

**Genetic relationships among naturally spawning Steelhead (*Oncorhynchus mykiss*) in lower Cowlitz River tributaries and hatchery Steelhead stocks released in the Cowlitz Basin: implications for recovery planning.**

Maureen P. Small, Anne Marshall, Julie Henning, and Jennifer Von Bargen  
Molecular Genetics Lab, Conservation Biology Unit, & Region 5 Fish Management  
600 Capitol Way N  
Washington Department of Fish and Wildlife  
Olympia, WA 98501  
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**Summary**

Natural-origin steelhead were sampled in tributaries of the lower Cowlitz basin and compared genetically to Cowlitz Hatchery steelhead broodstocks (summer, early-winter, and late-winter) to examine hatchery introgression into natural populations. Cowlitz tributary natural-origin adults were also compared to natural-origin steelhead collected in other nearby tributaries in the lower Columbia drainage to characterize existing genetic diversity. Lower Cowlitz tributary natural-origin steelhead had highest ancestry in a native gene pool and were genetically distinct from the three Cowlitz Hatchery stocks. However, we estimated ancestry or introgression from all three hatchery stocks in the natural-origin steelhead. The Cowlitz Hatchery early winter-run stock (non-native, Puget Sound origin) showed the highest introgression level among the three stocks. The eight marked, hatchery-origin adults collected during sampling appeared to originate from all three hatchery stocks, with the early-winter stock being the major contributor. Lower Cowlitz tributary natural-origin steelhead were most similar genetically to natural-origin steelhead in the Coweeman and Elochoman rivers, and were distinct from steelhead in the nearby Toutle River sub-basin. Introgression from hatchery stocks is a significant issue in recovery planning for the ESA-listed Lower Cowlitz population.

**Introduction**

Natural-origin steelhead in lower Cowlitz River tributaries are included as an independent population in the Lower Columbia River Steelhead Distinct Population Segment (DPS), which was ESA-listed as threatened in 1998. Within this DPS, there is a high degree of uncertainty regarding the existence of native populations or gene pools, and the impact of hatchery-origin steelhead on natural populations in terms of genetic diversity, population structuring, productivity, and viability or persistence. Busby et al. (1996) concluded that the major threat to genetic integrity of Lower Columbia steelhead occurred from past and present hatchery practices.

The late-winter steelhead stock produced at Cowlitz Trout Hatchery was derived from native Cowlitz Basin steelhead and may include a mixture of formerly distinct populations from drainages upstream of Mayfield Dam. Genetic characteristics (allozyme data) of the late-winter hatchery stock were distinctive compared to the non-native Cowlitz Hatchery early-winter and summer-run stocks, and to other Lower Columbia population samples (Phelps et al. 1997). The Cowlitz Hatchery early-winter stock was derived in 1967 from Chambers Creek (Puget Sound) winter-run hatchery stock. The Cowlitz summer-run stock was derived from the Skamania Hatchery summer stock. Both of these non-local hatchery stocks have been released in other lower Columbia tributaries. These stocks were produced to mitigate for the loss of fish due to hydroelectric dams on the Cowlitz River.

Here we examine genetic data for natural-origin steelhead adults in Lower Cowlitz mainstem tributaries (downstream of the Barrier and Mayfield dams, Figure 1a) and compare them to genetic data for the three Cowlitz Hatchery steelhead broodstocks, summer, early-winter, and late-winter (see Table 1). Due to past transplantation of non-native hatchery fish (7,456,769 summer-run released 1995-2008; 8,116,585 early-winter-run released 1995-2008) and high levels of on-station hatchery production (7,192,094 late-winter-run released 1995-2008), it is possible that Lower Cowlitz natural steelhead populations have been affected by interbreeding and/or ecological impacts from hatchery stocks. However, differences in spawn-timing and potential lower reproductive success of hatchery stocks could limit impacts on native wild-spawning populations.

The overall goal of this study is to genetically characterize natural-origin steelhead in Lower Cowlitz tributaries in order to identify remaining genetic resources and plan appropriate recovery actions. Our work is designed to test the following null hypotheses:

1. Un-marked (putative natural-origin) adult steelhead sampled from different tributaries of the Lower Cowlitz River are genetically distinct from hatchery-origin steelhead.
2. The genetic profiles of un-marked adult steelhead are distinct among different tributaries. In particular, natural-origin steelhead are genetically distinct between the Arkansas and Olequa tributary subbasins, based on all samples collected in 2008 and 2009 for each subbasin.
3. Lower Cowlitz tributary natural-origin steelhead are genetically distinct from steelhead in other Cowlitz sub-basins and Lower Columbia tributaries.
4. Cowlitz hatchery stocks are genetically distinct among themselves, such that 95% of fish assign back to their stock of origin with high probability.
5. Cowlitz hatchery stocks are genetically distinct from other lower Columbia hatchery stocks and wild populations.
6. Un-marked steelhead sampled at the barrier dam in 2005 and passed upstream are genetically distinct from the two non-local hatchery stocks, and most similar to the late-winter hatchery stock.

In this final report we estimate hatchery stock introgression in natural-origin steelhead sampled in 2008 and 2009, and resolve genetic relationships among all 2008 and 2009 samples and other Cowlitz and lower Columbia basin steelhead populations.

## **Materials and methods**

### Samples and sample processing

This study has a two-part phased sampling design to address the genetic impacts of hatchery steelhead stocks on natural-origin winter-run steelhead. During phase 1 tissue samples were collected from adult steelhead and in phase 2 we plan to collect DNA samples from juvenile steelhead that could be progeny of previously sampled naturally spawning adults. This report will discuss the results of phase 1 since no work has yet been completed on phase 2.

Phase 1, Years 1 and 2 (2008-2009): Adult steelhead in Lower Cowlitz tributaries were sampled using hook and line and dip net capture methods from March through May. Adult, non-adipose fin-clipped, presumed natural-origin, and adipose fin-clipped steelhead were sampled from multiple streams within tributary systems (Table 2; Figures 1a and 1b). The three tributary systems, Ostrander, Arkansas, and Olequa enter the lower Cowlitz mainstem between river miles 8.6 and 24.8. Sites within systems were chosen based on the contemporary population, stream condition, access, and the tributary drainage. It was important to sample any marked hatchery-origin steelhead encountered because these may be parents of a future generation.

A small fin clip was taken non-lethally from each fish, and sampling and biological data were recorded per individual. When risks from handling stress were low, scales were sampled to determine age, freshwater residency period, and check for absence of hatchery yearling release pattern to verify natural origin of unmarked fish. Fish handling was as minimal and non-invasive as possible, and all fish were released immediately post-sampling.

### Genetic data collection

Genetic data were collected over two years for the 449 fish shown in Table 1. Details on tributary-of-origin for the 08DC and 09CY natural spawners are given in Table 2. Genomic DNA was extracted from tissue and scale samples using silica membrane kits (Macherey-Nagel). Fish were genotyped at a suite of 16 microsatellite DNA loci (Table 3). The 16 loci have been standardized for genetic data collection among several laboratories (Stephenson et al. 2009), and is known as the “SPAN” (Stevan Phelps Allele Nomenclature) locus set. Microsatellite alleles were PCR-amplified using fluorescently labeled primers (see Table 3 for detailed PCR (polymerase chain reaction) information). Primers had a poly-a tail added to reverse primers (indicated by “+a” after primer name) to stabilize the reaction. The primer Oki10 was fluorescently labeled with a vector tail (V) in our lab and is identified in Table 3 by the label “V” and the concentration for the primer and the vector are given. The other primers were labeled at the factory when primers were constructed. PCRs were conducted in 384 well plates in 5 µl volumes employing 1 µl template with final concentrations of 1.5 mM MgCl<sub>2</sub>, 200µM of each dNTP, 0.05 µl Promega GoTaq and 1X Promega PCR buffer. After initial two minute denature at 94°, 37 cycles consisting of denature at 94° for 30 seconds, annealing (temperature in Table 3) for 30 seconds, extension at 72° for 60 seconds were followed by a 10-minute extension at 72°. Microsatellites were detected using an ABI 3730 automated DNA

Analyzer, and alleles were sized (to base pairs) and binned using an internal lane size standard (GS500Liz from Applied Biosystems) and GeneMapper software (Applied Biosystems).

### Genetic Data Analyses

Genotypic data per collection (Table 1) were examined to gather basic population information about the nature of the collections. We used the computer program FSTAT2.9.3 (Goudet 2001) to measure Hardy-Weinberg (HWE) equilibrium (genotypic proportions expected in a randomly mating population) expressed as  $F_{IS}$  values, allelic richness (number of alleles per population corrected for sample size), gene diversity (expected heterozygosity corrected for sample size – heterozygosity describes whether individuals are likely to have two different alleles at a locus), and allele frequencies. These descriptive statistics help identify sampling error, data collection error, and mixed-population samples. We assessed linkage disequilibrium (non-random genotypic associations between all possible pairs of loci) with a permutation method implemented in GENETIX (Belkhir et al. 2004) with 10,000 permutations. Linkage disequilibrium may arise if the collection includes family groups or migrants, if there is non-random mating, or genetic drift is large due to small population size, or loci are physically linked.

We used pairwise genotypic and  $F_{ST}$  tests in FSTAT with 10,000 permutations to determine whether Cowlitz tributary natural-origin steelhead and the three Cowlitz Hatchery stocks were genetically distinct from each other, and to assess their genetic relationships to winter- and summer-run steelhead in other drainages of the Cowlitz and lower Columbia River (Table 4; lower Columbia region steelhead genotypic data collected by T. Kassler and C. Dean, WDFW). If collections differ significantly in their genotypic distributions, this is an indication that they are reproductively isolated from each other and constitute distinct populations. Pairwise  $F_{ST}$  values are a ratio of the amount of genetic variance among or between populations over the total variance in the data set. Pairwise  $F_{ST}$  values that are significantly different from zero may indicate reproductive isolation among populations.

Natural spawners were sampled from several streams within a lower Cowlitz tributary system (Table 2; Figure 1b). Since most collections from a single stream of a tributary were too small for statistical tests we ran the tests with natural-origin spawners as a single group and divided into two tributary groups (Group 1 = Olequa, Stillwater and Campbell, and Group 2 = Arkansas, Monahan and Delameter. All hatchery-origin fish were excluded. Ostrander was excluded because a single fish was sampled). If the combined tributaries collection was out of HWE and tributary groups were in HWE, this would suggest some reproductive isolation among tributary groups. We also calculated the pairwise  $F_{ST}$  value for the tributary comparison. In one further assessment, we used self-assignment tests implemented in GeneClass2 (Piry et al. 2004, test detailed below), to calculate how well genotypes of individual fish matched those of other fish in their tributary group. If fish were genetically more similar to fish in their tributary group than to fish in the other tributary group this would also support reproductive isolation among the tributary groups.

We examined basic population structure among all winter- and summer-run steelhead samples using a dendrogram. Pairwise genetic chord distances (Cavalli-Sforza and Edwards 1967)

among collections were generated from allele frequencies using GENDIST in the program PHYLIP (Felsenstein 1993). A dendrogram ('tree') illustrating genetic relationships was constructed from pairwise chord distances using the neighbor-joining algorithm in the program NEIGHBOR in PHYLIP. To test the repeatability of tree branching, we made 10,000 bootstrap replicates of the pairwise chord distances using SEQBOOT in PHYLIP, tree topologies were created for all replicates using NEIGHBOR, and a consensus tree was produced using CONSENSE in PHYLIP.

We used the program GENETIX (Belkhir et al. 2004) to view genetic relationships among Lower Cowlitz tributary natural-origin spawners, adipose-clipped spawners, and the three Cowlitz Hatchery stocks, and among individuals within all collections from the Cowlitz basin. GENETIX performs a factorial correspondence analysis, which seeks the combination of allele frequencies that describes the most genetic variation among individuals. The program generates a plot of individuals in three dimensions according to their genotype (the first two dimensions generally encompass most of the genetic variance). Individuals that are genetically similar plot near each other and individuals that are genetically different plot distantly from each other. To view population centers, the program calculates the genetic center of each collection (*sur populations* option in GENETIX). In this function, the program also recalculates the position of individual fish in relation to the genetic center of its collection to better view collections with overlapping plots of individuals.

We used assignment tests and exclusion probabilities in the program GeneClass2 (Piry et al. 2004) to examine whether Cowlitz tributary natural-origin spawners were genetically distinct from Cowlitz Hatchery stocks. The assignment test assigns fish to the collection in which they have the highest likelihood of occurring, based on the fish's genotype and allele frequencies of all collections included as a baseline data set. The fish being tested is removed from its baseline collection and is compared to all baseline collections, which here included Cowlitz tributary natural-origin spawners and the three Cowlitz Hatchery stocks.

We conducted a first generation migrant analysis to examine whether Cowlitz tributary natural-origin spawners included recent descendants from Cowlitz Hatchery stocks. This test addressed the question of whether hatchery strays had spawned with each other or natural-origin fish in the previous generation. In this test, we used the Rannala and Mountain (1997) algorithm in GeneClass2 to calculate likelihoods that an individual fish originated in each of the four baseline collections. The program calculates the likelihood of drawing that individual's genotype from the collection where it was sampled ( $L_{\text{home}}$ ), based on the allele frequencies of the baseline collections (with the individual in question removed), and divides this likelihood by the highest assignment likelihood ( $L_{\text{max}}$ ) to any baseline collection (Paetkau et al. 2004). The program then computes the probability that each individual was a resident in its home collection with a Monte Carlo simulation (Paetkau et al. 2004). The simulation created 10,000 individuals for each baseline collection to simulate the genotypes likely to be encountered for that collection. Then it computed assignment likelihoods for simulated individuals (leaving out the simulated individual) and compared the likelihood of the genotype of the actual fish being tested to the distribution of the likelihoods for their simulated home collection. Fish were hypothesized as first generation migrants if their probability of

originating in their home collection was represented in less than 1% of the simulated values of their home collection.

We also used assignment tests to examine the origin of the adipose fin-clipped (“clipped”) fish that were collected in natural spawning areas. We used GeneClass2 with the Cowlitz tributary natural-origin and hatchery-origin collections for a baseline and then assigned the clipped fish as “unknown fish”. In this analysis the clipped fish were absent from the baseline and the program generates a likelihood for each fish of originating in each of the baseline collections, with the highest likelihood indicating the probable population of origin.

Previously, we reported our analysis of origins and ancestry of unmarked steelhead sampled in 2005 at the Cowlitz “Separator” just upstream from the Barrier Dam (Small et al. 2009). For this year’s analyses we retained the separator/Barrier Dam sample for region-wide analyses, but did not conduct specific tests regarding individual fish origins. The 2009 results showed that separator/Barrier Dam steelhead had nearly all of their ancestry in the Cowlitz Hatchery late-winter-run stock, which was expected due to the transportation restoration program in the upper watershed.

We used a Bayesian analysis implemented in the program STRUCTURE 2.2 (Pritchard et al. 2000) to estimate individual and population ancestry. STRUCTURE sorts individuals (or portions of individuals if they appear to have mixed ancestry) into a number of hypothetical clusters or populations (K) in order to minimize Hardy-Weinberg disequilibrium and linkage disequilibrium in the clusters or populations, since HWE and linkage equilibrium are characteristics of independent populations. The program calculates a likelihood value for the number of clusters or populations, given the data, with the highest likelihood value among the number of K’s tested indicating the number of genetically identifiable clusters in the data set. We included all Cowlitz tributary natural-origin spawners and hatchery collections and Coweeman River collections in one analysis and set the number of clusters or possible populations at 1 – 7. At K-value of 2 there are two possible clusters and we hypothesized that the genotypes would divide into a summer-run cluster and a winter-run cluster. For a K-value of 3 or 4, we hypothesized that the winter-run cluster would divide according to hatchery early- and late-run and natural-origin populations. Analyses were conducted in 5 independent runs that allowed admixture with 20,000 burn-ins and 230,000 iterations. In a second analysis we included eleven wild steelhead collections from other Cowlitz and lower Columbia drainages (Table 4) and set the number of clusters or possible populations at 2–11. In this analysis we were examining overall genetic structure among lower Columbia steelhead populations, looking for possible evidence of hatchery stock introgression. Hatchery introgression would be detected by portions of hatchery ancestry in natural-origin fish.

## **Results and Discussion**

### Basic 2008 and 2009 sample information

Fourteen fish failed to amplify at seven or more loci and were excluded from analyses (08DA0015, 06AP0010, 06AP0019, 06AP0022, 06AP0023, 06AP0031, 06AP0032,

06AP0034, 06AP0036, 06AP0042, 09AX0004, 05CD0014, 05CD0016, 05CD0017, 09CY0042). Four sets of fish had identical genotypes (08DC0018 and 08DC0030, 08DC0025 and 08DC0032; 06AP0048 and 06AP0051; 06AP0033 and 06AP0047), indicating that in four cases the same fish had been sampled twice. The first fish from each pair was included in analyses. Two fish were cutthroat trout or cutthroat-rainbow trout hybrids (05CD0020, cutthroat alleles at five loci; 06AP0016 cutthroat alleles at 6 loci) and were excluded from analyses. Hardy-Weinberg equilibrium values (HWE, as expressed by  $F_{IS}$ ) indicated significant homozygote excess in the 2008 Cowlitz Hatchery summer-run collection and in the two adult Coweeman collections (Table 5). HW disequilibrium was due mostly to excess homozygosity at a single locus, *One-102* (locus data not shown). An excess of homozygous genotypes could indicate that some related individuals were included or that larger alleles were not amplifying well in those collections (large allele drop-out). Gene diversity and allelic richness (based on 7 individuals, the smallest number of individuals with full genotypes) were significantly lower in the Cowlitz Hatchery late-winter-run collections ( $P$  values for Student's  $t$ -tests for lower diversity = 0.006 and 0.007, respectively, see Table 5), suggesting genetic drift in this population. Cowlitz tributary natural-origin spawners and hatchery collections had similar gene diversity and allelic richness (Table 5) compared to those characteristics in other Cowlitz and lower Columbia River steelhead collections, which averaged 0.809 and 10.45, respectively, among lower Columbia steelhead. Linkage equilibrium in each collection suggested that collections were from randomly mating populations but that the 08Cowlitz Hatchery summer-run collection and the 09Cowlitz Hatchery late-winter-run collection may have some source of disequilibrium (Table 5). Allele frequency differences were subtle between Cowlitz basin collections and among all steelhead collections from the lower Columbia River (data not shown).

We divided the Lower Cowlitz tributary natural-origin spawners into two groups representing fish from streams in the Olequa and Arkansas basins (see Table 2) and examined HWE and other statistics. Before division, the combined natural-origin spawner collection was out of HWE ( $F_{IS} = 0.07$ ,  $P = 0.04$ ) with a deficit of heterozygotes, suggesting cryptic subdivision in the combined group. When divided, Group 1 (Olequa system,  $N = 26$ ) was out of HWE for heterozygote excess and Group 2 (Arkansas system,  $N = 42$ ) was in HWE (Group 1  $F_{IS} = -0.041$ ,  $P = 0.97$  for homozygote excess and 0.02 for heterozygote excess; Group 2  $F_{IS} = 0.002$ ,  $P = 0.44$ ). These results support that the groups were each composed of individuals from a single population. The excess heterozygosity detected in Group 1 could be due to the small sample or population size. There was also significant genetic variance between the two groups (pairwise  $F_{ST}$  value = 0.011,  $P = 0.001$ ; pairwise genotypic test  $P = 0.001$ ). Gene diversity (Group 1 = 0.823, Group 2 = 0.826) and allelic richness (Group 1 = 9.68, Group 2 = 9.94) were not significantly different between the two groups (Student's  $t$ -test  $P = 0.4$  for both comparisons). In the assignment test (detailed below under "Assignment tests"), there was high self-assignment to each group (Figure 2) both with the criterion of accepting the highest assignment (76% Group 1 and 88% Group 2), and of a 90% threshold value (82% Group 1 and 94% Group 2). With the higher threshold there were some fish ( $N = 8$  and  $N = 7$ , respectively) that did not assign to a group. These fish plotted in the center of the cluster in Figure 2. We had a concern that the tributary groups were small and that the differentiation was the result of comparing two small groups that were different due to chance. Thus, as a further test, we randomly divided the natural-origin spawners into two groups and calculated genetic variance

(pairwise  $F_{ST}$  and genotypic tests), and neither was significant, supporting that genetic differences between the tributary groups were biologically significant rather than an artifact of comparing two small collections.

