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Western Alaska Salmon Stock Identification Program Technical Document 23: Chum Salmon SNP Selection Results

by

Nicholas A. DeCovich,

James R. Jasper,

Sara M. Turner,

Christopher Habicht

and

William D. Templin

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Alaska Department of Fish and Game Divisions of Sport Fish and Commercial Fisheries

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Weights and measures (metric)	
centimeter	cm
deciliter	dL
gram	g
hectare	ha
kilogram	kg
kilometer	km
liter	L
meter	m
milliliter	mL
millimeter	mm

Weights and measures (English)	
cubic feet per second	ft^3/s
foot	ft
gallon	gal
inch	in
mile	mi
nautical mile	nmi
ounce	oz
pound	lb
quart	qt
yard	yd

Time and temperature	
day	d
degrees Celsius	°C
degrees Fahrenheit	°F
degrees kelvin	K
hour	h
minute	min
second	s

Physics and chemistry	
all atomic symbols	
alternating current	AC
ampere	A
calorie	cal
direct current	DC
hertz	Hz
horsepower	hp
hydrogen ion activity (negative log of)	pH
parts per million	ppm
parts per thousand	ppt, ‰
volts	V
watts	W

General	
Alaska Administrative Code	AAC
all commonly accepted abbreviations	e.g., Mr., Mrs., AM, PM, etc.
all commonly accepted professional titles	e.g., Dr., Ph.D., R.N., etc.
at	@
compass directions:	
east	E
north	N
south	S
west	W
copyright	©
corporate suffixes:	
Company	Co.
Corporation	Corp.
Incorporated	Inc.
Limited	Ltd.
District of Columbia	D.C.
et alii (and others)	et al.
et cetera (and so forth)	etc.
exempli gratia (for example)	e.g.
Federal Information Code	FIC
id est (that is)	i.e.
latitude or longitude	lat. or long.
monetary symbols (U.S.)	$, ¢
months (tables and figures): first three letters	Jan,...,Dec
registered trademark	®
trademark	™
United States (adjective)	U.S.
United States of America (noun)	USA
U.S.C.	United States Code
U.S. state	use two-letter abbreviations (e.g., AK, WA)

Mathematics, statistics	
all standard mathematical signs, symbols and abbreviations	
alternate hypothesis	H_A
base of natural logarithm	*e*
catch per unit effort	CPUE
coefficient of variation	CV
common test statistics	(F, t, χ^2, etc.)
confidence interval	CI
correlation coefficient (multiple)	R
correlation coefficient (simple)	r
covariance	cov
degree (angular)	°
degrees of freedom	df
expected value	*E*
greater than	>
greater than or equal to	≥
harvest per unit effort	HPUE
less than	<
less than or equal to	≤
logarithm (natural)	ln
logarithm (base 10)	log
logarithm (specify base)	$\log_{2,}$ etc.
minute (angular)	'
not significant	NS
null hypothesis	H_O
percent	%
probability	P
probability of a type I error (rejection of the null hypothesis when true)	α
probability of a type II error (acceptance of the null hypothesis when false)	β
second (angular)	"
standard deviation	SD
standard error	SE
variance	
population	Var
sample	var

REGIONAL INFORMATION REPORT 5J12-25

WESTERN ALASKA SALMON STOCK IDENTIFICATION PROGRAM TECHNICAL DOCUMENT 23: CHUM SALMON SNP SELECTION RESULTS

by
Nicholas A. DeCovich, James R. Jasper, Sara M. Turner, Christopher Habicht, and William D. Templin
Alaska Department of Fish and Game, Division of Commercial Fisheries, Gene Conservation Laboratory, Anchorage

Alaska Department of Fish and Game
Division of Sport Fish, Research and Technical Services
333 Raspberry Road, Anchorage, Alaska, 99518-1565

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Nicholas A. DeCovich, James R. Jasper, Sara M. Turner, Christopher Habicht, and William D. Templin
Alaska Department of Fish and Game, Division of Commercial Fisheries, Gene Conservation Laboratory
333 Raspberry Road, Anchorage, Alaska, 99518-1565 USA

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ABSTRACT

Uncertainty about the magnitude, frequency, location, and timing of nonlocal harvest of sockeye and chum salmon in Western Alaska fisheries was the impetus for the Western Alaska Salmon Stock Identification Program (WASSIP). The program was designed to use genetic data in mixed stock analysis (MSA) to reduce this uncertainty. A baseline of allele frequencies is required for use in MSA to estimate the stock of origin of harvested fish. In 2008 the WASSIP Advisory Panel requested new baselines based upon 96 single nucleotide polymorphisms (SNPs) for chum salmon *Oncorhynchus keta* to improve the precision and accuracy of stock composition estimates. To meet the standards set by the Advisory Panel for increased resolution more emphasis was placed on selecting markers to distinguish among regional areas within Coastal Western Alaska. We investigated 188 SNPs developed by the Alaska Department of Fish and Game (ADF&G), contractors, or other laboratories to identify the best-performing SNPs for chum salmon MSA. Three measures were used to select the most useful markers from the WASSIP baseline: (1) gating measures (i.e. conformance to population genetic assumptions), (2) scored measures (assigning individual weights designed to select useful markers for WASSIP objectives), and (3) laboratory performance. We selected 96 of the 188 SNPs that perform better in the laboratory and will potentially distinguish among populations and regions more clearly than the previous set of 53 SNPs. For the purposes of WASSIP, we believe our method of selecting useful loci produced a panel of markers which will perform better than randomly selected loci for distinguishing among regions within Coastal Western Alaska and across the species range. This marker set should create consistent, reliable data on which to base further analyses for WASSIP.

Key words: Western Alaska Salmon Stock Identification Program, WASSIP, chum salmon, *Oncorhynchus keta*, mixed stock analysis, MSA, genetic baseline, marker selection, single nucleotide polymorphism, SNP

INTRODUCTION

Early in the development of the Western Alaska Salmon Stock Identification Program (WASSIP) it was clear that the resolution of chum salmon spawning in Coastal Western Alaska (CWAK) regional areas (Norton Sound, Lower Yukon, Lower Kuskokwim, Western Bristol Bay, and Eastern Bristol Bay) was not going to be sufficient to reach the 90% correct allocation level for defining these areas as reporting groups for mixed stock analyses (MSA; see Jasper et al. 2012 for the original panel of 53 SNPs). The WASSIP Memorandum of Understanding (ADF&G 2006) specifically mentions the need to develop a chum salmon baseline capable of identifying the origin of stocks within the Arctic-Yukon-Kuskokwim area, which includes many of the CWAK regional areas, in WASSIP fisheries. The WASSIP Advisory Panel (AP) requested that 96 single nucleotide polymorphism (SNP) markers be incorporated into the chum salmon baseline to improve the precision and accuracy of stock composition estimates at the joint AP/Technical Committee (TC) meeting on March 24, 2008.

To meet this request the department began the process of discovering additional SNP markers for chum salmon through a contract with the International Program for Salmon Ecological Genetics (IPSEG; http://www.fish.washington.edu/research/ipseg/research.html) at the University of Washington. These efforts were based on cDNA sequences from 2 chum salmon sampled from the Susitna and Delta rivers. This process has been described in a manuscript published in *Molecular Ecology Resources* (Seeb et al. 2011a) which was provided as Seeb et al. (2012). This process added 37 validated SNPs to the 53 already used by ADF&G for chum salmon (Jasper et al. 2012). Subsequent rounds of SNP development at the University of Washington were based on 16 fish from 4 populations from CWAK and increased the total number of described SNPs to 198 (Petrou et al. *In prep*). TaqMan™ assays were developed or available for all of these 198 SNPs including the original 53-marker set.

Markers were assayed by the IPSEG laboratory on 80–96 individuals from each of 30 collections (Table 1; Figure 1) chosen from across the species range. Ten of these collections were from

CWAK (Figure 2). Of the 198 markers surveyed, 188 markers were determined to perform adequately in the laboratory and were passed on to ADF&G for further consideration (Table 2).

The purpose of this technical document is to describe the methods (initially described in DeCovich et al. 2012) that the Gene Conservation Laboratory used to choose the set of 96 SNPs to be assayed in chum salmon for the WASSIP project. A similar process was completed with the selection of 96 SNPs for use with sockeye salmon and is described in Dann et al. (2012). However, the selection of chum salmon SNPs needed to be significantly different from that used for sockeye salmon: 1) there were many more SNPs available for chum salmon (188 SNPs) than were available for sockeye salmon (124 SNPs); and 2) more emphasis needed to be placed on selecting markers to distinguish among regional areas within CWAK for chum salmon, whereas resolution among regions important for management for sockeye salmon was already close to adequate with the original set of markers. For chum salmon, population discrimination factors contributed to the marker selection to a greater degree because we started from a larger pool of markers and the genetic divergence among chum salmon populations within the WASSIP study area is less than that for sockeye salmon in the current baselines. Whereas, for sockeye salmon, laboratory performance, conformance to Hardy-Weinberg Expectations (HWE), linkage among loci, and discrimination among pairs of populations of interest were the primary measures used in marker selection.

METHODS

We used a combination of gating and scored measures to select the 96 most useful markers for WASSIP (Figure 2). *Gating* measures were used to disqualify markers and included lack of conformance to Hardy-Weinberg Expectations and linkage disequilibrium. *Scored* measures were used to determine the relative usefulness of markers for MSA performance with individual weights designed to select useful markers for WASSIP objectives. Once the scored measures were used to rank the markers (most useful to least useful), laboratory performance was considered, and markers discarded due to poor laboratory performance were replaced with the next highest ranked marker.

GATING MEASURES

Conformance to Hardy-Weinberg Expectations

Nuclear markers were measured for conformance to HWE using the program Genetic Data Analysis (GDA; Lewis and Zaykin 2001 as described by Weir 1996). Collections out of HWE at $\alpha=0.05$ for more than 10% of the markers (19 markers) were excluded from further analysis because they likely do not represent a single population. The rest of the collections were assumed to be sampled from single populations. Markers out of HWE assessed across all populations ($\alpha=0.01$) were excluded. This overall p-value was calculated using the following equation:

$$x^2 = -2\sum_{i=1}^{k} log_e(p_i)$$

where k is the number of populations and p is the probability that marker i is out of HWE.

Mitochondrial markers were concatenated into a combined haplotype as described in Smith and Seeb (2008).

Linkage Disequilibrium

Linkage disequilibrium was measured with the program GDA. Marker pairs that exhibited linkage disequilibrium at $\alpha=0.05$ in more than 50% of populations examined were considered *associated*. Some markers were associated with more than one other marker, in which case all pairs with a common marker were assembled into *association blocks*. For marker sets considered associated (both associated pairs and association blocks), we determined whether it was more useful for MSA to combine linked markers or to use only a single marker from the set. For each set of associated markers we used the following process:

1) For each pair of associated markers we set up 3 treatment files:
    a. marker A combined with marker B (*composite phenotype*; Habicht et al. 2010);
    b. marker A retained and marker B excluded; and
    c. marker B retained and marker A excluded.

For associated blocks, we extended this method. For example, for an associated block of 3 markers where marker A and B are associated and marker A and C are associated, we set up 6 treatment files:

a. marker A combined with marker B and marker C excluded;
b. marker A combined with marker C and marker A excluded;
c. marker B combined with marker C and marker A excluded;
d. marker A retained and markers B and C excluded;
e. marker B retained and markers A and C excluded; and
f. marker C retained and markers A and B excluded.

2) The rate of correct allocation of simulated individuals to defined reporting groups based upon the markers in question was assessed using f_{ORCA} (Rosenberg 2005). Combinations of alleles from 2 or more markers can exist in more forms than single markers (for example, 2 markers produce frequencies for 9 possible composite phenotypes while each marker produces frequencies for only 2 alleles, and thus, composite markers generally have higher f_{ORCA} values than the single markers that form them). Simple comparisons of these values would often suggest combining linked pairs into composite markers. However, there are costs associated with composite markers:
    a. for a given sample size estimates of 9 phenotype frequencies are less precise than estimates of 1 allele frequency;
    b. two markers that are subsequently combined into a single locus displace 2 unassociated markers in the laboratory (i.e., it costs the same to screen 2 unassociated markers as 2 associated markers).

To account for these costs, and to ensure that only associated SNP pairs that provided significantly more information than the single SNPs were retained, the difference between f_{ORCA} values of the composite marker and the single SNP with the greater f_{ORCA} value in the pair were compared ($\Delta = f_{\text{ORCA-pair}} - \max(f_{\text{ORCA-single1}}, f_{\text{ORCA-single2}})$). This pair/single difference (Δ) was the test statistic.

3) Since the distribution of Δ was unknown, a sampled randomization test was conducted (Sokal and Rohlf 2005). One thousand SNP pairs were randomly selected, and Δ was calculated for each pair to empirically define the test statistic distribution. The 90th quantile of the distribution was set as a critical value (Δ_{90}). If Δ was greater than this critical value, the linked SNPs were combined into a composite phenotype. If Δ was less than the critical value the SNP with the lower f_{ORCA} was excluded from further analysis.

Once associated markers were either combined on excluded, the remaining markers or marker sets were considered loci.

SCORED MEASURES

Nine measures were used to score the effectiveness of loci for MSA. These measures were weighted to achieve two objectives: 1) to increase MSA performance to distinguish among CWAK regional areas, and 2) to maintain MSA performance to distinguish among regions throughout the rest of the species range. Weights were assigned to measures based on perceived benefit of the measure to achieve the objectives and the highest weights were placed on measures associated with the first objective (Figure 3). For each measure, j $(j = 1,2,\dots,J)$, raw values for each locus, l $(l = 1,2,\dots,L)$, were linearly scaled into scores between 0.0 (lowest) and 1.0 (highest) using the formula:

$$S'_{l,j} = \frac{S_{l,j} - S_{min,j}}{S_{max,j} - S_{min,j}}$$

Where, for measure j, $S_{l,j}$ is the raw value at locus l, $S_{min,j}$ is the minimum value across all loci, $S_{max,j}$ is the maximum value across all loci, and $S'_{l,j}$ is the scaled score for the one locus (ZeroOneScore). Weights were assigned for each measure to reflect WASSIP priorities (Figure 4). Scores for each locus were summarized across measures using the following formula:

$$\bar{S}_l = \sum_{j=i}^{J} \frac{w_j S'_{l,j}}{\sum_{l=1}^{L} S'_{l,j}}$$

Where w_j is the weight assigned to measure j, and $\bar{S}_l$ is the final score given to locus l. These scores were then ranked from highest to lowest.

Patterns in the scoring for each marker were visualized using a *heat map* created by using Microsoft Excel's conditional formatting on each column (measure) across rows (markers), and finally on the last column (sum of scores).

Measures to Distinguish Among CWAK Regional Areas

The first 4 of the 9 measures were CWAK-specific measures and accounted for 84% of the total weight. CWAK is the most difficult portion of the range to distinguish among populations, yet resolution within this area is central to the objectives of WASSIP. These 4 measures were aimed at selecting loci for differentiating both among CWAK populations and among CWAK regional areas.

The 1^{st} of the 9 measures, the overall F_{ST}, aimed at selecting loci that differentiate among the 10 CWAK populations. This measure was given 24% of the total weight.

The remaining measures aimed at selecting loci that differentiate among the 5 CWAK regional areas. The 2^{nd} of the 9 measures, overall θ_P (Weir and Cockerham 1984), is a variance-based estimation of F-statistics, was used as a measure of differentiation within regional areas when 2 populations were available in each regional area. θ_P for each marker was calculated via a 3-level hierarchical ANOVA (Weir 1996), in which the 10 populations from CWAK were organized into 5 regional areas (Table 1; Figure 2). The θ_P values calculated from individual markers were given 15% of the total weight.

The 3^{rd} of the 9 measures, f_{ORCA} (Rosenberg 2005), aimed at selecting loci for differentiating among the 5 CWAK regional areas with a backward elimination locus selection algorithm (Bromaghin 2008; Jasper and Templin, 2012). This method started with all loci, and then proceeded in a stepwise fashion to eliminate loci, one by one. At each step, the locus that provided the least information for distinguishing among selected regional areas was dropped. For this analysis, Norton Sound, Lower Yukon, and Kuskokwim were the selected regional areas because they have been shown in previous studies to be genetically similar (Jasper et al. 2012).

The f_{ORCA} with backward elimination loci selection algorithm has two components: 1) ranking loci from least to most informative, and 2) assigning f_{ORCA} values to each locus. The algorithm ranked individual loci as follows:

1) Remove one locus from the baseline and recompile the baseline with the remaining loci.
2) Select an individual fish without replacement from a randomly selected population from 1 of the 3 selected reporting groups in the baseline and assign it to one of the 15 reporting groups based on genotypic probability.
3) Repeat Step 2 10,000 times.
4) Calculate and record the fraction of correct assignments to reporting groups, f_{ORCA}, for the baseline excluding the locus.
5) Repeat Steps 1–4 for all loci in the baseline.
6) After all iterations were complete (one iteration for each excluded locus), the locus excluded in the iteration with the highest f_{ORCA} score was identified as the locus that contributed the least amount of information for distinguishing among selected reporting groups.
7) Recompile the reduced baseline (without the locus identified in Step 6) and repeat Steps 1–6.
8) Repeat this process until only one locus remains.

This method is similar to BELS (Bromaghin 2008) in that it starts with all markers and then sequentially eliminates the markers that provide the least amount of regional discrimination (Jasper and Templin 2012). Unfortunately, BELS was too time consuming and not practical for this application.

Each locus was scored by the change in f_{ORCA} caused by exclusion of the locus from the baseline (Δf_{ORCA}) with higher scores leading to higher rank. The Δf_{ORCA} scores can vary due to the stochastic nature of the method, so scores were *smoothed* by fitting a curve to the scores and using the fitted value for ranking loci. The f_{ORCA} scores were given 30% of the total weighting.

The 4th of the 9 measures, F_{ST} for population pairs, aimed at selecting loci that differentiate among the 5 CWAK regional areas using pairs from adjacent CWAK regional areas. F_{ST} for each marker was calculated using pairs of populations from adjacent regional areas. There were 4 population pairs possible from adjacent regional areas (see Figure 2 for regional areas), and pairs which provided the smallest pairwise F_{ST} were chosen for these tests. The average of the 4 F_{ST} values for each population pair was used as the final score for this section, and was given 15% of the total weight.

Measures to Distinguish Among Broad-scale Pacific Regions

The 5th and 6th of the 9 measures were aimed at differentiating among Pacific–wide regions. Together these measures received 10% of the total weight. Some WASSIP fisheries are known to intercept chum salmon from both the western and southeastern extent of the range. These measures ensured that broad-scale Pacific regions will be identifiable in WASSIP fishery samples. Principle component analysis (PCA) was used to measure the ability of each marker to distinguish Pacific regions. The 10% weight given to this section was divided between the first 2 principle components according to the proportion of overall variance that each explains. Thus, the amount of variation associated with each marker in the first principle component received 0-10% of the total weighting, and the amount of variation associated with each marker in the second principle component received the remaining weight.

Measures to Distinguish Among Specific Regions Outside of CWAK

The 7th, 8th, and 9th of the 9 measures aimed at selecting loci for differentiating among populations within regions outside CWAK (regional measures) received the remaining 6% of the total weighting. This ensured that markers important for distinguishing broad-scale population structure were considered and ensured a useable panel of SNPs for research in areas outside of CWAK (Figure 5). Population pairs selected from 3 regions of interest outside Alaska were used to calculate θ_P (Weir and Cockerham 1984) for individual markers. If no more than 1 population was available from a region, F_{ST} was calculated rather than θ_P. The 3 regions of interest included were: 1) Honshu and Hokkaido islands, 2) Southeast Alaska and British Columbia, and 3) British Columbia and Washington.

Postselection Laboratory Performance

Candidate SNPs were ordered from best to worst with respect to the measures above and laboratory performance was assessed on the best 96 candidates. As with the sockeye selection process (Dann et al. 2012), cluster tightness, alignment and drop-out rates were used as indicators of performance. Cluster tightness is a measure of the variation among individuals of a genotype; tight clusters indicate genotypes that were easier to score and produced more reliable data (Figure 6). Cluster alignment is a measure of the alignment of the genotype cluster relative to the origin; an assay with separated cluster alignment had distinct genotype clusters (Figure 7). Drop-out occurs when a sample is genotyped, but 1 or more alleles are not present, this can be due to DNA quality, mutation in the primer binding site, or alleles outside the normal calling range (Figure 8). Markers deemed unacceptable by consensus among 3 experienced genotypers based on any of these 3 measures, were discarded. When a marker was discarded due to laboratory performance, the next highest-rated marker was evaluated. The process was continued until 96 markers with adequate laboratory performance were selected. Laboratory performance was incorporated after the scored measures to avoid laboratory analysis of markers that provide little useful MSA information.

Laboratory performance was evaluated on DNA templates extracted from various tissue types. Further, assay performance was evaluated on DNA template that was both pre-amplified and not pre-amplified with the expectation that the pre-amplified templates would produce better results. This was expected to indicate assay robustness across varying template qualities. Assays were given a rating of poor, acceptable, good, or great. Those assays given a poor rating were discarded. This final step could result with a final selected SNP set falling below the target of 96 SNPs.

Ensuring No Loss in Baseline Performance

Final evaluation used simulations on the final locus set to test for any loss of MSA resolution for distinguishable regions (>90% correct allocation) generally outlined in Seeb et al. (2011b). Matching exact reporting groups was not possible, but reasonable approximations were tested. These reporting groups included (corresponding collection numbers from Table 1 in parentheses): Japan (1,2), Russia (3,4), Kotzebue Sound (5,6,), CWAK (7,8,9,10,13,14,15,16), Upper Yukon (11,12), Eastern Bristol Bay (17,18), North Alaska Peninsula (19,20), South Alaska Peninsula/Kodiak (21,22), Southcentral Alaska (23,24), Southeast Alaska/BC (26,27,28), and Washington (29,30). Correct allocations in Seeb et al. (2011) ranged from 85% to 99%, with the majority of reporting regions allocating above 90%. The correct allocation is expected to be higher for this study than those in Seeb et al. (2011b) because regions in this study are represented by only a few populations. Therefore, mean correct allocations to reporting groups below those reported by Seeb et al. (2011b) would trigger the addition of loci highly ranked for Pacific-wide and outside Alaska measures. If loci were added, the lowest-scored loci from the CWAK-specific measures would be dropped. Loci would be added and dropped following these rules until the resolution to these broader reporting groups exceeded 90%.

Simulations were performed using SPAM v3.7b (Debevec et al. 2000; Reynolds et al. 2001) using parametric bootstrapping with replacement. The simulations were based on 400 individuals using population-specific allele frequencies from every population within each reporting group and an equal number of fish were generated from each population within a reporting group. This process was repeated 1,000 times for each reporting group, and the mean and central 90% of the distribution of estimates were reported as the estimate and the 90% confidence interval. Simulated mixtures were analyzed using a maximum likelihood model. SPAM was used because of its ability to handle haplotype data.

RESULTS

GATING MEASURES

Conformance to Hardy-Weinberg Expectations

Deviations from HWE were observed in 1 collection from Southeast Alaska (24 Mile Creek from the Chilkat River drainage) at 30 loci (α=0.05). Further examination of this collection revealed negative F_{IS} values, consistent with the Wahlund effect, a reduction of heterozygosity due to a mixture of individuals from more than 1 population. The 24 Mile Creek collection was dropped from all subsequent analyses.

Five markers were out of HWE overall at the 29 remaining populations (α=0.01; Table 3). These 5 markers were excluded from subsequent analyses. There was a high, but not perfect, correspondence between the markers out of HWE overall and the markers out of HWE in multiple individual populations. All 5 of the excluded markers were also out of HWE (α=0.05) in 4 to 9 populations (14–31%). However, 2 of the markers that were not out of HWE overall, were out of HWE in 5 and 6 populations (17–21%). The 3 mitochondrial markers were concatenated into a combined haplotype.

Linkage Disequilibrium

Linkage disequilibrium analyses revealed 19 pairs of markers that were associated, evidenced by significant *p*-values (α=0.05) in more than 50% of the populations (Table 4). These 19 pairs segregated into 15 association blocks. The critical value, Δ_{90} = 0.041, was used to determine whether to retain associated SNPs as a pair or simply to retain the most informative SNP in the pair. Three marker pairs had Δ scores equal to or greater than this critical value and were retained as paired markers representing single loci (Table 4). These 3 pairs were renamed and used as composite phenotypes (loci) in all subsequent analyses.

SCORED MEASURES

Scored measure results were tabulated (Appendices A–H) and summarized in a heat map (Figure 9).

Measures to Distinguish Among CWAK Regional Areas

The 1st of the 4 measures intended to distinguish among CWAK regional areas was the overall F_{ST} among the 10 CWAK populations. Values for this measure ranged from –0.004 to 0.088 across individual loci (Appendix A). Values for the 2nd measure, θ_P among the 5 regions, ranged from -0.013 to 0.032 across individual loci (Appendix B). Values of F_{ST} and θ_P that are less than zero generally indicate no difference between the populations or regions measured.

The 3rd measure used backward elimination locus selection using f_{ORCA} as the measure of difference among populations of Norton Sound, Lower Yukon, and Kuskokwim. As expected from the backward-elimination algorithm, the f_{ORCA} curve was not monotonic (Figure 10) in that addition of some loci caused the curve to drop after it peaked at the optimal locus set. Therefore, to use this curve to assign meaningful scores to each locus, we regarded the change in the f_{ORCA} curve (Δf_{ORCA}) as the measure of the influence of a locus. Since each point on the f_{ORCA} curve was approximated instead of being calculated from closed form, the curve was not smooth making the Δf_{ORCA}'s somewhat noisy. Fortunately, the f_{ORCA} curve was approximately quadratic; making the Δf_{ORCA}'s approximately linear. We therefore fit a least-square regression line to the Δf_{ORCA}'s, and each locus was given a score based on the fitted value (Figure 11) prior to transformation into ZeroOneScores (Appendix C).

