESCSP	OtsWSNF_seg_sp22	Unassigned	1	-	-	-
07_DESCSP	OtsWSNF_seg_sp22	(blank)	(blank)	0	3	52
09_YAKIMA	OtsYRRD_int_sp22	OtsYRRD_seg_sp18	1	-	-	-
09_YAKIMA	OtsYRRD_int_sp22	Unassigned	1	4	-	-
09_YAKIMA	OtsYRRD_int_sp22	(blank)	(blank)	-	0	4
09_YAKIMA	OtsYRRD_seg_sp22	OtsYRRD_int_sp17	0.9943	-	-	-
09_YAKIMA	OtsYRRD_seg_sp22	OtsYRRD_int_sp18	0.9811	-	-	-
09_YAKIMA	OtsYRRD_seg_sp22	OtsYRRD_int_sp19	0.9936	-	-	-
09_YAKIMA	OtsYRRD_seg_sp22	OtsYRRD_seg_sp17	0.9807	-	-	-
09_YAKIMA	OtsYRRD_seg_sp22	OtsYRRD_seg_sp18	1	1	-	-
09_YAKIMA	OtsYRRD_seg_sp22	OtsYRRD_seg_sp19	1	1	-	-
09_YAKIMA	OtsYRRD_seg_sp22	Unassigned	1	1	-	-
09_YAKIMA	OtsYRRD_seg_sp22	(blank)	(blank)	-	0	2
10_UCOLSP	OtsCHJO_seg_sp22	OtsCARS_seg_sp18	1	-	-	-
10_UCOLSP	OtsCHJO_seg_sp22	OtsCHJO_seg_sp17	0.9209	-	-	-
10_UCOLSP	OtsCHJO_seg_sp22	OtsCHJO_seg_sp18	0.5658	1	-	-
10_UCOLSP	OtsCHJO_seg_sp22	OtsCHJO_seg_sp19	0.8227	-	-	-
10_UCOLSP	OtsCHJO_seg_sp22	OtsKOOS_seg_sp18	0.9429	-	-	-
10_UCOLSP	OtsCHJO_seg_sp22	OtsLNFH_seg_sp17	0.8606	-	-	-
10_UCOLSP	OtsCHJO_seg_sp22	OtsLNFH_seg_sp18	0.5506	25	-	-
10_UCOLSP	OtsCHJO_seg_sp22	OtsLWSN_seg_sp18	0.9392	-	-	-
10_UCOLSP	OtsCHJO_seg_sp22	OtsMETH_seg_sp18	0.7778	-	-	-
10_UCOLSP	OtsCHJO_seg_sp22	OtsTOUC_seg_sp18	0.9522	-	-	-
10_UCOLSP	OtsCHJO_seg_sp22	OtsWINT_seg_sp18	0.7993	-	-	-

10_UCOLSP	OtsCHJO_seg_sp22	OtsWINT_seg_sp19	0.989	-	-	-
10_UCOLSP	OtsCHJO_seg_sp22	Unassigned	1	59	-	-
10_UCOLSP	OtsCHJO_seg_sp22	(blank)	(blank)	-	0	45
10_UCOLSP	OtsEAST_seg_sp22	OtsEAST_seg_sp18	1	-	-	-
10_UCOLSP	OtsEAST_seg_sp22	Unassigned	1	-	-	-
10_UCOLSP	OtsEAST_seg_sp22	(blank)	(blank)	-	-	23
10_UCOLSP	OtsLNFH_seg_sp22	OtsEAST_seg_sp18	1	-	-	-
10_UCOLSP	OtsLNFH_seg_sp22	OtsLNFH_seg_sp17	0.8606	-	-	-
10_UCOLSP	OtsLNFH_seg_sp22	OtsLNFH_seg_sp18	0.5506	-	-	-
10_UCOLSP	OtsLNFH_seg_sp22	OtsLNFH_seg_sp19	1	-	-	-
10_UCOLSP	OtsLNFH_seg_sp22	Unassigned	1	-	-	-
10_UCOLSP	OtsLNFH_seg_sp22	(blank)	(blank)	0	0	52
10_UCOLSP	OtsMETH_seg_sp22	OtsMETH_seg_sp18	0.7778	-	-	-
10_UCOLSP	OtsMETH_seg_sp22	Unassigned	1	-	-	-
10_UCOLSP	OtsMETH_seg_sp22	(blank)	(blank)	0	1	0
10_UCOLSP	OtsWINT_seg_sp22	OtsMETH_seg_sp17	0.9051	-	-	-
10_UCOLSP	OtsWINT_seg_sp22	OtsMETH_seg_sp18	0.7778	-	-	-
10_UCOLSP	OtsWINT_seg_sp22	OtsMETH_seg_sp19	1	-	-	-
10_UCOLSP	OtsWINT_seg_sp22	OtsWINT_seg_sp18	0.7993	-	-	-
10_UCOLSP	OtsWINT_seg_sp22	Unassigned	1	-	-	-
10_UCOLSP	OtsWINT_seg_sp22	(blank)	(blank)	0	0	7
18_UCOLSF	OtsCHJO_int_su22	OtsCHJO_int_su16	0.9896	-	-	-
18_UCOLSF	OtsCHJO_int_su22	OtsCHJO_int_su17	0.7549	-	-	-
18_UCOLSF	OtsCHJO_int_su22	OtsCHJO_int_su19	0.9801	-	-	-
18_UCOLSF	OtsCHJO_int_su22	OtsCHJO_seg_su16	0.9915	-	-	-
18_UCOLSF	OtsCHJO_int_su22	OtsCHJO_seg_su17	0.9032	-	-	-
18_UCOLSF	OtsCHJO_int_su22	OtsCHJO_seg_su19	0.9623	-	-	-
18_UCOLSF	OtsCHJO_int_su22	OtsEAST_seg_su16	0.9831	-	-	-
18_UCOLSF	OtsCHJO_int_su22	OtsEAST_seg_su17	0.9661	-	-	-
18_UCOLSF	OtsCHJO_int_su22	OtsEAST_seg_su18	0.9917	-	-	-
18_UCOLSF	OtsCHJO_int_su22	OtsENFH_seg_su18	0.7628	-	-	-
18_UCOLSF	OtsCHJO_int_su22	OtsLYON_seg_fa18	0.8055	-	-	-
18_UCOLSF	OtsCHJO_int_su22	OtsWELL_seg_su17	0.8901	-	-	-
18_UCOLSF	OtsCHJO_int_su22	OtsWELL_seg_su18	0.8209	-	-	-
18_UCOLSF	OtsCHJO_int_su22	OtsWELL_seg_su19	1	-	-	-
18_UCOLSF	OtsCHJO_int_su22	Unassigned	1	-	-	-
18_UCOLSF	OtsCHJO_int_su22	(blank)	(blank)	0	1	37
18_UCOLSF	OtsCHJO_seg_su22	OtsCHJO_int_su16	0.9896	-	-	-
18_UCOLSF	OtsCHJO_seg_su22	OtsCHJO_int_su17	0.7549	-	-	-
18_UCOLSF	OtsCHJO_seg_su22	OtsCHJO_int_su19	0.9801	-	-	-
18_UCOLSF	OtsCHJO_seg_su22	OtsCHJO_seg_su16	0.9915	-	-	-
18_UCOLSF	OtsCHJO_seg_su22	OtsCHJO_seg_su17	0.9032	-	-	-
18_UCOLSF	OtsCHJO_seg_su22	OtsCHJO_seg_su19	0.9623	-	-	-
18_UCOLSF	OtsCHJO_seg_su22	OtsEAST_seg_su17	0.9661	-	-	-

18_UCOLSF	OtsCHJO_seg_su22	OtsEAST_seg_su18	0.9917	-	-	-
18_UCOLSF	OtsCHJO_seg_su22	OtsENFH_seg_su17	0.8393	-	-	-
18_UCOLSF	OtsCHJO_seg_su22	OtsENFH_seg_su18	0.7628	-	-	-
18_UCOLSF	OtsCHJO_seg_su22	OtsWELL_seg_su17	0.8901	-	-	-
18_UCOLSF	OtsCHJO_seg_su22	OtsWELL_seg_su18	0.8209	-	-	-
18_UCOLSF	OtsCHJO_seg_su22	OtsWELL_seg_su19	1	-	-	-
18_UCOLSF	OtsCHJO_seg_su22	Unassigned	1	-	-	-
18_UCOLSF	OtsCHJO_seg_su22	(blank)	(blank)	-	1	94
18_UCOLSF	(blank)	(blank)	(blank)	0	-	4
18_UCOLSF	OtsEAST_seg_su22	OtsCHJO_int_su17	0.7549	-	-	-
18_UCOLSF	OtsEAST_seg_su22	OtsCHJO_seg_su16	0.9915	-	-	-
18_UCOLSF	OtsEAST_seg_su22	OtsCHJO_seg_su17	0.9032	-	-	-
18_UCOLSF	OtsEAST_seg_su22	OtsEAST_seg_su16	0.9831	-	-	-
18_UCOLSF	OtsEAST_seg_su22	OtsEAST_seg_su17	0.9661	-	-	-
18_UCOLSF	OtsEAST_seg_su22	OtsEAST_seg_su18	0.9917	-	-	-
18_UCOLSF	OtsEAST_seg_su22	OtsENFH_seg_su17	0.8393	-	-	-
18_UCOLSF	OtsEAST_seg_su22	OtsLYON_seg_fa18	0.8055	-	-	-
18_UCOLSF	OtsEAST_seg_su22	OtsWELL_seg_su17	0.8901	-	-	-
18_UCOLSF	OtsEAST_seg_su22	OtsWELL_seg_su18	0.8209	-	-	-
18_UCOLSF	OtsEAST_seg_su22	Unassigned	1	-	-	-
18_UCOLSF	OtsEAST_seg_su22	(blank)	(blank)	0	0	20
18_UCOLSF	OtsENFH_seg_su22	OtsENFH_seg_su16	1	-	-	-
18_UCOLSF	OtsENFH_seg_su22	OtsENFH_seg_su17	0.8393	-	-	-
18_UCOLSF	OtsENFH_seg_su22	OtsENFH_seg_su18	0.7628	-	-	-
18_UCOLSF	OtsENFH_seg_su22	Unassigned	1	-	-	-
18_UCOLSF	OtsENFH_seg_su22	(blank)	(blank)	0	0	10
18_UCOLSF	OtsPRIE_seg_fa22	OtsEAST_seg_su18	0.9917	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsLWSN_seg_fa17	0.9595	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsLWSN_seg_fa19	1	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsLYON_seg_fa18	0.8055	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsLYON_seg_fa19	0.9597	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsNPFH_seg_fa18	0.8115	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsPRIE_seg_fa16	1	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsPRIE_seg_fa17	0.9095	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsPRIE_seg_fa18	0.8617	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsPRIE_seg_fa19	0.9615	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsPRIE_seg_fa20	0.745	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsPROS_seg_fa18	0.8668	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsRING_seg_fa17	0.934	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsRING_seg_fa19	0.9602	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsSPCR_seg_fa19	0.9068	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsUMAT_seg_fa18	0.9573	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	OtsUMAT_seg_fa19	1	-	-	-
18_UCOLSF	OtsPRIE_seg_fa22	Unassigned	1	-	-	-

18_UCOLSF	OtsPRIE_seg_fa22	(blank)	(blank)	0	9	163
18_UCOLSF	OtsPROS_seg_fa22	OtsLWSN_seg_fa17	0.9595	-	-	-
18_UCOLSF	OtsPROS_seg_fa22	OtsLWSN_seg_fa19	1	-	-	-
18_UCOLSF	OtsPROS_seg_fa22	OtsLYON_seg_fa18	0.8055	-	-	-
18_UCOLSF	OtsPROS_seg_fa22	OtsLYON_seg_fa20	0.9896	-	-	-
18_UCOLSF	OtsPROS_seg_fa22	OtsPROS_seg_fa17	0.3964	-	-	-
18_UCOLSF	OtsPROS_seg_fa22	OtsPROS_seg_fa20	0.9517	-	-	-
18_UCOLSF	OtsPROS_seg_fa22	OtsRING_seg_fa17	0.934	-	-	-
18_UCOLSF	OtsPROS_seg_fa22	OtsRING_seg_fa19	0.9602	-	-	-
18_UCOLSF	OtsPROS_seg_fa22	OtsUMAT_seg_fa18	0.9573	-	-	-
18_UCOLSF	OtsPROS_seg_fa22	OtsUMAT_seg_fa19	1	-	-	-
18_UCOLSF	OtsPROS_seg_fa22	Unassigned	1	-	-	-
18_UCOLSF	OtsPROS_seg_fa22	(blank)	(blank)	0	1	9
18_UCOLSF	OtsRING_seg_fa22	OtsPRIE_seg_fa17	0.9095	-	-	-
18_UCOLSF	OtsRING_seg_fa22	OtsPRIE_seg_fa18	0.8617	-	-	-
18_UCOLSF	OtsRING_seg_fa22	OtsPRIE_seg_fa19	0.9615	-	-	-
18_UCOLSF	OtsRING_seg_fa22	Unassigned	1	-	-	-
18_UCOLSF	OtsRING_seg_fa22	(blank)	(blank)	0	0	9
18_UCOLSF	OtsWELL_seg_su22	OtsCHJO_int_su16	0.9896	-	-	-
18_UCOLSF	OtsWELL_seg_su22	OtsCHJO_int_su17	0.7549	-	-	-
18_UCOLSF	OtsWELL_seg_su22	OtsCHJO_seg_su16	0.9915	-	-	-
18_UCOLSF	OtsWELL_seg_su22	OtsCHJO_seg_su17	0.9032	-	-	-
18_UCOLSF	OtsWELL_seg_su22	OtsEAST_seg_su16	0.9831	-	-	-
18_UCOLSF	OtsWELL_seg_su22	OtsEAST_seg_su17	0.9661	-	-	-
18_UCOLSF	OtsWELL_seg_su22	OtsEAST_seg_su18	0.9917	-	-	-
18_UCOLSF	OtsWELL_seg_su22	OtsENFH_seg_su16	1	-	-	-
18_UCOLSF	OtsWELL_seg_su22	OtsENFH_seg_su17	0.8393	-	-	-
18_UCOLSF	OtsWELL_seg_su22	OtsWELL_seg_su16	1	-	-	-
18_UCOLSF	OtsWELL_seg_su22	OtsWELL_seg_su17	0.8901	-	-	-
18_UCOLSF	OtsWELL_seg_su22	OtsWELL_seg_su18	0.8209	-	-	-
18_UCOLSF	OtsWELL_seg_su22	Unassigned	1	-	-	-
18_UCOLSF	OtsWELL_seg_su22	(blank)	(blank)	0	0	11
19_SRFALL	OtsNPFH_seg_fa22	OtsLYON_seg_fa17	0.7641	-	-	-
19_SRFALL	OtsNPFH_seg_fa22	OtsLYON_seg_fa18	0.8055	-	-	-
19_SRFALL	OtsNPFH_seg_fa22	OtsLYON_seg_fa19	0.9597	-	-	-
19_SRFALL	OtsNPFH_seg_fa22	OtsNPFH_seg_fa16	0.9726	-	-	-
19_SRFALL	OtsNPFH_seg_fa22	OtsNPFH_seg_fa17	0.9681	-	-	-
19_SRFALL	OtsNPFH_seg_fa22	OtsNPFH_seg_fa18	0.8115	-	-	-
19_SRFALL	OtsNPFH_seg_fa22	OtsPRIE_seg_fa17	0.9095	-	-	-
19_SRFALL	OtsNPFH_seg_fa22	OtsWELL_seg_su18	0.8209	-	-	-
19_SRFALL	OtsNPFH_seg_fa22	Unassigned	1	6	-	-
19_SRFALL	OtsNPFH_seg_fa22	(blank)	(blank)	-	0	5
20_BONPOOLSP	OtsCARS_seg_sp22	OtsCARS_seg_sp17	1			
20_BONPOOLSP	OtsCARS_seg_sp22	OtsCARS_seg_sp18	1			

20_BONPOOLSP	OtsCARS_seg_sp22	OtsCARS_seg_sp19	1			
20_BONPOOLSP	OtsCARS_seg_sp22	OtsLWSN_seg_sp18	1			
20_BONPOOLSP	OtsCARS_seg_sp22	OtsLWSN_seg_sp19	1			
20_BONPOOLSP	OtsCARS_seg_sp22	Unassigned	1			
20_BONPOOLSP	OtsCARS_seg_sp22	(blank)	1		1	4
20_BONPOOLSP	OtsLWSN_seg_sp22	OtsCARS_seg_sp18	1	-	-	-
20_BONPOOLSP	OtsLWSN_seg_sp22	OtsCARS_seg_sp19	1	-	-	-
20_BONPOOLSP	OtsLWSN_seg_sp22	OtsCLWH_seg_sp18	1	-	-	-
20_BONPOOLSP	OtsLWSN_seg_sp22	OtsDWOR_seg_sp18	0.9493	-	-	-
20_BONPOOLSP	OtsLWSN_seg_sp22	OtsLWSN_seg_sp17	0.9418	-	-	-
20_BONPOOLSP	OtsLWSN_seg_sp22	OtsLWSN_seg_sp18	0.9392	-	-	-
20_BONPOOLSP	OtsLWSN_seg_sp22	OtsLWSN_seg_sp19	0.9528	-	-	-
20_BONPOOLSP	OtsLWSN_seg_sp22	Unassigned	1	-	-	-
20_BONPOOLSP	OtsLWSN_seg_sp22	(blank)	(blank)	0	0	6
21_UMATILLASP	OtsUMAT_seg_sp22	OtsCARS_seg_sp17	0.9841	-	-	-
21_UMATILLASP	OtsUMAT_seg_sp22	OtsCARS_seg_sp18	1	-	-	-
21_UMATILLASP	OtsUMAT_seg_sp22	OtsCARS_seg_sp19	1	-	-	-
21_UMATILLASP	OtsUMAT_seg_sp22	OtsUMAT_seg_sp17	1	-	-	-
21_UMATILLASP	OtsUMAT_seg_sp22	OtsUMAT_seg_sp18	0.9913	-	-	-
21_UMATILLASP	OtsUMAT_seg_sp22	OtsUMAT_seg_sp19	1	-	-	-
21_UMATILLASP	OtsUMAT_seg_sp22	Unassigned	1	-	-	-
21_UMATILLASP	OtsUMAT_seg_sp22	(blank)	(blank)	0	0	45
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsKLIC_seg_fa19	0.565	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsLWSN_seg_fa16	1	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsLWSN_seg_fa17	0.9595	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsLWSN_seg_fa18	0.7313	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsLWSN_seg_fa19	1	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsLWSN_seg_fa20	0.9945	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsLYON_seg_fa19	0.9597	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsNPFH_seg_fa18	0.8115	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsPRIE_seg_fa18	0.8617	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsPRIE_seg_fa19	0.9615	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsRING_seg_fa17	0.934	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsRING_seg_fa18	0.832	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsRING_seg_fa19	0.9602	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsSPCR_seg_fa19	0.9068	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsUMAT_seg_fa18	0.9573	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	Unassigned	1	-	-	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	(blank)	(blank)	0	12	57
23_UMATILLA	OtsUMAT_seg_fa22	OtsLWSN_seg_fa19	1	-	-	-
23_UMATILLA	OtsUMAT_seg_fa22	OtsNPFH_seg_fa17	0.9681	-	-	-
23_UMATILLA	OtsUMAT_seg_fa22	OtsRING_seg_fa17	0.934	1	-	-
23_UMATILLA	OtsUMAT_seg_fa22	OtsRING_seg_fa19	0.9602	-	-	-
23_UMATILLA	OtsUMAT_seg_fa22	OtsUMAT_seg_fa18	0.9573	3	-	-



23_UMATILLA	OtsUMAT_seg_fa22	OtsUMAT_seg_fa19	1	-	-	-
23_UMATILLA	OtsUMAT_seg_fa22	Unassigned	1	1	-	-
23_UMATILLA	OtsUMAT_seg_fa22	(blank)	(blank)	-	0	1

Exp. GSI	Collection	PBT Source	Source Rate	Method						E
				Culled	Duplicate	Failed	GSI	PBT	Total	
02_WCASSP	OtsCOWL_seg_sp22	OtsCOWL_seg_fa18	0.5904	-	-	-	-	1	1	0.5
02_WCASSP	OtsCOWL_seg_sp22	OtsCOWL_seg_sp17	0.9369	-	-	-	-	222	222	207
02_WCASSP	OtsCOWL_seg_sp22	OtsCOWL_seg_sp18	0.8438	-	-	-	-	365	365	307
02_WCASSP	OtsCOWL_seg_sp22	OtsCOWL_seg_sp19	0.8965	-	-	-	-	6	6	5.3
02_WCASSP	OtsCOWL_seg_sp22	OtsKALA_seg_fa17	0.7518	-	-	-	-	1	1	0.7
02_WCASSP	OtsCOWL_seg_sp22	OtsKALA_seg_fa18	0.8585	-	-	-	-	17	17	14.
02_WCASSP	OtsCOWL_seg_sp22	OtsNSAN_seg_sp18	0.6524	-	-	-	-	7	7	4.5
02_WCASSP	OtsCOWL_seg_sp22	OtsNTOU_seg_fa18	0.6002	-	-	-	-	1	1	0.6
02_WCASSP	OtsCOWL_seg_sp22	OtsSPEE_seg_sp18	0.8331	-	-	-	-	1	1	0.8
02_WCASSP	OtsCOWL_seg_sp22	Unassigned	1	-	-	-	123	-	123	-
02_WCASSP	OtsCOWL_seg_sp22	(blank)	(blank)	0	5	571	-	-	576	0.8
02_WCASSP	OtsKALA_seg_sp22	OtsCOWL_seg_sp18	0.8438	-	-	-	-	3	3	2.5
02_WCASSP	OtsKALA_seg_sp22	OtsKALA_seg_fa18	0.8585	-	-	-	-	13	13	11.
02_WCASSP	OtsKALA_seg_sp22	OtsKALA_seg_sp16	0.7307	-	-	-	-	1	1	0.7
02_WCASSP	OtsKALA_seg_sp22	OtsKALA_seg_sp17	0.9707	-	-	-	-	334	334	324
02_WCASSP	OtsKALA_seg_sp22	OtsKALA_seg_sp18	0.5941	-	-	-	-	192	192	114
02_WCASSP	OtsKALA_seg_sp22	OtsKALA_seg_sp19	0.8563	-	-	-	-	1	1	0.8
02_WCASSP	OtsKALA_seg_sp22	OtsNSAN_seg_sp18	0.6524	-	-	-	-	4	4	2.6
02_WCASSP	OtsKALA_seg_sp22	OtsSPEE_seg_sp18	0.8331	-	-	-	-	1	1	0.8
02_WCASSP	OtsKALA_seg_sp22	OtsSSAN_seg_sp18	0.5355	-	-	-	-	1	1	0.5
02_WCASSP	OtsKALA_seg_sp22	Unassigned	1	-	-	-	61	-	61	-
02_WCASSP	OtsKALA_seg_sp22	(blank)	(blank)	0	18	21	-	-	39	0.8
02_WCASSP	OtsPARK_seg_sp22	OtsCARS_seg_sp18	1	-	-	-	-	1	1	1
02_WCASSP	OtsPARK_seg_sp22	OtsPARK_seg_sp17	0.9341	-	-	-	-	1	1	0.9
02_WCASSP	OtsPARK_seg_sp22	OtsPARK_seg_sp18	0.773	-	-	-	-	222	222	171
02_WCASSP	OtsPARK_seg_sp22	OtsPARK_seg_sp19	0.9797	-	-	-	-	8	8	7.8
02_WCASSP	OtsPARK_seg_sp22	Unassigned	1	-	-	-	47	-	47	-
02_WCASSP	OtsPARK_seg_sp22	(blank)	(blank)	0	1	3	-	-	4	0.7
02_WCASSP	OtsSPEE_seg_sp22	OtsSPEE_seg_sp17	0.5727	-	-	-	-	87	87	49.
02_WCASSP	OtsSPEE_seg_sp22	OtsSPEE_seg_sp18	0.8331	-	-	-	-	625	625	520
02_WCASSP	OtsSPEE_seg_sp22	OtsSPEE_seg_sp19	0.6836	-	-	-	-	11	11	7.5
02_WCASSP	OtsSPEE_seg_sp22	Unassigned	1	-	-	-	382	-	382	-
02_WCASSP	OtsSPEE_seg_sp22	(blank)	(blank)	0	10	20	-	-	30	0.7
03_WCASFA	OtsCOWL_seg_fa22	OtsCOWL_seg_fa16	0.7906	-	-	-	-	1	1	0.7
03_WCASFA	OtsCOWL_seg_fa22	OtsCOWL_seg_fa17	0.809	-	-	-	-	90	90	72.
03_WCASFA	OtsCOWL_seg_fa22	OtsCOWL_seg_fa18	0.5904	-	-	-	-	152	152	89.
03_WCASFA	OtsCOWL_seg_fa22	OtsCOWL_seg_fa19	0.9303	-	-	-	-	30	30	27.

03_WCASFA	OtsCOWL_seg_fa22	OtsCOWL_seg_fa20	0.7067	-	-	-	-	2	2	1.4
03_WCASFA	OtsCOWL_seg_fa22	OtsCOWL_seg_sp20	0.7656	-	-	-	-	1	1	0.7
03_WCASFA	OtsCOWL_seg_fa22	OtsKALA_seg_fa17	0.7518	-	-	-	-	4	4	3.0
03_WCASFA	OtsCOWL_seg_fa22	OtsKALA_seg_fa18	0.8585	-	-	-	-	22	22	18.5
03_WCASFA	OtsCOWL_seg_fa22	OtsKALA_seg_fa19	0.795	-	-	-	-	1	1	0.7
03_WCASFA	OtsCOWL_seg_fa22	OtsNSAN_seg_sp18	0.6524	-	-	-	-	2	2	1.3
03_WCASFA	OtsCOWL_seg_fa22	Unassigned	1	-	-	-	197	-	197	-
03_WCASFA	OtsCOWL_seg_fa22	(blank)	(blank)	0	2	211	-	-	213	0.7
03_WCASFA	OtsKALA_seg_fa22	OtsBIGC_seg_fa19	0.8693	-	-	-	-	2	2	1.7
03_WCASFA	OtsKALA_seg_fa22	OtsCOWL_seg_fa17	0.809	-	-	-	-	1	1	0.8
03_WCASFA	OtsKALA_seg_fa22	OtsCOWL_seg_fa19	0.9303	-	-	-	-	1	1	0.9
03_WCASFA	OtsKALA_seg_fa22	OtsKALA_seg_fa17	0.7518	-	-	-	-	61	61	45.5
03_WCASFA	OtsKALA_seg_fa22	OtsKALA_seg_fa18	0.8585	-	-	-	-	773	773	663.5
03_WCASFA	OtsKALA_seg_fa22	OtsKALA_seg_fa19	0.795	-	-	-	-	130	130	103.5
03_WCASFA	OtsKALA_seg_fa22	OtsKALA_seg_fa20	0.8621	-	-	-	-	8	8	6.8
03_WCASFA	OtsKALA_seg_fa22	OtsNSAN_seg_sp18	0.6524	-	-	-	-	3	3	1.9
03_WCASFA	OtsKALA_seg_fa22	OtsNTOU_seg_fa18	0.6002	-	-	-	-	2	2	1.2
03_WCASFA	OtsKALA_seg_fa22	OtsSPEE_seg_sp18	0.8331	-	-	-	-	2	2	1.6
03_WCASFA	OtsKALA_seg_fa22	Unassigned	1	-	-	-	205	-	205	-
03_WCASFA	OtsKALA_seg_fa22	(blank)	(blank)	0	43	166	-	-	209	0.8
03_WCASFA	OtsNTOU_seg_fa22	OtsKALA_seg_fa18	0.8585	-	-	-	-	3	3	2.5
03_WCASFA	OtsNTOU_seg_fa22	OtsNTOU_seg_fa17	0.7854	-	-	-	-	1	1	0.7
03_WCASFA	OtsNTOU_seg_fa22	OtsNTOU_seg_fa18	0.6002	-	-	-	-	38	38	22.5
03_WCASFA	OtsNTOU_seg_fa22	Unassigned	1	-	-	-	142	-	142	-
03_WCASFA	OtsNTOU_seg_fa22	(blank)	(blank)	0	6	20	-	-	26	0.6
03_WCASFA	OtsWASH_seg_fa22	OtsKALA_seg_fa18	0.8585	-	-	-	-	6	6	5.1
03_WCASFA	OtsWASH_seg_fa22	OtsWASH_seg_fa17	0.5004	-	-	-	-	19	19	9.5
03_WCASFA	OtsWASH_seg_fa22	OtsWASH_seg_fa18	0.577	-	-	-	-	236	236	136.5
03_WCASFA	OtsWASH_seg_fa22	OtsWASH_seg_fa19	0.4767	-	-	-	-	118	118	56.5
03_WCASFA	OtsWASH_seg_fa22	OtsWASH_seg_fa20	0.7237	-	-	-	-	6	6	4.3
03_WCASFA	OtsWASH_seg_fa22	Unassigned	1	-	-	-	378	-	378	-
03_WCASFA	OtsWASH_seg_fa22	(blank)	(blank)	0	39	144	-	-	183	0.5
04_WILLAM	OtsNSAN_seg_sp22	OtsNSAN_seg_sp18	0.6524	-	-	-	-	509	509	332.5
04_WILLAM	OtsNSAN_seg_sp22	OtsSSAN_seg_sp18	0.5355	-	-	-	-	2	2	1.0
04_WILLAM	OtsNSAN_seg_sp22	Unassigned	1	-	-	-	919	-	919	-
04_WILLAM	OtsNSAN_seg_sp22	(blank)	(blank)	0	18	109	-	-	127	0.6
04_WILLAM	OtsSSAN_seg_sp22	OtsSSAN_seg_sp18	0.5355	-	-	-	-	139	139	74.5
04_WILLAM	OtsSSAN_seg_sp22	Unassigned	1	-	-	-	426	-	426	-
04_WILLAM	OtsSSAN_seg_sp22	(blank)	(blank)	0	19	67	-	-	86	0.5
05_SPCRTU	OtsSPCR_seg_fa22	OtsBONN_seg_fa19	0.5676	-	-	-	-	6	6	3.4
05_SPCRTU	OtsSPCR_seg_fa22	OtsSPCR_seg_fa18	1	-	-	-	-	117	117	117
05_SPCRTU	OtsSPCR_seg_fa22	OtsSPCR_seg_fa19	0.9068	-	-	-	-	4821	4821	437.5
05_SPCRTU	OtsSPCR_seg_fa22	OtsSPCR_seg_fa20	1	-	-	-	-	58	58	58

05_SPCRTU	OtsSPCR_seg_fa22	Unassigned	1	-	-	-	1521	-	1521	-
05_SPCRTU	OtsSPCR_seg_fa22	(blank)	(blank)	0	83	135	-	-	218	0.9
06_KLICKR	OtsKLIC_seg_sp22	OtsKLIC_seg_sp17	0.9757	-	-	-	-	32	32	31.1
06_KLICKR	OtsKLIC_seg_sp22	OtsKLIC_seg_sp18	0.9665	-	-	-	-	547	547	528
06_KLICKR	OtsKLIC_seg_sp22	OtsKLIC_seg_sp19	1	-	-	-	-	4	4	4
06_KLICKR	OtsKLIC_seg_sp22	OtsLWSN_seg_sp18	0.9392	-	-	-	-	1	1	0.9
06_KLICKR	OtsKLIC_seg_sp22	OtsPARK_seg_sp18	0.773	-	-	-	-	1	1	0.7
06_KLICKR	OtsKLIC_seg_sp22	Unassigned	1	-	-	-	26	-	26	-
06_KLICKR	OtsKLIC_seg_sp22	(blank)	(blank)	0	1	3	-	-	4	0.9
07_DESCSP	OtsRBFH_seg_sp22	OtsDWOR_seg_sp18	0.9493	-	-	-	-	1	1	0.9
07_DESCSP	OtsRBFH_seg_sp22	OtsLOOK_seg_sp18	0.9276	-	-	-	-	1	1	0.9
07_DESCSP	OtsRBFH_seg_sp22	OtsMCCA_seg_ss18	0.9879	-	-	-	-	1	1	0.9
07_DESCSP	OtsRBFH_seg_sp22	OtsPARK_seg_sp18	0.773	-	-	-	-	2	2	1.5
07_DESCSP	OtsRBFH_seg_sp22	OtsRBFH_seg_sp17	0.8889	-	-	-	-	1	1	0.8
07_DESCSP	OtsRBFH_seg_sp22	OtsRBFH_seg_sp18	0.9603	-	-	-	-	444	444	426
07_DESCSP	OtsRBFH_seg_sp22	OtsRBFH_seg_sp19	0.9042	-	-	-	-	2	2	1.8
07_DESCSP	OtsRBFH_seg_sp22	Unassigned	1	-	-	-	18	-	18	-
07_DESCSP	OtsRBFH_seg_sp22	(blank)	(blank)	0	7	9	-	-	16	0.9
07_DESCSP	OtsWSNF_seg_sp22	OtsRBFH_seg_sp18	0.9603	-	-	-	-	4	4	3.8
07_DESCSP	OtsWSNF_seg_sp22	OtsWSNF_seg_sp17	0.7951	-	-	-	-	5	5	3.9
07_DESCSP	OtsWSNF_seg_sp22	OtsWSNF_seg_sp18	0.8985	-	-	-	-	108	108	97.8
07_DESCSP	OtsWSNF_seg_sp22	OtsWSNF_seg_sp19	0.8849	-	-	-	-	3	3	2.6
07_DESCSP	OtsWSNF_seg_sp22	Unassigned	1	-	-	-	54	-	54	-
07_DESCSP	OtsWSNF_seg_sp22	(blank)	(blank)	0	3	52	-	-	55	0.8
09_YAKIMA	OtsYRRD_int_sp22	OtsYRRD_seg_sp18	1	-	-	-	-	2	2	2
09_YAKIMA	OtsYRRD_int_sp22	Unassigned	1	4	-	-	377	-	381	-
09_YAKIMA	OtsYRRD_int_sp22	(blank)	(blank)	-	0	4	-	-	4	1
09_YAKIMA	OtsYRRD_seg_sp22	OtsYRRD_int_sp17	0.9943	-	-	-	-	1	1	0.9
09_YAKIMA	OtsYRRD_seg_sp22	OtsYRRD_int_sp18	0.9811	-	-	-	-	10	10	9.8
09_YAKIMA	OtsYRRD_seg_sp22	OtsYRRD_int_sp19	0.9936	-	-	-	-	3	3	2.9
09_YAKIMA	OtsYRRD_seg_sp22	OtsYRRD_seg_sp17	0.9807	-	-	-	-	1	1	0.9
09_YAKIMA	OtsYRRD_seg_sp22	OtsYRRD_seg_sp18	1	1	-	-	-	198	199	198
09_YAKIMA	OtsYRRD_seg_sp22	OtsYRRD_seg_sp19	1	1	-	-	-	21	22	21
09_YAKIMA	OtsYRRD_seg_sp22	Unassigned	1	1	-	-	8	-	9	-
09_YAKIMA	OtsYRRD_seg_sp22	(blank)	(blank)	-	0	2	-	-	2	0.9
10_UCOLSP	OtsCHJO_seg_sp22	OtsCARS_seg_sp18	1	-	-	-	-	2	2	2
10_UCOLSP	OtsCHJO_seg_sp22	OtsCHJO_seg_sp17	0.9209	-	-	-	-	4	4	3.6
10_UCOLSP	OtsCHJO_seg_sp22	OtsCHJO_seg_sp18	0.5658	1	-	-	-	2	3	1.1
10_UCOLSP	OtsCHJO_seg_sp22	OtsCHJO_seg_sp19	0.8227	-	-	-	-	3	3	2.4
10_UCOLSP	OtsCHJO_seg_sp22	OtsKOOS_seg_sp18	0.9429	-	-	-	-	1	1	0.9
10_UCOLSP	OtsCHJO_seg_sp22	OtsLNFH_seg_sp17	0.8606	-	-	-	-	1	1	0.8
10_UCOLSP	OtsCHJO_seg_sp22	OtsLNFH_seg_sp18	0.5506	25	-	-	-	238	263	131
10_UCOLSP	OtsCHJO_seg_sp22	OtsLWSN_seg_sp18	0.9392	-	-	-	-	3	3	2.8

10_UCOLSP	OtsCHJO_seg_sp22	OtsMETH_seg_sp18	0.7778	-	-	-	-	2	2	1.5
10_UCOLSP	OtsCHJO_seg_sp22	OtsTOUC_seg_sp18	0.9522	-	-	-	-	2	2	1.9
10_UCOLSP	OtsCHJO_seg_sp22	OtsWINT_seg_sp18	0.7993	-	-	-	-	3	3	2.3
10_UCOLSP	OtsCHJO_seg_sp22	OtsWINT_seg_sp19	0.989	-	-	-	-	1	1	0.9
10_UCOLSP	OtsCHJO_seg_sp22	Unassigned	1	59	-	-	211	-	270	-
10_UCOLSP	OtsCHJO_seg_sp22	(blank)	(blank)	-	0	45	-	-	45	0.5
10_UCOLSP	OtsEAST_seg_sp22	OtsEAST_seg_sp18	1	-	-	-	-	55	55	55
10_UCOLSP	OtsEAST_seg_sp22	Unassigned	1	-	-	-	120	-	120	-
10_UCOLSP	OtsEAST_seg_sp22	(blank)	(blank)	-	-	23	-	-	23	1
10_UCOLSP	OtsLNFH_seg_sp22	OtsEAST_seg_sp18	1	-	-	-	-	1	1	1
10_UCOLSP	OtsLNFH_seg_sp22	OtsLNFH_seg_sp17	0.8606	-	-	-	-	9	9	7.7
10_UCOLSP	OtsLNFH_seg_sp22	OtsLNFH_seg_sp18	0.5506	-	-	-	-	425	425	234
10_UCOLSP	OtsLNFH_seg_sp22	OtsLNFH_seg_sp19	1	-	-	-	-	10	10	10
10_UCOLSP	OtsLNFH_seg_sp22	Unassigned	1	-	-	-	410	-	410	-
10_UCOLSP	OtsLNFH_seg_sp22	(blank)	(blank)	0	0	52	-	-	52	0.5
10_UCOLSP	OtsMETH_seg_sp22	OtsMETH_seg_sp18	0.7778	-	-	-	-	7	7	5.4
10_UCOLSP	OtsMETH_seg_sp22	Unassigned	1	-	-	-	119	-	119	-
10_UCOLSP	OtsMETH_seg_sp22	(blank)	(blank)	0	1	0	-	-	1	0.7
10_UCOLSP	OtsWINT_seg_sp22	OtsMETH_seg_sp17	0.9051	-	-	-	-	1	1	0.9
10_UCOLSP	OtsWINT_seg_sp22	OtsMETH_seg_sp18	0.7778	-	-	-	-	306	306	238
10_UCOLSP	OtsWINT_seg_sp22	OtsMETH_seg_sp19	1	-	-	-	-	23	23	23
10_UCOLSP	OtsWINT_seg_sp22	OtsWINT_seg_sp18	0.7993	-	-	-	-	38	38	30.
10_UCOLSP	OtsWINT_seg_sp22	Unassigned	1	-	-	-	5	-	5	-
10_UCOLSP	OtsWINT_seg_sp22	(blank)	(blank)	0	0	7	-	-	7	0.7
18_UCOLSF	OtsCHJO_int_su22	OtsCHJO_int_su16	0.9896	-	-	-	-	1	1	0.9
18_UCOLSF	OtsCHJO_int_su22	OtsCHJO_int_su17	0.7549	-	-	-	-	88	88	66.
18_UCOLSF	OtsCHJO_int_su22	OtsCHJO_int_su19	0.9801	-	-	-	-	3	3	2.9
18_UCOLSF	OtsCHJO_int_su22	OtsCHJO_seg_su16	0.9915	-	-	-	-	1	1	0.9
18_UCOLSF	OtsCHJO_int_su22	OtsCHJO_seg_su17	0.9032	-	-	-	-	41	41	37.
18_UCOLSF	OtsCHJO_int_su22	OtsCHJO_seg_su19	0.9623	-	-	-	-	2	2	1.9
18_UCOLSF	OtsCHJO_int_su22	OtsEAST_seg_su16	0.9831	-	-	-	-	1	1	0.9
18_UCOLSF	OtsCHJO_int_su22	OtsEAST_seg_su17	0.9661	-	-	-	-	4	4	3.8
18_UCOLSF	OtsCHJO_int_su22	OtsEAST_seg_su18	0.9917	-	-	-	-	14	14	13.
18_UCOLSF	OtsCHJO_int_su22	OtsENFH_seg_su18	0.7628	-	-	-	-	3	3	2.2
18_UCOLSF	OtsCHJO_int_su22	OtsLYON_seg_fa18	0.8055	-	-	-	-	1	1	0.8
18_UCOLSF	OtsCHJO_int_su22	OtsWELL_seg_su17	0.8901	-	-	-	-	14	14	12.
18_UCOLSF	OtsCHJO_int_su22	OtsWELL_seg_su18	0.8209	-	-	-	-	12	12	9.8
18_UCOLSF	OtsCHJO_int_su22	OtsWELL_seg_su19	1	-	-	-	-	3	3	3
18_UCOLSF	OtsCHJO_int_su22	Unassigned	1	-	-	-	274	-	274	-
18_UCOLSF	OtsCHJO_int_su22	(blank)	(blank)	0	1	37	-	-	38	0.8
18_UCOLSF	OtsCHJO_seg_su22	OtsCHJO_int_su16	0.9896	-	-	-	-	4	4	3.9
18_UCOLSF	OtsCHJO_seg_su22	OtsCHJO_int_su17	0.7549	-	-	-	-	155	155	117
18_UCOLSF	OtsCHJO_seg_su22	OtsCHJO_int_su19	0.9801	-	-	-	-	2	2	1.9

18_UCOLSF	OtsCHJO_seg_su22	OtsCHJO_seg_su16	0.9915	-	-	-	-	2	2	1.9
18_UCOLSF	OtsCHJO_seg_su22	OtsCHJO_seg_su17	0.9032	-	-	-	-	34	34	30.
18_UCOLSF	OtsCHJO_seg_su22	OtsCHJO_seg_su19	0.9623	-	-	-	-	1	1	0.9
18_UCOLSF	OtsCHJO_seg_su22	OtsEAST_seg_su17	0.9661	-	-	-	-	11	11	10.
18_UCOLSF	OtsCHJO_seg_su22	OtsEAST_seg_su18	0.9917	-	-	-	-	38	38	37.
18_UCOLSF	OtsCHJO_seg_su22	OtsENFH_seg_su17	0.8393	-	-	-	-	3	3	2.5
18_UCOLSF	OtsCHJO_seg_su22	OtsENFH_seg_su18	0.7628	-	-	-	-	2	2	1.5
18_UCOLSF	OtsCHJO_seg_su22	OtsWELL_seg_su17	0.8901	-	-	-	-	17	17	15.
18_UCOLSF	OtsCHJO_seg_su22	OtsWELL_seg_su18	0.8209	-	-	-	-	12	12	9.8
18_UCOLSF	OtsCHJO_seg_su22	OtsWELL_seg_su19	1	-	-	-	-	1	1	1
18_UCOLSF	OtsCHJO_seg_su22	Unassigned	1	-	-	-	56	-	56	-
18_UCOLSF	OtsCHJO_seg_su22	(blank)	(blank)	-	1	94	-	-	95	-
18_UCOLSF	(blank)	(blank)	(blank)	0	-	4	-	-	4	0.8
18_UCOLSF	OtsEAST_seg_su22	OtsCHJO_int_su17	0.7549	-	-	-	-	3	3	2.2
18_UCOLSF	OtsEAST_seg_su22	OtsCHJO_seg_su16	0.9915	-	-	-	-	1	1	0.9
18_UCOLSF	OtsEAST_seg_su22	OtsCHJO_seg_su17	0.9032	-	-	-	-	4	4	3.6
18_UCOLSF	OtsEAST_seg_su22	OtsEAST_seg_su16	0.9831	-	-	-	-	2	2	1.9
18_UCOLSF	OtsEAST_seg_su22	OtsEAST_seg_su17	0.9661	-	-	-	-	82	82	79.
18_UCOLSF	OtsEAST_seg_su22	OtsEAST_seg_su18	0.9917	-	-	-	-	159	159	157
18_UCOLSF	OtsEAST_seg_su22	OtsENFH_seg_su17	0.8393	-	-	-	-	1	1	0.8
18_UCOLSF	OtsEAST_seg_su22	OtsLYON_seg_fa18	0.8055	-	-	-	-	2	2	1.6
18_UCOLSF	OtsEAST_seg_su22	OtsWELL_seg_su17	0.8901	-	-	-	-	38	38	33.
18_UCOLSF	OtsEAST_seg_su22	OtsWELL_seg_su18	0.8209	-	-	-	-	20	20	16.
18_UCOLSF	OtsEAST_seg_su22	Unassigned	1	-	-	-	366	-	366	-
18_UCOLSF	OtsEAST_seg_su22	(blank)	(blank)	0	0	20	-	-	20	0.9
18_UCOLSF	OtsENFH_seg_su22	OtsENFH_seg_su16	1	-	-	-	-	1	1	1
18_UCOLSF	OtsENFH_seg_su22	OtsENFH_seg_su17	0.8393	-	-	-	-	208	208	174
18_UCOLSF	OtsENFH_seg_su22	OtsENFH_seg_su18	0.7628	-	-	-	-	71	71	54.
18_UCOLSF	OtsENFH_seg_su22	Unassigned	1	-	-	-	43	-	43	-
18_UCOLSF	OtsENFH_seg_su22	(blank)	(blank)	0	0	10	-	-	10	0.8
18_UCOLSF	OtsPRIE_seg_fa22	OtsEAST_seg_su18	0.9917	-	-	-	-	1	1	0.9
18_UCOLSF	OtsPRIE_seg_fa22	OtsLWSN_seg_fa17	0.9595	-	-	-	-	2	2	1.9
18_UCOLSF	OtsPRIE_seg_fa22	OtsLWSN_seg_fa19	1	-	-	-	-	6	6	6
18_UCOLSF	OtsPRIE_seg_fa22	OtsLYON_seg_fa18	0.8055	-	-	-	-	3	3	2.4
18_UCOLSF	OtsPRIE_seg_fa22	OtsLYON_seg_fa19	0.9597	-	-	-	-	3	3	2.8
18_UCOLSF	OtsPRIE_seg_fa22	OtsNPFH_seg_fa18	0.8115	-	-	-	-	1	1	0.8
18_UCOLSF	OtsPRIE_seg_fa22	OtsPRIE_seg_fa16	1	-	-	-	-	1	1	1
18_UCOLSF	OtsPRIE_seg_fa22	OtsPRIE_seg_fa17	0.9095	-	-	-	-	968	968	880
18_UCOLSF	OtsPRIE_seg_fa22	OtsPRIE_seg_fa18	0.8617	-	-	-	-	2113	2113	182
18_UCOLSF	OtsPRIE_seg_fa22	OtsPRIE_seg_fa19	0.9615	-	-	-	-	1368	1368	131
18_UCOLSF	OtsPRIE_seg_fa22	OtsPRIE_seg_fa20	0.745	-	-	-	-	9	9	6.7
18_UCOLSF	OtsPRIE_seg_fa22	OtsPROS_seg_fa18	0.8668	-	-	-	-	1	1	0.8
18_UCOLSF	OtsPRIE_seg_fa22	OtsRING_seg_fa17	0.934	-	-	-	-	2	2	1.8

18_UCOLSF	OtsPRIE_seg_fa22	OtsRING_seg_fa19	0.9602	-	-	-	-	11	11	10.
18_UCOLSF	OtsPRIE_seg_fa22	OtsSPCR_seg_fa19	0.9068	-	-	-	-	1	1	0.9
18_UCOLSF	OtsPRIE_seg_fa22	OtsUMAT_seg_fa18	0.9573	-	-	-	-	31	31	29.
18_UCOLSF	OtsPRIE_seg_fa22	OtsUMAT_seg_fa19	1	-	-	-	-	3	3	3
18_UCOLSF	OtsPRIE_seg_fa22	Unassigned	1	-	-	-	1111	-	1111	-
18_UCOLSF	OtsPRIE_seg_fa22	(blank)	(blank)	0	9	163	-	-	172	0.9
18_UCOLSF	OtsPROS_seg_fa22	OtsLWSN_seg_fa17	0.9595	-	-	-	-	8	8	7.6
18_UCOLSF	OtsPROS_seg_fa22	OtsLWSN_seg_fa19	1	-	-	-	-	43	43	43
18_UCOLSF	OtsPROS_seg_fa22	OtsLYON_seg_fa18	0.8055	-	-	-	-	4	4	3.2
18_UCOLSF	OtsPROS_seg_fa22	OtsLYON_seg_fa20	0.9896	-	-	-	-	1	1	0.9
18_UCOLSF	OtsPROS_seg_fa22	OtsPROS_seg_fa17	0.3964	-	-	-	-	1	1	0.3
18_UCOLSF	OtsPROS_seg_fa22	OtsPROS_seg_fa20	0.9517	-	-	-	-	3	3	2.8
18_UCOLSF	OtsPROS_seg_fa22	OtsRING_seg_fa17	0.934	-	-	-	-	7	7	6.5
18_UCOLSF	OtsPROS_seg_fa22	OtsRING_seg_fa19	0.9602	-	-	-	-	6	6	5.7
18_UCOLSF	OtsPROS_seg_fa22	OtsUMAT_seg_fa18	0.9573	-	-	-	-	20	20	19.
18_UCOLSF	OtsPROS_seg_fa22	OtsUMAT_seg_fa19	1	-	-	-	-	3	3	3
18_UCOLSF	OtsPROS_seg_fa22	Unassigned	1	-	-	-	13	-	13	-
18_UCOLSF	OtsPROS_seg_fa22	(blank)	(blank)	0	1	9	-	-	10	0.9
18_UCOLSF	OtsRING_seg_fa22	OtsPRIE_seg_fa17	0.9095	-	-	-	-	23	23	20.
18_UCOLSF	OtsRING_seg_fa22	OtsPRIE_seg_fa18	0.8617	-	-	-	-	27	27	23.
18_UCOLSF	OtsRING_seg_fa22	OtsPRIE_seg_fa19	0.9615	-	-	-	-	94	94	90.
18_UCOLSF	OtsRING_seg_fa22	Unassigned	1	-	-	-	8	-	8	-
18_UCOLSF	OtsRING_seg_fa22	(blank)	(blank)	0	0	9	-	-	9	0.9
18_UCOLSF	OtsWELL_seg_su22	OtsCHJO_int_su16	0.9896	-	-	-	-	6	6	5.9
18_UCOLSF	OtsWELL_seg_su22	OtsCHJO_int_su17	0.7549	-	-	-	-	85	85	64.
18_UCOLSF	OtsWELL_seg_su22	OtsCHJO_seg_su16	0.9915	-	-	-	-	5	5	4.9
18_UCOLSF	OtsWELL_seg_su22	OtsCHJO_seg_su17	0.9032	-	-	-	-	69	69	62.
18_UCOLSF	OtsWELL_seg_su22	OtsEAST_seg_su16	0.9831	-	-	-	-	2	2	1.9
18_UCOLSF	OtsWELL_seg_su22	OtsEAST_seg_su17	0.9661	-	-	-	-	83	83	80.
18_UCOLSF	OtsWELL_seg_su22	OtsEAST_seg_su18	0.9917	-	-	-	-	6	6	5.9
18_UCOLSF	OtsWELL_seg_su22	OtsENFH_seg_su16	1	-	-	-	-	1	1	1
18_UCOLSF	OtsWELL_seg_su22	OtsENFH_seg_su17	0.8393	-	-	-	-	29	29	24.
18_UCOLSF	OtsWELL_seg_su22	OtsWELL_seg_su16	1	-	-	-	-	9	9	9
18_UCOLSF	OtsWELL_seg_su22	OtsWELL_seg_su17	0.8901	-	-	-	-	508	508	452
18_UCOLSF	OtsWELL_seg_su22	OtsWELL_seg_su18	0.8209	-	-	-	-	18	18	14.
18_UCOLSF	OtsWELL_seg_su22	Unassigned	1	-	-	-	139	-	139	-
18_UCOLSF	OtsWELL_seg_su22	(blank)	(blank)	0	0	11	-	-	11	0.8
19_SRFALL	OtsNPFH_seg_fa22	OtsLYON_seg_fa17	0.7641	-	-	-	-	17	17	12.
19_SRFALL	OtsNPFH_seg_fa22	OtsLYON_seg_fa18	0.8055	-	-	-	-	288	288	231
19_SRFALL	OtsNPFH_seg_fa22	OtsLYON_seg_fa19	0.9597	-	-	-	-	35	35	33.
19_SRFALL	OtsNPFH_seg_fa22	OtsNPFH_seg_fa16	0.9726	-	-	-	-	1	1	0.9
19_SRFALL	OtsNPFH_seg_fa22	OtsNPFH_seg_fa17	0.9681	-	-	-	-	31	31	30.
19_SRFALL	OtsNPFH_seg_fa22	OtsNPFH_seg_fa18	0.8115	-	-	-	-	98	98	79.

19_SRFALL	OtsNPFH_seg_fa22	OtsPRIE_seg_fa17	0.9095	-	-	-	-	1	1	0.9
19_SRFALL	OtsNPFH_seg_fa22	OtsWELL_seg_su18	0.8209	-	-	-	-	1	1	0.8
19_SRFALL	OtsNPFH_seg_fa22	Unassigned	1	6	-	-	229	-	235	-
19_SRFALL	OtsNPFH_seg_fa22	(blank)	(blank)	-	0	5	-	-	5	0.8
20_BONPOOLSP	OtsCARS_seg_sp22	OtsCARS_seg_sp17	1					21	21	21
20_BONPOOLSP	OtsCARS_seg_sp22	OtsCARS_seg_sp18	1					1199	1199	119
20_BONPOOLSP	OtsCARS_seg_sp22	OtsCARS_seg_sp19	1					22	22	22
20_BONPOOLSP	OtsCARS_seg_sp22	OtsLWSN_seg_sp18	1					4	4	4
20_BONPOOLSP	OtsCARS_seg_sp22	OtsLWSN_seg_sp19	1					1	1	1
20_BONPOOLSP	OtsCARS_seg_sp22	Unassigned	1				16		16	
20_BONPOOLSP	OtsCARS_seg_sp22	(blank)	1		1	4			5	1
20_BONPOOLSP	OtsLWSN_seg_sp22	OtsCARS_seg_sp18	1	-	-	-	-	255	255	255
20_BONPOOLSP	OtsLWSN_seg_sp22	OtsCARS_seg_sp19	1	-	-	-	-	1	1	1
20_BONPOOLSP	OtsLWSN_seg_sp22	OtsCLWH_seg_sp18	1	-	-	-	-	1	1	1
20_BONPOOLSP	OtsLWSN_seg_sp22	OtsDWOR_seg_sp18	0.9493	-	-	-	-	1	1	0.9
20_BONPOOLSP	OtsLWSN_seg_sp22	OtsLWSN_seg_sp17	0.9418	-	-	-	-	12	12	11.
20_BONPOOLSP	OtsLWSN_seg_sp22	OtsLWSN_seg_sp18	0.9392	-	-	-	-	697	697	654
20_BONPOOLSP	OtsLWSN_seg_sp22	OtsLWSN_seg_sp19	0.9528	-	-	-	-	10	10	9.5
20_BONPOOLSP	OtsLWSN_seg_sp22	Unassigned	1	-	-	-	53	-	53	-
20_BONPOOLSP	OtsLWSN_seg_sp22	(blank)	(blank)	0	0	6	-	-	6	0.9
21_UMATILLASP	OtsUMAT_seg_sp22	OtsCARS_seg_sp17	0.9841	-	-	-	-	1	1	0.9
21_UMATILLASP	OtsUMAT_seg_sp22	OtsCARS_seg_sp18	1	-	-	-	-	54	54	54
21_UMATILLASP	OtsUMAT_seg_sp22	OtsCARS_seg_sp19	1	-	-	-	-	1	1	1
21_UMATILLASP	OtsUMAT_seg_sp22	OtsUMAT_seg_sp17	1	-	-	-	-	5	5	5
21_UMATILLASP	OtsUMAT_seg_sp22	OtsUMAT_seg_sp18	0.9913	-	-	-	-	527	527	522
21_UMATILLASP	OtsUMAT_seg_sp22	OtsUMAT_seg_sp19	1	-	-	-	-	22	22	22
21_UMATILLASP	OtsUMAT_seg_sp22	Unassigned	1	-	-	-	17	-	17	-
21_UMATILLASP	OtsUMAT_seg_sp22	(blank)	(blank)	0	0	45	-	-	45	0.9
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsKLIC_seg_fa19	0.565	-	-	-	-	1	1	0.5
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsLWSN_seg_fa16	1	-	-	-	-	10	10	10
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsLWSN_seg_fa17	0.9595	-	-	-	-	1326	1326	127
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsLWSN_seg_fa18	0.7313	-	-	-	-	2732	2732	199
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsLWSN_seg_fa19	1	-	-	-	-	897	897	897
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsLWSN_seg_fa20	0.9945	-	-	-	-	34	34	33.
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsLYON_seg_fa19	0.9597	-	-	-	-	1	1	0.9
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsNPFH_seg_fa18	0.8115	-	-	-	-	1	1	0.8
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsPRIE_seg_fa18	0.8617	-	-	-	-	860	860	741
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsPRIE_seg_fa19	0.9615	-	-	-	-	4	4	3.8
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsRING_seg_fa17	0.934	-	-	-	-	1	1	0.9
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsRING_seg_fa18	0.832	-	-	-	-	109	109	90.
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsRING_seg_fa19	0.9602	-	-	-	-	1	1	0.9
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsSPCR_seg_fa19	0.9068	-	-	-	-	3	3	2.7
22_BONPOOLSFA	OtsLWSN_seg_fa22	OtsUMAT_seg_fa18	0.9573	-	-	-	-	2	2	1.9

22_BONPOOLSFA	OtsLWSN_seg_fa22	Unassigned	1	-	-	-	820	-	820	-
22_BONPOOLSFA	OtsLWSN_seg_fa22	(blank)	(blank)	0	12	57	-	-	69	0.8
23_UMATILLA	OtsUMAT_seg_fa22	OtsLWSN_seg_fa19	1	-	-	-	-	2	2	2
23_UMATILLA	OtsUMAT_seg_fa22	OtsNPFH_seg_fa17	0.9681	-	-	-	-	1	1	0.9
23_UMATILLA	OtsUMAT_seg_fa22	OtsRING_seg_fa17	0.934	1	-	-	-	1	2	0.9
23_UMATILLA	OtsUMAT_seg_fa22	OtsRING_seg_fa19	0.9602	-	-	-	-	5	5	4.8
23_UMATILLA	OtsUMAT_seg_fa22	OtsUMAT_seg_fa18	0.9573	3	-	-	-	48	51	45.
23_UMATILLA	OtsUMAT_seg_fa22	OtsUMAT_seg_fa19	1	-	-	-	-	3	3	3
23_UMATILLA	OtsUMAT_seg_fa22	Unassigned	1	1	-	-	3	-	4	-
23_UMATILLA	OtsUMAT_seg_fa22	(blank)	(blank)	-	0	1	-	-	1	0.9

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 SY2022 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 is one exception. The OtsPARK\_seg\_sp22 collection from Parkdale Hatchery on the Hood River had a correct assignment rate of 6.8%. 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. In some years, the Snake River Fall Chinook generally have high misassignment rates to the upper Columbia River su/fa (18\_UCOLSF) GSI group, which may explain cases where we observe low correct assignment of the Nez Perce Hatchery fall collections.



Table 8. GSI composition of the SY2022 Columbia River Chinook hatchery collections

Exp GSI	Collection	Observed GSI																	N A	Total	% Correct
		01_YOUNGS	02_WCASSP	03_WCASFA	04_WILLAM	05_SPCRTU	06_KLICKR	07_DESCSP	08_JOHNR	09_YAKIMA	10_UCOLSP	12_HELLSC	13_SFSALM	16_UPSALM	17_DESCFA	18_UCOLSF	19_SRFALL				
02_WCASSP	OtsCOWL_seg_sp22	-	702	27	15	-	-	-	-	-	-	-	-	-	-	-	-	-	744	94.4%	
	OtsKALA_seg_sp22	-	554	13	44	-	-	-	-	-	-	-	-	-	-	-	-	-	611	90.7%	
	OtsPARK_seg_sp22	-	19	-	17	-	34	14	1	-	-	37	31	-	-	-	-	-	279	6.8%	
	OtsSPEE_seg_sp22	-	1072	5	-	-	28	-	-	-	-	-	-	-	-	-	-	-	1105	97.0%	
03_WCASFA	OtsCOWL_seg_fa22	-	37	461	4	-	-	-	-	-	-	-	-	-	-	-	-	-	502	91.8%	
	OtsKALA_seg_fa22	-	-	1176	12	-	-	-	-	-	-	-	-	-	-	-	-	-	1188	99.0%	
	OtsNTOU_seg_fa22	2	1	181	-	-	-	-	-	-	-	-	-	-	-	-	-	-	184	98.4%	
	OtsWASH_seg_fa22	-	-	761	2	-	-	-	-	-	-	-	-	-	-	-	-	-	763	99.7%	
06_K 05_04_WILL LICK SPCAM R RTU	OtsNSAN_seg_sp22	-	-	-	1430	-	-	-	-	-	-	-	-	-	-	-	-	-	1430	100.0%	
	OtsSSAN_seg_sp22	-	-	-	565	-	-	-	-	-	-	-	-	-	-	-	-	-	565	100.0%	
	OtsSPCR_seg_fa22	-	-	-	-	6523	-	-	-	-	-	-	-	-	-	-	-	-	6523	100.0%	
	OtsKLIC_seg_sp22	-	-	-	-	-	60	7	-	1	3	-	-	-	-	-	-	-	611	99.3%	
07_DESCSP	OtsRBFH_seg_sp22	-	-	-	-	-	2	32	8	19	-	33	88	-	-	-	-	-	470	69.8%	
	OtsWSNF_seg_sp22	-	-	-	-	-	-	17	4	-	-	-	-	-	-	-	-	-	174	100.0%	
09_YAKIMA	OtsYRRD_int_sp22	-	-	-	-	-	-	-	1	38	1	-	-	-	-	1	-	-	383	99.5%	
	OtsYRRD_seg_sp22	-	-	-	-	-	-	-	1	24	4	-	-	-	-	-	-	-	245	99.6%	
10_UCOLSP	OtsCHJO_seg_sp22	-	-	-	-	-	-	-	-	-	488	7	24	2	-	-	-	-	521	93.7%	
	OtsEAST_seg_sp22	-	-	-	-	-	-	-	-	-	174	-	-	1	-	-	-	-	175	99.4%	
	OtsLNFH_seg_sp22	-	-	-	-	-	-	3	-	-	820	14	4	14	-	-	-	-	855	95.9%	
	OtsMETH_seg_sp22	-	-	-	-	-	-	-	-	-	126	-	-	-	-	-	-	-	126	100.0%	
18_UC OLS F	OtsWINT_seg_sp22	-	-	-	-	-	-	-	-	-	373	-	-	-	-	-	-	-	373	100.0%	
	OtsCHJO_int_su22	-	-	-	-	-	-	-	-	-	-	-	-	-	-	460	2	-	462	99.6%	

23_22_21_20_19_UM BO UM POOLSP ALL ATILNP ATIL LAS LAF OO	OtsCHJO_seg_su22	-	-	-	-	-	-	-	-	-	-	-	-	-	-	337	1	-	338	99.7%
	OtsEAST_seg_su22	-	-	-	-	-	-	-	-	-	-	-	-	1	-	677	-	-	678	99.9%
	OtsENFH_seg_su22	-	-	-	-	-	-	-	-	-	-	-	-	-	-	311	12	-	323	96.3%
	OtsPRIE_seg_fa22	-	-	-	-	1	-	-	-	-	-	-	-	-	-	5428	206	-	5635	96.3%
	OtsPROS_seg_fa22	-	-	-	-	-	-	-	-	-	-	-	-	-	-	98	11	-	109	89.9%
	OtsRING_seg_fa22	1	-	-	-	-	-	-	-	-	-	-	-	-	-	151	-	-	152	99.3%
	OtsWELL_seg_su22	-	-	-	-	-	-	-	-	-	-	-	-	-	-	960	-	-	960	100.0%
	OtsNPFH_seg_fa22	-	-	-	-	-	-	-	-	-	-	2	-	-	-	59	640	-	701	91.3%
	OtsCARS_seg_sp22	-	-	-	-	-	-	-	-	-	1004	58	1	-	-	-	-	-	1063	94.4%
	OtsLWSN_seg_sp22	-	-	-	-	-	-	-	-	-	1010	20	-	-	-	-	-	-	1030	98.1%
	OtsUMAT_seg_sp22	-	-	-	-	-	-	-	-	-	597	30	-	-	-	-	-	-	627	95.2%
	OtsLWSN_seg_fa22	-	-	15	-	3	-	-	-	-	-	-	-	-	-	6354	430	-	6802	93.4%
	OtsUMAT_seg_fa22	-	-	1	-	-	-	-	-	-	-	-	-	-	-	320	20	67	408	93.8%
Total		3	2385	2640	2089	6527	67	64	21	6	62	4665	8	31	18	0	15156	1322	67	37115

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 SY2022 steelhead broodstock collections that were genotyped by CRITFC primarily outside the Snake River basin and added to the PBT baseline in 2024 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 PBT assignment rate being similar to their observed PBT assignment rate and these assignment 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 (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 SY2022.

Table 9. PBT broodstock composition of the SY2022 Columbia River Steelhead hatchery collections

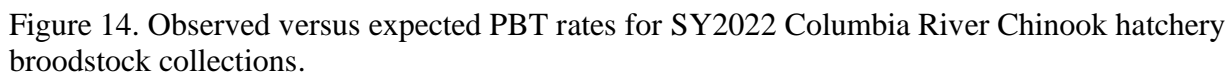
Exp. GSI	Collection	PBT Source	Source Rate	Method					PBT Rate	
				Duplicate	Failed	GSI	PBT	Total	Exp.	Obs.
03_SKAMAN	OmySKAM_su22	OmySKAM_su17	0.9400	-	-	-	40	40	37.6000	-
03_SKAMAN	OmySKAM_su22	OmySKAM_su18	0.9840	-	-	-	82	82	80.6880	-
03_SKAMAN	OmySKAM_su22	OmySKAM_su19	0.9869	-	-	-	5	5	4.9345	-
03_SKAMAN	OmySKAM_su22	Unassigned	N/A	-	-	10	-	10	-	-
03_SKAMAN	OmySKAM_su22	(blank)	(blank)	0	2	-	-	2	0.9703	0.9270
03_SKAMAN	OmySKAM_wi22	OmySKAM_wi18	0.6140	-	-	-	25	25	15.3500	-
03_SKAMAN	OmySKAM_wi22	OmySKAM_wi19	0.7071	-	-	-	37	37	26.1627	-
03_SKAMAN	OmySKAM_wi22	Unassigned	N/A	0	0	22	-	22	0.6696	0.7381
07_MGILCS	OmyMINT_su22	OmyMINT_su18	0.9760	-	-	-	5	5	4.8800	-
07_MGILCS	OmyMINT_su22	OmySFCR_su18	0.9470	-	-	-	1	1	0.9470	-
07_MGILCS	OmyMINT_su22	Unassigned	N/A	-	-	67	-	67	-	-
07_MGILCS	OmyMINT_su22	(blank)	(blank)	1	3	-	-	4	0.9712	0.0822
07_MGILCS	OmyROUN_su22	OmyROUN_su17	0.9980	-	-	-	13	13	12.9740	-
07_MGILCS	OmyROUN_su22	OmyROUN_su18	0.9850	-	-	-	201	201	197.9850	-
07_MGILCS	OmyROUN_su22	OmyROUN_su19	0.9583	-	-	-	217	217	207.9511	-
07_MGILCS	OmyROUN_su22	OmyWALL_su19	0.9969	-	-	-	1	1	0.9969	-
07_MGILCS	OmyROUN_su22	Unassigned	N/A	-	-	24	-	24	-	-
07_MGILCS	OmyROUN_su22	(blank)	(blank)	3	10	-	-	13	0.9720	0.9474
09_UPPCOL	OmyEAST_su22	OmyEAST_su17	1.0000	-	-	-	2	2	2.0000	-
09_UPPCOL	OmyEAST_su22	OmyEAST_su18	0.9460	-	-	-	12	12	11.3520	-
09_UPPCOL	OmyEAST_su22	OmyEAST_su19	0.9322	-	-	-	28	28	26.1016	-
09_UPPCOL	OmyEAST_su22	OmyWELL_su19	0.8468	-	-	-	1	1	0.8468	-
09_UPPCOL	OmyEAST_su22	Unassigned	N/A	-	-	47	-	47	-	-
09_UPPCOL	OmyEAST_su22	(blank)	(blank)	0	2	-	-	2	0.9372	0.4778
09_UPPCOL	OmyWELL_su22	OmyDWOS_su18	0.8640	-	-	-	1	1	0.8640	-
09_UPPCOL	OmyWELL_su22	OmyWELL_su18	0.6250	-	-	-	5	5	3.1250	-
09_UPPCOL	OmyWELL_su22	OmyWELL_su19	0.8468	-	-	-	70	70	59.2760	-
09_UPPCOL	OmyWELL_su22	OmyWINT_su17	1.0000	-	-	-	4	4	4.0000	-

09_UPPCOL	OmyWELL_su22	OmyWINT_su18	0.9700	-	-	-	55	55	53.3500	-
09_UPPCOL	OmyWELL_su22	OmyWINT_su19	0.8115	-	-	-	7	7	5.6805	-
09_UPPCOL	OmyWELL_su22	OmyWMET_su18	0.9660	-	-	-	23	23	22.2180	-
09_UPPCOL	OmyWELL_su22	OmyWOKA_su18	1.0000	-	-	-	7	7	7.0000	-
09_UPPCOL	OmyWELL_su22	OmyWOMA_su18	1.0000	-	-	-	1	1	1	-
09_UPPCOL	OmyWELL_su22	Unassigned	N/A	-	-	35	-	35	-	-
09_UPPCOL	OmyWELL_su22	(blank)	(blank)	0	13	-	-	13	0.904702	0.832
09_UPPCOL	OmyWINT_su22	OmyWINT_su18	0.97	-	-	-	3	3	2.91	
09_UPPCOL	OmyWINT_su22	Unassigned	N/A	0	0	106	-	106	0.97	0.028
<b>Total</b>				4	30	311	846	1191		

The GSI assignments of the steelhead SY2022 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\_su22 and OmyWINT\_su22) which typically have high rates of misassignment to the middle Columbia reporting group (07\_MGILCS).

Table 10. GSI composition of the SY2022 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_su22	-	136	-	-	-	-	-	-	-	-	-	-	3	139	100.0%
	OmySKAM_wi22	83	1	-	-	-	-	-	-	-	-	-	-	-	84	98.8%
07_MGILCS	OmyMINT_su22	-	-	-	-	57	-	1	2	-	-	-	7	10	77	85.1%
	OmyROUN_su22	-	-	-	-	421	-	3	-	-	-	-	26	19	469	93.6%
09_UPPCOL	OmyEAST_su22	-	-	-	-	38	-	38	-	-	-	-	8	8	92	45.2%
	OmyWELL_su22	-	-	-	-	109	-	53	2	-	-	-	27	13	204	27.7%
	OmyWINT_su22	-	-	-	-	56	-	36	-	-	-	-	15	2	109	33.6%
Total		83	137	0	0	681	0	131	4	0	0	0	83	55	1174	



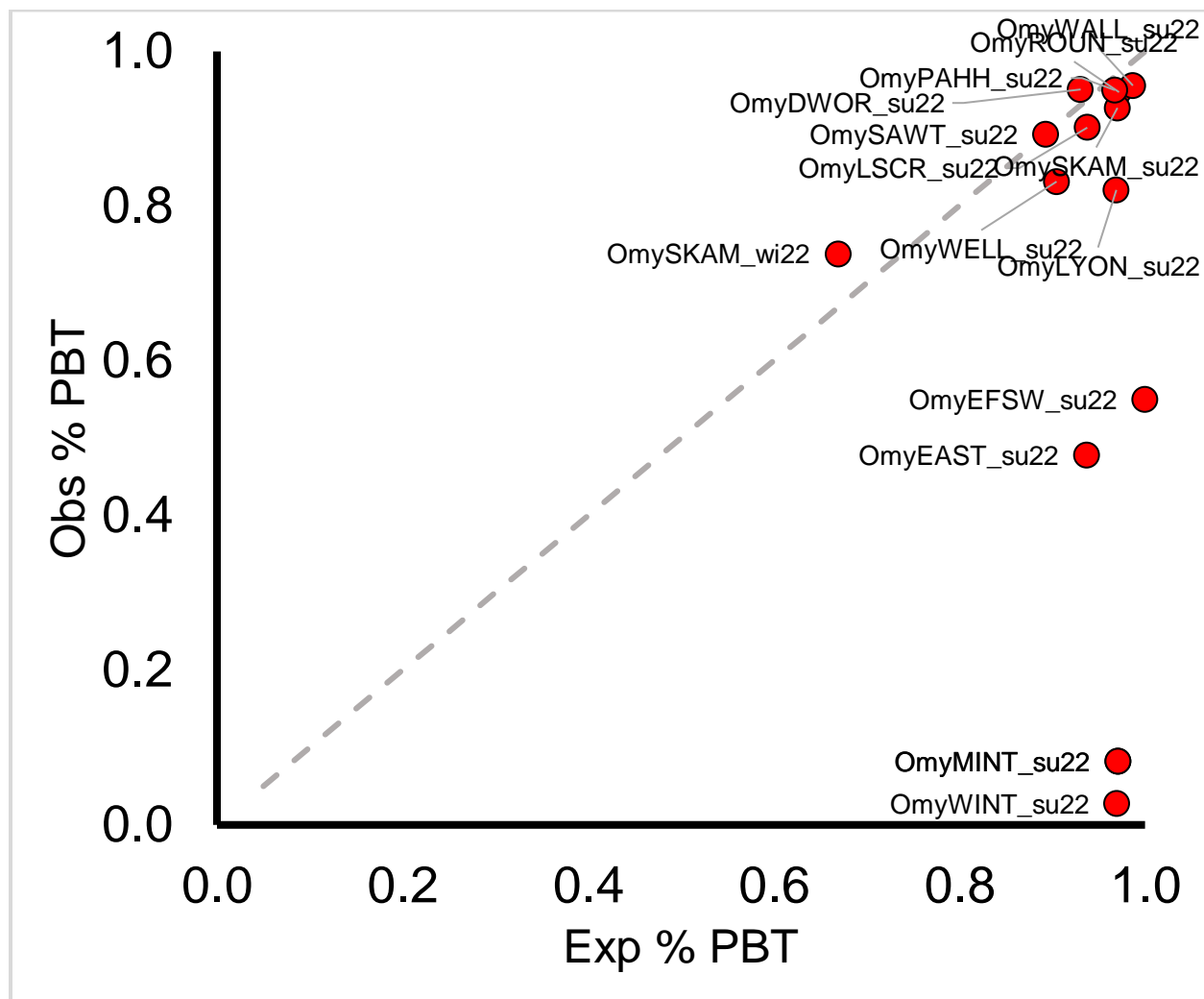


Figure 15. Observed versus expected PBT rates for SY2022 Columbia River Steelhead hatchery broodstock collections.

## 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.

Map ID	Spawning hatchery	Broodstock Code	Release group	Run type	Lineage	Region	Latitude	Longitude	1st SY	2024 genotyping	
										Current SY	Completed
1	Klaskanine (NF brood)	OtsKLNf_seg_fa	-	fall (tule)	LC	Col.	46.09000	#####	na	na	na
1	Klaskanine (SF brood)	OtsKLSF_seg_fa	-	fall (tule)	LC	Col.	46.09000	#####	na	na	na
2	Big Creek	OtsBIGC_seg_fa	-	fall (tule)	LC	Col.	46.14616	#####	2015	na	na
5	Cowlitz Salmon	OtsCOWL_seg_fa	-	fall (tule)	LC	Col.	46.51145	#####	2015	2023	552
5	Cowlitz Salmon	OtsCOWL_seg_sp	-	spring	LC	Col.	46.51145	#####	2015	2023	1240
6	North Toutle	OtsNTOU_seg_fa	-	fall (tule)	LC	Col.	46.37464	#####	2015	2023	459
7	Kalama Falls	OtsKALA_seg_fa	-	fall (tule)	LC	Col.	46.01624	#####	2016	2023	1294
7	Kalama Falls	OtsKALA_seg_sp	-	spring	LC	Col.	46.01624	#####	2015	2023	591
9	Speelyai (Lewis R)	OtsSPEE_seg_sp	-	spring	LC	Col.	45.98849	#####	2015	2023	1021
15	Clackamas	OtsCLAC_seg_sp	-	spring	LC	Col.	45.29600	#####	na	na	na
18	Marion Forks	OtsMARF_seg_sp	-	spring	LC	Col.	44.61200	#####	na	na	na
17	North Santiam	OtsNSAN_seg_sp	-	spring	LC	Col.	44.75790	#####	2020	2023	1448
19	South Santiam	OtsSSAN_seg_sp	-	spring	LC	Col.	44.41600	#####	2020	2023	865
20	McKenzie	OtsMCKE_seg_sp	-	spring	LC	Col.	44.11800	#####	2020	2023	551
21	Willamette	Ots_WILL_seg_sp	-	spring	LC	Col.	43.74500	#####	na	na	na
11	Washougal	OtsWASH_seg_fa	-	fall (tule)	LC	Col.	45.65344	#####	2015	2023	802
12	Bonneville, Tanner Cr.	OtsBONN_seg_fa	-	fall (tule)	LC	Col.	45.63300	#####	na	2023	2395
24	Spring Creek NFH	OtsSPRCR_seg_fa	-	fall (tule)	LC	Col.	45.72779	#####	2015	2023	7646
22	Little White Salmon NFH	OtsLWSN_seg_fa	OtsKLIC_seg_fa23	fall	IOT	Col.	45.72226	#####	2013	2023, 2024	2180
22	Little White Salmon NFH	OtsLWSN_seg_fa	OtsPROS_seg_fa23	fall	IOT	Col.	45.72226	#####	2013	2023, 2024	702
22	Little White Salmon NFH	OtsLWSN_seg_fa	-	fall	IOT	Col.	45.72226	#####	2013	2023, 2024	4202, 3757
29	Three Mile Dam	OtsUMAT_seg_fa	-	fall	IOT	Col.	45.88172	#####	2012	2023	1295
32	Prosser	OtsPROS_seg_fa	-	fall	IOT	Col.	46.21512	#####	2012	2023	335
35	Ringold Springs	OtsRING_seg_fa	-	fall	IOT	Col.	46.51401	#####	2016	2023	862
36	Priest Rapids	OtsPRIE_seg_fa	OtsKLIC_seg_fa23	fall	IOT	Col.	46.64728	#####	2012	2023	636
36	Priest Rapids	OtsPRIE_seg_fa	OtsPROS_seg_fa23	fall	IOT	Col.	46.64728	#####	2012	2023	521
36	Priest Rapids	OtsPRIE_seg_fa	-	fall	IOT	Col.	46.64728	#####	2012	2023	5680
44	Lyons Ferry	OtsLYON_seg_fa	-	fall	IOT	Snake	46.59725	#####	2011	2023	69
45	Nez Perce Tribal	OtsNPFH_seg_fa	-	fall	IOT	Snake	46.51954	#####	2011	2024	1000
38	Eastbank	OtsEAST_seg_su	-	summer	IOT	Col.	47.53367	#####	2012	2023	670
39	Entiat NFH	OtsENFH_seg_su	-	summer	IOT	Col.	47.69806	#####	2013	2023	328
40	Wells	OtsWELL_seg_su	-	summer	IOT	Col.	47.94582	#####	2012	2023	1034
41	Chief Joseph	OtsCHJO_SIN_su	OtsCHJO_int_sp23	summer	IOT	Col.	48.00060	#####	2013	2023	560
41	Chief Joseph	OtsCHJO_SIN_su	OtsCHJO_seg_sp23	summer	IOT	Col.	48.00060	#####	2013	2023	488
22	Little White Salmon NFH	OtsLWSN_seg_sp	Ots_LWSN_seg_sp23	spring	IST	Col.	45.72226	#####	2013	2023	786
22	Little White Salmon NFH	OtsLWSN_seg_sp	OtsTOUC_seg_sp23	spring	IST	Col.	45.72226	#####	2013	2023	231
31	South Fork Walla Walla	OtsUMAT_seg_sp	-	spring	IST	Col.	45.90200	#####	2012	2023	670
44	Lyons Ferry	OtsLYON_seg_sp	-	spring	IST	Snake	46.59725	#####	2008	2023	69
45	Nez Perce Tribal	OtsNPFH_seg_sp	-	spring	IST	Snake	46.51954	#####	2008	2023, 2024	273, 289
38	Eastbank	OtsEAST_seg_sp	-	spring	IST	Col.	47.53367	#####	2012	2023	196
41	Chief Joseph	OtsCHJO_seg_sp	-	spring	IST	Col.	48.00060	#####	2014	2023	547
13	Carson NFH	OtsCARS_seg_sp	-	spring	IST	Col.	45.86826	#####	2012	2023	1191
23	Parkdale	OtsPARK_seg_sp	-	spring	IST	Col.	45.52439	#####	2012	2023	210
25	Klickitat	OtsKLIC_seg_sp	OtsKLIC_seg_fa23	spring	IST	Col.	46.04236	#####	2008	2023	198
25	Klickitat	OtsKLIC_seg_sp	-	spring	IST	Col.	46.04236	#####	2008	2023	402
26	Warm Springs NFH	OtsWSNF_seg_sp	-	spring	IST	Col.	44.86201	#####	2012	2023	476
27	Round Butte	OtsRBFH_seg_sp	-	spring	IST	Col.	44.60503	#####	2012	2023	518
34	Cle Elum SRF	OtsYRRD_SIN_sp	OtsYRRD_int_sp23	spring	IST	Col.	47.18679	#####	2012	2023	427
34	Cle Elum SRF	OtsYRRD_SIN_sp	OtsYRRD_seg_sp23	spring	IST	Col.	47.18679	#####	2012	2023	322
37	Leavenworth NFH	OtsLNFH_seg_sp	-	spring	IST	Col.	47.55842	#####	2013	2023	789
42	Methow	OtsMETH_seg_sp	-	spring	IST	Col.	48.47703	#####	2012	2023	127
43	Winthrop NFH	OtsWINT_seg_sp	-	spring	IST	Col.	48.47366	#####	2013	2023	437
49	Lookingglass	OtsLOOK_seg_sp	-	spring	IST	Snake	45.73136	#####	2008	2023	616
47	Powell	OtsPOWP_seg_sp	-	spring	IST	Snake	46.50429	#####	2008	na	na
46	Dworshak NFH	OtsDWOR_seg_sp	-	spring	IST	Snake	46.50206	#####	2008	2023	1132
48	Kooskia	Ots_KOOS_seg_sp	-	spring	IST	Snake	46.50206	#####	2008	2023	421
47	Clearwater	OtsCLWH_seg_sp	-	spring	IST	Snake	46.50429	#####	2008	2023, 2024	2141, 2726
52	Rapid River	OtsRAPH_seg_ss	-	spring/summer	IST	Snake	45.35411	#####	2008	2023, 2024	2717, 2539
54	SF Salmon, McCall	OtsMCCA_seg_ss	-	spring/summer	IST	Snake	44.90777	#####	2008	na	na
54	Johnson Creek	OtsJHNW_int_ss	-	spring/summer	IST	Snake	44.90777	#####	2008	2023, 2024	90, 98
56	Pahsimeroi	OtsPAHH_seg_ss	-	spring/summer	IST	Snake	44.62284	#####	2008	na	na
55	Sawtooth	OtsSAWT_seg_ss	-	spring/summer	IST	Snake	44.15174	#####	2008	na	na

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, Coho and Sockeye Salmon hatchery broodstock sampled for PBT baselines.

Appendix 2: Steelhead, Coho and Sockeye Salmon hatchery broodstock sampled for FDI baselines.											
Map ID	Spawning hatchery	Broodstock Code	Release Group	Run type	Lineage	Region	Latitude	Longitude	1st SY	2024 genotyping Current SYCompleted	
	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_su	-	summer	coastal	Col.	45.62180	-122.21730	2023	2023	139
10	Skamania	OmySKAM_wi	-	winter	coastal	Col.	45.62180	-122.21730	2023	2023	54
23	Parkdale	OmyPARK_wi	-	winter	coastal	Col.	45.52440	-121.62160	2012	na	na
27	Round Butte	OmyROUN_su	-	summer	inland	Col.	44.60500	-121.27784	2013	2023	329
28	Umatilla	OmyUMAT_su	-	summer	inland	Col.	45.91300	-119.55200	2012	na	na
38	Eastbank	OmyEAST_su	-	summer	inland	Col.	47.53370	-120.28910	2012	2023	100
40	Wells	OmyWELL_su	OmyWMET_su23	summer	inland	Col.	47.94580	-119.87120	2013	2023	34
40	Wells	OmyWELL_su	OmyWOMA_su23	summer	inland	Col.	47.94580	-119.87120	2013	2023	8
40	Wells	OmyWELL_su	OmyWOKA_su23	summer	inland	Col.	47.94580	-119.87120	2013	2023	30
40	Wells	OmyWELL_su	-	summer	inland	Col.	47.94580	-119.87120	2013	2023	83
42	Methow (Twisp)	OmyMETH_su	-	summer	inland	Col.	48.47700	-120.20510	2013	na	na
43	Winthrop NFH	OmyWINT_su	-	summer	inland	Col.	48.47370	-120.20510	2013	2023	76
44	Lyons Ferry	OmyLYON_su	-	summer	inland	Snake	46.59730	-118.22820	2009	na	na
50	Wallowa	OmyWALL_su	-	summer	inland	Snake	45.41780	-117.30040	2009	na	na
53	Oxbow	OmyOXBO_su	-	summer	inland	Snake	44.97270	-116.85480	2008	na	na
46	Dworshak NFH	OmyDWOR_su	-	summer	inland	Snake	46.50210	-116.32320	2008	na	na
56	Pahsimeroi	OmyPAHH_su	-	summer	inland	Snake	44.62280	-113.98630	2008	na	na
55	Sawtooth	OmySAWT_su	-	summer	inland	Snake	45.15170	-114.88430	2008	na	na
51	Little Sheep Creek	OmyLSCR_su	-	summer	inland	Snake	45.47770	-116.93060	2008	na	na
30	Minthorn Springs	OmyMINT_su	-	summer	inland	Col.	45.69938	-118.39647	2012	2023	85
	Coho										
28	Umatilla	OkiUMA_seg_fa	-	fall	lower Col.	Col.	45.91300	-119.55200	2015	2023	933
32	Prosser	OkiPRO_seg_fa	-	fall	lower Col.	Col.	46.21510	-119.75960	2016	2023	622
37	Leavenworth NFH	OkiLNFH_seg_fa	-	fall	lower Col.	Col.	47.55840	-120.67380	2012	2023, 2024	1110, 994
43	Winthrop NFH	OkiWTP_seg_fa	-	fall	lower Col.	Col.	48.47370	-120.18910	2012	2023, 2024	626, 780
46	Dworshak NFH	OkiNPT_seg_fa	-	fall	lower Col.	Snake	46.50210	-116.32320	2015	2023	1387
16	Eagle Creek NFH	OkiEGLC_seg_fa	-	fall	lower Col.	Col.	45.27600	-122.20200	2019	2023	890
12	Bonneville	OkiBONN_seg_fa	-	fall	lower Col.	Col.	45.63300	-121.95700	2019	2023	870
33	Mel R Sampson	OkiMRS_SIN_fa	-	fall	lower Col.	Col.	47.04200	-120.62600	2022	2023	742
	Sockeye										
57	Penticton	OnePENT_seg	-	-	-	Col.	49.47889	-119.60611	2019	2023	2712

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

Note: The map ID indicates site locations corresponding with Figure 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.

☒ Chinook tissues genotyped using 351 SNPs

☒ Chinook tissues genotyped using 343 SNPs

☒ Chinook tissues genotyped using 298 SNPs

X Chinook tissues genotyped using 96 SNPs

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

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

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

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

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

N/A Stock discontinued/non-existent

\* Broodstock not sampled

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

† 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 2023.

Map num.	Hatchery	Species	Code	Run type	Lineage	Year						2017	2018	2019	2020	2021	2022	2023
						2011	2012	2013	2014	2015	2016							
29	Three Mile Dam, Umatilla River	Coho	OkiUMA_seg_fa22	Fall	Lower Columbia					X	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	X
46	Dworshak National Fish Hatchery	Coho	OkiNPT_seg_fa22	Fall	Lower Columbia			*	*	X	X	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	X	X
33	Mel R Sampson Hatchery	Coho	OkiMRS_int_fa22	Fall	Lower Columbia											X	X	X
43	Winthrop National Fish Hatchery	Coho	OkiWTP_seg_fa22	Fall	Lower Columbia		X	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	X
12	Bonneville Hatchery	Coho	OkiBONN_seg_fa22	Fall	Lower Columbia									X			X	X

Note: map numbers correspond to sites in Figure 13.  
X Coho tissues genotyped at 235 loci  
\* Samples received, but not genotyped.

### Section 3: Genetic Stock Identification of Chinook Salmon, Sockeye Salmon, Coho 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. Coho Salmon has become the most recent species to have a PBT baseline available for fisheries applications (Horn et al. 2024). Sampling of Coho Salmon in the Zone 6 fishery in future years will provide a demonstration of the utility of PBT for mixed stock fisheries management in the mainstem Columbia River. For the 2023 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, Coho, 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, Sockeye, and Coho 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 12<sup>th</sup> year of analysis of Sockeye salmon fisheries in the Columbia River mainstem, which consists of fish harvested in 2023 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. We have also recently completed genotyping of the first Sockeye hatchery program outside of the Snake River (Penticton Hatchery in the Okanagan River basin). Inclusion of the SY2019 –

2023 broodstocks from this hatchery program will allow PBT identification of these hatchery-origin fish in the future.

#### *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 2023 from a total of five different mixture sources: the spring period harvest of the 1) test fishery; 2) sport fishery (above and below Bonneville Dam); the summer period harvest of the 3) sport fishery (above and below Bonneville Dam); 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 16; Table 11). Typically for the summer management period fisheries, we may obtain samples from below Bonneville Dam in the recreational fishery, and above Bonneville Dam in the Zone 6 recreational fishery and the Treaty commercial fishery. In most cases, we analyzed all the random samples obtained from the various fisheries sampled above and below Bonneville Dam and included some non-random samples that were positive for a CWT to compare to our PBT assignments. For any fisheries in which we had to subsample the harvest, we selected fish randomly and with a balanced design across spatial regions. However, each subsample should be tailored to the way the catch is reported for each fishery to accurately represent the geographic and temporal stratification of the CREEL.

Stock proportions were estimated and expanded by the catch reported for each fishery source, such that stock abundance could be compared across fisheries. We use the following

four main geographic regions (Figure 16): Region A corresponds to our grouping of pre-existing Oregon and Washington state sport fishing sections 1-4 (or commercial zones 4-5), Region B corresponds to our grouping of sport sections 5-10 (or commercial zones 1-3). In the Zone 6, we typically distinguish Region 01 (Bonneville Pool) from Region 02 (Dalles and John Day Pools) because of the stock composition differences that can occur between the two regions particularly in the fall period when tules are observed in high proportions in Region 01. These sets of groupings were established for this study to achieve balanced sampling for analysis of these fishery datasets, as well as to best match the stratification of the reported catch.

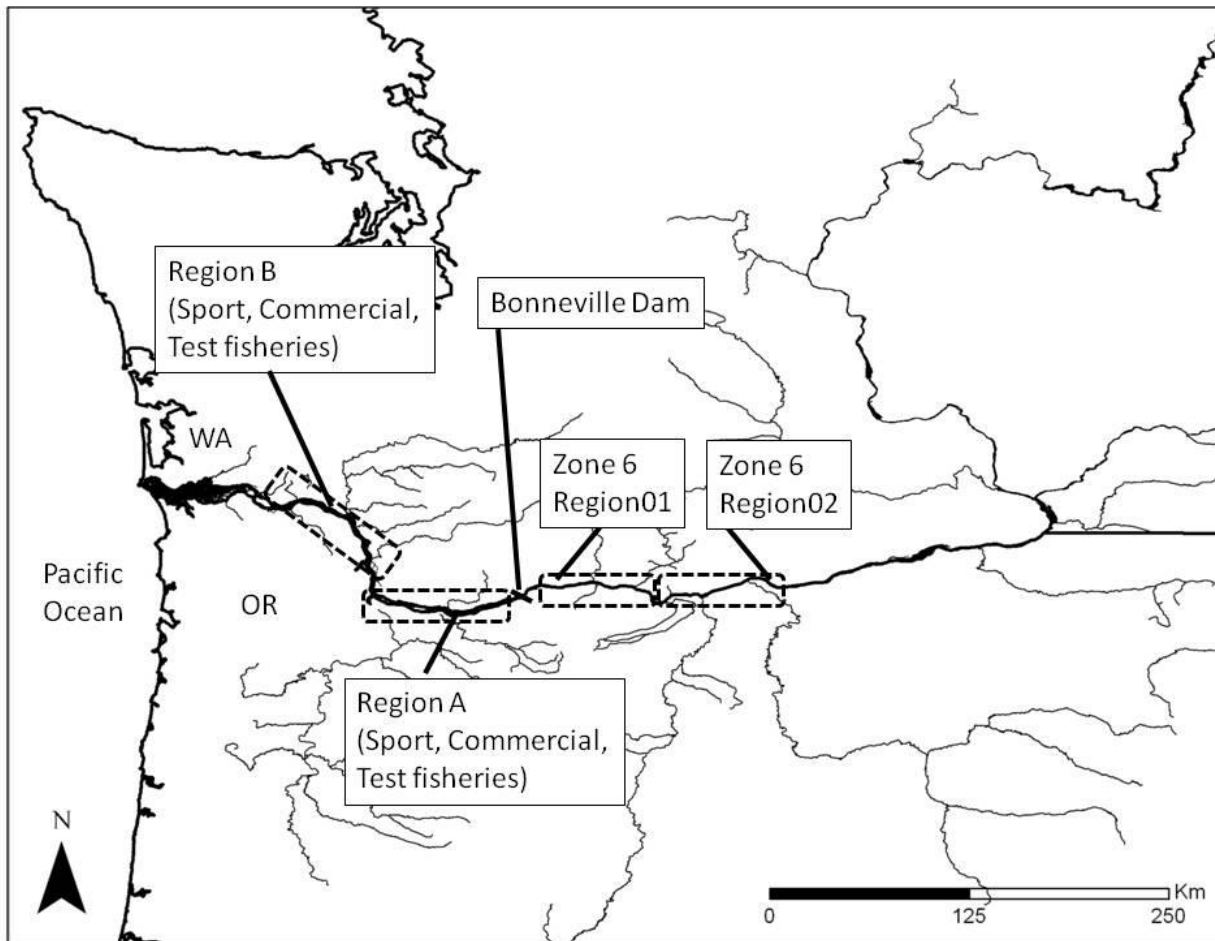
Non-Treaty fisheries during the spring management period for Chinook salmon are mark-selective based on absence or presence of the adipose fin to distinguish hatchery fish from natural origin fish, respectively. These adipose markings make it possible to have a mark-selective sport and commercial fishery 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 fisheries.

Tissues were sampled from Sockeye salmon in 2023 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 2023 are presented in the current report. This is the first year we have genotyped Coho salmon and include an analysis of the 2023 harvest from the Zone 6 Treaty commercial fishery. Samples were collected at the commercial buyers in Zone 6 as part of the CREEL conducted by WDFW; sources of the samples were unable to be resolved to a particular pool within Zone 6 but the sample could be stratified into weeks.

### *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.**

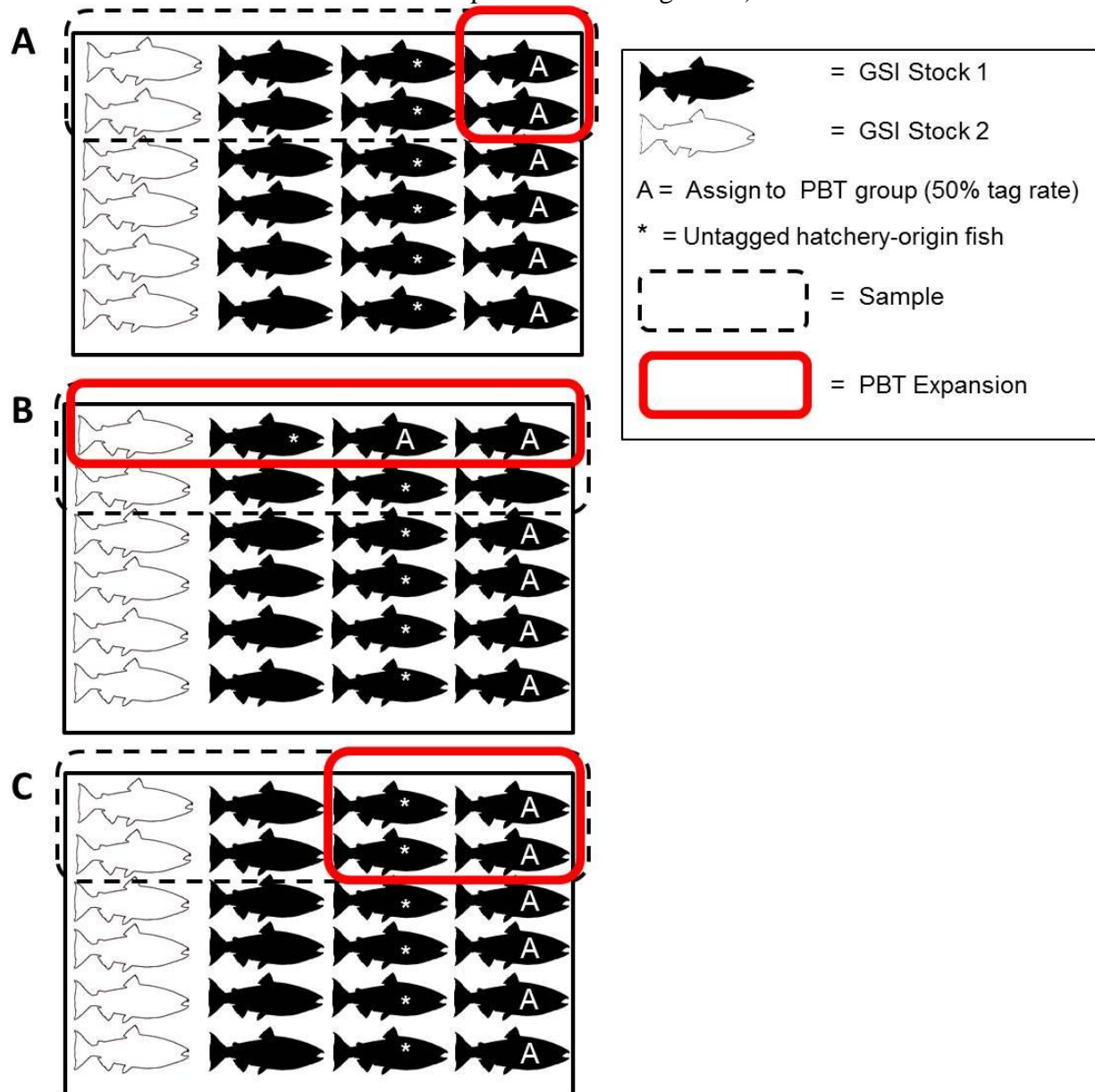


Table 11. Characteristics of Chinook, Sockeye, and Coho harvest samples by fishery, region, and adipose-clip status by weekly strata in 2023.

						Statistical weeks																																	
						Spring														Summer						Fall													
Chinook Period	Fishery	Region	Clip	Sampled	Genotyped	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	31	32	33	34	35	36	37	38	39	40	41	42	43	44	
Spring	Test	B	AD	277	262			1	2	9	20	53	58	52	31	20	8	2	6																				
			AI	38	34					3	6	5	9	5	2	4																							
	Sport	B	AD	188	171	4	3	1	23	75	16					3	30	16																					
		A	AD	121	108		4	2	4	8	11						33	43	3																				
		Sport	01 (Zone 6)	AD	13	13								1	7		1	4																					
	02 (Zone 6)		AD	77	63								11	26		14	12																						
Summer	Sport	B	AD	63	55															11	30	13		1															
		A	AD	41	37															13	13	10	1																
	Sport	02 (Zone 6)	AD	6	6															4	2																		
Fall	Sport	B	AD	168	150																				4	10	9	21	86	6	9	1	2	2					
			AI	318	277																				2	3	18	21	174	24	22	3	7	1	2				
		A	AD	159	142																				3	5	1	5	13	31	56	8		10	6	2	2		
			AI	511	478																						3	2	12	48	85	178	54	45	23	10	12	6	
	Sport	01 (Zone 6)	AD	166	151																							1	7	9	35	53	11	16	10	4	4	1	
			AI	556	529																							2	12	29	103	155	85	61	31	23	25	2	1
		02 (Zone 6)	AD	79	71																																		
			AI	276	256																								2	5	17	8	5	7	12	6	8	1	
	Commercial	B	AD	3	3																															3			
			AI	3	3																														3				
		A	AD	334	319																																		
			AI	252	224																																		
			Chinook fishery total				3649	3352	4	7	4	29	95	53	58	79	90	33	75	97	21	6	28	45	23	1	1	9	58	96	189	717	330	506	219	242	101	76	48
Summer	Sport	A&B	AD																				3	3															
			AI																		26	23	42		15	13	1												
Sockeye fishery total				135	126															26	23	42	0	18	16	1													
Fall	Treaty	Zone 6	AD		107																							1	8	23	35	33	7						
			AI		218																								1	36	51	62	26	42					
Coho fishery total				331	325																							2	44	74	97	59	49						

### *PBT Rate Expansion using SCOBIDEUX and SPIBETR functions*

The use of PBT adds complexity to analyses when each hatchery broodstock is genotyped at rates less than 100%. Expansion of hatchery-origin adipose-intact fish can lead to bias when we characterize natural-origin stocks by attributes (Figure 17). 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 SCOBIDEUX method provides.**

In Figure 17, 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 17, 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 17, B: yields an estimate of 50% hatchery origin, 37.5% natural-origin GSI stock 1, and 12.5% natural-origin GSI stock 2. Finally, using the corrections implemented by the SCOBIDEUX and SPIBETR functions, we are able to expand GSI stock 1 by PBT rates and correct this expansion by proportionally decreasing the GSI stock 1 in the remaining sample mixture, which yields scenario C (Figure 17): 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 12; Figure 18). 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 19). 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 20). 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.,  $\text{LOD} \geq 14$  &  $\text{FDR} \leq 0.1$ ) (See methods for [Parentage assignments using SNPPIT software v1.0](#), ID: 1341). For the remaining individuals, we used the best estimate of GSI assignments (regardless of the probability of assignment) provided by the program Rubias (Moran and Anderson 2019) to determine likely reporting group of origin (Method: [Assigning individual samples using Individual Assignment \(IA\) genetic methods v1.0](#), ID: 1334). In a previous report (Hess et al. 2022), we showed improvements in accuracy of assignments using Rubias compared to the program ONCOR and this was the first year since having made a switch between those assignment programs. For the assignment of sockeye, GSI via Rubias was used. We also have a baseline of candidate parents used in the reintroduction of Sockeye salmon which requires both SNPPIT and a program to perform single parentage assignments (SEQUOIA). For Chinook salmon, all age classes (3-, 4-, and 5+ year old fish) can be identified from Snake River and Columbia River stocks using PBT.

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

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

We made every effort to match representative DNA sampling of these harvest management strata, which is the approach we began implementing since the 2018 harvest analysis. Specifically, we describe our stratification for each fishery sample in the following section:

#### *The spring test fishery:*

This fishery is typically conducted in the early portion of the spring Chinook salmon management period and occurs in the commercial zones 2 and 3 (a portion of “Region B”). Chinook salmon are visually stock-identified (VSI) to lower river and upriver stock classifications. A fleet of boats conduct drift fishing each week and catch per unit effort (CPUE)

is estimated using the number of fish caught per number of drifts for each week. Tissue samples are obtained from both the clipped and unclipped fish caught in the test fishery at a high rate (>50%). We performed a final analysis of the 2023 test fishery. Similar to the 2021 test fishery (Hess et al. 2022), the CPUE estimated in the 2023 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 (Hess et al. 2024). 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 2023.**

Week	Drifts	Estimated # VSI-Upriver			CPUE of VSI-Upriver			Sample of VSI-Upriver			Sample Rate of VSI-Upriver		
		AD	AI	Total	AD	AI	Total	AD	AI	Total	AD	AI	Total
11	15	0.00	0.00	0.00	0.00	0.00	0.00				79.3%	59.1%	76.0%
12	14	0.00	0.00	0.00	0.00	0.00	0.00			0			
13	15	2.00	2.00	4.00	0.13	0.13	0.27	1		1			
14	15	10.93	1.21	12.14	0.73	0.08	0.81	8	1	9			
15	16	21.10	4.97	26.07	1.32	0.31	1.63	16	2	18			
16	15	42.37	6.05	48.42	2.82	0.40	3.23	34	4	38			
17	15	48.51	9.46	57.97	3.23	0.63	3.86	40	7	47	82.5%	74.0%	81.1%
18	16	48.56	2.56	51.11	3.03	0.16	3.19	36	3	39	81.2%	87.5%	81.7%
19	12	17.60	3.30	20.90	1.47	0.28	1.74	16	2	18			
20	9	3.00	1.00	4.00	0.33	0.11	0.44	4	1	5			
21	6	4.00	0.00	4.00	0.67	0.00	0.67	3		3			
22	8	1.00	0.00	1.00	0.13	0.00	0.13	1		1			
23	8	1.00	0.00	1.00	0.13	0.00	0.13	1		1			

**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 2023**

Week	Drifts	Estimated # VSI-Lower			CPUE of VSI-Lower			Sample of VSI-Lower			Sample Rate of VSI-Lower		
		AD	AI	Total	AD	AI	Total	AD	AI	Total	AD	AI	Total
11	15	0.00	0.00	0.00	0.00	0.00	0.00				71.1%	72.9%	71.4%
12	14	1.00	0.00	1.00	0.07	0.00	0.07	1		1			
13	15	2.00	0.00	2.00	0.13	0.00	0.13	1		1			
14	15	2.43	2.43	4.86	0.16	0.16	0.32	1	2	3			
15	16	4.97	4.97	9.93	0.31	0.31	0.62	3	4	7			
16	15	19.37	1.21	20.58	1.29	0.08	1.37	16	1	17			
17	15	23.66	2.37	26.03	1.58	0.16	1.74	16	1	17	67.6%	42.3%	65.3%
18	16	16.61	1.28	17.89	1.04	0.08	1.12	14	1	15	92.1%	87.8%	91.9%



19	12	12.10	0.00	12.10	1.01	0.00	1.01	11		11
20	9	8.00	1.00	9.00	0.89	0.11	1.00	8	1	9
21	6	5.00	0.00	5.00	0.83	0.00	0.83	5		5
22	8	0.00	0.00	0.00	0.00	0.00	0.00			0
23	8	5.00	0.00	5.00	0.63	0.00	0.63	5		5

*The Spring Chinook salmon sport fishery:*

This fishery is mark-selective, which means only the adipose-clipped fish are retained (“kept” fish). All the adipose-intact fish are released, and none of these released fish are tissue sampled, however, a portion of them are counted as mortalities. It may be possible in the future to use the sport test fishery unclipped chinook salmon stock composition to characterize the release mortalities from the spring sport fishery because the test fishery overlaps in timing and region with the spring sport fishery. Harvest is estimated and reported for the total lower Columbia mainstem instead of being geographically stratified into regions A and B. This lack of geographic stratification could be problematic and lead to bias in the genetic analysis unless all sampling is random and occurs at the same rate across regions. We have shown in the past that there are different compositions of stocks across regions (Hess et al. 2019). Sampling conducted by the joint states is typically random and sampling rates are even across the fishing zones, which may help minimize this bias. The 2023 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 2023 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 2023.**

	Total Adult Chinook			Sample of Total Adult Chinook Kept			
	Kept	Rel.	Rel. Mortality	regionA	regionB	total	rate
Jan-Feb Total	0	0	0				
March Total	457	84	8	9	29	38	0.08
April Total	2409	356	36	20	93	113	0.05
May Total	1825	679	68	64	43	107	0.06
June 1-15							
Total	0	0	0			0	
Season Total	4,691	1,119	112	93	165	258	0.05

Note: The released fish (“Rel.”) were not sampled for genetic analysis and so only the “kept” fish could be analyzed. The samples of kept fish usually come from both the regions A and B which was the case for 2023. 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 2023.**

Total Chinook			Sample of Total Chinook Kept			
Kept	Rel.	Rel. Mortality	region01	region02	total	rate
1059	514	51	11	57	68	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.

*The spring chinook salmon platform hook and line permit fishery:*

Yakama Nation typically executes this fishery below Bonneville Dam. However, sampling has not occurred since 2020. The spring chinook salmon zone 6 ceremonial permit fishery was also not analyzed due to the non-representative manner in which samples were obtained. Samples are difficult to obtain in general due to the use of these fish for ceremonies. Ideally, samples would be collected from the harvest of all four member tribes and temporal stratification would be applied; however, samples usually are only possible to obtain from the Yakama Nation harvest and the harvested fish are not possible to report on a weekly basis or by reservoir.

*The Summer Chinook salmon sport fishery:*

This fishery is similar to the spring sport fishery as it is also mark-selective, and the harvest is estimated and reported for the total lower Columbia mainstem instead of being geographically stratified into regions A and B. In 2023, we obtained samples from both regions of the lower Columbia mainstem, A and B (Table 17). We were also able to obtain a small portion of samples from the summer sport fishery above Bonneville Dam in Zone 6 (**Table 18**).

**Table 17. The sample rate and stratification for genetic analysis of the kept adipose clipped adult Chinook salmon from the lower river summer sport fishery in 2023.**

	Total Adult Chinook			Sample of Total Adult Chinook Kept			
	Kept	Rel.	Rel. Mortality	regionA	regionB	total	rate
June 16-30	2013	564	56	34	52	86	0.04
July 1-31	6	386	39				
Season Total	2,019	950	95	34	52	86	0.04

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.

**Table 18. The sample rate and stratification for genetic analysis of the kept adipose clipped adult Chinook salmon from the Zone 6 summer sport fishery in 2023**

	Total Adult Chinook			Sample of Total Adult Chinook Kept			
	Kept	Rel.	Rel. Mortality	zone01	zone02	total	rate
June 16-30					5	5	
July 1-31			0				
Season Total	120	104	10	0	5	5	0.04

Note: The season included openings between June 16 and July 31 and included the area from Bonneville Dam to the Oregon/Washington border.

*The fall Non-Treaty commercial fishery:*

This fishery occurred in two periods in the fall (early period = weeks 33 – 35; late period = weeks 38 – 42) 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 19). 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 19. The sample rate and stratification for genetic analysis of the adult and jack Chinook salmon from fall Non-Treaty commercial fishery in 2023.**

Region	Week	Harvest estimate adult+jack	Sample N			rate
			AD	AI	total	
A	32	407	12	25	37	0.02
A	33	1353	21	28	49	
A	34	4962	37	30	67	
A	35	20681	118	99	217	0.01
A	38	2163	2	4	6	0.01
A	39	1289	6	29	35	
A	40	471	0	4	4	
A	41	459				
A	42	560				
B	38	1044				
B	39	377				
B	40	150	3	3	6	
B	41	8				
B	42	8				

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 20). 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 2023, the sport fishery was also sampled in zone 6 from Bonneville Dam to McNary Dam (Table 21). We obtained samples of clipped and unclipped kept adults on a monthly basis and pooled this sample into a single stratum.

**Table 20. 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 2023.**

Catch Estimate				Sample of kept			
Month	kept Adult	Released	Release mortality(21%)	AD	AI	Total	rate
Aug	6,761	662	139	117	209	326	0.05
Sep	18,078	1459	306	138	460	598	0.03
Oct	2567	220	46	18	51	69	
Total	27,406	2341	492	273	720	993	0.04

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 21. 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 2023.**

Catch Estimate				Sample of kept			
Month	kept Adult	Released	Release mortality 21%	AD	AI	total	rate
August				21	33		
September				154	572		
October				28	98		
Total	15,992	1,857	390	203	703	906	0.06

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 2023 due to lack of resources, but is typically executed in zone 6 across several weeks of the fall management period. This fishery is monitored by visually identifying tules versus bright stocks and estimating each separately. Tissue collection is typically obtained from the fish identified as bright stocks, and very few tule stocks are sampled. Therefore, genetic analysis is constrained to estimating stock composition within the visually-identified bright harvest. However, in the future it may be possible to utilize genetic analysis as a way to estimate both tule and bright stocks as long as representative sampling of these morphologically distinct stocks can be carried out.

*The Sockeye Non-Treaty sport and commercial fishery:*

There was no Non-Treaty commercial fishery in 2023. Only the sport fishery occurred in 2023, and samples were pooled across months and treated as a single stratum (Table 22).

**Table 22. The sample rate and stratification for genetic analysis of the harvested Sockeye salmon from the sport fishery in 2023.**

Catch	Sample
-------	--------

Month	estimate	LBC	Osoyoos	Redfish	Wenatchee	Yakima	total	rate
June	981		53	3	26		82	0.00
July	384		25	8	10		43	0.11
total	1,365	0	78	11	36	0	125	0.09

*The Sockeye Treaty commercial fishery:*

This 2023 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.

*The Coho Treaty commercial fishery*

The 2023 Coho salmon Zone 6 Treaty commercial fishery was the first harvest we have been able to analyze for this species (**Table 23**). The samples were taken from commercial buyers and did not have exact locality data associated with the metadata. The catch summary does not split fish into clipped and unclipped groups and so the sample was used to estimate categories of hatchery clipped, hatchery unclipped, and putative natural-origin (wild) fish based on PBT assignments.

**Table 23. The sample rate and stratification for genetic analysis of the harvested Coho salmon from the fall Treaty Zone 6 commercial fishery in 2023.**

Harvest Estimate		Sample N			
Week	Total	AD	AI	Total	rate
32-34 Platforms	88			0	0.02
34	93			0	
35	416	1	1	2	
36	1,916	8	36	44	
37	2,715	23	51	74	0.03
38	2720	35	62	97	0.04
39	3793	33	26	59	0.01
40	3991	7	42	49	
41	462			0	
42	1584			0	
	17778			325	0.02

## 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 2024 run year of Chinook salmon.

*Comparison of Coded-wire tags and PBT assignments*

There were 285 coded-wire tags (CWTs) recovered and identified to hatchery stock and broodyear (BY) among the snouts obtained from the lower river fisheries (Table 24), and 226 of these CWTs also were PBT assigned (79%). Of the 226 fish with both CWT and PBT, there were 211 fish (93%) that appeared concordant with the PBT assignments according to both the hatchery source and the broodyear. There were 15 of the 226 fish with both CWT and PBT that were discordant for either just broodyear (N=1) or just hatchery source (N=12) or both hatchery source and broodyear (N=2). However, in some cases it may be that the CWT readings were wrong; e.g., a Puget Sound hatchery fish from CWT data was matched to a confident PBT assignment to Lyons Ferry Hatchery (“Discordant” rows, Table 24). Resolving these potential errors would increase the concordance rate even higher than 93%.

