GENETIC ASSESSMENT OF COLUMBIA RIVER STOCKS

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Executive Summary

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

Objective 1) discover and evaluate SNP markers in salmon and steelhead and other anadromous fishes. In the current year of this project we have continued our use of GT-seq protocols for SNP discovery. Our laboratory has designed SNP panels for five study species (Chinook salmon [*Oncorhychus tshawytscha*] – 299 loci; Steelhead trout [*O. mykiss*] – 390 loci; Sockeye salmon [*O. nerka*] – 382 loci; Coho salmon [*O. kisutch*] – 257 loci; and Pacific lamprey [*Entosphenus tridentata*] – 316 loci). The expanded panel for *O. mykiss* (from 379 to 390 markers) include markers associated with specific traits to enable identification of premature (early-arrival to spawning grounds, primarily summer-run) or mature (late-arrival to spawning grounds, primarily winter-run) steelhead.

In 2019, the total number of samples genotyped with GTseq was 157,319. The largest portion of samples were Chinook salmon (91,516), then Pacific lamprey (26,276), steelhead (23,144), coho (12,310), and sockeye (3,948) as shown in the full section for Objective 1.

Objective 2) expand and create genetic baselines for multiple species including Chinook Salmon (*Oncorhynchus tshawytscha*), steelhead trout (*O. mykiss*), Sockeye Salmon and kokanee (*O. nerka*), and Coho Salmon (*O. kisutch*). Objective two of this project describes efforts to evaluate genetic diversity among populations that will inform managers in the areas of harvest monitoring, and conservation monitoring. Our approach involves the collection, analysis, interpretation and distribution of genotypic data. These data are being compiled as species-specific reference baselines for characterizing Chinook salmon, steelhead trout, and *O. nerka* population structure specific to the Columbia River Basin. The collaborative, inter-agency application of genetic stock identification (GSI) tools continues to provide invaluable monitoring capabilities to understand relative stock proportions in sport, commercial and tribal harvests, as well as monitoring of stock specific run-timing at Bonneville Dam, Lower Granite Dam and other fish weirs in the basin. Moreover, GSI is being used in concert with parentage-based tagging (PBT; *O. tshawytscha, O. mykiss, O. kisutch*), providing the means to genetically assign individual fish to a hatchery broodstock-of-origin. PBT continues to be valuable for monitoring trends in hatchery production, harvest of hatchery fish, and population attributes of specific hatcheries (e.g., stray rates, survival/mortality, migratory behavior, hatchery/wild interactions). Major accomplishments in 2019 include expansion of our PBT baselines with the addition of several new hatcheries in the Columbia River Basin, both above and below Bonneville Dam. The current PBT baseline for Chinook salmon is shown in Figure 1. The GSI baseline for steelhead trout was substantially expanded 335 SNP markers after genotyping many of the original baseline collections with our revised GT-seq panel.
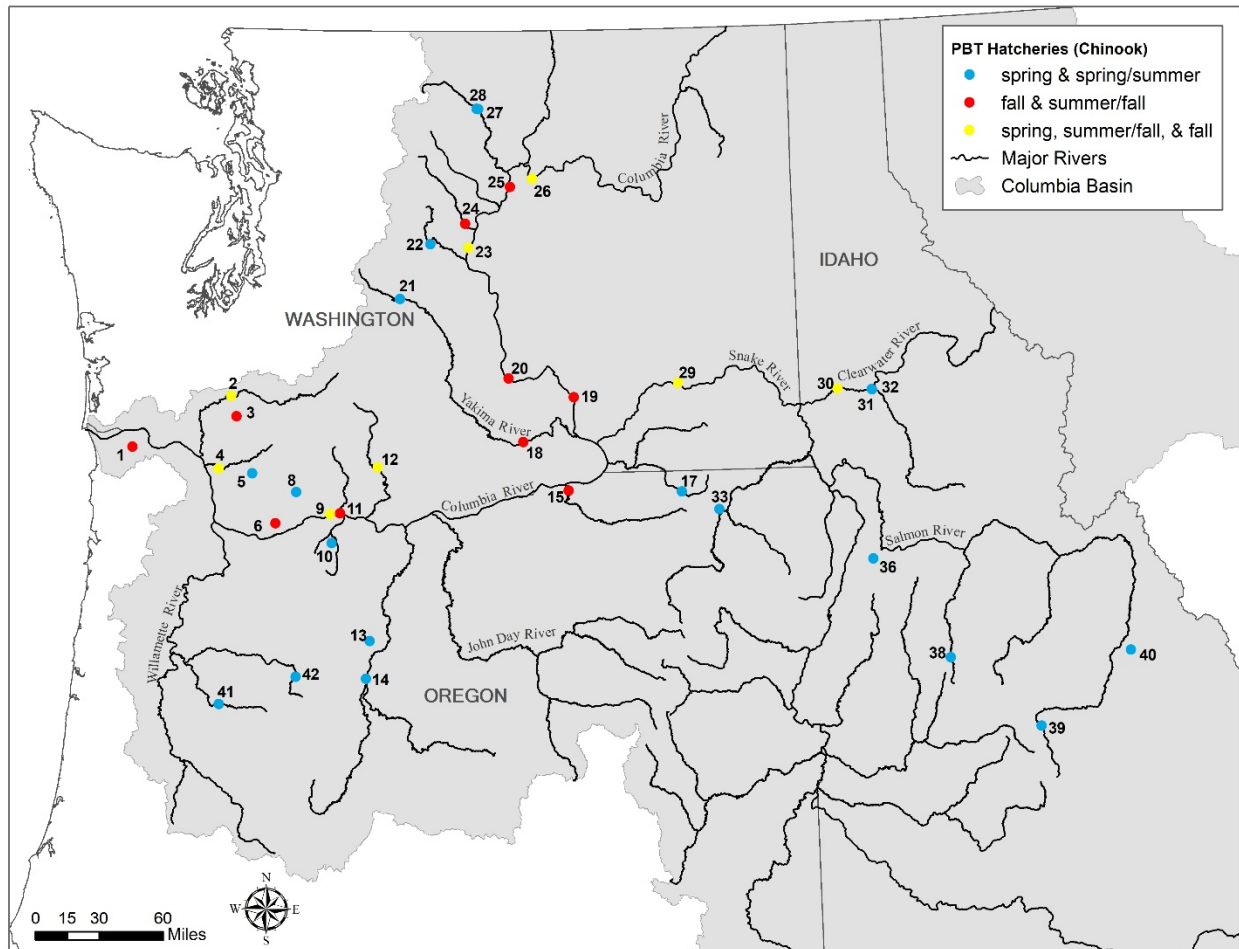
Figure 1. Chinook Salmon, PBT hatcheries. Numbers correspond to map ID and hatchery descriptions.

There are three projects that have begun to characterize reference baselines of millions of SNPs for Chinook Salmon, Coho Salmon, and *O. mykiss*. These new projects utilize whole genome resequencing methods that barcode pools of individuals that represent different collections and can generate allele frequencies across millions of SNP loci. We expect that in the near future there will be no shortage of genetic markers that can be used for GSI and PBT applications anywhere in the species range of our fish of interest. Specific SNPs may be targeted to improve GSI and PBT by incorporating them into GT-seq panels for high-throughput genotyping. In addition, projects will be able to utilize these SNPs for a number of other applications that involve elucidation of genetic mechanisms underlying fitness traits of interest.

Objective 3) implement GSI programs for mainstem Chinook salmon, Sockeye salmon, and steelhead fisheries. In this section, we first described a new method for estimating abundance from catch estimates and at Bonneville Dam using functions that minimize bias from expansion of PBT tag rates. This method allowed us to take PBT tag rates into account, and accurately estimate attributes of natural-origin fish without being influenced by the attributes of unmarked hatchery-origin fish that were not assigned with PBT. We have implemented this approach in all

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484 our harvest estimates for 2018. We have switched to a larger panel of SNP loci (254) that are a
485 subset of the most informative loci for PBT applications which we previously identified among a
486 set of 299 SNPs in Chinook salmon. Results have demonstrated this subset of 254 SNPs
487 improves accuracy of PBT assignments for all lineages of Chinook salmon and effectively
488 avoids crashing issues with SNPPIT, the software we use for PBT assignments.
489   We used a combination of PBT and GSI analyses to determine stock composition of
490 Chinook salmon harvested in 2018 in test, sport, commercial, and Treaty fisheries in the
491 mainstem Columbia River, and used PBT and GSI to estimate stock composition of sockeye
492 salmon harvested above and below Bonneville Dam in commercial, sport, and Treaty fisheries
493 during the spring, summer, and fall management periods (Figure 2). PBT is a new application
494 for Sockeye salmon and can identify fish that are part of the Yakima River reintroduction using a
495 baseline of translocated adults. This was the first year we analyzed the fall test fishery (pound
496 net) conducted in 2018.
497   There were 101 coded-wire tags (CWTs) recovered and identified to hatchery stock and
498 broodyear (BY) among the snouts recovered from the lower river fisheries, and 77 of these
499 CWTs also were PBT assigned (76%). Of the 77 fish with both CWT and PBT, there were 65
500 fish (84%) that appeared concordant with the PBT assignments according to both the hatchery
501 source and the broodyear.
502
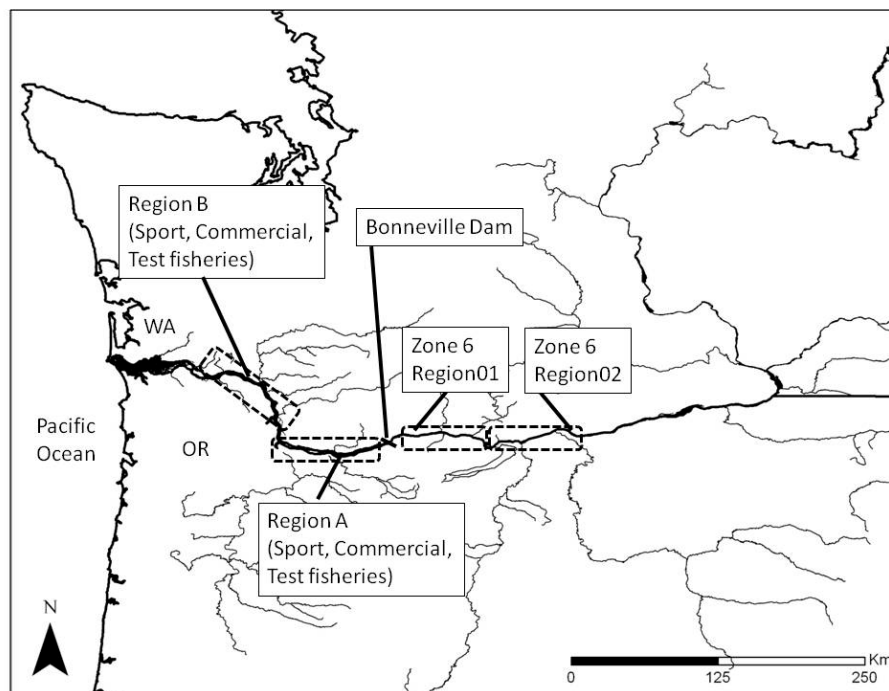
Figure 2. Sources of fishery mixtures in the lower Columbia River mainstem.

507   We examined one source of information that could potentially be useful to managers
508 particularly on years when the spring Chinook Salmon run is delayed. There is a test fishery that
509 is typically conducted by WDFW on Sundays each week in the early spring (February – May). If
510 the test fishery CPUE were lagged 13 days the peak in CPUE appears to correspond with a peak
511 in Bonneville weekly counts (Figure 3). So if the in-season genetic analysis includes the data

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512 from the test fishery, our report may be able to predict the abundance of particular hatchery and
513 natural-origin stocks that we can expect to pass Bonneville Dam up to 2 weeks later which would
514 be useful information for USvOR managers.

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516

517 **Figure 3. The relationship between the test fishery upriver Chinook Salmon CPUE (line)**
518 **and weekly fish counts at Bonneville Dam (solid gray) in 2018.**
519

520

521 Analysis of Chinook salmon fisheries in the summer management period (June 16 –
522 August 1) addressed the following objectives: 1) estimate stock composition for the mark
523 selective sport fishery in Region B and Region A below Bonneville Dam, and 2) compare stock
524 composition of adipose-clipped versus adipose-intact fish from the Tribal Zone 6 harvest above
525 Bonneville Dam.
526 The largest difference in the composition of these two fisheries is the presence of lower
527 river stocks (04_WILLAM) in the lower river fishery compared to the zone 6 fishery (**Figure 4**).
528 There were small but detectable abundances of Snake River spring stocks in both the Non-Treaty
529 and Treaty summer fisheries.

530

Figure 4. Genetic stock composition of the summer Chinook salmon fisheries analyzed in 2018.

The fall test fishery (pound net) may provide a relatively representative composition of the stocks present in the lower river. Comparison of the test fishery composition and the compositions of the commercial and sport harvests showed a dramatically lower abundance of "tules" in sport fishery compared to the other harvests (**Figure 5**). This difference may largely be due to sport fishers preferentially keeping the VSI bright fish over the tule fish.

Fall Non-Treaty sport fishery (kept adults)

Fall Test Fishery (kept=clipped, released=no clip)
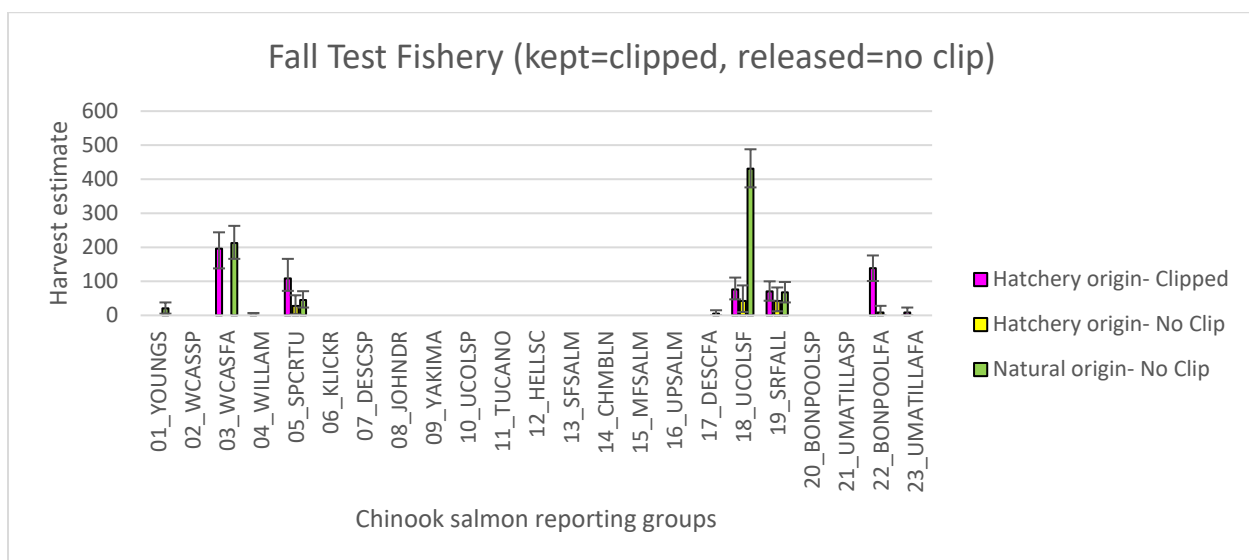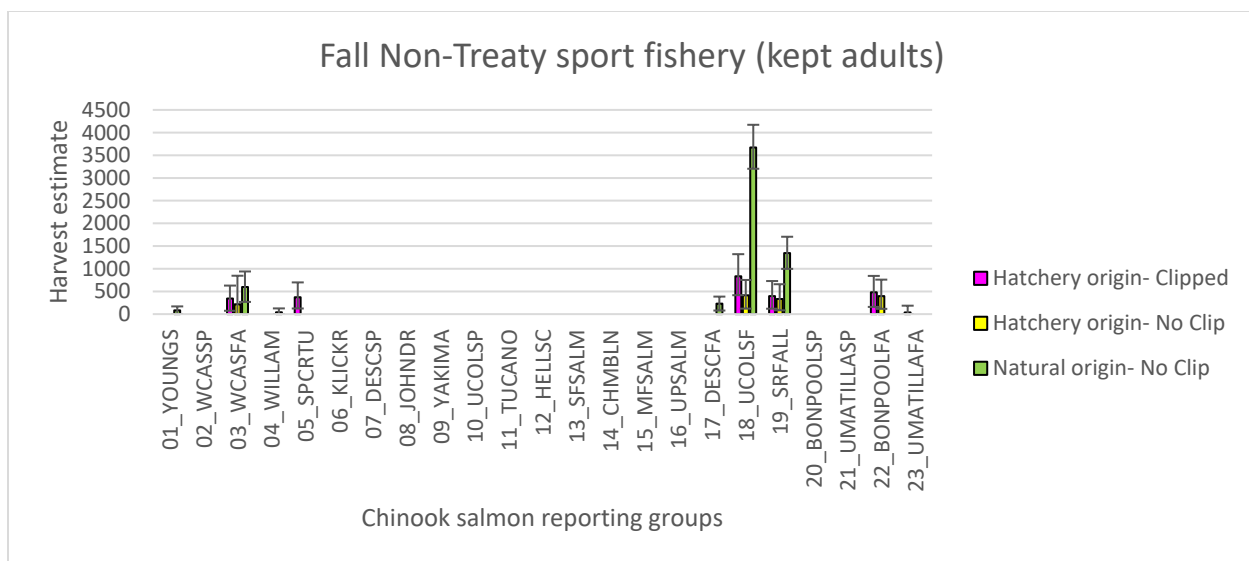
Figure 5. Genetic stock composition of the Non-Treaty fall test and sport Chinook salmon fisheries analyzed in 2018.

Analysis of stock composition of sockeye salmon fisheries included those from the lower Columbia River sport fishery below Bonneville Dam and the Zone 6 tribal fishery collected in 2018. The overall stock composition of sockeye salmon in these fisheries are shown in Table 1. The proportion of sockeye salmon stocks encountered at Bonneville Dam and in the Zone 6 tribal fishery differed most dramatically for the Wenatchee stock. For the first time, we estimated the number of reintroduced stock from the Yakima River that comprised the fishery (N=149, 2%).

17

556 **Table 1. Comparison of stock-specific abundance and percent composition among sockeye**
557 **salmon fisheries. The mean stock abundance estimate is provided for each fishery harvest**
558 **in 2018.**

Mixture source	Mean						Stock proportion					
	Okan ogan	Wenat chee	Sna ke	L B C	Yaki ma	oth er	Okan ogan	Wenat chee	Sna ke	LB C	Yaki ma	oth er
Sport	111	-	-	-	-	-	100.0 %	-	-	-	-	-
Treaty Zone 6	6,076	1,312	150	5	149	34	78.6%	17.0%	1.9 %	0.1 %	1.9%	0.4 %
Total Harvest	6,187	1,312	150	5	149	34	78.9%	16.7%	1.9 %	0.1 %	1.9%	0.4 %
Bonnevill e Dam	174,41 6	17,675	351	80	1,29 4	-	90.0%	9.1%	0.2 %	0.0 %	0.7%	-

559

560
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 and jack Chinook and adult steelhead during the spring, summer, and fall management periods, and 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 2018 (post-season analyses). Further, in-season analyses were completed for fish returning throughout 2019 and provided to regional fisheries managers such as the Technical Advisory Committee (TAC).

There were 7 major (i.e., abundance >1000 fish) Chinook salmon stocks represented in the total estimated relative abundance (N=124,854) of natural origin (i.e., adipose non-clipped fish that did not assign via PBT) Chinook salmon passing Bonneville Dam in 2018 (Figure 6). These non-clipped stocks in order of decreasing magnitude were 18_UCOLSF (92,425), 19_SRFALL (15,406), 12_HELLSC (4,833), 10_UCOLSP (3,607), 09_YAKIMA (2,240), 17_DESCFA (1,752), and 13_SFSALM (1,402). These stock abundance estimates were based on the stock proportions that were estimated in using SCOBI DEUX and SPIBETR functions and the estimates of clipped and unclipped adults distributed by TAC.

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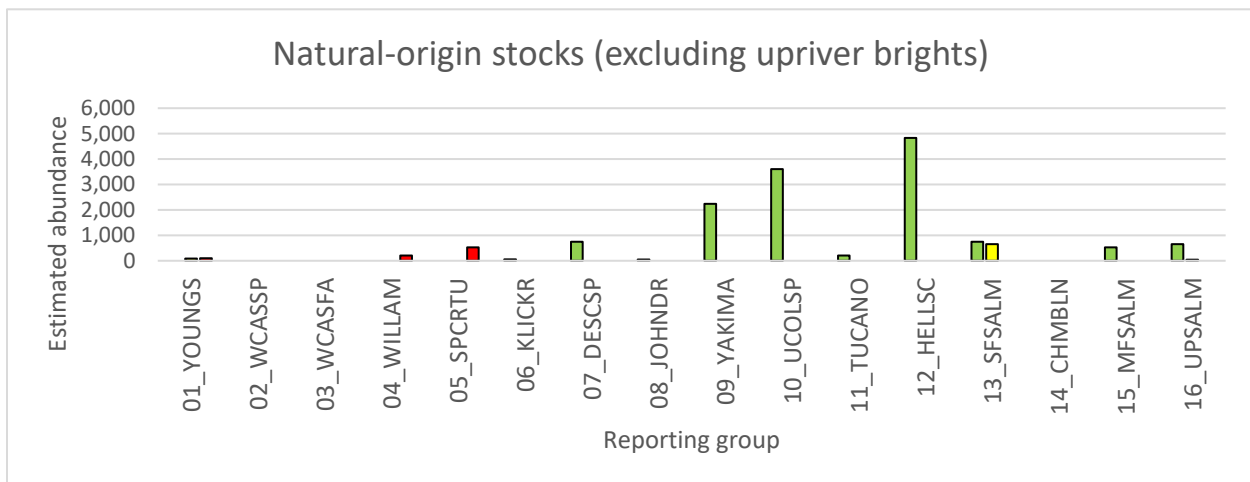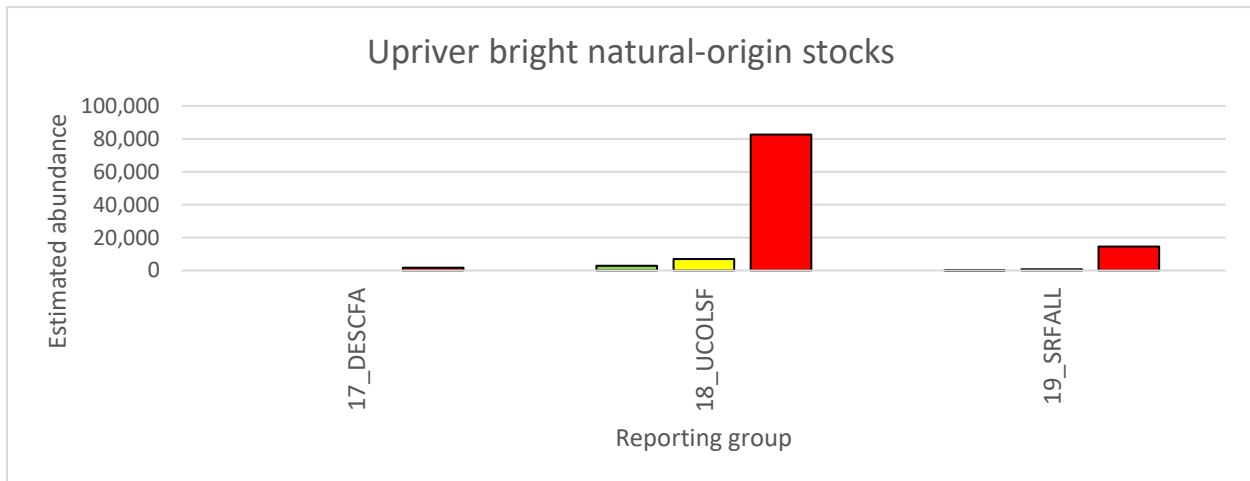
Figure 6. Estimated abundance of natural origin (excluding adipose-intact hatchery-origin fish) Chinook sampled at Bonneville Dam in 2018 assigned to genetic stock of origin. Upriver bright Chinook salmon reporting groups (top panel), and all other natural-origin Chinook reporting groups (bottom panel) are shown by spring (green), summer (yellow) and fall (red) management period.

There were five major stocks (abundance >1000) represented in the total estimated relative abundance (N=70,265) of hatchery origin steelhead passing Bonneville Dam in 2018. These stocks in order of decreasing magnitude were 10_SFCLWR (26,807), 07_MGILCS (18,878), 14_UPSALM (17,707), 09_UPPCOL (4,637), and 03_SKAMAN (2,101) (Figure 7). There were three major stocks (abundance >1000) represented in the total estimated relative abundance (N=23,735) of natural origin (excluding adipose unclipped hatchery-origin fish) steelhead passing Bonneville Dam in 2018 (Figure 7). These stocks in order of decreasing magnitude were 07_MGILCS (16,797), 09_UPPCOL (1,424), and 08_YAKIMA (1,321). Two major stocks in 2017 were no longer estimated with abundance >1000: 14_UPSALM (35, down from 2,286), and 06_KLICKR (942, down from 1,013). The 14_UPSALM stock appeared to have decreased dramatically but we feel this was a results of the SCOBI DEUX SPIBETR function that minimized bias from tag rate expansion of the unclipped hatchery-origin fish. This results underscores the importance of the SPIBETR method and using this function consistently on past years of data for better comparisons across years.

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B-Index Summer Steelhead
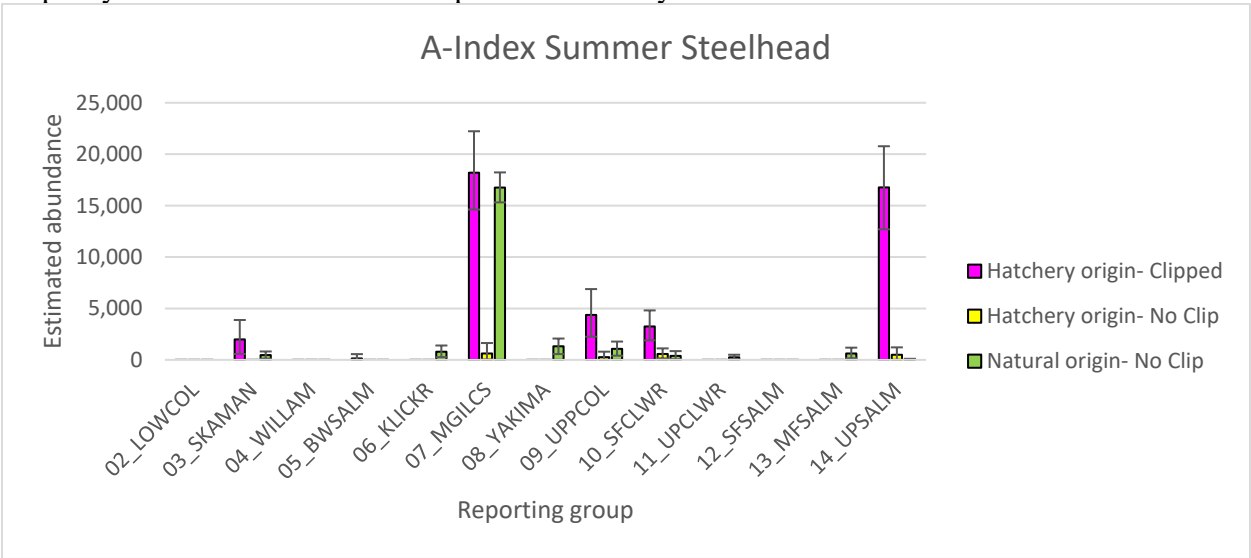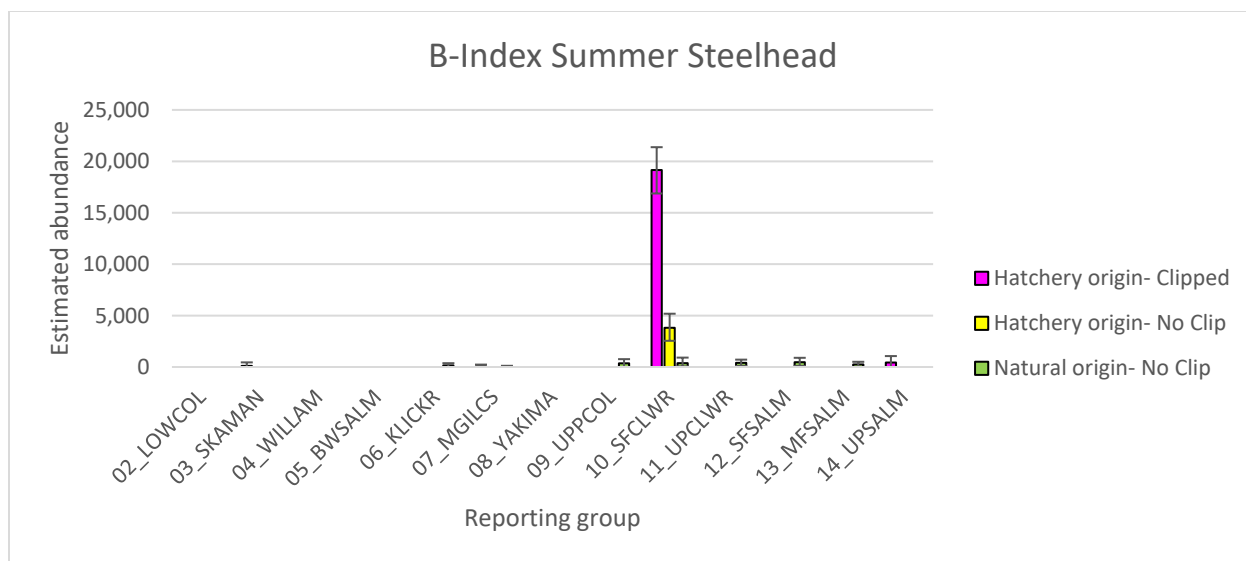
602
603
Figure 7. Estimated abundance (± 95% CI) of A-Index (<780mm FL, top) and B-Index
(>=780mm FL, bottom) hatchery origin (adipose clipped and unclipped) and natural-origin
steelhead assigned to genetic stock of origin that were sampled at Bonneville Dam in 2018.

608   Stock abundance for sockeye salmon was estimated over a course of 16 statistical weeks
609 (i.e. weeks 21-36). A total of 1,857 sockeye salmon were sampled at Bonneville Dam in 2018
610 and were assigned to one of four genetic stocks (i.e., Okanogan, Wenatchee, Snake, and Lake
611 Billy Chinook) using GSI and one reintroduced stock using PBT. The Okanogan stock had the
612 highest relative abundance (174,130), followed by the Wenatchee (17,675). The Snake and Lake
613 Billy Chinook stocks had estimated abundances < 500, but were based on relatively few genetic
614 assignments (<15) (Figure 8). The reintroduced stock from Yakima River was also low sample
615 size but we estimated 1,294 fish in 2018.

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Columbia River Sockeye stocks

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Low abundance Sockeye stocks
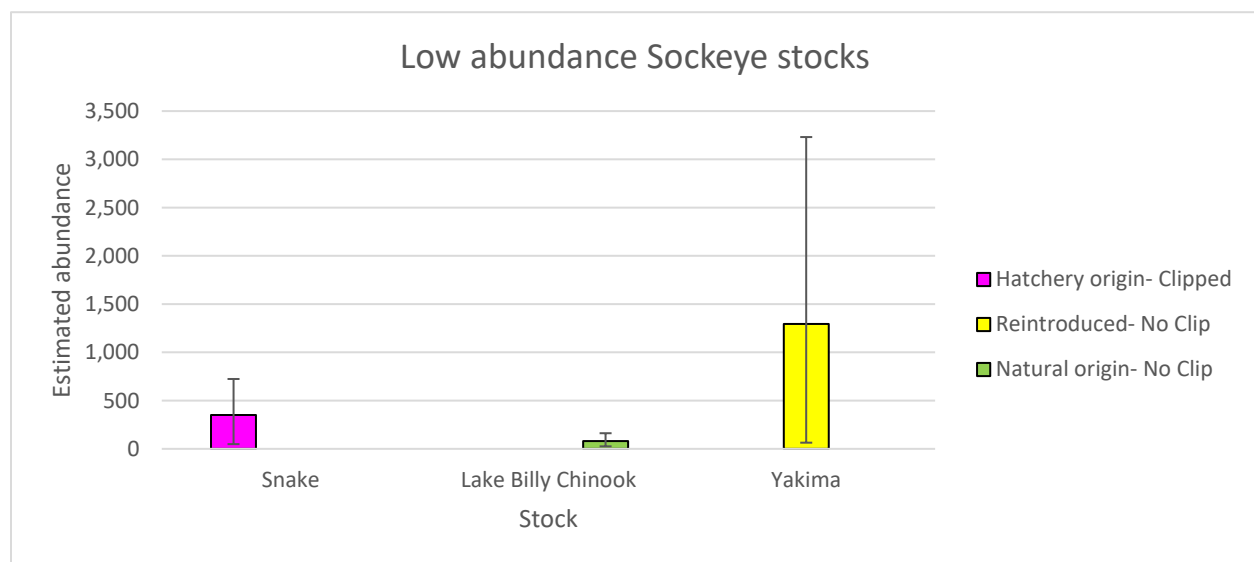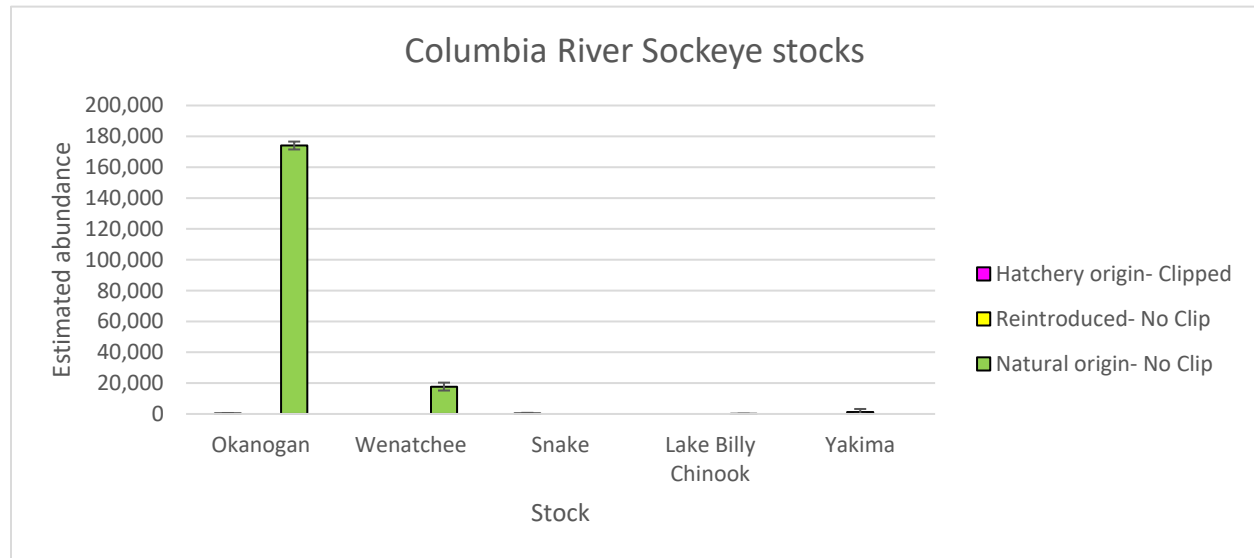
623
Figure 8. Estimated abundance (± 95% CI) of sockeye salmon stocks sampled at Bonneville
624
Dam in 2018.
625
626

627   While the run timing distributions of some hatchery origin and natural origin spring
628 Chinook salmon stocks terminated within the spring management period, several spring Chinook
629 salmon stocks extended well into the summer management period. For steelhead, the patterns
630 generally are consistent with past years. The late arriving natural-origin stocks with median dates
631 on or after August 25th were 10_SFCLWR 11_UPCLWR, 13_MFSALM, and 14_UPSALM.
632 We characterized run-timing by A-Index and B-Index categories for these stocks. For some
633 stocks that had earlier run-timing as A-Index sizes, these stocks were later arriving as B-Index
634 stocks. Run timing distributions for sockeye salmon sampled at Bonneville Dam broadly

635 overlapped in 2018, and we observed nearly identical run timing distributions for the Okanogan
636 and Wenatchee stocks (median date near 06/24/18).
637 Finally, we delivered reports to the U.S. v OR Technical Advisory Committee (TAC) on
638 in-season and timely post-season analyses of several runs and fish species passing Bonneville
639 Dam in 2019 (Table 2). The timely reporting of these preliminary analyses increased their
640 usefulness to the fisheries managers of these Columbia River stocks because the results were
641 available while the fishing seasons were being actively shaped or just prior to the TAC needing
642 information to perform their annual analytical tasks.
643 **Table 2. The in-season and post-season report timing and scope of the 2019 fish runs.**

Species	Management Period	Data coverage	Analysis begins	Report timing
Chinook	Spring	01/01/2019 – 05/03/2019	5/6/2019	5/10/2019
		01/01/2019 – 05/17/2019	5/20/2019	5/24/2019
		01/01/2019 – 06/01/2019	6/3/2019	6/7/2019
		01/01/2019 – 06/15/2019	6/17/2019	6/21/2019
	Summer	01/01/2019 – 07/05/2019	7/8/2019	7/12/2019
		01/01/2019 – 07/31/2019	8/5/2019	8/9/2019
	Fall	01/01/2019 – 10/25/2019	10/28/2019	11/1/2019
Steelhead	Skamania	04/01/2019 – 06/30/2019	7/8/2019	7/12/2019
	Summer A-/B-Index	07/01/2019 – 07/31/2019	8/5/2019	8/9/2019
		07/01/2019 – 10/25/2019	10/28/2019	11/1/2019
Sockeye	Total	01/01/2019 – 08/02/2019	8/5/2019	8/9/2019

644 Note: The data were reported as cumulative abundance estimates for each genetic stock during the Chinook Salmon
645 and Summer Steelhead A-/B-Index management periods. The report timing indicates the date these reports were
646 provided to the USvOR TAC chair Stuart Ellis for distribution to TAC members.
647
648 *Objective 5) Adaptive Genetic Variation associated with environment, landscape, and*
649 *phenotypic traits*
650
651 For Objective 5, work has progressed on sequencing Chinook salmon and steelhead
652 throughout the Columbia River Basin to evaluate neutral and adaptive genetic variation related to
653 environmental features. Our recent results indicate that environmental features are strong drivers
654 of adaptive genomic divergence in salmonid species and provide a foundation to investigate how
655 populations might respond to global environmental change (Matala et al. 2014; Hand et al. 2015;
656 Hecht et al. 2015; Micheletti et al. 2018a). Broad geographic patterns of neutral and non-neutral
657 variation demonstrated in these studies can be used to accommodate priorities for regional
658 management and inform long-term conservation of Chinook salmon and steelhead in the
659 Columbia River. Results from these studies indicate that temperature and precipitation are
660 consistently the main environmental factors influencing genetic variation in salmonids, but other
661 variables may also contribute for specific populations. Recent results also emphasize that
662 environmental conditions through the migratory corridor are stronger drivers of selection than
663 those at natal sites for steelhead in the Columbia River Basin (Micheletti et al. 2018a).
664

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

Objective 6) White Sturgeon Genetics

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

Acknowledgements

Introduction

This project combines multiple inter-related studies from the Fish & Wildlife Program Accords that address the following current and future objectives: 1) discover and evaluate SNP markers in salmon, steelhead, and lamprey; 2) expand and create genetic baselines for multiple species (Chinook, steelhead, sockeye, and coho); 3) implement Genetic Stock Identification (GSI) sampling programs for mainstem Chinook salmon, sockeye salmon, and steelhead fisheries, 4) GSI of fish passing Bonneville Dam (salmon and steelhead), 5) characterize adaptive genetic variation associated with environment, landscape, and phenotypic traits, 6) genetic diversity and structure of white sturgeon. These projects are highly related since SNP markers are needed to complete species-specific baselines, and these baselines are requisite to complete GSI. The results of these four 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 six fish species including: Chinook salmon, Steelhead trout, Sockeye salmon, Coho salmon, Pacific lamprey, and White Sturgeon. 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

771 the few ways to estimate the escapement of natural-origin stocks through run reconstruction of
772 these stocks passing Bonneville Dam.
773

774 ***Objectives 3 & 4) Genetic Stock Identification***
775   Genetic Stock Identification (GSI) methods have proven to be effective in determining
776 the proportion of stock origin in several mixed stock applications (Narum et al. 2008b, Hess et
777 al. 2011, Hess and Narum 2011). This study includes two GSI projects that will utilize genetic
778 baselines: 1) GSI to provide information about harvest; and 2) GSI of fish passing Bonneville
779 Dam.
780

781   This study includes GSI analysis of Chinook salmon and Sockeye salmon collected from
782 commercial, recreational, and tribal fisheries in the Columbia River. Subsequent years of the
783 study may include other species such as Coho salmon. Implementation of GSI technology could
784 make monitoring individual production units in mixed stock areas possible. Tissues will be
785 sampled annually from fisheries with existing programs in place with Washington Department of
786 Fish and Wildlife (WDFW), Oregon Department of Fish and Wildlife (ODFW), Yakama Nation
787 Fisheries Program (YNFP) and Confederated Tribes of the Warm Springs of Oregon
788 (CTWSRO). We plan to genotype representative samples from fisheries of primary interest.
789 The GSI estimates may help fill information gaps on natural-origin stocks.
790

791   The second application of GSI analysis in this study includes sampling unknown origin
792 salmon and steelhead at Bonneville Dam for genetic analysis. Samples will be collected over the
793 majority of the run on a weekly basis, and genetic baselines will be utilized to determine the
794 stock composition of these runs. Few studies have been able to determine the extent of overlap
795 among life history types of salmon and steelhead, but GSI of each life history type will allow us
796 to determine the stock composition of the different runs through Bonneville Dam which can be
797 compared to other methods such as using fish that were PIT-tagged as juveniles. Population
798 genetic methods and statistical assignment models have advanced dramatically in recent years,
799 and estimating stock composition is now possible using either Bayesian or Maximum Likelihood
800 methods (Anderson et al. 2008). Therefore, we plan to estimate stock composition of multiple
801 species passing Bonneville Dam and provide this information on a timely basis to fisheries
802 managers in the form of an annual report.
803

804   Finally, we continue to utilize a new genetic technology, parentage based tagging (PBT),
805 in combination with GSI to help augment and refine our stock identification results. PBT is an
806 efficient approach for mass-tagging of fish. The method is carried out by first genotyping a set
807 of potential parents which then provides the opportunity to assign a set of genotyped offspring to
808 their true parent pair. PBT is currently being utilized on a broad scale in the Columbia River
809 Basin to tag all Snake River Chinook salmon and steelhead hatchery broodstocks (Steele et al.
810 2011) and we now have a baseline that includes most Chinook salmon and steelhead hatcheries
811 located above Bonneville Dam. This application has effectively tagged all hatchery Chinook
812 salmon and steelhead above Bonneville Dam starting with the 2012 brood years. When parent
813 pairs of a hatchery fish are identified with PBT, we can provide accurate information including
814 age of the fish and the source hatchery in which its parents were spawned. We can now use PBT
815 in both Chinook salmon and steelhead GSI applications to identify all hatchery-origin fish, and

816   then we estimate stock-of-origin of all other hatchery fish that were not assigned with PBT (i.e.
817   the few hatcheries not in the PBT baseline) and all natural-origin fish using GSI. In this way
818   PBT and GSI are complimentary, and using them in combination takes full advantage of the
819   strengths of each method, while resolving or minimizing limitations. Exogenous stock transfers
820   by hatcheries have made hatchery-origin fish challenging to assign with GSI and represents a
821   main limitation that is addressed with PBT. Applications of PBT have been initiated in other
822   species such as Pacific lamprey, and are being used to monitor translocations of lamprey
823   throughout the interior of the Columbia River.
824

825   ***Objective 5) Adaptive Genetic Variation***

826

827   With increasing genomic information available for non-model organisms, single nucleotide
828   polymorphisms (SNPs) have begun to see increased use as genetic markers for population
829   genetic studies (e.g., Morin et al. 2004). These sequence polymorphisms are densely scattered
830   throughout the genome of most organisms, and are commonly observed in both coding and non-
831   coding regions of functional genes making them ideal markers to study adaptive molecular
832   variation (e.g., Akey et al. 2002). In a large suite of SNPs that are distributed across the genome
833   (e.g., Narum et al. 2018), it is possible to utilize both functionally neutral and adaptive markers
834   within a single study. This combination of information provides a powerful approach to study
835   questions in ecological genetics since both demographic processes (i.e., gene flow and genetic
836   drift) and local adaptation (i.e., selection) may be inferred.
837   Thus, genome scans with large numbers of SNP markers (e.g., RAD sequencing, Baird et al.
838   2008; Pool-seq, Schlotterer et al. 2014) and gene expression (e.g., RNA-seq) approaches may be
839   effective tools for identifying the genetic architecture underlying specific traits such as thermal
840   tolerance, run-timing/maturation, disease resistance, anadromy, and age-at-maturity. Underlying
841   genomic regions for these traits continue to be investigated and once identified, they can be
842   broadly screened in populations throughout the Columbia River Basin to facilitate management
843   for long term conservation and recovery of salmonids.
844
845

846   ***Objective 6) White Sturgeon Genetics***

847

848   The research for this project is specific to genetic monitoring of white sturgeon (*Acipenser*
849   *transmontanus*). The monitoring began in 2008 and has been focused on populations in the
850   impoundments upstream of four middle Columbia River dams: Bonneville, The Dalles, John
851   Day, and McNary. We have also incorporated collections from the lower Columbia River Below
852   Bonneville Dam and from several reaches of the Snake River Basin (Matala et al. 2017). This
853   research project directly addresses the following uncertainties: 1) What approaches to population
854   recovery and habitat restoration are most effective in regaining meta-population structure and
855   diversity that will increase viability of fish and wildlife in the Columbia River Basin?, 2) How do
856   artificial production and supplementation impact the maintenance or restoration of an
857   ecologically functional metapopulation structure?, and 3) What is the relationship between
858   genetic diversity and ecological and evolutionary performance, and to what extent does the loss
859   of stock diversity reduce the fitness, and hence survival rate and resilience of remaining

860 populations? Our monitoring objectives are aimed at providing answers for these uncertainties
861 that will inform long-term conservation and management of the species.
862

863 *Report Structure*
864   This report is divided into six sections, one for each of the objectives of the study. The
865 first section reports on SNP discovery efforts and the second section on genotyping SNP markers
866 in Chinook salmon, steelhead, and *O. nerka* to create genetic baselines. The third section
867 contains stock composition estimates of Chinook salmon and Sockeye salmon sampled in
868 mainstem fisheries in 2018. The fourth section includes analysis of run-timing distributions and
869 estimated abundance of adult Chinook salmon, Sockeye salmon, and steelhead stocks migrating
870 over Bonneville Dam in 2018. In addition, we have implemented in-season and timely post-
871 season analysis of the runs of Chinook salmon, Sockeye salmon and steelhead migrating over
872 Bonneville Dam in 2019. These in-season and post-season 2019 results were provided to
873 fisheries managers that participate on the USvOR Technical Advisory Committee and are
874 summarized in the fourth section of this report. The fifth section reports on progress to identify
875 adaptive variation associated with landscape, environment, and phenotypes. The sixth section
876 reports on updates to genetic analyses of white sturgeon.

Section 1: SNP Discovery

Introduction

Population genetic studies examine variation within the genomes of individuals in order to gain insights into the nature of those populations. For instance, genetic similarities among groups of individuals can indicate relatedness, recent population collapse, or barriers to migration. In the context of salmon conservation, population genetics can answer important questions directly related to fisheries management such as stock exploitation rates, effective population size, and rate of return. Other demographic information such as stock abundance estimates can also be made through analysis of samples taken from fish as they enter the Columbia River through genetic stock identification (GSI). These studies require genotype data from a suitably large and informative set of genetic markers for analysis. Likewise, the number of genotyped individuals must be suitably large to provide accurate results.

Next generation sequencing instruments can provide both a means to identify genetic variation and provide a platform for high-throughput sequencing. In the past, we have used methods such as restriction-site associated DNA sequencing (RAD-seq: https://www.monitoringmethods.org/Method/Details/4144) to identify and genotype thousands of single nucleotide polymorphisms (SNPs) within and among study populations. Recently reference genome assemblies have become publicly available for both Chinook salmon and steelhead, and these genome resources has enabled whole genome resequencing for investigating adaptive variation across a large portion of the genome (50-80%) in these species (whole genome resequencing: Whole Genome Resequencing: Poolseq Individual Barcode v1.0). Whole genome resequencing methods include individually barcoded samples, or pools of samples (Pool-seq, Whole Genome Resequencing: Poolseq Pooled v1.0; Schlotterer et al. 2014) depending on the study design. For both methods, sequence data is aligned to the reference genome assembly, and allele frequencies from millions of SNPs are analyzed to detect statistically significant regions of the genome associated with specific traits or adaptation to environmental factors. Putatively neutral regions of the genome are also useful for standard phylogeny and demographic analyses of populations. In most studies, allele frequencies are available for collections but sequencing depth is typically not high enough to provide individual genotypes. However, candidate SNPs may be developed into standard panels with Genotyping in Thousands by sequencing (GT-seq: https://www.monitoringresources.org/Document/Method/Details/5446) or other approaches to genotype many individuals to validate trait association, determine inheritance, and estimate linkage disequilibrium. GT-seq is a high throughput method that uses Illumina sequencers to rapidly genotype thousands of individual samples at hundreds of loci for less than ¼ the cost of previously used TaqMan assays (Campbell et al. 2015). Following the development of GT-seq, our laboratory has designed panels for 5 study species (Chinook salmon [*O. tshawytscha*] – 299 loci; Steelhead trout [*O. mykiss*] – 390 loci; Sockeye salmon [*O. nerka*] – 382 loci; Coho salmon [*O. kisutch*] – 257 loci; and Pacific lamprey [*E. tridentata*] – 316 loci). All of these GT-seq panels have been designed to a maximum of 75bp to allow for inexpensive sequencing runs on Illumina NextSeq 500. Recent additions of 11 SNPs were made to increase GT-seq panels for *O. mykiss* to 390 SNPs. The expanded panel for *O. mykiss* will improve our ability to identify specific traits of premature (summer-run) or mature (winter-run) steelhead (Micheletti et al. 2018).

922 *Methods*

923   For new SNP loci added to panels, the program Primer3 (Rozen and Skaletsky 2000) was
924 used to design primers flanking the target SNP locus for inclusion in existing GT-seq panels.
925 (GT-seq: https://www.monitoringresources.org/Document/Method/Details/5446) Parameters
926 used for primer design are as follows (product size range: 50-80 bases, optimal annealing
927 temperature: 60°C, primer size range: 18-24 bases, optimal GC content: 50%). The designed
928 primers were then modified by including the Illumina sequencing primer sites. The primers were
929 ordered from IDT (Integrated DNA technologies) at a concentration of 200μM at the 25nmole
930 synthesis scale. Testing was done by combining primers from previous loci for each species that
931 already worked for GT-seq with the newly designed primers. These new primer pools were then
932 used to create test libraries containing 96 samples using the GT-seq protocol (Campbell et al.
933 2015). Test libraries were "spiked" into an Illumina HiSeq lane with another sequencing library
934 such that each test library produced about 10 million reads of data for analysis. Since the test
935 library uses only a small percentage of the total reads on the flow cell the new library can be
936 sequenced very cheaply. The sequencing reads were analyzed for the presence of significant
937 numbers of hetero-dimers produced in multiplex PCR using custom perl scripts
938 (https://github.com/GTseq/GTseq-Pipeline/). Primers producing large numbers of sequencing
939 artifact reads through primer hetero-dimer interactions were flagged and omitted from the next
940 primer mix. Following this step, the primer mix was used for full scale genotyping using GT-seq
941 libraries containing 3,000-4,000 samples for a NextSeq flow cell.

942 *Results*

943   GT-seq primer pools are being used for all high throughput genotyping projects for 5
944 target species (Steelhead [O. mykiss] – 368 SNP loci including a sex determination marker,
945 Chinook [*O. tshawytscha*]-343 SNP loci including a sex determination marker, Coho [*O.*
946 *kisutch*]-257 SNP loci, Sockeye [*O. nerka*]-382 SNP loci, and Pacific Lamprey [*E. tridentata*]-
947 295 SNP loci). The remaining primer pools remain unchanged from last year's report but any
948 additional SNPs from Pool-seq data will be under development in the coming year (Paired-end
949 data assemblies, primer design, and testing). Our GT-seq panels have been used to genotype
950 over 157.319 samples as of Dec. 18th in the 2019 calendar year (Figure 9).

SAMPLES GENOTYPED BY GT-SEQ IN 2019 (TOTAL: 157,319)

A. transmontanus, 126
E. tridentatus, 26,275
O. kisutch, 12,310
O. tshawytscha, 91,516
O. mykiss, 23,144
O. nerka, 3,948
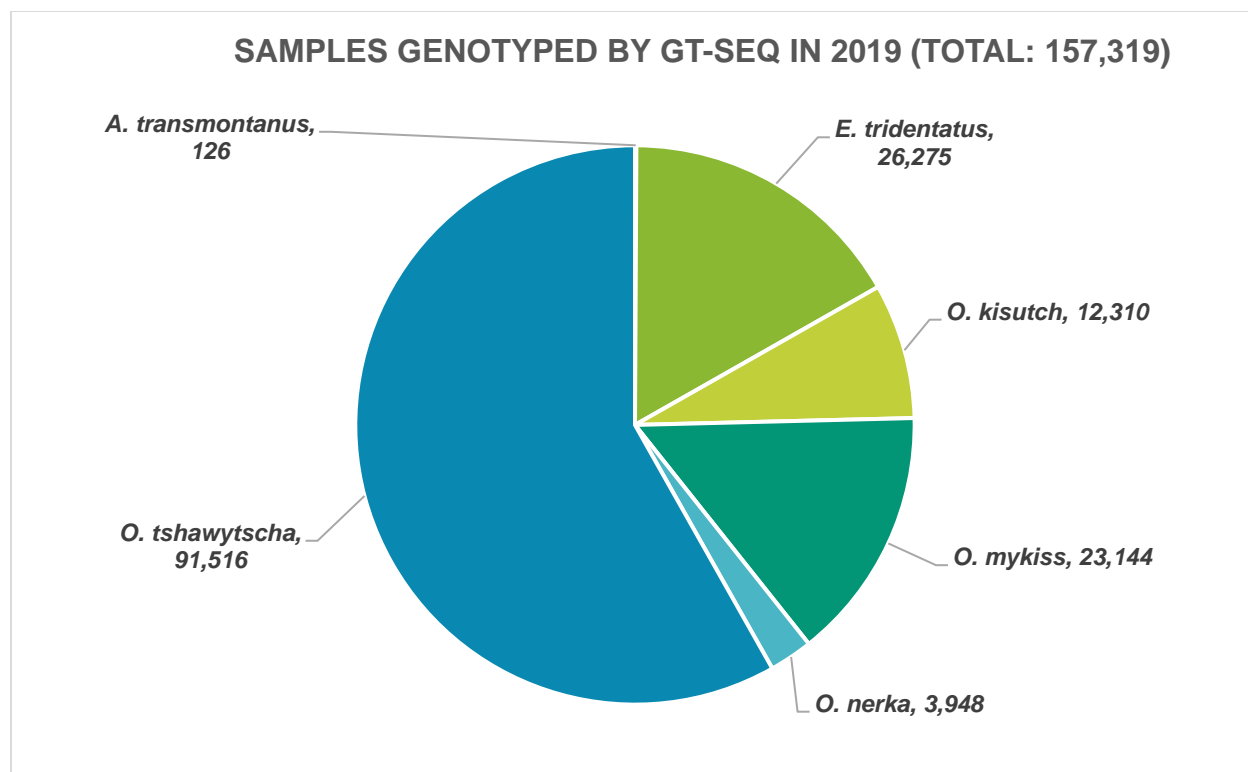
Figure 9. **Summary of Columbia River fish samples genotyped using GT-seq in calendar year 2019.**

Discussion

The GT-seq genotyping method has allowed for the genotyping of more samples in less time at more loci and at significantly cheaper cost than our previously used method (TaqMan genotyping assays). The total number of samples genotyped using this method has continued to increase from previous years but is expected to stay at a similar level in coming years of this project. The inclusion of more loci afforded by this method has also allowed for improved capabilities such as greater ability to discriminate between reporting groups in GSI and single parent assignments in PBT projects. Similarly, we can now take advantage of genetic markers associated with physical and behavioral traits of our study species by including them in our high-throughput panels. An example of this is our ability to distinguish between early- and late-spawning ground arrival timing in steelhead by including SNP loci found to be highly associated with this trait (Hess et al. 2016, Micheletti et al. 2018).

Expansion of our GT-seq panel for Sockeye salmon is also projected to greatly improve research capabilities in that species. The expanded panel contains 382 loci compared to the previous 93 loci, which should be sufficient for differentiation of Columbia River populations, but also provide statistical power for parentage analysis in this species.

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 (either HiSeq or NextSeq500) can be used as high throughput genotyping platforms while maintaining utility for other sequencing studies (whole-genome shotgun, RAD-seq, transcriptome sequencing, synthetic long read, etc.). This is

32

977 a key feature of the technique since it allows the multipurpose functionality of the laboratory
978 without investment in specialized equipment. Overall, GT-seq is a valuable tool for conservation
979 genetics studies allowing vastly improved statistical power, higher throughput, and prediction of
980 heritable traits at a lower cost.
981

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1003　　　　　　　Appendix 1. *GT-seq SNP panel for steelhead trout.*

Assay	A1	A2	Forward	Reverse	A1-Probe	A2-Probe	Allele Corrections	GCF_0021634 95.1 chromosome	GCF_0021634 95.1 SNP Coordinate
OmyY1_2SEXY	X	Y	GCGCATTTGTATGGTGAAAA	GCCTGGCATATGAGTGTTGA	NA	ATGTGTTCATATGCCAG	NA		
Omy_RAD72528-44	A	T	TGATGATCCGGACCCTCTCT	CCCGGATTCCCTCCACAGTT	TTGGAACAAACTGT	TTGGAACTAACTGT	0,0	omy01	7354513
OMS00078	T	C	GAGGGAAGCAGCCATAAACAGAATA	GTCTCACTATGGTCCATATCTGTGTAGA	TTCACATGCATAAGAGTG	TCACATGCATGAGAGTG	0,0	omy01	10499333
Omy_RAD65808-68	T	G	TCCTTCACTCTCGATCGGGA	TCAAACTGGGCCACTACTGT	ATCGGGATTCACTT	ATCGGGAGTCACTT	0,0	omy01	12187698
Omy_gadd45-332	T	C	AGAGAAGACTCACTGCTGTTTGC	AAATCAGTTCCCACGCTATGCT	TTGCTCCAAAATGG	TTGCTCCGAAATGG	0,0	omy01	12240053
Omy_107031-704	C	T	GGCTTTCGGATACTGAGCAACAA	TGAACTCACTGTTGGTATGGACTAGA	TGGACATGATTGCATAGAC	CTGGACATGATTACATAGAC	0,0	omy01	18131799
Omy_RAD73963-73	T	A	CCCTCTCAGGAAAGTGACCAC	GGATCATGTCAATCTGATGAGTTGG	TTTCTTTTGGA	TTTCTATTGGA	0,0	omy01	23729539
Omy_metA-161	T	G	CGCATGCACCAGTTGTAAGAAAG	AGTGCCACCAGCGATAAGAAAA	CAAGTAAGTGGTTATATTCT	CAAGTAAGTGGTTCTATTCT	0,0	omy01	24257340
Omy_RAD50632-21	C	T	CCTGCAGGCTGGGTCATTAT	GAGCCAGCTGTACCTTCTCC	TCAGCACCTCCAGCC	TCAGTACCTCCAGCC	0,0	omy01	38986533
Omy_RAD57916-29	A	C	GCAGGGCCTTAGAAACAGACT	TACACGCCTCACTGTTCTGC	CAGGGGCAAAACGG	CAGGGGCCAAACGG	0,0	omy01	44429931
OMS00070	T	C	CGTTCCTGCGGGACAGT	GTTTCTCTCACGTCCACAGATCT	CAAAATACGGAAATGCAG	AAATACGGGAATGCAG	0,0	omy01	55279296
OMS00003	T	G	GTGCCACTGATGAGGATGAGATCA	GTAATAAAGCCCTTTTGTGAGGAAAAACTAAT	CTTTACTGTCGACATTTTA	TACTGTCGCCATTTTA	0,0	omy01	59464348

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Omy_gdh-271	C	T	AGGTCAGTCTACTTACAGTATAAAGCAGT	GTCATGTCAACAGAGTAACATAATAAATCTGC	TCACCCTGAAGTGTAGAC	TCACCCTGAAATGTAGAC	0,0	omy01	63738413
Omy_cyp17-153	C	T	GCCCTCCAAGTTCCAAGTGAAAA	CAGGTCATTGATGAAACGTCAGAAC	ATACCTGAGTGTCATCG	ATACCTGAGTATCATCG	0,0	omy01	64509889
OMGH1PROM1-SNP1	A	T	TCAAACTGCATTTGATGGAAACAAACAT	AGGACAATTCTAAGTGACCTCAAACTG	TAGTGTTCACTGACTTCA	TAGTGTACACTGACTTCA	0,0	omy01	70466474
Omy_GH1P1_2	C	T	TGCATTTGATGGAAACAAACATAT-TTATAATGTGT	CAAAAACAAGGACAATTCTAAGTGACCTC	AAACTGTTGAACGGTAGTG	AAACTGTTGAACAGTAGTG	0,0	omy01	70466483
OMS00008	A	T	CCCTTTAAGGAGGATTTTAAATATGTGAGATAGAA	GGATACAGCGTTTTGGAATGAAACT	CTTCAAATATCCATAATTATATC	TCAAATATCCATAATAATATC	0,0	omy01	77384035
Omy_105385-406	T	C	GTAACCTACCCTCACCTGAACTTCA	GTCGCTCTTCTGGGCGTATCG	CTTGGAACCATTGCTAC	TTGGAACCGTTGCTAC	0,0	omy01	77446133
Omy_stat3-273	G	-	CAGACCTCCTCTATCTCCCTATGAG	ACCTCCTTTAAATTGTGCCCAAGAA	CCAGTTTG	TCAGTTTG	0,0	omy01	79XXXXXX
Omy_G3PD_2-371	C	A	GCAGGTAAGGTACACCATAGAGACA	CTCCCCCTGCCTTACCAAAC	AGACATGTGGATTGGCA	CAGACATGTGTATTGGCA	0,0	omy02	6083946
Omy_G3PD_2.246	C	T	TCATGTATCAATTAAGGCATTGTCTTGTCT	GTTAGACACAGTGACCACCTCTTT	AGTAAAGCCCATTGTTGAGT	AGTAAAGCCCATTATTGAGT	0,0	omy02	6084071
Omy_98683-165	A	C	GCCATTGCCAGAGAATTTGGTTAA	AACACACGCACCATCTTAAAGC	AGCCAGATACATATTTGT	CCAGATACAGATTTGT	0,0	omy02	8555140
OMS00156	A	T	GAGCAGAACACATAGAGGAAAGACT	GTAATCACCCTCTTAGCCTGTATGG	TGTGTGTCCTGCTGTAACA	TGTGTCCTGCAGTAACA	0,0	omy02	12397197
Omy_114587-480	T	G	CAGATTACGTTATTACGTTTGGGAAATTTTTAAGT	GTGAAAGAGTGGGAAATATAATTATAAGGTCAGA	CCTGTCCAAAATTGT	CCTGTCCACAATTGT	0,0	omy02	16204563
OMS00138	T	G	TCGGACCACATGAGCAGTTC	GTTCAACAGGTGCCCACAC	CTAACAATAACCAAAGACTG	CTAACAATAACCACAGACTG	0,0	omy02	22318448
Omy_NaKATPa3-50	A	C	GTTGAGCGTGTTATGGGAAAAGAG	TTGCATCGGCTTTCTGAAAACC	CACTCTGTTTCCTTTCTTT	TCTGTTTCCGTTCTTT	0,0	omy02	23893157
Omy_RAD25042-68	G	T	GCTGCTGAAACTGGTTTGCA	TCATGCAGATGAGCTTCCCTG	AATTTCTGCCCAAA	AATTTCTTCCCAAA	0,0	omy02	32793123

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Omy_cd59b-112	C	T	TTTGGATAAGATTGTCTTATATGACTAAAATGTCATGT	GCCAACGTCCTAGATATGGTGTAAT	CTAAAAGCCTATAGCAAACT	CTAAAAGCCTATAACAAACT	0,0.6	omy02	38922611
Omy_RAD27740-55	A	T	TCGGCCTGTACTAGTCTCACT	GCCTAAAATGGCCACTTTCATCA	TAACTTTAAAAAAA	TAACTTTTAAAAAA	0,0	omy02	42745963
Omy_u09-53.469	T	C	ACAGCCTGAGCGTTTGCA	GGAAACTGGGAGAGATCAAAGGA	TTGCAGCCCTTATTGTG	TTGCAGCCCTTGTTGTG	0,0	omy02	48859883
Omy_RAD20917-11	T	C	CGTTGTCGTCTCCAATCAGGA	ACCAGCTCGATGCCATTGC	AGGTTGCGAGGTC	AGGTCGCGAGGTC	0,0	omy02	52384497
Omy_metB-138	T	A	TCTGTCCCTGACGCTATAAAAACG	GAAGTATTTCAGCTTAATTTCACTGTTGAGTT	TTCGCCAAAGAGAAAT	TTCGCCAAAGTGAAAT	0,0	omy02	53792050
Omy_RAD9004-13	G	A	TATACCACGCCTTCCCTGGA	CAGAGAGAAATCCCCCACCC	TCATCTGAAGGGGG	TCATCTAAAGGGGG	0,0	omy02	54044836
Omy_lpl-220	C	G	TGACAATCACTGAGCAACTGAACTC	GTCCAGTCTTGCTTCAACTCATTCT	AGTGACAGTCA	AGTCACAGTCA	0,0	omy02	60022813
Omy_RAD16104-20	A	G	ATTCCAAAACCTGCAGGGGT	TCAGGATTTGGTAAGGTGGCC	AGGGCAAAG[AT]CAAAGG	AGGGCAAGG[AT]CAAAGG	0,0	omy02	67119313
Omy_RAD37816-68	A	T	CTCATTCCCTGGCCGTCTG	CCACTCACACTGGCTTATGC	GCGGCGTAAAAATG	GCGGCGTTAAAATG	0,0	omy02	73500031
Omy_RAD46314-35	A	G	ACTGCATCTTTTCCCCTGCA	TGAAGATACCCAGAGACACCA	TAGCAATGGT	TAGCGATGGT	0,0	omy02	78480158
Omy_RAD73204-63	G	C	CCTGGGCAATGACCTCCAC	AGCTCCCTTCTCTCTCCCTC	GTGCCCGCTCTCCACCG	GTGCCCCCTCTCCACCG	0,0	omy03	24670264
OMS00096	T	G	CATGAGAATGGATCAGTCTCCACAA	GATGAAATCTGAATGTGTTGACACTACAG	AAAGAGGAAGAGTCTCG	AAAGAGGAAGCGTCTCG	0,0	omy03	29109394
Omy_112301-202	T	G	GTAAACCCTGCCCACATAATTAGGT	CTGAGACACTGCTCCAAGGT	AATGCGAAGACAAACT	AATGCGAAGCCAAACT	0,0	omy03	37590554
Omy_RAD33798-24	T	C	CAGGAGGGTCAAGTGGAGTC	TTGGGCCCTCTCTTTTTGGG	GAGTCTATCAAGAT	GAGTCTACCAAGAT	1.4,0	omy03	38336651

Omy_RAD13499-13	T	C	GTTCACCTGACGACCAAGGT	GCTGGGGGAGCTTTACATGA	CGCCCTGTCCGCCA	CGCCCTGCCCGCCA	0,0	omy03	38408941
Omy_u09-54-311	C	T	GTGGCTCCCCAGGAACAAG	AAGTTTCATGTCACATTCCAGTTACCT	TGGTAATTATTCAACAGATCAGT	TGGTAATTATTCAACAAATCAGT	0,0	omy03	42920502
Omy_RAD58835-15	G	T	GTCTGCTAAGGTCCTGCAGG	GCCGACCATGAGAGACCTG	ATAGCTGCTGGGACCCA	ATAGCTTCTGGGACCCA	0,0.2	omy03	53735338
Omy_u07-79-166	G	T	CCCGCTATATTATTTGATCACCCTTGA	ATTTAAATCCATTTCTAAAAATAAGCAAACCTAACCA	ACTTGGGAATACCCCAGCC	CTTGGGAATAACCCAGCC	0,0	omy03	57523676
Omy_117815-81	C	T	CTGCTTTATGCACACCACATTGT	GCTCTTTCTGGAGAACAAGGTACTG	CTATACGGAGACCAGC	CTATACGGAAACCAGC	0,0	omy03	67894257
Omy_118654-91	A	G	CAGCGTAGACCGTTTCCTCATTAT	GCGCCGATGAGCAGCTT	TCAGCTTGTCTTGCCGC	CAGCTTGTCCTGCCGC	0,0	omy03	75458069
Omy_aromat-280	T	C	CTCCATTGATTCATGCCGAACATT	GGAGAGGTCAAACATAGCCTGGTA	TCTTGCAAACTCC	TCTTGCGAACTCC	1,0	omy04	3391469
Omy_105075-162	T	G	GGAGAAGGACAAGGACATTGGTAAT	AAAGCAGACCACACCATACTTCTC	CTTTCTCTCCTACTTTCC	CTTTCTCTCCTCCTTTCC	0,0	omy04	7635334
Omy_myoD-178	A	C	GGTCAAATATTTCATTTACGATTACACTTAGGC	TGGCAAAGCTGTCATTCCTTCTAAT	TTTTATGAGATATAATTTCC	TTTTATGAGATATCATTTCC	0,0	omy04	10520793
Omy_128923-433	T	C	CTATGTCCTTGGCAGAAGTCTACA	ACGTTTCTTTGGGCTGAGACTTATT	CTTCATTTTCATTCACTGTTTT	CATTTTCATTCGCTGTTTT	0,0	omy04	16436234
Omy_130524-160	C	G	CGAAGGTAGCGATTGGTCGTT	TGTCTGTTCTGCTGTGTGCTT	ATGGCTTGATCCTCA	ATGGCTTCATCCTCA	0,0	omy04	28889024
Omy_RAD77789-54	T	C	AGACAAAACCTGCAGGGGAC	AGCACGTTAAAACCAAACTGTCA	TAAATTATATTTGACAG	TAAATTACATTTGACAG	0,0	omy04	30976138
OMS00079	T	C	GTAACATTATGAATCTATCAGTTTCCCTAGCT	ACCTGCAACGTTAGAGCTGTTTATT	CTACTTTTCACAGTAACACAG	CTACTTTTCACAGTGACACAG	0,0	omy04	35250473
Omy_117286-374	A	T	TGATGTGTTGTTCCTCATGGCTTA	CTGTGCATTTATTCTTGTGATGCTAGG	CTTTCCTCATCATACTCTATGG	TCCTCATCATACACTATGG	0,0	omy04	52310165

OMS00 087	A	G	GCAAATTTCACCCTTAACGT GGTTT	GATTTGATGTGTGTGTA TTACCTCCTCTA	GTTA[CA]AAC TGACAAAGTG TG	GTTA[CA]AGC TGACAAAGTG T	0,0	omy04	525119 64
OMS00 111	T	C	CATGCGGACCTGCATAGCT	GCTTAGCCATTGACAGA GCATATCA	CAACCAGACT ACCATTC	AACCAGACTG CCATTC	0,0	omy04	630315 81
Omy_R AD9248 5-64	T	A	CCAGTCAGTCTTGCCTCAGG	GGTCACCACAGGATTGG AGG	GTGTAGATAT ACAT	GTGTAGAAAT ACAT	0,0	omy04	683184 64
OMS00 116	T	A	GCCTTTCTCCCATATCACATT CGA	AAACGCATCTTACACTG TGTTGTG	CTTTTACATTT TCAATATTCTG	TTTACATTTTC AATTTTCTG	0,0	omy05	113417 54
Omy_R AD1307 3-16	G	A	GTGAGGGATCACACCTGCAG	GCACCCATTCGTAATGT CCC	AAAGGGGACA TTACG	AAAAGGGAC ATTACG	0,0	omy05	139545 98
Omy_11 0362- 585	G	A	GCAGCCAAGATGAACGAAA ACTTC	CCGGCCTGGGTCTCAAT G	CACCGCCCTG CCCGT	CACCGCCTTG CCCGT	0,0	omy05	143072 79
OmyR2 4370	G	A	TCATTACCTACGCAGTGGAG	ATCTCTGGGCCTGAACA AT	ATTTAGCAGG AGGCCTCTCC A	ATTTAGCAGA AGGCCTCTCC A	0,0	omy05	285793 73
OmyR4 0252	T	A	ACTCTGAATTCCTCAGGCTT	TCGAACCAGCTGTCTTT CT	AATGCTATATT GAACCTTAA	AATGCTAAAT TGAACCTTAA	0,0	omy05	316752 78
OmyR1 9198	T	A	GTAACCATGACATCCACCAA TC	CCTATGCACAAAGCCTT CAC	ATCCCTGTTAT CTAATCATT	ATCCCTGTAA TCTAATCATT	0,0	omy05	349734 85
Omy_R AD2389 4-58	A	T	TGCAGAAAGGCTGTGTGGAT	TCTTAACACAGTCCTCA TGGAACA	GTGGATTAGG GG	GTGGATTTGG GG	0,0	omy05	409271 21
OmyR3 3562	G	A	CAGGAGTAATGCATCCCAAT G	CAAGTTGATAACGAGAC ATAAGGG	TAAGACTTGG CATAAGCATG	TAAGACTTAG CATAAGCATG	0,0	omy05	473375 40
Omy_bc AKala- 380rd	G	A	TTGCTCTCTTCTGGTTGCCTT A	CTTCAGGAGAAAGCGCT ACTGT	CATACCCATC CTATGTCAG	CATACTCATC CTATGTCAG	0,0	omy05	534692 95
OmyR1 4589	A	G	GGTGACTGAGCTGGATGT	TTTAGAGAATTTGGCAG TACGTC	GTGGTTACAA AGGGTCTGCA	GTGGTTACAA GGGGTCTGCA	0,0	omy05	561627 85
Omy_u0 9-61.043	A	T	TAGTCACATCCATAGTAATA CTTCC	TGTTCAGAAGCAGAAAA CCAATCTCT	CACTTGGTCCT TTTTCA	CTTGGTCCAT TTTTCA	0,0,4	omy05	588408 10
Omy_R AD3039 2-17	T	C	CCACTACTCACAGACCTGCA	GCTCAAGGACCAACAA AAAGCT	CTGAGACTGT GTGT	CTGAGACCGT GTGT	0,0	omy05	617726 69

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Omy_SECC22b-88	T	C	GGATCCCTCCTTTTAACACAAGACT	CTACAGGATGACTACCTAATTGCTAATAAAACA	CTGTCTGTCCATATATC	CTGTCTGTCCGTATATC	0,0	omy05	61828903
OmyR40319	C	T	AAAGATTGCTGCGATGTCTATAT	CGCAGAGAACAGAGGATGA	TGCAAGTGC[TA]GCCCTTTTAT	TGCAAGTGC[TA]GCCTTTTTAT	0,0	omy05	63158919
OMS00169	A	G	AGCACTTGACTCAAACTCACATAAATCA	CTGAGACAGGAAGAACAATGTTAACAAAA	CAAAAAGCATTGATATCAAT	AAAAGCATTGACATCAAT	0,0	omy05	67568174
Omy_RAD85131-35	T	C	TTCAATAACTACAGGCAGATGGT	AGTTCCCAAATGCACTGTACA	GATGGTATGGTGAG	GATGGTACGGTGAG	0,0	omy05	75534697
Omy_109525-403	A	G	CCTCATTCTCATTGGTGAGTTGTCT	TGTAAGATCTGACCACATGAGTATAACCA	CCTACACCTCTTTTTCCACA	CCTACACCTCTTTTCTCCACA	0,0	omy05	84224892
Omy_RAD43573-37	A	G	TGCAGGGAACGATGAAACCA	ACAGACACAGCATTGGCCAA	GAAAGAGAGAGTTT	GAAAGAGGGAGTTT	0,0	omy06	1745954
Omy_105714-265	C	T	CCACTCAGTGCAAGCATGGA	GCTTTCAATCCTTGGCTCCAATATC	CTGTTGTTTGAGGTTCAG	TGTTGTTTGAGATTCAG	0,0	omy06	7594847
Omy_107285-69	C	G	GCCCTTGTGACAATGCACTGTTATA	AGGTCTAGACAGTGTGCCATTTG	ATACGTTACTTTTGACCTTGT	ACGTTACTTTTCACCTTGT	0,0	omy06	9809156
OMS00013	A	G	GCCTTTGTTCTCCTTGGTGGTTA	AGAAAAGTGTGGACTGAGGTTGAG	CTTCTTTTCCCTTGCTACTC	CTTTTCCCTCGCTACTC	0,0	omy06	10325271
Omy_RAD35417-9	G	A	GCACTTGACCACATAGCTGG	ACTCCACACTCCACAAAGCA	TGCAGGACGTGCTTTGT	TGCAGGACATGCTTTGT	0,0	omy06	15867514
Omy_b9-164	T	-	GCACAGAACACAGCCAATATTAACA	GCCTTGACTCTCCCTTCATGAC	CCTACAACTTGATCTAACGTG	CCTACAACTTGATCTACGTG	0,0	omy06	17599731
Omy_RAD47955-51	G	T	AGTGTGCTAGAATGGGCCTG	ACCATGGGCAGTTCATTTCA	TTGGAATAGAATCTATA	TTGGAATATAATCTATA	0,0	omy06	23191748
Omy_vamp5-303	A	-	CTGCTTCCCAATTCAGTATCGTCTT	AGGCTGAAGCATTTCTGAGTATGAA	TGGCCGTAGTAGTTGGTCA	TGGCCGTAGTTGGTCA	0,0	omy06	33625138
Omy_star-206	A	G	CGTGTGCCAGCCCTTCT	GACCACTGAGATCATTGCTGTGA	TCTTTGGCACTATATCT	TTTGGCACCATATCT	0,0	omy06	36624863

Omy_RAD68634-40	A	C	TGCAGGACTCCTTTGAAACGT	TAACGCCAGCTGCATGATGA	CCTCTAAACTGAAT	CCTCTAACCTGAAT	0,0	omy06	40260800
Omy_RAD36952-53	C	A	TGTACGTCATTGGGGCTGAG	CCTACCAGACCACACGATGA	AGGACATCTTCATC	AGGACATATTCATC	0,0	omy06	40260970
Omy_IL1b-163	T	G	GGAACAACAGGATTAAGCCTACTCT	CCTAAAGGCCTAGGAAACTAAACTTCA	CTGAGGTCATAAAAATA	CTGAGGTCATACAAATA	0,0	omy06	42313129
Omy_RAD7016-31	C	A	GCAGGAATATTCACTGTTGCCA	TCTAAAATGTCGTTGGCGGC	ATAATTTCATTTAA	ATAATTTAATTTAA	0,0	omy06	51490760
Omy_RAD60135-12	C	G	AGCATACACACCTGCAGGAA	TGGTAGGAGGAGATGCTCTGT	GAACATACCGGAAC	GAACATAGCGGAAC	0,0	omy06	56110072
Omy_RAD35149-9	G	A	GAGTCAATAGAGCCCCCTGC	TGGTTAGCAGGAGCAATCTCA	GCGCGCTTATGTC	GCGCACTTATGTC	0,0	omy06	60182501
Omy_RAD39156-33	T	C	GGGTGTGACATGTGTGCAGA	ACTGCTTGTCCCCACCAAG	ACCGTAATGGAGAG	ACCGTAACGGAGAG	0,0	omy06	468XXXXX
Omy_RAD366-7	C	A	ACCAAATTAGAGCCTGCAGGA	GGAGAGGCCTTTCCGTGATC	CAGGACTTGCTTTT	CAGGAATTGCTTTT	0,1.4	omy07	6230066
Omy_mapK3-103	A	T	GAAGTCATTACTGGTCAGTGGTCAA	GCACAAAACATGAGGAAAGTTGAGA	AATTATTAAGCCTATTTTTTT	ATTATTAAGCCTAATTTTTT	0,0	omy07	10975716
Omy_Omyclmk438-96	A	C	CCCGACTCTACTTCACTACTTTCCT	GGCCTAGGACAATAGGACTGAAC	TACGCAAATTAGGTTAAA	CGCAAATTAGGGTTAAA	0,0	omy07	10976028
OMS00176	T	G	GTTGGAAGTTCCGGTGGTAGAG	CTGGGTCCTGAAGGAGCTT	TTCCAGCACTGCTGTC	CCAGCCCTGCTGTC	0,0	omy07	11029167
Omy_131460-646	C	T	GTGAAAAGGAATGGAGGAGTACAGT	TGCTAGGACAGGAAGATCATTTGTG	AATAAAGCAGAATTTGTTACTG	AAAGCAGAATTTATTACTG	0,0	omy07	36600038
Omy_RAD30619-61	T	A	CTGCAGGTCAATGGGTGCTA	ACACTGATCACATTTTTGTCACACT	CACTGTTAAA	CACTGTAAAA	0,0	omy07	42710419

Omy_RAD2567-8	A	T	CTGTCTGGATAGCCTTGCCC	TCTATCTCTGGGGAAAATAGCCC	GCAATGGGCTATTT	GCATTGGGCTATTT	0,0	omy07	43793241
Omy_pad-196	C	T	CAAACAACCACAGTAGTCCTCCAAT	GCTTTTCACCCTTTTGTAAATTAAGCCAAA	AAGACAAAGGTGTAATACC	AAGACAAAGGTATAATACC	0,0	omy07	44470619
Omy_RAD12439-64	G	A	GGAACTTTTCACATCATGTTGACTG	GCACAGAGAACTCCAGGCAA	CTTCTCCGATGTCA	CTTCTCCAATGTCA	0,0	omy07	44537893
OMS00064	T	G	GTGGATATGTAGTTCGATGGAACAGT	TTTACAACAATCTTCTTTTAATAAAAATATAGCCACTTAT	CAGGCAACATTTTATATAACTA	CAGGCAACATTTTATCTAACTA	0,0	omy07	45227750
Omy_RAD62596-38	A	T	GCAGGACACTGGTTCCCAAA	CCTGAGATTTGAGATCACTGGCT	TTAAAAAATATATATTA	TTAAAATATATATATTA	0.5,0	omy07	49977794
OMS00154	A	T	GATGTTGGCTGGAGGTGTAGT	TGGGAACACTTTGCCTACCC	ACAGGGCTTCTGATTGA	AGGGCTTCAGATTGA	0,0	omy07	56234573
Omy_sys1-188	C	A	CTTAAATGGTGCTGGTTGCTGTATT	AGTGATATCTTAGTGGGTCGAGGAAA	AAACATGTACGACCTGTC	TGTAAACATGTACTACCTGTC	0,0	omy07	56428776
Omy_arp-630	G	A	CTGCACAACTTGTTTCCTGCTATT	ACCAAGTGTCCCTGTAAGCC	CCGCTCCGTCTGCT	CCGCTCTGTCTGCT	0,0	omy07	57239751
Omy_myclarp404-111	T	G	GCTGTGGTGCTCATGGGTAAA	CCAGGGCAGGGTTGTTCTC	CAAAGCCATACGTGGCC	AAGCCATCCGTGGCC	0,0	omy07	57239957
Omy_RAD2976-26	G	A	AGGACTGTGATCCTCTCAGCT	AGCTCTGCTGAAACATCAGTCT	CAGCTGGGTTGAGA	CAGCTGGATTGAGA	0,0	omy07	58337126
Omy_97077-73	T	A	GTGTAAACAAAATGACTCTGGGATTCAG	AGAAGTGGCAATGGTGTGAAGTAT	TGGTGCAATAGAAATA	CATGGTGCAATAGTAATA	0,0	omy07	61875465
Omy_RAD7384-50	T	C	GACACGCCCTCAGCCAG	CTGGTACCTTCCTGCTGTGG	GCCTCTGGCAG	GCCTCCGGCAG	0,0	omy07	65241784
OMS00057	T	G	GAGAAAGGGAGCATGAGACAGA	GTTGGGCTCCGGTACGAT	CTCCACAGAACCTTG	CTCCACAGCACCTTG	0,0	omy07	67908135
Omy_105105-448	C	T	CAATTTGCAAGCAGGGAAAGGTTAT	GTGATGGGCTGCAATTGCTT	AAGGAGAATGCATAATC	TGAAAGGAGAATACATAATC	0,0	omy07	68303584
Omy_cd28-130	T	C	CACAACTCCACAGAGACAGTGA	GAGGACAAAACTGACCGTATGGT	CCTGTTCATTCACCC	CTGTTCGTTCACCC	0,2.7	omy07	190XXXXX

