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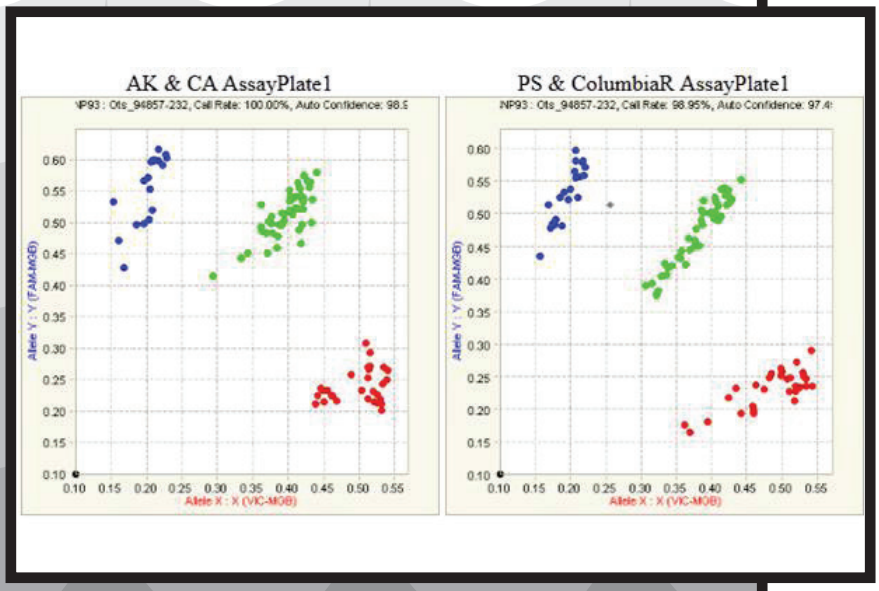
Moving GSI into the Next Decade: SNP Coordination for Pacific Salmon Treaty Fisheries



Principal Investigators:
Kenneth I. Warheit, (WDFW)
Lisa Seeb, (SAFS)
William D. Templin, (ADFG)
James Seeb, (SAFS)

Washington Department of
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FINAL REPORT

Pacific Salmon Commission's Chinook Technical Committee (US Section) for
Funding under the Letter of Agreement (LOA)

PROJECT TITLE:

N10-8 Moving GSI into the Next Decade: SNP Coordination for Pacific Salmon Treaty Fisheries

Principal Investigators
Kenneth I. Warheit, Washington Department of Fish and Wildlife (WDFW)
Lisa W. Seeb, University of Washington, School of Aquatic and Fishery Sciences (SAFS)
William D. Templin, Alaska Department of Fish and Game (ADFG)
James E. Seeb, University of Washington, School of Aquatic and Fishery Sciences (SAFS)

Executive Summary

Numerous projects, for both SNP genotyping and discovery, have been funded by the United States Chinook Technical Committee and the Northern and Southern Endowment funds of the Pacific Salmon Commission, as well as by a number of other funding sources. SNP applications are flourishing in local jurisdictions where dozens of new SNPs have been implemented to greatly improve resolving power. This project coordinated current efforts in SNP genotyping and discovery for Chinook salmon within the Pacific Salmon Commission area of interest and provided guidelines for the development of a common panel of 96 SNPs for coastwide use in genetic stock identification (GSI). First, a comprehensive list of over 288 SNPs was compiled in collaboration with other Pacific Salmon Commission investigators. Genotypes for all 288 SNPs were collected from four representative populations from across the range. Results for the four populations were evaluated by interested laboratories for resolution and information content to identify a subset of 192 SNPs that would work well in all laboratories. Next, an additional 38 populations ranging from the Central Valley of California to Northwest Alaska were genotyped for the 192 SNPs. Using the data from all 42 populations, SNPs were ranked for information content, and panels constructed using three separate techniques and two separate reporting group scenarios. F_{ST} and f_{ORCA} analyses produced different sets of 95 loci each for the population and the two reporting group analyses, while the principal component analysis (PCA) produced a single set of loci. We compared the results from each of these methods to the results from a random selection of 95 loci, treating the random sets of 95 loci as null hypotheses. [Standard SNP panels consist of 96 loci. We evaluated panels of 95 loci to reserve one spot for a SNP designed to identify the sex of the individual fish.] We evaluated each of the seven sets of loci by comparing their GSI performance (i.e., the proportion of correct assignments) to each other and to the random sets of loci.

All sets, including the random sets performed well. From these results, it is clear that there are many sets of 95 loci that would achieve the needed resolution for GSI analyses and fishery management. Furthermore, it is conceivable that less than 95 SNPs will be needed for assigning individual fish to, or for mixed stock analyses of, reporting groups. There are at least two new studies that are attempting to optimally construct combined GSI and PBT SNP panels (CRITFC and WDFW 2012 CTC-LOA projects). We recommend that these two studies use the results of this project as a starting point from which combined PBT and GSI panels are constructed.

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Introduction

This project was conceived to address the Chinook Technical Committee research theme of "Expansion of baseline information to address specific stock-separation issues relevant to PSC Chinook stocks". The project is a collaboration among three laboratories to coordinate existing SNP data to maximize the benefits from previous research and facilitate the transition to SNP markers during the next decade. This project builds on earlier studies funded by the Chinook Technical Committee including *N05-15 Development and Evaluation of Chinook salmon Single Nucleotide Polymorphism (SNP)*, which compared 37 SNPs to 13 microsatellites (Narum *et al.* 2008), and study *N06-12 SNP Development in Chinook salmon for Genetic Stock Identification of Mixed Fisheries* where additional SNPs were discovered and a set of 20 core populations were evaluated for 75 SNPs.

Results from those studies lead to *N08-09 SNP Assays for Baseline Genotyping*, in which 75 *TaqMan* assays for SNP genotyping were purchased in a large quantity and distributed to laboratories for baseline genotyping. In that same year, study *N08-12 High-resolution SNPs for identification of poorly differentiated stocks*, identified highly informative SNPs for poorly-differentiated stocks in Puget Sound and the Southeast Alaska Transboundary region (results reported here). Additional studies supported by the PSC for SNP discovery were also conducted (Miller et al. 2008b; Narum and Campbell 2010). The Miller et al. (2008) study at Canada Department of Fisheries and Oceans (CDFO) was a sister project to *N06-12* and included discovery of 11 new SNPs and analysis of the same individuals from the 20 core populations used in study *N06-12*.

Genotyping studies of baseline populations have also been supported by the LOA and Northern and Southern Endowment Funds with projects throughout the PSC area. These projects have supported work at ADFG, WDFW, CDFO, and Columbia River Inter-Tribal Fish Commission (CRITFC). This study draws on SNPs identified in all these previous studies.

Agencies and universities working with the PSC and CTC have independently made significant capital investments in SNP technology by standardizing on the Fluidigm instruments (http://www.fluidigm.com/applications/genotype-profiling.html). Unlike the first generation SNP technologies that required uniplex reactions, the Fluidigm instruments use high throughput dynamic arrays to simultaneously screen 96 samples for 96 *TaqMan* assays (Seeb *et al.* 2009). Consistent with this commitment, a large number of PSC and non-PSC projects, formerly based on microsatellites, have transitioned to SNPs. For example, the large Western Alaska Salmon Stock Identification Project (WASSIP; http://www.adfg.alaska.gov/index.cfm?adfg=wassip.main) conducted by ADFG is entirely SNP-based; the analysis of Southeast Alaska Chinook salmon fisheries (SEAK) is the only remaining microsatellite project within ADFG. SAFS and ADFG are funded by the Alaska Sustainable Salmon Fund (AKSSF) to develop a new 96-SNP panel for Alaska studies and other institutions are similarly transitioning into SNP-based studies with the discovery of dozens of new markers (Campbell and Narum 2008; Clemento et al. 2011).

This project addresses the need to standardize on a set of 96 SNPs for CTC fisheries. Where there were only 75 SNPs available from the early LOA studies, high-throughput assays for SNPs for Chinook salmon now number over 500. The objectives of this project were to: 1) Convene

an advisory panel of representatives from interested laboratories to assess the status of SNP discovery and genotyping for Chinook salmon in the PSC area and develop a comprehensive list of documented SNPs for Chinook, 2) Evaluate performance of 192 of the currently available SNPs using at least 40 core populations, and 3) conduct a statistical analysis using results from Objective 2 on 192 SNPs to identify high resolution panels of 96 SNPs for PSC fisheries.

Methodology & Design

Objective 1. SNP Coordination

At several time periods during the study, we convened meetings of interested PSC laboratories including members of the original GAPS group (Genetic Analysis of Pacific Salmon). The laboratories assessed the status of discovery and genotyping for Chinook salmon in the PSC area and developed a comprehensive list of SNPs and available *TaqMan* assays.

Objective 2. Core Populations and Evaluation of New SNPs

Collection of Core Populations

A total of 42 core populations represented by 48 individuals each was assembled by WDFW and ADFG working with collaborating laboratories (Table 1). Populations ranged from the Central Valley of California to the Yukon River in Alaska. Populations from the northern range of Chinook salmon beyond the PSC area of interest were included to facilitate high-seas and bycatch studies. DNA extraction was conducted at WDFW and ADFG following standard methods (Templin *et al.* 2011).

SNP Evaluation

The first phase of the evaluation was based on four core ascertainment populations representing the diversity of Chinook salmon across the range; ascertainment populations originated from the Coleman National Fish Hatchery (Sacramento Central Valley), McCall Fish Hatchery (Columbia River stream-type), Soos Creek Hatchery (Puget Sound fall), and Kanektok River (Western Alaska) (Table 1). These populations were genotyped for 288 SNPs identified under Objective 1 using *TaqMan* genotyping assays. Genotypes, allele frequencies, and HTML files of scatterplots were distributed to all interested PSC laboratories. Each laboratory ranked the SNPs based on resolution (Figure 1) and allele frequency range. Based on these rankings, a subset of 192 SNPs was chosen for evaluation under Phase II.

During Phase II of the SNP evaluation, the remaining 38 core populations were genotyped for the 192 SNPs identified above using two panels of 96 SNPs (Table 2).

Objective 3. Statistical Analysis and Panel Recommendation

Summary Statistics

We calculated summary statistics for the 42 core populations for the 192 SNPs. Statistics included allele frequency, expected and observed heterozygosity, fit to Hardy Weinberg equilibrium (HWE), and overall and regional F_{ST} values. Linkage disequilibrium (LD) analyses were also conducted. Analyses were conducted using Genepop (Rousset 2008), FSTAT (Goudet 2001), and the R Development Core Team (2008) packages *adegenet* (Jombart 2008*)* and *Hierfstat* (Goudet 2005). Based on these analyses, six loci had significant deviations from Hardy-Weinberg equilibrium (see Results and Conclusions), and were eliminated from further consideration, thereby reducing the pool of available loci to 185.

Reporting Groups

We constructed two sets of reporting groups, one based on the genetic data collected herein, and the other based on the PSC-CTC indicator stocks. These reporting groups aggregate populations using either genetic similarities or fishery management practices, respectively (Table 1).

For the reporting groups defined by genetic similarity, we aggregated populations into sets for which members of the set have greater similarity to each other than to populations outside the set. These reporting groups most closely matched the patterns of genetic diversity among populations of Chinook salmon. Principal components analysis was used initially to investigate patterns of genetic distinction in this dataset and to define reporting groups based on these distinctions.

For the reporting groups defined by fishery management practices, populations are placed in sets based on pre-defined distinctions used for management of the resource (e.g., national borders, watershed boundaries, or run timing). These reporting groups may not match well with the patterns of genetic diversity among populations of Chinook salmon. Management-based reporting groups were defined based on the population groupings used by the Chinook Technical Committee for Pacific Salmon Commission (e.g., Attachments I-V, Annex IV, Chapter 3, Pacific Salmon Treaty, Pacific Salmon Commission, January 2009).

SNP Ranking

We used three methods to rank the loci based on their collective ability to differentiate populations or reporting groups using a standard Genetic Stock Identification (GSI) process (e.g., individual assignments using conditional likelihood framework, as in the program ONCOR (S. Kalinowski)): F_{ST}, f_{ORCA} (Rosenberg *et al.* 2003; Rosenberg 2005) using backward elimination, and principal component analyses (PCA). In addition, we compared the results from each of these methods to the results from a random selection of 95 loci, treating the random sets of 95 loci as a null hypothesis.

Random Selection of SNPs

We randomly selected 95 loci from the collection of 185 loci as a null set to which we compared our selections of loci using F_{ST}, f_{ORCA}, and PCA. We then used the multilocus cross-validation method of Anderson et al. (2008) to determine discriminatory power of the three locus sets. Specifically, we developed and used a MATLAB (R2012a, The MathWorks, Inc.) script that randomly selected genotypes from 95 of the 185 loci, and then implemented the cross-validation method over gene copies (CV-GC) from Anderson et al. (2008). This is the same method as implemented in ONCOR, and described above, but was incorporated in the MATLAB script to automate the null hypothesis model. For each iteration, we created mixtures consisting of 200 individuals from only one population (100% mixtures) and calculated GSI accuracy as the percent correctly assigned back to that population, or that population's reporting group. GSI accuracy was calculated by repeating each analysis 100 times, for each population and randomly selected groups of 95 SNPs. This entire process was repeated 1000 times each with a different set of randomly selected 95 SNPs, generating for each population a distribution of GSI accuracy (for the population and the population's reporting group) based on randomly selected SNPs (see Figures 2-4).

F_{ST}

As a measure of the usefulness of individual loci to differentiate populations or reporting groups we used the F_{ST} of Weir and Cockerham as implemented in R in the software package *hierfstat*. For each locus, three F_{ST} values were calculated. The first measured the proportion of the total variation that was accounted for based on differences among the 42 populations for each individual locus. The second and third measured the proportion of the total variation that was among regions after we grouped populations into the genetic and PSC-CTC reporting groups, respectively. Loci were ranked in three sets based on the F_{ST} value for each measure (among populations, among genetic reporting groups, and among PSC-CTC reporting groups). For these analyses, F_{ST} could not be calculated for the locus *Ots_C3N3*, yet this locus is known to be diagnostic for distinguishing stream and ocean-type Chinook in the Columbia River. This locus was placed in every set of 95 loci used in this analysis.

f_{ORCA}

The second method we used to measure the usefulness of individual loci to differentiate populations or reporting was based on the "optimal rate of correct assignment" statistic (f_{ORCA}) as implemented in R. For each locus, three f_{ORCA} values were calculated based only on the information from that one locus. The first measured the potential rate of correct assignment of individuals to each of the 42 populations. The second measured the potential rate of correct assignment of individuals to genetic reporting groups. The third measured the potential rate of correct assignment of individuals to PSC-CTC reporting groups. Loci were ranked in three sets based on the f_{ORCA} value for each measure (populations, among genetic reporting groups, and among PSC-CTC reporting groups).

Principal Component Analysis

Finally, we conducted a PCA using individual-based allele frequencies from all 185 loci. Data were mean-centered, but not standardized to unit standard deviation (i.e., analysis based on variance-covariance matrix rather than correlation matrix). For each PCA axis, we conducted pairwise tests for differences in population means, using Bonferroni adjusted critical values, and eliminated all axes that did not have at least one population that was significantly different from 40 of the remaining 41 populations. This process resulted in 20 "significant" axes (Axes 1-17, 23, 24, 184), accounting for 43% of among-individual variance. We ranked SNP loci based on the absolute values of their coefficients (PC weights, or eigenvectors) for each PCA axis. Therefore, we selected a set of loci whose coefficients maximized the pairwise differences between populations. For each locus, we counted the number of times its coefficient (absolute value) was greater than both the 95^{th} and 99^{th} percentile for each of the 20 axes, and sorted the loci by these sums. In addition, weight was given to each locus that had the maximum coefficient (absolute value) for each of the 20 axes. We selected the top 95 loci based on these weighted sums. Three loci were vying for the 94^{th} and 95^{th} position. We selected the two loci with the highest mean and median coefficient.

SNP Panel Evaluation

The discriminatory power for genetic mixtures and individual assignment analyses was evaluated using recommendations and variations on the multilocus cross-validation method of Anderson et al. (2008, 2010). For each set of 95 loci generated from the F_{ST}, $f_{ORCA,}$ PCA we used the program ONCOR – mixture analysis, 100% simulations (S. Kalinowski; http://www.montana.edu/kalinowski/Software/ONCOR.htm) to evaluate GSI accuracy. This procedure implements the cross-validation method over gene copies (CV-GC) from Anderson et al. (2008). For each test we used 200 simulated individuals and 1000 simulations.

The population sample size of 48 was chosen to maximize the number of populations contributing to the study and is half of the sample size of 96 used in typical baseline studies. These small sample sizes precluded the use of separate training and holdout sets as described by Anderson (2010).

Results and Conclusions

Objective 1. SNP Coordination

Coordination meetings were held at the SNP Workshop (http://www.snpworkshop.org) in Blaine, Washington, in March 2010; at the Coastwide Salmon Genetics meeting (http://www.idahoafs.org/meeting_coastal.php) in Boise in June 2010; via teleconference in December 2010; and at the annual AFS National meeting in Seattle in September, 2011. Contributing laboratories included those of the three Principal Investigators (WDFW, ADFG, SAFS), three NOAA laboratories (Southwest Fisheries Science Center (SWFSC), Northwest Fisheries Science Center (NWFSC), and Auke Bay Laboratory (ABL)), Idaho Department of Fish and Game (IDFG), Columbia River Inter-Tribal Fish Commission (CRITFC), and US. Fish and Wildlife Abernathy Technology Center (USFWS).

A comprehensive list of SNPs (Box 1, Appendix 1) was compiled including those developed under Project N08-12 *High-resolution SNPs for identification of poorly differentiated stocks.*

Objective 2. Core Populations and Evaluation of New SNPs

Laboratories ranked the SNPs based on resolution and allele frequency range. Inclusion in existing GSI or parentage-based tagging panels (PBT) was also noted by some laboratories (Box 2, Appendix 1). After the initial evaluation of 288 SNPs, an additional nine SNPs were provided by CRITFC. These were added for a total of 297 SNPs, although genotyping for the four ascertainment populations was not conducted on the new CRITFC markers. Based on CRITFC experience, resolution was assumed to be acceptable for the new set. A sex-determining mark, *Ots_SEXY1*, was included in the new marker set.

SNPs with poor resolution and low minor allele frequencies were eliminated first. Further eliminations were based on rankings by laboratories with additional weight given to SNPs already included in existing panels.

Box 1. Origin 297 SNPs evaluated in this study. See also Appendix 1.

