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Sockeye Salmon Baseline for the Western Alaska Salmon Stock Identification Project

by

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

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Weights and measures (metric)

centimeter	cm
deciliter	dL
gram	g
hectare	ha
kilogram	kg
kilometer	km
liter	L
meter	m
milliliter	mL
millimeter	mm

Weights and measures (English)

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

Time and temperature

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

Physics and chemistry

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

General

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

Mathematics, statistics

all standard mathematical signs, symbols and abbreviations	
alternate hypothesis	H_A
base of natural logarithm	*e*
catch per unit effort	CPUE
coefficient of variation	CV
common test statistics	(F, t, χ^2, etc.)
confidence interval	CI
correlation coefficient (multiple)	R
correlation coefficient (simple)	r
covariance	cov
degree (angular)	°
degrees of freedom	df
expected value	*E*
greater than	>
greater than or equal to	≥
harvest per unit effort	HPUE
less than	<
less than or equal to	≤
logarithm (natural)	ln
logarithm (base 10)	log
logarithm (specify base)	$\log_2$, etc.
minute (angular)	'
not significant	NS
null hypothesis	H_O
percent	%
probability	P
probability of a type I error (rejection of the null hypothesis when true)	α
probability of a type II error (acceptance of the null hypothesis when false)	β
second (angular)	"
standard deviation	SD
standard error	SE
variance	
population	Var
sample	var

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by
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ABSTRACT

Uncertainty about the magnitude, frequency, location, and timing of the nonlocal harvest of sockeye and chum salmon in Western Alaska fisheries was the impetus for the Western Alaska Salmon Stock Identification Project (WASSIP). The project was designed to use genetic data in mixed stock analysis (MSA) to reduce this uncertainty. A baseline of allele frequencies is required for use in mixed stock analysis to estimate the stock of origin of harvested fish. This report describes the methodology we used to understand the population genetic structure and build a baseline for use in MSA, describes the performance of the baseline for MSA, and provides guidance on how to interpret biases documented in the MSA tests when evaluating future stock composition estimates of WASSIP mixtures. Of the 42,636 individuals from 485 collections selected to be genotyped, the final baseline was composed of 39,205 individuals from 450 collections representing 294 populations. Average population sample size was 133 individuals. We used 2 types of tests to measure the baseline's ability to correctly allocate to reporting groups: proof tests and escapement samples. Correct allocations for proof tests averaged 0.96, ranged from 0.81 to 0.99, and 21 of the 24 proof tests met our goal of 90% correct allocation. Correct allocations for escapement tests averaged 0.93, ranged from 0.49 to 0.99, and 28 of the 32 escapement tests met our goal of 90% correct allocation. The baseline tests provide bias information for interpreting stock composition estimates of WASSIP fisheries, especially for areas where sea/river ecotype sockeye are present. We believe this baseline will provide accurate and precise estimates of stock composition in Western Alaska sockeye salmon fisheries.

Key words Western Alaska Salmon Stock Identification Project, WASSIP, sockeye salmon, Oncorhynchus nerka, mixed stock analysis, genetic baseline

INTRODUCTION

Sockeye salmon (*Oncorhynchus nerka*) are Alaska's most commercially valuable salmonid, and the majority originate from and are harvested in Western Alaska (Eggers and Carroll 2011; Bugaev et al. 2008). The combination of sockeye salmon life history, migratory pathways and the geography of Western Alaska create the potential for the harvest of nonlocal populations as they return to natal streams. While a majority of the harvest of sockeye salmon in Western Alaska occurs in terminal fisheries, where nonlocal harvest is minimal (e.g., Bristol Bay; Dann et al. 2009), the harvest of nonlocal populations does occur and can bias estimates of total run and stock productivity. The relative impact of this bias depends on population size: less abundant populations are more affected by their nonlocal harvest than very abundant populations. Uncertainty about the magnitude, frequency, location, and timing of this nonlocal harvest was the impetus for the Western Alaska Salmon Stock Identification Project (WASSIP). WASSIP is a consensus-driven project with 11 signatories representing fishing, Alaska Native, and government interests who serve as the Advisory Panel (AP), a 4-member Technical Committee (TC), and is governed by a Memorandum of Understanding[1]. WASSIP was designed to use genetic data in mixed stock analysis (MSA) to try to reduce this uncertainty.

MSA has been used effectively for Pacific salmon and specifically for sockeye salmon for estimating stock compositions of mixtures of fish of unknown origin. The earliest work was based on allozymes and covered more restricted geographic ranges, while more recent work is based on microsatellites and/or single nucleotide polymorphisms (SNPs) and covers broader geographic ranges. Population structure and/or MSA has been investigated in sockeye within Bristol Bay (Habicht et al. 2007, Dann et al. 2009), within Cook Inlet (Grant et al. 1980, Seeb et al. 2000, Barclay et al. 2010), within Kuskokwim River (McPhee et al. 2009), within British

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[1] Western Alaska Salmon Stock Identification Program Memorandum of Understanding. Signed May 5, 2006 and revised March 24, 2008 by the following signatories: Alaska Department of Fish and Game, Aleut Corporation, Aleutians East Borough, Association of Village Council Presidents, Bering Sea Fishermen's Association, Bristol Bay Native Association, Concerned Area M Fishermen, Kawerak Incorporated, Lake and Peninsula Borough, Tanana Chiefs Conference, and Yukon Drainage Fisheries Association.

Columbia (Wood 1987a, 1987b, 1989, 1994), and throughout the Pacific Rim (Varnavskaya et al. 1994, Beacham et al. 2005 and 2006, Wood et al. 2008, Habicht 2010).

The foundation for genetic MSA of fishery samples is a genetic characterization of all the stocks that might contribute to the fishery. This characterization is accomplished by measuring allele frequencies at specific loci within populations representing stocks. Stocks are defined by stakeholders and might use information including sociological needs, population genetic structure, adequacy of representation in the baseline, and the expected number of fish from a stock potentially within a mixture. Estimating stock composition is accomplished by comparing genotypes of fish of unknown origin to a baseline of allele frequencies of potentially contributing stocks. Such baselines are defined by 2 components: populations of individuals and the genetic markers for which they have been genotyped. This document describes the baseline the Gene Conservation Laboratory has built, in consultation with the WASSIP AP and TC, for sockeye salmon for use in WASSIP. It comprises populations ranging from Salmon Lake on the Seward Peninsula to Bering Lake near Cape Suckling (along a coastline of approximately ~6,000 km) and 96 SNPs.

This baseline differs from the baseline previously presented to the WASSIP AP and TC (Dann et al. 20012a) in 3 primary ways: 1) the number and range of populations included, 2) the SNPs assayed in these populations, and 3) the methods used to build the baseline. The first 2 changes were driven by the AP's desire to increase the precision of stock composition estimates. We increased the number of populations represented within the WASSIP area and the number of SNPs from 45 to a set of 96 chosen specifically for WASSIP (Dann et al. 2012b). In order to accomplish these tasks and stay within budget, we genotyped a subset of collections from our library of tissues. This subset was chosen in an attempt to gain the greatest representative value from our genotyping efforts for a given cost. First, we limited the range of the baseline to include only collections ranging from Salmon Lake on the Seward Peninsula to Bering Lake near Cape Suckling. The original baseline included populations from throughout the Pacific Rim. Secondly, we used information from the 45 SNP baseline analysis to exclude redundant samples. The final difference was driven by the need to handle the increased numbers of potentially linked loci. As a byproduct of reanalyzing the baseline, we ended up with a quality control of both laboratory and statistical analyses reported by Dann et al. (2012c). A complete list of differences between this analysis and the original analysis from Dann et al. (2012c) is documented in Appendix A.

OBJECTIVES

Three objectives of this document are as follows:

1) describe the methodology we used to understand the population genetic structure and build a baseline for use in MSA,
2) describe the performance of the baseline for MSA, and
3) provide guidance on how to interpret biases documented in the MSA tests when evaluating future stock composition estimates of WASSIP mixtures.

DEFINITIONS

To reduce confusion associated with the methods, results, and interpretation of this study, basic definitions of commonly used genetic and salmon management terms are offered here.

Allele. Alternative form of a given gene or DNA sequence.

Bootstrapping. A method of resampling data with replacement to assess the variation of parameters of interest.

Brood (year). All salmon in a stock spawned in a specific year.

Credibility Interval. In Bayesian statistics, a credibility interval is a posterior probability interval. Credibility intervals differ from the confidence intervals in frequentist statistics in that they are a direct statement of probability: i.e. a 90% credibility interval has a 90% chance of containing the true answer.

District. Waters open to commercial salmon fishing. Commercial fishing districts, subdistricts and sections in WASSIP commercial fishing areas are defined in statutes listed below under 'Salmon administrative area'.

Effective population size (Ne). The size of an ideal population that would be affected by genetic drift at the same rate as the actual population. This idealized population has discrete generations, an even sex ratio, constant size, random union of gametes and random survivorship of offspring (Kalinowski and Waples 2002).

Escapement (or Spawning Abundance or Spawners). The annual estimated size of the spawning salmon stock; quality of escapement may be determined not only by numbers of spawners, but also factors such as sex ratio, age composition, temporal entry into the system, and spatial distribution with the salmon spawning habitat from 5 AAC 39.222(f)).

F-statistics. Measures used to partition genetic diversity within and among populations in a hierarchical fashion. Common measures include: F_{IS}, which is the average departure of genotype frequencies from Hardy-Weinberg expectations within populations; F_{ST}, which is the proportion of the variation due to allele frequency differences among populations; and F_{IT}, which is the departure of genotype frequencies from Hardy-Weinberg expectations relative to the entire population. In this common hierarchy, the subscripts refer to comparisons between levels in the hierarchy: $_{\mathrm{IS}}$ refers to individuals within populations, $_{\mathrm{ST}}$ to subpopulations within the total population, and $_{\mathrm{IT}}$ to individuals within the total population. Hierarchies and subscript notation can be extended to any level to accommodate different study designs.

Gametic Disequilibrium (or Linkage Disequilibrium). A state that exists in a population when alleles at different loci are not distributed independently in the population's gamete pool, often because the loci are physically linked.

Genetic Drift. Chance changes in allele frequency that result from the sampling of gametes from generation to generation in a finite population. The magnitude of these changes is inversely related to effective population size.

Genetic Marker. A known DNA sequence that can be identified by a simple assay.

Genotype. The set of alleles for one or more loci for an individual.

Hardy-Weinberg Expectations (HWE). The genotype frequencies that would be expected from given allele frequencies assuming: random mating, no mutation (the alleles do not change), no migration or emigration (no exchange of alleles between populations), infinitely large population size, and no selective pressure for or against any traits.

Harvest. The number of salmon or weight of salmon taken of a run from a specific stock.

Harvest Rate. The fraction harvest from a stock taken in a fishery.

Heterozygosity. The proportion of individuals in a population that are heterozygous at a particular marker; a measure of variability.

Lake Ecotype. The typical anadromous form of sockeye salmon which spends about half its life in a nursery lake before migrating seaward (Burgner 1991).

Locus (Loci, plural). A fixed position or region on a chromosome that may contain more than one genetic marker.

Mixed Stock Analysis (MSA). Method using allele frequencies from populations and genotypes from mixture samples to estimate stock compositions of mixtures.

Microsatellites. DNA sequences containing short (2–5 base pairs) tandem repeats of nucleotides (e.g., GTGTGTGT).

Polymerase Chain Reaction (PCR). Method which amplifies a single or few copies of a locus across several orders of magnitude, generating millions of copies of the DNA.

Reporting Group. A group of populations in a genetic baseline to which portions of a mixture are allocated during mixed stock analyses; constructed based on a combination of stakeholder needs and genetic distinction and approved by the WASSIP Technical Committee and Advisory Panel.

Run. The total number of salmon in a stock surviving to adulthood and returning to the vicinity of the natal stream in any calendar year, composed of both the harvest of adult salmon plus the escapement; the annual run in any calendar year With the exception of for pink salmon the run is composed of several age classes of mature fish from the stock, derived from the spawning of a number of previous brood years (from 5 AAC 39.222(f)).

Salmon Administrative Area (Area). Geographic areas used to administer the registration of commercial salmon fishing permits (from 20 AAC 05.230). Commercial salmon fishing areas are designated by letter code and are defined by the following Alaska administrative code: Chignik (Area L; 5 AAC 15.100); Aleutian Islands and Alaska Peninsula (Area M; 5 AAC 12.100, 5 AAC 09.100, and 5 AAC 11.101); Bristol Bay (Area T; 5 AAC 06.100); and Kuskokwim (Area W; 5 AAC 07.100). Districts and subdistricts within areas used to aid management are further defined by administrative code.

Salmon Stock. A locally interbreeding group of salmon that is distinguished by a distinct combination of genetic, phenotypic, life history, and habitat characteristics or an aggregation of 2 or more interbreeding groups, which occur in the same geographic area and is managed as a unit (from 5 AAC 39.222(f)). For purposes of this study, a “stock” is a composite of all populations within 15 major rivers and 9 adjacent regions that represent populations that might be observed in WASSIP fisheries.

Sea/river Ecotype. An anadromous form of sockeye salmon which does not spend any part of its life in a nursery lake before migrating seaward (Wood et al. 2008)

Single nucleotide polymorphism (SNP). DNA sequence variation occurring when a single nucleotide (A, T, C, or G) differs among individuals or within an individual between paired chromosomes.

METHODS

TISSUE SAMPLING

Baseline collections

We collected axillary processes, muscle, heart, or liver from sockeye salmon and preserved them in either 95% ethanol or by freezing them at -80°C. Target sample size for baseline collections was 95 individuals to achieve acceptable precision for estimating allele frequencies (Allendorf and Phelps 1981; Waples 1990a) and to accommodate our genotyping platform.