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OMS00132	A	T	GTTTATGACTCCATTGCCGAAATGATT	ACGCGACCTGCAATTCATCAATA	CAGCAGTCCTCTGTGTGG	AGCAGTCCTCAGTGTGG	0,0	omy08	9451350
Omy_hsp90BA-193	C	T	GGAATCGATGACGACGAAGTGATC	TTCCTCCATGCGTGATGCA	CCTCCGCGCCTGC	CCTCCGCACCTGC	0.5,0	omy08	1066761
OMS00153	T	G	ACTTTGCACCATAGGCTTGACAT	TGATAAGGATGATCAAAAAGCTGAAGTATGTA	ACAAAATGTAATTTTCC	CAAAATGTCATTTTCC	0,0	omy08	16303316
Omy_hsf2-146	A	-	CCAACAATTGCAGCCTCATCTTAAT	GGAGCAGAAAAAGGATTGGACCTT	ATAATCTACTA	ATAATCTAACA	0,0	omy08	17470364
OMS00068	A	G	GCACTAACTGGACAACATTTTTAAGAATGA	GGCAGTTGAGCATTTTGGGATATT	AATATGCCTCCTTCGTCTC	TATGCCTCCTCCGTCTC	0,0	omy08	17488038
Omy_srp09-37	C	T	TAGTTGTATTAACTCTTCTTTGAGTCTAGA	TCATTCCAGCTCCGTTCTCTTC	TTGTGCTATTGACGCCACAG	TTGTGCTATTGACACCACAG	0,0	omy08	21426823
OMS00151	A	G	CTAACGTCTTCCCAATGATATTTCACAAGATA	ACCGTGGAAATACAATTTTTATGCCAAT	TCATGACCTTGATAATC	ATGACCTCGATAATC	0,0	omy08	23949230
OMS00179	A	C	GTCATAACAAAATCAGGGCTTTCCAA	TGGGAGATTTGGGCTGCTTTAAA	TGCCTCTTCTCTTTTCTCAT	CCTCTTCTCTTGTCTCAT	0,0	omy08	25539930
Omy_RAD24287-74	A	G	ATTGTCTGTCTGCCGAGGTG	TGGCGACCTGTCACTAATGC	GGTCACTACCTCCC	GGTCACTGCCTCCC	0,0	omy08	28035734
Omy_120255-332	A	T	GCTAGCTAACATTGAAGGGTGGAAT	GGCTACAGGGACTTTACAATGGG	ACTATGCCATGAAGTTA	ACTATGCCAAGAAGTTA	0,0	omy08	29102820
Omy_RAD28236-38	T	C	GGCACACATCTGTCCCGTAG	GCACTAAGGTCTAGGAGCACG	ATCTGTCTTCGTGC	ATCTGTCCTCGTGC	0,0	omy08	40399499
Omy_RAD86706-72	C	T	TTCCCTGTAACTGTCACGCC	CCACATCACACCCTGACCTC	TACGTTTCATTTCT	TACGTTTTATTTCT	0,0	omy08	40479421
Omy_104519-624	T	C	CGTGTGAGTTTGCGGTAAAGAC	TGACGAGTCCGTCTTATCATCCT	CAGCAGGATACATCCGACT	AGCAGGATACGTCCGACT	0,0	omy08	42764123
Omy_108007-193	A	G	GTGAATACCACCCAGGCTTGT	GTCCCTTCCCCAGTTTCACTTAATT	ATGTTTTCTCCCTACTTAAC	TTTTCTCCCCACTTAAC	0,0	omy08	43671991
Omy_cox2-335	T	G	AGCTGGGCTGTATTTGTCAATACTT	CAGCCCGCCACTGTCT	CTTTAAAGACAAAGACTTTAT	TTTAAAGACAAAGCCTTTAT	0,0	omy08	50822629

Omy_RAD18903-48	A	G	GGGGATGAGTTCTTCGGTGG	CCACCAAATCCCCCGAAGAA	AGGAGACACCA	AGGAGGCACCA	0,0	omy08	6103920 8
Omy_nkef-241	C	A	AGTGTCATTGATGTCGGCCTATTTT	AAACGAATGTCCACCTCAGATGTT	CTTCTGTATCATTTTTG	TCTTCTGTATAATTTTTG	0,0	omy08	6942703 7
Omy_97865-196	A	G	TCCAGACTTCTGGTTTGTTCCATT	CCAGCCCCTATATTCACAATTAAGTGT	ATTAATTAACAAGCTC	ATTAATTGACAAGCT	0,0	omy08	8251334 4
Omy_rbm4b-203	-	T	CTGAAATTTGATGAATGGAAGCTGCA	CGTATTCAAGTCGATATACAGTCACGAT	CACGTTATTATGAAAAGGATGT	ACGTTATTATGAAAAGGATGT	0,0	omy09	1248511 7
Omy_112820-82	G	A	CCTTTCCTTTTGCATTTCCTCTACTTATTTATTT	AAATGAACTCACGTTGACCTCTGA	CGCCGCCAAGTTA	CGCCGCTAAGTTA	0,0	omy09	2186126 4
Omy_RAD65959-69	G	A	ACATTTTGGTGTTAACAACCCTGT	GCTAGCGAAGACCCTGAAGG	TTTTGTCGTTCCTT	TTTTGTCATTCCTT	0,0	omy09	3633847 2
OMS00103	A	T	GAGATCACTGTAGGATTGGCTGTTT	CCTCAGAGCAGCTCACAATGGCATC	CTCCACAGTAATTTTTTTT	CCACAGTAATTATTTTTT	0,0	omy09	3833569 2
OMS00056	T	C	TCAGGAAGTAAACTGAAAATTCCAATGTATGA	CCCCAACCATGCTTGTTATTGAAC	TAGCTTGACCAAATAGCA	CTTGACCGAATAGCA	0,0	omy09	4377132 5
OMS00175	T	C	TTGCGATATGGGACTGTATACATTTATTCC	ACTACCTCCAGTTAAAATAGTGTGGGAAA	ATCACTAGTTCAAATACAA	ATCACTAGTTCAGATACAA	0,0	omy09	5038170 7
Omy_tlr5-205	T	A	GAGCGTATCTGGTATGGTAACAACA	CTCCAGCAGCTTTAGAGAGTTTACA	CAGTAATATTTCAGTGCCCG	CAGTAATATTTCTGTGCCCG	0,0	omy09	6051048 3
Omy_114315-438	T	G	CCTCACCGATCTAGTCAACTTCATC	AGGAGGCTGAGGGAGATTCTAG	TTATGGGCTTAAGGGTC	TTATGGGCTTACGGGTC	0,0	omy09	6456450 8
Omy_gluR-79	C	T	GACTGTCTATAGCTATTCTTCTCAAACTGT	AGAAACTACCATTGTGATTAACAGATAGAAAATACAT	CAAGTATTTTGCGTAGGAAT	CAAGTATTTTGCATAGGAAT	0,0	omy10	7508221
Omy_RAD32139-58	G	A	GCAGGAAACAGGTACAAAGGA	TGGCTTCTTCCTTGCTGAGC	TCGACATGACCTGA	TCGACATAACCTGA	0,1	omy10	1077380 3
Omy_109894-185	T	C	GGGAGGAATTGGAATGACAGATTAAC	CGGTGTCATTATGGTTGTCATTGTG	CTCCCTGATCCCCC	CTCCCTGGTCCCCC	0,0,5	omy10	1085228 2
Omy_RAD66402-36	T	C	GGTGTGATACCTCAGAGCTCTG	CGTCTCCGGATCGTTCAGAG	AACCACTTCTCTG	AACCACCTCTCTG	0,2	omy10	3037208 4

M09AAE.082	T	G	CTATGTGCAGTGCCCTTCTCA	GGCTTACAAGTATGCATGACTAGCT	AGGTTGTTTTACAAATTTAA	AGGTTGTTTTACACATTTAA	0,0	omy10	32872704
OMS00095	A	T	CTCCAATGGCTGTCAACAATTAAATATAAGAC	GTGTGCTGGTCTCTTCTTTTATTCTCA	AGGCAACTATATATTTTTT	AGGCAACTATATATATTTTT	0.7,0	omy10	38704654
Omy_RAD26080-69	G	A	TGTGGGACAGCACATACTCC	CCAGGACACCAGTGGAGAAG	ATTAGTAGCATCATCGAG	ATTAGTAACATCATCGAG	0,0	omy10	40486618
Omy_RAD10733-10	A	G	TATAGACCCCCTGCCAGTCA	ACAGAGAAACCCCCGTCATT	AGGGTGAAGAACTG	AGGGTGAGGAACTG	0,0	omy10	41411754
Omy_ftzf1-217	A	T	ACAGGGATGGGCAACTTTGTT	GGATGACCCACGTGACACT	TCATGACGAGTTCTGATTT	TGACGAGTTCAGATTT	0,0	omy10	44060919
Omy_p53-262	T	A	CCCCAACATCCAGTATACAGTTTCA	CCCAAATTGGCAATTTTAATAGGATTCAGA	CAAGTAGTATGGAGCTCTAT	AAGTAGTATGGTGCTCTAT	0,0	omy10	46190822
Omy_tlr3-377	C	T	GTCGCTCCGGGTGCTT	GGCCCAAACACTTCCTTCCT	CGTGATTAGGTTCTTC	CGTGATTAGATTCTTC	0,0	omy10	56447078
OMS00106	T	G	CGTGTAGCATTCTTGAGGAAGCTT	TTTCCAACAGATGCCAGAATCCT	TCTGATGGAAACTTTC	TGATGGCAACTTTC	0,0	omy10	59855697
OMS00030	T	G	CCTCGTGACTACAGAGCTATACAAC	GATCTGATCGGTCGGGAGAGA	ATGAGGGTCCCTATACAGG	ATGAGGGTCCCTCTACAGG	0,0	omy10	60401405
Omy_UT16_2-173	C	T	ATTGACTCATTATCACCTTAGTTGTAGCTTCA	GCAGCTACTTGCTGTATCACATGTTTGT	ACAGTCAACAAGGGACTTAA	ACAGTCAATAAGGGACTTAA	0,0	omy10	61496264
Omy_RAD36848-7	G	A	CGAGGACGTTCATAGGGAGC	TCGATAAGTCCACCAGCTGG	TGCAGGGACACCACCCT	TGCAGGAACACCACCCT	0.5,0	omy10	63650747
Omy_RAD5374-56	A	C	GCTGTTACCGTGTGATGTTGA	AGAGTTCTGGCCTCTCCCTC	AGAGGGAAAGAGAG	AGAGGGACAGAGAG	0,0	omy11	6186937
Omy_g12-82	T	C	GATCAATTCGATCGCTCATGAAACTT	CTTCTCTCGTTCTCATTGTGTCTCA	CAAACTCTCAGGATTAG	AAACTCTCGGGATTAG	0,0	omy11	14764807
Omy_BAMBI4.238	T	C	CATGATGAGGAGGACCAAGATGAG	AGGTGTGGTTCAGGGCAG	CACCGCAATCACCG	ACCGCGATCACCG	0,0	omy11	24411085
Omy_MYC_2	T	C	CGGTTGCAGAACTCTCATGTTTG	CACGCCATGTCTTAACTTGCATTA	CATAGACTTTTGACCTTAT	CATAGACTTTTTGGCCTTAT	0,0	omy11	33841260

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Omy_RAD78502-57	T	G	GAGAGGCATCCTGTCTAGGG	ACCATGCTCTTTCTGTAGGTGT	GGAAATATCACACA	GGAAATAGCACACA	0,0	omy11	37031757
Omy_BAC-F5.284	C	T	CCTCATTTACTGTAGGACCATGCA	ACAACGCCAACAACTTTCTCTTG	CAGTAGGGCGGCAAG	ACAGTAGGACGGCAAG	0,0	omy11	42789302
Omy_cox1-221	T	A	CACTGAACTGTAAGCCATTGTGATT	GCAACATGGGAATGATTCATAAATGCA	CGGTAAGACCATTAAAA	CGGTAAGACCATTTAAA	0,0	omy11	47052310
OMS00120	A	G	GGCAGAAGAGGAGAGAGATATGATTG	CCTCAAATACCTCTGACATTGAAGGTT	C[GA]CCCACTAAAAC	C[GA]CCCACCAAAAC	0,0	omy11	51013177
Omy_RAD42793-59	T	C	CACGGCTAGTGGCATGTACC	CCACACCTGCATCAGTCTGT	CAGAGAATGCCAACAGA	CAGAGAACGCCAACAGA	0,0	omy11	51408522
Omy_102867-443	T	G	CATTTGTTTAATTTGATTTGGCACAACTTCA	CCCTAGTTCTGTAACACAAGACGTAA	TTTGGGTACATAATTTTT	TGGGTACATCATTTTT	0,0	omy11	55934332
Omy_oxct-85	A	T	CGTCACTGAAACATTACTGTAACATCCA	CATCATCACGCTGTTGGTTTCTTAA	CATCGCTTATTTATGC	CATCGCTAATTTATGC	0,0	omy11	68405894
Omy_117540-259	T	G	GGCAGGTTAACACAGTCATCTACTATAAA	CAGCATGTTGCTTTAATCCTTCACA	TGTCACTTCAAGTTTG	TGTCACTTCAACGTTTG	0,0	omy12	5079371
Omy_110201-359	T	G	GGTAAGGCCTGTCTGACTATTTTGA	AGAGGTCAATGGATGCCAGTTT	TTTGGCTATTGAAATTATCATT	TTGGCTATTGAAATTCTACATT	0,0	omy12	28727952
OMS00074	T	G	CCTGTTTATTCATCTAAACCAGTTCTTTAAAAT	AACTTAATTTAGCAAACAAATGTCTGAACAGAA	TGAAACAAAACAAATGTTCC	AAACAAAACACATGTTCC	0,0	omy12	31104727
Omy_hsc715-80	C	A	CCGGTCTACCCTATAGCTGTTG	AGTCAGTCAATTAGTGGTTTGAAATACTATCA	AACTGTATTTGGGAAAAT	ATAAACTGTATTTGTGAAAAT	0,0	omy12	40136309
Omy_RAD26691-36	A	G	TGCAGGAAACCGTCAATCTACA	CAGGAATTAATTGTATGGCCGGA	TCTCCTAACAGAAC	TCTCCTAGCAGAAC	0,0	omy12	47284987
Omy_RAD38406-19	T	A	CTGCAGGGGTATTAGGAGGC	AATGAGTTGTGGCGGTGAGT	AGGCTTTATATGGCC	AGGCATTATATGGCC	0,0	omy12	48181130
OMS00077	C	G	AATACCATCTTGAGCTCATTAGTAATTATTCAA	CCAGACTTACACACTCTTGACTGA	TTCCGGTGGTGAAGTT	CCGGTGCTGAAGTT	0,0	omy12	48861950

Omy_RAD1919-22	A	G	CAGGTCACAGACACACAGGG	CTACACCACCCCACGTTCTG	CAGGGAGGAGG	CAGGGGGGAGG	0,0	omy12	53383757
Omy_ndk-152	A	G	AAGAATTGAGGGATAAAAACAAAATAATATATAAACATGA	CAAACCTACATTCATTAAAGTCCAGTTTTGT	ACCCACTTTCAAAAC	ACCCACTCTCAAAAC	0,0	omy12	56277959
Omy_RAD76570-62	T	G	GCAGGTAGGTAGGAAGGAAAGC	TCTGACTGGTATTGAAAGGACCA	AGAGGTGTTCTGGT	AGAGGTGGTCTGGT	0,0	omy12	56297752
Omy_gh-475	C	T	AAGTTACCAGAATTTTGCAAACTCAACT	CCATATTTTGAGGTGTAGCTTTACCCT	CTGAAACTCATGGTATACA	CTGAAACTCATGATATACA	0,0	omy12	62308122
Omy_RAD33122-47	G	C	CAGGCTTTGTGGACATGTGC	GTGCTCTATCTTGCTCTTGGC	CCACAGGGTGGTGC	CCACAGGCTGGTGC	0,0.6	omy12	66078752
Omy_hsp70aPro-329	A	G	TGCGTATTATTGTTTTTCAAGGACTTTCAAA	TGAATATTTTCAAATACATGCCAATTCTTTCCAA	ACATTCCAATATTCAACTAT	CATTCCAATATCCAACTAT	0,0	omy12	66828836
OMS00053	T	C	GGAGCCAGGTCAAGGTGATC	GGATGTCTGGTGTGGCTGTAAA	ATTTATATGTATCAATCA	ATTTATACGTATCAATCA	0,0	omy12	66917868
OMS00112	A	T	TGGCAGCAAAAGGGATGCA	TCCTGAGCAACCAGTCAACATT	CCGGTTTCAAGTTTACTTGT	CGGTTTCAAGTATACTTGT	0,0	omy12	68382081
Omy_111666-301	T	A	GGGTGAAAAGAGTGGGACATTTACA	GTCAATTTCAAGGCACCAGACAAT	AGTATAACACAGTAAGACAAT	AGTATAACACAGTTAGACAAT	0,0	omy12	70990844
OMS00149	T	G	GGCATCATTGTTCTTGCTCTGTTTA	CCTGGGAGGGTTTATATCGGAGTAT	GCTAAATGCACAG	GCTAAAGGCACAG	0,0	omy12	6589XXXX
Omy_RAD66834-17	C	T	CTCCTGCAGGTCATCTCTGG	CTGTCTTGTGCTCAATGCCTG	TCTGGCTGACACCTTTA	TCTGGTTGACACCTTTA	0,0	omy13	10112620
Omy_118175-396	T	A	AGGCTTCACACACACATGCA	GACGCGCAACCTCTAGATTATACTT	CTCTTGCAGACATACCCGTA	CTCTTGCAGACATTCCCGTA	0,0	omy13	20282478
Omy_129870-756	C	T	TCGTTATTTTGCCTCGCGGTA	TCCCATGAAGATGTATACATGTTTTGTGA	ACAGGTATTTCGTGAAATG	CAGGTATTTCATGAAATG	0,0	omy13	22915161
Omy_113490-159	C	T	CATAGTACATTTACAGATAATGTTTTAAAGTGCATGT	CGAGATACCAAAATGCCACAGTTACAT	CATCTGTTTTGGTTTAGC	CATCTGTTTTAGTTTAGC	0,0	omy13	26494831

Omy_nach-200	A	T	CTCATGAAAAACGGGAGAGCAAAG	CAGCGGCTCTTCAGTAGTCT	AACTGACAGAGTCACAAC	CTGACAGAGACACAAC	0,0	omy13	30001796
OMS00180	T	G	GCGCCGAATGGCATTAGG	CACATTGCTGTCGTTTAGTTTGACT	CTAAAAGTGCATTAAGCC	CTAAAAGTGCCTTAAGCC	0,0	omy13	32462775
Omy_110064-419	T	G	GTGCAAGGGACCTAGCTAATCC	TCTGAACTGACACTGAAGAACAAAGAA	ACGTTAGCTTTTAATTTC	AACGTTAGCTTTTCATTTC	0,0	omy13	36272850
Omy_g1-103	T	C	AGTCGTGACAATGAGAAACAGTGTT	CTCAGCAAAAAGAAACGTCCCTTT	CCTTTTACAATGAAGATC	CTTTTACAGTGAAGATC	0,0	omy13	39287232
Omy_IL6-320	C	T	CGACTGATCTCCTGCAGACATG	CTTGTTCCTCGTTGTCTTCCTTCTA	CTATAGGAGAGAGGACAACA	ATAGGAGAGAAGACAACA	0,0	omy14	7102407
OMS00089	A	G	GCACCATTTGAATAAAAATCTGCTTTGT	GCAACCCAATTCAATATTAAGCACATGAT	ATGAATCCCAAATAAGAAC	AATCCCAAACAAGAAC	0,0	omy14	13150534
Omy_hsf1b-241	A	-	AGCCCGAACTATCCTAAAGCATTTT	AAATCAATAGCTCAGAGAATAATGAACACCA	CAGTGTTTTGTTTTTGTCATT	AGTGTTTTGTTTTTGTCATT	0,0	omy14	14516742
Omy_116733-349	C	T	GAAATGGACATGCCTACAAATTGCT	GATGTGATCAGTTTAGGCAAGGC	AGAGAATCTGATAGTATTTC	AGAGAATCTGATAATATTTC	0,0	omy14	18498042
Omy_ntl-27	G	A	GGTGTGTTACTGTAGTTGTGTCCTT	TGTGTAGCTAGTGATCCTGATTGTCT	CAGACAAGAGTACCCCAAGAC	CAGACAAGAGTACTCCAAGAC	0,0	omy14	22071034
Omy_txnip-343	T	C	CCTTCAAACTAACGCATCATAGACATG	GGTCACTTGGCTAATCCCCTTAT	AACTGAAGAGATCTG	AACTGAAGGGATCTG	0,0	omy14	24435825
Omy_UBA3b	A	T	GCCACTCAATGCATGTGTTTTCTAG	CAGCTAGCTTAAGTGGGATGCAA	TGGAGATAACGCTAACTATT	AGATAACGCAAACTATT	0,0	omy14	28552649
Omy_RAD55404-54	C	T	GCAGGGTGTCCACTACAGAC	AGGAGTCCTGAGAGTTGGGC	ATTGTTTCTGAAGG	ATTGTTTTTGAAGG	0,0	omy14	43876869
Omy_RAD12566-14	C	T	GTGGACATTCCTGCAGGGAT	TCCCACAAATATTTCATACGCACA	ATGTAAACAAATTG	ATGTAAATAAATTG	0,0	omy14	44125336
Omy_RAD3926-22	T	C	CGTTCCTGCAGGCTTTTCAC	TTGGCACAGAGAGTACGCAG	TTCACTTTTCCCTG	TTCACTTCTCCCTG	0,0	omy14	45345547
Omy_mcsf-268	T	C	CCAGCATTCGTTCCCATTTCC	CTTTTAATGTAGATTATATTCTTCTGTAGCCACTATGG	AAATAATAGATAAA[CT]CCT	AAATAACAGATAAA[CT]CCT	0,0	omy14	48758470

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Omy_101554-306	T	C	GCCTGTATTTCTCCTGTATGTGCAT	TCAACTTTTGCAAACTTTTTTATTCTTTGTCATTT	TGCTTCTCACATTTTTA	TGCTTCTCACGTTTTTA	0,0	omy14	53660117
Omy_RAD47444-53	C	T	GTCGTCTGGAGGAGCTGAAG	GGGTGACGTTTTCCTTCAGC	GGCGAGCTTGGCCCAAA	GGCGAGTTTGGCCCAAA	0,0	omy14	56051917
Omy_RAD17632-23	C	T	AAGCTCCTGCAGGTCATCTC	TCTGTGAACTGTCTTCTGCAAGT	CATGTGAGACCTTTGCA	CATGTGAGATCTTTGCA	0,0	omy14	56074485
OMS00072	A	G	GTGGGAGAGCTCGTCTATGG	ACAACAGGTCATTGGATGTGATCAG	TAGAAGGTCCATGTATCTC	AAGGTCCATGCATCTC	0,0	omy14	59971780
Omy_redd1-410	C	T	GTACTCCCACTAACATACAGTAGACTCA	GGCACCATTGTGTTTTAGGATGTAG	AAAATATCCTGCAAGGAAT	AATATCCTGCAAGAAAT	0,0	omy14	69044121
Omy_nxt2-273	C	T	CTTTAGAAAAGCCAAGGTATATTTTAACATACTTCT	CTGCTGCCCTCTAATGGTAAGATAG	AAGGCAC	AAGGCAT	0,0	omy14	71969784
Omy_110689-148	A	C	GTGTGTGGCAGAGAACTAACTGAT	GGTTAAGACATTAACATAACACTGGACTCT	CAAATGAACACATTATTTATC	ATGAACACATGATTTATC	0,0	omy14	7235XXXX
Omy_RAD88028-7	G	A	TAGCCCAGTTCGGTTCCAAC	AGTGTCTTTGGTGCGTCCTC	TGCAGGGGCTGG	TGCAGGAGCTGG	0,0	omy15	5676664
Omy_Ogo4-212	T	C	TGAAAGGTTTTATGCAGGTTATTTTCT	GTGTGTGTTAAATAAGCATTTGATGA	CATTTGATGAGACATCTT	ATTTGATGAGGCATCTT	0,0	omy15	12595806
Omy_hus1-52	G	A	CTTGCCGGAGGGTAGCT	CCACAACTTCTCAAATGAATGGAATGT	CCCATCCCTCCTCCTGG	CCCATCCCTTCTCCTGG	0,0.5	omy15	13042222
Omy_111084-526	A	C	CACCACACCAAGCAACTATTTCATT	ACCCAACTACTGTCCCATTTTTCAT	CCAGTGAAATTTATTTTT	CAGTGAAATGTATTTTT	0,0	omy15	17300850
Omy_111383-51	C	T	CACGCGCAATCTCTCGTTTTAC	TCTTTAGGCAACAAGCGTGTCA	AGCAAGCGCACT[AG]GGT	AGCAAGTGCACT[AG]GGT	0,0	omy15	21239768
Omy_carban1-264	G	A	GCAAAGCCTCATCTTCAATCATTTGT	GCAAAACACAAGTCAGGAATCACTTA	CATTAATATTGCTAATAACACCAAG	ATTAATATTGCTAATAACACTAAG	0,0	omy15	21454064
Omy_96222-125	T	C	GTAAGGAACTAATTGGCGCAACATT	CAGTTTGTCTAACACCCAGGCATAT	AACTACAACTGTAGCTAATT	CAACTGTGGCTAATT	0,0	omy15	24041111
Omy_RAD23577-43	T	C	AATAGGAACCAAGCCCCAGC	CAGAGCCTGAACCCATGGAG	TCTGGCTCTGTCGGTCT	TCTGGCTCCGTCGGTCT	0,0	omy15	26972288

Omy_RAD52812-28	C	G	AGGAGTCCTGTCCCATGTCA	GCTTAAGGCTGTGGTATGTGG	CAACCTC[TC]ATTCCACAT	CAACCTG[TC]ATTCCACAT	0,0	omy15	28623729
OMS00061	T	C	AAGTGGAGGCTGACCTGTTG	GCTGATGGCACCTGACAGTTAATT	CATTGCCATTTACAGACTT	TGCCATTTGCAGACTT	0,0	omy15	31231975
Omy_nips-299	T	-	GACAGGATAGGAACGGTTTCTCAAT	ATCAGAAGTTTAATTCAATATGTACACGATCCT	CTGGATTTCACATGTAATAC	CTGGATTTCACGTAATAC	0,0	omy15	39788784
Omy_LDHB-1_i2	C	T	ACGCACACTTATCCTTGACAATGTT	ACTGTGACAACAAATTCGGTGACA	ATGGGCAGTCATTCA	TGGGCAATCATTCA	0,0	omy15	44094440
OMS00143	T	C	GGAGGCACGCCCCAAA	TTTGTTAAAATAGAGCCCTTAGTGGGTTT	CCTGATCCAGAATCTAGA	CCTGATCCAGAGTCTAGA	0,0	omy15	59233015
Omy_97954-618	C	T	GCTCTGCTTCCTCGGCAAATA	CACAATTGGTTTTTGCACAAAAGTAAAGTATT	CAACGCTTACCGGTGTGT	CAACGCTTACCAGTGTGT	0,0	omy16	11433435
Omy_117370-400	A	G	TGCAAACACAGAGGAAAGGGATTT	GGCTTATTTGTTCCGTACTTGCATT	CAACTCCAATGAATTAA	AACTCCAACGAATTAA	0,0	omy16	14853962
OMS00062	T	C	ACCCTGGGAAGGCTACTGTAC	TGAACAGAGATCTGGAGAGTTGGAT	TTGACCAGCAGATGGTGTA	ACCAGCAGGTGGTGTA	0,0	omy16	14858081
Omy_RAD88122-32	G	A	TCAGTGGATGGAGTGTCCCT	GGTCTTTGGCCTTGTTGCTG	GCTGTGGAGATCAT[CT]CG	GCTGTGGAAATCAT[CT]CG	0,0	omy16	16334074
Omy_RAD40641-58	T	C	GGCAAACTGGCTTGTGAGTG	AAGGCTCTGCTTCTGCTTGA	AGTGATATCAAGTG	AGTGATACCAAGTG	0,0	omy16	17858278
OMS00041	G	C	GATTCTGTTCCATCCTCTTTCTGTCA	AAACATAAAAAAGGGCATGAAGGTGTC	CCACTCTATGCCTGCCCT	CACTCTATGCGTGCCCT	0,0	omy16	18279174
OMS00119	A	T	AGCGGCAGTTGTGTTAATGAGA	CTTCCTAAAGCCTGACAGTCTGT	CCACACAGCTGCCTGT	CACACAGCAGCCTGT	0,0	omy16	27506018
Omy_RAD116-59	T	C	GGAAGAAGTGAGAGCCCTGG	CTGTAGTCCACGATCCGCTC	CCACAATGTCAAC	CCACAACGTCAAC	0,0	omy16	33074866
Omy_RAD17849-16	G	C	GACTCCACAGCCTACATGGG	CCGTTAATGCCAGGGGAGTC	AGACGGACTCCCC	AGACCGACTCCCC	1.1,0	omy16	44116456
M09AAJ.163	G	A	TCCCATGGCCCTTACTCTATCAA	TTGAGGTGTATGTTGAAAAGTAAACTT	AACAAAGTGAAAGTGTCCT	CAAAGTGAAAGTGTCTT	0,0	omy16	44843440

OMS00018	T	G	AGAGTACATGTGTGGCTGCAA	GTCATAAATCAACACAATTATCTTCTTCACAGAA	AACCACATAATTAATAATTC	CCACATAATTCATAATTC	0,0	omy16	46432462
OMS00134	A	G	GAAACTGAAATGATCCCATCGTGTT	GCTAGCATAACAGCATTGCCATAT	TCTATAGCTGCAGTATATTA	TAGCTGCAGCATATTA	0,0	omy16	47743637
Omy_RAD31408-67	T	C	CAACCCTGCAGGCTACAGAA	TGGAGTGCCAACAAAAGAAGC	ACAGAATGCAGAAA	ACAGAACGCAGAAA	0,0	omy16	48341010
Omy_RAD79314-58	C	T	CACACTGACTCATCCCTCGC	GAGTGTCTTACCGAGCTGCC	AGACCTTGTC	AGACTTTGTC	0,0	omy16	62728432
Omy_RAD40132-55	A	C	TGCAGGGCCTGTATATTGCT	TCAAAGGACTGGGGAGAGGA	TCTGTGCAGTCCTC	TCTGTGCCGTCCTC	0,0	omy16	62784779
OMS00006	T	C	TCCACGTAGGACATAGTTTGAGCTA	TGTGGTGTCATGTTTGCCCTAC	CACTTACAAATACAAAATT	CTTACAAATGCAAAATT	0,0	omy16	63247944
Omy_anp-17	C	A	GGTAATGCCACATGCGGTAAATT	GGCGAAATCTGAAAATGTGCTGTTA	CTCTCATTGGTATAGTAACC	CTCATTGGTATATTAACC	0,0	omy16	3072XXXX
Omy_103705-558	T	C	CTCCAATCGCAAATACCCAGACT	CGCAGGAGACGGATGCC	AGACTTACCCAGAGTGAGAG	ACTTACCCAGGGTGAGAG	0,0	omy17	7065986
Omy_116938-264	A	G	GTTCATTCATGTTGAAGTGCGACAT	CTCTGCATGCTCCCATCCT	CCTTGTCTCAATTTTTCCTCT	CTTGTCTCAATTTCTCCTCT	0,0	omy17	7154463
OMS00128	T	G	ATGAAAGAACTCCCAGACACGTATTTT	ACATTTTAACACAGTAACACTAATACACACCA	ACTCTCAGAATTAATTATG	CACTCTCAGAATTCATTATG	0,0	omy17	14488587
Omy_101832-195	A	C	TGGCTCTGGACCTGTTGAGA	CGTCACAGCTATTTTAGGCGTAGT	TGTAGTCTTTCAGAGTAGTATG	TAGTCTTTCAGAGGAGTATG	0,0	omy17	17015658
Omy_RAD45104-18	A	G	TGGTGCTTCAGTGCTGTCAA	AGAGTGAAAACTGTGTGCGG	CAAGACACCGCACACAG	CAAGACGCCGCACACAG	0,0	omy17	20693754
Omy_101993-189	A	T	ACAAAACACAGTGGAATTACAATTAACGTT	GGAAGTTAAATTTCGCTTCGTCAGAA	CTTGATTTGCAGCTTGTCAA	TGATTTGCAGCATGTCAA	0,0	omy17	21491290
Omy_RAD22123-69	T	C	TGGGAAAGCATAGGAGGGGA	TGTGTGCCTGTCTTATAGCCC	CCAAAGATGTCAGA	CCAAAGACGTCAGA	0,0	omy17	23756920

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Omy_11 4976-223	T	G	GACAAACAGCACTTCATTGCAGTAA	GTTGCTCCAGCACCAGGT	ACCGATGGAACAATC	CCGATGGCACAATC	0,0	omy17	41462973
Omy_u09-56.119	T	C	CCAAGGTGGACCCACCAG	GCTGAGTTTATAGGTCAGTCATTATACATATTGA	AGTGAGCTGAAACAGAGCA	TGAGCTGAAGCAGAGCA	0,0	omy17	4169056
Omy_ca050-64	T	G	GTCATACAGAACTGTTTTGTTGTGTCAA	ACCTTGAATTGGTTCCTAATGCTATTGT	CAGTTTGAAGAATATACTC	CAGTTTGAAGACTATACTC	0,0	omy17	48651793
Omy_RAD43694-41	A	C	CCCCTCTCCCTGGCTAGAAT	TCAGGGGGTGTGCTTTTCC	AGGGAAGAGCGGAG	AGGGAAGCGCGGAG	0,1.1	omy17	57728549
Omy_RAD46672-27	C	G	TGCAGGAGGTCTTTTTCCTTGT	AACACATTCTTATTTGCAATGATGG	GTGGTAGCCCATCA	GTGGTAGGCCATCA	0,0	omy17	58256353
Omy_RAD58213-70	A	T	CCTGATGGGTGCTCTTCTCTC	AAACAGCATCATTATCCATAGTGTT	TTTTTT[TA]AAAATATACT	TTTTTT[AT]TAAAATATACT	0,0	omy17	58266227
Omy_U11_2b-154	T	C	GGGAAGCAGAAAAACTGGAAGTT	CCCTCTGTGGGCTTGATATTCA	AATGATACTTTTCAGATTGTAAC	TGATACTTTTCAGGTTGTAAC	0,0	omy17	59466696
Ocl_gshpx-357	T	G	GAGATCCTGAGGTCCCTGAAGTAT	AAGTGGAAATTTGGGCTCAAAGC	ATCCGTCCAGGAAATG	TCCGTCCCGGAAATG	0,0	omy17	64697703
Omy_GHSR-121	T	C	CTGTGTATAAGTTTATACAGTCAGCACAGT	TTCAGAGAGAGAAATGGCAGAAAGG	CCTAATAACCATGATAACAGC	AATAACCATGGTAACAGC	0,0	omy18	11662801
Omy_RAD59950-44	G	A	GGAGCTCATATCGCCGATGG	GAACTCTGTCACCCTGCCC	GGAGGGGAAGGG	GAAGGGGAAGGG	0,0	omy18	17292964
Omy_RAD42465-32	G	T	GTGGATCTTGGACTCCAGGC	TAGACATCGGCCCTCACAGA	CCAGGCTGGAAGAA	CCAGGCTTGAAGAA	0,0	omy18	25034287
Omy_RAD78776-10	T	C	CACAGCTTCCTGCAGGGTAA	GCTTGCATGGTCTCGCTAGT	GGGTAATCCTGGCT	GGGTAACCCTGGCT	0,0	omy18	25034326
Omy_sast-264	G	A	GAAGTAGGGTTTGTTGACCATGTGA	TGGATTCCATTTTAGGCTGTAATACATCTT	CTAGCCAATGCGTCTAA	ATCTAGCCAATGTGTCTAA	0,0	omy18	28252083
Omy_RAD43612-42	T	C	GTGGAGAGGGATTTTGGGGG	TGACAGGACAAACACAAGCCA	AAATGTGTATTTGTGTA	AAATGTGCATTTGTGTA	0,0	omy18	29118777

Omy_128996-481	T	G	CTCATCCACACTGTACAGTACAAGT	CATGCCTTCGTCTCATCAATAACAC	CAAACCTCAACCAC	CAAACCGCAACCAC	0,0	omy18	30802101
OMS00121	T	C	GGAAGGAGGTCCAGTGTGAGT	AAAATATGCAACACCACTAAAACTGGAAAA	ACAGCGTGATAAATT	CAGCGTGGTAAATT	0,0	omy18	34232991
OMS00127	T	G	CACCTTTCTCTCTCTCTCCATCTCA	AGTGTGCTACACAACCTTAAAAAATATATATCTATT	CACACACCCAAATGTA	ACACACCCCAATGTA	0,0	omy18	36268423
OMS00118	T	G	GCTTATTTAGAGTGCATGCCAGATG	TGGAACCAATGGGACAGTCCTA	GCGGGGTGTGC[AG]CATT	GCGGGGGGTGC[AG]CATT	0,0	omy18	42212299
Omy_RAD7210-8	C	A	ACACCACACTCCACAAAGCA	GCGCCTTGGTCTCCTTCATA	TGCAGGACTTGCTTTGT	TGCAGGAATTGCTTTGT	0,0	omy18	42558654
Omy_RAD19340-24	A	G	GCAGGGAGCAGCATATACATG	TGGGGTGATTTGAGTGACAC	CATGGAAATACATA	CATGGAGATACATA	0,0	omy18	42701841
Omy_RAD3209-10	A	G	CGGAGGAGTTTGAGCAGTCT	CTTCTACCACCACCTCGCTG	CGGTATCCCTGGC	CGGTGTCCCTGGC	0,0	omy18	50984953
M09AAD.076	T	C	ACTGTTACCACTCTCTCATCAACCT	GGGTCCAGGAGGTTTTTAAACAACAT	CACCAACCACTGGTGAA	CCAACCGCTGGTGAA	0,0	omy18	53717512
Omy_Il-1b_.028	T	C	ACTGTCTGGCTAGAGCACATTG	ATCTTCTACCACCGCACTGTTTTAA	CTGAGGCAACTTTTGT	TGAGGCAGCTTTTGT	0,0	omy19	10329530
OMS00092	A	C	TCTCCAGGTGTATCTTGAGAAGGT	AGGGTTCACACAGGGAAGATATCAT	CAGCTGAGAATAGGTTC	AGCTGAGAAGAGGTTC	0,0	omy19	12518551
OMS00017	A	G	ATTAAGTTCATACAAAAGTTCATCATAAATATTTTCCTTT	GGAGAACAAAGGGAAAGAGAAGACA	TAGACCTCGGTGCTGTAG	CCTCGGCGCTGTAG	0,0	omy19	19111591
OMS00105	T	G	ACATTTGAAGTCAGTATGGGTGTTGAG	GAACCTCACCACAGTACTAAATGCA	CTGCTATTCAAATTGCT	CTGCTATTCACATTGCT	0,0	omy19	20264968
OMS00133	A	G	GACCACTTCACTCATTCCTCCTTTT	TCCGGTTTACACACTTCATGCA	CGCCTCCATCTTTGTGGT	CGCCTCCATCTCTGTGGT	0,0	omy19	23702093
Omy_rapd-167	G	T	CCCAACATGCTCTATTGCAGCTA	AGTTGCATAAGATGAATCAATAAATTAAAAACACAGAT	AAACAATCCCCCCCAAA	AAACAATCCCACCCAAA	0,0	omy19	27362424
Omy_128693-455	T	C	GCCTGCAGGAGAAGGTAGAGTTA	GAAATGGAATGGACCCCAATCCT	CACTCAACTGATACCC	CTCAGCTGATACCC	0,1.4	omy19	32890059

Omy_RAD49111-35	T	C	GCAGGCTTAGCATTGCTGAC	GGAACCTGGGTGGGAGAATG	TTTCTTATATTTGA	TTTCTTACATTTGA	0,0	omy19	40050111
Omy_RAD739-59	C	G	ACGAGGCTTGTAAATGCAGT	TGCCTTTATACCAATGTCTGCTG	GAGTTGGCTATTTT	GAGTTGGGTATTTT	0,0	omy19	52923702
M09AAC.055	C	T	GTCTCCGACGTGTGGCT	TGGAACGAACCTGAGAACATAAGG	ACCTCCACGCTGTCC	ACCTCCACACTGTCC	0,0	omy19	53855167
OMY1011SNP	C	A	AGGCTGGTTTGGGATTCACTG	CGCCAAACACTAACTCTCTGTCT	CTTTACCTCGAAGACAAT	ACTTTACCTCTAAGACAAT	0,0.6	omy19	54446225
Omy_BAMBI2.312	G	T	CGAGCTCATGTCCGAAACTCAT	TTTGACAGCCTCAACTTCTAGGG	CCGAAAGTTCAACTTT	CCGAAAGTTAAACTTT	2.1,0	omy19	611XXXX
Omy_RAD29700-18	C	A	AATGGAATTGGCCCCAACCC	TCTCCATTGTGTGTAATCATGGT	ACAATTCAAATGATTTA	ACAATTAAAATGATTTA	0,0	omy20	1673196
OMS00039	A	G	GTCAGTACTGTGTGTGTCTGTGT	CCATCTACATTGTCAGCAGTGTGA	GTACGTGTCTCTGACC	GTGCGTGTCTCTGACC	0,0	omy20	4800495
OMS00114	T	G	GGATGATGCTGTGAGTCGAGAAG	ACCTTCGCCACCCATGTTTTATT	AAACGTTTCACATGCACC	AAACGTTTCACCTGCACC	0,0	omy21	11035495
Omy_99300-202	T	A	CAGTTTGACCCGATGGTGTGA	GATTATGGCGTGGCCTTTTGG	TCAGGCATGAGAGAAA	ATCAGGCATGTGAGAAA	0,0	omy21	14697073
Omy_cin-172	C	T	CGCATGGGACAGGTGTGT	GAGAAAGCCTGTAGAACCATGTCT	CGCTCACCGTGGTTAC	CGCTCACCATGGTTAC	0,0	omy21	21602618
Omy_vatf-406	T	C	TTGCTTCATTTTGTCATAACCTTGGG	TGCATGCTCTGACAAATGTTACACT	ATGACTATCCACA	ATGACTGTCCACA	0,0	omy21	23806220
Omy_LDHB-2_e5	T	C	TGCTAGGTGAGTCAGAGGTACATATT	GACTGGAAGGCCACCCATAAG	TTTACCTGTCAAC	CCTGTCGAC	0,0	omy21	24129907
Omy_LDHB-2_i6	G	T	TCCTCGCCAATACCATACATGTC	AGAGTGAAGCTAACACACACATTTCT	CTGTGTTTTGCTTCCCCA	CTGTGTTTTGATTCCCCA	0,0.5	omy21	24130559
Omy_104569-114	A	C	CCGAGGCCGACGTGATC	GCGCCTCGCTCATCATCA	CGCCACTCCGACGCC	CCACGCCGACGCC	0.5,0	omy21	32178517
Omy_zg57-91	C	A	CACTCATACACTCACTCACAAAGGA	AGCAGATAAGCCTTGTGAGTGAATCTT	CACAGACTGCACAGCC	CCACAGACTTCACAGCC	0,0	omy21	32766740

Omy_RAD35005-13	C	T	TGGTCAAAGTTGAGGGTGGT	CAGGGCCCTGATTAACCACT	CCAACTCCCGACGG	CCAACTCTCGACGG	0,0	omy21	37188435
Omy_b1-266	G	T	TCATGTGAACTTTAATTGACTAGGAAGTCG	GATATGAAAATATCTGAAGAGTTATATTTGGGAAATTGAC	TCTATAAACAACATTTTTC	TCTATAAACAAAATTTTTC	0,0	omy21	41255773
Omy_1004	A	T	GAGAATCGGAGCTAATCTTAGTTATTGTGA	CACTTTATTGAGCTACATGGCAAATCTG	CATGTGATGTTTTTTGC	ATGTGATGATTTTTGC	0,0	omy21	41944218
Omy_102505-102	A	G	CTGCAAACTGACATGGTAGCAAAA	TGCTTGCTTTTTAAAAACAATCTCCCA	AACAGGATGTTTTTGC	CAGGATGCTTTTGC	0,0	omy22	7759328
OMS00173	T	C	TGGAAGTAGCTACTTAACAGGAAATGG	AACACGTGTGCTTGTTTTGTCAA	CATTAGCTTGTGTATGAACT	ATTAGCTTGTGTGTGAACT	0,0	omy22	9105891
Omy_Ots249-227	C	T	CTATCTATCTATCTATCTATCTATCTATCTATCTATCTACTTACTGAGA	CCCCTAGATTAAACCTGTCCAGTCT	CCCTCTGAGAACTAC	CCTCTGAAAACTAC	0,0	omy22	18917430
OMS00058	A	G	GTGACATTTGGAGCCACTGC	GCTAGGAGACAGAGGGTGAAAG	CAACACTTTGTACCCCTC	CACTTTGCACCCCTC	0,0	omy22	19922139
Omy_RAD93580-37	T	G	AGGCAGAGGAGGGTTGTTTG	TGCAGAAGTCAAATCACGAACA	AGTCACCTGGGATT	AGTCACCGGGGATT	0,0	omy22	24247865
Omy_IL17-185	G	A	CCACCACACTCTGCAGCTT	TTGACGGGAATCCGAGACTTC	AAGAATCTCACCTGCCCAT	AAGAATCTCACCTGCCCAT	0,0	omy22	27226063
Omy_RAD103359-45	C	T	GGAGAAGGATGTGCTCCCTG	ATTTGGAGGTGGAGGGTCCA	CCTGTAACGCACAG	CCTGTAATGCACAG	0.4,0	omy22	40502475
Omy_RAD4848-14	G	T	TGTCCCTCTTCTGCACGATG	AGTTGGTAGCTCACTCTCTGT	GAGACAAGGACAGA	GAGACAATGACAGA	0,0	omy23	5493648
Omy_107806-34	C	T	TCTTTGTCCATGCACATTGATATT	AGCACATTTAGTTAGCAGTGATGGA	ATTGGATGTCAGTGTCATT	ATTGGATGTCAATGTCATT	0,0	omy23	10095418
Omy_RAD48799-69	A	G	GCTGAGCCACCTACACACAG	GTCTAACACTCGCAGCAGGT	CATCCTAGAATAGAAGT	CATCCTGGAATAGAAGT	0,0	omy23	21581080
Omy_187760-385	A	T	CGGCTATTCTCGCGTAAAAGCT	AAATGCAACCAGAAACGGAATGTC	TCCTTATCCAAAATTATTGTGC	CTTATCCAAAATAATTGTGC	0,0	omy23	23659737

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OMS00024	T	G	CACATACAACCATCACCCTTCCTAA	AGCATTGAGCGAAATTACCAAGAGT	AA[AC]CCCAAATTTTAC	AA[CA]CCCAATTTTAC	0,0	omy23	31418339
Omy_RAD3651-48	G	T	GAGTACAGTGCAGTGTGGGG	CCTTCCTCTTGCCACCATCA	GTTGGGAGAACTTT	GTTGGGATAACTTT	0,0	omy23	32029860
OMS00048	T	C	GGAAGAGCTGGAGAACAACGT	TGCAGTTGACAGAGGCTTTCTTT	CAGCTAAACTCAGCAAAA	AGCTAAACTCGGCAAAA	0,0	omy23	37125668
Omy_e1-147	G	T	GCACTGACTGTTACCAGGAAAGAG	GTACTGCAGTGTTGAGGCTATATCA	CCATCCTGAATCTGATTAA	CCATCCTGAATATGATTAA	0,0	omy23	38313338
Omy_109243-222	A	C	ATGTGCACCTCTTAAATTGTAAGTAAAATGT	ACCCTATATTCAGTGGCAAGATTGC	TGTTCATTAAATTGACTTTTT	TTCATTAAATGGACTTTTT	0,0	omy24	7009687
OMS00101	A	G	GCGTGTCGTGGGTCAGTTAAATA	GTGCAATCCAACCTATTAGTAGATATGCT	CTCTAGTAGCCTTATAGAAAG	CTAGTAGCCTTACAGAAAG	0,0	omy24	10475451
Omy_inos-97	C	A	GATGGACAGGGTCCTCTTCAC	CCTGTAGATAAACATGGTACCAGGTC	CCTTTCTTGATGGTATCC	TCCTTTCTTGATTGTATCC	0,0	omy24	24547687
Omy_RAD55997-10	A	C	CATTTTCTACCTGCAGGCTGC	AGCCTACATACATAAAGCCAACA	AGGCTGCAATGTTT	AGGCTGCCATGTTT	1,5,0	omy24	27405886
OMS00052	T	G	TGCGTTTTTCATCCCAATCATTCAC	GGCATCAGGCTCTTCTTCCT	CTTCCTTTTGAGAATAAT	CCTTTTGCGAATAAT	0,0	omy24	28174967
Omy_107336-170	C	G	GCCCTCTCACTCATGACATCAAC	GCTCCAGCCACTCGCA	CACTCCTGGGTGCAGAA	ACTCCTGCGTGCAGAA	0,0	omy25	30017455
Omy_RAD59758-41	T	C	GGCCCCCTTCTTTCAGGAAT	CACACACTCAACGGGTCAGT	TGATTGCTACTGAC	TGATTGCCACTGAC	0,0	omy25	40219356
OMS00174	A	C	TGACTAACTATGCAGCCTGAAAGG	GGGATACTCTTGTAATAAACTGTTGGTTAGTA	CAAGAACAGG[AC]TAAATGT	CAAGAACAGG[AC]GAAATGT	0,0	omy25	47325393
OMS00071	A	G	CCGGAGTGACCTCACATTTGG	GCATCGTACAGTTCACCTACCT	CTTGTTTGAGCTTTTTCT	TTGTTTGAGCCTTTTCT	0,0	omy25	48248474
Omy_ppie-232	C	T	CTGTTTTAGATTAGAATGTTTTTGGTCAGGT	CTGAACATAGGCTTTCATTTCAGACAT	AAATAGCGGAGAAAAT	AAAATAGCAGAGAAAAT	0,0	omy25	54990925

Omy_RAD14033-46	A	G	GCAGGAGATTTATTTGGCCCC	ACCCTTGTGATCACATACTGTCT	ATAGAGGAATAGAC	ATAGAGGGATAGAC	0,0	omy25	60064021
Omy_RAD1186-59	A	G	CACAGCCTGGATGTGGTTCT	ACAAGTTCCGGGAGTTTCCT	CCAGGACATCCAGG	CCAGGACGTCCAGG	0,0	omy25	70252314
OMS00002	A	C	TTTGATTTGATTTGTATCTGCTTCTT	CCAACATGCCTCACACAAAA	TGTTTTGCAGCGCTC	TGTTTGGCAGCGCT	0,0	omy25	82366395
Omy_RAD41594-34	A	G	TGCAGGGTTATAATGTGTCTTTGT	AAATCTCGGGCTGAGGAACG	CAGAGATACGTTCC	CAGAGATGCGTTCC	0,0	omy26	5600475
Omy_cd59-206	C	T	CGATTGGCCCAGATGTTTCCAT	GCTCCGTTGCATAGGTGACT	CAACAATCGAAGGTAAAT	CAACAATCAAAGGTAAAT	0,0	omy26	8028322
Omy_RAD13034-67	A	C	GAGTGATTCCCAGCCCTCC	TCTCTCCGTTGGCCAGAAAC	ATAAATCACAA	CTAAATCACAA	0,0	omy26	12537039
Omy_ada10-71	C	T	TCTTTGAGCGACAAAGTCCTTGT	ACCCACACATGAACGCAAAAG	CTTCCTGCGTCCAA	CTTCCTGCATCCAA	0,0	omy26	18315420
Omy_aspAT-123	T	C	GCCCATTTCACTGATGCTGTGA	AGGAGACCACTCCAAAGAGAACT	CCTTCCTAGGCAGTCAG	TTCCTGGGCAGTCAG	0,0	omy26	19289582
OMS00014	T	C	CTTACACACAAGGGCTTCATTCTG	GATGTCTCTGGGTGGTTGTCA	TGATTTGATGAATTAAACTTC	TTGATGAATTGAACTTC	0,0	omy27	6297526
OMS00015	A	T	TCAGACCCTATTTTTGGCACAAGT	GTCTAACTGATCCCACTTCTGCAT	CAAGTCACACTTTTAATGAA	CAAGTCACACTTATAATGAA	0,0	omy27	23730945
Omy_hsp47-86	T	A	CACATTAAGCACTCCCAGGGA	TTGCAAAGGCCAAACAGCATT	CAGGAGTGTAAATGTTT	ACAGGAGTGTATATGTTT	0,0	omy27	27944494
OMS00090	T	C	AGGGCACAACACCACTCTAAATT	TCGAAAAGCAACATCTGTCTCAGT	ACAACCACACAAGATT	AACCACGCAAGATT	0,0	omy28	4245997
Omy28_11607954	G	A	TGACACTGATCACAATGGTGAAAT	TAAACTGGAAGGAGAGAGCAAAAT	TGTGGGCTGCGAACATACTCA	TGTGGGCTGCAAACATACTCA	0,0	omy28	11607954
Omy_RAD52458-17	C	A	ACGTGTCCCTGAGGATGGTA	AGCTCTAGGTCTGGGTCCTG	ATGGCCCC[CT]AAGAACCC	ATGGCCCA[CT]AAGAACCC	0,0	omy28	11609794

Name	A1	A2	Seq1	Seq2	Probe1	Probe2		Chr	Pos
Omy_GREB1_05	T	G	TGGGCAGATATGGAAGAACGG	ACCTTCTAAATGGCCTCTGTGT	CGGTGGCTCTC	CGGTGGCTCGC	0,0	omy28	11618027
Omy28_11625241	A	G	CAACATTTAGGGAGAGGTTGCTAT	ATCATCAAGTTTGCCTACGACAC	CCTCCTCCCTATGGTTGTCTC	CCTCCTCCCTGTGGTTGTCTC	0,0	omy28	11625241
Omy28_11632591	G	A	GTAGAGGCCAAAGGCTTGAG	TGCTCTTATTACCTTCCAGACTCC	TGAGAAGAACACAGAGG	TGAGAAAAACACAGAGG	0,0	omy28	11632591
Omy_GREB1_09	T	G	CCAGTGGCAACCTCAGGTAG	GACTCCAGTCACCCAAGTCA	TCAATGGAGA	TCAAGGGAGA	0,0	omy28	11641623
Omy28_11658853	A	C	CAACATATGACCACTCGAAAACTC	ATTAATCACACCGTGAGACTCCTC	TGGTACAGACACGCACTAGCA	TGGTACAGACCCGCACTAGCA	0,0	omy28	11658853
Omy28_11667578	T	C	ACAGTAAACCCATTCAGGCATAGT	TTATCCTCTCAATCCACATCAAGA	GTATTGATCCTGTGGGAGACA	GTATTGATCCCGTGGGAGACA	0,0	omy28	11667578
Omy_RAD47080-54	A	G	TCAAAACCTGCAGGACTTGGA	TGGTTATATCTACAGTACAGTTCGT	TGCAAGACTTAAAACGA	TGCAAGGCTTAAAACGA	0,0	omy28	11667915
Omy_RAD15709-53	G	A	TGCAGGACTTGGATAACACAGA	TGGTTATATCTACAGTACAGTTCGT	ATGCAAGGCTTAAA	ATGCAAGACTTAAA	0,0	omy28	11667915
Omy28_11671116	C	T	AATTTCCCCAAATTTGAAACTCTT	GTGTACATTGTCAGGCAGAAACAT	CTGGTGAGAACAGGAATTACC	CTGGTGAGAATAGGAATTACC	0,0	omy28	11671116
Omy28_11676622	T	G	CGAATGCACTGTAGCTCATTCTAA	GCAGTAGAATGTCTCGCAAATACA	ACATGTCATTTATTGTTATCT	ACATGTCATTGATTGTTATCTT	0,0	omy28	11676622
Omy28_11683204	G	T	CAAGAAAGAAACAGATGTTGTCCA	TTGTGACTCAAATCTGCAACCTAT	ATGTAAAAAGGGCAGAAAA	ATGTAAAAAATGGCAGAAAA	0,0	omy28	11683204
Omy28_11773194	A	T	AGTTTGACACCCCTGTACTAGAGC	GTCTAACAAGCTCTGGGTGATTTA	GCAATTTTTTAAAATTACCGC	GCAATTTTTTTAAATTACCGC	0,0	omy28	11773194
Omy_RAD76060-20	C	T	TGCAGGGTGTCAGTATTGGG	TCCCATGCAAATTCCAAATGCT	GGGCGCTGTAGGCAA	GGGTGCTGTAGGCAA	0,0	omy28	21561303

OMS00129	C	G	GGAGATGATGAAATAAAAATTGAGGAAAAGATGA	TGTCTGGTGAATTATCGCAAATAACCA	TTGAACAACAAGAAAAA	TTGAACAACAACAAAAA	0,0	omy28	22531125
Omy_RAD46452-51	A	G	TGCAGGTAAGACTTGATCTGGA	TGACTCCAACCTAAGTGCATGT	TGAAGTCAGAAGTT	TGAAGTCGGAAGTT	0,0	omy28	27516610
Omy_97660-230	C	G	TCAGTTATGTGTAATCTCATTACCTCTCCAA	AACAGAAAAGGTCTCAATGTATTTTTTGCA	ACGTAACTTGTAGCGTTTT	ACGTAACTTGTACCGTTTT	0,0	omy28	35742946
Omy_impa1-55	C	T	CGCTGAGAGGATTGTCAA	TTTTCTTTGTTCAGTCTTCTGTCTCTG	CGAGATGATGCGTCTACA	CGAGATGATGCATCTACA	0,0	omy28	36390509
Omy_BAC-B4-324	G	T	CGTACTTTTCTTTTACAAAATTAAGTGGAGGAT	GCCTAATATTGGCCTAATGTCCTTCA	CATTGCCAAATACG	TACATTGACAAATACG	0,0	omy29	14528635
Omy_OmyP9-180	C	G	CTGGATGTGTAGTATCGGTGGAAAA	CACTGGGCACCTCTGATCTC	CTGTAGTAGTCCCCATTGT	CTGTAGTAGTCCGCATTGT	0,0	omy29	15673414
OMS00164	T	G	CAGAGGAGAGGAGAGCAAAATACTT	ACAACCTACTCATTGAAACTCATTGGA	CCAGATTCAATTAAATTTA	CAGATTCAATTCAATTTA	0,0	omy29	17249654
Omy_crb-106	G	T	GCTCAAAAGATTCTGCCAAATTCACA	ATTACAATGAAAGTACTTGAGTGTTTATGCAAA	TTGCAATGCGTCTTT	TTGCAATGAGTCTTT	0,0	omy29	30701374
Omy_118205-116	A	G	CTGCGGTGGGCTACACA	CGCAGCTGCGGATGAG	CTACTGAGGCTGAGTGCT	TACTGAGGCCGAGTGCT	0,0	omy29	33267127
Omy_sSOD-1	T	G	GCCGGACCCCACTTCAA	CAGACTAACCGAACAGCATCAGTGG	CCACAACAAGACCC	CCACAACCAGACCC	0,0	omy29	39802221
Omy_RAD19578-59	A	G	GGTTGGACACCTCCTGGTTA	TCAACCAAGCAACAGATTATAGCT	GGTTAAGAGTATTC	GGTTAAGGGTATTC	0,1.8	NA	NA
Omy_RAD40520-48	T	G	TGTTCATCTGATCAGCTGTCAG	ACACGTCGGTCTTCTTCTCC	GTCAGATTGCGCTG	GTCAGATGGCGCTG	0,0	NA	NA
Omy_RAD78147-27	C	T	GCATTTTAGCCCTCCCAAAGTC	CCTTCTTCCAGTTGTTAAAACCCA	CAAAGTCCCAGAGA	CAAAGTCTCAGAGA	0,2.6	NA	NA
Omy_RAD619-59	T	C	CATGGAGAAACAGACCCGCT	TGCTGTGTGTGTATCTGGGG	TGCTGGATCCCCCA	TGCTGGACCCCCCA	0,0	NA	NA

1004	Omy_R AD9871 5-53	T	G	CGTAACGGGGAGCTGATCTG	GCTGGTAAAATGCTGAG GGG	CAGGACTTCT CCCC	CAGGACTGCT CCCC	0,1.9	NA	NA

1005   Appendix 2. *GT-seq SNP panel for Chinook salmon.*

Assay	A1	A2	Forward	Reverse	A1-Probe	A2-Probe	Allele Corrections	Koop GCA_002872995.1 chromosome	Koop GCA_002872995.1 snp coordinate	Chi6 GCA_002831465.1 chromosome	Chi6 GCA_002831465.1 snp coordinate
Ots_SEXY3-1	X	Y	GGTCTTGCAGTCAGGAGAGG	CCAGGTGGTGAAGGTAGGAA	NA	TCAGCGAAGTGGAGAT	NA	NA	NA	NA	NA
Ots_myoD-364	T	G	GTGTGTGTGTGTGTGTGTCATCGT	TTTACACATATACAAAAATGGTCCTCTATTGTCAT	TCATCTTTTGTTATTTCCTTG	ATCTTTTGTTCTTTCCTTG	0.7, 0	Ots01	10134698	Ots01	7299784
Ots_u07-25.325	T	C	AGACAATCATGGTGTTTTGAGTCTTTCT	GCCTAGGCTTGATGGAGTCA	CCGCTTGAAAGTTTGA	CGCTTGAAGGTTTGA	0,0	Ots01	12626231	Ots01	9198721
Ots_110689-218	T	G	GTATAAACTAGAGTCCAGTGTTATGTTAATGTCTT	CATGGCAGACAACAGTAGAGAATATGA	CACCAATCAATTAATTATT	ACCAATCAATTCATTATT	0,0	Ots01	15276095	NA	NA
Ots_129458-451	T	C	TGGGACCCACATAAAGCAACTG	GACATAAGACCCATTTAGCCCCTTTT	CATCTGGCAATGCCTT	CATCTGGCAGTGCCTT	0,0	Ots01	15863134	Ots01	11080640
Ots_crRAD21115-24	C	T	TGCAGGTGGGACTTAAACACA	ACCTGTGGCAACGGTTGA	CACACACATGCACG	CACACATATGCACG	0,0	Ots01	27727076	Ots01	23499747
Ots_Prl2	A	G	CCTGGTCTGTTTGTGATCAAGATG	GGTTAACTCAAATAGAACATACTCTGACACA	ATGTATTGTTCATTTAATG	TGTATTGTTCGTTTAATG	0,0	Ots01	46840237	Ots01	40924770
Ots_Ikaros-250	G	A	GAGGCTGACTTGGACTTTGC	GGCCTGTCAGCCAAGGA	ACAGAAGATTTTCGGCTGC	ACAGAAGATTTTCGACTGC	0,0	Ots01	50283457	Ots01	45385098
Ots_107806-821	T	A	TGCAGTGCTGAATTAGAGATTAATTTTTGTG	CTCCCTTGCTTTTGGTCATTGG	CAAAGAAAATCAAAATTT	CAAAGAAAATCTAAATTT	0,0	Ots01	56999741	Ots01	51993828
Ots_127760-569	C	T	CTGCTGGCGCAGACATG	CGTTATAGAGGATAGTTTGGAGGAAGGA	CCGGTTTACCGATTTG	CGGTTTACCAATTTG	0,0	Ots01	70642723	Ots01	65444532
Ots_crRAD23631-48	G	A	GCCATATCCCGGGGCTTG	TGCCTCTGAGCACTGACTG	GGGCTTGGGGGCAT	GGGCTTAGGGGCAT	0,0	Ots01	73494810	Ots01	68018794

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

Ots_crRAD69327-53	G	T	GCCATTTGACCAACGGAGC	ACTCATACAGTATTTCCGCCTGT	ATAGGAGAATTGGA	ATAGGATAATTGGA	0,0	Ots02	52051529	Ots02	4708299
Ots_stk6-516	C	A	TGTGTTTAGGATTGAACTGACCATGTT	GTAAACTCCACCTGCAAGAAGGA	AACATAACGGACTCCC	TAGAACATAACTGACTCCC	0,0	Ots02	53397399	Ots02	3814527
Ots_cgo24-22	T	C	AGGTCCTCTGTCGCACCTA	GGAGGCGAGGTCTGGTG	CCAGATGAACAACTTCAC	CCAGATGAGCAACTTCAC	0,0	Ots03	9588638	Ots03	12326537
Ots_NOD1	C	G	GTGCTGCAGGAACCATGTG	CTGTGTGGACTGCTGTCTAAGG	CCAACGGCGACTTG	CCAACGCCGACTTG	0,0	Ots03	9598576	Ots12	23568768
Ots_113457-40R	C	T	CCCAAGTGGTGAGTGTCAGT	ACTACAACAGGTGTTGATAATAGAATCATTCTC	CCCT[AG]TTCTCCAATCCATAT	CCCT[AG]TTCTCTAATCCATATG	0,0	Ots03	17561381	Ots23	9447490
Ots_TNF	C	T	CCAAATCCTCATCCCACACACT	CCGTTGCACTTGACCCTAAAC	CTGGCTGTAAACGAAGA	TGGCTGTAAACAAAGA	2,0	Ots03	20344952	Ots03	21402560
Ots_112301-43	T	C	GCATGGCTGCCCTAGAACA	TCAGAACATTTCCTTCAGCTTCGT	CGTCGCATTCAGC	CGTCGCGTTCAGC	0,0	Ots03	33896915	Ots03	284XXXXX
Ots_u07-20.332	A	C	CGCGAGTTAGCTCGAATATTATGATTTC	TCAAGCTAGCATAGCAACTTCATCAA	ACCATTTGATATAACTGCGTTAG	CATTTGATATAACGGCGTTAG	0,0	Ots03	39126796	Ots03	33660993
Ots3_34894254	T	C	TGATATATTTTGCTGCAATGATCTG	AGAGGGAAGGTGGACAATGTT	TAACTTACAGTC	TAACTTACAGCC	0,0	Ots03	40436224	Ots03	34894254
Ots_118938-325	C	T	ATTTTCAAACAGGCATTTATCATTGGTGAA	GGTCTGTCCCTCATTCTTTGCA	AGAGATGCAAAGTGGAGTT	AGAGATGCAAAATGGAGTT	0,0	Ots03	48430243	Ots03	43610834
Ots3_57055518	T	C	TTAGCAGGCGATCTAATTCTGATT	ACACGCTAACTGCTGTATTCTCTG	TGATCATATCTCGTTCAGT	TGATCATACCTCGTTCAGT	0,0	Ots03	61138782	Ots03	57055518
Ots_100884-287	T	C	CGGAAGACCAGATTCTCCAAGAGTA	CGACCAAGTAGCGGCACTT	ATAGAACTACAATTCACATATAT	AACTACAATTCGCATATAT	0,0	Ots03	72097697	Ots09	34802127
Ots_94857-232R	T	C	GGCACTCTCCCTGGCTAGA	CCCCATCACTTCTCTGGCTTTAAAT	CAGGATAATAACAAACAAG	CAGGATAATAACGAACAAG	0,0	Ots03	2XXXXXXX	Ots03	27503532
Ots_107285-93	T	A	GCCCTTGTGACAATGCACTGTTATA	AACATACACCAATACTTAGGTCTAGACAGT	AAGTAACGTATCAAATGGC	AAAGTAACGTATCATATGGC	0,0	Ots04	6690909	Ots04	5852987

Ots_Ots311-101x	A	-	AAATGAGGCCGTCCTTTACACT	GCAATACAAGCCCTTGATAATGAAGT	CTGAGATCACTTTGAGCAC	ACTGAGATCACTGAGCAC	0,0	Ots04	20118827	Ots04	4070652
Ots_103122-180	T	C	CAAACGCGCACTCACACACA	TCACAATGGTACGATTTTACGACTCAA	CATCAACACAATCTGC	CATCAACACGATCTGC	0,0	Ots04	22443878	Ots04	16781457
Ots4_40942276	G	A	ATTAGTGCATATGAATCGGGCTAT	CCAAAAGGTTGAACGTACATATTG	GGAGTCAGATAC	GAAGTCAGATAC	0,0	Ots04	48716473	Ots04	40942276
Ots4_41638710	G	A	CAGCAGCTGTTTATGACTGACTTC	CTCGTGTAACCGATGTGAAATG	CCTGAGATTAGG	CCTGAGATTAAG	0,0	Ots04	49353548	Ots04	41638710
Ots4_42378741	C	T	CAGTTTAAGTGTTACCACCACGAG	GTGCAGGTGAGCGTTAACG	AGATGAACACCAACTGGCCGG	AGATGAACACTAACTGGCCGG	0,0	Ots04	50072182	Ots04	42378741
Ots_96500-180	G	T	CAGGTCTGGTCTACATCGAACAC	GATCATGTCAGATAGGATGCTGAAAGT	AAAACAAATCATTTTTG	AAAAACAAATAATTTTTCG	0,0	Ots04	53468710	Ots04	45636897
Ots4_64978818	C	A	AGAACCCATGCTTTCAGTACACTT	AAAATGGACAGAAATGTATCGCTC	TCAAGTGTTTCCTTTATTTTG	TCAAGTGTTTACTTTATTTTG	0,0	Ots04	71212183	Ots04	64978818
Ots11_11925999	G	T	TTTATATTCAGACATTCGCCAAAA	GATTGTCACAGTAACATAGAAATGGTTT	CATTTAAAATGGTAAAAATCA	CATTTAAAATTGTAAAAATCA	0,0	Ots04	71231942	Ots11	11925999
Ots_105401-325	G	T	GAACTGAGCGGCTGCTG	CGCCTCCTGGTGTCTATCCT	CCCGGACAAGATGAGACAG	CCCGGACAAGATGAGACCG	0,0	Ots04	1XXXXXXX	Ots04	12543170
Ots_HSP90B-100	C	T	CACCTTAGTTCCACGCAACATG	CTGCGTGTATTGTAGTGGTGACA	TCTATGGTGTGATTCATT	TTCTATGGTGTAATTCATTT	0,0	Ots05	7641577	Ots05	6866692
Ots_111681-657	G	T	CTGAGCTTTTTCAACTTACTTGTTGGA	GGCGCAGCAGCAACTG	TAGCGCAAACCCCGAACC	CGCAAACACCGAACC	0,0	Ots05	9439742	Ots05	8539947
Ots_128693-461	C	T	TCAATGTTCATCAATGCACTTCCTGTA	GCCTGCAGGAGAAGGTAGAGTTA	CTGGTACCCA	CTGATACCCA	0,0	Ots05	15919055	Ots11	29099828
Ots_crRAD66330-60	G	T	ACTCTCCCAGAAGGATTCAGAGA	TCCCAAAGCATCCTGCCA	AGAGAGGGGTCAAA	AGAGAGTGGTCAAA	0,0	Ots05	17933258	Ots05	14208918
Ots_u211-85	C	T	TGGTGAGAGCAGCTTTAAATGTCTT	ACCCATTCTTCTGTCTGGTTTAAGC	TCCCAAAGTCGAGTGTG	CCCAAAGTCAAGTGTG	0,0	Ots05	29079237	Ots05	34253781

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

Ots_Met A	T	A	GATCATTTATCAAGAC TATAGGCTATGGATAC G	AGTTGAGTTAAGTA ATTGGTAATTAGCC TGTT	CCTTAAGCA TATTTCT	CCTTAAGC GTATTTCT	1.6, 0	Ots06	21997 591	Ots06	20396 849
Ots_ZR-575	G	A	GCCTACCAGAAAGTAC CAATTGTGA	ACTTTTCACTGTCC TATTACAATTAGTA TTTGTGATAT	CC[GA]ACAC AATTTGT	CC[GA]ACA TAATTTTGT	0,0	Ots06	29177 962	Ots06	27576 884
Ots_crRA D46751-42	C	T	CAGGAACCTGCTTTAA TGCTCT	GCTTCTGCAGGGGG ACAA	TTTCTACTT AGTAA	TTTCTATTT AGTAA	0,0	Ots06	35130 855	NA	NA
Ots_9490 3-99R	G	T	CCGTCTGAGTAGGAGG ATCAATACA	TTTGGATCCAGCTC TCCGTATAGA	CAAACCAG CAAACAT	ACAAACCA GAAAACAT	0,0	Ots06	36076 090	Ots06	35539 172
Ots_1076 07-315	A	C	GTGATGAGAGGTTTCC GGAAAATCT	GTGTTCTGGATTCC ATTGTGCAAA	ATGGGAGA CAGATAACT	ATGGGAGA CATATAAC T	0,0	Ots06	36480 917	Ots06	36761 804
Ots_FGF 6B_1	A	C	GAGACAAAGGTTTGCA GGTTCATG	GGGAGCCATGCACT AATATATTGGA	CCTGTTATC AGACCCAA AT	CTGTTATCA GCCCCAAA T	0,0	Ots06	37585 917	Ots06	37250 687
Ots_u6-75	C	T	GAAAAAGTAAAGTAA AAGTAAAGTATTATAC CACTAAAGACAAT	GATCCACACTGTTG GTCTACTACAA	TTAGTCAAC TGTTGTTTT T	TTAGTCAA CTGTTATTT TT	0,0	Ots06	50534 743	NA	NA
Ots_crRA D73823-60	T	A	GCAGGAAGCAAAGTTC GGTG	AGCAACTCATCGCG TGGT	GCACGATG[CT]AGAAC	GCACGAAG [CT]AGAAC	0,0	Ots06	52896 472	Ots06	53325 628
Ots14_54 53033	G	A	ATTATTCAAACAGAGA TGGCGAAA	GAGGAGGTTTGCAT AGAACATGAT	TCTCTAAAA AGGTACAGT ATA	TCTCTAAA AAAGTACA GTATA	0,0	Ots06	55710 320	Ots14	54530 33
Ots_u07-53.133	C	T	AGCTAGGCTGTAAATG CAAGGAT	CAGTGCTTTCAATT CATGCTGTCAA	TAACACATG TTGGAGGTC	AACACATG TTAGAGGT C	0,0	Ots06	58232 274	NA	NA
Ots_GDH -81x	C	-	CTTTTCTGAATTAGTGC TGTGCTTGT	CCAACTTCTTCAAC TCTGTCAGTGA	TGTTACGGG ACATACT	TCTGTTACG GACATACT	0,0	Ots06	58688 462	Ots06	585X XXXX
Ots_GnR H-271	C	T	CAGATGAAAAATAAAT AATTGGGCCATTAGGA A	CAGAGAGACTGAG ACCATATGATGTAG T	CAATGAATA CAATATCTA ACCTAAT	AATGAATA CAATATCT AATCTAAT	0,0	Ots06	65879 558	Ots06	65660 176
Ots_1159 87-325	T	G	GGAGGTGTAGTGAAAT GGGAAGAT	GCATTCAGTGAACC AGTAGTGCTAT	ATGCATAAA AGGTAATTG TG	ATGCATAA AAGGTCAT TGTG	0,0	Ots06	66387 317	Ots06	66193 572
Ots_1053 85-421	A	G	GACTGTCTTGGAACCG TTGCTA	TCCCGGAACACACC AATGTC	CCTCCTGGG TATATCG	CTCCTGGG CATATCG	0,0	Ots06	73075 541	Ots06	73012 849

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Name											
Ots_map Kpr-151	A	T	TGTTGTCTCGGACTGC ATGAC	GAAGGCACAGAGA TGAAGGACAT	CGTATGTGC AATGCATG	CGTATGTG CATTGCAT G	0,0	Ots07	3593175	Ots07	5460143
Ots_map K-3'-309	T	G	GGCCACTGTCATAGAA TTAGGCATT	CGTGACCCTTGTAA CTGAAAAGC	ATGCTATTA AATGAATAT TC	ATGCTATT AAATGACT ATTC	0,0	Ots07	3608628	Ots07	5480042
Ots_1287 57-61R	A	-	CGTGTCCGGCTTCTTTT ATTTCATT	GATGGGTATGTTAA TCATATTACCAGCG TAA	TTGTGCATT TTCCCC	TGTGCATTT CCCCC	0,0	Ots07	6643830	NA	NA
Ots_1318 02-393	C	T	TGATTGTCTCATGGCC AATTGTCA	TGTAAATTCCACTT GGCAATCTTTGG	TGTTCGAGA ATGAAGAT GAGTAA	TCGAGAAT GAAGGTGA GTAA	0,0	Ots07	35733 706	Ots07	25665 994
Ots_1314 60-584	T	C	CCTATTTTTGATAGGTC ATAGTGAATGGGATAG	CTGTACTCCTCCAT TCCTTTTCACT	CTATCAAAG CAATACATT G	CTATCAAA GCAGTACA TTG	0,0	Ots07	42945 148	Ots07	31130 645
Ots_CHI 06048618 _5222	T	G	GCAATTACCCATGACT CTGTGA	GCCAAAAAGAGAC CGAATCA	ATTGTGCTT ATCACA	ATTGTGCTT AGCACA	0,0	Ots07	50130 039	Ots07	38043 969
Ots7_509 97124	G	T	AGATCAAGCTTGCTGA CTTCG	CATACACCACACTG TATTTTGCTG	GGGCCTTCG GGGTGCCTG TCC	GGGCCTTC GGTGTGCC TGTCC	0,0	Ots07	62901 252	Ots07	50997 124
Ots_nram p-321	G	A	GGCCATCTTTCAGGAC GTACAG	GCATGCTCTGCAAT ACGTTGAG	AAC[GT]GGC ATGAACGA CTT	AAC[GT]GG CATGAATG ACTT	0,0	Ots07	63847 460	Ots07	51336 125
Ots7_514 09415	T	C	ACAACTAGTCATCGTG GAATCTGA	ACATGCTAAAAGA AAGGAATGAGG	TGGTCTACT TTGTGC	TGGTCTACT TCGTGC	0,0	Ots07	63921 389	Ots07	51409 415
Ots9_289 75221	A	T	GCCTGCCCTACTTATCT CTTATCA	ACCTCTTCACTGTA AAATTTGCTG	TTTGCCAAA GAGTTCAGA TAC	TTTGCCAA AGTGTTCA GATAC	0,0	Ots07	64709 638	Ots09	28975 221
Ots_arp- 436	A	T	GCCCTGGAGAAGTACG TTTTAAACTAA	GCAACCATGTCAAC ATTGCACATAA	CTAGGTGAA ACTTTTTT AAA	CTAGGTGA AACTTTTTA AAAA	0,0	Ots07	65259 187	Ots07	52672 820
Ots7_532 91035	G	A	TCAAATTGAATGTAGA CAGATGGAA	AAATAGCTCGCAAA GCTAACATTA	GCTAGCAA ACGTCGCCA	GCTAGCAA ACATCGCC A	0,0	Ots07	66039 124	Ots07	53291 035
Ots7_536 31522	A	G	CTTATCTCAAAGGAAT GGGAATGA	CTACAGTATTTGGA TGCAGCTTTG	TGAGTTTTC AAGGGGTT	TGAGTTTTC AGGGGGTT	0,0	Ots07	66362 189	Ots07	53631 522
Ots7_542 12944	T	A	AAACCACGGTATCCTT TATTCATC	TTCCTAACCCCAAA ATATGTCTAAA	AATATATTT TTTATAGGC	AATATATA TTTTATAGG C	0,0	Ots07	66905 811	Ots07	54212 944

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Ots_97077-179R	G	T	CCTGAACAAATACTTAACGCTCCAGTT	GTAATAATACTTCACACCATTGCCACTTC	TCACAAATGTATCCTAAAGC	CACAAATGTATACTAAAGC	0,0	Ots07	70085972	Ots07	5632XXXX
Ots_105105-613	C	G	AGTACAAGTGCAGAGAATGACATCATG	GGTGTTTTATTTTCCCATATATCTTTTAACTTTAAGCT	CCGAGCTTGAGTTAGGA	CCGAGCTTGACTTAGGA	0,0	Ots07	77202120	Ots07	63322755
Ots_slc7a2-71	G	T	CCATTCCCATCGGCATCGT	GCAGCAGACACACCGAAGTA	GTCTCTGACGGTGTGCTTTC	GTCTCTGACTGTGTGCTTTC	0,0	Ots08	8668369	Ots08	61099332
Ots_crRAD34397-33	C	G	TGCCTAAACACTCCCAAGGT	GTTCCGTTTTTGTTCCGCGA	AA[GA]GTGCCTTCCCC	AA[GA]GTGGCTTCCCC	0,4,0	Ots08	10116544	Ots08	60161043
Ots_u07-64.221	G	C	GAGGATGACACTGTCCGTTTGT	CACAGTCCTTCGTATTCACCTTGAT	ATCGACCCTGTCATTAG	CGACCCTGTGATTAG	0,0	Ots08	12242337	Ots08	57998143
Ots_103041-52	G	A	ACCACCCACCTCCTCAGA	AGACAGAGAAAGTCGGGACACT	CATCCTGCTGGACCC	CATCCTGTTGGACCC	0,0	Ots08	15518130	Ots08	55669454
Ots_OTALDBINT1-SNP1	T	C	CGCTGGGCATGGATGAGT	GGCCAACACTGCTACTTCCT	CTACTGTTGTATTTTCTC	CTGTTGTGTTTTCTC	0,0	Ots08	16275426	NA	NA
Ots_101704-143	T	G	ACTTCTTGAGCCAATCGGATGATG	CCAGAGATAAACTAGTGGAGGAGATCA	CTTAGACGTCAGAGGTC	CTTAGACGTCCGAGGTC	0,0	Ots08	21039383	Ots08	51040180
Ots_102213-210	A	G	CATTCCATGACAATGATTGAAATCTAAAAACAC	GAGTATCTCAATTGCAACACTATGGTATGT	CTGTATACAGTAAGAGTATTAAT	ACAGTAAGAGCATTAAT	0,0	Ots08	26477291	Ots08	45XXXXXX
Ots_129170-683	C	A	AACCCTATGGGAACTCGTAGAACT	GCTAGGAGTTCTCAAAAGGGTTCT	ATTAGAACTCGTAGAACTAT	ATATTAGAACTCGTATAACTAT	0,6,0	Ots08	47390818	Ots17	11485501
Ots_ppie-245	C	A	TGTTTTTGGTCATGTATTTTCTGCTATTTTT	GGACTGGAGCTGCTGAACATA	ATGTCTGAAATGAAAGCC	AATGTCTGAAAATTAAAGCC	0,0	Ots08	50220193	Ots08	23260130
Ots_AsnRS-60	T	C	CCGACGCCTCACTGAGT	TGGTTTTTCAGGTCATGGTTTCCA	TGAGTCCCTGACCAGC	AGTCCCCGACCAGC	0,0	Ots09	2800047	Ots20	41784960
Ots_u1007-124	A	G	CGAAATAAGGGCCTGGTGTTTAAAA	TGTACCAGGTGGAAGCTTTGG	TGTCCTGTCCTCAGATCA	TCCTGTCCCCAGATCA	0,0	Ots09	11679141	Ots09	9430381
Ots9_16115048	G	A	ATAGAGCTTTTGGTGTTTCATTCC	AGTGTGTGTACTGTGTACTGGCCT	CCAGTGAGATGCTGTGTTGCA	CCAGTGAGATACTGTGTTGCA	0,0	Ots09	19855559	Ots09	16115048

Ots_P450-288	A	G	ATGTCAATATATTTCACTATAATGATTGGAAGCCA	CACTGAACTCGAAGCTGTTAGGA	CTATAAAGTTGGACAGTTGG	AAAGTTGGGCAGTTGG	0,0	Ots09	23147965	Ots09	19138835
Ots_102457-132	A	G	CCAGCAGAGACTGGGTTCAC	TTCCCTACCGGCGAAACC	TGGGGCAACGCACAATTGGCT	TGGGGCGACGCACAATTGGCT	0,0	Ots09	26992696	Ots09	23XXXXXX
Ots_110201-363	A	T	GTTTGGCTATTGAAATTATACATTAAAACATGTAGCT	CCATGGCATCCTGTAAAGAACAACA	TTTTAAAA+CTGGCATCCA	TTTTTAAACTGGCATCCA	0,0	Ots09	29017362	Ots09	25990000
Ots_hsp27b-150	G	A	TAGGAGTTGGAAAGACTGCACA	CCCATTGGTTCTTTGGTGTT	[CT]GATCTGGACCAGGCT	[CT]GATTTGGACCAGGCT	0,0	Ots09	67075478	Ots09	52471033
Ots_u1008-108	T	A	GGATGACTCCTACTAATAGACGGATGT	AGGACAGGAAAGAAGCAGCAAATA	TTGGTAAACCTGTTTATTGGTA	TGGTAAACCTGTTTTTTGGTA	0,0	Ots09	75362394	Ots09	62354402
Ots_FARSLA-220	G	A	GTTCGTGGGATTGTTCAATGTTCAT	CTTGGACAGGCTCACATTACCATA	CCTTGGATGGGA	CCTTGGATAGGA	0,0	Ots09	82809166	Ots09	68274964
Ots_hsc71-3'-488	C	T	TGCATCCATTCATACCTGACCAATT	TTTGGTTAGGCACACGATAATTTGC	TTTCCAATGGTATAGATATGA	TTTCCAATGATATAGATATGA	0,0	Ots09	XXXXXXXX	Ots09	37358812
Ots_Thio	T	C	TTTTAAAAATGGAGATAAACTCCTGACCTGAA	AATACCAAACCATGCCACTAATACCT	CAGTGTATTAGTCATTCTTA	CAGTGTATTAGTCGTTCTTA	0,0	Ots10	7144861	Ots10	5625322
Ots_112820-284	C	T	CATAGATGTTTATATGAAAAACCTCCCACTGT	GCATCCAAAAAGACGTGTGTGTTT	ACTCACACTCGAGTGACT	ACTCACACTCAAGTGACT	0,0	Ots10	18438064	Ots10	16907470
Ots_102414-395	A	G	GCCTACTGATAAATGTATGACAGTAATGGA	CAATAACAAACAAGCTAGGAACAAAAGTGT	CACATAGTGTAGCTTTACTAC	CACATAGTGTAGCTCTACTAC	0,0	Ots10	21873207	Ots10	20097469
Ots_108007-208	A	T	CAGGCTTGTGTTAAGTAGGGAGAAA	CATTGGACAAGACCGGGTAGTC	CAGTTTCACTTAATTTTAAAATG	TTTCACTTAATTTAAAAATG	0,0	Ots10	25247839	Ots20	4971142
Ots_129144-472	C	A	CTGTTAGTGCAGAAGACGTAGCT	GCAGAGCTATTGAGCCAAGTTACAA	TGGGTCTCGAGCCTGTA	TGGGTCTCGATCCTGTA	0,0	Ots10	30541697	Ots10	30704018
Ots_crRAD10447-25	C	T	CCGTTGCAGGACTCATCAGT	GCGTGGTTCAACAGCAGTG	AGCTAGCGCTCCTC	AGCTAGTGCTCCTC	0,0	Ots10	36392206	Ots10	36699634