GAPs[1]	75
ADFG	19
SWFSC	100
CRITFC	27
UW	34
UW/WDFW[1]	25
WDFW	6
CDFO[2]	10
Total	297

[1] Discovery partially funded by LOA
[2] Discovery funded by PSC Endowment

Box 2. Example of Phase I SNP evaluation. Resolution (1= very good, 2= good, 3 = poor, and 4= not evaluated) as scored by individual laboratories, laboratory vote, difference between minimum and maximum allele frequency across the study area, and information on contribution to existing panels are given. Laboratory vote includes: PROTECT, DROP, and no recommendation (NR). Full results are given in Appendix 1.

SNP NAME	UW Res	USFWS Res	WDFW Res	WDFW Vote	IDFG/CRITFC Vote	ADFG Vote	SWFSC Vote	(Max - Min) Allele Freq	SWFSC PBT	IDFG/CRITFC Panel
Ots_100884-287	1	1	1	NR	PROTECT	NR	NR	**0.22**	PBT	PBT
Ots_101119-381	1	1	1	NR	NR	NR	NR	**0.60**	PBT	
Ots_101554-407	1	2	1	NR	PROTECT	NR	NR	**0.66**		PBT
Ots_101704-143	1	2	1	NR	PROTECT	NR	NR	**0.42**	PBT	PBT
Ots_102213-210	2	1	1	NR	DROP	NR	PROTECT	**0.18**	PBT	
Ots_102414-395	1	1	1	NR	PROTECT	NR	NR	**0.19**	PBT	SNP/PBT

During Phase II of SNP evaluation, genotypes from all 42 populations (Table 1) were collected for the selected set of 192 SNPs (Table 2). Source references for each SNP are given in Table 2.

Objective 3. Statistical Analysis and Panel Evaluation

Summary Statistics

SNPs were evaluated for fit to HWE in all populations. SNPs were excluded if significant at an overall Fisher Exact Test (P<0.05). Six SNPs were eliminated: *Ots_111084b-619, Ots_113242-216, Ots_111666-408, Ots_113242-216, Ots_CCR7, Ots_DESMIN19-SNP1*. Two SNPs, *Ots_102457132* and *Ots_NAML12-SNP1*, that met the exclusion criteria were retained since the deviation was driven by only a few populations (< 10%). In tests for linkage disequilibrium, four linked pairs were also observed in the dataset: *Ots_HSP90B-385* and *Ots_HSP90B-100*, *Ots_FGF6B_1* and *Ots_FGF6A*, and *Ots_AldB1-122* and *Ots_aldb-177M*, and *Ots_Tnsf* and *Ots_Tf-3545*.

SNP Ranking

As described in the Methodology and Design section, we conducted three separate analyses for both the F_{ST} and f_{ORCA} methods, one each for the populations, genetic reporting groups, and PSC-CTC reporting groups. Therefore, each of these analyses (six in total) produced different sets of 95 loci, while the PCA analysis produced a single set of loci (Table 3). From these seven sets of 95 loci, 172 of the 185 loci were selected, reflecting the overall usefulness of each of the 185 loci. Eleven loci were selected in all seven sets, and another 27 loci occurred in six of seven sets. These 38 SNPs should be considered the most informative and be ranked the highest when constructing a final set of 96 SNPs. The F_{ST}-Population and F_{ST}-Genetics sets were most similar to each other sharing 91 of the 95 loci, while the f_{ORCA}-PSC-CTC set had the greatest number of singleton loci (four; a singleton locus is one that was selected by only one analysis). The PCA and f_{ORCA}-Population sets had three singleton loci each, while the F_{ST}-PSC-CTC and the f_{ORCA}-Genetics had two singleton loci each.

SNP Panel Evaluation

Random Selection of SNPs

The distribution of estimates from the 1000 iterations of randomly selected loci are presented for correct assignment to population (Figure 2), genetic reporting group (Figure 3), and PSC-CTC reporting group (Figure 4). Overall, and unexpectedly, random sets of 95 SNPs performed quite well with 35 of the 42 populations having correct assignment rates at or above 0.90 (Figure 2). The populations that did not make the 0.90 cutoff were Priest Rapids and Wells hatcheries, both Columbia River summer/fall-run populations; Clear Creek and Soos Creek hatcheries, closely related Puget Sound fall populations with a common broodstock origin (Green River); and three populations from western Alaska, Togiak, Kanektok, and George rivers. Assignments rates back to the correct reporting groups were particularly robust, especially for the genetic reporting groups (Figure 3). The poorer performance for the Priest Rapids and Wells hatcheries, and the Clear Creek and Soos Creek hatcheries for the PSC-CTC reporting groups was the result of the splitting of each genetically similar pair into different reporting groups (see Table 1).

Comparison Among SNP Sets

We evaluated each of the seven sets of loci by comparing their GSI performance (i.e., the proportion of correct assignments) to each other and to the random sets of loci. The overall performance for each set of loci was similar to each other, and for the most part, similar to the random sets (Figures 2-4). However, the F_{ST}-Population set performed better than the f_{ORCA}-Population, PCA, and random sets for assigning fish to the two Coleman Hatchery populations (Pops 1 and 2) and to Clear Creek (Pop 22) and Soos Creek (Pop 23) hatcheries (Figure 2). For the Togiak, Kanektok, and George rivers populations, the random sets out-performed the F_{ST}-Population, f_{ORCA}-Population, and PCA sets. There was slight improvement with the F_{ST}-PSC-CTC, f_{ORCA}-PSC-CTC, and PCA sets over the random sets for assigning fish from Priest Rapids and Wells hatcheries to their PSC-CTC regions, but even with these improvements, assignment rates were near 0.80 or less for all sets (Figure 4). Likewise, the F_{ST}-PSC-CTC, f_{ORCA}-PSC-CTC, and PCA sets were an improvement over the random sets for assigning fish to Clear Creek and Soos Creek hatcheries, especially for the f_{ORCA}-PSC-CTC set which provided near 100% correct assignments (Figure 4).

Overall, as stated above, each of these SNP sets performed very well, including the random sets, and there were little differences (except where noted above) among the sets in their ability to correctly assign individuals to populations or reporting groups.

Recommendations

All of 192 SNP loci are currently being used for either Chinook parentage based tagging (PBT) or GSI activities, and as such have already been through a vetting process at one or more laboratories. Therefore, it is not surprising that these SNPs, either in a random set or in one of the deliberate sets of 95, performed well in each of our GSI tests. In fact, even the collection of eleven loci in common to all seven sets (Table 3) did well as a set on its own in differentiating populations and the genetic and PSC-CTC reporting groups (median estimates, 0.81, 0.98, and 0.96, respectively; data not shown). We emphasize that not all 192 SNPs are equally informative, and we would rank the 38 SNP loci that occurred in six or seven of the seven sets (Table 3) as our highest priority SNPs.

From these results, it is clear that there are many sets of 95 loci that would achieve the needed resolution for GSI analyses and fishery management. Furthermore, it is conceivable that less than 95 SNPs will be needed for assigning individual fish to, or for mixed stock analyses of, reporting groups (e.g., the 38 highest priority SNPs, as described above). There are at least two new studies that are attempting to optimally construct combined GSI and PBT SNP panels (CRITFC and WDFW 2012 CTC-LOA projects). We recommend that these two studies use the results of this project as a starting point from which combined PBT and GSI panels are constructed. Furthermore, perhaps an appropriate strategy should be to construct a single 96-SNP panel (95 SNPs as above plus a sex-determination marker that is scorable and informative) for coastwide PBT/GSI analyses, and a second set of 96-SNP panel for local applications. This second panel would be specific to local (e.g., Columbia Basin, Puget Sound, SE Alaska) management needs. Furthermore, we recommend that GAPS laboratories share locus information from this second panel to ensure that GSI of fisheries in areas that aggregate many populations (e.g., SE Alaska) can make use of the regional-specific information.

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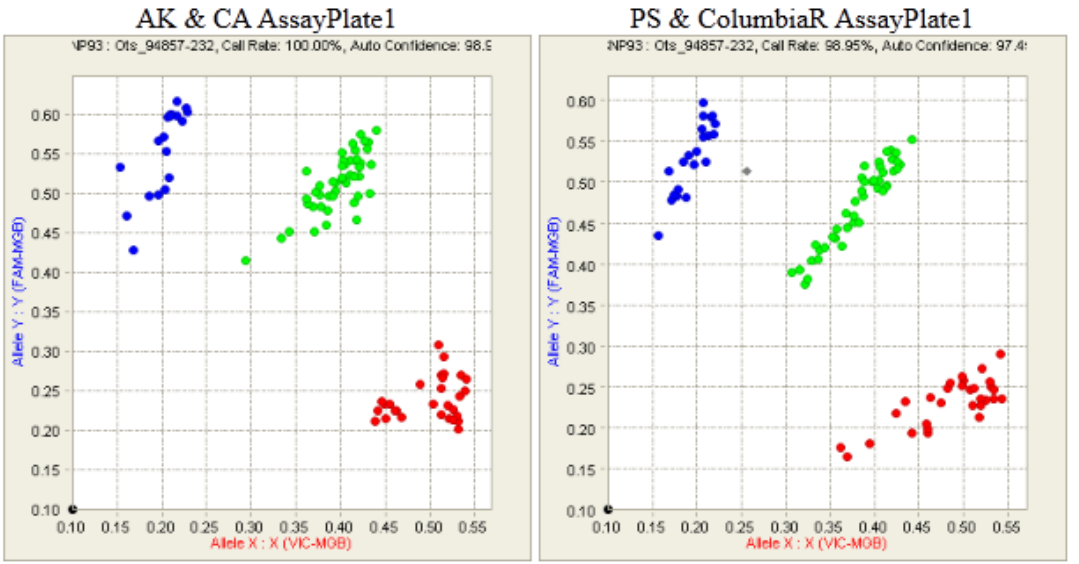
a. Ots 118175-479



b . Ots_nramp-321

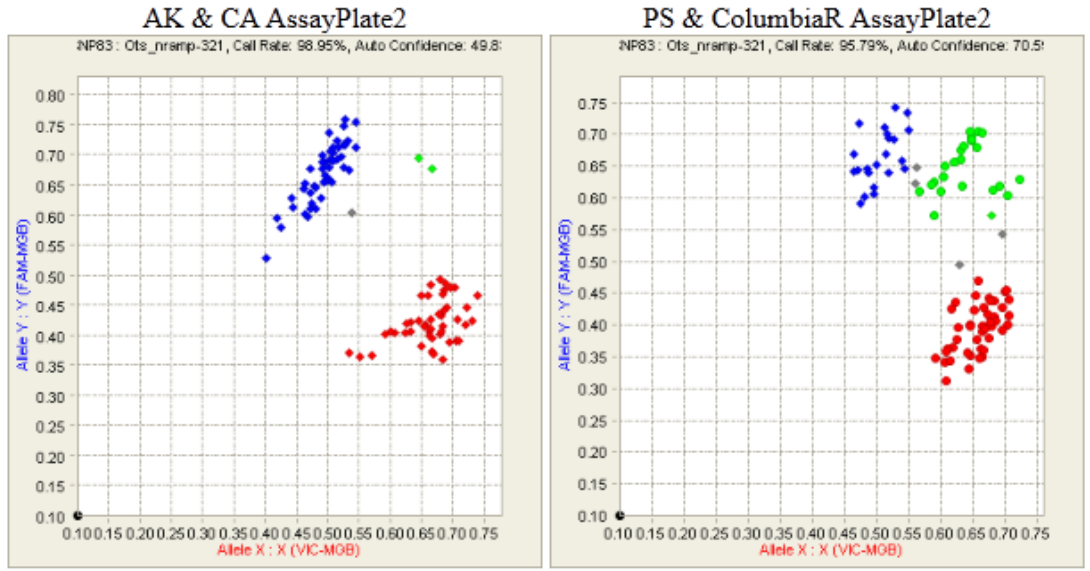


Figure 1. Scatterplots of SNPs with varying resolution. Two ascertainment populations are shown on each scatterplot. a) Scored by all laboratories as a "1" indicating very good resolution. b) Scored by all laboratories as a "3" indicating poor resolution.

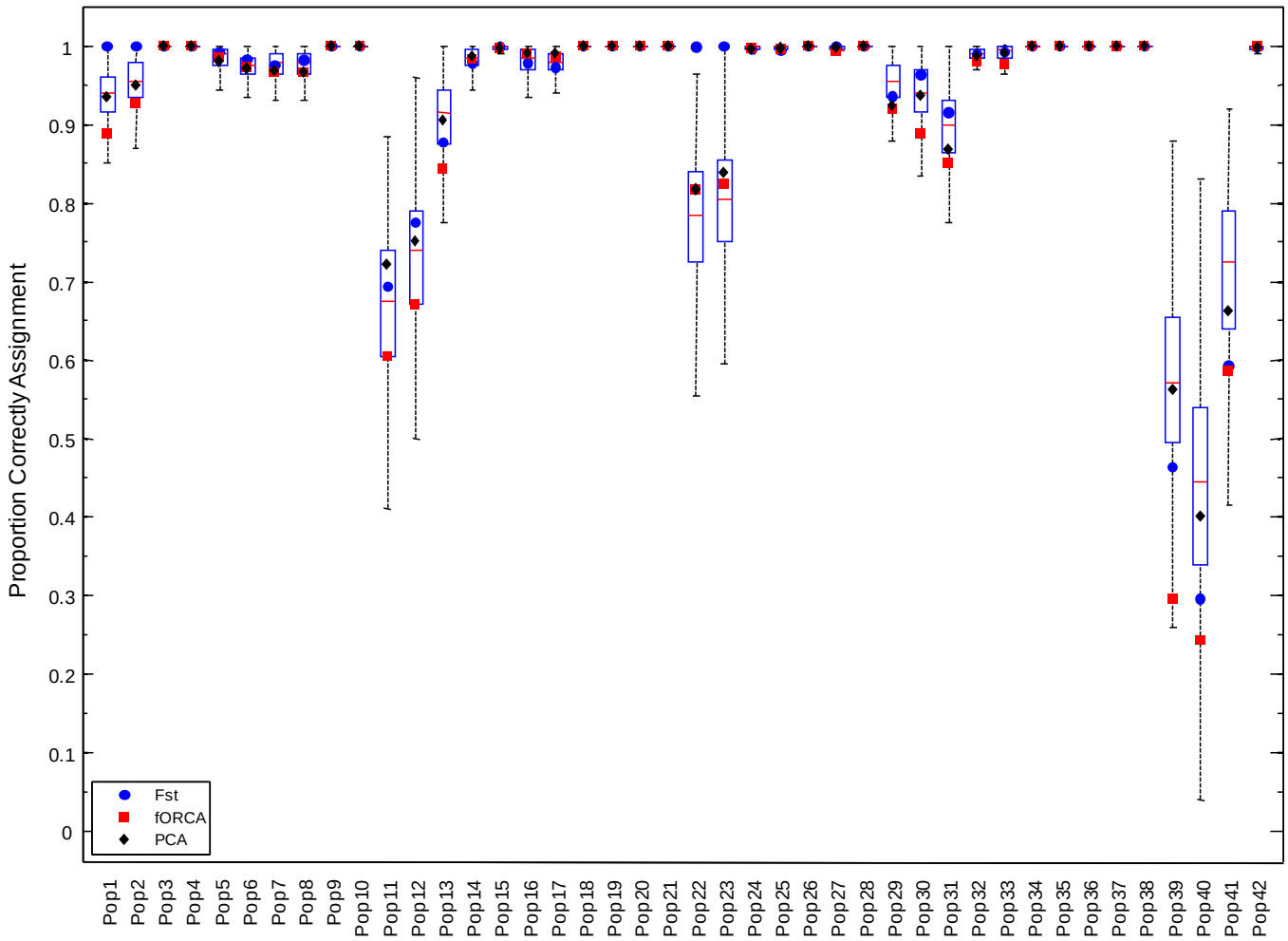


Figure 2. The proportion of correctly assigned simulated individuals from each population back to its population of origin. Populations are numbered sequentially and correspond to population numbers in Table 1. Box plots are for 1000 random sets of 95 SNP loci. Red line within each box is the median value, upper and lower parts of the box represent the 75th and 25th percentiles, respectively, and the tips of the box whiskers are ± 2.7 s (standard deviation) or roughly the 99% confidence interval. The symbols represent the mean estimate for correctly assigned individuals from 1000 ONCOR (S. Kalinowski) simulations (see text) for 95 SNP datasets established using F_{ST}, f_{ORCA} and PCA prioritized loci. See Table 4 for the specific loci used for each data set.

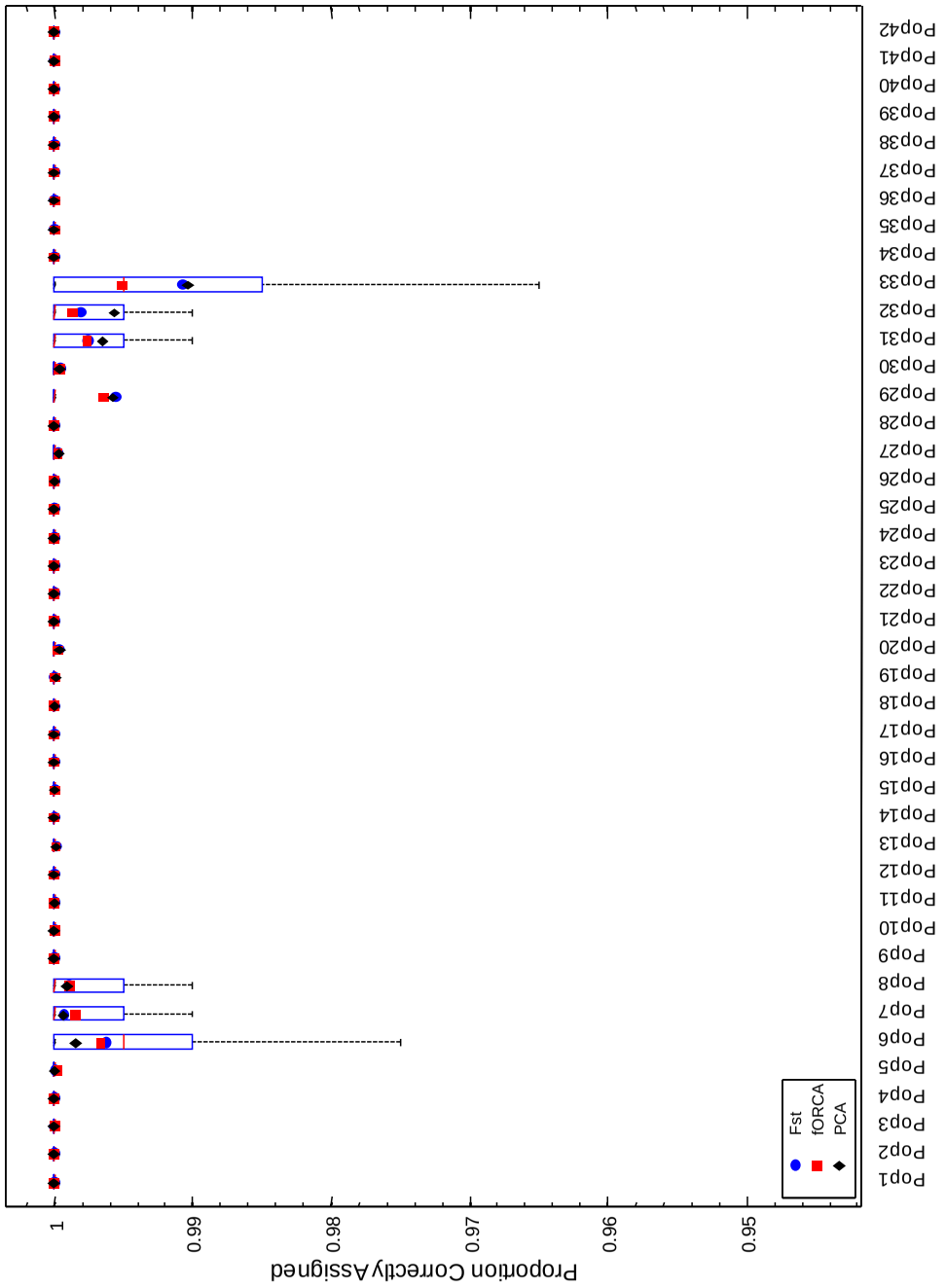


Figure 3. Same as Figure 2, except data represent proportion of correctly assigned simulated individuals from each population back to the population's Genetic Reporting Group.

