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Evaluating the genetics of naturally produced Chinook salmon (*Oncorhynchus tshawytscha*) captured in the Lower Rogue River (OR) in 2020

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Evaluating the genetics of naturally produced Chinook salmon (*Oncorhynchus tshawytscha*) captured in the Lower Rogue River (OR) in 2020

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INTRODUCTION

In the Rogue basin, the Oregon Department of Fish and Wildlife (ODFW) treats spring and fall Chinook salmon (*Oncorhynchus tshawytscha*) as distinct species management units (SMUs). Spring Chinook salmon in the lower river are defined as those adult Chinook salmon that enter freshwater during the period from February through mid-July. The goals and strategies for managing Rogue River spring Chinook salmon are documented in the Rogue Spring Chinook Salmon Conservation Plan which was adopted by the ODFW Fish and Wildlife Commission on September 7, 2007 and updated in 2019.

ODFW's management strategy for the spring Chinook salmon fishery in the Lower Rogue River is to protect natural-origin early run "spring" Chinook salmon while providing harvest opportunity on hatchery (i.e. adipose fin removed) spring Chinook salmon. To achieve this, regulations prohibit retention of naturally produced (i.e. adipose fin intact) Chinook salmon prior to June 1 from the river mouth upstream to Fishers Ferry boat ramp (old Gold Ray dam site). When the population reaches levels of abundance that meet desired status levels in the conservation plan, additional harvest opportunity will be provided on naturally produced fish.

As a result of improved returns of spring Chinook salmon following plan adoption, ODFW proposed a framework for providing additional fishery opportunities if population abundance continues to increase, even if abundance is below desired status. The proposed regulation changes would shift the date at which naturally produced Chinook salmon can be retained from June 1 to May 21, May 11, or April 1 (date and bag limit tied to abundance trigger – see pg. 32 in the updated plan for details).

Since the plan has been adopted and updated, there have been significant advances in our understanding of the genetic basis of adult run timing in anadromous salmonids. Several studies have reported that variation at a single genomic region on chromosome 28 has a strong statistical association with various measures of adult migration phenotypes in Chinook salmon and steelhead (*O. mykiss*) populations from coastal California and Oregon to the interior Columbia River, the Strait of Juan de Fuca, and Puget Sound (reviewed in Waples *et al.* 2022). In Rogue River Chinook salmon, two single nucleotide polymorphisms (SNPs) located between two genes, *greb1l* and *rock1*, on chromosome 28 appear to be highly diagnostic for adult run timing (Thompson *et al.* 2019). Spring Chinook salmon have two copies of the "early" run allele (homozygous spring) while fall Chinook salmon have two copies of the "late" run allele (homozygous fall). Chinook salmon that have one copy of the "early" run allele and one copy of the "late" run allele (heterozygous) tend to have intermediate run timing (Thompson *et al.* 2019).

These adult run timing genetic markers provide a useful tool to evaluate the effectiveness of management actions with respect to the metrics described in the Rogue Spring Chinook Salmon Conservation Plan. For example, to assess how angling regulations align with the genetic composition of Chinook salmon in the Lower Rogue River fishery, O'Malley *et al.* (2020a) genotyped 158 Chinook salmon caught from March 19 to July 8 in 2019 and reported that the

majority (~84%) of the naturally produced homozygous spring Chinook salmon were captured prior June 1, when retention is prohibited. In another study, O'Malley *et al.* (2020b) used the adult run timing markers to evaluate the spatial and temporal patterns of "early" and "late" run alleles across the entire spawning period of Chinook salmon in the Upper Rogue River (river kilometer 202.0-252.7; river mile 125.5-157) and reported significant temporal and spatial separation between homozygous spring and homozygous fall Chinook salmon, and, to a lesser extent, between homozygous spring and heterozygous fish. Furthermore, these genetic markers were also used to assess the genetic composition of a subsample of the spring Chinook salmon broodstock at the Cole M. Rivers Hatchery (CRH) in 2018. Results indicated that the majority (~88%) of the broodstock sampled were homozygous spring with four homozygous fall Chinook salmon collected after August 18 (O'Malley *et al.* 2020b). In 2020 and 2021 when the return of hatchery spring Chinook salmon was very low, a near real-time genotyping approach was implemented to incorporate an additional 106 and 40 Chinook salmon in 2020 and 2021, respectively into the CRH spring Chinook broodstock program while excluding homozygous fall Chinook salmon (O'Malley *et al.* 2022).

To expand on O'Malley *et al.* (2020a), ODFW collected samples from naturally produced Chinook salmon in the Lower Rogue River in 2020 using three approaches: volunteer anglers, creel surveys, and seining.

Objectives

1. Determine the genetic composition, based on two adult run timing markers, of naturally produced Chinook salmon captured in the Lower Rogue River in 2020.

2. Compare the 2020 results to those reported for naturally produced Chinook salmon captured in the Lower Rogue River in 2019 (O'Malley *et al.* 2020a).

METHODS

Sampling

Fin clips or operculum punches were taken from unmarked, presumed naturally produced Chinook salmon sampled in the Lower Rogue River by volunteer anglers, creel surveys, and seining from April 5 to September 30, 2020. Sample locations ranged from Rogue Bay upstream to Quosatana Creek (Figure 1).