The 4th measure, average F_{ST} between population pairs in CWAK, required us to identify the population pairs with the lowest F_{ST} from all possible pairs between adjacent groups. The populations chosen based on this criterion were; the Kwiniuk and East Fork Andreafsky rivers for the Norton Sound/Lower Yukon groups, the East Fork Andreafsky and Salmon rivers for the Lower Yukon/Lower Kuskokwim pairs, the Kanektok and Iowithla rivers for the Lower Kuskokwim/Western Bristol Bay pairs, and the Iowithla and Alagnak rivers for the Western Bristol Bay/Eastern Bristol Bay pairs (Figure 2, Appendix D).The average F_{ST} between population pairs ranged from –0.008 to 0.064 for the Norton Sound/Lower Yukon pair, –0.008 to 0.045 for the Lower Yukon/ Lower Kuskokwim pair, –0.006 to 0.085 for the Lower Kuskokwim/Western Bristol Bay pair, and –0.006 to 0.132 for the Western Bristol Bay/Eastern Bristol Bay pair. The average of the four ZeroOneScores was used to rank each locus for this measure. (Appendix E).

Measures to Distinguish Among Broad-scale Pacific Regions

The 5th and 6th measures were the first two principal components of a PCA which included all assessment populations to account for range-wide differences (Appendix F). Based upon the PCA, these two components accounted for 48% of the total variation in the dataset. Principal component 1 segregated populations from Japan to the Upper Yukon and principal component 2 segregated populations from Japan to Washington.

Measures to Distinguish Among Specific Regions Outside of CWAK

The 7th measure used the per-locus F_{ST} between Honshu (Tokachi River) and Hokkaido (Gakko River) populations. F_{ST} values ranged from –0.007 and 0.189 between these island populations (Appendix G).

The 8th measure used the per-locus F_{ST} between populations in Southeast Alaska (North Arm Creek) and British Columbia (Kitimat and Kitwanga rivers). These values ranged from -0.093 to 0.138 across the available loci (Appendix H). F_{ST} was used because only one population was available from Southeast Alaska.

The 9th measure was θ_P between the populations in British Columbia and Washington State (Nisqually River Hatchery and Elwha River). These values ranged from –0.101 to 0.393 across the available loci (Appendix I).

Post-selection Laboratory Performance

Seventeen of the 96 top-ranked loci were discarded and replaced with the next-highest scored markers due to poor performance in 1 or more of the laboratory measures (*Oke_RS9-379*, *Oke_U2017-87*, *Oke_U1027-89*, *Oke_U1028-100*, *Oke_col1a2-62*, *Oke_mcfd2-86*, *Oke_txnrd1-74*, *Oke_CO1A1-72*, *Oke_U2001-629*, *Oke_hmgb1-66*, *Oke_U1031-132*, *Oke_RPN1-80*, *Oke_GPH-78*, *Oke_CD123-62*, *Oke_U1020-75, Oke_U2022-101*, and *Oke_U2033-122*). One of the next highest-ranked markers was also removed due to poor performance (*Oke_PDIA3-475*) and the next highest marker was included. The 96 remaining markers were used in the chum salmon baseline panel (Table 2). After combining associated markers, the baseline panel contained 91 loci.

Ensuring No Loss in Baseline Performance

Simulation tests across regions outside of CWAK had mean allocation estimates ranging from 0.999 for the Japan region to 0.866 for the Eastern Bristol Bay region (Table 5). The Eastern Bristol Bay Region had the only mean allocation below 90%, and 9 out of 11 regions had mean allocations above 95%.

DISCUSSION

The gating measures (conformance to HWE, unassociated markers, and lab performance) ensured that the results obtained from the weighted measures were not due to artifacts associated with non-Mendelian inheritance, independence among loci, or laboratory genotyping errors.

For the purposes of WASSIP, we believe that these methods yielded a better set of loci than a random set. The selection of loci using these methods was clearly influenced by the measures used and the weights applied to the measures. The heat map shows that measures yielded different rankings of loci and that different measures or different weights would have resulted in the selection of a different set of loci. However, if we selected loci randomly we might expect to select approximately 51% (96/188) of the top 96 loci for any measure. As might be expected due to heavily weighting CWAK, we retained between 72% and 83% of the top-ranked 96 loci for measures designed to distinguish within this region. In addition, we also selected 61% of the top 96 loci ranked on their ability to distinguish among populations within Japan, 60% of the top 96 loci ranked on their ability to distinguish between populations from Southern British Columbia and Washington, and 56% of the top 96 loci ranked on their ability to distinguish between populations from Southeast Alaska and Northern British Columbia. Finally, for the PCA, which considers all populations, we retained 60% of the top 96 loci in PC1, and 59% of the top 96 loci PC2. We consider this evidence that our method of selecting useful loci produced a panel which will perform better than randomly selected loci for applications across the species range. This is also evidence that some loci are more useful than others, regardless of where resolution is needed. For example, *Oke_KPNA2-87* was the second highest scored locus, and performed well for measures concerning CWAK and those between Southeast Alaska and Northern British Columbia. The 7th highest scored locus, *Oke_RSPRY1-106*, also performed well for CWAK measures and those concerning Southern British Columbia and Washington populations.

The methods used here for chum salmon incorporated comments received from the TC for the locus selection in sockeye salmon (Dann et al. 2012), and chum salmon (DeCovich et al. 2012). First, we applied specific weights to measures rather than the *de facto* weighting scheme used in Dann et al. (2012), which was driven simply by the number of measures used. Secondly, we were careful to include measures that select loci that are strongly divergent around the Pacific Rim, such as the 3 regional measures listed at the end of the “Scored measures”, and we examined MSA performance of the final set to ensure no degradation in MSA performance from published analyses.

These methods also benefited from lessons learned during the SNP selection for sockeye salmon and outlined at the end of Dann et al. (2012). Among these were: 1) applying gating measures before applying ranking measures rather than having only ranking measures, 2) weighting ranking measures according to importance of the judge, and 3) scoring measures rather than ranking them.

The comparison of MSA performance reported in Seeb et al. (2011b) and by the set of loci identified in this project provides evidence that this panel of 96 SNPs provides better resolution than the previously-existing SNP panel. The only test that produced an estimate below 90% using the selected 91 loci was for Eastern Bristol Bay (87%; Table 5). In Seeb et al. (2011b), the Southern Bristol Bay regional area, which most closely approximates our Eastern Bristol Bay regional area, had a mean allocation estimate of 85% in simulation tests. Although these tests do not implement proper cross validation and therefore may be optimistic (Anderson 2010), both the Seeb et al. (2011b) and our tests used similar methods, so they are comparable.

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Stock Identification Program (WASSIP) TC during the implementation of the program. The authors would like to thank the WASSIP TC and Advisory Panel for their constructive input on each of the documents throughout the project. The authors would also like to thank Erica Chenoweth who coordinated and prepared the Technical Document series for publication and Publication Specialists Amy Carroll and Joanne MacClellan for implementing the series into Regional Information Reports.

TECHNICAL COMMITTEE COMMENTS

The Technical Committee commented extensively on Technical Document 8 (Decovich et al. 2012) which described the proposed methods for chum salmon SNP selection. Generally, the TC supported the approach and measures we proposed using. The TC also provided suggestions for improving some of the methods. We incorporated these comments into the final methods. Among the changes in methods instituted based on TC comments were:

1) Linkage Disequilibrium (LD) and Hardy-Weinberg Expectation (HWE): The TC noted that before using LD and HWE to exclude loci, we should check that the collections represent single populations. We added a test to detect collections that represented more than 1 population. We detected 1 collection from Southeast Alaska (24-Mile Creek from the Chilkat River drainage) that was out of HWE and we excluded this population from the locus selection analysis.
2) Lack of rationale for inclusion of measures for selecting loci that distinguish among collections outside Alaska: We provided a rationale for including each measure.

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TABLES

Table 1.–Collections of chum salmon screened for 188 SNPs (Table 2) and their associated region, sample size, and map number from Figure 1.

Region/regional areas	Collection	Sample size	Map Number
Japan	Tokachi River	80	1
	Gakko River late	80	2
Russia	Amur River summer	95	3
	Palana River	95	4
Kotzebue Sound	Kiana River	95	5
	Inmachuk River	95	6
Norton Sound[a]	Kwiniuk River	95	7
	Unalakleet River	95	8
Lower Yukon[a]	Andreafsky River - East Fork	95	9
	Nulato River	95	10
Upper Yukon	Fishing Branch	95	11
	Kluane River	95	12
Lower Kuskokwim[a]	Salmon River	95	13
	Kanektok River	95	14
Western Bristol Bay[a]	Osviak River	95	15
	Iowithla River	95	16
Eastern Bristol Bay[a]	Whale Mountain Creek	95	17
	Alagnak River	95	18
North Alaska Peninsula	Frosty Creek	95	19
	Sapsuk - Nelson River	95	20
South Alaska Peninsula/ Kodiak	Portage Creek	95	21
	Rough Creek	95	22
Southcentral Alaska	Little Susitna River	95	23
	Beartrap Creek	95	24
Southeast Alaska	Chilkat River – 24-Mile Creek[b]	95	25
	North Arm Creek	95	26
British Columbia	Kitimat River	95	27
	Kitwanga River	95	28
Washington	Nisqually River Hatchery	95	29
	Elwha River	95	30

[a] Regional areas included in Coastal Western Alaska (CWAK) region.

[b] Collection excluded from analyses due to deviation from Hardy-Weinberg expectations.

Table 2.–Forward and reverse primer sequences and VIC and FAM allele calls for 188 SNP assays screened for 30 collections (Table 1).

Assay name	Included in final set	VIC	FAM	Forward Primer Sequence	Reverse Primer Sequence
Oke_ACOT-100	X	C	G	TCAGGGACGATAAAGGGATCATCTT	GGGAGAGACACAGGTCTACCT
Oke_AhR1-278		T	A	GCGGACACCCTCTCACA	CCCACGGTAGTCGAAGCA
Oke_AhR1-78	X	G	A	AGCAGAACCAGCACCTACAG	GCTACTTGCCTTCTGCTGTTTG
Oke_APOB-60		C	T	CTGTGGATGGTATTCTGGATGCA	GGCACTACAAAAGAGGGAATCTCA
Oke_arf-319	X	T	C	TGCAGAAACTGATCATTGGTAGTGG	TCTGTTGTTACTCTGTTTCCTGCAA
Oke ATP5L-105	X	C	G	GTGCACACCAATCCATTTCTGAAT	TGTTTTAAGGTGTGACTTGCTGGTA
Oke_ATP5L-248		A	T	CTAGTGGATTGTGGCTTACGTCAA	GGATTCTGACTGTGGGTGTTTAACA
Oke_azin1-90	X	C	T	GGGAATAGTGTCATTTGGGATGCAT	GGTGAATGATATTCTGTAGTCATATTGCTTGA
Oke_brd2-118	X	C	T	CTCAAGCCCTCCACACTCA	GGGCCGTTTCCTGAAGCA
Oke_brp16-65	X	C	T	TCCACGTCACTCAGCATGATG	ACGGTCAACTTTTGGATTAGTGAAGA
Oke_CATB-60	X	C	T	GCTTCTATGGGTCCTACTACCGTAT	GCACTCCTCTTACACAACTCTGA
Oke_ccd16-77	X	A	C	TGTCTTCAGAATCCAATGCTTTCCT	GAGAAAGTTGCCGAGCTCAAG
Oke_CD123-62		A	G	GAACAGCAGTGAATCGGTTACCT	TTGACGCTGTGTGTCTTCGA
Oke_CD81-108	X	G	T	CAGTATCATCATACAGCACAGATACAACA	GCCTGCTTGTTATACTGACAGTCAA
Oke_CD81-173	X	A	C	GATGACTGGAGTCAGCTTGCA	TTTCCTTGGCTCATCTTGCTGTA
Oke_cjo57-86		A	C	CAGAAGGTCTAAAGGTCCTTAACAATCA	CAGATTGAACAGTGCCCAGAGA
Oke_CKS1-70		G	A	GCTACCTCTATCATACCGCCAATATT	ATGTACATCTCTCCATGTGTTTTGGT
Oke_CKS1-94	X	G	T	TCTTCGACATGTTTAATCGAACAGAAGT	CCAGCTTTCGCTTGTCAAAACG
Oke CKS-389	X	G	A	GGGCCATTCTCTGAGTTCAGT	GAGCACCGGTTGTCATGGA
Oke_CO1A1-72		G	A	CTGTCAATGGAGGGTGATCGAAAT	CACCTAAGGTCCTGCAAGCA
Oke_CO1A1-76		A	T	GAGGGTGATCGAAATTGTGCTACTA	ACGACTGACATCAAGATAAATCTGCTAATTT
Oke_col1a2-62		G	A	GCAGGAAACCACTCTCATTCTTACT	AGACTTAGGAAATTGCACCTGCTTA
Oke_Cr30	X	G	A	ACTACTCTCTGGCGGCTACA	AACCTTGGATTAGTGCTGATGTATGAG
Oke_Cr386	X	G	-	CTTAATGTAGTAAGAACCGACCAACGA	ACTTAGGAACCAAATGCCAGGAAT
Oke_ctgf-105	X	G	A	TGAGTCCATGTACTACAAGAAGATGCT	TCGGTTCAAGTTAAGAGTCATTGGTT
Oke_CTR2-82		C	T	GCAGCAGACACACCGAAGTA	CCATTCCCATCGGCATCGT
Oke_DBLOH-79		C	T	GCAGATATGCCTCAGGGATGT	GACAGTCAAAGGATCAAGCTACCT

-continued-

Table 2. Page 2 of 7.

Assay name	Included in final set	VIC	FAM	Forward Primer Sequence	Reverse Primer Sequence
Oke_DCXR-87	X	A	T	GTCACCCAGAACAATAGAATGAGTCT	TCTAACACACCCACAATCTGCAAAA
Oke_DM20-548		G	T	CACTCCCCTCGCTTACTGATATCTA	ACGGACAGCTCATTTACATACACAA
Oke_e2ig5-50	X	C	T	GCACTGCTCATTCTGTCACATG	GGGAGTTCTTAGTGTGACCATAGAG
Oke_EF2-394		C	T	GCTTAACTGCTGTTTCTGCTATAGG	GCAGTCTCCTCCTTCTTGAAGTT
Oke_eif4ebp2-64		G	A	CGAAAGAAGATGGCTGCTGTGA	TGGCTTGGCTTGTAGAAACCA
Oke_eif4g1-43	X	G	T	GCACCCAACAGTTCATCATGTAAGT	CCACCCCCAGTAGTCAATCCT
Oke_f5-71	X	C	T	CTCAAATTTCCCTTTGACATCAATTCATCA	GATCCTCATGCACATCCAAACG
Oke_FANK1-	X	C	T	ACTCACGTGTGGTAGAGACAGA	AGACTGAGAATCACAAGACCAACTG
Oke_FANK1-96		A	C	GGCTCACCTGGATGACATTATATAGG	CGTGAGTACACAACACTCTTTCAGT
Oke_FBXL5-61	X	G	A	TGGTGTGTAACGTCAGTGACTTAAG	CACCTCTAGAAATGACATGATCAGTGT
Oke_gdh1-191	X	A	G	GTGGAGACCAAACCCAGTAGAAC	GGGTTAGAGGTCAGGGTTAGAG
Oke_gdh1-234		C	T	CAAACCCAGTAGAACCCTGTGT	CTGGGAATGGTGATATATGTGTTCCT
Oke_gdh1-62	X	C	T	CCACGTGATACAGGGAGATGTG	CACACACACTGACACGTACTGT
Oke_GHII-3129	X	G	A	GTCAAGCTGATACCACTCAAATCTCA	AGAATCTGACTACAGTCACTTAAAGTGATT
Oke_glrx1-78	X	C	T	CGCTCCGTCCAGTGATGTC	GGCCAAAGAGGTATTGACAAAGTAC
Oke_GNMT-100		C	T	GCGTCCACGCTCGTCAT	AGCGTGGACTCCATCATGTTG
Oke_GnRH-373		C	A	CCTGAGGAGACAAGTGCACATG	ATTGGCCATTAGGAATACAATGAATACAAT
Oke_GPDH-191	X	T	A	CCTGTACCTATAGGGCAACTTCAC	TGCCCTCTGATGGTATGATGGT
Oke_GPH-105	X	T	G	CAGATCAACCCTGGAAAAATATCTGATGT	TGAACAAGCAGCCCAATTCTGT
Oke_GPH-78		G	T	GCAGCCCAATTCTGATATTTGTTTTACTAATT	TGAACAAGCAGCCCAATTCTGT
Oke_H2AX-72		C	T	AGGGCAACTACGCTCATAGAGTA	CGAGGACAGCAGCCATGTA
Oke_hmgb1-66		G	T	GGAAACAGAATAACTACTAAGACCCTACATT	ACGCCCCCATTGGAAACC
Oke_hnRNPL-		A	T	GAACGCAAGTAAGTGTTTGAAATCGA	GAAGAGAAAGACAGAAAGGGTTAGAAAA
Oke_HP-182	X	A	C	CCGATGACTCCAAAGAAGTTGCT	GTCTGAATATTGTTTGAAAGAGATGGTAAT
Oke_hsc71-199		G	C	CTGAAACTACCTCCCCCTAACAAG	ACAAGTCATGAGACTCAGACACAAG
Oke_HSP90BA-		G	A	CACATACCAGTGTCGACCTTGA	GCACAACGATGATGAGCAGTACAT
Oke_il-1racp-67	X	G	A	AATTGCTCCTCCTCGCTATTTCTC	CCATCATTCAGACGACAAGGAGTAT

-continued-

Table 2. Page 3 of 7.

Assay name	Included in final set	VIC	FAM	Forward Primer Sequence	Reverse Primer Sequence
Oke_IL8r2-406	X	A	G	GGATGGACATTCACAGTCTGGTT	TTTCCAATCCCTGGCATCGT
Oke_IL8r-272		T	G	AGGCTGAGGCAGTGACATG	ACCGACGCTTCTAGCAATGTAC
Oke_KPNA2-87	X	T	A	AGGCAGCCAGGTAAGTCAGTA	CAAAAGTAACGGTTAGGGACAGACA
Oke_lactb2-71		G	A	CGTCGTGAACCATGAGTGCAATA	TTCGCACAACTCTGGACGATAG
Oke_lamp2-138		G	A	GCATGTTACAGGACGGCAAGA	GGCTGGTATCACTGTGACATTCA
Oke_LAMP2-	X	A	G	TTCTAGCCATGACCCAATGAAAGG	AACTGCTCCAAATGCTGGTTAGTA
Oke_mcfd2-86		C	T	GGCTTGAGGGCCACATTG	GTCAAAACAAAATCTGTGCAACCCT
Oke_METK2-97		C	T	CCAGGACGAAGGTCAAAGTTCTT	GGCACATCCCAGAAGAGTGA
Oke_mgll-49	X	A	T	ACATTGTAATCTGTATTAGTCCAATGCAGAC	GGTACCACCTGCAACATCAAC
Oke_MLRN-63	X	G	A	CCATTTCAGCATTGCCAGATTTGAAA	GATGTCACAGACCAGTACCATGTTT
Oke_Moesin-160	X	T	G	TTTCAGCAAATGAAGAGAACATCAAACTG	GGGTTTCCAAACAAAGATGTCCTT
Oke_nc2b-148	X	A	C	CCAGCCTATTTCCTTTAGTGCATATGA	GCACCCTATTCCCTACATGGT
Oke_ND3-69	X	G	A	TGGTATTGAATTTGTCGTAGAAGGCAAA	CCACGGCCTACACGTAATCATC
Oke_ndub3-58		C	T	GAGGCTTCAGTCGTCCTGTATC	CAGCGAAGCCCCATTTAAAGC
Oke_NHERF-		G	T	AGGAGTGAGGGCGAGAGAA	GGAACGAACTCTTCAGTAACCT
Oke_NHERF-54		G	A	CCCTCAATTAGCACATGAAAATCACA	CTCCTTCTTTTGCTCTCTCTCTCAA
Oke_NUPR1-70	X	G	T	AGACGGTGAACTCTGCTGTAGA	TCCCTTCACTGAAGCTACAGTCA
Oke_PDIA3-475		A	G	CCCGGTTCCTCCAGTAGTTG	CTGGTGGCCTACTACGATGTG
Oke_PDIA3-82		A	C	TGCCTACGATGGACCCAGAA	ACTCAGCCCATCAGGACAAGA
Oke_pgap-111	X	C	T	TGCAGATCTCAATTTGAACGACCTAT	AGACGACCATTATGGCTAACGTT
Oke_pgap-92	X	C	G	TGCAGATCTCAATTTGAACGACCTAT	AGACGACCATTATGGCTAACGTT
Oke_pnrc2-78		G	A	CGTGACAGCAGGGAGATGA	CATCTCTAGGCATGCACCTTGA
Oke_PPA2-635	X	C	T	ACACAACTGACCATATTGACTTTCGA	TGGATAAAGATCTATATGGTGAATAAGGTC
Oke_psmd9-188		C	T	ACTGAGGCAATATTCTGCAGGTT	GGGCTTGCGAATTAGTGATGAAATC
Oke_psmd9-57	X	C	T	ACTGTAGTGACTGCATTTCATATTGCT	ACCAGTTGTATTTTATTGTGCCAAATGAC
Oke_rab5a-117	X	C	T	GGGAATAACAGTCATTGCAGCATTT	CCATTGTTGGAAACTGGACAGC
Oke_ras1-249	X	T	G	GGATGACTAAGAGCGACTGTATGTG	AATTTTATGACTGCTTGAAGATTGAGTGC

-continued-

Table 2. Page 4 of 7.

Assay name	Included in final set	VIC	FAM	Forward Primer Sequence	Reverse Primer Sequence
Oke_RFC2-618	X	G	A	GACAATGTGTTAGTGTAGGCTTCACT	ACACTGGAATACTTAAGTGCACAACA
Oke_RH1op-245	X	C	T	TGGCCGATCTCTTCATGGTAATC	TCCAAAGACGAAATAGCCATGCA
Oke_ROA1-209		A	G	CAGGGTTTGATTGGTTAACTTACATTGAAT	GCTGGATCTCTCATTACCTGTAGGT
Oke_RPN1-80		A	G	CACGCACCTTGCTAAGATAACAG	GGCTCTACCGCCAAGATAAAGTTAT
Oke_RS27-81	X	G	A	GCAACAAAGTGGACTATCACATTGAA	GCACCCAAGAAAGATTGATCCAGAA
Oke_RS27-94		G	A	CACTTCTAGATCAATCCGCTGTTTC	GCGACTCCAGCCTTGACA
Oke_RS9-379		A	T	GCAATCCTCCATACATTACCTGTCA	GTCTATAAGACTGCCCAGAACCAA
Oke_RSPRY1-	X	A	T	GTCCTCCCTATTCTTCCACTTACCT	GCAAAGAAGCCAGACCTGAGAAA
Oke_serpin-140	X	A	T	TCCACAGTGAGTAATAAAGTTGCACAT	GAGCAAAGACCTAGGCCTGAAG
Oke_slc1a3a-86	X	C	T	TGTCTTCATCTGTGGACTCCTACA	TCACCATGACAACTCACCTAGATGA
Oke_sylc-90	X	A	T	TTGAGGAAACCACTGGTCTTACAAG	GCATCCTTCCTACCTTCCTTGAG
Oke_TCP1-78	X	A	G	CTCCAGGGCATCAGCAAATG	TGCTCATTACCACCATCTCTCTCT
Oke_TCTA-202		A	C	AGTTTAGCACTTACCTTGTCGGT	CAGTCTCATTGCCATCCATTTCG
Oke_TCTA-99		C	G	GCTAGCACTTCATGGCAGCAT	GCCACCATCATCACGTTTAGTTCTA
Oke_Tf-278	X	C	A	GCCACAATTGTAATTCTAGATCCAGAGT	ACTGTACCTGGTGAGTTTTTAAAGCA
Oke_thic-84	X	C	T	GCTGCTGTCTTAAACCACATTCTACA	GCCTTCCTATTTGTCCTGTTCTCT
Oke_txnrd1-74		A	G	CACCCCATGTGCCTTTGGA	GACGTCCTGGCCCTTAACC
Oke_u0602-244		G	T	CAAGTATGCATGACTAGCTATGTGTATATCTT	TCTGCTATTGGTGGCCTATGTG
Oke_U1001-79		A	G	GACAGTCAAAGGATCAAGCTACCT	GCAGATATGCCTCAGGGATGT
Oke_U1002-165		C	G	GATTATTGGATCGAGAGAGTTAGAAGAGAGA	TCCTGCTGGAGCACATGTTC
Oke_U1002-262	X	G	T	CCTAGACCACTCCAGACTGTTG	GCTGTGAACTCAGAATTGCTGTGTA
Oke_U1008-83	X	A	G	GTCACCAAACATCCTGCGAATG	ACTGTAAAACAAATACAGAAGCTCACTCA
Oke_U1010-154		A	G	TCCCATGGCCCTTACTCTATCAATA	GGCTTTATAAATACATTTGATTGATTGAGG
Oke_U1010-251	X	A	G	CACCTCAATCAATCAAATGTATTTATAAAGC	ATCGTTGGGCCTAAACAAGGT
Oke_U1012-241	X	A	G	GCAGAGGTTATACCCATTTTAGATGCA	GTTGGCAGTCACGAACATTTGTTAT
Oke_U1012-60		A	G	TGTACTCCTCTGCTTGGCTGTATAT	GGTAACCTGCTTGCCAACAG
Oke_U1015-255	X	A	G	CAGAGTGCAGAGTAATACGCATACA	ACTCTGTCATCCTCACCAAGGTAA

-continued-

Table 2. Page 5 of 7.