**Table 24. Comparison of coded-wire tags with parentage-based tags that were identified in the lower river fisheries in 2023.**

Period	Coded-wire tag		Parentage-based tagging assignment			N
	Hatchery	BY	Hatchery	BY	Status	
Spring	Chief Joseph Hatchery	2019	Chief Joseph Hatchery	2019	Concordant	1
Spring	Clearwater Fish Hatchery	2019	Clearwater Fish Hatchery	2019	Concordant	1
Spring	Clearwater Fish Hatchery	2019	McCall Fish Hatchery	2019	BY	2
Spring	Clearwater Fish Hatchery	2019	Nez Perce Tribal Fish Hatchery	2019	Concordant	1
Spring	Clearwater Fish Hatchery	2020	Rapid River Fish Hatchery	2020	BY	1
Spring	Eastbank Fish Hatchery	2018	Eastbank Fish Hatchery	2018	Concordant	1
Spring	Kalama Falls Hatchery	2018	Kalama Falls Hatchery	2018	Concordant	3
Spring	Klickitat Hatchery	2020	Klickitat Hatchery	2020	Concordant	1
Spring	Leavenworth National Fish Hatchery	2019	Umatilla Fish Hatchery	2019	BY	1
Spring	Lewis River Hatchery	2020	Speelyai Fish Hatchery	2020	Concordant	1
Spring	Little White Salmon National Fish Hatchery	2019	Little White Salmon National Fish Hatchery	2019	Concordant	3
Spring	Lookingglass Fish Hatchery	2019	Lookingglass Fish Hatchery	2019	Concordant	4
Spring	Lookingglass Fish Hatchery	2019	Pahsimeroi Fish Hatchery	2019	BY	1
Spring	Round Butte Fish Hatchery	2019	Round Butte Fish Hatchery	2019	Concordant	1
Spring	Umatilla Fish Hatchery	2019	Umatilla Fish Hatchery	2019	Concordant	1
Spring	Warm Springs National Fish Hatchery	2019	Warm Springs National Fish Hatchery	2019	Concordant	3
Spring	Wells Fish Hatchery	2019	Wells Fish Hatchery	2019	Concordant	1
Spring	Willamette	2019	Cowlitz Salmon Hatchery	2018	Discordant	1
Spring	Willamette	2019	South Santiam Hatchery	2019	Concordant	1
Spring	Winthrop National Fish Hatchery	2019	Little White Salmon National Fish Hatchery	2019	BY	1

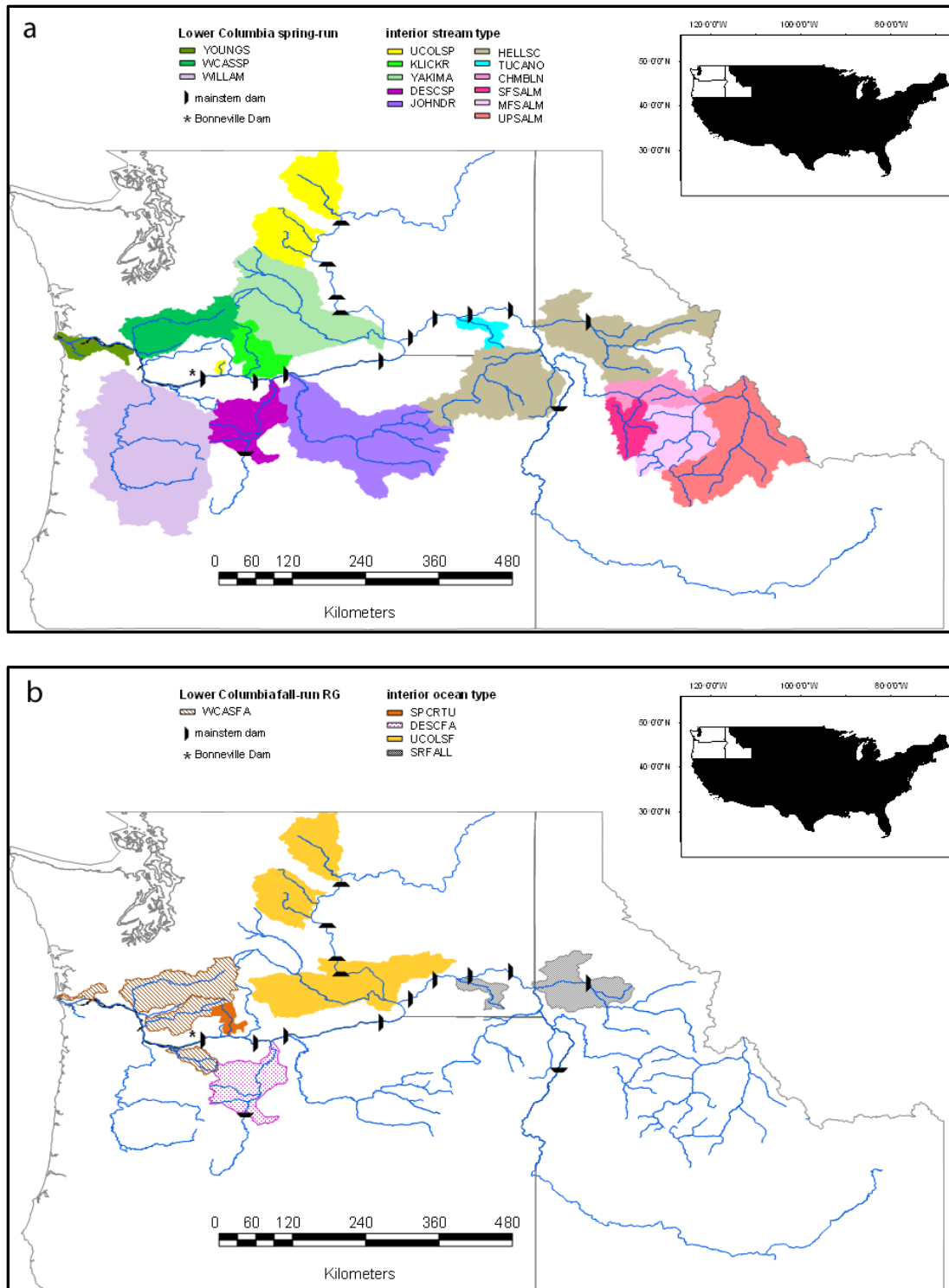


Spring	Winthrop National Fish Hatchery	2019	Winthrop National Fish Hatchery	2019	Concordant	2
Spring	Yakima River Roza Dam	2019	Yakima River Roza Dam	2019	Concordant	1
Spring	Yakima River Roza Dam	2020	Yakima River Roza Dam	2020	Concordant	1
Summer	Chief Joseph Hatchery	2019	Wells Fish Hatchery	2019	Concordant	1
Summer	Eastbank Fish Hatchery	2018	Eastbank Fish Hatchery	2018	Concordant	9
Summer	Eastbank Fish Hatchery	2018	South Santiam Hatchery	2018	BY	1
Summer	Eastbank Fish Hatchery	2019	Eastbank Fish Hatchery	2019	Concordant	1
Summer	Eastbank Fish Hatchery	2020	Yakima River Roza Dam	2020	Concordant	2
Summer	Entiat National Fish Hatchery	2018	Entiat National Fish Hatchery	2018	Concordant	2
Summer	Entiat National Fish Hatchery	2019	Entiat National Fish Hatchery	2019	Concordant	1
Summer	Entiat National Fish Hatchery	2020	Entiat National Fish Hatchery	2020	Concordant	1
Summer	Kalama Falls Hatchery	2019	Kalama Falls Hatchery	2019	Concordant	1
Summer	Lookingglass Fish Hatchery	2019	Lookingglass Fish Hatchery	2019	Concordant	1
Summer	Wells Fish Hatchery	2018	Eastbank Fish Hatchery	2018	Concordant	2
Summer	Wells Fish Hatchery	2018	Wells Fish Hatchery	2018	Concordant	2
Summer	Wells Fish Hatchery	2019	Eastbank Fish Hatchery	2019	Concordant	2
Summer	Wells Fish Hatchery	2019	Wells Fish Hatchery	2019	Concordant	3
Fall	Bonneville Hatchery	2019	Bonneville Hatchery	2019	Concordant	1
Fall	Bonneville Hatchery	2019	Spring Creek National Fish Hatchery	2019	Concordant	2
Fall	Bonneville Hatchery	2020	Bonneville Hatchery	2020	Concordant	2
Fall	Bonneville Hatchery	2020	Little White Salmon National Fish Hatchery	2019	BY	2
Fall	Bonneville Hatchery	2021	Little White Salmon National Fish Hatchery	2021	Concordant	3
Fall	Klickitat Fall	2018	Priest Rapids Hatchery	2018	Concordant	1
Fall	Little White Salmon National Fish Hatchery	2019	Little White Salmon National Fish Hatchery	2019	Concordant	2
Fall	Lyons Ferry Fish Hatchery	2018	Lyons Ferry Fish Hatchery	2018	Concordant	6
Fall	Lyons Ferry Fish Hatchery	2019	Little White Salmon National Fish Hatchery	2019	BY	1
Fall	Lyons Ferry Fish Hatchery	2019	Lyons Ferry Fish Hatchery	2018	Hatchery	1
Fall	Lyons Ferry Fish Hatchery	2019	Lyons Ferry Fish Hatchery	2019	Concordant	62
Fall	Lyons Ferry Fish Hatchery	2020	Lyons Ferry Fish Hatchery	2020	Concordant	6
Fall	Nez Perce Tribal Fish Hatchery	2018	Nez Perce Tribal Fish Hatchery	2018	Concordant	1
Fall	Nez Perce Tribal Fish Hatchery	2019	Nez Perce Tribal Fish Hatchery	2019	Concordant	4
Fall	Priest Rapids Hatchery	2018	Priest Rapids Hatchery	2018	Concordant	2

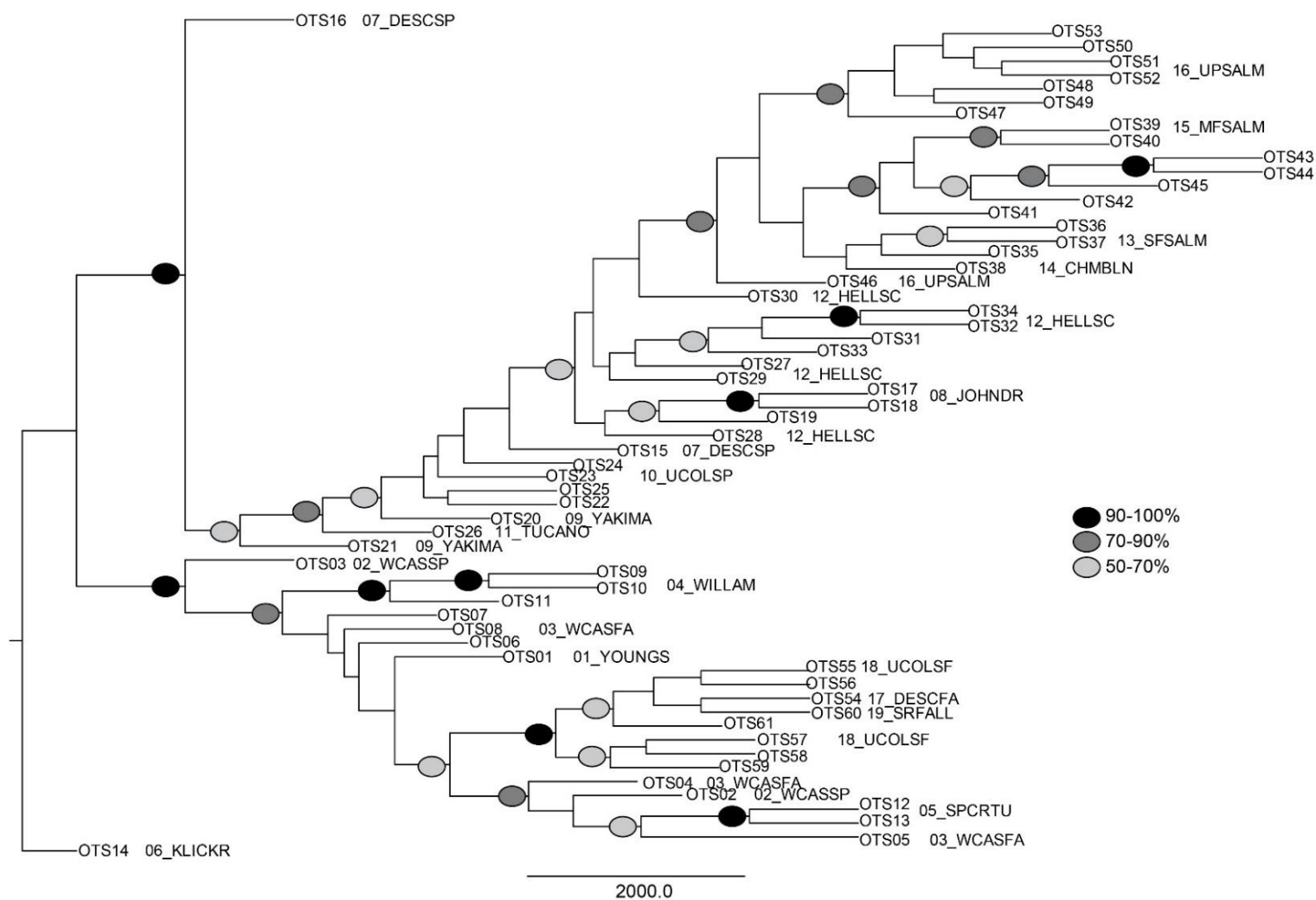
Fall	Priest Rapids Hatchery	2019	Priest Rapids Hatchery	2019	Concordant	8
Fall	Priest Rapids Hatchery	2020	Little White Salmon National Fish Hatchery	2019	Concordant	1
Fall	Priest Rapids Hatchery	2020	Priest Rapids Hatchery	2020	Concordant	2
Fall	Prosser Hatchery	2019	Little White Salmon National Fish Hatchery	2019	Concordant	3
Fall	Prosser Hatchery	2019	Spring Creek National Fish Hatchery	2019	BY	1
Fall	Puget Sound	2019	Lyons Ferry Fish Hatchery	2021	Discordant	1
Fall	Ringold Springs State Hatchery	2019	Priest Rapids Hatchery	2019	Concordant	13
Fall	Spring Creek National Fish Hatchery	2019	Lyons Ferry Fish Hatchery	2019	BY	1
Fall	Spring Creek National Fish Hatchery	2019	Spring Creek National Fish Hatchery	2019	Concordant	5
Fall	Spring Creek National Fish Hatchery	2020	Spring Creek National Fish Hatchery	2020	Concordant	18
Fall	Spring Creek National Fish Hatchery	2021	Spring Creek National Fish Hatchery	2021	Concordant	1
Fall	Umatilla Fish Hatchery	2018	Umatilla Fish Hatchery	2018	Concordant	2
Fall	Umatilla Fish Hatchery	2019	Priest Rapids Hatchery	2019	Concordant	3
Fall	Umatilla Fish Hatchery	2019	Ringold Springs State Hatchery	2019	Concordant	3
Fall	Umatilla Fish Hatchery	2020	Umatilla Fish Hatchery	2020	Concordant	2
Fall	Washougal Fish Hatchery	2019	Washougal Fish Hatchery	2019	Concordant	2
Fall	Willamette	2020	South Santiam Hatchery	2020	Concordant	1

Total	100.0%	226
Concordant	93.4%	211
Hatchery_Concordant	0.4%	1
BY_Concordant	5.3%	12
Discordant	0.9%	2
CWOnly_PBTFailed		30
CWOnly_PBT_Unassigned		29
PBT only		1710

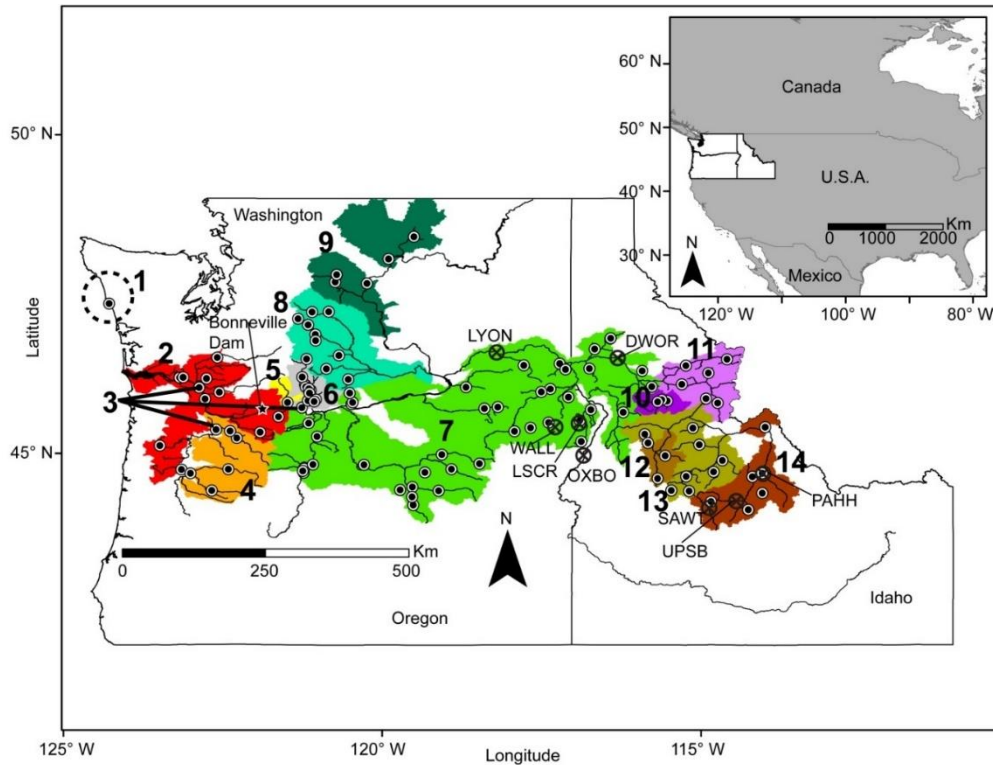
Note: \*Indicates that only the BY was concordant but these two samples in particular appear to have been switched. “Hatchery” under status indicates only the hatchery was concordant but not the BY. In some cases spawning hatcheries coordinate releases across multiple hatcheries and so in cases where 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.**



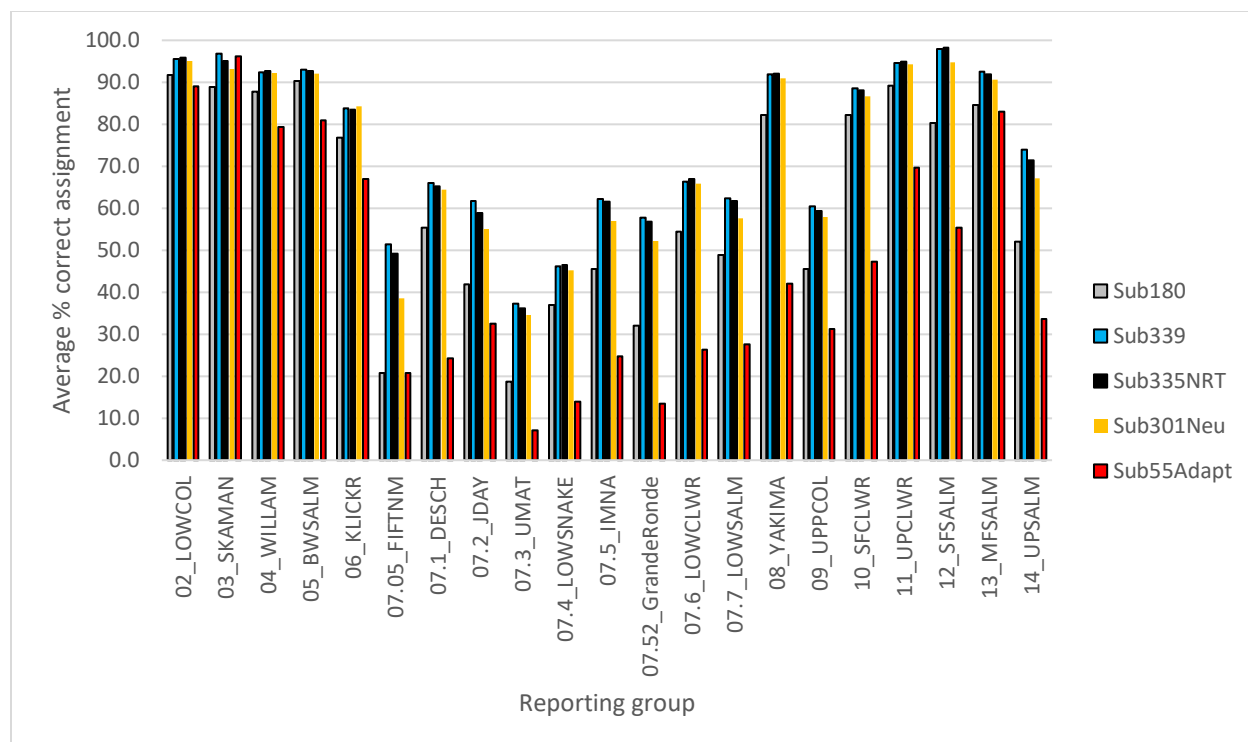
**Figure 20. Geographic distribution of collections represented in the Columbia River steelhead GSI and PBT genetic baselines.**

*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 21): 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 2023 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 (79%, Table 25).



**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 25. Comparison of PBT expected reporting groups versus the observed reporting groups using 177 SNPs (baseline 3.3) based on the assignments from the Bonneville 2023 mixture.**

PBT Expected GSI	Observed GSI						Total	%Correct
	03_SKAMAN	07_MGILCS	09_UPPCOL	10_SFCLWR	11_UPCLWR	14_UPSALM		
03_SKAMAN	15						15	100.0%
07_MGILCS	0	73	0	2		10	85	85.9%
09_UPPCOL		15	4			7	26	15.4%
10_SFCLWR				127			127	100.0%
14_UPSALM	0	16	2	6		88	112	78.6%
Grand Total	15	104	6	135	0	105	365	

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\_su20,21" and was spawned at the Pahsimeroi Hatchery. Removing these 6 fish recovers the "% Correct" assignment of this group to 83.0% 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 26). 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 ( $FDR = 6.6 \times 10^{-6}$ ) 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 26.** 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 and hatchery origin fish from Penticton Hatchery (348 SNPs)*

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 27). 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 (Table 27). This year we genotyped SY19 – 23 broodstocks from Penticton Hatchery; these additions and tag rates are shown in Table 28.

**Table 27. The numbers of candidate parents genotyped relative to the number of returning and translocated adult sockeye to the Yakima River each year.**

Year	Outplants	Prosser	Roza	O+P	O+R	Genotypes		Max YR	Tag rate	
						363	88		363	88
2009	1000	12	0	1012	1000	0	0	1012	0.0%	0.0%
2010	2500	11	40	2511	2540	0	0	2540	0.0%	0.0%
2011	4000	0	13	4000	4013	0	29	4013	0.0%	1.4%
2012	10000	47	154	10047	10154	985	985	10154	18.5%	18.5%
2013	4500	701	691	5201	5191	1168	1244	5201	39.9%	42.1%
2014	10000	2678	2576	12678	12576	2942	3146	12678	41.0%	43.5%
2015	10000	342	95	10342	10095	706	1182	10342	13.2%	21.6%
2016	10000	3742	3677	13742	13677	4633	4245	13742	56.1%	52.2%
2017	1000	372	375	1372	1375	426	422	1375	52.4%	52.0%
2018	4700	458	201	5158	4901	1377	1368	5158	46.3%	46.0%
2019	0	110	201	110	201	203	199	201	100.0%	100.0%
2020	10000	2549	4379	12549	14379	5895	-	14379	65.2%	
2021	2700	134	95	2834	2795	525	-	2834	33.6%	
2022	10000	157	510	10157	10510	1269	-	10510	22.7%	
2023	10000	104	424	10104	10424		-	10424	0.0%	

*Note: “Outplants” indicate the number of sockeye translocated into the Yakima River, and “Prosser” and “Roza” dam counts were summed (“O+P” or “O+R”) with the outplants to provide an estimate of the total escapement of spawners in the Yakima River each year. We used whichever number was greatest (“O+P” or “O+R”) to provide the maximum escapement of the Yakima River (“Max YR”). A portion of these spawners were successfully genotyped either using 363 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.*

**Table 28. The number of spawned individuals relative to the number of successfully genotyped adult Sockeye salmon from Penticton Hatchery that were used to develop the new PBT baseline.**

Year	Number of spawned individuals			Successful genotypes (348 SNPs)	Tag rate	
	Females	Males	Total		Single	Trio
2019	444	776	1220	410	56%	11.3%
2020	2377	2468	4845	959	36%	3.9%
2021	226	212	438	315	92%	51.7%
2022	2215	1607	3822	1028	47%	7.2%
2023	669	617	1286			

*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 29. Of the 3,649 harvested Chinook analyzed, there were 1,971 hatchery-origin individuals that could be confidently PBT assigned to 123 hatchery broodstock sources (i.e., 25 Lower Columbia, 5 Willamette, 30 Snake River, and 68 Columbia River hatchery broodstocks) spawned in 2017-2021. The majority of PBT assigned individuals (N=1326) were from the 2019 brood year (i.e., 4-years-old).

**Table 29. Summary of the Chinook salmon harvest samples by fishery, region, and fin clip in 2023.**

Fishery	Region	AdClip	Period			Analysis					
			Spring	Summer	Fall	GSI	PBT	duplicate	failed	Total	%PBT
Bon23	BONAFF	AD	1205	290	485	158	1801	3	18	1980	91.9%
		AI	417	152	1070	969	657	2	11	1639	40.4%
Test	B	AD	277			70	192		15	277	73.3%
		AI	38			27	7		4	38	20.6%
Sport	B	AD	188			51	120	2	15	188	70.2%
		AD	121			9	99	4	9	121	91.7%
Sport	01 (Zone 6)	AD	13				13			13	100.0%
	02 (Zone 6)	AD	77			3	60		14	77	95.2%
Sport	B	AD			63	9	46		8	63	83.6%
		AD			41	6	31	1	3	41	83.8%
Sport	02 (Zone 6)	AD			6	1	5			6	83.3%
Sport	B	AD		168		31	119		18	168	79.3%
		AI		318		185	92		41	318	33.2%
	A	AD		159		38	104	1	16	159	73.2%
		AI		511		321	157	16	17	511	32.8%
Sport	01 (Zone 6)	AD		166		33	118		15	166	78.1%
		AI		556		265	264	8	19	556	49.9%
	02 (Zone 6)	AD		79		6	65	1	7	79	91.5%
		AI		276		188	68		20	276	26.6%
Commercial	B	AD		3		1	2			3	66.7%
		AI		3		2	1			3	33.3%
	A	AD		334		36	283	1	14	334	88.7%
		AI		252		135	89		28	252	39.7%

## 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 83% (range = 67% – 100%, Table 29). The fishery(s) with the minimum and maximum assigned adipose-clipped Chinook salmon was the Non-Treaty commercial fishery in region B and the Non-Treaty Spring Zone 6 (region 01) Sport fishery, respectively. Among the adipose-intact fish, the average assignment via PBT was expectedly lower (average = 34%, range = 21% – 50%; Table 29). Among the fisheries with adipose-intact fish, the minimum and maximum PBT-assigned Chinook salmon was observed in the Spring Test fishery in (region B) and the Fall Sport fishery in Zone 6 (region 01), respectively.

### *The test fishery in the Chinook Salmon Spring Management Period of 2023*

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 22). 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.

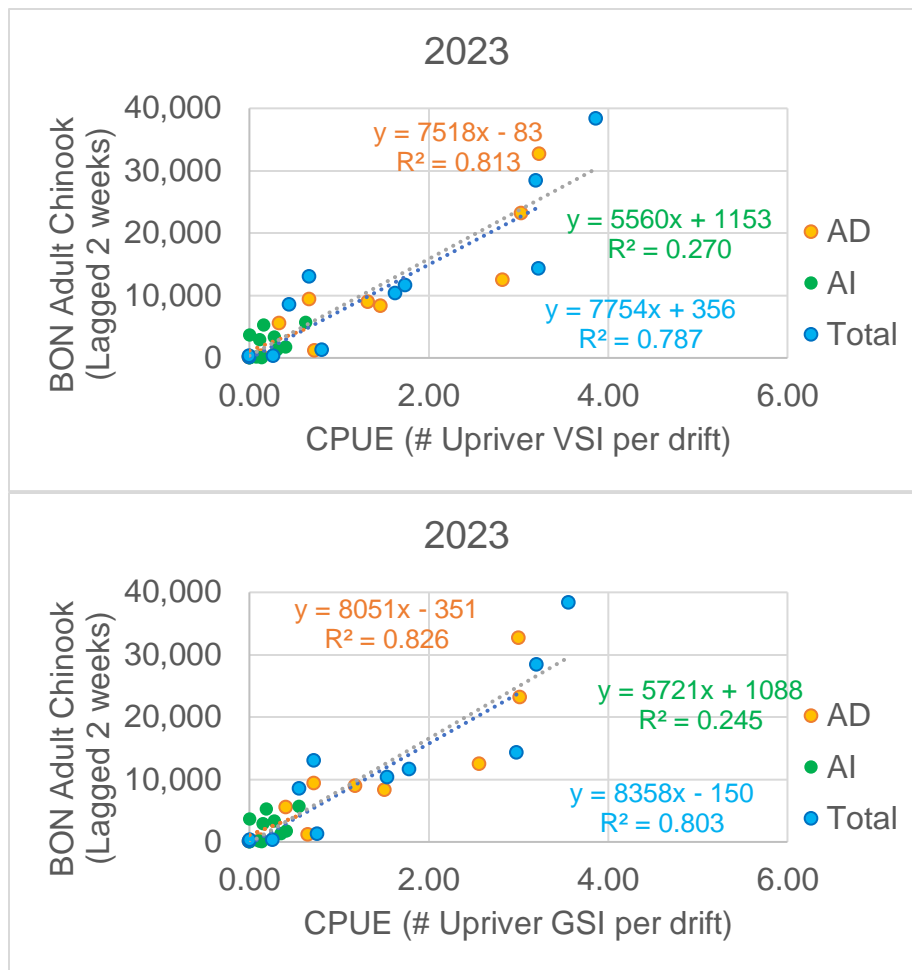
Here we show how the CPUE in the test fishery can be further resolved into finer stock units using genetic analysis and the reporting group level for the fish that had previously been only visually identified into two coarse level stocks, lower river and upriver (**Table 30**). The CPUE can be even resolved into finer units of hatchery broodstocks which could allow a high resolution of abundance prediction if this test fishery data were used in-season.

**Table 30. 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 2023 in units of catch-per-unit-effort (CPUE, # of fish per # of drifts).**

	GenStock	Lower (VSI)			Upriver (VSI)			Total
		H	HNC	W	H	HNC	W	
Lower	01_YOUNGS							0.0000
	02_WCASSP	1.9389			0.5459			2.4848
	03_WCASFA							0.0000
	04_WILLAM	5.4736		0.7565	0.4722		0.0789	6.7812
	Subtotal Lower							
Upriver	GenStock	7.4125	0.0000	0.7565	1.0181	0.0000	0.0789	9.2660
	05_SPCRTU							0.0000
	06_KLICKR	0.0000			0.0797			0.0797



07_DESCSP	0.0000			0.7098			0.7098
08_JOHNDR							0.0000
09_YAKIMA	0.0000		0.0000	0.1541		0.4229	0.5770
10_UCOLSP	0.0000	0.0000	0.0637	2.0540	0.2138	0.5547	2.8862
11_TUCANO							0.0000
12_HELLSC	0.1048	0.0815	0.0000	5.3647	0.2108	0.2720	6.0337
13_SFSALM	0.0000	0.0000		0.0787	0.0700		0.1487
14_CHMBLN							0.0000
15_MFSALM							0.0000
16_UPSALM	0.0000	0.0000	0.0000	0.5495	0.0704	0.2115	0.8313
17_DESCFA							0.0000
18_UCOLSF	0.3345			0.0000			0.3345
19_SRFALL							0.0000
20_BONPOOLSP	0.0876			3.4148			3.5025
21_UMATILLASP	0.0000			0.5673			0.5673
Subtotal Upriver GenStock	0.5270	0.0815	0.0637	12.9725	0.5649	1.4612	15.6707



**Figure 22. The relationship between the test fishery upriver Chinook Salmon CPUE and weekly fish counts at Bonneville Dam in 2023 with 2 week lag using VSI (top) and GSI (bottom) data.**

*The Non-Treaty sport fishery in the Chinook Salmon Spring Management Period of 2023*

We reported spring sport fishery results in the lower river below Bonneville Dam for reporting group level stock composition (Table 31) and the hatchery broodstock composition (Table 32) 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 33**) and broodstock units (**Table 34**) for the kept fish.

**Table 31. Summary of the stock composition at the reporting group level of the kept spring Chinook salmon in the Non-Treaty sport fishery of 2023 in units of reported catch.**

Run type	Reporting Group Code	Hatchery origin- Clipped	
		Estimated abundance	
		Mean	95% CI
Spring	01_YOUNGS		
Spring	02_WCASSP	386	207 – 563
Fall	03_WCASFA		
Spring	04_WILLAM	871	745 – 1022
Fall	05_SPCRTU		
Spring	06_KLICKR		
Spring	07_DESCSP	215	78 – 384
Spring	08_JOHNDR		
Spring	09_YAKIMA	73	18 – 160
Spring	10_UCOLSP	367	260 – 605
Spring	11_TUCANO		
Spring/Summer	12_HELLSC	1,304	1105 – 1651
Spring/Summer	13_SFSALM	402	199 – 570
Spring/Summer	14_CHMBLN		
Spring/Summer	15_MFSALM		
Spring/Summer	16_UPSALM	321	283 – 429
Fall	17_DESCFA		
Summer/Fall	18_UCOLSF	116	50 – 167
Fall	19_SRFALL		
Spring	20_BONPOOLSP	581	421 – 676
Spring	21_UMATILLASP	57	18 – 99
Fall	22_BONPOOLFA		
Fall	23_UMATILLAFA		
	<b>Total</b>	<b>4,691</b>	

**Table 32. Summary of the stock composition at the broodstock level of the kept adult spring Chinook salmon in the Non-Treaty sport fishery of 2023 in units of reported catch.**

Spring Sport Fishery 2023				Kept Adult Chinook AD			
Expected Run Time	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	GSI RepGrp
01Spring	Cowlitz Salmon Hatchery	OtsCOWL_seg_sp17	2017	13	0 – 39	0.3%	02_WCASSP
01Spring	Cowlitz Salmon Hatchery	OtsCOWL_seg_sp18	2018	29	0 – 71	0.6%	02_WCASSP
01Spring	Cowlitz Salmon Hatchery	OtsCOWL_seg_sp19	2019	19	0 – 57	0.4%	02_WCASSP
01Spring	Kalama Falls Hatchery	OtsKALA_seg_sp17	2017	12	0 – 37	0.3%	02_WCASSP
01Spring	Kalama Falls Hatchery	OtsKALA_seg_sp18	2018	185	72 – 322	4.0%	02_WCASSP
01Spring	Parkdale Fish Facility	OtsPARK_seg_sp19	2019	57	17 – 118	1.2%	02_WCASSP
01Spring	Speelyai Fish Hatchery	OtsSPEE_seg_sp17	2017	37	0 – 112	0.8%	02_WCASSP
01Spring	Speelyai Fish Hatchery	OtsSPEE_seg_sp19	2019	18	0 – 53	0.4%	02_WCASSP
01Spring	North Santiam Hatchery	OtsNSAN_seg_sp18	2018	88	18 – 162	1.9%	04_WILLAM
01Spring	South Santiam Hatchery	OtsSSAN_seg_sp18	2018	139	45 – 256	3.0%	04_WILLAM
01Spring	South Santiam Hatchery	OtsSSAN_seg_sp19	2019	106	24 – 201	2.3%	04_WILLAM
01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp19	2019	99	38 – 174	2.1%	07_DESCSP
01Spring	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp19	2019	116	43 – 212	2.5%	07_DESCSP
01Spring	Yakima River Roza Dam	OtsYRRD_int_sp19	2019	39	0 – 90	0.8%	09_YAKIMA
01Spring	Yakima River Roza Dam	OtsYRRD_seg_sp19	2019	34	0 – 69	0.7%	09_YAKIMA
01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp18	2018	77	0 – 194	1.7%	10_UCOLSP
01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp19	2019	203	108 – 300	4.3%	10_UCOLSP
01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp20	2020	18	0 – 54	0.4%	10_UCOLSP
01Spring	Winthrop National Fish Hatchery	OtsWINT_seg_sp19	2019	51	12 – 106	1.1%	10_UCOLSP
01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp19	2019	153	64 – 248	3.3%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsKOOS_seg_sp18	2018	23	0 – 68	0.5%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp19	2019	171	81 – 274	3.6%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsKOOS_seg_sp19	2019	109	41 – 200	2.3%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsLOOK_seg_sp19	2019	149	70 – 237	3.2%	12_HELLSC

01Spring	Nez Perce	OtsNPFH_seg_sp19	2019	67	22 – 134	1.4%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp18	2018	48	0 – 97	1.0%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp19	2019	541	382 – 703	11.5%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp20	2020	17	0 – 52	0.4%	12_HELLSC
01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp19	2019	139	56 – 230	3.0%	20_BONPOOLSP
01Spring	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp18	2018	23	0 – 68	0.5%	20_BONPOOLSP
01Spring	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp19	2019	419	274 – 568	8.9%	20_BONPOOLSP
01Spring	Umatilla Fish Hatchery	OtsUMAT_seg_sp19	2019	57	17 – 118	1.2%	21_UMATILLASP
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss19	2019	402	280 – 525	8.6%	13_SFSALM
02Spring/Summer	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss19	2019	86	34 – 154	1.8%	16_UPSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss19	2019	193	106 – 281	4.1%	16_UPSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss20	2020	17	0 – 52	0.4%	16_UPSALM
03Summer	Chief Joseph Hatchery	OtsCHJO_int_su19	2019	17	0 – 52	0.4%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su18	2018	34	0 – 86	0.7%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su18	2018	21	0 – 62	0.4%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su19	2019	17	0 – 51	0.4%	18_UCOLSF
#N/A	#N/A	Unassigned	#N/A	646	415 – 872	13.8%	#N/A
TOTAL				4,691	100.0%		

**Table 33. 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 2023 in units of reported catch.**

Run type	Reporting Group Code	Hatchery origin- Clipped	
		Estimated abundance	
		Mean	95% CI
Spring	01_YOUNGS		
Spring	02_WCASSP	16	0 – 63
Fall	03_WCASFA		
Spring	04_WILLAM		
Fall	05_SPCRTU		

Spring	06_KLICKR		
Spring	07_DESCSP	35	0 – 100
Spring	08_JOHNDR		
Spring	09_YAKIMA		
Spring	10_UCOLSP	214	106 – 382
Spring	11_TUCANO		
Spring/Summer	12_HELLSC	666	510 – 839
Spring/Summer	13_SFSALM		
Spring/Summer	14_CHMBLN		
Spring/Summer	15_MFSALM		
Spring/Summer	16_UPSALM	16	0 – 80
Fall	17_DESCFA		
Summer/Fall	18_UCOLSF		
Fall	19_SRFALL		
Spring	20_BONPOOLSP	65	8 – 137
Spring	21_UMATILLASP	48	0 – 119
Fall	22_BONPOOLFA		
Fall	23_UMATILLAFA		
	<b>Total</b>	<b>1,059</b>	

**Table 34. 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 2023 in units of reported catch**

Spring Zone 6 Sport Fishery 2023				Kept Adult Chinook AD			
Expected Run Time	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	GSI RepGrp
01Spring	Parkdale Fish Facility	OtsPARK_seg_sp19	2019	16	0 – 48	1.5%	02_WCASSP
01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp19	2019	17	0 – 52	1.6%	07_DESCSP
01Spring	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp19	2019	18	0 – 53	1.7%	07_DESCSP
01Spring	Chief Joseph Hatchery	OtsCHJO_seg_sp19	2019	19	0 – 54	1.8%	10_UCOLSP
01Spring	Eastbank Fish Hatchery	OtsEAST_seg_sp19	2019	17	0 – 51	1.6%	10_UCOLSP

01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp19	2019	159	80 – 239	15.1%	10_UCOLSP
01Spring	Winthrop National Fish Hatchery	OtsWINT_seg_sp19	2019	16	0 – 47	1.5%	10_UCOLSP
01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp18	2018	16	0 – 48	1.5%	12_HELLSC
01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp19	2019	31	0 – 62	2.9%	12_HELLSC
01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp20	2020	16	0 – 47	1.5%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp18	2018	16	0 – 49	1.6%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsKOOS_seg_sp19	2019	66	17 – 125	6.3%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp19	2019	78	31 – 140	7.4%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsLOOK_seg_sp19	2019	32	0 – 64	3.0%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp18	2018	18	0 – 52	1.7%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp19	2019	376	277 – 475	35.5%	12_HELLSC
01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp19	2019	32	0 – 64	3.0%	20_BONPOOLSP
01Spring	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp19	2019	33	0 – 65	3.1%	20_BONPOOLSP
01Spring	Umatilla Fish Hatchery	OtsUMAT_seg_sp19	2019	48	0 – 96	4.5%	21_UMATILLASP
02Spring/Summer	Lookingglass Fish Hatchery	OtsIMNW_seg_ss19	2019	16	0 – 48	1.5%	12_HELLSC
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss19	2019	16	0 – 48	1.5%	16_UPSALM
#N/A	#N/A	Unassigned	#N/A	2	0 – 51	0.2%	#N/A
		TOTAL	1,059		100.0%		

*The Non-Treaty sport fishery in the Chinook Salmon Summer Management Period of 2023*

In 2023, 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 35) and the hatchery broodstock composition (Table 36) of the kept fish (clipped hatchery-origin fish).

**Table 35. Summary of the stock composition at the reporting group level of the kept summer Chinook salmon in the Non-Treaty sport fishery of 2023 in units of reported catch.**

Run type	Reporting Group Code	Hatchery origin- Clipped	
		Estimated abundance	
		Mean	95% CI
Spring	01_YOUNGS		
Spring	02_WCASSP	27	0 – 133
Fall	03_WCASFA		
Spring	04_WILLAM	252	208 – 394
Fall	05_SPCRTU		
Spring	06_KLICKR		
Spring	07_DESCSP		
Spring	08_JOHNDR		
Spring	09_YAKIMA	24	0 – 70
Spring	10_UCOLSP	26	0 – 51
Spring	11_TUCANO		
Spring/Summer	12_HELLSC	24	0 – 72
Spring/Summer	13_SFSALM	94	47 – 208
Spring/Summer	14_CHMBLN		
Spring/Summer	15_MFSALM		
Spring/Summer	16_UPSALM	71	2 – 141
Fall	17_DESCFA		
Summer/Fall	18_UCOLSF	1,476	1290 – 1572
Fall	19_SRFALL		



Spring	20_BONPOOLSP	24	0 – 71
Spring	21_UMATILLASP		
Fall	22_BONPOOLFA		
Fall	23_UMATILLAFA		
<b>Total</b>		<b>2,019</b>	

**Table 36. Summary of the stock composition at the broodstock level of the kept adult summer Chinook salmon in the Non-Treaty sport fishery of 2023 in units of reported catch.**

Summer Sport Fishery 2023				Kept Adult Chinook AD			
Expected Run Time	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	GSI RepGrp
01Spring	Kalama Falls Hatchery	OtsKALA_seg_sp19	2019	27	0 – 82	1.4%	02_WCASSP
01Spring	North Santiam Hatchery	OtsNSAN_seg_sp18	2018	36	0 – 108	1.8%	04_WILLAM
01Spring	South Santiam Hatchery	OtsSSAN_seg_sp18	2018	88	0 – 175	4.3%	04_WILLAM
01Spring	South Santiam Hatchery	OtsSSAN_seg_sp19	2019	65	0 – 163	3.2%	04_WILLAM
01Spring	Yakima River Roza Dam	OtsYRRD_int_sp20	2020	24	0 – 71	1.2%	09_YAKIMA
01Spring	Eastbank Fish Hatchery	OtsEAST_seg_sp19	2019	26	0 – 79	1.3%	10_UCOLSP
01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp19	2019	24	0 – 72	1.2%	20_BONPOOLSP
02Spring/Summer	Lookingglass Fish Hatchery	OtsIMNW_seg_ss19	2019	24	0 – 73	1.2%	12_HELLSC
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss19	2019	72	24 – 145	3.6%	13_SFSALM
02Spring/Summer	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss19	2019	24	0 – 71	1.2%	16_UPSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss20	2020	47	0 – 119	2.3%	16_UPSALM
03Summer	Chief Joseph Hatchery	OtsCHJO_int_su19	2019	72	24 – 144	3.6%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su18	2018	568	426 – 734	28.1%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su19	2019	141	47 – 235	7.0%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su17	2017	28	0 – 84	1.4%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su18	2018	246	123 – 400	12.2%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su19	2019	50	0 – 100	2.5%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su20	2020	26	0 – 77	1.3%	18_UCOLSF

03Summer	Wells Fish Hatchery	OtsWELL_seg_su18	2018	86	29 – 172	4.2%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su19	2019	141	47 – 235	7.0%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELL_seg_su20	2020	24	0 – 72	1.2%	18_UCOLSF
#N/A	#N/A	Unassigned	#N/A	179	28 – 345	8.9%	#N/A
		TOTAL	2,019		100.0%		

*The Non-Treaty sport fishery in the Chinook Salmon Fall Management Period of 2023*

The 2023 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 37). We also reported the broodstock composition of the hatchery-origin Chinook salmon (Table 38). In 2023, 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 39, Table 40).

**Table 37. 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 2023 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					31	0 – 93
West Cascade Spring	Spring	02_WCASSP					144	62 – 247
West Cascade Fall	Fall	03_WCASFA	869	679 – 1020	141	80 – 286	1540	1234 – 1885
Willamette	Spring	04_WILLAM	144	62 – 246			159	72 – 262
Spring Creek Tule	Fall	05_SPCRTU	1113	856 – 1275	589	409 – 891	30	0 – 104
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	57	11 – 122			206	92 – 339

Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	3571	3205 – 4259	4191	3738 – 4763	8647	7956 – 9353
Snake River fall	Fall	19_SRFALL	755	600 – 987	966	805 – 1347	2091	1663 – 2487
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	568	242 – 815	1289	1098 – 1749		
Umatilla fall	Fall	23_UMATILLAFA	214	100 – 332	92	0 – 193		
<b>Total</b>			<b>7,290</b>		<b>7,268</b>		<b>12,848</b>	

**Table 38. 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 2023 in units of reported catch.**

Fall Sport Fishery 2023				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_sp19	2019	28	0 – 85	0.4%			0.0%	04_WILLAM
01Spring	South Santiam Hatchery	OtsSSAN_seg_sp20	2020	41	0 – 124	0.6%			0.0%	04_WILLAM
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su18	2018	21	0 – 62	0.3%			0.0%	18_UCOLSF
04Fall	Cowlitz Salmon Hatchery	OtsCOWL_seg_fa19	2019	55	0 – 133	0.8%			0.0%	03_WCASFA
04Fall	Cowlitz Salmon Hatchery	OtsCOWL_seg_fa20	2020	44	0 – 131	0.6%			0.0%	03_WCASFA
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa18	2018	48	0 – 120	0.7%			0.0%	03_WCASFA
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa19	2019	323	168 – 478	4.4%	26	0 – 78	0.4%	03_WCASFA
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa20	2020	167	72 – 286	2.3%	72	0 – 143	1.0%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa19	2019	129	0 – 259	1.8%	43	0 – 129	0.6%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa20	2020	43	0 – 128	0.6%			0.0%	03_WCASFA
04Fall	Bonneville Dam Hatchery	OtsBONN_seg_fa19	2019	272	91 – 472	3.7%			0.0%	05_SPCRTU
04Fall	Bonneville Dam Hatchery	OtsBONN_seg_fa20	2020	31	0 – 93	0.4%	31	0 – 93	0.4%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	2019	102	0 – 204	1.4%	363	204 – 544	5.0%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa20	2020	545	350 – 751	7.5%	195	82 – 319	2.7%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa21	2021	56	0 – 123	0.8%			0.0%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa18	2018	131	36 – 251	1.8%	191	72 – 322	2.6%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa19	2019	1989	1615 – 2386	27.3%	3016	2577 – 3498	41.5%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa20	2020	732	483 – 1022	10.0%	897	580 – 1229	12.3%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa21	#N/A	46	0 – 138	0.6%			0.0%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa17	2017	33	0 – 99	0.5%			0.0%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa19	2019	182	64 – 321	2.5%	54	0 – 118	0.7%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa20	2020	34	0 – 101	0.5%			0.0%	18_UCOLSF
04Fall	Yakima Nation Prosser Hatchery	OtsPROS_seg_fa20	2020			0.0%	32	0 – 97	0.4%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	2018	26	0 – 77	0.3%	38	0 – 115	0.5%	19_SRFALL

04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa19	2019	503	321 – 686	6.9%	675	460 – 900	9.3%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa20	2020	31	0 – 94	0.4%	114	42 – 218	1.6%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	2018	25	0 – 76	0.3%			0.0%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa19	2019			0.0%	74	21 – 149	1.0%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa20	2020			0.0%	64	0 – 128	0.9%	19_SRFALL
04Fall	Klickitat Hatchery	OtsKLIC_seg_fa18	2018			0.0%	57	0 – 171	0.8%	22_BONPOOLFA
04Fall	Klickitat Hatchery	OtsKLIC_seg_fa19	2019			0.0%	109	0 – 273	1.5%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	2018	42	0 – 127	0.6%	84	0 – 169	1.2%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa19	2019	401	236 – 576	5.5%	1008	751 – 1285	13.9%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa20	2020	93	31 – 186	1.3%	31	0 – 93	0.4%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa21	2021	31	0 – 94	0.4%			0.0%	22_BONPOOLFA
04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	2018	75	0 – 151	1.0%			0.0%	23_UMATILLFA
04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa20	2020	139	35 – 277	1.9%	92	23 – 196	1.3%	23_UMATILLFA
#N/A	#N/A	Unassigned	#N/A	872	482 – 1240	12.0%			0.0%	#N/A
TOTAL				7,290		100.0%	7,268		100.0%	

**Table 39. 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 2023 in units of reported catch.**

Reporting Group name	Run type	Reporting Group Code	Hatchery origin- Clipped		Hatchery origin- No Clip		Natural origin- No Clip	
			H		HNC		W	
			Est.	95% CI	Est.	95% CI	Est.	95% CI
Youngs Bay	Spring	01_YOUNGS						
West Cascade Spring	Spring	02_WCASSP						
West Cascade Fall	Fall	03_WCASFA					53	18 – 106
Willamette	Spring	04_WILLAM						
Spring Creek Tule	Fall	05_SPCRTU	582	370 – 759	245	85 – 388	72	16 – 139
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					194	106 – 300
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	1523	1079 – 1895	3450	2940 – 3930	4924	4490 – 5328
Snake River fall	Fall	19_SRFALL	624	438 – 845	751	501 – 982	1136	911 – 1373
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	591	354 – 824	1525	1082 – 2028		
Umatilla fall	Fall	23_UMATILLAFA	262	148 – 483	58	0 – 166		
<b>Total</b>			<b>3,583</b>		<b>6,030</b>		<b>6,379</b>	

**Table 40. 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 2023 in units of reported catch.**

Fall Sport BON Fishery 2023				Adult Chinook AD			Adult Chinook AI			
Expected Run Time	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	MLE	95% CI	Percent	GSI RepGrp
03Summer	Chief Joseph Hatchery	OtsCHJO_int_su17	2017	23	0 – 70	0.7%			0.0%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su18	2018	18	0 – 53	0.5%			0.0%	18_UCOLSF
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	2019	78	19 – 136	2.2%	58	19 – 117	1.0%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa20	2020	388	265 – 530	10.8%	53	18 – 106	0.9%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa21	2021			0.0%	134	57 – 211	2.2%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa18	2018	20	0 – 61	0.6%	41	0 – 82	0.7%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa19	2019	881	679 – 1083	24.6%	2845	2497 – 3213	47.2%	18_UCOLSF

04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa20	2020	403	261 – 569	11.2%	545	379 – 734	9.0%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa19	2019	18	0 – 55	0.5%			0.0%	18_UCOLSF
04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa20	2020	19	0 – 58	0.5%			0.0%	18_UCOLSF
04Fall	Yakima Nation Prosser Hatchery	OtsPROS_seg_fa20	2020	19	0 – 56	0.5%	19	0 – 56	0.3%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	2018	88	22 – 153	2.4%	22	0 – 66	0.4%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa19	2019	239	147 – 349	6.7%	460	331 – 625	7.6%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa20	2020	143	71 – 232	4.0%	178	89 – 285	3.0%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	2018	22	0 – 65	0.6%			0.0%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa19	2019	18	0 – 55	0.5%	36	0 – 73	0.6%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa20	2020			0.0%	55	18 – 110	0.9%	19_SRFALL
04Fall	Klickitat Hatchery	OtsKLIC_seg_fa19	2019			0.0%	219	94 – 375	3.6%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	2018	97	24 – 169	2.7%			0.0%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa19	2019	371	247 – 495	10.3%	1253	1006 – 1500	20.8%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa20	2020	124	53 – 213	3.5%	53	18 – 106	0.9%	22_BONPOOLFA
04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	2018	92	37 – 166	2.6%	18	0 – 55	0.3%	23_UMATILLAFA
04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa19	2019	71	18 – 124	2.0%			0.0%	23_UMATILLAFA
04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa20	2020	99	39 – 178	2.8%	40	0 – 99	0.7%	23_UMATILLAFA
#N/A	#N/A	Unassigned	#N/A	353	189 – 517	9.8%			0.0%	#N/A
		TOTAL		3,583		100.00%	6,030		100.00%	

### *The Non-Treaty commercial fishery in the Chinook Salmon Fall Management Period of 2023*

The fall Non-Treaty commercial fishery is shown by the composition of the combined adult and jack harvest using reporting group level (Table 41) and broodstock level (Table 42) 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 41. 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 2023 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					44	0 – 132
West Cascade Fall	Fall	03_WCASFA	547	227 – 1114			976	528 – 1479
Willamette	Spring	04_WILLAM	86	0 – 207			483	264 – 747
Spring Creek Tule	Fall	05_SPCRTU	10956	9448 – 12244	1828	1349 – 2652	929	468 – 1404
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					448	137 – 805
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	2127	1435 – 3304	2734	1865 – 3342	6809	5692 – 8059
Snake River fall	Fall	19_SRFALL	967	807 – 1211	1848	1482 – 2010	1075	579 – 1562
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	951	258 – 1146	894	357 – 1378		
Umatilla fall	Fall	23_UMATILLAFA	95	0 – 186	134	0 – 267		
<b>Total</b>			<b>15,730</b>		<b>7,438</b>		<b>10,764</b>	

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.

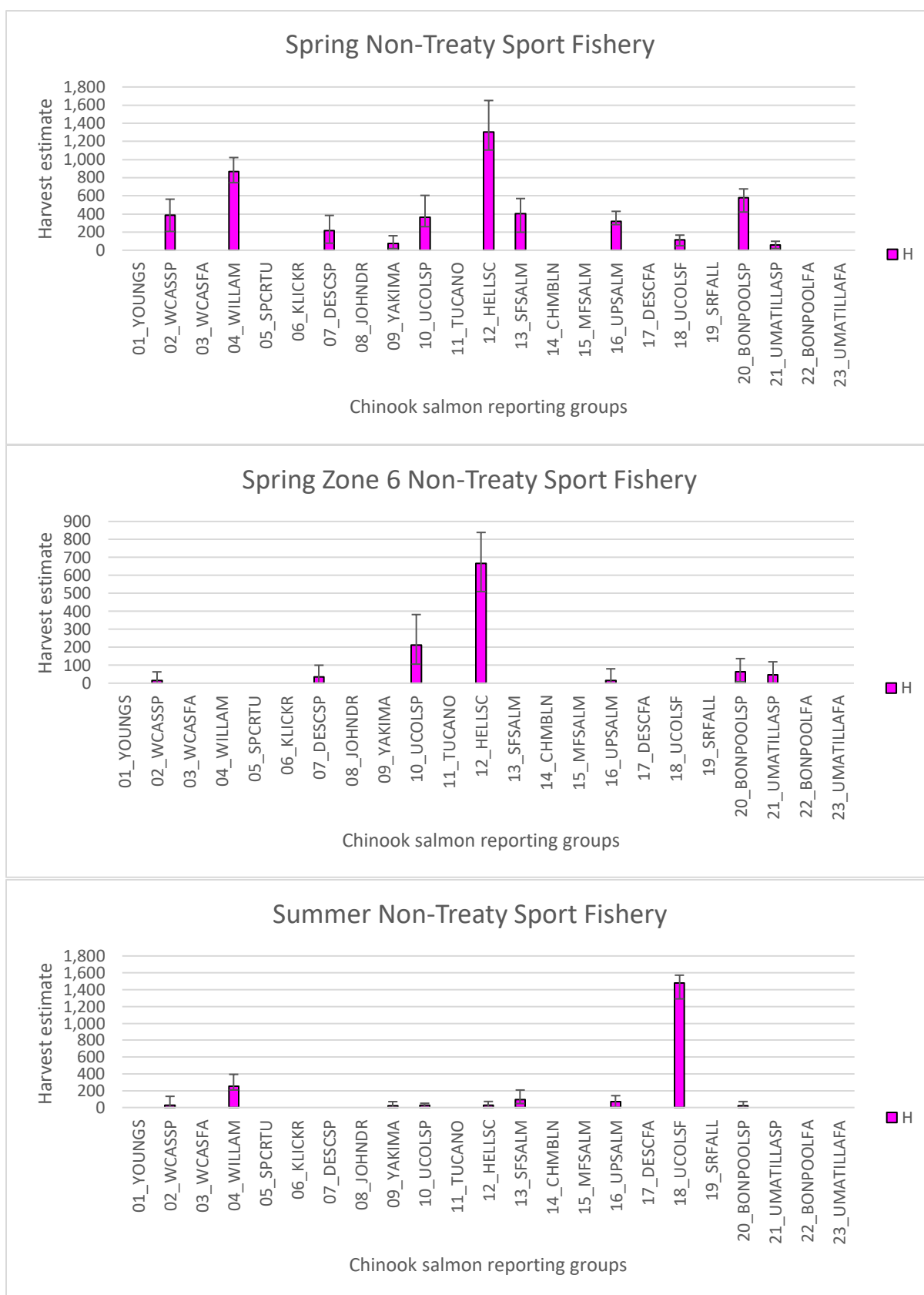
**Table 42. Summary of the stock composition at the broodstock level of the adult and jack Chinook salmon of the fall Non-Treaty commercial fishery below Bonneville Dam in 2023 in units of reported catch.**

Fall Commercial Fishery 2023				Adult/jack Chinook AD			Adult/jack Chinook AI			
Run	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	MLE	95% CI	Percent	GSI RepGrp
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa18	2018	51	0 – 154	0.3%			0.0%	03_WCASFA
04Fall	Kalama Falls Hatchery	OtsKALA_seg_fa19	2019	166	55 – 332	1.1%			0.0%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWASH_seg_fa19	2019	200	0 – 600	1.3%			0.0%	03_WCASFA
04Fall	Bonneville Dam Hatchery	OtsBONN_seg_fa19	2019	645	229 – 1149	4.1%			0.0%	05_SPCRTU
04Fall	Bonneville Dam Hatchery	OtsBONN_seg_fa20	2020	517	229 – 858	3.3%	44	0 – 133	0.6%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa18	2018	95	0 – 286	0.6%			0.0%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	2019	1742	1131 – 2440	11.1%	1127	622 – 1738	15.2%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa20	2020	7025	5944 – 8135	44.7%	506	227 – 835	6.8%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa21	2021			0.0%	151	0 – 358	2.0%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa18	2018	162	0 – 383	1.0%			0.0%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa19	2019	1402	871 – 2057	8.9%	2434	1596 – 3253	32.7%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa20	2020	344	0 – 746	2.2%	300	0 – 687	4.0%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	2018	55	0 – 164	0.3%	55	0 – 164	0.7%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa19	2019	771	382 – 1168	4.9%	1497	962 – 2077	20.1%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa20	2020	96	0 – 289	0.6%			0.0%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	2018			0.0%	108	0 – 217	1.5%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa19	2019	45	0 – 136	0.3%	189	45 – 422	2.5%	19_SRFALL
04Fall	Klickitat Hatchery	OtsKLIC_seg_fa19	2019			0.0%	169	0 – 506	2.3%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	2018	130	0 – 391	0.8%			0.0%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa19	2019	820	374 – 1341	5.2%	725	304 – 1204	9.7%	22_BONPOOLFA
04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	2018			0.0%	134	0 – 401	1.8%	23_UMATILLFA
04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa19	2019	95	0 – 286	0.6%			0.0%	23_UMATILLFA

#N/A	#N/A	Unassigned	#N/A	1367	641 – 2171	8.7%			0.0%	#N/A
		TOTAL		15,730		100.0%	7,438		100.0%	

*Comparison of stock composition of the clipped Chinook salmon stocks among spring-and summer-management period Chinook salmon sport fisheries in 2023*

The stock composition varied in expected ways across the Non-Treaty sport fisheries that were executed in the spring versus summer period (Figure 23). The largest difference in stock compositions across the spring and summer fisheries was the estimate of upper Columbia summer-run stock (18\_UCOLSF) which tends to be higher in the summer period compared to the spring period for the sport fishery (Figure 23). There can also be differences in the capture of Willamette River stock (04\_WILLAM) below Bonneville Dam compared to Zone 6 because the stock does not typically pass upstream of the dam in high numbers in the spring period. The 2023 harvest year showed both of these typical patterns. Deviations in these patterns sometimes occurs 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).

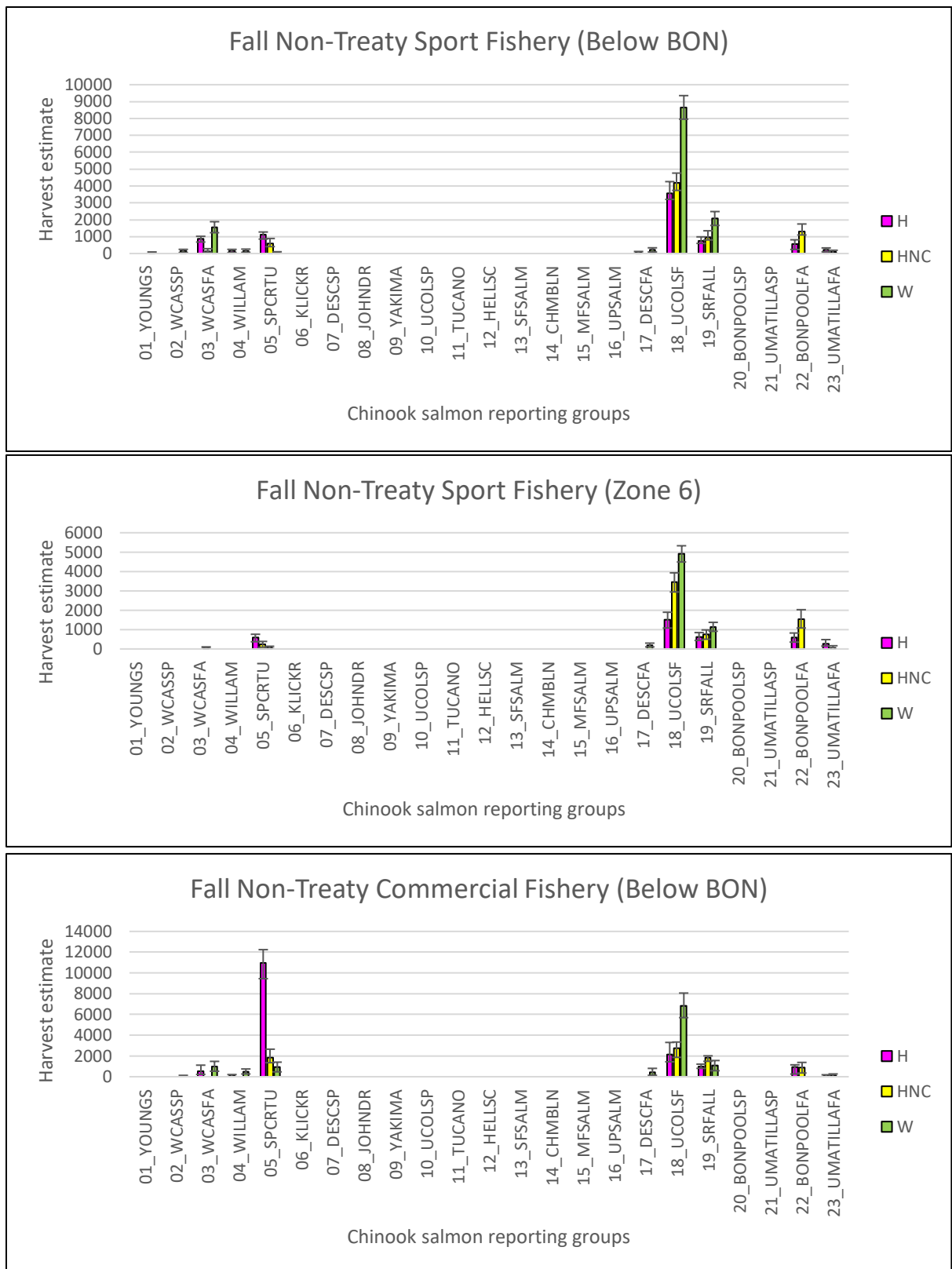


**Figure 23. Stock composition of spring and summer management period Chinook salmon harvest mixtures in 2023.**

*Comparison of stock composition of the clipped and unclipped Chinook salmon stocks among the Non-Treaty fall-management period fisheries in 2023*

The primary stock that distinguished the composition of the various Non-Treaty fall fisheries was the “tule” (05\_SPCRTU) stock (Figure 24). 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 compared to the Zone 6 sport fishery in the Bonneville Pool, and bright stocks were similarly found across both sport and commercial fisheries (Figure 24). 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).

We continue to find that despite both the Non-Treaty sport (above Bonneville, Figure 24) and commercial fishery (region A, Figure 24) being executed at similar times near Bonneville Dam, the sport fishery is comprised of dramatically lower abundance of “tules”. This difference may be largely due to sport fishers preferentially keeping the VSI bright fish over the tule fish.



**Figure 24. Genetic stock composition of the Fall Non-Treaty Chinook salmon fisheries analyzed in 2023.**

### *Comparison of stock composition among sockeye salmon fisheries from 2023*

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 43). 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 43).

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 43). In 2023, the stock proportions in the fishery deviated slightly from those estimated at Bonneville Dam. For example, Okanogan stock was 55% at Bonneville Dam compared to 62% in the fishery; Wenatchee stock was 44% at Bonneville Dam compared to 29% in the fishery; the Snake River stock was 1 % at Bonneville Dam compared to 9% in the fishery; and the Yakima reintroduced stock was close to 0% at Bonneville Dam and the fishery (Table 43). The 95% confidence intervals for all stock abundances in the Non-Treaty sport fishery were also estimated (Table 44). Despite small sample size for this fishery, our estimates captured a stock that typically has low abundance, Snake River stock.



**Table 43. Comparison of stock-specific abundance and percent composition among sockeye salmon fisheries. The mean stock abundance estimate is provided for each fishery harvest in 2023.**

Mixture source	Mean						Stock proportion					
	Okanogan	Wenatchee	Snake	LBC	Yakima	other	Okanogan	Wenatchee	Snake	LBC	Yakima	other
<b>Sport</b>	852	393	120	0	0	0	62.40%	28.80%	8.80%	0.00%	0.00%	0.00%
<b>Total Harvest</b>	852	393	120	0	0	0	62.40%	28.80%	8.80%	0.00%	0.00%	0.00%
<b>Bonneville Dam</b>	178,796	144,914	3,149	73	669	0	54.58%	44.23%	0.96%	0.02%	0.20%	0.00%

**Table 44. The reporting group composition of the Non-Treaty Sport Sockeye salmon fishery in 2023.**

Reporting Group name	Hatchery origin- Clipped		Reintroduction- No Clip		Natural origin- No Clip	
	Estimated abundance		Estimated abundance		Estimated abundance	
	Mean	95% CI	Mean	95% CI	Mean	95% CI
Okanogan					852	753 – 950
Wenatchee					393	295 – 480
Snake	66	22 – 109			55	22 – 98
Lake Billy Chinook						
Yakima						
Total	66		0		1299	

**Table 45. The reporting group composition of the Zone 6 Treaty Coho salmon fishery in 2023.**

	Hatchery origin- Clipped		Hatchery- No Clip		Natural origin- No Clip	
Reporting Group name	Estimated abundance		Estimated abundance		Estimated abundance	
	Mean	95% CI	Mean	95% CI	Mean	95% CI
OkiLNFH20			2102	1519 – 2696		
OkiNPT20	129	37 – 257	4454	3654 – 5178		
OkiNPT21			38	0 – 114		
OkiPRO20			759	403 – 1171		
OkiUMA20	627	290 – 1006	222	65 – 417		
OkiWTP20	38	0 – 113	1991	1443 – 2592		
Unassigned	5164	4365 – 6012			2254	1611 – 2949
Total	5958		9567		2254	

## *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 eleventh year in which we were able to assign all three major age classes of spring Chinook from Snake River hatcheries and the seventh 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 12th 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 expanded the baseline to now include Penticton Hatchery and the full baseline was completed through SY2022. In the future we can utilize this baseline to analyze both the reintroduced Yakima River stock and the hatchery stock from Penticton. 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 2023 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. Coho salmon is a new addition to the number of species we can analyze in the Columbia River fisheries. This is the first year we have analyzed the Treaty Zone 6 commercial Coho salmon fishery and intend to continue this analysis in the future to help determine hatchery- vs natural-origin stock proportions.

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 (SCOBIDEUX and SPIBETR programs, Delomas and Hess 2020) that are now available to perform tag rate expansions and balance those expansions by proportionally decreasing other stocks in the natural-origin category.

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

**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 2023, 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 2023 year of analysis of the sockeye salmon harvest in this current report. The 2023 Non-treaty sport fishery harvested slightly different composition of stocks compared to Bonneville Dam, which is typical across years although proportions do not always favor one particular stock. 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 2023 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. 25<sup>th</sup>), fork length (e.g., by definition, B-run fish are  $\geq 78$  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 2023. 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 2024 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 2024, 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 46 for the number and timing of reports for each species and run that were delivered in-season and post-season in 2024). 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 to serve as a placeholder for potential continuation of this effort in the future.

This is the first report where we document development of the mobile laboratory. We designed an innovative monitoring program intended to provide real-time genetic stock assessment of salmonids from priority fisheries during critical migration, spawning, and harvest periods. We developed a mobile laboratory where receipt of tissues, completed genotypes, and final PBT and GSI analyses are intended to be completed within a 24-hour period, providing the most up-to-date genetic assignments for monitoring trends across stocks in the Columbia River and its tributaries. This tool will help assess individuals from key migration and spawning sites by utilizing a mobile genetics laboratory. Designed in a custom trailer, the mobile laboratory will be fully equipped to process DNA samples from tissue collection through genotype, and results will be distributed to conservation managers in real time. Further, the laboratory will have the potential to run entirely off grid, providing capacity at remote sites where energy, power, and network settings may be otherwise prohibitive. The laboratory trailer has been designed and is in the final stages of approval before construction begins. Additionally, background research on DNA sequencing technologies capable of withstanding regular movement from site to site has been completed, and Illumina's MiSeq i100 Plus system has been identified as the optimal available platform to operate in the mobile lab setting. We plan to utilize this tool beginning with a series of preliminary deployments starting in late spring 2025.

#### **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 11<sup>th</sup> 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 9th year in which these can be assigned to some Columbia River hatcheries. This is the sixth 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 2025 features the final analyses of 2023, as well as the preliminary in-season and post-season analyses of 2024. 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 46. The in-season and post-season report timing and scope of the 2024 fish runs.**

Species	Management Period	Data coverage	Samples Arrive	Analysis begins	Report distributed
Chinook	Spring	01/01/2024 – 05/04/2024	5/6/2024	5/9/2024	5/13/2024
		01/01/2024 – 05/18/2024	5/20/2024	5/23/2024	5/27/2024
		01/01/2024 – 06/01/2024	6/3/2024	6/6/2024	6/10/2024
		01/01/2024 – 06/15/2024	6/17/2024	6/20/2024	6/24/2024
	Summer	06/16/2024 – 07/06/2024	7/8/2024	7/11/2024	7/12/2024
		06/16/2024 – 07/31/2024	8/5/2024	8/8/2024	8/12/2024
	Fall	08/01/2024 – 8/31/2024	9/2/2024	9/5/2024	9/9/2024
		08/01/2024 – 11/02/2024	11/4/2024	11/7/2024	11/11/2024
	Skamania	04/01/2024 – 06/30/2024	7/8/2024	7/11/2024	7/12/2024
Steelhead	Summer A-/B-Index	07/01/2024 – 08/04/2024	8/5/2024	8/8/2024	8/12/2024
		07/01/2024 – 09/01/2024	9/2/2024	9/5/2024	9/9/2024
		07/01/2024 – 10/31/2024	11/4/2024	11/7/2024	11/11/2024
Sockeye	Total	01/01/2024 – 08/03/2024	8/5/2024	8/8/2024	8/12/2024

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=561), Chinook (n=3,288), sockeye salmon (n=1,108) in 2023, 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 (04/23/23) and was completed on 10/14/23 (statistical week 41). Sampling occurred at the Adult

Fish Facility (AFF) located on the northern end of Bonneville Dam. Fish were sampled 4–5 d per statistical week (except when reduced due to restrictions on trap use or low run size at the beginning and end of the run) and for 4–6 h per day. A picket weir was used to divert migrating fish ascending the Washington shore fish ladder into the AFF collection pool. An attraction flow was used to draw fish through a false weir where they were selected for sampling. After sampling was completed and fish recovered from the anesthetic, they were returned to the Washington shore fish ladder above the picket weir. A small portion of the adult Chinook salmon run was missed prior to the statistical week in which sampling was initiated by April 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 2023. 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 2023 (Figure 25), 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 2023 for the spring and summer management periods was 1.0%, whereas the average sample rate for adult fall Chinook was 0.5% (Table 47).

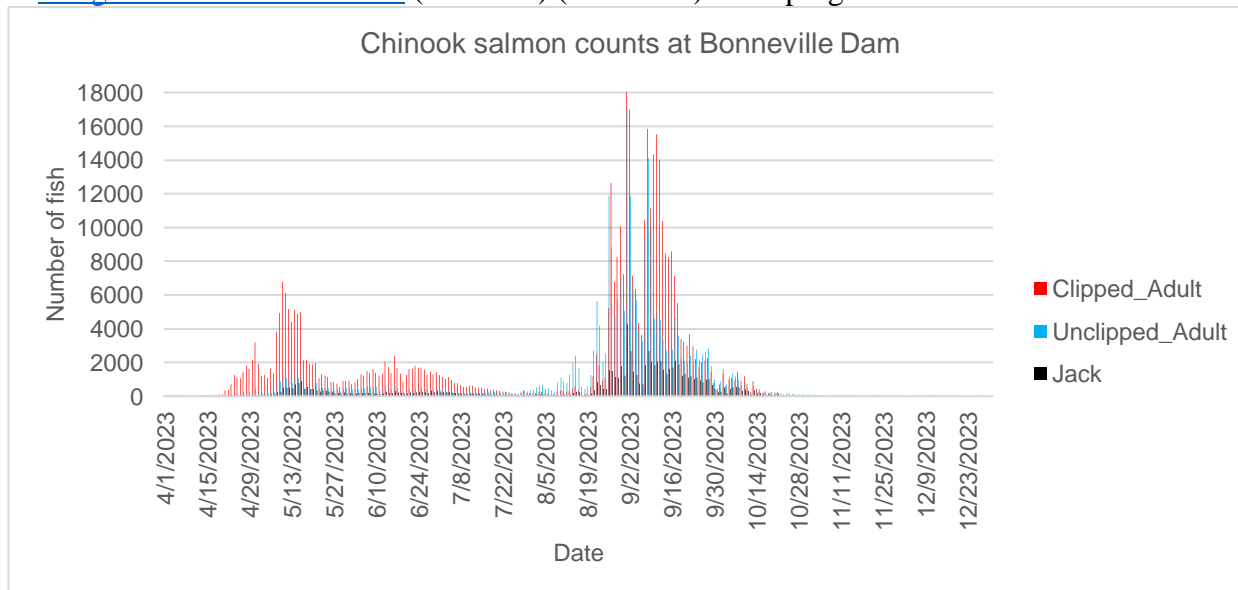
Based on numbers of fish collected, samples were pooled into a combination of weekly strata and multi-week strata for Chinook (Table 47), steelhead (Table 48), and sockeye salmon (Table 49) spanning the majority of the run-year from April to October. We followed a similar protocol as the Monitoring Methods [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, 2024).

**Figure 25. Daily passage of Chinook salmon (Clipped adults=red, Unclipped adult=blue, and jacks=black) at Bonneville Dam in 2023 (source: <https://www.fpc.org>; US v OR TAC).**

**Table 47. Sample numbers by weekly strata for adult-sized Chinook salmon that were DNA sampled or tallied for abundance at Bonneville Dam in 2023.**

		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	1,813	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	2,601	1,641	4	20	15	11	24	26	0.92%	1.58%
		30	1,541	1,354		8	9	1	8	10	0.52%	0.74%
		31	406	578		3	3		3	3	0.74%	0.52%
	Fall	31	1,068	2,595	2	16	6	6	18	12	1.69%	0.46%
		32	1,585	4,680		8	13	8	8	21	0.50%	0.45%
		33	2,143	8,920					0	0	0.00%	0.00%
		34	13,236	30,218	4	44	35	59	48	94	0.36%	0.31%
		35	86,405	60,346	3	41	33	51	44	84	0.05%	0.14%
		36	58,887	52,490	2	41	49	43	43	92	0.07%	0.18%
		37	79,534	25,564	9	68	93	73	77	166	0.10%	0.65%

		38	28,967	18,869	10	73	118	74	83	192	0.29%	1.02%
		39	12,597	15,695	6	50	89	34	56	123	0.44%	0.78%
		40	6,106	7,336	8	43	94	47	51	141	0.84%	1.92%
		41	5,882	3,922	2	23	67	28	25	95	0.42%	2.42%
		42-53	2,067	3,933					0	0	0.00%	0.00%
		Total	447,810	274,460	148	1,610	919	611	1,758	1,530	0.39%	0.56%

Note: Statistical weeks 1–16 are 1/1/23 – 4/22/23 and 42–53 is 10/15/23–12/31/23. ‘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 1<sup>st</sup> to June 15<sup>th</sup> (Spring management period), June 16<sup>th</sup> to July 31<sup>st</sup> (Summer management period), and August 1<sup>st</sup> 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 48. Sample numbers by monthly strata for steelhead that were DNA sampled or tallied for abundance at Bonneville Dam in 2023.**

				Sample (N)											
				A-Index				B-Index						Clipped	Non-clipped
		Clipped	Non-Clipped	Clipped		Non-clipped		Clipped		Non-clipped		Clipped	Non-clipped	Sample	Sample
	Strata	count	count	GSI	PBT	GSI	PBT	GSI	PBT	GSI	PBT	Total	Total	rate	rate
Skamania	14-27	1,706	1,498	0	15	14	0	0	1	0	0	16	14	0.94%	0.93%
A-/B-Index	27-31	11,842	12,936	2	41	41	2	0	1	1	0	44	44	0.37%	0.34%
	32-33	14,688	10,067	8	59	70	2	0	5	0	0	72	72	0.49%	0.72%
	34-37	31,321	11,131	5	51	12	1	1	23	2	4	80	19	0.26%	0.17%
	38-39	9,055	2,789	4	36	8	5	0	21	3	5	61	21	0.67%	0.75%
	40-45	4,855	2,003	7	59	17	16	0	14	1	4	80	38	1.65%	1.90%
Summer A-/B-Index subtotal		71,761	38,926	26	246	148	26	1	64	7	13	337	194	0.47%	0.50%
<b>Total</b>		73,467	40,424	26	261	162	26	1	65	7	13	353	208	0.48%	0.51%

Note: Statistical week 14-27 is 4/1/23–6/30/23 (Skamania Management Period) and 27-31 begins the A-/B-Index Period that runs from 7/1/2023-10/31/2023. ‘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 49. Sample numbers for genetic stock assignments of sockeye salmon that passed Bonneville Dam in 2023.**

Bonneville Dam in 2020									
Statistical week	Bonneville dam fish window count	Genetic stock						Total	Sample rate (%)
grouping		OKA	WEN	RED	LBC	Yakima			
						OKA	WEN		
1-22	137	2		1*				3	2.19%
23	1401	23	6					29	2.07%
24	19640	105	50					155	0.79%
25	70169	86	74				1	161	0.23%
26	119426	120	114	2				236	0.20%
27	78173	106	91	2				199	0.25%
28	29954	130	70	6				206	0.69%
29	6573	68	33	4		1		106	1.61%
30	1559	2	1					3	0.19%
31	413	4	2					6	1.45%
32	103	2	1	1				4	3.88%
33-37	52							0	0.00%
38-52	0							0	0.00%
Total	327600	648	442	15	1	1	0	1108	0.34%

Note: Statistical week 18 begins on 4/30/23 and 37 ends 9/16/23; 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). \*One fish assigned to “Alturas Lake” and was placed with “RED” stock. 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\_UMATILLFA 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.

There were 14 major (i.e., abundance >1000 fish) clipped hatchery origin Chinook salmon stocks represented in the total estimated abundance (N=447,80) of clipped hatchery Chinook salmon passing Bonneville Dam in 2023 (Table 50; Figure 26). These stocks in order of decreasing magnitude were 18\_UCOLSF (172,887), 05\_SPCRTU (86,387), 19\_SRFALL (55,914), 12\_HELLSC (38,496), 22\_BONPOOLFA (27,828), 20\_BONPOOLSP (23,295), 10\_UCOLSP (14,248), 16\_UPSALM (6,200), 13\_SFSALM (5,505), 23\_UMATILLAFA (5,403), 07\_DESCSP (4,132), 21\_UMATILLASP (3,010), 02\_WCASSP (1,329), and 04\_WILLAM (1,166) (Table 50).

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 50). Further, using PBT assignments we can now provide abundance and run-timing estimates for particular hatchery broodstocks (Table 51) which will allow for improved abundance estimates (Figure 26). In 2023, there were 79 different broodstocks of clipped hatchery-origin fish with abundances greater than 0 and 44 of them had abundance estimates >1000 fish (Table 51). The top five major clipped hatchery broodstocks were from Spring Creek, Priest Rapids, and Lyons Ferry hatcheries which were all fall run. The largest spring run clipped broodstock was represented by Rapid River Hatchery (SY2019; 16,020 fish), which is typically one of the largest spring run hatchery stocks.

**Table 50. Stock-specific abundance and run-timing of clipped hatchery origin adult Chinook salmon passing Bonneville Dam in 2023.**

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	0	0							
02_WCASSP	1,329	13	1,008	321	0	138	126	165	117	192	5/18/2023	39
03_WCASFA	251	2	0	0	251	278	276	279	274	280	10/5/2023	3
04_WILLAM	1,166	7	192	595	379	192	175	228	156	238	7/11/2023	53
05_SPCRTU	86,387	109	0	0	86,387	251	244	255	238	264	9/8/2023	11
06_KLICKR	452	4	452	0	0	130	122	133	114	138	5/10/2023	11
07_DESCSP	4,132	37	3,942	190	0	134	122	141.3	114	166	5/14/2023	19
08_JOHNDR	88	1	88	0	0	116	114	118	110.2	119	4/26/2023	4
09_YAKIMA	926	10	926	0	0	136	134	140	121	151	5/16/2023	6
10_UCOLSP	14,248	129	14,248	0	0	130	123	134	115	143	5/10/2023	11
11_TUCANO	294	2	294	0	0	130	126	131	121	133	5/10/2023	5
12_HELLSC	38,496	318	37,966	530	0	131	127	136	116	152	5/11/2023	9
13_SFSALM	5,505	76	4,680	825	0	155	147	164	140	183	6/4/2023	17
14_CHMBLN			0	0	0							
15_MFSALM			0	0	0							
16_UPSALM	6,200	73	5,876	324	0	144	135	158	123	167	5/24/2023	23
17_DESCFA			0	0	0							
18_UCOLSF	172,887	646	14,141	35,533	123,213	250	192	257	161	276	9/7/2023	65
19_SRFALL	55,914	73	0	898	55,016	244	240	251	230	259	9/1/2023	11
20_BONPOOLSP	23,295	175	23,295	0	0	130	125	134	114	141	5/10/2023	9
21_UMATILLASP	3,010	30	3,010	0	0	135	123	138	115	147	5/15/2023	15
22_BONPOOLFA	27,828	40	0	0	27,828	249	244	259	239	274	9/6/2023	15
23_UMATILLAFA	5,403	12	0	0	5,403	260	252	271	247	287	9/17/2023	19
Total	447,810	1,757	110,116	39,217	298,477							

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 51. Hatchery broodstock-specific abundance and run-timing distributions of clipped adult Chinook salmon passing Bonneville Dam in 2023.

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_sp19	12	1,184	1,008	176	0	136	125	149	117	176	5/16/2023	24
	02_WCASSP	Parkdale Fish Facility	OtsPARK_seg_sp20	1	145	0	145	0	191	186	198	183	209	7/10/2023	12
	04_WILLAM	North Santiam Hatchery	OtsNSAN_seg_sp18	1	373	0	0	373	235	229	238	217	238	8/23/2023	9
	04_WILLAM	North Santiam Hatchery	OtsNSAN_seg_sp19	2	427	147	280	0	186	164	194	157	207	7/5/2023	30
	06_KLICKR	Klickitat Hatchery	OtsKLIC_seg_sp19	2	317	317	0	0	129	118	131	113	133	5/9/2023	13
	07_DESCSP	Round Butte Fish Hatchery	OtsRBFH_seg_sp19	20	2,089	1,898	190	0	139	132	150	123	173	5/19/2023	18
	07_DESCSP	Round Butte Fish Hatchery	OtsRBFH_seg_sp20	1	78	78	0	0	161	158	164	155	166	6/10/2023	6
	07_DESCSP	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp19	16	1,965	1,965	0	0	124	117	135	111	140	5/4/2023	18
	09_YAKIMA	Yakima River Roza Dam	OtsYRRD_int_sp19	8	813	813	0	0	136	134	139	121	149	5/16/2023	5
	09_YAKIMA	Yakima River Roza Dam	OtsYRRD_seg_sp19	2	113	113	0	0	146	143	151	141	154	5/26/2023	8
	10_UCOLSP	Chief Joseph Hatchery	OtsCHJO_seg_sp19	7	1,108	1,108	0	0	135	131	137	116	142	5/15/2023	6
	10_UCOLSP	Eastbank Fish Hatchery	OtsEAST_seg_sp18	1	64	64	0	0	143	142	145	141	147	5/23/2023	3
	10_UCOLSP	Eastbank Fish Hatchery	OtsEAST_seg_sp19	8	1,142	1,142	0	0	134	130	136	123	147	5/14/2023	6
	10_UCOLSP	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp18	2	488	488	0	0	129	126	131	121	133	5/9/2023	5
	10_UCOLSP	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp19	65	7,550	7,550	0	0	129	121	133	114	140	5/9/2023	12
	10_UCOLSP	Winthrop National Fish Hatchery	OtsWINT_seg_sp19	24	3,139	3,139	0	0	131	129	135	121	144	5/11/2023	6
	11_TUCANO	Little White Salmon National Fish Hatchery	OtsTOUC_seg_sp19	2	294	294	0	0	130	126	131	121	133	5/10/2023	5
	12_HELLSC	Clearwater Fish Hatchery	OtsCLWH_seg_sp18	4	267	267	0	0	142	126	144	121	147	5/22/2023	18
	12_HELLSC	Clearwater Fish Hatchery	OtsCLWH_seg_sp19	49	6,508	6,508	0	0	132	129	135	120	143	5/12/2023	6
	12_HELLSC	Dworshak National Fish Hatchery	OtsDWOR_seg_sp18	2	171	171	0	0	118	115	143	111	146	4/28/2023	28
	12_HELLSC	Dworshak National Fish Hatchery	OtsKOOS_seg_sp18	1	144	144	0	0	136	135	138	134	140	5/16/2023	3
	12_HELLSC	Dworshak National Fish Hatchery	OtsDWOR_seg_sp19	40	4,923	4,751	172	0	133	128	137	115	163	5/13/2023	9
	12_HELLSC	Dworshak National Fish Hatchery	OtsKOOS_seg_sp19	32	4,115	4,115	0	0	132	124	136	115	140	5/12/2023	12
	12_HELLSC	Dworshak National Fish Hatchery	OtsDWOR_seg_sp20	1	70	70	0	0	143	142	145	141	147	5/23/2023	3
	12_HELLSC	Lookingglass Fish Hatchery	OtsLOOK_seg_sp18	1	230	230	0	0	130	129	132	128	133	5/10/2023	3
	12_HELLSC	Lookingglass Fish Hatchery	OtsLOOK_seg_sp19	21	2,167	2,167	0	0	136	131	148	116	164	5/16/2023	17
	12_HELLSC	Nez Perce	OtsNPFH_seg_sp19	13	2,086	2,086	0	0	130	128	132	116	136	5/10/2023	4
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH_seg_sp18	4	591	591	0	0	130	121	134	114	138	5/10/2023	13
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH_seg_sp19	131	16,020	16,020	0	0	130	124	135	117	145	5/10/2023	11
	20_BONPOOLSP	Carson National Fish Hatchery	OtsCARS_seg_sp18	2	149	149	0	0	118	115	150	111	153	4/28/2023	35

		20_BONPOOLSP	Carson National Fish Hatchery	OtsCARS_seg_sp19	69	9,823	9,823	0	0	131	129	135	117	141	5/11/2023	6
		20_BONPOOLSP	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp18	7	914	914	0	0	129	118	134	112	139	5/9/2023	16
		20_BONPOOLSP	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp19	97	12,408	12,408	0	0	130	122	133	114	141	5/10/2023	11
		21_UMATILLASP	Umatilla Fish Hatchery	OtsUMAT_seg_sp19	30	3,010	3,010	0	0	135	123	138	115	147	5/15/2023	15
02Spring/Summer		12_HELLSC	Lookingglass Fish Hatchery	OtsIMNW_seg_ss19	9	891	534	358	0	163	151	172	135	180	6/12/2023	21
		13_SFSALM	McCall Fish Hatchery	OtsMCCA_seg_ss18	1	50	50	0	0	151	150	153	148	154	5/31/2023	3
		13_SFSALM	McCall Fish Hatchery	OtsMCCA_seg_ss19	71	5,223	4,545	679	0	155	147	163	140	179	6/4/2023	16
		13_SFSALM	McCall Fish Hatchery	OtsMCCA_seg_ss20	1	147	0	147	0	192	186	199	183	210	7/11/2023	13
		16_UPSALM	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss18	2	127	127	0	0	157	152	162	148	165	6/6/2023	10
		16_UPSALM	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss19	12	889	889	0	0	147	142	160	135	165	5/27/2023	18
		16_UPSALM	Sawtooth Fish Hatchery	OtsSAWT_seg_ss19	52	4,712	4,534	177	0	141	135	155	125	166	5/21/2023	20
		16_UPSALM	Sawtooth Fish Hatchery	OtsSAWT_seg_ss20	2	224	77	147	0	186	164	195	157	207	7/5/2023	31
03Summer		18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_su17	1	85	85	0	0	161	158	164	155	166	6/10/2023	6
		18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_su18	1	145	0	145	0	191	186	198	183	209	7/10/2023	12
		18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_su19	15	1,974	448	1,526	0	174	167	182	156	199	6/23/2023	15
		18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_su19	28	4,235	362	3,127	746	187	177	202	161	238	7/6/2023	25
		18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su17	3	295	145	150	0	183	156	192	142	205	7/2/2023	36
		18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su18	150	18,735	4,574	12,932	1,229	176	167	187	155	228	6/25/2023	20
		18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su19	19	2,396	584	1,812	0	174	167	180	156	197	6/23/2023	13
		18_UCOLSF	Entiat National Fish Hatchery	OtsENFH_seg_su17	5	537	332	205	0	164	158	172	151	180	6/13/2023	14
		18_UCOLSF	Entiat National Fish Hatchery	OtsENFH_seg_su18	30	3,976	1,945	2,030	0	167	160	174	151	181	6/16/2023	14
		18_UCOLSF	Entiat National Fish Hatchery	OtsENFH_seg_su19	31	4,142	811	3,330	0	180	168	190	156	205	6/29/2023	22
		18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su18	27	3,980	1,144	2,836	0	172	165	179	156	194	6/21/2023	14
		18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su19	67	7,028	2,968	4,060	0	169	161	179	152	198	6/18/2023	18
		18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su20	2	228	79	149	0	186	164	194	157	207	7/5/2023	30
		18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su20	2	228	79	149	0	186	164	194	157	207	7/5/2023	30
04Fall		03_WCASFA	Washougal Fish Hatchery	OtsWASH_seg_fa19	1	251	0	0	251	278	276	279	274	280	10/5/2023	3
		05_SPCRTU	Bonneville Dam Hatchery	OtsBONN_seg_fa19	1	429	0	0	429	235	229	238	217	238	8/23/2023	9
		05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	20	19,835	0	0	19,835	249	244	254	238	261	9/6/2023	10
		05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa20	75	60,446	0	0	60,446	251	244	256	238	264	9/8/2023	12
		05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa21	2	1,750	0	0	1,750	250	246	251	233	252	9/7/2023	5
		18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa17	1	242	0	0	242	270	268	271	267	273	9/27/2023	3
		18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa18	5	4,817	0	0	4,817	246	244	252	239	265	9/3/2023	8
		18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa19	111	77,854	0	0	77,854	253	248	258	240	275	9/10/2023	10
		18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa20	55	29,613	0	0	29,613	259	253	270	241	285	9/16/2023	17
		18_UCOLSF	Ringold Springs State Hatchery	OtsRING_seg_fa19	9	4,418	0	0	4,418	254	250	261	234	283	9/11/2023	11

	18_UCOLSF	Ringold Springs State Hatchery	OtsRING_seg_fa20	4	1,623	0	0	1,623	257	254	269	253	279	9/14/2023	15
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa17	1	319	0	0	319	234	229	238	216	238	8/22/2023	9
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	7	6,508	0	180	6,328	245	240	251	225	257	9/2/2023	11
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa19	38	31,816	0	454	31,362	244	240	245	231	258	9/1/2023	5
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa20	11	7,167	0	147	7,020	249	242	255	227	263	9/6/2023	13
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa18	1	300	0	0	300	234	229	238	217	238	8/22/2023	9
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa19	7	6,163	0	0	6,163	244	241	253	236	281	9/1/2023	12
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa20	2	1,784	0	0	1,784	251	249	252	246	264	9/8/2023	3
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa17	1	125	0	0	125	278	276	279	274	280	10/5/2023	3
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	6	3,034	0	0	3,034	256	253	269	228	286	9/13/2023	16
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa19	21	18,875	0	0	18,875	244	242	254	239	271	9/1/2023	12
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa20	12	5,677	0	0	5,677	260	250	263	246	271	9/17/2023	13
	23_UMATILLAFA	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	7	4,122	0	0	4,122	256	251	265	247	286	9/13/2023	14
	23_UMATILLAFA	Umatilla Fish Hatchery	OtsUMAT_seg_fa20	5	1,245	0	0	1,245	272	265	281	260	290	9/29/2023	16
	#N/A	#N/A	Unassigned	166	14,494	2,335	3,662	8,497	244	174	256	119	264	9/1/2023	82
Total				1,776	447,810	110,116	39,217	298,477							

There were 7 major (i.e., abundance >1000 fish) *unclipped* hatchery origin Chinook salmon stocks represented in the total estimated abundance (N=142,043) of unclipped hatchery Chinook salmon passing Bonneville Dam in 2023 (Table 52; Figure 26). These stocks in order of decreasing magnitude were 18\_UCOLSF (66,393), 19\_SRFALL (37,311), 22\_BONPOOLFA (18,507), 05\_SPCRTU (11,314), 12\_HELLSC (2,762), 10\_UCOLSP (2,213), and 13\_SFSALM (1,323) (Table 52).

In 2023, there were 56 different broodstocks of unclipped hatchery-origin fish with abundances greater than 0 and 15 of them had abundance estimates >1000 fish (Table 53). The top five major unclipped hatchery broodstocks were from Priest Rapids Hatchery, Lyons Ferry, and Little White Salmon hatcheries which were all fall run. The largest spring run unclipped broodstock was represented by Methow Hatchery (SY2019, 1,112 fish).

**Table 52. Stock-specific abundance and run-timing of unclipped hatchery origin adult Chinook salmon passing Bonneville Dam in 2023.**

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							-
02_WCASSP	63	1	63	0	0	160	158	163	155.05	165.95	6/9/2023	5
03_WCASFA			0	0	0							-
04_WILLAM			0	0	0							-
05_SPCRTU	11,314	37	0	0	11,314	250	243	253	231	265	9/7/2023	10
06_Klickr			0	0	0							-
07_DESCSP	157	2	157	0	0	118	115	142	111	146	4/28/2023	27
08_JOHNDR			0	0	0							-
09_YAKIMA	109	1	109	0	0	136	135	138	134	140	5/16/2023	3
10_UCOLSP	2,213	28	2,126	86	0	134	129	142	120	162	5/14/2023	13
11_TUCANO			0	0	0							-
12_HELLSC	2,762	32	2,762	0	0	131	123	136	115	160	5/11/2023	13
13_SFSALM	1,323	25	1,212	111	0	151	146	158	141	173	5/31/2023	12
14_CHMBLN			0	0	0							-
15_MFSALM			0	0	0							-
16_UPSALM	806	11	521	285	0	155	141	178	124	205	6/4/2023	37
17_DESCFA			0	0	0							-
18_UCOLSF	66,393	301	1,504	4,702	60,187	246	241	256	176	278	9/3/2023	15
19_SRFALL	37,311	96	0	711	36,600	238	234	244	218	255	8/26/2023	10
20_BONPOOLSP	444	4	444	0	0	129	117	134	111	138	5/9/2023	17
21_UMATILLASP	482	7	482	0	0	130	121	141	114	151	5/10/2023	20
22_BONPOOLFA	18,507	51	0	0	18,507	245	241	251	231	266	9/2/2023	10
23_UMATILLAFA	160	2	0	0	160	264	261	276	260	280	9/21/2023	15
Total	142,043	598	9,380	5,895	126,768							

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 53. Hatchery broodstock-specific abundance and run-timing distributions of unclipped adult Chinook salmon passing Bonneville Dam in 2023.

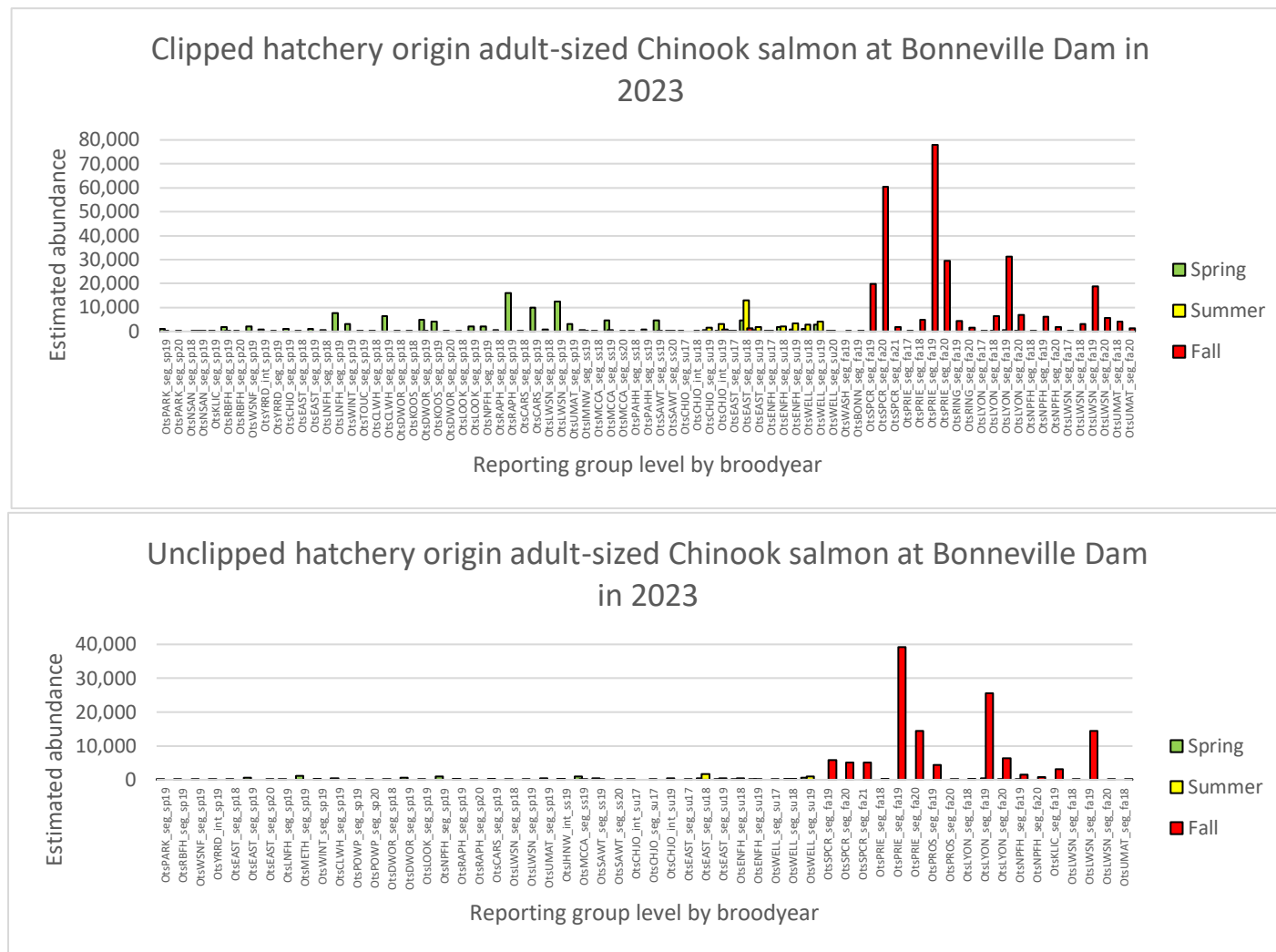
Run	GSI RepGrp	Hatchery	Brood stock	Sample N	Estimated abundance				Run-timing distribution						
					Total	Management Period			Ordinal day						Inter
						Spring	Summer	Fall		1st	3rd	5th	95th	Median	quartile
						Jan. 1 - Jun. 15	Jun. 16 - Jul. 31	Aug. 1 - Dec. 31	Median	quartile	quartile	%	%	date	range
01Spring	02_WCASSP	Parkdale Fish Facility	OtsPARK_seg_sp19	1	63	63	0	0	160	158	163	155	166	6/9/2023	5
	07_DESCSP	Round Butte Fish Hatchery	OtsRBFH_seg_sp19	1	101	101	0	0	116	114	118	109	119	4/26/2023	4
	07_DESCSP	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp19	1	56	56	0	0	143	142	145	141	147	5/23/2023	3
	09_YAKIMA	Yakima River Roza Dam	OtsYRRD_int_sp19	1	109	109	0	0	136	135	138	134	140	5/16/2023	3
	10_UCOLSP	Eastbank Fish Hatchery	OtsEAST_seg_sp18	2	152	152	0	0	137	135	148	134	153	5/17/2023	13
	10_UCOLSP	Eastbank Fish Hatchery	OtsEAST_seg_sp19	8	602	602	0	0	141	133	145	129	152	5/21/2023	12
	10_UCOLSP	Eastbank Fish Hatchery	OtsEAST_seg_sp20	1	86	0	86	0	197	190	204	184	211	7/16/2023	14
	10_UCOLSP	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp19	1	53	53	0	0	122	121	124	120	126	5/2/2023	3
	10_UCOLSP	Methow Fish Hatchery	OtsMETH_seg_sp19	13	1,112	1,112	0	0	132	129	136	121	144	5/12/2023	7
	10_UCOLSP	Winthrop National Fish Hatchery	OtsWINT_seg_sp19	3	208	208	0	0	121	117	157	112	164	5/1/2023	40
	12_HELLSC	Clearwater Fish Hatchery	OtsCLWH_seg_sp19	5	470	470	0	0	135	122	136	114	140	5/15/2023	14
	12_HELLSC	Clearwater Fish Hatchery	OtsPOWP_seg_sp19	3	149	149	0	0	154	151	159	148	165	6/3/2023	8
	12_HELLSC	Clearwater Fish Hatchery	OtsPOWP_seg_sp20	1	62	62	0	0	160	158	163	155	166	6/9/2023	5
	12_HELLSC	Dworshak National Fish Hatchery	OtsDWOR_seg_sp18	1	96	96	0	0	116	114	118	108	119	4/26/2023	4
	12_HELLSC	Dworshak National Fish Hatchery	OtsDWOR_seg_sp19	6	565	565	0	0	133	127	136	114	161	5/13/2023	10
	12_HELLSC	Lookingglass Fish Hatchery	OtsLOOK_seg_sp19	1	146	146	0	0	130	129	132	128	133	5/10/2023	3
	12_HELLSC	Nez Perce	OtsNPFH_seg_sp19	11	951	951	0	0	130	122	134	116	141	5/10/2023	12
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH_seg_sp19	3	260	260	0	0	128	123	131	120	133	5/8/2023	8
	12_HELLSC	Rapid River Fish Hatchery	OtsRAPH_seg_sp20	1	63	63	0	0	160	158	163	155	166	6/9/2023	5
	20_BONPOOLSP	Carson National Fish Hatchery	OtsCARS_seg_sp19	2	233	233	0	0	129	117	131	113	133	5/9/2023	14
	20_BONPOOLSP	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp18	1	97	97	0	0	116	114	118	108	119	4/26/2023	4
	20_BONPOOLSP	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp19	1	114	114	0	0	136	135	138	134	140	5/16/2023	3
	21_UMATILLASP	Umatilla Fish Hatchery	OtsUMAT_seg_sp19	7	482	482	0	0	130	121	141	114	151	5/10/2023	20
02Spring/Summer	13_SFSALM	McCall Fish Hatchery	OtsJHNW_int_ss19	6	274	274	0	0	149	145	152	141	154	5/29/2023	7
	13_SFSALM	McCall Fish Hatchery	OtsMCCA_seg_ss19	19	1,048	937	111	0	152	146	160	141	175	6/1/2023	14
	16_UPSALM	Sawtooth Fish Hatchery	OtsSAWT_seg_ss19	9	633	521	112	0	149	132	162	123	178	5/29/2023	30
	16_UPSALM	Sawtooth Fish Hatchery	OtsSAWT_seg_ss20	2	174	0	174	0	198	190	205	184	211	7/17/2023	15
03Summer	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_su17	1	82	82	0	0	160	158	164	155	166	6/9/2023	6
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_seg_su17	1	95	0	95	0	197	190	205	184	211	7/16/2023	15
	18_UCOLSF	Chief Joseph Hatchery	OtsCHJO_int_su19	5	507	0	507	0	179	173	191	167	209	6/28/2023	18

	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su17	1	112	0	112	0	174	170	178	167	182	6/23/2023	8
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su18	22	1,989	356	1,633	0	175	168	182	157	205	6/24/2023	14
	18_UCOLSF	Eastbank Fish Hatchery	OtsEAST_seg_su19	5	450	62	388	0	178	170	193	159	210	6/27/2023	23
	18_UCOLSF	Entiat National Fish Hatchery	OtsENFH_seg_su18	4	477	81	396	0	176	168	182	158	206	6/25/2023	14
	18_UCOLSF	Entiat National Fish Hatchery	OtsENFH_seg_su19	2	158	66	92	0	186	161	199	156	210	7/5/2023	38
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su17	1	122	0	122	0	175	170	178	167	182	6/24/2023	8
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su18	6	567	226	341	0	174	162	192	156	209	6/23/2023	30
	18_UCOLSF	Wells Fish Hatchery	OtsWELL_seg_su19	21	1,647	632	1,015	0	170	161	179	150	202	6/19/2023	18
04Fall	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	18	5,760	0	0	5,760	250	246	252	237	265	9/7/2023	6
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa20	19	5,171	0	0	5,171	246	239	254	227	265	9/3/2023	15
	05_SPCRTU	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa21	13	5,076	0	0	5,076	239	234	245	222	262	8/27/2023	11
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa18	3	299	0	0	299	258	255	276	253	280	9/15/2023	21
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa19	158	39,200	0	0	39,200	249	244	256	235	276	9/6/2023	12
	18_UCOLSF	Priest Rapids Hatchery	OtsPRIE_seg_fa20	67	14,396	0	0	14,396	254	245	269	239	283	9/11/2023	24
	18_UCOLSF	Yakima Nation Prosser Hatchery	OtsPROS_seg_fa19	3	4,346	0	0	4,346	242	239	244	227	245	8/30/2023	5
	18_UCOLSF	Yakima Nation Prosser Hatchery	OtsPROS_seg_fa20	1	87	0	0	87	287	283	293	281	303	10/14/2023	10
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa18	1	191	0	0	191	255	254	257	253	259	9/12/2023	3
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa19	68	26,050	0	448	25,602	238	233	244	218	254	8/26/2023	11
	19_SRFALL	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa20	20	6,569	0	174	6,395	241	236	245	219	261	8/29/2023	9
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa19	5	1,594	0	89	1,505	234	226	237	210	238	8/22/2023	11
	19_SRFALL	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa20	2	752	0	0	752	251	249	252	246	257	9/8/2023	3
	22_BONPOOLFA	Klickitat Hatchery	OtsKLIC_seg_fa19	4	3,102	0	0	3,102	244	239	250	227	260	9/1/2023	11
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa18	1	134	0	0	134	262	261	264	260	266	9/19/2023	3
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa19	45	14,494	0	0	14,494	245	241	252	233	268	9/2/2023	11
	22_BONPOOLFA	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa20	1	99	0	0	99	262	261	264	260	266	9/19/2023	3
	23_UMATILLFA	Umatilla Fish Hatchery	OtsUMAT_seg_fa18	2	157	0	0	157	264	261	276	260	280	9/21/2023	15
Total				611	142,043	9,380	5,895	126,768							

**Table 54. Stock-specific abundance and run-timing of natural origin adult Chinook salmon passing Bonneville Dam in 2023.**

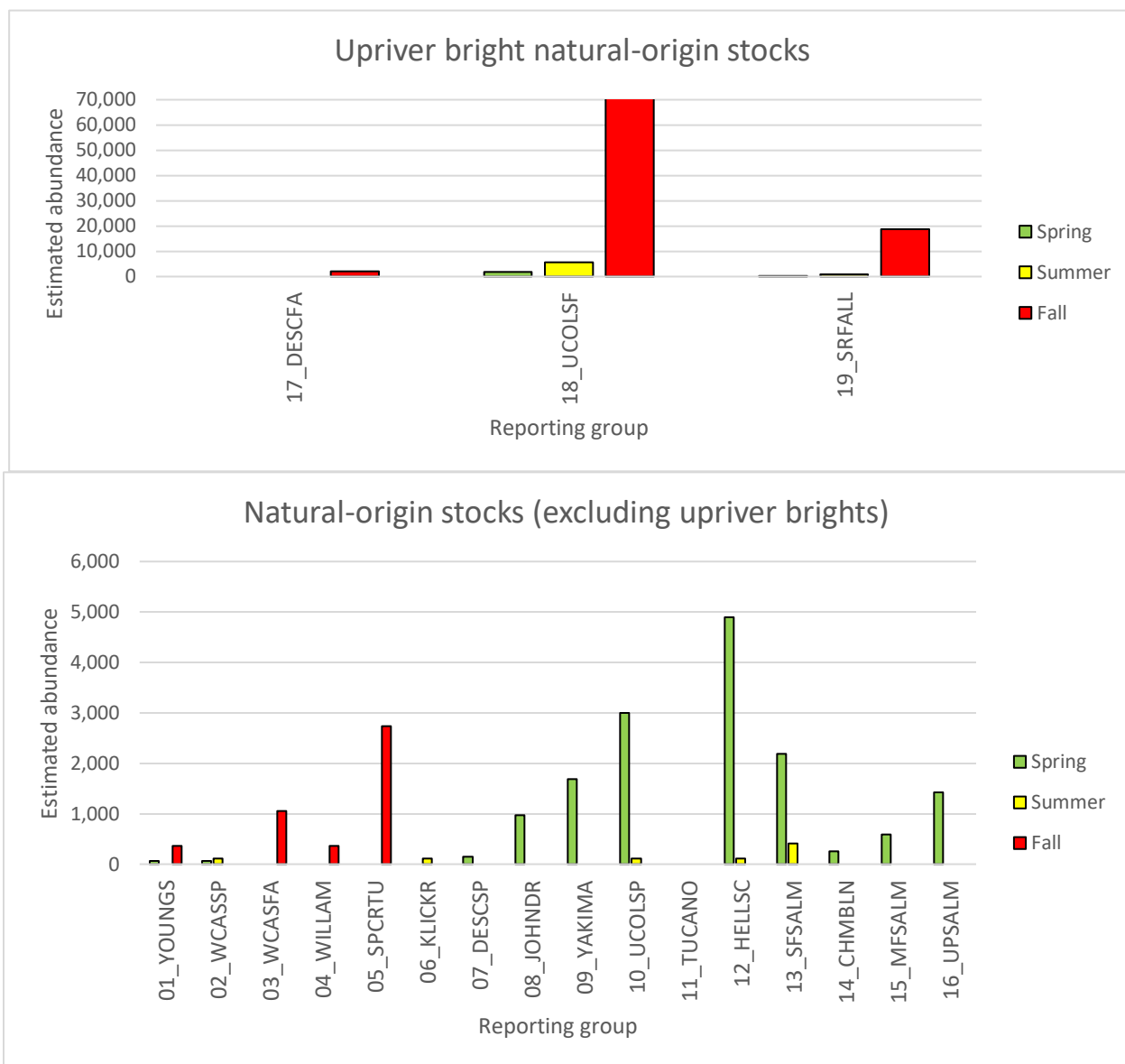
Reporting Group	Estimated abundance					Run-timing distribution						
	Mean	Sample N	Management Period			Ordinal day						
			Spring	Summer	Fall		1st	3rd	5th	95th	Median	Interquartile
			Jan. 1-Jun. 15	Jun. 16-Jul. 31	Aug. 1-Dec. 1	Median	quartile	quartile	percentile	percentile	date	range (days)
01_YOUNGS	427	2	62	0	365	233	223	237	159	238	8/21/2023	14
02_WCASSP	170	2	62	108	0	169	162.5	176	156.5	181	6/18/2023	14
03_WCASFA	1,055	5	0	0	1,055	237	232	261	219	270	8/25/2023	29
04_WILLAM	365	1	0	0	365	234	227	238	217	238	8/22/2023	11
05_SPCRTU	2,733	10	0	0	2,733	244	241	245	238	263	9/1/2023	4
06_Klickr	108	1	0	108	0	175	170	178	167	181.6	6/24/2023	8
07_DESCSP	144	2	144	0	0	118	115	121	111	125	4/28/2023	6
08_JOHNDR	972	14	972	0	0	135	124	140	117	151	5/15/2023	16
09_YAKIMA	1,692	17	1,692	0	0	133	130	138	119	158	5/13/2023	8
10_UCOLSP	3,106	44	2,998	108	0	136	130	145	120	161	5/16/2023	15
11_TUCANO	0		0	0	0							
12_HELLSC	5,006	61	4,898	108	0	136	131	154	121	165	5/16/2023	23
13_SFSALM	2,601	40	2,193	407	0	151	141	162	129.2	180	5/31/2023	21
14_CHMBLN	250	4	250	0	0	142	118	147	113	164	5/22/2023	29
15_MFSALM	587	7	587	0	0	135	130	140	115	152	5/15/2023	10
16_UPSALM	1,420	20	1,420	0	0	138	133	151	124	163	5/18/2023	18
17_DESCFA	2,044	13	0	0	2,044	245	240	264	228	289	9/2/2023	24
18_UCOLSF	90,098	581	1,926	5,723	82,449	251	240	261	183	280	9/8/2023	21
19_SRFALL	19,639	95	85	765	18,789	246	241	255	217	276	9/3/2023	14
20_BONPOOLSP	-	-	0	0	0	-	-	-	-	-	-	-
21_UMATILLASP	-	-	0	0	0	-	-	-	-	-	-	-
22_BONPOOLFA	-	-	0	0	0	-	-	-	-	-	-	-
23_UMATILLAFA	-	-	0	0	0	-	-	-	-	-	-	-
Total	132,417	919	17,289	7,327	107,800							

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 26. 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 2023 during spring (green), summer (yellow) and fall (red) management periods.**

There were 10 major (i.e., abundance >1000 fish) Chinook salmon stocks represented in the total estimated relative abundance (N=132,417) of natural-origin (i.e., excluding unclipped hatchery-origin fish) Chinook salmon passing Bonneville Dam in 2023 (Table 54;Figure 27). These natural-origin stocks in order of decreasing magnitude were 18\_UCOLSF (90,098), 19\_SRFALL (19,639), 12\_HELLSC (5,006), 10\_UCOLSP (3,106), 05\_SPCRTU (2,733), 13\_SFSALM (2,601), 17\_DESCFA (2,044), 09\_YAKIMA(1,692), 16\_UPSALM (1,420), and 03\_WCASFA (1,055). These stock abundance estimates were generated using SCOBIDEUX and SPIBETR functions and the estimates of clipped and unclipped adults distributed by TAC (Table 47).



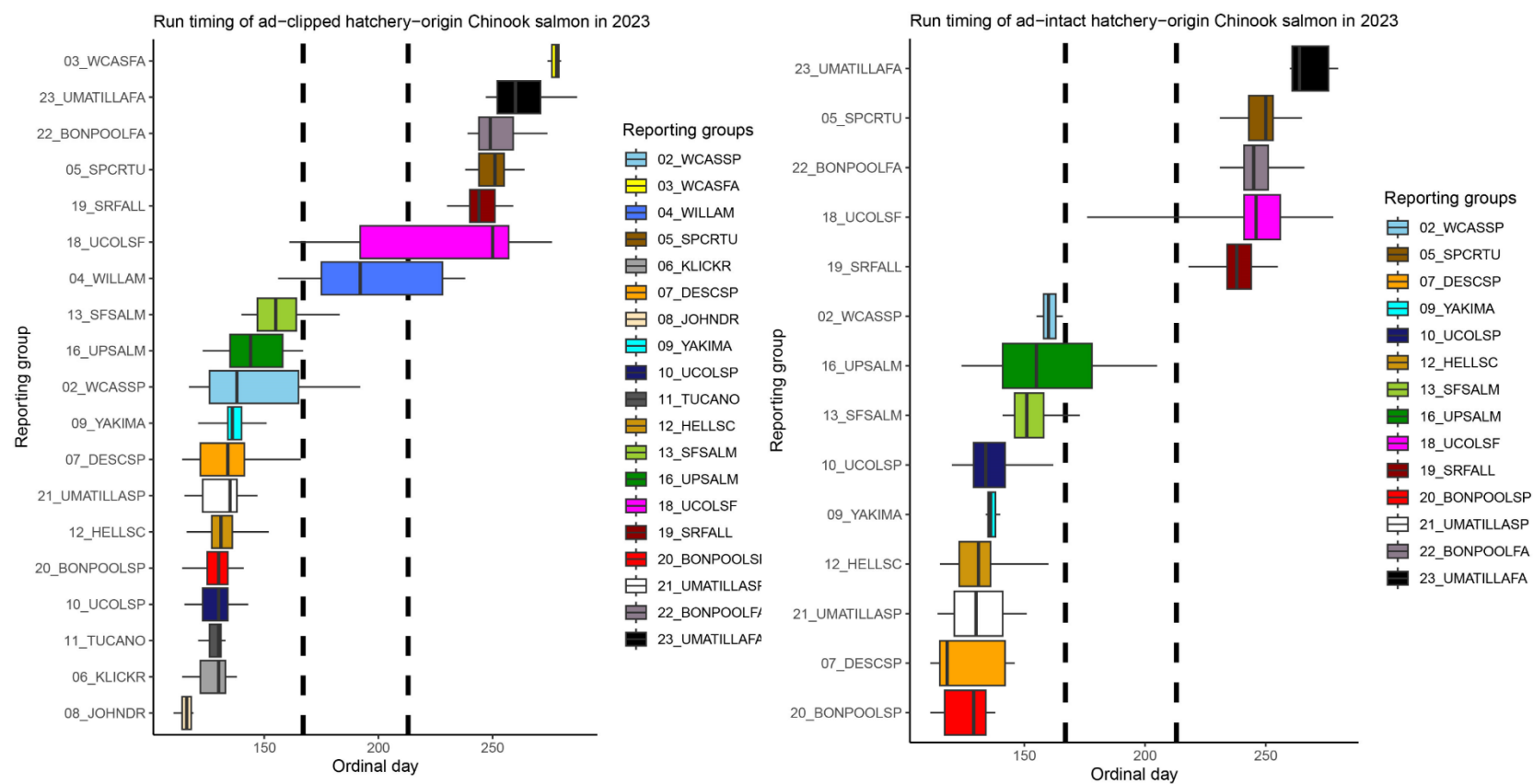
**Figure 27. Estimated abundance of natural origin reporting groups (excluding unclipped hatchery-origin fish) of adult-sized Chinook salmon sampled at Bonneville Dam in 2023 during the spring (green), summer (yellow), and fall (red) management periods. Upriver bright Chinook salmon reporting groups (top panel), and all other natural-origin Chinook reporting groups (bottom panel) are shown separately.**

### *Run-timing of Chinook salmon stocks in 2023*

We plotted the run-timing distributions of the clipped and unclipped hatchery-origin Chinook salmon reporting group stocks (Figure 28) and provided the subtotals of reporting group abundance for each management period (clipped Table 50, unclipped Table 52). 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 02\_WCASSP, 04\_WILLAM, 07\_DESCSP, 12\_HELLSC, 13\_SFSALM, and 16\_UPSALM was found to extend beyond the spring management period (total abundance in the summer period was 2,786 fish). We estimated that 98% of all hatchery origin spring stocks passed Bonneville Dam in the spring period and 2% of the spring stock abundance passed in the summer period (Table 50, Table 52). 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 28% (15,645 fish) and 72% (40,235 fish) of the total abundance estimated in those two periods, respectively.

