Report to Southern Fund Panel

Award Number: SF-2012-1-13B

WDFW number: 12-1284

Amount of Grant: $150,000

Project Title: Chum Salmon Southern Area Genetic Baseline Enhancement

Grantees: Kit Rawson, John Candy, Terry Beacham, Lisa Seeb, Maureen Small, Kenneth Warheit, Gary Winans

Affiliations: Tulalip Tribes, CDFO, UW, WDFW, NOAA

Project Start and End Date: 07/01/2012 - 06/31/2014

Abstract

This project developed SNP loci and genotyped Chum salmon populations from the US and CAN Southern Boundary region to increase resolution of genetic stock identification in this region in support of regional and international Chum salmon fisheries management. Twenty Chum salmon population collections were genotyped with 186 single nucleotide polymorphism loci (described in this report) and with 28 microsatellite loci (described in attached report). Overall F_{ST} value with SNP data was 0.032, with individual locus values ranging from 0.001 to 0.128. Baseline collections were added to existing datasets to more precisely and accurately manage Chum salmon fisheries Washington and British Columbia. In 100% simulations with SNP data, assignments to individual populations averaged 77%, with a range from 40% to 99%, assignments to regional groups averaged 94%, with a range from 69% to 99%, and assignments to country group were 95% or greater. Populations clustered by geographic region and in all mixed fishery simulations mixture components assigned to their country of origin with precision and accuracy. The genetic data can be used by American (Washington) and Canadian managers and co-managers to shape fisheries and to facilitate the sustainability and productivity of Chum salmon. These data were added to interagency databases now in use to study bycatch of Chum salmon in trawl fisheries in the Bering Sea.

Executive Summary

This project supported the development, evaluation, and improvement of single nucleotide polymorphism (SNP) and microsatellite (mSAT) data for identifying southern Chum salmon stocks in mixed-stock fisheries. We conducted an updated survey of genetic variation in representative population samples of Chum salmon from southern British Columbia (SBC) and Washington State (WA) to enhance Chum salmon population genetic baselines for better stock assessment, management, and research. Tissue samples were collected from representative stocks (20 stocks for initial evaluation) and genotyped at 186 SNP loci and 28 mSAT loci.

This study enhanced the existing SNP baseline and improved accuracy in international estimates. This study enhanced the existing mSAT baseline, particularly in the US, and improved the accuracy of assessments using the mSAT baseline in international fishery estimates. The study filled population gaps in the SBC SNP baseline and in the WA mSAT baseline. The enhanced SNP baseline builds on the SNP panels developed by UW, ADFG, and WDFW for Chum salmon originating from British Columbia, Washington, and Alaska. The SNP and mSAT baselines were compared individually for resolving power for mixed stock fisheries and other fishery management questions through simulations. This report focuses on the development of SNP loci, the enhancement of the SNP baseline, and the performance of SNP loci in resolving simulated mixed fishery samples.

Contents

List of Tables

List of Figures

Overview:

The primary application of the Chum salmon SNP genetic data is to resolve the stock composition of mixed stock fisheries. Genetic baselines will also be used to develop a new management-oriented fisheries model that incorporates genetic and environmental information. Other uses of the genetic baselines include improving the scientific understanding of factors limiting Chum salmon recovery and production, analyses of relative reproductive success of hatchery- and natural-origin spawners and the impact of supplementation programs on wild populations, improved abundance estimations, and identifying origins of juvenile Chum salmon that use coastal nursery areas.

Stock:

Stocks were selected by the Chum TC to represent important US and Canadian stock groups including Puget Sound fall and winter Chum salmon, and Hood Canal fall Chum salmon (Table 1). Canadian stock groups include fall Chum salmon from East and West Coast Vancouver Island, Fraser River, and Mainland Coastal (including Johnston Strait and inlet stocks).

Conservation Level:

Chum salmon abundance levels in the US and Southern BC have trended downward for the past 10 years in most stocks along the Southern boundary creating a medium level of concern for these stocks. In response to concerns over stock abundance levels, commercial and recreational fisheries were reduced or suspended in some areas and years. The expanded baselines will improve the ability of both countries and co-managers to manage populations of low abundance and improve survival rate estimates for cohort reconstruction.

Bilateral Fishery Relevance:

The improved baselines will allow the Chum TC to address its obligations under the Pacific Salmon Treaty, Annex IV Chapter 6 to estimate and document the stock composition and exploitation rates in fisheries of concern to the treaty, evaluate stock composition information for fisheries using bilaterally agreed upon methods and manage for catch composition in mixed stock fisheries.

Fishery Benefits:

The genetic baselines provide a foundation for all international and domestic Chum salmon fisheries management. Benefits include the ability to manage fishery exploitation of individual stocks and manage stocks on a regional basis (eg. distinguish Fraser River stocks from Puget Sound stocks in a mixture from Northern Puget Sound). This ability to distinguish between stock

groups provides information that may prevent over-exploitation of stocks of concern and prevent restricting fisheries unnecessarily.

Context:

During the past five years the number of SNPs available for stock identification of Pacific salmon has increased considerably (Narum et al. 2008, Abadia-Cardosa et al. 2011, Campbell and Narum 2011, Seeb et al. 2011b, Templin et al. 2011, Seeb et al. 2014b, Warheit et al. 2014). All laboratories currently working in the PSC area are now using SNP technology.

SNPs are based directly on the DNA sequence and are scored as a digit (letter A, C, G, and T). Therefore they are precisely scored automatically and the data are easily transferable between laboratories (Morin et al. 2004, Morin and McCarthy 2007, Seeb et al. 2007). SNPs may be located in coding regions for genes under selection and thus may also survey adaptive as well as neutral variation. Adaptive variation may be particularly valuable in achieving the Chum TC goal of incorporating genetic and environmental information to manage fisheries.

The current SNP project builds on ongoing projects conducted by UW and WDFW through PACSNP (Seeb et al. 2011b) and in collaboration with Alaska Department of Fish and Game's Western Alaska Salmon Stock Identification Program (WASSIP http://www.adfg.alaska.gov/index.cfm?adfg=wassip.main). In addition, UW and WDFW recently completed a SNP project funded by a NOAA Saltonstall-Kennedy grant to develop and evaluate SNPs specifically to differentiate populations of Chum salmon in the Southern Boundary area (Seeb et al. 2014a). Those SNPs were ascertained from populations from southern British Columbia and Washington State that were chosen by the Chum Technical Committee in 2011.

Replicate surveys of SNP and mSAT variation in the standard set of populations were conducted, SNPs and mSATs were assembled for each individual surveyed, and an evaluation was conducted of the efficacy for stock identification of both marker types. Analyses included mixed stock fishery simulations with both marker types.

Objective 1. Baseline genotyping of 20 populations from Washington and British Columbia for 28 mSATs. This Objective was completed by Department of Fisheries and Oceans (Candy et al. 2014)

Objective 2. Baseline genotyping of 20 populations from Washington and British Columbia for 96 SNPs (this report).

Samples: The target sample size was 95 for each population. The sample size was 50 from the Skagit River and 80 more samples were collected from the river in fall 2013. These additional Skagit samples are scheduled to be SNP-genotyped at WDFW in summer 2014. Tissue samples from spawning Chum salmon were collected from most populations during 2010 and 2011

(Southgate was an archived sample collected in 2003, see Figure 1 for map of sample locations). Samples were collected from Cheakamus River in fall 2013, after SNP genotyping ended. The Cheakamus sample is scheduled to be SNP-genotyped at WDFW in summer 2014. Collections across years from the same site were pooled. We also pooled collections from two sampling sites within drainages for Grovers and Chico creeks, and Skookum and Mill creeks (Table 1). Samples were obtained from 22 collections resulting in 19 populations (excluding Cheakamus). Chum salmon DNA was extracted with a silica membrane protocol following manufacturer's instructions (Macherey-Nagel). Each SNP locus was scored independently by two researchers and discrepancies were resolved before exporting final scores.

SNP selection: The SNP selection process (described in Seeb et al. 2014) was conducted in with 259 candidate SNPs. Of these SNPs, 75 were novel SNPs developed under a companion Salton-Stall Kennedy project (Seeb et al. 2014a) focusing on the Southern Boundary region, and 60 were previously described (Smith et al. 2005, Elfstrom et al. 2007) (Table 2). In addition, we tested 124 newly developed SNPs that became available from study of Alaskan Chum salmon conducted in the Seeb laboratory (Seeb et al. 2011a, Petrou et al. 2013, Petrou et al. 2014). The SNP rankings were based on overall F_{ST} across boundary region populations and selected SNPs with high resolving power. A final panel of 192 SNPs was identified for population genotyping that included three mitochondrial and 189 nuclear SNPs.

SNP genotyping: SNP genotyping was performed using the BioMark 96.96 Dynamic Array (Fluidigm http://www.fluidigm.com/ biomark_genotyping.htm) installed at the University of Washington and following the general protocols of Seeb et al. (2011). Genotypes will be entered into the Progeny database (Progeny Software, South Bend, Indiana) installed at SAFS and WDFW and made publically available on a web-based application. Quality control measures included: reanalysis of 4% of each collection for all SNP markers to ensure that genotypes were reproducible and to identify laboratory errors and measure rates of inconsistencies during repeated analyses.

Statistics: A total of 1756 Chum salmon were SNP-genotyped for the 19 populations. Two of the novel assays failed to perform properly, leaving genotypes for 190 SNPs. We tested for deviation from Hardy-Weinberg expectations, as expressed by F_{IS}, at each locus and across all loci using FSTAT 2.9.3 ((Nei 1987), Goudet 2001) with 1000 permutations: loci out of equilibrium in > 50% of the populations ($P < 0.01$) were removed. Departure from HWE can be an indication that collections contain the following: family groups, a strong year class, more than one subpopulation, related parents in the previous generation, or the locus may have been under selection. We tested whether genotypes at each locus were independent of each other with Fisher's tests for genotypic linkage disequilibrium using GENETIX (Belkhir et al. 2001) with 100 permutations. Loci were tested for linkage between each pair of loci within and across samples. Linkage disequilibrium can be an indication that the collection contains family groups, that the population or locus is under selection, or that allele frequencies drifted because of small

population size: if a locus pair was linked in all collections, one locus was removed from all collections. We calculated basic genetic diversity measures, Nei's (1987) estimate of heterozygosity and allelic richness (based on minimum 31 individuals), using FSTAT. Results for HWE tests were adjusted for multiple comparisons (sequential Bonferroni correction, (Rice 1989)) to an alpha level of 0.05. Because there were 16471 simultaneous pairwise tests for linkage per population, we report the number of permutations that were larger than or equal to the actual linkage values at 5% and 1%.

Pairwise tests: We conducted pairwise genotypic tests to evaluate population differentiation using FSTAT. We also used FSTAT to calculate the amount of genetic variance among samples (pairwise F_{ST} values (Weir and Cockerham 1984)) and the amount of genetic variance over all samples at each locus (G_{ST}', Nei's estimate of F_{ST} corrected for population size differences, hereafter referred to as F_{ST}). Genetic structure among collections was assessed in a principal coordinates plot based on pairwise F_{ST} values using GenAlEx (Peakall and Smouse 2006) and in a neighbor-joining tree based on Nei's genetic distances using PHYLIP (Felsenstein 2004).

Assignment tests: In another assessment of genetic structure, we conducted genetic assignment tests using the methods implemented in the program ONCOR (Kalinowski , Anderson et al. 2008). Because we expected genetic similarity among collections based on geographic proximity and we were interested in resolution at the country level, we clustered collections into "reporting groups" according to country, US and CAN. We used 100% simulation tests (with sample sizes same as baseline option) as a first examination of the power of the loci for genetic assignments. In this test, the program simulated fishery samples composed of 100% individuals from a single collection (200 fish were simulated per collection in turn and 100 simulations were conducted per collection) and assigned those individuals to the genetic baseline. In assignment tests, the collections constitute the genetic baseline and each individual is assigned a likelihood of being sampled from each baseline collection, based on the genotype of the individual and allele frequencies of the baseline collections. The assignment is to the collection with the highest likelihood. If data are structured at the local level, individuals assign to their collection of origin and if data are structured at the regional level, individuals may not assign to their collection of origin, but assign to a collection within their reporting group (country or regional group). The 100% simulation is an unrealistic best case fishery scenario in which a collection is unmixed, but it tells about the information content of the loci and what might be expected for genetic resolution of components in a mixed fishery. We also conducted "leave-one-out" assignment tests on the baseline collections. In this test, each individual was assigned to the baseline, based on the genotype of the fish and the allele frequencies of the baseline collections, with the fish in question removed from its collection when allele frequencies are calculated. Similar to the 100% simulation, the collection with the highest likelihood was the assignment for the individual fish. In contrast to the 100% simulation, the likelihoods were conditioned on the mixture proportions calculated for the collection in which the fish was sampled. In this test only individuals with full genotypes were assigned.

Mixed fishery simulations: We used ONCOR to simulate mixed fishery samples for mixtures expected at a test fishing site along the coast to examine loci for performance in a mixed fishery. We set up a series of simulated mixed fisheries of 200 fish each and ran simulations 1000 times for each simulated mixture to generate average mixture proportions, standard deviations, and 95% confidence intervals (see Tables 5-7 for mixture proportions). Simulations began with a test case involving the two US and Canadian samples that had the smallest pairwise F_{ST} value (Nooksack and Puntledge) in which the actual proportions were 9:1, 7.5:2.5, and 1:1 as the most difficult challenge to examine the resolving power of the SNP loci. The next series of simulations added Hopedale to Nooksack and Puntledge with actual proportions ranging from equal proportions (0.33 each) to 0.9:0.05:0.05 to increase the complexity of the analysis and move towards mixtures that might be encountered in fishery samples. The next series of simulations added Stillaguamish to the mixtures that ranged from equal proportions to 7:1:1:1, to similarly increase complexity and realism for the analysis.

Results for Objective 2: The SNP genotyping was enlarged with supplementary funding to include additional populations and additional SNPs. We successfully genotyped 190 SNPs in 19 populations. Successful genotypes were from three mitochondrial (mtDNA) and 187 nuclear SNPs (Table 2, Appendix 1).

Two of the mtDNA SNPs were monomorphic (*Oke-C30* and *Oke_Cr386*) and the third (*Oke_ND3-69*) had a frequency of < 0.02; all mtDNA SNPs were dropped from further analyses for this study. However, these mtDNA loci distinguish southern populations from those that originate in Alaska and Asia and will be extremely useful for Pacific Rim-wide analyses (Seeb et al. 2014a). We also excluded two SNPs that deviated significantly from Hardy-Weinberg equilibrium (*Oke_RSPRY1-106, Oke_XBP1-82)* and excluded two individual SNPs from pairs of SNPs that showed significant linkage disequilibrium (excluded SNP in bold: *Oke_RAD14962 /* ***Oke_RAD15073;*** *Oke_DBLOH-79/* ***Oke_u0602-244****)*. This resulted in a final total for analyses of 183 SNPs.

Sample statistics: Genetic diversity measures, allelic richness and gene diversity (heterozygosity), were correlated in populations (Table 3) and diversity tended to be higher in northern populations and decrease towards the south (Table 3, Figure 2, Figure 3). Because samples were genotyped with SNPs and there are only two alleles per SNP locus, allelic richness (average number of alleles per locus) was low. Similarly, gene diversity was lower than in microsatellites and also because one allele is often at higher frequency (major allele), rather than evenly distributed, such that heterozygosity is lower at SNP loci. However, populations tended to have higher heterozygosity than expected under Hardy-Weinberg proportions. Collections were fixed at an average of around 4% of the loci and fewer than 5% of locus pairs were in linkage at the 1% level in all collections.

Population relationships: Results were concordant between pairwise genotypic and F_{ST} results, with the exception that Hopedale and Squawkum were undifferentiated with the pairwise genotypic test but their pairwise F_{ST} value was significant. The pairwise F_{ST} values showed significant genetic variance among most samples (Table 4) with some non-significant values among geographically close populations (Figure 1). The samples from Georgia Strait and Phillips River in Johnstone Strait were undifferentiated and the samples from North Puget Sound were undifferentiated. The Skagit River sample was half the size of most other samples (N = 50), which may have contributed to the lack of significant genetic variance in comparisons if 50 individuals was insufficient to capture the majority of genetic diversity in the population. The overall average F_{ST} value among Canadian samples was 0.02 and among US samples was 0.03 and between Canadian and US samples was 0.04, supporting strong differentiation across the Southern Boundary Region. Relationships among the populations are represented in a principle coordinates analysis (PCoA) plot based on pairwise F_{ST} values (Figure 4) and in a neighbor-joining tree (Figure 5) based on Nei's unbiased distance. In both analyses the samples collected in south Puget Sound and Hood Canal cluster together (100% bootstrap support in the tree) and the samples collected in northern locations cluster together (unsupported branch in the tree). The two samples from the Fraser River, Squawkum and Hopedale, clustered closely and the PCoA suggested subgroups consisting of North Puget Sound collections and collections from Vancouver Island and coastal British Columbia. Interestingly, the winter run Chum salmon from Puyallup Hatchery clustered with Lilliwaup in the PCoA and plotted on its own in the NJ tree. These relationships among populations were concordant with results based on microsatellites (Small et al. 2006, Beacham et al. 2008, Beacham et al. 2009, Small et al. 2009, and Beacham et al. 2014) and allozymes (Phelps et al. 1994, Johnson et al. 1997) showing regional clustering, although differences in marker systems, populations and sample sizes preclude direct comparisons.