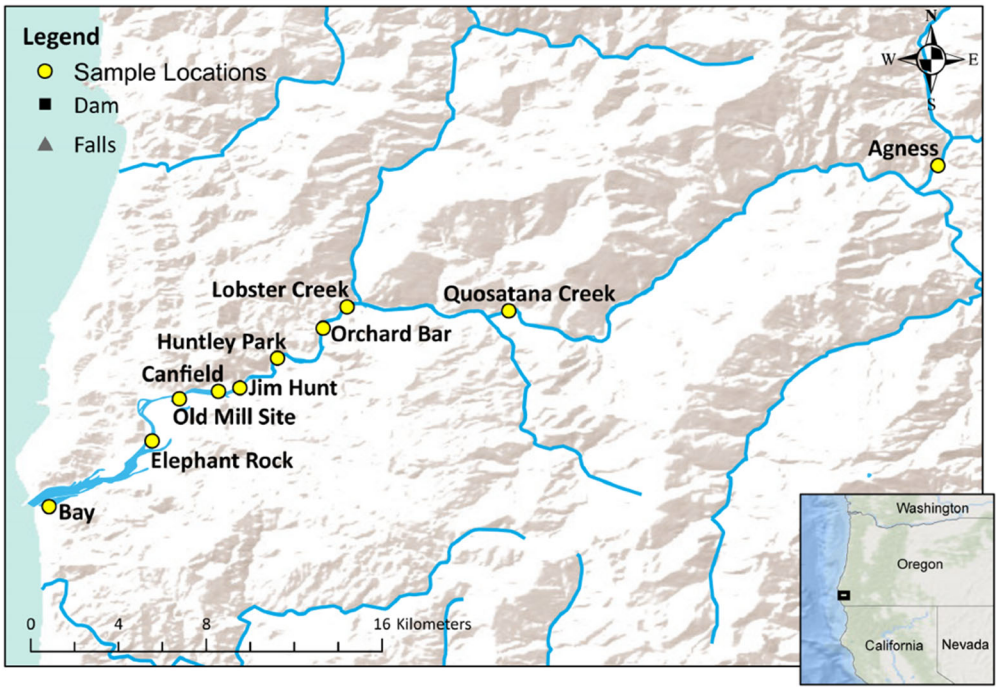

Figure 1. Map of the sample locations in the Lower Rogue River, Oregon. Samples were not collected at Canfield, Jim Hunt, Orchard Bar or Agness in 2020.

Volunteer anglers were asked to take tissue samples from any unmarked, presumed naturally produced Chinook salmon beginning March 2, 2020. Volunteer anglers were issued sampling kits containing written instructions, individually labeled vials containing ethanol, and a paper hole punch for extracting caudal fin tissue. Additionally, the kits contained the following instructions:

- Minimize handling (keep fish in net on side of boat and close to the water surface)
- Work with a partner (one person holds fish, other holds net and collects sample)
- Use paper hole punch to extract fin tissue sample from caudal fin (imagine the tail fin is a piece of paper)
- Gently release fish back into river
- Very carefully remove tissue sample from the hole punch's "chip guard" and place into sample vial. Be sure that sample is completely immersed in the liquid and close the cap snugly.
- Place vial into resealable bag. With a sharpie, record date, angler (collector), and location on bag's exterior.
- Rinse the hole punch in clean water
- Store sample in safe place away from heat for the duration of the fishing trip
- Drop samples off with Gold Beach ODFW staff directly or at one of the five Drop boxes* and then notify ODFW

*Drop boxes were located at Rogue Outdoor Store, ODFW Gold Beach office, Mill Site, Lobster Creek Campground, and Quosatana Creek Campgrounds.

The Drop boxes were set up prior to March 1. ODFW staff collected samples from the boxes daily, or, at a minimum, weekly during the study period. The returned sample vials were organized chronologically and stored at the Gold Beach ODFW office for the duration of the project. All samples were stored at room temperature away from sunlight. The ethanol in each vial was replaced one week after samples were collected. At that time, each vial was labeled externally with a sample-ID number. Additionally, a small piece of Rite-in-the-Rain paper with the sample-ID number recorded with pencil was placed inside the vial with the tissue sample. Data records for each sample were entered into an Excel spreadsheet and included sample-ID number, collection date, collection area, collector, and collection method. All volunteer angler-caught individuals were sampled from April 5 to June 20.

Creel survey samples were taken from the fish cleaning station at the Port of Gold Beach and all samples were reported to have been captured in the Bay from July 8 to July 19. Seined individuals were sampled by ODFW staff at Huntley Park from July 21 to September 30.

Environmental Data

Rogue River discharge and temperature data were collected from the United States Geological Survey (USGS) National Water Information System. Data were downloaded from monitoring station 14372300 near Agness, OR in 15-minute intervals through 2019 and 2020 and daily mean values were calculated for each variable.

Genotyping

Tissue samples were transferred to the State Fisheries Genomics Lab in Newport, OR where DNA was extracted from fin clips or operculum punches using the method of Ivanova *et al.* (2006). Using the Genotyping-in-Thousands by sequencing method (GT-seq; Campbell *et al.* 2015), all samples were genotyped at 353 single nucleotide polymorphisms (SNPs) (Hess *et al.* 2016), including a sex marker and two adult run timing SNPs (Ots37124_12277401 and Ots37124_12310649) that are ~33 kb apart on the Otsh_v1.0 (GCA_002872995.1) genome assembly, and located in the intergenic region between *greb1l* and *rock1*. These latter two SNPs are hereafter referred to as *greb1l* SNP1 and SNP2, respectively. In Rogue River and Klamath River populations of Chinook salmon, *greb1l* SNP1 is reportedly more diagnostic of adult migration phenotype than *greb1l* SNP2 (T. Thompson, pers. comm.).

The genotyping protocol followed Campbell *et al.* (2015), except the second polymerase chain reaction (PCR) used Ultra II Q5 master mix (New England Biolabs) to add i5 and i7 adapters. Negative and positive controls, as well as replicates were genotyped. Amplicons were sequenced on an Illumina NextSeq500 at the University of Oregon Genomics & Cell

Characterization Core Facility. We used modified genotyping scripts previously developed by Campbell *et al.* (2015), which are available at https://github.com/State-Fisheries-Genomics-Lab/GT-seq/tree/main/GT-seq_scripts. Genotype quality control was assessed using fastqc, replicate samples and negative controls.