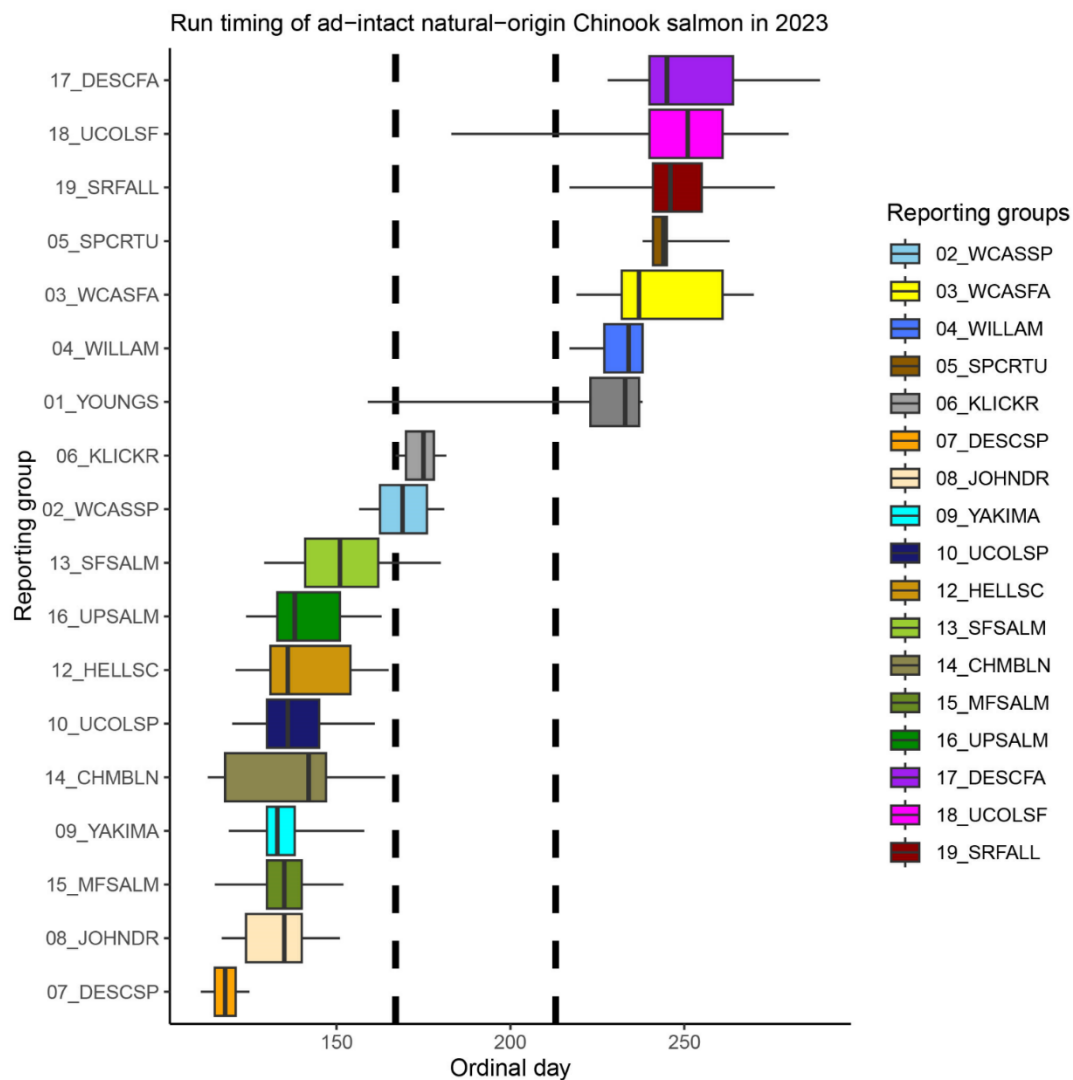
We also plotted run-timing distributions for each broodstock of clipped (Figure 30) and unclipped (Figure 31) hatchery origins and provided the subtotals of these broodstock abundance estimates for each management period (clipped Table 51, unclipped Table 53). Although most stocks with sample sizes  $\geq 5$  had median dates that fit within their expected management period, there was one summer run Upper Columbia clipped broodstock from Entiat Hatchery that had a median date in the spring (Figure 30); there were no spring/summer run hatchery clipped broodstock with sample size  $\geq 5$  that had median dates in the summer.

We plotted the run-timing distributions of the natural-origin (excluding adipose unclipped hatchery-origin fish, Figure 29) Chinook salmon stocks and provide subtotals of abundance for each management period (Table 54). 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-timings for 02\_WCASSP, 06\_KLICKR, 10\_UCOLSP, 12\_HELLSC, and 13\_SFSALM were found to extend beyond the spring management period (total estimated abundance in the summer period for these stocks was 839 fish). We also estimated that 95% (15,154 fish) of the natural origin spring stocks passed Bonneville Dam in the spring period and 5% (731 fish) of the spring stock abundance passed in the summer period (Table 54). 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 25% (1,926 fish) and 75% (5,723 fish) of the total abundance estimated in those two periods, respectively.



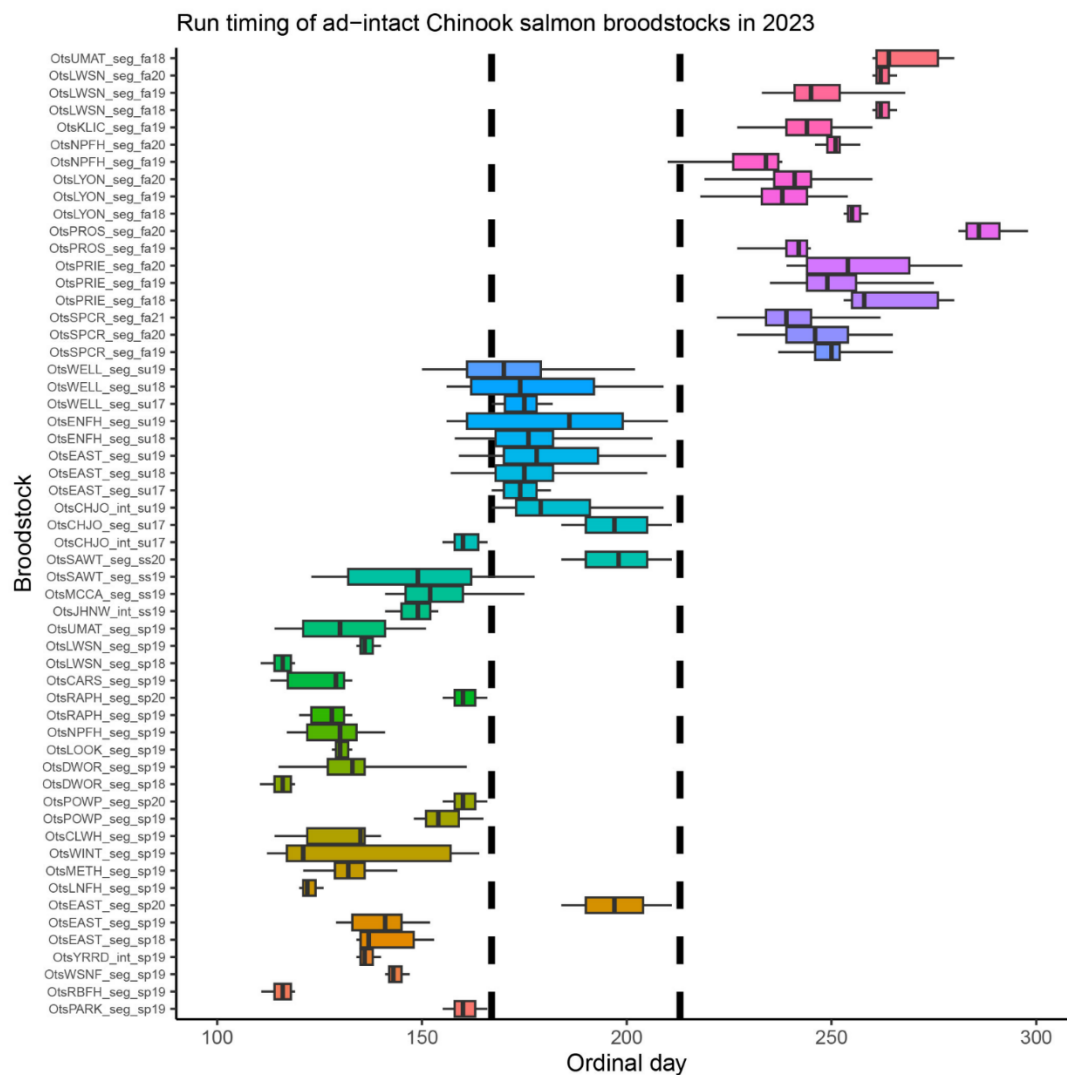
**Figure 28. Reporting group-level run-timing distributions (median ordinal day, interquartile range, and 5<sup>th</sup> and 95<sup>th</sup> percentile) for clipped and unclipped hatchery-origin adult-sized Chinook salmon that were sampled at Bonneville Dam in 2023 during the spring, summer, and fall management periods (separated by dashed lines).**





**Figure 29.** Reporting group-level run-timing distributions (median ordinal day, interquartile range, and 5<sup>th</sup> and 95<sup>th</sup> percentile) for natural-origin adult-sized Chinook salmon that were sampled at Bonneville Dam in 2023 during the spring, summer, and fall management periods (separated by dashed lines).



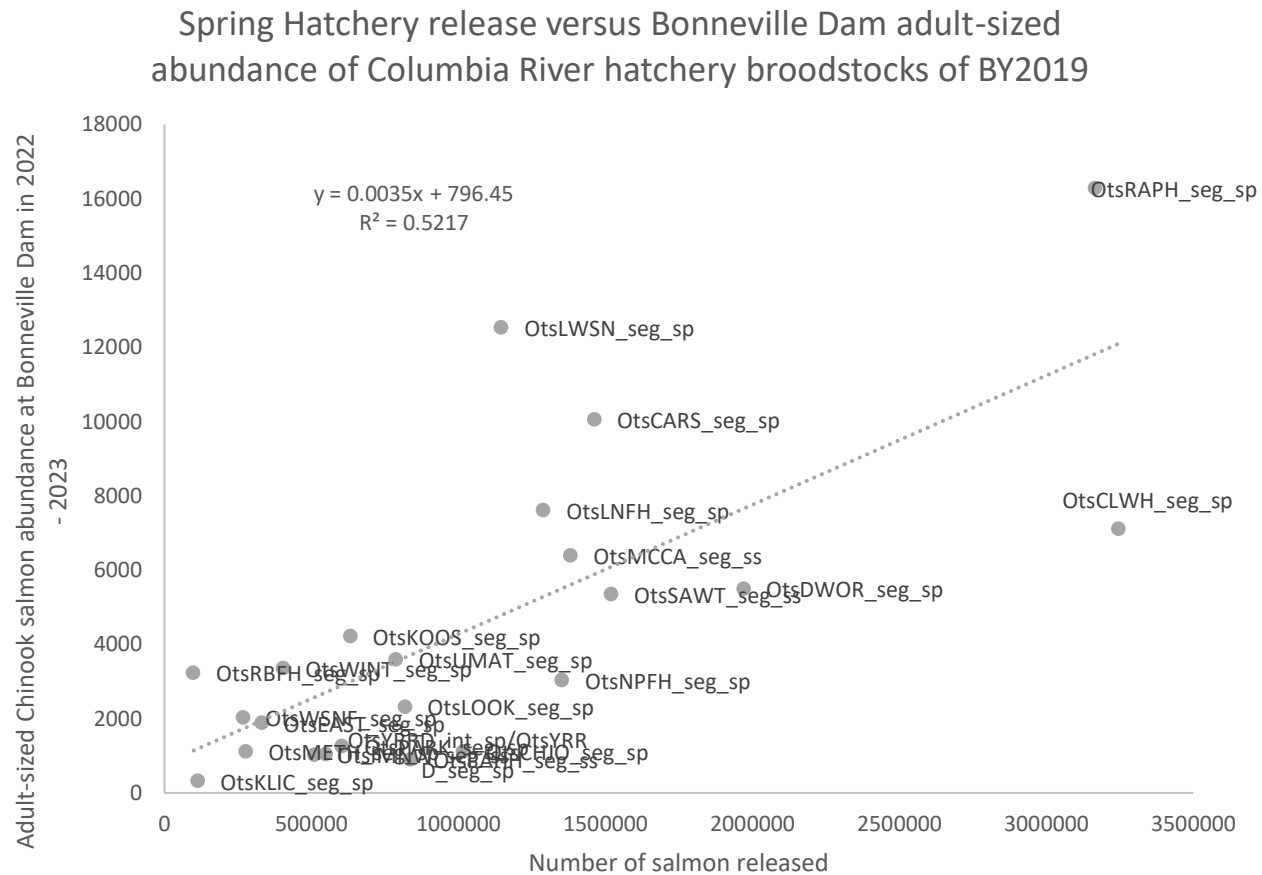


**Figure 31. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5<sup>th</sup> and 95<sup>th</sup> percentile) for unclipped adult-sized Chinook salmon that were sampled at Bonneville Dam in 2023 during the spring, summer, and fall management periods (separated by dashed lines).**

*Demonstration of PBT to estimate smolt-to-adult survival using the adult Spring- and Summer-Run Chinook salmon clipped and unclipped hatchery-origin stocks that passed Bonneville Dam in 2022 – 2023*

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 2019 (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 SY2019 broodstocks that returned to Bonneville Dam as adults in 2022 and 2023 (i.e., 3- and 4-year-olds, respectively). Inclusion of the abundance estimates from 2022 would be more 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  $R^2$  (0.52) of the linear trend (Figure 32).

This smolt-to-adult survival type of analysis may be highly beneficial for management of these hatchery stocks in the future and we will continue using the hatchery release information and PBT abundance estimates in this kind of analysis. This is the third 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 286 Spring Chinook salmon smolts released converted to 1 adult-sized Spring Chinook salmon that returned to Bonneville Dam in 2022 and 2023.



**Figure 32. Smolt release numbers of hatchery-origin Spring Chinook salmon of BY2019 from Columbia River hatcheries above Bonneville Dam versus the estimated abundance of BY2019 adult-sized fish that passed Bonneville Dam in 2022 – 2023.**

### *Estimated relative abundance of steelhead stocks in 2023*

Daily passage of summer A-/B-Index steelhead at Bonneville Dam in 2023 is provided in Figure 33. Among clipped hatchery-origin summer A-/B-Index steelhead, there were five major stocks (abundance >1000) represented in the total estimated abundance (N=71,761) of clipped hatchery origin steelhead passing Bonneville Dam in 2022 (Table 55). These stocks in order of decreasing magnitude were 07\_MGILCS (20,050), 10\_SFCLWR (14,274, B-Index; 6,244, A-Index), 14\_UPSALM (23,286), 09\_UPPCOL (6,513), and 03\_SKAMAN (1,016) (Table 55; Figure 34). All of these major clipped stocks were A-Index size fish except for 10\_SFCLWR which had a combination of both A-Index and B-Index fish.

Among the unclipped hatchery-origin summer A-/B-Index steelhead, there was a single major stock (abundance >1000) represented in the total estimated abundance (N=6,717) of unclipped hatchery origin steelhead passing Bonneville Dam in 2023 (Table 56; Figure 34). This stock was 10\_SFCLWR (3,225, B-Index; 1,061, A-Index).

Using PBT assignments we can now provide abundance (Table 58; Figure 35) and run-timing estimates for each of the clipped and unclipped hatchery broodstocks (Table 58). There were 17 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 2023 (Table 58).

These stocks with greater than 1,000 abundance were OmyDWOC\_su20 (A-Index = 1,958 and B-Index = 11,736), OmySAWT\_su21 (A-Index = 7,796), OmyWELL\_su21 (A-Index = 4,200), OmyOXBO\_su21 (A-Index = 4,198), OmyPAHH\_su20 (A-Index = 3,950), OmyWALL\_su21 (A-Index = 3,805), OmyPAHH\_su21 (A-Index = 3,351 and B-Index = 62), OmyCGRW\_su20 (A-Index = 3,092), OmyWALL\_su20 (A-Index = 2,928), OmyLSCR\_su21 (A-Index = 2,562), OmySFCR\_su20 (A-Index = 513 and B-Index = 2,538), OmyCGRW\_su21 (A-Index = 2,362), OmyOXBO\_su20 (A-Index = 1,980), OmyMINT\_su21 (A-Index = 1,520), OmyWELL\_su20 (A-Index = 1,503), OmyDWOC\_su21 (A-Index = 1,418), and OmySFCR\_su21 (A-Index = 1,113). Almost all of these abundances were dominated by A-Index fish except for the stocks OmyDWOC\_su20 and OmySFCR\_su20, which had notable B-Index contributions.

There were five major stocks (abundance >1000) represented in the total estimated abundance (N=32,209) of natural origin (excluding adipose unclipped hatchery-origin fish) summer A-/B-Index steelhead passing Bonneville Dam in 2023 (Table 57). These stocks in order of decreasing magnitude were 07\_MGILCS (20,213 A-Index), 14\_UPSALM (3,720 A-Index), 09\_UPPCOL (2,783 A-Index), 10\_SFCLWR (1,423 A-Index), and 08\_YAKIMA (1,159 A-Index). This year there were no major stocks of natural-origin B-Index.

Table 55. Stock-specific abundance and run-timing by A-/B-Index categories of clipped hatchery-origin summer A-/B-Index steelhead passing Bonneville Dam in 2023.

Size	Hatchery origin- Clipped		Sample N	Estimated abundance		Run-timing distribution							
	Reporting Group name	Reporting Group Code		Mean		95% CI		Ordinal day					
				Median	1st quartile	3rd quartile	5th percentile	95th percentile	Median date	Interquartile range (days)			
A-INDEX	Lower Columbia	02_LOWCOL										-	
	Skamania	03_SKAMAN	4	1,016	476 – 1900	203	194	220	186	254	7/22/2023	26	
	Willamette	04_WILLAM										-	
	Big White Salmon	05_BWSALM										-	
	Klickitat	06_KLICKR										-	
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	90	20,050	16310 – 22069	221	202	243	188	260	8/9/2023	41	
	Yakima	08_YAKIMA										-	
	upper Columbia	09_UPPCOL	25	6,513	4760 – 8248	215	202	240	188	258	8/3/2023	38	
	SF Clearwater	10_SFCLWR	46	6,244	4300 – 7283	254	244	263	232	277	9/11/2023	19	
	upper Clearwater	11_UPCLWR										-	
	SF Salmon	12_SFSALM										-	
	MF Salmon	13_MFSALM										-	
	upper Salmon	14_UPSALM	106	23,286	21495 – 27601	224	206	243	189	264	8/12/2023	37	
	A-INDEX Subtotal		271	57,109									
B-INDEX	Lower Columbia	02_LOWCOL										-	
	Skamania	03_SKAMAN		0	0 – 0	195	190	200	184	204.2	7/14/2023	10	
	Willamette	04_WILLAM										-	
	Big White Salmon	05_BWSALM										-	
	Klickitat	06_KLICKR										-	

mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	1	257	0 – 1045							-
Yakima	08_YAKIMA										-
upper Columbia	09_UPPCOL		0	0 – 0	233	228	252	191	262	8/21/2023	24
SF Clearwater	10_SFCLWR	62	14,274	12848 – 16979	255	244	264	229	279	9/12/2023	20
upper Clearwater	11_UPCLWR										-
SF Salmon	12_SFSALM										-
MF Salmon	13_MFSALM										-
upper Salmon	14_UPSALM	2	122	3 – 299	261	251	268	241	281	9/18/2023	17
	<b>B-INDEX Subtotal</b>	<b>65</b>	<b>14,652</b>								

**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 56. Stock-specific abundance and run-timing by A-/B-Index categories of unclipped hatchery-origin summer A-/B-Index steelhead passing Bonneville Dam in 2023.

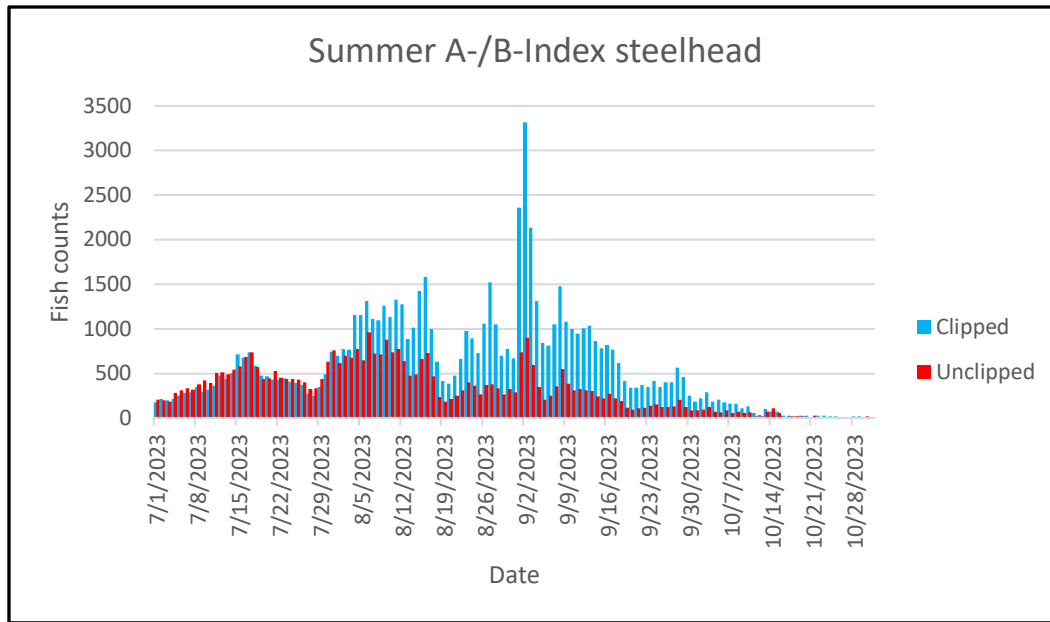
Size	Hatchery origin- Unclipped		Sample N	Estimated abundance		Run-timing distribution						
						Ordinal day						
	Reporting Group name	Reporting Group Code		Mean	95% CI	Median	1st quartile	3rd quartile	5th percentile	95th percentile	Median date	Interquartile range (days)
A-INDEX	Lower Columbia	02_LOWCOL										
	Skamania	03_SKAMAN										
	Willamette	04_WILLAM										
	Big White Salmon	05_BWSALM										
	Klickitat	06_KLICKR		52	0 – 102	276	271	281	268	287	10/2/2023	10
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	4	684	55 – 1390	213	199	220	187	271	8/1/2023	21
	Yakima	08_YAKIMA										
	upper Columbia	09_UPPCOL	2	639	7 – 1327	242	233	247	227	272	8/30/2023	14
	SF Clearwater	10_SFCLWR	14	1,061	740 – 1275	267	258	276	254	288	9/24/2023	18
	upper Clearwater	11_UPCLWR										
	SF Salmon	12_SFSALM										
	MF Salmon	13_MFSALM										
	upper Salmon	14_UPSALM	6	762	355 – 1292	260	201	274	188	288	9/17/2023	73
		A-INDEX Subtotal	26	3,198								
B-INDEX	Lower Columbia	02_LOWCOL										
	Skamania	03_SKAMAN										
	Willamette	04_WILLAM										
	Big White Salmon	05_BWSALM										
	Klickitat	06_KLICKR										

mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS		294	0 – 869	198	192	204	185	210	7/17/2023	12
Yakima	08_YAKIMA										
upper Columbia	09_UPPCOL										
SF Clearwater	10_SFCLWR	13	3,225	1724 – 4437	245	235	254	227	271	9/2/2023	19
upper Clearwater	11_UPCLWR										
SF Salmon	12_SFSALM										
MF Salmon	13_MFSALM										
upper Salmon	14_UPSALM										
	<b>B-INDEX Subtotal</b>	<b>13</b>	<b>3,519</b>								

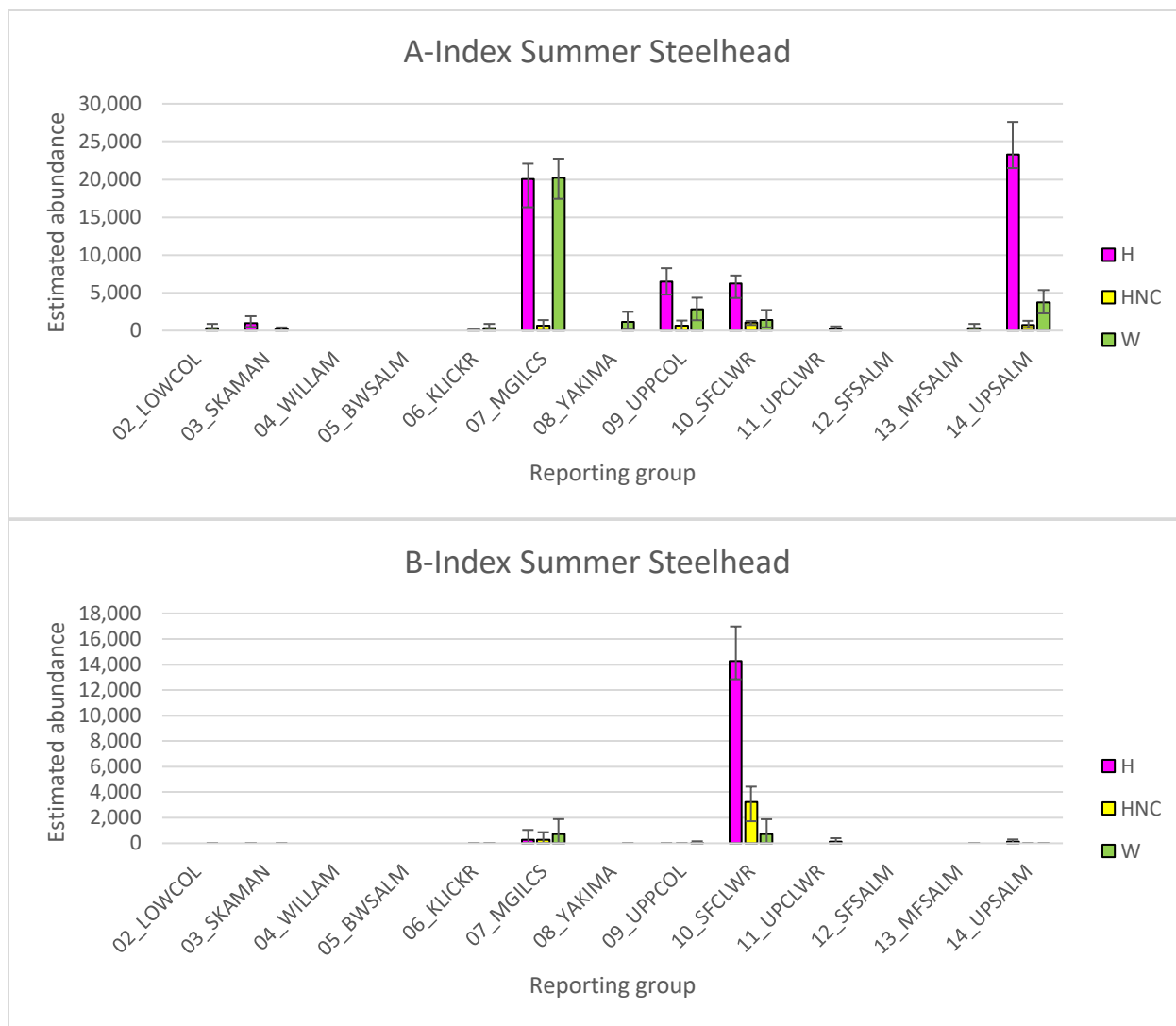
Table 57. Stock-specific abundance and run-timing by A-/B-Index categories of unclipped natural-origin summer A-/B-Index steelhead passing Bonneville Dam in 2023.

Size						Run-timing distribution						
	Natural origin- No Clip					Ordinal day						
	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	1	294	0 – 882	198	192	204	185	210	7/17/2023	12
	Skamania	03_SKAMAN	1	140	0 – 419	218	215	222	212	224	45,144	7
	Willamette	04_WILLAM				-	-	-	-	-	-	-
	Big White Salmon	05_BWSALM				-	-	-	-	-	-	-
	Klickitat	06_KLICKR	2	294	0 – 882	198	192	204	185	210	7/17/2023	12
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	99	20,213	17417 – 22744	215	200	225	188	253	8/3/2023	25
	Yakima	08_YAKIMA	4	1,159	140 – 2471	226	211	240	190	251	8/14/2023	29
	upper Columbia	09_UPPCOL	12	2,783	1370 – 4340	225	213	243	192	256	8/13/2023	30
	SF Clearwater	10_SFCLWR	6	1,423	422 – 2722	231	215	249	192	261	8/19/2023	34
	upper Clearwater	11_UPCLWR	2	273	0 – 552	225	218	258	213	265	8/13/2023	40
	SF Salmon	12_SFSALM				-	-	-	-	-	-	-
	MF Salmon	13_MFSALM	1	294	0 – 882	198	192	204	185	210	7/17/2023	12
	upper Salmon	14_UPSALM	20	3,720	2273 – 5353	216	201	224	188	256	8/4/2023	23
			A-INDEX Subtotal	148	30,593							
B-INDEX	Lower Columbia	02_LOWCOL				-	-	-	-	-	-	-
	Skamania	03_SKAMAN				-	-	-	-	-	-	-
	Willamette	04_WILLAM				-	-	-	-	-	-	-
	Big White Salmon	05_BWSALM				-	-	-	-	-	-	-
	Klickitat	06_KLICKR				-	-	-	-	-	-	-
	mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	3	719	0 – 1890	244	234	251	227	261	9/1/2023	17
	Yakima	08_YAKIMA				-	-	-	-	-	-	-

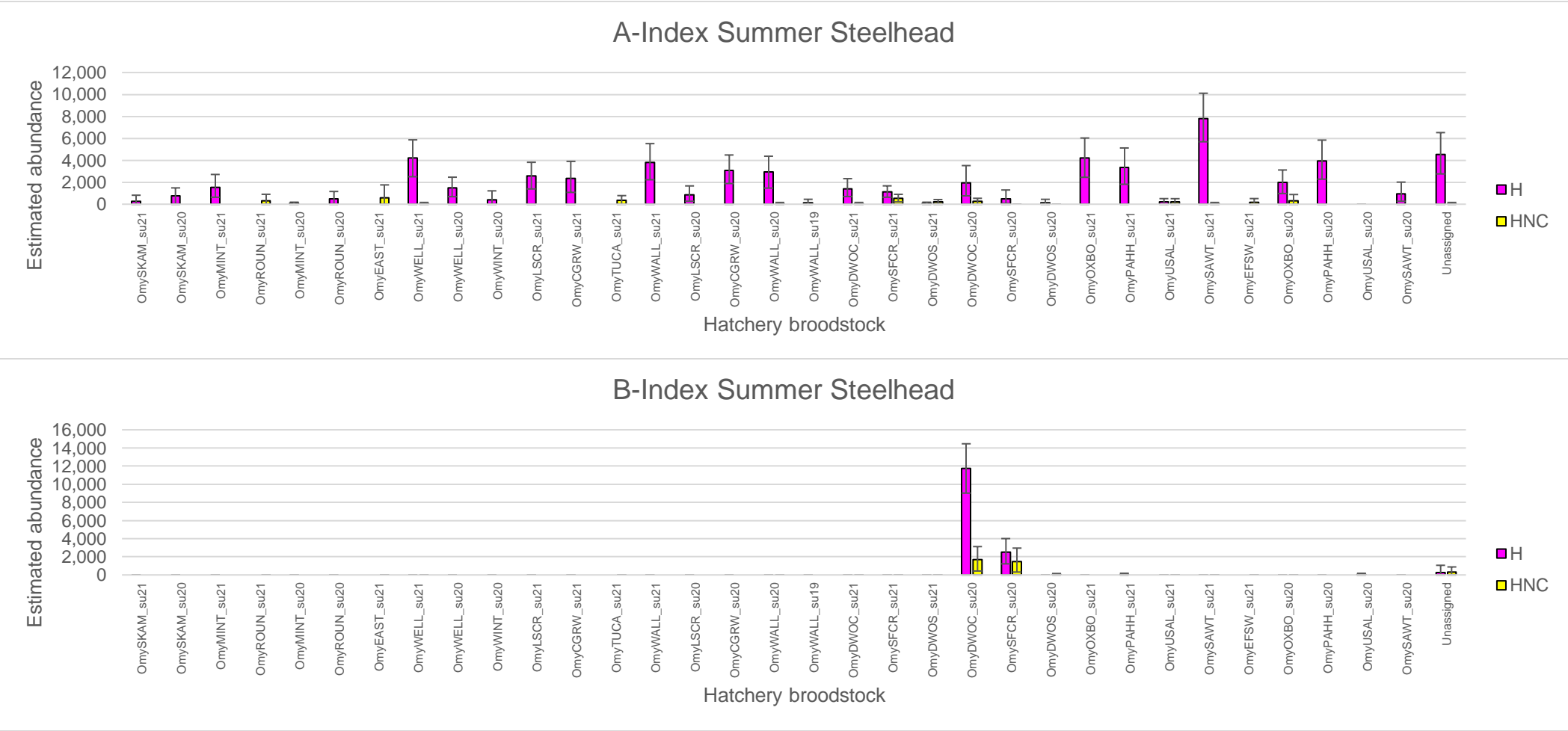
	upper Columbia	09_UPPCOL	1	51	0 – 155	276	271	281	268	287	45,201	10
	SF Clearwater	10_SFCLWR	2	714	0 – 1883	244	234	251	227	261	9/1/2023	17
	upper Clearwater	11_UPCLWR	1	133	0 – 398	258	256	261	254	266	9/15/2023	5
	SF Salmon	12_SFSALM				-	-	-	-	-	-	-
	MF Salmon	13_MFSALM				-	-	-	-	-	-	-
	upper Salmon	14_UPSALM				-	-	-	-	-	-	-
		<b>B-INDEX Subtotal</b>	<b>7</b>	<b>1,616</b>								



**Figure 33. Daily passage of clipped (blue) and unclipped (red) steelhead at Bonneville Dam in 2023 during the summer A-/B-Index management period (source: <https://www.fpc.org>).**



**Figure 34. Estimated abundance ( $\pm$  95% CI) of A-Index (<780mm FL, top) and B-Index ( $\geq$ 780mm FL, bottom) hatchery origin (clipped “H” and unclipped “HNC”) and natural-origin (“W”) steelhead assigned to genetic stock of origin that were sampled at Bonneville Dam in 2023.**



**Figure 35. 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 2023.**

**Key to broodstock collection is presented in Appendix 4.**

Table 58. Hatchery broodstock-specific estimated abundance of clipped and unclipped A-Index and B-Index PBT-assigned steelhead passing Bonneville Dam in 2023.

					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	

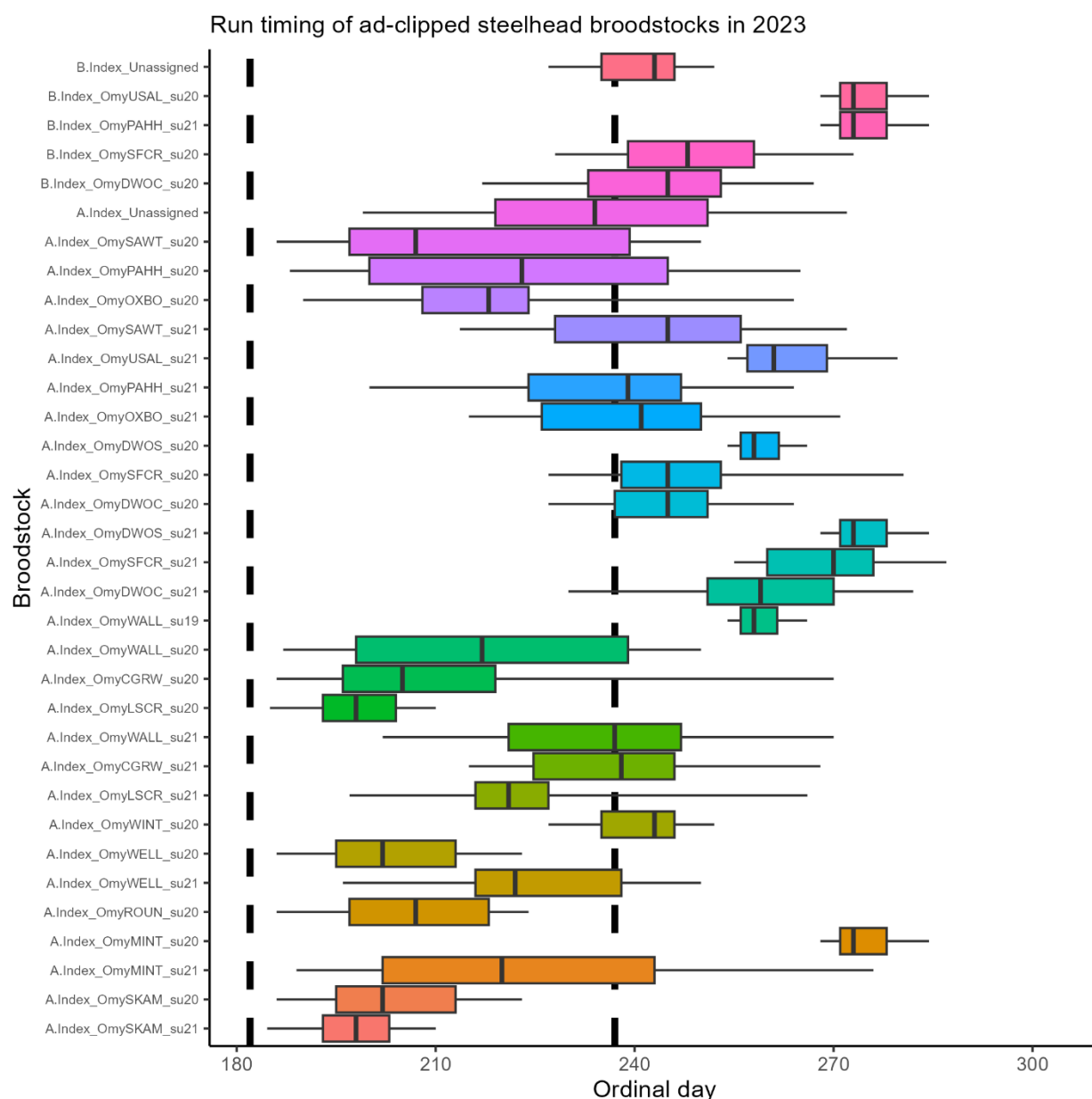
**Note:** These abundance estimates were calculated using a method to estimate abundance of each stock based on temporally stratified stock proportions and total numbers of clipped and unclipped steelhead that passed the Bonneville Dam at the fish counting window. Key to broodstock collection is presented in Appendix 4.



### *Run-timing of steelhead stocks in 2023*

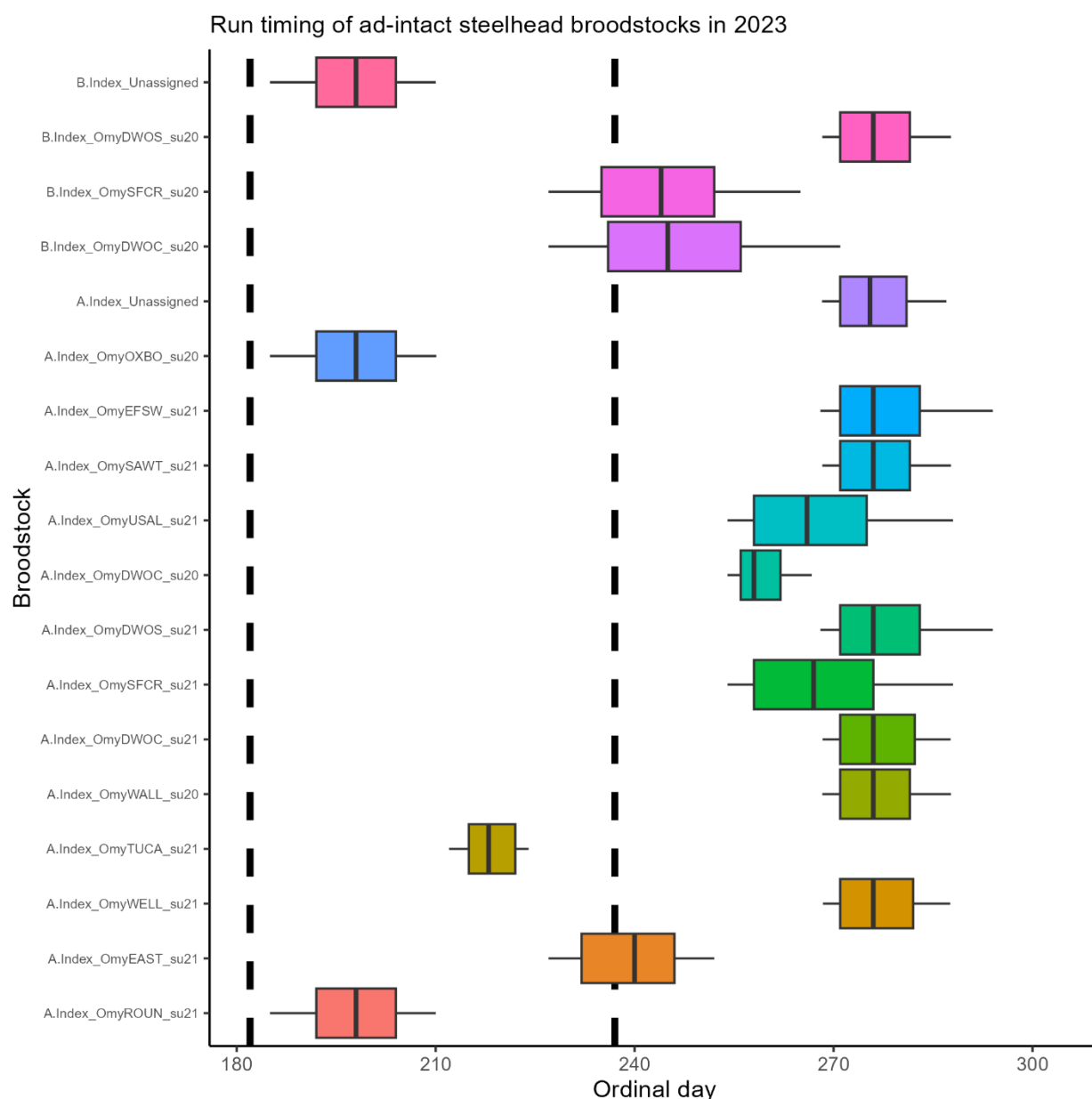
We were able to characterize the run-timing distributions at the broodstock level for the clipped (Figure 36) and unclipped (Figure 37) hatchery steelhead stocks arriving during the summer A-/B-Index management period. Very few winter-run steelhead stocks exist above Bonneville Dam and our sampling program 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 4/1/2023 – 6/30/2023, and the summer A-/B-Index period begins on 7/1/2023 and lasts until 10/31/2023. 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 25<sup>th</sup> (Ordinal day 237) at Bonneville Dam (Figure 36). There were a total of 29 different clipped hatchery broodstocks and of these 29 broodstocks, there were 14 broodstocks (OmySKAM\_su21, OmySKAM\_su20, OmyMINT\_su20, OmyWELL\_su21, OmyWINT\_su20, OmyCGRW\_su21, OmyWALL\_su21, OmyWALL\_su19, OmyDWOC\_su21, OmySFCR\_su21, OmyDWOS\_su21, OmySFCR\_su20, OmyPAHH\_su21, and OmyUSAL\_su21) that had median dates observed after August 25<sup>th</sup> in 2023. 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 16 unique broodstocks, and 11 of them had a median run date after August 25<sup>th</sup>. (Figure 37).

We characterized the run-timing distributions for natural-origin steelhead stocks (Figure 38); the patterns generally are consistent with past years. The late arriving stocks with median dates on or after August 25<sup>th</sup> were 07\_MGILCS (B-Index), 10\_SFCLWR (both A-Index and B-Index), 11\_UPCLWR (B-Index), and 09\_UPPCOL (B-Index). For the four 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 (10\_SFCLWR).



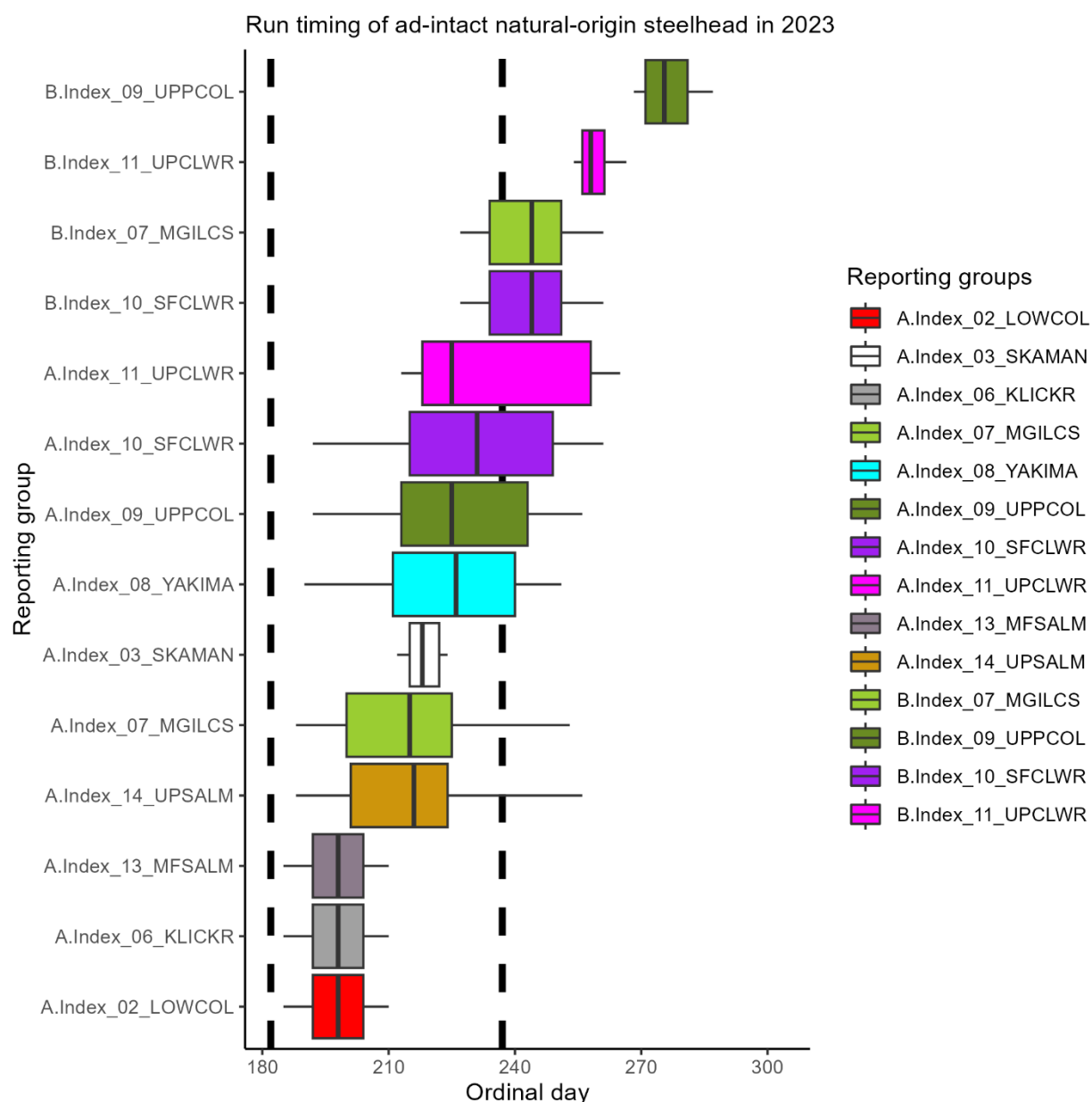
**Figure 36. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5<sup>th</sup> and 95<sup>th</sup> percentile) for clipped hatchery-origin steelhead that were sampled at Bonneville Dam in 2023 and reported by A-Index and B-Index size category.**

**Key to broodstock collection is presented in Appendix 4.**



**Figure 37. PBT hatchery broodstock-level run-timing distributions (median ordinal day, interquartile range, and 5<sup>th</sup> and 95<sup>th</sup> percentile) for unclipped hatchery-origin steelhead that were sampled at Bonneville Dam in 2023 and reported by A-Index and B-Index size category.**

**Key to broodstock collection is presented in Appendix 4.**

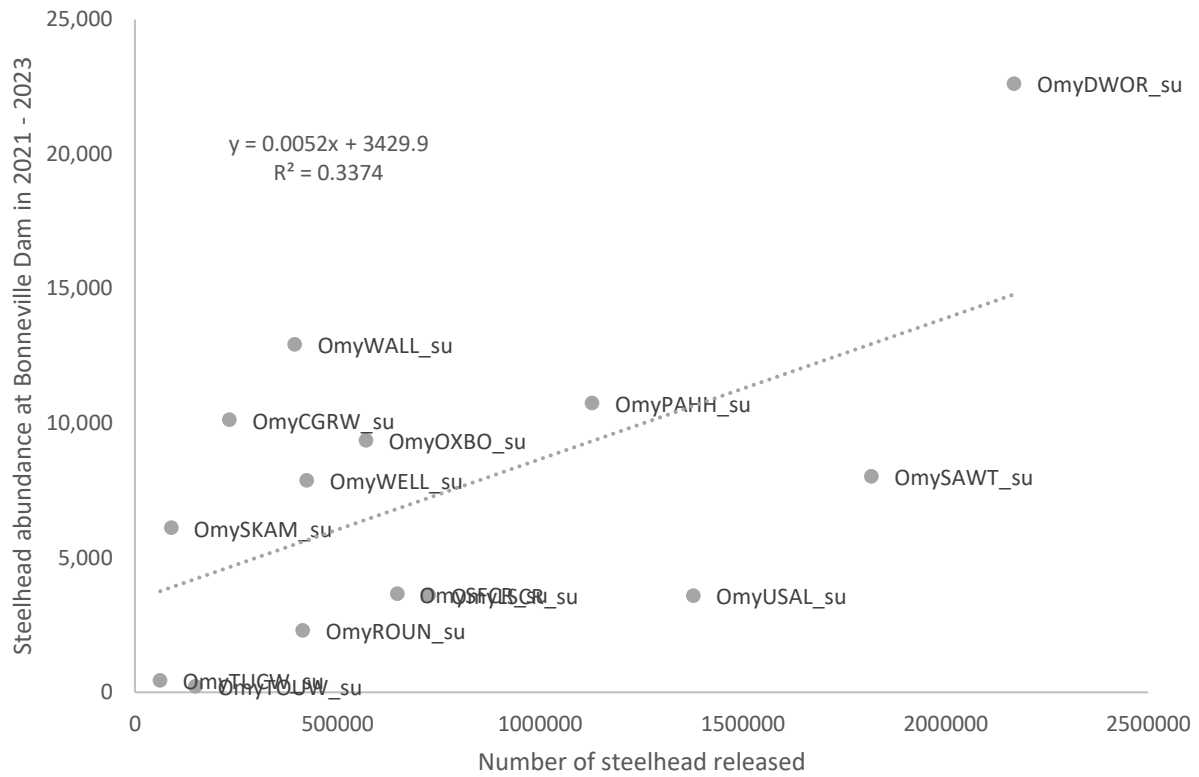


**Figure 38. Reporting group level run-timing distributions (median ordinal day, interquartile range, and 5<sup>th</sup> and 95<sup>th</sup> percentile) for natural-origin steelhead (unclipped hatchery-origin fish excluded) that were sampled at Bonneville Dam in 2023 and split by A-Index and B-Index size category.**

*Demonstration of PBT to estimate smolt-to-adult survival using the A-/B-Index Summer steelhead clipped and unclipped hatchery-origin stocks that passed Bonneville Dam in 2021 – 2023*

We obtained the release information for clipped and unclipped hatchery-origin steelhead from Columbia River hatcheries located upstream of Bonneville Dam from Brood Year 2019 (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 steelhead with the corresponding abundance we estimated for the SY2019 broodstocks that returned to Bonneville Dam as adults in 2021 – 2023 (i.e., 1- 2- and 3-ocean ages). There was moderate correspondence of number of clipped and unclipped releases versus Bonneville Dam abundance estimates for Spring-run stocks based on the  $R^2$  (0.33) of the linear trend (**Figure 39**). This smolt-to-adult survival type of analysis may be highly beneficial for management of these hatchery stocks in the future and we will continue using the hatchery release information and PBT abundance estimates in this kind of analysis. This is the first analysis that we have performed using steelhead. This current analysis demonstrated a trend of 192 steelhead smolts released converted to 1 Summer Steelhead that returned to Bonneville Dam between 2021 and 2023.

### Steelhead Hatchery juvenile release versus Bonneville Dam adult abundance of Columbia River hatchery broodstocks of BY2019



**Figure 39. Smolt release numbers of hatchery-origin Steelhead of BY2019 from Columbia River hatcheries versus the estimated abundance of BY2019 fish that passed Bonneville Dam during the Summer Period.**

*Estimated abundance and run-timing of Sockeye salmon stocks in 2023*

Daily passage of Sockeye salmon at Bonneville Dam in 2023 is provided in Figure 40. Stock abundance for sockeye salmon was estimated over a course of 18 statistical weeks (i.e. weeks 19 – 37). A total of 1,108 sockeye salmon were sampled at Bonneville Dam in 2023 and were assigned to one of four genetic stocks (i.e., Okanogan, Wenatchee, Snake (and Alturas), and Lake Billy Chinook) using GSI and one reintroduced stock (Yakima) using PBT (Table 49). The Okanogan stock had the highest relative abundance (178,796), followed by the Wenatchee (144,914) (Table 59). This year there were a small number of sockeye estimated from Snake River (3,036). The Lake Billy Chinook stock had 73 and the reintroduced stock from Yakima River had 669 estimated abundance (Table 59, Figure 41).

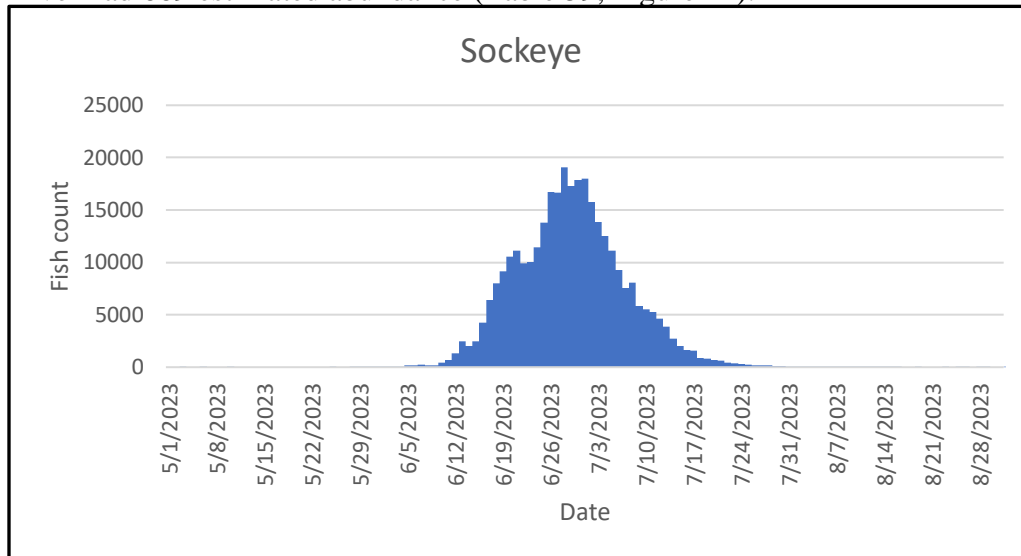
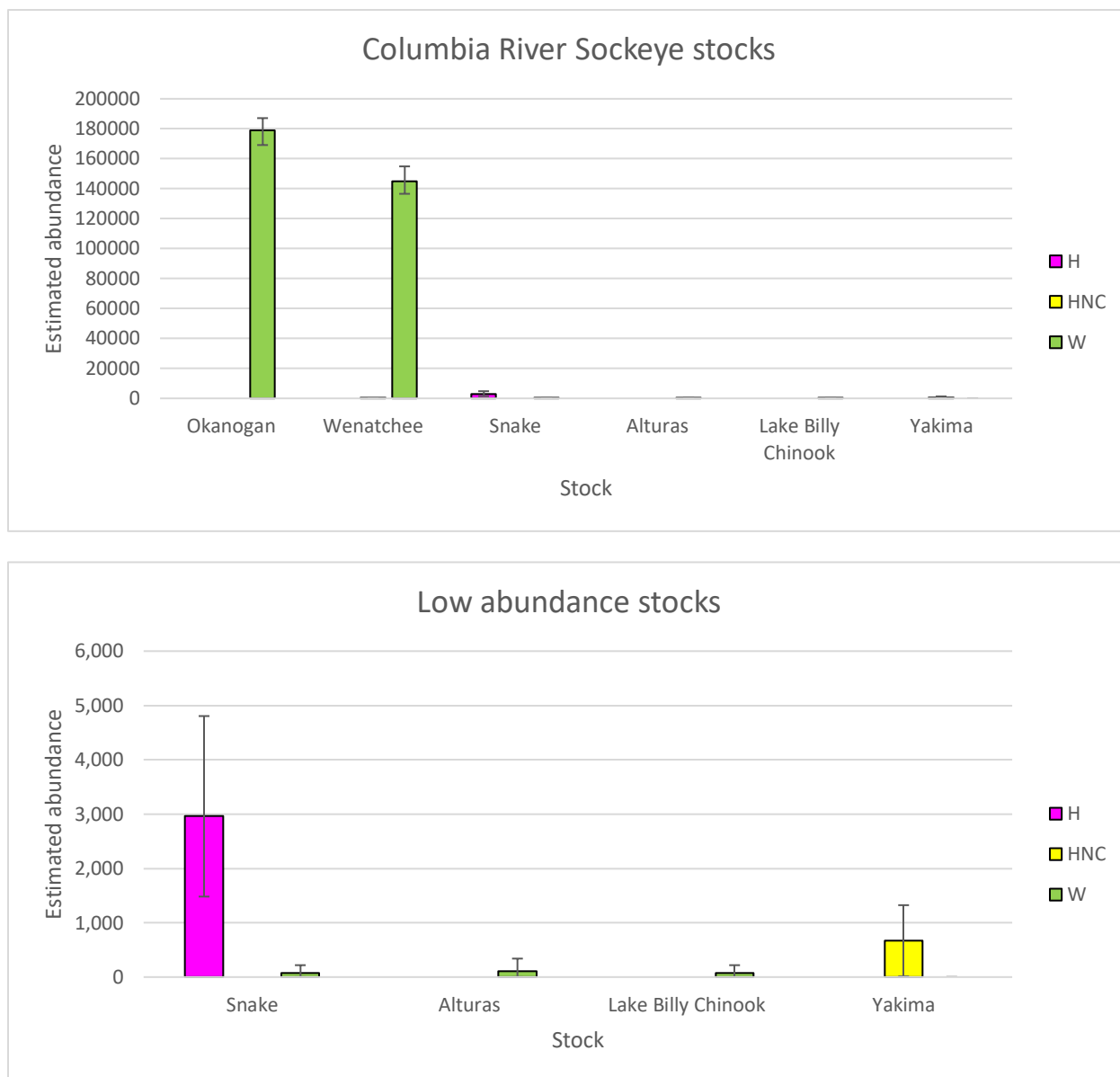


Figure 40. Daily passage of sockeye at Bonneville Dam in 2023 (source: <https://www.fpc.org>).



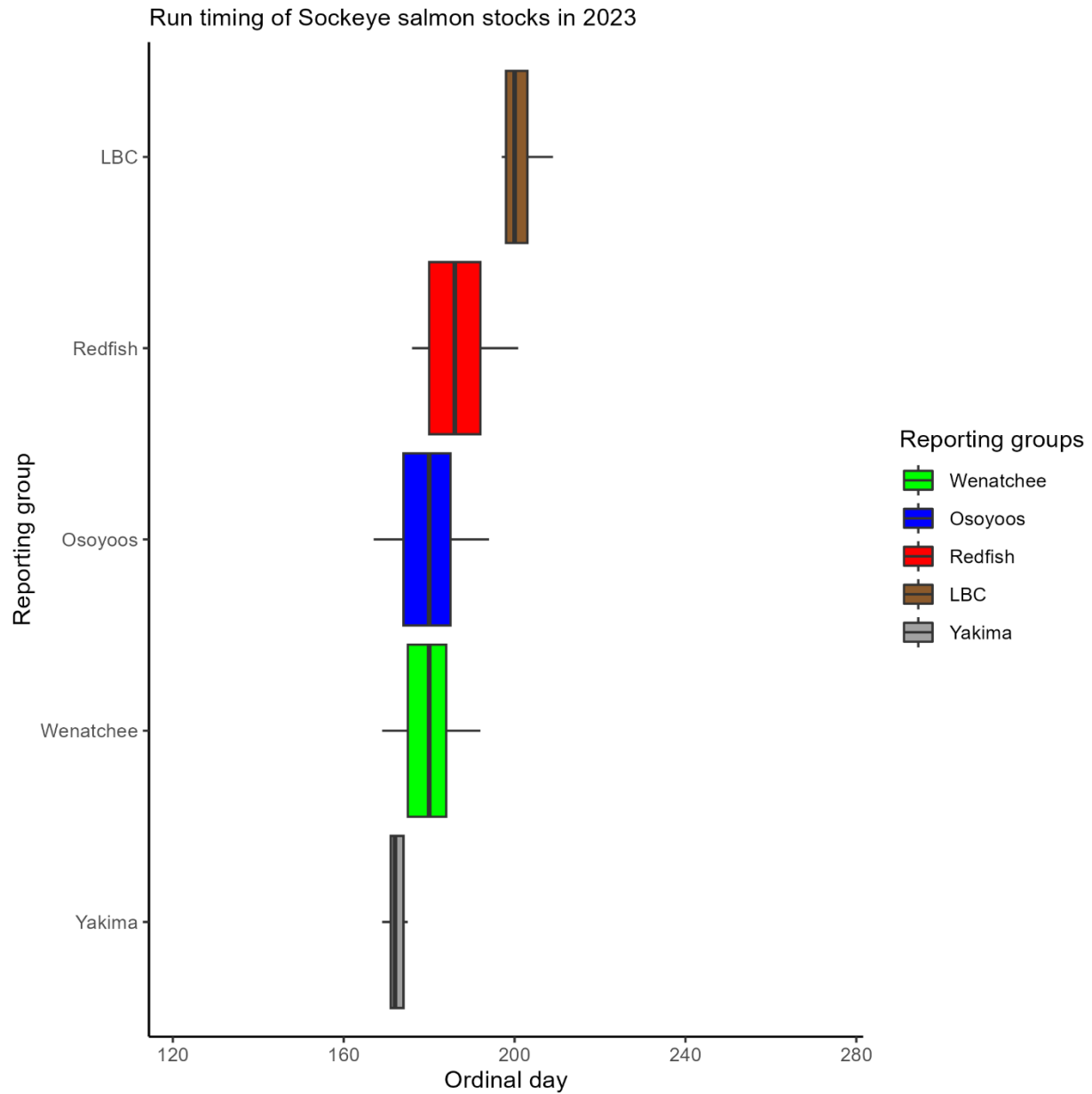
**Figure 41. Estimated abundance ( $\pm$  95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2023.**

We characterized the run-timing distributions for all detected sockeye salmon stocks (Figure 42). The Wenatchee and Okanogan stocks had nearly identical run timing distributions with the same median date on 06/29/23. Snake River stock was relatively later timed (median date of 7/5/2023 and Yakima was earlier timed (6/21/2023 median date, Figure 42).



**Table 59. Estimated abundance of sockeye salmon stocks passing Bonneville Dam in 2023.**

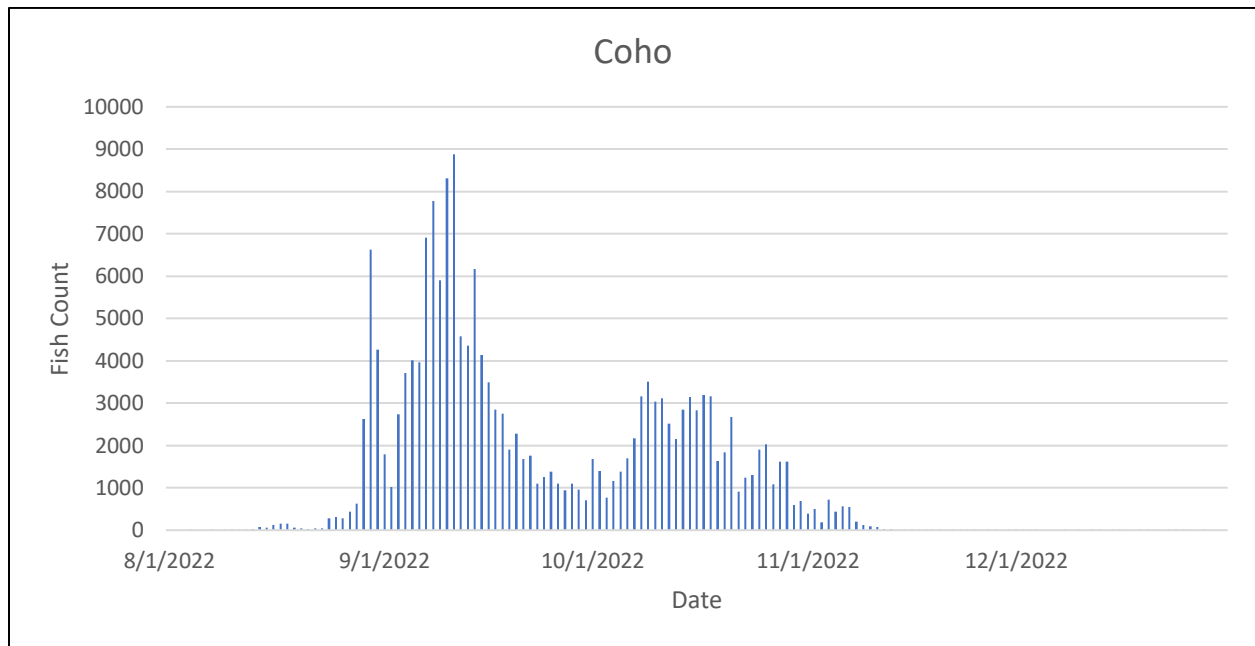
Reporting Group name	Estimated abundance					
	H		HNC		W	
	Est.	95% CI	Est.	95% CI	Est.	95% CI
Okanogan					178,796	169131 – 187099
Wenatchee			73	0 – 73	144,840	136573 – 154893
Snake	2,963	1482 – 4805			73	0 – 219
Alturas					113	0 – 340
Lake Billy Chinook					73	0 – 219
Yakima			669	13 – 1324	0	0
Total	2,963		742		323,896	



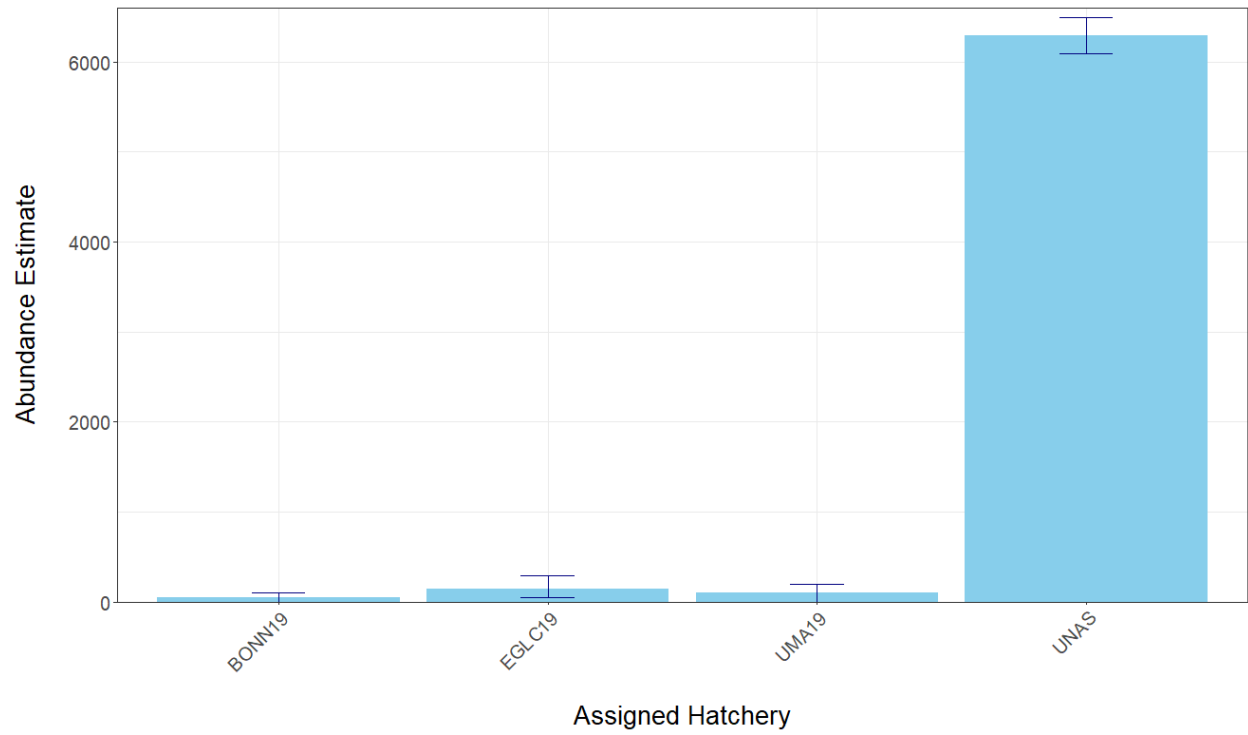
**Figure 42. Run-timing distributions (median ordinal day, interquartile range, and 5<sup>th</sup> and 95<sup>th</sup> percentile) for the major stocks of sockeye salmon that were sampled at Bonneville Dam in 2023 and assigned to stock of origin.**

*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.**

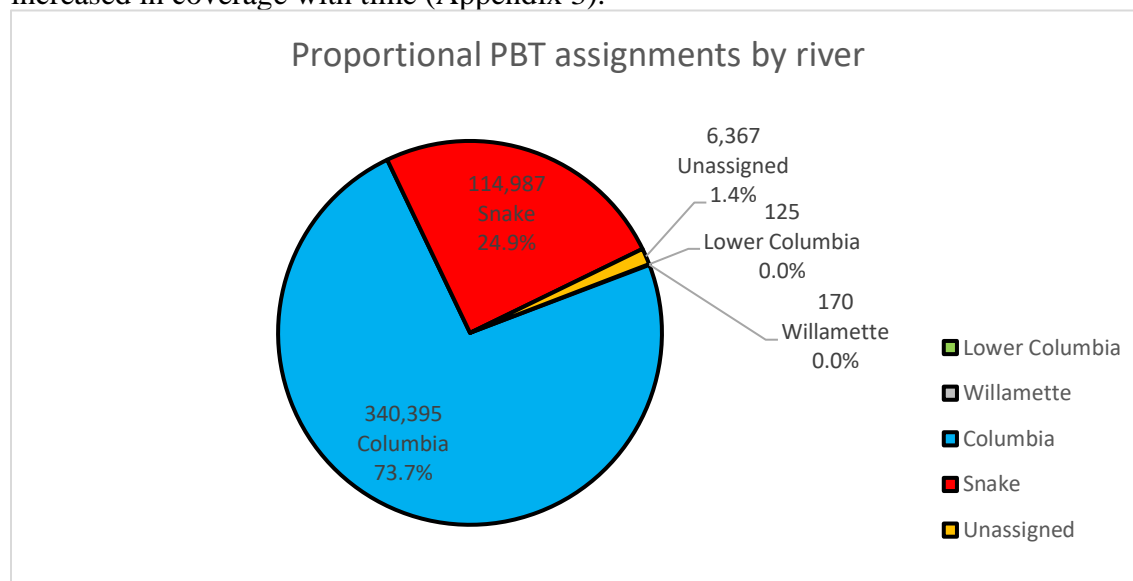
### *In-season analysis of Chinook salmon passing Bonneville Dam in 2024*

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 2023 across all management periods (Table 46). The first report was distributed to members of the U.S. v OR TAC on May 13, 2024. 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 2023. We use window counts of the adult-sized fish 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 2,862 adult-sized Chinook Salmon were collected and analyzed for the 2024 in-season reports (Table 60). 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 11, 2024 provided sub-totals for each stock that were broken out by management period (clipped hatchery-origin stocks, Table 61; unclipped hatchery-origin stocks, Table 62; natural-origin stocks, Table 63). 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 63) and upper Columbia River spring Chinook Salmon stocks (Reporting group 10\_UCOLSP, Table 63). 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 86 unique hatchery broodstocks in 2024 (Table 64). The total estimated abundances of these clipped and unclipped broodstocks were comprised of 0.2% Lower Columbia, 0.3% Willamette, 19.3% Snake River, and 57.1% 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 2024. 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 65). In fact, in 2024, the percentage of adipose-clipped fish abundance that were estimated to be PBT broodstock were 99.1%, 95.0%, and 97.8% 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). Consistent with recent 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 2024.**

**Table 60. The sample sizes of Chinook salmon at the Bonneville Dam AFF during the spring, summer, and fall management periods of 2024.**

		Statistical week	TAC		Sample (N)						
					Clipped		Unclipped		Subtotal		Rate
			clip count	unclip count	H	HNC	W	clip	unclip	clip	unclip
Management period	Spring	1-16	2,995	335				0	0	0.00%	0.00%
		17	10,645	1,305	50	48	13	50	61	0.47%	4.68%
		18	19,349	2,603	167	4	18	167	22	0.86%	0.85%
		19	24,337	4,036	138	13	15	138	28	0.57%	0.69%
		20	10,914	3,113	101	13	15	101	28	0.93%	0.90%
		21	4,426	2,343	65	14	36	65	50	1.47%	2.13%
		22	3,345	2,554	15	7	15	15	22	0.45%	0.86%
		23	4,617	2,181	51	9	15	51	24	1.10%	1.10%
		24	8,830	3,282	63	14	12	63	26	0.71%	0.79%
	Summer	25	8,979	3,011	20	4	1	20	5	0.22%	0.17%
		26	8,576	1,888	18	3	1	18	4	0.21%	0.21%
		27	5,959	1,381	47	3	7	47	10	0.79%	0.72%
		28	3,043	1,057	32		7	32	7	1.05%	0.66%
		29	2,005	1,089	25	4	12	25	16	1.25%	1.47%
		30	1,357	1,244	18	2	13	18	15	1.33%	1.21%
		31	744	1,229	6	6	4	6	10	0.81%	0.81%
	Fall	31	725	1,198	4	2	1	4	3	0.55%	0.25%
		32	1,919	3,528	13	16	14	13	30	0.68%	0.85%
		33	4,301	10,120	13	15	16	13	31	0.30%	0.31%
		34	27,484	31,212	53	38	36	53	74	0.19%	0.24%
		35	48,502	63,084	75	68	97	75	165	0.15%	0.26%
		36	44,109	72,136	88	78	102	88	180	0.20%	0.25%
		37	25,214	55,645	82	61	88	82	149	0.33%	0.27%
		38	13,680	31,457	78	63	120	78	183	0.57%	0.58%
		39	9,695	21,206	69	44	113	69	157	0.71%	0.74%
		40	5,981	10,275	39	27	83	39	110	0.65%	1.07%
		41	1,866	5,177	13	15	84	13	99	0.70%	1.91%
		42	1,260	2,445	2		8	2	8	0.16%	0.33%
		43-44	1,120	2,422				0	0	0.00%	0.00%
		<b>Total</b>	<b>305,974</b>	<b>342,559</b>	<b>1,345</b>	<b>571</b>	<b>946</b>	<b>1,345</b>	<b>1,517</b>	<b>0.44%</b>	<b>0.44%</b>

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 and unclipped adult abundance. The AFF sample is broken into adipose-clipped and unclipped categories and then further indicate whether an unclipped fish with a PBT assignment (PBT) is Hatchery unclipped “HNC” or putatively natural origin (“W”). 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 61. 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 2024.**

		H	Spring		Summer		Fall		Cumulative total date Nov. 2
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	
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_UMATILLFA					4,320	2037 – 7706	4,320
<b>Total</b>			<b>110,116</b>		<b>39,212</b>		<b>278,042</b>		<b>427,371</b>

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 2, 2024 are provided. Bonneville 2023 spring, summer, and fall management period Chinook PBT/GSI analyses that corresponds with statistical weeks 1 – 24 (01/01/24-06/15/24: spring), 24 – 31 (6/16/24-7/31/24:summer) and 31 – 44 (8/1/2024-11/2/2024:fall).

**Table 62. 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 2024.**

		HNC	Spring		Summer		Fall		Cumulative total date Nov. 2
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							0
West Cascade Fall	Fall	03_WCASFA							0
Willamette	Spring	04_WILLAM							0
Spring Creek Tule	Fall	05_SPCRTU					20,268	15352 - 27247	20,268
Klickitat	Spring	06_KLICKR	48	0 - 141					48
Deschutes spring	Spring	07_DESCSP	417	301 - 939					417
John Day	Spring	08_JOHNDR							0
Yakima	Spring	09_YAKIMA	112	5 - 332					112
Upper Columbia spring	Spring	10_UCOLSP	2,234	1315 - 2497	661	15 - 1307			2,895
Tucannon	Spring	11_TUCANO							0
Hells Canyon	Spring/Summer	12_HELLSC	2,784	1995 - 4132					2,784
South Fork Salmon	Spring/Summer	13_SFSALM	904	531 - 1393					904
Chamberlain Creek	Spring/Summer	14_CHMBLN							0
Middle Fork Salmon	Spring/Summer	15_MFSALM							0
Upper Salmon	Spring/Summer	16_UPSALM	463	143 - 938	666	15 - 1316			1,129
Deschutes fall	Fall	17_DESCFA							0
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	1,577	1288 - 2373	2,118	1335 - 3407	71,756	66240 - 89231	75,452

Snake River fall	Fall	19_SRFALL			1,079	686 - 1363	33,371	29031 - 36624	34,451
Bonneville Pool spring	Spring	20_BONPOOLSP	362	195 - 498					362
Umatilla spring	Spring	21_UMATILLASP	673	69 - 1007					673
Bonneville Pool fall	Fall	22_BONPOOLFA					16,404	12960 - 21641	16,404
Umatilla fall	Fall	23_UMATILLAFA					172	0 - 508	172
<b>Total</b>			<b>9,574</b>		<b>4,524</b>		<b>141,971</b>		<b>156,069</b>

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 02, 2024 are provided.

**Table 63. Preliminary in-season reporting of natural-origin stock-specific abundance estimates of adult-sized Chinook Salmon passing Bonneville Dam across all management periods in 2024.**

		W	Spring		Summer		Fall		Cumulative total date Nov. 2
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	NA	NA					0
West Cascade Spring	Spring	02_WCASSP	NA	NA					0
West Cascade Fall	Fall	03_WCASFA	NA	NA					0
Willamette	Spring	04_WILLAM	NA	NA	96	0 - 289			96
Spring Creek Tule	Fall	05_SPCRTU	NA	NA	96	0 - 289	6,180	3716 - 9280	6,276
Klickitat	Spring	06_KLICKR	NA	NA					0
Deschutes spring	Spring	07_DESCSP	NA	NA					0
John Day	Spring	08_JOHNDR	118	0 - 290					118
Yakima	Spring	09_YAKIMA	380	101 - 720					380
Upper Columbia spring	Spring	10_UCOLSP	1,810	1154 - 2632	330	0 - 990			2,140
Tucannon	Spring	11_TUCANO	237	0 - 473					237
Hells Canyon	Spring/Summer	12_HELLSC	4,787	3781 - 5795	330	0 - 991			5,117
South Fork Salmon	Spring/Summer	13_SFSALM	1,298	771 - 1902	330	0 - 990			1,628

Chamberlain Creek	Spring/Summer	14_CHMBLN	274	47 - 558					274
Middle Fork Salmon	Spring/Summer	15_MFSALM	906	441 - 1466					906
Upper Salmon	Spring/Summer	16_UPSALM	1,063	520 - 1626					1,063
Deschutes fall	Fall	17_DESCFA	NA	NA	96	0 - 289	3,183	1725 - 4856	3,279
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	1,308	775 - 1933	4,622	3380 - 5927	128,369	119408 - 136989	134,299
Snake River fall	Fall	19_SRFALL	NA	NA	475	180 - 859	30,202	24886 - 35251	30,676
<b>Total</b>			<b>12,180</b>		<b>6,376</b>		<b>167,934</b>		<b>186,490</b>

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 02, 2024 are provided.

**Table 64. The estimated abundances of the clipped and unclipped adult-sized Chinook salmon assigned to PBT hatchery broodstock that passed Bonneville Dam in 2024 (1/01/2024 – 11/02/2024).**

						Abundance estimate				
Period	Expected Run Time	Hatchery	Broodstock	Brood year	GSI RepGrp	Clipped		Unclipped		Total
						Est.	95% C.I.	Est.	95% C.I.	
Spring	01Spring	Parkdale Fish Facility	OtsPARK_seg_sp20	2020	02_WCASSP	730	231 - 1301			730
	01Spring	Speelyai Fish Hatchery	OtsSPEE_seg_sp20	2020	02_WCASSP	125	0 - 347			125
	01Spring	Klickitat Hatchery	OtsKLIC_seg_sp20	2020	06_KLICKR	212	0 - 497	48	0 - 143	260
	01Spring	Round Butte Fish Hatchery	OtsRBFH_seg_sp20	2020	07_DESCSP	109	0 - 326			109
	01Spring	Warm Springs National Fish Hatchery	OtsWSNF_seg_sp20	2020	07_DESCSP	184	0 - 552	417	116 - 833	600
	01Spring	Yakima River Roza Dam	OtsYRRD_int_sp20	2020	09_YAKIMA	1,625	809 - 2526	112	0 - 337	1,738
	01Spring	Yakima River Roza Dam	OtsYRRD_seg_sp20	2020	09_YAKIMA	108	0 - 324			108
	01Spring	Chief Joseph Hatchery	OtsCHJO_seg_sp20	2020	10_UCOLSP	1,568	733 - 2438	355	85 - 658	1,923
	01Spring	Eastbank Fish Hatchery	OtsEAST_seg_sp20	2020	10_UCOLSP	530	108 - 1066	1,133	616 - 1701	1,663
	01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp19	2019	10_UCOLSP	232	0 - 579			232
	01Spring	Leavenworth National Fish Hatchery	OtsLNFH_seg_sp20	2020	10_UCOLSP	6,572	4854 - 8211	411	172 - 708	6,983
	01Spring	Methow Fish Hatchery	OtsMETH_seg_sp20	2020	10_UCOLSP			284	0 - 851	284
	01Spring	Methow Fish Hatchery	OtsMETH_seg_sp21	2021	10_UCOLSP			51	0 - 154	51
	01Spring	Winthrop National Fish Hatchery	OtsWINT_seg_sp19	2019	10_UCOLSP	117	0 - 351			117
	01Spring	Winthrop National Fish Hatchery	OtsWINT_seg_sp20	2020	10_UCOLSP	1,522	787 - 2307			1,522
	01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp19	2019	12_HELLSC	450	0 - 996			450
	01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp20	2020	12_HELLSC	9,381	7415 - 11381	81	0 - 162	9,462
	01Spring	Clearwater Fish Hatchery	OtsPOWP_seg_sp20	2020	12_HELLSC			602	222 - 1032	602
	01Spring	Clearwater Fish Hatchery	OtsCLWH_seg_sp21	2021	12_HELLSC	91	0 - 272			91
	01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp19	2019	12_HELLSC	232	0 - 579	144	0 - 433	376
	01Spring	Dworshak National Fish Hatchery	OtsKOOS_seg_sp19	2019	12_HELLSC	123	0 - 364	57	0 - 143	180
	01Spring	Dworshak National Fish Hatchery	OtsDWOR_seg_sp20	2020	12_HELLSC	10,734	8635 - 12779	88	28 - 177	10,822
	01Spring	Dworshak National Fish Hatchery	OtsKOOS_seg_sp20	2020	12_HELLSC	1,355	558 - 2302			1,355

01Spring	Lookingglass Fish Hatchery	OtsLOOK_seg_sp20	2020	12_HELLSC	3,111	1962 - 4238	617	206 - 1137	3,728
01Spring	Lookingglass Fish Hatchery	OtsLOOK_seg_sp21	2021	12_HELLSC	108	0 - 324			108
01Spring	Nez Perce	OtsNPFH_seg_sp19	2019	12_HELLSC	587	117 - 1260			587
01Spring	Nez Perce	OtsNPFH_seg_sp20	2020	12_HELLSC			172	0 - 462	172
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp19	2019	12_HELLSC	193	0 - 437			193
01Spring	Rapid River Fish Hatchery	OtsRAPH_seg_sp20	2020	12_HELLSC	12,471	10473 - 14571	1,021	531 - 1500	13,491
01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp19	2019	20_BONPOOLSP	108	0 - 324			108
01Spring	Carson National Fish Hatchery	OtsCARS_seg_sp20	2020	20_BONPOOLSP	10,985	9057 - 13208	108	27 - 188	11,093
01Spring	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp19	2019	20_BONPOOLSP			28	0 - 85	28
01Spring	Little White Salmon National Fish Hatchery	OtsLWSN_seg_sp20	2020	20_BONPOOLSP	6,548	4849 - 8095	226	113 - 339	6,774
01Spring	Umatilla Fish Hatchery	OtsUMAT_seg_sp20	2020	21_UMATILLASP	969	385 - 1599	673	256 - 1166	1,642
01Spring	Umatilla Fish Hatchery	OtsUMAT_seg_sp21	2021	21_UMATILLASP	121	0 - 363			121
02Spring/Summer	Lookingglass Fish Hatchery	OtsIMNW_seg_ss20	2020	12_HELLSC	691	216 - 1249			691
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss19	2019	13_SFSALM			48	0 - 144	48
02Spring/Summer	McCall Fish Hatchery	OtsJHNW_int_ss20	2020	13_SFSALM			429	116 - 874	429
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss20	2020	13_SFSALM	1,424	811 - 2174	427	95 - 791	1,851
02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss21	2021	13_SFSALM	91	0 - 272			91
02Spring/Summer	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss19	2019	16_UPSALM	108	0 - 325			108
02Spring/Summer	Pahsimeroi Fish Hatchery	OtsPAHH_seg_ss20	2020	16_UPSALM	646	251 - 1092			646
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss19	2019	16_UPSALM	383	0 - 819			383
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss20	2020	16_UPSALM	2,344	1486 - 3323	463	160 - 811	2,808
03Summer	Chief Joseph Hatchery	OtsCHJO_int_su19	2019	18_UCOLSF	755	286 - 1275	129	0 - 386	883
03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su19	2019	18_UCOLSF	146	0 - 437			146
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su18	2018	18_UCOLSF	225	0 - 675			225
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su19	2019	18_UCOLSF	1,942	1222 - 2752	242	0 - 591	2,184
03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su20	2020	18_UCOLSF	841	280 - 1402			841
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su18	2018	18_UCOLSF	184	0 - 551			184
03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su19	2019	18_UCOLSF	2,347	1395 - 3221	232	0 - 539	2,579

	03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su20	2020	18_UCOLSF	557	154 - 1041	139	0 - 417	696
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su19	2019	18_UCOLSF	3,447	2584 - 4364	576	207 - 1015	4,023
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su20	2020	18_UCOLSF	1,355	686 - 2038	260	0 - 520	1,614
	NA	NA	Unassigned	NA	NA	773	318 - 2124			773
			Spring Subtotal			89,456		9,574		99,030
Summer	01Spring	Parkdale Fish Facility	OtsPARK_seg_sp21	2021	02_WCASSP	88	0 - 265			88
	01Spring	North Santiam Hatchery	OtsNSAN_seg_sp19	2019	04_WILLAM	170	0 - 510			170
	01Spring	Eastbank Fish Hatchery	OtsEAST_seg_sp20	2020	10_UCOLSP			661	0 - 1322	661
	02Spring/Summer	McCall Fish Hatchery	OtsMCCA_seg_ss20	2020	13_SFSALM	839	277 - 1679			839
	02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss20	2020	16_UPSALM			334	0 - 1001	334
	02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT_seg_ss21	2021	16_UPSALM			332	0 - 996	332
	03Summer	Chief Joseph Hatchery	OtsCHJO_int_su18	2018	18_UCOLSF	88	0 - 265			88
	03Summer	Chief Joseph Hatchery	OtsCHJO_int_su19	2019	18_UCOLSF	3,891	2581 - 5393	337	0 - 1012	4,228
	03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su19	2019	18_UCOLSF	1,425	563 - 2446	343	0 - 1030	1,768
	03Summer	Chief Joseph Hatchery	OtsCHJO_int_su20	2020	18_UCOLSF	674	125 - 1479			674
	03Summer	Chief Joseph Hatchery	OtsCHJO_seg_su20	2020	18_UCOLSF	1,487	633 - 2561	113	0 - 338	1,599
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su18	2018	18_UCOLSF	736	178 - 1561	333	0 - 1000	1,069
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su19	2019	18_UCOLSF	2,478	1282 - 3688	661	0 - 1322	3,139
	03Summer	Eastbank Fish Hatchery	OtsEAST_seg_su20	2020	18_UCOLSF	2,995	1813 - 4379	331	0 - 992	3,326
	03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su19	2019	18_UCOLSF	5,009	3331 - 6596			5,009
	03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su20	2020	18_UCOLSF	1,923	803 - 3141			1,923
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su18	2018	18_UCOLSF	108	0 - 323			108
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su19	2019	18_UCOLSF	4,226	2743 - 5962			4,226
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su20	2020	18_UCOLSF	2,162	1036 - 3316			2,162
	03Summer	Wells Fish Hatchery	OtsWELL_seg_su21	2021	18_UCOLSF	195	0 - 390			195
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa19	2019	19_SRFALL			201	0 - 401	201
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa20	2020	19_SRFALL	535	178 - 892	584	195 - 973	1,119
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa21	2021	19_SRFALL	90	0 - 270	196	0 - 392	286
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa19	2019	19_SRFALL			99	0 - 297	99

			Unassigned			1,542	525 - 3006			1,542
			Summer Subtotal			30,662		4,524		35,186
Fall	03Summer	Chief Joseph Hatchery	OtsCHJO_int_su19	2019	18_UCOLSF	472	0 - 945			472
	03Summer	Chief Joseph Hatchery	OtsCHJO_int_su20	2020	18_UCOLSF	344	0 - 1033			344
	03Summer	Entiat National Fish Hatchery	OtsENFH_seg_su20	2020	18_UCOLSF			255	0 - 766	255
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa19	2019	05_SPCRTU	713	0 - 2139	190	0 - 569	903
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa20	2020	05_SPCRTU	12,730	8954 - 16504	2,238	861 - 3691	14,968
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa21	2021	05_SPCRTU	3,468	1534 - 5786	13,580	9926 - 17521	17,048
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR_seg_fa22	2022	05_SPCRTU	24,785	18809 - 29597	4,260	2067 - 6665	29,045
	04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa19	2019	18_UCOLSF	11,615	8166 - 15453	19,968	15661 - 24533	31,583
	04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa20	2020	18_UCOLSF	41,642	34777 - 47390	35,703	29432 - 41792	77,345
	04Fall	Priest Rapids Hatchery	OtsPRIE_seg_fa21	2021	18_UCOLSF	15,100	10880 - 18776	14,085	9992 - 18226	29,185
	04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa19	2019	18_UCOLSF	2,317	714 - 4389			2,317
	04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa20	2020	18_UCOLSF	1,749	523 - 3306	187	0 - 560	1,936
	04Fall	Ringold Springs State Hatchery	OtsRING_seg_fa21	2021	18_UCOLSF	900	248 - 1873	716	0 - 1696	1,616
	04Fall	Yakima Nation Prosser Hatchery	OtsPROS_seg_fa20	2020	18_UCOLSF	323	0 - 962	842	0 - 2105	1,165
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa19	2019	19_SRFALL	3,648	1517 - 5893	5,128	2995 - 7472	8,777
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa20	2020	19_SRFALL	17,341	13076 - 22041	15,469	12042 - 19008	32,811
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON_seg_fa21	2021	19_SRFALL	4,503	2190 - 6867	6,839	4239 - 9394	11,342
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa19	2019	19_SRFALL	666	0 - 1998	478	0 - 1194	1,144
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa20	2020	19_SRFALL	2,917	912 - 5126	4,656	2549 - 6855	7,574
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH_seg_fa21	2021	19_SRFALL	658	0 - 1974	800	175 - 1663	1,458
	04Fall	Klickitat Hatchery	OtsKLIC_seg_fa19	2019	22_BONPOOLFA			677	0 - 2030	677
	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa19	2019	22_BONPOOLFA	3,810	1661 - 5973	9,936	7086 - 13164	13,746
	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa20	2020	22_BONPOOLFA	21,107	16438 - 25880	2,784	1276 - 4429	23,891
	04Fall	Little White Salmon National Fish Hatchery	OtsLWSN_seg_fa21	2021	22_BONPOOLFA	6,176	3905 - 8912	3,007	1630 - 4687	9,183
	04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa19	2019	23_UMATILLFA			172	0 - 516	172



	04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa20	2020	23_UMATILLAFA	2,370	756 - 4158			2,370
	04Fall	Umatilla Fish Hatchery	OtsUMAT_seg_fa21	2021	23_UMATILLAFA	2,448	1049 - 3963			2,448
			Unassigned			4,052	2572 - 10551			4,052
			Fall Subtotal			185,856		141,971		327,827

**Table 65. Expanded abundance of PBT-unassigned Chinook Salmon stocks across management periods in 2024.**

Management period	Clipped adult abundance		% PBT of Clipped fish
	Unassigned	Subtotal	
Spring	773	89,456	99.1%
Summer	1,542	30,662	95.0%
Fall	4,052	185,856	97.8%

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% for each management period.

*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 (7/1/2024 – 10/31/2024, Table 46). The Skamania Management Period (4/1/2024 – 6/30/2024) had a single report that covered the entire Skamania period. There was a total of 722 clipped and 426 unclipped steelhead that were sampled at the Bonneville Dam AFF and genotyped in 2024 (Table 66). 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 66). 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 67, Table 68, Table 69). We also incorporate tag rate expansion to account for the percentage of each hatchery stock that has been successfully genotyped. Tag rate expansions have been used previously in all of our genetic analyses for Chinook salmon, Sockeye salmon and steelhead. However, one feature that has been missing from our tag rate expansion methods in the past is a way to balance the numbers of fish that are expanded in the PBT broodstock categories by subtracting an equal set of fish from the sample. This issue is now resolved through our implementation of SCOBIDEUX and SPIBETR methodologies described previously (Section 3). Finally, as we have demonstrated in our post-season analyses, the preliminary analysis reports for 2024 include a breakdown of all the A- and B-Index steelhead abundance by broodstock for both clipped and unclipped hatchery-origin groups (Table 70).

**Table 66. The sample sizes of Summer Steelhead at the Bonneville Dam AFF during the Skamania and A-/B-Index management periods of 2024.**

		Sample (N)														
		Statistical				A-Index				B-Index				Clipped	Unclipped	
						Clipped	Unclipped	Clipped	Unclipped	Sample	Sample					
week	Strata	count	count	Clipped	Unclipped	H	HNC	W	Total	H	HNC	W	Total	rate	rate	
Management period	Skamania	14	1	21	98										0.00%	0.00%
		15	1	10	58										0.00%	0.00%
		16	1	30	60										0.00%	0.00%
		17	1	71	62	1	2		3						1.41%	3.23%
		18	1	80	41	2		1	3	1				1	3.75%	2.44%
		19	1	126	53	3		5	8						2.38%	9.43%
		20	1	237	89	10		3	13						4.22%	3.37%
		21	1	164	82	1		3	4						0.61%	3.66%
		22	1	293	113	3		1	4						1.02%	0.88%
		23	1	327	168	10		1	11						3.06%	0.60%
		24	1	906	595	8	1	2	11	1				1	0.99%	0.50%
		25	1	1353	1,137	1			1						0.07%	0.00%
		26	1	1654	1,581	2			2						0.12%	0.00%
		Subtotal Skamania		5272	4137	41	3	16	60	2	0	0	2			
	A-/B-Index	27	1	3137	2,748	10	1	10	21	1				1	0.35%	0.40%
		28	1	3969	4,096	30	1	19	50	1			1	2	0.78%	0.51%
		29	1	5001	5,552	36	4	51	91				1	1	0.72%	1.01%
		30	2	6637	6,068	32	3	28	63	2			1	3	0.51%	0.53%
		31	2	8128	6,123	36	1	23	60	3				3	0.48%	0.39%
		32	3	8374	4,999	62	2	53	117	2	2	2		6	0.76%	1.18%
		33	4	5758	2,565	50	3	25	78	6	2	5		13	0.97%	1.36%
		34	4	15358	6,133	11	1	3	15	2			1	3	0.08%	0.08%
		35	5	11,010	3,857	32	1	8	41	14			2	16	0.42%	0.29%
		36	5	13,375	4,607	24	5	5	34	17	7	3		27	0.31%	0.43%

		37	6	10,989	3,883	12	4	4	20	39	10	2	51	0.46%	0.52%
		38	6	10,225	3,415	28	4	2	34	68	21	2	91	0.94%	0.85%
		39	7	6,412	2,056	20	11	4	35	49	28	1	78	1.08%	2.14%
		40	8	1,766	698	13	4	2	19	31	8	1	40	2.49%	2.15%
		41	8	914	413	21	3	9	33	21	7	3	31	4.60%	5.33%
		42	8	431	222	3	1		4	3	1	1	5	1.39%	1.35%
		43	8	296	161										
		44	8	187	182										
Summer A-/B-Index subtotal				111,967	57,778	420	49	246	715	259	86	26	371		
<b>Total</b>				<b>117,239</b>	<b>61,915</b>	<b>461</b>	<b>52</b>	<b>262</b>	<b>775</b>	<b>261</b>	<b>86</b>	<b>26</b>	<b>373</b>		

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 to indicate whether the fish were clipped hatchery-origin (H), unclipped hatchery-origin (HNC), or natural-origin (W). Sample rate relates the total sample for a particular stratum to the total fish counted at the window.

**Table 67. Estimated abundance of clipped hatchery-origin stocks of Summer Steelhead that passed Bonneville Dam in 2024 during the Skamania and A-/B-Index Management Periods.**

Reporting Group name	Reporting Group Code	H		Subtotal for Skamania Period (Apr 1 - Jun 30)		Subtotal for Skamania Period (Apr 1 - Jun 30)		Subtotal for A-/B-Index Period (Jul 01 - Oct 31)		Subtotal for A-/B-Index Period (Jul 01 - Oct 31)	
		A-Index		B-Index		A-Index		B-Index			
		Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI
Lower Columbia	02_LOWCOL	51	0 - 292	0	0 - 0						
Skamania	03_SKAMAN	4,730	4238 - 5095	245	6 - 490	4,785	3571 - 5640	715	470 - 1939		
Willamette	04_WILLAM										
Big White Salmon	05_BWSALM										
Klickitat	06_KLICKR										
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	246	6 - 608	0	0 - 0	15,523	12472 - 18025	39	0 - 112		
Yakima	08_YAKIMA										

upper Columbia	09_UPPCOL					9,334	8684 - 11785	2,217	963 - 3283
SF Clearwater	10_SFCLWR					5,502	4368 - 7604	28,642	26596 - 31572
upper Clearwater	11_UPCLWR								
SF Salmon	12_SFSALM								
MF Salmon	13_MFSALM								
upper Salmon	14_UPSALM					41,959	38723 - 45149	3,251	2380 - 4285
<b>Total</b>		<b>5,027</b>		<b>245</b>		<b>77,103</b>		<b>34,864</b>	

Note: Based on the sample data described in Table 66 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 68. Estimated abundance of unclipped hatchery-origin stocks of Summer Steelhead that passed Bonneville Dam in 2024 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)	
Reporting Group name	Reporting Group Code	A-Index		B-Index		A-Index		B-Index	
		Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI
Lower Columbia	02_LOWCOL								
Skamania	03_SKAMAN	435	0 - 643			286	0 - 429	0	0 - 0
Willamette	04_WILLAM								
Big White Salmon	05_BWSAL M								
Klickitat	06_KLICKR								
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS					2,092	1119 - 3140	0	0 - 0
Yakima	08_YAKIMA								
upper Columbia	09_UPPCOL	218	0 - 218			1,535	717 - 3697	100	0 - 200
SF Clearwater	10_SFCLWR					1,712	721 - 2935	5,586	4408 - 7231
upper Clearwater	11_UPCLWR								
SF Salmon	12_SFSALM								
MF Salmon	13_MFSALM								
upper Salmon	14_UPSALM					2,309	1131 - 3769	3,509	2307 - 4714
<b>Total</b>		<b>653</b>		<b>0</b>		<b>7,934</b>		<b>9,195</b>	

Note: Based on the sample data described in Table 66 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 69. Estimated abundance of natural-origin stocks (excluding unclipped hatchery-origin) of Summer Steelhead that passed Bonneville Dam in 2024 during the Skamania and A-/B-Index Management Periods.**

	W	Subtotal for Skamania Period (Apr 1 - Jun 30)		Subtotal for Skamania Period (Apr 1 - Jun 30)		Subtotal for A-/B-Index Period (Jul 01 - Oct 31)		Subtotal for A-/B-Index Period (Jul 01 - Oct 31)	
Reporting Group name	Reporting Group Code	A-Index		B-Index		A-Index		B-Index	
		Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI
Lower Columbia	02_LOWCOL	653	218 - 1306			618	140 - 1152	0	0 - 0
Skamania	03_SKAMAN	1,524	871 - 2395			720	223 - 1277	0	0 - 0
Willamette	04_WILLAM								
Big White Salmon	05_BWSAL M								
Klickitat	06_KLICKR	218	0 - 653			669	225 - 1217	0	0 - 0
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	435	0 - 871			23,145	20846 - 25911	645	141 - 1305
Yakima	08_YAKIMA	218	0 - 653			2,947	1873 - 4070	141	0 - 423
upper Columbia	09_UPPCOL	218	0 - 653			1,563	846 - 2329	149	0 - 447
SF Clearwater	10_SFCLWR					1,539	663 - 2522	1,818	875 - 2837
upper Clearwater	11_UPCLWR	218	0 - 653			0	0 - 0	507	36 - 1080
SF Salmon	12_SFSALM					0	0 - 0	357	42 - 903
MF Salmon	13_MFSALM					1,091	403 - 1828	273	0 - 819
upper Salmon	14_UPSALM					4,252	2891 - 5770	217	0 - 652
	<b>Total</b>	<b>3,484</b>		<b>0</b>		<b>36,542</b>		<b>4,107</b>	

Note: Based on the sample data described in Table 66 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 70. Estimated abundance of clipped and unclipped hatchery-origin A-/B-Index Summer Steelhead that passed Bonneville Dam in 2024 (July 1 – Oct 31) and were assigned to PBT broodstocks.**

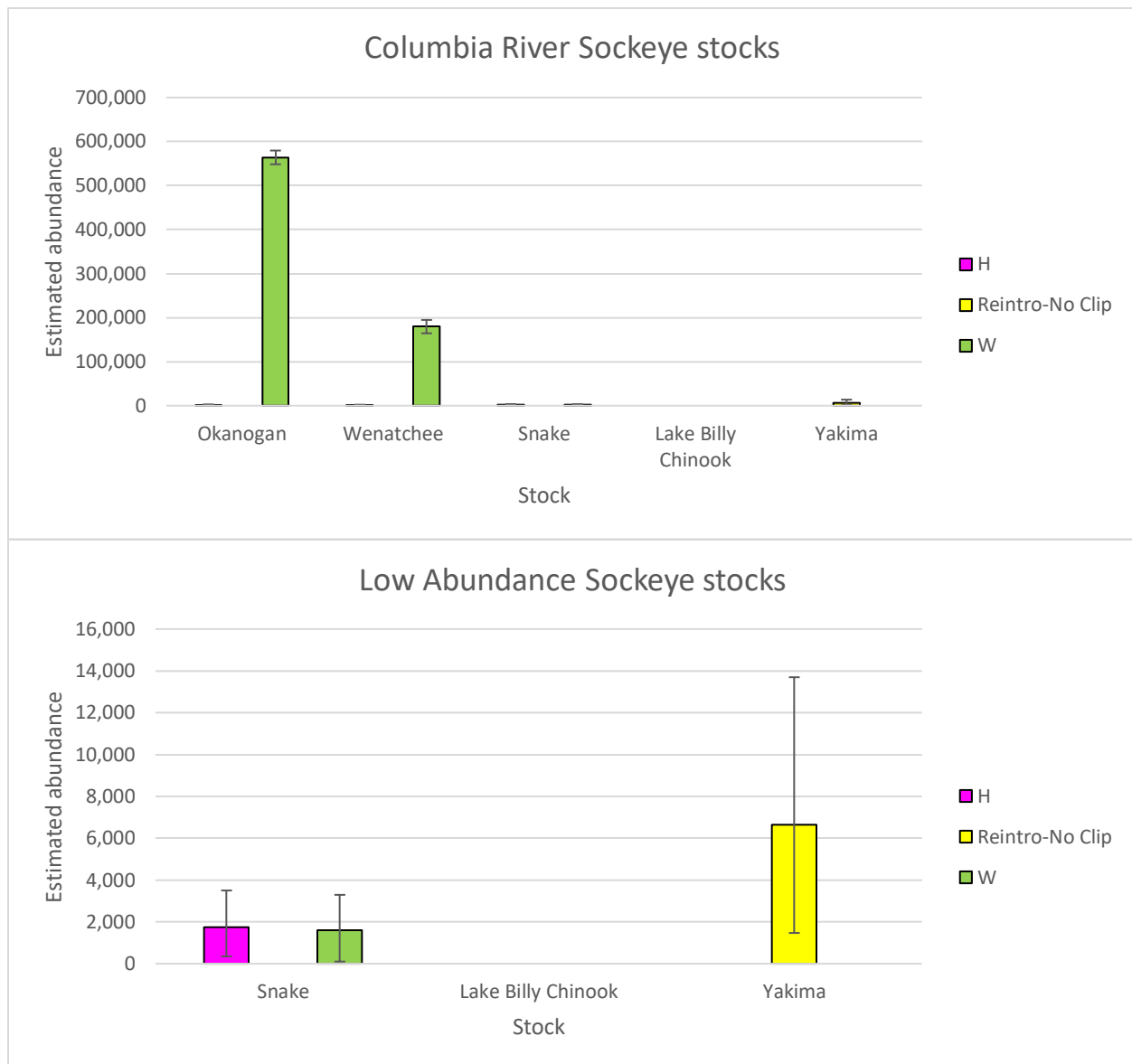
					Hatchery clipped				Hatchery unclipped			
					A-INDEX		B-INDEX		A-INDEX		B-INDEX	
Hatchery	Stock	GSI RepGrp	Broodstock	Brood year	Est.	95% CI	MLE	95% CI	MLE	95% CI	MLE	95% CI
Skamania Hatchery	Summer	03_SKAMAN	OmySKAM_su21	2021	4,129	2883 - 5352	715	202 - 1383	286	0 - 715	0	0 - 0
Little Sheep Satellite	Imnaha	07_MGILCS	OmyLSCR_su21	2021	1,913	974 - 2916	0	0 - 0				
Little Sheep Satellite	Imnaha	07_MGILCS	OmyLSCR_su22	2022	1,403	551 - 2390	0	0 - 0				
Lyons Ferry Hatchery	Wallowa stock -trapped/spawned at Cottonwood, released at Cottonwood and other Washington sites	07_MGILCS	OmyCGRW_su21	2021	1,080	319 - 1980	0	0 - 0				
Lyons Ferry Hatchery	Tucannon	07_MGILCS	OmyTUCA_su21	2021					701	0 - 2102	0	0 - 0
Lyons Ferry Hatchery	Wallowa stock -trapped/spawned at Cottonwood, released at Cottonwood and other Washington sites	07_MGILCS	OmyCGRW_su22	2022	1,515	571 - 2617	0	0 - 0				
Minthorn Springs Satellite	Minthorn Springs	07_MGILCS	OmyMINT_su21	2021	1,127	357 - 2044	0	0 - 0				
Minthorn Springs Satellite	Minthorn Springs	07_MGILCS	OmyMINT_su22	2022	332	0 - 918	0	0 - 0				
Round Butte	Deschutes River	07_MGILCS	OmyROUN_su21	2021	1,471	658 - 2390	0	0 - 0	741	282 - 1326	0	0 - 0
Wallowa Fish Hatchery	Wallowa stock -released at Cottonwood and other Washington sites	07_MGILCS	OmyCGRW_su19	2019	145	0 - 434	0	0 - 0				
Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGILCS	OmyWALL_su21	2021	4,927	3328 - 6534	0	0 - 0	493	0 - 1098	0	0 - 0
Wallowa Fish Hatchery	Wallowa-Oregon released (assumed)	07_MGILCS	OmyWALL_su22	2022	887	303 - 1586	0	0 - 0				
Eastbank	Wenatchee	09_UPPCOL	OmyEAST_su21	2021					218	0 - 653	100	0 - 300
Wells Fish Hatchery	WMET/WOKA/WOMA/WELLS	09_UPPCOL	OmyWELL_su21	2021	2,980	1708 - 4292	1,605	697 - 2648	221	0 - 662	0	0 - 0
Wells Fish Hatchery	Methow Safety-Net	09_UPPCOL	OmyWMET_su21	2021	1,939	826 - 3153	306	0 - 918				
Wells Fish Hatchery	Okanogan; Natural origin Omak released; Hatchery origin Okanogan tribs	09_UPPCOL	OmyWOKA_su21	2021	279	0 - 580	306	0 - 918				
Wells Fish Hatchery	Okanogan; Natural origin Omak released	09_UPPCOL	OmyWOMA_su21	2021					226	0 - 536	0	0 - 0
Wells Fish Hatchery	WELLS; Columbia Safety-Net	09_UPPCOL	OmyWELL_su22	2022	547	39 - 1258	0	0 - 0				
Wells Fish Hatchery	Methow Safety-Net	09_UPPCOL	OmyWMET_su22	2022	1,402	606 - 2332	0	0 - 0				
Wells Fish Hatchery	Okanogan; Natural origin Omak released; Hatchery origin Okanogan tribs	09_UPPCOL	OmyWOKA_su22	2022	280	0 - 841	0	0 - 0				



Winthrop NFH	Methow River	09_UPPCOL	OmyWINT_su20	2020	736	199 - 1473	0	0 - 0				
Winthrop NFH	Methow River	09_UPPCOL	OmyWINT_su21	2021	440	0 - 1320	0	0 - 0	513	0 - 1286	0	0 - 0
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su20	2020	0	0 - 0	293	0 - 587				
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su21	2021	3,613	2250 - 5019	20,560	17835 - 23055	819	291 - 1526	3,423	2401 - 4542
Dworshak NFH	All Dworshak stocks	10_SFCLWR	OmyDWOR_su21	2021	0	0 - 0	144	0 - 433				
Dworshak NFH	Dworshak stock-trapped and spawned at Dworshak, reared at Magic Valley FH, released in Salmon basin	10_SFCLWR	OmyDWOS_su21	2021	0	0 - 0	183	0 - 511	135	42 - 275	628	308 - 964
Dworshak NFH	SF Clearwater	10_SFCLWR	OmySFCR_su21	2021	950	330 - 1732	5,995	4533 - 7715	664	185 - 1267	1,495	807 - 2316
Dworshak NFH	Dworshak-Clearwater basin trapped, spawned, reared, and released	10_SFCLWR	OmyDWOC_su22	2022	135	0 - 324	0	0 - 0	48	0 - 140	0	0 - 0
Dworshak NFH	SF Clearwater	10_SFCLWR	OmySFCR_su22	2022	190	0 - 488	0	0 - 0				
Oxbow (IDFG)	Oxbow	14_UPSALM	OmyOXBO_su21	2021	12,019	9575 - 14596	455	0 - 1065				
Oxbow (IDFG)	Oxbow	14_UPSALM	OmyOXBO_su22	2022	631	133 - 1241	0	0 - 0				
Pahsimeroi	Pahsimeroi	14_UPSALM	OmyPAHH_su21	2021	11,787	9260 - 14441	780	119 - 1536				
Pahsimeroi	Upper Salmon	14_UPSALM	OmyUSAL_su21	2021	1,646	859 - 2506	1,871	1068 - 2809	1,520	734 - 2419	3,509	2369 - 4761
Pahsimeroi	Pahsimeroi	14_UPSALM	OmyPAHH_su22	2022	226	40 - 480	0	0 - 0				
Pahsimeroi	Upper Salmon	14_UPSALM	OmyUSAL_su22	2022					301	42 - 736	0	0 - 0
Sawtooth	Sawtooth	14_UPSALM	OmySAWT_su21	2021	11,700	9420 - 14282	144	0 - 433	218	0 - 653	0	0 - 0
Sawtooth	Sawtooth	14_UPSALM	OmySAWT_su22	2022	2,777	1569 - 4152	0	0 - 0				
			Unassigned		3,896	2572 - 5547	1,505	767 - 2395	830	179 - 1704	41	0 - 124
TOTAL					77,103		34,864		7,934		9,195	

*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 3, 2024 (Table 46). 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 2024, there were 1,660 Sockeye Salmon that were sampled at the AFF and genotyped for this analysis (Table 71). This year we estimated low but non-zero abundance for the ESA listed stock (Redfish Lake Sockeye Salmon from the Snake River, abundance=3,342) (Table 71, 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 2024, we estimated zero abundance of the Lake Billy Chinook stock. Importantly, we have the ability to estimate the reintroduced stock from the Yakima River using our PBT baseline and the stock abundance estimate for 2024 was 6,644 fish (identified as BY2020). This is a relatively high abundance. Although run years 2020 and 2021 had produced abundance estimates of the Yakima stock that were greater than 3,000 fish, recent years appeared to decline. However, 2020 – 2021 run years combined with this 2024 run year, have 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 ( $\pm$  95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2024.**

**Table 71. Estimated abundance of Sockeye Salmon genetic stocks that passed Bonneville Dam in 2024.**

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	1,278	0 – 2864			564,102	548378 – 579575	2		1,250	1,252
Wenatchee	749	0 – 2248			179,793	164338 – 194749	1		387	388
Snake	1,753	351 – 3502			1,590	102 – 3293	4		4	8
Lake Billy Chinook										0
Yakima			6,644	1471 – 13698				12		12
Total	3,780		6,644		745,485		7	12	1,641	1,660

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 93% of fish that were clipped hatchery-origin summer A-/B-Index steelhead at Bonneville Dam in 2023 to 33 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 2024 (95%).

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 2024. Namely, the percentage of adipose-clipped fish abundance that were estimated to be PBT broodstock were 99.1%, 95.0%, and 97.8% 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.

This year's report continued recent analysis where 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 (2019). The trend suggested 286 smolts were needed to be released to equal 1 adult-sized Spring Chinook that returned to Bonneville Dam in 2022 and 2023. Further, we estimated smolt-to-adult survival for BY2019 steelhead as well and found that approximately 192 steelhead smolts were needed to equal 1 adult Summer Steelhead at Bonneville Dam between 2021 and 2023. Future work could sum all abundance of the SY2019 adult return across age-classes 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 and steelhead 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, Coho, and Sockeye salmon and provide this data to fisheries managers.

We were able to address the following **F&W Program Management Questions:**

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

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

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

We identified 14 major clipped Chinook salmon hatchery-origin stocks (79 clipped hatchery broodstock sources), 7 major unclipped hatchery-origin stocks (56 unclipped hatchery broodstock sources) and 10 natural-origin stocks estimated to have relative abundances  $\geq 1,000$  fish passing Bonneville Dam in 2023. The Spring Chinook stocks of 2023 were observed to spillover into the summer period by 2% for hatchery-origin stocks and 5% 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 (25 – 28%) 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  $\geq 1,000$  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 2023, the relatively large ( $\geq 78$  cm) steelhead were found primarily to originate from Dworshak hatchery broodstock (OmyDWOC\_su20, OmySFCR\_su20). 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 Pahsimeroi in the upper Salmon River (OmyPAHH\_su21) that was a source of B-sized 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 twelfth 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 2023 and found that the Okanogan stock has the greatest relative abundance followed by the Wenatchee stock. We found 3,036 fish from the Snake River stock, estimated 73 fish from Lake Billy Chinook and 669 from 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 (2024) we continued an increased frequency of in-season reporting as we planned in the past three years during the Chinook Salmon spring and summer management periods, and we have offered timely post-season reports for the fall management period of Chinook Salmon, as well as Skamania and A-/B-Index Summer Steelhead Management Periods, and Sockeye Salmon. For steelhead and sockeye, our genetic analyses have become officially integrated into the routine analyses that U.S. v OR TAC performs. In all cases, the genetic analyses are a complement to the data that fisheries managers have available to gain insights into the biological characteristics of fisheries. The genetic analysis of the Spring Chinook Salmon test fishery data may begin to play a particularly important role in the in-season analyses because of its potential predictive power for stock abundance and timing at Bonneville Dam weeks in advance of the arrival of the run.

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## Section 5: Local adaptation in salmonids

### Introduction

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

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

Molecular techniques such as RNA-seq (Wolf 2013) also provide the opportunity to investigate transcriptional response to thermal stress and further identify mechanisms for thermal adaptation. Patterns of gene expression under heat stress are important to determining evolutionary adaptation among conspecific populations that occupy various environments. Multiple genes have been shown to be involved in heat tolerance across many species, including highly conserved heat shock proteins (hsps) that are upregulated under stressful conditions such as exposure to heat (Morimoto et al. 1992; Sorensen et al. 2003). An adaptive heat shock response has additionally been shown to occur among conspecific populations that occupy variable environments (e.g., Dahlhoff and Rank 2000; Sorensen et al. 2001). However, many genes are known to have a role in regulating the effects of temperature and are likely to be involved in thermal adaptation (Sorensen et al. 2005; Kassahn et al. 2007). Thus, RNA-seq provides the opportunity to



investigate differential expression across the transcriptome and identify biological pathways involved in evolutionary response to thermal stress.

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

### ***Fish Population RM&E***

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

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

### **Uncertainty Research**

See Appendix A for table of critical uncertainties research.

### **Project Map:**

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

### **Contract Map(s):**

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

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

## **Methods: Protocols, Study Designs, and Study Area**

### **Method Title:** Whole Genome Resequencing

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

### **Method Summary:**

With reference genome assemblies now publicly available for both Chinook salmon and steelhead, this enables whole genome resequencing for investigating adaptive variation across a large portion of the genome (50-80%) in these species. Whole genome resequencing methods include individually barcoded samples, or pools of samples (Pool-seq; Schlotterer et al. 2014) depending on the study design. For both methods, sequence data is aligned to the reference genome assembly, and allele frequencies from millions of SNPs are analyzed to detect statistically significant regions of the genome associated with specific traits or adaptation to environmental factors. Putatively neutral regions of the

genome are also useful for standard phylogeny and demographic analyses of populations. In most studies, allele frequencies are available for collections but sequencing depth is typically not high enough to provide individual genotypes. However, candidate SNPs may be developed into standard panels with GTseq or other approaches to genotype many individuals to validate trait association, determine inheritance, and estimate linkage disequilibrium.