The F_{ST} values were calculated over all populations for all SNPs as well as observed heterozygosity (Table 2). For the full panel of 183 SNPs, the overall F_{ST} values ranged from 0.001 (*Oke_GHII-3129*) to 0.128 (*Oke_U502-241*) with an overall average of 0.033 (in comparison, the overall average for the mSAT data was 0.011 (Beacham et al. 2014)). We plotted the five SNP loci with the highest F_{ST} values to illustrate frequency differences along a latitudinal gradient (Figure 6). This suite of SNP loci shows promise for high-resolution discrimination among Chum salmon populations in the Salish Sea.

Assignment and mixed fishery: Simulation studies employing ONCOR demonstrated the accuracy and precision of the SNP dataset for genetic stock identification. In the 100% simulation (Table 5), the best-case scenario of a single, unmixed stock, the assignment accuracy to population of origin ranged from 40% (Big Qualicum) to 99% (Puyallup and Nitinat). Mis-assignments were to other populations within regions: the lowest assignment to region of origin was 69% (Lang) and assignment to region was 76% for Big Qualicum. Based on the mis-assignment patterns for the single, unmixed stock analysis and geographic proximity, we tried a

regional grouping that clustered the Strait of Georgia collections into a single region (Big Qualicum, Lang and Puntledge): Big Qualicum regional assignment increased to 94%, Lang regional assignment increased to 86%, and Puntledge regional assignment increased to 92%. Assignment to country of origin was 95% or greater for all populations (Table 5).

In comparison to 100% assignment simulations with the mSAT data, assignment power for individual populations varied between marker sets: for some populations SNPs had better assignment power (eg. Skookum) and for some populations mSATs had better assignment power (eg. Big Qualicum, see Beacham et al. 2014 for mSAT assignment data). There was no significant difference in assignments between the marker types in a paired t-test ($p = 0.101$ for SNP comparison with 14 mSAT loci and $p = 0.45$ for SNP comparison with 28 mSAT loci).

We first performed simulated mixed fisheries with the two populations from U.S. and Canada that had the lowest pairwise F_{ST} value, Nooksack and Puntledge and examined mixture allocations to populations and summarized to country of origin (Table 6, Figure 7). Allocations to original populations were below actual values because proportions were also allocated to closely related populations. However, in all simulations estimated allocations to country of origin were indistinguishable from actual allocations. The next simulated mixed fishery series involved three populations, Nooksack from US and two Canadian populations, Puntledge and Hopedale (Table 7, Figure 8). The final simulated mixed fishery series involved four populations, Nooksack and Stillaguamish from US and Puntledge and Hopedale from Canada (Table 8, Figure 9). Results with increased numbers of populations were similar to the simulations with two populations in that allocations to original populations were lower than actual values but allocations to country were indistinguishable from actual allocations. Simulated mixed fishery results with SNPs were comparable to simulations with mSATs (see Beacham et al. 2014), as expected from the similar power displayed in the 100% assignments.

Upon completion of this project, the SNP baseline will be available for distribution to the international scientific community through the Pacific Salmon Commission and the North Pacific Anadromous Fish Commission. Results were presented to managers and the fishing community through the Chum Technical Committee Meetings held in Vancouver, British Columbia, and Olympia Washington, in early 2013, with updates provided in February, 2014.

Evaluation: Project objectives for SNP genotyping were mostly attained or surpassed. Our objective originally was to develop a novel 36-SNP panel for Chum salmon to accommodate the then current (2012) needs of management. We developed 75 novel SNPs. Objective 2 was originally to genotype 20 populations from Washington and British Columbia for 96 SNPs. We screened 19 populations for 192 SNPs and the remaining population is scheduled to be genotyped. The new data will be freely available to the international scientific community and are currently used by the University of Washington and Washington Department of Fish and Wildlife.

We made modifications described above because agencies are increasing the sizes of assay panels as more SNPs become available (see for example Jasper et al. 2013, Petrou et al. 2013). We felt that the original 36-SNP target for this study may not completely meet the needs of management, especially given that we developed 75 novel assays and had dozens of additional assays available from sister studies. We were able to expand the scope of the project by leveraging funds made available by the Gordon and Betty Moore Foundation to support discretionary genotyping research in Pacific salmon and with Salton-Stall Kennedy funding. Washington Department of Fish and Wildlife supplied the extra chips used to assay the additional populations and additional SNPs, and the project benefitted from an ongoing initiative to develop genetic databases for Chum salmon by the Chum Technical Committee of the Pacific Salmon Commission with funding from the Southern Endowment Fund.

Acknowledgements:

We thank the Chum Technical Committee of the Pacific Salmon Commission for help with sample coordination. Tissue samples originated from a number of sources including the Washington Department of Fish Wildlife, the U.S. Fish and Wildlife Service, the Tulalip Tribe, Alaska Department of Fish and Game, and the Canadian Department of Fisheries and Oceans. We thank the Southern Endowment Fund of the Pacific Salmon Commission for funding this project. The scope of the SNP project was increased as a result of funding from the Washington Department of Fish and Wildlife, the Gordon and Betty Moore Foundation. Special thanks to Carita Pascal of the University of Washington who contributed significantly to the success of this SNP project.

References:

Abadia-Cardoso, A., A. J. Clemento, and J. C. Garza. 2011. Discovery and characterization of single-nucleotide polymorphisms in steelhead/rainbow trout, Oncorhynchus mykiss. Molecular Ecology Resources 11:31-49.

Anderson, E. C., R. S. Waples, and S. T. Kalinowski. 2008. An improved method for predicting the accuracy of genetic stock identification. Canadian Journal of Fisheries and Aquatic Sciences 65:1475-1486.

Beacham, T. D., J. R. Candy, C. Wallace, S. Urawa, S. Sato, N. V. Varnavskaya, K. D. Le, and M. Wetklo. 2009. Microsatellite stock identification of Chum salmon on a Pacific Rim basis. North American Journal of Fisheries Management 29:1757-1776.

Beacham, T. D., B. Spilsted, K. D. Le, and M. Wetklo. 2008. Population structure and stock identification of Chum salmon (Oncorhynchus keta) from British Columbia determined with microsatellite DNA variation. Canadian Journal of Zoology 86:1002-1014.

Beacham, T. D., K. D. Le, C. Wallace, and J. R. Candy. 2014. Chum salmon stock identification in southern British Columbia and Puget Sound using microsatellites. Report to the Southern Fund Panel.

Belkhir, K., P. Borsa, L. Chikhi, N. Raufaste, and F. Bonhomme. 2001. GENETIX 4.05, logiciel sous Windows ™ pour la genetique des populations. Laboratoire Genome, Populations, Interactions, CNRS UMR 5000, Universite de Montpellier II, Montpellier (France).

Campbell, N. R., and S. R. Narum. 2011. Development of 54 novel single-nucleotide polymorphism (SNP) assays for sockeye and coho salmon and assessment of available SNPs to differentiate stocks within the Columbia River. Molecular Ecology Resources 11:20-30.

Elfstrom, C. M., C. T. Smith, and L. W. Seeb. 2007. Thirty-eight single nucleotide polymorphism markers for high-throughput genotyping of Chum salmon. Molecular Ecology Notes 7:1211-1215.

Felsenstein, J. 2004. Inferring phylogenies. http://evolution.genetics.washington.edu/phylip.html

Jasper, J. R., C. Habicht, S. Moffitt, R. Brenner, J. Marsh, B. Lewis, E. C. Fox, Z. Grauvogel, S. D. R. Olive, and W. S. Grant. 2013. Source-Sink Estimates of Genetic Introgression Show Influence of Hatchery Strays on Wild Chum Salmon Populations in Prince William Sound, Alaska. PLoS ONE 8.

Johnson, O. W., W. S. Grant, R. G. Cope, K. Neely, F. W. Waknitz, and R. S. Waples. 1997. Status review of Chum salmon from Washington, Oregon, and California U. S. Dept. Commer., NOAA Tech. Memo. NMFS-NWFSC-32, 280 p.

Kalinowski, S. ONCOR. http://www.montana.edu/kalinowski/Software.htm

Morin, P. A., G. Luikart, and R. K. Wayne. 2004. SNPs in ecology, evolution and conservation. Trends in Ecology & Evolution 19:208-216.

Morin, P. A. and M. McCarthy. 2007. Highly accurate SNP genotyping from historical and low-quality samples. Molecular Ecology Notes 7:937-946.

Narum, S. R., M. Banks, T. D. Beacham, M. R. Bellinger, M. R. Campbell, J. Dekoning, A. Elz, C. M. Guthrie Iii, C. Kozfkay, K. M. Miller, P. Moran, R. Phillips, L. W. Seeb, C. T. Smith, K. Warheit, S. F. Young, and J. C. Garza. 2008. Differentiating salmon populations at broad and fine geographical scales with microsatellites and single nucleotide polymorphisms. Molecular Ecology 17:3464-3477.

Nei, M. 1987. Molecular evolutionary genetics. Columbia University Press, New York.

Peakall, R. O. D. and P. E. Smouse. 2006. genalex 6: genetic analysis in Excel. Population genetic software for teaching and research. Molecular Ecology Notes 6:288-295.

Petrou, E. L., L. Hauser, R. S. Waples, J. E. Seeb, W. D. Templin, D. Gomez-Uchida, and L. W. Seeb. 2013. Secondary contact and changes in coastal habitat availability influence the nonequilibrium population structure of a salmonid (Oncorhynchus keta). Molecular Ecology:n/a-n/a.

Petrou, E. L., J. E. Seeb, L. Hauser, M. J. Witteveen, W. D. Templin, and L. W. Seeb. 2014. Fine-scale sampling reveals distinct isolation by distance patterns in Chum salmon (Oncorhynchus keta) populations occupying a glacially dynamic environment. Conservation Genetics 15:229-243.

Phelps, S. R., L. L. Leclair, S. Young, and H. L. Blankenship. 1994. Genetic diversity patterns of Chum salmon in the Pacific Northwest. Canadian Journal of Fisheries and Aquatic Sciences 51:65-83.

Rice, W. R. 1989. Analyzing tables of statistical tests. Evolution 43:223-225.

Seeb, J. E., C. E. Pascal, E. D. Grau, L. W. Seeb, W. D. Templin, T. Harkins, and S. B. Roberts. 2011a. Transcriptome sequencing and high-resolution melt analysis advance single nucleotide polymorphism discovery in duplicated salmonids. Molecular Ecology Resources 11:335-348.

Seeb, L. W., A. Antonovich, M. Banks, T. Beacham, R. Bellinger, S. Blankenship, M. Campbell, N. Decovich, J. C. Garza, C. Guthrie, T. Lundrigan, P. Moran, S. Narum, J. Stephenson, J. Supernault, D. Teel, W. D. Templin, J. K. Wenburg, S. Young, and C. T. Smith. 2007. Development of a standardized DNA Database for Chinook salmon. Fisheries 32 540-552.

Seeb, L. W., J. Seeb, and K. Warheit. 2014a. Development of high resolution DNA markers to manage fishery interactions of Chum salmon in Western Washington.33.

Seeb, L. W., R. K. Waples, M. T. Limborg, K. I. Warheit, C. E. Pascal, and J. E. Seeb. 2014b. Parallel signatures of selection in temporally-isolated lineages of pink salmon. Molecular Ecology in press.

Seeb, L. W., W. D. Templin, S. Sato, S. Abe, K. Warheit, J. Y. Park, and J. E. Seeb. 2011b. Single nucleotide polymorphisms across a species' range: implications for conservation studies of Pacific salmon. Molecular Ecology Resources 11:195-217.

Small, M. P., K. Currens, T. H. Johnson, A. E. Frye, and J. F. Von Bargen. 2009. Impacts of supplementation: genetic diversity in supplemented and unsupplemented populations of summer

Chum salmon (Oncorhynchus keta) in Puget Sound (Washington, USA). Canadian Journal of Fisheries and Aquatic Sciences 66:1216-1229.

Small, M. P., A. E. Frye, J. F. Von Bargen, and S. F. Young. 2006. Genetic structure of Chum salmon (Oncorhynchus keta) populations in the lower Columbia River: are Chum salmon in Cascade tributaries remnant populations? Conservation Genetics 7:65-78.

Smith, C. T., C. M. Elfstrom, L. W. Seeb, and J. E. Seeb. 2005. Use of sequence data from rainbow trout and Atlantic salmon for SNP detection in Pacific salmon. Molecular Ecology 14:4193-4203.

Templin, W. D., J. E. Seeb, J. R. Jasper, A. W. Barclay, and L. W. Seeb. 2011. Genetic differentiation of Alaska Chum Salmon Southern Area Genetic Baseline Enhancement Chinook salmon: the missing link for migratory studies. Molecular Ecology Resources 11:226-246.

Warheit, K. I., L. W. Seeb, W. D. Templin, and J. Seeb. 2014. N10-8 Moving GSI into the Next Decade: SNP Coordination for Pacific Salmon Treaty Fisheries. Page 47 + iii Final Report: Pacific Salmon Commission's Chinook Technical Committee (US Section) for Funding under the Letter of Agreement (LOA). Washington Department of Fish and Wildlife, Olympia, WA.

Weir, B. S. and C. C. Cockerham. 1984. Estimating F-statistics for the analysis of population-structure. Evolution 38:1358-1370.

Table 1. Information on Chum salmon baseline collections including country, map number, region, tributary, collection year(s), number of samples in collection (N), the latitude and longitude for the collection site, and the name used in tables and figures. Cheakamus River is listed but has not yet been genotyped with SNPs.

Country	map number	Region	Tributary	Year	N	Lat	Long	name
CAN	1	Johnstone Strait	Nimpkish River	2010	95	50.567	-126.983	Nimpkish
CAN	2	Southern mainland	Southgate River	2003	95	50.531	-124.470	Southgate
CAN	3	Southern mainland	Phillips River	2011	95	50.340	-125.210	Phillips
CAN	4	East Vancouver Island	Puntledge River	2010	95	49.700	-125.000	Puntledge
CAN	5	Southern mainland	Lang Creek	2011	95	49.460	-124.220	Lang
CAN	6	East Vancouver Island	Big Qualicum River	2010	95	49.400	-124.617	BigQualicum
CAN	7	Southern mainland	Cheakamus River	2013		49.465	-123.100	Cheakamus
CAN	8	Lower Fraser	Squawkum River	2010	95	49.233	-122.000	Squawkum
CAN	9	Lower Fraser	Hopedale Slough	2011	95	49.097	-122.023	Hopedale
CAN	10	West Vancouver Island	Nitinat River	2010	95	48.822	-124.681	Nitinat
USA	11	North Puget Sound	North Fork Nooksack River	2010	95	48.810	-122.200	Nooksack
USA	12	North Puget Sound	Skagit Mainstem River	2010	50	48.387	-122.367	Skagit
USA	13	North Puget Sound	North Fork Stillaguamish	2010	95	48.204	-122.127	Stillaguamish
USA	14	North Puget Sound	Snohomish River	2010	95	47.830	-122.047	Snohomish
USA	15	Hood Canal	Big Beef Creek	2010, 2011	78, 17	47.652	-122.783	BigBeef
USA	16	Hood Canal	Lilliwaup River	2011	91	47.463	-123.112	Lilliwaup
USA	17	Central Puget Sound	Grovers Creek/Chico Creek	2010	14, 81	47.603	-122.705	Grovers_Chico
USA	18	South Puget Sound	Puyallup Hatchery	2011	95	47.200	-122.342	Puyallup
USA	19	South Puget Sound	Skookum/Mill Creek	2010, 2011	69, 26	47.180	-123.065	Skookum_Mill
USA	20	South Puget Sound	Kennedy Creek	2010, 2011	44, 51	47.095	-123.090	Kennedy

Table 2. The overall F_{ST} (five highest values in pink cells) and mean observed heterozygosity (Ho) for final 183 SNPs.