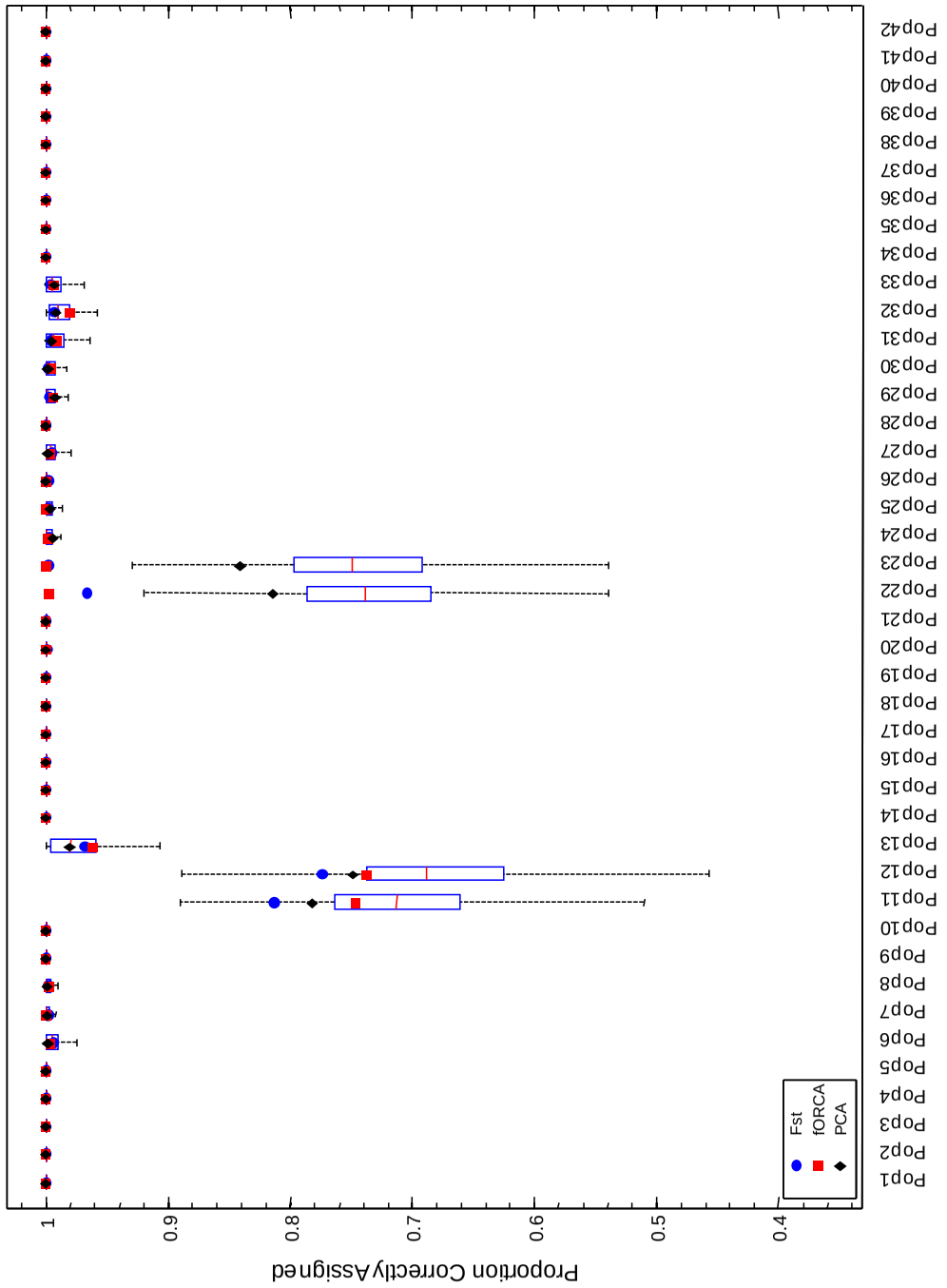


Figure 4. Same as Figure 2, except data represent proportion of correctly assigned simulated individuals from each population back to the population's PSC-CTC Reporting Group.

Table 1. Population ID, name, collection date, and sample size for the 42 core populations of Chinook salmon analyzed for 192 SNPs. The four ascertainment populations analyzed for the full 288 SNPs in Phase I of the evaluation are denoted with an asterisk (*). Genetics and CTC regions used in SNP evaluation are given.

Pop ID	Population Name	Date	N	Genetics Region		PSC-CTC Region	
				Region ID	Region Name	Region ID	Name
1	Coleman NFH Sacramento River*	2006	48	1	Central Valley	1	Central Valley
2	Coleman Hatchery - Battle Creek Late-fall Chinook	2010	48	1	Central Valley	1	Central Valley
3	Eel River	2010	48	2	Eel	2	No. CA Coast
4	Trinity River Hatchery	2010	48	3	OR/CA Coast	3	Klamath
5	Cole M. Rivers Hatchery- Rogue River	2010	48	3	OR/CA Coast	4	So. OR Coast
6	Rock Creek Hatchery	2010	48	3	OR/CA Coast	4	So. OR Coast
7	Cowlitz Hatchery	2010	48	4	LColR/Willamette	5	Columbia R. Fall
8	NF Lewis River	2004	48	4	LColR/Willamette	5	Columbia R. Fall
9	Spring Creek Hatchery	2010	48	4	LColR/Willamette	5	Columbia R. Fall
10	McKenzie Hatchery	2010	48	4	LColR/Willamette	5	Columbia R. Fall
11	Priest Rapids Hatchery	2010	48	5	CR_OceanType/Deschutes	5	Columbia R. Fall
12	Wells Hatchery	2008	48	5	CR_OceanType/Deschutes	6	Columbia R. SU
13	Lyons Ferry Hatchery	2010	48	5	CR_OceanType/Deschutes	5	Columbia R. Fall
14	Wenatchee River Spring	2010	48	6	CR_StreamType	7	Columbia R. Stream-type
15	Cle Elum River	2010	48	6	CR_StreamType	7	Columbia R. Stream-type
16	Johnson/McCall Fish Hatchery*	2010	48	6	CR_StreamType	7	Columbia R. Stream-type
17	Rapid River Hatchery	2010	48	6	CR_StreamType	7	Columbia R. Stream-type
18	Nestucca River	2010	48	7	PNW Coast/W VI	8	Far N. Migrating OR Fall
19	Quinault Lake Hatchery	2010	48	7	PNW Coast/W VI	9	WA Coastal
20	Robertson Creek Hatchery	2010	48	7	PNW Coast/W VI	10	WCVI
21	Middle Shuswap, South Thompson	1997	48	8	South Thompson	11	Fraser Early
22	Clear Creek Hatchery - Nisqually River	2005	47	9	Puget Sound/S BC	12	South Puget Sound
23	Soos Creek Hatchery*	2010	48	9	Puget Sound/S BC	13	N. PS SU/Fall
24	Kendall Creek Hatchery	2010	48	9	Puget Sound/S BC	14	N. PS Spring
25	Marblemount Hatchery	2010	48	9	Puget Sound/S BC	13	N. PS SU/Fall

Table 1 (con't)

Pop ID	Population Name	Date	N	Genetics Region		PSC-CTC Region	
				Region ID	Region Name	Region ID	Name
26	Big Qualicum Hatchery	2010	48	9	Puget Sound/S BC	15	L. Strait Georgia
27	Harrison River	2010	48	9	Puget Sound/S BC	16	Fraser Late
28	Morkill River	2001	48	10	U Fraser	11	Fraser Early
29	Morice River	2010	48	11	N BC/SEAK	17	North/Central BC
30	Kitsumkalum River	2010	48	11	N BC/SEAK	17	North/Central BC
31	Kitwanga River	2009	48	11	N BC/SEAK	17	North/Central BC
32	Little Port Walter-Unuk River	2009	48	11	N BC/SEAK	18	SEAK
33	Little Tatsamenie/Tatsatua - Taku	2007	48	12	TransB/Tahini	18	SEAK
34	Pullen Creek Hatchery	2005	48	12	TransB/Tahini	18	SEAK
35	Alsek Goat Creek	2007	48	13	Alsek/Copper	19	Alsek/Copper
36	Sinona Creek	2005	48	13	Alsek/Copper	19	Alsek/Copper
37	Montana Creek	2009	48	14	Western Alaska	20	W. AK
38	Karluk River	2006	48	14	Western Alaska	20	W. AK
39	Togiak River weir	2009	48	14	Western Alaska	20	W. AK
40	Kanektok River*	2005	48	14	Western Alaska	20	W. AK
41	George River weir	2005	48	14	Western Alaska	20	W. AK
42	Kantishna River	2005	48	14	Western Alaska	20	W. AK

Table 2. List of 192 SNPs evaluated for 42 baseline populations.

No.	Assay	VIC/ FAM	Primer Sequences	Probe Sequences	Ref
1	*Ots_100884-287*	T/C	F: CGGAAGACCAGATTCTCCAAGAGTA	VIC-ATAGAACTACAATTCACATATAT	5
			R: CGACCAAGTAGCGGCACTT	FAM-AACTACAATTCGCATATAT	
2	*Ots_101119-381*	T/C	F: TTTTCTAGGACAGGTTGCTTGCA	VIC-TGCCACATGATAATTGA	5
			R: CCAGGTTTCTTTAGCCTACTTATTCTTTACA	FAM-CCACATGGTAATTGA	
3	*Ots_101554-407*	C/G	F: TGAAAGATATCAATTGTAGTAGTGGTGGTG	VIC-ATGGAGGATTGTGGTTGT	5
			R: ACACGCCAGTCCACAAGT	FAM-ATGGAGGATTCTGGTTGT	
4	*Ots_101704-143*	T/G	F: ACTTCTTGAGCCAATCGGATGATG	VIC-CTTAGACGTCAGAGGTC	5
			R: CCAGAGATAAACTAGTGGAGGAGATCA	FAM-CTTAGACGTCCGAGGTC	
5	*Ots_102213-210*	A/G	F: CATTCCATGACAATGATTGAAATCTAAAAACAC	VIC-CTGTATACAGTAAGAGTATTAAT	5
			R: GAGTATCTCAATTGCAACACTATGGTATGT	FAM-ACAGTAAGAGCATTAAT	
6	*Ots_102414-395*	A/G	F: GCCTACTGATAAATGTATGACAGTAATGGA	VIC-CACATAGTGTAGCTTTACTAC	5
			R: CAATAACAAACAAGCTAGGAACAAAAGTGT	FAM-CACATAGTGTAGCTCTACTAC	
7	*Ots_102420-494*	T/G	F: TGCCAACCTGGCCAGTTAC	VIC-CATGTGAACAACAAGCG	5
			R: GCTTCCCTGCTTCCATGGT	FAM-CATGTGAACACCAAGCG	
8	*Ots_102457-132*	A/G	F: CCAGCAGAGACTGGGTTCAC	VIC-CAATTGTGCGTTGCCCCA	5
			R: TTCCCTACCGGCGAAACC	FAM-ATTGTGCGTCGCCCCA	
9	*Ots_102801-308*	C/A	F: TGGGACAGAGGTGGGAATTGA	VIC-AGGGACAGTTTCGCAGACG	5
			R: CCCAAAGATGCTTAACTGAAGATGTG	FAM-AAGGGACAGTTTCTCAGACG	
10	*Ots_102867-609*	A/G	F: CTCTGCCATTCATTTGGGCTTTG	VIC-ACAGAGAGAAGTCCCAGGTG	5
			R: GTCTAAAGTGGTCCCCTTGGAT	FAM-AGAGAGAAGCCCCAGGTG	
11	*Ots_103041-52*	G/A	F: ACCACCCACCTCCTCAGA	VIC-CATCCTGCTGGACCC	5
			R: AGACAGAGAAAGTCGGGACACT	FAM-CATCCTGTTGGACCC	
12	*Ots_103122-180*	T/C	F: CAAACGCGCACTCACACA	VIC-CATCAACACAATCTGC	5
			R: TCACAATGGTACGATTTTACGACTCAA	FAM-CATCAACACGATCTGC	
13	*Ots_104063-132*	C/T	F: GCGTTACTGGTGTTATAAACGTTAGC	VIC-CTTTCGTCCTTAGCACATAG	5
			R: GTTTATTTAATTATGAAGGACGATGTTGAAGTCA	FAM-CTTTCGTCCTTAACACATAG	
14	*Ots_104415-88*	C/T	F: CCTGAGCATCCCAGTTGAACT	VIC-TCCTGAAAAACGACATCC	5
			R: TGTTTTCAATACACTGCAATTTAGTTTTGGT	FAM-CTGAAAAACAACATCC	

Table 2 (con't)

No.	Assay	VIC/ FAM	Primer Sequences	Probe Sequences	Ref
15	*Ots_104569-86*	T/G	F: CCTGCATGTTGTTCACGTTGTC	VIC-TGGTCGCAGATGCC	5
			R: CGGCCGGAGGGATCAC	FAM-TGGTCGCCGATGCC	
16	*Ots_105105-613*	C/G	F: AGTACAAGTGCAGAGAATGACATCATG	VIC-CCGAGCTTGAGTTAGGA	5
			R: GGTGTTTTATTTTCCCATATATCTTTTAACTTTAAGCT	FAM-CCGAGCTTGACTTAGGA	
17	*Ots_105132-200*	G/T	F: CGATGTACTGAGGGCAGTGT	VIC-CAAGAGTGGCATAAAA	5
			R: GAGTGGAGTTCCTTAATAATCATTGACCTT	FAM-CAAGAGTGGAATAAAA	
18	*Ots_105385-421*	A/G	F: GACTGTCTTGGAACCGTTGCTA	VIC-CCTCCTGGGTATATCG	5
			R: TCCCGGAACACACCAATGTC	FAM-CTCCTGGGCATATCG	
19	*Ots_105407-117*	T/A	F: TGTGTACATCCGCGTAAATATTGAAGATAA	VIC-CAGGTTAGGAATGGTTG	5
			R: CTGTGAGCTGCTGCAAACC	FAM-CAGGTTAGGATTGGTTG	
20	*Ots_106499-70*	C/G	F: ACTCTATCATCGGCAGGACCAT	VIC-CTCATTTTTCAGAATTGTATTC	5
			R: ACCGTAAGTGTGGTTGTGTTCATTA	FAM-CTCATTTTTCAGAATTCTATTC	
21	*Ots_106747-239*	C/A	F: ATCGAGGATGCCTCAAAGACATC	VIC-CCCGCGGTGAGTAT	5
			R: GTTAGACCCACCACCAGTCATC	FAM-CCCGCTGTGAGTAT	
22	*Ots_107074-284*	A/T	F: CCCACTTCCAGAGCCTGAA	VIC-ACCGTAGCTGCACCTG	5
			R: TTTTCCATGGCTGTGTGTACTGT	FAM-CGTAGCAGCACCTG	
23	*Ots_107285-93*	T/A	F: GCCCTTGTGACAATGCACTGTTATA	VIC-AAGTAACGTATCAAATGGC	5
			R: AACATACACCAATACTTAGGTCTAGACAGT	FAM-AAAGTAACGTATCATATGGC	
24	*Ots_107806-821*	T/A	F: CTCCCTTGCTTTTGGTCATTGG	VIC-CAAAGAAAATCAAAATTT	5
			R: TGCAGTGCTGAATTAGAGATTAATTTTTGTG	FAM-CAAAGAAAATCTAAATTT	
25	*Ots_108007-208*	A/T	F: CAGGCTTGTGTTAAGTAGGGAGAAA	VIC-CAGTTTCACTTAATTTTAAAATG	5
			R: CATTGGACAAGACCGGGTAGTC	FAM-TTTCACTTAATTTAAAAATG	
26	*Ots_108390-329*	G/C	F: GAGGTTTGTTACTGTCACCCATAGA	VIC-CTACTTATGTAGCATTTTAA	5
			R: CCTGCTGTAGCAAACTGTCTCAAA	FAM-CTACTTATGTAGGATTTTAA	
27	*Ots_108735-302*	C/T	F: CCTTTTTCTTATTAGTTTTACTTCCCCAGAGA	VIC-AAACAAACAACGCCTCATG	5
			R: CAATTCCATTCTTGATTCTGTTTAACGGT	FAM-AACAAACAACACCTCATG	
28	*Ots_108820-336*	G/A	F: TGAAATAAATTGTTCTGTTGATATGTGAATTTTGGA	VIC-ATTGCCCATCTCAGAATA	5
			R: CAACGACACACCAACAACGT	FAM-AATTGCCCATCTTAGAATA	

Table 2 (con't)