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Ots_crRAD18937-60	G	A	GGCACAGCGACAGGAGTT	TGAGCTGGTGCGTCTGAG	CTCCTCAGGTGGGC	CTCCTCAAGTGGGC	0,0	Ots10	50635181	Ots10	51017984
Ots_nkef-192	C	T	CATTTAGCAGACACTCTTATCTTAGTGTCA	CGAATGTCCACCTCAGATGTTACAA	AATAGGCCGACATCAA	AAATAGGCCAACATCAA	0,0	Ots10	51361376	Ots10	51394567
Ots_crRAD26165-69	C	T	GGGCCACGGGGTTGTAAA	TCCCAGGATGCAATGGGA	CTCT[GA]CCCCTGGAC	CTCT[GA]CTCCTGGAC	0,0	Ots10	52149501	Ots16	20109332
Ots_u07-57.120	A	T	GGTTTGAGCCAATCAGTTGTGTT	CGGTCTAATGTCCATTGCTCATGTT	GTGACAAGGTAGGGGTTG	GTGACATGGTAGGGGTTG	0,0	Ots11	12974126	Ots11	16346192
Ots_106313-729	A	G	TTGTTCAATGGGCATTAATGCATGTT	TGCTTATGTGCAGATACTTGAGACAAA	AAGAGTCCAGCGTTACTT	AAGAGTCCAGTGTTACTT	0,0	Ots11	16517829	NA	NA
Ots_108735-302	C	T	CCTTTTTCTTATTAGTTTTACTTCCCCAGAGA	CAATTCCATTCTTGATTCTGTTTAACGGT	AAACAAACAACGCCTCATG	AACAAACAACACCTCATG	0,0	Ots11	17583626	Ots11	21337974
Ots_crRAD76512-28	A	T	GCAGGGACAGGGCCCT	TGGTGCTGGGTGCTGTAC	TAAAAAAATATAAA	TAAAAATATATAAA	0.3,0	Ots11	25425413	Ots11	32328258
Ots11_32418659	A	T	CAATTGTAGCCCTCTAACTTTTCC	ATACGACACACAAAGCCAATTGTA	AGCCAATTGTAGCCTTAGTGC	AGCCAATTGTTGCCTTAGTGC	0,0	Ots11	25519430	Ots11	32418659
Ots11_32468959	G	C	AACACAGATCAAATGTTTTCACAC	AACACAGGAAAAACAGAATGTTGA	GTGATAGTTTGATAGTTTTAT	GTGATAGTTTCATAGTTTTAT	0,0	Ots11	25588829	NA	NA
Ots_crRAD9615-69	T	C	GAATGCAGGGCCAGGGAG	ACTCCCAGACCATCCAGCT	TATTGGTCAGGGAA	TATTGGCCAGGGAA	0,0	Ots11	25656094	NA	NA
Ots_crRAD36072-29	T	C	TGCAGGACCAACTTTCTCAT	GGCTGACTGGTGAAGGGG	AACCTGTGTGATTT	AACCTGCGTGATTT	0,0	Ots11	29147224	Ots11	36019633
Ots_crRAD61523-71	A	G	GCCAAGTGATCAAGTGCTTGT	CCAGCAGTTCAGTTGCGG	CAGAGCATGTGCTG	CAGAGCGTGTGCTG	0.2,0	Ots11	35352564	Ots11	41149096
Ots_GPH-318	C	T	GGTGATAACAGGTGTTGCACCAA	TCAGGTGGTGGTGGACAAC	ATCAAGCTGACGAACCA	CAAGCTGACAAACCA	0,0	Ots11	40844253	Ots11	46176184
Ots_crRAD20376-66	G	A	GGGAGGCAGGCAAAAGGT	GGTTCACCACCAGCCTTCT	GGGA[TA]GGAGTATTT	GGGA[TA]GAAGTATTT	0,0	Ots11	41283424	Ots11	46457753

Ots_zn593-346	A	T	CTACGCGAGAAATAACACTTTTCAAAACT	GGCGAGTTTATTACGGTGTTATGAC	TCTTGCAATCATTTTTAAC	CTTGCAATCATATTTAAC	0,0	Ots11	41292800	Ots11	46464971
Ots_IsoT	T	C	GACTCAGGTAAGGAAACATCAATGTCA	GAAAGCAAAGCATTTTATCCACCACTA	AACCAGTAGAATAACC	CAGTGGAATAACC	0.5,0	Ots12	10323252	Ots12	9121489
Ots_crRAD55400-59	C	T	CGCAATGAGCCAACCCCT	CTGGTTTGTTCCCGGGCT	CTAACCCGGA[CA][GA]AC	CTAACCTGGA[CA][GA]AC	0,0	Ots12	18236712	Ots12	17250308
Ots_102867-609	A	G	CTCTGCCATTCATTTGGGCTTTG	GTCTAAAGTGGTCCCCTTGGAT	ACAGAGAGAAGTCCCAGGTG	AGAGAGAAGCCCCAGGTG	0,0	Ots12	21101745	Ots12	204XXXXX
Ots_131906-141	A	T	GGCTCGAACCACCCAGTTTA	TGCCCAACTGGTTTGCAATC	CACGGTTTACACTCCTATTA	ACGGTTTACACTCCAATTA	0,0	Ots12	21773920	NA	NA
Ots12_23066874	A	G	CTCTTTCAGTTGTCTTTGCTCTTG	ATTATGAAAAGGCATGAACAGGGT	TCCCCACCAAAATTAAGCAAA	TCCCCACCAAGATTAAGCAAA	0,0	Ots12	25387620	Ots12	23066874
Ots_pop5-96	T	C	CTCTTGCTACTTGCAGTGTATCTCA	AGTTTGAGGGCTCTATTCTGTCATG	TTCTGTTACTGGAC	CTGTTACTGGGC	0,0	Ots12	29307827	Ots12	27353346
Ots_u07-49.290	G	A	GCTGAGGAAGGATTCTGTATTTGCT	TCGGACAGAGCGCATCC	CTTTCCCCGTGTTGGT	ACTTTCCCTGTGTTGGT	0,0	Ots12	31470258	Ots12	30314171
Ots_cox1-241	C	T	CACTGAACTGTAAGCCATTGTGATT	GTAAATGTAGTATACAGTATAGGCATCGTAGGT	CACTACGGTAAGACCAT	CACTACAGTAAGACCAT	0,0	Ots12	31570301	Ots12	30421258
Ots_ETIF1A	A	C	TCTGAACTCACCAAAGGAACACTTG	GAGAGAAAAGGAGAAATGATTGCCATT	CAACTGAAGAAAATAATATG	CTGAAGAAAAGAATATG	0,0	Ots12	38462855	Ots12	34678104
Ots_GCSH	C	T	GTTCTTTTTAATGATGACTACAGGTCTTTCAC	GCTACTTTACATAATACCATTTGAGCTGAGA	TATCTGGGCGGGCTG	CTATCTGGACGGGCTG	0,0	Ots12	65634622	Ots12	58052588
Ots_96899-357R	T	A	TCTCCTGAACTAATTTAGACCTCTGAATGT	CCTCATATTGCTTTCATCTGAAGAGAGA	CTGAATGTTTTTTTAATCTTT	CTGAATGTTTTTTTTATCTTT	0,0	Ots12	67888781	Ots15	21523451
Ots_aspat-196	G	C	CCTGAACAGGTACACACAAACGA	TCCAACTGATGAATATGACCAACATGAAT	CACTCTTTATATCCACACC[GA]	CAGTCTTTATATCCACACC[GA]	0,0	Ots12	68043508	Ots12	60406597
Ots_P450	T	A	TGAGCGAGATTTATCAAACTGTCAAAGA	CCCAAGCGGGAGAACTTACAG	CCCCGAAGTACTTTT	CCCGAAGAACTTTT	0,0	Ots12	72832053	Ots12	65154384
Ots_brp16-64	T	C	ACTCTGGGTCCAGGAGGTTTT	CTGACGAGACCATGCACCAA	AAGTCAGCATCTTTCA	AGTCAGCGTCTTTCA	0,0	Ots13	4293254	Ots13	4383923

Ots_106419b-618	G	T	CAAGGGCACATTGGCAGATTTT	ACCGGACCAAAGCACACA	CAATGATTAATGATTAATCCTTC	TGATTAATGATTCATCCTTC	0,0	Ots13	11736968	Ots13	11463845
Ots_HFABP-34	C	T	CAAGAACACCGAGATCTCCTTCA	TCGGCGGTGGTCTCG	TCGAACTCCGCTCCTAG	TCGAACTCCACTCCTAG	0,0	Ots13	12380464	NA	NA
Ots_TAPBP	C	T	TTTCTCATCCTTCTCTCTTCCAGTCT	GGACAAACCAGCACTCCAGAA	CAGCTGTCCAGTTCTG	CAGTTGTCCAGTTCTG	0,0	Ots13	26128999	Ots30	34770823
Ots_crRAD27164-55	A	T	GGAGGCTCTACGTAGGCCT	ACAATATCTGACACTGACTTGGTCA	AATTTGAATGACCA	AATTTGTATGACCA	0,0	Ots13	27591014	Ots13	25285990
Ots_mybp-85	C	T	CAAGGGATGTGACAAATTAATCAAACACATAA	AAGAGGTCTAATAAATCTCCAATGTAAAAACGT	AGAGCATGTAGTTTTG	AGCATGTAATTTTG	0,0	Ots13	31784059	Ots13	29231079
Ots_crRAD17527-58	C	T	TGCCGCTGGATTTATTGACA	GCGTCAGATCAGCTGGTCT	TAGCTCCGAGCTAA	TAGCTCTGAGCTAA	0,0	Ots13	36124810	Ots11	37324165
Ots_112419-131	A	T	GTGGGTAATCGATGCCAAAGAGAT	TGGCAGTGTTTTCAACTAGCTTTG	AAGCGACTTGATTATC	AGCGACATGATTATC	0,0	Ots13	45350303	Ots32	7853251
Ots_hnRNPL-533	A	T	TCTTTGATATTGAGCTCATAAAAGCAAGGT	TCCTTGTTCATCCATCAGGCATAAAA	CATTTACCAGTTCTCACACAC	TTTACCAGTTCACACACAC	0,0	Ots13	46418615	Ots13	46705374
Ots_SL	A	G	AATATTGGCTTTCTGAGAATGCATTTGG	CCAAGATACTTCCTTTAACTTCTCTGTCA	TCAAAGATATGATTCAATTAA	AAGATATGGTTCAATTAA	0,0	Ots13	62174556	NA	NA
Ots_crRAD35313-66	A	G	TGCAGGAAGAGTTCAGAGAAATCT	GCTCGTTGCAGGTAGAAATGT	TTTAAGATGTAGTT	TTTAAGGTGTAGTT	0,0	Ots13	70298983	Ots13	65139272
Ots_U2567-104	G	A	CATAGTATAGTGATTCGAGTCTGGAGTCT	CGGGCTTTCTTAGGATATTTTCCTGA	GAGACTGTTGAGAC	GAGACTATTGAGAC	0,0	Ots13	73139521	Ots13	68622537
Ots_IL8R_C8	C	T	CGTGGTGTTCGCCTTCCT	TGTCGGCCATCACTGTCATG	CTGGACGCCGTTACA	TGGACGCCATTACA	0,5, 0	Ots14	1429870	NA	NA
Ots_GPDH-338	G	A	CACTAAATATTCCTTATCATTTCATACTAAGTCTGAAGAA	AGCTGATACACAATCAAAACACAAAACAT	CCACTACTTAACGTGCTTT	CCACTACTTAACATGCTTT	1,0	Ots14	7996596	Ots14	11576466
Ots_CHI06035945_4547	C	T	AGCGAGGCTTGCGTTTTACT	GTGCAGTCTGGGCTTGTCTT	CCGCAACAGATC	CTGCAACAGATC	0,0	Ots14	8787979	Ots14	12373492

Ots_U5049-250	G	T	CAATGTCTAAAGTAATGGTGGTATTCTTGC	TCTTTGACACACCATCTGCCAATT	TGGAATGGGTAAGGTGTA	TGGAATGTGTAAGGTGTA	0,0	Ots14	21359050	Ots14	2257XXXX
Ots_crRAD18492-65	C	T	GCAGGGCGCAAAGTTCTT	CAGTGAGCGACTGTAATCTGA	TTATGGCTATTATT	TTATGGTTATTATT	0,0	Ots14	43620612	Ots14	424XXXXX
Ots_crRAD57687-34	T	G	TGCAGGGACGGGGCT	TGCTGTTGTCTTGGGTCTCTC	ACAAATTAATTAAA	ACAAATGAATTAAA	0,0.7	Ots14	3XXXXXXX	Ots14	31889864
Ots_104063-132	C	T	GCGTTACTGGTGTTATAAACGTTAGC	GTTTATTTAATTATGAAGGACGATGTTGAAGTCA	CTTTCGTCCTTAGCACATAG	CTTTCGTCCTTAACACATAG	0.5,0	Ots15	2747251	NA	NA
Ots_NFYB-147	C	T	CAGATGATAGCTTCAGTAAGTGGTTCA	CCGTCCACAGCACAAGACTATAATA	TGTTCCAATGTAAAATGTATGC	TTCCAATGTAAAATATATGC	0,0	Ots15	5313010	NA	NA
Ots_124774-477	T	C	AGTTGTTCTTTTTATATTGTGTTTTTATTCCATTCCA	GCCAAATAAAAACAAAGCATGAACACA	CCACCGCCATCTGATA	CACCGCCGTCTGATA	0,0	Ots15	10921418	Ots15	15167502
Ots_vatf-251	G	-	CTTTTCGGGTTATTCATGCTGTTGT	GCAAGCATTTGAAAAACAGACTGGAT	AGACCACAAGATACAGTACC	AGACCACAAGATAGTACC	0,0	Ots15	13005607	Ots17	7664045
Ots_112208-722	C	A	CTGCATGAACGTTAACTCAAATAAAAGGT	AATGAGTTCTACTGACATTGTATACTAGAATAAGTATCA	TGTGAGGGCGGTCTT	ATGTGAGGTCGGTCTT	0,0	Ots15	13348552	Ots15	17637330
Ots15_18157381	C	T	TCTCAATGTGATTGAAATGGATGT	TGTCTGTAGTTTGTGTGTACGGTG	CCCTGGAGATCT	CTCTGGAGATCT	0,0	Ots15	13993075	Ots15	18157381
Ots_crRAD20887-70	G	A	CTGCTTGTAGCCGTTCAGC	AGAACACATCTGGCCAGGT	GAACTCGTCGTTGG	GAACTCATCGTTGG	0,0	Ots15	17832008	Ots20	7378067
Ots_CHI06027687_143477	G	A	GCGAGTGTTAAAAGGGTCAAA	TCTCAAGCCATAAGACGGGTA	GGAGATAGTCAGGG	GGAAATAGTCAGGG	0,0	Ots15	17999857	Ots01	34155766
Ots_102801-308	C	A	TGGGACAGAGGTGGGAATTGA	CCCAAAGATGCTTAACTGAAGATGTG	AGGGACAGTTTCGCAGACG	AAGGGACAGTTTCTCAGACG	0,0	Ots15	19904397	Ots15	19971476
Ots5_70908626	T	C	TACGGTAGGAAGACTGAATGAGTG	CCCTACCTCTCCAGATAGCTTGTA	AGCCTCTTCCTCTCTG	AGCCTCTTCCCCTCTG	0,0	Ots15	36201712	Ots05	70908626
Ots_117259-271	T	G	ACACCCACTTCAACCTCCATAAC	GCCTCAGAGCTTAGCTTGGA	CTCTCCTGATCACTCTGT	CTCTCCTGATCCCTCTGT	0,0	Ots16	11947135	Ots16	11458685

ID	A1	A2	Forward	Reverse	Probe1	Probe2	Value	Chr	Pos	Chr2	Pos2
Ots_117242-136	A	G	GTGACAGGAGACAGAAAGAGACATT	TGGTCCTCCCTGTCTCTATCTACTA	CAGCACATAACTTGACCTC	AGCACATAACCTGACCTC	0,0	Ots16	29941952	Ots16	29333295
Ots_unk526	A	G	TCAAGACTGTGCTGTAGTTGTCTAC	CCTCCCCCTTTTCCACATCAG	CAACATTCCAGTCTGAAAC	CATTCCAGCCTGAAAC	0,0	Ots16	30269244	Ots16	29699840
Ots_Myc-366	T	C	CCTTAGCTGCTCTTTGAAGTTGACT	GGCTATAGAGTGTATTTACAGCATGCA	TCTCTGCTCATCTGTC	CTCTGCTCGTCTGTC	0,0	Ots16	30269853	Ots16	29700449
Ots_unk1832-39	C	T	GAAACGTCTATGCTGTCCCCTTTAA	CTGCAGTATTAGCTCTAGTTGAATCCA	CACCACTAGAACTCTC	CACCACTAAAACTCTC	0,0	Ots16	37061421	NA	NA
Ots17_885364	C	A	GTAAAGAAACATGACCTTTTCTGAG	CAGGTTATGGCCATCATAGTTAAA	TAGCCTTAAGCGCTTCCTGCC	TAGCCTTAAGAGCTTCCTGCC	0,0	Ots17	1405257	Ots17	885364
Ots_104415-88	C	T	CCTGAGCATCCCAGTTGAACT	TGTTTTCAATACACTGCAATTTAGTTTTGGT	TCCTGAAAAACGACATCC	CTGAAAAACAACATCC	0,0	Ots17	5993649	Ots17	5512367
Ots_SWS1op-182	T	A	TCAAAGACATCGAACACAAGAACGA	GCAGGTAAATTCAAACGTCATCATAAGAA	ATGTACTTTAACGATTCATTT	ATGTACTTTAACGTTTCATTT	0,0	Ots17	8656175	Ots17	7365688
Ots_crRAD16540-50	C	T	TGTGTATTCGTCGACCGGA	TCACCTGACCAAAGCACTGG	ATTAAACGT[CA]TGGA	ATTAAATGT[CA]TGGA	0,0	Ots17	11570673	Ots17	9728418
Ots_crRAD2806-42	C	A	GCAGGGGCAGACTGAAGG	ACTTCATGCCAATCTCACTAAACA	GTTTGGCATAAAGT	GTTTGGAATAAAGT	0,0	Ots17	15937591	Ots17	14222969
Ots_crRAD22960-32	C	T	ATCAGGTCTGGGGCGACA	TTCACCTCTGCCATCGCC	CGACACCACTTACA	CGACACTACTTACA	0,0	Ots17	15937659	Ots17	14223038
Ots_IGF-I.1-76	A	T	GGTAGGCCGTCAGTGTAAAATAAGT	GATGGAGGCCACTGTGTTCTTA	CTGCCTAGTTAAATAAAATA	CTGCCTAGTTAAATTAAATA	0,0	Ots17	17781778	Ots18	4150743
Ots18_3541813	T	C	CCCCAAAAACATCAAGAAGTCTAA	ACATGGTGAGGAAAAGGTAGACTAA	CTACCTACCTTAGTGCTC	CTACCTACCTCAGTGCTC	0,0	Ots18	458745	Ots18	3541813
Ots18_3550047	A	G	ATCATCTCTGCTCAGAGGCTATTC	AGAGTGGAAGGAACGTCTTACACT	TCATTTTTGCAGAGAGAGAAT	TCATTTTTGCGGAGAGAGAAT	0,0	Ots18	467661	Ots18	3550047
Ots_crRAD92420-25	G	T	AGTGCAGGTCTCCAGATTTACA	ACCGAAGTGTATGTAAACTTCCGA	CAATCGGAAGTCGG	CAATCGTAAGTCGG	0,0	Ots18	2423432	Ots18	6695198

Ots_crRAD33491-71	C	T	CAGTTCGCTTCTCCAGGGA	TGTGGGTAGCAGACTGACG	GAGAGCCGAGCTTT	GAGAGCTGAGCTTT	0,0	Ots18	6100851	Ots18	2699387
Ots_crRAD12037-39	A	G	TGCAGGAACTTGCTATGCT	TGTGGAAAAAGTCAAGGGGTCT	CATTCAAAAAGTAT	CATTCAGAAAGTAT	0,0	Ots18	9770315	Ots18	10327070
Ots_crRAD55475-26	T	G	TGCAGGGTTGGGGACAATT	AGTCTATTTCCCGATTTGACTGGA	CCATTTTAATTCCA	CCATTTGAATTCCA	0,0	Ots18	17529243	Ots18	17929277
Ots18_29943476	A	G	GTTCATTTTGAAATAACTGCATCG	CTCTACAAGGTCCATGCACATTAG	GCCTGACTGGACAACCATTTG	GCCTGACTGGGCAACCATTTG	0,0	Ots18	30949170	Ots18	29943476
Ots18_30099101	C	T	CAAATGTAAGGATACGCTTGAATG	GAGTTGCAAGCGATTACATGTATT	ATTGCATACTCGAGTCATCCA	ATTGCATACTTGAGTCATCCA	0,0	Ots18	32296859	Ots18	30099101
Ots_Hsp90a	G	C	GTCGTTTTTCATAGAAAATAGCTCACAGTT	ACAGTATACCGGCTGCCTATTCATA	ATTTGACTTGTCTTTTT	ATTTGACTTGTGTTTTT	0,0	Ots18	32303237	Ots18	30105519
Ots_S7-1	T	C	TGCCATCATAAACAACCTAACAAGTAACT	CCTGGTTTAAAAACGGCCAACTG	TACAGGAGATAAGGTCGCA	CAGGAGATAGGGTCGCA	0,0	Ots18	33195644	Ots18	31651991
Ots18_32088284	T	C	CATGAGACACCCTGGAGAAAA	ATTTTGATAGTACCTTCTTGGGGC	ATGTTACATGTA	ACGTTACATGTA	0,0	Ots18	33781780	Ots18	32088284
Ots_pigh-105	A	-	GCATTACTAAAAACTGGTGTGTGGAA	GTTTGGAATGTTTCTCTGATTGTGTTAACAA	TGACCTGAAAATA[TC]ATATTTTT	ACCTGAAAATA[TC]ATTTTTTT	0,0	Ots18	38228583	Ots18	35641063
Ots_CD59-2	G	A	CATGTTACCCAGCTAAAAGTCTATAGCA	TGTTTATCTCTGAGTGAAAAGGTGTGT	CTAAAATGTCATGTAAATAT	ACTAAAATGTCATATAAATAT	0,5,0	Ots19	9550712	Ots19	9312796
Ots_RAG3	C	T	CATTTCCACGAAAAGCCAGATGAC	ACAGAATAAAGTATCTTCCTCTTACATCACTACTAAT	CTCTACAGTATG	CTCTACAATATG	0,0	Ots19	36242326	Ots19	34427967
Ots_110381-164	A	G	CTCTTGTTTGCTATGGGAGATGTAGT	CCGTATCCTAAACCCTTCACTGTT	ATTTGCGTCTTCTCCC	TTGCGTCCTCTCCC	0,0	Ots19	36960028	Ots19	35228582
Ots_RAS1	C	T	TCATAAACATGGTGTCTTTCAGTCAGTT	CTGACATGTGAAACTACTAAAGCATTTAATCAC	CAATCTATCATCGACCAGC	CAATCTATCATCAACCAGC	0,0	Ots19	37925628	Ots19	36275840
Ots_95442b-204	A	T	GTCTCTCTCTCTTTGCATCATTACACT	GGACTCTTGAGCTGTCTGGCTATAT	TGGTTCCCCAAATTT	TGATGGTTCCCCTAATTT	0,0	Ots19	40912881	Ots19	39212513

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Ots19_46172133	C	T	CACATGGCTCTTTGCTCAAAAT	GCCTACCATTATGTGTTGAATGTT	GCAAATCTCCGATGTAAAGT	GCAAATCTCTGATGTAAAGT	1,0	Ots19	47135055	Ots19	46172133
Ots19_46172427	G	A	CAGTTCCTGACATTCACCAAAATA	GCAAACAACCCATCACTAATACAG	TATTCAAAAGGAGCAGTTCAT	TATTCAAAAGAAGCAGTTCAT	0.8,0	Ots19	47135348	Ots19	46172427
Ots_crRAD20262-46	A	G	CCTCTGCTGAGTTTGAGGGG	TGAGCAGAGCCTATGAGGACT	GGTTACA[TC]CCCAAA	GGTTACG[TC]CCCAAA	0,0	Ots19	47358507	Ots19	46397112
Ots10_21244146	A	C	CTTCCAGGAGGTATTGTTGGTTAT	TGAACGTAGGTTTGCCATATACAG	CCATTATCATTAT	CCCTTATCATTAT	0,0	Ots19	53906684	Ots10	21244146
Ots_Est740	T	C	GGACTCGTGCTTGAGGAAGATG	TGCATGGCTCCAACTCCTT	TCTGGATGGAACCGTTAG	CTGGATGGAGCCGTTAG	0,0	Ots20	3751056	Ots20	39254576
Ots_crRAD44588-67	C	T	CGCAAGTCAGCAGGGTGA	TGGGGTTTTAGGCTGGGT	GTGA[AG]CCAATCAAT	GTGA[AG]CTAATCAAT	0,0	Ots20	20333782	Ots20	25774788
Ots_AldoB4-183	T	A	TTTGTGCGTAAAGTCAGGTAGTGT	GTGCATGCCATGAGAACTTTGTTT	CTGTGTGTCTAAGACAAT	CTGTGTGTCTATGACAAT	0,0	Ots21	6477138	Ots21	5252021
Ots_AldB1-122	C	T	GCCATGGAGGACTGGATGA	GCCACCACTACTTGCTGAGAAAATA	TGTTGGCGAAGTG[GT]GT	TGTTGGTGAAGTG[GT]GT	0,0	Ots21	6480172	Ots21	5255056
Ots_105132-200	G	T	CGATGTACTGAGGGCAGTGT	GAGTGGAGTTCCTTAATAATCATTGACCTT	CAAGAGTGGCATAAAA	CAAGAGTGGAATAAAA	0,0	Ots21	11799043	Ots21	9585379
Ots_101554-407	C	G	TGAAAGATATCAATTGTAGTAGTGGTGGTG	ACACGCCAGTCCACAAGT	ATGGAGGATTGTGGTTGT	ATGGAGGATTCTGGTTGT	0,0	Ots21	12050017	Ots21	9784111
Ots_GST-375	C	T	CAGCCCGTCCCAAAATCAAG	CAGGAATATCACTGTTTGCCATTGC	TTTCTTGTAGGCGTCAGAG	TCTTGTAGGCATCAGAG	0,0	Ots21	20087626	Ots21	18672650
Ots_GST-207	G	A	GGAGAACATGCATCACCATTCAAG	TCAGCAAACGAAGGCTATGTAGAAT	ATGAGAGAGTCTTTCTCTGTT	ATGAGAGAGTCTTTTTCTGTT	0,0	Ots21	20087794	Ots21	18672818
Ots_redd1-187	A	G	TTCTGGGTTGCCATACTCTTTCAAT	AGTTGAGACCTTCAGTTCTTAGGGTAT	ATTCTGACAGCTGTTTTG	CTGACAGCCGTTTTG	0,0	Ots21	27483610	Ots01	9939318

Ots_E2-275	A	G	GGTGCCACTTTAGTAT AGCTGCTTA	CCCTACCCCCTGTG TTCCA	CCCCCATAT TGCTG	CCCCACAT TGCTG	0,0	Ots22	6419264	Ots22	5457012
Ots_1230 48-521	A	C	CTCAACAGTGCACCTC CCTTAATT	CCAAACACACCCTT CCATAATCTCT	TCACATCCA ACTCAGTAC T	CATCCAAC GCAGTACT	0,0	Ots22	9478478	Ots22	8033323
Ots_parp 3-286	A	G	AGTCAGTGTTGGTGTA GTGAAGAGA	CATTTGTGGAGTGT TTATTGAACAGTAA CA	AGTTACAAG TGGTGTTTC A	ACAAGTGG CGTTTCA	0,0	Ots22	10728055	Ots22	9505120
Ots_u07-17.135	A	G	CTCGCCTCTGTCATTGT ATTACCTT	TGACACACGAGCCA TTTTGATGAT	AAAATGTAC CACATACTT GT	AAATGTAC CACATACT CGT	0,0	Ots22	12134293	Ots22	11164448
Ots_CD6 3	A	C	TGCATGTTTTCTAACTG TGTTTTTGTGT	TGAATGCCCCCCAT CAACA	AGATCATGG GAATCATAT	ATCATGGG CATCATAT	0,0	Ots22	14629707	Ots22	13378891
Ots_1105 51-64	C	A	GAGTGGTCAAGGTTTC AGTTTCTG	GAAATGGACAGAC ACAAGGTCAAAC	ACGCTCGGA ACATT	ACGCTCTG AACATT	0,0	Ots22	15838315	Ots22	14420914
Ots_u100 2-75	T	C	CCGCCTTTCCCACCTTC TC	TCAAACGAGAACA CACTAAGGTTGT	ATGGCCCTT ACACTATC	TGGCCCTT ACGCTATC	0,0	Ots22	16981803	Ots22	15468014
Ots_tpx2-125	C	T	TGTTGTAATCTTTCTGA ATATTTGCTTGCTT	TCTTCCAAATTGAG CACAAAAGCAT	CAGGCGGTT CTCC	CAGGCAGT TCTCC	0,0	Ots22	21879673	Ots22	20362912
Ots22_32 650802	G	A	AAGGAGCAGGAGATG TTATTGAAG	ACTAGGTACTTCAC TGGTCCACTG	GGGAGAGG AGGCCTGTC TTTA	GGGAGAGG AGACCTGT CTTTA	0,0	Ots22	34412033	Ots22	32650802
Ots_CHI 06105101 _16717	C	T	AAGGCCGTGAACATCT GTG	ATCGCAGGCTAGCT TTTCAA	CCTCACATA CTCCCTT	CCTCATAT ACTCCCTT	0,0	Ots23	18000122	Ots23	5124325
Ots_CHI 06105101 _18523	A	G	GCGGTGGGATACCTCC TCTA	GCGAGAAAAGCAC TGAATGA	GGCGGCTCG GAAAATTAT TTT	GGCGGCTC GGGAAATT ATTTT	0,0	Ots23	18003825	NA	NA
Ots_1067 47-239	C	A	ATCGAGGATGCCTCAA AGACATC	GTTAGACCCACCAC CAGTCATC	CCCGCGGTG AGTAT	CCCGCTGT GAGTAT	0,0	Ots24	9568130	Ots24	17321046
Ots_PEM T	C	T	AGAGCATTCAATTTAA AAGCTGAAAACGA	CTTTGATCCCTGCT TGCAGTATTT	TGC[AT]TTG CTAAGACTT G	TGC[AT]TTG TTAAGACT TG	0,0	Ots24	10785871	Ots24	15921271
Ots_1173 70-471	G	T	GTTGGCTCCTTCAATTC AATTTGGA	TGCAAACACAGAG GAAAGGGATTT	ACGGAACA AATAAGAC ATTT	CGGAACAA ATAAGCCA TTT	0,0	Ots24	12157474	Ots24	14581248
Ots_1070 74-284	A	T	CCCACTTCCAGAGCCT GAA	TTTTCCATGGCTGT GTGTACTGT	ACCGTAGCT GCACCTG	CGTAGCAG CACCTG	0,0	Ots25	8142848	Ots11	16750220

Ots_GTH 2B-550	C	G	CACAGGAAGGACGTGTTTTGATG	TGACTACCCGTTGTACCAATGAAC	ATAACATCTGCAGCATTAA	ATAACATGTGCAGCATTAA	0,0	Ots25	26054245	Ots25	27327552
Ots_myo1a-384	A	C	CTCCCCCCTGGACTTTGG	GCTCTATTGCACCGTGTTCTG	ACAGATCCATCCACCACT	AGATCCAGCCACCACT	0,0	Ots26	10237957	Ots03	39283854
Ots_112876-371	C	A	GCCTACAGCAAATTCAGCTACACAT	TGGACCTTCAATCATCACAGCTT	CATCACAACGATGTGTG	CACATCACAACTATGTGTG	0,0	Ots26	30XXXXXX	Ots26	29108047
Ots17_22360456	T	G	ATGGTTAAATTGACTCCTCCCTAT	GCCTACTACTGTTCTGTCATCTGC	AGTCTGTCGTTGT	AGGCTGTCGTTGT	0,0	Ots27	14067908	Ots17	22360456
Ots_RAD4543-52	T	C	TCTTTGGACTGTGTATACCAGGTGTA	GCCAGATGCTGTGTGTGTTT	TACATATGACTAATGAAA	TACATACGACTAATGAAA	0,0	Ots27	17341235	Ots27	12866217
Ots_EndoRB1-486	G	A	CCTTTGGGTCTGCTTGAGGTT	GGAGCCAAATCCTAATGCTGAAGTA	TCCTTCTCACGCTTCT	CTCCTTCTCATGCTTCT	0,0	Ots28	9310115	Ots28	8187490
Ots_108820-336	G	A	TGAAATAAATTGTTCTGTTGATATGTGAATTTTGGA	CAACGACACACCAACAACGT	ATTGCCCATCTCAGAATA	AATTGCCCATCTTAGAATAATA	0,0	Ots28	12014613	Ots28	10815622
Ots28_11023212	A	G	AGAAAGCCATCATCATGAGACC	ACAAACAAACAAAAATGGTCAGAA	AACGTGACACAAT	AACGTGACACGAT	0,0	Ots28	12231157	Ots28	11023212
Ots28_11025336	A	C	TGCAATATAGAACAAATCCGAAAA	AATAACCCTTGGCTTCACATACAT	CAATGAAGTTAATTTAATTGG	CAATGAAGTTCATTTAATTGG	0,0	Ots28	12233225	Ots28	11025336
Ots28_11033282	G	A	GGCTTTCTGATGATCTTGAACTTT	AGTGTGAGAGAGAGGAAGTCCCTA	TAAAAATGGTTGATATGTA	TAAAAATGATTGATATGTA	0,0	Ots28	12241662	Ots28	11033282
Ots28_11062192	C	G	AGATGATATGGATTTGCTGTGTGT	TTGAACATAACGATCAGAGAAAGA	TTCTCAAGTCCTACTCAACTG	TTCTCAAGTCGTACTCAACTG	0,0	Ots28	12266158	Ots28	11062192
Ots28_11070757	A	G	TTTTGGAACCCTTTTTACTACGAG	ACATCAGTATAGCAGAGGAGAGGG	ACCCATGAATAAGGACGAGAG	ACCCATGAATGAGGACGAGAG	0,0	Ots28	12274804	Ots28	11070757
Ots28_11071377	T	C	ATTTGCTGTGTGTGGAGTGAAT	GTAGTGACAGATGCTCTTGGAGG	CATCTTAGCCTCTCTGACCCC	CATCTTAGCCCCTCTGACCCC	0,0	Ots28	12275402	Ots28	11071377
Ots28_11072994	C	T	GGGAGACTTAAAACAACCTCAAAA	ACCTGCAACCTTCTATTCAACAGT	CCATATGTCGCTTGT	CCATATGTCGTTTGT	0,0	Ots28	12277000	Ots28	11072994
Ots28_11073102	T	A	GGTGAGCCATTCATAACAATCTT	TGTTATCCTGGATCATTCAAGAGA	ACATTACTTTTCAAAAATATT	ACATTACTTTACAAAAATATT	0,0	Ots28	12277108	Ots28	11073102

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Ots28_11073668	T	A	CCTAAGAGGAGACGAGCATTACAG	GGTAAATCAACATATGACCACTCG	TACAGTTTCCTGTCTGA	TACAGTTTCCAGTCTGA	0,0	Ots28	12277674	Ots28	11073668
Ots28_11075348	G	A	CATTTCAAAATTAGGAGGTTAGGG	AGATGAGAGCTGTGGCCTGT	GTGTGAAAGGGGAGAAGGGCT	GTGTGAAAGGAGAGAAGGGCT	0,0	Ots28	12279292	Ots28	11075348
Ots28_11075712	C	T	GCTTAAACAGCTGCTATTAGGACA	TAAGGATTTGTTGCCAGCTCTAAT	GAAAACTCTGCCCTG	GAAAACTCTGTCCTG	0,0	Ots28	12279656	Ots28	11075712
Ots28_11077016	C	T	AAAATATGTGCAACATCCAATGTC	ACACAAGCTGGCTGAAGCTAAT	GTCAAACCAACTTTGCCAAGG	GTCAAACCAATTTTGCCAAGG	0,0	Ots28	12280918	Ots28	11076976
Ots28_11077172	G	A	GTTTTGCCAGAGAGAATGTACAAA	TAGTGGTTAGAGCATTGGACTAGC	ACACACACAAGAGACACCCAC	ACACACACAAAAGACACCCAC	0,0.4	Ots28	12281112	Ots28	11077172
Ots28_11077576	A	G	TGTGCGGAATTACTGATAATTGAC	GCTCTGCATTTTACAACACTGCT	GAAGGCCAAATAAAATTG	GAAGGCCGAATAAAATTG	0,0	Ots28	12281512	Ots28	11077576
Ots28_11095755	A	T	CCAATGGTGATTTTAGAACCATTAC	AAAACAGAGTATGGATCAACAGCA	AGAGTTGAATGGC	AGTGTTGAATGGC	0,0	Ots28	12299996	Ots28	11095755
Ots28_11143508	G	A	ACCTTTTAGCCAGTGACAACATTT	ATGCAAGAAACTCTCGACGATAG	TTCACGTACGGCCCAT	TTCACATACGGCCCAT	0,0	Ots28	12341541	Ots28	11143508
Ots28_11160599	G	T	GTGCATATTTTACGTGGTTGAAGT	ATTCCATTTCACCCATATGAATTT	CTCTCTGCTTGCGTT	CTCTCTGCTTTCGTT	0,0	Ots28	12359222	Ots28	11160599
Ots28_11164637	C	A	TGATTTGACTTTTTGTGGTGTTTT	GTTCCAATCTGTTTTTGCTCTCTT	CTGGCGGGGTCTGGG	CTGGCGGGGTATGGG	0,0	Ots28	12363212	Ots28	11164637
Ots28_11186543	A	T	GGCTTGCCTTTAGATAGAATCTTG	AAATCTCACAAGTCCAAAAACAAA	AAAGCTGATTAAAAA	AAAGCTGATTTTAAAA	0,0	Ots28	12385919	Ots28	11186543
Ots28_11201129	T	G	TGCGAGATTTATCTACTTGTCCAG	GGTAGTTTTGTACGCAATTGCTAA	ACTGAAGGAATTTAAC	ACTGAAGGAAGTTAAC	0,0	Ots28	12400459	Ots28	11201129
Ots28_11202190	T	C	GCTAAATGTAAATCGAGTGGCTGT	TACATGGGTCCTCTCAGTGTTCTA	CAAAAGTCTGTATTTTCAAAA	CAAAAGTCTTGCATTTTCAAAA	0,0	Ots28	12401520	Ots28	11202190
Ots28_11202400	C	T	CCCTCCAAAAAGAAAACATTTGAT	AAATTGGCTAATCAAACACTGGTT	GACACACTCACGA	GACACACTCCATGA	0,0	Ots28	12401729	Ots28	11202400
Ots28_11202863	C	A	GAGGATGGATGAGACTTTTCAGAT	GCTCTTTACCGGGTTTATATGAAG	ATAAAAAATTCTGCGTGAATG	ATAAAAAATTTATGCGTGAATG	0,0	Ots28	12402193	Ots28	11202863

Ots28_11205423	A	G	TTAAATCACCCAGAGCTTGTTAGA	ACCTGACCTAGATAACAACCACAA	CCTGCACACATGTCAAACCG	CCTGCACACGTGTCAAACCG	0,0	Ots28	12404734	Ots28	11205423
Ots28_11205993	C	T	GCTGCTATTTCCGACCTTACAATA	ATCAAGACAAAACACTCACCAGAA	GCTATTAAAAGG	GTTATTAAAAGG	0,0	Ots28	12405298	Ots28	11205993
Ots28_11206740	T	C	ACTTTGAGGACTTACTCCTGTCCT	CTGGAGAAAGACAAGATGATGATC	CCTTCCCTCCTAGGGCAACGT	CCTTCCCTCCCAGGGCAACGT	0,0	Ots28	12406045	Ots28	11206740
Ots28_11207428	T	G	TATACCTTTGTAGCATCCCTCTCC	CATATAAAGTGGACAGCGTTTGAC	GTTGGGAGCGTCCCAAAATGG	GTTGGGAGCGGCCCAAAATGG	0,5,0	Ots28	12406663	Ots28	11207428
Ots_trnau1ap-86	G	T	GGACAAGTTGAAACAGATCAGGAAGT	GCCACTGGATACCATCACTTCAAA	AATCCCTCCTTTTTCC	TCCCTCATTTTTCC	0,0	Ots28	18849666	Ots28	17646942
Ots_OTSTF1-SNP1	G	T	CGGACAAAGAGCTACAGAAATGC	CGTCCCTCTTCACGCATGA	CCGCCACCTTGGCT	CGCCACATTGGCT	0,0	Ots28	27509692	Ots28	25845386
Ots_122414-56	C	T	GCACCGTATCAACGAGCTCAT	TGCATGGATTTCCTTTGTGTTGTTG	TGTATGACCTCTGACCTGT	TGTATGACCTCTAACCTGT	0,0	Ots28	28489780	Ots28	26647710
Ots_CCR7	C	T	CTGCTCACCTGCATCAGTGT	CCATGGTGGTCTGGACGAT	CCACGTAGCGATCG	ACCACATAGCGATCG	0,0	Ots28	37080463	Ots28	34762262
Ots_97660-56	A	T	TTCCCTAATCTGACGTACTACCAACT	CGCCACTGACGTTCATTCCA	ACGAGACAGATATTC	ACGAGACTGATATTC	0,0	Ots28	37155946	Ots28	34830271
Ots_crRAD18289-33	T	C	GCAGGGAAAACTGGTCAGGA	AGGTGAACCTCCGTCCCA	GAATGGTGTTAAAT	GAATGGCGTTAAAT	0,0	Ots29	7893296	Ots34	8970778
Ots29_23344676	T	C	GAACTATCCTGACTCCCATTGAAA	CTGAGTTCCTCCTGGTTGTTATG	TGCAAGTCCTTCAAAGGCTCA	TGCAAGTCCTCCAAAGGCTCA	0,0	Ots29	12582492	Ots29	23344676
Ots_111084b-619	C	A	TTGTGGAATTACACCTTCAGAGTTCAAT	GCCTGTTTGGCTTTCTTAAACTGAT	TCCATGG[AT]AACGGACAAT	TCCATGG[AT]AACTGACAAT	0,0	Ots29	16022207	Ots29	19749885
Ots29_18791740	T	G	GTTTTGGTGTGGTCTCAAATCC	CGGCACCTGGAAACAGTC	CCTATGAAGTT	CCGATGAAGTT	0,0	Ots29	17054573	Ots29	18791748
Ots_108390-329	G	C	GAGGTTTGTTACTGTCACCCATAGA	CCTGCTGTAGCAAACTGTCTCAAA	CTACTTATGTAGCATTTTAA	CTACTTATGTAGGATTTTAA	0,0	Ots29	19105883	Ots29	16533976

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

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Ots_crRAD57520-66	T	G	ACAGAGCTGTGTCTACCAGA	ACCCTCTCTTGGCCTTGC	TTTTTGTTCAAAAG	TTTTTGGTCAAAAG	0,0	Ots30	39954606	Ots30	1332375
Ots_P53	G	A	GGAACTTCCTCTCCCGTTCTG	GCACACACACGCACCTCAA	CTGGGTCGGCGCT	TGGGTCGACGCTC	0,0	Ots30	40916627	Ots30	2417591
Ots_109693-392	T	G	TCTCCCTCATTCCCATGTCATATCA	GGGAACGTATCAGGTGAGTGT	TCCGTTAGTTCATCCTGG	TCCGTTAGTTCCTCCTGG	0,0	Ots31	9369378	Ots13	7402550
Ots_unk1104-38	C	T	TAACCATGACTTCTATCAATCACCCC	CCTCCATACATCGTCAAAGCTGTA	CCACTAAGGATTACGTTACG	CACTAAGGATTACATTACG	0,0	Ots31	14800538	Ots31	21291286
Ots_ntl-255	T	A	TGCAGTTACAAGCCTAAGACAATCT	CAACTAAAGTAACACACCAGCAACTG	ATTCTTCCTC[TC]ACAATTG	ATACTTCCTC[TC]ACAATTG	0,0	Ots31	20616326	Ots31	15370000
Ots_101119-381	T	C	TTTTCTAGGACAGGTTGCTTGCA	CCAGGTTTCTTTAGCCTACTTATTCTTTACA	TGCCACATGATAATTGA	CCACATGGTAATTGA	0,0	Ots31	21772790	Ots02	58361347
Ots_txnip-321	T	C	CCTTCAAACTAACACATCATAGACATGCTT	TTATCAAACTGAAGGCGGATTACTGA	TCTGGCGGATTTACA	CTGGCGGGTTTACA	0,0	Ots31	23141496	Ots31	13146728
Ots_113242-216	C	T	GAGGCCTAATGTCTCTTGTGACT	GACATCTTCAACAAGTGTTCATTCACC	ATTACCAACGGAGAACC	TTACCAACAGAGAACC	0,0	Ots31	31397037	NA	NA
Ots_sept9-78	G	A	GTCGATTACCGTTAGCTTCATCCT	ATTTCTCCTGTGTCTCTCTGTCT	CTCTTCGATGTCTAGACA	CTCTTCAATGTCTAGACA	0,0	Ots32	5543176	Ots32	9390357
Ots_DDX5-171	C	T	ATGACCAATTGAAGAGTTCTTCCGT	CAAAGCCAAACGTCACATTTACACT	TTCATAATTGAACGATTTCA	CATAATTGAACAATTTCA	0,0	Ots32	7183341	Ots32	5948580
Ots_118175-479	C	T	TGCGCGTCTCATTCAACCAT	ACCTTACGTCCTAGGTAGGAAACA	AGAATGAAGTGAAAAGAA	AGAATGAAGTAAAAGAA	0,0	Ots32	7631574	Ots32	5436160
Ots_129870-55	A	T	GCATGTAACACATTATTTGGCATATGTACT	CAGTACACTGGAGATTTGCAATGTT	ATGCATTCACCTGTATTAT	TGCATTCACCAGTATTAT	0,0	Ots32	10246920	Ots32	2979852
Ots_Ostm1	C	G	CCAGCCCCGTAACACACAT	GAGAGGAAGCAGAAAGGTCGTTTAA	CCGTGGTATTGTTTCAA	CCGTGGTATTCTTTCAA	0,0	Ots33	2743227	Ots33	4569955
Ots_NAML12-SNP1	A	G	TGCCACCTCAGTTTTAGTGTTATATCC	AGCGCCAACCTGTCACT	AAACCATTTTCATTCTTTTG	CCATTTTCACTCTTTTG	0,0	Ots33	8523757	Ots33	9777802
Ots_CRB211	A	C	CAACGCGGGAATGGCTTTTAA	GCCAGAGTCGCCAAAATAGTAGAAT	CTACCGTACTGAACTC	CCGTACGGAACTC	0,0	Ots33	28420240	Ots33	29785703

Ots_TGFB	C	T	GCCTCACATTTTACTGATGTCACTTC	GAGCAGATCTCTTCAGTAGTGGTTT	AGCCTAGCTCTCGGAAG	AGCCTAGTTCTCGGAAGG	0,0	Ots33	28445695	Ots33	29760263
Ots_106499-70	C	G	ACTCTATCATCGGCAGGACCAT	ACCGTAAGTGTGGTTGTGTTCATTA	CATTTTTCAGAATTGTATTC	CATTTTTCAGAATTCTATTC	0,0	Ots33	37411470	NA	NA
Ots_TLR3	C	T	TGCACCTGCGAGAGCAT	CTGGCGTTTGTTCCGTTCAG	CTGTGGTTTGTGGCGTG	CTGTGGTTTGTAGCGTG	0,0	Ots34	7234189	Ots34	7365214
Ots_crRAD24807-74	A	T	TGCAGGAGAGCAGGGTAGA	CGTGCCTAACATCATGTGCA	ATGATAAT	ATGATATT	0.8,0	Ots4	44035017	Ots04	36172590
Ots_crRAD36152-44	C	T	CAAAGTGCAGGTGCTGGC	CCAGCCAGGTGTTGAGCA	CTGCCACCCTTTGA	CTGCCATCCTTTGA	0,0	NA	NA	Ots12	13203734
Ots_afmid-196	G	C	CGTGGAGTAGGTGGTTACAGTTTAT	CTCGTAACAAGCTACTGTAGTGTACT	CAAAGTCAAAGATCCTATTAAA	AAGTCAAAGATCGTATTAAA	2,0	NA	NA	Ots32	17096334
Ots_126619-400	C	T	GGATGGTTGTCATTTCTCTGCAAA	CCGGGATACAATAATAATATTTGGTTAAGAGTTTTTT	AGAAAGTTCTAGAAATAATT	AAAGTTCTAGGAATAATT	2,0	NA	NA	NA	NA
Ots_Est1363	A	T	GGTGATTTTGCCACAGAGTAGAGAT	AGTGTTAAATGTAACTTGCATATACAGGCAAT	CCATCCTGTCTTGTCTG	CATCCTGTCATGTCTG	0,0	NA	NA	Ots03	8292351
Ots_U2305-63	T	-	TGTCATCTCTATTGCAATCTCAGTAGATTTCTAT	CCAGGTCGTCTTTATTGCAGATTATCA	AATGTCATATAGAAATCTAC	AATGTCATAGAAATCTACTG	2,0	NA	NA	Ots14	398XXXX
Ots_u07-07.161	C	T	GTCAACAAATGCAGGTAACATAAATGGT	GATGCAAACACCTGTGAAATTGTGA	ATCAGTGACATAAGTTGTCCA	TCAGTGACATAAATTGTCCA	0,0	NA	NA	Ots04	37799853
Ots_u202-161	T	A	CACTTTTGACTTTACATGGAACTTAACTCAT	GGGACTTCACTTTCTACAAACATGTCA	AGCTAGTGCTTAGCAGCTA[AC]	AGCTAGTGCATAGCAGCTA[AC]	1.5,0	NA	NA	NA	NA
Ots_Cath_D141	T	C	CACTTGTTCTGCACACTACTTGTC	CACACATGGATTTTGCCTGTCTAAA	TGGGAAGCAATCAA	AATTGGGAAGCAGTCAA	0,2	NA	NA	NA	NA
Ots_110495-380	G	C	GCCTAGGTATGTACGAAACTTCACA	AGGCTTTTTCAGATGGTCGTATGA	CATAGAC[AG]GGGGCCAT	CATACAC[AG]GGGGCCAT	1.9,0	NA	NA	NA	NA
Ots18_3417174	A	C	TGAGGTATTACTTGCTGAGTTTGC	CAAGAAGATGTGAACTAATTCCCA	CTGAATCCTGTAAG	CTGCATCCTGTAAG	0,0	NA	NA	Ots18	3417174

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Ots_1239 21-111	A	G	TCGCTAGGCAGAAATA TAGGGTTCT	GAGCATGGCGCTTG CA	TGCTAAATG GCATATATT AT	CTAAATGG CACATATT AT	0,0	NA	NA	Ots18	25247 852
Ots_unk7 936-50	C	G	ATGGGTTGGGATTATG GTTCATTGT	CAAAATGGTTACTT GCATAGTCTTTTGT	AGACATGTA GCTATGTAG GTAA	AGACATGT AGCTATCT AGGTAA	0,0	NA	NA	NA	NA
Ots_9955 0-204	C	T	TGACAGATTTCACCTT TAACTAGCTAAGC	GCAACCTCTTTCAC ACTTCAGTAAC	AAGGCTTTG GTTGTTTG	AAGGCTTT GATTGTTTG	0,0	NA	NA	NA	NA
Ots_crRA D60614- 46	G	T	TGCCGTGAGAAACTGG TCA	TTTCCTCCTCTCTGC CTCA	AAGATGGT ATGTAT	AAGATGTT ATGTAT	0,0	NA	NA	Ots12	72156 356
Ots_OTD ESMIN1 9-SNP1	C	A	GGTCTGTCTGTCTGTCT ATCTGTCAATG	TGTGTGTCTTTGTTC ATTCCTACCA	CCAGTCATG GGTCATT	TCCAGTCA TTGGTCATT	0,0	NA	NA	NA	NA
Ots_TCT A-58	C	T	ACCAGTACCTAAACGT TAGAAAGCAA	CGTTAGTTAGCTAT GTCTGAAAGGCA	CTGCCATGA AGTGCTAG	TGCCATGA AATGCTAG	0,0	NA	NA	Ots02	89930 26
Ots_MH C2	T	G	GTCCTCAGCTGGGTCA AGAG	GTAGTGGAGAGCA GCGTTAGG	CTGGAGCGT TTCTGTA	CTGGAGCG TGTCTGTA	0.5, 0	NA	NA	NA	NA
Ots_1100 64-383	C	T	AACAAAGAATGTTAAA CACCAAACAGGAA	GTGCAAGGGACCTA GCTAATCC	CTACGTAAT GAACGTTAG CT	ACGTAATG AACATTAG CT	0,0	NA	NA	Ots27	81410 61
Ots_U21 2-158	G	A	CCCCATATGAGACGCT ACAGTAATG	CAAATGCCCTCTAA GCAGACCTT	CTGGAAGA AGGCCTC	CTGGAAAA AGGCCTC	1.5, 0	NA	NA	Ots27	14522 192
Ots33_19 359879	T	C	AGCGCCTGTTTTACAT AAACACTT	GTGAGTACCGTAAA GACTGAGCAA	AAATAAAC GCTGGGTCT AATT	AAATAAAC GCCGGGTC TAATT	0,0	NA	NA	Ots33	19359 879
Ots2_382 64269	A	C	GTATGAGTTGTGTGGT TGCAATGT	CTCTAGCCTATTGC ACAATGTCC	TCCCTTGTC TATGGTATA TCT	TCCCTTGTC TCTGGTAT ATCT	0,0	NA	NA	Ots02	38264 269
Ots18_34 26299	T	A	TTATTTTGGGCTTCATA TGGTTCT	GGTCATGATGTTGA TATTTTTGGA	AATGCCATT TTGT	AAAGCCAT TTTGT	0,0	NA	NA	Ots18	34262 99
Ots_U51 21-34	A	G	CCAGAGGTTAGATGGC CCTTT	CTGAGCCAGAACCA CAAATTGAATT	AGGGTCTCA TGCTCCCT	AGGGTCTC GTGCTCCCT	0,0	NA	NA	Ots05	20893 356
Ots_crRA D60620- 51	A	G	CAGGCAGTCACTGAGT CCG	TTTGAGCACCGTTT CCGA	GTACGGAA AAAACA	GTACGGGA AAAACA	0,0	NA	NA	Ots21	24004 835
Ots_ARN T	G	T	CCACTGGCTGTGGAGC TT	GGGTTCAGTGATAG TTGGGCAAAT	TACAGATGT CATTTTAC	CTACAGAT GTAATTTTA C	2.2, 0	NA	NA	Ots23	24857 375

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Ots_GH2	A	T	GCGTACTGAGCCTGGATGACA	CCCCCAGGTTCTGGTAGTAGTTC	TGACTCTCAGCA[TA]CTG	TGACTCTCTGCA[TA]CTG	1.8,0	NA	NA	NA	NA
Ots_IL11	T	C	CCTCCAGATGAGACCCACTCT	CAAAATGGTGCTCAAACGACTTCA	AGCTCCATGCGGACT	AGCTCCACGCGGACT	0,0	NA	NA	Ots20	20625334
Ots_118205-61	T	C	CCATACAGCCAGTCCAGGTG	ACTGGACAGGGCTGGGT	TAGTAGCCCCTACACCTC	TAGCCCCTGCACCTC	0,0.4	NA	NA	Ots33	32594959
Ots_crRAD26081-28	T	G	GGGAGAGGGAGACGTGGA	TCACCAGCTCCTCCTCCTC	TGGAGGTGGAGGAG	TGGAGGGGGAGGAG	0,0	NA	NA	NA	NA
Ots28_11210919	C	T	AGTGCTCCATGCTGGAGTTT	GATGAAGCAGAAGGAGAGGCT	GACCTCAAGCAGTCAG	GACCTTAAGCAGTCAG	0,0	NA	NA	Ots28	11210919

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Section 2: Genetic Baseline Expansion

Introduction

Distinct population aggregates of Chinook Salmon (*Oncorhynchus tshawytscha*), steelhead trout (*O. mykiss*), and the species *O. nerka* (Sockeye Salmon and kokanee)*,* have evolved through the cumulative effects of selection and genetic drift (Waples 1991). The homing behavior (philopatry) displayed by Pacific Salmon means that fish typically return to spawn in their natal rearing sites or stream of origin. This distinctive life history attribute can significantly restrict gene flow, shape regional variation, and influence demographics among naturally reproducing populations (Hasler and Scholz 1983; McIssac and Quinn 1988; Quinn *et al.* 1991). Genetic differentiation is most easily resolved among populations that are geographically distant, where degree of gene flow is generally correlated with relative migration distances and adjacency in stream networks. However, local adaptations and the distribution of suitable spawning habitat within stream networks may influence finer (regional) scale genetic structure among watersheds in close proximity (Beacham *et al.* 2006; Matala et al. 2012). The natural phenomenon of immigration or straying (a homing miscue) buffers the loss of genetic diversity in salmon populations (Milner and Bailey 1989), but the rate of straying exhibited by wild fish is generally low (Quinn 1993; Heard *et al.* 1995) and genetic structure between populations may persist despite moderate gene flow from straying (e.g., Neville *et al.* 2007). Some evidence indicates that hatchery-origin fish exhibit a higher rate of straying which may be affected by changes is fish passage protocols, transport through the hydro system, artificial rearing practices, or inadequate acclimation (imprinting to natal waters by juvenile salmon). An elevated rate of immigration between populations may erode local adaptations, and lead to changes in spatial and temporal variability within and/or among populations (Hess and Matala 2013; Hess et al. 2016a; Matala et al. 2017).

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

habitats such as variation in local climates or temperatures (Dionne et al. 2008; Narum et al. 2008a; Micheletti et al. 2017). Although local adaptation may be inferred from landscape genetics (Olsen et al. 2010; Blankenship et al. 2011), inferences based primarily on neutral genetic differentiation risk incorrectly identifying the underlying processes affecting population distinctions (Funk et al. 2012; Landguth & Balkenhol 2012). Techniques such as outlier detection methods, and genome wide association studies (GWAS) based on DNA sequence variation provide evidence of non-neutral population structure or adaptive variation (markers associated with run timing; Hess et al. 2016b). Such applications in genetic monitoring allow a more resolved understanding of genetic differentiation beyond what can be concluded from neutral loci alone (Narum et al. 2010b; Matala et al. 2011; Ackerman et al. 2012, Bourret et al. 2013). Putative non-neutral population differentiation can then be interpreted in the context of contemporary risks and vulnerabilities (e.g., climate change) for salmonid populations in the Columbia River Basin, revealing highly correlative relationships between genetic variation and the physical environment (see Limborg et al 2011). This additional information may ultimately influence conservation criteria for delineating populations across diverse landscapes.

Project objectives, time line 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, 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. myiss*), have been well characterized and have been used extensively for genetic stock identification (GSI) as described in Hess et al. (2015) and Hasselman et al. (2016). Our most recent efforts focus on expanding genetic characterizations throughout the basin that will provide information about adaptive potentials and natural selective forces contributing to stock structure. Next generation sequencing technologies continue to be employed by the CRITFC genetics lab in order to expand SNP panels for Chinook Salmon, Coho Salmon, Sockeye Salmon, steelhead trout and Pacific lamprey (Hess et al. 2016c). Methods for genotyping by sequencing (GT-seq) are described in Campbell et al. (2015), and protocols for whole genome resequencing are shown below. Detailed laboratory methods are available in Monitoring Methods: https://www.monitoringmethods.org/Protocol/Details/230 (ID#230; owner Matthew Campbell) and Hess et al. (2012). Methods for whole genome resequencing (Whole Genome Resequencing: Poolseq Individual Barcode v1.0) utilize PoolParty v0.8 (Micheletti and Narum 2018), a bioinformatic pipeline based on bash and R to identify and process SNPs. High-quality SNPs were then used to assess population structure based on principal component analyses (PCA) and pairwise genetic distance displayed in neighbor joining (NJ) trees using the 'adegenet' package in R (Jombart & Ahmed 2011) or in GenAlEx v6.5 (Peakall and Smouse 2006).

Expansion and status of reference baselines for GSI:

Our three primary goals for expanding, maintaining, and evaluating each species-specific baseline are threefold. First, we used genetic stock identification (GSI) analyses for monitoring of fishery returns through the migratory corridor of the Columbia River, including harvest GSI in the lower Columbia River, and fish passage GSI at Bonneville and Lower Granite dams (see sections 3 & 4 of this report). Second, PBT broodstock sampling and genotyping of Columbia River Basin hatcheries has been updated to include the most recent years for continued evaluation of hatchery stock composition in various fisheries and to more accurately account for abundance of natural-origin stocks by identifying unmarked hatchery fish. Third, the sequence/genotypic data are also being applied in various analyses to evaluate selection, including investigations of landscape genetics, and adaptive differentiation among populations.

The GT-seq primer pools developed from RAD-seq data are currently being used for all high throughput genotyping projects, including 5 target species: steelhead trout, Chinook Salmon, Coho Salmon, Sockeye Salmon, and Pacific Lamprey. Currently we do not utilize reference baselines for GSI of either Coho Salmon or Pacific Lamprey, and in 2019 there were no updates to the reference populations in our GSI baseline for Chinook Salmon and Sockeye Salmon. The most recent marker panels are described in Section 1. Testing of the reference baseline for GSI based on the expanded SNP marker panel for steelhead trout is described in Section 3.

In addition, we are using whole genome resequencing methods that pool samples (Pool-seq; Schlotterer et al. 2014) to generate reference baselines with millions of SNPs for several species, Chinook Salmon (Table 3), Coho Salmon (Table 4), and *O. mykiss* (Table 5). Allele frequencies from millions of SNPs will be analyzed to detect statistically significant regions of the genome associated with specific traits or adaptation to environmental factors. Putatively neutral regions of the genome are also useful for standard phylogeny and demographic analyses of populations. Therefore, there are multiple objectives that can be accomplished with these Pool-seq reference baselines including identifying novel SNPs that can be used for improved accuracy and precision of future GSI and PBT applications. These reference baselines comprised of millions of SNPs thus fit two of the main objectives for this project: SNP discovery and expand and create baselines.

Table 3. Creation of a Chinook Salmon SNP baseline by whole genome resequencing of pools of samples

Pool Seq Library ID	Number of reads (R1)	Mean Coverage	ID	Collection	(n)	Lineage	Reporting Groups
L-0730	438,161,235	35.02	OTS01	Big Creek Tule	71	Rogue	01_YOUNGS
L-0731	203,076,142	16.26	OTS03	Kalama R spring-run	93	LC	02_WCASSP
L-1037	203,899,979	16.07	OTS05	Elochoman R fall-run	86	LC	03_WCASFA
L-0732	241,863,213	14.64	OTS06	Lewis R fall-run	68	LC	03_WCASFA
L-1067	214,421,199	19.45	OTS12	White Salmon fall-run	78	LC	05_SPCRTU
L-0736/L-0736_2	751,365,978	64.28	OTS13	Spring Creek NFH tule fall-run	94	LC	05_SPCRTU
L-0737	248,031,203	21.27	OTS16	Warm Springs R spring-run	93	ST	07_DESCSP
L-0756	148,429,490	11.86	OTS17	John Day North Fork-Main Stem	52	ST	08_JOHNDR
L-0739	479,879,641	36.47	OTS18	Middle Fork John Day R spring-run	36	ST	08_JOHNDR
L-0740	139,194,175	9.99	OTS19	North Fork John Day R spring-run	39	ST	08_JOHNDR
L-0741_A	196,168,023	12.61	OTS20	American R spring-run	62	ST	09_YAKIMA
L-0906/L-0733/L-0733_Test/L-0876	208,041,237	16.89	-	Methow R spring-run	87	ST	10_UCOLSP
L-0742	340,007,427	14.54	OTS22	Winthrop NFH spring-run	83	ST	10_UCOLSP
L-0743	277,739,324	24.25	OTS24	Wenatchee R spring-run	51	ST	10_UCOLSP
L-0745	221,784,271	16.25	OTS26	Tucannon River spring-run	52	ST	11_TUCANO
L-1038	205,605,681	17.82	OTS28	Lostine R spring-run	41	ST	12_HELLSC
L-0747	279,162,633	21.60	OTS29	Grande Ronde R spring-run	30	ST	12_HELLSC

L-1069	195,959,654	16.30	OTS32	Red R spring-run	45	ST	12_HELLSC
L-0749	468,738,121	36.61	OTS33	Powell R spring-run	94	ST	12_HELLSC
L-0748	212,015,624	18.42	OTS30	Imnaha R spring-run	76	ST	12_HELLSC
L-1068	200,911,545	15.92	OTS31	Lolo Cr spring-run	48	ST	12_HELLSC
L-1087	194,515,174	17.94	OTS34	Rapid R Hatchery	96	ST	12_HELLSC
L-1070	217,481,702	19.89	OTS35	South Forth Salmon R spring-run	45	ST	13_SFSALM
L-0751	248,736,026	18.17	OTS37	Secesh R spring-run	90	ST	13_SFSALM
L-0752	570,363,043	49.47	OTS38	Chamberlain Cr spring-run	78	ST	14_CHMBLN
L-0753	238,267,170	10.02	OTS39	Big Cr spring-run	48	ST	15_MFSALM
L-1059	248,813,713	21.73	OTS41	Loon Cr spring-run	42	ST	15_MFSALM
L-0754	189,279,625	14.94	OTS43	Bear Valley Cr spring-run	33	ST	15_MFSALM
L-0755	218,687,602	20.14	OTS45	Marsh Cr spring-run	44	ST	15_MFSALM
L-1085	207,691,679	14.92	OTS40	Camas Cr spring-run	60	ST	15_MFSALM
L-1086	608,135,302	54.51	OTS42	Sulphur Cr spring-run	35	ST	15_MFSALM
L-1105	210,570,014	18.39	OTS44	Capehorn Cr spring-run	60	ST	15_MFSALM
L-0757	188,391,901	17.82	OTS47	Lemhi R spring-run	95	ST	16_UPSALM
L-0758	141,386,850	9.71	OTS48	Pahsimeroi R spring-run	92	ST	16_UPSALM
L-1057	203,885,206	18.56	OTS49	East Fork Salmon R spring-run	96	ST	16_UPSALM
L-1080	243,282,312	20.16	OTS50	Salmon R spring-run	61	ST	16_UPSALM
L-1060	239,722,545	14.02	OTS51	West Fork Yankee Fork spring-run	93	ST	16_UPSALM
L-0760	276,701,035	18.50	OTS53	Sawtooth Hatchery weir spring-run	91	ST	16_UPSALM
L-1106	208,349,688	20.87	OTS52	Valley Cr spring-run	42	ST	16_UPSALM
L-0761	503,337,440	32.75	OTS55	lower Yakima R fall-run	46	OT	18_UCOLSF
L-0762/L-0966/L-0967	476,295,447	32.01	OTS57	Wenatchee R summer-run	122	OT	18_UCOLSF
L-0763/L-0877/L-0897/L-0904	482,651,780	24.78	OTS59	Methow R summer-run	136	OT	18_UCOLSF
L-0764	215,478,389	17.03	OTS60	Lyons Ferry weir fall-run	92	OT	19_SRFALL

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

Stock	n	Location	Region (BPA subbasin)	Lineage
Wenatchee	282	Leavenworth NFH	Wenatchee	Oki-Lower Columbia
Bonneville Dam	175	Bonneville Dam	Mixed	Mixed

Table 5. 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	Prop. Geno. @ Dep.*	
Coastal	02_LOWCOL	L. Columbia	Cowlitz	Cowlitz	Cowlitz R, Coweeman R	95	257,455,270	0.61	1
Coastal	02_LOWCOL	L. Columbia	Hood	EF Hood	EF Hood R	48	260,113,702	0.62	1
Coastal	02_LOWCOL	L. Columbia	Hood	EF Hood	Parkdale Fish Facility	83	219,546,080	0.51	1
Coastal	02_LOWCOL	L. Columbia	Hood	WF Hood	WF Hood R	79	212,615,249	0.45	2
Coastal	02_LOWCOL	L. Columbia	Lewis	Lewis	EF Lewis R	78	325,463,369	0.65	1
Coastal	03_SKAMAN	L. Columbia	Washougal	Washougal	Skamania Stock	60	250,089,125	0.58	1
Coastal	04_WILLAM	L. Columbia	Willamette	Willamette	Eagle Cr	61	254,529,741	0.58	1
Coastal	04_WILLAM	L. Columbia	Willamette	Willamette	Little Rock, Mad Crks	50	265,050,782	0.55	1
Coastal	05_BWSALM	L. Columbia	Big White Salmon	Big White Salmon	Big White Salmon R	95	194,626,391	0.48	2
Inter-mediate	06_KLICKR	L. Columbia	Klickitat	Klickitat	Swale, Brush, Dead Canyon, Synder, White, Tepee, Fish Lake Crks	95	227,020,456	0.52	2
Inland	07_MGILCS	L. Columbia	Columbia Gorge	Columbia Gorge	Mill Cr	96	232,750,154	0.56	1
Inland	07_MGILCS	L. Columbia	Columbia Gorge	Columbia Gorge	Fifteenmile Cr	92	170,322,546	0.62	3
Inland	07_MGILCS	L. Columbia	Deschutes	Deschutes	Warm Springs R	95	262,227,329	0.61	1
Inland	07_MGILCS	L. Columbia	John Day	John Day	MF John Day R, Granite, Rudio, Wall, Trail Crks	95	285,409,446	0.58	1
Inland	07_MGILCS	L. Columbia	John Day	MF John Day	Upper John Day R, Beech, Belshaw, Canyon Crks	69	246,704,439	0.57	1
Inland	07_MGILCS	L. Columbia	John Day	SF John Day	Murderers, Deer, Black Canyon Crks	96	224,529,764	0.57	1
Inland	07_MGILCS	L. Columbia	Middle Columbia	Middle Columbia	Rock, Squaw Crks	91	216,427,544	0.61	3
Inland	07_MGILCS	L. Columbia	Umatilla	Umatilla	Umatilla R	70	236,157,293	0.54	2
Inland	07_MGILCS	L. Columbia	Walla Walla	Walla Walla	Walla Walla R, Touchet R, Yellowhawk Cr	95	158,223,069	0.48	3
Inland	07_MGILCS	Snake	Asotin	Asotin	Asotin Cr	60	227,071,819	0.57	1
Inland	07_MGILCS	Snake	Asotin	Asotin	George Creek	58	321,868,839	0.66	1
Inland	07_MGILCS	Snake	Clearwater	L Clearwater	Little Bear Cr	46	267,109,802	0.60	1
Inland	07_MGILCS	Snake	Clearwater	L Clearwater	Sweetwater Cr	51	224,853,521	0.53	1
Inland	07_MGILCS	Snake	Clearwater	L Clearwater	Potlatch R	50	217,298,385	0.51	1
Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	Big Canyon Cr	95	251,726,901	0.59	1

Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	Catherine Cr	91	199,865,574	0.53	2
Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	Joseph Cr	88	240,989,824	0.52	1
Inland	07_MGILCS	Snake	Grande Ronde	Grande Ronde	upper Grande Ronde R	58	190,569,290	0.61	3
Inland	07_MGILCS	Snake	Imnaha	Imnaha	Gumboot Cr	38	233,911,089	0.54	1
Inland	07_MGILCS	Snake	Imnaha	Imnaha	Lightning Cr	95	319,903,348	0.66	1
Inland	07_MGILCS	Snake	Imnaha	Imnaha	Little Sheep Cr	76	235,566,015	0.53	1
Inland	07_MGILCS	Snake	Lower Snake	Lower Snake	Alpowa Cr	53	287,842,645	0.63	1
Inland	07_MGILCS	Snake	Salmon	L Salmon	Little Salmon R, Hazard, Boulder Crks	95	248,041,850	0.59	1
Inland	07_MGILCS	Snake	Salmon	L Salmon	White Bird Cr	50	200,302,136	0.46	2
Inland	07_MGILCS	Snake	Tucannon	Tucannon	Tucannon R	42	214,476,660	0.55	1
Inland	07_MGILCS	Snake	Umatilla	Umatilla	Minthorn Springs	74	222,263,607	0.54	1
Inland	08_YAKIMA	U. Columbia	Yakima	Yakima	Naches R, Nile Cr	38	181,114,635	0.49	3
Inland	08_YAKIMA	U. Columbia	Yakima	Yakima	Satus R	67	208,951,362	0.49	2
Inland	08_YAKIMA	U. Columbia	Yakima	Yakima	Teanaway R, Big Cr, Roza Dam	95	384,909,116	0.69	1
Inland	09_UPPCOL	U. Columbia	Entiat	Entiat	Entiat R	43	336,470,474	0.65	1
Inland	09_UPPCOL	U. Columbia	Methow	Methow	Winthrop NFH	93	180,992,366	0.46	2
Inland	09_UPPCOL	U. Columbia	Okanogan	Okanogan	Bonaparte, Salmon, Omak Crks	95	278,354,930	0.58	1
Inland	09_UPPCOL	U. Columbia	Wenatchee	Wenatchee	Chiwaukum Cr	54	227,418,107	0.56	1
Inland	10_SFCLWR	Snake	Clearwater	SF Clearwater	Clear Cr	61	243,826,940	0.59	1
Inland	10_SFCLWR	Snake	Clearwater	SF Clearwater	Crooked R	86	216,426,527	0.51	1
Inland	10_SFCLWR	Snake	Clearwater	SF Clearwater	Tenmile Cr	60	288,038,275	0.64	1
Inland	11_UPCLWR	Snake	Clearwater	Lochsa	Canyon, Deadman Crks	68	285,197,311	0.61	1
Inland	11_UPCLWR	Snake	Clearwater	Lochsa	upper Lochsa R	72	129,797,910	0.57	3
Inland	11_UPCLWR	Snake	Clearwater	Selway	Little Clearwater R	65	236,963,840	0.55	1
Inland	11_UPCLWR	Snake	Clearwater	Selway	upper Selway R	51	111,568,814	0.49	3
Inland	11_UPCLWR	Snake	Clearwater	Selway	White Cap Cr	72	264,031,261	0.60	1
Inland	12_SFSALM	Snake	Salmon	SF Salmon	Johnson Cr	95	201,270,498	0.48	2
Inland	12_SFSALM	Snake	Salmon	SF Salmon	Lick Cr	70	200,066,360	0.56	2
Inland	12_SFSALM	Snake	Salmon	SF Salmon	Secesh R	30	263,042,376	0.60	1
Inland	12_SFSALM	Snake	Salmon	SF Salmon	East Fork SF Salmon R	53	126,942,745	0.56	3
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Bargamin Cr	60	189,953,336	0.53	2
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Big, Rush Crks	95	328,230,174	0.67	1
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Loon Cr	51	320,069,394	0.65	1
Inland	13_MFSALM	Snake	Salmon	MF Salmon	Marsh Cr	60	334,274,383	0.67	2
Inland	14_UPSALM	Snake	Salmon	NF Salmon	Sawtooth Hatchery	47	241,483,030	0.57	1
Inland	14_UPSALM	Snake	Salmon	NF Salmon	EF Salmon R	51	304,068,477	0.64	1
Inland	14_UPSALM	Snake	Salmon	NF Salmon	Yankee Fork Salmon R	58	191,268,742	0.52	2

| Inland | 14_UPSALM | Snake | Salmon | NF Salmon | Morgan Cr | 39 | 109,730,025 | 0.50 | [3] |
| Inland | 14_UPSALM | Snake | Salmon | NFSalmon | Lemhi R, Bear Valley Cr | 95 | 225,800,707 | 0.51 | [2] |

*proportion of draft genome covered at a given depth of 10X:
[1] 100bp trim, min depth 15; [2] 50bp trim, min depth 15; [3] 50bp trim, min depth 10

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 10, Figure 14, Appendix 6, Appendix 7, and Appendix 8) to include Chinook Salmon, steelhead, and Coho Salmon broodstocks in all hatcheries above Bonneville Dam using expanded SNP panels of 343 loci for Chinook Salmon, 368 loci for steelhead trout and 257 loci for Coho Salmon. Each year the expansion effort is integrated with existing PBT baselines as data comes available (e.g., Chinook salmon, Appendix 4).

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 10. Chinook Salmon, PBT hatcheries. Numbers correspond to map ID and hatchery descriptions (Appendix 6).

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 2019 report period included spawn year 2017 for some lower Columbia River hatcheries, but primarily broodyear 2018 was genotyped for most hatcheries. The total numbers of fish genotyped for PBT baselines in 2019 included n=16,529 spring Chinook Salmon, n=2,563 upper Columbia summer Chinook Salmon, n=28,514 fall Chinook Salmon (Appendix 4), n=4,722 steelhead trout (Appendix 5), and n=1,758 Coho Salmon (Appendix 5). DNA was extracted using modified Chelex extractions and Qiagen DNeasy 96 kits. Extracted genomic DNA was genotyped at 343 SNP loci for Chinook Salmon, 368 SNP loci for steelhead trout, and 257 SNP loci for Coho Salmon using a GTseq protocol: (https://www.monitoringresources.org/Document/Method/Details/5446).
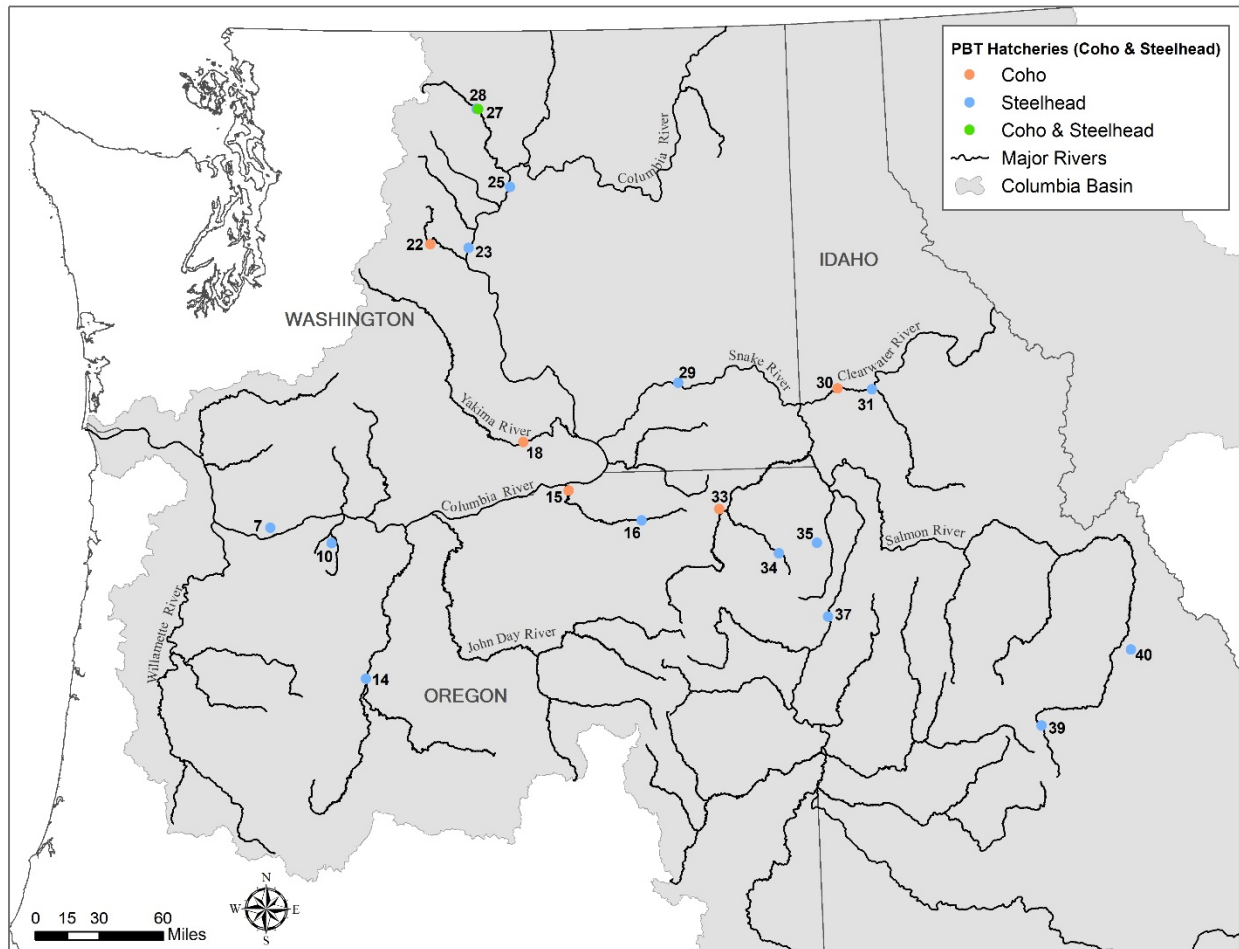
Figure 11. Steelhead and Coho Salmon, PBT hatcheries. Numbers correspond to map ID and hatchery descriptions (Appendix 7, Appendix 8).

Hatchery offspring that are subsequently sampled either as juveniles or adults (e.g., in a fishery) are then PBT assigned back to spawned parents which provides the individual age and specific hatchery of origin for each offspring.

Discussion

1. Over the course of the Genetic Assessment project we have compiled extensive data sets
2. of SNP genotypes for Chinook Salmon steelhead trout and *O. nerka,* and continue to improve
3. resources for Coho Salmon and Pacific Lamprey. The populations we have evaluated span
4. diverse regions in the Columbia River Basin (including the Snake River Basin). We continue to
5. update and maintain SNP reference baselines for evaluation of these species in future
6. generations. This long-term strategy informs harvest management and assures the greatest
7. likelihood of discerning temporal variation among reproductively distinct species aggregates
8. (Waples 1991), while monitoring population viability related to demographic trends that occur
9. locally and/or regionally. Philopatry (Quinn et al. 1991, Hendry et al. 2003) and hatchery
10. supplementation activities (Ford et al. 2006; Hard & Heard 1999) play a major role in how
11. genetic divergence and differentiation is distributed geographically. For managing sustainable
12. fisheries, it is necessary to understand the magnitude of influence that these and other factors
13. have on our ability to differentiate populations, both qualitatively (phenotypes; landscapes) and
14. quantitatively (e.g., genetic stock identification). This becomes particularly important where
15. mixed stock fisheries may consist of both ESA listed and unlisted populations, and where
16. differential harvest may have the greatest impact on specific populations. Our current efforts
17. have largely focused on expanding numbers of markers and non-neutral markers associated with
18. maturation. However, loci for adaptive divergence (landscape genetics) remains as one of our
19. primary objectives for strengthening our understanding of non-neutral genetic variation among
20. populations. Data collected through whole genome resequening and GT-seq techniques has
21. yielded large numbers of potential SNPs, and demonstrated their utility for characterizing
22. adaptive variation, and identifying environmental and life history related variables that are likely
23. to have significant influence on allele frequencies (e.g., precipitation, temperature, run-timing.;
24. Hecht et al. 2015, Hess et al. 2016b; Micheletti et al. 2017; Narum et al. 2018; Micheletti et al.
25. 2018).The expansion efforts reported here also provided improved ability to differentiate stocks
26. on regional and local scales through application of GSI and PBT methods.
27. Collections of *O. tshawytscha*, *O. mykiss*, and *O. nerka* have been chosen for baseline
28. expansion based on availability, novelty, and in accordance with our goal of reaching complete
29. coverage of extant stocks within the Columbia River Basin. Priority collections for all three
30. species have been identified as those important to basin-wide harvest and hatchery management,
31. particularly in tribal fisheries. This includes major supplementation stocks for all three species:
32. lower Columbia, ocean-type, and stream-type lineages of Chinook Salmon, inland and coastal
33. lineages of steelhead trout, and the anadromous (Sockeye Salmon) and land-locked (kokanee)
34. forms of *O. nerka*. Species-specific reference baselines may include life history variants such as
35. potentially distinct populations of resident *O. mykiss* (Narum et al. 2008a; Narum et al. 2011).
36. The application of GSI in fisheries continues to inform managers on several fronts, including:
37. harvest management, abundance estimates, life history distinctions and conservation needs.
38. Moreover, PBT is being used for multiple purposes including validation of assigned origins
39. using GSI. In fact, PBT frequently reveals substantial numbers of unmarked hatchery-origin fish
40. that are incorrectly identified as wild in the field. Future efforts for baseline expansion include
41. compiling allele frequencies for millions of SNPs from whole genome resequencing that can be
42. drawn from at any time should the need for more markers be necessary. An example of such
43. need is basin-wide coverage to account for stock transfers or reintroductions throughout the
44. basin.