Selection of baseline collections to genotype

We selected a subset of collections to include in the WASSIP baseline to reflect 4 goals to efficiently represent: 1) population abundance, 2) geographic coverage of populations, 3) genetic diversity, and 4) among-year variation of allele frequencies within populations. We used information from fishery managers and researchers, area residents, and WASSIP AP members to evaluate population abundance and geographic coverage to target sampling locations and timings. We restricted the range of collections for the WASSIP baseline to spawning locations between Cape Prince of Wales to Cape Suckling (Figure 1). We used population structure information from Dann et al. (2012a) to include samples that represented known population genetic structure and to exclude redundant samples. We used all samples that had similar location and calendar collection dates, but differed by collection year, to examine among-year variation.

Escapement collections

We collected samples from the escapement of sockeye salmon to rivers within the WASSIP area to test the baseline. These were commonly collected at escapement enumeration sites, which were generally located well below spawning grounds, but above the tidal influence in each system and were expected to only capture fish destined to spawn within the river system.

LABORATORY ANALYSIS

Developing and ascertaining SNPs for WASSIP

We contracted the development of at least 55 SNP markers that were targeted to differentiate among populations spawning within western Alaska and the Alaska Peninsula drainages and we requested novel SNPs developed by other laboratories (Dann et al. 2012b). We chose 24 populations from across the species range to represent the regions that produce the majority of sockeye salmon as well as the geographic and genetic diversity observed in previous analyses (Habicht et al. 2010). In addition to these production and diversity criteria, we included populations where collections met the following criteria: 1) fin, heart or liver tissue was available, 2) 8-10 DNA extractions worth of tissue was available for future analyses, and 3) 95 individuals were available for adequate estimates of allele frequencies. We intended this set of 24 populations to serve as a set of test populations for all laboratories interested in the population genetics of Pacific Rim sockeye salmon. In addition to one pair of populations in the set of 24 test populations, we included an additional 6 pairs of populations that were of interest to the department for a total of 36 populations. Each pair of populations represented 2 regions which the department desired greater genetic divergence to aid in MSA for management purposes.

Populations were assigned to fine- and broad-scale regions for use in regional measures of diversity. We assayed these 36 populations for available SNPs to assess their utility for WASSIP.

We evaluated these SNPs for 30 measures in our marker selection. Laboratory performance, conformance to Hardy-Weinberg expectations (HWE), and linkage among SNPs were primary factors in marker selection, but we also included measures of genetic variation among wide and narrow geographic scales as well as between the pairs of populations of interest. The contribution of each category of information to the 30 measures was as follows: laboratory performance (3), population genetic assumptions (HWE and linkage disequilibrium; 2), principal component analysis (3), F_{ST} (3), differences between pairs of populations of interest (2 measures for each pair=14), and f_{ORCA} (Rosenberg 2005; 1). We adopted a nonparametric approach to summarizing each SNP's performance for the 30 measures we evaluated. We ranked each SNP for each measure and summed the ranks in an approach based on Kendall's coefficient of concordance (*W*; Sokal and Rohlf 1995). *W* measures the agreement among rankings of different judges, but since we were more interested in an overall measure of performance across judges we chose the sum of ranks as our overall measure of marker performance. After final sums of ranks were tallied, we evaluated the best 96 SNPs (those with the lowest sum of ranks) for laboratory performance so that we only included SNPs that would provide reliable genotypic data. Finally, we considered correspondence from other laboratories in an attempt to maximize the efficiency of SNP data collection and standardize data sets across the Pacific Rim. A more complete description of this process is described by Dann et al. (2012b).

Assaying genotypes

We extracted genomic DNA from tissue samples using a DNeasy® 96 Tissue Kit by QIAGEN® (Valencia, CA). We screened 96 SNP markers (Table 1) using Fluidigm® 96.96 Dynamic Arrays (http://www.fluidigm.com). The Fluidigm® 96.96 Dynamic Array contains a matrix of integrated channels and valves housed in an input frame. On one side of the frame are 96 inlets to accept the sample DNA from individual fish and on the other are 96 inlets to accept the assays for 96 SNP markers. Once in the wells, the components are pressurized into the chip using the IFC Controller HX (Fluidigm). The 96 samples and 96 assays are then systematically combined into 9,216 parallel reactions. Each reaction is a mixture of 4µl of assay mix (1×DA Assay Loading Buffer (Fluidigm), 10×TaqMan® SNP Genotyping Assay (Applied Biosystems), and 2.5×ROX (Invitrogen)) and 5µl of sample mix (1×TaqMan® Universal Buffer (Applied Biosystems), 0.05x AmpliTaq® Gold DNA Polymerase (Applied Biosystems), 1x GT Sample Loading Reagent (Fluidigm) and 60-400ng/µl DNA) combined in a 7.2nL chamber. Thermal cycling was performed on an Eppendorf IFC Thermal Cycler as follows: 70°C for 30 min for "Hot-Mix" step, initial denaturation of 10 min at 96°C followed by 40 cycles of 96° for 15 s and 60° for 1 min. The Dynamic Arrays were read on a Fluidigm® EP1TM System or BioMarkTM System after amplification and scored using Fluidigm® SNP Genotyping Analysis software.

Assays that failed to amplify on the Fluidigm system were reanalyzed on the Applied Biosystems platform. Each reaction on this platform was performed in 384-well reaction plates in a 5µL volume consisting of 5–40ng/µl of template DNA, 1×TaqMan® Universal PCR Master Mix (Applied Biosystems), and 1×TaqMan® SNP Genotyping Assay (Applied Biosystems). Thermal cycling was performed on a Dual 384-Well GeneAmp® PCR System 9700 (Applied Biosystems) as follows: an initial denaturation of 10 min at 95°C followed by 50 cycles of 92°C for 1 s and annealing/extension temperature for 1 min. The plates were scanned on an Applied

Biosystems Prism 7900HT Sequence Detection System after amplification and scored using Applied Biosystems' Sequence Detection Software (SDS) version 2.2.

Genotypes produced on both platforms were imported and archived in the Gene Conservation Laboratory Oracle database, LOKI.

Laboratory quality control

We conducted a quality control analysis (QC) to identify laboratory errors and to measure the background discrepancy rate of our genotyping process. The QC analyses were performed by staff not involved in the original genotyping. We applied 4 methods to the QC depending on the type of collection and when it was genotyped. We have termed these the "Old", "Assay", "39" and "New" QC methods.

The "Old" QC method was how we conducted QC prior to WASSIP. This method consists of re-genotyping 8% of the fish genotyped in the original project using the same DNA extraction for the same SNPs assayed in the original project. Discrepancy rates were calculated as the number of conflicting genotypes, divided by the total number of genotypes compared. These discrepancy rates describe the difference between original project data and QC data for all SNPs and are capable of identifying assay plate errors, but cannot detect DNA extraction plate errors (rotations, etc.) since they are based upon the same extractions.

The "39" QC method compared new and old genotypes for the 39 SNPs common to our current and previous baselines (Dann et al. 2012a). Since we assayed collections for all 96 SNPs at once, we were able to compare genotypes for 39 SNPs for 100% of individuals in a collection. Discrepancy rates were calculated as above; these rates describe the difference between our old data for these 39 SNPs and new data for these same SNPs and are capable of identifying errors associated with these SNPs, but cannot detect DNA extraction errors since they are based upon the same extractions.

The "Assay" QC method compared all 96 SNPs for original project genotypes with QC genotypes based upon the same DNA extraction. We instituted this QC method as a complement to the "39" method since the "39" method is incapable of detecting errors associated with the 57 new SNPs on each assay plate. Errors associated with these new loci were detected by genotyping the 96 loci from previously extracted DNA on one chip of 96 previously genotyped and quality controlled individuals every time an assay tray was assembled. The new genotypes from these 96 fish were then compared with the genotypes in the database to ensure that the assay tray was assembled without error. Discrepancy rates were calculated as above; these rates describe the difference between original project data and QC data for all SNPs but are based on the same DNA plate and so are incapable of detecting DNA plate errors.

The "New" QC method is our current QC method and consists of re-extracting 8% of project fish and genotyping them for the same SNPs assayed in the original. Discrepancy rates were described as above; these rates describe the difference between original project data and QC data for all SNPs and are capable of identifying extraction, assay plate, and genotyping errors. This QC method is the best representation of the error rate of our current genotype production.

For all QC methods, assuming that the discrepancies among analyses were due equally to errors during the original genotyping and during quality control, error rates in the original genotyping can be estimated as half the rate of discrepancies.

STATISTICAL ANALYSIS

Data retrieval and quality control

We retrieved genotypes from LOKI and imported them into *R* (R Development Core Team 2010). All subsequent analyses were performed in *R* unless otherwise noted. Prior to statistical analysis, we performed 3 analyses to confirm the quality of the data used. First we identified SNP markers that were invariant in all individuals. We excluded these markers from further statistical analyses.

Second, we removed individuals that were missing substantial genotypic data from further analyses. We used what we refer to as the "80% rule" which excludes individuals missing genotypes for 20% or more of loci, because these individuals likely have poor-quality DNA. The inclusion of individuals with poor-quality DNA might introduce genotyping errors into the baseline and reduce the accuracies of MSA.

The final data confirmation analysis identified individuals with duplicate genotypes and removed them from further analyses. Duplicate genotypes can occur as a result of sampling or extracting the same individual twice, and were defined as pairs of individuals sharing the same alleles in 95% of loci screened. The individual with the most missing data from each duplicate pair was removed from further analyses.

Hardy-Weinberg Equilibrium

After calculating allelic frequencies for each locus, we tested observed genotype frequencies for each baseline collection for conformance to HWE at each locus by Monte Carlo simulation with 10,000 iterations using the *adegenet* package (Jombart 2008). We combined probabilities for each collection across loci using Fisher's method (Sokal and Rohlf 1995) and examined the frequency of departures from HWE to identify collections that exhibited substantially more departures than others. We removed collections from subsequent analyses if they departed significantly from HWE after correcting for multiple tests with Bonferroni's method ($\alpha = 0.05$ / no. of collections) or if they departed from HWE substantially more frequently than others.

Pooling collections into populations

When appropriate we pooled collections to obtain better estimates of allele frequencies following a step-wise protocol. First, we pooled collections from the same geographic location, sampled at similar calendar dates but in different years, as suggested by Waples (1990b). We then tested for differences in allele frequencies between pairs of geographically proximate collections that were collected at similar calendar dates and might represent the same population. We used Fisher's exact test (Sokal and Rohlf 1995) of allele frequency homogeneity and based our decisions on a summary across loci using Fisher's method. When these tests indicated no difference between collections ($P > 0.01$), we pooled them. When these pooled collections were near other collections we followed the same protocol until we found significant differences between the pairs of collections being tested. After this pooling protocol, we considered these final collections to be populations. Finally, we tested populations for conformance to HWE following the same protocol described above to ensure that our pooling was appropriate, and that tests for linkage disequilibrium would not result in falsely positive results due to departure from HWE.

Process for defining reporting groups

We defined groups of populations to be used as reporting groups for MSA. Defining reporting groups was an iterative process that took into account the following: 1) sociological needs (stakeholder and fishery management needs), 2) genetic population structure (MSA potential), 3) adequacy of representation in the baseline (number of individuals and representative value of genetic variation within groups), and 4) the expected number of fish from a reporting group potentially within a mixture (Habicht et al. 2012). We used the following metrics of these 4 factors as guidelines when evaluating potential reporting groups: 1) utility of information for fishery managers and stakeholders, 2) 90% correct allocation in tests of the baselines ability to allocate to reporting groups, 3) 400 individuals from enough different collections to adequately represent the genetic diversity present within a reporting group, and 4) an expected contribution to a given mixture of 5%, or 20 fish for the 400 fish mixtures proposed for WASSIP. The definition of reporting groups heavily depends on information gained from the "Testing reporting groups for MSA and identifying biases" section described below.

One way to meet the criteria of having adequate numbers of fish from a reporting group potentially within a mixture, was to report stock composition with 2 levels of reporting groups and to use the levels for reporting in the context of the fishery. This was termed "dynamic reporting group" method and allows for reporting of subregional reporting groups for fisheries within the region and regional reporting groups for fisheries outside the region. Final regional and subregional reporting groups were defined in consultation with the AP and TC and are summarized in Table 2.

Removal of collections from the baseline

We removed some collections from further analysis for different reasons. These reasons included collections not meeting our desired minimum sample size of 75 individuals and not pooling with others that were appropriate to pool with. Similarly, we removed collections that did not pool with geographically close collections and lacked reliable metadata to discern their exact sample date and location.

We removed collections from the Yukon River subregional group following the recommendation of the AP at the March 2011 meeting[2]. This recommendation was based upon 4 factors: 1) the Yukon River supports a small escapement that appears to be newly colonizing, and the expected contribution of any Yukon River component is expected to fall below 5% of any WASSIP mixture; 2) the number of sockeye salmon returning to the Kuskokwim is much higher than to the Yukon River; 3) genetic similarity between collections from the Yukon and Kuskokwim rivers would likely result in misallocation of Kuskokwim River fish to a Yukon River reporting group; and 4) the Yukon River drainage would be represented by fewer than the 400 fish goal for reporting groups (142 fish, Table 3).

We also removed collections that were believed to be mixtures of multiple populations and not representative of single, spawning populations. We removed hatchery broodstock collections that were believed to not represent either the hatchery or original population. Finally, we identified collections of escapement samples that were previously used as baseline but were no longer

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[2] Western Alaska Salmon Stock Identification Project. Joint Meeting of Advisory Panel and Technical Committee. March 17, 2011. Anchorage, AK.

needed to represent spawning populations because more representative collections replaced them. We subsequently used these collections as tests of the baseline.

Linkage disequilibrium

We tested for linkage disequilibrium between each pair of nuclear SNPs in each population to ensure that subsequent baseline and MSA would be based on independent markers. We used the program *Genepop* version 4.0.11 (Rousset 2008) with 100 batches of 5,000 iterations for these tests. We summarized the frequency of significant linkage disequilibrium between pairs of SNPs ($P < 0.05$), and further investigated pairs that exhibited linkage in a substantial number of populations. We considered pairs to be linked if they exhibited linkage in more than half of all populations or if they exhibited linkage in less than half of populations but in substantially more populations than a majority of SNP pairs. We defined “substantially more” by examining a histogram of the frequency of the number of populations in which pairs were linked. We also examined the correlation coefficient r between the first alphabetical allele in each linked pair of SNPs in each population to visualize the pattern of linkage across the geographic range of the baseline. We used the *BRugs* package to estimate the error around these correlation coefficient estimates (Thomas et al. 2006).