Locus	F_{ST}	Ho	Locus	F_{ST}	Ho
Oke_ACOT-100	0.016	0.177	*Oke_RAD4787*	0.017	0.118
Oke_arf-319	0.044	0.323	*Oke_RAD4864*	0.016	0.519
Oke_azin1-90	0.023	0.444	*Oke_RAD4875*	0.026	0.486
Oke_ccd16-77	0.037	0.283	*Oke_RAD5156*	0.090	0.374
Oke_CD123-62	0.026	0.302	*Oke_RAD5162*	0.019	0.503
Oke_cjo57-86	0.052	0.456	*Oke_RAD5276*	0.055	0.251
Oke_CKS1-94	0.028	0.302	*Oke_RAD5734*	0.098	0.394
Oke_CKS-389	0.005	0.217	*Oke_RAD5951*	0.031	0.149
Oke_col1a2-62	0.047	0.443	*Oke_RAD618*	0.053	0.249
Oke_CTR2-82	0.010	0.485	*Oke_RAD7067*	0.032	0.352
Oke_DBLOH-79	0.034	0.507	*Oke_RAD7178*	0.046	0.381
Oke_DCXR-87	0.008	0.008	*Oke_RAD7431*	0.050	0.499
Oke_DM20-548	0.025	0.530	*Oke_RAD7744*	0.017	0.275
Oke_EF2-394	0.024	0.445	*Oke_RAD8326*	0.010	0.518
Oke_eif4ebp2-64	0.012	0.419	*Oke_RAD8335*	0.094	0.078
Oke_eif4g1-43	0.023	0.353	*Oke_RAD8372*	0.032	0.403
Oke_FANK1-166	0.027	0.385	*Oke_RAD8698*	0.022	0.253
Oke_FBXL5-61	0.018	0.264	*Oke_RAD8799*	0.092	0.435
Oke_gdh1-234	0.034	0.314	*Oke_RAD8814*	0.100	0.301
Oke_GHII-3129	0.004	0.097	*Oke_RAD8930*	0.053	0.132
Oke_GNMT-100	0.022	0.456	*Oke_RAD9447*	0.027	0.501
Oke_GPDH-191	0.031	0.396	*Oke_RAD9864*	0.044	0.176
Oke_GPH-105	0.020	0.489	*Oke_ras1-249*	0.034	0.451
Oke_GPH-78	0.036	0.465	*Oke_RFC2-618*	0.005	0.008
Oke_hmgb1-66	0.022	0.500	*Oke_RH1op-245*	0.015	0.192
Oke_HP-182	0.021	0.126	*Oke_ROA1-209*	0.033	0.405
Oke_hsc71-199	0.011	0.182	*Oke_RPN1-80*	0.022	0.294
Oke_il-1racp-67	0.007	0.287	*Oke_RS27-94*	0.014	0.265
Oke_IL8r-272	0.008	0.059	*Oke_serpin-140*	0.014	0.376
Oke_KPNA2-87	0.013	0.257	*Oke_slc1a3a-86*	0.025	0.254
Oke_lactb2-71	0.041	0.536	*Oke_sylc-90*	0.008	0.414
Oke_LAMP2-186	0.031	0.267	*Oke_TCP1-78*	0.016	0.179
Oke_mcfd2-86	0.074	0.490	*Oke_TCTA-202*	0.020	0.472
Oke_METK2-97	0.069	0.319	*Oke_Tf-278*	0.015	0.475
Oke_mgll-49	0.024	0.452	*Oke_thic-84*	0.056	0.473
Oke_MLRN-63	0.019	0.551	*Oke_U1002-262*	0.053	0.326
Oke_nc2b-148	0.015	0.383	*Oke_U1008-83*	0.018	0.417
Oke_pnrc2-78	0.023	0.503	*Oke_U1010-251*	0.025	0.380
Oke_PPA2-635	0.027	0.144	*Oke_U1015-255*	0.013	0.139

Locus	F_{ST}	Ho	Locus	F_{ST}	Ho
Oke_psmd9-188	0.022	0.434	*Oke_U1016-154*	0.022	0.548
Oke_rab5a-117	0.007	0.537	*Oke_U1017-52*	0.017	0.335
Oke_RAD10605	0.060	0.340	*Oke_U1019-218*	0.019	0.014
Oke_RAD10719	0.035	0.530	*Oke_U1021-102*	0.030	0.524
Oke_RAD11183	0.093	0.295	*Oke_U1022-139*	0.059	0.239
Oke_RAD11379	0.018	0.258	*Oke_U1023-147*	0.006	0.491
Oke_RAD11500	0.019	0.109	*Oke_U1024-113*	0.016	0.090
Oke_RAD1168	0.036	0.399	*Oke_U1028-100*	0.095	0.401
Oke_RAD11690	0.020	0.375	*Oke_U1031-132*	0.035	0.191
Oke_RAD11918	0.017	0.341	*Oke_u1-519*	0.037	0.509
Oke_RAD11928	0.029	0.310	*Oke_U2001-629*	0.028	0.217
Oke_RAD11999	0.042	0.172	*Oke_U2002-200*	0.009	0.481
Oke_RAD12038	0.019	0.212	*Oke_u200-385*	0.004	0.520
Oke_RAD12294	0.106	0.157	*Oke_U2005-62*	0.011	0.522
Oke_RAD12415	0.091	0.329	*Oke_U2006-109*	0.016	0.390
Oke_RAD12909	0.036	0.315	*Oke_U2010-94*	0.035	0.480
Oke_RAD14679	0.019	0.101	*Oke_U2015-151*	0.005	0.003
Oke_RAD14852	0.064	0.280	*Oke_U2016-118*	0.019	0.094
Oke_RAD14962	0.035	0.269	*Oke_U2017-87*	0.009	0.124
Oke_RAD15315	0.015	0.072	*Oke_U2021-86*	0.021	0.380
Oke_RAD16205	0.027	0.128	*Oke_U2022-101*	0.023	0.062
Oke_RAD1635	0.080	0.196	*Oke_U2023-99*	0.019	0.085
Oke_RAD16431	0.030	0.243	*Oke_U2025-86*	0.015	0.384
Oke_RAD16718	0.030	0.029	*Oke_U2026-64*	0.052	0.213
Oke_RAD16763	0.023	0.256	*Oke_U2029-79*	0.025	0.246
Oke_RAD16805	0.034	0.202	*Oke_U2031-37*	0.011	0.178
Oke_RAD17316	0.016	0.259	*Oke_U2032-74*	0.014	0.136
Oke_RAD19121	0.105	0.417	*Oke_U2033-122*	0.030	0.534
Oke_RAD20162	0.013	0.125	*Oke_U2034-55*	0.030	0.401
Oke_RAD2158	0.023	0.485	*Oke_U2035-54*	0.063	0.375
Oke_RAD2414	0.031	0.401	*Oke_U2037-76*	0.023	0.126
Oke_RAD24191	0.047	0.125	*Oke_U2040-77*	0.013	0.415
Oke_RAD27585	0.021	0.012	*Oke_U2041-84*	0.053	0.427
Oke_RAD27616	0.040	0.041	*Oke_U2043-51*	0.026	0.166
Oke_RAD27694	0.037	0.070	*Oke_U2048-91*	0.011	0.386
Oke_RAD27721	0.033	0.032	*Oke_U2049-99*	0.050	0.463
Oke_RAD2812	0.055	0.366	*Oke_U2052-56*	0.038	0.220
Oke_RAD2827	0.020	0.424	*Oke_U2053-60*	0.017	0.429
Oke_RAD28497	0.015	0.436	*Oke_U2056-90*	0.022	0.518
Oke_RAD30079	0.028	0.058	*Oke_U2057-80*	0.023	0.488
Oke_RAD3131	0.056	0.192	*Oke_U212-87*	0.000	0.000
Oke_RAD3143	0.007	0.392	*Oke_U302-195*	0.031	0.026
Oke_RAD3480	0.054	0.368	*Oke_U305-130*	0.022	0.482

Locus	F_{ST}	Ho	Locus	F_{ST}	Ho
Oke_RAD3490	0.030	0.508	*Oke_U305-307*	0.029	0.033
Oke_RAD3693	0.041	0.477	*Oke_U401-143*	0.011	0.060
Oke_RAD369	0.040	0.420	*Oke_U401-220*	0.017	0.064
Oke_RAD3715	0.039	0.428	*Oke_U502-241*	0.128	0.349
Oke_RAD3861	0.021	0.419	*Oke_U504-228*	0.014	0.451
Oke_RAD3938	0.038	0.182	*Oke_U506-110*	0.020	0.069
Oke_RAD39	0.012	0.458	*Oke_U507-286*	0.025	0.462
Oke_RAD4286	0.040	0.436	*Oke_U509-219*	0.014	0.509
Oke_RAD4426	0.045	0.459	*Oke_U511-271*	0.050	0.183
			Oke_zn593-152	0.009	0.465

Table 3. Genetic statistics for population collections (183 SNPs). The collection number precedes sample name. Gene diversity (Gene Div) is an estimate of heterozygosity per sample with correction for unequal sample sizes, Hardy-Weinberg Equilbrium value as expressed by F_{IS} with p values for tests of excess homozygotes (hom) and heterozygotes (het), fixed loci are the number of loci with a single allele and the number of pairs of loci (out of 16471 total pairs) in linkage disequilibrium at the 5% level and the 1% level are under "linkage". Significant values are in bold type.

				excess hom	excess het		linkage	
	N alleles	Gene Div	F_{IS}	*p* value	*p* value	fixed loci	5%	1%
1_Nimpkish	1.94	0.306	-0.042	1.0000	**0.0000**	6	768	178
2_Southgate	1.92	0.302	-0.001	0.5267	0.4745	8	639	137
3_Phillips	1.94	0.303	-0.012	0.9102	0.0902	5	753	153
4_Puntledge	1.92	0.297	-0.008	0.8224	0.1779	10	694	141
5_Lang	1.93	0.304	-0.101	1.0000	**0.0000**	7	828	170
6_BigQualicum	1.93	0.296	-0.009	0.8528	0.1477	8	685	146
8_Squawkum	1.95	0.303	0.003	0.3789	0.6219	4	762	154
9_Hopedale	1.94	0.306	-0.128	1.0000	**0.0000**	4	**898**	197
10_Nitinat	1.94	0.307	0.008	0.1683	0.8331	6	664	128
11_Nooksack	1.93	0.298	-0.100	1.0000	**0.0000**	9	**881**	174
12_Skagit	1.94	0.318	-0.142	1.0000	**0.0000**	9	**947**	206
13_Stillaguamish	1.92	0.293	-0.053	1.0000	**0.0000**	8	728	143
14_Snohomish	1.92	0.302	-0.094	1.0000	**0.0000**	7	**906**	222
15_BigBeef	1.93	0.290	-0.013	0.9322	0.0682	8	667	136
16_Lilliwaup	1.93	0.284	-0.037	1.0000	**0.0000**	8	742	155
17_Grovers_Chico	1.91	0.283	-0.004	0.6879	0.3133	9	654	141
18_Puyallup	1.92	0.282	-0.014	0.9371	0.0632	7	720	129
19_Skookum_Mill	1.93	0.284	-0.011	0.8927	0.1077	6	697	128
20_Kennedy	1.91	0.279	-0.002	0.6103	0.3907	9	638	136
average	1.93	0.297				7	751	157

Table 4. Pairwise F_{ST} values (non-significant values in purple) in lower triangular matrix and associated p values in upper triangular matrix (non-significant values in green). Pairwise F_{ST} value in yellow was significant but the pairwise genotypic test was not, all other pairwise test results were congruent. Sample names at top are abbreviated to decrease column width, sample numbers follow Table 1.

	1_Nimp	2_South	3_Phill	4_Punt	5_Lang	6_BigQ	8_Squawk	9_Hope	10_Nitin	11_Nook	12_Skagit	13_Stillag	14_Snoho	15_BigB	16_Lilli	17_Gr_Ch	18_Puya	19_Skook_M	20_Kenn
1_Nimpkish		0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
2_Southgate	0.0199		0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
3_Phillips	0.0115	0.0090		0.0001	0.3222	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
4_Puntledge	0.0129	0.0104	0.0030		0.5126	0.2991	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
5_Lang	0.0153	0.0113	0.0029	0.0031		0.3152	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
6_BigQualicum	0.0134	0.0144	0.0035	0.0003	0.0024		0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
8_Squawkum	0.0324	0.0312	0.0251	0.0221	0.0225	0.0226		0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
9_Hopedale	0.0335	0.0340	0.0279	0.0235	0.0244	0.0253	0.0044		0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
10_Nitinat	0.0302	0.0348	0.0209	0.0270	0.0264	0.0268	0.0456	0.0465		0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
11_Nooksack	0.0193	0.0243	0.0145	0.0108	0.0171	0.0128	0.0230	0.0205	0.0309		0.0043	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
12_Skagit	0.0228	0.0265	0.0183	0.0169	0.0177	0.0173	0.0188	0.0180	0.0250	0.0119		0.0211	0.0033	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
13_Stillaguamish	0.0202	0.0254	0.0172	0.0148	0.0183	0.0152	0.0165	0.0180	0.0349	0.0082	0.0085		0.0008	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
14_Snohomish	0.0225	0.0266	0.0187	0.0136	0.0172	0.0150	0.0156	0.0131	0.0346	0.0081	0.0078	0.0025		0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
15_BigBeef	0.0424	0.0474	0.0379	0.0352	0.0385	0.0369	0.0438	0.0426	0.0482	0.0321	0.0301	0.0291	0.0235		0.0993	0.0001	0.0001	0.0001	0.0001
16_Lilliwaup	0.0507	0.0547	0.0443	0.0427	0.0460	0.0438	0.0453	0.0460	0.0550	0.0374	0.0344	0.0325	0.0266	0.0018		0.0001	0.0001	0.0001	0.0001
17_Grovers_Chico	0.0578	0.0602	0.0504	0.0486	0.0504	0.0498	0.0554	0.0502	0.0592	0.0409	0.0401	0.0368	0.0336	0.0203	0.0240		0.0001	0.0001	0.0001
18_Puyallup	0.0525	0.0565	0.0484	0.0425	0.0474	0.0442	0.0494	0.0455	0.0539	0.0375	0.0348	0.0310	0.0267	0.0261	0.0310	0.0203		0.0001	0.0001
19_Skookum_Mill	0.0631	0.0683	0.0578	0.0537	0.0572	0.0548	0.0599	0.0554	0.0618	0.0477	0.0468	0.0456	0.0397	0.0232	0.0309	0.0079	0.0241		0.0001
20_Kennedy	0.0669	0.0751	0.0642	0.0602	0.0645	0.0615	0.0671	0.0637	0.0717	0.0541	0.0541	0.0502	0.0487	0.0306	0.0376	0.0129	0.0317	0.0053	

Table 5. Estimates from 100% simulations in ONCOR for Chum salmon populations genotyped with 183 SNP loci to population (pop), regional reporting groups listed in Table 1, and to country of origin.

	Pop		Region		Country	
	AVG	ST DEV	AVG	ST DEV	AVG	ST DEV
1_Nimpkish	0.9539	0.0175	0.9548	0.0212	0.9940	0.0064
2_Southgate	0.9578	0.0219	0.9889	0.0115	0.9992	0.0019
3_Phillips	0.6376	0.0536	0.8160	0.0457	0.9934	0.0086
4_Puntledge	0.4943	0.0541	0.8654	0.0483	0.9759	0.0168
5_Lang	0.5671	0.0546	0.6933	0.0591	0.9953	0.0056
6_BigQualicum	0.4068	0.0603	0.7617	0.0537	0.9880	0.0103
8_Squawkum	0.7845	0.0408	0.9916	0.0073	0.9940	0.0062
9_Hopedale	0.8205	0.0475	0.9853	0.0101	0.9886	0.0103
10_Nitinat	0.9928	0.0073	0.9940	0.0067	0.9982	0.0032
11_Nooksack	0.8652	0.0403	0.9511	0.0227	0.9460	0.0244
12_Skagit	0.7282	0.0401	0.9600	0.0199	0.9641	0.0170
13_Stillaguamish	0.7107	0.0491	0.9880	0.0112	0.9888	0.0107
14_Snohomish	0.7190	0.0525	0.9718	0.0166	0.9785	0.0138
15_BigBeef	0.7083	0.0477	0.9941	0.0065	0.9992	0.0017
16_Lilliwaup	0.6640	0.0415	0.9986	0.0028	0.9998	0.0008
17_Grovers_Chico	0.9260	0.0284	0.9263	0.0297	0.9998	0.0008
18_Puyallup	0.9925	0.0074	0.9935	0.0065	0.9998	0.0008
19_Skookum_Mill	0.8160	0.0448	0.9328	0.0302	0.9999	0.0007
20_Kennedy	0.8904	0.0327	0.9900	0.0113	1.0000	0.0000
	0.7706	0.0397	0.9346	0.0222	0.9896	0.0074

Table 6. Estimates from mixture simulations (2 populations) in ONCOR for Chum salmon populations genotyped with 183 SNP loci. Mixture proportions were estimated for populations (top portion) and for country of origin (bottom portion). Results are plotted in Figure 7.