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Appendix 3. *Populations represented in the expanded GT-seq SNP panel for steelhead trout.*

pop	subbasin	location	latitude	longitude
Coastal Lineage				
Grays	Grays	Gray R.	46.2121	-123.3634
Elochoman	Elochoman	Elochoman R.	46.2267	-123.3304
Mill	Elochoman	Mill Cr.	46.1885	-123.1773
Abernathy	Elochoman	AFTC weir	46.2256	-123.1481
Germany	Elochoman	Germany Cr.	46.1901	-123.1238
Cowlitz	Cowlitz	Cowlitz R. at Barrier Dam	46.5026	-122.5881
Kalama (SUM)	Kalama	Kalama R.	46.0329	-122.8703
Kalama (WIN)	Kalama	Kalama R.	46.0329	-122.8703
Lewis	Lewis	North Fork Lewis @ Merwin Dam	45.9568	-122.5551
Eagle	Willamette	Clackamas R. - Eagle Cr.	45.3514	-122.3840
Clackamas (SUM)	Willamette	Clackamas R. - North Fork Dam	45.2417	-122.2817
Clackamas (WIN)	Willamette	Clackamas R. - Eagle Cr.	45.3514	-122.3840
	Willamette	Clackamas R. - Timber Park	45.2994	-122.3506
	Willamette	Columbia R. - mainstem	45.3724	-122.6044
N. Santiam	Willamette	Rock Cr.	44.7467	-122.3953
S. Santiam	Willamette	Wiley Cr.	44.4150	-122.6739
Sandy	Sandy	Still Cr.	45.3309	-121.9158
Washougal	Washougal	Washougal R.	45.3909	-122.0960
BWS Rattlesnake	Big White Salmon	Rattlesnake Cr.	45.7993	-121.4843
	Big White Salmon	BWS screw trap	45.7476	-121.5211
BWS mainstem	Big White Salmon	mainstem (Dam6 relocation)	45.7993	-121.4843
	Big White Salmon	BWS screw trap	45.7476	-121.5211
Skamania	Washougal	Skamania Hatchery	45.6227	-122.2175
Inland Lineage				
Fifteenmile	Fifteenmile	Fifteenmile Cr.	45.4509	-121.1244
Deschutes	Deschutes	Deschutes R. - Trout Cr.	44.8214	-121.0872
	Deschutes	Warm Springs R.	44.8609	-121.2444
	Deschutes	Warm Springs R. - Mill Cr.	44.8647	-121.4222
Klickitat	Klickitat	Dillacort Cr.	45.7414	-121.2222
	Klickitat	Wheeler Cr.	45.7951	-121.1928
	Klickitat	Swale Cr.	45.8091	-121.0652
	Klickitat	Snyder Cr.	45.8247	-121.1565
	Klickitat	Little Klickitat R.	45.8271	-120.8181
	Klickitat	Bowman Cr.	45.8452	-121.0421
	Klickitat	Dead Canyon	45.9423	-121.1439
	Klickitat	Summit Cr.	45.9876	-121.1255
	Klickitat	White Cr.	46.0133	-121.1500
	Klickitat	Trout Cr.	46.0378	-121.1994
JohnDay	John Day	Beech Cr.	44.4113	-119.1160
	John Day	Black Canyon Cr.	44.3314	-119.5657
	John Day	Murderer's Cr.	44.3173	-119.5310
	John Day	Deer Cr.	44.1890	-119.5139
	John Day	Middle Fork John Day	44.9129	-119.2964
	John Day	Fox Cr.	44.6156	-119.2941
	John Day	Belshaw Cr.	44.4370	-119.2930
	John Day	Desolation Cr.	44.9397	-118.8379
	John Day	Camp Cr.	44.6891	-118.7966
	John Day	Clear Cr.	44.5888	-118.5068
	John Day	Granite Cr.	44.8383	-118.4770
Umatilla	Umatilla	Iskuulpa Cr.	45.6994	-118.3965
Ahtanum	Yakima	Ahtanum R.	46.5318	-120.6815
Cowiche	Yakima	Cowiche Cr.	46.6288	-120.5708
Naches	Yakima	Little Rattlesnake Cr.	46.7680	-121.0464
	Yakima	N.F. Little Naches R.	47.1090	-121.3201

	Yakima	Pile Up Cr.	46.3274	-121.1537
	Yakima	Nile Cr.	46.8618	-121.0489
	Yakima	Quartz Cr.	45.9457	-120.5097
Satus	Yakima	Dry Cr.	46.1929	-120.6138
	Yakima	Satus Cr.	46.0432	-120.5716
Toppenish	Yakima	Toppenish Cr.	46.3227	-120.8749
Wenatchee	Wenatchee	Levenworth NFH	47.5591	-120.6742
	Wenatchee	Nason Cr.	47.8019	-120.7150
	Wenatchee	Wells Hatchery (LNFH Stock)	47.5591	-120.6742
Methow	Methow	Methow R.	48.0495	-119.9012
Entiat	Entiat	Entiat R. - screw trap	47.6641	-120.2417
Omak	Okanogan	Omak Cr. Adult Weir	48.3957	-119.5043
Touchet	Walla Walla	Touchet R.	46.0340	-118.6836
Dworshak	Clearwater	Dworshak National Fish Hatchery	46.5025	-116.3205
Lochsa	Clearwater	Fish Cr.	46.3316	-115.3461
S. F. Clearwater	Clearwater	South Fork Clearwater R.	46.5061	-116.5491
Catherine	Grande Ronde	Catherine Cr.	45.3070	-117.8660
Joseph	Grande Ronde	Joseph Cr.	46.0416	-117.0017
UpperGR	Grande Ronde	Upper Grande Ronde Adult Trap	45.7314	-117.8640
Wenaha	Grande Ronde	Wenaha R.	45.9453	-117.4513
Lightning	Imnaha	Lightning Cr. Weir	45.6554	-116.7265
Rapid	Salmon	Little Salmon R. - Rapid R.	45.3547	-116.3915
N. F. Salmon	Salmon	North Fork Salmon R.	45.4099	-113.9919
Pahsimeroi	Salmon	Pahsimeroi Fish Hatchery	44.6845	-114.0404
	total			

305 Note: *Each locality is identified by the lineage, subbasin- specific location (e.g. tributary) with*
306 *geographic coordinates, origin, and sample size (n).*

307 **Appendix 4. Chinook Salmon hatchery broodstock sampled for PBT baselines.**

Map ID	Spawning hatchery	Run type	Lineage	Region	Latitude	Longitude	2019 genotyping Year	Sampled	Completed
	Klaskanine (NF brood)	fall (tule)	LC	Col.	46.09	-123.718	na	na	na
	Klaskanine (SF brood)	fall (tule)	LC	Col.	46.09	-123.718	na	na	na
1	Big Creek	fall (tule)	LC	Col.	46.147	-123.581	2015	2018	1886
2	Cowlitz Salmon	fall (tule)	LC	Col.	46.511	-122.629	2015	2017	1929
2	Cowlitz Salmon	spring	LC	Col.	46.511	-122.629	2015	2017	1649
3	Toutle	fall (tule)	LC	Col.	46.375	-122.572	2015	2017	167
4	Kalama Falls	fall (tule)	LC	Col.	46.017	-122.733	2016	2017	3460
4	Kalama Falls	spring	LC	Col.	46.017	-122.733	2015	2017	342
5	Lewis River	spring	LC	Col.	45.937	-122.616	2015	2017	964
	Clackamas	spring	LC	Col.	45.296	-122.362	na	na	na
42	Marion Forks	spring	LC	Col.	44.612	-121.948	2018	2018	920
41	South Santiam	spring	LC	Col.	44.416	-122.675	2015	2018	3159
	McKenzie	spring	LC	Col.	44.118	-122.637	na	na	na
	Willamette	spring	LC	Col.	43.745	-122.444	na	na	na
6	Washougal	fall (tule)	LC	Col.	45.653	-122.169	2015	2017	1177
	Bonneville, Tanner Cr.	fall (tule)	LC	Col.	45.633	-121.957	na	na	na
11	Spring Creek NFH	fall (tule)	LC	Col.	45.728	-121.544	2015	2018	6524
9	Little White Salmon NFH	fall	IOT	Col.	45.719	-121.645	2013	2018	1743
15	Umatilla	fall	IOT	Col.	45.913	-119.552	2012	2018	968
12	Klickitat	fall	IOT	Col.	46.041	-121.183	2018	2018	491
18	Prosser	fall	IOT	Col.	46.215	-119.76	2012	2018	87
19	Ringold Springs	fall	IOT	Col.	46.514	-119.259	2016	2018	455
20	Priest Rapids	fall	IOT	Col.	46.647	-119.899	2012	2018	6937
29	Lyons Ferry	fall	IOT	Snake	46.598	-118.226	2011	2018	1879
30	Nez Perce Tribal	fall	IOT	Snake	46.52	-116.66	2011	2018	811
23	Eastbank	summer	IOT	Col.	47.53	-120.293	2012	2018	723
24	Entiat NFH	summer	IOT	Col.	47.698	-120.323	2013	2018	309
25	Wells	summer	IOT	Col.	47.947	-119.871	2012	2018	777
26	Chief Joseph	summer	IOT	Col.	48.001	-119.647	2013	2018	754
9	Little White Salmon NFH	spring	IST	Col.	45.719	-121.645	2013	2018	1644
15	Umatilla	spring	IST	Col.	45.913	-119.552	2012	2018	459
29	Lyons Ferry	spring	IST	Snake	46.598	-118.226	2008	2018	IDFG
30	Nez Perce Tribal	spring	IST	Snake	46.52	-116.66	2008	2018	188
23	Eastbank	spring	IST	Col.	47.53	-120.293	2012	2018	272
26	Chief Joseph	spring	IST	Col.	48.001	-119.647	2014	2018	229
8	Carson NFH	spring	IST	Col.	45.868	-121.974	2012	2018	850
10	Parkdale	spring	IST	Col.	45.525	-121.622	2012	2018	194
12	Klickitat	spring	IST	Col.	46.041	-121.183	2008	2018	197
13	Warm Springs NFH	spring	IST	Col.	44.861	-121.246	2012	2018	307
14	Round Butte	spring	IST	Col.	44.605	-121.277	2012	2018	696
21	Cle Elum SRF	spring	IST	Col.	47.187	-120.976	2012	2018	511
22	Leavenworth NFH	spring	IST	Col.	47.558	-120.674	2013	2018	721
27	Methow	spring	IST	Col.	48.477	-120.205	2012	2018	129
28	Winthrop NFH	spring	IST	Col.	47.558	-120.675	2013	2018	387
33	Lookingglass	spring	IST	Snake	45.732	-117.865	2008	2018	761
31	Dworshak NFH	spring	IST	Snake	46.504	-116.328	2008	2018	IDFG
32	Clearwater	spring	IST	Snake	46.504	-116.328	2008	2018	IDFG
36	Rapid River	spring/summer	IST	Snake	45.354	-116.394	2008	2018	1855
38	SF Salmon, McCall	spring/summer	IST	Snake	44.908	-116.117	2008	2018	IDFG
38	SF Salmon, Johnson Creek	spring/summer	IST	Snake	44.899	-115.492	2008	2018	95
40	Pahsimeroi	spring/summer	IST	Snake	44.684	-114.039	2008	2018	IDFG
39	Sawtooth	spring/summer	IST	Snake	44.15	-114.883	2008	2018	IDFG

308
309
310 * In 2017 adult broodstock for Umatilla were collected/spawned at Ringold Springs.
311 Note: The Map ID indicates the sites of the hatcheries corresponding to Figure 13. Genetic lineage is lower Col.
312 (LC), interior ocean-type (IOT), and interior stream-type (IST). Year refers to the first year of PBT sampling for

313 each hatchery: na – not currently a PBT hatchery. For some hatchery PBT samples, genotyping efforts have begun
314 to backdate collections that were initially archived- the "sampled" field indicates which collection years were
315 genotyped in 2018. The project collaborators at Idaho Department of Fish and Game (IDFG) were responsible for
316 genotyping of Snake River hatcheries (see "completed" column).

Appendix 5. Steelhead and Coho Salmon hatchery broodstock sampled for PBT baselines.

Map ID	Spawning hatchery	Run type	Lineage	Region	Latitude	Longitude	Year	2019 Genotyping Sampled	Completed
1	Big Creek	winter	coastal	Col.	46.147	-123.581	na	na	na
	Abernathy FTC	winter	coastal	Col.	46.226	-123.153	2012	archived	0
	Cowlitz Trout	winter	coastal	Col.	46.511	-122.629	na	na	na
4	Kalama Falls	winter	coastal	Col.	46.017	-122.733	na	na	na
	Merwin	winter	coastal	Col.	45.954	-122.564	na	na	na
	Clackamas	winter	coastal	Col.	45.296	-122.362	na	na	na
	Eagle Creek NFH	winter	coastal	Col.	45.276	-122.202	na	na	na
	Sandy	winter	coastal	Col.	45.407	-122.254	na	na	na
7	Skamania	summer/winter	coastal	Col.	45.652	-122.168	2013	2018	346
10	Parkdale	winter	coastal	Col.	45.525	-121.622	2012	2018	41
14	Round Butte	summer	inland	Col.	44.605	-121.277	2013	2018	906
15	Umatilla	summer	inland	Col.	45.913	-119.552	2012	2018	83
23	Eastbank	summer	inland	Col.	47.53	-120.293	2012	2018	145
25	Wells	summer	inland	Col.	47.947	-119.871	2013	2018	238
27	Methow (Twisp)	summer	inland	Col.	48.477	-120.205	2013	2018	na*
28	Winthrop NFH	summer	inland	Col.	48.477	-120.205	2012	2018	132
29	Lyons Ferry	summer	inland	Snake	46.598	-118.226	2009	2018	IDFG
34	Wallowa	summer	inland	Snake	45.418	-117.302	2009	2018	IDFG
37	Oxbow	summer	inland	Snake	44.971	-116.853	2008	2018	IDFG
31	Dworshak NFH	summer	inland	Snake	46.504	-116.328	2008	2018	1792
40	Pahsimeroi	summer	inland	Snake	44.684	-114.039	2008	2018	1039
39	Sawtooth	summer	inland	Snake	44.15	-114.883	2008	2018	IDFG
35	Little Sheep Creek	summer	inland	Snake	45.477	-116.928	2008	2018	IDFG
	Coho								
15	Umatilla	na	na	Col.	45.913	-119.552	2012	2018	589
18	Prosser	na	na	Col.	46.215	-119.76	2016	2018	579
22	Leavenworth NFH	na	na	Col.	47.558	-120.674	2012	2018	na
28	Winthrop NFH	na	na	Col.	48.477	-120.205	2012	2018	na
31	Dworshak NFH	na	na	Snake	46.504	-116.328	2012	2018	590

* Steelhead Methow Hatchery Twisp stock spawned at Winthrop NFH starting in 2017; not distiguished from Winthrop stock.
Note: The map ID indicates site locations corresponding with Figure 13. Genetic lineage is coastal or inland. Year refers to the first year of PBT sampling for each hatchery: na – not currently a PBT hatchery. Some 2017 PBT samples have been archived awaiting shipment to the Hagerman Genetics Laboratory as of the drafting of this report. The project collaborators at Idaho Department of Fish and Game (IDFG) were responsible for genotyping of Snake River hatcheries (see "completed" column). All Coho broodstocks sampled for PBT broodstock were designated for release of fish upstream of Bonneville Dam.

Appendix 6. Checklist of PBT broodstock collections that comprise the PBT baselines for Chinook salmon from 2008 through 2018.

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

Note: Species-specific collections code along with run type and genetic lineage are provided for both species. Map numbers correspond with Figure 13.
X   Chinook tissues genotyped using 343 SNPs
X   Chinook tissues genotyped using 298 SNPs
X   Chinook tissues genotyped using 96 SNPs
~   Chinook broodstock sampled, spawned at another hatchery and genotyped using 298 SNPs
a   Chinook Lyons Ferry stock consolidated under 'OtsLYON' starting in 2012
b   Chinook Umatilla fall stock spawned at Little White Salmon Hatchery in 2015 & 2016; not distinguished from LWS stock. Broodstock collected/spawned at Ringold Springs in 2017; not distiguished from Ringold stock.
c   Chinook typically spawned at Little White Salmon NFH, but due to low returns in 2018 they were spawned at Klickitat Hatchery.
h   Chinook Warm Springs NFH spring stock spawned at Little White Salmon Hatchery starting in 2015-2017.
N/A   Stock discontinued/non-existent
*   Broodstock not sampled
**   Broodstock sampled, tissues archived until funding identified for processing

Appendix 7. Checklist of PBT broodstock collections that comprise the PBT baselines for steelhead from 2008 through 2018.

Map num.	Hatchery	Species	Code	Run type	Lineage	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018
31	Dworshak National Fish Hatchery	Steelhead	OmyDWOR	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X
35	Little Sheep Creek Hatchery	Steelhead	OmyLSCR	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X
29	Lyons Ferry Fish Hatchery- Touchet	Steelhead	OmyTOUW c	Summer	Interior	*	X	X	X	X	X	X	X	X	X	X
29	Lyons Ferry Fish Hatchery	Steelhead	OmyLYON d	Summer	Interior	*	X	X	X	X	N/A	N/A	N/A	N/A	N/A	N/A
29	Lyons Ferry Fish Hatchery - Grande Ronde	Steelhead	OmyCGRW c	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X
29	Lyons Ferry Fish Hatchery - Tucannon	Steelhead	OmyTUCW c	Summer	Interior	*	X	X	X	X	X	X	X	X	X	X
29	Lyons Ferry Fish Hatchery - Wallowa	Steelhead	OmyWALW	Summer	Interior	N/A	N/A	N/A	N/A	N/A	N/A	N/A	X	N/A	N/A	N/A
37	Oxbow	Steelhead	OmyOXBO	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X
39	Sawtooth Fish Hatchery	Steelhead	OmySAWT	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X
39	Sawtooth Fish Hatchery - East Fork Salmon	Steelhead	OmyEFSW e	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X
39	Sawtooth Fish Hatchery - Squaw Creek	Steelhead	OmySQUW f	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X
40	Pahsimeroi Fish Hatchery	Steelhead	OmyPAHH	Summer	Interior	X	X	X	X	X	X	X	X	X	X	X
34	Wallowa Fish Hatchery	Steelhead	OmyWALL	Summer	Interior	*	X	X	X	X	X	X	X	X	X	X
23	Eastbank Hatchery	Steelhead	OmyEASTBK	Summer	Interior	*	*	*	*	X	X	X	X	X	X	X
27	Methow Hatchery (Twisp)	Steelhead	OmyTWP i	Summer	Interior	*	*	*	*	*	X	X	X	X	~	~
10	Parkdale Fish Facility	Steelhead	OmyPFF	Winter	Coastal	*	*	*	*	X	X	X	X	X	X	X
14	Round Butte Fish Hatchery	Steelhead	OmyRB	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X
7	Skamania Hatchery (Summer)	Steelhead	OmySKH_su g	Summer	Coastal	*	*	*	*	*	X	X	X	X	X	X
7	Skamania Hatchery (Winter)	Steelhead	OmySKH_wi g	Winter	Coastal	*	*	*	*	*	X	X	X	X	X	X
16	Minthorn Springs	Steelhead	OmyUMA	Summer	Interior	*	*	*	*	X	X	X	X	X	X	X
25	Wells Hatchery - On Station	Steelhead	Omy_WEL	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X
25	Wells Hatchery - Okanogan stock	Steelhead	OmyWEL_OKA	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X
25	Wells Hatchery - Omak stock	Steelhead	OmyWEL_OMA	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X
25	Wells Hatchery - Methow stock	Steelhead	OmyWEL_MET	Summer	Interior	*	*	*	*	*	X	X	X	X	X	X
28	Winthrop National Fish Hatchery	Steelhead	OmyWTP	Summer	Interior	*	*	*	*	X	X	X	X	X	X	X

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

360 **Appendix 8. Checklist of PBT broodstock collections that comprise the PBT baselines for Coho Salmon from 2008 through 2018.**

361

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

362 Note: map numbers correspond to sites in Figure 13.
363 X   Coho tissues genotyped at 257 loci
364 *   Samples received, but not genotyped.

365   Section 3: Genetic Stock Identification of Chinook Salmon, Sockeye Salmon, and
366   Steelhead Harvest Mixtures in the Mainstem Columbia River
367

368   ***Introduction***

369   Genetic Stock Identification (GSI) methods have proven to be effective in determining
370   the proportion of stock origin in mixed stock applications of salmonids (Shaklee et al. 1999,
371   Winans et al. 2004, Beacham et al. 2006, and Beacham et al. 2011). These methods have been
372   demonstrated to be useful even at relatively fine geographic scales within the Columbia River
373   Basin (CRB) (Hess et al. 2011, Hess and Narum 2011, Hess et al. 2014). Within the CRB,
374   Chinook salmon consist of three major genetic lineages and steelhead consist of two major
375   genetic lineages that can be further divided into populations that are genetically structured on a
376   finer spatial scale (e.g., Waples et al. 2004; Narum et al. 2010; Blankenship et al. 2011). In this
377   study, we used separate groups of SNP markers to discriminate 19 reporting groups for Chinook
378   salmon, 14 reporting groups for steelhead, and four reporting groups for sockeye salmon.
379   Despite continuous improvements of the power of our Chinook salmon and steelhead
380   baselines in GSI applications (Hess et al. 2014), we have determined that further improvement in
381   the detail of data and accuracy of stock assignments could be made by utilizing a recently
382   developed genetic technology (i.e., parentage based tagging (PBT)), in combination with GSI, in
383   a tiered approach for stock identification (Hess et al. 2016). PBT is an efficient approach for
384   mass tagging of fish. The method is carried out by first genotyping a set of potential parents
385   which then provides the opportunity to assign a set of genotyped offspring to their true parent
386   pair. PBT is currently being utilized on a broad scale in the Columbia River Basin, and was
387   recently (i.e., 2012-present) expanded beyond Snake River hatcheries (Steele et al. 2011) to tag
388   all Chinook salmon and steelhead hatchery broodstock from hatcheries in the CRB above
389   Bonneville Dam. This application has effectively tagged all Snake River hatchery Chinook
390   salmon and steelhead starting with the 2008 brood years, and elsewhere in the CRB above
391   Bonneville Dam beginning with the 2012 brood year. When parent pairs of hatchery fish are
392   identified with PBT, we can provide accurate information including age of the fish and the
393   source hatchery in which its parents were spawned (Steele et al. 2011). We use PBT in this
394   harvest study to identify hatchery-origin fish, and then use GSI to estimate stock-of-origin of all
395   other hatchery fish that were not assigned with PBT and for all natural-origin fish. For sockeye
396   salmon, we no longer rely solely on GSI to determine stock of origin because PBT can be used to
397   identify reintroduced fish to the Yakima River. For the 2018 Chinook harvest, multiple age
398   classes (3-, 4-, and 5-year old fish) can be identified from Lower Columbia, Middle Columbia,
399   and Snake River stocks using PBT (Appendix 6).
400   We continue to employ the genotyping-in-thousands by sequencing (GT-seq) approach
401   that has been developed in our laboratory (Campbell et al. 2015). This approach has increased
402   the cost-effectiveness for genotyping moderate numbers of SNP loci (100s) for relatively large
403   numbers of individuals (1000s), which allows us to run all SNP loci regardless of whether we
404   intend to use primarily PBT analyses or a combination of PBT and GSI. Thus, our projects now
405   benefit from the additional data that comes from genotyping with all available markers (i.e.,
406   increased power for statistical assignment of individuals).
407   Fisheries conducted in the mainstem of the lower and middle Columbia River provide an
408   important application of genetic stock analyses because the fish harvested consist of mixtures of
409   stocks throughout the CRB. Further, mainstem Chinook and Sockeye salmon fisheries represent

410 a majority of the CRB harvest of this species taken by the commercial, sport, and tribal
411 fishermen. In order to help support sustainable fisheries, PBT and GSI can be used to address
412 two primary questions: 1) how are Chinook salmon stocks temporally and spatially distributed in
413 the mainstem Columbia River; and 2) how are these stocks temporally and spatially distributed
414 in the harvests of fisheries. Importantly, we can now estimate abundance of all genetic stocks
415 using the reported catch estimates of each fishery.
416
417
418 *Project objectives and higher-level harvest management questions*
419   Our study had three primary objectives: 1) utilize a combination of PBT and GSI
420 analyses to determine stock composition of Chinook salmon harvested in sport, commercial, and
421 tribal fisheries in the mainstem Columbia River, 2) utilize GSI to estimate stock composition of
422 sockeye salmon harvested above and below Bonneville Dam in commercial, sport, and tribal
423 fisheries, 3) estimate abundance of all stocks based on catch estimates for each fishery. Results
424 from these objectives were used to address:
425
426 **Harvest RM&E: F&W Program Management Question: What are your in-river**
427 **monitoring results and what are your estimates of stock composition and stock-specific**
428 **abundance, escapement, catch, and age distribution?**
429
430   Increasingly, we are tailoring our analyses to address specific questions that fisheries
431 managers have presented to us. For example, in 2012 managers proposed extending the
432 geographic boundary of one of the mark selective spring-run Chinook salmon sport fisheries
433 above Bonneville Dam that occurs at the mouth of the Wind River. This extension created a
434 larger "bubble" boundary at the mouth of the Wind River and was intended to increase Columbia
435 River mainstem fishing access while maintaining targeted focus on Wind River spring-run
436 Chinook salmon. For 2012-2016, we examined the stock composition of the Wind River sport
437 harvest and provided context by comparing stock proportions among the various samples from
438 other fisheries and Bonneville Dam that were analyzed that same year. The Wind River sport
439 fishery has not been sampled since 2017 and could not be included in analyses. However, there
440 is a new research gear (pound net) being tested by the joint states in the fall fisheries below
441 Bonneville Dam. We have included analysis of the 2018 fall pound net fishery to estimate stock
442 abundance of fall Chinook salmon among the clipped fish that were retained (kept) and the
443 unclipped fish that were released. We included in this report the 6th year of analysis of Sockeye
444 salmon fisheries in the Columbia River mainstem. Differences in relative abundance of the three
445 main stocks (Okanagan, Wenatchee, and Snake) present challenges to managing lower river
446 harvest, because of the desire to harvest the highly abundant Okanagan stock around the much
447 less abundant Snake River stock and moderately abundant Wenatchee River stock. Stock
448 composition estimates are expected to help determine how harvest is impacting these various
449 stocks. This year, we identified a stock of reintroduced Sockeye salmon to the Yakima River
450 using PBT and can now estimate the contribution of this reintroduced stock to each harvest of
451 Sockeye salmon and the run at large.
452
453
454 *Time line for completion of objectives*

111

455　　　　Objectives will be ongoing and PBT/GSI results updated each year for harvest analyses
456　of salmonids throughout the accords-funding. As new genetic techniques are developed, they
457　will be applied to this project and results will be compared between years to determine the extent
458　of improvements.
459
460　Our study was not designed to address the following question:
461　**Harvest RM&E: F&W Program Management Question: Can selective fisheries targeting**
462　**hatchery fish or healthy populations reduce impacts on ESA-listed populations?**
463
464　*Accuracy testing of PBT and GSI baselines*
465　　　　Prior to conducting analyses for fisheries harvest collections and mixture samples
466　encountered at Bonneville Dam (Section 4), we assessed the accuracy of our PBT and GSI
467　baselines in assigning Chinook salmon and steelhead to their hatchery brood or reporting group
468　of origin (see Results section).
469

470　***Methods***
471　Methods for estimating stock composition are available at
472　(https://www.monitoringmethods.org/Protocol/Details/229). The Monitoring Methods Protocol
473　is entitled Snake River steelhead and Chinook salmon stock composition estimates (2010-026-
474　00) v1.0.
475
476　*Tissue collection of Chinook salmon and Sockeye salmon*
477　　　　Tissues were sampled from Chinook salmon in 2018 from a total of 9 different mixture
478　sources: the spring-run seasons of the following fisheries: 1) lower river test, 2) lower river sport,
479　and 3) Zone 6 Treaty ceremonial permit, the summer management period harvests of the
480　following fisheries:4) lower river sport, and 5) Zone 6 tribal summer, and the fall-run harvest
481　from 6) the lower river test (pound net), 7) lower river commercial, 8) lower river sport, and 9)
482　Zone 6 tribal fall fishery. Tissues are also collected from steelhead, Chinook salmon, and
483　Sockeye salmon at Bonneville Dam for stock ID (see Section 4). While fisheries generally
484　harvest jack sized Chinook salmon at low rates and do not have specific harvest limits on jacks,
485　jacks do comprise part of the harvest and may be sampled if encountered. Jacks are sampled at
486　the Bonneville AFF trap in the proportion that they are encountered in the sampling. Sampling
487　restrictions at the AFF can result in biases in the size of fish sampled compared to the run at
488　large. Therefore, we split the AFF sample of Chinook salmon into adults and jacks and analyze
489　them separately. Harvest tissues were collected in coordination with existing monitoring
490　programs led by Washington Department of Fish and Wildlife (WDFW) and Oregon Department
491　of Fish and Wildlife (ODFW) and the Yakama Nation. The spring management period Chinook
492　salmon fisheries were sampled below Bonneville Dam in the sport, test fishery, and in the Treaty
493　permit fishery (Figure 12; Table 6). The summer management period fisheries were sampled
494　below Bonneville Dam in the sport fishery, and above Bonneville Dam in the Zone 6 Treaty
495　commercial fishery. Due to limited funds, we analyzed a subset of samples obtained from the
496　various fisheries sampled above and below Bonneville Dam. For all fisheries in which we had to
497　subsample the harvest, we selected fish randomly and with a balanced design across spatial
498　regions. However, each subsample should be tailored to the way the catch is reported for each
499　fishery to accurately represent the geographic and temporal stratification of the CREEL.

500   Stock proportions were estimated and expanded by the catch reported for each fishery
501   source, such that stock abundance could be compared across fisheries. We use the following
502   four main geographic regions (Figure 12): Region A corresponds to our grouping of pre-existing
503   Oregon and Washington state sport fishing zones 1-4 (or commercial zones 4-5), Region B
504   corresponds to our grouping of sport zones 5-10 (or commercial zones 1-3). Here, we do not
505   discriminate between Region 01 and Region 02 in the Zone 6 fishery, because that information
506   did not accompany the samples we received. These sets of groupings were established for this
507   study in order to achieve balanced sampling for analysis of these fishery datasets, as well as to
508   best match the stratification of the reported catch.
509   Non-Treaty fisheries during the spring management period for Chinook salmon are mark-
510   selective based on absence or presence of the adipose fin to distinguish hatchery fish from
511   natural origin fish, respectively. These adipose markings make it possible to have a mark-
512   selective sport and commercial fishery in which only fish with missing adipose fins (hatchery-
513   origin) are legally retained. Fish with intact adipose fins that are caught in these fisheries are
514   released, but mortality rates are unknown from these releases. In addition to sampling hatchery-
515   origin fish from the mark selective commercial and sport fisheries, we were able to obtain
516   samples from non-clipped hatchery and natural origin fish from Bonneville Dam and the Treaty
517   Zone 6 fishery above Bonneville Dam.
518   Tissues were sampled from sockeye salmon in 2018 from three fishery mixture sources:
519   1) lower river sport, 2) Bonneville Dam (see Section 4), and 3) the Treaty fishery in Zone 6. All
520   samples obtained from these fisheries were analyzed.
521
522   *Molecular data*
523   Methods for DNA extraction, DNA amplification, and genotyping of SNP assays using
524   genotyping-in-thousands by sequencing (GT-seq) are available at
525   (https://www.monitoringresources.org/Document/Method/Details/5446). Additional details
526   regarding how 192 SNPs were reduced to 186 SNPs can be found in Hess et al. (2012, 2013).
527   Subsequently, we have reduced our Chinook salmon GSI baseline from 186 SNPs to 179 SNPs
528   (Hess et al. 2019), and further reduced from 179 SNPs to 177 SNPs because we were unable to
529   transition the full set of 186 SNPs to GT-seq protocols and subsequent iterations of our active
530   GT-seq panels. These 177 SNP markers were used for GSI, and for PBT analyses, we used 93 of
531   the SNPs (legacy panel) as well as an expanded panel of 254 SNPs. We used 363 SNP markers
532   for GSI and PBT of sockeye mixtures.
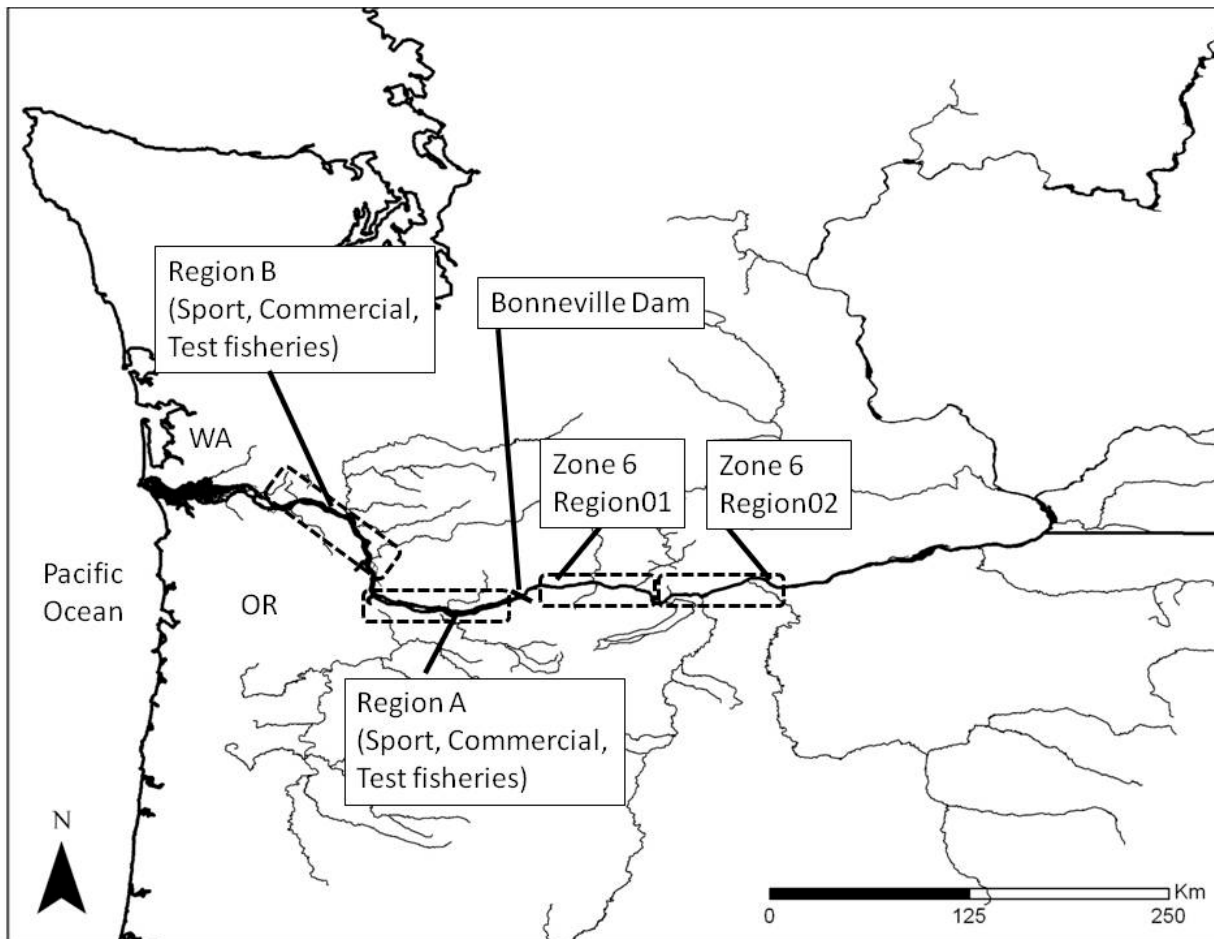
Figure 12. Project scope showing sources of Chinook salmon and Sockeye salmon harvest mixtures that were analyzed using PBT/GSI.

Table 6. Characteristics of Chinook salmon harvest samples by fishery, region, and adipose-clip status by weekly strata in 2018.

Period	Fishery	Region	Clip	Sampled	Genotyped												Spring						Summer										Fall						
						10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
Spring	Sport	A	AD	354	347		8	15	86	125	44						11	27	9	22																
		B	AD	527	526	1	12	46	62	300	35						7	8	16	39																
	Test	B	AD	571	567			2	5	15	37	78	154	191	82	3																					
			AI	86	83				1	7	2	20	21	26	6																						
	Ceremonial	Below_BON	AD	240	235								26	165	44																						
			AI	39	38								2	30	6																						
		ZN6	AD	139	139								6	43	60	30																					
			AI	29	29								2	10	8	9																					
Summer	Sport	A	AD	31	30																7	22				1										
		B	AD	43	42																11	28	2				1									
	Treaty	ZN6	AD	166	165																66	41	30	23	3	2										
			AI	59	58																24	15	13	3		3										
Fall	Commercial	A	AD	291	198																									87	111					
			AI	240	100																									50	50					
	Sport	A	AD	45	45																							2	3		3	23	14			
			AI	174	119																							1	2	2	16	49	49			
		B	AD	33	32																							2	3	10	13	4				
			AI	80	79																							1	17	25	29	6	1			
	Test	B	AD	646	299																								1	190	53	53	2		
			AI	1050	172																								21	88	28	33	2		
	Treaty	ZN6	AD	370	234																							2		2	25	50	66	32	42	15
			AI	1387	456																							3	6	1	53	51	100	89	99	54
				6600	3993	1	22	67	170	464	177	175	253	336	121	39	18	35	25	61	108	106	45	26	3	6	1	11	31	199	578	264	316	125	141	69

539 *PBT Rate Expansion using SCOBI DEUX and SPIBETR functions*
540　　　　The use of PBT adds complexity to analyses when each hatchery broodstock is
541 genotyped at rates less than 100%. Expansion of hatchery-origin adipose-intact fish can lead to
542 bias when we characterize natural-origin stocks by attributes (Figure 13). We have developed
543 and implemented a fully automated method which minimizes the bias that PBT rate expansion
544 can impose (Delomas and Hess, In review). The correction implemented by this method
545 (SPIBETR, Salmonid Prior Information to Balance Expansion from Tag Rates) is illustrated
546 below:
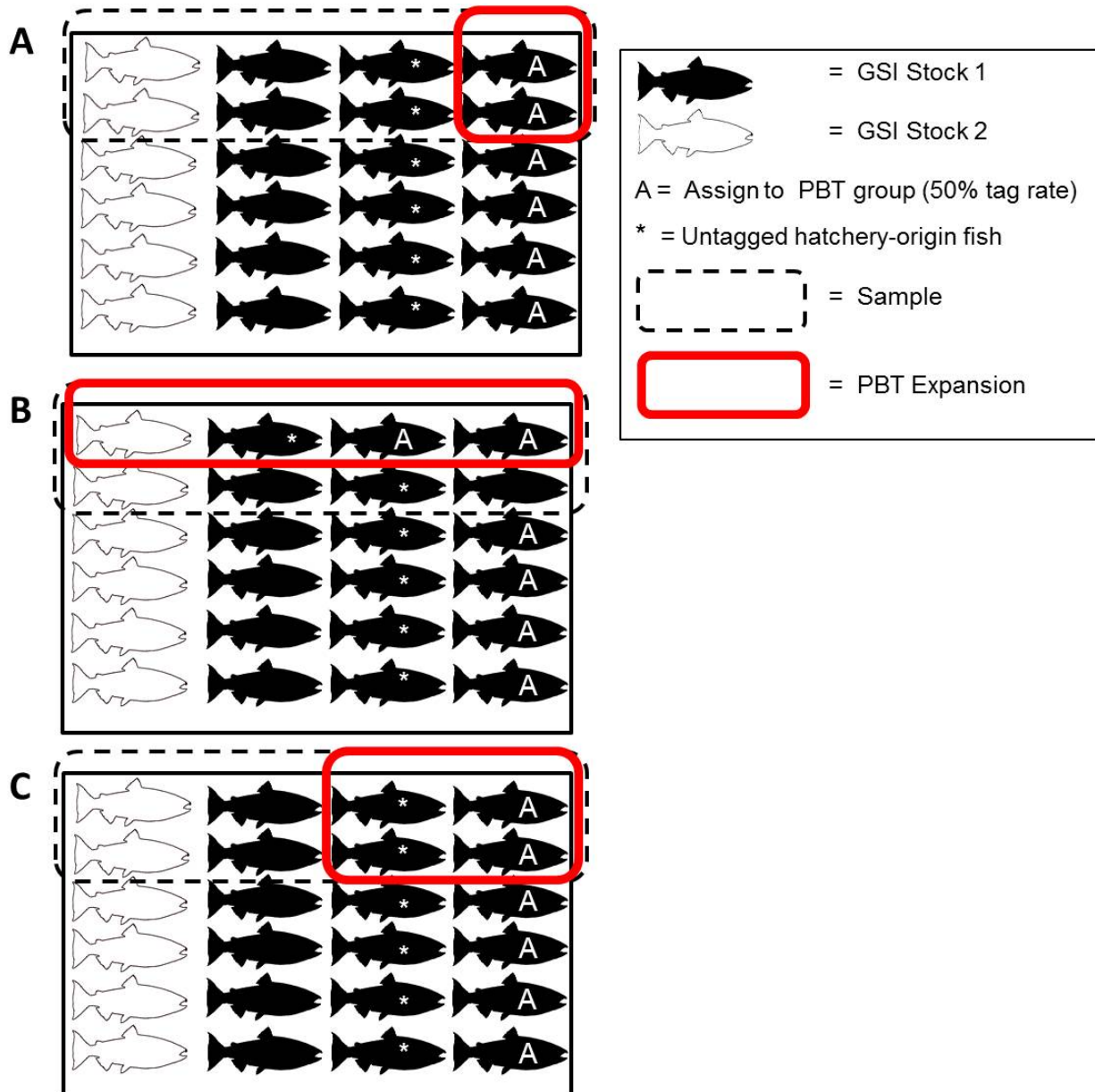
547
548 **Figure 13. Conceptual illustration of the bias correction the SCOBI DEUX method**
549 **provides.**

550

551 In **Figure 13**, each pane shows a mixture of fish consisting of two natural-origin stocks (GSI
552 Stock 1 and 2) and one PBT group with a 50% tag rate. The true proportions are 50% hatchery

116

553 origin, 25% natural-origin GSI stock 1, and 25% natural-origin GSI stock 2. When PBT rates
554 are ignored, we would estimate the mixture to be 25% hatchery origin, 50% natural-origin GSI
555 stock 1, and 25% natural-origin GSI stock 2 (**Figure 13**, A); this estimate is biased low toward
556 the hatchery-origin fish. However, if we were to take PBT rates into account but did not adjust
557 for the GSI information in the mixture, we could end up with estimates that accurately reflect the
558 true proportion of hatchery-origin fish but do not accurately reflect the true stock composition of
559 the natural-origin fish: e.g., **Figure 13**, B: yields an estimate of 50% hatchery origin, 37.5%
560 natural-origin GSI stock 1, and 12.5% natural-origin GSI stock 2. Finally, using the corrections
561 implemented by the SCOBI DEUX and SPIBETR functions, we are able to expand GSI stock 1
562 by PBT rates and correct this expansion by proportionally decreasing the GSI stock 1 in the
563 remaining sample mixture, which yields scenario C (**Figure 13**): the mixture would be estimated
564 to be 50% hatchery origin, 25% natural-origin GSI stock 1, and 25% natural-origin GSI stock 2.
565
566
567 *GSI baselines for Chinook salmon, sockeye salmon, and steelhead*
568
569   Chinook salmon GSI analyses were performed using the updated baseline referred to as
570 "Columbia River Basin Chinook salmon GSI baseline version 3.1" and is available on the
571 FishGen website (https://www.fishgen.net). However, we made on slight modification and
572 decreased the number of SNP markers to 177 that were included in the latest iteration of the GT-
573 seq panel. This baseline consists of 61 collections that are delineated into the following 19
574 reporting groups: Columbia Rogue "01_YOUNGS", West Cascade spring-run "02_WCASSP",
575 West Cascade fall-run "03_WCASFA", Willamette River spring-run "04_WILLAM", Spring
576 Creek Group Tule fall-run "05_SPCRTU", Klickitat River spring-run "06_KLICKR", Deschutes
577 River spring-run "07_DESCSP", John Day River spring-run "08_JOHNDR", Yakima River
578 spring-run "09_YAKIMA", upper Columbia River spring-run "10_UCOLSP", Tucannon River
579 spring-run "11_TUCANO", Hells Canyon spring-run "12_HELLSC", South Fork Salmon River
580 spring-run "13_SFSALM", Chamberlain Creek spring-run "14_CHMBLN", Middle Fork
581 Salmon River spring-run "15_MFSALM", upper Salmon River spring-run "16_UPSALM",
582 Deschutes River fall-run "17_DESCFA", upper Columbia River summer-/fall-run
583 "18_UCOLSF", and Snake River fall-run "19_SRFALL" (Table 7; Figure 14). Reporting groups
584 were primarily determined by the relative genetic similarity among populations according to a
585 phylogenetic analysis, and our previous results demonstrate sufficient power to discern three
586 reporting groups (17_DESCFA, 18_UCOLSF, and 19_SRFALL) among the interior ocean-type
587 collections. In one year, we had grouped all interior ocean-type collections into a single
588 reporting group "Interior_Columbia_R_su/fa" (Hess et al. 2013). Genetic distances were
589 computed from allele frequencies based on Nei's (1972) genetic distance, with the PHYLIP v
590 3.69 (Felsenstein 1989) and 1000 bootstrap replicates were performed. Distances were clustered
591 using the Neighbor – Joining method (Saitou and Nei, 1987), and a consensus tree was
592 constructed (http://evolution.genetics.washington.edu/phylip/) (Figure 15). The clusters are
593 labeled with names of reporting groups used to aggregate the collections based on a combination
594 of factors including genetic similarity, life history, and geographic proximity. Bootstrap support
595 is shown with shaded ovals (Source: Hess et al. 2015).
596   The 10_UCOLSP reporting group includes the following Bonneville pool hatchery
597 stocks: Carson stock (Ots22), and Little White Salmon R. (Ots23) because they are genetically
598 indistinguishable from Upper Columbia R. spring Chinook salmon (includes Walla Walla and

599 Umatilla River stocks). This composite group is notable because inclusion of these Bonneville
600 pool stocks explains why a large proportion of fish from the Wind R. sport fishery should assign
601 to this 10_UCOLSP reporting group. However, the PBT baseline is now able to specifically
602 identify fish from Carson Hatchery and Little White Salmon Hatchery allowing them to be
603 distinguished from fish returning to the upper Columbia R. The 01_YOUNGS reporting group
604 represents an out-of-basin genetic stock (originating from the Rogue R., OR) that is reared within
605 the Columbia R. at Youngs Bay. Basic QAQC was performed to remove duplicate individuals
606 and strays from the reference populations in the baseline. The baseline and reporting group data
607 is available on FishGen.
608   GSI analyses for *O. nerka* utilized a baseline that included sockeye salmon and kokanee
609 populations from throughout the Columbia River basin. This baseline included sockeye
610 populations from the Osoyoos (i.e., Okanogan), Wenatchee, and Redfish Lake (i.e., Snake), and
611 a kokanee population from Lake Whatcom that were included in "Sockeye GSI baseline v1.0,
612 and were shown to accurately discriminate among these major stock (Hess et al 2013). We
613 updated our baseline to included additional kokanee populations from Alturas Lake, Fishhook
614 Creek, Lake Billy Chinook, Meadow Creek, Suttle Creek, Cougar, Gold, North Fork Tieton,
615 Odell, Speylai, Stanley, Warm, Wizard, Wallowa River, and Wallowa Lake, and refer to this as
616 "Sockeye GSI baseline v3.0". The transition to GT-seq required omission of a few loci due to
617 poor genotyping quality with the new protocols. A total of 363 SNPs was used for these
618 analyses.
619   For steelhead, we have the following two GSI baselines available: 1) GSI baseline
620 version 3.3 with 177 SNPs and 2) a new GSI baseline with 335 SNPs. The GSI version 3.3
621 comprises 116 collections from throughout the Columbia River basin that are partitioned into the
622 following 14 reporting groups: 01_WCOAST (Quinault River), 02_LOWCOL (lower Columbia
623 River), 03_SKAMAN (Skamania hatchery releases at three sites in lower Columbia River,
624 Willamette River, and Klickitat River), 04_ WILLAM (Willamette River), 05_BWSALM (Big
625 White Salmon River), 06_KLICKR (Klickitat River), 07_MGILCS (middle Columbia River,
626 Grande Ronde River, Imnaha River, lower Snake River, lower Clearwater River, and lower
627 Salmon River), 08_YAKIMA (Yakima River), 09_UPPCOL (upper Columbia River),
628 10_SFCLWR (South Fork Clearwater River), 11_UPCLWR (upper Clearwater River),
629 12_SFSALM (South Fork Salmon River), 13_MFSALM (Middle Fork Salmon River), and
630 14_UPSALM (upper Salmon River) (see Table 8; Figure 16). Genetic distances were computed
631 from allele frequencies based on Nei's (1972) genetic distance, with the PHYLIP v 3.69
632 (Felsenstein 1989) and 1000 bootstrap replicates were performed. Distances were clustered
633 using the Neighbor – Joining method (Saitou and Nei, 1987), and a consensus tree was
634 constructed (http://evolution.genetics.washington.edu/phylip/) (Hess et al. 2019). The GSI
635 baseline with 335 SNPs comprises 128 collections throughout the Columbia River that are
636 partitioned into 13 reporting groups (**Table 9**), which are all the reporting groups listed in
637 version 3.3 except 01_WCOAST (Quinault River). This 335 SNP baseline is still in the testing
638 phase and will be considered for exclusive use of GSI applications only if it is determined to be
639 more accurate than the existing version 3.3. baseline.
640

641 **Table 7. 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

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Table 8. Results of the leave-one-out analysis for the steelhead GSI 335 SNP baseline.

Reporting group	02_LOWCOL	03_SKAMAN	04_WILLAM	05_BWSALM	06_KLICKR	07.05_FIFTNM	07.1_DESCH	07.2_JDAY	07.3_UMAT	07.4_LOWSNAKE	07.5_IMNA	07.52_GrandeRonde	07.6_LOWCLWR	07.7_LOWSALM	08_YAKIMA	09_UPPCOL	10_SFCLWR	11_UPCLWR	12_SFSALM	13_MFSALM	14_UPSALM	Self	MCGILCS
02_LOWCOL	95.9	3.4	0.4	0.1	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	95.9	
03_SKAMAN	4.8	95.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	95.1	
04_WILLAM	2.7	4.6	92.7	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	92.7	
05_BWSALM	1.5	0.0	0.6	92.7	3.3	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	92.7	
06_KLICKR	1.3	4.3	0.0	1.2	83.5	4.5	0.8	0.0	0.2	1.4	0.0	0.3	0.1	0.1	0.6	0.8	0.2	0.0	0.0	0.0	0.6	83.5	
07.05_FIFTNM	0.7	0.0	0.1	1.1	5.7	49.2	7.4	0.7	2.9	9.9	4.0	5.1	1.6	1.7	1.4	1.8	0.0	0.8	0.0	1.6	4.1	49.2	82.6
07.1_DESCH	0.0	0.0	0.0	0.3	0.4	3.2	65.2	4.1	3.5	5.8	1.2	7.8	2.1	1.0	0.8	2.5	0.2	0.0	0.0	0.2	1.8	65.2	93.9
07.2_JDAY	0.0	0.0	0.0	0.0	0.0	0.8	4.1	58.9	9.0	7.4	3.1	11.0	2.0	0.4	0.8	1.1	0.2	0.0	0.2	0.0	0.8	58.9	96.8
07.3_UMAT	0.0	0.0	0.0	0.0	0.0	1.1	7.2	13.5	36.1	16.7	0.3	12.1	4.1	0.8	4.6	2.5	0.1	0.0	0.0	0.0	0.7	36.1	92.0
07.4_LOWSNAKE	0.0	0.0	0.0	0.0	0.0	1.8	3.8	4.0	8.0	46.5	1.9	11.9	4.9	2.7	1.6	8.1	0.4	0.1	0.0	0.1	4.2	46.5	85.5
07.5_IMNA	0.0	0.0	0.0	0.0	0.0	0.5	3.0	3.2	2.6	9.6	61.6	8.1	2.3	4.5	0.4	1.0	0.5	0.0	0.0	1.0	1.6	61.6	95.5
07.52_GrandeRonde	0.0	0.0	0.0	0.0	0.0	1.2	5.9	8.5	6.0	10.9	2.0	56.8	2.4	1.3	0.3	3.1	0.0	0.1	0.0	0.3	1.2	56.8	95.0
07.6_LOWCLWR	0.0	0.0	0.0	0.0	0.0	0.6	2.8	1.5	3.7	9.3	1.1	9.2	67.0	0.5	0.3	2.1	0.7	0.6	0.1	0.1	0.5	67.0	95.7
07.7_LOWSALM	0.0	0.0	0.0	0.0	0.0	0.2	2.5	0.3	1.8	13.2	3.5	5.3	1.4	61.8	0.0	1.4	0.1	0.0	0.7	2.7	5.1	61.8	90.0
08_YAKIMA	0.0	0.0	0.0	0.0	0.2	0.6	0.8	1.2	1.1	1.3	0.1	1.1	0.4	0.1	92.0	0.9	0.0	0.0	0.0	0.0	0.1	92.0	
09_UPPCOL	0.0	0.0	0.0	0.4	0.6	2.0	2.4	1.4	2.1	15.9	0.9	6.7	2.3	1.4	2.3	59.4	0.0	0.0	0.1	2.2		59.4	
10_SFCLWR	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	88.0	8.9	0.0	0.0	0.3	88.0	
11_UPCLWR	0.0	0.0	0.0	0.0	0.0	0.2	0.1	0.0	0.0	0.1	0.0	0.0	0.6	0.0	0.0	0.0	3.7	94.9	0.0	0.0	0.4	94.9	
12_SFSALM	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.1	0.1	0.2	0.0	0.0	0.0	0.9	0.0	0.0	98.2	0.2	0.1	98.2	
13_MFSALM	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.3	0.3	2.1	0.5	0.4	0.0	0.0	0.0	0.1	0.0	0.0	0.0	91.9	2.8	91.9	
14_UPSALM	0.0	0.0	0.0	0.0	0.2	0.6	1.1	0.3	0.3	7.6	1.5	2.8	1.6	3.7	1.9	3.0	0.4	0.1	0.0	3.5	71.5	71.5	

Note: Reporting group, population ID, population name and samples size used in analysis are provided for each collection in the baseline. The number of correct assignments to reporting group for each population in the baseline are reported (gray shading) and are tallied to provide the number of correct assignments for the reporting group overall (yellow shading). The average proportion of correct assignments to reporting group (across collections) is provided along the diagonal. MCGILCS has been challenging to discriminate smaller groups that comprise the large region. This baseline of 335 SNPs had limited ability (correct assignment <70%) to accurately resolve smaller groups (groups with "07" notation) within MCGILCS. Therefore we also report the correct assignments to the MCGILCS group as a whole (far right column;"MCGILCS").

Table 9. Sample sizes, locations, and reporting groups of steelhead baseline populations for the new panel of 335 SNPs.

Reporting Group	Population	Name	Latitude	Longitude	N
02_LOWCOL	POP001.1	ElochomanR	46.226734	-123.330417	55
	POP001.2	AbernathyCr	46.225600	-123.148100	96
	POP002	CowlitzR	46.502611	-122.588094	131
	POP003	GermanyCr	46.190147	-123.123783	43
	POP004	GraysR	46.367836	-123.581335	40
	POP005	KalamaR_wi	46.032897	-122.870311	41
	POP006	MillCr	46.188517	-123.177297	40
	POP007	NFLewisR	45.956781	-122.555108	92
	POP008	StillCr	45.330870	-121.915750	13
	POP009	WashougalR	45.585126	-122.393031	49
03_SKAMAN	POP010	ClackamasR_su	45.241700	-122.281700	47
	POP011	KalamaR_su	46.032897	-122.870311	42
	POP012	KlickitatRSkamania_su	45.818764	-121.235121	271
04_WILLAM	POP013	ClackamasR_wi	45.317613	-122.413773	261
	POP014	EagleCr	45.351428	-122.384017	23
	POP015	NSantiamR	44.750042	-122.403872	32
	POP016	NFEagleCr	45.351428	-122.384017	25
	POP017	SFSantiamR	44.415003	-122.673942	74
05_BWSALM	POP019	BuckCr_above	45.799317	-121.484314	44
	POP020	BuckCr_below	45.799317	-121.484314	38
	POP022	LRattlesnakeCr	45.799317	-121.484314	39
	POP023	BigWhiteSalmonR_mainstem	45.799317	-121.484314	36
	POP024	MidRattlesnakeCr	45.799317	-121.484314	31
	POP025	BigWhiteSalmonR_above	45.799317	-121.484314	24
	POP026	RattlesnakeCr	45.799317	-121.484314	41
	POP028	BigWhiteSalmonR_Husum	45.799550	-121.485590	14
06_KLICKR	POP031	BowmanCr	45.845210	-121.042110	99
	POP032	DeadCanyonCr	45.942280	-121.143940	34
	POP033	DillacortCr	45.741407	-121.222239	26
	POP034	WheelerCr	45.795093	-121.192829	8
	POP035	SnyderCr	45.824664	-121.156523	29
	POP036	SwaleCr	45.809090	-121.065160	91
	POP037	LKlickitatR	45.841340	-121.003888	77
	POP038	LowSummitCr	45.935701	-121.101827	64
	POP039	LowTroutCr	46.037760	-121.199420	74
	POP040	LowWhiteCr	46.013280	-121.150020	36
	POP042	SurveyorsCr	46.196480	-121.254910	35
	POP043	UpTroutCr	46.077410	-121.212210	51
07.05_FIFTNM	POP044	FifteenmileCr_wi	45.450900	-121.124360	125
07.1_DESCH	POP045	UpDeschutesR	45.261809	-121.034665	95

	POP046	DRTroutCr	44.821430	-121.087210	14
	POP047	WarmSpringsR	44.860900	-121.244380	50
	POP048	WarmSpringsRMillCr	44.865417	-121.447637	159
	POP049	WarmSpringsR_trap	44.860900	-121.244380	50
07.2_JDAY	POP053	LowJohnDayR	44.742749	-120.171219	36
	POP054	SFJohnDayR	44.286801	-119.542160	97
	POP055	NFJohnDayR	44.779154	-119.014929	41
	POP060	MFJohnDayR	44.577569	-118.805415	37
	POP063	UpJohnDayR	44.451083	-119.035553	78
07.3_UMAT	POP064	IskuulpaCr	45.699380	-118.396470	71
	POP065	UmatillaR_Minthorn	45.699380	-118.396470	74
07.4_LOWSNAKE	POP066	TouchetR	46.033994	-118.683625	58
	POP088	Alpowa Cr. '10	46.407620	-117.219784	51
	POP089	Asotin Cr. '10			59
	POP108	George Cr. '10	46.302906	-117.116818	53
	POP136	Sheep Cr. '14	45.467700	-116.555300	47
	POP143	Tucannon R. '10	46.309733	-117.657180	29
	POP144	Tucannon R. '11	46.309733	-117.657180	25
	POP145	Tucannon R. '13	46.309733	-117.657180	35
07.5_IMNA	POP068	LightningCr	45.655370	-116.726530	76
	POP109	Gumboot Cr. '12			17
	POP110	Gumboot Cr. '13			21
	POP124	Mahogany Cr. '11			6
	POP125	Mahogany Cr. '13			8
07.52_GrandeRonde	POP067	JosephCr	46.041552	-117.001710	45
	POP069	UpGrandeRondeR	45.370986	-117.865698	325
	POP070	WenahaR	45.945347	-117.451303	77
	POP112	Joseph Cr. '11	46.027769	-117.017715	55
07.6_LOWCLWR	POP091	Big Bear Cr. '12	46.630629	-116.656189	9
	POP102	E.F. Potlatch R. '16	46.798444	-116.419441	52
	POP113	Little Bear Cr. '12	46.637226	-116.677980	67
	POP123	Lapwai Cr. '13	46.334260	-116.603210	32
	POP126	Mission Cr. '13	46.317070	-116.711300	50
	POP140	Sweetwater Cr. '13	46.294630	-116.856500	65
	POP146	Webb Cr. '13	46.313980	-116.809080	30
	POP148	Potlatch R., W.F. '10	46.805376	-116.418187	50
07.7_LOWSALM	POP094	Boulder Cr. '14	45.154090	-116.395400	46
	POP137	Slate Cr. '13	45.639380	-116.120170	28
	POP149	Whitebird Cr. '14	45.770490	-116.290730	47
08_YAKIMA	POP071	AhtanumCr	46.531800	-120.681500	85
	POP072	CowicheCrowCr	46.628791	-120.570774	74
	POP073	LRattlesnakeCr	46.766026	-121.046083	70
	POP074	NFLNachesR	47.109039	-121.320081	66

	POP075	NileCr	46.861839	-121.048875	97
	POP077	QuartzCr	45.945650	-120.509653	96
	POP078	SatusCr	46.067822	-120.592854	442
	POP079.1	TaneumCr	47.092889	-120.831758	12
	POP079.2	TeanawayR	47.285885	-120.899339	17
	POP080	ToppenishCr	46.322706	-120.874878	134
09_UPPCOL	POP081	EntiatR	47.664071	-120.241689	43
	POP082	IcicleCr	47.559120	-120.674150	10
	POP083	MethowR	48.049472	-119.901200	49
	POP084	MethowH	48.476859	-120.205384	25
	POP085	NasonCr	47.801890	-120.715010	19
	POP086	OmakCr	48.395658	-119.504272	125
	POP087	WellsH	47.559120	-120.674150	11
10_SFCLWR	POP099	Clear Cr. '15			23
	POP100	Crooked R. '13	45.822237	-115.526680	56
	POP122	Lolo Cr. '12			46
	POP128	Newsome Cr. '12	45.836560	-115.615180	48
	POP141	Tenmile Cr. '13			51
11_UPCLWR	POP092	Bear Cr. '12	46.019020	-114.837580	27
	POP096	Canyon Cr. '04	46.216135	-115.555865	45
	POP097	Lochsa R. Crooked Fork '00	46.525108	-114.678649	46
	POP101	E.F. Moose Cr. '12	46.173560	-114.886080	44
	POP107	Gedney Cr. '04	46.058216	-115.313589	51
	POP114	Little Clearwater R. '08	45.753673	-114.774752	57
	POP129	Ohara Cr. '13	46.048060	-115.516940	28
	POP138	Selway R. '08			47
	POP142	Three Links Cr. '12	46.111200	-115.071900	34
	POP150	White Cap Cr. '08	45.868734	-114.728378	55
12_SFSALM	POP103	Salmon R. S.F., E.F. '09	45.012862	-115.713109	25
	POP104	Salmon R. S.F., E.F. '10			22
	POP135	Secesh R. '11			63
13_MFSALM	POP090	Bargamin Cr. '15	45.721674	-115.034530	56
	POP093	Big Cr. '11	45.092594	-114.732175	47
	POP095	Bear Valley Cr. '11			35
	POP098	Chamberlain Cr. '16			50
	POP106	Elk Cr. '11			47
	POP131	Pistol Cr. '12	44.723520	-115.150140	38
	POP132	Rapid R. '12	44.680060	-115.152270	32
	POP147	W.F. Chamberlain Cr. '16			50
14_UPSALM	POP105	Salmon R. E.F. '16	44.115434	-114.429996	65
	POP111	Hayden Cr. '17	44.861600	-113.631880	53
	POP127	Morgan Cr. '12	44.667570	-114.230070	47
	POP130	Panther Cr. '13	45.034940	-114.299490	51

POP133	Salmon R. '18	44.163590	-114.886786	2
POP134	Salmon R. '16	44.150558	-114.885088	50
Grand Total				7422

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679 *Combined application of PBT and GSI*
680   We combined PBT and GSI results together by first accepting all confident PBT
681 assignments to hatchery broodstock (i.e., LOD≥14 & FDR≤0.1) (See methods for Parentage
682 assignments using SNPPIT software v1.0, ID: 1341). For the remaining individuals, we used the
683 best estimate of GSI assignments (regardless of the probability of assignment) provided by the
684 program ONCOR to determine likely reporting group of origin (Method: Assigning individual
685 samples using Individual Assignment (IA) genetic methods v1.0, ID: 1334). For the assignment
686 of sockeye, GSI via ONCOR was used. We also have a baseline of candidate parents used in the
687 reintroduction of Sockeye salmon which requires both SNPPIT and a program to perform single
688 parentage assignments (SEQUOIA). For Chinook salmon, all age classes (3-, 4-, and 5+ year old
689 fish) can be identified from Snake River and Columbia River stocks using PBT.
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691 *Use of SCOBI DEUX and SPIBETR functions to expand PBT and GSI for abundance in harvest*
692 *samples*
693   After combining PBT and GSI assignments, we examined the stratification of the harvest
694 samples for the way in which harvest managers stratify the data to perform CREEL estimates of
695 total harvested fish. In some cases, fisheries are mark selective and so only adipose clipped fish
696 are necessary to sample to estimate the stock-specific abundances in the harvest. We also pooled
697 our sample into the same temporal and spatial stratification in which harvest managers report
698 CREEL estimates. For example, if the total harvested fish is only estimated for the entire catch
699 without further breakdown into weeks or months, we had to treat our harvest sample as a single
700 stratum. Ideally, fish are sampled randomly to acquire the DNA tissue samples in the same
701 stratification units that harvest managers report. However, there are several ways in which the
702 selection of the harvest samples has been non-random in the past. For example, the harvest
703 monitors that work for the joint states (ODFW and WDFW) classify their samples into 3 "sample
704 categories" in which samples can either be random without a CWT, random with a CWT, or non-
705 random with a CWT. Because, the current management of the fisheries rely on CWT data, fish
706 that are not part of the normal random sample for the CREEL estimates will be wanded for the
707 presence of CWTs and if there is a positive CWT detection that fish will get sampled with
708 biodata and genetic tissue collection. For genetic analysis, the non-random CWT fish should be
709 excluded to obtain a random sample, but could be used for purposes of comparing CWT and
710 PBT stock ID results. In past years, we may have inadvertently subsampled both random and
711 non-random samples and used both types in our analyses.
712   We made every effort to match representative DNA sampling of these harvest
713 management strata, which is a difference in this year's analysis compared to previous years.
714 Specifically, we describe our stratification for each fishery sample in the following section:
715   *The spring test fishery:*
716   This fishery is conducted in the early portion of the spring Chinook salmon management
717 period and occurs in the commercial sections 2 and 3 (a portion of "Region B"). Chinook
718 salmon are visually stock-identified (VSI) to lower river and upriver stock classifications. A
719 fleet of boats conduct drift fishing each week and catch per unit effort (CPUE) is estimated using

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720 the number of fish caught per number of drifts for each week. Tissue samples are obtained from
721 both the adipose clipped and adipose intact fish caught in the test fishery at a high rate (>50%).
722 The CPUE has appeared to be a good predictor for the timing and strength of the first peak of the
723 run of spring chinook at Bonneville Dam (Hess et al. 2019), and in this report we established a
724 new strategy for analysis of this sample to obtain stock-specific CPUE for both the adipose
725 clipped and adipose intact upriver chinook salmon. For our sample, we used only the VSI-
726 upriver chinook salmon that were caught in sections 2 and 3 of the test fishery, and stratified into
727 pools of weekly drifts (as indicated in Table 10). Weeks were pooled to obtain sample sizes >10
728 fish for most strata. We applied these stratified samples to the appropriate CPUE estimated for
729 the respective temporal strata for each of the adipose clipped and unclipped observed VIS-
730 upriver test fish.

732 **Table 10. The sample rate and stratification for genetic analysis of the VSI-upriver**
733 **adipose clipped and unclipped adult Chinook salmon from the spring test fishery in 2018.**

		Observed Upriver AD			SAMPLE (Upriver VSI AD)			Observed Upriver AD-intact			SAMPLE (Upriver VSI AD-intact)		
Week	Drifts	N	Pooled N	CPUE	N	Pooled N	Rate	N	Pooled N	CPUE	N	Pooled N	Rate
12	15	1	17	0.36	1	15	0.88	0	6	0.13	0	3	0.50
13	17	8			7			4			3		
14	15	8			7			2			0		
15	16	12	79	2.47	11	64	0.81	6	16	0.50	6	14	0.88
16	16	67			53			10			8		
17	16	73	121	4.32	68	116	0.96	13	26	0.93	10	11	0.42
18	12	48			48			13			1		
		217	**217**		**195**	**195**		**48**	**48**		**28**	**28**	

734 Note: Only the visual stock identified (VSI) upriver Chinook salmon were analyzed from the spring test
735 fishery. The Catch per Unit Effort (CPUE) was calculated from the number of fish observed / the number of "Drifts"
736 made total for the fleet of boats used in the test fishery.

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

Table 11. The sample rate and stratification for genetic analysis of the kept adipose clipped adult Chinook salmon from the spring sport fishery in 2018.

	Total Adult Chinook			Sample of Total Adult Chinook Kept			
	Kept	Rel.	Rel. Mortality	regionA	regionB	total	rate
Jan-Feb Total	18	0	0				0.12
March Total	1,871	278	28	109	121	230	
April Total	4,119	581	58	169	335	504	0.12
May Total	468	355	36	29	14	43	0.09
June 1-15 Total	1,033	316	32	40	56	96	0.09
Season Total	7,509	1,530	154	347	526	873	0.12

Note: The released fish ("Rel.") were not sampled for genetic analysis and so only the "kept" fish could be analyzed. The samples of kept fish came from both the regions A and B but for the analysis the sample was treated as a single region for compatibility with the way the catch is reported. Monthly strata were used and the first stratum was pooled to include all fish harvested from January through March as indicated by the outlines in the table.

The spring chinook salmon platform hook and line permit fishery:
Yakama Nation executed this fishery in 2018 below Bonneville Dam. The total catch was 454 adult spring chinook salmon and samples obtained for the entire period were 273 or a sample rate of 60.1%. All samples were pooled and the catch was estimated by adipose clipped and intact stocks.

The spring chinook salmon zone 6 ceremonial permit fishery was 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 (total ceremonial harvest in 2018 = 8,718) and temporal stratification would be applied; however, samples were gathered from the Yakama Nation harvest exclusively in 2018 (N=168, Table 6) and the harvested fish are not possible to report on a weekly basis or by reservoir.

The summer chinook salmon sport fishery is mark-selective similar to the spring sport fishery. The total adult fish that were kept in 2018 were 1,027 fish and of those, we obtained 72 tissue samples from adipose clipped fish across regions A and B. The summer chinook salmon are mostly destined for the upper Columbia and so stock composition should be similar across regions A and B. We pooled all 72 tissue samples which were all random (sample rate = 7%) and used the pooled sample to estimate stock composition in the fishery. There were 750 fish that were released and of those, 15% (113 fish) were assumed to be release mortalities. We did not estimate the stock composition of these release mortalities, although this could be done since the composition should be similar to the kept fish.

The summer chinook salmon Treaty fishery in zone 6 is estimated by adipose clipped and unclipped adults by statistical week (Table 12). We split our sample by adipose clip and pooled samples across weeks to obtain a minimum of 10 fish per stratum to analyze the stock composition of this harvest.

787   **Table 12. The sample rate and stratification for genetic analysis of the adipose**
788 **clipped and unclipped adult Chinook salmon from the zone 6 summer Treaty fishery in**
789 **2018.**

	Harvest Estimate		Sample N		Sample rate	
Week	AD	AI	AD	AI	AD	AI
24	280	77			0.02	0.03
25	3,083	628	66	24		
26	2,228	550	41	15		
27	1,375	315	30	13	0.02	0.03
28	961	149	23	2		
29	120	34	3			
30-31	43	12	2	2		

790   Note: The adipose clipped (AD) and unclipped/intact (AI) fish shown by harvest estimate and sample size.
791 Samples were pooled across weeks as indicated by the boxed samples in the table.
792
793   *The fall Non-Treaty commercial fishery:*
794   This fishery occurred in two separate weeks in August in region A and was reported by
795 total adults and jacks. We obtained random samples of both adipose clipped and unclipped
796 chinook salmon (both adults and jacks) and stratified by weeks to analyze the genetic stock
797 composition of this harvest (**Table 13**). However, limited funds required subsampling.
798 Subsampling did not keep adipose clipped and unclipped fish in the same ratios as compared to
799 the total sample, which may have introduced some bias into the final estimates of total clipped
800 and unclipped genetic stocks.
801
802   **Table 13. The sample rate and stratification for genetic analysis of the adult and**
803 **jack Chinook salmon from fall Non-Treaty commercial fishery in 2018.**

	Harvest estimate	Total Sample N				SubSample N			
Week	adult+jack	AD	AI	total	rate	AD	AI	total	rate
34	3351	94	100	194	0.06	57	50	107	0.03
35	4969	109	135	244	0.05	53	50	103	0.02

804   Note: The harvest estimate combines both adults and jacks and does not distinguish clipped and unclipped
805 fish. The total sample was originally a random sample of the harvest but limited funds required subsampling.
806 Subsampling did not keep adipose clipped and unclipped fish in the same ratios as compared to the total sample,
807 which may have introduced some bias into the final estimates of total clipped and unclipped genetic stocks.
808
809   *The fall Non-Treaty sport fishery:*
810   This fishery is not mark-selective and the stock composition of the released fish is
811 assumed to be similar to the kept fish. We stratified the samples of kept fish by month and
812 estimated the stock composition of the adipose clipped and adipose intact fish using the sample
813 data (Table 14). The catch estimate for this fishery is reported by month for the adult fish and
814 further is not stratified geographically into regions. We recorded geographic region in the sample
815 data and so this geographic stratification could be applied if the harvest estimates were stratified
816 similarly. This geographic stratification should only be necessary if the sample were not obtained
817 randomly with respect to time and region. However, we used only the random samples obtained
818 from this fishery.

821 **Table 14. The sample rate and stratification for genetic analysis of the kept adult**
822 **Chinook salmon from the fall Non-Treaty sport fishery in 2018.**

	Catch Estimate			Sample of kept		
Month	kept Adult	Released	Release mortality	AD	AI	rate
Aug	4119	232	35	26	72	0.02
Sep	5683	645	97	37	115	0.03
	9802			63	187	0.03

823 Note: The sample numbers of the kept Chinook salmon were stratified by month and adipose clip data was
824 used to estimate the stock composition of both adipose clipped (AD) and adiposed intact (AI) stocks.
825
826 *The fall Treaty commercial fishery*:
827 This fishery occured in zone 6 across several weeks of the fall management period. This
828 fishery is monitored by visually identifying tules versus bright stocks and estimating each
829 separately (Table 15). Tissue collection is mostly obtained from the fish identified as bright
830 stocks, and very few tule stocks are sampled. Therefore, genetic analysis was constrained to
831 estimating stock composition within the visually-identified bright harvest.
832
833
834 **Table 15. The sample rate and stratification for genetic analysis of the adult bright**
835 **Chinook salmon from fall Treaty zone 6 commercial fishery in 2018.**

	Harvest estimate		Sample of Brights		
Week	Brights	Tules	AD	AI	rate
31 - 34	652	19	3	9	0.01
35	5,365	3319	25	53	
36	11,530	6110	49	51	0.01
37	10,717	3102	65	100	0.02
38	5,941	1206	32	89	0.02
39	3,962	940	39	98	0.03
40	2,786	493	15	54	0.02
total	40,953	15,189	228	454	0.02

836
837
838 *The fall test fishery or pound net fishery*:
839 The pound net is a relatively recent gear type that is being developed by the joint states.
840 In 2018, the fall pound net fishery was conducted in the Cathlamet Channel (area 83) and the
841 numbers and genetic samples of the kept (Table 16) and released (Table 17) Chinook salmon
842 were stratified to obtain at least 10 fish in each stratum. The Chinook jacks were not expanded
843 for stock composition due to the low sample size.
844
845 **Table 16. The sample rate and stratification for genetic analysis of the kept adipose**
846 **clipped Chinook salmon from the fall pound net fishery in 2018.**

2018 Pound Net Trap Kept Catch Summary (all adipose-clipped)

Week	Chin Adults	Sample Chin Adults	Rate	Chin Jacks	Sample Chin Jacks	Rate
34	47	1	0.46	2		0.21
35	353	182		28	8	
36	105	52	0.50	5	1	
37	92	52	0.57	13	1	
38	3	2	0.67	0		
	600	289	0.48	48	10	0.21

Note: The "Sample" indicates numbers of successfully genotyped fish in each stratum. The weekly strata were pooled as indicated by the outlined boxes to obtain at least 10 fish in each stratum. The "Rate" is the sample rate attained for each pooled stratum.

Table 17. The sample rate and stratification for genetic analysis of the released adipose unclipped adult Chinook salmon from the fall pound net fishery in 2018

2018 Pound Net Trap Released Catch Summary (adipose unclipped)

Week	Chin Adults No Ad-clip	Sample	
34	70	21	0.30
35	445	88	0.20
36	152	28	0.18
37	223	33	0.15
38	11	2	
41	0		
42	1		
43	1		
	903	172	0.19

Note: The "Sample" indicates numbers of successfully genotyped fish in each stratum. The weekly strata were pooled as indicated by the outlined boxes to obtain at least 10 fish in each stratum. The "Rate" is the sample rate attained for each pooled stratum.

The Sockeye Non-Treaty sport fishery:

This fishery was estimated to have 73 and 212 kept and released fish, respectively, for a total mortality of 111 sockeye. We successfully genotyped a total of 9 of the kept fish which were assumed representative of the total mortality (sample rate = 8.1% of the total mortality). All samples were pooled to estimate stock composition of this harvest. Every fish in the sample assigned to the Osoyoos stock (i.e., 100% of the 111 sockeye mortalities were estimated to be Osoyoos).

The Sockeye Treaty commercial fishery:

This fishery occurred in zone 6 and catch estimates were reported by week in the summer and additional estimates of sockeye were reported in zone 6 during the spring and fall periods as well as below Bonneville Dam. All Sockeye salmon catch estimates were combined for the total harvest (**Table 18**).

Table 18. The sample rate and stratification for genetic analysis of the harvested Sockeye salmon from the Treaty fishery in 2018.

Week	Harvest estimate	LBC	Odell	Osoyoos	Redfish	Wenatchee	Yakima	total	rate
21-24	299			4				4	0.02
25	2,346			40		11		51	
26	2,494			33	3	13	1	50	0.02
27	1,546		1	40		4		45	0.03
28	837			32		2		34	0.04
29	121	1		25		3	2	31	0.19
30	83			7		1		8	
31	0								
total	7,727	1	1	181	3	34	3	223	0.03

Results

Information content of the 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 has recently become problematic (Hess et al. 2019) is that there are individual genotypes that have been causing the software SNPPIT to crash. We rely on this software for our PBT analyses and so resolving this problem is critical to the effectiveness of PBT applications in the long term. We examined a set of 299 SNPs in the GT-seq panel for information content (observed heterozygosity) in each of the three major lineages of Chinook Salmon represented by a set of broodstocks collected in 2015 (Hess et al. 2019). We first discovered that among the original 93 SNPs, there were 92 that were found above an observed heterozygosity of 10% for the stream-type lineage broodstocks of spawn year 2015 (Table 12 in Hess et al. 2019). In contrast, there were 72 and 64 SNPs with observed heterozygosities >10% for the ocean-type and Lower Columbia lineages, respectively. According to Steele et al. (2013), less than 72 highly polymorphic SNPs is the point at which accuracy for PBT was observed to decline. We suspect that it is the lack of sufficient numbers of SNP markers with high information content (i.e. observed heterozygosity) that has been causing SNPPIT to crash when we analyze parent-offspring pairs from ocean-type and Lower Columbia River broodstocks with low polymorphism at these 93 SNPs.

To resolve this issue, we recommend the use of a larger set of SNP markers (~200) that have greater than 10% observed heterozygosity in each of the major lineages of Chinook Salmon. Our evaluation of the broodstocks from SY2015 indicated a set of 269 SNP loci that had >10% observed heterozygosity for at least 1 major lineage, and within this panel of 269 loci there were 193, 218, and 195 SNPs with >10% observed heterozygosity for each of the major lineages stream-type, ocean-type, and Lower Columbia, respectively (Hess et al. 2019). Based on this analysis, a set of 254 SNPs were chosen from these 269 loci and overlap with our current GT-seq panel (Table 19).

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.

904　This result confirmed that the source of the crashing issue was likely related to the lack of
905　sufficient numbers of SNPs with high information content that is primarily affecting ocean-type
906　broodstocks. Further, the higher number of SNP loci requires decreased computational time to
907　run the parentage analyses, which is extremely helpful for the relatively short time available to
908　process in-season samples.

909 **Table 19. The "legacy set" of 93 SNP loci and the set of 254 SNP loci with high information**
910 **content used for PBT applications of the three major genetic lineages of Columbia River**
911 **Chinook salmon.**

SNP93 order	Best 254	Locus
1	1	Ots_100884287
2	2	Ots_101554407
3	3	Ots_101704143
4	4	Ots_102414395
5	5	Ots_102801308
6	6	Ots_103122180
7	7	Ots_10441588
8	8	Ots_105105613
9	9	Ots_105132200
10	10	Ots_105385421
11	11	Ots_105407117
12	12	Ots_108820336
13	13	Ots_109525816
14	14	Ots_110064383
15	15	Ots_110201363
16	16	Ots_110495380
17	17	Ots_11055164
18	18	Ots_110689218
19	19	Ots_11230143
20	20	Ots_112419131
21	21	Ots_112820284
22	22	Ots_112876371
23	23	Ots_113242216
24	24	Ots_115987325
25	25	Ots_117432409
26	26	Ots_11820561
27	27	Ots_118938325
28	28	Ots_123921111
29	29	Ots_124774477
30	30	Ots_12875761R
31	31	Ots_129458451
32	32	Ots_94857232R
33	33	Ots_9490399R
34	34	Ots_96500180
35	35	Ots_96899357R
36	36	Ots_ARNT
37	37	Ots_AsnRS60
38	38	Ots_brp1664

39	39	Ots_CD592
40	40	Ots_CirpA
41	41	Ots_cox1241
42	42	Ots_E2275
43	43	Ots_Est740
44	44	Ots_ETIF1A
45	45	Ots_FGF6B_1
46	46	Ots_GCSH
47	47	Ots_GDH81x
48	48	Ots_GPH318
49	49	Ots_GTH2B550
50	50	Ots_HMGB173
51	51	Ots_hsc713488
52	52	Ots_HSP90B100
53	53	Ots_IGFI176
54	54	Ots_Ikaros250
55	55	Ots_IL8R_C8
56	56	Ots_mapK3309
57	57	Ots_mapKpr151
58	58	Ots_MHC2
59	59	Ots_mybp85
60	60	Ots_NFYB147
61	61	Ots_nkef192
62	62	Ots_NOD1
63	63	Ots_ntl255
64	64	Ots_OTALDBINT1SNP1
65	65	Ots_OTDESMIN19SNP1
66	66	Ots_OTSTF1SNP1
67	67	Ots_P53
68	68	Ots_parp3286
69	70	Ots_pop596
70	71	Ots_ppie245
71	72	Ots_Prl2
72	73	Ots_RAG3
73	74	Ots_redd1187
74	75	Ots_S71
75	76	Ots_SClkF2R2135
76	77	Ots_SWS1op182
77	78	Ots_TAPBP
78	79	Ots_TGFB
79	80	Ots_Thio
80	81	Ots_TLR3
81	82	Ots_tpx2125

82	83	Ots_txnip321
83	84	Ots_u0707161
84	85	Ots_u0717135
85	86	Ots_u0718378
86	87	Ots_u0725325
87	88	Ots_u0749290
88	89	Ots_u100275
89	90	Ots_u21185
90	91	Ots_u492
91	92	Ots_u675
92	93	Ots_unk526
93	94	Ots_vatf251
	69	Ots_pigh105
	95	Ots_106747239
	96	Ots_11345740R
	97	Ots_123048521
	98	Ots_96222525
	99	Ots_97077179R
	100	Ots_AldB1122
	101	Ots_arp436
	102	Ots_aspat196
	103	Ots_Cath_D141
	104	Ots_CD63
	105	Ots_CRB211
	106	Ots_EndoRB1486
	107	Ots_EP529
	108	Ots_FARSLA220
	109	Ots_GST207
	110	Ots_GST375
	111	Ots_hsp27b150
	112	Ots_IL11
	113	Ots_myo1a384
	114	Ots_myoD364
	115	Ots_nramp321
	116	Ots_Ots311101x
	117	Ots_P450
	118	Ots_PGK54
	119	Ots_RFC2558
	120	Ots_SL
	121	Ots_u0720332
	122	Ots_u0753133
	123	Ots_u0757120
	124	Ots_u202161

125	Ots_ZR575
126	Ots_LWSop638
127	Ots_u1008108
128	Ots_IsoT
129	Ots_101119381
130	Ots_102213210
131	Ots_102457132
132	Ots_102867609
133	Ots_10649970
134	Ots_107074284
135	Ots_10728593
136	Ots_107806821
137	Ots_108007208
138	Ots_108390329
139	Ots_108735302
140	Ots_109693392
141	Ots_111681657
142	Ots_112208722
143	Ots_117242136
144	Ots_117259271
145	Ots_118175479
146	Ots_12241456
147	Ots_12723662
148	Ots_12830257
149	Ots_128693461
150	Ots_129144472
151	Ots_13072099
152	Ots_131460584
153	Ots_131906141
154	Ots_99550204
155	Ots_DDX5171
156	Ots_Est1363
157	Ots_HFABP34
158	Ots_hnRNPL533
159	Ots_Hsp90a
160	Ots_nelfd163
161	Ots_OTSMTASNP1
162	Ots_P450288
163	Ots_stk6516
164	Ots_TCTA58
165	Ots_u1007124
166	Ots_U2362227
167	Ots_U2362330

168	Ots_U2446123
169	Ots_unk110438
170	Ots_unk183239
171	Ots_unk351349
172	Ots_unk793650
173	Ots_unk948051
175	Ots_104063132
176	Ots_105401325
177	Ots_106313729
178	Ots_106419b618
179	Ots_107607315
180	Ots_110381164
181	Ots_117370471
182	Ots_120950417
183	Ots_126619400
184	Ots_127760569
185	Ots_12987055
186	Ots_131802393
187	Ots_95442b204
188	Ots_9766056
189	Ots_afmid196
190	Ots_AldoB4183
191	Ots_BMP2SNP1
192	Ots_cgo2422
193	Ots_crRAD1044725
194	Ots_crRAD1162055
195	Ots_crRAD1203739
196	Ots_crRAD1372551
197	Ots_crRAD1654050
198	Ots_crRAD1752758
199	Ots_crRAD1849265
200	Ots_crRAD1893760
201	Ots_crRAD2026246
202	Ots_crRAD2037666
203	Ots_crRAD2088770
204	Ots_crRAD2111524
205	Ots_crRAD2296032
206	Ots_crRAD2480774
207	Ots_crRAD2536750
208	Ots_crRAD25559
209	Ots_crRAD2616569
211	Ots_crRAD2716455
212	Ots_crRAD2751569

213	Ots_crRAD280642
214	Ots_crRAD3349171
215	Ots_crRAD3439733
216	Ots_crRAD3531366
217	Ots_crRAD3607229
218	Ots_crRAD3615244
219	Ots_crRAD4458867
220	Ots_crRAD4608156
221	Ots_crRAD4675142
222	Ots_crRAD4729755
223	Ots_crRAD5547526
224	Ots_crRAD5752066
225	Ots_crRAD5768734
226	Ots_crRAD6061446
227	Ots_crRAD6062051
228	Ots_crRAD6152371
229	Ots_crRAD6633060
230	Ots_crRAD6932753
231	Ots_crRAD7382360
232	Ots_crRAD7476628
233	Ots_crRAD7558170
234	Ots_crRAD7651228
235	Ots_crRAD7896846
236	Ots_crRAD9242025
237	Ots_crRAD961569
238	Ots_MetA
239	Ots_NAML12SNP1
240	Ots_Ostm1
241	Ots_PEMT
242	Ots_RAD454352
243	Ots_sept978
244	Ots_slc7a271
245	Ots_trnau1ap86
247	Ots_U212158
248	Ots_U230563
249	Ots_U2567104
250	Ots_U5049250
251	Ots_U512134
252	Ots_crRAD1828933
253	Ots_crRAD5540059
254	Ots_crRAD5737668
255	Ots_10304152
256	Ots_111084b619

257	Ots_129170683

912   Note: The loci are sorted by their order in the original panel of 93SNPs used for PBT applications, and "Best 254"
913   indicates the group of 254 SNPs that were observed with a heterozygosity >10% for at least one of the major genetic
914   lineages based on hatchery broodstock of spawn year 2015 (Hess et al. 2019).