**Method Title:** RAD sequencing v1.0

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

**Method Summary:**

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

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

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

**Method Summary:**

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

## ***Results***

### **Objective 1) Environment & Landscape Genetics**

*Hypotheses:*

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

Hypothesis 2: Environmental drivers of selection act on specific genes resulting in different allelic and genotypic frequencies among adapted populations. Genome scans

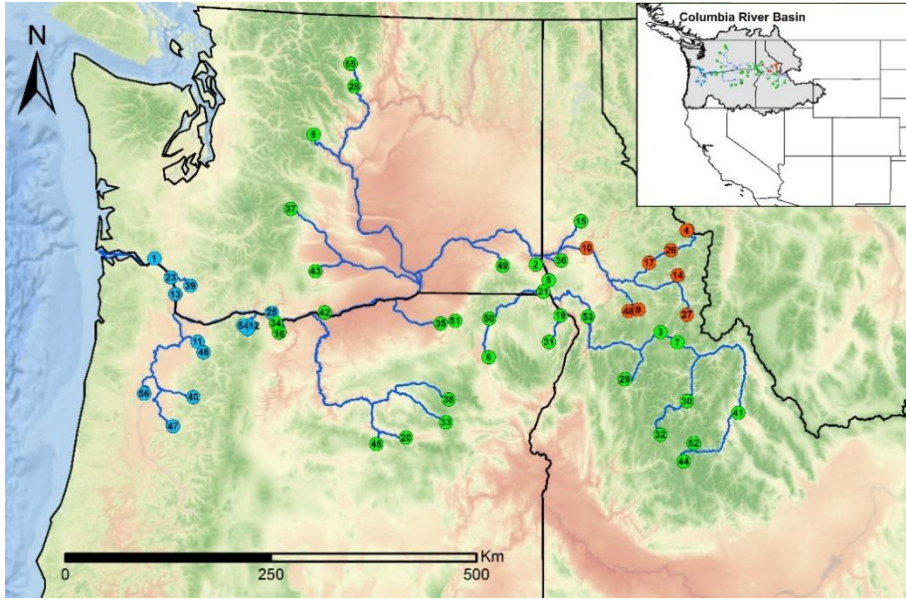
can identify candidate genes involved in local adaptation of fish populations across heterogeneous landscapes.

*Activities implemented:*

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

For steelhead, landscape genetics work has been done at both fine and broad scales. Fine scale landscape genetics approaches were used to identify ecological patterns of residence vs anadromy and found consistent evidence that certain landscape features have led to prevalence of certain life history types in *O. mykiss* (Narum et al. 2008a) but also *O. nerka* (Nichols et al. 2016). Broad scale studies were initially done with panel of 188 SNP markers to investigate patterns of landscape genetics across 145 populations in the Columbia River Basin (Matala et al. 2014). Results indicated that precipitation and temperature were the primary environmental drivers of local adaptation and neutral genetic structure largely reflected isolation by distance. These results were shown to be robust due to replication of multiple populations representing each distinct genetic unit (Hand et al. 2016). A follow-up study (Micheletti et al. 2018a) was done with a much larger number of genetic markers (~20K SNPs) at broad scale and found evidence that the mainstem Columbia River migratory corridor exhibits greater selective pressure on steelhead than natal tributaries (Figure 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 72). 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

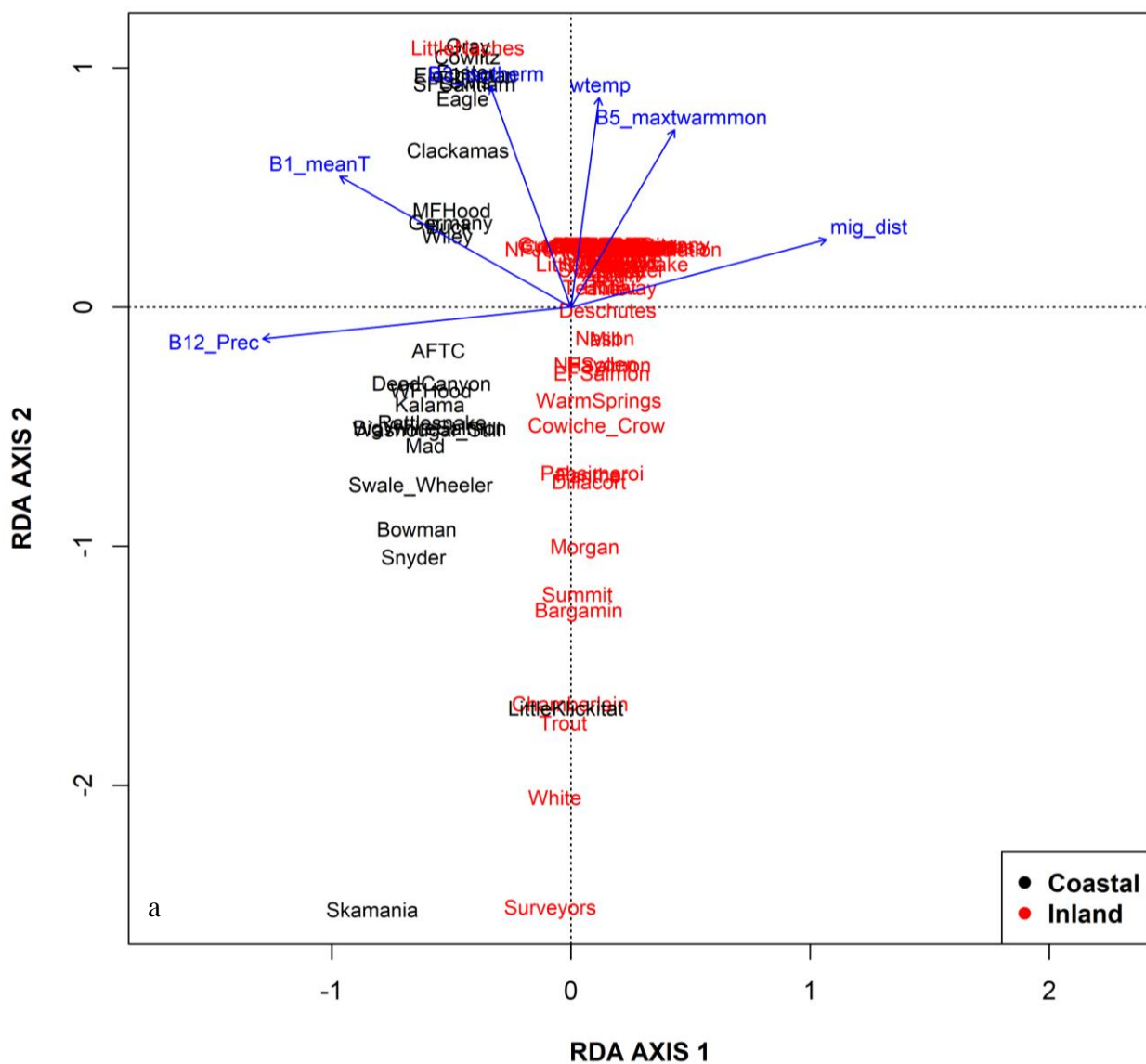
month, annual precipitation, and migration distance. Additional studies are underway to further pinpoint candidate genes through whole genome resequencing.



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

Notation	Description	Unit	Res. (m)	Class	Source	Retained in model
mig_dist	Migration Distance	km	30	Topography	USGS	Y
elev_mean	Elevation	m	30	Topography	USGS	N
wtemp	Water Temp	°C	30	Temperature	NorWeST	Y
hli	Heat Load Index	hli	30	Temperature	ESRI	N
B1_meanT	Annual Mean Temp	°C	1000	Temperature	WorldClim	Y
B2_meanrange	Mean Diurnal Range	°C	1000	Temperature	WorldClim	N
B3_isotherm	Isothermality	°C	1000	Temperature	WorldClim	Y
B4_tseason	Temp Seasonality	°C	1000	Temperature	WorldClim	N
B5_maxtwarmmon	Max Temp Warmest Month	°C	1000	Temperature	WorldClim	Y
B6_mintcoldmon	Min Temp Coldest Month	°C	1000	Temperature	WorldClim	N
B7_trange	Temp Annual Range	°C	1000	Temperature	WorldClim	N
B8_meantwetq	Mean Temp Wettest Quarter	°C	1000	Temperature	WorldClim	N
B9_meantdryq	Mean Temp Driest Quarter	°C	1000	Temperature	WorldClim	N
B10_meantwarmq	Mean Temp Warmest Quarter	°C	1000	Temperature	WorldClim	N
B11_meantcoldq	Mean Temp Coldest Quarter	°C	1000	Temperature	WorldClim	Y
B12_Prec	Annual Precip	mm	1000	Precipitation	WorldClim	Y
B13_precwetmon	Precip Wettest Month	mm	1000	Precipitation	WorldClim	Y
B14_precdrymon	Precip Driest Month	mm	1000	Precipitation	WorldClim	N
B15_precseason	Precip Seasonality	mm	1000	Precipitation	WorldClim	N
B16_precwetq	Precip Wettest Quarter	mm	1000	Precipitation	WorldClim	N
B17_precdryq	Precip Driest Quarter	mm	1000	Precipitation	WorldClim	N
B18_precwarmq	Precip Warmest Quarter	mm	1000	Precipitation	WorldClim	N
B19_preccoldq	Precip Coldest Quarter	mm	1000	Precipitation	WorldClim	N



**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.

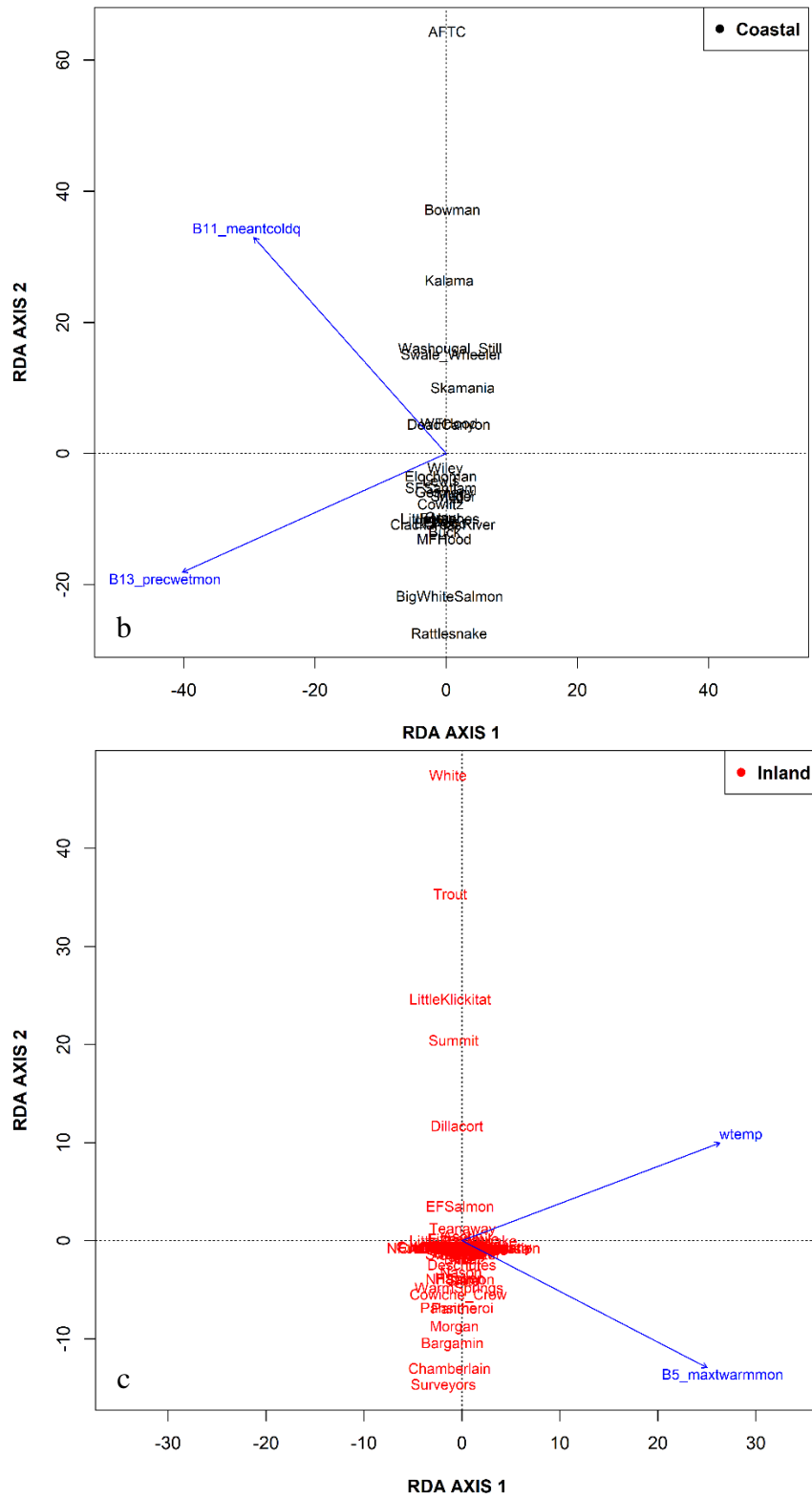
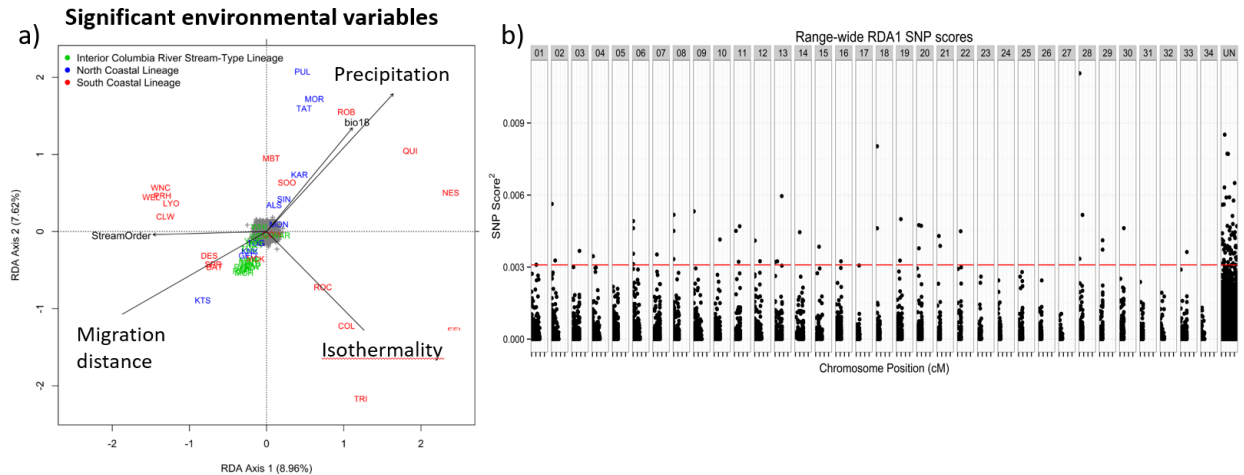


Figure 48 b-c.

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 49a). Several candidate markers were associated with local adaptation within and among lineages (Figure 49b; 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:*

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

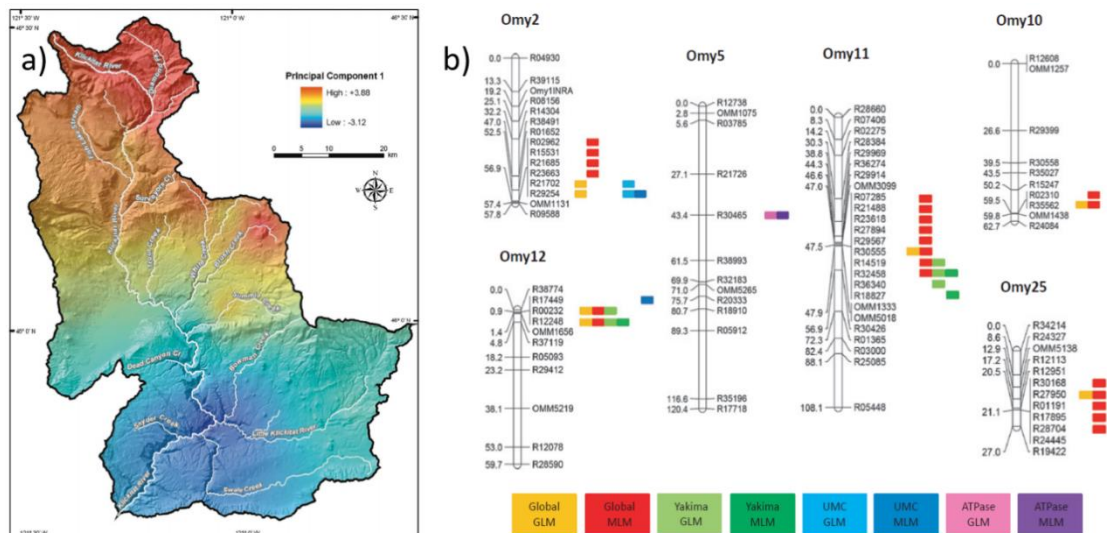
Hypothesis 2: Markers from candidate genes can be developed into cost efficient assays for genotyping large numbers of individuals to monitor genetic variation for phenotypic

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

#### Activities implemented:

Multiple studies have been initiated to investigate the genetic basis for multiple phenotypic traits using association mapping or gene expression approaches. Work has focused on genomic regions associated with several different traits.

Work on resident vs. anadromous *O. mykiss* (Narum et al. 2008a; Hecht et al. 2013) has revealed that a combination of environmental and genetic factors contribute to determination of these life history types (Figure 50).



**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 region on Chr. 12 may represent a minor effect gene for male anadromy and suggests that this life history variation is more strongly driven by other mechanisms related to environmental rearing such as epigenetic modification, gene expression, and phenotypic plasticity. However, the candidate SNPs from Chr. 12 will be developed for further validation in GTseq panels. Primer design is complicated in this region by structural variation but testing is ongoing to develop markers.

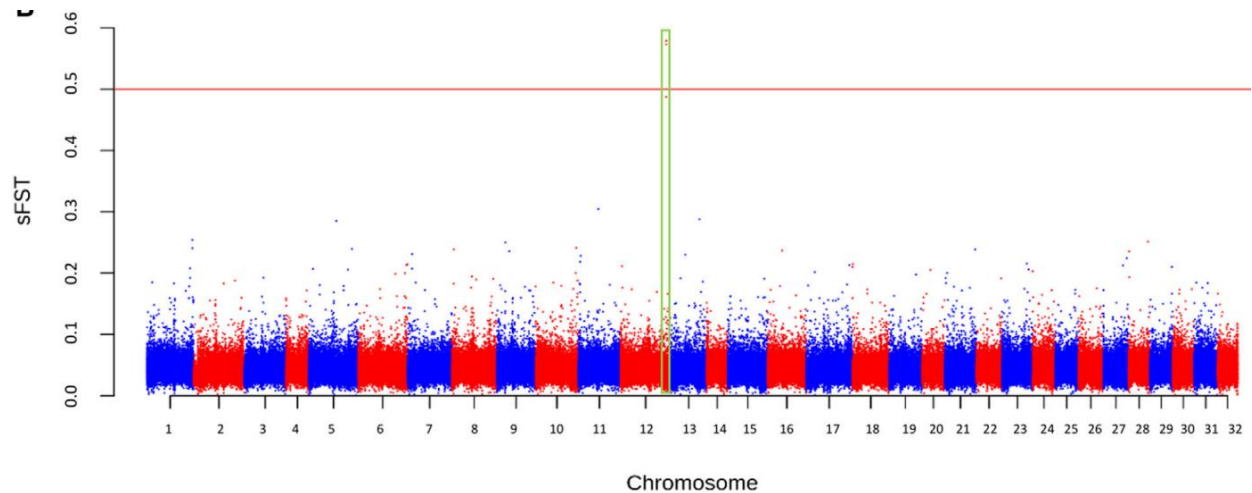
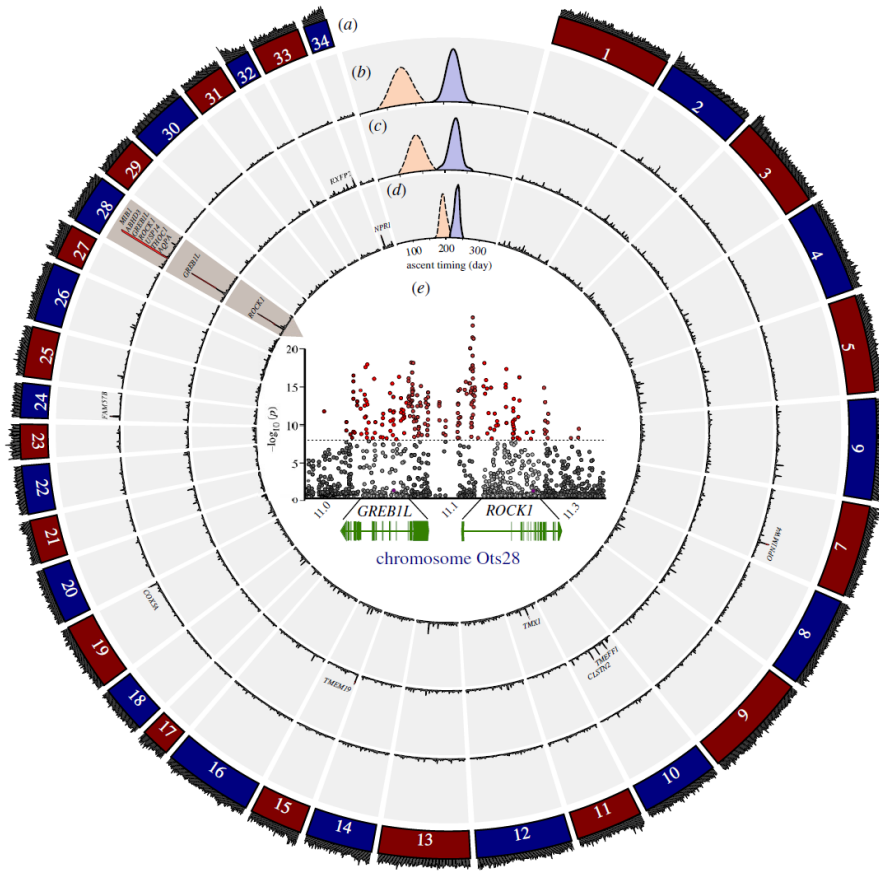


Figure 51. Manhattan plot of differences in allele frequencies between resident and anadromous collections across the genome based on sliding window FST (sFST). The minimum coverage threshold was 15 reads and the minor allele frequency was  $\geq 0.05$ . (from Collins et al. 2022)

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 *GREB1L*, *ROCK1*, and intergenic regions with significance based on CMH tests.

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

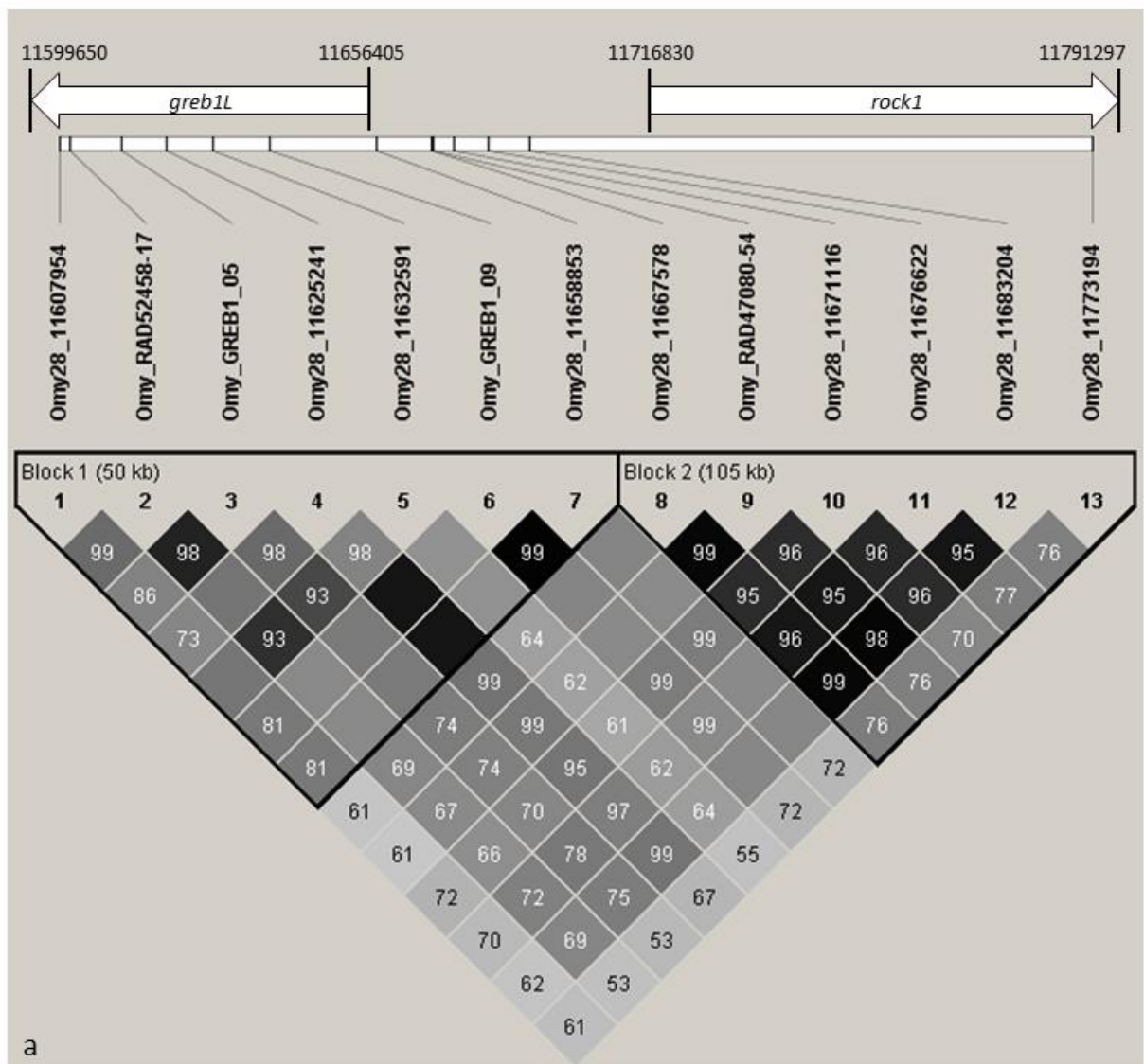
The distribution of genetic variation underlying adult migration timing in steelhead across the landscape was described by genotype frequencies (Collins et al. 2020). We examined 13 markers occurring on chromosome 28 within the *greb1L*, *rock1*, and intergenic region between *greb1L* and *rock1* that were previously shown to be strongly associated with adult migration timing (Hess et al. 2016; Micheletti et al. 2018c; Table 73). 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 association with run-timing phenotypes and genotypes from Chr28 was demonstrated in Willis et al. (2020).

**Table 73.** Adult steelhead migration timing associated candidate marker information. The ‘Order ID’ column corresponds to the SNP order, according to the physical position within the genome assembly. SNP names, chromosome number, position, gene, primers, probes, and orientation are also listed and are based on the genome assembly NCBI accession GCF\_002163495.1. The premature allele is indicated in the probe column with an underline.

Order ID	SNP	Chr	Position	Gene	Forward primer	Reverse primer	Probe	Orientation
1	Omy28_11607954	28	11607954	<i>greb1L</i>	TGACACTGATCACAATGGTGAAAT	TAAACTGGAAGGAGAGAGCAAAAT	TGTGGGCTGC[A/G]AACATACTCA	+
2	Omy_RAD52458-17	28	11609794	<i>greb1L</i>	ACGTGTCCCTGAGGATGGTA	AGCTCTAGGTCTGGGTCCTG	ATGGCCC[C/A][CT]AAGAACCC	-
3	Omy_GREB1_05	28	11618027	<i>greb1L</i>	TGGGCAGATATGGAAGAACGG	ACCTTCTAAATGGCCTCTGTGT	CGGTGGCTC[T/G]C	+
4	Omy28_11625241	28	11625241	<i>greb1L</i>	CAACATTAGGGAGAGGTTGCTAT	ATCATCAAGTTGCCTACGACAC	CCTCCTCCCT[A/G]TGGTTGTCTC	+
5	Omy28_11632591	28	11632591	<i>greb1L</i>	GTAGAGGCCAAAGGCTTGAG	TGCTCTTATTACCTCCAGACTCC	TGAGAA[G/A]AACACAGAGG	+
6	Omy_GREB1_09	28	11641623	<i>greb1L</i>	CCAGTGGCAACCTCAGGTAG	GACTCCAGTCACCAAGTCA	TCAA[T/G]GGAGA	+
7	Omy28_11658853	28	11658853	intergenic	CAACATATGACCACTCGAAAACCTC	ATTAATCACACCGTGAGACTCCTC	TGGTACAGAC[A/C]CGCACTAGCA	+
8	Omy28_11667578	28	11667578	intergenic	ACAGTAAACCCATTAGGCATAGT	TTATCCTCTCAATCCACATCAAGA	GTATTGATCC[T/C]GTGGGAGACA	+
9	Omy_RAD47080-54	28	11667915	intergenic	TCAAAACCTGCAGGACTTGGA	TGGTTATATCTACAGTACAGTTCGT	TGCAAG[A/G]CTTAAACGA	+
10	Omy28_11671116	28	11671116	intergenic	AATTTCCCAAATTTGAAACTCTT	GTGTACATTGTGAGCAGAAACAT	CTGGTGAGAA[C/T]AGGAATTACC	+
11	Omy28_11676622	28	11676622	intergenic	CGAATGCACTGTAGCTATTCTAA	GCAGTAGAATGTCTCGAAATACA	ACATGTCATT[T/G]ATTGTTATCT	+
12	Omy28_11683204	28	11683204	intergenic	CAAGAAAGAAACAGATGTTGTCCA	TTGTGACTCAAATCTGCAACCTAT	ATGTAAAAAA[G/T]GGCAGAAAA	+
13	Omy28_11773194	28	11773194	<i>rock1</i>	AGTTTGACACCCCTGTACTAGAGC	GTCTAACAAGCTCTGGGTGATTTA	GCAATTTTT[T/A]AAATTACCGC	+

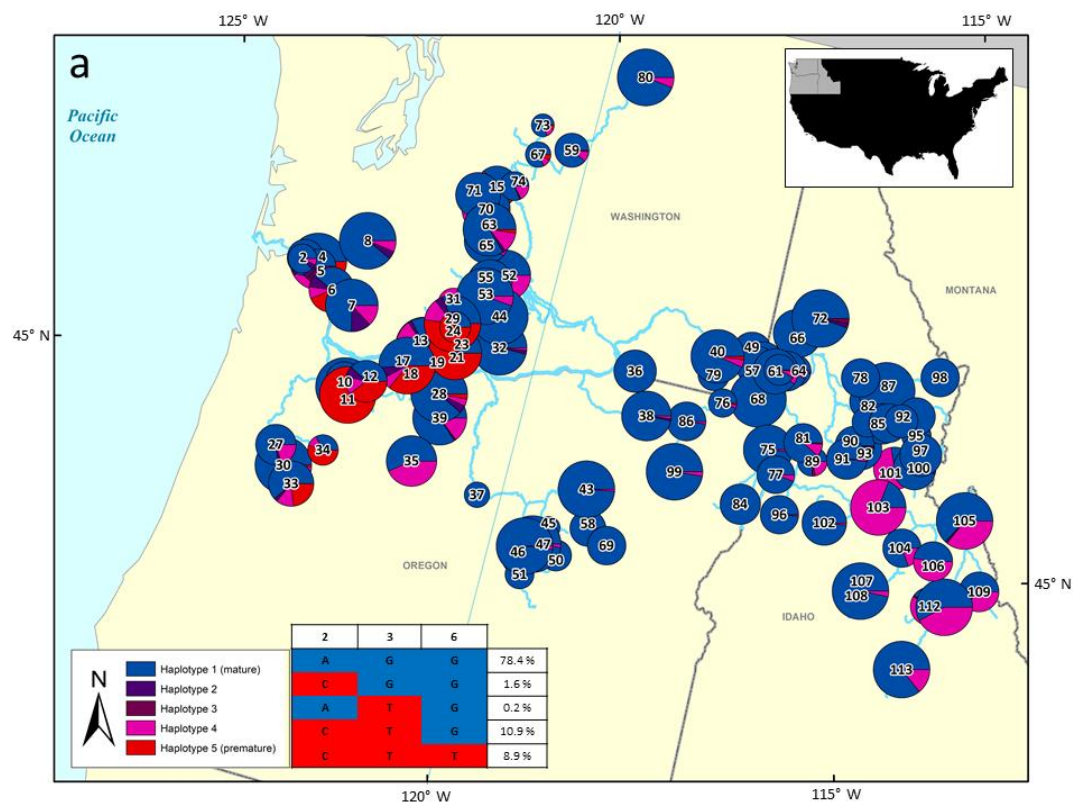
We assessed linkage disequilibrium (LD) within the 13 candidate markers to identify haplotype blocks that would be informative for estimating frequencies of adult migration types. Candidate markers were analyzed for all sampling locations in Haploview with solid spine and this resulted in two haploblocks,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

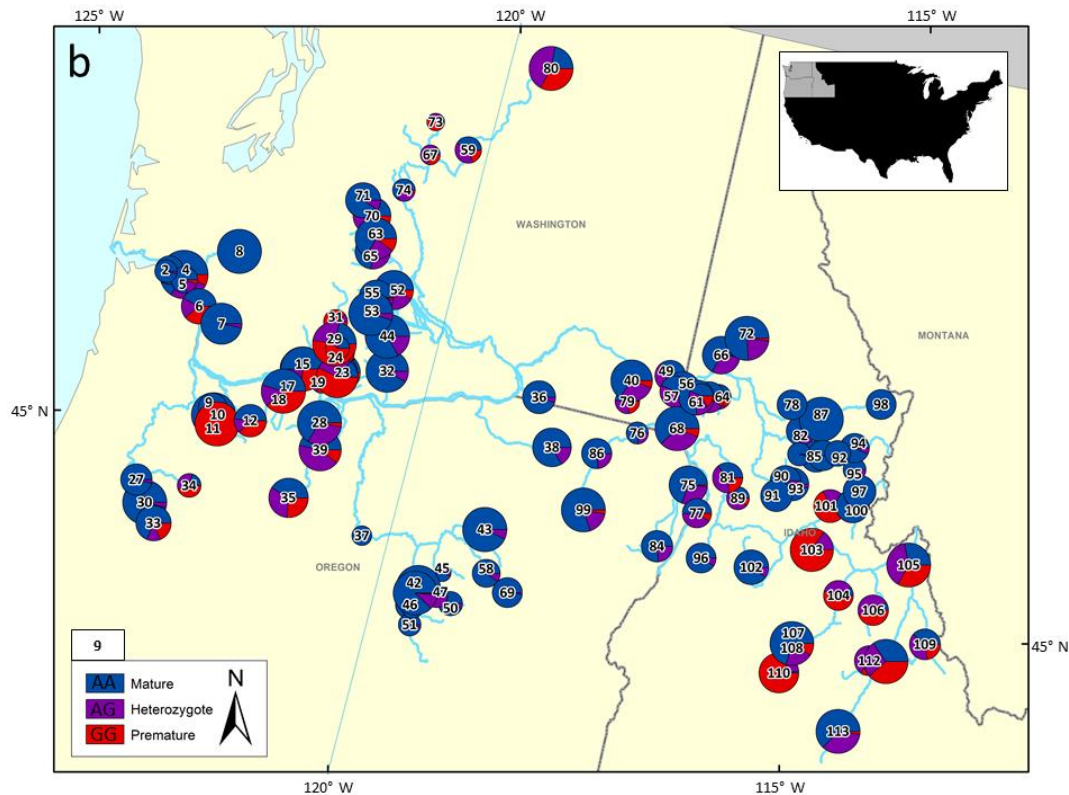
Genotypes were assessed across the Columbia River basin with the migration timing associated markers. The haplotypes representative of the heterozygote genotype are depicted as a gradient corresponding to the number of markers that match either fixed genotype and the percentage of individuals with each 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).





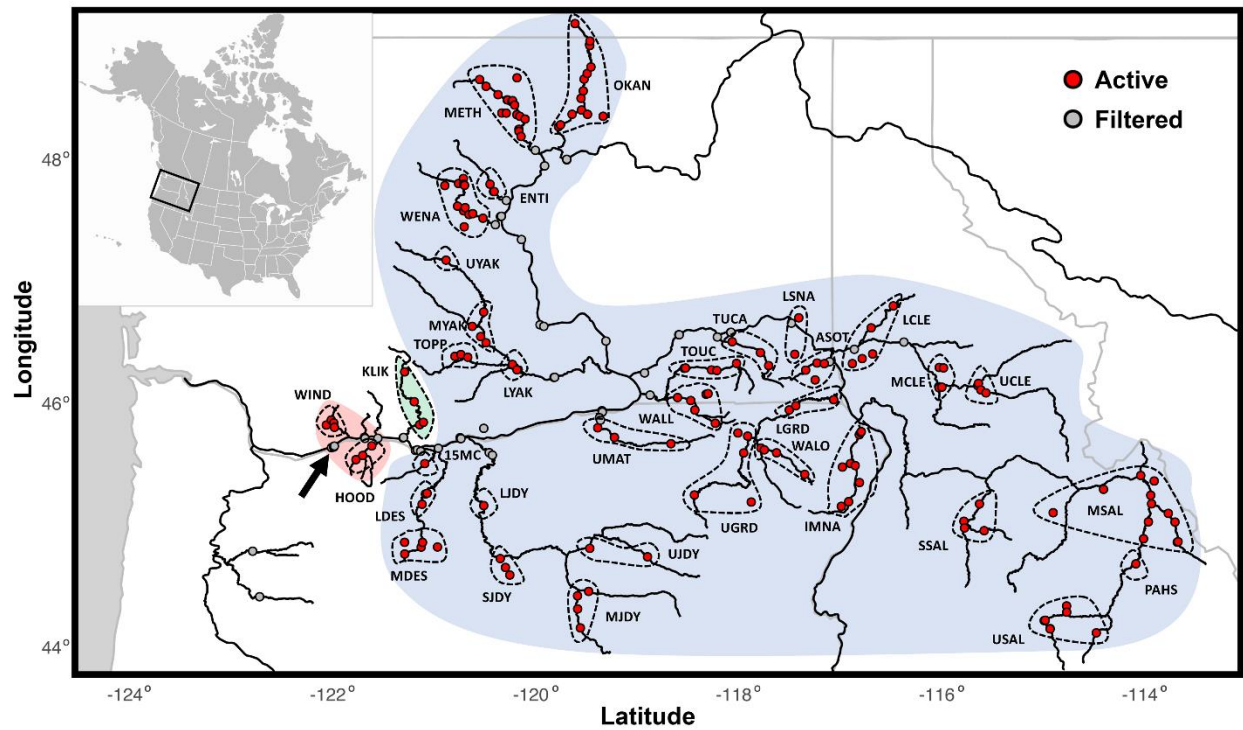
**Figure 54a.**

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.

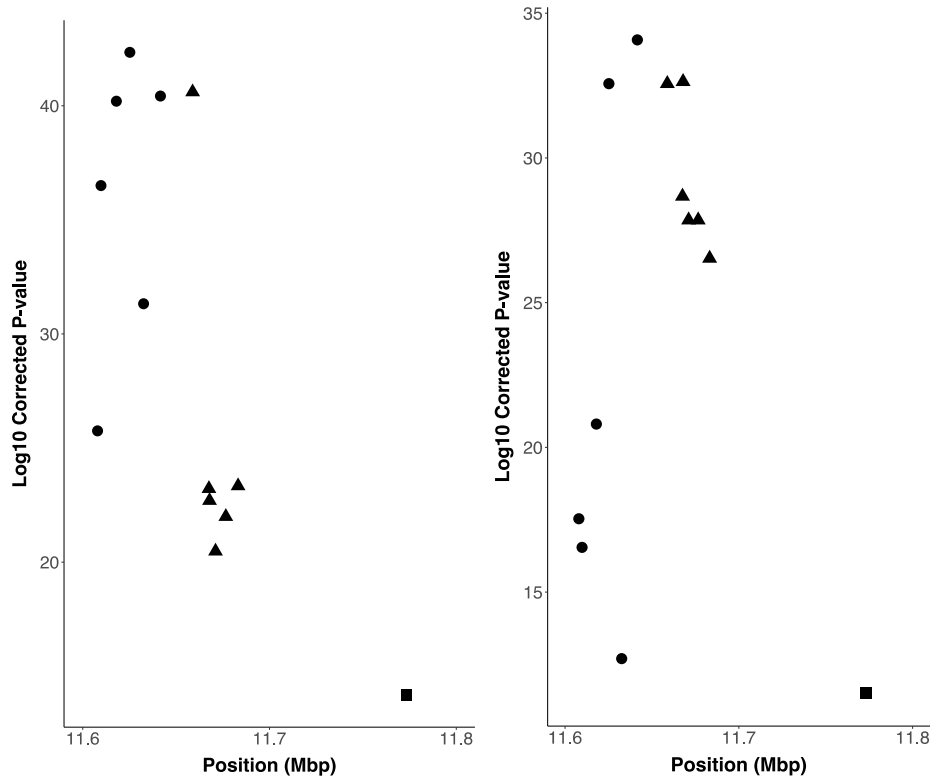


**Figure 54b.**

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.



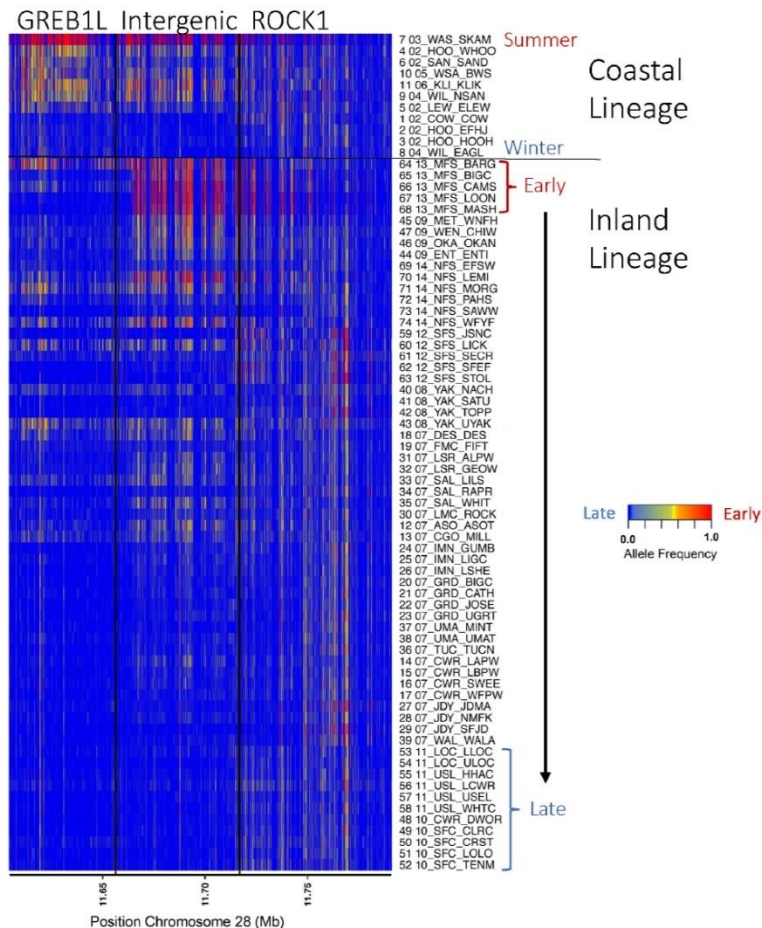
**Figure 55. Columbia River Basin with active and filtered passive integrated transponder arrays. River courses in black; borders and coast in gray. Hydrological unit groupings, identified by dashed lines, are organized into lineages and sub-basins as follows: coastal lineage in Red, intermediate lineage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



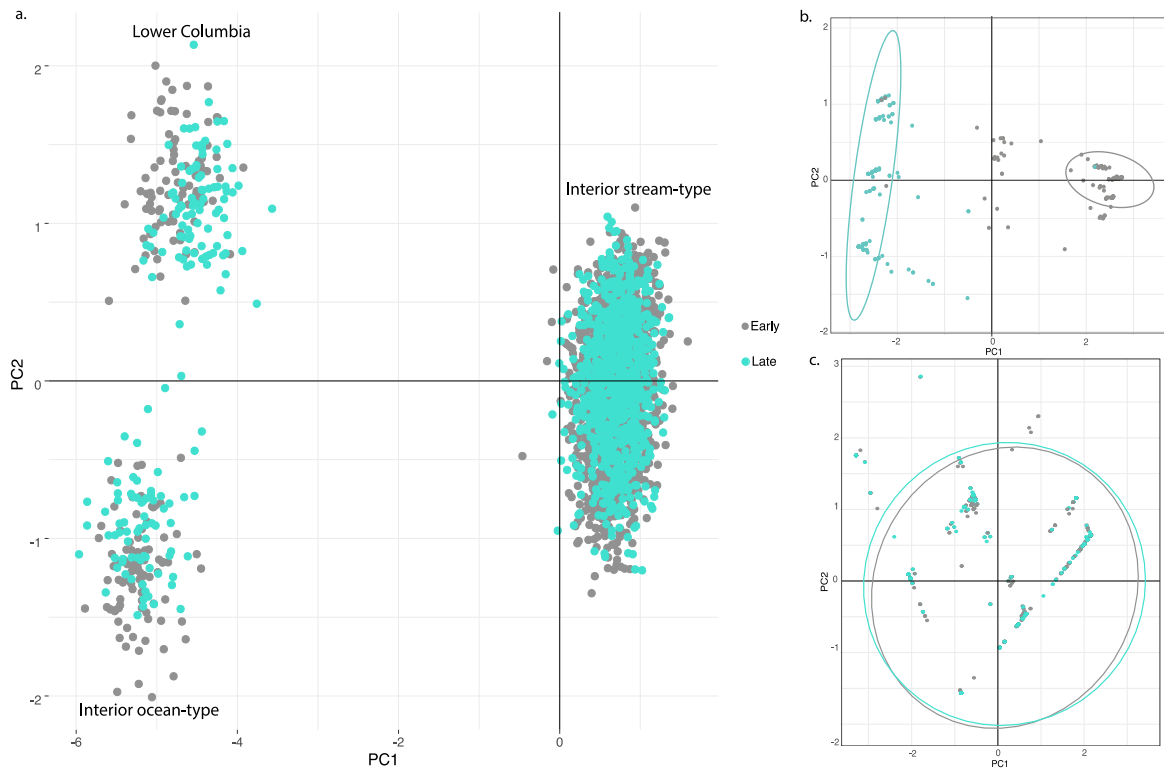
**Figure 57. Allele frequencies for hundreds of SNPs spanning GREB1 through ROCK1 for 74 populations of Steelhead based on wholegenome sequencing (Willis et al., 2023). Populations are sorted within each lineage by early at the top and late at the bottom. The coastal lineage includes the Skamania stock 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 developed that span 220kb on chromosome 28 including candidate genes greb1L and rock1 for adult migration timing (Koch and Narum 2020). Using individual-level genotypes from these candidate markers, we tested for an association with migration phenotypes across three distinct lineages that demonstrate both an early and late migration phenotype. We then used pedigree data from one of the populations, which enabled association tests between the candidate

markers and fitness. Estimates of fitness were based on previous estimates of reproductive success from Janowitz-Koch et al. (2019).

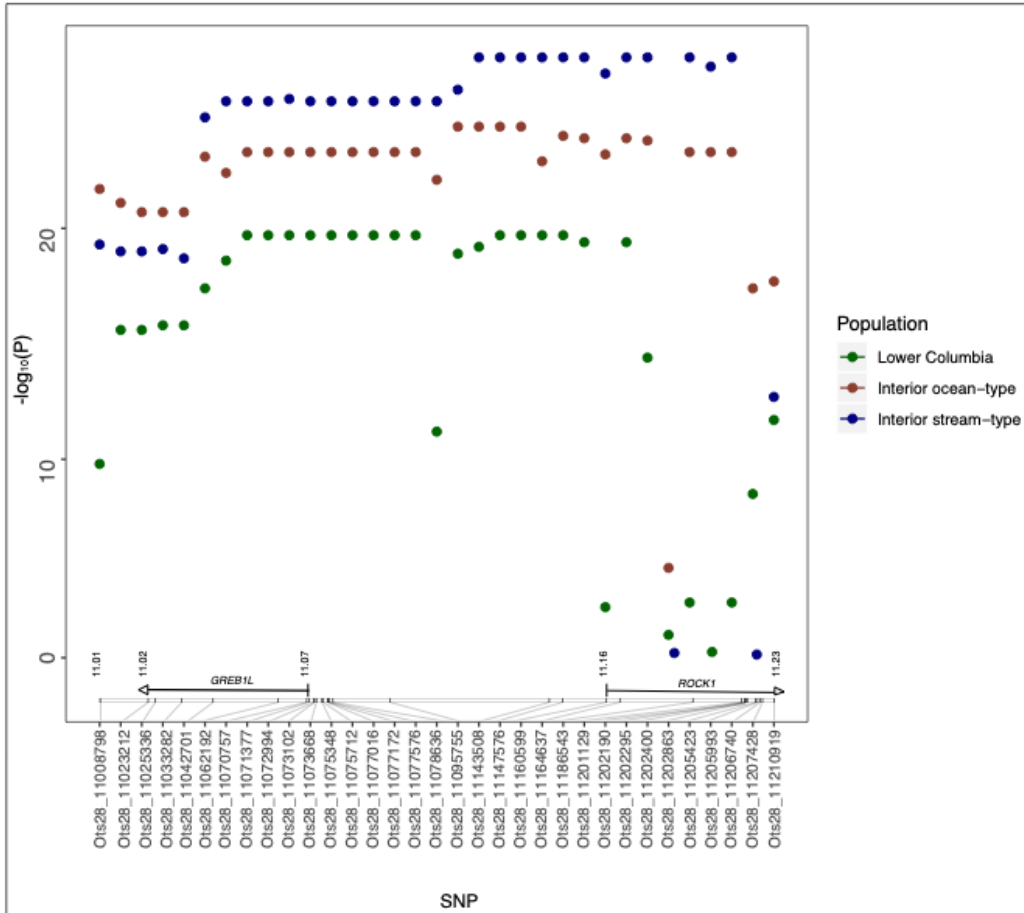
A series of PCA results demonstrated clear differences in clustering between putatively neutral markers and those associated with adult migration timing in both the Lower Columbia and Interior ocean-type lineages (Figure 58). The pattern was investigated separately for the larger set of individual samples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

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

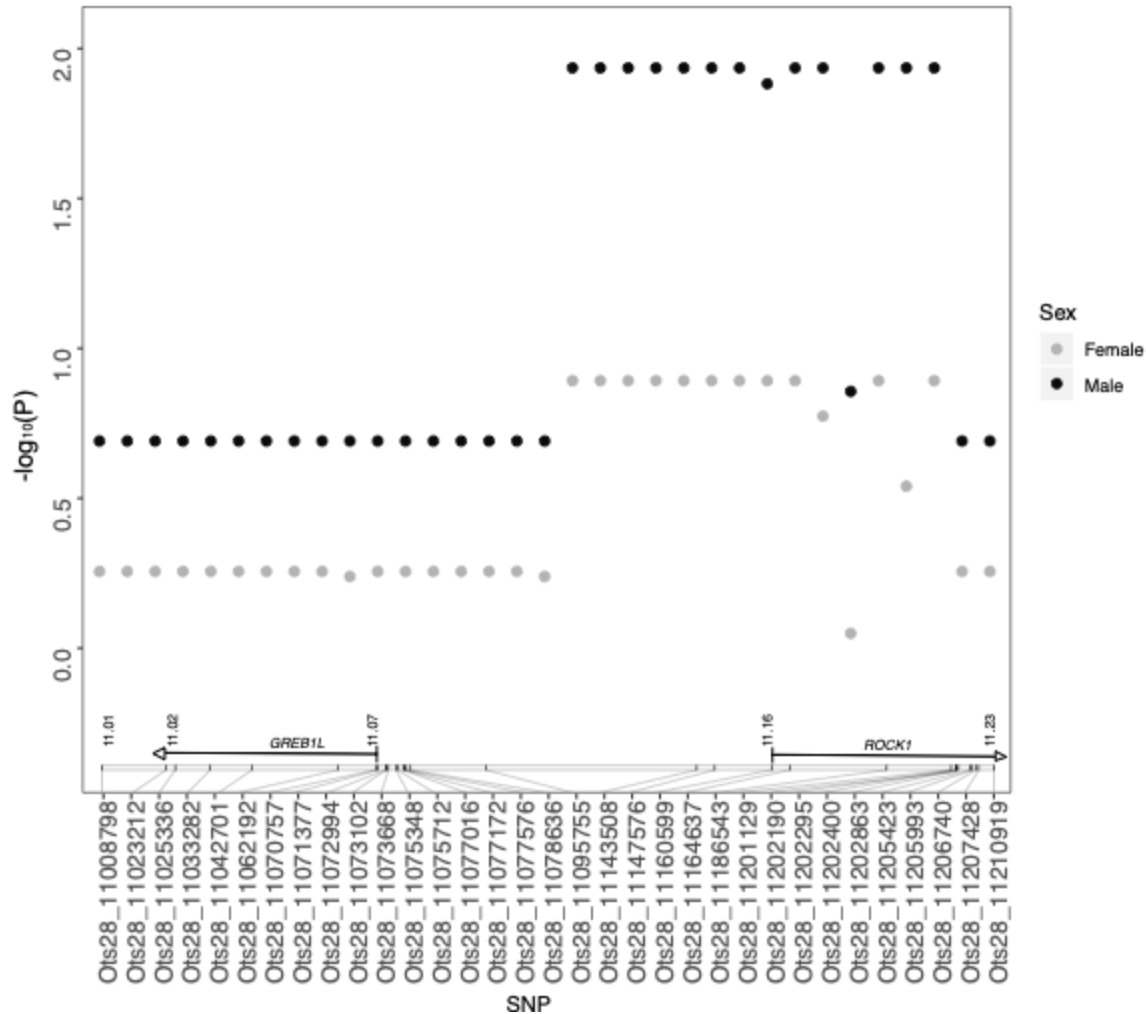


**Figure 58. PCA of genetic variation in Chinook Salmon (from Koch and Narum 2020). Results presented represent A) 185 neutral SNP markers, B) 33 chromosome 28 markers for the Lower Columbia and Interior ocean-type populations combined, and C) 33 chromosome 28 markers for the Interior stream-type population.**





**Figure 59.** Association of each candidate SNP marker with migration timing within three lineages of Chinook Salmon (from Koch and Narum 2020). The colored dots for each lineage represent sliding windows for consecutive pairs of SNPs along the candidate genomic region. SNP number on the x-axis corresponds to the 33 candidate markers, while the genome position of markers on chromosome 28 (NCBI accession GCA\_002831465.1) is depicted in the gene diagrams above the x-axis. Y-axis represents  $-\log_{10}(\text{FDR-corrected p-value})$ .

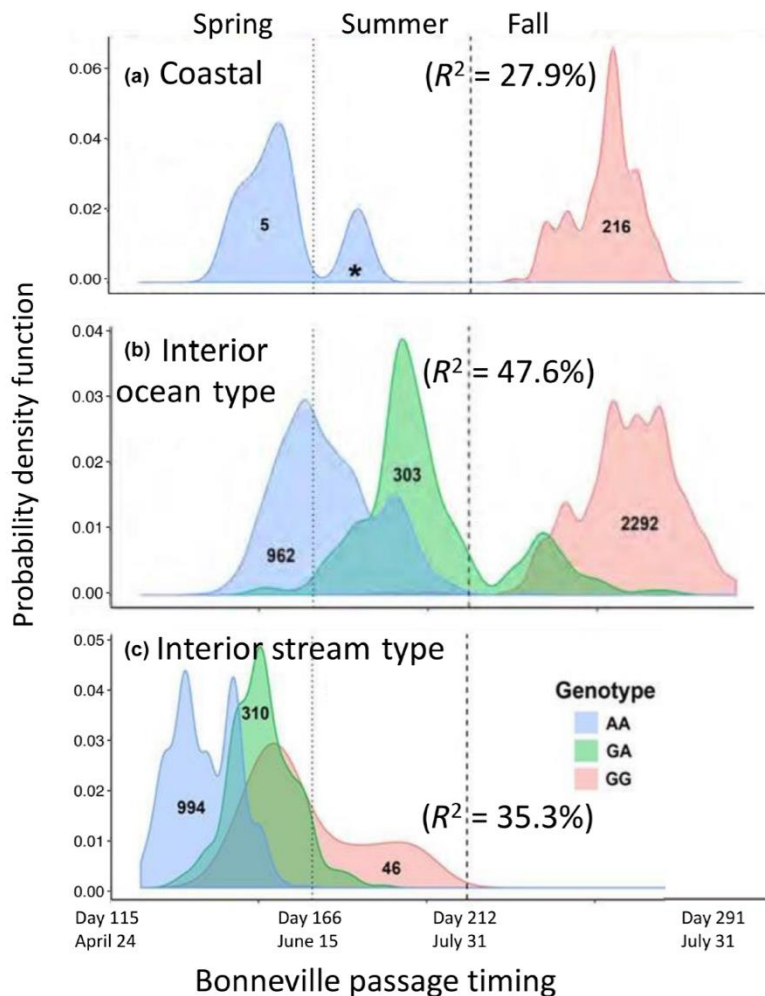


**Figure 60. Association of each candidate SNP marker with fitness within the Interior stream-type population. The dots represent sliding windows for consecutive pairs of SNPs along the candidate genomic region with sexes presented separately. SNP number on the x-axis corresponds to the 33 candidate markers, while the genome position of markers on chromosome 28 (NCBI accession GCA\_002831465.1) is depicted in the gene diagrams above the x-axis. Y-axis represents  $-\log_{10}(\text{FDR-corrected p-value})$ .**

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

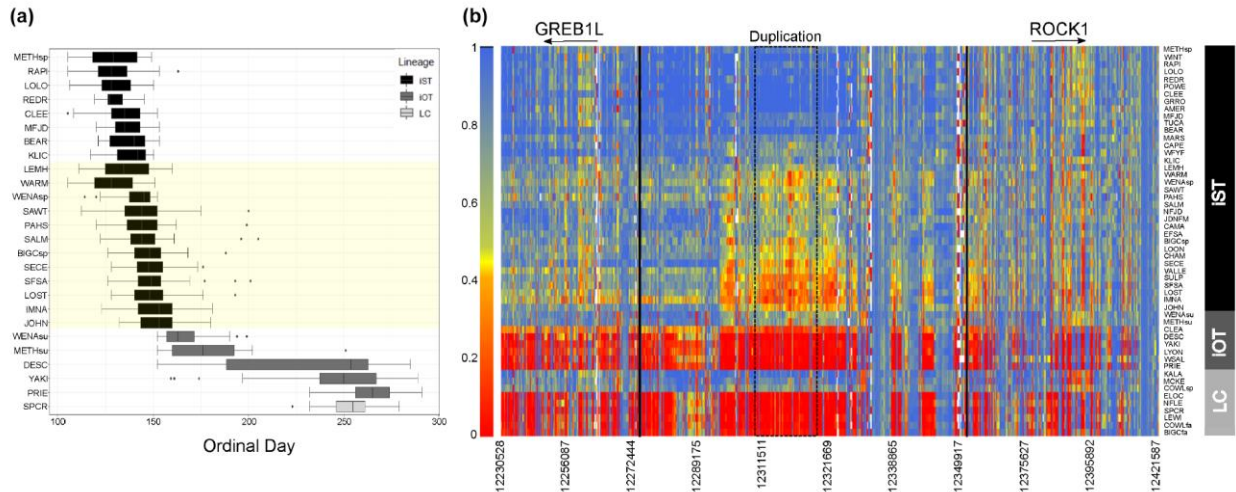


in the chromosome 28 region that were significantly associated with adult migration timing phenotypes. This is particularly notable for the interior stream-type lineage, which exhibits an earlier and more constrained freshwater entry than the other lineages. In both interior stream-type and interior 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 64) 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.

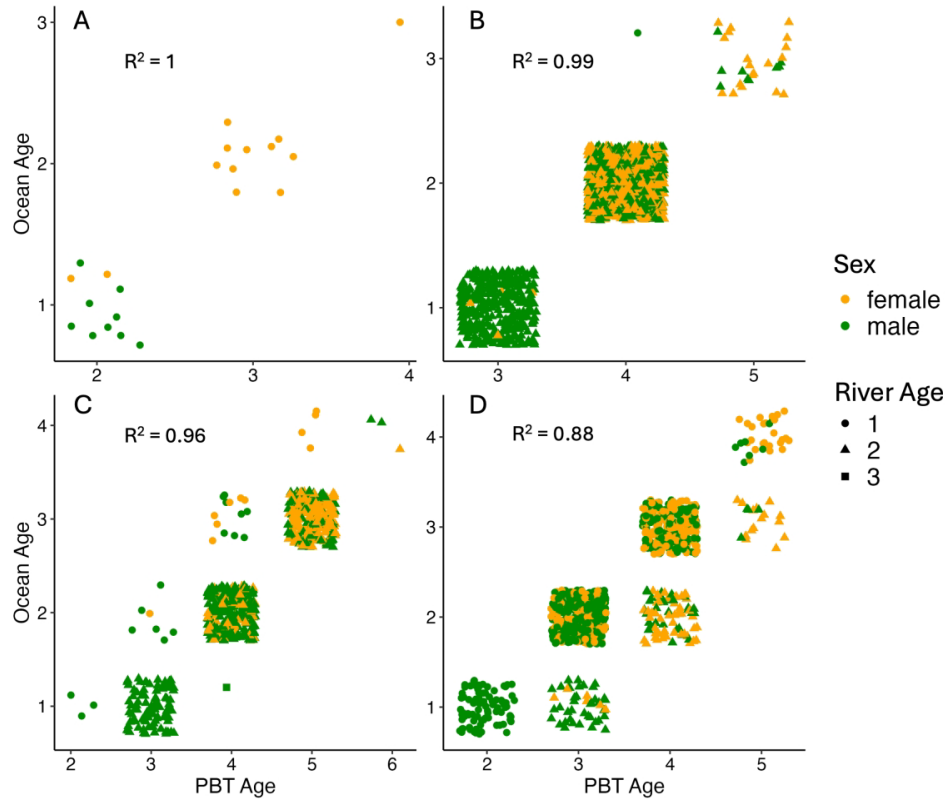


**Figure 62. Allele frequencies for hundreds of SNPs spanning GREB1 through ROCK1 for 53 populations of Chinook Salmon based on whole genome sequencing (Horn and Narum 2023). A) Populations are sorted within each lineage by adult migration timing with early at the top and late at the bottom. Lineages 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 has been investigated in multiple studies over decades to determine the genetic and environmental factors that contribute to this trait. The total age at maturity is considered to include the combination of years spent in freshwater and marine environments prior to spawning, with total age for Chinook Salmon typically ranging from 2-5 years for males and 3-5 years for females for each of the three lineages in the Columbia River (Hess et al., 2014; Myers et al., 1998; Willis et al. 2021, **Figure 63**). However, exceptions are observed, with interior ocean-type lineage fish of either sex occasionally returning at 6-years-old. A critical aspect of variation in age-at-maturity is the degree to which this trait is environmentally or genetically controlled, since these factors determine the opportunity for anthropogenic selection to permanently alter life history variation (e.g., Oke et al., 2020). Studies have suggested a classic model of phenotypic variance (gene (G) + environment (E) + GxE interactions) for growth rates and the consequences of those growth rates on the phenotype of age-at-maturity in salmonids (e.g., Carlson & Seamons). While estimates of heritability have been observed to be relatively high in previous studies (e.g.,  $h^2$  males = 0.49-0.57,  $h^2$  females = 0.39-0.41; Hankin et al., 1993), individuals that grow quickly at early life stages tend to mature at younger ages (Hankin et al., 1993; Hutchings & Jones, 1998; Hutchings & Myers, 1994; Silverstein et al., 1998; Vøllestad et al., 2004). Moreover, while heritability for age-at-maturity or propensity-to-jack appears to be strong for males, there is conflicting evidence for the degree of heritability among females or correlation between age-at-maturity in opposite-sex parents and offspring (Forest et al., 2016; Gamble & Calsbeek, 2023; Hankin et al., 1993; Heath et al., 1994).

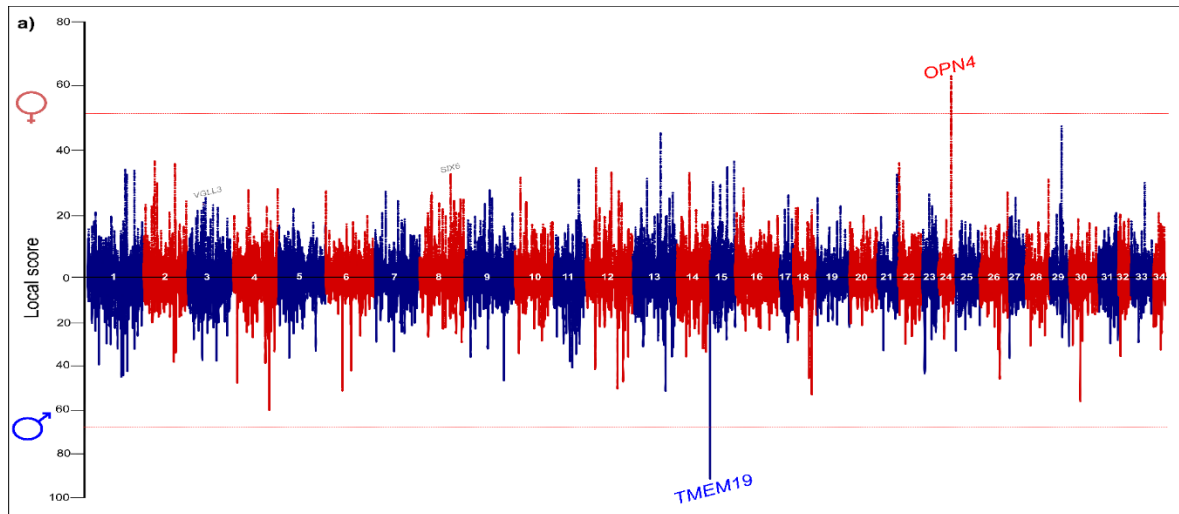
Initial studies have not identified genes of major effect for Chinook Salmon (Micheletti & Narum, 2018; Waters et al., 2021), though evidence points to a strong influence of sex-chromosome-linked variation (McKinney et al., 2020, 2021), consistent with the high heritability of jacking and age-at-maturity in males. However, evidence for major genomic association in hatchery-reared fish has been lacking, presumably due to maturity phenotypes that were more strongly driven by rapid growth in the artificial rearing environment (McKinney et al., 2021). Based on co-location of markers showing sex-linked variation, chromosome 17 (OtsLG17) is thought to be the sex-chromosome for most Chinook Salmon populations (Phillips et al., 2005; Stein et al., 2001). However, McKinney et al. (2020, 2021) identified two chromosomes associated with sex in Chinook Salmon from Alaska and the Columbia River, OtsLG17 and OtsLG18, and that males with different nucleotide variant combinations (haplotypes) from the short arms of these chromosomes differed in their age-at-maturity.

An initial genome wide study indicated that age at maturity appeared to be a polygenic trait but genes of greatest effect differ between sexes (Figure 64; females = OPN4, males = TMEM19; Micheletti and Narum 2018b). Recent studies by other labs have identified Y-linked haplotypes on Chromosome 17 associated with age-at-maturity in Chinook salmon (e.g., McKinney et al. 2020) and markers have been developed to genotype large numbers of individuals to test whether this pattern of association can be verified for the three major lineages of Chinook salmon in the Columbia River. Initial genotyping of these Y-linked markers from McKinney et al. 2020 in approximately 1200 samples from each lineage indicated that SNPs and haplotypes based on these markers are nearly fixed in all Chinook salmon from the Columbia River. With minor allele frequencies < 0.1% across all populations, these Y-linked markers were not effective and the pattern of association reported by McKinney et al. (2020) was not validated. However, additional markers from Chr17 based on variation from Micheletti and Narum (2018b) have been incorporated into GTseq panels for further testing. Extensive genome scans are also underway for regions associated with age-at-maturity in Chinook salmon from multiple populations representing each of the lineages in the Columbia River. Initial results support high heritability of this trait across populations of all lineages, and several significant regions of the genome including those from Chr17 and Chr18. Further analyses are ongoing.

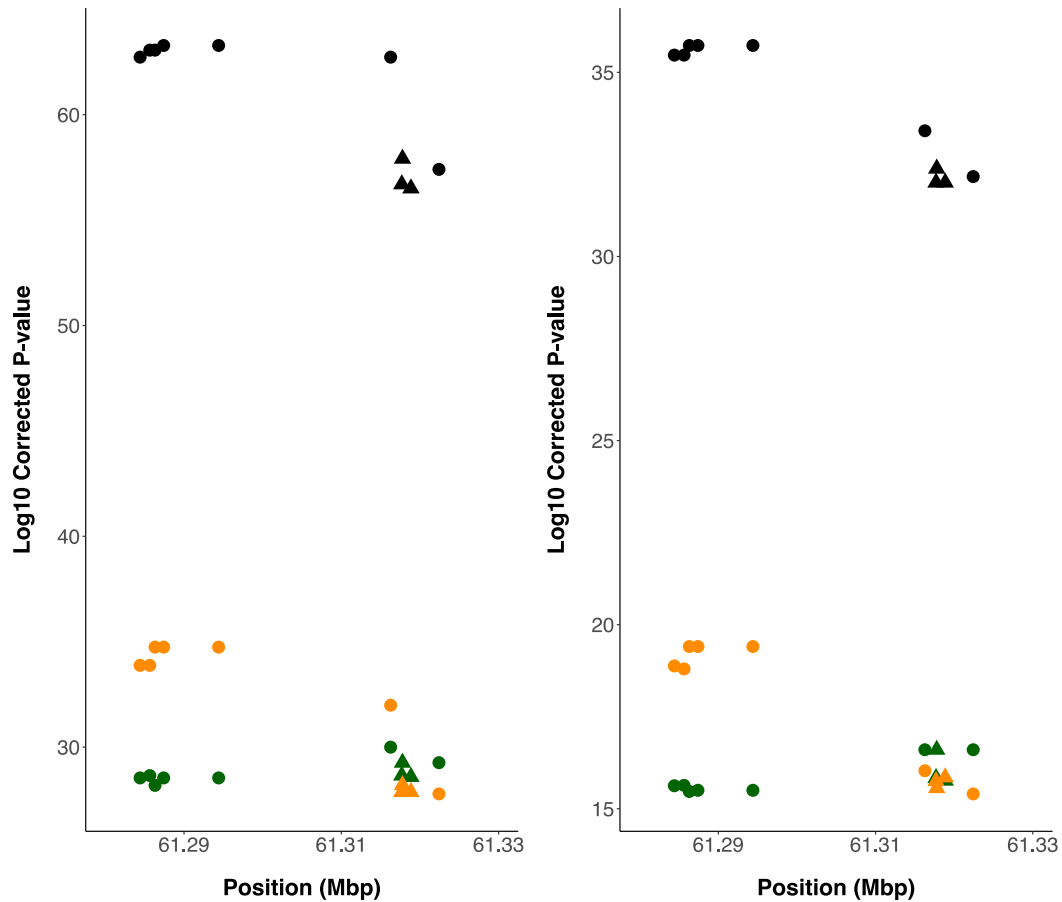


**Figure 63.** Ocean age from scales (years) versus parentage-based tagging age (years) for hatchery-origin (PBT-assigned) Chinook salmon sampled ( $N = 2,938$ ) at Bonneville Dam from 2014 to 2019 (data from Willis et al. 2021). A) Coastal; B) Interior stream-type; C) Interior ocean-type, summer run; D) Interior ocean-type, fall run.

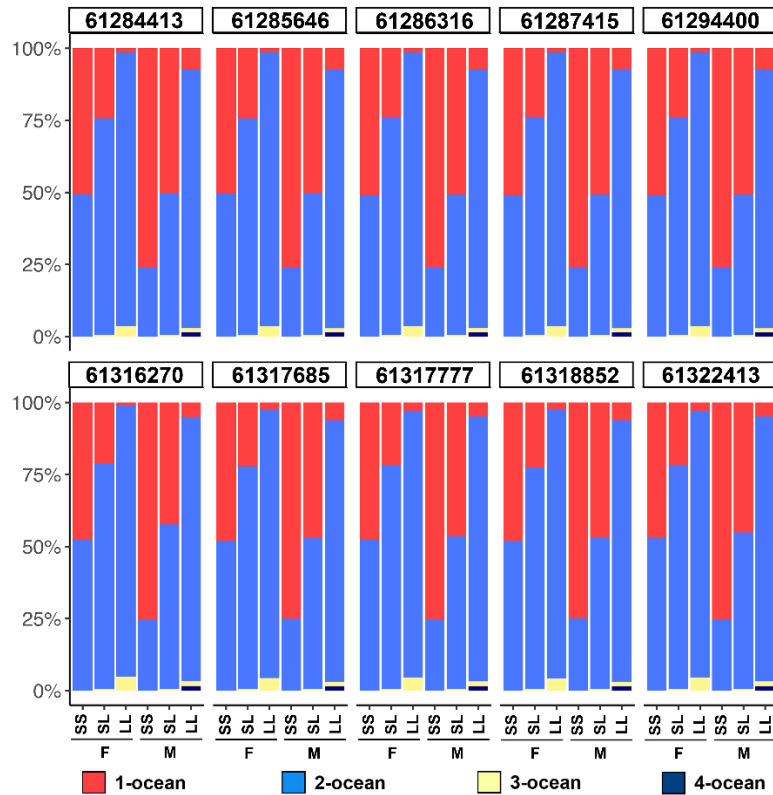
In steelhead, we confirmed the association of markers on chromosome 25 recently identified by a paper in publication (Waters et al. 2021), which pointed to a region containing the SIX6 gene (Willis et al. 2020). In the same Bonneville Adult Fish Facility steelhead described above, we found that variation 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 65). 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 66).



**Figure 64.** Manhattan plot (from Micheletti and Narum 2018b) illustrating differentiated regions within age classes of females (top; 4- vs. 5-year-olds) and males (bottom; 3- vs. 4- vs. 5-year-olds). Red dashed lines indicate  $\alpha = 0.01$  significance threshold for the local score test with Bonferroni correction. Only the opsin 4 (OPN4) gene in females and transmembrane protein 19 (TMEM19) in males were significant using Bonferroni corrected thresholds. Relative locations of the VGLL3 (Ch3) and SIX6 (Chr8) genes which correspond to age at maturity in Atlantic salmon, are displayed in grey and were not significant.



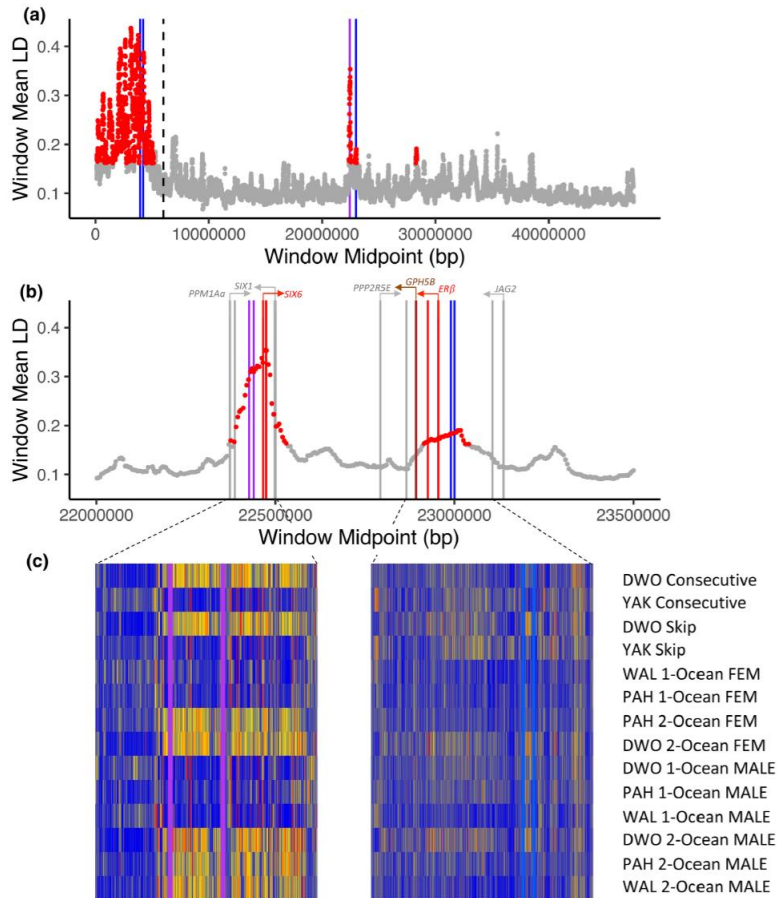
**Figure 65. Significance of association of chromosome 25 markers with fork length (left) and ocean age (right) in BONAFF steelhead. Position refers to SNP locus position on chromosome 25. Circle: Intergenic, triangle: SIX6; orange: female; green: male; black: combined male and female.**



**Figure 66. 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 ( $ER\beta$ ) 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).

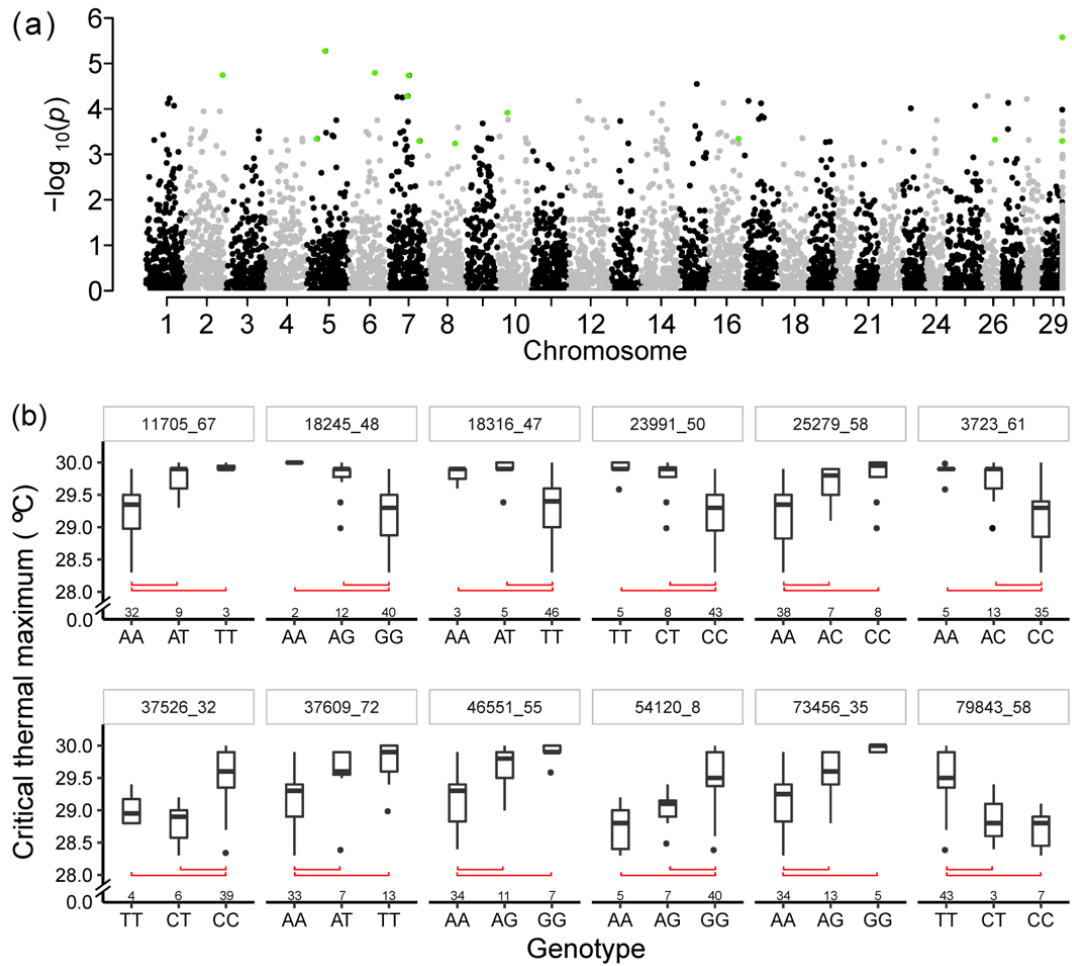




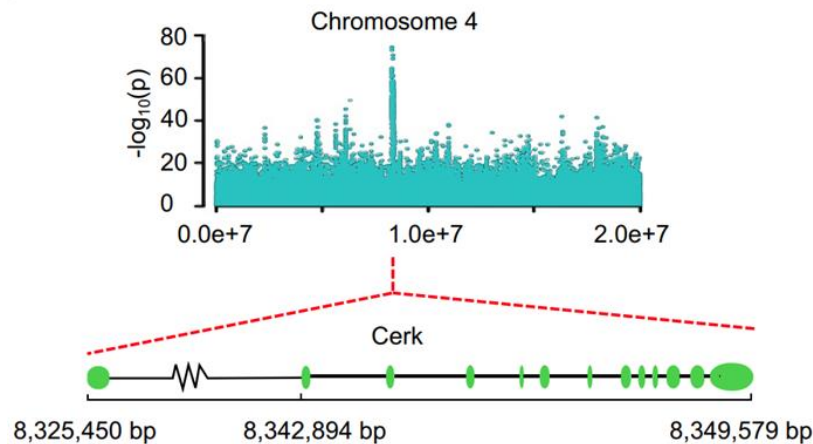
**Figure 67. Mean linkage disequilibrium among sites on Omy25 q-arm in sliding windows of 100Kbp and steps of 5Kbp, with LD outlier windows (red) identified as  $\geq 2 \times \text{IQR}$  after excluding the centromeric region (bounds indicated by dashed line) in consecutive and skip spawning female 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 *ERβ/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 68; 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 69), and markers were developed from this candidate gene for further validation. As these candidate genes for traits have begun to be identified (Figure 68; 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 68.** Results from Chen et al. (2018a) that demonstrate association of loci with thermal tolerance in natural populations of redband trout from desert, cool montane, and cold montane environments. Outlier loci and the association with critical thermal maximum (CTMAX). (a) Manhattan plot of calibrated p values, which were derived from the median z-score of results. Outliers identified by at least two analyses are in green. (b) significant associations between CTMAX and genotypes of candidate outlier loci (locus name above each panel). Red brackets indicate significant differences at the level of  $\alpha=0.05$  in one-way ANOVA on ranks with subsequent Dunn's post-hoc test. Numbers above genotypes represent the sample size.



**Figure 69.** 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*

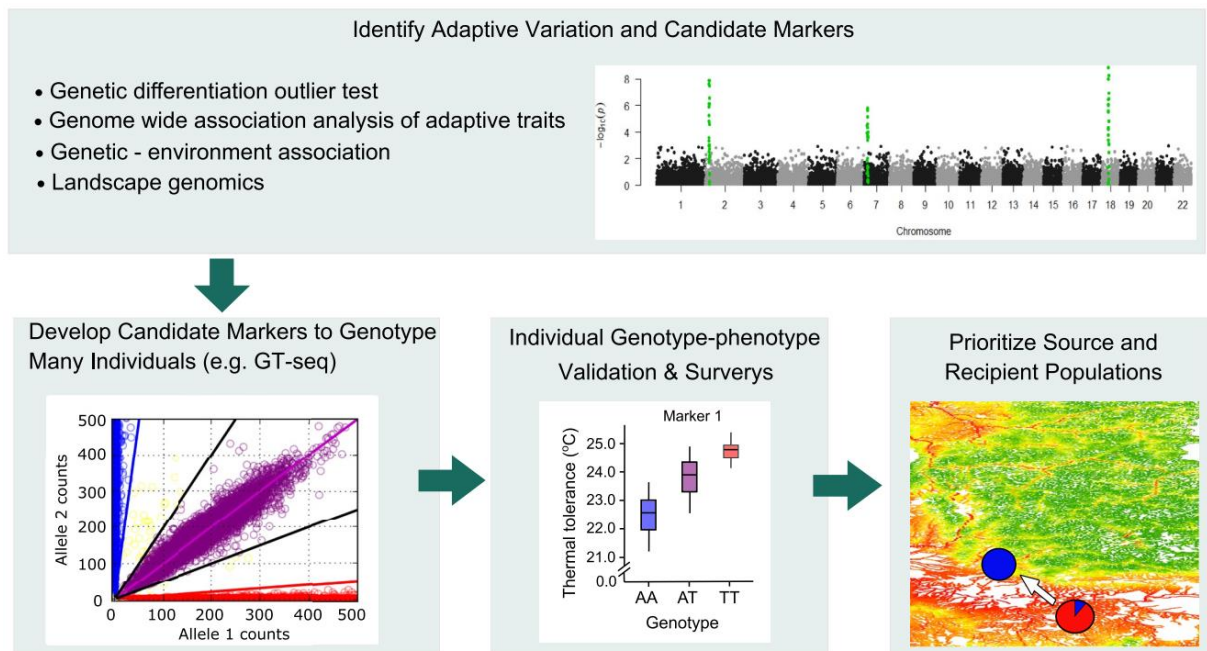
#### **Management questions/decisions and anticipated outcomes**

##### *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

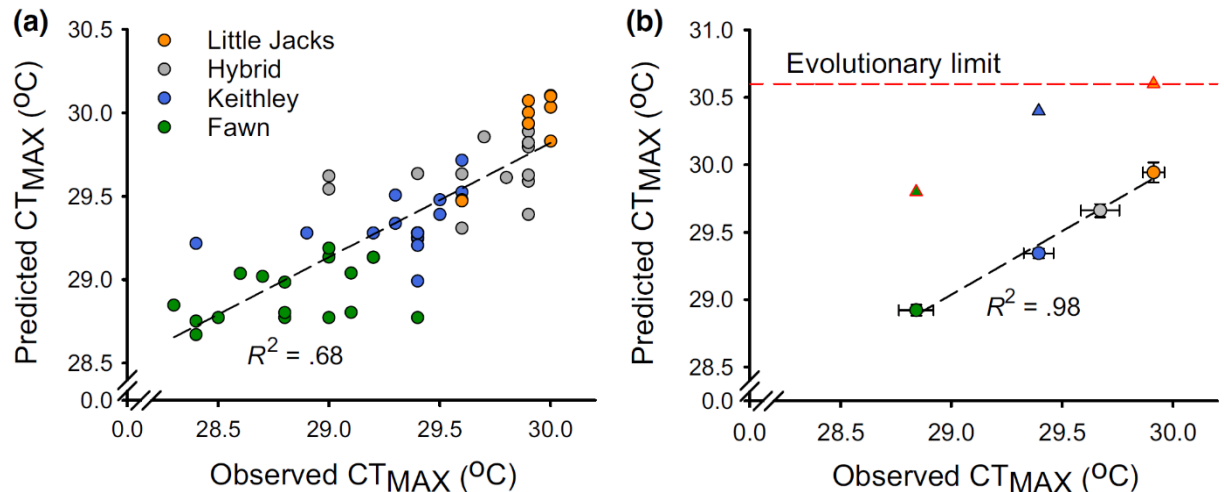
species and populations will be able to adapt to future environmental changes, especially for freshwater ectotherms with limited migratory opportunities. Local extirpation events might occur if populations experience extreme temperatures above their maximum adaptive capacity from existing genomic variation. 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 71). 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 70) if warranted, as described in a recent review (Chen et al. 2021).



**Figure 70.** 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 71.** 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

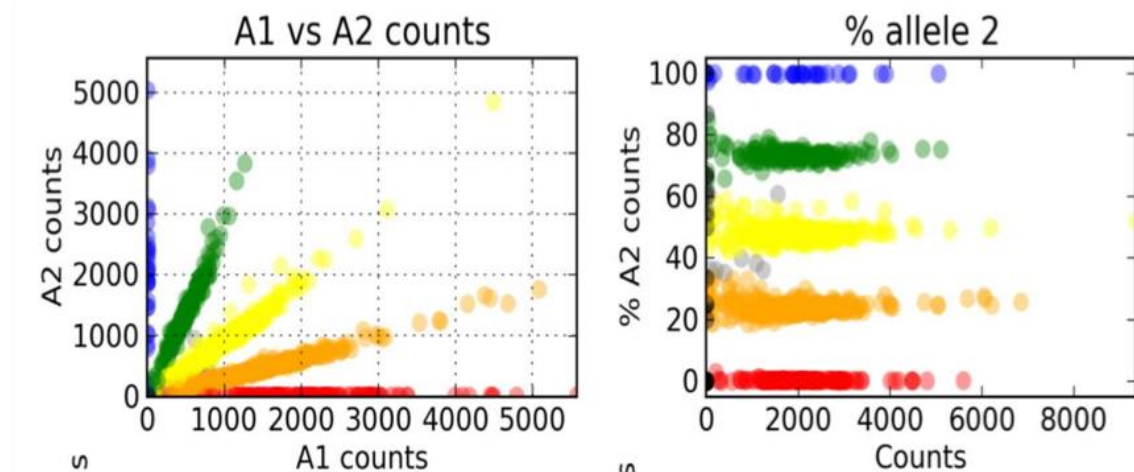
White sturgeon are a long-lived amphidromous species that historically ranged throughout the Columbia River Basin, occurring as broadly distributed, overlapping meta-populations (Parsley 2007; Beamesderfer et al. 2012). Overfishing is believed to have contributed heavily to decreased productivity and 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 ploidy-sensitive pipeline to conduct and publish analyses of population structure of white sturgeon in the Columbia and other stronghold river basins (Willis et al. 2022). In 2024, we genotyped

broodstock candidates collected for use at the Yakama Nation Fisheries (YNF) sturgeon hatchery. We also analyzed data from 541 sturgeon from population surveys conducted in the mid-upper Columbia (Priest Rapids to Wells dams; largely in 2022 and 2023), where the majority of fish now consist of progeny of previous YNF broodstock released in these reaches by the adjoining public utility districts. Analysis of these data is ongoing, but some results are discussed below. Finally, in 2024 we also completed incorporation of linkage maps from two full-sibling families of white sturgeon to further improve our draft genome assembly for white sturgeon.

## Methods

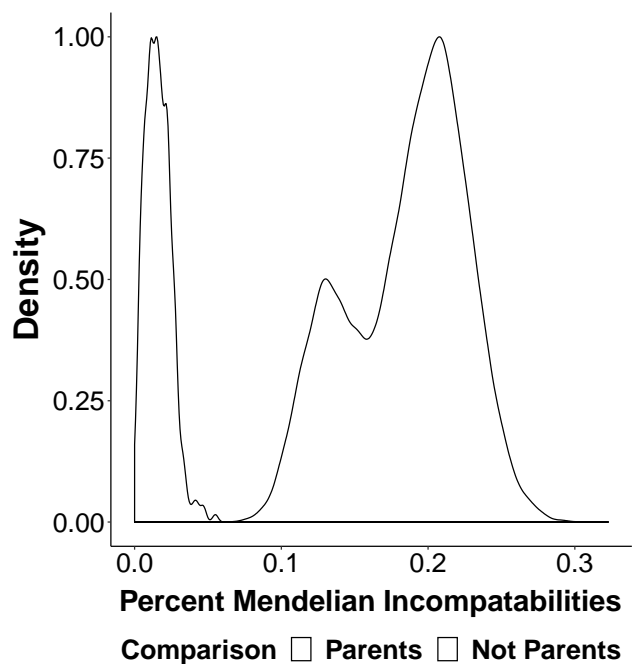
Our SNP panel consists of 325 loci that met or exceeded quality control criteria, including minor allele frequencies above 5%, and at least 80% genotyping success among samples (Matala et al. 2017). The SNPs were designed using extensive genomic sequence data, and the panel was designed to be genotyped using the GT-seq high throughput sequencing method (Campbell et al. 2015). 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, ABAB, BBBB) (Figure 72).



**Figure 72. Example of a locus GT-seq plot from octoploid (functionally tetraploid) white sturgeon.**

However, individuals that are greater ploidy (functionally 5N, 6N) exhibit some distinct and exclusive read ratios (e.g. AAABB, ABABBB), 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 (<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 (Delomas et al. 2021).

The genotyping panel was previously tested using a set of known parent-offspring pairs from two sets of 6 reciprocal pairings (6 males x 6 females from two spawn years, 2017 and 2022) of white sturgeon created by Yakama Nation Fisheries. Using these known relationships, we were able to establish that the majority of loci exhibited the expected mendelian inheritance patterns (Figure 73).



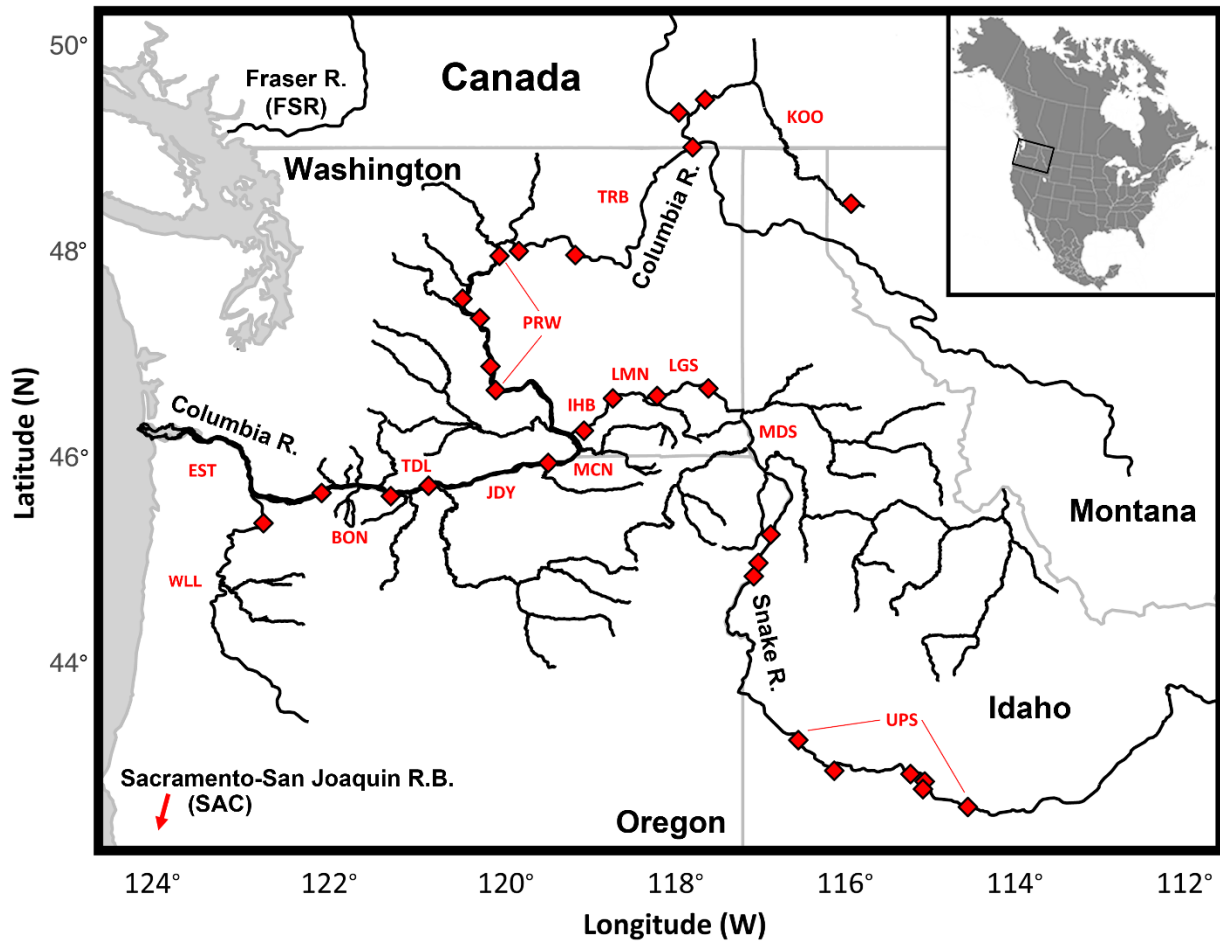
**Figure 73. Distribution of Mendelian incompatibilities (parents and offspring with mismatched alleles) observed among all offspring in six reciprocal crosses of white sturgeon.**

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.

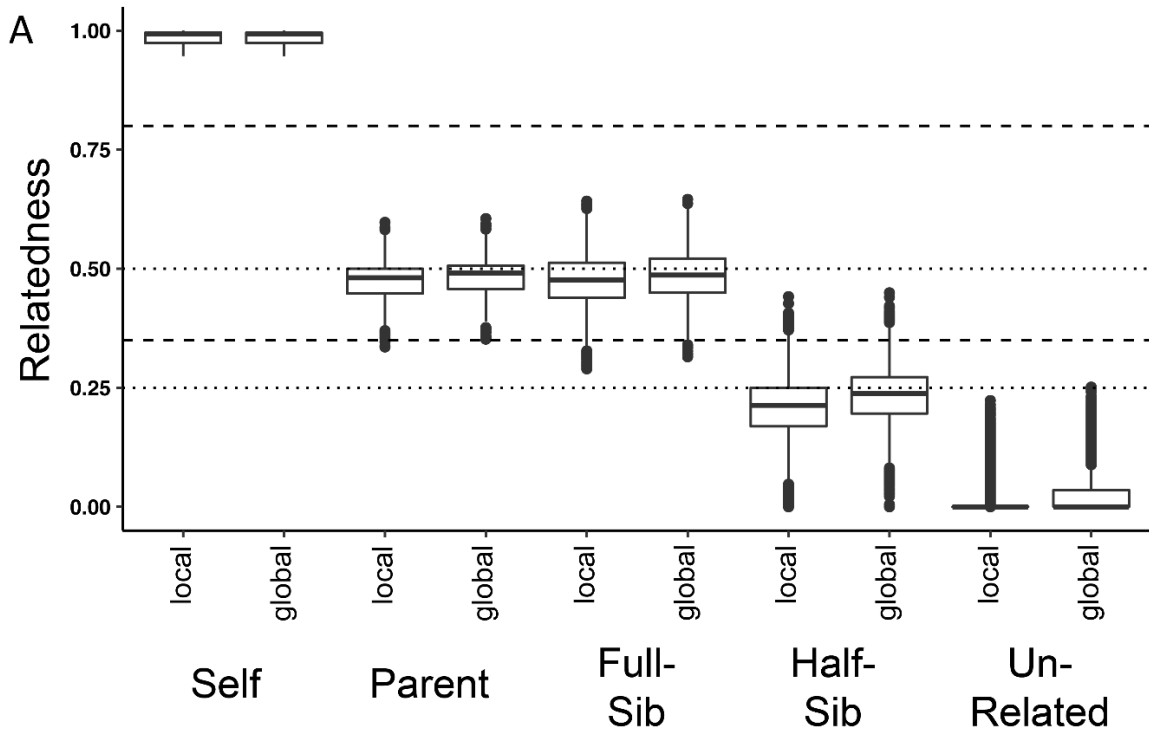
### Results:

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 74). 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). Using these data, we are able to identify first-degree relatives using values from individuals with known relationships from a known-cross families with parents collected from John Day Reservoir and provided by Yakama Nation Fisheries (Figure 75).





**Figure 74. 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.



**Figure 75. Maximum likelihood estimation of relatedness in known full- and half-sib families from broodstock collected in John Day Reservoir.** 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.



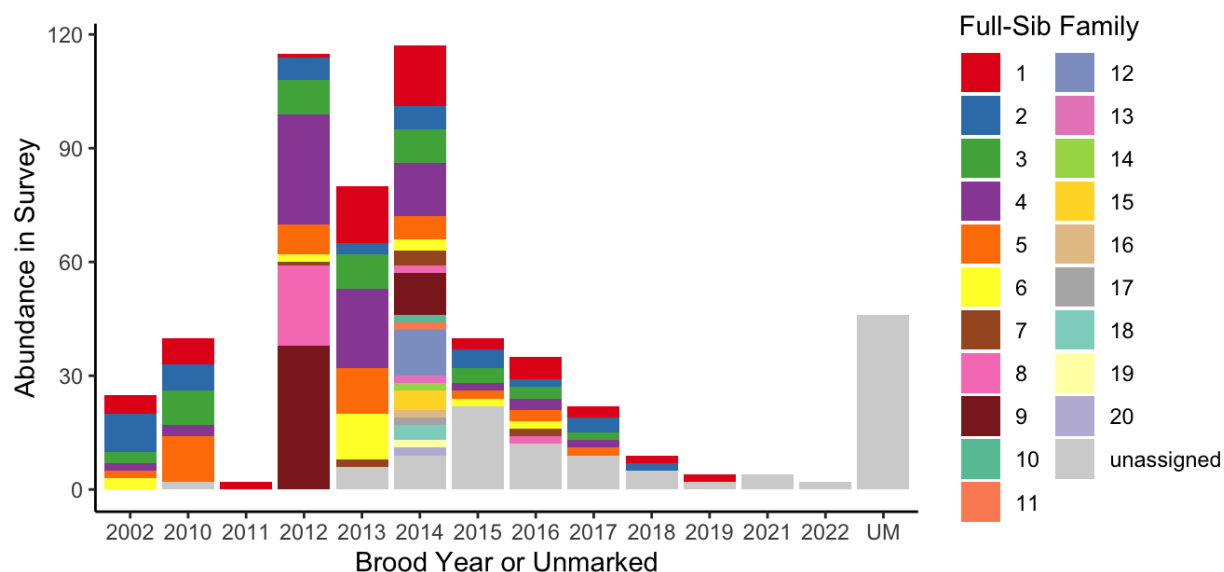
Genotyping efforts in recent years have focused on providing a robust sample of young-of-year fish from multiple years in each lower Columbia River reach, which reflect the genetic diversity of the breeders that contribute to each cohort, and a robust sample of the adult population in each reach (as well as McNary, from which recruits could disperse downstream) (**Table 74**). 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. Analysis of these data is ongoing.

As another product of our annual genotyping of the broodstock candidates collected from John Day Reservoir for Yakama Nation Fisheries, we are able to identify the parents of the white sturgeon collected in population surveys of the upper-mid Columbia reaches made by contractors for the public utility districts. While most of the released offspring are tagged with PIT transponders identifying their brood year, relatedness and parentage from genetic data allow us to discriminate shed-tag from natural-origin or hatchery-backcross individuals, as well as to assess if survivorship across full-sibling hatchery families (sharing both parents) remains similar to the proportions at release (**Figure 76**). Changes in family proportions may imply differential survivorship related to domestication, a phenomenon of significant concern to hatchery managers.



Young-of-year (<30cm)	Collection Year														Totals
	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2021	2022	
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	Collection Year														Totals
	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2021	2022	
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 74. Sample sizes of individuals genotyped at 80% completeness and ploidy confidence of 10LLR across year and life stage for the lower Columbia River reaches. Adult totals do not include 126 individuals genotyped from Yakama Nation Fisheries broodstock collections in 2023 and 2024.**



**Figure 76. Abundance of brood year and full-sibling families in 541 white sturgeon collected in the mid-upper Columbia reaches**

Our continuing efforts with white sturgeon have included the development of a draft genome assembly. While extensive whole genome data provided draft contig sequences, the majority of the genome remained poorly anchored from initial assembly. To overcome this, we have been

working closely with collaborators to generate linkage maps to assist in ordering and orienting (anchoring) smaller scaffolds into chromosomes. In 2024, we were able to incorporate two linkage maps derived from restriction-site associated (RAD-seq) libraries of a Fraser River white sturgeon family and messenger RNA (RNA-seq) libraries of a white sturgeon family from the Snake River. These linkage maps have allowed us to increase the size of the largest scaffolds in the assembly, although even the further-anchored assembly remains largely fragmented (**Table 75**).

<b>Total Length:</b> 6,265,289,666bp
<b>Scaffold Count:</b> 832,145
<b>Mean Scaffold Size:</b> 7,529.08bp
<b>Largest Scaffold:</b> 55,262,319bp
<b>N50:</b> 415,779bp with 1976 scaffolds
<b>N90:</b> 2,016bp with 399,337 scaffolds
<b>Scaffolding Gaps:</b> 514,997

**Table 75.** Statistics of the draft genome assembly of white sturgeon further anchored using linkage maps from Fraser River and Snake River families

## 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 72). 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 73), we continue to explore more robust methods to fully utilize the information content of tetraploid genotypes.

Our research is guided by previous results from microsatellite data which indicate a regional distinction between upper and lower reach Columbia River populations is evident (Matala et al. 2017), and published results with SNP data are consistent with this while providing additional detail. More broadly, current demographic trends and genetic variation may be a consequence of diminished rearing and/or spawning habitat coincident with stream fragmentation and limited connectivity. Ongoing efforts for this project are designed to further resolve the dynamics of recruitment and population demographic trends in the context of regional population structure and local adaptation and evolutionary potential, particularly in the John Day reach, where Tribal efforts are underway to identify efficient stock supplementation techniques. While supplementation is a natural proposal for reaches where adult carrying capacity appears to exceed *in situ* recruitment rates, the effects of different rates and types of supplementation remain unclear (e.g. hatchery spawning vs. repatriation). In addition to the traditional questions about the preservation of native genetic diversity, the incidence of spontaneous autopolyploidy (increases to 6N from 4N) may well be greater in hatchery spawned fish (Van Eenennaam et al. 2019), and as the fertility of 6N and backcross (5N) fish has yet to be clarified, there remains a chance that supplementation could have counterintuitive consequences for populations with already diminished recruitment. To this end, our ongoing examination of genetic diversity and rates of ploidy variation in these different reaches across life stages will help clarify natural rates of spontaneous autopolyploidy and of variation in genetic diversity between cohorts, as well as between recruits and the adult population.

Our continuing efforts with white sturgeon include the development of a draft genome assembly. While extensive whole genome data has provided draft contig sequences, the majority of the genome remains insufficiently anchored for publication due to the challenges of scaffolding a 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 in part 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. 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.

Our future investigation of white sturgeon also depend on the construction of a high-quality genome assembly which 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). While linkage mapping provided improvements on our initial assembly, the majority of the genome remains fragmented due to the challenges of scaffolding a genome with extensive and complex patterns of paralogy and homeology (white sturgeon are ancestrally octoploid and functionally tetraploid). Fortunately, since our initial sequencing of the white sturgeon genome, sequencing technologies that produce very long sequencing reads, reads capable of crossing the large, ambiguously homologous regions of the sturgeon genome, have become significantly more feasible in price and accuracy. We anticipate that application of this technology will enable not only an improved genome assembly for Columbia River white sturgeon, but also a pan-genome resource that will represent the structural genomic variation present within and among white sturgeon populations in different Pacific coast basins.

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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, Coho salmon, and steelhead (Objective 3), and stock composition of Chinook salmon, Sockeye salmon, Coho salmon, and steelhead passing Bonneville Dam (Objective 4). Chinook, Sockeye, and Coho 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. Coho salmon analysis in the Zone 6 Treaty fishery will help to test the new PBT baseline available for this species and has potential to be a helpful management tool.