Briefly, we filtered genotypes based on missingness, sample duplication and the individual fuzziness index (IFI), which estimates the amount of cross-contamination in each individual. We also removed sites with poorly calibrated allele correction values or more than three clusters of allele ratios suggestive of a paralogous sequence variant. We took an iterative approach to missingness and IFI filtering and recalculated missingness for all individuals and genotypes between each step (O'Leary *et al.* 2018). We began filtering by removing negative controls and replicate individuals (retained replicate with highest number of on-target reads). Then we removed individuals with more than 30% missing data, then SNPs with greater than 50% data, and individuals with IFI greater than 10 (i.e., greater than 10% putative background reads). In our second round of filtering, we removed individuals with more than 10% missing data, then removed SNPs with greater than 20% missing data, and individuals with IFI greater than 2.5. We then examined any SNP with greater than 10% missing data and skewed or high variance in allele ratios among uncalled and heterozygous samples by plotting corrected read counts of alternative alleles. SNPs with a strong bias towards one allele among heterozygotes, more than three clusters of allele ratios, or indistinct clusters of allele ratios were removed from the dataset. After genotype quality filtering was complete, we removed monomorphic loci. Of the 353 SNPs genotyped, we focused on only *greb1l* SNP1 and SNP2 for this report.

We also estimated the degree of dominance (D_F) at *greb1l* SNP1. D_F is a metric that describes the deviation of the heterozygous phenotype from that under complete additivity and is provided by the equation below.

$$D_F = \frac{z_{het} - \bar{z}}{z_{spring} - \bar{z}}$$

Where z_{het} is the average phenotype (Julian day of sampling) of the heterozygote, z_{spring} is the average phenotype of the spring homozygote, and $\bar{z}$ is the midpoint between the spring and fall homozygote phenotype. A value of 1 denotes complete dominance of the spring allele, while a value of -1 denotes complete dominance of the fall allele and a value of 0 denotes additivity between the two alleles.

RESULTS

Sample Collection

Volunteer anglers sampled 67 unmarked, presumed naturally produced Chinook salmon throughout the Lower Rogue River. Twelve individuals were sampled in Rogue Bay through creel surveys and 132 individuals were sampled at Huntley Park through seining (Table 1). In

contrast to 2019, there were no highwater events and samples were collected from volunteer anglers consistently from April 5 to June 20 (Figure 2).

	Sampling Method		
	Angler, N = 67	**Creel Survey**, N = 12	**Seine**, N = 132
Location			
Rogue Bay	0 (0%)	12 (100%)	0 (0%)
Elephant Rock	4 (6.0%)	0 (0%)	0 (0%)
Mill Site	16 (24%)	0 (0%)	0 (0%)
Huntley Park	0 (0%)	0 (0%)	132 (100%)
Lobster Creek	25 (37%)	0 (0%)	0 (0%)
Quosatana	22 (33%)	0 (0%)	0 (0%)
Age			
Adult	67 (100%)	7 (58%)	132 (100%)
Jack	0 (0%)	5 (42%)	0 (0%)

Table 1. Number of samples (N) collected based on the sampling method and location. Number of samples (N) collected from adult or jack salmon. Chinook salmon less than 575 mm fork length were identified as jacks.

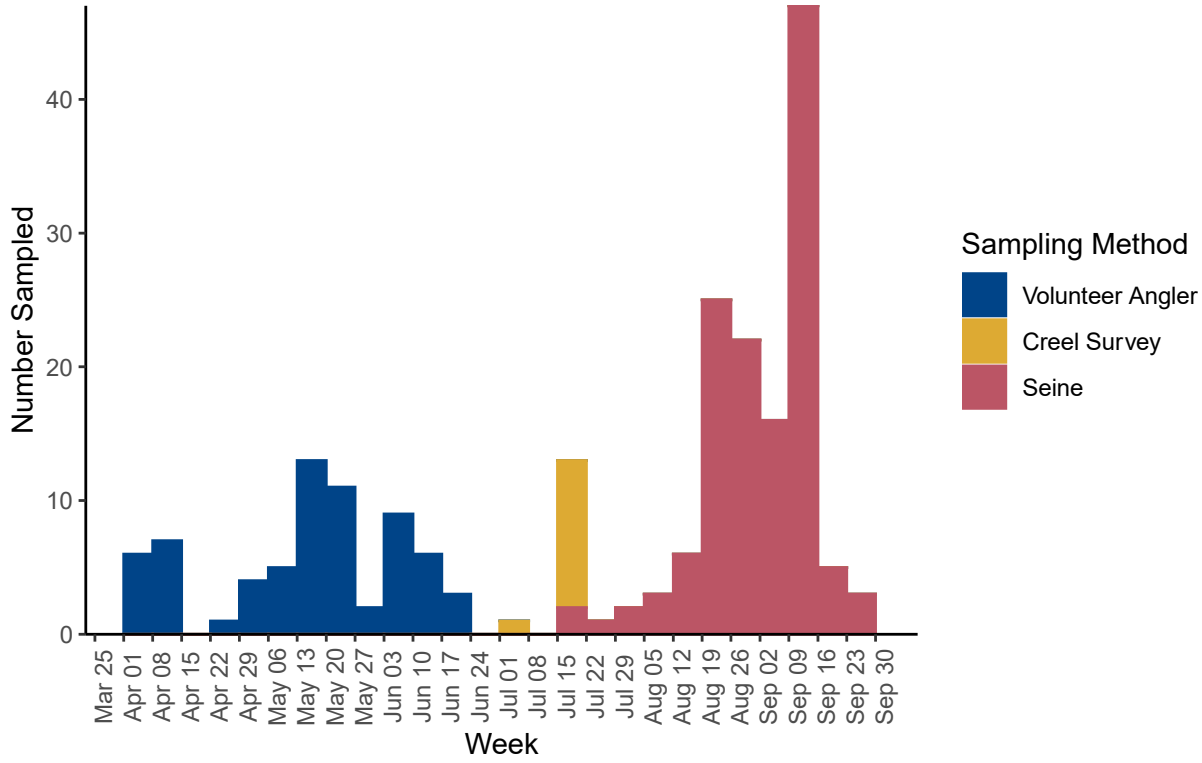

Figure 2. Number of individuals sampled by volunteer anglers, creel survey (cleaning station) or seine. Counts are binned into weeklong intervals bounded by dates on the x-axis.