915 *Comparison of Coded-wire tags and PBT assignments*
916   There were 101 coded-wire tags (CWTs) recovered and identified to hatchery stock and broodyear (BY) among the snouts
917 recovered from the lower river fisheries (Table 20), and 77 of these CWTs also were PBT assigned (76%). Of the 77 fish with both
918 CWT and PBT, there were 65 fish (84%) that appeared concordant with the PBT assignments according to both the hatchery source
919 and the broodyear. There were 12 of the 77 fish with both CWT and PBT that were discordant for either hatchery source (N=6) or
920 broodyear (N=5), and a single fish that was discordant for both hatchery source and broodyear information.
921
922   **Table 20. Comparison of coded-wire tags with parentage-based tags that were identified in the lower river fisheries in**
923 **2018.**

	Coded-wire tag			Parentage-based tagging assignment				HatcheryCorrect	BYCorrect	Missing
Period	Hatchery	BY	Code	Hatchery	BY	N				
01Spring	CHELAN FALLS HATCHERY	2012	OtsEASTBK12_su	Eastbank Fish Hatchery	2012	1		Y	Y	0
01Spring	CHELAN FALLS HATCHERY	2014	OtsEASTBK14_su	Eastbank Fish Hatchery	2014	4		Y	Y	0
01Spring	CHIEF JOSEPH HATCHERY	2013	OtsCJH13int_su	Chief Joseph Hatchery	2013	1		Y	Y	0
01Spring	CLE ELUM HATCHERY	2014	OtsYR14int_sp	Yakima River Roza Dam	2014	1		Y	Y	0
01Spring	DRYDEN POND	2014	OtsEASTBK14_su	Eastbank Fish Hatchery	2014	1		Y	Y	0
01Spring	LOOKINGGLASS HATCH	2014	OtsLSTW14S_sp	Lookingglass Fish Hatchery	2014	1		Y	Y	0
01Spring	LOOKINGGLASS HATCH	2015	OtsLSTW15S_sp	Lookingglass Fish Hatchery	2015	1		Y	Y	0
01Spring	MCCALL HATCHERY	2014	OtsMCCA14S_spsu	McCall Fish Hatchery	2014	2		Y	Y	0
01Spring	NASON CREEK ACC FACILITY	2015	OtsEASTBK15_sp	Eastbank Fish Hatchery	2015	1		Y	Y	0
01Spring	ROUND BUTTE HATCHERY	2014	OtsPFF14_sp	Parkdale Fish Facility	2014	2		Y	Y	0
01Spring	SIMILKAMEEN HATCHERY	2012	OtsEASTBK12_su	Eastbank Fish Hatchery	2012	1		Y	Y	0
01Spring	SIMILKAMEEN HATCHERY	2014	OtsCJH14int_su	Chief Joseph Hatchery	2014	4		Y	Y	0
01Spring	WELLS HATCHERY	2013	OtsWELLS13_su	Wells Fish Hatchery	2013	1		Y	Y	0
01Spring	WELLS HATCHERY	2014	OtsWELLS14_su	Wells Fish Hatchery	2014	12		Y	Y	0

139

02Summer	Carlton Acclimaition Pond (Methow R)	2014	OtsEASTBK14_su	Eastbank Fish Hatchery	2014	1	Y	Y	0
02Summer	Carlton Acclimaiton Pond (Methow R)	2013	OtsEASTBK13_su	Eastbank Fish Hatchery	2013	1	Y	Y	0
02Summer	CHELAN FALLS HATCHERY	2012	OtsEASTBK12_su	Eastbank Fish Hatchery	2012	1	Y	Y	0
02Summer	CHELAN FALLS HATCHERY	2014	OtsEASTBK14_su	Eastbank Fish Hatchery	2014	4	Y	Y	0
02Summer	CHELAN FALLS HATCHERY	2015	OtsEASTBK15_su	Eastbank Fish Hatchery	2015	1	Y	Y	0
02Summer	CHIEF JOSEPH HATCHERY	2013	OtsCJH13seg_su	Chief Joseph Hatchery	2013	1	Y	Y	0
02Summer	CHIEF JOSEPH HATCHERY	2014	OtsCJH14seg_su	Chief Joseph Hatchery	2014	1	Y	Y	0
02Summer	DRYDEN POND	2013	OtsEASTBK13_su	Eastbank Fish Hatchery	2013	1	Y	Y	0
02Summer	DRYDEN POND	2014	OtsEASTBK14_su	Eastbank Fish Hatchery	2014	2	Y	Y	0
02Summer	ENTIAT NFH	2014	OtsENFH14_su	Entiat National Fish Hatchery	2014	2	Y	Y	0
02Summer	MCCALL HATCHERY	2014	OtsMCCA14S_spsu	McCall Fish Hatchery	2014	1	Y	Y	0
02Summer	SIMILKAMEEN HATCHERY	2014	OtsCJH14int_su	Chief Joseph Hatchery	2014	2	Y	Y	0
02Summer	WELLS HATCHERY	2013	OtsWELLS13_su	Wells Fish Hatchery	2013	1	Y	Y	0
02Summer	WELLS HATCHERY	2014	OtsWELLS14_su	Wells Fish Hatchery	2014	1	Y	Y	0
03Fall	Bonneville Hatchery	2014	OtsLWS14_fa	Little White Salmon National Fish Hatchery	2014	2	Y	Y	0
03Fall	CHIEF JOSEPH HATCHERY	2014	OtsCJH14seg_su	Chief Joseph Hatchery	2014	1	Y	Y	0
03Fall	Irrigon Hatchery	2016	OtsLYON16S_1_fa	Lyons Ferry Fish Hatchery	2016	1	Y	Y	0
03Fall	Klickitat Hatchery	2015	OtsLWS15_fa	Little White Salmon National Fish Hatchery	2015	1	Y	Y	0
03Fall	Lyons Ferry Hatchery	2014	OtsLYON14S_1_fa	Lyons Ferry Fish Hatchery	2014	4	Y	Y	0
03Fall	Priest Rapids Hatchery	2015	OtsPRH15_fa	Priest Rapids Hatchery	2015	1	Y	Y	0
03Fall	Spring Creek Hatchery	2015	OtsSPCR15_fa	Spring Creek National Fish Hatchery	2015	1	Y	Y	0
03Fall	Umatilla Hatchery	2015	OtsLWS15_fa	Little White Salmon National Fish Hatchery	2015	1	Y	Y	0
01Spring	WELLS HATCHERY	2013	OtsWELLS14_su	Wells Fish Hatchery	2014	1	Y	N	0
01Spring	WELLS HATCHERY	2014	OtsWELLS13_su	Wells Fish Hatchery	2013	1	Y	N	0
02Summer	Carlton Acclimaiton Pond (Methow R)	2013	OtsCJH14int_su	Chief Joseph Hatchery	2014	1	Y	N	0
02Summer	DRYDEN POND	2013	OtsEASTBK12_su	Eastbank Fish Hatchery	2012	1	Y	N	0
02Summer	SIMILKAMEEN HATCHERY	2014	OtsEASTBK13_su	Eastbank Fish Hatchery	2013	1	Y	N	0
01Spring	CHELAN FALLS HATCHERY	2014	OtsCJH14int_su	Chief Joseph Hatchery	2014	1	N	Y	0
01Spring	LOOKINGGLASS HATCH	2014	OtsPFF14_sp	Parkdale Fish Facility	2014	1	N	Y	0

02Summer	Sandy Hatchery	2014	OtsEASTBK14_su	Eastbank Fish Hatchery	2014	2	N	Y	0
02Summer	Sandy Hatchery	2014	OtsENFH14_su	Entiat National Fish Hatchery	2014	1	N	Y	0
03Fall	Bonneville Hatchery	2014	OtsLYON14S_1_fa	Lyons Ferry Fish Hatchery	2014	1	N	Y	0
02Summer	MCKENZIE HATCHERY	2013	OtsENFH14_su	Entiat National Fish Hatchery	2014	1	N	N	0
01Spring	DRYDEN POND	2013	NA	NA	NA	1			1
01Spring	ENTIAT NFH	2014	NA	NA	NA	1			1
01Spring	LEWIS RIVER HATCHERY	2015	NA	NA	NA	1			1
01Spring	LOOKINGGLASS HATCH	2014	NA	NA	NA	1			1
01Spring	MCKENZIE HATCHERY	2014	NA	NA	NA	1			1
02Summer	CHELAN FALLS HATCHERY	2013	NA	NA	NA	1			1
02Summer	Colitz Salmon Hatchery	2014	NA	NA	NA	1			1
02Summer	DRYDEN POND	2013	NA	NA	NA	1			1
02Summer	MCKENZIE HATCHERY	2013	NA	NA	NA	1			1
02Summer	Minto Ponds (N Santiam R)	2013	NA	NA	NA	1			1
03Fall	Klickitat Hatchery	2013	NA	NA	NA	1			1
03Fall	Sandy Hatchery	2016	NA	NA	NA	1			1
01Spring	Sandy Hatchery	2014	NA	NA	NA	2			2
01Spring	CHELAN FALLS HATCHERY	2013	NA	NA	NA	4			4
02Summer	Sandy Hatchery	2014	NA	NA	NA	6			6

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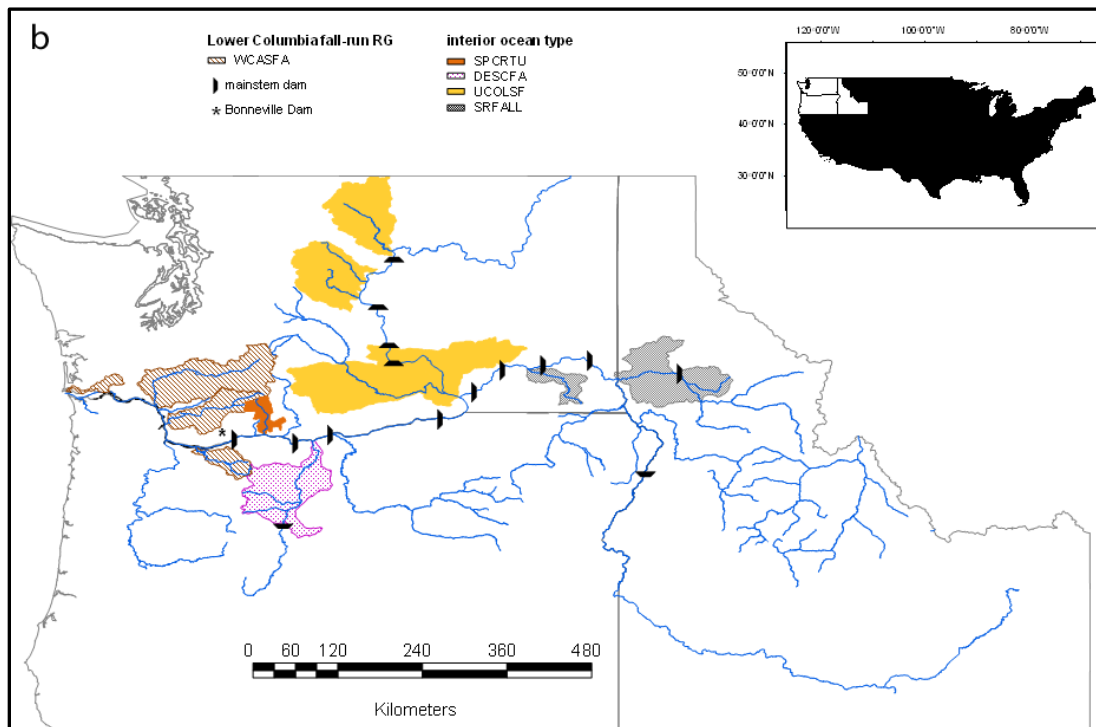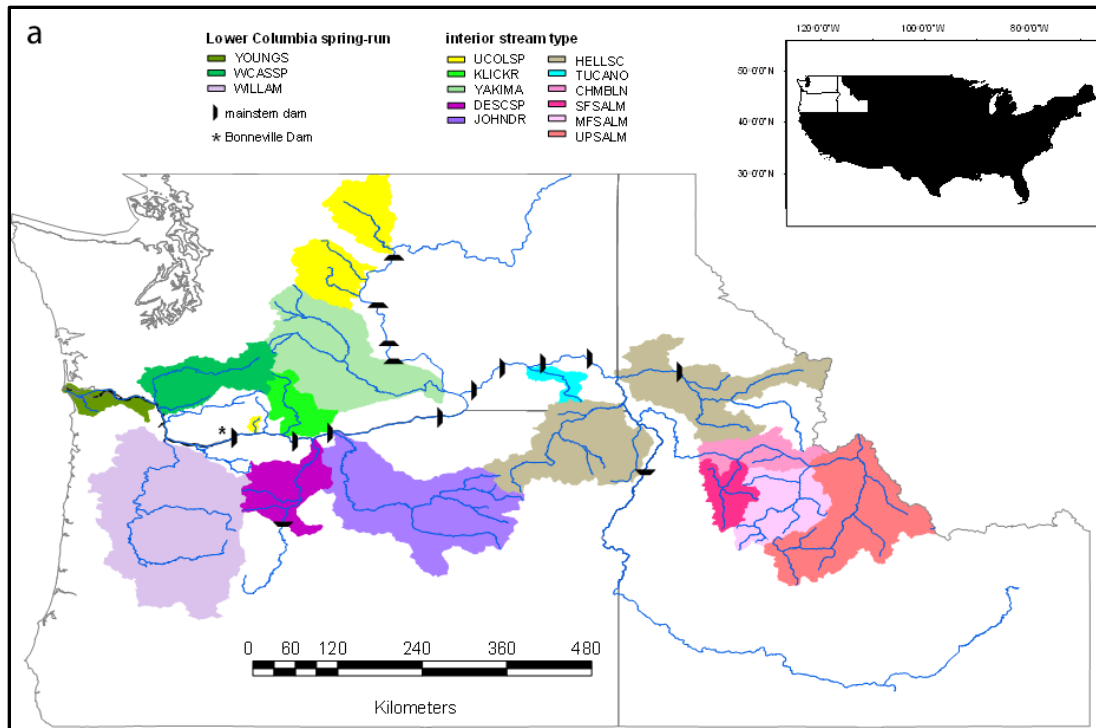
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928 **Figure 14. Map of Chinook salmon GSI reporting groups for a) Lower Columbia (LC) and**
929 **interior stream type (ST) lineage, and b) interior ocean type (OT) lineage.**

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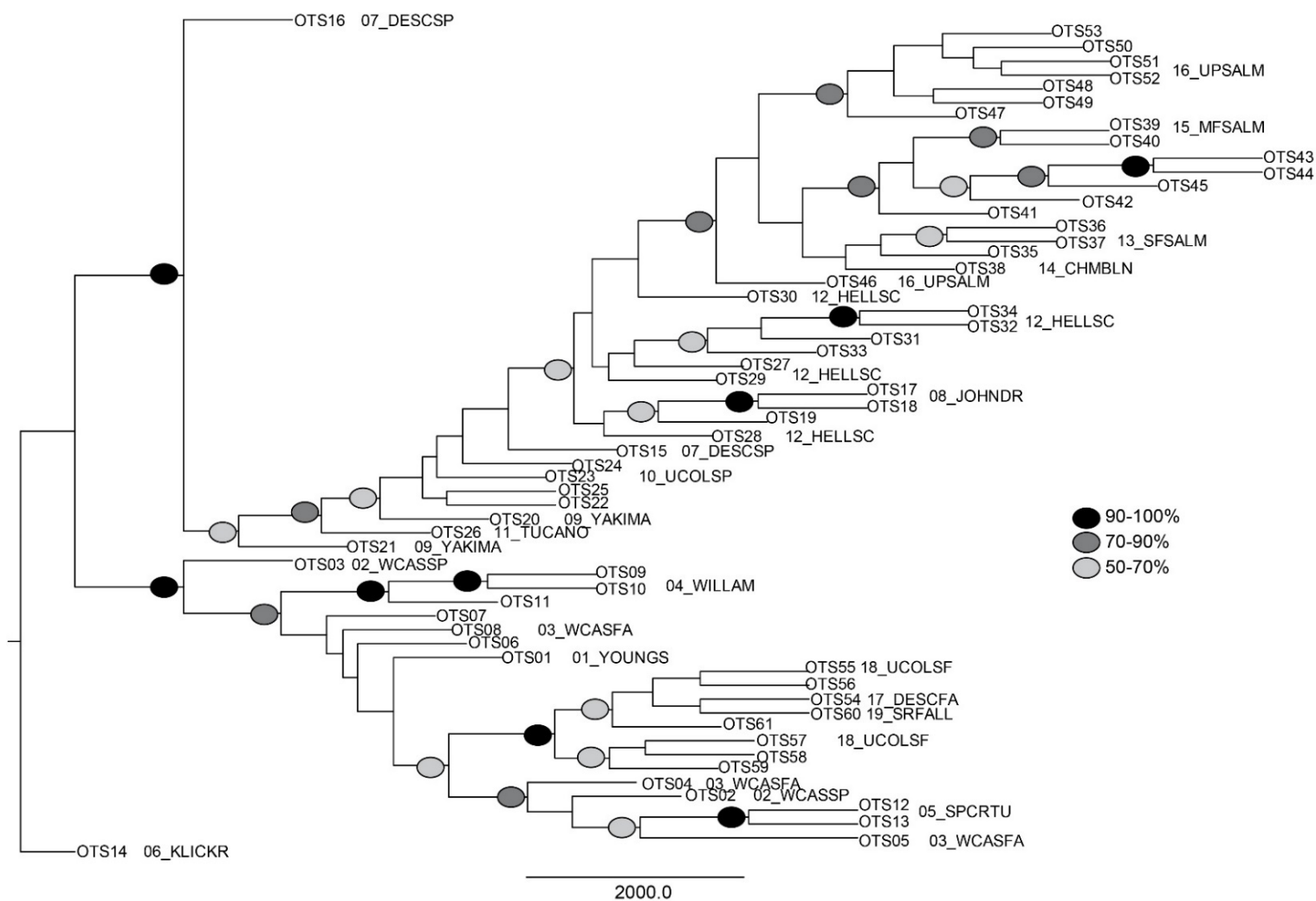
Figure 15. Neighbor-joining tree of Chinook salmon baseline populations using Nei's 1972 genetic distance of 179 SNP loci.

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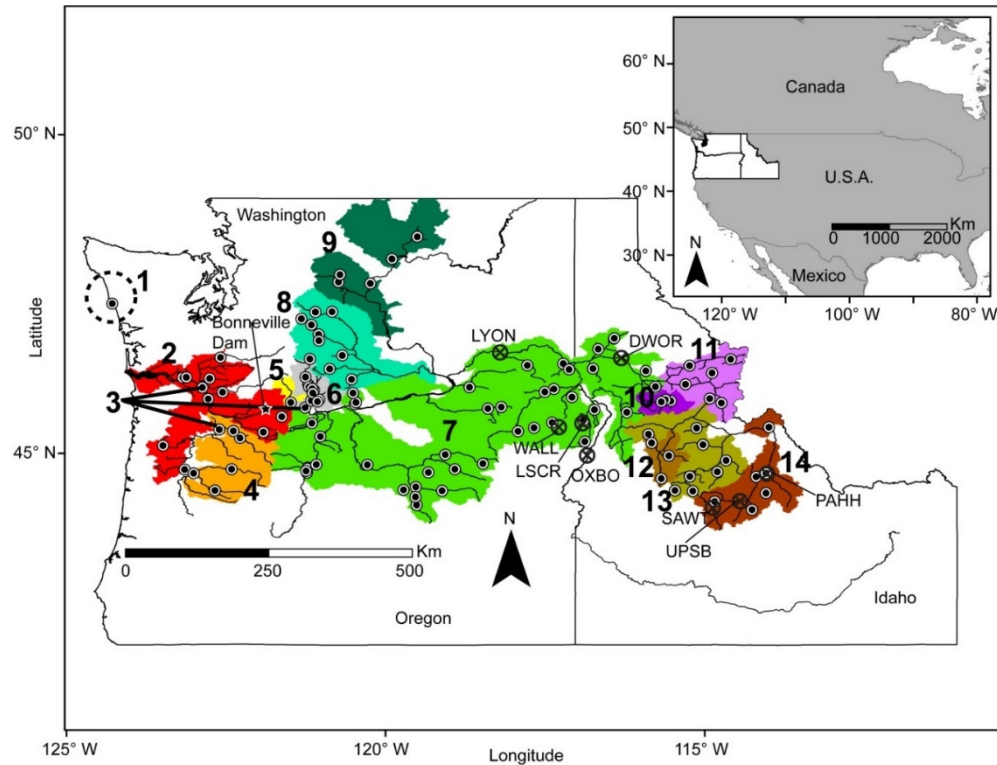
**Figure 16. Geographic distribution of collections represented in the Columbia River
steelhead GSI and PBT genetic baselines.**

In Figure 16, the shape overlay represents the geographic extent of the following 14 reporting
groups in the GSI baseline: 1) Quinault (WCOAST), 2) lower Columbia River (LOWCOL), 3)
Skamania hatchery releases at three sites in lower Columbia River, Willamette River, and
Klickitat River (SKAMAN), 4) Willamette River (WILLAM), 5) Big White Salmon River
(BWSALM), 6) Klickitat River (KLICKR), 7) middle Columbia River, Grande Ronde River,
Imnaha River, lower Snake River, lower Clearwater River, and lower Salmon River (MGILCS),
8) Yakima River (YAKIMA), 9) upper Columbia River (UPPCOL), 10) South Fork Clearwater
River (SFCLWR), 11) upper Clearwater River (UPCLWR), 12) South Fork Salmon River
(SFSALM), 13) Middle Fork Salmon River (MFSALM), and 14) upper Salmon River
(UPSALM). There are 116 collections (filled circles) categorized into reporting groups. The
PBT baseline is indicated as 8 stocks (crossed circles) corresponding to the following sites where
fish are collected and spawned for broodstock: Lyons Ferry Hatchery (LYON), Wallowa
(WALL), Little Sheep Creek (LSCR), Oxbow Hatchery (OXBO), Dworshak Hatchery (DWOR),
upper Salmon River B-run (UPSB), Sawtooth Hatchery (SAWT), and Pahsimeroi Hatchery
(PAHH). Bonneville Dam (star) is the site where fish were non-lethally sampled for the mixed-
stock analysis.

Steelhead 177 SNP and 335 SNP baselines

For steelhead, we have used GSI baseline v3.3 that comprises 116 collections from throughout the Columbia River basin that are partitioned into 14 reporting groups (N= 9991) (Figure 16). However, a set of 335 SNP loci is now available for a similar set of collections representing 13 of the 14 reporting groups (N=7422 individuals, **Table 9**). We tested the accuracy of this new panel of 335 SNP loci by performing leave-1-out tests. Specifically, we generated the following different subsets of loci (Figure 17): 180 SNPs from baseline v3.3 ("Sub180"), 339 SNPs that include putatively neutral and adaptive loci ("Sub339"), 335 SNPs that exclude the run timing candidate SNPs ("Sub335NRT"), 301 SNPs that were putatively neutral ("Sub301Neu"), and 55 SNPs that were putatively adaptive ("Sub55Adapt"). We found that the 335 and 339 SNPs both performed best, but we felt it would be better to exclude the run timing candidate SNPs to avoid any unintended bias for stocks containing within population variation in run timing. Therefore, we propose testing of the 335 SNP baseline to determine whether it can replace the original 177 SNP v3.3. baseline.

However, recent testing using comparisons of PBT and GSI assignments have highlighted some potential accuracy issues with the new 335 SNP baseline. First, this new baseline is not able to accurately assign smaller subgroups within the MCGILCS reporting group (Table 8), 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, **Table 21**, **Table 22**). Although assignment accuracies to the other reporting groups we could analyze in this way were similar between SNP panels (**Table 22**), 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.

We detected samples (n=28, 1.5%) from the coastal lineage (i.e., 01_WCOAST – 06_KLICKR reporting groups) that were incorrectly assigned to reporting groups of the inland lineage (i.e., 07_MGILCS – 14_UPSALM reporting groups (**Table 20**Figure 17). We similarly detected samples (n=29, 0.34%) from reporting groups from the inland lineage were incorrectly assigned to coastal lineage reporting groups (**Table 20**). Incorrect assignments were typically distributed across multiple reporting groups, but the largest proportion of incorrect assignments were consistently to three reporting groups (07_MGILCS, 06_KLICKR, and 05_BWSALM). Samples from the geographically large 07_MGILCS reporting group were incorrectly assigned to every reporting group except 01_WCOAST, 03_SKAMAN, and 04_WILLAM (**Table 20**).
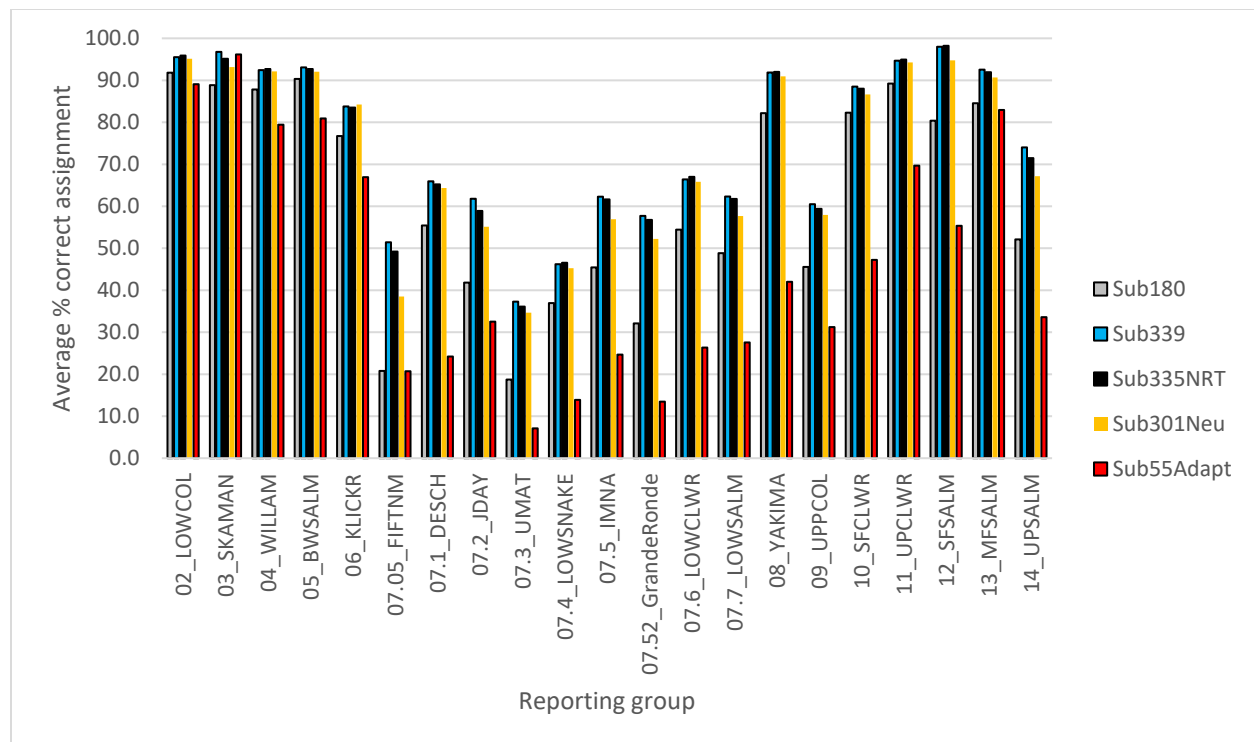
Figure 17. Proportion of steelhead in leave-one-out tests that assigned correctly for each reporting group by lineage using the following subsets of SNPs: 180 SNPs from baseline v3.3 ("Sub180"), 339 SNPs that include putatively neutral and adaptive loci ("Sub339"), 335 SNPs that exclude the run timing candidate SNPs ("Sub335NRT"), 301 SNPs that were putatively neutral ("Sub301Neu"), and 55 SNPs that were putatively adaptive ("Sub55Adapt").

996 **Table 21. Comparison of PBT expected reporting groups versus the observed reporting groups using 177 SNPs (baseline 3.3)**
997 **based on the assignments from the Bonneville 2019 mixture.**

	Observed GSI							
PBT Expected GSI	03_SKAMAN	07_MGILCS	09_UPPCOL	10_SFCLWR	11_UPCLWR	14_UPSALM	Total	Correct%
03_SKAMAN	22						22	100.0%
07_MGILCS		100	2			13	115	87.0%
09_UPPCOL		5	4			1	10	40.0%
10_SFCLWR		7		209	1	3	220	95.0%
14_UPSALM		17	1	1		88	107	82.2%

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999 **Table 22. Comparison of PBT expected reporting groups versus the observed reporting groups using 335 SNPs (new baseline)**
1000 **based on the assignments from the Bonneville 2019 mixture.**

	Observed GSI							
PBT Expected GSI	03_SKAMAN	07_MGILCS	09_UPPCOL	10_SFCLWR	11_UPCLWR	14_UPSALM	Total	Correct%
03_SKAMAN	22						22	100.0%
07_MGILCS		112	2	1			115	97.4%
09_UPPCOL		3	7				10	70.0%
10_SFCLWR		3		216	1		220	98.2%
14_UPSALM		68	2			37	107	34.6%

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1003 *Sockeye (363 SNPs) parent baseline for identifying reintroduced stocks from Yakima River*
1004   This is the first year we have been able to utilize candidate parents that were genotyped from tissues collected from carcass
1005 spawning surveys and directly from the fish translocated from Priest Rapids Dam and released into the Yakima River (**Table 23**). A
1006 combination of parent-pair assignments (trio assignment) and single parent assignments were performed to obtain as large of a sample
1007 of offspring as possible. Tag rates assumed the ability to perform single parent assignments.
1008
1009
1010 **Table 23. The numbers of candidate parents genotyped relative to the number of returning and translocated adult sockeye to**
1011 **the Yakima River each year.**

						Genotypes		Max	Tag rate	
Year	Outplants	Prosser	Roza	O+P	O+R	383	88	YR	383	88
2009	1000	12	17	1012	1017	0	0	1017	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	0	985	10154	0.0%	18.5%
2013	4500	696	691	5196	5191	1165	1244	5196	39.8%	42.2%
2014	10000	2678	2576	12678	12576	2906	3146	12678	40.6%	43.5%
2015	10000	342	95	10342	10095	698	1182	10342	13.0%	21.6%
2016	10000	3742	3949	13742	13949	4245	4245	13949	51.6%	51.6%
2017	1000	372	137	1372	1137	422	422	1372	52.1%	52.1%
2018	4700	456	201	5156	4901	1368	1368	5156	46.0%	46.0%
2019	0	110	201	110	201	199	199	201	100.0%	100.0%

1012 *Note: "Outplants" indicate the number of sockeye translocated into the Yakima River, and "Prosser" and "Roza" dam counts were*
1013 *summed ("O+P" or "O+R") with the outplants to provide an estimate of the total escapement of spawners in the Yakima River each*
1014 *year. We used whichever number was greatest ("O+P" or "O+R") to provide the maximum escapement of the Yakima River ("Max*
1015 *YR"). A portion of these spawners were successfully genotyped either using 383 or 88 (the legacy panel) SNPs and tag rates were*
1016 *calculated using the Max YR as the denominator. When cross information and the gender of the broodstock samples is unknown, then*
1017 *the tag rate for single parentage is : $1-(f\_t)^2$, where f_t is the fraction of the total broodstock not genotyped.*

1018   *Parentage based tagging assignments of Chinook salmon in harvest mixtures*
1019   A summary of the Chinook harvest samples that were genotyped (derived from Table 6)
1020   is presented in Table 24. Of the 3,993 harvest Chinook analyzed, PBT identified 1,944 hatchery-
1021   origin individuals that could be confidently assigned back to 79 hatchery broodstock sources
1022   (i.e., 3 Lower Columbia, 25 Snake River, and 51 Columbia River hatchery broodstocks) spawned
1023   in 2012-2016. The majority of PBT assigned individuals were from the 2014 brood year (i.e., 4-
1024   years-old).

1025 **Table 24. Summary of the Chinook salmon harvest samples by fishery, region, and fin clip**
1026 **in 2018.**

Fishery	Region	Clip	Spring	Summer	Fall	GSI	PBT	Total	%PBT
Sport	A	AD	347			157	190	347	54.8%
	B	AD	526			273	253	526	48.1%
Test		AD	567			283	284	567	50.1%
	B	AI	83			58	25	83	30.1%
Ceremonial	Below_BON	AD	235			79	156	235	66.4%
		AI	38			25	13	38	34.2%
	ZN6	AD	139			50	89	139	64.0%
		AI	29			16	13	29	44.8%
Sport	A	AD		30		12	18	30	60.0%
	B	AD		42		13	29	42	69.0%
Treaty	ZN6	AD		165		31	134	165	81.2%
		AI		58		44	14	58	24.1%
Commercial	A	AD			198	53	145	198	73.2%
		AI			100	81	19	100	19.0%
Sport	A	AD			45	17	28	45	62.2%
		AI			119	94	25	119	21.0%
	B	AD			32	12	20	32	62.5%
		AI			79	67	12	79	15.2%
Test	B	AD			299	115	184	299	61.5%
		AI			172	147	25	172	14.5%
Treaty	ZN6	AD			234	44	190	234	81.2%
		AI			456	378	78	456	17.1%
						2049	1944	3993	48.7%

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Comparison of proportion of PBT assignments among Chinook salmon fisheries

The average of adipose-clipped Chinook salmon from fishery mixtures across all periods was that were assigned via PBT was 64% (range = 48% – 81%, Table 24). The fishery(s) with the minimum and maximum assigned adipose-clipped Chinook salmon was the spring sport fishery in region B and both summer and fall Treaty zone 6 fisheries, respectively. Among the adipose-intact fish, the average assignment via PBT was expectedly lower (average = 24%, range = 14% – 45%; Table 24). Among the fisheries with adipose-intact fish, the minimum and maximum PBT-assigned Chinook salmon was observed in the fall test and the spring ceremonial fishery, respectively. For both adipose-clipped and adipose-intact fish, the collections with the minimum PBT-assigned fish were due to areas that receive higher proportions of lower river hatchery fish that are not as well covered in the PBT baseline.

The test fishery in the Chinook Salmon Spring Management Period of 2018

We examined one source of information that could potentially be useful to managers particularly on years when the spring Chinook Salmon run is delayed. There is a test fishery that is typically conducted by WDFW on Sundays each week in the early spring (February – May). Four boats are contracted to perform a series of drifts (typically four drifts per boat) through the commercial zones 1-3 near the mouth of the Columbia River. The drifts are targeted for Spring Chinook and biodata and a tissue for genetic analysis is collected. Visual Stock ID classifies fish as lower river (West Cascade Spring and Willamette River stocks) versus upriver (all stocks destined above Bonneville Dam). Genetic Analysis can refine the initial Visual Stock ID calls and more accurately classify these fish into lower and upriver stocks. For example, we characterized reporting groups among the hatchery clipped, hatchery unclipped, and natural-origin VSI-upriver fish caught in the test fishery (Table 25, **Table 26**). We use a catch per unit effort (CPUE) metric in the test fishery that is based on the number of upriver Chinook handled per test fishery drift. If the test fishery CPUE were lagged 13 days the peak in CPUE appears to correspond with a peak in Bonneville weekly counts (Figure 21). So if the in-season genetic analysis includes the data from the test fishery, our report may be able to predict the abundance of particular hatchery and natural-origin stocks that we can expect to pass Bonneville Dam up to 2 weeks later which would be useful information for USvOR managers. In fact, comparison of the relative proportions of the hatchery broodstocks that were estimated in the test fishery and Bonneville Dam showed that these samples from these two sources have very similar compositions of stocks (Figure 19). Further, there is high correlation between the estimated CPUE of each hatchery broodstock in the test fishery and the estimated abundance of the same broodstocks passing Bonneville Dam in weeks lagged 13 days after the test fishery.

Table 25. Summary of the stock composition at the reporting group level of the VSI-identified upriver spring Chinook salmon in the test fishery of 2018 in units of catch-per-unit-effort (CPUE, # of fish per # of drifts).

		Hatchery origin-Clipped	Hatchery origin-No Clip	Natural origin- No Clip
Run type	**Reporting Group Code**	**Estimated abundance**	**Estimated abundance**	**Estimated abundance**

		Mean	95% CI	Mean	95% CI	Mean	95% CI
Spring	01_YOUNGS						
Spring	02_WCASSP	0.29	0.08 – 0.57				
Fall	03_WCASFA	0.04	0 – 0.15				
Spring	04_WILLAM	0.58	0.26 – 1				
Fall	05_SPCRTU						
Spring	06_KLICKR	0.04	0 – 0.15				
Spring	07_DESCSP	0.12	0 – 0.31			0.15	0.03 – 0.31
Spring	08_JOHNDR					0.04	0 – 0.09
Spring	09_YAKIMA	0.17	0 – 0.41			0.20	0.03 – 0.4
Spring	10_UCOLSP	0.61	0.22 – 1.07	0.13	0 – 0.4	0.23	0.06 – 0.44
Spring	11_TUCANO			0.08	0 – 0.24		
Spring/Summer	12_HELLSC	2.37	1.74 – 2.98	0.28	0 – 0.58	0.24	0.07 – 0.45
Spring/Summer	13_SFSALM	0.09	0 – 0.3				
Spring/Summer	14_CHMBLN						
Spring/Summer	15_MFSALM						
Spring/Summer	16_UPSALM	0.26	0.07 – 0.53				
Fall	17_DESCFA						
Summer/Fall	18_UCOLSF						
Fall	19_SRFALL						
Spring	20_BONPOOLSP	2.05	1.38 – 2.66	0.13	0 – 0.39		
Spring	21_UMATILLASP	0.54	0.24 – 0.91	0.07	0 – 0.21		
Fall	22_BONPOOLFA						
Fall	23_UMATILLAFA						
	Total	**7.15**		**0.70**		**0.86**	

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1071   **Table 26. Summary of the stock composition at the broodstock level of the hatchery-origin VSI-identified upriver**

1072   **spring Chinook salmon in the test fishery of 2018 in units of catch-per-unit-effort (CPUE, # of fish per # of drifts).**

Expected Run Time	Hatchery	code	Brood year	Adult Chinook AD			Adult Chinook AI			GSI RepGrp
				MLE	95% CI	Percent	MLE	95% CI	Percent	
01Spring	Parkdale Fish Facility	OtsPFF14_sp	2014	0.08	0 – 0.2	1.1%			0.0%	02_WCASSP
01Spring	Klickitat Hatchery	OtsKH14_sp	2014	0.04	0 – 0.12	0.5%			0.0%	06_KLICKR
01Spring	Round Butte Fish Hatchery	OtsRB14_sp	2014	0.08	0 – 0.19	1.1%			0.0%	07_DESCSP
01Spring	Yakima River Roza Dam	OtsYR14int_sp	2014	0.11	0 – 0.23	1.6%			0.0%	09_YAKIMA
01Spring	Yakima River Roza Dam	OtsYR14seg_sp	2014	0.06	0 – 0.17	0.8%			0.0%	09_YAKIMA
01Spring	Chief Joseph Hatchery	OtsCJH14_sp	2014	0.04	0 – 0.13	0.6%			0.0%	10_UCOLSP
01Spring	Leavenworth National Fish Hatchery	OtsLNFH14_sp	2014	0.08	0 – 0.15	1.1%			0.0%	10_UCOLSP
01Spring	Winthrop National Fish Hatchery	OtsWTP14_sp	2014	0.15	0.04 – 0.28	2.1%	0.13	0 – 0.31	18.5%	10_UCOLSP
01Spring	Winthrop National Fish Hatchery	OtsWTP15_sp	2015	0.04	0 – 0.11	0.5%			0.0%	10_UCOLSP
01Spring	Lyons Ferry Fish Hatchery	OtsTUCW14S_sp	2014			0.0%	0.08	0 – 0.16	11.5%	11_TUCANO
01Spring	Clearwater Fish Hatchery	OtsCLWH14S_sp	2014	0.66	0.43 – 0.89	9.3%			0.0%	12_HELLSC
01Spring	Clearwater Fish Hatchery	OtsCLWH15S_sp	2015	0.04	0 – 0.11	0.5%			0.0%	12_HELLSC
01Spring	Clearwater Fish Hatchery	OtsPOWP14S_sp	2014	0.38	0.19 – 0.57	5.3%	0.12	0 – 0.29	17.5%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsDWOR15S_sp	2015	0.08	0 – 0.2	1.1%	0.04	0 – 0.12	5.6%	12_HELLSC

Run	Hatchery	Stock	Year							Group
01Spring	Lookingglass Fish Hatchery	OtsCTHW14S_sp	2014	0.04	0 – 0.13	0.6%			0.0%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsGRUW14S_sp	2014	0.04	0 – 0.12	0.5%	0.09	0 – 0.26	12.3%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsLOOK14S_sp	2014	0.08	0 – 0.17	1.1%			0.0%	12_HELLSC
01Spring	Nez Perce	OtsNPFH14S_sp	2014			0.0%	0.04	0 – 0.11	5.3%	12_HELLSC
01Spring	Carson National Fish Hatchery	OtsCAR13_sp	2013	0.05	0 – 0.14	0.7%			0.0%	20_BONPOOLSP
01Spring	Carson National Fish Hatchery	OtsCAR14_sp	2014	0.61	0.38 – 0.86	8.5%	0.05	0 – 0.1	6.9%	20_BONPOOLSP
01Spring	Little White Salmon National Fish Hatchery	OtsLWS13_sp	2013	0.06	0 – 0.14	0.9%			0.0%	20_BONPOOLSP
01Spring	Little White Salmon National Fish Hatchery	OtsLWS14_sp	2014	1.33	1 – 1.65	18.6%	0.08	0 – 0.25	12.1%	20_BONPOOLSP
01Spring	Umatilla Fish Hatchery	OtsUMA14_sp	2014	0.50	0.3 – 0.74	7.0%	0.07	0 – 0.14	10.3%	21_UMATILLASP
01Spring	Umatilla Fish Hatchery	OtsUMA15_sp	2015	0.04	0 – 0.12	0.5%			0.0%	21_UMATILLASP
02Spring/Summer	McCall Fish Hatchery	OtsMCCA14S_spsu	2014	0.05	0 – 0.16	0.7%			0.0%	13_SFSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT14S_spsu	2014	0.26	0.11 – 0.45	3.7%			0.0%	16_UPSALM
#N/A	#N/A	Unassigned	#N/A	2.26	1.85 – 2.66	31.6%			0.0%	#N/A
		TOTAL		7.15		100.0%	0.70		100.0%	

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1075   .
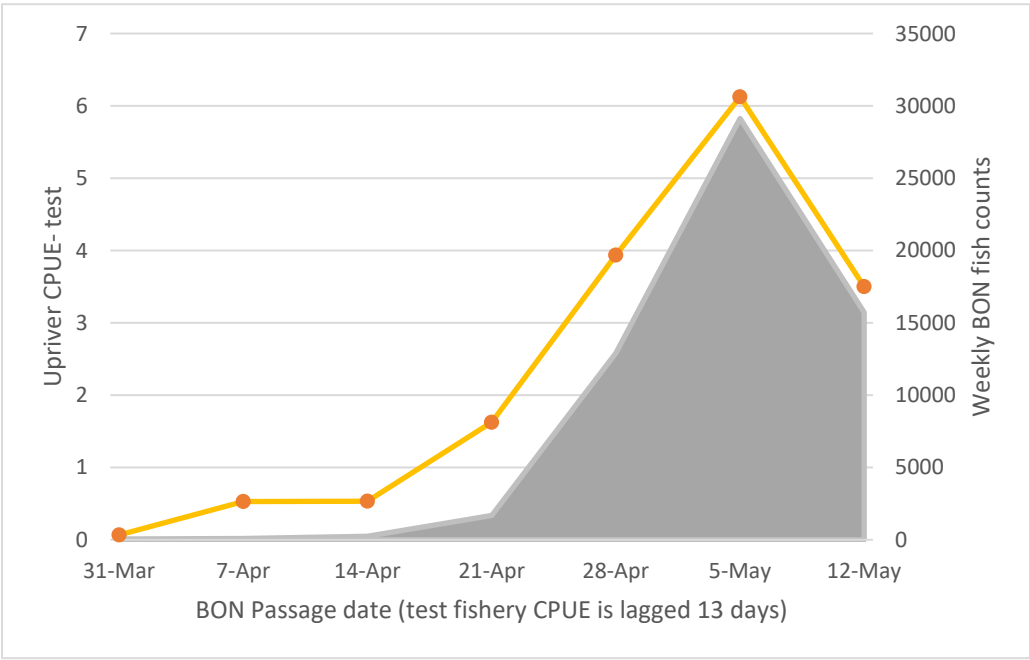
Figure 18. The relationship between the test fishery upriver Chinook Salmon CPUE (line) and weekly fish counts at Bonneville Dam (solid gray) in 2018.

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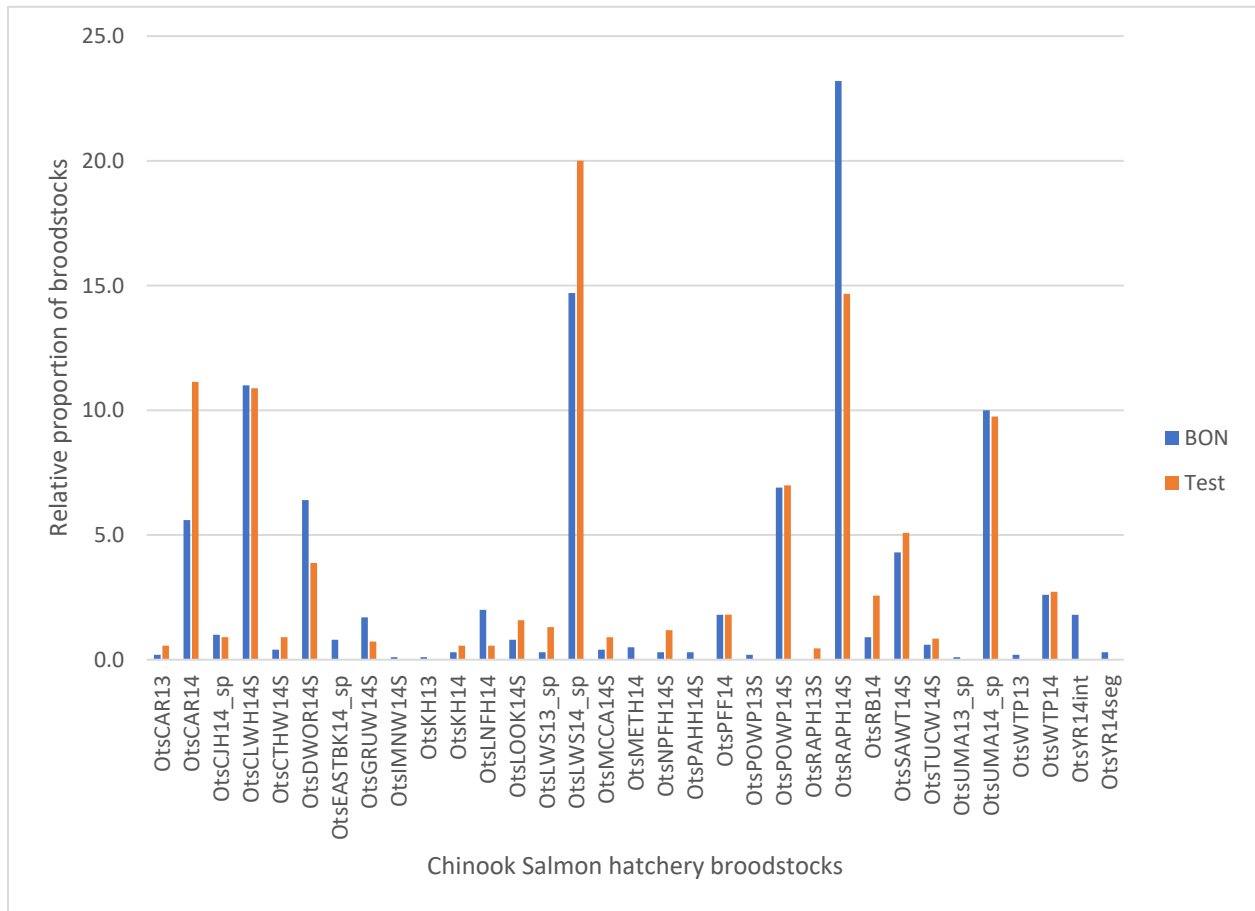
Figure 19. Relative proportions of hatchery broodstocks of upriver Chinook Salmon caught in the test fishery (March 18 – April 29) compared to Chinook Salmon that passed Bonneville Dam in corresponding weeks lagged 13 days from the test fishery (March 31 – May 12) in 2018.
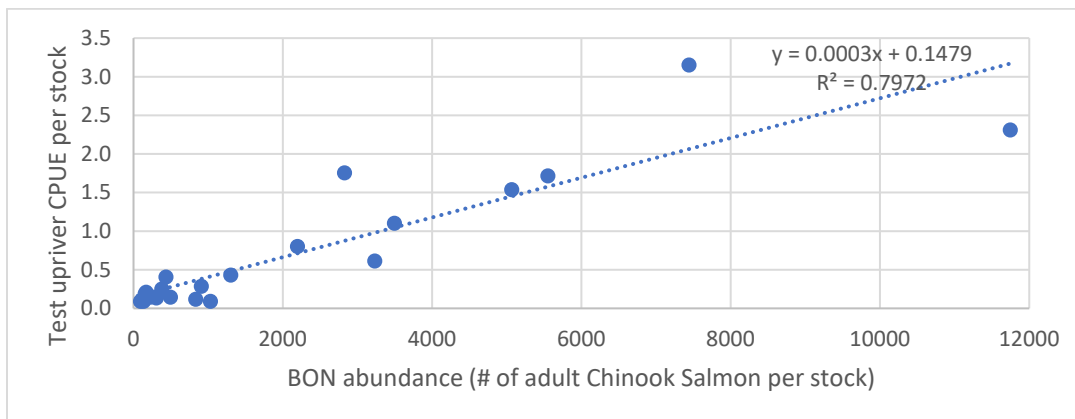
Figure 20. Correlation of the test fishery CPUE with the estimated abundance passing Bonneville Dam of hatchery broodstocks identified by PBT analysis in 2018.

1089   We reported spring sport fishery results for reporting group level stock composition
1090 (Table 27) and the hatchery broodstock composition (**Table 28**) of the kept fish (clipped
1091 hatchery-origin fish).
1092
1093 **Table 27. Summary of the stock composition at the reporting group level of the kept spring**
1094 **Chinook salmon in the Non-Treaty sport fishery of 2018 in units of reported catch.**

		Hatchery origin-Clipped	
		Estimated abundance	
Run type	Reporting Group Code	Mean	95% CI
Spring	01_YOUNGS		
Spring	02_WCASSP	675	489 – 871
Fall	03_WCASFA	36	0 – 91
Spring	04_WILLAM	1,133	905 – 1368
Fall	05_SPCRTU		
Spring	06_KLICKR	94	29 – 170
Spring	07_DESCSP	60	9 – 122
Spring	08_JOHNDR		
Spring	09_YAKIMA	96	24 – 199
Spring	10_UCOLSP	459	296 – 634
Spring	11_TUCANO		
Spring/Summer	12_HELLSC	1,884	1607 – 2186
Spring/Summer	13_SFSALM	369	214 – 549
Spring/Summer	14_CHMBLN		
Spring/Summer	15_MFSALM		
Spring/Summer	16_UPSALM	80	19 – 159
Fall	17_DESCFA		
Summer/Fall	18_UCOLSF	718	558 – 858
Fall	19_SRFALL	7	0 – 44
Spring	20_BONPOOLSP	1,579	1299 – 1829
Spring	21_UMATILLASP	319	201 – 447
Fall	22_BONPOOLFA		
Fall	23_UMATILLAFA		
	Total	**7,509**	

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1099   **Table 28. Summary of the stock composition at the broodstock level of the kept spring Chinook salmon in the Non-**
1100   **Treaty sport fishery of 2018 in units of reported catch.**

| Expected Run Time | Hatchery | Broodstock | Broodyear | Adult Chinook AD | | | |
				MLE	95% CI	Percent	GSI RepGrp
01Spring	Parkdale Fish Facility	OtsPFF13_sp	2013	13	0 – 39	0.2%	02_WCASSP
01Spring	Parkdale Fish Facility	OtsPFF14_sp	2014	104	59 – 161	1.4%	02_WCASSP
01Spring	Klickitat Hatchery	OtsKH13_sp	2013	37	9 – 71	0.5%	06_KLICKR
01Spring	Klickitat Hatchery	OtsKH14_sp	2014	29	9 – 59	0.4%	06_KLICKR
01Spring	Round Butte Fish Hatchery	OtsRB14_sp	2014	47	18 – 84	0.6%	07_DESCSP
01Spring	Round Butte Fish Hatchery	OtsRB15_sp	2015	12	0 – 37	0.2%	07_DESCSP
01Spring	Yakima River Roza Dam	OtsYR14seg_sp	2014	71	27 – 125	0.9%	09_YAKIMA
01Spring	Yakima River Roza Dam	OtsYR14int_sp	2014	20	0 – 43	0.3%	09_YAKIMA
01Spring	Chief Joseph Hatchery	OtsCJH14_sp	2014	41	10 – 82	0.5%	10_UCOLSP
01Spring	Eastbank Fish Hatchery	OtsEASTBK14_sp	2014	18	0 – 37	0.2%	10_UCOLSP
01Spring	Eastbank Fish Hatchery	OtsEASTBK15_sp	2015	23	0 – 46	0.3%	10_UCOLSP
01Spring	Leavenworth National Fish Hatchery	OtsLNFH14_sp	2014	64	28 – 110	0.9%	10_UCOLSP
01Spring	Winthrop National Fish Hatchery	OtsWTP14_sp	2014	29	0 – 59	0.4%	10_UCOLSP
01Spring	Clearwater Fish Hatchery	OtsCLWH14S_sp	2014	476	368 – 587	6.3%	12_HELLSC
01Spring	Clearwater Fish Hatchery	OtsPOWP14S_sp	2014	168	110 – 232	2.2%	12_HELLSC
01Spring	Dworshak National Fish Hatchery	OtsDWOR15S_sp	2015	12	0 – 35	0.2%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsCTHW14S_sp	2014	32	10 – 63	0.4%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsLOOK14S_sp	2014	62	29 – 104	0.8%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsLSTW14S_sp	2014	30	0 – 74	0.4%	12_HELLSC
01Spring	Carson National Fish Hatchery	OtsCAR13_sp	2013	44	11 – 89	0.6%	20_BONPOOLSP
01Spring	Carson National Fish Hatchery	OtsCAR14_sp	2014	625	504 – 751	8.3%	20_BONPOOLSP
01Spring	Little White Salmon National Fish Hatchery	OtsLWS13_sp	2013	54	18 – 91	0.7%	20_BONPOOLSP
01Spring	Little White Salmon National Fish Hatchery	OtsLWS14_sp	2014	856	718 – 994	11.4%	20_BONPOOLSP
01Spring	Umatilla Fish Hatchery	OtsUMA13_sp	2013	9	0 – 28	0.1%	21_UMATILLASP
01Spring	Umatilla Fish Hatchery	OtsUMA14_sp	2014	309	227 – 398	4.1%	21_UMATILLASP

02Spring/Summer	McCall Fish Hatchery	OtsMCCA14S_spsu	2014	307	212 – 416	4.1%	13_SFSALM
02Spring/Summer	McCall Fish Hatchery	OtsMCCA15S_spsu	2015	25	0 – 51	0.3%	13_SFSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT14S_spsu	2014	31	9 – 61	0.4%	16_UPSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT15S_spsu	2015	11	0 – 33	0.1%	16_UPSALM
03Summer	Chief Joseph Hatchery	OtsCJH13int_su	2013	16	0 – 49	0.2%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCJH14int_su	2014	76	38 – 127	1.0%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEASTBK12_su	2012	34	11 – 68	0.5%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEASTBK13_su	2013	45	11 – 80	0.6%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEASTBK14_su	2014	90	45 – 136	1.2%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH14_su	2014	92	31 – 154	1.2%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELLS13_su	2013	55	21 – 98	0.7%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELLS14_su	2014	113	57 – 170	1.5%	18_UCOLSF
#N/A	#N/A	Unassigned	#N/A	3428	3191 – 3669	45.7%	
		TOTAL		7,509		100.0%	

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1104   Our analyses of the spring Treaty permit fishery below Bonneville Dam, allowed us to estimate the portion of stocks that were
1105 natural-origin (8.8%) compared to the total catch that included clipped and unclipped hatchery-origin Chinook salmon (Table 29).
1106 We could further estimate abundances of hatchery broodstocks among the hatchery-origin fish (**Table 30**).
1107
1108 **Table 29. Summary of the stock composition at the reporting group level of the Yakama Nation permit fishery below**
1109 **Bonneville Dam in 2018 in units of reported catch.**

Reporting Group name	Run type	Reporting Group Code	Hatchery origin- Clipped Estimated abundance		Hatchery origin- No Clip Estimated abundance		Natural origin- No Clip Estimated abundance	
			Mean	95% CI	Mean	95% CI	Mean	95% CI
Youngs Bay	Spring	01_YOUNGS						
West Cascade Spring	Spring	02_WCASSP	7	0 – 16				
West Cascade Fall	Fall	03_WCASFA						
Willamette	Spring	04_WILLAM						
Spring Creek Tule	Fall	05_SPCRTU						
Klickitat	Spring	06_KLICKR	2	0 – 7				
Deschutes spring	Spring	07_DESCSP	8	2 – 18			2	0 – 5
John Day	Spring	08_JOHNDR	2	0 – 7			3	0 – 7
Yakima	Spring	09_YAKIMA	5	0 – 15			2	0 – 5
Upper Columbia spring	Spring	10_UCOLSP	41	22 – 64	5	0 – 14	9	3 – 16
Tucannon	Spring	11_TUCANO			4	0 – 11		
Hells Canyon	Spring/Summer	12_HELLSC	192	156 – 225	10	2 – 24	13	6 – 21
South Fork Salmon	Spring/Summer	13_SFSALM	5	0 – 13			2	0 – 5
Chamberlain Creek	Spring/Summer	14_CHMBLN						
Middle Fork Salmon	Spring/Summer	15_MFSALM					3	0 – 7
Upper Salmon	Spring/Summer	16_UPSALM	18	7 – 34			7	2 – 13

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Deschutes fall	Fall	17_DESCFA						
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF						
Snake River fall	Fall	19_SRFALL						
Bonneville Pool spring	Spring	20_BONPOOLSP	84	57 – 111	4	0 – 12		
Umatilla spring	Spring	21_UMATILLASP	28	12 – 46				
Bonneville Pool fall	Fall	22_BONPOOLFA						
Umatilla fall	Fall	23_UMATILLAFA						
		Total	**391**		**23**		**40**	

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Table 30. Summary of the stock composition at the broodstock level of the Yakama Nation permit fishery below
Bonneville Dam of 2018 in units of reported catch.

Expected Run Time	Hatchery	Broodstock	Broody ear	Adult Chinook AD			Adult Chinook AI			GSI RepGrp
				MLE	95% CI	Percent	MLE	95% CI	Percent	
01Spring	Parkdale Fish Facility	OtsPFF14_sp	2014	7	2 – 14	1.8%			0.0%	02_WCASSP
01Spring	Round Butte Fish Hatchery	OtsRB14_sp	2014	8	3 – 15	2.1%			0.0%	07_DESCSP
01Spring	Yakima River Roza Dam	OtsYR14int_sp	2014	5	2 – 10	1.3%			0.0%	09_YAKIMA
01Spring	Chief Joseph Hatchery	OtsCJH15_sp	2015			0.0%	2	0 – 5	7.3%	10_UCOLSP
01Spring	Eastbank Fish Hatchery	OtsEASTBK14_sp	2014	5	0 – 10	1.3%			0.0%	10_UCOLSP
01Spring	Leavenworth National Fish Hatchery	OtsLNFH14_sp	2014	8	3 – 15	2.1%			0.0%	10_UCOLSP
01Spring	Winthrop National Fish Hatchery	OtsWTP14_sp	2014	7	2 – 12	1.8%	4	0 – 9	15.6%	10_UCOLSP
01Spring	Lyons Ferry Fish Hatchery	OtsTUCW14S_sp	2014			0.0%	4	0 – 9	16.3%	11_TUCANO
01Spring	Clearwater Fish Hatchery	OtsCLWH14S_sp	2014	60	43 – 76	15.4%			0.0%	12_HELLSC
01Spring	Clearwater Fish Hatchery	OtsPOWP14S_sp	2014	22	12 – 32	5.6%	3	0 – 7	14.8%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsCTHW14S_sp	2014	4	0 – 8	1.0%	2	0 – 6	8.4%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsGRUW14S_sp	2014	2	0 – 5	0.4%	3	0 – 8	14.7%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsLOOK14S_sp	2014	9	4 – 16	2.3%			0.0%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsCTHW15S_sp	2015	2	0 – 5	0.4%			0.0%	12_HELLSC
01Spring	Nez Perce	OtsNPFH14S_sp	2014			0.0%	2	0 – 5	7.5%	12_HELLSC
01Spring	Rapid River Fish Hatchery	OtsRAPH15S_sp	2015	2	0 – 5	0.5%			0.0%	12_HELLSC

01Spring	Carson National Fish Hatchery	OtsCAR14_sp	2014	35	24 – 49	9.1%	2	0 – 6	8.2%	20_BONPOOLSP
01Spring	Carson National Fish Hatchery	OtsCAR15_sp	2015	2	0 – 5	0.4%			0.0%	20_BONPOOLSP
01Spring	Little White Salmon National Fish Hatchery	OtsLWS14_sp	2014	46	31 – 60	11.9%	2	0 – 5	7.3%	20_BONPOOLSP
01Spring	Umatilla Fish Hatchery	OtsUMA14_sp	2014	28	18 – 40	7.2%			0.0%	21_UMATILLASP
02Spring/Summer	McCall Fish Hatchery	OtsMCCA14S_spsu	2014	2	0 – 7	0.6%			0.0%	13_SFSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT14S_spsu	2014	13	7 – 22	3.4%			0.0%	16_UPSALM
#N/A	#N/A	Unassigned	#N/A	123	101 – 146	31.5%			0.0%	#N/A
		TOTAL		391		100.0%	23		100.0%	

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1118   For the summer Non-Treaty sport fishery below Bonneville Dam, we estimated report
1119 group composition (Table 31) of the kept fish (clipped hatchery-origin), and further broke these
1120 groups into abundance estimates of broodstocks (**Table 32**).
1121
1122 **Table 31. Summary of the stock composition at the reporting group level of the summer**
1123 **Non-Treaty sport fishery below Bonneville Dam in 2018 in units of reported catch.**

Reporting Group name	Run type	Reporting Group Code	Hatchery origin-Clipped Estimated abundance	
			Mean	95% CI
Youngs Bay	Spring	01_YOUNGS		
West Cascade Spring	Spring	02_WCASSP	14	0 – 56
West Cascade Fall	Fall	03_WCASFA		
Willamette	Spring	04_WILLAM	180	56 – 309
Spring Creek Tule	Fall	05_SPCRTU		
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	17	0 – 66
South Fork Salmon	Spring/Summer	13_SFSALM	40	0 – 119
Chamberlain Creek	Spring/Summer	14_CHMBLN		
Middle Fork Salmon	Spring/Summer	15_MFSALM		
Upper Salmon	Spring/Summer	16_UPSALM	22	0 – 83
Deschutes fall	Fall	17_DESCFA		
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	755	627 – 925
Snake River fall	Fall	19_SRFALL		
Bonneville Pool spring	Spring	20_BONPOOLSP		
Umatilla spring	Spring	21_UMATILLASP		
Bonneville Pool fall	Fall	22_BONPOOLFA		
Umatilla fall	Fall	23_UMATILLAFA		
		Total	**1,027**	

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1127 **Table 32. Summary of the stock composition at the broodstock level of the summer Non-Treaty sport fishery below**
1128 **Bonneville Dam of 2018 in units of reported catch.**

Summer Sport Fishery 2018				Adult Chinook AD			
Expected Run Time	**Hatchery**	**Broodstock**	**Broodyear**	**MLE**	**95% CI**	**Percent**	**GSI RepGrp**
01Spring	South Santiam Hatchery	OtsSSANT16_sp	2016	15	0 – 45	1.5%	04_WILLAM
02Spring/Summer	Lookingglass Fish Hatchery	OtsIMNW15S_spsu	2015	17	0 – 50	1.6%	12_HELLSC
02Spring/Summer	McCall Fish Hatchery	OtsMCCA14S_spsu	2014	40	0 – 79	3.9%	13_SFSALM
03Summer	Chief Joseph Hatchery	OtsCJH13seg_su	2013	48	16 – 96	4.7%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCJH13int_su	2013	61	20 – 123	6.0%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCJH14int_su	2014	128	64 – 208	12.5%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCJH14seg_su	2014	65	0 – 162	6.3%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEASTBK12_su	2012	29	0 – 57	2.8%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEASTBK13_su	2013	57	14 – 100	5.6%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEASTBK14_su	2014	143	71 – 214	13.9%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEASTBK15_su	2015	14	0 – 43	1.4%	18_UCOLSF
03Summer	Entiat National Fish Hatchery	OtsENFH14_su	2014	136	58 – 214	13.3%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELLS13_su	2013	14	0 – 43	1.4%	18_UCOLSF
03Summer	Wells Fish Hatchery	OtsWELLS14_su	2014	29	0 – 71	2.8%	18_UCOLSF
#N/A	#N/A	Unassigned	#N/A	232	120 – 346	22.6%	#N/A
		TOTAL		1,027		100.0%	

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1130   The stock composition of the summer Treaty zone 6 commercial fishery was characterized by reporting group level of the
1131   clipped and unclipped hatchery-origin and the natural-origin Chinook salmon (Table 33). We further categorized hatchery-origin
1132   stocks by broodstock (**Table 34**).

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1134   **Table 33. Summary of the stock composition at the reporting group level of the summer Treaty Zone 6 commercial fishery in**
1135   **2018 in units of reported catch.**

		Hatchery origin- Clipped		Hatchery origin- No Clip		Natural origin- No Clip	
		Estimated abundance		Estimated abundance		Estimated abundance	
Run type	**Reporting Group Code**	**Mean**	**95% CI**	**Mean**	**95% CI**	**Mean**	**95% CI**
Spring	01_YOUNGS						
Spring	02_WCASSP						
Fall	03_WCASFA						
Spring	04_WILLAM	35	0 – 170			28	0 – 85
Fall	05_SPCRTU						
Spring	06_KLICKR						
Spring	07_DESCSP					31	0 – 91
Spring	08_JOHNDR						
Spring	09_YAKIMA						
Spring	10_UCOLSP	36	0 – 249	48	0 – 193	28	0 – 85
Spring	11_TUCANO						
Spring/Summer	12_HELLSC	397	58 – 815	33	0 – 131	28	0 – 85
Spring/Summer	13_SFSALM	291	0 – 730	179	0 – 403	80	6 – 179
Spring/Summer	14_CHMBLN						
Spring/Summer	15_MFSALM						
Spring/Summer	16_UPSALM	105	0 – 419			49	0 – 125
Fall	17_DESCFA						
Summer/Fall	18_UCOLSF	7,226	6573 – 7710	271	68 – 545	961	748 – 1158
Fall	19_SRFALL					28	0 – 85
Spring	20_BONPOOLSP						

Expected Run Time		Broodstock		
Spring	21_UMATILLASP			
Fall	22_BONPOOLFA			
Fall	23_UMATILLAFA			
	Total	**8,090**	**531**	**1,234**

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1138 **Table 34. Summary of the stock composition at the broodstock level of the summer Treaty Zone 6 commercial fishery of 2018**

1139 **in units of reported catch.**

Summer Treaty Fishery 2018				Adult Chinook AD			Adult Chinook AI			
Expected Run Time	Hatchery	Broodstock	Broody ear	MLE	95% CI	Percent	MLE	95% CI	Percent	GSI RepGrp
01Spring	Eastbank Fish Hatchery	OtsEASTBK14_sp	2014			0.0%	48	0 – 145	9.1%	10_UCOLSP
01Spring	Clearwater Fish Hatchery	OtsCLWH14S_sp	2014	54	0 – 163	0.7%			0.0%	12_HELLSC
01Spring	Clearwater Fish Hatchery	OtsPOWP14S_sp	2014			0.0%	33	0 – 98	6.2%	12_HELLSC
01Spring	Lookingglass Fish Hatchery	OtsLSTW14S_sp	2014	342	124 – 595	4.2%			0.0%	12_HELLSC
02Spring/Summer	McCall Fish Hatchery	OtsMCCA14S_spsu	2014	291	73 – 528	3.6%	179	45 – 313	33.7%	13_SFSALM
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT14S_spsu	2014	105	0 – 262	1.3%			0.0%	16_UPSALM
03Summer	Chief Joseph Hatchery	OtsCJH13seg_su	2013	645	364 – 920	8.0%	32	0 – 96	6.0%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCJH13int_su	2013	185	0 – 350	2.3%			0.0%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCJH14int_su	2014	914	592 – 1265	11.3%	36	0 – 108	6.8%	18_UCOLSF
03Summer	Chief Joseph Hatchery	OtsCJH14seg_su	2014	766	314 – 1180	9.5%			0.0%	18_UCOLSF
03Summer	Eastbank Fish Hatchery	OtsEASTBK12_su	2012	154	45 – 309	1.9%			0.0%	18_UCOLSF

03Summer	Eastbank Fish Hatchery	OtsEASTBK13_su	2013	332	121 – 553	4.1%	75	0 – 149	14.1%	18_UCOL SF
03Summer	Eastbank Fish Hatchery	OtsEASTBK14_su	2014	1,340	930 – 1722	16.6%	99	30 – 199	18.7%	18_UCOL SF
03Summer	Entiat National Fish Hatchery	OtsENFH13_su	2013	58	0 – 174	0.7%			0.0%	18_UCOL SF
03Summer	Entiat National Fish Hatchery	OtsENFH14_su	2014	1,422	959 – 1850	17.6%			0.0%	18_UCOL SF
03Summer	Entiat National Fish Hatchery	OtsENFH15_su	2015	59	0 – 177	0.7%			0.0%	18_UCOL SF
03Summer	Wells Fish Hatchery	OtsWELLS13_su	2013	401	186 – 641	5.0%			0.0%	18_UCOL SF
03Summer	Wells Fish Hatchery	OtsWELLS14_su	2014	929	604 – 1276	11.5%	29	0 – 87	5.5%	18_UCOL SF
#N/A	#N/A	Unassigned	#N/A	92	0 – 682	1.1%			0.0%	#N/A
		TOTAL		8,090		100.0%	531		100.0%	

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1142   The fall test (pound net) fishery reported a total of 600 kept Chinook salmon (all clipped hatchery-origin), which were
1143 comprised of a third lower river stocks (primarily 03_WCASFA), and 2/3 upriver stocks (18% Spring Creek tules and the remaining
1144 were upriver brights). Among the released stocks, 25% were lower river and the rest were upriver stocks (Table 35). The hatchery-
1145 origin fish were identified by broodstock (**Table 36**), and the lower river stocks were found to be comprised of Big Creek, Cowlitz
1146 Salmon Hatchery, North Toutle Hatchery, and Washougal Fish Hatchery.
1147
1148 **Table 35. Summary of the stock composition at the reporting group level of the fall test fishery in 2018 in units of reported**
1149 **catch.**

			Hatchery-origin Kept- Clipped		Hatchery origin- No Clip (RELEASED Chinook salmon)		Natural origin- No Clip	
Reporting Group name	**Run type**	**Reporting Group Code**	**Estimated abundance**		**Estimated abundance**		**Estimated abundance**	
			Mean	**95% CI**	**Mean**	**95% CI**	**Mean**	**95% CI**
Youngs Bay	Spring	01_YOUNGS					21	5 – 38
West Cascade Spring	Spring	02_WCASSP						
West Cascade Fall	Fall	03_WCASFA	196	138 – 244			212	166 – 263
Willamette	Spring	04_WILLAM	2	0 – 7				
Spring Creek Tule	Fall	05_SPCRTU	109	72 – 166	28	3 – 59	45	23 – 71
Klickitat	Spring	06_KLICKR						
Deschutes spring	Spring	07_DESCSP						
John Day	Spring	08_JOHNDR						
Yakima	Spring	09_YAKIMA						
Upper Columbia spring	Spring	10_UCOLSP						
Tucannon	Spring	11_TUCANO						
Hells Canyon	Spring/Summer	12_HELLSC						
South Fork Salmon	Spring/Summer	13_SFSALM						
Chamberlain Creek	Spring/Summer	14_CHMBLN						
Middle Fork Salmon	Spring/Summer	15_MFSALM						
Upper Salmon	Spring/Summer	16_UPSALM						
Deschutes fall	Fall	17_DESCFA					5	0 – 15

Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	76	47 – 111	42	10 – 88	431	376 – 488
Snake River fall	Fall	19_SRFALL	71	43 – 100	42	12 – 82	68	38 – 98
Bonneville Pool spring	Spring	20_BONPOOLSP						
Umatilla spring	Spring	21_UMATILLASP						
Bonneville Pool fall	Fall	22_BONPOOLFA	139	101 – 176	9	0 – 28		
Umatilla fall	Fall	23_UMATILLAFA	8	0 – 23				
		Total	**600**		**121**		**782**	

1150

1152 **Table 36. Summary of the stock composition at the broodstock level of the fall test fishery of 2018 in units of reported**
1153 **catch.**

Fall Pound Net (Test Fishery 2018)				Kept Chinook AD			Released Chinook AI			
Expected Run Time	Hatchery	Broodstock	Broody ear	MLE	95% CI	Percent	MLE	95% CI	Percent	GSI RepGrp
04Fall	Big Creek Hatchery	OtsBIG15_fa	2015	41	14 – 81	6.8%			0.0%	03_WCASFA
04Fall	Cowlitz Salmon Hatchery	OtsCOW15_fa	2015	2	0 – 7	0.4%			0.0%	03_WCASFA
04Fall	North Toutle Hatchery	OtsTOU15_fa	2015	10	2 – 17	1.6%			0.0%	03_WCASFA
04Fall	Washougal Fish Hatchery	OtsWAS15_fa	2015	10	0 – 30	1.7%			0.0%	03_WCASFA
04Fall	Spring Creek National Fish Hatchery	OtsSPCR15_fa	2015	85	65 – 107	14.2%	28	10 – 47	22.9%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR16_fa	2016	7	0 – 14	1.1%			0.0%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRH13_fa	2013	2	0 – 5	0.3%	7	0 – 20	5.6%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRH14_fa	2014	28	16 – 41	4.7%	9	0 – 20	7.2%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRH15_fa	2015	29	17 – 42	4.8%	27	10 – 47	22.3%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON14S_1_fa	2014	27	15 – 39	4.5%	8	0 – 20	7.0%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON15S_1_fa	2015	25	13 – 38	4.1%	16	5 – 33	13.5%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH14S_1_fa	2014	8	2 – 16	1.4%	9	0 – 21	7.2%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH15S_1_fa	2015	2	0 – 7	0.4%	9	0 – 21	7.2%	19_SRFALL
04Fall	Little White Salmon National Fish Hatchery	OtsLWS13_fa	2013	18	9 – 29	3.0%			0.0%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWS14_fa	2014	45	31 – 61	7.5%	3	0 – 10	2.8%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWS15_fa	2015	76	56 – 96	12.7%	5	0 – 16	4.4%	22_BONPOOLFA
04Fall	Umatilla Fish Hatchery	OtsUMA13_fa	2013	4	0 – 11	0.7%			0.0%	23_UMATILLAFA

04Fall	Umatilla Fish Hatchery	OtsUMA14_fa	2014	4	0 – 9	0.7%			0.0%	23_UMATILL AFA
#N/A	#N/A	Unassigned	#N/A	177	129 – 221	29.6%			0.0%	#N/A
		TOTAL		600		100.0 %	121		100.0 %	

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1155   The fall Non-Treaty sport fishery was not mark-selective and could be characterized by reporting group composition of clipped
1156 and unclipped hatchery-origin and natural-origin stocks (**Table 37**). We also reported the broodstock composition of the hatchery-
1157 origin Chinook salmon (**Table 38**).
1158
1159   **Table 37. Summary of the stock composition at the reporting group level of the kept adult Chinook salmon of the fall**
1160 **Non-Treaty sport fishery in 2018 in units of reported catch.**

Reporting Group name	Run type	Reporting Group Code	Hatchery origin- Clipped Estimated abundance		Hatchery origin- No Clip Estimated abundance		Natural origin- No Clip Estimated abundance	
			Mean	95% CI	Mean	95% CI	Mean	95% CI
Youngs Bay	Spring	01_YOUNGS					84	0 – 170
West Cascade Spring	Spring	02_WCASSP						
West Cascade Fall	Fall	03_WCASFA	344	74 – 629	218	0 – 846	597	269 – 940
Willamette	Spring	04_WILLAM					42	0 – 126
Spring Creek Tule	Fall	05_SPCRTU	371	124 – 699				
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				233	79 – 386
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	835	417 – 1321	413	121 – 753	3,674	3203 – 4172
Snake River fall	Fall	19_SRFALL	398	119 – 729	332	84 – 659	1,346	997 – 1705
Bonneville Pool spring	Spring	20_BONPOOLSP					
Umatilla spring	Spring	21_UMATILLASP					
Bonneville Pool fall	Fall	22_BONPOOLFA	482	159 – 842	397	116 – 760	
Umatilla fall	Fall	23_UMATILLAFA	37	0 – 186			
		Total	**2,467**		**1,360**		**5,975**	

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1163   **Table 38. Summary of the stock composition at the broodstock level of the kept adult Chinook salmon of the fall Non-**
1164   **Treaty sport fishery in 2018 in units of reported catch.**

Fall Sport Fishery 2018					Adult Chinook AD			Adult Chinook AI			
Order	Expected Run Time	Hatchery	Broodstock	Brood year	MLE	95% CI	Percent	MLE	95% CI	Percent	GSI RepGrp
	03Summer	Chief Joseph Hatchery	OtsCJH14seg_su	2014	95	0 – 286	3.9%			0.0%	18_UCOLSF
	04Fall	North Toutle Hatchery	OtsTOU15_fa	2015			0.0%	48	0 – 145	3.6%	03_WCASFA
	04Fall	Washougal Fish Hatchery	OtsWAS15_fa	2015			0.0%	169	0 – 508	12.4%	03_WCASFA
	04Fall	Spring Creek National Fish Hatchery	OtsSPCR15_fa	2015	298	130 – 476	12.1%			0.0%	05_SPCRTU
	04Fall	Priest Rapids Hatchery	OtsPRH13_fa	2013	37	0 – 111	1.5%			0.0%	18_UCOLSF
	04Fall	Priest Rapids Hatchery	OtsPRH14_fa	2014	238	84 – 396	9.6%	265	116 – 446	19.5%	18_UCOLSF
	04Fall	Priest Rapids Hatchery	OtsPRH15_fa	2015	116	37 – 233	4.7%	149	37 – 260	10.9%	18_UCOLSF
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON13S_1_fa	2013			0.0%	82	0 – 201	6.0%	19_SRFALL
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON14S_1_fa	2014	202	75 – 366	8.2%	85	0 – 169	6.2%	19_SRFALL
	04Fall	Lyons Ferry Fish Hatchery	OtsLYON15S_1_fa	2015	85	0 – 175	3.4%	85	0 – 210	6.3%	19_SRFALL
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH14S_1_fa	2014			0.0%	42	0 – 126	3.1%	19_SRFALL
	04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH15S_1_fa	2015			0.0%	38	0 – 115	2.8%	19_SRFALL
	04Fall	Little White Salmon National Fish Hatchery	OtsLWS13_fa	2013	116	37 – 233	4.7%	163	42 – 294	12.0%	22_BONPOOLFA
	04Fall	Little White Salmon National Fish Hatchery	OtsLWS14_fa	2014	126	42 – 252	5.1%	111	0 – 223	8.2%	22_BONPOOLFA

04Fall	Little White Salmon National Fish Hatchery	OtsLWS15_fa	2015	239	83 – 406	9.7%	122	0 – 245	9.0%	22_BONPOOLFA
04Fall	Umatilla Fish Hatchery	OtsUMA13_fa	2013	37	0 – 111	1.5%			0.0%	23_UMATILLAFA
#N/A	#N/A	Unassigned	#N/A	877	598 – 1198	35.5%			0.0%	#N/A
		TOTAL		2,467		100.0%	1,360		100.0%	

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1167   The fall Non-Treaty commercial fishery is shown by the composition of the combined adult and jack harvest using reporting
1168 group level (**Table 39**) and broodstock level (**Table 40**) resolution.
1169
1170   **Table 39. Summary of the stock composition at the reporting group level of the adult and jack Chinook salmon of the**
1171 **fall Non-Treaty commercial fishery in 2018 in units of reported catch.**

Reporting Group name	Run type	Reporting Group Code	Hatchery origin- Clipped Estimated abundance		Hatchery origin- No Clip Estimated abundance		Natural origin- No Clip Estimated abundance	
			Mean	95% CI	Mean	95% CI	Mean	95% CI
Youngs Bay	Spring	01_YOUNGS						
West Cascade Spring	Spring	02_WCASSP						
West Cascade Fall	Fall	03_WCASFA	190	31 – 647			413	206 – 634
Willamette	Spring	04_WILLAM	30	0 – 124			31	0 – 93
Spring Creek Tule	Fall	05_SPCRTU	3,124	2343 – 3890	146	0 – 387		
Klickitat	Spring	06_KLICKR						
Deschutes spring	Spring	07_DESCSP						
John Day	Spring	08_JOHNDR						
Yakima	Spring	09_YAKIMA						
Upper Columbia spring	Spring	10_UCOLSP						
Tucannon	Spring	11_TUCANO						
Hells Canyon	Spring/Summer	12_HELLSC						
South Fork Salmon	Spring/Summer	13_SFSALM						
Chamberlain Creek	Spring/Summer	14_CHMBLN						
Middle Fork Salmon	Spring/Summer	15_MFSALM						
Upper Salmon	Spring/Summer	16_UPSALM						
Deschutes fall	Fall	17_DESCFA						
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	259	26 – 539	176	0 – 434	2,245	1822 – 2663
Snake River fall	Fall	19_SRFALL	268	32 – 537	391	111 – 744	501	298 – 734
Bonneville Pool spring	Spring	20_BONPOOLSP						

Umatilla spring	Spring	21_UMATILLASP					
Bonneville Pool fall	Fall	22_BONPOOLFA	486	145 – 938	62	0 – 186	
Umatilla fall	Fall	23_UMATILLAFA					
		Total	4,356		774		3,190	

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1174 **Table 40. Summary of the stock composition at the broodstock level of the adult and jack Chinook salmon of the fall**
1175 **Non-Treaty commercial fishery of 2018 in units of reported catch**

Fall Commercial Fishery 2018				Adult/jack Chinook AD			Adult/jack Chinook AI			
Expected Run Time	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	MLE	95% CI	Percent	GSI RepGrp
04Fall	Washougal Fish Hatchery	OtsWAS15_fa	2015	141	0 – 424	3.2%			0.0%	03_WCASFA
04Fall	Spring Creek National Fish Hatchery	OtsSPCR15_fa	2015	2,056	1634 – 2483	47.2%	146	32 – 291	18.8%	05_SPCRTU
04Fall	Spring Creek National Fish Hatchery	OtsSPCR16_fa	2016	429	152 – 728	9.9%			0.0%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRH14_fa	2014	96	0 – 241	2.2%	128	31 – 266	16.5%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRH15_fa	2015			0.0%	48	0 – 145	6.2%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON13S_1_fa	2013	32	0 – 96	0.7%			0.0%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON14S_1_fa	2014	142	31 – 271	3.3%	257	97 – 434	33.2%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON15S_1_fa	2015	52	0 – 156	1.2%	85	0 – 189	11.0%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH12S_1_fa	2012			0.0%	49	0 – 146	6.3%	19_SRFALL
04Fall	Little White Salmon National Fish Hatchery	OtsLWS13_fa	2013	176	48 – 338	4.0%	62	0 – 155	8.0%	22_BONPOOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWS14_fa	2014	159	48 – 303	3.6%			0.0%	22_BONPOOLFA

04Fall	Little White Salmon National Fish Hatchery	OtsLWS15_fa	2015	152	0 – 304	3.5%			0.0%	22_BONPO OLFA
		Unassigned		920	515 – 1329	21.1%			0.0%	
		TOTAL		4,356		100.0%	774		100.0%	

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1177   The fall Treaty Zone 6 commercial fishery is reported by "tule" (i.e. Spring Creek
1178 Hatchery tules) and "bright" (upriver bright stocks include 17_DESCFA, 18_UCOLSF, and
1179 19_SRFALL) stocks. The YN monitors sample only the bright stock for DNA analysis and so
1180 we provide estimated abundances of the stocks that comprise this Visual Stock Identification
1181 "bright" group of fish. It was expected that there would be a small portion of "tule" fish within
1182 this group due to some misidentification of the stock using VSI. We estimated 842 tules
1183 (05_SPCRTU) which comprised 4% of the total clipped and unclipped hatchery-origin catch.
1184 The broodstock composition estimates identified a number of jacks that were included in this
1185 harvest from Priest Rapids, Lyons Ferry, and Little White Salmon hatcheries (Broodyear 2016,
1186 **Table 42**)
1187
1188   **Table 41. Summary of the stock composition at the reporting group level of the**
1189 **adult VSI-bright Chinook salmon of the fall Treaty zone 6 commercial fishery in 2018 in**
1190 **units of reported catch.**
1191

| Reporting Group name | Run type | Reporting Group Code | Hatchery origin- Clipped | | Hatchery origin |
| | | | Estimated abundance | | Estimated ab |
			Mean	95% CI	Mean	9
Youngs Bay	Spring	01_YOUNGS				
West Cascade Spring	Spring	02_WCASSP				
West Cascade Fall	Fall	03_WCASFA				
Willamette	Spring	04_WILLAM				
Spring Creek Tule	Fall	05_SPCRTU	773	189 – 1612	69	0
Klickitat	Spring	06_KLICKR				
Deschutes spring	Spring	07_DESCSP				
John Day	Spring	08_JOHNDR				
Yakima	Spring	09_YAKIMA				
Upper Columbia spring	Spring	10_UCOLSP				
Tucannon	Spring	11_TUCANO				
Hells Canyon	Spring/Summer	12_HELLSC				
South Fork Salmon	Spring/Summer	13_SFSALM				
Chamberlain Creek	Spring/Summer	14_CHMBLN				
Middle Fork Salmon	Spring/Summer	15_MFSALM				
Upper Salmon	Spring/Summer	16_UPSALM				
Deschutes fall	Fall	17_DESCFA				
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	6,538	4869 – 8149	1,972	106
Snake River fall	Fall	19_SRFALL	3,942	2597 – 5443	2,283	124
Bonneville Pool spring	Spring	20_BONPOOLSP				
Umatilla spring	Spring	21_UMATILLASP				
Bonneville Pool fall	Fall	22_BONPOOLFA	3,572	2367 – 4734	516	132
Umatilla fall	Fall	23_UMATILLAFA	167	0 – 475		
		Total	**14,992**		**4,840**	

Table 42. Summary of the stock composition at the broodstock level of the adult VSI-bright Chinook salmon of the fall Treaty zone 6 commercial fishery in 2018 in units of reported catch

Fall Treaty Fishery 2018				VSI-Bright Chinook AD			VSI-Bright Chinook AI			
Expected Run Time	Hatchery	Broodstock	Broodyear	MLE	95% CI	Percent	MLE	95% CI	Percent	GSI RepGrp
04Fall	Spring Creek National Fish Hatchery	OtsSPCR15_fa	2015	656	262 – 1080	4.4%	69	0 – 207	1.4%	05_SPCRTU
04Fall	Priest Rapids Hatchery	OtsPRH12_fa	2012	187	0 – 560	1.2%			0.0%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRH13_fa	2013	833	429 – 1269	5.6%	125	37 – 264	2.6%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRH14_fa	2014	2,019	1390 – 2659	13.5%	1,245	778 – 1783	25.7%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRH15_fa	2015	1,517	1024 – 2093	10.1%	572	250 – 962	11.8%	18_UCOLSF
04Fall	Priest Rapids Hatchery	OtsPRH16_fa	2016	29	0 – 87	0.2%	29	0 – 87	0.6%	18_UCOLSF
04Fall	Lyons Ferry Fish Hatchery	OtsLYON13S_1_fa	2013	69	0 – 207	0.5%			0.0%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON14S_1_fa	2014	1,939	1277 – 2604	12.9%	1,269	777 – 1802	26.2%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON15S_1_fa	2015	972	502 – 1470	6.5%	295	101 – 536	6.1%	19_SRFALL
04Fall	Lyons Ferry Fish Hatchery	OtsLYON16S_1_fa	2016	122	0 – 365	0.8%	69	0 – 208	1.4%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH13S_1_fa	2013	166	49 – 333	1.1%	382	135 – 652	7.9%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH14S_1_fa	2014	297	67 – 576	2.0%	201	67 – 401	4.1%	19_SRFALL
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH15S_1_fa	2015	169	0 – 404	1.1%	67	0 – 201	1.4%	19_SRFALL

04Fall	Little White Salmon National Fish Hatchery	OtsLWS13_fa	2013	447	183 – 764	3.0%	149	0 – 373	3.1%	22_BON POOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWS14_fa	2014	1,991	1403 – 2630	13.3%	315	107 – 571	6.5%	22_BON POOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWS15_fa	2015	1,085	692 – 1544	7.2%	52	0 – 155	1.1%	22_BON POOLFA
04Fall	Little White Salmon National Fish Hatchery	OtsLWS16_fa	2016	49	0 – 147	0.3%			0.0%	22_BON POOLFA
04Fall	Umatilla Fish Hatchery	OtsUMA13_fa	2013	167	44 – 333	1.1%			0.0%	23_UMATILLA FA
#N/A	#N/A	Unassigned	#N/A	2,281	1574 – 3052	15.2%			0.0%	#N/A
		TOTAL		14,992		100.0%	4,840		100.0%	

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1200   The Treaty Sockeye salmon fishery was estimated by clipped hatchery-origin and other
1201 unclipped categories ("reintroduced" and natural-origin). We estimated that there were two
1202 clipped hatchery stocks, Snake River and Okanogan River stocks (**Table 43**). For the first time,
1203 we estimated the number of reintroduced stock from the Yakima River that comprised the fishery
1204 (N=149, 2%; **Table 43**). The Yakima River reintroduced stock could be further broken down
1205 into broodyear and genetic stock, and was comprised of mostly Wenatchee genetic stock from
1206 brood year 2014 (4-year-olds, **Table 44**). The Yakima River sample was small and our
1207 confidence intervals overlapped 0. The estimate for these fish at Bonneville Dam was ~1300
1208 fish and so the stock specific harvest rate on this stock would be estimated ~10%. The Treaty
1209 harvest rate for the whole run of the sockeye was approximately 4%, and so these numbers seem
1210 reasonable given this context

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1214   **Table 43. Summary of the stock composition at the reporting group level of the**
1215 **sockeye salmon of theTreary fishery in 2018 in units of reported catch**

	Hatchery origin-Clipped		Reintroduction- No Clip		Natural origin- No Clip	
	Estimated abundance		Estimated abundance		Estimated abundance	
Reporting Group name	**Mean**	**95% CI**	**Mean**	**95% CI**	**Mean**	**95% CI**
Okanogan	25	0 – 74			6,052	5654 – 6418
Wenatchee					1,312	932 – 1729
Snake	150	50 – 299				
Lake Billy Chinook					5	0 – 16

Yakima		149	0 – 558	
Odell				34	0 – 103
Total	174	149	7,369	

Table 44. Summary of the stock composition at the broodstock level for the reintroduced sockeye salmon from the Yakima River caught in the Treaty fishery in 2018 in units of reported catch

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

Comparison of stock composition among sockeye salmon fisheries

Sockeye salmon were sampled from the lower Columbia River below Bonneville Dam in the lower river sport and above Bonneville Dam in the Zone 6 tribal fishery, and were assigned to five major Columbia River sockeye genetic stocks (Table 45, an additional kokanee stock "Odell" was detected). The lower river commercial harvest did not occur in 2018, and there was no Zone 6 sport fishery in 2018. Low sample numbers of *O. nerka* make it difficult to estimate narrow confidence intervals for abundance estimates of the Yakima River, Snake River, and Lake Billy Chinook stocks (Table 46).