Assay name	Included in final set	VIC	FAM	Forward Primer Sequence	Reverse Primer Sequence
Oke_U1016-154	X	C	T	GCAGGTTGCTAAGTCATGTTACACA	ACGATAGGCACTAGGCAACATAAAG
Oke_U1017-52	X	C	T	TGGCAATGGGATGTCAAGTTATGA	CCAAGGAGTCCATGGTAATAAGCAA
Oke_U1018-50	X	C	T	TCCAGGTTGCTGACAATGTAAAAGT	TGTGTTGCACAATATCCACTACTTTGA
Oke_U1019-218		C	T	GCAGTCACACATTTTCTTCATCACA	TTCCTACAGAGGCAGATGCTAGT
Oke_U1020-75		C	G	GCCAATCGCGGAAGTCTCA	GTTCACAAACGGCACAACAGTAC
Oke_U1021-102	X	G	T	TCGAGGATTTGAGGATTAGGCTACT	AGCAAAATCACTAAGTCTCTCGTGTT
Oke_U1022-114		A	G	GGAGTACTGCAATTGTCGCTTTTTAA	CAGTCCACCACGTGTTTGTG
Oke_U1022-139	X	A	G	AACATTAAAACTGTGGTTTTGACCTCTTG	CAGTCCACCACGTGTTTGTG
Oke_U1023-147	X	A	C	TCTTAAAATGGAGAGAGCGATTAATGAAGG	GGCTTCAGTTGACCATGTACTCATA
Oke_U1024-113	X	A	G	CATGCTGGTGAATTATTGGACAATGT	CTGCTACATATGAAACTAGAGAACACACT
Oke_U1025-135	X	G	T	GGCTAGGGTTCTATTTGGACCAT	CAGTAGTGTTCTGTCCTGTAGTTCAA
Oke_U1027-89		A	G	GCTCTGAAAAATATCTGACGTGATTGG	ATCTAGGGTCAGCCATCAGGAA
Oke_U1028-100		A	C	CCTACTATTTCAGAGGCTTGACACA	CCCTCCAAGTCCCCAGTCA
Oke_U1031-132		C	T	ACTAGAGCAGGCTTTTCTGTTTAGC	CGGTTATGCCTTAAATCTTTACCCATAAAT
Oke_U1103-150		C	A	ACCTCTCGACTTATTCCAAATTTTGTTACA	ĜĜT̂ÂTTGTGTGTAGTGGTTAAAGGG
Oke_u1-519		A	T	AGGTTTGTATGCGGCTGCTT	CAACTCAGCACAAGAACTGTTCAC
Oke_U2001-629		C	T	CCCCACTCCTTCTACTCATCCAT	TTAGTACAAATGAACGAGGGTTGGAA
Oke_U2002-200		A	C	CCAGTGTTGTAGAAAACATGTGCTCTA	GCGCTTACGCTTCAATTTGCA
Oke_U2003-142		C	T	CTCCTCACTAACAGTAGCTGCAATT	CCTTGAAAGTGAGATATCTGTAGTTCGT
Oke_u200-385	X	G	T	CCCATAATTTTGCAACCCTAGTCACA	CCTTTCCCCATATCCTGTCACTTTT
Oke_U2005-62		A	G	GTACAGCAGAGACTAAAGCTATACAACA	GAGGTCAAGGCTTCAACATCAC
Oke_U2006-109	X	G	T	CCAACACCACTTTCCATTAATAAGCA	GCACACCCTAATTGACAAACAAACC
Oke_U2007-190	X	C	G	ACAGGCTGTGATGAGTTAACAATGTAAA	CATGTCGTCTACTTTGATGCCAATT
Oke_U2010-94		C	T	CCGCAGACAGTGGTCAATACT	GCCCTTCTCTTTCTCCATACTTTTCT
Oke_U2011-107	X	G	T	CCGTTTCTGTCAGACTCTGGTAAA	CTGGAGTGACTCAGGATCATAGC
Oke_U2015-151	X	C	T	GCATTTTATCCTCAAACTTTTCAACTGACA	ACGAATCCACCTAAAATCCACCAAA
Oke_U2016-118		C	T	ACGTGTCCTGTTCAAATTAGCAGTA	GAGGTGCATGCTTTTGTTCCA

-continued-

Table 2. Page 6 of 7.

Assay name	Included in final set	VIC	FAM	Forward Primer Sequence	Reverse Primer Sequence
Oke_U2017-87		A	C	CAGGAGCCATTGGAAGAGTAGAG	CCATGATTTGAAAAGAGCTGAACCAT
Oke_U2019-112		A	C	GAATTTGACTGCCTGGCGAAAG	CGTACTGCTGATCCCAAATGATTTT
Oke_u202-131		C	T	GCTCTGGTCCAGGTCGTT	ACGTTCTTCGCCTCATGTTACATTA
Oke_u202-131		A	C	GCTATGACACTGCACTTTTGACTTT	GCAATTAGCTGCTAAGCACTAGCT
Oke_U2021-86		A	C	TGTGGCTCCAGCCAAAGTT	GCATCCTCAGTTCCAGCATAATGAT
Oke_U2022-101		G	C	TGTCCTAATGACAGGCCTTGC	GTCACTGCAGCCTAACGTTATATTG
Oke_U2023-99		C	T	CACTATTTTGACAAGTGTTAAGATCATTTTGTCT	TGTGATCAACAGTTTTACACTCAATGGA
Oke_U2024-93		C	T	CGTCTTTCCAATACCACAGAGATACA	GAAGTGTTGACCTCTGCTCCTT
Oke_U2025-86	X	A	G	AAATCCCCATGGAGAAACACAATGA	ATTGTCCTTCCGCAGTGGT
Oke_U2026-64		G	T	CTTCCCACGTCTTTTCTGTCTCA	GCCTCTCACGTTACACTGTCATTTT
Oke_U2029-79	X	C	T	GGTTTGATTTCGTCGCGATTTGA	AAATCCCAGGGAGCGAAAGTC
Oke_U2031-37	X	A	T	CACACTTTCAATCAAATGTTGTGCAG	CGTTTGAGACGCCCTTCACT
Oke_U2032-74	X	G	A	GCTATTCCAATGTAAATCCTGTACTGTGT	AACCCTATCTGCTCATTGGTCATG
Oke_U2033-122		G	T	ACGCCCTTCCCCGATTC	GGCCTGGGTATGACTCAACATG
Oke_U2034-55	X	C	T	GGGAAGAAAAGCCTACCATAAACAG	CCCAGAGCGAATGCCAACA
Oke_U2035-54	X	G	A	CGCCAATAACGCTCCAACAAC	CTTCACACCCTGAGAACTGGTTTTA
Oke_U2037-76	X	C	G	CATATCAGGTGTGTCTCAACAGTCT	GGCATTCACTACATCACATGACCTT
Oke_U2038-32		C	T	CGACTTCCTGGCGTCATCTTC	GGGTACTTTCATACAGTACAGCTCT
Oke_U2040-77		A	C	GGGCTAGAATTCTACTTGGTGACA	CCTTCCACAGTCTCATTTTGCTCTT
Oke_U2041-84	X	G	T	CCAGACCATGTGCTTGTTTGTCATA	GTGAATATTTTGGCAAGCCTGTACA
Oke_U2042-61		C	T	GCAATGCACATCTGAAATCTGCTAT	ACTCATTTTCAGATGTTCTTCCTTTGTCT
Oke_U2043-51	X	G	A	CACAAACCTACTACAGACAGCAGTT	GCCAGCTTTGTAGTCTTGTGGAAA
Oke_U2045-43		G	A	GACCCCGGGTCACCAC	CCAGGTGTGGCAGTGGAT
Oke_U2047-49		G	A	TTAGCTAGTATGTTAGCGTAGCACTT	TGCTGAATTTGAGGAACTAAACGTTAGT
Oke_U2048-91	X	A	C	AGTTGGGTCTTAAAGATGATCATTTGCT	GGACTCTTGACGGCCATCTTA
Oke_U2049-99		C	T	CATTGTAGCAGAGGGTCAACGATAT	ACACACGGCATTGCAAACTC
Oke_U2050-101	X	C	T	CTCTGAGTGTCACAATCACATATCGT	GTGTAAACGCATTCGAAGTCCTTT

-continued-

Table 2. Page 7 of 7.

Assay name	Included in final set	VIC	FAM	Forward Primer Sequence	Reverse Primer Sequence
Oke_U2052-56		C	T	GTGCCATGTTAGCCAAAAAGTTTCA	TCCATGTTAGCAGCGAACGTT
Oke_U2053-60	X	C	T	TCTGCTTTTGTCGTCTCACCAA	CACACGAGGGTGGACTTAGTT
Oke_U2054-58	X	C	T	CGTCTCATTCAGCTCTTTGATGTC	TTGGTTCAAGATGACACTGGTGT
Oke_U2056-90	X	G	T	CCATCACGTCACCATTACACTGT	GACATTAGCTGGCAGTCTGATCA
Oke_U2057-80	X	A	G	GCAGTTGTCATGGCAGTAAGG	GCCCCTCGTTCATTTTCAGATG
Oke_U212-87	X	C	A	TTGATTCATACTCAAGGTGAGCAGATT	GCTGGTGGCCCTTGTGA
Oke_u216-222		G	A	CGCAATATTAAGTGCGTCATACTTGT	CCCAGATGTTATTGTTTAAACTAGAGAATG C
Oke_u217-172	X	T	C	GGATGGAAGAAGTTAGTTGTGTCAGA	CAAGTGGCAAAGTTTAAGAGTATAAAAAC CTAA
Oke_U302-195	X	C	A	GACCCTCAGCTATTTTAAGAACCTCAA	ACCTACCTCCTGCCAAGTTTTAAAC
Oke_U401-143		T	A	GCACTGGAAAGCACTCATCCTT	GCAGTCAGACACCATGCAAAA
Oke_U401-220		G	A	TGACTGCATTCACTACTGACAAAGT	TGCAGCAAATGCTTGAGACTTACT
Oke_U502-241	X	G	A	ATGATCATTACACAGATGCACCTTGT	GCCAATTACACACTCACTCACAACT
Oke_U503-272		C	T	GCAGAGAGAGGTCTGAATGAAACAG	CACGTCCTTTATCTTGCCTCTGTAT
Oke_U504-228	X	A	G	CTTAACTCAGTCACACCAACTCACT	GTGAGTTACAATGAGCTGCATGAG
Oke_U505-112		T	G	GAATACAGCATTGTGGGTAA	CTCAGTTGGTGCAGTAGGA
Oke_U506-110	X	C	T	CGTGGTTGGTTTCATTGACTCTCA	CGTTTCTCAAGATGTTCCTCTCCAA
Oke_U507-286	X	T	G	TGGTCATAGCTTGCACTGTACAAA	CCTAACTGTTCTTGCCCATATAGTGAA
Oke_U507-87		G	T	GAAGACTGGACACACACGATATGT	GGCTGAGGCCATTCTATTCCC
Oke_U509-219	X	C	T	GCACCCCACCTGGCTT	TCACTCACTCTGCGTCTCTCT
Oke_U510-204		G	T	GCTCCCTGGACGGGTATATATG	CATCCGCCAATACTTCCTCGTA
Oke_U511-271		T	A	GACACAACGTTTTGGGACATTCAG	CGATGAGAAGGTGTCCACATACTTT
Oke_U514-150		C	T	GCATCATTAGTAAGGCGTCATTGG	GGCCAAGGATTATAGAGACAACACT
Oke_UBA3-245		C	T	GAGAGGTGATAAGACAATGAGAAGTGTTA	GCGTTGAGTATGTCAGAATGCTACA
Oke_uqcrfs-69		C	G	CGCTGCTCTCCTGAGAAGATTTC	GCAGTCCGATTCGCTCACA
Oke_XBP1-82		C	T	TCTGCTCCGGAGTCTTCTGTAT	AAGGAGAGTGTTTAACAAAATTATACAGG ATCT
Oke_zn593-152		A	C	GTTTTGAAAAGTTATTTCTCGCGTAGATTAAG A	AACTAGCTAGTTATCTAGTAGTAGCTAAAT TAGCT

Table 3.–Overall *P*-values and number of populations that failed to conform to Hardy-Weinberg expectations (HWE) for 188 SNP assays screened for 29 populations (Table 1; excluding Chilkat River – 24-Mile Creek which was removed due to evidence of a Wahlund effect; α = 0.05).

Assay	Overall *P*-value	# of populations out of HWE at α =0.05
Oke ACOT-100	0.9981	0
Oke_AhR1-278	1.0000	1
Oke_AhR1-78	0.5936	1
Oke_APOB-60	0.9875	0
Oke_arf-319	0.8778	1
Oke_ATP5L-105	0.6802	1
Oke_ATP5L-248	0.6918	0
Oke_azin1-90	0.5763	3
Oke_brd2-118	0.8405	1
Oke_brp16-65	0.8567	1
Oke_CATB-60	0.9919	2
Oke_ccd16-77	0.0619	4
Oke_CD123-62	0.5147	1
Oke_CD81-108	0.9992	1
Oke_CD81-173	0.4379	3
Oke_cjo57-86	0.3294	4
Oke_CKS1-70	0.5925	3
Oke_CKS1-94	0.5160	2
Oke_CKS-389	0.9909	0
Oke_CO1A1-72	0.5492	2
Oke_CO1A1-76	1.0000	0
Oke_col1a2-62	0.5174	2
Oke_ctgf-105	0.9972	1
Oke_CTR2-82	0.3413	3
Oke_DBLOH-79	0.9599	0
Oke_DCXR-87	0.9998	0
Oke_DM20-548	0.5432	2
Oke_e2ig5-50	0.0790	2
Oke_EF2-394	1.0000	1
Oke_eif4ebp2-64	1.0000	0
Oke_eif4g1-43	0.9958	0
Oke_f5-71	0.3646	2
Oke_FANK1-166	0.9980	0
Oke_FANK1-96	0.9962	1
Oke_FBXL5-61	0.9270	1
Oke_gdh1-191	0.8487	1
Oke_gdh1-234	0.4138	3
Oke_gdh1-62	0.0309	4

-continued-

Table 3. Page 2 of 5.

Assay	Overall *P*-value	# of populations out of HWE at α =0.05
Oke_GHII-3129	0.2241	3
Oke_glrx1-78	0.8752	1
Oke_GNMT-100	0.9053	0
Oke_GnRH-373	0.2854	2
Oke_GPDH-191	0.9496	1
Oke_GPH-105	0.8992	1
Oke_GPH-78	0.3047	4
Oke_H2AX-72	0.8694	1
Oke_hmgb1-66	0.5620	3
Oke_hnRNPL-239	1.0000	0
Oke_HP-182	0.9790	2
Oke_hsc71-199	1.0000	1
Oke_HSP90BA-299	1.0000	1
Oke_il-1racp-67	0.9493	1
Oke_IL8r2-406	1.0000	0
Oke_IL8r-272	0.7479	1
Oke_KPNA2-87	0.9916	1
Oke_lactb2-71	0.8141	1
Oke_lamp2-138	1.0000	0
Oke_LAMP2-186	0.9869	0
Oke_mcfd2-86	0.8576	0
Oke_METK2-97	0.9620	1
Oke_mgll-49	0.5136	0
Oke_MLRN-63	0.9898	0
Oke_Moesin-160	0.9957	1
Oke_nc2b-148	0.9153	1
Oke_ndub3-58	0.2729	3
Oke_NHERF-123	0.8726	0
Oke_NHERF-54	0.8959	0
Oke_NUPR1-70	0.7919	3
Oke_PDIA3-475	0.5841	0
Oke_PDIA3-82	0.9712	0
Oke_pgap-111	0.2488	1
Oke_pgap-92	0.5462	1
Oke_pnrc2-78	0.7158	2
Oke_PPA2-635	0.9488	0
Oke_psmd9-188	0.5337	2
Oke_psmd9-57	0.8052	2
Oke_rab5a-117	0.9200	3
Oke_ras1-249	0.9953	0

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Table 3. Page 3 of 5.

Assay	Overall *P*-value	# of populations out of HWE at α =0.05
Oke_RFC2-618	1.0000	0
Oke_RH1op-245	0.9708	4
Oke_ROA1-209	0.4019	2
Oke_RPN1-80	0.6250	2
Oke_RS27-81	0.4124	1
Oke_RS27-94[a]	0.0000	8
Oke_RS9-379	0.0212	5
Oke_RSPRY1-106	0.7958	1
Oke_serpin-140	0.9192	1
Oke_slc1a3a-86	0.8389	0
Oke_sylc-90	0.4604	2
Oke_TCP1-78	0.9739	1
Oke_TCTA-202	0.6765	2
Oke_TCTA-99	0.9442	1
Oke_Tf-278	0.9338	0
Oke_thic-84	0.6852	1
Oke_txnrd1-74	0.8981	2
Oke_u0602-244	0.4252	1
Oke_U1001-79	0.9857	0
Oke_U1002-165	0.9786	1
Oke_U1002-262	0.9352	0
Oke_U1008-83	1.0000	1
Oke_U1010-154	1.0000	0
Oke_U1010-251	0.0414	3
Oke_U1012-241	0.9848	0
Oke_U1012-60	0.9883	0
Oke_U1015-255	0.9503	0
Oke_U1016-154	0.6140	0
Oke_U1017-52	0.7574	2
Oke_U1018-50	0.9612	0
Oke_U1019-218	0.9292	3
Oke_U1020-75	0.9900	0
Oke_U1021-102	0.5443	3
Oke_U1022-114	0.7127	0
Oke_U1022-139	0.6993	2
Oke_U1023-147	0.8875	1
Oke_U1024-113	0.9515	0
Oke_U1025-135	1.0000	1
Oke_U1027-89	0.5566	4
Oke_U1028-100	0.2772	3

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Table 3. Page 4 of 5.

Assay	Overall *P*-value	# of populations out of HWE at α =0.05
Oke_U1031-132	0.5473	2
Oke_U1103-150 [a]	0.0001	6
Oke_u1-519	0.8056	0
Oke_U2001-629	0.6696	1
Oke_U2002-200	0.8931	1
Oke_U2003-142	1.0000	1
Oke_u200-385	0.8790	2
Oke_U2005-62	0.9200	0
Oke_U2006-109	0.0582	2
Oke_U2007-190	0.7421	1
Oke_U2010-94	0.6136	0
Oke_U2011-107	0.8741	2
Oke_U2015-151	0.9998	0
Oke_U2016-118	0.5700	1
Oke_U2017-87	0.9985	1
Oke_U2019-112	0.6769	2
Oke_u2020-51	0.9338	2
Oke_u202-131	1.0000	1
Oke_U2021-86	0.3065	3
Oke_U2022-101	0.2853	2
Oke_U2023-99	0.9890	0
Oke_U2024-93	0.8776	1
Oke_U2025-86	0.9937	1
Oke_U2026-64	0.9520	0
Oke_U2029-79	0.5835	1
Oke_U2031-37	0.9884	0
Oke_U2032-74	0.9810	0
Oke_U2033-122	0.8152	2
Oke_U2034-55	0.6745	1
Oke_U2035-54	0.9256	2
Oke_U2037-76	0.9294	1
Oke_U2038-32 [a]	0.0001	7
Oke_U2040-77 [a]	0.0000	9
Oke_U2041-84	0.8063	2
Oke_U2042-61	0.9315	2
Oke_U2043-51	0.9686	0
Oke_U2045-43	0.1017	2
Oke_U2047-49	0.0473	3
Oke_U2048-91	0.5658	0
Oke_U2049-99	0.7893	0

-continued-

Table 3. Page 5 of 5.

Assay	Overall *P*-value	# of populations out of HWE at α =0.05
Oke_U2050-101	1.0000	1
Oke_U2052-56	0.4868	2
Oke_U2053-60	0.8569	0
Oke_U2054-58	0.9848	1
Oke_U2056-90	0.3998	1
Oke_U2057-80	0.9851	1
Oke_U212-87	1.0000	0
Oke_u216-222	0.9975	0
Oke_u217-172	0.4417	3
Oke_U302-195	0.0738	6
Oke_U401-143	1.0000	0
Oke_U401-220	0.3713	2
Oke_U502-241	0.9532	0
Oke_U503-272	0.9998	0
Oke_U504-228	0.8380	1
Oke_U505-112	0.1447	1
Oke_U506-110	0.8801	1
Oke_U507-286	0.4256	1
Oke_U507-87	0.1185	3
Oke_U509-219	0.1058	3
Oke_U510-204	0.9562	1
Oke_U511-271	1.0000	1
Oke_U514-150	1.0000	0
Oke_UBA3-245	0.6753	2
Oke_uqcrfs-69	1.0000	0
Oke_XBP1-82 [a]	0.0053	4
Oke_zn593-152	0.9398	0

[a] Markers out of HWE assessed across all populations (α=0.01) and excluded from further analyses.

Table 4.–Locus pairs (α=0.05) that are significantly associated in more than 50% of the populations, and their respective association blocks that were formed from grouped pairs. For each SNP block, the f_{ORCA} value for the single and composite SNP and the pair/single differences (Δ) are reported (see text for details). For combined SNP pairs that provided significantly more information than single SNPs as determined by the Δ_{90} (0.041), composite phenotype names are provided.

Association block	SNP pair	Locus name	f_{ORCA}	Δ	Composite name
1	*Oke_DBLOH-79 / Oke_u0602-244*	*Oke_DBLOH-79*[a]	0.116		
	Oke_DBLOH-79 / Oke_U1001-79	*Oke_u0602-244*	0.106		
	Oke_u0602-244 / Oke_U1001-79	*Oke_U1001-79*	0.095		
		Oke_DBLOH-79 /Oke_u0602-244	0.113	-0.003	
		Oke_DBLOH-79 /Oke_U1001-79	0.097	-0.019	
		Oke_u0602-244/Oke_U1001-79	0.136	0.030	
2	*Oke_U1021-102 / Oke_U1022-139*	*Oke_U1022-114*	0.088		
	Oke_U1022-114 / Oke_U1022-139	*Oke_U1022-139*	0.083		
		Oke_U1021-102	0.082		
		Oke_U1022-114 / Oke_U1022-139	0.129	0.041	
		Oke_U1021-102 / Oke_U1022-139[a]	0.131	0.048	*U102Comb*
3	*Oke_gdh1-191 / Oke_gdh1-62*	*Oke_gdh1-234*	0.085		
	Oke_gdh1-234 / Oke_gdh1-62	*Oke_gdh1-62*	0.104		
		Oke_gdh1-191	0.096		
		Oke_gdh1-234/Oke_gdh1-62	0.101	-0.003	
		Oke_gdh1-62/Oke_gdh1-191[a]	0.150	0.046	*gdhComb*
4	*Oke_U1002-165 / Oke_U1002-262*	*Oke_U1002-165*	0.068		
		Oke_U1002-262	0.108		
		Oke_U1002-165 / Oke_U1002-262	0.141	0.033	
5	*Oke_U1012-241 / Oke_U1012-60*	*Oke_U1012-241*[a]	0.087		
		Oke_U1012-60	0.076		
		Oke_U1012-241 / Oke_U1012-60	0.097	0.010	
6	*Oke_U507-286 / Oke_U507-87*	*Oke_U507-286*[a]	0.099		
		Oke_U507-87	0.072		
		Oke_U507-286 / Oke_U507-87	0.112	0.013	

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Table 4. Page 2 of 2.

Association block	SNP pair	Locus name	f_{ORCA}	Δ	Composite name
7	*Oke_U1010-251 / Oke_UBA3-245*	*Oke_U1010-251*[a]	0.083		
		Oke_UBA3-245	0.074		
		Oke_U1010-251 / Oke_UBA3-245	0.106	0.023	
8	*Oke_U401-143 / Oke_U401-220*	*Oke_U401-143*[a]	0.084		
		Oke_U401-220	0.076		
		Oke_U401-143 / Oke_U401-220	0.102	0.018	
9	*Oke_PDIA3-475 / Oke_PDIA3-82*	*Oke_PDIA3-475*[a]	0.091		
		Oke_PDIA3-82	0.087		
		Oke_PDIA3-475 / Oke_PDIA3-82	0.118	0.027	
10	*Oke_TCTA-202 / Oke_TCTA-99*	*Oke_TCTA-202*[a]	0.105		
		Oke_TCTA-99	0.086		
		Oke_TCTA-202 / Oke_TCTA-99	0.104	-0.001	
11	*Oke_ATP5L-105 / Oke_ATP5L-248*	*Oke_ATP5L-105*[a]	0.105		
		Oke_ATP5L-248	0.088		
		Oke_ATP5L-105 / Oke_ATP5L-248	0.112	0.007	
12	*Oke_NHERF-123 / Oke_NHERF-54*	*Oke_NHERF-123*	0.084		
		Oke_NHERF-54[a]	0.103		
		Oke_NHERF-123 / Oke_NHERF-54	0.139	0.036	
13	*Oke_psmd9-188 / Oke_psmd9-57*	*Oke_psmd9-188*	0.055		
		Oke_psmd9-57[a]	0.084		
		Oke_psmd9-188 / Oke_psmd9-57	0.097	0.013	
14	*Oke_pgap-111 / Oke_pgap-92*	*Oke_pgap-111*	0.071		
		Oke_pgap-92	0.084		
		Oke_pgap-111 / Oke_pgap-92[a]	0.125	0.041	*pgapComb*
15	*Oke_IL8r-272 / Oke_IL8r2-406*	*Oke_IL8r-272*	0.088		
		Oke_IL8r2-406[a]	0.101		
		Oke_IL8r-272 / Oke_IL8r2-406	0.102	0.001	

[a] This locus was retained for further analysis.

Table 5.–Estimated proportional contributions (Est), standard deviations (SD), and 90% confidence intervals by reporting group (CI) for simulation tests of allocation to correct regions.

