Western Alaska Salmon Stock Identification Program **Technical Document**:[1] 6

Title: Selection of the 96 SNP marker set for sockeye salmon **Version:** 1.0
Authors: T. Dann, J. Jasper, H. Hoyt, H. Hildebrand, and C. Habicht
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Introduction

The WASSIP Advisory Panel requested that 96 single nucleotide polymorphism (SNP) markers be incorporated into the baselines for both sockeye salmon (*Oncorhynchus nerka*) and chum salmon (*O. keta*) to improve the precision and accuracy of stock composition estimates (March 24, 2008). To meet this request for sockeye salmon, we contracted the development of at least 55 SNP markers that were targeted to differentiate among populations spawning within western Alaska and the Alaska Peninsula drainages (forthcoming SNP Discovery Technical Document) and we requested novel SNPs developed by other laboratories. Through these sources, we received a total of 79 novel SNPs. Here we present the methodology for how the best-performing SNP markers for sockeye salmon were selected for WASSIP. These selected markers are being screened in baseline collections at this time and the new baseline genotypes should be complete by the end of July, 2010.

The purpose of this technical document is to describe the methods that the Gene Conservation Laboratory (GCL) used to choose the set of SNPs to be assayed in sockeye salmon for the WASSIP project. We intend to gather feedback from the Technical Committee on the methodology for marker selection in chum salmon. We anticipate having more markers to select from in chum salmon (i.e., 240 SNPs) than we did for sockeye salmon (i.e., 124 SNPs). For sockeye salmon, laboratory performance, conformance to Hardy-Weinberg expectations, linkage among loci, and discrimination among pairs of populations of interest were the primary judges used in marker selection. For chum salmon, we anticipate that population-discrimination factors

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will contribute to the marker selection to a greater degree because we will be starting 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.

Methods

Choice of test populations

We chose 24 populations from across the species range to represent the regions that produce the majority of sockeye salmon as well as the geographic and genetic diversity observed in previous analyses (Habicht et al. 2010). In addition to these production and diversity criteria, we included populations where collections met the following criteria: 1) fin, heart or liver tissue was available, 2) 8-10 DNA extractions worth of tissue was available for future analyses, and 3) 95 individuals were available for adequate estimates of allele frequencies. We intended this set of 24 populations to serve as a set of test populations for all laboratories interested in the population genetics of Pacific Rim sockeye salmon. In addition to one pair of populations in the set of 24 test populations, we included an additional 6 pairs of populations that were of interest to ADF&G for a total of 36 populations. Each pair of populations represented two regions which the Department desired greater genetic divergence between to aid in mixed stock analyses (MSA) for management purposes. Populations were assigned to fine- and broad-scale regions for use in regional measures of diversity.

Laboratory measures

Assaying Genotypes

Genomic DNA for more recent collections was extracted using a DNeasy® 96 Tissue Kit by QIAGEN® (Valencia, CA), while an inorganic method was used for some older collections. We screened the 45 current sockeye salmon SNP markers as well as 77 new SNP markers performed using Fluidigm® 96.96 Dynamic Arrays (http://www.fluidigm.com) and 1 current and 1 new marker on the Applied Biosystems platform. The Fluidigm® 96.96 Dynamic Array contains a matrix of integrated channels and valves housed in an input frame. On one side of the frame are 96 inlets to accept the sample DNA from each individual fish and on the other are 96 inlets to accept the assays for each SNP marker. Once in the wells, the components are pressurized into the chip using the IFC Controller HX (Fluidigm). The 96 samples and 96 assays are then systematically combined into 9,216 parallel reactions. In this study, 122 assays were loaded on two separate arrays. Each reaction is a mixture of 4µl of assay mix (1x DA Assay Loading Buffer (Fluidigm), 10x TaqMan® SNP Genotyping Assay (Applied Biosystems), and 2.5x ROX (Invitrogen)) and 5µl of sample mix (1x TaqMan® Universal Buffer (Applied Biosystems), 0.05x AmpliTaq® Gold DNA Polymerase (Applied Biosystems), 1x GT Sample Loading Reagent (Fluidigm) and 60-400ng/µl DNA) combined in a 7.2nL chamber. Thermal cycling was performed on an Eppendorf IFC Thermal Cycler as follows: 70°C for 30 min for "Hot-Mix" step, initial denaturation of 10 min at 96°C followed by 40 cycles of 96° for 15 s and 60° for 1 min. The Dynamic Arrays were read on a Fluidigm® EP1™ System after amplification and scored using Fluidigm® SNP Genotyping Analysis software.

The 2 assays genotyped on the Applied Biosystems platform was performed in 384-well reaction plates. Each reaction was conducted in a 5µL volume consisting of 5-40ng/µl of template DNA, 1x TaqMan® Universal PCR Master Mix (Applied Biosystems), and 1x TaqMan® SNP Genotyping Assay (Applied Biosystems). Thermal cycling was performed on a Dual 384-Well GeneAmp® PCR System 9700 (Applied Biosystems) as follows: an initial denaturation of 10 min at 95°C followed by 50 cycles of 92°C for 1s and annealing/extension temperature for 1 min. The plates were scanned on an Applied Biosystems Prism 7900HT Sequence Detection System after amplification and scored using Applied Biosystems' Sequence Detection Software (SDS) version 2.2.

Scoring Genotypes and Rating Assays

The most important measure of an assay's utility was the genotyping performance on our platform. We assessed the performance of these assays in our laboratory to determine their utility as markers used in the future for MSA.

Dynamic Arrays that experienced the same DNA and assay loading and PCR process were combined for scoring purposes, and are referred to as combined chip runs. Two Dynamic Arrays always experienced these same conditions on our platform, and so we scored 18 combined chip runs independently that serve as repeated measures for further laboratory performance judges. We entered collected genotypes into the GCL Oracle database, LOKI, for access for further analyses.

During the scoring process, we rated each combined chip run for 3 measures to judge laboratory performance. These measures were: 1) the spread of, 2) the space between, and 3) the alignment of genotype clusters. The spread of a genotype cluster was a measure of the variation among individuals of a genotype; an assay with very little variability in genotype clusters spread had tight genotype clusters that were easier to score and produced more reliable data (Figure 2). The space between genotype clusters was a measure of the distance between the edges of genotype clusters; an assay with large spacing between clusters had distinct clusters that were easier to score and produced more reliable data (Figure 3). The alignment of genotype clusters was a measure of the alignment of genotype clusters relative to the origin; an assay with separated cluster alignment from the origin had distinct genotype clusters. This measure is correlated with the space between clusters but can differ depending upon the distance from the origin (Figure 4).

For each of these measures, we gave each combined chip run a subjective score ranging between 1 (worst) and 5 (best). To avoid scoring and rating bias, each combined chip run was scored and rated by two people, one of which was always our most senior laboratory staff member for consistency and the other was one of the three other laboratory staff members involved with this project. In addition to these measures, we also calculated the success rate of an assay as the number of successfully genotyped individuals divided by the total number amplified. We tabulated the mean, variance and coefficient of variation (CV) for each of these measures of each assay and ranked each assay by its mean and CV for each measure. Rankings for all judges in this study were corrected for ties when necessary.

Population genetics measures

Conformance to Hardy-Weinberg Expectations

We tested population genotype frequencies at each marker for conformance to Hardy-Weinberg expectations (HWE) using GDA (Lewis and Zaykin 2001). We tabulated the number of populations that failed to conform to HWE for three levels of significance ($\alpha = 0.05$, 0.01, and 0.001), and ranked each marker based upon the number of populations that failed to conform to HWE for $\alpha = 0.05$. The number of the 36 test populations expected to fail to conform to HWE by chance at these three criteria are approximately 2, 0 and 0, respectively.

Linkage disequilibrium

We tested all pairs of nuclear markers for gametic disequilibrium within each collection using GDA (Lewis and Zaykin 2001). We defined a pair of markers to be significantly out of gametic equilibrium if tests for gametic disequilibrium were significant ($P < 0.01$) for greater than half of all collections. When gametic linkage was significant, we examined the distribution of the linkage across the range of the test populations to determine if there was a pattern to the phase of linkage that might be useful for MSA. We used the measure of linkage r (Hedrick 2005), which is D as described by Hill (1975) but corrected for allele frequency, to assess the phasing of linkage. We also estimated the haplotype frequencies as described by Hill (1975), and, if a haplotype was missing, we interpreted this as indicating the loci were in phase, in which case one locus provides the same amount of information as both linked loci. When a pair of loci were linked, and no pattern in the phase of linkage was observed, we chose which locus to keep for further analyses based upon ratings for the laboratory measures described above and observed heterozygosities. We did not rank markers based upon linkage; rather, we treated this measure as a “gating measure” beyond which only unlinked or usefully linked markers were allowed to continue on for ranking in further analyses.

Principal component analysis

We conducted a principal component analysis as a measure of how much of the overall genetic variation each marker explained. We calculated the contribution of each marker to the first and second principal components (PC1 and PC2, respectively), as well as the average contribution to the principal components that explained 80% of total variation. We ranked each marker based upon these three judges of informational content.

Measures of population divergence based upon F_{ST}

We calculated three measures of F_{ST} to assess how each marker described differentiation among populations and regions using the Weir and Cockerham measure of F_{ST} (θ) calculated in GDA (Lewis and Zaykin 2001). These measured variation partitioned among populations within fine-scale regions (θ_{S}), among fine-scale regions within broad-scale regions (θ_{P}), and between populations within pairs of populations of interest (θ_{Pairs}). We ranked each marker based upon each of these three F_{ST} measures; the marker with the highest F_{ST} value received the top rank.

Measures of population divergence among pairs of populations of interest

We used two measures to examine the divergence among pairs of populations of interest to assess how each marker differentiated populations of interest to ADF&G. These measures were the log likelihood ratio G statistic (Sokal and Rohlf 1995) from a test of the homogeneity of allele frequencies and f_{ORCA}. f_{ORCA} is a measure of informativeness described by Rosenberg (2005; Rosenberg et al. 2003) that indicates how well each marker assigns individuals back to their population of origin. The two measures differ in that the G test is based solely upon differences in population allele frequencies of a marker while f_{ORCA} measures a markers utility for population assignment.

Overall f_{ORCA}

We implemented the univariate accumulation algorithm described by Rosenberg (2005), using the Optimal Rate of Correct Assignment as a performance function (f_{ORCA}; Rosenberg et al. 2003; Rosenberg 2005). While the univariate accumulation method does not consider synergies between markers, Rosenberg (2005) demonstrated that it performs as well as methods that do consider synergies.

Sum of rankings and selection of final marker set

We investigated a nonparametric approach to determine how concordant rankings among differing measures of marker performance were. Specifically, we examined Kendall's coefficient of concordance (*W*), which measures the agreement among rankings of different judges (Sokal and Rohlf 1995). It is calculated as:

$$W = \frac{X^2}{k(n-1)} \qquad \text{(Eq. 1)}$$

where *k* is the number of variables or judges, *n* is the number of items per variable or items being ranked, and X^2 is a component of Friedman's method for randomized blocks, the nonparametric analog of a randomized block ANOVA (Sokal and Rohlf 1995). The statistic X^2 is calculated as:

$$X^2 = \left[\frac{12}{ab(a+1)}\sum^a \left(\sum^b R_{ij}\right)^2\right] - 3b(a+1) \qquad \text{(Eq. 2)}$$

where *a* is the number of treatments and is equal to *n* in Equation 1, *b* is the number of blocks and is equal to *k* in Equation 1, and R_{ij} is the sum of ranks across *b* blocks.

We were more interested in an overall measure of performance across many different judges, so we chose the R_{ij} of Equation 2 as our overall measure of marker performance. Markers were ranked based upon their R_{ij} values with the lowest value receiving the highest ranking. Some Markers lacked scores for some judges for various reasons (e.g., *G* tests when the marker was fixed between the populations being tested), and these markers were given rankings equal to the worst ranking for these judges. In contrast, mitochondrial SNPs (*One_CO1*, *One_Cytb_17*, and *One_Cytb_26*) were given rankings equal to the highest ranking for our Hardy-Weinberg judge, and both the mitochondrial SNPs and the two linked MHC SNPs (*One_MHC2_190* and

One_MHC2_251) were given the rankings that their combined haplotype/phenotype marker received.

We examined the top-ranked 96 markers from this final list with senior laboratory staff to ensure that their performance in the lab would produce reliable data. When it was deemed necessary, we replaced SNPs that performed very poorly with the next highest ranked SNP that we believed would produce reliable data.

The final consideration in choosing 96 markers was correspondence with stakeholder laboratories. We distributed our methodology and final list of 96 SNPs to these laboratories to see if any of the SNPs we chose to remove were highly valuable to other laboratories and could be easily replaced to maximize the efficiency of SNP data collection and standardize data sets across the Pacific Rim.

Population genetics measures not included in the ranking of SNPs

We conducted three other analyses of genetic variation among test populations that we ultimately did not include as judges for final rankings and marker selection. We present those analyses here for completeness and to help guide the methodology to be employed for chum salmon marker selection.

Backward elimination locus selection

We examined the marker contribution to correct individual assignment with the backward elimination locus selection algorithm incorporated in the program BELS (Bromaghin 2008). We did not define reporting groups as our regional groupings and numbers of populations within regions for this project were not representative of the reporting groups we have used in the past or intend to use with the sockeye baseline currently in production. Instead, we chose to maximize the mean individual assignment accuracy as our measure of performance and set a minimum performance of 0. We chose to resample baseline data, with equal baseline collection sample sizes of 95 individuals, to accurately represent our baseline for sockeye salmon. We chose to simulate genotypes for individual assignment from baseline allele frequencies with a fixed number of individuals per population. We set this number of individuals to be 190, which is representative of our desired minimum sample size for mixtures, and conducted 250 replications. Since the analysis took 54 days to complete with these parameters, and was not nearing completion when we chose our marker set, we did not include BELS rankings as a judge but report them here for completeness.

Hierarchical log-likelihood analysis

We examined the homogeneity of allele frequencies among populations within 9 fine-scale regions (Table 1) using a hierarchical log-likelihood ratio test (*G* test; Sokal and Rohlf, 1995). We included data from all independent nuclear markers and haplotype data for the mitochondrial SNPs and the two linked MHC SNPs. As the number of populations within regions differed greatly (i.e., 3 populations in the North Peninsula region, 7 populations in the Cook Inlet region), we divided *G* statistics by degrees of freedom to examine a measure of regional diversity less biased by sampling effort.

Nei's gene diversity analysis

Finally, we examined how diversity was distributed among the different hierarchical levels described above with Nei's Gene Diversity analysis (Nei 1987). We tabulated the percentage of variation attributable to allele frequency differences within populations (G_{WP}), among populations within fine-scale regions (G_{PF}), among fine-scale regions within broad-scale regions (G_{FB}), and among broad-scale regions within the total (G_{BT}) for each of the 124 SNPs (Tables 2 and 3) screened for 36 test populations (Table 1) of sockeye salmon.

Results

Choice of test populations

The 36 populations chosen as test populations represent regions producing the majority of sockeye salmon (Bristol Bay – 8 populations; Kamchatka Peninsula – 4 populations; Eggers and

Irvine 2007; Bugaev et al. 2008), much of the genetic diversity that has been observed (6 populations from the Alaska Peninsula and Kodiak; 8 populations from Southeast Alaska and British Columbia; Habicht et al. 2010), and a broad expanse of the species' range (Table 1; Figure 1). The pairs of populations of interest include 3 pairs of populations from Bristol Bay where the GCL has noted a lack of genetic divergence between reporting groups in the past (i.e., Igushik and Wood rivers, Egegik and Ugashik rivers, and Ugashik and Meshik rivers; Habicht et al. 2007; Dann et al. 2009), and where we hoped to find new discriminating markers. Similar reporting group overlap was identified in the Chignik River system (i.e., Black and Chignik lakes; Creelman et al. *In Prep*), in Cook Inlet (i.e., Yentna and Susitna river sloughs; Larson and Mama and Papa Bear lakes; Barclay et al. 2010), and in southern Southeast Alaska (i.e., McDonald and Hugh Smith lakes; GCL unpublished data). With the exception of Glacial Lake in the Norton Sound region, all of our regional groupings are represented by multiple populations; Norton Sound was subsequently included with the western Bristol Bay region.

Laboratory measures

Assaying Genotypes

A total of 3,447 fish from the 36 test populations (Table 1) were genotyped for the 124 markers included in this study (Table 2). When all markers were included, individuals were genotyped with a failure rate of 4.11%, but this is inflated artificially high because some markers failed in the laboratory and their genotypes for all individuals were zeroed out during the scoring process (see Scoring Genotypes and Rating Assays below). After correcting for these two markers, individuals were genotyped with a failure rate of 2.52%, which is common for our laboratory. A comparison of genotypes for the 45 SNPs previously genotyped for these collections and genotypes produced in this project revealed a low discrepancy rate of 0.30%. Assuming an equal error rate in the original and current genotyping process, and that this project accurately represents our genotyping process, these collections were genotyped with a process that produced genotypes with an error rate of 0.15%.

Scoring Genotypes and Rating Assays

A majority of assays performed well in our laboratory. The average cluster tightness was 3.7, and in general, ratings were normally distributed. Five assays were always rated 5 (best), few were rated very poorly (i.e., 5 assays rated < 3), and many assays were rated intermediate producing a 'broad shoulder' of intermediate ratings (Table 4; Figure 5). A more left-skewed distribution was observed for the measure of space between genotype clusters. (i.e. 26 assays rated < 3), with an average rating of 3.3 (Table 4; Figure 6). In contrast, a majority of assays produced genotype clusters with good alignment from the origin, with an average rating of 4.3, 34 with a rating of 5 and only 8 with a rating below 3 (Table 4; Figure 7). Three assays failed in the laboratory; two that exhibited multiple clusters, indicative of multiple SNPs (*One_PPM1K-118* and *One_U1207-231*) and one due to massive drop-outs (*One_UCA-24*). These assays were removed from further analyses.

Population genetics measures

Conformance to Hardy-Weinberg Expectations

Forty-one markers conformed to HWE in all populations, 38 for all but 1 population, and 26 for all but 2 populations at α = 0.05 (Table 5; Figure 9). The few variates observed for this measure resulted in many tied ranks (e.g., markers out of HWE for 1 population were ranked 60.5). While 12 markers failed to conform to HWE at more than 2 populations (α = 0.05), only one showed a considerable departure indicative of major problems (i.e., *One_ U1021-57*; 14 populations). As a result, we removed this SNP from further analyses.

Linkage disequilibrium

Three pairs of SNPs exhibited significant linkage disequilibrium in a majority of populations. These were *One_aldB-152*/*One_ALDOB-135* (36 populations at $\alpha = 0.05$), *One_GPH-414*/ *One_GTHa* (36 populations at $\alpha = 0.05$), and *One_MHC2_190*/ *One_MHC2_251* (26 populations at $\alpha = 0.05$) (Table 6). The linked MHC SNPs exhibit a pattern of linkage that is useful for MSA (i.e., a different phasing of linkage across regions) whereas the other two pairs do not (Figure 10; Supplement A.113). For the two pairs of SNPs without a useful pattern of linkage, we chose one SNP to retain for further analyses based upon laboratory ratings and observed heterozygosity (*One_aldB-152* and *One_GTHa*). For the remaining pair of linked nuclear SNPs and the triplet of mitochondrial SNPs (*One_CO1*, *One_Cytb_17*, and *One_Cytb_26*), genotypes from each locus were pooled to form phenotype/haplotype markers: *One_MHC2_190_251* and *One_CO1_Cytb17_26*, respectively.

Principal component analysis

The first 2 principal components, PC1 and PC2, explained 25% and 10% of the overall variation, respectively, while the first 12 principal components explained 80% of total variation. Marker contributions to PC1 and PC2 exhibited similar distributions, with few markers contributing greater than 2% to each PC (9 and 10 markers, respectively) and a sharply dropping tail of marker contribution (Table 7; Figures 11 and 12). In contrast, most markers had a similar contribution to the 12 PC's that explained 80% of the overall variation (64 markers 0.5-1%), with one exception: the combined MHC marker contributed 3.9% (Table 7; Figure 13).

Measures of population divergence based upon F_{ST}

The distribution of marker F_{ST} values among populations within fine-scale region and among fine-scale regions within broad-scale regions were very similar, with few markers having relatively high values, a rapidly declining tail to many intermediate values, and some very small values (Table 8; Figures 14 and 15). F_{ST} values were greater among populations than among regions, and the distribution of F_{ST} values reflect marked differences of allele frequencies among populations and regions for a few markers and small differences for many markers. For example, *One_U1103* exhibited nearly fixed allele frequencies west of the Copper River but highly variable frequencies among populations in the Eastern Gulf region ($\theta_{\mathrm{P}} = 0.261$; rank = 1; Supplement A.82).

The distribution of marker F_{ST} values between populations within pairs of populations was different from the other two measures in that one marker had a high F_{ST} while most were of intermediate values (Table 8; Figure 16). *One_U1004-184* exhibited substantial variation between these pairs of populations and had an F_{ST} of 0.49 (Rank = 1; Supplement A.71), while 87 markers had an F_{ST} between 0 and 0.1. However, some markers (e.g., *One_U404-229*) showed highly divergent allele frequencies between some pairs of populations (McDonald Lake minor allele frequency (MAF) = 0.214, Hugh Smith Lake MAF = 0.096), but were either fixed (Ualik – Pick) or showed very small differences in MAF for other pairs of populations (maximum MAF difference for other 5 pairs = 0.035; Supplement A.101).

Measures of population divergence among pairs of populations of interest

Log-likelihood ratio (G) statistics and f_{ORCA} generally gave very similar marker rankings (Tables 9 and 10). Markers were generally either good at discriminating between pairs of populations or they were not; that is, markers were either ranked in the top 96 for many population discriminating judges or they were ranked in the top 96 for very few (Figure 17). Notably, *One_U1004-184* exhibited substantial allele frequency differences between populations in 5 of the 7 pairs, and was the top ranked marker in 6 judges (both G-statistic and f_{ORCA} for Ualik-Pick, Deer-Cinder, and Broadway-Hatchery comparisons; Supplement A.71).

Overall f_{ORCA}

The combined MHC and mtDNA markers were the top and second-ranked markers as measured by overall f_{ORCA}, and *One_U1004-183* ranked third (Table 11). This may be explained by the fact that MHC and mtDNA, the top and second-ranked markers, were the only two with more than two alleles.

Sum of rankings and selection of final marker set

Some of our judges produced very different rankings, and so the nonparametric measure of concordance suggested little agreement among judges (e.g., Figure 18). For example, measures of laboratory performance were often not highly correlated with measures of diversity across broad-scale regions.

One hundred fifteen markers passed each of the gating judges and were ranked for each of the 30 judges. The distribution of the summed rankings was approximately normal with an average of 1,704 (SD = 363), and ranged from a low of 704.5 (*One_MHC2_251*) to a high of 2,697 (*One_serpin*) (Table 12; Figure 19). The top-ranked markers (i.e., those with the lowest sum of ranks) included 5 markers with sum of ranks lower than 1,000, 10 markers with sum of ranks between 1,000 and 1,500, and 81 markers with sum of ranks greater than 1,500.

The final examination of the 96 markers with the lowest sum of ranks revealed 2 that performed poorly in the laboratory. These were: *One_dds-529* (original rank 90; loose, poorly separated genotype clusters) and *One_psme2-354* (original rank 91; indistinct separation between heterozygote and minor allele homozygote clusters). We replaced these with markers originally ranked 97 and 99 (*One_U1205-57* and *One_c3-98*; sum of ranks 2,064 and 2,083, respectively), which performed much better in the laboratory and will likely produce much more accurate and repeatable genotypic data.

Following our correspondence with stakeholder laboratories, we exchanged 1 SNP with its linked complementary SNP to maximize marker set alignment with other laboratories. This exchange was of *One_GPH-414* for *One_GTHa*, which was a relatively benign transition, as the 2 SNPs had very similar observed heterozygosities (0.38 for both) and average cluster tightness (3.2 and 3.6, respectively), space between (3.9 and 4.2, respectively), alignment (4.4 and 4.7, respectively), and success rate (98% for both) ratings.

Population genetics measures not included in the ranking of SNPs

Backward elimination locus selection

The BELS analysis indicated that the average individual assignment accuracy was 89% with all 114 markers included in the analysis (Table 13; Figure 14). The first markers dropped contributed little to individual assignment accuracy, with 5 contributing less than 1% individually and 87 contributing 1%. Only 2 markers contributed greater than 7% (combined *One_MHC2-190_251* = 14%) and the mitochondrial marker contributed 7% (*One_CO1_Cytb17_26*).

Hierarchical log-likelihood analysis

The *G* statistics scaled by degrees of freedom varied considerably among markers within a region and among regions (Table 14). As measured by this scaled *G*, the greatest diversity was observed in the British Columbia – Washington region (average *G*/df across markers of 23.72), while the least diversity was observed in the Eastern Bristol Bay region (4.31; average across all markers and all regions = 10.94). When averaged across regions for individual markers, the distribution of *G*/df was approximately normal and *One_U1004-183* exhibited the greatest intra-regional allele frequency diversity (28.9; Supplement A.71).

Nei's gene diversity analysis

Overall, 88% of total allele frequency variation was attributed to within populations, with 6% among populations within fine-scale regions, 2% among fine-scale regions within broad-scale regions and 5% among broad-scale regions within the total. *One_ppie-74* had the largest percent of variation attributable to among populations within regions (25%), although this was largely due to a drastically different allele frequency for the Issaquah population relative to other British Columbia/Washington populations (Table 15; Supplement A.44). The combined *One_MHC2-190_251* (18%), *One_U1214-107* (15%), the combined *One_CO1_Cytb17_26* (14%), *One_metA-253* (11%), and *One_U1004-183* (11%) were the other markers with greater than 10% attributable to frequency variation among populations within regions. *One_HpaI-99* (11%), *One_metA-253* (6%), *One_STC-410* (5%) and *One_STR07* (5%) were the markers that varied the most among fine-scale regions within broad-scale regions.

Discussion

Laboratory performance, conformance to Hardy-Weinberg expectations, and linkage among SNPs were the primary factors in marker selection for sockeye salmon. These factors played the dominant role in marker selection because they were gating factors and we were selecting from a small set of markers (124 SNPs) that was only 29% larger than our targeted number of 96 SNPs to run for the full baseline. In other words, after exclusion based on these factors, there were few loci to exclude based on other factors to achieve our target of 96 SNPs. Of the 124 SNPs we screened, 6 were excluded outright based on these 3 factors and 3 SNPs were excluded due to fixation. An additional 10 markers were excluded primarily due to low rankings heavily influenced by poor laboratory performance (Figures 18 and 19).

Other factors that influenced marker selection included both positive and negative factors. The positive factors included large allele frequency differences at both wide and narrow geographic scales and a premium on selecting markers that would allow standardization among laboratories. The two MHC SNPs (*One_MHC2-190* and *One_MHC2-251*), for example, had relatively poor but acceptable laboratory performance, yet rated at the top based on high measures of genetic variation both on the wide (F_{ST} and overall f_{ORCA}) and narrow (pairwise *G* and f_{ORCA}) geographic scales (Figure 18). We also selected *One_GPH-414*, which was the lower laboratory-ranked locus of the linked locus pair that included *One_GTHa*. We selected *One_GPH-414* because it is part of the standard set used by Canadian Department of Fisheries and Oceans (CDFO). CDFO is one of the stakeholder laboratories that analyze SNPs in sockeye salmon. Both of these two loci had acceptable laboratory performance, and this change would allow for data sharing across laboratories.

Aside from the three primary factors, the largest negative factor that affected marker selection was low levels of genetic variation. Low variation at all levels was the main factor in the exclusion of an additional 8 markers (Tables 7, 8, 14, and 15). These excluded markers either had very low levels of variability within populations, among populations within fine-scale regions, among fine-scale regions within broad-scale regions, and/or among broad-scale regions within the total. Little variation also heavily influenced some measures as divergent allele frequencies for 'outlier' populations provided great contrast from most populations. For example, *One_metA-253* was the highest ranking SNP as measured by PC1 due to near fixation for all populations west and north of the Copper River, but a frequency of approximately 0.2 for Meziadin Beach in British Columbia (Supplement A.36).

The choice of populations to test SNPs on could impact the ranking of loci due to differences in genetic variation at each of these levels based on different test populations. We chose populations that represented large sockeye salmon producing regions (e.g., Bristol Bay and the Kamchatka Peninsula) and genetic diversity on different geographic scales (e.g., North Alaska Peninsula and the Eastern Gulf of Alaska). Some populations were chosen to ensure that the full Pacific Rim was represented so that we could identify loci that might differentiate among populations from throughout the range of the species. Other collections were included to identify loci that were likely to provide discriminating power between specific populations. How these populations are chosen and how they are grouped into regional groups clearly has substantial influence on marker selection based upon differing population and regional allele frequencies. For example, we included the Glacial Lake population from the Seward Peninsula for geographic representation but did not include other Norton Sound area populations. So we grouped that population with others from the nearest regional group (western Bristol Bay) for analyses of measures based upon regional diversity. This may have artificially inflated the relative intra-regional diversity for that region, and corresponding rankings for measures based upon this diversity, due to this necessary inclusion of a distantly related population.

Similarly, the methodology used for the final selection of loci can introduce potential bias. Test statistics and scores for the 30 judges we chose to include were on different scales, and instead of ranking each independently and summing ranks we could have unitized all scores to a common range. Some of our judges exhibited very little variability (e.g., the number of populations failing to conform to HWE at $\alpha = 0.05$), so a difference of one variate had profound consequences on rankings when corrections for ties were made. Such a unitizing across judges would have allowed us to include a weighting scheme if we wanted.

After gating judges were considered, we weighted our sockeye salmon SNP selection methodology based upon the number of judges from a category of analyses. For example, because the genetic diversity among populations in Western Alaska is greater for sockeye salmon (e.g., Technical Document 5) than that for chum salmon (e.g., Technical Document 4), we focused our sockeye salmon SNP selection on discriminating between populations from the few reporting groups that still misallocate to one another. By defining half of our judges (i.e., 15 of 30) to be measures of discrimination between these pairs of populations, we weighted our methodology heavily towards this effort (Figures 18 and 20). Our next most important focus was laboratory performance (8 judges) and, lastly, information content of genetic variation among populations, regional groupings and overall (6 judges). Our thinking was that if we selected the loci with the most genetic variation between populations within fine-scale regions, we would select loci that would also be useful at the larger geographic scales. This hypothesis seems to be graphically borne out in Figure 18, where the distribution of good (green) and poor (red) performing loci appear to be correlated between the PCA and F_{ST} columns and the “Pairs of population measures” columns. Cases where these measures scored high but the loci scored low overall were driven by poor laboratory performance scores.

The set of 96 SNPs we have chosen appear very useful for our needs. The new marker set performs much better in our laboratory than our previous set of 45 SNPs, which will create more consistent, reliable data to base analyses on. Similarly, the new marker set distinguishes among populations and regions better than the old set, and improves the correct assignment as measured by f_{ORCA} (Figure 20). The rate of improvement to correct assignment with each additional SNP was slightly greater for our chosen 96 SNPs than it was for the original 45 SNPs, indicating that the intermediate SNPs in the 96 SNP set contributed to correct assignment more than the intermediate SNPs in the 45 SNP set. Furthermore, the correct-assignment curve asymptotes at a much higher correct assignment (i.e., 91% compared to ~72%; Figure 20). In general, it appears as though this set of SNPs should provide adequate power to correctly identify reporting groups in mixed stock analyses of WASSIP area fisheries.

Incorporating lessons on SNP selection from sockeye salmon to chum salmon

The development and application of methods to select SNP loci in sockeye salmon provides insights into the most appropriate methods to select SNP loci for chum salmon. Higher numbers of loci available for selection for chum salmon, differences among life histories between the two species that lead to different population structure, and different management needs will all factor into the best methodology. One of the likely parallels between these two methods will be the incorporation of first gating judges (including Hardy-Weinberg equilibrium expectations, linkage disequilibrium, acceptable laboratory performance) and then ranking judges (including laboratory performance, principal component analysis, measures of population divergence based upon F_{ST}, measures of population divergence among pairs of populations of interest, overall f_{ORCA}, backward elimination locus selection, hierarchical log-likelihood analysis, and Nei's gene diversity analysis). The likely differences will be in the focus and weighting of the ranking variables. These ranking judges will be more important for chum salmon than sockeye salmon SNP selection because of the larger number of loci likely available to chose from in chum salmon. Retaining markers to increase correspondence of marker sets among stakeholder laboratories will affect the final marker selection process but only for markers with intermediate scores (all critical top-scoring markers will be retained and markers that do not pass gating judges will be excluded).

We anticipate focusing the selection of test populations based on a hierarchy of discrimination. At the highest level of the hierarchy, we will score loci based on their among-continent variation (Asia, North America), then move to among coast-wide areas (Japan, Russia, Western Alaska, Alaska Peninsula, Cook Inlet and Prince William Sound, Southeast Alaska, British Columbia, Washington), then among Western Alaska/Alaska Peninsula regions (Alaska Peninsula, eastern Bristol Bay, western Bristol Bay, Kuskokwim River summer, Kuskokwim River fall, Yukon River summer, Yukon River fall, Norton Sound, Kotzebue Sound) and finally within Western Alaska/Alaska Peninsula regions (two populations within each region). Based on known population structure of chum salmon, we expect to find adequate genetic differentiation for the two levels of this hierarchy and to distinguish among the Yukon River fall, Kuskokwim River fall and Alaska Peninsula regions and coastal Western Alaska combined regions. Therefore we propose to emphasize loci that are particularly powerful at discriminating among coastal Western Alaska regions (eastern Bristol Bay, western Bristol Bay, Kuskokwim River summer, Yukon River summer, Norton Sound and Kotzebue Sound). The proposed list of test populations along with our objectives will be shared with the Advisory Panel for comment.