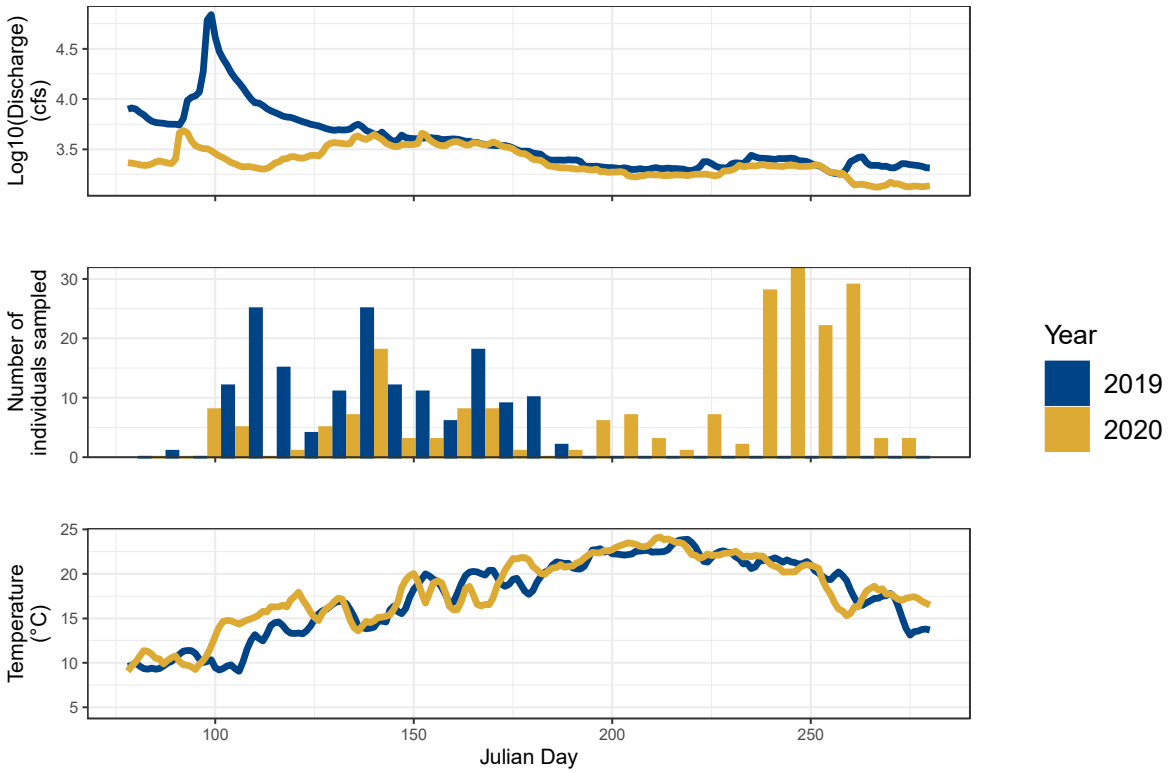

Figure 3. Average daily discharge (Log10 transformed cubic feet per second (cfs)) and river temperature (°C) at USGS Agness gauge (number 14372300), and number of Chinook salmon sampled by anglers binned into weeklong intervals in 2019 (O'Malley *et al.* 2020a)(blue) and 2020 (yellow).

Genotyping

Two of the 211 samples were excluded during filtering. Of the remaining 209 samples, 49 samples were genotyped homozygous spring, 35 samples were genotyped heterozygous, 121 samples were genotyped homozygous fall and four samples had discordant genotypes across the two *greb1l* SNPs (Table S1, Figure 3). Discordant genotypes are those that disagree at *greb1l* SNP1 and SNP2.

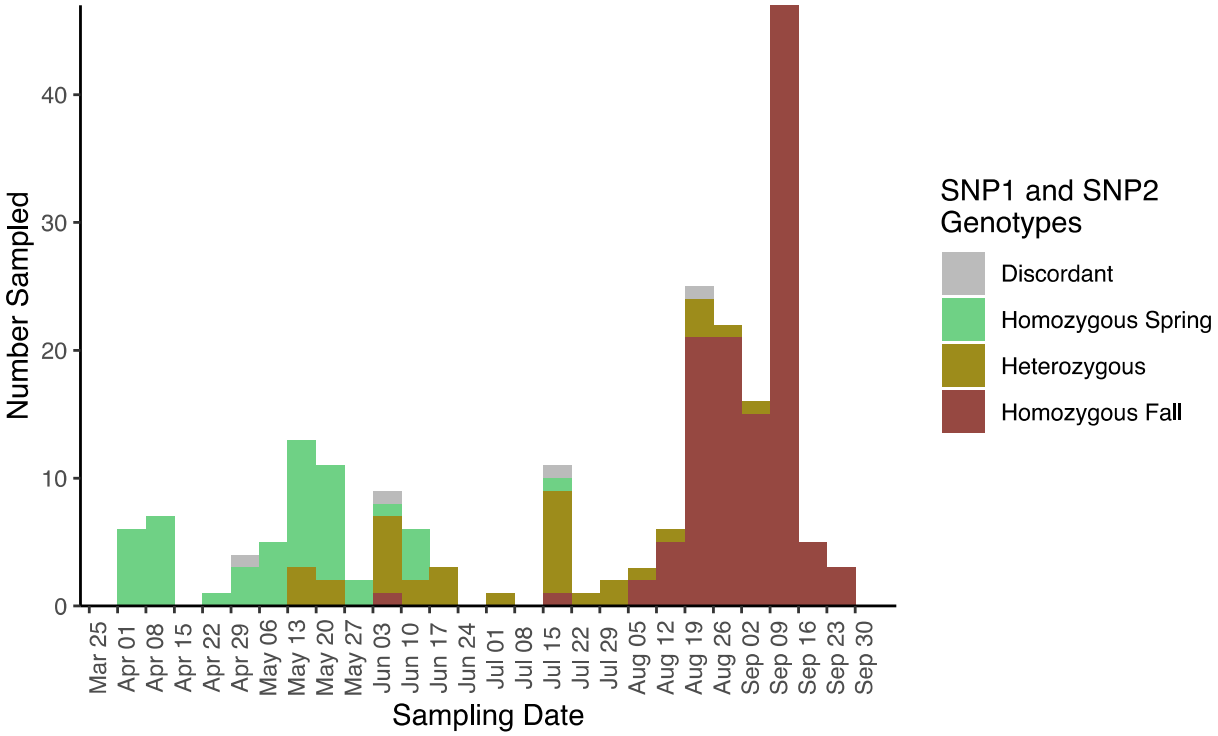

Figure 4. Number of individuals sampled in 2020 with homozygous spring, heterozygous, homozygous fall, and discordant genotypes at *greb1l* SNP1 and SNP2 binned into weeklong intervals bounded by the dates on the x-axis. Discordant genotypes are those that disagree at *greb1l* SNP1 and SNP2.

