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# Abstract

This project discovered, developed, and genotyped single nucleotide polymorphism (SNP) loci in Chum salmon genomic libraries using restriction-site associated DNA tag sequences. The project implemented a developing SNP genotyping technology (GTseq) to efficiently genotype hundreds of Chum salmon at hundreds of SNP loci in single sequencing runs. The effort expanded the Chum salmon baseline in the Southern Boundary Region in support of regional and international Chum salmon fisheries management. In initial genotyping, 2064 individuals in 37 populations were genotyped at 724 SNP loci in two GTseq panels. Because locus performances were uneven in high-throughput genotyping, the most variable 350 loci were reorganized into a single GTseq panel for a final genotyping of 2466 individuals in 43 Chum salmon populations. The overall FST value was 0.043 (SD 0.028) and individual locus FST values ranged from 0.0004 to 0.1651, with 13 loci showing positive signals for selection. Populations clustered by region and run-group. In 100% simulations, the baseline averaged 64% assignment back to population and 98% assignment to region. In mixed fishery simulations, assignments to population were relatively low but assignments to region and country of origin were accurate and precise. The baseline is now available for fisheries managers to investigate catch composition in domestic and international fisheries to manage Chum salmon in the Southern Boundary region.

# Executive Summary

Samples from 43 Chum salmon populations in Washington and southern British Columbia were collected and genotyped to expand the Chum SNP genetic baseline. In fall 2014, WDFW prepared 192 Chum salmon sample libraries for RAD sequencing, completed in winter 2015 on contract to the University of Oregon. WDFW conducted bioinformatics on the RAD sequences in spring 2015, developed a Chum RAD catalogue of sequences and compared the catalogue to a UW Chum RAD catalogue developed from populations from different locations. The comparison identified matching and different SNPs and SNPs with high resolving power for Southern Boundary region populations, resulting in a “white list” of 5000 candidate SNPs from the WDFW Chum RAD catalogue for primer development and amplicon (SNP) panel construction. In initial efforts, UW developed two amplicon panels, one with 335 loci that included 130 SNPs that were originally TaqMan assays plus 205 newly developed SNPs from the RAD catalogue, and a second panel of 389 newly developed SNPs, for 724 total SNPs and developed a GTseq protocol to genotype samples with the two panels. When the project shifted into high-throughput genotyping at WDFW, the two GTseq panels produced uneven results with some loci and some collections failing. WDFW conducted experiments to identify factors contributing to failures and found that the GTseq protocol was highly sensitive to DNA quantity and purity. To develop a robust baseline, WDFW reorganized the two panels into a single panel composed of 350 loci (Oke\_GTseq350), re-extracted and concentrated DNA from failed samples, and re-genotyped the baseline for a total of 43 populations in the baseline. Because of unexpected costs associated with the project and initial genotyping failures, we genotyped generally half the proposed number of samples per collection. Genotypic data clustered regionally, following groupings previously identified with other genetic markers. In assignment tests, the proportion of correct assignments to population varied from low to high and assignments to regional groups was universally high. In simulated mixed fisheries in the Southern Boundary Region, assignments to individual populations averaged 57% correct and assignments to regional groups and country averaged 98% correct, confirming that the SNP data will be useful for Southern Boundary region fisheries management. This report documents the development of new SNP loci, the enhancement of the SNP baseline, and the performance of SNP loci in resolving simulated mixed fishery samples.

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# Introduction

This project discovered, developed, and genotyped single nucleotide polymorphisms (SNPs) with the power to discriminate among Southern Boundary region Chum salmon populations (Figure 1). One goal was to differentiate geographically close populations within countries, such as the lower and upper Skagit rivers Chum salmon populations in North Puget Sound, to support managing Chum salmon on a local scale. Another goal was to differentiate geographically close populations that are located on either side of the international border, such as the lower Fraser and Nooksack rivers Chum salmon populations. This would support managing cross-border region Chum salmon. Because existing SNPs had been developed over a wider geographic region ([Rawson et al. 2014](#_ENREF_8)), this development effort in this project focused on Chum salmon populations that had been difficult to distinguish genetically with the fewer SNPs available in the range-wide SNP panel. The project developed amplicon sequencing technology (GTseq) for 724 SNPs, culminating in a final panel of 350 SNPs, genotyped 43 Chum salmon populations with the GTseq SNP panel, and compared the amplicon results to TaqMan results.

# Methods

## SNP ascertainment panel

To expand the geographic scope of British Columbia samples from our earlier work (Rawson et al. 2014, Seeb et al., 2014) we designed a new ascertainment panel to included 192 samples from four Chum salmon collections selected to sequence for the SNP development (Table 1). Ascertainment refers to the samples used for the SNP discovery because the sequencing detects SNPs that are variable and informative in the samples under investigation. The ascertainment panel is designed to answer a genetic question with the SNP development; here the question is fine-scale population structure among Chum salmon populations in the Southern Boundary region (Table 2).

### Genomic Library Preparation

We used restriction-site associated DNA (RAD) tag sequences (Miller et al. 2007, Baird et al. 2008) to discover and genotype SNPs in in the ascertainment panel. RAD tags are short DNA sequences adjacent to restriction enzyme recognition sites and can characterize genome-wide molecular diversity (e.g., Miller et al. 2007, Baird et al. 2008, Hohenlohe et al. 2010, Narum et al. 2013). We extracted and isolated genomic DNA from tissue using Qiagen DNEasy ® kits (Qiagen Inc., Valencia, CA), following the recommended protocol for animal tissues. DNA was quantitated using Quant-It ™ BR assay kit (Life Technologies) and a QuantiFluor® ds DNA system (Promega) to normalize or standardize DNA from all individuals at 1µg/40µL. Quantitated genomic DNA was digested using the enzyme *Sbf* I-HF® (New England Biolabs) at 50 µL reaction volumes (400 U/ml *Sbf*I-HF®, 1X Cutsmart™ buffer). Digests were conducted at 37°C for 3h followed by 65°C for 20m. P1 adapters (Integrated DNA Technologies), which included a DNA barcode specific to each individual fish – the unique DNA barcode allows sequence libraries from multiple fish to be pooled and separated later- were ligated to digested DNA in 60 µL reaction volumes (8.3 nM P1 adapters, 0.17X NEBuffer 2 (New England Biolabs), 1 nM rATP (Promega), 16,666.7 U/ml T4 DNA Ligase (New England Bioloabs). The reaction was incubated at room temperature for 1h followed by 65°C for 20m, after which DNA from individuals was pooled into a single reaction. Pooled DNA was sheared using a Bioruptor ® (Diagenode) for 4 to 9 cycles of 30s of shearing and 59s resting, depending on DNA quality. Sheared DNA was purified and size selected using Agencourt® AMPure® XP PCR purification kits (Beckman Coulter Inc.), following manufacturers’ protocol. Genomic libraries were prepared, including the ligation of the P2 adapter (primer for the complimentary DNA strand), using the KAPA LTP Library Preparation Kit for Illumina® platforms (KAPA Biosystems) following manufacturers’ protocol with the optional final PCR amplification step, annealing at 68°C. Library DNA concentrations were evaluated using qPCR with the KAPA Library Quantification Kit for Illumina® platforms and an Applied Biosystems™ 7900 real-time PCR system (Life Technologies) following manufacturers’ protocol. Libraries were normalized to10 nM and sent to University of Oregon Genomics Core Facility (UOGCF), where they were run on an Illumina® HiSeq 2000 sequencer. After the first round of sequencing, the sequence data were processed using algorithms in the “*process\_radtags”* module of *Stacks* ([Catchen Julian et al. 2013a](#_ENREF_2), [Catchen Julian M. et al. 2011b](#_ENREF_4)) to evaluate average depth of coverage per individual. To increase total yield per individual, individual libraries were normalized again at the P1 ligation step based on the average depth of coverage such that DNA was reduced from individuals with high depth of coverage and DNA was increased from individuals with low depth of coverage. Library preparation proceeded as described above and the new libraries were submitted to the UOGCF for the second round of sequencing on the HiSeq 2000.

### RAD-seq bioinformatics

WDFW has a virtual machine on a dedicated server to process RAD-seq data. The sequence data are processed through the *STACKs* software package ([Catchen J. et al. 2011a](#_ENREF_1), [Catchen J. et al. 2013b](#_ENREF_3)), using Perl scripts to run the data through the components of *Stacks*. The program processes the data in several modules to associate individual ID codes with sequences, screen out sequencing errors, find the same SNP loci in all individuals, calculate statistics for SNP loci, and construct SNP genotypes for statistical analyses. The software is run iteratively to initially clean the data and eventually develop a set of candidate SNPs fitting criteria for the study. The sequence data was processed using Perl scripts written by Sewall Young (WDFW) and Ken Warheit. As described above, the barcodes associated with the raw sequence data from UOGCF are replaced with the individual WDFW ID using *process\_radtags* with the sliding window of the read length (w) set at 15 and the score limit (s) set at 10 (sequences below the score limit threshold are discarded). In this study, data from the two sequencing rounds were combined for each individual into a single data set per individual. The “*ustacks*” module merges sequences with SNPs into SNP loci. In an exploratory run, *Ustacks* was run with stack depth parameter (m) set to 2 (minimum number of sequences with the same SNP detected in the same individual at a single locus to form a “stack” of matched copies of those sequences), and the mismatch parameter (M) set to 2 (maximum number of nucleotides mismatching between two “stacks” of sequences to merge them into a single locus). In the final run, *Ustacks* parameters m and M were set at 3 and 4, respectively. In both runs, the bounded SNP model was used with alpha = 0.05 and the upper bound for epsilon, ε = 0.1. The SNP loci from all individuals were merged into a “catalogue” of SNP loci, a consensus of loci with all alleles detected, using the “*cstacks*” module. Next, the “*sstacks*” module matches SNP loci from individuals to the catalogue of SNP loci and identifies the allelic state for individuals at each SNP locus (homozygous for either allele or heterozygote), creating SNP genotypes for each individual. Next, the “*populations*” module tabulates alleles within and among population samples, calculates overall genetic statistics, and outputs genotypes in formats that can be used in other software programs (e.g. *GENEPOP* and *STRUCTURE*) that we used to further screen SNP loci. To compile data within and among populations in the *populations* module we included a population map that identified the population origin for each sample. To compile data only on SNP loci over all populations, the population map identified each sample as belonging to the same population.

The SNP catalogue from this effort was compared to the Chum salmon SNP catalogue developed from geographically wide ranging Chum salmon populations ([Waples 2015](#_ENREF_10), [Waples et al. 2015](#_ENREF_11)). Comparing catalogues identified matching SNPs detected in both RAD-seq libraries and SNPs unique to each library. Newly discovered SNPs from the Southern Boundary RAD-seq library developed for addition to the Chum SNP amplicon panel.

The “*populations*” output includes a “*sumstats.tsv*” file with basic statistics about each locus in each population as well as a column number which describes the exact basepair location for the SNP in relation to the ends of the sequence. We used column information to screen for SNPs that were at least 20 basepairs from both ends of the sequence to allow space for primer DNA in TaqMan assay development. The *sumstats* calculates the minor allele (less common allele) frequency and we initially selected only SNP loci with a minor allele frequency of 0.01 or above over all populations. The *populations* output includes a “*hapstats*” file that tabulates the number of alleles per locus. Some SNP loci had more than 2 alleles and were excluded from further consideration. The *populations* output includes a “*phistats*” file with the overall FST value for each SNP and we initially selected SNP loci with FST values of at least 0.0005. Loci fulfilling these described criteria (N = 18,113) constituted our first “whitelist”, or list of acceptable loci based on the first screening. The *populations* module was run again with the first whitelist. Genotypes were screened in *GENEPOP* for conformance to Hardy-Weinberg equilibrium (HWE) expectations and pairwise FST values were calculated between populations and *populations* was run six more times with increasingly stringent whitelists. Our final whitelist (N=2236) included loci that were in HWE, that had minor allele frequencies of at least 0.05, and with overall FST values of at least 0.01. These loci will be screened further to identify primer sequences for TaqMan assays.

The sequencing generated nearly 500 million total sequences with 141,852,135 reads retained after screening for ambiguous barcodes, low quality sequences, and ambiguous RAD-tags. Sequence quality was below threshold values for 15 Campbell River samples (Table 1) and in one or more samples from the other collections. After additional QA/QC protocols and ranking the loci for their capacity to differentiate populations, 389 loci were selected for amplicon panel 2 (Small et al. 2017).

## Combined Amplicon Panel Development and GTseq protocol

Primer Design*:* Illumina sequencing primer tails were added to the 5’ end of the current TaqMan primers (Campbell et al. 2015). The primers were ordered in 96-well plates at a concentration of 200 µM (Integrated DNA Technologies). Primers amplifying nuclear loci were pooled and diluted to 250 nM per primer (PrimerPool1). Primers amplifying mitochondrial loci were added to the pool and diluted to 2.5 nM per primer (PrimerPool1). PrimerPool1 contained 334 primer pairs and primerPool2 contained 389 primer pairs. Ninety-six Illumina i5 tagging primers, each containing a unique 6-base barcode and one i7 primer were diluted to 10 nM ([Seeb et al. 2014](#_ENREF_9)). After initially genotyping 2000 individuals with mixed success detailed in Small et al (2017), Amelia Louden at WDFW conducted tests to identify variable loci that amplified consistently together, and reorganized 350 of the most useful primers into a single primer pool, Oke\_GTseq350. The 2000 individuals were re-genotyped with this single primer pool (Table 3).

GTseq protocol*:* Panels 1 and 2, and the new Oke\_GTseq350 panel were genotyped using a cost effective method based on custom amplicon sequencing called Genotyping in Thousands (GTseq) (Campbell et al. 2015). The GTseq is an efficient genotyping method that amplifies pools of targeted SNPs and then indexes individual samples. The pools are sequenced, de-multiplexed, and genotyped by generating a ratio of allele counts for each individual. The entire process can be broken down into four segments; extraction, library preparation, sequencing, and genotyping.

To extract and isolate genomic DNA from tissue, 30uL of 10% Chelex (Sigman Aldrich, C7901) and 5uL of Proteinase K solution (Qiagen, 1018332) were added to the fin and incubated overnight at 55°C. To start the library preparation, an ExoSAP cleanup was performed on10uL of extracted DNA. 1.3uL of Exonuclease I (New England BioLabs, M0293L), 0.3 uL of SAP (New England BioLabs, M0371L), 0.15uL of Exonuclease 1 Buffer (New England BioLabs, B0293S), and 1.25uL of nuclease free water were added to the extracted DNA for a combined volume of 13uL. Thermal cycling was conducted in 96-well PCR plates for all reactions and had the following conditions for the ExoSAP reaction: 37°C-60 min, 80°C-20 min, 4°C-hold. Following the ExoSAP reaction, amplification of the multiplexed pool of targeted loci was performed. The multiplex PCR cocktail reaction was 2uL of cleaned DNA extract, 3.5uL of Qiagen Multiplex PCR Plus mix (Qiagen, 10672201), and 1.5uL pooled primer mix (IDT, Tables 3 and 4, final volume = 7uL; final primer concentrations at each locus = 54nM). Thermal cycling conditions were as follows: 95°C-15 min; 5 cycles [95°C – 30 s, 5% ramp down to 57°C – 30 s, 72°C – 2 min]; 10 cycles [95°C – 30 s, 65°C – 30 s, 72°C – 30 s]; 4°C hold. Following the multiplex PCR, the amplified samples were diluted 20-fold. 3uL of diluted multiplex PCR product was then used in the barcoding PCR. The barcoding PCR is used to add indexes that identify each sample by well and by plate. For the barcoding PCR, 1uL of 10uM well-specific i5 tagging primer (IDT) and 1uL of 10uM plate-specific i7 tagging primer were added to the 3uL of amplified sample. 5uL of Qiagen Multiplex PCR Plus mix (Qiagen, 10672201) was then added for a final reaction volume of 10uL. Thermal cycling conditions were: 95°C – 15 min; 10 cycles [98°C – 10 s, 65°C – 30 s, 72°C – 30 s]; 72°C – 5 min; 4°C hold. Following the barcode PCR, each plate of samples (library) was normalized using the SequalPrepTM Normalization Plate Kit (Applied Biosystems, A1051001) according to the manufacturer’s instructions. Upon completion of normalization, 10uL of each sample per 96-well plates was pooled into a 1.5mL tube constituting a library.

A purification step was then performed on each library with Agencourt AMPure® XP magnetic beads (Agencourt, A63881) according to the manufacturer’s instructions for size selection with a 2:1 and 1.43:1 ratio of library to beads. The purified libraries were then eluted with 15uL of TE pH 8.0. In order to complete the final process of library preparation, each library was quantified and normalized. The libraries were quantified using a Qubit 3 Fluorometer (Invitrogen) and QubitTMdsDNA HS Assay Kit reagents (Invitrogen, Q32854) according to the manufacturer’s instructions. Following the quantification, the concentration of each library was calculated using the molecular weight specific to the multiplex pool used (SEWA187 or SW269). Then each library was normalized to 4nM and pooled with other libraries that were sequenced on the same sequencing run. Pooled libraries were then sequenced at a 2.5pM loading concentration on an Illumnia NextSeq 500 instrument of a single-end read flow cell using 111 cycles with dual-index reads of six cycles each. To genotype the samples a bioinformatics pipeline was used. This pipeline is explained and available online at <https://github.com/GTseq/GTseq-Pipeline> (Campbell et al. 2015). Essentially, there are a series of custom perl scripts that ultimately create individual fastq files and genotype files for every individual that can be compiled a number of ways for further analysis. The genotyping is performed with a simple perl script which counts amplicon-specific sequences for each allele, and allele ratios are used to determine the genotypes.

Data Analysis Treatment**:** The quality of the sequences was analyzed using FastQC, downloaded from <http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>.

Perl scripts were downloaded from <https://github.com/GTseq/GTseq-Pipeline> (Campbell et al, 2015). The numbers of unique reads per individual were counted and hashed using GTseq\_HashSeqs.pl. The output from this script was used to count the occurrence of the forward primer sequence, the TaqMan probe sequence, and when both occur in the same read. This will identify primer pairs that amplify “off-target” sequences and will need to be removed from the primer pool.

SNP genotyping was done using GTseq\_Genotyper.pl and compiled using GTseq\_GenoCompile.pl. The genotypes were compared to existing TaqMan or SNPtype genotypes.

Southern Boundary Chum salmon SNP baseline expansion: Over 2000 tissue samples from Southern Boundary Area Chum salmon were genotyped with SNPs from panels 1 and 2 (Table 2) in summer 2017 (Small et al. 2017). Samples with incomplete genotypes were re-genotyped in summer 2017. Remaining samples with incomplete genotypes were re-extracted and re-genotyped in spring 2018 with the reorganized SNP panel (Oke\_GTseq350). Additional samples from Hood Canal and Lower Columbia River were genotyped with Oke\_GTseq350 during the redevelopment in winter 2018, and added to the baseline (Table 2) to provide a broader context for the Southern Boundary Chum salmon populations. Our final complete dataset now consists of 350 SNPs (Table 3) genotyped using either panels 1 and 2 (Small et al. 2017 and this report) or Oke\_GTseq350 (this report).

Genotyping troubleshooting: Genotyping success was assessed per individual per SNP locus, per collection per SNP panel, and examined for age of tissue, DNA extraction method, age of DNA extraction, technician performing DNA extraction, and day of DNA extraction. Because success differed between collections, extraction methods and SNP panels, and appeared to be sensitive to DNA extraction method, WDFW conducted an experiment where DNA was newly extracted from the same 379 individuals with Chelex and with Qiagen and individuals were re-genotyped at both panels.

Genetic analyses:Data were prepared for analyses using R scripts written by Sarah Brown (WDFW). Genetic statistics for genotypic data were generated using GenAlEx, an Excel addin ([Peakall and Smouse 2012](#_ENREF_7)) and Arlequin 3.5 (Excoffier and Lischer 2010). GenAlEx calculated Hardy-Weinberg Equilibrium (HWE) values for each locus in each population and for each locus over all populations. Arlequin generated pairwise FST values between collections and conducted a permutation test of their significance from zero. We conducted a locus by locus analysis of molecular variance (AMOVA) using Arlequin and tested loci for selection using the hierarchical island model (Excoffier et al. 2009). Genotypic data were formatted in GenAlEx for tree-building in PHYLIP (Felsenstein 2004), and for assignment tests and mixed fishery analyses in ONCOR. We also conducted a principal coordinates analysis of the data in GenAlEx.

# Results

Genotyping and troubleshooting*:* In the genotyping effort in summer 2017 there were more successful genotypes with panel 1 than with panel 2 and some collections failed to amplify at panel 1 while others failed to amplify with panel 2 (see Appendix I, Appendix II, Small et al. 2017). Where additional samples existed for collections that mostly failed at either or both panels, these additional samples were extracted and genotyped to increase collection sizes, but failures remained unacceptably high. There was higher success for samples extracted with Qiagen in 2014 and mixed success for samples extracted with Chelex in summer 2017. In the test with samples freshly extracted with Chelex, there was an effort to cut larger tissue pieces and these samples had higher genotyping success, suggesting DNA quantity was limited in some failed DNA extracts. Because there was too much missing data in most collections from the original genotyping effort with two panels and running two SNP panels doubled genotyping costs, Amelia Louden (WDFW) reorganized the 724 SNPs from the two panels into a single panel composed of the best performing SNPs from both panels (Oke\_GTseq350, see Table 3). Most of the loci on panel 1 were first developed and vetted as TaqMan assays before transforming them into a GTseq panel. The loci on panel 2 were selected for information content in the RADseq process and transformed directly into a GTseq panel. Because the GTseq panels requires compatibility among hundreds of primer sets, SNPs from TaqMan assays were generally easier to employ having been through more thorough testing. The final panel, Oke\_GTseq350, included 130 loci from panel 1 and 220 loci from panel 2. To complete the baseline genotyping effort, tissue samples were re-extracted with Chelex, taking care to cut larger pieces, and genotyping success was higher with Oke\_GTseq350. In the final genotyping, 1843 of the 2466 samples from 43 populations had >80% data and were included in the analysis (Table 4).

Genetic statistics: GenAlEx calculated observed and expected heterozygosity and the Hardy-Weinberg Equilibrium (HWE) value over all loci, as expressed by FIS (Table 4). In general, observed heterozygosity was higher than expected heterozygosity, as indicated by mostly negative FIS values over all loci (excess heterozygosity) for each population. The percentage of polymorphic loci was 95%. Over all collections and all loci, loci at both panels tended towards excess heterozygosity (average FIS = -0.0086). With the large number of loci, the tests for linkage among loci are still running and results are unavailable. Loci were tested for departures from expected heterozygosity under HWE. With no correction for multiple tests, there were generally more loci out of HWE than expected by chance (average 5.9%), with the highest percentage in the Nanaimo River collection and the lowest in Dungeness River collection. After correcting for multiple tests, no collections had more loci out of HWE than expected by chance (not shown).

AMOVA**:** We tested loci for genetic variation with an AMOVA (Table 3). Because Hood Canal Summer Chum salmon (HCSCS) belong to their own Evolutionary Significant Unit and are highly differentiated from other Chum salmon (Small et al. 2015), we conducted AMOVAs both excluding and including the HCSCS (Table 3) to gain a better understanding of the genetic variation. The average FST over all loci without HCSCS was 0.036 (SD 0.025) and with HCSCS was 0.043 (SD 0.028). Without HCSCS, 27 loci had FST values that were > 2 SD higher than average and with HCSCS, 41 loci had FST values that were > 2 SD higher than average.

Selection: We tested loci for signals of selection using the hierarchical island model in Arlequin with 20,000 permutations (Figure 2). Seven loci showed signs of positive selection both with and without HCSCS (Table 3). Six loci showed signs of positive selection only when HCSCS were included and four loci showed signs of positive selection only when HCSCS were excluded. One locus appeared to be under balancing selection regardless of whether HCSCS were included or excluded.

Pairwise FST: The pairwise FST values among regions showed high variation between HCSCS and all other regions and run groups (Table 5). The next highest variation was between South Puget Sound falls and winters, and the Canadian regions. Because our main interest in this report is fall and winter-run Chum salmon in the Southern Boundary region, we present only pairwise FST values between the Southern Boundary region collections (Table 5). Among Georgia Strait collections, there was relatively little variation but 37/55 of the comparisons were significantly different from zero. The Hood Canal fall Chum salmon populations are from a more restricted geographic distribution than Georgia Strait (Figure 1) and there was relatively low variation among them. However, comparisons to the Hamma Hamma (and some Duckabush) falls were significantly different from zero. However the Hamma Hamma falls were the smallest collection in the baseline (N = 19) and we suspect the differences were because the collection did not fully characterize the genetic variation in the population. The North Puget Sound Chum salmon were distributed geographically at a level between Georgia Strait and Hood Canal populations (Figure 1). Genetic variation was low among the populations and comparisons to Lower Skagit and Nooksack rivers (and most comparisons to Lower Sauk River), were significantly different from zero. There was an intermediate amount of genetic variation between the Dungeness and Sooke collections on the south and north sides of the Strait of Juan de Fuca and the collections from Georgia Strait and North Puget Sound. The Strait of Juan de Fuca is located between Georgia Strait and North Puget Sound.

Genetic Structure: The SNP genotypic data had similar geographic structure found previously with other genetic marker sets (Rawson et al. 2014, Small et al. 2015). In the principal coordinates analysis (PCoA) plot, the HCSCS and Lower Columbia populations were excluded because their inclusion compressed the other populations into corners of the plot. The variation explained by the axes was distributed slightly differently when they were included (36.6% on axis 1 and 16.2% on axis 2). In the PCoA (Figure 3), populations from the same region clustered together, and axis 1 explained 38% of the variation in the data. Populations separated along axis 1 according to a longitudinal gradient from north to south: northern population were on the left and southern populations on the right of axis 1. The second axis explained 13% of the variation and separated the northern regional populations from each other. This geographic structure was similar in the neighbor-joining tree (Figure 4) where northern populations clustered at the right of the tree and southern populations clustered at the left, except for the Lower Columbia Chum salmon populations, which clustered closer to the northern fall-run collections. In the tree, regional groups were further clustered on sub-branches with mostly strong (>60%) bootstrap support. For instance, the southern Puget Sound populations cluster with 73% bootstrap support and within that grouping, the winter-runs form a sub-branch with 81% bootstrap support, the Hood Canal falls form a sub-branch with 67% bootstrap support, the South Puget Sound falls form a sub-branch with 80% bootstrap support, and the South Puget Sound winters form a sub-branch with 78% bootstrap support.