One other change we might propose for chum salmon is to change the methods for the scored variables from the ranking method used in sockeye salmon (1 for the best to 124 for the worst) to a rating based on the score for the variable scaled to 1. Let us take the measures of population divergence based upon F_{ST} among populations within fine-scale regions (Table 8; Figure 14) to demonstrate the difference in methods. For sockeye, we simply ranked each marker and gave a rank value to each marker. However, in looking at the distribution of F_{ST} across ranked markers, we do not see a linear increase in F_{ST} from the poorest to best-performing loci. Rather the curve is S-shaped with an initial steep increase in F_{ST}, followed by a much flatter increase through the middle-raked markers followed by a steep increase in F_{ST} for the highest-ranked markers. The ranking method used for sockeye salmon does not take this non-linear information into account. For example the 19th ranked marker is ranked 92 rankings higher than the 111th marker (111-19), even though it only had a 32% higher scaled F_{ST} value ((0.163-0.036)/0.398). On the other hand, the highest ranked marker was ranked only slightly higher (110 rankings higher) than the 19th marker even though it has a 91% higher scaled F_{ST} value ((0.398-0.036)/0.398). Using the scaled F_{ST} values will add this information into the marker rating methods. Most of the scored variables did not have linear relationships (see Figures 5-8 and 11-17) and should benefit from the scaled rating method.

Future analyses

1. **Finish running the baseline.** We have currently genotyped approximately 30,500 individuals from 324 populations, and have approximately another 5,700 from 60 populations to genotype.
2. Identify changes to the marker selection methodology used for sockeye salmon to be employed for chum salmon.

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Technical Committee review and comments

Document 6: Selection of the 96 SNP marker set for sockeye salmon

Comments on this document appear to be somewhat moot, as the 96-locus panel has already been selected and implemented for sockeye. However, many of the issues are relevant for the parallel exercise for chum.

In general, the approach seems logical and well thought out. Each of the ‘judges’ has some potential value in helping to screen candidate loci, but the criteria differ in the types of information they provide. Some criteria are directly relevant only to local WASSIP issues, while others address issues of broader coastwide relevance. It should be recognized that the number of criteria used for each category produces a *de facto* weighting scheme, and those involved should carefully examine this to ensure that the results adequately reflect the relative importance of different overlapping goals. We believe that substantial coastwide benefits, at little cost to local resolution within WASSIP, can be achieved by giving some consideration to loci that are strongly divergent around the Pacific Rim but relatively homogeneous within WASSIP.

We agree with the general idea that an important initial screening should eliminate from consideration loci that cannot reliably be resolved in the laboratory. From the information presented, however, it is difficult to determine exactly how the tolerance level for error was set.

We also agree with the idea to create a common scale for each of the criteria (e.g., each locus gets a score from 0 to 1). This should facilitate a quantitative rating scale that summarizes information across criteria.

Specific comments keyed to line number:

Line 183: It is not clear why this would be a general result

291: failure rate of ~2.5% in getting genotypes. The key is whether this is random or whether the probability of failure depends on the genotype. If, for example, heterozygotes are more likely to be scored as "failed," this would bias genotypic and allele frequencies.

299: estimated error rate of 0.15%. Actually, this is not a measure of absolute error rate, which would require knowing what the true genotype is. What has been quantified is a measure of *consistency*. For example, independent runs or scorers could get the same answer but both be wrong.

318, and Table 5: How many total HWE departures were there? How does this compare with the number expected by chance?

423: BELS appears to be an appropriate method to select informative loci from a larger set of candidate loci. However, because they do not implement proper cross-validation, BELS and other commonly used programs provide an overly optimistic assessment of assignment success of the selected loci; see Anderson (2010).

Tables

Table 1. Populations of sockeye salmon screened for 124 SNPs (Tables 2 and 3) and their associated map number, pair number, and fine- and broad-scale regional groupings.

Population	Map number	Pair number	Fine-scale region	Broad-scale region
Palana River	1		Russia	Russia
Ozernaya River - Kuril Lake	2		Russia	Russia
Kamchatka River	3		Russia	Russia
Severnaya Lagoon	4		Russia	Russia
Glacial Lake	5		Norton Sound and western Bristol Bay	Western Alaska
Ualik Lake	6	1	Norton Sound and western Bristol Bay	Western Alaska
Pick Creek	7	1	Norton Sound and western Bristol Bay	Western Alaska
Upper Nushagak-Klutapuk Creek	8		Norton Sound and western Bristol Bay	Western Alaska
Tikchik River	9		Norton Sound and western Bristol Bay	Western Alaska
Upper Talarik Creek	10		Eastern Bristol Bay	Western Alaska
Margot Creek	11		Eastern Bristol Bay	Western Alaska
Becharof Creek	12	2	Eastern Bristol Bay	Western Alaska
Deer Creek	13	2, 3	Eastern Bristol Bay	Western Alaska
Mainstem - Cinder River	14	3	North Peninsula	Alaska Peninsula and Kodiak
Bear Lake	15		North Peninsula	Alaska Peninsula and Kodiak
Outer Marker Lake	16		North Peninsula	Alaska Peninsula and Kodiak
Broadway Creek, Black Lake	17	4	Chignik and Kodiak	Alaska Peninsula and Kodiak
Hatchery Beach, Chignik Lake	18	4	Chignik and Kodiak	Alaska Peninsula and Kodiak
Lower Thumb River, Karluk Lake	19		Chignik and Kodiak	Alaska Peninsula and Kodiak
Pyramid Creek - Crescent Lake	20		Cook Inlet	Cook Inlet
West Fork Yentna River	21	5	Cook Inlet	Cook Inlet
Susitna River Slough	22	5	Cook Inlet	Cook Inlet
Larson Lake	23	6	Cook Inlet	Cook Inlet

Table 1. (Page 2 of 2).

Population	Map number	Pair number	Fine-scale region	Broad-scale region
Mama and Papa Bear Lakes	24	6	Cook Inlet	Cook Inlet
Kenai River	25		Cook Inlet	Cook Inlet
Moose Creek	26		Cook Inlet	Cook Inlet
Mahlo River	27		Copper River and northern Southeast Alaska	Eastern Gulf of Alaska
Klukshu River, Alsek	28		Copper River and northern Southeast Alaska	Eastern Gulf of Alaska
Taku River	29		Copper River and northern Southeast Alaska	Eastern Gulf of Alaska
Scud River, Stikine	30		Southern Southeast Alaska	Eastern Gulf of Alaska
McDonald Lake	31	7	Southern Southeast Alaska	Eastern Gulf of Alaska
Hugh Smith Lake	32	7	Southern Southeast Alaska	Eastern Gulf of Alaska
Meziadin Beach, Nass	33		British Columbia and Washington	Eastern Gulf of Alaska
Slamgeesh River, Skeena	34		British Columbia and Washington	Eastern Gulf of Alaska
Kitlope Lake, Central	35		British Columbia and Washington	Eastern Gulf of Alaska
Issaquah Creek	36		British Columbia and Washington	Eastern Gulf of Alaska

Table 2. Forward and reverse primer sequences for 124 SNP assays screened for 36 test populations (Table 1).

Assay	Forward sequence	Reverse sequence
One_ACBP-79[a]	GAGGTGTGGGCTGACCA	TCGACCGCTGGCAGTG
One_agt-132[b]	GACCCAGATCAACAACTTCATCCA	TGGTTGAGCTAAGGTCCTTGAAC
One_aldB-152[c]	CGATCAGGTGACGCTAAAATTAACTC	GTGGCTTCCTCTTCACTCTGA
One_ALDOB-135[a]	CCCGTGCCGGACTTGTT	TCAGCCATGTCAATTGGAATGTGA
One_apoe-83[b]	CGCCATGGACAAGGTCAAG	GGCACAGTGCTTCCAAACC
One_bckB-137[c]	TCATCTCTCCCTCTCACCAATATCTC	CATTGGGCGGAGTGTATTTCC
One_c3-98[b]	GAGTGTGGAACTGGTTCTTGTTG	GCCGGCAGGGCATCA
One_ccd16-131[b]	CCGTGACCTGTTGAACTTTGTTTAG	TCACGTTCTTGGAAAACAGC
One_CD9-269[b]	ACGCTCTGAGGTGATATGAAACAC	CATCCGACGTCAACATCCAAAC
One_cetn1-167[b]	CAGAAATCCTGACTGTTAAAACAATGCA	CTGCTCGTTGATCTCTCCATCTC
One_CFP1[d]	CGCAGGTCAAAGTAGTACTTAGCAT	GAGCGTCACTTCCTGGAACTT
One_cin-177[c]	CCTCAGACTAGTGACCGTACCTA	CGCTCACCGTGGTTACGT
One_CO1[a]	CATAGTAATGCCTGCTGCTAGGA	CCACTTTTTGTTTGAGCTGTGCTAA
One_ctgf-301[a]	AAGGACAGAAACATATATGCGTATATTCAATGT	CTGTCTTTCGTCCCCTCTTTAGG
One_Cytb_17[a]	CCTGGGAGATCCAGACAATTTTA	CGTAAGCGAAAAGGAAGTATCACTCT
One_Cytb_26[a]	CCTGGGAGATCCAGACAATTTTA	CGTAAGCGAAAAGGAAGTATCACTCT
One_dds-529[c]	CATAATGCTCCCCATCTTGAATTGG	CACTCAGCCCTTTAGGGAAGA
One_DDX5-86[b]	CTCCCACATTGATCTGGACGTA	TGCCACTTGGCCCAAAGAG
One_E2-65[a]	GTGGCACCCCCTTTCTCT	TGCAAACCTCAGTGGAGAACC
One_gadd45-269[c]	AGTTCTCATCCTCTGCGGAAAG	CCAAAATGGCTGGGCAAACAG
One_gdh-212[c]	CCTGTGTTGAAGTGGAGTAGGTTAA	GCTTTATACTGTAAGTGGACTGACCTT
One_GHII-2165[a]	GGCATCAACCTGCTCATCGA	TGCACAAAGTGCGGCAC

Table 2. (Page 2 of 6).

Assay	Forward sequence	Reverse sequence
One_ghsR-66[c]	TGTAACAATACAAGGATAATGCAAATAATGTAGGT	GGTTATTAGGTTACTGTGCTGACTGT
One_GPDH-201[a]	GAAGCTGATCCTAGACCTGTACCTA	TGGTATGATGGTGCTACTGGAAGT
One_GPDH2-187[a]	TCACATCCTTGAGTCGTGTTTGTC	GGGCGTAACCGCAAGGT
One_GPH-414[a]	CAAGAAGAATCAAGAGAAAGAGAGATGGT	CCTAGTGTCATGCACATAACGTGTA
One_GTHa[d]	CAAGAAGAATCAAGAGAAAGAGAGATGGT	CCTAGTGTCATGCACATAACGTGTA
One_HGFA-49[a]	ACTTGCTACTTCAGGGTTTTTGTGA	TGGCAGAACAATTCCTCAATGCATA
One_HpaI-71[a]	TGTTGTTCCTAGGCTGTCATTGAAA	CCCTGCGTATTACTAAGGCCATATTTATT
One_HpaI-99[a]	CCTGAGTTGTGTTCAATGGGCATAA	TGGGTCATGTTCATTAGAGCACAAA
One_hsc71-220[a]	ACAGCGAAACTATTGATTTAAGGCTCAT	CGCAGGTAAATCACTGATCATGTTT
One_Hsp47[d]	CGTTCAAATAAATGCTGTTTGGCCTTT	GTGGTGTTCGGATTTTTCCTGAAA
One_Ig-90[b]	GGATTGTGGTAACTCTGACAGTAGT	CATCTAAATTCAGTGGCAGTGGGTTA
One_IL8r-362[a]	TTGCTAGAAGCGTTGGTTATGATGA	CAGCAAAATTGAGAAGTCACTAGGAAAA
One_ins-107[a]	GGAACCCTGCAAGAGGAGAAAA	GAAATGAATGTGAAGGCAATGATGAGA
One_KCT1-453[b]	GGGAAAGTATGCTGTGGGATCAG	GGTTCCTCAGTGAGTGTTCTCTATG
One_KPNA-422[a]	TGGGCCCTGGGAAACATC	CCATAGCCACTTTCGATACAGGTAA
One_LEI-87[a]	ACAGCGCATCCCCATAATGG	GCCTTTGTGGAGGTCAACGA
One_leptin-92[c]	CAGTTGCGCTAAACAGACTCAAG	CAGTTGCTCAGTGATTGTCAACATT
One_lpp1-44[b]	GGTCCAATAGGGAGCTCAGACA	GGGAATGAACCAGACATGTGAATG
One_MARCKS-241[a]	CCTATCACAGCTTGGTTGAGTTCAA	TCCACCCGCTCATTTTTGTAAGAT
One_metA-253[c]	TTCTTATCGCTGGTGGCACTTT	GACCAAAGACTATTTAGTTGCCACCTA
One_MHC2_190[a]	GTATGGTGTGAAGAATGCA	GCTCACCTGTCTTGTCCAGTA
One_MHC2_251[a]	CTGGACAAGACAGGTGAGCA	AAAGTAATGGTCTTGACTTGATCA

Table 2. (Page 3 of 6).

Assay	Forward sequence	Reverse sequence
One_Mkpro-129[c]	TGACGTATGTGCAATGCATGTCTAT	AGATGAAGGACATGGCTGAAAACAT
One_ODC1-196[b]	CCGAGGTGGGATTCAACATGAC	TGTCCTCAGACCCAGGGAAA
One_Ots208-234[c]	CAGCCGACATGCATCAGTTA	TGACCCCATGTTTCATGCT
One_Ots213-181[a]	CCATAGTGTATCACACAATACTCATGTCT	TCTATCATCTGCAAATCTGTGTACTAGACT
One_p53-534[a]	GACAATCTTAAAGCGGTGGTCTTG	AACCTTTATCAGCCATCATCCAACT
One_parp3-170[c]	TGTGCACCGTTGCCTTTCT	ACAGTAACAAACCAGAGTTACAAGTGG
One_pax7-248[c]	AGTAAAGGTAGTGATGCAATGATGCA	AACCGCATAGGACGTAAAGCA
One_PIP[d]	ACAGAGTCAGGACTTGATATGTACAGA	CCTGACGAGGGTCTACTACACT
One_ppie-74[c]	GTTGATTCCACCTTCTCTGTGATGT	GTGAAATTGACACAGAAGCTGTTCA
One_PPM1K-118[b]	GGGATCCAAGCTAACCACAACTT	CACATCAACGCAGGGTTACATTATT
One_Prl2[a]	ACCTCTCTCTCTCTCAGGACTCTCA	GAGGAGGTGTGACACATAGATGGA
One_psme2-354[b]	TGGTCCTTCAGGTACTTTTCAGAGA	CAAATGCCAATTCTCACCACATGA
One_rab1a-76[b]	TCGCCATATTCTCTCTCCCTATCC	ATCCACTCAGACCCATATCTACCAA
One_RAG1-103[a]	AGCTCACACATACAACAAATATGATCTAATGT	GTGAACTGCATCTTTGAACAAATGC
One_RAG3-93[a]	AGATAAAGATGGTTTCAAAGTCACCCA	GGGCTGCCATCTAAAAAATATTGCT
One_redd1-414[c]	GTTGGCTACATCCTAAAACACAATGG	CAGCCCTGGAGTACTGAATCAG
One_RFC2-102[a]	TCCAGGAGCTGCATTTTGAGTTAAA	AAGGTGGATGACAATGTGTTAGTGT
One_RFC2-285[a]	GGATGAGGCTGACAGGTAAGTC	ACAGTCGTTATAGGTACAGGTACACT
One_RH2op-395[a]	GCTGCTAGGTCAAACTCGAAGAG	CAGCCTTGTTCAACCCCATTATCTA
One_rpo2j-261[c]	GATTCTGAGATCATACAGTGGATTGGT	GCTTGTCATCTTTCAGCACATACCTA
One_sast-211[c]	TGTACTTAGTCCAATAAGCATTTCAACAGT	TGGCTAGATTCACATGGTCAACAAA
One_serpin-75[a]	ACACCTGCAACCAAATTATCATTGC	AACAGGCCTTAACCAATTTCCATCT

Table 2. (Page 4 of 6).

Assay	Forward sequence	Reverse sequence
One_spf30-207[c]	AGCATTTCAGTTTTGTACATTTACAGTAAAACA	ACCTACTCGTAATTTCAGGGCAAAA
One_srp09-127[c]	CGGAGCTGGAATGACGACAT	AGGTTCAGCAAATCCCTCTTTAGAG
One_ssrd-135[c]	TGGAAACTCCTAGTGTACTTCATTCTCA	CGTTCCACGCTCCCTAGAATAGA
One_STC-410[a]	CAACACAACATCAACATCATTAATAAACATTCTG	AACATCCCCGTTTTGACCACTTAT
One_STR07[a]	CACACCTGAGGCACAAGCT	GTATGTCTACCAGAGAGGTCAAGGA
One_SUMO1-6[c]	GCACAAGCCAAAAAGTTTTCTCCAT	GGACATAGTTGGAGGCAGACAAAA
One_sys1-230[c]	CTACCTGTCTAACAGTGAATGCTAACTT	TGAAACCATTAAGCTCTTTGTAGGACAA
One_taf12-248[c]	ACCTTCAATATGGTGGTGGTTACC	ACTAAACGCACAACAGCAAACG
One_Tf_ex11-750[a]	AGCAGGTGTAAGCATGTGTACTT	CCTGCTCTGCCTCAACAATGTTAA
One_Tf_in3-182[a]	GCCCTTAGCACTTCAGTTGCA	CAGACAGAAACCATTTGATCCGATTC
One_tshB-92[c]	GCATTGTCGTACTCGTGTGTTTG	CACAACAGCAACAATACATGTCACA
One_txnip-401[c]	GCCAGATCCCTTCAGTTGGA	GGCCATTTCAAAAGGCTGCAT
One_U1002-101[b]	GCCAACCCTATACTGTACGGATTTTT	TCCGTTGCATTGTCCATCCA
One_U1003-75[b]	TCACGAGCCCCAGTCAGA	CGGGTTTCGGTGGTTTAGTATTCTA
One_U1004-183[b]	GGTGTGACTGCTGTGTTTAATTGC	ACCATCATTACACAGCAATTCTGAGT
One_U1009-91[b]	CTCTGTCCTTGAACTGTTGTCTGTT	GCCGCTGCTACTCTTCCT
One_U1010-81[b]	CAGCCCCTCGAGGTAACTG	GTTGAGACAACAAAACGTCTACTGT
One_U1012-68[b]	TCTATTACCATACAGGCCCAGTACA	CCTTTTGTGTCTTCCAGTCATGTGA
One_U1013-108[b]	TCTGTGCTCTCCTCCAGGAT	CGAAACTGAGGAGTGCTCTGA
One_U1014-74[b]	TCCCCTGCAGCAACTGTTTT	GGCAGAGACGGCATCCT
One_U1016-115[b]	GGATTTTTGACTTGACCGTTTTGTGT	ATTAACATGTGCAAAGGGAGAATGC
One_U1017-62[b]	CAGAGAAGGACGTACCATTGATACAT	CCGGTAGATTGGCGTTGCT

Table 2. (Page 5 of 6).

Assay	Forward sequence	Reverse sequence
One_U1021-57[b]	ACAGTGCTACAGGGAGAGAGATTT	GATGGTCAGCGTAGAGAAGCAA
One_U1024-197[b]	CTGAACTGATCTACCGCTCTGT	GGAACAGATACTCCAGGAGAGATGA
One_U1101[b]	CTATGACATGTTTATTTTAATTAGCCACCAACT	AGTATAGCTAGGGAACCTTTCGATCTT
One_U1102-220[b]	TCCCTCTGCTGGAGAACTACAG	GGAACAGCAGTCCTGAGTACAG
One_U1103[b]	CCCAGCCGCCATGTGTA	TGTAGTTCAGCCACCATCTTTGG
One_U1104-138[b]	GGAACAGAACACTGAGAATGAATGC	GGGAATATGTCGACTGCTCACT
One_U1105[b]	GCCTTAATAGTGTCTTCTGATCCCTTT	CCCTCTGTTGTCCAGACTCTTAG
One_U1201-492[b]	GCTTATGACGGAGAAGAGATGCA	AGGATACTGAAGCCCAGAGACA
One_U1202-1052[b]	CGATTTGAGTCTCCAATGGTCTCT	ATTCCTATGGTTAACATCAATTCTATAAAGTCAT
One_U1203-175[b]	CCCGGAGACATACTTGATGCA	GGAGGACCTGCAGGATCAC
One_U1204-53[b]	GTAAAACCCTTCATGTTGGCCATT	CTCCATGTCTGAATGTCCCATCA
One_U1205-57[b]	AGTAAATGGTTATTCACGTAACGGATAAG	CAGGACAGTTCCACATTCTAACAGA
One_U1206-108[b]	CTGAGATGGTGCTTTCTGAGGATA	TGGATGAAAGGGAAATTCTGTCAACA
One_U1207-231[b]	GGCCAAACTGACAGGGATCTATTAA	GGGTCCAGTCTGTACACCATCTAT
One_U1208-67[b]	ACTTGAATGTCTGTTTCGTAGGTGAT	ACACAGTTGACAGTGGAGCAA
One_U1209-111[b]	GTCACGTAATCACGAGAAAGATACTAAATGT	TCTGCGTCTCCAGAGAGGTT
One_U1210-173[b]	ACAAAGTCTCTCTCTGAGTAGGAGTAC	CAAAGTATCTCAGAGTGCTGATCTAGGA
One_U1211-97[b]	GCGTGTCCTCCCATTAGAAGA	CTGCAGAAGTACAGCATCTATCTGA
One_U1212-106[b]	CGTAATGACCTACCACCATATCAGT	TGGCATGACTTTAACAATTCCCAAAAAA
One_U1214-107[b]	CCAAATGTACTCCATGTTGGTTAGC	TGCCTGAGTATTAAGCTATATCATTGAAGTTTT
One_U1215-82[b]	GTTGCTTGGTTTCGTTTGGAGTAG	CTCCAGAAGAGGAATACCACAGTTC
One_U1216-230[b]	TGGGATCGGACGTCAATAGATTTC	GTAATACAGAGTGAGCGTGATACATTGT

Table 2. (Page 6 of 6).

Assay	Forward sequence	Reverse sequence
One_U301-92[a]	AGCCAGTAGCCGATAATGTTTGTC	CCCCTCCCAAATTGCTAGCT
One_U401-224[a]	GGGTGGAGACGAACGGATTC	GTACGATTTTTTTGTAGCCCCAAGT
One_U404-229[a]	GTTTGTGTGTTGGTGTTTGTCCTT	CATTTATCTTGGTGGACGTGTGAGT
One_U502-167[a]	GCTTTTGTGCAATAGCTATGTTGCT	GCAAAGGTAGGCAGCAGATTG
One_U503-170[a]	GATTCAGAATTGCCACGACAAAGAA	GTGATTGGTACATGTCTGTCGAGTT
One_U504-141[a]	GCTATAGCTCACAGAGGATCCCA	TATTGGCGGGTGAGGGATG
One_U508-533[a]	AGGCACAACCTCACATTTGGAA	CTCAAAGGGTCTGAATACTTATGTAAATAAGGT
One_UCA-24[b]	AACTCTGCGTCTGTCTGCTT	TCAGATGGTTCATTATGACAGCAACA
One_vamp5-255[c]	GGTTGACTTTTCTTAACTTTTTAATCTGTGATATTGT	GCTGAGCTAGTGATGGTACCATTT
One_vatf-214[c]	TCATTCCTTTGCCTGGAGCATT	GGCATACAGCAAAACAATTCAACCA
One_VIM-569[a]	TTCTGGGTGGACTCATTGATCAC	ATGCGTTATACCTGTAATCTGCAAGT
One_zn706-68[c]	CCACTCTACGTACATCCCATATTCC	GCAGTATACAGATGAGAAAAAGTAGCAAAAAAA
One_ZNF-61[a]	CCATTCATGTTCTATTCAGATATATTTTGTGCA	CCTAGCTAGAGCTCAACAATATGCA
One_Zp3b-49[a]	TCCTCGTGGTTATAGTTATAAAGATGTCAGT	TTGGCTCTGCACTCGGTTTA

[a] Assay developed by the Gene Conservation Laboratory of the Alaska Department of Fish and Game (Elfstrom et al. 2006; Smith et al. 2005).
[b] Assay developed by the International Program for Salmon Ecological Genetics at the University of Washington.
[c] Assay developed by the Hagerman Genetics Laboratory of the Columbia River Inter-Tribal Fish Commission.
[d] Assay developed by the Molecular Genetics Laboratory at the Canadian Department of Fisheries and Oceans.

Table 3. VIC and FAM definitions and sequences for 124 SNP assays (Table 2) screened for 36 test populations (Table 1) and observed heterozygosities (H_O).

Assay	VIC	FAM	VIC sequence	FAM sequence	H_O
One_ACBP-79[a]	G	A	CAGAGGTCATGGTTCTA	CAGAGGTCATAGTTCTA	0.433
One_agt-132[b]	A	C	ACAGGAAAATCACGAGCCT	CAGGAAAATCCCGAGCCT	0.425
One_aldB-152[c]	A	G	CTCAGGCATTACCTTC	CAGGCATCACCTTC	0.369
One_ALDOB-135[a]	G	A	ACAGCACGAAATTA	ACAGCACAAAATTA	0.300
One_apoe-83[b]	C	T	TTTAGACGGCGGTCTC	ATTTAGACAGCGGTCTC	0.328
One_bckB-137[c]	T	G	TTGATGTAGTTAAGATTATTG	TGATGTAGTTAAGCTTATTG	0.000
One_c3-98[b]	C	T	GTTGATGGACCACCTGGT	TTGATGGACCACTTGGT	0.135
One_ccd16-131[b]	C	T	AAGGAGAAAGTTGCCGAGCT	ATAAGGAGAAAGTTACCGAGCT	0.002
One_CD9-269[b]	C	T	TGGAATGGAGAAATC	ATGGAATGAAGAAATC	0.353
One_cetn1-167[b]	A	C	TTGACGAAGCAGACCGA	TTGACGAAGCCGACCGA	0.442
One_CFP1[d]	C	T	TGCAGTTCAACATCAA	CTGCAGTTCAATATCAA	0.235
One_cin-177[c]	C	T	TCACGCACGGGACAG	CACGCACGGAACAG	0.466
One_CO1[a]	T	C	ACTTCTACTACTTTCCC	ACTTCTACTACTCTCCC	N/A[e]
One_ctgf-301[a]	G	T	TGATGGATGTGTAGGGC	TGATGGATGTTTAGGGC	0.047
One_Cytb_17[a]	A	G	CAACCCGCTAGTTAC	AACCCGCTGGTTAC	N/A[e]
One_Cytb_26[a]	A	G	TTTGATATGAGGTGGAGTAA	TGATATGAGGTGGGGTAA	N/A[e]
One_dds-529[c]	A	G	AGCAATCCCATCTCTC	AGCAACCCCATCTCTC	0.405
One_DDX5-86[b]	C	T	AGGACTTCCTGAAGGAC	AGGACTTCCTAAAGGAC	0.441
One_E2-65[a]	C	T	CATTGTCCCTAGGAAAG	ATTGTCCCTAGAAAAG	0.280
One_gadd45-269[c]	G	C	CTCCAGCCGATACTT	TCCAGCGGATACTT	0.001
One_gdh-212[c]	C	A	ATCTGTTACCAGAATGTTT	ATCTGTTACCATAATGTTT	0.451

Table 3. (Page 2 of 6).

Assay	VIC	FAM	VIC sequence	FAM sequence	H_O
One_GHII-2165[a]	T	A	CACAAATGGAAATTGA	CACAAATGGTAATTGA	0.213
One_ghsR-66[c]	A	T	AGGTTAAGCTGTGTATAAGT	TTAAGCTGTGAATAAGT	0.389
One_GPDH-201[a]	T	C	CTTCACCCCTGGAGCC	CACCCCCGGAGCC	0.438
One_GPDH2-187[a]	G	C	CCTTGGAGGTCTTG	ACCTTGGACGTCTTG	0.187
One_GPH-414[a]	C	T	AAGAACTAGAATGGAACAGA	AAGAACTAGAATGAAACAGA	0.381
One_GTHa[d]	A	G	CAAGAACTAGAATGAAACAGA	AAGAACTAGAATGGAACAGA	0.381
One_HGFA-49[a]	A	T	CTAAAGCACCATGTTGC	ACTAAAGCACCTTGTTGC	0.275
One_HpaI-71[a]	A	T	TCAGTTAAGAACTAATTCT	AGTTAAGAACAAATTCT	0.392
One_HpaI-99[a]	C	T	AACGGAAGAAACCCCTCAA	AACGGAAGAAACTCCTCAA	0.157
One_hsc71-220[a]	C	A	ATTGGCCACAGCGC	ATTGGCAACAGCGC	0.352
One_Hsp47[d]	A	G	TTATTGACTATGGCACATTG	TTGACTATGGCGCATTG	0.307
One_Ig-90[b]	C	G	CTCCTGCATCTTCAGCC	CCTGCATGTTCAGCC	0.056
One_IL8r-362[a]	C	T	CAGCCAAAGAAGAGTC	AGCCAAAAAAGAGTC	0.150
One_ins-107[a]	C	T	ATATGTTGTATGGACTACTG	ATATGTTGTATGAACTACTG	0.435
One_KCT1-453[b]	G	T	TGGTCAGGGTATCGCCATA	TGGTCAGGGTATCTCCATA	0.198
One_KPNA-422[a]	A	G	CTGGTATGAGAAGGCACA	TGGTATGAGGAGGCACA	0.350
One_LEI-87[a]	A	G	ACTCGCCACCTCTGT	TCGCCGCCTCTGT	0.430
One_leptin-92[c]	T	A	CTGATCCAGGTTCAGTAGTA	CTGATCCAGGTTCTGTAGTA	0.000
One_lpp1-44[b]	C	T	TTGTGCTTTCCTGACCTAT	TTGTGCTTTCCTAACCTAT	0.371
One_MARCKS-241[a]	T	A	TTGCTTAAAAGGTCTTCC	TTGCTTAAAAGGTCATCC	0.035
One_metA-253[c]	C	G	AGGCAATTGAGGTTAAT	AGGCAATTGACGTTAAT	0.094
One_MHC2_190[a]	G	T	CTGCTATCGACTACAGC	CGCTGCTATCTACTACAG	0.298

Table 3. (Page 3 of 6).

Assay	VIC	FAM	VIC sequence	FAM sequence	H_O
One_MHC2_251[a]	C	T	CACTTACAGGCCCCTG	CACTTACAGGCCTCTG	0.322
One_Mkpro-129[c]	A	G	ATGCATATACATGTAATATAT	TGCATATACATGTAACATAT	0.432
One_ODC1-196[b]	C	T	CCACCTCCGATGTCC	CACCTCCAATGTCC	0.416
One_Ots208-234[c]	-	A	CACACGTTACATCAGATAACT	CACACAATGTTACATCAGATAAC	0.192
One_Ots213-181[a]	T	A	CTTTGAATTAAAAACATTTTT	CTTTGAATTAAAAACTTTTTT	0.267
One_p53-534[a]	C	A	ATGTCCAAAGATCTGG	AATGTCCAAATATCTGG	0.059
One_parp3-170[c]	T	A	ACACAGGAAAAGTTG	ACACAGGTAAAGTTG	0.000
One_pax7-248[c]	C	A	AATTCAAAACGAAATGTG	TGAATTCAAAACTAAATGTG	0.212
One_PIP[d]	C	T	AACACACATTTCTCAACACA	ACACACATTTTTCAACACA	0.448
One_ppie-74[c]	-	A	TGCAAACACTTTTTTTATAATG	TGCAAACACTTTTTTTTATAATG	0.033
One_PPM1K-118[b]	G	T	ATCTCACTTATGGTGCTTC	ATATCTCACTTATTGTGCTTC	N/A[f]
One_Prl2[a]	G	T	ACCAATGGGACGAGTG	CCACCAATTGGACGAG	0.448
One_psme2-354[b]	A	G	TGATGCAGTAGCTAAAG	ATGCAGTGGCTAAAG	0.373
One_rab1a-76[b]	G	T	TGTGGAGCAAGGTAACT	TGTGGAGCAATGTAACT	0.193
One_RAG1-103[a]	T	A	CGAATCTCAACAATAAGT	CTCGAATCTCAACTATAAGT	0.079
One_RAG3-93[a]	C	T	CATTTTGGACTTCGGGACC	CATTTTGGACTTTGGGACC	0.148
One_redd1-414[c]	T	C	CCTAAGTCAGTCACTGTAG	CCCAAGTCAGTCACTGTA	0.410
One_RFC2-102[a]	A	G	ATCACGTTGTATTTCTTT	CACGTTGTGTTTCTTT	0.290
One_RFC2-285[a]	A	T	CACGACATCTAAGCTGAA	CACGACATCTATGCTGAA	0.064
One_RH2op-395[a]	G	T	TGGGAACATCATTTTTTAA	TTGGGAACATAATTTTTTAA	0.016
One_rpo2j-261[c]	G	T	CACATGTTTTACTCATTTGA	CACATGTTTTACTAATTTGA	0.312
One_sast-211[c]	G	T	CATCATTTGCATTATTG	CATCATTTGAATTATTG	0.073

Table 3. (Page 4 of 6).