### Pairwise tests

Pairwise genotypic and  $F_{ST}$  test results were congruent and nearly all indicated significant differences among Cowlitz basin collections but not between 2008 and 2009 collections from the same population (Table 6). Cowlitz collections were also significantly different from summer and winter steelhead collections from other lower Columbia localities, with the exception of the comparison between the 2008 Cowlitz Hatchery late-winter broodstock sample and natural-origin steelhead sampled at the Cowlitz Barrier Dam/separator in 2005. Although the 2008 and 2009 collections of Cowlitz Hatchery late-winter broodstock were not differentiated from each other, the 2009 Cowlitz Hatchery late-winter broodstock sample was differentiated from the Cowlitz Barrier Dam natural-origin steelhead sample. However, the genetic variance between the 2009 hatchery and natural-origin steelhead was minimal (0.0074 or less than 1%). The average pairwise  $F_{ST}$  values for comparisons between Cowlitz Hatchery collections and the 12 lower Columbia region natural-origin steelhead collections were: summer-run 0.0227, early-winter 0.0241, and late-winter 0.0277. Average pairwise  $F_{ST}$  values were significantly less for the summer-run in comparison to late-winter (Student's t-test  $P = 0.006$ ) suggesting that natural-origin steelhead from lower Columbia tributaries had closer genetic relationships with Cowlitz Hatchery summer-run stock than with the late-winter-run stock.

Results from pairwise tests suggested that Cowlitz Hatchery late-winter steelhead are reproducing successfully upstream of the Barrier Dam (where they have been transported) due to little or low genetic divergence from natural-origin steelhead handled at the separator. While we did not determine whether pairwise  $F_{ST}$  values are significantly different from each other ( $P$  values evaluate whether the pairwise  $F_{ST}$  is significantly different from 0), the magnitude of the pairwise  $F_{ST}$  values suggested that the 2008 and 2009 Cowlitz tributary natural-origin spawner collections were genetically more similar to Cowlitz Hatchery early-winter and summer stocks than to the late-winter stock (Table 6). Average pairwise  $F_{ST}$  values in comparisons of natural-origin spawners to early-winter and to summer stocks were comparable and these were significantly lower than comparison to late-winter stocks. We used Student's t-tests to compare the average  $F_{ST}$  in comparisons of natural-origin spawners to early (0.020) versus late-winter stocks (0.030) and in comparisons of natural-origin spawners to summer (0.019) versus late-winter (0.030) stocks ( $P = 0.022$  and  $0.001$ , respectively). More variance (higher  $F_{ST}$ ) indicates less geneflow (or higher genetic drift) between two groups, such as between natural spawning populations and hatchery broodstocks. There were also temporal differences in comparisons between the Cowlitz tributary natural-origin spawners and the 2008 and 2009 early-winter-run broodstock samples (2008 early winter run average pairwise  $F_{ST} = 0.0152$ ; 2009 early-winter run average pairwise  $F_{ST} = 0.0251$ , Student's t-test  $P = 0.025$ ). These differences in comparisons to hatchery broodstocks may indicate different levels of hatchery introgression in different years into natural spawning populations or some inclusion of natural-origin fish in hatchery broodstocks. Overall it appears that Cowlitz hatchery fish derived from non-local broodstocks (Skamania and Chambers) have likely

strayed into natural spawning areas and reproduced successfully, including interbreeding with native steelhead.

### Dendrogram

The dendrogram illustrated some discrete clusters and some notable sample groupings among summer- and winter-run steelhead collections from the lower Columbia region (Figure 3). The tree gives information about genetic distances among collections, temporal stability and genetic drift. In general, the closer the branch connections (nodes), the more similar the collections and these similarities correspond with levels of variance presented in pairwise  $F_{ST}$  tests (Table 6). Temporal samples from each Cowlitz hatchery stock clustered together with 100% bootstrap support. Relatively long branch lengths and placement at branch terminuses suggested some genetic drift in hatchery collections, possibly from restricting broodstocks to marked fish collected within restricted time windows. Cowlitz separator/Barrier Dam steelhead clustered with the Cowlitz hatchery late-winter stock with 100% support, confirming last year's results. The 2008 and 2009 Cowlitz tributary natural-origin spawner collections clustered together on their own branch, and Elochoman steelhead grouped closest with them, although with moderate ( $\geq 70\%$ ) bootstrap support. There was moderate bootstrap support (77%) for a branch that included Cowlitz Hatchery summer-run, Kalama natural-origin summer-run, and Washougal and East Fork Lewis natural winter-runs. Cedar Creek trap steelhead (North Fork Lewis) grouped with 79% bootstrap support with Cowlitz Hatchery early-winter-runs. North Fork Lewis steelhead collected at Merwin Dam grouped with the Cedar Creek collection at a subsequent node. Toutle River steelhead samples (North Fork, South Fork and Green) formed a distinct cluster, and grouped most closely with Kalama wild winter-runs. The Coweeman smolt collection clustered closely with the 2006 Coweeman adult collection and the 2005 Coweeman adult collection did not appear to be as closely associated with them as one might expect, although this could be due to small sample size ( $N=19$ ).

### Factorial correspondence analysis

The factorial correspondence analysis (FCA) plot of the Cowlitz tributary natural spawners and Cowlitz hatchery collections illustrated differences estimated by pairwise  $F_{ST}$  values (Figure 4a and Figure 4b). The two temporal samples from each hatchery stock grouped together and each stock occupied distinct space. Tributary natural-origin spawners centered in their own space between the summer and early-winter-run hatchery fish and overlapped both groups. The clipped fish collected in tributaries plotted mainly with early-winter-run hatchery fish. When all steelhead collections from the lower Columbia region were plotted by FCA, overlap was high and the plot was uninformative (Figure 5a). This may reflect gene flow and common ancestry as suggested by genetic distance values and the dendrogram clustering (Figure 3), and the moderate to low pairwise  $F_{ST}$  values (Table 6). When population centers were viewed (Figure 5b), the Cowlitz Hatchery summer and late-winter collections plotted on opposite sides of the first axis and on the periphery of the second axis, supporting their genetic distinction. The Cowlitz Hatchery early-winter collection plotted on the periphery of the second axis but closer to the central cluster of lower Columbia region steelhead along the first axis, which included Cowlitz tributary natural spawners (Figure 5b), suggesting some genetic influence from Chambers Creek-origin hatchery stocks in these lower Columbia samples. The 2005

Coweeman adult collection plotted distantly from the 2005 Coweeman smolt and the 2006 Coweeman adult collections (Figure 5b), suggesting some source of temporal divergence or a small sample size effect.

### Assignment tests

GeneClass assignments and first generation migrant tests further supported genetic distinctions among Cowlitz hatchery stocks and tributary natural-origin spawners (Table 7a and 7b). We used 90% relative likelihood score as the cutoff value for a positive assignment (negative log likelihood values are under the ‘first generation migrant test’ columns in Table 7b; lowest number is the highest likelihood since they are negative values). Fish with assignment values below 90% were considered unassigned. For assigned fish (those with positive assignments), Cowlitz Hatchery steelhead had high (95-100%) correct self-assignment (assignment to their collection of origin, or “home” group). With the additional 2009 baseline collections in this year’s analysis, Cowlitz tributary natural-origin spawners had high correct self-assignment, among fish with positive assignments. Roughly 6% (3 of 47 2008 and 2009 fish positively assigned; Table 7a) of Cowlitz tributary natural-origin spawners assigned to Cowlitz Hatchery early-winter stock (but see first generation migrant discussion below). These hatchery-assigned fish support the presence of possibly unmarked hatchery fish in spawning areas (presumed natural-origin fish that assign to hatchery collections), or gene flow from that hatchery stock (true natural-origin fish that look genetically like hatchery fish), and suggested that hatchery input varied over time – mis-assigned fish were only in the 2008 collection. However, 15 fish (36%) in the 2009 tributaries sample could not be positively assigned to a group (Table 7a), suggesting higher genotypic variance in this sample.

The Cowlitz Hatchery late-winter-run steelhead had the lowest percentage (8%) of unassigned fish overall, and the Cowlitz tributary natural-origin spawners had the highest percentage of unassigned fish overall (31%; Table 7a). When fish are unassigned, they have similar assignment likelihoods to two or more collections such that they assign weakly (ratio is less than 90%) to a single collection. This could occur for several reasons, including if there is gene flow among spawning groups or one-way gene flow from a hatchery into natural spawning areas through straying. In sum, the high self-assignments and low “mis-assignments” support genetic distinction among hatchery groups and lower Cowlitz tributary natural-origin spawners.

To further assess the possibility of hatchery fish straying into natural spawning areas we conducted a first-generation migrant test (Table 7b). For Cowlitz tributary natural-origin spawners, most of the likelihoods of their assignments were within the simulated values for their home collection, with the exception of two fish (08DC0003, 09CY0018). In the assignment test 08DC0003 assigned to the Cowlitz Hatchery early-winter stock and 09CY0018 assigned weakly (below 90% cutoff) to the Cowlitz Hatchery summer stock (Table 7b), suggesting that they were actual, or descendants of, hatchery strays. Two other fish (08DC0014, 08DC0022) assigned to Cowlitz Hatchery early-winter stock in the assignment test but were above the 1% probability threshold of arising from Cowlitz tributary natural-origin spawners in the first generation migrant test (Table 7b). The simulation generated 10,000 genotypes that might be expected from Cowlitz tributary natural-origin spawners and

the genotypes for these two fish were within the 99% expectation interval for genotypes for natural-origin spawners, even though the assignment likelihood was higher to the hatchery stock.

The clipped fish collected in natural spawning areas in Lower Cowlitz tributaries were assigned as unknown fish using the same baseline as above analyses (Table 7b at end of table). Five assigned as early-winter-run hatchery fish, one assigned as a late-winter-run hatchery fish and two assigned below the threshold value, one as late-winter-run and one as summer-run. Thus, about 63% of the hatchery strays were early-winter stock origin. The presence of hatchery fish in natural spawning areas corroborates the signals of introgression from hatchery fish suggested in other analyses.

### STRUCTURE analysis

GeneClass and STRUCTURE are similar in that they assign individuals to populations. However, they differ in that GeneClass calculates assignment likelihoods for the whole individual to user-defined baseline populations. STRUCTURE uses no *a priori* knowledge about populations to divide up all the alleles in the dataset into clusters or populations and may assign portions of an individual to different populations if its alleles at some loci are more common in different population clusters. We use both analyses to examine relationships among populations and identify individuals with mixed ancestry.

STRUCTURE results can be difficult to interpret. Adding population data can alter relationships estimated among collections in a previous analysis since the gene pool is altered and the program works on partitioning the total gene pool. Closely related populations may be significantly different by other measures but indistinct using STRUCTURE (STRUCTURE can resolve differences associated with a pairwise  $F_{ST}$  value of 0.03 or greater (Latch et al. 2006), when there are less than ten distinct genetic groups in the data set (Pritchard et al. 2000). Pritchard et al. (2000) did not specify the level of genetic distinction that can be resolved but empirical evidence (Small, unpublished data) indicates that increasing the number of populations in the data set increases the challenge to resolve population structure. Results are best interpreted in concert with those from other analyses. Thus, where STRUCTURE indicates an individual may have mixed ancestry, the individual is often unassigned in GeneClass due to similar assignment likelihoods to more than one population, which supports mixed ancestry for this individual. But the actual ancestry values (F1 hybrid? or beyond?) are more difficult to quantify and confidence intervals are generally wide for ancestry values (Small, unpublished data). More loci would likely increase the precision and accuracy for ancestry values but the locus set we employ is useful for general resolution.

The STRUCTURE analysis supported results from other analyses as described above. STRUCTURE sorts individuals (or portions of individuals if they are of mixed ancestry) into genetically similar clusters. In this analysis, we used membership in a cluster to identify genetically distinct populations – if most individuals from a putative population or group (e.g., Cowlitz Hatchery summers) occupy one cluster, this cluster is identified and named as that population or group. Membership (“ancestry”) in each hypothetical cluster is calculated for each individual, and results per individual are given as the percentage of membership in each

cluster. These same results are also presented graphically, with individuals represented by bars of color, with different colors corresponding to the different clusters (individuals with ancestry in multiple clusters would have multiple colors in their bar of color).

We analyzed the data from  $K = 1$  to 6 with only 2008 and 2009 Cowlitz hatchery and tributary collections and then analyzed data from  $K = 3$  to 7 adding Coweeman collections. In the analysis with only the 2008 and 2009 Cowlitz collections the likelihood values were essentially the same at  $K = 3-5$  (2: -22797; 3: -22483; 4: -22494; 5: -22478; 6: -22594). We included Coweeman collections to examine genetic grouping in the presence of other natural-origin steelhead in the Cowlitz basin. This inclusion altered the analysis such that the likelihood values peaked sharply at  $K = 4$  (3: -32205; **4: -31914**; 5: -32180; 6: -32326; 7: -32450) and allowed better resolution between natural-origin and hatchery-origin fish in the Cowlitz basin. At  $K = 3$  (data not shown) the three hatchery groups each occupied their own cluster and natural-origin fish from Lower Cowlitz tributaries and Coweeman divided between summer and early-winter clusters. At  $K = 4$  the Cowlitz tributary natural-origin spawners clustered with Coweeman individuals and together formed a definitive group showing some level of ancestry shared with hatchery collections (Figure 6). The clipped fish were predominantly hatchery early-winter ancestry. Each collection included individuals with ancestry primarily in another cluster. For instance, in the 2009 Cowlitz Hatchery early-winter-run collection (represented by green in Figure 6), there were four individuals with at least 50% ancestry in another cluster indicated by different colors (not green) in their color bar. A few 'mostly green or blue' individuals in the Cowlitz Hatchery summer and early-winter collections and a few 'mostly blue or red' individuals in the Cowlitz Hatchery late-winter collection suggested that some individuals with alternative or mixed ancestry were included in broodstock samples (Figure 6). Most of these fish were unassigned or assigned out of their home collection in the GeneClass assignment test (see individuals in Table 7b).

There were temporal differences in ancestry portions between the Cowlitz tributary natural-origin spawner collections. The 2008 collection had more summer-run ancestry than the 2009 collection (Figure 6 and Table 8). In the 2008 collection 8/26 individuals had at least 30% ancestry in the summer-run cluster, and in the 2009 collection 8/42 individuals had at least 30% ancestry in the summer-run cluster. Early-winter-run ancestry was similar between collection years. Cowlitz tributary natural-origin spawner collections had 54 to 61% ancestry in a cluster that also contained Coweeman samples (Table 8). Hatchery collections had roughly 80% or higher ancestry in a single cluster (Table 8). The lower ancestry in a single cluster for the natural-origin fish and ancestry shared with hatchery clusters suggests some introgression by hatchery stocks into natural spawning populations.

We also conducted a STRUCTURE analysis including all the lower Columbia region steelhead collections (Table 4). Results are shown as a color bar chart in Figure 7 and summarized in Table 9. In this analysis  $K = 5$  had the highest likelihood value (-92,934) but was only slightly higher than  $K = 4$  (-93,023), so we present summaries for both  $K = 4$  and  $K = 5$ . At  $K = 4$ , the collections with the highest membership in the four hypothetical clusters were Cowlitz Hatchery early-winter in cluster 1 (~75%), Cowlitz Hatchery late-winters in cluster 2 (~81%), Cowlitz Hatchery summers in cluster 3 (~68%), and North Fork Toutle winters in cluster 4 (~61%). These four collections were also at branch terminuses in the dendrogram (Figure 3).

The cluster occupied by North Fork Toutle winters included substantial portions of natural spawners from nearby tributaries (Table 9). At  $K = 4$  Cowlitz tributary natural-origin spawners, Coweeman adults and juveniles, and Elochoman natural spawners had nearly equal ancestry in the early-winter-run and the North Fork Toutle clusters (Table 9).

At  $K = 5$ , the hatchery collections remained primary occupants of their respective clusters, Coweeman fish became primary occupants of a fourth cluster and Toutle fish remained primary occupants of a fifth cluster (Table 9). Cowlitz and Elochoman natural spawners had roughly 30% ancestry in the cluster that was now occupied primarily by Coweeman, roughly 30% ancestry in the early-winter-run cluster, and roughly 20% ancestry in the North Fork Toutle cluster. As found in Small et al. (2009) estimated ancestry of the Cowlitz Barrier Dam/separator collection was very similar to that of Cowlitz Hatchery late-winter-run collection (Table 9), supporting that they are derived from the same population with little genetic input from non-local hatchery broodstocks.

Different STRUCTURE analyses estimated different levels of ancestry in Cowlitz tributary natural-origin steelhead, as shown in Tables 8 and 9. For example, in the analysis with few populations Cowlitz Hatchery early-winter stock ancestry was estimated at about 19% and 18% in the 2008 and 2009 tributary samples, respectively, with  $K = 4$  (Table 8). In the context of multiple lower Columbia region population samples Cowlitz Hatchery early-winter stock ancestry was estimated at 30% and 44% in the 2008 and 2009 tributary samples, respectively, with  $K = 4$  (Table 9). This same analysis with  $K = 5$  estimated different ancestry values from those resolved at  $K = 4$  (Table 9). As described earlier, STRUCTURE results are likely to vary when the total gene pool assessed is larger. Also, if genetic relationship among collections or putative populations added to a data set are relatively close (e.g., low  $F_{ST}$  values), ancestry will be more difficult to resolve. Regarding hatchery early-winter stock ancestry in tributary natural-origin steelhead, STRUCTURE results overall suggested that it was substantial even though a value was not precisely estimated.

As discussed in Small et al. (2009), there was more genetic structure among the collections than is described in the STRUCTURE analysis. The program has limits to its resolving power and was used here to explore general structure and possible hatchery stock introgression in lower Columbia region steelhead populations. All collections of natural-origin (un-clipped) steelhead shared some ancestry with the three hatchery stocks used in our analyses, but North Fork Toutle collection appeared to share the least ancestry with hatchery stocks (Table 9). Since most hatchery populations throughout this region were founded with out-of-basin broodstocks, this shared ancestry likely indicates various levels of hatchery stock introgression into natural spawning populations.

## Conclusions

Natural-origin steelhead collected in lower Cowlitz River tributaries were genetically distinct from Cowlitz Hatchery broodstocks but showed genetic influence from hatchery stocks, in particular the non-local early-winter stock. Among Cowlitz natural-origin spawners three fish assigned to the early-winter stock with high likelihood, and of the hatchery ancestry detected in

the STRUCTURE analysis at  $K = 5$ , the highest proportion was with the “early-winter” cluster. There was likely a component of the hatchery summer stock in the natural-origin spawners collection, suggested by the roughly 12% portion of ancestry in the “summer” cluster in the STRUCTURE analysis. The lower assignment rate to collection of origin for Cowlitz tributary natural-origin spawners also supported mixed ancestry. In this case, some fish assigned to hatchery early-winters and others were nearly equally likely to have originated in a natural-origin and hatchery-origin collection and thus did not assign with confidence to a single collection.

As a group, lower Cowlitz tributary natural-origin spawners were genetically distinct from all other steelhead collections from the lower Columbia region, including the unmarked, natural origin fish collected at the Cowlitz Barrier Dam/separator. Pairwise  $F_{ST}$  values, the dendrogram and the STRUCTURE analysis suggested that Lower Cowlitz tributary steelhead were most similar to Elochoman and Coweeman natural-origin steelhead. There was also genetic distinction between natural-origin steelhead spawning in the two major Cowlitz tributary groups represented in the dataset.

The risk of future introgression and/or ecological impacts appeared to be greatest from the hatchery early-winter run stock. The majority of adipose fin-clipped fish sampled in lower Cowlitz tributaries originated from the early-winter stock. Our tributary sampling did not begin until late March, thus we would not have observed any hatchery early-winter run fish that may have been in the tributaries during their typical early return period between December and February. A more complete assessment of hatchery stock impacts should include observations and sampling during the early winter.

In addition to adult sampling in expanded time frames, we think it is worth considering the Phase 2, juvenile sampling, aspect of the project. In our study proposal, we anticipated that a second phase might be useful for further evaluation of hatchery stock impacts. Phase 2 was framed as follows: “If it is found that hatchery fish are entering the spawning grounds but little or no introgression is found in natural origin adults from the previous brood years, then juvenile sampling should begin”. This phase is important for determining whether (1) hatchery fish are producing offspring in the tributary where they were captured, (2) introgression is occurring and can be detected in juveniles, and (3) the level of juvenile production among hatchery-origin fish may pose an ecological risk to natural populations. We think our current results show that introgression has occurred. Juvenile sampling could be most useful for addressing issues 1, hatchery fish acting as a temporally separate breeding group, and 3, ecological risks posed by offspring of hatchery parents, above. If juvenile sampling were conducted, the timeframe and geographical coverage may need to be extensive, in order to account for life-history and rearing habitat diversity.