Assignment tests: The self-assignment tests and mixed fishery analyses with ONCOR further illustrated the geographic structure to the SNP genetic data. We conducted 100% mixture simulations simulating 200 fish from a single population 100 times and estimated the mixture proportions in comparison to the full baseline. While this is an unrealistic scenario (100% of the fish in a fishery sample of 200 fish all from the same population), it gives an indication of whether individuals from a population can be assigned reliably back to their population. Estimates to individual populations and to regions were averaged over the 100 simulations (Table 6 and Figure 5). The average assignment back to home population was 57% and average assignment back to region was 98% indicating that genetic variation partitions strongly among regions. The lowest average assignment back to home population was for Campbell River (9%), but they assigned well to home region (99%). The Campbell River simulated fish assigned better to Phillips and Puntledge collections (26% and 22%, respectively), underscoring the close relationship among these populations. The highest average assignment back to home population was for Nisqually (winter-runs) at 99% and their regional assignment was 100%. There was a positive relationship between baseline collection size and assignment back to home population (R2 = 22% in a regression of percent correct assignment on collection size) and an error decomposition in ONCOR suggested that precision would be improved by increasing collections sizes. Assignments to regions were universally high (Table 6 and Figure 5) and the three collections with less than 93% assignment were in transitional locations geographically, Sooke and Dungeness on the Strait of Juan de Fuca, and lower Skagit in North Puget Sound. For all three of these collections, the next highest region of assignment was to Georgia Strait (Sooke 28%, Dungeness 8%, and lower Skagit 10%).

Mixed Fishery: We conducted mixed fishery simulations with ONCOR (Table 7) to examine the power of the SNPs to resolve a mixed fishery composed of fish from nearby US and CAN populations across the Southern Boundary. We simulated varying proportions of Hopedale, Puntledge, Nooksack and Stillaguamish rivers fish in a fishery sample of 200 fish 100 times; 0.25:0.25:0.25:0.25 and 0.7:0.1:0.1:0.1, with each of the four collections at highest representation in turn. Estimated values for populations were all lower than the actual values because fish assigned to other populations in their regional group. However, estimations to region were close to the actual values. The Nooksack contribution was better estimated than the other components and within two standard deviations of the actual value. The average estimated values for the other collections were within two standard deviations of the actual value, with the exception of the first mixture with equal proportions where all but Nooksack were lower. When rolled up by region, mixture estimates improved and were within two standard deviations of the true values.

We also conducted mixed fishery simulations for pairs of geographically close populations across the border and within the US and CAN (Table 8). In the tests for mixes of fish from Hopedale River, a tributary of the Fraser River and Nooksack River in North Puget Sound, Hopedale fish were underestimated because nearly half of those fish assigned to Peach, a nearby tributary in the Fraser River. The Nooksack fish were underestimated to a lesser degree, and a portion assigned to other North Puget Sound populations and a small portion assigned to Georgia Strait populations. In the tests for mixes of fish from the upper and lower Skagit River, in the equal mixture the upper Skagit fish portion was better estimated than the lower Skagit fish (Table 8), and the remaining portion assigned mainly to Georgia Strait and a small amount to the Fraser. The mis-assigned portions varied according to the mix and then the lower Skagit was at 75% actual value, there was a higher portion attributed to the Georgia Strait (Table 8). In the tests for mixes of fish from Big and Little Qualicum rivers (not shown), most of the fish assigned correctly back to population (37/50 Big Qualicum, 34/50 Little Qualicum) with the remaining fish partitioned among other Georgia Strait collections. Assignment to region was 99%, as expected since they were from the same region and mis-assigned fish were attributed to other populations in Georgia Strait.

Comparisons to TaqMan data: In comparisons to genotypic data previously obtained from 89 TaqMan assays developed from Chum salmon across their range (Small et al. 2015), there were increases in the genetic variation detected in the Southern Boundary Region. The regional pairwise FST value between the Fraser and North Puget Sound increased from 0.009 with the TaqMan data to 0.019 with GTseq data, and the regional pairwise FST value between the Georgia Strait and North Puget Sound increased from 0.006 to 0.015 (Table 5). In comparisons to genotypic data previously obtained from 183 TaqMan assays developed for the Southern Boundary Region (Rawson et al. 2014), results varied. The regional pairwise FST value between the Fraser and North Puget Sound increased from 0.018 with the 183 TaqMan assays to 0.019 with GTseq data, and the regional pairwise FST value between the Georgia Strait and North Puget Sound decreased from 0.018 to 0.015.

The increases in genetic variation detected with 89 TaqMan assays versus 350 SNP loci with GTseq genotyping were expected because the ascertainment panel for the GTseq SNP development included collections that were difficult to resolve and some of the selected SNPs were variable among closely related populations. The decrease from genetic variation detected with 183 TaqMan assays to the GTseq data was likely because the collection sizes with 183 TaqMan assays averaged more than twice the size (Rawson et al. 2014) of the collections in the GTseq data set (92 versus 43, respectively), and captured more of the genetic variation than the smaller collections. Further, although collections were from the same regions, there were different populations represented in the two data sets, which also contributed to different results.

We also compared results for self-assignment to population and to region with the 89 TaqMan assays (Small et al. 2015), 183 TaqMan assays (Rawson et al. 2014) and 350 SNP loci in the GTseq panel (this study). Because there were different collections in the different data sets, we compare only the average self-assignment and assignment to region as an indication of the genetic resolution of the data sets. The average self-assignment was the same over all collections for the 89 TaqMan assays (58%) and 350 SNP loci (57%) and higher for the 183 TaqMan assays (77%). The average assignment to region was highest for the 350 SNP loci (98%), lowest for the 183 TaqMan assays (93%), and intermediate for the 89 TaqMan assays (95%).

In summary, the 350 SNP loci in the emerging Chum salmon baseline improves our ability in some comparisons to resolve contributions of Chum salmon originating in US and CAN tributaries in the Southern Boundary Region. Increasing representation both of individual populations and of populations within regions will enhance our ability to manage international and domestic fisheries.

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Table 1. List of collections sequenced for Southern Boundary Chum salmon RAD SNP development and the number of successful libraries.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Collection year | Tributary | WDFW code | N selected | N libraries |
| 2010 | Little Qualicum River | 10OU | 48 | 47 |
| 2011 | Campbell River | 11OL | 48 | 32 |
| 2012 | Conuma River | 12OM | 48 | 43 |
| 2012 | Cheakamus River | 12ON | 48 | 42 |
|  |  | Total | 192 | 164 |

**Table 2. List of collections genotyped with 350 SNPs to expand the Southern Boundary Chum SNP baseline. The region column has the regional groupings used in ONCOR analyses. The total number of samples run for each collection is under “N Run”. Samples with 80% or more loci in their genotypes were included in analyses (run number differs from final N in Table 4.)**

| Country | region | Collections | N Run | WDFW code |
| --- | --- | --- | --- | --- |
| US | HoodCanal\_F | Anderson | 48 | 11MD |
| US | HoodCanal\_F | Big Beef | 48 | 10LY |
| US | HoodCanal\_F | Dewatto | 48 | 11KN |
| US | HoodCanal\_F | Duckabush\_F | 48 | 11MF |
| US | HoodCanal\_F | Lilliwaup | 48 | 10LZ |
| US | HoodCanal\_F | HammaHamma\_F | 70 | 12AN |
| US | HoodCanal\_F | NF Skokomish | 19 | 10LO |
| US | HoodCanal\_F | NF Skokomish | 48 | 11KQ |
| US | HoodCanal\_S | Dosewallips\_S | 18 | 12HR |
| US | HoodCanal\_S | Dosewallips\_S | 18 | 14MB |
| US | HoodCanal\_S | HammaHamma\_S | 25 | 12AN |
| US | HoodCanal\_S | HammaHamma\_S | 11 | 14PI |
| US | HoodCanal\_S | Duckabush\_S | 48 | 14MC |
| US | NorthPS | Lower\_Sauk | 48 | 14QN |
| US | NorthPS | Nooksack | 48 | 10LT |
| US | NorthPS | Skagit\_lower\_mainstem | 48 | 14QM |
| US | NorthPS | Snohomish | 48 | 10PB |
| US | NorthPS | Stillaguamish | 48 | 10PC |
| US | NorthPS | upper\_Skagit | 48 | 10LR |
| US | NorthPS | upper\_Skagit | 80 | 14DB |
| US | SJF | Dungeness (Beebe Cr) | 48 | 10LK |
| US | SouthPS | Chico/Grovers | 48 | 10MA |
| US | SouthPS | Chico/Grovers | 66 | 15TJ |
| US | SouthPS | Green River Hatchery | 96 | 07LB |
| US | SouthPS | Kennedy | 48 | 11KS |
| US | SouthPS | Skookum | 48 | 10MH |
| US | SouthPS\_W | DIRU\_Puyallup H | 48 | 11KR |
| US | SouthPS\_W | Nisqually | 75 | 11KV |
| US | LowColumbia | I\_205 | 95 | 16MN |
| US | LowColumbia | Horsetail | 26 | 16MQ |
| US | LowColumbia | Ives Island | 68 | 16MR |
| CAN | Fraser | Hopedale | 48 | 11NS |
| CAN | Fraser | Peach | 48 | 10OT |
| CAN | Fraser | Squawkum | 48 | 10QT |
| CAN | GeorgiaSt | Big Qualicum | 48 | 10OV |
| CAN | GeorgiaSt | Campbell | 34 | 11OL |
| CAN | GeorgiaSt | Cheakamus | 43 | 12ON |
| CAN | GeorgiaSt | Cowichan | 48 | 11OJ |
| CAN | GeorgiaSt | Lang | 48 | 11NU |
| CAN | GeorgiaSt | Little Qualicum | 96 | 10OU |
| CAN | GeorgiaSt | Nanaimo | 96 | 10OP |
| CAN | GeorgiaSt | Phillips | 48 | 11NT |
| CAN | GeorgiaSt | Puntledge | 48 | 10OQ |
| CAN | GeorgiaSt | Snake | 48 | 10OS |
| CAN | GeorgiaSt | Southgate | 48 | 03AA |
| CAN | JohnstoneSt | Nimpkish | 48 | 10OR |
| CAN | WCVI | Conuma | 43 | 12OM |
| CAN | WCVI | Nitinat | 48 | 10OW |
| CAN | WCVI | Sooke | 47 | 11OK |
|  |  |  | 2466 |  |

Table 3. List of loci in final GTseq panel (Oke\_GTseq350) and their overall FST values with and without Hood Canal Summer Chum salmon (HCSCS) in the baseline (from an AMOVA in ARLEQUIN). The FST is the magnitude of the variation among collections and the P-values indicate which variation was significantly different from zero. The average FST over all collections and the standard deviation is at the bottom of the table for calculations with and without HCSCS. Blue cells highlight loci that were significant only with HCSCS included in the baseline. In the Arlequin hierarchical test for selection, yellow cells had positive signals with or without HCSCS, orange cells had positive signals only with HCSCS, and green cells had positive signals only without HCSCS. Purple cell appeared to be under balancing selection.