Focusing only on *greb1l* SNP1, 50 individuals were genotyped homozygous spring, 37 were genotyped heterozygous, and 122 were genotyped homozygous fall (Figure 5). The first heterozygous sample was collected on May 5. The first homozygous fall sample was collected on June 9. Samples shifted from majority homozygous spring to majority heterozygous in the period from June 3 to June 10 and from majority heterozygous to majority homozygous fall in the period from August 5 to August 12. July 19 was the last day that a homozygous spring individual was observed, and September 4 was the last day that a heterozygous individual was observed.

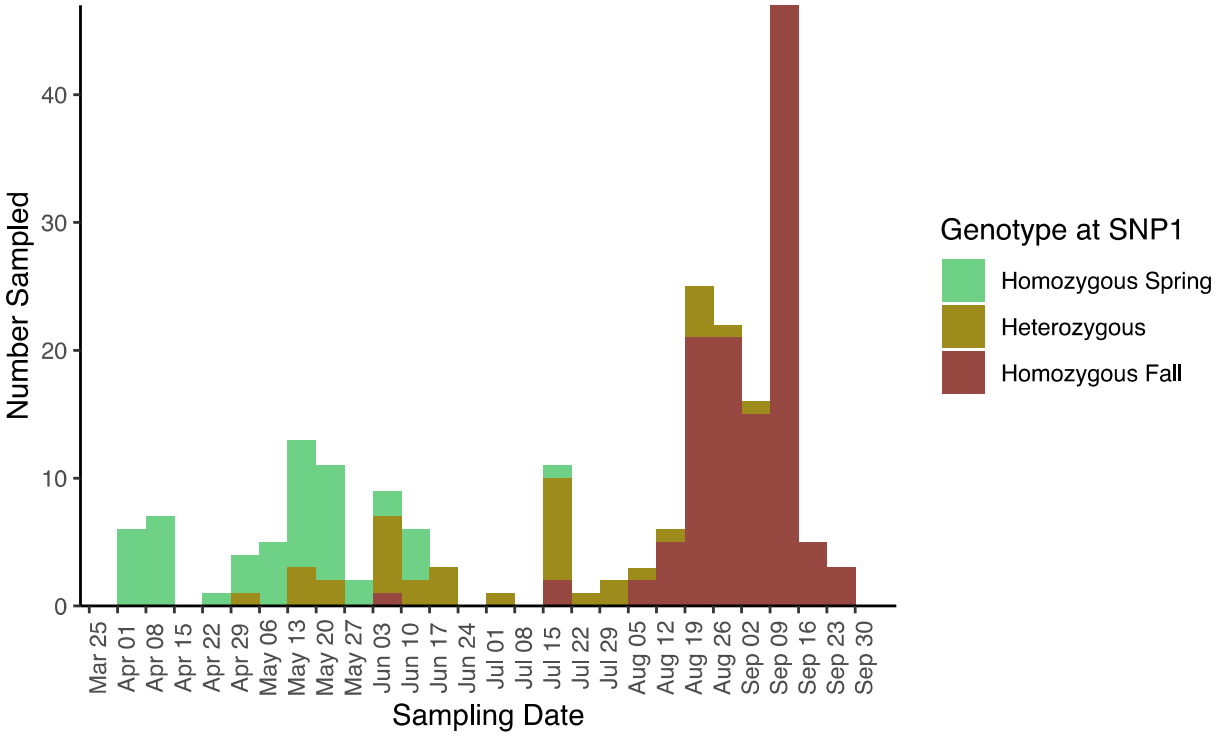

Figure 5. Number of individuals sampled in 2020 with homozygous spring, heterozygous, and homozygous fall genotypes at *greb1l* SNP1 binned into weeklong intervals bounded by the dates on the x-axis.

The mean sampling date of homozygous spring, heterozygous, and homozygous fall individuals at *greb1l* SNP1 was May 12, July 6 and September 4, respectively (Figure 6). The midpoint between mean homozygous spring and homozygous fall sampling date was July 8, corresponding to a degree of dominance of 0.038 for the “early” run allele.