Assay	VIC	FAM	VIC sequence	FAM sequence	H_O
One_serpin-75[a]	G	T	CAGTGTGTAATTTAATGATATAT	ACAGTGTGTAATTTAATTATATAT	0.039
One_spf30-207[c]	G	T	AGGGACATCTTACCTCAAAA	AGGGACATCTTACCTAAAAA	0.295
One_srp09-127[c]	T	A	CAGCGAAGGATATGCT	CAGCGAAGGTTATGCT	0.082
One_ssrd-135[c]	-	T	CTGCGGCTTTGTCTTG	TGCGGCTTTTGTCTTG	0.475
One_STC-410[a]	T	C	CCGATGGGTATATTATTATA	CCGATGGGTATATTGTTATA	0.336
One_STR07[a]	G	C	ACGCACACTGTCCTT	ACGCACACTCTCCTT	0.399
One_SUMO1-6[c]	C	A	CAAGATTGAAATTGGTTTGC	CAAGATTGAAATTTGTTTGC	0.297
One_sys1-230[c]	T	G	CAAAGCAAGTGATATATTAGTG	AAAGCAAGTGATATCTTAGTG	0.413
One_taf12-248[c]	C	T	CCAGACAAAATCAAATTA	CCAGACAAAATAAAATTA	0.047
One_Tf_ex11-750[a]	G	A	CAGGGTCGCTGCAC	CCAGGGTCACTGCAC	0.380
One_Tf_in3-182[a]	A	G	AACAGAAAGTCTACACTTT	ACAGAAAGTCTGCACTTT	0.109
One_tshB-92[c]	A	C	ACCACCCTGTAGCTCA	CACCCTGGAGCTCA	0.111
One_txnip-401[c]	C	T	TGACTGCACTAGTTTAGAC	TGACTGCACTAATTTAGAC	0.047
One_U1002-101[b]	G	T	TCGTTCCAAAGAATGTTGTG	CGTTCCAAAGAATTTTGTG	0.009
One_U1003-75[b]	C	T	AGAGACTACTTCCTTTTTG	AGAGACTACTTCTTTTTTG	0.294
One_U1004-183[b]	A	G	AAGTTCCCTGTATTTCTT	TCCCTGCATTTCTT	0.345
One_U1009-91[b]	A	G	CATGTTCTGTATGGACCC	TGTTCTGTGTGGACCC	0.283
One_U1010-81[b]	A	G	CACACCAACGTTATGTAGAG	CACCAACGTTGTGTAGAG	0.064
One_U1012-68[b]	C	T	TGACGGGTGTTCCTGATAA	TGACGGGTGTTCTTGATAA	0.251
One_U1013-108[b]	G	T	ACGGAATTCCTGTTGCCCT	ACGGAATTCCTTTTGCCCT	0.250
One_U1014-74[b]	C	T	TTGACCTGCGCCAGTAT	TTTTGACCTGCACCAGTAT	0.212
One_U1016-115[b]	-	T	AATGGCAGTTTTTTATTTGA	ATGGCAGTTTTTTTATTTGA	0.402

Table 3. (Page 5 of 6).

Assay	VIC	FAM	VIC sequence	FAM sequence	H_O
One_U1017-62[b]	A	T	CAGAAAAACTGGTACTTGTT	CAGAAAAACTGGTTCTTGTT	0.031
One_U1021-57[b]	A	G	AGTTGAACGTTTGGTTTGA	GTTGAACGTTCGGTTTGA	0.414
One_U1024-197[b]	G	T	ACCTGACCCAACAAA	ACCTGACACAACAAA	0.199
One_U1101[b]	C	A	TGGACGTATGTCATATTT	TGGACGTATGTAATATTT	0.303
One_U1102-220[b]	C	T	CCAGTAGTGTTTTCTG	CAGTAGTGCTTTCTG	0.168
One_U1103[b]	G	A	TCGGCGAAAACT	TCGGCAAAAACT	0.050
One_U1104-138[b]	G	T	CCTTCTCAGAGGGTAGAGA	CCTTCTCAGAGGTTAGAGA	0.009
One_U1105[b]	T	A	CCTGTTTTTTTTAAAAGAC	TCCTGTTTTTTTTTAAAGAC	0.332
One_U1201-492[b]	A	G	AAGACTTCCTCCAGGCTC	ACTTCCCCCAGGCTC	0.445
One_U1202-1052[b]	T	C	CAAACTTTTTCATCTACATTTA	ACTTTTTCATCCACATTTA	0.370
One_U1203-175[b]	G	A	CCATAGTTGCTGGGCTT	CTCCATAGTTACTGGGCTT	0.397
One_U1204-53[b]	C	T	ATGCATACACGCTGATGC	ATGCATACACACTGATGC	0.318
One_U1205-57[b]	A	G	AGTTATCATGGTCATCTCT	AGTTATCATGGTCGTCTCT	0.049
One_U1206-108[b]	G	T	AACATTGAGCTTCCC	ATAACATTGATCTTCCC	0.300
One_U1207-231[b]	C	T	ACATTCCTTGGCATTGC	CATTCCTTGACATTGC	N/A[f]
One_U1208-67[b]	A	C	CCCAATGTGATTGTCAC	CCAATGTGCTTGTCAC	0.398
One_U1209-111[b]	C	T	CTCACATCGAGATGATC	TCACATCGAAATGATC	0.170
One_U1210-173[b]	A	G	CCCTCCTATTCATTATGATTGT	CCTCCTATTCATTACGATTGT	0.149
One_U1211-97[b]	C	T	CTGTTTCAGTGTGCTTG	CTGTTTCAGTATGCTTG	0.165
One_U1212-106[b]	A	G	TTTTGACATACAAAAAATA	TTTGACATACAGAAAATA	0.445
One_U1214-107[b]	A	C	TAGTGACCTATTAAATTGC	TGACCTATTCAATTGC	0.137
One_U1215-82[b]	A	C	AATGAGACAAAGTATTTGGT	AATGAGACAAAGTCTTTGGT	0.469

Table 3. (Page 6 of 6).

Assay	VIC	FAM	VIC sequence	FAM sequence	H_O
One_U1216-230[b]	A	T	CCTGGCTACTAAGTAAC	CTGGCTACAAAGTAAC	0.452
One_U301-92[a]	T	G	CCATGGATTAAAATATTT	CCATGGATTAAACTATTT	0.230
One_U401-224[a]	C	A	CACCTGGAAAGGACTGA	ACACCTGGAAATGACTGA	0.439
One_U404-229[a]	C	T	CATGTTCTTCAGTGAACC	ATGTTCTTCAATGAACC	0.108
One_U502-167[a]	A	G	CTTCTTGATCAATAACG	CTTCTTGATCGATAACG	0.034
One_U503-170[a]	T	G	AAGTACTAAAATCAGTTTTACATTG	TACTAAAATCAGTTGTACATTG	0.231
One_U504-141[a]	C	A	TCAAGGACACAAACAA	TCAAGGACAAAAACAA	0.362
One_U508-533[a]	C	T	ACACTACAGCCTTATTC	ACACTACAGCTTTATTC	0.090
One_UCA-24[b]	C	T	CGAACAGGGCTGGATG	CGAACAGGACTGGATG	N/A[f]
One_vamp5-255[c]	C	T	TAGGCTCCGTGCTCAGT	TAGGCTCCGTACTCAGT	0.309
One_vatf-214[c]	C	A	TGGTATTACTGTGCATTGAC	ATGGTATTACTGTTCATTGAC	0.089
One_VIM-569[a]	G	A	AAGTGTTTCCATACTCACTATA	AAGTGTTTCCATATTCACTATA	0.207
One_zn706-68[c]	C	T	ATTAAGTGAAGGGAGCAGC	AAGTGAAGGAAGCAGC	0.002
One_ZNF-61[a]	C	A	CTATGGACATGATCTTT	TTCTATGGACATTATCTTT	0.342
One_Zp3b-49[a]	C	A	AGGCCCAATCCTT	AGGCCAAATCCTT	0.182

[a] Assay developed by the Gene Conservation Laboratory of the Alaska Department of Fish and Game (Elfstrom et al. 2006; Smith et al. 2005).
[b] Assay developed by the International Program for Salmon Ecological Genetics at the University of Washington.
[c] Assay developed by the Hagerman Genetics Laboratory of the Columbia River Inter-Tribal Fish Commission.
[d] Assay developed by the Molecular Genetics Laboratory at the Canadian Department of Fisheries and Oceans.
[e] These assays are mitochondrial SNPs and were not measured for heterozygosity.
[f] These assays failed in the laboratory and were not measured for heterozygosity.

Table 4. Summary of the average, coefficient of variation (CV) and associated ranks for four measures of laboratory performance of 124 assays (Tables 2 and 3) screened for 36 test populations (Table 1). See footnotes for explanations of the lack of scores or rankings.

	Cluster tightness				Space between clusters				Cluster alignment				Success rate			
	Average		CV		Average		CV		Average		CV		Average		CV	
Assay	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank
One_ACBP-79	3.28	90	0.14	23	3.67	55	0.23	51	4.56	58	0.11	41.5	97.69	79	0.02	73
One_agt-132	3.39	77.5	0.18	58	3.72	53	0.20	33	4.28	81	0.19	90	98.04	56	0.02	74
One_aldB-152	3.39	77.5	0.21	85.5	3.89	47	0.25	60	4.44	71	0.12	47.5	98.08	52	0.02	59
One_ALDOB-135	2.89	111.5	0.16	42	2.83	91.5	0.33	78	3.89	99	0.21	96	96.01	107	0.09	109
One_apoe-83	3.78	44.5	0.21	89	4.44	14.5	0.19	23.5	4.78	31	0.09	26	98.26	48	0.01	16
One_bckB-137[a]	4.89	10	0.10	11.5	1.00	117.5	N/A	N/A	4.89	20	0.10	30	99.50	3	0.01	2
One_c3-98	3.89	37.5	0.20	68.5	3.56	63	0.34	80	4.17	87	0.22	101	99.25	9	0.01	12
One_ccd16-131	4.94	7.5	0.05	7.5	0.28	115.5	4.24	115.5	4.94	12	0.05	12	99.54	1	0.01	6
One_CD9-269	3.39	77.5	0.21	85.5	4.28	19.5	0.19	25	4.78	31	0.09	26	97.97	59	0.01	33
One_cetn1-167	3.61	56.5	0.17	43.5	3.56	63	0.24	56.5	4.00	94	0.19	89	97.84	70	0.02	76
One_CFP1	3.67	52	0.23	101	4.17	24	0.24	54	4.56	58	0.15	75.5	98.26	47	0.01	48
One_cin-177	3.56	61.5	0.20	72.5	3.28	78.5	0.29	77	3.83	101.5	0.22	102	97.37	92	0.02	64
One_CO1	5.00	3.5	0.00	3.5	5.00	1.5	0.00	1.5	4.94	12	0.05	12	99.13	15	0.01	24
One_CTGF-301	4.00	32.5	0.23	98	3.33	75	0.58	97	4.67	45	0.13	53	97.01	98	0.09	110
One_Cytb_17	5.00	3.5	0.00	3.5	5.00	1.5	0.00	1.5	5.00	4.5	0.00	4.5	99.54	2	0.01	1
One_Cytb_26	5.00	3.5	0.00	3.5	4.94	3	0.05	3	5.00	4.5	0.00	4.5	99.10	16	0.01	15
One_dds-529	2.50	119	0.25	111	2.00	105.5	0.34	82	2.11	118.5	0.32	110	97.62	83	0.01	29
One_DDX5-86	3.33	84.5	0.25	112	2.78	95	0.40	86	3.67	104	0.25	106	96.91	101	0.02	90
One_E2-65	3.28	90	0.14	23	3.50	67.5	0.20	34	4.44	71	0.14	69	95.23	112	0.11	114
One_gadd45-269	5.00	3.5	0.00	3.5	1.00	118.5	N/A	115.5	4.89	20	0.10	30	99.20	13	0.01	14
One_gdh-212	3.50	67.5	0.18	52	4.00	35.5	0.27	69.5	4.61	51	0.13	56.5	97.81	72	0.01	20
One_GHII-2165	3.72	47.5	0.24	107	4.56	8	0.17	15	4.78	31	0.09	26	98.62	34	0.02	58
One_ghsR-66	3.39	77.5	0.23	104	4.00	35.5	0.27	69.5	4.56	58	0.14	62	97.94	63	0.01	21

Table 4. (Page 2 of 6).

	Cluster tightness				Space between clusters				Cluster alignment				Success rate			
	Average		CV		Average		CV		Average		CV		Average		CV	
Assay	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank
One_GPDH-201	3.72	47.5	0.22	93	3.94	40.5	0.24	55	4.44	71	0.14	69	98.41	43	0.01	46
One_GPDH2-187	3.11	99.5	0.24	109	2.78	95	0.42	89	4.11	88.5	0.20	93	98.74	32	0.01	8
One_GPH-414	3.22	94	0.13	19	3.89	47	0.20	27	4.39	75.5	0.16	79	97.95	61	0.01	38
One_GTHa	3.61	56.5	0.22	91	4.17	24	0.17	13	4.72	38.5	0.10	34	98.06	54	0.01	41
One_HGFA-49	2.94	109	0.14	26	3.28	78.5	0.23	52	4.56	58	0.14	62	97.60	86	0.05	100
One_HpaI-71	2.89	112.5	0.11	14	2.89	90	0.20	31.5	3.83	101.5	0.16	80	96.11	106	0.04	96
One_HpaI-99	3.39	77.5	0.21	85.5	3.56	63	0.20	29	3.94	98	0.22	100	95.71	111	0.10	111
One_hsc71-220	3.61	56.5	0.17	43.5	2.33	103	0.36	83	3.28	111	0.34	112	98.24	49	0.02	52
One_Hsp47	3.83	41.5	0.22	95.5	4.06	32	0.25	59	4.33	78	0.19	91	98.46	41	0.01	42
One_Ig-90	4.50	16.5	0.21	82	1.78	107	1.23	111	4.67	45	0.15	72	99.34	7	0.01	7
One_IL8r-362	3.83	41.5	0.22	95.5	4.44	14.5	0.18	17	4.72	38.5	0.10	34	99.02	18	0.01	27
One_ins-107	3.00	105	0.16	41	3.28	78.5	0.27	71.5	4.00	94	0.17	82	95.12	113	0.06	104
One_KCT1-453	3.89	37.5	0.15	31	3.89	47	0.21	42.5	4.28	81	0.22	103	98.48	40	0.02	71
One_KPNA-422	3.22	94	0.17	45	3.94	40.5	0.20	35	4.67	45	0.13	53	97.96	60	0.02	57
One_LEI-87	3.89	37.5	0.20	68.5	3.61	58	0.32	78	4.50	64.5	0.17	84	98.29	45	0.02	53
One_leptin-92[a]	5.00	3.5	0.00	3.5	1.00	117.5	N/A	N/A	5.00	4.5	0.00	4.5	99.49	4	0.01	9
One_lpp1-44	3.67	52	0.23	101	4.56	8	0.15	9	4.83	26	0.08	22.5	98.01	57	0.01	32
One_MARCKS-241	3.22	94	0.27	115	2.50	101	0.48	92	3.00	113	0.36	114	95.77	110	0.12	115
One_metA-253	4.56	14.5	0.17	47	3.17	85	0.74	105	4.94	12	0.05	12	98.84	23	0.01	44
One_MHC2_190	2.78	116.5	0.20	70	2.78	95	0.36	84	3.56	106	0.22	99	94.95	115	0.07	106
One_MHC2_251	3.94	34.5	0.18	59.5	3.89	47	0.21	42.5	4.22	84.5	0.19	87.5	97.93	64	0.02	85
One_Mkpro-129	3.33	84.5	0.23	105	3.67	55	0.26	66	4.50	64.5	0.14	65	96.75	102	0.04	99
One_ODC1-196	3.06	103	0.08	10	3.22	83	0.23	49	4.06	90.5	0.13	59.5	97.89	67	0.02	79
One_Ots208-234[b]	N/A	61.5	N/A	60.5	N/A	63	N/A	58.5	N/A	58	N/A	60.75	N/A	60.5	N/A	60.5

Table 4. (Page 3 of 6).

	Cluster tightness				Space between clusters				Cluster alignment				Success rate			
	Average		CV		Average		CV		Average		CV		Average		CV	
Assay	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank
One_Ots213-181	3.50	67.5	0.18	52	3.89	47	0.21	42.5	4.61	51	0.13	56.5	96.35	104	0.08	107
One_p53-534	4.22	25.5	0.19	64	2.83	92.5	0.84	107	4.89	20	0.07	18.5	95.99	108	0.10	113
One_parp3-170[a]	5.00	3.5	0.00	3.5	1.00	117.5	N/A	N/A	5.00	4.5	0.00	4.5	98.82	25	0.02	66
One_pax7-248	4.22	25.5	0.17	48.5	4.50	11	0.27	67	4.89	20	0.07	18.5	98.74	31	0.02	65
One_PIP	3.11	99.5	0.15	33	3.50	67.5	0.18	18	4.06	90.5	0.13	59.5	97.04	96	0.03	91
One_ppie-74	4.06	30.5	0.27	116	1.22	111	1.21	110	3.61	105	0.40	117	93.63	117	0.25	118
One_PPM1K-118[c]	1.72	N/A	0.65	N/A	1.33	N/A	0.68	N/A	2.11	N/A	0.58	N/A	5.44	N/A	4.24	N/A
One_Prl2	3.11	99.5	0.15	33	3.56	63	0.24	56.5	4.56	58	0.14	62	96.93	100	0.02	82
One_psme2-354	2.94	109	0.27	114	2.56	99.5	0.52	95	3.28	111	0.33	111	97.01	97	0.04	97
One_rab1a-76	3.28	90	0.23	103	4.06	32	0.20	28	4.44	71	0.12	47.5	97.62	84	0.02	51
One_RAG1-103	4.33	22	0.18	54	3.94	40.5	0.47	91	4.89	20	0.07	18.5	98.08	53	0.04	98
One_RAG3-93	3.50	67.5	0.22	97	3.39	73	0.34	81	4.00	94	0.24	105	96.13	105	0.10	112
One_redd1-414	3.33	84.5	0.18	55.5	2.89	90	0.26	65	3.28	111	0.31	109	97.75	75	0.02	61
One_RFC2-102	4.00	32.5	0.17	46	4.11	28	0.22	45.5	4.50	64.5	0.16	77	98.61	35	0.01	28
One_RFC2-285	4.39	20	0.16	40	3.94	40.5	0.40	87	4.61	51	0.15	73	99.36	6	0.01	10
One_RH2op-395	4.50	16.5	0.16	38	3.11	86	0.74	104	4.78	31	0.11	44.5	97.81	71	0.06	103
One_rpo2j-261	3.56	61.5	0.20	72.5	4.11	28	0.16	12	4.72	38.5	0.10	34	97.61	85	0.01	36
One_sast-211	3.56	61.5	0.28	117	4.11	28	0.29	76	4.72	38.5	0.12	50.5	98.87	22	0.01	25
One_serpin-75	2.83	114.5	0.39	119	1.72	108	0.77	106	2.50	116.5	0.42	118	85.94	120	0.31	120
One_spf30-207	3.56	61.5	0.20	72.5	4.22	21.5	0.19	22	4.61	51	0.11	39.5	98.52	39	0.01	40
One_srp09-127	4.22	25.5	0.17	48.5	3.67	55	0.56	96	4.94	12	0.05	12	98.91	21	0.01	49
One_ssrd-135	3.44	72	0.20	80.5	4.11	28	0.18	21	4.61	51	0.11	39.5	97.56	88	0.02	78
One_STC-410	2.94	109	0.25	110	1.67	109	0.41	88	2.61	115	0.37	115	90.47	119	0.13	116
One_STR07	2.78	116.5	0.15	36	3.28	78.5	0.27	71.5	3.94	98	0.16	81	97.20	93	0.02	80

Table 4. (Page 4 of 6).

	Cluster tightness				Space between clusters				Cluster alignment				Success rate			
	Average		CV		Average		CV		Average		CV		Average		CV	
Assay	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank
One_SUMO1-6	3.17	96	0.22	94	3.61	58	0.25	62	4.56	58	0.11	41.5	97.64	82	0.02	70
One_sys1-230	3.39	77.5	0.21	85.5	3.83	51.5	0.22	48	4.67	45	0.10	37	97.89	66	0.01	35
One_taf12-248	4.28	23	0.18	50	2.22	104	1.05	109	4.83	26	0.08	22.5	99.09	17	0.01	13
One_Tf_ex11-750	3.39	77.5	0.15	29.5	4.00	35.5	0.21	40	4.44	71	0.12	47.5	95.89	109	0.07	105
One_Tf_in3-182	4.22	25.5	0.15	35	4.44	14.5	0.28	74	4.83	26	0.11	38	99.15	14	0.01	19
One_tshB-92	3.67	52	0.19	63	4.06	32	0.18	19	4.44	71	0.14	69	98.77	27	0.01	11
One_txnip-401	4.72	13	0.12	18	1.61	110	1.46	112	5.00	4.5	0.00	4.5	99.40	5	0.01	5
One_U1002-101	4.89	10	0.07	9	0.83	113	2.30	113	5.00	4.5	0.00	4.5	99.28	8	0.01	23
One_U1003-75	3.33	84.5	0.18	55.5	3.94	40.5	0.18	20	4.44	71	0.12	47.5	97.92	65	0.02	83
One_U1004-183	3.50	67.5	0.15	28	3.56	63	0.28	73	4.28	81	0.18	85	98.20	50	0.02	63
One_U1009-91	3.72	47.5	0.15	37	4.67	5	0.13	6	4.94	12	0.05	12	98.28	46	0.02	55
One_U1010-81	4.56	14.5	0.11	15	4.33	18	0.37	85	4.94	12	0.05	12	98.83	24	0.01	37
One_U1012-68	4.06	30.5	0.16	39	4.50	11	0.11	5	4.78	31	0.09	26	98.74	33	0.01	39
One_U1013-108	3.67	52	0.23	101	4.00	35.5	0.26	63	4.72	38.5	0.10	34	97.88	68	0.02	67
One_U1014-74	3.78	44.5	0.19	67	4.39	17	0.19	26	4.78	31	0.11	44.5	98.04	55	0.02	69
One_U1016-115	3.11	99.5	0.10	13	2.00	105.5	0.17	14	2.11	118.5	0.15	74	97.86	69	0.01	45
One_U1017-62	4.44	18	0.19	65	3.22	83	0.73	103	5.00	4.5	0.00	4.5	98.75	29	0.02	54
One_U1021-57	2.56	117	0.24	107	2.44	101	0.25	60	3.33	108	0.21	93	97.17	94	0.02	75
One_U1024-197	3.44	72	0.20	80.5	3.89	47	0.17	16	4.22	84.5	0.19	87.5	98.57	36	0.01	34
One_U1101	3.11	99.5	0.22	92	3.89	47	0.21	42.5	4.50	64.5	0.11	43	97.94	62	0.02	88
One_U1102-220	3.00	105	0.23	99	2.56	99.5	0.63	101	2.50	116.5	0.68	120	98.46	42	0.01	18
One_U1103	4.39	20	0.11	16.5	3.22	83	0.66	102	4.72	38.5	0.12	50.5	98.97	19	0.01	4
One_U1104-138	4.78	12	0.14	21	0.78	114	2.31	114	4.89	20	0.10	30	99.23	10	0.01	17
One_U1105	3.11	99.5	0.15	33	3.28	78.5	0.20	36	3.94	98	0.18	86	97.74	77	0.02	56

Table 4. (Page 5 of 6).

	Cluster tightness				Space between clusters				Cluster alignment				Success rate			
	Average		CV		Average		CV		Average		CV		Average		CV	
Assay	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank
One_U1201-492	3.33	84.5	0.21	83	3.44	70	0.27	68	4.22	84.5	0.17	83	97.67	80	0.02	81
One_U1202-1052	2.83	114.5	0.14	20	2.89	90	0.20	31.5	3.50	107	0.26	108	97.55	89	0.02	86
One_U1203-175	3.44	72	0.18	57	4.17	24	0.21	37	4.89	20	0.07	18.5	98.36	44	0.02	68
One_U1204-53	3.50	67.5	0.20	77	4.22	21.5	0.21	39	4.78	31	0.09	26	97.77	74	0.02	84
One_U1205-57	4.11	28.5	0.23	106	3.28	78.5	0.59	99	4.33	78	0.21	96	98.94	20	0.01	22
One_U1206-108	2.94	109	0.14	26	3.39	73	0.21	38	3.78	103	0.25	107	92.54	118	0.25	119
One_U1207-231[c]	1.56	N/A	0.63	N/A	1.72	N/A	0.74	N/A	2.67	N/A	0.66	N/A	5.32	N/A	4.24	N/A
One_U1208-67	3.67	52	0.21	88	4.56	8	0.14	8	4.89	20	0.07	18.5	97.38	91	0.02	62
One_U1209-111	3.83	41.5	0.18	61.5	4.72	4	0.10	4	4.72	38.5	0.10	34	98.77	26	0.01	43
One_U1210-173	3.56	61.5	0.20	72.5	3.61	58	0.24	53	4.00	94	0.23	104	98.76	28	0.01	31
One_U1211-97	3.33	84.5	0.29	118	2.67	98	0.50	93	3.44	108	0.35	113	97.74	76	0.02	89
One_U1212-106	3.28	90	0.14	23	3.56	63	0.22	47	4.39	75.5	0.14	67	96.97	99	0.03	94
One_U1214-107	3.61	56.5	0.19	66	4.28	19.5	0.29	75	4.50	64.5	0.14	65	98.56	38	0.01	47
One_U1215-82	2.11	120	0.46	120	1.17	112	0.61	100	1.94	120	0.54	119	95.12	114	0.03	92
One_U1216-230	3.28	90	0.20	79	4.11	28	0.22	45.5	4.67	45	0.13	53	97.44	90	0.02	87
One_U301-92	3.94	34.5	0.18	59.5	4.44	14.5	0.19	23.5	4.72	38.5	0.14	71	96.64	103	0.08	108
One_U401-224	3.39	77.5	0.15	29.5	3.83	51.5	0.24	58	4.50	64.5	0.14	65	97.57	87	0.01	50
One_U404-229	4.11	28.5	0.20	78	3.44	70	0.51	94	4.56	58	0.15	75.5	98.75	30	0.02	77
One_U502-167	4.94	7.5	0.05	7.5	2.72	97	0.92	108	4.94	12	0.05	12	99.21	11	0.01	30
One_U503-170	4.39	20	0.11	16.5	4.61	6	0.13	7	4.61	51	0.13	56.5	97.73	78	0.05	101
One_U504-141	2.94	109	0.14	26	3.44	70	0.23	50	4.33	78	0.16	78	97.66	81	0.02	60
One_U508-533[d]	3.00	105	0.2	75	3.00	87	0.2	30	4.00	94	0.2	92	93.7	116	0.2	117
One_UCA-24[c]	3.39	N/A	0.27	N/A	3.28	N/A	0.29	N/A	3.06	N/A	0.38	N/A	67.08	N/A	0.18	N/A
One_vamp5-255	3.50	67.5	0.18	52	3.56	63	0.26	64	4.11	88.5	0.22	98	97.79	73	0.02	72

Table 4. (Page 6 of 6).

	Cluster tightness				Space between clusters				Cluster alignment				Success rate			
	Average		CV		Average		CV		Average		CV		Average		CV	
Assay	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank	Score	Rank
One_vatf-214	3.89	37.5	0.21	90	3.39	73	0.58	98	4.61	51	0.13	56.5	99.21	12	0.01	3
One_VIM-569	3.83	41.5	0.18	61.5	3.94	40.5	0.16	11	4.22	84.5	0.21	95	98.14	51	0.03	93
One_zn706-68	4.89	10	0.10	11.5	0.28	115.5	4.24	115.5	5.00	4.5	0.00	4.5	98.00	58	0.03	95
One_ZNF-61	3.72	47.5	0.20	76	4.50	11	0.16	10	4.89	20	0.07	18.5	97.16	95	0.05	102
One_Zp3b-49	3.56	61.5	0.26	113	2.94	88	0.46	90	2.78	114	0.40	116	98.56	37	0.01	26

[a] This marker was excluded from subsequent analyses due to fixation in 36 test populations.

[b] This marker was screened on the ABI platform for the 36 test populations and was given median rankings for each laboratory measure.

[c] These markers were not given ratings or included in subsequent analyses due to massive laboratory failure or the appearance of excessive clusters.

[d] This marker was screened on the ABI platform for the 36 test populations and was given ratings based upon previous analyses of other populations on the Biomark platform.

Table 5. The number of populations that failed to conform to Hardy-Weinberg expectations for 124 SNP assays (Tables 2 and 3) screened for 36 test populations (Table 1) at three levels of significance (α = 0.001, 0.01, and 0.05), and rankings based upon the number of populations at α = 0.05.

	α = 0.001	α = 0.01	α = 0.05	
Assay	Number	Number	Number	Rank
One_ACBP-79	0	1	1	60.5
One_agt-132	0	2	3	109.5
One_aldB-152	0	0	1	60.5
One_ALDOB-135	0	1	1	60.5
One_apoe-83	1	1	1	60.5
One_bckB-137	0	0	0	21
One_c3-98	1	1	2	92.5
One_ccd16-131	0	0	0	21
One_CD9-269	0	0	2	92.5
One_cetn1-167	0	0	3	109.5
One_CFP1	0	1	2	92.5
One_cin-177	0	1	2	92.5
One_CO1[a]	N/A	N/A	N/A	21
One_CTGF-301	0	0	0	21
One_Cytb_17[a]	N/A	N/A	N/A	21
One_Cytb_26[a]	N/A	N/A	N/A	21
One_dds-529	0	0	2	92.5
One_DDX5-86	1	1	4	114.5
One_E2-65	0	0	0	21
One_gadd45-269	0	0	0	21
One_gdh-212	0	0	1	60.5
One_GHII-2165	1	1	3	109.5
One_ghsR-66	0	0	0	21
One_GPDH-201	0	0	0	21
One_GPDH2-187	0	0	1	60.5
One_GPH-414	0	0	1	60.5
One_GTHa	0	0	1	60.5
One_HGFA-49	0	0	1	60.5
One_HpaI-71	0	0	0	21
One_HpaI-99	0	1	1	60.5
One_hsc71-220	0	0	1	60.5
One_Hsp47	0	0	0	21
One_Ig-90	1	1	1	60.5

Table 5. (Page 2 of 4).

	α = 0.001	α = 0.01	α = 0.05	
Assay	Number	Number	Number	Rank
One_IL8r-362	0	0	0	21
One_ins-107	0	2	5	116
One_KCT1-453	0	0	2	92.5
One_KPNA-422	0	0	3	109.5
One_LEI-87	0	0	2	92.5
One_leptin-92	0	0	0	21
One_lpp1-44	0	0	1	60.5
One_MARCKS-241	0	0	0	21
One_metA-253	0	0	0	21
One_MHC2_190	0	1	2	92.5
One_MHC2_251	0	0	2	92.5
One_Mkpro-129	0	1	3	109.5
One_ODC1-196	0	0	0	21
One_Ots208-234	0	0	2	92.5
One_Ots213-181	0	0	0	21
One_p53-534	0	0	0	21
One_parp3-170[b]	N/A	N/A	N/A	N/A
One_pax7-248	0	0	0	21
One_PIP	0	0	1	60.5
One_ppie-74	0	0	0	21
One_PPM1K-118[b]	N/A	N/A	N/A	N/A
One_Prl2	0	2	2	92.5
One_psme2-354	0	0	2	92.5
One_rab1a-76	0	0	2	92.5
One_RAG1-103	0	0	0	21
One_RAG3-93	0	0	0	21
One_redd1-414	0	0	0	21
One_RFC2-102	0	0	0	21
One_RFC2-285	0	0	0	21
One_RH2op-395	0	0	1	60.5
One_rpo2j-261	0	0	2	92.5
One_sast-211	0	0	0	21
One_serpin-75	0	0	0	21
One_spf30-207	0	0	0	21
One_srp09-127	0	0	1	60.5
One_ssrd-135	0	0	1	60.5

Table 5. (Page 3 of 4).

	$\alpha = 0.001$	$\alpha = 0.01$	$\alpha = 0.05$	
Assay	Number	Number	Number	Rank
One_STC-410	0	1	2	92.5
One_STR07	0	0	1	60.5
One_SUMO1-6	0	0	1	92.5
One_sys1-230	0	1	2	92.5
One_taf12-248	0	0	2	60.5
One_Tf_ex11-750	0	0	0	21
One_Tf_in3-182	0	0	0	21
One_tshB-92	0	0	2	92.5
One_txnip-401	1	1	1	60.5
One_U1002-101	0	0	0	21
One_U1003-75	0	0	0	21
One_U1004-183	0	0	4	114.5
One_U1009-91	0	0	0	21
One_U1010-81	0	0	0	21
One_U1012-68	0	0	1	60.5
One_U1013-108	1	1	2	92.5
One_U1014-74	1	1	1	60.5
One_U1016-115	0	0	1	60.5
One_U1017-62	0	0	0	21
One_U1021-57	8	12	14	117
One_U1024-197	0	0	2	92.5
One_U1101	0	0	2	92.5
One_U1102-220	2	2	3	109.5
One_U1103	0	0	0	21
One_U1104-138	0	0	0	21
One_U1105	1	1	1	60.5
One_U1201-492	0	0	2	92.5
One_U1202-1052	1	1	1	60.5
One_U1203-175	1	1	1	60.5
One_U1204-53	0	0	2	92.5
One_U1205-57	0	0	2	92.5
One_U1206-108	0	0	1	60.5
One_U1207-231[b]	N/A	N/A	N/A	N/A
One_U1208-67	0	0	2	92.5
One_U1209-111	0	0	0	21
One_U1210-173	0	1	1	60.5
One_U1211-97	0	0	1	60.5

Table 5. (Page 4 of 4).