No.	Assay	VIC/ FAM	Primer Sequences	Probe Sequences	Ref
29	*Ots_109525-816*	C/T	F: GCCAGATAGTAGCGTACATCATGAG	VIC-CATGAGGCGTTCGGC	5
			R: CTCCCCATGTCCCTGAGTCT	FAM-ATGAGGCATTCGGC	
30	*Ots_109693-392*	T/G	F: TCTCCCTCATTCCCATGTCATATCA	VIC-TCCGTTAGTTCATCCTGG	5
			R: GGGAACGTATCAGGTGAGTGT	FAM-TCCGTTAGTTCCTCCTGG	
31	*Ots_110064-383*	C/T	F: AACAAAGAATGTTAAACACCAAACAGGAA	VIC-CTACGTAATGAACGTTAGCT	5
			R: GTGCAAGGGACCTAGCTAATCC	FAM-ACGTAATGAACATTAGCT	
32	*Ots_110201-363*	A/T	F: GTTTGGCTATTGAAATTATACATTAAAACATGTAGCT	VIC-TGGATGCCAGTTTTAAAA	5
			R: CCATGGCATCCTGTAAAGAACAACA	FAM-TGGATGCCAGTTTAAAAA	
33	*Ots_110495-380*	G/C	F: GCCTAGGTATGTACGAAACTTCACA	VIC-ATGGCCCCTGTCTATG	5
			R: AGGCTTTTTCAGATGGTCGTATGA	FAM-ATGGCCCCTGTGTATG	
34	*Ots_110551-64*	C/A	F: GAGTGGTCAAGGTTTCAGTTTCTG	VIC-ACGCTCGGAACATT	5
			R: GAAATGGACAGACACAAGGTCAAAC	FAM-ACGCTCTGAACATT	
35	*Ots_110689-218*	T/G	F: GTATAAACTAGAGTCCAGTGTTATGTTAATGTCTT	VIC-CACCAATCAATTAATTATT	5
			R: CATGGCAGACAACAGTAGAGAATATGA	FAM-ACCAATCAATTCATTATT	
36	*Ots_111084b-619*	C/A	F: TTGTGGAATTACACCTTCAGAGTTCAAT	VIC-CCATGGAAACGGACAAT	5
			R: GCCTGTTTGGCTTTCTTAAACTGAT	FAM-TCCATGGAAACTGACAAT	
37	*Ots_111666-408*	C/T	F: GAGAATCTGGGATTGGTACATCCAT	VIC-ATAGTATCACTAGTTAAAAAT	5
			R: AAGCTCATGATACATGTATGAGTTATATTCTTCAAG	FAM-ATAGTATCACTAATTAAAAAT	
38	*Ots_111681-657*	G/T	F: CTGAGCTTTTTCAACTTACTTGTTGGA	VIC-TAGCGCAAACCCCGAACC	5
			R: GGCGCAGCAGCAACTG	FAM-CGCAAACACCGAACC	
39	*Ots_112301-43*	T/C	F: GCATGGCTGCCCTAGAACA	VIC-CGTCGCATTCAGC	5
			R: TCAGAACATTTCCTTCAGCTTCGT	FAM-CGTCGCGTTCAGC	
40	*Ots_112419-131*	A/T	F: GTGGGTAATCGATGCCAAAGAGAT	VIC-AAGCGACTTGATTATC	5
			R: TGGCAGTGTTTTCAACTAGCTTTG	FAM-AGCGACATGATTATC	
41	*Ots_112820-284*	C/T	F: CATAGATGTTTATATGAAAAACCTCCCACTGT	VIC-ACTCACACTCGAGTGACT	5
			R: GCATCCAAAAAGACGTGTGTGTTT	FAM-ACTCACACTCAAGTGACT	
42	*Ots_112876-371*	C/A	F: GCCTACAGCAAATTCAGCTACACAT	VIC-CATCACAACGATGTGTG	5
			R: TGGACCTTCAATCATCACAGCTT	FAM-CACATCACAACTATGTGTG	

Table 2 (con't)

No.	Assay	VIC/ FAM	Primer Sequences	Probe Sequences	Ref
43	*Ots_113242-216*	C/T	F: GAGGCCTAATGTCTCTTGTGACT	VIC-ATTACCAACGGAGAACC	5
			R: GACATCTTCAACAAGTGTTCATTCACC	FAM-TTACCAACAGAGAACC	
44	*Ots_113457-40*	C/T	F: CCCAAGTGGTGAGTGTCAGT	VIC-ATATGGATTGGAGAATAG	5
			R: ACTACAACAGGTGTTGATAATAGAATCATTCTC	FAM-CATATGGATTAGAGAATAG	
45	*Ots_115987-325*	T/G	F: GGAGGTGTAGTGAAATGGGAAGAT	VIC-ATGCATAAAAGGTAATTGTG	5
			R: GCATTCAGTGAACCAGTAGTGCTAT	FAM-ATGCATAAAAGGTCATTGTG	
46	*Ots_117242-136*	A/G	F: GTGACAGGAGACAGAAAGAGACATT	VIC-CAGCACATAACTTGACCTC	5
			R: TGGTCCTCCCTGTCTCTATCTACTA	FAM-AGCACATAACCTGACCTC	
47	*Ots_117259-271*	T/C	F: ACACCCACTTCAACCTCCATAAC	VIC-CTCTCCTGATCACTCTGT	5
			R: GCCTCAGAGCTTAGCTTGGA	FAM-CTCTCCTGATCCCTCTGT	
48	*Ots_117432-409*	A/G	F: TCATCAAAACATGCCTCTTCTGTGT	VIC-TTTAGACTTTGCTCTATAACAG	5
			R: TGTTGAACCTGTCACTCTGTCTTC	FAM-ACTTTGCTCCATAACAG	
49	*Ots_118175-479*	C/T	F: TGCGCGTCTCATTCAACCAT	VIC-AGAATGAAGTGAAAAGAA	5
			R: ACCTTACGTCCTAGGTAGGAAACA	FAM-AGAATGAAGTAAAAAGAA	
50	*Ots_118205-61*	T/C	F: CCATACAGCCAGTCCAGGTG	VIC-TAGTAGCCCCTACACCTC	5
			R: ACTGGACAGGGCTGGGT	FAM-TAGCCCCTGCACCTC	
51	*Ots_122414-56*	C/T	F: GCACCGTATCAACGAGCTCAT	VIC-TGTATGACCTCTGACCTGT	5
			R: TGCATGGATTTCCTTTGTGTTGTTG	FAM-TGTATGACCTCTAACCTGT	
52	*Ots_123048-521*	A/C	F: CTCAACAGTGCACCTCCCTTAATT	VIC-TCACATCCAACTCAGTACT	5
			R: CCAAACACACCCTTCCATAATCTCT	FAM-CATCCAACGCAGTACT	
53	*Ots_123921-111*	A/G	F: TCGCTAGGCAGAAATATAGGGTTCT	VIC-TGCTAAATGGCATATATTAT	5
			R: GAGCATGGCGCTTGCA	FAM-CTAAATGGCACATATTAT	
54	*Ots_124774-477*	T/C	F: AGTTGTTCTTTTTATATTGTGTTTTTATTCCATTCCA	VIC-CCACCGCCATCTGATA	5
			R: GCCAAATAAAAACAAAGCATGAACACA	FAM-CACCGCCGTCTGATA	
55	*Ots_127236-62*	T/A	F: TGGAGAACTTGCACTGAATGTGAAA	VIC-TCTCTTATCTGAGTTCTGC	5
			R: GCTGTTGGACCTTGACTTTAACAAATT	FAM-CTCTTATCTGTGTTCTGC	
56	*Ots_127760-569*	C/T	F: CTGCTGGCGCAGACATG	VIC-CCGGTTTACCGATTTG	5
			R: CGTTATAGAGGATAGTTTGGAGGAAGGA	FAM-CGGTTTACCAATTTG	

Table 2 (con't)

No.	Assay	VIC/ FAM	Primer Sequences	Probe Sequences	Ref
57	*Ots_128302-57*	C/T	F: GGTTGCAGGGCAGAACTGT	VIC-CCTGCAATACGACCAAC	5
			R: ACCCATCCAATAACCCATTTTCCTT	FAM-CTGCAATACAACCAAC	
58	*Ots_128693-461*	C/T	F: TCAATGTTCATCAATGCACTTCCTGTA	VIC-CACTCAGCTGGTACCCA	5
			R: GCCTGCAGGAGAAGGTAGAGTTA	FAM-ACTCAGCTGATACCCA	
59	*Ots_128757-61*	A/-	F: CGTGTCCGGCTTCTTTTATTTCATT	VIC-TTGTGCATTTTCCCC	5
			R: GATGGGTATGTTAATCATATTACCAGCGTAA	FAM-TGTGCATTTCCCCC	
60	*Ots_129144-472*	C/A	F: CTGTTAGTGCAGAAGACGTAGCT	VIC-TGGGTCTCGAGCCTGTA	5
			R: GCAGAGCTATTGAGCCAAGTTACAA	FAM-TGGGTCTCGATCCTGTA	
61	*Ots_129170-683*	C/A	F: AACCCTATGGGAACTCGTAGAACT	VIC-ATTAGAACTCGTAGAACTAT	5
			R: GCTAGGAGTTCTCAAAAGGGTTCT	FAM-ATATTAGAACTCGTATAACTAT	
62	*Ots_129458-451*	T/C	F: TGGGACCCACATAAAGCAACTG	VIC-CATCTGGCAATGCCTT	5
			R: GACATAAGACCCATTTAGCCCCTTTT	FAM-CATCTGGCAGTGCCTT	
63	*Ots_130720-99*	A/G	F: CGGTCATTGTAAATGTCAACGGTTT	VIC-CCTGTCTCATTCCC	5
			R: TGCTTGCATGTTCTTGGTGTAGTAA	FAM-CTGTCCCATTCCC	
64	*Ots_131460-584*	T/C	F: CCTATTTTTGATAGGTCATAGTGAATGGGATAG	VIC-CTATCAAAGCAATACATTG	5
			R: CTGTACTCCTCCATTCCTTTTCACT	FAM-CTATCAAAGCAGTACATTG	
65	*Ots_131906-141*	A/T	F: GGCTCGAACCACCCAGTTTA	VIC-CACGGTTTACACTCCTATTA	5
			R: TGCCCAACTGGTTTGCAATC	FAM-ACGGTTTACACTCCAATTA	
66	*Ots_94857-232*	T/C	F: GGCACTCTCCCTGGCTAGA	VIC-CAGGATAATAACAAACAAG	5
			R: CCCCATCACTTCTCTGGCTTTAAAT	FAM-CAGGATAATAACGAACAAG	
67	*Ots_94903-99*	G/T	F: CCGTCTGAGTAGGAGGATCAATACA	VIC-CAAACCAGCAAACAT	5
			R: TTTGGATCCAGCTCTCCGTATAGA	FAM-ACAAACCAGAAAACAT	
68	*Ots_96222-525*	C/T	F: GCTCTTGCCCATCTGTAGGAT	VIC-TGTAGCTAATTTTAAGTTCTC	5
			R: GGCGCAACATATGTATTAAGCAACT	FAM-AGCTAATTTTAAATTCTC	
69	*Ots_96500-180*	G/T	F: GATCATGTCAGATAGGATGCTGAAAGT	VIC-AAAACAAATCATTTTTCG	5
			R: CAGGTCTGGTCTACATCGAACAC	FAM-AAAAACAAATAATTTTTCG	
70	*Ots_96899-357*	T/A	F: TCTCCTGAACTAATTTAGACCTCTGAATGT	VIC-CTGAATGTTTTTTTTAATCTTT	5
			R: CCTCATATTGCTTTCATCTGAAGAGAGA	FAM-CTGAATGTTTTTTTTTATCTTT	

Table 2 (con't)

No.	Assay	VIC/ FAM	Primer Sequences	Probe Sequences	Ref
71	*Ots_97077-179*	G/T	F: CCTGAACAAATACTTAACGCTCCAGTT	VIC-TCACAAATGTATCCTAAAGC	5
			R: GTAATAATACTTCACACCATTGCCACTTC	FAM-CACAAATGTATACTAAAGC	
72	*Ots_99550-204*	C/T	F: TGACAGATTTCACCTTTAACTAGCTAAGC	VIC-AAGGCTTTGGTTGTTTG	5
			R: GCAACCTCTTTCACACTTCAGTAAC	FAM-AAGGCTTTGATTGTTTG	
73	*Ots_AldB1-122*	C/T	F: GCCATGGAGGACTGGATGA	VIC-ACCCACTTCGCCAACA	5
			R: GCCACCACTACTTGCTGAGAAAATA	FAM-ACCCACTTCACCAACA	
74	*Ots_aldb-177M*	T/A	F: GCGATCAGGTGACGCTAAAATGA	VIC-CCAAATTGCTTAACCC	4
			R: AGGAAGGTGATGCCTGAGAGA	FAM-CCAAATTGCTTTATCC	
75	*Ots_ARNT*	G/T	F: CCACTGGCTGTGGAGCTT	VIC-TACAGATGTCATTTTAC	9
			R: GGGTTCAGTGATAGTTGGGCAAAT	FAM-CTACAGATGTAATTTTAC	
76	*Ots_arp-436*	A/T	F: GCCCTGGAGAAGTACGTTTTAAACTAA	VIC-CTAGGTGAAACTTTTTTTAAA	11
			R: GCAACCATGTCAACATTGCACATAA	FAM-CTAGGTGAAACTTTTTAAAAA	
77	*Ots_AsnRS-60*	T/C	F: CCGACGCCTCACTGAGT	VIC-TGAGTCCCTGACCAGC	2
			R: TGGTTTTTCAGGTCATGGTTTCCA	FAM-AGTCCCCGACCAGC	
78	*Ots_aspat-196*	G/C	F: CCTGAACAGGTACACACAAACGA	VIC-CACACCCACTCTTTAT	4
			R: TCCAACTGATGAATATGACCAACATGAAT	FAM-CACACCCAGTCTTTAT	
79	*Ots_brp16-64*	T/C	F: ACTCTGGGTCCAGGAGGTTTT	VIC-AAGTCAGCATCTTTCA	15
			R: CTGACGAGACCATGCACCAA	FAM-AGTCAGCGTCTTTCA	
80	*Ots_C3N3*	T/G	F: CCGGATTCCATGGCCTACAC	VIC-CTAGAAAGGTTGATCCAATAA	1
			R: GCCAAAATGATGTTCGGATGTAAAGT	FAM-AAAGGTTGAGCCAATAA	
81	*Ots_Cath_D141*	T/C	F: CACTTGTTCTGCACACTACTTGTC	VIC-TGGGAAGCAATCAA	5
			R: CACACATGGATTTTGCCTGTCTAAA	FAM-AATTGGGAAGCAGTCAA	
82	*Ots_CCR7*	C/T	F: CTGCTCACCTGCATCAGTGT	VIC-CCACGTAGCGATCG	9
			R: CCATGGTGGTCTGGACGAT	FAM-ACCACATAGCGATCG	
83	*Ots_CD59-2*	G/A	F: TGTTTATCTCTGAGTGAAAAAGGTGTGT	VIC-CTAAAATGTCATGTAAATAT	9
			R: CATGTTACCCAGCTAAAAGTCTATAGCA	FAM-ACTAAAATGTCATATAAATAT	
84	*Ots_CD63*	A/C	F: TGCATGTTTTCTAACTGTGTTTTTGTGT	VIC-AGATCATGGGAATCATAT	9
			R: TGAATGCCCCCCATCAACA	FAM-ATCATGGGCATCATAT	

Table 2 (con't)

No.	Assay	VIC/ FAM	Primer Sequences	Probe Sequences	Ref
85	*Ots_CirpA*	C/T	F: GCTGTGATTGTGCTCTAAAGACATG	VIC-AATGCATTACAGAACTGA	12
			R: CTCCCACTTAGCATTCCTACCTT	FAM-AATGCATTACAAAACTGA	
86	*Ots_cox1-241*	C/T	F: CACTGAACTGTAAGCCATTGTGATT	VIC-CACTACGGTAAGACCAT	4
			R: GTAAATGTAGTATACAGTATAGGCATCGTAGGT	FAM-CACTACAGTAAGACCAT	
87	*Ots_DDX5-171*	C/T	F: ATGACCAATTGAAGAGTTCTTCCGT	VIC-TTCATAATTGAACGATTTCA	16
			R: CAAAGCCAAACGTCACATTTACACT	FAM-CATAATTGAACAATTTCA	
88	*Ots_E2-275*	A/G	F: GGTGCCACTTTAGTATAGCTGCTTA	VIC-CCCCCATATTGCTG	2
			R: CCCTACCCCCTGTGTTCCA	FAM-CCCCACATTGCTG	
89	*Ots_EndoRB1-486*	G/A	F: CCTTTGGGTCTGCTTGAGGTT	VIC-TCCTTCTCACGCTTCT	5
			R: GGAGCCAAATCCTAATGCTGAAGTA	FAM-CTCCTTCTCATGCTTCT	
90	*Ots_EP-529*	A/G	F: GCCCTGCCTGCAACTTC	VIC-CAGTGTCATTTTCGGC	10
			R: GAAACCAACGTCTTGATGTAGACCTA	FAM-ATCAGTGTCATCTTCGGC	
91	*Ots_Est1363*	A/T	F: GGTGATTTTGCCACAGAGTAGAGAT	VIC-CCATCCTGTCTTGTCTG	12
			R: AGTGTTAAATGTAACTTGCATATACAGGCAAT	FAM-CATCCTGTCATGTCTG	
92	*Ots_Est740*	T/C	F: GGACTCGTGCTTGAGGAAGATG	VIC-TCTGGATGGAACCGTTAG	12
			R: TGCATGGCTCCAACTCCTT	FAM-CTGGATGGAGCCGTTAG	
93	*Ots_ETIF1A*	A/C	F: TCTGAACTCACCAAAGGAACACTTG	VIC-CAACTGAAGAAAATAATATG	9
			R: GAGAGAAAAGGAGAAATGATTGCCATT	FAM-CTGAAGAAAAGAATATG	
94	*Ots_FARSLA-220*	G/A	F: GTTCGTGGGATTGTTCAATGTTCAT	VIC-CCTTGGATGGGATGTG	3
			R: CTTGGACAGGCTCACATTACCATA	FAM-CCTTGGATAGGATGTG	
95	*Ots_FGF6A*	G/T	F: TCAAAAATGTCTATCCAACAAATACTCTGAAAAATATTG	VIC-CACGATTAGCAATGAACAA	7
			R: CTTGTGCGCACCTTGCA	FAM-CACGATTAGCAATTAACAA	
96	*Ots_FGF6B_1*	A/C	F: GAGACAAAGGTTTGCAGGTTCATG	VIC-CCTGTTATCAGACCCAAAT	7
			R: GGGAGCCATGCACTAATATATTGGA	FAM-CTGTTATCAGCCCCAAAT	
97	*Ots_GCSH*	C/T	F: GTTCTTTTTAATGATGACTACAGGTCTTTCAC	VIC-TATCTGGGCGGGCTG	12
			R: GCTACTTTACATAATACCATTTGAGCTGAGA	FAM-CTATCTGGACGGGCTG	
98	*Ots_GDH-81x*	C/-	F: CTTTTCTGAATTAGTGCTGTGCTTGT	VIC-TGTTACGGGACATACT	4
			R: CCAACTTCTTCAACTCTGTCAGTGA	FAM-TCTGTTACGGACATACT	