Region	Est	SD	Lower 90% CI	Upper 90% CI
Japan	0.9994	0.0012	0.9975	1.0000
Russia	0.9965	0.0032	0.9903	1.0000
Kotzebue Sound	0.9541	0.0190	0.9205	0.9817
CWAK	0.9484	0.0310	0.8913	0.9860
Upper Yukon	0.9970	0.0031	0.9911	1.0000
Eastern Bristol Bay	0.8660	0.0908	0.6682	0.9479
North Alaska Peninsula	0.9933	0.0052	0.9837	0.9999
South Alaska Peninsula/Kodiak	0.9893	0.0072	0.9759	0.9989
Southcentral Alaska	0.9855	0.0089	0.9687	0.9973
Southeast Alaska / British Columbia	0.9917	0.0062	0.9798	0.9999
Washington	0.9950	0.0047	0.9858	1.0000

FIGURES

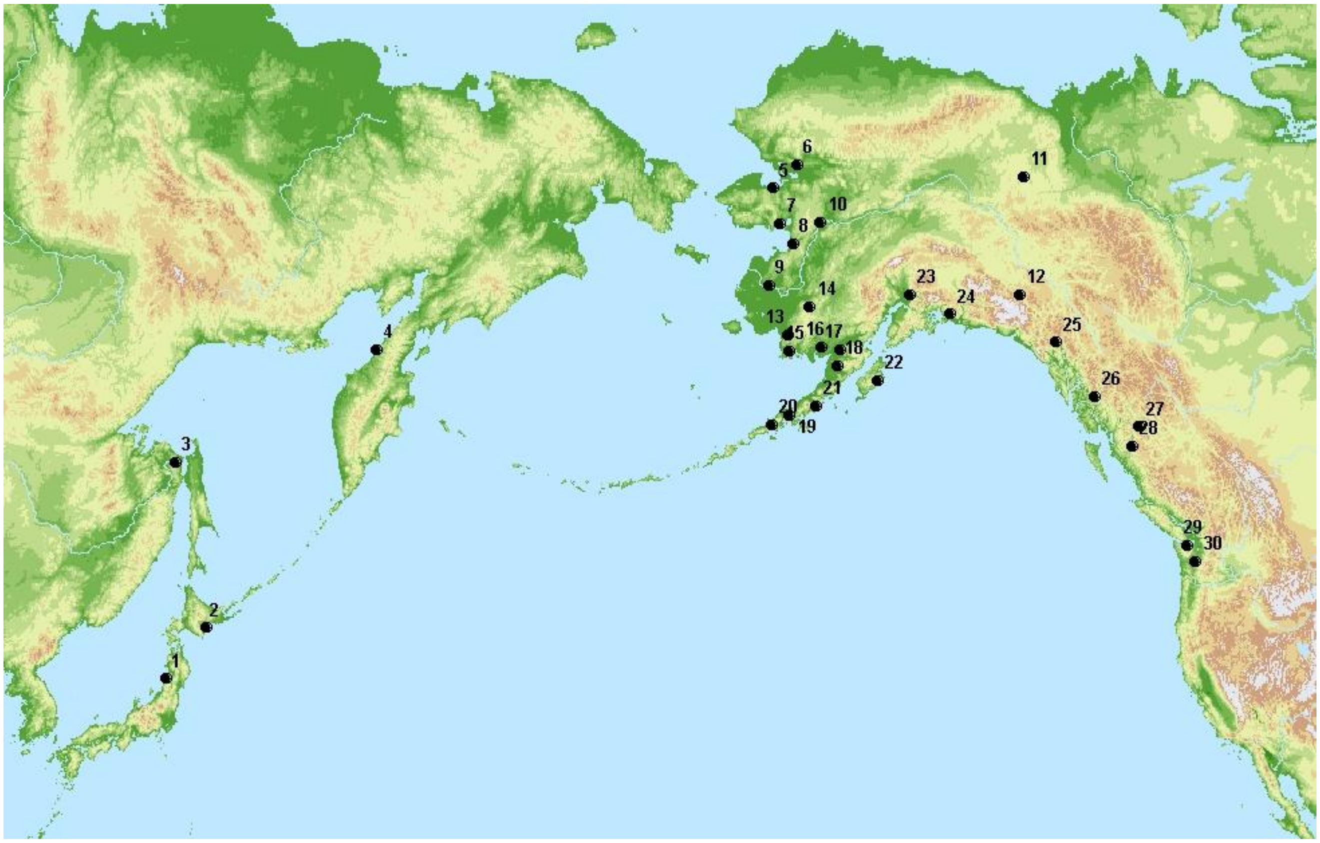


Figure 1.–Map of chum salmon populations used in the SNP-selection process. Map numbers correspond to populations in Table 1.

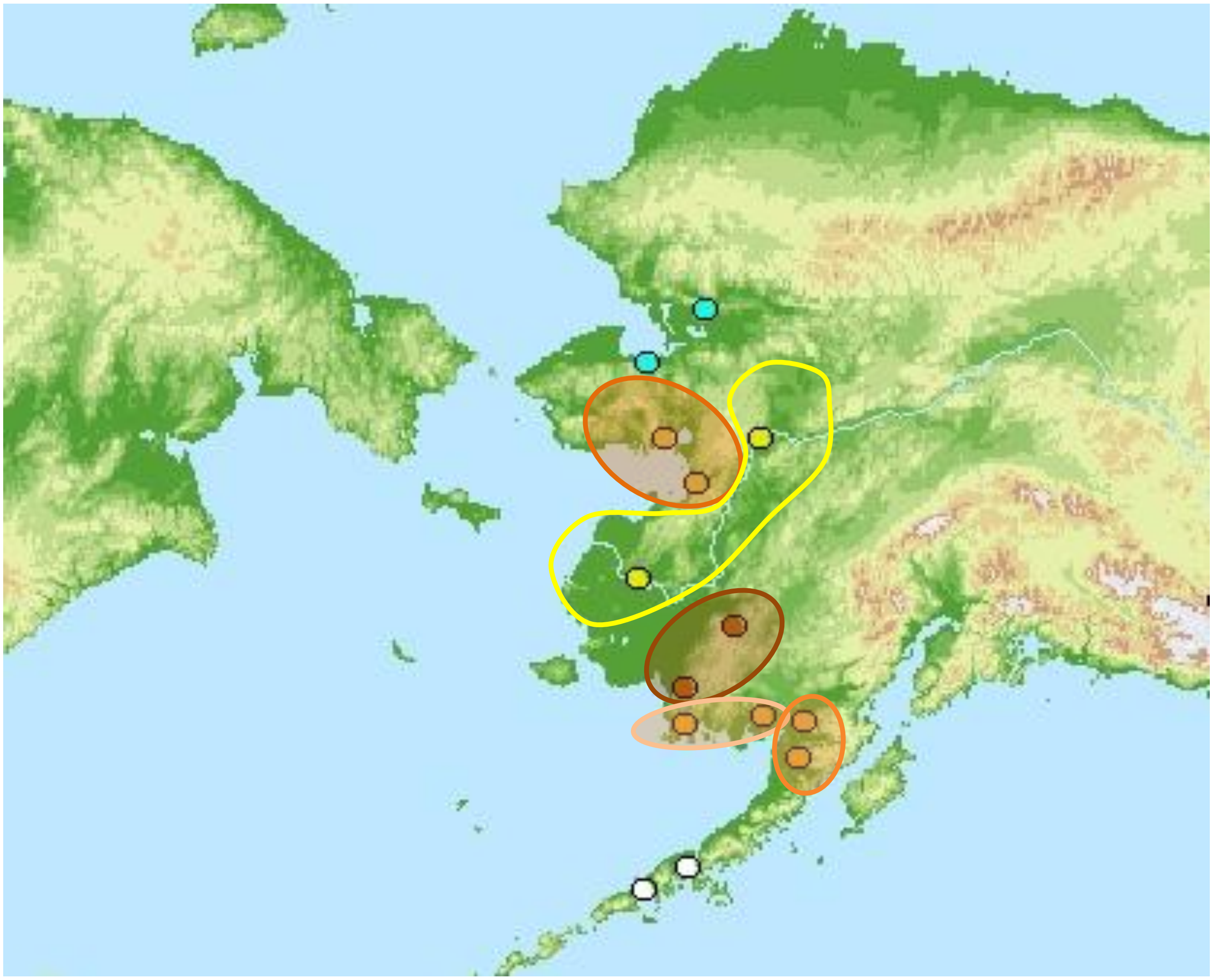


Figure 2.–Locations of chum salmon collections within Western Alaska. The 5 regional areas within Coastal Western Alaska to be measured using overall F_{ST} are indicated by the ellipses.

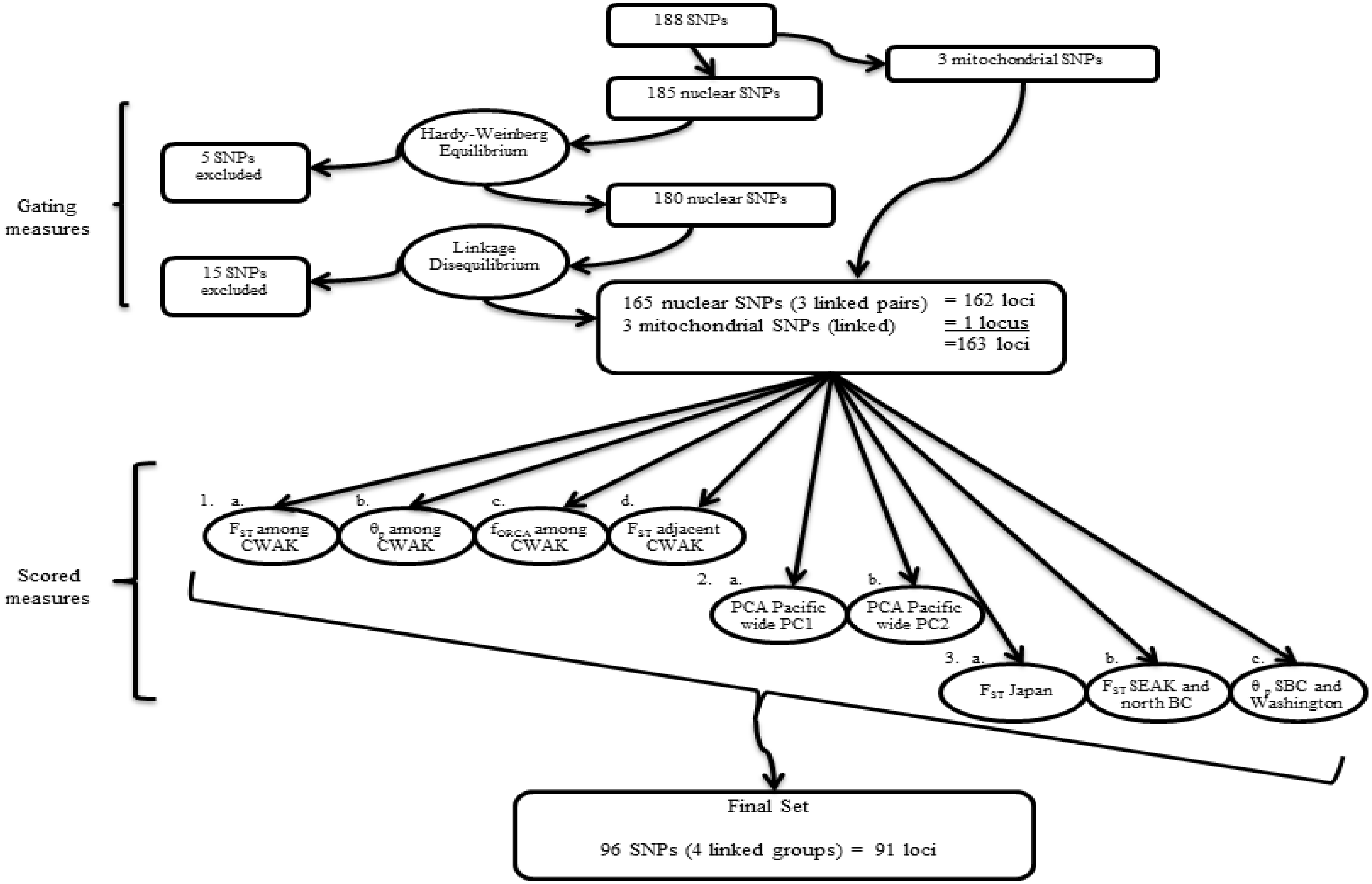


Figure 3.–Flow chart depicting the SNP-selection protocol; starting with 188 SNP markers at the top and ending with 91 loci at the end. Gating measures were used to eliminate markers from further evaluation and combine linked markers. Scored measures were divided into 3 categories: 1) measures to distinguish among Coastal Western Alaska (CWAK) regional areas and populations, 2) measures to distinguish among broad Pacific-coast regions, and 3) measures to distinguish among specific regions outside of CWAK. Weights for the scored measures are shown in Figure 4.

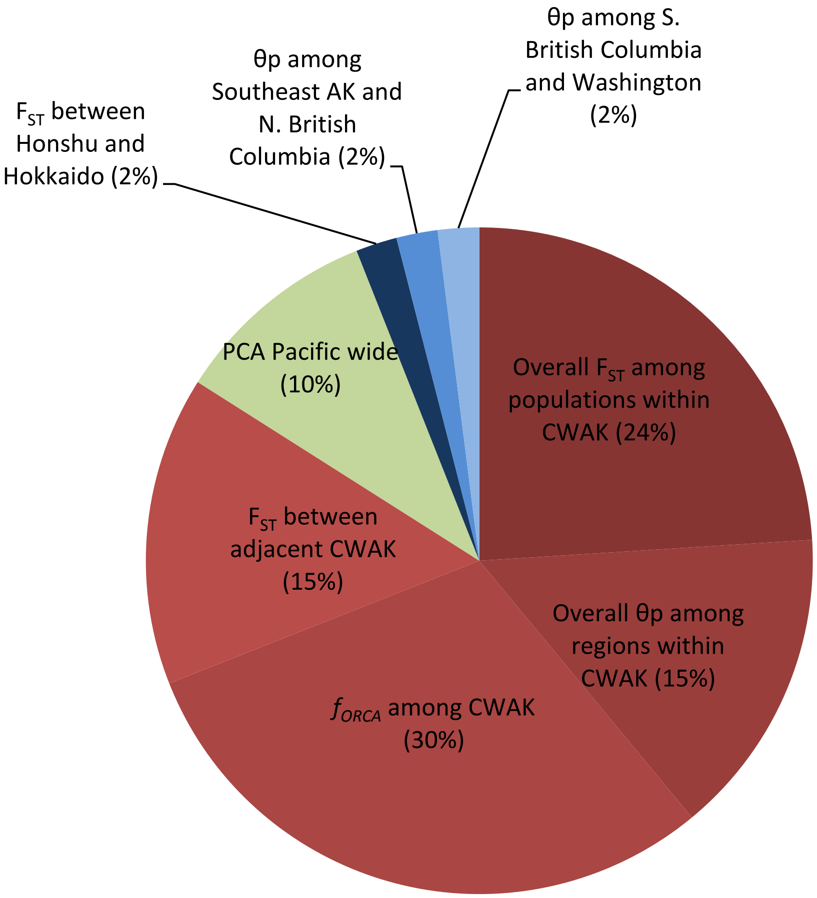


Figure 4.–Weights (in percent) given to scored measures of population structure and MSA performance.

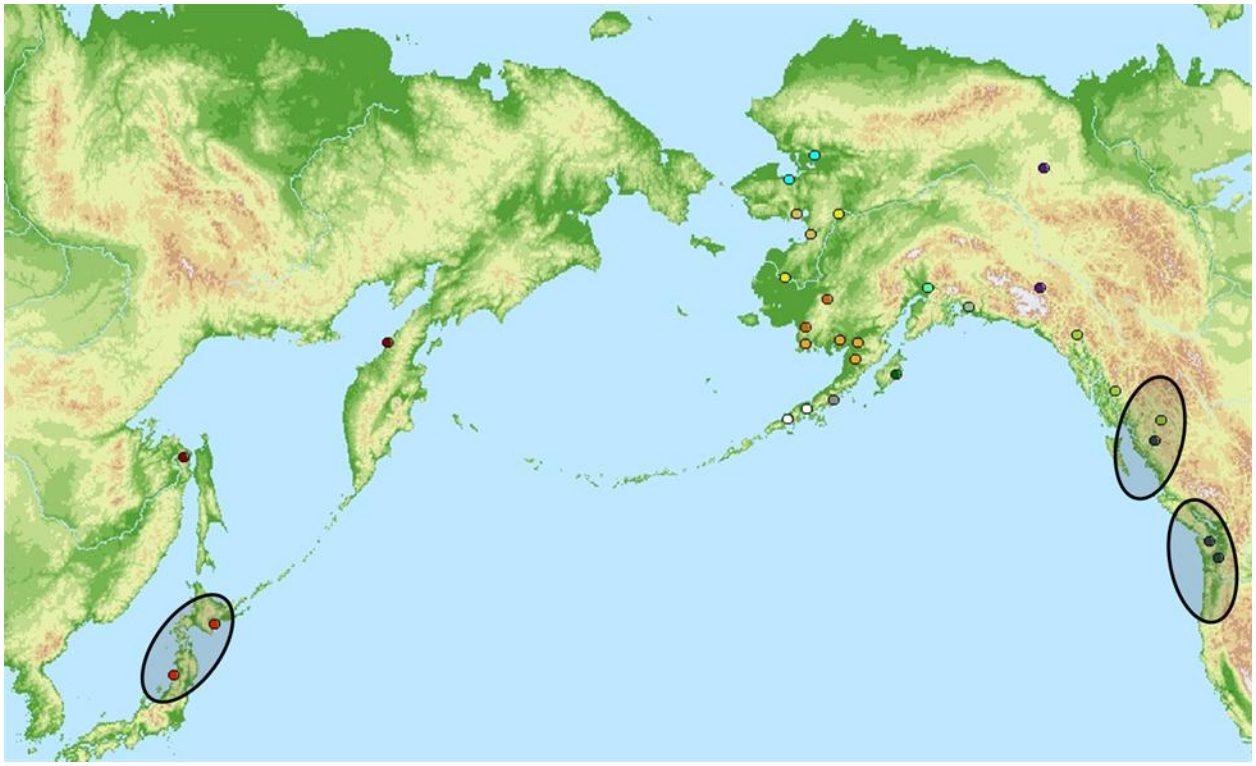
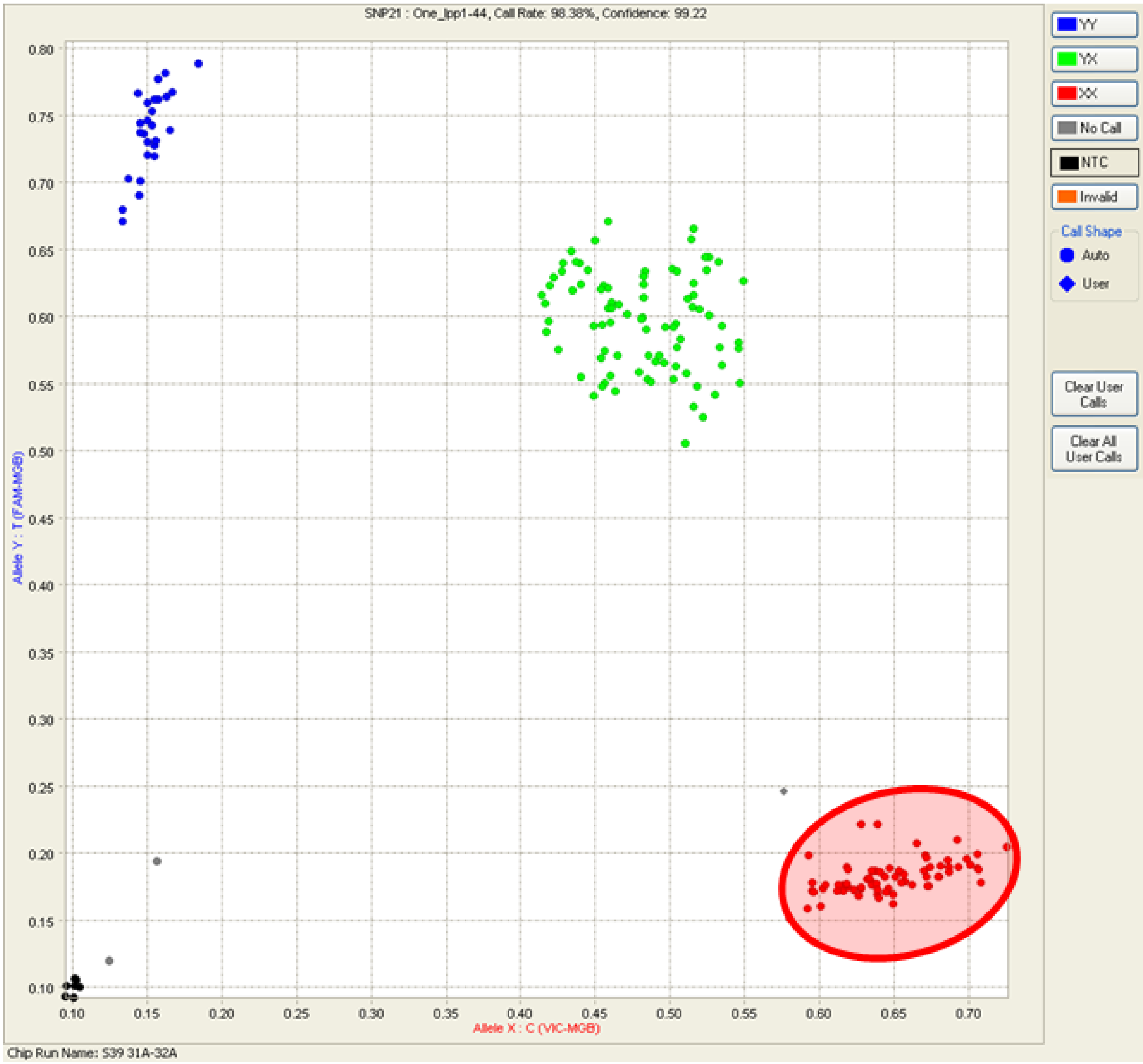


Figure 5.–Chum salmon populations used in SNP selection process highlighting the 3 population pairs (in ovals) of chum salmon chosen to measure F_{ST} within regions of interest to research groups outside of Alaska.



SNP21 : One_lpp1-44, Call Rate: 98.38%, Confidence: 99.22

Chip Run Name: S39 31A-32A

Figure 6.–Screen capture of a scatter plot from genotyping software. Each point represents a single fish. The 3 clusters represent each possible genotype (TT homozygote - blue, TC heterozygote - green, and CC homozygote - red). The size of the shaded area for the CC homozygote distribution is an indication of cluster tightness.

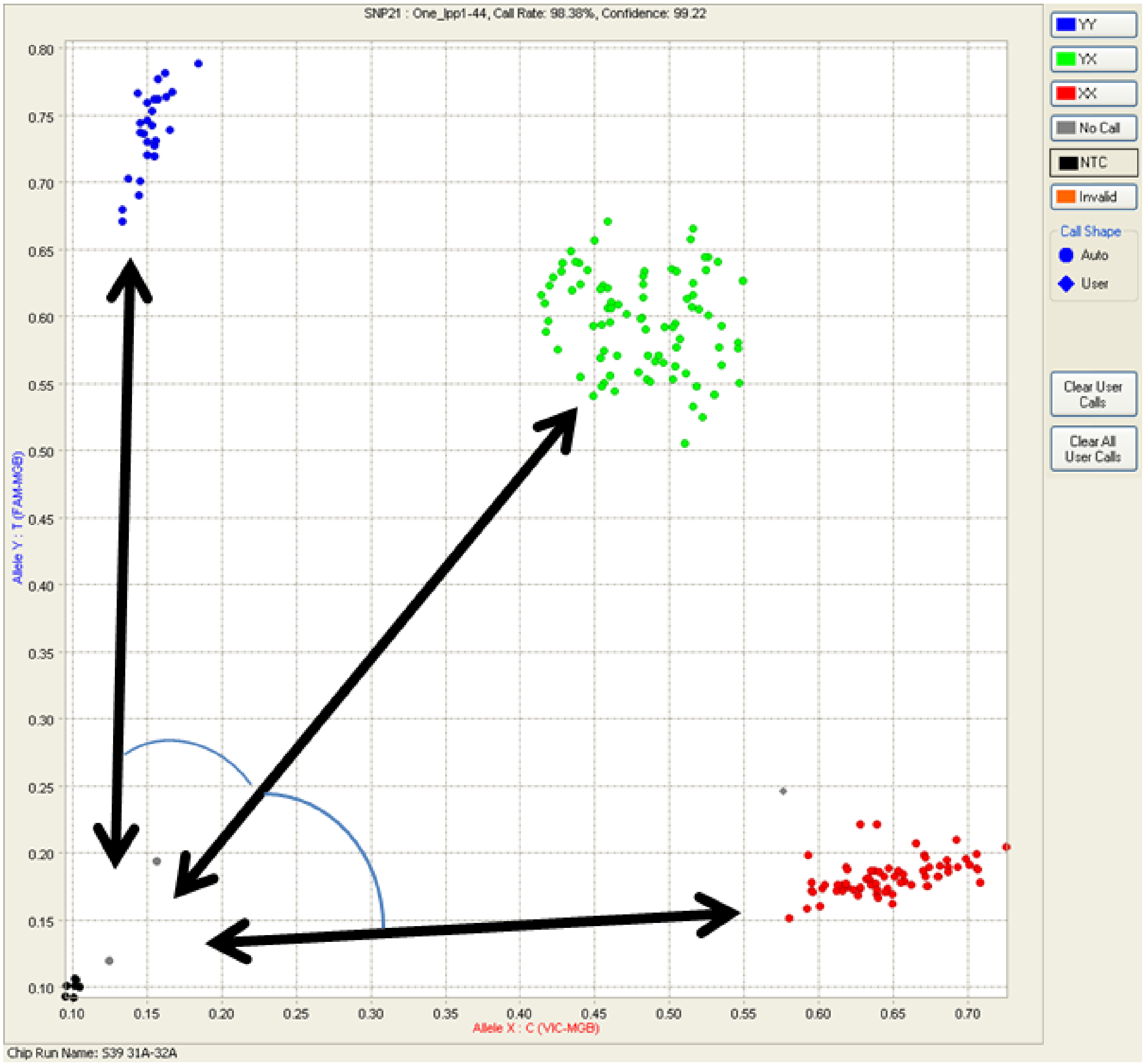


Figure 7.–Screen capture of a scatter plot from genotyping software. Each point represents a single fish. The 3 clusters represent each possible genotype (TT homozygote - blue, TC heterozygote - green, and CC homozygote - red). The angle between the double-ended arrows is an indication of cluster alignment.