|  | *with HC summer* | |  | NO HC summer | |  |  | *with HC summer* | |  | NO HC summer | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| SNP name | *FST* | *P-value* |  | FST | P-value |  | SNP name | *FST* | *P-value* |  | FST | P-value |
| Oke\_ACOT\_100 | *0.0219* | *0* |  | 0.0218 | 0 |  | Oke\_RDDFW48705\_55 | *0.0560* | *0* |  | 0.0289 | 0 |
| Oke\_APOB\_60 | *0.0436* | *0* |  | 0.0427 | 0 |  | Oke\_RDDFW49372\_62 | *0.1089* | *0* |  | 0.0296 | 0 |
| Oke\_ATP5L\_105 | *0.0314* | *0* |  | 0.0242 | 0 |  | Oke\_RDDFW50553\_28 | *0.0302* | *0* |  | 0.0130 | 0 |
| Oke\_AhR1\_278 | *0.0077* | *0.01075* |  | 0.0091 | 0.00684 |  | Oke\_RDDFW51270\_33 | *0.0926* | *0* |  | 0.0725 | 0 |
| Oke\_CATB\_60 | *0.0130* | *0* |  | 0.0124 | 0.00098 |  | Oke\_RDDFW51705\_44 | *0.0762* | *0* |  | 0.0733 | 0 |
| Oke\_CD123\_62 | *0.0579* | *0* |  | 0.0387 | 0 |  | Oke\_RDDFW52567\_35 | *0.0113* | *0.00196* |  | 0.0070 | 0.02542 |
| Oke\_CKS1\_70 | *0.0377* | *0* |  | 0.0418 | 0 |  | Oke\_RDDFW52773\_67 | *0.0268* | *0* |  | 0.0282 | 0 |
| Oke\_CKS\_389 | *0.0188* | *0* |  | 0.0155 | 0 |  | Oke\_RDDFW53380\_67 | *0.0169* | *0* |  | 0.0176 | 0 |
| Oke\_CO1A1\_72 | *0.0172* | *0* |  | 0.0141 | 0.00098 |  | Oke\_RDDFW54241\_69 | *0.0248* | *0* |  | 0.0237 | 0 |
| Oke\_CTR2\_82 | *0.0427* | *0* |  | 0.0212 | 0 |  | Oke\_RDDFW57028\_36 | *0.0756* | *0* |  | 0.0150 | 0 |
| Oke\_DBLOH\_79 | *0.0501* | *0* |  | 0.0432 | 0 |  | Oke\_RDDFW57213\_78 | *0.0240* | *0* |  | 0.0260 | 0 |
| Oke\_DCXR\_87 | *0.0132* | *0.00293* |  | 0.0142 | 0.00293 |  | Oke\_RDDFW58551\_52 | *0.0231* | *0* |  | 0.0215 | 0 |
| Oke\_DM20\_548 | *0.0253* | *0* |  | 0.0221 | 0 |  | Oke\_RDDFW58967\_48 | *0.0596* | *0* |  | 0.0143 | 0.00098 |
| Oke\_EF2\_394 | *0.0626* | *0* |  | 0.0435 | 0 |  | Oke\_RDDFW59084\_41 | *0.0319* | *0* |  | 0.0344 | 0 |
| Oke\_GNMT\_100 | *0.0208* | *0* |  | 0.0216 | 0 |  | Oke\_RDDFW59113\_30 | *0.0589* | *0* |  | 0.0502 | 0 |
| Oke\_GPDH\_191 | *0.0235* | *0* |  | 0.0287 | 0 |  | Oke\_RDDFW6089\_75 | *0.0596* | *0* |  | 0.0189 | 0 |
| Oke\_H2AX\_72 | *0.0308* | *0* |  | 0.0173 | 0 |  | Oke\_RDDFW61097\_36 | *0.1033* | *0* |  | 0.0455 | 0 |
| Oke\_HP\_182 | *0.0093* | *0.00098* |  | 0.0105 | 0.00098 |  | Oke\_RDDFW61270\_26 | *0.0353* | *0* |  | 0.0391 | 0 |
| Oke\_IL8r2\_406 | *0.0077* | *0.00880* |  | 0.0087 | 0.00587 |  | Oke\_RDDFW61351\_74 | *0.0006* | *0.41642* |  | 0.0013 | 0.32845 |
| Oke\_IL8r\_272 | *0.0117* | *0* |  | 0.0032 | 0.17791 |  | Oke\_RDDFW61394\_55 | *0.0509* | *0* |  | 0.0236 | 0 |
| Oke\_LAMP2\_186 | *0.0191* | *0* |  | 0.0156 | 0 |  | Oke\_RDDFW62184\_66 | *0.0857* | *0* |  | 0.0479 | 0 |
| Oke\_METK2\_97 | *0.0529* | *0* |  | 0.0412 | 0 |  | Oke\_RDDFW63326\_23 | *0.0337* | *0* |  | 0.0262 | 0 |
| Oke\_MLRN\_63 | *0.0215* | *0* |  | 0.0237 | 0 |  | Oke\_RDDFW63766\_37 | *0.0607* | *0* |  | 0.0418 | 0 |
| Oke\_PDIA3\_082 | *0.0090* | *0.00489* |  | 0.0106 | 0.00196 |  | Oke\_RDDFW64078\_73 | *0.0922* | *0* |  | 0.0802 | 0 |
| Oke\_PDIA3\_475 | *0.0128* | *0* |  | 0.0150 | 0 |  | Oke\_RDDFW64969\_46 | *0.0384* | *0* |  | 0.0313 | 0 |
| Oke\_PPA2\_635 | *0.0304* | *0* |  | 0.0286 | 0 |  | Oke\_RDDFW65679\_48 | *0.0452* | *0* |  | 0.0255 | 0 |
| Oke\_RAD10028\_44 | *0.0128* | *0* |  | 0.0114 | 0.00098 |  | Oke\_RDDFW65809\_61 | *0.0882* | *0* |  | 0.0758 | 0 |
| Oke\_RAD10173\_41 | *0.0125* | *0* |  | 0.0128 | 0.00098 |  | Oke\_RDDFW65817\_59 | *0.0544* | *0* |  | 0.0523 | 0 |
| Oke\_RAD10459\_85 | *0.0657* | *0* |  | 0.0720 | 0 |  | Oke\_RDDFW6606\_46 | *0.0674* | *0* |  | 0.0530 | 0 |
| Oke\_RAD10591\_67 | *0.0292* | *0* |  | 0.0114 | 0.00196 |  | Oke\_RDDFW66307\_18 | *0.0687* | *0* |  | 0.0763 | 0 |
| Oke\_RAD10676\_50 | *0.0067* | *0.02053* |  | 0.0050 | 0.07429 |  | Oke\_RDDFW66740\_41 | *0.0487* | *0* |  | 0.0530 | 0 |
| Oke\_RAD10719\_31 | *0.0578* | *0* |  | 0.0550 | 0 |  | Oke\_RDDFW67033\_73 | *0.0838* | *0* |  | 0.0915 | 0 |
| Oke\_RAD11183\_63 | *0.1258* | *0* |  | 0.1107 | 0 |  | Oke\_RDDFW6714\_54 | *0.0384* | *0* |  | 0.0425 | 0 |
| Oke\_RAD11379\_85 | *0.0297* | *0* |  | 0.0255 | 0 |  | Oke\_RDDFW67894\_45 | *0.0297* | *0* |  | 0.0296 | 0 |
| Oke\_RAD11444\_75 | *0.0052* | *0.08407* |  | 0.0061 | 0.04888 |  | Oke\_RDDFW68590\_61 | *0.0284* | *0* |  | 0.0310 | 0 |
| Oke\_RAD11500\_80 | *0.0238* | *0* |  | 0.0204 | 0 |  | Oke\_RDDFW6872\_56 | *0.1316* | *0* |  | 0.0922 | 0 |
| Oke\_RAD11690\_33 | *0.0751* | *0* |  | 0.0246 | 0 |  | Oke\_RDDFW69367\_28 | *0.0315* | *0* |  | 0.0348 | 0 |
| Oke\_RAD11918\_57 | *0.0300* | *0* |  | 0.0106 | 0.00098 |  | Oke\_RDDFW69501\_76 | *0.0350* | *0* |  | 0.0343 | 0 |
| Oke\_RAD11928\_30 | *0.0236* | *0* |  | 0.0207 | 0 |  | Oke\_RDDFW69741\_55 | *0.0469* | *0* |  | 0.0196 | 0 |
| Oke\_RAD11999\_36 | *0.0626* | *0* |  | 0.0638 | 0 |  | Oke\_RDDFW69778\_62 | *0.0284* | *0* |  | 0.0175 | 0 |
| Oke\_RAD12038\_34 | *0.0215* | *0* |  | 0.0160 | 0 |  | Oke\_RDDFW69792\_54 | *0.0928* | *0* |  | 0.0598 | 0 |
| Oke\_RAD12294\_71 | *0.0979* | *0* |  | 0.1103 | 0 |  | Oke\_RDDFW70556\_28 | *0.0257* | *0* |  | 0.0256 | 0 |
| Oke\_RAD12377\_41 | *0.0409* | *0* |  | 0.0229 | 0 |  | Oke\_RDDFW70829\_40 | *0.0637* | *0* |  | 0.0239 | 0 |
| Oke\_RAD12415\_71 | *0.1408* | *0* |  | 0.1296 | 0 |  | Oke\_RDDFW70902\_20 | *0.0339* | *0* |  | 0.0349 | 0 |
| Oke\_RAD12909\_51 | *0.0413* | *0* |  | 0.0405 | 0 |  | Oke\_RDDFW71171\_55 | *0.0328* | *0* |  | 0.0267 | 0 |
| Oke\_RAD13522\_47 | *0.0305* | *0* |  | 0.0232 | 0 |  | Oke\_RDDFW71319\_78 | *0.0104* | *0* |  | 0.0103 | 0 |
| Oke\_RAD14303\_73 | *0.0251* | *0* |  | 0.0159 | 0 |  | Oke\_RDDFW71747\_19 | *0.0424* | *0* |  | 0.0433 | 0 |
| Oke\_RAD14679\_56 | *0.0244* | *0* |  | 0.0261 | 0 |  | Oke\_RDDFW71866\_73 | *0.0328* | *0* |  | 0.0351 | 0 |
| Oke\_RAD14852\_56 | *0.0827* | *0* |  | 0.0809 | 0 |  | Oke\_RDDFW72082\_30 | *0.1204* | *0* |  | 0.0075 | 0.01075 |
| Oke\_RAD14962\_45 | *0.1015* | *0* |  | 0.0993 | 0 |  | Oke\_RDDFW72091\_54 | *0.0446* | *0* |  | 0.0468 | 0 |
| Oke\_RAD16205\_61 | *0.0213* | *0* |  | 0.0180 | 0 |  | Oke\_RDDFW72178\_38 | *0.0263* | *0* |  | 0.0219 | 0 |
| Oke\_RAD1635\_77 | *0.0682* | *0* |  | 0.0639 | 0 |  | Oke\_RDDFW72464\_65 | *0.0468* | *0* |  | 0.0295 | 0 |
| Oke\_RAD16763\_78 | *0.0189* | *0* |  | 0.0183 | 0 |  | Oke\_RDDFW72515\_22 | *0.0286* | *0* |  | 0.0265 | 0 |
| Oke\_RAD16805\_31 | *0.0397* | *0* |  | 0.0373 | 0 |  | Oke\_RDDFW72580\_61 | *0.0453* | *0* |  | 0.0445 | 0 |
| Oke\_RAD17085\_70 | *0.0232* | *0* |  | 0.0168 | 0 |  | Oke\_RDDFW73626\_31 | *0.0400* | *0* |  | 0.0430 | 0 |
| Oke\_RAD17316\_60 | *0.0330* | *0* |  | 0.0307 | 0 |  | Oke\_RDDFW73828\_41 | *0.0438* | *0* |  | 0.0316 | 0 |
| Oke\_RAD17332\_67 | *0.0380* | *0* |  | 0.0361 | 0 |  | Oke\_RDDFW74107\_70 | *0.0729* | *0* |  | 0.0434 | 0 |
| Oke\_RAD19121\_72 | *0.1142* | *0* |  | 0.1052 | 0 |  | Oke\_RDDFW75268\_70 | *0.0198* | *0* |  | 0.0057 | 0.04888 |
| Oke\_RAD19883\_47 | *0.0269* | *0* |  | 0.0242 | 0 |  | Oke\_RDDFW75348\_40 | *0.0737* | *0* |  | 0.0783 | 0 |
| Oke\_RAD21307\_43 | *0.0192* | *0* |  | 0.0160 | 0 |  | Oke\_RDDFW76878\_51 | *0.0333* | *0* |  | 0.0207 | 0 |
| Oke\_RAD2158\_44 | *0.0149* | *0* |  | 0.0121 | 0 |  | Oke\_RDDFW78157\_36 | *0.0524* | *0* |  | 0.0412 | 0 |
| Oke\_RAD22662\_43 | *0.0391* | *0* |  | 0.0307 | 0 |  | Oke\_RDDFW78789\_24 | *0.0934* | *0* |  | 0.0836 | 0 |
| Oke\_RAD2414\_54 | *0.0223* | *0* |  | 0.0230 | 0 |  | Oke\_RDDFW80154\_68 | *0.0142* | *0.00196* |  | 0.0148 | 0 |
| Oke\_RAD24191\_34 | *0.0355* | *0* |  | 0.0308 | 0 |  | Oke\_RDDFW80662\_52 | *0.0557* | *0* |  | 0.0577 | 0 |
| Oke\_RAD2522\_75 | *0.0117* | *0* |  | 0.0085 | 0.00684 |  | Oke\_RDDFW89343\_75 | *0.0247* | *0* |  | 0.0090 | 0.00782 |
| Oke\_RAD27585\_82 | *0.0482* | *0* |  | 0.0484 | 0 |  | Oke\_RDDFW89357\_49 | *0.0915* | *0* |  | 0.0837 | 0 |
| Oke\_RAD27616\_72 | *0.0277* | *0* |  | 0.0264 | 0 |  | Oke\_RDDFW89443\_55 | *0.0781* | *0* |  | 0.0213 | 0 |
| Oke\_RAD2772\_76 | *0.0459* | *0* |  | 0.0416 | 0 |  | Oke\_RDDFW90259\_25 | *0.0205* | *0* |  | 0.0111 | 0.00293 |
| Oke\_RAD2812\_43 | *0.0823* | *0* |  | 0.0765 | 0 |  | Oke\_RDDFW90437\_74 | *0.0234* | *0* |  | 0.0187 | 0 |
| Oke\_RAD2827\_56 | *0.0195* | *0* |  | 0.0205 | 0 |  | Oke\_RDDFW91049\_44 | *0.0251* | *0* |  | 0.0263 | 0 |
| Oke\_RAD3131\_64 | *0.0523* | *0* |  | 0.0576 | 0 |  | Oke\_RDDFW91108\_63 | *0.0188* | *0* |  | 0.0186 | 0 |
| Oke\_RAD3143\_30 | *0.0365* | *0* |  | 0.0327 | 0 |  | Oke\_RDDFW9156\_37 | *0.0175* | *0* |  | 0.0121 | 0.00098 |
| Oke\_RAD3223\_33 | *0.0225* | *0* |  | 0.0137 | 0 |  | Oke\_RDDFW92495\_48 | *0.0182* | *0* |  | 0.0131 | 0 |
| Oke\_RAD3480\_76 | *0.0558* | *0* |  | 0.0610 | 0 |  | Oke\_RDDFW92671\_68 | *0.0366* | *0* |  | 0.0337 | 0 |
| Oke\_RAD3664\_73 | *0.0312* | *0* |  | 0.0218 | 0 |  | Oke\_RDDFW92833\_41 | *0.0465* | *0* |  | 0.0333 | 0 |
| Oke\_RAD3693\_30 | *0.0770* | *0* |  | 0.0647 | 0 |  | Oke\_RDDFW93115\_22 | *0.0977* | *0* |  | 0.0852 | 0 |
| Oke\_RAD369\_38 | *0.0423* | *0* |  | 0.0410 | 0 |  | Oke\_RDDFW93316\_60 | *0.0231* | *0* |  | 0.0213 | 0 |
| Oke\_RAD3715\_76 | *0.0437* | *0* |  | 0.0463 | 0 |  | Oke\_RDDFW945\_50 | *0.0357* | *0* |  | 0.0314 | 0 |
| Oke\_RAD3762\_78 | *0.0396* | *0* |  | 0.0263 | 0 |  | Oke\_RDDFW94768\_76 | *0.0342* | *0* |  | 0.0210 | 0 |
| Oke\_RAD3861\_38 | *0.0221* | *0* |  | 0.0223 | 0 |  | Oke\_RDDFW95768\_60 | *0.0238* | *0* |  | 0.0203 | 0 |
| Oke\_RAD3907\_37 | *0.0728* | *0* |  | 0.0663 | 0 |  | Oke\_RDDFW96549\_63 | *0.0840* | *0* |  | 0.0933 | 0 |
| Oke\_RAD3938\_71 | *0.0241* | *0* |  | 0.0275 | 0 |  | Oke\_RDDFW97046\_68 | *0.0330* | *0* |  | 0.0294 | 0 |
| Oke\_RAD3995\_44 | *0.0201* | *0* |  | 0.0212 | 0 |  | Oke\_RDDFW97566\_28 | *0.0572* | *0* |  | 0.0492 | 0 |
| Oke\_RAD4286\_77 | *0.0297* | *0* |  | 0.0227 | 0 |  | Oke\_RDDFW97971\_30 | *0.0315* | *0* |  | 0.0276 | 0 |
| Oke\_RAD4538\_78 | *0.0544* | *0* |  | 0.0580 | 0 |  | Oke\_RDDFW98640\_53 | *0.0670* | *0* |  | 0.0495 | 0 |
| Oke\_RAD4787\_63 | *0.0181* | *0* |  | 0.0171 | 0 |  | Oke\_RDDFW9886\_52 | *0.0433* | *0* |  | 0.0464 | 0 |
| Oke\_RAD4875\_62 | *0.0173* | *0* |  | 0.0198 | 0 |  | Oke\_RFC2\_618 | *0.0006* | *0.53763* |  | 0.0008 | 0.57869 |
| Oke\_RAD5156\_68 | *0.0753* | *0* |  | 0.0806 | 0 |  | Oke\_RH1op\_245 | *0.0134* | *0* |  | 0.0145 | 0 |
| Oke\_RAD5276\_66 | *0.0514* | *0* |  | 0.0528 | 0 |  | Oke\_RS9\_379 | *0.0284* | *0* |  | 0.0108 | 0 |
| Oke\_RAD5434\_50 | *0.0134* | *0* |  | 0.0023 | 0.11339 |  | Oke\_RSPRY1\_106 | *0.0414* | *0* |  | 0.0399 | 0 |
| Oke\_RAD5457\_49 | *0.0409* | *0* |  | 0.0431 | 0 |  | Oke\_TCP1\_78 | *0.0170* | *0* |  | 0.0095 | 0.00196 |
| Oke\_RAD5615\_34 | *0.0243* | *0* |  | 0.0071 | 0.02737 |  | Oke\_TCTA\_99 | *0.0232* | *0* |  | 0.0243 | 0 |
| Oke\_RAD5734\_46 | *0.0768* | *0* |  | 0.0819 | 0 |  | Oke\_U1002\_165 | *0.0542* | *0* |  | 0.0486 | 0 |
| Oke\_RAD5951\_44 | *0.0378* | *0* |  | 0.0329 | 0 |  | Oke\_U1002\_262 | *0.1277* | *0* |  | 0.1228 | 0 |
| Oke\_RAD7067\_53 | *0.0303* | *0* |  | 0.0254 | 0 |  | Oke\_U1008\_83 | *0.0244* | *0* |  | 0.0260 | 0 |
| Oke\_RAD715\_49 | *0.0422* | *0* |  | 0.0358 | 0 |  | Oke\_U1015\_255 | *0.0160* | *0* |  | 0.0127 | 0 |
| Oke\_RAD7431\_40 | *0.0751* | *0* |  | 0.0803 | 0 |  | Oke\_U1017\_52 | *0.0358* | *0* |  | 0.0199 | 0 |
| Oke\_RAD7512\_33 | *0.0564* | *0* |  | 0.0487 | 0 |  | Oke\_U1019\_218 | *0.0175* | *0.00098* |  | 0.0173 | 0.00098 |
| Oke\_RAD7883\_49 | *0.0237* | *0* |  | 0.0074 | 0.00391 |  | Oke\_U1020\_75 | *0.0054* | *0.02639* |  | 0.0043 | 0.05474 |
| Oke\_RAD7936\_41 | *0.0471* | *0* |  | 0.0486 | 0 |  | Oke\_U1021\_102 | *0.0508* | *0* |  | 0.0341 | 0 |
| Oke\_RAD8018\_38 | *0.0097* | *0.00196* |  | 0.0108 | 0 |  | Oke\_U1023\_147 | *0.0115* | *0.00293* |  | 0.0070 | 0.01760 |
| Oke\_RAD8326\_32 | *0.0121* | *0* |  | 0.0087 | 0 |  | Oke\_U1024\_113 | *0.0004* | *0.42131* |  | 0.0012 | 0.31378 |
| Oke\_RAD8335\_79 | *0.0866* | *0* |  | 0.0962 | 0 |  | Oke\_U1028\_100 | *0.1036* | *0* |  | 0.1099 | 0 |
| Oke\_RAD8372\_31 | *0.0434* | *0* |  | 0.0348 | 0 |  | Oke\_U2001\_629 | *0.0513* | *0* |  | 0.0541 | 0 |
| Oke\_RAD8698\_82 | *0.0368* | *0* |  | 0.0387 | 0 |  | Oke\_U2003\_142 | *0.0026* | *0.17498* |  | 0.0020 | 0.24047 |
| Oke\_RAD8799\_30 | *0.1272* | *0* |  | 0.1154 | 0 |  | Oke\_U2005\_62 | *0.0333* | *0* |  | 0.0112 | 0.00098 |
| Oke\_RAD8814\_56 | *0.0696* | *0* |  | 0.0712 | 0 |  | Oke\_U2006\_109 | *0.0243* | *0* |  | 0.0172 | 0 |
| Oke\_RAD8930\_48 | *0.0981* | *0* |  | 0.0499 | 0 |  | Oke\_U2010\_94 | *0.0639* | *0* |  | 0.0439 | 0 |
| Oke\_RAD905\_85 | *0.0229* | *0* |  | 0.0184 | 0 |  | Oke\_U2011\_107 | *0.0123* | *0* |  | 0.0128 | 0 |
| Oke\_RAD9273\_49 | *0.0379* | *0* |  | 0.0385 | 0 |  | Oke\_U2016\_118 | *0.0235* | *0* |  | 0.0214 | 0 |
| Oke\_RAD9447\_73 | *0.0433* | *0* |  | 0.0451 | 0 |  | Oke\_U2017\_87 | *0.0717* | *0* |  | 0.0685 | 0 |
| Oke\_RDDFW10186\_42 | *0.0454* | *0* |  | 0.0381 | 0 |  | Oke\_U2019\_112 | *0.0136* | *0* |  | 0.0133 | 0 |
| Oke\_RDDFW112\_17 | *0.0369* | *0* |  | 0.0352 | 0 |  | Oke\_U2020\_51 | *0.0255* | *0* |  | 0.0139 | 0.00098 |
| Oke\_RDDFW13161\_74 | *0.1235* | *0* |  | 0.0685 | 0 |  | Oke\_U2022\_101 | *0.0886* | *0* |  | 0.0887 | 0 |
| Oke\_RDDFW13803\_76 | *0.0402* | *0* |  | 0.0364 | 0 |  | Oke\_U2024\_93 | *0.0357* | *0* |  | 0.0314 | 0 |
| Oke\_RDDFW14498\_66 | *0.0550* | *0* |  | 0.0281 | 0 |  | Oke\_U2025\_86 | *0.0254* | *0* |  | 0.0149 | 0 |
| Oke\_RDDFW14591\_59 | *0.0881* | *0* |  | 0.0791 | 0 |  | Oke\_U2026\_64 | *0.0314* | *0* |  | 0.0337 | 0 |
| Oke\_RDDFW14903\_53 | *0.0341* | *0* |  | 0.0327 | 0 |  | Oke\_U2029\_79 | *0.0393* | *0* |  | 0.0328 | 0 |
| Oke\_RDDFW15717\_46 | *0.0403* | *0* |  | 0.0424 | 0 |  | Oke\_U2031\_37 | *0.0122* | *0* |  | 0.0074 | 0.00587 |
| Oke\_RDDFW16518\_29 | *0.0045* | *0.16422* |  | 0.0044 | 0.18475 |  | Oke\_U2032\_74 | *0.0158* | *0* |  | 0.0178 | 0 |
| Oke\_RDDFW16781\_68 | *0.0462* | *0* |  | 0.0421 | 0 |  | Oke\_U2033\_122 | *0.0524* | *0* |  | 0.0555 | 0 |
| Oke\_RDDFW16886\_37 | *0.1134* | *0* |  | 0.1065 | 0 |  | Oke\_U2034\_55 | *0.0473* | *0* |  | 0.0508 | 0 |
| Oke\_RDDFW17423\_60 | *0.0909* | *0* |  | 0.0850 | 0 |  | Oke\_U2035\_54 | *0.0819* | *0* |  | 0.0493 | 0 |
| Oke\_RDDFW17478\_56 | *0.0983* | *0* |  | 0.0834 | 0 |  | Oke\_U2037\_76 | *0.0255* | *0* |  | 0.0281 | 0 |
| Oke\_RDDFW18411\_78 | *fixed* |  |  |  |  |  | Oke\_U2041\_84 | *0.0373* | *0* |  | 0.0415 | 0 |
| Oke\_RDDFW19534\_51 | *0.0215* | *0* |  | 0.0200 | 0 |  | Oke\_U2043\_51 | *0.0280* | *0* |  | 0.0244 | 0 |
| Oke\_RDDFW19665\_62 | *0.0516* | *0* |  | 0.0496 | 0 |  | Oke\_U2045\_43 | *0.0110* | *0.00196* |  | 0.0087 | 0.00587 |
| Oke\_RDDFW19805\_61 | *0.0456* | *0* |  | 0.0455 | 0 |  | Oke\_U2048\_91 | *0.0169* | *0* |  | 0.0176 | 0 |
| Oke\_RDDFW19807\_50 | *0.0193* | *0* |  | 0.0220 | 0 |  | Oke\_U2049\_99 | *0.0464* | *0* |  | 0.0423 | 0 |
| Oke\_RDDFW19817\_73 | *0.0151* | *0* |  | 0.0141 | 0 |  | Oke\_U2053\_60 | *0.0227* | *0* |  | 0.0192 | 0 |
| Oke\_RDDFW19905\_31 | *0.0851* | *0* |  | 0.0894 | 0 |  | Oke\_U2054\_58 | *0.0244* | *0* |  | 0.0196 | 0 |
| Oke\_RDDFW20179\_61 | *0.0421* | *0* |  | 0.0316 | 0 |  | Oke\_U2056\_90 | *0.0434* | *0* |  | 0.0270 | 0 |
| Oke\_RDDFW20811\_77 | *0.0422* | *0* |  | 0.0233 | 0 |  | Oke\_U2057\_80 | *0.0265* | *0* |  | 0.0286 | 0 |
| Oke\_RDDFW20999\_31 | *0.0557* | *0* |  | 0.0581 | 0 |  | Oke\_U305\_307 | *0.0367* | *0* |  | 0.0355 | 0 |
| Oke\_RDDFW21285\_59 | *0.0423* | *0* |  | 0.0270 | 0 |  | Oke\_U504\_228 | *0.0367* | *0* |  | 0.0204 | 0 |
| Oke\_RDDFW21890\_73 | *0.0245* | *0* |  | 0.0260 | 0 |  | Oke\_U506\_110 | *0.0278* | *0* |  | 0.0250 | 0 |
| Oke\_RDDFW23444\_56 | *0.1252* | *0* |  | 0.0861 | 0 |  | Oke\_U507\_087 | *0.0278* | *0* |  | 0.0163 | 0 |
| Oke\_RDDFW24615\_60 | *0.0480* | *0* |  | 0.0319 | 0 |  | Oke\_U507\_286 | *0.0325* | *0* |  | 0.0348 | 0 |
| Oke\_RDDFW24690\_58 | *0.0617* | *0* |  | 0.0627 | 0 |  | Oke\_U509\_219 | *0.0507* | *0* |  | 0.0433 | 0 |
| Oke\_RDDFW25476\_76 | *0.0259* | *0* |  | 0.0206 | 0 |  | Oke\_U511\_271 | *0.1188* | *0* |  | 0.1320 | 0 |
| Oke\_RDDFW25539\_63 | *0.0357* | *0* |  | 0.0285 | 0 |  | Oke\_U514\_150 | *0.0343* | *0* |  | 0.0392 | 0 |
| Oke\_RDDFW27843\_66 | *0.0509* | *0* |  | 0.0516 | 0 |  | Oke\_arf\_319 | *0.0319* | *0* |  | 0.0304 | 0 |
| Oke\_RDDFW28182\_57 | *0.0507* | *0* |  | 0.0428 | 0 |  | Oke\_brd2\_118 | *0.0083* | *0.00587* |  | 0.0063 | 0.02053 |
| Oke\_RDDFW28560\_20 | *0.0337* | *0* |  | 0.0308 | 0 |  | Oke\_brp16\_65 | *0.0125* | *0* |  | 0.0102 | 0.00098 |
| Oke\_RDDFW29139\_38 | *0.0631* | *0* |  | 0.0317 | 0 |  | Oke\_ccd16\_77 | *0.0438* | *0* |  | 0.0446 | 0 |
| Oke\_RDDFW29994\_56 | *0.0476* | *0* |  | 0.0513 | 0 |  | Oke\_cjo57\_86 | *0.0581* | *0* |  | 0.0626 | 0 |
| Oke\_RDDFW30681\_49 | *0.0392* | *0* |  | 0.0368 | 0 |  | Oke\_ctgf\_105 | *0.0630* | *0* |  | 0.0629 | 0 |
| Oke\_RDDFW32214\_64 | *0.0167* | *0* |  | 0.0128 | 0 |  | Oke\_e2ig5\_50 | *0.0231* | *0* |  | 0.0234 | 0 |
| Oke\_RDDFW35061\_72 | *0.0286* | *0* |  | 0.0302 | 0 |  | Oke\_eif4ebp2\_64 | *0.0486* | *0* |  | 0.0322 | 0 |
| Oke\_RDDFW36545\_52 | *0.0861* | *0* |  | 0.0518 | 0 |  | Oke\_eif4g1\_43 | *0.0412* | *0* |  | 0.0334 | 0 |
| Oke\_RDDFW36920\_78 | *0.0670* | *0* |  | 0.0713 | 0 |  | Oke\_f5\_71 | *0.0143* | *0* |  | 0.0069 | 0.02542 |
| Oke\_RDDFW37304\_51 | *0.0507* | *0* |  | 0.0540 | 0 |  | Oke\_glrx1\_78 | *0.0290* | *0* |  | 0.0264 | 0 |
| Oke\_RDDFW37547\_71 | *0.0309* | *0* |  | 0.0182 | 0 |  | Oke\_hsc71\_199 | *0.0325* | *0* |  | 0.0257 | 0 |
| Oke\_RDDFW37906\_35 | *0.0444* | *0* |  | 0.0386 | 0 |  | Oke\_il\_1racp\_67 | *0.0114* | *0* |  | 0.0122 | 0.00196 |
| Oke\_RDDFW37977\_64 | *0.0242* | *0* |  | 0.0089 | 0.00587 |  | Oke\_lactb2\_71 | *0.0472* | *0* |  | 0.0410 | 0 |
| Oke\_RDDFW38189\_70 | *0.1651* | *0* |  | 0.0753 | 0 |  | Oke\_mcfd2\_86 | *0.0656* | *0* |  | 0.0712 | 0 |
| Oke\_RDDFW38998\_48 | *0.0355* | *0* |  | 0.0380 | 0 |  | Oke\_mgll\_49 | *0.0130* | *0* |  | 0.0121 | 0.00196 |
| Oke\_RDDFW39056\_71 | *0.0570* | *0* |  | 0.0558 | 0 |  | Oke\_nc2b\_148 | *0.0266* | *0* |  | 0.0187 | 0 |
| Oke\_RDDFW39550\_74 | *0.0278* | *0* |  | 0.0116 | 0.00098 |  | Oke\_ndub3\_58 | *0.0105* | *0* |  | 0.0084 | 0.00391 |
| Oke\_RDDFW41741\_28 | *0.0753* | *0* |  | 0.0723 | 0 |  | Oke\_pgap\_92 | *0.0303* | *0* |  | 0.0317 | 0 |
| Oke\_RDDFW41894\_64 | *0.0591* | *0* |  | 0.0225 | 0 |  | Oke\_pnrc2\_78 | *0.0249* | *0* |  | 0.0170 | 0 |
| Oke\_RDDFW41968\_67 | *0.0422* | *0* |  | 0.0463 | 0 |  | Oke\_psmd9\_057 | *0.0085* | *0.00489* |  | 0.0078 | 0.01466 |
| Oke\_RDDFW44691\_36 | *0.0667* | *0* |  | 0.0725 | 0 |  | Oke\_psmd9\_188 | *0.0551* | *0* |  | 0.0440 | 0 |
| Oke\_RDDFW45450\_75 | *0.0507* | *0* |  | 0.0507 | 0 |  | Oke\_rab5a\_117 | *0.0057* | *0.02053* |  | 0.0075 | 0.00391 |
| Oke\_RDDFW46094\_46 | *0.0176* | *0* |  | 0.0169 | 0 |  | Oke\_ras1\_249 | *0.0680* | *0* |  | 0.0368 | 0 |
| Oke\_RDDFW4669\_39 | *0.0327* | *0* |  | 0.0345 | 0 |  | Oke\_serpin\_140 | *0.0833* | *0* |  | 0.0145 | 0 |
| Oke\_RDDFW46886\_62 | *0.0492* | *0* |  | 0.0514 | 0 |  | Oke\_slc1a3a\_86 | *0.0216* | *0* |  | 0.0173 | 0 |
| Oke\_RDDFW47500\_38 | *0.0427* | *0* |  | 0.0434 | 0 |  | Oke\_sylc\_90 | *0.0202* | *0* |  | 0.0234 | 0 |
| Oke\_RDDFW47666\_40 | *0.1060* | *0* |  | 0.0593 | 0 |  | Oke\_thic\_84 | *0.0888* | *0* |  | 0.0666 | 0 |
| Oke\_RDDFW47763\_68 | *0.0355* | *0* |  | 0.0257 | 0 |  | Oke\_txnrd1\_74 | *0.0192* | *0* |  | 0.0133 | 0 |
| Oke\_RDDFW47838\_76 | *0.0215* | *0* |  | 0.0229 | 0 |  | Oke\_u1\_519 | *0.0567* | *0* |  | 0.0361 | 0 |
| Oke\_RDDFW48220\_71 | *0.0304* | *0* |  | 0.0308 | 0 |  | Oke\_u200\_385 | *0.0159* | *0* |  | 0.0050 | 0.09775 |
| Oke\_RDDFW48558\_66 | *0.0444* | *0* |  | 0.0395 | 0 |  | Oke\_u216\_222 | *0.0244* | *0* |  | 0.0213 | 0 |
| Oke\_RDDFW48576\_24 | *0.0719* | *0* |  | 0.0489 | 0 |  | avg | *0.0431* |  |  | 0.0359 |  |
| Oke\_RDDFW48705\_55 | *0.0560* | *0* |  | 0.0289 | 0 |  | SD | *0.0283* |  |  | 0.0250 |  |

Table 4. Final number (N) of samples per collection included in analyses and genetic statistics for each collection, including: number of fixed loci and loci deviating from Hardy-Weinberg Equilibrium (HWE) expectations, the percent of polymorphic and loci out of HWE, observed and unbiased expected heterozygosity (Ho and uHe), the fixation index (FIS), and number on map in Figure 1.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  | % | <0.05 | % |  |  |  |
| Map | Region\_run | Populations | Final N | fixed loci | polymorphic | N out of HWE | out of HWE | Ho | uHe | FIS |
| 1 | Fraser | Hopedale | 39 | 17 | 95.11 | 22 | 6.65 | 0.3214 | 0.3142 | -0.0285 |
| 2 | Fraser | Peach | 43 | 19 | 94.54 | 16 | 4.86 | 0.3157 | 0.3209 | 0.0031 |
| 3 | Fraser | Squawkum | 32 | 15 | 95.69 | 21 | 6.31 | 0.3074 | 0.3171 | 0.0084 |
| 4 | GeorgiaSt | Big Qualicum | 48 | 14 | 95.98 | 20 | 5.99 | 0.3165 | 0.3208 | 0.0036 |
| 5 | GeorgiaSt | Campbell | 32 | 14 | 95.98 | 12 | 3.59 | 0.3343 | 0.3282 | -0.0359 |
| 6 | GeorgiaSt | Cheakamus | 42 | 11 | 96.84 | 18 | 5.34 | 0.3198 | 0.3228 | -0.0060 |
| 7 | GeorgiaSt | Cowichan | 25 | 15 | 95.69 | 17 | 5.11 | 0.3165 | 0.3220 | -0.0097 |
| 8 | GeorgiaSt | Lang | 33 | 13 | 96.26 | 12 | 3.58 | 0.3191 | 0.3225 | -0.0098 |
| 9 | GeorgiaSt | Little Qualicum | 46 | 13 | 96.26 | 17 | 5.07 | 0.3255 | 0.3221 | -0.0165 |
| 10 | GeorgiaSt | Nanaimo | 50 | 12 | 96.55 | 39 | 11.61 | 0.3253 | 0.3274 | -0.0067 |
| 11 | GeorgiaSt | Phillips | 44 | 12 | 96.55 | 21 | 6.25 | 0.3279 | 0.3244 | -0.0195 |
| 12 | GeorgiaSt | Puntledge | 48 | 12 | 96.55 | 33 | 9.82 | 0.3183 | 0.3244 | 0.0082 |
| 13 | GeorgiaSt | Snake | 44 | 11 | 96.84 | 27 | 8.01 | 0.3364 | 0.3270 | -0.0330 |
| 14 | GeorgiaSt | Southgate R | 48 | 10 | 97.13 | 16 | 4.73 | 0.3172 | 0.3190 | -0.0047 |
| 15 | HoodCanal\_F | Anderson | 48 | 14 | 95.98 | 26 | 7.78 | 0.3089 | 0.3166 | 0.0078 |
| 16 | HoodCanal\_F | Big Beef | 47 | 12 | 96.55 | 18 | 5.36 | 0.3215 | 0.3192 | -0.0141 |
| 17 | HoodCanal\_F | Dewatto | 47 | 13 | 96.26 | 17 | 5.07 | 0.3184 | 0.3180 | -0.0167 |
| 18 | HoodCanal\_F | Duckabush\_F | 46 | 15 | 95.69 | 12 | 3.60 | 0.3134 | 0.3167 | -0.0042 |
| 19 | HoodCanal\_F | HammaHamma\_F | 19 | 21 | 93.97 | 25 | 7.65 | 0.2914 | 0.3047 | 0.0127 |
| 20 | HoodCanal\_F | Lilliwaup\_F | 47 | 15 | 95.69 | 19 | 5.71 | 0.3123 | 0.3138 | -0.0053 |
| 21 | HoodCanal\_F | NF\_Skokomish | 30 | 20 | 94.25 | 22 | 6.71 | 0.3065 | 0.3136 | 0.0010 |
| 22 | HoodCanal\_S | Dosewallips\_S | 36 | 29 | 91.67 | 23 | 7.21 | 0.2732 | 0.2807 | 0.0097 |
| 23 | HoodCanal\_S | HammaHamma\_S | 59 | 25 | 92.82 | 30 | 9.29 | 0.2645 | 0.2764 | 0.0259 |
| 24 | HoodCanal\_S | Duckabush\_S | 47 | 23 | 93.39 | 15 | 4.62 | 0.2744 | 0.2794 | 0.0052 |
| 25 | JohnstoneSt | Nimpkish | 41 | 11 | 96.84 | 20 | 5.93 | 0.3244 | 0.3161 | -0.0388 |
| 26 | LowColumbia | I\_205 | 91 | 10 | 97.13 | 25 | 7.40 | 0.3073 | 0.3126 | 0.0082 |
| 27 | LowColumbia | Horsetail | 26 | 30 | 91.38 | 15 | 4.72 | 0.3119 | 0.3074 | -0.0310 |
| 28 | LowColumbia | Ives Island | 64 | 13 | 96.26 | 21 | 6.27 | 0.3029 | 0.3087 | 0.0098 |
| 29 | NorthPS | Lower\_Sauk | 24 | 15 | 95.69 | 14 | 4.20 | 0.3133 | 0.3132 | -0.0176 |
| 30 | NorthPS | Nooksack | 32 | 13 | 96.26 | 20 | 5.97 | 0.3243 | 0.3032 | -0.0700 |
| 31 | NorthPS | Skagit\_lower\_mainstem | 29 | 15 | 95.69 | 23 | 6.91 | 0.3110 | 0.3158 | -0.0078 |
| 32 | NorthPS | Snohomish | 34 | 16 | 95.40 | 15 | 4.52 | 0.3221 | 0.3221 | -0.0118 |
| 33 | NorthPS | Stillaguamish | 39 | 16 | 95.40 | 16 | 4.82 | 0.3127 | 0.3152 | -0.0077 |
| 34 | NorthPS | upper\_Skagit | 45 | 11 | 96.84 | 20 | 5.93 | 0.3134 | 0.3178 | 0.0044 |
| 35 | SJF | Dungeness (Beebe Cr) | 38 | 12 | 96.55 | 12 | 3.57 | 0.3245 | 0.3254 | -0.0183 |
| 36 | SouthPS | Chico/Grovers | 55 | 13 | 96.26 | 21 | 6.27 | 0.3058 | 0.3145 | 0.0173 |
| 37 | SouthPS | Kennedy | 47 | 19 | 94.54 | 14 | 4.26 | 0.3094 | 0.3099 | -0.0119 |
| 38 | SouthPS | Skookum | 37 | 20 | 94.25 | 21 | 6.40 | 0.3061 | 0.3124 | 0.0073 |
| 39 | SouthPS\_W | DIRU\_Puyallup H | 43 | 14 | 95.98 | 15 | 4.49 | 0.3139 | 0.3134 | -0.0186 |
| 40 | SouthPS\_W | Nisqually | 74 | 17 | 95.11 | 27 | 8.16 | 0.3137 | 0.3169 | 0.0051 |
| 41 | WCVI | Conuma | 44 | 15 | 95.69 | 18 | 5.41 | 0.3201 | 0.3225 | -0.0061 |
| 42 | WCVI | Nitinat | 48 | 12 | 96.55 | 14 | 4.17 | 0.3197 | 0.3206 | -0.0118 |
| 43 | WCVI | Sooke | 32 | 15 | 95.69 | 19 | 5.71 | 0.3290 | 0.3214 | -0.0424 |
|  |  | Grand Total or avg | 1843 | 15.4 | 95.58 | 19.7 | 5.93 | 0.3133 | 0.3149 | -0.0086 |
|  |  | Standard error |  |  |  |  |  | 0.0014 | 0.0013 | 0.0014 |