Table 2 (con't)

No.	Assay	VIC/ FAM	Primer Sequences	Probe Sequences	Ref
99	*Ots_GH2*	A/T	F: GCGTACTGAGCCTGGATGACA	VIC-TGACTCTCAGCATCT	1
			R: CCCCCAGGTTCTGGTAGTAGTTC	FAM-TGACTCTCTGCATCTG	
100	*Ots_GPDH-338*	G/A	F: CACTAAATATTCCTTATCATTTCATACTAAGTCTGAAGAA	VIC-CCACTACTTAACGTGCTTT	2
			R: AGCTGATACACAATCAAAACACAAAACAT	FAM-CCACTACTTAACATGCTTT	
101	*Ots_GPH-318*	C/T	F: GGTGATAACAGGTGTTGCACCAA	VIC-ATCAAGCTGACGAACCA	3
			R: TCAGGTGGTGGTGGACAAC	FAM-CAAGCTGACAAACCA	
102	*Ots_GST-207*	G/A	F: GGAGAACATGCATCACCATTCAAG	VIC-ATGAGAGAGTCTTTCTCTGTT	3
			R: TCAGCAAACGAAGGCTATGTAGAAT	FAM-ATGAGAGAGTCTTTTTCTGTT	
103	*Ots_GTH2B-550*	C/G	F: TGACTACCCGTTGTACCAATGAAC	VIC-TTAATGCTGCAGATGTTAT	7
			R: CACAGGAAGGACGTGTTTTGATG	FAM-ATGCTGCACATGTTAT	
104	*Ots_HFABP-34*	C/T	F: CAAGAACACCGAGATCTCCTTCA	VIC-TCGAACTCCGCTCCTAG	16
			R: TCGGCGGTGGTCTCG	FAM-TCGAACTCCACTCCTAG	
105	*Ots_HMGB1-73*	G/T	F: TGCTTCAGTGAAAATAAGCGTGAGA	VIC-ACTGTATATGTTACGTTTTC	15
			R: GTCGAGCGGTATGAATACTTTCTGA	FAM-ACTGTATATGTTAAGTTTTC	
106	*Ots_hnRNPL-533*	A/T	F: TCTTTGATATTGAGCTCATAAAAGCAAGGT	VIC-CATTTACCAGTTCTCACACAC	3
			R: TCCTTGTTCATCCATCAGGCATAAAA	FAM-TTTACCAGTTCACACACAC	
107	*Ots_hsc71-5'-453*	C/T	F: TTGAGAACATGTGGTAATTAACTACAATGACTAA	VIC-CTGAGGTGGCAAAAT	6
			R: GTACGAAGTTGCGCCTTGTC	FAM-TGAGGTGACAAAAT	
108	*Ots_hsp27b-150*	G/A	F: TAGGAGTTGGAAAGACTGCACA	VIC-YGATCTGGACCAGGCT	6
			R: CCCATTGGTTCTTTGGTGTT	FAM-YGATTTGGACCAGGCT	
109	*Ots_Hsp90a*	G/C	F: ACAGTATACCGGCTGCCTATTCATA	VIC-ATTTGACTTGTCTTTTTG	5
			R: GTCGTTTTTCATAGAAAATAGCTCACAGTT	FAM-TTTGACTTGTGTTTTTG	
110	*Ots_HSP90B-100*	C/T	F: CACCTTAGTTCCACGCAACATG	VIC-TCTATGGTGTGATTCATT	3
			R: CTGCGTGTATTGTAGTGGTGACA	FAM-TTCTATGGTGTAATTCATT	
111	*Ots_HSP90B-385*	G/A	F: CCCTCTCAGCCACCAGGTA	VIC-ACCCACGCCAAACT	3
			R: CTAGGCTGGAGCTGACATCTC	FAM-AAACCCACACCAAACT	
112	*Ots_IGF-I.1-76*	A/T	F: GGTAGGCCGTCAGTGTAAAATAAGT	VIC-CTGCCTAGTTAAATAAAATA	2
			R: GATGGAGGCCACTGTGTTCTTA	FAM-CTGCCTAGTTAAATTAAATA	

Table 2 (con't)

No.	Assay	VIC/ FAM	Primer Sequences	Probe Sequences	Ref
113	*Ots_Ikaros-250*	G/A	F: GAGGCTGACTTGGACTTTGC	VIC-ACAGAAGATTTTCGGCTGC	2
			R: GGCCTGTCAGCCAAGGA	FAM-ACAGAAGATTTTCGACTGC	
114	*Ots_IL11*	T/C	F: CCTCCAGATGAGACCCACTCT	VIC-AGTCCGCATGGAGCT	9
			R: CAAAATGGTGCTCAAACGACTTCA	FAM-TCCGCGTGGAGCT	
115	*Ots_il13Ra2B-37*	T/G	F: AGGACTGGCTGCACATTCA	VIC-CCAGGGAATCTATCCCAG	16
			R: GAGGAGCTGTTCACACATATGTTG	FAM-CCAGGGAATCTCTCCCAG	
116	*Ots_il-1racp-166*	G/T	F: GCCAAGAAAGTGTAGCTCCAACATA	VIC-CCACATTCGTTTTTC	2
			R: AAGCAGAAACCCAGTAAGAAGGAAA	FAM-ACCACATTAGTTTTTC	
117	*Ots_IL8R_C8*	C/T	F: CGTGGTGTTCGCCTTCCT	VIC-CTGGACGCCGTTACA	9
			R: TGTCGGCCATCACTGTCATG	FAM-TGGACGCCATTACA	
118	*Ots_IsoT*	T/C	F: GACTCAGGTAAGGAAACATCAATGTCA	VIC-AACCAGTAGAATAACC	12
			R: GAAAGCAAAGCATTTTATCCACCACTA	FAM-CAGTGGAATAACC	
119	*Ots_LWSop-638*	T/C	F: CAATTACTCTTTCTCAGCCCTGTGT	VIC-TTTAACAAGAAAATTATACATTTC	2
			R: GCGGTAAGATGCAGTTTTACATGGA	FAM-CAAGAAAGTTATACATTTC	
120	*Ots_mapK-3'-309*	T/G	F: CGTGACCCTTGTAACTGAAAAGC	VIC-ATGCTATTAAATGAATATTC	11
			R: GGCCACTGTCATAGAATTAGGCATT	FAM-ATGCTATTAAATGACTATTC	
121	*Ots_mapKpr-151*	A/T	F: TGTTGTCTCGGACTGCATGAC	VIC-CATGCATTGCACATAC	11
			R: GAAGGCACAGAGATGAAGGACAT	FAM-CATGCAATGCACATAC	
122	*Ots_MHC1*	G/A	F: GTCCACATTCTCCAGTACATGTATGG	VIC-CATCATCCCGTGAGCAG	1
			R: CAAACCCCTCTGTCTGTTCAGT	FAM-TCATCATCCCATGAGCAG	
123	*Ots_MHC2*	T/G	F: GTCCTCAGCTGGGTCAAGAG	VIC-CTGGAGCGTTTCTGTA	1
			R: GTAGTGGAGAGCAGCGTTAGG	FAM-CTGGAGCGTGTCTGTA	
124	*Ots_mybp-85*	C/T	F: CAAGGGATGTGACAAATTAATCAAACACATAA	VIC-AGAGCATGTAGTTTTG	9
			R: AAGAGGTCTAATAAATCTCCAATGTAAAAACGT	FAM-AGCATGTAATTTTG	
125	*Ots_Myc-366*	T/C	F: CCTTAGCTGCTCTTTGAAGTTGACT	VIC-TCTCTGCTCATCTGTC	5
			R: GGCTATAGAGTGTATTTACAGCATGCA	FAM-CTCTGCTCGTCTGTC	
126	*Ots_myo1a-384*	A/C	F: CTCCCCCCTGGACTTTGG	VIC-ACAGATCCATCCACCACT	4
			R: GCTCTATTGCACCGTGTTCTG	FAM-AGATCCAGCCACCACT	

Table 2 (con't)

No.	Assay	VIC/ FAM	Primer Sequences	Probe Sequences	Ref
127	*Ots_myoD-364*	T/G	F: GTGTGTGTGTGTGTGTCATC	VIC-TCATCTTTTGTTATTTCCTTG	4
			R: TTTACACATATACAAAAATGGTCCTCTATTGTCAT	FAM-ATCTTTTGTTCTTTCCTTG	
128	*Ots_nelfd-163*	A/G	F: CTCACTGCAAATCCAACTTCATCAT	VIC-ACCCACCAGTGTCATT	15
			R: CCACTACATCCTCATCCAAGGTT	FAM-CCACCAGCGTCATT	
129	*Ots_NFYB-147*	C/T	F: CCGTCCACAGCACAAGACTATAATA	VIC-TGTTCCAATGTAAAATGTATGC	15
			R: CAGATGATAGCTTCAGTAAGTGGTTCA	FAM-TTCCAATGTAAAATATATGC	
130	*Ots_nkef-192*	C/T	F: CATTTAGCAGACACTCTTATCTTAGTGTCA	VIC-AATAGGCCGACATCAA	4
			R: CGAATGTCCACCTCAGATGTTACAA	FAM-AAATAGGCCAACATCAA	
131	*Ots_NOD1*	C/G	F: GTGCTGCAGGAACCATGTG	VIC-CCAACGGCGACTTG	7
			R: CTGTGTGGACTGCTGTCTAAGG	FAM-CCAACGCCGACTTG	
132	*Ots_ntl-255*	T/A	F: TGCAGTTACAAGCCTAAGACAATCT	VIC-TTGTAGAGGAAGAATATTC	11
			R: CAACTAAAGTAACACACCAGCAACTG	FAM-TTGTAGAGGAAGTATATTC	
133	*Ots_ALDBINT1-SNP1*	T/C	F: CGCTGGGCATGGATGAGT	VIC-CTACTGTTGTATTTTCTC	5
			R: GGCCAACACTGCTACTTCCT	FAM-CTGTTGTGTTTTCTC	
134	*Ots_DESMIN19-SNP1*	C/A	F: GGTCTGTCTGTCTGTCTATCTGTCA	VIC-CCAGTCATGGGTCATT	5
			R: TGTGTGTCTTTGTTCATTCCTACCA	FAM-TCCAGTCATTGGTCATT	
135	*Ots_NAML12-SNP1*	A/G	F: TGCCACCTCAGTTTTAGTGTTATATCC	VIC-AAACCATTTTCATTCTTTTG	5
			R: AGCGCCAACCTGTCACT	FAM-CCATTTTCACTCTTTTG	
136	*Ots_Ots311-101x*	A/-	F: AAATGAGGCCGTCCTTTACACT	VIC-CTGAGATCACTTTGAGCAC	4
			R: GCAATACAAGCCCTTGATAATGAAGT	FAM-ACTGAGATCACTGAGCAC	
137	*Ots_BMP2-SNP1*	C/T	F: ACTGCCACAGACACGAACTC	VIC-CCCACTTCGCTGAAGT	5
			R: GCCACTATCCACTCGTTCCA	FAM-CCCACTTCACTGAAGT	
138	*Ots_MTA-SNP1*	C/T	F: GCCGAAAAATAAGCGATTAGTGATGA	VIC-AATTGCCTCATTGGGTG	5
			R: GCCCCATGGTAAACCTAATTAACCT	FAM-AATTGCCTCATTAGGTG	
139	*Ots_TF1-SNP1*	G/T	F: CGGACAAAGAGCTACAGAAATGC	VIC-CCGCCACCTTGGCT	5
			R: CGTCCCTCTTCACGCATGA	FAM-CGCCACATTGGCT	
140	*Ots_P450*	T/A	F: TGAGCGAGATTTATCAAACTGTCAAAGA	VIC-CCCCGAAGTACTTTT	1
			R: CCCAAGCGGGAGAACTTACAG	FAM-CCCGAAGAACTTTT	

Table 2 (con't)

No.	Assay	VIC/ FAM	Primer Sequences	Probe Sequences	Ref
141	*Ots_P450-288*	A/G	F: ATGTCAATATATTTCACTATAATGATTGGAAGCCA	VIC-CTATAAAGTTGGACAGTTGG	14
			R: CACTGAACTCGAAGCTGTTAGGA	FAM-AAAGTTGGGCAGTTGG	
142	*Ots_P53*	G/A	F: GGAACTTCCTCTCCCGTTCTG	VIC-CTGGGTCGGCGCT	1
			R: GCACACACACGCACCTCAA	FAM-TGGGTCGACGCTC	
143	*Ots_parp3-286*	A/G	F: AGTCAGTGTTGGTGTAGTGAAGAGA	VIC-AGTTACAAGTGGTGTTTCA	11
			R: CATTTGTGGAGTGTTTATTGAACAGTAACA	FAM-ACAAGTGGCGTTTCA	
144	*Ots_PGK-54*	T/A	F: CTCATACTTTGTACCTGTGTGTTCCA	VIC-CCACCATCAAGCACTG	7
			R: CGACCCAAGTGGCTCATCAG	FAM-CCACCATCATGCACTG	
145	*Ots_pop5-96*	T/C	F: CTCTTGCTACTTGCAGTGTATCTCA	VIC-TTCTGTTACTGGACTGATG	11
			R: AGTTTGAGGGCTCTATTCTGTCATG	FAM-CTGTTACTGGGCTGATG	
146	*Ots_ppie-245*	C/A	F: TGTTTTTGGTCATGTATTTTCTCTGCTATTTTT	VIC-ATGTCTGAAATGAAAGCC	11
			R: GGACTGGAGCTGCTGAACATA	FAM-AATGTCTGAAATTAAAGCC	
147	*Ots_Prl2*	A/G	F: CCTGGTCTGTTTGTGATCAAGATG	VIC-ATGTATTGTTCATTTAATG	1
			R: GGTTAACTCAAATAGAACATACTCTGACACA	FAM-TGTATTGTTCGTTTAATG	
148	*Ots_RAG3*	C/T	F: CATTTCCACGAAAAGCCAGATGAC	VIC-CTCTACAGTATGAACTATG	7
			R: ACAGAATAAAGTATCTTCCTCTTACATCACTACTAAT	FAM-CTCTACAATATGAACTATG	
149	*Ots_redd1-187*	A/G	F: TTCTGGGTTGCCATACTCTTTCAAT	VIC-ATTCTGACAGCTGTTTTG	11
			R: AGTTGAGACCTTCAGTTCTTAGGGTAT	FAM-CTGACAGCCGTTTTG	
150	*Ots_RFC2-558*	A/-	F: GTAAGGTCTACTCCGGTTGTATTCG	VIC-TGCATGTAACAAATAACAT	2
			R: CAATACGACAGTACCGGTGTTAAACT	FAM-TGCATGTAACATAACAT	
151	*Ots_S7-1*	T/C	F: TGCCATCATAAACAACCTAACAAGTAACT	VIC-TACAGGAGATAAGGTCGCA	7
			R: CCTGGTTTAAAAACGGCCAACTG	FAM-CAGGAGATAGGGTCGCA	
152	*Ots_SClkF2R2-135*	A/T	F: CCAAATACAGACCAGCTACTTGTGT	VIC-ATTCAAAGTCAAATTTT	2
			R: CTTCAAGTCCCTGAATAATGGTACGT	FAM-ATTCAAAGTCTAATTTT	
153	*Ots_SL*	A/G	F: AATATTGGCTTTCTGAGAATGCATTTGG	VIC-TCAAAGATATGATTCAATTAA	1
			R: CCAAGATACTTCCTTTAACTTCTCTGTCA	FAM-AAGATATGGTTCAATTAA	
154	*Ots_stk6-516*	C/A	F: TGTGTTTAGGATTGAACTGACCATGTT	VIC-AACATAACGGACTCCC	15
			R: GTAAACTCCACCTGCAAGAAGGA	FAM-TAGAACATAACTGACTCCC	

Table 2 (con't)

No.	Assay	VIC/ FAM	Primer Sequences	Probe Sequences	Ref
155	*Ots_SWS1op-182*	T/A	F: TCAAAGACATCGAACACAAGAACGA	VIC-ATGTACTTTAACGATTCATTT	2
			R: GCAGGTAAATTCAAACGTCATCATAAGAA	FAM-ATGTACTTTAACGTTTCATTT	
156	*Ots_TAPBP*	C/T	F: TTTCTCATCCTTCTCTCTTCCAGTCT	VIC-CTGGACAGCTGGTCC	9
			R: GGACAAACCAGCACTCCAGAA	FAM-CTGGACAACTGGTCC	
157	*Ots_TCTA-58*	C/T	F: ACCAGTACCTAAACGTTAGAAAGCAA	VIC-CTGCCATGAAGTGCTAG	16
			R: CGTTAGTTAGCTATGTCTGAAAGGCA	FAM-TGCCATGAAATGCTAG	
158	*Ots_Tf-3545*	C/G	F: TGCTCTAAGGCTCAACTGATCCTA	VIC-CTGGTCATGGCTGTCA	14
			R: GCTGATGGCCCTCAAGGTA	FAM-CTGGTCATCGCTGTCA	
159	*Ots_TGFB*	C/T	F: GCCTCACATTTTACTGATGTCACTTC	VIC-CTTCCGAGAGCTAGGCT	9
			R: GAGCAGATCTCTTCAGTAGTGGTTT	FAM-CTTCCGAGAACTAGGCT	
160	*Ots_Thio*	T/C	F: TTTTAAAAATGGAGATAAACTCCTGACCTGAA	VIC-CAGTGTATTAGTCATTCTTA	12
			R: AATACCAAACCATGCCACTAATACCT	FAM-CAGTGTATTAGTCGTTCTTA	
161	*Ots_TLR3*	C/T	F: TGCACCTGCGAGAGCAT	VIC-CTGTGGTTTGTGGCGTG	9
			R: CTGGCGTTTGTTCCGTTCAG	FAM-CTGTGGTTTGTAGCGTG	
162	*Ots_Tnsf*	A/G	F: GCCAATACGGGTTCTGAACTGT	VIC-TGCTCCAGATCTC	1
			R: CGGAATAGTCATAGTAGGGCTCGTT	FAM-TGCTCCAGGTCTC	
163	*Ots_tpx2-125*	C/T	F: TGTTGTAATCTTTCTGAATATTTGCTTGCTT	VIC-CAGGCGGTTCTCC	15
			R: TCTTCCAAATTGAGCACAAAAGCAT	FAM-CAGGCAGTTCTCC	
164	*Ots_txnip-321*	T/C	F: CCTTCAAACTAACACATCATAGACATGCTT	VIC-TCTGGCGGATTTACA	11
			R: TTATCAAACTGAAGGCGGATTTACTGA	FAM-CTGGCGGGTTTACA	
165	*Ots_u07-07.161*	C/T	F: GTCAACAAATGCAGGTAACATAAATGGT	VIC-ATCAGTGACATAAGTTGTCCA	8
			R: GATGCAAACACCTGTGAAATTGTGA	FAM-TCAGTGACATAAATTGTCCA	
166	*Ots_u07-17.135*	A/G	F: CTCGCCTCTGTCATTGTATTACCTT	VIC-AAAATGTACCACATACTTGT	8
			R: TGACACACGAGCCATTTTGATGAT	FAM-AAATGTACCACATACTCGT	
167	*Ots_u07-18.378*	A/T	F: GGAAACCAGCTAGGATTCAGGAA	VIC-ATATGGTATGTAGAGGCTAGTTA	8
			R: CGTTATATGGTTTGCTTGTTTGCGATA	FAM-TATGTAGAGGCAAGTTA	
168	*Ots_u07-19.260*	C/T	F: GGATGTAGAGTGAAATCACCTTCGA	VIC-CTTTAGACTGGTGGACTC	8
			R: GCAGACTGACTGGTTTAGTTTAACG	FAM-CTTTAGACTAGTGGACTC	