The Cowlitz Hatchery stocks were genetically distinct from each other. However, the assignment test and the STRUCTURE analysis suggested that some fish in hatchery collections had mixed ancestry and thus did not assign with high probability to their home hatchery collection. The assignment test also identified a few fish in the Cowlitz Hatchery summer-run collection as Cowlitz Hatchery early-winter-run fish or Cowlitz tributary natural-origin fish, suggesting some early-winter-run and natural-origin fish had been included in the summer-run

broodstock. The Cowlitz Hatchery stocks were also distinct from other Cowlitz and lower Columbia region steelhead collections, with the exception of the comparison between the Cowlitz Hatchery late-winter and Barrier Dam/separator natural-origin collections.

Findings relative to the study's hypotheses are as follows:

1. *Un-marked (putative natural-origin) adult steelhead sampled from different tributaries of the Lower Cowlitz River are genetically distinct from hatchery-origin steelhead.*

- Results showed that, although there has been some hatchery introgression, the natural-origin tributary spawners were different from the hatchery broodstocks.

2. *The genetic profiles of un-marked adult steelhead are distinct among different tributaries.*

- Steelhead from the Arkansas and Olequa basins are distinct from each other.

3. *Lower Cowlitz tributary natural-origin steelhead are genetically distinct from steelhead in other Cowlitz sub-basins and Lower Columbia tributaries.*

-The Cowlitz tributary natural-origin steelhead were genetically distinct from all other steelhead in other Cowlitz sub-basin and Lower Columbia tributaries. They were closest genetically to the Coweeman and Elochoman collections. This genetic similarity may be due to sharing founders from the same ancestral population and gene flow among lower Cowlitz tributary groups, and some similarity may be due to introgression in natural spawning populations from a common out-of-basin hatchery stock, particularly the early-winter-run stock founded from Chambers Creek in Puget Sound.

4. *Cowlitz hatchery stocks are genetically distinct among themselves, such that 95% of fish assign back to their stock of origin with high probability.*

-The hatchery stocks were genetically distinct among themselves and if only fish with greater than 90% relative likelihood of assignment are considered, 95 to 100% of fish assigned back to their stock of origin with high probability. If all fish sampled per broodstock are considered (positively assigned with 90% relative likelihood and ambiguously assigned with less than 90% relative likelihood), the percentage of fish assigning back to their stock of origin changed to: 88% for Cowlitz Hatchery late-winter-run; 86% for Cowlitz Hatchery summer-run; 79% for Cowlitz Hatchery early-winter-run.

5. *Cowlitz hatchery stocks are genetically distinct from other lower Columbia hatchery stocks and wild populations.*

- The three Cowlitz Hatchery stocks were distinct from the eleven wild or natural-origin steelhead population samples we had for testing. We did not have samples from any other lower Columbia region hatcheries to test.

6. *Un-marked steelhead sampled at the barrier dam in 2005 and passed upstream are genetically distinct from the two non-local hatchery stocks, and most similar to the late-winter hatchery stock.*

-This hypothesis was correct.

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Figure 1a. Map of lower Cowlitz Basin, steelhead distribution, and other drainages or features referred to in the report. Note that steelhead distribution is shown in yellow and may be obscured by overlaid blue drainage outlines at the scale of this image.

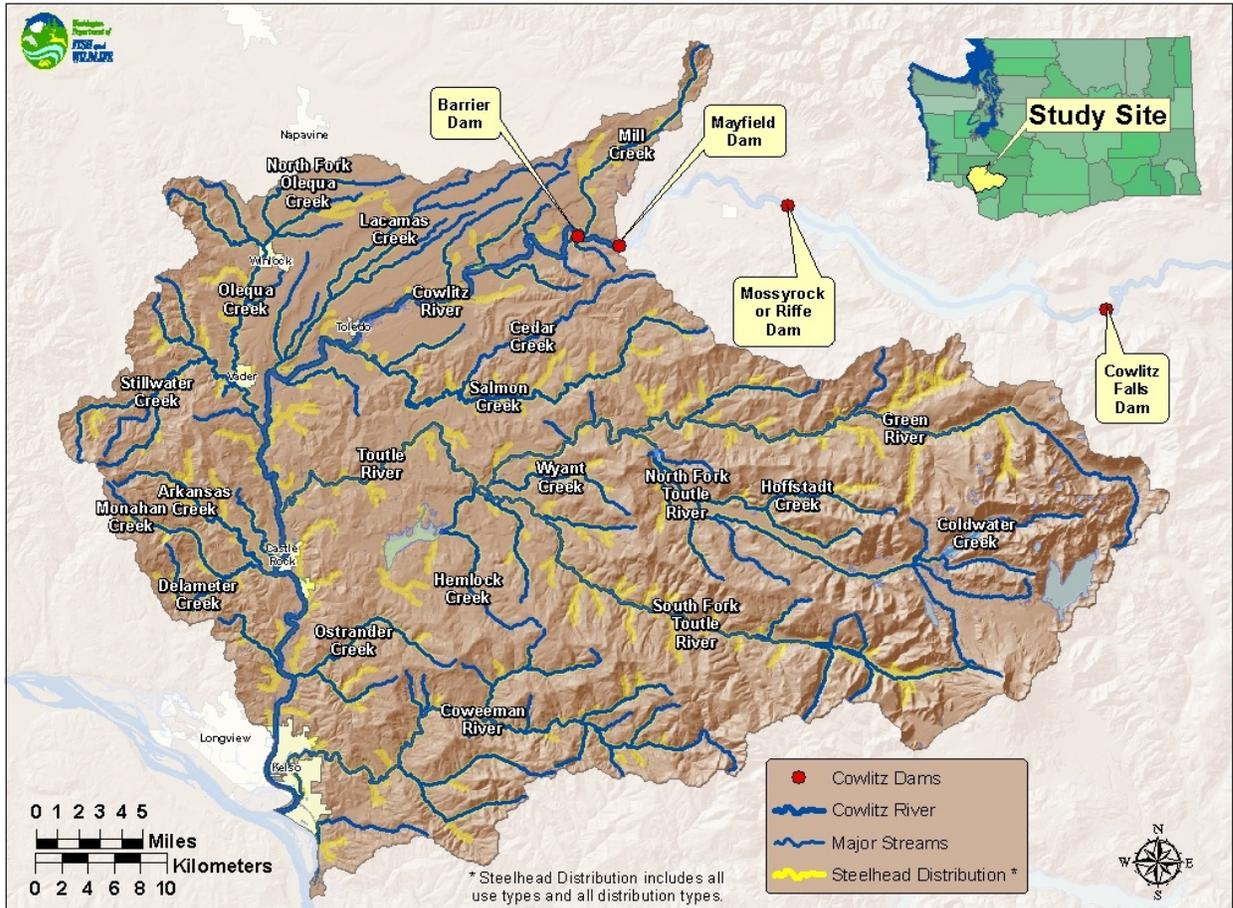


Figure 1b. Fine-scale map of tributaries in the Lower Cowlitz basin where natural spawning steelhead were collected 2008-2009. Circles roughly enclose tributary groups (see Table 2).

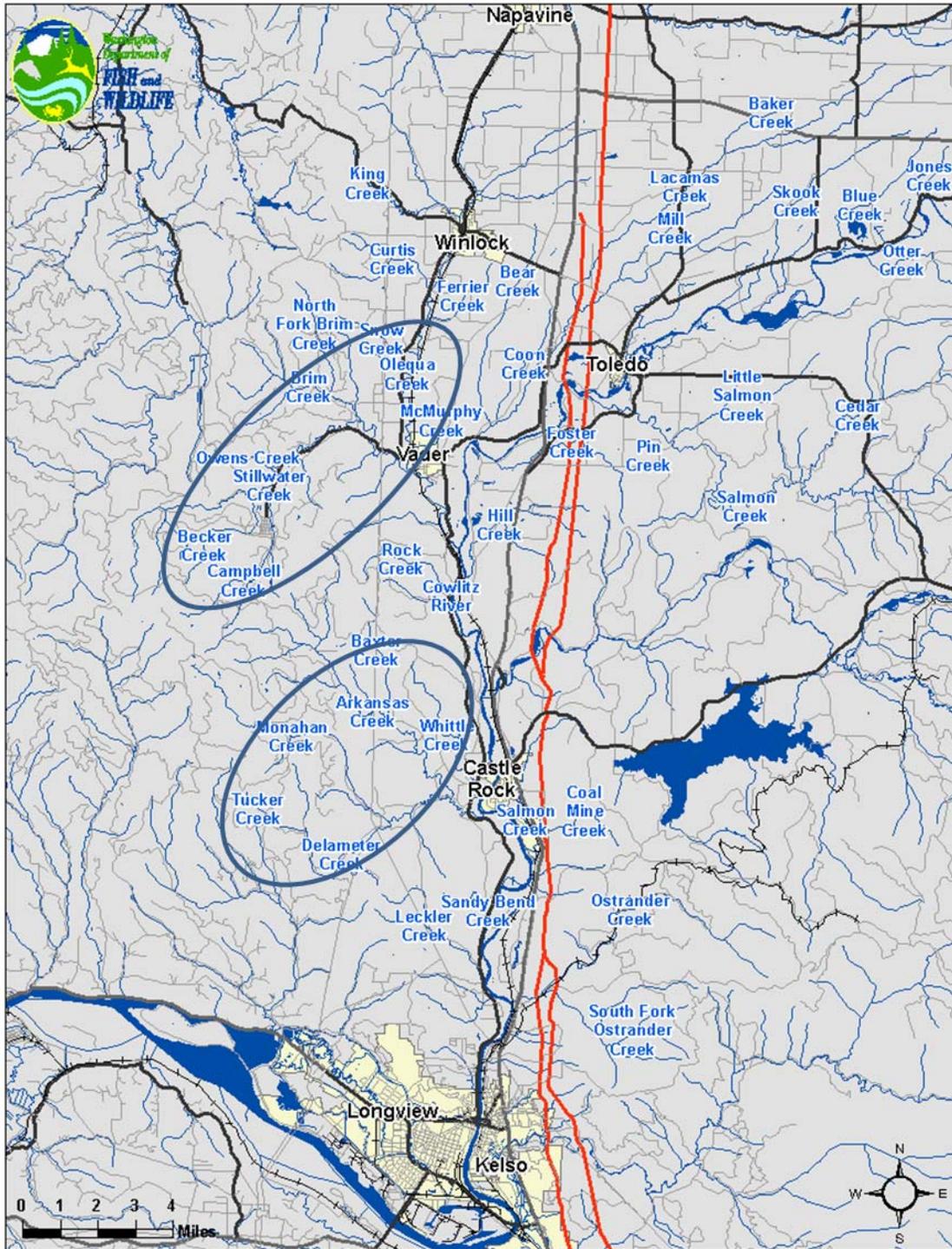


Figure 2. Plot of the GeneClass assignment values for Group 1 and Group 2, the tributary groups composed of natural-origin spawners (Group 1 = Olequa, Stillwater and Campbell, and Group 2 = Arkansas, Monahan and Delameter, all hatchery-origin fish excluded). The plot shows some overlap among assignment values but also distinction between the groups.

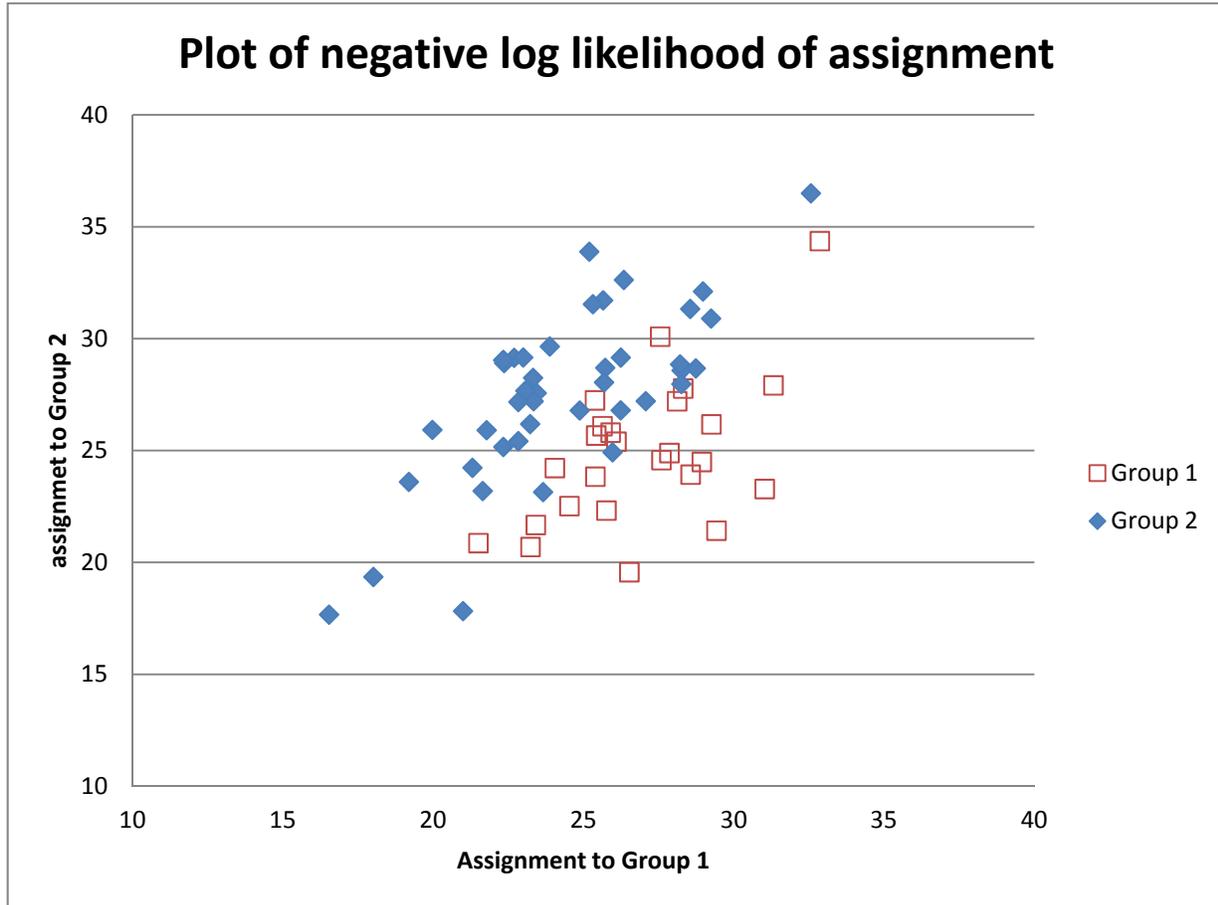


Figure 3. Neighbor-joining dendrogram of genetic distances among Cowlitz and lower Columbia region steelhead collections (see Tables 1 and 4 for collection details). Numbers at the nodes are bootstrap values or the percentage of trees in which the collections beyond the node occurred together in the consensus tree of 1000 trees.

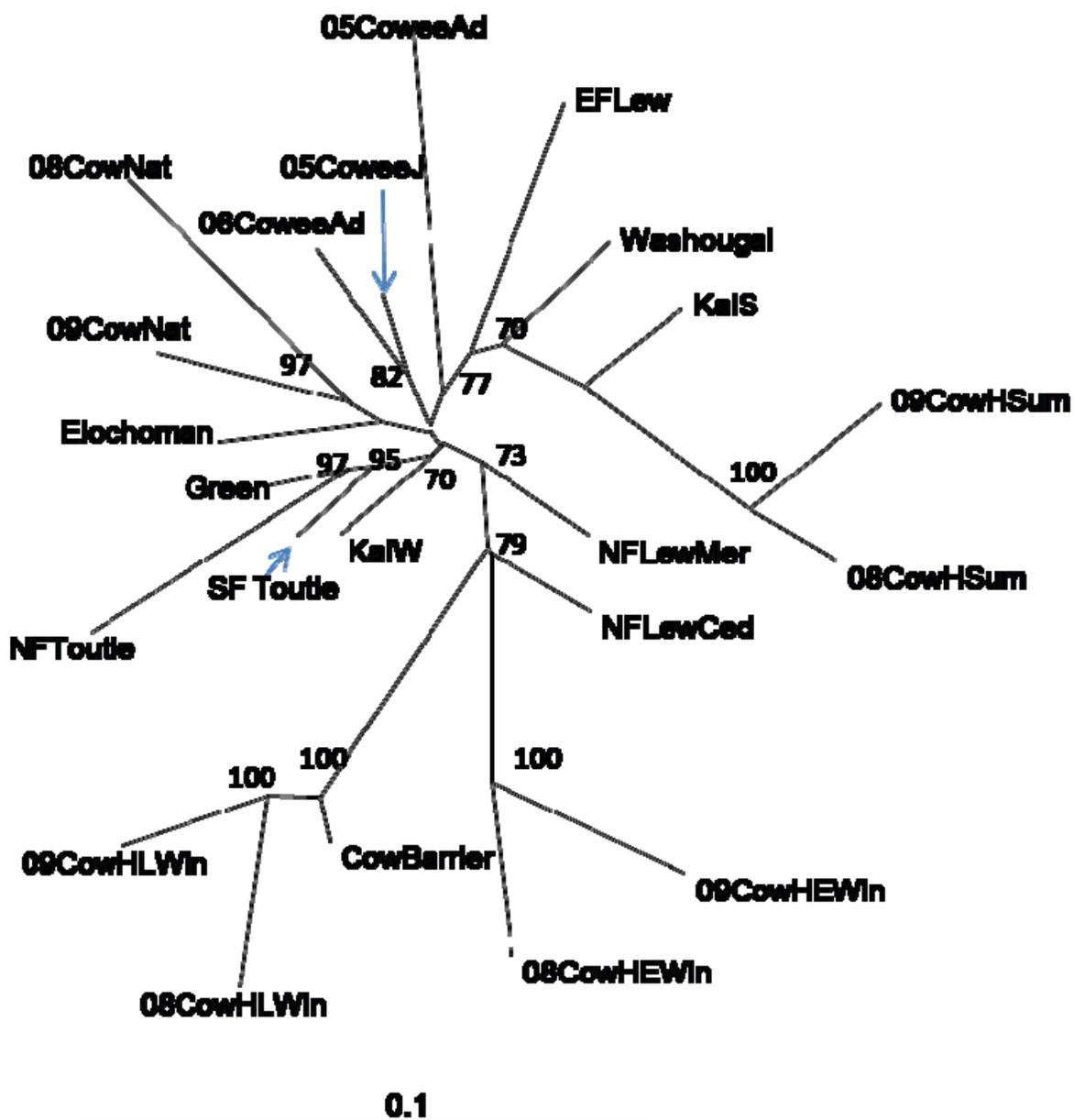


Figure 4a and 4b. Factorial correspondence analysis plot of 2008 and 2009 Cowlitz basin individuals (Figure 4a) and sample collection centers (Figure 4b). See Table 1 for sample names and details.

Figure 4a.

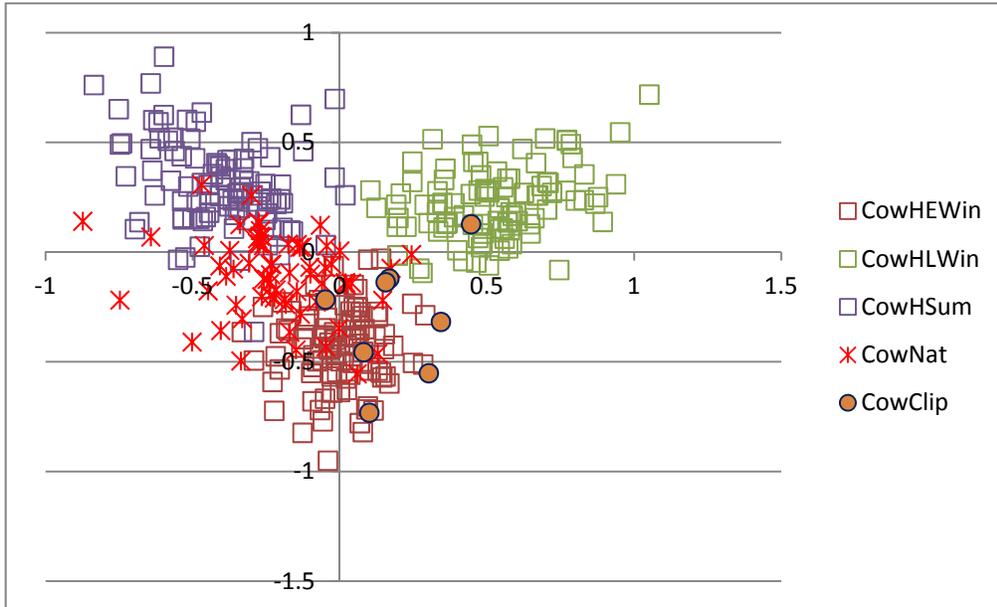


Figure 4b.