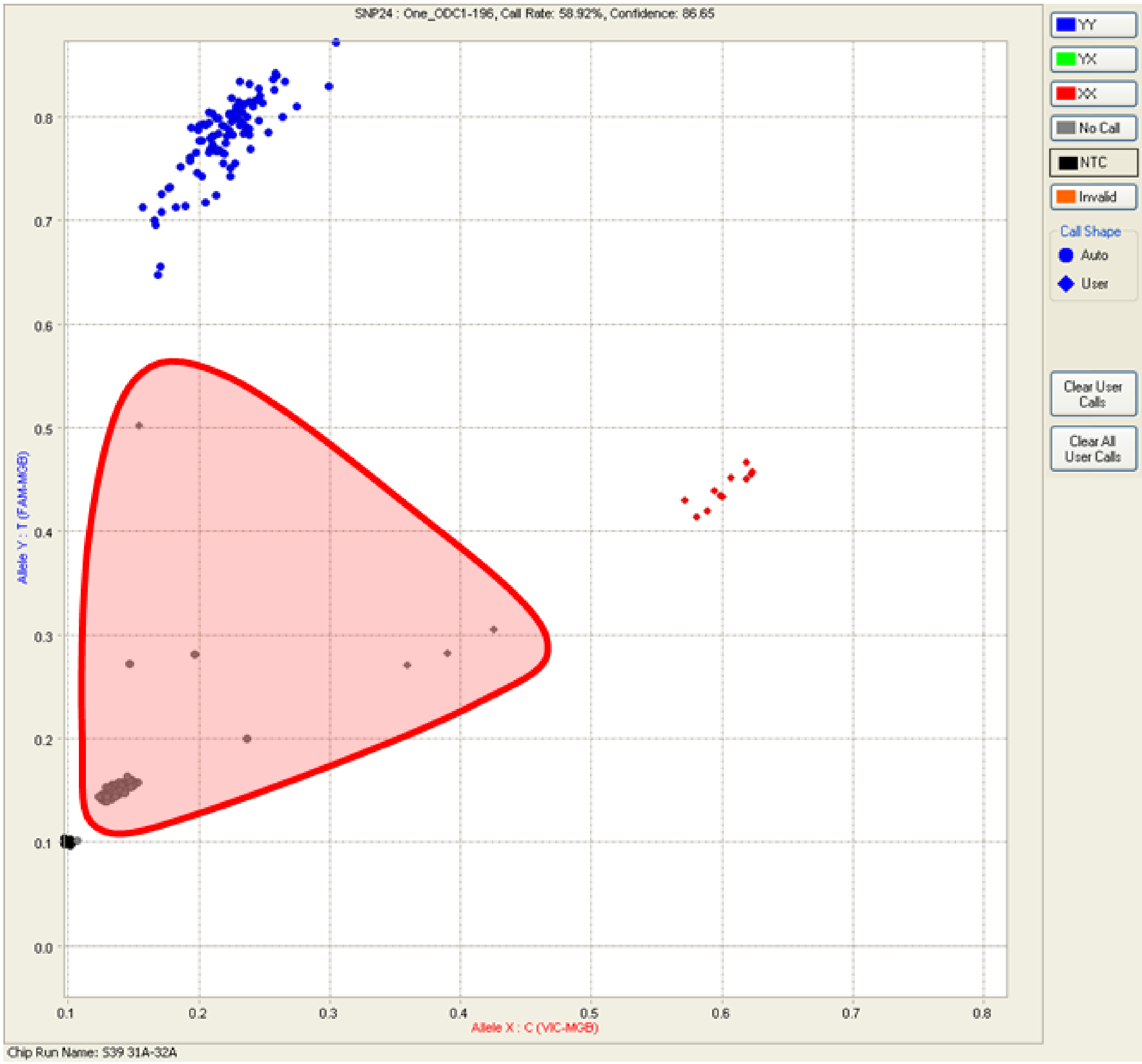


Figure 8.–Screen capture of a scatter plot from genotyping software. Each point represents a single fish. This is for a mitochondrial SNP marker with only 1 allele per fish. The 2 clusters represent each possible genotype (T - blue and C - red). The shaded area represents fish for which the assay failed.

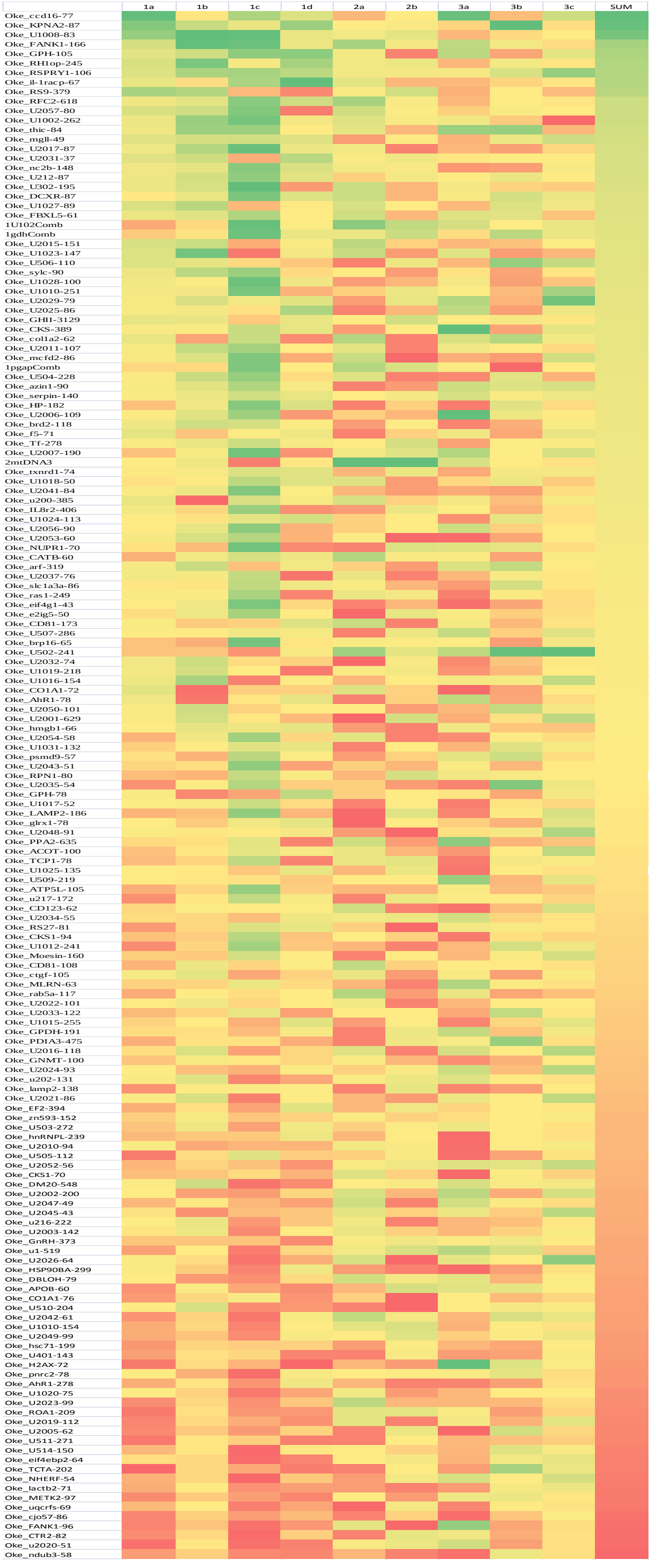


Figure 9.–Heat map depicting scoring of 163 SNP loci, green is the best scoring and red the worst. Loci are listed in overall ranked order (right column; most informative to least informative) based on weighted scored measures outlined in Figure 3.

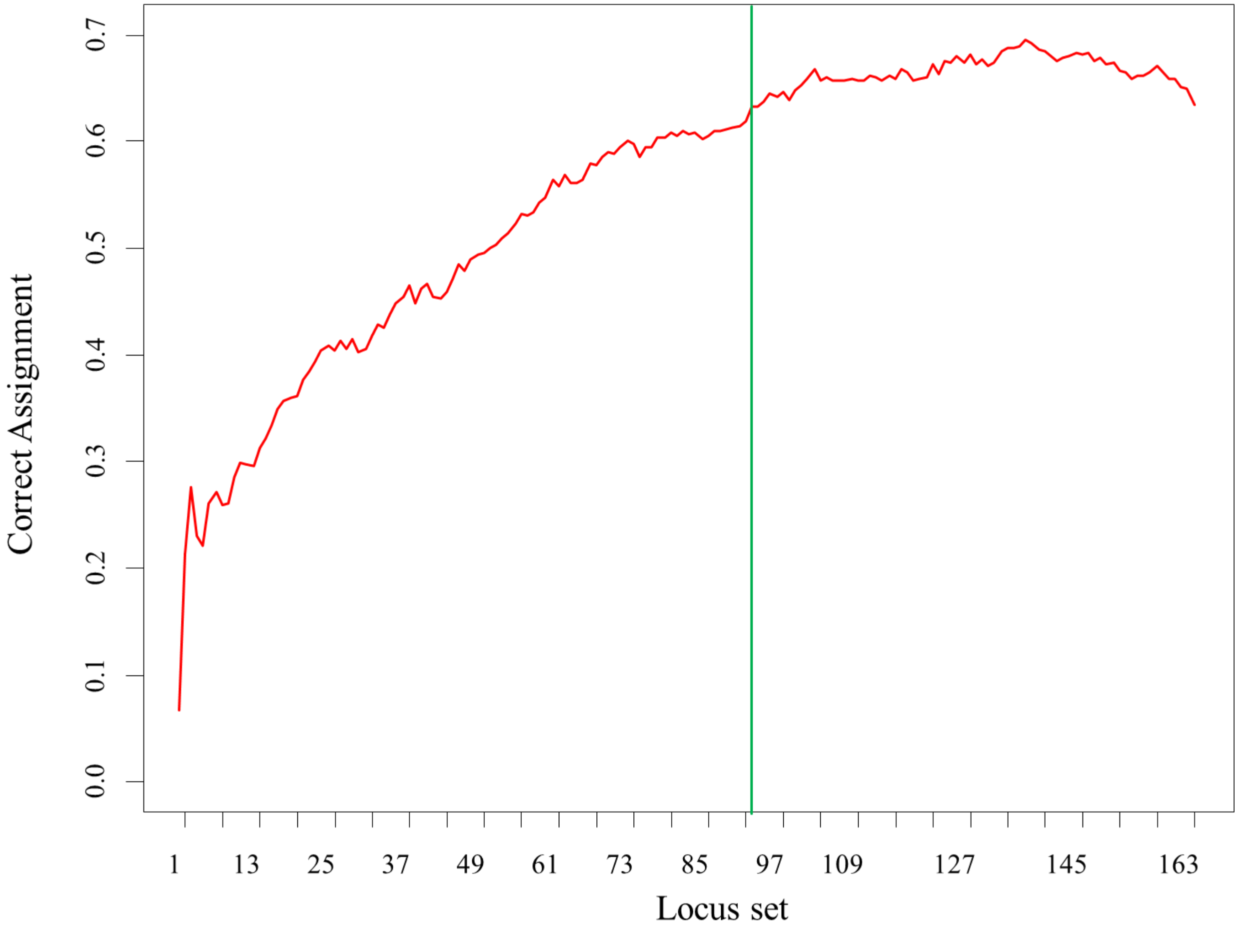


Figure 10.–The estimated optimal correct assignment (f_{ORCA}) to 3 of the Coastal Western Alaska regional areas (Norton Sound, Lower Yukon, Lower Kuskokwim) for sets of SNP loci defined by the backwards elimination locus selection algorithm. Locus sets are listed in ranked, accumulating order such that the set on the far left includes only the highest ranked locus and subsequent sets to the right include the next most informative locus until all loci are included in the final set. The vertical line indicates the cut-off value for the optimal set of 91 loci.

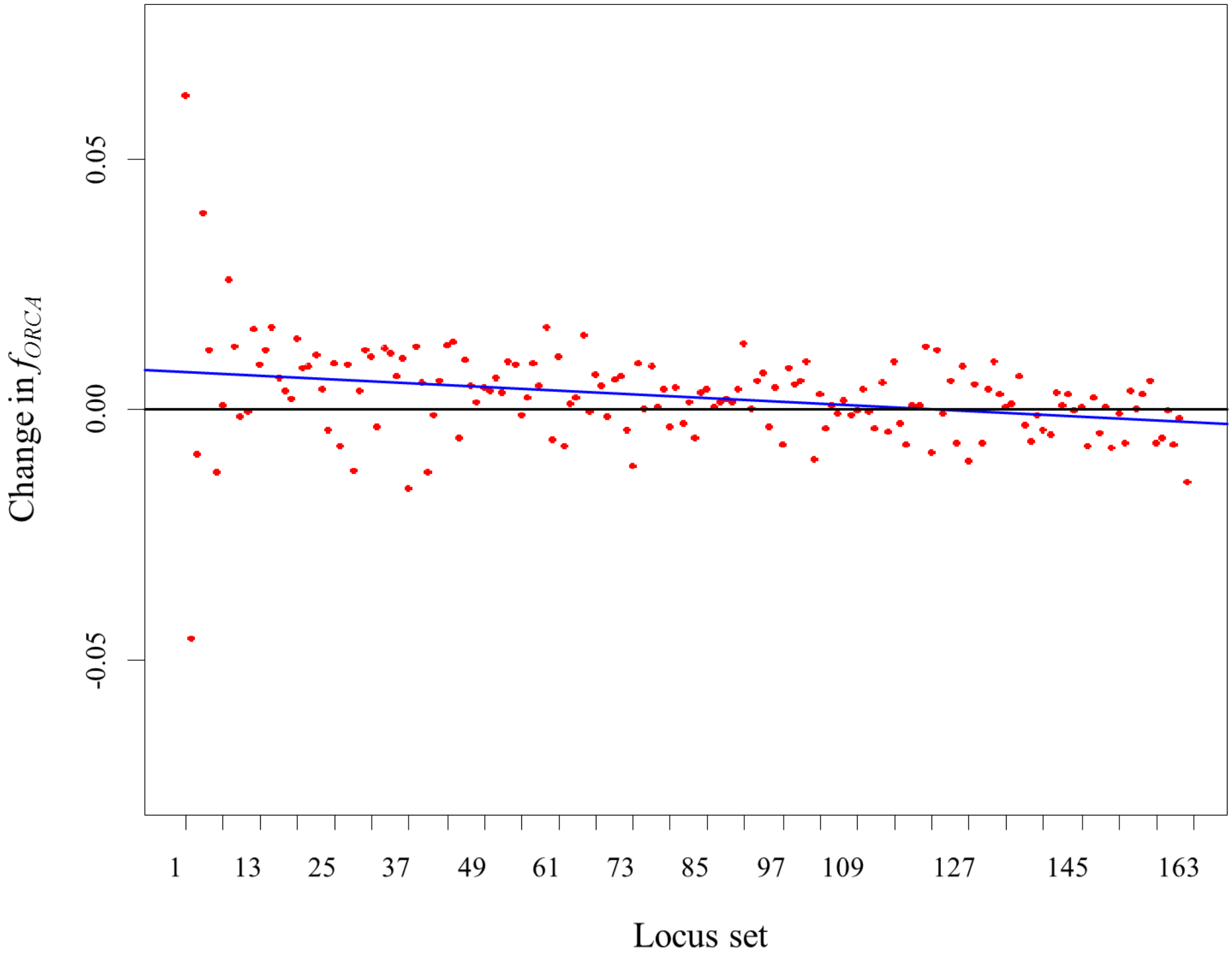


Figure 11.–The estimated change in optimal correct assignment (f_{ORCA}) to 3 of the Coastal Western Alaska regional areas (Norton Sound, Lower Yukon, Lower Kuskokwim) for sets of SNP loci defined by the backwards elimination locus selection algorithm. Locus sets are listed in ranked, accumulating order such that the set on the far left includes only the highest ranked locus and subsequent sets to the right include the next most informative locus until all loci are included in the final set. The regression line indicates the fitted value used to measure the change in assignment attributable to each successive locus.

APPENDICES

Appendix A.–Overall F_{ST} among the 10 Coastal Western Alaska populations and ZeroOneScores (values scaled linearly between 0.0 (lowest) and 1.0 (highest)). Measured value 1.a. as outlined in Figure 3 – see text for methods.

Marker	F_{ST}	ZeroOneScores
Oke_ACOT-100	0.0012	0.057
Oke_AhR1-278	0.0001	0.046
Oke_AhR1-78	0.0114	0.167
Oke_APOB-60	-0.0016	0.027
Oke_arf-319	0.0091	0.143
Oke_ATP5L-105	0.0002	0.046
Oke_azin1-90	0.0085	0.136
Oke_brd2-118	0.0124	0.179
Oke_brp16-65	0.0014	0.059
Oke_CATB-60	0.0003	0.048
Oke_ccd16-77	0.0880	1.000
Oke_CD123-62	0.0024	0.071
Oke_CD81-108	0.0004	0.049
Oke_CD81-173	0.0071	0.121
Oke_cjo57-86	-0.0023	0.019
Oke_CKS1-70	0.0011	0.056
Oke_CKS1-94	0.0013	0.058
Oke_CKS-389	0.0080	0.131
Oke_CO1A1-72	0.0193	0.254
Oke_CO1A1-76	-0.0011	0.033
Oke_col1a2-62	0.0164	0.223
Oke_ctgf-105	0.0091	0.144
Oke_CTR2-82	-0.0020	0.023
Oke_DBLOH-79	0.0038	0.086
Oke_DCXR-87	0.0035	0.082
Oke_DM20-548	0.0062	0.111
Oke_e2ig5-50	0.0029	0.075
Oke_EF2-394	0.0001	0.045
Oke_eif4ebp2-64	0.0029	0.076
Oke_eif4g1-43	0.0037	0.084
Oke_f5-71	0.0185	0.245
Oke_FANK1-166	0.0269	0.336
Oke_FANK1-96	-0.0023	0.019
Oke_FBXL5-61	0.0149	0.206
gdhComb[a]	0.0017	0.063
Oke_GHII-3129	0.0163	0.221
Oke_glrx1-78	0.0044	0.092
Oke_GNMT-100	0.0014	0.059
Oke_GnRH-373	0.0015	0.061

-continued-

Appendix A. Page 2 of 5.

Marker	F_{ST}	ZeroOneScores
Oke_GPDH-191	0.0029	0.075
Oke_GPH-105	0.0197	0.259
Oke_GPH-78	0.0074	0.125
Oke_H2AX-72	-0.0030	0.011
Oke_hmgb1-66	0.0038	0.085
Oke_hnRNPL-239	0.0008	0.053
Oke_HP-182	0.0013	0.058
Oke_hsc71-199	-0.0013	0.030
Oke_HSP90BA-299	0.0069	0.119
Oke_il-1racp-67	0.0157	0.215
Oke_IL8r2-406	0.0109	0.163
Oke_KPNA2-87	0.0708	0.813
Oke_lactb2-71	0.0000	0.045
Oke_lamp2-138	-0.0015	0.028
Oke_LAMP2-186	0.0005	0.049
Oke_mcfd2-86	0.0076	0.127
Oke_METK2-97	-0.0020	0.022
Oke_mgll-49	0.0208	0.271
Oke_MLRN-63	0.0022	0.068
Oke_Moesin-160	0.0020	0.065
mtDNA3[b]	0.0040	0.087
Oke_nc2b-148	0.0123	0.178
Oke_ndub3-58	-0.0010	0.033
Oke_NHERF-54	0.0002	0.047
Oke_NUPR1-70	0.0031	0.078
Oke_PDIA3-475	0.0001	0.045
pgapComb[a]	0.0026	0.072
Oke_pnrc2-78	0.0041	0.089
Oke_PPA2-635	0.0027	0.074
Oke_psmd9-57	0.0031	0.078
Oke_rab5a-117	0.0000	0.044
Oke_ras1-249	0.0062	0.112
Oke_RFC2-618	0.0121	0.175
Oke_RH1op-245	0.0252	0.318
Oke_ROA1-209	-0.0030	0.011
Oke_RPN1-80	0.0010	0.055
Oke_RS27-81	-0.0011	0.032
Oke_RS9-379	0.0506	0.594
Oke_RSPRY1-106	0.0222	0.285
Oke_serpin-140	0.0064	0.113
Oke_slc1a3a-86	0.0034	0.081

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Appendix A. Page 3 of 5.

Marker	F_{ST}	ZeroOneScores
Oke_sylc-90	0.0138	0.194
Oke_TCP1-78	0.0009	0.054
Oke_TCTA-202	-0.0041	0.000
Oke_Tf-278	0.0072	0.122
Oke_thic-84	0.0129	0.184
Oke_txnrd1-74	0.0063	0.113
Oke_U1002-262	0.0140	0.197
Oke_U1008-83	0.0609	0.706
Oke_U1010-154	0.0000	0.044
Oke_U1010-251	0.0105	0.158
Oke_U1015-255	0.0136	0.192
Oke_U1016-154	0.0053	0.102
Oke_U1017-52	0.0031	0.078
Oke_U1018-50	0.0101	0.154
Oke_U1019-218	0.0055	0.104
Oke_U1020-75	-0.0019	0.023
Oke_U1012-241	0.0023	0.069
Oke_U1023-147	0.0226	0.290
Oke_U1024-113	0.0046	0.094
Oke_U1025-135	0.0050	0.098
Oke_U1027-89	0.0251	0.317
Oke_U1028-100	0.0114	0.168
U102Comb[a]	-0.0002	0.042
Oke_U1031-132	0.0021	0.066
Oke_u1-519	-0.0007	0.036
Oke_U2001-629	0.0062	0.112
Oke_U2002-200	0.0042	0.090
Oke_U2003-142	0.0034	0.081
Oke_u200-385	0.0159	0.217
Oke_U2005-62	-0.0021	0.022
Oke_U2006-109	0.0056	0.105
Oke_U2007-190	0.0012	0.058
Oke_U2010-94	0.0070	0.120
Oke_U2011-107	0.0088	0.140
Oke_U2015-151	0.0249	0.314
Oke_U2016-118	0.0029	0.076
Oke_U2017-87	0.0125	0.180
Oke_U2019-112	-0.0023	0.019
Oke_u2020-51	-0.0036	0.006
Oke_u202-131	0.0071	0.121
Oke_U2021-86	0.0068	0.118

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Appendix A. Page 4 of 5.

Marker	F_{ST}	ZeroOneScores
Oke_U2022-101	0.0036	0.084
Oke_U2023-99	-0.0019	0.024
Oke_U2024-93	0.0040	0.088
Oke_U2025-86	0.0081	0.132
Oke_U2026-64	0.0066	0.116
Oke_U2029-79	0.0086	0.138
Oke_U2031-37	0.0206	0.268
Oke_U2032-74	0.0114	0.167
Oke_U2033-122	0.0008	0.052
Oke_U2034-55	0.0029	0.075
Oke_U2035-54	-0.0016	0.027
Oke_U2037-76	0.0111	0.164
Oke_U2041-84	0.0068	0.118
Oke_U2042-61	-0.0015	0.028
Oke_U2043-51	0.0024	0.070
Oke_U2045-43	0.0031	0.078
Oke_U2047-49	0.0007	0.052
Oke_U2048-91	0.0068	0.118
Oke_U2049-99	0.0000	0.044
Oke_U2050-101	0.0073	0.124
Oke_U2052-56	0.0005	0.050
Oke_U2053-60	0.0090	0.142
Oke_U2054-58	0.0004	0.049
Oke_U2056-90	0.0036	0.083
Oke_U2057-80	0.0249	0.314
Oke_U212-87	0.0130	0.186
Oke_u216-222	0.0050	0.098
Oke_u217-172	-0.0018	0.025
Oke_U302-195	0.0140	0.196
Oke_U401-143	-0.0008	0.036
Oke_U502-241	0.0013	0.059
Oke_U503-272	0.0014	0.059
Oke_U504-228	0.0064	0.113
Oke_U505-112	-0.0029	0.012
Oke_U506-110	0.0224	0.287
Oke_U507-286	0.0058	0.107
Oke_U509-219	0.0043	0.091
Oke_U510-204	0.0057	0.106
Oke_U511-271	-0.0031	0.011
Oke_U514-150	0.0007	0.052
Oke_uqcrfs-69	0.0008	0.053

-continued-

Appendix A. Page 5 of 5.

Marker	F_{ST}	ZeroOneScores
Oke_zn593-152	0.0020	0.066
Marker	F_{ST}	ZeroOneScores

[a] Nuclear SNP composite phenotypes.

[b] Mitochondrial SNP composite phenotype.

Appendix B.–Overall θ_P among the 5 Coastal Western Alaska regional areas calculated via a 3-level hierarchical ANOVA (Weir, 1995; Table 1; Figure 2). The θ_P values calculated from individual loci were linearly scaled between 0.0 and 1.0 and used as scores. Measured value 1.b. as outlined in Figure 3 – see text for methods.