**Table 5. Pairwise FST values among regions (top) with pairwise values among populations at bottom (please zoom to see details, Hood Canal Summers and Lower Columbia Falls excluded). Values are colored with a heat map with low values in green, high values in red and intermediate values in yellow. Pink cells are p-values > 0.01.**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | HoodCanal\_S | LowColumbia | GeorgiaSt | SJF | HoodCanal\_F | NorthPS | SouthPS\_F | JohnstoneSt | Fraser | WCVI | SouthPS\_W |
| HoodCanal\_S |  |  |  |  |  |  |  |  |  |  |  |
| LowColumbia | 0.0969 |  |  |  |  |  |  |  |  |  |  |
| GeorgiaSt | 0.0963 | 0.0371 |  |  |  |  |  |  |  |  |  |
| SJF | 0.0824 | 0.0300 | 0.0125 |  |  |  |  |  |  |  |  |
| HoodCanal\_F | 0.0694 | 0.0419 | 0.0376 | 0.0237 |  |  |  |  |  |  |  |
| NorthPS | 0.0869 | 0.0279 | 0.0148 | 0.0114 | 0.0300 |  |  |  |  |  |  |
| SouthPS\_F | 0.0750 | 0.0561 | 0.0562 | 0.0426 | 0.0265 | 0.0472 |  |  |  |  |  |
| JohnstoneSt | 0.1048 | 0.0433 | 0.0185 | 0.0200 | 0.0484 | 0.0262 | 0.0633 |  |  |  |  |
| Fraser | 0.1013 | 0.0358 | 0.0240 | 0.0248 | 0.0448 | 0.0189 | 0.0631 | 0.0375 |  |  |  |
| WCVI | 0.1039 | 0.0497 | 0.0263 | 0.0264 | 0.0548 | 0.0338 | 0.0668 | 0.0245 | 0.0442 |  |  |
| SouthPS\_W | 0.0742 | 0.0482 | 0.0483 | 0.0351 | 0.0254 | 0.0377 | 0.0278 | 0.0574 | 0.0532 | 0.0635 |  |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 4 |  | Southgate | Nanaimo | Puntledge | LilQual | BigQual | Snake | Phillips | Lang | Cowichan | Campbell | Cheakamus | Dungeness | NFSkok | HammaF | BigBeef | Lilli\_F | Dewatto | Anderson | Duckabush | UpSkagit | Nooksack | Snohomish | Stillaguamish | LoSkagit | LoSauk | ChicGrov | Skookum | Kennedy | Nimpkish | Peach | Squawkum | Hopedale | Nitnat | Sooke | Conuma | PuyallupH | Nisqually |
| GeorgiaSt | Southgate | \* | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| GeorgiaSt | Nanaimo | 0.0194 | - | 0.0024 | 0.0006 | 0.0056 | 0.0002 | 0.0004 | 0.0762 | 0.1201 | 0.0456 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| GeorgiaSt | Puntledge | 0.0152 | 0.0044 | \* | 0.0014 | 0.0015 | 0.0001 | 0.0004 | 0.1177 | 0.0324 | 0.0929 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0001 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| GeorgiaSt | LilQual | 0.0150 | 0.0044 | 0.0037 | - | 0.4017 | 0.0002 | 0.0000 | 0.0942 | 0.5128 | 0.0126 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| GeorgiaSt | BigQual | 0.0150 | 0.0035 | 0.0037 | 0.0001 | \* | 0.0000 | 0.0002 | 0.0016 | 0.0503 | 0.0022 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| GeorgiaSt | Snake | 0.0130 | 0.0056 | 0.0056 | 0.0040 | 0.0047 | - | 0.0000 | 0.0122 | 0.0002 | 0.0056 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| GeorgiaSt | Phillips | 0.0109 | 0.0051 | 0.0046 | 0.0037 | 0.0038 | 0.0047 | \* | 0.0287 | 0.0275 | 0.1919 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| GeorgiaSt | Lang | 0.0136 | 0.0023 | 0.0017 | 0.0014 | 0.0035 | 0.0026 | 0.0020 | - | 0.1276 | 0.4197 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| GeorgiaSt | Cowichan | 0.0139 | 0.0024 | 0.0037 | -0.0004 | 0.0025 | 0.0067 | 0.0027 | 0.0017 | \* | 0.1946 | 0.0055 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0001 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| GeorgiaSt | Campbell | 0.0110 | 0.0029 | 0.0019 | 0.0026 | 0.0034 | 0.0028 | 0.0007 | -0.0001 | 0.0011 | - | 0.0028 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0002 | 0.0000 | 0.0000 | 0.0000 |
| GeorgiaSt | Cheakamus | 0.0119 | 0.0072 | 0.0056 | 0.0079 | 0.0058 | 0.0050 | 0.0046 | 0.0059 | 0.0039 | 0.0035 | \* | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| SJF | Dungeness | 0.0236 | 0.0110 | 0.0127 | 0.0109 | 0.0110 | 0.0115 | 0.0112 | 0.0123 | 0.0097 | 0.0109 | 0.0128 | - | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0002 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| HoodCanal\_F | NFSkok | 0.0385 | 0.0316 | 0.0309 | 0.0309 | 0.0289 | 0.0294 | 0.0323 | 0.0332 | 0.0277 | 0.0331 | 0.0325 | 0.0167 | \* | 0.0370 | 0.8312 | 0.1958 | 0.9506 | 0.0404 | 0.8453 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| HoodCanal\_F | HammaF | 0.0525 | 0.0434 | 0.0412 | 0.0409 | 0.0420 | 0.0419 | 0.0485 | 0.0452 | 0.0420 | 0.0439 | 0.0437 | 0.0263 | 0.0042 | - | 0.0048 | 0.0003 | 0.0017 | 0.0003 | 0.0020 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| HoodCanal\_F | BigBeef | 0.0440 | 0.0355 | 0.0364 | 0.0363 | 0.0353 | 0.0347 | 0.0392 | 0.0349 | 0.0305 | 0.0373 | 0.0392 | 0.0225 | -0.0013 | 0.0051 | \* | 0.0238 | 0.4609 | 0.2341 | 0.0489 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| HoodCanal\_F | Lilli\_F | 0.0504 | 0.0407 | 0.0414 | 0.0420 | 0.0399 | 0.0413 | 0.0446 | 0.0431 | 0.0401 | 0.0440 | 0.0465 | 0.0262 | 0.0010 | 0.0082 | 0.0019 | - | 0.1046 | 0.2312 | 0.0003 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| HoodCanal\_F | Dewatto | 0.0453 | 0.0350 | 0.0354 | 0.0354 | 0.0360 | 0.0362 | 0.0385 | 0.0338 | 0.0302 | 0.0368 | 0.0402 | 0.0249 | -0.0022 | 0.0059 | -0.0001 | 0.0011 | \* | 0.3613 | 0.1026 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| HoodCanal\_F | Anderson | 0.0491 | 0.0415 | 0.0386 | 0.0386 | 0.0388 | 0.0401 | 0.0422 | 0.0406 | 0.0375 | 0.0407 | 0.0445 | 0.0256 | 0.0024 | 0.0078 | 0.0006 | 0.0007 | 0.0003 | - | 0.0030 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| HoodCanal\_F | Duckabush | 0.0483 | 0.0386 | 0.0370 | 0.0370 | 0.0372 | 0.0373 | 0.0396 | 0.0386 | 0.0362 | 0.0395 | 0.0411 | 0.0236 | -0.0016 | 0.0065 | 0.0015 | 0.0040 | 0.0012 | 0.0029 | \* | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| NorthPS | UpSkagit | 0.0254 | 0.0175 | 0.0159 | 0.0161 | 0.0156 | 0.0183 | 0.0183 | 0.0198 | 0.0160 | 0.0145 | 0.0127 | 0.0124 | 0.0173 | 0.0304 | 0.0256 | 0.0281 | 0.0262 | 0.0299 | 0.0282 | - | 0.0000 | 0.0646 | 0.4228 | 0.0000 | 0.1794 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| NorthPS | Nooksack | 0.0195 | 0.0134 | 0.0059 | 0.0056 | 0.0097 | 0.0113 | 0.0111 | 0.0146 | 0.0121 | 0.0069 | 0.0086 | 0.0043 | 0.0262 | 0.0499 | 0.0312 | 0.0396 | 0.0304 | 0.0384 | 0.0337 | 0.0078 | \* | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| NorthPS | Snohomish | 0.0256 | 0.0129 | 0.0122 | 0.0147 | 0.0134 | 0.0132 | 0.0137 | 0.0138 | 0.0128 | 0.0110 | 0.0106 | 0.0108 | 0.0181 | 0.0291 | 0.0256 | 0.0288 | 0.0244 | 0.0285 | 0.0276 | 0.0016 | 0.0066 | - | 0.2484 | 0.0000 | 0.0046 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| NorthPS | Stillaguamish | 0.0220 | 0.0151 | 0.0147 | 0.0140 | 0.0143 | 0.0156 | 0.0171 | 0.0168 | 0.0128 | 0.0139 | 0.0135 | 0.0111 | 0.0185 | 0.0329 | 0.0271 | 0.0320 | 0.0271 | 0.0319 | 0.0296 | -0.0002 | 0.0054 | 0.0004 | \* | 0.0000 | 0.0060 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| NorthPS | LoSkagit | 0.0182 | 0.0130 | 0.0101 | 0.0099 | 0.0127 | 0.0144 | 0.0103 | 0.0121 | 0.0091 | 0.0110 | 0.0117 | 0.0141 | 0.0257 | 0.0445 | 0.0314 | 0.0355 | 0.0306 | 0.0365 | 0.0338 | 0.0079 | 0.0126 | 0.0095 | 0.0072 | - | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| NorthPS | LoSauk | 0.0302 | 0.0203 | 0.0169 | 0.0196 | 0.0193 | 0.0218 | 0.0225 | 0.0238 | 0.0206 | 0.0182 | 0.0168 | 0.0155 | 0.0213 | 0.0326 | 0.0276 | 0.0315 | 0.0270 | 0.0340 | 0.0306 | 0.0010 | 0.0088 | 0.0042 | 0.0034 | 0.0126 | \* | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| SouthPS | ChicGrov | 0.0637 | 0.0519 | 0.0537 | 0.0527 | 0.0521 | 0.0502 | 0.0525 | 0.0505 | 0.0468 | 0.0528 | 0.0539 | 0.0398 | 0.0186 | 0.0254 | 0.0206 | 0.0224 | 0.0221 | 0.0240 | 0.0192 | 0.0359 | 0.0470 | 0.0366 | 0.0362 | 0.0442 | 0.0363 | - | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| SouthPS | Skookum | 0.0660 | 0.0559 | 0.0584 | 0.0586 | 0.0547 | 0.0538 | 0.0547 | 0.0579 | 0.0514 | 0.0586 | 0.0575 | 0.0408 | 0.0249 | 0.0371 | 0.0230 | 0.0294 | 0.0268 | 0.0286 | 0.0266 | 0.0476 | 0.0583 | 0.0461 | 0.0491 | 0.0541 | 0.0520 | 0.0125 | \* | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| SouthPS | Kennedy | 0.0728 | 0.0631 | 0.0619 | 0.0619 | 0.0608 | 0.0598 | 0.0621 | 0.0618 | 0.0543 | 0.0633 | 0.0643 | 0.0471 | 0.0251 | 0.0327 | 0.0285 | 0.0314 | 0.0296 | 0.0310 | 0.0297 | 0.0492 | 0.0559 | 0.0482 | 0.0489 | 0.0567 | 0.0470 | 0.0107 | 0.0053 | - | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| Johnstone | Nimpkish | 0.0268 | 0.0218 | 0.0184 | 0.0172 | 0.0173 | 0.0164 | 0.0140 | 0.0193 | 0.0178 | 0.0152 | 0.0184 | 0.0200 | 0.0403 | 0.0548 | 0.0465 | 0.0523 | 0.0478 | 0.0489 | 0.0483 | 0.0267 | 0.0241 | 0.0249 | 0.0252 | 0.0248 | 0.0315 | 0.0578 | 0.0643 | 0.0678 | \* | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| Fraser | Peach | 0.0337 | 0.0261 | 0.0235 | 0.0275 | 0.0280 | 0.0259 | 0.0260 | 0.0259 | 0.0240 | 0.0220 | 0.0256 | 0.0270 | 0.0383 | 0.0520 | 0.0446 | 0.0474 | 0.0419 | 0.0458 | 0.0476 | 0.0226 | 0.0207 | 0.0186 | 0.0221 | 0.0133 | 0.0220 | 0.0583 | 0.0628 | 0.0666 | 0.0400 | - | 0.0669 | 0.1843 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| Fraser | Squawkum | 0.0286 | 0.0206 | 0.0177 | 0.0198 | 0.0226 | 0.0204 | 0.0217 | 0.0203 | 0.0201 | 0.0166 | 0.0207 | 0.0216 | 0.0387 | 0.0490 | 0.0411 | 0.0464 | 0.0420 | 0.0437 | 0.0458 | 0.0202 | 0.0183 | 0.0164 | 0.0200 | 0.0114 | 0.0175 | 0.0592 | 0.0661 | 0.0692 | 0.0335 | 0.0020 | \* | 0.0018 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| Fraser | Hopedale | 0.0337 | 0.0255 | 0.0222 | 0.0258 | 0.0273 | 0.0229 | 0.0250 | 0.0245 | 0.0238 | 0.0204 | 0.0214 | 0.0257 | 0.0366 | 0.0526 | 0.0436 | 0.0477 | 0.0413 | 0.0463 | 0.0480 | 0.0222 | 0.0223 | 0.0169 | 0.0210 | 0.0142 | 0.0206 | 0.0568 | 0.0644 | 0.0646 | 0.0390 | 0.0006 | 0.0037 | - | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| WCVI | Nitnat | 0.0384 | 0.0349 | 0.0326 | 0.0342 | 0.0311 | 0.0333 | 0.0254 | 0.0323 | 0.0359 | 0.0304 | 0.0375 | 0.0330 | 0.0522 | 0.0656 | 0.0591 | 0.0658 | 0.0600 | 0.0624 | 0.0618 | 0.0401 | 0.0356 | 0.0368 | 0.0397 | 0.0341 | 0.0461 | 0.0703 | 0.0695 | 0.0773 | 0.0276 | 0.0525 | 0.0489 | 0.0502 | \* | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| WCVI | Sooke | 0.0174 | 0.0109 | 0.0075 | 0.0062 | 0.0078 | 0.0102 | 0.0054 | 0.0104 | 0.0090 | 0.0053 | 0.0113 | 0.0125 | 0.0334 | 0.0493 | 0.0344 | 0.0428 | 0.0344 | 0.0379 | 0.0385 | 0.0210 | 0.0171 | 0.0156 | 0.0189 | 0.0143 | 0.0256 | 0.0478 | 0.0543 | 0.0551 | 0.0171 | 0.0305 | 0.0251 | 0.0307 | 0.0156 | - | 0.0000 | 0.0000 | 0.0000 |
| WCVI | Conuma | 0.0400 | 0.0387 | 0.0360 | 0.0380 | 0.0372 | 0.0373 | 0.0287 | 0.0369 | 0.0366 | 0.0322 | 0.0394 | 0.0338 | 0.0571 | 0.0707 | 0.0626 | 0.0691 | 0.0641 | 0.0635 | 0.0660 | 0.0449 | 0.0410 | 0.0397 | 0.0450 | 0.0404 | 0.0520 | 0.0731 | 0.0726 | 0.0815 | 0.0288 | 0.0550 | 0.0499 | 0.0554 | 0.0059 | 0.0147 | \* | 0.0000 | 0.0000 |
| SouthPS\_W | PuyallupH | 0.0568 | 0.0477 | 0.0477 | 0.0464 | 0.0427 | 0.0433 | 0.0451 | 0.0456 | 0.0433 | 0.0460 | 0.0457 | 0.0326 | 0.0138 | 0.0248 | 0.0187 | 0.0238 | 0.0241 | 0.0246 | 0.0214 | 0.0311 | 0.0437 | 0.0308 | 0.0320 | 0.0418 | 0.0342 | 0.0195 | 0.0258 | 0.0285 | 0.0538 | 0.0525 | 0.0518 | 0.0488 | 0.0679 | 0.0412 | 0.0717 | - | 0.0000 |
| SouthPS\_W | Nisqually | 0.0633 | 0.0541 | 0.0544 | 0.0520 | 0.0497 | 0.0506 | 0.0519 | 0.0505 | 0.0483 | 0.0531 | 0.0521 | 0.0375 | 0.0212 | 0.0312 | 0.0296 | 0.0324 | 0.0305 | 0.0323 | 0.0279 | 0.0374 | 0.0460 | 0.0353 | 0.0358 | 0.0451 | 0.0387 | 0.0293 | 0.0318 | 0.0319 | 0.0610 | 0.0550 | 0.0583 | 0.0529 | 0.0730 | 0.0507 | 0.0766 | 0.0112 | - |

Table 6. ONCOR assignment results for assignment to population of origin (pop) in first column, and assignment to regional group along diagonal. Percentage of assignment to populations are colored with a heat map from low (green) to high (red) and assignments to region are red.

|  |  |  | regional group | | | | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| region | population | pop | HoodCanalF | HoodCanalS | NorthPS | SJF | SouthPS | SouthPSW | LowColumbia | Fraser | GeorgiaSt | JohnstoneSt | WCVI |
| HoodCanal\_F | Anderson | 0.3130 | 0.9995 | 0 | 0.0002 | 0.0001 | 0.0002 | 0.0001 | 0 | 0 | 0 | 0 | 0 |
| HoodCanal\_F | BigBeef\_F | 0.3494 | 0.9990 | 0 | 0 | 0.0001 | 0.0003 | 0.0006 | 0 | 0 | 0.0001 | 0 | 0.0001 |
| HoodCanal\_F | Dewatto | 0.2813 | 0.9991 | 0 | 0.0001 | 0.0003 | 0.0004 | 0.0002 | 0 | 0 | 0 | 0 | 0 |
| HoodCanal\_F | Duckabush\_F | 0.4907 | 0.9979 | 0 | 0.0003 | 0.0001 | 0.0012 | 0.0006 | 0 | 0 | 0 | 0 | 0.0001 |
| HoodCanal\_F | Lilliwaup\_F | 0.4000 | 0.9995 | 0 | 0.0003 | 0.0001 | 0.0002 | 0.0001 | 0 | 0 | 0 | 0 | 0 |
| HoodCanal\_F | HammaHamma\_F | 0.3943 | 0.9979 | 0 | 0.0008 | 0.0002 | 0.0005 | 0.0006 | 0 | 0 | 0.0001 | 0 | 0 |
| HoodCanal\_F | NF\_Skokomish | 0.0884 | 0.9907 | 0 | 0.0032 | 0.0004 | 0.0011 | 0.0045 | 0.0002 | 0 | 0.0001 | 0 | 0 |
| HoodCanal\_S | Dosewallips\_S | 0.3741 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HoodCanal\_S | HammaHamma\_S | 0.8280 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| HoodCanal\_S | Duckabush\_S | 0.5637 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| NorthPS | Lower\_Sauk | 0.1810 | 0.0006 | 0 | 0.9930 | 0.0012 | 0.0001 | 0.0001 | 0.0005 | 0.0022 | 0.0021 | 0.0001 | 0.0004 |
| NorthPS | Nooksack | 0.8474 | 0.0002 | 0 | 0.9483 | 0.0116 | 0 | 0 | 0.0001 | 0.0008 | 0.0359 | 0.0004 | 0.0029 |
| NorthPS | Skagit\_lower\_main | 0.6577 | 0.0005 | 0 | 0.8494 | 0.0028 | 0 | 0 | 0.0011 | 0.0374 | 0.1002 | 0.0003 | 0.0085 |
| NorthPS | Snohomish | 0.4057 | 0.0020 | 0 | 0.9380 | 0.0065 | 0.0001 | 0.0002 | 0.0005 | 0.0069 | 0.0438 | 0.0003 | 0.0020 |
| NorthPS | Stillaguamish | 0.4095 | 0.0003 | 0 | 0.9828 | 0.0021 | 0.0001 | 0.0001 | 0.0004 | 0.0008 | 0.0130 | 0.0004 | 0.0002 |
| NorthPS | upper\_Skagit | 0.5854 | 0.0009 | 0 | 0.9886 | 0.0022 | 0.0001 | 0.0002 | 0.0006 | 0.0010 | 0.0064 | 0.0001 | 0.0003 |
| SJF | Dungeness | 0.8723 | 0.0049 | 0 | 0.0329 | 0.8723 | 0.0001 | 0.0001 | 0.0006 | 0.0004 | 0.0833 | 0.0009 | 0.0047 |
| SouthPS | Chico/Grovers | 0.9758 | 0.0039 | 0 | 0.0001 | 0 | 0.9944 | 0.0017 | 0 | 0 | 0 | 0 | 0 |
| SouthPS | Kennedy | 0.9119 | 0.0004 | 0 | 0 | 0 | 0.9989 | 0.0008 | 0 | 0 | 0 | 0 | 0 |
| SouthPS | Skookum | 0.7790 | 0.0019 | 0 | 0 | 0.0001 | 0.9971 | 0.0010 | 0 | 0 | 0 | 0 | 0 |
| SouthPS\_W | DIRU\_Puyallup | 0.9426 | 0.0062 | 0 | 0.0004 | 0.0001 | 0.0055 | 0.9878 | 0 | 0 | 0 | 0 | 0.0001 |
| SouthPS\_W | Nisqually | 0.9964 | 0.0003 | 0 | 0.0001 | 0.0001 | 0.0003 | 0.9994 | 0 | 0 | 0 | 0 | 0 |
| LowColumbia | I 205 | 0.8563 | 0.0001 | 0 | 0.0004 | 0.0002 | 0 | 0 | 0.9993 | 0 | 0.0001 | 0 | 0 |
| LowColumbia | Horsetail | 0.5125 | 0 | 0 | 0.0002 | 0 | 0 | 0 | 0.9998 | 0.0001 | 0 | 0 | 0 |
| LowColumbia | IvesIs | 0.5993 | 0.0001 | 0 | 0.0003 | 0.0001 | 0 | 0 | 0.9994 | 0.0001 | 0.0001 | 0 | 0 |
| Fraser | Hopedale | 0.5165 | 0 | 0 | 0.0030 | 0 | 0 | 0 | 0.0002 | 0.9949 | 0.0019 | 0 | 0.0001 |
| Fraser | Peach | 0.6339 | 0 | 0 | 0.0024 | 0.0001 | 0 | 0 | 0 | 0.9970 | 0.0005 | 0 | 0.0001 |
| Fraser | Squawkum | 0.4997 | 0 | 0 | 0.0101 | 0.0004 | 0 | 0 | 0.0001 | 0.9812 | 0.0079 | 0.0001 | 0.0003 |
| GeorgiaSt | BigQualicum | 0.3729 | 0.0001 | 0 | 0.0032 | 0.0006 | 0 | 0 | 0 | 0.0002 | 0.9937 | 0.0005 | 0.0018 |
| GeorgiaSt | Campbell | 0.0865 | 0.0001 | 0 | 0.0045 | 0.0006 | 0 | 0.0001 | 0 | 0.0007 | 0.9866 | 0.0010 | 0.0067 |
| GeorgiaSt | Cheakamus | 0.6415 | 0 | 0 | 0.0095 | 0.0014 | 0 | 0.0001 | 0.0002 | 0.0006 | 0.9867 | 0.0010 | 0.0007 |
| GeorgiaSt | Cowichan | 0.0901 | 0.0003 | 0 | 0.0149 | 0.0023 | 0.0001 | 0 | 0.0002 | 0.0007 | 0.9721 | 0.0004 | 0.0093 |
| GeorgiaSt | Lang | 0.2002 | 0.0001 | 0 | 0.0021 | 0.0005 | 0 | 0 | 0.0001 | 0.0006 | 0.9952 | 0.0002 | 0.0014 |
| GeorgiaSt | LittleQualicum | 0.3532 | 0.0002 | 0 | 0.0030 | 0.0010 | 0 | 0 | 0 | 0.0002 | 0.9924 | 0.0006 | 0.0028 |
| GeorgiaSt | Nanaimo | 0.6507 | 0.0001 | 0 | 0.0030 | 0.0019 | 0 | 0.0001 | 0 | 0.0003 | 0.9937 | 0.0002 | 0.0010 |
| GeorgiaSt | Phillips | 0.4866 | 0 | 0 | 0.0025 | 0.0021 | 0 | 0 | 0 | 0.0004 | 0.9871 | 0.0021 | 0.0060 |
| GeorgiaSt | Puntledge | 0.5402 | 0 | 0 | 0.0039 | 0.0010 | 0 | 0 | 0 | 0.0006 | 0.9927 | 0.0003 | 0.0016 |
| GeorgiaSt | Snake | 0.6193 | 0.0001 | 0 | 0.0036 | 0.0025 | 0 | 0 | 0 | 0.0005 | 0.9910 | 0.0009 | 0.0016 |
| GeorgiaSt | Southgate | 0.9702 | 0 | 0 | 0.0007 | 0.0001 | 0 | 0 | 0 | 0.0003 | 0.9985 | 0.0001 | 0.0005 |
| JohnstoneSt | Nimpkish | 0.9692 | 0.0001 | 0 | 0.0017 | 0.0007 | 0 | 0 | 0 | 0.0002 | 0.0270 | 0.9692 | 0.0014 |
| WCVI | Conuma | 0.8644 | 0 | 0 | 0.0001 | 0.0001 | 0 | 0 | 0 | 0 | 0.0008 | 0 | 0.9992 |
| WCVI | Nitinat | 0.9024 | 0 | 0 | 0.0002 | 0.0001 | 0 | 0 | 0 | 0 | 0.0006 | 0.0002 | 0.9991 |
| WCVI | Sooke | 0.6845 | 0.0003 | 0 | 0.0116 | 0.0086 | 0.0001 | 0.0001 | 0 | 0.0005 | 0.2764 | 0.0011 | 0.7016 |