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 2023. 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 2023, 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 2024. 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	Primary Flag	Rev Primer
OmyY1_2SEXY	X	Y		ATGTGTTCATATGCCAG	GCGCATTTGTATGGTGAAAA		0	GCCTGGCATATGAGTGTTGA
M09AAC.055	C	T	ACCTCCACGTGTCC	ACCTCCACACTGTCC	GTCTCCGACGTGTGGCT	(0,0)	1	TGGAACGAACCTGAGAACATAAGG
M09AAD.076	T	C	CACCAACCACTGGTGAA	CCAACCGCTGGTGAA	ACTGTTACCACTCTCTCATCAACCT	(0,0)	1	GGGTCCAGGAGGTTTTAAACAACAT
M09AAE.082	T	G	AGGTTGTTTTACAAATTTAA	AGGTTGTTTTACACATTTAA	CTATGTGCAGTGCCCTTCTCA	(0,0)	1	GGCTTACAAGTATGCATGACTAGCT
M09AAJ.163	G	A	AACAAAGTGAAAGTGTCTT	CAAAGTGAAAGTGTCTT	TCCCATGGCCCTTACTCTATCAA	(0,0)	1	TTGAGGTGTATGTTGAAAAGTAACTT
Ocl_gshpx-357	T	G	ATCCGTCCAGGAAATG	TCCGTCCCGGAAATG	GAGATCCTGAGGTCCCTGAAGTAT	(0,0)	3	AAGTGGAATTTGGGCTCAAAGC
Oki_101419-103-27	A	C	AATCCACTTCC	AATCCCCCTTCC	CCCAATTGGAGACCAGGGTT	(0,0)	3	TCATTGAGACAGTTGGGAGACA
Oki_101419-103-44	T	C	GTTCTCTACT	GTTCTCCACT	CCCAATTGGAGACCAGGGTT	(0,0)	4	
Oki_105105-245-23	T	G	GCCTTTTCCAT	GCCTTGTCAT	GCGTATCAAGCATCAACGCC	(0,0)	3	TCTTTCAGCAAGGTTGGGCA
Oki_105105-245-56	G	A	CTCATGCCAA	CTCATACCAA	GCGTATCAAGCATCAACGCC	(0,0)	4	
Oki_106172-60-38	C	T	GTGCGCATCAA	GTGCGTATCAA	ACTACTTGGCGTGTGTGTGGG	(0,0)	3	TCCACTGAGAGGATGAGGCA
Oki_106172-60-47	G	A	AACGCGTGAC	AACGCACTGAC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_106172-60-47c	A	C	AACGCACTGAC	AACGCCCTGAC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_106172-60-53	C	T	CTGACCGCYGC	CTGACTGICYGC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_111681-407-38	C	T	AGAAACTGCAA	AGAAACTGTAA	TTCATCCCATTGGAAGCCCC	(0,0)	3	ACAGCCTATATCTGTGCGCT
Oki_120255mod-105	C	T	AACGTCAGTTA	AACGTTAGTTA	GGGTAGGCTAAAACATAAATTACTCAA	(0,0)	4	
Oki_120255mod-113	G	A	AGTTACTGG	AGTTACTAG	GGGTAGGCTAAAACATAAATTACTCAA	(0,0)	4	
Oki_120255mod-115	G	T	TTACTRGGGTA	TTACTRGTGTA	GGGTAGGCTAAAACATAAATTACTCAA	(0,0)	4	
Oki_120255mod-119	G	A	GTAGYTTCTWTG	GTAAYTTCWTG	GGGTAGGCTAAAACATAAATTACTCAA	(0,0)	4	
Oki_120255mod-120	C	T	CTTCWTGGCAT	TTTCWTGGCAT	GGGTAGGCTAAAACATAAATTACTCAA	(0,0)	4	
Oki_120255mod-133	T	C	TGGCATAGTC	TGGCATAGCC	GGGTAGGCTAAAACATAAATTACTCAA	(0,0)	4	
Oki_120255mod-135	A	C	GGCATAGYCAT	GGCATAGYCCT	GGGTAGGCTAAAACATAAATTACTCAA	(0,0)	4	
Oki_120255mod-137	A	T	ATAGYCMTAGAT	ATAGYCMTTGAT	GGGTAGGCTAAAACATAAATTACTCAA	(0,0)	4	
Oki_120255mod-141	A	G	ATAGYCMTWGATA	ATAGYCMTWGATG	GGGTAGGCTAAAACATAAATTACTCAA	(0,0)	4	
Oki_120255mod-99	A	C	GACTAAAACGT	GACTACAACGT	GGGTAGGCTAAAACATAAATTACTCAA	(0,0)	3	CATTGAAGGGTGAATTGAAG

Oki_126619-265-31	A	C	GGATTGKGCAC	GGATTGKGCC	TGCGTAGTTAATTTACCTCGG	(0,0)	3	TACGCAGCACTGAAGACTGG
Oki_126619-265-35	A	G	CAGCACAGCTG	CGGCACAGCTG	TGCGTAGTTAATTTACCTCGG	(0,0)	4	
Oki_126619-265-50	G	T	GATTCTGCAGT	GATTCTCCAGT	TGCGTAGTTAATTTACCTCGG	(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	TGGATACCCCAACTCTCCA
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	AGCTCGGCTG	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	TTKGTGAGCA	ACTTTCTAGTAGGCGTGTGGC	(0,0)	4	
OMGH1PROM1-SNP1	A	T	TAGTGTTCACTGACTTCA	TAGGTACACTGACTTCA	TCAAATGCATTTGATGGAAACAACAT	(0,0)	1	AGGACAATTCTAAGTGACCTCAAACTG
OMS00002	A	C	TGTTTGCAGCGCTC	TGTTTGGCAGCGCT	TTTGATTGATTGTATCTGCTTCTT	(0,0)	1	CCAACATGCCTCACAAAA
OMS00003	T	G	CTTACTGTCGACATTTTA	TACTGTCGCCATTTTA	GTGCCACTGATGAGGATGAGATCA	(0,0)	1	GTAATAAAGCCCTTTTGTGAGGAAAACTAAT
OMS00006	T	C	CACCTACAAATACAAAATT	CTTACAAATGCAAAATT	TCCACGTAGGACATAGTTTGAGCTA	(0,0)	1	TGTGGTGTATCTTTGTCCTAC
OMS00008	A	T	CTTCAAATATCCATAATTATATC	TCAAATATCCATAATAATATC	CCCTTTAAGGAGGATTTTAAATATGTGAGATAGAA	(0,0)	1	GGATACAGCGTTTTTGAATGAAACT
OMS00013	A	G	CTTCTTTCCTTGCTACTC	CTTTCCTCGTACTC	GCCTTGTCTCTTGGTGGTTA	(0,0)	1	AGAAAAGTGTGGACTGAGGTTGAG
OMS00014	T	C	TGATTGATGAATTAACCTTC	TTGATGAATTGAACCTC	CTTACACACAAGGGCTTCATTCTG	(0,0)	1	GATGTCTCTGGGTGGTTGTCA
OMS00015	A	T	CAAGTCACACTTTTAATGAA	CAAGTCACACTTATAATGAA	TCAGACCCTATTTTGGCACAAGT	(0,0)	1	GTCTAACTGATCCACTTCTGCAT
OMS00017	A	G	TAGACCTCGGTGCTGTAG	CCTCGGCGCTGTAG	ATTAAGTTCATACAAAAGTTCATCATAAATATTTTCCTT	(0,0)	1	GGAGAACAAAGGGAAAGAGAAGACA
OMS00018	T	G	AACCACATAATTAATAATTC	CCACATAATTCATAATTC	AGAGTACATGTGTGGCTGCAA	(0,0)	1	GTCATAAATCAACACAATTATCTTCTCACAGAA
OMS00024	T	G	AA[AC]CCCAATTTTAC	AA[CA]CCCAATTTTAC	CACATACAACCATCACCTTCCTAA	(0,0)	1	AGCATTGAGCGAAATTACCAAGAGT
OMS00030	T	G	ATGAGGGTCCCTATACAGG	ATGAGGGTCCCTCTACAGG	CCTCTGACTACAGAGCTATACAAC	(0,0)	1	GATCTGATCGGTGGGAGAGA
OMS00039	A	G	GTACGTGTCTGTACC	GTGCGTGTCTGTACC	GTCACTACTGTGTGTCTGTGT	(0,0)	1	CCATCTACATTGTGAGCAGTGTGA
OMS00041	G	C	CCACTCTATGCTGCCCT	CACTCTATGCGTGCCCT	GATTCTGTCCATCCTCTTCTGTCA	(0,0)	1	AAACATAAAAAAGGGCATGAAGGTGTC
OMS00048	T	C	CAGCTAAACTCAGAAAA	AGCTAAACTCGGCAAAA	GGAAGAGCTGGAGAACACGT	(0,0)	1	TGCAGTTGACAGAGGCTTCTCTT
OMS00052	T	G	CTTCCTTTTGAGAATAAT	CCTTTTGCGAATAAT	TGCGTTTTCATCCCAATCATTAC	(0,0)	1	GGCATCAGGCTCTTCTCCT
OMS00053	T	C	ATTTATATGTATCAATCA	ATTTATACGTATCAATCA	GGAGCCAGGTCAAGGTGATC	(0,0)	1	GGATGTCTGGTGGCTGTAAA

OMS00056	T	C	TAGCTTGACCAATAGCA	CTTGACCGAATAGCA	TCAGGAAGTAACTGAAATTCGAATGTATGA	(0,0)	1	CCCCAACCATGCTTGTTATTGAAC
OMS00057	T	G	CTCCACAGAACCTTG	CTCCACAGACCTTG	GAGAAAGGGAGCATGAGACAGA	(0,0)	1	GTGGGGTCCGGTACGAT
OMS00058	A	G	CAACACTTTGTACCCCTC	CACTTTGCACCCCTC	GTGACATTTGGAGCCACTGC	(0,0)	1	GCTAGGAGACAGAGGGGTGAAAG
OMS00061	T	C	CATTGCCATTTACAGACTT	TGCCATTTGCAGACTT	AAGTGGAGGCTGACCTGTTG	(0,0)	1	GCTGATGGCACTTGACAGTTAATT
OMS00062	T	C	TTGACCAGCAGATGGTGTA	ACCAGCAGGTGGTGTA	ACCCTGGGAAGGCTACTGTAC	(0,0)	1	TGAACAGAGATCTGGAGAGTTGGAT
OMS00064	T	G	CAGGCAACATTTTATATACTA	CAGGCAACATTTTATCTAATA	GTGGATATGTAGTTCGATGGAACAGT	(0,0)	1	TTTACAACATCTCTTTTAAATAAATATAGCCACTTAT
OMS00068	A	G	AATATGCCTCCTCGTCTC	TATGCCTCCTCGTCTC	GCACTAACTGGACAACATTTTAAAGAATGA	(0,0)	1	GGCAGTTGAGCATTTTGGGATATT
OMS00070	T	C	CAAAATACGGAATGCAG	AAATACGGGAATGCAG	CGTTCCTGCGGGACAGT	(0,0)	1	GTTTCTCTCAGTCCACAGATCT
OMS00071	A	G	CTGTTTGAGCTTTTCT	TTGTTTGAGCTTTTCT	CCGGAGTGACCTCACATTTGG	(0,0)	1	GCATCGTACAGTTCACTACCT
OMS00072	A	G	TAGAAGGTCCATGTATCTC	AAGGTCCATGCATCTC	GTGGGAGAGCTCGTCTATGG	(0,0)	1	ACAACAGGTCATTGGATGTGATCAG
OMS00074	T	G	TGAACAAAACAAATGTTCC	AAACAAAACACATGTTCC	CCTGTTTATTCATCTAAACAGTTCTTTAAAT	(0,0)	1	AACTTAATTTAGCAAAACAAATGTCTGAACAGAA
OMS00077	C	G	TTCCGGTGGTAAGTT	CCGGTGCTGAAGTT	AATACCATCTTGAGCTCATTAGTAATTATCAA	(0,0)	1	CCAGACTTTACACACTCTTGACTGA
OMS00078	T	C	TTCACATGCATAAGAGTG	TCACATGCATGAGAGTG	GAGGGAAGCAGCCATAAACAGAATA	(0,0)	1	GTCTCACTATGGTCATATCTGTGTAGA
OMS00079	T	C	CTACTTTTCACAGTAACACAG	CTACTTTTCACAGTGACACAG	GTAACATTATGAATCTATCAGTTTCCCTAGCT	(0,0)	1	ACCTGCAACGTTAGAGCTGTTATT
OMS00087	A	G	GTTA[CA]AACTGACAAAGTGTG	GTTA[CA]AGCTGACAAAGTGT	GCAAAATTCACCCCTAACGTGGTGT	(0,0)	1	GATTTGATGTGTGTATTACCTCCTCTA
OMS00089	A	G	ATGAATCCCAATAAGAAC	AATCCCAACAAGAAC	GCACCATTTGAATAAAAAATCTGCTTTGT	(0,0)	1	GCAACCCAATTCAATATTAAGCACATGAT
OMS00090	T	C	ACAACCACACAAGATT	AACCACGCAAGATT	AGGGCACACACCACTCTAAATT	(0,0)	1	TCGAAAAGCAACATCTGTCTCAGT
OMS00092	A	C	CAGCTGAGAATAGGTTT	AGCTGAGAAGAGGTTT	TCTCCAGGTGTATCTTGAGAAGGT	(0,0)	1	AGGGTTCACACAGGGAAGATATCAT
OMS00095	A	T	AGGCAACTATATATTTTTT	AGGCAACTATATATTTTTT	CTCCAATGGCTGTCAACAATTAATATAAGAC	(0,7,0)	1	GTGTGCTGCTCTCTCTTTATTCTCA
OMS00096	T	G	AAAGAGGAAGAGTCTCG	AAAGAGGAAGCGTCTCG	CATGAGAATGGATCAGTCTCCACAA	(0,0)	1	GATGAAATCTGAATGTGTGACACTACAG
OMS00101	A	G	CTCTAGTAGCCTTATAGAAAG	CTAGTAGCCTTACAGAAAG	GCGTGTCTGGGTACAGTTAAATA	(0,0)	1	GTGCAATCCAACCTATTAGTAGATATGCT
OMS00103	A	T	CTCCACAGTAATTTTTTTT	CCACAGTAATTTTTTTT	GAGATCACTGTAGGATTGGCTGTTT	(0,0)	1	CCTCAGAGCAGCTCAATGGCATC
OMS00105	T	G	CTGCTATTCAAATTGCT	CTGCTATTACATTGCT	ACATTTGAAGTCAGTATGGGTGTTGAG	(0,0)	1	GAACCTCACCACAGTACTAAATGCA
OMS00106	T	G	TCTGATGGAACTTTC	TGATGGCACTTTC	CGTGTAGCATTTCTTGAGGAAGCTT	(0,0)	1	TTTCCAACAGATGCCAGAATCCT
OMS00111	T	C	CAACCAGACTACCATTC	AACCAGACTGCCATTTC	CATGCGGACCTGCATAGCT	(0,0)	1	GCTTAGCCATTGACAGAGCATATCA
OMS00112	A	T	CGGTTTCAAGTTTACTTGT	CGGTTTCAAGTATACTTGT	TGGCAGCAAAAGGGATGCA	(0,0)	1	TCCTGAGCAACCAAGTCAACATT
OMS00114	T	G	AAACGTTTCACATGCACC	AAACGTTTCACCTGCACC	GGATGATGCTGTGAGTCGAGAAG	(0,0)	1	ACCTTCGCCACCATGTTTTATT
OMS00116	T	A	CTTTTACATTTTCAATATTCTG	TTTACATTTTCAATTTTCTG	GCCTTCTCCCATATCATTTCGA	(0,0)	1	AAACGCATCTTACACTGTGTGTG
OMS00118	T	G	GCGGGGTGTGC[AG]CATT	GCGGGGGTGC[AG]CATT	GCTTATTTAGAGTGCATGCCAGATG	(0,0)	1	TGGAACCAATGGGACAGTCTTA

OMS00119	A	T	CCACACAGTGCCTGT	CACACAGCAGCCTGT	AGCGGCAGTTGTGTTAATGAGA	(0,0)	1	CTTCCTAAAGCCTGACAGTCTGT
OMS00120	A	G	C[GA]CCCACATAAAC	C[GA]CCCACAAAAAC	GGCAGAAGAGGAGAGATATGATTG	(0,0)	1	CCTCAATAACCTCTGACATTGAAGGTT
OMS00121	T	C	ACAGCGTGATAAATT	CAGCGTGGTAAATT	GGAAGGAGGTCCAGTGTGAGT	(0,0)	1	AAAATATGCAACACCACTAAACTGGAAAA
OMS00127	T	G	CACACACCCAAATGTA	ACACACCCCAATGTA	CACCTTCTCTCTCTCCATCTCA	(0,0)	1	AGTGTGCTACACACCTTAAAAATATATCTATT
OMS00128	T	G	ACTCTCAGAAATTAATTATG	CACTCTCAGAAATTCATTATG	ATGAAAGAACTCCCAGACACGTATTTT	(0,0)	1	ACATTTTAAACAGTAACACTAATACACCA
OMS00129	C	G	TTGAACAACAAGAAAAA	TTGAACAACAACAAAAA	GGAGATGATGAAATAAAAATTGAGGAAAGATGA	(0,0)	1	TGCTCTGGTGAATTATCGCAATAACCA
OMS00132	A	T	CAGCAGTCCTCTGTGTGG	AGCAGTCCTCAGTGTGG	GTTTATGACTCCATTGCCGAAATGATT	(0,0)	1	ACGCGACCTGCAATTTCATCAATA
OMS00133	A	G	CGCCTCCATCTTTGTGGT	CGCCTCCATCTCTGTGGT	GACCACTCACTCATTCTCCTTTT	(0,0)	1	TCCGGTTTACACACTTCATGCA
OMS00134	A	G	TCTATAGCTGCAGTATATTA	TAGCTGCAGCATATTA	GAAACTGAAATGATCCATCGTGTT	(0,0)	1	GCTAGCATAACAGCATTGCCATAT
OMS00138	T	G	CTAACAATAACCAAGAGCTG	CTAACAATAACCACAGACTG	TCGGACCACATGAGCAGTTC	(0,0)	1	GTTCACACGGTGCCACAC
OMS00143	T	C	CCTGATCCAGAATCTAGA	CCTGATCCAGAGTCTAGA	GGAGGCACGCCCCAAA	(0,0)	1	TTTGTAAAAATAGAGCCCTTAGTGGGTTT
OMS00149	T	G	GCTAAATGCACAG	GCTAAAGGCACAG	GGCATCATTGTTCTTGCTCTGTTA	(0,0)	1	CCTGGGAGGGTTTATATCGGAGTAT
OMS00151	A	G	TCATGACCTTGATAATC	ATGACCTCGATAATC	CTAAGCTCTTCCCAATGATATTTACAAAGATA	(0,0)	1	ACCGTGGAATACAAATTTTTATGCCAAT
OMS00153	T	G	ACAAAATGTAATTTTCC	CAAAATGTCATTTTCC	ACTTTGACCATAGGCTTGACAT	(0,0)	1	TGATAAGGATGATCAAAAAGCTGAAGTATGTA
OMS00154	A	T	ACAGGGCTTCTGATTGA	AGGGCTTCAGATTGA	GATGTGGCTGGAGGTGTAGT	(0,0)	1	TGGGAACACTTTTGCTACCC
OMS00156	A	T	TGTGTGCTCTGCTGTAACA	TGTGTCTGCAGTAACA	GAGCAGAACACATAGAGGAAAGACT	(0,0)	1	GTAATCACCTCTTAGCTGTATGG
OMS00164	T	G	CCAGATTCAATTAATTTA	CAGATTCAATTCAATTTA	CAGAGGAGAGGAGAGCAAAATACTT	(0,0)	1	ACAACCTACTCATTGAAACTATTGGA
OMS00169	A	G	CAAAAAGCATTGATATCAAT	AAAAGCATTGACATCAAT	AGCACTTGACTCAAACTCACATAAATCA	(0,0)	1	CTGAGACAGGAAGAACAATGTTAACAAAA
OMS00173	T	C	CATTAGCTTGTGTATGAACT	ATTAGCTTGTGTGAACT	TGGAAGTAGCTACTTAACAGGAAATGG	(0,0)	1	AACACGTGTGCTGTTTGTGCAA
OMS00174	A	C	CAAGAACAGG[AC]TAAATGT	CAAGAACAGG[AC]GAAATGT	TGACTAACTATGCAGCCTGAAAGG	(0,0)	1	GGGATACTCTTGTAATAAACTGTTGGTTAGTA
OMS00175	T	C	ATCACTAGTTCAAATACAA	ATCACTAGTTCAGATACAA	TTGCGATATGGGACTGTATACATTATTCC	(0,0)	1	ACTACCTCCAGTTAAAAATAGTGGGAAA
OMS00176	T	G	TTCCAGCAGCTGTGTC	CCAGCCCTGCTGTC	GTTGGAAGTTCGGTGGTAGAG	(0,0)	1	CTGGGCTCCTGAAGGAGCTT
OMS00179	A	C	TGCTCTTCTCTTTCTCAT	CCTCTTCTCTGTCTCAT	GTCATAACAAAATCAGGGCTTTCCAA	(0,0)	1	TGGGAGATTTGGGCTGCTTTAAA
OMS00180	T	G	CTAAAAGTGCATTAAGCC	CTAAAAGTGCCTTAAGCC	GCGCCGAATGGCATTAGG	(0,0)	1	CACATTGCTGTCGTTTAGTTTGACT
Omy_1004	A	T	CATGTGATGTTTTTIGC	ATGTGATGATTTTTGC	GAGAATCGGAGCTAATCTTAGTTATTGTGA	(0,0)	1	CACTTTATTGAGCTACATGGCAATCTG
Omy_101554-306	T	C	TGCTTCTCACATTTTAA	TGCTTCTCACGTTTTTAA	GCCTGTATTTCTCTGTATGTGCAT	(0,0)	1	TCAACTTTTGCAAATTTTTATTCTTTGTCATTT
Omy_101832-195	A	C	TGTAGTCTTTCAGAGTAGTATG	TAGTCTTTTCAGAGGAGTATG	TGGCTCTGGACCTGTTGAGA	(0,0)	1	CGTCACAGCTATTTTAGGCGTAGT
Omy_101993-189	A	T	CTTGATTTCAGAGTGTCAA	TGATTTCAGCATGTCAA	ACAAAACACAGTGGAAATTACAATTAACGTT	(0,0)	1	GGAAGTTAAATTCGCTTCGTGAGAA
Omy_102505-102	A	G	AACAGGATGTTTTTGC	CAGGATGCTTTTTGC	CTGCAAACTGACATGGTAGCAAAA	(0,0)	1	TGCTTGCTTTTTAAAAACAATCTCCA

Omy_102867-443	T	G	TTGGGTACATAATTTTT	TGGGTACATCATTTTT	CATTGTGTTAATTTGATTGGCACAACTCA	(0,0)	1	CCCTAGTCTGTAAACAAAGACGTAA
Omy_103705-558	T	C	AGACTTACCAGAGTGAGAG	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	GCGCCTCGTCATCATCA
Omy_105075-162	T	G	CTTCTCTCTACTTTCC	CTTCTCTCTCTTTCC	GGAGAAGGACAAGGACATTGGTAAT	(0,0)	1	AAAGCAGACCACACATACTTCTC
Omy_105105-448	C	T	AAGGAGAATGCATAATC	TGAAAGGAGAATACATAATC	CAATTGCAAGCAGGGAAGGTTAT	(0,0)	1	GTGATGGGCTGCAATTGCCT
Omy_105385-406	T	C	CTTGAACCATTTGCTAC	TTGGAACCGTTGCTAC	GTAACCTACCTCACCTGAATTCA	(0,0)	1	GTCGCTCTTCTGGCGTATCG
Omy_105714-265	C	T	CTGTTGTTGAGGTTTAC	TGTTGTTTGAGATTCAG	CCACTCAGTGCAAGCATGGA	(0,0)	1	GCTTCAATCTTGGCTCCAATATC
Omy_107031-704	C	T	TGGACATGATTGCATAGAC	CTGGACATGATTACATAGAC	GGCTTTCGGATACTGAGCAACAA	(0,0)	1	TGAACTCACTGTTGGTATGGACTAGA
Omy_107285-69	C	G	ATACGTTACTTTTGACCTTGT	ACGTTACTTTTACCTTGT	GCCCTTGTGACAATGCACCTGTTATA	(0,0)	1	AGGTCTAGACAGTGTGCCATTG
Omy_107336-170	C	G	CACTCTGGGTGCAGAA	ACTCTGCGTGCAGAA	GCCCTCTCACTCATGACATCAAC	(0,0)	1	GCTCCAGCCACTCGCA
Omy_107806-34	C	T	ATGGATGTCAGTGTCTT	ATGGATGTCATGTCTT	TCITTTGCCATGCATTGATATT	(0,0)	1	AGCACATTTAGTTAGCAGTATGGA
Omy_108007-193	A	G	ATGTTTCTCCCTACTTAAC	TTTTCTCCCACTTAAC	GTGAATACCACCCAGGCTTGT	(0,0)	1	GTCCCTTCCCAAGTTTCACTTAAT
Omy_109243-222	A	C	TGTTCAATAAATTGACTTTTT	TTCATTAATGGACTTTTT	ATGTGCACCTCTTAATTTGTAAGTAAATGT	(0,0)	1	ACCCTATATTCAGTGGCAAGATTGC
Omy_109525-403	A	G	CCTACACCTCTTTTCCACA	CCTACACCTCTTTTCCACA	CCTATTCTCATTGGTGAGTTGTCT	(0,0)	1	TGTAAGATCTGACCACATGAGTATAACCA
Omy_109894-185	T	C	CTCCGTGATCCCC	CTCCGTGATCCCC	GGGAGGAATTGGAATGACAGATTAAAC	(0,0,7)	1	CGGTGTCATTATGGTTGTCATTGTG
Omy_110064-419	T	G	ACGTTAGCTTTTAATTC	AACGTTAGCTTTTATTC	GTGCAAGGGACCTAGCTAATCC	(0,0)	1	TCTGAACTGACACTGAAGAACAAAGAA
Omy_110201-359	T	G	TTGGCTATTGAAATTATACATT	TTGGCTATTGAAATTCTACATT	GGTAAGGCCTGTCTGACTATTTTGA	(0,0)	1	AGAGGTCAATGGATGCCAGTTT
Omy_110362-585	G	A	CACCGCCTGCCGT	CACCGCCTGCCGT	GCAGCCAAGATGAACGAAACTTC	(0,0)	1	CCGGCCTGGGTCTCAATG
Omy_110689-148	A	C	CAATGAACACATTATTTATC	ATGAACACATGATTTATC	GTGTGTGCGAGAGAACTAATGAT	(0,0)	1	GGTTAAGACATTAAACATAACTGGACTCT
Omy_111084-526	A	C	CCAGTGAAATTTATTTTT	CAGTGAAATGTATTTTT	CACCACCAACGAACTATTTTCATT	(0,0)	1	ACCAACTACTGTCCCATTTTTCAT
Omy_111383-51	C	T	AGCAAGCGCACTJAGJGGT	AGCAAGTGCCTJAGJGGT	CACGCGCAATCTCTGTTTTAC	(0,0)	1	TCTTTAGGCAACAGCGTGTCA
Omy_111666-301	T	A	AGTATAACACAGTAAGACAAT	AGTATAACACAGTTAGACAAT	GGGTGAAAAGAGTGGGACATTTACA	(0,0)	1	GTCAATTTCAAGGCACAGACAAT
Omy_112301-202	T	G	AATGCGAAGACAAACT	AATGCGAAGCCAAACT	GTAACCTTGCCACATAATTAGGT	(0,0)	1	CTGAGACTGTCTCAAGGT
Omy_112820-82	G	A	CGCCGCAAGTTA	CGCCGCTAAGTTA	CCTTCTCTTTGCAATTCCTACTATTTAATT	(0,0)	1	AAATGAACTCACGTTGACCTCTGA
Omy_113490-159	C	T	CATCTGTTTGGTTTAGC	CATCTGTTTAGTTTAGC	CATAGTACATTTACAGATAATGTTTAAAGTGCATGT	(0,0)	1	CGAGATACCAAAATGCCACAGTTACAT
Omy_114315-438	T	G	TTATGGGCTTAAGGGTC	TTATGGGCTTACGGGTC	CCTCACCAGTCTAGTCAACTTCATC	(0,0)	1	AGGAGGCTGAGGGAGATTCTAG
Omy_114587-480	T	G	CCTGTCCAAAATTGT	CCTGTCCAAAATTGT	CAGATTACGTTATTACGTTTGGGAAATTTTAAAGT	(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	CCTTGTCTCAATTTTCTCTCT	CTTGTCTCAATTTCTCTCTCT	GTTCAATTCATGTTGAAGTGCACAT	(0,0)	1	CTCTGCATGCTCCCATCCT
Omy_117286-374	A	T	CTTTCCTCATCATCTCTATGG	TCCTCATCATACACTATGG	TGATGTGTGTTCTCATGGCTTA	(0,0)	1	CTGTGCATTATTCTGTGTAGCTAGG
Omy_117370-400	A	G	CAACTCCAATGAATTAA	AACTCCAACGAATTAA	TGCAAAACACAGAGGAAAGGGATT	(0,0)	1	GGCTATTTGTTCCTACTTGCA
Omy_117540-259	T	G	TGTCACCTCAAAAGTTTG	TGTCACCTCAACGTTTG	GGCAGGTTAACACAGTCATCTACTATAAA	(0,0)	1	CAGCATGTTGCTTAACTCTTACA
Omy_117815-81	C	T	CTATACGGAGACCAGC	CTATACGGAAACCAGC	CTGCTTTATGCACACCACATTGT	(0,0)	1	GCTCTTCTGGAGAACCAAGGTACTG
Omy_118175-396	T	A	CTCTTGACAGACATACCCGTA	CTCTTGACAGACATTCCCGTA	AGGCTTACACACACATGCA	(0,0)	1	GACGCGCAACCTCTAGATTACTT
Omy_118205-116	A	G	CTACTGAGGCTGAGTGCT	TACTGAGGCCGAGTGCT	CTGCGGTGGGTACACA	(0,0)	1	CGCAGCTGCGGATGAG
Omy_118654-91	A	G	TCAGCTTGCTTGCCGC	CAGCTTGCTTGCCGC	CAGCGTAGACCGTTTCTCTATTAT	(0,0)	1	GCGCCGATGAGCAGCTT
Omy_120255-332	A	T	ACTATGCCATGAAGTTA	ACTATGCCAAGAAGTTA	GCTAGCTAACATTGAAGGTGGAAT	(0,0)	1	GGCTACAGGCACTTACAATGGG
Omy_128693-455	T	C	CACTCAACTGATACCC	CTCAGCTGATACCC	GCCTGCAGGAGAAGGTAGAGTTA	(0,0.8)	1	GAAATGGAATGGACCCCAATCCT
Omy_128923-433	T	C	CTTCATTTTCATTCTGTTTT	CATTTTCATTCTGTTTT	CTATGTCCTTGCGAGAAGTCTACA	(0,0)	1	ACGTTTCTTGGGTGAGACTTATT
Omy_128996-481	T	G	CAAACCTCAACCAC	CAAACCGCAACCAC	CTCATCCACACTGTACAGTACAAGT	(0,0.6)	1	CATGCCTCTGCTCATCAATAACAC
Omy_129870-756	C	T	ACAGGTATTTCTGAAATG	CAGGTATTTTCATGAAATG	TCGTTATTTTGCTCTCGCGTA	(0,0)	1	TCCCATGAAGATGTATACATGTTTTGTGA
Omy_130524-160	C	G	ATGGCTTGATCCTCA	ATGGCTTCATCCTCA	CGAAGGTAGCGATTGGTCGTT	(0,0)	1	TGCTGTCTGCTGTGTGCTT
Omy_131460-646	C	T	AATAAAGCAGAATTTGTACTG	AAAGCAGAATTTATTACTG	GTGAAAAGGAATGGAGAGTACAGT	(0,0)	1	TGCTAGGACAGGAAGATCAATTTGTG
Omy_187760-385	A	T	TCCTTATCCAAAATTATTGTGC	CTTATCCAAAATAATTGTGC	CGGCTATTCTCGCGTAAAAGCT	(0,0)	1	AAATGCAACCGAAACGGAATGTC
Omy_96222-125	T	C	AACTACAACCTGTAGCTAATT	CAACTGTGGCTAATT	GTAAGGAACCTAATTGGCGCAACATT	(0,0)	1	CAGTTTGTCTAACACCCAGGCATAT
Omy_97077-73	T	A	TGGTGCAATAGAAAATA	CATGGTGCAATAGTAATA	GTGTAACAAAATGACTCTGGGATTGAG	(0,0)	1	AGAAGTGGCAATGGTGTGAAGTAT
Omy_97660-230	C	G	ACGTAACCTGTAGCGTTTT	ACGTAACCTGTACCGTTTT	TCAGTTATGTGTAATCTCAATACCTTCCAA	(0,0)	1	AACAGAAAAGGTCTCAATGTATTTTTGCA
Omy_97865-196	A	G	ATTAATTAACAAGCTC	ATTAATTGACAAGCT	TCCAGACTTCTGGTTGTTCATT	(0,0.2)	1	CCAGCCCTATATTACAATTAAGTGT
Omy_97954-618	C	T	CAACGCTTACCGGTGTGT	CAACGCTTACCAGTGTGT	GCTCTGCTTCCTCGGCAAAATA	(0,0)	1	CACAATTGGTTTTTGACAAAAGTAAAGTATT
Omy_98683-165	A	C	AGCCAGATACATATTGT	CCAGATACAGATTGT	GCCATTGCCAGAGAATTTGGTTAA	(0,0)	1	AACACACGCACCATCTTAAAGC
Omy_99300-202	T	A	TCAGGCATGAGAGAAA	ATCAGGCATGTGAGAAA	CAGTTTGACCCGATGGTGTGA	(0,0)	1	GATTATGGCGTGGCCTTTTGG
Omy_ada10-71	C	T	CTTCTGCGTCCAA	CTTCTGCATCCAA	TCTTTGAGCGACAAAGTCTTGT	(0,0)	1	ACCCACACATGAACGCAAAAG
Omy_arp-17	C	A	CTCTATTGGTATAGTAACC	CTCATTGGTATATTAACC	GGTAATGCCACATGCGGTAAATT	(0,0)	1	GGCGAAATCTGAAAATGTGCTGTGA
Omy_aromat-280	T	C	TCTTGCAAACCTC	TCTTGCGAACTCC	CTCCATTGATTATGCGCAACATT	(1,0)	1	GGAGAGGTCAACATAGCCTGGTA
Omy_arp-630	G	A	CCGCTCCGTCTGCT	CCGCTCTGTCTGCT	CTGCACAACTGTTTCTGCTATT	(0,0)	1	ACCAAGTGTCCCTGTGAAGCC
Omy_aspAT-123	T	C	CCTTCCTAGGCAGTCAG	TTCCTGGGCAGTCAG	GCCCATTCTACTGATGCTGTGA	(0,0)	1	AGGAGACCACTCCAAGAGAACT



Omy_b1-266	G	T	TCATATAACAACATTTTTC	TCATATAACAAAATTTTTC	TCATGTGAACTTTAATTGACTAGGAAGTCG	(0,0)	1	GATATGAAAATATCTGAAGAGTTATATTTGGGAAATTGAC
Omy_b9-164	T	-	CCTACAACCTGATCTAACGTG	CCTACAACCTGATCTACGTG	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	ACAACGCCAACAACTTCTCTTG
Omy_BAMB12-312	G	T	CCGAAAGTTCAACTTT	CCGAAAGTTAACTTT	CGAGCTCATGTCCGAAACTCAT	(2.1,0)	1	TTTGACAGCCTCAACTTCTAGGG
Omy_BAMB14-238	T	C	CACCGCAATCACCG	ACCGCGATCACCG	CATGATGAGGAGGACCAAGATGAG	(0,0)	1	AGGTGTGGTTCAGGGCAG
Omy_bcAKala-380rd	G	A	CATACCCATCCTATGTCAG	CATACTATCCTATGTCAG	TTGCTCTCTTCTGGTTGCCTTA	(0,0)	1	CTTCAGGAGAAAGCGCTACTGT
Omy_ca050-64	T	G	CAGTTTGAAGAATATACTC	CAGTTTGAAGACTATACTC	GTCATACAGAACTGTTTTGTGTGTCAA	(0,0)	1	ACCTTGAATTGGTTCCTAATGCCTATTGT
Omy_carban1-264	G	A	CATTAAATTGCTAATAACACCAAG	ATTAATATTGCTAATAACACTAAG	GCAAAGCCTCATCTTCAATCATTTGT	(0,0)	1	GCAAAACACAAGTCAGGAATCACTTA
Omy_cd28-130	T	C	CCTGTTCAATCACCC	CTGTTCTGTTACCC	CACAACTCCACAGAGACAGTGA	(0.2,7)	1	GAGGACAAAAGTACCCTATGGT
Omy_cd59-206	C	T	CAACAATCGAAGGTAAT	CAACAATCAAAGGTAAT	CGATTGGCCAGATGTTCCAT	(0,0)	1	GCTCCGTGTCATAGGTGACT
Omy_cd59b-112	C	T	CTAAAGCCTATAGCAAAC	CTAAAGCCTATAACAACT	TTTGATAAGATTGCTTATATGACTAAATGTCATGT	(0.0,6)	1	GCCAACTGTCATAGATATGGTGAAT
Omy_cin-172	C	T	CGCTACCGTGGTTAC	CGCTACCATGGTTAC	CGCATGGGACAGGTGTGT	(0,0)	1	GAGAAAGCCTGTAGAACCATGTCT
Omy_cox1-221	T	A	CGGTAAGACCATTAATA	CGGTAAGACCATTTAAA	CACTGAACGTGAAGCCATTGTGATT	(0,0)	1	GCAACATGGGAATGATTCATAAATGCA
Omy_cox2-335	T	G	CTTTAAAGACAAAGACTTAT	TTTAAAGACAAAGCCTTAT	AGCTGGGCTGTATTGTCAACTCT	(0,0)	1	CAGCCCGCCACTGTCT
Omy_crb-106	G	T	TTGCAATGCGTCTTT	TTGCAATGAGTCTTT	GCTCAAAAAGATTCTGCAAATTCACA	(0,0)	1	ATTACAATGAAAGTACTTGAGTGTTTATGCAAA
Omy_cyp17-153	C	T	ATACCTGAGTGTCATCG	ATACCTGAGTATCATCG	GCCCTCCAAGTCCAAGTGAAAA	(0,0)	1	CAGGTCAATTGATGAAACGTCAGAAC
Omy_e1-147	G	T	CCATCCTGAATCTGATTAA	CCATCCTGAATATGATTAA	GCACTGACTGTTACCAGGAAAGAG	(0,0)	1	GTAATGCAAGTGTGAGGCTATATCA
Omy_ftzf1-217	A	T	TCATGACGAGTTCGATTT	TGACGAGTTCAGATTT	ACAGGGATGGCAACTTTGTT	(0,0)	1	GGATGACCCACGTGACACT
Omy_g1-103	T	C	CCTTTTACAATGAAGATC	CTTTTACAGTGAAGATC	AGTCGTGACAATGAGAAACAGTGTT	(0,0)	1	CTCAGCAAAAAGAAACGTCCCTTT
Omy_g12-82	T	C	CAAACCTCAGGATTAG	AAACTCTCGGATTAG	GATCAATTCGATCGCTCATGAAACTT	(0,0)	1	CTTCTCTGTTCTCATTTGTGTCTCA
Omy_G3PD_2-246	C	T	AGTAAAGCCATTGTTGAGT	AGTAAAGCCATTATTGAGT	TCATGTATCAATTAAGGCATTGCTTGTCT	(0,0)	1	GTTAGACACAGTGACCACCTCTTT
Omy_G3PD_2-371	C	A	AGACATGTGGATTGGCA	CAGACATGTGTATTGGCA	GCAGGTAAGGTACACCATAGAGACA	(0,0)	1	CTCCCCCTGCCTTACCAAC
Omy_gadd45-332	T	C	TTGCTCCAAAATGG	TTGCTCCGAAAATGG	AGAGAAGACTCACTGCTGTTTGC	(0,0)	1	AAATCAGTCCACGCTATGCT
Omy_gdh-271	C	T	TCACCCTGAAGTGATAGC	TCACCCTGAAATGTAGAC	AGGTGACTGTACTACAGTATAAAGCAGT	(0,0)	1	GTCATGTCAACAGAGTAACATAATAAATCTGC
Omy_GHIP1_2	C	T	AAACTGTTGAACGGTAGTG	AAACTGTTGAACAGTAGTG	TGCATTTGATGGAACAAACATATTTATAATGTGT	(0,0)	1	CAAAAACAAGGACAATTCTAAGTGACCTC
Omy_gh-475	C	T	CTGAAACTCATGGTATACA	CTGAAACTCATGATATACA	AAGTTACCAGAAATTTGCAAACTCACT	(0,0)	1	CCATATTTTGAGGTGTAGCTTTACCT
Omy_GHSR-121	T	C	CCTAATAACCATGATAACAGC	AATAACCATGGTAACAGC	CTGTGTATAAGTTTATACAGTCAGCACAGT	(0,0)	1	TTCAGAGAGAGAAATGCGAGAAAGG
Omy_gluR-79	C	T	CAAGTATTTTGCCTAGGAAT	CAAGTATTTGCATAGGAAT	GACTGTCTATAGCTATTCTTCTCAAACTGT	(0,0)	1	AGAAACTACCATTTGTGATTAACAGATAGAAAATACAT

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_GREB1_09_USDA	T	G	TCMATGGAGA	TCMAGGGAGA	CCAGTGGCAACCTCAGGTAG	(0,0)	2	
Omy_GTA0162575	G	T	CTGATAACATCTGCC	CTGATAACATCTGCA	TGCTTTGATAACGCGTCTTCATG	(0,0)	1	GTGGCGCCACGTGCA
Omy_GTA0162621	A	G	TGTCTAAACTGGACA	TGTCTAAACTGGACG	CGCATAAGGCTTGGACTGTT	(0,0)	1	CTGGACTAGTGTGCATGCCCA
Omy_GTA0246634	A	G	GAATCTGTACTAGA	GAATCTGTACTAGG	TCGTCACGTAGCCCAGC	(0,0)	1	AGGGTACTACCAGCATCCACAATG
Omy_GTA0262322	A	G	GCTAGCACTGCAGTA	GCTAGCACTGCAGTG	AATGAATCTACTACTGAAAAATAAGCTAC	(0,0)	1	CCCTCTCTTTGAGTGAACACTGACA
Omy_GTA0262327	G	T	TAGCACAGGCTCTAC	TAGCACAGGCTCTAA	TGCCCTTTTATTACTGACAACATCA	(0,0)	1	CAGGGATTTAGGGATTTGATGCATCT
Omy_GTA0266143	C	A	AAGTAGTGCATATC	AAGTAGTGCATATA	GCCCATAGTGTCTGTGICAAA	(0,0)	1	GGGCTGCATCTCAAGTGG
Omy_hsc715-80	C	A	AACTGTATTGGGAAAAT	ATAAACTGTATTGTGAAAAT	CCGGTCTACCTATAGCTGTG	(0,0)	1	AGTCAGTCAATTAGTGGTTTGAAATACTATCA
Omy_hsf1b-241	A	-	CAGTGTTTGTTTTTGTCAAT	AGTGTTTGTTTTTGTCAAT	AGCCCGAACTATCCTAAAGCATTTT	(0,0)	1	AAATCAATAGCTCAGAGAATAATGAACACCA
Omy_hsf2-146	A	-	ATAATCTACTA	ATAATCTAACA	CCAACAATTGCAGCCTCATCTTAAT	(0,0)	1	GGAGCAGAAAAAGGATTGGACCTT
Omy_hsp47-86	T	A	CAGGAGTGTAAATGTTT	ACAGGAGTGTATATGTTT	CACATTAGCACTCCAGGGA	(0,0)	1	TTGCAAGGCCAAACAGCAAT
Omy_hsp70aPro-329	A	G	ACATTCCAATATTCAACTAT	CATTCCAATATCCAATAT	TGCGTATTATTGTTTTCAAGGACTTTCAAA	(0,0)	1	TGAATATTTTCAAATACATGCCAATCTTTCCAA
Omy_hsp90BA-193	C	T	CCTCCGCGCCTGC	CCTCCGCACTGC	GGAATCGATGACGACGAAGTGATC	(0,2,0)	1	TTCTCCATGCGTGTATGCA
Omy_hus1-52	G	A	CCCATCCCTCTCTCTGG	CCCATCCCTTCTCTCTGG	CTTGCCGGAGGGTAGCT	(0,0,5)	1	CCACAACCTTCTCAAATGAATGGAATGT
Omy_IL17-185	G	A	AAGAATCTCACTGCCCAT	AAGAATCTCACTTGCCCAT	CCACCACACTCTGCAGCTT	(0,0)	1	TTGACGGGAATCCGAGACTTC
Omy_IL1b_028	T	C	CTGAGGCAACTTTTGT	TGAGGCAGCTTTTGT	ACTGTCTGGCTAGAGCACATTG	(0,0)	1	ATCTTCTACCACTGCTGTTTAA
Omy_IL1b-163	T	G	CTGAGGTCATAAAAATA	CTGAGGTCATACAAATA	GGAACAACAGGATTAAGCCTACTCT	(0,0)	1	CCTAAAGGCCTAGGAACTAAACTTCA
Omy_IL6-320	C	T	CTATAGGAGAGAGACAACA	ATAGGAGAGAAGACAACA	CGACTGATCTCCTGCAGACATG	(0,0)	1	CTTGTTCTCGTTGTCTTCTCTCTA
Omy_imp1-55	C	T	CGAGATGATGCGTCTACA	CGAGATGATGCATCTACA	CGCTGAGAGGATTGTCAA	(0,0)	1	TTTTCTTTGTICAGTCTTCTGTCTCTG
Omy_inos-97	C	A	CCTTCTTGATGGTATCC	TCCTTCTTGATTGTATCC	GATGGACAGGTCTCTTTCAC	(0,0)	1	CCTGTAGATAAAACATGGTACCAGGTC
Omy_LDHB-1_i2	C	T	ATGGGCAGTCATTCA	TGGGCAATCATTCA	ACGCACACTTATCCTTGACAATGTT	(0,0)	1	ACTGTGACAACAAATTCGGTGACA
Omy_LDHB-2_e5	T	C	TTTACCTGTCAAC	CCTGTGAC	TGCTAGGTGAGTCAGAGGTACATATT	(0,0)	1	GACTGGAAGGCCACCCATAAG
Omy_LDHB-2_i6	G	T	CTGTGTTTGTCTCCCA	CTGTGTTTGTATCCCA	TCCTCGCAATACCATACATGTC	(0,0,5)	1	AGAGTGAAGCTAACACACACTTCT
Omy_lpl-220	C	G	AGTGACAGTCA	AGTCACAGTCA	TGACAATCACTGAGCAACTGAACTC	(0,0)	1	GTCCAGTCTTGCTTCAACTATTCT
Omy_mapK3-103	A	T	AATTATTAAGCCTATTTTTT	ATTATTAAGCCTAATTTTTT	GAAGTCATTACTGGTCACTGGTICAA	(0,0)	1	GCACAAAACATGAGGAAAGTTGAGA
Omy_mcsf-268	T	C	AAATAATAGATAAA[CT]CCT	AAATAACAGATAAA[CT]CCT	CCAGCATCTCGTCCCATTTCC	(0,0)	1	CTTTAATGTAGATTATATTCTTCTGTAGCCACTATGG
Omy_metA-161	T	G	CAAGTAAGTGGTATATTCT	CAAGTAAGTGGTCTATTCT	CGCATGCACCAGTTGTAAGAAAG	(0,0)	1	AGTGCCACCAGCGATAAGAAAA

Omy_metB-138	T	A	TTCGCCAAAGAGAAAT	TTCGCCAAAGTGAAAT	TCTGTCCCTGACGCTATAAAAACG	(0,0)	1	GAAGTATTTACAGCTTAATTTCACTGTTGAGTT
Omy_MYC_2	T	C	CATAGACTTTTGGACCTTAT	CATAGACTTTTGGCCTTAT	CGGTGCGAGAACTCTCATGTTTG	(0,0)	1	CACGCCATGTCTTAACCTGCATTA
Omy_myclarp404-111	T	G	CAAAGCCATACGTGGCC	AAGCCATCCGTGGCC	GCTGTGGTGCTCATGGGAAA	(0,0)	3	CCAGGGCAGGGTGTGCTC
Omy_myoD-178	A	C	TTTTATGAGATATAATTTCC	TTTTATGAGATATCATTTC	GGTCAAATATTTCAATTACGATTACCTAGGC	(0,0)	1	TGGCAAAGCTGTCACTTCCTCTAAT
Omy_nach-200	A	T	AACTGACAGAGTCACAAC	CTGACAGAGACACAAC	CTCATGAAAAACGGGAGAGCAAAG	(0,0)	1	CAGCGGCTCTTCAGTAGTCT
Omy_NaKATPa3-50	A	C	CACTCTGTTTCCTTTCTTT	TCTGTTCCGTTCTTT	GTTGAGCGTGTTATGGGAAAAGAG	(0,0)	1	TTGCATCGGCTTTCTGAAAAAC
Omy_ndk-152	A	G	ACCCACTTTCAAAAC	ACCCACTCTCAAAAC	AAGAATTGAGGGATAAAAACAAAATAATATATAAACATGA	(0,0)	1	CAAACCTACATTCATTAAGTCCAGTTTGT
Omy_nips-299	T	-	CTGGATTTCACATGTAATAC	CTGGATTTCACGTAATAC	GACAGGATAGGAACGGTTTCTCAAT	(0,0)	1	ATCAGAAAGTTTAATTCAATATGTACACGATCCT
Omy_nkef-241	C	A	CTTCTGATCATTTTTTG	TCTTCTGTATAATTTTTG	AGTGTCAATTGATGTCGGCCTATTTT	(0,0)	1	AAACGAATGTCCACCTCAGATGTT
Omy_ntl-27	G	A	CAGACAAGAGTACCCCAAGAC	CAGACAAGAGTACTCCAAGAC	GGTGTGTTACTGTAGTTGTGTCCTT	(0,0)	1	TGTGTAGCTAGTGATCCTGATTGTCT
Omy_nxt2-273	C	T	AAGGCAC	AAGGCAT	CTTTAGAAAAGCCAAGGTATATTTTAACTACTTCT	(0,0)	1	CTGCTGCCCTCTAATGGTAAGATAG
Omy_Ogo4-212	T	C	CATTGATGAGACATCTT	ATTTGATGAGGCATCTT	TGAAAGGTTTATGCAAGTTATTTTCT	(0,0)	1	GTGTGTGTTAAATAAGCATTGATGA
Omy_Omyclmk438-96	A	C	TACGCAAATTAGGTTTAAA	CGCAAATTAGGGTTAAA	CCCGACTCTACTTCACTACTTTCCT	(0,0)	3	GGCTAGGACAATAAGGACTGAAC
Omy_OmyP9-180	C	G	CTGTAGTAGTCCCATTGT	CTGTAGTAGTCCGATTGT	CTGGATGTGTAGTATCGGTGAAAA	(0,0)	1	CACTGGCACCTCTGATCTC
Omy_Ots249-227	C	T	CCCTCTGAGAACTAC	CCTCTGAAAACCTAC	CTATCTATCTATCTATCTATCTATCTATCTACTACTGAGA	(0,0)	1	CCCTAGATTAAACCTGTCCAGICT
Omy_oxct-85	A	T	CATCGCTTATTTATGC	CATCGCTAATTTATGC	CGTCACTGAAACATTACTGTAACATCCA	(0,0)	1	CATCATCACGCTGTGGTTTCTTAA
Omy_p53-262	T	A	CAAGTAGTATGGAGCTCTAT	AAGTAGTATGGTGCTCTAT	CCCCAACATCCAGTATACAGTTTCA	(0,0)	1	CCCAATTGGCAATTTTAAATAGGATTGAGA
Omy_pad-196	C	T	AAGACAAAGGTGTAATACC	AAGACAAAGGTATAATACC	CAAACAACCACAGTAGTCTCTCAAT	(0,0)	1	GCTTTTCACCCCTTTGTAAATTAAGCCAAA
Omy_ppie-232	C	T	AAATAGCGGAGAAAAT	AAAATAGCAGAGAAAAT	CTGTTTGTAGATTAGAATGTTTTTGGTCAGGT	(0,0)	1	CTGAACATAGGCTTTCATTTGAGACAT
Omy_RAD103359-45	C	T	CCTGTAACGCACAG	CCTGTAATGCACAG	GGAGAAGGATGTGCTCCCTG	(0,4,0)	1	ATTTGGAGGTGGAGGGTCCA
Omy_RAD10733-10	A	G	AGGGTGAAGAACTG	AGGGTGAGGAACTG	TATAGACCCCTGCCAGTCA	(0,0)	1	ACAGAGAAAAACCCGTCATT
Omy_RAD116-59	T	C	CCACAATGTCAAC	CCACAACGTCAAC	GGAAGAAGTGAGAGCCCTGG	(0,0)	1	CTGTAGTCCACGATCCGCTC
Omy_RAD1186-59	A	G	CCAGGACATCCAGG	CCAGGACGTCCAGG	CACAGCCTGGATGTGGTTCT	(0,0)	1	ACAAGTCCGGGAGTTTCCT
Omy_RAD12439-64	G	A	CTTCTCCGATGICA	CTTCTCCAATGICA	GGAACTTTTCACATCATGTTGACTG	(0,0)	1	GCACAGAGAACTCCAGGCAA
Omy_RAD12566-14	C	T	ATGTAAACAAATTG	ATGTAAATAAATTG	GTGGACATTCCTGCAGGGAT	(0,0)	1	TCCACAAAATATTTATACGCACA
Omy_RAD13034-67	A	C	ATAATCACAA	CTAAATCACAA	GAGTGATTCCCAGCCCTCC	(0,0)	1	TCCTCCGTTGGCCAGAAAC
Omy_RAD13034-67-21	C	T	CTCCCGAACC	CTCCCTGAACC	GAGTGATTCCCAGCCCTCC	(0,0)	4	
Omy_RAD13034-67-35	A	T	CTGAGTGGACA	CTGTGTGGACA	GAGTGATTCCCAGCCCTCC	(0,0)	4	
Omy_RAD13073-16	G	A	AAAGGGGACATTACG	AAAAGGGGACATTACG	GTGAGGGATCACACCTGCAG	(0,0)	1	GCACCAATTCGTAATGTCCC

Omy_RAD13499-13	T	C	CGCCCTGTCCGCCA	CGCCCTGCCCGCCA	GTTACCTGACGACCAAGGT	(0,0)	1	GCTGGGGAGCTTTACATGA
Omy_RAD14033-46	A	G	ATAGAGGAATAGAC	ATAGAGGGATAGAC	GCAGGAGATTTATTGGCCCC	(0,0)	1	ACCTTGTGATCACATACTGTCT
Omy_RAD15709-53	G	A	ATGCAAGGCTTAAA	ATGCAAGACTTAAA	TGCAGGACTTGGATAACACAGA	(0,0)	1	TGGTTATATCTACAGTACAGTTCGT
Omy_RAD16104-20	A	G	AGGGCAAAG[AT]CAAAGG	AGGGCAAAG[AT]CAAAGG	ATTCCAAAACCTGCAGGGGT	(0,0)	1	TCAGGATTTGGTAAGGTGGCC
Omy_RAD17632-23	C	T	CATGTGAGACCTTTGCA	CATGTGAGATCTTTGCA	AAGCTCTGCAGGTCATCTC	(0,0)	1	TCTGTGAAGTGTCTTCTGCAAGT
Omy_RAD17849-16	G	C	AGACGGACTCCCC	AGACCGACTCCCC	GACTCCACAGCCTACATGGG	(0,9,0)	1	CCGTTAATGCCAGGGGAGTC
Omy_RAD18903-48	A	G	AGGAGACACCA	AGGAGGCACCA	GGGGATGAGTTCTTCGGTGG	(0,0)	1	CCACCAAATCCCCGAAGAA
Omy_RAD1919-22	A	G	CAGGGAGGAGG	CAGGGGGGAGG	CAGGTCACAGACACAGGG	(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	TGTGTGCTGTCTTATAGCCC
Omy_RAD23577-43	T	C	TCTGGCTCTGTCGGTCT	TCTGGCTCCGTCGGTCT	AATAGGAACCAAGCCCCAGC	(0,0)	1	CAGAGCCTGAACCATGGAG
Omy_RAD23894-58	A	T	GTGGATTAGGGG	GTGGATTGGGG	TGCAGAAAGGCTGTGTGGAT	(0,0)	1	TCCTAACACAGTCTCATGGAACA
Omy_RAD24287-74	A	G	GGTCACTACCTCCC	GGTCACTGCCTCCC	ATTGCTGTCTGCCGAGGTG	(0,0)	1	TGGCGACCTGTCACTAATGC
Omy_RAD25042-68	G	T	AATTTCTGCCCAA	AATTTCTTCCCAA	GCTGTGAAACTGGTTTGCA	(0,0)	1	TCATGCAGATGAGCTTCCTG
Omy_RAD2567-8	A	T	GCAATGGGCTATTT	GCAATGGGCTATTT	CTGTCTGGATAGCCTTGCCC	(0,0)	1	TCTATCTTGGGGAAAATAGCCC
Omy_RAD26080-69	G	A	ATTAGTAGCATCATCGAG	ATTAGTAACATCATCGAG	TGTGGGACAGCACATACTCC	(0,0)	1	CCAGGACACCAGTGGAGAAG
Omy_RAD26691-36	A	G	TCTCTAACAGAAC	TCTCTAGCAGAAC	TGCAGGAAACCGTCAATCTACA	(0,0)	1	CAGGAATTAATTGTATGGCCGGA
Omy_RAD27740-55	A	T	TAACTTTAAAAAAA	TAACTTTAAAAAAA	TCGGCCTGTACTAGTCTCACT	(0,0)	1	GCCTAAAATGGCCACTTTCATCA
Omy_RAD28236-38	T	C	ATCTGTCTTCGTGC	ATCTGTCTCTGTGC	GGCACACATCTGTCCCGTAG	(0,0)	1	GCCTAAGGTCTAGGAGCACG
Omy_RAD29700-18	C	A	ACAATTCAAATGATTTA	ACAATTAATGATTTA	AATGGAATTGGCCCCAACCC	(0,0)	1	TCTCCATTGTGTGAATCATGGT
Omy_RAD2976-26	G	A	CAGCTGGGTTGAGA	CAGCTGGATTGAGA	AGGACTGTGATCCTCTCAGCT	(0,0)	1	AGCTCTGTGAAACATCAGTCT
Omy_RAD30392-17	T	C	CTGAGACTGTGTGT	CTGAGACCGTGTGT	CCACTACTCAGACACTGCA	(0,0)	1	GCTCAAGGACCAACAAAAGCT
Omy_RAD30619-61	T	A	CACTGTAAAA	CACTGTAAAA	CTGAGGTCAATTGGGTGCTA	(0,0)	1	ACACTGATCACATTTTGTACACT
Omy_RAD31408-67	T	C	ACAGAATGCAGAAA	ACAGAACGCAGAAA	CAACCCATGCAGGTACAGAA	(0,0)	1	TGGAGTGCCAAACAAAAGAGC
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	CAGGCTTTGTGACATGTGC	(0,0,6)	1	GTGCTCTATCTTGCTCTTGGC

Omy_RAD33798-24	T	C	GAGTCTATCAAGAT	GAGTCTACCAAGAT	CAGGAGGGTCAAGTGGAGTC	(1,0)	1	TTGGGCCCTCTCTTTTGGG
Omy_RAD35005-13	C	T	CCAACTCCCACGG	CCAACTCTCGACGG	TGGTCAAAGTTGAGGGTGGT	(0,0)	1	CAGGGCCTGATTAACCACT
Omy_RAD35149-9	G	A	GCGCGCTTATGTC	GCGCACTTATGTC	GAGTCAATAGAGCCCCCTGC	(0,0)	1	TGGTTAGCAGGAGCAATCTCA
Omy_RAD35417-9	G	A	TGCAGGACGTGCTTTGT	TGCAGGACATGCTTTGT	GCACTTGACCACATAGCTGG	(0,0)	1	ACTCCACACTCCAAAAGCA
Omy_RAD3651-48	G	T	GTGGGGAGAACTTT	GTGGGGATAACTTT	GAGTACAGTGCAGTGTGGGG	(0,0)	1	CCTTCCTCTTGCCACCATCA
Omy_RAD366-7	C	A	CAGGACTTGCTTTT	CAGGAATTGCTTTT	ACCAAATTAGAGCTGCAGGA	(0,0.2)	1	GGAGAGGCCTTTCCTGTATC
Omy_RAD36848-7	G	A	TGCAGGGACACCACCT	TGCAGGAACACCACCT	CGAGGACGTTTCATAGGGAGC	(0.5,0)	1	TCGATAAGTCCACCACTGG
Omy_RAD36952-53	C	A	AGGACATCTTCATC	AGGACATATTCATC	TGTACGTATTGGGGCTGAG	(0,0)	1	CCTACCAGACCACACGATGA
Omy_RAD37816-68	A	T	GCGGCGTAAAAATG	GCGGCGTTAAAAATG	CTCATTCCTTGCCCGTCTG	(0,0)	1	CCACTCACACTGGCTTATGC
Omy_RAD38406-19	T	A	AGGCTTTATATGGCC	AGGCATTATATGGCC	CTGAGGGGTATTAGGAGGC	(0,0)	1	AATGAGTTGTGGCGGTGAGT
Omy_RAD39156-33	T	C	ACCGTAATGGAGAG	ACCGTAACGGAGAG	GGGTGTGACATGTGTGCAGA	(0,0)	1	ACTGCTTGTCCCCACCAAG
Omy_RAD3926-22	T	C	TTCACCTTTCCCTG	TTCACTTCTCCCTG	CGTTCCTGCAGGCTTTTAC	(0,0)	1	TTGGCACAGAGTACGCAG
Omy_RAD40132-55	A	C	TCTGTGCAGTCCTC	TCTGTGCCCTCCTC	TGCAGGGCTGTATATTGCT	(0.8,0)	1	TCAAAGGACTGGGGAGAGGA
Omy_RAD40520-48	T	G	GTGAGATTGCGCTG	GTGAGATGGCGCTG	TGTTATCTGTATCAGTGTGAG	(0,0)	1	ACACGTCGGTCTTCTTCTCC
Omy_RAD40641-58	T	C	AGTGATATCAAGTG	AGTGATACCAAGTG	GGCAAATGGCTTGTGAGTG	(0,0)	1	AAGGCTCTGCTTCTGCTTGA
Omy_RAD41594-34	A	G	CAGAGATACGTTCC	CAGAGATGCGTTCC	TGCAGGGTTATAATGTGTCTTTGT	(0,0)	1	AAATCTCGGGTGAAGGAACG
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	GTGAGAGGGATTTTGGGGG	(0,0)	1	TGACAGGACAAACACAAGCCA
Omy_RAD43694-41	A	C	AGGGAAGAGCGGAG	AGGGAAGCGCGGAG	CCCCTCTCCCTGGCTAGAAT	(0.1,1)	1	TCAGGGGGTGTGCTTTTCC
Omy_RAD45104-18	A	G	CAAGACACCGCACACAG	CAAGACCGCGCACACAG	TGGTGCTTCACTGTGTCAA	(0,0)	1	AGAGTGAAAACTGTGTGCGG
Omy_RAD46314-35	A	G	TAGCAATGGT	TAGCGATGGT	ACTGCATCTTTCCCTGCA	(0,0)	1	TGAAGATACCCAGAGACACCA
Omy_RAD46452-51	A	G	TGAAGTCAGAAGTT	TGAAGTCGAAGTT	TGCAGGTAAGACTTGATCTGGA	(0,0)	1	TGACTCCAACCTAAGTGCATGT
Omy_RAD46672-27	C	G	GTGGTAGCCCATCA	GTGGTAGGCCATCA	TGCAGGAGGCTTTTCTCTGT	(0,0)	1	AACACATTCTTATTGCAATGATGG
Omy_RAD47080-54	A	G	TGCAAGACTTAAACGA	TGCAAGGCTTAAACGA	TCAAAACCTGCAGGACTTGGA	(0,0)	1	TGGTTATATCTACAGTACAGTTCGT
Omy_RAD47444-53	C	T	GGCGAGCTTGGCCAAA	GGCGAGTTTGGCCAAA	GTCGTCTGGAGGAGCTGAA	(0,0)	1	GGGTGACGTTTCTTTCAGC
Omy_RAD47955-51	G	T	TTGGAATAGAATCTATA	TTGGAATATAATCTATA	AGTGTGCTAGAATGGGCTG	(0,0)	1	ACCATGGGAGTTCATTCA
Omy_RAD4848-14	G	T	GAGACAAGGACAGA	GAGACAATGACAGA	TGTCCTCTTCTGCACGATG	(0,0)	1	AGTTGGTAGTCACTCTCTGT

Omy_RAD48799-69	A	G	CATCCTAGAATAGAAGT	CATCCTGGAATAGAAGT	GCTGAGCCACCTACACACAG	(0,0)	1	GTCTAACACTCGCAGCAGT
Omy_RAD49111-35	T	C	TTTCTTATATTGA	TTTCTTACATTGA	GCAGGCTTAGCATTGCTGAC	(0,0)	1	GGAACCTGGGTGGGAGAATG
Omy_RAD50632-21	C	T	TCAGCACCTCCAGCC	TCAGTACCTCCAGCC	CCTGCAGGCTGGGTCAATT	(0,0)	1	GAGCCAGCTGTACCTTCTCC
Omy_RAD52458-17	C	A	ATGGCCCC[CT]AAGAACCC	ATGGCCCA[CT]AAGAACCC	ACGTGTCCTGAGGATGGTA	(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	AGAGGGAAGAGAG	AGAGGGACAGAGAG	GCTGTTACCGTGTGATGTTGA	(0,0)	1	AGAGTTCGGCCTCTCCCTC
Omy_RAD55404-54	C	T	ATTGTTTCTGAAGG	ATTGTTTTTGAAGG	GCAGGGTGCTCCATACAGAC	(0,0)	1	AGGAGTCCTGAGAGTTGGGC
Omy_RAD55997-10	A	C	AGGCTGCAATGTTT	AGGCTGCCATGTTT	CATTTTCTACCTGCAGGCTGC	(0.9,0)	1	AGCCTACATACATAAGCCAACA
Omy_RAD57916-29	A	C	CAGGGGCAAAACGG	CAGGGGCCAAACGG	GCAGGGCCTAGAAACAGACT	(0,0)	1	TACACGCCTCACTGTTCTGC
Omy_RAD58213-70	A	T	TTTTTT[TA]AAAATATACT	TTTTTT[AT]TAAATATACT	CCTGATGGGTGCTCTTCTCTC	(0,0)	1	AAACAGCATCATTATCCATAGTGT
Omy_RAD58835-15	G	T	ATAGCTGCTGGGACCCA	ATAGCTTCTGGGACCCA	GTCTGCTAAGGTCTGCAGG	(0,0.2)	1	GCCGACCATGAGAGACCTG
Omy_RAD59758-41	T	C	TGATTGCTACTGAC	TGATTGCCACTGAC	GGCCCCCTTCTTCAGGAAT	(0,0)	1	CACACACTCAACGGGTCAGT
Omy_RAD59950-44	G	A	GGAGGGGAAGGG	GAAGGGGAAGGG	GGAGCTCATATCGCCGATGG	(0,0)	1	GAACTCTGTCACCTGCC
Omy_RAD60135-12	C	G	GAACATACCGGAAC	GAACATAGCGGAAC	AGCATACACCTGCAGGAA	(0,0)	1	TGGTAGGAGGAGATGCTCTGT
Omy_RAD619-59	T	C	TGCTGGATCCCCCA	TGCTGGACCCCCCA	CATGGAGAAACAGACCCGCT	(0,0)	1	TGCTGTGTGTGTATCTGGGG
Omy_RAD62596-38	A	T	TTAAAAATATATATTA	TTAAATATATATATTA	GCAGGACACTGGTTCCTCAA	(0.5,0)	1	CCTGAGATTGAGATCACTGGCT
Omy_RAD65808-68	T	G	ATCGGGATTCACCT	ATCGGGAGTCACCT	TCTTCACTCTCGATCGGGA	(0,0)	1	TCAAACCTGGGCCACTACTGT
Omy_RAD65959-69	G	A	TTTTGTCGTTCTT	TTTTGTCATTCTT	ACATTTTGGTGTAAACACCTGT	(0,0)	1	GCTAGCGAAGACCTGAAGG
Omy_RAD66402-36	T	C	AACCACTTCTCTG	AACCACTTCTCTG	GGTGTGATACCTCAGAGCTCTG	(0.1,7)	1	CGTCTCCGGATCGTTCAGAG
Omy_RAD66834-17	C	T	TCTGGCTGACACCTTTA	TCTGGTTGACACCTTTA	CTCCTGCAGGTCATCTCTGG	(0,0)	1	CTGCTTGTGCTCAATGCCTG
Omy_RAD68634-40	A	C	CCTCTAAACTGAAT	CCTCTAACCTGAAT	TGCAGGACTCCTTTGAAACGT	(0,0)	1	TAACGCCAGCTGCATGATGA
Omy_RAD7016-31	C	A	ATAATTTCATTTAA	ATAATTTAATTTAA	GCAGGAATATTCATCTGTGCCA	(0,0)	1	TCTAAATATGCTGTGCGGGC
Omy_RAD7210-8	C	A	TGCAGGACTTGCTTTGT	TGCAGGAATTGCTTTGT	ACACCACACTCCACAAAGCA	(0,0)	1	GCGCCTTGGTCTCTTCATA
Omy_RAD72528-44	A	T	TTGGAACAACTGT	TTGGAACCTAACTGT	TGATGATCCGGACCTCTCT	(0,0)	1	CCCGATTCCCTCCACAGTT
Omy_RAD73204-63	G	C	GTGCCGCTCTCCACCG	GTGCCCTCTCTCCACCG	CCTGGGCAATGACCTCCAC	(0,0)	1	AGTCCCTTCTCTCTCCCTC
Omy_RAD7384-50	T	C	GCCTCTGGCAG	GCCTCCGGCAG	GACACGCCCTCAGCCAG	(0,0)	1	CTGGTACCTTCTGCTGTGG
Omy_RAD739-59	C	G	GAGTTGGCTATTTT	GAGTTGGGTATTTT	ACGAGGCTTGTAATGCAGT	(0,0)	1	TGCCTTTATACCAATGTCTGCTG
Omy_RAD73963-73	T	A	TTTCTTTTGA	TTTCTATTGGA	CCCTCTCAGGAAAGTGACCAC	(0,0)	1	GGATCATGTCAATCTGATGAGTTGG
Omy_RAD76060-20	C	T	GGGCGCTGTAGGCAA	GGGTGCTGTAGGCAA	TGCAGGGTGTGAGTATTGGG	(0,0)	1	TCCCATGCAAAATCCAAATGCT

Omy_RAD76570-62	T	G	AGAGGTGTTCTGGT	AGAGGTGGTCTGGT	GCAGGTAGGTAGGAAGGAAAGC	(0,0)	1	TCTGACTGGTATTGAAAGGACCA
Omy_RAD77789-54	T	C	TAAATTATATTGACAG	TAAATTACATTGACAG	AGACAAAACCTGCAGGGGAC	(0,0)	1	AGCACGTAAAAACCAAACTGTCA
Omy_RAD78147-27	C	T	CAAAGTCCCAGAGA	CAAAGTCTCAGAGA	GCATTTTAGCCCTCCCAAAGTC	(0,2,6)	1	CCTTCTTCCAGTTGTAAAAACCCA
Omy_RAD78502-57	T	G	GGAAATACACACA	GGAAATAGCACACA	GAGAGGCATCCTGTCTAGGG	(0,0)	1	ACCATGCTCTTCTGTAGGTGT
Omy_RAD78776-10	T	C	GGGTAATCCTGGCT	GGGTAACCTGGCT	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	CAGTGCAACC	CAGTGTCAAAC	CACACTGACTCATCCCTCGC	(0,0)	4	
Omy_RAD85131-35	T	C	GATGGTATGGTGAG	GATGGTACGGTGAG	TTCAATAACTACAGGCAGATGGT	(0,0)	1	AGTTCCTCAATGCACTGTACA
Omy_RAD86706-72	C	T	TACGTTTCATTCT	TACGTTTATTCT	TTCCCTGTAACTGTCAACGCC	(0,0)	1	CCACATCACACCTGACCTC
Omy_RAD88028-7	G	A	TGCAGGGGCTGG	TGCAGGAGCTGG	TAGCCAGTTTCGGTTCCAAC	(0,0)	1	AGTGTCTTTGGTGCCTCTC
Omy_RAD88122-32	G	A	GCTGTGGAGATCAT[CT]CG	GCTGTGGAAATCAT[CT]CG	TCAGTGGATGGAGTGTCCCT	(0,0)	1	GGTCTTTGGCCTTGTGTCTG
Omy_RAD9004-13	G	A	TCATCTGAAGGGGG	TCATCTAAAGGGGG	TATACCAACGCTTCCCTGGA	(0,0)	1	CAGAGAGAAATCCCCACCC
Omy_RAD92485-64	T	A	GTGTAGATATACAT	GTGTAGAAATACAT	CCAGTCAGTCTTGCTCAGG	(0,0)	1	GGTCAACACAGGATTGGAGG
Omy_RAD93580-37	T	G	AGTCACCTGGGATT	AGTCACCGGGATT	AGGCAGAGGAGGGTTGTTTG	(0,0)	1	TGCAGAAGTCAAATCACGAACA
Omy_RAD98715-53	T	G	CAGGACTTCTCCCC	CAGGACTGCTCCCC	CGTAACGGGGAGCTGATCTG	(0,1,9)	1	GCTGGTAAAAATGCTGAGGGG
Omy_rapd-167	G	T	AAACAATCCCCCACA	AAACAATCCCACCCAAA	CCCAACATGTCTATTGCAGCTA	(0,0)	1	AGTTGCATAAGATGAATCAATAAATTAACACAGAT
Omy_rbm4b-203	-	T	CACGTTATTATGAAAAGGATGT	ACGTTATTATGAAAAAGGATGT	CTGAAATTGATGAATGGAAGCTGCA	(0,0)	1	CGTATTCAAGTCGATATACAGTCACGAT
Omy_redd1-410	C	T	AAAATATCCTGCAAGGAAT	AATATCCTGCAAGAAAT	GTAATCCCACTAACATACAGTAGACTCA	(0,0)	1	GGCACCATTGTGTTTTAGGATGTAG
Omy_sast-264	G	A	CTAGCCAATGCGTCTAA	ATCTAGCCAATGTGTCTAA	GAAGTAGGGTTGTTGACCATGTGA	(0,0)	1	TGGATTCCATTTTAGGCTGTAATACATCTT
Omy_SECC22b-88	T	C	CTGTCGTCCATATATC	CTGTCGTCCGTATATC	GGATCCCTCCTTTTAACACAAGACT	(0,0)	1	CTACAGGATGACTACCTAATTGCTAATAAAACA
Omy_srp09-37	C	T	TTGTGCTATTGACGCCACAG	TTGTGCTATTGACACCACAG	TAGTTGTATTAACCTTCTTTGAGTCTAGA	(0,0)	1	TCATTCCAGCTCCGTCTCTCTC
Omy_sSOD-1	T	G	CCACAACAAGACCC	CCACAACCAGACCC	GCCGGAGCCCACTTCAA	(0,0)	1	CAGACTAACCGAACAGCATCAGTGG
Omy_star-206	A	G	TCTTTGGCACTATATCT	TTTGGCACCATATCT	CGTGTGCCAGCCCTTCT	(0,0)	1	GACCACTGAGATCATGTGTGTGA
Omy_stat3-273	G	-	CCAGTTTG	TCAGTTTG	CAGACCTCTCTATCTCCCTATGAG	(0,0)	1	ACCTCCTTTAAATTGTGCCCAAGAA
Omy_sys1-188	C	A	AAACATGTACGACCTGTC	TGTAAACATGTACTACCTGTC	CTTAATAGGTGCTGGTTGCTGTATT	(0,0)	1	AGTGATATCTTAGTGGGTCGAGGAAA
Omy_tlr3-377	C	T	CGTGATTAGGTTCTTC	CGTGATTAGATTCTTC	GTCGCTCCGGGTGCTT	(0,0)	1	GGCCCAAACTTCCTTCCT

Omy_tlr5-205	T	A	CAGTAATATTTCTAGTGCCCG	CAGTAATATTTCTGTGCCCG	GAGCGTATCTGGTATGGTAACAACA	(0,0)	1	CTCCAGCAGCTTTAGAGAGTTTACA
Omy_txnip-343	T	C	AACTGAAGAGATCTG	AACTGAAGGGATCTG	CCTTCAAACAAACGCATCATAGACATG	(0,0)	1	GGTCACTTGGCTAATCCCTTAT
Omy_u07-79-166	G	T	ACTTGGGAATACCCAGCC	CTTGGGAATAACCCAGCC	CCCCTATATTATTGATCACCCTTGA	(0,0)	1	ATTTAAATCCATTCTAAAAATAAGCAAACCTAACCA
Omy_u09-53.469	T	C	TTGCAGCCCTTATTGTG	TTGCAGCCCTTGTGTG	ACAGCTGAGCGTTTGCA	(0,0)	1	GGAAACTGGGAGAGATCAAAGGA
Omy_u09-54-311	C	T	TGGTAATTATTCAACAGATCAGT	TGGTAATTATTCAACAAATCAGT	GTGGCTCCCCAGGAACAAG	(0,0)	1	AAGTTTCATGTCACATTCAGTTACCT
Omy_u09-56.119	T	C	AGTGAGCTGAACAGAGCA	TGAGCTGAAGCAGAGCA	CCAAGTGGACCCACCAG	(0,0)	1	GCTGAGTTTATAGGTCAGTCATTATACATATTGA
Omy_u09-61.043	A	T	CACTTGTCTCTTTTCA	CTTGGTCCATTTTCA	TAGTCACATCCATAGTAATACTTCC	(0,0.4)	1	TGTTCAGAAGCAGAAAAACCAATCTCT
Omy_U11_2b-154	T	C	AATGATACTTTTCAGATTGTAAC	TGATACTTTTCAGGTTGTAAC	GGGAAGCAGAAAAACTGGAAAGTT	(0,0)	1	CCCTCTGTGGGCTTGATATCA
Omy_UBA3b	A	T	TGGAGATAACGCTAACTATT	AGATAACGCAAACTATT	GCCACTCAATGCATGTGTTTCTAG	(0,0)	1	CAGCTAGCTTAAGTGGGATGCAA
Omy_UT16_2-173	C	T	ACAGTCAACAAGGGACTTAA	ACAGTCAATAAGGGACTTAA	ATTGACTCATTATCACCTTAGTTGTAGCTTCA	(0,0)	1	GCAGCTACTTGCTGTATCACATGTTTGT
Omy_vamp5-303	A	-	TGGCCGTAGTAGTTGGTCA	TGGCCGTAGTTGGTCA	CTGCTTCCAATTCTAGTATCGTCTT	(0,0)	1	AGGCTGAAGCATTTCTGAGTATGAA
Omy_vatf-406	T	C	ATGACTATCCACA	ATGACTGTCCACA	TTGCTCATTTTGTGCATAACCTTGGG	(0,0)	1	TGCATGCTCTGACAAATGTTACACT
Omy_VGLL3-1_AT	A	T	ATAGTAATGGC	ATTGTAATGGC	GGTGCCAGACTAGACGAA	(0,0)	1	CGTGCGTAAAACGCCAAT
Omy_VGLL3-1_GT	G	T	TGTGTTCGAAT	TGTGTTCTAAT	GGTGTCAGACTAGACGAA	(0,0)	2	
Omy_VGLL3-6_AT	A	T	ATATTATTGTTCAA	ATATTTTGTTCAA	TGAAATTGTTGCATGTTGCGT	(0,0)	1	TGTAGGTGAGCCTTGAACTTT
Omy_VGLL3-6_CT	C	T	TACACACCAATA	TACACATCAATA	AGATGTAGGGCATGATTGCCA	(0,0)	1	GCCTAGTGTCTGTATGTGTGGA
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	TGTTTGGTTTTATGGGCTGA
Omy25_61285646	C	A	AGAATGTCTATT	AGAATGTATATT	TTGACACTGGTCTGAGAATG	(0,0)	1	AAGCAGAGGGGTGCACTG
Omy25_61286316	T	G	ATGCTAACCTT	ATGCTAACCTG	GGCCTCCTGAAGAGGAAAAA	(0,0)	1	AGGGACTTGTGCCAGATTGA
Omy25_61287415	T	C	TACCATTCCTG	TACCATTCCTG	TGTTCTGGTGATGTTGCTCT	(0,0)	1	ACCTGACGTGGCTCTCTGTA
Omy25_61294400	A	G	GCTGGTCAGCACATGCTTTGA	GCTGGTCAGCGCATGCTTTGA	GACAGATTATCTTGGCGTTTGG	(0,0)	1	AAACGGATTACCAGGACACG
Omy25_61316270	G	T	AGGCCTATAGTT	AGTCCTATAGTT	ATCGACTGTGCCCTATCTGG	(0,0)	1	ATCAATGGGTCTCTTCGTT
Omy25_61317685	A	G	TCTGATTAAACCAC	TCTGATTAGCCAC	TGGGCTAGATTTTCAGTCTGC	(0,0)	1	ATGCATCTCTTGAATGGTG
Omy25_61317777	A	G	AATTTAAAAACGGTATGCTT	AATTTAAAAAGCGGTATGCTT	TTCGTTCTCTGTTGTTTTATTCTG	(0,0)	1	CAAGCAGCAGGCATGACA
Omy25_61318852	A	G	AAAAAAGGGAGCTCG	AAAAAGAGGGAGCTCG	TACGCGAATGGTACTTGCAG	(0,0)	1	TTTCCGACTTGTGTGGGAGT
Omy25_61322413	C	G	CTAGGGGACACA	CTAGGGGACAGA	ATCAGGGCAACTAGGGGACA	(0,0)	1	CCGCATCATTAGTGCTGATT
Omy28_11607954	G	A	TGTGGGCTGCGAACATACTCA	TGTGGGCTGCAACATACTCA	TGACACTGATCACAATGGTGAAT	(0,0)	1	TAAACTGGAAGGAGAGAGCAAAAT



Omy28_11625241	A	G	CCTCCTCCCTATGGTTGTCTC	CCTCCTCCCTGTGGTTGTCTC	CAACATTTAGGGAGAGGTTGCTAT	(0,0)	1	ATCATCAAGTTTGCCTACGACAC
Omy28_11625241_USDA	A	G	CCTCCTCCCTATGGTTGTCT	CCTCCTCCCTGTGGTTGTCT	CAACATTTAGGGAGAGGTTGCTAT	(0,0)	2	
Omy28_11632591	G	A	TGAGAAGAACACAGAGG	TGAGAAAAACACAGAGG	GTAGAGGCCAAAGGCTTGAG	(0,0)	1	TGCTCTTATTACCTTCCAGACTCC
Omy28_11658853	A	C	TGGTACAGACACGCACTAGCA	TGGTACAGACCCGCACTAGCA	CAACATATGACCATCTCGAAACTC	(0,0)	1	ATTAATCACACCGTGAGACTCCTC
Omy28_11667578	T	C	GTATTGATCCTGTGGGAGACA	GTATTGATCCCGTGGGAGACA	ACAGTAAACCCATTCAGGCATAGT	(0,0)	1	TTATCCTCTCAATCCACATCAAGA
Omy28_11671116	C	T	CTGGTGAGAACAGGAATTACC	CTGGTGAGAATAGGAATTACC	AATTCCCCAAATTGAAACTCTT	(0,0)	1	GTGTACATTGTCAGGCAGAAACAT
Omy28_11671116_USDA	C	T	CTGGTGAGAACAGG	CTGGTGAGAATAGG	AATTCCCCAAATTGAAACTCTT	(0,0)	2	
Omy28_11676622	T	G	ACATGTCATTTAATTGTATCT	ACATGTCATTGATTGTATCT	CGAATGCACGTGAGCTCATCTAA	(0,0)	1	GCAGTAGAATGTCTCGCAATACA
Omy28_11683204	G	T	ATGTAAAAAAGGGCAGAAAA	ATGTAAAAAATGGCAGAAAA	CAAGAAAGAAACAGATGTTGTCCA	(0,0)	1	TTGTGACTCAAATCTGCAACCTAT
Omy28_11773194	A	T	GCAATTTTTTAAATTACCGC	GCAATTTTTTAAATTACCGC	AGTTTGACACCCCTGTACTAGAGC	(0,0)	1	GTCTAACAGCTCTGGTGATTTA
Omy4_8260712	G	C	GAGGTACCATGATCAACCAAT	GAGGTACCATCATCAACCAAT	AGATCCCGAATTTCCCACTT	(0,0)	1	GAAACCTGGCGCCTTAAATTAG
Omy4_8261223	A	G	ATATATGGTCCA	ATGTATGGTCCA	CACATGGGATGTGGTTAATGT	(0,0)	1	GTTCGATACGCCTATTTCATGG
Omy4_8269484	A	C	CAATGTAT	CCATGTAT	GCCCAACTCCCTATTAAAGGTC	(0,0)	1	AAGGTACTTCATTCTTACCAGAAA
Omy4_8325040	G	A	CTGCAGCTACGGAATGCTTAC	CTGCAGCTACAGAATGCTTAC	AGCCAAGTTTGCGCATTTACT	(0,0)	1	TGGATCAGCCAATGAATTACAC
Omy4_8343709	C	A	GGTGAATTAATCACC	GGTGAATTAATAACC	TTTGCAATTGTGTTTAGGGTA	(0,0)	1	AGTCTGCTTTCCACCAGACACT
Omy4_8345868	A	C	ATTGTTTAAATGTCTAAC	ATTGTTTCAATGTCTAAC	TCAAATAATTCCTTTGGGTACAA	(0,0)	1	AAGCATTTTCATATAAAGAAGTCTG
OmyR14589Pearse	T	A	ATCCCTGTTATCTAATCATT	ATCCCTGTAATCTAATCATT	GTAACCATGACATCCACCAATC	(0,0)	1	CCTATGCACAAAGCCTTCAC
OmyR19198Pearse	G	A	ATTAGCAGGAGGCCTCTCCA	ATTAGCAGAAGGCCTCTCCA	TCATTACCTACGCAGTGGAG	(0,0)	1	ATCTCTGGGCCTGAACAAT
OmyR24370Pearse	G	A	TAAGACTTGGCATAAGCATG	TAAGACTTAGCATAAGCATG	CAGGAGTAATGCATCCCAATG	(0,0)	1	CAAGTTGATAACGAGACATAAGGG
OmyR33562Pearse	A	G	GTGGTTACAAAGGGTCTGCA	GTGGTTACAAGGGTCTGCA	GGTGACTGAGCTGGATGT	(0,0)	1	TTTAGAGAAATTTGGCAGTACGTC
OmyR40252Pearse	T	A	AATGCTATATTGAACCTTAA	AATGCTAAATTGAACCTTAA	ACTCTGAATTCCTCAGGCTT	(0,0)	1	TCGAACCAGCTGTCTTTCT
OmyR40319Pearse	C	T	TGCAAGTGC[TA]GCCCTTTTAT	TGCAAGTGC[TA]GCCCTTTTAT	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	GGGTTTCAGTGATAGTTGGCAAAT
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	CACCAATTACCA	CTCCCCCTGGACTTTGG	(0,0)	3	GCTCTATTGCACCGTGTCTG
Ots_myo1a-384-57	C	T	CTGCAGAACAC	CTGCAGAATAC	CTCCCCCTGGACTTTGG	(0,0)	4	
Ots_P53-25	G	T	TTCTGCAGGGG	TTCTGCAGTGG	GGAACCTCCTCTCCCGTTCTG	(0,0)	3	GCACACACGCACCTCAA
Ots_P53-28	G	C	GGCAGCTCCT	GGCCAGCTCCT	GGAACCTCCTCTCCCGTTCTG	(0,0)	4	
Ots_P53-40	T	C	CTCCTGGGTCG	CTCCTGGGCCG	GGAACCTCCTCTCCCGTTCTG	(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	Primary Flag	Rev Primer
Ots_SEXY3-1	X	Y	NA	TCAGCGAAGTGGAGAT	GGTCTTGCAAGTCAAGGAGAGG	NA	0	CCAGGTGGTGAAGGTAGGAA
Oki_101419-103-27	A	C	AATCCACTTCC	AATCCCCCTCC	CCCAATTGGAGACCAGGGTT	(0,0)	3	TCATTGAGACAGTTGGGAGACA
Oki_101419-103-44	T	C	GTTCCTCTACT	GTTCCTCCACT	CCCAATTGGAGACCAGGGTT	(0,0)	4	
Oki_105105-245-23	T	G	GCCTTTTCCAT	GCCTTGTCAT	GCGTATCAAGCATCAACGCC	(0,0)	3	TCTTTCAGCAAGGTGGGCA
Oki_105105-245-56	G	A	CTCATGCCAA	CTCATACCCA	GCGTATCAAGCATCAACGCC	(0,0)	4	
Oki_106172-60-38	C	T	GTGCGCATCAA	GTGCGTATCAA	ACTACTGGCGTGTGTGTGGG	(0,0)	3	TCCACTGAGAGGATGAGGCA
Oki_106172-60-47	G	A	AACGCGCTGAC	AACGCACTGAC	ACTACTGGCGTGTGTGTGGG	(0,0)	4	
Oki_106172-60-47c	A	C	AACGCACTGAC	AACGCCCTGAC	ACTACTGGCGTGTGTGTGGG	(0,0)	4	
Oki_106172-60-53	C	T	CTGACCGCYGC	CTGACTGCYGC	ACTACTGGCGTGTGTGTGGG	(0,0)	4	
Oki_111681-407-38	C	T	AGAACTGCAA	AGAACTGTAA	TTCATCCCATTGGAAGCCCC	(0,0)	3	ACAGCCTATATCTGTGCGCT
Oki_120255mod-105	C	T	AACGTCAGTTA	AACGTTAGTTA	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-113	G	A	AGTTACTGG	AGTTACTAG	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-115	G	T	TTACTRGGGTA	TTACTRGTGTA	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-119	G	A	GTAGYTTCWTG	GTAAYTTCWTG	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-120	C	T	CTTCWTGGCAT	TTTCWTGGCAT	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-133	T	C	TGGCATAGTC	TGGCATAGCC	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-135	A	C	GGCATAGYCAT	GGCATAGYCCT	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-137	A	T	ATAGYCMTAGAT	ATAGYCMTTGAT	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-141	A	G	ATAGYCMTWGATA	ATAGYCMTWGATG	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-99	A	C	GACTAAAACGT	GACTACAACGT	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	3	CATTGAAGGGTGAATTGAAG
Oki_126619-265-31	A	C	GGATTGKGCAC	GGATTGKGCCC	TGCGTAGTTAATTTACCTCGG	(0,0)	3	TACGCAGCACTGAAGACTGG
Oki_126619-265-35	A	G	CAGCACAGCTG	CGGCACAGCTG	TGCGTAGTTAATTTACCTCGG	(0,0)	4	
Oki_126619-265-50	G	T	GATTGCCAGT	GATTCTCCAGT	TGCGTAGTTAATTTACCTCGG	(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	TGGATACCCCACTCTCCA

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	CAAAACCTTGGCGTTGCAAG
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	GCTGTGGTGCTCATGGGTAAG	(0,0)	3	CCAGGGCAGGGTTGTTCTC
Omy_RAD13034-67-21	C	T	CTCCCGAACC	CTCCCTGAACC	GAGTGATTCCAGCCCTCC	(0,0)	3	TCTCTCCGTTGGCCAGAAAC
Omy_RAD13034-67-35	A	T	CTGAGTGGACA	CTGTGTGGACA	GAGTGATTCCAGCCCTCC	(0,0)	4	
Omy_RAD79314-58-25	C	T	CTCGCCTGCG	CTCGCCTGTG	CACACTGACTCATCCCTCGC	(0,0)	3	GAGTGTCTTACCGAGCTGCC
Omy_RAD79314-58-27	T	C	GTCACRCCTGC	GCCACRCCTGC	CACACTGACTCATCCCTCGC	(0,0)	4	
Omy_RAD79314-58-31	G	A	ACGCTTGCCT	ACACCTGCCT	CACACTGACTCATCCCTCGC	(0,0)	4	
Omy_RAD79314-58-66	C	A	CAGTGTCAAAC	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	TTCCTAGGGG	TTCCTAGGGG	TGCCCTGTTGTGATGAGCAT	(0,0)	4	
Ots_100884-287	T	C	ATAGAACTACAATTCACATATAT	AACTACAATTCGATATAT	CGGAAGACCAGATTCTCCAAGAGTA	(0,0)	1	CGACCAAGTAGCGCACTT
Ots_101119-381	T	C	TGCCACATGATAATTGA	CCACATGGTAATTGA	TTTCTAGGACAGGTTGCTTGCA	(0,0)	1	CCAGGTTCTTTAGCCTACTTATTCTTTACA
Ots_101554-407	C	G	ATGGAGGATTGTGGTTGT	ATGGAGGATTCTGGTTGT	TGAAAGATATCAATTGTAGTAGTGGTGGTG	(0,0)	1	ACACGCCAGTCCACAAGT
Ots_101704-143	T	G	CTTAGACGTCAGAGGTC	CTTAGACGTCAGAGGTC	ACTTCTTGAGCCAATCGGATGATG	(0,0)	1	CCAGAGATAAACTAGTGGAGGAGATCA
Ots_102213-210	A	G	CTGTATACAGTAAGAGTATTAAT	ACAGTAAGAGCATTAAAT	CATTCCATGACAATGATTGAAATCTAAAAACAC	(0,0)	1	GAGTATCTCAATTGCACACTATGGTATGT
Ots_102414-395	A	G	CACATAGTGTAGCTTTACTAC	CACATAGTGTAGCTTACTAC	GCCTACTGATAAATGTATGACAGTAATGGA	(0,0)	1	CAATAACAAACAAGCTAGGAACAAAAGTGT
Ots_102457-132	A	G	TGGGGCAACGCACAATTGGCT	TGGGGCGACGCACAATTGGCT	CCAGCAGAGACTGGGTTAC	(0,0)	1	TTCCTACCGCGCAACC
Ots_102801-308	C	A	AGGGACAGTTTCGACAGCG	AAGGGACAGTTTCTCAGACG	TGGGACAGAGGTGGGAATTGA	(0,0)	1	CCCAAGATGCTTAAGTGAAGATGTG

Ots_102867-609	A	G	ACAGAGAGAAGTCCCAGGTG	AGAGAGAAGCCCCAGGTG	CTCTGCCATTCAATTGGGCTTTG	(0,0)	1	GTCTAAAGTGGTCCCCTTGGAT
Ots_103041-52	G	A	CATCTGCTGGACCC	CATCTGTTGGACCC	ACCACCACCTCCTCAGA	(0,0)	1	AGACAGAGAAAGTCGGGACACT
Ots_103122-180	T	C	CATCAACACAATCTGC	CATCAACACGATCTGC	CAAACGCGACTCACACACA	(0,0)	1	TCACAATGGTACGATTTTACACTCAA
Ots_104063-132	C	T	CTTTCGTCCTTAGCACATAG	CTTTCGTCCTTAACACATAG	GCGTTACTGTTGTTATAAACGTTAGC	(0,5,0)	1	GTTTATTTAATTATGAAGGACGATGTTGAAGTCA
Ots_104415-88	C	T	TCCTGAAAAACGACATCC	CTGAAAAACAACATCC	CCTGAGCATCCCAGTTGAACT	(0,0)	1	TGTTTTCAATACACTGCAATTTAGTTTGGT
Ots_105105-613	C	G	CCGAGCTTGAGTTAGGA	CCGAGCTTGACTTAGGA	AGTACAAGTGCAGAGAATGACATCATG	(0,0)	1	GGTGTTTATTTTCCCATATATCTTTAACTTTAAGCT
Ots_105132-200	G	T	CAAGAGTGGCATAAAA	CAAGAGTGGAATAAAA	CGATGTACTGAGGGCAGTGT	(0,0)	1	GAGTGGAGTTCCTTAATAATCATTGACCTT
Ots_105385-421	A	G	CCTCTGGGTATATCG	CTCCTGGGCATATCG	GACTGTCTTGGAACCGTTGCTA	(0,0)	1	TCCCGGAACACACCAATGTC
Ots_105401-325	G	T	CCCGACAAGATGAGACAG	CCCGACAAGATGAGACCG	GAAGTCTGAGCGGTGCTG	(0,0)	1	CGCTCTCTGGTGCTATCCT
Ots_105407-117	T	A	CAGGTTAGGAATGGTTG	CAGGTTAGGATTGGTTG	TGTGTACATCCGCGTAAATATTGAAGATAA	(0,0,2)	1	CTGTGAGCTGCTGCAAAACC
Ots_106313-729	A	G	AAGAGTCCAGCGTACTT	AAGAGTCCAGTGTACTT	TTGTTCAATGGGCATTAAATGCATGTT	(0,0)	1	TGCTTATGTGCAGATCTTGAGACAAA
Ots_106419b-618	G	T	CAATGATTAATGATTAATCCTTC	TGATTAATGATTATCCTTC	CAAGGGCACATTGGCAGATTTT	(0,0)	1	ACCGGACCAAGCACACA
Ots_106499-70	C	G	CATTTTTCAGAAATTGTATTC	CATTTTTCAGAAATTCTATTC	ACTCTATCATCGGCAGGACCAT	(0,0)	1	ACCGTAAGTGTGGTTGTGTTTATTA
Ots_106747-239	C	A	CCCGCGGTGAGTAT	CCCGCTGTGAGTAT	ATCGAGGATGCCTCAAAGACATC	(0,0)	1	GTTAGACCCACCACAGTCATC
Ots_107074-284	A	T	ACCGTAGCTGCACCTG	CGTAGCAGCACCTG	CCCAGTCCAGAGCCTGAA	(0,0)	1	TTTCCATGGCTGTGTACTGT
Ots_107285-93	T	A	AAGTAACGTATCAAAATGGC	AAAGTAACGTATCATATGGC	GCCCTTGTGACAATGCAGTGTATA	(0,0)	1	AACATACACCAATACTAGGTCTAGACAGT
Ots_107607-315	A	C	ATGGGAGACAGATAACT	ATGGGAGACATATAACT	GTGATGAGAGGTTCCGGAAAACTCT	(0,0)	1	GTGTTCTGGATTCCATTGTGCAAA
Ots_107806-821	T	A	CAAAGAAAATCAAAATTT	CAAAGAAAATCTAAATTT	TGCAGTGTGAATTAGAGATTAATTTTGTG	(0,0)	1	CTCCCTTGCTTTTGGTCAATGG
Ots_108007-208	A	T	CAGTTTCACTTAATTTTAAAATG	TTTCACTTAATTTTAAAATG	CAGGCTTGTGTTAAGTAGGGAGAAA	(0,0)	1	CATTGGACAAGACGGGTAGTC
Ots_108390-329	G	C	CTACTTATGTAGCATTTTAA	CTACTTATGTAGGATTTTAA	GAGGTTTGTACTGTCACCATAGA	(0,0)	1	CCTGCTGTAGCAAACTGTCTCAAA
Ots_108735-302	C	T	AAACAAACAACGCCTCATG	AACAAACAACACCTCATG	CCTTTTCTTATTAGTTTTACTTCCCCAGAGA	(0,0)	1	CAATTCCATTCTTGATTCTGTTTACGGT
Ots_108820-336	G	A	ATTGCCATCTCAGAATA	AATTGCCATCTTGAATA	TGAAATAAATTGTTCTGTTGATATGTGAATTTTGA	(0,0)	1	CAACGACACACCAACAACGT
Ots_109525-816	C	T	CATGAGGCGTTCGGC	ATGAGGCATTCGGC	GCCAGATAGTAGCGTACATCATGAG	(0,0)	1	CTCCCCATGTCCTGAGTCT
Ots_109693-392	T	G	TCCGTTAGTTCATCCTGG	TCCGTTAGTTCCTCCTGG	TCTCCCTCATTCCCATGTCATATCA	(0,0)	1	GGGAACGTATCAGGTGAGTGT
Ots_110064-383	C	T	CTACGTAATGAACGTTAGCT	ACGTAATGAACATTAGCT	AACAAAGAATTGTTAAACACCAACAGGAA	(0,0)	1	GTGCAAGGGACCTAGCTAATCC
Ots_110201-363	A	T	TTTTAAAA+CTGGCATCCA	TTTTTAAACTGGCATCCA	GTTTGGCTATTGAAATTATACATTAACATGTAGCT	(0,0)	1	CCATGGCATCCTGTAAAGAACACA
Ots_110381-164	A	G	ATTGCGTCTTCTCCC	TGCGTCTCTCTCCC	CTCTTGTTTGTATGGGAGATGTAGT	(0,0)	1	CCGTATCCTAAACCTTCACTGTT
Ots_110495-380	G	C	CATAGAC[AG]GGGGCCAT	CATACAC[AG]GGGGCCAT	GCCTAGGTATGTACGAAACTTCACA	(1,8,0)	1	AGGCTTTTTCAGATGGTCGTATGA
Ots_110551-64	C	A	ACGCTCGAACATT	ACGCTCTGAACATT	GAGTGGTCAAGGTTTCAGTTTCTG	(0,0)	1	GAAATGGACAGACACAAGGTCAAAC

Ots_110689-218	T	G	CACCAATCAATTAATTATT	ACCAATCAATTCATTATT	GTATAAAGTAGAGTCCAGTGTTATGTTAATGTCTT	(0,0)	1	CATGGCAGACAACAGTAGAGAATATGA
Ots_111084b-619	C	A	TCCATGG[AT]AACGACAAT	TCCATGG[AT]AACTGACAAT	TTGTGGAATTACACCTTCAGAGTTCAAT	(0,0)	1	GCCTGTTGGCTTTCTTAACTGAT
Ots_111681-657	G	T	TAGCGCAAACCCGAACC	CGCAAACCCGAACC	CTGAGCTTTTCAACTTACTTGTGGA	(0,0)	1	GGCGCAGCAGCAACTG
Ots_112208-722	C	A	TGTGAGGCGGTCTT	ATGTGAGGTCGGTCTT	CTGCATGAACGTTAACTCAAATAAAAGGT	(0,0)	1	AATGAGTCTACTGACATTGTATACTAGAATAAGTATC A
Ots_112301-43	T	C	CGTCGATTTCAGC	CGTCGCTTCAGC	GCATGGCTGCCCTAGAACA	(0,0)	1	TCAGAACATTTCCCTTCAGCTTCGT
Ots_112419-131	A	T	AAGCGACTTGATTATC	AGCGACATGATTATC	GTGGGTAATCGATGCCAAAGAGAT	(0,0)	1	TGGCAGTGTTTCAACTAGCTTTG
Ots_112820-284	C	T	ACTCACATCGAGTGACT	ACTCACATCAAGTGACT	CATAGATGTTTATATGAAAAACCTCCCACTGT	(0,0)	1	GCATCCAAAAAGACGTGTGTGTTT
Ots_112876-371	C	A	CATCACAACGATGTGTG	CACATCACAACATGTGTG	GCCTACAGCAAATTCAGTCAACAT	(0,0)	1	TGGACCTTCAATCATCAGACTT
Ots_113242-216	C	T	ATTACCAACGGAGAACC	TTACCAACAGAGAACC	GAGGCCTAATGTCTCTTGTGACT	(0,0)	1	GACATCTTCAACAAGTGTTCAATTCACC
Ots_113457-40R	C	T	CCCT[AG]TTCTCCAATCCATAT	CCCT[AG]TTCTCTAATCCATATG	CCCAAGTGGTGAGTGTCAGT	(0,0)	1	ACTACAACAGGTGTTGATAATAGAATCATTTCTC
Ots_115987-325	T	G	ATGCATAAAAGGTAATTGTG	ATGCATAAAAGGTCAATTGTG	GGAGGTGTAGTGAATGGGAAGAT	(0,0)	1	GCATTTCAGTGAACAGTAGTGCTAT
Ots_117242-136	A	G	CAGCATAACTTGACCTC	AGCACATAACCTGACCTC	GTGACAGGAGACAGAAAGAGACATT	(0,0)	1	TGGTCTCCCTGTCTCTATCTACTA
Ots_117259-271	T	G	CTCTCCTGATCACTCTGT	CTCTCCTGATCCCTCTGT	ACACCCACTTCAACCTCCATAAC	(0,0)	1	GCCTCAGAGCTTAGCTTGA
Ots_117370-471	G	T	ACGGAACAAATAAGCATTT	CGGAACAAATAAGCCATTT	GTTGGCTCCTTCAATTCAATTTGGA	(0,0)	1	TGCAAAACAGAGGAAAGGGATTT
Ots_117432-409	A	G	TTTAGACTTTGCTCTATAACAG	ACTTTGCTCCATAACAG	TCATCAAAACATGCCTCTCTGTGT	(0,0)	1	TGTTGAACCTGTCACTCTGTCTTC
Ots_118175-479	C	T	AGAATGAAGTGAAAGAA	AGAATGAAGTAAAAAGAA	TGCGCTCTCATTTCAACCAT	(0,0)	1	ACCTTACGTCTAGTAGGAAACA
Ots_118205-61	T	C	TAGTAGCCCTACACCTC	TAGCCCTGCACCTC	CCATACAGCCAGTCCAGGTG	(0,0.4)	1	ACTGGACAGGGCTGGGT
Ots_118938-325	C	T	AGAGATGCAAAGTGGAGTT	AGAGATGCAAAATGGAGTT	ATTTTCAACAGGCATTTATCATTGGTGAA	(0,0)	1	GGTCTGTCCCTCAATCTTTGCA
Ots_120950-417	A	T	CTGGACCAGAATCTGA	CTGGACCAGATCTCTGA	CAGACAGGTACCATCACACT	(0,0)	1	TGGTGAAGCTGTAGGAGAAGGA
Ots_122414-56	C	T	TGTATGACCTCTGACCTGT	TGTATGACCTCTAACCTGT	GCACCGTATCAACGAGCTCAT	(0,0)	1	TGCATGGATTTCCCTTGTGTGTTG
Ots_123048-521	A	C	TCACATCCAACCTCAGTACT	CATCCAACGCAGTACT	CTCAACAGTGCACCTCCCTTAATT	(0,0)	1	CCAAACACACCTTCCATAATCTCT
Ots_123921-111	A	G	TGCTAAATGGCATATATTAT	CTAAATGGCACATATTAT	TCGCTAGGCAGAAATATAGGGTTCT	(0,0)	1	GAGCATGGCGCTTGCA
Ots_124774-477	T	C	CCACGCCATCTGATA	CACCGCGCTCTGATA	AGTTGTCTTTTATATTGTGTTTTATTCCATTCCA	(0,0)	1	GCCAAATAAAACAAAGCATGAACACA
Ots_126619-400	C	T	AGAAAGTTCTAGAAATAATT	AAAGTTCTAGGAATAATT	GGATGGTTGTCAATTTCTCTGCAAA	(2,0)	1	CCGGGATACAATAATAATTTGGTTAAGAGTTTTTT
Ots_127236-62	T	A	TCTCTATCTGAGTCTGTC	CTCTTATCTGTGTTCTGC	TGGAGAAGTGCAGTGAATGTGAAA	(0,0)	1	GCTGTTGGACCTTGACTTTAACAATT
Ots_127760-569	C	T	CCGGTTTACCGATTG	CGGTTTACCAATTG	CTGCTGGCGCAGACATG	(0,0)	1	CGTTATAGAGGATAGTTTGGAGGAAGGA
Ots_128302-57	C	T	CCTGCAATACGACCAAC	CTGCAATACAACCAAC	GGTTGCAGGGCAGAACTGT	(0,0)	1	ACCCATCCAATAACCATTTTCCCT
Ots_128693-461	C	T	CTGGTACCCA	CTGATACCCA	TCAATGTTCAATGCACCTTCCTGTA	(0,0)	1	GCCTGCAGGAGAAGGTAGAGTTA
Ots_128757-61R	A	-	TTGTGCATTTTCCCC	TGTGCATTTCCCC	CGTGCCGGCTCTTTTATTTCATT	(0,0)	1	GATGGGTATGTTAATCATATTACCAGCGTAA

Ots_129144-472	C	A	TGGGTCTCGAGCCTGTA	TGGGTCTCGATCCTGTA	CTGTTAGTGCAGAAGACGTAGCT	(0,0)	1	GCAGAGCTATTGAGCCAAGTTACAA
Ots_129170-683	C	A	ATTAGAACTCGTAGAATAT	ATATTAGAACTCGTATAACTAT	AACCTATGGGAACTCGTAGAACT	(0,6,0)	1	GCTAGGAGTTCTCAAAGGGTTCT
Ots_129458-451	T	C	CATCTGGCAATGCCTT	CATCTGGCAGTGCCTT	TGGGACCCACATAAGCAACTG	(0,0)	1	GACATAAGACCCATTTAGCCCTTTT
Ots_129870-55	A	T	ATGCATTACCTGTATTAT	TGCATTACCAAGTATTAT	GCATGTAACACATTATTTGGCATATGTA	(0,0)	1	CAGTACACTGGAGATTGCAATGTT
Ots_130720-99	A	G	CCTGTCTCATTCCC	CTGTCCCATTCCC	CGGTCAATTGTAATGTCAACGGTTT	(0,0)	1	TGCTTGCATGTTCTTGGTGTAGTAA
Ots_131460-584	T	C	CTATCAAAGCAATACATTG	CTATCAAAGCAGTACATTG	CCTATTTTGTAGAGTCATAGTGAATGGGATAG	(0,0)	1	CTGTAATCTCCATTCCTTTTCACT
Ots_131802-393	C	T	TGTTGAGAAATGAAGATGAGTAA	TCGAGAAATGAAGGTGAGTAA	TGATTGTCTCATGGCCAATTGTCA	(0,0)	1	TGTAAATCCACTTGGCAATCTTTGG
Ots_131906-141	A	T	CACGGTTTACACTCCTATTA	ACGGTTTACACTCCAATTA	GGCTCGAACCACCCAGTTTA	(0,0)	1	TGCCCAACTGGTTTGCATC
Ots_94857-232R	T	C	CAGGATAATAACAACAAG	CAGGATAATAACGAACAAG	GGCACTCTCCCTGGCTAGA	(0,0)	1	CCCCATCACTTCTCTGGCTTTAAAT
Ots_94903-99R	G	T	CAAAACGACAAACAT	ACAAACGAGAAAACAT	CCGTCTGAGTAGGAGGATCAATACA	(0,0)	1	TTGGATCCAGCTCTCCGTATAGA
Ots_95442b-204	A	T	TGGTTCCTCCAAATTT	TGATGGTTCCTCAATTT	GTCTCTCTCTCTTTGCATCATTACACT	(0,0)	1	GGACTCTTGAGCTGTCTGGCTATAT
Ots_96222-525	C	T	TGTAGCTAATTTAAGTTCTC	AGCTAATTTTAAATCTC	GCTCTGGCCATCTGTAGGAT	(0,0)	1	GGCGCAACATATGTATTAAAGCACT
Ots_96500-180	G	T	AAAACAAATCATTTTTCG	AAAAACAAATAATTTTCG	CAGGTCTGGTCTACATCGAACAC	(0,0)	1	GATCATGTCAGATAGGATGTGAAAGT
Ots_96899-357R	T	A	CTGAATGTTTTTTTAAATCTTT	CTGAATGTTTTTTTATCTTT	TCTCTGAACTAATTTAGACCTCTGAATGT	(0,0)	1	CCTCATATTGCTTTTATCTGAAGAGAGA
Ots_97077-179R	G	T	TCACAAATGTATCTAAAGC	CACAAATGTATACTAAAGC	CCTGAACAAATCTTAAACGCTCCAGTT	(0,0)	1	GTAATAACTTACACATTGCCACTTC
Ots_97660-56	A	T	ACGAGACAGATATTC	ACGAGACTGATATTC	TTCCTAATCTGACGTACTACCAACT	(0,0)	1	CGCCACTGACGTTTATCCA
Ots_99550-204	C	T	AAGGCTTTGGTTGTTTG	AAGGCTTTGATTGTTTG	TGACAGATTTACCTTTAACTAGCTAAGC	(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	GCCACCCTACTTGTGAGAAAAATA
Ots_AldB4-183	T	A	CTGTGTGTCTAAGACAAT	CTGTGTGTCTATGACAAT	TTTGTGCGTAAAGTCAGGTAGTGT	(0,0)	1	GTGCATGCCATGAGAACTTTGTTT
Ots_ARNT	G	T	TACAGATGTATTTTAC	CTACAGATGTATTTTAC	CCACTGGCTGTGGAGCTT	(2,2,0)	1	GGGTTCACTGATAGTTGGGCAAT
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	CTAGGTGAAACTTTTTTAAA	CTAGGTGAAACTTTTTAAAA	GCCCTGGAGAAAGTACGTTTTAACTAA	(0,0)	1	GCAACCATGTCAACATTGCACATAA
Ots_AsnRS-60	T	C	TGAGTCCCTGACCAGC	AGTCCCCGACCAGC	CCGACGCTCACTGAGT	(0,0)	1	TGGTTTTTCAGGTATGGTTTCCA
Ots_aspat-196	G	C	CACTCTTTATATCCACAC[GA]	CAGTCTTTATATCCACAC[GA]	CCTGAACAGGTACACACAAACGA	(0,0)	1	TCCAACCTGATGAATATGACCAACATGAAT
Ots_BMP2-SNP1	C	T	CCCACTTCGCTGAAGT	CCCACTTCACTGAAGT	ACTGCCACAGACACGAACTC	(0,0)	1	GCCACTATCCACTCGTTCCA
Ots_brp16-64	T	C	AAGTCAGATCTTTCA	AGTCAGCGTCTTTCA	ACTCTGGGTCTCAGGAGGTTTT	(0,0)	1	CTGACGAGACCATGCACCAA
Ots_Cath_D141	T	C	TGGGAAGCAATCAA	AATTGGGAAGCAGTCAA	CACCTGTTCTGCACACTACTTGTC	(0,2)	1	CACACATGGATTTTGCTGTCTAAA

Ots_CCR7	C	T	CCACGTAGCGATCG	ACCACATAGCGATCG	CTGCTCACCTGCATCAGTGT	(0,0)	1	CCATGGTGGTCTGGACGAT
Ots_CD59-2	G	A	CTAAATGTCATGTAATAT	ACTAAATGTCATATAATAT	CATGTTACCCAGCTAAAAGTCTATAGCA	(0.5,0)	1	TGTTTATCTCTGAGTGAAAAGGTGTGT
Ots_CD63	A	C	AGATCATGGGAATCATAT	ATCATGGGCATCATAT	TGCATGTTTCTAACTGTGTTTTGTGT	(0,0)	1	TGAATGCCCCCATCAACA
Ots_ego24-22	T	C	CCAGATGAACAACCTCAC	CCAGATGAGCAACTTCAC	AGGTCCTCTGTGCACCTA	(0,0)	1	GGAGGCGAGGCTGTGGTG
Ots_CHI06027687_143477	G	A	GGAGATAGTCAGGG	GGAAATAGTCAGGG	GCGAGTGTTAAAAGGGTCAAA	(0,0)	1	TCTCAAGCCATAAGACGGGTA
Ots_CHI06035945_4547	C	T	CCGCAACAGATC	CTGCAACAGATC	AGCGAGGCTTGC GTTTTACT	(0,0)	1	GTGCAGTCTGGGCTTGCTCT
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	GGCGGCTCGGAAAATTATTT	GGCGGCTCGGAAAATTATTT	GCGGTGGGATACCTCCTCTA	(0,0)	1	GCGAGAAAAGCATGAATGA
Ots_CirpA	C	T	CAGTTCTGTAATGCATT	CAGTTTTGTAATGCATT	GCTGTGATTGTGCTCTAAAGACATG	(0,0)	1	CTCCCACTTAGCATCTACCTT
Ots_cox1-241	C	T	CACTACGGTAAGACCAT	CACTACAGTAAGACCAT	CACTGAACTGTAAGCCATTGTGATT	(0,0)	1	GTAAATGTAGTATACAGTATAGGCATCGTAGGT
Ots_CRB211	A	C	CTACCGTACTGAACTC	CCGTACGGAATC	CAACGCGGGAATGGCTTTTAA	(0,0)	1	GCCAGAGTCGCAAAATAGTAGAAT
Ots_crRAD10447-25	C	T	AGCTAGCGCTCCTC	AGCTAGTGCTCCTC	CCGTGTCAGGACTCATCAGT	(0,0)	1	GCGTGGTTCAACAGCAGTG
Ots_crRAD11620-55	C	T	AGAAGCCCAGCTCC	AGAAGCTCAGCTCC	TGGGATAGAACAGGAGCTTAAACA	(0,0)	1	TGTCTTGGTCGCGCAGTT
Ots_crRAD12037-39	A	G	CATTCAAAAAGTAT	CATTCAAAAAGTAT	TGCAGGAACTTGCTATGCT	(0,0)	1	TGTGAAAAAAGTCAAGGGGTCT
Ots_crRAD13725-51	C	A	GAGGCCACAGATTC	GAGGCCACAGATTC	TGCAGGAGGAGGAAGGCA	(0,0)	1	AGAGCTGCCAGGTGGAGT
Ots_crRAD16540-50	C	T	ATTAAACGT[CA]TGGA	ATTAAATGT[CA]TGGA	TGTGTATTCTGTCGACCGGA	(0,0)	1	TCACCTGACCAAAAGCACTGG
Ots_crRAD17527-58	C	T	TAGCTCCGAGCTAA	TAGCTCTGAGCTAA	TGCCGTGGATTATTGACA	(0,0)	1	GCGTCAGATCAGCTGGTCT
Ots_crRAD18289-33	T	C	GAATGGTGTAAAT	GAATGGCGTTAAAT	GCAGGGAAAAGTGTACGGA	(0,0)	1	AGGTGAACCTCCGTCCA
Ots_crRAD18492-65	C	T	TTATGGCTATTATT	TTATGGTTATTATT	GCAGGGCGCAAAGTCTCT	(0,0)	1	CAGTGAGCGACTGTAACTCTGA
Ots_crRAD18937-60	G	A	CTCCTCAGGTGGGC	CTCCTCAAGTGGGC	GGCACAGCGACAGGAGTT	(0,0)	1	TGAGCTGGTGCCTCTGAG
Ots_crRAD20262-46	A	G	GGTTACA[TC]CCCCAA	GGTTACG[TC]CCCCAA	CCTCTGCTGAGTTTGAGGGG	(0,0)	1	TGAGCAGAGCCTATGAGGACT
Ots_crRAD20376-66	G	A	GGGA[TA]GGAGTATT	GGGA[TA]GAAGTATT	GGGAGGCAGGCAAAAGGT	(0,0)	1	GGTTCACCACAGCCTTCT
Ots_crRAD20887-70	G	A	GAATCTGTCGTTGG	GAATCATCGTTGG	CTGCTGTGAGCCGTTACGC	(0,0)	1	AGAACACATCTGGCCAGGT
Ots_crRAD21115-24	C	T	CACACATATGCACG	CACACATATGCACG	TGCAGGTGGGACTTAAACACA	(0,0)	1	ACCTGTGCAACGGTTGA
Ots_crRAD22960-32	C	T	CGACCACTTACA	CGACACTACTTACA	ATCAGGTCTGGGCGACA	(0,0)	1	TTCACCTCTGCCATCGCC
Ots_crRAD23631-48	G	A	GGGCTTGGGGGCAT	GGGCTTAGGGGCAT	GCCATATCCGGGGCTTG	(0,0)	1	TGCCTCTGAGCACTGACTG
Ots_crRAD24807-74	A	T	ATGATAAT	ATGATATT	TGCAGGAGAGCAGGGTAGA	(0.8,0)	1	CGTGCCTAACATCATGTGCA
Ots_crRAD25367-50	T	G	GTATATTAGAATG	GTATATGTAGAATG	ACTGCAGGCGTCATGCTT	(0,0)	1	TGGACAAAAGACCACAGGCT



Ots_crRAD255-59	T	C	AACTGTTCAAACCC	AACTGTCAAACCC	TGCAGGAGCTGTGATGGG	(0,0)	1	GTACGGAGCGTCACTGCT
Ots_crRAD26081-28	T	G	TGGAGGTGGAGGAG	TGGAGGGGAGGAG	GGGAGAGGGAGACGTGGA	(0,0)	1	TCACCAGCTCCTCTCCTC
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	GCATTTAAAAATC	CAGATGGTGCAGGCCGAA	(0,0)	1	ACTCGTTGTGATTCCAGCCA
Ots_crRAD2806-42	C	A	GTTTGGCATAAAGT	GTTTGAATAAAGT	GCAGGGCAGACTGAAGG	(0,0)	1	ACTTCATGCCAATCTCACTAAACA
Ots_crRAD33491-71	C	T	GAGAGCCGAGCTTT	GAGAGCTGAGCTTT	CAGTTCGCTTCTCCAGGGA	(0,0)	1	TGTGGGTAGCAGACTGACG
Ots_crRAD34397-33	C	G	AA[GA]GTGCCCTCCCC	AA[GA]GTGGCTTCCCC	TGCCTAAACACTCCC AAGGT	(0,4,0)	1	GTTCCGTTTTTGTCCCGCA
Ots_crRAD35313-66	A	G	TTTAAGATGTAGTT	TTTAAGGTGTAGTT	TGCAGGAAGAGTTT CAGAGAAATCT	(0,0)	1	GCTCGTGCAGGTAGAAATGT
Ots_crRAD36072-29	T	C	AACCTGTGTGATTT	AACCTGCGTGATTT	TGCAGGACCAACTTTCTCAT	(0,0)	1	GGCTGACTGGTGAAGGGG
Ots_crRAD36152-44	C	T	CTGCCACCTTTGA	CTGCCATCCTTTGA	CAAAGTGCAGGTGCTGGC	(0,0)	1	CCAGCCAGGTGTGAGCA
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	TAGCCGTACCCGAT	TAGCCGCCACCGAT	CTCCTGTTCGTAGCCG	(0,0)	1	GGACGACCAAAGGTAGAACCC
Ots_crRAD55400-59	C	T	CTAACCCGGA[CA][GA]AC	CTAACCTGGA[CA][GA]AC	CGCAATGAGCCAACCCCT	(0,0)	1	CTGGTTTGTCCCGGGCT
Ots_crRAD55475-26	T	G	CCATTTTAATTCCA	CCATTTGAATTCCA	TGCAGGGTTGGGACAATT	(0,0)	1	AGTCTATTTCCGATTTGACTGGA
Ots_crRAD57376-68	T	C	ATAAAGTGTGTTAT	ATAAAGCGTGTTAT	TGCAGGCATCATGCTTAATAACT	(0,0)	1	ACGTGACACAGGTCTGGG
Ots_crRAD57520-66	T	G	TTTTTGTTCAAAG	TTTTTGTTCAAAG	ACAGAGCTGTGTCTACCAGA	(0,0)	1	ACCCCTCTTGGCCTTGC
Ots_crRAD57687-34	T	G	ACAAATTAATTAAA	ACAAATGAATTAAA	TGCAGGGACGGGGCT	(0,0,7)	1	TGCTGTTGTCTGGGTCTCTC
Ots_crRAD60614-46	G	T	AAGATGGTATGTAT	AAGATGTTATGTAT	TGCCGTGAGAACTGGTCA	(0,0)	1	TTCTCTCTCTCTGCCTCA
Ots_crRAD60620-51	A	G	GTACGGAAAAACA	GTACGGGAAAAACA	CAGGCAGTCACTGAGTCG	(0,0)	1	TTTGAGCACCGTTTCCGA
Ots_crRAD61523-71	A	G	CAGAGCATGTGCTG	CAGAGCGTGTGCTG	GCCAAGTGATCAAGTGCTTGT	(0,2,0)	1	CCAGCAGTTCAGTTGCGG
Ots_crRAD66330-60	G	T	AGAGAGGGGTCAAA	AGAGAGTGGTCAAA	ACTCTCCCAAGGATTCAGAGA	(0,0)	1	TCCCAAAGCATCTGCCA
Ots_crRAD69327-53	G	T	ATAGGAGAATTGGA	ATAGGATAATTGGA	GCCATTTGACCAACGGAGC	(0,0)	1	ACTCATACAGATTTCGCCTGT
Ots_crRAD73823-60	T	A	GCACGATG[CT]JAGAAC	GCACGAAG[CT]JAGAAC	GCAGGAAGCAAAGTTCGGTG	(0,0)	1	AGCAACTCATCGGTGGT
Ots_crRAD74766-28	G	A	AGACTGATAAAAG[AT]	AGACTGATAAAAG[AT]	GCTGACCACCGACCACAG	(0,0)	1	AGCTCTGCAGTAACAATGGGA
Ots_crRAD75581-70	A	G	GAACTTAAACACT	GAACTTGAAACACT	ACACATGGCTCGTCTGCA	(0,0)	1	GGAGCTCAGGGTGCAGGA
Ots_crRAD76512-28	A	T	TAAAAAATATATAA	TAAAAATATATAA	GCAGGGACAGGGCCCT	(0,3,0)	1	TGGTGCTGGGTGCTGTAC

Ots_crRAD78968-46	C	T	AG[CA]AATC[CA]CACAGC	AG[CA]AATT[CA]CACAGC	CCTGCTCTGTCTGGGC	(0,0)	1	GTGAAGACGACCCCGTG
Ots_crRAD92420-25	G	T	CAATCGGAAGTCGG	CAATCGTAAGTCGG	AGTGCAGGTCTCCAGATTACA	(0,0)	1	ACCGAAGTGATGTAACTTCCGA
Ots_crRAD9615-69	T	C	TATTGGTCAGGGAA	TATTGGCCAGGGAA	GAATGCAGGGCCAGGGAG	(0,0)	1	ACTCCCAGACCATCCAGT
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	TTCATAATTGAACGATTTC	CATAATTGAACAATTTC	ATGACCAATTGAAGAGTTCTCCGT	(0,0)	1	CAAAGCCAAACGTCACATTACACT
Ots_E2-275	A	G	CCCCCATATTGCTG	CCCCACATTGCTG	GGTGCCACTTTAGTATAGCTGCTTA	(0,0)	1	CCCTACCCCTGTGTTCCA
Ots_EndoRB1-486	G	A	TCCTTCTCACGCTTCT	CTCCTTCTCATGCTTCT	CCTTTGGGTCTGCTTGAGGTT	(0,0)	1	GGAGCCAAATCCTAATGCTGAAGTA
Ots_EP-529	A	G	CAGTGTCATTTTCGGC	ATCAGTGTCATCTTCGGC	GCCCTGCCTGCAACTTC	(0,0)	1	GAAACCAACGCTTGATGTAGACCTA
Ots_Est1363	A	T	CCATCCTGTCTTGICTG	CATCCTGTCTGTCTG	GGTGATTTTGCCACAGAGTAGAGAT	(0,0)	1	AGTGTTAAATGTAACCTGCATATACAGGCAAT
Ots_Est740	T	C	TCTGGATGGAACGTTAG	CTGGATGGAGCCGTTAG	GGACTCGTGCTTGAGGAAGATG	(0,0)	1	TGCATGGCTCCAACCTCTT
Ots_ETIF1A	A	C	CAACTGAAGAAAAATATG	CTGAAGAAAAGAATATG	TCTGAACCTACCAAAGGAACACTTG	(0,0)	1	GAGAGAAAAGGAGAAATGATTGCCATT
Ots_FARSLA-220	G	A	CCTTGGATGGGA	CCTTGGATAGGA	GTTCTGGGATTGTCAATGTTTCAT	(0,0)	1	CTTGGACAGGCTCACATTACCATA
Ots_FGF6B_1	A	C	CCTGTTATCAGACCCAAAT	CTGTTATCAGCCCCAAAT	GAGACAAAGGTTTGACAGTTTCATG	(0,0)	1	GGGAGCCATGCACATAATATTGGA
Ots_GCSH	C	T	TATCTGGGCGGGCTG	CTATCTGGACGGGCTG	GTCTTTTTAATGATGACTACAGGCTTTCAC	(0,0)	1	GCTACTTACATAATACCAATTGAGCTGAGA
Ots_GDH-81x	C	-	TGTTACGGACATACT	TCTGTTACGGACATACT	CTTTTCTGAATTAGTGCTGTGCTTGT	(0,0)	1	CCAACCTCTCAACTCTGTCAGTGA
Ots_GH2	A	T	TGACTCTCAGCA[TA]CTG	TGACTCTCTGCA[TA]CTG	GCGTACTGAGCCTGGATGACA	(1,8,0)	1	CCCCCAGGTTCTGGTAGTAGTTC
Ots_GnRH-271	C	T	CAATGAATACAATATCTAACCTAA T	AATGAATACAATATCTAATCTAA T	CAGATGAAAAATAAATAATTGGGCCATTAGGAA	(0,0)	1	CAGAGAGACTGAGACCATATGATGTAGT
Ots_GPDH-338	G	A	CCACTACTTAACGTGCTTT	CCACTACTTAACATGCTTT	CACTAAATATTCCTTATCATTTCATACTAAGTCTGAAGAA	(1,0)	1	AGCTGATACACAATAAAAACAAAAACAT
Ots_GPH-318	C	T	ATCAAGCTGACGAACCA	CAAGCTGACAAACCA	GGTGATAACAGGTGTGCACCAA	(0,0)	1	TCAGGTGGTGGTGACAAC
Ots_GST-207	G	A	ATGAGAGAGTCTTTCTCTGTT	ATGAGAGAGTCTTTTCTGTT	GGAGAACATGCATCACCATTCAAG	(0,0)	1	TCAGCAAACGAAGGCTATGTAGAAT
Ots_GST-375	C	T	TTTCTGTAGGCGTCAGAG	TCTGTAGGCATCAGAG	CAGCCCGTCCCAAAATCAAG	(0,0)	1	CAGGAATATCACTGTTTGCCATTGC
Ots_GTH2B-550	C	G	ATAACATCTGCAGCATTAA	ATAACATGTGCAGCATTAA	CACAGGAAGGACGTGTTTGATG	(0,0)	1	TGACTACCCGTGTACCAATGAAC
Ots_HFABP-34	C	T	TCGAACTCCGCTCCTAG	TCGAACTCCACTCCTAG	CAAGAACCCGAGATCTCCTCA	(0,0)	1	TCGGCGGTGGTCTCG
Ots_HMGB1-73	G	T	ACTGTATATGTTACGTTTTTC	ACTGTATATGTTAAGTTTTTC	TGCTTCAGTGAAAATAAGCGTGAGA	(0,0)	1	GTCGAGCGGTATGAATACTTTCTGA
Ots_hnRNPL-533	A	T	CATTTACCAGTTCTCACACAC	TTTACCAGTTCACACACAC	TCTTTGATATTGAGCTCATAAAAGCAAGGT	(0,0)	1	TCCTTGTTCAATCCATCAGGCATAAAA
Ots_hsc71-3'-488	C	T	TTTCCAATGGTATAGATATGA	TTTCCAATGATATAGATATGA	TGCATCCATTACACTGTACCAATT	(0,0)	1	TTTGTTAGGCACACGATAATTGTC
Ots_hsp27b-150	G	A	[CT]GATCTGGACAGGCT	[CT]GATTTGGACAGGCT	TAGGAGTTGGAAAGACTGCACA	(0,0)	1	CCCATTGGTCTTTGGTGTT
Ots_Hsp90a	G	C	ATTTGACTTGTCTTTTT	ATTTGACTTGTGTTTTT	GTCGTTTTTCATAGAAAATAGCTCACAGTT	(0,0)	1	ACAGTATACCGGCTGCCTATTCATA