Marker	θ_P	ZeroOneScores
Oke_ACOT-100	0.0018	0.329
Oke_AhR1-278	0.0015	0.321
Oke_AhR1-78	-0.0113	0.039
Oke_APOB-60	0.0035	0.365
Oke_arf-319	0.0127	0.571
Oke_ATP5L-105	-0.0003	0.282
Oke_azin1-90	0.0076	0.457
Oke_brd2-118	0.0114	0.542
Oke_brp16-65	-0.0047	0.184
Oke_CATB-60	0.0048	0.395
Oke_ccd16-77	0.0015	0.322
Oke_CD123-62	0.0030	0.354
Oke_CD81-108	0.0058	0.419
Oke_CD81-173	-0.0014	0.257
Oke_cjo57-86	-0.0009	0.269
Oke_CKS1-70	-0.0021	0.241
Oke_CKS1-94	-0.0014	0.258
Oke_CKS-389	0.0034	0.365
Oke_CO1A1-72	-0.0120	0.022
Oke_CO1A1-76	0.0000	0.288
Oke_col1a2-62	-0.0060	0.155
Oke_ctgf-105	0.0072	0.449
Oke_CTR2-82	0.0002	0.293
Oke_DBLOH-79	-0.0072	0.130
Oke_DCXR-87	0.0065	0.433
Oke_DM20-548	0.0116	0.547
Oke_e2ig5-50	0.0053	0.406
Oke_EF2-394	0.0009	0.309
Oke_eif4ebp2-64	-0.0001	0.285
Oke_eif4g1-43	0.0052	0.404
Oke_f5-71	-0.0022	0.239
Oke_FANK1-166	0.0319	0.996
Oke_FANK1-96	-0.0024	0.236
Oke_FBXL5-61	0.0082	0.471
gdhComb[a]	0.0013	0.317
Oke_GHII-3129	0.0062	0.425

-continued-

Appendix B. Page 2 of 5.

Marker	θ_P	ZeroOneScores
Oke_glrx1-78	-0.0015	0.256
Oke_GNMT-100	0.0040	0.378
Oke_GnRH-373	-0.0023	0.238
Oke_GPDH-191	0.0009	0.309
Oke_GPH-105	0.0115	0.545
Oke_GPH-78	-0.0090	0.088
Oke_H2AX-72	0.0004	0.298
Oke_hmgb1-66	0.0069	0.442
Oke_hnRNPL-239	-0.0020	0.245
Oke_HP-182	0.0050	0.400
Oke_hsc71-199	-0.0003	0.282
Oke_HSP90BA-299	-0.0013	0.261
Oke_il-1racp-67	0.0005	0.301
Oke_IL8r2-406	0.0000	0.288
Oke_KPNA2-87	0.0131	0.579
Oke_lactb2-71	0.0021	0.336
Oke_lamp2-138	0.0031	0.358
Oke_LAMP2-186	-0.0028	0.227
Oke_mcfd2-86	0.0089	0.487
Oke_METK2-97	-0.0014	0.257
Oke_mgll-49	0.0104	0.519
Oke_MLRN-63	-0.0004	0.279
Oke_Moesin-160	-0.0017	0.252
mtDNA3[b]	0.0057	0.416
Oke_nc2b-148	0.0071	0.446
Oke_ndub3-58	-0.0010	0.266
Oke_NHERF-54	-0.0001	0.287
Oke_NUPR1-70	-0.0033	0.214
Oke_PDIA3-475	0.0012	0.316
pgapComb[a]	0.0002	0.292
Oke_pnrc2-78	-0.0044	0.190
Oke_PPA2-635	0.0009	0.309
Oke_psmd9-57	-0.0042	0.195
Oke_rab5a-117	0.0022	0.338
Oke_ras1-249	0.0028	0.351
Oke_RFC2-618	0.0078	0.463
Oke_RH1op-245	0.0273	0.895
Oke_ROA1-209	0.0009	0.309
Oke_RPN1-80	-0.0041	0.198

-continued-

Appendix B. Page 3 of 5.

Marker	θ_P	ZeroOneScores
Oke_RS27-81	-0.0002	0.283
Oke_RS9-379	0.0169	0.665
Oke_RSPRY1-106	0.0182	0.693
Oke_serpin-140	0.0057	0.416
Oke_slc1a3a-86	0.0013	0.318
Oke_sylc-90	0.0154	0.630
Oke_TCP1-78	-0.0003	0.282
Oke_TCTA-202	0.0001	0.291
Oke_Tf-278	0.0064	0.430
Oke_thic-84	0.0211	0.757
Oke_txnrd1-74	0.0038	0.372
Oke_U1002-262	0.0216	0.768
Oke_U1008-83	0.0320	1.000
Oke_U1010-154	0.0000	0.289
Oke_U1010-251	0.0049	0.397
Oke_U1015-255	0.0190	0.710
Oke_U1016-154	0.0031	0.357
Oke_U1017-52	0.0029	0.354
Oke_U1018-50	0.0104	0.519
Oke_U1019-218	-0.0007	0.272
Oke_U1020-75	-0.0003	0.281
Oke_U1012-241	0.0024	0.343
Oke_U1023-147	0.0286	0.924
Oke_U1024-113	0.0012	0.315
Oke_U1025-135	0.0019	0.330
Oke_U1027-89	0.0156	0.634
Oke_U1028-100	0.0029	0.354
U102Comb[a]	0.0001	0.291
Oke_U1031-132	0.0025	0.344
Oke_u1-519	0.0024	0.342
Oke_U2001-629	0.0106	0.525
Oke_U2002-200	-0.0063	0.149
Oke_U2003-142	0.0058	0.418
Oke_u200-385	-0.0130	0.000
Oke_U2005-62	-0.0017	0.250
Oke_U2006-109	0.0086	0.479
Oke_U2007-190	0.0038	0.374
Oke_U2010-94	-0.0053	0.170
Oke_U2011-107	0.0137	0.593

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Marker	θ_P	ZeroOneScores
Oke_U2015-151	0.0127	0.572
Oke_U2016-118	0.0094	0.497
Oke_U2017-87	0.0166	0.658
Oke_U2019-112	0.0000	0.290
Oke_u2020-51	0.0018	0.328
Oke_u202-131	0.0085	0.478
Oke_U2021-86	0.0098	0.507
Oke_U2022-101	0.0051	0.402
Oke_U2023-99	0.0001	0.290
Oke_U2024-93	-0.0029	0.224
Oke_U2025-86	0.0043	0.385
Oke_U2026-64	0.0004	0.297
Oke_U2029-79	0.0097	0.503
Oke_U2031-37	0.0116	0.547
Oke_U2032-74	0.0117	0.549
Oke_U2033-122	-0.0003	0.283
Oke_U2034-55	-0.0002	0.284
Oke_U2035-54	0.0029	0.352
Oke_U2037-76	0.0039	0.376
Oke_U2041-84	0.0059	0.420
Oke_U2042-61	-0.0006	0.276
Oke_U2043-51	0.0008	0.306
Oke_U2045-43	-0.0081	0.108
Oke_U2047-49	0.0019	0.331
Oke_U2048-91	0.0018	0.328
Oke_U2049-99	-0.0022	0.240
Oke_U2050-101	0.0118	0.550
Oke_U2052-56	-0.0004	0.279
Oke_U2053-60	0.0098	0.505
Oke_U2054-58	0.0050	0.400
Oke_U2056-90	0.0067	0.437
Oke_U2057-80	0.0116	0.546
Oke_U212-87	0.0105	0.522
Oke_u216-222	0.0064	0.431
Oke_u217-172	0.0017	0.326
Oke_U302-195	0.0099	0.508
Oke_U401-143	0.0011	0.313
Oke_U502-241	-0.0020	0.244
Oke_U503-272	0.0055	0.412

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Appendix B. Page 5 of 5.

Marker	θ_P	ZeroOneScores
Oke_U504-228	0.0124	0.565
Oke_U505-112	0.0003	0.296
Oke_U506-110	0.0071	0.446
Oke_U507-286	0.0021	0.336
Oke_U509-219	0.0017	0.327
Oke_U510-204	0.0100	0.511
Oke_U511-271	0.0016	0.324
Oke_U514-150	0.0016	0.323
Oke_uqcrfs-69	0.0023	0.339
Oke_zn593-152	0.0042	0.381

[a] Nuclear SNP composite phenotypes.

[b] Mitochondrial SNP composite phenotype.

Appendix C.–f_{ORCA} with backward elimination using 3 of the Coastal Western Alaska regional areas (Norton Sound, Lower Yukon, Lower Kuskokwim), locus rank based on fitted Δf_{ORCA}, and ZeroOneScores, scaled values were scaled linearly between 0.0 (lowest) and 1.0 (highest). Measured value 1.c. as outlined in Figure 3 – see text for methods.

Marker	Δf_{ORCA} score	Rank	ZeroOneScores
Oke_ACOT-100	0.0033	69	0.580
Oke_AhR1-278	-0.0006	135	0.173
Oke_AhR1-78	0.0023	86	0.475
Oke_APOB-60	0.0001	123	0.247
Oke_arf-319	0.0010	108	0.340
Oke_ATP5L-105	0.0058	28	0.833
Oke_azin1-90	0.0050	42	0.747
Oke_brd2-118	0.0039	60	0.636
Oke_brp16-65	0.0069	10	0.944
Oke_CATB-60	0.0038	61	0.630
Oke_ccd16-77	0.0051	40	0.759
Oke_CD123-62	0.0026	81	0.506
Oke_CD81-108	0.0017	96	0.414
Oke_CD81-173	0.0016	98	0.401
Oke_cjo57-86	-0.0003	130	0.204
Oke_CKS1-70	0.0020	92	0.438
Oke_CKS1-94	0.0048	45	0.728
Oke_CKS-389	0.0043	53	0.679
Oke_CO1A1-72	0.0015	100	0.389
Oke_CO1A1-76	0.0028	78	0.525
Oke_col1a2-62	0.0042	54	0.673
Oke_ctgf-105	0.0000	124	0.241
Oke_CTR2-82	-0.0021	160	0.019
Oke_DBLOH-79	-0.0009	139	0.148
Oke_DCXR-87	0.0067	13	0.926
Oke_DM20-548	-0.0018	155	0.049
Oke_e2ig5-50	0.0053	37	0.778
Oke_EF2-394	-0.0001	126	0.228
Oke_eif4ebp2-64	-0.0022	161	0.012
Oke_eif4g1-43	0.0066	14	0.920
Oke_f5-71	0.0027	80	0.512
Oke_FANK1-166	0.0072	5	0.975
Oke_FANK1-96	-0.0019	157	0.037
Oke_FBXL5-61	0.0050	41	0.753
gdhComb[a]	0.0071	7	0.963
Oke_GHII-3129	0.0013	103	0.370
Oke_glrx1-78	0.0030	75	0.543
Oke_GNMT-100	0.0024	84	0.488

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Marker	Δf_{ORCA} score	Rank	ZeroOneScores
Oke_GnRH-373	0.0011	106	0.352
Oke_GPDH-191	0.0008	111	0.321
Oke_GPH-105	0.0061	23	0.864
Oke_GPH-78	0.0000	125	0.235
Oke_H2AX-72	0.0005	116	0.290
Oke_hmgb1-66	0.0031	73	0.556
Oke_hnRNPL-239	0.0014	102	0.377
Oke_HP-182	0.0063	19	0.889
Oke_hsc71-199	0.0014	101	0.383
Oke_HSP90BA-299	-0.0013	146	0.105
Oke_il-1racp-67	0.0051	39	0.765
Oke_IL8r2-406	0.0057	29	0.827
Oke_KPNA2-87	0.0032	71	0.568
Oke_lactb2-71	-0.0007	137	0.160
Oke_lamp2-138	0.0027	79	0.519
Oke_LAMP2-186	0.0059	26	0.846
Oke_mcfd2-86	0.0065	16	0.907
Oke_METK2-97	-0.0003	129	0.210
Oke_mgll-49	0.0040	58	0.648
Oke_MLRN-63	0.0032	72	0.562
Oke_Moesin-160	0.0039	59	0.642
mtDNA3[b]	-0.0015	150	0.080
Oke_nc2b-148	0.0063	20	0.883
Oke_ndub3-58	-0.0011	143	0.123
Oke_NHERF-54	-0.0023	163	0.000
Oke_NUPR1-70	0.0070	8	0.957
Oke_PDIA3-475	0.0023	87	0.469
pgapComb[a]	0.0066	15	0.914
Oke_pnrc2-78	-0.0021	159	0.025
Oke_PPA2-635	0.0035	67	0.593
Oke_psmd9-57	0.0047	46	0.722
Oke_rab5a-117	0.0021	90	0.451
Oke_ras1-249	0.0052	38	0.772
Oke_RFC2-618	0.0062	21	0.877
Oke_RH1op-245	0.0029	77	0.531
Oke_ROA1-209	-0.0006	134	0.179
Oke_RPN1-80	0.0044	52	0.685
Oke_RS27-81	0.0036	64	0.611
Oke_RS9-379	0.0008	112	0.315
Oke_RSPRY1-106	0.0053	36	0.784
Oke_serpin-140	0.0041	57	0.654

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Marker	Δf_{ORCA} score	Rank	ZeroOneScores
Oke_slc1a3a-86	0.0045	49	0.704
Oke_sylc-90	0.0057	30	0.821
Oke_TCP1-78	0.0046	48	0.710
Oke_TCTA-202	0.0002	122	0.253
Oke_Tf-278	0.0041	56	0.660
Oke_thic-84	0.0056	31	0.815
Oke_txnrd1-74	0.0037	63	0.617
Oke_U1002-262	0.0068	11	0.938
Oke_U1008-83	0.0074	2	0.994
Oke_U1010-154	-0.0012	145	0.111
Oke_U1010-251	0.0068	12	0.932
Oke_U1012-241	0.0004	118	0.278
Oke_U1015-255	-0.0014	148	0.093
Oke_U1016-154	0.0042	55	0.667
Oke_U1017-52	0.0047	47	0.716
Oke_U1018-50	0.0026	82	0.500
Oke_U1019-218	-0.0017	153	0.062
Oke_U1020-75	0.0054	34	0.796
Oke_U1023-147	-0.0016	152	0.068
Oke_U1024-113	0.0034	68	0.586
Oke_U1025-135	0.0012	104	0.364
Oke_U1027-89	0.0007	113	0.309
Oke_U1028-100	0.0071	6	0.969
U102Comb[a]	0.0073	3	0.988
Oke_U1031-132	0.0035	66	0.599
Oke_u1-519	-0.0016	151	0.074
Oke_U2001-629	0.0024	85	0.481
Oke_U2002-200	-0.0004	131	0.198
Oke_U2003-142	-0.0010	142	0.130
Oke_u200-385	0.0038	62	0.623
Oke_U2005-62	-0.0004	132	0.191
Oke_U2006-109	0.0056	32	0.809
Oke_U2007-190	0.0069	9	0.951
Oke_U2010-94	0.0006	115	0.296
Oke_U2011-107	0.0054	35	0.790
Oke_U2015-151	0.0002	121	0.259
Oke_U2016-118	-0.0002	128	0.216
Oke_U2017-87	0.0072	4	0.981
Oke_U2019-112	0.0003	120	0.265
Oke_u2020-51	-0.0020	158	0.031
Oke_u202-131	-0.0012	144	0.117

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Marker	Δf_{ORCA} score	Rank	ZeroOneScores
Oke_U2021-86	-0.0013	147	0.099
Oke_U2022-101	0.0018	95	0.420
Oke_U2023-99	-0.0008	138	0.154
Oke_U2024-93	0.0005	117	0.284
Oke_U2025-86	0.0021	89	0.457
Oke_U2026-64	-0.0019	156	0.043
Oke_U2029-79	0.0029	76	0.537
Oke_U2031-37	0.0003	119	0.272
Oke_U2032-74	0.0020	91	0.444
Oke_U2033-122	0.0033	70	0.574
Oke_U2034-55	0.0009	110	0.327
Oke_U2035-54	0.0049	43	0.741
Oke_U2037-76	0.0044	51	0.691
Oke_U2041-84	0.0065	17	0.901
Oke_U2042-61	-0.0018	154	0.056
Oke_U2043-51	0.0060	24	0.858
Oke_U2045-43	0.0009	109	0.333
Oke_U2047-49	0.0006	114	0.302
Oke_U2048-91	0.0025	83	0.494
Oke_U2049-99	-0.0010	141	0.136
Oke_U2050-101	0.0017	97	0.407
Oke_U2052-56	0.0011	107	0.346
Oke_U2053-60	0.0048	44	0.735
Oke_U2054-58	0.0055	33	0.802
Oke_U2056-90	0.0062	22	0.870
Oke_U2057-80	0.0064	18	0.895
Oke_U212-87	0.0060	25	0.852
Oke_u216-222	-0.0005	133	0.185
Oke_u217-172	0.0045	50	0.698
Oke_U302-195	0.0074	1	1.000
Oke_U401-143	0.0018	94	0.426
Oke_U502-241	-0.0007	136	0.167
Oke_U503-272	-0.0001	127	0.222
Oke_U504-228	0.0059	27	0.840
Oke_U505-112	0.0036	65	0.605
Oke_U506-110	0.0019	93	0.432
Oke_U507-286	0.0030	74	0.549
Oke_U509-219	0.0022	88	0.463
Oke_U510-204	-0.0009	140	0.142
Oke_U511-271	0.0015	99	0.395
Oke_U514-150	-0.0022	162	0.006

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Marker	Δf_{ORCA} score	Rank	ZeroOneScores
Oke_uqcrfs-69	-0.0015	149	0.086
Oke_zn593-152	0.0012	105	0.358

[a] Nuclear SNP composite phenotypes.

[b] Mitochondrial SNP composite phenotype.

Appendix D.–F_{ST} for population pairs with the smallest pairwise F_{ST} from adjacent CWAK regional areas – see text for methods.

Region pair	Lowest F_{ST} value	Population 1	Population 2
Norton Sound / Lower Yukon	0.00053	Kwiniuk River	Andreafsky River - East Fork
Lower Yukon / Lower Kuskokwim	0.00004	Andreafsky River - East Fork	Salmon River
Lower Kuskokwim / Western Bristol Bay	0.00237	Kanektok River	Iowithla River
Western Bristol Bay / Eastern Bristol Bay	0.00563	Iowithla River	Alagnak River

Appendix E.–F_{ST} between the populations listed in Appendix D, and ZeroOneScores. The average of the ZeroOneScores is given in the far right column and this value was scaled linearly between 0.0 (lowest) and 1.0 (highest). Measured value 1.d. as outlined in Figure 3 – see text for methods.

	Norton Sound / Lower Yukon		Lower Yukon / Lower Kuskokwim		Lower Kuskokwim / Western Bristol Bay		Western Bristol Bay / Eastern Bristol Bay		
Locus	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	Avg. ZeroOneScores
Oke_ACOT-100	-0.0048	0.042	0.0014	0.173	0.0154	0.230	-0.0053	0.001	0.111
Oke_AhR1-278	0.0014	0.128	-0.0027	0.095	0.0218	0.300	-0.0038	0.012	0.134
Oke_AhR1-78	0.0169	0.345	-0.0052	0.046	-0.0037	0.019	0.0302	0.260	0.167
Oke_APOB-60	-0.0053	0.035	-0.0052	0.046	0.0005	0.066	-0.0034	0.015	0.041
Oke_arf-319	-0.0049	0.040	0.0001	0.147	-0.0048	0.008	0.0359	0.301	0.124
Oke_ATP5L-105	0.0040	0.165	-0.0052	0.046	0.0013	0.074	-0.0053	0.001	0.072
Oke_azin1-90	0.0012	0.126	-0.0011	0.126	0.0090	0.159	-0.0008	0.034	0.111
Oke_brd2-118	-0.0040	0.054	-0.0004	0.137	0.0108	0.179	-0.0035	0.014	0.096
Oke_brp16-65	0.0033	0.156	-0.0028	0.093	0.0004	0.065	-0.0032	0.017	0.083
Oke_CATB-60	-0.0022	0.078	0.0047	0.237	0.0024	0.087	0.0160	0.156	0.139
Oke_ccd16-77	-0.0053	0.035	0.0011	0.167	0.0465	0.573	-0.0017	0.028	0.201
Oke_CD123-62	0.0135	0.298	-0.0049	0.052	-0.0031	0.027	-0.0054	0.001	0.094
Oke_CD81-108	-0.0019	0.082	0.0067	0.274	-0.0053	0.002	-0.0019	0.026	0.096
Oke_CD81-173	-0.0049	0.040	-0.0028	0.092	0.0352	0.448	0.0197	0.184	0.191
Oke_cjo57-86	-0.0017	0.085	0.0003	0.151	-0.0044	0.011	-0.0051	0.002	0.062
Oke_CKS1-70	-0.0049	0.040	-0.0009	0.128	0.0000	0.060	-0.0044	0.008	0.059
Oke_CKS1-94	-0.0012	0.092	-0.0052	0.048	-0.0036	0.021	0.0092	0.107	0.067
Oke_CKS-389	-0.0004	0.104	-0.0052	0.047	0.0047	0.113	0.0472	0.384	0.162
Oke_CO1A1-72	-0.0048	0.043	-0.0048	0.055	0.0027	0.090	0.0090	0.105	0.073
Oke_CO1A1-76	-0.0041	0.052	-0.0050	0.051	0.0001	0.061	-0.0038	0.012	0.044
Oke_col1a2-62	-0.0034	0.062	-0.0045	0.061	-0.0022	0.036	-0.0051	0.003	0.040
Oke_ctgf-105	-0.0050	0.039	-0.0033	0.083	0.0072	0.139	-0.0011	0.032	0.073

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	Norton Sound / Lower Yukon		Lower Yukon / Lower Kuskokwim		Lower Kuskokwim / Western Bristol Bay		Western Bristol Bay / Eastern Bristol Bay		
Locus	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	Avg. ZeroOneScores
Oke_CTR2-82	-0.0026	0.073	-0.0007	0.132	-0.0038	0.018	0.0032	0.063	0.072
Oke_DBLOH-79	-0.0044	0.047	-0.0022	0.104	0.0081	0.149	-0.0040	0.010	0.078
Oke_DCXR-87	-0.0047	0.043	0.0303	0.724	-0.0054	0.001	-0.0032	0.017	0.196
Oke_DM20-548	-0.0054	0.034	-0.0029	0.091	-0.0053	0.002	-0.0008	0.034	0.040
Oke_e2ig5-50	-0.0048	0.043	-0.0002	0.143	0.0073	0.140	-0.0014	0.030	0.089
Oke_EF2-394	0.0092	0.237	0.0128	0.390	-0.0036	0.020	0.0071	0.091	0.185
Oke_eif4ebp2-64	-0.0040	0.053	-0.0051	0.048	-0.0039	0.018	-0.0019	0.026	0.036
Oke_eif4g1-43	-0.0053	0.035	0.0031	0.205	-0.0054	0.001	0.0030	0.062	0.076
Oke_f5-71	-0.0053	0.035	0.0060	0.260	0.0147	0.222	0.0002	0.041	0.140
Oke_FANK1-166	0.0016	0.131	0.0016	0.176	0.0009	0.070	0.0208	0.191	0.142
Oke_FANK1-96	-0.0053	0.034	-0.0003	0.140	-0.0053	0.001	-0.0045	0.007	0.046
Oke_FBXL5-61	-0.0050	0.039	-0.0043	0.064	0.0140	0.214	-0.0021	0.024	0.085
gdhComb[a]	0.0039	0.163	0.0124	0.383	-0.0035	0.022	-0.0002	0.039	0.152
Oke_GHII-3129	0.0281	0.503	-0.0044	0.062	-0.0049	0.006	0.0020	0.054	0.156
Oke_glrx1-78	0.0180	0.360	0.0020	0.184	-0.0035	0.022	0.0095	0.109	0.169
Oke_GNMT-100	-0.0036	0.058	0.0028	0.199	-0.0014	0.045	-0.0052	0.002	0.076
Oke_GnRH-373	-0.0032	0.065	-0.0050	0.051	-0.0018	0.040	-0.0055	0.000	0.039
Oke_GPDH-191	0.0113	0.267	0.0018	0.180	-0.0051	0.004	-0.0035	0.014	0.116
Oke_GPH-105	-0.0046	0.045	0.0011	0.167	0.0489	0.599	0.1319	1.000	0.453
Oke_GPH-78	-0.0034	0.061	0.0447	1.000	0.0028	0.091	-0.0054	0.001	0.288
Oke_H2AX-72	-0.0052	0.036	-0.0051	0.049	-0.0049	0.006	-0.0053	0.001	0.023
Oke_hmgb1-66	0.0335	0.577	-0.0044	0.063	-0.0045	0.011	-0.0054	0.001	0.163
Oke_hnRNPL-239	-0.0021	0.079	0.0140	0.414	0.0012	0.074	-0.0047	0.006	0.143
Oke_HP-182	0.0200	0.389	0.0038	0.218	0.0074	0.142	0.0039	0.068	0.204
Oke_hsc71-199	-0.0048	0.042	-0.0010	0.127	0.0057	0.123	-0.0053	0.001	0.073

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Locus	Norton Sound / Lower Yukon		Lower Yukon / Lower Kuskokwim		Lower Kuskokwim / Western Bristol Bay		Western Bristol Bay / Eastern Bristol Bay		Avg. ZeroOneScores
	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	
Oke_HSP90BA-299	0.0000	0.109	0.0106	0.348	0.0000	0.060	0.0000	0.040	0.139
Oke_il-1racp-67	0.0357	0.609	0.0410	0.928	0.0403	0.504	0.0366	0.306	0.587
Oke_IL8r2-406	-0.0039	0.055	-0.0050	0.050	-0.0001	0.059	-0.0047	0.006	0.042
Oke_KPNA2-87	0.0637	1.000	0.0234	0.593	-0.0053	0.002	-0.0003	0.037	0.408
Oke_lactb2-71	-0.0039	0.055	-0.0017	0.114	-0.0031	0.026	-0.0053	0.001	0.049
Oke_lamp2-138	-0.0025	0.074	0.0028	0.200	-0.0043	0.013	0.0079	0.097	0.096
Oke_LAMP2-186	-0.0049	0.040	-0.0038	0.073	0.0061	0.128	-0.0053	0.001	0.061
Oke_mcfd2-86	-0.0047	0.044	-0.0013	0.121	-0.0024	0.034	-0.0019	0.026	0.056
Oke_METK2-97	-0.0046	0.044	-0.0047	0.056	-0.0034	0.022	-0.0015	0.029	0.038
Oke_mgll-49	0.0184	0.366	0.0099	0.335	-0.0050	0.005	0.0030	0.062	0.192
Oke_MLRN-63	-0.0044	0.048	-0.0052	0.046	0.0109	0.180	-0.0002	0.038	0.078
Oke_Moesin-160	-0.0051	0.038	0.0008	0.162	0.0001	0.062	0.0087	0.103	0.091
mtDNA3[b]	-0.0078	0.000	0.0006	0.158	-0.0001	0.059	0.0109	0.119	0.084
Oke_nc2b-148	-0.0006	0.100	0.0057	0.255	-0.0014	0.045	0.0537	0.431	0.208
Oke_ndub3-58	-0.0052	0.036	-0.0053	0.045	-0.0025	0.032	-0.0003	0.038	0.038
Oke_NHERF-54	-0.0039	0.054	-0.0022	0.104	-0.0008	0.051	0.0041	0.070	0.070
Oke_NUPR1-70	-0.0037	0.058	-0.0030	0.089	-0.0054	0.001	-0.0047	0.006	0.039
Oke_PDIA3-475	-0.0018	0.084	-0.0056	0.040	0.0031	0.094	-0.0045	0.007	0.056
pgapComb[a]	0.0035	0.158	-0.0077	0.000	0.0038	0.102	0.0074	0.093	0.088
Oke_pnrc2-78	0.0033	0.156	0.0056	0.253	-0.0048	0.007	-0.0032	0.016	0.108
Oke_PPA2-635	-0.0034	0.062	-0.0043	0.063	-0.0048	0.007	-0.0034	0.015	0.037
Oke_psmd9-57	-0.0053	0.035	0.0101	0.339	-0.0049	0.006	-0.0053	0.001	0.095
Oke_rab5a-117	0.0132	0.293	-0.0051	0.048	-0.0051	0.004	-0.0034	0.015	0.090
Oke_ras1-249	-0.0051	0.038	-0.0042	0.066	-0.0052	0.003	0.0001	0.041	0.037
Oke_RFC2-618	0.0124	0.282	0.0124	0.382	0.0149	0.224	0.0055	0.080	0.242

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Appendix E. Page 4 of 7.