Table 2 (con't)

No.	Assay	VIC/ FAM	Primer Sequences	Probe Sequences	Ref
169	*Ots_u07-25.325*	T/C	F: AGACAATCATGGTGTTTTGAGTCTTTCT	VIC-CCGCTTGAAAGTTTGA	8
			R: GCCTAGGCTTGATGGAGTCA	FAM-CGCTTGAAGGTTTGA	
170	*Ots_u07-49.290*	G/A	F: GCTGAGGAAGGATTCTGTATTTGCT	VIC-CTTTCCCCGTGTTGGT	8
			R: TCGGACAGAGCGCATCC	FAM-ACTTTCCCTGTGTTGGT	
171	*Ots_u07-53.133*	C/T	F: AGCTAGGCTGTAAATGCAAGGAT	VIC-TAACACATGTTGGAGGTC	8
			R: CAGTGCTTTCAATTCATGCTGTCAA	FAM-AACACATGTTAGAGGTC	
172	*Ots_u07-57.120*	A/T	F: GGTTTGAGCCAATCAGTTGTGTT	VIC-CAACCCCTACCTTGTCAC	8
			R: CGGTCTAATGTCCATTGCTCATGTT	FAM-CCCCTACCATGTCAC	
173	*Ots_u1002-75*	T/C	F: CCGCCTTTCCCACCTTCTC	VIC-ATGGCCCTTACACTATC	15
			R: TCAAACGAGAACACACTAAGGTTGT	FAM-TGGCCCTTACGCTATC	
174	*Ots_u1007-124*	A/G	F: CGAAATAAGGGCCTGGTGTTTAAAA	VIC-TGTCCTGTCCTCAGATCA	15
			R: TGTACCAGGTGGAAGCTTTGG	FAM-TCCTGTCCCCAGATCA	
175	*Ots_u202-161*	T/A	F: CACTTTTGACTTTACATGGAACTTAACTCAT	VIC-ATTAGCTGCTAAGCACTAG	2
			R: GGGACTTCACTTTCTACAAACATGTCA	FAM-ATTAGCTGCTATGCACTAG	
176	*Ots_u211-85*	C/T	F: TGGTGAGAGCAGCTTTAAATGTCTT	VIC-TCCCAAAGTCGAGTGTG	2
			R: ACCCATTCTTCTGTCTGGTTTAAGC	FAM-CCCAAAGTCAAGTGTG	
177	*Ots_U2362-227*	A/T	F: TCGTGGATTGTGGCTTACGT	VIC-CTTAAGAAGCATTTTTTTG	16
			R: GGGTGTTTAACAAGTAGTCCCTTCA	FAM-AAGAAGCATTTATTTTTG	
178	*Ots_U2362-330*	A/G	F: AATGGGTAACAAAGAAATAGCTAGCTACTT	VIC-ACTGGGAAGATTGTTTG	16
			R: GACAGACCACAGTGAAGGTGAAA	FAM-CTGGGAAGACTGTTTG	
179	*Ots_U2446-123*	C/A	F: CTGGTCTGTGACGTCAAAATGATG	VIC-CTGCAACTCGACGCAAG	16
			R: AGCTAGACCAGGCCATTTGAG	FAM-ACTGCAACTCTACGCAAG	
180	*Ots_u6-75*	C/T	F: GAAAAAGTAAAGTAAAAGTAAAGTATTATACCACTAAAGACAAT	VIC-TTAGTCAACTGTTGTTTTT	2
			R: GATCCACACTGTTGGTCTACTACAA	FAM-TTAGTCAACTGTTATTTTT	
181	*Ots_unk1104-38*	C/T	F: TAACCATGACTTCTATCAATCACCCC	VIC-CCACTAAGGATTACGTTACG	16
			R: CCTCCATACATCGTCAAAGCTGTA	FAM-CACTAAGGATTACATTACG	
182	*Ots_unk1832-39*	C/T	F: GAAACGTCTATGCTGTCCCCTTTAA	VIC-CACCACTAGAACTCTC	16
			R: CTGCAGTATTAGCTCTAGTTGAATCCA	FAM-CACCACTAAAACTCTC	

Table 2 (con't)

No.	Assay	VIC/ FAM	Primer Sequences	Probe Sequences	Ref
183	*Ots_unk3513-49*	C/T	F: TTTGAGTGAGTCACTGCACCAA	VIC-AGTGCGAAGAACC	16
			R: CAGCTCCACAGTGTCACCAT	FAM-AGTGCAAAGAACC	
184	*Ots_unk526*	A/G	F: TCAAGACTGTGCTGTAGTTGTCTAC	VIC-CAACATTCCAGTCTGAAAC	7
			R: CCTCCCCCTTTTCCACATCAG	FAM-CATTCCAGCCTGAAAC	
185	*Ots_unk7936-50*	C/G	F: ATGGGTTGGGATTATGGTTCATTGT	VIC-AGACATGTAGCTATGTAGGTAA	16
			R: CAAAATGGTTACTTGCATAGTCTTTTGT	FAM-AGACATGTAGCTATCTAGGTAA	
186	*Ots_unk8200-45*	A/G	F: TCAGGAGTGAAGCTGGTCTCT	VIC-CAGTTTAAAGTGTATTCTCC	16
			R: TTCCATAGTAACTGACCTCAGTGTCT	FAM-TTTAAAGTGCATTCTCC	
187	*Ots_unk9480-51*	G/C	F: CAAATCAGAACAAAACCTCCCACAA	VIC-CTCCCACAAACCC	16
			R: GGAAGTCTGTCTGAATGGTTGTCTT	FAM-TCCCAGAAACCC	
188	*Ots_USMG5-67*	C/T	F: GGGCAATGGTGGCTATGCT	VIC-TCTTGCTCACGTATGCA	15
			R: CGTATGTTGTTCTGTCCACAGTGT	FAM-CTTGCTCACATATGCA	
189	*Ots_vatf-251*	G/-	F: CTTTTCGGGTTATTCATGCTGTTGT	VIC-AGACCACAAGATACAGTACC	11
			R: GCAAGCATTTGAAAAACAGACTGGAT	FAM-AGACCACAAGATA--GTACC	
190	*Ots_zn593-346*	A/T	F: CTACGCGAGAAATAACACTTTTCAAAACT	VIC-TCTTGCAATCATTTTTAAC	15
			R: GGCGAGTTTATTACGGTGTTATGAC	FAM-CTTGCAATCATATTTAAC	
191	*Ots_zP3b-215*	G/T	F: TGCTGAGGACCATCTGCAATTC	VIC-CCAAATATCCTACCCGTGATG	2
			R: AGGTCCATGAATAACTGAAAATGTACAAGT	FAM-CAAATATCCTACCAGTGATG	
192	*Ots_SEXY3-1*	X/Y	F: GGTCTTGCAGTCAGGAGAGG		13
			R: CCAGGTGGTGAAGGTAGGAA	FAM-ATCTCCACTTCGCTGA	
	Ots_SEXY3-1 AC		F: TCCTTGTGTCTAAAGGGCTTTGAG	VIC-CAGAATTAGCTTTGGACATT	
			R: GGGCTTGCTAGTCCTAAACAGATC		

1- Smith et al. (2005b); 2- Smith et al. (2005a); 3- Smith et al. (2007); 4- Campbell and Narum (2008); 5- Clemento et al. (2011); 6- Campbell and Narum (2009); 7-Unpublished Northwest Fisheries Science Center. Contact Anna Elz - Anna.Elz@noaa.gov ; 8-Unpublished Washinton Department of Fish and Wildlife. Contact Sewall Young - Sewall.Young@wdfw.wa.gov
9-Unpublished Washington State University - Vancouver. Contact Jennifer DeKoning - dekoning@vancouver.wsu.edu ;' 10-Unpublished Oregon State University. Contact Renee Bellinger renee.bellinger@oregonstate.edu; 11-Unpublished Columbia River Inter-Tribal Fish Commission. Contact Nathan Campbell - camn@critfc.org ;12-Miller et al. (2008a) ; 13-Sex determination marker-based on GenBank sequence DQ393586.; 14-Unpublished Alaska Department of Fish and Game. Contact Bill Templin - Bill.Templin@alaska.gov 15-Unpublished University of Washington & Washington Department of Fish and Wildlife. Contact - Lseeb@uw.edu 16-Unpublished University of Washington. Contact Lisa Seeb - Lseeb@uw.edu

Table 3. SNPs used in each evaluation panel. The count of the number of included panels for each SNP is also given.

SNP Number	SNP Name	F_{ST}			f_{ORCA}			PCA	Count
		Pop	Genetics	PSC-CTC	Pop	Genetics	PSC-CTC		
1	*Ots_100884-287*							X	1
2	*Ots_101119-381*	X	X	X	X	X	X		6
3	*Ots_101554-407*	X	X		X	X	X		5
4	*Ots_101704-143*	X	X			X		X	4
5	*Ots_102213-210*				X		X		2
6	*Ots_102414-395*			X	X		X	X	4
7	*Ots_102420-494*			X	X	X		X	4
8	*Ots_102457-132*	X	X	X			X	X	5
9	*Ots_102801-308*			X	X		X		3
10	*Ots_102867-609*				X	X			2
11	*Ots_103041-52*	X	X	X		X	X		5
12	*Ots_103122-180*	X	X	X	X	X		X	6
13	*Ots_104063-132*			X			X		2
14	*Ots_104415-88*	X	X		X	X			4
15	*Ots_104569-86*			X		X	X		3
16	*Ots_105105-613*	X	X			X	X	X	5
17	*Ots_105132-200*	X	X	X	X	X	X	X	7
18	*Ots_105385-421*	X	X	X	X	X	X		6
19	*Ots_105407-117*				X				1
20	*Ots_106499-70*				X			X	2
21	*Ots_106747-239*				X			X	2
22	*Ots_107074-284*		X					X	2
23	*Ots_107285-93*			X			X		2
24	*Ots_107806-821*				X		X	X	3
25	*Ots_108007-208*	X	X		X	X	X		5
26	*Ots_108390-329*			X	X	X	X		4
27	*Ots_108735-302*	X	X	X	X	X	X	X	7
28	*Ots_108820-336*	X	X	X	X	X		X	6
29	*Ots_109525-816*						X		1
30	*Ots_109693-392*			X					1
31	*Ots_110064-383*			X		X	X	X	4
32	*Ots_110201-363*			X			X	X	3
33	*Ots_110495-380*	X	X	X	X	X	X	X	7
34	*Ots_110551-64*								0
35	*Ots_110689-218*						X		1
36	*Ots_111681-657*			X					1
37	*Ots_112301-43*	X	X	X		X	X	X	6
38	*Ots_112419-131*		X	X		X	X		4
39	*Ots_112820-284*								0
40	*Ots_112876-371*			X	X	X	X	X	5
41	*Ots_113457-40*	X	X		X	X		X	5
42	*Ots_115987-325*	X	X		X	X		X	5
43	*Ots_117242-136*			X			X		2

Table 3 (con't)

SNP Number	SNP Name	F_{ST}			f_{ORCA}			PCA	Count
		Pop	Genetics	PSC-CTC	Pop	Genetics	PSC-CTC		
44	*Ots_117259-271*	X	X		X	X	X	X	6
45	*Ots_117432-409*				X			X	2
46	*Ots_118175-479*			X	X		X		3
47	*Ots_118205-61*								0
48	*Ots_122414-56*	X	X	X	X	X	X	X	7
49	*Ots_123048-521*				X	X			2
50	*Ots_123921-111*								0
51	*Ots_124774-477*	X	X	X		X			4
52	*Ots_127236-62*	X	X			X		X	4
53	*Ots_127760-569*	X	X		X	X			4
54	*Ots_128302-57*	X	X	X	X	X	X		6
55	*Ots_128693-461*				X			X	2
56	*Ots_128757-61*			X			X	X	3
57	*Ots_129144-472*	X	X		X		X		4
58	*Ots_129170-683*						X		1
59	*Ots_129458-451*	X	X			X			3
60	*Ots_130720-99*	X	X	X	X	X		X	6
61	*Ots_131460-584*	X	X		X	X		X	5
62	*Ots_131906-141*						X	X	2
63	*Ots_94857-232*			X	X		X	X	4
64	*Ots_94903-99*			X	X			X	3
65	*Ots_96222-525*			X				X	2
66	*Ots_96500-180*	X	X	X		X		X	5
67	*Ots_96899-357*	X	X						2
68	*Ots_97077-179*	X	X	X	X		X		5
69	*Ots_99550-204*					X			1
70	*Ots_AldB1-122*				X				1
71	*Ots_aldb-177M*	X	X		X		X	X	5
72	*Ots_ALDBINT1-SNP1*	X	X		X	X	X	X	6
73	*Ots_ARNT*	X	X	X	X	X			5
74	*Ots_arp-436*	X	X		X		X		4
75	*Ots_AsnRS-60*			X	X			X	3
76	*Ots_aspat-196*	X	X		X				3
77	*Ots_BMP2-SNP1*				X				1
78	*Ots_brp16-64*				X	X		X	3
79	*Ots_C3N3*	X	X	X	X	X		X	6
80	*Ots_Cath_D141*			X			X	X	3
81	*Ots_CD59-2*			X			X	X	3
82	*Ots_CD63*	X	X					X	3
83	*Ots_CirpA*	X	X	X	X	X		X	6
84	*Ots_cox1-241*	X	X	X	X	X	X	X	7
85	*Ots_DDX5-171*	X	X	X	X	X	X		6
86	*Ots_E2-275*	X	X	X	X	X	X	X	7
87	*Ots_EP-529*						X		1

Table 3 (con't)

SNP Number	SNP Name	F_{ST}			f_{ORCA}			PCA	Count
		Pop	Genetics	PSC-CTC	Pop	Genetics	PSC-CTC		
88	*Ots_Est1363*	X	X			X	X	X	5
89	*Ots_Est740*			X				X	2
90	*Ots_ETIF1A*	X	X		X	X		X	5
91	*Ots_FARSLA-220*	X	X	X	X	X	X	X	7
92	*Ots_FGF6A*	X	X	X	X	X	X	X	7
93	*Ots_FGF6B_1*			X		X	X	X	4
94	*Ots_GCSH*	X	X		X	X	X	X	6
95	*Ots_GDH-81x*				X	X			2
96	*Ots_GH2*	X	X			X	X		4
97	*Ots_GPDH-338*	X		X					2
98	*Ots_GPH-318*								0
99	*Ots_GST-207*			X	X				2
100	*Ots_GTH2B-550*	X	X			X	X		4
101	*Ots_HFABP-34*								0
102	*Ots_HMGB1-73*	X	X	X		X			4
103	*Ots_hnRNPL-533*	X	X	X		X	X	X	6
104	*Ots_hsc71-5'-453*	X	X						2
105	*Ots_hsp27b-150*	X	X	X		X		X	5
106	*Ots_Hsp90a*	X	X		X	X	X	X	6
107	*Ots_HSP90B-100*	X	X			X	X	X	5
108	*Ots_HSP90B-385*			X		X	X	X	4
109	*Ots_IGF-I.1-76*	X	X			X	X		4
110	*Ots_Ikaros-250*	X	X	X			X		4
111	*Ots_IL11*	X					X	X	3
112	*Ots_il13Ra2B-37*							X	1
113	*Ots_il-1racp-166*								0
114	*Ots_IL8R_C8*	X	X		X	X		X	5
115	*Ots_IsoT*	X	X				X		3
116	*Ots_LWSop-638*	X	X						2
117	*Ots_mapK-3'-309*	X	X	X	X	X	X	X	7
118	*Ots_mapKpr-151*	X	X	X		X	X	X	6
119	*Ots_MHC1*	X	X	X		X	X	X	6
120	*Ots_MHC2*	X	X			X	X	X	5
121	*Ots_MTA-SNP1*			X	X		X		3
122	*Ots_mybp-85*			X		X	X	X	4
123	*Ots_Myc-366*								0
124	*Ots_myo1a-384*			X	X		X		3
125	*Ots_myoD-364*	X	X	X	X	X		X	6
126	*Ots_NAML12-SNP1*			X	X		X	X	4
127	*Ots_nelfd-163*	X	X	X	X	X		X	6
128	*Ots_NFYB-147*	X		X	X		X		4
129	*Ots_nkef-192*	X	X			X		X	4
130	*Ots_NOD1*	X	X		X	X			4
131	*Ots_ntl-255*			X	X	X			3

Table 3 (con't)