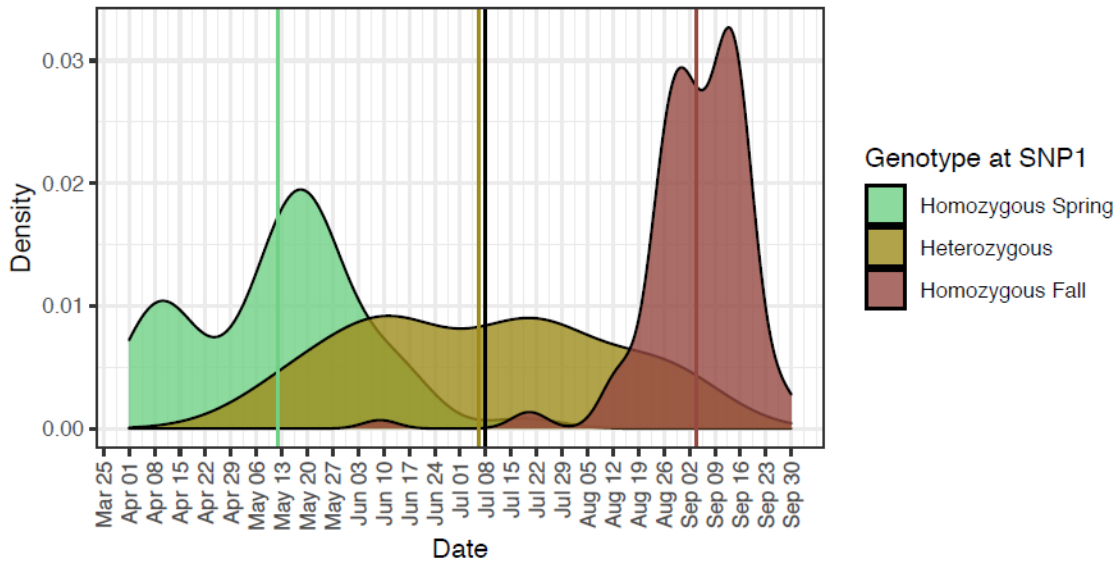

Figure 6. Density plot of sampling date across genotypes at *greb1l* SNP1. Mean sampling date for each genotype displayed as vertical line in corresponding color, black vertical line is the midpoint between mean sampling dates of the two homozygous genotypes.

Given the absence of any evidence of strong dominance of the "early" or "late" run allele, we also considered the cumulative proportion of observed "early" run alleles in the dataset (Figure 7).

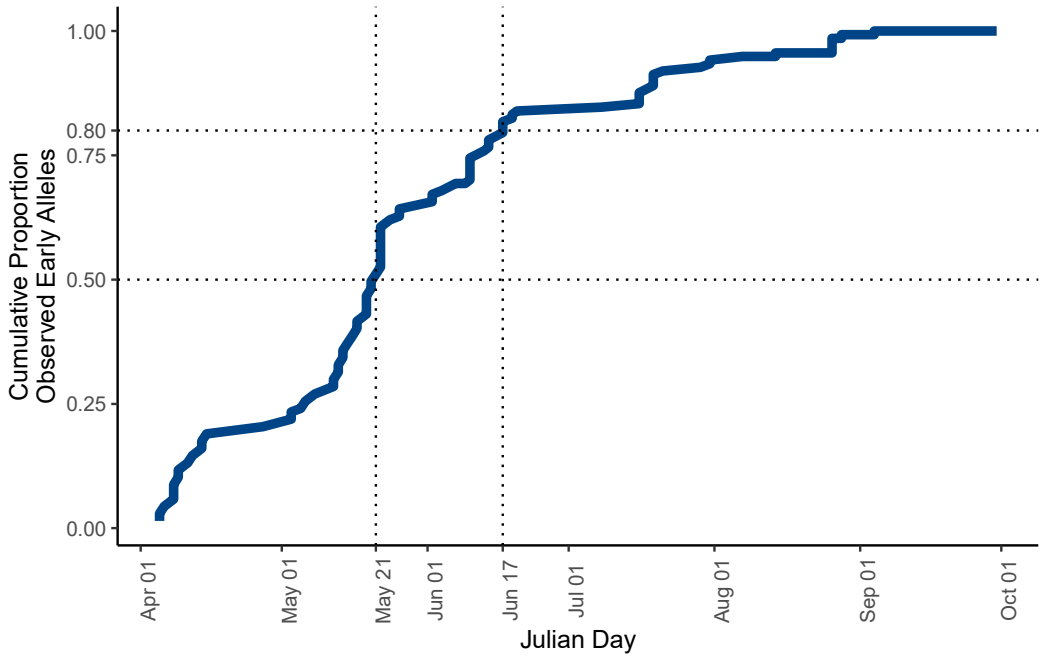

Figure 7. Cumulative proportion of all "early" run alleles observed by date with milestones at 50% and 80% of total number of "early" run alleles highlighted.

DISCUSSION

Here we provide the second consecutive year of results for Chinook salmon caught in the Lower Rogue River, revealing relationships between adult run timing and genotypes at two SNPs. Sampling effort was expanded in 2020 to include creel surveys and seining in addition to volunteer anglers, which was the only approach used in 2019. With this increased effort, samples were collected up until September 30, 2020, whereas sampling ended on July 8 in 2019. As a result, 211 naturally produced Chinook salmon were sampled in 2020 compared to 162 naturally produced Chinook salmon in 2019.

In summarizing the findings, it is important to acknowledge that the values reported here are likely affected by an uneven distribution of sampling effort over time. For example, milestones such as the first and last dates at which certain genotypes are observed are sensitive to effort. Increased sampling effort will generally lead to earlier first observations and later last observations of genotypes until sample size approaches census size, and uneven sampling effort through time will bias one observation more than the other.

Based on *greb1l* SNP1, the majority of naturally produced homozygous spring Chinook salmon (82%; 41 out of 50 fish) genotyped in this study were captured during the period when retention of unmarked Chinook salmon was prohibited (April 5-May 31). The remaining nine homozygous spring Chinook salmon were captured between June 2 and July 19. During this same period, 19 heterozygous and two homozygous fall fish were caught by anglers or sampled at the cleaning station. The majority of naturally produced Chinook salmon collected at Huntley Park from July 21 to Sept 30 were homozygous fall Chinook salmon (91%; 120 out of 132 fish). The remaining fish were heterozygous at *greb1l* SNP1. It is important to note that heterozygous fish may serve as a potential reservoir for "early" run alleles.

In both years, more than 80% of the fish sampled prior to June 1 were homozygous spring Chinook salmon based on *greb1l* SNP1. It is important to note that in 2019, 37% (19 out of 52 fish) of the naturally produced Chinook salmon sampled from June 1 to July 8, the last day of sample collection, were homozygous spring. Similarly in 2020, 38% (eight out of 21 fish) of the naturally produced Chinook salmon sampled during the same period were homozygous spring.

The migration timing expressed by fish with homozygous spring, heterozygous, and homozygous fall genotypes depends on the dominance pattern of *greb1l* SNP1 and linked genetic variants. Complete dominance of "early" run alleles would lead to heterozygotes expressing the same phenotype as homozygous spring fish. In contrast, under complete

additivity, heterozygotes express intermediate adult migration timing relative to homozygous spring and homozygous fall fish.