For each linked SNP pair, we either removed one of the linked SNPs or combined the pair into a composite, haploid marker in further analyses if the pattern of linkage provided information useful for MSA. We used f_{ORCA} as our measure of information. f_{ORCA} assesses the rate of correct allocation of simulated individuals to defined reporting groups based upon the markers in question (Rosenberg 2005). Because combinations of alleles from 2 or more markers can exist in more forms than single markers (9 possible phenotypes vs. 4 alleles for a pair of SNPs), composite markers generally have higher f_{ORCA} values than the single markers that form them. Simple comparisons of these values would always suggest combining linked pairs into composite markers. However, there is a cost associated with combining linked pairs as estimates of 8 phenotype frequencies are less precise than estimates of one allele frequency at 2 loci for a given sample size.

To account for this cost, and to ensure that we combined only SNP pairs that provided significantly more information than the single SNPs in question, we compared the difference between f_{ORCA} values of the composite marker and the single SNP with the greater f_{ORCA} value in the pair ($\Delta = f_{\mathrm{ORCA\text{-}pair}} - \max(f_{\mathrm{ORCA\text{-}single1}}, f_{\mathrm{ORCA\text{-}single2}})$). This difference ($\Delta$) was our test statistic. Since we did not know the distribution of Δ, we conducted a sampled randomization test (Sokal and Rohlf 2005). We randomly selected 1,000 SNP pairs, calculated Δ for each pair to empirically define the test statistic distribution, and set the 90th quantile of the distribution as a critical value (Δ_{90}). We then either combined linked SNPs into composite, haploid markers if Δ was greater than this critical value or dropped the SNP with the lower f_{ORCA} value if Δ was less than the critical value.

Analysis of genetic structure

Analysis of temporal variance

We examined the among-year temporal variation of allele frequencies with a hierarchical, 4-level Analysis of Variance (ANOVA). We treated the temporal samples as sub-subpopulations, populations as subpopulations, and regional reporting groups as populations based on the method described in Weir (1996). This method allowed the quantification of the sources of total allelic variation and permitted the calculation of the between-collection component of variance and the assessment of its magnitude relative to among-population and among-region components of variance. This analysis was conducted using the software package *GDA* (Lewis and Zaykin 2001).

Visualization of genetic distances

We visualized pairwise F_{ST} estimates among collections from the final set of independent markers estimated with the package *hierfstat* (Goudet 2006). We constructed 1,000 bootstrapped Neighbor-Joining trees by resampling loci with replacement to assess the stability of tree nodes across markers. We plotted the consensus tree with the *FigTree* program (Rambaut 2007). These trees provided insight into the variability of the genetic structure of these populations.

Testing reporting groups for MSA and identifying biases

We assessed the identifiability of subregional reporting groups in mixtures. These tests were used to determine if the underlying genetic structure supported using proposed subregional reporting groups for MSA. These tests also provide insights into potential biases in misallocation. The results of these tests will provide key insights in interpreting MSA results from WASSIP mixtures.

To assess the identifiability of subregional reporting groups in mixtures we conducted 2 types of tests. The first were “100% proof tests”, where we sampled 200 individuals without replacement from each subregional reporting group and analyzed them as a mixture against the reduced baseline. These tests provided an indication of the power of the baseline for MSA under the assumption that all the populations from a reporting group were represented in the baseline. The second were “escapement tests”, where we analyzed samples of the escapement to a river within a subregional reporting group as an independent mixture against the full baseline. These tests assumed that the fish sampled at escapement enumeration projects were destined to spawn upstream from where they were sampled. The AP and TC set a guideline that correct allocation for these single-reporting group tests should exceed 90% to be considered adequate, as is generally accepted (Seeb et al. 2000).

For both types of tests, we summarized the results following the dynamic reporting groups protocol (described in Habicht et al. 2012). For example, for tests of a subregional reporting group within the Bristol Bay region, we summarized estimates to all 9 Bristol Bay subregional groups as well as the 6 other regional groups, but for tests of subregional groups outside of Bristol Bay only a regional Bristol Bay estimate was summarized.

BAYES protocol

Stock compositions of these test mixtures were estimated with the program *BAYES* (Pella and Masuda 2001). The Bayesian model implemented by *BAYES* places a Dirichlet distribution as the prior distribution for the stock proportions, and the parameters for this distribution must be specified. We defined prior parameters for each subreporting group to be equal (i.e., a “flat” prior) with the prior for each reporting group subsequently divided equally to populations within that reporting group. We set the sum of all prior parameters to 1 (prior weight), which is equivalent to adding one fish to each mixture (Pella and Masuda 2001). We ran 5 independent Markov Chain Monte Carlo (MCMC) chains of 40,000 iterations with different starting values and discarded the first 20,000 iterations to remove the influences of the initial start values. We defined the starting values for the first chain such that the first 1/5 of the baseline populations summed to 0.9 and the remaining populations summed to 0.1. Each chain had a different 1/5 of baseline populations sum to 0.9.

We combined the second half of each chain to form the posterior distribution and tabulated mean estimates and 90% credibility intervals from a total of 100,000 iterations. We also assessed the within- and among-chain convergence of these estimates using the Raftery-Lewis and Gelman-Rubin diagnostics, respectively. These compare variation of estimates within a chain (Raftery and Lewis 1996) and within a chain to the total variation among chains (Gelman and Rubin 1992), respectively. If the Gelman-Rubin diagnostic for any stock group estimate was greater than 1.2 and the Raftery-Lewis diagnostic suggested each chain had not converged to stable estimates, we reanalyzed the mixture with 80,000-iteration chains following the same protocol. However, if the Raftery-Lewis diagnostic suggested each chain had converged to stable estimates we did not reanalyze the mixture further. Instead we examined estimates among chains, and if only one chain differed from the other 4, we assessed the shrink factors for the 4 similar chains and tabulated mean estimates and 90% credibility intervals from these chains if the shrink factor was not greater than 1.2. If the shrink factor was greater than 1.2, we examined changes in baseline allele frequencies and tabulated mean estimates and 90% credibility intervals from chains that had the least amount of allele frequency change between the original baseline and the *BAYES* posterior allele frequencies. We repeated this procedure for each reporting group mixture. A critical level of 90% correct allocation was used to determine if the reporting group was acceptably identifiable (Seeb et al. 2000). We visualized these results as barplots using the *gplots* package (Warnes 2010).

RESULTS

TISSUE SAMPLING

Baseline collections

We compiled a library of quality baseline tissues from 99,176 sockeye salmon in 903 collections. These samples were collected from 1991 through 2011 and ranged from the Kamchatka Peninsula in Russia to Washington State.

Selection of baseline collections to genotype

We chose to restrict the area of our baseline to include only those populations likely to be present in WASSIP mixtures, so we chose a subset of collections from this library ranging from Salmon Lake on the Seward Peninsula to Bering Lake near Cape Suckling (Figures 1–11). These collections spanned the years 1991–2011 (Table 3) and totaled 42,636 sockeye salmon from 485 collections.

A majority of the baseline collections chosen for WASSIP were located in the WASSIP study area (23,612 individuals; 55% of total). The Bristol Bay regional reporting group comprised the majority of these individuals, with 12,844 chosen to be genotyped for 96 SNPs (30% of total).

Escapement samples

A total of 6,614 sockeye salmon from 32 collections of the escapement to 14 different rivers within the WASSIP study area were successfully genotyped (Figure 1; Table 4). These samples were collected between 2001 and 2010 and provided tests of 14 of the 24 subregional reporting groups.

LABORATORY ANALYSIS

Developing and ascertaining SNPs for WASSIP

Seventy-nine novel SNPs from various sources were added to the existing 45 SNPs and screened for the 36 representative populations (Dann et al. 2012b). A total of 3,447 fish from the 36 test populations were genotyped for the 124 markers included in marker selection. A majority of assays performed well in our laboratory, but 3 failed and were removed from further analysis. Similarly, a majority of markers conformed to HWE, but one showed frequent departures from HWE ($P < 0.05$ in 14 populations) and was removed from further analyses. Three pairs of SNPs exhibited significant linkage disequilibrium in a majority of populations. One pair (*One_MHC*2-190 and *One_MHC*2-251) exhibited a useful pattern of linkage so both SNPs were retained. One SNP from each of the other 2 pairs were removed based upon laboratory performance and observed heterozygosity. Few SNPs contributed significantly to the principal component measures while a majority contributed little. Rankings for F_{ST} measures were generally concordant, but some variation was observed for measures of genetic differentiation between pairs of populations. G and f_{ORCA} rankings were very similar to the rankings for F_{ST} between pairs of populations.

One hundred fifteen markers passed each of the gating judges (lab performance, HWE and linkage disequilibrium) and were ranked for all 30 judges. The distribution of the summed rankings was approximately normal with an average of 1,704 (SD = 363), and ranged from a low of 704.5 (*One_MHC*2_251) to a high of 2,697 (*One_serpin*) (Table 5; Figure 12). The top-ranked 96 markers (i.e., those with the lowest sum of ranks) included 5 markers with sum of ranks lower than 1,000, 10 markers with sum of ranks between 1,000 and 1,500, and 81 markers with sum of ranks greater than 1,500. Final examination of the 96 markers with the lowest sum of ranks revealed 2 that performed poorly in the laboratory. These were replaced with markers originally ranked 97 and 99 that performed much better in the laboratory and were more likely to produce accurate and repeatable genotypic data. Following our correspondence with stakeholder laboratories, we exchanged 1 SNP with its linked complementary SNP to maximize marker set alignment with other laboratories. This exchange which was a relatively benign transition, as the 2 SNPs had very similar observed heterozygosities (0.38 for both) and average laboratory performance.

Assaying genotypes

A majority of genotypes were produced on the Biomark platform. The number of individuals genotyped from baseline collections ranged from 6 to 190 and averaged 88 individuals (Table 3). Within the WASSIP study area, the number of individuals genotyped ranged from 7 to 190 and averaged 90 individuals. Baseline collections from East of WASSIP ranged from 6 to 190 individuals with an average of 85. The number of individuals genotyped from the escapement collections ranged from 95 to 475, averaged 208, and totaled 6,685, although it should be noted that 7 of these collections (762 individuals) were originally included as baseline.

Quality control

Quality control demonstrated a low overall discrepancy rate of 0.34% and 0.25% for WASSIP sockeye salmon baseline and escapement collections, respectively (Tables 6 and 7). A majority of discrepancies were between homozygotes and heterozygotes, and very few homozygote-homozygote discrepancies were observed (total of 295 out of 1,343,236 baseline genotypes compared; 22 out of 201,921 escapement genotypes compared). Assuming that half the errors occurred in the QC and half in the original genotyping, baseline collections of sockeye salmon were genotyped with a process that produced genotypes with an error rate of 0.12% for “Old”, 0.12% for “New”, 0.18% for “39”, 0.07% for “Assay” QC method collections and an overall rate of 0.17%. With the same assumption, escapement collections were genotyped with a process that produced genotypes with an error rate of 0.01% for “New”, 0.15% for “39”, 0.04% for “Assay” QC method collections and an overall rate of 0.12%.

STATISTICAL ANALYSIS

Data retrieval and quality control

All SNPs were variant for populations in the WASSIP study area. A total of 590 individuals from WASSIP baseline collections were missing genotypes from greater than 20% of the loci (19 SNPs) and were removed from further analyses (Table 3). Of these, 388 were from within the WASSIP study area and 202 were from East of WASSIP collections. For baseline collections within the WASSIP area, 27 individuals were removed from the Norton Sound reporting group (5.24%), 50 individuals from Kuskokwim Bay (1.31%), 275 individuals from Bristol Bay (2.14%), 17 individuals from North Peninsula (0.45%), 6 individuals from South Peninsula (0.71%), and 13 individuals from Chignik (0.72%).

There were 148 duplicate individuals identified in WASSIP baseline collections, 107 in the WASSIP area collections and 41 from East of WASSIP collections. For baseline collections within the WASSIP study area, 2 duplicate individuals were removed from Norton Sound (0.39%), 30 individuals from Kuskokwim Bay (0.79%), 43 individuals from Bristol Bay (0.33%), 26 individuals from North Peninsula (0.69%), 0 individuals from South Peninsula (0.00%), and 6 individuals from Chignik (0.33%).

Hardy-Weinberg Equilibrium

Five baseline collections deviated from HWE and were removed from further analyses (Table 3). Four of these collections came from the Eastside of Bristol Bay while the fifth came from the Kuskokwim River. We observed no pattern in the deviation from HWE among loci. Four of the 5 collections that were removed had Fisher’s summary probabilities less than the Bonferroni adjusted α (1.03×10^{-4}). We removed the fifth collection because its Fisher’s summary probability was not much greater than the adjusted α ($P=1.5\times10^{-4}$), it exhibited significant ($P < 0.05$) departures from HWE for 13 loci (14% of total), and we had another collection from the same location to represent the local population (SNANU04; Nanuktuk Creek; Table 3).

Pooling collections into populations

Four hundred and fifty collections pooled into 294 populations (Table 3). Populations comprised of pooled collections ranged from Necons River in the Kuskokwim River to Kushtaka Lake near Cape Suckling. The geographic distance between pooled collections was often small (< 5 km).

Removal of collections from the baseline

In our pooling tests, we discovered 7 collections that did not pool with others and were too small to include in the baseline (2 of these lacked reliable metadata and were not pooled; Table 3). Nine collections lacked reliable metadata or were believed to be mixtures of populations and were not included in pooling tests. We removed 3 collections from the Yukon River subregional reporting group following the AP decision at the March 2011 meeting. The Main Bay collection

(SMAIN91; collection # 426) came from multiple broodstocks for a hatchery and was thought to not represent either the hatchery or original population and was removed from further analyses. We identified 8 collections of escapement samples that were previously used as baseline but were no longer needed to represent spawning populations because more representative collections replaced them. These collections were subsequently used as tests of the baseline (Table 4), except for 1 small collection (SGOOD91, n = 46; Table 3).