Ots_HSP90B-100	C	T	TCTATGGTGTGATTCATT	TTCTATGGTGTAATTCATT	CACCTTAGTTCACGCAACATG	(0,0)	1	CTGCGTGATTGTAGTGGTGACA
Ots_IGF-L1-76	A	T	CTGCCTAGTTAAATAAAATA	CTGCCTAGTTAAATTAATA	GGTAGGCCGTCAAGTAAAAAAGT	(0,0)	1	GATGGAGGCCACTGTGTTCTTA
Ots_Ikaros-250	G	A	ACAGAAGATTTTCGGCTGC	ACAGAAGATTTTCGACTGC	GAGGCTGACTTGGACTTTGC	(0,0)	1	GGCCTGTCACGCAAGGA
Ots_IL11	T	C	AGTCCATGCGGACT	AGTCCACGCGGACT	CCTCCAGATGAGACCACTCT	(0,0)	1	CAAAATGGTGCTCAAACGACTCA
Ots_IL8R_C8	C	T	CTGGACGCCGTTACA	TGGACGCCATTACA	CGTGGTGTCGCCTTCCT	(0,5,0)	1	TGTCGGCCATCACTGTCATG
Ots_IsoT	T	C	AACCAGTAGAATAACC	CAGTGAATAAACC	GACTCAGGTAAGGAAACATCAATGTCA	(0,5,0)	1	GAAAGCAAAGCATTTTATCCACCACTA
Ots_LWSop-638	T	C	TTTAACAAGAAAATTATACATTTT	CAAGAAAGTTATACATTTT	CAATTACTCTTTCTCAGCCCTGTGT	(0,0)	1	GCGGTAAGATGCAGTTTATCATGGA
Ots_mapK-3'-309	T	G	ATGCTATTAAATGAATATTC	ATGCTATTAAATGACTATTC	GGCCACTGTCATAGAATTAGGCATT	(0,0)	1	CGTGACCCTTGTAAGTAAAAAGC
Ots_mapKpr-151	A	T	CGTATGTGCAATGCATG	CGTATGTGCATTGCATG	TGTTGTCTCGGACTGCATGAC	(0,0)	1	GAAGGCACAGAGATGAAGGACAT
Ots_MetA	T	A	CCTTAAGCATATTTCT	CCTTAAGCGTATTTCT	GATCATTATCAAGACTATAGGCTATGGATACG	(1,8,0)	1	AGTTGAGTTAAGTAATTGGTAATTAGCCTGTT
Ots_MHC2	T	G	CTGGAGCGTTTCTGTA	CTGGAGCGTGTCGTA	GTCTCAGCTGGGTCAAGAG	(0,5,0)	1	GTAGTGGAGAGCAGCGTTAGG
Ots_mybp-85	C	T	AGAGCATGTAGTTTIG	AGCATGTAATTTIG	CAAGGGATGTGACAAATTAATCAACACATAA	(0,0)	1	AAGAGGTCTAATAATCTCCAATGTAAAAACGT
Ots_Myc-366	T	C	TCTCTGCTCATCTGTC	CTCTGCTCGTCTGTC	CCTTAGCTGCTCTTTGAAGTTGACT	(0,0)	1	GGCTATAGAGTGTATTTACAGCATGCA
Ots_myo1a-384	A	C	ACAGATCCATCCACCACT	AGATCCAGCCACCACT	CTCCCCCTGGACTTTGG	(0,0)	1	GCTCTATTGCACCGTGTCTTG
Ots_myo1a-384-36	C	T	CACCACTACCA	CACCATACCA	CTCCCCCTGGACTTTGG	(0,0)	4	
Ots_myo1a-384-57	C	T	CTGCAGAACAC	CTGCAGAATAC	CTCCCCCTGGACTTTGG	(0,0)	4	
Ots_myoD-364	T	G	TCATCTTTTGTTATTTCTTG	ATCTTTTGTTCTTTCTTG	GTGTGTGTGTGTGTGTGCATCGT	(0,9,0)	1	TTTACACATATACAAAAATGGTCTCTATTGTGCAT
Ots_NAML12-SNP1	A	G	AAACCATTTTCATTCTTTIG	CCATTTTCACTCTTTIG	TGCCACCTCAGTTTTAGTGTATATCC	(0,0)	1	AGCGCCAACTGTCACT
Ots_nelfd-163	A	G	ACCCACCAGTGCATT	CCACCAGCGTATT	CTCACTGCAATCCAACCTCATCAT	(0,0)	1	CCACTACATCTCTCAAGGTT
Ots_NFYB-147	C	T	TGTTCCAATGTAAAAATGTATGC	TTCCAATGTAAAAATATATGC	CAGATGATAGCTTCAGTAAGTGGTTCA	(0,0)	1	CCGTCCACAGCACAAGACTATAATA
Ots_nkef-192	C	T	AATAGCCGACATCAA	AAATAGGCCAACATCAA	CATTTAGCAGACACTCTTATCTTAGTGTA	(0,0)	1	CGAATGTCCACCTCAGATGTTACAA
Ots_NOD1	C	G	CCAACGCCGACTTG	CCAACGCCGACTTG	GTGCTGCAGGAACCATGTG	(0,0)	1	CTGTGTGGACTGTGTCTAAGG
Ots_nramp-321	G	A	AAC[G]TJGGCATGAACGACTT	AAC[G]TJGGCATGAATGACTT	GGCCATCTTTCAGGACGTACAG	(0,0)	1	GCATGCTCTGCAATACGTTGAG
Ots_ntl-255	T	A	ATTCTTCTC[TC]ACAATTG	ATACTTCTC[TC]ACAATTG	TGCAGTTACAAGCCTAAGACAATCT	(0,0)	1	CAACTAAAGTAACACACCAGCAACTG
Ots_Ostm1	C	G	CCGTGGTATTGTTTCAA	CCGTGGTATTCTTTCAA	CCAGCCCCGTAACACACAT	(0,0)	1	GAGAGGAAGCAGAAAGGTCGTTTAA
Ots_OTALDBINT1-SNP1	T	C	CTACTGTTGTATTTCTC	CTGTTGTGTTTCTC	CGCTGGGCATGGATGAGT	(0,0)	1	GGCCAACTGCTACTTCTCT
Ots_OTDESMIN19-SNP1	C	A	CCAGTCATGGGTCACT	TCCAGTCATTGGTCACT	GGTCTGTCTGTCTGTCTATCTGTCAATG	(0,0)	1	TGTGTGTCTTTGTTCATTCTACCA
Ots_Ots311-101x	A	-	CTGAGATCACTTTGAGCAC	ACTGAGATCACTGAGCAC	AAATGAGGCCGTCTTTACACT	(0,0)	1	GCAATACAAGCCCTTGATAATGAAGT
Ots_OTSMTA-SNP1	C	T	AATTGCCTCAATGGGTG	AATTGCCTCATTAGGTG	GCCGAAAAATAAGCGATTAGTGATGA	(0,0)	1	GCCCCATGGTAAACCTAATTAACCT

Ots_OTSTF1-SNP1	G	T	CCGCCACCTTGGCT	CGCCACATTGGCT	CGGACAAAGAGCTACAGAAATGC	(0,0)	1	CGTCCCTCTTCACGCATGA
Ots_P450	T	A	CCCCGAAGTACTTTT	CCCGAAGAACTTTT	TGACGCGAGATTATCAAAGTGTCAAAGA	(0,0)	1	CCCCAAGCGGAGAACTTACAG
Ots_P450-288	A	G	CTATAAAGTTGGACAGTTGG	AAAGTTGGGCAGTTGG	ATGTCATATATTCTACTATAATGATTGGAAGCCA	(0,0)	1	CAGTGAAGTGAAGCTGTTAGGA
Ots_P53	G	A	CTGGGTCGGCGCT	TGGGTCGACGCTC	GGAAGTCTCTCTCCGTTCTG	(0,0)	1	GCACACACACGCACCTCAA
Ots_P53-25	G	T	TTCTGCAGGGG	TTCTGCAGTGG	GGAAGTCTCTCTCCGTTCTG	(0,0)	4	
Ots_P53-28	G	C	GGGCAGCTCCT	GGCCAGCTCCT	GGAAGTCTCTCTCCGTTCTG	(0,0)	4	
Ots_P53-40	T	C	CTCCTGGGTCG	CTCCTGGGCCG	GGAAGTCTCTCTCCGTTCTG	(0,0)	4	
Ots_parp3-286	A	G	AGTTACAAGTGGTGTTC	ACAAGTGGCGTTTCA	AGTCAGTGTGGTGTAGTGAAGAGA	(0,0)	1	CATTGTGGAGTGTATTGAACAGTAACA
Ots_PEMT	C	T	TGC[AT]TTGCTAAGACTTG	TGC[AT]TTGTTAAGACTTG	AGAGCATCAATTTAAAGCTGAAAACGA	(0,0)	1	CTTGATCCCTGCTGCAGTATTTT
Ots_PGK-54	T	A	CCACCATCAAGCACTG	CCACCATCATGCACTG	CTCATACTTTGTACCTGTGTGTCCA	(0,0)	1	CGACCAAGTGGCTCATCAG
Ots_pigh-105	A	-	TGACCTGAAAATA[TC]ATATTTT	ACCTGAAAATA[TC]ATTTTTT	GCATTACTAAAACTGGTGTGTGGAA	(0,0)	1	GTTTGAATGTTTCTCTGATTGTGTTAACA
Ots_pop5-96	T	C	TTCTGTTACTGGAC	CTGTTACTGGC	CTCTGCTACTTGCAGTGTATCTCA	(0,0)	1	AGTTTGAGGGCTCTATCTGTCTCATG
Ots_ppie-245	C	A	ATGTCTGAAATGAAAGCC	AATGTCTGAAATGAAAGCC	TGTTTTTGGTCATGTATTTCTCTGCTATTTTT	(0,0)	1	GGACTGGAGCTGCTGAACATA
Ots_Prl2	A	G	ATGTATTGTTCAATTAATG	TGTATTGTTCGTTTAATG	CCTGGTCTGTTTGTGATCAAGATG	(0,0)	1	GGTTAACTCAATAGAACATACTCTGACACA
Ots_RAD4543-52	T	C	TACATATGACTAATGAAA	TACATACGACTAATGAAA	TCTTTGGACTGTGTATACCAGGTGTA	(0,0)	1	GCCAGATGCTGTGTGTGTTT
Ots_RAG3	C	T	CTCTACAGTATG	CTCTACAATATG	CATTTCCACGAAAAGCCAGATGAC	(0,0)	1	ACAGAATAAAGTATCTCTCTTACACTACTAAT
Ots_RAS1	C	T	CAATCTATCATCGACCAGC	CAATCTATCATCAACCAGC	TCATAAACATGGTGTCTTTCAGTCAGTT	(0,0)	1	CTGACATGTGAACTACTAAAGCATTTAATCAC
Ots_redd1-187	A	G	ATTCTGACAGCTGTTTTG	CTGACAGCCGTTTTG	TTCCTGGGTGCCATACTCTTTCAAT	(0,0)	1	AGTTGAGACCTTCAGTTCTTAGGGTAT
Ots_RFC2-558	A	-	TGCATGTAACAAATAACAT	TGCATGTAACATAACAT	AAGGTCTACTCCGGTGTATTTCGGT	(0,0)	1	CAATACGACAGTACCGGTGTAAACT
Ots_S7-1	T	C	TACAGGAGATAAGGTCGCA	CAGGAGATAGGGTCGCA	TGCCATCATAAACACCTAACAGTAACT	(0,0)	1	CCTGGTTTAAAAACGGCAACTG
Ots_SClkF2R2-135	A	T	ATTCAAAGTCAAATTTT	ATTCAAAGTCTAATTTT	CCAAATACAGACCAGCTACTTGTGT	(0,0)	1	CTCAAGTCCCTGAATAATGGTACGT
Ots_sept9-78	G	A	CTCTCGATGTCTAGACA	CTCTCAATGTCTAGACA	GTCGATTACCGTTAGCTTCATCCT	(0,0)	1	ATTTCTCTGTGTCTCTCTGTCT
Ots_Six6-3_AG	A	G	AGTAAATGTATGA	AGTAAAGTGTATGA	GACACCATAAACGCTGTAGCC	(0,0)	1	TCAACTTTGCAATGAAAATGACAAG
Ots_Six6-3_AT	A	T	GAGTAAACATTGAA	GAGTAAACTTTGAA	GCGAGCAATTATTCGGGCAA	(0,0)	1	AAGGTAAGTGAATATAGGGTAGC
Ots_SL	A	G	TCAAAGATATGATTCAATTA	AAGATATGGTTCAATTA	AATATTGGCTTCTGAGAATGCATTGG	(0,4,0)	1	CCAAGATACTCTCTTAACTCTCTGTCA
Ots_slc7a2-71	G	T	GTCTCTGACGGTGTGCTTTC	GTCTCTGACTGTGTGCTTTC	CCATTCCCATCGGCATCGT	(0,0)	1	GCAGCAGACACCCGAAGTA
Ots_stk6-516	C	A	AACATAACGGACTCCC	TAGAACATAACTGACTCCC	TGTGTTTAGGATTGAAGTACCATGTT	(0,0)	1	GTAAACTCCACCTGCAAGAAGGA
Ots_SWS1op-182	T	A	ATGTACTTTAACGATTCATTT	ATGTACTTTAACGTTTCATTT	TCAAAGACATCGAACACAAGACGA	(0,0)	1	GCAGGTAAATCAACGTCATCATAAGAA
Ots_TAPBP	C	T	CAGCTGTCCAGTTCTG	CAGTTGTCCAGTTCTG	TTTCTATCCTTCTCTCTCCAGTCT	(0,0)	1	GGACAACCAGCACTCCAGAA

Ots_TCTA-58	C	T	CTGCCATGAAGTGCTAG	TGCCATGAAATGCTAG	ACCACTACCTAAACGTTAGAAAGCAA	(0,0)	1	CGTTAGTTAGCTATGTCTGAAAGGCA
Ots_TGFB	C	T	AGCTAGCTCTCGGAAG	AGCTAGTTCTCGGAAG	GCCTCACATTTTACTAGTGCACTTC	(0,0)	1	GAGCAGATCTCTCAGTAGTGGTTT
Ots_Thio	T	C	CAGTGATTAGTCATTCTTA	CAGTGATTAGTCGTTCTTA	TTTAAAAATGGAGATAAATCCTGACCTGAA	(0,0)	1	AATACCAAACCATGCCACTAATACCT
Ots_TLR3	C	T	CTGTGGTTGTGGCGTG	CTGTGGTTGTAGCGTG	TGCACCTGCGAGAGCAT	(0,0)	1	CTGGCGTTGTTCCTTGTCAG
Ots_TNF	C	T	CTGGCTGTAAACGAAGA	TGGCTGTAAACAAAGA	CCAAATCCTCATCCCACACACT	(2,0)	1	CCGTTGCACTTGACCCTAAAC
Ots_tpx2-125	C	T	CAGGCGGTTCTCC	CAGGCAGTTCTCC	TGTTGTAATCTTCTGAATATTGCTTGCTT	(0,0)	1	TCTTCCAAATTGAGCACAAAAGCAT
Ots_trnau1ap-86	G	T	AATCCCTCCTTTTTCC	TCCCTCATTTTTCC	GGACAAGTTGAAACAGATCAGGAAGT	(0,0)	1	GCCACTGGATACCATCACTTCAAA
Ots_txnip-321	T	C	TCTGGCGGATTTACA	CTGGCGGGTTTACA	CCTTCAAACCTAACACATCATAGACATGCTT	(0,0)	1	TTATCAAACCTGAAGCGGATTACTGA
Ots_u07-07.161	C	T	ATCAGTGACATAAGTTGTCCA	TCAGTGACATAAATTGTCCA	GTCACAAATGCAGGTAAACATAAATGGT	(0,0)	1	GATGCAAAACACCTGTGAAATTGTGA
Ots_u07-17.135	A	G	AAAATGTACCACATACTTGT	AAATGTACCACATACTCGT	CTCGCTCTGTCAATTGTATTACCTT	(0,0)	1	TGACACACGAGCCATTTTGATGAT
Ots_u07-18.378	A	T	ATATGGTATGTAGAGGCTAGTTA	TATGTAGAGGCAAGTTA	GGAAACCAGCTAGGATTCAAGAA	(0,0)	1	CGTTATATGGTTTGCTTTGTTCGATA
Ots_u07-20.332	A	C	ACCATTGATATAAATGCGTTAG	CATTTGATATAACGGCGTTAG	CGCGAGTTAGCTCGAATATTATGATTTC	(0,0)	1	TCAAGCTAGCATAGCAACTTCATCAA
Ots_u07-25.325	T	C	CCGCTTGAAAGTTTGA	CGCTTGAAGGTTTGA	AGACAATCATGGTGTTTGAGTCTTTCT	(0,0)	1	GCCTAGGCTTGATGGAGTCA
Ots_u07-49.290	G	A	CTTCCCGGTGTTGGT	ACTTCCCTGTGTTGGT	GCTGAGGAAGGATTCTGTATTGCT	(0,0)	1	TCGGACAGAGCGCATCC
Ots_u07-53.133	C	T	TAACACATGTTGAGGTC	AACACATGTTAGAGGTC	AGCTAGGCTGTAATGCAGGAT	(0,0)	1	CAGTGCTTCAATTCAATGCTGTCAA
Ots_u07-57.120	A	T	GTGACAAGGTAGGGGTTG	GTGACATGGTAGGGGTTG	GGTTTGAGCCAATCAGTTGTGTT	(0,0)	1	CGGTCTAATGTCCATTGCTCATGTT
Ots_u07-64.221	G	C	ATCGACCTGTCAATTAG	CGACCTGTGATTAG	GAGGATGACACTGTCCGTTTGT	(0,0)	1	CACAGTCCTTCGTATTACCTTGAT
Ots_u1002-75	T	C	ATGGCCCTTACACTATC	TGGCCCTTACGCTATC	CCGCCTTCCCACCTTCTC	(0,0)	1	TCAAACGAGAACACACTAAGGTTGT
Ots_u1007-124	A	G	TGTCCTGTCTCAGATCA	TCCTGTCCCCAGATCA	CGAAATAAGGGCTGGTGTTAAAA	(0,0)	1	TGTACCAGGTGGAAGCTTTGG
Ots_u1008-108	T	A	TTGGTAAACCTGTTTATTGGTA	TGGTAAACCTGTTTTTTGGTA	GGATGACTCTACTAATAGACGGATGT	(0,0)	1	AGGACAGGAAAGAAGCAGCAATA
Ots_u202-161	T	A	AGCTAGTGCTTAGCAGCTA[AC]	AGCTAGTGCATAGCAGCTA[AC]	CACTTTTGACTTTACATGGAACTTAACAT	(1,4,0)	1	GGGACTTCACTTTTACAAACATGTCA
Ots_u211-85	C	T	TCCCAAAGTCGAGTGTG	CCCAAAGTCAAGTGTG	TGGTGAGAGCAGCTTAAATGTCTT	(0,0)	1	ACCCATTCTCTGTCTGGTTTAAGC
Ots_U212-158	G	A	CTGGAAGAAGGCCTC	CTGGAAAAAGGCCTC	CCCCATATGAGACGCTACAGTAATG	(1,5,0)	1	CAAATGCCCTCTAAGCAGACCTT
Ots_U2305-63	T	-	AATGTCATATAGAAATCTAC	AATGTCATAGAAATCTACTG	TGTCATCTCTATTGCAATCTCAGTAGATTCTAT	(2,0)	1	CCAGGTCGCTTTATTGCAGATTATCA
Ots_U2362-227	A	T	AAGAAGCATTTTT[GT][GT]	AAGAAGCATTTATTT	TCGTGGATTGTGCTTACGT	(0,0)	1	GGGTGTTTAAACAAGTAGTCCTTCA
Ots_U2362-330	A	G	ACTGGGAAGATTGTTTG	CTGGGAAGACTGTTTG	AATGGGTAAACAAGAAATAGCTAGCTACTT	(0,0)	1	GACAGACCACAGTGAAGGTGAAA
Ots_U2446-123	C	A	CTGCAACTCGACGCAAG	ACTGCAACTCTACGCAAG	CTGGTCTGTGACGTCAAAATGATG	(0,0)	1	AGCTAGACCAGGCCATTTGAG
Ots_U2567-104	G	A	GAGACTGTTGAGAC	GAGACTATTGAGAC	CATAGTATAGTATTCCGAGTCTGGAGTCT	(0,0)	1	CGGGCTTTCTTAGGATATTTCTCTGA
Ots_u4-92	T	C	CTGTGTTGAATTTAACATAAT	TCTGTGTTGAATTTAACGTAAT	ATCCAAGGAGCCCCATTAAGATTT	(0,0)	1	CGTACCAGAGTTGTAGAAGCATCT

Ots_U5049-250	G	T	TGGAATGGGTAAGGTGTA	TGGAATGTGTAAGGTGTA	CAATGTCTAAAGTAATGGTGGTATTCTTGC	(0,0)	1	TCTTTGACACACCATCTGCCAATT
Ots_U5121-34	A	G	AGGGTCTCATGTCCT	AGGGTCTCGTCTCCT	CCAGAGGTTAGATGGCCCTTT	(0,0)	1	CTGAGCCAGAACCAAAATGAATT
Ots_u6-75	C	T	TTAGTCAACTGTGTTTT	TTAGTCAACTGTATTTTT	GAAAAAGTAAAGTAAAGTAAAGTATTATACCACTAAAGACAA T	(0,0)	1	GATCCACACTGTTGGTCTACTACAA
Ots_unk1104-38	C	T	CCACTAAGGATTACGTTACG	CACTAAGGATTACATTACG	TAACCATGACTTCTATCAATACCC	(0,0)	1	CCTCCATACATCGTCAAAGCTGTA
Ots_unk1832-39	C	T	CACCACTAGAACTCTC	CACCACTAAAACCTCTC	GAAACGTCTATGCTGTCCCTTTAA	(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	CCTCCCCCTTTCCACATCAG
Ots_unk7936-50	C	G	AGACATGTAGCTATGTAGGTAA	AGACATGTAGCTATCTAGGTAA	ATGGGTTGGGATTATGGTTCATTGT	(0,0)	1	CAAAATGGTTACTTGCATAGTCTTTTGT
Ots_unk9480-51	G	C	CTCCACAAACCC	TCCACGAAACCC	CAAATCAGAACAAACCTCCACAA	(0,0)	1	GGAAGTCTGTCTGAATGGTTGTCTT
Ots_unk9480-51-38	T	C	TCCASAAACT	TCCASAAACC	CAAATCAGAACAAACCTCCACAA	(0,0)	4	
Ots_unk9480-51-39	C	A	CTAAGGAGACC	ATAAGGAGACC	CAAATCAGAACAAACCTCCACAA	(0,0)	4	
Ots_vatf-251	G	-	AGACCACAAGATACAGTACC	AGACCACAAGATAGTACC	CTTTCCGGGTATTATCATGCTGTTGT	(0,0)	1	GCAAGCATTTGAAAAACAGACTGGAT
Ots_VGLL3-1	C	A	ACCTGCTCTAATA	ACCTGATCTAATA	AGGAGTCCGAGTCACTCT	(0,0)	1	AGATGTGGGTGTACAGAACTC
Ots_wenYhap_25067_92	A	G	GCATAGTTTGG	GCATGGTTTGG	ATAATGTTCTCTGACATGTTGGTG	(0,0)	1	AAGTGAAGGTCAAGCCATGAGT
Ots_wenYhap_71572	C	T	GCCACACTGTT	GCCATACTGTT	CTAGTCTGACATGTAGGCTCATC	(0,0)	1	GAAATCATGCACAGAATGAACAGT
Ots_zn593-346	A	T	TCTTGCAATCATTTTAAC	CTTGCAATCATATTTAAC	CTACGCGAGAAATAACACTTTTCAAACT	(0,0)	1	GGCAGGTTTATTACGGTGTATTGAC
Ots_ZR-575	G	A	CC[GA]ACAAATTTGT	CC[GA]ACATAATTTGT	GCCTACCAGAAAGTACCAATGTGA	(0,0)	1	ACTTTTCACTGCTCTATTACAATTAGTATTTGTGATAT
Ots1_72858599	A	G	GGTGGAGGGGAAAAGCAGTG	GGTGGAGGGGAAAAGCAGTG	AACCATTGTTCTGTATTCTGCT	(0,0)	1	CCATCCTTTCATTCGTCTTTTAC
Ots10_21244146	A	C	CCATTATCATTAT	CCCTTATCATTAT	CTTCCAGGAGGTATTGTTGTTAT	(0,0)	1	CTGTATATGGCAAACCTACGTTCA
Ots11_11925999	G	T	CATTTAAAAATGGTAAAAATCA	CATTTAAAAATGTAAAAATCA	TTTATATTCAGACATTGCGCAAAA	(0,0)	1	AAACCATTTCTATGTTACTGTGACAA
Ots11_32418659	A	T	AGCCAATTGTAGCCTTAGTGC	AGCCAATTGTGCTTAGTGC	CAATTGTAGCCCTCTAACTTTTCC	(0,0)	1	TACAATTGGCTTTGTGTGTCGTAT
Ots11_32468959	G	C	GTGATAGTTTGATAGTTTAT	GTGATAGTTTCATAGTTTAT	AACACAGATCAATGTTTCACAC	(0,0)	1	TCAACATTCTGTTTTCTGTGTT
Ots12_23066874	A	G	TCCCCACCAAAATTAAGCAAA	TCCCCACCAAGATTAAGCAAA	CTCTTTCAGTTGTCTTTGCTCTTG	(0,0)	1	ACCTGTTCATGCCTTTTCATAAT
Ots14_5453033	G	A	TCCTAAAAAGGTACAGTATA	TCCTAAAAAGGTACAGTATA	ATTATTCAAAACAGAGATGGCGAAA	(0,0)	1	ATCATGTCTATGCAAAACCTCCTC
Ots15_18157381	C	T	CCCTGGAGATCT	CTCTGGAGATCT	TCTCAATGTGATTGAAATGGATGT	(0,0)	1	CACCGTACACACAACTACAGACA
Ots17_1486479_C6	G	A	CTGTAGTGACGCGCAACAC	CTGTAGTGACACGCAACAC	GTCACGATCAGCAATGAGACAG	(0,0)	1	GGACTAAGGCACTGCATTGAA
Ots17_22360456	T	G	AGTCTGTCGTTGT	AGGCTGTCGTTGT	ATGGTTAAATTGACTCTCCCTAT	(0,0)	1	GCAGATGACAGAAACAGTAGTAGGC
Ots17_885364	C	A	TAGCCTTAAGCGCTTCTGCC	TAGCCTTAAGAGCTTCTGCC	GTAAAGAAACATGACCTTTTCTGAG	(0,0)	1	TTTAACTATGATGGCCATAACCTG
Ots18_29943476	A	G	GCCTGACTGGACAACCATTTG	GCCTGACTGGGCAACCATTTG	GTTCATTTTGAAATAACTGCATCG	(0,0)	1	CTAATGTGCATGGACCTTGTAGAG

Ots18_30099101	C	T	ATTGCATACTCGAGTCATCCA	ATTGCATACTTGAGTCATCCA	CAAAATGTAAGGATACGCTTGAATG	(0,0)	1	AATACATGTAATCGTTGCAACTC
Ots18_32088284	T	C	ATGTTACATGTA	ACGTTACATGTA	CATGAGACACCCCTGGAGAAAA	(0,0)	1	GCCCCAAGAAGGTACTATCAAAAT
Ots18_3417174	A	C	CTGAATCCTGTAAG	CTGCATCCTGTAAG	TGAGGTATTACTTGCTGAGTTTGC	(0,0)	1	TGGGAATTAGTTCACATCTTCTTG
Ots18_3426299	T	A	AATGCCATTTTGT	AAAGCCATTTTGT	TTATTTTGGGGTTCATATGGTTCT	(0,0)	1	TCCAAAAATATCAACATCATGACC
Ots18_3541813	T	C	CTACCTACCTTAGTGCTC	CTACCTACCTCAGTGCTC	CCCCAAAAACATCAAGAACTCTAA	(0,0)	1	TTAGTCTACCTTTTCTCACCATGT
Ots18_3550047	A	G	TCATTTTTCAGAGAGAGAAT	TCATTTTTCGGGAGAGAGAAT	ATCATCTCTGCTCAGAGGCTATTCT	(0,0)	1	AGTGTAAAGACGTTCCCTCCACTCT
Ots19_46172133	C	T	GCAAATCTCCGATGTAAAGT	GCAAATCTCTGATGTAAAGT	CACATGGCTCTTTGCTCAAAAT	(1,0)	1	AACATTCAACACATAATGGTAGGC
Ots19_46172427	G	A	TATTCAAAAGGAGCAGTTCAT	TATTCAAAAGAAGCAGTTCAT	CAGTTCCTGACATTACCAAAAATA	(0,8,0)	1	CTGTATTAGTGATGGGTTGTTTGC
Ots2_38264269	A	C	TCCCTTGTCTATGGTATATCT	TCCCTTGTCTCTGGTATATCT	GTATGAGTTGTGTGGTTGCAATGT	(0,0)	1	GGACATTGTGCAATAGGCTAGAG
Ots2_42405643	G	T	CAGGTTGTGGTTGTT	CAGGTTGTGTTTGT	GAGAGAGTGCATTCTTCATCAAGTT	(0,0)	1	ATTGGGAAAAACCCGTACTGA
Ots22_32650802	G	A	GGGAGAGGAGCCCTGTCTTTA	GGGAGAGGAGACCTGTCTTTA	AAGGAGCAGGAGATGTTATTGAAG	(0,0)	1	CAGTGGACCAGTGAAGTACCTAGT
Ots28_11023212	A	G	AACGTGACACAAT	AACGTGACACGAT	AGAAAGCCATCATCATGAGACC	(0,0)	1	TTCTGACCATTTTTGTGTTTGT
Ots28_11025336	A	C	CAATGAAGTTAATTTAATTGG	CAATGAAGTTCATTTAATTGG	TGCAATATAGAACAAATCCGAAAA	(0,0)	1	ATGTATGTGAAGCCAAGGGTTATT
Ots28_11033282	G	A	TAAAAATGGTGATATGTA	TAAAAATGATTGATATGTA	GGCTTTCTGATGATCTTGAACCTT	(0,0)	1	TAGGGACTTCCTCTCTCACACT
Ots28_11062192	C	G	TTCTCAAGTCCTACTCAACTG	TTCTCAAGTCGACTCAACTG	AGATGATATGGATTGCTGTGTGT	(0,0)	1	TCTTTCTCTGATCGTTATGTTCAA
Ots28_11070757	A	G	ACCCATGAATAAGGACGAGAG	ACCCATGAATGAGGACGAGAG	TTTGGAAACCTTTTACTACGAG	(0,0)	1	CCCTCTCTCTGTATACTGATGT
Ots28_11071377	T	C	CATCTTAGCCTCTCTGACCCC	CATCTTAGCCCCCTCTGACCCC	ATTTGCTGTGTGTGGAGTGAAT	(0,0)	1	CCTCCAAGAGCATCTGTCACTAC
Ots28_11072994	C	T	CCATATGTCGCTTGT	CCATATGTCGTTTGT	GGGAGACTTAAACAACCTCAAAA	(0,0)	1	ACTGTTGAATAGAAGGTTGCAGGT
Ots28_11073102	T	A	ACATTACTTTTCAAAAATATT	ACATTACTTTACAAAATATT	GGTGAGCCATTCATAACAATCTT	(0,0)	1	TCTCTTGAATGATCCAGGATAACA
Ots28_11073668	T	A	TACAGTTTCTGTCTGA	TACAGTTTCCAGTCTGA	CCTAAGAGGAGACGAGCATTACAG	(0,0)	1	CGAGTGGTCATATGTTGATTACC
Ots28_11075348	G	A	GTGTGAAAGGGGAGAAGGGCT	GTGTGAAAGGAGAGAAGGGCT	CATTTCAAAATTAGGAGTTAGGG	(0,0)	1	ACAGGCCACAGCTCTCATCT
Ots28_11075712	C	T	GAAAACCTTGCCCTG	GAAAACCTCTGTCCTG	GCTTAAACAGCTGCTATTAGGACA	(0,0)	1	ATTAGAGCTGGCAACAAATCCTTA
Ots28_11077016	C	T	GTCAAACCACTTTGCCAAGG	GTCAAACCAATTTGCCAAGG	AAAATATGTGCAACATCCAATGTC	(0,0)	1	ATTAGCTTCAGCCAGCTTGTTGT
Ots28_11077172	G	A	ACACACACAAGAGACACCAC	ACACACACAAAAGACACCAC	GTTTTGCCAGAGAGAATGTACAAA	(0,0,4)	1	GCTAGTCCAATGCTCTAACCCTA
Ots28_11077576	A	G	GAAGGCCAATAAAATTG	GAAGGCCGAATAAAATTG	TGTGCGGAATTACTGATAATTGAC	(0,0)	1	AGCAGTGTGTAAAAATGCAGAGC
Ots28_11095755	A	T	AGAGTTGAATGGC	AGTGTTGAATGGC	CCAATGGTGATTTAGAACATTAC	(0,0)	1	TGCTGTTGATCCATACTCTGTTTT
Ots28_11143508	G	A	TTCACGTACGGCCCAT	TTCACATACGGCCCAT	ACCTTTTAGCCAGTGACAACATTT	(0,0)	1	CTATCGTCGAGAGTTCTTGCAT
Ots28_11160599	G	T	CTCTCTGCTGCGTT	CTCTCTGCTTTCGTT	GTGCATATTTACGTGGTTGAAGT	(0,0)	1	AAATTCATATGGGTGAAATGGAAT
Ots28_11164637	C	A	CTGGCGGGTCTGGG	CTGGCGGGGTATGGG	TGATTTGACTTTTGTGGTGT	(0,0)	1	AAGAGAGCAAAAACAGATTGGAAC

Ots28_11186543	A	T	AAAGCTGATTAAAA	AAAGCTGATTAAAA	GGCTTGCCTTTAGATAGAATCTTG	(0,0)	1	TTTGTTTTGGACTTGTGAGATTT
Ots28_11201129	T	G	ACTGAAGGAATTTAAC	ACTGAAGGAAGTTAAC	TGCAGATTTATCTACTTGTCCAG	(0,0)	1	TTAGCAATTGCGTACAAAACACC
Ots28_11202190	T	C	CAAAAGTCTGTATTTCAAAA	CAAAAGTCTGCATTTTCAAAA	GCTAAATGTAAATCGAGTGGCTGT	(0,0)	1	TAGAACACTGAGAGGACCATGTA
Ots28_11202400	C	T	GACACACTCACGA	GACACACTCATGA	CCCTCCAAAAAGAAAACATTGAT	(0,0)	1	AACCAGTGTGTTGATTAGCCAATTT
Ots28_11202863	C	A	ATAAAAAATTCTGCGTGAATG	ATAAAAAATTATGCGTGAATG	GAGGATGGATGAGACTTTTCAGAT	(0,0)	1	CTTCATATAAACCCGGTAAAGAGC
Ots28_11205423	A	G	CCTGCACACATGTCAAACCG	CCTGCACACGTGTCAAACCG	TTAAATACCCAGAGCTTGTAGA	(0,0)	1	TGTGGTGTATCTAGGTCAGGT
Ots28_11205993	C	T	GCTATTAAGG	GTTATTAAGG	GCTGCTATTTCCGACCTTACAATA	(0,0)	1	TTCTGTTGAGTGTGTTGTCTTGAT
Ots28_11206740	T	C	CCTTCCCTCTAGGGCAACGT	CCTTCCCTCCAGGGCAACGT	ACTTTGAGGACTTACTCTGTCTT	(0,0)	1	GATCATCATCTTGTCTTCTCCAG
Ots28_11207428	T	G	GTTGGAGCGTCCCAAATGG	GTTGGAGCGGCCCAAATGG	TATACCTTTGTAGCATCCCTCTCC	(0,5,0)	1	GTCAAACGCTGCCACTTTATATG
Ots28_11210919	C	T	GACCTCAAGCAGTCAG	GACCTTAAGCAGTCAG	AGTGCTCCATGCTGGAGTTT	(0,0)	1	AGCCTCTCCTTCTGCTTCATC
Ots29_18791740	T	G	CCTATGAAGTT	CCGATGAAGTT	GTTTTGGTGGTCTCAAAATCC	(0,0)	1	CGGCACCTGGAACAGTC
Ots29_23344676	T	C	TGCAAGTCCTTCAAAGGCTCA	TGCAAGTCCTCCAAGGCTCA	GAACATCTCTGACTCCCATGAAA	(0,0)	1	CATAACAACGAGGAGAACTCAG
Ots3_34894254	T	C	TAACCTACAGTC	TAACCTACAGCC	TGATATATTTTGTGCAATGATCTG	(0,0)	1	AACATTGTCCACCTTCCCTCT
Ots3_57055518	T	C	TGATCATATCTCGTTCAGT	TGATCATACCTCGTTCAGT	TTAGCAGGCGATCTAATTCTGATT	(0,0)	1	CAGAGAATACAGCAGTTAGCGTGT
Ots30_17330452	G	C	CATGTCAGTGC	CATGTCAGTGC	CACAAATGTGACCGTTTTCATC	(0,0)	1	TTGAACAGGGTGTCTGTAGTG
Ots30_17330688	T	C	TGTGTCTGAGA	TGTGTCCGAGA	CTGACAAAAGTATGCTGCCTGA	(0,0)	1	TGCTTGGTTACACAGTTTGACA
Ots33_19359879	T	C	AAATAAACGCTGGGTCTAATT	AAATAAACGCCGGGTCTAATT	AGCGCTGTTTTACATAAACACTT	(0,0)	1	TTGCTCAGTCTTACGGTACTCAC
Ots4_40942276	G	A	GGAGTCAGATAC	GAAGTCAGATAC	ATTAGTGCATATGAATCGGGCTAT	(0,0)	1	CAATATGTACGTTCAACCTTTTGG
Ots4_41638710	G	A	CCTGAGATTAGG	CCTGAGATTAAG	CAGCAGCTGTTTATGACTGACTTC	(0,0)	1	CATTTACATCGGTTACACGAG
Ots4_42378741	C	T	AGATGAACACCAACTGGCCGG	AGATGAACACTAACTGGCCGG	CAGTTTAAGTGTTACCACCACGAG	(0,0)	1	CGTTAACGCTCACCTGCAC
Ots4_64978818	C	A	TCAAGTGTTTCTTTATTTTG	TCAAGTGTTTACTTTATTTTG	AGAACCCATGCTTTCAGTACACTT	(0,0)	1	GAGCGATACATTTCTGTCCATTTT
Ots5_44795073	C	T	TTTTTGTTGCCCATGAATT	TTTTTGTTCTGCCATGAATT	GCACTGTATACAAAATCGTGTGGT	(0,0)	1	TATTGGGCATTGTCTGTCTAATG
Ots5_70908626	T	C	AGCCTCTTCTCTCTG	AGCCTCTTCCCCTCTG	TACGGTAGGAAGACTGAATGAGTG	(0,0)	1	TACAAGCTATCTGGAGGTTAGGG
Ots6_10904949	C	T	CCTTTGTCACCGCTCATCAGC	CCTTTGTCAGTCTCATCAGC	AAATCACCCCACTTCTTTTGTG	(0,0)	1	TGCTTATGCATCACCTTTCTAC
Ots6_33505144	T	A	AACATATGAGTTGTAATGCC	AACATATGAGATGTAATGCC	CCCACCATACAATAAGGCATGT	(0,0)	1	TGGGTATTGTTTATGGGAGAGAT
Ots7_50997124	G	T	GGGCCTTCGGGGTGCTGTCC	GGGCCTTCGGGTGCTGTCC	AGATCAAGCTTGCTGACTTCG	(0,0)	1	CAGCAAAATACAGTGGGTGTATG
Ots7_51409415	T	C	TGGTCTACTTTGTGC	TGGTCTACTTCGTGC	ACAACTAGTCATCGTGAATCTGA	(0,0)	1	CCTCATTCCTTTCTTTAGCATGT
Ots7_53291035	G	A	GCTAGCAAACGTCGCCA	GCTAGCAAACATCGCCA	TCAAATGAATGTAGACAGATGGAA	(0,0)	1	TAATGTTAGCTTTGCGAGCTATTT
Ots7_53631522	A	G	TGAGTTTTCAAGGGGT	TGAGTTTTCAGGGGT	CTTATCTCAAAGGAATGGGAATGA	(0,0)	1	CAAAGCTGCATCCAATACTGTAG



Ots7_54212944	T	A	AATATATTTTTATAGGC	AATATATTTTTATAGGC	AAACCACGGTATCCTTTATTCATC	(0,0)	1	TTTAGACATATTTGGGGTTAGGAA
Ots9_16115048	G	A	CCAGTGAGATGCTGTGTGCA	CCAGTGAGATACTGTGTGCA	ATAGAGCTTTTGGTGTTCATTCC	(0,0)	1	AGGCCAGTACACAGTACACACT
Ots9_28975221	A	T	TTTGCCAAAGAGTTCAGATAC	TTTGCCAAAGTGTTCAGATAC	GCCTGCCCTACTTATCTCTATCA	(0,0)	1	CAGCAATTTACAGTGAAGAGGT
Ots1_27140162	A	G	AGTGCCAACATAAAA	AGTGCCAACGTAAA	ATCTGGCAGACAAATCCGGTTT	(0,0)	1	CCAAACCATGAAAAACAGCCCA
Ots1_66076738	A	G	WTAAGATAAATGCAC	WTAAGATGAATGCAC	TGTTGACGAAAATTATCCCGCT	(0,0)	1	CTTCGTTCAACTGTCGTACCTT
Ots1_70387503	C	T	GTATTACTCTGGGG	GTATTATTCTGGGG	CCAAAGCTGCTTCCACCAA	(0,0)	1	ACAATTTACACAACCTACTCCCA
Ots1_76687317	A	G	CTGACTGACTAATCT	CTGACTGGCTAATCT	AGGGTGACGACGAAATTAGTC	(0,0)	1	CAGAAGCTGGACTATGTGGAGT
Ots10_30585920	C	T	CTCAAAACTGAAGGT	CTCAAAATTGAAGGT	CATGCTGGTTCAAACTTCAAGGT	(0,0)	1	ACAAGGTCGCACTGTACATCTT
Ots10_9122143	C	T	ACAGTAGCGAGGCTA	ACAGTAGTGAGGCTA	TAAAAATGAACGTGGCGAGGC	(0,0)	1	CGACTAAGTGGTGCCTGTATGT
Ots11_25464702	A	G	ATCCCCCAAAGTCGG	ATCCCCGAAGTCGG	GTACGACTGTGTGCCCCATTGT	(0,0)	1	ATGAAAAATGGAGCAGCGATGG
Ots13_59820108	C	T	GCTTGCTCTCCGACC	GCTTGCTCTCCGACC	TACATGGCACGCTGTAAATTTGT	(0,0)	1	TGACTCTGCTTTACAAGGGGTG
Ots17_2812224	A	C	GAAGTGAGCATAGAA	GAAGTGAGCATAGAC	GTGATCAGAGTCTCCGGAACA	(0,0)	1	CAGTGACATGAGCCTACCACAT
Ots2_10023971	A	G	AATAATGTAGACTG	AATAATGTAGCGCTG	TGAACAGCTTTGTATGAACATAACA	(0,0)	1	CCATTCAAAACCCAGGCAATGAC
Ots21_11292994	C	T	GTCAGACTTACAAC	GTCAGATTTACAAC	ACCGATAAAGCCTAATCCAGT	(0,0)	1	TGGTCCTGCAGTTATGTTCACT
Ots31_8676501	C	T	AAAGAGACGCATACA	AAAGAGATGCATACA	AGGTTACTTGTACATCTCTGGGA	(0,0)	1	ACGAGTTACTGATTTTGTGTGTGA
Ots33_22128145	C	T	ATAACTACTACGCAT	ATAACTATTACGCAT	TACACAGCACACCGTAATTTGG	(0,0)	1	CAGTTGTCGCGTTGGTAAGAAG
Ots4_26584430	A	T	AAGCACAAGCATTTT	AAGCACATGCATTTT	ATATTACTGCACAGCCGGAAC	(0,0)	1	GCACGTTTGTGAGAATAGAGCA
Ots4_69260400	C	T	AAGTTTACATTTGAA	AAGTTTATATTTGAA	CGTCCCTACCCATTGAAGTTT	(0,0)	1	ATAGAGTGTAGCTGGGGTTGG
Ots5_15328967	C	G	GGTAACACAGTCACA	GGTAACAGAGTCACA	ACACTCCACCAATCACACAGTT	(0,0)	1	TGATTGAATGACCAGTGCAGGA
Ots5_6600890	G	T	GTTTGAAGCTTTCTG	GTTTGAATCTTTCTG	ACCAAGTTAGCTACATCCATACCA	(0,0)	1	TGTGATCATGCTGTACTTGCCT
Ots6_74160204	A	T	CTAGTAGACCGGCAA	CTAGTAGTCCGGCAA	AAAGACAAAACAAGTGGACCCG	(0,0)	1	TTCTTCTGAAGTCGGTGCCTC
Ots7_78097510	A	G	ATTCTGCAAAAGTTA	ATTCTGTCGAAAGTTA	CGAAGTCACCGCTACAATCCT	(0,0)	1	TCCGACTTCAACTGTACACACT
Ots11_25009447	A	T	TTTTGTTATATTTTG	TTTTGTTTTATTTTG	TCAGATTGAAAGCAGGTACACT	(0,0)	1	AGGCTAAAGGACTGATGAGCAA
Ots16_62110135	A	G	GAAAAATAAGTTTTA	GAAAAATGAGTTTTA	GTACACTCAGTGTACAGTCGAAAG	(0,0)	1	CACAAAGTAGATGCTCAACCGAT
Ots22_37910995	A	T	TTTATATACAATCTT	TTTATATTCAATCTT	TTACAAGGTTATTATCCGGTTGAAA	(0,0)	1	GCTCAAACGCAGTCACAACAG
Ots26_22091974	A	G	TAGTTGCAGATCAGA	TAGTTGCGGATCAGA	TGGTCCAAAATCTTCTGACC	(0,0.3)	1	GGTGGGAAAAGTATGTGAACCA
Ots31_7150057	C	T	TGTCAGCAGGTATG	TGTCAGTAGGTATG	GGTGGGAAGGAAGCATTGTGTT	(0,0)	1	CGTTCTTGACTGCACTGAAATGT
Ots34_7961260	A	C	ATTCTGAAATTTTAT	ATTCTGACATTTTAT	AATTGATTAAGGCTGCTTTTACAAG	(0,0)	1	TGTTCAAGTAAGTGGCTGTTGA
Ots6_17852464	A	C	ATATGTAATGRGTTT	ATATGTACTGRGTTT	ACAGCTTGGAAAATCCAGAAAATA	(0,0)	1	TTCTTACAGCATTTTACAACGT

Ots6_71457825	C	T	AATCTGATAATTTCG	AATCTGATAATTTG	GGAACCTCCGAGTTGAAATATGTG	(0,0)	1	ACTCGGAACTGGAAACTCAGA
Ots7_76804229	A	G	CAGTGAAGGAAATC	CAGTGAAGGGAAATC	GGCTAGGCCATTAGTTCAGT	(0,0.5)	1	CCTTGCTTTGTGCGCTGAAA

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

Assay	A1	A2	A1-Probe	A2-Probe	FWD Primer	Corr	Primary Flag	Rev Primer
One_SEXsdY-F19R20	X	Y		CTCCAACCTGTGT	CCCAACACCTTCCTATCTCC		0	CCTTCCTCCTAGAGCTTAAAC
One_1a.11217-58	C	T	ACCTAACCTAACC	ACCTAACTAACC	AGCTGACAGCCACAAAGTCA	(0,0)	1	AGGTAGCAGTGCTTTAAGGT
One_1a.11387-56	C	T	TGGCTTCCGATGT	TGGCTTCTGGATGT	CAGTCACCAAGTTCCTCCA	(0,0)	1	TGACCATGCTCCTTAACATCC
One_1a.12158-56	G	T	CTAAAAAGAACTTA	CTAAATTAACCTTA	TCTGACCCACGACGCTCTAT	(0,0)	1	TTCCAGACGCACACAGTTCA
One_1a.12851-49	C	T	AATCTGCCCTGCTA	AATCTGCTCTGCTA	CCAGACCGTACAGAATCTGC	(0,0)	1	ACCAATCACAGGCTGCTTTG
One_1a.13961-31	A	T	ATTACAAAGAAATAT	ATTACACTGAATAT	TGCAGGTTAGTGAAGATAAATGGGA	(0,0)	1	TGTCACAGAAACCACAGTCTGA
One_1a.14403-38	C	T	TAGAGCGCATGAG	TAGAGCGTATGAG	CACCCAGCCTGCCACAAG	(1,0)	1	ACCAGGCTGTGCATAACCG
One_1a.14866-33	C	G	AGGAGGACTTTTGT	AGGAGGAGTTTTGT	TTGTGTGTGGGTGCAGGAG	(0,0)	1	CCGAGCTATGAGGTCAAGAGT
One_1a.15933-53	A	G	GCCCTGCACTGCC	GCCCTGCGCTGCC	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	TGCAGGGTATGTCTGTTTTGT	(0,0)	1	GCACAACGTAGCCAAATTC
One_1a.20814-68	A	G	AAGGTCCATTACAA	AAGGTCCGTACAA	ACATTCAGAAAGGGGAAGGTCC	(0,0)	1	CTACTTCCCCTTCCCATGCC
One_1a.22268-41	C	T	GGCATCACGAGGGA	GGCATCATGAGGGA	GAGGGACTGGTCACTTCAC	(1,5,0)	1	TCCTCATTTTCCCTCCCTC
One_1a.22351-67	C	T	CAGACATCGCTCAG	CAGACATTGCTCAG	GGAGGCTATCAGCTTCTGCA	(0,0)	1	TCCAGTAGTATGTCTTGAGCT
One_1a.23491-46	A	G	TTGGCCCAACAGTC	TTGGCCCGACAGTC	GCAGGTTTTCACCTCAACCC	(0,0)	1	AGTTATGTTACGGGTCTCATTACCA
One_1a.23626-48	A	C	TGAAAAAACCCCTTC	TGAAAAACCCCTTC	ATGCAAGGGAAGGGAAGTGA	(0,0)	1	CATCTCTCTGTGTGTAAGAAGGG
One_1a.24137-66	G	T	AGAGAGAGATGTTG	AGAGAGATATGTTG	ACTCTCTCTCCACTCTGCA	(0,0)	1	TCTTGGATGTCAGTACTACAACA
One_1a.25746-65	C	T	TGGCTGCCTGCAA	TGGCTGTCTGCAA	ATGAATCACATTGGCCATGCA	(0,0)	1	AACGTTCAAGTTCGTTGAG
One_1a.25904-44	A	C	ATAAAAAAATTTCA	ATAAAAAACATTTCA	GCAGGTGCATCTTAAGGGTG	(0,0)	1	TCACTCAAGAGGTAGAGCTGC
One_1a.27200-35	A	C	TGAGAGTATTGTGA	TGAGAGTCTTTGTGA	TGCAGGCCAGTTATAGATCA	(0,0)	1	TCTTCATCATCTTTATGCTTTCGTT
One_1a.27760-67	C	T	TGGTGCTCAACGAG	TGGTGCTTAACGAG	GACCTGCAGTCCACATCCC	(0,0)	1	ACCTCTGCGTAATTGGCTC
One_1a.28530-58	C	T	GCTGGCACACTAGC	GCTGGCATACTAGC	GGCCAGGTGTATGGACCCTA	(0,0)	1	TCCAACAGAGCAGTGTGTGT
One_1a.29135-58	A	G	ATCTGCAATCGTTT	ATCTGCAGTCGTTT	GCCCCGGGTCTCTTTAATC	(0,0)	1	TGCAGGATGAAGAGGAGGAA
One_1a.30563-32	C	T	TGAACTGCGTTTCC	TGAACTGTGTTTCC	TGCAGGCTTATTCGGGTTT	(0,0)	1	GCTTAACACGGAAGCCAAGC
One_1a.32514-40	C	G	ACCTTCCCTCCAC	ACCTTCCGCTCCAC	CAGCCACACCCACCAGAC	(0,0)	1	CCTGAGCAGCTATGGAGTGG
One_1a.35102-40	C	T	CTTTTACCGTACGA	CTTTTACTGTACGA	GGTTCATGCTTTACAACAGGGG	(0,0)	1	TAGCACCTCCCACCAGAACA

One_la.36888-37	A	G	TTTTGGATATTGA	TTTTGGGTATTGA	TGCAGGTTACGGGAAGAAA	(0,0)	1	AGTCATTGACTCTCGTGATCA
One_la.37709-28	G	T	ACGAGAGGCTCGGC	ACGAGAGTCTCGGC	GCAGGAGAGACGGTGGTTTA	(0,0)	1	CCCGAGGGATGTGAGTACTG
One_la.39597-30	G	T	TCTTGATGATTGAC	TCTTGATTATTGAC	TGCAGGCTCTGGGTTTATCT	(0,0)	1	ACTAGGTCCTTCTTGCGGC
One_la.39667-45	A	C	TGTAACAAAGATGA	TGTAACACAGATGA	ACCACATGGGAGGAGGATGT	(0,0)	1	AACAAAGATGCCAGGGTCC
One_la.40490-31	A	G	TGGATTTAAATGGA	TGGATTTGAATGGA	TGCAGGCACCATAAGCACTA	(0,0)	1	AGCCTACTTGCATAGCCTTCTC
One_la.40540-34	A	G	AGTAGCAATAGCAG	AGTAGCAGTAGCAG	TGCAGGACTCTAATTCATTGAGA	(0,0)	1	AACGGCAGACTGGGTACATG
One_la.40596-58	A	C	AACCCAAAACCCCTG	AACCCAACCCCTG	ATGAGTACTGTACGTGCGGC	(0,0)	1	TCGGTCAGTTGGTTGGACAC
One_la.41039-32	A	T	AAATAAAAAATAA	AAATAATAAAATAA	AGGGAAGGGAGCTGGGATTT	(0,0)	1	CTCTCTGTCGGGATGTGTGT
One_la.41570-62	C	G	GGTCACGCAAGGT	GGTCACGGCAAGGT	TTTGCAGAGAACGACAGGCT	(0.8,0)	1	CCTGCATCCTACCAGAGTGC
One_la.41669-43	C	T	TAATGCACAGCGTT	TAATGCATAGCGTT	GGAGGTTTCCCTGTAATGCA	(0,0)	1	GACTGCCTGCAATGACAAGC
One_la.42159-31	C	T	AGTTCCTCTCTACG	AGTTCCTTCTACG	AAGCATGCAGAGCTCCAGTT	(1.9,0)	1	ATGGGGGTGTATCCTGGGTG
One_la.42211-64	A	T	ATCTAAGAGGATGT	ATCTAAGTGGATGT	CCAACCACGTCAACTGAGCA	(0,0)	1	TGCATTAAATGTTAAACCGTTAGCT
One_la.44788-39	A	G	CACTGAGATGGATG	CACTGAGGTGGATG	TGCAGGTGGAGATGTGGTG	(0,0)	1	GCACAAACAGACTGGAACGTG
One_la.45935-29	A	C	TGGAAGGAGAAGCT	TGGAAGGCGAAGCT	GCTATATGAGCGACCGGTGG	(0,0)	1	CCCCCAGCTAAATAACAATGAGG
One_la.48100-30	C	G	CACAATACAAATGG	CACAATAGAAATGG	AGGATCTGCAAGTTGTACACA	(0,0)	1	CCCTCGCTGTATCATGTGCT
One_la.4900-40	A	G	TTTGTCTACCCCAT	TTTGTCTGCCCAT	TGCAGGATATTAACTTTAAAGCTGT	(0,0)	1	TCCATGCTAATTCTTGCAATTCT
One_la.51402-35	A	G	TGTTATCATGATAG	TGTTATCTGATAG	TGCAGGGGAGAGAACAGAATG	(0,0)	1	TGGTACACTGTAGGGCTACA
One_la.5313-43	A	G	GGGAAGGACCAGGA	GGGAAGGGCCAGGA	TGGCCATGAGGGTTTACTGG	(0,0)	1	AGGGTGCCATTTGGGATACA
One_la.53797-66	A	T	CAACTTTAAAAAAA	CAACTTTTAAAAAA	TGTTACAGACGGTGCCAACT	(0,0)	1	AGGCATTTTCTGAAGACGT
One_la.5407-55	A	T	GCAAGAGATTATTG	GCAAGAGTTTATTG	GCAGGAGGGGATAGTTGCC	(0,0)	1	ACAGAAACACAGCTAGCCCA
One_la.54542-52	A	G	TTGACCAAAAGGGG	TTGACCAGAAGGGG	GCAGGTTGTGATCGTGACCA	(0,2)	1	TGAAGAGACTACGCCCCCTT
One_la.55218-55	C	T	GGCCCAACTTCAAC	GGCCCAATTCAAC	CAGGCCATACTGAACCGAG	(0,0)	1	CCTTGGGTGCGGTTGAA
One_lb.56018-52	C	T	GAAGAAACGTGTGT	GAAGAAATGTGTGT	AAGCATGACGAGTGTCCGT	(0,0)	1	GCACTCCCTGCCCTATACA
One_lb.56276-30	A	G	CTAGAGCATGATAA	CTAGAGCGTGATAA	CTGGCCCTGAGTCGTAGAG	(0,0)	1	AATAGGCCGAGTGTTGCCG
One_lb.56339-60	C	T	GTGGCATCTCATTA	GTGGCATTTCATTA	CCGAAACTTTGGAGCGAACC	(0,0)	1	TCCTTTAACTGTGAGACACCT
One_lb.56528-40	G	T	TAGAAATGATGAGG	TAGAAATTATGAGG	GCAGGGTTGTGGCTGTTCTA	(0,0)	1	CCAAAGATGAAACCAAGTTCCTGT
One_lb.56760-39	G	T	TGTAAATGAATATA	TGTAAATTAATATA	TGCAGGTTCTGAGAAGAAATCAA	(0,0)	1	ACTTCATCAACCAACCCAT
One_lb.5780-62	C	G	TGTTTCGCCCCCT	TGTTTCGCCCCCT	TTGTGTCTGGCAGTGTTTCG	(0,0)	1	CAGTGGCAGGCACAATGATG
One_lb.5833-45	A	G	CATCACTAAGACCA	CATCACTGAGACCA	CGGCCTTATCGTCAGTCTCC	(0,0)	1	TGAAGTTGCATGGAAGTCATCA

One_lb.58946-27	C	G	TCTGCTGCCTTAGG	TCTGTGGCTTAGG	TGCAGGCCAAACAAGTTATTCT	(0,0)	1	ACACACACACTCCAAGCT
One_lb.58981-44	A	G	AGAACTCATTAATC	AGAACTCGTTAATC	CAGCCGATTCTGCTTTTGA	(0,0)	1	CCTCTGGACGGCATCAATCT
One_lb.59232-51	A	G	TGCAGTGATGCCAT	TGCAGTGGTGCCAT	ATTCTGCGTCCATCAGACC	(0,0)	1	TCCGGGATAGCCAGAACTCA
One_lb.60577-60	A	G	TGGACGAAGACTGA	TGGACGAGGACTGA	ATCGCACACAGGCCTCAG	(0,0)	1	ACATTGAGGTCGTGTCCT
One_lb.60684-45	G	T	GACGTTTGAGTTAA	GACGTTTAGTTAA	CGGGAGGAGCAACACAGTA	(0,0)	1	CATTGACTGACCCCTGCTT
One_lb.61920-50	C	T	TTTTTTCAAACCG	TTTTTTTAAACCG	GCAGGAAAGGTGAATTATTTCTGG	(0,0)	1	TCTGTCAAGACGTCATTACCA
One_lb.61967-31	A	G	GGCGTTCACGCAAT	GGCGTTCGCGCAAT	AACCTAGGACCTTGGCGTTC	(0,0)	1	GACGGAGGGAAGCATGGAG
One_lb.63191-29	A	G	TATTCCAATGTATA	TATTCCAGTGTATA	GCAGGAAAGTAGCATCTTCGC	(0,0)	1	GCAAGATAGCCTATCCAGTATACA
One_lb.63942-34	G	T	AGAGGGGAGTTGC	AGAGGGGTAGTTGC	CAGGATCAGTGGCTGTGTGA	(0,0)	1	AGTAGCATTGGTTCTGGCCC
One_lb.64367-65	A	C	GTGGACTAATACTT	GTGGACTCATACTT	ATGAGGCTCTGGGATGTGGA	(0,0)	1	CCTGCAATCTCATTACATAACGCA
One_lb.64886-42	C	T	ACCTACGCCTCACG	ACCTACGTCTCACG	CGCATGGCAGTGACATACCT	(0,0)	1	TGCATCTTAAGCCAGGGGAA
One_lb.67122-29	A	G	CCTCCGGATCATCT	CCTCCGGGTATCT	AGGTCACTAGGTCTCTCG	(0,0)	1	TAGGGTGTCTGCCTGAG
One_lb.68250-26	A	G	TGGAGGAAGAAGAG	TGGAGGAGGAAGAG	TTGCCCTCGTCTTGGAG	(0,0)	1	TTAACGGTGATGGAGCTGGC
One_lb.6939-43	C	T	GTGATGCGGGGGT	GTGATGTGGGGGT	GGCCTCAGAACCTGTTTGA	(0,0)	1	TCTGCATTCTGGTGATGGCT
One_lb.70246-46	C	T	GCTATGCGGACTCC	GCTATGGTGACTCC	TTTGTGGAGAGCCTGCGTAG	(0,0)	1	GTACGAGAAGGCTGGCAGG
One_lb.70297-45	C	G	GGGCCGGAAGTGG	GGGCCGGAAGTGG	CAGTGGGCTGTAAAGAGGGG	(0,0)	1	GCAGAGGAAGGGGGTTCTTC
One_lb.70694-28	C	T	CAACAAGTGCTTA	CAACAAGTTGCTTA	TGCAGGCTTGACTGGAAGG	(0,0)	1	ACTCCGGTATCTCTGTGCT
One_lb.70768-40	A	G	GTCTACTACTGGAG	GTCTACTGTGGAG	GGGCCAAGTTTACCCGTCTA	(0,0)	1	CCGTAATCGTCTGGCAGTT
One_lb.72136-33	C	T	CCTAAACCTCTACT	CCTAAACTCTACT	TGCAGGATGATGTCATGGTGT	(0,0)	1	ACAGTACAGGTTAGGCTGTAAGA
One_lb.72637-54	A	T	AGCGAGAACAAACA	AGCGAGATCAAACA	TCCACACTGAACTGGTTGCC	(0,0)	1	AGTGCACAGAAAACCTTGGGC
One_lb.72787-38	G	T	TTCTGGGGTTTGT	TTCTGGGTTTGT	CGTGAGCAGTCTACAGTATCAAC	(0,0)	1	TGTGTACCATGGGCATTGT
One_lb.72992-37	A	G	CAGAAGTACATGAC	CAGAAGTGCATGAC	TGCAGGTTTTAGCAAAGCCA	(0,0)	1	TCCCATATTTAGTCGAATTGGT
One_lb.73420-52	C	T	GAACTTTCGATTAA	GAACTTTTGATTAA	AGGTTGCAACATTTGGGA	(0,0)	1	AGGGAATCTGGAATCCTCCGA
One_lb.73656-45	C	T	TACAGTACGTATAT	TACAGTATGTATAT	ACTTCCAGGGGGATCTCTGT	(0,0)	1	TGCATTCTCAAAGACGGCT
One_lb.74472-27	C	T	CACTGCCCTGTGT	CACTGCCTCTGTGT	TGCAGGTTTCAAAGTAGACCA	(0,0)	1	CAGACCAGACAGAGGCATG
One_lb.74818-26	C	G	AAAACACCAGACGA	AAAACACGAGACGA	TGCAGGAAACAAAGAGACA	(0,0)	1	TGTAAATCTACTGCCCCATCGT
One_lb.75116-33	G	T	CGAAAAGCTTCAT	CGAAAATCTTCAT	TGCAGGGCTGAATTCAATTCA	(0,0)	1	TGTGTGATGTGAGCCTCA
One_lb.76686-31	A	C	ATAGTTTAATATTC	ATAGTTTCATATTC	TGCAGGTGATGTATGTGTGT	(0,0)	1	CATGGCCTTTGTGAGGGAGT
One_lb.76828-42	A	C	AGTCACCACCATAG	AGTCACCCCATAG	CAGGAGGGAAGGTTGGAGG	(0,1.2)	1	AGTTTACTACCACACCCCG

One_lb.77679-43	A	C	GAGATCCAACGACC	GAGATCCCACGACC	CCAAGCTGAGCTTCGGAGAT	(0,0)	1	GAAACCCAGGTAGCCAGTCC
One_lb.78278-49	C	T	TACATCACCTAGTA	TACATCATCTAGTA	AGCATTACCAAAAGATAGCATGG	(0,0)	1	CAAAAGCCAAAACGTGCAGC
One_lb.78365-62	A	C	GGCATCCATGTCAA	GGCATCCCTGTCAA	CGTCACGTGATGTCCCCATA	(0,0)	1	CTTCAGGTGCCATCTTGGA
One_lb.79240-40	A	G	TTCTTGCACTCTAG	TTCTTGCGCTCTAG	TTGCCCAATGAGGAAAGGCC	(0,0)	1	CAGCTGGAGAGGGCCATG
One_lb.79575-35	C	T	TTGTGGTCGCCTGA	TTGTGGTTGCCTGA	TTGGCTACACAAAGGACGGT	(0,0)	1	GACGGGTGCTAAGGTCAGG
One_lb.80431-46	C	T	GAAACCACAATGAC	GAAACCATAATGAC	TACTGGCCCCCTAGCTACAG	(0,0)	1	TGTCTGTTCTGTTCTTGCTTGT
One_lb.80929-65	A	G	AGACATGAGATTAC	AGACATGGGATTAC	CCAAAGGGGACAGACAGCTT	(0,0)	1	ATGAGCGGGAGAATGTAGCT
One_lb.83667-61	A	C	CCAAGTCATCCTGC	CCAAGTCCTCCTGC	GCAGGATGTCACGACACAGA	(0,0)	1	CGCAGGAGTCCCTAGAGGA
One_lb.85587-38	C	G	AGAGTGTCTTTTG	AGAGTGTGTTTGT	GCAGGCAGTCAGGATGTCTC	(0,0)	1	AGGCAGTCTTAATGACAAGTCCT
One_lb.88442-61	A	G	CGTTCAAATACCA	CGTTCAAGTACCA	AGTAACCAAAAAGTCTCTCGTTCA	(0,0)	1	GGCTTGCTCAAGTGTGACA
One_lb.8859-52	A	G	TGGGAGAAGGAGGG	TGGGAGAGGGAGGG	AGGGACTTGGCTTTCAGCTG	(0,0)	1	CTCTCTCCCCCTTCTCCCTC
One_lb.89789-50	A	C	CTGTGCCAATTGA	CTGTGCCCATTGA	CCAGACGGTCACTGTGCC	(0,0)	1	GGACAGGCAGCATGTGTGA
One_lb.90162-56	A	C	CGCAAGCATGCTAA	CGCAAGCCTGCTAA	TCAAGCGACCACCATGAC	(0,0)	1	CCGTGGCTCTTCCCTTTTAA
One_lb.90239-52	A	G	CCATCGCACAAACA	CCATCGCGCAAACA	CAACCTCTACCACGACCCAC	(0,0)	1	AGTTGTAAAAGAGGAGAGAAGTGT
One_lb.9134-28	C	T	CTCATTACGCATGG	CTCATTATGCATGG	TGCAGGACGTTGCTTATCA	(0,0)	1	AATGGCAAGGTCCCAGTTGG
One_lb.9362-41	C	T	AAGGTAGCTGTCAT	AAGGTAGTGTGCAT	GCAGGCTCTGGTAGTATTCACA	(0,0)	1	CGGGGTGCTATTCTCCACTC
One_lc.34041-34	C	G	GATGAACCAGACTG	GATGAACGAGACTG	GCGTTTGGAATATGCTCCA	(0,0)	1	ACAAGACCTCAGAGTGCTGT
One_lc.51810-33	C	G	CAGAGGACGAGCCG	CAGAGGAGGAGCCG	TGCAGGAGGAACCGCC	(0.5,0)	1	GCAAAATGGAGTGTACGGC
One_lc.5765-39	G	T	GTACGCCCGCAGCG	GTACGCCTCCAGCG	CACAGAGGCTGCTCAGTAC	(0,0)	1	TCCTACCTTGACCAACTCCGA
One_lc.70294-64	A	T	GAATGTAATAAAAA	GAATGTATTAAAAA	AACAAAAGGAACCTTGAACAACT	(0,0)	1	CTTTCGTTGCGCCACAGTG
One_lc.85338-32	C	T	ACAAAAGCTACTAC	ACAAAAGTTACTAC	TGCAGGCCTATTGTTGATGICT	(0,0)	1	TCCTCCTTTGCACTCTCT
One_lc.87896-59	C	T	AGGTAGTCGATTA	AGGTAGTTGCATTA	GAGGGAGAAGCATCAGAGGT	(0,0)	1	CCTGGCCCTTACACCAAGT
One_ld.80954-64	A	T	CACTCACACACACA	CACTCACTCACACA	CTGCGGGACTGATGTCTAC	(0,0)	1	GGGAGTTACCACACACTGCA
One_2.10623-54	G	T	GATTCTTGTGGGC	GATTCTTTTGGGC	GCTAATGTGAAACGTGCCTGA	(0,0)	1	TAGCCTGTTGCACAAACCT
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	GGTGGTGGCGACA	ACCAGCTGTCAGAGATGCAC	(0,0)	1	GGCATCCTTCTCTCTGTCGG
One_2.15628-38	A	C	CGGATACAGCAGCC	CGGATACCGCAGCC	CAACTCTCTGTCCAGCGGAT	(0,0)	1	CAATCTCCAGTCCCACAGG
One_2.16766-45	A	G	CTCCCCGATGCTTA	CTCCCCGGTGCTTA	GCCTCGATAAAGCCTGGGTC	(0,0)	1	TCCGGCAGTTCGATTTACA

One_2.20011-31	A	G	TTTCGGAAGACGCA	TTTCGGAGGACGCA	TCACGCCGGTCACGTTTC	(0,0)	1	GGGAGAGGCAAAGGTCAAGT
One_2.20130-27	A	T	TGTGCTAAATACAA	TGTGCTATATACAA	TGCAGGCTTTACTCTCTGGT	(0,0)	1	GGCATTAAAGAGAGCGAGGT
One_2.21362-59	A	C	ATAGATTACAAAAA	ATAGATTCCAAAAA	GCAGGGACACACACACTA	(0,0)	1	TCTTCCCTTGTGACTCTTCTTT
One_2.21498-40	A	C	AACATTTAAGCAAG	AACATTTAGCAAG	TCAGAGGTATGGCAGCCTA	(0,0)	1	AGCGCACAGATCTGGGAATT
One_2.21735-50	C	T	GGAGGCTCGTGTTA	GGAGGCTTGTGTTA	TGCAGGAGAGGGGCTTTA	(0,0)	1	TCCTCTGAATCAGTATCTCTCT
One_2.21990-53	A	T	TACTCTTACCAACA	TACTCTTCCAACA	GAAGTCGATGTGTGCAGCA	(0,0)	1	TGCAAAATTCGCATGAATTGATT
One_2.23230-33	G	T	GTTCTCAGTGCAT	GTTCTCATGTGCAT	GGTGTAAATCCAAAAACAGCCCT	(0,0)	1	TCAGAGATGTGCTCTGATATACAGT
One_2.24434-33	A	C	TATAGAGAGAGAGA	TATAGAGCGAGAGA	AGACTCTCTCCCTTCTGCAGT	(0,0)	1	TCAGTTCTTAAGTTCTGTGAGGT
One_2.24795-33	C	T	CAGCTAACTGGGTC	CAGCTAATTGGGTC	ACAGTCAATCAAGTCGAGC	(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	ACGACCTTTCTCAAGTGGC	(0,0)	1	GGCCAGCCAACAGAGAGTT
One_2.28376-51	G	T	TGTGCATGGGCAGT	TGTGCATTGGCAGT	CTGTGATACCCGATACCCGC	(0,0)	1	AGAGAAACAAGAGAGAACTGCC
One_2.28955-38	C	T	CCGCTCTCGGGCAC	CCGCTCTTGGGCAC	ATCAGCACTCGCCGCTC	(0,0)	1	CCCATGTATTTGGTTTGACGGA
One_2.29037-65	A	G	TGTCCTAAGCCCG	TGTCCTGAGCCCG	TCTCTCTGCAGAGTGTGA	(0,0)	1	GTCCGGGAGACACATGAAT
One_2.30761-49	G	T	ATGTGGGTTTTC	ATGTGGTTTTTTC	ACCTTGGACAGCTGTGAAA	(0,0)	1	CCTGGTGAGGACAACAAGCA
One_2.32804-64	A	T	GGATATAATAACA	GGATATAATTAACA	TCGGATTGGGAGTGTGTGG	(0,0)	1	GGATGGATCGGATGGCATGT
One_2.34398-57	C	G	ACCATCTCGGTCAG	ACCATCTGGGTCAG	GCTCTTAATCTTGACCCCA	(0,0)	1	CTTGGCGGTGATAGAGACGG
One_2.34943-66	A	C	TTTACATATTTTAA	TTTACATCTTTTAA	TGGTTAGATCTTAGGATAATGCAAC	(0,0)	1	TGTCTTAAACCTGGACCCCA
One_2.35396-68	A	G	TCATGGAATCACAC	TCATGGAGTCACAC	GTGAGAGTGGAGCTGTAGGC	(0,0)	1	GGGGAAGTGTGTCTGTGTGA
One_2.38070-37	A	G	ATATTCCAATAGTT	ATATTCCGATAGTT	GCAGGGAATGTTGTAGAAACACA	(0,0)	1	CTGCGAGACTGCTCACAAC
One_2.38869-26	A	G	TGTTAAGACAAAGG	TGTTAAGGCAAAGG	GGACAGTCTTGAGGGTGTTA	(0,0)	1	TCTCTCTCTCCAGAGCAGAC
One_2.39254-69	A	T	AGAACACACTCTCT	AGAACACTCTCTCT	GGTTCCTGGAGCTACATCG	(0,0)	1	TGACAAAGAGGAGGTGGCTC
One_2.39727-26	C	T	CGGGGAACATGGTG	CGGGGAATATGGTG	AGGTAGTGTGAATAGACGGGGA	(0,0)	1	CACCAACCATGATCCAGTG
One_2.40976-37	A	G	GCCATGTACACTTC	GCCATGTGCACTTC	CATGTGTGTGTGAGACGGG	(0,0)	1	CCCCACTTCTCTGCGAGTTG
One_2.41128-67	C	T	TGAATAGCGTCTCT	TGAATAGTGTCTCT	AGTGGCTGCCCTTGTCTCT	(0,0)	1	TCAGTCAGCTGCACAGAGAC
One_2.41231-65	C	T	CAAGCTACTGAGGC	CAAGCTATTGAGGC	TCAACCTGAGTTTCTGAGGC	(0,0)	1	GGATCGGGATGGTATAGCCC
One_2.41371-35	G	T	CCCTTCAGGTTTCAT	CCCTTCATGTTTCAT	GGATGTTATCCTTAGAGTATCCCTT	(0,0)	1	ATCATTTTCTGCTGGGCCA
One_2.44103-35	A	G	GAGAGTAAACATG	GAGAGTAGAAAATG	GGAGGAAGGAGAGGATGGGA	(0,0)	1	GGGCTTCTTTCCTTGATGTGA
One_2.45396-65	A	T	CCCCACATGTATA	CCCCACTTGTATA	AGTTCGAAGGAGAAAACCCCC	(0,0)	1	AGTGTTTGAGGACTTCACTGT

One_2.45475-58	A	C	GCAGGGTAACGCCA	GCAGGGTCACGCCA	ACAAGGTGTTGTGCAAGGT	(0,0)	1	AGACCTCTGCATCACGGTTG
One_2.45776-68	A	G	CGGAGACATCCTAG	CGGAGACGTCTAG	ATTGTGCAAGGTAGACGCCTC	(0,0)	1	AGAGAATAGGCCTCTCCGCT
One_2.45877-55	A	G	AGTATTATATGTC	AGTATTTGTATGTC	TCCCAATAATCGCAACCGT	(0,0)	1	GAGTGGAGCCACGACAAT
One_2.45957-54	C	T	GGTATATCGC	GGTATATTGC	CGTTGTGTCGGAATCTTCTCT	(0,0)	1	TTTCCATCCGCACAGTAGG
One_2.46012-53	C	G	CCTACTTCGAACAG	CCTACTTGGAACAG	GTCTCCAGAGGGTTGTGCAT	(0,0)	1	GCTCAGCTGACAGACAGGAG
One_2.46152-39	G	T	GTGCCCTGGTTCCC	GTGCCCTGTGTTCCC	TTTGTGCTGAGCAAGGTGC	(0,0)	1	GACCCATGCATCCATCTGCT
One_2.48609-47	A	G	GGTCCTCATGTGAG	GGTCCTCGTGTGAG	AGTTAGGCAAACCAACCGG	(0,0)	1	AAGGTGGCCAATAGCAAGAC
One_2.48637-56	A	C	TTGATTAAGGACAG	TTGATTACGGACAG	GCTTTTGCAGTGGCATGTC	(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	GCTCAATCGAAATCACCTTCA
One_2.51190-49	A	G	TTCTATCACCTCAA	TTCTATCGCCTCAA	AGCACCTAACCTGTAACTCT	(0,0)	1	AGGTGTTCTTAATGTTTGTACT
One_2.52203-44	G	T	CCAATTTGGTTGTT	CCAATTTTGTGTT	GCAGGTACAGTGAGCTCCAG	(0,0)	1	TGTCCTTGATCATTACAGAGCCA
One_2.52394-28	C	G	TCCCATACAGCACC	TCCCATAGAGCACC	GAGACAGGTCGCTCCATA	(0,0)	1	CCCTGGTCAGAAGATGTGCA
One_2.5338-43	G	T	GAAGTTAGTGCAGT	GAAGTTATTGCAGT	ACCACAGTACGTAGCTATGAAGT	(0,0)	1	ACATTTCCTGAAGCCATTACTGC
One_2.53715-43	G	T	AGCTGGTGCCAAA	AGCTGGTTGCCAAA	AGCTTCTTTCACAGGCAGCT	(0,0)	1	TGGTCCATCTCTTAACCCCT
One_2.54344-58	A	G	TGGACGAATGTATG	TGGACGAGTGTATG	CTCCCACCAATGGCGTGAT	(0,2)	1	AAACAACTGCATGGCGCTC
One_2.5654-67	C	G	GCACTTACTCAAAA	GCACTTAGTCAAAA	GGATGTGCCTGAGACCTACC	(0,0)	1	AGGGATTGATGATTATTGTTGT
One_2.5744-26	A	C	ATCATAAAAAAAAA	ATCATAACAAAAA	GGACGGAGGCTGGGATCATA	(0,0)	1	GTCCCTCATGTCGTGATGTGT
One_2.58200-50	A	T	TCAAAAAACATGTT	TCAAAAATCATGTT	TCTGTGGGGTATAGAGATACGGT	(0,0)	1	TAACCCCGCTGTACCAAC
One_2.58880-45	G	T	TTGAGACGCTCATC	TTGAGACTCTCATC	GGACAGCCTGGTGTGAGA	(0,0)	1	AGCAGGCTGATGTAGTGCTG
One_2.59897-41	C	T	CCACCGTCAGGGTG	CCACCGTTAGGGTG	CGGAGTTTTCCCTGGCACA	(0,0)	1	GCACCACCTAGACTGAACA
One_2.62240-45	C	G	TGTTTGCTCTTTT	TGTTTGCCTCTTTT	TGGAGAGGTATTGGTTCAAGGT	(0,0)	1	GCTACTAAATAACTCTCCATCAGTG
One_2.6248-65	A	T	TCTATTAGAAGGG	TCTCATTTGAAGGG	GGGAAAGAGGGAGGAGCCTA	(0,0)	1	ACTCAACCATGCCTCCTTGC
One_2.63402-51	C	G	CCATTAGCAGTTTG	CCATTAGGAGTTTG	CCAGAGCCAAGCCAGGTAG	(0,0)	1	GATCCCAGACCTGTCACTGC
One_2.63762-51	A	G	TCATTTAATGGACT	TCATTAGTGGACT	TGTGCTGTTGTGCTGATA	(0,0)	1	GGAATATTCCCCCTATGCTTTTGT
One_2.63984-53	A	G	AGCTCACAGATCCA	AGCTCACGGATCCA	GTCACAGACATACAGGAGCTCA	(0,0)	1	TCCACGTAACAACAGGCCTG
One_2.64150-27	A	G	AATAAAACAGTCA	AATAAAAGCAGTCA	TGCAGGAGAGAGGAGGAATGA	(0,0)	1	CCACAGGTCTGGAGGTGTA
One_2.6529-40	C	G	TCACCGTCTGTGAC	TCACCGTGTGTGAC	CAGGGTGCCTCCACAAC	(0,0)	1	CCACCTGGAGCAGTCAC
One_2.65369-59	A	G	AATAACAA.GAGCA	AATAACAG.GAGCA	GCAGGGGACACAACAACAAC	(0,0)	1	AGCTTGTCTGTTGTTGCTC



One_2.65998-48	G	T	CAGAGCCCTGCGC	CAGAGCCTCTGCGC	CAGGCTCTCACACTCCTGG	(0,0)	1	GCATGCACCTTTACGCTGA
One_2.66468-68	A	G	TGTATCCAAACATG	TGTATCCGAACATG	TGCTTGTGCCTCGCATCAA	(0,0)	1	TGAGGACACTTTATGGATTCTCC
One_2.70711-39	C	T	AGGTGCTCGTGCGT	AGGTGCTTGTGCGT	TGCCCTGTGTGATGAGCAT	(0,0)	1	GGCTGTGTAGAACGACCCC
One_2.71025-65	A	C	ATTACCCAGTGTGT	ATTACCCGTGTGT	TATGAATCCTCCCGAGCC	(0,0)	1	TTATGGATGAGCTGGGAGGC
One_2.71512-50	C	T	TTTGATTCAATCCA	TTTGATTATTCCA	ACCTTCTCATTTGTGGATTGAT	(0,0)	1	CTGCCAAGTCGATGTTCAAACA
One_2.72182-45	G	T	GCCATGTGGTGAAG	GCCATGTTGTGAAG	TCTTGATTAGTGCCAGCCATGT	(0,0)	1	TGTGTCGCTCTGTTCTGGAC
One_2.73281-30	A	G	TCTGTCCACATTCG	TCTGTCCGATTCG	GCAGGTGACAAAGTCTCTACA	(0,0)	1	CCACTGTACATAAACCATGCAGA
One_2.73487-56	A	G	AGCGCACATACTGC	AGCGCACGTACTGC	CTGTTCACACCCCTCCATC	(0,0)	1	GTTCTGTCATGTCCACCCCC
One_2.74998-68	A	G	ATTGTTGAGGTGCT	ATTGTTGGGGTGCT	TGCAGGGACACAAGGAGAGA	(0,0)	1	CCTGCAGTGTTCAAAGCACC
One_2.75586-34	A	G	AAATTAACTGAGG	AAATTAACTGAGG	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	GCCCCAGGATCATGTTGTA	(0,0)	1	AGAACTATTCTGGGTGCTGCA
One_2.76328-30	C	T	GCTGAGCCCTGTGA	GCTGAGCTCTGTGA	TGCACACCATACTCTGCTG	(0,0)	1	AAGAACGTCCAGAACACGCT
One_2.76532-58	C	G	GGAAATGCTTTCAC	GGAAATGGTTTCAC	TGCAGAATACCAATTCATACATCA	(0,0)	1	CTCTCGCCCCTTTACTGTG
One_2.77164-35	A	C	AGGCATCAGCCCTG	AGGCATCCGCCCTG	AGGGGGACCATTCAGACTA	(0,0)	1	AATGAGGAGAAGCTTGGCCC
One_2.78198-36	C	T	CTGTCAGCGTTGAT	CTGTCAGTGTGAT	TGTACTACACATTCCTGTCAG	(0,0)	1	CGTCCCAGAACAAACCTCT
One_2.80177-55	C	T	CGATTGACCAACG	CGATTGATCAACG	CTTACGGGATCGGTGACCC	(0,0)	1	ACTTACAACCTCATGCTAATCACA
One_2.80525-35	A	G	TGTTAGAACGCAAT	TGTTAGAGCGCAAT	CCTGCCACAAGGGGTGTGTA	(0,0)	1	GTTTGGCCCGCCTTACTTG
One_2.81573-50	C	G	AGAAGAGCAAAGAG	AGAAGAGGAAAGAG	CCTGCACACCTGAGGAGAAG	(0,0)	1	AATAGTTCAGTCCTTACATTCTCT
One_2.84041-67	C	T	CCTGGGCCGACCAC	CCTGGGCTGACCAC	CCTGGCCTACTCTGTGTACG	(0,0)	1	GCTCTGCTGGTCTCTGTCG
One_2.8522-64	A	G	ATGTAAGATAATCT	ATGTAAGGTAATCT	ACCAGACCTTCCCGAGATCA	(0,0)	1	TGAGCTGTGTGACATTATCCACA
One_2.85340-30	A	G	GCTTCACAAGGGAC	GCTTCACGAGGGAC	GCTGAAGGAGCGTCGG	(0,0)	1	CTGGCTGACCCCATGACATT
One_2.86889-62	A	T	CCAACATATGTGTT	CCAACATTGTGTGTT	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	CATCAGTACAGGTCCCCAC
One_2.90371-33	A	C	GTAACCTAATTAC	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	GGGTAAGAACAGATTGCGT	(0,0)	1	AAACAATGTTAACTCGAGGTTTGA
One_3RFP.12866-45	A	C	GCTTCTCATGCTGC	GCTTCTCTGCTGC	GAGCTTTGTGATTGGGGGAGA	(1,8,0)	1	TCTGACCAATCGCAGAGCAG

One_3RFP.18602-33	A	G	CTATCACAAGCAGC	CTATCAGCAGCAGC	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	TCTGTTTTGAGGACATTCAAGTTGT
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	GAGTTGGAGTGGTCCCAGT
One_3RFP.25184-65	A	G	CATCGCCACTTTGT	CATCGCCGCTTTGT	GCAGGTCGACGCTTTTAAAG	(0,0)	1	TCCCTCAGCTGTTACCAAC
One_3RFP.25749-53	A	G	GCACAGCATTGAGA	GCACAGCGTTGAGA	GCCACCACATTAGGAGGAG	(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	ACTGAGGTGATGT	GTCACCTGGACAGTTGATGGA	(0,0)	1	GCCAATCAGAATGTTTTCCCA
One_3RFP.28357-29	C	T	GCTCCAAGTCTCT	GCTCCAATTGCTCT	CAGGCTGGGTAGCTCCA	(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	GCAGGCCAACACATCAAG	(0,0)	1	GCGGTGTGCGTGTGTAC
One_3RFP.39193-43	C	T	GAGGATGCTCTCC	GAGGATGTCCTCC	AGAGTCTGTTCCCTGAGGG	(0,0)	1	ACCTTCTATTTCAGTGTGAGGA
One_3RFP.40708-40	A	C	ACACTCCAGTGGCT	ACACTCCCGTGGCT	TGTTAACACACTCTTCACACTCC	(0,0)	1	CCTTCCATCCTTGCTGCAGA
One_3RFP.43935-63	C	T	AACACATCGGTTAC	AACACATTGGTTAC	CACACCTCTCTCTAGCCAC	(0,0)	1	ATGCAATGGCCAGTGTGAT
One_3RFP.46202-49	A	C	CGTTAGTAGTTTTT	CGTTAGTCGTTTTT	GGGACGGGTGAGTAAGGTGA	(0,0)	1	CAGGCAGGAATGTACAAGCG
One_3RFP.46608-58	G	T	CCTTCATGAACTGT	CCTTCATTAAGTGT	TGGTGCATGAACACTGAGCT	(0,0)	1	TTCCGGATTGCTCTCACACC
One_3RFP.47148-54	A	G	CATGAATAGAAGGG	CATGAATGGAAGGG	GCCTTCTCAGCGATGACTC	(0,1,1)	1	ACCGTAGCTACACAATTCCC
One_3RFP.50303-37	C	T	TCTCTGCCTGCAA	TCTCTGGTCTGCAA	GCTTCAGCTCTCCACAACA	(0,0)	1	GGCACTGCAAAGATCTCCA
One_3RFP.52579-51	A	G	ATTATTAAC.TAAC	ATTATTAGC.TAAC	CACCTTGCTCTCTGCCTGTA	(0,2,1)	1	TCTGCTCTCCATGGTAGCT
One_3RFP.53804-31	A	G	ACGGATAAGGGGCA	ACGGATAGGGGGCA	GGTACTTCTTCTCTGGACGG	(0,0)	1	GACCTTGGTGTGCGTCTCAA
One_3RFP.53932-47	C	T	AACTAATCCATCAT	AACTAATCATCAT	TGTTGCCAAGTTGACTAAAGAACT	(0,0)	1	ACAGTGGATTATCTACCAACAGTAC
One_3RFP.56125-30	C	T	CAATTGTCTTATAT	CAATTGTTTTATAT	TGCAGGAGTTAACAGGAAGTCA	(0,0)	1	AGCCAATGTGTACTAGTGCCA
One_3RFP.60219-36	C	T	ATIGTTTCTCCGA	ATIGTTTTCTCCGA	TGACCTTGGTTGTCAGGTGA	(0,0)	1	CTTAAGCCGGAAGCCAGCT
One_3RFP.60536-30	C	G	GTGGTTTCATTGG	GTGGTTTGATTGG	CTGAATTTGGCTGGGGGT	(0,0)	1	TGTTTTGTCTCAAACTGGGGG
One_3RFP.62278-33	C	G	CCTCAATCCCATGG	CCTCAATGCCATGG	CACCACCGCTGTCTCAAT	(0,0)	1	TTCTCTCCCTGTTCCCCC
One_3RFP.6937-57	A	G	TTGCAAAATCCAAC	TTGCAAAGTCCAAC	TGGTTTACAGATGCATTGCAAA	(0,0)	1	ATGGTTTTAAGAGCTGGTTTGG
One_3RFP.70374-61	A	T	GCTCATGATTGGCT	GCTCATGTTTGGCT	GGGACTGATCATCAGGCTC	(0,0)	1	TCTTCAGTTGTGGTGAGCC
One_3RFP.70898-49	C	G	CTTATATCGTTTTT	CTTATATGGTTTTT	GCACCTTCGGCAATGTGAC	(0,0)	1	ACCTGGAGAACCTGACCATTC

One_3RFP.70952-46	A	G	TACATGGAGTTAA	TACATGGGTGTAA	GTAAGCTTTGAGGCCTTCA	(0,0)	1	TGCGAACCTGGAACATTGT
One_3RFP.71744-45	C	T	TGT.TGGCCGGCAG	TGT.TGGTCGGCAG	AGGCAACCAGAGTTTCTCTC	(0,0.4)	1	CACGGCTGCTCTTCTCTC
One_3RFP.72056-60	A	C	TTTTAATAATACTG	TTTTAATCATACTG	TCAGCCAACGCCTTGATCTT	(0,0)	1	ACCCAAGGACATCTAACCAGA
One_3RFP.72689-27	A	C	ACAGTGGAGACTAC	ACAGTGGCGACTAC	GCCACCCGAAGAAGAACAGT	(1.75,0)	1	CCTGTGAATCGTGGTGAGT
One_3RFP.74551-60	A	C	AACAACAAAACAC	AACAACAAAACAC	ACGGTCTCTCAGTTCCTCT	(0,0)	1	GCCAAGATATCCAGTTCAGT
One_3RFP.7464-69	A	G	CCACAGGATTCTC	CCACAGGGTTTCTC	TGCTGAGTACACACGTCCT	(0,0)	1	TGGCAGAATTAAACCACTGTTT
One_3RFP.76568-44	A	T	CCCTAGTACTTCTC	CCCTAGTCTTCTC	GAACCTTCGCCAGAGCTC	(0,0)	1	TTGGGGCTGGAACAAACAG
One_3RFP.77278-58	A	T	CAACAAAAATGGAA	CAACAAATATGGAA	TTTCCAGCCCAGAGTTGAG	(0,0)	1	CCATCACATCGGCACAAAGC
One_3RFP.80015-44	A	C	TAAAAATATAGGAT	TAAAAATCTAGGAT	TGCAGGGACAGGGGATTAAA	(0,0)	1	GTGGTGTCTCTTGGTCGTG
One_3RFP.80215-59	A	C	TTTCCGGAGTCCAT	TTTCCGGCGTCCAT	ACTATGCAGCTAAACGCCCT	(0,0)	1	ACAGCTGGATGGGATTTC
One_3RFP.81817-50	G	T	TGCTTTGGGCACCT	TGCTTTGTGCACCT	ATCCGGCCCAAGATGCTTTG	(0,0)	1	CAACAAGGACAGTGCCTCT
One_3RFP.83488-50	A	C	CTCACTTAATTTTG	CTCACTTCATTTTG	AGGATTTAGGGCTTGACCAG	(0,0)	1	GTGTTCTTTCTCTCTCAGGAAGGC
One_3RFP.89355-44	C	G	TCTGGGACGCGTC	TCTGGGAGGCGTC	TCTATCTTCTCCATGTTCTGGGA	(0,2)	1	AGTCAGGGAGCATGCAGAAC
One_4a.12382-55	A	T	CTACGCCAGAGCAG	CTACGCTGAGCAG	GGTGCAAAAGGAGTCAATGT	(0,0)	1	AGTGCACCCACACAACCATA
One_4a.13104-68	C	G	CTCCCCTCTGACAT	CTCCCCTGTGACAT	AACCGAAAAGTGTCTCCCC	(0,0)	1	ATCCACTTTCCACAGCTGGA
One_4a.14909-37	A	T	TTATAACACTTCT	TTATAACTTCTCT	GCAGGACTGTCACAGCTTCT	(0,0)	1	AATGCAGTCCAGGTGCG
One_4a.19795-33	G	T	CACGCGGAATCTG	CACGCGTAATCTG	TGAATGGTTTGTACAGCGG	(0,0)	1	TGCAACAGAGGTGGTTGGT
One_4a.21799-29	A	G	GGTGGGGAAGCTCT	GGTGGGGAGCTCT	GTGTGCGTCGCTGGAG	(0,0)	1	GCTGTGAAGTAAACCAGCGC
One_4a.22514-58	A	G	TTGTGTTATCTCG	TTGTGTGTCTCTCG	CCACTGTAGTGTCTGTGT	(0,0)	1	GGTGACGCTCCACATACAA
One_4a.24016-53	C	T	GTTCTTCAAGATG	GTTCTTTAAGATG	AGCAGCACACTAGCATGAGC	(0,0)	1	TTGCAACCAGGAAATGACCA
One_4a.25035-26	G	T	GGCTACAGATGTAC	GGCTACATATGTAC	TGCAGGAGCCATAGGAATG	(0,0)	1	AGTTCTCTGCAACATGGTGA
One_4a.25174-68	C	T	AAGGGGGCGGCAGG	AAGGGGGTGGCAGG	GCACCTCCGTGAACCTTGAT	(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	TGCAGGACTTTTGGCCACAT	(0,0)	1	GACCACTGCATCACTCAGGA
One_4a.32895-28	A	G	ATAGCTTATGGGAC	ATAGCTTGTGGGAC	TGCAGGAAAAGCTAGACTAGAAT	(0,0)	1	AGCTTGCTCCCTTGGAATA
One_4a.32932-27	A	C	GACTGATAGACCTG	GACTGATCGACCTG	TGCAGGTTAGTCACTTGATAGACT	(0,0)	1	TCTGTCAAGAGCTAACCTACAGG
One_4a.40410-31	A	C	ATTCAATTAATTT	ATTCAATCATATT	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	TGTGTAACCATCTCTTGCTGT

One_4a.44564-40	G	T	GCTGAGAGGGCAGT	GCTGAGATGGCAGT	TGCAGGAGTGAAAAATAGATTCTGT	(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	AGGAACATGGTGCATCTCTGG	(0,0)	1	ACTGTGTGTGTGTGCGTACA
One_4a.47733-44	A	C	ACCTCCAAACTCCT	ACCTCCACACTCCT	CTGACCACCTCTCTCAAACC	(0,0)	1	GGTATGTTCAGGGCCCTGTCT
One_4a.5042-49	C	T	GAAGCATCGGGGAT	GAAGCATTGGGGAT	GGGGCAAGGGAAGAGGA	(1.3,0)	1	TTGCCGTCACAACTTCTCT
One_4a.51425-41	C	T	GAACGAGCTGCGTG	GAACGAGTTGCGTG	GATGAACACGGCGCTGAAC	(0,0)	1	AGGGTGTCCAGCACAAACATC
One_4a.52596-64	A	G	C.TTCAGACTTCGG	C.TTCAGGCTTCGG	TGCAGGGAACAAGGTGTGA	(0,0)	1	GCCTTACTCGGCCCGAAG
One_4a.53531-43	A	G	CCGTGACACTTATT	CCGTGACGCTTATT	TGCACTGCAGAGGAGGGG	(0,0)	1	AGAGACGATAGCAGCAACATT
One_4a.58187-48	A	T	AGGTCAAATTCTCTG	AGGTCAATTCTCTG	TATCTGGGCTGGAGGAGAG	(0,0)	1	AGATGGCTCAGCTGAAGCAA
One_4a.59326-51	A	C	CAATACAATGGGTA	CAATACACTGGGTA	GCAGGACATAAATGGGCCT	(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	CACTGTTGAGAGCCGTCCT	(0,0)	1	TGGGACTAAGTTAAGAGAGTGTGT
One_4a.6566-43	G	T	TGTAACAGGACAAA	TGTAACATGACAAA	TGCAGGTGTCTCAGAGGGAT	(0,0)	1	CCATACCCCTACCCCTTATCA
One_4a.67550-44	C	T	AGATAGACCTGCAA	AGATAGATCTGCAA	GTGAAGAGCTCTGCCTCCAG	(0,0)	1	GCCTGAGGTCTCTGACGATG
One_4a.7119-57	A	C	TCAGAAAAAGTGAC	TCAGAAACAGTGAC	TGCAGGGTAAGTTGAATCAAAA	(0,0)	1	CCCCCAGACCATAAAGCCAC
One_4a.84616-28	A	T	AGTATCAAGTCTCT	AGTATCATGTCTCT	TGCAGGACGGAATACAGAGT	(0,1.3)	1	AGGCAGGAGGACATGATACT
One_4a.9496-33	A	C	GATTGTCTAGAGCTA	GATTGTCCGAGCTA	TGCAGGAGAAGCTTAGCAGG	(0,0)	1	GCTGAAGACATGCTTGGCC
One_ACBP-79	G	A	CAGAGGTCATGGTTCTA	CAGAGGTCATAGTTCTA	GAGGTGTGGGTGACCA	(0,0)	1	TCGACCGTGGCAGTG
One_agt-132	A	C	ACAGGAAAATCACGAGCCT	CAGGAAAATCCCGAGCCT	GACCCAGATCAACAACCTCATCCA	(0,0)	1	TGGTTGAGCTAAGGTCTTTGAAC
One_aldB-152	A	G	CTCAGGCATTACCTTC	CAGGCATCACCTTC	CGATCAGGTGACGCTAAAATTAATC	(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	TGCAGTTC AACATCAA	CTGCAGTTCAATATCAA	CGCAGGTCAAAGTAGTACTTAGCAT	(0,0)	1	GAGCGTCACTTCTGGAACCTT
One_cin-177	C	T	TCACGCACGGGACAG	CACGCACGGAACAG	CCTCAGACTAGTGACCGTACCTA	(0,0)	1	CGCTACCGTGGTTACGT
One_dds-529	A	G	AGCAATCCCATCTCTC	AGCAACCCCATCTCTC	CATAATGCTCCCCATCTTGAATTGG	(0,0)	1	CACTCAGCCCTTTAGGGAAGA
One_DDX5-86	C	T	AGGACTTCCTGAAGGAC	AGGACTTCCTAAAGGAC	CTCCACATTGATCTGGACGTA	(0,0)	1	TGCCACTTGGCCCAAGAG
One_E2-65	C	T	CATTGTCCCTAGGAAAG	ATTGTCCCTAGAAAAG	GTGGCACCCCTTTCTCT	(0,0)	1	TGCAACCTCAGTGGAGAACC
One_gdh-212	C	A	ATCTGTTACCAGAATGTTT	ATCTGTTACCATAATGTTT	CCTGTGTTGAAGTGGAGTAGGTTAA	(0,0)	1	GCTTTATACTGTAAGTGGACTGACCTT

One_GHII-2165	T	A	CACAAATGGAAATTGA	CACAAATGGTAATTGA	GGCATCAACCTGCTCATCGA	(0,0)	1	TGCACAAAGTGC GGAC
One_ghsR-66	A	T	AGGTTAAGCTGTGTATAAGT	TTAAGCTGTGAATAAGT	TGTAACAATACAAGGATAATGCAAATAATGTAGGT	(0,0)	1	GGTTATTAGGTTACTGTGCTGACTGT
One_GPDH-201	T	C	CTTCAACCTGGAGCC	CACCCCGGAGCC	GAAGCTGATCTAGACCTGTACCTA	(0,0)	1	TGGTATGATGGTGCTACTGGAAGT
One_GTHa	A	G	CAAGAACTAGAATGAAACAGA	AAGAACTAGAATGGAACAGA	CAAGAAGAATCAAGAGAAAGAGAGATGGT	(0,0)	1	CCTAGTGTATGCACATAACGTGTA
One_HGFA-49	A	T	CTAAAGCACCATTGTTGC	ACTAAAGCACCTTGTGTC	ACTTGCTACTTCAGGGTTTTGTGA	(0,0)	1	TGGCAGAACAAATCCTCAATGCATA
One_HpaI-99	C	T	AACGGAAGAAACCCCTCAA	AACGGAAGAACTCCTCAA	CCTGAGTTGTGTTCAATGGGCATAA	(0,0)	1	TGGGTCAATGTTTATTAGAGACAAAA
One_hsc71-220	C	A	ATTGGCCACAGCGC	ATTGGCAACAGCGC	ACAGCGAACTATTGATTTAAGGCTCAT	(2,0)	1	CGCAGGTAAATCACTGATCATGTTT
One_Hsp47	A	G	TTATTGACTATGGCACATTG	TTGACTATGGCGCATTG	CGTTCAAATAAATGCTGTTTGCCCTTT	(0,0)	1	GTGGTGTTTCGGATTTTTCTGAAA
One_IL8r-362	C	T	CAGCCAAAGAAGAGTC	AGCCAAAAAGAGTC	TGCTAGAAGCGTTGGTTATGATGA	(0,0)	1	CAGCAAAATTGAGAAGTCACTAGGAAAA
One_Ins-107	C	T	TACAGTAGTCCATACAACATA	ATACAGTAGTTCATACAACATAT	TTGAAATGAATGTGAAGGCA	(0,0)	1	GAACCTGCAAGAGGAGAA
One_KCT1-453	G	T	TGGTCAGGGTATCGCCATA	TGGTCAGGGTATCTCCATA	GGGAAAGTATGCTGTGGGATCAG	(0,0)	1	GGTTCTCAGTGAGTGTCTCTATG
One_KPNA-422	A	G	CTGGTATGAGAAGGCACA	TGGTATGAGGAGGCACA	TGGGCCCTGGGAAACATC	(0,0)	1	CCATAGCCACTTTCGATACAGGTAA
One_LEI-87	A	G	ACTCGCCACCTCTGT	TCGCCGCTCTGT	ACAGCGCATCCCCATAATGG	(0,0)	1	GCCTTTGTGGAGGTCAACGA
One_lpp1-44	C	T	TTGTGCTTTCTGACCTAT	TTGTGCTTTCTTAACCTAT	GGTCCAATAGGAGCTCAGACA	(0,0)	1	GGGAATGAACCAGACATGTGAATG
One_LRRC9_68810	T	G	CTTGGATGAAAAATATCA	CTTGGATGAAACATATCA	TGCAGGGAAATTACTTATGTGATCAT	(0,0)	1	AAGACAGATCAGTCCGAGAAAA
One_MARCKS-241	T	A	TTGCTTAAAGGTCTTCC	TTGCTTAAAGGTCTATCC	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	AGATGAAGGACATGGGTGAAAAAT
One_ODC1-196	C	T	CCACTCCGATGTCC	CACCTCCAATGTCC	CCGAGGTGGGATTCAACATGAC	(0,0)	1	TGTCCTCAGACCCAGGGAAA
One_Ots208-234	-	A	CACACGTTACATCAGATAACT	CACACAATGTTACATCAGATAAC	CAGCCGACATGCATCAGTTA	(0,0)	1	TGACCCCATGTTTCATGCT
One_Ots213-181	T	A	CTTTGAATTA AAAACATTTTT	CTTTGAATTA AAAAATTTTT	CCATAGTGATCACACAATACTCATGICT	(0,0)	1	TCTATCATCTGCAATCTGTGTACTAGACT
One_p53-534	C	A	TCCAAAGATCTGG	TCCAAATATCTGG	GACAATCTTAAAGCGTGGTCTTG	(0,0)	1	AACCTTTATCAGCCATCATCCAAT
One_pax7-248	C	A	AATTCAAAACGAAATGTG	TGAATCAAAACTAAATGTG	AGTAAAGGTAGTGATGCAATGATGCA	(0,0)	1	AACCGCATAGGACGTAAAGCA
One_PIP_3	C	T	AACACACATTCTCAACACA	ACACACATTTTCAACACA	ACAGAGTCAGGACTTGATATGTACAGA	(0,0)	1	CCTGACGAGGGTCTACTACACT
One_Prl2	G	T	ACCAATGGGACGAGTG	CCACCAATTGGACGAG	ACCTCTCTCTCTCAGGACTCTCA	(0,0)	1	GAGGAGGTGTGACACATAGATGGA
One_psme2-354	A	G	TGATGCAGTAGCTAAAG	ATGCAGTGGCTAAAG	TGGTCCTTCAGGTACTTTTCAGAGA	(0,1.8)	1	CAATGCCAATCTCACCACATGA
One_rab1a-76	G	T	TGTGGAGCAAGGTAAT	TGTGGAGCAATGTAAT	TCGCCATATTCTCTCCCTATCC	(0,0)	1	ATCCACTCAGACCCATATCTACCAA
One_RAG3-93	C	T	CATTTGGACTTCGGGACC	CATTTGGACTTTGGGACC	AGATAAAGATGGTTTCAAAGTCACCCA	(0,0)	1	GGGTGCCATCTAAAAAATATTGCT
One_redd1-414rd	A	G	CCTAAGTCAGTCACTGTAG	CCCAAGTCAGTCACTGTA	GTTGGCTACATCTTAAACACAATGG	(0,0)	1	CAGCCCTGGAGTACTGAATCAG

One_RFC2-102	A	G	ATCACGTGTATTCTTT	CACGTTGTGTTCTTT	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	CAGCCTTGTTCAACCCCATATCTA
One_rpo2j-261	G	T	CACATGTTTTACTCATTTGA	CACATGTTTTACTAATTTGA	GATTCTGAGATCATACAGTGGATTGGT	(0,0)	1	GCTTGTCTCTTTCAGCATACCTA
One_sast-211	G	T	CATCATTTGCATTATTG	CATCATTTGAATTATTG	TGTACTTAGTCCAATAAGCATTTCACAGT	(0,0)	1	TGGCTAGATTACATGGTCAACAAA
One_Six6-3	A	C	TAATATTACGGAA	TAATCTTTACGGAA	AGGCTACCTATAGTTCAGTTACC	(0,0)	1	GGCTACAGCGTTTATGGTGTC
One_spf30-207	G	T	AGGGACATCTTACCTCAAAA	AGGGACATCTTACCTAAAAA	AGCATTTACAGTTTTGTACATTTACAGTAAACA	(0,0)	1	ACCTACTCGTAATTTACAGGCAAAA
One_srp09-127	T	A	CAGCGAAGGATATGCT	CAGCGAAGGTTATGCT	CGGAGCTGGAATGACGACAT	(0,0)	1	AGGTTACAGAAATCCCTCTTAGAG
One_ssrd-135	-	T	CTGCGGCTTTGICTTG	TGCGGCTTTTGTCTTG	TGGAACCTCTAGTGTACTTCATTCTCA	(0,0)	1	CGTTCACGCTCCCTAGAAAGA
One_STR07	G	C	ACGCACACTGTCCTT	ACGCACACTCTCCTT	CACACCTGAGGCACAAGCT	(0,0)	1	GTATGTCTACCAGAGAGGTCAAGGA
One_SUM01-6	C	A	CAAGAT[AT]GAAATTGGTTTGC	CAAGATTGAAATTTGTTTGC	GCACAAGCCAAAAAGTTTCTCCAT	(0,0)	1	GGACATAGTTGGAGGCAGACAAAA
One_sys1-230	T	G	CAAAGCAAGTGATATATTAGTG	AAAGCAAGTGATATCTTAGTG	CTACCTGTCTAACAGTGAATGCTAACTT	(0,0)	1	TGAAACCATTAAAGCTCTTTGTAGGACAA
One_taf12-248	G	T	CCAGACAAAATCAAATTA	CCAGACAAAATAAAATTA	ACCTTCAATATGTTGGTGGTTACC	(0,0)	1	ACTAAACGCACAACAGCAACG
One_Tf_ex11-750	G	A	CAGGGTCGCTGCAC	CCAGGGTCACTGCAC	AGCAGGTGTAAGCATGTGTACTT	(0,0)	1	CCTGCTCTGCCTCAACAATGTTAA
One_txnlp-401	C	T	TGACTGCACTAGTTTAGAC	TGACTGCACTAATTTAGAC	GCCAGATCCCTTCAGTTGGA	(0,0)	1	GGCCATTTCAAAAGGCTGCAT
One_U1003-75	C	T	AGAGACTACTTCCTTTTTG	AGAGACTACTTCTTTTTTG	TCACGAGCCCCAGTCAGA	(0,0)	1	CGGGTTTCGGTGGTTAGTATTCTA
One_U1004-183	A	G	AAGTCCCTGTATTCTT	TCCCTGCATTCTT	GGTGTGACTGCTGTGTTTAATTGC	(0,0)	1	ACCATCATTACACAGCAATTCTGAGT
One_U1009-91	A	G	CATGTCTGTATGGACCC	TGTTCTGTGTGGACCC	CTCTGTCTTGAACGTGTGTCTGTT	(0,0)	1	GCCGCTGCTACTCTTCCT
One_U1010-81	A	G	CACACCAACGTTATGTAGAG	CACCAACGTGTGTAGAG	CAGCCCCTCAGGTAACGT	(0,0)	1	GTTGAGACAACAAAACGTCTACTGT
One_U1012-68	C	T	TGACGGGTGTTCTTGATAA	TGACGGGTGTTCTTGATAA	TCTATTACCATACAGGCCAGTACA	(0,0)	1	CCTTTGTGTCTTCCAGTCATGTGA
One_U1013-108	G	T	ACGGAATTCCTGTTGCCCT	ACGGAATTCCTTTTGCCCT	TCTGTGCTCTCCTCCAGGAT	(0,0)	1	CGAAACTGAGGAGTGCTCTGA
One_U1014-74	C	T	TTGACCTGCGCCAGTAT	TTTTGACCTGCACAGTAT	TCCCCTGCAGCAACTGTTTT	(0,0)	1	GGCAGAGACGGCATCCT
One_U1024-197	G	T	ACCTGACCCAACAAA	ACCTGACACAACAAA	CTGAACTGATCTACCGCTCTGT	(0,0.5)	1	GGAACAGATACTCCAGGAGAGATGA
One_U1101	C	A	TGGACGTATGCATATTT	TGGACGTATGTAATATTT	CTATGACATGTTATTTTAATTAGCCACCAACT	(0,0)	1	AGTATAGTAGGGAACCTTTTCGATCTT
One_U1105	T	A	CCTGTTTTTTTTAAAGAC	TCCTGTTTTTTTTAAAGAC	GCCTTAATAGTGTCCTCTGATCCCTTT	(0,0)	1	CCCTCTGTTGTCCAGACTCTTAG
One_U1201-492	A	G	AAGACTTCCTCCAGGCTC	ACTTCCCCAGGCTC	GCTTATGACGAGAGAAGAGATGCA	(0,0)	1	AGGATACTGAAGCCCAGAGACA
One_U1202-1052	T	C	CAAACCTTTTTCATCTACATTTA	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	GTAACCCCTTCATGTTGGCCATT	(0,0)	1	CTCCATGTCTGAATGTCCCATCA

One_U1205-57	A	G	AGTTATCATGGTCATCTCT	AGTTATCATGGTCGTCTCT	AGTAAATGGTTATTACGTAACGGATAAG	(0,0.8)	1	CAGGACAGTTCACATTCTAACAGA
One_U1206-108	G	T	AACATTGAGCTTCCC	ATAACATTGATCTTCCC	CTGAGATGGTGCTTTCTGAGGATA	(0,0)	1	TGGATGAAAGGGAAATTCTGTCAACA
One_U1207-231	C	T	ACATTCCTTGGCATTGC	CATTCTTGACATTGC	GGCCAAACTGACAGGGATCTATTAA	(0,0)	1	GGGTCCAGTCTGTACACCATCTAT
One_U1208-67	A	C	CCCAATGTGATTGTCAC	CCAATGTGCTGTCAC	ACTTGAATGTCTGTTCTGAGGTGAT	(0,0)	1	ACACAGTTGACAGTGGAGCAA
One_U1209-111	C	T	CTCACATCGAGATGATC	TCACATCGAAATGATC	GTCACGTAATCACGAGAAAGATACTAAATGT	(0,0)	1	TCTGCGTCTCCAGAGAGGTT
One_U1212-106	A	G	TTTTGACATACAAAAATA	TTTGACATACAGAAAAATA	CGTAATGACCTACCACCATATCAGT	(0,0)	1	TGGCATGACTTTAAACAATCCCAAAAAA
One_U1214-107	A	C	TAGTGACCTATTAAATTGC	TGACCTATTCAATTGC	CCAAATGTACTCCATGTTGGTTAGC	(0,0)	1	TGCCTGAGTATTAAGCTATATCATTGAAGTTTT
One_U1215-82	A	C	AATGAGACAAAGTATTTGGT	AATGAGACAAAGTCTTTGGT	GTTGCTTGGTTTCTGTTGGAGTAG	(0,1.9)	1	CTCCAGAAGAGGAATACCACAGTTC
One_U1216-230	A	T	CCTGGCTACTAAGTAAC	CTGGCTACAAAGTAAC	TGGGATCGGACGCTCAATAGATTTC	(0,0)	1	GTAATACAGAGTGAGCGTGATACATTGT
One_U301-92	T	G	CCATGGATTAAAATATTT	CCATGGATTAAACTATTT	AGCCAGTAGCCGATAATGTTTGTGTC	(0,0)	1	CCCTCCCAAATTGCTAGCT
One_U401-224	C	A	CACCTGGAAAGGACTGA	ACACCTGGAAATGACTGA	GGGTGGAGACGAACGGATTTC	(0,0)	1	GTACGATTTTTTTGTAGCCCCAAGT
One_U502-167	A	G	CTTCTTGATCAATAACG	CTTCTTGATCGATAACG	GCTTTTGTGCAATAGCTATGTTGCTTA	(0,0)	1	GCAAAGGTAGGCAGCAGATTG
One_U503-170	T	G	AAGTACTAAATC[AT]GTTTTACATTG	TACTAAAATCAGTTGTACATTG	GATTTCAGAATTGCCACGACAAGAA	(0,0)	1	GTGATTGGTACATGTCTGTGCGAGTT
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	TAGGCTCCGTCTCAGT	TAGGCTCCGTACTCAGT	GGTTGACTTTTCTTAACTTTAAATCTGTGATATTGT	(0,0)	1	GCTGAGCTAGTGATGGTACCATT
One_vatf-214	C	A	TGGTATTACTGTGCATTGAC	ATG[CG]TATT[A][AC]TGTTCAATTGAC	TCATTCTTTGCTGGAGCATT	(0,0)	1	GGCATACAGCAAAACAATTCAACCA
One_VIM-569	G	A	AAGTGTTTCCATACTCACTATA	AAGTGTTTCCATATTCACATA	TTCTGGGTGGACTCATTGATCAC	(0,0)	1	ATGCGTTATACCTGTAATCTGCAAGT
One_ZNF-61	C	A	CTATGGACATGATCTTT	TTCTATGGACATTATCTTT	CCATTTCATGTTCTATTACAGATATATTTGTGCA	(0,0)	1	CCTAGCTAGAGCTCAACAATATGCA
One_Zp3b-49	C	A	AGGCCCAATCCTT	AGGCCAAATCCTT	TCCTCGTGGTTATAGTTATAAAGATGTCAGT	(0,0)	1	TTGGCTCTGCACTCGGTTTA
Oki_101419-103-27	A	C	AATCCACTTCC	AATCCCCTTCC	CCCAATTGGAGACCAGGGTT	(0,0)	3	TCATTACAGACAGTTGGGAGACA
Oki_105105-245-23	T	G	GCCTTTTCCAT	GCCTTGTCAT	GCGTATCAAGCATCAACGCC	(0,0)	3	TCITTCAGCAAGGTTGGGCA
Oki_106172-60-38	C	T	GTGCGCATCAA	GTGCGTATCAA	ACTACTTGGCGTGTGTGTTGGG	(0,0)	3	TCCACTGAGAGGATGAGGCA
Oki_111681-407-38	C	T	AGAAACTGCAA	AGAAACTGTAA	TTCATCCCATTGGAAGCCCC	(0,0)	3	ACAGCTATATCTGTGCGCT
Oki_120255mod-99	A	C	GACTAAAACGT	GACTACAACGT	GGGTAGGCTAAACTAAATTACTCAAA	(0,0)	3	CATTGAAGGGTGGAATTGAAG
Oki_126619-265-31	A	C	GGATTGKGCAC	GGATTGKGCC	TGCGTAGTTAATTTACCTCGG	(0,0)	3	TACGCAGCACTGAAGACTGG
Oki_aspAT-273-37	C	T	CTGGACACAAT	CTGGATACAAT	ATGCTGGGAGAAACAGTGGG	(0,0)	3	CTCCTCTGTAAGGGTGGGT
Oki_RAD41030-31-36	C	T	GAAGGYCRGGG	GAAGGYTRGGG	GCTGAGCCTGGTCTGGG	(0,0)	3	TGGATACCCCAACTCTCTCA
Oki_RAD51585-47-25	C	G	GTGGCTCACTT	GTGGCTCAGTT	ACTTTCTAGTAGGCGTGTGGC	(0,0)	3	CAAAACCTGGCGTTGCAAG