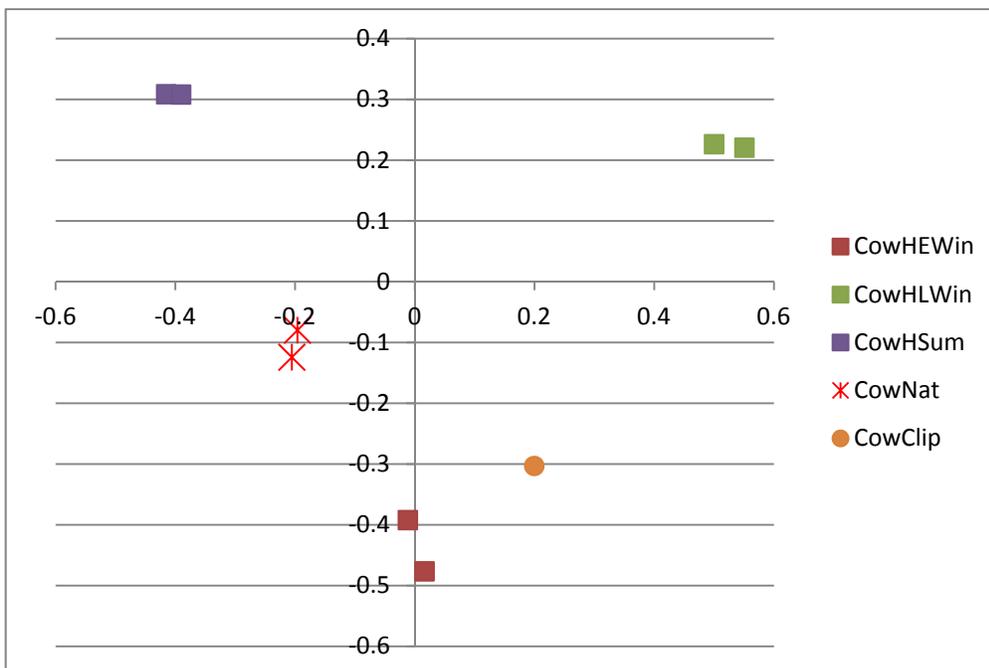


Figure 5a. Factorial correspondence analysis plot of all lower Columbia region steelhead collections, as described in tables 1 and 4. The Cowlitz basin samples have their own symbols and the rest of the lower Columbia basin samples are identified with blue diamonds.

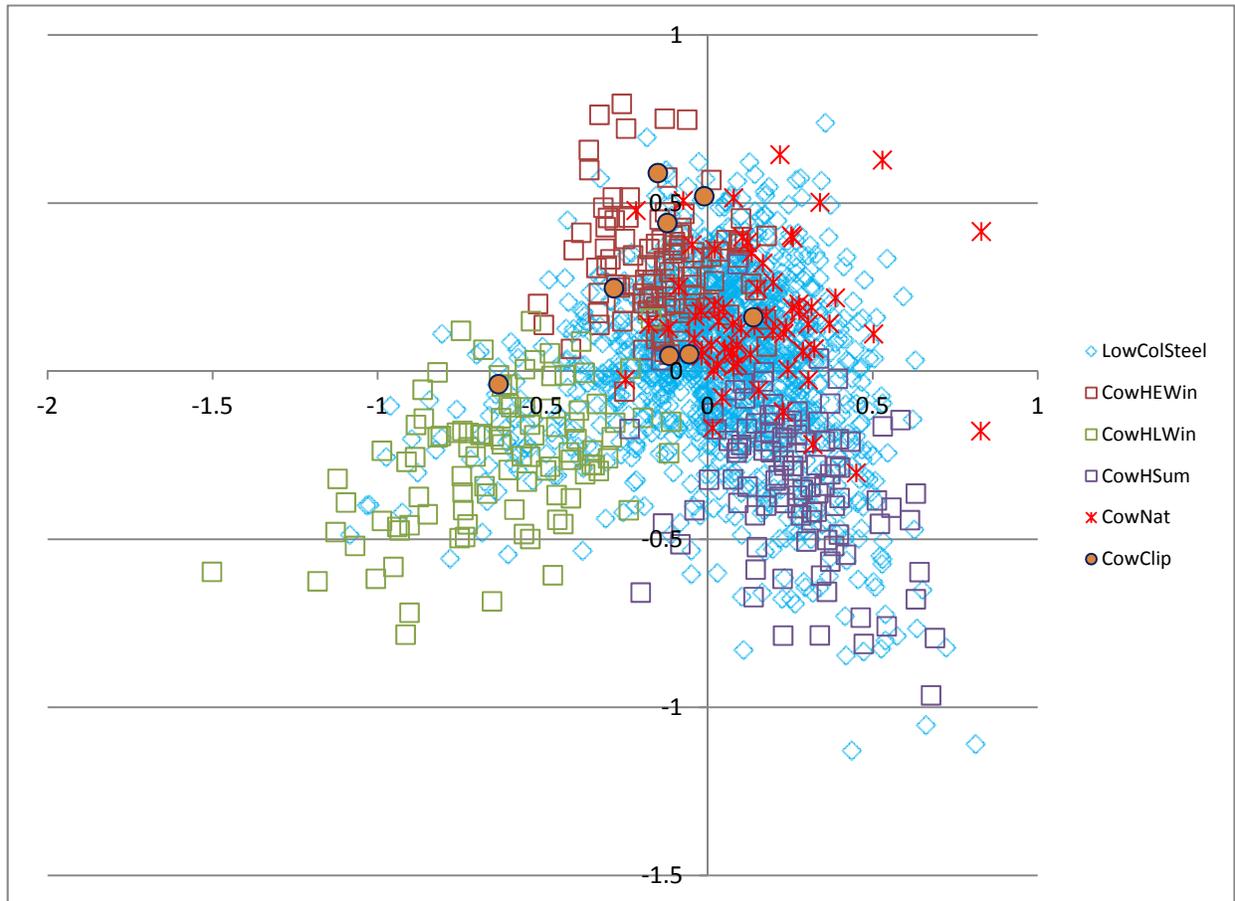
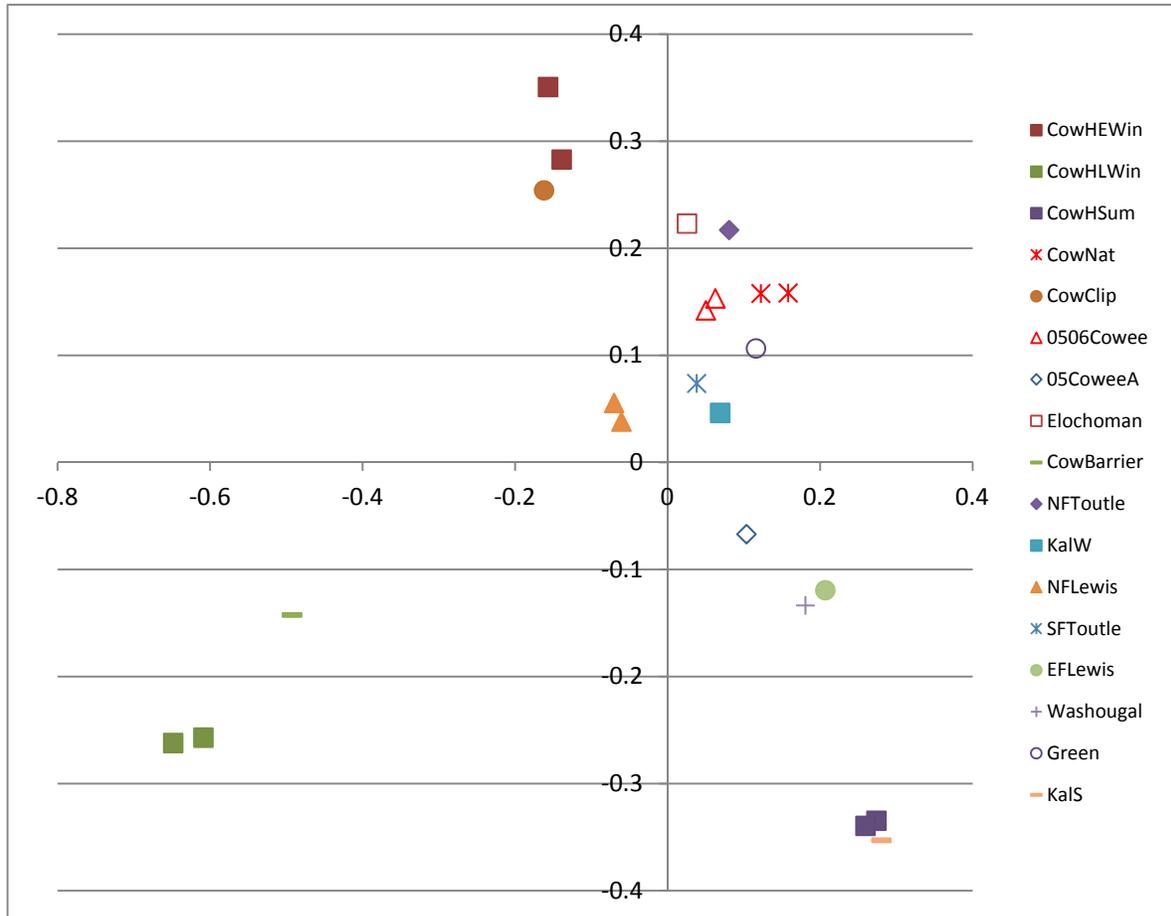


Figure 5b. Factorial correspondence analysis plot of collection centers from Figure 5a for lower Columbia steelhead. These points are the centers of the clusters of individual points for each collection in Figure 5a (individual Lower Columbia steelhead population centers identified).



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Figure 6. Individual ancestry values for 2008 and 2009 Cowlitz basin collections from STRUCTURE at  $K = 4$ , the most likely number of clusters. Each individual within a collection is represented by a bar of color. The bar of color is associated with a cluster; single color suggests pure ancestry and multiple colors suggests mixed ancestry (ancestry in more than one cluster). Collections are decomposed into cluster memberships below top combined color bar. Table 8 has percentage of ancestry values (percentage of color) in numerical format for each individual and presents the average ancestries over all individuals in each collection.

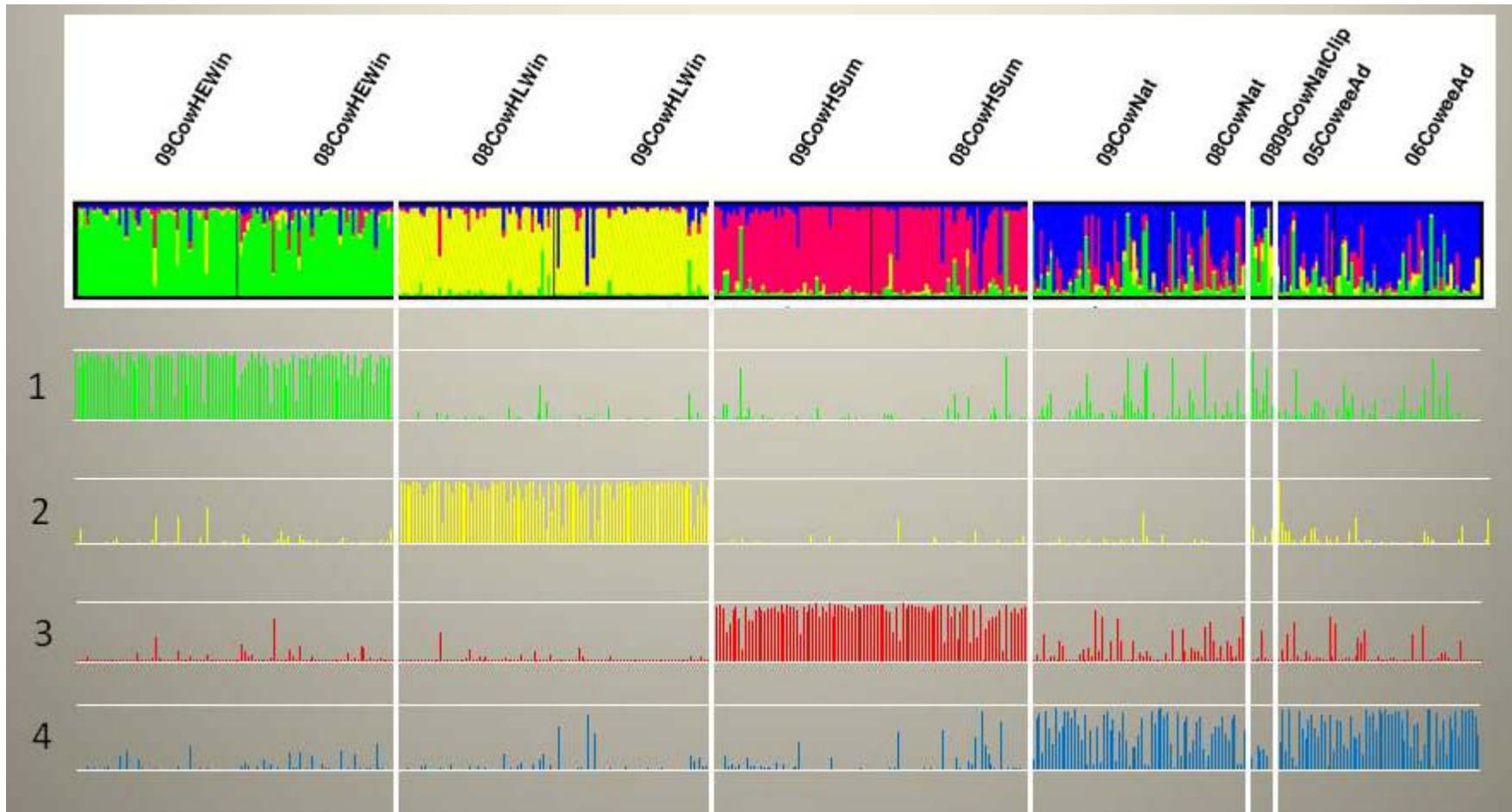
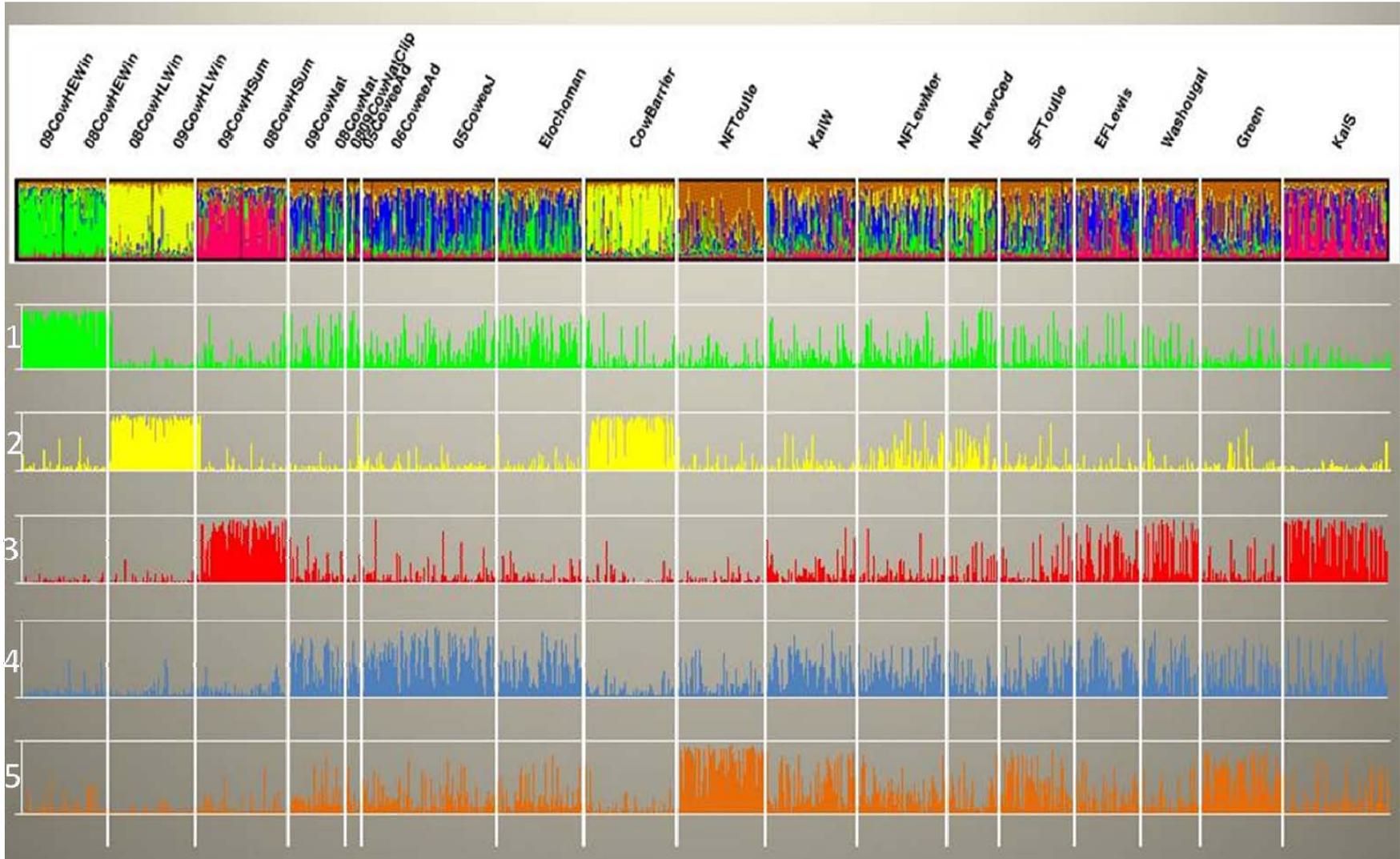


Figure 7. Individual ancestry values for all lower Columbia R. collections from STRUCTURE at  $K = 5$ . Each individual within a collection is represented by a bar of color. The bar of color is associated with a cluster; single color suggests pure ancestry and multiple colors suggests mixed ancestry (ancestry in more than one cluster). Table 9 has percentage of ancestry values (percentage of color) averaged over all individuals in each collection in numerical format.



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Table 1. Cowlitz steelhead samples for lab analysis in 2008 and 2009; N is number of fish analyzed.

WDFW Code	Sample Name	N	Comments	Abbreviation
08DA	Cowlitz Hatchery early-winter-run adults	49	Chambers Creek stock origin	08CowHEWin
09AW	Cowlitz Hatchery early-winter-run adults	50	Chambers Creek stock origin	09CowHEWin
08DD	Cowlitz Hatchery late-winter-run adults	50	Cowlitz native-origin	08CowHLWin
09AX	Cowlitz Hatchery late-winter-run adults	50	Cowlitz native-origin	09CowHLWin
08CB	Cowlitz summer-run adults	50	Skamania Hatchery stock origin	08CowHSum
09AY	Cowlitz summer-run adults	50	Skamania Hatchery stock origin	09CowHSum
08DC	Cowlitz tributaries natural-origin adults	26	multiple tributaries	08CowNat
09CY	Cowlitz tributaries natural-origin adults	42	multiple tributaries	09CowNat
08DC & 09CY	Cowlitz tributaries clipped adults	4,4	unknown hatchery origin	0809CowClip
05CD	Coweeman adults	19	natural origin	05CoweeAd
06AP	Coweeman adults	55	natural origin	06CoweeAd
	<b>Total</b>	<b>449</b>		

Table 2. 2008-2009 Lower Cowlitz tributary Steelhead sampling summary and sample data. Origin for clipped samples from GeneClass assignments in Table 7b.