Of the 42,636 individuals from 485 collections selected to be genotyped, the final baseline was composed of 39,205 individuals from 450 collections representing 294 populations. Average population sample size was 133 individuals (range: 74–567; Table 3).

Linkage disequilibrium

Three SNP pairs were significantly linked in a majority of WASSIP area sockeye salmon populations in tests for LD. Two pairs were linked in greater than half of all populations (*One_MHC*2_190 & *One_MHC*2_251, $P < 0.05$ for 71% of populations; *One_GPDH*-201 & *One_GPDH*2-1872, 57% of populations), while one other pair was linked in substantially more populations than most other pairs (*One_Tf_ex*11-750 & *One_Tf_in*3-182, 40% of populations; Figure 13). The 90% critical value of the f_{ORCA} difference distribution (Δ_{90}) was 0.017, which was greater than Δ for 2 of the linked pairs (*One_GPDH*-201 & *One_GPDH*2-1872: $\Delta = 0.009$; *One_Tf_ex*11-750 & *One_Tf_in*3-182: $\Delta = 0.000$; Table 8 and Figure 14). Δ_{90} was less than Δ for the third pair (*One_MHC*2_190 & *One_MHC*2_251: $\Delta = 0.028$) and an examination of the correlation coefficient *r* of alleles at the 2 SNPs suggested a useful pattern in the linkage across reporting groups (Figure 15). So we dropped the SNP with the lowest f_{ORCA} value in 2 pairs (*One_GPDH2*-1872 and *One_Tf_ex*11-750) and combined the MHC SNPs.

Analysis of genetic structure

Analysis of temporal variance

We included 127 collections belonging to 60 populations in the analysis of temporal variance using the 4-level ANOVA (Table 9). We attempted to include collections that were taken at a similar location and at a similar Julian date to control for differences in locality and run timing. These collections ranged from the Necons River in the Kuskokwim River drainage to Kushtaka Lake near Cape Suckling and represented 4 of the 7 regional reporting groups. The ANOVA indicated that the variation among temporal collections within populations (Temporal *F*) was negligible, and that the variation among populations within regions was 2.75 greater than variation among regions ($\sigma^2_{\mathrm{SS}} = -0.89$; $\sigma^2_{\mathrm{S}} = 3.26$; $\sigma^2_{\mathrm{P}} = 1.18$; Temporal $F = -0.03$; Table 10).

Visualization of genetic distances

The neighbor-joining tree of pairwise F_{ST} indicated that sockeye salmon from the East of WASSIP group exhibit the greatest diversity among populations included in the baseline (Figure 16), and that substantial genetic structure existed within WASSIP-area groups for use in MSA (Figure 17). We observed high concordance among loci for many population groupings, in particular for populations spawning in lacustrine environments (e.g., Upper Kuskokwim River lakes, Lake Clark, Alagnak), but also for some sea/river ecotype populations (e.g., Kuskokwim River populations; Figure 17). Interestingly, some population groupings were defined more by life history and habitat usage than by geography (e.g., sea/river ecotype sockeye salmon from the Kuskokwim and Nushagak drainages). The tree of genetic distances indicated weak structuring among less abundant populations of the North and South Peninsula (e.g., Nelson River, NW

District-Black Hills, South Peninsula) but more defined structure for some of the more abundant populations of lake-type sockeye salmon from the North Peninsula (e.g., Bear).

Baseline evaluation for MSA

Proof Tests

Correct allocations for proof tests averaged 0.96 and ranged from 0.81 to 0.99 (Tables 11–15; Appendix B; Figure 18). Twenty-two of the 24 proof tests met our goal of 90% correct allocation.

For Norton Sound, South Peninsula, and East of WASSIP reporting groups, correct allocations in the proof tests were 0.93 (Norton Sound), 0.98 (South Peninsula), and 0.97 (East of WASSIP; Table 11; Figure 18). Within Kuskokwim Bay, correct allocations averaged 0.93 and ranged from 0.89 to 0.98 across the 3 tests (Table 12; Figure 18). One proof test did not reach the 90% correct allocation level: Goodnews (correct allocation = 0.89, misallocation to Bristol Bay = 0.10; Table 12). Within the Bristol Bay regional reporting group, proof test correct allocations averaged 0.95 and ranged from 0.81 to 0.99 across the 9 tests (Table 13). One proof test did not reach the 90% correct allocation level: Togiak (correct allocation = 0.81, misallocation to Kuskokwim Bay = 0.18; Table 13). Within the North Peninsula, proof test correct allocations averaged 0.97 and ranged from 0.94 to 0.99 across the 7 tests (Table 14). Within Chignik, correct allocations to the 2 Chignik regional reporting groups (Black and Chignik lakes) were both 0.99 (Table 15).

Escapement Tests

Correct allocations for escapement tests averaged 0.93 and ranged from 0.49 to 0.99 (Tables 16–18; Appendix C; Figure 19). Twenty-eight of the 32 escapement tests met our goal of 90% correct allocation.

Within Kuskokwim Bay, correct allocations in the escapement tests averaged 0.89 and ranged from 0.49 to 0.99 with 8 of the 10 tests correctly allocating at 0.91 or greater (Table 16; Figure 19). Two escapement tests did not meet the 90% correct allocation goal: Kwethluk River weir 2007 (correct allocation = 0.49, misallocation to Nushagak River populations within the Bristol Bay reporting group = 0.48; Table 16), and Goodnews River weir 2001 (correct allocation = 0.83, misallocation to Togiak populations within the Bristol Bay reporting group = 0.15; Table 16).

Within Bristol Bay, correct allocations in the escapement tests averaged 0.95 and ranged from 0.81 to 0.99 across the 20 tests (Table 17; Figure 19). Two escapement tests did not meet the 90% correct allocation goal: Togiak Subsistence 2008 (correct allocation = 0.81, misallocation to Goodnews River populations within the Kuskokwim Bay reporting group = 0.18), and the Nushagak Radio Telemetry 2005 test (correct allocation = 0.84, misallocation to Kuskokwim River populations within the Kuskokwim Bay reporting group = 0.12; Table 17).

Within Chignik, correct allocations for the 2 escapement tests were 0.98 and 0.92 for the early (6/14–21/2010) and late (7/23–30/2010) runs, respectively (Table 18; Figure 19).

DISCUSSION

This baseline represents the most complete baseline for sockeye salmon in Alaska west of Cape Suckling and was specifically designed for MSA of WASSIP fisheries. This baseline contains more than 10,000 additional fish and twice the number of markers as the previously-published baseline (Habicht et al. 2010). These additional markers were selected with specific focus on discrimination among reporting groups that were previously difficult to detect in mixtures. In addition, this baseline represents additional collections, through 2011, in drainages where baseline tests and population genetic structure indicated gaps. This baseline is the foundation for estimates of stock composition in WASSIP fisheries and the estimates of stock-specific harvests and harvest rates based upon them. As such, we have strived for transparency in describing the methods used and decisions made assembling the baseline.

The process by which this baseline was assembled was also unprecedented. All major decisions surrounding the baseline construction were reviewed by the TC and approved through consensus by the AP. Among the most substantive of these decisions were 1) to use SNP,; 2) to double the number of markers and obtain additional funding to do so, and 3) to help define reporting groups. This process required considerable time and effort from both the TC and AP in creating, reviewing, and commenting on technical documents as well as attending and contributing to meetings. The results from this process, however, will outweigh the costs. The stakeholders not only had significant influence on the direction and priorities of the analysis, they also have gained a better understanding of the process, the strengths and weaknesses of the analyses, and a sense of ownership.

We set out to describe the methodology we used to understand the population genetic structure and build a baseline for use in MSA, describe the performance of the baseline for MSA, and provide guidance on how to interpret biases documented in the MSA tests when evaluating future stock composition estimates of WASSIP mixtures. This discussion will focus primarily on interpreting the results of the population structure and on how to use MSA performance tests when evaluating stock composition estimates in future WASSIP reports.

GENETIC VARIATION AMONG SOCKEYE SALMON CONTRIBUTING TO WASSIP AREA FISHERIES

The distribution of variation observed in this baseline (Figure 17) is concordant with that previously observed using 45 SNPs (Habicht et al. 2010). As previously observed among sockeye salmon populations throughout the Pacific Rim, genetic variation was distributed generally among regions and within regions among nursery lakes (Varnavskaya 1994, Wood et al. 2008, Habicht et al. 2010). This pattern is well suited for MSA for WASSIP fisheries because the reporting groups desired by the AP were either regional, single, or multidrainage reporting groups that correspond to the distribution of genetic variation.

However, we also observed deviations from these patterns, which in some cases resulted in lower MSA performance. The deviant patterns in genetic variation appeared to be influenced by either ecotype (sea/river vs. lake ecotype) or a combination of geographic proximity and small population sizes (Figure 17). These patterns are not unique to this study.

The ecotype influence is evidenced by the intermingling of populations in the tree from the Togiak, Goodnews, Nushagak, and Kuskokwim rivers. These are the only drainages representing Western Alaska in our baseline that are known to support sea/river ecotype sockeye salmon. Sea/river ecotype sockeye salmon populations within and across drainages have been shown to be more similar to each other than lake ecotype populations (Wood et al. 1989; 1994). Wood et al. (2008) hypothesized that sea/river ecotypes colonize new drainages and lake ecotype populations evolve recurrently from these colonizations. As a result more migration occurs among sea/river ecotype populations than among lake ecotype populations resulting in higher genetic variation within and smaller genetic variation among populations of sea/river ecotypes than lake ecotypes. Wood termed this the 'recurrent evolution' hypothesis. Recently, McPhee et al. (2009) found further evidence for this hypothesis within the Kuskokwim River based upon microsatellite markers. Some of McPhee's collections are included in this baseline, which provides SNP evidence supporting the recurrent evolution hypothesis.

The pattern produced by the combination of geographic proximity and small population sizes is evidenced by the intermingling of populations in the tree from the north and south Alaska Peninsula. Populations along the Alaska Peninsula are generally small in number and are separated by salt water. The separation by salt water produces relatively low migration among populations. Less abundant populations also generally have smaller effective population sizes, which are more influenced by the effect of genetic drift on allele frequencies than more abundant populations (Hedrick 2005). This low migration coupled with high rates of genetic drift can result in a deviation from the pattern of increasing genetic distance with geographic distance. Add to that, the AP desire to split reporting groups at the end of the Alaska Peninsula, and you end up with intermingling of populations between these reporting groups on the tree. A similar pattern of high interpopulation diversity has been observed in southeast Alaska for sockeye salmon, where population sizes are small and each drainage is separated by salt water (Wood et al. 1994).

Fortunately, the genetic diversity among these populations is so high that the genetic relationships among them, as evidenced by the intermingling in the tree, does not affect MSA performance. These populations are so distinct from one another that more that 90% of allocations go to the right populations and therefore the correct reporting groups. In other areas, where diversity within reporting groups is smaller, the correct allocation to populations may be lower but the misallocations go to other populations within the same reporting group and MSA performance still meets 90% correct allocation.

EFFECT OF GENETIC SIMILARITY AMONG SEA/RIVER ECOTYPE SOCKEYE SALMON ON MSA PERFORMANCE

The similarity among sea/river ecotype populations, however, produces challenges for MSA. The Kwethluk River weir test of the Kuskokwim River reporting group had the lowest correct allocation of any of the baseline evaluation tests (49%; Table 16). This weir collection (#28; Table 3) was included in previous baselines, but was removed from this baseline and used as an escapement test because we received more representative baseline collections from spawning aggregations higher in the drainage. However, the collection of sea/river ecotype sockeye from the Kwethluk River (Collection #26; Table 3) was removed due to small sample size (n = 51). The low correct allocation of this test is likely the result of the sample containing many sea/river ecotype sockeye salmon, the absence of sea/river ecotype sockeye salmon from the Kwethluk River in the baseline, and the genetic similarity among sea/river ecotype sockeye salmon populations observed elsewhere (e.g., Wood et al. 2008; McPhee et al. 2009). These findings are supported by the misallocation to Nushagak populations within the Bristol Bay reporting group, similar misallocations between reporting groups with genetically similar sea/river ecotype sockeye salmon (e.g., Goodnews River and Togiak; Tables 12, 13, 16, and 17), and a reciprocal misallocation from the Nushagak reporting group to the Kuskokwim Bay reporting group in escapement test # 18 (Nushagak radio telemetry 2005 – correct allocation = 84%, misallocation to Kuskokwim = 12%; Table 17). However, the small contribution of the Kwethluk River to the overall Kuskokwim River escapement (2000–2009 Kwethluk weir average = 3,235; Bavilla et al. 2010), combined with the high correct allocations of other tests of this reporting group (99%, 94%, 94%, 94%, 91%; Table 16), and the small sample size of the test (n = 141) suggest that results of this test should be interpreted with caution.

The poor performance of 2 tests of the Goodnews and Togiak reporting groups was previously described in a Technical Document to the AP and TC (Dann et al 2012d). This is likely the result of genetic similarity among populations along the drainage divide and the previous absence of sea/river ecotype sockeye from the Togiak reporting group in the baseline. Sockeye salmon spawning in the mainstem of the Togiak River are believed to contribute an average of 43.5% of the escapement to the drainage, as estimated by aerial surveys (average of 1988–2007; Salomone et al. 2009). In August of 2011 we collected sea/river ecotype sockeye from the mainstem of the Togiak River as well as sockeye from a tributary of the Togiak River that was believed to contribute a large portion of the Togiak drainage escapement (9% to Pungokepuk Lake; Salomone et al. 2009).