	$\alpha = 0.001$	$\alpha = 0.01$	$\alpha = 0.05$	
Assay	Number	Number	Number	Rank
One_U1212-106	0	1	1	60.5
One_U1214-107	0	0	2	92.5
One_U1215-82	0	0	1	60.5
One_U1216-230	0	0	3	109.5
One_U301-92	0	1	1	60.5
One_U401-224	0	0	1	60.5
One_U404-229	0	1	1	60.5
One_U502-167	0	0	0	21
One_U503-170	0	0	0	21
One_U504-141	0	0	1	60.5
One_U508-533	0	0	1	60.5
One_UCA-24[b]	N/A	N/A	N/A	N/A
One_vamp5-255	0	0	1	60.5
One_vatf-214	0	0	0	21
One_VIM-569	0	0	1	60.5
One_zn706-68	0	0	0	21
One_ZNF-61	0	0	3	109.5
One_Zp3b-49	0	0	0	21

[a] These mitochondrial assays were not included in tests of conformance to Hardy-Weinberg expectations, and were given rankings equal to the highest rank for this judge.

[b] These assays were not included in tests of conformance to Hardy-Weinberg expectations due to poor laboratory performance.

Table 6. Percent of total test populations of sockeye salmon (Table 1) exhibiting significant (α = 0.001, 0.01, and 0.05) gametic disequilibrium for the pairs of loci for which disequilibrium was most commonly observed.

Pair of loci		α = 0.001		α = 0.01		α = 0.05	
		Number of populations	Percentage of total	Number of populations	Percentage of total	Number of populations	Percentage of total
One_aldB-152	*One_ALDOB-135*	34	94%	34	94%	36	100%
One_GPH-414	*One_GTHa*	35	97%	36	100%	36	100%
One_MHC2_190	*One_MHC2_251*	16	44%	23	64%	26	72%

Table 7. The contribution (%) to the first (PC1) and second (PC2) principal components, the average contribution to the first 12 principal components that explained 80% of total variation, and associated rankings for 124 sockeye salmon SNPs (Tables 2 and 3) screened for 36 test populations (Table 1).

	PC1		PC2		Average contribution	
Assay	%	Rank	%	Rank	%	Rank
One_ACBP-79	0.8	48	1.5	25.5	0.9	21
One_agt-132	0.5	72	1.3	29	0.7	49.5
One_aldB-152	0.6	62.5	0.2	91	0.5	89
One_ALDOB-135[a]	N/A	N/A	N/A	N/A	N/A	N/A
One_apoe-83	2.1	9	0.9	44.5	1.1	11
One_bckB-137[b]	N/A	N/A	N/A	N/A	N/A	N/A
One_c3-98	0.4	84	0.8	50.5	0.5	89
One_ccd16-131	0.2	100	0.1	101	0.2	109.5
One_CD9-269	0.2	100	0	109	0.3	107.5
One_cetn1-167	0.5	72	0	109	0.5	89
One_CFP1	1.5	20.5	2.4	5	1	14.5
One_cin-177	0.4	84	1.2	32	0.6	69
One_CO1[c]	2.3	7	1.8	17.5	1.8	2
One_CTGF-301	0.4	84	0.6	60.5	0.4	102
One_Cytb_17c	2.3	7	1.8	17.5	1.8	2
One_Cytb_26c	2.3	7	1.8	17.5	1.8	2
One_dds-529	0.7	55	1.1	35.5	0.6	69
One_DDX5-86	0	110	0.2	91	0.4	102
One_E2-65	0.2	100	0.9	44.5	0.5	89
One_gadd45-269	0	110	0	109	0.1	111.5
One_gdh-212	0.6	62.5	1.9	14	0.7	49.5
One_GHII-2165	2.9	3	1.2	32	1.4	3.5
One_ghsR-66	0.7	55	1.3	29	0.6	69
One_GPDH-201	1.4	26	0.6	60.5	0.7	49.5
One_GPDH2-187	1.8	12.5	0.1	101	0.9	21
One_GPH-414[a]	N/A	N/A	N/A	N/A	N/A	N/A
One_GTHa	1.1	35	0.8	50.5	0.7	49.5
One_HGFA-49	0.3	93.5	0.4	71	0.4	102
One_HpaI-71	0.8	48	1	39	0.9	21
One_HpaI-99	2.4	5.5	1.5	25.5	1.3	5.5
One_hsc71-220	0.7	55	0.3	81	0.7	49.5
One_Hsp47	0.4	84	2.1	9	0.7	49.5
One_Ig-90	1.6	16.5	0.9	44.5	0.8	33.5

Table 7. (Page 2 of 4).

	PC1		PC2		Average contribution	
Assay	%	Rank	%	Rank	%	Rank
One_IL8r-362	0.4	84	0.6	60.5	0.6	69
One_ins-107	0.7	55	0.6	60.5	0.5	89
One_KCT1-453	0.6	62.5	0.7	55	0.6	69
One_KPNA-422	0.3	93.5	0.8	50.5	0.4	102
One_LEI-87	1.3	30	0.3	81	0.9	21
One_leptin-92[b]	N/A	N/A	N/A	N/A	N/A	N/A
One_lpp1-44	0.7	55	0.4	71	0.8	33.5
One_MARCKS-241	0.4	84	0.6	60.5	0.4	102
One_metA-253	3.3	1	2.7	4	1.4	3.5
One_MHC2_190[d]	3.1	2	3.7	1.5	3.9	1
One_MHC2_251[d]	3.1	2	3.7	1.5	3.9	1
One_Mkpro-129	1.0	37	1.7	20.5	1	14.5
One_ODC1-196	0.3	93.5	1.8	17.5	0.6	69
One_Ots208-234	2.4	5.5	0.4	71	0.9	21
One_Ots213-181	1.6	16.5	0.2	91	0.7	49.5
One_p53-534	1.4	26	2.1	9	0.8	33.5
One_parp3-170[b]	N/A	N/A	N/A	N/A	N/A	N/A
One_pax7-248	0.7	55	0.1	101	0.6	69
One_PIP	0	110	0.7	55	0.5	89
One_ppie-74	1.4	26	3.4	3	1.3	5.5
One_PPM1K-118[e]	N/A	N/A	N/A	N/A	N/A	N/A
One_Prl2	0.1	105.5	2.0	11.5	0.7	49.5
One_psme2-354	0.4	84	0.3	81	0.6	69
One_rab1a-76	0.4	84	0.9	44.5	0.6	69
One_RAG1-103	0.1	105.5	1.5	25.5	0.7	49.5
One_RAG3-93	0.5	72	0.6	60.5	0.6	69
One_redd1-414	1.6	16.5	0.4	71	1	14.5
One_RFC2-102	0.5	72	0.5	64.5	0.5	89
One_RFC2-285	0.6	62.5	0.9	44.5	0.5	89
One_RH2op-395	0	110	0	109	0.2	109.5
One_rpo2j-261	0.4	84	1.8	17.5	0.6	69
One_sast-211	0.5	72	0.2	91	0.5	89
One_serpin-75	0.2	100	0	109	0.3	107.5
One_spf30-207	0.7	55	1.1	35.5	0.6	69
One_srp09-127	1.7	14	0.5	64.5	0.7	49.5

Table 7. (Page 3 of 4).

	PC1		PC2		Average contribution	
Assay	%	Rank	%	Rank	%	Rank
One_ssrd-135	0.6	62.5	1	39	0.6	69
One_STC-410	1.4	26	0.8	50.5	1.2	8
One_STR07	0.8	48	1.7	20.5	0.9	21
One_SUMO1-6	1	37	0.4	71	0.7	49.5
One_sys1-230	0	110	0.2	91	0.5	89
One_taf12-248	1.5	20.5	1.5	25.5	0.8	33.5
One_Tf_ex11-750	1.9	10.5	0.4	71	1.2	8
One_Tf_in3-182	0.2	100	1.3	29	0.9	21
One_tshB-92	0.2	100	0.3	81	0.4	102
One_txnip-401	1.9	10.5	0.1	101	0.8	33.5
One_U1002-101	0.5	72	0.4	71	0.5	89
One_U1003-75	2.2	8	0.3	81	1.1	11
One_U1004-183	0.6	62.5	2.3	6	1.1	11
One_U1009-91	0.5	72	1.1	35.5	0.7	49.5
One_U1010-81	0.6	62.5	1.8	17.5	0.6	69
One_U1012-68	0.6	62.5	0.7	55	0.8	33.5
One_U1013-108	0.5	72	0.9	44.5	0.5	89
One_U1014-74	0.5	72	0.9	44.5	0.5	89
One_U1016-115	1.2	32.5	0.3	81	0.9	21
One_U1017-62	0.9	41.5	1	39	0.5	89
One_U1021-57[f]	N/A	N/A	N/A	N/A	N/A	N/A
One_U1024-197	1.2	32.5	0.9	44.5	0.8	33.5
One_U1101	0.2	100	2	11.5	0.6	69
One_U1102-220	1.5	20.5	0.4	71	0.8	33.5
One_U1103	0.9	41.5	0.2	91	0.7	49.5
One_U1104-138	0.3	93.5	0	109	0.4	102
One_U1105	1.5	20.5	0.7	55	0.8	33.5
One_U1201-492	0.3	93.5	1.6	22.5	0.6	69
One_U1202-1052	1.4	26	0.4	71	0.7	49.5
One_U1203-175	0.8	48	0.1	101	0.5	89
One_U1204-53	0.5	72	1.9	14	0.7	49.5
One_U1205-57	0.4	84	0.2	91	0.4	102
One_U1206-108	0.9	41.5	0.1	101	0.6	69
One_U1207-231[e]	N/A	N/A	N/A	N/A	N/A	N/A
One_U1208-67	1.4	26	0.3	81	0.8	33.5
One_U1209-111	0.8	48	0.7	55	0.8	33.5

Table 7. (Page 4 of 4).

	PC1		PC2		Average contribution	
Assay	%	Rank	%	Rank	%	Rank
One_U1210-173	0.9	41.5	0.2	91	0.6	69
One_U1211-97	1.2	32.5	0.3	81	0.6	69
One_U1212-106	0.4	84	2.2	7	0.6	69
One_U1214-107	1.4	26	3.7	1.5	1.2	8
One_U1215-82	0.3	93.5	0	109	0.4	102
One_U1216-230	0.5	72	0.1	101	0.5	89
One_U301-92	0.1	105.5	0.3	81	0.5	89
One_U401-224	1.6	16.5	0.2	91	0.8	33.5
One_U404-229	1.8	12.5	1.2	32	0.9	21
One_U502-167	0.9	41.5	1.9	14	0.8	33.5
One_U503-170	0.4	84	0.1	101	0.6	69
One_U504-141	0.4	84	2.1	9	0.7	49.5
One_U508-533	0.8	48	0.2	91	0.6	69
One_UCA-24[e]	N/A	N/A	N/A	N/A	N/A	N/A
One_vamp5-255	0.8	48	1.1	35.5	0.8	33.5
One_vatf-214	0.9	41.5	1.6	22.5	0.8	33.5
One_VIM-569	1	37	0.4	71	0.6	69
One_zn706-68	0.1	105.5	0.1	101	0.1	111.5
One_ZNF-61	1.2	32.5	0.2	91	0.8	33.5
One_Zp3b-49	2.6	4	0.4	71	1	14.5

[a] These assays were dropped due to significant linkage and were not included in this analysis.

[b] These assays were dropped due to fixation in the 36 test populations and were not included in this analysis.

[c] These assays are linked and were included as a haplotype marker in this analysis.

[d] These assays are linked and were included as a haplotype marker in this analysis.

[e] These assays were dropped due to laboratory failure and were not included in this analysis.

[f] This assay was dropped due to failure to conform to Hardy-Weinberg expectations and was not included in this analysis.

Table 8. F_{ST} values and associated rankings among populations within fine-scale regions (θ_{S}), among fine-scale regions within broad-scale regions (θ_{P}), and between populations within pairs of populations of interest (θ_{Pairs}) for 124 assays (Tables 2 and 3) screened for 36 test populations (Table 1) using the Weir and Cockerham method (1984).

	θ_{S}		θ_{P}		θ_{Pairs}	
Assay	Statistic	Rank	Statistic	Rank	Statistic	Rank
One_ACBP-79	0.125	31	0.012	90	0.166	9
One_agt-132	0.112	43	0.016	81	0.049	78
One_aldB-152	0.090	64	0.018	76	0.065	56
One_ALDOB-135[a]	N/A	N/A	N/A	N/A	N/A	N/A
One_apoe-83	0.225	11	0.116	12	0.062	60
One_bckB-137[b]	N/A	N/A	N/A	N/A	N/A	N/A
One_c3-98	0.066	86	-0.014	111	0.037	86
One_ccd16-131	0.014	109	0.017	77	N/A[g]	112
One_CD9-269	0.048	99	0.078	24	0.061	63
One_cetn1-167	0.096	58	0.002	105	0.082	37
One_CFP1	0.152	18	0.013	88	0.091	30
One_cin-177	0.079	77	0.136	10	0.032	95
One_CO1[c]	0.243	8	0.016	79	0.203	4
One_CTGF-301	0.036	108	0.020	69	0.026	99
One_Cytb_17c	0.243	8	0.016	79	0.203	4
One_Cytb_26c	0.243	8	0.016	79	0.203	4
One_dds-529	0.052	98	0.017	78	0.036	89
One_DDX5-86	0.058	94	0.006	96	0.071	49
One_E2-65	0.080	76	0.188	4	0.085	36
One_gadd45-269	0.000	112	0.087	19	0.000	111
One_gdh-212	0.081	72	0.024	63	0.019	101
One_GHII-2165	0.314	3	0.161	7	0.156	12
One_ghsR-66	0.120	36	0.034	50	0.074	48
One_GPDH-201	0.093	60	0.035	49	0.063	57
One_GPDH2-187	0.141	25	0.009	95	0.200	6
One_GPH-414[a]	N/A	N/A	N/A	N/A	N/A	N/A
One_GTHa	0.109	46	0.097	14	0.065	55
One_HGFA-49	0.038	106	0.054	40	0.026	98
One_HpaI-71	0.163	16	0.092	15	0.115	22
One_HpaI-99	0.277	5	-0.001	108	0.055	71
One_hsc71-220	0.104	51	0.079	23	0.122	19
One_Hsp47	0.111	44	0.005	98	0.126	18

Table 8. (Page 2 of 4).

	θ_S		θ_P		θ_{Pairs}	
Assay	Statistic	Rank	Statistic	Rank	Statistic	Rank
One_Ig-90	0.124	32	0.030	57	0.081	38
One_IL8r-362	0.083	69	0.011	92	0.058	67
One_ins-107	0.052	97	0.018	75	0.031	96
One_KCT1-453	0.082	71	0.029	60	0.035	90
One_KPNA-422	0.054	96	0.020	68	0.048	80
One_LEI-87	0.146	21	0.088	17	0.079	42
One_leptin-92[b]	N/A	N/A	N/A	N/A	N/A	N/A
One_lpp1-44	0.127	30	0.021	67	0.087	34
One_MARCKS-241	0.036	107	0.237	2	0.008	108
One_metA-253	0.398	1	0.024	64	0.041	85
One_MHC2_190[d]	0.255	7	0.073	26	0.146	14
One_MHC2_251[d]	0.255	7	0.073	26	0.146	14
One_Mkpro-129	0.150	19	0.030	58	0.063	58
One_ODC1-196	0.100	54	0.023	65	0.093	28
One_Ots208-234	0.205	15	0.013	85	0.142	15
One_Ots213-181	0.104	49	0.031	54	0.077	44
One_p53-534	0.121	35	0.012	89	0.200	5
One_parp3-170[b]	N/A	N/A	N/A	N/A	N/A	N/A
One_pax7-248	0.078	79	0.152	9	0.004	110
One_PIP	0.058	93	0.083	21	0.057	68
One_ppie-74	0.292	4	0.050	41	0.037	87
One_PPM1K-118[e]	N/A	N/A	N/A	N/A	N/A	N/A
One_Prl2	0.097	57	0.020	70	0.074	47
One_psme2-354	0.110	45	-0.009	109	0.122	20
One_rab1a-76	0.081	73	0.002	104	0.052	75
One_RAG1-103	0.142	24	-0.023	112	0.177	8
One_RAG3-93	0.065	87	0.016	80	0.079	41
One_redd1-414	0.160	17	0.013	86	0.067	52
One_RFC2-102	0.081	74	0.022	66	0.061	64
One_RFC2-285	0.056	95	0.089	16	0.095	27
One_RH2op-395	0.012	110	0.063	31	0.008	107
One_rpo2j-261	0.089	65	0.055	38	0.107	23
One_sast-211	0.059	91	0.065	30	0.075	46
One_serpin-75	0.040	104	0.020	72	0.015	105

Table 8. (Page 3 of 4).

	θ_S		θ_P		θ_{Pairs}	
Assay	Statistic	Rank	Statistic	Rank	Statistic	Rank
One_spf30-207	0.085	68	0.028	61	0.090	31
One_srp09-127	0.120	37	0.027	62	0.086	35
One_ssrd-135	0.059	92	0.154	8	0.016	103
One_STC-410	0.233	9	0.046	43	0.196	7
One_STR07	0.135	27	0.082	22	0.135	17
One_SUMO1-6	0.097	56	0.060	32	0.034	93
One_sys1-230	0.094	59	0.032	53	0.056	70
One_taf12-248	0.109	47	0.088	18	0.121	21
One_Tf_ex11-750	0.233	10	0.039	47	0.251	3
One_Tf_in3-182	0.212	13	0.084	20	0.295	2
One_tshB-92	0.045	101	0.200	3	0.046	81
One_txnip-401	0.149	20	0.010	93	0.147	13
One_U1002-101	0.045	103	0.014	84	0.049	79
One_U1003-75	0.221	12	-0.009	110	0.061	62
One_U1004-183	0.323	2	0.068	29	0.490	1
One_U1009-91	0.090	63	0.055	39	0.096	26
One_U1010-81	0.063	88	0.036	48	0.052	77
One_U1012-68	0.107	48	0.032	52	0.097	25
One_U1013-108	0.076	82	0.068	28	0.032	94
One_U1014-74	0.061	90	0.019	73	0.034	92
One_U1016-115	0.142	23	0.059	35	0.135	16
One_U1017-62	0.062	89	0.020	71	0.009	106
One_U1021-57[f]	N/A	N/A	N/A	N/A	N/A	N/A
One_U1024-197	0.083	70	0.058	36	0.088	33
One_U1101	0.075	83	0.168	5	0.053	73
One_U1102-220	0.116	38	0.002	103	0.037	88
One_U1103	0.135	28	0.261	1	0.062	61
One_U1104-138	0.045	102	0.060	33	0.060	65
One_U1105	0.135	26	0.005	99	0.090	32
One_U1201-492	0.092	62	-0.001	107	0.046	82
One_U1202-1052	0.115	40	0.130	11	0.078	43
One_U1203-175	0.072	85	0.031	56	0.053	74
One_U1204-53	0.078	81	0.059	34	0.065	54
One_U1205-57	0.039	105	0.106	13	0.034	91
One_U1206-108	0.088	66	0.077	25	0.071	50

Table 8. (Page 4 of 4).

	θ_S		θ_P		θ_{Pairs}	
Assay	Statistic	Rank	Statistic	Rank	Statistic	Rank
One_U1207-231[e]	N/A	N/A	N/A	N/A	N/A	N/A
One_U1208-67	0.122	33	0.000	106	0.044	83
One_U1209-111	0.112	42	0.029	59	0.070	51
One_U1210-173	0.074	84	0.002	102	0.052	76
One_U1211-97	0.081	75	0.031	55	0.057	69
One_U1212-106	0.121	34	0.013	87	0.066	53
One_U1214-107	0.271	6	0.015	83	0.043	84
One_U1215-82	0.047	100	0.057	37	0.017	102
One_U1216-230	0.087	67	0.005	97	0.027	97
One_U301-92	0.079	78	0.019	74	0.063	59
One_U401-224	0.113	41	0.011	91	0.025	100
One_U404-229	0.144	22	0.009	94	0.080	39
One_U502-167	0.102	53	0.043	45	0.016	104
One_U503-170	0.092	61	0.070	27	0.054	72
One_U504-141	0.097	55	0.045	44	0.058	66
One_U508-533	0.115	39	0.015	82	0.102	24
One_UCA-24[e]	N/A	N/A	N/A	N/A	N/A	N/A
One_vamp5-255	0.104	50	0.003	101	0.076	45
One_vatf-214	0.103	52	0.033	51	0.165	10
One_VIM-569	0.078	80	0.165	6	0.080	40
One_zn706-68	0.006	111	0.004	100	0.006	109
One_ZNF-61	0.129	29	0.040	46	0.162	11
One_Zp3b-49	0.205	14	0.049	42	0.091	29

[a] These assays were dropped due to significant linkage and were not included in this analysis.

[b] These assays were dropped due to fixation in the 36 test populations and were not included in this analysis.

[c] These assays are linked and were included as a haplotype marker in this analysis.

[d] These assays are linked and were included as a haplotype marker in this analysis.

[e] These assays were dropped due to laboratory failure and were not included in this analysis.

[f] This assay was dropped due to failure to conform to Hardy-Weinberg expectations and was not included in this analysis.

[g] This assay was fixed for both populations in each pair and was given a rating equal to the worst.

Table 9. Test statistics and rankings based upon log-likelihood ratio (*G*) tests that describe the power of 124 SNPs (Tables 2 and 3) to discriminate between 7 pairs of sockeye salmon populations of interest (Table 1).

	Ualik-Pick		Becharof-Deer		Deer-Cinder		Broadway-Hatchery		Yentna-Susitna		Larson-Mama		McDonald-Hugh	
Assay	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank
One_ACBP-79	3.39	30	0.4	71	0.23	87	0.39	71	6.82	22	0.07	71	7.86	13
One_agt-132	0.52	66	0.32	74.5	9.31	18	1.38	43	0.33	83	1.12	40	6.18	19
One_aldB-152	5.4	17	0.46	66	0.99	70	4.14	17	3.46	35	0.27	58	5.53	21
One_ALDOB-135[a]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_apoe-83	4.95	19	0.05	97.5	10.7	16	0	93	8.16	18	5.83	4	5.38	22
One_bckB-137[b]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_c3-98	0	94.5	1.68	37	0.2	92.5	1.66	38	2.25	50	1.29	35	0.03	93
One_ccd16-131	N/A[g]	94.5	N/A[g]	104.5	N/A[g]	92.5	N/A[g]	93	N/A[g]	93	N/A[g]	90	N/A[g]	93
One_CD9-269	0	94.5	7.96	7	17.98	12	0.27	77	14.76	4	0.01	85	0.68	67
One_cetn1-167	0.22	80	0.24	83	1.06	69	0.85	59.5	2.96	39.5	2.99	11	0.36	78
One_CFP1	2.26	42	0.82	53	0.05	92.5	2.26	30	0.6	78	0.04	75.5	4.21	28
One_cin-177	4.9	20	1.2	47	11.1	15	0.01	91	0.22	87	2.47	21	3.17	34
One_CO1[c]	1.26	55	0.05	97.5	2.8	37	2.8	22	1.89	58	0.03	78.5	32.65	2
One_CTGF-301	N/A[g]	94.5	0.41	69.5	1.29	61.5	2.02	33	9.23	14.5	2.6	17.5	4.15	29
One_Cytb_17[c]	1.26	55	0.05	97.5	2.8	37	2.8	22	1.89	58	0.03	78.5	32.65	2
One_Cytb_26[c]	1.26	55	0.05	97.5	2.8	37	2.8	22	1.89	58	0.03	78.5	32.65	2
One_dds-529	3.42	28	1.52	40	0.22	89.5	4.33	14	10.08	12	0.74	44	0.05	93
One_DDX5-86	3.4	29	0.57	61	0.55	77	0	93	2.01	56	0.26	60	3.95	30
One_E2-65	3.38	31	1.63	39	2.66	40	0.85	59.5	0.15	91.5	0.21	66.5	0.01	93
One_gadd45-269	N/A[g]	94.5	N/A[g]	104.5	N/A[g]	92.5	N/A[g]	93	1.48	63.5	N/A[g]	90	1.37	55
One_gdh-212	7.42	12	0.6	59.5	0.53	78	0.7	62.5	2.57	46	0	90	0.56	70
One_GHII-2165	0.65	62	0.11	90.5	0.81	73.5	1.08	52	0.22	87	10.05	2	0.06	93
One_ghsR-66	0.98	59	6.48	10	2.69	39	0.96	55	0.22	87	2.53	20	2.35	38
One_GPDH-201	8.11	9	0.8	54.5	0.09	92.5	6.58	7	0.66	74	1.91	26	0.93	62

Table 9. (Page 2 of 6).

	Ualik-Pick		Becharof-Deer		Deer-Cinder		Broadway-Hatchery		Yentna-Susitna		Larson-Mama		McDonald-Hugh	
Assay	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank
One_GPDH2-187	0.48	68	1.92	36	6.11	22	2.76	23	5.81	27.5	0.06	72.5	6.46	18
One_GPH-414[a]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_GTHa	8.26	8	8.29	6	18.52	11	0.11	81	4.47	32	0	90	13.85	5
One_HGFA-49	0.46	69.5	0.38	72	3.5	32	5.73	8	6.52	24	0.54	49	8.89	11
One_HpaI-71	1.44	50	0.41	69.5	1.54	52	1.77	36	5	30	0.02	82	1.11	58.5
One_HpaI-99	0.2	82	1.19	48	2.54	42	1.01	54	0.37	81.5	1.34	32	3.81	32
One_hsc71-220	4.73	21	0.07	95	1.14	65	1.72	37	4.52	31	2.76	16	0.15	89.5
One_Hsp47	0.06	88	0.02	100	3.74	30	2.41	25	31.91	1	1.19	38	1.56	50
One_Ig-90	N/A[g]	94.5	N/A[g]	104.5	N/A[g]	92.5	N/A[g]	93	N/A[g]	93	N/A[g]	90	1.07	61
One_IL8r-362	5.12	18	30.05	2	34.25	4	3.85	18	1.83	59	0	90	2.1	43
One_ins-107	2.93	32	1.13	49.5	0	92.5	4.41	13	2.1	55	0.02	82	1.09	60
One_KCT1-453	0.03	89.5	2.89	21.5	3.34	34	1.14	50.5	3.78	34	4.55	7	0.13	91.5
One_KPNA-422	3.54	27	0.14	86	3.6	31	0.54	65	3.16	38	0.1	70	8.68	12
One_LEI-87	2.53	38	3.18	15	0.91	71	0.01	91	1.77	60.5	0.51	50	6.65	17
One_leptin-92[b]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_lpp1-44	1.14	56	16.31	3	10.27	17	0.05	83	1	70	2.91	14	0.32	80
One_MARCKS-241	N/A[g]	94.5	2.68	26.5	0	92.5	N/A[g]	93	3.99	33	N/A[g]	90	3.09	35
One_metA-253	N/A[g]	94.5	1.34	45	1.37	58	N/A[g]	93	2.23	51.5	5.96	3	4.67	26
One_MHC2_190[d]	20.19	3	158.28	1	37.4	3	53.39	2	9.29	13	14.01	1	37.13	1
One_MHC2_251[d]	20.19	3	158.28	1	37.4	3	53.39	2	9.29	13	14.01	1	37.13	1
One_Mkpro-129	7.57	11	0.52	63	1.47	53	3.81	19	0.03	93	1.71	28	0.3	81.5
One_ODC1-196	25.2	2	0.01	101.5	0.17	92.5	8.78	6	1.48	63.5	0.62	47	2.12	42
One_Ots208-234	0.99	58	1.21	46	0.52	79	4.22	15	2.8	43	0.33	55	0.02	93
One_Ots213-181	2.12	44	2.22	30.5	1.24	63	1.28	47	6.78	23	1.96	23	0.04	93
One_p53-534	N/A[g]	94.5	2.89	21.5	1.41	54.5	N/A[g]	93	N/A[g]	93	N/A[g]	90	0.39	76

Table 9. (Page 3 of 6).

	Ualik-Pick		Becharof-Deer		Deer-Cinder		Broadway-Hatchery		Yentna-Susitna		Larson-Mama		McDonald-Hugh	
Assay	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank
One_parp3-170[b]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_pax7-248	0.15	84	2.84	24	0.81	73.5	1.88	35	9.05	16	1.03	42	0.07	93
One_PIP	0.56	64	0.64	56	23.14	9	0.02	88	2.79	44	0.35	54	3.89	31
One_ppie-74	N/A[g]	94.5	2.78	25	1.32	60	1.39	41.5	0.01	93	N/A[g]	90	0.23	85
One_PPM1K-118[e]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_Prl2	0.66	61	0.11	90.5	6.86	20	0.04	85	0	93	0.72	45	0.41	73
One_psme2-354	0.01	92	7.71	8	15.93	13	4.91	12	0.16	90	0	90	10.57	6
One_rab1a-76	0.22	80	0	104.5	0.2	92.5	0.19	78	0.01	93	0.03	78.5	0	93
One_RAG1-103	2.87	33	1.35	43.5	1.08	67.5	4.15	16	14.11	6	1.51	29	1.27	57
One_RAG3-93	4.65	22	6.65	9	1.08	67.5	1.36	44	0.02	93	2.97	12.5	5.86	20
One_redd1-414	8.52	7	0.12	88.5	0.38	82	0.9	57.5	7.48	21	1.25	37	0.52	72
One_RFC2-102	1.82	46	2.92	19.5	1.2	64	0.01	91	17.87	2	0.03	78.5	9.33	10
One_RFC2-285	2.7	36	4.35	13.5	30.81	5	1.14	50.5	2.96	39.5	N/A[g]	90	1.92	46
One_RH2op-395	0	94.5	0.36	73	1.4	56	N/A[g]	93	1.31	66	N/A[g]	90	7.22	16
One_rpo2j-261	4.38	23	1.48	41	1.36	59	1.15	49	10.98	10	0.6	48	0.12	93
One_sast-211	0.29	78	2.15	33	5.29	24	0	93	9.23	14.5	0.26	60	2.85	36
One_serpin-75	1.1	57	0.18	84.5	0.66	76	13.02	4	0	93	N/A[g]	90	0.74	65
One_spf30-207	0.5	67	0	104.5	2.31	45.5	0	93	14.65	5	0.04	75.5	0.29	83
One_srp09-127	1.36	53	4.43	12	1.29	61.5	0.34	74	1.11	69	1.3	34	0.4	74.5
One_ssrd-135	1.28	54	3.1	17	0.9	72	1.34	45	5.28	29	1.86	27	4.71	25
One_STC-410	5.87	15	0.49	65	24.82	7	0.92	56	0.04	93	3.52	8	1.59	49
One_STR07	5.95	14	0.54	62	44.39	2	0.35	72.5	10.27	11	0.01	85	0.35	79
One_SUMO1-6	0.33	77	2.34	29	0.02	92.5	0.02	88	2.54	48	0.25	62	0.68	67
One_sys1-230	0.02	91	1.13	49.5	5.27	25	3.37	20	0	93	0.05	74	0.68	67
One_taf12-248	N/A[g]	94.5	N/A[g]	104.5	1.41	54.5	0.35	72.5	N/A[g]	93	0.31	56	0.57	69

Table 9. (Page 4 of 6).

	Ualik-Pick		Becharof-Deer		Deer-Cinder		Broadway-Hatchery		Yentna-Susitna		Larson-Mama		McDonald-Hugh	
Assay	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank
One_Tf_ex11-750	0.14	85	0.29	78.5	0	92.5	12.81	5	0.14	93	1.4	31	1.55	51
One_Tf_in3-182	0.11	86	0.94	52	3.18	35	39.95	3	0.29	85	N/A[g]	90	0	93
One_tshB-92	4.32	24	1.4	42	0.05	92.5	2.14	32	8.42	17	1.16	39	1.28	56
One_txnip-401	N/A[g]	94.5	0.29	78.5	2.74	38	N/A[g]	93	N/A[g]	93	N/A[g]	90	0.15	89.5
One_U1002-101	N/A[g]	94.5	N/A[g]	104.5	N/A[g]	92.5	N/A[g]	93	N/A[g]	93	N/A[g]	90	4.64	27
One_U1003-75	1.52	48	0.18	84.5	2.55	41	5.21	11	0.9	72	0.39	52	9.67	9
One_U1004-183	73.74	1	0.3	77	46.52	1	137.5	1	13.52	7	0.03	78.5	7.85	14
One_U1009-91	2.8	34	0.05	97.5	0.11	92.5	2.31	28	1.59	62	0.01	85	0.03	93
One_U1010-81	N/A[g]	94.5	0.6	59.5	2.95	36	0.3	76	11.54	9	0.37	53	2.25	41
One_U1012-68	10.9	5	14.36	4	0.43	81	0.9	57.5	0	93	0.26	60	1.44	52
One_U1013-108	0.85	60	0.08	94	0.51	80	0.15	79	0.12	93	5.08	5	2.34	39
One_U1014-74	0.54	65	0.61	57.5	12.05	14	2.39	26	2.91	42	0	90	1.93	45
One_U1016-115	11.29	4	2.22	30.5	1.62	50	1.22	48	0.44	79	0.22	65	4.75	24
One_U1017-62	N/A[g]	94.5	1.35	43.5	1.38	57	0	93	N/A[g]	93	N/A[g]	90	0	93
One_U1021-57[f]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_U1024-197	2.49	39	0.31	76	4.03	28	0	93	2.13	54	0.18	68.5	9.79	8
One_U1101	0.45	71	2.18	32	0.17	92.5	0.58	64	15.23	3	3.47	10	5.17	23
One_U1102-220	0	94.5	2.68	26.5	0	92.5	0	93	0.82	73	0.29	57	2.41	37
One_U1103	1.43	51.5	0	104.5	2.02	47	0.05	83	2.59	45	2.6	17.5	26.37	3
One_U1104-138	0.61	63	2.92	19.5	N/A[g]	92.5	N/A[g]	93	N/A[g]	93	N/A[g]	90	N/A[g]	93
One_U1105	3.95	25	1.65	38	0.22	89.5	2.23	31	6.07	25	1.26	36	0.19	86
One_U1201-492	0.03	89.5	8.48	5	0	92.5	1.56	40	2	57	3.49	9	1.81	47
One_U1202-1052	0.37	75	2.88	23	4.84	26	0.05	83	0.65	75.5	1.98	22	0.06	93
One_U1203-175	0.08	87	0.09	93	28.28	6	2.58	24	0.92	71	2.87	15	2	44
One_U1204-53	0.46	69.5	0.44	67	2.31	45.5	0.03	86	2.54	48	4.69	6	0.91	63

Table 9. (Page 5 of 6).