2008	Group	Stream	Section	Sample #	Date	Sex	Size Inches	Ad-clipped	Origin	Age from Scale data	Spawning	
	Group 2	Monahan	M-2	08DC0001	19-Mar	M	24	No			Unknown	
	Group 2		M-2	08DC0012	8-Apr	M	24	No		R.1+	Unknown	
	Group 2		M-3	08DC0016	10-Apr	M	27	No		2.1+	Unknown	
	Group 2		M-3	08DC0018	15-Apr	M	Unknown	Unknown			Unknown	
	Group 2		M-3	08DC0023	22-Apr	M	Unknown	Unknown			Unknown	
	Group 2		M-3	08DC0024	23-Apr	M	25	Yes	CowEWin	1.1+	Unknown	
	Group 2		M-3	08DC0025	24-Apr	F	28	No		R.1+	Unspawned	
	Group 2		M-3	08DC0026	24-Apr	Unknown	Unknown	Unknown			Unknown	
	Group 2		M-3	08DC0027	28-Apr	M	25	No		R.1+	Ripe	
	Group 2		M-3	08DC0028	30-Apr	M	31	No		2.1+	Ripe	
	Group 2		M-3	08DC0029	30-Apr	M	30	Yes	CowSum	1.1+	Ripe	
	Group 2		M-3	08DC0030	12-May	M	29	No		R.1+	Ripe	
	Group 2		M-3	08DC0031	12-May	M	28	No		R.1+	Ripe	
	Group 2	M-3	08DC0032	24-Apr	Unknown	Unknown	Unknown			Unknown		
	Group 1	Olequa	O-3	08DC0017	11-Apr	F	27	No		2.1+	½ Spawned	
			O-7	08DC0020	19-Apr	F	24	Yes	CowEWin		Not ripe	
	Group 1		O-8/O-9	08DC0011	8-Apr	F	32	No		2.1+	Unspawned	
	Group 1		O-10	08DC0006	29-Mar	M	28	No			Unknown	
	Group 1		O-10	08DC0008	1-Apr	M	27	No		R.1+	Ripe	
	Group 1		O-11	08DC0022	22-Apr	M	27	No		Unknown	Ripe	
	Group 1		O-12	08DC0002	24-Mar	M	18	No		R.+	Unknown	
	Group 1		O-12	08DC0004	26-Mar	F	25	No		R	Spawned out	
	Group 2		Delameter	D-3	08DC0010	2-Apr	F	25	No		R.1+	Spawned out
	Group 2			D-3	08DC0013	8-Apr	M	32	No		2.1+	Unknown
	Group 2	D-3		08DC0019	19-Apr	M	30	No		Unknown	Ripe	
	Group 2	D-3		08DC0021	20-Apr	M	29	No			Unknown	
	Group 1	Stillwater	S-6	08DC0007	31-Mar	M	32	No		R.1+S+S+	Ripe	
	Group 1		S-6	08DC0015	9-Apr	M	39	No		R.2+	Ripe	
	Group 1		S-8	08DC0005	29-Mar	M	28	No		R.1+	Ripe	
	Group 1	Campbell	C-2	08DC0014	9-Apr	M	36	No		2.2+	Ripe	
			Baxter	Culver Coyote Rd	08DC0009	1-Apr	M	26	Yes	CowEWin	1.1+	Ripe
	Group 3	Ostrander	O-1	08DC0003	25-Mar	M	24	No		2.1+	Ripe	

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2009	Group	Stream	Sample #	Date	Sex	Size Inches	Ad-clipped	Origin	Age from Scale data	SCALE CARD #	
	Group 2	Arkansas	09CY0004	12-Mar-09	M	27	no		R.1+	3367	
	Group 2		09CY0016	31-Mar-09	M	31	no		2.1+S+	3368	
	Group 1	Campbell	09CY0002	5-Mar-09	M	27	no		2.1+	3367	
	Group 1		09CY0003	5-Mar-09	M	28	no		2.1+	3367	
	Group 1		09CY0005	16-Mar-09	F	31	no		2.1+S+	3367	
	Group 1		09CY0007	19-Mar-09	M	35	no		W1.2+	3367	
	Group 1		09CY0013	27-Mar-09	M	27	no		R.1+	3368	
	Group 2	Delameter	09CY0010	25-Mar-09	M	28	no		2.1+	3368	
	Group 2		09CY0020	7-Apr-09	M	24	no		2.1+	3368	
	Group 2		09CY0023	9-Apr-09	M	30	no		2.1+	3369	
	Group 2		09CY0029	15-Apr-09	M	19	yes	CowEWin	1.+	3369	
			09CY0035	22-Apr-09	M	29	no		2.1+	3371	
	Group 2	Monahan	09CY0001	4-Mar-09	M	18	no		2.+	3367	
	Group 2		09CY0012	25-Mar-09	M	27	no		2.1+	3368	
	Group 2		09CY0015	30-Mar-09	F	28	no		2.1+	3368	
	Group 2		09CY0022	9-Apr-09	M	32	no		2.1+S+	3369	
			09CY0024	10-Apr-09	F	32	yes	CowEWin	1.1+	3369	
	Group 2		09CY0025	10-Apr-09	M	29	no		3.1+	3369	
	Group 2		09CY0026	10-Apr-09	F	30	no		2.1+	3369	
	Group 2		09CY0027	10-Apr-09	M	27	no		2.1+	3369	
	Group 2		09CY0030	15-Apr-09	M	24	no		2.1+	3369	
	Group 2		09CY0031	16-Apr-09	M	32	no		R.1+S+	3371	
	Group 2		09CY0032	21-Apr-09	M	30	no		2.1+	3371	
			09CY0033	21-Apr-09	M	19	yes	CowLWin	1.+	3371	
	Group 2		09CY0034	21-Apr-09	M	26	yes	CowLWin	R.1+	3371	
			09CY0036	23-Apr-09	M		unk		R.1+	3371	
	Group 2		09CY0037	23-Apr-09	M	26	no		2.1+	3371	
	Group 2		09CY0038	23-Apr-09	M	27	no		3.1+	3371	
	Group 2		09CY0039	23-Apr-09	M	27	no		2.1+	3371	
	Group 2		09CY0040	27-Apr-09	M	32	no		2.2+	3371	
	Group 2		09CY0041	27-Apr-09	M	30	no		2.1+	3371	
			09CY0042	27-Apr-09			no	no data	2.1+		
	Group 2		09CY0043	28-Apr-09	M	30	no		2.1+	3372	
	Group 2		09CY0044	28-Apr-09	M	21	no		2.+	3372	
	Group 2	09CY0045	29-Apr-09	M	31	no		2.1+	3372		
	Group 2	09CY0046	12-May-09	F	30	no		2.1+	3372		
	Group 2	09CY0047	12-May-09	M	28	no		2.1+	3372		
	Group 1	Olequa	09CY0006	17-Mar-09	M	27	no		R.1+	3367	
	Group 1		09CY0008	24-Mar-09	M	30	no		W1.1+	3367	
	Group 1		09CY0009	24-Mar-09	M	27	no		W1.1+	3367	
	Group 1		09CY0011	25-Mar-09	M	27	no		2.1+	3368	
	Group 1		09CY0014	27-Mar-09	M	26	no		W1.1+	3368	
	Group 1		09CY0017	31-Mar-09	M	32	no		2.1+	3368	
	Group 1		09CY0018	31-Mar-09	M	30	no		2.1+	3368	
	Group 1		09CY0019	2-Apr-09	M	24	no		R.1+	3368	
	Group 1		09CY0028	14-Apr-09	M	21	no		2.+	3369	
	Group 1		Stillwater	09CY0021	8-Apr-09	M	32	no		W1.1+	3369

Table 3. Information for microsatellite multiplexes and loci including annealing temperature (°C) and primer and vector concentration. References for primer sequences are under Citation. The +a indicated a poly-a tail on the primer.

multiplex	primer	molarity	Annealing temp	citation
OmyL	One102+a	0.1	47°	Olsen et al. 2000
	Oke4+a	0.055		Buchholz et al. 1999
	Ots100 +a	0.067		Nelson and Beacham 1999
OmyM	Oki23MMBL +a	0.07	55°	Smith et al. 1998
	Omy7iNRA +a	0.1		K. Gharbi, unpublished
	Ssa408 +a	0.13		Cairney et al. 2000
OmyN	Ots4 +a	0.05	59°	Banks et al. 1999
	Omy1011 +a	0.06		Spies et al. 2005
OmyO	Omy1001 +a	0.07	49°	Spies et al. 2005
	Ots3M +a	0.035		Greig and Banks 1999
OmyP	Ssa407 +a	0.08	59°	Cairney et al. 2000
	Ogo4 +a	0.05		Olsen et al. 1998
	One14 +a	0.12		Scribner et al. 1996
OmyQ	Ssa289 +a	0.11	50°	McConnell et al. 1995
	Oki10+a	0.12		Smith et al. 1998
	V4	0.06		

Table 4. Other Cowlitz and lower Columbia wild winter and summer-run steelhead population samples used in comparative analyses (from Kassler and Dean 2007). All samples (except 2005 Coweeman smolts) were from adults, and were winter-run unless otherwise indicated.

WDFW Code	Sample Name	<i>N</i>	Abbreviation
03AM & 04AW & 06AR	Elochoman R.	101	Elochoman
03OB	Kalama R. summer-run	118	KalS
05CJ	Coweeman R. - smolts	91	05CoweJ
05BL	N. F. Toutle R.	99	NFToutle
06AK	Green R. (N.F. Toutle)	96	Green
05CE & 06AM & 07BB	S. F. Toutle R.	73	SFToutle
05BK	Cowlitz R. at Barrier Dam	98	CowBarrier
05BM	Kalama R. winter-run	100	KalW
05BN & 06AT	N. F. Lewis R. @ Merwin Dam	98	NFLewMer
05BO & 06AV	N. F. Lewis R. @ Cedar Cr trap	59	NFLewCed
05CG & 06AO	E. F. Lewis R.	77	EFLew
05CH & 06AL	Washougal R.	71	Washougal

Table 5. Descriptive genetic statistics: N is the number of samples included in analyses (clipped fish removed from Cowlitz tributary natural origin spawners), gene diversity (Gene Div) is expected heterozygosity corrected for sample size, allelic richness (Rich) is the average number of alleles per locus corrected for a sample size of seven fish (the lowest number of fish with complete genotypes in a single collection), linkage disequilibrium (% link) is the percentage of locus pairs where genotypes were not independent,  $F_{IS}$  is the Hardy Weinberg equilibrium value followed by its probability,  $P$ -value in the next column (significant value in bold type). See Table 1 for collection abbreviations.

	N	Gene Div	Rich	% link	$F_{IS}$	$P$ val
08CowHSum	50	0.811	6.27	5	<b>0.049</b>	0.002
09CowHSum	50	0.806	6.22	1	0.025	0.060
08CowHEWin	49	0.807	6.23	2	0.002	0.463
09CowHEWin	50	0.794	6.02	1	-0.004	0.592
08CowHLWin	50	0.776	5.71	0	-0.036	0.983
09CowHLWin	50	0.785	5.79	6	<u>0.039</u>	0.013
08CowNat	26	0.828	6.66	1	-0.012	0.704
09CowNat	42	0.826	6.74	0	-0.007	0.667
05CoweeAd	19	0.832	6.79	0	<b>0.074</b>	0.003
06CoweeAd	55	0.805	6.32	4	<b>0.079</b>	0.000

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Table 6. Pairwise genotypic tests and pairwise  $F_{ST}$  values. The upper triangular matrix contains the  $P$ -values for the pairwise genotypic tests (bold type values NOT significant) and the lower triangular matrix contains the pairwise  $F_{ST}$  values – all values were significant except for the values in bold type. See Tables 1 and 4 for collection details and abbreviations.

	08CowHS	09CowHS	08CowHEW	09CowHEW	08CowHLW	09CowHLW	08CowNat	09CowNat	Elochoman	0506Cowee	CowBarrier	NFToutle	Green	SFToutle	KalW	NFLewMer	NFLewCed	EFLewis	Washougal	KalS
08CowHS		<b>0.58040</b>	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001
09CowHS	<b>0.0010</b>		0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001
08CowHEW	0.0265	0.0314		<b>0.00131</b>	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001
09CowHEW	0.0322	0.0385	<b>0.0072</b>		0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001
08CowHLW	0.0403	0.0440	0.0298	0.0376		<b>0.00119</b>	0.00001	0.00001	0.00001	0.00001	<b>0.05513</b>	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001
09CowHLW	0.0370	0.0421	0.0320	0.0325	<b>0.0071</b>		0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001
08CowNat	0.0144	0.0205	0.0153	0.0261	0.0299	0.0281		<b>0.26797</b>	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001
09CowNat	0.0195	0.0234	0.0150	0.0242	0.0302	0.0307	<b>0.0036</b>		0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00006	0.00001	0.00001	0.00001
Elochoman	0.0245	0.0275	0.0151	0.0224	0.0306	0.0300	0.0089	0.0073		0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001
0506Cowee	0.0195	0.0233	0.0184	0.0166	0.0260	0.0225	0.0066	0.0075	0.0092		0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001
CowBarrier	0.0376	0.0393	0.0253	0.0267	<b>0.0038</b>	0.0074	0.0269	0.0224	0.0246	0.0196		0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001
NFToutle	0.0241	0.0271	0.0295	0.0336	0.0391	0.0378	0.0156	0.0177	0.0189	0.0174	0.0336		0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001
Green	0.0171	0.0170	0.0219	0.0258	0.0353	0.0281	0.0082	0.0081	0.0121	0.0080	0.0259	0.0101		<b>0.00039</b>	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001
SFToutle	0.0220	0.0208	0.0233	0.0251	0.0314	0.0273	0.0098	0.0096	0.0117	0.0073	0.0196	0.0120	<b>0.0018</b>		0.00001	0.00001	0.00001	0.00001	0.00001	0.00001
KalW	0.0183	0.0202	0.0226	0.0211	0.0303	0.0240	0.0109	0.0097	0.0121	0.0052	0.0204	0.0152	0.0065	0.0053		0.00001	0.00001	0.00001	0.00001	0.00001
NFLewMer	0.0225	0.0228	0.0196	0.0227	0.0240	0.0211	0.0127	0.0122	0.0100	0.0078	0.0177	0.0197	0.0086	0.0058	0.0065		0.00001	0.00001	0.00001	0.00001
NFLewCed	0.0202	0.0228	0.0113	0.0152	0.0198	0.0202	0.0155	0.0097	0.0107	0.0080	0.0129	0.0202	0.0118	0.0100	0.0077	0.0080		0.00001	0.00001	0.00001
EFLew	0.0169	0.0220	0.0281	0.0357	0.0362	0.0321	0.0130	0.0112	0.0159	0.0139	0.0338	0.0234	0.0129	0.0146	0.0153	0.0154	0.0182		0.00001	0.00001
Washougal	0.0160	0.0185	0.0259	0.0237	0.0355	0.0277	0.0122	0.0110	0.0155	0.0079	0.0264	0.0251	0.0111	0.0104	0.0078	0.0101	0.0135	0.0118		0.00001
KalS	0.0109	0.0117	0.0346	0.0345	0.0394	0.0343	0.0167	0.0143	0.0210	0.0134	0.0329	0.0252	0.0121	0.0133	0.0084	0.0152	0.0177	0.0125	0.0058	

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Table 7a and 7b. Table 7a is a summary of the results from the GeneClass assignment test for the Cowlitz basin collections (left side of Table 7b below, clipped fish assignments at end of table). Results reflect samples with over 90% relative assignment likelihood (values in blue). See Table 1 for name abbreviations. Boxed assignments had over 90% relative assignment likelihood to a collection different from the collection of origin. The right side of Table 7b presents the GeneClass first generation migrant test data. The “HOME” column has the name of the collection of origin. The second column has the negative logarithm of the likelihood of the assignment to the home collection ( $L_{home}$ ) divided by the highest likelihood of assignment ( $L_{max}$ ). Since these are logarithms, if the assignment to the home collection is also the highest likelihood, this value would be the log of 1, which is 0. The next column has the probability of the assignment likelihood ratio from the simulation (values over 1% or 0.01 in blue) and the next four columns have the actual negative log likelihoods of assignment.

Table 7a	>90% relative assignment likelihood							Total
	CowSum	CowEWin	CowLWin	CowNat	Assign	unassign	%unassign	
08CowHSum	41	2	0	1	44	6	12.00	50
09CowHSum	45	1	0	0	46	4	8.00	50
08CowHEWin	0	34	0	0	34	15	30.61	49
09CowHEWin	0	45	0	0	45	5	10.00	50
08CowHLWin	0	0	43	0	43	7	14.00	50
09CowHLWin	0	0	45	3	48	1	2.04	49
08CowNat	0	3	0	17	20	6	23.08	26
09CowNat	0	0	0	27	27	15	35.71	42
Total assign	90	79	91	47				
correct	86	79	88	44				
%correct	95.56	100.00	96.70	93.62				

Table 7b.	Assignment test				First Generation Migrant Test				
	sample	ASSIGN TO	score	HOME	$L_{home}/L_{max}$	probability	CowSum '-log(L)	CowEWin '-log(L)	CowLWin '-log(L)
08CB0001	CowSum	100.00	CowSum	0	0.520	25.24	30.90	36.13	31.75
08CB0002	CowSum	100.00	CowSum	0	0.515	23.71	29.42	33.80	29.31
08CB0003	CowSum	100.00	CowSum	0	0.519	20.66	26.90	29.71	27.76
08CB0004	CowSum	100.00	CowSum	0	0.517	21.78	26.65	30.91	26.39
08CB0005	CowSum	96.67	CowSum	0	0.517	22.03	24.92	33.60	23.51
08CB0006	CowSum	99.04	CowSum	0	0.540	17.50	19.55	23.48	20.58
08CB0007	CowSum	92.19	CowSum	0	0.523	21.70	24.34	22.84	23.72
08CB0008	CowSum	99.99	CowSum	0	0.518	22.37	26.63	28.35	26.49
08CB0009	CowSum	99.96	CowSum	0	0.519	23.24	28.26	31.55	26.60
08CB0010	CowSum	99.97	CowSum	0	0.516	19.28	28.97	27.93	22.81
08CB0011	CowSum	99.66	CowSum	0	0.524	23.87	30.53	35.61	26.34
08CB0012	CowSum	100.00	CowSum	0	0.520	22.02	33.55	32.97	26.97
08CB0013	CowSum	99.97	CowSum	0	0.520	18.58	22.17	25.27	23.37
08CB0014	CowSum	99.45	CowSum	0	0.519	17.32	20.31	22.40	19.66
08CB0015	CowSum	56.48	CowSum	0	0.519	23.40	30.91	29.42	23.52
08CB0016	CowSum	97.66	CowSum	0	0.523	20.51	25.62	26.48	22.13
08CB0017	CowSum	99.96	CowSum	0	0.519	18.45	21.88	25.33	22.96
08CB0018	CowSum	98.04	CowSum	0	0.517	21.91	25.06	23.62	26.08
08CB0019	CowSum	99.98	CowSum	0	0.517	22.77	26.55	27.99	27.12
08CB0020	CowSum	99.93	CowSum	0	0.513	25.15	28.62	39.25	28.60
08CB0021	CowSum	98.68	CowSum	0	0.523	23.97	29.80	34.48	25.84
08CB0022	CowSum	100.00	CowSum	0	0.523	20.19	27.99	29.39	25.40
08CB0023	CowSum	71.91	CowSum	0	0.519	21.87	26.97	26.64	22.28
08CB0024	CowSum	99.99	CowSum	0	0.518	20.53	24.91	31.31	24.72
08CB0025	CowSum	99.81	CowSum	0	0.519	23.11	27.92	28.57	25.84