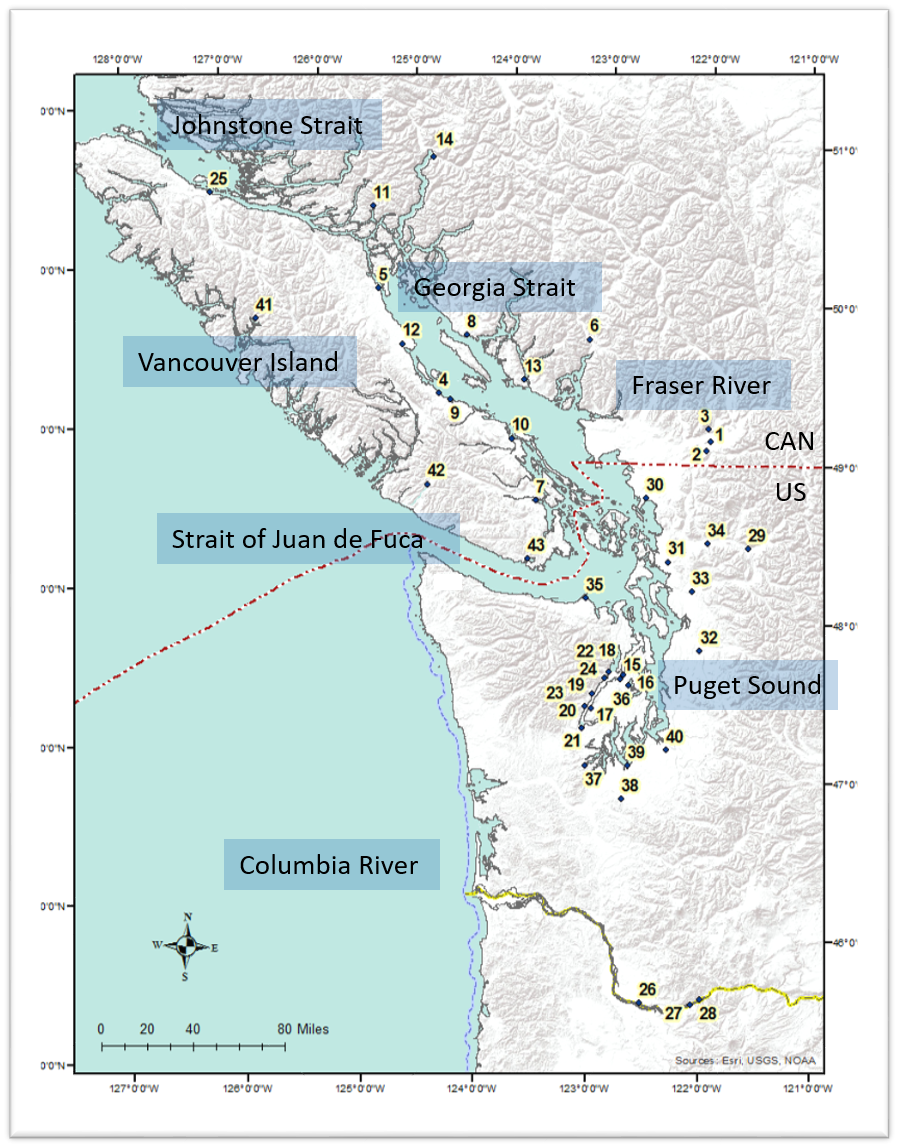
**Table 7. Simulated mixed fishery analysis with ONCOR with a mix of fish from Georgia Strait and North Puget Sound. The actual population proportions for simulations are under “Actual value”, followed by the average estimated proportion, and the standard deviation for the estimates. Average estimated proportions per regional group are at the bottom of the table.**

|  |  | ACTUAL | ESTIMATES | |  | ACTUAL | ESTIMATES | |  | ACTUAL | ESTIMATES | |  | ACTUAL | ESTIMATES | |  | ACTUAL | ESTIMATES | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | VALUE | AVG | SD |  | VALUE | AVG | SD |  | VALUE | AVG | SD |  | VALUE | AVG | SD |  | VALUE | AVG | SD |
| Fraser | Hopedale | 0.25 | 0.1316 | 0.0298 |  | 0.7 | 0.3558 | 0.0416 |  | 0.1 | 0.0531 | 0.0197 |  | 0.1 | 0.0492 | 0.0176 |  | 0.1 | 0.0492 | 0.0182 |
| Fraser | Peach | 0 | 0.1059 | 0.0281 |  | 0 | 0.3025 | 0.0363 |  | 0 | 0.0438 | 0.0169 |  | 0 | 0.0439 | 0.0192 |  | 0 | 0.0386 | 0.0163 |
| Fraser | Squawkum | 0 | 0.0116 | 0.0106 |  | 0 | 0.0348 | 0.0166 |  | 0 | 0.0048 | 0.0062 |  | 0 | 0.0056 | 0.0067 |  | 0 | 0.0058 | 0.0062 |
| GeorgiaSt | BigQualicum | 0 | 0.0419 | 0.0223 |  | 0 | 0.0143 | 0.0114 |  | 0 | 0.1059 | 0.0298 |  | 0 | 0.0156 | 0.0129 |  | 0 | 0.0190 | 0.0135 |
| GeorgiaSt | Campbell | 0 | 0.0212 | 0.0130 |  | 0 | 0.0107 | 0.0091 |  | 0 | 0.0587 | 0.0246 |  | 0 | 0.0136 | 0.0120 |  | 0 | 0.0078 | 0.0083 |
| GeorgiaSt | Cheakamus | 0 | 0.0093 | 0.0096 |  | 0 | 0.0037 | 0.0055 |  | 0 | 0.0221 | 0.0137 |  | 0 | 0.0050 | 0.0066 |  | 0 | 0.0044 | 0.0059 |
| GeorgiaSt | Cowichan | 0 | 0.0019 | 0.0036 |  | 0 | 0.0009 | 0.0027 |  | 0 | 0.0024 | 0.0041 |  | 0 | 0.0023 | 0.0043 |  | 0 | 0.0015 | 0.0029 |
| GeorgiaSt | Lang | 0 | 0.0081 | 0.0080 |  | 0 | 0.0026 | 0.0036 |  | 0 | 0.0188 | 0.0138 |  | 0 | 0.0056 | 0.0068 |  | 0 | 0.0041 | 0.0052 |
| GeorgiaSt | LittleQualicum | 0 | 0.0340 | 0.0171 |  | 0 | 0.0139 | 0.0109 |  | 0 | 0.0786 | 0.0247 |  | 0 | 0.0226 | 0.0145 |  | 0 | 0.0167 | 0.0120 |
| GeorgiaSt | Nanaimo | 0 | 0.0120 | 0.0098 |  | 0 | 0.0053 | 0.0070 |  | 0 | 0.0368 | 0.0180 |  | 0 | 0.0064 | 0.0080 |  | 0 | 0.0065 | 0.0072 |
| GeorgiaSt | Phillips | 0 | 0.0109 | 0.0106 |  | 0 | 0.0049 | 0.0061 |  | 0 | 0.0282 | 0.0187 |  | 0 | 0.0058 | 0.0082 |  | 0 | 0.0042 | 0.0060 |
| GeorgiaSt | Puntledge | 0.25 | 0.1325 | 0.0297 |  | 0.1 | 0.0514 | 0.0179 |  | 0.7 | 0.3416 | 0.0399 |  | 0.1 | 0.0591 | 0.0186 |  | 0.1 | 0.0547 | 0.0197 |
| GeorgiaSt | Snake | 0 | 0.0072 | 0.0076 |  | 0 | 0.0032 | 0.0048 |  | 0 | 0.0118 | 0.0108 |  | 0 | 0.0039 | 0.0062 |  | 0 | 0.0047 | 0.0071 |
| GeorgiaSt | Southgate | 0 | 0.0004 | 0.0015 |  | 0 | 0.0002 | 0.0010 |  | 0 | 0.0006 | 0.0014 |  | 0 | 0.0001 | 0.0004 |  | 0 | 0.0004 | 0.0015 |
| JohnstoneSt | Nimpkish | 0 | 0.0004 | 0.0014 |  | 0 | 0 | 0.0002 |  | 0 | 0.0001 | 0.0006 |  | 0 | 0.0004 | 0.0013 |  | 0 | 0.0002 | 0.0010 |
| WCVI | Conuma | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0.0003 |  | 0 | 0 | 0.0002 |  | 0 | 0 | 0 |
| WCVI | Nitinat | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0.0003 |  | 0 | 0 | 0.0001 |  | 0 | 0 | 0.0005 |
| WCVI | Sooke | 0 | 0.0015 | 0.0029 |  | 0 | 0.0008 | 0.0023 |  | 0 | 0.0025 | 0.0038 |  | 0 | 0.0034 | 0.0049 |  | 0 | 0.0009 | 0.0022 |
| HoodCanal\_F | Anderson | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0.0001 |  | 0 | 0 | 0 |  | 0 | 0.0001 | 0.0005 |
| HoodCanal\_F | BigBeef\_F | 0 | 0 | 0.0005 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0.0001 | 0.0005 |
| HoodCanal\_F | Dewatto | 0 | 0 | 0.0001 |  | 0 | 0 | 0 |  | 0 | 0 | 0.0004 |  | 0 | 0 | 0.0003 |  | 0 | 0 | 0.0003 |
| HoodCanal\_F | Duckabush\_F | 0 | 0 | 0.0001 |  | 0 | 0 | 0 |  | 0 | 0 | 0.0002 |  | 0 | 0 | 0.0001 |  | 0 | 0 | 0 |
| HoodCanal\_F | HammaHamma\_F | 0 | 0 | 0.0004 |  | 0 | 0 | 0.0003 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| HoodCanal\_F | Lilliwaup\_F | 0 | 0 | 0.0002 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| HoodCanal\_F | NFSkokomish | 0 | 0.0002 | 0.0009 |  | 0 | 0 | 0 |  | 0 | 0 | 0.0002 |  | 0 | 0 | 0.0003 |  | 0 | 0 | 0 |
| HoodCanal\_S | Dosewallips\_S | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| HoodCanal\_S | HammaHamma\_S | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| HoodCanal\_S | Duckabush\_S | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| NorthPS | Lower\_Sauk | 0 | 0.0038 | 0.0053 |  | 0 | 0.0021 | 0.0039 |  | 0 | 0.0020 | 0.0035 |  | 0 | 0.0053 | 0.0065 |  | 0 | 0.0075 | 0.0091 |
| NorthPS | Nooksack | 0.25 | 0.1828 | 0.0330 |  | 0.1 | 0.0718 | 0.0190 |  | 0.1 | 0.0715 | 0.0191 |  | 0.7 | 0.5510 | 0.0391 |  | 0.1 | 0.0722 | 0.0182 |
| NorthPS | Skagit\_lower\_mainstem | 0 | 0.0038 | 0.0052 |  | 0 | 0.0030 | 0.0045 |  | 0 | 0.0020 | 0.0041 |  | 0 | 0.0027 | 0.0042 |  | 0 | 0.0071 | 0.0089 |
| NorthPS | Snohomish | 0 | 0.0536 | 0.0190 |  | 0 | 0.0242 | 0.0142 |  | 0 | 0.0220 | 0.0131 |  | 0 | 0.0316 | 0.0175 |  | 0 | 0.1257 | 0.0319 |
| NorthPS | Stillaguamish | 0.25 | 0.1140 | 0.0287 |  | 0.1 | 0.0476 | 0.0180 |  | 0.1 | 0.0482 | 0.0187 |  | 0.1 | 0.0816 | 0.0269 |  | 0.7 | 0.2923 | 0.0373 |
| NorthPS | upper\_Skagit | 0 | 0.1073 | 0.0265 |  | 0 | 0.0439 | 0.0168 |  | 0 | 0.0412 | 0.0173 |  | 0 | 0.0749 | 0.0263 |  | 0 | 0.2714 | 0.0404 |
| SJF | Dungeness | 0 | 0.0035 | 0.0048 |  | 0 | 0.0021 | 0.0033 |  | 0 | 0.0029 | 0.0054 |  | 0 | 0.0100 | 0.0106 |  | 0 | 0.0045 | 0.0059 |
| SouthPS | Chico/Grovers | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| SouthPS | Kennedy | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0.0005 |  | 0 | 0 | 0 |
| SouthPS | Skookum | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| SouthPS\_W | DIRU\_Puyallup | 0 | 0 | 0.0002 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0.0005 |
| SouthPS\_W | Nisqually | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0.0003 |  | 0 | 0 | 0.0005 |  | 0 | 0 | 0.0003 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | GROUPS |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CAN | Fraser | 0.25 | 0.2491 | 0.0316 |  | 0.7 | 0.6931 | 0.0318 |  | 0.1 | 0.1017 | 0.0216 |  | 0.1 | 0.0987 | 0.0214 |  | 0.1 | 0.0936 | 0.0222 |
| CAN | GeorgiaSt | 0.25 | 0.2795 | 0.0319 |  | 0.1 | 0.1112 | 0.026 |  | 0.7 | 0.7055 | 0.0318 |  | 0.1 | 0.1400 | 0.0282 |  | 0.1 | 0.1240 | 0.0241 |
| CAN | JohnstoneSt | 0 | 0.0004 | 0.0014 |  | 0 | 0 | 0.0002 |  | 0 | 0.0001 | 0.0006 |  | 0 | 0.0004 | 0.0013 |  | 0 | 0.0002 | 0.0010 |
| CAN | WCVI | 0 | 0.0015 | 0.0029 |  | 0 | 0.0008 | 0.0023 |  | 0 | 0.0026 | 0.0039 |  | 0 | 0.0035 | 0.0049 |  | 0 | 0.0009 | 0.0023 |
| US | HoodCanal\_F | 0 | 0.0003 | 0.0011 |  | 0 | 0 | 0.0003 |  | 0 | 0.0001 | 0.0005 |  | 0 | 0.0001 | 0.0004 |  | 0 | 0.0001 | 0.0008 |
| US | HoodCanal\_S | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| US | NorthPS | 0.5 | 0.4654 | 0.0362 |  | 0.2 | 0.1926 | 0.0269 |  | 0.2 | 0.1870 | 0.0267 |  | 0.8 | 0.7470 | 0.0341 |  | 0.8 | 0.7762 | 0.0321 |
| US | SJF | 0 | 0.0035 | 0.0048 |  | 0 | 0.0021 | 0.0033 |  | 0 | 0.0029 | 0.0054 |  | 0 | 0.0100 | 0.0106 |  | 0 | 0.0045 | 0.0059 |
| US | SouthPS | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0.0005 |  | 0 | 0 | 0 |
| US | SouthPS\_W | 0 | 0 | 0.0002 |  | 0 | 0 | 0 |  | 0 | 0 | 0.0003 |  | 0 | 0 | 0.0005 |  | 0 | 0.0001 | 0.0005 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

**Table 8. Simulated mixed fishery analysis with ONCOR with an international mix of fish from a pair of nearby populations in Georgia Strait and North Puget Sound and a domestic mix of fish from a pair of nearby populations within North Puget Sound. The actual population proportions for simulations are under “Actual value”, followed by the average estimated proportion, and the standard deviation for the estimates. Average estimated proportions per regional group are at the bottom of the table.**

|  |  |  |  |  |  | International |  |  |  |  |  |  |  |  |  |  |  | US Domestic |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | ACTUAL |  |  |  | ACTUAL |  |  |  | ACTUAL |  |  |  | ACTUAL |  |  |  | ACTUAL |  |  |  | ACTUAL |  |  |
|  |  | VALUE | AVG | ST DEV |  | VALUE | AVG | ST DEV |  | VALUE | AVG | ST DEV |  | VALUE | AVG | ST DEV |  | VALUE | AVG | ST DEV |  | VALUE | AVG | ST DEV |
| Fraser | Hopedale | 0.5 | 0.2615 | 0.0363 |  | 0.25 | 0.1336 | 0.0280 |  | 0.75 | 0.3881 | 0.0400 |  | 0 | 0.0029 | 0.0043 |  | 0 | 0.0050 | 0.0066 |  | 0 | 0.0016 | 0.0028 |
| Fraser | Peach | 0 | 0.2150 | 0.0319 |  | 0 | 0.1087 | 0.0244 |  | 0 | 0.3243 | 0.0384 |  | 0 | 0.0065 | 0.0069 |  | 0 | 0.0105 | 0.0097 |  | 0 | 0.0033 | 0.0046 |
| Fraser | Squawkum | 0 | 0.0231 | 0.0138 |  | 0 | 0.0121 | 0.0103 |  | 0 | 0.0349 | 0.0150 |  | 0 | 0.0078 | 0.0077 |  | 0 | 0.0101 | 0.0098 |  | 0 | 0.0028 | 0.0042 |
| GeorgiaSt | BigQualicum | 0 | 0.0009 | 0.0026 |  | 0 | 0.0026 | 0.0041 |  | 0 | 0.0006 | 0.0018 |  | 0 | 0.0048 | 0.0065 |  | 0 | 0.0064 | 0.0077 |  | 0 | 0.0037 | 0.0050 |
| GeorgiaSt | Campbell | 0 | 0.0033 | 0.0053 |  | 0 | 0.0049 | 0.0061 |  | 0 | 0.0017 | 0.0036 |  | 0 | 0.0018 | 0.0038 |  | 0 | 0.0028 | 0.0047 |  | 0 | 0.0012 | 0.0023 |
| GeorgiaSt | Cheakamus | 0 | 0.0013 | 0.0029 |  | 0 | 0.0022 | 0.0037 |  | 0 | 0.0009 | 0.0020 |  | 0 | 0.0031 | 0.0055 |  | 0 | 0.0029 | 0.0042 |  | 0 | 0.0025 | 0.0040 |
| GeorgiaSt | Cowichan | 0 | 0.0015 | 0.0029 |  | 0 | 0.0020 | 0.0038 |  | 0 | 0.0008 | 0.0019 |  | 0 | 0.0057 | 0.0073 |  | 0 | 0.0105 | 0.0099 |  | 0 | 0.0031 | 0.0045 |
| GeorgiaSt | Lang | 0 | 0.0009 | 0.0023 |  | 0 | 0.0008 | 0.0021 |  | 0 | 0.0005 | 0.0016 |  | 0 | 0.0023 | 0.0042 |  | 0 | 0.0035 | 0.0059 |  | 0 | 0.0013 | 0.0026 |
| GeorgiaSt | LittleQualicum | 0 | 0.0077 | 0.0081 |  | 0 | 0.0093 | 0.0084 |  | 0 | 0.0032 | 0.0046 |  | 0 | 0.0095 | 0.0108 |  | 0 | 0.0157 | 0.0131 |  | 0 | 0.0042 | 0.0058 |
| GeorgiaSt | Nanaimo | 0 | 0.0014 | 0.0033 |  | 0 | 0.0014 | 0.0026 |  | 0 | 0.0004 | 0.0014 |  | 0 | 0.0033 | 0.0054 |  | 0 | 0.0039 | 0.0057 |  | 0 | 0.0021 | 0.0041 |
| GeorgiaSt | Phillips | 0 | 0.0012 | 0.0029 |  | 0 | 0.0009 | 0.0024 |  | 0 | 0.0005 | 0.0015 |  | 0 | 0.0049 | 0.0068 |  | 0 | 0.0081 | 0.0088 |  | 0 | 0.0025 | 0.0044 |
| GeorgiaSt | Puntledge | 0 | 0.0033 | 0.0048 |  | 0 | 0.0055 | 0.0070 |  | 0 | 0.0018 | 0.0037 |  | 0 | 0.0124 | 0.0104 |  | 0 | 0.0178 | 0.0138 |  | 0 | 0.0052 | 0.0066 |
| GeorgiaSt | Snake | 0 | 0.0012 | 0.0027 |  | 0 | 0.0023 | 0.0044 |  | 0 | 0.0008 | 0.0024 |  | 0 | 0.0015 | 0.0028 |  | 0 | 0.0024 | 0.0044 |  | 0 | 0.0010 | 0.0021 |
| GeorgiaSt | Southgate | 0 | 0.0002 | 0.0009 |  | 0 | 0.0002 | 0.0008 |  | 0 | 0 | 0.0002 |  | 0 | 0.0009 | 0.0028 |  | 0 | 0.0019 | 0.0030 |  | 0 | 0.0005 | 0.0015 |
| JohnstoneSt | Nimpkish | 0 | 0.0002 | 0.0007 |  | 0 | 0.0002 | 0.0008 |  | 0 | 0.0003 | 0.0011 |  | 0 | 0.0003 | 0.0010 |  | 0 | 0.0003 | 0.0012 |  | 0 | 0.0002 | 0.0008 |
| WCVI | Conuma | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| WCVI | Nitinat | 0 | 0 | 0 |  | 0 | 0.0001 | 0.0007 |  | 0 | 0 | 0 |  | 0 | 0 | 0.0003 |  | 0 | 0 | 0 |  | 0 | 0.0001 | 0.0006 |
| WCVI | Sooke | 0 | 0.0015 | 0.0033 |  | 0 | 0.0025 | 0.0045 |  | 0 | 0.0013 | 0.0026 |  | 0 | 0.0032 | 0.0051 |  | 0 | 0.0048 | 0.0066 |  | 0 | 0.0018 | 0.0037 |
| HoodCanal\_F | Anderson | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0.0001 | 0.0006 |  | 0 | 0 | 0.0003 |  | 0 | 0.0001 | 0.0007 |
| HoodCanal\_F | BigBeef\_F | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0.0001 | 0.0006 |  | 0 | 0.0001 | 0.0007 |  | 0 | 0.0001 | 0.0007 |
| HoodCanal\_F | Dewatto | 0 | 0 | 0.0004 |  | 0 | 0 | 0.0001 |  | 0 | 0 | 0 |  | 0 | 0.0002 | 0.0010 |  | 0 | 0.0001 | 0.0004 |  | 0 | 0.0002 | 0.0010 |
| HoodCanal\_F | Duckabush\_F | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0.0001 | 0.0005 |  | 0 | 0.0001 | 0.0007 |  | 0 | 0.0002 | 0.0008 |
| HoodCanal\_F | HammaHamma\_F | 0 | 0 | 0.0003 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| HoodCanal\_F | Lilliwaup\_F | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0.0003 | 0.0012 |  | 0 | 0.0002 | 0.0008 |  | 0 | 0 | 0.0001 |
| HoodCanal\_F | NFSkokomish | 0 | 0.0001 | 0.0005 |  | 0 | 0.0001 | 0.0006 |  | 0 | 0 | 0.0004 |  | 0 | 0.0002 | 0.0010 |  | 0 | 0.0002 | 0.0010 |  | 0 | 0.0008 | 0.0020 |
| HoodCanal\_S | Dosewallips\_S | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| HoodCanal\_S | HammaHamma\_S | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| HoodCanal\_S | Duckabush\_S | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| NorthPS | Lower\_Sauk | 0 | 0.0036 | 0.0051 |  | 0 | 0.0057 | 0.0065 |  | 0 | 0.0026 | 0.0040 |  | 0 | 0.0368 | 0.0153 |  | 0 | 0.0213 | 0.0139 |  | 0 | 0.0543 | 0.0235 |
| NorthPS | Nooksack | 0.5 | 0.4074 | 0.0366 |  | 0.75 | 0.6113 | 0.0408 |  | 0.25 | 0.2017 | 0.0290 |  | 0 | 0.0010 | 0.0024 |  | 0 | 0.0027 | 0.0040 |  | 0 | 0.0018 | 0.0030 |
| NorthPS | Skagit\_lower\_mainstem | 0 | 0.0024 | 0.0040 |  | 0 | 0.0022 | 0.0036 |  | 0 | 0.0021 | 0.0036 |  | 0.5 | 0.2949 | 0.0307 |  | 0.75 | 0.4568 | 0.0364 |  | 0.25 | 0.1454 | 0.0289 |
| NorthPS | Snohomish | 0 | 0.0100 | 0.0108 |  | 0 | 0.0138 | 0.0113 |  | 0 | 0.0060 | 0.0075 |  | 0 | 0.0501 | 0.0212 |  | 0 | 0.0346 | 0.0183 |  | 0 | 0.0616 | 0.0234 |
| NorthPS | Stillaguamish | 0 | 0.0268 | 0.0141 |  | 0 | 0.0406 | 0.0196 |  | 0 | 0.0136 | 0.0115 |  | 0 | 0.2024 | 0.0336 |  | 0 | 0.1525 | 0.0311 |  | 0 | 0.2367 | 0.0411 |
| NorthPS | upper\_Skagit | 0 | 0.0186 | 0.0126 |  | 0 | 0.0263 | 0.0176 |  | 0 | 0.0095 | 0.0079 |  | 0.5 | 0.3392 | 0.0399 |  | 0.25 | 0.2208 | 0.0354 |  | 0.75 | 0.4582 | 0.0459 |
| SJF | Dungeness | 0 | 0.0068 | 0.0078 |  | 0 | 0.0106 | 0.0102 |  | 0 | 0.0043 | 0.0054 |  | 0 | 0.0032 | 0.0052 |  | 0 | 0.0030 | 0.0044 |  | 0 | 0.0026 | 0.0040 |
| SouthPS | Chico/Grovers | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| SouthPS | Kennedy | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| SouthPS | Skookum | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| SouthPS\_W | DIRU\_Puyallup | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0.0005 |  | 0 | 0.0001 | 0.0006 |  | 0 | 0 | 0.0004 |
| SouthPS\_W | Nisqually | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0.0001 | 0.0004 |  | 0 | 0 | 0 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | GROUPS |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CAN | Fraser | 0.5 | 0.4996 | 0.0361 |  | 0.25 | 0.2544 | 0.0303 |  | 0.75 | 0.7473 | 0.0325 |  | 0 | 0.0171 | 0.0118 |  | 0 | 0.0257 | 0.0154 |  | 0 | 0.0078 | 0.0069 |
| CAN | GeorgiaSt | 0 | 0.0229 | 0.0109 |  | 0 | 0.0321 | 0.0146 |  | 0 | 0.0113 | 0.0080 |  | 0 | 0.0501 | 0.0191 |  | 0 | 0.0759 | 0.0237 |  | 0 | 0.0274 | 0.0125 |
| CAN | JohnstoneSt | 0 | 0.0002 | 0.0007 |  | 0 | 0.0002 | 0.0008 |  | 0 | 0.0003 | 0.0011 |  | 0 | 0.0003 | 0.0010 |  | 0 | 0.0003 | 0.0012 |  | 0 | 0.0002 | 0.0008 |
| CAN | WCVI | 0 | 0.0015 | 0.0033 |  | 0 | 0.0026 | 0.0045 |  | 0 | 0.0013 | 0.0026 |  | 0 | 0.0032 | 0.0051 |  | 0 | 0.0048 | 0.0066 |  | 0 | 0.0019 | 0.0037 |
| US | HoodCanal\_F | 0 | 0.0001 | 0.0007 |  | 0 | 0.0001 | 0.0006 |  | 0 | 0 | 0.0004 |  | 0 | 0.0009 | 0.0020 |  | 0 | 0.0007 | 0.0017 |  | 0 | 0.0014 | 0.0025 |
| US | HoodCanal\_S | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| US | NorthPS | 0.5 | 0.4688 | 0.0351 |  | 0.75 | 0.6999 | 0.0357 |  | 0.25 | 0.2355 | 0.0322 |  | 1 | 0.9243 | 0.0223 |  | 1 | 0.8886 | 0.0274 |  | 1 | 0.9580 | 0.0149 |
| US | SJF | 0 | 0.0068 | 0.0078 |  | 0 | 0.0106 | 0.0102 |  | 0 | 0.0043 | 0.0054 |  | 0 | 0.0032 | 0.0052 |  | 0 | 0.0030 | 0.0044 |  | 0 | 0.0026 | 0.0040 |
| US | SouthPS | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |
| US | SouthPS\_W | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0 |  | 0 | 0 | 0.0005 |  | 0 | 0.0001 | 0.0007 |  | 0 | 0 | 0.0004 |