	Norton Sound / Lower Yukon		Lower Yukon / Lower Kuskokwim		Lower Kuskokwim / Western Bristol Bay		Western Bristol Bay / Eastern Bristol Bay		
Locus	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	Avg. ZeroOneScores
Oke_RH1op-245	0.0265	0.479	0.0265	0.651	0.0002	0.062	0.0354	0.298	0.372
Oke_ROA1-209	-0.0052	0.037	-0.0048	0.054	-0.0039	0.018	0.0049	0.075	0.046
Oke_RPN1-80	-0.0052	0.036	0.0115	0.365	-0.0055	0.000	-0.0041	0.010	0.103
Oke_RS27-81	0.0022	0.140	0.0149	0.430	-0.0040	0.016	0.0019	0.054	0.160
Oke_RS9-379	-0.0055	0.032	-0.0032	0.085	-0.0022	0.037	-0.0053	0.001	0.039
Oke_RSPRY1-106	0.0019	0.135	-0.0024	0.101	0.0163	0.240	0.0958	0.737	0.303
Oke_serpin-140	-0.0007	0.099	-0.0048	0.055	-0.0028	0.030	0.0582	0.463	0.162
Oke_slc1a3a-86	-0.0026	0.073	0.0067	0.274	0.0024	0.087	0.0077	0.096	0.132
Oke_sylc-90	-0.0044	0.048	-0.0054	0.043	0.0014	0.076	0.0137	0.140	0.077
Oke_TCP1-78	-0.0046	0.045	-0.0046	0.057	-0.0020	0.038	-0.0052	0.002	0.036
Oke_TCTA-202	-0.0052	0.037	-0.0046	0.057	-0.0026	0.032	-0.0047	0.006	0.033
Oke_Tf-278	-0.0054	0.034	0.0053	0.247	-0.0024	0.034	0.0137	0.139	0.114
Oke_thic-84	-0.0039	0.054	-0.0008	0.131	-0.0053	0.002	0.0162	0.158	0.086
Oke_txnrd1-74	0.0072	0.210	0.0052	0.246	0.0089	0.159	0.0108	0.119	0.183
Oke_U1002-262	-0.0048	0.041	0.0090	0.318	-0.0039	0.017	0.0117	0.125	0.125
Oke_U1008-83	0.0000	0.109	0.0000	0.146	0.0108	0.179	0.0220	0.200	0.159
Oke_U1010-154	0.0000	0.109	0.0000	0.146	0.0000	0.060	0.0000	0.040	0.089
Oke_U1010-251	-0.0051	0.038	-0.0006	0.135	0.0001	0.061	-0.0053	0.001	0.059
Oke_U1015-255	-0.0043	0.050	0.0021	0.186	-0.0053	0.002	0.0147	0.147	0.096
Oke_U1016-154	0.0047	0.175	-0.0051	0.050	-0.0028	0.029	0.0021	0.055	0.077
Oke_U1017-52	0.0003	0.114	0.0113	0.362	0.0018	0.080	0.0216	0.197	0.188
Oke_U1018-50	-0.0036	0.059	-0.0049	0.052	-0.0052	0.003	-0.0036	0.014	0.032
Oke_U1019-218	-0.0034	0.062	-0.0004	0.139	-0.0053	0.001	-0.0041	0.010	0.053
Oke_U1020-75	-0.0019	0.082	0.0022	0.188	-0.0050	0.005	-0.0053	0.001	0.069
Oke_U1012-241	0.0079	0.220	0.0033	0.208	0.0107	0.179	0.0118	0.125	0.183
Oke_U1023-147	0.0039	0.164	-0.0036	0.078	-0.0025	0.033	0.0249	0.221	0.124

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Appendix E. Page 5 of 7.

	Norton Sound / Lower Yukon		Lower Yukon / Lower Kuskokwim		Lower Kuskokwim / Western Bristol Bay		Western Bristol Bay / Eastern Bristol Bay		
Locus	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	Avg. ZeroOneScores
Oke_U1024-113	0.0352	0.601	0.0053	0.248	-0.0023	0.035	-0.0037	0.013	0.224
Oke_U1025-135	0.0143	0.310	0.0077	0.293	-0.0035	0.021	-0.0035	0.014	0.160
Oke_U1027-89	-0.0053	0.035	-0.0023	0.102	0.0006	0.067	0.0131	0.135	0.085
Oke_U1028-100	-0.0053	0.035	-0.0014	0.119	0.0291	0.381	-0.0053	0.001	0.134
U102Comb[a]	0.0063	0.197	-0.0042	0.067	0.0005	0.066	0.0016	0.052	0.095
Oke_U1031-132	-0.0043	0.049	0.0219	0.564	-0.0041	0.015	-0.0049	0.004	0.158
Oke_u1-519	-0.0048	0.042	0.0044	0.229	-0.0027	0.030	-0.0052	0.002	0.076
Oke_U2001-629	-0.0055	0.032	-0.0019	0.110	-0.0053	0.001	0.0093	0.107	0.063
Oke_U2002-200	0.0015	0.131	-0.0052	0.046	0.0018	0.080	0.0010	0.047	0.076
Oke_U2003-142	-0.0044	0.047	-0.0046	0.058	-0.0039	0.017	0.0264	0.232	0.089
Oke_u200-385	0.0003	0.113	-0.0003	0.139	-0.0051	0.004	0.0218	0.198	0.114
Oke_U2005-62	0.0004	0.114	-0.0044	0.062	0.0041	0.105	-0.0035	0.015	0.074
Oke_U2006-109	-0.0016	0.087	-0.0035	0.079	-0.0042	0.014	-0.0045	0.007	0.047
Oke_U2007-190	-0.0048	0.041	-0.0055	0.042	0.0006	0.066	-0.0022	0.024	0.043
Oke_U2010-94	-0.0026	0.072	-0.0032	0.084	-0.0006	0.053	-0.0014	0.029	0.060
Oke_U2011-107	-0.0055	0.032	0.0073	0.285	-0.0033	0.023	-0.0052	0.002	0.086
Oke_U2015-151	-0.0044	0.047	-0.0052	0.046	0.0101	0.171	0.0147	0.147	0.103
Oke_U2016-118	-0.0051	0.037	0.0009	0.164	0.0025	0.087	-0.0032	0.017	0.076
Oke_U2017-87	0.0023	0.142	0.0017	0.178	0.0189	0.268	-0.0047	0.006	0.148
Oke_U2019-112	-0.0041	0.052	-0.0037	0.076	-0.0053	0.001	0.0003	0.042	0.043
Oke_u2020-51	-0.0037	0.057	-0.0052	0.046	-0.0035	0.022	-0.0036	0.014	0.035
Oke_u202-131	-0.0042	0.051	-0.0044	0.063	0.0032	0.095	-0.0049	0.004	0.053
Oke_U2021-86	-0.0014	0.090	-0.0012	0.123	-0.0054	0.001	0.0157	0.154	0.092
Oke_U2022-101	0.0065	0.200	-0.0029	0.091	0.0006	0.067	-0.0053	0.001	0.090
Oke_U2023-99	-0.0026	0.073	0.0021	0.187	-0.0051	0.004	-0.0044	0.008	0.068

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Appendix E. Page 6 of 7.

Locus	Norton Sound / Lower Yukon		Lower Yukon / Lower Kuskokwim		Lower Kuskokwim / Western Bristol Bay		Western Bristol Bay / Eastern Bristol Bay		Avg. ZeroOneScores
	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	
Oke_U2024-93	-0.0050	0.040	0.0007	0.159	-0.0049	0.006	0.0249	0.221	0.106
Oke_U2025-86	0.0159	0.331	0.0004	0.154	0.0500	0.611	0.0341	0.288	0.346
Oke_U2026-64	0.0001	0.110	-0.0052	0.046	-0.0003	0.057	-0.0035	0.014	0.057
Oke_U2029-79	0.0254	0.464	-0.0013	0.122	-0.0016	0.042	0.0088	0.104	0.183
Oke_U2031-37	-0.0044	0.048	-0.0046	0.059	0.0853	1.000	0.0117	0.125	0.308
Oke_U2032-74	-0.0038	0.056	-0.0029	0.091	0.0001	0.062	0.0061	0.084	0.073
Oke_U2033-122	-0.0053	0.034	-0.0046	0.059	0.0037	0.101	-0.0044	0.008	0.050
Oke_U2034-55	-0.0053	0.035	-0.0013	0.121	0.0123	0.196	0.0230	0.207	0.140
Oke_U2035-54	-0.0044	0.048	-0.0006	0.135	0.0036	0.100	-0.0050	0.003	0.072
Oke_U2037-76	-0.0053	0.035	-0.0049	0.053	-0.0029	0.028	-0.0053	0.001	0.029
Oke_U2041-84	0.0065	0.200	-0.0032	0.085	-0.0031	0.026	0.0027	0.060	0.093
Oke_U2042-61	0.0028	0.149	0.0073	0.286	-0.0039	0.017	-0.0052	0.002	0.113
Oke_U2043-51	-0.0022	0.079	-0.0052	0.047	-0.0008	0.051	-0.0019	0.026	0.051
Oke_U2045-43	-0.0032	0.064	-0.0017	0.114	-0.0052	0.003	0.0070	0.091	0.068
Oke_U2047-49	0.0027	0.147	-0.0051	0.049	-0.0048	0.007	-0.0054	0.001	0.051
Oke_U2048-91	-0.0052	0.036	-0.0017	0.114	0.0181	0.260	0.0039	0.068	0.119
Oke_U2049-99	0.0022	0.140	-0.0052	0.046	0.0156	0.232	-0.0019	0.026	0.111
Oke_U2050-101	0.0008	0.120	0.0000	0.147	-0.0051	0.004	0.0048	0.075	0.086
Oke_U2052-56	-0.0037	0.057	-0.0040	0.069	-0.0014	0.045	-0.0049	0.004	0.044
Oke_U2053-60	-0.0053	0.035	-0.0047	0.055	-0.0033	0.024	0.0112	0.122	0.059
Oke_U2054-58	-0.0045	0.047	0.0016	0.177	-0.0024	0.034	0.0010	0.047	0.076
Oke_U2056-90	0.0003	0.114	-0.0053	0.045	-0.0051	0.004	0.0044	0.072	0.059
Oke_U2057-80	-0.0040	0.054	-0.0051	0.049	-0.0046	0.009	-0.0027	0.020	0.033
Oke_U212-87	0.0052	0.182	0.0159	0.449	0.0015	0.076	-0.0053	0.001	0.177
Oke_u216-222	-0.0049	0.041	-0.0029	0.090	-0.0027	0.031	0.0096	0.110	0.068
Oke_u217-172	0.0072	0.210	0.0044	0.231	-0.0052	0.003	-0.0036	0.014	0.114

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Appendix E. Page 7 of 7.

	Norton Sound / Lower Yukon		Lower Yukon / Lower Kuskokwim		Lower Kuskokwim / Western Bristol Bay		Western Bristol Bay / Eastern Bristol Bay		
Locus	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	F_{ST}	ZeroOneScores	Avg. ZeroOneScores
Oke_U302-195	-0.0051	0.038	-0.0047	0.056	0.0031	0.094	-0.0053	0.001	0.048
Oke_U401-143	-0.0047	0.043	-0.0052	0.047	-0.0018	0.041	-0.0033	0.016	0.037
Oke_U502-241	0.0101	0.250	-0.0048	0.055	0.0059	0.125	-0.0036	0.013	0.111
Oke_U503-272	0.0129	0.289	-0.0008	0.130	-0.0003	0.057	-0.0006	0.035	0.128
Oke_U504-228	0.0043	0.170	-0.0024	0.099	-0.0051	0.004	0.0004	0.042	0.079
Oke_U505-112	-0.0016	0.086	0.0010	0.166	-0.0039	0.017	-0.0031	0.017	0.072
Oke_U506-110	-0.0051	0.037	-0.0052	0.046	0.0029	0.092	0.0081	0.099	0.069
Oke_U507-286	-0.0007	0.099	0.0005	0.155	0.0127	0.200	-0.0045	0.007	0.115
Oke_U509-219	-0.0038	0.057	-0.0017	0.114	0.0042	0.106	-0.0052	0.002	0.070
Oke_U510-204	-0.0042	0.050	-0.0052	0.047	-0.0043	0.013	0.0049	0.076	0.046
Oke_U511-271	-0.0045	0.046	-0.0038	0.074	-0.0051	0.003	-0.0032	0.017	0.035
Oke_U514-150	0.0096	0.243	-0.0054	0.043	-0.0044	0.011	-0.0002	0.038	0.084
Oke_uqcrfs-69	-0.0017	0.085	-0.0042	0.065	-0.0001	0.059	-0.0053	0.001	0.053
Oke_zn593-152	0.0012	0.126	-0.0038	0.073	0.0031	0.094	-0.0054	0.000	0.073

[a] Nuclear SNP composite phenotypes.

[b] Mitochondrial SNP composite phenotype.

Appendix F.–The amount of variation explained by each of the first 2 components (PC 1 and PC 2) of the principal component analysis, and ZeroOneScores, scaled values were scaled linearly between 0.0 (lowest) and 1.0 (highest). Measured value 2.a. and 2.b. as outlined in Figure 3 – see text for methods.

Marker	PC 1	ZeroOneScores	PC 2	ZeroOneScores
Oke_ACOT-100	0.8	0.286	0.3	0.067
Oke_AhR1-278	0.3	0.107	0.1	0.022
Oke_AhR1-78	0.1	0.036	0.4	0.089
Oke_APOB-60	0.3	0.107	1.6	0.356
Oke_arf-319	0.4	0.143	0.2	0.044
Oke_ATP5L-105	0.3	0.107	0.3	0.067
Oke_azin1-90	0.1	0.036	0.2	0.044
Oke_brd2-118	0.2	0.071	0.6	0.133
Oke_brp16-65	0.6	0.214	0.6	0.133
Oke_CATB-60	1.6	0.571	0.7	0.156
Oke_ccd16-77	0.3	0.107	0.5	0.111
Oke_CD123-62	1.2	0.429	0.1	0.022
Oke_CD81-108	1.4	0.500	0.4	0.089
Oke_CD81-173	1.3	0.464	0.1	0.022
Oke_cjo57-86	0.1	0.036	0.4	0.089
Oke_CKS1-70	1.0	0.357	0.4	0.089
Oke_CKS1-94	0.5	0.179	0.4	0.089
Oke_CKS-389	0.2	0.071	0.5	0.111
Oke_CO1A1-72	1.0	0.357	0.4	0.089
Oke_CO1A1-76	0.4	0.143	0.0	0.000
Oke_col1a2-62	1.6	0.571	0.1	0.022
Oke_ctgf-105	0.8	0.286	0.2	0.044
Oke_CTR2-82	0.1	0.036	1.1	0.244
Oke_DBLOH-79	1.2	0.429	0.8	0.178
Oke_DCXR-87	1.3	0.464	0.3	0.067
Oke_DM20-548	0.5	0.179	0.7	0.156
Oke_e2ig5-50	0.0	0.000	1.1	0.244
Oke_EF2-394	0.3	0.107	0.9	0.200
Oke_eif4ebp2-64	0.5	0.179	0.8	0.178
Oke_eif4g1-43	0.1	0.036	0.3	0.067
Oke_f5-71	0.1	0.036	0.4	0.089
Oke_FANK1-166	1.8	0.643	0.8	0.178
Oke_FANK1-96	0.9	0.321	0.0	0.000
Oke_FBXL5-61	1.2	0.429	0.3	0.067
gdhComb[a]	0.8	0.286	1.9	0.422

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Appendix F. Page 2 of 5.

Marker	PC 1	ZeroOneScores	PC 2	ZeroOneScores
Oke_GHII-3129	0.5	0.179	1.7	0.378
Oke_glrx1-78	0.0	0.000	0.5	0.111
Oke_GNMT-100	0.6	0.214	0.3	0.067
Oke_GnRH-373	0.6	0.214	0.9	0.200
Oke_GPDH-191	0.1	0.036	1.0	0.222
Oke_GPH-105	0.7	0.250	0.1	0.022
Oke_GPH-78	0.4	0.143	0.5	0.111
Oke_H2AX-72	0.3	0.107	0.2	0.044
Oke_hmgb1-66	0.2	0.071	0.1	0.022
Oke_hnRNPL-239	0.3	0.107	0.5	0.111
Oke_HP-182	0.1	0.036	0.4	0.089
Oke_hsc71-199	0.2	0.071	0.6	0.133
Oke_HSP90BA-299	0.2	0.071	0.1	0.022
Oke_il-1racp-67	0.9	0.321	0.3	0.067
Oke_IL8r2-406	0.2	0.071	1.0	0.222
Oke_KPNA2-87	0.5	0.179	0.7	0.156
Oke_lactb2-71	0.2	0.071	0.1	0.022
Oke_lamp2-138	0.1	0.036	1.1	0.244
Oke_LAMP2-186	0.0	0.000	1.3	0.289
Oke_mcfd2-86	1.3	0.464	0.0	0.000
Oke_METK2-97	0.5	0.179	0.2	0.044
Oke_mgll-49	0.2	0.071	0.6	0.133
Oke_MLRN-63	0.3	0.107	0.1	0.022
Oke_Moesin-160	0.1	0.036	0.5	0.111
mtDNA3[b]	2.8	1.000	4.5	1.000
Oke_nc2b-148	0.7	0.250	0.7	0.156
Oke_ndub3-58	0.3	0.107	0.1	0.022
Oke_NHERF-54	0.2	0.071	0.8	0.178
Oke_NUPR1-70	0.1	0.036	1.4	0.311
Oke_PDIA3-475	0.1	0.036	0.9	0.200
pgapComb[a]	1.6	0.571	1.5	0.333
Oke_pnrc2-78	0.5	0.179	0.6	0.133
Oke_PPA2-635	1.2	0.429	0.2	0.044
Oke_psmd9-57	0.2	0.071	0.4	0.089
Oke_rab5a-117	1.6	0.571	0.2	0.044
Oke_ras1-249	0.8	0.286	0.8	0.178
Oke_RFC2-618	1.8	0.643	0.7	0.156

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Appendix F. Page 3 of 5.

Marker	PC 1	ZeroOneScores	PC 2	ZeroOneScores
Oke_RH1op-245	0.7	0.250	1.0	0.222
Oke_ROA1-209	0.9	0.321	1.2	0.267
Oke_RPN1-80	0.3	0.107	1.6	0.356
Oke_RS27-81	0.4	0.143	0.0	0.000
Oke_RS9-379	0.6	0.214	1.7	0.378
Oke_RSPRY1-106	0.7	0.250	0.8	0.178
Oke_serpin-140	0.5	0.179	0.8	0.178
Oke_slc1a3a-86	0.6	0.214	0.3	0.067
Oke_sylc-90	0.5	0.179	0.2	0.044
Oke_TCP1-78	0.8	0.286	1.2	0.267
Oke_TCTA-202	0.1	0.036	0.5	0.111
Oke_Tf-278	0.5	0.179	1.6	0.356
Oke_thic-84	0.9	0.321	0.3	0.067
Oke_txnrd1-74	0.3	0.107	1.0	0.222
Oke_U1002-262	1.0	0.357	0.7	0.156
Oke_U1008-83	0.7	0.250	1.2	0.267
Oke_U1010-154	0.9	0.321	1.5	0.333
Oke_U1010-251	0.4	0.143	1.0	0.222
Oke_U1015-255	0.3	0.107	0.5	0.111
Oke_U1016-154	0.1	0.036	0.6	0.133
Oke_U1017-52	1.0	0.357	0.2	0.044
Oke_U1018-50	0.6	0.214	0.8	0.178
Oke_U1019-218	0.7	0.250	0.2	0.044
Oke_U1020-75	0.3	0.107	0.1	0.022
Oke_U1012-241	0.2	0.071	0.6	0.133
Oke_U1023-147	1.3	0.464	0.2	0.044
Oke_U1024-113	0.4	0.143	0.5	0.111
Oke_U1025-135	0.3	0.107	1.0	0.222
Oke_U1027-89	1.1	0.393	0.5	0.111
Oke_U1028-100	0.2	0.071	0.3	0.067
U102Comb[a]	2.2	0.786	2.1	0.467
Oke_U1031-132	0.1	0.036	0.5	0.111
Oke_u1-519	0.7	0.250	1.5	0.333
Oke_U2001-629	0.0	0.000	1.6	0.356
Oke_U2002-200	1.1	0.393	0.3	0.067
Oke_U2003-142	0.8	0.286	0.4	0.089
Oke_u200-385	1.1	0.393	0.4	0.089
Oke_U2005-62	0.1	0.036	1.0	0.222

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Appendix F. Page 4 of 5.

Marker	PC 1	ZeroOneScores	PC 2	ZeroOneScores
Oke_U2006-109	0.4	0.143	0.3	0.067
Oke_U2007-190	0.7	0.250	1.3	0.289
Oke_U2010-94	0.7	0.250	0.7	0.156
Oke_U2011-107	0.9	0.321	0.1	0.022
Oke_U2015-151	1.5	0.536	0.4	0.089
Oke_U2016-118	1.0	0.357	0.1	0.022
Oke_U2017-87	0.7	0.250	0.1	0.022
Oke_U2019-112	0.9	0.321	0.1	0.022
Oke_u2020-51	0.6	0.214	1.0	0.222
Oke_u202-131	0.6	0.214	1.0	0.222
Oke_U2021-86	0.3	0.107	0.2	0.044
Oke_U2022-101	0.7	0.250	0.1	0.022
Oke_U2023-99	1.5	0.536	0.3	0.067
Oke_U2024-93	0.4	0.143	0.7	0.156
Oke_U2025-86	0.1	0.036	0.3	0.067
Oke_U2026-64	1.1	0.393	0.0	0.000
Oke_U2029-79	0.2	0.071	1.1	0.244
Oke_U2031-37	0.6	0.214	0.9	0.200
Oke_U2032-74	0.0	0.000	0.7	0.156
Oke_U2033-122	0.5	0.179	0.5	0.111
Oke_U2034-55	0.7	0.250	1.0	0.222
Oke_U2035-54	0.4	0.143	0.2	0.044
Oke_U2037-76	0.8	0.286	0.1	0.022
Oke_U2041-84	0.3	0.107	0.2	0.044
Oke_U2042-61	1.4	0.500	0.8	0.178
Oke_U2043-51	0.4	0.143	0.3	0.067
Oke_U2045-43	0.9	0.321	0.4	0.089
Oke_U2047-49	1.2	0.429	0.1	0.022
Oke_U2048-91	0.2	0.071	0.0	0.000
Oke_U2049-99	0.5	0.179	1.3	0.289
Oke_U2050-101	0.5	0.179	0.2	0.044
Oke_U2052-56	0.6	0.214	0.9	0.200
Oke_U2053-60	0.6	0.214	0.0	0.000
Oke_U2054-58	0.9	0.321	0.1	0.022
Oke_U2056-90	0.4	0.143	0.5	0.111
Oke_U2057-80	1.2	0.429	0.6	0.133
Oke_U212-87	0.4	0.143	0.8	0.178
Oke_u216-222	0.7	0.250	0.1	0.022

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Appendix F. Page 5 of 5.

Marker	PC 1	ZeroOneScores	PC 2	ZeroOneScores
Oke_u217-172	0.1	0.036	1.0	0.222
Oke_U302-195	1.3	0.464	0.3	0.067
Oke_U401-143	0.1	0.036	0.7	0.156
Oke_U502-241	1.9	0.679	1.2	0.267
Oke_U503-272	0.4	0.143	0.6	0.133
Oke_U504-228	1.0	0.357	0.1	0.022
Oke_U505-112	0.4	0.143	0.7	0.156
Oke_U506-110	0.1	0.036	1.0	0.222
Oke_U507-286	0.1	0.036	1.0	0.222
Oke_U509-219	0.5	0.179	0.5	0.111
Oke_U510-204	0.1	0.036	0.0	0.000
Oke_U511-271	0.1	0.036	0.5	0.111
Oke_U514-150	0.5	0.179	0.4	0.089
Oke_uqcrfs-69	0.0	0.000	0.8	0.178
Oke_zn593-152	0.6	0.214	0.4	0.089

[a] Nuclear SNP composite phenotypes.