	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
1_Nimpkish	0	0.0031	0.0054	0	0.0043	0.0067	0	0.0035	0.0057	0	0.0053	0.0077	0	0.0045	0.0072
2_Southgate	0	0.0010	0.0026	0	0.0030	0.0053	0	0.0019	0.0041	0	0.0042	0.0069	0	0.0049	0.0077
3_Phillips	0	0.0089	0.0117	0	0.0245	0.0213	0	0.0157	0.0159	0	0.0350	0.0264	0	0.0423	0.0287
4_Puntledge	0.1	0.0878	0.0339	0.5	0.2786	0.0514	0.25	0.1626	0.0423	0.75	0.3863	0.0575	0.9	0.4521	0.0598
5_Lang	0	0.0046	0.0079	0	0.0215	0.0207	0	0.0109	0.0139	0	0.0337	0.0265	0	0.0416	0.0298
6_BigQualicum	0	0.0510	0.0278	0	0.1949	0.0455	0	0.1045	0.0370	0	0.2847	0.0547	0	0.3394	0.0591
8_Squawkum	0	0.0005	0.0018	0	0.0004	0.0015	0	0.0005	0.0017	0	0.0004	0.0015	0	0.0004	0.0015
9_Hopedale	0	0.0011	0.0028	0	0.0010	0.0025	0	0.0010	0.0027	0	0.0009	0.0024	0	0.0008	0.0022
10_Nitinat	0	0.0003	0.0012	0	0.0003	0.0012	0	0.0004	0.0015	0	0.0003	0.0013	0	0.0003	0.0011
11_Nooksack	0.9	0.7718	0.0395	0.5	0.4338	0.0440	0.75	0.6429	0.0466	0.25	0.2271	0.0379	0.1	0.1018	0.0287
12_Skagit	0	0.0036	0.0059	0	0.0023	0.0044	0	0.0030	0.0054	0	0.0016	0.0035	0	0.0010	0.0026
13_Stillaguamish	0	0.0302	0.0211	0	0.0156	0.0153	0	0.0243	0.0186	0	0.0084	0.0108	0	0.0047	0.0075
14_Snohomish	0	0.0356	0.0227	0	0.0192	0.0169	0	0.0283	0.0205	0	0.0118	0.0126	0	0.0058	0.0085
15_BigBeef	0	0.0002	0.0010	0	0.0002	0.0009	0	0.0001	0.0008	0	0.0001	0.0008	0	0.0002	0.0009
16_Lilliwaup	0	0.0001	0.0006	0	0.0001	0.0006	0	0.0001	0.0005	0	0.0001	0.0005	0	0.0001	0.0005
17_Grovers_Chico	0	0.0001	0.0005	0	0.0000	0.0004	0	0.0001	0.0005	0	0.0000	0.0004	0	0.0000	0.0003
18_Puyallup	0	0.0001	0.0007	0	0.0001	0.0007	0	0.0001	0.0007	0	0.0001	0.0006	0	0.0001	0.0005
19_Skookum_Mill	0	0.0001	0.0006	0	0.0000	0.0002	0	0.0000	0.0003	0	0.0000	0.0004	0	0.0000	0.0001
20_Kennedy	0	0.0000	0.0001	0	0.0000	0.0002	0	0.0000	0.0003	0	0.0000	0.0002	0	0.0000	0.0001
GROUPS															
CAN	0.1	0.1584	0.0332	0.5	0.5287	0.0426	0.25	0.3011	0.0424	0.75	0.7508	0.0379	0.9	0.8863	0.0297
US	0.9	0.8416	0.0332	0.5	0.4713	0.0426	0.75	0.6989	0.0424	0.25	0.2492	0.0379	0.1	0.1137	0.0297

Table 7. Estimates from mixture simulations (three populations) in ONCOR for Chum salmon populations genotyped with 183 SNP loci. Mixture proportions were estimated for populations (top portion) and for country of origin (bottom portion). Results are plotted in Figure 8.

	ACTUAL			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	VALUE	AVG	ST DEV
1_Nimpkish	0	0.0031	0.0056	0	0.0024	0.0046	0	0.0026	0.0047	0	0.0034	0.0060	0	0.0029	0.0052	0	0.0027	0.0052	0	0.0029	0.0050
2_Southgate	0	0.0020	0.0042	0	0.0025	0.0044	0	0.0018	0.0039	0	0.0023	0.0044	0	0.0015	0.0034	0	0.0012	0.0028	0	0.0007	0.0020
3_Phillips	0	0.0171	0.0175	0	0.0131	0.0151	0	0.0106	0.0132	0	0.0153	0.0158	0	0.0123	0.0142	0	0.0085	0.0109	0	0.0066	0.0093
4_Puntledge	0.33	0.1831	0.0449	0.3	0.1555	0.0406	0.2	0.1098	0.0348	0.3	0.1716	0.0424	0.2	0.1303	0.0373	0.1	0.0839	0.0336	0.05	0.0599	0.0292
5_Lang	0	0.0167	0.0176	0	0.0170	0.0169	0	0.0123	0.0142	0	0.0143	0.0156	0	0.0099	0.0128	0	0.0057	0.0091	0	0.0033	0.0064
6_BigQualicum	0	0.1254	0.0375	0	0.1107	0.0362	0	0.0758	0.0326	0	0.1173	0.0383	0	0.0814	0.0326	0	0.0487	0.0277	0	0.0309	0.0221
8_Squawkum	0	0.0492	0.0246	0	0.0900	0.0313	0	0.0882	0.0316	0	0.0443	0.0232	0	0.0282	0.0191	0	0.0143	0.0131	0	0.0078	0.0088
9_Hopedale	0.34	0.2793	0.0391	0.6	0.4924	0.0433	0.6	0.4946	0.0453	0.3	0.2467	0.0374	0.2	0.1630	0.0314	0.1	0.0832	0.0230	0.05	0.0416	0.0174
10_Nitinat	0	0.0003	0.0012	0	0.0002	0.0010	0	0.0003	0.0011	0	0.0003	0.0013	0	0.0003	0.0013	0	0.0004	0.0014	0	0.0004	0.0014
11_Nooksack	0.33	0.2868	0.0409	0.1	0.0934	0.0268	0.2	0.1736	0.0328	0.4	0.3415	0.0410	0.6	0.5151	0.0435	0.8	0.6848	0.0427	0.9	0.7722	0.0415
12_Skagit	0	0.0028	0.0050	0	0.0023	0.0044	0	0.0025	0.0049	0	0.0030	0.0053	0	0.0032	0.0058	0	0.0037	0.0065	0	0.0040	0.0064
13_Stillaguamish	0	0.0110	0.0125	0	0.0049	0.0077	0	0.0074	0.0099	0	0.0136	0.0147	0	0.0197	0.0169	0	0.0255	0.0200	0	0.0295	0.0218
14_Snohomish	0	0.0227	0.0183	0	0.0151	0.0144	0	0.0202	0.0172	0	0.0260	0.0196	0	0.0316	0.0216	0	0.0370	0.0245	0	0.0397	0.0253
15_BigBeef	0	0.0002	0.0009	0	0.0001	0.0008	0	0.0001	0.0006	0	0.0002	0.0010	0	0.0002	0.0010	0	0.0002	0.0011	0	0.0002	0.0010
16_Lilliwaup	0	0.0001	0.0006	0	0.0001	0.0005	0	0.0000	0.0004	0	0.0001	0.0005	0	0.0001	0.0005	0	0.0001	0.0006	0	0.0001	0.0007
17_Grovers_Chico	0	0.0000	0.0004	0	0.0000	0.0005	0	0.0000	0.0004	0	0.0001	0.0004	0	0.0001	0.0005	0	0.0001	0.0005	0	0.0001	0.0005
18_Puyallup	0	0.0001	0.0007	0	0.0001	0.0006	0	0.0001	0.0007	0	0.0001	0.0006	0	0.0001	0.0006	0	0.0001	0.0007	0	0.0001	0.0005
19_Skookum_Mill	0	0.0000	0.0003	0	0.0000	0.0003	0	0.0000	0.0005	0	0.0000	0.0003	0	0.0000	0.0005	0	0.0000	0.0004	0	0.0000	0.0004
20_Kennedy	0	0.0000	0.0000	0	0.0000	0.0001	0	0.0000	0.0001	0	0.0000	0.0003	0	0.0000	0.0003	0	0.0000	0.0002	0	0.0000	0.0002
Groups																					
CAN	0.67	0.6763	0.0413	0.9	0.8839	0.0289	0.8	0.7960	0.0337	0.6	0.6155	0.0420	0.4	0.4298	0.0413	0.2	0.2485	0.0382	0.1	0.1541	0.0344
US	0.33	0.3237	0.0413	0.1	0.1161	0.0289	0.2	0.2040	0.0337	0.4	0.3845	0.0420	0.6	0.5702	0.0413	0.8	0.7515	0.0382	0.9	0.8459	0.0344

Table 8. Estimates from mixture simulations (four populations) in ONCOR for Chum salmon populations genotyped with 183 SNP loci. Mixture proportions were estimated for populations (top portion) and for country of origin (bottom portion). Results are plotted in Figure 9.

	VALUE	AVG	ST DEV	VALUE	AVG	ST DEV	VALUE	AVG	ST DEV	VALUE	AVG	ST DEV	VALUE	AVG	ST DEV
1_Nimpkish	0	0.0031	0.0055	0	0.0018	0.0037	0	0.0028	0.0049	0	0.0046	0.0070	0	0.0023	0.0046
2_Southgate	0	0.0019	0.0039	0	0.0012	0.0029	0	0.0010	0.0026	0	0.0040	0.0065	0	0.0013	0.0029
3_Phillips	0	0.0138	0.0146	0	0.0057	0.0085	0	0.0085	0.0113	0	0.0320	0.0245	0	0.0077	0.0100
4_Puntledge	0.25	0.1356	0.0380	0.1	0.0547	0.0255	0.1	0.0791	0.0330	0.7	0.3482	0.0529	0.1	0.0528	0.0257
5_Lang	0	0.0123	0.0138	0	0.0070	0.0098	0	0.0058	0.0093	0	0.0349	0.0264	0	0.0068	0.0097
6_BigQualicum	0	0.0989	0.0350	0	0.0377	0.0221	0	0.0481	0.0286	0	0.2648	0.0522	0	0.0417	0.0250
8_Squawkum	0	0.0383	0.0208	0	0.1065	0.0347	0	0.0144	0.0132	0	0.0152	0.0130	0	0.0168	0.0138
9_Hopedale	0.25	0.2007	0.0345	0.7	0.5717	0.0461	0.1	0.0814	0.0236	0.1	0.0806	0.0234	0.1	0.0769	0.0240
10_Nitinat	0	0.0003	0.0012	0	0.0001	0.0008	0	0.0004	0.0013	0	0.0003	0.0013	0	0.0002	0.0011
11_Nooksack	0.25	0.2239	0.0402	0.1	0.0935	0.0264	0.7	0.5929	0.0461	0.1	0.1074	0.0305	0.1	0.1173	0.0325
12_Skagit	0	0.0040	0.0065	0	0.0031	0.0055	0	0.0044	0.0069	0	0.0024	0.0050	0	0.0052	0.0077
13_Stillaguamish	0.25	0.1755	0.0377	0.1	0.0664	0.0252	0.1	0.0933	0.0322	0.1	0.0671	0.0256	0.7	0.4872	0.0503
14_Snohomish	0	0.0911	0.0336	0	0.0502	0.0252	0	0.0672	0.0297	0	0.0379	0.0229	0	0.1832	0.0434
15_BigBeef	0	0.0002	0.0008	0	0.0002	0.0008	0	0.0002	0.0010	0	0.0002	0.0010	0	0.0002	0.0011
16_Lilliwaup	0	0.0001	0.0006	0	0.0001	0.0004	0	0.0001	0.0006	0	0.0001	0.0007	0	0.0002	0.0008
17_Grovers_Chico	0	0.0001	0.0007	0	0.0000	0.0004	0	0.0001	0.0005	0	0.0001	0.0006	0	0.0001	0.0006
18_Puyallup	0	0.0001	0.0007	0	0.0001	0.0007	0	0.0001	0.0006	0	0.0001	0.0005	0	0.0002	0.0009
19_Skookum_Mill	0	0.0000	0.0004	0	0.0000	0.0003	0	0.0000	0.0004	0	0.0000	0.0003	0	0.0000	0.0003
20_Kennedy	0	0.0000	0.0003	0	0.0000	0.0001	0	0.0000	0.0003	0	0.0000	0.0003	0	0.0000	0.0004
CAN	0.5	0.5050	0.0417	0.8	0.7865	0.0341	0.2	0.2416	0.0370	0.8	0.7847	0.0362	0.2	0.2064	0.0333
US	0.5	0.4950	0.0417	0.2	0.2135	0.0341	0.8	0.7584	0.0370	0.2	0.2153	0.0362	0.8	0.7936	0.0333

Figure 1. Map of sample locations for Chum salmon collected in the Southern Boundary area. Numbers corresponding to sample location names are in Table 1.

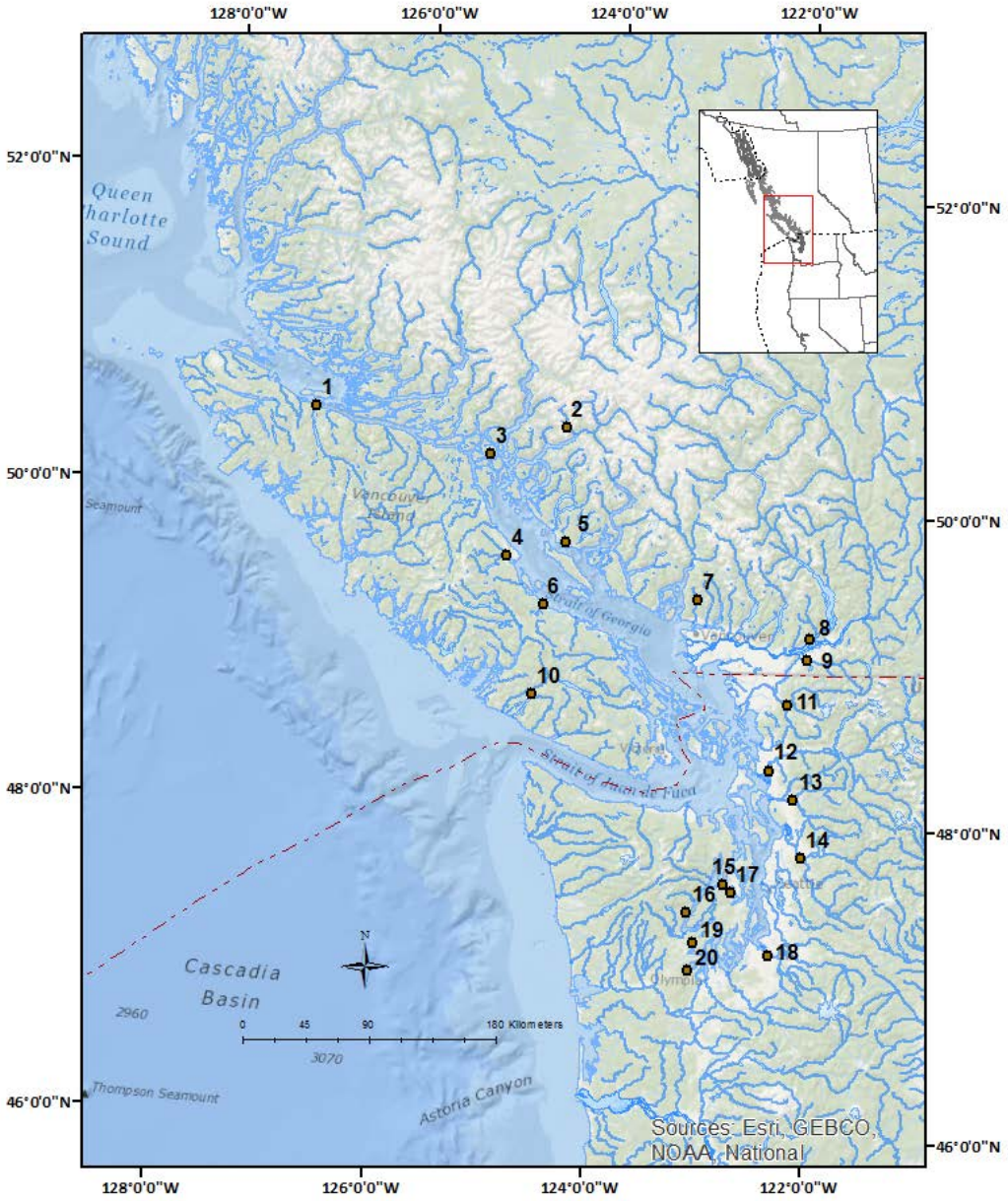
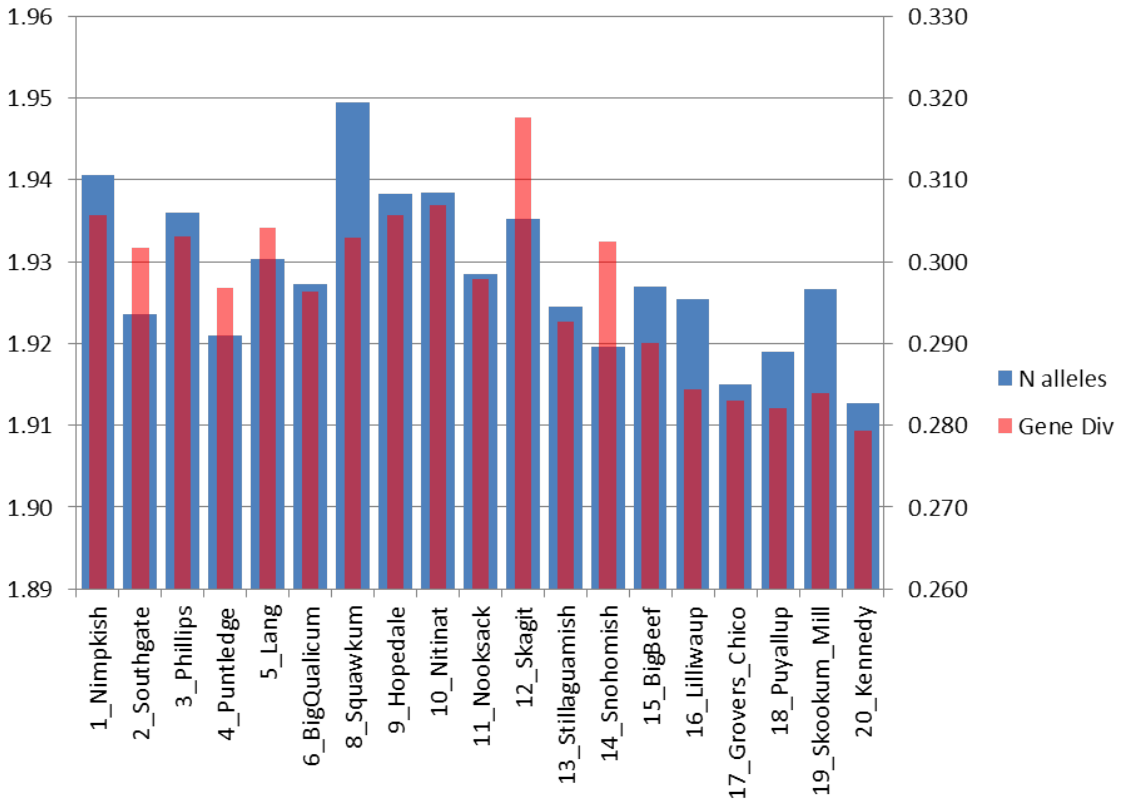


Figure 2. Plot of genetic diversity measures: allelic richness (N alleles) and heterozygosity (Gene div). Collection numbers precede sample names (see Table 1 for sample numbers) and are arranged from North on the left to South on the right.