Figure 1. Map of Southern Boundary Chum salmon collection locations. The red dotted line indicates the international boundary. Population numbers follow Table 4.

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**Figure 2. Plot of simulated FST values versus heterozygosity and 99% confidence interval for simulated values with (orange circles) and without (blue circles) Hood Canal Summer Chum salmon (HCSCS). Observed FST values are plotted versus observed heterozygosity with (red filled circles) and without (black filled circles) HCSCS. Observed FST values plotting above the 99% CI indicate loci possibly under positive selection (see Table 3).**

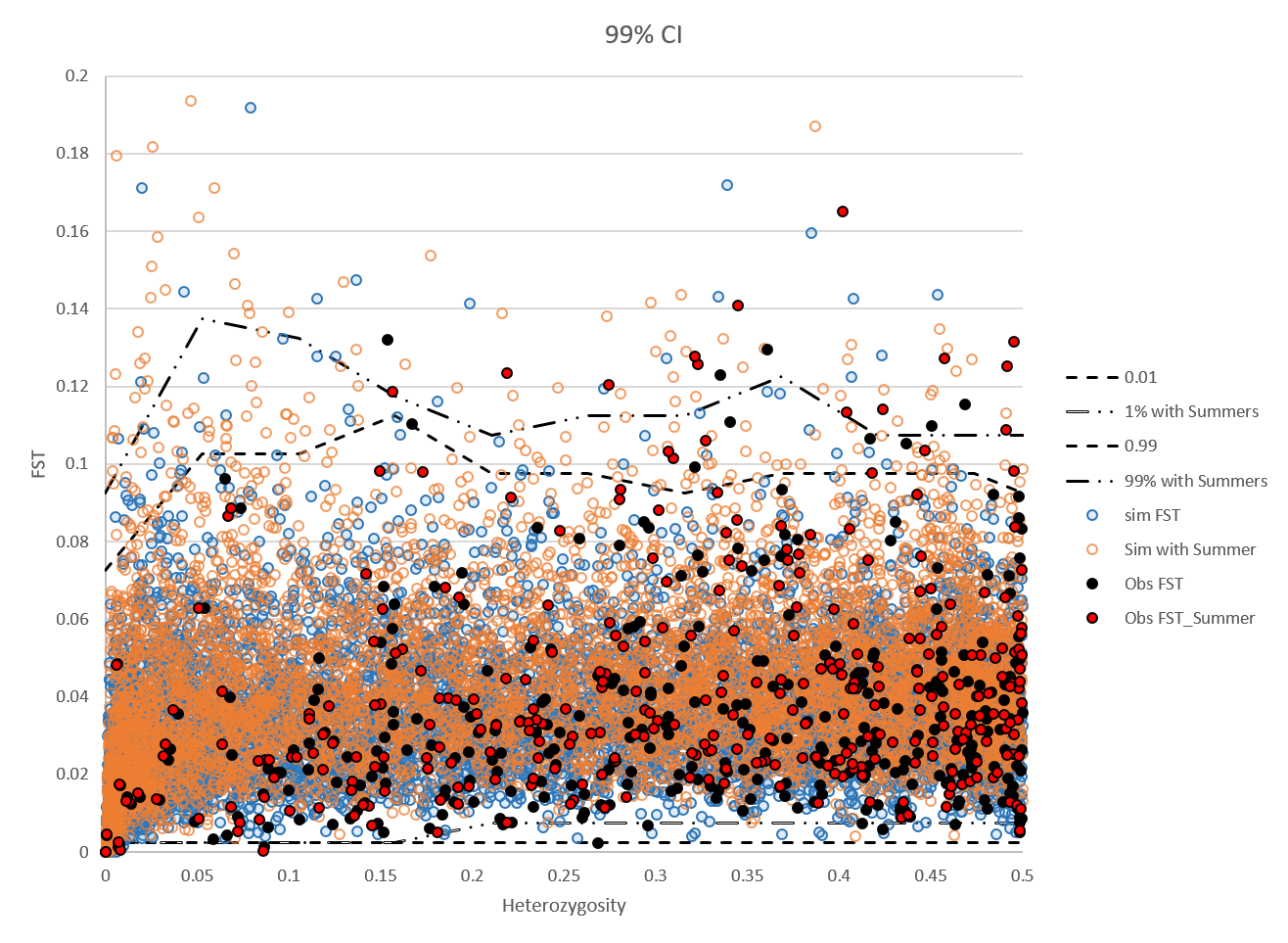


Figure 3. Principal coordinates analysis plot of Chum salmon populations without Hood Canal Summer Chum salmon or Lower Columbia Chum salmon.

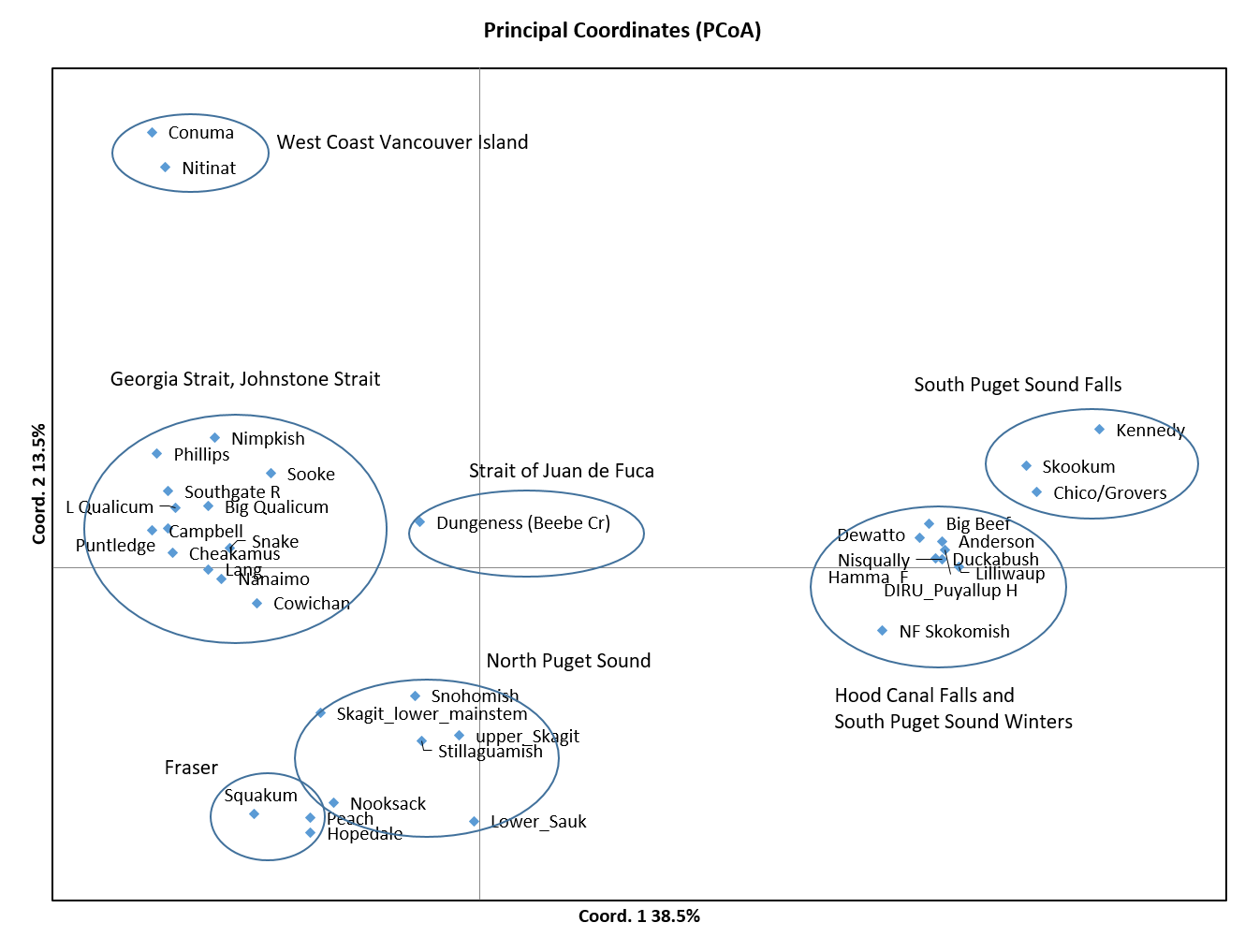


Figure 4. Neighbor-joining tree of Nei’s genetic distances among Chum salmon collections with bootstrap values based on 10,000 trees (only values >60% shown).

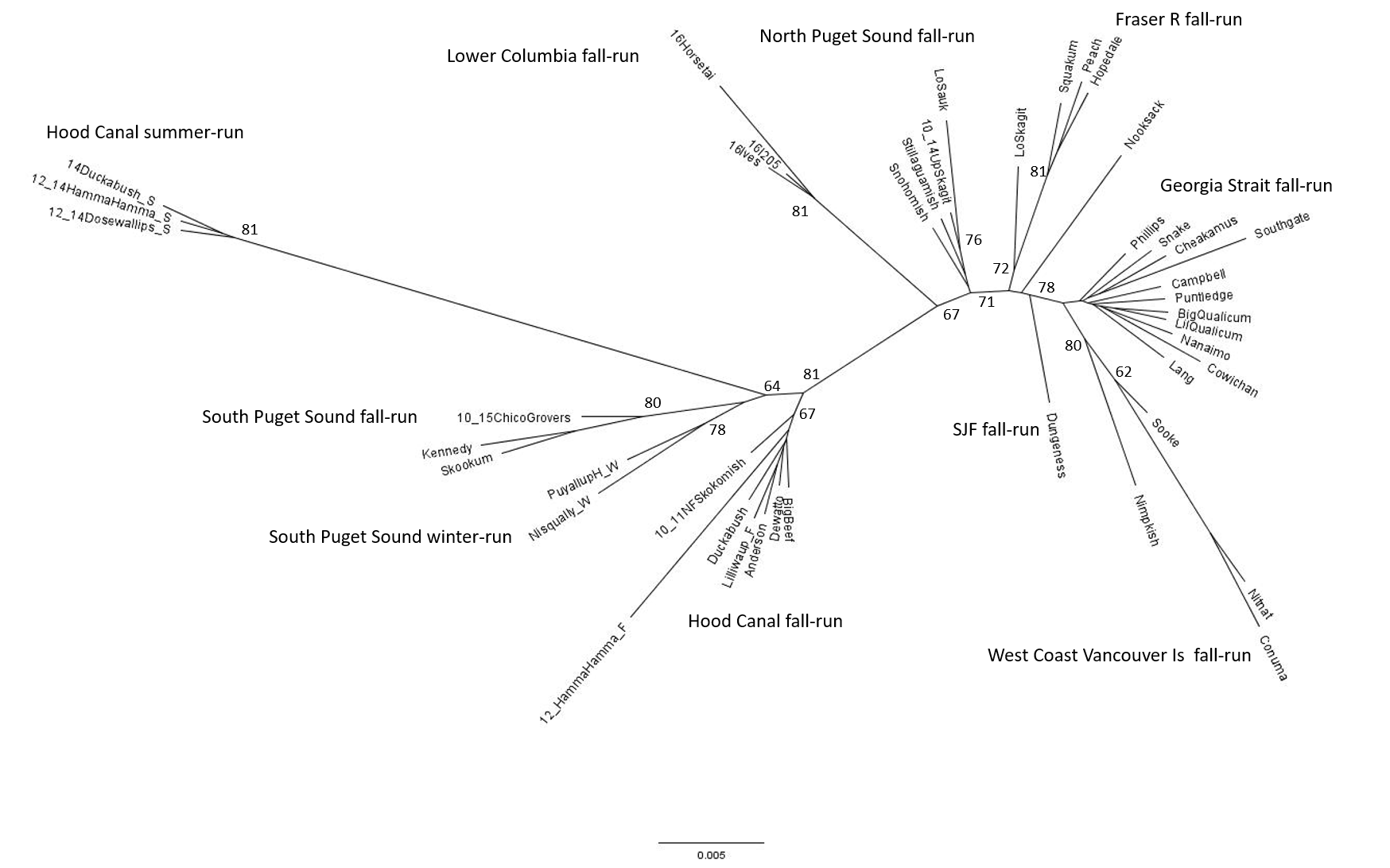
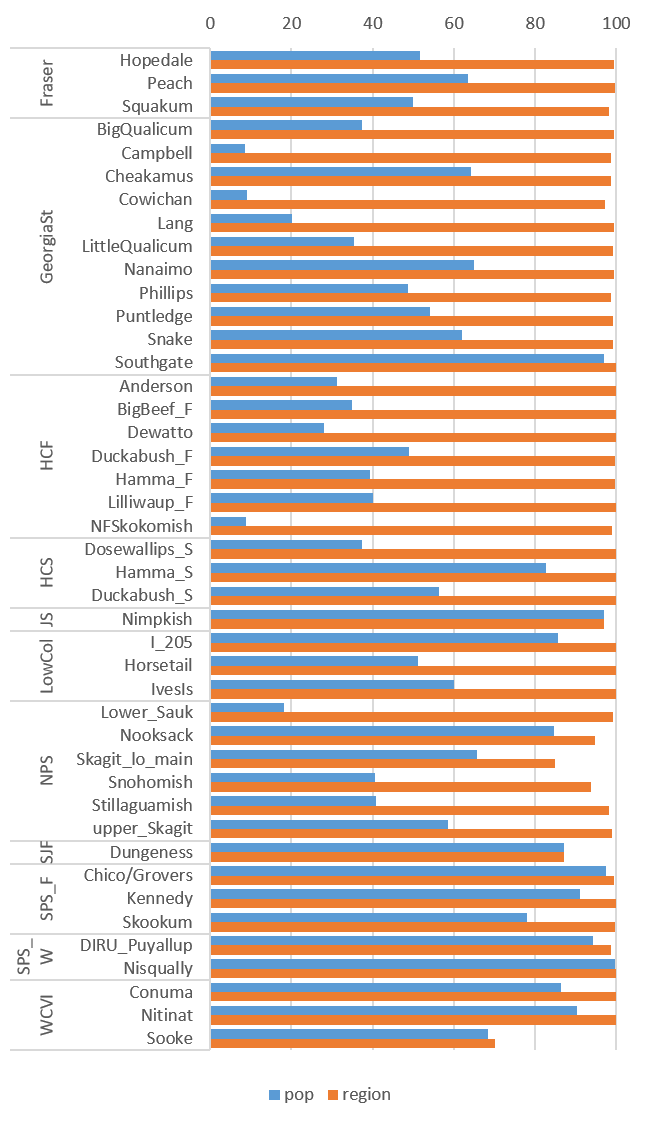


Figure 5. Plot of ONCOR assignments to collection of origin (pop) and to region of origin (region). The actual values are in Table 6.