These new 2011 collections greatly improved our representation of sockeye salmon from the Togiak River drainage and our measures of the accuracy and precision of estimates of the Togiak and Goodnews reporting groups in future MSA. Correct allocations from proof tests and escapement samples reflect this and have changed from those based on the baseline lacking these collections and reported previously (Dann et al 2012d). In proof tests the correct allocation to the Goodnews reporting group increased from 0.82 to 0.89, while for the Togiak it reduced from 0.97 to 0.81, reflecting a more realistic assessment of the genetic distinction between the 2 groups of populations (Tables 12 and 13). Correct allocations for escapement tests also changed but in different ways (Togiak subsistence increased from 0.79 to 0.81; Goodnews 2001 reduced from 0.95 to 0.83; and Goodnews 2007 improved from 0.83 to 0.96; Tables 16 and 17). The different responses to the new additions to the baseline likely reflect the composition of the escapement samples; the presence of sea/river ecotype vs. lake-type sockeye in the samples.

MSA PERFORMANCE

Conservative tests

We used 2 types of tests to evaluate the baseline’s accuracy and precision in estimating stock compositions for the 24 subregional reporting groups: proof tests and escapement samples. Proof tests assume that all populations from a reporting group are present in the baseline but provide a conservative measure of the power of the baseline for MSA. Escapement tests assume that the fish sampled at escapement enumeration projects were not strays and provided an independent measure of the power of the full baseline for MSA. Both types of tests of MSA performance of the baseline (proof and escapement) were performed with fewer fish than the sampling goal for WASSIP mixed fisheries strata (400 individuals). These tests also used flat priors. As a result, estimates of correct allocations to reporting groups may be conservative, especially estimates from tests with small sample sizes.

Proof tests were performed with 200, and in a few cases 100, individuals to avoid depopulating the baseline for reporting groups represented by fewer individuals (the minimum target size for a reporting group was set at 400 fish; see section: “Process for defining reporting groups”). Escapement tests were performed with single-year collections to allow for the inspection of year-to-year variation in performance within drainages. These tests always contained fewer than 400 fish, and sometimes as few as 95 fish. Results of escapement tests containing fewer than 190 fish should be interpreted with caution.

Using a flat prior in baseline evaluation tests is also conservative as we anticipate using an informative prior (sequential prior based on the posterior distribution of similar mixtures) in the MSA of WASSIP mixtures. The use of a flat prior in both the proof and escapement tests is likely to have the most negative impact on the correct assignments for reporting groups that have populations with similar allele frequencies, such as sea/river ecotype sockeye salmon (see below). We anticipate that an informed prior, such as the sequential prior, will improve the performance of the baseline.

Baseline representation versus population size affects proof tests

The poor performance of the Egegik proof test is likely due to an artifact of the sampling procedure used in our proof tests, coupled with highly divergent population sizes and a genetic outlier population. The proof test for the Egegik reporting group had a lower correct allocation (89%; Table 13) than previously reported results and the results of the escapement tests for Egegik (97% and 99%; Table 17). These previous results included proof tests based upon an older baseline comprising fewer collections and 45 SNPs (correct allocation 96%; Dann et al. 2009). The 96 SNPs used in the current baseline are the result of marker selection that specifically included measures to improve MSA distinction between the Egegik and Ugashik reporting groups (see section: "Developing and ascertaining SNPs for WASSIP"). We believe the lower than expected correct allocation is a result of sampling individuals from an Egegik population (Becharof Lake south, Collection # 187, Table 3; Figure 5) with very divergent MHC frequencies. The contribution to the proof test sample from the population in question was greater than the contribution the population represents to the total escapement to the Egegik River (P. Salomone, Egegik/Ugashik Area Management Biologist, ADF&G, Anchorage, personal communication). This explains the discrepancy between the low correct allocation of the proof test and high correct allocations of the escapement tests (97% and 99%, Table 17) and reinforces the importance of adequately representing population abundances in a baseline.

Baseline is adequate for WASSIP objectives

We believe that the baseline we have built for sockeye salmon for use in WASSIP meets the goals of accurately describing the genetic structure among populations within the WASSIP area as well as consistently meeting our goal of 90% correct allocation in MSA applications. We are confident in the methods used to build the baseline as well as the product of those methods, and believe that this baseline will provide accurate and precise estimates of stock composition in WASSIP fisheries.

MSA TEST BIASES AND INTERPRETING STOCK COMPOSITION ESTIMATES

The baseline tests not only provided a basis of determining if the genetic variation among populations was adequate to support the reporting groups important to the AP, they also provided information useful when interpreting future stock composition estimates. This context will be especially useful when mixtures allocate large proportions to reporting groups that performed worse in the tests than a majority of reporting groups (<95% correct allocation). A great example of these reporting groups are those containing sea/river ecotype sockeye salmon (see Discussion section: "Effect of genetic similarity among sea/river ecotype sockeye salmon on MSA performance"). In many of these tests, misallocation occurred among reporting groups that contained sea/river ecotype salmon (Kuskokwim, Goodnews, Togiak, and Nushagak rivers; Tables 12, 13, 16 and 17). Therefore, when interpreting results that contain these reporting groups, keep in mind that misallocation is likely to occur among them. Since many of the fisheries that will contain significant contributions from these reporting groups are terminal fisheries and therefore might be expected to contain close to 100% of the local stock (Kuskokwim River districts W1 and W2, Goodnews Bay district W5, Togiak and Nushagak districts), the baseline evaluation tests are especially useful. These tests provide the expected misallocation to the other reporting groups if the full mixture is all from one reporting group. For example, in the Togiak fishery, a misallocation to Kuskokwim of 18% is expected due to the genetic similarity among populations within these reporting groups (Tables 13 and 17). On the other hand, an allocation from a mixture collected in this fishery to Naknek, for example, would not be reasonably attributed to misallocation based upon genetic structure. Errors in sampling and other nongenetic sources of error could also explain such aberrant results.

RESPONSE TO TECHNICAL COMMITTEE COMMENTS

TC members provided comments on 4 technical documents that have bearing on this baseline: an investigation of temporal variation (Jasper et al. 2012); the sockeye salmon baseline based upon 45 SNPs (Dann et al. 2012a); the selection of the 96 SNP panel for sockeye salmon (Dann et al. 2012b); and the sockeye salmon baseline based upon 96 SNPs (Dann et al. 2012c). We have incorporated comments from the TC on documents relevant to this baseline and believe that TC concerns have been addressed in this report.

We made an error interpreting marker summary statistics in previous baselines, and appreciate the discovery of this error by TC members. We were interpreting the average allele frequencies across all populations in the baseline as the mean of expected heterozygosity values for each population. We mistakenly attributed the discrepancy we had observed between observed and expected heterozygosity to a genotype scoring bias against individuals with heterozygous genotypes. We were actually observing the Wahlund effect, the deficiency of heterozygotes due to combining subpopulations with differing allele frequencies together in a sample (Hedrick 2005). The error was simply the result of misinterpreting an output file from the program GDA, and we have since taken steps to summarize marker statistics more directly. While this error was unfortunate, we now know that our genotyping process does not appear to bias genotypic and allele frequencies as we previously believed.

We have provided more details on the results of tests of HWE to indicate why 5 collections were removed. All other collections that were not removed conformed to HWE. Similarly, we provide more details as to why the 3 Yukon River collections were removed from the baseline. In response to Jasper et al. (2009), the TC suggested that intragenerational evaluations of temporal variation might be more stringent comparisons to assess temporal variation in allele frequencies. We have included 60 interannual comparisons ranging from 1 to 18 years, with many representing intracohort as well as parent-offspring and multigenerational variation.

We investigated the leave one out method of evaluating the baseline potential for MSA proposed by Anderson et al. (2008) but, as TC members noted, the core software currently doesn’t accommodate mixed marker sets (diploid and phenotypic markers). However, the primary benefit of the leave one out method (cross-validation) is accomplished by the proof tests reported here, which provide conservative estimates of the baseline’s accuracy and precision to discriminate among reporting groups due to the depopulation of baseline sample sizes.

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TABLES AND FIGURES

Table 1.– Source, observed heterozygosity, F_{IS} and F_{ST} for the 96 single nucleotide polymorphisms (SNPs) used to analyze the population genetic structure of sockeye salmon in the WASSIP study area. Weir and Cockerham estimates of F_{ST} (1984) are also provided for the 2 sets of linked loci combined as haplotypes. Statistics for each marker are based on the 294 populations within the area. Overall summary statistics are estimates from the final marker set; overall H_O is the average value across loci and overall F_{IS} and F_{ST} are estimated following Weir and Cockerham.

Assay	Source[a]	H_O	F_{IS}	F_{ST}
One_ACBP-79	A	0.396	0.026	0.110
One_agt-132	B	0.382	0.003	0.085
One_aldB-152	C	0.351	0.003	0.103
One_apoe-83	B	0.329	0.007	0.126
One_c3-98	B	0.125	-0.139	0.062
One_CD9-269	B	0.347	0.002	0.094
One_cetn1-167	B	0.435	0.013	0.114
One_CFP1	D	0.214	0.004	0.065
One_cin-177	C	0.459	0.004	0.060
One_CO1[b]	A	N/A	N/A	0.234
One_ctgf-301	A	0.036	-0.004	0.034
One_Cytb_17[b]	A	N/A	N/A	0.532
One_Cytb_26[b]	A	N/A	N/A	0.242
One_E2-65	A	0.322	-0.005	0.088
One_gdh-212	C	0.426	0.007	0.076
One_GHII-2165	A	0.190	0.008	0.238
One_ghsR-66	C	0.378	0.003	0.154
One_GPDH-201	A	0.458	0.003	0.071
One_GPDH2-187[c]	A	0.136	0.009	0.106
One_GPH-414	A	0.397	-0.001	0.107
One_HGFA-49	A	0.249	0.018	0.066
One_HpaI-71	A	0.403	0.006	0.104
One_HpaI-99	A	0.138	0.009	0.204
One_hsc71-220	A	0.297	0.003	0.091
One_Hsp47	D	0.284	0.007	0.113
One_IL8r-362	A	0.112	-0.016	0.095
One_KCT1-453	B	0.203	0.006	0.091
One_KPNA-422	A	0.334	0.006	0.096
One_LEI-87	A	0.427	0.006	0.114
One_lpp1-44	B	0.373	0.005	0.166
One_metA-253	C	0.048	0.005	0.389
One_MHC2_190[b]	A	0.308	0.025	0.351
One_MHC2_251[b]	A	0.347	0.011	0.290
One_Mkpro-129	C	0.443	0.006	0.113
One_ODC1-196	B	0.429	-0.001	0.112
One_Ots208-234	C	0.142	0.007	0.108
One_Ots213-181	A	0.236	0.015	0.106
One_p53-534	A	0.040	0.005	0.145
One_pax7-248	C	0.225	0.007	0.080
One_PIP	D	0.432	0.006	0.083
One_Prl2	A	0.451	-0.004	0.098
One_rab1a-76	B	0.222	0.014	0.097
One_RAG1-103	A	0.042	-0.008	0.115
One_RAG3-93	A	0.125	0.007	0.062
One_redd1-414	C	0.422	0.015	0.145
One_RFC2-102	A	0.283	0.011	0.091
One_RFC2-285	A	0.072	0.005	0.081
One_rpo2j-261	C	0.310	0.007	0.069
One_sast-211	C	0.069	0.030	0.034
One_spf30-207	C	0.330	-0.001	0.090
One_srp09-127	C	0.028	0.010	0.039
One_ssrd-135	C	0.460	-0.010	0.080
One_STC-410	A	0.365	0.019	0.207
One_STR07	A	0.384	-0.003	0.129
One_SUMO1-6	C	0.314	0.006	0.068
One_sys1-230	C	0.432	0.003	0.131
One_taf12-248	C	0.020	0.007	0.087
One_Tf_ex11-750[c]	A	0.402	0.004	0.193
One_Tf_in3-182	A	0.110	0.011	0.290
One_tshB-92	C	0.121	0.003	0.114
One_txnip-401	C	0.003	0.024	0.039
One_U1003-75	B	0.228	0.010	0.183
One_U1004-183	B	0.358	-0.002	0.311
One_U1009-91	B	0.254	0.002	0.141
One_U1010-81	B	0.055	0.008	0.052
One_U1012-68	B	0.220	0.014	0.114
One_U1013-108	B	0.238	0.019	0.069
One_U1014-74	B	0.255	0.009	0.074
One_U1016-115	B	0.410	0.016	0.104
One_U1024-197	B	0.167	0.002	0.059

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Table 1. Page 2 of 2.

Assay	Source[a]	H_O	F_{IS}	F_{ST}
One_U1101	B	0.324	0.006	0.064
One_U1103	B	0.042	0.015	0.127
One_U1105	B	0.324	0.020	0.161
One_U1201-492	B	0.429	-0.004	0.056
One_U1202-1052	B	0.410	0.022	0.075
One_U1203-175	B	0.405	0.005	0.098
One_U1204-53	B	0.319	0.014	0.074
One_U1205-57	B	0.058	0.020	0.144
One_U1206-108	B	0.301	0.011	0.055
One_U1208-67	B	0.402	-0.009	0.076
One_U1209-111	B	0.225	0.009	0.110
One_U1210-173	B	0.181	0.011	0.053
One_U1212-106	B	0.418	0.003	0.140
One_U1214-107	B	0.090	0.007	0.080
One_U1216-230	B	0.402	0.014	0.113
One_U301-92	A	0.258	0.004	0.093
One_U401-224	A	0.438	-0.003	0.084
One_U404-229	A	0.069	0.014	0.122
One_U502-167	A	0.044	-0.012	0.041
One_U503-170	A	0.237	-0.003	0.090
One_U504-141	A	0.359	0.008	0.067
One_vamp5-255	C	0.346	0.001	0.085
One_vatf-214	C	0.055	0.000	0.120
One_VIM-569	A	0.185	0.018	0.083
One_ZNF-61	A	0.373	-0.002	0.148
One_Zp3b-49	A	0.135	0.005	0.322
One_CO1_Cytb17_26[b]		N/A	N/A	0.266
One_MHC2_190_251[b]		N/A	N/A	0.244
Average/Overall		0.266	0.005	0.118

[a] A) Gene Conservation Laboratory of the Alaska Department of Fish and Game; Smith et al. 2005; Elfstrom et al. 2006; B) International Program for Salmon Ecological Genetics at the University of Washington; Storer et al.; C) Hagerman Genetics Laboratory of the Columbia River Inter-Tribal Fish Commission; Campbell and Narum 2011; and D) Molecular Genetics Laboratory at the Canadian Department of Fisheries and Oceans.