	Ualik-Pick		Becharof-Deer		Deer-Cinder		Broadway-Hatchery		Yentna-Susitna		Larson-Mama		McDonald-Hugh	
Assay	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank
One_U1205-57	2.09	45	4.35	13.5	5.67	23	1.06	53	1.3	67	N/A[g]	90	1.65	48
One_U1206-108	8.04	10	0.26	81.5	1.13	66	2.36	27	0.18	89	1.92	25	0.3	81.5
One_U1207-231[e]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_U1208-67	0.22	80	1.06	51	6.53	21	0.53	66	5.81	27.5	0.06	72.5	0.12	93
One_U1209-111	0.37	75	4.96	11	8.56	19	0.82	61	3.35	36	0.45	51	0.13	91.5
One_U1210-173	2.46	40	2.54	28	1.93	48	5.38	10	2.16	53	1.08	41	1.42	53
One_U1211-97	3.66	26	0.26	81.5	3.36	33	0.31	75	12.88	8	0.85	43	0	93
One_U1212-106	0.38	72.5	0.42	68	1.57	51	0.44	69	7.69	20	0	90	3.76	33
One_U1214-107	1.77	47	0	104.5	24.17	8	1.39	41.5	0.37	81.5	1.47	30	7.29	15
One_U1215-82	0.38	72.5	0.05	97.5	0.29	86	1.32	46	0.38	80	1.93	24	1.11	58.5
One_U1216-230	10.27	6	3.07	18	19.24	10	0	93	0.15	91.5	2.57	19	0.4	74.5
One_U301-92	1.45	49	0.12	88.5	0.17	92.5	2.29	29	1.77	60.5	1.31	33	0.09	93
One_U401-224	0.18	83	3.12	16	0.35	84	1.96	34	1.18	68	0.02	82	0.75	64
One_U404-229	N/A[g]	94.5	2.12	34	2.32	44	0.5	68	1.34	65	2.97	12.5	10.16	7
One_U502-167	5.82	16	0.51	64	0.67	75	0.52	67	5.9	26	N/A[g]	90	14.47	4
One_U503-170	2.54	37	2.1	35	1.8	49	1.64	39	0.62	77	0.21	66.5	0.28	84
One_U504-141	2.16	43	0.01	101.5	0.22	89.5	0.42	70	0.32	84	0.18	68.5	0.54	71
One_U508-533	2.79	35	0.1	92	0.22	89.5	N/A[g]	93	7.87	19	0	90	0.17	87.5
One_UCA-24[e]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_vamp5-255	0.37	75	0.61	57.5	0.37	83	0.02	88	0.07	93	0.68	46	2.31	40
One_vatf-214	N/A[g]	94.5	0.8	54.5	0.33	85	2.85	21	2.54	48	N/A[g]	90	0.37	77
One_VIM-569	2.37	41	0.13	87	3.82	29	0.13	80	3.23	37	0.23	63.5	0.17	87.5
One_zn706-68	N/A[g]	94.5	N/A[g]	104.5	N/A[g]	92.5	N/A[g]	93	2.94	41	N/A[g]	90	N/A[g]	93
One_ZNF-61	6.54	13	0.28	80	2.53	43	5.61	9	0.65	75.5	0.23	63.5	0.07	93

Table 9. (Page 6 of 6).

	Ualik-Pick		Becharof-Deer		Deer-Cinder		Broadway-Hatchery		Yentna-Susitna		Larson-Mama		McDonald-Hugh	
Assay	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank	*G*	Rank
One_Zp3b-49	1.43	51.5	0.32	74.5	4.22	27	0.7	62.5	2.23	51.5	N/A[g]	90	1.41	54

[a] These assays were dropped due to significant linkage and were not included in this analysis.

[b] These assays were dropped due to fixation in the 36 test populations and were not included in this analysis.

[c] These assays are linked and were included as a haplotype marker in this analysis.

[d] These assays are linked and were included as a haplotype marker in this analysis.

[e] These assays were dropped due to laboratory failure and were not included in this analysis.

[f] This assay was dropped due to failure to conform to Hardy-Weinberg expectations and was not included in this analysis.

[g] Some SNPs were homozygous for both populations in some G tests and lack a test statistic. These SNPs were given a ranking equal to the worst rank for the test in question.

Table 10. Rankings based upon f_{ORCA} that describe the power of 124 SNPs (Tables 2 and 3) to discriminate between 7 pairs of sockeye salmon populations of interest (Table 1).

Assay	Ualik-Pick	Becharof-Deer	Deer-Cinder	Broadway-Hatchery	Yentna-Susitna	Larson-Mama	McDonald-Hugh
One_ACBP-79	20	61	72	59	20	64	13
One_agt-132	46	45	16	48	62	29	16
One_aldB-152	16	60	51	10	31	47	21
One_ALDOB-135[a]	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_apoe-83	21	103	14	109	15	5	19
One_bckB-137[b]	108	112	104	100	103	57	109
One_c3-98	110	34	84	39	57	92	92
One_ccd16-131	114	106	113	92	110	108	101
One_CD9-269	109	7	7	67	5	87	59
One_cetn1-167	78	50	55	68	44	8	79
One_CFP1	43	44	105	27	68	105	26
One_cin-177	27	32	18	71	73	16	31
One_CO1[c]	44	110	22	30	66	58	1
One_CTGF-301	92	95	76	66	30	53	51
One_Cytb_17[c]	44	110	22	30	66	58	1
One_Cytb_26[c]	44	110	22	30	66	58	1
One_dds-529	30	26	63	13	12	38	99
One_DDX5-86	33	54	79	110	46	61	28
One_E2-65	23	27	30	45	89	59	114
One_gadd45-269	97	108	109	103	95	85	87
One_gdh-212	7	48	65	56	27	102	54
One_GHII-2165	67	77	66	47	75	2	100
One_ghsR-66	45	8	31	44	82	13	32
One_GPDH-201	11	40	91	6	76	18	42

Table 10. (Page 2 of 6).

Assay	Ualik-Pick	Becharof-Deer	Deer-Cinder	Broadway-Hatchery	Yentna-Susitna	Larson-Mama	McDonald-Hugh
One_GPDH2-187	60	72	38	51	34	73	15
One_GPH-414[a]	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_GTHa	8	6	10	69	29	109	5
One_HGFA-49	86	66	28	11	16	49	8
One_HpaI-71	37	59	48	38	22	77	55
One_HpaI-99	100	51	44	37	105	33	25
One_hsc71-220	17	114	52	23	25	17	95
One_Hsp47	84	99	23	35	1	27	46
One_Ig-90	105	113	114	114	112	89	67
One_IL8r-362	22	2	6	24	51	76	36
One_ins-107	35	35	106	12	52	72	56
One_KCT1-453	82	13	34	65	43	32	89
One_KPNA-422	28	82	26	64	39	60	10
One_LEI-87	36	21	54	113	40	41	11
One_leptin-92[b]	95	87	107	112	109	84	105
One_lpp1-44	39	3	15	73	54	21	66
One_MARCKS-241	93	85	111	95	69	110	77
One_metA-253	103	79	103	87	74	42	37
One_MHC2_190[d]	3	1	3	2	19	1	2
One_MHC2_251[d]	3	1	3	2	19	1	2
One_Mkpro-129	10	47	56	14	92	19	82
One_ODC1-196	2	92	80	5	59	40	41
One_Ots208-234	80	49	94	21	41	36	108
One_Ots213-181	40	36	40	32	21	14	102
One_p53-534	96	81	88	93	91	88	72

Table 10. (Page 3 of 6).

Assay	Ualik-Pick	Becharof-Deer	Deer-Cinder	Broadway-Hatchery	Yentna-Susitna	Larson-Mama	McDonald-Hugh
One_parp3-170[b]	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_pax7-248	72	20	49	33	10	34	96
One_PIP	64	38	8	76	42	37	30
One_ppie-74	102	55	71	72	101	112	88
One_PPM1K-118[e]	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_Prl2	49	56	20	79	96	31	83
One_psme2-354	94	5	9	7	70	93	12
One_rab1a-76	68	88	97	85	106	114	113
One_RAG1-103	62	98	81	62	2	24	76
One_RAG3-93	19	22	78	31	104	50	17
One_redd1-414	13	78	67	46	18	26	86
One_RFC2-102	42	15	53	80	6	97	14
One_RFC2-285	75	65	17	54	86	99	43
One_RH2op-395	101	68	90	101	88	113	57
One_rpo2j-261	18	25	47	43	8	52	93
One_sast-211	71	84	59	105	55	74	33
One_serpin-75	83	105	96	29	113	80	74
One_spf30-207	69	75	32	99	3	70	94
One_srp09-127	79	28	77	88	72	111	84
One_ssrd-135	47	14	62	40	26	15	22
One_STC-410	14	43	5	58	100	9	47
One_STR07	9	53	2	70	9	94	85
One_SUMO1-6	59	18	86	97	35	45	62
One_sys1-230	90	30	25	18	99	71	60
One_taf12-248	104	111	101	94	111	75	68

Table 10. (Page 4 of 6).

Assay	Ualik-Pick	Becharof-Deer	Deer-Cinder	Broadway-Hatchery	Yentna-Susitna	Larson-Mama	McDonald-Hugh
One_Tf_ex11-750	88	58	102	4	71	30	44
One_Tf_in3-182	85	37	35	3	98	107	104
One_tshB-92	52	46	95	52	38	25	53
One_txnip-401	106	96	85	98	114	101	80
One_U1002-101	89	90	112	77	108	95	34
One_U1003-75	74	80	43	8	63	35	6
One_U1004-183	1	83	1	1	11	98	9
One_U1009-91	25	89	87	19	45	79	98
One_U1010-81	111	73	60	82	24	51	39
One_U1012-68	15	4	69	53	97	90	35
One_U1013-108	50	62	64	74	90	23	52
One_U1014-74	57	42	12	25	33	82	45
One_U1016-115	4	12	45	34	64	44	18
One_U1017-62	113	109	98	104	107	96	111
One_U1021-57[f]	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_U1024-197	48	67	36	90	61	55	4
One_U1101	56	23	73	61	4	7	20
One_U1102-220	99	94	108	91	67	43	49
One_U1103	81	107	75	96	81	63	3
One_U1104-138	73	63	93	111	102	81	112
One_U1105	29	33	82	26	17	28	70
One_U1201-492	98	9	110	36	47	6	40
One_U1202-1052	61	11	24	75	53	10	110
One_U1203-175	58	97	4	17	49	3	38
One_U1204-53	70	71	39	78	36	4	58

Table 10. (Page 5 of 6).

Assay	Ualik-Pick	Becharof-Deer	Deer-Cinder	Broadway-Hatchery	Yentna-Susitna	Larson-Mama	McDonald-Hugh
One_U1205-57	54	70	57	86	77	104	69
One_U1206-108	6	57	41	28	87	11	71
One_U1207-231[e]	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_U1208-67	65	29	19	60	13	67	64
One_U1209-111	53	19	21	63	28	56	91
One_U1210-173	38	17	29	15	37	39	106
One_U1211-97	26	64	27	57	7	46	90
One_U1212-106	55	41	42	81	23	78	23
One_U1214-107	63	104	13	102	93	83	24
One_U1215-82	51	74	68	41	79	20	61
One_U1216-230	5	10	11	108	83	12	73
One_U301-92	34	91	74	16	48	22	103
One_U401-224	76	16	83	22	50	86	50
One_U404-229	91	31	58	55	80	68	7
One_U502-167	41	69	89	89	60	69	27
One_U503-170	31	24	46	42	58	65	97
One_U504-141	24	100	70	50	78	54	63
One_U508-533	66	102	92	107	14	100	81
One_UCA-24[e]	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_vamp5-255	77	39	61	84	94	66	29
One_vatf-214	112	76	100	20	84	91	65
One_VIM-569	32	86	50	83	32	62	75
One_zn706-68	107	101	99	106	85	103	78
One_ZNF-61	12	52	33	9	56	48	107

Table 10. (Page 6 of 6).

Assay	Ualik-Pick	Becharof-Deer	Deer-Cinder	Broadway-Hatchery	Yentna-Susitna	Larson-Mama	McDonald-Hugh
One_Zp3b-49	87	93	37	49	65	106	48

[a] These assays were dropped due to significant linkage and were not included in this analysis.
[b] These assays were dropped due to fixation in the 36 test populations and were not included in this analysis.
[c] These assays are linked and were included as a haplotype marker in this analysis.
[d] These assays are linked and were included as a haplotype marker in this analysis.
[e] These assays were dropped due to laboratory failure and were not included in this analysis.
[f] This assay was dropped due to failure to conform to Hardy-Weinberg expectations and was not included in this analysis.

Table 11. Rankings based upon f_{ORCA} that describe the power of each of 124 SNPs (Tables 2 and 3) to discriminate among 36 sockeye salmon populations of interest (Table 1).

Assay	f_{ORCA} rank	Assay	f_{ORCA} rank
One_ACBP-79	41	*One_KCT1-453*	83
One_agt-132	25	*One_KPNA-422*	58
One_aldB-152	47	*One_LEI-87*	17
One_ALDOB-135[a]	N/A	*One_leptin-92*[b]	114
One_apoe-83	12	*One_lpp1-44*	26
One_bckB-137[b]	112	*One_MARCKS-241*	104
One_c3-98	78	*One_metA-253*	7
One_ccd16-131	113	*One_MHC2_190*[d]	1
One_CD9-269	74	*One_MHC2_251*[d]	1
One_cetn1-167	56	*One_Mkpro-129*	11
One_CFP1	16	*One_ODC1-196*	29
One_cin-177	18	*One_Ots208-234*	38
One_CO1[c]	2	*One_Ots213-181*	48
One_CTGF-301	105	*One_p53-534*	97
One_Cytb_17[c]	2	*One_parp3-170*[b]	N/A
One_Cytb_26[c]	2	*One_pax7-248*	75
One_dds-529	79	*One_PIP*	84
One_DDX5-86	71	*One_ppie-74*	30
One_E2-65	86	*One_PPM1K-118*[e]	N/A
One_gadd45-269	110	*One_Prl2*	43
One_gdh-212	42	*One_psme2-354*	21
One_GHII-2165	4	*One_rab1a-76*	73
One_ghsR-66	27	*One_RAG1-103*	90
One_GPDH-201	33	*One_RAG3-93*	93
One_GPDH2-187	63	*One_redd1-414*	6
One_GPH-414[a]	N/A	*One_RFC2-102*	81
One_GTHa	28	*One_RFC2-285*	103
One_HGFA-49	69	*One_RH2op-395*	106
One_HpaI-71	14	*One_rpo2j-261*	64
One_HpaI-99	24	*One_sast-211*	100
One_hsc71-220	65	*One_serpin-75*	107
One_Hsp47	70	*One_spf30-207*	76
One_Ig-90	92	*One_srp09-127*	77
One_IL8r-362	62	*One_ssrd-135*	57
One_ins-107	61	*One_STC-410*	9

Table 11. (Page 2 of 2).

Assay	f_{ORCA} rank	Assay	f_{ORCA} rank
One_STR07	10	*One_U1203-175*	60
One_SUMO1-6	32	*One_U1204-53*	68
One_sys1-230	22	*One_U1205-57*	101
One_taf12-248	85	*One_U1206-108*	37
One_Tf_ex11-750	20	*One_U1207-231*[e]	N/A
One_Tf_in3-182	45	*One_U1208-67*	13
One_tshB-92	98	*One_U1209-111*	54
One_txnip-401	99	*One_U1210-173*	66
One_U1002-101	108	*One_U1211-97*	94
One_U1003-75	19	*One_U1212-106*	59
One_U1004-183	3	*One_U1214-107*	8
One_U1009-91	44	*One_U1215-82*	34
One_U1010-81	91	*One_U1216-230*	67
One_U1012-68	51	*One_U301-92*	55
One_U1013-108	50	*One_U401-224*	23
One_U1014-74	96	*One_U404-229*	72
One_U1016-115	5	*One_U502-167*	88
One_U1017-62	102	*One_U503-170*	46
One_U1021-57[f]	N/A	*One_U504-141*	39
One_U1024-197	80	*One_U508-533*	89
One_U1101	35	*One_UCA-24*[e]	N/A
One_U1102-220	52	*One_vamp5-255*	49
One_U1103	95	*One_vatf-214*	87
One_U1104-138	109	*One_VIM-569*	82
One_U1105	15	*One_zn706-68*	111
One_U1201-492	36	*One_ZNF-61*	31
One_U1202-1052	53	*One_Zp3b-49*	40

[a] These assays were dropped due to significant linkage and were not included in this analysis.

[b] These assays were dropped due to fixation in the 36 test populations and were not included in this analysis.

[c] These assays are linked and were included as a haplotype marker in this analysis.

[d] These assays are linked and were included as a haplotype marker in this analysis.

[e] These assays were dropped due to laboratory failure and were not included in this analysis.

[f] This assay was dropped due to failure to conform to Hardy-Weinberg expectations and was not included in this analysis.

Table 12. Sum of rankings and final ADF&G rank for 124 SNPs (Tables 2 and 3) screened for 36 test populations (Table 1).

Assay	Sum of ranks	Final rank	Assay	Sum of ranks	Final rank
One_ACBP-79	1470.5	24	*One_KCT1-453*	1722	65
One_agt-132	1615	51	*One_KPNA-422*	1725	66
One_aldB-152	1565.5	43	*One_LEI-87*	1468.5	23
One_ALDOB-135[a]	N/A	N/A	*One_leptin-92*[b]	N/A	N/A
One_apoe-83	1068	6	*One_lpp1-44*	1278.5	10
One_bckB-137[b]	N/A	N/A	*One_MARCKS-241*	2547	114
One_c3-98	2083	96	*One_metA-253*	1425	18
One_ccd16-131	2424	112	*One_MHC2_190*[e]	991.5	5
One_CD9-269	1713	64	*One_MHC2_251*[e]	704.5	1
One_cetn1-167	1986	91	*One_Mkpro-129*	1637	55
One_CFP1	1561	42	*One_ODC1-196*	1591.5	47
One_cin-177	1709.5	62	*One_Ots208-234*	1644.25	56
One_CO1[c]	894.5	4	*One_Ots213-181*	1509	32
One_CTGF-301	2039.5	94	*One_p53-534*	1995.5	93
One_Cytb_17[c]	843.5	2	*One_parp3-170*[b]	N/A	N/A
One_Cytb_26[c]	874.5	3	*One_pax7-248*	1487	26
One_dds-529	1955.5	97	*One_PIP*	1776.5	74
One_DDX5-86	2323	108	*One_ppie-74*	2132	101
One_E2-65	1844.5	79	*One_PPM1K-118*[f]	N/A	N/A
One_gadd45-269	2298.5	107	*One_Prl2*	1911.5	86
One_gdh-212	1665.5	58	*One_psme2-354*	1956	98
One_GHII-2165	1394.5	15	*One_rab1a-76*	2412	111
One_ghsR-66	1388.5	14	*One_RAG1-103*	1489.5	27
One_GPDH-201	1430	20	*One_RAG3-93*	1847	81
One_GPDH2-187	1608	50	*One_redd1-414*	1634	53
One_GPH-414[a,d]	N/A	N/A	*One_RFC2-102*	1506	31
One_GTHa[d]	1159.5	8	*One_RFC2-285*	1505	30
One_HGFA-49	1741	67	*One_RH2op-395*	2343.5	109
One_HpaI-71	1541.5	38	*One_rpo2j-261*	1429.5	19
One_HpaI-99	1746.5	69	*One_sast-211*	1778	76
One_hsc71-220	1711.5	63	*One_serpin-75*	2697	115
One_Hsp47	1520.5	34	*One_spf30-207*	1679	60
One_Ig-90	2164	103	*One_srp09-127*	1635.5	54
One_IL8r-362	1261.5	9	*One_ssrd-135*	1444	21
One_ins-107	2090.5	99	*One_STC-410*	1695	61

Table 12. (Page 2 of 2).

Assay	Sum of ranks	Final rank	Assay	Sum of ranks	Final rank
One_STR07	1528	36	*One_U1203-175*	1520	33
One_SUMO1-6	1858	82	*One_U1204-53*	1626	52
One_sys1-230	1844.5	80	*One_U1205-57*	2064	95
One_taf12-248	1915.5	87	*One_U1206-108*	1824	77
One_Tf_ex11-750	1538.5	37	*One_U1207-231*[f]	N/A	N/A
One_Tf_in3-182	1410	16	*One_U1208-67*	1543.5	39
One_tshB-92	1666	59	*One_U1209-111*	1291.5	11
One_txnip-401	1959	90	*One_U1210-173*	1646	57
One_U1002-101	2111.5	100	*One_U1211-97*	1992	92
One_U1003-75	1417.5	17	*One_U1212-106*	1758.5	72
One_U1004-183	1123	7	*One_U1214-107*	1550	41
One_U1009-91	1504.5	29	*One_U1215-82*	2393.5	110
One_U1010-81	1500.5	28	*One_U1216-230*	1831	78
One_U1012-68	1317.5	12	*One_U301-92*	1888	85
One_U1013-108	1876	83	*One_U401-224*	1753.5	70
One_U1014-74	1606.5	48	*One_U404-229*	1579	46
One_U1016-115	1334	13	*One_U502-167*	1471	25
One_U1017-62	2221.5	104	*One_U503-170*	1567.5	44
One_U1021-57[g]	N/A	N/A	*One_U504-141*	1925.5	88
One_U1024-197	1607	49	*One_U508-533*	2286.5	106
One_U1101	1547	40	*One_UCA-24*[f]	N/A	N/A
One_U1102-220	2241	105	*One_vamp5-255*	1933	89
One_U1103	1579	45	*One_vatf-214*	1757.5	71
One_U1104-138	2151.5	102	*One_VIM-569*	1768.5	73
One_U1105	1521	35	*One_zn706-68*	2472	113
One_U1201-492	1884.5	84	*One_ZNF-61*	1457.5	22
One_U1202-1052	1741.5	68	*One_Zp3b-49*	1777	75

[a] These assays were dropped due to significant linkage and were not included in this analysis.

[b] These assays were dropped due to fixation in the 36 test populations and were not included in this analysis.

[c] These assays are linked and were included as a haplotype marker in some analyses.

[d] These two linked assays have nearly identical allele frequencies for the 36 test populations and are expected to provide similar test statistics and rankings for all measures except laboratory performance. These were exchanged to provide additional overlap among markers run by stakeholder laboratories (i.e., CDFO). See text for details.

[e] These assays are linked and were included as a haplotype marker in some analyses.

[f] These assays were dropped due to laboratory failure and were not included in this analysis.

[g] This assay was dropped due to failure to conform to Hardy-Weinberg expectations and was not included in this analysis.

Table 13. Cumulative performance measure (mean individual assignment accuracy), contribution to performance measure and rank based upon performance measure for 124 SNPs (Table 2) screened for 36 test populations (Table 1) from a Backwards Elimination Locus Selection (BELS) algorithm. See text for details.

Assay	Performance Measure	Contribution	Rank
One_ACBP-79	0.73	0.01	33
One_agt-132	0.80	0.00	49
One_aldB-152	0.68	0.01	26
One_ALDOB-135[a]	N/A	N/A	N/A
One_apoe-83	0.34	0.03	6
One_bckB-137	0.89	0.00	110
One_c3-98	0.87	0.00	77
One_ccd16-131	0.89	0.00	112
One_CD9-269	0.78	0.00	42
One_cetn1-167	0.66	0.01	24
One_CFP1	0.88	0.00	95
One_cin-177	0.86	0.00	73
One_CO1[b]	0.14	0.07	2
One_CTGF-301	0.88	0.00	84
One_Cytb_17[b]	0.14	0.07	2
One_Cytb_26[b]	0.14	0.07	2
One_dds-529	0.87	0.00	81
One_DDX5-86	0.76	0.00	37
One_E2-65	0.76	0.00	39
One_gadd45-269	0.89	0.00	107
One_gdh-212	0.87	0.00	83
One_GHII-2165	0.46	0.02	10
One_ghsR-66	0.52	0.02	13
One_GPDH-201	0.86	0.00	75
One_GPDH2-187	0.82	0.00	55
One_GPH-414[a]	N/A	N/A	N/A
One_GTHa	0.63	0.01	21
One_hsc71-220	0.78	0.00	43
One_HGFA-49	0.88	0.00	87
One_HpaI-71	0.54	0.02	14
One_HpaI-99	0.56	0.02	15
One_Hsp47	0.60	0.01	18
One_Ig-90	0.89	0.00	111
One_IL8r-362	0.80	0.00	48

Table 13. (Page 2 of 4).

Assay	Performance Measure	Contribution	Rank
One_KCT1-453	0.77	0.00	41
One_KPNA-422	0.83	0.00	60
One_LEI-87	0.84	0.00	62
One_leptin-92	0.89	0.00	108
One_lpp1-44	0.48	0.02	11
One_MARCKS-241	0.89	0.00	104
One_metA-253	0.88	0.00	89
One_MHC2_190[c]	0.00	0.14	1
One_MHC2_251[c]	0.00	0.14	1
One_Mkpro-129	0.59	0.01	17
One_ODC1-196	0.66	0.01	23
One_Ots208-234	0.81	0.00	51
One_Ots213-181	0.79	0.00	45
One_p53-534	0.89	0.00	99
One_parp3-170[d]	N/A	N/A	N/A
One_pax7-248	0.80	0.00	47
One_pIns	0.89	0.00	96
One_PIP	0.84	0.00	61
One_ppie-74	0.89	0.00	109
One_PPM1K-118[e]	N/A	N/A	N/A
One_Prl2	0.70	0.01	29
One_psme2-354	0.75	0.01	36
One_rab1a-76	0.85	0.00	65
One_RAG1-103	0.82	0.00	53
One_RAG3-93	0.85	0.00	66
One_redd1-414	0.41	0.03	8
One_RFC2-102	0.67	0.01	25
One_RFC2-285	0.87	0.00	78
One_RH2op395	0.89	0.00	102
One_rpo2j-261	0.83	0.00	56
One_sast-211	0.88	0.00	86
One_serpin	0.88	0.00	85
One_spf30-207	0.81	0.00	52
One_srp09-127	0.89	0.00	97
One_ssrd-135	0.87	0.00	82
One_STC-410	0.38	0.03	7
One_STR07	0.50	0.02	12

Table 13. (Page 3 of 4).

Assay	Performance Measure	Contribution	Rank
One_taf12-248	0.89	0.00	98
One_SUMO1-6	0.86	0.00	70
One_sys1-230	0.01	0.01	20
One_Tf_ex11-750	0.04	0.04	5
One_Tf_in3-182	0.02	0.02	9
One_tshB-92	0.00	0.00	94
One_txnip-401	0.00	0.00	103
One_U1002-101	0.00	0.00	106
One_U1003-75	0.05	0.05	3
One_U1004-183	0.04	0.04	4
One_U1009-91	0.00	0.00	59
One_U1010-81	0.00	0.00	92
One_U1012-68	0.01	0.01	16
One_U1013-108	0.00	0.00	50
One_U1014-74	0.00	0.00	57
One_U1016-115	0.01	0.01	19
One_U1017-62	0.00	0.00	113
One_U1021-57[f]	N/A	N/A	N/A
One_U1024-197	0.00	0.00	88
One_U1101	0.00	0.00	54
One_U1102-220	0.01	0.01	32
One_U1103	0.00	0.00	76
One_U1104-138	0.00	0.00	105
One_U1105	0.01	0.01	30
One_U1201-492	0.01	0.01	35
One_U1202-1052	0.00	0.00	79
One_U1203-175	0.00	0.00	44
One_U1204-53	0.00	0.00	69
One_U1205-57	0.00	0.00	93
One_U1206-108	0.00	0.00	74
One_U1207-231[e]	N/A	N/A	N/A
One_U1208-67	0.00	0.00	72
One_U1209-111	0.01	0.01	22
One_U1210-173	0.00	0.00	90
One_U1211-97	0.00	0.00	58
One_U1212-106	0.01	0.01	34
One_U1214-107	0.00	0.00	38

Table 13. (Page 4 of 4).

Assay	Performance Measure	Contribution	Rank
One_U1215-82	0.89	0.00	101
One_U1216-230	0.70	0.01	28
One_U301-92	0.86	0.00	71
One_U401-224	0.87	0.00	80
One_U404-229	0.77	0.00	40
One_U502-167	0.88	0.00	91
One_U503-170	0.72	0.01	31
One_U504-141	0.84	0.00	63
One_U508-533	0.85	0.00	68
One_UCA-24[e]	N/A	N/A	N/A
One_vamp5-255	0.79	0.00	46
One_vatf-214	0.89	0.00	100
One_VIM-569	0.85	0.00	67
One_zn706-68	0.89	0.00	114
One_ZNF-61	0.69	0.01	27
One_Zp3b-49	0.84	0.00	64

[a] These assays were dropped due to significant linkage and were not included in this analysis.

[b] These assays are linked and were included as a haplotype marker in this analysis.

[c] These assays are linked and were included as a haplotype marker in this analysis.

[d] These assays were dropped due to fixation in the 36 test populations and were not included in this analysis.

[e] These assays were dropped due to laboratory failure and were not included in this analysis.

[f] This assay was dropped due to failure to conform to Hardy-Weinberg expectations and was not included in this analysis.

Table 14. Log-likelihood ratio test statistics (*G*) divided by degrees of freedom for 124 SNPs (Tables 2 and 3) screened for 36 test populations (Table 1) from a hierarchical analysis of allele frequency homogeneity among populations within 9 fine-scale regions (Table 1). Fine-scale regions are abbreviated as follows: Russia (R), Norton Sound and western Bristol Bay (NS/WBB), Eastern Bristol Bay (EBB), North Peninsula (NP), Chignik and Kodiak (C/K), Cook Inlet (CI), Copper River and northern Southeast Alaska (CR/NSE), Southern Southeast Alaska (SSE), and British Columbia and Washington (BC/WA).

Assay	R	NS/WBB	EBB	NP	C/K	CI	CR/NSE	SSE	BC/WA
One_ACBP-79	12.89	1.81	2.66	2.87	24.51	9.53	1.98	4.84	15.44
One_agt-132	8.73	2.97	2.71	10.58	1.01	15.91	44.57	3.61	67.97
One_aldB-152	24.41	2.17	6.73	18.84	5.14	24.65	17.75	2.85	24.98
One_ALDOB-135[a]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_apoe-83	22.32	26.00	0.88	29.82	0.40	11.57	2.05	19.80	64.40
One_bckB-137[b]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_c3-98	7.39	4.74	3.43	12.81	7.46	15.23	41.38	0.05	2.35
One_ccd16-131	0.00	0.00	0.00	0.00	0.00	0.00	4.39	3.43	0.00
One_CD9-269	20.09	6.69	16.27	8.78	0.56	9.67	7.12	0.46	7.90
One_cetn1-167	17.26	39.25	0.93	23.19	0.54	15.13	19.55	0.82	4.75
One_CFP1	1.13	0.81	0.48	16.82	1.13	12.13	29.99	2.12	66.87
One_cin-177	1.20	12.66	2.99	30.81	4.52	6.30	3.54	5.35	30.90
One_CO1[c]	4.33	0.35	0.32	4.26	2.55	8.20	3.89	10.46	20.27
One_CTGF-301	0.00	9.50	2.26	0.70	3.26	5.53	2.13	2.82	9.84
One_Cytb_17[c]	4.33	0.35	0.32	4.26	2.55	8.20	3.89	10.46	20.27
One_Cytb_26[c]	4.33	0.35	0.32	4.26	2.55	8.20	3.89	10.46	20.27
One_dds-529	5.73	6.54	2.15	4.53	3.93	8.33	35.99	0.75	10.46
One_DDX5-86	4.10	4.48	1.04	0.79	0.90	13.60	26.14	16.87	10.64
One_E2-65	20.04	12.74	3.40	6.50	0.66	25.88	6.93	1.23	24.73
One_gadd45-269	0.97	0.00	0.00	0.00	0.00	0.68	0.00	1.07	0.00
One_gdh-212	5.07	14.31	7.51	0.28	2.12	1.19	11.27	2.43	52.50
One_GHII-2165	11.32	3.45	1.65	6.82	0.82	15.18	80.25	0.85	20.93
One_ghsR-66	11.63	55.95	28.79	13.97	24.58	7.48	31.11	1.19	20.87
One_GPDH-201	9.63	10.99	0.33	4.57	15.52	4.37	17.69	4.62	23.75
One_GPDH2-187	16.64	1.98	1.91	8.44	3.76	7.57	4.75	9.47	11.23
One_GPH-414[a]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_GTHa	60.03	3.29	3.00	8.93	56.05	7.82	14.06	17.57	33.57
One_HGFA-49	10.25	8.50	2.67	5.00	4.50	1.85	2.98	4.57	12.98
One_HpaI-71	16.76	5.59	7.27	41.53	6.39	19.75	13.48	2.45	91.20
One_HpaI-99	5.37	3.38	1.40	5.93	44.04	7.24	15.01	2.56	26.45
One_hsc71-220	23.08	8.36	3.21	28.03	17.07	22.33	2.80	19.95	25.38

Table 14. (Page 2 of 4).