Appendix I. **List of loci in panel 1 and panel 2 (Small et al. 2017), their status in genotypes (fixed for one allele, failed, missing too much data), and statistics for loci included in analyses including their Hardy-Weinberg equilibrium value over all loci as expressed by FIS and the percentage of variation among populations (FST).**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| 336 loci |  |  |  | 389 loci |  |  |
| **Panel 1** | **Fis** | **Fst** |  | **Panel 2** | **Fis** | **Fst** |
| Oke\_ACOT\_100 | 0.002 | 0.032 |  | Oke\_RDDFW10186\_42 | -0.018 | 0.039 |
| Oke\_APOB\_60 | -0.011 | 0.021 |  | Oke\_RDDFW10693\_22 | missing too much data |  |
| Oke\_ATP5L\_105 | -0.007 | 0.030 |  | Oke\_RDDFW10693\_57 | fixed for one allele |  |
| Oke\_ATP5L\_248 | failed in all |  |  | Oke\_RDDFW10914\_20 | fixed for one allele |  |
| Oke\_AhR1\_278 | 0.024 | 0.021 |  | Oke\_RDDFW10914\_38 | missing too much data |  |
| Oke\_CATB\_60 | -0.036 | 0.027 |  | Oke\_RDDFW112\_17 | -0.017 | 0.024 |
| Oke\_CD123\_62 | -0.016 | 0.040 |  | Oke\_RDDFW11601\_32 | 0.038 | 0.059 |
| Oke\_CD81\_108 | fixed for one allele |  |  | Oke\_RDDFW12818\_72 | missing too much data |  |
| Oke\_CKS\_389 | -0.051 | 0.022 |  | Oke\_RDDFW12847\_41 | fixed for one allele |  |
| Oke\_CKS1\_70 | -0.029 | 0.017 |  | Oke\_RDDFW12847\_63 | missing too much data |  |
| Oke\_CKS1\_94 | 0.019 | 0.034 |  | Oke\_RDDFW13161\_74 | -0.036 | 0.059 |
| Oke\_CO1A1\_72 | -0.160 | 0.018 |  | Oke\_RDDFW13211\_57 | -0.038 | 0.021 |
| Oke\_CTR2\_82 | -0.025 | 0.033 |  | Oke\_RDDFW13211\_64 | fixed for one allele |  |
| Oke\_DBLOH\_79 | -0.027 | 0.029 |  | Oke\_RDDFW13652\_53 | missing too much data |  |
| Oke\_DCXR\_87 | -0.025 | 0.021 |  | Oke\_RDDFW13803\_76 | 0.073 | 0.043 |
| Oke\_DM20\_548 | -0.036 | 0.029 |  | Oke\_RDDFW14151\_28 | -0.066 | 0.020 |
| Oke\_EF2\_394 | -0.034 | 0.047 |  | Oke\_RDDFW14151\_40 | fixed for one allele |  |
| Oke\_FANK1-96 | failed in all |  |  | Oke\_RDDFW14498\_66 | -0.002 | 0.028 |
| Oke\_FBXL5\_61 | -0.042 | 0.042 |  | Oke\_RDDFW14591\_59 | -0.083 | 0.077 |
| Oke\_GHII\_2943 | missing too much data |  |  | Oke\_RDDFW14903\_26 | fixed for one allele |  |
| Oke\_GHII\_3129 | -0.035 | 0.024 |  | Oke\_RDDFW14903\_53 | -0.020 | 0.036 |
| Oke\_GNMT\_100 | -0.002 | 0.036 |  | Oke\_RDDFW15665\_35 | fixed for one allele |  |
| Oke\_GPDH\_191 | -0.036 | 0.028 |  | Oke\_RDDFW15665\_57 | fixed for one allele |  |
| Oke\_GPH\_78 | -0.100 | 0.047 |  | Oke\_RDDFW15665\_59 | fixed for one allele |  |
| Oke\_GnRH\_373 | -0.066 | 0.035 |  | Oke\_RDDFW15717\_46 | 0.008 | 0.059 |
| Oke\_GnRH\_527 | missing too much data |  |  | Oke\_RDDFW16060\_68 | missing too much data |  |
| Oke\_H2AX\_72 | 0.021 | 0.029 |  | Oke\_RDDFW16224\_65 | missing too much data |  |
| Oke\_HP\_182 | -0.067 | 0.028 |  | Oke\_RDDFW16518\_29 | -0.017 | 0.016 |
| Oke\_HSP90BA\_299 | fixed for one allele |  |  | Oke\_RDDFW16781\_68 | 0.334 | 0.042 |
| Oke\_IL8r\_272 | -0.031 | 0.018 |  | Oke\_RDDFW16886\_37 | -0.034 | 0.113 |
| Oke\_IL8r2\_406 | -0.037 | 0.019 |  | Oke\_RDDFW17423\_60 | -0.060 | 0.078 |
| Oke\_KPNA2\_87 | -0.025 | 0.031 |  | Oke\_RDDFW17478\_56 | 0.007 | 0.069 |
| Oke\_LAMP2\_138 | fixed for one allele |  |  | Oke\_RDDFW18238\_31 | -0.028 | 0.121 |
| Oke\_LAMP2\_186 | -0.050 | 0.026 |  | Oke\_RDDFW18238\_48 | fixed for one allele |  |
| Oke\_METK2\_97 | 0.002 | 0.046 |  | Oke\_RDDFW18411\_76 | fixed for one allele |  |
| Oke\_MLRN\_63 | -0.012 | 0.032 |  | Oke\_RDDFW18411\_78 | -0.011 | 0.021 |
| Oke\_Moesin\_160 | fixed for one allele |  |  | Oke\_RDDFW18744\_69 | missing too much data |  |
| Oke\_NHERF\_54 | missing too much data |  |  | Oke\_RDDFW18744\_74 | fixed for one allele |  |
| Oke\_NUPR1\_70 | 0.266 | 0.033 |  | Oke\_RDDFW19534\_51 | 0.008 | 0.032 |
| Oke\_PDIA3\_082 | -0.017 | 0.022 |  | Oke\_RDDFW19665\_33 | fixed for one allele |  |
| Oke\_PDIA3\_475 | -0.007 | 0.025 |  | Oke\_RDDFW19665\_35 | fixed for one allele |  |
| Oke\_PPA2\_635 | -0.027 | 0.044 |  | Oke\_RDDFW19665\_62 | -0.077 | 0.062 |
| Oke\_RAD10028\_44 | 0.019 | 0.020 |  | Oke\_RDDFW19805\_61 | 0.171 | 0.050 |
| Oke\_RAD10173\_41 | -0.055 | 0.024 |  | Oke\_RDDFW19807\_50 | -0.050 | 0.034 |
| Oke\_RAD10345\_57 | -0.064 | 0.030 |  | Oke\_RDDFW19817\_72 | -0.001 | 0.056 |
| Oke\_RAD10459\_85 | -0.072 | 0.080 |  | Oke\_RDDFW19817\_73 | -0.039 | 0.026 |
| Oke\_RAD10591\_67 | 0.028 | 0.025 |  | Oke\_RDDFW19840\_72 | -0.160 | 0.032 |
| Oke\_RAD10676\_50 | -0.023 | 0.019 |  | Oke\_RDDFW19905\_31 | -0.027 | 0.100 |
| Oke\_RAD10719\_31 | -0.045 | 0.030 |  | Oke\_RDDFW20161\_36 | -0.015 | 0.028 |
| Oke\_RAD11183\_63 | 0.014 | 0.104 |  | Oke\_RDDFW20161\_39 | fixed for one allele |  |
| Oke\_RAD11379\_85 | -0.006 | 0.022 |  | Oke\_RDDFW20179\_61 | -0.001 | 0.047 |
| Oke\_RAD11444\_75 | -0.001 | 0.019 |  | Oke\_RDDFW20811\_59 | -0.036 | 0.027 |
| Oke\_RAD11500\_80 | -0.084 | 0.023 |  | Oke\_RDDFW20811\_77 | -0.052 | 0.031 |
| Oke\_RAD11690\_33 | -0.033 | 0.024 |  | Oke\_RDDFW20999\_31 | -0.026 | 0.061 |
| Oke\_RAD11918\_57 | -0.022 | 0.017 |  | Oke\_RDDFW21285\_40 | fixed for one allele |  |
| Oke\_RAD11928\_30 | -0.043 | 0.031 |  | Oke\_RDDFW21285\_59 | -0.013 | 0.039 |
| Oke\_RAD11999\_36 | -0.021 | 0.053 |  | Oke\_RDDFW21890\_33 | 0.052 | 0.093 |
| Oke\_RAD12038\_34 | -0.020 | 0.028 |  | Oke\_RDDFW21890\_70 | -0.016 | 0.012 |
| Oke\_RAD12294\_71 | 0.007 | 0.098 |  | Oke\_RDDFW21890\_73 | -0.048 | 0.037 |
| Oke\_RAD12377\_41 | -0.062 | 0.028 |  | Oke\_RDDFW22279\_22 | 0.028 | 0.040 |
| Oke\_RAD12415\_71 | -0.011 | 0.107 |  | Oke\_RDDFW22279\_27 | fixed for one allele |  |
| Oke\_RAD12909\_51 | -0.010 | 0.043 |  | Oke\_RDDFW23398\_37 | missing too much data |  |
| Oke\_RAD13522\_47 | -0.056 | 0.032 |  | Oke\_RDDFW23398\_50 | missing too much data |  |
| Oke\_RAD14303\_73 | -0.046 | 0.021 |  | Oke\_RDDFW23444\_20 | fixed for one allele |  |
| Oke\_RAD14679\_56 | -0.046 | 0.034 |  | Oke\_RDDFW23444\_56 | -0.005 | 0.088 |
| Oke\_RAD14714\_35 | -0.014 | 0.029 |  | Oke\_RDDFW24027\_36 | -0.052 | 0.061 |
| Oke\_RAD14852\_56 | -0.055 | 0.064 |  | Oke\_RDDFW24027\_43 | fixed for one allele |  |
| Oke\_RAD14962\_45 | -0.002 | 0.034 |  | Oke\_RDDFW24027\_64 | fixed for one allele |  |
| Oke\_RAD15073\_41 | 0.001 | 0.050 |  | Oke\_RDDFW24615\_47 | fixed for one allele |  |
| Oke\_RAD16205\_61 | 0.039 | 0.028 |  | Oke\_RDDFW24615\_60 | -0.020 | 0.032 |
| Oke\_RAD1635\_77 | -0.038 | 0.068 |  | Oke\_RDDFW24690\_58 | -0.082 | 0.055 |
| Oke\_RAD16718\_63 | 0.032 | 0.040 |  | Oke\_RDDFW25476\_76 | -0.066 | 0.016 |
| Oke\_RAD16763\_78 | -0.119 | 0.024 |  | Oke\_RDDFW25539\_63 | -0.027 | 0.033 |
| Oke\_RAD16805\_31 | 0.035 | 0.041 |  | Oke\_RDDFW26052\_19 | fixed for one allele |  |
| Oke\_RAD17085\_70 | -0.086 | 0.028 |  | Oke\_RDDFW26052\_31 | fixed for one allele |  |
| Oke\_RAD17316\_60 | 0.012 | 0.033 |  | Oke\_RDDFW26052\_64 | missing too much data |  |
| Oke\_RAD17332\_67 | -0.060 | 0.033 |  | Oke\_RDDFW26817\_29 | missing too much data |  |
| Oke\_RAD19121\_72 | -0.044 | 0.109 |  | Oke\_RDDFW26862\_22 | -0.034 | 0.071 |
| Oke\_RAD19883\_47 | 0.007 | 0.026 |  | Oke\_RDDFW26862\_37 | fixed for one allele |  |
| Oke\_RAD20162\_46 | -0.010 | 0.019 |  | Oke\_RDDFW27446\_69 | 0.028 | 0.033 |
| Oke\_RAD21307\_43 | -0.057 | 0.027 |  | Oke\_RDDFW27536\_70 | -0.072 | 0.056 |
| Oke\_RAD2158\_44 | -0.036 | 0.026 |  | Oke\_RDDFW27843\_52 | fixed for one allele |  |
| Oke\_RAD22662\_43 | 0.003 | 0.029 |  | Oke\_RDDFW27843\_66 | -0.015 | 0.047 |
| Oke\_RAD2414\_54 | 0.017 | 0.031 |  | Oke\_RDDFW28182\_52 | fixed for one allele |  |
| Oke\_RAD24191\_34 | -0.010 | 0.034 |  | Oke\_RDDFW28182\_57 | -0.026 | 0.052 |
| Oke\_RAD2522\_75 | -0.035 | 0.023 |  | Oke\_RDDFW28560\_20 | -0.007 | 0.035 |
| Oke\_RAD2633\_36 | missing too much data |  |  | Oke\_RDDFW28666\_54 | fixed for one allele |  |
| Oke\_RAD27585\_82 | 0.209 | 0.061 |  | Oke\_RDDFW28666\_75 | fixed for one allele |  |
| Oke\_RAD27616\_72 | 0.013 | 0.032 |  | Oke\_RDDFW29139\_38 | -0.050 | 0.029 |
| Oke\_RAD27694\_79 | -0.053 | 0.026 |  | Oke\_RDDFW29874\_52 | -0.068 | 0.033 |
| Oke\_RAD2772\_76 | 0.027 | 0.039 |  | Oke\_RDDFW29874\_55 | fixed for one allele |  |
| Oke\_RAD27721\_75 | -0.053 | 0.036 |  | Oke\_RDDFW29989\_29 | fixed for one allele |  |
| Oke\_RAD2812\_43 | -0.051 | 0.074 |  | Oke\_RDDFW29994\_56 | 0.003 | 0.051 |
| Oke\_RAD2827\_56 | 0.037 | 0.031 |  | Oke\_RDDFW29999\_39 | missing too much data |  |
| Oke\_RAD28497\_70 | -0.010 | 0.018 |  | Oke\_RDDFW30681\_41 | fixed for one allele |  |
| Oke\_RAD3055\_58 | -0.044 | 0.059 |  | Oke\_RDDFW30681\_49 | 0.009 | 0.064 |
| Oke\_RAD3131\_64 | 0.006 | 0.063 |  | Oke\_RDDFW31371\_31 | fixed for one allele |  |
| Oke\_RAD3143\_30 | -0.160 | 0.025 |  | Oke\_RDDFW31371\_56 | failed in most |  |
| Oke\_RAD3223\_33 | -0.067 | 0.022 |  | Oke\_RDDFW32036\_76 | missing too much data |  |
| Oke\_RAD3375\_60 | -0.068 | 0.033 |  | Oke\_RDDFW32214\_64 | -0.025 | 0.022 |
| Oke\_RAD3480\_76 | 0.008 | 0.070 |  | Oke\_RDDFW32254\_59 | failed in most |  |
| Oke\_RAD3490\_31 | -0.011 | 0.049 |  | Oke\_RDDFW32254\_60 | failed in most |  |
| Oke\_RAD3664\_73 | -0.040 | 0.038 |  | Oke\_RDDFW32254\_70 | fixed for one allele, lots missing |  |
| Oke\_RAD369\_38 | -0.026 | 0.042 |  | Oke\_RDDFW32345\_49 | -0.054 | 0.043 |
| Oke\_RAD3693\_30 | -0.015 | 0.057 |  | Oke\_RDDFW3253\_50 | -0.016 | 0.071 |
| Oke\_RAD3715\_76 | 0.036 | 0.054 |  | Oke\_RDDFW32868\_20 | missing too much data |  |
| Oke\_RAD3762\_78 | -0.025 | 0.039 |  | Oke\_RDDFW33509\_23 | fixed for one allele |  |
| Oke\_RAD3861\_38 | 0.023 | 0.028 |  | Oke\_RDDFW33509\_72 | failed in most |  |
| Oke\_RAD39\_44 | 0.004 | 0.032 |  | Oke\_RDDFW33525\_53 | -0.006 | 0.039 |
| Oke\_RAD3907\_37 | 0.352 | 0.058 |  | Oke\_RDDFW34023\_59 | missing too much data |  |
| Oke\_RAD3938\_71 | -0.056 | 0.039 |  | Oke\_RDDFW34023\_62 | missing too much data |  |
| Oke\_RAD3995\_44 | 0.019 | 0.027 |  | Oke\_RDDFW34164\_40 | fixed for one allele |  |
| Oke\_RAD4286\_77 | -0.020 | 0.033 |  | Oke\_RDDFW34164\_44 | missing too much data |  |
| Oke\_RAD4538\_78 | 0.050 | 0.026 |  | Oke\_RDDFW34164\_69 | fixed for one allele |  |
| Oke\_RAD4746\_56 | missing too much data |  |  | Oke\_RDDFW35061\_72 | 0.013 | 0.030 |
| Oke\_RAD4787\_63 | -0.026 | 0.022 |  | Oke\_RDDFW36545\_52 | -0.038 | 0.050 |
| Oke\_RAD4875\_62 | 0.022 | 0.033 |  | Oke\_RDDFW36646\_46 | -0.003 | 0.038 |
| Oke\_RAD5156\_68 | -0.022 | 0.087 |  | Oke\_RDDFW36646\_61 | fixed for one allele |  |
| Oke\_RAD5162\_76 | -0.013 | 0.029 |  | Oke\_RDDFW36920\_78 | -0.013 | 0.068 |
| Oke\_RAD5248\_62 | fixed for one allele |  |  | Oke\_RDDFW37304\_51 | -0.008 | 0.044 |
| Oke\_RAD5276\_66 | -0.027 | 0.059 |  | Oke\_RDDFW37547\_71 | -0.063 | 0.029 |
| Oke\_RAD5434\_50 | -0.105 | 0.014 |  | Oke\_RDDFW37906\_35 | 0.101 | 0.040 |
| Oke\_RAD5457\_49 | -0.053 | 0.053 |  | Oke\_RDDFW37977\_48 | fixed for one allele |  |
| Oke\_RAD5615\_34 | -0.010 | 0.013 |  | Oke\_RDDFW37977\_64 | -0.004 | 0.015 |
| Oke\_RAD5734\_46 | 0.031 | 0.087 |  | Oke\_RDDFW38189\_39 | fixed for one allele |  |
| Oke\_RAD5951\_44 | 0.003 | 0.034 |  | Oke\_RDDFW38189\_70 | -0.043 | 0.070 |
| Oke\_RAD618\_35 | -0.006 | 0.056 |  | Oke\_RDDFW38998\_48 | -0.052 | 0.035 |
| Oke\_RAD7067\_53 | -0.029 | 0.036 |  | Oke\_RDDFW39056\_71 | 0.053 | 0.071 |
| Oke\_RAD7080\_44 | -0.023 | 0.028 |  | Oke\_RDDFW39550\_23 | fixed for one allele |  |
| Oke\_RAD715\_49 | -0.013 | 0.039 |  | Oke\_RDDFW39550\_74 | 0.013 | 0.027 |
| Oke\_RAD7178\_80 | -0.001 | 0.049 |  | Oke\_RDDFW40127\_73 | missing too much data |  |
| Oke\_RAD7431\_40 | 0.022 | 0.068 |  | Oke\_RDDFW40127\_78 | fixed for one allele |  |
| Oke\_RAD7512\_33 | 0.279 | 0.048 |  | Oke\_RDDFW41741\_28 | -0.111 | 0.083 |
| Oke\_RAD7638\_81 | 0.006 | 0.043 |  | Oke\_RDDFW41894\_19 | fixed for one allele |  |
| Oke\_RAD7744\_46 | missing too much data |  |  | Oke\_RDDFW41894\_64 | -0.002 | 0.036 |
| Oke\_RAD7883\_49 | -0.036 | 0.016 |  | Oke\_RDDFW41968\_67 | -0.003 | 0.050 |
| Oke\_RAD7936\_41 | -0.061 | 0.034 |  | Oke\_RDDFW44199\_25 | -0.089 | 0.063 |
| Oke\_RAD8018\_38 | -0.049 | 0.017 |  | Oke\_RDDFW4437\_66 | missing too much data |  |
| Oke\_RAD8326\_32 | -0.055 | 0.021 |  | Oke\_RDDFW44691\_36 | -0.061 | 0.069 |
| Oke\_RAD8335\_79 | -0.041 | 0.095 |  | Oke\_RDDFW45296\_28 | -0.036 | 0.023 |
| Oke\_RAD8372\_31 | -0.036 | 0.028 |  | Oke\_RDDFW45319\_50 | fixed for one allele |  |
| Oke\_RAD859\_84 | -0.047 | 0.023 |  | Oke\_RDDFW45450\_75 | 0.008 | 0.058 |
| Oke\_RAD8698\_82 | 0.017 | 0.034 |  | Oke\_RDDFW45583\_44 | fixed for one allele |  |
| Oke\_RAD8799\_30 | -0.006 | 0.112 |  | Oke\_RDDFW45583\_55 | 0.014 | 0.035 |
| Oke\_RAD8814\_56 | -0.033 | 0.077 |  | Oke\_RDDFW45583\_70 | fixed for one allele |  |
| Oke\_RAD8930\_48 | -0.015 | 0.053 |  | Oke\_RDDFW4577\_49 | missing too much data |  |
| Oke\_RAD905\_85 | -0.034 | 0.029 |  | Oke\_RDDFW46094\_46 | -0.014 | 0.028 |
| Oke\_RAD9273\_49 | -0.016 | 0.043 |  | Oke\_RDDFW46682\_21 | -0.063 | 0.042 |
| Oke\_RAD9447\_73 | 0.021 | 0.050 |  | Oke\_RDDFW46682\_22 | fixed for one allele |  |
| Oke\_RAD9641\_41 | -0.031 | 0.183 |  | Oke\_RDDFW4669\_39 | -0.001 | 0.046 |
| Oke\_RDDFW112379\_31 | 0.211 | 0.049 |  | Oke\_RDDFW46886\_62 | 0.038 | 0.063 |
| Oke\_RDDFW90896\_32 | fixed for one allele |  |  | Oke\_RDDFW46897\_65 | 0.002 | 0.042 |
| Oke\_RDDFW91049\_44 | 0.201 | 0.036 |  | Oke\_RDDFW47294\_38 | missing too much data |  |
| Oke\_RDDFW91108\_63 | -0.005 | 0.029 |  | Oke\_RDDFW47500\_38 | -0.071 | 0.051 |
| Oke\_RDDFW91681\_39 | fixed for one allele |  |  | Oke\_RDDFW47666\_40 | -0.037 | 0.072 |
| Oke\_RDDFW91687\_49 | fixed for one allele |  |  | Oke\_RDDFW47763\_49 | fixed for one allele |  |
| Oke\_RDDFW92272\_22 | failed in all |  |  | Oke\_RDDFW47763\_61 | fixed for one allele |  |
| Oke\_RDDFW92495\_48 | -0.033 | 0.025 |  | Oke\_RDDFW47763\_68 | -0.102 | 0.033 |
| Oke\_RDDFW92659\_20 | -0.010 | 0.046 |  | Oke\_RDDFW47838\_76 | -0.039 | 0.036 |
| Oke\_RDDFW92671\_68 | -0.027 | 0.044 |  | Oke\_RDDFW48220\_71 | 0.060 | 0.041 |
| Oke\_RDDFW92833\_41 | -0.009 | 0.044 |  | Oke\_RDDFW48458\_45 | -0.014 | 0.054 |
| Oke\_RDDFW93000\_33 | -0.020 | 0.068 |  | Oke\_RDDFW48458\_47 | fixed for one allele |  |
| Oke\_RDDFW93115\_22 | -0.043 | 0.087 |  | Oke\_RDDFW48558\_66 | -0.017 | 0.049 |
| Oke\_RDDFW93316\_60 | 0.033 | 0.027 |  | Oke\_RDDFW48576\_24 | 0.088 | 0.051 |
| Oke\_RDDFW93593\_60 | fixed for one allele |  |  | Oke\_RDDFW48705\_55 | -0.030 | 0.040 |
| Oke\_RDDFW93735\_64 | 0.186 | 0.031 |  | Oke\_RDDFW48742\_64 | -0.041 | 0.023 |
| Oke\_RDDFW94378\_52 | missing too much data |  |  | Oke\_RDDFW48742\_74 | fixed for one allele |  |
| Oke\_RDDFW94768\_76 | -0.046 | 0.022 |  | Oke\_RDDFW49372\_62 | -0.019 | 0.038 |
| Oke\_RDDFW95538\_72 | -0.132 | 0.045 |  | Oke\_RDDFW50136\_27 | failed in most |  |
| Oke\_RDDFW95768\_60 | 0.020 | 0.038 |  | Oke\_RDDFW50136\_29 | -0.332 | 0.035 |
| Oke\_RDDFW96264\_54 | fixed for one allele |  |  | Oke\_RDDFW50160\_63 | fixed for one allele |  |
| Oke\_RDDFW96549\_63 | -0.042 | 0.081 |  | Oke\_RDDFW50351\_49 | missing too much data |  |
| Oke\_RDDFW97046\_68 | -0.052 | 0.039 |  | Oke\_RDDFW50351\_61 | fixed for one allele |  |
| Oke\_RDDFW97519\_38 | -0.023 | 0.016 |  | Oke\_RDDFW50553\_28 | 0.002 | 0.022 |
| Oke\_RDDFW97562\_38 | fixed for one allele |  |  | Oke\_RDDFW50712\_32 | fixed for one allele |  |
| Oke\_RDDFW97566\_28 | -0.005 | 0.052 |  | Oke\_RDDFW50712\_39 | 0.004 | 0.053 |
| Oke\_RDDFW97971\_30 | -0.050 | 0.031 |  | Oke\_RDDFW50942\_63 | -0.032 | 0.082 |
| Oke\_RDDFW98343\_20 | -0.036 | 0.029 |  | Oke\_RDDFW51270\_27 | fixed for one allele |  |
| Oke\_RDDFW98639\_62 | fixed for one allele |  |  | Oke\_RDDFW51270\_33 | -0.047 | 0.075 |
| Oke\_RDDFW98640\_53 | -0.051 | 0.054 |  | Oke\_RDDFW51705\_44 | -0.077 | 0.060 |
| Oke\_RDDFW98823\_20 | fixed for one allele |  |  | Oke\_RDDFW51953\_71 | missing too much data |  |
| Oke\_RFC2\_618 | -0.011 | 0.009 |  | Oke\_RDDFW52567\_26 | -0.047 | 0.034 |
| Oke\_RH1op\_245 | 0.022 | 0.028 |  | Oke\_RDDFW52567\_35 | 0.024 | 0.020 |
| Oke\_ROA1\_209 | -0.055 | 0.045 |  | Oke\_RDDFW52773\_33 | fixed for one allele |  |
| Oke\_RPN1\_80 | 0.118 | 0.027 |  | Oke\_RDDFW52773\_67 | 0.010 | 0.030 |
| Oke\_RS27\_81 | 0.005 | 0.024 |  | Oke\_RDDFW53380\_67 | 0.002 | 0.027 |
| Oke\_RS9\_379 | -0.003 | 0.027 |  | Oke\_RDDFW54241\_23 | 0.014 | 0.049 |
| Oke\_RSPRY1\_106 | -0.035 | 0.041 |  | Oke\_RDDFW54241\_69 | -0.020 | 0.034 |
| Oke\_TCP1\_78 | -0.010 | 0.027 |  | Oke\_RDDFW54728\_73 | fixed for one allele |  |
| Oke\_TCTA\_202 | missing too much data |  |  | Oke\_RDDFW55482\_64 | fixed for one allele |  |
| Oke\_TCTA\_99 | 0.004 | 0.030 |  | Oke\_RDDFW55482\_66 | missing too much data |  |
| Oke\_Tf\_278 | -0.080 | 0.033 |  | Oke\_RDDFW55482\_68 | fixed for one allele |  |
| Oke\_U1002\_165 | -0.007 | 0.052 |  | Oke\_RDDFW55554\_29 | fixed for one allele |  |
| Oke\_U1002\_262 | -0.009 | 0.098 |  | Oke\_RDDFW55554\_52 | missing too much data |  |
| Oke\_U1008\_83 | -0.066 | 0.025 |  | Oke\_RDDFW55883\_46 | 0.039 | 0.020 |
| Oke\_U1010\_251 | missing too much data |  |  | Oke\_RDDFW55883\_69 | fixed for one allele |  |
| Oke\_U1012\_241 | -0.001 | 0.027 |  | Oke\_RDDFW56753\_61 | fixed for one allele |  |
| Oke\_U1012\_60 | missing too much data |  |  | Oke\_RDDFW56753\_68 | missing too much data |  |
| Oke\_U1015\_255 | -0.018 | 0.022 |  | Oke\_RDDFW56934\_32 | -0.043 | 0.062 |
| Oke\_U1016\_154 | -0.009 | 0.038 |  | Oke\_RDDFW56934\_34 | fixed for one allele |  |
| Oke\_U1017\_52 | 0.014 | 0.026 |  | Oke\_RDDFW56934\_50 | fixed for one allele |  |
| Oke\_U1018\_50 | -0.037 | 0.023 |  | Oke\_RDDFW57028\_36 | 0.002 | 0.027 |
| Oke\_U1019\_218 | -0.030 | 0.025 |  | Oke\_RDDFW57213\_78 | -0.024 | 0.031 |
| Oke\_U1020\_75 | 0.024 | 0.020 |  | Oke\_RDDFW57684\_65 | -0.021 | 0.047 |
| Oke\_U1021\_102 | -0.008 | 0.033 |  | Oke\_RDDFW57684\_67 | fixed for one allele |  |
| Oke\_U1022\_253 | -0.061 | 0.038 |  | Oke\_RDDFW58551\_39 | fixed for one allele |  |
| Oke\_U1023\_147 | -0.068 | 0.012 |  | Oke\_RDDFW58551\_52 | -0.073 | 0.033 |
| Oke\_U1024\_113 | -0.009 | 0.015 |  | Oke\_RDDFW58967\_26 | fixed for one allele |  |
| Oke\_U1025\_135 | fixed for one allele |  |  | Oke\_RDDFW58967\_39 | fixed for one allele |  |
| Oke\_U1027\_89 | 0.034 | 0.032 |  | Oke\_RDDFW58967\_48 | 0.014 | 0.023 |
| Oke\_U1028\_100 | 0.008 | 0.078 |  | Oke\_RDDFW59084\_41 | -0.121 | 0.046 |
| Oke\_U1031\_132 | -0.056 | 0.054 |  | Oke\_RDDFW59113\_30 | -0.084 | 0.052 |
| Oke\_U2001\_629 | missing too much data |  |  | Oke\_RDDFW60209\_22 | 0.029 | 0.027 |
| Oke\_U2002\_200 | -0.020 | 0.024 |  | Oke\_RDDFW60597\_26 | -0.023 | 0.020 |
| Oke\_U2003\_142 | -0.014 | 0.011 |  | Oke\_RDDFW60597\_28 | -0.025 | 0.021 |
| Oke\_U2005\_62 | -0.040 | 0.019 |  | Oke\_RDDFW60645\_53 | -0.006 | 0.035 |
| Oke\_U2006\_109 | -0.033 | 0.022 |  | Oke\_RDDFW6089\_53 | fixed for one allele |  |
| Oke\_U2007\_190 | -0.021 | 0.033 |  | Oke\_RDDFW6089\_67 | -0.061 | 0.035 |
| Oke\_U2010\_94 | -0.067 | 0.048 |  | Oke\_RDDFW6089\_75 | -0.059 | 0.034 |
| Oke\_U2011\_107 | -0.017 | 0.023 |  | Oke\_RDDFW61097\_29 | fixed for one allele |  |
| Oke\_U2015\_151 | fixed for one allele |  |  | Oke\_RDDFW61097\_36 | 0.015 | 0.051 |
| Oke\_U2016\_118 | -0.044 | 0.034 |  | Oke\_RDDFW61270\_26 | -0.011 | 0.044 |
| Oke\_U2017\_87 | -0.002 | 0.018 |  | Oke\_RDDFW61351\_74 | -0.017 | 0.014 |
| Oke\_U2019\_112 | -0.043 | 0.025 |  | Oke\_RDDFW61394\_35 | fixed for one allele |  |
| Oke\_U2020\_51 | 0.000 | 0.026 |  | Oke\_RDDFW61394\_55 | -0.057 | 0.032 |
| Oke\_U2021\_86 | -0.002 | 0.038 |  | Oke\_RDDFW62057\_23 | -0.020 | 0.059 |
| Oke\_U2022\_101 | fixed for one allele |  |  | Oke\_RDDFW62057\_46 | 0.064 | 0.015 |
| Oke\_U2023\_99 | -0.050 | 0.029 |  | Oke\_RDDFW62184\_66 | 0.025 | 0.035 |
| Oke\_U2024\_93 | 0.031 | 0.038 |  | Oke\_RDDFW62197\_61 | -0.048 | 0.040 |
| Oke\_U2025\_86 | -0.019 | 0.023 |  | Oke\_RDDFW62296\_25 | 0.005 | 0.050 |
| Oke\_U2026\_64 | -0.013 | 0.040 |  | Oke\_RDDFW62296\_27 | fixed for one allele |  |
| Oke\_U2029\_79 | -0.026 | 0.039 |  | Oke\_RDDFW62806\_57 | 0.022 | 0.079 |
| Oke\_U2031\_37 | -0.026 | 0.022 |  | Oke\_RDDFW62943\_70 | missing too much data |  |
| Oke\_U2032\_74 | -0.011 | 0.028 |  | Oke\_RDDFW62948\_20 | -0.046 | 0.051 |
| Oke\_U2033\_122 | -0.084 | 0.039 |  | Oke\_RDDFW62971\_46 | -0.012 | 0.050 |
| Oke\_U2034\_55 | -0.016 | 0.045 |  | Oke\_RDDFW62971\_59 | fixed for one allele |  |
| Oke\_U2035\_54 | -0.036 | 0.060 |  | Oke\_RDDFW63326\_23 | -0.031 | 0.037 |
| Oke\_U2037\_76 | -0.048 | 0.039 |  | Oke\_RDDFW63375\_38 | missing too much data |  |
| Oke\_U2038\_32 | fixed for one allele |  |  | Oke\_RDDFW63391\_32 | -0.006 | 0.042 |
| Oke\_U2040\_77 | missing too much data |  |  | Oke\_RDDFW63711\_77 | missing too much data |  |
| Oke\_U2041\_84 | 0.000 | 0.059 |  | Oke\_RDDFW63766\_37 | -0.029 | 0.062 |
| Oke\_U2042\_61 | -0.028 | 0.019 |  | Oke\_RDDFW63813\_60 | 0.035 | 0.040 |
| Oke\_U2043\_51 | 0.031 | 0.031 |  | Oke\_RDDFW64078\_73 | -0.040 | 0.081 |
| Oke\_U2045\_43 | -0.070 | 0.024 |  | Oke\_RDDFW64719\_73 | missing too much data |  |
| Oke\_U2047\_49 | 0.000 | 0.044 |  | Oke\_RDDFW64969\_46 | -0.032 | 0.031 |
| Oke\_U2048\_91 | -0.070 | 0.031 |  | Oke\_RDDFW65679\_48 | -0.001 | 0.037 |
| Oke\_U2049\_99 | -0.050 | 0.057 |  | Oke\_RDDFW65723\_42 | fixed and missing in most |  |
| Oke\_U2050\_101 | fixed for one allele |  |  | Oke\_RDDFW65723\_43 | missing in most |  |
| Oke\_U2053\_60 | -0.020 | 0.035 |  | Oke\_RDDFW65723\_58 | missing in most |  |
| Oke\_U2054\_58 | -0.045 | 0.039 |  | Oke\_RDDFW65809\_22 | fixed for one allele |  |
| Oke\_U2056\_90 | -0.072 | 0.028 |  | Oke\_RDDFW65809\_61 | -0.024 | 0.056 |
| Oke\_U2057\_80 | -0.047 | 0.022 |  | Oke\_RDDFW65817\_41 | fixed for one allele |  |
| Oke\_U212\_87 | fixed for one allele |  |  | Oke\_RDDFW65817\_59 | -0.006 | 0.045 |
| Oke\_U302\_195 | -0.006 | 0.055 |  | Oke\_RDDFW6606\_46 | -0.039 | 0.061 |
| Oke\_U305\_307 | -0.052 | 0.036 |  | Oke\_RDDFW66307\_18 | 0.009 | 0.076 |
| Oke\_U401\_143 | -0.005 | 0.018 |  | Oke\_RDDFW66355\_30 | missing too much data |  |
| Oke\_U503\_272 | -0.029 | 0.027 |  | Oke\_RDDFW66355\_43 | fixed for one allele |  |
| Oke\_U504\_228 | -0.001 | 0.034 |  | Oke\_RDDFW66355\_58 | fixed for one allele |  |
| Oke\_U505\_112 | -0.070 | 0.012 |  | Oke\_RDDFW66423\_44 | fixed for one allele |  |
| Oke\_U506\_110 | 0.073 | 0.040 |  | Oke\_RDDFW66423\_68 | 0.242 | 0.038 |
| Oke\_U507\_087 | -0.015 | 0.026 |  | Oke\_RDDFW66423\_71 | fixed for one allele |  |
| Oke\_U507\_286 | -0.011 | 0.031 |  | Oke\_RDDFW66598\_48 | fixed for one allele |  |
| Oke\_U509\_219 | -0.067 | 0.044 |  | Oke\_RDDFW66598\_49 | -0.044 | 0.033 |
| Oke\_U510\_204 | -0.025 | 0.018 |  | Oke\_RDDFW66716\_44 | missing too much data |  |
| Oke\_U511\_271 | missing too much data |  |  | Oke\_RDDFW66740\_41 | -0.022 | 0.046 |
| Oke\_U514\_150 | 0.017 | 0.037 |  | Oke\_RDDFW66747\_32 | failed in all |  |
| Oke\_UBA3\_245 | 0.027 | 0.036 |  | Oke\_RDDFW67033\_73 | -0.043 | 0.087 |
| Oke\_XBP1\_82 | missing too much data |  |  | Oke\_RDDFW6714\_54 | -0.040 | 0.045 |
| Oke\_arf\_319 | -0.011 | 0.041 |  | Oke\_RDDFW6788\_43 | missing too much data |  |
| Oke\_azin1\_90 | -0.067 | 0.030 |  | Oke\_RDDFW67894\_45 | -0.013 | 0.039 |
| Oke\_brd2\_118 | -0.054 | 0.013 |  | Oke\_RDDFW6801\_63 | fixed for one allele |  |
| Oke\_brp16\_65 | 0.001 | 0.024 |  | Oke\_RDDFW6801\_65 | fixed for one allele |  |
| Oke\_ccd16\_77 | -0.034 | 0.050 |  | Oke\_RDDFW68166\_78 | missing too much data |  |
| Oke\_cjo57\_86 | -0.028 | 0.059 |  | Oke\_RDDFW68211\_50 | missing too much data |  |
| Oke\_col1a2\_62 | -0.021 | 0.051 |  | Oke\_RDDFW68211\_62 | fixed for one allele |  |
| Oke\_ctgf\_105 | -0.023 | 0.044 |  | Oke\_RDDFW68590\_54 | fixed for one allele |  |
| Oke\_e2ig5\_50 | 0.005 | 0.034 |  | Oke\_RDDFW68590\_61 | -0.031 | 0.036 |
| Oke\_eif4ebp2\_64 | -0.032 | 0.024 |  | Oke\_RDDFW6872\_56 | 0.023 | 0.069 |
| Oke\_eif4g1\_43 | -0.050 | 0.033 |  | Oke\_RDDFW69177\_36 | failed in all |  |
| Oke\_f5\_71 | -0.055 | 0.017 |  | Oke\_RDDFW69177\_76 | failed in all |  |
| Oke\_gdh1\_191 | missing too much data |  |  | Oke\_RDDFW69329\_52 | fixed for one allele |  |
| Oke\_gdh1\_62 | 0.045 | 0.063 |  | Oke\_RDDFW69329\_56 | missing too much data |  |
| Oke\_glrx1\_78 | -0.014 | 0.033 |  | Oke\_RDDFW69367\_21 | fixed for one allele |  |
| Oke\_hmgb1\_66 | -0.025 | 0.027 |  | Oke\_RDDFW69367\_28 | -0.016 | 0.038 |
| Oke\_hnRNPL\_239 | fixed for one allele |  |  | Oke\_RDDFW69501\_76 | -0.074 | 0.038 |
| Oke\_hsc71\_199 | -0.014 | 0.036 |  | Oke\_RDDFW69669\_47 | 0.026 | 0.025 |
| Oke\_il\_1racp\_67 | -0.030 | 0.028 |  | Oke\_RDDFW69669\_50 | fixed for one allele |  |
| Oke\_lactb2\_71 | -0.069 | 0.049 |  | Oke\_RDDFW69741\_48 | 0.007 | 0.044 |
| Oke\_mcfd2\_86 | -0.031 | 0.065 |  | Oke\_RDDFW69741\_54 | fixed for one allele |  |
| Oke\_mgll\_49 | -0.011 | 0.024 |  | Oke\_RDDFW69741\_55 | -0.034 | 0.021 |
| Oke\_nc2b\_148 | -0.039 | 0.026 |  | Oke\_RDDFW69778\_62 | 0.003 | 0.026 |
| Oke\_ndub3\_58 | -0.007 | 0.034 |  | Oke\_RDDFW69792\_54 | -0.076 | 0.066 |
| Oke\_pgap\_92 | 0.010 | 0.025 |  | Oke\_RDDFW69799\_59 | -0.055 | 0.034 |
| Oke\_pnrc2\_78 | -0.009 | 0.030 |  | Oke\_RDDFW69799\_78 | fixed for one allele |  |
| Oke\_psmd9\_057 | -0.020 | 0.021 |  | Oke\_RDDFW70556\_28 | 0.024 | 0.036 |
| Oke\_psmd9\_188 | -0.053 | 0.027 |  | Oke\_RDDFW70829\_40 | 0.003 | 0.019 |
| Oke\_rab5a\_117 | -0.113 | 0.015 |  | Oke\_RDDFW7083\_70 | missing too much data |  |
| Oke\_ras1\_249 | 0.031 | 0.034 |  | Oke\_RDDFW70902\_20 | -0.040 | 0.047 |
| Oke\_serpin\_140 | -0.020 | 0.024 |  | Oke\_RDDFW71171\_44 | fixed for one allele |  |
| Oke\_slc1a3a\_86 | 0.026 | 0.027 |  | Oke\_RDDFW71171\_55 | -0.026 | 0.041 |
| Oke\_sylc\_90 | 0.003 | 0.017 |  | Oke\_RDDFW71319\_56 | fixed for one allele |  |
| Oke\_thic\_84 | -0.001 | 0.074 |  | Oke\_RDDFW71319\_78 | -0.017 | 0.029 |
| Oke\_txnrd1\_74 | -0.033 | 0.019 |  | Oke\_RDDFW71430\_54 | 0.004 | 0.033 |
| Oke\_u0602\_244 | missing too much data |  |  | Oke\_RDDFW71430\_63 | #N/A | #N/A |
| Oke\_u1\_519 | -0.054 | 0.048 |  | Oke\_RDDFW71450\_69 | missing too much data |  |
| Oke\_u200\_385 | -0.020 | 0.018 |  | Oke\_RDDFW71747\_19 | 0.127 | 0.045 |
| Oke\_u202\_131 | fixed for one allele |  |  | Oke\_RDDFW71866\_73 | 0.091 | 0.051 |
| Oke\_u216\_222 | -0.061 | 0.023 |  | Oke\_RDDFW72082\_30 | -0.038 | 0.015 |
| Oke\_u217\_172 | -0.020 | 0.019 |  | Oke\_RDDFW72091\_54 | -0.040 | 0.051 |
| Oke\_uqcrfs\_69 | fixed for one allele |  |  | Oke\_RDDFW72178\_20 | fixed for one allele |  |
| Oke\_zn593\_152 | -0.056 | 0.024 |  | Oke\_RDDFW72178\_38 | -0.004 | 0.030 |
| Oke\_CO1A1\_76 | -0.040 | 0.019 |  | Oke\_RDDFW72400\_36 | missing too much data |  |
| Oke\_FANK1\_166 | missing too much data |  |  | Oke\_RDDFW72400\_37 | missing too much data |  |
| Oke\_GPH\_105 | -0.088 | 0.029 |  | Oke\_RDDFW72458\_46 | fixed for one allele |  |
| Oke\_NHERF123 | failed in all |  |  | Oke\_RDDFW72458\_49 | -0.008 | 0.032 |
| Oke\_RDDFW91687\_75 | fixed for one allele |  |  | Oke\_RDDFW72464\_55 | 0.014 | 0.036 |
| Oke\_RDDFW92272\_27 | failed in all |  |  | Oke\_RDDFW72464\_65 | -0.009 | 0.029 |
| Oke\_RDDFW92495\_53 | fixed for one allele |  |  | Oke\_RDDFW72515\_22 | 0.102 | 0.045 |
| Oke\_RDDFW93115\_34 | fixed for one allele |  |  | Oke\_RDDFW72556\_23 | fixed for one allele |  |
| Oke\_RDDFW93593\_65 | -0.045 | 0.028 |  | Oke\_RDDFW72556\_29 | -0.036 | 0.051 |
| Oke\_RDDFW93735\_66 | -0.043 | 0.039 |  | Oke\_RDDFW72580\_61 | -0.046 | 0.054 |
| Oke\_RDDFW95768\_62 | missing too much data |  |  | Oke\_RDDFW73104\_50 | 0.126 | 0.035 |
| Oke\_RDDFW96264\_56 | -0.034 | 0.029 |  | Oke\_RDDFW73104\_57 | fixed for one allele |  |
| Oke\_RDDFW96549\_67 | fixed for one allele |  |  | Oke\_RDDFW73104\_59 | fixed for one allele |  |
| Oke\_RDDFW97519\_39 | -0.044 | 0.043 |  | Oke\_RDDFW73204\_40 | missing too much data |  |
| Oke\_RDDFW97562\_72 | -0.005 | 0.109 |  | Oke\_RDDFW73408\_68 | fixed for one allele |  |
| Oke\_RDDFW98639\_71 | missing too much data |  |  | Oke\_RDDFW73408\_78 | -0.054 | 0.065 |
| Oke\_RDDFW98823\_72 | -0.056 | 0.059 |  | Oke\_RDDFW73626\_31 | -0.011 | 0.047 |
| Oke\_U1022\_278 | -0.062 | 0.041 |  | Oke\_RDDFW7364\_35 | missing too much data |  |
| Oke\_U401\_220 | failed in all |  |  | Oke\_RDDFW7364\_61 | fixed for one allele |  |
| Oke\_gdh1\_234 | -0.020 | 0.054 |  | Oke\_RDDFW73828\_41 | -0.047 | 0.044 |
| Oke\_pgap\_111 | -0.026 | 0.037 |  | Oke\_RDDFW74107\_70 | -0.004 | 0.053 |
| Oke\_RDDFW93735\_70 | fixed for one allele |  |  | Oke\_RDDFW74836\_19 | fixed for one allele |  |
| Oke\_RDDFW96264\_75 | fixed for one allele |  |  | Oke\_RDDFW74836\_67 | missing too much data |  |
| Oke\_RDDFW98823\_76 | fixed for one allele |  |  | Oke\_RDDFW74938\_31 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW75108\_61 | missing too much data |  |
|  |  |  |  | Oke\_RDDFW75110\_36 | -0.006 | 0.036 |
|  |  |  |  | Oke\_RDDFW75110\_51 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW75268\_70 | -0.049 | 0.019 |
|  |  |  |  | Oke\_RDDFW75348\_40 | -0.044 | 0.080 |
|  |  |  |  | Oke\_RDDFW75830\_40 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW75830\_48 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW75830\_66 | -0.019 | 0.067 |
|  |  |  |  | Oke\_RDDFW75958\_27 | 0.002 | 0.033 |
|  |  |  |  | Oke\_RDDFW75958\_28 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW76713\_16 | -0.041 | 0.033 |
|  |  |  |  | Oke\_RDDFW76713\_26 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW76878\_51 | -0.004 | 0.035 |
|  |  |  |  | Oke\_RDDFW76918\_38 | failed in all |  |
|  |  |  |  | Oke\_RDDFW76918\_55 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW76972\_26 | -0.031 | 0.025 |
|  |  |  |  | Oke\_RDDFW77053\_53 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW77053\_64 | -0.011 | 0.052 |
|  |  |  |  | Oke\_RDDFW77343\_67 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW77343\_71 | missing too much data |  |
|  |  |  |  | Oke\_RDDFW77508\_44 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW77508\_50 | 0.005 | 0.031 |
|  |  |  |  | Oke\_RDDFW77508\_53 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW78157\_34 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW78157\_36 | -0.006 | 0.051 |
|  |  |  |  | Oke\_RDDFW78789\_24 | -0.077 | 0.082 |
|  |  |  |  | Oke\_RDDFW78882\_33 | missing too much data |  |
|  |  |  |  | Oke\_RDDFW78935\_20 | missing too much data |  |
|  |  |  |  | Oke\_RDDFW79716\_69 | -0.121 | 0.025 |
|  |  |  |  | Oke\_RDDFW80059\_43 | 0.009 | 0.022 |
|  |  |  |  | Oke\_RDDFW80154\_43 | 0.048 | 0.061 |
|  |  |  |  | Oke\_RDDFW80154\_68 | -0.037 | 0.016 |
|  |  |  |  | Oke\_RDDFW80429\_45 | 0.066 | 0.026 |
|  |  |  |  | Oke\_RDDFW80429\_56 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW80662\_52 | -0.001 | 0.068 |
|  |  |  |  | Oke\_RDDFW80789\_39 | missing too much data |  |
|  |  |  |  | Oke\_RDDFW83497\_50 | 0.010 | 0.021 |
|  |  |  |  | Oke\_RDDFW83497\_58 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW88286\_45 | missing too much data |  |
|  |  |  |  | Oke\_RDDFW88286\_69 | missing too much data |  |
|  |  |  |  | Oke\_RDDFW89343\_75 | 0.008 | 0.025 |
|  |  |  |  | Oke\_RDDFW89357\_30 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW89357\_49 | -0.040 | 0.079 |
|  |  |  |  | Oke\_RDDFW89443\_28 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW89443\_55 | -0.042 | 0.033 |
|  |  |  |  | Oke\_RDDFW90259\_25 | -0.004 | 0.019 |
|  |  |  |  | Oke\_RDDFW90437\_74 | -0.024 | 0.036 |
|  |  |  |  | Oke\_RDDFW9156\_37 | -0.055 | 0.026 |
|  |  |  |  | Oke\_RDDFW945\_42 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW945\_50 | 0.007 | 0.025 |
|  |  |  |  | Oke\_RDDFW9723\_23 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW9723\_32 | fixed for one allele |  |
|  |  |  |  | Oke\_RDDFW9723\_42 | missing too much data |  |
|  |  |  |  | Oke\_RDDFW9886\_52 | -0.010 | 0.052 |