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sample	Assignment test		HOME	L <sub>home</sub> /L <sub>max</sub>	probability	First Generation Migrant Test			
	ASSIGN TO	score				CowSum	CowEWin	CowLWin	CowNat
08CB0026	CowSum	99.98	CowSum	0	0.517	22.29	27.88	27.49	25.92
08CB0027	CowEWin	96.79	CowSum	1.646	0.009	25.61	23.96	29.91	25.94
08CB0028	CowSum	99.36	CowSum	0	0.520	22.03	24.52	30.90	24.52
08CB0029	CowSum	100.00	CowSum	0	0.517	20.18	29.85	28.99	24.85
08CB0030	CowSum	100.00	CowSum	0	0.518	27.26	33.87	37.05	32.74
08CB0031	CowEWin	46.83	CowSum	0.006	0.027	25.73	25.72	28.29	26.55
08CB0032	CowSum	97.24	CowSum	0	0.525	23.81	34.70	33.35	25.36
08CB0033	CowSum	86.48	CowSum	0	0.517	26.83	29.07	30.64	27.65
08CB0034	CowSum	100.00	CowSum	0	0.518	20.82	27.94	31.34	28.57
08CB0035	CowNat	98.70	CowSum	1.881	0.005	27.76	34.82	30.71	25.88
08CB0036	CowSum	99.90	CowSum	0	0.517	22.65	25.68	29.11	26.70
08CB0037	CowSum	99.96	CowSum	0	0.517	25.35	29.73	36.19	28.75
08CB0038	CowSum	99.84	CowSum	0	0.522	25.47	28.40	29.43	28.99
08CB0039	CowSum	99.44	CowSum	0	0.518	24.29	26.61	37.47	27.31
08CB0040	CowSum	97.94	CowSum	0	0.521	23.75	25.43	32.64	28.59
08CB0041	CowSum	70.17	CowSum	0	0.520	22.84	25.51	26.11	23.21
08CB0042	CowSum	98.64	CowSum	0	0.519	23.91	32.55	35.46	25.77
08CB0043	CowEWin	98.65	CowSum	5.1	0.000	29.77	24.67	35.68	26.53
08CB0044	CowSum	97.43	CowSum	0	0.519	23.95	26.34	31.31	25.60
08CB0045	CowSum	100.00	CowSum	0	0.517	25.47	34.47	35.33	30.52
08CB0046	CowSum	84.64	CowSum	0	0.519	23.26	31.38	24.57	24.14
08CB0047	CowSum	99.94	CowSum	0	0.521	23.37	28.55	39.12	26.60
08CB0048	CowSum	95.96	CowSum	0	0.533	17.07	19.93	23.12	18.46
08CB0049	CowSum	100.00	CowSum	0	0.519	22.17	28.96	31.43	28.39
08CB0050	CowSum	100.00	CowSum	0	0.532	21.95	30.87	27.75	29.48
09AY0001	CowSum	99.81	CowSum	0	0.519	21.13	27.21	32.48	23.84
09AY0002	CowSum	100.00	CowSum	0	0.520	25.48	32.79	32.30	29.88
09AY0003	CowSum	99.94	CowSum	0	0.517	23.12	29.53	34.58	26.36
09AY0004	CowSum	99.98	CowSum	0	0.518	23.30	27.09	32.64	27.39
09AY0005	CowNat	82.37	CowSum	0.671	0.034	19.76	22.15	26.80	19.08
09AY0006	CowSum	90.94	CowSum	0	0.522	23.68	25.47	26.15	24.78
09AY0007	CowSum	100.00	CowSum	0	0.516	25.62	34.90	35.80	30.34
09AY0008	CowSum	99.87	CowSum	0	0.519	23.58	29.28	31.98	26.47
09AY0009	CowSum	78.59	CowSum	0	0.515	27.85	28.51	34.22	29.13
09AY0010	CowEWin	97.61	CowSum	1.651	0.007	27.26	25.60	36.08	28.27
09AY0011	CowSum	99.96	CowSum	0	0.517	23.18	26.63	29.26	29.84
09AY0012	CowSum	99.94	CowSum	0	0.520	21.88	25.64	26.22	25.32
09AY0013	CowSum	98.22	CowSum	0	0.520	20.71	22.46	24.03	25.40
09AY0014	CowSum	99.01	CowSum	0	0.521	21.37	24.83	27.41	23.38
09AY0015	CowSum	99.99	CowSum	0	0.519	22.95	28.80	36.81	26.80
09AY0016	CowSum	99.89	CowSum	0	0.521	22.08	27.83	32.33	25.05
09AY0017	CowSum	76.05	CowSum	0	0.517	28.56	30.14	38.00	29.10
09AY0018	CowSum	99.92	CowSum	0	0.521	27.16	34.38	34.64	30.25
09AY0019	CowSum	99.20	CowSum	0	0.519	23.28	28.46	38.43	25.38
09AY0020	CowSum	91.05	CowSum	0	0.514	21.31	24.94	31.36	22.32
09AY0021	CowSum	100.00	CowSum	0	0.519	21.35	27.50	32.37	26.95
09AY0022	CowSum	99.28	CowSum	0	0.518	20.14	22.30	27.90	23.75
09AY0023	CowSum	98.26	CowSum	0	0.519	22.40	27.47	29.32	24.15
09AY0024	CowSum	100.00	CowSum	0	0.519	24.71	33.65	33.07	34.22
09AY0025	CowSum	100.00	CowSum	0	0.523	21.69	27.37	31.16	26.07
09AY0026	CowSum	98.51	CowSum	0	0.518	21.56	25.10	30.57	23.39
09AY0027	CowSum	94.67	CowSum	0	0.521	23.28	29.77	30.19	24.53
09AY0028	CowSum	99.98	CowSum	0	0.518	23.74	29.56	30.80	27.52
09AY0029	CowSum	100.00	CowSum	0	0.519	23.97	30.51	29.41	32.73
09AY0030	CowSum	99.85	CowSum	0	0.525	16.86	23.25	19.67	23.95
09AY0031	CowSum	100.00	CowSum	0	0.521	21.08	26.38	32.69	28.64
09AY0032	CowSum	99.92	CowSum	0	0.520	22.64	25.75	30.08	29.88
09AY0033	CowSum	100.00	CowSum	0	0.519	21.33	32.82	33.61	30.02
09AY0034	CowSum	62.74	CowSum	0	0.518	20.37	20.60	26.60	22.68

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sample	Assignment test			First Generation Migrant Test					
	ASSIGN TO	score	HOME	$L_{home}/L_{max}$	probability	CowSum -log(L)	CowEWin -log(L)	CowLWin -log(L)	CowNat -log(L)
09AY0035	CowSum	99.92	CowSum	0	0.519	19.60	22.72	25.32	25.24
09AY0036	CowSum	99.98	CowSum	0	0.520	21.17	27.16	24.99	26.52
09AY0037	CowSum	100.00	CowSum	0	0.519	18.87	26.24	29.45	23.18
09AY0038	CowSum	99.97	CowSum	0	0.521	23.81	30.95	33.51	27.26
09AY0039	CowSum	99.98	CowSum	0	0.519	21.15	24.86	36.33	25.76
09AY0040	CowSum	100.00	CowSum	0	0.519	19.15	24.87	26.10	25.32
09AY0041	CowSum	100.00	CowSum	0	0.519	23.32	34.65	36.14	29.22
09AY0042	CowSum	99.62	CowSum	0	0.540	14.89	17.32	24.27	19.03
09AY0043	CowSum	99.18	CowSum	0	0.521	22.28	24.36	28.49	26.98
09AY0044	CowSum	99.98	CowSum	0	0.518	22.46	27.64	29.20	26.07
09AY0045	CowSum	100.00	CowSum	0	0.522	21.07	29.06	34.07	28.97
09AY0046	CowSum	99.98	CowSum	0	0.517	23.81	27.52	33.98	28.04
09AY0047	CowSum	99.41	CowSum	0	0.517	22.28	30.68	29.19	24.51
09AY0048	CowSum	100.00	CowSum	0	0.517	27.28	34.69	36.51	31.95
09AY0049	CowSum	100.00	CowSum	0	0.519	21.87	30.63	32.78	26.72
09AY0050	CowSum	99.87	CowSum	0	0.520	21.54	25.13	34.98	24.49
08DA0001	CowEWin	99.66	CowEWin	0	0.514	26.73	23.52	34.12	26.07
08DA0002	CowEWin	99.81	CowEWin	0	0.516	29.77	27.06	31.72	33.17
08DA0003	CowEWin	78.23	CowEWin	0	0.514	23.61	22.59	29.18	23.33
08DA0004	CowEWin	99.06	CowEWin	0	0.520	24.88	22.65	25.10	26.39
08DA0005	CowEWin	85.84	CowEWin	0	0.516	22.04	21.13	25.04	22.50
08DA0006	CowEWin	100.00	CowEWin	0	0.514	28.27	21.73	28.70	27.03
08DA0007	CowEWin	84.40	CowEWin	0	0.513	31.69	26.75	35.50	27.48
08DA0008	CowEWin	81.85	CowEWin	0	0.515	29.21	24.50	34.73	25.16
08DA0009	CowEWin	81.44	CowEWin	0	0.514	27.55	22.16	30.65	22.80
08DA0010	CowEWin	99.97	CowEWin	0	0.516	24.88	21.23	25.22	25.97
08DA0011	CowNat	90.00	CowEWin	0.964	0.012	25.76	24.10	28.35	23.14
08DA0012	CowEWin	92.90	CowEWin	0	0.517	25.06	23.94	34.09	28.64
08DA0013	CowNat	78.11	CowEWin	0.645	0.013	30.80	26.71	27.33	26.06
08DA0014	CowEWin	81.45	CowEWin	0	0.517	28.67	20.42	21.06	22.92
08DA0016	CowEWin	99.90	CowEWin	0	0.518	28.23	22.44	25.44	26.96
08DA0017	CowEWin	92.08	CowEWin	0	0.518	27.12	23.96	27.48	25.03
08DA0018	CowEWin	77.91	CowEWin	0	0.521	25.90	25.07	30.10	25.94
08DA0019	CowEWin	82.89	CowEWin	0	0.514	22.53	20.69	25.17	21.41
08DA0020	CowEWin	99.95	CowEWin	0	0.516	33.62	28.40	34.95	31.68
08DA0021	CowNat	70.04	CowEWin	1.671	0.005	24.77	26.05	28.90	24.38
08DA0022	CowEWin	99.98	CowEWin	0	0.516	28.13	22.47	26.30	26.63
08DA0023	CowEWin	99.99	CowEWin	0	0.516	32.86	26.68	32.09	30.78
08DA0024	CowEWin	100.00	CowEWin	0	0.512	37.70	26.85	33.19	33.85
08DA0025	CowEWin	94.24	CowEWin	0	0.518	31.42	29.64	41.44	31.00
08DA0026	CowEWin	96.62	CowEWin	0	0.515	23.55	20.39	22.36	22.01
08DA0027	CowEWin	100.00	CowEWin	0	0.516	25.39	18.81	27.81	24.27
08DA0028	CowEWin	99.99	CowEWin	0	0.519	33.88	24.97	29.09	29.69
08DA0029	CowEWin	62.96	CowEWin	0	0.519	30.66	24.26	30.66	24.49
08DA0030	CowEWin	99.91	CowEWin	0	0.516	27.54	19.77	24.44	22.85
08DA0031	CowEWin	100.00	CowEWin	0	0.516	26.70	21.24	29.19	26.80
08DA0032	CowEWin	98.98	CowEWin	0	0.515	28.31	23.32	28.26	25.31
08DA0033	CowEWin	99.98	CowEWin	0	0.516	23.80	20.00	25.92	25.20
08DA0034	CowEWin	99.94	CowEWin	0	0.514	27.61	23.94	29.04	27.39
08DA0035	CowEWin	99.99	CowEWin	0	0.516	24.78	19.90	27.84	23.90
08DA0036	CowEWin	99.95	CowEWin	0	0.516	27.69	21.99	31.30	25.29
08DA0037	CowEWin	99.01	CowEWin	0	0.517	23.28	19.65	28.16	21.66
08DA0038	CowEWin	64.16	CowEWin	0	0.518	26.88	26.12	32.13	26.53
08DA0039	CowEWin	100.00	CowEWin	0	0.515	28.89	21.89	30.07	26.93
08DA0040	CowEWin	91.98	CowEWin	0	0.515	24.51	23.13	30.37	24.47
08DA0041	CowEWin	99.07	CowEWin	0	0.514	23.53	21.36	33.08	23.95
08DA0042	CowEWin	99.80	CowEWin	0	0.515	26.29	21.89	25.98	24.62
08DA0043	CowNat	84.61	CowEWin	0.74	0.016	29.64	25.89	32.17	25.15
08DA0044	CowEWin	99.98	CowEWin	0	0.516	26.49	21.86	26.95	25.59
08DA0045	CowEWin	98.36	CowEWin	0	0.515	28.27	25.63	31.33	27.47

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sample	Assignment test		HOME	L <sub>home</sub> /L <sub>max</sub>	probability	First Generation Migrant Test			
	ASSIGN TO	score				CowSum	CowEWin	CowLWin	CowNat
08DA0046	CowEWin	99.99	CowEWin	0	0.520	23.87	19.76	25.59	25.08
08DA0047	CowEWin	96.37	CowEWin	0	0.517	24.33	18.75	27.55	20.17
08DA0048	CowEWin	99.93	CowEWin	0	0.515	30.31	23.82	27.33	27.25
08DA0049	CowEWin	83.90	CowEWin	0	0.512	38.32	27.77	31.22	28.49
08DA0050	CowEWin	99.92	CowEWin	0	0.517	28.14	23.55	34.05	26.65
09AW0001	CowEWin	99.98	CowEWin	0	0.516	22.79	18.65	22.51	23.23
09AW0002	CowEWin	99.89	CowEWin	0	0.514	32.74	24.12	30.46	27.06
09AW0003	CowEWin	99.84	CowEWin	0	0.516	33.37	23.21	35.25	26.02
09AW0004	CowEWin	83.62	CowEWin	0	0.515	26.88	24.13	26.24	24.86
09AW0005	CowEWin	100.00	CowEWin	0	0.517	25.87	19.92	27.19	25.09
09AW0006	CowEWin	99.47	CowEWin	0	0.516	26.53	20.31	26.49	22.59
09AW0007	CowEWin	100.00	CowEWin	0	0.516	27.75	20.19	28.94	24.91
09AW0008	CowEWin	99.97	CowEWin	0	0.515	33.64	25.39	34.74	28.88
09AW0009	CowEWin	99.88	CowEWin	0	0.519	25.53	20.86	26.44	23.80
09AW0010	CowEWin	97.70	CowEWin	0	0.513	21.30	18.49	20.39	20.53
09AW0011	CowEWin	99.65	CowEWin	0	0.514	24.22	19.71	25.05	22.17
09AW0012	CowEWin	99.99	CowEWin	0	0.516	31.60	21.51	30.12	25.68
09AW0013	CowEWin	100.00	CowEWin	0	0.516	32.13	25.78	32.93	31.73
09AW0014	CowEWin	94.94	CowEWin	0	0.519	36.64	25.13	36.22	26.41
09AW0015	CowEWin	99.97	CowEWin	0	0.517	23.15	19.22	25.19	22.97
09AW0016	CowNat	79.92	CowEWin	0.627	0.019	32.17	30.99	36.19	30.36
09AW0017	CowEWin	100.00	CowEWin	0	0.519	24.59	19.44	25.92	26.77
09AW0018	CowEWin	99.64	CowEWin	0	0.516	26.86	21.35	28.86	23.80
09AW0019	CowEWin	100.00	CowEWin	0	0.515	27.90	22.40	35.88	28.87
09AW0020	CowEWin	97.59	CowEWin	0	0.514	27.51	25.17	26.92	27.85
09AW0021	CowEWin	99.99	CowEWin	0	0.513	26.50	21.45	27.21	25.79
09AW0022	CowEWin	99.99	CowEWin	0	0.516	27.00	20.42	33.53	24.34
09AW0023	CowEWin	100.00	CowEWin	0	0.515	28.73	22.32	29.83	27.04
09AW0024	CowEWin	99.94	CowEWin	0	0.517	25.34	22.11	29.14	26.50
09AW0025	CowEWin	57.14	CowEWin	0	0.520	29.81	29.60	30.56	31.17
09AW0026	CowEWin	99.78	CowEWin	0	0.520	22.79	19.82	29.35	22.78
09AW0027	CowEWin	99.99	CowEWin	0	0.515	26.58	21.78	31.00	26.02
09AW0028	CowEWin	100.00	CowEWin	0	0.515	35.11	23.18	32.25	31.33
09AW0029	CowEWin	100.00	CowEWin	0	0.519	36.07	25.48	38.47	29.79
09AW0030	CowEWin	96.14	CowEWin	0	0.517	31.73	25.49	35.09	26.88
09AW0031	CowEWin	99.54	CowEWin	0	0.514	21.39	19.04	23.30	22.98
09AW0032	CowEWin	68.26	CowEWin	0	0.514	22.13	20.04	20.38	23.47
09AW0033	CowEWin	99.99	CowEWin	0	0.516	27.68	20.42	30.95	24.34
09AW0034	CowEWin	100.00	CowEWin	0	0.523	26.68	18.37	25.36	24.33
09AW0035	CowEWin	99.98	CowEWin	0	0.516	29.01	22.36	30.86	25.96
09AW0036	CowEWin	98.78	CowEWin	0	0.515	25.04	22.94	27.61	25.30
09AW0037	CowEWin	99.96	CowEWin	0	0.516	36.91	25.42	33.42	28.80
09AW0038	CowEWin	98.58	CowEWin	0	0.519	27.17	22.89	29.91	24.73
09AW0039	CowEWin	99.94	CowEWin	0	0.516	33.32	25.47	29.42	28.75
09AW0040	CowEWin	99.98	CowEWin	0	0.515	26.45	22.04	32.28	25.84
09AW0041	CowEWin	83.02	CowEWin	0	0.514	22.15	20.81	22.04	21.81
09AW0042	CowEWin	99.94	CowEWin	0	0.524	21.15	17.94	23.74	23.63
09AW0043	CowEWin	100.00	CowEWin	0	0.514	32.27	22.46	35.50	30.39
09AW0044	CowEWin	100.00	CowEWin	0	0.515	26.82	19.35	24.81	25.98
09AW0045	CowEWin	100.00	CowEWin	0	0.517	29.67	20.83	28.82	26.05
09AW0046	CowEWin	99.99	CowEWin	0	0.514	24.47	20.53	26.81	29.67
09AW0047	CowEWin	100.00	CowEWin	0	0.515	29.00	21.71	29.99	31.46
09AW0048	CowEWin	99.99	CowEWin	0	0.514	23.86	19.65	26.24	26.77
09AW0049	CowEWin	99.97	CowEWin	0	0.521	22.46	18.95	24.50	25.39
09AW0050	CowEWin	100.00	CowEWin	0	0.515	28.75	23.72	31.50	29.37
08DD0001	CowLWin	98.42	CowLWin	0	0.510	28.92	24.30	22.51	27.07
08DD0002	CowLWin	100.00	CowLWin	0	0.509	33.06	34.94	21.63	31.25
08DD0003	CowLWin	100.00	CowLWin	0	0.513	23.82	25.73	18.57	23.42
08DD0004	CowLWin	99.45	CowLWin	0	0.508	24.39	21.71	19.45	24.07
08DD0005	CowLWin	99.70	CowLWin	0	0.510	23.51	24.13	19.99	22.57