The timing of the sockeye salmon fisheries may influence the harvested proportion of each stock. The Wenatchee stock has an early shifted run in some years like 2018. The Snake River stock (i.e., Redfish Lake) was only represented by 3 fish in the Zone 6 tribal fishery sample (Table 45) making run-timing estimates imprecise for this stock. Of the 3 Snake River fish identified with GSI, all fish were sampled in week 26. Notable difference in stock proportions between Bonneville Dam and the Zone 6 tribal harvest were observed for the Okanogan stock (90% vs. 79%) and for the Wenatchee stock (9% vs. 17%) in the Bonneville Dam *vs*. harvest mixture samples, respectively (Table 46).

Table 45. Summary of sample sizes and stock assignments for the 2018 sockeye salmon fisheries by weekly strata.

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

Table 46. Comparison of stock-specific abundance and percent composition among sockeye salmon fisheries. The mean stock abundance estimate is provided for each fishery harvest in 2018.

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

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1248 **Figure 21. Stock composition of spring management period clipped and unclipped Chinook**
1249 **salmon harvest mixtures in 2018.**

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1252 *Comparison of stock composition of the clipped and unclipped Chinook salmon stocks among*
1253 *spring-management period Chinook salmon fisheries*
1254   The stock composition of the test fishery and the YN permit fishery below Bonneville
1255 Dam were very similar (Figure 21) providing further support for the use of the test fishery as a
1256 way to predict the upstream stock composition. The sport fishery contained more of the lower
1257 river stocks (02_WCASSP and 04_WILLAM) as would be expected given the location of the
1258 fishing effort in both regions A and B.
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1262 *Comparison of stock composition of the clipped and unclipped Chinook salmon stocks between*
1263 *the Treaty and Non-Treaty summer-management period fisheries*
1264   Analysis of Chinook salmon fisheries in the summer management period (June 16 –
1265 August 1) addressed the following objectives: 1) estimate stock composition for the mark
1266 selective sport fishery in Region B and Region A below Bonneville Dam, and 2) compare stock
1267 composition of adipose-clipped versus adipose-intact fish from the Tribal Zone 6 harvest above
1268 Bonneville Dam. Due to closure of the commercial fishery during the summer management
1269 period in 2018, there was no Non-Treaty commercial harvest to compare.
1270   The largest difference in the composition of these two fisheries is the presence of lower
1271 river stocks (04_WILLAM) in the lower river fishery compared to the zone 6 fishery (Figure 22).
1272 There were small but detectable abundances of Snake River spring stocks in both the Non-Treaty
1273 and Treaty summer fisheries.
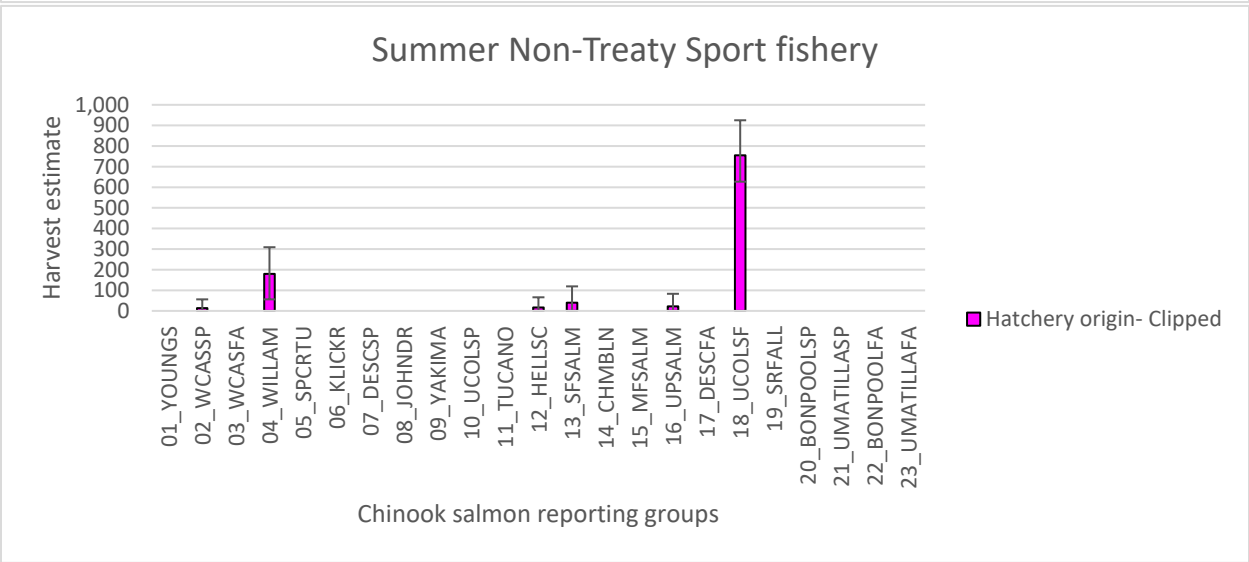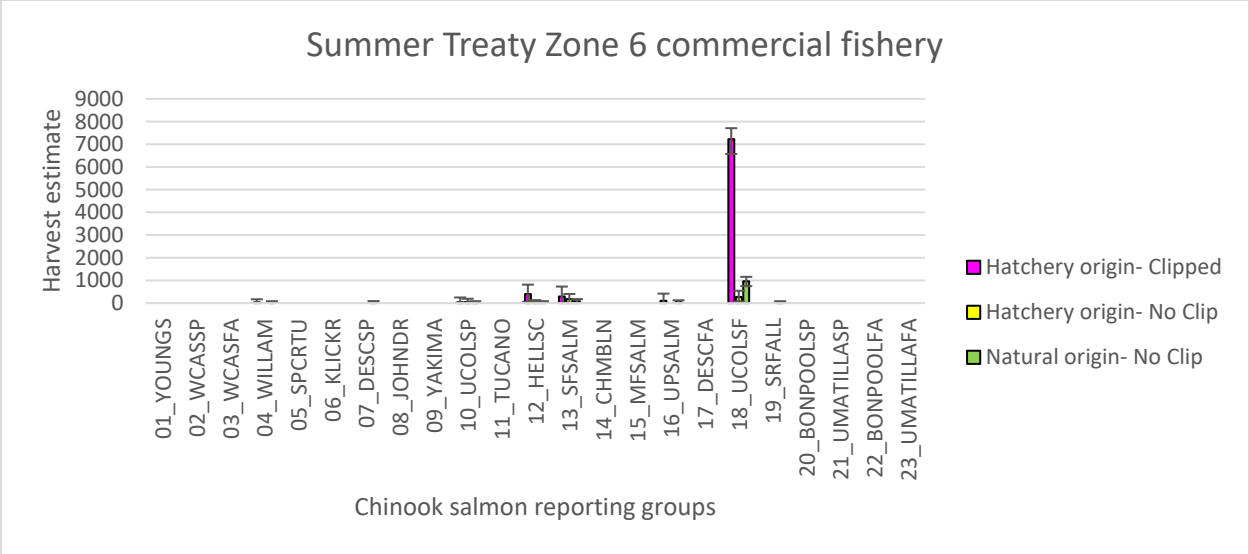
Figure 22. Genetic stock composition of the summer Chinook salmon fisheries analyzed in 2018.

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

One of the stocks that distinguished the composition of these fall fisheries was the "tule" (05_SPCRTU) stock (Figure 23). There were very low numbers of this stock present in the Treaty Zone 6 fishery due to the way that it was sampled; monitors visually assessed fish as belonging to either "tule" or "bright" category and only DNA sampled the "bright" stock. As such, the Treaty harvest composition can only be used to assess the relative abundance of stocks within the VSI-bright group of fish. However, the fall test fishery (pound net) does provide a more representative composition of the stocks present in the lower river. Comparison of the test fishery composition and the compositions of the commercial and sport harvests showed a

1290   dramatically lower abundance of "tules" in sport fishery compared to the other harvests. This
1291   difference is largely due to sport fishers preferentially keeping the VSI bright fish over the tule
1292   fish.

1293

Fall Treaty Zone 6 commercial fishery (adult VSI-bright)

1294

Fall Non-Treaty commercial fishery (adults + jacks)
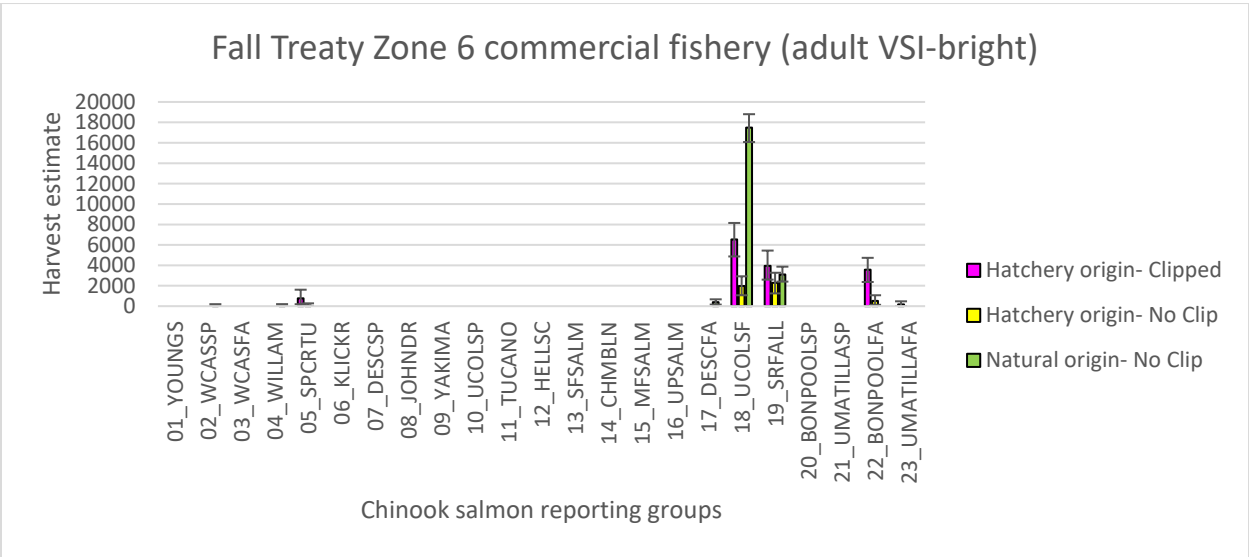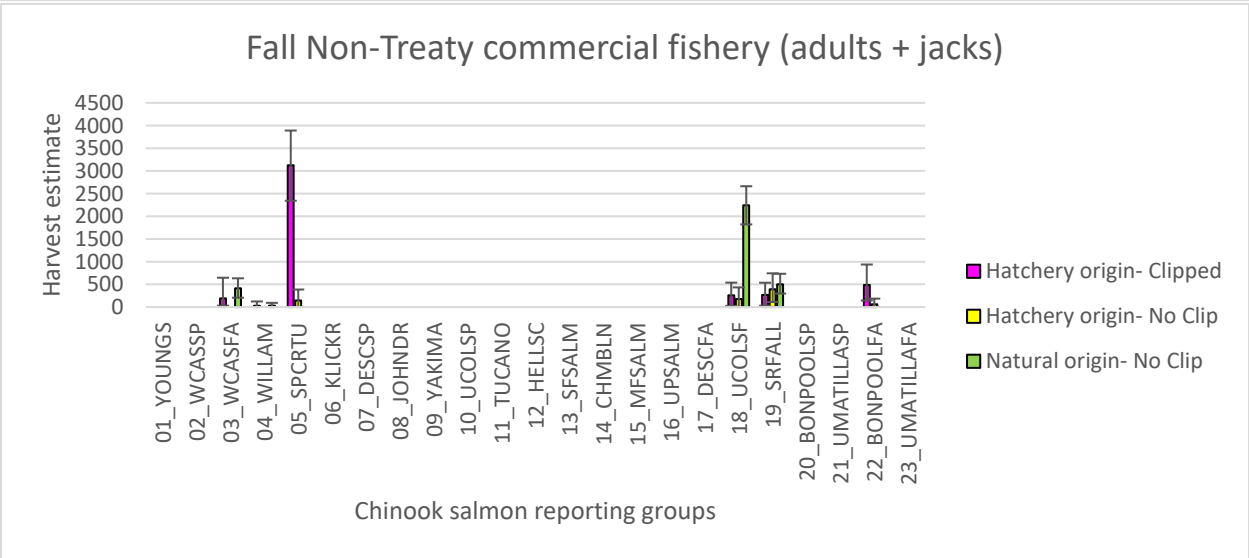
1295
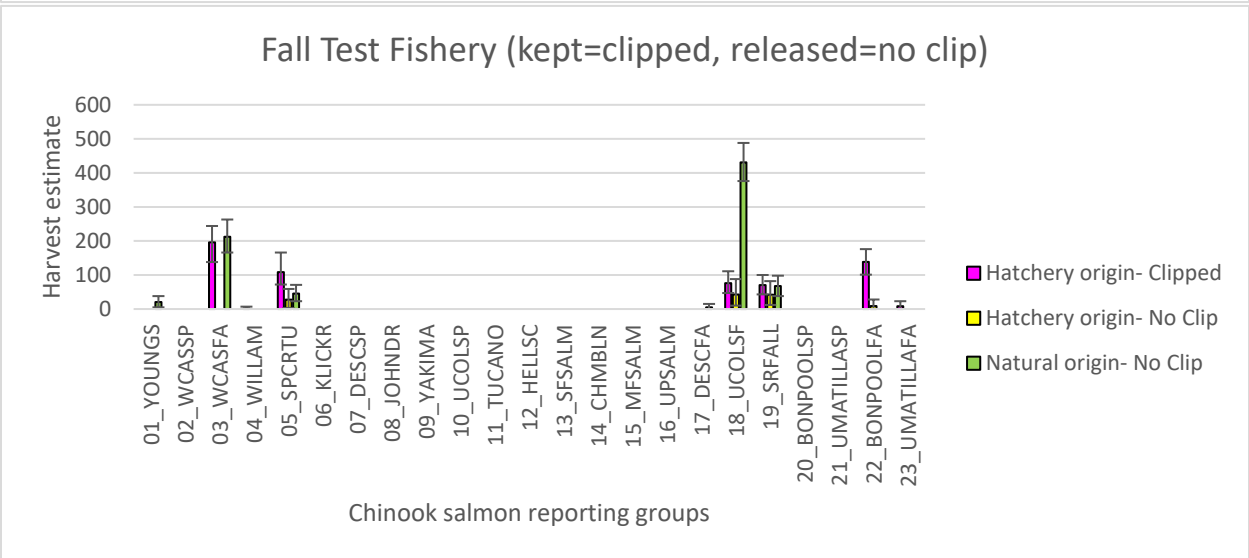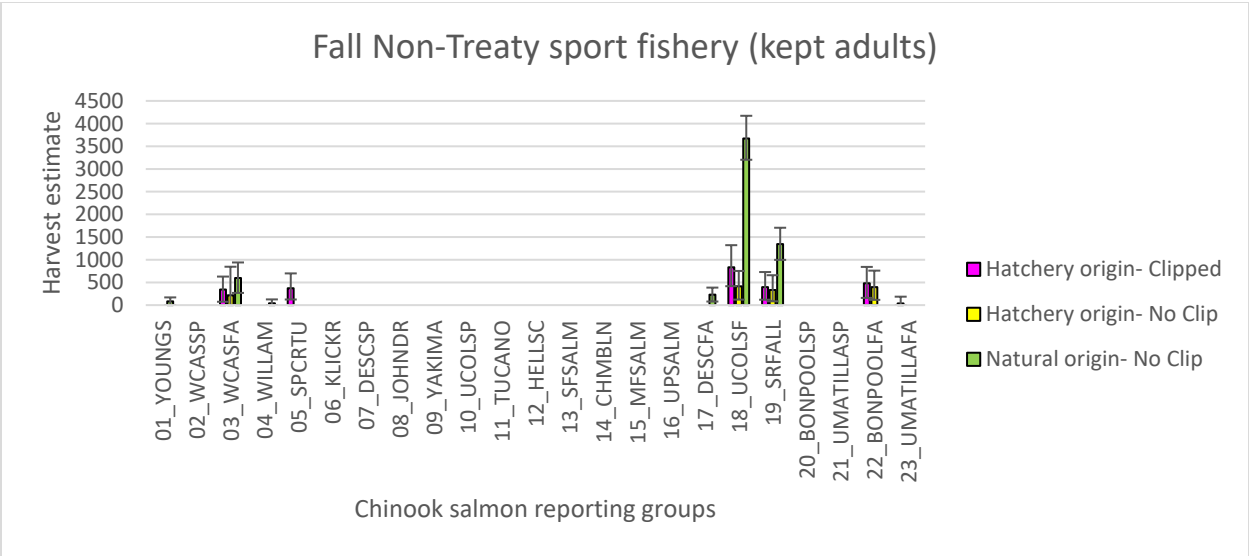
Figure 23. Genetic stock composition of the fall Chinook salmon fisheries analyzed in 2018.

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 sixth year in which we were able to assign all three major age classes of spring Chinook from Snake River hatcheries and the second year in which we could assign 3-, 4-, and 5-year old fish to Columbia River hatcheries as a consequence of our expanded PBT baseline. Ongoing expansion of the PBT baseline has now allowed the ability to assign all yearling hatchery jacks and subyearling 4-year-olds originating above Bonneville Dam (complete spawn years date back to 2015), and so future years of analyses will contain all major year classes. Expansion of the PBT baseline to include not only hatcheries of Chinook salmon

1312 and steelhead above Bonneville Dam, but also hatcheries throughout the range of these species
1313 could eventually lead to replacing the coded wire tag program for monitoring of in-river harvest
1314 stock composition of these species if increases in funding were available and fishery managers
1315 thought it were needed. We understand there will be benefit to not only increasing the number of
1316 broodstocks represented in the baseline but also expanding the number of SNP loci that we use
1317 for PBT applications. A new subset of 254 SNP loci is now being utilized in this report because
1318 of its optimal information content across the three major genetic lineages of Chinook Salmon
1319 found in the Columbia River Basin and now most broodstocks have complete genotypes. This
1320 report includes the sixth genetic analysis on sockeye salmon harvest. This is the first year we
1321 have been able to utilize a PBT baseline that can identify offspring of parents from the Yakima
1322 River reintroduction. Our results demonstrated differences in stock composition of the sockeye
1323 salmon harvest as compared to the total run estimated at Bonneville Dam, but there are questions
1324 about the validity of the estimates especially at Bonneville given the potential for sampling error
1325 around rare stocks like Snake River sockeye salmon. We will continue to perform PBT and GSI
1326 on sockeye salmon harvest in the future to gain further insight into these patterns.
1327   Our most significant achievement in this year, is our ability to expand estimated genetic
1328 stock proportions by the reported catch estimates for each fishery. This improvement required
1329 tailoring each analysis to the way in which catch is stratified and reported. Our analyses take
1330 advantage of new methods (SCOBI DEUX and SPIBETR programs, Delomas and Hess 2020)
1331 that are now available to perform tag rate expansions and balance those expansions by
1332 proportionally decreasing other stocks in the natural-origin category.
1333
1334 One higher level management question was possible to address in this section:
1335   **1) Harvest RM&E: F&W Program Management Question: What are your in-river**
1336   **monitoring results and what are your estimates of stock composition and stock-**
1337   **specific abundance, escapement, catch, and age distribution?**
1338
1339   The in-river estimates of stock composition, stock-specific abundance, escapement,
1340 catch, and age distribution were addressed for part of the treaty mainstem spring-management
1341 period fisheries Chinook salmon harvests below Bonneville Dam, the spring-management test
1342 fishery, the non-treaty spring-management sport fishery, the non-treaty and treaty summer-
1343 management fisheries, the non-treaty and treaty mainstem fall-management fisheries, and the
1344 mainstem treaty sockeye salmon harvests above and non-treaty harvest below Bonneville Dam.
1345 For the spring management period of Chinook salmon, we continue to observe a spatial pattern
1346 for the stock composition of lower Columbia River stocks which appear more abundant
1347 downstream from the Willamette River mouth as compared to upstream of this point which is
1348 consistent with a long history of CWT data. We observed differences in the composition of
1349 hatchery stocks represented in spring vs. summer management period harvest of Chinook
1350 salmon, and run-timing plays an important role in this difference (i.e., late-running stocks appear
1351 more abundant among the upriver spring-type lineage that are caught in the summer management
1352 period). This pattern is consistent when compared to known origin PIT tagged adult and jack
1353 fish tagged as juveniles. Known origin adult age upriver spring and Snake River spring Chinook
1354 salmon are almost all past Bonneville by June 15 in most years.
1355   The sockeye salmon tribal fishery is managed in a way that attempts to harvest as many
1356 harvestable sockeye salmon as possible under the allowed harvest rate schedule in the U.S. v.
1357 Oregon Management Agreement. This 2018 year of analysis of the sockeye salmon harvest

1358   corroborates harvest analyses from previous years, which suggested there may be some over
1359   representation of the Wenatchee sockeye stocks in the Zone 6 harvest as compared to the stock
1360   proportions that are present at Bonneville Dam. The results for Snake River sockeye salmon are
1361   dependent upon representative sampling at Bonneville Dam, but low sample rate and the rarity of
1362   this stock led to uncertainty and high variation around estimates of Snake River sockeye salmon
1363   from Bonneville Dam. Sampling protocols at Bonneville Dam may have higher representation of
1364   young fish as compared to harvest mixtures. Timing of the fishery may also influence the
1365   proportion of each stock, and is consistent with run-timing distributions we observed in previous
1366   reports; the Wenatchee stock has relatively early run-timing but the timing of the Snake River
1367   stock is uncertain due to inconsistent results between PIT-tag and GSI methods. Future analysis
1368   will be needed to examine these patterns for consistency and delve into explanations.
1369   Importantly, we estimated that the Yakima River reintroduction of sockeye has a measurable
1370   (albeit small, ~2%) impact on the Treaty fishery in zone 6.
1371

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1478 Section 4: Characterization of Chinook salmon, sockeye salmon, and steelhead
1479 run-timing and abundance at Bonneville Dam

1480 ***Introduction***

1481   The Columbia River Basin supports ESA listed natural-origin stocks of Chinook salmon
1482 and steelhead as well as hatchery supplemented populations. Both Chinook salmon and
1483 steelhead have been declining in the Columbia River Basin for several reasons including climate
1484 change, habitat degradation, hydropower, hatchery practices, and over-harvesting. Along with
1485 abundance estimates, basic information related to the way in which stocks of salmonids are
1486 spatiotemporally distributed are needed by fisheries managers to achieve sustainable fisheries.
1487   As evident from the genetic stock identification (GSI and PBT) analyses of Chinook and
1488 Sockeye salmon fisheries harvests in Section 3, certain stocks seem to have strong spatial and
1489 temporal associations. However, because the type of fishing gear, harvest regulations, and the
1490 locations targeted varies considerably among fisheries, samples from a representative mixture of
1491 all hatchery- and natural-origin stocks at a fixed location is expected to more accurately estimate
1492 relative abundance and characterize run-timing distributions of stocks. One potentially ideal
1493 fixed location for such sampling is Bonneville Dam, but trapping limitations at this location
1494 continue to pose a major challenge for sampling. In addition to information on abundance and
1495 run-timing, biological data including fork length and age can be examined with estimated stock
1496 of origin to characterize life history differences among stocks. This type of examination is
1497 especially important for steelhead, which has been managed using two life-history categories
1498 (i.e., A- and B-run). These life-history categories have been observed to be differentially
1499 characterized by run-timing at Bonneville Dam (e.g., B-run typically arrives after Aug. 25th),
1500 fork length (e.g., by definition, B-run fish are >=78 cm), and ocean age (e.g., most B-run fish
1501 tend to spend 2 or more years in saltwater) and all of these types of data have been collected for
1502 steelhead in this study.
1503 *Project objectives and higher level harvest management questions*
1504   Here we analyze fish across the entire run of steelhead, Chinook and Sockeye salmon
1505 from April to October to estimate temporally stratified proportions of stocks and extrapolate
1506 abundance using a daily census that is conducted at the Bonneville Dam fish counting window.
1507 We examine steelhead, Chinook salmon, and Sockeye salmon using sets of species-specific SNP
1508 assays for up to 390 loci per species. Although there are some methodological differences
1509 among these species-specific applications (e.g., different temporal strata), the general approach
1510 to estimating abundance and characterizing run-timing distributions was applied consistently
1511 post-season across species in 2018. For all three species, we have demonstrated that these genetic
1512 baselines are generally accurate for assigning fish of unknown origin, but the genetic similarity
1513 of some stocks requires large reporting groups comprised of broad geographic areas (i.e., mid-
1514 Columbia R. and lower Snake R. for spring Chinook salmon). Since Bonneville Dam is the most
1515 downstream dam on the Columbia River, the mixture samples obtained here represent the
1516 majority of upriver/interior Columbia River Basin stocks. This ongoing study offers a rare
1517 opportunity to monitor populations of multiple species of salmonids from a broad geographic
1518 range over several years. This long-term study will allow us to characterize trends in run timing
1519 and abundance of steelhead, Chinook and sockeye salmon and provide this data to fisheries
1520 managers. However, the genetic stock units ('reporting groups') are not the same units that
1521 groups of fish are currently managed for due to levels of genetic differentiation that can be
1522 detected among baseline stocks (see results under Objective 2 for details). Thus, fisheries

1523 managers continue to explore how to best incorporate genetic monitoring results with more
1524 traditional monitoring/tagging programs.
1525   One of the newest features of our analyses is an in-season analysis that was first
1526 conducted on Chinook Salmon during the 2017 spring and summer management periods. We
1527 have continued offering in-season reports for Chinook Salmon on an approximately bi-weekly
1528 report timing schedule during the 2019 spring and summer management periods. Other species
1529 and runs have been reported to U.S. v OR Technical Advisory Committee (TAC) members on a
1530 timely basis near the end of each management period. Specifically, in 2019, we provided timely
1531 post-season reports for steelhead after the Skamania Management Period and the Summer A-/B-
1532 Index Management Period, Sockeye Salmon, and Chinook Salmon after the Fall Management
1533 Period (see Table 47 for the number and timing of reports for each species and run that were
1534 delivered in-season and post-season in 2019).
1535 **Harvest RM&E: F&W Program Management Questions:**
1536   **i)   What are the status and trend of adult productivity of fish populations?**
1537   **ii)   What are your in-river monitoring results and what are your estimates of stock**
1538   **composition and stock-specific abundance, escapement, catch, and age**
1539   **distribution?**
1540   Analysis of the 2011 dataset by Hess et al. (2012) was the first year we were able to apply
1541 Parentage Based Tagging (PBT) to assign a portion of Snake River hatchery-origin spring-run
1542 Chinook salmon and summer-run steelhead back to their hatchery parents (Steele et al. 2011).
1543 This powerful genetic tool provides the opportunity to obtain additional types of data including
1544 accurate age of fish, quantification of the number of non-adipose clipped hatchery-origin fish,
1545 and precise assignments of fish to their hatchery broodstock (Steele et al. 2013). The ability of
1546 PBT to assign fish to their hatchery broodstock has been shown to be equally accurate as
1547 traditional tags (e.g., CWTs; Steele et al. 2013), and PBT provides assignments to specific
1548 hatchery broodstocks rather than larger reporting groups used in GSI methods. However, these
1549 tools can provide the greatest benefit when applied in combination, as GSI has the ability to
1550 provide information on natural-origin fish throughout the Columbia River basin, while PBT is
1551 most effective for hatchery-origin fish. The current PBT baseline was recently expanded beyond
1552 Snake River hatcheries to include others above Bonneville Dam. However, this effort is
1553 ongoing, and while hatcheries continue to be added to our PBT baseline annually, GSI remains a
1554 necessary tool for both hatchery- and natural-origin fish that originate from outside the Snake
1555 River basin. This report is the 6th year in which all major age classes of steelhead (i.e. 1-, 2-, and
1556 3- ocean ages) and Chinook salmon (3-, 4-, and 5-year olds) can be assigned using the PBT
1557 baseline of Snake River hatcheries, and the 4th year in which these can be assigned to some
1558 Columbia River hatcheries. This is the first year that Sockeye salmon from the Yakima River
1559 reintroduction can be assigned to candidate parents, allowing this stock to be identified in
1560 fisheries and at Bonneville Dam. This study integrates PBT and GSI results to provide the
1561 greatest amount of stock-specific information available for hatchery- and natural-origin
1562 steelhead, Sockeye and Chinook salmon passing Bonneville Dam.
1563
1564 *Time line for completion of objectives*
1565   Objectives will be ongoing and GSI results updated each year for analyses of salmon and
1566 steelhead throughout the accords-funding. This report that is written in January 2020 features
1567 the final analyses of 2018, as well as the preliminary in-season and post-season analyses of 2019.

1568 As new genetic techniques are developed they will be applied to this project and results will be
1569 compared between years to determine the extent of improvements.
1570
1571 **Table 47. The in-season and post-season report timing and scope of the 2019 fish runs.**

Species	Management Period	Data coverage	Analysis begins	Report timing
Chinook	Spring	01/01/2019 – 05/03/2019	5/6/2019	5/10/2019
		01/01/2019 – 05/17/2019	5/20/2019	5/24/2019
		01/01/2019 – 06/01/2019	6/3/2019	6/7/2019
		01/01/2019 – 06/15/2019	6/17/2019	6/21/2019
	Summer	01/01/2019 – 07/05/2019	7/8/2019	7/12/2019
		01/01/2019 – 07/31/2019	8/5/2019	8/9/2019
	Fall	01/01/2019 – 10/25/2019	10/28/2019	11/1/2019
Steelhead	Skamania	04/01/2019 – 06/30/2019	7/8/2019	7/12/2019
	Summer A-/B-Index	07/01/2019 – 07/31/2019	8/5/2019	8/9/2019
		07/01/2019 – 10/25/2019	10/28/2019	11/1/2019
Sockeye	Total	01/01/2019 – 08/02/2019	8/5/2019	8/9/2019

1572 Note: The data were reported as cumulative abundance estimates for each genetic stock during the Chinook Salmon
1573 and Summer Steelhead A-/B-Index management periods. The report timing indicates the date these reports were
1574 provided to the USvOR TAC chair Stuart Ellis for distribution to TAC members.

1575 *Methods*

1576 *Sample Collection*

1577   Tissue samples were obtained from adult steelhead (n=878), Chinook (n=3,019) and
1578 sockeye salmon (n=1,857) adults in 2018 during migration runs at Bonneville Dam. This
1579 sampling effort is covered under the 2008 – 2017 *U.S. vs.* Oregon harvest biological opinion for
1580 sampling at Bonneville Dam.
1581 Sampling for Chinook salmon at Bonneville Dam began during statistical week 17 (04/22/18)
1582 and was completed on 10/13/18 (statistical week 41). Sampling occurred at the Adult Fish
1583 Facility (AFF) located on the northern end of Bonneville Dam. Fish were sampled 4–5 d per
1584 statistical week (except when reduced due to restrictions on trap use or low run size at the
1585 beginning and end of the run) and for 4–6 h per day. A picket weir was used to divert migrating
1586 fish ascending the Washington shore fish ladder into the AFF collection pool. An attraction flow
1587 was used to draw fish through a false weir where they were selected for sampling. After
1588 sampling was completed and fish recovered from the anesthetic, they were returned to the
1589 Washington shore fish ladder above the picket weir. Only 0.1% of the total Spring management
1590 period (i.e., January 1-June 15) adult Chinook salmon count had passed Bonneville by the
1591 sampling start date (April 16). In previous years, 2.0-2.5% of the total Spring management
1592 period adult Chinook salmon count had passed Bonneville by the sampling start date. However,
1593 the adult migration run was delayed passing Bonneville Dam in the spring of 2018 (
1594
1595 **Figure 24**) and resulted in a lower proportion of unsampled fish. Nonetheless, some early timed
1596 stocks may be slightly under-estimated in the results. Restrictions imposed by USACE and
1597 NMFS on sampling at the Bonneville AFF result in sample rates for Chinook, sockeye, and

198

1598 steelhead that are often low. The average sample rate for the adult spring Chinook run in 2018
1599 for the spring and summer management periods was 1.3%, whereas the average sample rate for
1600 adult fall Chinook was 0.7% (Table 48).
1601   Based on numbers of fish collected, samples were pooled into weekly strata for Chinook
1602 (Table 48), monthly strata for steelhead (Table 49), or a combination thereof for sockeye salmon
1603 (Table 50) spanning the majority of the run-year from April to October. We followed a similar
1604 protocol as the Monitoring Methods Protocol "Snake River steelhead and Chinook salmon stock
1605 composition estimates (2010-026-00) v1.0".
1606
1607 *Molecular markers*
1608   Expanded panels of genetic markers for steelhead, Sockeye and Chinook salmon are
1609 provided in Section 1.
1610 *Statistical analyses*
1611   Snake River Chinook salmon and steelhead were analyzed for Parentage assignments
1612 using SNPPIT software v1.0 (ID: 1341) (Published). The program ONCOR was used to estimate
1613 the most likely population-of-origin for the sockeye salmon samples. Individuals were assigned
1614 using a 'best estimate' approach Assigning individual samples using Individual Assignment (IA)
1615 genetic methods v1.0 (ID: 1334) (Published). We used GSIsim for Mixture modeling to estimate
1616 stock proportions v1.0 (ID: 1333) (Published) to estimate stock composition of Bonneville Dam
1617 mixture strata for Chinook salmon and steelhead. Additional detail regarding the specific
1618 application to Bonneville Dam are published in Hess et al. (2013).
1619
1620
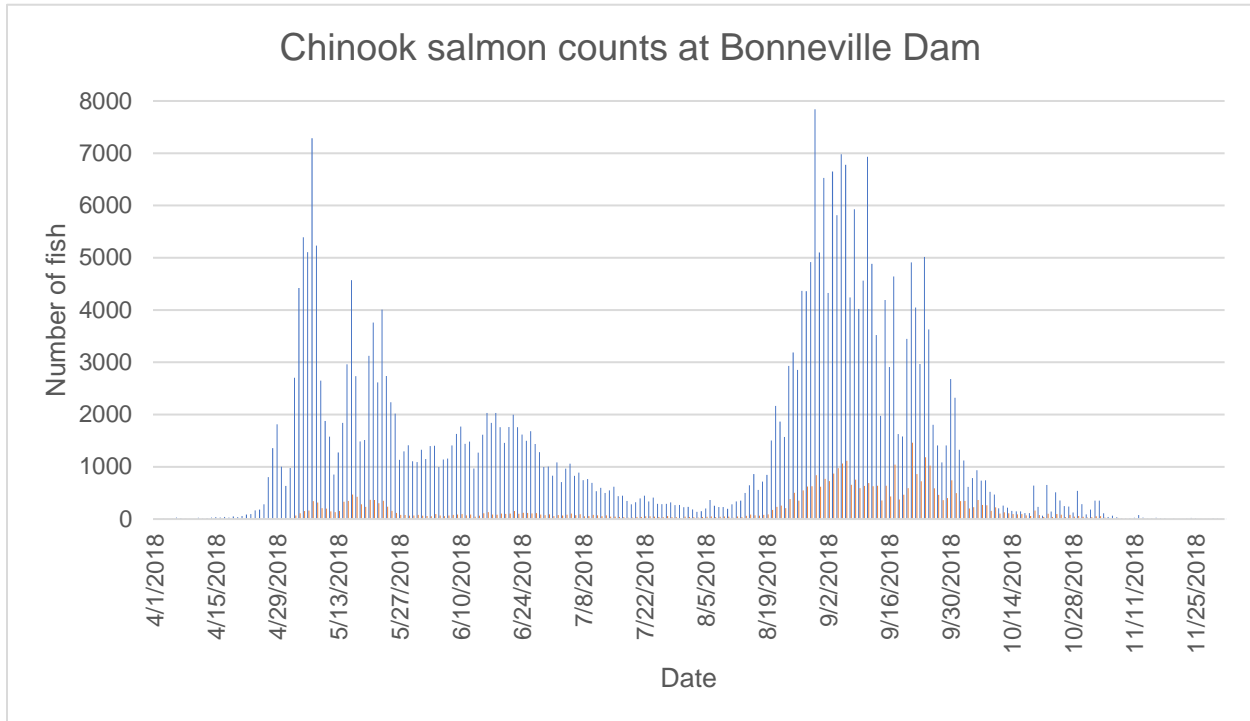
1621 **Figure 24. Daily passage of Chinook salmon (adults=blue and jacks=red) at Bonneville**
1622 **Dam in 2018 (source: www.fpc.org).**

Table 48. Sample numbers by weekly strata for Chinook salmon that were DNA sampled or tallied for abundance at Bonneville Dam in 2018.

Management period		Statistical week	TAC clip count	TAC unclip count	Clipped GSI	Clipped PBT	Non-clipped GSI	Non-clipped PBT	Subtotal clip	Subtotal unclip	Rate clip	Rate unclip
	Spring	1-17	3,088	352	4	52	4	2	56	6	1.8%	1.7%
		18	14,384	2,559	9	142	32	18	151	50	1.0%	2.0%
		19	20,576	4,011	9	186	39	26	195	65	0.9%	1.6%
		20	12,988	3,397	10	158	43	12	168	55	1.3%	1.6%
		21	15,044	5,457	24	181	82	22	205	104	1.4%	1.9%
		22	5,659	2,852	15	64	33	15	79	48	1.4%	1.7%
		23	5,992	3,140	18	81	37	13	99	50	1.7%	1.6%
		24sp	6,058	2,488	13	48	26	7	61	33	1.0%	1.3%
	Summer	24su-25	11,091	3,546	11	45	14	1	56	15	0.5%	0.4%
		26	7,490	2,028	12	38	13	3	50	16	0.7%	0.8%
		27	5,276	1,087	4	17	4	2	21	6	0.4%	0.6%
		28	2,941	1,444	5	37	13	4	42	17	1.4%	1.2%
		29	1,947	909	8	34	19	3	42	22	2.2%	2.4%
		30-31	1,794	1,353	3	25	9	2	28	11	1.6%	0.8%
	Fall	31-34	6,608	13,913	6	18	49	19	24	68	0.4%	0.5%
		35	16,665	19,301	21	71	138	30	92	168	0.6%	0.9%
		36	16,709	24,013	6	32	97	21	38	118	0.2%	0.5%
		37	10,960	19,128	15	52	174	24	67	198	0.6%	1.0%
		38	6,421	16,743	5	34	121	23	39	144	0.6%	0.9%
		39	4,478	12,839	7	28	101	16	35	117	0.8%	0.9%
		40	2,450	7,329	3	20	81	10	23	91	0.9%	1.2%

		41-53	2,226	7,296	1	5	35	5	6	40	0.3%	0.5%
		Total	180,846	155,184	209	1,368	1,164	278	1,577	1,442	0.9%	0.9%

1625 Note: Statistical weeks 1–17 are 1/1/18 – 4/28/18 and 41–53 is 10/7/18–12/31/18. 'TAC count' is based on the estimates of clip and unclipped adult
1626 Chinook salmon provided by US v OR Technical Advisory Committee using data from the Fish Passage Center (http://www.fpc.org) observed by the
1627 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
1628 sample rate. The management periods approximate the date ranges from January 1st to June 15th (Spring management period), June 16th to July 31st
1629 (Summer management period), and August 1st to December 31 (Fall management period) which are used to categorize spring-, summer-, and fall-run
1630 Chinook salmon, respectively. The number of sampled fish that were assigned via PBT or GSI are shown.

Table 49. Sample numbers by monthly strata for steelhead that were DNA sampled or tallied for abundance at Bonneville Dam in 2018.

				Sample (N)											
		Clipped count	Non-Clipped count	A-Index				B-Index				Clipped Total	Non-clipped Total	Clipped Sample rate	Non-clipped Sample rate
				Clipped		Non-clipped		Clipped		Non-clipped					
	Strata			GSI	PBT	GSI	PBT	GSI	PBT	GSI	PBT				
Skamania	14-26	7,258	5,708	7	43	29	0	0	4	3	0	54	32	0.7%	0.6%
A-/B-Index	27-29	7,515	6,999	17	46	57	2	0	3	1	0	66	60	0.9%	0.9%
	30-34	21,768	12,602	11	69	59	2	0	0	1	0	80	62	0.4%	0.5%
	35-36	14,088	3,684	11	57	13	2	1	32	5	4	101	24	0.7%	0.7%
	37-38	11,626	3,034	1	34	5	2	6	67	7	10	108	24	0.9%	0.8%
	39-40	6,653	1,998	0	26	6	6	9	85	6	20	120	38	1.8%	1.9%
	41-44	2,836	1,197	2	27	8	8	7	39	5	13	75	34	2.6%	2.8%
Summer A-/B-Index subtotal		64,486	29,514	42	259	148	22	23	226	25	47	550	242	0.9%	0.8%
Total		71,744	35,222	49	302	177	22	23	230	28	47	604	274	0.8%	0.8%

Note: Statistical week 14-16 is 4/1/18–6/30/18 (Skamania Management Period) and 27-29 begins the A-/B-Index Period that runs from 7/1/2018-10/31/2018. '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.

202

1639 **Table 50. Sample numbers for genetic stock assignments of sockeye salmon that passed**
1640 **Bonneville Dam in 2018.**

Statistical week grouping	Bonneville dam fish window count	Genetic stock					Total	Sample rate (%)
		OKA	WEN	RED	LBC	Yakima		
21-23	3290	84	1				85	2.6%
24	17831	214	14				228	1.3%
25	59289	313	37			1	351	0.6%
26	62984	414	42	2		2	460	0.7%
27	34044	277	33				310	0.9%
28	10880	200	20	1			221	2.0%
29	3201	103	7	1	1	1	113	3.5%
30-36	2297	75	10		2	2	89	3.9%
Total	193816	1680	164	4	3	6	1857	1.0%

1641 Note: Statistical week 21 begins on 5/20/18 and 36 ends 9/8/18; there were no sockeye counted
1642 before or after these dates. 'Fish count' is based on tallies of sockeye salmon adults provided by
1643 the Fish Passage Center (http://www.fpc.org) observed by the Corps of Engineers at their fish
1644 counting window. GSI stocks are Okanagan (OKA), Wenatchee (WEN), Snake River (RED),
1645 and Lake Billy Chinook (LBC) and PBT can identify fish from the Yakima reintroduction. The
1646 number of samples for a given statistical week or pooled stratum was used to calculate sample
1647 rate. Relatively few sockeye salmon were sampled from the RED, LBC, and Yakima stocks, and
1648 limits inference regarding run-timing and abundance of these stocks.
1649

1650 *Results*
1651 *Estimated relative abundance of Chinook salmon stocks in 2018*
1652 In previous years the 10_UCOLSP reporting group included Carson Hatchery for
1653 estimates of relative abundance due to genetic similarity in GSI assignments, so the abundance
1654 estimates for this reporting group did not represent actual returns specifically to the upper
1655 Columbia River. Beginning in 2017, we have categorized several hatcheries as their own
1656 reporting groups to alleviate this issue and so that a more accurate assessment of the number of
1657 Chinook returning to the upper Columbia River can be determined. To that end, we have
1658 included the following reporting groups that are comprised of collections from our PBT baseline.
1659 The 20_BONPOOLSP reporting group includes spring Chinook from Caron Hatchery and Little
1660 White Salmon Hatchery. The 21_UMATILLASP reporting group includes spring Chinook from
1661 the Umatilla Hatchery. The 22_BONPOOLFA reporting group includes fall Chinook from the
1662 Little White Salmon Hatchery. The 22_UMATILLAFA reporting group includes fall Chinook
1663 from the Umatilla Hatchery.

1664　　　　　There were 13 major (i.e., abundance >1000 fish) hatchery origin Chinook salmon stocks
1665　　represented in the total estimated abundance (N=211,176) of hatchery Chinook salmon passing
1666　　Bonneville Dam in 2018 (Table 51; Figure 25). These stocks in order of decreasing magnitude
1667　　were 18_UCOLSF (62,113), 12_HELLSC (35,203), 05_SPCRTU (24,290), 22_BONPOOLFA
1668　　(22,109), , 19_SRFALL (20,264), , 20_BONPOOLSP (14,028), 16_UPSALM (7,563),
1669　　21_UMATILLASP (7,358), 10_UCOLSP (5,592), 13_SFSALM (4,290), 09_YAKIMA (2,943),
1670　　02_WCASSP (2,062), and 07_DESCP (1,704) (Table 51; Figure 25). One stocks
1671　　(13_MFSALM) that was considered major in 2016 did not meet the abundance threshold
1672　　(>1000) to be considered a major stock in 2017 (Table 51).
1673　　　　　With the exception of reporting groups 20_BONPOOLSP, 21_UMATILLASP,
1674　　22_BONPOOLFA, and 23_UMATILLAFA), abundance estimates include abundance for PBT-
1675　　assigned fish (adipose clipped and non-clipped) and adipose clipped fish that were assigned via
1676　　GSI. PBT assignments improved our ability to accurately identify hatchery origin fish and
1677　　estimate total stock abundance (Table 51). Further, using PBT assignments we can now provide
1678　　abundance and run-timing estimates for particular hatchery broodstocks (Table 51) which will
1679　　allow for much improved abundance estimates.

Table 51. Stock-specific abundance of hatchery origin (adipose clipped and intact) Chinook salmon passing Bonneville Dam in 2018.

Hatchery	Broodstock	Brood year	Adult Chinook AD						Adult Chinook AI						GSI RepGrp
			Spring	Summer	Fall	MLE	95% CI	Percent	Spring	Summer	Fall	MLE	95% CI	Percent	
Parkdale Fish Facility	OtsPFF14_sp	2014	2,062	0	0	2,062	1443 – 2732	1.1%	55	0	0	55	0 – 165	0.2%	02_WCASSP
Klickitat Hatchery	OtsKH13_sp	2013	132	0	0	132	0 – 302	0.1%						0.0%	06_KLICKR
Klickitat Hatchery	OtsKH14_sp	2014	722	0	0	722	377 – 1155	0.4%						0.0%	06_KLICKR
Round Butte Fish Hatchery	OtsRB14_sp	2014	1,240	0	0	1,240	728 – 1778	0.7%	52	0	0	52	0 – 157	0.2%	07_DESCSP
Warm Springs National Fish Hatchery	OtsWSNFH14_sp	2014						0.0%	195	0	0	195	0 – 586	0.6%	07_DESCSP
Yakima River Roza Dam	OtsYR14int_sp	2014	2,492	0	0	2,492	1784 – 3252	1.4%						0.0%	09_YAKIMA
Yakima River Roza Dam	OtsYR14seg_sp	2014	451	0	0	451	109 – 851	0.2%						0.0%	09_YAKIMA
Chief Joseph Hatchery	OtsCJH14_sp	2014	477	0	0	477	164 – 828	0.3%	126	0	0	126	0 – 265	0.4%	10_UCOLSP
Eastbank Fish Hatchery	OtsEASTBK14_sp	2014	640	0	0	640	231 – 1080	0.4%	261	0	0	261	0 – 522	0.9%	10_UCOLSP
Eastbank Fish Hatchery	OtsEASTBK15_sp	2015						0.0%	107	0	0	107	0 – 320	0.4%	10_UCOLSP
Leavenworth National Fish Hatchery	OtsLNFH14_sp	2014	1,435	0	0	1,435	820 – 2054	0.8%	73	0	0	73	0 – 219	0.2%	10_UCOLSP
Methow Fish Hatchery	OtsMETH14_sp	2014						0.0%	220	0	0	220	52 – 423	0.7%	10_UCOLSP
Winthrop National Fish Hatchery	OtsWTP13_sp	2013	118	0	0	118	0 – 355	0.1%						0.0%	10_UCOLSP
Winthrop National Fish Hatchery	OtsWTP14_sp	2014	1,574	0	0	1,574	995 – 2161	0.9%	540	0	0	540	289 – 863	1.8%	10_UCOLSP
Lyons Ferry Fish Hatchery	OtsTUCW14S_sp	2014						0.0%	500	0	0	500	231 – 768	1.6%	11_TUCANO
Clearwater Fish Hatchery	OtsPOWP13S_sp	2013	108	0	0	108	0 – 322	0.1%						0.0%	12_HELLSC
Clearwater Fish Hatchery	OtsCLWH14S_sp	2014	7,712	0	0	7,712	6449 – 8974	4.3%	866	43	0	909	547 – 1286	3.0%	12_HELLSC
Clearwater Fish Hatchery	OtsPOWP14S_sp	2014	3,897	0	0	3,897	2961 – 4861	2.2%	434	0	0	434	186 – 685	1.4%	12_HELLSC
Dworshak National Fish Hatchery	OtsDWOR14S_sp	2014	3,841	0	0	3,841	2960 – 4791	2.1%	165	0	0	165	51 – 320	0.5%	12_HELLSC
Lookingglass Fish Hatchery	OtsLOOK14S_sp	2014	540	0	0	540	199 – 913	0.3%	54	0	0	54	0 – 163	0.2%	12_HELLSC
Lookingglass Fish Hatchery	OtsCTHW14S_sp	2014	271	0	0	271	76 – 563	0.2%						0.0%	12_HELLSC
Lookingglass Fish Hatchery	OtsGRUW14S_sp	2014	446	0	0	446	156 – 815	0.2%	302	0	0	302	114 – 542	1.0%	12_HELLSC
Lookingglass Fish Hatchery	OtsLSTW14S_sp	2014	264	0	0	264	82 – 528	0.1%						0.0%	12_HELLSC

Hatchery	Code	Year						%						%	Group
Nez Perce	OtsNPFH14S_sp	2014						0.0%	128	0	0	128	0 – 319	0.4%	12_HELLSC
Rapid River Fish Hatchery	OtsRAPH13S_sp	2013	74	0	0	74	0 – 223	0.0%						0.0%	12_HELLSC
Rapid River Fish Hatchery	OtsRAPH14S_sp	2014	15,160	0	0	15,160	13285 – 17001	8.4%	233	0	0	233	75 – 466	0.8%	12_HELLSC
Carson National Fish Hatchery	OtsCAR13_sp	2013	116	0	0	116	0 – 346	0.1%						0.0%	20_BONPOOLSP
Carson National Fish Hatchery	OtsCAR14_sp	2014	4,086	0	0	4,086	3123 – 5122	2.3%	265	0	0	265	67 – 510	0.9%	20_BONPOOLSP
Little White Salmon National Fish Hatchery	OtsLWS13_sp	2013	275	0	0	275	0 – 575	0.2%						0.0%	20_BONPOOLSP
Little White Salmon National Fish Hatchery	OtsLWS14_sp	2014	8,647	226	0	8,873	7408 – 10285	4.9%	412	0	0	412	142 – 695	1.4%	20_BONPOOLSP
Umatilla Fish Hatchery	OtsUMA13_sp	2013	156	0	0	156	0 – 386	0.1%	55	0	0	55	0 – 164	0.2%	21_UMATILLASP
Umatilla Fish Hatchery	OtsUMA14_sp	2014	6,528	0	0	6,528	5402 – 7684	3.6%	620	0	0	620	332 – 926	2.0%	21_UMATILLASP
Lookingglass Fish Hatchery	OtsIMNW14S_sp su	2014	628	0	0	628	305 – 1017	0.3%						0.0%	12_HELLSC
McCall Fish Hatchery	OtsMCCA14S_sp su	2014	2,920	394	0	3,314	2372 – 4208	1.8%	696	0	0	696	334 – 1124	2.3%	13_SFSALM
McCall Fish Hatchery	OtsJHNW14S_sp su	2014						0.0%	201	0	0	201	0 – 402	0.7%	13_SFSALM
Pahsimeroi Fish Hatchery	OtsPAHH14S_sp su	2014	1,766	397	0	2,163	1461 – 2911	1.2%						0.0%	16_UPSALM
Sawtooth Fish Hatchery	OtsSAWT14S_sp su	2014	5,058	0	0	5,058	4048 – 6090	2.8%	331	0	0	331	114 – 574	1.1%	16_UPSALM
Chief Joseph Hatchery	OtsCJH13seg_su	2013	292	1,626	0	1,918	1095 – 2781	1.1%	0	330	0	330	96 – 660	1.1%	18_UCOLSF
Chief Joseph Hatchery	OtsCJH13int_su	2013	143	783	0	925	318 – 1606	0.5%						0.0%	18_UCOLSF
Chief Joseph Hatchery	OtsCJH14seg_su	2014	1,424	6,713	0	8,137	5520 – 9726	4.5%						0.0%	18_UCOLSF
Chief Joseph Hatchery	OtsCJH14int_su	2014	574	3,902	0	4,476	3277 – 5724	2.5%	141	548	0	689	213 – 1237	2.3%	18_UCOLSF
Chief Joseph Hatchery	OtsCJH15int_su	2015	0	0	489	489	0 – 1466	0.3%						0.0%	18_UCOLSF
Eastbank Fish Hatchery	OtsEASTBK12_su	2012	312	261	0	573	104 – 1136	0.3%						0.0%	18_UCOLSF
Eastbank Fish Hatchery	OtsEASTBK13_su	2013	614	1,411	0	2,025	1195 – 2928	1.1%	73	246	0	318	73 – 638	1.0%	18_UCOLSF
Eastbank Fish Hatchery	OtsEASTBK14_su	2014	1,594	3,749	194	5,537	4173 – 6796	3.1%	148	135	0	283	81 – 533	0.9%	18_UCOLSF
Entiat National Fish Hatchery	OtsENFH13_su	2013	0	164	0	164	0 – 486	0.1%	0	141	0	141	0 – 424	0.5%	18_UCOLSF
Entiat National Fish Hatchery	OtsENFH14_su	2014	737	5,768	0	6,505	4667 – 8078	3.6%	174	0	0	174	0 – 411	0.6%	18_UCOLSF
Wells Fish Hatchery	OtsWELLS12_su	2012						0.0%	63	0	0	63	0 – 190	0.2%	18_UCOLSF
Wells Fish Hatchery	OtsWELLS13_su	2013	1,646	274	0	1,919	1300 – 2646	1.1%	77	0	0	77	0 – 232	0.3%	18_UCOLSF
Wells Fish Hatchery	OtsWELLS14_su	2014	1,155	4,581	0	5,736	4376 – 7136	3.2%	77	243	0	320	0 – 806	1.1%	18_UCOLSF

Hatchery	Code	Year													
Wells Fish Hatchery	OtsWELLS15_su	2015	63	154	0	217	0 – 524	0.1%						0.0%	18_UCOLSF
Spring Creek National Fish Hatchery	OtsSPCR15_fa	2015	0	0	15,555	15,555	12630 – 18525	8.6%	0	0	867	867	237 – 1589	2.9%	05_SPCRTU
Spring Creek National Fish Hatchery	OtsSPCR16_fa	2016	0	0	2,989	2,989	1345 – 4999	1.7%	0	0	321	321	0 – 962	1.1%	05_SPCRTU
Priest Rapids Hatchery	OtsPRH13_fa	2013	0	0	1,145	1,145	487 – 1822	0.6%	0	0	995	995	405 – 1696	3.3%	18_UCOLSF
Priest Rapids Hatchery	OtsPRH14_fa	2014	0	0	2,979	2,979	1674 – 4294	1.6%	0	0	3,079	3,079	2136 – 4310	10.2%	18_UCOLSF
Priest Rapids Hatchery	OtsPRH15_fa	2015	0	0	3,900	3,900	2604 – 5323	2.2%	0	0	3,602	3,602	2421 – 4813	11.9%	18_UCOLSF
Lyons Ferry Fish Hatchery	OtsLYON13S_1_fa	2013	0	0	844	844	187 – 1501	0.5%	0	0	547	547	118 – 1027	1.8%	19_SRFALL
Lyons Ferry Fish Hatchery	OtsLYON14S_1_fa	2014	0	64	3,452	3,516	2201 – 5055	1.9%	0	165	3,289	3,455	2360 – 4636	11.4%	19_SRFALL
Lyons Ferry Fish Hatchery	OtsLYON15S_1_fa	2015	0	0	5,085	5,085	3121 – 7089	2.8%	0	0	1,580	1,580	890 – 2357	5.2%	19_SRFALL
Lyons Ferry Fish Hatchery	OtsLYON16S_1_fa	2016						0.0%	0	0	217	217	0 – 651	0.7%	19_SRFALL
Nez Perce Tribal Fish Hatchery	OtsNPFH13S_1_fa	2013						0.0%	0	0	205	205	0 – 615	0.7%	19_SRFALL
Nez Perce Tribal Fish Hatchery	OtsNPFH14S_1_fa	2014	0	0	1,172	1,172	440 – 2092	0.6%	0	0	1,248	1,248	525 – 2088	4.1%	19_SRFALL
Nez Perce Tribal Fish Hatchery	OtsNPFH15S_1_fa	2015	0	65	170	235	0 – 575	0.1%	0	0	1,602	1,602	770 – 2472	5.3%	19_SRFALL
Little White Salmon National Fish Hatchery	OtsLWS13_fa	2013	0	0	4,848	4,848	2925 – 6881	2.7%	0	0	1,311	1,311	589 – 2087	4.3%	22_BONPOOLFA
Little White Salmon National Fish Hatchery	OtsLWS14_fa	2014	0	0	6,839	6,839	5093 – 8681	3.8%	0	0	1,628	1,628	942 – 2434	5.4%	22_BONPOOLFA
Little White Salmon National Fish Hatchery	OtsLWS15_fa	2015	0	0	7,144	7,144	5375 – 8960	4.0%	0	0	339	339	102 – 685	1.1%	22_BONPOOLFA
#N/A	Unassigned	#N/A	1,403	8	9,711	11,122	8963 – 15354	6.1%						0.0%	#N/A
	TOTAL		83,790	30,539	66,516	180,846		100.0%	7,647	1,852	20,831	30,330		100.0%	

1681 **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
1682 estimates of clipped and unclipped Chinook salmon that passed Bonneville Dam at the fish counting window. Abundance was reported for each stock as subtotals that passed within each
1683 management period.
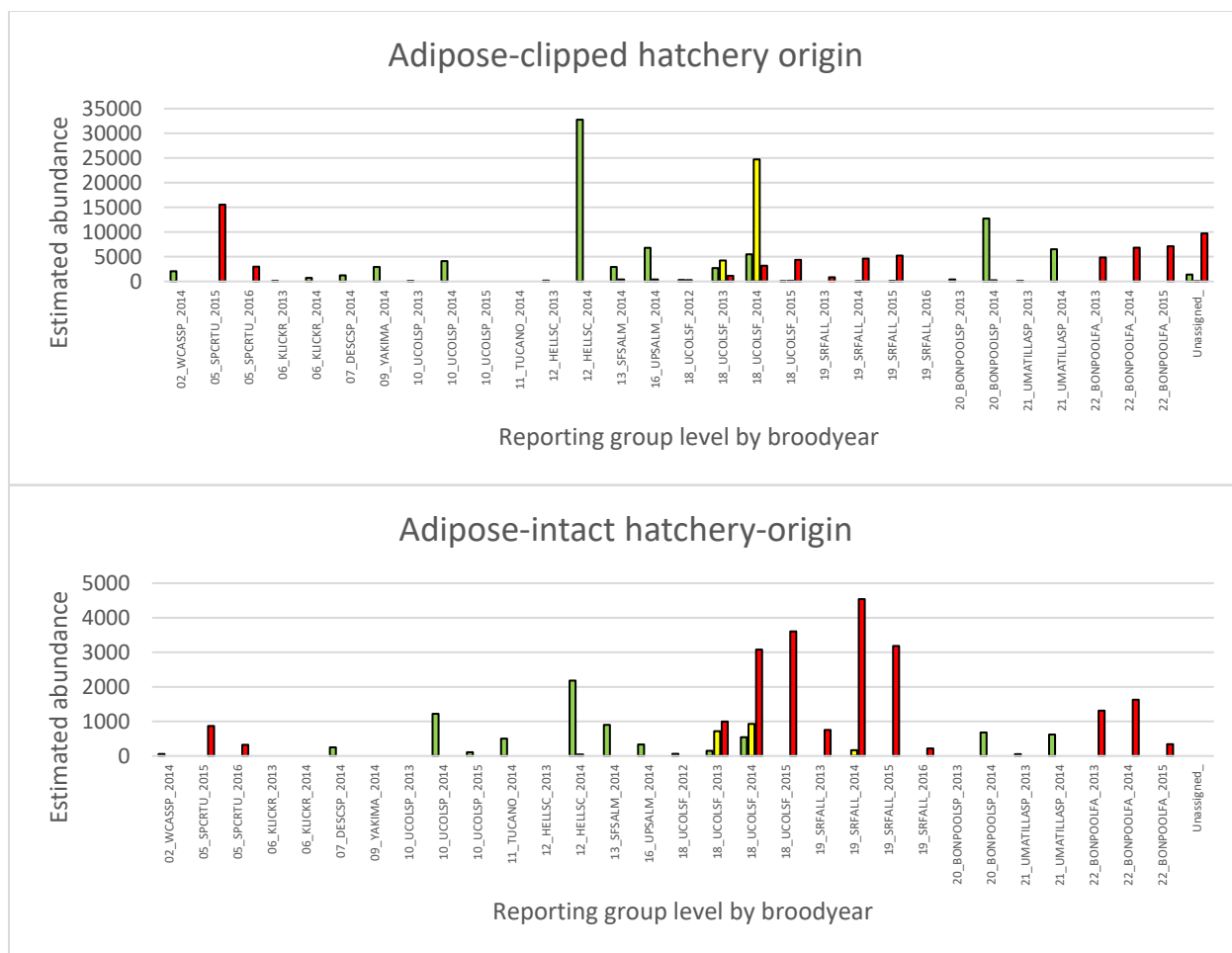
Figure 25. Estimated abundance of hatchery origin adipose-clipped (top) and adipose-intact (bottom) Chinook assigned by PBT reporting groups and broodyears that were sampled at Bonneville Dam in 2018 during spring (green), summer (yellow) and fall (red) management periods.

In Figure 25, there are several new reporting groups that have been created and are populated based on hatchery fish assigned via PBT, which were subsequently categorized into higher level groups to complement the GSI reporting groups. For example, 20_BONPOOLSP reporting group includes PBT assignments of spring Chinook to Carson Hatchery and Little White Salmon Hatchery. The 21_UMATILLASP reporting group includes PBT assignments of spring Chinook to the Umatilla Hatchery. The 22_BONPOOLFA reporting group includes PBT assignments of fall Chinook to the Little White Salmon Hatchery. The 22_UMATILLAFA reporting group includes PBT assignments of fall Chinook to the Umatilla Hatchery. These reporting groups serve the purpose of distinguishing these hatchery broodstocks apart from other reporting groups that share genetic affinity with these hatcheries but are part of ESA listed groups. For example, 20_BONPOOLSP broodstocks share genetic similarity with upper Columbia River spring Chinook Salmon, but only hatchery fish from the latter group are ESA listed.

We detected PBT assignments for 19.3% (278/1442) of adipose non-clipped (i.e., presumed natural-origin) Chinook salmon sampled at Bonneville Dam in 2017. There were 7

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1706   major (i.e., abundance >1000 fish) Chinook salmon stocks represented in the total estimated
1707   relative abundance (N=124,854) of natural origin (i.e., adipose non-clipped fish that did not
1708   assign via PBT) Chinook salmon passing Bonneville Dam in 2018 (Table 52; Figure 26). These
1709   non-clipped stocks in order of decreasing magnitude were 18_UCOLSF (92,425), 19_SRFALL
1710   (15,406), 12_HELLSC (4,833), 10_UCOLSP (3,607), 09_YAKIMA (2,240), 17_DESCFA
1711   (1,752), and 13_SFSALM (1,402). These stock abundance estimates were based on the stock
1712   proportions that were estimated in using SCOBI DEUX and SPIBETR functions and the
1713   estimates of clipped and unclipped adults distributed by TAC (Table 48).

1714 **Table 52. Estimated abundance of natural origin Chinook salmon stocks passing**
1715 **Bonneville Dam in 2018.**

Reporting Group name	Run type	Reporting Group Code	Spring	Summer	Fall	Natural origin- No Clip Estimated abundance Mean	95% CI
Youngs Bay	Spring	01_YOUNGS	0	85	97	182	0 – 448
West Cascade Spring	Spring	02_WCASSP					
West Cascade Fall	Fall	03_WCASFA					
Willamette	Spring	04_WILLAM	0	0	204	204	0 – 613
Spring Creek Tule	Fall	05_SPCRTU	0	0	526	526	160 – 1071
Klickitat	Spring	06_KLICKR	52	0	0	52	0 – 157
Deschutes spring	Spring	07_DESCSP	745	0	0	745	427 – 1060
John Day	Spring	08_JOHNDR	51	0	0	51	0 – 154
Yakima	Spring	09_YAKIMA	2,240	0	0	2,240	1685 – 2815
Upper Columbia spring	Spring	10_UCOLSP	3,607	0	0	3,607	2862 – 4306
Tucannon	Spring	11_TUCANO	207	0	0	207	51 – 400
Hells Canyon	Spring/Summer	12_HELLSC	4,833	0	0	4,833	4104 – 5611
South Fork Salmon	Spring/Summer	13_SFSALM	748	654	0	1,402	779 – 2103
Chamberlain Creek	Spring/Summer	14_CHMBLN					
Middle Fork Salmon	Spring/Summer	15_MFSALM	525	0	0	525	278 – 827
Upper Salmon	Spring/Summer	16_UPSALM	655	41	0	696	385 – 1025
Deschutes fall	Fall	17_DESCFA	0	0	1,752	1,752	1060 – 2478
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	2,885	6,950	82,590	92,425	88839 – 95299
Snake River fall	Fall	19_SRFALL	59	785	14,562	15,406	13193 – 17744
		Total	16,608	8,515	99,731	124,854	

1716 Note: Abundance of natural-origin stocks is shown by subtotals that passed Bonneville Dam in
1717 each management period (spring, summer, and fall) and the total mean estimate with 95% C.I.
1718 Natural-origin estimates exclude abundance of adipose-intact hatchery-origin fish.
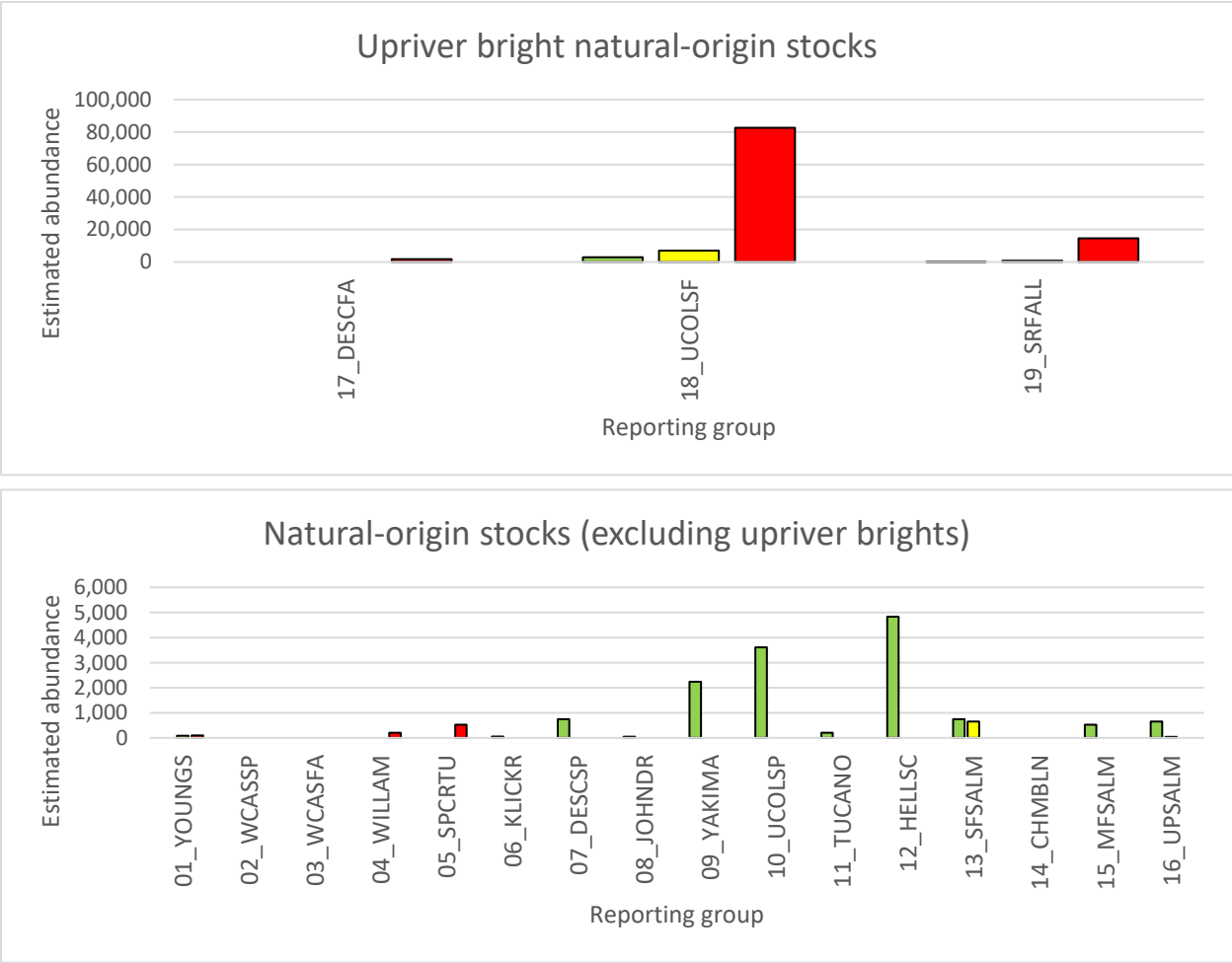
Figure 26. Estimated abundance of natural origin (excluding adipose-intact hatchery-origin fish) Chinook sampled at Bonneville Dam in 2018 assigned to genetic stock of origin. Upriver bright Chinook salmon reporting groups (top panel), and all other natural-origin Chinook reporting groups (bottom panel) are shown by spring (green), summer (yellow) and fall (red) management period.

1725 *Run-timing of Chinook salmon stocks in 2018*
1726   We plotted the run-timing distributions of the natural-origin (excluding adipose unclipped
1727 hatchery-origin fish) Chinook salmon stocks and provide subtotals of abundance for each
1728 management period (Table 52; **Figure 27**). While the median date of passage for all natural-
1729 origin spring Chinook stocks occurred well within the spring management period, the run-timing
1730 for 13_SFSALM and 16_UPSALM was found to extend beyond the spring management period
1731 (i.e., the 95th percentile of their run distribution occurred after 6/16/17; ordinal day 166). We
1732 estimated that 47% and 6% of the total abundance of these two spring stocks arrived during the
1733 summer management period for 3_SFSALM and 16_UPSALM, respectively (Table 52). The
1734 run-timing for one natural-origin summer/fall Chinook stock (i.e., 18_UCOLSF) and three
1735 natural-origin fall Chinook salmon stocks (i.e., 05_SPCRTU, 17_DESCFA, and 19_SRFALL)
1736 all had median dates on or after ordinal day 241 (8/29/18, **Figure 27**). We estimated that for the
1737 18_UCOLSF stock abundance that arrives during the spring and summer management periods,
1738 approximately 29% arrives during the spring (Table 52).
1739
1740

1741
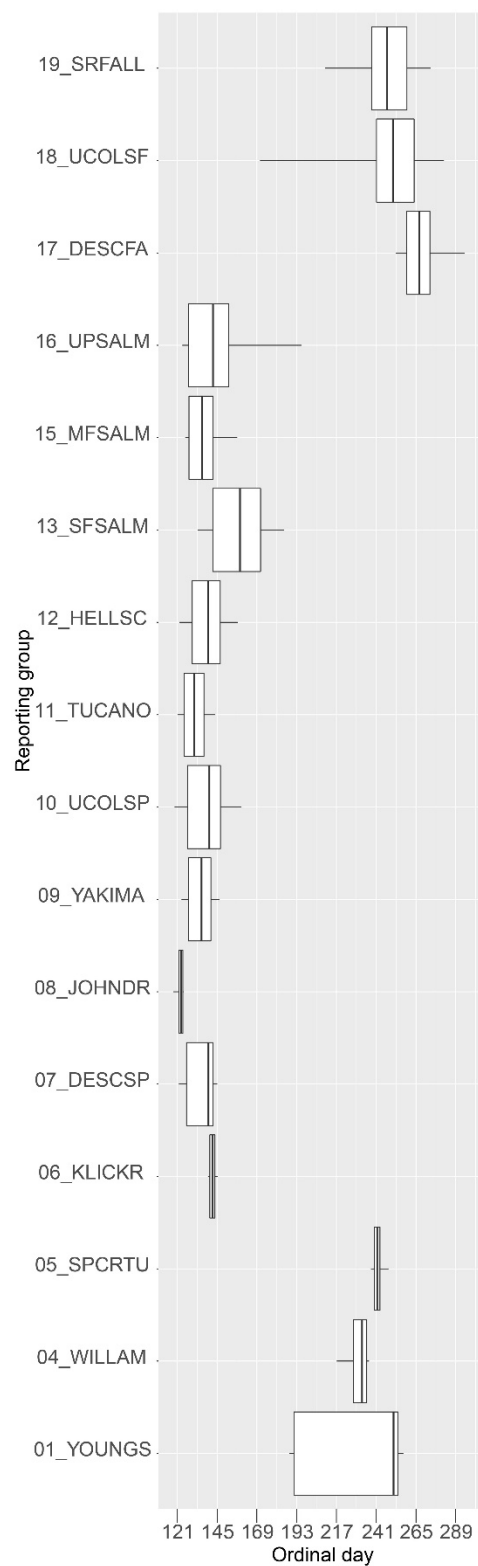
Figure 27. Run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for natural origin Chinook (excluding all adipose-intact hatchery-origin fish) assigned to reporting group of origin that were sampled at Bonneville Dam in 2018.

1745 *Estimated relative abundance of steelhead stocks in 2018*
1746   Daily passage of steelhead at Bonneville Dam in 2018 is provided in Figure 28. There
1747 were five major stocks (abundance >1000) represented in the total estimated relative abundance
1748 (N=70,265) of hatchery origin steelhead passing Bonneville Dam in 2018 (Table 53). These
1749 stocks in order of decreasing magnitude were 10_SFCLWR (26,807), 07_MGILCS (18,878),
1750 14_UPSALM (17,707), 09_UPPCOL (4,637), and 03_SKAMAN (2,101) (Table 53; Figure 29).
1751 These same stocks were identified as being of major abundance in 2016 and 2017. These
1752 estimates include relative abundance estimated from PBT-assigned fish that were mostly adipose
1753 clipped; however, a portion of the PBT-assigned fish were found to be non-clipped. Therefore,
1754 PBT assignments improved our ability to accurately identify hatchery-origin steelhead and
1755 estimate total stock relative abundance. Further, using PBT assignments we can now provide
1756 abundance (Table 54; Figure 30) and run-timing estimates for particular hatchery broodstocks
1757 (Table 54). There were 12 major hatchery broodstock sources (abundance >1000) represented in
1758 the total estimated abundance of hatchery-origin steelhead passing Bonneville Dam in 2018
1759 (Table 54). These stocks in order of decreasing magnitude were OmyDWOR15S (25,501),
1760 OmyLYON16S (5,657), OmyWALL15S (4,461), OmyOXBO16S (4,395), OmyPAHH16S
1761 (3,533), OmyOXBO15S (3,433), OmyLYON15S (2,822), OmySAWT16S (2,784),
1762 OmyWEL_OKA15 (2,516), OmyPAHH15S (2,288), OmySKH14_su (1,386), and OmyRB15
1763 (1,167).
1764   We detected PBT assignments for 28.5% (69/242) of adipose non-clipped (i.e., presumed
1765 natural-origin) steelhead sampled at Bonneville Dam in 2018. There were three major stocks
1766 (abundance >1000) represented in the total estimated relative abundance (N=23,735) of natural
1767 origin (excluding adipose unclipped hatchery-origin fish) steelhead passing Bonneville Dam in
1768 2018 (Table 53). These stocks in order of decreasing magnitude were 07_MGILCS (16,797),
1769 09_UPPCOL (1,424), and 08_YAKIMA (1,321). Two major stocks in 2017 were no longer
1770 estimated with abundance >1000: 14_UPSALM (35, down from 2,286), and 06_KLICKR (942,
1771 down from 1,013). The 14_UPSALM stock appeared to have decreased dramatically but we feel
1772 this was a results of the SCOBI DEUX SPIBETR function that minimized bias from tag rate
1773 expansion of the unclipped hatchery-origin fish. This results underscores the importance of the
1774 SPIBETR method and using this function consistently on past years of data for better
1775 comparisons across years.