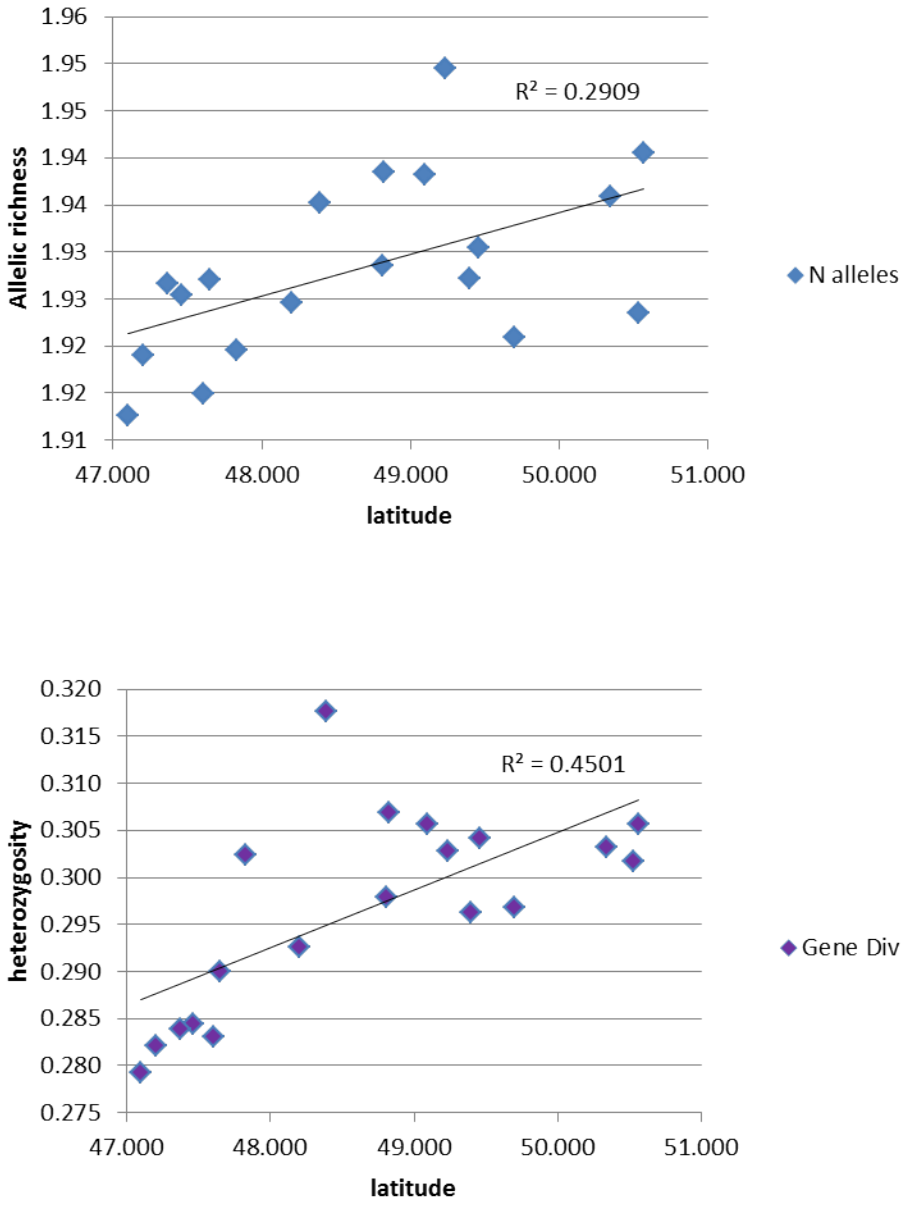


Figure 3 Plots of genetic diversity measures including allelic richness (N alleles) and heterozygosity (Gene Div) versus latitude.

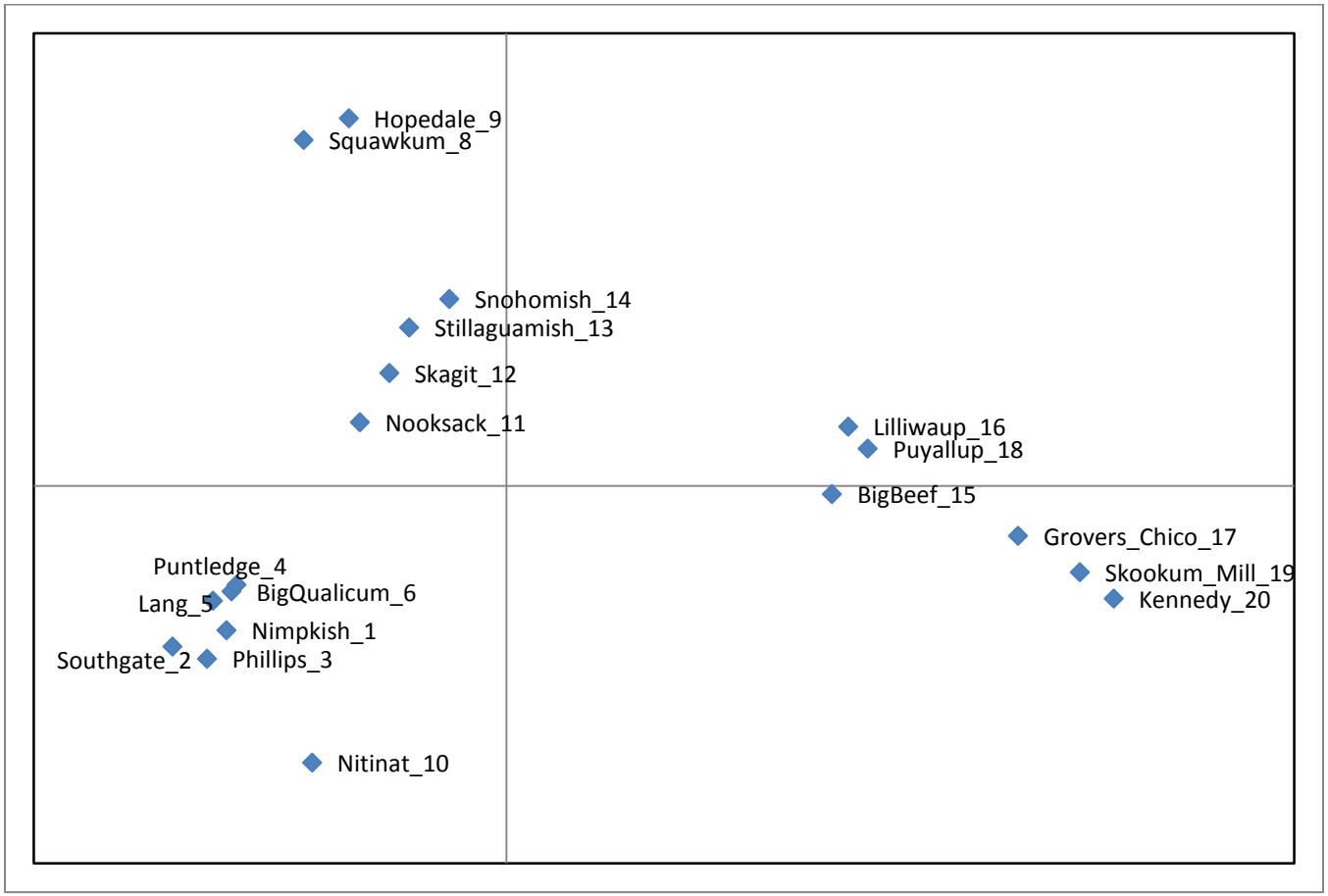


Figure 4. Principle coordinates plot of populations from GenAlEx, based on pairwise F_{ST} values. Population numbers are given in Table 1.

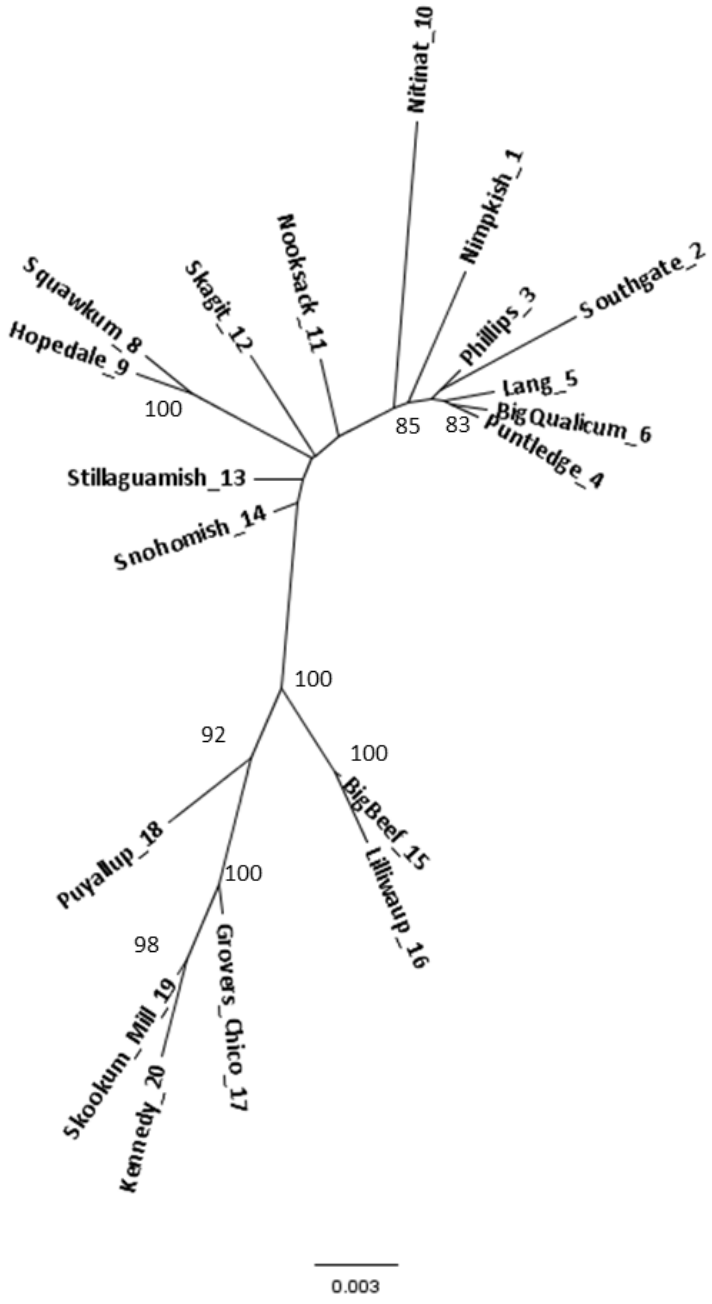


Figure 5. Neighbor-joining tree based on Nei's unbiased genetic distance for SNP data. Numbers following names are from Table 1 and plotted in the map in Figure 1. Numbers at the nodes are the percentage of 1000 trees where collections beyond the node clustered together. Only percentage values over 80% are shown.

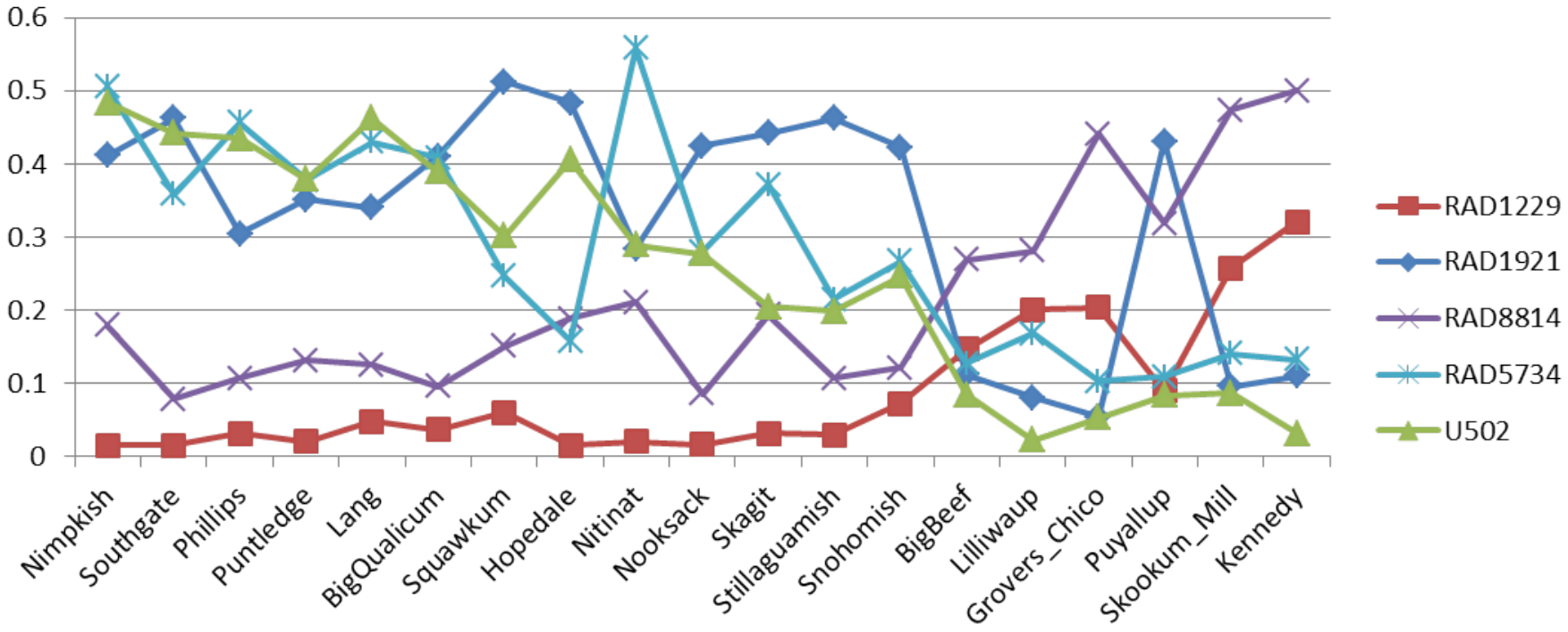


Figure 6. Plot of allele frequencies for SNP loci with the highest overall F_{ST} values in the Southern Boundary Chum salmon data. Samples are arranged from North (left) to South (right) and names follow Table 1.

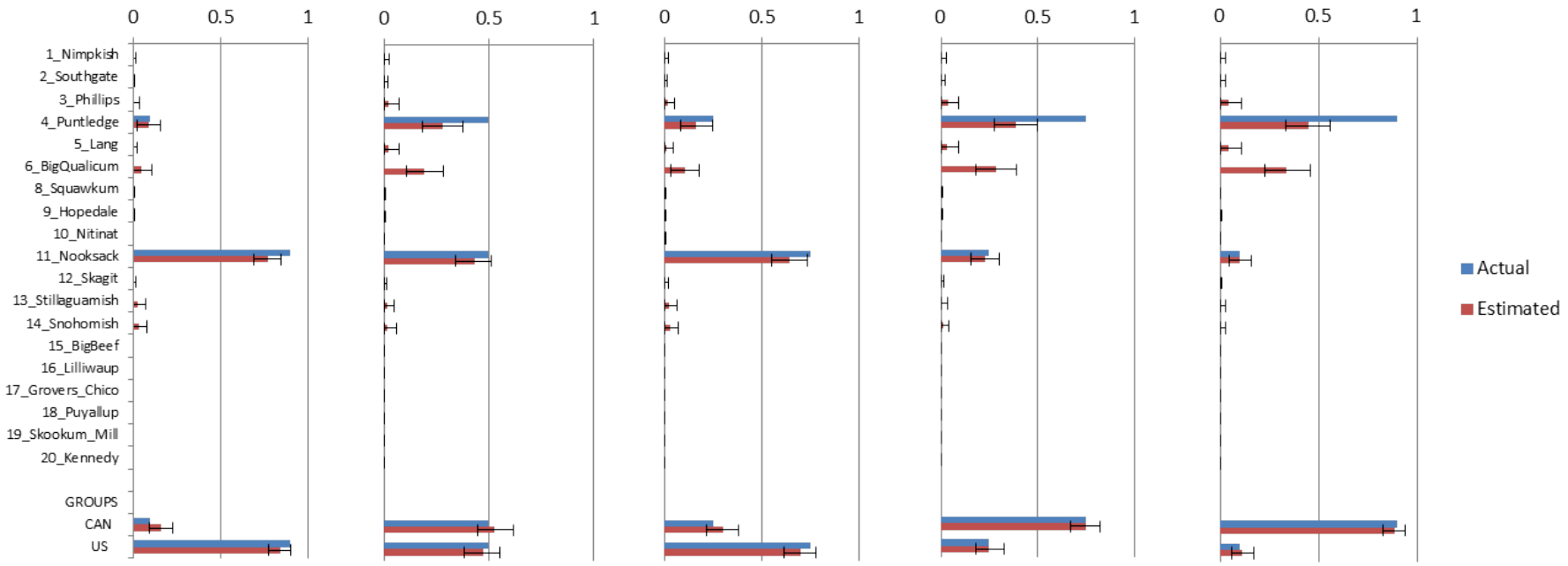


Figure 7. Plot of mixture simulation results (two populations) and their 95% confidence intervals compared with actual values; numerical values presented in Table 6.