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sample	Assignment test		HOME	L <sub>home</sub> /L <sub>max</sub>	probability	First Generation Migrant Test			
	ASSIGN TO	score				CowSum	CowEWin	CowLWin	CowNat
08DD0006	CowLWin	100.00	CowLWin	0	0.512	25.55	27.73	17.72	25.02
08DD0007	CowLWin	100.00	CowLWin	0	0.512	34.50	29.41	20.81	29.24
08DD0008	CowLWin	100.00	CowLWin	0	0.510	30.52	25.42	20.47	24.86
08DD0009	CowLWin	96.52	CowLWin	0	0.512	28.60	25.22	23.65	25.68
08DD0010	CowLWin	99.99	CowLWin	0	0.512	30.95	32.78	21.16	25.28
08DD0011	CowLWin	100.00	CowLWin	0	0.510	28.98	26.99	19.74	26.21
08DD0012	CowLWin	100.00	CowLWin	0	0.510	33.62	26.58	18.73	27.38
08DD0013	CowLWin	99.99	CowLWin	0	0.509	22.14	21.15	17.21	22.79
08DD0014	CowLWin	100.00	CowLWin	0	0.509	35.97	36.37	21.13	33.19
08DD0015	CowLWin	64.21	CowLWin	0	0.508	25.63	26.38	25.29	27.03
08DD0016	CowLWin	100.00	CowLWin	0	0.508	29.01	26.17	17.91	26.59
08DD0017	CowLWin	99.99	CowLWin	0	0.507	27.65	24.49	18.93	22.98
08DD0018	CowLWin	99.89	CowLWin	0	0.511	30.30	26.66	22.81	25.82
08DD0019	CowLWin	100.00	CowLWin	0	0.509	26.27	23.55	17.90	25.55
08DD0020	CowLWin	100.00	CowLWin	0	0.511	29.87	25.54	19.50	27.59
08DD0021	CowLWin	99.94	CowLWin	0	0.510	26.61	24.17	20.06	23.37
08DD0022	CowLWin	99.95	CowLWin	0	0.508	30.91	25.13	21.83	28.48
08DD0023	CowLWin	99.98	CowLWin	0	0.509	26.70	29.54	22.70	26.94
08DD0024	CowLWin	83.93	CowLWin	0	0.509	22.70	23.19	21.58	22.62
08DD0025	CowLWin	99.97	CowLWin	0	0.509	29.61	24.33	20.76	31.20
08DD0026	CowLWin	99.99	CowLWin	0	0.513	27.60	23.41	19.34	24.64
08DD0027	CowLWin	99.98	CowLWin	0	0.509	27.30	25.53	21.59	25.46
08DD0028	CowLWin	98.80	CowLWin	0	0.506	26.06	22.35	20.43	24.80
08DD0029	CowLWin	99.97	CowLWin	0	0.508	24.14	24.74	20.33	24.28
08DD0030	CowLWin	100.00	CowLWin	0	0.508	27.62	24.67	19.52	26.58
08DD0031	CowLWin	99.98	CowLWin	0	0.509	29.19	24.27	20.55	29.45
08DD0032	CowLWin	100.00	CowLWin	0	0.510	30.68	24.46	19.99	25.99
08DD0033	CowLWin	100.00	CowLWin	0	0.508	26.13	23.07	17.48	22.92
08DD0034	CowLWin	100.00	CowLWin	0	0.508	30.31	27.70	20.56	28.17
08DD0035	CowLWin	95.56	CowLWin	0	0.509	26.99	25.86	20.97	22.30
08DD0036	CowLWin	100.00	CowLWin	0	0.510	25.37	27.05	19.61	27.73
08DD0037	CowLWin	89.28	CowLWin	0	0.525	18.86	15.20	14.19	15.83
08DD0038	CowLWin	100.00	CowLWin	0	0.508	31.28	30.41	21.89	33.61
08DD0039	CowLWin	97.97	CowLWin	0	0.509	31.91	28.08	24.11	25.79
08DD0040	CowLWin	99.02	CowLWin	0	0.508	24.26	23.50	21.36	24.21
08DD0041	CowLWin	99.91	CowLWin	0	0.507	26.12	24.65	19.88	22.95
08DD0042	CowLWin	100.00	CowLWin	0	0.510	20.82	21.46	16.14	22.06
08DD0043	CowLWin	100.00	CowLWin	0	0.513	25.10	24.23	17.20	22.12
08DD0044	CowLWin	61.32	CowLWin	0	0.516	21.27	25.10	21.07	26.05
08DD0045	CowLWin	100.00	CowLWin	0	0.511	36.53	37.26	23.99	34.70
08DD0046	CowLWin	78.22	CowLWin	0	0.510	27.47	23.32	22.67	23.90
08DD0047	CowEWin	61.72	CowLWin	0.291	0.011	25.34	20.42	20.71	21.38
08DD0048	CowLWin	99.97	CowLWin	0	0.510	29.67	25.21	21.75	27.99
08DD0049	CowLWin	62.99	CowLWin	0	0.509	28.54	25.09	23.07	23.31
08DD0050	CowLWin	100.00	CowLWin	0	0.513	27.94	26.11	20.15	30.65
09AX0001	CowLWin	100.00	CowLWin	0	0.507	26.81	25.02	20.16	28.58
09AX0002	CowLWin	99.81	CowLWin	0	0.511	30.90	28.27	23.76	26.49
09AX0003	CowLWin	99.83	CowLWin	0	0.508	31.38	25.53	22.77	28.73
09AX0005	CowLWin	100.00	CowLWin	0	0.517	24.83	22.75	15.54	24.29
09AX0006	CowLWin	100.00	CowLWin	0	0.509	30.31	27.16	20.10	28.01
09AX0007	CowLWin	100.00	CowLWin	0	0.507	23.97	24.52	16.69	25.59
09AX0008	CowLWin	100.00	CowLWin	0	0.510	33.48	30.43	24.51	31.61
09AX0009	CowLWin	99.84	CowLWin	0	0.506	23.66	25.30	20.84	26.47
09AX0010	CowLWin	99.04	CowLWin	0	0.511	24.20	22.93	20.64	23.01
09AX0011	CowLWin	100.00	CowLWin	0	0.508	28.77	26.24	20.58	26.95
09AX0012	CowNat	99.59	CowLWin	2.771	0.001	27.73	28.45	27.80	25.03
09AX0013	CowLWin	98.19	CowLWin	0	0.507	27.04	21.49	19.76	23.90
09AX0014	CowNat	64.64	CowLWin	0.262	0.015	27.60	26.99	22.76	22.50
09AX0015	CowLWin	100.00	CowLWin	0	0.512	27.75	25.67	21.07	27.92

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sample	Assignment test		HOME	L <sub>home</sub> /L <sub>max</sub>	probability	First Generation Migrant Test			
	ASSIGN TO	score				CowSum	CowEWin	CowLWin	CowNat
09AX0016	CowLWin	100.00	CowLWin	0	0.509	31.29	28.98	22.43	31.71
09AX0017	CowLWin	99.99	CowLWin	0	0.511	27.92	22.34	18.37	23.14
09AX0018	CowLWin	100.00	CowLWin	0	0.510	33.00	27.66	21.08	28.86
09AX0019	CowLWin	98.17	CowLWin	0	0.508	24.44	22.93	21.18	25.11
09AX0020	CowLWin	99.34	CowLWin	0	0.510	26.69	23.29	21.12	25.82
09AX0021	CowLWin	100.00	CowLWin	0	0.506	29.06	29.92	23.77	32.73
09AX0022	CowLWin	100.00	CowLWin	0	0.510	36.08	28.92	20.54	29.10
09AX0023	CowLWin	100.00	CowLWin	0	0.509	27.13	25.56	17.28	28.27
09AX0024	CowLWin	100.00	CowLWin	0	0.512	29.79	27.32	20.79	26.25
09AX0025	CowLWin	100.00	CowLWin	0	0.510	29.63	23.39	19.10	29.16
09AX0026	CowLWin	100.00	CowLWin	0	0.507	30.99	29.14	24.33	29.54
09AX0027	CowLWin	100.00	CowLWin	0	0.510	24.87	23.93	18.89	25.00
09AX0028	CowLWin	100.00	CowLWin	0	0.510	28.48	25.50	19.75	29.62
09AX0029	CowLWin	100.00	CowLWin	0	0.510	25.19	24.12	18.31	25.81
09AX0030	CowLWin	99.99	CowLWin	0	0.507	27.35	23.79	19.68	24.11
09AX0031	CowLWin	100.00	CowLWin	0	0.507	35.02	30.27	24.64	31.44
09AX0032	CowLWin	100.00	CowLWin	0	0.510	34.77	30.66	23.01	33.91
09AX0033	CowLWin	100.00	CowLWin	0	0.506	30.51	25.26	20.22	27.72
09AX0034	CowLWin	100.00	CowLWin	0	0.510	31.43	28.09	19.60	31.50
09AX0035	CowLWin	100.00	CowLWin	0	0.511	28.18	26.12	20.64	29.67
09AX0036	CowLWin	100.00	CowLWin	0	0.509	31.42	29.79	21.27	30.74
09AX0037	CowLWin	99.96	CowLWin	0	0.508	23.87	22.53	19.12	26.96
09AX0038	CowLWin	99.96	CowLWin	0	0.510	28.43	25.10	21.73	26.65
09AX0039	CowLWin	99.92	CowLWin	0	0.515	30.64	26.87	23.24	26.50
09AX0040	CowLWin	99.50	CowLWin	0	0.510	28.00	25.14	22.31	24.76
09AX0041	CowLWin	100.00	CowLWin	0	0.509	31.53	27.73	23.12	29.05
09AX0042	CowLWin	100.00	CowLWin	0	0.510	31.87	29.83	20.70	36.45
09AX0043	CowLWin	100.00	CowLWin	0	0.510	29.72	27.87	22.29	28.16
09AX0044	CowNat	64.21	CowLWin	0.276	0.016	26.73	24.77	23.47	23.20
09AX0045	CowLWin	100.00	CowLWin	0	0.510	36.43	32.45	24.95	31.03
09AX0046	CowLWin	100.00	CowLWin	0	0.509	29.97	28.56	20.64	29.37
09AX0047	CowLWin	43.04	CowLWin	0	0.510	23.77	21.74	21.59	21.80
09AX0048	CowLWin	99.91	CowLWin	0	0.506	31.36	26.24	23.17	27.44
09AX0049	CowLWin	99.99	CowLWin	0	0.510	26.25	27.15	21.61	25.91
09AX0050	CowLWin	100.00	CowLWin	0	0.507	30.71	25.71	19.28	27.38
08DC0001	CowNat	100.00	CowNat	0	0.537	31.78	28.12	30.40	23.34
08DC0002	CowNat	92.35	CowNat	0	0.544	25.38	29.69	32.21	24.29
08DC0003	CowEWin	100.00	CowNat	4.741	0.002	36.65	25.07	33.40	29.81
08DC0004	CowNat	100.00	CowNat	0	0.543	29.56	31.24	34.55	24.71
08DC0005	CowNat	74.61	CowNat	0	0.547	24.36	26.26	35.68	23.88
08DC0006	CowNat	99.99	CowNat	0	0.540	26.88	28.43	32.61	22.97
08DC0007	CowNat	99.85	CowNat	0	0.549	27.70	25.72	27.83	22.91
08DC0008	CowNat	82.66	CowNat	0	0.547	26.10	25.56	31.63	24.77
08DC0010	CowNat	98.89	CowNat	0	0.539	24.27	23.76	27.47	21.69
08DC0011	CowNat	99.98	CowNat	0	0.550	27.57	28.73	30.98	23.75
08DC0012	CowNat	99.56	CowNat	0	0.545	28.16	31.59	35.80	25.81
08DC0013	CowNat	99.90	CowNat	0	0.545	26.61	29.27	30.01	23.63
08DC0014	CowEWin	96.21	CowNat	1.405	0.027	35.04	25.79	30.68	27.20
08DC0015	CowNat	93.44	CowNat	0	0.538	22.68	26.26	32.42	21.53
08DC0016	CowNat	86.55	CowNat	0	0.540	25.99	30.23	34.71	25.18
08DC0017	CowNat	99.91	CowNat	0	0.545	28.55	28.39	34.52	25.09
08DC0018	CowNat	99.89	CowNat	0	0.536	28.46	32.35	33.98	25.49
08DC0019	CowNat	100.00	CowNat	0	0.544	32.67	31.51	33.46	27.07
08DC0021	CowNat	99.11	CowNat	0	0.551	28.03	29.97	35.24	25.98
08DC0022	CowEWin	91.49	CowNat	1.269	0.033	27.50	26.10	33.07	27.37
08DC0023	CowNat	100.00	CowNat	0	0.551	32.65	27.99	28.98	23.10
08DC0025	CowNat	100.00	CowNat	0	0.540	33.63	35.15	35.51	26.00
08DC0026	CowSum	65.54	CowNat	0.281	0.066	25.82	28.53	30.38	26.10
08DC0027	CowSum	50.85	CowNat	0.017	0.078	23.69	26.01	28.52	23.71

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Assignment test					First Generation Migrant Test				
sample	ASSIGN TO	score	HOME	L <sub>home</sub> /L <sub>max</sub>	probability	CowSum -log(L)	CowEWin -log(L)	CowLWin -log(L)	CowNat -log(L)
08DC0028	CowNat	95.90	CowNat	0	0.541	25.85	24.85	24.65	23.05
08DC0029	CowNat	86.57	CowNat	0	0.537	31.99	23.47	28.63	22.66
09CY0001	CowNat	86.13	CowNat	0	0.555	28.85	24.74	32.65	23.95
09CY0002	CowNat	100.00	CowNat	0	0.549	29.16	29.80	32.47	24.25
09CY0003	CowNat	99.27	CowNat	0	0.542	27.16	26.68	31.79	24.43
09CY0004	CowSum	43.90	CowNat	0.045	0.077	24.03	24.46	26.55	24.08
09CY0005	CowNat	84.00	CowNat	0	0.550	34.72	32.12	38.64	31.40
09CY0006	CowNat	91.96	CowNat	0	0.543	28.88	26.39	31.45	25.33
09CY0007	CowNat	68.30	CowNat	0	0.538	30.04	28.36	28.45	27.76
09CY0008	CowNat	100.00	CowNat	0	0.539	33.70	30.91	32.29	23.43
09CY0009	CowNat	99.39	CowNat	0	0.543	26.56	29.14	27.99	24.34
09CY0010	CowNat	99.97	CowNat	0	0.568	21.25	23.99	26.07	17.75
09CY0011	CowNat	100.00	CowNat	0	0.541	34.59	31.55	39.10	22.86
09CY0012	CowNat	100.00	CowNat	0	0.544	29.67	30.65	34.52	23.11
09CY0013	CowNat	99.80	CowNat	0	0.535	30.98	28.10	31.23	25.39
09CY0014	CowNat	100.00	CowNat	0	0.546	33.74	32.43	42.71	24.85
09CY0015	CowNat	100.00	CowNat	0	0.549	27.91	27.07	30.86	20.41
09CY0016	CowNat	99.64	CowNat	0	0.542	28.91	29.06	31.88	26.24
09CY0017	CowNat	99.90	CowNat	0	0.542	23.72	25.20	24.77	20.65
09CY0018	CowSum	53.33	CowNat	2.271	0.010	23.69	23.75	29.14	25.96
09CY0019	CowNat	97.18	CowNat	0	0.549	24.41	23.55	25.99	21.95
09CY0020	CowSum	86.29	CowNat	0.799	0.055	20.93	27.48	27.19	21.73
09CY0021	CowNat	99.97	CowNat	0	0.546	27.88	28.70	25.74	22.20
09CY0022	CowNat	99.84	CowNat	0	0.560	22.63	25.08	25.12	19.83
09CY0023	CowNat	100.00	CowNat	0	0.543	36.79	33.52	36.01	28.66
09CY0025	CowSum	45.93	CowNat	0.206	0.069	26.88	27.14	30.11	27.09
09CY0026	CowNat	64.30	CowNat	0	0.547	23.47	30.56	38.77	23.21
09CY0027	CowNat	75.87	CowNat	0	0.541	31.93	30.02	28.71	28.19
09CY0028	CowNat	99.51	CowNat	0	0.543	23.78	23.46	24.35	20.94
09CY0030	CowNat	80.57	CowNat	0	0.560	19.65	26.70	22.39	19.03
09CY0031	CowNat	100.00	CowNat	0	0.548	31.78	28.12	30.40	23.34
09CY0032	CowNat	99.43	CowNat	0	0.543	26.80	25.26	27.80	23.01
09CY0035	CowEWin	84.93	CowNat	0.751	0.049	35.10	30.72	36.01	31.47
09CY0036	CowNat	88.93	CowNat	0	0.586	16.43	19.87	22.95	15.52
09CY0037	CowNat	98.06	CowNat	0	0.544	29.93	27.53	26.61	24.85
09CY0038	CowSum	84.48	CowNat	0.851	0.047	25.38	26.77	28.15	26.23
09CY0039	CowNat	99.97	CowNat	0	0.539	27.76	28.29	32.02	24.13
09CY0040	CowNat	100.00	CowNat	0	0.534	30.31	29.78	34.78	23.33
09CY0041	CowEWin	67.95	CowNat	0.392	0.061	27.11	25.93	33.24	26.32
09CY0043	CowNat	100.00	CowNat	0	0.544	29.74	29.25	31.96	23.43
09CY0044	CowNat	90.95	CowNat	0	0.538	32.01	27.69	28.20	26.57
09CY0045	CowNat	99.90	CowNat	0	0.546	31.45	30.11	35.76	27.11
09CY0046	CowNat	100.00	CowNat	0	0.541	30.05	28.54	29.45	23.60
09CY0047	CowNat	88.27	CowNat	0	0.570	22.86	27.53	32.38	21.99

Clipped fish	Assign to	score	No simulation	CowSum -log(L)	CowEWin -log(L)	CowLWin -log(L)	CowNat -log(L)
08DC0009*	CowEWin	97.36		33.36	26.26	27.88	28.80
08DC0020*	CowEWin	99.65		32.84	25.31	33.95	27.77
08DC0024*	CowEWin	99.46		29.42	24.60	26.89	28.08
08DC0029*	CowNat	55.93		20.22	20.56	22.93	19.96
09CY0024*	CowEWin	91.73		29.39	23.81	27.26	24.86
09CY0029*	CowEWin	99.94		33.04	28.12	35.16	31.35
09CY0033*	CowLWin	99.98		26.08	20.60	17.00	23.84
09CY0034*	CowNat	94.78		34.74	27.90	27.67	26.21

Table 8. Collection (Population) and individual ancestry values for STRUCTURE analysis for K = 4 (see Figure 6 for graphic results of individual ancestry) with 2008 and 2009 Cowlitz basin samples and Coweeman samples. The top portion of the table has the ancestry values in each cluster for collections averaged over all individuals (individual values in lower portion) with the number of individuals in each collection under N (individual values for Coweeman not included). Order is the same as in Figure 6. Ad-clipped spawners are indicated by asterisks. Colored cells (colors match clusters in Figure 6) are values over 30%.

Collection Average	Population	Clusters			
		1	2	3	4
	09CowHEWin	0.858	0.055	0.040	0.047
	08CowHEWin	0.805	0.045	0.077	0.073
	08CowHLWin	0.046	0.867	0.043	0.044
	09CowHLWin	0.035	0.861	0.028	0.075
	09CowHSum	0.057	0.024	0.864	0.055
	08CowHSum	0.068	0.034	0.786	0.113
	09CowNat	0.182	0.044	0.162	0.612
	08CowNat	0.191	0.035	0.235	0.540
	0809CowClip	0.452	0.218	0.087	0.243
	05CoweAd	0.124	0.086	0.186	0.605
	06CoweAd	0.145	0.058	0.096	0.701
	05CoweJ	0.193	0.054	0.096	0.657
Individual values	individual	CowHEW	CowHLW	CowHS	CowNat
CowHEW	09AW0001	0.955	0.013	0.015	0.017
	09AW0002	0.732	0.231	0.022	0.015
	09AW0003	0.963	0.007	0.006	0.024
	09AW0004	0.792	0.024	0.097	0.087
	09AW0005	0.968	0.008	0.014	0.010
	09AW0006	0.911	0.025	0.019	0.045
	09AW0007	0.964	0.012	0.014	0.010
	09AW0008	0.929	0.027	0.012	0.032
	09AW0009	0.921	0.011	0.023	0.046
	09AW0010	0.834	0.055	0.025	0.086
	09AW0011	0.929	0.017	0.033	0.022
	09AW0012	0.926	0.032	0.017	0.026
	09AW0013	0.864	0.094	0.017	0.025
	09AW0014	0.749	0.016	0.008	0.227
	09AW0015	0.952	0.013	0.025	0.009
	09AW0016	0.633	0.017	0.031	0.319
	09AW0017	0.965	0.013	0.012	0.011
	09AW0018	0.959	0.007	0.012	0.022
	09AW0019	0.831	0.014	0.146	0.010
	09AW0020	0.747	0.042	0.041	0.170
	09AW0021	0.933	0.015	0.013	0.039
	09AW0022	0.961	0.008	0.020	0.011
	09AW0023	0.930	0.027	0.023	0.020
	09AW0024	0.854	0.057	0.069	0.020
	09AW0025	0.132	0.409	0.412	0.047
	09AW0026	0.917	0.011	0.055	0.017
	09AW0027	0.945	0.011	0.020	0.024
	09AW0028	0.910	0.037	0.022	0.031
	09AW0029	0.946	0.010	0.012	0.032
	09AW0030	0.936	0.018	0.018	0.028
	09AW0031	0.899	0.034	0.049	0.019
	09AW0032	0.333	0.407	0.188	0.072
	09AW0033	0.953	0.008	0.008	0.031

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Individual values	individual	CowHEW	CowHLW	CowHS	CowNat
CowHEW cont.	09AW0034	0.959	0.013	0.009	0.020
	09AW0035	0.935	0.017	0.021	0.028
	09AW0036	0.502	0.025	0.083	0.390
	09AW0037	0.939	0.021	0.009	0.031
	09AW0038	0.924	0.023	0.019	0.034
	09AW0039	0.854	0.088	0.012	0.046
	09AW0040	0.938	0.013	0.019	0.030
	09AW0041	0.265	0.575	0.120	0.041
	09AW0042	0.951	0.016	0.021	0.012
	09AW0043	0.964	0.009	0.015	0.011
	09AW0044	0.955	0.023	0.011	0.011
	09AW0045	0.951	0.013	0.011	0.025
	09AW0046	0.895	0.052	0.039	0.015
	09AW0047	0.929	0.035	0.025	0.011
	09AW0048	0.953	0.024	0.014	0.009
	09AW0049	0.909	0.036	0.027	0.028
	09AW0050	0.917	0.027	0.040	0.016
	08DA0001	0.955	0.007	0.016	0.022
	08DA0002	0.467	0.146	0.309	0.079
	08DA0003	0.672	0.040	0.172	0.116
	08DA0004	0.734	0.092	0.097	0.077
	08DA0005	0.842	0.015	0.114	0.029
	08DA0006	0.968	0.011	0.009	0.012
	08DA0007	0.892	0.017	0.015	0.077
	08DA0008	0.952	0.019	0.011	0.018
	08DA0009	0.768	0.029	0.024	0.178
	08DA0010	0.904	0.020	0.037	0.039
	08DA0011	0.821	0.013	0.073	0.093
	08DA0012	0.225	0.040	0.725	0.010
	08DA0013	0.836	0.074	0.031	0.059
	08DA0014	0.743	0.206	0.019	0.032
	08DA0016	0.902	0.058	0.014	0.026
	08DA0017	0.799	0.132	0.040	0.029
	08DA0018	0.492	0.014	0.215	0.280
	08DA0019	0.821	0.020	0.104	0.054
	08DA0020	0.947	0.009	0.008	0.036
	08DA0021	0.293	0.152	0.282	0.274
	08DA0022	0.895	0.058	0.022	0.025
	08DA0023	0.854	0.053	0.032	0.061
	08DA0024	0.922	0.041	0.018	0.020
	08DA0025	0.647	0.014	0.109	0.230
	08DA0026	0.897	0.065	0.022	0.017
	08DA0027	0.968	0.010	0.012	0.010
	08DA0028	0.845	0.030	0.013	0.112
	08DA0029	0.917	0.023	0.014	0.046
	08DA0030	0.930	0.024	0.009	0.036
	08DA0031	0.960	0.010	0.019	0.011
	08DA0032	0.924	0.021	0.021	0.034
	08DA0033	0.910	0.038	0.028	0.023
	08DA0034	0.581	0.084	0.030	0.306
	08DA0035	0.965	0.012	0.013	0.009
	08DA0036	0.792	0.013	0.152	0.043
	08DA0037	0.919	0.030	0.026	0.025
	08DA0038	0.652	0.016	0.065	0.267
	08DA0039	0.944	0.019	0.014	0.023
	08DA0040	0.628	0.055	0.266	0.051
	08DA0041	0.730	0.012	0.243	0.014
	08DA0042	0.885	0.039	0.033	0.043