1776 **Table 53. Stock-specific abundance by A-/B-Index categories of hatchery- (adipose clipped and non-clipped) and natural-origin summer A-/B-Index steelhead passing**
1777 **Bonneville Dam in 2018.**

Reporting Group name	Reporting Group Code	Hatchery origin- Clipped				Hatchery origin- No Clip				Natural origin- No Clip			
		A-INDEX		B-INDEX		A-INDEX		B-INDEX		A-INDEX		B-INDEX	
		Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI
Lower Columbia	02_LOWCOL	0	0 – 0	0	0 – 0	0	0 – 0	0	0 – 0	0	0 – 0	0	0 – 0
Skamania	03_SKAMAN	1,995	572 – 3876	107	0 – 449	0	0 – 0	0	0 – 0	467	117 – 817	0	0 – 0
Willamette	04_WILLAM	0	0 – 0	0	0 – 0	0	0 – 0	0	0 – 0	0	0 – 0	0	0 – 0
Big White Salmon	05_BWSALM	139	0 – 558	0	0 – 0	0	0 – 0	0	0 – 0	0	0 – 0	0	0 – 0
Klickitat	06_KLICKR	0	0 – 0	0	0 – 0	0	0 – 0	0	0 – 0	792	266 – 1396	151	0 – 371
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	18,199	14618 – 22230	58	0 – 233	621	36 – 1637	0	0 – 0	16,760	15310 – 18228	36	0 – 117
Yakima	08_YAKIMA	0	0 – 0	0	0 – 0	0	0 – 0	0	0 – 0	1,321	560 – 2073	0	0 – 0
upper Columbia	09_UPPCOL	4,372	2254 – 6883	0	0 – 0	265	0 – 796	0	0 – 0	1,067	407 – 1780	357	0 – 763
SF Clearwater	10_SFCLWR	3,253	1897 – 4809	19,159	16873 – 21374	576	139 – 1117	3,819	2546 – 5181	386	62 – 851	370	60 – 913
upper Clearwater	11_UPCLWR	0	0 – 0	0	0 – 0	0	0 – 0	0	0 – 0	248	51 – 498	398	107 – 716
SF Salmon	12_SFSALM	0	0 – 0	0	0 – 0	0	0 – 0	0	0 – 0	0	0 – 0	467	105 – 894
MF Salmon	13_MFSALM	0	0 – 0	0	0 – 0	0	0 – 0	0	0 – 0	627	153 – 1187	253	0 – 506
upper Salmon	14_UPSALM	16,773	12692 – 20773	430	0 – 1062	498	0 – 1215	0	0 – 0	35	0 – 104	0	0 – 0
	Total	**44,732**		**19,754**		**1,960**		**3,819**		**21,703**		**2,032**	

1778 **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
1779 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
1780 by uneven sampling.
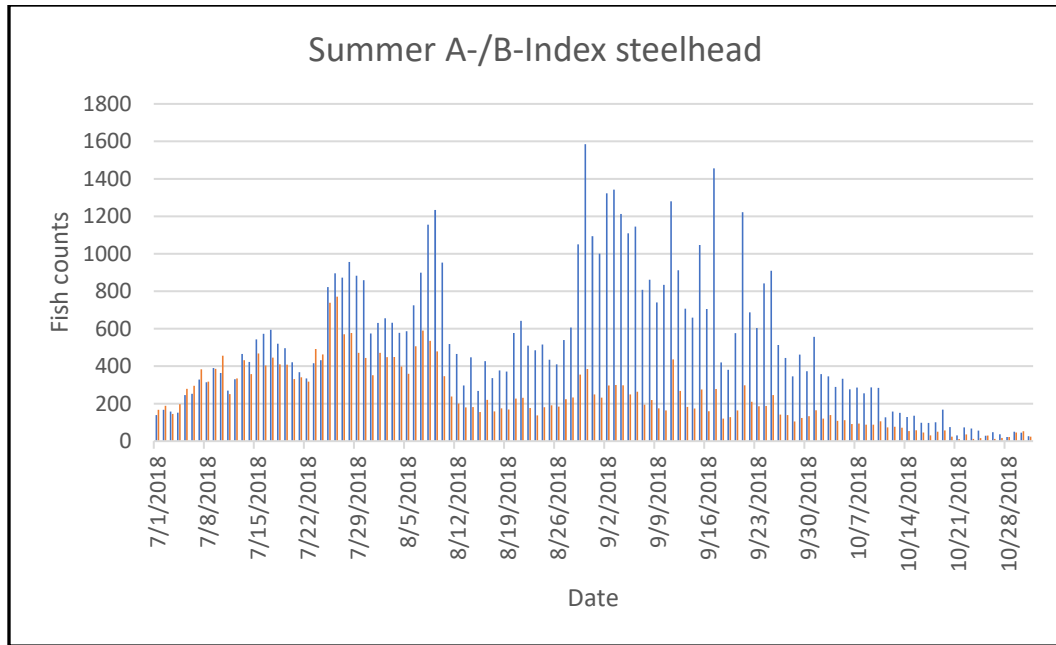
Figure 28. Daily passage of clipped (blue) and unclipped (red) steelhead at Bonneville Dam in 2018 during the summer A-/B-Index management period (source: www.fpc.org).

1785

1786
1787 **Figure 29. Estimated abundance (± 95% CI) of A-Index (<780mm FL, top) and B-Index**
1788 **(>=780mm FL, bottom) hatchery origin (adipose clipped and unclipped) and natural-origin**
1789 **steelhead assigned to genetic stock of origin that were sampled at Bonneville Dam in 2018.**

1790

A-Index Summer Steelhead

1791

B-Index Summer Steelhead
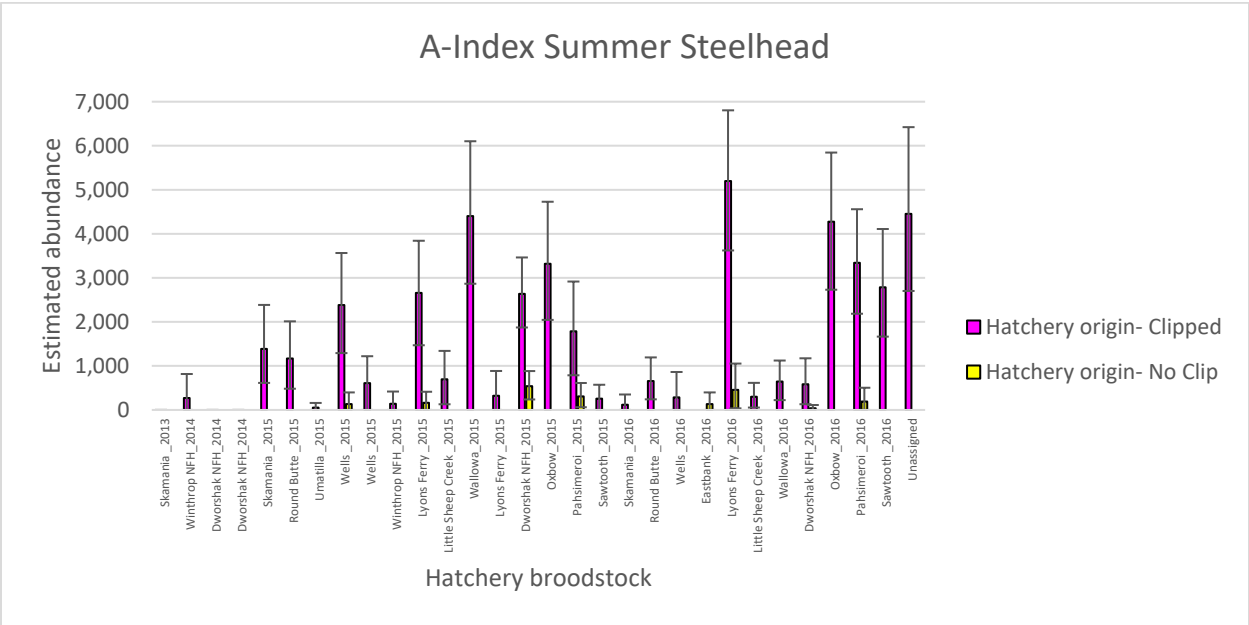
1792
Figure 30. Estimated abundance (± 95% CI) of A-Index (<780mm FL, top) and B-Index (>=780mm FL, bottom) hatchery origin steelhead (adipose clipped and unclipped) sampled at Bonneville Dam in 2018 that assigned via PBT to 29 hatchery broodstocks of origin. The 2016 age-class (1-ocean fish), 2015 age-class (2-ocean fish), and 2014 age class (3-ocean fish) are shown. Key to broodstock collection is presented in Appendix 7.

1798 **Table 54. Hatchery broodstock-specific estimated abundance of A-Index and B-Index adipose clipped and non-clipped PBT-assigned steelhead passing Bonneville Dam in 2018.**

| | | | | | Hatchery clipped | | | | Hatchery Unclipped | | | |
| | | | | | A-INDEX | | B-INDEX | | A-INDEX | | B-INDEX | |
Hatchery	Stock	GSI RepGrp	Broodstock	Broodyear	MLE	95% CI	MLE	95% CI	MLE	95% CI	MLE	95% CI
Skamania	Summer	03_SKAMAN	OmySKH12_su	2013	0	0 – 0	107	0 – 326				
Skamania	Summer	03_SKAMAN	OmySKH14_su	2015	1,386	614 – 2385	0	0 – 0				
Skamania	Summer	03_SKAMAN	OmySKH15_su	2016	117	0 – 351	0	0 – 0				
Round Butte	Deschutes River	07_MGILCS	OmyRB15	2015	1,167	482 – 2012	0	0 – 0				
Umatilla	Minthorn Springs	07_MGILCS	OmyUMA15	2015	53	0 – 159	0	0 – 0				
Lyons Ferry	Mixed origins (Snake + UpC)	07_MGILCS	OmyLYON15S	2015	2,659	1469 – 3842	0	0 – 0	163	0 – 413	0	0 – 0
Little Sheep Creek	-	07_MGILCS	OmyLSCR15S	2015	696	129 – 1341	0	0 – 0				
Wallowa	-	07_MGILCS	OmyWALL15S	2015	4,403	2866 – 6102	58	0 – 173				
Lyons Ferry	Wallowa	07_MGILCS	OmyWALW15S	2015	321	0 – 885	0	0 – 0				
Round Butte	Deschutes River	07_MGILCS	OmyRB16	2016	657	241 – 1193	0	0 – 0				
Lyons Ferry	Mixed origins (Snake + UpC)	07_MGILCS	OmyLYON16S	2016	5,199	3622 – 6804	0	0 – 0	458	36 – 1053	0	0 – 0
Little Sheep Creek	-	07_MGILCS	OmyLSCR16S	2016	301	54 – 615	0	0 – 0				
Wallowa	-	07_MGILCS	OmyWALL16S	2016	647	223 – 1122	0	0 – 0				
Winthrop NFH	Methow River	09_UPPCOL	OmyWTP14	2014	272	0 – 816	0	0 – 0				
Wells	Okanogan Stock	09_UPPCOL	OmyWEL_OKA15	2015	2,383	1291 – 3564	0	0 – 0	133	0 – 398	0	0 – 0
Wells	Omak Stock	09_UPPCOL	OmyWEL_OMA15	2015	610	0 – 1220	0	0 – 0				
Winthrop NFH	Methow River	09_UPPCOL	OmyWTP15	2015	139	0 – 418	0	0 – 0				
Wells	On Station	09_UPPCOL	OmyWEL16S	2016	287	0 – 862	0	0 – 0				
Eastbank	Chelan/Methow/Okanogan/Wenatchee	09_UPPCOL	OmyEASTBK16	2016					133	0 – 398	0	0 – 0
Dworshak NFH	Clearwater River	10_SFCLWR	OmyDWOR14S_1	2014	0	0 – 0	220	0 – 444				
Dworshak NFH	Clearwater River	10_SFCLWR	OmyDWOR14S	2014	0	0 – 0	166	0 – 388				
Dworshak NFH	Clearwater River	10_SFCLWR	OmyDWOR15S	2015	2,636	1873 – 3463	18,508	17028 – 19905	538	238 – 883	3,819	3025 – 4694
Dworshak NFH	Clearwater River	10_SFCLWR	OmyDWOR16S	2016	584	130 – 1173	0	0 – 0	37	0 – 112	0	0 – 0
Oxbow	-	14_UPSALM	OmyOXBO15S	2015	3,319	2045 – 4728	114	0 – 342				
Pahsimeroi	Salmon River	14_UPSALM	OmyPAHH15S	2015	1,786	787 – 2916	196	0 – 482	306	62 – 612	0	0 – 0
Sawtooth	Salmon River	14_UPSALM	OmySAWT15S	2015	257	0 – 572	0	0 – 0				
Oxbow	-	14_UPSALM	OmyOXBO16S	2016	4,274	2730 – 5845	121	0 – 354				
Pahsimeroi	Salmon River	14_UPSALM	OmyPAHH16S	2016	3,341	2185 – 4558	0	0 – 0	192	0 – 504	0	0 – 0
Sawtooth	Salmon River	14_UPSALM	OmySAWT16S	2016	2,784	1665 – 4109	0	0 – 0				
#N/A	#N/A	#N/A	Unassigned	#N/A	4,454	2702 – 6422	265	109 – 582				

1799 **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
1800 passed the Bonneville Dam at the fish counting window. Key to broodstock collection is presented in Appendix 7.

1801   *Run-timing of steelhead stocks in 2018*
1802   We were able to characterize the run-timing distributions for hatchery origin clipped and
1803   unclipped steelhead stocks (Figure 31). Very few winter-run steelhead stocks exist above
1804   Bonneville Dam and our sampling program at Bonneville AFF does not trap or collect fish
1805   between December and March when winter-run steelhead would be most likely to occur. The
1806   Skamania summer steelhead period is 4/1/2018 – 6/30/ 2018, and the summer A-/B-Index period
1807   begins on 7/1/2018 and lasts until 10/31/2018. We examined run-timing of the stocks arriving in
1808   the A-/B-Index period (Figure 31). The broodstock that typically has late run-timing is the
1809   Dworshak stock, which often arrives after August 25th at Bonneville Dam (Figure 31).
1810   We characterized the run-timing distributions for natural-origin steelhead stocks (Figure
1811   32); the patterns generally are consistent with past years. The late arriving stocks with median
1812   dates on or after August 25th were 10_SFCLWR 11_UPCLWR, 13_MFSALM, and
1813   14_UPSALM. We characterized run-timing by A-Index and B-Index categories for these stocks.
1814   For some stocks that had earlier run-timing as A-Index sizes, these stocks were later arriving as
1815   B-Index stocks (Figure 32).

1816
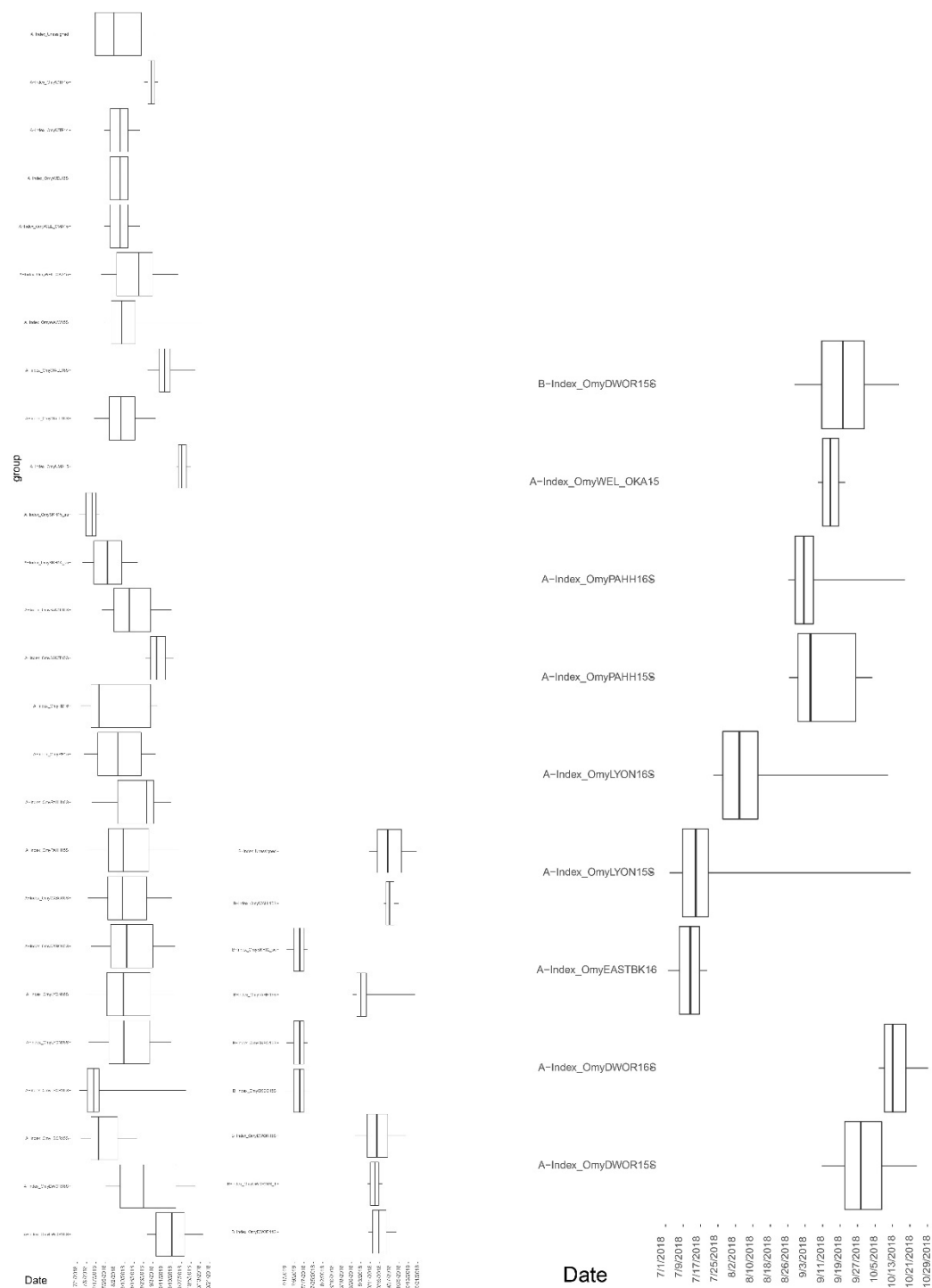
1817

1818 **Figure 31. Run-timing distributions (median ordinal day, interquartile range, and 5th and**
1819 **95th percentile) for hatchery-origin steelhead (adipose clipped, left; adipose unclipped,**
1820 **right) that were sampled at Bonneville Dam in 2018 and assigned to broodstock of origin.**
1821 **Each broodstock is shown by A-Index and B-Index size category. Key to broodstock**
1822 **collection is presented in Appendix 7.**
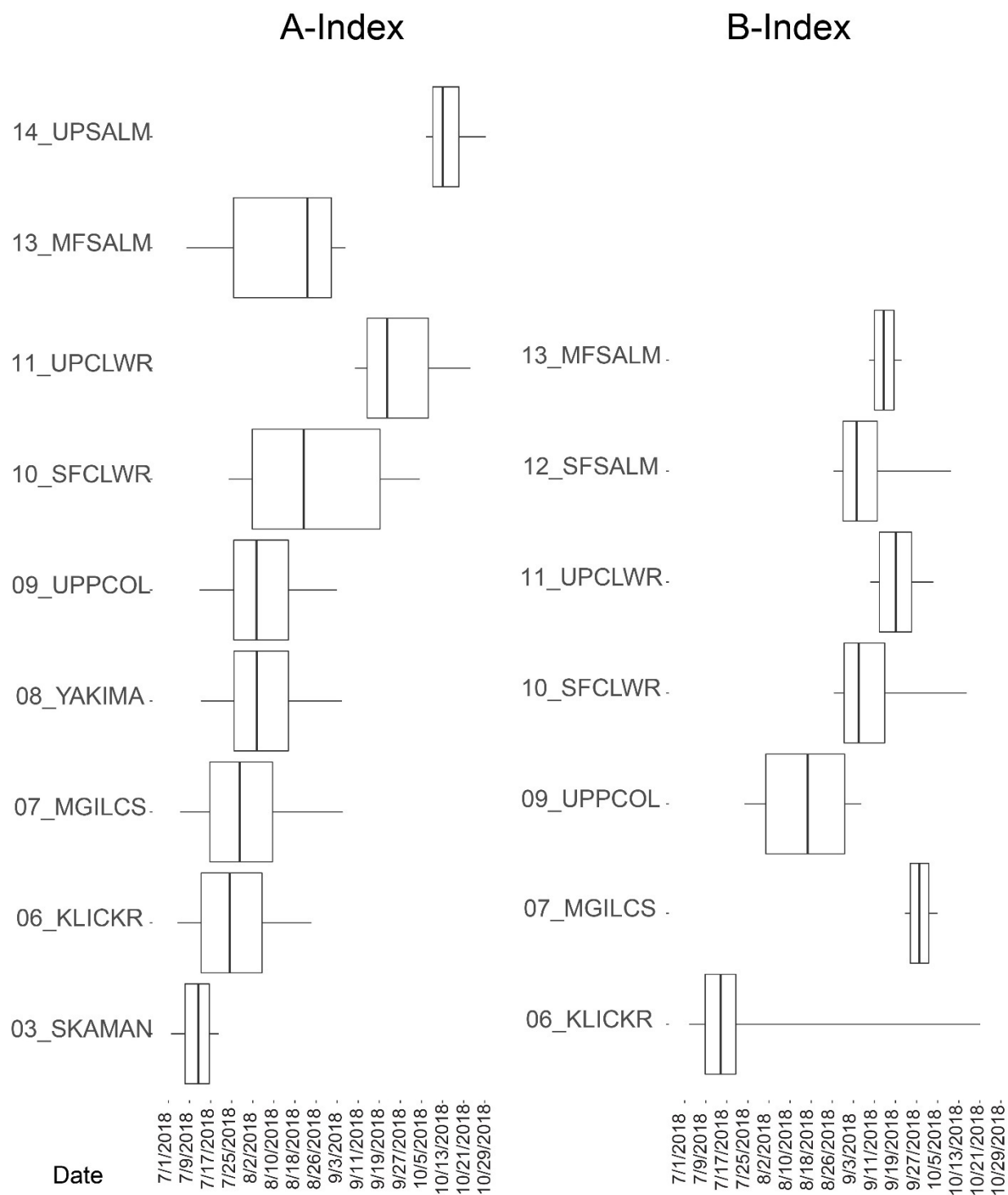
Figure 32. Run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for natural-origin steelhead (all hatchery-origin adipose-unclipped fish excluded) that were sampled at Bonneville Dam in 2018 and assigned to stock of origin. Each stock is shown by A-Index (left) and B-Index (right) size category

1828   *Estimated abundance and run-timing of Sockeye salmon stocks in 2018*
1829   Daily passage of Sockeye salmon at Bonneville Dam in 2018 is provided in **Figure 33**. Stock
1830   abundance for sockeye salmon was estimated over a course of 16 statistical weeks (i.e. weeks
1831   21-36). A total of 1,857 sockeye salmon were sampled at Bonneville Dam in 2018 and were
1832   assigned to one of four genetic stocks (i.e., Okanogan, Wenatchee, Snake, and Lake Billy
1833   Chinook) using GSI and one reintroduced stock using PBT (Table 55). The Okanogan stock had
1834   the highest relative abundance (174,130), followed by the Wenatchee (17,675) (Table 55). The
1835   Snake and Lake Billy Chinook stocks had estimated abundances < 500, but were based on
1836   relatively few genetic assignments (<15) (Table 55, **Figure 34**). The reintroduced stock from
1837   Yakima River was also low sample size but we estimated 1,294 fish in 2018.
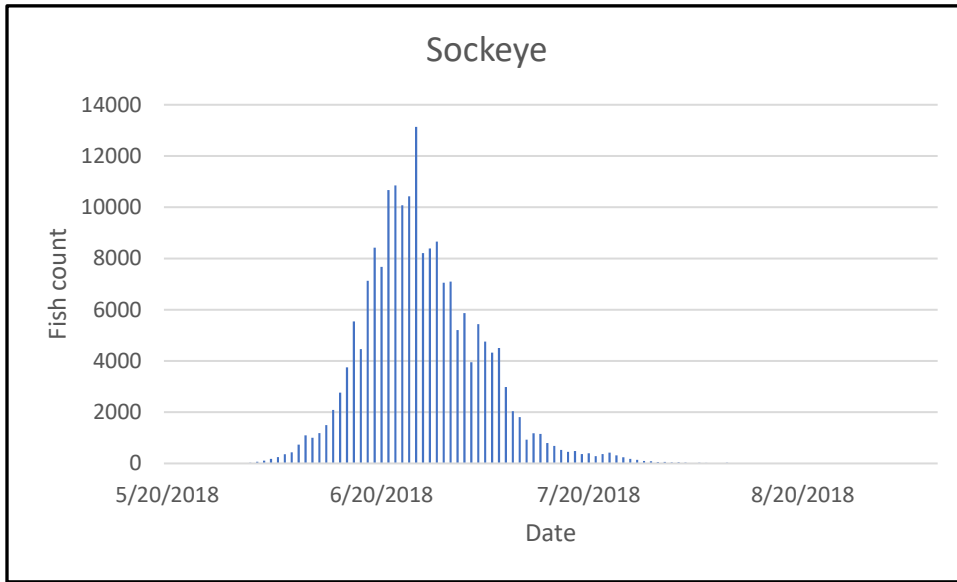
1838
1839   **Figure 33. Daily passage of sockeye at Bonneville Dam in 2018 (source: www.fpc.org).**
1840
1841
1842   We characterized the run-timing distributions for the two major sockeye salmon stocks
1843   (Table 55, Figure 35). The Wenatchee and Okanogan stocks had nearly identical run timing
1844   distributions each with a median date near 06/24/18 (Figure 35).
1845
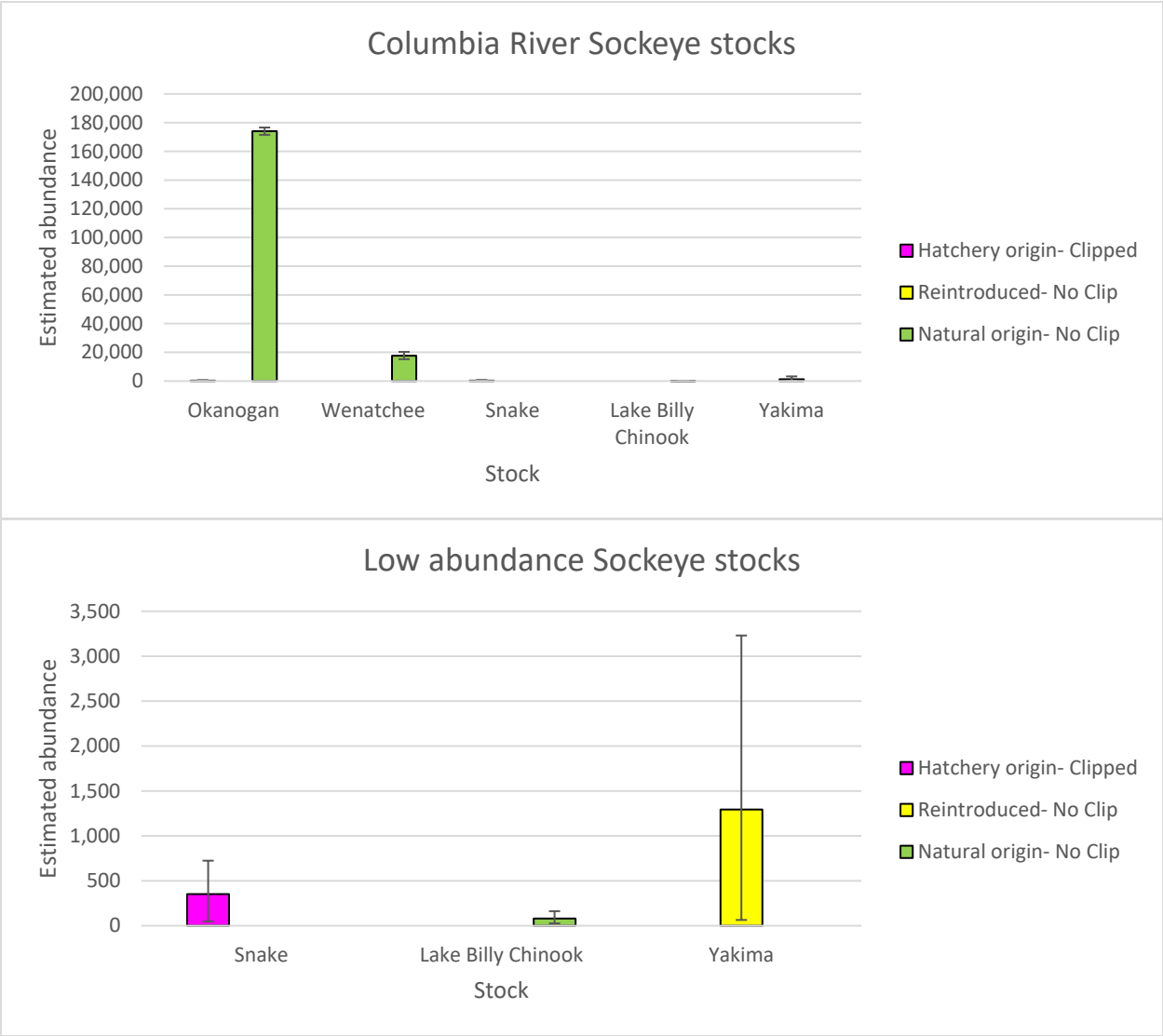
Figure 34. Estimated abundance (± 95% CI) of sockeye salmon stocks sampled at Bonneville Dam in 2018.

1850 **Table 55. Estimated abundance of sockeye salmon stocks passing Bonneville Dam in 2018.**

Reporting Group name	Estimated abundance					
	Hatchery origin- Clipped		Reintroduction- No Clip		Natural origin- No Clip	
	Mean	95% CI	Mean	95% CI	Mean	95% CI
Okanogan	285	0 – 630			174,130	171500 – 176606
Wenatchee					17,675	15190 – 20307
Snake	351	49 – 724				
Lake Billy Chinook					80	26 – 162
Yakima			1,294	64 – 3231		

1851
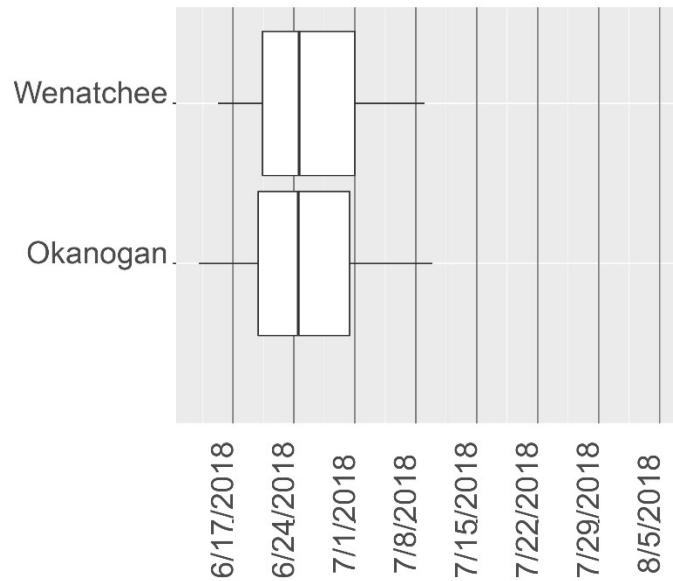
Figure 35. Run-timing distributions (median ordinal day, interquartile range, and 5th and 95th percentile) for the major stocks of sockeye salmon that were sampled at Bonneville Dam in 2018 and assigned to stock of origin.

1857 *In-season analysis of Chinook salmon passing Bonneville Dam in 2019*
1858   There were four in-season reports covering data on Chinook Salmon that passed
1859 Bonneville Dam during the Spring Management Period (Table 47), and a total of seven in-season
1860 reports for Chinook Salmon in 2019 across all management periods (Table 56). The first report
1861 was distributed to members of the USvOR TAC on May 10, 2019 and included an analysis of
1862 data on Chinook Salmon sampled at the Bonneville Dam AFF from the date on which the first
1863 Chinook Salmon was sampled (April 25, 2019) until May 3, 2019 (Table 47). We had originally
1864 planned to offer reports on approximately a bi-weekly reporting schedule after mid-April when
1865 sampling typically begins at the Bonneville Dam AFF, however, the 2019 run of Spring Chinook
1866 Salmon was delayed relative to the 10 year average-timed run. The goal for analysis is to have at
1867 least two weeks of sample sizes greater than 50 fish per week before in-season reporting is
1868 initiated. Each report used a new analysis similar to the reporting for the Bonneville Dam post-
1869 season report for run year 2018. However, there was one important change to the post-season
1870 methods that we implemented in-season to improve the suitability of the results for managers.
1871 Specifically, we used window counts of only the adult-sized fish in order to estimate stock-
1872 specific abundances of adult-size Chinook Salmon. In the past, our BPA reports included stock-
1873 specific abundance and run-timing estimates of all Chinook Salmon, including jack-sized fish.
1874 Management of Chinook Salmon fisheries in the Columbia River is based solely on adult-sized
1875 Chinook Salmon (>560 mm fork length), and so we restricted our sample to this fork length
1876 threshold for our in-season analysis. Further, we used TAC estimates of the clipped and
1877 unclipped adult Chinook salmon and expanded genetic stock proportions with those estimates.
1878   A total of 3,148 adult-sized Chinook Salmon were collected and analyzed for the 2019
1879 in-season reports (Table 56). Estimates of stock-specific abundances of natural-origin stocks
1880 (i.e., those fish that were adipose unclipped and did not have a PBT-assignment) and hatchery-
1881 origin stocks (i.e. adipose-clipped fish and/or those fish that were PBT-assigned) were provided
1882 in each in-season report. Each subsequent report provided cumulative stock-specific abundances
1883 and the final report issued on November 1, 2019 provided sub-totals for each stock that were
1884 broken out by management period (hatchery-origin stocks, Table 57; natural-origin stocks, Table
1885 59). Two of the stocks that were of particular interest this year were the natural-origin Snake
1886 River spring/summer run (Reporting groups 11_TUCANO, 12_HELLSC, 13_SFSALM,
1887 14_CHMBLN, 15_MFSALM, and 16_UPSALM; Table 59) and upper Columbia River spring
1888 Chinook Salmon stocks (Reporting group 10_UCOLSP, Table 59). These ESA listed stocks can
1889 affect the overall harvest rates that pertain to the Treaty and Non-Treaty fisheries on the
1890 mainstem Columbia River. Another aspect of this in-season analysis that was useful to managers
1891 was the ability to determine the approximate abundance of stream-type lineage stocks (the
1892 spring-run and Snake River spring/summer run stocks) that continue to pass Bonneville Dam
1893 during the summer management period. Further, there are non-ESA listed upper Columbia River
1894 summer-run (reporting group 18_UCOLSF) that can pass Bonneville Dam before the summer
1895 management period. The delineation of these management periods is known by managers to not
1896 provide complete separation of these mixed stocks (i.e., interior Columbia River stream-type
1897 versus ocean-type genetic lineages), however the dates of the management periods are the result
1898 of policy decisions that in part consider a trade-off between over- and under-utilization of ESA
1899 and non-ESA listed Chinook Salmon stocks. This in-season genetic analysis can be used in
1900 addition to other data by managers to help evaluate options for shaping the fisheries in a way that
1901 balances objectives of the USvOR Management Agreement.

1902   PBT assignments during the Chinook Salmon management periods allowed classification
1903   of 80 unique hatchery broodstocks in 2019 (Table 60). These broodstocks were comprised of
1904   20% of hatcheries from the Snake River and 75% of hatcheries from the rest of the Columbia
1905   River above Bonneville Dam (Figure 36). Similar to the natural- and hatchery-origin abundance
1906   estimates, the subtotals of these hatchery broodstock abundances were provided to USvOR TAC
1907   for each management period and bi-weekly strata for the in-season reporting in 2019. We
1908   observed that this run year of Chinook Salmon at Bonneville Dam was one of the best in terms of
1909   coverage of hatchery broodstock in the PBT baseline. One measure of the level of coverage of
1910   the PBT baseline is the percentage of clipped adult-sized Chinook Salmon that were estimated to
1911   belong to a PBT hatchery broodstock. If all hatchery broodstock above Bonneville Dam are
1912   included in the PBT baseline AND our estimated tag rates are accurate for each hatchery
1913   broodstock, then this percentage is expected to be 100% across all strata in the all the
1914   management periods (Table 61). In fact, in 2019, the percentage of adipose-clipped fish
1915   abundance that were estimated to be PBT broodstock ranged from 85-100%, 94-100%, and 82-
1916   100% in the spring, summer, and fall management periods, respectively. One reason that the
1917   early fall management period had some of the lowest estimated percentages of PBT-assigned
1918   clipped fish was likely due to the fact that a major hatchery component of the run during this
1919   time, Spring Creek Hatchery, has only recently been added to the PBT baseline and not all
1920   broodyears are covered yet (Appendix 6). We expect that even the fall management period will
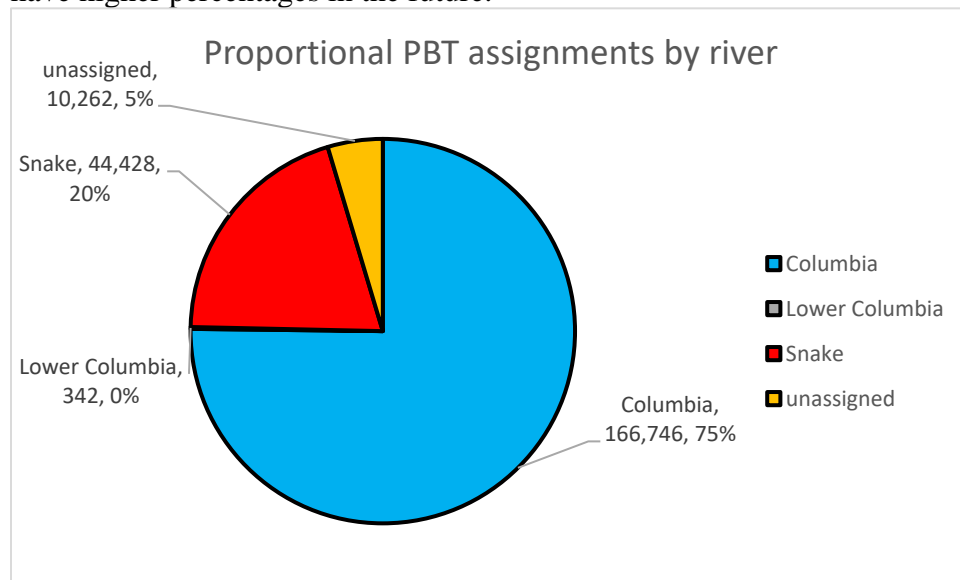1921   have higher percentages in the future.

1922
1923   **Figure 36. Proportion of hatchery broodstocks from the Snake River versus the rest of the**
1924   **Columbia River above Bonneville Dam in 2019.**

1925 **Table 56. The sample sizes of Chinook salmon at the Bonneville Dam AFF during the**
1926 **spring, summer, and fall management periods of 2019.**

Management period		Statistical week	TAC-Estimate Clipped Fish	TAC-Estimate Unclipped Fish	Fish count	Sample (N)					Sample rate
						Clipped		Non-clipped		Total	
						GSI	PBT	GSI	PBT		
	Spring	1-17	1,867	228	2,095	1	10	2	3	16	0.76%
		18	11,741	2,606	14,347	42	215	38	20	315	2.20%
		19	14,090	4,357	18,447	19	193	58	13	283	1.53%
		20	6,268	3,269	9,537	20	95	35	22	172	1.80%
		21	4,144	2,012	6,156	14	91	43	18	166	2.70%
		22	3,316	1,621	4,937	8	58	26	9	101	2.05%
		23	4,922	1,618	6,540	19	63	27	7	116	1.77%
		24	7,107	2,064	9,171	8	97	27	9	141	1.54%
	Summer	25	7278	1276	8,554	14	67	14	4	99	1.16%
		26	6502	1590	8,092	8	62	16	4	90	1.11%
		27	5193	1374	6,567	5	34	22	2	63	0.96%
		28	3150	972	4,122	4	51	25	4	84	2.04%
		29	2044	1128	3,172	3	35	22		60	1.89%
		30	1496	1245	2,741	1	17	13	2	33	1.20%
		31	501	724	1,225	1	9	17	1	28	2.29%
	Fall	31	412	629	1,041		6	7		13	1.25%
		32	781	1,663	2,444					0	0.00%
		33	1,630	3,320	4,950		5	12	4	21	0.42%
		34	4,405	6,997	11,402	3	24	44	9	80	0.70%
		35	12,083	18,788	30,871	3	22	54	11	90	0.29%
		36	17,106	30,167	47,273	6	34	57	14	111	0.23%
		37	23,583	45,451	69,034	31	81	106	36	254	0.37%
		38	16,304	27,628	43,932	20	69	178	37	304	0.69%
		39	10,371	20,080	30,451	12	57	150	28	247	0.81%
		40	6,403	8,569	14,972	1	10	28	6	45	0.30%
		41	2,089	5,784	7,873		22	93	20	135	1.71%
		42-48	3,137	8,686	11,823	2	14	58	7	81	0.69%
		Total	177,923	203,846	381,769	245	1,441	1,172	290	3,148	0.82%

1927 Note: The fish counts indicate the number of adult-sized Chinook Salmon at the fish ladder
1928 windows at Bonneville Dam and the sample (N) indicates the numbers of adult-sized Chinook
1929 Salmon (>560 mm fork length) that were collected at the AFF. TAC provides estimates of the
1930 total clipped an unclipped adult abundance. The AFF sample is broken into adipose-clipped and
1931 non-clipped categories and then further indicate whether a PBT assignment (PBT) was

1932   confirmed or if it was not assigned with PBT (GSI). Sample rate relates the total sample for a
1933   particular stratum to the total fish counted at the window. The alternating gray and clear rows
1934   indicate the breakpoints in the weekly strata at which time one of the seven total in-season
1935   analyses was performed (Table 47).

Table 57. Preliminary in-season reporting of clipped hatchery-origin stock-specific abundance estimates of Chinook Salmon passing Bonneville Dam across all management periods in 2019.

Reporting Group name	Run type	Reporting Group Code	Hatchery origin (Clipped)		Spring Estimated abundance		Summer Estimated abundance		Fall Estimated abundance		Cumulative total date Dec 31 Estimated abundance
				Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean
Youngs Bay	Spring	01_YOUNGS		0	0 – 0	0	0 – 0	0	0 – 0	0
West Cascade Spring	Spring	02_WCASSP		932	530 – 1368	0	0 – 0	0	0 – 0	932
West Cascade Fall*	Fall	03_WCASFA		0	0 – 0	0	0 – 0	763	0 – 2111	763
Willamette	Spring	04_WILLAM		0	0 – 0	0	0 – 251	0	0 – 0	0
Spring Creek Tule	Fall	05_SPCRTU		0	0 – 0	0	0 – 0	27,986	21706 – 34298	27,986
Klickitat	Spring	06_KLICKR		73	0 – 218	0	0 – 0	0	0 – 0	73
Deschutes spring	Spring	07_DESCSP		577	278 – 900	0	0 – 0	0	0 – 0	577
John Day	Spring	08_JOHNDR		0	0 – 0	0	0 – 0	0	0 – 0	0
Yakima	Spring	09_YAKIMA		941	554 – 1361	0	0 – 0	0	0 – 0	941
Upper Columbia spring	Spring	10_UCOLSP		5,926	5061 – 6903	0	0 – 0	0	0 – 0	5,926
Tucannon	Spring	11_TUCANO		0	0 – 0	0	0 – 0	0	0 – 0	0
Hells Canyon	Spring/Summer	12_HELLSC		18,639	17297 – 19844	270	0 – 855	0	0 – 0	18,909
South Fork Salmon	Spring/Summer	13_SFSALM		2,442	1801 – 3065	335	0 – 948	0	0 – 0	2,777
Chamberlain Creek	Spring/Summer	14_CHMBLN		0	0 – 0	0	0 – 0	0	0 – 0	0
Middle Fork Salmon	Spring/Summer	15_MFSALM		0	0 – 0	0	0 – 0	0	0 – 0	0
Upper Salmon	Spring/Summer	16_UPSALM		2,105	1580 – 2729	92	0 – 454	0	0 – 0	2,196

Deschutes fall	Fall	17_DESCFA	0	0 – 0	0	0 – 0	0	0 – 0	0
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	12,976	12317 – 13587	25,167	24163 – 25916	21,153	16605 – 27655	59,296
Snake River fall	Fall	19_SRFALL	0	0 – 0	300	0 – 795	9,958	6182 – 14213	10,258
Bonneville Pool spring	Spring	20_BONPOOLSP	8,493	7429 – 9556	0	0 – 0	0	0 – 0	8,493
Umatilla spring	Spring	21_UMATILLASP	351	136 – 613	0	0 – 0	0	0 – 0	351
Bonneville Pool fall	Fall	22_BONPOOLFA	0	0 – 0	0	0 – 0	38,446	32517 – 45044	38,446
Umatilla fall	Fall	23_UMATILLAFA	0	0 – 0	0	0 – 0	0	0 – 0	0
		Total	53,455		26,164		98,305		177,923

1938 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
1939 31) management periods and the cumulative total through the window counts on Dec 31, 2019 are provided.
1940
1941

1942 **Table 58. Preliminary in-season reporting of unclipped hatchery-origin stock-specific abundance estimates of Chinook Salmon**
1943 **passing Bonneville Dam across all management periods in 2019**.
1944

Hatchery origin (No Clip)			Spring		Summer		Fall		Cumulative total date Dec 31
Reporting Group name	Run type	Reporting Group Code	Estimated abundance		Estimated abundance		Estimated abundance		Estimated abundance
			Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean
Youngs Bay	Spring	01_YOUNGS	0	0 – 0	0	0 – 0	0	0 – 0	0
West Cascade Spring	Spring	02_WCASSP	34	0 – 103	0	0 – 0	0	0 – 0	34
West Cascade Fall*	Fall	03_WCASFA	0	0 – 0	0	0 – 0	0	0 – 0	0
Willamette	Spring	04_WILLAM	0	0 – 0	95	0 – 286	0	0 – 0	95
Spring Creek Tule	Fall	05_SPCRTU	0	0 – 0	0	0 – 0	3,869	1079 – 7481	3,869
Klickitat	Spring	06_KLICKR	0	0 – 0	0	0 – 0	0	0 – 0	0

Deschutes spring	Spring	07_DESCSP	117	0 – 286	0	0 – 0	0	0 – 0	117
John Day	Spring	08_JOHNDR	0	0 – 0	0	0 – 0	0	0 – 0	0
Yakima	Spring	09_YAKIMA	34	0 – 102	0	0 – 0	0	0 – 0	34
Upper Columbia spring	Spring	10_UCOLSP	2,634	2005 – 3285	0	0 – 0	0	0 – 0	2,634
Tucannon	Spring	11_TUCANO	127	0 – 292	0	0 – 0	0	0 – 0	127
Hells Canyon	Spring/Summer	12_HELLSC	885	541 – 1245	80	0 – 240	0	0 – 0	965
South Fork Salmon	Spring/Summer	13_SFSALM	793	462 – 1150	0	0 – 0	0	0 – 0	793
Chamberlain Creek	Spring/Summer	14_CHMBLN	0	0 – 0	0	0 – 0	0	0 – 0	0
Middle Fork Salmon	Spring/Summer	15_MFSALM	0	0 – 0	0	0 – 0	0	0 – 0	0
Upper Salmon	Spring/Summer	16_UPSALM	0	0 – 0	0	0 – 0	0	0 – 0	0
Deschutes fall	Fall	17_DESCFA	0	0 – 0	0	0 – 0	0	0 – 0	0
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	497	256 – 746	863	532 – 1230	14,900	10588 – 19209	16,260
Snake River fall	Fall	19_SRFALL	0	0 – 0	64	0 – 192	10,315	6247 – 15066	10,379
Bonneville Pool spring	Spring	20_BONPOOLSP	191	46 – 342	0	0 – 0	0	0 – 0	191
Umatilla spring	Spring	21_UMATILLASP	632	343 – 954	0	0 – 0	0	0 – 0	632
Bonneville Pool fall	Fall	22_BONPOOLFA	0	0 – 0	0	0 – 0	7,697	4554 – 10950	7,697
Umatilla fall	Fall	23_UMATILLAFA	0	0 – 0	0	0 – 0	0	0 – 0	0
		Total	**5,944**		**1,103**		**36,781**		**43,827**

1945 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
1946 31) management periods and the cumulative total through the window counts on Dec 31, 2019 are provided.
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1949 **Table 59. Preliminary in-season reporting of natural-origin stock-specific abundance estimates of Chinook Salmon passing**
1950 **Bonneville Dam across all management periods in 2019**

Reporting Group name	Run type	Reporting Group Code	Natural origin-No Clip		Spring		Summer		Fall		Cumulative total date Dec 31
			Estimated abundance		Estimated abundance		Estimated abundance				Estimated abundance
			Mean	95% CI	Mean	95% CI	Mean	95% CI			Mean
Youngs Bay	Spring	01_YOUNGS	0	0 – 0	0	0 – 0	0	0 – 0			0
West Cascade Spring	Spring	02_WCASSP	0	0 – 0	0	0 – 0	0	0 – 0			0
West Cascade Fall*	Fall	03_WCASFA	0	0 – 0	0	0 – 0	1,271	478 – 2256			1,271
Willamette	Spring	04_WILLAM	0	0 – 0	0	0 – 0	0	0 – 0			0
Spring Creek Tule	Fall	05_SPCRTU	0	0 – 0	0	0 – 0	1,214	408 – 2934			1,214
Klickitat	Spring	06_KLICKR	0	0 – 0	0	0 – 0	0	0 – 0			0
Deschutes spring	Spring	07_DESCSP	468	226 – 748	0	0 – 0	0	0 – 0			468
John Day	Spring	08_JOHNDR	674	401 – 976	0	0 – 0	0	0 – 0			674
Yakima	Spring	09_YAKIMA	928	609 – 1295	51	0 – 154	0	0 – 0			979
Upper Columbia spring	Spring	10_UCOLSP	1,712	1207 – 2328	0	0 – 0	0	0 – 0			1,712
Tucannon	Spring	11_TUCANO	91	0 – 183	0	0 – 0	0	0 – 0			91
Hells Canyon	Spring/Summer	12_HELLSC	3,584	2941 – 4225	78	0 – 235	0	0 – 0			3,662
South Fork Salmon	Spring/Summer	13_SFSALM	779	455 – 1109	78	0 – 236	0	0 – 0			857
Chamberlain Creek	Spring/Summer	14_CHMBLN	0	0 – 0	0	0 – 0	0	0 – 0			0
Middle Fork Salmon	Spring/Summer	15_MFSALM	353	151 – 591	0	0 – 0	0	0 – 0			353
Upper Salmon	Spring/Summer	16_UPSALM	914	604 – 1252	57	0 – 172	0	0 – 0			971

Deschutes fall	Fall	17_DESCFA	0	0 – 0	0	0 – 0	2,801	1706 – 4128	2,801
Upper Columbia summer/fall	Summer/Fall	18_UCOLSF	2,273	1824 – 2680	6,653	6158 – 7137	115,574	109979 – 120502	124,500
Snake River fall	Fall	19_SRFALL	55	0 – 164	289	93 – 527	20,120	16799 – 23652	20,464
		Total	**11,831**		**7,207**		**140,980**		**160,018**

1951   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
1952   31) management periods and the cumulative total through the window counts on Dec 31, 2019 are provided.
1953
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Table 60. The estimated abundances of the clipped and unclipped PBT hatchery broodstock that passed Bonneville Dam in 2019 (1/1/2019 – 12/31/2019)

Expected Run Time	Hatchery	Broodstock	Brood year	Lineage	GSI RepGrp	Snake / Columbia	MLE Clipped	MLE Unclipped	MLE Total
01Spring	Parkdale Fish Facility	OtsPFF14	2014	Lower Columbia	02_WCASSP	Columbia	70	0	70
01Spring	Parkdale Fish Facility	OtsPFF15	2015	Lower Columbia	02_WCASSP	Columbia	772	34	807
01Spring	South Santiam Hatchery	OtsSSANT15S	2015	Lower Columbia	04_WILLAM	Columbia Lower	0	86	86
01Spring	Klickitat State Fish Hatchery	OtsKH14	2014	Interior stream type	06_KLICKR	Columbia	71	0	71
01Spring	Round Butte Fish Hatchery	OtsRB15	2015	Interior stream type	07_DESCSP	Columbia	424	117	541
01Spring	Warm Springs National Fish Hatchery	OtsWSNFH15	2015	Interior stream type	07_DESCSP	Columbia	501	0	501
01Spring	Levi George/Cle Elum (Integrated)	OtsYR15int	2015	Interior stream type	09_YAKIMA	Columbia	722	34	756
01Spring	Levi George/Cle Elum (Segregated)	OtsYR15seg	2015	Interior stream type	09_YAKIMA	Columbia	125	0	125
01Spring	Chief Joseph Hatchery (Spring)	OtsCJH15_sp	2015	Interior stream type	10_UCOLSP	Columbia	1,666	58	1,723
01Spring	Eastbank Fish Hatchery (Spring)	OtsEASTBK14_sp	2014	Interior stream type	10_UCOLSP	Columbia	0	86	86
01Spring	Eastbank Fish Hatchery (Spring)	OtsEASTBK15_sp	2015	Interior stream type	10_UCOLSP	Columbia	468	1,047	1,515
01Spring	Eastbank Fish Hatchery (Spring)	OtsEASTBK16S_sp	2016	Interior stream type	10_UCOLSP	Columbia	0	98	98
01Spring	Leavenworth National Fish Hatchery	OtsLNFH15	2015	Interior stream type	10_UCOLSP	Columbia	1,772	53	1,825
01Spring	Methow State Fish Hatchery	OtsMETH14	2014	Interior stream type	10_UCOLSP	Columbia	0	46	46
01Spring	Methow State Fish Hatchery	OtsMETH15	2015	Interior stream type	10_UCOLSP	Columbia	0	411	411

01Spring	Winthrop National Fish Hatchery	OtsWTP15	2015	Interior stream type	10_UCOLSP	Columbia	1,764	835	2,599
01Spring	Lyons Ferry Fish Hatchery (Spring)	OtsLYON15S	2015	Interior stream type	11_TUCANO	Snake	0	127	127
01Spring	Clearwater Fish Hatchery	OtsCLWH14S	2014	Interior stream type	12_HELLSC	Snake	293	0	293
01Spring	Clearwater Fish Hatchery	OtsCLWH15S	2015	Interior stream type	12_HELLSC	Snake	2,891	198	3,089
01Spring	Clearwater Fish Hatchery - Powell Facility	OtsPOWP14S	2014	Interior stream type	12_HELLSC	Snake	114	0	114
01Spring	Clearwater Fish Hatchery - Powell Facility	OtsPOWP16S	2016	Interior stream type	12_HELLSC	Snake	0	86	86
01Spring	Dworshak National Fish Hatchery	OtsDWOR14S	2014	Interior stream type	12_HELLSC	Snake	86	0	86
01Spring	Dworshak National Fish Hatchery	OtsDWOR15S	2015	Interior stream type	12_HELLSC	Snake	2,808	164	2,972
01Spring	Lookingglass Fish Hatchery - Catherine Creek	OtsCTHW15S	2015	Interior stream type	12_HELLSC	Snake	449	0	449
01Spring	Lookingglass Fish Hatchery - Grande Ronde	OtsGRUW15S	2015	Interior stream type	12_HELLSC	Snake	257	231	488
01Spring	Lookingglass Fish Hatchery - Lookingglass Creek	OtsLOOK14S	2014	Interior stream type	12_HELLSC	Snake	49	0	49
01Spring	Lookingglass Fish Hatchery - Lookingglass Creek	OtsLOOK15S	2015	Interior stream type	12_HELLSC	Snake	676	0	676
01Spring	Lookingglass Fish Hatchery - Lostine River	OtsLSTW14S	2014	Interior stream type	12_HELLSC	Snake	54	0	54
01Spring	Lookingglass Fish Hatchery - Lostine River	OtsLSTW15S	2015	Interior stream type	12_HELLSC	Snake	250	0	250
01Spring	Rapid River Fish Hatchery	OtsRAPH14S	2014	Interior stream type	12_HELLSC	Snake	377	0	377
01Spring	Rapid River Fish Hatchery	OtsRAPH15S	2015	Interior stream type	12_HELLSC	Snake	8,592	253	8,845

01Spring	Carson National Fish Hatchery	OtsCAR14	2014	Interior stream type	20_BONPOOL SP	Columbia	239	0	239
01Spring	Carson National Fish Hatchery	OtsCAR15	2015	Interior stream type	20_BONPOOL SP	Columbia	3,396	139	3,535
01Spring	Little White Salmon National Fish Hatchery (Spring)	OtsLWS14_ sp	2014	Interior stream type	20_BONPOOL SP	Columbia	605	0	605
01Spring	Little White Salmon National Fish Hatchery (Spring)	OtsLWS15_ sp	2015	Interior stream type	20_BONPOOL SP	Columbia	3,865	52	3,917
01Spring	Umatilla Fish Hatchery (Spring)	OtsUMA14_ sp	2014	Interior stream type	21_UMATILL ASP	Columbia	67	0	67
01Spring	Umatilla Fish Hatchery (Spring)	OtsUMA15_ sp	2015	Interior stream type	21_UMATILL ASP	Columbia	244	632	876
02Spring/Summer	Lookingglass Fish Hatchery - Imnaha River	OtsIMNW14 S	2014	Interior stream type	12_HELLSC	Snake	43	0	43
02Spring/Summer	Lookingglass Fish Hatchery - Imnaha River	OtsIMNW15 S	2015	Interior stream type	12_HELLSC	Snake	430	38	468
02Spring/Summer	Lookingglass Fish Hatchery - Imnaha River	OtsIMNW16 S	2016	Interior stream type	12_HELLSC	Snake	194	0	194
02Spring/Summer	McCall Fish Hatchery - South Fork Salmon	OtsMCCA1 5S	2015	Interior stream type	13_SFSALM	Snake	2,510	793	3,302
02Spring/Summer	McCall Fish Hatchery - South Fork Salmon	OtsMCCA1 6S	2016	Interior stream type	13_SFSALM	Snake	228	0	228
02Spring/Summer	Pahsimeroi Fish Hatchery	OtsPAHH14 S	2014	Interior stream type	16_UPSALM	Snake	46	0	46
02Spring/Summer	Pahsimeroi Fish Hatchery	OtsPAHH15 S	2015	Interior stream type	16_UPSALM	Snake	612	0	612
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT14 S	2014	Interior stream type	16_UPSALM	Snake	176	0	176
02Spring/Summer	Sawtooth Fish Hatchery	OtsSAWT15 S	2015	Interior stream type	16_UPSALM	Snake	1,068	0	1,068
03Summer	Chief Joseph Hatchery	OtsCJH14int _su	2014	Interior ocean type	18_UCOLSF	Columbia	513		513
03Summer	Chief Joseph Hatchery	OtsCJH15int _su	2015	Interior ocean type	18_UCOLSF	Columbia	813		813

03Summer	Chief Joseph Hatchery	OtsCJH16int _su	2016	Interior ocean type	18_UCOLSF	Columbia	257		257
03Summer	Chief Joseph Hatchery (Summer/Fall) - Integrated	OtsCJH14int _sufa	2014	Interior ocean type	18_UCOLSF	Columbia	4,716	224	4,940
03Summer	Chief Joseph Hatchery (Summer/Fall) - Integrated	OtsCJH15int _sufa	2015	Interior ocean type	18_UCOLSF	Columbia	2,388	164	2,552
03Summer	Chief Joseph Hatchery (Summer/Fall) - Integrated	OtsCJH16int _sufa	2016	Interior ocean type	18_UCOLSF	Columbia	346	86	432
03Summer	Chief Joseph Hatchery (Summer/Fall) - Segregated	OtsCJH13se g_sufa	2013	Interior ocean type	18_UCOLSF	Columbia	169	0	169
03Summer	Chief Joseph Hatchery (Summer/Fall) - Segregated	OtsCJH14se g_sufa	2014	Interior ocean type	18_UCOLSF	Columbia	4,211	0	4,211
03Summer	Chief Joseph Hatchery (Summer/Fall) - Segregated	OtsCJH15se g_sufa	2015	Interior ocean type	18_UCOLSF	Columbia	2,021	209	2,230
03Summer	Chief Joseph Hatchery (Summer/Fall) - Segregated	OtsCJH16se g_sufa	2016	Interior ocean type	18_UCOLSF	Columbia	54	0	54
03Summer	Eastbank Fish Hatchery	OtsEASTBK 15_su	2015	Interior ocean type	18_UCOLSF	Columbia	997		997
03Summer	Eastbank Fish Hatchery (Summer)	OtsEASTBK 13_su	2013	Interior ocean type	18_UCOLSF	Columbia	133	0	133
03Summer	Eastbank Fish Hatchery (Summer)	OtsEASTBK 14_su	2014	Interior ocean type	18_UCOLSF	Columbia	6,077	61	6,138
03Summer	Eastbank Fish Hatchery (Summer)	OtsEASTBK 15_su	2015	Interior ocean type	18_UCOLSF	Columbia	4,570	184	4,754
03Summer	Entiat National Fish Hatchery (Summer)	OtsENFH14	2014	Interior ocean type	18_UCOLSF	Columbia	2,076	0	2,076
03Summer	Entiat National Fish Hatchery (Summer)	OtsENFH15	2015	Interior ocean type	18_UCOLSF	Columbia	3,578	0	3,578
03Summer	Wells Fish Hatchery	OtsWELLS1 4	2014	Interior ocean type	18_UCOLSF	Columbia	4,530	109	4,640
03Summer	Wells Fish Hatchery	OtsWELLS1 5	2015	Interior ocean type	18_UCOLSF	Columbia	2,470	343	2,813

04Fall	Washougal Fish Hatchery	OtsWAS15_fa	2015	Lower Columbia	03_WCASFA	Lower Columbia	257		257
04Fall	Spring Creek National Fish Hatchery	OtsSPCR15_fa	2015	Lower Columbia	05_SPCRTU	Columbia	1,083	285	1,368
04Fall	Spring Creek National Fish Hatchery	OtsSPCR16_fa	2016	Lower Columbia	05_SPCRTU	Columbia	11,235	2,010	13,244
04Fall	Spring Creek National Fish Hatchery	OtsSPCR17_fa	2017	Lower Columbia	05_SPCRTU	Columbia	11,949	1,575	13,524
04Fall	Little White Salmon National Fish Hatchery	OtsLWS14_fa	2014	Interior ocean type	18_UCOLSF	Columbia	835	596	1,431
04Fall	Little White Salmon National Fish Hatchery	OtsLWS15_fa	2015	Interior ocean type	18_UCOLSF	Columbia	23,428	1,911	25,339
04Fall	Little White Salmon National Fish Hatchery	OtsLWS16_fa	2016	Interior ocean type	18_UCOLSF	Columbia	14,183	5,189	19,372
04Fall	Priest Rapids Hatchery	OtsPRH14_fa	2014	Interior ocean type	18_UCOLSF	Columbia		51	51
04Fall	Priest Rapids Hatchery	OtsPRH15_fa	2015	Interior ocean type	18_UCOLSF	Columbia	7,189	6,932	14,121
04Fall	Priest Rapids Hatchery	OtsPRH16_fa	2016	Interior ocean type	18_UCOLSF	Columbia	8,664	7,917	16,581
04Fall	Lyons Ferry Fish Hatchery	OtsLYON14S_1_fa	2014	Interior ocean type	19_SRFALL	Snake	257	1,033	1,290
04Fall	Lyons Ferry Fish Hatchery	OtsLYON15S_1_fa	2015	Interior ocean type	19_SRFALL	Snake	4,147	3,012	7,158
04Fall	Lyons Ferry Fish Hatchery	OtsLYON16S_1_fa	2016	Interior ocean type	19_SRFALL	Snake	3,944	2,612	6,556
04Fall	Lyons Ferry Fish Hatchery (Fall)	OtsLYON15S_1	2015	Interior ocean type	19_SRFALL	Snake	227	74	301
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH15S_1_fa	2015	Interior ocean type	19_SRFALL	Snake	613	2,425	3,038
04Fall	Nez Perce Tribal Fish Hatchery	OtsNPFH16S_1_fa	2016	Interior ocean type	19_SRFALL	Snake	685	1,234	1,919
04Fall	Nez Perce Tribal Fish Hatchery (Fall)	OtsNPFH16S_1	2016	Interior ocean type	19_SRFALL	Snake	73	0	73
#N/A	#N/A	Unassigned	#N/A	#N/A	#N/A	#N/A	10,262	0	10,262
Grand Total							177,923	43,854	221,778

1960

240

Table 61. Expanded abundance of PBT-assigned Chinook Salmon stocks across management periods in 2019

		Sample (Tag-rate-Corrected abundance)						% PBT of Clipped fish
	Statistical week	Clipped		Non-clipped		Total GSI	Total PBT	
		GSI	PBT	GSI	PBT			
Management period	Spring	1-17	33	1,833	64	164	98	1,997	98.2%
		18	1,106	10,635	1,591	1,015	2,697	11,650	90.6%
		19	415	13,676	3,492	864	3,907	14,540	97.1%
		20	693	5,575	1,843	1,426	2,535	7,002	89.0%
		21	236	3,908	1,277	736	1,512	4,644	94.3%
		22	-62	3,378	1,057	563	995	3,942	101.9%
		23	728	4,193	1,245	374	1,973	4,567	85.2%
		24	-262	7,369	1,449	615	1,187	7,984	103.7%
	Summer	25	430	6,848	977	299	1,407	7,147	94.1%
		26	-148	6,650	1,247	343	1,099	6,993	102.3%
		27	-166	5,359	1,253	121	1,087	5,480	103.2%
		28	-291	3,441	827	145	536	3,586	109.2%
		29	-167	2,211	1,128	0	961	2,211	108.2%
		30	-77	1,573	1,066	179	989	1,752	105.2%
		31	18	483	681	43	699	526	96.4%
	Fall	31 32	-28	509	561	0	532	509	105.9%
		33	-247	635	1,647	882	1,400	1,518	163.7%
		34	-357	1,843	3,463	1,173	3,106	3,016	124.0%
		35	-638	3,994	11,110	2,459	10,473	6,453	119.0%
		36	-134	6,298	14,397	4,899	14,263	11,197	102.2%
		37	1,862	8,537	18,477	6,933	20,339	15,469	82.1%
		38	622	4,151	15,937	3,602	16,560	7,753	87.0%
		39	243	2,654	12,095	2,375	12,339	5,029	91.6%
		40	128	1,437	5,332	1,143	5,460	2,579	91.8%
		41	-22	363	3,934	907	3,912	1,270	106.6%
		42-48	76	544	6,215	756	6,290	1,300	87.8%

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% across all strata.

*The % values above 100% can occur when PBT expansion is greater than the total count of clipped fish in a stratum.

1971   *In-season analysis of steelhead passing Bonneville Dam in 2019*
1972   There were three reports provided to USvOR TAC during the steelhead management periods:
1973   Skamania Management Period (4/1/2019 – 6/30/2019) and summer A-/B-Index Management
1974   Period (7/1/2019 – 10/31/2019, Table 47). There were a total of 471 adipose clipped and 371
1975   adipose unclipped steelhead that were sampled at the Bonneville Dam AFF and genotyped in
1976   2019 (Table 62). The methods described for the analysis of the 2017 sample of steelhead at
1977   Bonneville Dam are not as useful to fisheries managers that serve on USvOR TAC because the
1978   size groups (A-/B-Index) have not been fully integrated into the results. Therefore, we revised
1979   these methods and provided a breakdown of those A-/B-Index groups in addition to the adipose
1980   clipped and unclipped categories (Table 62). One of the important features of the genetic
1981   analyses of steelhead at Bonneville Dam is that they can identify unmarked hatchery fish via
1982   PBT assignments. The identification of unmarked hatchery fish is critical for accurate
1983   calculations of ESA impacts on steelhead stocks. The methods we are using provide a means to
1984   estimate the abundance of six categories of steelhead; i.e., clipped hatchery (H), unclipped
1985   hatchery (HNC), and natural-origin (W) for A-Index and B-Index fish (Table 63). We also
1986   incorporate tag rate expansion to account for the percentage of each hatchery stock that has been
1987   successfully genotyped. Tag rate expansions have been used previously in all of our genetic
1988   analyses for Chinook Salmon and steelhead. However, one feature that has been missing from
1989   our tag rate expansion methods in the past is a way to balance the numbers of fish that are
1990   expanded in the PBT broodstock categories by subtracting an equal set of fish from the sample.
1991   This is issue is now resolved through our implementation of SCOBI DEUX and SPIBETR
1992   methodologies described previously (Section 3).

1993
1994

Table 62. The sample sizes of Summer Steelhead at the Bonneville Dam AFF during the Skamania and A-/B-Index management periods of 2019.

		Statistical week	Strata	Clipped count	Non-Clipped count	A-Index Clipped GSI	A-Index Clipped PBT	A-Index Non-clipped GSI	A-Index Non-clipped PBT	B-Index Clipped GSI	B-Index Clipped PBT	B-Index Non-clipped GSI	B-Index Non-clipped PBT	Clipped Total	Non-clipped Total	Clipped Sample rate	Non-clipped Sample rate
Management period	Skamania	14	1	67	105									0	0	0.00%	0.00%
		15	1	53	76									0	0	0.00%	0.00%
		16	1	44	46									0	0	0.00%	0.00%
		17	1	42	26	1		1						1	1	2.38%	3.85%
		18	1	92	28									0	0	0.00%	0.00%
		19	1	81	37			1						0	1	0.00%	2.70%
		20	1	62	28				2					0	2	0.00%	7.14%
		21	1	57	23	1		1						1	1	1.75%	4.35%
		22	1	70	56	1	1							2	0	2.86%	0.00%
		23	1	129	53	4								4	0	3.10%	0.00%
		24	1	106	135			1				1		0	2	0.00%	1.48%
		25	1	235	288	1		4						1	4	0.43%	1.39%
		26	1	457	738	5		3						5	3	1.09%	0.41%

243

A-/B-Index															
Subtotal Skamania	1	1495	1639	1	13	13	0	0	0	1	0	14	14	0.94%	0.85%
27	1	1160	1,745	1	5	8				1		6	9	0.52%	0.52%
28	1	1445	2,516	4	8	18						12	18	0.83%	0.72%
29	1	2205	3,503	4	19	36				2		23	38	1.04%	1.08%
30	2	2754	4,089	2	15	25						17	25	0.62%	0.61%
31	2	3170	4,167	3	29	37						32	37	1.01%	0.89%
32	2	3837	4,529									0	0	0.00%	0.00%
33	3	4185	4,051	2	21	33	1					23	34	0.55%	0.84%
34	3	2878	1,911	7	33	34				1		40	35	1.39%	1.83%
35	4	2779	1,704	5	27	21	1		1			33	22	1.19%	1.29%
36	4	2011	1,166	1	12	7	2		1		1	14	10	0.70%	0.86%
37	4	2108	1,131	3	16	5	2		2	1	1	21	9	1.00%	0.80%
38	5	2960	1,328	2	28	10	3		17	3	3	47	19	1.59%	1.43%
39	5	1569	633	1	10	6	2		10	2		21	10	1.34%	1.58%
40	6	1366	606	2	19	7	5	1	21	3	11	43	26	3.15%	4.29%
41	6	1708	825		36	10	9		30	3	5	66	27	3.86%	3.27%
42	7	929	474	1	32	11	7		12	2	4	45	24	4.84%	5.06%

43	7	510	285								0	0	0.00%	0.00%
44	7	147	82								0	0	0.00%	0.00%
Summer A-/B-Index subtotal	37,721	34,745	38	310	268	32	1	94	18	25	443	343	1.17%	0.99%
Total	40,711	38,023	40	336	294	32	1	94	20	25	471	371	1.16%	0.98%

Note: The clipped and non-clipped counts indicate the number of adipose clipped and unclipped steelhead at the fish ladder windows at Bonneville Dam and the sample (N) indicates the numbers of A- and B-sized (<580 mm and ≥580 mm fork length, respectively) that were collected at the AFF. The AFF sample is broken into A- and B-sized and adipose-clipped and non-clipped categories and then further indicate whether a PBT assignment (PBT) was confirmed or if it was not assigned with PBT (GSI). Sample rate relates the total sample for a particular stratum to the total fish counted at the window. The alternating gray and clear rows indicate the breakpoints in the weekly strata at which time one of the three total in-season analyses was performed (Table 47).

Table 63. Estimated abundance of hatchery-origin clipped stocks of Summer Steelhead that passed Bonneville Dam in 2019 during the Skamania and A-/B-Index Management Periods.

	Hatchery origin-Clipped	**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 Code	**Estimated abundance**		**A-INDEX: Estimated abundance**		**B-INDEX: Estimated abundance**	
Reporting Group name		**Mean**	**95% CI**	**Mean**	**95% CI**	**Mean**	**95% CI**
Lower Columbia	02_LOWCOL	0	0 – 0	0	0 – 0	0	0 – 0
Skamania	03_SKAMAN	1,281	854 – 1495	3,082	1480 – 4553	0	0 – 0
Willamette	04_WILLAM	0	0 – 0	0	0 – 0	0	0 – 0

Reporting Group name	Code	Mean	95% CI	Mean	95% CI	Mean	95% CI
Big White Salmon	05_BWSALM	0	0 – 0	0	0 – 0	0	0 – 0
Klickitat	06_KLICKR	0	0 – 0	0	0 – 0	0	0 – 0
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	0	0 – 0	14,240	11754 – 17247	0	0 – 0
Yakima	08_YAKIMA	0	0 – 0	0	0 – 0	0	0 – 0
upper Columbia	09_UPPCOL	214	0 – 641	990	219 – 1929	0	0 – 0
SF Clearwater	10_SFCLWR	0	0 – 0	3,783	2655 – 4894	4,029	3096 – 4977
upper Clearwater	11_UPCLWR	0	0 – 0	34	0 – 223	0	0 – 0
SF Salmon	12_SFSALM	0	0 – 0	34	0 – 219	0	0 – 0
MF Salmon	13_MFSALM	0	0 – 0	0	0 – 0	0	0 – 0
upper Salmon	14_UPSALM	0	0 – 0	11,465	8909 – 14418	64	0 – 263
	Total	**1,495**		**33,628**		**4,093**	

Note: Based on the sample data described in Table 62 we estimated abundances of six categories of steelhead; i.e., clipped hatchery (H), unclipped hatchery (HNC), and natural-origin (W) for A-Index and B-Index fish. The sample was divided into the most strata possible maintaining a minimum sample of 100 clipped and unclipped steelhead per stratum in the A-/B-Index period. All weeks were pooled into a single stratum in the Skamania period.

Table 64. Estimated abundance of hatchery-origin unclipped stocks of Summer Steelhead that passed Bonneville Dam in 2019 during the Skamania and A-/B-Index Management Periods.

	Hatchery origin- No Clip	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)	
		Estimated abundance		A-INDEX: Estimated abundance		B-INDEX: Estimated abundance	
Reporting Group name	**Reporting Group Code**	**Mean**	**95% CI**	**Mean**	**95% CI**	**Mean**	**95% CI**

Reporting Group name	Code	Mean	95% CI	Mean	95% CI	Mean	95% CI
Lower Columbia	02_LOWCOL	0	0 – 0	0	0 – 0	0	0 – 0
Skamania	03_SKAMAN	0	0 – 0	0	0 – 0	0	0 – 0
Willamette	04_WILLAM	0	0 – 0	0	0 – 0	0	0 – 0
Big White Salmon	05_BWSALM	0	0 – 0	0	0 – 0	0	0 – 0
Klickitat	06_KLICKR	0	0 – 0	0	0 – 0	0	0 – 0
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	0	0 – 0	309	0 – 812	0	0 – 0
Yakima	08_YAKIMA	0	0 – 0	0	0 – 0	0	0 – 0
upper Columbia	09_UPPCOL	0	0 – 0	98	0 – 390	0	0 – 0
SF Clearwater	10_SFCLWR	0	0 – 0	1,120	627 – 1686	1,029	499 – 1640
upper Clearwater	11_UPCLWR	0	0 – 0	0	0 – 0	0	0 – 0
SF Salmon	12_SFSALM	0	0 – 0	0	0 – 0	0	0 – 0
MF Salmon	13_MFSALM	0	0 – 0	0	0 – 0	0	0 – 0
upper Salmon	14_UPSALM	0	0 – 0	193	0 – 578	0	0 – 0
Total		**0**		**1,719**		**1,029**	

Note: Based on the sample data described in Table 62 we estimated abundances of six categories of steelhead; i.e., clipped hatchery (H), unclipped hatchery (HNC), and natural-origin (W) for A-Index and B-Index fish. The sample was divided into the most strata possible maintaining a minimum sample of 100 clipped and unclipped steelhead per stratum in the A-/B-Index period. All weeks were pooled into a single stratum in the Skamania period.

Table 65. Estimated abundance of natural-origin unclipped stocks (excluding hatchery-origin unclipped) of Summer Steelhead that passed Bonneville Dam in 2019 during the Skamania and A-/B-Index Management Periods.

	Natural origin- No Clip	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 Code	**Estimated abundance**		**A-INDEX: Estimated abundance**		**B-INDEX: Estimated abundance**	
Reporting Group name		**Mean**	**95% CI**	**Mean**	**95% CI**	**Mean**	**95% CI**
Lower Columbia	02_LOWCOL	234	0 – 468	0	0 – 0	119	0 – 358
Skamania	03_SKAMAN	585*	117 – 820	857	326 – 1476	119	0 – 358

Willamette	04_WILLAM	0	0 – 0	0	0 – 0	0	0 – 0
Big White Salmon	05_BWSALM	0	0 – 0	0	0 – 0	0	0 – 0
Klickitat	06_KLICKR	351	117 – 702	924	439 – 1538	0	0 – 0
mid Columbia/Grande Ronde/Imnaha/lower Clearwater/lower Snake/lower Salmon	07_MGILCS	351	117 – 702	19,996	18209 – 21593	214	0 – 478
Yakima	08_YAKIMA	0	0 – 0	1,390	731 – 2154	0	0 – 0
upper Columbia	09_UPPCOL	0	0 – 0	1,050	465 – 1668	0	0 – 0
SF Clearwater	10_SFCLWR	0	0 – 0	434	168 – 728	498	230 – 817
upper Clearwater	11_UPCLWR	0	0 – 0	206	54 – 418	0	0 – 0
SF Salmon	12_SFSALM	0	0 – 0	68	0 – 203	35	0 – 101
MF Salmon	13_MFSALM	0	0 – 0	704	281 – 1233	0	0 – 0
upper Salmon	14_UPSALM	117	0 – 351	5,314	4010 – 6628	68	0 – 203
	Total	**1,639**		**30,943**		**1,054**	

2019 Note: Based on the sample data described in Table 62 we estimated abundances of six categories of steelhead; i.e., clipped hatchery (H), unclipped hatchery
2020 (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
2021 clipped and unclipped steelhead per stratum in the A-/B-Index period. All weeks were pooled into a single stratum in the Skamania period.
2022 *A small number (N=117) were estimated to be B-Index size.
2023
2024
2025 Table 66. Estimated abundance of hatchery-origin clipped and unclipped broodstocks of A-/B-Index Summer Steelhead that passed
2026 Bonneville Dam in 2019 (July 1 – Oct 31).

					Hatchery clipped				Hatchery unclipped			
					A-INDEX		B-INDEX		A-INDEX		B-INDEX	
Hatchery	**Stock**	**GSI RepGrp**	**Broodstock**	**Brood year**	**MLE**	**95% CI**	**MLE**	**95% CI**	**MLE**	**95% CI**	**MLE**	**95% CI**

Skamania	Summer	03_SKA MAN	OmySKH16_su	2016	2,893	1732 – 3772	0	0 – 0	0	0 – 0	0	0 – 0
Round Butte	Deschutes River	07_MGI LCS	OmyRB17	2017	235	0 – 634	0	0 – 0	0	0 – 0	0	0 – 0
Umatilla	Minthorn Springs	07_MGI LCS	OmyUMA 17	2017	220	0 – 450	0	0 – 0	0	0 – 0	0	0 – 0
Round Butte	Deschutes River	07_MGI LCS	OmyRB16	2016	616	203 – 1119	0	0 – 0	98	0 – 293	0	0 – 0
Eastbank	Chelan/Methow/Okanogan/Wenatchee	09_UPP COL	OmyEAST BK17	2017	0	0 – 0	0	0 – 0	98	0 – 293	0	0 – 0
Wells	On Station	09_UPP COL	OmyWEL 17	2017	118	0 – 355	0	0 – 0	0	0 – 0	0	0 – 0
Wells	On Station	09_UPP COL	OmyWEL 16	2016	670	225 – 1226	0	0 – 0	0	0 – 0	0	0 – 0
Winthrop NFH	Methow River	09_UPP COL	OmyWTP16	2016	112	0 – 336	0	0 – 0	0	0 – 0	0	0 – 0
Little Sheep Creek	-	07_MGI LCS	OmyLSCR 17S	2017	1,346	678 – 2067	0	0 – 0	0	0 – 0	0	0 – 0
Lyons Ferry	Grande Ronde	07_MGI LCS	OmyCGR W17S	2017	4,823	3533 – 6077	0	0 – 0	0	0 – 0	0	0 – 0
Lyons Ferry	Wallowa	07_MGI LCS	OmyWAL W17S	2017	1,830	1087 – 2681	0	0 – 0	0	0 – 0	0	0 – 0
Lyons Ferry	Tucannon	07_MGI LCS	OmyTUC W17S	2017	623	112 – 1196	0	0 – 0	86	0 – 259	0	0 – 0
Lyons Ferry	Touchet	07_MGI LCS	OmyTOU W17S	2017	0	0 – 0	0	0 – 0	27	0 – 81	0	0 – 0
Little Sheep Creek	-	07_MGI LCS	OmyLSCR 16S	2016	1,097	456 – 1864	0	0 – 0	0	0 – 0	0	0 – 0
Lyons Ferry	Grande Ronde	07_MGI LCS	OmyCGR W16S	2016	1,536	860 – 2264	0	0 – 0	0	0 – 0	0	0 – 0
Lyons Ferry	Wallowa	07_MGI LCS	OmyWAL W16S	2016	1,244	584 – 2002	0	0 – 0	0	0 – 0	0	0 – 0
Lyons Ferry	Tucannon	07_MGI LCS	OmyTUC W16S	2016	0	0 – 0	0	0 – 0	98	0 – 293	0	0 – 0
Dworshak NFH	Clearwater River	10_SFCL WR	OmyDWO C17S	2017	1,095	762 – 1479	0	0 – 0	280	146 – 439	0	0 – 0

Hatchery	River	Code	Omy	Year								
Dworshak NFH	SF Clearwater	10_SFCLWR	OmySFCW17S	2017	306	148 – 503	0	0 – 0	81	27 – 162	0	0 – 0
Dworshak NFH	Upper Salmon	10_SFCLWR	OmyUSAL17S	2017	0	0 – 0	0	0 – 0	35	0 – 105	0	0 – 0
Dworshak NFH	Upper Salmon	10_SFCLWR	OmyUSAL16S	2016	506	230 – 806	211	57 – 387	429	153 – 721	0	0 – 0
Dworshak NFH	Clearwater River	10_SFCLWR	OmyDWOC16S	2016	1,876	1269 – 2420	3,818	3242 – 4452	295	115 – 505	1,029	685 – 1423
Oxbow	-	14_UPSALM	OmyOXBO17S	2017	2,032	1035 – 3058	0	0 – 0	0	0 – 0	0	0 – 0
Pahsimeroi	Salmon River	14_UPSALM	OmyPAHH17S	2017	2,044	1355 – 2813	0	0 – 0	0	0 – 0	0	0 – 0
Sawtooth	Salmon River	14_UPSALM	OmySAWT17S	2017	2,953	2062 – 3833	0	0 – 0	0	0 – 0	0	0 – 0
Sawtooth	East Fork Salmon River	14_UPSALM	OmyEFSW17S	2017	0	0 – 0	0	0 – 0	193	0 – 485	0	0 – 0
Oxbow	-	14_UPSALM	OmyOXBO16S	2016	1,899	1067 – 2696	0	0 – 0	0	0 – 0	0	0 – 0
Pahsimeroi	Salmon River	14_UPSALM	OmyPAHH16S	2016	1,209	662 – 1838	64	0 – 193	0	0 – 0	0	0 – 0
Sawtooth	Salmon River	14_UPSALM	OmySAWT16S	2016	1,166	552 – 1881	0	0 – 0	0	0 – 0	0	0 – 0
#N/A	#N/A	#N/A	Unassigned	#N/A	1,180	608 – 2553	0	0 – 23	0	0 – 0	0	0 – 0
			TOTAL		33,628		4,093		1,719		1,029	

2027

2028 *Post-season analysis of Sockeye Salmon passing Bonneville Dam in 2019*
2029   We provided a timely post-season analysis of Sockeye Salmon once the majority of
2030 samples had been collected at the Bonneville Dam AFF in mid-August and distributed the report
2031 to USvOR TAC on August 9, 2019 (Table 47). In recent years, the results of our genetic analysis
2032 have become an official component of the post-season run reconstruction and pre-season
2033 forecasting that TAC performs in November of each year. Therefore, timely reporting of the
2034 individual assignments of the Bonneville Dam sample of Sockeye Salmon to GSI reporting
2035 groups is critical for efficient execution of fisheries management of this species in the Columbia
2036 River. In 2019, there were 1,857 Sockeye Salmon that were sampled at the AFF and genotyped
2037 for this analysis (Table 67). For the first year since we began genetic analysis of Sockeye
2038 salmon, we estimated zero abundance for the ESA listed stock (Redfish Lake Sockeye Salmon
2039 from the Snake River) (Table 67, Figure 37). The genetic analyses provide additional
2040 information that cannot be obtained by conventional tagging methods. For example, PIT-tags
2041 placed in adults at the Bonneville Dam AFF can identify the stock-of-origin only for fish that
2042 survive and are detected at upstream dams. However, the genetic analysis can provide stock-of-
2043 origin on most fish regardless of whether they survive further upstream of Bonneville Dam. This
2044 ability has allowed greater numbers of fish to be detected from the relatively rare ESA listed
2045 Snake River stock, which improves accuracy and precision of abundance estimates. In addition,
2046 the Lake Billy Chinook stock from the Deschutes River is rare and difficult to detect with PIT-
2047 tags because of limited arrays in the Deschutes River. Therefore, the ability for the genetic
2048 baseline to identify individuals from this stock provides the only way to effectively monitor this
2049 stock's abundance in the mainstem Columbia River. In 2019, we estimated the Lake Billy
2050 Chinook stock was 264 (95% C.I.: 143 – 409) fish. Similar to the 2018 year, we were able to
2051 estimate the reintroduced stock from the Yakima River using our PBT baseline; the stock
2052 abundance in 2019 was 265 (95% C.I.: 0 – 1103).