Assay	R	NS/WBB	EBB	NP	C/K	CI	CR/NSE	SSE	BC/WA
One_Hsp47	3.77	17.09	4.99	16.76	12.45	10.64	6.52	14.80	34.47
One_Ig-90	0.00	0.00	0.00	2.20	0.00	0.00	5.41	1.54	18.28
One_IL8r-362	7.06	33.75	17.55	7.81	2.01	4.78	21.33	3.31	0.35
One_ins-107	32.68	3.22	0.79	5.03	2.61	8.92	11.34	0.92	12.95
One_KCT1-453	10.95	33.70	2.98	10.93	1.80	11.10	0.25	4.45	15.90
One_KPNA-422	3.23	17.29	1.78	0.76	9.51	7.35	3.71	9.22	14.25
One_LEI-87	28.90	19.12	2.18	6.58	0.69	14.25	10.29	3.57	18.66
One_leptin-92[b]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_lpp1-44	9.89	60.50	10.34	11.26	33.29	5.80	0.95	0.68	14.00
One_MARCKS-241	5.11	0.00	1.15	11.66	2.50	5.44	8.21	1.98	9.38
One_metA-253	0.00	0.00	0.93	0.00	2.50	1.96	12.91	11.29	66.93
One_MHC2_190[d]	17.93	14.68	13.71	11.78	4.23	10.02	9.30	7.12	12.94
One_MHC2_251[d]	17.93	14.68	13.71	11.78	4.23	10.02	9.30	7.12	12.94
One_Mkpro-129	10.86	9.28	4.03	2.37	7.07	20.88	28.62	8.19	36.77
One_ODC1-196	3.88	20.63	0.90	1.30	5.46	10.26	8.94	2.03	43.37
One_Ots208-234	1.08	5.38	1.45	13.56	2.28	5.85	8.90	0.73	34.37
One_Ots213-181	6.69	11.36	4.53	3.69	4.72	4.86	5.88	2.27	26.65
One_p53-534	0.00	0.00	1.52	2.13	17.81	4.84	12.72	3.47	16.32
One_parp3-170[b]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_pax7-248	46.23	4.50	8.62	26.26	6.96	8.97	25.16	4.19	16.08
One_PIP	22.78	1.78	0.49	10.90	0.07	9.82	15.40	2.23	13.57
One_ppie-74	10.37	0.00	2.52	2.14	6.84	5.92	3.02	9.67	102.87
One_PPM1K-118[e]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_Prl2	15.15	33.50	3.60	5.56	0.64	10.44	11.37	7.44	44.37
One_psme2-354	2.40	2.99	7.54	7.70	7.29	12.60	34.13	9.10	21.43
One_rab1a-76	1.31	9.08	4.85	7.88	25.91	20.87	14.00	13.61	22.75
One_RAG1-103	0.00	7.23	0.92	2.97	4.05	36.33	5.60	4.59	17.07
One_RAG3-93	10.88	3.31	2.64	19.39	8.71	14.78	13.53	3.40	17.55
One_redd1-414	29.63	10.60	6.49	24.63	19.87	19.73	0.79	6.55	26.62
One_RFC2-102	7.02	8.79	2.36	16.56	0.86	44.87	3.28	19.30	38.30
One_RFC2-285	6.82	2.35	2.24	12.76	0.76	6.84	9.67	9.32	2.88
One_RH2op-395	0.12	4.43	1.49	3.01	0.00	0.65	4.93	4.33	1.63
One_rpo2j-261	7.28	6.01	1.58	14.50	15.67	27.18	15.53	16.81	35.43
One_sast-211	1.16	2.10	3.93	5.39	1.39	7.26	21.80	3.76	2.32
One_serpin-75	6.18	2.66	4.98	3.36	8.30	6.20	7.72	0.47	13.09
One_spf30-207	24.09	10.10	4.19	12.44	1.30	15.68	6.30	0.19	56.20

Table 14. (Page 3 of 4).

Assay	R	NS/WBB	EBB	NP	C/K	CI	CR/NSE	SSE	BC/WA
One_srp09-127	4.51	0.81	4.80	6.99	1.19	4.52	9.87	0.77	10.54
One_ssrd-135	7.13	9.21	2.37	19.05	2.98	5.07	20.38	9.98	19.79
One_STC-410	27.25	8.26	19.24	26.89	3.60	11.39	0.43	39.58	1.43
One_STR07	3.39	5.54	10.34	3.50	1.66	15.12	54.10	24.02	27.15
One_SUMO1-6	22.02	18.09	1.64	3.01	0.01	4.39	4.74	0.65	24.43
One_sys1-230	36.93	2.86	4.12	13.53	3.74	5.66	29.15	0.36	8.88
One_taf12-248	0.92	1.45	2.87	0.81	3.86	1.82	6.66	1.30	11.92
One_Tf_ex11-750	45.93	15.14	8.82	19.24	6.86	21.73	7.87	2.94	9.74
One_Tf_in3-182	2.75	2.88	17.15	11.36	22.07	2.72	2.80	0.03	23.19
One_tshB-92	7.64	31.63	0.50	1.58	1.67	9.93	5.93	0.77	8.73
One_txnip-401	0.00	0.91	1.06	0.00	0.00	0.65	13.36	13.63	7.38
One_U1002-101	0.00	0.00	0.00	0.00	0.00	0.00	7.96	8.60	0.00
One_U1003-75	58.23	6.22	3.39	11.79	14.06	18.25	14.33	6.11	20.80
One_U1004-183	27.21	24.10	1.91	14.74	74.95	68.95	20.16	5.87	22.06
One_U1009-91	18.37	11.24	7.64	15.54	2.78	3.02	30.25	15.31	33.67
One_U1010-81	7.34	0.00	6.05	0.26	2.53	7.36	4.30	6.96	19.85
One_U1012-68	14.50	13.21	11.78	0.09	5.07	35.02	39.50	5.42	48.40
One_U1013-108	23.55	0.56	2.77	11.14	1.35	13.98	2.26	25.82	13.63
One_U1014-74	8.18	9.69	2.53	7.98	4.21	7.77	6.85	1.01	17.62
One_U1016-115	38.40	7.13	2.72	5.11	11.40	18.82	26.83	16.03	36.37
One_U1017-62	5.54	0.00	0.91	2.20	0.68	12.27	5.68	1.64	11.22
One_U1021-57[f]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_U1024-197	10.94	4.51	1.50	5.51	0.49	2.21	12.96	9.64	32.59
One_U1101	13.18	7.55	7.30	2.21	2.73	7.11	4.35	10.77	74.97
One_U1102-220	8.86	4.16	14.34	19.23	6.28	8.19	0.37	9.31	10.15
One_U1103	6.32	0.82	0.92	4.41	3.48	2.37	36.34	19.26	10.94
One_U1104-138	0.00	7.32	1.89	1.10	0.00	0.00	0.00	0.00	0.00
One_U1105	32.03	17.16	11.44	7.54	1.33	26.95	3.65	8.15	8.00
One_U1201-492	22.33	9.76	12.18	7.78	10.80	13.86	3.10	2.54	75.70
One_U1202-1052	33.23	5.67	3.97	4.05	0.92	11.92	2.67	0.28	18.21
One_U1203-175	12.56	1.97	0.39	0.24	3.79	14.07	0.85	16.19	17.19
One_U1204-53	7.83	11.95	1.28	1.74	0.98	17.05	0.22	15.51	14.31
One_U1205-57	2.63	3.13	6.25	1.00	8.75	2.51	26.65	3.86	7.50
One_U1206-108	41.67	9.01	0.59	1.23	1.35	6.19	21.16	25.49	26.41
One_U1207-231[e]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_U1208-67	3.36	7.40	3.09	13.18	16.55	15.60	31.43	0.07	24.71
One_U1209-111	1.38	30.75	6.80	13.85	14.12	4.00	13.92	0.51	19.76

Table 14. (Page 4 of 4).

Assay	R	NS/WBB	EBB	NP	C/K	CI	CR/NSE	SSE	BC/WA
One_U1210-173	6.72	9.23	3.65	30.52	6.46	9.93	6.80	4.17	6.00
One_U1211-97	2.77	3.05	2.65	11.73	7.45	17.07	0.96	0.28	0.00
One_U1212-106	24.66	7.25	7.06	11.17	5.89	12.46	58.15	6.62	51.47
One_U1214-107	27.38	24.27	1.50	8.48	2.64	4.80	14.05	8.63	93.53
One_U1215-82	6.45	8.43	0.10	55.15	1.16	2.37	19.00	4.26	9.11
One_U1216-230	12.17	12.08	9.78	0.80	21.67	7.40	0.33	6.65	37.13
One_U301-92	1.11	15.98	4.54	1.39	4.39	4.94	24.47	23.16	12.99
One_U401-224	8.38	4.01	1.82	9.83	1.11	1.17	17.77	6.08	16.32
One_U404-229	0.91	0.00	6.55	5.73	0.34	4.46	38.87	8.00	6.97
One_U502-167	0.00	5.89	2.93	2.20	1.09	4.37	11.03	7.27	42.73
One_U503-170	29.31	14.79	5.32	36.69	2.21	24.25	13.37	6.10	19.16
One_U504-141	11.30	5.82	12.64	0.39	3.70	6.14	29.59	17.21	64.50
One_U508-533	2.17	0.86	4.13	4.15	0.00	16.62	29.26	4.21	26.10
One_UCA-24[e]	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
One_vamp5-255	1.38	34.58	0.28	16.87	3.49	26.03	27.93	1.61	18.58
One_vatf-214	5.80	0.80	0.73	1.23	1.44	14.24	9.05	8.26	11.94
One_VIM-569	40.20	16.58	0.36	18.06	2.93	17.90	5.19	0.16	8.59
One_zn706-68	0.00	0.00	0.00	1.10	2.68	1.34	0.00	0.00	0.00
One_ZNF-61	28.86	41.23	1.10	17.48	7.50	8.61	2.11	0.11	20.99
One_Zp3b-49	0.90	2.92	0.22	9.16	13.07	19.40	1.04	6.15	22.49
Average	12.58	9.70	4.31	9.55	6.81	11.15	13.78	6.85	23.72

[a] These assays were dropped due to significant linkage and were not included in this analysis.

[b] These assays were dropped due to fixation in the 36 test populations and were not included in this analysis.

[c] These assays are linked and were included as a haplotype marker in this analysis.

[d] These assays are linked and were included as a haplotype marker in this analysis.

[e] These assays were dropped due to laboratory failure and were not included in this analysis.

[f] This assay was dropped due to failure to conform to Hardy-Weinberg expectations and was not included in this analysis.

Table 15. The percentage of variation attributable to allele frequency differences within populations (G_{WP}), among populations within fine-scale regions (G_{PF}), among fine-scale regions within broad-scale regions (G_{FB}), and among broad-scale regions within the total (G_{BT}) for 124 SNPs (Tables 2 and 3) screened for 36 test populations (Table 1) of sockeye salmon.

Assay	G_{WP}	G_{PF}	G_{FB}	G_{BT}
One_ACBP-79	88%	3%	0%	8%
One_agt-132	89%	7%	0%	4%
One_aldB-152	91%	6%	1%	1%
One_ALDOB-135[a]	N/A	N/A	N/A	N/A
One_apoe-83	78%	8%	3%	11%
One_bckB-137[b]	N/A	N/A	N/A	N/A
One_c3-98	93%	4%	1%	1%
One_ccd16-131	100%	0%	0%	0%
One_CD9-269	95%	4%	0%	1%
One_cetn1-167	90%	6%	1%	3%
One_CFP1	85%	7%	2%	6%
One_cin-177	92%	4%	3%	1%
One_CO1[c]	76%	14%	3%	7%
One_CTGF-301	96%	2%	1%	1%
One_Cytb_17[c]	76%	14%	3%	7%
One_Cytb_26[c]	76%	14%	3%	7%
One_dds-529	95%	3%	1%	1%
One_DDX5-86	94%	3%	1%	2%
One_E2-65	92%	5%	2%	1%
One_gadd45-269	100%	0%	0%	0%
One_gdh-212	92%	4%	1%	3%
One_GHII-2165	71%	6%	3%	21%
One_ghsR-66	88%	9%	2%	2%
One_GPDH-201	91%	3%	1%	5%
One_GPDH2-187	87%	3%	1%	10%
One_GPH-414[a]	N/A	N/A	N/A	N/A
One_GTHa	89%	7%	2%	2%
One_HGFA-49	96%	2%	1%	1%
One_HpaI-71	84%	8%	2%	5%
One_HpaI-99	72%	7%	11%	10%
One_hsc71-220	90%	7%	1%	2%
One_Hsp47	89%	5%	1%	5%
One_Ig-90	88%	4%	1%	7%
One_IL8r-362	92%	5%	1%	2%

Table 15. (Page 2 of 4).

Assay	G_{WP}	G_{PR}	G_{RB}	G_{BT}
One_ins-107	94%	4%	1%	1%
One_KCT1-453	92%	5%	2%	1%
One_KPNA-422	94%	3%	2%	1%
One_LEI-87	86%	5%	1%	8%
One_leptin-92[b]	N/A	N/A	N/A	N/A
One_lpp1-44	87%	7%	1%	4%
One_MARCKS-241	96%	3%	1%	1%
One_metA-253	63%	11%	6%	20%
One_MHC2_190[d]	73%	18%	4%	5%
One_MHC2_251[d]	73%	18%	4%	5%
One_Mkpro-129	86%	5%	2%	7%
One_ODC1-196	90%	4%	1%	5%
One_Ots208-234	81%	4%	1%	14%
One_Ots213-181	90%	3%	0%	7%
One_p53-534	88%	3%	2%	6%
One_parp3-170[b]	N/A	N/A	N/A	N/A
One_pax7-248	92%	6%	0%	2%
One_PIP	94%	3%	2%	1%
One_ppie-74	69%	25%	3%	3%
One_PPM1K-118[e]	N/A	N/A	N/A	N/A
One_Prl2	90%	6%	3%	1%
One_psme2-354	89%	4%	4%	2%
One_rab1a-76	92%	6%	1%	1%
One_RAG1-103	86%	8%	0%	6%
One_RAG3-93	93%	4%	1%	2%
One_redd1-414	85%	6%	1%	8%
One_RFC2-102	92%	7%	0%	1%
One_RFC2-285	95%	2%	1%	2%
One_RH2op-395	99%	1%	0%	0%
One_rpo2j-261	91%	6%	2%	1%
One_sast-211	94%	3%	2%	2%
One_serpin-75	96%	2%	1%	0%
One_spf30-207	91%	6%	0%	2%
One_srp09-127	89%	2%	2%	7%
One_ssrd-135	94%	4%	1%	1%
One_STC-410	78%	5%	5%	12%

Table 15. (Page 3 of 4).

Assay	G_{WP}	G_{PR}	G_{RB}	G_{BT}
One_STR07	87%	5%	5%	3%
One_SUMO1-6	91%	3%	1%	5%
One_sys1-230	91%	4%	1%	4%
One_taf12-248	90%	2%	3%	5%
One_Tf_ex11-750	78%	5%	0%	16%
One_Tf_in3-182	80%	5%	2%	13%
One_tshB-92	95%	4%	0%	0%
One_txnip-401	86%	3%	3%	7%
One_U1002-101	95%	2%	1%	1%
One_U1003-75	79%	7%	2%	12%
One_U1004-183	69%	11%	3%	17%
One_U1009-91	91%	5%	2%	2%
One_U1010-81	94%	4%	2%	1%
One_U1012-68	89%	8%	0%	2%
One_U1013-108	92%	4%	1%	2%
One_U1014-74	94%	3%	1%	2%
One_U1016-115	86%	7%	3%	4%
One_U1017-62	93%	4%	1%	2%
One_U1021-57[f]	N/A	N/A	N/A	N/A
One_U1024-197	91%	5%	0%	4%
One_U1101	92%	6%	1%	1%
One_U1102-220	89%	3%	3%	5%
One_U1103	87%	6%	4%	3%
One_U1104-138	95%	2%	1%	1%
One_U1105	87%	6%	1%	5%
One_U1201-492	91%	7%	1%	1%
One_U1202-1052	89%	4%	0%	7%
One_U1203-175	93%	3%	1%	3%
One_U1204-53	92%	4%	1%	2%
One_U1205-57	96%	3%	0%	1%
One_U1206-108	91%	6%	0%	3%
One_U1207-231[e]	N/A	N/A	N/A	N/A
One_U1208-67	88%	5%	2%	5%
One_U1209-111	89%	5%	2%	4%
One_U1210-173	92%	4%	0%	3%
One_U1211-97	92%	3%	0%	4%
One_U1212-106	88%	7%	2%	2%

Table 15. (Page 4 of 4).

Assay	G_{WP}	G_{PR}	G_{RB}	G_{BT}
One_U1214-107	74%	15%	4%	7%
One_U1215-82	95%	4%	0%	1%
One_U1216-230	91%	5%	2%	2%
One_U301-92	92%	4%	3%	1%
One_U401-224	89%	2%	2%	6%
One_U404-229	86%	4%	1%	9%
One_U502-167	89%	9%	1%	2%
One_U503-170	91%	7%	1%	2%
One_U504-141	90%	7%	2%	1%
One_U508-533	89%	6%	1%	4%
One_UCA-24[e]	N/A	N/A	N/A	N/A
One_vamp5-255	90%	7%	1%	2%
One_vatf-214	90%	3%	4%	4%
One_VIM-569	92%	5%	1%	2%
One_zn706-68	94%	0%	0%	0%
One_ZNF-61	87%	6%	0%	6%
One_Zp3b-49	81%	4%	1%	14%

[a] These assays were dropped due to significant linkage and were not included in this analysis.
[b] These assays were dropped due to fixation in the 36 test populations and were not included in this analysis.
[c] These assays are linked and were included as a haplotype marker in this analysis.
[d] These assays are linked and were included as a haplotype marker in this analysis.
[e] These assays were dropped due to laboratory failure and were not included in this analysis.
[f] This assay was dropped due to failure to conform to Hardy-Weinberg expectations and was not included in this analysis.

Table 16. Proposed test collections for marker selection in chum salmon.

Region	Population	Collection	Sample size	Lat.	Long.
Japan					
	Tokachi River	CMTOKA02	80	42.6950	-143.6653
	Gakko River early	CMGAKK03E	80	39.0525	-139.8864
Russia					
	Amur River summer	CMAMU01	95	53.1100	-140.7400
	Palana River	CMPALA98	95	59.0667	-159.8333
Kotzebue Sound					
	Kiana River	CMKIAN04	95	66.9728	-160.4269
	Kelly Lake	CMKEL91	95	67.9187	-162.3501
Norton Sound					
	American River	CMAMER04	95	65.4245	-165.7849
	Unalakleet River	CMUNAL04	95	63.8703	-160.7859
Yukon summer					
	Anvik River	CMOTT93	95	63.2425	-160.6972
	Nulato River	CMNUL03	95	64.7356	-158.1870
Yukon fall					
	Pelly River	CMPEL93	84	62.5500	-136.7500
	Kluane River	CMKLUA01	95	61.6222	-139.3912
Kuskokwim summer					
	George River	CMGEO96	95	61.8975	-157.7135
	Goodnews River weir	CMGOO91	95	59.1028	-161.5610
Kuskokwim fall					
	Windy Fork	CMWINDF08	95	62.6944	-154.5926
	Big River	CMBIGR08	95	62.6063	-155.0135
Western Bristol Bay					
	Togiak River	CMTOG93	95	59.0783	-160.3372
	Mulchatna River	CMMUL94	95	59.6449	-157.1168
Eastern Bristol Bay					
	Naknek River (Big Cr)	CMBRIB93	80	58.2926	-157.5340
	Meshik River	CMMES92	78	56.7910	-158.6617
Alaska Peninsula					
	Frosty Creek	CMFRO92	95	55.1933	-162.8604
	Canoe Bay Creek	CMCAN92	95	55.7250	-161.2188
Southcentral Alaska					
	Lake Creek	CMLAK96	95	61.9060	-150.9089
	Olsen Creek	CMPWS95A	95	60.7596	-146.1747
Southeast Alaska					
	Chilkat River - 24Mile	CM24MI06	95	59.4204	-135.9495
	North Arm Creek	CMNARM06S	95	56.6855	-132.3081
British Columbia					
	Kitimat River	CMKITIM06	95	54.0000	-128.6667
	Kitwanga River	CMKITW06	95	55.1000	-128.0834
Washington					
	Nisqually River Hatchery	CMNISQ04	95	47.0959	-122.6960
	Elwha River	CMELWH04	95	48.1452	-123.5640

Figures

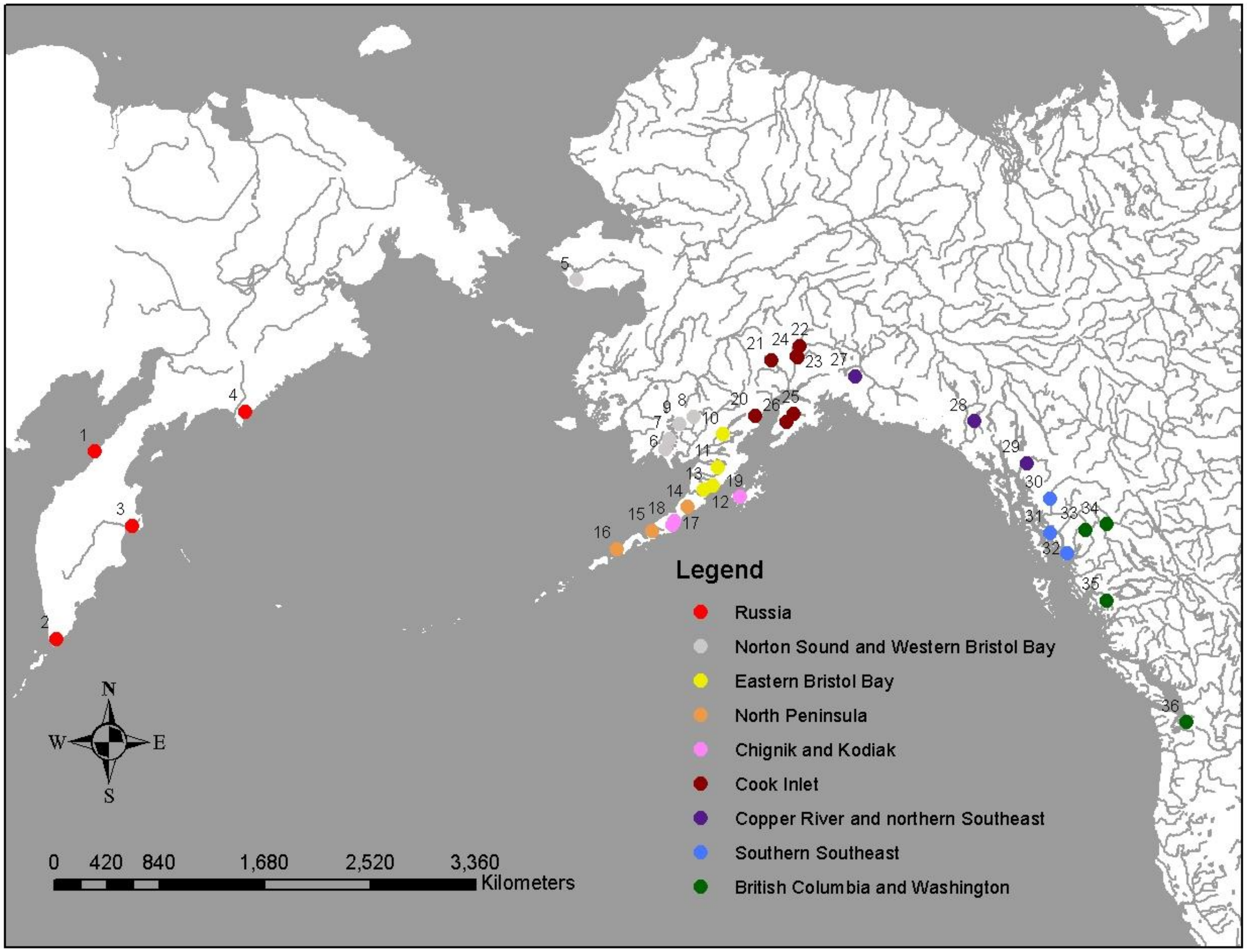


Figure 1. Backbone collections from 9 fine-scale geographic regions (Table 1) genotyped for 124 SNPs (Table 2). See text and Table 1 for details.

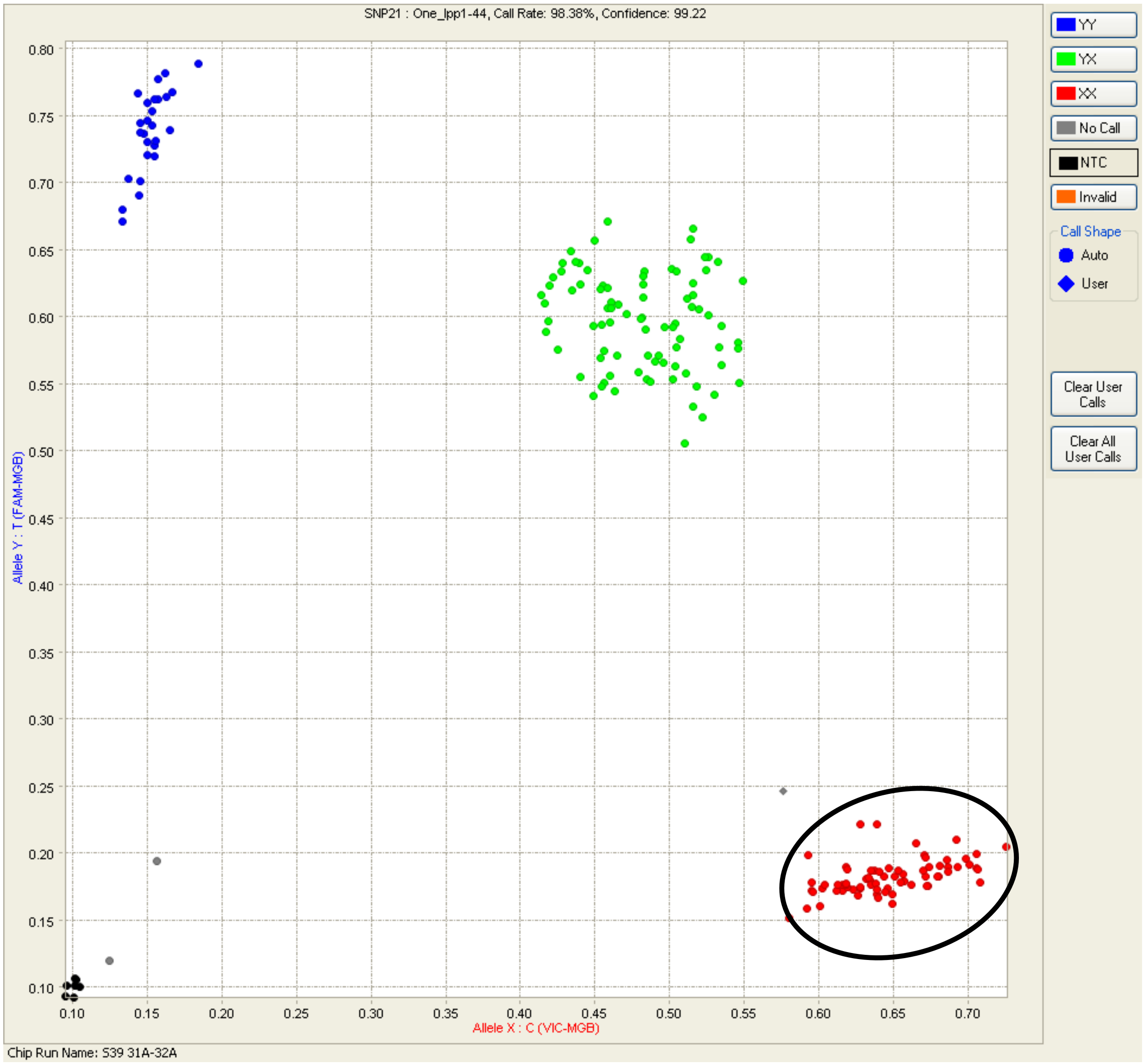
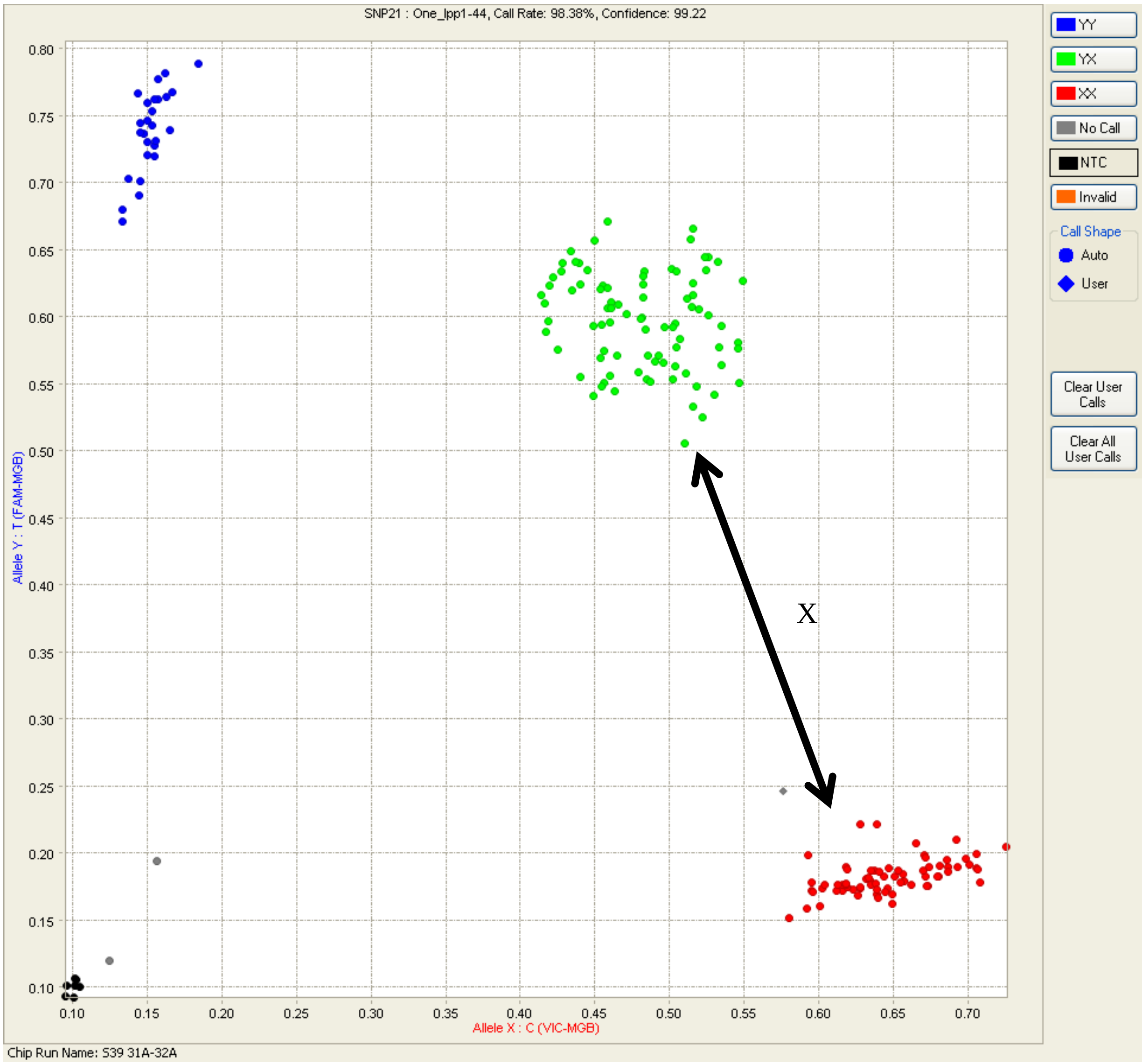


Figure 2. An image from our genotyping software exhibiting an assay with tight genotype clusters (circle), i.e., one in which the spatial variation among individuals of a genotype is low. Individuals homozygous for genotype AA are colored red, heterozygous for AB are green, and homozygous for BB are blue. Individuals that failed to amplify or are of an uncertain genotype are grey and no template controls (no DNA) are black.



Chip Run Name: 539 31A-32A

Figure 3. An image from our genotyping software exhibiting an assay with widely separated genotype clusters, i.e., one in which the separation between cluster edges (X) is high.