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Individual values	individual	CowHEW	CowHLW	CowHS	CowNat
CowHEWcont	08DA0043	0.892	0.017	0.056	0.036
	08DA0044	0.943	0.016	0.013	0.028
	08DA0045	0.518	0.011	0.042	0.429
	08DA0046	0.808	0.082	0.068	0.041
	08DA0047	0.923	0.016	0.018	0.044
	08DA0048	0.902	0.036	0.029	0.032
	08DA0049	0.744	0.218	0.015	0.024
	08DA0050	0.915	0.017	0.050	0.018
CowHLW	08DD0001	0.046	0.911	0.028	0.015
	08DD0002	0.009	0.971	0.010	0.010
	08DD0003	0.014	0.932	0.035	0.019
	08DD0004	0.035	0.911	0.039	0.015
	08DD0005	0.024	0.894	0.035	0.046
	08DD0006	0.007	0.968	0.015	0.009
	08DD0007	0.018	0.956	0.008	0.019
	08DD0008	0.022	0.955	0.008	0.014
	08DD0009	0.138	0.763	0.033	0.066
	08DD0010	0.009	0.868	0.035	0.088
	08DD0011	0.025	0.949	0.011	0.015
	08DD0012	0.010	0.977	0.005	0.007
	08DD0013	0.014	0.958	0.017	0.011
	08DD0014	0.005	0.982	0.006	0.007
	08DD0015	0.104	0.346	0.503	0.048
	08DD0016	0.006	0.979	0.008	0.007
	08DD0017	0.022	0.941	0.010	0.028
	08DD0018	0.083	0.772	0.031	0.114
	08DD0019	0.011	0.970	0.008	0.011
	08DD0020	0.016	0.963	0.009	0.012
	08DD0021	0.044	0.929	0.011	0.016
	08DD0022	0.025	0.934	0.013	0.028
	08DD0023	0.015	0.892	0.076	0.018
	08DD0024	0.074	0.653	0.200	0.073
	08DD0025	0.018	0.962	0.012	0.009
	08DD0026	0.046	0.917	0.016	0.020
	08DD0027	0.023	0.832	0.083	0.062
	08DD0028	0.067	0.897	0.015	0.021
	08DD0029	0.032	0.838	0.092	0.038
	08DD0030	0.009	0.971	0.009	0.011
	08DD0031	0.018	0.955	0.011	0.015
	08DD0032	0.023	0.948	0.009	0.021
08DD0033	0.010	0.970	0.010	0.010	
08DD0034	0.010	0.968	0.010	0.012	
08DD0035	0.021	0.641	0.075	0.263	
08DD0036	0.010	0.970	0.010	0.010	
08DD0037	0.174	0.731	0.035	0.059	
08DD0038	0.011	0.973	0.009	0.007	
08DD0039	0.034	0.859	0.045	0.062	
08DD0040	0.061	0.668	0.133	0.138	
08DD0041	0.046	0.920	0.017	0.017	
08DD0042	0.009	0.973	0.009	0.009	
08DD0043	0.010	0.968	0.008	0.014	
08DD0044	0.020	0.684	0.185	0.110	
08DD0045	0.014	0.952	0.010	0.024	
08DD0046	0.091	0.719	0.012	0.179	
08DD0047	0.508	0.220	0.022	0.250	
08DD0048	0.020	0.951	0.010	0.019	
08DD0049	0.245	0.522	0.127	0.106	
08DD0050	0.017	0.960	0.012	0.011	

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Individual values	individual	CowHEW	CowHLW	CowHS	CowNat
CowHLW cont.	09AX0001	0.029	0.926	0.030	0.015
	09AX0002	0.020	0.278	0.014	0.689
	09AX0003	0.028	0.938	0.014	0.020
	09AX0005	0.010	0.970	0.008	0.012
	09AX0006	0.010	0.967	0.010	0.013
	09AX0007	0.013	0.959	0.012	0.015
	09AX0008	0.015	0.924	0.035	0.026
	09AX0009	0.017	0.698	0.245	0.040
	09AX0010	0.060	0.801	0.097	0.043
	09AX0011	0.022	0.951	0.010	0.017
	09AX0012	0.043	0.058	0.022	0.876
	09AX0013	0.043	0.928	0.012	0.018
	09AX0014	0.040	0.363	0.021	0.576
	09AX0015	0.044	0.918	0.017	0.021
	09AX0016	0.010	0.965	0.013	0.012
	09AX0017	0.014	0.962	0.013	0.011
	09AX0018	0.025	0.953	0.011	0.011
	09AX0019	0.172	0.694	0.097	0.037
	09AX0020	0.025	0.931	0.026	0.018
	09AX0021	0.016	0.929	0.035	0.020
	09AX0022	0.008	0.979	0.006	0.006
	09AX0023	0.009	0.967	0.016	0.008
	09AX0024	0.018	0.887	0.011	0.084
	09AX0025	0.037	0.944	0.009	0.009
	09AX0026	0.036	0.923	0.012	0.028
	09AX0027	0.016	0.949	0.020	0.014
	09AX0028	0.009	0.979	0.007	0.006
	09AX0029	0.016	0.964	0.011	0.009
	09AX0030	0.020	0.958	0.010	0.012
	09AX0031	0.030	0.909	0.021	0.040
	09AX0032	0.032	0.937	0.018	0.013
	09AX0033	0.021	0.945	0.014	0.019
	09AX0034	0.011	0.973	0.006	0.010
	09AX0035	0.016	0.932	0.017	0.036
	09AX0036	0.009	0.963	0.017	0.011
	09AX0037	0.019	0.929	0.033	0.019
	09AX0038	0.023	0.962	0.008	0.008
	09AX0039	0.024	0.932	0.012	0.031
	09AX0040	0.033	0.904	0.037	0.026
	09AX0041	0.035	0.886	0.046	0.033
	09AX0042	0.007	0.976	0.011	0.006
	09AX0043	0.015	0.952	0.019	0.014
	09AX0044	0.390	0.276	0.094	0.239
	09AX0045	0.054	0.768	0.021	0.157
	09AX0046	0.009	0.959	0.012	0.019
	09AX0047	0.107	0.588	0.099	0.206
	09AX0048	0.033	0.893	0.009	0.065
	09AX0049	0.018	0.874	0.036	0.071
	09AX0050	0.010	0.971	0.008	0.010
CowHSum	09AY0001	0.018	0.012	0.957	0.013
	09AY0002	0.050	0.013	0.918	0.019
	09AY0003	0.010	0.006	0.969	0.015
	09AY0004	0.037	0.021	0.907	0.035
	09AY0005	0.236	0.034	0.492	0.238
	09AY0006	0.237	0.060	0.641	0.062
	09AY0007	0.014	0.012	0.871	0.103
	09AY0008	0.028	0.014	0.919	0.039
	09AY0009	0.066	0.094	0.736	0.105

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Individual values	individual	CowHEW	CowHLW	CowHS	CowNat
CowSum cont.	09AY0010	0.749	0.021	0.202	0.028
	09AY0011	0.026	0.018	0.946	0.010
	09AY0012	0.072	0.020	0.696	0.212
	09AY0013	0.173	0.031	0.715	0.081
	09AY0014	0.029	0.041	0.863	0.067
	09AY0015	0.017	0.010	0.941	0.032
	09AY0016	0.012	0.026	0.874	0.087
	09AY0017	0.090	0.029	0.836	0.045
	09AY0018	0.015	0.011	0.917	0.057
	09AY0019	0.029	0.006	0.904	0.061
	09AY0020	0.027	0.011	0.934	0.028
	09AY0021	0.016	0.008	0.838	0.138
	09AY0022	0.024	0.013	0.948	0.015
	09AY0023	0.049	0.021	0.819	0.112
	09AY0024	0.008	0.015	0.962	0.015
	09AY0025	0.019	0.015	0.944	0.022
	09AY0026	0.017	0.012	0.930	0.041
	09AY0027	0.015	0.029	0.881	0.076
	09AY0028	0.052	0.019	0.478	0.451
	09AY0029	0.022	0.017	0.946	0.014
	09AY0030	0.008	0.136	0.844	0.012
	09AY0031	0.021	0.010	0.955	0.015
	09AY0032	0.049	0.028	0.905	0.018
	09AY0033	0.006	0.007	0.982	0.006
	09AY0034	0.190	0.025	0.769	0.016
	09AY0035	0.034	0.024	0.930	0.012
	09AY0036	0.020	0.115	0.856	0.009
	09AY0037	0.007	0.007	0.977	0.010
	09AY0038	0.024	0.012	0.747	0.217
	09AY0039	0.024	0.011	0.957	0.008
	09AY0040	0.016	0.010	0.965	0.010
	09AY0041	0.011	0.006	0.973	0.010
	09AY0042	0.030	0.012	0.942	0.016
	09AY0043	0.043	0.049	0.890	0.019
	09AY0044	0.084	0.036	0.846	0.034
	09AY0045	0.008	0.008	0.970	0.014
	09AY0046	0.048	0.011	0.924	0.017
	09AY0047	0.018	0.016	0.908	0.058
	09AY0048	0.021	0.016	0.948	0.015
	09AY0049	0.018	0.010	0.951	0.022
	09AY0050	0.023	0.011	0.958	0.009
	08CB0001	0.012	0.017	0.961	0.009
	08CB0002	0.011	0.014	0.965	0.010
	08CB0003	0.010	0.010	0.972	0.009
	08CB0004	0.016	0.007	0.969	0.008
	08CB0005	0.095	0.007	0.878	0.020
	08CB0006	0.079	0.029	0.838	0.054
	08CB0007	0.076	0.391	0.502	0.030
	08CB0008	0.029	0.017	0.918	0.036
	08CB0009	0.022	0.015	0.365	0.598
	08CB0010	0.009	0.007	0.977	0.008
	08CB0011	0.048	0.024	0.904	0.024
	08CB0012	0.007	0.007	0.973	0.012
	08CB0013	0.015	0.013	0.958	0.013
	08CB0014	0.024	0.023	0.923	0.030
	08CB0015	0.024	0.019	0.934	0.024
	08CB0016	0.013	0.029	0.939	0.019
	08CB0017	0.033	0.021	0.910	0.036

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Individual values	individual	CowHEW	CowHLW	CowHS	CowNat
CowHSum cont.	08CB0018	0.028	0.111	0.845	0.016
	08CB0019	0.019	0.069	0.871	0.041
	08CB0020	0.029	0.007	0.943	0.020
	08CB0021	0.016	0.017	0.948	0.020
	08CB0022	0.013	0.014	0.964	0.009
	08CB0023	0.015	0.025	0.340	0.619
	08CB0024	0.017	0.010	0.958	0.015
	08CB0025	0.175	0.031	0.763	0.032
	08CB0026	0.014	0.035	0.939	0.012
	08CB0027	0.370	0.038	0.391	0.202
	08CB0028	0.108	0.008	0.842	0.042
	08CB0029	0.008	0.013	0.968	0.011
	08CB0030	0.014	0.007	0.965	0.014
	08CB0031	0.331	0.189	0.316	0.165
	08CB0032	0.006	0.007	0.882	0.105
	08CB0033	0.040	0.013	0.418	0.528
	08CB0034	0.012	0.009	0.950	0.029
	08CB0035	0.019	0.016	0.048	0.917
	08CB0036	0.043	0.023	0.548	0.386
	08CB0037	0.024	0.008	0.698	0.270
	08CB0038	0.088	0.066	0.745	0.100
	08CB0039	0.195	0.007	0.754	0.045
	08CB0040	0.089	0.030	0.864	0.016
	08CB0041	0.039	0.029	0.177	0.755
	08CB0042	0.010	0.009	0.964	0.017
	08CB0043	0.910	0.010	0.035	0.045
	08CB0044	0.081	0.039	0.846	0.034
	08CB0045	0.011	0.022	0.917	0.050
	08CB0046	0.008	0.116	0.825	0.051
	08CB0047	0.048	0.008	0.895	0.049
08CB0048	0.031	0.016	0.924	0.030	
08CB0049	0.039	0.019	0.925	0.017	
08CB0050	0.015	0.020	0.941	0.025	
CowNat	09CY0001	0.776	0.017	0.035	0.173
	09CY0002	0.036	0.011	0.134	0.819
	09CY0003	0.058	0.015	0.034	0.892
	09CY0004	0.192	0.048	0.479	0.281
	09CY0005	0.059	0.010	0.012	0.920
	09CY0006	0.223	0.043	0.081	0.653
	09CY0007	0.390	0.089	0.109	0.412
	09CY0008	0.015	0.010	0.015	0.960
	09CY0009	0.040	0.020	0.351	0.588
	09CY0010	0.022	0.011	0.280	0.687
	09CY0011	0.049	0.008	0.023	0.920
	09CY0012	0.021	0.017	0.042	0.920
	09CY0013	0.124	0.042	0.033	0.800
	09CY0014	0.028	0.006	0.014	0.952
	09CY0015	0.171	0.011	0.123	0.695
	09CY0016	0.251	0.060	0.208	0.481
	09CY0017	0.064	0.013	0.047	0.877
	09CY0018	0.658	0.015	0.225	0.102
	09CY0019	0.246	0.027	0.105	0.622
	09CY0020	0.017	0.018	0.870	0.096
	09CY0021	0.037	0.102	0.172	0.689
	09CY0022	0.078	0.039	0.754	0.129
	09CY0023	0.100	0.010	0.016	0.874
	09CY0025	0.018	0.038	0.030	0.914
	09CY0026	0.014	0.006	0.342	0.638

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Individual values	individual	CowHEW	CowHLW	CowHS	CowNat
CowNat cont.	09CY0027	0.123	0.064	0.040	0.773
	09CY0028	0.090	0.039	0.719	0.152
	09CY0030	0.013	0.024	0.358	0.606
	09CY0031	0.059	0.027	0.012	0.902
	09CY0032	0.387	0.104	0.028	0.481
	09CY0035	0.890	0.027	0.018	0.066
	09CY0036	0.292	0.012	0.344	0.352
	09CY0037	0.114	0.488	0.031	0.367
	09CY0038	0.191	0.116	0.139	0.554
	09CY0039	0.075	0.043	0.082	0.800
	09CY0040	0.713	0.009	0.179	0.099
	09CY0041	0.817	0.018	0.081	0.084
	09CY0043	0.024	0.015	0.048	0.914
	09CY0044	0.106	0.156	0.015	0.722
	09CY0045	0.018	0.018	0.029	0.936
	09CY0046	0.014	0.014	0.010	0.962
	09CY0047	0.016	0.007	0.140	0.838
	08DC0001	0.062	0.028	0.012	0.899
	08DC0002	0.020	0.029	0.542	0.409
	08DC0003	0.900	0.027	0.012	0.061
	08DC0004	0.064	0.008	0.034	0.894
	08DC0005	0.184	0.015	0.559	0.242
	08DC0006	0.037	0.012	0.183	0.767
	08DC0007	0.064	0.074	0.031	0.831
	08DC0008	0.430	0.026	0.251	0.293
	08DC0010	0.271	0.058	0.191	0.479
	08DC0011	0.026	0.031	0.190	0.753
	08DC0012	0.026	0.033	0.106	0.834
	08DC0013	0.042	0.028	0.590	0.340
	08DC0014	0.930	0.013	0.012	0.045
	08DC0015	0.087	0.013	0.658	0.243
	08DC0016	0.043	0.025	0.348	0.584
	08DC0017	0.248	0.020	0.055	0.677
08DC0018	0.025	0.029	0.263	0.683	
08DC0019	0.093	0.016	0.047	0.844	
08DC0021	0.058	0.017	0.356	0.568	
08DC0022	0.248	0.018	0.255	0.479	
08DC0023	0.103	0.017	0.074	0.806	
08DC0025	0.023	0.014	0.100	0.862	
08DC0026	0.454	0.033	0.409	0.104	
08DC0027	0.096	0.024	0.771	0.109	
08DC0028	0.079	0.269	0.038	0.614	
08DC0031	0.343	0.027	0.016	0.614	
CowClip	08DC0009*	0.743	0.041	0.010	0.206
	08DC0020*	0.954	0.011	0.011	0.024
	08DC0024*	0.443	0.121	0.053	0.382
	08DC0029*	0.134	0.027	0.516	0.323
	09CY0024*	0.379	0.217	0.055	0.350
	09CY0029*	0.734	0.016	0.020	0.230
	09CY0033*	0.011	0.969	0.011	0.009
09CY0034*	0.214	0.340	0.024	0.422	

Table 9. Collection and individual ancestry values for STRUCTURE analysis for K = 4 and K = 5 (see Figure 6 for graphic results of individual ancestry) with all lower Columbia region steelhead samples (see Tables 1 and 4 for name abbreviations). The table has the ancestry values for collections averaged over all individuals. Values from 0.15 to 0.29 are in light green cells, values from 0.3 to 0.39 are in olive cells, and values over 0.4 are in bright green cells.

Population	K = 4				K = 5					Individuals
	1	2	3	4	1	2	3	4	5	
08CowHEWin	0.732	0.117	0.069	0.081	0.737	0.071	0.042	0.076	0.074	49
09CowHEWin	0.756	0.111	0.063	0.071	0.783	0.067	0.038	0.046	0.066	50
08CowHLWin	0.067	0.818	0.068	0.048	0.050	0.832	0.047	0.039	0.033	50
09CowHLWin	0.074	0.797	0.064	0.065	0.049	0.804	0.041	0.063	0.043	49
08CowHSum	0.151	0.080	0.674	0.095	0.122	0.051	0.671	0.084	0.073	50
09CowHSum	0.139	0.078	0.691	0.092	0.111	0.049	0.686	0.072	0.081	50
08CowNat	0.443	0.074	0.169	0.314	0.372	0.044	0.110	0.269	0.205	26
09CowNat	0.300	0.092	0.228	0.380	0.221	0.056	0.136	0.386	0.202	42
0809CowClip	0.515	0.221	0.096	0.167	0.384	0.184	0.045	0.292	0.094	8
Elochoman	0.439	0.121	0.136	0.304	0.330	0.077	0.079	0.311	0.203	101
05CoweeAd	0.241	0.128	0.321	0.310	0.148	0.076	0.193	0.421	0.163	19
06CoweeAd	0.315	0.121	0.149	0.415	0.192	0.079	0.080	0.466	0.183	45
05CoweeJ	0.338	0.116	0.171	0.376	0.245	0.071	0.094	0.435	0.154	91
CowBarrier	0.120	0.723	0.078	0.078	0.103	0.720	0.054	0.064	0.060	99
NFToutle	0.169	0.120	0.097	0.614	0.095	0.069	0.052	0.128	0.656	99
Green	0.196	0.121	0.201	0.482	0.119	0.081	0.132	0.253	0.415	95
SFToutle	0.239	0.153	0.175	0.433	0.170	0.102	0.117	0.241	0.370	73
KalW	0.260	0.139	0.223	0.378	0.170	0.096	0.140	0.306	0.288	100
NFLewMer	0.280	0.231	0.177	0.311	0.199	0.182	0.111	0.286	0.223	97
NFLewCed	0.334	0.249	0.195	0.222	0.294	0.203	0.142	0.181	0.181	60
EFLew	0.194	0.092	0.411	0.303	0.136	0.058	0.302	0.325	0.179	76
Washougal	0.196	0.105	0.432	0.266	0.140	0.068	0.350	0.304	0.137	71
KalS	0.109	0.085	0.595	0.211	0.068	0.053	0.546	0.192	0.142	118