2053
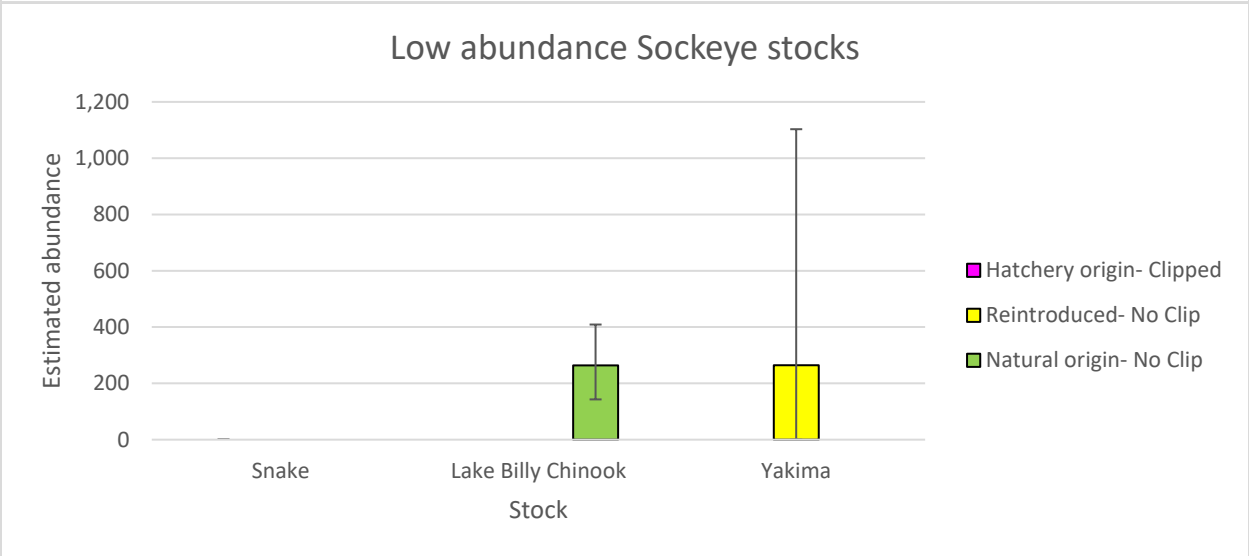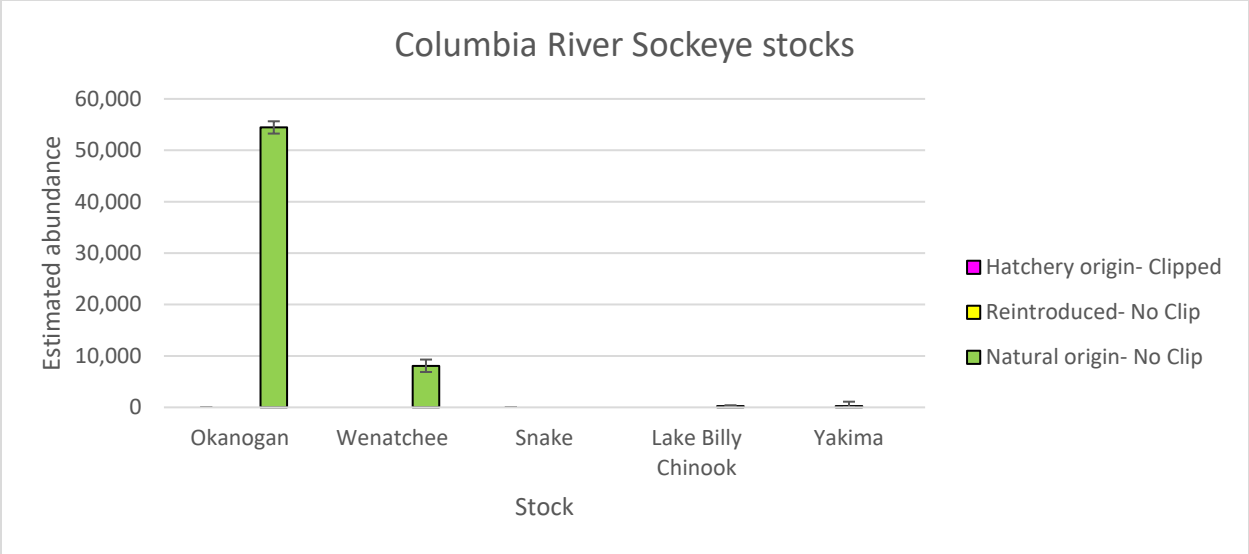
2054
2055 **Figure 37. Abundance estimates of Sockeye Salmon stocks passing Bonneville Dam in 2019.**

2056 **Table 67. Estimated abundance of Sockeye Salmon genetic stocks that passed Bonneville Dam in 2019.**

Reporting Group name	Hatchery origin-Clipped Estimated abundance		Reintroduction- No Clip Estimated abundance		Natural origin- No Clip Estimated abundance	
	Mean	95% CI	Mean	95% CI	Mean	95% CI
Okanogan	0	0 – 0			54,466	53254 – 55645
Wenatchee					8,052	6878 – 9299
Snake	0	0 – 0				
Lake Billy Chinook					264	143 – 409
Yakima			265	0 – 1103		
Total	0		265		62,781	

2057 Note: The abundance is estimated from the total fish counts at the fish ladder windows at Bonneville Dam. Most stocks are identified
2058 by GSI assignment, however this year we were able to use PBT to identify Yakima fish that were reintroduced.

253

Discussion

Parentage based tagging (PBT) and genetic stock identification (GSI) may be considered as methods that could replace the central functions of the coded wire tag program and could be a replacement for adipose fin marking to identify hatchery origin fish. However, this replacement would be contingent on continued genotyping of hatchery broodstock, fish passing Bonneville Dam, and harvested fish. For ocean fisheries management, additional hatcheries throughout the range of Chinook salmon would have to contribute broodstock samples to this PBT baseline in order for the method to serve ocean fisheries management and the need to monitor total fishery impacts for stocks including Columbia River stocks of fall Chinook (tules and upriver brights) harvested in ocean fisheries. The genetic methods provide a substantial amount of information when they are combined and used to analyze Columbia River Chinook salmon and steelhead passing Bonneville Dam. PBT improves the accuracy for defining hatchery-origin and by subtraction, total natural-origin stocks. Expansion of our PBT baseline to include hatcheries in the Columbia River has increased the proportion of hatchery origin fish passing Bonneville Dam that can be assigned to their broodstock source. We were able to assign the 78% of fish that were hatchery-origin summer A-/B-Index steelhead at Bonneville Dam in 2018 to 29 broodstock sources. As this effort continues to expand, we anticipate a corresponding increase in the proportion of hatchery origin fish that can be confidently assigned to their hatchery broodstock source. We have observed at least one sign of improved PBT coverage based upon our in-season analyses of Chinook Salmon that passed Bonneville Dam in 2019. Namely, the percentage of adipose-clipped fish abundance that was identified as PBT broodstock ranged from 85-100%, 94-100%, and 82-100% in the spring, summer, and fall management periods, respectively. We would expect these percentages to be high (~100%) only if all hatchery broodstock above Bonneville Dam are included in the PBT baseline AND our estimated tag rates are accurate for each hatchery broodstock. The fact that the management periods mostly attained high percentages gives us confidence that the PBT baseline coverage is nearly complete for Chinook Salmon above Bonneville Dam.

Genetic monitoring combining PBT and GSI is one of a number of possible tools that can be used to identify hatchery and natural fish at various resolutions. Other methods include, CWTs, PIT tags, VIE tags, and otolith marks. Adipose fin clips can be used to differentiate hatchery fish from wild fish either when fish are clipped at 100% or through expansions if stocks are not clipped at 100%. PBT can further discriminate among hatchery stocks within the reporting groups that we use for GSI analyses, and so we can now characterize different age-classes from particular hatcheries by run-timing distributions and estimate their abundance at Bonneville Dam. GSI continues to provide information that would not be possible with PBT, especially for natural-origin stocks.

This long-term study will allow us to characterize trends in run timing and abundance of steelhead and Chinook and Sockeye salmon and provide this data to fisheries managers. We were able to address the following **F&W Program Management Questions:**
What are the status and trend of adult productivity of fish populations?
What are your in-river monitoring results and what are your estimates of stock composition and stock-specific abundance, escapement, catch, and age distribution?

Trapping at Bonneville Dam can only be done at very low rates due to restrictions placed on trap operations by USACE and NFMS. Low sample rates inhibit getting a representative

2103 sample of various stocks of fish. Higher sample rates would improve the precision of the
2104 estimates of fish at Bonneville Dam. Some fisheries were also sampled at very low rates.
2105 We identified 13 Chinook salmon hatchery-origin stocks (66 hatchery broodstock
2106 sources) and 7 natural-origin stocks estimated to have relative abundances ≥1,000 fish passing
2107 Bonneville Dam in 2018. The migratory delays observed at Bonneville Dam in the spring of
2108 2018 appear to have affected the run-timing distributions for several hatchery-origin and natural-
2109 origin stocks. These delays likely contributed to the broad overlap in the temporal distributions
2110 of spring, summer/fall, and fall Chinook stocks, and our detection of spring stocks passing
2111 Bonneville Dam well into the summer management period.
2112 We identified five steelhead hatchery-origin stocks (29 hatchery broodstock sources) and
2113 five natural-origin stocks estimated to have relative abundances ≥1,000 fish passing Bonneville
2114 Dam in 2018. We found that genetic stocks seemed to fit well into the historical management
2115 categories, particularly the hatchery-origin stocks. B-Index fish appeared to have later run-
2116 timing compared to A-Index fish from the same stock.
2117 Characteristics of steelhead that assigned to Snake River hatchery broodstock sources
2118 generally support the typical A-run and B-run steelhead life history categories. The relatively
2119 large (≥78 cm) steelhead were found primarily to originate from Dworshak hatchery broodstock.
2120 These fish were also relatively old (2- and 3-ocean-age) and were derived from the Clearwater
2121 R., which is one of the regions expected to produce "B-run" steelhead. It is notable that the
2122 MGILCS reporting group represents some fish both within and outside the Snake River steelhead
2123 DPS, but does not represent all of the fish within the Snake River DPS.
2124 This was the seventh year that we were able to analyze sockeye salmon using GSI, and
2125 similar to analyses for 2017, in 2018, we used a GSI baseline that included kokanee samples
2126 from the Deschutes River drainage, Wallowa Lake, and other locations on the Snake River. We
2127 estimated relative stock composition and stock abundance for sockeye passing Bonneville Dam
2128 in 2018, and found that the Okanogan stock has the greatest relative abundance followed by the
2129 Wenatchee stock. We found fewer fish from the Snake River stock compared to previous years,
2130 and identified fish from Lake Billy Chinook and even from the reintroduced stock in Yakima
2131 River using a PBT baseline. We also found that the migratory run timing for the Okanogan and
2132 Wenatchee stocks overlaps broadly at Bonneville Dam, with the Snake stock migrating slightly
2133 later in the year.
2134 This year (2019) we continued the increased frequency of in-season reporting as we
2135 performed in 2018 during the Chinook Salmon spring and summer management periods, and we
2136 have offered timely post-season reports for the fall management period of Chinook Salmon, as
2137 well as Skamania and A-/B-Index Summer Steelhead Management Periods, and Sockeye
2138 Salmon. For steelhead and sockeye, our genetic analyses have become officially integrated into
2139 the routine analyses that U.S. v OR TAC performs. In all cases, the genetic analyses are a
2140 complement to the data that fisheries managers have available to gain insights into the biological
2141 characteristics of fisheries. The genetic analysis of the Spring Chinook Salmon test fishery data
2142 may begin to play a particularly important role in the in-season analyses because of its potential
2143 predictive power for stock abundance and timing at Bonneville Dam weeks in advance of the
2144 arrival of the run.
2145

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2161 mon.pdf
2162

Introduction

2165   Environmental and landscape features can greatly contribute to the population structure,
2166   life history diversification, and local adaptation of organisms in aquatic habitats
2167   (reviewed in Storfer et al. 2006). Geographic barriers to dispersal include recent events
2168   that may have been human induced (e.g., dams) as well as ancient events such as
2169   glaciations and formation of mountain chains (e.g., Castric et al. 2001). However, other
2170   environmental characteristics such as elevation, temperature, forest cover, and
2171   precipitation may influence distribution, adaptation, and gene flow of species (Dionne et
2172   al. 2008; Narum et al. 2008). For example, the geographic distributions of species
2173   ranges' are often determined by thermal tolerance (Brannon et al. 2004) and may
2174   necessitate adaptations for survival in extreme environments (Rodnick et al. 2004).

2176   Screening with many genetic markers provides the opportunity to investigate local
2177   adaptation in natural populations and identify candidate genes under selection (Beaumont
2178   and Nichols 1996; Beaumont and Balding 2004; Excoffier et al. 2009). This has become
2179   a commonly employed approach in ecological and population genetics studies to detect
2180   outlier loci that are putatively under selection (e.g., Vasemagi and Primmer 2005; Nosil
2181   et al. 2008). Additionally, correlation methods can be highly informative to identify
2182   markers in coding and cis-regulatory regions of known functional genes that are
2183   associated with specific selective pressures or phenotypes (Lyman and Mackay 1998;
2184   Chase et al. 2009; Torgerson et al. 2009). With increasing genomic information available
2185   for non-model organisms, single nucleotide polymorphisms (SNPs) have begun to see
2186   increased use as genetic markers for population genetic studies (e.g., Morin et al. 2004).
2187   These sequence polymorphisms are densely scattered throughout the genome of most
2188   organisms, and are commonly observed in both coding and non-coding regions of
2189   functional genes making them ideal markers to study adaptive molecular variation (e.g.,
2190   Akey et al. 2002). In a large suite of SNPs that are distributed across the genome (e.g.,
2191   Narum et al. 2018), it is possible to utilize both functionally neutral and adaptive markers
2192   within a single study. This combination of information provides a powerful approach to
2193   study questions in ecological genetics since both demographic processes (i.e., gene flow
2194   and genetic drift) and local adaptation (i.e., selection) may be inferred.

2196   Molecular techniques such as RNA-seq (Wolf 2013) also provide the opportunity to
2197   investigate transcriptional response to thermal stress and further identify mechanisms for
2198   thermal adaptation. Patterns of gene expression under heat stress are important to
2199   determining evolutionary adaptation among conspecific populations that occupy various
2200   environments. Multiple genes have been shown to be involved in heat tolerance across
2201   many species, including highly conserved heat shock proteins (hsps) that are upregulated
2202   under stressful conditions such as exposure to heat (Morimoto et al. 1992; Sorensen et al.
2203   2003). An adaptive heat shock response has additionally been shown to occur among
2204   conspecific populations that occupy variable environments (e.g., Dahlhoff and Rank
2205   2000; Sorensen et al. 2001). However, many genes are known to have a role in
2206   regulating the effects of temperature and are likely to be involved in thermal adaptation

2207 (Sorensen et al. 2005; Kassahn et al. 2007). Thus, RNA-seq provides the opportunity to
2208 investigate differential expression across the transcriptome and identify biological
2209 pathways involved in evolutionary response to thermal stress.
2210
2211 Thus, genome scans with large numbers of SNP markers (e.g., RAD sequencing, Baird et
2212 al. 2008; Pool-seq, Schlotterer et al. 2014) and gene expression (e.g., RNA-seq)
2213 approaches may be effective tools for identifying the genetic architecture underlying
2214 specific traits such as thermal tolerance, run-timing/maturation, disease resistance,
2215 anadromy, and age-at-maturity. Once these underlying genomic regions are identified,
2216 they can be broadly screened in populations throughout the Columbia River Basin to
2217 facilitate management for long term conservation and recovery of salmonids.
2218
2219

2220 *Fish Population RM&E*
2221 **F&W Program Strategy:** Assess the status and trend of diversity of natural and
2222 hatchery origin fish populations.
2223 **F&W Program Management Question:** What are the status and trend of diversity
2224 of natural and hatchery origin fish populations?

2225 **Uncertainty Research**
2226 See Appendix A for table of critical uncertainties research.
2227
2228 **Project Map:**
2229 *http://www.cbfish.org/Project.mvc/Map/2009-005-00*
2230 **Contract Map(s):**
2231 *http://www.cbfish.org/Contract.mvc/Map/61839*
2232 *http://www.cbfish.org/Contract.mvc/Map/65575*

2233 **Methods: Protocols, Study Designs, and Study Area**
2234 **Method Title:** Whole Genome Resequencing

2235 • **Method Link:**
2236 • [Whole Genome Resequencing: Poolseq Individual Barcode v1.0](#) (ID: 6754) Published
2237 • [Whole Genome Resequencing: Poolseq Pooled v1.0](#) (ID: 6775) Published

2238 **Method Summary:**
2239 With reference genome assemblies now publicly available for both Chinook salmon and
2240 steelhead, this enables whole genome resequencing for investigating adaptive variation
2241 across a large portion of the genome (50-80%) in these species. Whole genome
2242 resequencing methods include individually barcoded samples, or pools of samples (Pool-
2243 seq; Schlotterer et al. 2014) depending on the study design. For both methods, sequence
2244 data is aligned to the reference genome assembly, and allele frequencies from millions of
2245 SNPs are analyzed to detect statistically significant regions of the genome associated with

2246	specific traits or adaptation to environmental factors. Putatively neutral regions of the
2247	genome are also useful for standard phylogeny and demographic analyses of populations.
2248	In most studies, allele frequencies are available for collections but sequencing depth is
2249	typically not high enough to provide individual genotypes. However, candidate SNPs
2250	may be developed into standard panels with GTseq or other approaches to genotype
2251	many individuals to validate trait association, determine inheritance, and estimate linkage
2252	disequilibrium.

2253

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 38). 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). Additional studies are underway to further pinpoint candidate genes through whole genome resequencing.
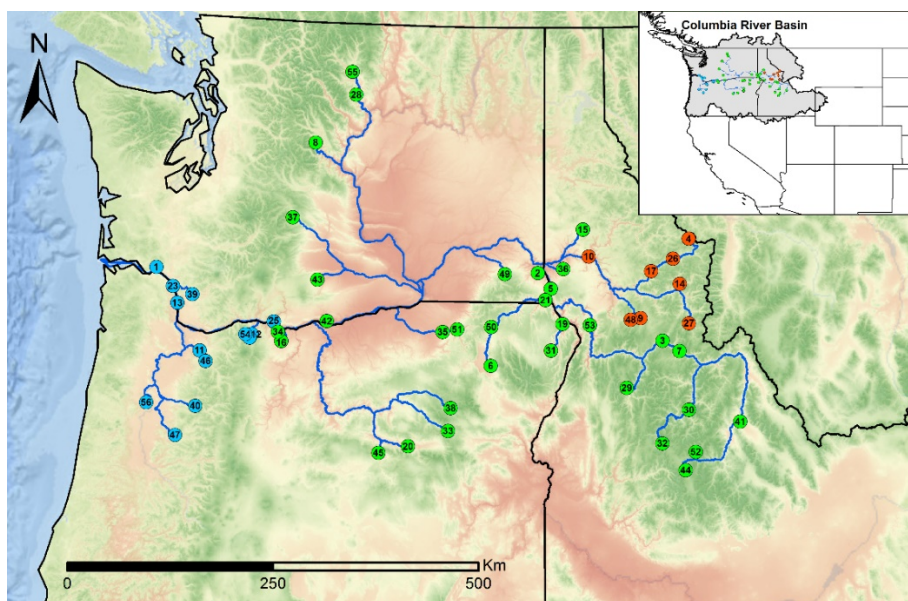
Figure 38. Steelhead collection localities colored by genetic cluster (from Micheletti et al. 2018a). blue = coastal, green = inland, red = inland-Clearwater. Blue lines indicate each population's migration path to the ocean. Map layer shows mean annual temperature for the warmest quarter with transition from colder (green) to warmer (red).

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 39**a). Several candidate markers were associated with local adaptation within and among lineages (**Figure 39**b; Hecht et al. 2015). A follow-up study to investigate local adaptation through whole genome resequencing has demonstrated that a broad portfolio of diversity persists in Chinook salmon and candidate genes for local adaptation are widespread throughout the genome within and among lineages (Narum et al. 2018). Additional studies are underway to represent genome wide variation for a more thorough set of populations throughout the Columbia River Basin.
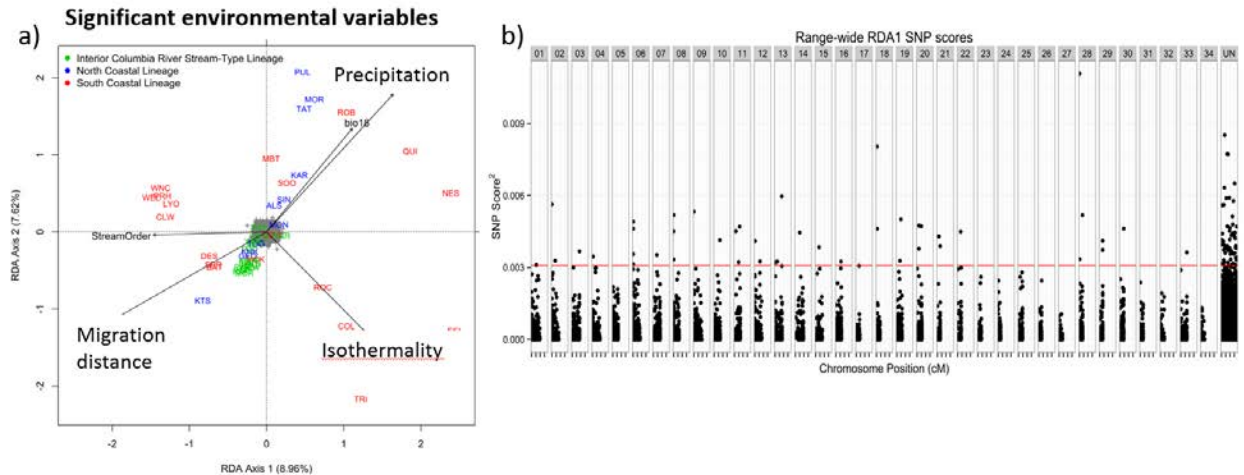
Figure 39. a) Environmental drivers of selection and b) candidate markers for local adaptation in Chinook salmon (from Hecht et al. 2015). a) Population scores for canonical RDA axis 1 and 2 are represented by the three-letter abbreviation for each population, coloured to represent the lineage assignment of that population. SNP variance is indicated by the position of grey '+' symbols radiating from the plot centroid, each representing a different locus. Environmental factors are depicted as black vectors (arrows), where the length of the vector is a representation of the magnitude of the contribution of that environmental variable in explaining SNP variance. The angle between environmental variable vectors is a representation of the correlation between those variables. Vectors and points are plotted with symmetrical scaling (scale = 3) to preserve the relationship between scores, without focusing on a single score.

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 11 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).

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 3 & Table 5) that will also be used for baseline allele frequencies. Landscape genomics analyses for both Chinook salmon and steelhead are ongoing.

Objective 2) Genetic Basis for Phenotypic Expression of Traits
Hypotheses:

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

Hypothesis 2: Markers from candidate genes can be developed into cost efficient assays for genotyping large numbers of individuals to monitor genetic variation for phenotypic traits at broad scales, with the potential to predict resiliency of populations to environmental changes.

Activities implemented:

Multiple studies have been initiated to investigate the genetic basis for multiple phenotypic traits using association mapping or gene expression approaches. Work has focused on genomic regions associated with several different traits. Work on resident vs. anadromous *O. mykiss* (Narum et al. 2008a; Hecht et al. 2013) has revealed that a combination of environmental and genetic factors contribute to determination of these life history types (Figure 43).
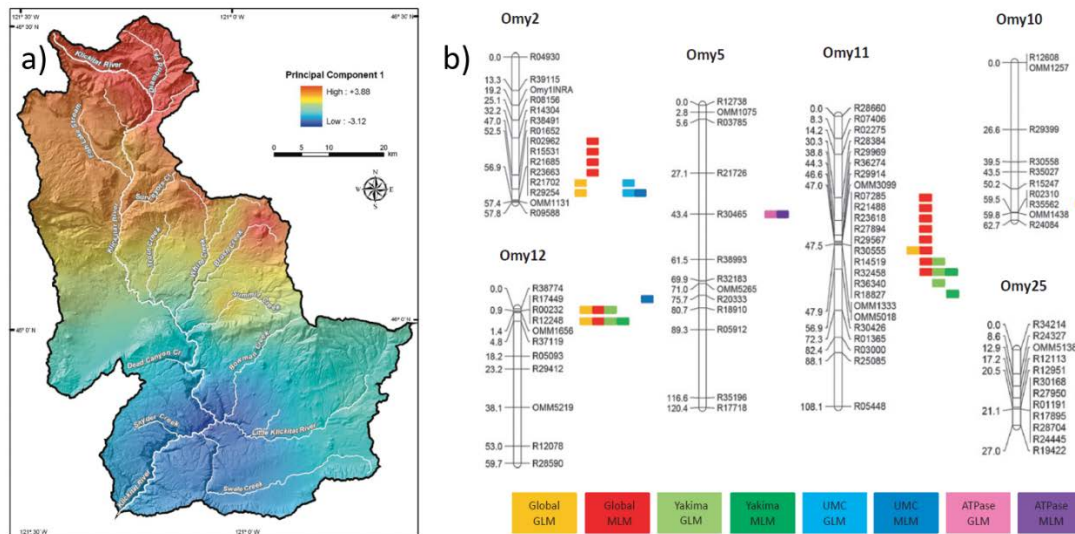
Figure 40. **a) Synthesis map illustrating interpolation principal component (PC1) that accounts for 59% of variation in resident (red) vs anadromous (red) life history (from Narum et al. 2008a). b) Significant loci detected from eight individual association tests, where each test is represented by a different colored pill and placed to the right of the linkage group. GLM, general linear model; MLM, mixed linear model (from Hecht et al. 2013).**

Run-timing related to maturity in steelhead (Hess et al. 2016; Micheletti et al. 2018c) and Chinook salmon (Hess and Narum 2011; Narum et al. 2018) 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 41).
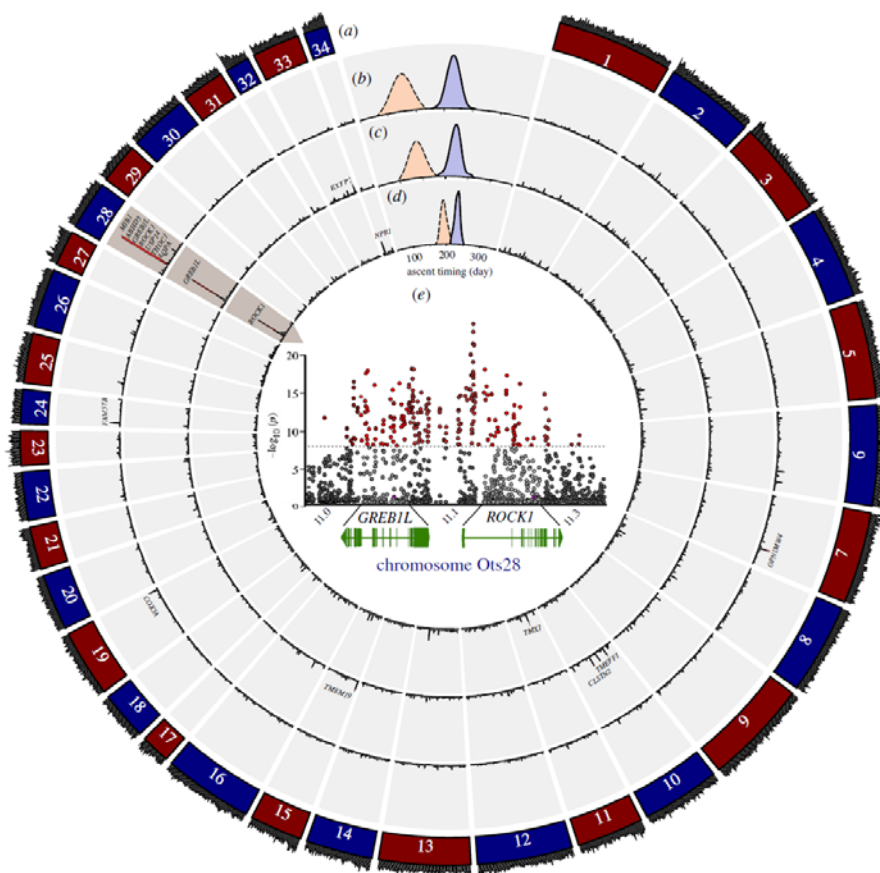
Figure 41. Manhattan plot for premature and mature collections of Chinook salmon (from Narum et al. 2018). (a) Sequence coverage (black outer ring) for each chromosome. (b) Significant divergence between premature (spring-run) and mature (fall-run) migrating Chinook salmon in the Cowlitz River of the coastal lineage. (c) Significant divergence between premature (Methow River summer-run) and mature (Priest Rapids fall-run) migrating Chinook salmon within the interior ocean-type lineage. (d) Significant divergence for Chinook salmon returning to Johnson Creek (interior stream-type) that enter freshwater premature (spring/summer-run), 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 11.022 and 11.225 Mb (GREB1 L, ROCK1, and intergenic regions) with significance based on CMH tests. Significant genes are labelled. Timing of ascent to spawning grounds for premature (dashed line, orange) and mature (solid line, blue) collection pairs are shown within the ring for each lineage (b–d). Purple dots show two non-synonymous SNPs.

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.

A principal component analysis (PCA) of allele frequencies of putatively neutral markers, without linkage disequilibrium (LD), will be plotted for all populations. Putatively neutral markers will be assessed to detect underlying population structure, which we expect to coincide with coastal and inland lineages. The PCA of putatively neutral markers will accompany a discriminate analysis of principal components (DAPC) with the R package adegenet 2.1.0 to assign probability of individual membership to genetic

groups, K, revealed with the putative neutral marker PCA (Jombart 2008, Jombart and Ahmed 2011). The DAPC recovers maximum genetic variation between groups, while minimizing genetic variation within groups (Jombart, 2008; Jombart and Ahmed, 2011). The 'find.clusters' adegenet function will run for 25 instances for K=1 through K=10. The Bayesian information criterion (BIC) will be averaged and scaled by the standard deviation for each K value. The most appropriate number of genetic groups will be determined with the greatest ΔK value as described in Evanno et al. (2005). A total of 13 markers will be evaluated on chromosome 28 within the *GREB1L, rock1*, and intergenic region between *GREB1L* and *ROCK1* (Hess et al. 2016, Micheletti et al. 2018a). Premature, mature, and heterozygote genotypes migration-timing will be established based on genotypes from previous studies and the Skamania stock genotype, which is a hatchery-strain intensively selected for premature migration and cultured since 1956 with steelhead from the Washougal and Klickitat Rivers (Chilcote et al. 1986). Premature, mature, and heterozygote migration timing genotype proportions will be assessed across all collection locations. A PCA of allele frequencies of adaptive markers will also be conducted for all collection locations to assess genetic grouping based on migration-timing.

We seek to identify subsets of the markers, or haplotype blocks, most associated with migration-timing. Additionally, we will assess linkage disequilibrium (LD) within the 13 markers. Haplotype blocks of the 13 chromosome 28 markers will be defined with solid spine LD analysis in the Java Runtime Environment software, Haploview 4.2, across all collection locations (Barrett et al. 2005). The same markers will be assessed for LD in individuals from coastal and inland lineages (as delineated by DAPC) separately. The number and frequency of haplotypes across the basin will be compared between haplotype blocks. Variation of genotype proportions will also be evaluated with various sets of adaptive, chromosome 28 markers.

Redundancy analyses (RDA) will be conducted for all Columbia River basin sites to model the degree to which the variation in environmental variables explains the variation in allele frequencies of adaptive markers included in the haplotype blocks (Borcard et al. 1992; Kierepka and Latch 2015). Vegan 2.5-6 R package (Oksanen et al. 2019) will be used to analyze all populations together and each lineage separately. We will use environmental variables significantly associated with adaptive genetic variation in a previous study (Micheletti et al. 2018b). When two highly correlated (>0.75 pairwise correlation; Asuero et al. 2006) environmental variables are identified, one will be removed from further analyses and the variable kept will be determined from biological relevance to salmonids according to previous studies (Hecht et al. 2015; Olsen et al. 2011; Micheletti et al. 2018b). One-way analysis of variance (ANOVA) with a Tukey's range test (Tukey 1949) will identify significant variability in salmonid habitat. Environmental variables will be analyzed with the "envfit" PCA function of the vegan R package. The ANOVA test and PCA together determine significant environmental variables within and among *O. mykiss* habitats that will be measured in this study. The final RDAs will be run with significant (α=0.05) environmental variables retained from permutation tests with 1000 permutations. Frequency of alleles in the haplotype block associated with migration-timing are correlated to environmental variables with RDA

2479 constraint scores. Constraint scores indicate the degree of correlation and whether there is
2480 a positive or negative relationship between environmental variables and allelic
2481 frequencies.
2482
2483 We are also analyzing a large sample of steelhead collected at Bonneville Adult Fish
2484 Facility (N=1,538) and in the Hood River (N=354) for patterns of association of the 13
2485 chromosome 28 (*GREB1/ROCK1*) markers with two attributes of run-timing: the day
2486 each fish passed Bonneville dam and the day each fish was recorded at their most
2487 upstream passive integrated transponder (PIT) array (Figure 42). These samples were
2488 filtered from a larger set of complete PIT histories using custom R code, and consist of
2489 those samples for which the arrival to spawning tributary could be reliably inferred.
2490 Filtering was designed to exclude iteroparous spawning fish (kelts) with incomplete
2491 histories, "dip-in" fish that seek temporary thermal refuge in rivers other than their
2492 spawning destination, "overshoots" that travel farther upstream than necessary in higher
2493 order rivers but later regress, as well as fish only recorded at sites from which precision
2494 in arrival time could not be expected (e.g. dams and arrays in higher order rivers). While
2495 the Bonneville fish include mostly Interior Lineage fish, and are thus almost exclusively
2496 "summer-run" fish, the Hood River data inludes both cannonical "summer-run" and
2497 "winter-run" fish.
2498 For Bonneville samples, in addition to the two raw measures of run time, we will
2499 calculate two compound measures, the lag time between Bonneville passage day and
2500 upstream arrival day, and the effective speed, which is the former compound statistic
2501 divided by the river distance between Bonneville Dam and the respective PIT array.
2502 Finally, we will also examine several relative measures: the Bonneville passage day or
2503 upstream arrival day relative to the median or last of such day within a sub-basin or
2504 hydrological unit, both within and across measures. In all, we will examine genetic
2505 association with 20 total measures of run timing.
2506 From both sets of steelhead samples, we will infer patterns of linkage and haplotype
2507 frequencies using Haploview (Barrett, Fry, Maller, & Daly, 2005), which implements an
2508 expectation-maximization algorithm, and Shapeit, which utilizes a hidden-markov model
2509 and graph based algorithm (Delaneau, Marchini, & Zagury, 2012). Genetic association in
2510 these data will utilize both SNP-based and haplotype-based association analyses,
2511 including both the "mixed-linear" and "BLINK" models of GAPIT (Lipka et al., 2012)
2512 and the GLM-based haplotype score permutation routine of Haplo.stats (Sinnwell P &
2513 Schaid J, 2005). We expect these analyses to indicate 1) if the association of run timing
2514 with chromosome 28 markers is consistent between Coastal Lineage and Interior Lineage
2515 steelhead, 2) if the degree and pattern of correlation across the candidate region is the
2516 same, 3) whether heterozygotes for chromosome 28 markers have a phenotypic indicative
2517 of additive or dominant expression patterns, and 4) which markers or haplotypes are most
2518 strongly associated with run timing and may be most predictive of run timing from

2519   genetic surveys, not unlike the results from Chinook salmon, discussed below.
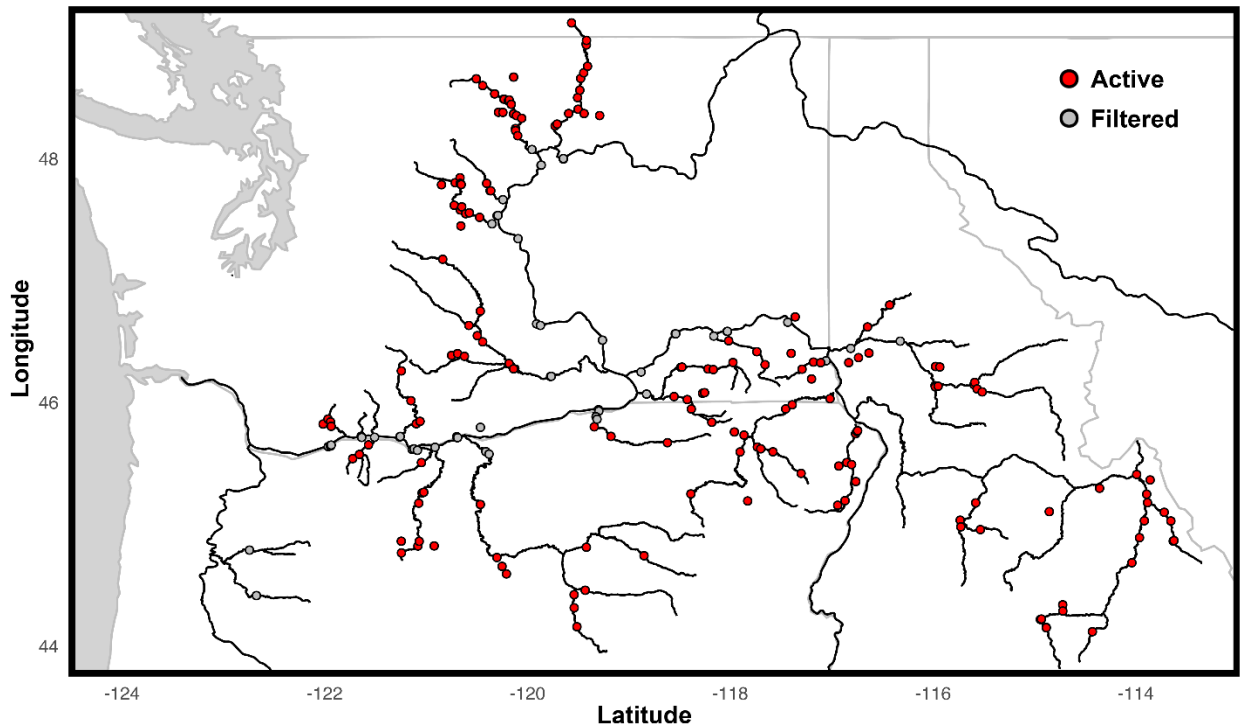

2520
Figure 42. Map of passive integrated transponder (PIT) arrays at which steelhead passing and tagged at Bonneville Dam in 2013 to 2018 were later recorded. Filtered sites are those for which precise upstream arrival time could not be ensured, while fish recorded at the remaining active sites (N=1,538 samples) provide run-timing phenotype data for genetic association analyses.

For Chinook salmon, 33 candidate markers were devloped that span 220kb on chromosome 28 including candidate genes greb1L and rock1 for adult migration timing. 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 43). 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 43).

Association tests validated that the majority of markers were significantly associated with migration timing for all three lineages (Figure 44). The strongest association was consistently observed for markers within or upstream of the rock1 gene, closely followed

2546   by markers located within or upstream of greb1L. Out of the 33 candidate SNPs, 13 SNPs
2547   were significantly associated with fitness (
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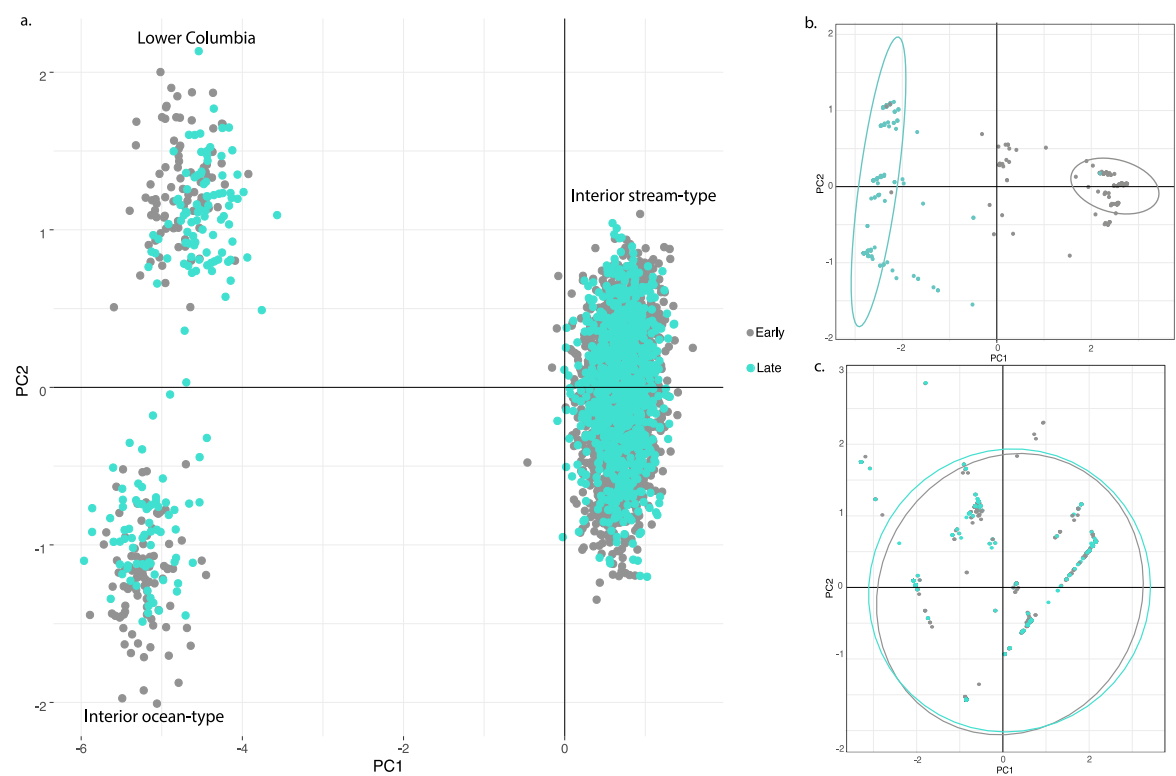2566
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2570   **Figure 45**).

Figure 43. PCA of genetic variation in Chinook Salmon. 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.
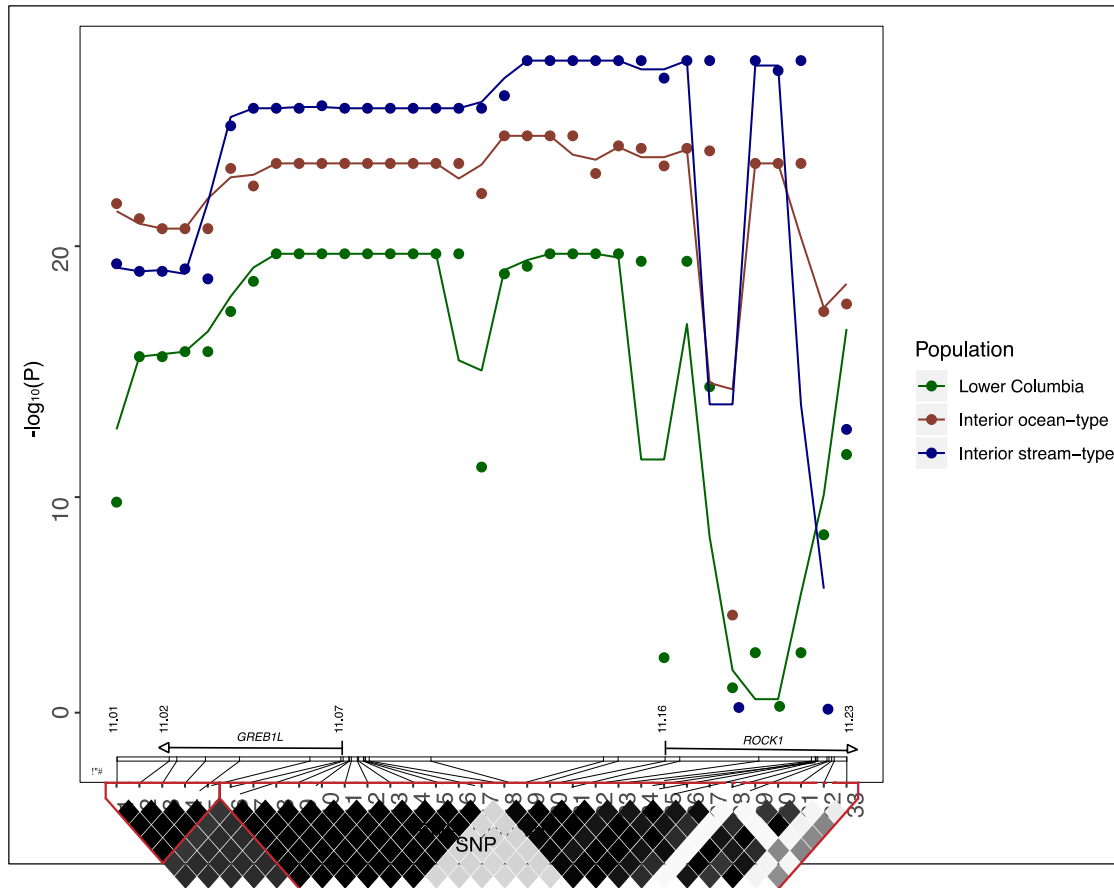
Figure 44. Association of each candidate SNP marker with migration timing within three lineages of Chinook Salmon. The colored lines for each lineage represent sliding windows for consecutive pairs of SNPs along the candidate genomic region. SNP number on the x-axis corresponds to the 33 candidate markers, while the genome position of markers on chromosome 28 (NCBI accession GCA_002831465.1) is depicted in the gene diagrams above the x-axis. Y-axis represents −log$_{10}$(FDR-corrected p-value).
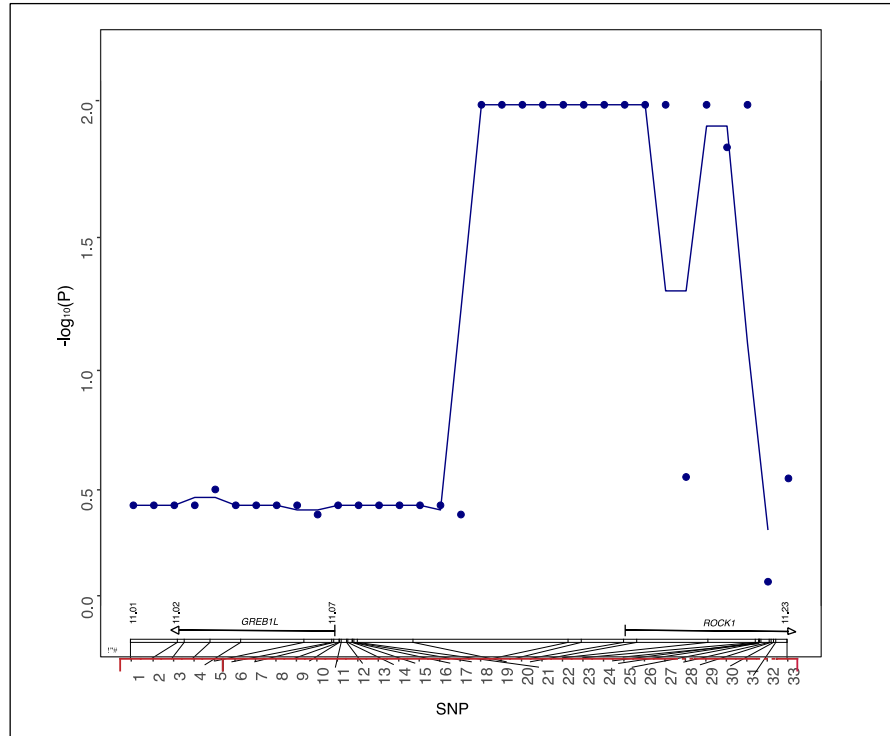
Figure 45. Association of each candidate SNP marker with fitness within the Interior stream-type population. The lines represent sliding windows for consecutive pairs of SNPs along the candidate genomic region. SNP number on the x-axis corresponds to the 33 candidate markers, while the genome position of markers on chromosome 28 (NCBI accession GCA_002831465.1) is depicted in the gene diagrams above the x-axis. Y-axis represents −log$_{10}$(FDR-corrected p-value).

Age at maturity in Chinook salmon appears to be a polygenic trait but genes of greatest effect differ between sexes (females = OPN4, males = TMEM19; Figure 46; Micheletti and Narum 2018b). We continue to investigate ocean age/size at maturity for steelhead with whole genome resequencing data for distinct 1-ocean vs 2-ocean phenotypes in multiple populations. Disease resistance in *O. mykiss* appears to be highly complex with several genes involved (Campbell and Narum 2015).
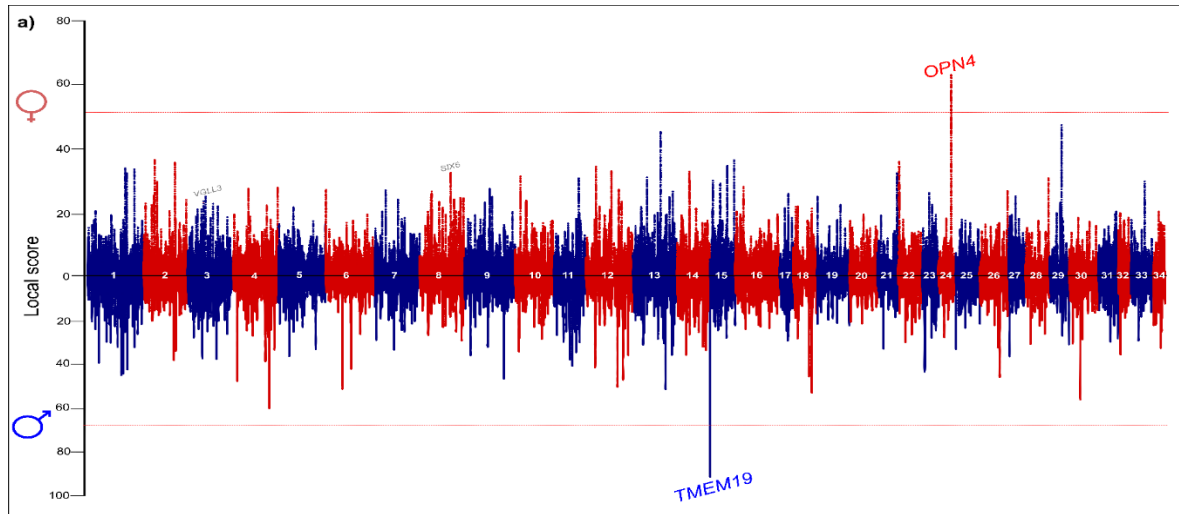
Figure 46. Manhattan plot (from Micheletti and Narum 2018b) illustrating differentiated regions within age classes of females (top; 4- vs. 5-year-olds) and males (bottom; 3- vs. 4- vs. 5-year-olds). Red dashed lines indicate $\alpha = 0.01$ significance threshold for the local score test with Bonferroni 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.

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; Chen et al. 2018b). As these candidate genes for traits have begun to be identified (Figure 50; Chen et al. 2018a), 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.
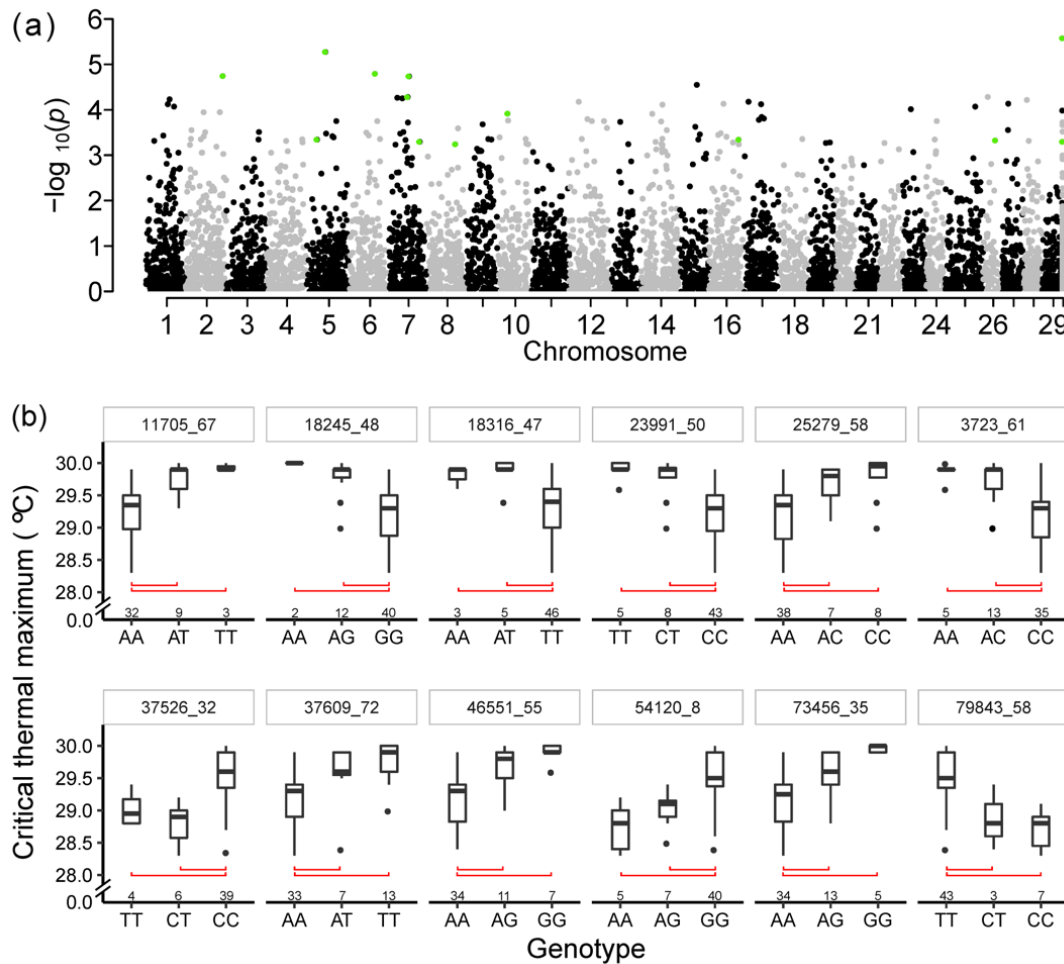
Figure 47. Results from Chen et al. (2018a) that demonstrate association of loci with thermal tolerance in natural populations of redband trout from desert, cool montane, and cold montane environments. Outlier loci and the association with critical thermal maximum (CTMAX). (a) Manhattan plot of calibrated p values, which were derived from the median z-score of results from Lositan, outFLANK and PCAdapt (François et al., 2016). Outliers identified by at least two analyses are in green. (b) significant associations between CTMAX and genotypes of candidate outlier loci (locus name above each panel). Red brackets indicate significant differences at the level of α=0.05 in one-way ANOVA on ranks with subsequent Dunn's post−hoc test. Numbers above genotypes represent the sample size. Results published in Chen et al. (2018a).

Summary of accomplishments & lessons learned:

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

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

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Synthesis of Findings: Discussion/Conclusions

Fish Population RM&E

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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 51). However, populations that currently live in warm environments may have a narrow safety margin, and therefore are more vulnerable and may need conservation attention. Thus, phenotypic plasticity and behavioral thermoregulation, such as seeking thermal refugia (e.g. deep pools, cool springs and upwelling groundwater), will become critically important for them to temporarily survive or avoid extreme temperatures in the future. To predict the rate and limits of evolutionary adaptation more acutely in the future, more advanced niche models need to incorporate additional factors such as the intensity of selection, effective population size, heritability and phenotypic plasticity. This information can be incorporated into robust adaptive networks that include a broad portfolio of adaptive diversity, connectivity, and meta-population scale management for long-term persistence.

Markers that are associated with specific phenotypic traits will also enable monitoring of genetic variation for traits that are considered important to managers. In particular, markers have been developed for premature vs. mature arrival to spawning grounds (e.g., migration/maturation timing) to monitor genetic variation for this trait in the Columbia Basin.
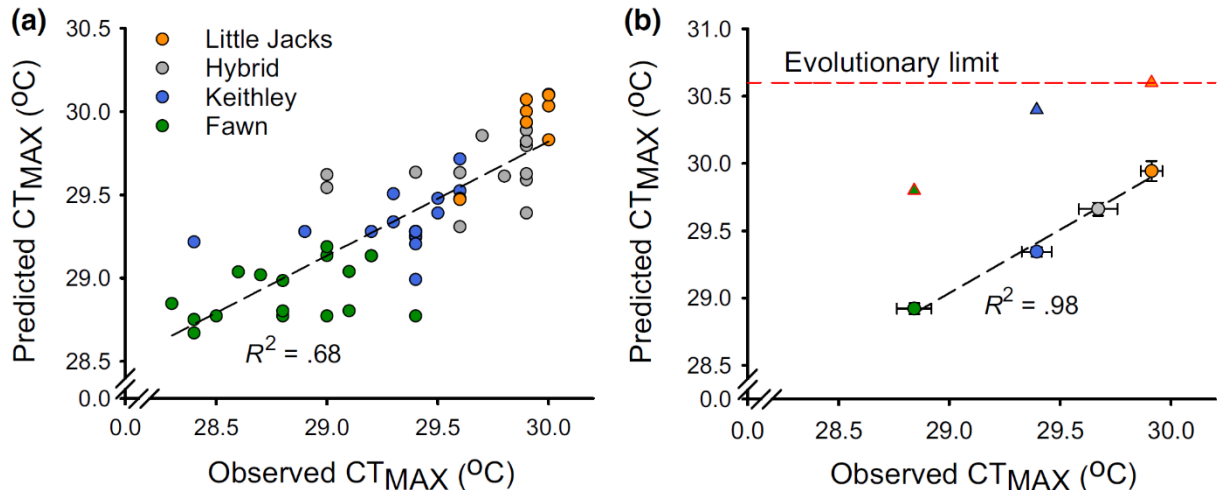
Figure 48. Critical thermal maximum (CTMAX) prediction (from Chen et al. 2018a). (a) Correlation between observed and predicted individual CTMAX values. (b) Prediction of population mean CTMAX (SEM) and evolutionary limits for populations (triangle) and species (dash line).

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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2949 Section 6: Sturgeon genetics
2950 **Introduction**
2951 White sturgeon are a long-lived amphidromous species that historically ranged throughout the
2952 Columbia River Basin, occurring as broadly distributed, overlapping meta-populations (Parsley
2953 2007; Beamesderfer et al. 2012). Overfishing is believed to have contributed heavily to
2954 decreased productivity and declining population abundances as early as the late 1880's (Mallette
2955 2008). Moreover, impacts on white sturgeon populations and trending declines in abundances
2956 have been linked to factors associated with the construction of dams (e.g., the hydropower
2957 system) in the mainstem Columbia River and its tributaries. Impounding of the Columbia River
2958 has significantly fragmented populations (see Nelson et al. 2013). Regional flow regimes and
2959 hydrology have been altered and diminished from their natural states (Barton et al. 2010),
2960 affecting availability and quality of preferred spawning and rearing habitat for white sturgeon
2961 over a large geographic range (Parsley et al. 1993; Rien et al. 2005; Parsley 2007). Most notably,
2962 dams have greatly restricted migration through the Columbia River corridor, and fish passage has
2963 not provided the same benefit for sturgeon that has been afforded to salmon species
2964 (Beamesderfer et al. 2011: Beamesderfer et al. 2012). By some estimates, as many as 24
2965 functionally discrete white sturgeon populations have arisen as a result (Parsley 2007). It is also
2966 important to recognize that altered habitat has severely impacted recruitment, predator and prey
2967 interactions, and population genetic variability throughout much of the Columbia River Basin
2968 (Nelson et al 2012). Considerable monitoring and evaluation efforts have been initiated in the
2969 Columbia (KTOI 2007; Drauch-Schreier et al 2012; Drauch-Schreier et al. 2013), and Snake
2970 River region (IPC 2005), where sturgeon populations have experienced some of the greatest
2971 declines, and where little to no recruitment has been observed in recent years. There have been
2972 similar and concerted attempts to characterize white sturgeon population status where relatively
2973 larger numbers of sturgeon still persist (e.g., Bonneville Reservoir and the lower Columbia
2974 River) but where long-term impacts to habitat and productivity remain a concern for long-term
2975 viability and genetic diversity (Mallette 2008; Chapman and Jones 2010).
2976 　　　　Since 2008, Tribal managers and CRITFC scientists have been monitoring the genetic
2977 population structure of white sturgeon residing in reservoirs impounded by Bonneville Dam, The
2978 Dalles Dam, John Day Dam and McNary Dam in the Middle Columbia River. A long-term
2979 monitoring effort was initiated in order to assess previously described risks to contemporary
2980 population status, including concerns for limited migration potential, declining or low genetic
2981 diversity, small effective population sizes, and poor productivity. This report provides a
2982 summary of ongoing efforts in 2019 to understand of local demographics and resolve population
2983 structure. Previously, we reported on our success in overcoming the octoploid nature of the white
2984 sturgeon genome, which created difficulties in scoring traditional microsatellite markers, by
2985 developing a panel of single nucleotide markers (SNPs) that we are able to genotype as
2986 functionally-tetraploid markers. Because the inheritance pattern of these markers is more
2987 interpretable than data from microsatellite markers, these data are more amenable to a wider
2988 variety of genetic analyses.
2989
2990 **Methods**
2991 Our SNP panel consists of 325 loci that met or exceeded quality control criteria, including minor
2992 allele frequencies above 5%, and at least 80% genotyping success among samples (Matala et al.
2993 2017). The SNPs were designed using extended sequence data, and the panel was genotyped
2994 using the GT-seq high throughput sequencing method (Campbell et al. 2015;

2995 . Genotypes of white
2996 sturgeon segregate into five distinct clusters indicative of four alleles at each locus (tetraploidy)
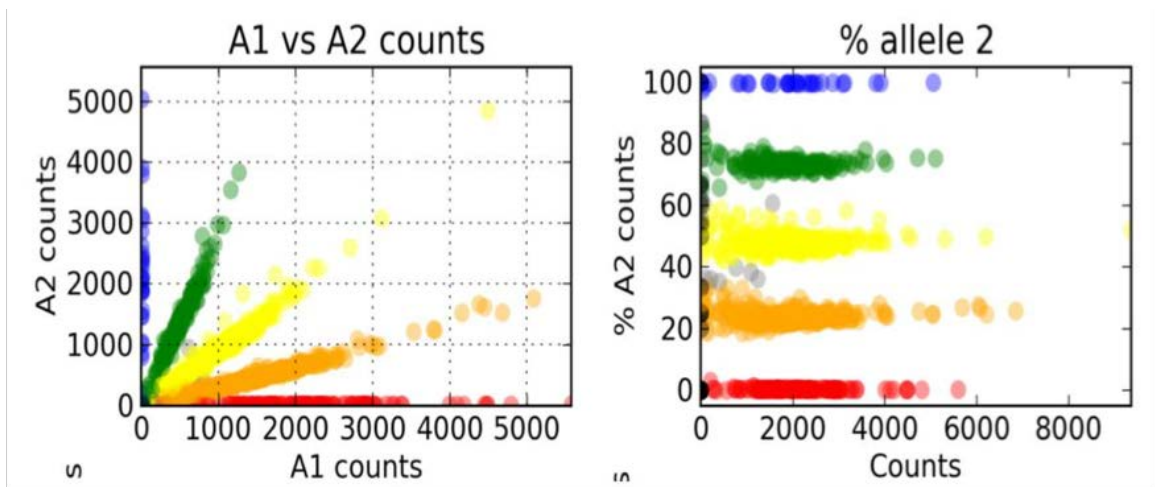2997 (e.g. AAAA, AAAB, AABB, ABBB, BBBB) (**Figure 49**).
2998

2999
3000 **Figure 49. Example of a tetraploid locus GT-seq plot.**
3001
3002 This genotyping panel was tested using a set of known parent-offspring pairs from 3 reciprocal
3003 pairings (3 males x 3 females) contributed by our collaborator at the University of California-
3004 Davis (Dr. Andrea Drauch-Schreier). Using these known relationships, we were able to establish
3005 that the majority of loci exhibited the expected mendelian inheritance patterns, while flagging a
3006 handful of loci for re-evaluation (**Figure 50**). Though statistical parentage assignment remains
3007 challenging (see Discussion), these data also appeared promising for identifying the most likely
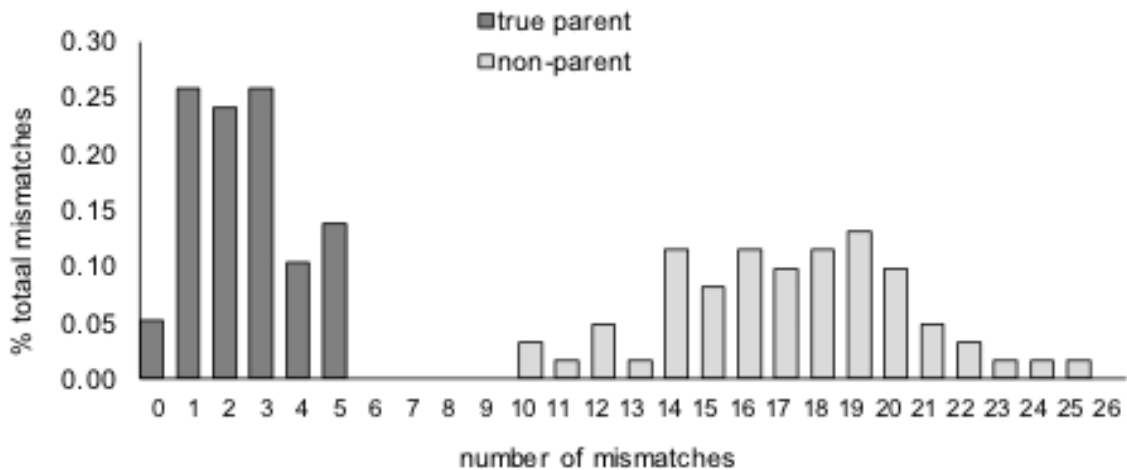3008 parents among a set of candidates.
3009

3010
3011 **Figure 50. Distribution of proportional discrepancies (numbers of mismatched loci)**
3012 **observed among all offspring assigned to a non-parent pair compared to offspring assigned**
3013 **to a known (i.e. true) parent pair.**
3014
3015 Given the success in developing this genotyping panel (described in more detail in our 2018
3016 report), in 2019, in collaboration with sturgeon experts at Cramer Fish Sciences (P. Anders), we

3017 undertook to organize and expand our tissue holdings for white sturgeon. We were specifically
3018 interested to identify representation in our holdings sufficient to meet our continuing objectives,
3019 including understanding the relationship of genetic diversity to local adaptation and evolutionary
3020 potential in the context of regional and local population structure, as well as local demographic
3021 trends in recruitment and spawning success, their relationship to recent environmental
3022 conditions, and their amenability to stock supplementation.
3023
3024 **Results:**
3025 Our tissue holdings include 10,697 unique samples from white sturgeon from the Columbia
3026 Basin, as well as 116 from other Pacific versants. We categorized these based on the Columbia
3027 River reach from which they were collected (**Figure 50**), and where known, the life stage of the
3028 individual (Table 68).
3029
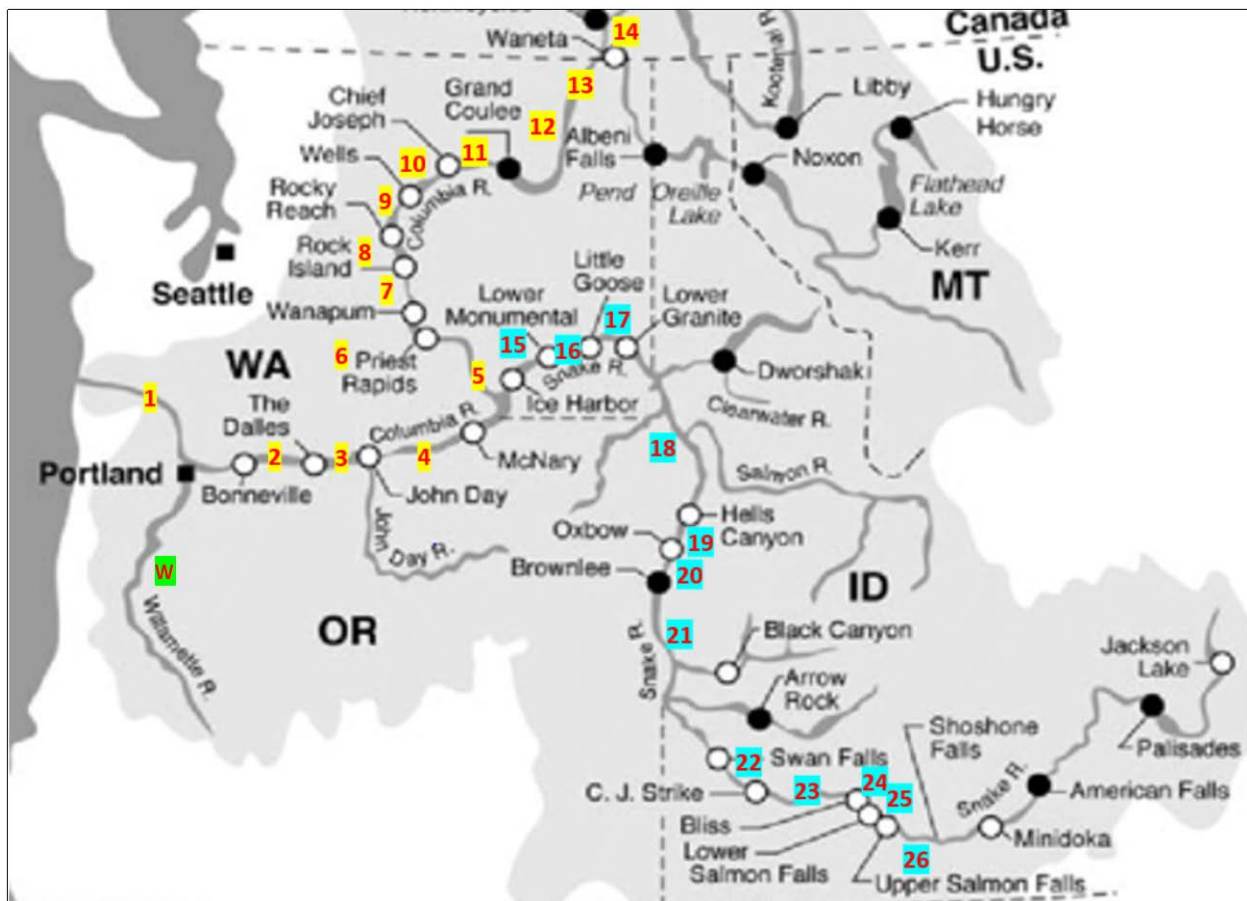
3031 **Figure 51. Locations in the Columbia Basin where white sturgeon are or historically were**
3032 **present.**
3033
3034
3035 **Table 68. White sturgeon from the Columbia Basin in the CRITFC collection. Life stages**
3036 **are defined as Adult (>136cm), Sub-adult (100-136cm), and Juvenile (<100cm).**

Loc	Region	Reach	Adult	Sub-adult	Juvenile	Unk	Totals
1	Lower Columbia River	Lower Columba River	159	49	813	41	1,062
2	Lower River Pools	Bonneville Pool	78	6	2,931	342	3,357
3		The Dalles Pool	46	1	1,800	56	1,903
4		John Day Pool	606	492	1,219	851	3,168
5	Mid-Columbia Pools	McNary Pool	50	68	56	53	227
6		Priest Rapids Pool	0	0	0	0	0
7		Wanapum Pool	0	0	0	0	0
8	Upper-Mid C Pools	Rock Island Pool	0	0	0	0	0
9		Rocky Reach Pool	3	6	28	0	37
10		Wells Pool	0	0	0	0	0
11		Chief Joseph Pool	0	0	0	0	0
12	Upper Columbia	Grand Coulee Reservoir	99	1	126	0	226
13		Upper Columbia River	0	0	0	0	0
14		Upper Columbia (BC)	0	0	0	0	0
15	Lower Snake	Ice Harbor Pool	25	33	65	4	127
16		Lower Monumental Pool	67	52	25	0	144
17		Little Goose Pool	62	42	27	0	131
18		Lower Granite Pool	24	10	32	30	96
19	Middle Snake	Hells Canyon Reservoir	0	0	0	0	0
20		Oxbow Reservoir	0	0	0	0	0
21		Brownlee Reservoir	0	0	0	0	0
22		Swan Falls Reservoir	0	0	0	0	0
23		CJ Strike Reservoir	11	4	0	78	93
24	Upper Snake	Bliss Reservoir	0	0	0	0	0
25		Lower Salmon Falls Res.	0	0	0	0	0
26		Upper Salmon Falls Res.	0	0	0	112	112
W	Willamette	Santiam River	0	0	0	14	14
			1,230	764	7,122	1,581	10,697

Tallying using meta-data characteristics in this manner allowed us to assess the strengths of this collection, as well as to identify areas for additional sampling and tissue loans, although in general the abundance of samples in our collection reflects where there remain moderate to robust populations of white sturgeon in the Columbia Basin (Beamesderfer, et al. 2012). From this parsing, we were able to identify a subset of 3,006 samples to genotype in the 2020 calendar year that will allow us to assess, using the more robust 325 marker panel, population genetic structure in the Columbia Basin, and the Columbia relative to other drainages, as well as variations in genetic diversity across life stages indicative of differing and potentially problematic patterns of recruitment (Table 69).

Table 69. White sturgeon targeted for genotyping in calendar year 2020. Life stages are defined as above, except that fish less than 30cm are identified as young-of-year (YOY).

	Region	Reach	Adult	Sub-Adults + Juveniles	YOY	Unk	Totals
1	Below Bonneville	Lower Columbia River	85	68	223	3	**379**
2	Lower Columbia	Bonneville	36	5	264	0	**305**
3	Lower Columbia	The Dalles	18	8	327	1	**354**
4	Lower Columbia	John Day	249	421	81	142	**893**
5	Middle Columbia	McNary	46	97	14	55	**212**
9	Upper-Mid Columbia	Rocky Reach	3	34	0	0	**37**
12	Upper Columbia	Grand Coulee/FDR	99	27	100	0	**226**
15	lower Snake	Ice Harbor	26	87	0	4	**117**
16	lower Snake	Little Goose	66	54	0	0	**120**
17	lower Snake	Lower Monumental	68	74	0	0	**142**
18	lower Snake	Lower Granite	22	3	0	18	**43**
23	middle Snake	CJ Strike	8	1	0	75	**84**
26	upper Snake	Upper Salmon Falls	0	0	0	96	**96**
W	Willamette	Santiam	0	0	0	14	**14**
	Outside Columbia	Nechako River	0	0	0	5	**5**
	Outside Columbia	Sacramento-San Joaquin River	6	0	0	3	**9**
	Outside Columbia	Fraser River	0	0	0	10	**10**

3051
3052
3053 **Discussion:**
3054 Our research is guided by previous results which indicate that white sturgeon in the Middle
3055 Columbia River have experienced a significant genetic bottleneck and decreased diversity as a
3056 result of dramatically restricted migration, altered flow regimes, and loss of spawning and
3057 rearing habitat. In addition, little to no genetic differentiation between impoundments in the
3058 Middle Columbia River has been observed, although a regional distinction between Snake River
3059 and Columbia River populations is evident (Matala et al. 2017). The accumulation of genetic
3060 monitoring results (2008-2018) for White Surgeon in the Middle Columbia River and Snake
3061 River are similar to evaluations of population structure reported for similar large systems like the
3062 Fraser River in British Columbia Canada. Current demographic trends and genetic variation may
3063 be a consequence of diminished rearing and/or spawning habitat coincident with stream
3064 fragmentation and limited connectivity. Ongoing efforts for this project are designed to further
3065 resolve the dynamics of recruitment and population demographic trends in the context of
3066 regional population structure and local adaptation and evolutionary potential, particularly in the
3067 John Day and Grand Coulee Reservoirs, where Tribal efforts are underway to identify efficient
3068 stock supplementation techniques (Table 69).
3069 To this end, a robust parentage baseline will provide confident estimates of the size of spawning
3070 populations (i.e. numbers of adults contributing to recruitment) based on levels of kinship among
3071 juvenile age groups. However, one of the ongoing challenges with this objective is the nature of
3072 genetic data from white sturgeon. Although technically octoploid (8 of each chromosome),
3073 following an evolutionarily recent genome duplication from an putatively tetraploid ancestral
3074 state (4 copies of each chromosome), the white sturgeon appears to have regained a functional
3075 tetraploid status, as indicated by the mendelian segregation of four alleles at the majority of SNP
3076 loci (**Figure 49**). Nonetheless, while the optimization of markers accurately rendering genotypes

3077 of the functional tetraploid chromosomal segments empowers our ability to glean information
3078 about population genetic structure and diversity, the majority of statistical parentage programs
3079 remain designed to process only diploid data (two copies of each chromosome, like humans).
3080 While we have garnered some success in identifying likely parent candidates using ad hoc (e.g.
3081 mismatch distribution) methods (**Figure 50**), we continue to develop and explore more robust
3082 methods to fully utilize the information content of tetraploid genotypes.
3083 Robust information on recruitment dynamics will be valuable to managers concerned with
3084 reversing decreasing trends in productivity, and in hatchery operations focused on maximizing
3085 genetic variation and family contributions in supplementation or translocation programs.
3086 Distance and numbers of barriers that currently sequester populations in the Snake River region
3087 and Middle Columbia may profoundly influence genetic variability. Some of the highest levels
3088 of genetic diversity in our long-term analyses were observed in the Lower Columbia River
3089 population of relatively high abundance. However, where historical migration between regions
3090 has been restricted, the effective isolation of larger and older mature fish means the opportunities
3091 for populations to repopulate or recolonize will take decades following recruitment. Therefore,
3092 understanding the origins and abundances of local spawners is vital for estimating demographic
3093 trends, the potential to improve genetic variability, and the efficacy of supplementation.
3094 Targeting of both YOY and older (mature) fish will continue in subsequent years to allow for
3095 implementation of additional kinds of proposed analyses defined in the overall objectives of this
3096 project.
3097 In addition, our continuing efforts with white sturgeon include the development of a draft
3098 genome assembly. While extensive whole genome data has provided draft contig sequences, the
3099 majority of the genome remains insufficiently anchored for publication due to the challenges of
3100 scaffolding a high repetitive (octoploid) genome. To overcome this, we are working closely with
3101 collaborators to generate a linkage map from a reduced ploidy line of white sturgeon, which will
3102 assist to order or orient (anchor) smaller scaffolds into chromosomes. The draft genome, once
3103 complete, will allow us to use genome-level sequencing data to survey genetic variants
3104 underlying phenotypic traits and local adaptation, a type of analysis that the lab has had
3105 extensive success completing for other Columbia Basin species (e.g. Micheletti et al. 2018).
3106 Since White Sturgeon are long lived and require many years to reach sexual maturity, the value
3107 of data generated by this project are largely defined by the project's long-term implementation. It
3108 began in 2008 and continues to present, with samples collected and archived on an annual basis.
3109 Among other things, this affords the opportunity to monitor cohorts through various age-classes
3110 or life history stages. It also provides more robust analysis as data accumulates. For example,
3111 fish that were sampled as subadults in 2008 are reaching (or have reached) sexual maturity and
3112 are available to screen as potential parents of juvenile fish sampled in recent or upcoming years.
3113 Work on our most current objective (genome sequencing to discover a sex-linked marker for
3114 gender ID) has only just begun, and we anticipate long-term applicability of the data produced,
3115 particularly with continued collaborations and data sharing with co-managers in the basin.
3116
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3204
3205

3206
Overall Conclusion
3208
3209   This project combines four inter-related studies from the Fish & Wildlife Program
3210 Accords that address the following current and future objectives: 1) discover and evaluate SNP
3211 markers in salmon and steelhead and other anadromous fishes; 2) expand and create genetic
3212 baselines for multiple species including Chinook salmon, steelhead, sockeye salmon and
3213 kokanee, and coho salmon; 3) implement Genetic Stock Identification (GSI)/PBT programs for
3214 mainstem Chinook salmon, sockeye salmon, and steelhead fisheries and 4) GSI/PBT of fish
3215 passing Bonneville Dam (steelhead, sockeye, and Chinook salmon).
3216   As described in Section 1, SNP panels continue to be expanded with GTseq that enables
3217 genotyping large sample sizes (>157,000 fish genotyped in 2019). This genotyping protocol has
3218 greatly increased our laboratory's efficiency by allowing large numbers of fish to be genotyped
3219 with large numbers of SNP loci but at lower costs. For genetic baseline expansion (Objective 2),
3220 PBT hatcheries above Bonneville were genotyped to enable more thorough assignment of
3221 hatchery origin fish. In addition, GSI baselines are being developed with whole genome
3222 resequencing to provide allele frequency estimates for millions of SNPs in Chinook salmon and
3223 steelhead. SNPs identified through current efforts involving whole genome resequencing will be
3224 useful in characterizing genetic diversity of hatchery and wild Chinook salmon and steelhead
3225 stocks. This study included two broad applications of stock identification; namely, stock
3226 composition of fisheries for Chinook salmon, sockeye salmon, and steelhead (Objective 3), and
3227 stock composition of Chinook salmon, sockeye salmon, and steelhead passing Bonneville Dam
3228 (Objective 4). Chinook salmon and steelhead fishery applications of GSI were integrated with
3229 the new genetic technology of parentage based tagging (PBT). The challenge imposed by long
3230 histories of exogenous stock transfers from specific hatchery programs often prevents effective
3231 application of GSI in assigning hatchery fish. However, as the role of PBT is expanding to tag all
3232 hatchery fish, the role of GSI will be focused on identifying stocks of natural-origin fish.
3233   Our GSI analyses of harvest included stock composition results for the spring, summer,
3234 and fall management periods of Chinook salmon fisheries in the lower Columbia River
3235 mainstem. Sockeye salmon fisheries were analyzed and our stock composition results will
3236 provide additional information to managers of these fisheries. However, the sockeye salmon
3237 results indicate an increase in sample size may be warranted to make accurate estimates of rare
3238 stocks such as Snake River sockeye salmon.
3239   For Objective 4, we used a combination of GSI and PBT to estimate run-timing
3240 distributions and relative abundance of hatchery and wild Chinook salmon and steelhead stocks
3241 in 2019. For sockeye salmon, we used GSI to estimate relative stock abundance and run-timing
3242 distributions. The stock-specific data on abundance and run-timing of these species were used as
3243 a context for interpreting harvest stock composition. We continue timely post-season reporting of
3244 genetic analysis of Chinook, steelhead and Sockeye Salmon at Bonneville Dam in 2019, but we
3245 also continue to provide in-season results at bi-weekly intervals during the spring and summer
3246 management periods of Chinook Salmon, and approximately monthly for the summer and fall
3247 runs of steelhead and Chinook Salmon. The timely updates of the genetic analyses for these runs
3248 and species of Columbia River fishes improves their utility for fisheries managers such as the
3249 Technical Advisory Committee (TAC).
3250   For Objective 5 on local adaptation, candidate genes for several traits have been
3251 identified in both steelhead and Chinook salmon. As these candidate genes for traits have begun

3252 to be identified, SNP markers from these regions are being incorporated in standard genotyping
3253 panels with GTseq to validate and monitor genetic variation for these traits in large numbers of
3254 individuals. Inclusion of candidate markers associated with specific traits allows more detailed
3255 genetic monitoring of stocks in the Columbia Basin. Extensive programs are in place that enable
3256 genetic identification of the origin of individual fish, but candidate markers from this study also
3257 provide the ability to monitor genetic variation for specific traits that are expected to be
3258 necessary to maintain life history variation for long term persistence of populations.
3259   For Objective 6 on white sturgeon genetics, the accumulation of genetic monitoring
3260 results (2008-2018) for White Surgeon in the Middle Columbia River and Snake River are
3261 similar to evaluations of population structure reported for similar large systems like the Fraser
3262 River in British Columbia Canada. Current demographic trends and genetic variation may be a
3263 consequence of diminished rearing and/or spawning habitat coincident with stream
3264 fragmentation and limited connectivity. Ongoing efforts for this project are designed to utilize
3265 SNP markers that were developed for this species to further resolve regional population structure
3266 and parentage analyses to support tribal efforts to supplement white sturgeon in the Columbia
3267 Basin.