[b] These SNPs were combined into haplotypes and treated together as single loci, *One_CO1_Cytb17_26* and *One_MHC2-190_251*.

[c] These SNPs were dropped due to linkage.

Table 2.– Geographic boundaries of the regional and subregional reporting groups defined for use in mixed stock analysis of sockeye salmon for WASSIP.

Regional	Subregional	Start point	Stop point
Norton Sound	Norton Sound	Cape Prince of Wales	Point Romanof
Kuskokwim Bay	Kuskokwim River	Naskonat Peninsula	Warehouse Bluff
	Kanektok	Warehouse Bluff	Jacksmith Bay
	Goodnews	Jacksmith Bay	Cape Newenham
Bristol Bay	Togiak	Cape Newenham	Cape Constantine
	Igushik	Cape Constantine	Coffee Point
	Wood	Coffee Point	Black Slough
	Nushagak	Black slough	Etolin Point
	Kvichak	Etolin Point	Pederson Point (excluding Alagnak River)
	Alagnak	Alagnak River headwaters	Alagnak River mouth
	Naknek	Pederson Point	Cape Chichagof
	Egegik	Cape Chichagof	Cape Greig
	Ugashik	Cape Greig	Cape Menshikof
North Peninsula	Cinder	Cape Menshikof	Coastline at 158° 20.00' W
	Meshik	Coastline at 158° 20.00' W	Stroganof Point
	Ilnik	Stroganof Point	Cape Seniavin
	Sandy	Cape Seniavin	Coastline at 56° 12.00' N
	Bear	Coastline at 56° 12.00' N	Cape Rozhnof
	Nelson	Cape Rozhnof	Frank's Point
	Northwestern District-Black Hills	Frank's Point	Scotch Cap
South Peninsula	South Peninsula	Scotch Cap	Kupreanof Point
Chignik	Black Lake	Tributaries of Black River	Black Lake outlet
	Chignik Lake	Kupreanof Point	Cape Kumlik (excluding Black Lake)[a]
East of WASSIP	East of WASSIP	Cape Kumlik	Cape Suckling

Note: A Yukon River subregional group was removed, see text for details.

[a] The Chignik Lake reporting group does not include Surprise Lake (Collection #263), which was placed in the East of WASSIP reporting group at the request of the AP.

Table 3.–Regional and subregional reporting group, ADF&G collection code, location, collection and population number, collection date, and the numbers of sockeye salmon used to describe the genetic structure of sockeye salmon in the WASSIP study area and estimate the stock composition of WASSIP mixed fisheries. The number of individuals includes the number of individuals initially genotyped for the set of 96 SNPs (Initial), the numbers removed because of missing loci (Missing) and duplicate individuals (Duplicate), and the number of individuals incorporated into the baseline (Final). Collection names contain population names in parentheses when they differ from final population names (e.g. Figure 17).

Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
North of Kuskokwim Bay	Norton Sound	SSALM01	Salmon Lake	1	1	8/3/2001	88	5	0	83
		SGLAC04	Glacial Lake	2	2	8/15/2004	190	3	0	187
		SUNA07	Unalakleet River	3	3	8/22/2007	95	5	0	90
						Norton Sound Total	373	13	0	360
	Yukon River	SANDRE05[a]	Andreafsky River	4		7/12/2005	47	13	1	0
		SANDRE06[a]		5		6/28/2006	48	1	0	0
		SANDRE08[a]		6		7/19/2008	47	0	1	0
						Yukon River Total	142	14	2	0
						North of Kuskokwim Bay Total	515	27	2	360
Kuskokwim Bay	Kuskokwim River	SUTAK06[b]	Upper Takotna River	7		2006	40	4	0	0
		SNECO06	Necons River	8	4	8/1/2006	55	0	0	55
		SNECO07		9	4	7/28/2007	95	2	0	93
		STELA03	Telaquana Lake outlet	10	5	8/14/2003	96	0	0	96
		STELA05	Telaquana Lake - east beach	11	6	10/4/2005	95	0	0	95
		STELA09	Telaquana Lake outlet	12	5	8/29/2009	94	0	1	93
		STELABC209	Telaquana Lake - Bear Creek	13	7	8/30/2009	95	0	0	95
		STELAUB09	Telaquana Lake - east beach	14	6	8/31/2009	93	0	0	93
		STELASWB09	Telaquana Lake - southwest beach	15	6	9/3/2009	94	1	2	91
		STELAPC09	Telaquana Lake - Phylis Creek	16	7	9/2/2009	89	2	6	81
		SKOGR08	Kogrukluk River	17	8	8/4/2008	71	0	0	71
		SKOGR01[c]		18		7/6/2001	96	5	0	0
		SKOGR07[c]		19		7/24/2007	95	0	0	0
		SCHUKO08	Chukowan River (Kogrukluk River)	20	8	8/7/2008	75	0	0	75
		SHOLI08	Holitna River (Kogrukluk River)	21	8	8/9/2008	75	0	0	75
		SSALMR06[d]	Salmon River (Aniak River)	22		8/2/2006	142	2	0	0
		SATSAK09	Atsaksovluk Creek (Aniak River)	23	9	8/6/2009	95	0	6	89

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Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
Kuskokwim Bay	Kuskokwim River	STULU08	Tuluksak River	24	10	7/4/2008	75	0	1	74
		SKWETL06	Kwethluk River lakes	25	11	8/8/2006	68	14	4	50
		SKWETR06[b]	Kwethluk River	26		8/8/2006	57	6	0	0
		SKWETR07	Kwethluk River lakes	27	11	8/5/2007	50	1	0	49
		SKWET07[c]	Kwethluk River	28		2007	142	0	1	0
					Kuskokwim River Total		1,887	37	21	1,275
	Kanektok	SKAGF09	Kagati Lake tributary	29	12	8/9/2009	95	1	0	94
		SPEGF09	Pegati Lake tributary	30	12	8/8/2009	95	0	0	95
		SKAGB09	Kagati Lake beach	31	13	8/9/2009	95	0	0	95
		SPEGB09	Pegati Lake beach	32	13	8/8/2009	95	0	1	94
		SKAGO09	Kagati-Pegati Lake outlet	33	14	8/10/2009	95	0	0	95
		SKANE09	Kanektok River	34	15	8/12/2009	95	2	0	93
		SKANE02[c]	Kanektok River	35		7/16/2002	95	0	0	0
		SKANE07[c]	Kanektok River	36		7/10/2007	96	0	0	0
						Kanektok Total	761	3	1	566
	Goodnews	SGOODSO10NF	Goodnews River - North Fork lake tributary	37	16	8/12/2010	95	0	3	92
		SGOODB10NF	Goodnews River - North Fork lake beach	38	17	8/12/2010	95	0	0	95
		SGOODO10NF	Goodnews River - North Fork lake outlet	39	17	8/12/2010	95	0	1	94
		SGOODR10NF	Goodnews River - North Fork river	40	18	8/13/2010	95	0	1	94
		SGOOD02		41	18	7/23/2002	95	4	0	91
		SGOOD06		42	18	7/20/2006	48	2	1	45
		SGOODSO10MF	Goodnews River - Middle Fork lake tributary	43	19	8/8/2010	95	0	2	93
		SGOODB10MF	Goodnews River - Middle Fork lake beach	44	19	8/8/2010	95	0	0	95
		SGOODO10MF	Goodnews River - Middle Fork lake outlet	45	19	8/8/2010	95	0	0	95
		SGOODR10MF	Goodnews River - Middle Fork river	46	20	9/14/2010	69	0	0	69
		SGOODR11MF		47	20	8/7/2011	7	0	0	7
		SGOOD91[c]		48		8/1/1991	48	2	0	0
		SGOOD01[c]		49		7/15/2001	96	0	0	0

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Table 3. Page 3 of 18.

Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
Kuskokwim Bay	Goodnews	SGOOD07[c]		50		2007	142	2	0	0
						Goodnews Total	1,170	10	8	870
						Kuskokwim Bay Total	3,818	50	30	2,711
Bristol Bay	Togiak	SSLUG10	Slug River	51	21	8/8/2010	108	1	0	107
		SOSVIAK10	Osviak River	52	21	8/8/2010	75	0	0	75
		STOGL00	Sunday Creek (Togiak Lake)	53	22	8/21/2000	95	1	1	93
		STOGT06	Togiak Tower (Togiak Lake)	54	22	7/27/2006	95	0	0	95
		STOGRM11	Togiak River	55	23	8/19/2011	95	1	0	94
		SONGI06	Ongivinuk Lake	56	24	8/24/2006	95	0	0	95
		SNENE06	Nenevok Lake	57	25	8/24/2006	95	1	0	94
		SPUNGO11	Pungokepuk Lake	58	26	8/23/2011	95	1	0	94
		SGECH00	Gechiak Lake	59	27	8/21/2000	96	1	0	95
		SKULU06	Kulukak River Lake	60	28	8/24/2006	95	0	1	94
						Togiak Total	944	6	2	936
	Igushik	SUALI03	Ualik Lake	61	29	8/14/2003	99	1	0	98
		SUALI03f		62	29	8/14/2003	30	0	0	30
		SONGU07	Ongoke River - Upper	63	30	8/27/2007	95	6	1	88
		SONGL07	Ongoke River - Lower	64	30	8/28/2007	95	0	0	95
		SAMAN03	Amanka Lake	65	31	8/14/2003	100	1	2	97
		SAMAN03f		66	31	8/14/2003	57	1	0	56
		SSNAKLKB10	Snake Lake beach	67	32	8/11/2010	89	1	0	88
		SSNAKLKO10	Snake Lake outlet	68	32	8/11/2010	83	0	0	83
						Igushik Total	648	10	3	635
	Wood	SLKUL07	Lake Kulik East beach	69	33	9/10/2007	95	4	0	91
		SGRANT07	Grant River	70	34	8/22/2007	95	9	3	83
		SKULIK01	Lake Kulik West beach	71	35	8/1/2001	96	2	0	94
		SMIKCH09	Mikchalk Lake	72	36	9/10/2009	95	1	0	94
		SSILVH07	Silver Horn beaches	73	37	9/10/2007	95	0	0	95
		SHARDL07	Hardluck Bay beaches	74	38	9/10/2007	95	0	0	95
		SMOOSCK09	Moose Creek	75	39	8/17/2009	95	1	1	93
		SAGULU01	Agulukpak River	76	40	8/21/2001	94	2	0	92

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Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
Bristol Bay	Wood	SANVI06	Anvil Bay Beach	77	41	8/20/2006	95	0	1	94
		SSIXCK08	Sixth Creek	78	42	2008	95	1	0	94
		SN4BE06	N4 Beach	79	43	8/11/2006	95	0	1	94
		SABEA04	A Beach - Little Togiak Lake	80	44	8/8/2004	65	0	0	65
		SABEA05		81	44	8/10/2005	30	2	0	28
		SLTOG08	Little Togiak River	82	45	2008	95	13	0	82
		SPICK01	Pick Creek	83	46	8/3/2001	95	1	2	92
		SPICK08		84	46	7/22/2008	93	1	5	87
		SLYNXLK09	Lynx Lake	85	47	9/9/2009	95	2	1	92
		SLYNX06	Lynx Beach	86	48	8/11/2006	95	0	0	95
		SLYNXCKT09	Lynx Creek - Cold Tributary	87	49	8/12/2009	81	2	0	79
		SLYNX01	Lynx Creek	88	50	8/22/2001	95	1	0	94
		SLYNXCK09		89	50	8/21/2009	109	1	1	107
		SAGULO01	Agulowok River	90	51	8/22/2001	95	0	0	95
		SICEL07	Ice Creek	91	52	8/9/2007	95	6	0	89
		SHAPP01	Happy Creek	92	53	7/30/2001	95	0	0	95
		SHANS04	Hansen Creek	93	54	8/4/2004	95	0	0	95
		SBEAR01	Bear Creek	94	55	8/2/2001	96	2	0	94
		SEAGL07	Eagle Creek	95	56	8/12/2007	93	1	0	92
		SYAKOB06	Yako Beach	96	57	8/19/2006	95	0	0	95
		SMISS98	Mission Creek	97	58	1998	94	2	1	91
		SWOOD09	Wood River	98	59	9/5/2009	95	3	0	92
						Wood Total	2,751	57	16	2,678
	Nushagak	SFISHT10	Fish Trap Lake	99	60	9/4/2010	80	1	0	79
		SMULC01B	Upper Mulchatna River	100	61	8/27/2001	65	0	0	65
		SMULC01A		101	61	8/27/2001	95	8	0	87
		SKOKT00	Koktuli River	102	62	8/13/2000	96	3	0	93
		SSTUY00	Stuyahok River	103	63	8/14/2000	96	2	0	94
		SUPNK01	Klutapuk Creek (Upper Nushagak River)	104	64	8/18/2001	95	0	0	95
		SKING01	King Salmon River (Upper Nushagak River)	105	64	8/18/2001	48	0	0	48
		SCHAU01	Chauekuktuli Lake beach	106	65	8/22/2001	96	0	0	96