[b] Mitochondrial SNP composite phenotype.

Appendix G.–F_{ST} between populations from Honshu and Hokkaido islands and ZeroOneScores, scaled values were scaled linearly between 0.0 (lowest) and 1.0 (highest). Measured value 3.a. as outlined in Figure 3 – see text for methods.

Marker	F_{ST}	ZeroOneScores
Oke_ACOT-100	-0.0027	0.020
Oke_AhR1-278	-0.0042	0.012
Oke_AhR1-78	0.0793	0.439
Oke_APOB-60	0.0409	0.242
Oke_arf-319	0.0468	0.273
Oke_ATP5L-105	0.0128	0.099
Oke_azin1-90	0.0643	0.362
Oke_brd2-118	-0.0044	0.011
Oke_brp16-65	0.0065	0.067
Oke_CATB-60	0.0100	0.084
Oke_ccd16-77	0.1812	0.960
Oke_CD123-62	-0.0057	0.004
Oke_CD81-108	0.0065	0.067
Oke_CD81-173	0.0164	0.118
Oke_cjo57-86	-0.0061	0.003
Oke_CKS1-70	-0.0065	0.000
Oke_CKS1-94	-0.0051	0.008
Oke_CKS-389	0.1890	1.000
Oke_CO1A1-72	-0.0063	0.001
Oke_CO1A1-76	0.0063	0.066
Oke_col1a2-62	0.0503	0.291
Oke_ctgf-105	0.0129	0.099
Oke_CTR2-82	0.0213	0.142
Oke_DBLOH-79	0.0362	0.218
Oke_DCXR-87	0.0129	0.099
Oke_DM20-548	0.0543	0.311
Oke_e2ig5-50	0.0090	0.080
Oke_EF2-394	0.0024	0.046
Oke_eif4ebp2-64	-0.0004	0.032
Oke_eif4g1-43	-0.0059	0.003
Oke_f5-71	0.0222	0.147
Oke_FANK1-166	0.0824	0.455
Oke_FANK1-96	0.1312	0.705
Oke_FBXL5-61	0.0442	0.259
gdhComb[a]	0.0030	0.049
Oke_GHII-3129	0.0050	0.059
Oke_glrx1-78	0.0019	0.043
Oke_GNMT-100	-0.0033	0.016
Oke_GnRH-373	0.0094	0.082

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Appendix G. Page 2 of 5.

Marker	F_{ST}	ZeroOneScores
Oke_GPDH-191	0.0749	0.417
Oke_GPH-105	0.0856	0.471
Oke_GPH-78	0.0037	0.052
Oke_H2AX-72	0.1878	0.994
Oke_hmgb1-66	0.0234	0.153
Oke_hnRNPL-239	-0.0063	0.001
Oke_HP-182	-0.0049	0.008
Oke_hsc71-199	0.0000	0.033
Oke_HSP90BA-299	-0.0063	0.001
Oke_il-1racp-67	0.0000	0.033
Oke_IL8r2-406	0.0069	0.069
Oke_KPNA2-87	0.0025	0.046
Oke_lactb2-71	-0.0022	0.022
Oke_lamp2-138	-0.0041	0.012
Oke_LAMP2-186	-0.0041	0.012
Oke_mcfd2-86	-0.0007	0.030
Oke_METK2-97	0.0237	0.155
Oke_mgll-49	-0.0004	0.031
Oke_MLRN-63	0.0973	0.531
Oke_Moesin-160	0.0000	0.033
mtDNA3[b]	0.0523	0.301
Oke_nc2b-148	-0.0025	0.020
Oke_ndub3-58	-0.0058	0.004
Oke_NHERF-54	0.0537	0.308
Oke_NUPR1-70	0.0402	0.239
Oke_PDIA3-475	0.0138	0.104
pgapComb[a]	0.0093	0.081
Oke_pnrc2-78	0.0116	0.093
Oke_PPA2-635	0.1384	0.741
Oke_psmd9-57	0.0368	0.222
Oke_rab5a-117	0.0314	0.194
Oke_ras1-249	-0.0046	0.010
Oke_RFC2-618	0.0000	0.033
Oke_RH1op-245	0.0000	0.033
Oke_ROA1-209	0.0115	0.092
Oke_RPN1-80	0.0216	0.144
Oke_RS27-81	0.0183	0.127
Oke_RS9-379	-0.0006	0.030
Oke_RSPRY1-106	0.0152	0.111
Oke_serpin-140	0.0538	0.309
Oke_slc1a3a-86	-0.0024	0.021

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Marker	F_{ST}	ZeroOneScores
Oke_sylc-90	0.0035	0.052
Oke_TCP1-78	-0.0050	0.008
Oke_TCTA-202	-0.0023	0.022
Oke_Tf-278	-0.0018	0.024
Oke_thic-84	0.1217	0.656
Oke_txnrd1-74	-0.0012	0.027
Oke_U1002-262	0.0210	0.141
Oke_U1008-83	0.0000	0.033
Oke_U1010-154	-0.0003	0.032
Oke_U1010-251	0.0081	0.075
Oke_U1015-255	0.0190	0.131
Oke_U1016-154	-0.0048	0.009
Oke_U1017-52	0.0027	0.047
Oke_U1018-50	-0.0029	0.018
Oke_U1019-218	0.0001	0.034
Oke_U1020-75	0.0001	0.034
Oke_U1012-241	-0.0042	0.012
Oke_U1023-147	0.0390	0.233
Oke_U1024-113	-0.0032	0.017
Oke_U1025-135	-0.0054	0.006
Oke_U1027-89	0.0001	0.034
Oke_U1028-100	0.0167	0.119
U102Comb[a]	0.0543	0.311
Oke_U1031-132	-0.0002	0.033
Oke_u1-519	0.0881	0.484
Oke_U2001-629	-0.0008	0.030
Oke_U2002-200	0.0852	0.469
Oke_U2003-142	0.0002	0.034
Oke_u200-385	0.0173	0.122
Oke_U2005-62	-0.0065	0.000
Oke_U2006-109	0.1885	0.997
Oke_U2007-190	0.0944	0.516
Oke_U2010-94	-0.0061	0.002
Oke_U2011-107	0.0223	0.148
Oke_U2015-151	0.0000	0.033
Oke_U2016-118	0.0534	0.306
Oke_U2017-87	0.0000	0.033
Oke_U2019-112	0.0174	0.122
Oke_u2020-51	0.0602	0.341
Oke_u202-131	0.0443	0.260
Oke_U2021-86	0.0259	0.166

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Marker	F_{ST}	ZeroOneScores
Oke_U2022-101	0.0000	0.033
Oke_U2023-99	0.0000	0.033
Oke_U2024-93	0.0654	0.368
Oke_U2025-86	0.0778	0.431
Oke_U2026-64	0.0330	0.202
Oke_U2029-79	0.0932	0.510
Oke_U2031-37	0.0039	0.053
Oke_U2032-74	-0.0037	0.015
Oke_U2033-122	-0.0012	0.027
Oke_U2034-55	0.0552	0.316
Oke_U2035-54	-0.0043	0.012
Oke_U2037-76	0.0001	0.034
Oke_U2041-84	-0.0011	0.028
Oke_U2042-61	0.0000	0.033
Oke_U2043-51	0.0115	0.092
Oke_U2045-43	0.0275	0.174
Oke_U2047-49	0.0593	0.336
Oke_U2048-91	0.0033	0.051
Oke_U2049-99	0.0020	0.043
Oke_U2050-101	0.0000	0.033
Oke_U2052-56	0.0440	0.259
Oke_U2053-60	-0.0061	0.002
Oke_U2054-58	-0.0036	0.015
Oke_U2056-90	0.0656	0.369
Oke_U2057-80	0.0020	0.044
Oke_U212-87	0.0043	0.056
Oke_u216-222	0.0000	0.033
Oke_u217-172	0.0084	0.076
Oke_U302-195	0.0189	0.130
Oke_U401-143	-0.0022	0.022
Oke_U502-241	0.0811	0.448
Oke_U503-272	0.0258	0.165
Oke_U504-228	-0.0037	0.014
Oke_U505-112	-0.0061	0.002
Oke_U506-110	0.0000	0.033
Oke_U507-286	0.0731	0.407
Oke_U509-219	0.1240	0.668
Oke_U510-204	0.0042	0.055
Oke_U511-271	0.0000	0.033
Oke_U514-150	-0.0001	0.033
Oke_uqcrfs-69	-0.0041	0.012

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Marker	F_{ST}	ZeroOneScores
Oke_zn593-152	0.0032	0.050

[a] Nuclear SNP composite phenotypes.

[b] Mitochondrial SNP composite phenotype.

Appendix H.–F_{ST} between populations from Southeast Alaska and Northern British Columbia and ZeroOneScores, scaled values were scaled linearly between 0.0 (lowest) and 1.0 (highest). Measured value 3.b. as outlined in Figure 3 – see text for methods.

Marker	F_{ST}	ZeroOneScores
Oke_ACOT-100	0.0009	0.070
Oke_AhR1-278	-0.0053	0.027
Oke_AhR1-78	-0.0048	0.031
Oke_APOB-60	0.0217	0.211
Oke_arf-319	0.0531	0.425
Oke_ATP5L-105	-0.0033	0.041
Oke_azin1-90	0.0304	0.270
Oke_brd2-118	-0.0043	0.035
Oke_brp16-65	-0.0054	0.027
Oke_CATB-60	-0.0050	0.030
Oke_ccd16-77	-0.0032	0.041
Oke_CD123-62	-0.0032	0.042
Oke_CD81-108	-0.0001	0.063
Oke_CD81-173	-0.0035	0.040
Oke_cjo57-86	-0.0026	0.046
Oke_CKS1-70	0.0040	0.091
Oke_CKS1-94	-0.0007	0.059
Oke_CKS-389	-0.0050	0.029
Oke_CO1A1-72	-0.0049	0.030
Oke_CO1A1-76	-0.0034	0.041
Oke_col1a2-62	0.0649	0.505
Oke_ctgf-105	-0.0053	0.027
Oke_CTR2-82	-0.0045	0.033
Oke_DBLOH-79	-0.0038	0.037
Oke_DCXR-87	0.0390	0.329
Oke_DM20-548	0.0073	0.113
Oke_e2ig5-50	-0.0020	0.050
Oke_EF2-394	0.0017	0.075
Oke_eif4ebp2-64	0.0114	0.141
Oke_eif4g1-43	-0.0049	0.030
Oke_f5-71	-0.0048	0.031
Oke_FANK1-166	0.0112	0.140
Oke_FANK1-96	-0.0049	0.030
Oke_FBXL5-61	0.0279	0.253
gdhComb[a]	0.0601	0.472
Oke_GHII-3129	0.0092	0.126
Oke_glrx1-78	-0.0039	0.037
Oke_GNMT-100	-0.0040	0.036
Oke_GnRH-373	0.0132	0.153

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Appendix H. Page 2 of 5.

Marker	F_{ST}	ZeroOneScores
Oke_GPDH-191	-0.0028	0.044
Oke_GPH-105	-0.0049	0.030
Oke_GPH-78	-0.0046	0.032
Oke_H2AX-72	0.0303	0.269
Oke_hmgb1-66	-0.0026	0.046
Oke_hnRNPL-239	0.0000	0.063
Oke_HP-182	0.0280	0.254
Oke_hsc71-199	-0.0048	0.031
Oke_HSP90BA-299	-0.0053	0.027
Oke_il-1racp-67	-0.0015	0.053
Oke_IL8r2-406	-0.0039	0.037
Oke_KPNA2-87	0.1377	1.000
Oke_lactb2-71	0.0083	0.120
Oke_lamp2-138	-0.0054	0.027
Oke_LAMP2-186	0.0027	0.082
Oke_mcfd2-86	-0.0056	0.025
Oke_METK2-97	0.0174	0.182
Oke_mgll-49	0.0172	0.180
Oke_MLRN-63	0.0047	0.096
Oke_Moesin-160	0.0037	0.088
mtDNA3[b]	0.0000	0.063
Oke_nc2b-148	-0.0055	0.026
Oke_ndub3-58	0.0165	0.176
Oke_NHERF-54	0.0010	0.070
Oke_NUPR1-70	0.0228	0.219
Oke_PDIA3-475	0.0906	0.680
pgapComb[a]	-0.0093	0.000
Oke_pnrc2-78	0.0232	0.221
Oke_PPA2-635	-0.0038	0.038
Oke_psmd9-57	0.0449	0.369
Oke_rab5a-117	-0.0048	0.031
Oke_ras1-249	0.0038	0.089
Oke_RFC2-618	0.0002	0.065
Oke_RH1op-245	0.0119	0.145
Oke_ROA1-209	-0.0055	0.026
Oke_RPN1-80	0.0069	0.110
Oke_RS27-81	0.0075	0.115
Oke_RS9-379	0.0016	0.074
Oke_RSPRY1-106	0.0354	0.304
Oke_serpin-140	0.0043	0.093
Oke_slc1a3a-86	0.0389	0.328

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Marker	F_{ST}	ZeroOneScores
Oke_sylc-90	-0.0049	0.030
Oke_TCP1-78	0.0094	0.128
Oke_TCTA-202	0.0775	0.591
Oke_Tf-278	0.0025	0.081
Oke_thic-84	0.0899	0.675
Oke_txnrd1-74	0.0094	0.127
Oke_U1002-262	-0.0022	0.048
Oke_U1008-83	-0.0012	0.055
Oke_U1010-154	0.0000	0.063
Oke_U1010-251	-0.0034	0.041
Oke_U1015-255	0.0089	0.124
Oke_U1016-154	-0.0005	0.060
Oke_U1017-52	0.0165	0.176
Oke_U1018-50	-0.0036	0.039
Oke_U1019-218	0.0003	0.066
Oke_U1020-75	0.0388	0.328
Oke_U1012-241	-0.0014	0.054
Oke_U1023-147	-0.0054	0.027
Oke_U1024-113	0.0215	0.209
Oke_U1025-135	0.0000	0.063
Oke_U1027-89	0.0311	0.275
Oke_U1028-100	-0.0053	0.027
U102Comb[a]	0.0016	0.074
Oke_U1031-132	0.0290	0.261
Oke_u1-519	0.0321	0.282
Oke_U2001-629	-0.0006	0.059
Oke_U2002-200	-0.0045	0.033
Oke_U2003-142	-0.0017	0.052
Oke_u200-385	-0.0031	0.042
Oke_U2005-62	0.0414	0.345
Oke_U2006-109	0.0175	0.182
Oke_U2007-190	0.0019	0.076
Oke_U2010-94	0.0034	0.087
Oke_U2011-107	0.0005	0.067
Oke_U2015-151	-0.0028	0.044
Oke_U2016-118	0.0016	0.074
Oke_U2017-87	-0.0053	0.027
Oke_U2019-112	-0.0040	0.036
Oke_u2020-51	-0.0053	0.027
Oke_u202-131	0.0000	0.063
Oke_U2021-86	0.0002	0.065

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Marker	F_{ST}	ZeroOneScores
Oke_U2022-101	0.0005	0.067
Oke_U2023-99	-0.0036	0.039
Oke_U2024-93	-0.0031	0.042
Oke_U2025-86	-0.0053	0.027
Oke_U2026-64	0.0000	0.063
Oke_U2029-79	-0.0039	0.037
Oke_U2031-37	0.0021	0.077
Oke_U2032-74	-0.0027	0.045
Oke_U2033-122	0.0547	0.435
Oke_U2034-55	-0.0015	0.053
Oke_U2035-54	0.1089	0.804
Oke_U2037-76	0.0071	0.112
Oke_U2041-84	-0.0053	0.027
Oke_U2042-61	0.0341	0.296
Oke_U2043-51	-0.0037	0.039
Oke_U2045-43	-0.0022	0.049
Oke_U2047-49	0.0037	0.088
Oke_U2048-91	0.0096	0.129
Oke_U2049-99	0.0042	0.092
Oke_U2050-101	0.0531	0.425
Oke_U2052-56	0.0255	0.237
Oke_U2053-60	-0.0048	0.031
Oke_U2054-58	0.0029	0.083
Oke_U2056-90	-0.0018	0.051
Oke_U2057-80	0.0056	0.102
Oke_U212-87	0.0184	0.189
Oke_u216-222	-0.0030	0.043
Oke_u217-172	0.0007	0.068
Oke_U302-195	-0.0016	0.053
Oke_U401-143	-0.0051	0.029
Oke_U502-241	0.1340	0.975
Oke_U503-272	0.0001	0.064
Oke_U504-228	0.0255	0.237
Oke_U505-112	-0.0050	0.030
Oke_U506-110	0.0920	0.690
Oke_U507-286	-0.0019	0.050
Oke_U509-219	-0.0036	0.039
Oke_U510-204	0.0095	0.128
Oke_U511-271	-0.0029	0.044
Oke_U514-150	0.0270	0.247
Oke_uqcrfs-69	0.0000	0.063

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Appendix H. Page 5 of 5.

Marker	F_{ST}	ZeroOneScores
Oke_zn593-152	0.0013	0.072

[a] Nuclear SNP composite phenotypes.

[b] Mitochondrial SNP composite phenotype.

Appendix I.–θ_p between population pairs from British Columbia and Washington and ZeroOneScores, scaled values were scaled linearly between 0.0 (lowest) and 1.0 (highest). Measured value 3.c. as outlined in Figure 3 – see text for methods.

Marker	θ_P	ZeroOneScores
Oke_ACOT-100	0.1726	0.554
Oke_AhR1-278	0.0004	0.205
Oke_AhR1-78	-0.0059	0.192
Oke_APOB-60	0.0141	0.233
Oke_arf-319	0.0076	0.220
Oke_ATP5L-105	-0.0195	0.165
Oke_azin1-90	0.1072	0.421
Oke_brd2-118	0.0231	0.251
Oke_brp16-65	0.0344	0.274
Oke_CATB-60	0.0217	0.248
Oke_ccd16-77	0.1300	0.467
Oke_CD123-62	0.1113	0.430
Oke_CD81-108	0.0000	0.204
Oke_CD81-173	0.0015	0.207
Oke_cjo57-86	0.0180	0.241
Oke_CKS1-70	-0.0125	0.179
Oke_CKS1-94	-0.0108	0.182
Oke_CKS-389	0.0688	0.344
Oke_CO1A1-72	0.0087	0.222
Oke_CO1A1-76	-0.0084	0.187
Oke_col1a2-62	0.0412	0.288
Oke_ctgf-105	0.0243	0.254
Oke_CTR2-82	0.0007	0.206
Oke_DBLOH-79	0.0178	0.240
Oke_DCXR-87	0.0560	0.318
Oke_DM20-548	0.0372	0.280
Oke_e2ig5-50	-0.0011	0.202
Oke_EF2-394	0.0048	0.214
Oke_eif4ebp2-64	0.0718	0.350
Oke_eif4g1-43	-0.0055	0.193
Oke_f5-71	0.0612	0.328
Oke_FANK1-166	-0.0058	0.193
Oke_FANK1-96	-0.0025	0.199
Oke_FBXL5-61	-0.0248	0.154
gdhComb[a]	0.0595	0.325
Oke_GHII-3129	0.0049	0.214
Oke_glrx1-78	0.0785	0.363
Oke_GNMT-100	0.0071	0.219
Oke_GnRH-373	0.0080	0.221

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Appendix I. Page 2 of 5.

Marker	θ_P	ZeroOneScores
Oke_GPDH-191	0.0355	0.276
Oke_GPH-105	0.0752	0.357
Oke_GPH-78	0.0378	0.281
Oke_H2AX-72	0.0172	0.239
Oke_hmgb1-66	-0.0243	0.155
Oke_hnRNPL-239	0.0000	0.204
Oke_HP-182	-0.0057	0.193
Oke_hsc71-199	0.0093	0.223
Oke_HSP90BA-299	0.0008	0.206
Oke_il-1racp-67	0.0057	0.216
Oke_IL8r2-406	-0.0014	0.202
Oke_KPNA2-87	-0.0020	0.200
Oke_lactb2-71	0.0540	0.314
Oke_lamp2-138	0.0076	0.220
Oke_LAMP2-186	0.1052	0.417
Oke_mcfd2-86	0.1211	0.449
Oke_METK2-97	0.0043	0.213
Oke_mgll-49	0.1313	0.470
Oke_MLRN-63	0.0006	0.205
Oke_Moesin-160	0.1127	0.433
mtDNA3[b]	0.0000	0.204
Oke_nc2b-148	0.0273	0.260
Oke_ndub3-58	-0.0007	0.203
Oke_NHERF-54	0.1143	0.436
Oke_NUPR1-70	-0.0030	0.198
Oke_PDIA3-475	-0.0012	0.202
pgapComb[a]	0.0104	0.225
Oke_pnrc2-78	-0.0038	0.197
Oke_PPA2-635	-0.0244	0.155
Oke_psmd9-57	-0.0034	0.197
Oke_rab5a-117	-0.0275	0.149
Oke_ras1-249	-0.0032	0.198
Oke_RFC2-618	0.0025	0.209
Oke_RH1op-245	0.0035	0.211
Oke_ROA1-209	-0.0096	0.185
Oke_RPN1-80	0.0091	0.223
Oke_RS27-81	0.0032	0.211
Oke_RS9-379	-0.0305	0.142
Oke_RSPRY1-106	0.2649	0.741
Oke_serpin-140	0.0505	0.306
Oke_slc1a3a-86	0.0047	0.214

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Appendix I. Page 3 of 5.

Marker	θ_P	ZeroOneScores
Oke_sylc-90	0.0048	0.214
Oke_TCP1-78	0.0214	0.248
Oke_TCTA-202	0.0574	0.321
Oke_Tf-278	0.0230	0.251
Oke_thic-84	-0.0339	0.136
Oke_txnrd1-74	0.0339	0.273
Oke_U1002-262	-0.1009	0.000
Oke_U1008-83	0.0093	0.223
Oke_U1010-154	0.0000	0.204
Oke_U1010-251	0.2342	0.679
Oke_U1015-255	0.1611	0.531
Oke_U1016-154	-0.0092	0.186
Oke_U1017-52	-0.0175	0.169
Oke_U1018-50	0.0082	0.221
Oke_U1019-218	0.0106	0.226
Oke_U1020-75	0.0472	0.300
Oke_U1012-241	0.0753	0.357
Oke_U1023-147	-0.0352	0.133
Oke_U1024-113	-0.0006	0.203
Oke_U1025-135	0.0000	0.204
Oke_U1027-89	0.0430	0.291
Oke_U1028-100	-0.0245	0.155
U102Comb[a]	0.0609	0.328
Oke_U1031-132	0.0327	0.271
Oke_u1-519	-0.0173	0.169
Oke_U2001-629	0.1723	0.553
Oke_U2002-200	0.1116	0.430
Oke_U2003-142	0.0247	0.254
Oke_u200-385	0.0295	0.264
Oke_U2005-62	-0.0088	0.187
Oke_U2006-109	0.0081	0.221
Oke_U2007-190	0.1084	0.424
Oke_U2010-94	0.0290	0.263
Oke_U2011-107	-0.0063	0.192
Oke_U2015-151	0.0145	0.234
Oke_U2016-118	0.1888	0.587
Oke_U2017-87	-0.0093	0.185
Oke_U2019-112	0.0816	0.369
Oke_u2020-51	-0.0003	0.204
Oke_u202-131	0.0000	0.204
Oke_U2021-86	0.1657	0.540

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Appendix I. Page 4 of 5.

Marker	θ_P	ZeroOneScores
Oke_U2022-101	0.0084	0.221
Oke_U2023-99	-0.0032	0.198
Oke_U2024-93	0.1869	0.583
Oke_U2025-86	0.0494	0.304
Oke_U2026-64	0.2893	0.790
Oke_U2029-79	0.3518	0.917
Oke_U2031-37	0.0081	0.221
Oke_U2032-74	0.0062	0.217
Oke_U2033-122	0.0056	0.216
Oke_U2034-55	0.0031	0.211
Oke_U2035-54	0.0525	0.311
Oke_U2037-76	0.0041	0.213
Oke_U2041-84	-0.0023	0.200
Oke_U2042-61	0.0637	0.333
Oke_U2043-51	0.0069	0.218
Oke_U2045-43	0.1764	0.561
Oke_U2047-49	-0.0035	0.197
Oke_U2048-91	0.2031	0.616
Oke_U2049-99	0.0511	0.308
Oke_U2050-101	0.0354	0.276
Oke_U2052-56	0.1497	0.507
Oke_U2053-60	0.0079	0.220
Oke_U2054-58	-0.0032	0.198
Oke_U2056-90	0.0070	0.218
Oke_U2057-80	0.0091	0.223
Oke_U212-87	0.0090	0.223
Oke_u216-222	0.0049	0.214
Oke_u217-172	-0.0107	0.183
Oke_U302-195	-0.0174	0.169
Oke_U401-143	0.0200	0.245
Oke_U502-241	0.3929	1.000
Oke_U503-272	0.0008	0.206
Oke_U504-228	-0.0383	0.127
Oke_U505-112	0.0010	0.206
Oke_U506-110	0.1507	0.510
Oke_U507-286	0.0865	0.379
Oke_U509-219	0.0704	0.347
Oke_U510-204	0.0207	0.246
Oke_U511-271	-0.0158	0.172
Oke_U514-150	0.0264	0.258
Oke_uqcrfs-69	0.0000	0.204

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Appendix I. Page 5 of 5.

Marker	θ_P	ZeroOneScores
Oke_zn593-152	0.0221	0.249

[a] Nuclear SNP composite phenotypes.

[b] Mitochondrial SNP composite phenotype.