SNP Number	SNP Name	F_{ST}			f_{ORCA}			PCA	Count
		Pop	Genetics	PSC-CTC	Pop	Genetics	PSC-CTC		
132	*Ots_Ots311-101x*	X	X						2
133	*Ots_P450-288*	X	X		X	X	X	X	6
134	*Ots_P450*	X	X	X	X	X	X		6
135	*Ots_P53*						X	X	2
136	*Ots_parp3-286*			X	X		X		3
137	*Ots_PGK-54*	X	X		X	X	X	X	6
138	*Ots_pop5-96*			X			X		2
139	*Ots_ppie-245*	X	X	X	X	X		X	6
140	*Ots_Prl2*						X	X	2
141	*Ots_RAG3*	X	X			X			3
142	*Ots_redd1-187*					X			1
143	*Ots_RFC2-558*	X	X	X		X			4
144	*Ots_S7-1*							X	1
145	*Ots_SClkF2R2-135*			X				X	2
146	*Ots_SL*	X	X	X	X	X	X	X	7
147	*Ots_stk6-516*								0
148	*Ots_SWS1op-182*			X			X	X	3
149	*Ots_TAPBP*	X	X	X	X	X	X	X	7
150	*Ots_TCTA-58*		X	X	X		X		4
151	*Ots_TF1-SNP1*	X	X		X	X		X	5
152	*Ots_Tf-3545*			X	X				2
153	*Ots_TGFB*				X			X	2
154	*Ots_Thio*			X				X	2
155	*Ots_TLR3*			X		X	X	X	4
156	*Ots_Tnsf*	X	X		X	X	X	X	6
157	*Ots_tpx2-125*	X	X						2
158	*Ots_txnip-321*			X	X		X		3
159	*Ots_u07-07.161*			X	X			X	3
160	*Ots_u07-17.135*			X	X		X		3
161	*Ots_u07-18.378*	X	X		X	X			4
162	*Ots_u07-19.260*			X			X	X	3
163	*Ots_u07-25.325*	X	X			X	X		4
164	*Ots_u07-49.290*						X	X	2
165	*Ots_u07-53.133*	X	X	X	X		X	X	6
166	*Ots_u07-57.120*	X	X	X		X		X	5
167	*Ots_u1002-75*			X			X	X	3
168	*Ots_u1007-124*								0
169	*Ots_u202-161*	X	X	X		X			4
170	*Ots_u211-85*	X	X	X	X	X		X	6
171	*Ots_U2362-227*			X		X	X		3
172	*Ots_U2362-330*	X	X		X	X			4
173	*Ots_U2446-123*	X	X	X	X	X		X	6
174	*Ots_u6-75*								0
175	*Ots_unk1104-38*	X	X		X	X		X	5

Table 3 (con't)

SNP Number	SNP Name	F_{ST}			f_{ORCA}			PCA	Count
		Pop	Genetics	PSC-CTC	Pop	Genetics	PSC-CTC		
176	*Ots_unk1832-39*	X			X	X		X	4
177	*Ots_unk3513-49*		X		X	X		X	4
178	*Ots_unk526*			X	X		X		3
179	*Ots_unk7936-50*			X	X		X		3
180	*Ots_unk8200-45*	X	X	X			X		4
181	*Ots_unk9480-51*	X	X	X		X			4
182	*Ots_USMG5-67*								0
183	*Ots_vatf-251*	X	X		X	X	X		5
184	*Ots_zn593-346*			X	X		X		3
185	*Ots_zP3b-215*								0

Appendix 1. SNPs initially evaluated during Phase I. SNPs included in the 192 for Phase II evaluation are marked with an "X". Source of the assay, resolution (1= very good, 2= good, 3 = poor, and 4 = not evaluated) as scored by individual laboratories, laboratory vote, difference between minimum and maximum allele frequency across the study area, and information on contribution to existing panels are given. Laboratory vote includes: PROTECT, DROP, and NR (no recommendation).

SNP Name	Assay Source[1]	Included in 192	Resolution[1]			Laboratory Vote[1]				Allele Freq (Max - Min)	Existing Panels[1]	
			UW	USFWS	WDFW	WDFW	IDFG/CRITFC	ADFG	SWFSC		SWFSC	IDFG/CRITFC
Ots_100884-287	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.22	PBT	PBT
Ots_101119-381	swfsc103	X	1	1	1	NR	NR	NR	NR	0.60	PBT	
Ots_101554-407	swfsc103	X	1	2	1	NR	PROTECT	NR	NR	0.66		PBT
Ots_101704-143	swfsc103	X	1	2	1	NR	PROTECT	NR	NR	0.42	PBT	PBT
Ots_102213-210	swfsc103	X	2	1	1	NR	DROP	NR	PROTECT	0.18	PBT	
Ots_102414-395	critfc21v3.0	X	1	1	1	NR	PROTECT	NR	NR	0.19	PBT	SNP/PBT
Ots_102420-494	swfsc103	X	3	3	3	DROP	DROP	DROP	PROTECT	0.38	PBT	
Ots_102457-132	swfsc103	X	1	1	1	NR	NR	NR	NR	0.63	PBT	
Ots_102801-308	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.37	PBT	PBT
Ots_102867-609	swfsc103	X	3	2	2	NR	DROP	DROP	PROTECT	0.54	PBT	
Ots_103041-52	swfsc103	X	1	1	1	NR	NR	NR	NR	0.61	PBT	
Ots_103122-180	swfsc103	X	1	2	1	NR	PROTECT	NR	NR	0.99		PBT
Ots_104063-132	swfsc103	X	3	3	2-3	DROP	DROP	DROP	PROTECT	0.25	PBT	
Ots_104415-88	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.56		PBT
Ots_104569-86	swfsc103	X	2	2	2	NR	DROP	NR	PROTECT	0.38	PBT	
Ots_105105-613	critfc21v3.0	X	1	1	1	NR	PROTECT	NR	NR	0.22	PBT	SNP/PBT
Ots_105132-200	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.59	PBT	PBT
Ots_105385-421	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.41		PBT
Ots_105407-117	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.25	PBT	PBT
Ots_106499-70	swfsc103	X	1	2	1	NR	NR	NR	NR	0.46	PBT	
Ots_106747-239	critfc21v3.0	X	1	1	1	NR	PROTECT	NR	NR	0.46	PBT	SNP
Ots_107074-284	swfsc103	X	1	1	1	NR	NR	NR	NR	0.77	PBT	
Ots_107285-93	swfsc103	X	1	2	1	NR	NR	NR	NR	0.37	PBT	
Ots_107806-821	swfsc103	X	3	3	2	NR	DROP	DROP	PROTECT	0.25	PBT	
Ots_108007-208	swfsc103	X	1	1	1	NR	NR	NR	NR	0.68	PBT	
Ots_108390-329	swfsc103	X	1	1	1	NR	NR	NR	NR	0.49	PBT	
Ots_108735-302	swfsc103	X	3	3	2	NR	DROP	DROP	PROTECT	0.29	PBT	
Ots_108820-336	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.66		PBT
Ots_109525-816	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.20		PBT

Appendix 1 (con't)

SNP Name	Assay Source[1]	Included in 192	Resolution[1]			Laboratory Vote[1]				Allele Freq (Max - Min)	Existing Panels[1]	
			UW	USFWS	WDFW	WDFW	IDFG/CRITFC	ADFG	SWFSC		SWFSC	IDFG/CRITFC
Ots_109693-392	swfsc103	X	1	2	1	NR	NR	NR	NR	0.27	PBT	
Ots_110064-383	critfc21v3.0	X	1	1	1	NR	PROTECT	NR	NR	0.09	PBT	SNP/PBT
Ots_110201-363	swfsc103	X	1	2	1	NR	PROTECT	NR	NR	0.39	PBT	PBT
Ots_110495-380	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.66	PBT	PBT
Ots_110551-64	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.06	PBT	PBT
Ots_110689-218	swfsc103	X	3	3	2	NR	PROTECT	NR	DROP	0.15	PBT	PBT
Ots_111084b-619	swfsc103	X	1	1	1	NR	NR	NR	NR	0.82		
Ots_111666-408	swfsc103	X	3	3	3	DROP	DROP	DROP	PROTECT	0.54	PBT	
Ots_111681-657	swfsc103	X	1	1	1	NR	NR	NR	NR	0.43	PBT	
Ots_112301-43	swfsc103	X	1	2	1	NR	PROTECT	NR	NR	0.35	PBT	PBT
Ots_112419-131	swfsc103	X	1	2	1	NR	PROTECT	NR	NR	0.58	PBT	PBT
Ots_112820-284	swfsc103	X	1	2	1	NR	PROTECT	NR	NR	0.49	PBT	PBT
Ots_112876-371	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.53	PBT	PBT
Ots_113242-216	gaps75	X	1	2	2	PROTECT	PROTECT	NR	NR	0.44	PBT	SNP/PBT
Ots_113457-40	gaps75	X	3	3	2	PROTECT	PROTECT	NR	PROTECT	0.72	PBT	SNP
Ots_115987-325	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.87		PBT
Ots_117242-136	swfsc103	X	1	2	1	NR	NR	NR	NR	0.34	PBT	
Ots_117259-271	swfsc103	X	1	2	1	NR	NR	NR	NR	1.00		
Ots_117432-409	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.41	PBT	PBT
Ots_118175-479	swfsc103	X	3	3	2	NR	DROP	DROP	PROTECT	0.18	PBT	
Ots_118205-61	swfsc103	X	1	2	1	NR	PROTECT	NR	NR	0.30	PBT	PBT
Ots_122414-56	swfsc103	X	1	1	1	NR	NR	NR	NR	0.80	PBT	
Ots_123048-521	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.41	PBT	SNP
Ots_123921-111	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.19	PBT	PBT
Ots_124774-477	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.56	PBT	PBT
Ots_127236-62	swfsc103	X	1	2	1	NR	NR	NR	NR	0.79	PBT	
Ots_127760-569	swfsc103	X	1	1	1	NR	NR	NR	NR	0.50		
Ots_128302-57	swfsc103	X	1	2	1	NR	NR	NR	NR	0.92	PBT	
Ots_128693-461	swfsc103	X	1	1	1	NR	NR	NR	NR	0.43	PBT	
Ots_128757-61	gaps75	X	1	2	1	PROTECT	PROTECT	NR	NR	0.28	PBT	SNP/PBT
Ots_129144-472	swfsc103	X	3	3	3	DROP	DROP	DROP	PROTECT	0.39	PBT	

Appendix 1 (con't)

SNP Name	Assay Source[1]	Included in 192	Resolution[1]			Laboratory Vote[1]				Allele Freq (Max - Min)	Existing Panels[1]	
			UW	USFWS	WDFW	WDFW	IDFG/CRITFC	ADFG	SWFSC		SWFSC	IDFG/CRITFC
Ots_129170-683	swfsc103	X	3	3	3	DROP	DROP	DROP	PROTECT	0.13	PBT	
Ots_129458-451	swfsc103	X	1	1	1	NR	PROTECT	NR	NR	0.52	PBT	PBT
Ots_130720-99	swfsc103	X	3	3	2	NR	DROP	DROP	PROTECT	0.90	PBT	
Ots_131460-584	swfsc103	X	1	2	1	NR	NR	NR	NR	0.79	PBT	
Ots_131906-141	swfsc103	X	1	1	1	NR	NR	NR	NR	0.48	PBT	
Ots_94857-232	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.35	PBT	SNP/PBT
Ots_94903-99	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.51		SNP/PBT
Ots_96222-525	gaps75	X	1	2	1	PROTECT	PROTECT	NR	NR	0.70	PBT	SNP
Ots_96500-180	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.79	PBT	SNP/PBT
Ots_96899-357	gaps75	X	1	2	1	DROP	PROTECT	NR	NR	0.34		SNP/PBT
Ots_97077-179	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.28	PBT	SNP
Ots_99550-204	swfsc103	X	1	2	1	NR	NR	NR	NR	0.33	PBT	
Ots_AldB1-122	gaps75	X	1	2	1	PROTECT	PROTECT	NR	NR	0.28	PBT	SNP
Ots_aldb-177M	gaps75	X	2	2	2	PROTECT	PROTECT	NR	NR	0.79		SNP
Ots_ARNT	critfc21v3.0	X	3	3	2-3	DROP	PROTECT	NR	PROTECT	0.81		SNP/PBT
Ots_arp-436	critfc21v3.0	X	2	2	2	NR	PROTECT	NR	NR	0.45		SNP
Ots_AsnRS-60	gaps75	X	1	1	1	DROP	PROTECT	NR	NR	0.14	PBT	SNP/PBT
Ots_aspat-196	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.29	PBT	SNP
Ots_brp16-64	uw/wdfw	X	1	1	1	NR	PROTECT	NR	NR	0.17		PBT
Ots_C3N3	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	1.00		SNP
Ots_Cath_D141	critfc21v3.0	X	2	4	2	NR	PROTECT	NR	NR	0.04		SNP
Ots_CCR7	critfc21v3.0	X	1	1	1	NR	PROTECT	NR	NR	0.56		SNP
Ots_CD59-2	gaps75	X	2	2	1	PROTECT	PROTECT	NR	NR	0.35	PBT	SNP/PBT
Ots_CD63	gaps75	X	2	2	1	DROP	PROTECT	NR	PROTECT	0.53	PBT	SNP
Ots_CirpA	dfo	X	1	1	1	NR	PROTECT	NR	NR	0.54		PBT
Ots_cox1-241	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.88		SNP/PBT
Ots_DDX5-171	uw	X	1	1	1	NR	NR	NR	NR	0.68		
Ots_E2-275	ADFG	X	1	1	1	NR	PROTECT	PROTECT	NR	0.61		SNP/PBT
Ots_EndoRB1-486	gaps75	X	2	2	2	DROP	PROTECT	NR	NR	0.27		SNP
Ots_EP-529	gaps75	X	1	2	1	PROTECT	PROTECT	NR	NR	0.12	PBT	SNP
Ots_Est1363	dfo	X	1	1	1	NR	NR	NR	NR	1.00		
Ots_Est740	dfo	X	1	2	1	NR	PROTECT	NR	NR	0.53		PBT
Ots_ETIF1A	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.70		SNP/PBT
Ots_FARSLA-220	gaps75	X	2	3	2	PROTECT	PROTECT	NR	NR	0.98		SNP
Ots_FGF6A	gaps75	X	1	1	1	PROTECT	DROP	PROTECT	NR	0.44		SNP

Appendix 1 (con't)

SNP Name	Assay Source[1]	Included in 192	Resolution[1]			Laboratory Vote[1]				Allele Freq (Max - Min)	Existing Panels[1]	
			UW	USFWS	WDFW	WDFW	IDFG/CRITFC	ADFG	SWFSC		SWFSC	IDFG/CRITFC
Ots_FGF6B_1	gaps75	X	2	2	2	DROP	PROTECT	DROP	NR	0.36		SNP/PBT
Ots_GCSH	dfo	X	3	2	2-3	DROP	PROTECT	DROP	NR	0.98		PBT
Ots_GDH-81x	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.29	PBT	SNP/PBT
Ots_GH2	gaps75	X	1	2	1	DROP	PROTECT	PROTECT	NR	0.32		SNP
Ots_GPDH-338	gaps75	X	1	2	1	DROP	PROTECT	PROTECT	NR	0.11		SNP
Ots_GPH-318	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.39		SNP/PBT
Ots_GST-207	ADFG	X	1	2	1	PROTECT	PROTECT	PROTECT	NR	0.30		SNP
Ots_GTH2B-550	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.63		SNP/PBT
Ots_HFABP-34	uw	X	1	2	2	NR	NR	NR	NR	0.42		
Ots_HMGB1-73	uw/wdfw	X	1	1	1	NR	PROTECT	NR	NR	0.72		PBT
Ots_hnRNPL-533	ADFG	X	1	1	1	PROTECT	NR	PROTECT	NR	0.68		
Ots_hsc71-5'-453	critfc21v3.0	X	1	1	1	NR	PROTECT	NR	NR	0.38		SNP
Ots_hsp27b-150	critfc21v3.0	X	1	1	1	NR	PROTECT	NR	NR	0.62		SNP
Ots_Hsp90a	swfsc15more	X	1	1	1	NR	NR	NR	NR	0.96		
Ots_HSP90B-100	gaps75	X	1	1	1	PROTECT	PROTECT	PROTECT	NR	0.92		SNP/PBT
Ots_HSP90B-385	ADFG	X	1	2	1	PROTECT	NR	DROP	NR	0.17	PBT	
Ots_IGF-I.1-76	gaps75	X	1	2	1	DROP	PROTECT	PROTECT	NR	0.55		SNP/PBT
Ots_Ikaros-250	gaps75	X	3	3	2-3	DROP	PROTECT	PROTECT	NR	0.75		SNP/PBT
Ots_IL11	gaps75	X	2	4	2	DROP	PROTECT	NR	NR	0.17		SNP
Ots_il13Ra2B-37	uw	X	1	2	2	NR	NR	NR	NR	0.46		
Ots_il-1racp-166	ADFG	X	1	1	1	NR	NR	PROTECT	NR	0.57		
Ots_IL8R_C8	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.93		SNP/PBT
Ots_IsoT	dfo	X	1	1	1	NR	NR	NR	NR	0.56		
Ots_LWSop-638	gaps75	X	1	4	1	PROTECT	PROTECT	PROTECT	NR	0.03		SNP
Ots_mapK-3'-309	critfc21v3.0	X	1	2	1	NR	PROTECT	NR	NR	0.81		SNP/PBT
Ots_mapKpr-151	critfc21v3.0	X	1	2	1	NR	PROTECT	NR	NR	0.70		SNP/PBT
Ots_MHC1	gaps75	X	1	2	1	PROTECT	PROTECT	PROTECT	NR	0.88	PBT	SNP/PBT
Ots_MHC2	gaps75	X	3	3	2-3	DROP	PROTECT	PROTECT	NR	0.68		SNP/PBT
Ots_mybp-85	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.51	PBT	SNP/PBT
Ots_Myc-366	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.27	PBT	SNP
Ots_myo1a-384	gaps75	X	1	2	1	PROTECT	PROTECT	NR	NR	0.15		SNP
Ots_myoD-364	gaps75	X	2	2	1-2	DROP	PROTECT	NR	PROTECT	0.78	PBT	SNP
Ots_nelfd-163	uw/wdfw	X	1	2	1	NR	NR	NR	NR	0.96		
Ots_NFYB-147	uw/wdfw	X	1	2	1	NR	PROTECT	NR	NR	0.19		PBT
Ots_nkef-192	gaps75	X	1	2	1	PROTECT	PROTECT	NR	NR	0.88		SNP/PBT

Appendix 1 (con't)