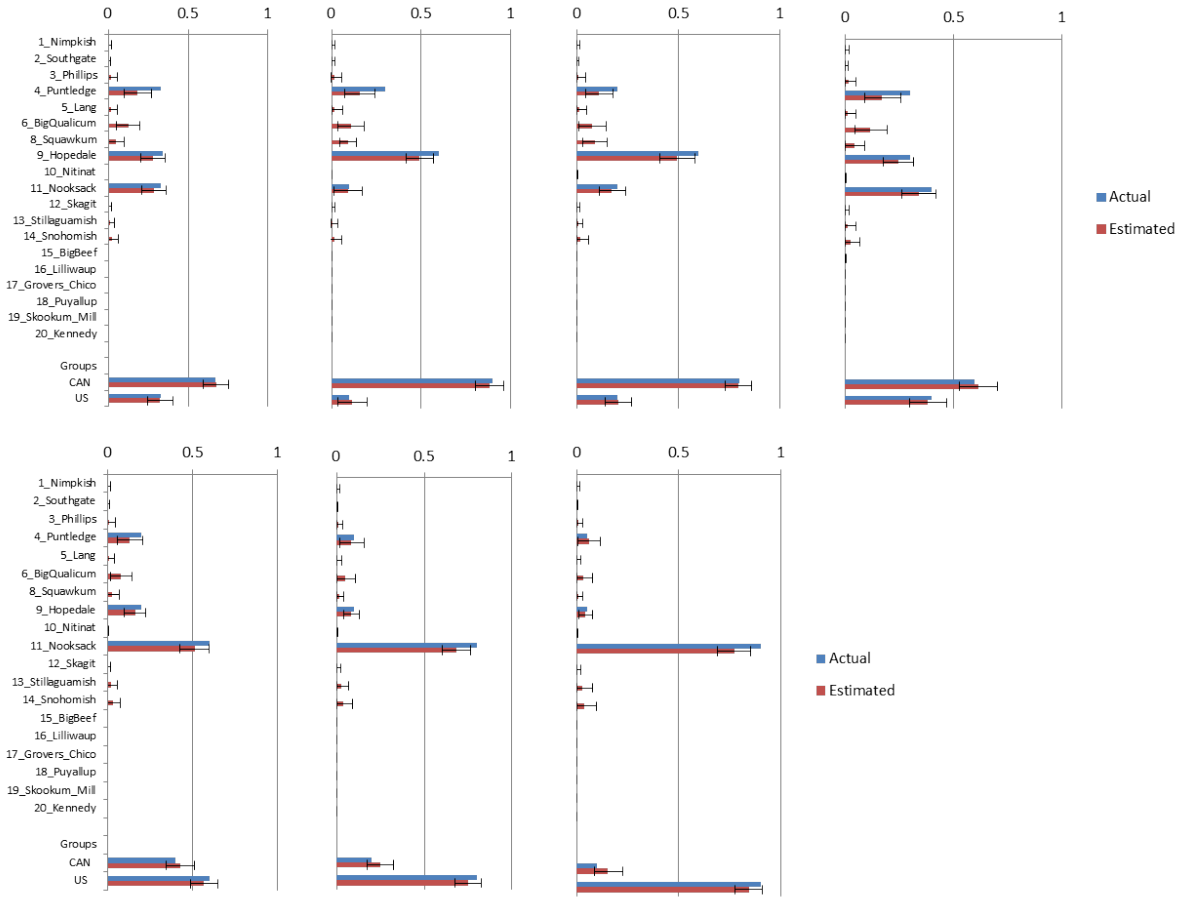


Figure 8. Plot of mixture simulation results (three populations) and their 95% confidence intervals compared with actual values; numerical values presented in Table 7.

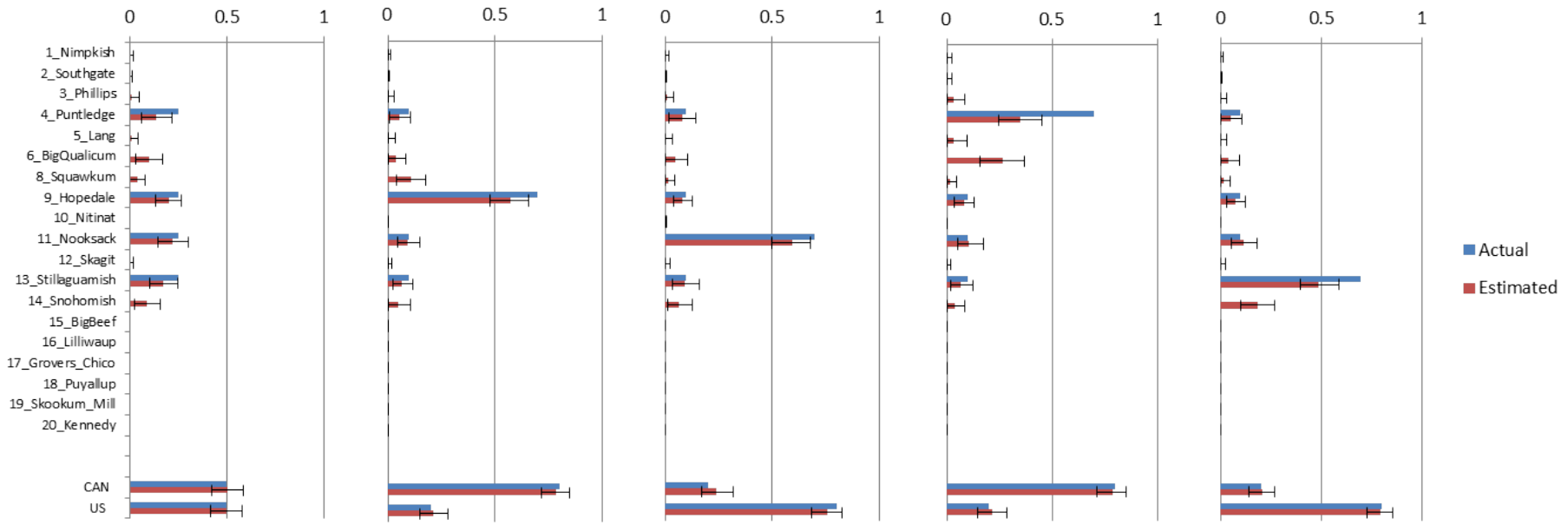


Figure 9. Plot of mixture simulation results (four populations) and their 95% confidence intervals compared with actual values; numerical values presented in Table 8.

Appendix 1. Description of SNPs and 5'-nuclease reaction assays analyzed in this study, including three mitochondrial SNPs.

SNP	VIC Allele	FAM Allele	Forward Primer Sequence	Reverse Primer Sequence	VIC Probe Sequence	FAM Probe Sequence	Citation [2]
Oke_ACOT-100	C	G	TCAGGGACGATAAAGGGATCATCTT	GGGAGAGACACAGGTCTACCT	CTTCCGCTCTCTACTCC	TTCCGCTCTGTACTCC	2
Oke_arf-319	T	C	TGCAGAAACTGATCATTGGTAGTGG	TCTGTTGTTACTCTGTTTCCTGCAA	CTGTGTGAATTGCCTC	CTGTGTGAACTGCCTC	4
Oke_azin1-90	C	T	GGGAATAGTGTCATTTGGGATGCAT	GGTGAATGATATTCTGTAGTCATATTGCTTGA	CCTTTATCTGAGGAACTG	CCTTTATCTGAAGAACTG	2
Oke_ccd16-77	A	C	TGTCTTCAGAATCCAATGCTTTCCT	GAGAAAGTTGCCGAGCTCAAG	CCAGCCCCCTCTGAAA	AGCCCCCGCTGAAA	3
Oke_CD123-62	A	G	GAACAGCAGTGAATCGGTTACCT	TTGACGCTGTGTGTCTTCGA	CTGATCGATTTCAACCC	TGATCGATCTCAACCC	2
Oke_cjo57-86	A	C	CAGAAGGTCTAAAGGTCCTTAACAATCA	CAGATTGAACAGTGCCCAGAGA	TGTTGTAAGTTATTTAATTTATG	TTGTAAGTTATTTCATTTATG	2
Oke_CKS1-94	G	T	TCTTCGACATGTTTAATCGAACAGAAGT	CCAGCTTTCGCTTGTCAAAACG	TCTGGATAAATTTGTGTATTC	TTCTGGATAAATTTTTGTATTC	2
Oke_CKS-389	G	A	GGGCCATTCTCTGAGTTCAGT	GAGCACCGGTTGTCATGGA	AAATGAATGATAATGTGTTCTG	AAATGAATGATAATATGTTCTG	4
Oke_col1a2-62	G	A	GCAGGAAACCACTCTCATTCTTACT	AGACTTAGGAAATTGCACCTGCTTA	TTTGTATTGACTGAGTCTTG	TTTGTATTGACTAAGTCTTG	2
Oke_Cr30[1]	G	A	ACTACTCTCTGGCGGCTACA	AACCTTGGATTAGTGCTGATGTATGAG	CAAGTTATGGCATTTACA	TTACAAGTTATAGCATTTACA	4
Oke_Cr386[1]	G	-	CTTAATGTAGTAAGAACCGACCAACGA	ACTTAGGAACCAAATGCCAGGAAT	ATCGTATTAGGTCGCATCT	AAATCGTATTAGTCGCATCT	4
Oke_CTR2-82	C	T	GCAGCAGACACACCGAAGTA	CCATTCCCATCGGCATCGT	CTCTGACGGTGTGCTT	TCTCTGACAGTGTGCTT	2
Oke_DBLOH-79	C	T	GCAGATATGCCTCAGGGATGT	GACAGTCAAAGGATCAAGCTACCT	CTGCCATGGAGGAAG	CTGCCATAGAGGAAG	2
Oke_DCXR-87	A	T	GTCACCCAGAACAATAGAATGAGTCT	TCTAACACACCCACAATCTGCAAAA	CCTGTTTGTTGAAACCGTA	CCTGTTTGTTGTAACCGTA	2
Oke_DM20-548	G	T	CACTCCCCTCGCTTACTGATATCTA	ACGGACAGCTCATTTACATACACAA	CTAGATCATGTTCACTATCTATA	TAGATCATGTTCACTATATATA	4
Oke_EF2-394	C	T	GCTTAACTGCTGTTTCTGCTATAGG	GCAGTCTCCTCCTTCTTGAAGTT	CATGATGGCGTCAAAC	ATGATGGCATCAAAC	2
Oke_eif4ebp2-64	G	A	CGAAAGAAGATGGCTGCTGTGA	TGGCTTGGCTTGTAGAAACCA	TGATGTGAGAGCTCA	TGATGTGAAAGCTCA	4
Oke_eif4g1-43	G	T	GCACCCAACAGTTCATCATGTAAGT	CCACCCCCAGTAGTCAATCCT	CTGAGATTCTTCATCTTTTAC	TGAGATTCTTCATATTTTAC	2
Oke_FANK1-166	C	T	ACTCACGTGTGGTAGAGACAGA	AGACTGAGAATCACAAGACCAACTG	CTACAGCCCGGCTGTG	CTACAGCCCAGCTGTG	2
Oke_FBXL5-61	G	A	TGGTGTGTAACGTCAGTGACTTAAG	CACCTCTAGAAATGACATGATCAGTGT	TCTGAGGGAAACTGC	TCTGAGGAAAACTGC	2
Oke_gdh1-234	C	T	CAAACCCAGTAGAACCCTGTGT	CTGGGAATGGTGATATATGTGTTCCT	CCTCTAACCCCGCTGCG	CCTCTAACCCTGCTGCG	2
Oke_GHII-3129	G	A	GTCAAGCTGATACCACTCAAATCTCA	AGAATCTGACTACAGTCACTTAAAGTGATTTT	CAGGGCGACTCTAT	ACAGGGCAACTCTAT	1
Oke_GNMT-100	C	T	GCGTCCACGCTCGTCAT	AGCGTGGACTCCATCATGTTG	TTGAGGAGGGATTTAA	TTGAGGAAGGATTTAA	2
Oke_GPDH-191	T	A	CCTGTACCTATAGGGCAACTTCAC	TGCCCTCTGATGGTATGATGGT	CGGAGCCACTTCCAGTA	CGGAGCCACTACCAGTA	4
Oke_GPH-105	T	G	CAGATCAACCCTGGAAAAATATCTGATGT	TGAACAAGCAGCCCAATTCTGT	CCAGTAATTGGTATTTTGA	CCAGTAATTGGTCTTTTGA	1
Oke_GPH-78	G	T	GCAGCCCAATTCTGATATTTGTTTTACTAATT	TGAACAAGCAGCCCAATTCTGT	ATATCTGATGTGAGAAGAG	AAATATCTGATGTTAGAAGAG	1
Oke_hmgb1-66	G	T	GGAAACAGAATAACTACTAAGACCCTACATTATAAC	ACGCCCCCATTGGAAACC	ACTGCTTGCTAAGGCA	CACTGCTTTCTAAGGCA	2
Oke_HP-182	A	C	CCGATGACTCCAAAGAAGTTGCT	GTCTGAATATTGTTTGAAAGAGATGGTAATGG	AGAAAAGGTGAGCTAGTATG	AAAAGGTGAGCTCGTATG	1
Oke_hsc71-199	G	C	CTGAAACTACCTCCCCCTAACAAG	ACAAGTCATGAGACTCAGACACAAG	AAAGTTTGAAATGTGTTCTAC	AAAGTTTGAAATGTCTTCTAC	4
Oke_il-1racp-67	G	A	AATTGCTCCTCCTCGCTATTTCTC	CCATCATTCAGACGACAAGGAGTAT	CGTACGAGATGTAGATGT	CGTACGAGATATAGATGT	4
Oke_IL8r-272	A	G	AGGCTGAGGCAGTGACATG	ACCGACGCTTCTAGCAATGTAC	CAAGAGGTCTTTGTCGACAT	AAGAGGTCTTTGCCGACAT	4
Oke_KPNA2-87	T	A	AGGCAGCCAGGTAAGTCAGTA	CAAAAGTAACGGTTAGGGACAGACA	ACAGAACAGAAACAGTG	AACAGAACAGTAACAGTG	1
Oke_lactb2-71	G	A	CGTCGTGAACCATGAGTGCAATA	TTCGCACAACTCTGGACGATAG	CTCCCTCGTGTCGAGCA	CTCCCTCGTATCGAGCA	2
Oke_LAMP2-186	A	G	TTCTAGCCATGACCCAATGAAAGG	AACTGCTCCAAATGCTGGTTAGTA	CTAACTTTACAAAGACACTGC	AACTTTACAAAGGCACTGC	2
Oke_mcfd2-86	C	T	GGCTTGAGGGCCACATTG	GTCAAAACAAAATCTGTGCAACCCT	TTGAATTTCGAAAATCC	TTGAATTTCAAAAATCC	2
Oke_METK2-97	C	T	CCAGGACGAAGGTCAAAGTTCTT	GGCACATCCCAGAAGAGTGA	AGGGAGCTGCTGGACA	AGGGAGCTACTGGACA	2