Omy_myclarp404-111	T	G	CAAAGCCATACGTGGCC	AAGCCATCCGTGGCC	GCTGTGGTCTCATGGGTAAA	(0,0)	3	CCAGGGCAGGGTTGTCTC
Omy_RAD13034-67-21	C	T	CTCCCCGAACC	CTCCTGAACC	GAGTGATTCACGCCCTCC	(0,0)	3	TCTCTCCGTGGCCAGAAAC
Omy_RAD79314-58-25	C	T	CTCGCCCTGCG	CTCGCCCTGTG	CACACTGACTCATCCCTCGC	(0,0)	3	GAGTGTCTTACCGAGCTGCC
Ots_ARNT-29	A	G	GTGCTAGCTAC	GTGCTGGCTAC	CCACTGGCTGTGGAGCTT	(0,0)	3	GGGTTCAGTGATAGTTGGGCAAAT
Ots_crRAD9615-69-19	T	A	GGGAGTGGGAG	GGGAGAGGGAG	GAATGCAGGGCCAGGGAG	(0,0)	3	ACTCCAGACCATCCAGCT
Ots_myo1a-384-36	C	T	CACCACTACCA	CACCATTACCA	CTCCCCCTGGACTTTGG	(0,0)	3	GCTCTATTGCACCGTGTCTG
Ots_P53-25	G	T	TTCTGCAGGGG	TTCTGCAGTGG	GGAACTTCTCTCCCGTCTG	(0,0)	3	GCACACACACGCACCTCAA
Ots_unk9480-51-38	T	C	TCCASAAACT	TCCASAAACC	CAATCAGAACAAAACCTCCACAA	(0,0)	3	GGAAGTCTGTCTGAATGTTGTCTT
Oki_101419-103-44	T	C	GTICTCTACT	GTICTCCACT	CCCAATTGGAGACCAGGGTT	(0,0)	4	
Oki_105105-245-56	G	A	CTCATGCCAA	CTCATACCAA	GCGTATCAAGCATCAACGCC	(0,0)	4	
Oki_106172-60-47	G	A	AACGCGCTGAC	AACGCACTGAC	ACTACTTGGCGTGTGTGGG	(0,0)	4	
Oki_106172-60-47c	A	C	AACGCACTGAC	AACGCCCTGAC	ACTACTTGGCGTGTGTGGG	(0,0)	4	
Oki_106172-60-53	C	T	CTGACCGCYGC	CTGACTGCYGC	ACTACTTGGCGTGTGTGGG	(0,0)	4	
Oki_120255mod-105	C	T	AACGTCAGTTA	AACGTTAGTTA	GGGTAGGCTAAAATAAATTACTCAA	(0,0)	4	
Oki_120255mod-113	G	A	AGTTACTGG	AGTTACTAG	GGGTAGGCTAAAATAAATTACTCAA	(0,0)	4	
Oki_120255mod-115	G	T	TTACTRGGGTA	TTACTRGTGTA	GGGTAGGCTAAAATAAATTACTCAA	(0,0)	4	
Oki_120255mod-119	G	A	GTAGYTTCTWG	GTAAYTTCTWG	GGGTAGGCTAAAATAAATTACTCAA	(0,0)	4	
Oki_120255mod-120	C	T	CTTCWTGGCAT	TTTCWTGGCAT	GGGTAGGCTAAAATAAATTACTCAA	(0,0)	4	
Oki_120255mod-133	T	C	TGGCATAGTC	TGGCATAGCC	GGGTAGGCTAAAATAAATTACTCAA	(0,0)	4	
Oki_120255mod-135	A	C	GGCATAGYCAT	GGCATAGYCCT	GGGTAGGCTAAAATAAATTACTCAA	(0,0)	4	
Oki_120255mod-137	A	T	ATAGYCMTAGAT	ATAGYCMTTGAT	GGGTAGGCTAAAATAAATTACTCAA	(0,0)	4	
Oki_120255mod-141	A	G	ATAGYCMTWGATA	ATAGYCMTWGATG	GGGTAGGCTAAAATAAATTACTCAA	(0,0)	4	
Oki_126619-265-35	A	G	CAGCACAGCTG	CGGCACAGCTG	TGCGTAGTTAATTTACCTCGG	(0,0)	4	
Oki_126619-265-50	G	T	GATTCCGCACT	GATTCTCAGT	TGCGTAGTTAATTTACCTCGG	(0,0)	4	
Oki_aspAT-273-45	T	A	AATCCTTAACA	AATCCATAACA	ATGCTGGGAGAACAGTGGG	(0,0)	4	
Oki_RAD41030-31-37	G	A	GGGGSTCTGTG	AGGGSTCTGTG	GCTGAGCCTGGTCTGGG	(0,0)	4	
Oki_RAD41030-31-41	G	C	GGGTCTGTGG	GGGCTCTGTGG	GCTGAGCCTGGTCTGGG	(0,0)	4	
Oki_RAD41030-31-55	G	T	AGCTCGGGCTG	AGCTCTGGCTG	GCTGAGCCTGGTCTGGG	(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	
Omy_RAD13034-67-35	A	T	CTGAGTGGACA	CTGTGTGGACA	GAGTGATTCCCAGCCCTCC	(0,0)	4	
Omy_RAD79314-58-27	T	C	GTACRCCTGC	GCCACRCCTGC	CACACTGACTCATCCCTCGC	(0,0)	4	
Omy_RAD79314-58-31	G	A	ACGCTGCCCT	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	GCCTTGTGITT	GCAGGTGTGATCGTGACCA	(0,0)	4	
One_1a.54542-52-47	G	C	TTGACCAGAAG	TTCACCAGAAG	GCAGGTGTGATCGTGACCA	(0,0)	4	
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	
Ots_ARNT-29c	A	C	GTGCTAGCTAC	GTGCTCGCTAC	CCACTGGCTGTGGAGCTT	(0,0)	4	
Ots_crRAD9615-69-50	A	T	CTGGGAGGAGA	CTGGGTGGAGA	GAATGCAGGGCCAGGGAG	(0,0)	4	
Ots_myola-384-57	C	T	CTGCAGAACAC	CTGCAGAATAC	CTCCCCCTGGACTTTGG	(0,0)	4	
Ots_P53-28	G	C	GGCAGCTCCT	GGCCAGCTCCT	GGAACTTCCTCTCCGTTCTG	(0,0)	4	
Ots_P53-40	T	C	CTCCTGGGTCG	CTCCTGGGCCG	GGAACTTCCTCTCCGTTCTG	(0,0)	4	
Ots_unk9480-51-39	C	A	CTAAGGAGACC	ATAAGGAGACC	CAAATCAGAACAAAACCTCCACAA	(0,0)	4	

## Appendix 9. GT-seq SNP panel for Coho salmon

Assay	A1	A2	A1-Probe	A2-Probe	FWD Primer	Corr	Primary Flag	Rev Primer
Oki_101419-103	C	A	CTACTTGCCTGTCT	CTACTTGACTGTCT	CCCAATTGGAGACCAGGGTT	(0,0)	1	TCATTGAGACAGTTGGGAGACA
Oki_101419-103-27	A	C	AATCCACTTCC	AATCCCCCTTCC	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	ACACTTGATTACCATTGCGT	(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	AGTTATGACAGATT	AGACAACTAAGCAACCTCTGAGA	(0,0)	1	TCATCCAGCGCTGCAAATG
Oki_103577-70	A	T	ATGTGAAATGTGGA	ATGTGAATTGTGGA	AGCGAGAGGGCCTACAGTTA	(0,0)	1	CACATGAAGAATTCCTCCACA
Oki_103713-182	A	G	TGAAATGAAGATAC	TGAAATGGAGATAC	CACCAAGGCAGAGAGCTCTC	(0,0)	1	TTGTGGCACAATCTACTGT
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	ATGTAACCTCTCAA	ATGTAACGCTCAA	GCGTATCAAGCATCAACGCC	(0,0)	1	TCTTTCAGCAAGGTTGGGCA
Oki_105105-245-23	T	G	GCCTTTTCCAT	GCCTTGTCAT	GCGTATCAAGCATCAACGCC	(0,0)	4	
Oki_105105-245-56	G	A	CTCATGCCAA	CTCATACCAA	GCGTATCAAGCATCAACGCC	(0,0)	4	
Oki_105115-49	T	G	CTTTAAGTTATTTTC	CTTTAAGGTATTTTC	TGGGGTAACACTTTCGTAGCT	(0,0)	1	GCGTTGAGGTGACATGTAGC
Oki_105132-169	C	T	CACGATGCACTGAG	CACGATGTACTGAG	TGCCCTGAACCACATGTCAA	(0,0)	1	TGGAATAAAAACTGCAGACACTG
Oki_105407-161	C	T	CAGCCTTCGTTTGT	CAGCCTTTGTTTGT	GCAGCAGCTCACAGCCTT	(0,2)	1	TGTCCTGACAGCCTATAGGAT
Oki_106172-60	C	T	AACCTCTCATCGTG	AACCTCTATCGTG	ACTACTTGGCGTGTGTGTGGG	(0,0)	1	TCCACTGAGAGGATGAGGCA
Oki_106172-60-38	C	T	GTGCGATCAA	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	CTGACTGICYGC	ACTACTTGGCGTGTGTGTGGG	(0,0)	4	
Oki_106313-353	A	G	ACTTACCAACTGTT	ACTTACCGACTGTT	TCCCCATTACAATATGTCCCTGAC	(0,0)	1	TGAGTTTTCCAACCTGTGTG
Oki_106419-292	T	G	CTAAAACTGAAAGG	CTAAACGGAAAGG	TGCATCTGTAAGTAGCTCTGGA	(0,0)	1	AGTCTACCATCTACAAGTTCCTT

Oki_106479-278	A	G	ACTACACAGATGCA	ACTACACGGATGCA	CCCTCTAGGCTTTAGCAAACACT	(0,0)	1	TCAGTCAATTTGTTACGTGCTGT
Oki_107031-314	A	T	TTTTTGATTACT	TTTTGTTTTACT	AAAAACAGCCAGCGAAGGGA	(0,1,4)	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	TGAGCAGCAAGTCTACACC
Oki_109651-152	A	T	TTTTTTAAAGCTA	TTTTTTTAAGCTA	GGCTGTTGTCATATCATCCCG	(0,0)	1	GTCTACACACAGCCCAGGTT
Oki_109894-418	C	A	CTGGTTGCTGAAC	CTGGTTGATTGAAC	GGAGGTACCAGGTGAGCTCA	(0,0)	1	GACCAGACCATAGACATTGCCT
Oki_110078-191	T	G	TACACTCTAATGTC	TACACTCGAATGTC	ACACACAACTCGCTCTAGC	(0,0)	1	ACAGTGTCTGAAAGGGCCA
Oki_110381-77	A	G	GGGTTTAAGATACG	GGGTTTAGGATACG	TGAAACGTCCCAACTTCCC	(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	ACCAGCAACTCTTCTCTCC
Oki_114250-187	T	G	CGA.TAGTCTTTT	CGA.TAGGTCTTTT	GGCGATTAGAGCAGGTGCTAT	(0,0)	1	TGGGAAATGTGTTGAATGTCCT
Oki_114448-101	C	T	CACTGCACCCGTCA	CACTGCATCCGTCA	ATGTTGATCAACCACTGCA	(0,0)	1	CCTCTGCTGGACTAGGCTA
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	TTCTCTTAACCAACCGCAGC	(0,0)	1	ACCAAGACTATGCAAGGCC
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	ACCATAATTCACAAACGAGGCC	(0,0)	1	AGCAGAGGTCGAATGAACGG
Oki_120255mod-105	C	T	AACGTCAGTTA	AACGTTAGTTA	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-113	G	A	AGTTACTGG	AGTTACTAG	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-115	G	T	TTACTRGGGTA	TTACTRGTGTA	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-119	G	A	GTAAYTTCWTG	GTAAYTTCWTG	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-120	C	T	CTTCWTGGCAT	TTTCWTGGCAT	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-133	T	C	TGGCATAGTC	TGGCATAGCC	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-135	A	C	GGCATAGYCAT	GGCATAGYCCT	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-137	A	T	ATAGYCMTAGAT	ATAGYCMTTGAT	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	

Oki_120255mod-141	A	G	ATAGYCMTWGATA	ATAGYCMTWGATG	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	4	
Oki_120255mod-99	A	C	GACTAAACGT	GACTACAACGT	GGGTAGGCTAAACTAAATTACTCAA	(0,0)	3	
Oki_121006-412	C	A	CAAAACCTCAACC	CAAAACATCAACC	AGGCAGAGGACAGTGACTCT	(0,0)	1	TGCAGTACTCCAAGGGTTGA
Oki_122593-430	A	G	TCTCACCAGTCTTT	TCTCACCAGTCTTT	TCTGGGTAAAGTGTGCCTTT	(0,0)	1	TCGATTCCAGGGTCTCAAAAGA
Oki_123044-68	C	A	TT.AAAACGTTTT	TT.AAAAAGTTTT	ACTGCCATATCAGTATTGGGGG	(0,0)	1	TGCTATGTTAACTAAACCGGAATCA
Oki_123921-90	A	G	ATTGTAAATTATCT	ATTGTAAGTTATCT	GGCGACGGAGATGAAGGTAT	(0,0)	1	CCAAGCCTGAACCTTAGGG
Oki_124162-62	A	T	AGCAAAAATATAAA	AGCAAAAATATAAA	GAACTGCCAGGTGTCAAGTG	(0,0)	1	ACCTTTTTGTGCACCTTACATGT
Oki_125998-340	T	G	AACATACTGAGGGC	AACATACGGAGGGC	CGCAGGTCTTCTTAAGCAG	(0,0)	1	TCACCTTTATTCGTACAGGCCCT
Oki_126160-142	C	T	TTTGATCTAAAT	TTTGATCTGAAT	TGCTACCAACACCTGTTTG	(0,0)	1	TCCGGTCACTCCCTTGTACA
Oki_126619-265	T	G	CGGATTGTGCACAC	CGGATTGGGCACAC	TGCGTAGTTAATTTTACCTCGG	(0,2)	1	TACGCAGCACTGAAGACTGG
Oki_126619-265-31	A	C	GGATTGKGCAC	GGATTGKCCC	TGCGTAGTTAATTTTACCTCGG	(0,0)	4	
Oki_126619-265-35	A	G	CAGCACAGCTG	CGGCACAGCTG	TGCGTAGTTAATTTTACCTCGG	(0,0)	4	
Oki_126619-265-50	G	T	GATTCTCCAGT	GATTCTCCAGT	TGCGTAGTTAATTTTACCTCGG	(0,0)	4	
Oki_127645-235	C	A	GTGGCTAAAAA	GTGGCATAAAAA	TTGGTTGGATCTGGTGCTC	(0,0)	1	GCTACTTGTATGAACCTTGTATCGCT
Oki_128302-547	A	G	AACAAATAGGGATG	AACAAATGGGGATG	AGCTGGAGGGGATTCAGTA	(0,0)	1	GGGATAAGAGGGTTTACAGTAAAGT
Oki_128693-70	C	A	AGAATTACATTTTC	AGAATTAAATTTTC	AGAGGTCAAGGGTCAAGAGG	(0,0)	1	CATGTCCCCACCAAACTGGA
Oki_128757-232	A	T	TTTGGGAAAGCTTT	TTTGGGATAGCTTT	TCAAAACGTTATTGTACGATGACCT	(0,0)	1	GACCGGGTGCAACACAAAAA
Oki_128851-185	A	G	TAACCAGACTCCCT	TAACCAGGCTCCCT	CTCCAGTCTCCAGTTTACACA	(0,0)	1	GGCCCTCTCTGGAGAAAAC
Oki_129870-552	A	G	TGCTATTATGTTTT	TGCTATTGTGTTTT	AGGGAGACAGGCTGACATCA	(0,0)	1	AGGAACAGAAATGTTGCGTCA
Oki_130113-304	T	G	TACAAATTTATCGT	TACAAATGTATCGT	GGGAGAGTGTGGAATCCCC	(0,0)	1	CTTGTTCAAGGGCAGAACGA
Oki_130295-48	A	G	AAGCAATAAACAGT	AAGCAATGAACAGT	TGAGCACAAATATAATGTGGCTGT	(0,0)	1	AGAAAAATATTCTGTGTCCCT
Oki_130524-184	C	T	CAGGAAGCTGACTC	CAGGAAGTTGACTC	CGATTGGCTGTGGCATGAC	(0,0)	1	TGCTCTGCTGTGTGCTTACA
Oki_131147-353	T	G	AAAA.ATTTTTGGG	AAAA.ATGTTTGGG	GGCCTTTGTCAAAAGTAGTGCA	(0,0)	1	CCAGTCTCTTTGCGTCCAA
Oki_131460-243	C	A	TTTCCTTCTACATC	TTTCCTTATACATC	GGAACAATCGAGCAAGGAGC	(0,0)	1	GCTTGCCATGATAACCTCA
Oki_94903-192	A	T	AATTTAAAGTCAAT	AATTTAATGTCAAT	TCCAAACCGCATCGTAAAGT	(0,0)	1	CCGACATATGTGAATGCGAGA
Oki_95318-100	C	T	TTGAAGGCTGTAA	TTGAAGGTTGTAA	CGCCTGCACTAAATATGTAGACA	(0,0)	1	GGGTGAAGTGCCCTTTAAC
Oki_96158-278	A	G	CTATTGTAGGGTCG	CTATTGTGGGTCG	CCACCTCATCTCTTCGG	(0,0)	1	ACTGTCCAGTTTGTGACGGG
Oki_96376-63	A	T	GAGAGTTAAAAAA	GAGAGTTTAAAAAA	CTGCTACGTGTTGACAGTGA	(0,0)	1	TGTGGAACATGAACCTAAACGT
Oki_97660-149	T	G	GGTTACATACAGGG	GGTTACAGACAGGG	CACTGGTCCGGTCCAATGA	(0,0)	1	CTGTTACTCCCCAACCTGT

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	TGAAAGCTTGTGGGCTCTT
Oki_arp-105	C	T	GCTTGTGCACTACT	GCTTGTGTAGTACT	TGGCATTGACAAAGCAGGT	(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	AGTTCCCACTACTAC	ACGACACCCACAAGTTCCC	(0,0)	1	GCAATCAAACCTAAGGCCACACA
Oki_gdh-189	T	A	.ATTTTTTCTGTGA	.ATTTTATCTGTGA	CCTGTGTTGAAGTGGAGTAGGT	(0,0)	1	GCTTTATACTGTAAAGTGGACTGACC
Oki_gh-183	A	G	CATCAATACAATTT	CATCAATGCAATTT	ATGTGTTACTGGCTCAAACCT	(0,0)	1	TGCAGTAGAGCATGCTTGGT
Oki_gshpx-152	A	C	TTGCAACATTGTAG	TTGCAACCTTGTAG	TGTAGTTTGTGCGAGTTGTTG	(0,0)	1	GTTTCAATGATGAGTCCAAAAGT
Oki_hsc713-56	C	T	TGAGTCTGTGACT	TGAGTCTGTGACT	TGTGTTCTACCTCTTGTGTCTG	(0,0)	1	TCAAATTTCACTCCTTGACAAGTCA
Oki_hsc71p-313	T	G	TGTTTATTAACCTAC	TGTTTATGAACCTAC	TGAATGTGCCATGTAGTAGGT	(0,0)	1	GGGGCAGGCATAAAAGTAGA
Oki_itpa-85	G	T	TAAATAAGTTGTTT	TAAATAATTTGTTT	ACCACACTCCGTCTCCATA	(0,0)	1	AGCGACTTGACTCTGAACAGA
Oki_nips-159	G	T	TCAAAATGACATGC	TCAAAATTACATGC	TCTTCTCTGTGTCGGCATCAA	(0,0)	1	TCCAAGTCTGGTTAGAGCCCT
Oki_parp3-19	-	T	CCAATTTAAAGCC	CCAATTTTAAAGCC	AGCTTTGCCTCTAGACTTGTGT	(0,0)	1	ACCTTGAAGATCCATCTGGC
Oki_pigh-33	T	A	GTTAACAATTTCCA	GTTAACAATTTCCA	ACCGCATACCAAGTCATGCA	(0,0)	1	TCATCAGTTTTTCTTTCCATTGGGA
Oki_pop5-265	G	T	TACTCCTGGAATAG	TACTCCTTGAATAG	AGAAAACCATGAGGCTCCGG	(0,0)	1	CAGCTGCATTGAAGCACCAG
Oki_RAD100310-36	T	C	TAAAAATGCCGAGC	TAAAAACGCCGAGC	TGCAGGACTTGTGTTTACTG	(0,0)	1	TGGGAGAGAAAGGTATGTCTGT
Oki_RAD100331-48	G	A	CAGACCGCTCTCA	CAGACCACGCTCTCA	CGCCACCCAAATAACCCAGA	(0,0)	1	TTCCCAGGCAGTTCTGAGAC
Oki_RAD100388-66	A	G	AAACAGATAGTACC	AAACAGGTAGTACC	CGATTGTGTGAGGGGCCCTA	(0,0)	1	AATATTCCTCCAGGCACGC
Oki_RAD100479-50	G	A	ATGGACGTGTTTTT	ATGGACATGTTTTT	GGTCTTTTCCACACTGTCTGC	(0,0)	1	TCCAGAGAAAGGGCTCATCC
Oki_RAD100507-58	T	G	TTCTCTTACAAGCT	TTCTCTGACAAGCT	TGCAGGCTGTATAGTGGAG	(0,0)	1	CAGCTGGTCCACTGTCTATCA
Oki_RAD101032-66	C	T	TATGCGCTGATTTA	TATGCGTTGATTTA	TTGCACCATCTGGAGACTGG	(0,0)	1	CCCCACTACCAATCGAAGA
Oki_RAD101136-60	A	G	ACTGACAGTCTAAA	ACTGACGGTCTAAA	TGCAGGCCTCAATGTCTAAA	(0,0)	1	TGGTCACTTGTAACCTGTAGCTGT
Oki_RAD101478-57	C	T	AACCACCATTAACC	AACCACTATTAACC	AGAGCATATGCCACGTCTG	(0,0)	1	GCTCTCTCTCGCCACAAC
Oki_RAD101607-49	C	T	GAGATGCGTCCGTG	GAGATGTGTCCGTG	CCGGGGCTTTCAGAGAGATG	(0,0)	1	TGTTTTCCCCCTTTTGCCCT
Oki_RAD104180-61	G	T	AAAATGGCAGGATG	AAAATGTCAGGATG	ATATAGGCTGGGAGGGGAGGAG	(1.5,0)	1	ACAGCTGTGACTTGAACCCACA
Oki_RAD104335-44	T	C	CCGCTGTGAGGGGA	CCGCTGCGAGGGGA	GTAGTGCAAAGCTGAACGCC	(0,0)	1	TCACCTTGTCCGGTTCTTGG
Oki_RAD104946-41	C	T	GAGGGGCGCCCTGG	GAGGGGTGCCCTGG	CATGTGGCTGTAGTGGAGGGG	(0,0)	1	GCCCTGAATGACAGCTCAG

Oki_RAD106191-62	T	C	GAGAAGTGATCACC	GAGAAGCGATCACC	TGAGATCGAGCTTGCTGTGG	(0,0)	1	CCCTCCCGAGCCTCAAAATA
Oki_RAD106666-44	T	C	CGGCTATACACAGG	CGGCTACACACAGG	ACGCCAGTCTGATTGGAGTC	(0,0)	1	CGGTTTTGATTACCTGGCCG
Oki_RAD109528-59	T	A	ATTATGTTATTTTC	ATTATGATATTTTC	GGCCTCAAAGAGAAAGAGCA	(0,0)	1	GGAACCTCTGGAGAAGGTAAAGAA
Oki_RAD111744-32	A	T	GGGTCGAAGGTCCG	GGGTCGTAGGTCCG	CTTTGACAGACAGGGTGGGGT	(0,0)	1	CCATGCTCCAGAGTCTCGAC
Oki_RAD115799-69	C	G	ATCCTGCTCCGGCA	ATCCTGGTCCGGCA	CTGCATCGGTAGTGGTCGATG	(0,0)	1	CCAGGAGTTTGCCTGGAAT
Oki_RAD11844-57	T	G	AAACACTGACATAA	AAACACGGACATAA	TGCAGGTATTTCGGCTACACT	(0,0)	1	TCGCAGAAGGCCATTTTATGT
Oki_RAD12124-45	A	C	TCGAAAACTGTAAT	TCGAAACCTGTAAT	TGCAGGAACCTGATGATCTGA	(0,0)	1	CCAGGATTTGGTTCATTGCTT
Oki_RAD16167-62	C	T	GCGTGTCCAACAAA	GCGTGTTCACAAA	GGAGTCGGCTGTCTTGACT	(0,0)	1	GCAAACAGCATTTCTGTCGA
Oki_RAD23788-32	C	A	TATTATCTAAACA	TATTATACTAAACA	AGGGGGCTTAAACACAGCAT	(0,0)	1	TCTTTGAAATTGTTGCATGTTGC
Oki_RAD25212-35	G	C	TTCTGGGACATCCC	TTCTGGCACATCCC	TGCTAGTTCACAGCTTGTTCT	(0,0)	1	TGGAGAACCATCGAGCAACG
Oki_RAD27801-45	T	A	CACAGCTAACCGCA	CACAGCAAACCGCA	GCAGGTAGCGATGTGGAAGT	(0,0)	1	CCTCTTTGGTATTCTGTGCGG
Oki_RAD29028-42	A	T	ACTTCAGGAATTA	ACTTCCTGGAATTA	GTCACCTCTGAAGTAGCTGCACT	(0,0)	1	AGCCACAGGAATAGAAAGCAA
Oki_RAD29136-50	T	G	GTAAGGTTTCTCA	GTAAGGGTTCTCA	CCTTCACAAAGACAACATGACTGT	(0,0)	1	AGCAACGGAAATAGGCAAGGA
Oki_RAD34432-38	T	G	TGTGAATAGATGGC	TGTGAAGAGATGGC	TGCAGGATTTTGTGGAGAGGA	(0,0)	1	TCATCGGTCTACCTGACGGT
Oki_RAD345-59	G	A	CAGAGGGGCTTCCT	CAGAGGAGCTTCCT	GACACTTCTACTAGCGGCC	(0,0)	1	TGACTCACTACCGCTGAGGA
Oki_RAD35219-62	T	C	AGGATATGGCTCAT	AGGATACGGCTCAT	ACCGAACGGAGGTGAGGATA	(0,0)	1	TCAGCCACAGTCTTGGTGTG
Oki_RAD35990-63	A	C	CTCAAGAGGGGTAA	CTCAAGCGGGGTAA	TCAAGACATACAACAAAAGTGGT	(0,0)	1	CACAGTTAAAGACCCATTGCGG
Oki_RAD36669-48	A	G	CTTCCTATCAGTGT	CTTCCTGTCAGTGT	GGTCTCCTGTCTCTTCCT	(0,0)	1	AGAGGGCAAGCAGTCAGTTC
Oki_RAD37278-54	T	C	TTTTGGTGATTTGG	TTTTGGCGATTTGG	AGCGTGGTGTAACCTCAGAGG	(0,0)	1	CTCAAGTTAGGATTACGCCCA
Oki_RAD37493-51	G	A	CCAGCCGGGAACAC	CCAGCCAGGAACAC	ACGCATCACAGTGAGACCAG	(0,0)	1	AAAGTAACCGCTCACCGAG
Oki_RAD37537-45	T	C	ATGTACTCACAGTA	ATGTACCCACAGTA	AGTCCAATTGTAACACCATGT	(0,0)	1	TCCACCCATTACCACGAACC
Oki_RAD37698-60	T	G	A[GA]TTTTGGGAGTA	A[GA]TTTTGGGGAGTA	TGCTGAGGTCTTTCTGTGTC	(0,0)	1	TCTCTCTGGATAAGGTGAGTTTT
Oki_RAD37979-59	G	T	TATGAAGACATTCC	TATGAATACATTCC	GGGGTCTCTGTCATCAAAGGA	(0,0.5)	1	TCACTGTGTTTTCCCAAGGAA
Oki_RAD40179-68	T	C	CTGAAGTTGACTAC	CTGAAGCTGACTAC	AATGCCACCATCTACAGCA	(0,0)	1	AGAGCAGCACATAGGGTTTGT
Oki_RAD41030-31	T	C	GGGGCCTAGGGGCT	GGGGCCAGGGGCT	GCTGAGCCTGGTCTGGG	(0,0)	1	TGGATACCCCACTCCTCCA
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	ATTCAGCACATT[GA]	ATTCAGTACATT[GA]	TGCAGGGAGAGGAGAAGGAA	(0,0)	1	AGGTTGTGCGTAAGGTACAGT
Oki_RAD43051-33	G	A	CAGCCGGCTGAGCA	CAGCCGACTGAGCA	AGGAGTTGGTAAAGCCCTG	(1,0)	1	ACCAAGTTTCGGCTACATGCT
Oki_RAD43627-30	T	A	CATTTTAAAAATTA	CATTTTAAAAATTA	GCAGGCAGCATGTGTTTAAA	(0,0)	1	AGGACACACAGATAAGAGACAGA
Oki_RAD44268-51	T	C	TGAGTTACAAAAC	TGAGTTCACAAAAC	ACAGACAATGACCTACACTGAGT	(0,0)	1	AGTGCCTTTGAACAGGGTGT
Oki_RAD44444-52	G	A	TTACATGTAGGTCA	TTACATATAGGTCA	TGCCAGTAGGTAGCTCAGGT	(0,0)	1	AGGCCTCAAAGTGTAGCACAA
Oki_RAD45691-45	T	G	GAGTACTGCATG[TA]C	GAGTACGGCATG[TA]C	GGGCCCAGCTTATCTGATTA	(0,0)	1	CTGATTCGGTCTGGCCTGAA
Oki_RAD45878-53	G	T	ACAGGGGTTTCGAGA	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	GCAGGCCGATGGTATTGTT	(0,0)	1	GTTTCATGCCTTCCTGCCAG
Oki_RAD46974-68	T	G	CATTTTGAATGTTA	CATTTTGAATGTTA	TGGAACGGTTCACCAATTT	(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	CAAAGCGAGCGAT	CAAAGCAGAGCGAT	AGCCCTCTCTACGTGTCTCA	(0,0)	1	AACAAACGCACAAACATCGCT
Oki_RAD51428-47	A	G	GTTATAACAGCAGT	GTTATAGCAGCAGT	CTGCAGCCAGGGAGGTTATA	(0,0)	1	CCAGAGGAAACCCAGCAGAG
Oki_RAD51585-47	G	T	TCACTTGGTAGAGC	TCACTTTGTAGAGC	ACTTTCTAGTAGGCGTGTGGC	(0,0)	1	CAAAACCTGGCGTTGCAAG
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	CGCCCAACCAACACTAACCCCT	(0,0)	1	AGTGGCCTAACTTTAATTGACACA
Oki_RAD52785-52	C	A	GCAAC[AT]CGGCCACT	GCAAC[AT]AGGCCACT	CTAAACACAAAGCCCTGGCA	(0,0)	1	TTTAATTATCTACCTGTTCACTGGC
Oki_RAD53121-66	C	T	CATTCCCTCATTCC	CATTCTTCTATTCC	CTCTAAATACCCGGGTGCC	(0,0)	1	CACATTCTTGAGACAAGCAAGGG
Oki_RAD53655-42	T	C	GGGGATTTGAGAAA	GGGGATCTGAGAAA	GGTGAAGGTTTCAGAGGGGG	(0,0)	1	GCGCTCTCCGTGATCTCATT
Oki_RAD53703-50	C	T	GCCTCACGAGTGGT	GCCTCATGAGTGGT	TGCAGGAGGACACAACACA	(0,0)	1	CACAGCCTTAGACCACTGCA
Oki_RAD53750-45	A	G	CGTGACAGTAGAAA	CGTGACGGTAGAAA	CAGAGGAGGGGCCGTGA	(0,0)	1	CCCTGTATCAACCGGTGCT
Oki_RAD54918-40	T	C	TCATCTGAGGCCA	TCATCCCAGGCCA	CAGGCCAGCTGTGAGTAAA	(0,0)	1	ATAGGGTGCCATCTTGACG
Oki_RAD55090-49	C	A	GAGAGCCGGACGGG	GAGAGCAGGACGGG	ATCGCAGCAGGCTCTATG	(0,0)	1	CTCCATCTCCTTGGGGCTGG
Oki_RAD55690-46	A	C	GTAAAGACCCCTAA	GTAAAGCCCTTAA	CCACAAGGGCACAATGAGTC	(0,0)	1	GACCAGTAGTCGATAGGGC
Oki_RAD56094-43	G	T	CGCACCGTTCCTTC	CGCACCTTTCCTTC	AAGAGGTATGCCACGATCCC	(0,0)	1	AAACGAACCTCAACCTCCA

Oki_RAD57307-33	A	G	CTCAAGATTTTAAA	CTCAAGGTTTAAA	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	TTTTGTAAAAAAA	TTTTGTAAAAAAA	TGATTGAATACCTAGTCTCCCTATG	(0,0)	1	CGCCACTCAGAAGCCAATA
Oki_RAD59556-32	T	C	CATTAGTGTAAATA	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	GCTCTCTTTGTTC	GCTCTCTTTGTTC	CAGTGGATGAGAGGCTTGG	(0,0)	1	CCAAGACCAGCCCTGAGC
Oki_RAD60246-68	A	C	ATTCTCACGAAGTG	ATTCTCCCGAAGTG	GCAGCCCTACCTACCATTCT	(0,0)	1	GAACATCGCAGGCATTGAA
Oki_RAD61746-62	C	T	GCTATTGGAAAGA	GCTATTGGAAAGA	TTGGGGAGAACTGTGTGTGG	(0,0)	1	CGCCCATGCACTGTTGATC
Oki_RAD61821-61	A	T	TAAATAAACTCAA	TAAATAAACTCAA	TGCAGGCTAAACAGTACTT	(0,0)	1	TGACCAGAAGACCCCTCTGT
Oki_RAD64084-65	C	A	AATATACGTTTTAG	AATATAAGTTTTAG	AGGCAATTTTACATAGATGGCAA	(0,0)	1	TCGCAAGATCATTATCCAGTGGT
Oki_RAD64627-67	T	A	AATAAATAGGCTCC	AATAAAAAGGCTCC	GGTCTCTCTTGGTATTGGT	(0,0)	1	GGTTACATCCTCAATGGGTCCA
Oki_RAD65234-35	T	G	CCAGATTTTTTGT	CCAGATGTTTTGT	TGCAGGAAGAGGTTAGAAAAAGA	(0,0)	1	ATGTATGGACTTGACAAACAACA
Oki_RAD65388-37	C	A	AAAAAACCATGTGG	AAAAAACATGTGG	GTGTTGGTGGTCAGAGACAG	(0,0)	1	AAGCTGATTTCCTGGCAAAAT
Oki_RAD65610-58	A	T	GTTATTACCTGTGC	GTTATTCTGTGC	TGCAGGCCAGTTCAGTGTT	(0,0)	1	GGCAGTTAATCACGTGCACA
Oki_RAD65902-30	C	T	CTTGCCGGAAAAA	CTTGCTGGAAAAA	CCTTGTTACCAGGCTTTC	(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	AAGCCTCCTCTCACAGCTA
Oki_RAD67081-48	G	A	TGATGCGGTGACAT	TGATGCGGTGACAT	GGCTGTCGGTGTTCACAAT	(0,0)	1	AGCAATTCGATGACCATAGCT
Oki_RAD67114-64	T	A	ATGATATGTACAGA	ATGATAAGTACAGA	AGTCAGGTGAGACTCAAATCCT	(0,0)	1	GACAGGAGTCTACCTGGTT
Oki_RAD67674-60	C	T	ATCTTCAATTTAGG	ATCTTCAATTTAGG	TGCAGGAGTAAACAACCA	(0,0)	1	AGCACCAGCTGTTGCTCAAT
Oki_RAD68033-63	A	G	TATCACAATGTAGG	TATCAGATGTAGG	CCTGAACAAAACATTAGGAATCA	(0,0)	1	TCTCTCAATTCACTAGCCACT
Oki_RAD68190-55	G	A	GCTAGGGACGTGGG	GCTAGGAACGTGGG	TGAGGGGGTTGGGAGGGG	(0,0)	1	CCCCCATTAAGTCTCCACG
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	CTTAACCTTATCC	CTTAACACTTATCC	GCAGGATAAGGCACCTACG	(0,0)	1	CAGCACTGAATCATGCGCAG
Oki_RAD70600-60	G	A	AAAAAGGGACATCG	AAAAAGAGACATCG	CTGCACCTACCACCAACAGT	(0,0)	1	ACGATAAAGTCTGCACTCCGA



Oki_RAD70812-52	A	T	AGTATGATAAACTA	AGTATGTAAACTA	TGCAGGGGTGTTGATGTTA	(0,0)	1	AGACGACCCAGAGATTCTCA
Oki_RAD70820-47	A	T	ATACGGAGGTGATT	ATACGGTGGTGATT	TACCGACAACCTTGCTCTC	(0,0)	1	CAGACCCCATCCCAATCAC
Oki_RAD70963-47	A	G	GCAACAACCTGGTTA	GCAACAGCTGGTTA	GGTCAGACCTGCCTTATCTGA	(0,0)	1	CAGATCAGATGAGCCGACA
Oki_RAD71346-63	T	C	AGAGGATGTTGGGC	AGAGGACGTGGGC	ATGGGACTGGATTGTGCT	(0,0)	1	CGACTCATTTGCAACCTTGGT
Oki_RAD71442-69	G	A	TGAATGGAAGTTTA	TGAATGAAAGTTTA	AGGGGTGTCTTCAGTATGACA	(0,0)	1	AGACAGTGCACCAACGTTGT
Oki_RAD71948-56	A	G	TTATTGAAATCTAC	TTATTGGAATCTAC	AGGACCAGCTTAGCCTCTCC	(0,0)	1	CATCAGGTCGAGGTAGGAG
Oki_RAD72095-45	A	C	AAAATAAATGGAGC	AAAATACATGGAGC	GGACACACAAATCACAGGGGA	(0,0)	1	GCAGCATTGCCCTGAAGTA
Oki_RAD72101-67	A	G	GCTTGCACAGAGCA	GCTTGCAGAGCA	TGCAGGTGCGAGAAACAAGA	(0,0)	1	GCAGGAGTGGTTGGAATTGC
Oki_RAD72759-48	A	G	CATGAGACTGTAAC	CATGAGGCTGTAAC	CCAGGTTCAATGGTAGCTAGCT	(0,0)	1	AGGGGGTGAATACTTTCGCA
Oki_RAD72979-40	G	A	GAGAATGATGAAGT	GAGAATAATGAAGT	TGCAGGTGTGTAAAGGACTC	(0,0)	1	TCGGGTGATTCTGAGGCTA
Oki_RAD73094-68	A	G	AAACACATACGCAC	AAACAGTACGCAC	AGCGCCACCAGAACTAAACA	(0,0)	1	TGCATGTACGTATGTGTGCG
Oki_RAD73130-59	T	C	AATACCTCCTAACG	AATACCCCTAACG	TCAGCCTGGTGAGCAAAACA	(0,0)	1	TAGCAACAACAGGAGGCAG
Oki_RAD73234-42	T	C	TCTCGCTTCGATT	TCTCGCTTCGATT	TTGGGCCAGTTATCCCTCT	(0,0)	1	TAACAGGGTGCAACCACAA
Oki_RAD75909-38	T	C	GGTGGATGTTCTGC	GGTGGACGTTCTGC	CCAGTCTACTTCCAGCTGGTGG	(0,0)	1	AGTCTGTCTCTGAGGGAAG
Oki_RAD75911-69	G	T	GACCTTGAAGGCAA	GACCTTTAAGGCAA	ACTAATCAGCGGCTCACCAC	(0,0)	1	TACCCTGTGTAGCACCCCT
Oki_RAD76218-42	T	G	ACCATTTCCCAGG	ACCATTGCCCAGG	CCACAACCAGATCAGACCA	(0,0)	1	AGCCTGTGGAGTTGAGGTG
Oki_RAD77207-61	A	G	GGAACATTTAGGA	GGAACGTTTAGGA	GACGGTCTGACTGTGAGGG	(0,0)	1	CCTGGGGCTTGGCATTAGAT
Oki_RAD77210-64	A	T	GTGCAAGA[TC]ATTA	GTGCAATGA[TC]ATTA	TGAACAGCCCTGCTCAAGAA	(0,0)	1	TGTTTTGCCATTGTGTTCCCT
Oki_RAD77803-60	G	A	TCATATGTTGTAT	TCATATATTGTAT	TGAATGTGTCTGCTAAGTGCA	(0,6,0)	1	TCTTCTGTAGCGTCGTTGG
Oki_RAD77883-62	C	G	TGGGGGCTCGTACA	TGGGGGTCGTACA	CACCAGCGCTCAAAATTGT	(0,0)	1	TGCATCGGCTGTGAGATTAA
Oki_RAD78112-64	T	G	AATAAATGCACGAG	AATAAAGGCACGAG	ACCCGCATCATACTTAGCA	(0,0)	1	CTGTGTCCAGGCATGTGGTA
Oki_RAD78543-33	A	G	CTCATCAGCATTCA	CTCATCGCATTCA	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	GCACAGTGACG	TGCAGGGAGGATAGACAACC	(0,0)	1	TGCTGTTATTACCCCTCGT
Oki_RAD80982-68	T	C	GCCGGGTATCGTCG	GCCGGCATCGTCG	CAGCCTAGTGACACCTGC	(0,0)	1	GTCCCCACCGTCTCCATAAC
Oki_RAD81387-37	G	A	CTATCTGACTAGTT	CTATCTAACTAGTT	GCAGGAGTCCATGTCTACTCAG	(0,0)	1	AGTCCAATGGCTCCTGCAAT
Oki_RAD82856-48	C	T	CGCTACCACTCGA	CGCTATCAGTCGA	TGCACATGACCAGTACTCGC	(0,0)	1	GATCCACTGCATGCTCCAGT
Oki_RAD83766-63	T	A	AAAGACTGAGGAAA	AAAGACAGAGGAAA	AGCAACATGACCACGTCCT	(0,0)	1	TTGTTTGTCCGGCTCCTGT

Oki_RAD83875-36	G	A	TGTGATGTAGCTGC	TGTGATATAGCTGC	AGCTTGGCAAGGAAGTCTGT	(0,0)	1	GAAGTGGGCTAAACGCTCCT
Oki_RAD84577-58	T	G	ACCTACTTCTGCCA	ACCTACGTCTGCCA	CAGAGAGAAGCACAGCACCTA	(0,0)	1	TGCTCTGCTTCCTGTGTTT
Oki_RAD85448-48	A	T	ATGGAGATATCTAC	ATGGAGTTATCTAC	AGGCAAGCAATGGAGTGGA	(0,5,0)	1	GGAGGCATCTCTGAAATGCTG
Oki_RAD85949-47	G	A	TAACACGCGTTCTA	TAACACACGTTCTA	TCAGTTAGTGGGTCTCCTCTCT	(0,0)	1	TCGTCAACAGTGCAGTAGGC
Oki_RAD86627-60	A	T	AGCATTATCACTTT	AGCATTTTCACTTT	TCCTCCAAACCTGCTTCG	(0,0)	1	CTTGGGTAGCAAATCAGCCA
Oki_RAD87141-55	T	C	AGCTCATTCTTTT	AGCTCACTCTTTT	ACCACCCAGTAAGGCTCCTA	(0,0)	1	TCTGTCTCCAGACTCCTGT
Oki_RAD87446-62	G	A	GTGTATGCAATCCC	GTGTATACAATCCC	TGTGTGAGAGAGTGTGCGTG	(0,0)	1	GGGGAGCCCTGCATTAAGG
Oki_RAD87621-67	T	G	C[CT]GCATTGTGCTA	C[CT]GCATGGCTGCTA	TGCCCCAAGGAATGACTACC	(0,0)	1	CAGCCCTGGTTGCATCCTTA
Oki_RAD87777-48	A	T	GCCAAACAAGACTT	GCCAACTAAGACTT	TCGTAAATAAGCGCGCCAA	(0,0)	1	AGGCTCTAGTCTATCTGGGT
Oki_RAD88551-51	A	G	GAAAGCATTGTCAT	GAAAGCGTTGTCAT	GGCTAAGGGCTACGTAACC	(0,0)	1	TGGCTCCCGAGATTCTGAGA
Oki_RAD89259-51	T	G	TATTACTGAACAAT	TATTACGGAACAAT	GCAGGGTATCTGAGGCACAT	(0,0)	1	GGCAAAGAACAGCTATTATGACCA
Oki_RAD89374-40	T	G	GTACTTCCAAGAT	GTACTTGCCAAGAT	TGCAGGCAAGGGAAGTTAAC	(0,0)	1	CTGGTACTTAAGCCAGCAGGT
Oki_RAD91362-68	C	A	ATGGCACAATTTT	ATGGCAAATATTTT	GCAGCAGAAGAGGCACAAGA	(0,0)	1	ACTGTAGAATTGCTAAATCCCACA
Oki_RAD91430-44	A	G	GCTGCTACAAATGG	GCTGCTGCAATGG	TGCGAGGCCCTTCAATGTTA	(0,0)	1	AGTCTCACAACCCCTCTCT
Oki_RAD91470-66	C	A	AGGTCACTGCTGAG	AGGTCAATGCTGAG	GGACCTGAACAAGTGGAGCT	(0,0)	1	TGCAATGCATGGAACCTCTCA
Oki_RAD91478-52	T	C	CGGCTATAGCTGTG	CGGCTACAGCTGTG	TGTAGCAGTCTAATGACCGGC	(0,0)	1	GCCTAGTTGCTGACAATGC
Oki_RAD91907-38	T	G	ACTGGTTGTGAGAC	ACTGGTGGTGAGAC	ACAGAGGAGCACACTGGT	(0,0)	1	GGGCAGAAGGTAAGATATCAGACT
Oki_RAD92875-31	C	T	ACACCACGCCGCTC	ACACCATGCCGCTC	CCAAGAGGGTGTCCATCGAC	(0,0)	1	TCGCCAACCCATCTCAACAT
Oki_RAD93028-59	A	G	GCTCACAGAACTCA	GCTCACGGAATCA	GGTGTGTAACTGTCTGGACA	(0,0)	1	GCCAAGCCAATTAGCTGTGC
Oki_RAD94215-66	A	G	GAGGATAAGGCGGA	GAGGATGAGGCGGA	AAGGAGACACGATGGGAGGA	(0,0)	1	CTGCAGCTCCAGATGATCGA
Oki_RAD94241-30	C	G	CAGTAGCCTTTAT	CAGTAGGCTCTTAT	TGCAGGTGGGCAACAAGATT	(0,0)	1	CTGTATCTCTGGACCATGCAGT
Oki_RAD96072-42	A	G	TGAAGGATAAGCAC	TGAAGGGTAAGCAC	AGGGCACAGGAGGAGTCATT	(0,0)	1	GCAGTGGGAGTTTGTGTGC
Oki_RAD96498-69	C	A	GCCAAACGCATCCT	GCCAAAAGCATCCT	CCACAAGGAGTTGCAAGAGCAT	(0,0)	1	CATAGGGCGCCGCATAATTG
Oki_RAD97325-35	T	A	TCTTGGTCAGCTCC	TCTTGGACAGCTCC	TGCAGGGAGCTACAATGGTA	(0,0)	1	GCTCACCTCTTAGCCCTCT
Oki_RAD97993-40	C	T	TGGTTCCGTAATAC	TGGTTCTGTAATAC	GCTGCCCTGAGAACAGAGTT	(0,0)	1	CCTGTCTGTGTATGAGGTGG
Oki_RAD98280-45	G	C	TTTACAGTTGGTTT	TTTACACTTGGTTT	GGTCACGAGTCTCTTGAGC	(0,0)	1	GGTGTGATGTGGCTGAAACC
Oki_RAD98485-66	A	G	TATTCTAATTGGCA	TATTCTGATTGGCA	GGGACCTTGACTGTTAAATTCAA	(0,0)	1	AGCACATGTGAAAGCCGAGA
Oki_RAD99931-47	T	C	TTACCATCAATATG	TTACCACCAATATG	GCTCCAGAGGCTCCCTTTTC	(0,0)	1	CGCTCACTCCCTCCATCAAT
Oki_sast-230	A	G	AAGTAGTATTGTGT	AAGTAGTGTGTGT	ACAGTAGTATCTATGCCTTTGAGCA	(0,0)	1	CGCATTGGCTAGATTACATGG

Oki_SECC22-67	T	G	TCCCAACTGTCTGT	TCCCAACGGTCTGT	ACTGTTGAAGACTTGTTTTCCA	(0,0)	1	ACCACTACAGGATGACTACCT
Oki_Six6-3	C	T	ATTAGATTCAAAT	ATTAGATTTAAAT	ACAGCTCTATTCAATGTTACTCG	(0,0)	1	GCGAGCAATTATTCGGGCAA
Oki_srp09-107	A	G	TGAGAGGAGAAATC	TGAGAGGGGAAATC	AACGGAAGAGAACGGAGCTG	(0,0)	1	GCAGCGAAGGTTATGCTCTC
Oki_sys1-141	T	G	TGGAAATTAAGTGA	TGGAAATGAAGTGA	TGGAAACATTGCACACCTCTCA	(0,0)	1	GCAACCAGCACCATTTCAGT
Oki_taf12-40	-	T	CCTTTTTAATGCT	CCTTTTTAATGCT	GTGTGTGATTGTGAGCTCCAC	(0,0)	1	GAGTGTGTGATTTGGCCAGT
Oki_thyK-100	T	G	ATTACCATTAGACT	ATTACCAGTAGACT	CCACCCTGCAACTCTGATCA	(2,0)	1	CCAATCCAAGTCAACTCCCC
Oki_txnlp-35	C	G	AGCTCTCTCTGTG	AGCTCTCTCTGTG	GGCAGGACCAAGGTCTTCC	(0.5,0)	1	GATGGTCTTCCCTGCCAGG
Oki30_5473492	C	T	TCCTTTGTACAGC	TCTTTTGTACAGC	TCTGGAAGCACACCAATGAA	(0,0)	1	TCAGTTTTGCGCATAGAAATTG
Oki30_5551409	T	C	TTTAACAGCTTG	TTTAACAGCTCG	CAGGGAAGAGGACAGTGTGA	(0,0)	1	CTGAACAAGGAGGTACCAGGA
Omy_myclarp404-111	T	G	CAAGCCATACGTGGCC	AAGCCATCCGTGGCC	GCTGTGGTGCTCATGGGTAAA	(0,0)	3	CCAGGGCAGGGTTGTCTC
Omy_RAD13034-67-21	C	T	CTCCCCGAACC	CTCCCTGAACC	GAGTGATTCCCAGCCCTCC	(0,0)	3	TCTCTCCGTTGGCCAGAAAC
Omy_RAD13034-67-35	A	T	CTGAGTGGACA	CTGTGTGGACA	GAGTGATCCCAGCCCTCC	(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	CAGTGTCGAACC	CAGTGTCGAAC	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	TTACCAGAAG	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	GGGTTCAGTGATAGTTGGGCAAT
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	CACCAATTACCA	CTCCCCCTGGACTTTGG	(0,0)	3	GCTCTATTGCACCGTGTCTG

Ots_myola-384-57	C	T	CTGCAGAACAC	CTGCAGAATAC	CTCCCCCTGGACTTTGG	(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	CAAATCAGAACAAAACCTCCACAA	(0,0)	3	GGAAGTCTGTCTGAATGGTTGTCTT
Ots_unk9480-51-39	C	A	CTAAGGAGACC	ATAAGGAGACC	CAAATCAGAACAAAACCTCCACAA	(0,0)	4	

## Appendix 10. GT-seq SNP panel for Pacific lamprey

Assay	A1	A2	A1-Probe	A2-Probe	FWD Primer	Corr	Primary Flag	Rev Primer
Etr_1004	A	T	TGCGATTACGGTTCC	TGCGATTATCGGTTCC	CGCCACGCGTGTTCAC	(0,0)	1	CGACCGCTTTCTCTCTGCAAA
Etr_1007	C	T	CACTCATCAGCGAGCCT	CACTCATCAACGAGCCT	ACACGAACACCCAAAAGTGATGT	(0,0)	1	ATGACTACTGACGATTCCCATTGAC
Etr_1022	C	T	TTTGCTCTGGTGATCTG	ATTTTGGTCTAGTGATCTG	GCACGAAAGCACTGAAGCT	(0,0)	1	TCAGGAAGGTTTGCATTGATACCA
Etr_1034	T	G	CCGAATCCTTGAGCTG	CCGAATCCTGGAGCTG	CAGCAGCAGAACCGAATCCT	(0,0)	1	ACCTTGATGGTCCATGGGG
Etr_1060	A	G	ACTCGCCACATTGC	CTCGCCGATTGC	TCGCACGCACTCACGTTA	(0,0)	1	GTGAAGTCCGTCGTCTTACCTTTT
Etr_1068	G	A	CCTCAACAGACTCTTGG	CCTCAACAGATTCTTGG	GGGCCCTGGAGGGTCAC	(0,0)	1	GCACACGCAATACAAAGATTCCT
Etr_1104	A	G	GGGAATGACACACAA	GGGAATGACGACACAA	AGCAGAGGGGGAAGAGGAAA	(0,0)	1	CCACTTGAGCTGCAATGTTGA
Etr_1106	T	C	GAAACCCAGTAGAATTA	GAAACCCAGCAGAATTA	TCCCTAGTCTCTGAGAAACCCAG	(0,0)	1	AAGGTCGCATCGTCAGTGT
Etr_1131	C	T	GAGCTATCTCTGCAGA	GAGCTATCTTTGCAGA	TTAACGGCGTGCATGCATG	(0,0)	1	AAACTGGTGGAAAAATGTGGG
Etr_1163	A	T	TGCAACCGTGTTTATAGAG	CAACCGTGTTTTATAGAG	TGCAGGAACGCGTAAAC	(0,0)	1	TCTGACGCTTGATGGAATCTGTTC
Etr_1181	G	A	CACTCCACAGAAACGGG	CACTCCACAAAAACGGG	AGTCGACCACCTTGTGAAGC	(0,0)	1	GGGCAGCTGTCCCGTTT
Etr_1184	A	G	CCAGGCGACATGAGCTC	CCAGGCGACGTGAGCTC	CTTGACAGCCACGGCGAC	(0,0)	1	GCTGCTTTGTTTTTCGGGGT
Etr_1187	C	G	GCTGCAAACTCT	GCTGCAAAATGT	ACAAAAGCTGTCTGGCCTGA	(0,0)	1	CAAAGACCGGGCTCTGTC
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	GATCTGGCAGAAGGCAACAG	(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	TCCAACCGTGATATG	TGCAGGAATAACATTCGAATTTCTACTC	(0,0)	1	GACATGACAGTCGCTAGATTCCT
Etr_1349	G	C	CCTGGGTTCAACCC	CCTGGCTTCAACCC	CGGTGAGCAGCCTCTGG	(0,0)	1	GGTGAAACCCCTTCATTGTGTGA
Etr_1359	T	A	TCGCAGACTTGCG	TCGCAGACTAGCG	CTGTATTGGTTGCTGTCGA	(0,0)	1	GTCACCTTCAATGCCGCTT
Etr_1376	C	A	CTGCATGTTCTGACACTG	CCTGCATGTTCTTACACTG	GCAACTCAGTGGGAAACG	(0,0)	1	GCGGTCCAGATGAGATTCCA
Etr_1378	G	C	TCGAGATGTGGAAGCC	TCGAGATGTGGAAGCC	ACACAAAGACTGGAGCAATGG	(0,0)	1	CTCCCATAGGCTTGCTCGAG
Etr_1383	G	A	TCAAGCCGAACGTTG	TCAAGCCAAACGTTG	GGAGAGGACAGGTCCAAGGT	(0,0)	1	CGTAGAGCCTGCGAAAGTGTT

Etr_140	A	C	AACACAGTTGCTACTGCT	ACAGTTGGCACTGCT	TGCGTGGTATCTATACGACGAT	(0,0)	1	ACACACACCAAGTACCACT
Etr_1428	T	C	TTGCGGTGATGATGC	TTGCGGTGCTGATGC	CAGCAGGGATATCATCACCTTCTT	(0,0)	1	ATGGCACGGGCAGAGAA
Etr_1507	C	T	ACGGCAGCGCGCGGGGC	ACGGCAGCGTGC GGGC	AAGGGACAATCTGAGAGCGC	(0,0)	1	CAAAACCGGACAGTGGCAA
Etr_1509	A	C	TATATGTATATCTCCAC	TATATGTATCTCCAC	CCACGGGTGGGTATGCATAT	(0,0)	1	CCGAGGCCTAATTCACACCA
Etr_1522	T	C	CGCGATCCTACCGC	CGCGATCCCCACCGC	TTTGCCGTGCTCATGTATCTACA	(0,0)	1	GACCTTGCGGTGATCACA
Etr_1548	T	C	ATATTGCACTGACT	ATATTGCACCGACT	GCCCTAGCTATTAATGCCGT	(0,0)	1	CTGGCACACAACGGCCTA
Etr_1551	C	G	CTACAAACCCCGGCAA	CTACAAACGCCCGGCAA	GCGTAGAACAACAGGCCCTA	(0,0)	1	ACCCGGCTGTACCTGAGATA
Etr_1556	A	G	TGGCTGGAGACGCTGCC	TGGCTGGAGCGCTGCC	AGCGACATGGCTGGAG	(0,0)	1	GGTGCTCTGGATCAGGAACC
Etr_1561	A	G	GCCAAAGTCACGCTGTT	GCCAAAGTCGCGCTGTT	GTCGAAGAAGACGCCAAAGTC	(0,0)	1	TCGCCTTTTCTTAATGCGCG
Etr_1567	T	A	ACAGTTCGAAAGCCAG	ACAGTTCGTAAGCCAG	TTGCACCACTCCTTGCT	(0,0)	1	GTAATGGTGGGACAATGCAAAGG
Etr_1569	A	T	TTGTTGCTGATTTTATT	TTGTTGCTGTTTATT	CGGGGTGAAGCAGTTTCCA	(0,0)	1	AAGTCACAACTCTCTGGGT
Etr_1589	G	A	AACCGCAGGACACACA	AACCGCAGAACACACA	TGTGACCGGTGAGCAGCA	(0,0)	1	CTTTGACTCCGTGCTCTCT
Etr_1613	C	G	CCCCTGCCACCGTCC	CCCCTGCCAGCGTCC	CGCTTACGACCCAGTGCATA	(0,0)	1	TTTACTGGTAGCAGCTCCT
Etr_162	T	C	CTGACCCCAACGACC	TCTGACCCCGACGACC	CGAGGCCTTCGTGAGAA	(0,0)	1	CTGCGGTGACATGAAGTTGAAT
Etr_1667	A	C	GTTATTGCCACAAATT	GTTATTGCCCAAAATT	CGACACGGCACATCATTATAAGG	(0,0)	1	AGGTCAGCAAGGTATTGTGGT
Etr_1684	T	C	TGAGAGCCTTTCCATCGC	AGAGCCTTCCCATCGC	GAGGAACCTGCGGAGAGAAG	(0,0)	1	TGTGTTTGGTGGAGGAGATG
Etr_1696	G	A	CCCGCGGCCGCC	CCCGCAGCCGCC	CCGTGTAGAGGTGGACATAGG	(0,0)	1	TGGCCATCTGCATGTTGGT
Etr_172	T	C	TGTCCCTATAAAGGAGG	TGTCCCTACAAGGAGG	CTCACGCTGCCCCAGG	(0,0)	1	TACACGAGCAGCTCCTCCTT
Etr_1762	A	C	CCCCCTCTCATCTGGGG	CCCCCTCTCTCTGGGG	TGTACCAAGAACCCCTCTC	(0,0)	1	CACCCCTCCTGAGAAATGCC
Etr_1765	C	T	TTGGAGTCCCAAGCACG	TTGGAGTCCTAAGCACG	CGCACCGATAACTAGACGA	(0,0)	1	ACCAAAAAGAGGGGGCTCAA
Etr_1773	A	G	TTCACTGAAACGTGGT	TTCACTGAAGACGTGGT	GGTCTGGCTGAACGACAAAT	(0,0)	1	CAAACACATGGTGCCACACA
Etr_1795	C	T	GCGAGATCCCAATGGG	GCGAGATCCTAAATGGG	CAGCGGGTGAACGTAGCTAC	(0,0)	1	ATTCAACACCTGCCACCAT
Etr_1806	A	G	AACACTGACAATATCTAAAG	CACTGACAATGTCTAAAG	GTAATGGCGTGTCCGTTTG	(0,0)	1	CGAGTACTACTCTGGCCATGTAG
Etr_181	C	A	TCTCATCTCTCGCTGCT	CTCTCATCTCTCTCTGCT	GAGCGGATGGGCGACTT	(0,0)	1	GCGGCGAGCACACA
Etr_1843	C	G	GTGCGACCCCAACGAAA	GTGCGACCCGAACGAAA	TTACGGCAGCAAAAACAGCC	(0,0)	1	GCCCTGTGAGTTCAATGC
Etr_1848	G	A	TCTACATATGCATGTGG	TCTACATATACATGTGG	ACCGAATAAAGTGTGTCTAGCA	(0,0)	1	TACACTGCACCCCACTC
Etr_1857	G	T	GGTCTCCGTGGCTGTGT	GGTCTCCGTGTGTGTGT	CTGCTGTTGCGGTGTGT	(0,0)	1	GGAGATGATCTGCATGCAGC
Etr_1875	C	A	CACCGAAGCCCAATATC	CACCGAAGCACAATATC	CGACTTCCACATTAGCACCG	(0,0)	1	GTGCATTATTCCAGCATTCCT

Etr_1882	G	T	GGCGCGTTAGGATCTAC	GGCGCGTTATGATCTAC	TGCTCTGCTTTCCACAGACG	(0,0)	1	GGGTTTGCCACGTAATGATG
Etr_190	A	G	CTGACATTACAATGTTTAT	TGACATTACAGTGTTTAT	GCAGGAGACCCTTGCTTGTC	(0,0)	1	AGGTGGCACACGAAAGTATCAAAT
Etr_1944	C	T	AAGGCTATCCGTGC	AAGGCTATCTGTGC	TGAAGTAGGTCTCCCAAAGGC	(0,0)	1	CCCACAGGTACGCAAAGGTA
Etr_1975	C	A	GCAGCCCTGCAACTGCT	GCAGCCCTGAAACTGCT	TGTTAGATGTGTAAAGCGCAG	(0,0)	1	AGAGGTCACAAACAGCCCTC
Etr_2013	C	T	TCAAGAATCACAGGCAGAG	TCAAGAATCACAAAGCAGAG	CGTGGCGTCGCTTTCC	(0,0)	1	CCGACGCTCCGAGTGAAA
Etr_2015	C	T	GCTCGATGACGAGACCG	GCTCGATGATGAGACCG	GGGCTTCGGTCGCTTATAA	(0,0)	1	AGTCCTTCTTCTGCTGCG
Etr_2016-70	C	T	TCGACTTCCCACAAATTT	TCGACTTCTGACAATTT	TTTCATTATTTCTTGACGCTTG TG	(0,0)	1	GGATAGACGCCTCTGCTGAG
Etr_2050	T	C	GCTGTGCATGGAGGAG	GCTGTGCAGCGGAGGAG	CCCATGTCTAAACAGCAGCT	(0,0)	1	GCACCTCACACATCTGCTCT
Etr_2066	G	A	CGCCTGCTCGCGCTCCT	CGCCTGCTCACGCTCCT	GAACCTGTGCCCTCACTCC	(0,0)	1	GCGCAGGATGAAATTGCAGA
Etr_2068	C	T	GTGCGCACGCGGAATGT	GTGCGCACGTGGAATGT	CAGCACTGCATCGACGTG	(0,0)	1	CAGCTCTACTCGTACCTGGC
Etr_2071	A	C	GGCACAGGCACGACACA	GGCACAGGCCCGACACA	CACAGGTTCACTTGGGTGG	(0,0)	1	AGAGCTGCTCATTGGTTTCA
Etr_2097	C	T	CAGGTCTGGGAGCCGA	CAGGTCTGAGGCCGA	GGGCGTGCGGACATACT	(0,0)	1	GCGAACATGGTCAACGAATGC
Etr_2099	G	A	ACCCGCGCGGACACGTG	ACCCGCGCAACACGTG	AAGACCCACGGCGATTCACT	(0,0)	1	CCCTCAACAGCCTTGCCATA
Etr_2107	C	T	CGAACGGCGCGAGAAGC	CGAACGGCGTGAGAAGC	TGACCACACGGCGTCTTCG	(0,0.6)	1	AAGCACGAGAGCGCGTT
Etr_211B	T	G	GCGTAACCTTGAGCACT	GCGTAACCTGGAGCACT	GGGTGGAGGAGCGTAACCT	(0,0)	1	GTGCACGTAGTTGCGGTTG
Etr_212	A	G	TGCTTCTCTACTTTTGC	TGCTTCTCTGCTTTTGC	TCTTTCCCGTGTGCTTCTC	(0,0)	1	GCGACACGAGGGTATTTCGAT
Etr_2126	A	G	CCGTCCCAATTCGCGCA	CGTCCCAACTCGCGCA	GAGACCGTGGGCGACT	(0,0)	1	GACGCGGCGATGTAGGT
Etr_2193	C	G	TGCGGCTGGAGACG	TGCGGCTGCAGACG	GGTTCATCTGGGAGCTTTTGC	(0,0)	1	AAGCCACACAGAGAAGTGACATC
Etr_2226	T	C	TTTGGCTTCTCGACGCT	TTTGGCTTCCCAGCGCT	GCAAAACGCCGTACACCTTT	(0,0)	1	TAGTTGCGTTGAAAGCGAGC
Etr_223	A	G	CTATTGGTTATGAGGTT	CTATTGGTTGTGAGGTT	GTAAGGCGTGGGCTATTGGT	(0,0)	1	AGTTACTGAGATGACCGAGGA
Etr_225	C	G	CACTGGCATTGTICG	CACTGCCATTGTICG	TGGTTGAATCCAGTGCGGATAAA	(0,0)	1	GTGCAAAACCGGTCTCTAATG
Etr_2272	A	C	GAGAGAAGGAAT	GAGAGAAGGCAT	AAGGGGACGGGAGAGAAGG	(0,0)	1	ACAACAAGAACTGCAGCAGTG
Etr_2287	T	G	CTGCTTGTATCTCCCCT	CTGCTTGTAGTCCCCT	TTCATGTGACACCTGCTGCT	(0,0)	1	GAGGCGGGTGTACACAGAG
Etr_2304	G	A	CGTGCTGTAGAGAGA	CGTGCTGTAAAGAGA	ATCGGCACATTTCTTCCCGT	(0,0)	1	GCTAAAGAAGCGCATGGAC
Etr_231	G	A	ACGATGCCGTCCGCC	CGATGCCATCCGCC	CCAGGAATAAGGACACGGTTTGG	(0,0)	1	CGTCCCTCCCTCCTTGT
Etr_2334	C	T	TTCGCTCAGCTCCCCG	TCGCTCAACTCCCCG	CCAGCCACCACGTCAAGT	(0,0)	1	GTGCGGTTGGCAGAGATG
Etr_234	T	C	CCCCAGTGTGACACC	CCCAGTGCGACACC	CTCCTCCACGGCGATGTT	(0,0)	1	TGCACTACGAGAACAACCTCTCC
Etr_2409	G	T	CCGCACGGGAGGTCCA	CCGCACGGGTAGGTCCA	CCAGGTGCTGAAGGGCCG	(0,0)	1	GCTCTCGGCTGGACAAC

Etr_2414	A	G	GCCAAGCGGACCCCTCT	GCCAAGCGGGCCCTCT	AGACCATTCCTCTGCCAAGC	(0,0)	1	CCCCAGGGTGCTCTTAAACA
Etr_2416	C	T	TGGTGCGGTGCACGC	TGGTGCGGTACACGC	TCATTACAGGAAGCCTCGTTCAG	(0,0)	1	CGGAGCCCTCCCTGTGT
Etr_2418	C	T	TAATCTTACCAAGTTTC	TAATCTTACTAAGTTTC	TCGGCTATTAACTCCGTGC	(0,0)	1	TGGGTACTGCGAGGAGAGAA
Etr_2451	C	A	TATACCTGTCGCCCCA	TATACCTGTAGCCCCA	GTGAGGGAGAGAGGGAAGAGT	(0,0)	1	CGAGAACACATACTGGGGC
Etr_2460	T	C	CTGGCGGCTTCGCACGG	CTGGCGGCTCCGCACGG	CATGCAGCCGACAACTGG	(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	TGCACTTGAACATGGGTTACAAAC
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	GCTCCAAACCGCAT	AGAGATCCCTGTGGTCCAA	(0,0)	1	TCGTGTCATCGTCGTCATC
Etr_2675	G	A	AAGACGACGATTCCT	AAGACGACAATTCCT	GCTGGATAATTGGCATCTCACACA	(0,0)	1	CTCAATCGTCTGTTGCCAAAC
Etr_2730	G	A	GTTGAACCCGTAGCGCG	GTTGAACCCATAGCGCG	CAGCCACCTCGAGAGCTG	(0,0)	1	ATGGGAGGGCATTGAGGTG
Etr_2765	C	T	TTAATCATGCCAATGCC	TTAATCATGTCAATGCC	ATCTGCACAAGCTTCAGGTT	(0,0)	1	ACGTGTTAAACCGAGCCACT
Etr_2776	A	C	GGAGCACCCAAAC	GGAGCACCCAAAC	GTACCTGGACGTCAAGCACA	(0,0.6)	1	CGACAGCTGCATTGACATCG
Etr_2791	A	G	CCCAGAGAAACAGCAGA	CCCAGAGAAAGCAGCAGA	AGGTGGTACTGCAATGGACC	(0,0)	1	GCTCCGTCCATACCATCATATGT
Etr_2823	C	T	CGCACGCGCCGAGCAGT	CGCACGCGCTGAGCAGT	ATGTGCGCCATGCCGAT	(0,0)	1	CACACGGGGATCTTTGTCT
Etr_2841	G	A	CGCATCTTTGTCCCTGC	CGCATCTTTATCCCTGC	ACAGGTAGTACTGCAACGCA	(0,0)	1	GCTGGATGCTTGGAGACCAT
Etr_2858	T	G	GAAAAGAAATGGTTTGA	GAAAAGAAAGGGTTTGA	GGCAGAGATCCTTGAGAGCA	(0,0)	1	CTCCACTATTCGCATCGTGA
Etr_2878	C	T	CTTGTCAACTCCACGA	CTTGTCAAATTCACGA	AGCTTGCATCCGTGACTTCA	(0,0)	1	GGTTGTC AAGTTCTCGTGA
Etr_2915	C	G	ACAGCTCCCTTCCAC	AGCTTCGTTCCAC	GCCCTTCAAGTTCAGTTCAC	(0,0)	1	GTTACAGTAGATCTTGACCTTCA
Etr_292	A	G	CAATAAACACACACACA	CAATAAACGCCACACA	ACATGCAGAATAGGGACAGAAACA	(0,0)	1	CGTGTGCCTCAGATGAGAA
Etr_2937	T	C	GGCCACGTTTTTCCGCG	GGCCACGTTCTCCGCG	CTTCGTGCTGGTGATCGGTC	(0,0)	1	CACCACCTCCACGTAGCAG
Etr_2971	T	A	CATTGAGGGTGCA	CATTGAGGGAGCA	AAGCTTACGTGCAGGCTCA	(0,0)	1	CAGCACCACTTTTCCGTG
Etr_2974	G	A	CGCCTGCCCGCACACCT	CGCCTGCCACACACCT	TGAGACCAGCGCACCTG	(0,0)	1	TGAGTGTGCATGGTGAGTGT
Etr_2990	A	G	CTCAGAGACATCCTCGG	CTCAGAGACGTCTCCTCGG	GAGCCTCTGGGTGATCTCCT	(0,0)	1	GGAGAACCCGTTGCGTTTC
Etr_3007	G	A	GGTTGTAAGGGTTGGGA	GGTTGTAAGAGTTGGGA	CGGTGTGAAATCAGACGGG	(0,0)	1	CCGGTIGGCCTCACATAACT
Etr_3037-68	A	G	TCTGCAAAAGACACAGA	TCTGCAAAAGACACGGA	CACCTTCAGGAAGCACACGA	(0,0)	1	GGGTACGCACAACCTTTGGG
Etr_3038	G	A	TTTCTACTCGGCTCTAC	TTTCTACTCAGCTCTAC	AGTCGACCCCTCAACCACAATT	(0,0)	1	ACGTAGTGAACAGTAGAGC



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	GGGACACTTGGGAAGGACACC	(0,0)	1	AGGATTCCGACCACCTCACA
Etr_3145	C	T	GGTGCCCATCGGAGGA	GGTGCCCATTTGGAGGA	TGGTGATGACGATCGTGGTGCC	(0,0)	1	TTCATCATCTTCCGCACGGT
Etr_3169	C	T	AAGCCGGTGCACCGAG	AAGCCGGTGTACCGAG	ATAATGGTTCGCGACAGGCA	(0,0)	1	ATAACACCGCAGCATCTCGG
Etr_3189	C	T	CACGCGCGCACGC	CACGCGCACACGC	CAGGTGCAGTACGCACTCA	(0,0)	1	GCGCCAACCGCTACAC
Etr_3234	T	C	TGATTCTTCTAGCTCCT	TGATTCTTCTAGCTCCT	CCAAGTGCTAAGTACTCACTCTGT	(0,0)	1	TGTTTCATGAAGGGCACTGAGA
Etr_3240	T	C	AAACCTGGGTGTGGGCC	AAACCTGGGCGTGGGCC	ACCTGCGTCAGTGAAAAAC	(0,0)	1	AAAACCATTTCGTTGAGGGCC
Etr_3253	A	G	CGAGTTCACACGCGAA	CGAGTTCACGCGCGAA	CAGGAGCAAGAGCAGTCTCA	(0,0)	1	CCACTTGAGCTTAAGTTCGCG
Etr_3255	C	T	GTGGGGTCTCCGATGG	GTGGGGTCTCCGATGG	CAGCCACTCCACCACCATG	(0,0)	1	TTCGAGTGCCAGATGACGC
Etr_3262	C	A	CCAAGAATGCT	CCAAGAATGAT	AGGTGCCTCCTTCCAAAAGT	(0,0)	1	ACTGTACCAGCTTAAGTGAAA
Etr_3292	G	A	TGCTCTCAAACGTGTCCA	TGCTCTCAAACATGTCCA	GCAGGTGAAGTATTTCATGTATCCA	(0,0)	1	GAGCGGCAGCCTAGGAA
Etr_3330	G	A	GAAGTGTAGGTTTGGG	GAAGTGTAGTTTGGG	ACTGGGAAATGTGAAGTTGA	(0,0)	1	ACAACCCCTTGTGTCGTCAA
Etr_3350	G	T	AGCAGGCCGCTCTGTC	AGCAGGCCTTCTGTC	GGCAGGCAATAGATCCTCATTCAG	(0,0)	1	TGATTTTGGGCGAAGATTACGT
Etr_3356	T	G	GCATACACGTACAACAG	GCATACACGACAACAG	GTCATTGCTCCACACACGTG	(0,0)	1	CGGTGCTCGAAAAAGAGAG
Etr_337	T	C	AGGTGAGTCTTTGT	AGGTGAGTCTTTGT	ATCGTCAGGAGGAGCCAG	(0,0)	1	CTGGGTGGCAGGTTTCACAA
Etr_3383	T	G	CACCCGTTATAGAAAC	CACCCGTTCTAGAAAC	GGTCGTCTCGAGGTGTTGG	(0,0)	1	GCACGCACGCGTCAA
Etr_3403	T	C	CGTATCCTTTCATGGGG	CGTATCCTTCCATGGGG	GCAAACCCAAATACGCATCGT	(0,0)	1	TTCCAGACAGCAAGGGCAG
Etr_3411	G	C	GCCGACCCCGACGCCG	GCCGACCCCCAGGCCG	ATGTCGCACCTCCACATGAG	(0,0)	1	CGGGATAACTACGGGCTG
Etr_346	G	A	TGAATTTTCGGCCATAC	TGAATTTTCAGCCATAC	TGGCGTGATCGGTAGAACT	(0,0)	1	TGCAGCAATATAGACCTTACCTGT
Etr_3466	G	T	AATGGACACGATTCCAC	AATGGACACTATTCCAC	TGCCCCGAACATTGTAATGGA	(0,0)	1	ACGTAGCCATTTCGACCACTT
Etr_3502	A	T	AACCCAAAAAATGCTT	AACCCAAAAATAATGCTT	TACAGCGCTACACATGCACAA	(0,0)	1	GTCTTTAACGTGAAAGAACCTCCA
Etr_3549	A	G	CCCGTACATGGTCACC	CCGTACACGGTCACC	CAACCGCATGCTTGCA	(0,0)	1	CTGCCGCTCGGGTCT
Etr_3555	C	T	CACCAACCGTGCAAT	CACCAACCATGCAAT	GCCCCATCGCTCGTTTAC	(0,0)	1	GCAGTGCGCCAACCATAA
Etr_360	G	T	TGGTGCGTTGGTGGTGC	TGGTGCGTTTGGTGGTGC	TGCTTTCCATGAGTGGTGGT	(0,0)	1	AAGTGTGCGCATTTTCATCCG
Etr_3601	T	A	CCCAAATAATAAACTTT	CCCAAATAAAAACTTT	TGGCTCTCCACTATCCCAAA	(0,0)	1	GCCTTTGTTTGTATTACAAGAGCA
Etr_3638	C	T	ATTGTAGACCGAGCTGC	ATTGTAGACTGAGCTGC	TGTGCACGTTCTTAGGTCAGA	(0,0)	1	ATTAGTTGTGCACGAGCTC

Etr_3725	T	C	TAGGTATCTAGTCCA	TAGGTATCCAGTCCA	ACACTGCTCCAGTAGGTATCC	(0,0)	1	AGATAGGGCCCAGACAGCA
Etr_378	G	T	AGTCAAAATGTATTTA	AGTCAAAATTTATTTA	CTGAGAGGCTGTCTGCAGAG	(0,0)	1	GCCCTACATTTGGGGAGTCA
Etr_3837	C	T	GACAATTGTACGTGCC	GACAATTGTACGTGCC	TGCCCTAAAGTGTACATCCGT	(0,0)	1	CCAGAAAGAATAAGCGCGGG
Etr_384	G	T	CCAAGATTTGTAATCTC	CCAAGATTTTAAATCTC	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	CCCAGAAGGATGTTGTGTGT	(0,0)	1	GCATTGCGGTTAGAGCACTG
Etr_4000	T	C	TTGCACGTCTAAC	TTGCACGTCCAAC	CAGCGCTCTGGATTGCAC	(0,0)	1	TAGGCCCAGGAGGAAGCC
Etr_4015	G	A	TCTCGTCTCGGGGACTG	TCTCGTCTCAGGGACTG	ACTGTCGTATTCCCTTCTCGT	(0,0)	1	CGGTAATCGTGCATTGGGC
Etr_4028	T	C	ATAAATCAATGTGCCCC	ATAAATCAACGTGCCCC	TGCCTTGGAATCCGACACC	(0,0)	1	TGTTGTCCGTGGGCGAC
Etr_4037	G	T	TCACAAAATGAAC TTGA	TCACAAAATTAAC TTGA	TCCTGGTCTCTTTATTTCTCACAA	(0,0)	1	GCTTTCTCACAGCACTTGCC
Etr_4079	G	A	CTACATTCAGTTTAAATG	CTACATTCATTTAAATG	TCATGGGTGATTGCCATGTT	(0,0)	1	TGCACCAATCTTACCACGGA
Etr_412	G	A	CCTCGAAGCAGCTTT	CCTCGAAACAGCTTT	GGTAGCTTCCCCCTAATGCT	(0,0)	1	TGGTGAGAAAGAAGTCAACATGCA
Etr_4130	A	G	ACGATGGCAACGACG	ACGATGGCGACGACG	CAGGCCGTTCTTGCG	(0,0)	1	GCTCCCTCGGAAGCC
Etr_4142	T	C	TGTGCAAGCTGCCTTCA	TGTGCAAGCCGCTTCA	CATCTGTGGTGTGCACCTG	(0,0)	1	GAGACGATGTTGCTGAAGGC
Etr_4156	A	G	TAGCAGCTCAGGGTGCA	TAGCAGCTCGGGTGCA	GTAGCGGTTGGTGTCTAGCA	(0,0)	1	GACGTCATCCTCAACGGCC
Etr_4165	C	A	GCCAATATTCTC	GCCAATATTATC	ACTTCTCTATCTTGCGCCA	(0,0)	1	GGAGACCGAACAGAGATGGG
Etr_4173	A	G	CCAATGCATAAGTAATC	CAATGCATGAGTAATC	GCACAACAATGTTATAACGGCACAA	(0,0)	1	GACGCCATGTCAGAGAGACT
Etr_4194	A	C	TGCGAATCAAAC TTCAA	TGCGAATCACAC TTCAA	ACTTTCCAATGTGCCATGCG	(0,0)	1	ACTCCATCGTAACTGCAGTGA
Etr_4214	C	T	TGCGTTCACGTT CATAG	TGCGTTCACATTCATAG	TGGGTTCTCGCACTGTTAG	(0,0.4)	1	TTCACGTTCTAATGCTGTCTGA
Etr_4215	A	G	GATGTAGCGATACGTGA	GATGTAGCGGTACGTGA	TCCTCGTGGATGATGTAGCG	(0,0)	1	GGGCTGCACCAATACCTCTT
Etr_4254	G	A	CTTTCCCATGTGTGCCT	CTTTCCCATATGTGCCT	ATTCTGCTGTGACACGCTT	(0,0)	1	CGAGAGCCTTCACGCCTAAT
Etr_4281	A	T	ACGTGGCATGCTATG	ACGTGGCTGTCTATG	TGCAGGAGGACTACACCAACT	(0,0)	1	GCACGGTTAGTCATTGGGTCAA
Etr_4288	A	T	AAGGATGATAG	AAGGATGATTG	AGCCACATTGCTCTCATGT	(0,0)	1	TGGTGATCGACTGAACCAGC
Etr_4390	T	C	CGGTGGTCATGGGTCAT	CGGTGGTCACGGGTCAT	ACGTAATAGTTGGCGGTGGT	(0,0)	1	GGGCCTCACCTGGTTTCAA
Etr_4414	G	C	AGGAGGCCGCCGAG	AGGAGCCGCCCGAG	CTCCGATTAACCCCTTTGTC	(0,0)	1	GCGCGTGTGTCCAAAATTG
Etr_4455	T	C	GTCTGAGCTTGGGGGG	GTCTGAGCTCGGGGGG	TCGTTCCGGGGGTCTGAG	(0,0)	1	GCCGTAGCTATTTGAGTCACG

Etr_4479	C	T	CATGATGCCCTTCTTGC	CATGATGCCTTCTTGC	AATGATGTCGGCGCTGTACT	(0,0)	1	CTTGCGTGGGAGTACCGC
Etr_4498	T	C	GCAAGGGGTTGGT	GCAAGGGGTCGGT	TGGCAAGTGCGGTAATTCT	(0,0)	1	AATGAATCGTGGCCCTCTC
Etr_4504	C	T	CTGATTGTCCACACAA	CTGATTGTCTACACAA	TCAGACACTCTGAGATCCCA	(0,0)	1	TTCATGGGTGGGAGTGGGAT
Etr_4521	C	A	GGTTGCACGCAAAGTCC	GGTTGCACGAAAAGTCC	GTAGCACAGCGGATCTCCG	(0,0)	1	CCTCGTCTCGCTGGACTTT
Etr_4531	G	A	CCGCACGCGCTCG	CCGCACACGCTCG	GTTTGAGTTTGCGAAAGGTACGA	(0,0)	1	GTACGTAGCGAGCGTGTGT
Etr_4544	G	C	TGTGATTACAGAACCTT	TGTGATTCACCAACCCT	GGCACACTGGTTCCATCTCT	(0,0)	1	GAATTCGGGGTGTGGAGGTT
Etr_4574	G	T	CTTCCAAAGGCCCTGGT	CTTCCAAAGTCCCTGGT	CGGCGCACATCTTCCAAAG	(0,0)	1	GAGTGAAGACGACGTCTCG
Etr_4633	G	A	CTGGGCAACGAAAGCA	CTGGGCAACAAAAGCA	GAAGGGACGAGGAGGAGAGGT	(0,0)	1	CATGTCCAAGTCGCTGCTTT
Etr_464	C	A	TAGCGCTTCACCCGTCCA	CGCTTCACACCGTCCA	TGCAGGGACCGCGTTAC	(0,0)	1	GTGCCCCACCGGTCT
Etr_4670	G	A	CCGTAACACTGTCCCGG	CGTAACACTGTCCCGG	AGGATCCGAGCCCATATGAGA	(0,0)	1	GTTTGGTCGACATCGGAAAAGG
Etr_4686	T	C	GGTCTGCTATTCGGTG	GGTCTGCTACTCGGTG	CTAGGATAGCAGCACCGACGC	(0,0)	1	CCAAGGCCCTATGCGTAAA
Etr_4694	A	C	ATCACATACATAAA	ATCACATACCTAAA	GCACCATGACGCTTCATTC	(0,0)	1	TCTGTTGAGTGGTGTGATATGCA
Etr_4716	G	A	CATCAGAACGATAGCCC	CATCAGAACAATAGCCC	GCCGACACGAGCATCAGAA	(0,0)	1	CCTGACTGTCCTGCACGTA
Etr_4750	T	G	AGTCGTTTTTC	AGTCGTTTGC	CAAGGTAAGCGGCAGTCAGA	(0,0)	1	ACTGCAATATACACTGTCCTT
Etr_477	C	T	AGCTGCAGATCACCA	AGCTGCAATCACCA	AAGTGGGTGCTGGACTGGC	(0,0)	1	TCGCTGGTCCAGTAGATGGT
Etr_4800	G	A	ACCTGGTGCAGAACCGG	ACCTGGTGCAGAACCGG	GCGCTGGGTTTCTTGTTGA	(0,0)	1	CTGCTGCTGCTGATTGAGTG
Etr_480-67	C	T	TTACGAACACTCG	TTACGAACATTCG	CGCACGTGCCTTGTTATGT	(0,0)	1	TCCGACAATTCGCAAGTCGA
Etr_4845	G	T	AGATGTCCAGTCGGGGC	AGATGTCCATTCGGGGC	AGGAATCCGATGAGCTACGA	(0,0)	1	CGTACGTCGGACACCACTG
Etr_485	A	G	CACCAATTAAGCAATTGTATT	CCAATTAAGCGTTGTATT	CAGCCACCGTCGACACA	(0,0)	1	AACTGCTGAAGTTACTGATGTTACA
Etr_4853	C	T	CGTCGAAGGCCTCCAGC	CGTCGAAGGTCTCCAGC	CCTCGCACGGGGGTCTATA	(2,2,0)	1	GTGCAGGTTCACTCTCCCC
Etr_4859	C	G	CACAGGGATCGATGGCA	CACAGGGATGGATGGCA	CCCTGACCACCCACTCACAG	(0,0)	1	AGCTTATATTAACGCAAGCGGC
Etr_4889	T	C	AGGTTATGTTATGAAGG	AGGTTATGTCATGAAGG	TGTTGGGAACAGGGCACAAA	(0,0)	1	CTTTGTTGCGCCTTCGTTC
Etr_49	A	T	TTGTGATGCAACTTCGT	TTGTGATGCATCTTCGT	TGGGTGAGCGAGGATGGT	(0,0)	1	CGTCCACACTGCGTTCAAC
Etr_4965	T	C	CCACCGAGTTGGCTAC	CACCGAGTCGGCTAC	GCGCCAGGTGAGGAGA	(0,0)	1	CTCTCTTCTCTGTTGCAACTT
Etr_5020	A	C	TGCAACGAAATAATTAC	TGCAACGAAATCATTTAC	CCCCACGTGACGCA	(0,0)	1	GCTGCAATGTGGAGACCTTT
Etr_5043	A	C	AACAACTTTAATTCGGC	AACAACTTTCATTTCGGC	TGCAGGGTTTATATTGCCAAATCA	(0,0)	1	GGCGAATGGCGGTTGTTATT
Etr_5112	C	T	TTGGGGGTGCCCTTAGA	TTGGGGGTGTCCTTAGA	AGAACAGCTTGCAATGGGGG	(0,0)	1	GGCGTCTCGGAGCAAGTTAT
Etr_518	C	G	TCAGCGGTGCCAGGTCG	TCAGCGGTGGCAGGTCG	CCGGATTTCGAATTCGGGT	(0,0)	1	CCTGAGCAGCCCGATGG

Etr_5193	T	G	TGGTTAATTCACCAGAAGTA	TGGTTAATTCACCCGAAGTA	ATTGCCGCCCTCATGAA	(0,0)	1	ATACACTGTGAAGCAGATGGAACCT
Etr_5197	C	T	ATATATTTACGCGATCTAAC	ATATTTACGCAATCTAAC	GCAGGTGATTTGTCCATAAGAGGTT	(0,0)	1	GTGGTGGGTTTAACGACACATTT
Etr_5267	G	T	GAGACGCGCGGCATGC	GAGACGCGTGGCATGC	GGAAAGAGGCTCCGGCTG	(0,0)	1	AGTTGTCCATCATCGCGCTCA
Etr_527	A	C	CAGCAGAAAAAGCA	AGCAGCAAAAGCA	GGTACTCGGTGGTATCACACA	(0,0)	1	GGCAATGCTGCTGCTTCTG
Etr_5272	C	T	GCGCGCAAACGATGCTC	GCGCGCAAATGATGCTC	CACCGTGTCCGAGTCGTG	(0,0)	1	GAGGACAGAGCGTGAAGGAG
Etr_5317	A	C	CACGAAATTTTGAACTTT	ACGAAATTTTGCACTTT	CGGATTTTCACCTTTTCTGCGTTTC	(0,0)	1	CAGTTCACGAGCCAGACTACAG
Etr_534	T	C	CCGTGCTCGTACAA	CCGTGCTCGCACAA	CTCCACGGTCTGCGTGAACCG	(0,0)	1	CGGGTTAGCCTTCAAGGGAG
Etr_5346	T	C	AAGGCTCAATAATGC	AAGGCTCAGTAATGC	TGTGTGGGAAATGACAATCCAT	(0,0)	1	GACATACGGTGTGTGTACTACAAT
Etr_5352	A	G	AGAATCTGGACAATGGC	AGAATCTGGGCAATGGC	ACAGGATCTATGGTGTGCAGAG	(0,0)	1	ACCCGTGAGACTCGTGAAAA
Etr_5465	A	G	CCGCGTGTCCAGC	CGCGTGTCCAGC	CGACTGCCCTTCGATGCA	(0,0)	1	TTGACCTTGACGGATTGGATCTC
Etr_5510	A	G	TCGTGTTGACCTCTTCAGTA	CGTGTGACCTCCTCAGTA	TGCAGGAAGTAACTGTGTAATTAACG	(0,0)	1	GCGACGTAAATATGCTGCAAGTTT
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	CAGGAGACGTAGCCCTCTA	(0,0)	1	GAGTAGACAAGAGAAGACGAATTCACA
Etr_5603	G	A	GATACTCCAGCTCCTTG	GATACTCCAACCTCTTG	CGCTCCACATTGTTGAGAGC	(0,0)	1	GTTGTGTGAGCTGTGTGC
Etr_5626	T	C	TGTGTGATGTATTGGGC	TGTGTGATGCATTGGGC	ACGTTTTTGATAAAGGTCCGC	(0,0)	1	GTCTGAATTTTCTGTGCCCA
Etr_5654	T	G	TGAGGAATGTAAAACTG	TGAGGAATGGAAAACTG	AGGAGATCGAGAGGCTCACA	(0,0)	1	TGAGACAAGGGTTCACGTGG
Etr_57	A	G	ATTAGCACACGTGCCG	ATTAGCACAGCGTGCCG	GCGCCAATTGTGTTTTGTGA	(0,0)	1	CCCCTCGGAGGTTTATTGCA
Etr_5711	C	G	CTCCTCTGCCGCGCGCA	CTCCTCTGCGGCGCGCA	CTCAGGCTGGATCGATGTCTG	(0,0)	1	TTAACGCACGGACATCACCA
Etr_5757	A	G	GGTGCCAGGAAAGG	GGTGCCAGGGAAAGG	TAACCAGCATCGCTTCGGAC	(0,0)	1	ATGTCCACATCGTCTGCAG
Etr_5762	C	G	GCGCGACACCAACGACG	GCGCGACACGAACGACG	GGTAAACGTGGAAAGAGCGC	(0,0)	1	AAAGTCCCCGTCTCTCGTC
Etr_5780	T	G	TTGTGATCTTCAGTATT	TTGTGATCTGCAGTATT	AGCTGGGTGGTTGAGTTGAG	(0,0)	1	ACAATGCGTGTGTTCAACCG
Etr_5831	A	G	GCAATGCGCATGCGCGC	GCAATGCGCGTGC	GCGTCTCGATCCCTTGTTA	(0,0)	1	ATAAACTTCGGGTGGCCAG
Etr_5960	C	A	ACTCGTCCACCAAACAT	ACTCGTCCAACAAACAT	TGAAGCCAAACTCGTCCA	(0,0)	1	ACATGGAGGGCATGCAATG
Etr_5993	T	A	TGGAGTCGATTGGAAC	TGGAGTCGAATGGAAC	GACACGTCCACCACAGGG	(0,0)	1	TGTCAGTGTTTTCGCAACGAC
Etr_6026	C	T	TCCACCCAGCCCTACC	TCCACCCAGTCTTACC	TCGGGAGGCACGTTCTTC	(0,0)	1	GCATAAAATCGGCAGAAATGAGAGA
Etr_603	G	A	AGGTGTTCCAAGTTTGT	AGGTGTTCCAAATTTGT	CAGGAGGAGAAGCCGTGG	(0,0)	1	GGGAGGGGAAGAAGTGAGT

Etr_6076	T	C	AGGAGAAATTCCTCAGC	AGGAGAAATCCCTCAGC	GCTGAGCATTTCTCCGAGGT	(0,0)	1	TCAGCCAGCCACTTATAGGC
Etr_615	A	G	CACGGCACGGTCG	ACGGCGCGGTCTG	GCGGCTTGGGATGTTATCTTCAATA	(0,3,0)	1	GCCTGGGCGGCCTATC
Etr_6179	T	C	AGCTCGCAGTGAC	AGCTCGCAGCGAC	ATGCCAGGACACAAGTTCGT	(0,0)	1	CTGCTCATGTCCACAGGTC
Etr_6229	A	G	TTTGGTGCAAACCTTACC	TTTGGTGCAAGCTTACC	CCCCAAACATTGCTTTGGT	(0,0)	1	ATGCTGGTTGGGCTCTTACC
Etr_6318-70	C	T	TGCCCGACGCGACTC	GTGCCCGATGCGACTC	GACTTGTTCCGGCACTACCC	(0,0)	1	GCCGTGAAAGAGAGCGTGAG
Etr_6363	A	G	CTAAAGTATAATTAAG	CTAAAGTATGATTAAG	CACGATGCCACAAACATGTCA	(0,0)	1	GC GTTTCATTTTCATTGGATCCC
Etr_6369	C	T	GCTGGTGACAAGCAGA	GCTGGTGATAAGCAGA	GAGCAGGACAAAGCAGGAG	(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	AGGACTTTCTTTTAGGTTGTAGCCAAT
Etr_640	G	A	AAGTAGGATGGTGGCCT	AAGTAGGATAGTGGCCT	AGGTAGCACAGCAAGTAGGA	(0,0)	1	AATGCCCAAAAATCCGTGG
Etr_642	G	T	TGCAAGGTTGGAA	TGCAAGGTTTGAA	GACGCTCACTGCATGCAAG	(0,0)	1	ACCATTTTCATGCCACCCCA
Etr_6436	G	A	GTCACAATGTGCGACA	GTCACAATATGCGACA	CAGGGAGCACTCGTCAACAA	(0,0)	1	GATGTGGCCAGTGACAGACT
Etr_6440	G	A	ACAGCGGTTGTCTCAG	ACAGCGGTTATCTCAG	AGTCAGTACATTGAGTTCCAAT	(0,0)	1	ATCCCTCATCCCCATGGTCA
Etr_668	A	G	CGCAACCAATGCCGC	CGCAACCAAGTCCGC	GTCCCGTGGACAAGAGTCA	(0,0)	1	GCTGCCAGGCACTTGTG
Etr_673	C	T	CGGCCGCTTCTCT	CGGCCACTTCTCT	GCCGACAGCTGCTTCTCT	(0,0,5)	1	CCACGTTGCTGTTGTTTGTC
Etr_678	G	T	GGTAGGTCAGGTCCGCT	GGTAGGTCATGTCGCT	AAACTGGGCTGGTAGGTCA	(0,0)	1	ATTCTTGACGTCGGCTGTC
Etr_681	C	T	AGCACGAGACGAGCGG	CACGAGACAAGCGG	CGGTCGCCATAGGTGTT	(0,0)	1	CAAGCACATGCTCAGCAACAG
Etr_687	C	T	TCGCCACTTCATTACC	TCGCCACTTTATTACC	AAGAAGCTCCATCGCCACTT	(0,0)	1	CGTGGTTTCAGTTGCGAAGG
Etr_705	G	A	CCGCTATCTCCGGCTGG	CCGCTATCTCCAGCTGG	AGCAGAGACACGCAACGTAATA	(0,0)	1	GGTTGTGCTGGACATTGTTATTGA
Etr_7081	T	C	ACATTGTTCTATTCTCA	ACATTGTTCCATTCTCA	GGAAGAAAGAGGGAGGCCTG	(0,0)	1	AGCACAAATCGTCGTAAAGGG
Etr_7142	G	A	GGTCTTGGCGCCACGGT	GGTCTTGGCACACGGT	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	TGGTAAATTTACT	TGGTAAATGTACT	CAGAAGTGATTGGAATCGGCA	(0,0)	1	GGCCTTCTCTGCATATATACCAGT
Etr_73	T	C	CGCTGTCATGTTCC	CGCTGTCGTGTTCC	TGGCAGGTGTGGAAAGCA	(0,0)	1	CTCGCGCTGTTAAACCTCTTG
Etr_7358	T	C	GCCAGTGAATGTGAACG	GCCAGTGAACGTGAACG	GAAACACAACCGACGCG	(0,0)	1	TGGCGTTACAGTGTGTTGTC
Etr_7382	C	G	CAGTGGAGGCAGTTAGA	CAGTGGAGGGAGTTAGA	AGGTGGTAGGGTTAAGCGA	(0,0)	1	TCCTCAAACACCCGATTGC

Etr_7387	G	T	AAGGAGTGGCGGTGTAA	TGAAGGAGTGGCTGTGTAA	CGGTGGTCGAGGCGAATG	(0,0)	1	CGTCTCCGCGGAAGGT
Etr_7416	T	C	CTCCTGTGACATCCAG	TCCTGTGGCATCCAG	GTGTCGGCAAGGGTGAGATAT	(0,0)	1	AGGAGCTTGACAAAACAAAACAGATTATTATC
Etr_7443	T	G	TCCTAGGTTTG	TCCTAGGTTGG	GCCTCGATCAGGTCTTAGGT	(0,0)	1	CCTCTTCACCCCTCCCTCTT
Etr_752	A	G	GTGCGTGATAAA	GTGCGTGATGAA	TGGGTGGGTGAGTTTGTGAG	(0,0)	1	GCTGTTAGCGAGCACACAAC
Etr_754	T	C	CTCGTTCCGTTCTGCCT	TCGTTTCCGCTCTGCCT	CAATTATAGCCGAGGAGCCCATCT	(0,0)	1	AAGATCGGTGAGGCAGAGAGA
Etr_7649	G	A	ACGAGTGGGAGCCTG	CGAGTGAGAGCCTG	CCTCCCAGACAGAGGTTGGA	(0,0)	1	GGCAACACGCACCTGTAG
Etr_766	T	C	ACGATCTGTTCTCTAGTAGC	CGATCTGTTCTCTAGTAGC	GGAAGCTGACAGCCAACATTG	(0,0)	1	GGCTGCGAGACATTGAGT
Etr_7781	T	C	GGGGAGTGTGGCTGTC	GGGGAGTGTGGCTGTC	CTCCCTGCAACCCTGAC	(0,0)	1	CACGTACTCAGCTCACAGCC
Etr_781	C	A	CTGGAAGAAATGATTCTC	ACTGGAAGAAATATTCTC	GCCACTCTGTGCTTAACCTGA	(0,0)	1	CGGGCTTGGTAGGATATGTC
Etr_785	C	T	TTGGTGCAGGAAGTGA	TTGGTGCAGAAAGTGA	GGACGCGTGCCAATTGAG	(0,0)	1	GCCCGATTGGCCACCAT
Etr_786	A	T	TGCTTCCCCAGCAATTT	TGCTTCCCCTGCAATTT	TCCTCTTCTGTGTCTCCCC	(0,0)	1	AACGAGCTCGGAAAAGAGG
Etr_7872	T	C	GGAATTCTATGGAGGCT	GGAATTCTACGGAGGCT	GCACAATGCAACAAGGCTG	(0,0)	1	GCACTGGAAGCCCTTACACT
Etr_7918	T	C	CCGACGGGATATCCGAG	CCGACGGGACATCCGAG	TACGGACCCAAGCAGGTTG	(0,0)	1	AGCTCACTCCTCACTCCTC
Etr_7974-70	C	T	TTCGTGTCGACACC	TTCGTGTCGATACC	CTTCAGCGCCAGTCTCAG	(0,0)	1	AATTACAGCAGGAGAGCCTC
Etr_8064	A	G	GATCTGTCCACCATTGG	GATCTGTCCGCCATTGG	GTGTGATGCTTCTGATCTGTCC	(0,0)	1	GCGCAAAGTGTGAAAACTGG
Etr_810	A	G	CCAAAGGCACCCCTCC	CAAAGGCGCCCTCC	CAGGTAGTTGATGGTGACCCA	(0,0)	1	GCAGCGCTCGCATCCT
Etr_814	C	T	TTTCTGCCCAACACC	TTTCTGTGCCAACACC	GGTCCACGGTCCGATGTG	(0,0)	1	ATGAGATGACTTAACAAACAAAGATTGCA
Etr_8196	A	C	AGAAGGACCTCAAATAGAT	AAGGACCTCCAATAGAT	GCTTGTCTGCTCACGACACT	(0,0)	1	ACCTCGAACTCGTTGCT
Etr_824	C	G	ACCGATGTTCTGGCCG	ACCGATGTTGGTGGCCG	TGCAGATGTTCTGTCACCGAT	(0,0)	1	CGACCCAGCCTCAAATGAGT
Etr_8281	G	A	CCTTCTGCAGCCTTCGC	CCTTCTGCAACCTTCGC	GGAGAGTATTCTCGTGCCG	(0,0)	1	ACAGACTGGTGAGGCAAGTG
Etr_8298	G	A	GAACGAGCAGAGCTGGT	GAACGAGCAAGCTGGT	TCTGCTGAAGTGAAATCCGGT	(0,0)	1	AGCAATTAAGCAGGACCCCT
Etr_832	C	T	ACGAGTTCTCGACGTTCA	ACGAGTTCTCAACGTTCA	GCAGGTCAAAGTAGACAGTCTTGIG	(0,0)	1	GCACCTACGAGATCTGCTTCAG
Etr_833	G	T	GCAGCATGTGGGGCAG	GCAGCATGTGGGGCAG	CTTCGGGAGGCAGCATGT	(0,0)	1	AGCTGTTTCGTGGGCCATTA
Etr_836	A	G	ACGTGATCACTGCCGTC	CGTGATCACCGCCGTC	ACGCAGTGCTCTCTGATTG	(0,0)	1	GTGCCGCTCAACAGCAT
Etr_84	A	G	CTGAAGTCTCTAGTTACG	AAGTCTCTGGTTACG	TGCAGGTAAATAGAGGTGTGATCCA	(0,0)	1	CCCTGTGCTGATGTGTGTAGAA
Etr_8649	G	A	AAGGCACCGGGAGCAAC	AAGGCACCGAGAGCAAC	TCTCAGGAGGCTGGGTAAAG	(0,0)	1	GCCAAGGCAAGTAAACAGTGT
Etr_8681	T	C	GACGCAGGCTGGTTGGC	GACGCAGGCCGTTGGC	CTTACACGGACCCAGCTGGAC	(0,0.5)	1	CGACCGTGTGATTTGCATCG
Etr_874	C	T	GAGTGGCGTCGACGCAT	GAGTGGCGTTGACGCAT	AGGGAGAGCCTCAAGAGCAT	(0,0)	1	TGAGAGTGATGGTTCTCAGGA

Etr_875	C	T	AGCGCGCTCGTC	CAGCGCACCTCGTC	TGCAGGCAACGGTTGTAGAG	(0,0)	1	CCCAACGGGACGAGGTTTT
Etr_8780	T	C	GCATAAACTTCAAATC	GCATAAACTCAAATC	TCGTTGTTGAAACATTGGCAT	(0,0)	1	ACATCTCGGCGTAAGTGATTG
Etr_8960	G	A	CAATGCCCCGAATGGTG	CAATGCCCCAAATGGTG	TTCAAAACGCCTCGCCAATG	(0,0)	1	AGTGGCAGTGTCCGAAAA
Etr_899	A	G	CATTGCGCACTTGCT	ATTGCGCCTTGCT	ACGGTGACATAGTCTCTGGTA	(0,0)	1	GGCACTGGATTACACCATGA
Etr_905	C	T	GTGCGTGTCTCCCGCA	GTGCGTGTCTCCCGCA	GCTTCTGAGGGAGTCTTGT	(0,0)	1	TGAAGTCTCTGCGGTACCAC
Etr_906	G	A	CACCGTCTTGATGCT	CACCGTCTTAATGCT	AGCCAGAGTTTGCTCACCA	(0,0)	1	GCATGCGAAGGCCAAGAAAT
Etr_9113	C	A	ATATGCGTCGATAGTT	ATATGCGTCAGATAGTT	CTGCAACACGGCTCGAAATA	(0,0)	1	ATCACTTGCATGCCCCGAA
Etr_917	G	A	TGAGGAAATCTGGACACTC	TGAGGAAATCTAGACACTC	CAGGTGGCACCGTTGGAT	(0,0.3)	1	CCACAAATATTGAACACAATAAGACACAT
Etr_9189	G	A	AGGACACACGTAACATC	AGGACACACATAACATC	GACACGTGTACCCCTGTCTG	(0,0)	1	TGTAATAATGTTTTACGCAAGATGT
Etr_930-35	G	C	TGACGGGAGCGGTAAGG	TGACGGGAGCCGTAAGG	GAAGCATCAGGGAGGGTGAC	(0,0)	1	TGCACACGTCTGATTGATCAC
Etr_951	G	A	TCATTTGCTGGTTGG	TCATTTGCTAGTTGG	TCCCTCAAAACGAATGTTCAATT	(0,0)	1	GGGTGTCAGTGTGAAACAT
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	TCGCACTGAATCAGTGACA	(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	CCCAGGGGTGTCGG	CAGGAGTAGGCCGAGTAG	(0,0)	3	CGCTGTGCTGTGTGAGAT
LampSD_700	G	T	ACGACGCAAAGCG	CGACGAAAAGCG	TGCGATCGCTGATGCTGAG	(0,0)	3	GACCCATACCGGTTTCACCAT
LampSD_1589	G	T	AGGGAGCCGATATTG	CAGGGAGCCTATATTG	CGACGTTGGGCAATCGTT	(0,0)	3	TCACTGTTCCATCGCAGTACTTATTTAA

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

Assay	A1	A2	A1-Probe	A2-Probe	FWD Primer	Corr	Primary Flag	Rev Primer
LampSD_1589	G	T	AGGGAGCCGATATTG	CAGGGAGCCTATATTG	CGACGTTGGGCAATCGTT	(0,0)	3	TCACTGTTTCCATCGCAGTACTTATATAA
LampSD_327	A	G	AAGTAGGTGTCTCAGTAAAA	AGGTGTCTCGGTAAAA	GCCTAAACCACTCGGATGCA	(0,0)	3	ATGTCAACAAACACAATCCACACAATT
LampSD_478	G	A	CCCAGGGCGTGCCG	CCCAGGGGTGCGG	CAGGAGTAGGCCGCAGTAG	(0,0)	3	CGCTGTGCCTGTGTCAGAT
LampSD_700	G	T	ACGACGCAAAAGCG	CGACGAAAAGCG	TGCGATCGCTGATGCTGTAG	(0,0)	3	GACCCATACCGGTTTACCAT
Lri100P121189	A	G	CACAGGCTCCGG	CGCAGGCTCCGG	GGGGAGGGAGAACACCACT	(0,0)	1	GCCGATGAGCTGTATCTGCTT
Lri101P1393771	C	T	GGTACGGGGCGGT	GGTACGGGTGGT	CTGCAGGAACCATGTAAATC	(0,0)	1	CGGTGGCATATTTGTTTGAC
Lri102P1900277	G	T	AAATCCTTGCGGC	AAATCCTTGCTGC	CTAGTGTGGGGGTACAGCAGAC	(0,0)	1	AGCTCTCCTGCCTGGGTATAG
Lri1046P6449	C	T	GCTCCAGACGGCG	GCTTCAGACGGCG	CAAAGCGGGGTGTTTTGT	(0,0)	1	GTACACGCACCGCACAG
Lri104P686936	G	A	AGGACTTCTCGGA	AGGACTTCTCAGA	CAGCAGCGCTTTGAGCAC	(0,0)	1	CAGGCGATGATCTGGAGGT
Lri105P1231914	G	A	TCACGGCCCTGGA	TCACGGCCCTAGA	GACAACCAGCTGGAGAGTCTG	(0,0)	1	CTCACCTTAAGCGGTTTCC
Lri106P1252618	C	T	AGCGTGAACGCAT	AGCGTGAACGTAT	AAGCTACAGTCGTGCACATT	(0,0)	1	CAGGGTTGGCTAGGTGAATG
Lri106P1790668	A	G	AATTGGGGTC	AGTTGGGGTC	AGACATGGTGCAGAATTATACA	(0,0)	1	GCTCAGATCGGTTTTAATTGTG
Lri107P679417	A	G	GCCTGCAGGAT	GCCTGCAGGGT	CTTGATATCGCTGCCAGT	(0,0)	1	AGTCGCGTGCAGTTGGAAT
Lri108P658763	C	A	GGGCGCCGGCATG	GGGCGCAGGCATG	CTGAGACCATGCGATCGAG	(0,0)	1	CAGCAACCCACTTGCTGTACT
Lri109P766527	A	G	CATTAATAATAGA	CATTAATAGTAGA	GAGAAGCACTGTCTAGGCCATAA	(0,0)	1	CCAGAATCATCATTTGTCAGTGG
Lri10P1667154	C	T	TCCGTCCGGCCGG	TCCGTCTGGCCGG	CTGCAGGAGCAGCTCGAC	(0,0)	1	CGAAAGAAGTTCAACACACGTA
Lri10P6216903	C	T	CAGGGCGTGCTCG	CAGGGGTGCTCG	TGGAAGAGTAGGCCAAAAACAC	(0,0)	1	CAACAACATCCTCACAGACACC
Lri10P8084542	G	A	CTTAAACCAAGAC	CTTAAACCAAAAC	CTGCAGGTGCTGTGTTAATATAGG	(0,0)	1	GTGCCTGGGAAAATGAGAGAC
Lri10P8119699	G	A	CAATGACACGGGA	CAATGACACGAGGA	GTTCTCCGAGAGTCCAC	(0,0)	1	CAGCTCTGTAGCAGGGTTGAC
Lri10P9580222	T	C	CAGAGTACCACCC	CAGAGCACCACCC	CTCCTTGCCAGCTTTCGTAAC	(0,0)	1	CACCAAAAGCACCAGCAGAT
Lri112P1524062	G	A	CCAACGAGCCGCG	CCAACGAGCCACG	ATAGATGAGCACCGGGACGA	(0,0)	1	ATGAAGGCGTCGATGTAGTC
Lri113P109152	C	T	TTGACATGACCTC	TTGACATGACTTC	TCCACTCAGAAGAATTGACTCC	(0,0)	1	GGATGAGTGGCTGCTGCT
Lri11433P5520TD58	A	G	CGTCTATTCA	CGTCTGTTCA	CTGCACTCACTACACGAGGT	(0,0)	1	AGTTGATGCTGCCGGATG
Lri11465P555	C	T	CTGCAGGGCTC	CTGCAGGGCTT	CCACTGAAGGTTGTGAAAGGTT	(0,0)	1	TGCATCAATAATTACGTGTTGG
Lri117P1107147	A	G	GGCGCTCGGTACCT	GGCGCTCGGTGCCT	ATGATGAAGCCATGTCTGACC	(0,0)	1	CTGCAGGAGAGCGATAGTGAC



Lri118P1477521	G	T	AATGCCTGCAGGAA	AATTCCTGCAGGAA	ACGGCATCTATTAGTCCACCTC	(0,0)	1	CGAGCGAGGTAGTTTGATGTTT
Lri118P434131	A	G	CAAGTGTTGGCA	CAGGTGTTGGCA	CCCAGGATGGACACGTTG	(0,0)	1	GAGTCGGCTGGGATTTTCT
Lri119P1436785	A	T	TTTGACAGCACAC	TTTGACTGCACAC	CCTGCAGGAAAAAGTGAGTT	(0,0)	1	TTTGTTTGAGAGTGCACGTTGT
Lri11P11536190	A	G	CGCTCAGACCGCTG	CGCTCGGACCGCTG	ACCCCTTCAAAGCAGTGGAT	(0,0)	1	TTAGTGGCGGGTTTTAAAGTG
Lri11P11704965	A	G	GTAACGTTCAAAT	GTGACGTTCAAAT	ACAGTCGTTCGGCTCAATG	(0,0)	1	TCAGTCCCAACCAACAAGT
Lri11P2066282	T	C	TTATAAACACAA	TTACAAACCACAA	TAATGGGAAGACAGACGACGAT	(0,0)	1	CCAAACTTCCACAAGTTCACCT
Lri11P311028	A	G	GCGGCTCCTCACG	GCGGCTCCTCGCG	TACTTCCAGCGAAGAAAGTCT	(0,0)	1	ACGGCGTCACCAACAAC
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	TCGCTCGCAGGTCAAAAG	(0,0)	1	GATGATCCCTTCCACAGG
Lri12696P1650	C	A	CTTGGGACTG	CTTGGGAATG	ACCAATATCAAAACTGGGGTTG	(0,0)	1	GTTCAATTGCTCTGCAGGTTGT
Lri128P486601	C	T	CTGTGGTGGAC	CTGTGGTGGAT	ACGTCTGCACACGAGGTCAT	(0,0)	1	GGACCCCTGCAGGAGAGGAC
Lri12P11460075	G	A	CCCTCGCCGCTCG	CCCTCGCCACTCG	GCACCTGCAGGAGATTCATTTA	(0,0)	1	AGTATCGTGGGTGTGATT
Lri12P1774736	C	G	GACTGTCGTTACG	GACTGTCGTTGAGC	CACCTCCACTCAGCCTTGTT	(0,0)	1	AATTTCCCTGCACAAGAACAC
Lri12P182981	A	C	CTAAGAAACATG	CTCACGAAACATG	GCGGCATACGACTATTAGGG	(0,0)	1	CAATTTCATGCACAAATACAA
Lri12P183087	A	G	TGTGGCAATACA	TGTGGCGAATGCA	ATTGTACGCAAAAACAATGTGC	(0,0)	1	GTGTCTCGTCTGCATAGTTTCC
Lri12P1838366	G	A	GTGCCGAAGCGTT	GTGCCGAAGCAATT	CAAGGCGGTACCTTTCACCT	(0,0)	1	GACGATGGGATGGCGAAG
Lri12P279478	G	A	TCCAACAAGGAG	TCCAACAAGAGAG	GCATTTTATCATGCGCCTATT	(0,0)	1	GTGTCATGCAGTGTGAAAAA
Lri12P3082762	G	A	GGTGGCTAACGAC	GGTGGCTAACAAAC	AAATGAATTGCGTGCAAGAGA	(0,0)	1	GGCAAAACAAAACAAGGAGAG
Lri12P5470970	A	G	TCCCACGCTGACG	TCCCACGCTGGCG	AAAATGTGCGTTTAGATTATTTGG	(0,0)	1	AGCTCTTTTCAATGGTGACCT
Lri12P6060911	T	C	CAGTCGCCCTTCAG	CAGTCGCCCTCCAG	TCAAGATCGACCTTTGTAGAGGA	(0,0)	1	TCTTTCCCTCCTACTTTGTG
Lri12P7199624	G	A	GGTGTACAAAA	AGTGTACAAAA	TTATTGTGAGGGCGATGTTAT	(0,0)	1	GGGCTAACTCTCTTGAAGTTG
Lri12P8386432	C	G	TCTTTAGCAACGT	TCTTTAGCAAGGT	AAAGACCTGCAGGCTCATAAAG	(0,0)	1	AACAGCTCCGGTATTCTCTT
Lri12P9648016	G	A	GCAGGCAGCAGAG	GCAGGCAGCAAAG	TCGTCGCACACAACATCC	(0,0)	1	CTCTGTCTGCGTGAAGGTAG
Lri131P901089	C	A	GAGAAAAACAGCAAT	GAGAAAACAGAAAT	TATTTACACCACAATTGTCAGCA	(0,0)	1	GTTACGGTCAGTAGAGGCGAGT
Lri134P444626	G	A	ATCGAGCCGAGTC	ATCGAGCCGAATC	GCAGGGTCTTGTTATTATTGG	(0,0)	1	AGACATCGTCCACCATTTGAC
Lri137P957664	A	C	TCAACCACAAATA	TCAACCACAACTA	GTAGCAAACAGAGGGGAAAAAT	(0,0)	1	TCGTAGTAGTTATTGTTACAGGTGTGT
Lri139P639349	G	A	GACCGGAGGGCTG	GACCGGAAGGCTG	ATTTTCGAGCCAGTGTGACAAAT	(0,0)	1	GCTCCAGTACGCACTGCTTGT
Lri13P10838895	C	T	GTGTCAGGTCCCG	GTGTCAGGTCTCG	CCCTATTATAAGCGCCTAGTGG	(0,0)	1	AGGGAGTGACATACCAATACC