SNP Name	Assay Source[1]	Included in 192	Resolution[1]			Laboratory Vote[1]				Allele Freq (Max - Min)	Existing Panels[1]	
			UW	USFWS	WDFW	WDFW	IDFG/CRITFC	ADFG	SWFSC		SWFSC	IDFG/CRITFC
Ots_NOD1	gaps75	X	1	1	1	PROTECT	PROTECT	PROTECT	NR	0.76		SNP/PBT
Ots_ntl-255	CRITFC new	X	1			NR	NR	NR	NR	?		PBT
Ots_ALDBINT1-SNP1	swfsc15more	X	1	1	1	NR	PROTECT	NR	NR	0.88	PBT	PBT
Ots_DESMIN19-SNP1	swfsc15more	X	1	1	1	NR	PROTECT	NR	NR	0.56		
Ots_NAML12-SNP1	swfsc15more	X	1	1	1	NR	NR	NR	NR	0.69	PBT	SNP
Ots_Ots311-101x	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.46	PBT	
Ots_BMP2-SNP1	swfsc15more	X	1	1	1	NR	NR	NR	NR	0.14	PBT	
Ots_MTA-SNP1	swfsc15more	X	1	1	1	NR	NR	NR	NR	0.36		PBT
Ots_TF1-SNP1	swfsc15more	X	1	1	1	NR	PROTECT	NR	NR	0.84	PBT	SNP
Ots_P450	gaps75	X	1	1	1	PROTECT	PROTECT	PROTECT	NR	0.95		
Ots_P450-288	ADFG	X	2	2	1	PROTECT	DROP	PROTECT	NR	0.67		SNP/PBT
Ots_P53	gaps75	X	2	3	2	PROTECT	PROTECT	NR	NR	0.26		SNP
Ots_parp3-286	CRITFC new	X	1			NR	NR	NR	NR	?		SNP/PBT
Ots_PGK-54	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.54	PBT	SNP/PBT
Ots_pop5-96	CRITFC new	X	2			NR	NR	NR	NR	?		SNP
Ots_ppie-245	CRITFC new	X	1			NR	NR	NR	NR	?		SNP/PBT
Ots_Prl2	gaps75	X	1	2	1-2	PROTECT	PROTECT	PROTECT	NR	0.67	PBT	SNP/PBT
Ots_RAG3	gaps75	X	1	2	1-2	PROTECT	PROTECT	PROTECT	NR	0.65	PBT	SNP
Ots_redd1-187	CRITFC new	X	1			NR	NR	NR	NR	?		
Ots_RFC2-558	gaps75	X	1	2	1	PROTECT	PROTECT	PROTECT	NR	0.75	PBT	SNP/PBT
Ots_S7-1	gaps75	X	3	3	3	DROP	PROTECT	PROTECT	PROTECT	0.30		SNP/PBT
Ots_SClkF2R2-135	gaps75	X	1	1	1	PROTECT	PROTECT	PROTECT	NR	0.31	PBT	
Ots_SEXY1	CRITFC new	X				NR	NR	NR	NR	?		
Ots_SL	gaps75	X	1	2	2	DROP	PROTECT	PROTECT	NR	0.96		SNP/PBT
Ots_stk6-516	uw/wdfw	X	1	4	1	NR	NR	NR	NR	0.05		PBT
Ots_SWS1op-182	gaps75	X	1	2	1	PROTECT	PROTECT	PROTECT	NR	0.56	PBT	SNP/PBT
Ots_TAPBP	gaps75	X	1	1	1	DROP	PROTECT	PROTECT	NR	0.83	PBT	SNP
Ots_TCTA-58	uw	X	1	1	1	NR	NR	NR	NR	0.55		PBT
Ots_Tf-3545	ADFG	X	1	4	1	PROTECT	NR	DROP	NR	0.04		SNP/PBT
Ots_TGFB	gaps75	X	3	2	2-3	PROTECT	PROTECT	DROP	NR	0.46		SNP/PBT
Ots_Thio	dfo	X	2	2	2	NR	PROTECT	DROP	NR	0.44		SNP/PBT
Ots_TLR3	gaps75	X	3	3	2-3	DROP	PROTECT	DROP	NR	0.58		
Ots_Tnsf	gaps75	X	1	2	1	DROP	PROTECT	PROTECT	NR	0.84		SNP/PBT
Ots_tpx2-125	uw/wdfw	X	1	4	1	NR	PROTECT	NR	NR	0.07		SNP/PBT
Ots_txnip-321	CRITFC new	X	1			NR	NR	NR	NR	?		SNP

Appendix 1 (con't)

SNP Name	Assay Source[1]	Included in 192	Resolution[1]			Laboratory Vote[1]				Allele Freq (Max - Min)	Existing Panels[1]	
			UW	USFWS	WDFW	WDFW	IDFG/CRITFC	ADFG	SWFSC		SWFSC	IDFG/CRITFC
Ots_u07-07.161	gaps75	X	1	2	1	PROTECT	PROTECT	NR	NR	0.50	PBT	SNP
Ots_u07-17.135	wdfw	X	1	4	1	DROP	PROTECT	NR	NR	0.09		PBT
Ots_u07-18.378	gaps75	X	2	2	2	PROTECT	PROTECT	NR	NR	0.50		
Ots_u07-19.260	wdfw	X	1	4	1	PROTECT	NR	NR	NR	0.08		SNP
Ots_u07-25.325	gaps75	X	1	2	2	PROTECT	PROTECT	NR	NR	0.54		SNP/PBT
Ots_u07-49.290	gaps75	X	1	1	1	PROTECT	PROTECT	NR	NR	0.59	PBT	
Ots_u07-53.133	gaps75	X	2	2	2	PROTECT	PROTECT	NR	NR	0.75		
Ots_u07-57.120	gaps75	X	1	3	2-3	DROP	PROTECT	NR	NR	0.98		
Ots_u1002-75	uw/wdfw	X	1	2	1-2	NR	PROTECT	NR	NR	0.33		SNP/PBT
Ots_u1007-124	uw/wdfw	X	1	2	1-2	NR	NR	NR	NR	0.27		
Ots_u202-161	gaps75	X	1	3	3	DROP	PROTECT	NR	NR	0.99		
Ots_u211-85	gaps75	X	1	2	3	DROP	PROTECT	NR	NR	0.98		
Ots_U2362-227	uw	X	1	2	2	NR	NR	NR	NR	0.34		SNP/PBT
Ots_U2362-330	uw	X	1	2	2	NR	NR	NR	NR	0.52		
Ots_U2446-123	uw	X	1	1	1	NR	NR	NR	NR	0.60		
Ots_u6-75	gaps75	X	3	2	3	PROTECT	PROTECT	PROTECT	NR	0.16		
Ots_RAD1104-38	uw	X	1	1	1	NR	NR	NR	NR	0.59		
Ots_RAD1832-39	uw	X	1	2	1-2	NR	NR	NR	NR	0.68		
Ots_RAD3513-49	uw	X	1	2	1	NR	NR	NR	NR	0.36		SNP
Ots_unk526	gaps75	X	1	2	2	DROP	PROTECT	NR	NR	0.20	PBT	PBT
Ots_RAD7936-50	uw	X	1	2	2	NR	NR	NR	NR	0.26		PBT
Ots_RAD8200-45	uw	X	1	2	1	NR	NR	NR	NR	0.37		PBT
Ots_RAD9480-51	uw	X	1	1	1	NR	NR	NR	NR	0.75		PBT
Ots_USMG5-67	uw/wdfw	X	1	4	3	DROP	NR	NR	NR	0.05		PBT
Ots_vatf-251	CRITFC new	X	1			NR	NR	NR	NR	?		PBT?
Ots_zn593-346	uw/wdfw	X	1	1	1	NR	NR	NR	NR	0.09		PBT
Ots_zP3b-215	gaps75	X	3	4	3	DROP	DROP	PROTECT	NR	0.04		PBT
Omy_1005	uw		3	3	3	DROP	DROP	DROP	NR	0.15		
Ots_101770-82	swfsc103		1	1	1	NR	NR	NR	NR	0.16		
Ots_102195-157	swfsc103		2	4	1	NR	DROP	NR	NR	0.04		
Ots_104084-194	swfsc103		3	3	3	DROP	DROP	DROP	DROP	0.24		
Ots_104216-70	swfsc103		1	4	1	DROP	NR	DROP	NR	0.02		
Ots_105401-325	swfsc103		3	3	3	DROP	DROP	DROP	DROP	0.27	PBT	
Ots_105897-124	swfsc103		1	2	1	NR	NR	NR	NR	0.06		
Ots_106172-425	swfsc103		4	4	3	DROP	DROP	DROP	DROP	0.00		

Appendix 1 (con't)

SNP Name	Assay Source[1]	Included in 192	Resolution[1]			Laboratory Vote[1]				Allele Freq (Max - Min)	Existing Panels[1]	
			UW	USFWS	WDFW	WDFW	IDFG/CRITFC	ADFG	SWFSC		SWFSC	IDFG/CRITFC
Ots_106313-729	swfsc103		2	3	2-3	DROP	DROP	NR	NR	0.07		
Ots_106419b-618	swfsc103		3	3	2	NR	DROP	DROP	DROP	0.87		
Ots_107220-70	swfsc103		4	4	2	DROP	DROP	DROP	DROP	0.00		
Ots_107607-315	swfsc103		2	3	1-2	NR	DROP	NR	NR	0.32		
Ots_109243-285	swfsc103		3	3	2	NR	DROP	DROP	DROP	0.43		
Ots_110381-164	swfsc103		3	3	2	NR	DROP	DROP	DROP	0.36		
Ots_111084-96	swfsc103		3	3	2	NR	DROP	NR	DROP	0.48		
Ots_111312-435	swfsc103		3	3	2	NR	DROP	DROP	DROP	0.99	PBT	
Ots_112208-722	swfsc103		1	2	1	NR	NR	NR	NR	0.51	PBT	
Ots_117043-255	swfsc103		3	3	2	NR	DROP	NR	DROP	0.66	PBT	
Ots_117138-545	swfsc103		4	4	1	NR	DROP	DROP	DROP	0.00		
Ots_117370-471	swfsc103		3	3	3	DROP	DROP	DROP	DROP	0.16		
Ots_118938-325	swfsc103		3	3	2	NR	PROTECT	DROP	PROTECT			
Ots_120950-417	swfsc103		1	2	1	NR	NR	NR	NR	0.36		
Ots_123205-61	swfsc103		4	4	1	DROP	DROP	DROP	DROP	0.00		
Ots_126619-400	swfsc103		3	3	3	DROP	DROP	DROP	DROP	0.39		
Ots_128495b-45	swfsc103		3	3	3	DROP	DROP	DROP	DROP	0.18		
Ots_129303b-54	swfsc103		3	3	2	NR	DROP	DROP	DROP	0.30		
Ots_129870-55	swfsc103		1	2	2	NR	NR	NR	NR	0.30		
Ots_131802-393	swfsc103		1	2	1	NR	NR	NR	NR	0.24		
Ots_95442b-204	swfsc103		2	2	2	NR	DROP	NR	NR	0.92		
Ots_97660-56	swfsc103		1	1	1	NR	NR	NR	NR	0.24		
Ots_98409-850	swfsc103		1	4	1	NR	NR	NR	NR	0.09		
Ots_98683-796	swfsc103		1	4	1	NR	NR	NR	NR	0.13		
Ots_afmid-196	uw/wdfw		2	2	2	NR	DROP	NR	NR	0.15		
Ots_AldoB4-183	swfsc15more		1	1	1	NR	NR	NR	NR	0.21	PBT	
Ots_apoc1-47	uw		2	2	3	DROP	DROP	NR	NR	0.10		
Ots_arf-188	ADFG		1	4	1	NR	NR	DROP	NR	0.02		
Ots_casp9-99	uw/wdfw		4	4	1	DROP	DROP	DROP	DROP	0.00		
Ots_cd59-51	uw		2	2	3	DROP	DROP	NR	NR	0.96		
Ots_cgo24-22	uw		3	3	3	DROP	DROP	DROP	NR	0.82		
Ots_Chin30up-211	swfsc15more		1	4	2-3	DROP	DROP	NR	NR	0.08		
Ots_CRB211	swfsc15more		4	4	1	DROP	DROP	DROP	DROP	0.00		SNP
Ots_DBLOH-73	uw/wdfw		4	4	1	NR	DROP	DROP	DROP	0.00		
Ots_E9BAC	ADFG		4	4	1	DROP	DROP	DROP	DROP	0.00		

Appendix 1 (con't)

SNP Name	Assay Source[1]	Included in 192	Resolution[1]			Laboratory Vote[1]				Allele Freq (Max - Min)	Existing Panels[1]	
			UW	USFWS	WDFW	WDFW	IDFG/CRITFC	ADFG	SWFSC		SWFSC	IDFG/CRITFC
Ots_Est803	dfo		1	1	1	NR	NR	NR	NR	0.38		
Ots_GnRH-271	gaps75		2	4	2	DROP	PROTECT	NR	NR			
Ots_GST-375	gaps75		1	4	1	DROP	DROP	DROP	NR	0.09		SNP
Ots_HGFA-446	ADFG		4	4	1	NR	DROP	PROTECT	DROP			
Ots_hsc71-3'-488	critfc21v3.0		3	3	3	DROP	NR	DROP	NR	0.74		SNP/PBT
Ots_hsp47-339	critfc21v3.0_2more		4	4	1	DROP	DROP	DROP	DROP	0.00		
Ots_hsp90BA-252	critfc21v3.0_2more		3	3	3	DROP	DROP	DROP	NR	0.78		
Ots_HSP90BB-88	uw/wdfw		4	4	1	NR	DROP	DROP	DROP	0.00		
Ots_ins-115	ADFG		2	4	1	NR	DROP	DROP	NR			
Ots_LEI-292	ADFG		1	4	1	DROP	NR	DROP	NR			
Ots_MetA	ADFG		3	3	3	DROP	DROP	DROP	NR	0.61		
Ots_nramp-321	gaps75		3	3	3	DROP	PROTECT	DROP	NR			
Ots_Ostm1	dfo		4	4	3	DROP	DROP	DROP	DROP	0.00		
Ots_NAML12-SNP2	swfsc15more		1	2	1	NR	NR	NR	NR	0.34		
Ots_Ots2	ADFG		3	3	3	DROP	DROP	DROP	NR	0.58		
Ots_PEMT	dfo		3	3	2	NR	DROP	DROP	NR	0.61		
Ots_Phos	dfo		2	3	2	NR	DROP	DROP	NR	0.14		
Ots_picalm-175	uw/wdfw		3	3	3	DROP	DROP	DROP	NR	0.12		
Ots_pigh-105	CRITFC new		2			NR	NR	NR	NR	?		PBT
Ots_PSMB1-197	ADFG		4	4	1	DROP	DROP	DROP	DROP	0.00		
Ots_RAS1	critfc21v3.0		4	4	1	DROP	DROP	DROP	DROP	0.00		SNP
Ots_sept9-78	uw		2	2	2	NR	DROP	NR	NR	0.39		
Ots_SERPC1-209	gaps75/ADFG		1	4	3	DROP	NR	DROP	NR			
Ots_slc7a2-71	uw		3	3	2-3	DROP	DROP	NR	NR	0.34		
Ots_TNF	critfc21v3.0		1	4	1	NR	DROP	NR	NR	0.09		SNP
Ots_trnau1ap-86	uw/wdfw		1	2	2	NR	NR	NR	NR	0.09		
Ots_TUBA-454	ADFG		1	2	2	DROP	NR	drop	NR			
Ots_u07-17.373	wdfw		2	3	3	DROP	DROP	DROP	NR	0.09		
Ots_u07-20.332	wdfw		1	4	1	DROP	PROTECT	NR	NR			
Ots_u07-24.441	wdfw		4	4	1	DROP	DROP	DROP	DROP	0.00		
Ots_u07-53.185	wdfw		3	3	3	DROP	DROP	DROP	NR	0.65		
Ots_u07-64.221	critfc21v3.0		1	4	1	NR	DROP	NR	NR	0.06		SNP
Ots_u1001-110	uw/wdfw		4	4	2	DROP	DROP	DROP	DROP	0.00		
Ots_u1001-73	uw/wdfw		1	4	2	DROP	DROP	NR	NR	0.03		
Ots_u1004-117	uw/wdfw		1	4	1	NR	NR	NR	NR	0.02		

Appendix 1 (con't)

SNP Name	Assay Source[1]	Included in 192	Resolution[1]			Laboratory Vote[1]				Allele Freq (Max - Min)	Existing Panels[1]	
			UW	USFWS	WDFW	WDFW	IDFG/CRITFC	ADFG	SWFSC		SWFSC	IDFG/CRITFC
Ots_u1005-108	uw/wdfw		4	4	1	NR	DROP	DROP	DROP	0.00		
Ots_u1006-171	uw/wdfw		2	2	3	DROP	DROP	NR	NR	0.19		
Ots_u1008-108	uw/wdfw		1	2	1	NR	NR	NR	NR	0.22		
Ots_u1010-110	uw/wdfw		4	4	2	NR	DROP	DROP	DROP	0.00		
Ots_u1011-76	uw/wdfw		1	4	2	NR	DROP	NR	NR	0.01		
Ots_u1012-34	uw/wdfw		4	4	2-3	DROP	DROP	DROP	DROP	0.00		
Ots_U212-158	ADFG		1	4	1	NR	NR	NR	NR			
Ots_U2305-63	uw		3	3	3	DROP	DROP	DROP	NR	0.36		
Ots_U2387-124	uw		3	4	3	DROP	DROP	DROP	NR	0.02		
Ots_U2481-39	uw		3	4	3	DROP	DROP	DROP	NR	0.11		
Ots_U2514-60	uw		2	2	2	NR	DROP	DROP	NR	0.50		
Ots_U2567-104	uw		2	2	2	NR	DROP	DROP	NR	0.22		
Ots_U2637-32	uw		1	2	1	NR	NR	NR	NR	0.07		
Ots_u4-92	gaps75		3	2	3	DROP	PROTECT	NR	PROTECT			
Ots_U5049-250	uw		3	3	3	DROP	DROP	DROP	NR	0.40		
Ots_U5051-29	uw		2	3	2-3	DROP	DROP	NR	NR	0.14		
Ots_U5056-57	uw		1	4	3	DROP	NR	NR	NR	0.04		
Ots_U5121-34	uw		2	2	2-3	DROP	DROP	DROP	NR	0.29		
Ots_U608-861	ADFG		2	2	3	DROP	DROP	DROP	NR	0.31		
Ots_unc119-59	uw		3	3	2	NR	DROP	DROP	NR	0.91		
Ots_RAD10261-46	uw		3	3	2-3	DROP	DROP	DROP	NR	0.49		
Ots_RAD12380-39	uw		2	2	2-3	DROP	DROP	DROP	NR	0.08		
Ots_RAD4543-52	uw		2	2	2	NR	DROP	NR	NR	0.41		
Ots_RAD8207-62	uw		4	4	2	DROP	DROP	DROP	DROP	0.00		
Ots_USMG5-56	uw		1	4	2-3	DROP	NR	DROP	NR	0.05		
Ots_ZNF330-181	ADFG		1	4	1	DROP	NR	NR	NR	0.02		

[1] Abbreviations: ADFG-Alaska Department of Fish and Game, CRITFC-Columbia River Inter-Tribal Fish Commission, DFO-Department of Fisheries and Ocean, IDFG-Idaho Department of Fish and Game, SWFSC-Southwest Fisheries Science Center, GAPS75--Genetic Analysis of Pacific Salmon 75 SNP panel, USFWS-US. Fish and Wildlife Abernathy Technology Center, UW-University of Washington, and WDFW-Washington Department of Fish and Wildlife.