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Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
Bristol Bay	Nushagak	SALLE00	Allen River beach	107	66	8/17/2000	96	4	1	91
		SALLE01	Allen River	108	67	8/22/2001	95	1	0	94
		SNUYL00	Nuyakuk Lake	109	68	8/16/2000	95	4	0	91
		SNUYA01	Nuyakuk Lake - south beach	110	68	8/23/2001	94	0	0	94
		STIKC01	Tikchik River	111	69	8/18/2001	95	2	0	93
		STIKC00	Tikchik Lake Creek	112	70	8/18/2000	95	1	0	94
						Nushagak Total	1,241	26	1	1,214
	Kvichak	STLGF99	Upper Tlikakila River - Glacier Fork	113	71	10/6/1999	47	0	0	47
		SUTLIK01	Upper Tlikakila River	114	71	9/24/2001	96	0	0	96
		SLLCL99	Little Lake Clark	115	72	10/9/1999	95	0	0	95
		SKIJI01	Kijik River	116	73	9/19/2001	96	9	0	87
		SLKIJ01	Lower Kijik River	117	74	9/18/2001	96	1	0	95
		SCHLB99	Chulitna Lodge beach	118	75	10/5/1999	96	1	0	95
		SCHLP99	Chulitna Lodge ponds	119	75	10/1/1999	48	0	1	47
		SSUCK07	Sucker Bay Lake	120	76	9/14/2007	95	0	0	95
		STAZI01	Tazimina River (Sixmile Lake)	121	77	8/29/2001	95	0	0	95
		SNHAL02	Newhalen River (Sixmile Lake)	122	77	9/3/2002	96	0	0	96
		STOMK00	Tomkok Creek	123	78	8/24/2000	95	0	0	95
		STOMK02		124	78	8/28/2002	48	8	0	40
		SKNUT00	Knutson Bay	125	79	8/27/2000	96	13	0	83
		SKNUT99L		126	79	10/16/1999	95	0	0	95
		SPEDR99	Pedro Ponds	127	80	1999	47	0	0	47
		SBEAR99L[b]	Pedro Ponds - Bear Pond late	128		10/17/1999	47	0	0	0
		SGRAS99L	Pedro Ponds - Grass Pond late	129	80	10/15/1999	44	0	0	44
		SCHIN00	Chinkelyes Creek (Iliamna River)	130	81	8/28/2000	96	1	0	95
		SILIA04B	Iliamna River	131	81	8/21/2004	95	0	3	92
		SILIA99L	Iliamna River - late	132	82	10/17/1999	96	10	0	86
		SFING00	Finger Beach 1 (Pile Bay)	133	83	8/24/2000	84	1	0	83
		SSOUT99	Southeast Creek beach (Pile Bay)	134	83	8/26/1999	95	0	0	95
		SPORC99	Porcupine Island (Iliamna Lake islands)	135	84	1999	48	0	0	48
		SFUEL00	Fuel Dump Island (Iliamna Lake islands)	136	84	8/28/2000	96	4	0	92

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Table 3. Page 6 of 18.

Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
Bristol Bay	Kvichak	SWOOD01	Woody Island (Iliamna Lake islands)	137	84	8/19/2001	96	1	0	95
		STRIA00	Triangle Island (Iliamna Lake islands)	138	84	8/16/2000	96	1	0	95
		STOMM00	Tommy Creek	139	85	8/24/2000	96	4	0	92
		STOMM02		140	85	8/19/2002	48	0	1	47
		SCOPP00	Copper River	141	86	8/28/2000	96	0	0	96
		SCOPP99		142	86	8/23/1999	47	0	0	47
		SNICK00	Nick N Creek	143	87	8/25/2000	96	4	0	92
		SSECK00	Southeast Creek (Gibralter Lake)	144	88	8/26/2000	96	2	0	94
		SDREA01	Dream Creek (Gibralter Lake)	145	88	8/22/2001	95	1	0	94
		SGIBR00	Gibralter River	146	89	8/25/2000	90	11	0	79
		SGIBR99		147	89	8/23/1999	95	0	1	94
		SDENN00	Dennis Creek (South Iliamna Lake)	148	90	8/23/2000	96	0	0	96
		SBELI00	Belinda Creek (South Iliamna Lake)	149	90	8/25/2000	95	12	0	83
		SUTAL04	Upper Talarik Creek	150	91	8/15/2004	95	4	1	90
		SUTAL06		151	91	8/10/2006	95	0	2	93
		SLTAL00	Lower Talarik Creek	152	92	8/26/2000	95	0	0	95
		SLTAL01		153	92	8/23/2001	70	1	0	69
						Kvichak Total	3,439	89	9	3,294
	Alagnak	SFUNN04E[d]	Funnel Creek	154		8/8/2004	96	0	0	0
		SMORA04E	Moraine Creek	155	93	8/8/2004	96	0	0	96
		SBATT01	Battle Creek	156	94	9/4/2001	96	4	0	92
		SBATL04T	Battle Lake tributary	157	94	9/11/2004	96	0	0	96
		SBATL04B	Battle Lake beach	158	94	9/11/2004	96	0	0	96
		SNANU04E[d]	Nanuktuk Creek	159		8/9/2004	96	3	0	0
		SNANU04		160	95	9/9/2004	96	1	0	95
		SKULI01	Kulik River	161	96	9/5/2001	96	6	0	90
		SKULI04		162	96	9/8/2004	96	0	0	96
						Alagnak Total	864	14	0	661
	Naknek	SAMER00	American River	163	97	8/22/2000	92	2	1	89
		SAMER01		164	97	8/17/2001	96	9	1	86
		SGROS03	Grosvenor Lake	165	98	8/12/2003	96	2	0	94

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Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
Bristol Bay	Naknek	SHARD03	Hardscrabble Creek	166	99	8/12/2003	96	0	1	95
		SELAGOR06[b]	East La Gorce Creek	167		8/27/2006	47	0	0	0
		SKATO106[d]	Katolinat Creek beach	168		9/17/2006	75	1	0	0
		SMARG01	Margot Creek	169	100	8/15/2001	95	0	1	94
		SHEAD01	Headwater Creek (Brooks Lake)	170	101	7/22/2001	93	19	0	74
		SBRLK00	Brooks Lake	171	101	8/22/2000	96	0	0	96
		SCHARL06[b]	Charlene Creek	172		9/11/2006	47	0	0	0
		SLQTIP06	Lower Q-Tip Lake	173	102	9/12/2006	86	0	0	86
		SIDAV00	Idavain Creek	174	103	8/23/2000	95	2	0	93
		SIDAV06		175	103	8/29/2006	48	0	0	48
		SDUMP306	Dumpling Creek beach	176	104	9/17/2006	83	0	0	83
						Naknek Total	1,145	35	4	938
	Egegik	SCABI00	Cabin Creek (East Becharof)	177	105	8/15/2000	96	1	0	95
		SRUTH00[d]	Ruth Lake outlet	178		8/12/2000	96	7	1	0
		SSALCR06	Salmon Creek (East Becharof)	179	105	8/16/2006	95	7	0	88
		SBURL06	Burls Creek (East Becharof)	180	105	8/16/2006	95	1	2	92
		SCLEO01	Cleo Creek (East Becharof)	181	105	8/16/2001	48	0	0	48
		SFEAT01	Featherly Creek (East Becharof)	182	105	8/16/2001	48	0	0	48
		SBECH00	Becharof Creek (East Becharof)	183	105	8/11/2000	94	3	0	91
		SKEJU00	Kejulik River -Upper	184	106	8/8/2000	96	0	2	94
		SKEJU01	Kejulik River	185	106	8/17/2001	96	0	0	96
		SBECH08NT	Becharof Lake north	186	107	8/11/2008	95	1	1	93
		SBECH08SB	Becharof Lake south	187	108	8/11/2008	95	1	1	93
						Egegik Total	954	21	7	838
	Ugashik	SUGAS01	Ugashik Creek	188	109	7/21/2001	96	7	0	89
		SCROCK05	Crooked Creek (Upper Ugashik creeks)	189	110	8/24/2005	95	0	0	95
		SDEER01	Deer Creek (Upper Ugashik creeks)	190	110	7/20/2001	96	0	0	96
		SUGAS00	Ugashik Narrows	191	111	8/24/2000	96	0	0	96
		SBLACKU05	Black Creek (Lower Ugashik creeks)	192	112	8/24/2005	95	1	0	94
		SECRE05	E Creek (Lower Ugashik creeks)	193	112	8/8/2005	95	0	0	95

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Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
Bristol Bay	Ugashik	SOUTL00	Outlet Stream	194	113	8/26/2000	95	4	0	91
		SFIGU05	Figure 8 Creek	195	114	8/22/2005	95	4	1	90
		SOLDH05	Old Ham Creek	196	115	8/22/2005	95	1	0	94
						Ugashik Total	858	17	1	840
						Bristol Bay Total	12,844	275	43	12,034
North Peninsula	Cinder	SWIGGC05	Wiggly Creek (Upper Cinder River)	197	116	7/29/2005	90	0	10	80
		SMAINC05	Mainstem Cinder River (Upper Cinder River)	198	116	7/29/2005	95	1	0	94
		SLAVA04	Lava Creek	199	117	7/23/2004	95	0	3	92
		SMUDA05	Mud Creek	200	118	7/30/2005	95	0	0	95
						Cinder Total	375	1	13	361
	Meshik	SMESLK05	Meshik Lake beach	201	119	7/30/2005	95	0	0	95
		SMESLKO05	Meshik Lake outlet	202	119	7/30/2005	95	0	0	95
		SMESHL05	L Creek (Upper Meshik River)	203	120	7/30/2005	95	1	0	94
		SMESH202	Blue Violet Creek (Upper Meshik River)	204	120	7/29/2002	93	0	2	91
		SMESH102	Landlock Creek (Lower Meshik River)	205	121	7/29/2002	96	0	0	96
		SREDBC05	Red Bluff Creek	206	122	7/30/2005	95	0	0	95
						Meshik Total	569	1	2	566
	Ilnik	SNPEN01	Willie Creek (Ocean River)	207	123	8/27/2001	81	1	0	80
		SOCEA01	Ocean River	208	123	2001	96	1	0	95
		SILNIK07	Ilnik River	209	124	7/7/2007	190	1	1	188
		SWILD05	Wildman Lake	210	125	7/30/2005	95	0	1	94
						Ilnik Total	462	3	2	457
	Sandy	SSAND00	Sandy Lake	211	126	6/30/2000	95	0	0	95
		SSANDR07	Sandy River	212	126	7/8/2007	190	0	0	190
						Sandy Total	285	0	0	285
	Bear	SBEAR00E	Bear River - Early 1	213	127	6/30/2000	95	0	0	95
		SBEARR07	Bear River - Early 2	214	128	7/7/2007	95	0	0	95
		SCUB04	Cub Creek (Upper Bear creeks)	215	129	8/15/2004	95	0	0	95
		SREDC04	Red Creek (Upper Bear creeks)	216	129	8/15/2004	95	0	0	95
		SBEARS05	Bear Lake beach	217	130	8/29/2005	95	1	0	94

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Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
North Peninsula	Bear	SBEARO05	Bear Lake outlet	218	131	8/29/2005	95	0	0	95
		SBEAR00L	Bear River - Late	219	132	8/18/2000	96	2	0	94
						Bear Total	666	3	0	663
	Nelson	SHOOD01	Sapsuk Lake	220	133	7/31/2001	95	1	0	94
		SHOOD05	Sapsuk Lake beach	221	133	7/31/2005	95	1	0	94
		SNELSR07	Sapsuk River	222	133	7/1/2007	47	0	0	47
		SDAVI05	Davids River	223	134	7/31/2005	95	0	0	95
		SHOOD00[e]	Sapsuk River	224		7/5/2000	96	0	0	0
						Nelson Total	428	2	0	330
	NW District/ Black Hills	SNCREK07	North Creek	225	135	7/25/2007	95	1	4	90
		SMOF09	Moffett Creek	226	136	8/18/2009	95	0	3	92
		SMOFF02	Paul Hansen tributary	227	137	7/30/2002	95	2	0	93
		SOUTE04	Outer Marker Lake (Izembek Lagoon lakes)	228	138	9/9/2004	95	2	0	93
		SBLUE04	Blue Bill Lake (Izembek Lagoon lakes)	229	138	9/7/2004	95	0	1	94
		SSWANL08	Swansons Lagoon	230	139	8/25/2008	95	1	0	94
		SPETELA05	Peterson Lagoon	231	140	8/2/2005	95	1	0	94
		SWHAL02	Whaleback Mountain Creek	232	141	7/30/2002	96	0	0	96
		SMCLE04	McLees Lake	233	142	6/4/2004	143	0	1	142
		SSUMM99	Summer Bay Lake	234	143	8/25/1999	96	0	0	96
						Northwestern District/Black Hills Total	1,000	7	9	984
						North Peninsula Total	3,785	17	26	3,646
South Peninsula	South Peninsula	SSANA08	Sanak Island	235	144	8/24/2008	86	0	0	86
		SHANLK05	Hansen Lake	236	145	8/2/2005	95	0	0	95
		SMIDL04	Morzhovoi Bay - Middle Lagoon	237	146	7/28/2004	95	2	0	93
		STHIN05	Thin Point Lagoon	238	147	8/1/2005	95	1	0	94
		SMORT04	Mortensen's Lagoon	239	148	8/2/2004	95	0	0	95
		SLONGJ05	Long John Lagoon	240	149	8/1/2005	95	0	0	95
		SCANBR08	Canoe Bay River	241	150	8/26/2008	95	1	0	94
		SARCH05	Archeredin Lake	242	151	8/3/2005	95	1	0	94
		SORZI00	Orzinski	243	152	7/1/2000	94	1	0	93
						South Peninsula Total	845	6	0	839