Lri13P11116125	C	T	TGCTCCATGGC	TGTTCCATGGC	AGTGCTGTTGCTGGTGAG	(0,0)	1	ATGCGAAGGCCAAGAAATAC
Lri13P4766961	T	G	GTTATGATATTT	GTTATGATATGT	CAAGAGGATGCAGTGGTGT	(0,0)	1	GTTGAGGAGCACTGGGCTATC
Lri13P6132767	A	C	GTGTACAGACCGT	GTGTACAGCCCGT	CTGACACTGCTCCAGCACCT	(0,0)	1	TGCCCTCGACATGTTTGTG
Lri13P6221318	C	T	ACGCTGCTGCACG	ACGCTGCTGTACG	CTCTCGCAGCTCTCCAA	(0,0)	1	CAGAGGACCAGGATGAGACTG
Lri13P6230623	T	G	AAATAGAGACTCG	AAATAGAGACGCG	TTGTCCTCCACTGCTAGGCTAT	(0,0)	1	CCTGCAGCCGTATGTGT
Lri13P7256497	G	A	TTATGCCTTTGAC	TTATGCCTTTAAC	AACCATCGGTATTATCCAGTC	(0,0)	1	CCACCTGCAGGTTTTAGAATA
Lri140P591452	C	T	GGGCCGATGACAG	GGGCCGATGATAG	GCCTGTAGCACGGCACCT	(0,0)	1	GTGTCATGTGTCACGTGTGTG
Lri1432P16471	A	G	TGCCATCAGAATC	TGCCATCAGAGTC	GGAACAACACTTTGCTTTGAT	(0,0)	1	GAAAGCCAATTTAAAGAGGTGA
Lri144P657672	C	T	TCAGTCACCTTGTG	TCAGTCACCTTGTG	CCTGCAGGTCCACTGACTC	(0,0)	1	AGAGACTGATGCCCCCTTG
Lri148P462863	G	C	TTACGCACTCAAT	TTACCCACTCAAT	TAGGCAAGTGGTAAAGGGTGAT	(0,0)	1	GGTGAGTGGGTGAAGTCTGTG
Lri149P787096	T	G	GGATGGCATGTCT	GGATGGCATGGCT	TTGTCTCGATGTGAGCAAGACT	(0,0)	1	GCGCCTATAGAGACACTCG
Lri14P11709110	A	G	CACTCCACCAAGT	CACTCCACCAGGT	CACACTCAGCTCCGTCTTCA	(0,0)	1	CTCCAGCCTTGACCCATGT
Lri14P2900879	G	A	CCTCTGGGCGAG	CCTCTGGGCAAG	ATCGAAGGCACCTTGGTAGTT	(0,0)	1	GACTACCTGGTGGTAGCCAGTC
Lri14P3595836	C	G	TGCAGGTGCTC	TGCAGGTGCTG	GTGAATGCCGCCAGTAAGAC	(0,0)	1	CGCTGCAGGAATTGTAAATA
Lri14P3895562	T	G	CTTATTTTATTT	CGTATTTTATTT	TGGTGTGTTGCTGTACATTG	(0,0)	1	CGCTGTTTATTGCAGATTCA
Lri14P3943878	G	T	AGGAAACATTGT	ATGAAACATTGT	GCCAAGTACGTCGATCAT	(0,0)	1	TTACCGTGGGAGTCTGAGATTA
Lri14P4079387	C	A	AAAAGTAATGCTA	AAAAGTAATGATA	AAATCCCAGGTATAAGCCTTTG	(0,0)	1	TTACAGTTGGCACCATTGAAAC
Lri14P4102727	G	A	GAGCCATTCCGGC	GAGCCATTCCAGC	AATAGCTATCTTCTGCGCATC	(0,0)	1	GGGCGTACAATAAATGGTTTG
Lri14P4106054	G	A	GACGAGATCTGGC	GACGAGATCTAGC	AACACGACATGTCTGCAGAGTC	(0,0)	1	TCTAACACCATTCATGAACAA
Lri14P4985173	A	C	AAGGACAGGGAAC	AAGGACAGGGCAC	TCAACAACTTAAACTCACCGTAT	(0,0)	1	CCTGCAGGTTATCATCAAGAAG
Lri151P237159	A	C	CGTCACATACCA	CGTCACATCCCA	GGCCAAACCATTTGAACAGT	(0,0)	1	AGCCCCATGACAAGACTCC
Lri159P658357	T	C	AGCGCGGCCGTAC	AGCGCGGCCGCAC	GTTTGTAGCCCTTGCCAAC	(0,0)	1	CGGTGACAAAAGAGTTTCAGAG
Lri15P1409554	T	A	GAGTTTGAATCCG	GAGTTTGAAAACCG	GCAGGTTGAAATTGGAGGTTAC	(0,0)	1	AACCTTCTTGCTGGGATG
Lri15P2172074	A	G	AAATTGTAATTA	AGATTGTAATTA	CGCACTGGGAAAGTTGAGTAA	(0,0)	1	TCAAGACAAGTGTTACCAATG
Lri15P6598748	G	A	GTAATGTGCAC	ATAATGTGCAC	ATGTGTCCGTGTGTCTATGGT	(0,0)	1	GCAGGGAGAAATCCTTCAATA
Lri16103P3900	T	C	AGCAGACCTATGC	AGCAGACCTACGC	TTCAGCCACTTCAAGGAGAACT	(0,0)	1	CTGGTAAATGGCCTTCTGTAG
Lri162P690722	C	T	CTCCAAATCAG	TTCCAAATCAG	ATTGCGTGTGTGCTGTCT	(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	CTCGCGACAGGAGGTCT	(0,0)	1	TCAGGACTGTTAGAGTGTGGA
Lri177P26697	A	C	ACCAGCATGGA	ACCAGCATGGC	ACGGACAGCTCGTCGTTG	(0,0)	1	CCGCAGGACCTTAACCTGAT
Lri178P237573	A	C	ATTGGTGAGATCTA	ATTGGTGAGCTCTA	GTTCCGTTATTTCGACTTCC	(0,0)	1	GTC AAGTGGCGCATTTCAT
Lri178P423530	G	A	TGGAGCCGTGTGA	TGAAGCCGTGTGA	AGTGGATAAAATTGACGCCGTAT	(0,0)	1	CGTAGATCGCACCACCAAC
Lri17P2957024	G	A	TCTCGATGATCAG	TCTCGATAATCAG	CATCACCCTCCAGAGTCAG	(0,0)	1	GGAAACCTTCATCCAACAGT
Lri17P3232763	A	G	TCGCACACCGACT	TCGCACACCGGCT	CTGTGCTGCATCCAACAAG	(0,0)	1	AAATGCCCCGAGGGATAAT
Lri17P385674	T	C	ATGACGTGATACG	ATGACGTGACACG	GGGATCGCAGTGCCTAT	(0,0)	1	CTCGTCTCCGTCCAGGT
Lri17P5047059	T	G	CGACCAAGGGTTT	CGACCAAGGGGTT	CAAGGTATATCGGCAGTGTGC	(0,0)	1	GTAATGCTGGTTTGAATGTTCG
Lri17P6620172	T	C	AATTGTCGTG	AATTGTCGCG	CCCGGTGATGAAAATTGC	(0,0)	1	AAC TTGTGGAAAGTCAGGTTTTT
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	CCTGGCTTCTCTGTGTTC	(0,0)	1	ACTCACTTGTGGTGGTGAACG
Lri17P8999134	T	G	GATGAATCCACAT	GATGAATGCCACAT	CAGCCATGATCTATCAACTTGTG	(0,0)	1	CAGGGCTAGATGGATTGTTAC
Lri17P9471416	G	A	GCAGGTGTGCCCC	GCAGGTATGCCCC	TGAATGGTCTCTGCACGATCT	(0,0)	1	GCCTGGCGAGAGACACTTTTAT
Lri18P1201819	A	G	GGCCAGCCACTTC	GGCCGGCCACTTC	AAGCGCACGTCGAGGTCT	(0,0)	1	AGTCGCACACTGTGAGAAGTC
Lri18P163972	G	A	ACTTGTGGCGTGC	ACTTGTGGCATGC	GTCGAAGGCTGCACGTT	(0,0)	1	GAGAGGTCTACTGGTCCGACTG
Lri18P3516203	A	C	CATTTATCAAT	CATTTATCACT	GCTGGTGTATGCCTGTAAACAA	(0,0)	1	CAGCCCTGCAGGTTTGAG
Lri18P4745725	A	G	ATTGTGCTGTATC	ATTGTGCTGTGTC	TGGGACCGAATTCTGAGTGTAT	(0,0)	1	AAAACCGACGTCCTCTTAGC
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	TTGTTCCGGTTCTG	AGTGCCTGCAGGACGTGT	(0,0)	1	GCAGAAGGAGAGATGGACAGAC
Lri18P8805776	A	G	AGTCCCTGCA	GGCTCCCTGCA	GCCAGATCACGGAGAGAAATAA	(0,0)	1	CTCCGGCCGTGTGAAATC
Lri18P9016369	A	G	CATTTGGTGCA	CATTTGGTGCG	TGTACATACCCAACCTGTCTAA	(0,0)	1	CTCGCCACAAACATCACCT
Lri19P6892352	C	G	GCGTCTCGGCCAC	GCGTCTCGGCAC	GAGCTGCCCCATCGTCTC	(0,0)	1	GGCTGCTCAGACGTCACTT
Lri19P7387400	T	C	TGTGCACAGCT	CGTGACAGCT	CAGCGTGACGAGTCCTG	(0,0)	1	ACTAGGATGACATGGACCTGGA
Lri19P9473436	C	T	TCCCTGGTGTCCA	TCTCTGGTGTCCA	GGTTAGTACAGATTGGTGAAAGTGG	(0,0)	1	GGTGTCTGGTCTGGAAGG
Lri19P9852768TD53	A	T	GATA[GT]ATTCAT	GATA[GT]TTTCAT	ATTGCCTGCAGGTTGGAAT	(0,0)	1	ACATTCAACAATGACCACGTT

Lri1P11647852	C	A	TTGTCACACACT	TTGTCACACAAT	GTGCTCTCCAAGCTCTAACCTG	(0,0)	1	GTGACCACCACCCCATCAC
Lri1P16171976	G	A	AGTAAAAGGA	AGTAAAAGA	GTTTGACACGCGTTTGAGAT	(0,0)	1	CAAGACCCTTTGCTTCTCTGT
Lri1P17366484	T	A	GCTGATCTCTCA	GCTGATCTCCACA	CCTCCGGCAAGAAAACAAG	(0,0)	1	CTGAGGTCCACAGTTCATTG
Lri1P17392168	T	A	GAACGTCTGTGTC	GAACGTCTGCAGC	TTTATGAACACCAGTGCAACCT	(0,0)	1	CAGGTGAGTGGCGCTGTAT
Lri1P17477528	G	A	CCAACGCAGCGGC	CCAACGCAGCAGC	GGCAATTGCAAAGATCGTG	(0,0)	1	CCACCTCTCTCTGAACAC
Lri1P6957846	G	T	GGGGGCCACTGCG	GGGGGCCACTTCG	ACACCCTGCAGGATCAGC	(0,0)	1	AGCAGCATCGGAATGAAATC
Lri1P8709918	T	C	GCTTTTCCTAGCT	GCTTTCCCTAGCT	GCACAACTACTCTGGTGCTTTG	(0,0)	1	TGCAACCTCATCTTCTTACCA
Lri20P3277044	C	T	ATCTTCTCCAGG	ATCTTCTCCAGG	CGGAGTCTCTGACGAACTCTAT	(0,0)	1	GCTTCCCAACCCCTCTT
Lri21P4463586	T	G	AAAAGCATTGAGA	AAAAGCATGGAGA	GAAATGGAACAGAAGCTGAAAA	(0,0)	1	AGCATTGTACGTAATCCTTGT
Lri21P5493330	T	C	GCAATCCTGTTGT	GCAATCCTGTCGT	GGAGGTGACCGATATTGTGAGT	(0,0)	1	CTCACTATGCCCAAATGATGCT
Lri21P6647296	G	A	GGTCCGGCTGGAA	GGTCCGGCTGAAA	TTCTAACTGTTCTCTTGACG	(0,0)	1	GAGGCAGGGAGACTTAAGTGAG
Lri21P702243	G	A	GGGTGAGCGCGGT	GGGTGAGCGCAGT	TCCCTGACGAGCTCGAC	(0,0)	1	CTCGACGCACTTGGACATAAT
Lri21P9294857	G	A	TGTTGTTGTGCA	TGTTGTTGTACA	ACACAAACCCCACTGCAAG	(0,0)	1	AATGTCCTGCAGGTGACTGAG
Lri222P307512	C	T	AGCCTTTGCGCAA	AGCCTTTGCGTAA	ATTAGGGCTTAATCACCTGGAG	(0,0)	1	CGGCGAGTGGTTTAATTTAC
Lri22434P974	G	C	GCTCTCTCTCT	CCTCTCTCTCT	CTGCAAGGTGGTGGTGAC	(0,0)	1	CGACGAGGATCCAGTAGTAGTTG
Lri22P1323692	C	T	ATCATCATCCCGT	ATCATCATCTGT	TCGTCATTAGCAGCAATAGCAT	(0,0)	1	TGTGTGTTGTCTGAGTAGTATTGTGA
Lri22P3313925	G	C	GCTTGACGCGTG	GCTTGACGCCTG	GTCGACAATAACCTGGGGAAAC	(0,0)	1	GCAATATCACCCACCAAACTGT
Lri22P7082523	A	C	CGCTGCAGGACAA	CGCTGCAGGCCAA	AGCAGGGGGAAACACACAG	(0,0)	1	ACCGCTGCACACTCGATA
Lri22P7625675	T	C	TTGGAAGGTTTC	CTGGAAGGTTTC	CATGGCAAAAGGATTTCCTTC	(0,0)	1	CACAGTGGTACTCATTGTATCAGC
Lri22P8175926	G	A	CCCCTGCAGGGTG	CCCCTGCAGGATG	ACTAGGGCAAGTCATCACATCA	(0,0)	1	CCTGGAATCTAGGAGTGATTCTG
Lri23P3389463	G	A	GGCTCGTGCAACG	GGCTCATGCAACG	CAGGCTTGCCACTTTTGAC	(0,0)	1	GACAGCGTAGTAGCACCAGTT
Lri23P8725518	A	C	CGACATCACAATG	CGACATCACCATG	GTTGAACCGTAGCGATGAACTC	(0,0)	1	GGCTATGCGTGTGACGTTT
Lri23P9526641	T	C	GAAGTTTGCGCGT	GAAGCTTGCGCGT	CATCTCCACCCCAAGGAT	(0,0)	1	CGACTGTGCCAGGACCTT
Lri24296P1937	C	T	GAATTGGTTTCAC	GAATTGGTTTAC	GGGGAGCACACGATTAC	(0,0)	1	CAGCCTGTTGTATTGCCAGA
Lri2481P8393	G	A	GTGAGAGCAGGCA	GTGAGAGCAGCA	CAGGATGGACCCTGGAGAC	(0,0)	1	CTGAGGGGACTCTTCCTCATCT
Lri24P3183281	A	C	GTTCCCAACTAA	GTTCCCAACTCA	CCGACAATCTATTGAACTC	(0,0)	1	AGCCAACCGTGCTAATAAGAAG
Lri24P3549440	A	C	CCCACCTGAATA	CCCACTGAATC	CAGCTAAGTTCGCACTGTAG	(0,0)	1	ATTGCAACCCGATACAATCT
Lri24P3934915	A	C	TCCACCACCACT	TCCACCACCCT	AGGTAGCCTTACCCTACTGC	(0,0)	1	TTGAGAGGTACATCCAGGATCA
Lri24P4354883	T	A	AATTTTACTATT	AATATTACTATT	CAAAGCCCACTGGCAATTACT	(0,0)	1	GCAACCACCATTTATTTCAA

Lri24P4954513	G	A	AGAGACAAGGCCAC	AGAAACAAGGCCAC	GGGCTGTGGCACTGTAATAAT	(0,0)	1	ACATTGTAGCCATTATGAAGCA
Lri24P6514737	G	A	CATTAAAGAAATAA	CATTAAAAATAA	TAAATGCATGTGAGCCATTTC	(0,0)	1	GAITTTTCCCACTTGTGGTTTT
Lri24P6808546	T	A	GCACTTTTAATT	GCACTTTTAAAT	GAAATAGACCGTGTACAGTATTGA	(0,0)	1	CGGTGGAAGGACAACAACTA
Lri24P7481704	A	G	CTACGTTTTIACG	CTACGTTTTTGCG	AAGCAGGTAAAGAGGGTTCACA	(0,0)	1	TGAAAACAATACAAGTTCACAACAA
Lri24P7765916	T	G	CATCACCTCTTCT	CATCACCGCTTCT	CTTCCTTAGCTGCCATTTCATT	(0,0)	1	TAAATGGACTTGGGTAGGGACA
Lri25061P2542	C	T	TTTGCCACGGCCA	TTTGCCATGGCCA	GTCCTGACGGGTTCGTAGAGT	(0,0)	1	TGTAGCTCCTTCGCGTTAGAT
Lri25P2230291	G	A	GTCTGTAGGCGGA	GTCTGTAGGCAGA	TTCTTGTGTAGATTCCACCT	(0,0)	1	TTGTCAATAACACTGCCTTTGG
Lri25P7373093	C	T	GGCTATACAT	GGTTATACAT	TTTCAAGCACGGTGAATACTG	(0,0)	1	TTCTCGAAGCTTTCATTAGTTGG
Lri25P8275961	A	G	GCATGGTTCCTGG	GCGTGGTTCCTGG	GACAACCACAAGGCAGACATC	(0,0)	1	ATGATGGCTCACCGATGAAGT
Lri25P8435093	T	A	TTTTTTTATTT	TTTTTTAATTT	CAGGCTGTGGGTGCAGTA	(0,0)	1	CTTGCTCACAGAACTGTACGA
Lri25P8849487	A	T	GTCAGTCAGCACCT	GTCAGTCAGCTCCT	GCAATGTTCAATTCCACCTG	(0,0)	1	CTTGTCGTGATGTACATTCTGC
Lri26245P408	A	C	CAACAGGAAAAAG	CAACAGGAAACAG	TTAAATTAATTTGGGCCTTAGCC	(0,0)	1	GACTTCGCCTGTGACTCG
Lri262P62290	T	C	ATTTACAGCATGC	ATTTACAGCACGC	CGTTATAAACACACGCGTTCC	(0,0)	1	TATAGCGCCACGTGTTGTATTC
Lri26500P1136	T	C	AATATGCGTCTGA	AATATGCGTCCGA	GATCAATTTGCTTGACCTG	(0,0)	1	AAGCAGTATCCATCACTTTGCAT
Lri26P4406096	A	G	GGAAGTGGCGTT	GGAAGTGGCGGTT	CTGCAGGTGATGCTTGAGAC	(0,0)	1	TACAACCTGACGGTGCACAT
Lri26P6719186	C	T	GCAACAGCTTCAG	GCAACAGCTTTAG	ATCCTGAACCAACCGATGT	(0,0)	1	AGGCTGGTGTGAAGTATACATA
Lri2718P13929	C	T	AGTAGCCCGCTGA	AGTAGTCCGCTGA	TTTTGGCTTTTATAAGACAGTACATTA	(0,0)	1	AAACTGAAAGGCATGCAGAAAC
Lri27P6150884	T	C	TTACTCAAGATTC	TTACTCAAGACTC	CATCAGGGTTGTGTTTGAGAT	(0,0)	1	CCACACACAAGACATTATCAAC
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	AAATTTCCCTGTGCCCATTT	(0,0)	1	TGCTGCGTCTGGTAGTTGTCTA
Lri28P628762	C	T	GTGAGTTACCTTC	GTGAGTTATCTTC	ACGTCTCCGGCTTCGTTAG	(0,0)	1	CCAAAGACAAGGGTCCCAAC
Lri29P1902704	C	T	CGGGGTAGGCCGG	CGGGGTAGGCTGG	GGAGAGCGTGCCTTCTGG	(0,0)	1	CCATTTCTCTCACCTTCATCTC
Lri29P2715537	C	T	ACCCACCGGTTGGC	ACCTACCGGTTGGC	TATCCGACATGCCAACTACAC	(0,0)	1	ACACCCGAGACGGCTTTT
Lri29P3853819	T	C	TGGGGTACACTGT	TGGGGTACACCGT	GTCCGATAGCATTTTGCTCACT	(0,0)	1	ATCCATGGAATAACACGATCC
Lri2P10660681	A	T	GGAGGAGGGAACG	GGAGGAGGGATCG	GTTGACATCATCTCGGCTGTAA	(0,0)	1	GAGCGAGGTGTCTCGTCTG
Lri2P10747040	C	T	TCAGTTAGTTCCT	TCAGTTAGTTTCT	ATACAAAAGGGACCTTGCGTTG	(0,0)	1	AGATGGAGCGGGTGGTAAT
Lri2P10948512	T	C	GGTAGAGTGGTCG	GGTAGAGTGGCCG	GACGTGATCTGCACCTCCTC	(0,0)	1	GTCAACCCCATCATCTACTCC
Lri2P11971110	A	C	GGCTCTTATA	GGCTCTTATC	GACAGATTCAAAATGGATGTGG	(0,0)	1	GCAGGAGACACGCCAACT

Lri2P12835756TD51	A	G	AGACCACTGTG	AGACCGCTGTG	AGCAGTATTTGTCGATTCTGT	(0,0)	1	TTCTCTGCCACCTTGGCTAC
Lri2P14986968	T	C	TACCACGGTCT	CACCACGGTCT	CTCCCGAGGGGCTCATAC	(0,0)	1	GCAGAGCTGCTGCTTGTTT
Lri2P16247548	A	T	TCCACGAACAATG	TCCACGTACAATG	GCACCGTATTTGGACAACG	(0,0)	1	ATCGTTCAGATCCGGCAAG
Lri2P16250399	T	C	AAATCATAGATAA	AAATCAGAGATAA	ACTCATCACTTTGCCACTACCC	(0,0)	1	GGTATGCAACTCGCAAAAGTTA
Lri2P16333005	T	A	TCCTACATCCT	TCCTACATCCA	CAACGTAAATGGACAAATGATGG	(0,0)	1	CGCTTTACAGAAGGATGATGTG
Lri2P16367064	A	G	ACAATCTGTCTAG	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	TGTGTTACTCGTA	TGTGTTACTCTTA	TTCCGGAGCATGCTATAACC	(0,0)	1	GAGTGAATTACTCTACCTGACATGAA
Lri2P697855	C	G	TTGCTCATGTGGG	TTGCTCATGTGGG	CCAGATCAGTATTGTTTGTGTGA	(0,0)	1	TTTATTGAGGTAACGAGCATGG
Lri2P7179941	A	G	GGTGCTTGGAAATA	GGTGCTTGGAGTA	AGGTTCTGCAGGACATCAAAAGT	(0,0)	1	CACCTGCCCCAAAAGTTCAT
Lri2P7418446	T	G	TATATGCTCTT	GATATGCTCTT	AGGGCATGTGCAAAACCAT	(0,0)	1	AGTCTTAACCCAGGGGAATCAA
Lri2P9432908	T	C	CATAAGACACCAA	CACAAGACACCAA	CAATTGTGTTTCATGTGGATT	(0,0)	1	GCCTACTGACCACCTCTTAGCC
Lri30P2608358	G	A	GAGACCGTGGTTT	GAGACCGTAGTTT	GGCCTCCCACTTCGAATC	(0,0)	1	TGTTGTTGCCAAGTCGAAAATA
Lri30P2645807	C	T	AAGTGCCCTCCTG	AAGTGCCCTCTTG	GCTACATCATTTGCTGTTGGT	(0,0)	1	GAGAGCGTGCAACAGATCCT
Lri31P1720639	T	C	CCTTGACTGCCTGC	CCTCGACTGCCTGC	GTGGTAGTAAACATCGCGACA	(0,0)	1	GTGCTGTTGGTGAGTGAATGAT
Lri31P2117932	A	G	CCATCCGTTT	CCGTCCGTTT	ATGAATTGTCACGATACGTGGT	(0,0)	1	GCAAACGAAACAGAAGGGAATA
Lri31P2211794	T	C	GGGCCCTTCCACA	GGGCCCTCCACA	TGTGTGTCATGTTACAGACCT	(0,0)	1	GATGAAATGCAGCCAGATCAC
Lri32744P2002	T	C	TGATGCAGGGTGG	TGATGCAGGGCGG	CAGGTATGGTGTGCGTGCT	(0,0)	1	CATGTTGTAGAGCTCGTGAAG
Lri32P2538291	T	C	ATTTAGTTGCTGA	ATTTAGTTGCCGA	CATACGTGTGCATATGTTGTCA	(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	CTTCCTGCAGGTCTGTGTGT	(0,0)	1	CTCAAAGTGAACGAAGCCGTAG
Lri34P1263783	T	A	TCCGTAGCTCGGC	TCCGAAGCTCGGC	GCAAAGCACTCTCCCTACACT	(0,0)	1	GTCTTTGTGTTGCAGGCACTC
Lri34P1457601	G	T	TGCCGGACTCGCG	TGCCGGACTCTCG	GGCGGTGCCCTTGTAGAC	(0,0)	1	CCCATGGACTGCGTCAAG
Lri35P1746600	G	T	CTGTTGTGGGAA	CTGTTGTGGGAA	GTCGATCACATTACTCGTACCG	(0,0)	1	CTCCTCGCTCAAATGAGCACT
Lri35P3483061	G	A	CTACACCGATGTA	CTACACCAATGTA	TATTGGTCTGTGCTACATCG	(0,0)	1	CCGGATAGCCTGTAAACAACTG
Lri3691P10383	A	C	AGGGTCTGTTA	AGGGTCTGTTC	CCTGCAAGTCACTCTCAATCAGT	(0,0.3)	1	ACTGCTGTGCCAGGCTAGGT
Lri36P402209	A	G	GAACATCAGAGAG	GAACATCGAGAG	AGTCCTTAGAAGAAGCGATCC	(0,0)	1	AGGAACCGATCCATCTTCATAC

Lri37P1167580	G	T	CACCTGGCCAGAT	CACCTGTCCAGAT	GGCAACAGTTTGCTTACGATT	(0,0)	1	CCTCCAGGCACTGTGATTTTAT
Lri37P1334668	A	T	AATATTCTCATA	AATATTCTCTTA	GGACCCTGAGTCTGTGCTTG	(0,0)	1	GTTC AATTCTCTGGTTACCCCTCA
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	CCTGCAGGTTGAG	GAGTGGTGAGGATACGGTTGTT	(0,0)	1	GGAGGCTGACACAATGAGATT
Lri39P2374814	G	C	GCAGCGAGCTG	GCAGCGAGCTC	GTACGAACCTGAATCCCGACT	(0,0)	1	GGGTTTTTGGTCGGCTTG
Lri39P3784671	C	G	ATTCAAGGCACAG	ATTCAAGGCAGAG	GAACACCAAGCCCCATTGT	(0,0)	1	CGTGCGAGGATGAGGTCT
Lri39P4974575	C	T	TTTCTTTTATTACA	TTTTTTTATTACA	GACACTGCCAGCCCAAAATA	(0,0)	1	GGCTTTTCTGGGTAATAAGAAAAT
Lri39P5026600	T	C	CCGACGGGCATGG	CCGACGGGCACGG	GAGTGGGGCTTCCAGCAG	(0,0)	1	CACGCGAAGTTGTGAGAGT
Lri3P10860799	A	G	ACACAGCGTAGTG	ACACAGCGTGGTG	CGGGTTTTCTGTACATATCCT	(0,0)	1	GAGTTTAAACATACACGTGGCATT
Lri3P11837289	G	C	AGGGGCATCTTT	AGGGGCATCTTT	CTGGCCAGTGTGCAAGAAC	(0,0)	1	GAAGGCTTTCCACCAAGAGAG
Lri3P13239723	T	G	TGCCTCCTGCA	GGCCTCCTGCA	TGAGCTCATCCTTTTCACAGAG	(0,0)	1	AAGCGAGTGGTGACGTG
Lri3P15907151	T	C	TGAGAAGGCATGC	TGAGAAGGCACGC	GTCCCAAGATTACCAAGGAGA	(0,0)	1	CATCCACGGTTAACAAAAATCC
Lri3P169003	T	A	AGGGTTGTTGTGT	AGGGTAGTTGTGT	GCAAGCAGGAGTTGAATCAAAC	(0,0)	1	CCTGCAGCGTAAATATGACCTT
Lri3P5546698	T	G	TGGCTTTGTTTG	TGGCTTTGTTGG	ATGTGGTTCAACTAAGCAATGG	(0,0)	1	GAAGGCAGATAAACCAACGAC
Lri3P9055258	C	T	AAACCCAGGCCCA	AAACTCAGGCCCA	GTGCTGGACTCGGGAAAC	(0,0)	1	CGGTGATGACACTCGTGACT
Lri3P9532051	G	T	TGCTTCCCACGT	TGCTTCCCCTT	CAGGCTGAGGACGACAATG	(0,0)	1	TTCTGCCAGCAATGACACC
Lri40P5376191	C	A	GCTCCTCGGCCGA	GCTCCTCGGCAGA	AAGACACGGCTTCATCATC	(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	GATGGCATAGAGCAAAATCGAC	(0,0)	1	TTGAGTGCCTGCTGCTAAA
Lri44P3432223	T	C	TTATTTTAGCT	TTATTTTAGCC	CTGCAGGTTGCGTCTTCTT	(0,0)	1	CCTGGCGACCTCTTCGTAT
Lri44P3836279	A	T	AGACGCCTCCA	AGACGCCTCCT	CCCTTATTTAAATCCCCGAGA	(0,0)	1	GTGCACTGTTGCTATTGCGTA

Lri44P527021	A	G	GATCAGACCTGC	GGTCAGACCTGC	GACACCCTGGGGTTTGTG	(0,0)	1	CTCCTGCAGGCACCAAAT
Lri45P1246569	C	G	GACGGACAGGCA	GACGGACAGGGA	CACCGCTCCACAACTG	(0,0)	1	GTGACAGGTGAGGGTGAGAGT
Lri4631P8667TD39	G	T	TGGCTGGGACC	TGGCTTGGACC	AAGAGCAACCCCAAACATTAC	(0,0)	1	CTATAGCACGGACGACTTACCC
Lri46P2660109	C	T	CGCGGAACGCAGA	CGTGGAACGCAGA	GTTGCGCATGGAGGAAGT	(0,0)	1	GATGATGGCGAAGGTGTAGAC
Lri46P2937100	T	C	CGTCGTGGAGTGG	CGTCGTGGAGCGG	AGGAAATGGTGAAGGTCATCC	(0,0)	1	GCATCTCTTCGTTGTCATCT
Lri46P4260004	T	C	TGCAGGGCTCCT	TGCAGGGCCCT	CTCAATCAAGTGCAATTTCGTC	(0,0)	1	ATGCATATTCACACGCACACAC
Lri47P1274188	A	G	CACGCACGGCAA	CACGCACGGCGA	CACCAAAGCGTATATCTGCCTA	(0,0)	1	CCACTGACGGATCATTAGC
Lri47P4802446	A	G	CGCCGTGTTTATG	CGCCGTGTTTGTG	CTGCAGGTGTTGCCGTCT	(0,0)	1	GGATAAAATTAATAGTCCCACTCG
Lri47P580971	G	T	GCAGGTCAAAGCG	GCAGGTCAAATCG	GACACTCCGACTTTGTTCCTC	(0,0)	1	CTTGTGGTGGTGGTGGTTTT
Lri487P66561	T	C	GGGCAAACTACCGC	GGGCAAAACCACGC	CCTGCCTGACGATTGAT	(0,0)	1	CTTTGGAGCGCAAACATTG
Lri48P1014973	T	C	CCGACCATGAT	CCGACCATGAC	TGCAGTTTACTCTGGCTTTGA	(0,0)	1	GGTCGTAGTGCATGTTGGTCAT
Lri4P11912704	C	T	GGGTATCCGCGTC	GGGTATCTGCGTC	ATCTTAATCCGGCCCTGCAT	(0,0)	1	GAAGCTGCCACGGTCAT
Lri4P12290187	T	C	GGATGGACTGTAC	GGATGGACTGCAC	CTCCAGGCTGAACCTCG	(0,0)	1	ATAACCCATTGACACATTGCAG
Lri4P14283823	A	C	TGCAGGGCCCAAGT	TGCAGGGCCCCAGT	CTCGAGCTTCCAGAGACTTCC	(0,0)	1	CCTCCTCTCAAACCTCAACTC
Lri4P1741698	C	G	AGGCCTTGTGCAC	AGGCCTTGTGGAC	GGGGATCACTATGCTGGTATTG	(0,0)	1	CCTTTGGTGACCTATGCAGTG
Lri4P2731292	G	A	TGTGACATGTCC	TATGACATGTCC	CCATTACCTGCTGCAAGTTGAC	(0,0)	1	GGCTTGCCTTCTCTGCTACTTA
Lri4P3128860	T	C	AGTTGGAAGCTAG	AGTTGGAAGCCAG	AAGCCCTTTCTTTAAATGTCA	(0,0)	1	CCTGCCTGCAGGGTACTACTAA
Lri4P5424460	T	C	GGTAATTGTAT	GGTAATTGTAC	AGCATCCTTGGACGACATTACT	(0,0)	1	GCGAAATTGTCCACAGC
Lri4P8684156	C	T	CACACACAACCC	CACACACAACCTCC	CCGAATGATAAAGCGGACAA	(0,0)	1	CTGCAGGGCATGAGAATAGAT
Lri4P8958596	C	T	TGCAGGCAAGCCA	TGCAGGCAAGTCA	ACGCTATACGTGACATTTGTGG	(0,0)	1	ACCCTGTGTTAAGGCCAACTC
Lri4P9222922	T	C	TGGCCTTAAGTCC	TGGCCTTAAGCCC	TTCCACATCATGGTCAAGTACC	(0,0)	1	GGGATACATGAACCTCATACCC
Lri4P982449	T	A	CACAGCCACAT	CACAGCCACAA	AACTGTAGGTGGAAAGGTCACA	(0,0)	1	CACATTTTCAGGCAGCTGAT
Lri50P1221681	G	C	TTGCCACGTAG	TTCCCCACGTAG	AAGATCTGGCCACACCAAAT	(0,0)	1	GCATCTGTTCTCCAGCTCTA
Lri50P1657665	T	C	TTTCTCCAACT	TTTCCCAACT	GCGTAACAAGGTCTCATTATTGC	(0,0)	1	CTGAAAGCTGTCCAGTAGGTT
Lri51P900701	A	G	TGCTCAATGAAGA	TGCTCAATGAGGA	AGGATGAGAAGCACCAGCTCT	(0,0)	1	CCCTCACTCTGTCTTGTATCT
Lri5215P4376	C	G	CATGCCGCTCTCA	CATGCCGCTGTCA	AGTCCTCTTGCCACCCATC	(0,0)	1	TCCGTCTTCGACACGTCAG
Lri5229P1229	A	C	TTCCACACCAAC	TTCCACACCCAC	AAGGCAACAAAACACCCCTTC	(0,0)	1	AATGAAGGCTACCCATGTTTC
Lri5244P5218	T	A	GTAGTAATAATA	GTAGTAATAAAA	CGTTGTAGACCACAGAACGAAC	(0,0)	1	GCAGGCACGAAAGTTTCAA
Lri5270P9970	A	T	ACGATATAACAAC	ACGATTTAACAAC	AATGTCCACGTTTCATATGTGC	(0,0)	1	ATTACCAAGAGCATTGACCAAC



Lri5345P10185	T	A	GAACGGTGTAGTC	GAACGGTGAAGTC	TGCAGGTATAAACTAACCTCGT	(0,0)	1	CTGTGGTCTACATTGGGATG
Lri53P1124643	G	C	GGCATTTTGAGTG	GGCATTTTGACTG	TGCAGGTTAGGGGAAATGAGTA	(0,0)	1	GGAGAAGTGCTGCTCGAAAG
Lri53P2383812	A	G	TGCAAAATACACCC	TGCGAAATACACCC	ACTGCCTCAGGAATTCATCAT	(0,0)	1	GCAGCTTAAGTTAACACAAATTGTAA
Lri53P2456049	A	G	TTGCAAGGTTAAA	TTGCAAGGTTAAA	TTAACGGTCTCCCTCTCCAG	(0,0)	1	GATGTAAGCCGCTTGTACAG
Lri53P338003	G	C	CTGACCGTCTGCTG	CTGACCGTCTCCTG	AAGCCGTACCGGTGTTTC	(0,0)	1	GTCAGTGGCACCTGCTC
Lri54P1001845	A	G	CGGGCGCAAGAGA	CGGGCGCAAGGGA	TTCTCGGGTCTCTTGAAGT	(0,0)	1	GATCATCTGGCTGGGTCTGTA
Lri55P2165401	G	A	CTGCAGGCGAGTC	CTGCAGGCGAATC	CCGTCTTGTCTGATCCTTCTT	(0,0)	1	ACGCTTTCCCAAAGTTAAG
Lri55P3190566	C	T	ATCTTAAAACTC	ATCTTAAAAATTC	ACTCACTCGCTGTGGTCATAGA	(0,0)	1	CGTTTTGGAGAACAGGAGGAT
Lri563P38486	G	A	AGAACTCTGCGCC	AGAACTCTGCACC	TTGGGAGTGAATGTTGTCTAG	(0,0)	1	TAAGACGTGGACGTCAAACC
Lri5898P7578	C	A	CAGGCGCGGAT	CAGGAGCGGAT	GATTAGCTTCCGTCAACGTCT	(0,0)	1	ATCGTCTAACCGTTACCTC
Lri5P1244864	G	C	CGGCAATCCAG	CCGCAATCCAG	TTTGATGTCGTTCTGATAAGG	(0,0)	1	CTGTCATACGTCACCTTAC
Lri5P12934722	G	C	CCTGGAGCTGGAGC	CCTCGAGCTGGAGC	GTACCTTCCAGTACCGCAAAT	(0,0)	1	TTAGAACAAAGGGGATTGTCA
Lri5P13075196	G	C	ATTCCGATGCTAT	ATTCCGATCCTAT	GCAATAAAAGGCCACGAAATTA	(0,0)	1	ACCTCTGGTACCTCAGGGTCA
Lri5P13191816	T	G	TGGCTCTGCATCT	TGGCTCTGCAGCT	GCAATAATTGTGCCATCATGC	(0,0)	1	CTGCAGGGGTGCTTGTCTA
Lri5P14389115	C	T	GCACGGGCACAC	GTACGGGCACAC	GTGCCCCGGTTACTGATG	(0,0)	1	GTGGGCAGCGTTGTGAGA
Lri5P14629399	G	T	TGCGACCTTGGCT	TGCGACCTTGCTCT	AGCTCTGTCTCGCCCTCT	(0,0)	1	TGTTACCAATTAATAACACAAATCTCG
Lri5P2456252	T	C	TTTTTGCTAGAA	TTTTTGTCAGAA	ATCTGCCTGCAGGAATTGAT	(0,0)	1	TAGTCGTTTCACTGGACACTG
Lri5P3706885	G	A	TTTGACTTGGCA	TTTGACTTGACA	TTTTTCTATGTTTGAAGGAG	(0,0)	1	ACAGGTACAAGCAGGCTCTGG
Lri5P4043379	C	G	TTAAGGCTGACT	TTAAGGCTGAGT	CACGTAGACACTCATCTTTTGC	(0,0)	1	ACAGTATAAAACAAATGCCTCCA
Lri5P4269100	A	G	TCCTCATCCTC	TCCTCGTCTC	CTGGTCGTCTCTCTGCTC	(0,0)	1	TCCTCGCCGTGGATTTTC
Lri5P4640927	A	T	TCTTCATTCCAGC	TCTTCTTCCAGC	TGAAAAAATGGGTCCCTAACA	(0,0)	1	TCCTCAGGGTACAAACATACA
Lri5P5071040	T	A	ATTATTCTCTCA	ATTATTCTCACA	GTCACAAGGCTTATGCAAATGT	(0,0)	1	AGACTTCACGAATATGGCAACC
Lri5P7155011	T	C	GTGAATGTGTTGG	GTGAATGTGTCGG	AATTCGCATCAGGGTCTCAG	(0,0)	1	ATTGTTGTGTTGCATTATCT
Lri5P9200047	G	T	GAGAGAATCTGCG	GAGAGAATCTTCG	AAACCTTAACATTTCAGCACTCG	(0,0)	1	GACCTGGAAGGAGTGTCACTTT
Lri5P9366468	T	A	GAAAAAGTTACGT	GAAAAAGTAACGT	GCAGGCAGAATAGTGAATGTT	(0,0)	1	TTGCTTCAATCAGAAGCTGAAG
Lri5P9979583	C	T	TGCAGGTAATCGTG	TGCAGGTAATTGTG	TTGATCAAACTACATACAACCAA	(0,0)	1	CTGTCAACAGAGCCAACATCAT
Lri60P1197606	C	T	AGGTACAACGTGT	AGGTACAATGTGT	TGCAAGGCTTGTTAAGTCAGTG	(0,0)	1	CAGCTGCCACGGTTTCAA
Lri60P2434871	G	A	CGGTGGTACGGC	CGGTGGTACAGC	TGCAGAGTGAGCAGAGCAAG	(0,0)	1	CAGTAGGACGCCACAGC
Lri61P3097033	T	C	CGCTCTCATCTGC	CGCTCTCATCCGC	GTTTCGTGGACAGTAGTGAGA	(0,0)	1	CTTGCCCGTGTGGTTGTAG

Lri61P414412	G	A	ATGGAGTAACTAA	ATGGAATAACTAA	CTGCAGGCCAGTATACAACATT	(0,0)	1	AGTTTAATTCGGGCATTGGAT
Lri63P1075345	T	C	CCTGCAGGCATACA	CCTGCAGGCACACA	ACAAATGAGTTCGTGCCATAAG	(0,0)	1	CAATTGCAAGATGATTCCAGA
Lri64P1877052	C	T	ACACTAATTCATA	ACACTAATTTATA	AATATGTGGTCTCTGGGTTTGC	(0,0)	1	CATGCCTGCAGGGGAAAT
Lri64P3699994	C	G	ACCGGTGGGGGGG	ACGGGTGGGGGGG	CTGCAGGATTGTGAAGGCTAC	(0,0)	1	GCGATCTCCTCTGAGACAC
Lri65P1192162	T	C	TCTCAGAGCTC	CCTCAGAGCTC	GAGGGCCACATCAACCAC	(0,0)	1	TGCTCATTGGCGTTGTAGAC
Lri65P2520673	A	G	AATTGATAGGT	GATTGATAGGT	GAGGGAATTCCGAAGTTGAGTA	(0,0)	1	CGTATGGTGCAAAAGAAAGTTCA
Lri65P2642230	T	C	TGCACAGCAAG	CGCACAGCAAG	AACCTCTACGTGACCTCGATCT	(0.5,0)	1	GTGAAGTGCTCCACGATGTTT
Lri66P303856	C	A	AAACACACCCCGG	AAACACACCCAGG	AGAATGTCGGGACATCATGC	(0,0)	1	TTCATCAGGCAAAACACACG
Lri67P441125	A	G	GGTGCAATGGA	GGTGCAATGGG	AGCGAGGACAAGAAGACCTG	(0,0)	1	AGAGGGTCGTGCTTACTTCTC
Lri69P3566988	C	T	TAAACATGTCCT	TAAACATGTTCT	GCTGGCTATCATCCCTTCTAAA	(0,0)	1	TGCTCTGAAGTAAAGTGGGCTTG
Lri6P10286942	T	A	AAGTAATGTATCT	AAGTAATGTA ACT	GTGTGCATTGATTGACAGGTT	(0,0)	1	CTAATGGGGAGCCAATAAAC
Lri6P10328882	T	A	GGAAACCTTTTTC	GGAAACCATTTTC	AGTTGGGTGGCCTCAATGT	(0,0)	1	GAAGCTCCGTCTCTAGAAGTGC
Lri6P10383294	C	G	GCATGCATCCCGT	GCATGCATCCGGT	TGTTTAATGTGAGCAGTTAATCGTG	(0,0)	1	TTTCACTCGATTACCCCTCTGT
Lri6P10474030	C	T	AATCCCTCCCATGA	AATTCCTCCCATGA	CCGAATCGTCACCGATCATA	(0,0)	1	TCAAATGCAATGCCACTAGAAC
Lri6P10581411	T	C	TTTCTCACAGTAT	TTTCTCACAGCAT	AGATAGGGACAATAATTGGGTCA	(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	TTGTGGCGTCCA	TTGTGGCGGTTCA	TCACGAATTCACCTCGTGTACT	(0,0)	1	GGCAAGGGTTGGTGGATT
Lri6P5524704	T	C	GGCATTTCGAGTCC	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	CAAGCGCTGTCTGA	CAAGCGCTTTCTGA	ACAAAACGTGGCCTCGTG	(0,0)	1	GATGATGGTGGTGGTGATGAT
Lri6P8338530	T	C	GCTCTGAAGAG	GCTCCGAAGAG	GCAACAACACCGAGGACCAAC	(0,0)	1	CGCCTATCTCCCAACCAAT
Lri7079P1000	T	A	ATCACATATCTT	ATCACATATCAT	GTCTTGATGGTGGAACTTACC	(0,0)	1	AGAGCCGTCGCCTAACCT
Lri70P1263023	G	A	TTCACCGTTC	TTCACCATTTC	TGCAAAAGTAATTTATTATGGAAATG	(0,0)	1	AGAACTACACCTGCAGGCACAT
Lri71P1277485	C	G	ACGCTGCATGCC	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	TTTAAATAGCGA	TTTAAATAGGTGA	AGTGCCAGAACTAGGGGGTA	(0,0)	1	AATTGAGGAGGTAATGGTTCGAT
Lri76P1581919	C	T	GTCAGCGGGATA	GTCAGTGGGATA	GATTGGTGAATGACGCAAAAC	(0,0)	1	CTCCCTCTGCAGGTAATTCAT
Lri76P839426	T	C	CACAACCTCCATGG	CACAACCTCCACGG	CCTGCAGGTACCTTATTGATGG	(0,0)	1	AGGTAGGGGTGGTGGAGAGA
Lri76P849517	T	G	TAAGGCACCTTAT	TAAGGCACCTGAT	CTGCAGGAAACATGCAGAATAG	(0,0)	1	ATATCTGGGGAAAAATGGCAAG
Lri77P239810	T	C	CTTGTGCTGGTTC	CTTGTGCTGGCTC	GGATTGATCACGGCTGATG	(0,0)	1	TCGACTCTGAGCGAGTACAAG
Lri78P1108359	G	C	GTTTATACACGC	GTTTATACACCC	TGCACCTCTATATGCGGTGT	(0,0)	1	AGGTGATCTGTTCCCTCCT
Lri78P1274279	G	A	AGCGCGAGACGTG	AGCGCGAGACATG	GAAGCCCTGCCAAACGAC	(0,0)	1	ATTGTCGGAGCGCGTTGT
Lri78P1520535	A	G	AGTAAGCAAGATG	AGTAAGCAAGGTG	TGGTAGGGTTAAGCGGATTAAA	(0,0)	1	CCTTAACCACTGGCTTCTTCAC
Lri78P2370671	G	T	ACCTGCAGGCGGC	ACCTGCAGGCTGC	TAACCACACTTTAACCCACCAT	(0,0)	1	ACCCTGGTTAAATAATAGACATCG
Lri78P482602	T	C	CCACCATGCACTT	CCACCACGCACTT	CACCTCTCCGTACCTGCTTCTG	(0,0)	1	CTGCCCTGCTGGATGTACC
Lri79P2948990	A	G	ACTGTCCGTAACA	ACTGTCCGTAGCA	AGTAGATCACTGCAACGACAG	(0,0)	1	GAGCTCAATTCCCAACGTTATT
Lri7P12869891	T	C	GCCATGTTTCCCC	GCCATGCTTCCCC	AGGAATGAACCCCTTTCTGTGT	(0,0)	1	AAAAGTTTAGTTTAAAGACCACGATG
Lri7P1684065	G	C	AAGAACCCAGGGG	AAGAACCCAGCGG	TGCAGGGAGAGACTGATTA AAA	(0,0)	1	GTGGTTCAGGTATTGGGTGATT
Lri7P2921566	C	T	GCACTGCCCCGCT	GCACTGCCCTGCT	TTCTCTTCTGGTTCATTCTC	(0,0)	1	CTTGGATGGCTCTGGGAAG
Lri7P474819	A	T	TAAAAATACCCT	TTAAAAATACCCT	AGATGCGGATAAGCAAAACAAAG	(0,0)	1	CAGCGGCAGAAACAAATAATA
Lri80P1637884	G	T	TGGCTGACGGTG	TTGCTGACGGTG	CATGCTTCTTTGTGAGCTTTC	(0,0)	1	CACATAATCTGCTCGCCCACT
Lri82P53126	G	T	CGAGCAGCTGGTT	CGAGCAGCTGTTT	CAGGAAGGAGAGTGGGTCCT	(0,0)	1	ATCCAGGCGGCCATAACT
Lri83P1195764	T	C	TATTTCCGAGTGG	TATTTCCGAGCGG	AGCTGCCCTCTGCACAGTT	(0,0)	1	GAAAAAGGGTGGCTGACTTTTA
Lri83P1335304	G	A	ACAGGGGGCGGAG	ACAGGGGGCGAGAG	CCTGCAGGCTCTTGATCGT	(0,0)	1	AAGACGGAGGGCAAGACC
Lri83P2068917	C	A	TCCGTGGCTACGAC	TCCGTGGCTAAGAC	ACTCCCTTTGTAGAGCGTGTGA	(0,0)	1	GAGTACTTTGGGAACGTCCTTG
Lri83P564737	G	A	GAAATGAGAAT	AAAATGAGAAT	GCACAACCGTGAAACCT	(0,0)	1	CCTGCAGGACATTTCCAAATTA
Lri84P170406	A	G	CTTTGTTATGCTA	CTTTGTTGTGCTA	ATTTTCATAAATGAGGGGGATG	(0,0)	1	AGACGCTCCACACTCACCAC
Lri84P876835	T	A	CGCAAGCGGGTAA	CGCAAGCGGGAAA	TACCTGTTTAGGCCCTTTCAG	(0,0)	1	CGCCAAGCTTTTGTGCTCTA
Lri84P876852	G	T	TGCAGGAGAGAT	TGCAGGATAGAT	AGCAGAAACCGCTGAAAGTG	(0,0)	1	CTAATTCTGCCTCAAGCTTTT
Lri85P2050795	G	A	GAAGCAGTTTT	AAAGCAGTTTT	CGAGTGGCCAGGGAGTA	(0,0)	1	GTTGGAAAACAGCCTGAAAGAT
Lri85P2095420	T	C	CTCAACGACGTCC	CTCAACGACGCCC	GCGTCGATACCAATGGATG	(0,0)	1	GAAAGATTTGCACGGTCCTAAG
Lri85P213759	C	G	AGGCCAGGGCGT	AGGCCAGGGGGGT	GACCGTGGTCTGTATGCATCT	(0,0)	1	GGTCATGTGACCGTCATGG
Lri85P891582	C	T	GGCCCCGGCGTTC	GGTCCCGCGTTC	GCGATGACATCTACCAGCAATA	(0,0)	1	GTTACCGGCACGGTGATG

Lri85P956410	G	A	TCCGCCGCCTGGA	TCCGCCGCCTAGA	TGGTGCAGTGTTCACGTC	(0,0)	1	TTTACCTGCTGGTAGATCTCG
Lri86P103182	T	G	AAGCGTAGCGTGA	AAGCGTAGCGGGA	TTAGGTCTGCACCCAAAAATAA	(0,0)	1	CAATTAGGCATGAAAGCATTG
Lri88P1164318	T	C	GCCCATTAGTCC	GCCCATTAGCCC	CTCTCCAGCCCATCTCAC	(0,0)	1	CTGGGTCCAATGAACTTCTGTT
Lri89P2322061	A	G	TTTCCGACAAGC	TTTCCGACAGGC	TTTTTGTCTCCACATTGCAC	(0,0)	1	GCTCTTACAACGTTTGGAGCAT
Lri8P1441255	A	T	GTGTCTGACA	GTGTCTGGACT	GGTGAAGATGCTGTCGTCAGAG	(0,0)	1	CACAGCTGGGCTGAAGT
Lri8P4138772	A	T	GTATGTATTTA	GTATGTATTTT	ACAGCTCCACCCAGCTTCATA	(0,0)	1	ATGCGACTCAAACCACTACTCA
Lri8P4295266	T	G	CATCATGCAATA	CATCATGCAAGA	TAATTTTCCATGAGGTGTTGA	(0,0)	1	GATTGTGATCACCCAGAACAGA
Lri8P9543505	A	G	CTCCACAGCTAAT	CTCCACAGCTGAT	CGATGCAGTAGTGC GTCT	(0,0)	1	ACAGCATGGCGAGCATGA
Lri90P257157	A	C	AGCATTTCATC	CGCATTTCATC	TGATTATGATGTCATCGGTAAAG	(0,0)	1	TGCAGGTTATGTTTGTCTCCTG
Lri90P618248	A	G	ACATCACCGCC	GCATCACCGCC	ACGACGCGATAGAGCAGGT	(0,3,0)	1	CGATTGTTCTCTGCAGGTGT
Lri91P204352	T	A	AAGAGTATTCTG	AAGAGTATTCAG	TCACGCAGGTAACCTATTTCAT	(0,0)	1	GATGTCACAGTGGTTCACAGGT
Lri91P2342186	T	C	GTGTCCAGGGG	GTGCCAGGGG	CTGAAATTAATCCCTGTCTCCAG	(0,0)	1	GGCACACCTGGACACATCT
Lri91P730506	C	A	GACGCATTTTCTA	GACGCATTTTATA	GCTACCGAACCCGTGACTT	(0,0)	1	TTAATAACACGCATCAAAGATACATT
Lri93P1340289	A	G	AGAAGCAGAAAC	AGAAGCAGAAAGC	GAGCGATTCTCTCCGTACCAT	(0,0)	1	CAGGAACAGCTCCTTGTGTGAA
Lri96P1067926TD50	T	C	AA[CT]GTGGGTT	AA[CT]GTCGGGTT	GCTAGCTGAACCCGTTACACAT	(0,0)	1	GCATATTGCGGAATACACCAC
Lri98P763276	A	C	AGGGTCGCGCAGC	AGGGTCGCGCCGC	GCGTCTTCAAACCTCATCGAGAC	(0,0)	1	GCGTACGGATGTGAGTCTTAG
Lri99P330522	A	G	GCAGGTTGCAAG	GCAGGTTGCAGG	TTAGTAACCTTTTCCCAGATG	(0,0)	1	CCTGAATAAAATGAACGCTGA
Lri9P10378057	C	T	GATCGGGTCTC	GATCGGGTCTT	ACAAAGGTGGCCAGACATGA	(0,0)	1	GGCTACTTATAACCCACGTTCG
Lri9P1124057	G	T	AAAACACGGTGCA	AAAACACGGTTCA	TGTGAACCTCGGGGAAG	(0,5,0)	1	ATGAAATGCGGTAGTGTCTCTG
Lri9P12500977	T	G	AGTGAGGTGGTCG	AGTGAGGTGGGCG	GTGAGGTGGGCCAGCAGT	(0,0)	1	CCTCCATCTCCAGCTCGTC
Lri9P4476882	A	G	GTCAGCACGCA	GTCAGCACGCG	GGTTTCCACTATCTGGTGTGT	(0,0)	1	GCATACCAGCGTTCAATAAACA

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

Assay	A1	A2	A1-Probe	A2-Probe	FWD Primer	Primary Flag	Rev Primer
Atr_10304-61	G	A	TGGCTTGGCAGTGG	TGGCTTGACAGTGG	GCCTTTGTTCTCCAGCTTGC	1	TCTAAACAGACCAATCCCACTG
Atr_10322-43	G	A	GCAGCGAAACAAAGA	GCAGCAAAACAAAGA	TGCAGGGGCTATCAGAGACT	1	AATCAGTGTGGGAGCTCAGC
Atr_10428-71	T	A	AGAGAGCTAGCA	AGAGAGCAAGCA	CGCACACACACAAAGAGAGC	1	GGATCCAGAGCCACAGTGTC
Atr_10437-26	T	G	TTTTTTGGCAACTGT	TTTTTGGGCAACTGT	TGCAGGTGGGTTATGGGTIG	1	TGAATTAACAGGTACAGTTGCAGA
Atr_10672-61	C	T	GACCACACTGGGCAG	GACCATACTGGGCAG	GC AAAATTGGCAGGGATGGT	1	GCAGGTGTTTGTCTGAGCTC
Atr_10867-69	C	T	TGGTATACAATGAA	TGGTATATAATGAA	AGGACTGGGTAGGGAGCATT	1	ACCGAGCTGGATGACTTGAA
Atr_10998-72	T	C	AGTAATGTGTT	AGTAATGCGTT	CAAAGCGCCCATGATTGTCA	1	TTAGCAGGCACAACTGACAA
Atr_11046-75	T	A	GGCCCAAT	GGCCCAAA	GGAGGGCCTGGGAATCCT	1	TTCAGGGGAACAAGGTGAG
Atr_11104-35	T	C	TGCACTGTCGTGTCT	TGCACCGTCGTGTCT	CGCTAGTAGTGAAGTGAAGTGC	1	CCCTCTCAGGTGCTGTTTAC
Atr_11585-33	C	T	TAAAGCCAAGTTTGT	TAAAGTCAAGTTTGT	GGTTGGTAGTTTTCGGCATT	1	AGTGGAGTTCTCCGATCCCA
Atr_11787-73	G	A	CTAACCCGCG	CTAACCCACG	ACAGTCCCTACAGGCATTGC	1	GATTCCAGAGGGAGTGTGCG
Atr_11864-68	T	C	ATATCGCTGACCAC	ATATCGCGGACCAC	GGTACCACCGCAATATCGC	1	CAGAGCTGCTGGTTGTTTCG
Atr_12219-56	A	C	ATAGTATATGCGGG	ATAGTATCTGCGGG	GCAGGGAAGTCTAAACCCCA	1	AATTGTGTTCTTTGCCCGC
Atr_12616-36	G	A	GCCGTTCTGTGAAGC	GCCGTTCTATGAAGC	TCCTGCCATGTAGCAAGAG	1	TCCACCGGCTATTCTCTTT
Atr_12677-44	A	G	ATGTACTATTAGC	ATGTACTGTTAGC	TGCAGGAGAGGATGTATACGTC	1	ACTTCAAACAACAAAGGCTGCT
Atr_13073-61	T	A	TTTAAATTGCATT	TTTAAATATGCATT	GCTGCAGCTTACAGTCTTCA	1	TGCAGAGCTCAATCCAAACCT
Atr_13132-45	G	A	GCCACGAAGAACATG	GCCACAAAGAACATG	GTGACCAGCATGACCACCAT	1	TATCACAGGGAGCTGGGGAT
Atr_13476-65	A	T	TTATCAGTATGCAGC	TTATCTGTATGCAGC	CGTTTTCCAGCACCACAGGT	1	CTGACCTTTGGCTTGTGTGC
Atr_13706-54	A	T	GTGAGAGAAGACTA	GTGAGAGTAGACTA	AGGCTACTTGCACTGCCAG	1	TCATAAGAGCTGTCTGAACTGA
Atr_13729-47	T	C	GCACAAGTTTTTTT	GCACAAGCTTTTTT	CCATAGCTTTTGTGCAGACA	1	TGCCTTTATGTTGACAGGGTCA
Atr_13917-71	C	A	AACTACTCATCA	AACTACTAATCA	CCTTCCAGGGAGCTTGATG	1	CAGAAATGCAAGTACACTGTTGA
Atr_13930-72	A	T	GTTTTATAAGC	GTTTTATTAGC	TGTTTTAGTGGGACCAAGTCT	1	TGCAAAATAAAACACTGTGGAAAAA
Atr_13996-43	T	C	TATICTGTAATGTTT	TATTCGTAATGTTT	CAGGTCTGTGTGTGTGACA	1	TCAAGTTCACCTCGACAGCA
Atr_14410-52	T	A	GAAGCAATCCCCAG	GAAGCAAAACCCAG	ACAGGTGGTTCATCTGCAAAAC	1	TGGCATTGTTCCACTGGGG
Atr_14635-67	C	A	GGAGCACAAAAAC	GGAGCACAAAAAC	ATCCCCAGCTGATTTGCCTC	1	ACCACTTTAATGCATCTCTGG
Atr_14824-32	A	G	TTAACATGAAAGTCA	TTAACGTGAAAGTCA	TGCAGGGATCCACAGAAATGT	1	AAGCAGCTGAACACAATGGG

Atr_14862-38	T	C	TTGACTCCCTTTAAG	TTGACCCCTTTAAG	CGCCTCCCAGGACTATTTT	1	TTTCCTGTGGCCATTTTATTGT
Atr_14917-56	C	T	AACACATCTTAACA	AACACATTTTAACA	TGCGCCACCTAGAAACACAT	1	TGCACAAAGAAAGGTCCTGGT
Atr_15179-54	G	T	TTCAAATGACCCCA	TTCAAATTACCCCA	GCAGGGTAAGTTAGTTTAAGCGC	1	GGTGCAGCTTGTATGGGGT
Atr_15201-45	A	C	TTACTGAAACACAT	TTACTGACACACAT	GGGTACAGTGC AAGAAATGGC	1	TAGTCAGGTTGGCTGTGAGC
Atr_15273-44	T	G	ATAGATCCTGTCCTA	ATAGAGCCTGTCCTA	GGGAATGTTTCTCTGTTTGGAT	1	ACTCCAGTCTGGACATAAACTCA
Atr_15294-66	T	A	TGGGATAGAATTTTC	TGGGAAAGAATTTTC	TGTATTGTTGCGATGAATTGGGA	1	TCTGATGTAGAACTCTGTGTAGTT
Atr_15298-72	G	A	TCTCACTGTAT	TCTCACTATAT	TCTCAGCATCTTCACTACCCA	1	TGATAAAGCAACCTTGAGCCCT
Atr_15875-62	C	T	CCTGCCCCGTGGAA	CCTGCCCTGTGGAA	TCCATCAGAGCTCACCAGGA	1	AGTGTTCATTGGCTCTGGA
Atr_16803-66	C	T	GGCAGCACGCCTCT	GGCAGCATGCCTCT	CATGTTGTGTGTCCGGTGC	1	TCCCTGGAATTGGTGC AAA
Atr_1720-33	C	A	GGGGGCTTTGAGAGC	GGGGGATTGAGAGC	GGCAAAGCAGAAGGGGG	1	TGTGTGTATCTGCTGTGTGGT
Atr_17710-71	T	C	CAGGATGCCC	CAGGACGCCC	GCTCTCCCATCTTTTGCAGC	1	ACACTGACGGCAGCTATTCC
Atr_18133-56	G	A	TGGGTTTGTGTAT	TGGGTTTATGTAT	AGTCAAGTGTGTGTGTGGGT	1	AGCAGGGAAGATACTGGTTGC
Atr_18295-67	T	C	ACCTGCATGGCAAA	ACCTGCACGGCAAA	CTCGTCTTGAGGCACCTGC	1	TGAAAACCTGGCAGCTTTGTGA
Atr_18334-74	A	G	ATGGTGGAC	ATGGTGGGC	GGAA GTTGGTCTCAGAGGC	1	AATGAGTGCCATCAGCCACT
Atr_18403-29	C	G	AGATCCATGAAGCTC	AGATCGATGAAGCTC	TGCAGGTAATGAATGTTGCCT	1	TGCGTCTGTTTCATCCCTCT
Atr_19496-44	A	G	GAGTGAAGGCTATTGG	GAGTGGGGCTATTGG	CACACCTAGGGGCACATTGA	1	TCAACAGCGAGAAGGGTTGT
Atr_19666-61	G	T	ACATTCAGGGCATA	ACATTCATGGCATA	CAGGGCTCAAGCTCTTCTGT	1	TGTAGTGAGGTTACCTTATTATGCC
Atr_19783-57	C	A	TCTAAATGGACATC	TCTAAATGGACATC	TCTTCTCTGGAATGATTACATCCA	1	GACAGTGAAGCAAGAGAAATCCA
Atr_20013-55	C	T	GCCTGCTCCCTCG	GCCTGCTTCCCTCG	GATGCTAACCTGGCTCTGGG	1	CCGAATATCCGCGGAAGAA
Atr_20037-39	G	A	AGAACGTGTTCTCTGC	AGAACATGTTCTCTGC	GCAGCGTAGAGTTACAGCA	1	ACAGTAGACGTCAACGGGAT
Atr_20117-55	A	G	GCTTCACCCCAGGCA	GCTTCGCCCCAGGCA	CCTGCTCCCAACAGGACAA	1	TCAGATGGGCTGTGTGAAAC
Atr_20219-65	A	G	ATGCCAGGCTTTCTA	ATGCCGGGCTTTCTA	TGGACCTTATTAGAAGCTTAATGCC	1	GCACCTCTATGGCACTTTTGG
Atr_20252-35	T	C	ATGGGGGTTGTAAT	ATGGGGGCTGTAAT	ACTTGGACGAGGCATCATGG	1	GCCAAATTC AACTGCTGGGA
Atr_20332-60	T	A	GTATAACTAGAACA	GTATAACAAGAACA	ACATTGCTACACCTCACCC	1	TTTGACTGCCACAAGCTCCT
Atr_20482-41	C	T	CGGGAGCCGAGCTT	CGGGAGCTGAGCTT	CTCATTTGCAATTGGGCTCGG	1	GCAGCCTAGCAGGATCTCAT
Atr_20529-52	A	G	GCACAACTTTTACA	GCACAGCTTTTACA	ATCGCAGCTTGACAGTGAGT	1	AGTAATTCC AAAAGCCCACTGG
Atr_20740-65	T	C	ATTGCTCTCTGCCCT	ATTGCCCTCTGCCCT	AACATCATCCCTTCTCTGCG	1	GAGTTCAGAGCCAGCACAGA
Atr_2084-45	A	G	GGTTTGAAAATGTT	GGTTTGAGAATGTT	TGAGGTAGCCAGCAGGTTTG	1	AATGATGCCAGAGCCTGTAT
Atr_20952-49	T	C	ACACTACTCTGCCC	ACACTACCTTGCCC	TCCCCAGCTGACATGAACAC	1	CACAA TTGCCAAGTGCTGC

Atr_21685-29	A	G	GTGCTGAAGGCTCC	GTGCTGAGGGCTCC	TGCAGGTTTGTTCTCTGTTT	1	CCACCAGCCAAAGAGACAGT
Atr_22008-56	C	T	TACTGAACAGTGAT	TACTGAATAGTGAT	GGGCAAGAAAAGACCCAAACC	1	GCCTTCTGGTCTCTAATATAAAGTGC
Atr_22727-31	C	T	TTTGCCAGATTTCAG	TTTGCTAGATTTCAG	GCAGGAAACCATGATGCACC	1	TGACTTACTAGACATCTGCAACTGA
Atr_23070-31	C	A	CAGTCTCCGCATTT	CAGTCTCAGCATTT	GCCTTTGCCCTCCAGTCTC	1	TCCTCTGATCCCACGACCTT
Atr_24146-56	A	C	ACATGTTAATCTTG	ACATGTTTCATCTTG	TGGCTAAAGATCTAGAACACATGT	1	TCAACCGAGCTCTGTTGCTT
Atr_25159-57	T	C	TATTTTAGTGGAAGC	TATTTCAGTGGAAGC	CCTGAGTGTGTGAACCAGCT	1	ACATGTTAGCCAAGAGTTGCA
Atr_2540-75	A	C	TCTGGTAA	TCTGTGAC	TCAAGCATGCTAAGTGTCTGTT	1	TGTTCCCGGGTGCCAAAAA
Atr_25540-60	C	T	AATTCCCAGCTATGC	AATTCTCAGCTATGC	AGCAGACCACTGGCATGAAT	1	TCTATCATGGGCATCTGCAAA
Atr_25562-47	A	G	CGGCAAGCAATAAAA	CGGCAGGCAATAAAA	CGGTTATAGGATTAGTATGCGGC	1	GCAGAGTGCAGTGAATAGCC
Atr_25884-65	T	G	AAAATTTTCCCGAA	AAAATGTTTCCCGAA	GCAGGGAGATTGGGAAGTCA	1	AACAGCAAAATTTAAATTCGGGAAA
Atr_25905-72	G	A	AAACCCAGGAA	AAACCCAGAAA	TGAGGGGAAGTTGAGGTGTT	1	TTCTCTTGACCTTTCAATTGATC
Atr_26310-63	A	C	GAACGAAGCTTAGTT	GAACGCAGCTTAGTT	CAAAATGCCCGATCACCCAC	1	TTTGCCTGTTTGACCTCTG
Atr_2684-39	A	T	ACTGGACAGAGATC	ACTGGACTGAGATC	CAGGAGACGCAGGGAGAAAAG	1	GCCCACACTGTCATTGAGCT
Atr_27072-33	T	A	TTTATGATAGTGAT	TTTATGAAAAGTGAT	GCAGGTGATTGGTGGAAATAGC	1	TGGACTCGCATCACCTTCAC
Atr_27367-69	T	C	AAATAAATACACAG	AAATAAACACACAG	CGTTTCCACAGTGGCAATCA	1	TGTGTGAATTTGGATTCTCTGTGT
Atr_27395-73	C	T	CAGG[GA]CGC	CAGG[GA]TGC	TGCGACTCTGCTGTGTATGA	1	GACATTTTGCTGTCCAGAAGGG
Atr_27430-71	A	G	ATTGCCCATGCC	ATTGCCCGTGCC	CTGGTCTGGTCAGCAATTGC	1	AGTGCCCAACACAGTATGG
Atr_2768-35	C	T	CGCCTGGCCAGTTG	CGCCTGGTCAGTTG	TGCAGGTGTTTCAGTTGAGCA	1	AGACAATACAGCAGACCCAAT
Atr_28175-70	T	G	TTTAGTTTTGC	TTTAGGTTTGC	AGGTAGGCTAGAAATCGGTTCA	1	TGGTCTTGATTAAGGGGTGCA
Atr_28280-63	A	G	TGATCAGAAACCTT	TGATCAGGAACCTT	TCCACTTTGAACTCACCGGG	1	ACTGTACACTTTGCTTGTCTTACA
Atr_28411-65	A	G	GTGCCCAACAGGAC	GTGCCAGCAGGAC	AAACCAAGCAGCGTCTGGAA	1	GCAGCTCTGTCAGTCTCAGG
Atr_2858-58	C	G	ACCAGCTGTGCCGGG	ACCAGGTGTGCCGGG	TGCAGGCATTTTGTGGACC	1	CACAGTACCATGGGAGTCCC
Atr_28609-62	A	T	CAAACATATCATTG	CAAACATTTTCATTG	GCAGCAGGGTAAGGATGACA	1	AAGCAGGGAAATACAATACAATGA
Atr_28746-28	T	A	AGGTTCTTCACTTT	AGGTTCTACACTTT	AGGGGTTGTTGGGCATAAGG	1	AGTAAGCACAGGATATAACAAAGTG
Atr_28834-39	T	A	ATGTAGGTGACAGT	ATGTAGGAGACAGT	TGCAGGAGTGATCACAAGATGT	1	TGTGAATACCCCGACTGCTG
Atr_28861-59	T	A	GACCCTGGTGCAGAT	GACCCAGGTGCAGAT	ACCCAGGACCAAAGGGAGAT	1	GTGTGACTCACATCTGCACC
Atr_29024-55	A	G	CTCTCAAGTCTTGA	CTCTCAGTCTTGA	TCCAAAGGCCGGTAACCTAC	1	AAGGCCAGTGAACCCACAAT
Atr_29086-33	C	T	TTGTCAACGGGTTT	TTGTCAATGGGTTT	GGTTTGGTTCAACCGCACAG	1	AGAGAGCGCTGTAGACAGT
Atr_29277-35	C	G	TGAAACAGCAGTATG	TGAAAGAGCAGTATG	GGATCGTCTCTGCTTGTGA	1	TGCCAAGCCCTAACTGCTAG

Atr_29302-34	C	T	CTGCTC[GA]TCTACAGT	CTGCTT[GA]TCTACAGT	GCAGGCTGTATAGTGAAACTGG	1	TTACTACTCACCTCACCTGAAAAA
Atr_29414-61	C	T	TTCCAACCGGGGAT	TTCCAAC TGGGGAT	CAGGGCTGGGGTCTGGA	1	GGCGCACTCTGTCTCCAAAT
Atr_30145-46	T	C	AAGGAAATACTTGC	AAGGAAACACTTGC	TGCAGGTGCCCATTTGATCA	1	TATTCTACTGCGCTCTGGC
Atr_30271-58	G	A	AGGAGTCGTATTTC	AGGAGTCATATTTC	ATGCAGAATCCACAGGAGTC	1	AAGGAGCTTAGACACTGCCA
Atr_30376-68	C	T	CAGGAAACGACTCA	CAGGAAATGACTCA	CCGCCAGCAGTCAGGAAA	1	TTGGTCCACAATCCCCATC
Atr_30916-62	G	A	GACTGGGGCTATTT	GACTGGGACTATTT	AGGTCGTGCTGTATTGGTCA	1	CAGGTGTGATGAGGGGAAAT
Atr_30992-26	C	T	TAATGGTCGTTAAT	TAATGGTTGTTAAT	GCAGGTCTGAAATGAGGTAATGG	1	GCTCCCTTTTATTGTGTGACT
Atr_31917-28	T	C	AAAAC TGGTCGCTCA	AAAACCGTTCGCTCA	TGCAGGACCAAGTGGGATTA	1	TTACAGAGGAAGGTGAGCGAC
Atr_32234-71	C	T	CACGCCACGGGG	CACGCCATGGGG	CTCAGGAGGATGGCCATTCT	1	TGTTACAAAAGGTCTCATCCCC
Atr_32382-60	G	A	TATACTCGGAAACA	TATACTAGAAACA	CAAACCTGGTCCCTTGGTC	1	GGGACTGCAGTGCACCTAG
Atr_32545-55	A	G	ACTCAACACGCCCT	ACTCAACCGCCCT	TCCACTTGGGATGATCTAATCTCC	1	TTGAGAACCAAGTTGGGCACT
Atr_32551-51	G	A	AGGTCGAAGTAGTGG	AGGTCAAAGTAGTGG	GCTCTCCAGGTGTGCTTGA	1	AGAGTCCAGCGGGCTAC
Atr_32840-74	T	A	TTCATTA	TTCATAA	TGGCACAGCTTTACCGGTTT	1	GTCCACAGAGTTGTTGTGAAA
Atr_32945-42	G	T	AAAAGAAGAGTTCC	AAAAGAATAGTTCC	TGCTCTTTCAAATCCTATGACTCA	1	AGCAGAAATCGTTTTACAAGGAAC
Atr_33123-54	T	C	AAAGCAATGATTAA	AAAGCAACGATTAA	ACTGTGTTCAGAGACCATTGGA	1	AGAGTTTTTACAATTATTGCCCT
Atr_33645-66	G	C	TCGCTCTGTGAGGT	TCGCTCTGTGAGGT	TGCGTGTCTGCATCTCCAAT	1	GGCAGCACAGACCATACAGT
Atr_33798-72	G	T	GTGCCGCTG	GTGCCTCTG	ATTTTGGTTGTGGCGGTGC	1	GGTTTCCCATTTCTCCAGC
Atr_33803-28	G	T	AGCTGCAGGGATGG	AGCTGCATGGATGG	GGAATGTAATGTGACCAGCTGC	1	ACCAGGAATGGATCAAATGCT
Atr_34-41	G	C	GTCTGCAATGCTGT	GTCTCCAATGCTGT	CCTGCCTGTGTGAATTCAG	1	CCGTGAAGCCACTACAGCAT
Atr_34454-29	G	A	GACCAGGGTTGCCT	GACCAGGATTGCCT	GATTGTGGCACTCCAGGACC	1	ACCCGAAAAGTAGAAGCCCT
Atr_34497-36	C	T	GATAGTTCGCTCTT	GATAGTTTCTCTT	GGAGGTGCTGCTGGTGATAG	1	GCTTGGTGGTTGTAGGTGCT
Atr_3451-52	T	G	GTGCTTTACCAACAT	GTGCTGTACCAACAT	GGTTTGGAGGAAGTTTGTGCT	1	CTCTGTCCCTCAATTGGAGGA
Atr_35415-62	C	A	CAGAACGTTAAAAATT	CAGAAAGTTAAAAATT	GGAAGTTGGTCTTATGATTAGTGTT	1	AAACAAGATGTTGGAGTACAAAAGT
Atr_35440-36	A	T	ATACCATACATACA	ATACCATTCATACA	CAGGTCCTACCACTGCTGAC	1	TGCAAAGTGTGTTCTCTGTATG
Atr_3581-53	T	A	TTTTATTTTTCATA	TTTTATTATTCATA	AGCTCCAGTTCACAAAGCCT	1	TGCAGCTTCTTGGGGATCA
Atr_36194-59	T	C	CTTCTGTTCTCAGA	CTTCCGTTCTCAGA	CCATCTGCAGTGTGGAATCCT	1	GCCGCTTCTTCTCTCTGAG
Atr_3627-31	A	T	GTCTATTAGTGTTT	GTCTATTGTGTTT	GTTCAAACCACACAACTGTCTAT	1	ACTGCAATGAGACACAGATGT
Atr_36331-53	C	T	TGTGGCTCGAGGGC	TGTGGCTTGAGGGC	CGGAAGGCCTCAGATTGTGG	1	AGTCCGCTGCCTGAACTAC
Atr_36485-28	C	T	CCTCATCCTAGCCC	CCTCATCTTAGCCC	GGTGCTAGCAGCCCTCATC	1	CACAGACCAATCATGCCCT



Atr_36740-33	G	A	TAGAAAGTGTAGATGA	TAGAAATGTAGATGA	TGCAGGCTAATATAAAGTAGAAAGC	1	ACAAGTTCCTGGTTAAAAACAGCT
Atr_36960-37	A	G	CCATGCCAGTCCGT	CCATGCCGGTCCGT	CTTGACGCCAGCTGCAGAA	1	TGAGGGTGAGGAGCCATACT
Atr_37068-70	C	T	TTTGTCTTCG	TTTGTITTCG	ATAAAGCATGAACACCACATGG	1	GGCTGTTTGTCTCAGTGTGT
Atr_37739-28	T	C	ATAGCTGGTACAGGT	ATAGCCGGTACAGGT	GCAGGATCATGCATGCGC	1	TGAACCCAGACAAGAAGGACA
Atr_37898-35	C	A	GCTGGCTTGGTCGTG	GCTGGATTGGTCGTG	CAGGCTGGCCTTTGTCCATA	1	TTAAGGTTCACTGGGCGTCC
Atr_38278-50	C	A	GTGCATGCAAATA	GTGCATGAAATA	TCCTCAAACACAGTGTGC	1	TACAGTGCATGCCTTCCTGG
Atr_38591-73	A	T	CCGTCATT	CCGTCTTT	GCTGAAGTATAACAACATCACCGT	1	AATTGGGAGAACTTTACAGTCCT
Atr_39018-58	C	A	AAAAGACCAATTTCA	AAAAGACAATTTCA	GGTTCAGACCCACTGTGTATCA	1	AGCCAGCCTAAGGTTTTGAA
Atr_39023-56	C	T	AGTGACACGGAGAG	AGTGACATGGAGAG	GGTCCACCTGTCAATAATGGC	1	TCGAGAGAGAGAGCCCTCAC
Atr_3903-41	G	A	AGCTGGTGAATCGGA	AGCTGATGAATCGGA	TGCAGGTTGAGTTCAGATTGT	1	GATAGGGGTGCTGCATCCG
Atr_39071-73	G	A	CTTCACAGAC	CTTCACAAAA	ATAGCCCAGGTGGATGCATG	1	TGGATAAGCGGTTCTGCAGA
Atr_39081-73	C	T	TTTAGATCAG	TTTAGATTAG	TGGATGGAGGTTTAATAGGACCA	1	GGGCCCTTCCAGTTGAGATT
Atr_39125-48	T	C	ATAGTGTGAAACT	ATAGTGTGAAACT	GCAACATCGTGAAACGCCA	1	TGATTCAAAGGAATGCTTGGCA
Atr_40110-57	G	A	TAGGGCCGATGCA	TAGGGCCACATGCA	GCACTGTGCCACTGACATAT	1	CAATCGCTATTGATTGCTGCA
Atr_40169-65	C	T	AGACCCAGTTGTGGC	AGACCTAGTTGTGGC	GGGTGGTTCCTACATGACGT	1	TGCCCTGTAACACCCCTGT
Atr_40316-51	A	T	ATTAAAGAAAAATA	ATTAAAGTAAAAATA	TGCAGGTTTGTTCTGTGAATGG	1	CTCTGTCAAGGCCACAGA
Atr_40343-66	G	A	CTGCTTCGTTAGGG	CTGCTTCATTAGGG	CAGCAACGCTTACAGCACAG	1	AACAAGCATCGTCTCTCCCT
Atr_40774-37	A	G	ACTCAACTCTGACCC	ACTCAGCTCTGACCC	TGCAGGCAACAGTCTTAGAC	1	CCTGGACTGGATTGGATCTCG
Atr_40954-66	G	T	ATTGGGGGTAAAAT	ATTGGGGTTAAAAT	TTGGACATTGCAAAATGGGG	1	TGCATGACTATGGGCGTGTT
Atr_40974-63	G	A	GAGATGTGATCTGT	GAGATGTAATCTGT	GGACCACAGATGAGATCCG	1	GCAAAGCATGCGAAACAGAT
Atr_41828-27	A	C	TAAAGGGAACAGT	TAAAGGGCAACAGT	GCAGGAGTCTACAAAGTTAAAGG	1	TGTTTTACATGCTTTACGGTCA
Atr_41948-31	A	G	GAATTGAAGAAGTA	GAATTGAGGAAGTA	TGCAGGGAGGGACATCTCTT	1	TCATGTTTCGAGTCAAGGAGCT
Atr_41986-71	G	T	AGTGGCAGAATG	AGTGGCATAATG	ATTGTATGGCGCTTCCTGCT	1	AGAAGGGTTGAGCATGTCCC
Atr_42039-63	T	C	AGGCCAGTGGCGAG	AGGCCAGCGCGAG	ACCAATCCAATCAGCCTCGG	1	TCTGTCCGTGCTGGTTTGG
Atr_42405-55	C	A	CCCCAGTCCCTTAA	CCCCAGTACCTTAA	CAACACTGACAGACCCCGAG	1	TGCAGCACAGCGTGATCTAT
Atr_42741-51	T	A	CGTCATTTTGAAATT	CGTCAATTTTGAAATT	TGTGCAGACTAAAAGCATGCG	1	ACTCAGGAGTCTAACTGAAGCC
Atr_43107-50	G	A	ATCTGCTGTAGCAC	ATCTGCTATAGCAC	GGTGTCTGCTGTAGCTCAAT	1	GAGGCAAACTGGCAATGACT
Atr_43402-63	A	T	AGATCACTCAACAAA	AGATCTCTCAACAAA	GCAGGTTTGACTTGCTGGG	1	GTCAGGCCAATGTCCACTT
Atr_43414-51	C	T	TATGAGCCGAGTCT	TATGAGCTGAGTCT	AGTCTTCCGAGGGACAGTT	1	CCCTTTCGTAAATGAGGCCCT

Atr_43531-74	G	A	GTGCGCCGC	GTGCGCCAC	AACGTTCAGTGAAGTGCGC	1	CCAACTGAGCCCCAACATA
Atr_43571-39	C	A	TACATCTATCTGGTT	TACATATATCTGGTT	TGCAGGGATATAGTATGTCACTTT	1	TGCACCCCTATTCTGAAGTG
Atr_43809-42	A	T	AAAATA[AT]AAAAAATA	AAAAT[AT]AAAAAATA	GCAGGGCGTATCGACAGATT	1	GCCAACTGCTCACCCTTA
Atr_44473-38	T	C	ACATTGATATCTCA	ACATTGACATCTCA	GCAGGTGGTGGAGCTCATAG	1	CTCCTTCTGCAGCATACCA
Atr_44513-72	T	C	GTGGCTCTAGA	GTGGCTCCAGA	CAAACGATATGAAAGCTGTGGC	1	GGTCCATTCTAGTCAGCTCGT
Atr_44873-44	C	T	GCTGACATCTGTCAT	GCTGATATCTGTCAT	ATGGTCTTTTCCCCCTGGG	1	AGCTCAGCCAATCAGCACAA
Atr_45074-45	T	G	GTGCATTTCAGCAG	GTGCATTGCAGCAG	GGAGAAACACACCAAGCG	1	AGTCTGCTTCTACTCCAGT
Atr_45494-35	G	T	CATTCAGTCGAGG	CATTTCATTCGAGG	GCAGGACATACACGGTGGAA	1	TCCAGAGCTACACACCTCGA
Atr_457-66	G	A	TCAACTGGGACCAT	TCAACTGAGACCAT	GAAGGGCTGAAGTGATGGCT	1	ACCCTCATGTACAAATGTAAAAGA
Atr_45890-59	G	T	GTGAGGAGACCTGT	GTGAGGATACCTGT	TAAGGGCTGCAGTGGTGAAG	1	CCACGGTACCTGTGCTGATT
Atr_46006-31	C	A	TGCTGCATGCTTCAC	TGCTGAATGCTTCAC	TGCAGGATATAATAGTAAAGGGGTC	1	CCCCCTCATGTGAAAAAGTGT
Atr_46088-36	T	C	TCATCTGTAATATG	TCATCTGCAATATG	GGCAGTCATGATATAAAGCGGG	1	TCTAGTGACCTCTGGTGGCT
Atr_46134-46	T	C	TCCCTGCTGATTTT	TCCCTGCCGATTTT	TGCTTGACCTAGCCAGTAGTG	1	TGGGGGCTAGGGAGACAAA
Atr_46229-66	G	A	TTGCTCCGTACAAA	TTGCTCCATACAAA	AGTGACAGGGAATTGTATGCCT	1	ATGTCACACTCCCAGGGAC
Atr_46247-56	C	T	TAAACCGGGGCTCTG	TAAACTGGGGCTCTG	GTCAGGGACTCGTGGACTTC	1	AAGGGAGCTGGAGGAAGAGT
Atr_4643-39	A	G	TATGTATACCTGAG	TATGTATGCCTGAG	GGCAAGAGAGAGCATCAGCA	1	TCATTCAAGCCCACCACCTC
Atr_4661-28	C	T	GTTAGTCCGGGGCA	GTTAGTCTGGGGCA	GCAGGTAGATCTCCAGCTGG	1	CTTGCCAGTGCGGTTGAAA
Atr_46637-57	C	G	AGCGTCACAGGCTA	AGCGTCAGAGGCTA	CATAAGCGCTGGGATAGGGG	1	TGCAGGAGCTGACCTTTGAG
Atr_46690-29	A	C	CTGCCAAAGGATCT	CTGCCAACGGATCT	GGCTCTCAGAGTAATTACTGCCA	1	TTCCCTCACTCCAAGAGCA
Atr_46720-39	G	A	GTAGAGCTGTATTAT	GTAGAACTGTATTAT	TGTTTACAGCTTGCTCCTAGT	1	ACATTGCTGCATGGCATATGA
Atr_4674-42	C	A	TTCTCTCTCCTTATC	TTCTACTCCTTATC	GGTGTCTGCTTTGAGCTTGG	1	CTTCAGAAGGAGCATGCA
Atr_4677-47	C	G	TCCCGGACCGGGCC	TCCCGGAGCGGGCC	CCTGACACTGGCACTCAACA	1	CACCAAGGCTGGAGAGGTTTG
Atr_46983-45	T	A	GTTCTGTTTCTACAG	GTTCTGTTACTACAG	CCTGGTAGCATGTGGGTGTT	1	TGCCTCATTGTAATCATATCAGGAC
Atr_47163-58	C	T	TGCAGCGGCACATGG	TGCAGTGGCACATGG	ATCCATCTGTCCCTCCAGCT	1	GCACTTCACCATCCGGAAG
Atr_47195-73	T	C	AAGCCGTAA	AAGCCGTCAA	GAAACGCTCAGGAGTGAAC	1	CAGTGGGCGTGTTACGTAAG
Atr_47352-72	A	G	GCCGAGCACTC	GCCGAGCGCTC	CTCATGCCGCTCTCCTTCAC	1	TTGTGTTCTGGTCCCAGCG
Atr_47484-45	T	C	GTAGGGGTTGCTCT	GTAGGGGTGCTCT	GCAGGGGTCTGTTAGAGCTC	1	AATCAGCAGTCACCTCACCG
Atr_47529-73	C	A	TAAGCAACTT	TAAGCAAAAT	GCTGCCATTAATGATCTTGTCCT	1	CGCAGGACCAAGAAGATGTT
Atr_47979-72	T	A	GCCTTTATATC	GCCTTTAAATC	AGGCAGAACTAAATACAGCACTG	1	AGGGAACGAAGGGAACATTT

Atr_48754-60	G	A	CTGCAACGACGTGT	CTGCAACAACGTGT	GCTTTCCTCTTCAGTGGCC	1	TCCACGACACATACACGT
Atr_49388-52	G	A	CATGTGTGTCTGTC	CATGTGTATCTGTC	GGGACCCATGTATAAGATGGCC	1	AGTTTGGTGAAGATTGGCAGT
Atr_49532-44	T	G	AAACTTTAT[CA]GTCTG	AAACTGTAT[CA]GTCTG	GCAGGAACCTTTGCAACTACTGT	1	AGCATTACTGTGTAGGCTTTACAGA
Atr_49629-71	G	A	CATGCCTGGGA	CATGCCTAGGGA	CCAGCAGAGCCATGGGAATC	1	CGGAGGCAGGTGCAACAG
Atr_49790-61	C	A	TGCACTACTCTTCT	TGCACTAATCTTCT	GCTACAGTACCACCTGCACT	1	CCCCCCAGAAATCAGGAGTC
Atr_50179-30	T	C	GCCAATGGGTGAAG	GCCAACGGGTGAAG	TGCAGGCCTCTTAGCTGTTG	1	AGCATCTTGCCACATCCACA
Atr_5019-45	C	T	TCCTGCAGC[TA]TTCCT	TCCTGTAGC[TA]TTCCT	GCACCGCTGAATGCTACATC	1	TTTCGTGCAGGCTGAGACAT
Atr_50212-69	C	A	AGAGACTATGGC	AGAGAATATGGC	TCACTACAGAATGTGTTCACTCA	1	TGCAATTATGATGTTCTCAGCCA
Atr_50642-59	C	G	CCCTACTTAATGACA	CCCTAGTTAATGACA	CAGGATCGTGGTGCTCCAG	1	GCAGTAGGCCATCACTGTCA
Atr_51176-35	G	T	AAAAGTTGCACAAC	AAAAGTTTCACAAC	TGCAGGTGAGATGAGGTTACTG	1	ACTCCAGCACATAAGAGCAGT
Atr_51458-37	T	A	CTCGCACTGTTGGC	CTCGCACAGTTGGC	TCAATCTGATGCTGGGCTC	1	GACTGAGGAGCCGCCAAAT
Atr_51832-58	A	C	CAGTCAATGC[TC]GATT	CAGTCCATGC[TC]GATT	GCTGTAGGGTCCACGGTAGA	1	TGGGGATTCCAGAGTGAGTA
Atr_51999-44	A	G	AATATAATGGGTAAG	AATATGATGGGTAAG	TAGGGTCCCAGGGCAGTTTA	1	GGTGTGCAACCCAATGAATACA
Atr_52021-40	C	T	AGATGCACTGCATTA	AGATGTACTGCATTA	TGCAGGTGTCACATTCACGTGT	1	ACTGACCACAACCTAAACTGT
Atr_52164-31	A	T	TTTTTTTAAAGAGC	TTTTTTTAAAGAGC	TGCAGGGATAAGCCAAAGC	1	AGCTTGGTGGAAATCCAGGTG
Atr_525-66	G	C	AACAAGAAGCAAAGA	AACAACAAGCAAAGA	TCCAGCATGACCATCTCTGC	1	GGGTCACTGTGTCTCTTTGCT
Atr_52650-66	A	G	AGACAGTATGTTTG	AGACAGTGTGTTTG	CCCTTGCTGTGGCTCTTCAA	1	AGCCCTATAGTCTCCACCA
Atr_52666-51	A	G	AAAGGGTAGTTATT	AAAGGGTGGTTATT	GCAGGCCTTCTGTATGTAAACC	1	TGCTTCTTAGAATTTAAGGCTGCA
Atr_52675-47	C	T	TGAACCGCACCTC	TGAACCGTGACCTC	CAGTTTGTGAGCCGGTGTG	1	CTCCACCAAGAGAGTGCTG
Atr_52715-59	C	T	AGTATACCCCTTGT	AGTATACTCCTTGT	ACTGTAGTGTGGTTATGTGGTT	1	TGAAGATTGTATGTTGTTGGCACA
Atr_52868-38	C	T	TTGCAAACGGAGCA	TTGCAAAATGGAGCA	CAGGGTCCCAGCTGAAGAG	1	CGCAAGAAGCTGATGTGCTC
Atr_53157-67	G	C	GACAAGAGAGACAG	GACAAGACAGACAG	CCAGCCTAGCCATGGACAAG	1	TCACATCCAACCTTGCCAGT
Atr_53210-55	C	T	AGAAGCCAATAGGTG	AGAAGTCAATAGGTG	TCTTGCAATGCTTACCAGT	1	ACGCTTCATGGCATTTTGTGT
Atr_5336-58	A	T	AAACCACAGCATT	AAACCACATGCATT	CTCACCTCACAGGCTACACC	1	CTTTCAGTGCAGTCAGAAATGC
Atr_53521-30	C	T	ATCCCTTCTACCG	ATCCCTTCTACCG	TGCAGGTGATCATCTGAACAAGA	1	ACCAATCCTCTGACAGTTTGT
Atr_53686-72	A	C	AATACAAAT	AATACCAAT	CCCGTGGTTTGTAAAGCAGGA	1	CTGGGGACTACTTGAGCTGC
Atr_53904-44	A	G	AGTCAATTAGTCAAG	AGTCAGTTAGTCAAG	TGCAGGAGACCGTGAAATGT	1	GGTATCCTCCCTGGCTTGAC
Atr_54038-48	A	G	CCGGGGAAAGGATG	CTGGGGAGAGGATG	CACAGGTATGCCACAGGACA	1	AGGAAGCTAAACACAATCTACCA
Atr_54041-38	C	T	TTTGAATCTTAAGA	TTTGAATTTTAAGA	ACTGTCTTGGTGGCAAACT	1	ACCTAACTCGGAAATGTGATTGT

Atr_54160-70	T	C	TCATTTTGGGTC	TCATTTTCGGGC	TTGCGGTTCCAGATGTGGGT	1	AGAGCACACAAAACATTTTCGGT
Atr_54266-27	G	A	GTTACTTGATTGG	GTTACTTATATTGG	TGCAGGCTTCACTACATAGGT	1	ACATCCACCCTCAACAAGCT
Atr_54764-45	G	A	AGCACTCGTCCCA	AGCACTCACTCCCA	TGGGGAGCCAAGTAATGAGC	1	AACCAGAGAGGCCCGAGTAT
Atr_54795-72	G	A	CATTTGTAT	CATTTATAT	TGCACGTATGATGAAGGTGT	1	GCAATTTTAAAGGTGTGGAGACA
Atr_55583-67	G	A	TTACCGGATTGAC	TTACCAGGATTGAC	ACGAGGCATTGATTAAGTCCAGT	1	AACGCTACTGACTTGAGGCC
Atr_55892-54	G	A	ATCTCGTAGACCTCA	ATCTCATAGACCTCA	AGCCTGTCACTTCCAATGAGG	1	TGAACACCCCTCTGAGGTCT
Atr_56024-45	C	A	CAAGTAGCGATCAG	CAAGTAGAGATCAG	AGGTCAGCCCGTCCCTATAA	1	TGGTCTTCTCTCAAGATGTGCT
Atr_56033-37	C	T	GCTACAGCTTTATT	GCTACAGTTTATT	TCTAGTCCCTCCGCTACAG	1	ATGGCCCGATAGTTTGGCA
Atr_5610-27	A	G	GTGACACAAGATTA	GTGACACGAGATTA	TGCAGGTACAAGCAGAGCAG	1	GCCACTTGCAACTGGGAAA
Atr_56109-40	C	T	CAGAACTCGCCCTG	CAGAACTTGCCCTG	CGCATGCGTCCGATAGCC	1	ATAGAGAACTGCAGAGGGC
Atr_56854-26	A	C	GGAAAGTAGGGGTA	GGAAAGTCGGGGTA	GACGTGCACGGGTGGAAA	1	CACAGCCTCAGTGCTTCAGA
Atr_57018-28	C	T	GCGTTGTCTCCGA	GCGTTGTCTCCGA	CTTGCCTGTAAGCTGCGTTG	1	TTTACACTGCAGGCCCTT
Atr_57542-29	A	T	CCAGAAAATGGCTC	CCAGAAATTGGCTC	CTGGCCTTTGTCTCCAGAA	1	CAGTGTGTCTCTCCGATCC
Atr_57756-67	C	T	CAATCAACGAGCAG	CAATCAATGAGCAG	TGCAGGTAAGGGCAGATGAC	1	TTTCCATGGGTCTGCTGCT
Atr_5779-55	T	G	TTTTTCTTTCCCT	TTTTTCTGTCCCT	TGCAGGTATTGAAGACATTCTCTGA	1	GACGTGAATGGAGGGGTCAG
Atr_57832-69	C	A	GAACACGCTGACAC	GAACACGATGACAC	ACCAGTTCAGAGATATGGGTG	1	GGGCGCTTTATCACAAAGGA
Atr_57870-70	A	C	ACTACCTAACCAG	ACTACCTACCAG	TTACCTTACATATGTGTCACTACCT	1	CTCACGTGAGAGTTGCTCTGT
Atr_58305-70	G	A	CCACTGTGGTG	CCACTATGGTG	TGTTACAGTTGTTACATGTCCA	1	GCCATGTCCAGCTTTTACACC
Atr_58342-71	T	C	TCCTTCTTCTG	TCCTTCTCTCTG	GGGTGTGTTGTCTCTCTTCT	1	GACTGAGGAAATAGCAAAGCGT
Atr_58434-42	G	A	CCAGTCCGTTTCC	CCAGTCCATTTCC	GCAGAACCAACCCAGTCC	1	GAGGGCGAGGAACCAAGC
Atr_58562-59	G	T	TATAATTGACCTCT	TATAATTTACCTCT	GACAGGATCCACCACACT	1	AAAGAGGACCGGTCAAGAGG
Atr_58720-60	A	G	TTCCTATAGTTTAG	TTCCTATGGTTTAG	CCAGTCAAGTGCAAGGGTGA	1	TGAACTTGAAACTCATTTTGACCA
Atr_58831-60	G	A	GTAATAATGACGGC	GTAATAATATACGGC	TGCGTGTTTATCTTGAGAAACCG	1	TCTTTTATGAGCACTGCCGT
Atr_5890-29	T	C	CTTCGTATGAGATG	CTTCGTACGAGATG	CAGGTGTAAACCCCGAGTC	1	TCGTTCCGAGCAACAGGAC
Atr_5892-46	A	C	TCATTCCAGAATCC	TCATTCCCAGAATCC	CAATAGCATGGCCGCACTTC	1	TGGACACAGCACAAAGAAGAGT
Atr_59201-47	G	A	CAGCAGGGTCCACT	CAGCAGGATCCACC	GCTTGATTTCACCTGGGTGCC	1	ACCAGGCACTCACAATGACA
Atr_59284-42	G	T	CAGAGATGAATTTT	CAGAGATTAATTTT	AACCTCGTCAACCTCTCTCA	1	GCTCAAGCAGAGGTTTGTGG
Atr_59310-44	A	C	CTCAGCGAGCACTC	CTCAGCGCGCACTC	GCAGTTTGGTGAAGCTCAGC	1	GAAGCCTCAGGAAGCAACAG
Atr_59487-73	C	T	ATAAACGT	ATAAATGT	ACTTGAGCAAAAGGAATGCAGA	1	TGAACCTCTACTCTTATTTGCACA

Atr_59800-43	C	G	ACAGTCCCTAACTAT	ACAGTGCCTAACTAT	CACGTGACGAGGGTGACGAG	1	TCTGCGGTTTACAGAGGCAA
Atr_59842-43	G	A	GGCGGTGAACACAG	GGCGGTAAACACAG	CATCTCTCTTGTGAGGGCGG	1	TCCAGCTACATTGCCTGTGG
Atr_60162-29	T	A	TTTTTTTAAATTG	TTTTTTTAAATTG	TGCAGGCAGGACTGTTTC	1	GAACAGTCCACACGCTAGG
Atr_60265-55	C	A	GGCTTCCAGTGTG	GGCTTCCAAGTGTG	AGGGGTCGGATTAGCCACTA	1	AGGTGGACATTCTAGGTGAGGA
Atr_60368-72	A	T	AGGAACAGCA	AGGAACCTGCA	CGATGGCCTCCAAGGAACC	1	CCCTATCATTCTGTCACTCGT
Atr_60688-70	C	T	GAACCAGCGGTTG	GAACCAGTGGTTG	CCTCCAATGACCTACTGAACCA	1	GGTGTGGTGGCTAACTGAT
Atr_60859-44	T	C	AATTCAATTGACCC	AATTCAACTGACCC	AGGGGTCAGAATCTGCATGC	1	AAGTGTCATCGCTTGTGGG
Atr_61062-75	C	A	ATCTGGGC	ATCTGGGA	TGCCCTGAAAGAGGTCAGTT	1	TGACTGTATGAAAGAAGGCAGT
Atr_61171-66	C	T	GATGTGACTGCACG	GATGTGATTGCACG	CCGACGCTGTAAGTTCTGGA	1	TGTCCTCCGAAACGACTGC
Atr_61911-75	C	G	ATTGCC	ATTGCG	AGTGGCAGCTCCTTCACTTC	1	GCGCCGTTACACTTTCAGTA
Atr_62330-56	A	C	AGGGTGAAAGTCCCA	AGGGTGACGTCCCA	GGGCCAGGAAGGAAAAGCAT	1	ACTACAGGAGCTTTTGGGAC
Atr_62419-71	G	A	CTGCAACGACAC	CTGCAACAACAC	CCTGCAGAGAGACACAGACG	1	GGCCAGACAAAGGAAGGACA
Atr_62463-34	C	T	TGCAGAGCGTTCAC	TGCAGAGTGTTCAC	GCAGGGATAGAAATAAGACTCTGGT	1	GCTTGTTACGTATACACTGGCA
Atr_6251-29	G	T	TCAGGGGGAGATGCA	TCAGGTGGAGATGCA	TGCAGGGACACAAGAGCTTC	1	GCTTCTTGACTTGCTGCC
Atr_62952-34	T	C	TTCCTCTGTGGTG	TTCCTCTGTGGTG	GGATTGGAAGCAACGTTTCTCC	1	AGGACCAGGAATGAAATGGCA
Atr_63042-40	T	C	ACTCATTGACCTCTG	ACTCACTGACCTCTG	GTCTTTGCCCTCCATGAGCT	1	TCCAGGTACTCCACAGCAGA
Atr_63076-27	T	A	ACAAATTTCATTCA	ACAAATTACATTCA	GCAGGCAACAACAACCTCAC	1	ACAGTATCATAGTGGAGGTGAATG
Atr_63101-44	A	G	ACCAGGCAAATTC	ACCAGGCGAATTC	CCATTGTTACAGGGTTTGGGG	1	TGTCGGACATAACCTGGAAACT
Atr_63246-38	A	G	GTGTATTATGTATC	GTGTATTGTGTATC	CAGTCAGCTGCATTGTGTGT	1	AACTCACTATGCTGCCTGGG
Atr_63885-66	C	T	GCTGCCGTCGGTCAG	GCTGCTGTCGGTCAG	TGTTACCCAAGCTGTGTCAG	1	TGCTAATTTTCTTCTCTGACCGA
Atr_64006-52	C	T	GGTTTACCCTGAAG	GGTTTACTCTGAAG	CTGGATGGGGAGCGGTTTAC	1	CAGCTCCCAACCACTGTAAG
Atr_64217-68	A	G	CCTTAAATTCGAG	CCTTAGATTTCGAG	TGTTAACAAGGGAACGCCG	1	TTTTTAGTTACCCCTACCCAGG
Atr_6456-50	G	A	GTTCAGACTGCAGGT	GTTCAAACTGCAGGT	GCATTGCTGCCAGGTTAACA	1	GGAAAACACAACCTGTGCGC
Atr_64706-45	T	A	CACTGACTGCTGTA	CACTGACAGCTGTA	TGCAGGGATGGTCCTTGTGTG	1	ATGACCAAGCCAACTGCCTT
Atr_65094-30	A	G	AGAGCAGACGCCAGT	AGAGCGGACGCCAGT	GCAGGGCTGTCTCGAGAG	1	GACCAAGCTGCCTCTTCCA
Atr_65359-46	T	C	CATCTTCAATCAG[CT]T	CATCTCCAATCAG[CT]T	GTAGTTCCCTGCTTGCAT	1	ATCGCTCTGTGTTGGACCC
Atr_65377-56	G	A	TAACAGGATAATAGG	TAACAAGATAATAGG	CTGGTGATCCCTGCTGTAGG	1	CTGCAGAACCCAGAGACCTG
Atr_65729-42	T	G	GTTACCATCTCTAC	GTTACCAGCTCTAC	TTAATTCACAATGTAGCAGTTACCA	1	GCGCACCCTCTATTTCAAACT
Atr_65843-52	G	T	GCGTCAGGTGGGAA	GCGTCAGTTGGGAA	AATGTGAGTAAGGGGGCGTC	1	CACTTTCAAAGCAAATGTTGGTCA

Atr_6612-39	A	C	TGCCCATATACATGG	TGCCCTATACATGG	TGCAGGGATGCCTATTGTACA	1	GGGATCCCAGGTCATTTC
Atr_66563-34	A	G	AACCTCTATACAGT	AACCTCTGTACAGT	TGCAGGTTAAATGTCCACATCA	1	GGCTCCCAACCACATCGTTA
Atr_66664-59	C	T	CTCAGAGTCCCTG	CTCAGAGTCCCTG	AGGTACCCCTTGCCAAATGG	1	TGCAAAGTAGAAGGCAGGGA
Atr_66806-52	T	C	TTACCTGTTTGAGA	TTACCTGCTTGAGA	AGCCCTGCTTTAACAGTGGT	1	TAACCCCTCATCCCTCAGG
Atr_67534-27	C	T	CATAACTACAAATAT	CATAATTACAAATAT	GCAGGCAAGTGCAACATCAA	1	GCTGTGCAGAGTGTAGGAG
Atr_67759-28	G	A	GGCACGGCACAAAAC	GGCACAGCACAAAAC	AGGGGAAGAGCCAGTGAGAG	1	AATTGCTGTGCTTGCCATGG
Atr_68186-72	C	T	ACAGTCCCTGC	ACAGTCCTTGC	TACCAAGTCGCTGACCAGTA	1	TCTGCCTCTCCACAGGTTA
Atr_68680-72	T	C	CATGATCAG	CATGACCAG	TTACCAAGGAAACCAGGGGC	1	ACATGCTAAAGTGGCTGCTG
Atr_68762-59	A	T	CTCAGATAGTGAGA	CTCAGATTGTGAGA	GGGTGCAGCAAGGATGGTAT	1	CCTGCACCAAGGTAAGCTCT
Atr_68808-31	A	T	GTATTAAAGCTGGC	GTATTATGCTGGC	GGTAATGCCTCCCACTTGT	1	GGAGGAGTTTATTGAAAGCAGGC
Atr_69047-33	A	G	TAATTATATGAAAG	TAATTATGTGAAAG	GCAGGCTGCTACTGTAGTCT	1	GTGAAAACAGTCCTTTCCCT
Atr_69217-58	A	G	TCAAAGCACCCGAG	TCAAAGCGCCCGAG	AAGCCCCTTCTGCTTCTC	1	ACTGCTTCGTAGTAGAAAGT
Atr_6988-51	T	C	TTAACTTTAGATCA	TTAACTTCAGATCA	TGGTCTGGCAGGAACAC	1	TGCTTGATGTTACCTGATTTGAT
Atr_7001-57	T	C	CACATTATTTCTGT	CACATTACTTCTGT	CCAGAGTGATGTGCATAAAGCC	1	TGCTGTGCTTCTGTTCTGT
Atr_70139-39	G	A	ATTACAGTCCCCCA	ATTACAATCCCCCA	GGAGTCCTACAAGTTAAAGGGC	1	CACGTTAATGAAGTGTGGGG
Atr_70167-40	C	T	CAGACCTCGTCTG	CAGACCTTGTCTG	GCATGCATCAGATAGCCAGC	1	ACTATATTGCACTGTAGCAGGAC
Atr_7026-63	C	A	AATTACCAAGTTT	AATTCACAAAGTTT	GGGTGCCCCAAATATATTGCA	1	AGAGTTGCTGCTTGTTAACTT
Atr_70459-55	C	T	TCTGTTTCACATTG	TCTGTTTACATTG	GGAAGATTCCGATGACAGAACT	1	GCAGAGAAAAGAGCCGCAAT
Atr_70467-53	A	G	TAAGCACTTCAGAAT	TAAGCGCTTCAGAAT	TGACACACCTGAAAAACACCAC	1	TTAGCTGTGGGATCATGCCA
Atr_70479-48	T	A	CATAGATTGCTTCA	CATAGATAGCTTCA	GTCTGGGAAATGTCTGGGCA	1	CAGCCTAGGTCTCTGTTTGCA
Atr_70609-65	A	T	TCTGGACAGATTAA	TCTGGACTGATTAA	GCAATGGCTAAACATCTGGAACA	1	TCATTCCACCGAGTCTCTCT
Atr_7072-61	C	T	AAGGACGTTGCTCGC	AAGGATGTTGCTCGC	ACGCACCTCAAACAGTTGA	1	GCTGGGGTGGATAAAATGG
Atr_70880-74	T	C	CCCTCACTT	CCCTCACCT	GCTTTCTTTGGCCCAAGGG	1	GCATGCAGCGGGAACATTTT
Atr_71195-60	A	T	CAGAAAGATGGGGTG	CAGAATGATGGGGTG	TGATGTTGAAGCCTCTACACCA	1	ACGATACTTCATCCACCCCA
Atr_72165-47	C	A	GGTCTCGGGTTTCC	GGTCTAGGGTTTCC	GGGTGCTCTACCTCTGGTCT	1	GTGGCTGATCACATCCCTT
Atr_72251-33	A	C	TTAGGAGATGCTGA	TTAGGAGCTGCTGA	AGAAGCTGGGAGTGGTTAGGA	1	TGGGGTTTTAAAGCTATACACCA
Atr_72558-41	C	T	TCCATGTCGTCTAA	TCCATGTTGTCTAA	GCAGGGCTAGTGACTCTTCA	1	TCTGTCTTATCTGTAGTGTGATCAC
Atr_72693-61	A	G	TTAAGGCATACATA	TTAAGGCGTACATA	CGGTGTGCTGCTATTTAAGGC	1	TCCTGAAGACATTGACTAGAGGA
Atr_7298-56	C	T	GTCCCGACCAAGGCG	GTCCCGATCAGGCG	CGGTCAGTATGGCTCCTGTC	1	GCAGTGCCCCCTGATGTATT

Atr_73438-69	T	C	TGAAATAAACAA	TGAAACAAACAA	AGCTGCACCCCTTTTAACT	1	CCCTGCATGAAGTCCAAGGT
Atr_73505-52	A	T	CATTCAAAACACAC	CATTCAATACACAC	GCAGGAAAAACAAGCCAGGG	1	AGAACGAATGGTCATTGTGTGT
Atr_73608-61	C	T	CGACCCGGGTCTATT	CGACCTGGGTCTATT	TGCATTTTGCTTCGCTCGAC	1	CTGCTTAACCCAGGTCCCAG
Atr_73740-69	T	C	ACATTTCTGTGC	ACATTCCTGTGC	CCTTTCGTAGGCACACTAGACA	1	AGTCATTCAACCTTTCATGGCAC
Atr_73905-66	A	T	AAGTTTTAAACTG	AAGTTTTAAACTG	AGGTTCTCCTGTTTACAAGTT	1	GGTACAGGCTCGCTCGTAAT
Atr_73987-49	G	A	GCATGGCCAGTTATA	GCATGACCAGTTATA	CTTACCCTCCACTGCTAGCTG	1	CCGGCAAAACACTACACCA
Atr_73994-27	C	T	CAAGACTATGAAGAG	CAAGATTATGAAGAG	TGCAGGTCTATTTTCTAACAGCA	1	ACCAGTGGACATGCTTACGG
Atr_74094-36	G	A	TGCCCCGCATTATGC	TGCCCATCATTATGC	GGATGTGCAAGCATGGAACC	1	GCACATGCGATACTCCAGCA
Atr_74322-45	A	G	GGTTTATACACATG	GGTTTATGCACATG	CAGAGGGCAGGTCCAAGAAA	1	AGCCACCCCTGAATCATCATGT
Atr_74662-68	T	C	AAAAGTTCCCCCT	AAAAGTTC CCCCT	AGGGGAGTGCTGTGTTGTG	1	ATGGTGGCTCAGTCCCAAAG
Atr_74730-29	G	A	AAGCCGCAGAAAGAC	AAGCCACAGAAAGAC	GCAGGTCAGAGGGAGTTTGA	1	TGCTGCTGTGTTACAGAGAGG
Atr_74747-45	C	T	CAATTGTCTATCAG	CAATTGTTATCAG	TGCAGGCAAAACAAGACAGAC	1	GCCTGGAAGTACTGAAGTGA
Atr_74844-59	T	A	CCTTTGTGTGTACA	CCTTTAGTTGTACA	GTGAACCACACTGTCTTTCTGT	1	TGACTGTTTTGTCCACGTTGT
Atr_74987-50	T	C	TTTACTTCAAACACTAC	TTTACCTCAAACACTAC	GCAGGGCGAATTCTCAATATGG	1	AGGTATGGTGTCCTTGTAGTTTGA
Atr_75140-58	C	T	GAGTATGCTTTCAT	GAGAATGTTTTCAT	CACCAGAGTGCTTTAAGGTTTATAA	1	CTGTTGTTTCATGAGCCGTATAAT
Atr_75407-53	G	T	ACAGACAGGGTCTC	ACAGACATGGTCTC	GGAAAGGTACAGTACAGGGCA	1	AAGCCCTGAAGCAATCGGAA
Atr_756-60	T	A	ATCTAACTACTGAC	ATCTAACAACCTGAC	TGCAGGCATTCTATAAACACG	1	AGAGGGCTTTGAGATGAAGGA
Atr_75982-70	G	T	ATGAAGAAGAT	ATGAATAAGAT	CAGGAAGATCCGGCAAAAGA	1	TGCTGCCTCTTGCTCATCTT
Atr_76253-44	G	A	CTGTCTCGCCTCTC	CTGTCTCACCTCTC	AGGTTCTTATTACATGCCTCTGTCT	1	GGGTCTGGTGCTGTGATTA
Atr_76409-55	G	A	CAGCCGCAGGAGAGC	CAGCCACAGGAGAGC	TCAGCGAGTGAGTGGACAAC	1	TGATCATAAATGTAAACTGCTCTCC
Atr_76418-65	A	T	CCGGCTTATCTGAA	CCGGCTTTTCTGAA	GGTAATGCGTGGGTGGTGTT	1	ACCAGCAATAACGTCTTCCTGT
Atr_76571-26	C	A	CGATGTTACGTGC	CGATGCTAACGTGC	GAGGGTCCGCTAGCGATG	1	GCACTGCTCTCTATCTGGGG
Atr_76791-46	G	A	TATCCGCTGTAGCAC	TATCCACTGTAGCAC	GTCCCTGAGCTACCAAG	1	ATTGAGGCAAAACCAGCAGG
Atr_76888-43	C	T	TGTCAAGCGATTGA	TGTC AAGTATTGA	ACAAACAATCAGGGCTGTICA	1	TGTGAATGAGACGGATGCAGT
Atr_76890-36	G	A	TTCTCGATCTCGCTT	TTCTCAATCTCGCTT	CAGTCGCCGAATCCTGTTCT	1	GATACGTGCTAGGACCTGC
Atr_769-65	C	T	CCTCTCAAACATAAAA	CCTCTTAAACATAAAA	GTCCACACAGTACTTGGCCT	1	TCATGCTAAGGACCTTGATTACGA
Atr_77778-67	C	T	AGTAGATCACCAGA	AGTAGATTACCAGA	TTGCTTACCCCTGCTTTAGC	1	AAACTGTGCAAGTGGACACA
Atr_7793-68	C	A	CGGTACTCAAATAA	CGGTACTAAAATAA	TAGGGAAAGGGAGTCAGCCA	1	ACTTCCATTCCACAGCTAATGA
Atr_78173-42	T	C	GGCATTGGAAC[CG]GTC	GGCATCGGAAC[CG]GTC	CTCAGGTCACCCAGCAGAG	1	GTTGAGCCGCTTGCAATCTC

Atr_7817-58	G	A	ACAC[CT]GTTCATCAGC	ACAC[CT]ATTCATCAGC	GCCTCAGCTGAAAACACAAGA	1	CCGTGTGAGTTTGCTGCTG
Atr_78413-36	G	T	TACCCGAGTCTAAA	TACCCGATTCTAAA	TGCAGGTGTGTATTGCTGACA	1	AGCAGATATGAGTAAACATTGCCT
Atr_78571-74	A	C	AAGTGAGAC	AAGTGAGCC	GACTTGCAGGTGTTCTGGAGT	1	AGTTCGGCTTGCTTGTTTT
Atr_78600-73	C	A	CCCAGCTCAG	CCCAGCTAAG	AATAAGGAGCAAGCCCAGCT	1	GTCGACTTTGGGGAGCAAGG
Atr_78858-41	A	G	CATGAACCATTTTT	CATGAGCCATTTTT	AGCTGACAACGACATCATGA	1	TCCGCATGAGTCAAAATCATACT
Atr_7928-34	C	A	GTCATAACTGCTCA	GTCATAAATGCTCA	GGGGTTGCAGTACCTTGAGG	1	TCAAAGGCATCAACAGGAGT
Atr_7944-51	C	A	GGCAGCTCGCGGCC	GGCAGCTAGCGGCC	GTGACCAGTACGTGACCCAG	1	GTCTTCTCTCGTCTCGGC
Atr_8314-34	T	A	GATATTGTATGTGGC	GATATAGTATGTGGC	TGCAGGATTCTTTACAGAAGA	1	TGAACAGCTCTGGATGCACG
Atr_9723-56	C	T	ATGCGCAGTCTGTAG	ATGCGTAGTCTGTAG	TGATGGGCCATCTTTCACGG	1	GAGAAGCCTTGGAGTGGACC



### Appendix 13. Species Associations for Species Diagnostic Markers

Locus	A1	A2	SpeciesA1	SpeciesA2	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;Sfo;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;Sfo	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_myclar404-111	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_myol1a-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