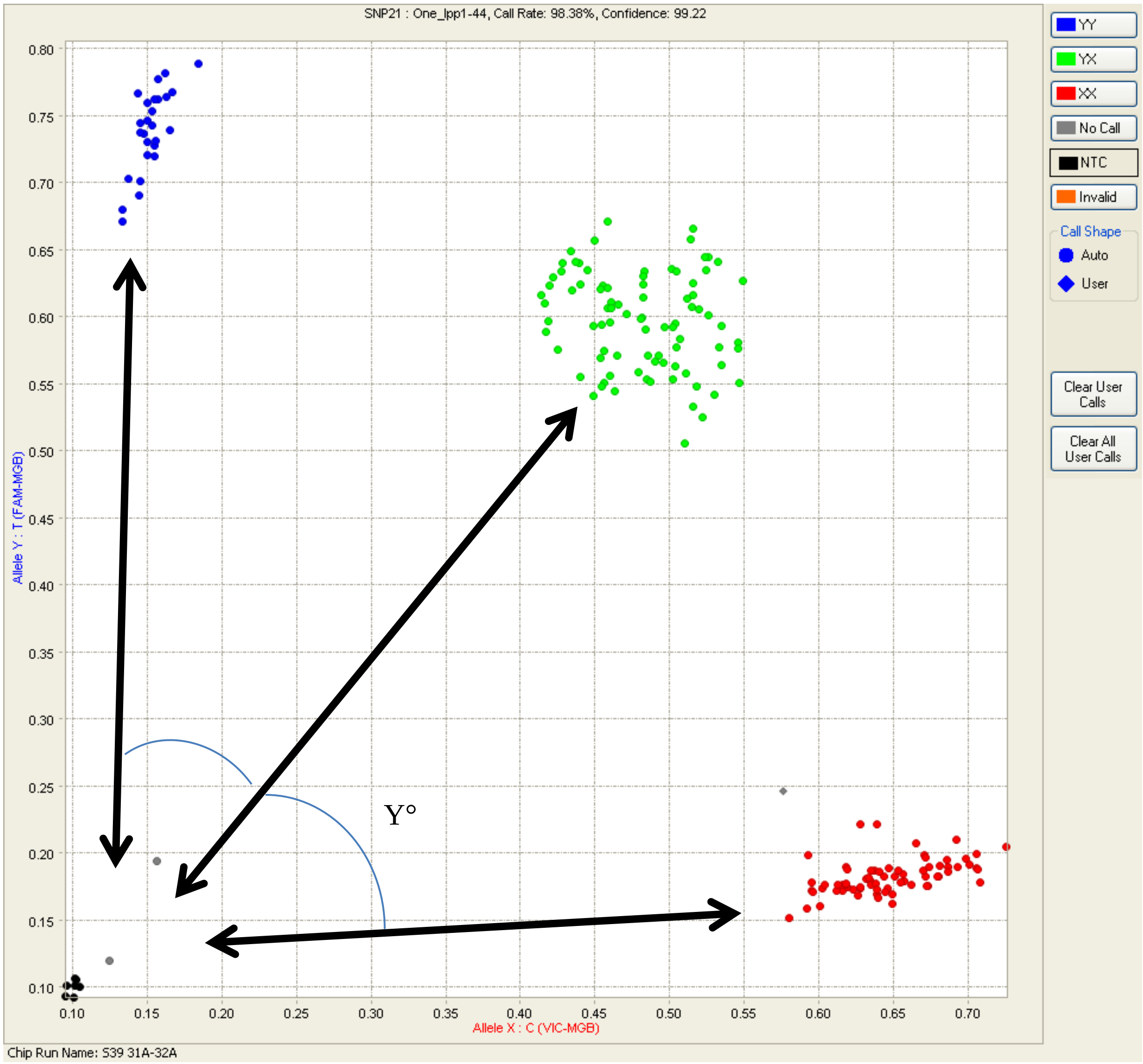


Figure 4. An image from our genotyping software exhibiting an assay with widely separated genotype cluster alignment, i.e., one in which the degree of separation between cluster axes from the origin (Y) is high.

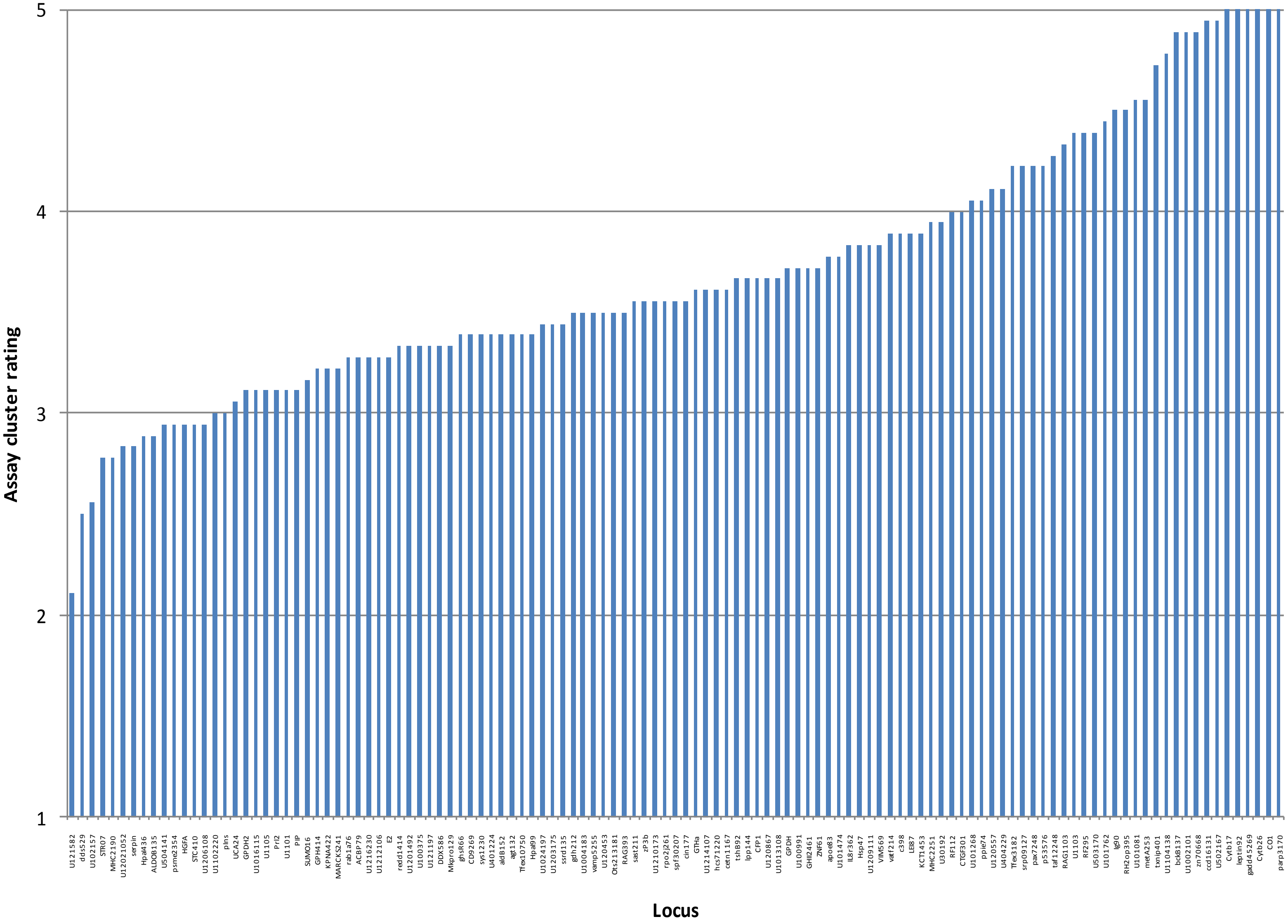


Figure 5. The average cluster tightness rating of 124 SNPs (Tables 2 and 3) screened for 36 test populations (Table 1) ordered from lowest rating (Left) to highest rating (Right).

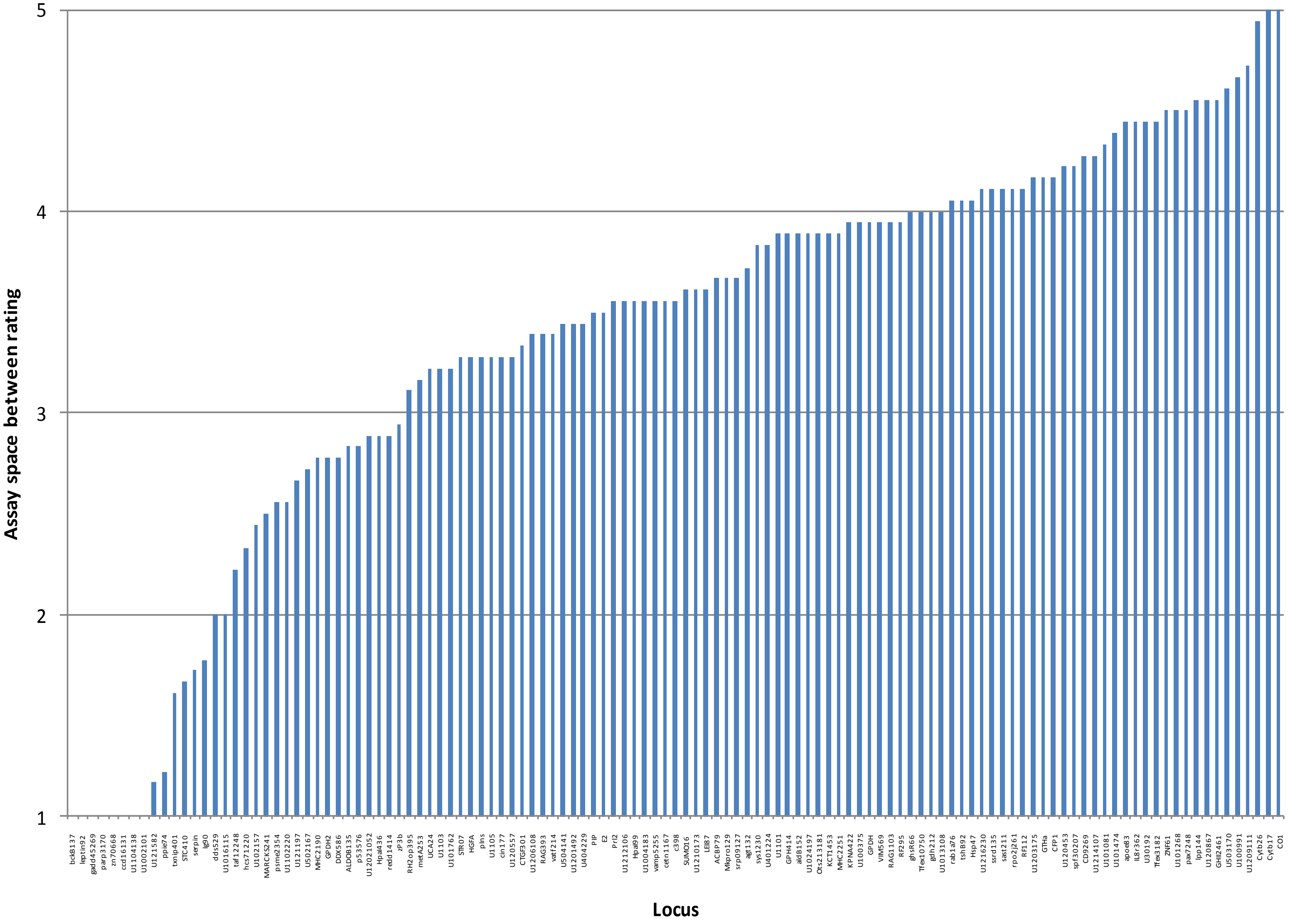


Figure 6. The average space between cluster rating of 124 SNPs (Tables 2 and 3) screened for 36 test populations (Table 1) ordered from lowest rating (Left) to highest rating (Right).

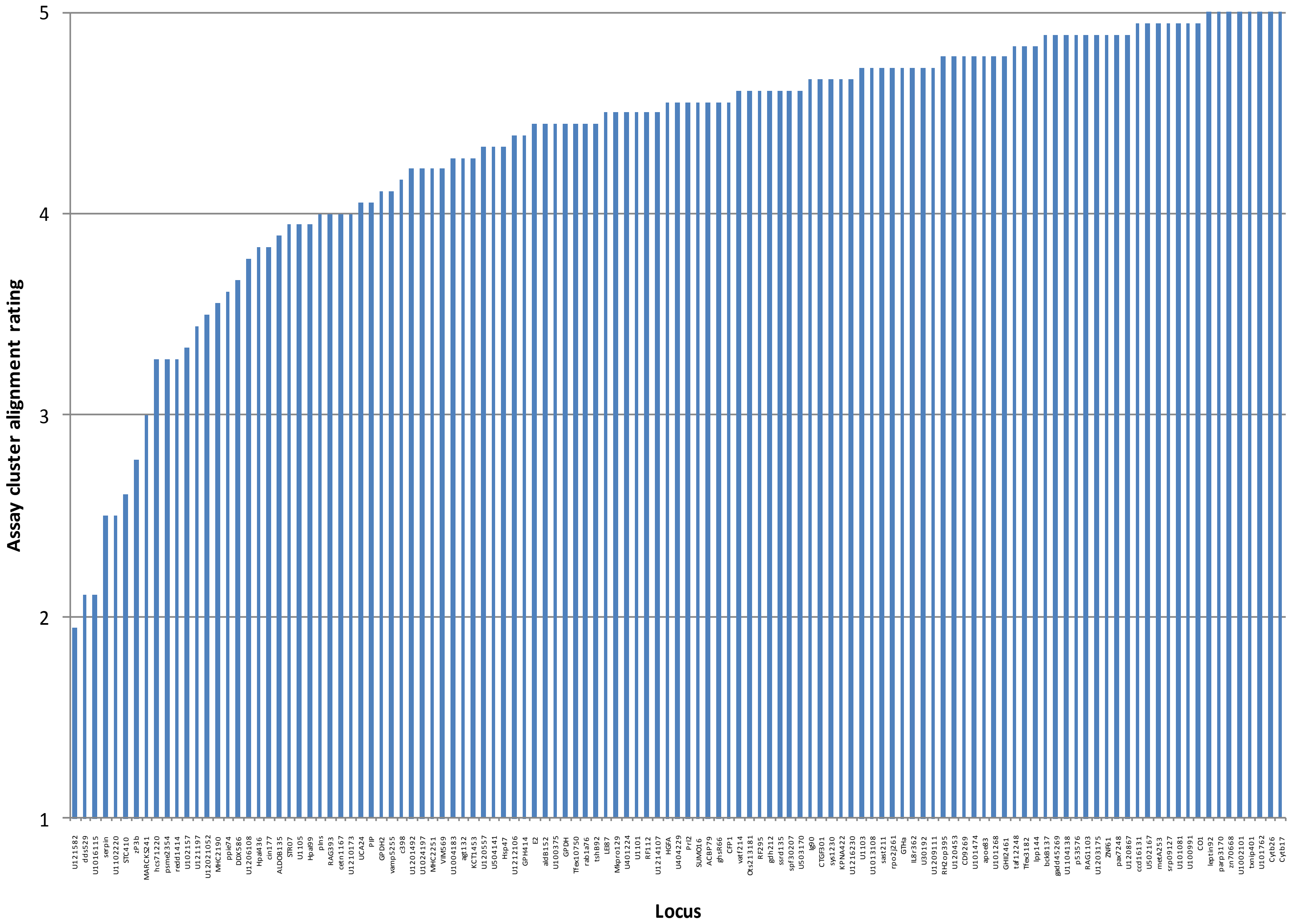


Figure 7. The average cluster alignment rating of 124 SNPs (Tables 2 and 3) screened for 36 test populations (Table 1) ordered from lowest rating (Left) to highest rating (Right).

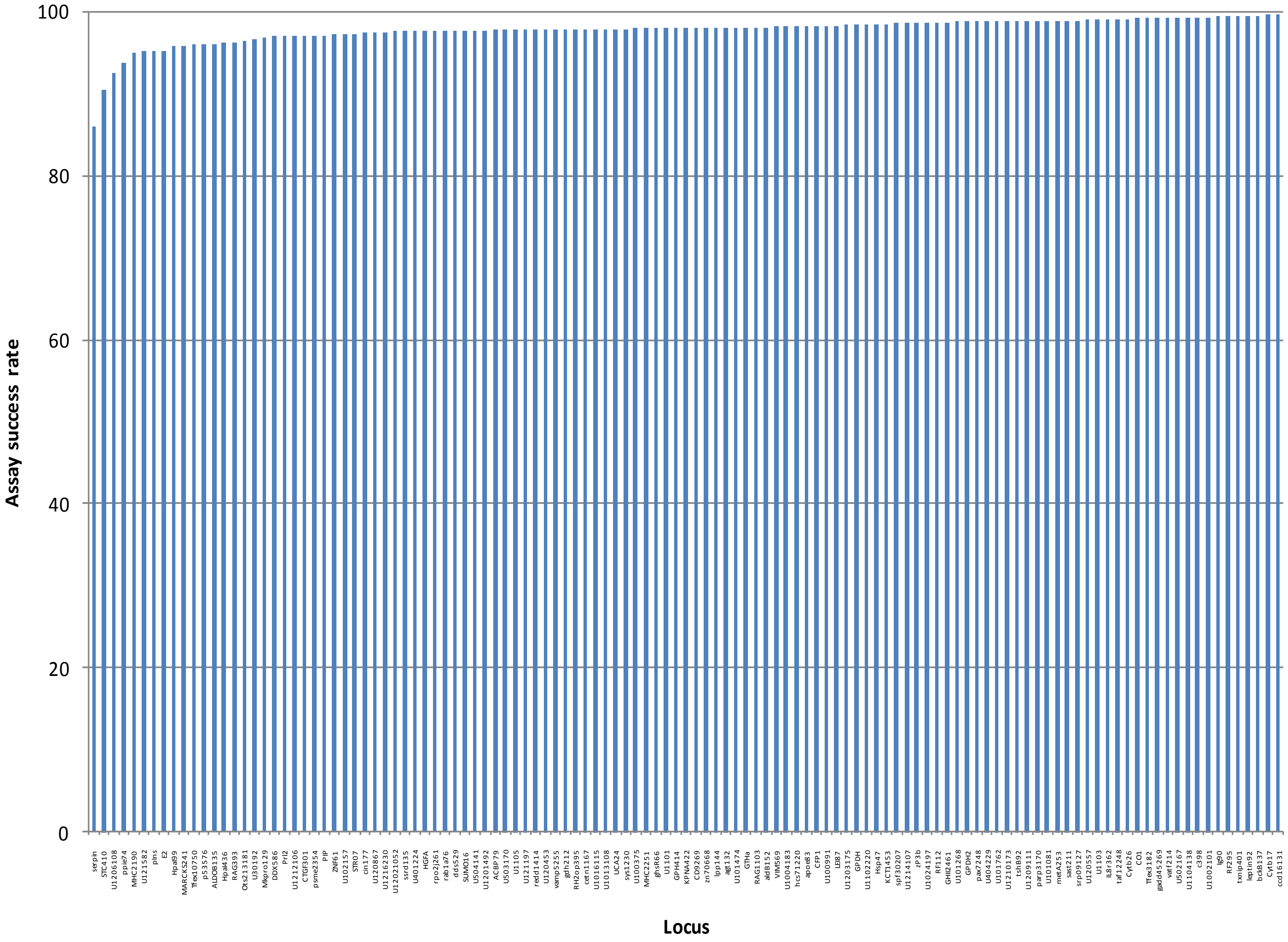


Figure 8. The average success rate (%) of 124 SNPs (Tables 2 and 3) screened for 36 test populations (Table 1) ordered from lowest rating (Left) to highest rating (Right).

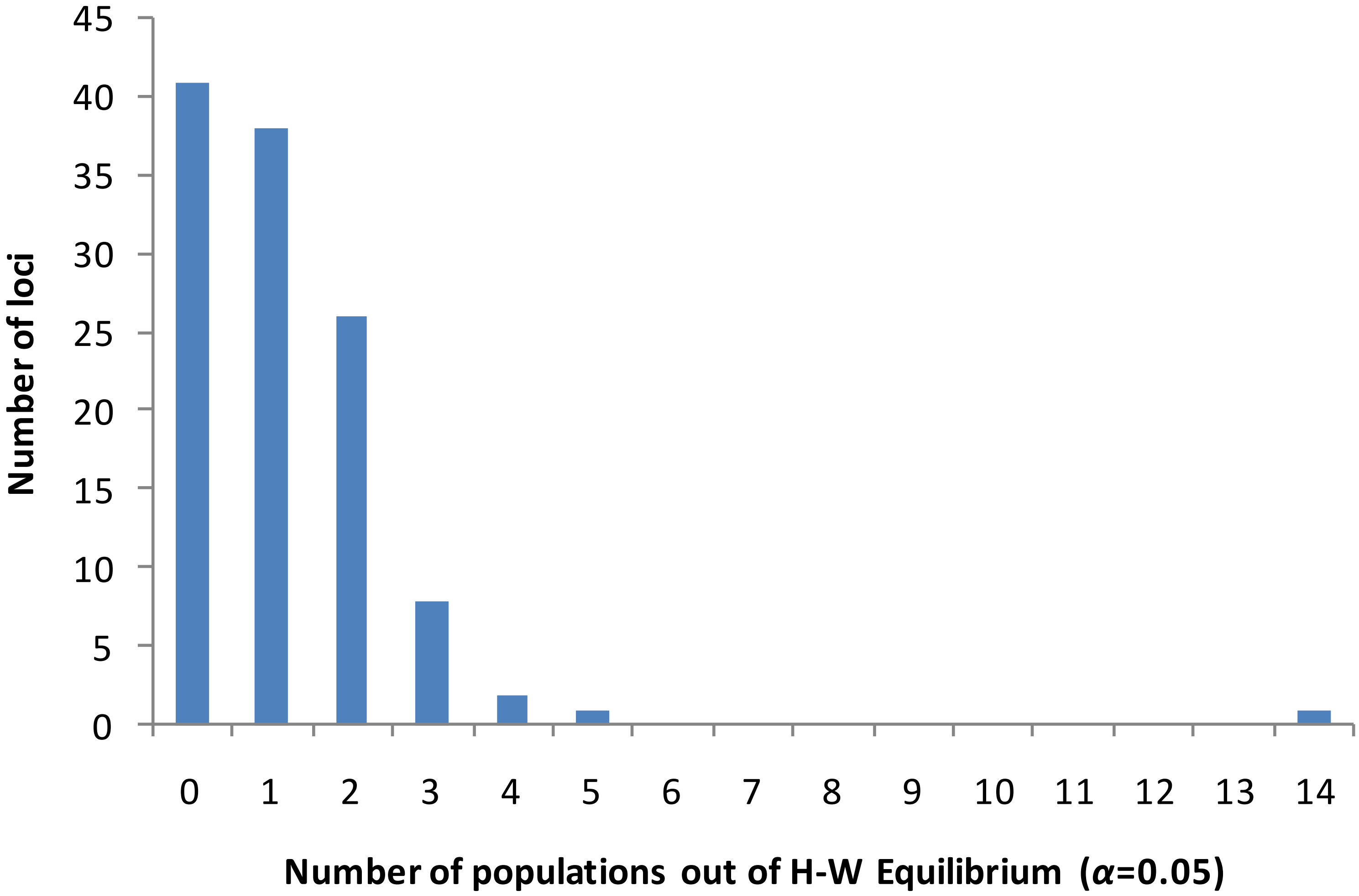


Figure 9. Number of markers that were out of H-W equilibrium (α = 0.05) for 0 to 14 populations. By chance, the one would expect 1.8 populations to be out of H-W expectation at this criterion (i.e., 36 populations * 0.05).

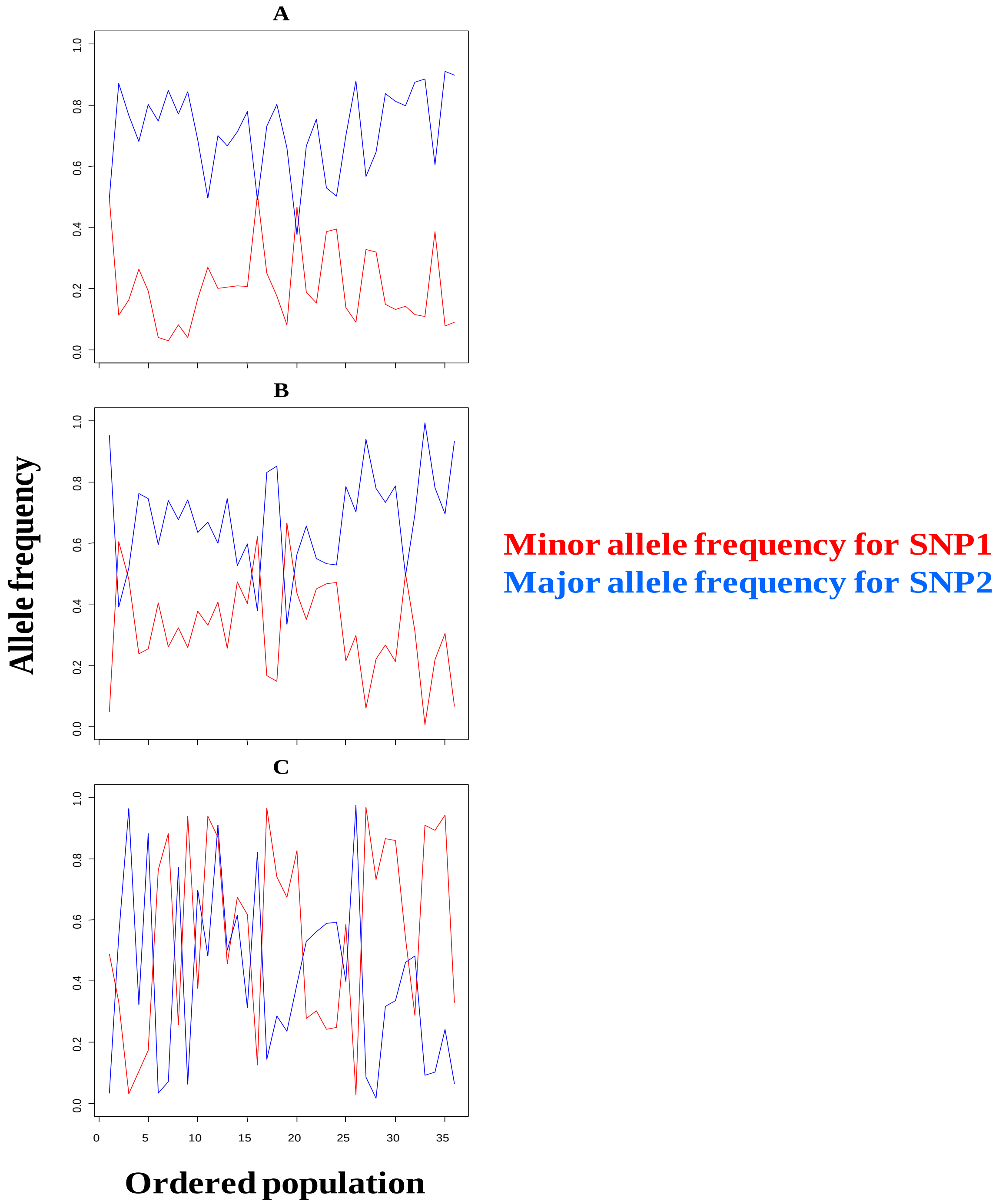


Figure 10. Minor (SNP1 in red) and major (SNP2 in blue) allele frequencies for three pairs of SNPs exhibiting linkage disequilibrium: *One_aldB-152*/*One_ALDOB-135* (A), *One_GPH-414*/ *One_GTHa* (B), and *One_MHC2_190*/ *One_MHC2_251* (C). Note that the frequencies of these two alleles for the first two pairs of loci are mirror images of each other, indicating close-to-perfect phasing, whereas the last locus set does not. The lack of tight phasing between linked loci is indicative of locus pairs that are useful in MSA as a combined set.

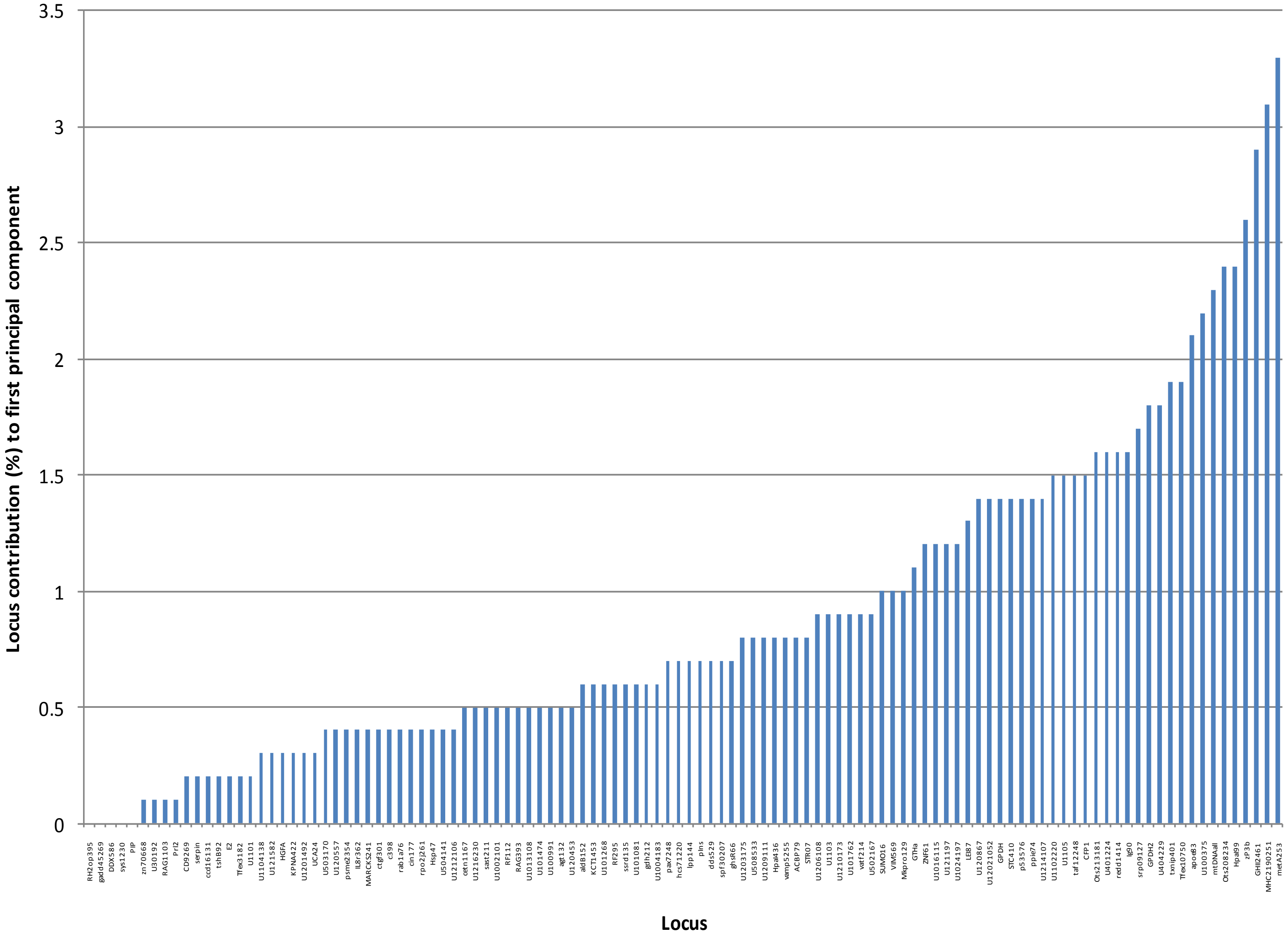
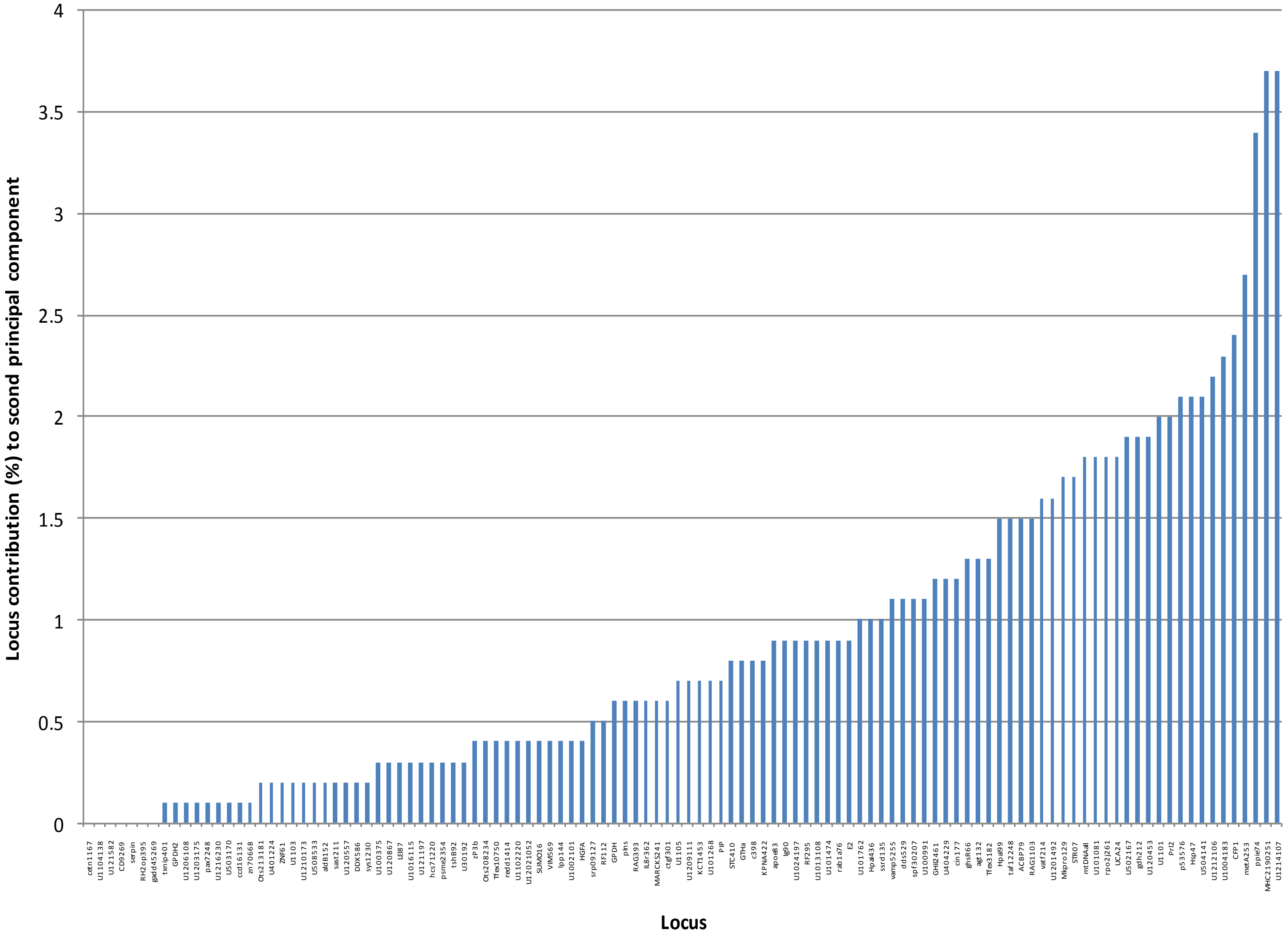


Figure 11. The contribution to principal component 1 (%) for each of 114 SNPs included in a principle component analysis of 36 test populations (Table 1) ordered from lowest contribution (Left) to highest contribution (Right). See text and Table 7 for details.