SNP	VIC Allele	FAM Allele	Forward Primer Sequence	Reverse Primer Sequence	VIC Probe Sequence	FAM Probe Sequence	Citation [2]
Oke_mgll-49	A	T	ACATTGTAATCTGTATTAGTCCAATGCAGAC	GGTACCACCTGCAACATCAAC	ATTTATGGGTGTTCCCC	TTATGGGAGTTCCCC	2
Oke_MLRN-63	G	A	CCATTTCAGCATTGCCAGATTTGAAA	GATGTCACAGACCAGTACCATGTTT	CTGGTGATTGACGATCC	CTGGTGATTAACGATCC	2
Oke_nc2b-148	A	C	CCAGCCTATTTCCTTTAGTGCATATGA	GCACCCTATTCCCTACATGGT	TTTAGTTCTAGTCAAAAGTAG	TAGTTCTAGTCCAAAGTAG	2
Oke_ND3-69[1]	G	A	TGGTATTGAATTTGTCGTAGAAGGCAAA	CCACGGCCTACACGTAATCATC	CAGCCAGAAAGGTAGAG	CAGCCAGAAAAGTAGAG	4
Oke_pnrc2-78	G	A	CGTGACAGCAGGGAGATGA	CATCTCTAGGCATGCACCTTGA	TGGCCTTCCAGCTGAA	TGGCCTTCCAACTGAA	2
Oke_PPA2-635	C	T	ACACAACTGACCATATTGACTTTCGA	TGGATAAAGATCTATATGGTGAATAAGGTCACA	TTGCCTCCCCCGCTC	TTATTGCCTCTCCCGCTC	1
Oke_psmd9-188	C	T	ACTGAGGCAATATTCTGCAGGTT	GGGCTTGCGAATTAGTGATGAAATC	CAGGAAGTTCCCCGTGTTG	CAGGAAGTTCCCTGTGTTG	2
Oke_rab5a-117	C	T	GGGAATAACAGTCATTGCAGCATTT	CCATTGTTGGAAACTGGACAGC	CAGCTGTTTTTCTTGTAGCCT	AGCTGTTTTTCTTATAGCCT	2
Oke_RAD10605	C	G	CGCCACAATGAGTCACTAGAGT	GCACAATTGGCCCAAAGTCTTG	ATGAGCCAACTAAAGC	TGAGCCAAGTAAAGC	5
Oke_RAD10719	C	T	ATGCAGGTCAACTGAGGTAAA	GTTCCCAAAAACTGTAGAGGTGTCT	CAGCCACCTCGATGAA	CAGCCACCTTGATGAA	5
Oke_RAD11183	A	C	TCTGTCAACAACCACCAGAATAGTG	CTTGGTCACATCTGTCCATAGACT	TTGTAACGGACCTTCCCCT	AACGGACCGTCCCCT	5
Oke_RAD11379	C	G	CTCATTGGATATCTCATTGGCAGACA	ACCTTGGCATTGAATACTACACACA	CAGAGTGAACTGTATGATC	CAGAGTGAACTCTATGATC	5
Oke_RAD11500	C	T	TTGTCCAACAGGGCTTGTCT	AAGGACCAAAGCTGTACTGATGAAA	TCCAAGAGGCTGCGCC	TCCAAGAGGCTACGCC	5
Oke_RAD1168	G	T	GCTGCAGCTGGCCTAGAA	TGCATAGTATTGATATTAGCCCTCTGACT	AGACCGGCAGGTTT	CAGACCGTCAGGTTT	5
Oke_RAD11690	A	G	GGCCCCCAACCATCCT	GGGAGCGTACAGGATTTGAATCA	CTGCTTTTCAGTCTCTCCAA	TGCTTTTCAGTCCCTCCAA	5
Oke_RAD11918	C	T	ACTTCTGGAGTGTGGCATCAAAA	CTGTCATGGTCAAAACATATTGGTTCAA	AGAGGTCTGTCCGTGATAA	AGAGGTCTGTCCATGATAA	5
Oke_RAD11928	A	T	GGGTGATGGTGGTGCCA	GCTGCTGGCACTTCTTACG	AATAGCCCTGTCCTTCAA	TAGCCCTGACCTTCAA	5
Oke_RAD11999	A	G	TTCGATAAGCTAGACCTGTGGGA	GGCCCAGGGACGTAATAAAACTAAA	CAGGCAATTATAAGCTATCCCA	AGGCAATTATAAGCCATCCCA	5
Oke_RAD12038	A	T	CCAGGTCTTCCGTGCTGAAT	ACGGCCCAGCAAACACA	CTACACACACTCTCACACAC	CACACACTCACACACAC	5
Oke_RAD12294	A	C	CTTGATTTAGCTTAATTGTCTGGTGTGC	CAGAACAACAGAGCCAATGGAATT	TGCACATCAGTCGACCTG	CACATCAGGCGACCTG	5
Oke_RAD12415	A	C	CACCGCACATGGCAGAAC	TCCTAGTCGACTCGGCTACTG	CTCCATCCCAAGATAGA	CTCCATCCCACGATAGA	5
Oke_RAD12909	G	T	AGGAAAATAAACACACAGCACACCTA	TGTAGTATATCTGAAAAATATGCAGGAT	TGCACATTGTGACATTC	CTGCACATTGTTACATTC	5
Oke_RAD14679	G	T	GGCCTCCACATCGACTTCTC	ATGCTGGGAGTTGGAGATACC	CGGGACGCTCCATG	CCGGGACTCTCCATG	5
Oke_RAD14852	A	C	CCCTGTGGGTTCATACTGTAACT	GGCAGAATTGTTGCATTACACTG	CTGTTTTGTACCATGACTTG	CTGTTTTGTACCCTGACTTG	5
Oke_RAD14962	C	T	TGCTGGATGTGCTCAGACAA	GCCCCTGACCTGTGCA	TTGACCGCTCTTTCTGT	TTGACCGCTTTTTCTGT	5
Oke_RAD15073	A	G	GGGTCGTCGAGAACAACGT	GGCACTTAAAACACCTCTTCCAAAA	CCATTTCTCCCACCATGAT	ATTTCTCCCGCCATGAT	5
Oke_RAD15315	C	T	GGTCCTGGGCTGGTTACAC	TGGCAGTCCGTCCAACTG	CACAGAACCGAAGAAT	CACAGAACCAAAGAAT	5
Oke_RAD16205	A	G	GCACCTCCCAATGGCTTTCT	GGCTCCATTGGAAGAAGACACA	CATCAGTGCCACCCCCA	TCAGTGCCGCCCCCA	5
Oke_RAD1635	C	G	ACTGTGACTGAGTGTGCAATGTTAT	CATTCTACAGGGCTAAGAGATTCAGT	AAACAGAGATATGGTATGGC	AACAGAGATATGCTATGGC	5
Oke_RAD16431	C	T	GTGCTGGCGTGGTTACAC	CATTATAAATATTCGCTTACCTTTGATGATCTTCA	ACTCCTGGGAATCC	CACTCCTAGGAATCC	5
Oke_RAD16718	A	C	CAGTGCTTTGATGTTTGCAGAGAA	CTGCTCAAAGACCATCACAGTTG	TCACTCCAAGGTTATTT	ACTCCACGGTTATTT	5
Oke_RAD16763	C	T	CCACATATACCGTGCCTTCAGAAAA	GTGTGTATATGGGTGAGAGAAATGCATAT	CATACCCCTCGACTTAT	CATACCCCTTGACTTAT	5
Oke_RAD16805	A	G	ATGCAGGATATCTGCTCCGG	CGGTGAAAGGTGAATGTGACAAAC	ATCCGAAATCACAGCCAT	CGAAATCGCAGCCAT	5
Oke_RAD17316	C	G	GCTGAGGGCTTCTGTTGCTAATTA	CCAAGAAAGAGTGAAACAGGTCACA	TTGTCCCCCAGGAATG	TTGTCCCCCACGAATG	5
Oke_RAD19121	G	T	GCGGCTGACGATGAGGAA	GTATGGCCTGCGCAGTAAGT	CTGCCCTGGCCGTATG	CCTGCCCTGTCCGTATG	5
Oke_RAD20162	A	T	GACGATGCATCTTGGAAAACATGAG	ATATTGAGTCAAATATGTTTAGTAAATGGATAA	AGCATATTTCTGCAATGAGTA	AAGCATATTTCTGCTATGAGTA	5
Oke_RAD2158	C	T	CGGTTGTCAGTTGAACAGTGTTT	CAACTCCCCAACGAACTTAGGA	TCGAGATGTGTCAAAAG	TCGAGATGTATCAAAAG	5
Oke_RAD2414	C	T	CTGGCAGGGTGTTGATCCA	GAGCAGGTGTGGTATGATCTACATG	CCTCTCAGCTGGGCTG	CCTCTCAGCTAGGCTG	5
Oke_RAD24191	A	C	GCAGGACGATGGCAGATACAG	CGTTTTGAATTCAGGCTGTAACACA	AGCCTTCAGAAAGTATTC	CCTTCAGAACGTATTC	5

SNP	VIC Allele	FAM Allele	Forward Primer Sequence	Reverse Primer Sequence	VIC Probe Sequence	FAM Probe Sequence	Citation [2]
Oke_RAD27585	A	C	TGGTCCTACAGACACAAAGAAACAA	ACTTTCAGGACCCTCTTTCTCTCT	TCTTTTTGTGTGTTTCTCTT	TTTTTGTGTGTGTCTCTT	5
Oke_RAD27616	A	G	CCCCAGCAAATGACTTTAGGTGTAT	GCAGCAGCTCTGGATCCT	CTCTGCAACCTGTTCAG	TCTGCAACCCGTTCAG	5
Oke_RAD27694	A	C	GCCTGGGATGATGTCCTTTTATGT	GCGAGGCTTTTATAAGAGCACATTT	CATACATCTAATCTCCC	ATACATCTCATCTCCC	5
Oke_RAD27721	C	T	AGTAGCTGATGTAATGGAGCGAAC	AGCTGCCTAAACAACGTATTGGT	ACAGGCACGTTATCAG	ACAGGCACATTATCAG	5
Oke_RAD2812	A	T	CCCACCCTGGACAGAGATAAAG	AGTAGGAGCCCTATCAGTAGTATTTGG	CTAGTTCCTCTCTACTTCCA	CTAGTTCCTCTCTTCTTCCA	5
Oke_RAD2827	A	C	GCCGCACCTCACACTAGT	CAATAAACAGGGAGCTGGAACAAAC	TTGGTGACCAGTAATTT	TTGGTGACCAGTCATTT	5
Oke_RAD28497	A	G	GCACAATACTGTGCATTTGGAAAGT	CCATTTAAGGCTGTAATGTAACAGAATGTG	ACCCCTCAACTTTTT	CCCTCGACTTTTT	5
Oke_RAD30079	A	C	TGAGGACCAAACACACACACA	ATGCAACTTTGTCTGGTTCTCTCT	ACTCCACCCCTTACTATG	CCACCCCTGACTATG	5
Oke_RAD3131	A	C	GCACCATACAGCTCCACACAA	TTTCCTTCTCTCTGGCTGTGATG	CCCCTGGGTTTGTGTAT	CCCTGGGTGTGTGTAT	5
Oke_RAD3143	A	G	GCAGGCTGTCTCGTCATTGTT	GTGTGCCTTGAATTCTAAATAAAATGAGTGT	AGTAGTAGGCTTGATTACC	TAGTAGGCTCGATTACC	5
Oke_RAD3480	A	C	CGTCATCAGATTTGAAAAGGCTTTGC	GTGACAGTTACAAGGCATTGACATT	CACCGAAATAGAATTT	CCGAAAGAGAATTT	5
Oke_RAD3490	A	G	GCAGGAGCCAGCTAGTATTGATC	ACCCTTTCTGTCACCCTTTTATTGTAA	CAACCAACAATCTC	AACCAGCAATCTC	5
Oke_RAD369	A	T	GGGCAGTGTCCTACAAG	CCCCTGGAAGGCCAAATCC	AAGACCATCACTTTTGCCTG	ACCATCACTATTGCCTG	5
Oke_RAD3693	C	T	TGCAGGTAACATCAGAGCACAAA	TCTGGTCATAGGAATAACTCCGGAAAT	ATGAGAGAATATCGAAGAAT	ATGAGAGAATATCAAAGAAT	5
Oke_RAD3715	A	G	GGCCCGGCCTTGCT	CGCAACACGTGAACCTTCTC	CATGTAACTGATTGAACAAA	ATGTAACTGATCGAACAAA	5
Oke_RAD3861	A	C	GGCATGCGAATGTTAACCTGTTTA	TGTTCCAAACGACTGTGTGATCTC	CCGACGTGATTAAGAC	CGACGTGAGTAAGAC	5
Oke_RAD39	A	G	CAGGTGGTCATGCATACAGGAT	CCTGCATCCTTTTCTACAGTATTTCAATAAC	AATCTGTCCACTAATAAA	CTGTCCACCAATAAA	5
Oke_RAD3938	C	G	GCTCCTCTCTGCCTGGTT	GCCATAAACAGAGATACCGTTGGAT	TCCAACGTCTGCGCTAT	TTCCAACGTCTCCGCTAT	5
Oke_RAD4286	A	G	CAGTTGTAACTAACCTGGCTCTGAT	GAGCTACCGCCCTGTATGTT	TAGATTAGGCTCAGAGTTTA	ATTAGGCTCGGAGTTTA	5
Oke_RAD4426	G	T	ACGTGTCTAACAGAATGTCCATGAC	CGCCGGACCACTTAAAATGACTAG	TGAGTACTAGCGAGCTGC	CTGAGTACTAGCTAGCTGC	5
Oke_RAD4787	A	G	GCTATCAACGCACAACGTGTT	ACGAAGTATCTCCTAGGCATGGT	TCGTTCATACATTGCTTG	CGTTCATACACTGCTTG	5
Oke_RAD4864	C	T	AAAGATGAACGGAGCAAAGTACAGA	GCAAGCTCTGTCAGGTTAAATGG	AGCAATTTACAGGTTTTC	AGCAATTTACAAGTTTTC	5
Oke_RAD4875	A	C	GTTCGTTGCAATCGAGTCAATAGTG	GCAGGAGCAATTGTTCAAAACGTA	CTGAAATACACAATTTCT	CTGAAATACACCATTTCT	5
Oke_RAD5156	A	T	CAGAGATGCGTCCGTGGT	CCTGTGCATTTGCTGCTTTCATATTT	CATGAGTGTGATATGGG	CATGAGTGTGTTATGGG	5
Oke_RAD5162	A	G	CTTGTAAGGAGAAGAGTATTTTTGTTTAAATTGGT	CTGTTCAAAAGTAGTGCACTATATAGGGAAT	AAGTAATCACAACGGAAGTG	AATCACAGCGGAAGTG	5
Oke_RAD5276	G	T	CAATCTGACCTAGTCTTCCAAGCC	CTGAAACATCGAAGACACTACTCTCA	TGGGAGATTTTATTATGGAACTT	TGGGAGATTTTATTATTGAACTT	5
Oke_RAD5734	C	T	GGTGGACTTTGGCAAACTGTTT	GGAGATGATGACTTCTGGGTTGATC	AGGAAGCAAATGACCCCT	AGGAAGCAAATAACCCCT	5
Oke_RAD5951	A	G	TGCAGGCAGACTATAATGTCATCAA	GCACTCTGAGTTTGTGGAGGTG	AGAGTGGAGCATTCAG	AGAGTGGAGCGTTCAG	5
Oke_RAD618	A	G	TGCAGGGTTCGGTAGGTTACTTTAT	AAGTTACATTACTGATTACAATTTTGGACAGGTA	ACCAGTAACTAATGGATTAC	CAGTAACTAACGGATTAC	5
Oke_RAD7067	A	T	GAGTTGAATGCAGGGAGAATAGGT	CCAGATGCCACAGATCAGTGAT	CACCATGCCTGCGATAA	ACCATGCCAGCGATAA	5
Oke_RAD7178	A	C	ACCTTTTTACAAGCAGACTAAATCCTAAAGT	TGAGATAATATGTTCTATCCCATTGCTATGGT	AGACTGAATAGATTATTATCC	AGACTGAATAGATTAGTATCC	5
Oke_RAD7431	G	T	GTGCTCTATTTCTGAGTTGGTGTGA	AGACCAGTGTGGACAGGTAGTC	CCTGACCCCAACCAA	CCTGACCCAAACCAA	5
Oke_RAD7744	G	T	GGGTCCTAAAATTCTAAATCAAATAGCT	TTTCTACTAAGCTATATGGAATTGTTTCAAGAT	AAATCATCCTTGGTATGACC	AAATCATCCTTGTTATGACC	5
Oke_RAD8326	A	C	TGCAGGTTAGCTTGGTTGGTTAA	CATTGAGAAAGTGGGCATAGATCGA	CTTCCGTTCAAATCTAAAA	TCCGTTCAAAGCTAAAA	5
Oke_RAD8335	A	G	TGCTCGGGCTCCAAATGAC	AGCAGAGAAAACCCCGAATCC	ATCGAGCCAAAACT	CTATCGAGCCGAAACT	5
Oke_RAD8372	A	G	TGCAGGAGGAACCGCC	CCGACCATCAAGGTTTTGCAA	CCTGACAGTAAGATATATCAA	CTGACAGTAAGATGTATCAA	5
Oke_RAD8698	C	T	GAAGGCTCTCCCCCTTTCTG	TGTGTGTGTGTGTGTTTACTTACGA	CTCCCATATAGGCGTAGTAG	CCCATATAGGCATAGTAG	5
Oke_RAD8799	G	T	GCAGGAGTGAGTCACTGCTTTA	CCCCTCCCAGAGTGCCATAT	CCCTGTCATTCAAACAT	CCCTGTCATTAAAACAT	5
Oke_RAD8814	A	C	GACCAAATCCTTCACGTCACTGA	GTTGCTGTTTCAATCTGCATTACG	CCTGAAAACAGACAAACA	CCTGAAAACAGCCAAACA	5