Appendix II. **List of collections and the number of samples genotyped initially at the two panels with statistics and data for collections at panel 1 and panel 2 (from Small et al. 2017). Green River Hatchery was eliminated because of missing data. Statistics include the number of loci out of Hardy-Weinberg Equilibrium (Loci out HWE), the percentage of loci out of HWE, the number of loci fixed for a single allele (Fixed/282, Fixed/209) and the percentage of polymorphic loci (% poly loci), as well as the number of samples in each collection meeting the 66% genotype threshold of data (Final N).**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | Final N | Loci out | Panel 1 stats | Fixed/ |  |  |  | Loci out | Panel 2 stats | Fixed/ |  |
| region | Collections | panel 1 | HWE | % out HWE | 282 | % poly loci |  | Final N | HWE | % out HWE | 209 | % poly loci |
| HoodCanal | Anderson | 47 | 13 | 4.92 | 19 | 93.29% |  | 41 | 11 | 5.47 | 8 | 96.17% |
| HoodCanal | BigBeef | 43 | 14 | 5.24 | 16 | 94.35% |  | 35 | 8 | 3.98 | 8 | 96.17% |
| HoodCanal | Dewatto | 48 | 17 | 6.39 | 17 | 93.99% |  | 30 | 13 | 6.50 | 9 | 95.69% |
| HoodCanal | Duckabush | 47 | 11 | 4.21 | 22 | 92.23% |  | 42 | 7 | 3.52 | 10 | 95.22% |
| HoodCanal | Lilliwaup | 42 | 12 | 4.53 | 18 | 93.64% |  | 33 | 12 | 6.03 | 10 | 95.22% |
| HoodCanal | NFSkokomish | 23 | 16 | 6.25 | 27 | 90.46% |  | 47 | 7 | 3.47 | 7 | 96.65% |
| NorthPS | Lower\_Sauk | 23 | 18 | 6.72 | 15 | 94.70% |  | 19 | 8 | 3.98 | 8 | 96.17% |
| NorthPS | Nooksack | 32 | 23 | 8.75 | 20 | 92.93% |  | 34 | 22 | 10.95 | 8 | 96.17% |
| NorthPS | Skagit\_lo\_main | 31 | 18 | 6.84 | 20 | 92.93% |  | 26 | 14 | 7.00 | 9 | 95.69% |
| NorthPS | Snohomish | 40 | 13 | 4.92 | 19 | 93.29% |  | 37 | 9 | 4.48 | 8 | 96.17% |
| NorthPS | Stillaguamish | 41 | 12 | 4.60 | 22 | 92.23% |  | 34 | 9 | 4.48 | 8 | 96.17% |
| NorthPS | upper\_Skagit | 33 | 15 | 5.64 | 17 | 93.99% |  | 30 | 13 | 6.47 | 8 | 96.17% |
| SJF | Dungeness | 46 | 14 | 5.24 | 16 | 94.35% |  | 0 |  |  |  |  |
| SouthPS | Chico/Grovers | 50 | 15 | 5.70 | 20 | 92.93% |  | 39 | 14 | 6.90 | 6 | 97.13% |
| SouthPS | Green River Hatchery | 8 |  |  |  |  |  | 0 |  |  |  |  |
| SouthPS | Kennedy | 47 | 13 | 5.02 | 24 | 91.52% |  | 47 | 9 | 4.50 | 9 | 95.69% |
| SouthPS | Skookum | 39 | 14 | 5.41 | 24 | 91.52% |  | 37 | 11 | 5.42 | 6 | 97.13% |
| SouthPS\_W | DIRU\_PuyallupH | 46 | 9 | 3.40 | 18 | 93.64% |  | 44 | 13 | 6.40 | 6 | 97.13% |
| SouthPS\_W | Nisqually\_W | 65 | 19 | 7.20 | 19 | 93.29% |  | 59 | 18 | 8.87 | 6 | 97.13% |
| Fraser | Hopedale | 46 | 19 | 7.17 | 18 | 93.64% |  | 45 | 15 | 7.46 | 8 | 96.17% |
| Fraser | Peach | 37 | 9 | 3.45 | 22 | 92.23% |  | 0 |  |  |  |  |
| Fraser | Squawkum | 38 | 15 | 5.58 | 14 | 95.05% |  | 31 | 10 | 5.00 | 9 | 95.69% |
| GeorgiaSt | BigQualicum | 48 | 15 | 5.68 | 19 | 93.29% |  | 48 | 14 | 6.80 | 3 | 98.56% |
| GeorgiaSt | Campbell | 34 | 13 | 4.91 | 18 | 93.64% |  | 33 | 5 | 2.48 | 7 | 96.65% |
| GeorgiaSt | Cheakamus | 43 | 12 | 4.43 | 12 | 95.76% |  | 43 | 17 | 8.29 | 4 | 98.09% |
| GeorgiaSt | Cowichan | 29 | 18 | 6.82 | 19 | 93.29% |  | 24 | 10 | 4.98 | 8 | 96.17% |
| GeorgiaSt | Lang | 34 | 8 | 3.01 | 17 | 93.99% |  | 36 | 8 | 3.92 | 5 | 97.61% |
| GeorgiaSt | LittleQualicum | 48 | 11 | 4.21 | 22 | 92.23% |  | 48 | 13 | 6.40 | 6 | 97.13% |
| GeorgiaSt | Nanaimo | 48 | 19 | 7.14 | 17 | 93.99% |  | 34 | 15 | 7.46 | 8 | 96.17% |
| GeorgiaSt | Phillips | 45 | 16 | 5.99 | 16 | 94.35% |  | 46 | 13 | 6.34 | 4 | 98.09% |
| GeorgiaSt | Puntledge | 48 | 29 | 10.86 | 16 | 94.35% |  | 48 | 15 | 7.35 | 5 | 97.61% |
| GeorgiaSt | Snake | 35 | 18 | 6.72 | 15 | 94.70% |  | 35 | 10 | 4.93 | 6 | 97.13% |
| GeorgiaSt | Southgate | 47 | 13 | 4.96 | 21 | 92.58% |  | 45 | 10 | 4.93 | 6 | 97.13% |
| JohnstoneSt | Nimpkish | 47 | 15 | 5.54 | 12 | 95.76% |  | 47 | 18 | 8.82 | 5 | 97.61% |
| WCVI | Conuma | 45 | 12 | 4.48 | 15 | 94.70% |  | 45 | 15 | 7.46 | 8 | 96.17% |
| WCVI | Nitinat | 48 | 14 | 5.22 | 15 | 94.70% |  | 48 | 6 | 2.99 | 8 | 96.17% |
| WCVI | Sooke | 31 | 11 | 4.17 | 19 | 93.29% |  | 27 | 8 | 4.00 | 9 | 95.69% |
|  | mean |  | 14.8 | 5.59 | 18.3 | 93.52% |  |  | 11.8 | 5.82 | 7.1 | 96.58% |
|  | SE |  | 4.1 | 1.5 | 3.3 | 0.20% |  |  | 3.9 | 1.9 | 1.8 | 0.14% |