1042

1043 Figure 12. The contribution to principal component 2 (%) for each of 114 SNPs included in a principle component analysis of 36 test

1044 populations (Table 1) ordered from lowest contribution (Left) to highest contribution (Right). See text and Table 7 for details.

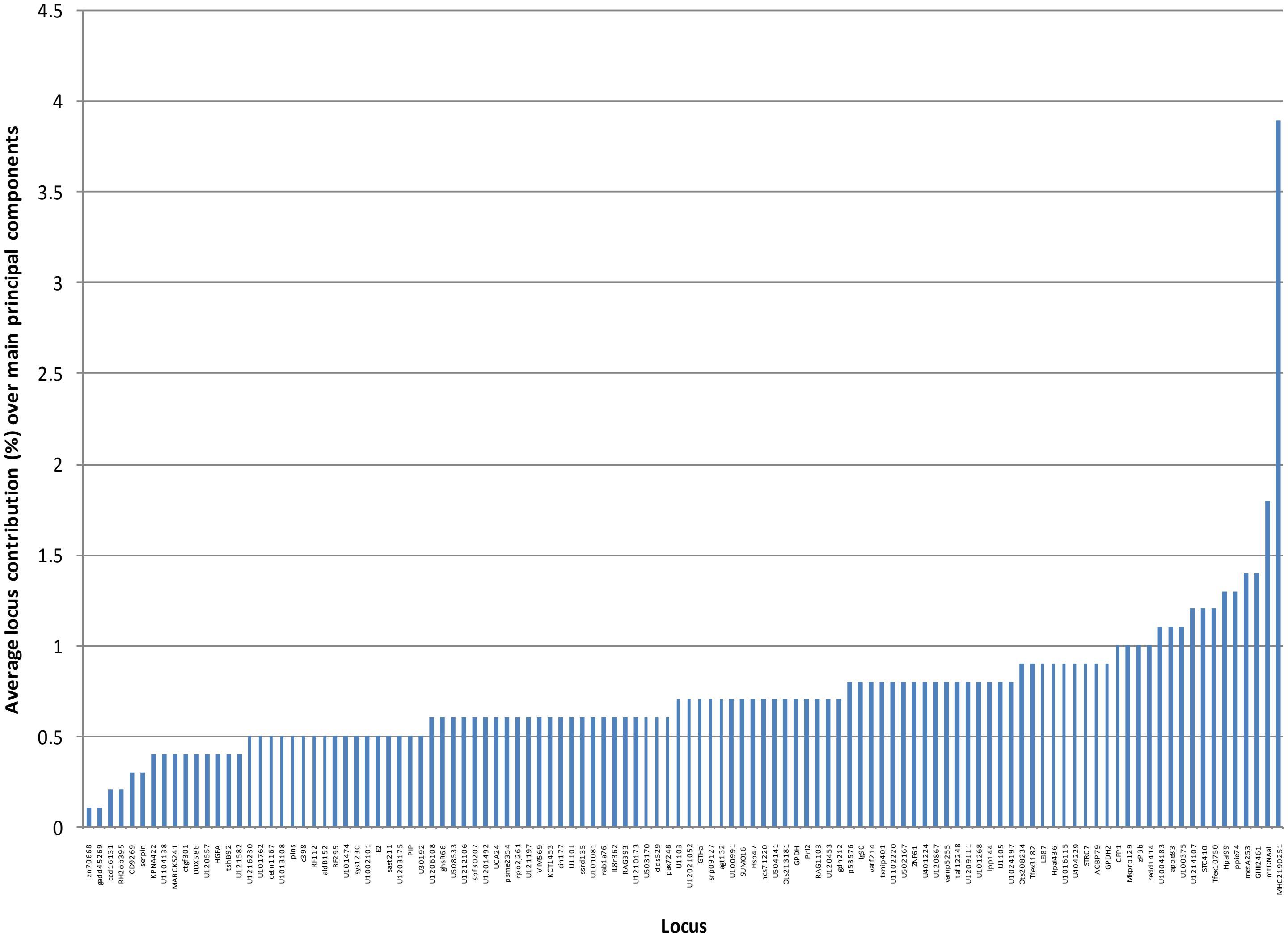
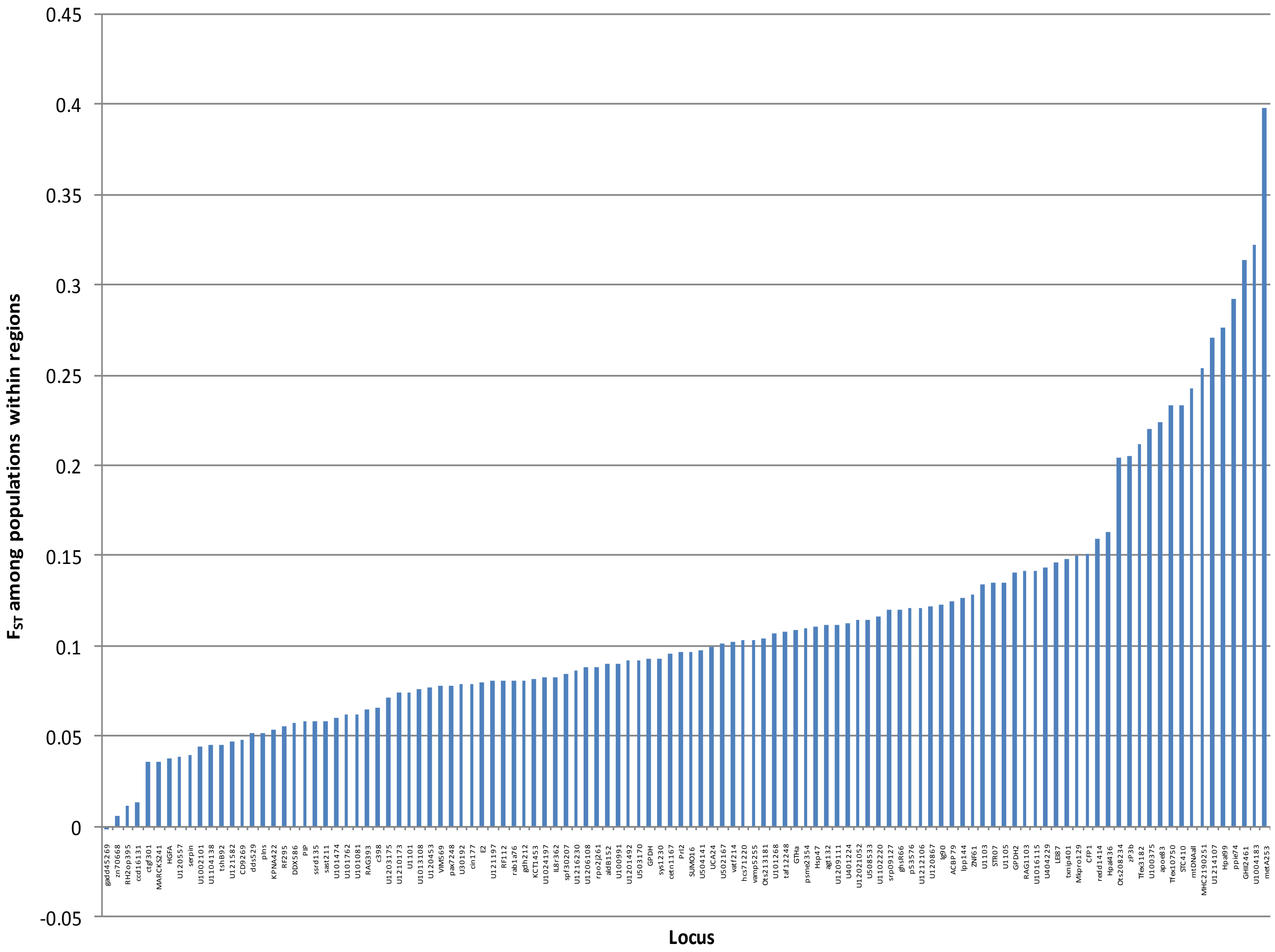
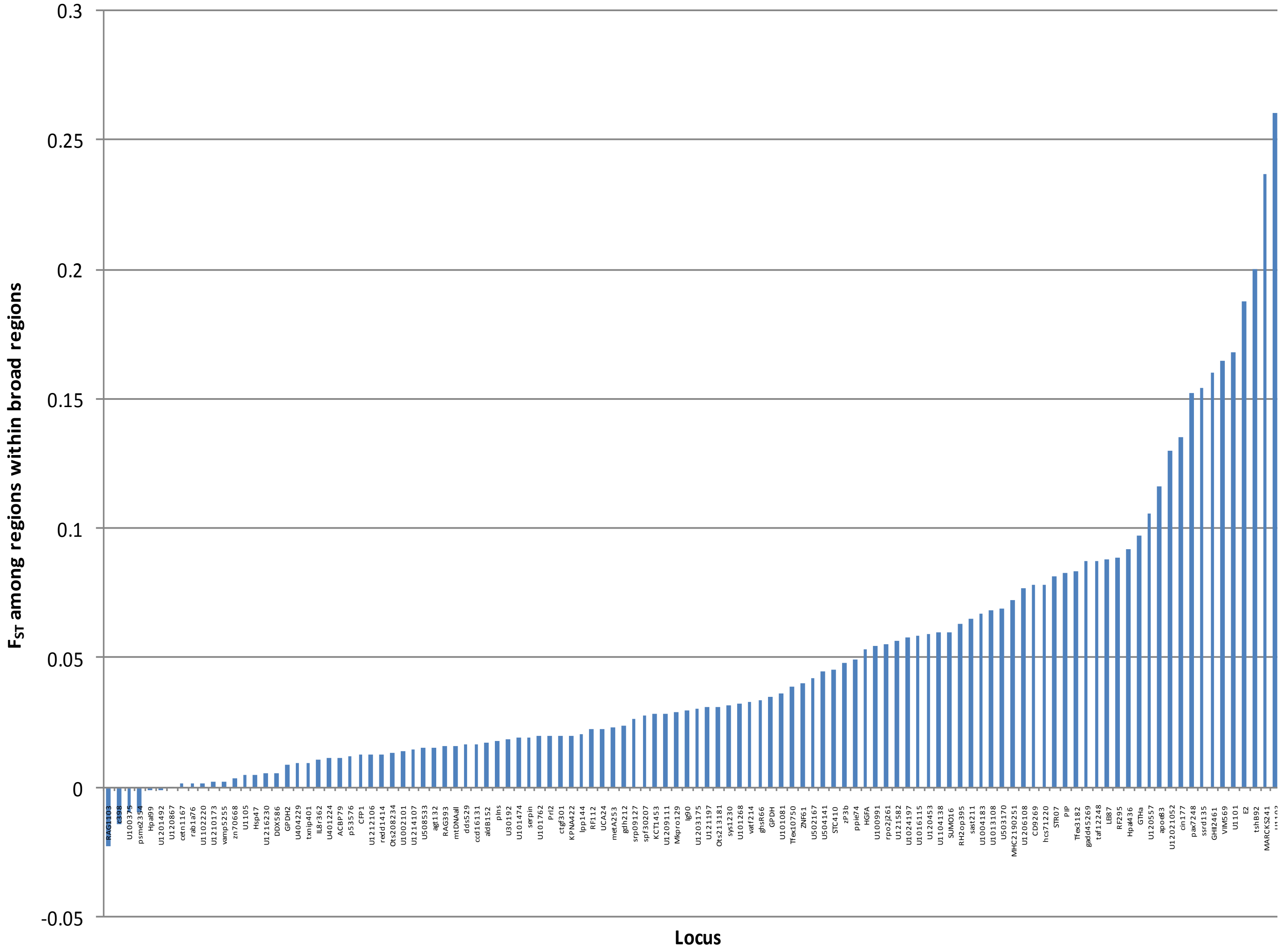


Figure 13. The average contribution (%) to the first 12 principal components that explained 80% of the total variation for each of 114 SNPs included in a principle component analysis of 36 test populations (Table 1) ordered from lowest contribution (Left) to highest contribution (Right). See text and Table 7 for details.



1049

1050 Figure 14. Weir and Cockerham's F_{ST} (1984) among populations within fine-scale regions (θ_S) of 36 test populations (Table 1)
1051 ordered from lowest (Left) to highest (Right). See text and Table 8 for details.



1052

1053 Figure 15. Weir and Cockerham's F_{ST} (1984) among fine-scale regions within broad-scale regions (θ_P) of 36 test populations (Table
1054 1) ordered from lowest (Left) to highest (Right). See text and Table 8 for details.

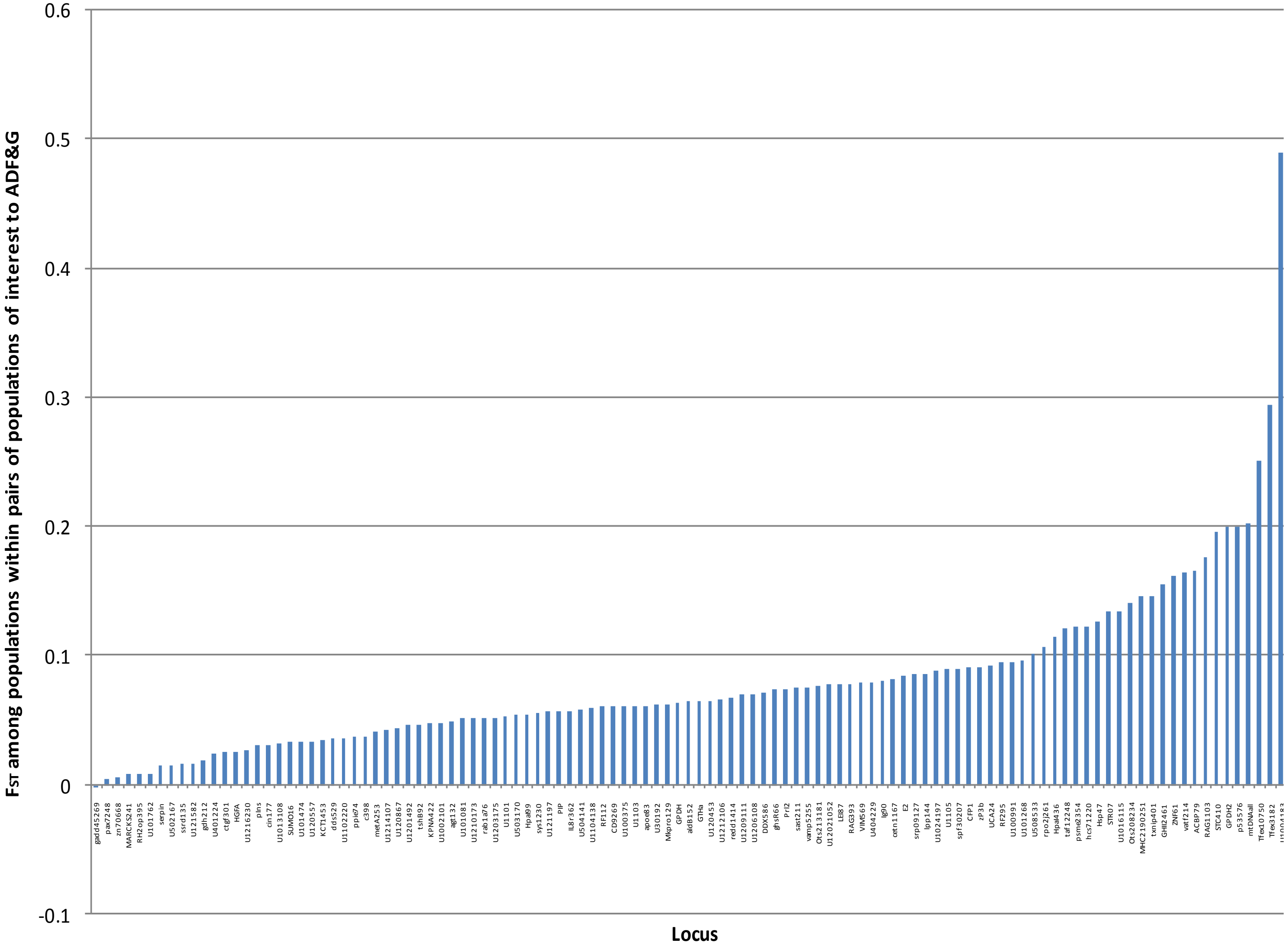
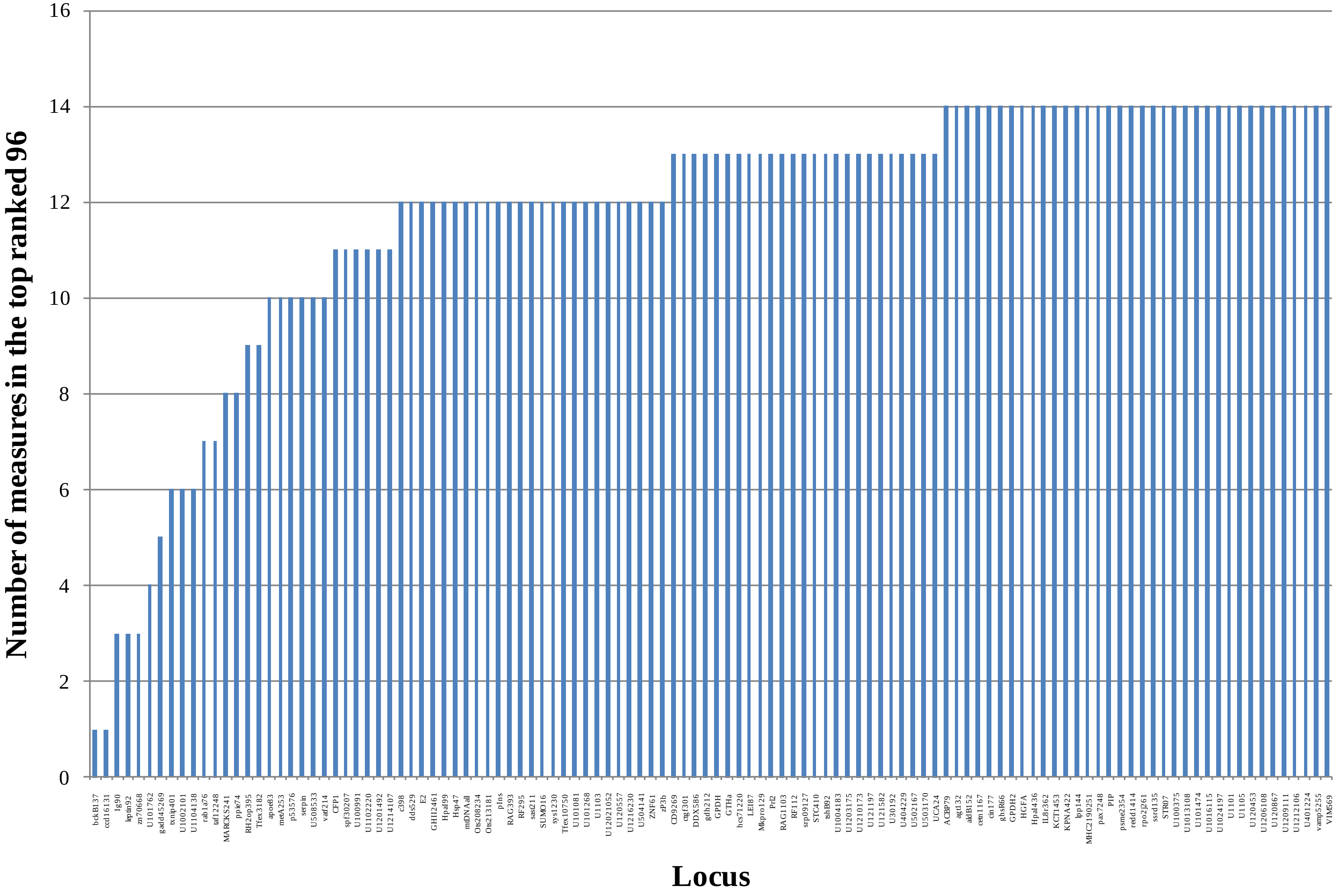


Figure 16. Weir and Cockerham's F_{ST} (1984) between populations within pairs of populations (θ_{Pairs}) of 36 test populations (Table 1) ordered from lowest (Left) to highest (Right). See text and Table 8 for details.



1058

1059 Figure 17. The number of measures of differentiation (of 14 total) between 7 pairs of populations (Table 1) that each of 124 SNPs
1060 (Table 2) ranked in the top 96 for, ordered from lowest (Left) to highest (Right). See text and Tables 9 and 10 for details.

Figure 18. A color-coded representation of rankings ordered by sum of ranks vertically (Top – Bottom: lowest sum of ranks to highest sum of ranks) and category of judges horizontally (Left – Right: Laboratory measures, Hardy-Weinberg, principle component analyses, F_{ST}s and measures of differentiation between pairs of populations of interest) for the 115 SNPs that were not removed from consideration. Note the horizontal break separating the 96 SNPs with the lowest sum of ranks above and the 19 SNPs selected for removal below the break.

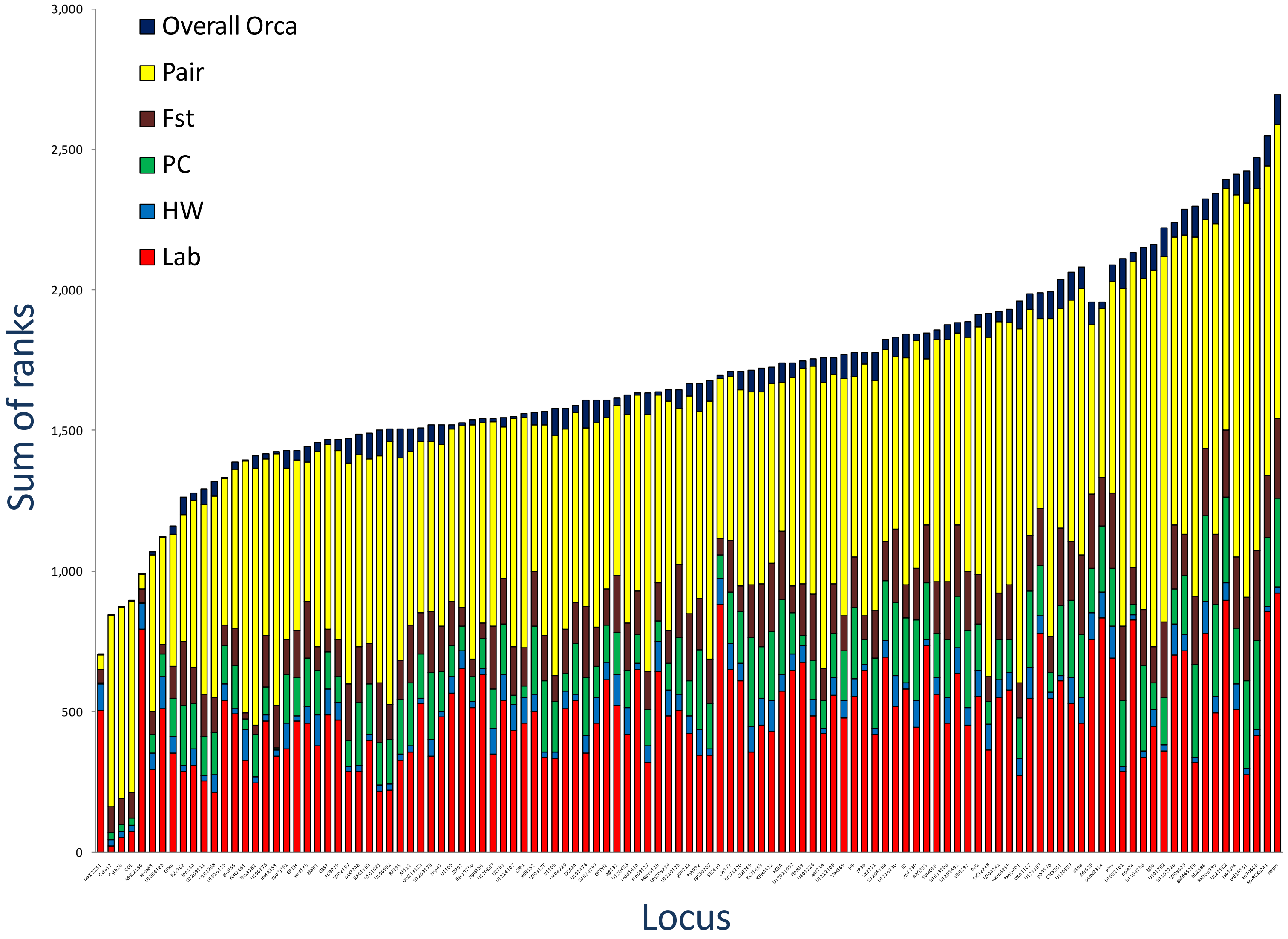


Figure 19. The sum of rankings for the 115 SNPs that were not removed from consideration and color-coded by category of judge: Overall Orca = Overall f_{ORCA} measure, Pair = 14 measures of pairwise differentiation, Fst = three measures of θ_{ST}, PC = 3 measures from principal component analysis, HW = Hardy-Weinberg Equilibrium measure, and Lab = 8 measures of laboratory performance.

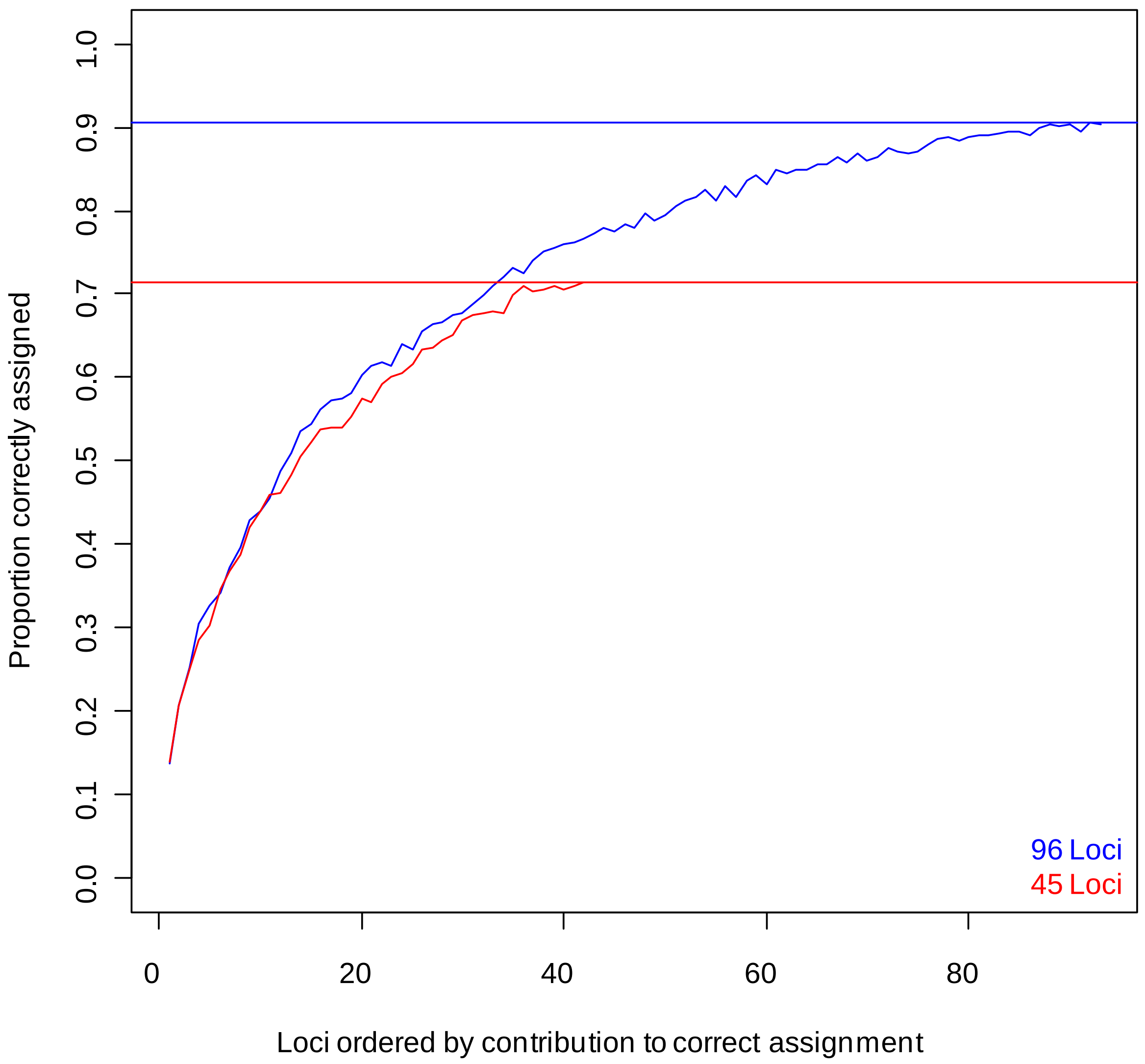


Figure 20. Assignment curves based upon f_{ORCA} for the 45 SNPs that comprised our previous baseline for sockeye salmon and the 96 SNPs chosen to represent our future baseline. See text for details.

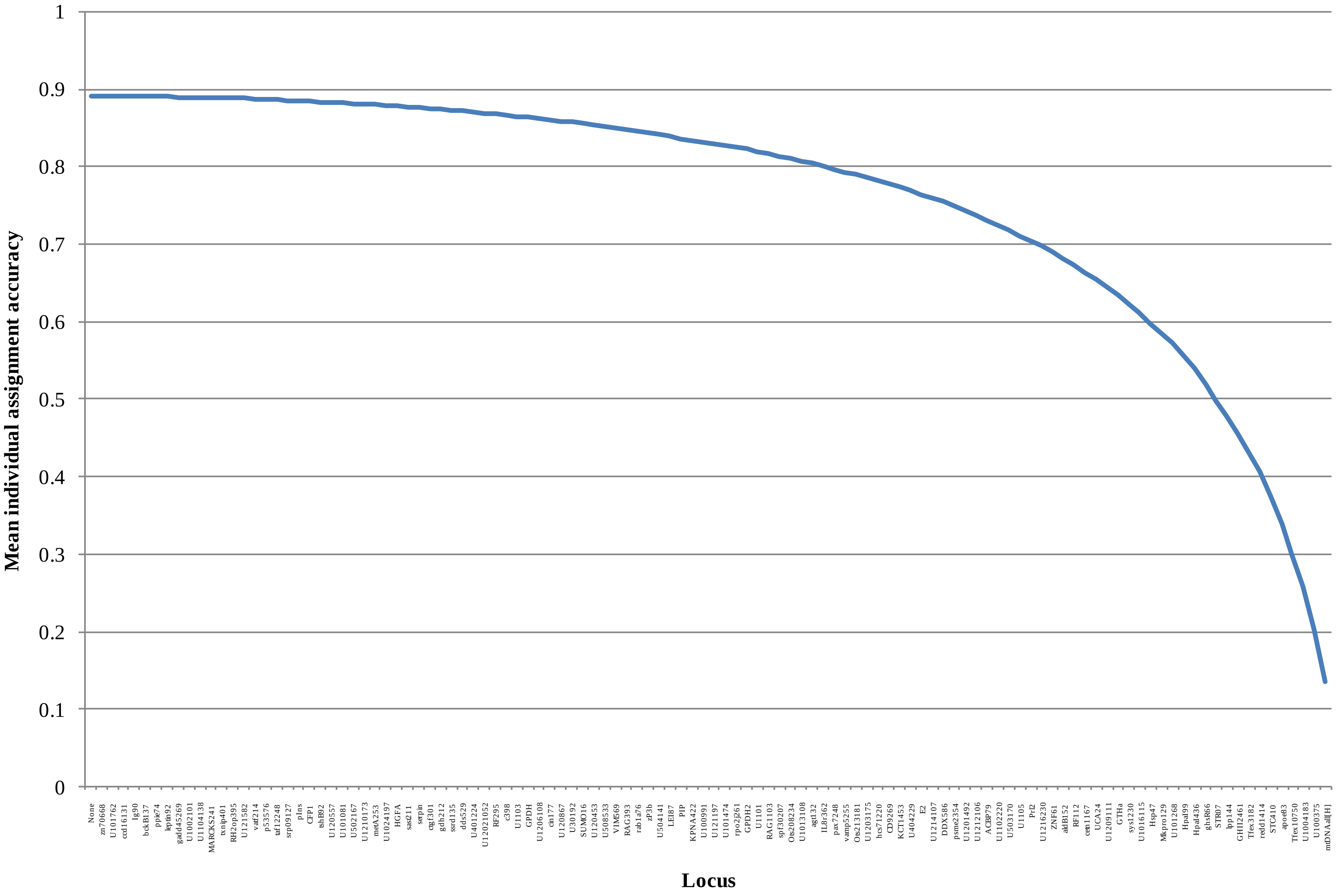


Figure 21. Cumulative performance measure (mean individual assignment accuracy) for 124 SNPs (Table 2) screened for 36 test populations (Table 1) from a Backwards Elimination Locus Selection (BELS) algorithm. See text for details.