SNP	VIC Allele	FAM Allele	Forward Primer Sequence	Reverse Primer Sequence	VIC Probe Sequence	FAM Probe Sequence	Citation [2]
Oke_RAD8930	G	T	GCTCGACCTTATTCATGGTTTCCT	CTGTTTTCTGACGTTGACTTAACTCT	TGAAGGTGGTGGAATTA	TGAAGGTGTTGGAATTA	5
Oke_RAD9447	A	C	TGATGAAACTGTGGCCTTGCA	CGTAGATGAGACGGTTTCTGACA	CAATTCATATCTGAACCAAC	CAATTCATATCTGCACCAAC	5
Oke_RAD9864	C	T	CTGAGCTGGCGTGGCTA	GCAATTACATCCAACCGGCCT	CACAATTGCAGGCCATGTA	CACAATTGCAGACCATGTA	5
Oke_ras1-249	T	G	GGATGACTAAGAGCGACTGTATGTG	AATTTTATGACTGCTTGAAGATTGAGTGC	CACCAAGGTAAAAAT	CCAAGGGAAAAAT	1
Oke_RFC2-618	G	A	GACAATGTGTTAGTGTAGGCTTCACT	ACACTGGAATACTTAAGTGCACAACA	CAGCTCCTGGACTCA	CAGCTCCTAGACTCA	4
Oke_RH1op-245	C	T	TGGCCGATCTCTTCATGGTAATC	TCCAAAGACGAAATAGCCATGCA	AGTGGTGAAGCCTC	TAGTGGTAAAGCCTC	4
Oke_ROA1-209	G	A	CAGGGTTTGATTGGTTAACTTACATTGAAT	GCTGGATCTCTCATTACCTGTAGGT	TAGAGAGTAATGCAAAAAT	ATAGAGAGTAATGTAAAAAT	2
Oke_RPN1-80	G	A	CACGCACCTTGCTAAGATAACAG	GGCTCTACCGCCAAGATAAAGTTAT	CCGTGTCTCCCTGATTT	CCGTGTCTCCTTGATTT	2
Oke_RS27-94	G	A	CACTTCTAGATCAATCCGCTGTTTC	GCGACTCCAGCCTTGACA	ATGCAGGGACTGCTG	ATGCAGGAACTGCTG	2
Oke_RSPRY1-106	A	T	GTCCTCCCTATTCTTCCACTTACCT	GCAAAGAAGCCAGACCTGAGAAA	TAGTCTCTTTACATAATCTC	TAGTCTCTTTACTTAATCTC	3
Oke_serpin-140	A	T	TCCACAGTGAGTAATAAAGTTGCACAT	GAGCAAAGACCTAGGCCTGAAG	CAAGAACTGACCTTAGACAC	AAGAACTGACCTTTGACAC	4
Oke_slc1a3a-86	C	T	TGTCTTCATCTGTGGACTCCTACA	TCACCATGACAACTCACCTAGATGA	CCCAACGCGGTGATG	CCCAACGCAGTGATG	2
Oke_sylc-90	A	T	TTGAGGAAACCACTGGTCTTACAAG	GCATCCTTCCTACCTTCCTTGAG	ATATCTTTGAGACTAGATTAA	CTTTGAGACAAGATTAA	2
Oke_TCP1-78	A	G	CTCCAGGGCATCAGCAAATG	TGCTCATTACCACCATCTCTCTCT	ATACTGCTCCAGAGACG	CTGCTCCAGGGACG	1
Oke_TCTA-202	A	C	AGTTTAGCACTTACCTTGTCGGT	CAGTCTCATTGCCATCCATTTCG	ATCGTTCACAGTGTTTC	TCGTTCACCGTGTTTC	2
Oke_Tf-278	C	A	GCCACAATTGTAATTCTAGATCCAGAGT	ACTGTACCTGGTGAGTTTTTAAAGCA	ATTTTACAGTTGACATTCAA	TTTTACAGTTGAAATTCAA	1
Oke_thic-84	C	T	GCTGCTGTCTTAAACCACATTCTACA	GCCTTCCTATTTGTCCTGTTCTCT	ATGGAATGACAGCAATGT	ATGGAATGACAACAATGT	2
Oke_u0602-244	G	T	CAAGTATGCATGACTAGCTATGTGTATATCTT	TCTGCTATTGGTGGCCTATGTG	CAGTGCCCTTCTCACA	CAGTGCCCTTATCACA	3
Oke_U1002-262	G	T	CCTAGACCACTCCAGACTGTTG	GCTGTGAACTCAGAATTGCTGTGTA	AAGCTTGATTTCTTTTCTT	AAGCTTGATTTATTTTCTT	3
Oke_U1008-83	A	G	GTCACCAAACATCCTGCGAATG	ACTGTAAAACAAATACAGAAGCTCACTCA	CCGTTCTCTTCTTGGACAC	CGTTCTCTTCCTGGACAC	3
Oke_U1010-251	A	G	CACCTCAATCAATCAAATGTATTTATAAAGCCA	ATCGTTGGGCCTAAACAAGGT	ATAGAGGTGAGCATTGACAT	TAGAGGTGAGCACTGACAT	3
Oke_U1015-255	A	G	CAGAGTGCAGAGTAATACGCATACA	ACTCTGTCATCCTCACCAAGGTAA	CAAACACACACAGAGCC	AACACACGCAGAGCC	3
Oke_U1016-154	C	T	GCAGGTTGCTAAGTCATGTTACACA	ACGATAGGCACTAGGCAACATAAAG	CCATGTTTGCGGTATGT	CCATGTTTGCAGTATGT	3
Oke_U1017-52	C	T	TGGCAATGGGATGTCAAGTTATGA	CCAAGGAGTCCATGGTAATAAGCAA	AGAGAGTTGTCGTTCATC	AGAGAGTTGTCATTCATC	3
Oke_U1019-218	C	T	GCAGTCACACATTTTCTTCATCACA	TTCCTACAGAGGCAGATGCTAGT	ACTGGTGAAGGGATATT	CTGGTGAAGAGATATT	3
Oke_U1021-102	G	T	TCGAGGATTTGAGGATTAGGCTACT	AGCAAAATCACTAAGTCTCTCGTGTT	TGTTTCCACAAGAACTGA	TGTTTCCACAATAACTGA	3
Oke_U1022-139	A	G	AACATTAAAACTGTGGTTTTGACCTCTTG	CAGTCCACCACGTGTTTGTG	CTGGAACATGAAGCAAA	TGGAACATGGAGCAAA	3
Oke_U1023-147	A	C	TCTTAAAATGGAGAGAGCGATTAATGAAGG	GGCTTCAGTTGACCATGTACTCATA	CATCAGGGAAAGCCTACAAA	AGGGAAAGCCGACAAA	3
Oke_U1024-113	A	G	CATGCTGGTGAATTATTGGACAATGT	CTGCTACATATGAAACTAGAGAACACACT	CCAGAAACAACTTAATTAT	CAGAAACAACTCAATTAT	3
Oke_U1028-100	A	C	CCTACTATTTCAGAGGCTTGACACA	CCCTCCAAGTCCCCAGTCA	AATTGTGAAGCAGAGGAG	AATTGTGAAGCCGAGGAG	3
Oke_U1031-132	C	T	ACTAGAGCAGGCTTTTCTGTTTAGC	CGGTTATGCCTTAAATCTTTACCCATAAATAAAA	TTGTTAAAAACGGCATAGTT	ATTGTTAAAAACAGCATAGTT	3
Oke_u1-519	A	T	AGGTTTGTATGCGGCTGCTT	CAACTCAGCACAAGAACTGTTCAC	TCATGAAATGGGTTTCTAT	ATGAAATGGGATTCTAT	4
Oke_U2001-629	C	T	CCCCACTCCTTCTACTCATCCAT	TTAGTACAAATGAACGAGGGTTGGAA	AGCCTTTCACATCCCCA	CAGCCTTTCATATCCCCA	2
Oke_U2002-200	A	C	CCAGTGTTGTAGAAAACATGTGCTCTA	GCGCTTACGCTTCAATTTGCA	AAAGCTGTGGTATATAAT	AAAGCTGTGGTCTATAAT	2
Oke_u200-385	G	T	CCCATAATTTTGCAACCCTAGTCACA	CCTTTCCCCATATCCTGTCACTTTT	CATTATCTCCCTGAATGTA	CATTATCTCCATGAATGTA	4
Oke_U2005-62	A	G	GTACAGCAGAGACTAAAGCTATACAACA	GAGGTCAAGGCTTCAACATCAC	TGACTGACTGCATAGTTGT	ACTGACTGCGTAGTTGT	2
Oke_U2006-109	G	T	CCAACACCACTTTCCATTAATAAGCA	GCACACCCTAATTGACAAACAAACC	AAACAAAGGCAAAGTC	AAAACAAAGGAAAAGTC	2
Oke_U2010-94	C	T	CCGCAGACAGTGGTCAATACT	GCCCTTCTCTTTCTCCATACTTTTCT	CTCTCCTCGGTGTTGC	CTCTCCTCAGTGTTGC	2
Oke_U2015-151	C	T	GCATTTTATCCTCAAACTTTTCAACTGACA	ACGAATCCACCTAAAATCCACCAAA	AATTGATCACGATCATTC	ATTGATCACAATCATTC	2

SNP	VIC Allele	FAM Allele	Forward Primer Sequence	Reverse Primer Sequence	VIC Probe Sequence	FAM Probe Sequence	Citation [2]
Oke_U2016-118	C	T	ACGTGTCCTGTTCAAATTAGCAGTA	GAGGTGCATGCTTTTGTTCCA	CCAGCTATAACAGCCTTG	CAGCTATAACAACCTTG	2
Oke_U2017-87	A	C	CAGGAGCCATTGGAAGAGTAGAG	CCATGATTTGAAAAGAGCTGAACCAT	CGTTGGTGTGAAGTACAGAT	TTGGTGTGAAGGACAGAT	2
Oke_U2021-86	A	C	TGTGGCTCCAGCCAAAGTT	GCATCCTCAGTTCCAGCATAATGAT	AAACATTTCCTGTACATTAA	CATTTCCTGGACATTAA	2
Oke_U2022-101	G	C	TGTCCTAATGACAGGCCTTGC	GTCACTGCAGCCTAACGTTATATTG	AGCTGGTTACGTGTCGTG	CTGGTTACGTCTCGTG	2
Oke_U2023-99	C	T	CACTATTTTGACAAGTGTTAAGATCATTTTGTGT	TGTGATCAACAGTTTTACACTCAATGGA	CACTTTTATTGCGGTATAGAT	CACTTTTATTGCGATATAGAT	2
Oke_U2025-86	G	A	AAATCCCCATGGAGAAACACAATGA	ATTGTCCTTCCGCAGTGGT	ACTTTTTTGTCGTTTTTTT	ACTTTTTTGTCATTTTTTT	2
Oke_U2026-64	G	T	CTTCCCACGTCTTTTCTGTCTCA	GCCTCTCACGTTACACTGTCATTTT	CAGATCAAATTGTAAAACT	CAGATCAAATTTTAAAACT	2
Oke_U2029-79	C	T	GGTTTGATTTCGTCGCGATTTGA	AAATCCCAGGGAGCGAAAGTC	AGGTGTACTGAAGAGAC	AGGTGTACTAAAGAGAC	2
Oke_U2031-37	A	T	CACACTTTCAATCAAATGTTGTGCAG	CGTTTGAGACGCCCTTCACT	CATTCACACTGATCTGC	TTCACACAGATCTGC	2
Oke_U2032-74	G	A	GCTATTCCAATGTAAATCCTGTACTGTGT	AACCCTATCTGCTCATTGGTCATG	CAATAAAGTGCTAGGTGTCC	CAATAAAGTGCTAAGTGTCC	2
Oke_U2033-122	G	T	ACGCCCTTCCCCGATTC	GGCCTGGGTATGACTCAACATG	CGACGTCAATGACTTTG	CGACGTCAATTACTTTG	2
Oke_U2034-55	C	T	GGGAAGAAAAGCCTACCATAAACAG	CCCAGAGCGAATGCCAACA	ATGTCAAATCACGCTGATG	ATGTCAAATCACACTGATG	2
Oke_U2035-54	G	A	CGCCAATAACGCTCCAACAAC	CTTCACACCCTGAGAACTGGTTTTA	CACCAATAACGTCCTAATC	CACCAATAACATCCTAATC	2
Oke_U2037-76	C	G	CATATCAGGTGTGTCTCAACAGTCT	GGCATTCACTACATCACATGACCTT	TCGAGTCTGGAGTCTTGA	CGAGTCTGGACTCTTGA	2
Oke_U2040-77	A	C	GGGCTAGAATTCTACTTGGTGACA	CCTTCCACAGTCTCATTTTGCTCTT	CCAGACGACTTACTCTC	AGACGACGTACTCTC	2
Oke_U2041-84	G	T	CCAGACCATGTGCTTGTTTGTCATA	GTGAATATTTTGGCAAGCCTGTACA	CAGATCCGGTGTATGC	ACAGATCCTGTGTATGC	2
Oke_U2043-51	G	A	CACAAACCTACTACAGACAGCAGTT	GCCAGCTTTGTAGTCTTGTGGAAA	TCTGGAGGCGTATTGG	CTGGAGGCATATTGG	2
Oke_U2048-91	A	C	AGTTGGGTCTTAAAGATGATCATTTGCT	GGACTCTTGACGGCCATCTTA	CAGCCTCATAAGATGTTTA	CAGCCTCATAAGCTGTTTA	2
Oke_U2049-99	C	T	CATTGTAGCAGAGGGTCAACGATAT	ACACACGGCATTGCAAACTC	AAACTAGTATTTCCCGTCTATG	ACTAGTATTTCCCATCTATG	2
Oke_U2052-56	C	T	GTGCCATGTTAGCCAAAAAGTTTCA	TCCATGTTAGCAGCGAACGTT	CATGACGGGAGGATTA	CATGACGGAAGGATTA	2
Oke_U2053-60	C	T	TCTGCTTTTGTCGTCTCACCAA	CACACGAGGGTGGACTTAGTT	CACACATATGAGATGCC	CACACATATAAGATGCC	2
Oke_U2056-90	G	T	CCATCACGTCACCATTACACTGT	GACATTAGCTGGCAGTCTGATCA	CGAAGTGATGAAGGTGACAA	CGAAGTGATGAATGTGACAA	2
Oke_U2057-80	A	G	GCAGTTGTCATGGCAGTAAGG	GCCCCTCGTTCATTTTCAGATG	CACGTTTTCTCTTTTCTC	ACGTTTTCTCCTTTCTC	2
Oke_U212-87	C	A	TTGATTCATACTCAAGGTGAGCAGATT	GCTGGTGGCCCTTGTGA	CTTGTGACATTCCTCTCT	CTTGTGACATTACTCTCT	4
Oke_U302-195	C	A	GACCCTCAGCTATTTTAAGAACCTCAA	ACCTACCTCCTGCCAAGTTTTAAAC	TTGTCAAAGGAATCATTT	TGTCAAAGGAATAATTT	1
Oke_U305-130	G	C	GGGTGGATCTAATTTTGGCTGTAGT	GGAGAATCATTATTGTCTTTACCGGAGAA	TCTTCCACCCGATTGG	TTCCACGCGATTGG	1
Oke_U305-307	G	T	TTTGGAAACGTGTGGGATTAATTTTGT	CACGGCTGTCCATTTGCAAT	ACAAACGGGCCAGTTG	CAAACGGGACAGTTG	1
Oke_U401-143	T	A	GCACTGGAAAGCACTCATCCTT	GCAGTCAGACACCATGCAAAA	CATTTTCACTCCTACTACTC	CATTTTCACTCCTTCTACTC	1
Oke_U401-220	G	A	TGACTGCATTCACTACTGACAAAGT	TGCAGCAAATGCTTGAGACTTACT	CCATGCCTTGTACAATA	TCCATGCCTTATACAATA	1
Oke_U502-241	G	A	ATGATCATTACACAGATGCACCTTGT	GCCAATTACACACTCACTCACAACT	CCACTCTCCGTTTTAT	CCACTCTCCATTTTAT	1
Oke_U504-228	A	G	CTTAACTCAGTCACACCAACTCACT	GTGAGTTACAATGAGCTGCATGAG	TGGCTCAAACTTG	TTGGCTCGAACTTG	1
Oke_U506-110	C	T	CGTGGTTGGTTTCATTGACTCTCA	CGTTTCTCAAGATGTTCCTCTCCAA	TTGTAAGTTGTGGCTAAAA	TTGTAAGTTGTGACTAAAA	1
Oke_U507-286	T	G	TGGTCATAGCTTGCACTGTACAAA	CCTAACTGTTCTTGCCCATATAGTGAA	CTGCTGTTCATAAAAGTA	CTGCTGTTCATACAAGTA	1
Oke_U509-219	C	T	GCACCCCACCTGGCTT	TCACTCACTCTGCGTCTCTCT	CCTCTCTGCAGGGCT	CCCTCTCTACAGGGCT	1
Oke_U511-271	T	A	GACACAACGTTTTGGGACATTCAG	CGATGAGAAGGTGTCCACATACTTT	ACAGAAATACAGTATATAACCT	CAGAAATACAGTAAATAACCT	1
Oke_XBP1-82	C	T	TCTGCTCCGGAGTCTTCTGTAT	AAGGAGAGTGTTTAACAAAATTATACAGGATGT	CCTTTATACATACGGAAACAG	CCTTTATACATACAGAAACAG	2
Oke_zn593-152	A	C	GTTTTGAAAAGTTATTTCTCGCGTAGATTAAGA	AACTAGCTAGTTATCTAGTAGTAGCTAAATTAGCT	AGTTACTGAGACATAAACCA	CTGAGACAGAAACCA	2

[1]MtDNA SNPs

SNP	VIC Allele	FAM Allele	Forward Primer Sequence	Reverse Primer Sequence	VIC Probe Sequence	FAM Probe Sequence	Citation [2]

[2]Citation:

1 Elfstrom et al. (2007)

2 Petrou et al. (2014)

3 Seeb et al. (2011a)

4 Smith et al. (2005)

5 Seeb et al. 2014)