Our results suggest a completely additive model is a close fit to the data. The mean sampling date of heterozygotes is intermediate between the two homozygotes (i.e. only about two days earlier than the exact midpoint between the mean homozygous spring and homozygous fall). However, individuals may hold in the lower river resulting in a potential disconnect between sampling date and freshwater entry timing thus reducing our confidence in this estimate (Waples *et al*. 2022).

Assuming a completely additive model, we could pay particular attention to escapement of "early" run alleles rather than the genotype (i.e. – homozygous v. heterozygous) of individuals. From this perspective, half of all "early" run alleles at *greb1l* SNP1 in the dataset are observed by the third week of May and 80% of all "early" run alleles are observed by the third week of June. When the population reaches conservation status or faces uncertain river conditions, harvest could be delayed to the third week of June to protect the "early" run allele. As stated above, this observation is sensitive to uneven sampling effort over time, and the time at which these thresholds are crossed in the river may vary from these estimates.

ACKNOWLEDGMENTS

We appreciate the effort from all participating anglers. Without your contributions, this project would not have been as successful. We thank the University of Oregon Genomics & Cell Characterization Core Facility for DNA sequencing the Rogue River Chinook salmon samples and the Oregon State University Center for Quantitative Life Sciences for use of the computational infrastructure. This report benefitted from review by Peter Stevens, Marc Johnson, and Dan Van Dyke of ODFW. K. O'Malley used startup funds to conduct this research.

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SUPPLEMENTAL INFORMATION

Sample	Date	Julian Day	Location	Detailed Location	Sampling Method	Ots37124-12277401	Ots37124-12310649	*greb1l* SNP1 Genotype	*greb1l* SNP2 Genotype	Two SNP Genotype
OtsAC20ROGR_0001	4/5/20	96	Quosatana	Quosatana	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0002	4/5/20	96	Quosatana	Quosatana	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0003	4/6/20	97	Port	Elephant Rock	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0004	4/8/20	99	Quosatana	Quosatana	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0005	4/8/20	99	Mill Site	Willows	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0006	4/8/20	99	Mill Site	Willows	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0007	4/9/20	100	Lobster Creek	Dunk	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0008	4/9/20	100	Quosatana	Cole Riffle	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0009	4/11/20	102	Lobster Creek	Shallow Riffle	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0010	4/12/20	103	Mill Site	Elephant Rock	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0011	4/14/20	105	Quosatana	Cole Riffle	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0012	4/14/20	105	Quosatana	Cole Riffle	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0013	4/15/20	106	Lobster Creek	Lobster	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0014	4/27/20	118	Lobster Creek	Dunk	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0015	5/3/20	124	Lobster Creek	Lobster	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0016	5/3/20	124	Mill Site	Snag Patch	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0017	5/5/20	126	Lobster Creek	Dunk	angler	TA	AA	heterozygote	homozygous_spring	discordant
OtsAC20ROGR_0018	5/6/20	127	Mill Site	Clay Banks	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0019	5/8/20	129	Mill Site	226	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0020	5/12/20	133	Quosatana	226	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0021	5/12/20	133	Mill Site	Clay Banks	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0022	5/13/20	134	Lobster Creek	Lobster	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0023	5/13/20	134	Lobster Creek	Lobster	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0024	5/14/20	135	Mill Site	Elephant Rock	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0025	5/14/20	135	Mill Site	Willows	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0026	5/15/20	136	Mill Site	Elephant Rock	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0027	5/16/20	137	Mill Site	Willows	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0028	5/17/20	138	Mill Site	226	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0029	5/17/20	138	Lobster Creek	Lobster	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0030	5/17/20	138	Lobster Creek	Lobster	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0031	5/19/20	140	Quosatana	Quosatana	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0032	5/19/20	140	Port	Elephant Rock	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0033	5/19/20	140	Port	Elephant Rock	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0034	5/19/20	140	Lobster Creek	Lobster	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0035	5/20/20	141	Lobster Creek	Lobster	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0036	5/20/20	141	Port	Elephant Rock	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0037	5/21/20	142	Lobster Creek	Dunk	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0038	5/22/20	143	Lobster Creek	Lobster	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0039	5/22/20	143	Lobster Creek	Lobster	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0040	5/22/20	143	Lobster Creek	Dunk	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0041	5/22/20	143	Quosatana	Quosatana	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0042	5/22/20	143	Mill Site	Elephant Rock	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0043	5/22/20	143	Lobster Creek	Lobster	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0044	5/22/20	143	Lobster Creek	Lobster	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0045	5/24/20	145	Mill Site	Willows	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0046	5/26/20	147	Quosatana	Quosatana	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0047	5/26/20	147	Mill Site	Clay Banks	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0048	6/2/20	154	Lobster Creek	Lobster	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring

Sample	Date	Julian Day	Location	Detailed Location	Sampling Method	Ots37124-12277401	Ots37124-12310649	*greb1l* SNP1 Genotype	*greb1l* SNP2 Genotype	Two SNP Genotype
OtsAC20ROGR_0049	6/2/20	154	Lobster Creek	Lobster	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0050	6/4/20	156	Lobster Creek	Lobster	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0051	6/7/20	159	Quosatana	Quosatana	angler	TT	AT	homozygous_spring	heterozygote	discordant
OtsAC20ROGR_0052	6/9/20	161	Lobster Creek	Dunk	angler	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0053	6/10/20	162	Mill Site	Upper Rogue	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0054	6/10/20	162	Quosatana	Quosatana	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0055	6/10/20	162	Quosatana	Quosatana	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0056	6/10/20	162	Lobster Creek	Lobster	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0057	6/10/20	162	Lobster Creek	Lobster	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0058	6/10/20	162	Lobster Creek	Lobster	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0059	6/13/20	165	Quosatana	Quosatana	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0060	6/14/20	166	Quosatana	Quosatana	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0061	6/14/20	166	Quosatana	Quosatana	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0062	6/17/20	169	Quosatana	Quosatana	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0063	6/17/20	169	Quosatana	Quosatana	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0064	6/17/20	169	Quosatana	Quosatana	angler	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0065	6/19/20	171	Quosatana	Quosatana	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0066	6/19/20	171	Quosatana	Quosatana	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0067	6/20/20	172	Quosatana	Quosatana	angler	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0068	7/8/20	190	Rogue Bay	Rogue Bay	cleaning station	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0069	7/16/20	198	Rogue Bay	Rogue Bay	cleaning station	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0070	7/16/20	198	Rogue Bay	Rogue Bay	cleaning station	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0071	7/16/20	198	Rogue Bay	Rogue Bay	cleaning station	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0073	7/16/20	198	Rogue Bay	Rogue Bay	cleaning station	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0075	7/19/20	201	Rogue Bay	Rogue Bay	cleaning station	TT	AA	homozygous_spring	homozygous_spring	homozygous_spring
OtsAC20ROGR_0076	7/19/20	201	Rogue Bay	Rogue Bay	cleaning station	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0077	7/19/20	201	Rogue Bay	Rogue Bay	cleaning station	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0078	7/19/20	201	Rogue Bay	Rogue Bay	cleaning station	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0079	7/19/20	201	Rogue Bay	Rogue Bay	cleaning station	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0080	7/21/20	203	Huntley Park	Huntley Park	seine	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0081	7/21/20	203	Huntley Park	Huntley Park	seine	AA	AT	homozygous_fall	heterozygote	discordant
OtsAC20ROGR_0082	7/29/20	211	Huntley Park	Huntley Park	seine	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0083	7/31/20	213	Huntley Park	Huntley Park	seine	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0084	7/31/20	213	Huntley Park	Huntley Park	seine	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0085	8/7/20	220	Huntley Park	Huntley Park	seine	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0086	8/12/20	225	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0087	8/12/20	225	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0088	8/14/20	227	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0089	8/14/20	227	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0090	8/14/20	227	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0091	8/14/20	227	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0092	8/14/20	227	Huntley Park	Huntley Park	seine	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0093	8/19/20	232	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0094	8/21/20	234	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0095	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0096	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0097	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0098	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall

Sample	Date	Julian Day	Location	Detailed Location	Sampling Method	Ots37124-12277401	Ots37124-12310649	*greb1l* SNP1 Genotype	*greb1l* SNP2 Genotype	Two SNP Genotype
OtsAC20ROGR_0099	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0100	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0101	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0102	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0103	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0104	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0105	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0106	8/26/20	239	Huntley Park	Huntley Park	seine	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0107	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0108	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0109	8/26/20	239	Huntley Park	Huntley Park	seine	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0110	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0111	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0112	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0113	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0114	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0115	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0116	8/26/20	239	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0117	8/26/20	239	Huntley Park	Huntley Park	seine	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0118	8/26/20	239	Huntley Park	Huntley Park	seine	TA	TT	heterozygote	homozygous_fall	discordant
OtsAC20ROGR_0119	8/28/20	241	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0120	8/28/20	241	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0121	8/28/20	241	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0122	8/28/20	241	Huntley Park	Huntley Park	seine	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0123	8/31/20	244	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0124	8/31/20	244	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0125	8/31/20	244	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0126	8/31/20	244	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0127	8/31/20	244	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0128	8/31/20	244	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0129	8/31/20	244	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0130	8/31/20	244	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0131	8/31/20	244	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0132	8/31/20	244	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0133	8/31/20	244	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0134	8/31/20	244	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0135	8/31/20	244	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0136	8/31/20	244	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0137	9/2/20	246	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0138	9/2/20	246	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0139	9/2/20	246	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0140	9/2/20	246	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0141	9/4/20	248	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0142	9/4/20	248	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0143	9/4/20	248	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0144	9/4/20	248	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0145	9/4/20	248	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0146	9/4/20	248	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall

Sample	Date	Julian Day	Location	Detailed Location	Sampling Method	Ots37124-12277401	Ots37124-12310649	*greb1l* SNP1 Genotype	*greb1l* SNP2 Genotype	Two SNP Genotype
OtsAC20ROGR_0147	9/4/20	248	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0148	9/4/20	248	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0149	9/4/20	248	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0150	9/4/20	248	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0151	9/4/20	248	Huntley Park	Huntley Park	seine	TA	AT	heterozygote	heterozygote	heterozygote
OtsAC20ROGR_0152	9/4/20	248	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0153	9/4/20	248	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0154	9/4/20	248	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0155	9/9/20	253	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0156	9/9/20	253	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0157	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0158	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0159	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0160	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0161	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0162	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0163	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0164	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0165	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0166	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0167	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0168	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0169	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0170	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0171	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0172	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0173	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0174	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0175	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0176	9/11/20	255	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0177	9/14/20	258	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0178	9/14/20	258	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0179	9/14/20	258	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0180	9/14/20	258	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0181	9/14/20	258	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0182	9/14/20	258	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0183	9/14/20	258	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0184	9/14/20	258	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0185	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0186	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0187	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0188	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0189	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0190	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0191	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0192	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0193	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0194	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall

Sample	Date	Julian Day	Location	Detailed Location	Sampling Method	Ots37124-12277401	Ots37124-12310649	*greb1l* SNP1 Genotype	*greb1l* SNP2 Genotype	Two SNP Genotype
OtsAC20ROGR_0195	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0196	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0197	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0198	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0199	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0200	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0201	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0202	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0203	9/16/20	260	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0204	9/18/20	262	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0205	9/18/20	262	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0206	9/21/20	265	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0207	9/23/20	267	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0208	9/23/20	267	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0209	9/28/20	272	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0210	9/28/20	272	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall
OtsAC20ROGR_0211	9/30/20	274	Huntley Park	Huntley Park	seine	AA	TT	homozygous_fall	homozygous_fall	homozygous_fall

Table S1. The full dataset used for the analyses which consists of 209 Chinook salmon samples collected in the Lower Rogue River in 2020. Two of the Rogue Bay cleaning station samples were excluded during genotype filtering due to high missingness.

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