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Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
Chignik	Black Lake	SBROAD97	Broad Creek (Black Lake)	244	153	9/1/1997	96	1	2	93
		SBSPR97	Big Spring (Black Lake)	245	153	1997	95	2	0	93
		SBOUL97	Boulevard Creek (Black Lake)	246	153	9/1/1997	95	0	0	95
		SFAN97	Fan Creek (Black Lake)	247	153	1997	95	0	0	95
		SALEC97	Alec River (Black Lake)	248	153	9/1/1997	96	0	0	96
						Black Lake Total	477	3	2	472
	Chignik Lake	SCHIA08	Chiaktuak Creek	249	154	8/29/2008	95	2	0	93
		SCHIA97E		250	154	1997	95	0	1	94
		SCHIA97M		251	154	9/18/1997	94	1	0	93
		SWESTF97[e]	West Fork Chignik River	252		1997	95	0	0	0
		SWESTF08		253	155	8/28/2008	95	1	0	94
		SCUCU08	Cucumber Creek (Early Chignik Lake)	254	156	8/29/2008	95	0	1	94
		SHAT08E	Hatchery Beach (Early Chignik Lake)	255	156	8/29/2008	95	1	2	92
		SHAT96	Hatchery Beach (Late Chignik Lake)	256	157	10/18/1996	95	0	0	95
		SHAT97E	Hatchery Beach (Early Chignik Lake)	257	156	9/15/1997	94	0	0	94
		SCLARK08	Clark River - Early	258	158	8/28/2008	94	3	0	91
		SCLARK96	Clark River (Late Chignik Lake)	259	157	10/19/1996	95	0	0	95
		SCLRK97E	Clark River - Early	260	158	9/16/1997	96	1	0	95
		SCHIG08	Chignik River	261	159	8/30/2008	95	1	0	94
		SCHIG98		262	159	8/22/1998	95	0	0	95
						Chignik Lake Total	1,328	10	4	1,219
						Chignik Total	1,805	13	6	1,691
East of WASSIP	East of WASSIP	SSURPL08	Surprise Lake	263	160	8/22/2008	95	0	0	95
		SOCEAB06	Ocean Beach	264	161	8/29/2006	95	0	0	95
		SHORS05	Horse Marine Lake	265	162	9/2/2005	95	0	0	95
		SPINNM08	Pinnell Creek (Frazer Lake upper creeks)	266	163	8/21/2008	78	0	0	78
		SSTUM08	Stumble Creek (Frazer Lake upper creeks)	267	163	8/21/2008	95	1	0	94
		SCOUR08	Courts Shoreline (Frazer Lake beaches)	268	164	8/21/2008	95	7	0	88
		SMIDWM08	Midway Creek (Frazer Lake middle creeks)	269	165	8/21/2008	93	1	0	92
		SMIDWS08	Midway beach (Frazer Lake beaches)	270	164	8/21/2008	95	4	0	91
		SLINDM08	Linda Creek (Frazer Lake middle creeks)	271	165	8/22/2008	95	5	0	90

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Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
East of WASSIP	East of WASSIP	SHOLFS08	Hollow Fox beach (Frazer Lake beaches)	272	164	8/22/2008	95	1	0	94
		SVALA08	Valarian Creek - Frazer Lake	273	166	8/21/2008	95	0	0	95
		SOUTS08	Outlet beach - Frazer Lake	274	167	8/20/2008	95	10	0	85
		SDOGSC08	Dog Salmon Creek	275	168	8/22/2008	95	3	0	92
		SAKAL05L	Akalura Lagoon	276	169	9/2/2005	95	0	0	95
		SUPS00E	Upper Station - Early	277	170	6/15/2000	95	0	0	95
		SUPUP93	Upper Station - Upper	278	171	9/1/1993	95	0	0	95
		SLUPS93	Upper Station - Lower	279	172	1993	95	1	0	94
		SAYAK00	Ayakulik River	280	173	7/26/2000	96	1	2	93
		SAYAK08L		281	173	8/14/2008	95	3	1	91
		SOMALL99	Karluk Lake - O'Malley River (Late Karluk)	282	174	9/30/1999	95	1	2	92
		SUTHU00E	Karluk Lake - Upper Thumb Lake	283	175	7/24/2000	95	0	0	95
		SLTHUM99	Karluk Lake - Lower Thumb River (Late Karluk)	284	174	9/30/1999	95	19	0	76
		SLRIV97	Little River Lake	285	176	7/15/1997	96	1	0	95
		SUGAN97	Uganik Lake	286	177	7/15/1997	95	0	0	95
		SBUSK05	Buskin Lake	287	178	6/26/2005	95	1	0	94
		SBUSKL10		288	178	6/13/2010	95	0	1	94
		SLKLOU05	Lake Louise - Buskin River	289	179	8/3/2005	95	0	0	95
		SLKLOU10		290	179	7/19/2010	95	0	2	93
		SPASA05	Pasagshak Lake	291	180	7/15/2005	95	0	0	95
		SLMIA05	Lake Miam	292	181	9/2/2005	95	0	1	94
		SSALT94	Saltery Lake	293	182	1994	95	2	0	93
		SSALT99		294	182	8/26/1999	95	1	0	94
		SAFOG93	Afognak Lake	295	183	8/15/1993	79	0	1	78
		SMALI93	Malina	296	184	8/15/1993	80	1	1	78
		STHOR06	Thorsheim Lake	297	185	8/23/2006	83	0	0	83
		SPORT98	Portage Lake	298	186	1998	96	0	0	96
		SLKIT93	Little Kitoi	299	187	9/10/1993	95	0	0	95
		SKAFL08	Kaflia Lake	300	188	8/27/2008	95	1	0	94
		SWACK09	Wackton Creek - Lake Fork Crescent River	301	189	8/13/2009	95	2	0	93
		SPYRAM09	Pyramid Creek - Crescent Lake	302	190	8/13/2009	95	0	0	95

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Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
East of WASSIP	East of WASSIP	SCRES941[e]	Crescent Lake	303		1994	48	0	0	0
		SCREE942[e]		304		1994	47	0	0	0
		SCRESL09[f]	Crescent Lake outlet	305		8/12/2009	95	0	0	0
		SLJACK06	Little Jack Creek	306	191	9/6/2006	95	1	0	94
		SPACK92	Packers Lake	307	192	7/1/1992	95	0	0	95
		SSFBIG07	South Fork Big River	308	193	8/14/2007	123	0	0	123
		SSFBIGF09	South Fork Big River Falls	309	193	7/7/2009	48	0	0	48
		SWOLV93	Wolverine Creek - Big River	310	194	7/5/1993	95	1	0	94
		SBLACSC07	Black Sand Creek	311	195	8/13/2007	95	0	0	95
		SFARR07	Farro Lake Creek	312	196	8/13/2007	95	0	0	95
		SMCCA93	McArthur River	313	197	1993	95	0	1	94
		SCHIL92	Chilligan River	314	198	1992	48	0	0	48
		SCHIL94		315	198	1994	48	0	0	48
		SCHAK08	Chakachatna Slough	316	199	8/27/2008	95	0	1	94
		SCOAS09	Coal Creek - Spring	317	200	8/21/2009	48	0	0	48
		SCOAW09	Coal Creek - West Fork	318	200	8/21/2009	47	0	0	47
		SMOOSE07	Moose Creek - Skwentna	319	201	8/27/2007	95	0	1	94
		SPUNT06	Puntilla Lake	320	202	9/6/2006	95	0	0	95
		SREDSA06	Red Salmon Lake	321	203	9/7/2006	95	2	0	93
		STRIM107[b,e]	Trimble River	322		9/17/2007	61	0	0	0
		STRIM109[b,e]		323		9/1/2009	18	1	0	0
		STRIM207		324	204	9/17/2007	47	0	0	47
		STRIM209		325	204	9/1/2009	48	0	0	48
		SHAYT08	Hayes River tributary	326	205	9/2/2008	48	0	1	47
		SHAYT09		327	205	8/28/2009	47	0	0	47
		SSKWEN07	Skwentna River	328	206	9/20/2007	108	0	0	108
		SCANYC07	Canyon Creek (Skwentna River)	329	206	9/20/2007	65	0	0	65
		SJUDD06	Judd Lake	330	207	7/26/2006	94	2	0	92
		SJUDD09		331	207	2009	95	2	0	93
		SJUDD93		332	207	8/23/1993	96	0	0	96

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Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
East of WASSIP	East of WASSIP	STRIN09	Trinity Lake - inlet	333	208	8/22/2009	95	0	0	95
		STRIN92	Trinity Lake	334	208	8/1/1992	48	0	1	47
		SSHEL06	Shell Lake	335	209	7/24/2006	95	1	0	94
		SSHEL09		336	209	2009	95	2	0	93
		SSHEL93		337	209	9/3/1993	48	0	0	48
		SWHISK06	Whiskey Lake Outlet (Hewitt Lakes)	338	210	9/2/2006	58	0	0	58
		SWHISK09		339	210	9/1/2009	47	0	0	47
		SHEWI06	Hewitt Lake	340	210	8/2/2006	65	4	0	61
		SHEWI92[e]		341		8/1/1992	47	0	0	0
		SJOHNCK09	Johnson Creek	342	211	8/28/2009	95	0	2	93
		SKICH107	Kichatna River	343	211	8/27/2007	95	0	0	95
		SYENW92	West Fork Yentna River	344	212	9/1/1992	96	8	0	88
		SYENW93		345	212	9/10/1993	100	3	1	96
		SCHEL06	Chelatna Lake	346	213	7/27/2006	95	0	0	95
		SCHEL09		347	213	8/7/2009	95	0	0	95
		SCHEL93		348	213	8/28/1993	95	0	0	95
		SBYER07	Byers Lake	349	214	8/13/2007	95	3	0	92
		SBYER93		350	214	1993	48	1	0	47
		SSPINK08	Spink Creek	351	215	8/30/2008	95	2	0	93
		SSWALK06	Swan Lake	352	216	9/2/2006	95	0	0	95
		SSWALK09		353	216	9/8/2009	48	0	1	47
		SSWLK07		354	216	8/15/2007	47	4	0	43
		SSUS9511	Susitna River sloughs	355	217	1995	50	2	0	48
		SSUS9611		356	217	9/5/1996	6	0	0	6
		SSUS97		357	217	9/5/1997	94	0	0	94
		SSTEP07	Stephan Lake	358	218	7/28/2007	95	0	0	95
		SSTEP93		359	218	9/2/1993	48	0	0	48
		SLARS06	Larson Lake - east beach	360	219	7/23/2006	95	1	0	94
		SLARS93	Larson Lake - outlet	361	220	9/1/1993	95	0	0	95
		SLARS11E	Larson Lake - east beach	362	219	9/7/2011	90	0	0	90
		SLARS11O	Larson Lake - outlet	363	220	9/7/2011	126	1	0	125

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Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
East of WASSIP	East of WASSIP	SMAMA97	Mama and Papa Bear Lakes	364	221	9/3/1997	50	0	0	50
		SPAPA07		365	221	8/28/2007	54	0	1	53
		STALK97	Talkeetna River sloughs (Mama and Papa L.)	366	221	9/4/1997	79	11	0	68
		SBIRC07	Birch Creek	367	222	8/28/2007	95	0	1	94
		SBIRC93[e]		368		1993	67	2	0	0
		SSHEEP08	Sheep River	369	223	8/30/2008	95	0	0	95
		SNANC10	Nancy Lake	370	224	9/3/2010	95	0	0	95
		SNANC93		371	224	8/27/1993	95	0	0	95
		SLMEAD09	Little Meadow Creek (Upper Fish Creek)	372	225	8/8/2009	142	0	0	142
		SFISH93[f]	Upper Fish Creek	373		1993	95	0	0	0
		SFISH94		374	225	8/15/1994	94	0	0	94
		SBIGL11	Big Lake Outlet	375	226	8/30/2011	190	2	0	188
		SBIGL92[e]		376		8/1/1992	95	0	0	0
		SCOTT93	Cottonwood Creek (Wasilla Creek)	377	227	1993	95	0	0	95
		SWASI98	Wasilla Creek	378	227	1998	71	5	0	66
		SESKA06	Eska Creek	379	228	9/5/2006	95	0	0	95
		SJIM97	Jim Creek	380	229	9/2/1997	95	1	0	94
		SJIMLK11		381	229	9/1/2011	67	0	1	66
		SBODE06	Bodenburg Creek	382	230	8/30/2006	95	1	0	94
		SEAGLR11	Eagle River	383	231	8/23/2011	95	0	0	95
		SSIXM08	Sixmile Creek	384	232	7/30/2008	95	0	1	94
		SCARMLK10	Carmen Lake	385	233	8/23/2010	95	0	0	95
		SWILLIW06	Williwaw Creek	386	234	9/7/2006	39	0	0	39
		SWILLIW07		387	234	8/23/2007	69	0	0	69
		SCHICK10	Chickaloon River	388	235	7/13/2010	95	0	0	95
		SSWAN97	Swanson River	389	236	8/21/1997	95	0	0	95
		SBISH93	Bishop Creek	390	237	1993	95	0	0	95
		SDANI93	Daniels Lake	391	238	1993	95	2	0	93
		SRAIL97	Railroad Creek (Trail Creek)	392	239	8/13/1997	48	0	0	48
		SJOHN97	Johnson Creek (Trail Creek)	393	239	8/12/1997	88	1	0	87
		SMOOK93	Moose Creek	394	240	7/27/1993	47	0	0	47

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Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
East of WASSIP	East of WASSIP	SMOOK94	Moose Creek	395	240	1994	95	0	0	95
		SPTAR92		396	241	8/1/1992	47	1	0	46
		SPTAR93	Ptarmigan Creek	397	241	1993	95	1	0	94
		STERN92	Tern Lake	398	242	9/1/1992	48	0	1	47
		STERN93		399	242	1993	48	0	0	48
		SQUAR93	Quartz Creek	400	243	8/6/1993	94	1	0	93
		SURGOAT09E	Upper Russian Lake - Goat Creek (Early)	401	244	7/20/2009	95	2	0	93
		SURGOATM09	Upper Russian Lake - Goat Creek	402	245	9/3/2009	95	1	0	94
		SURUS97	Upper Russian Lake - Goat Creek (Early)	403	244	8/19/1997	95	0	0	95
		SRBEAR09	Upper Russian Lake - Bear Creek	404	246	9/3/2009	95	1	1	93
		SURSHOAL09	Upper Russian Lake shoal	405	247	9/4/2009	95	0	0	95
		SUPRUS99	Upper Russian Lake South shoal	406	247	9/16/1999	95	0	1	94
		SURUSA99	Upper Russian Lake outlet	407	248	9/17/1999	95	1	0	94
		SUROUT09		408	248	9/2/2009	95	0	0	95
		SRUSA92E	Russian River above falls (Early)	409	244	7/1/1992	96	0	0	96
		SRUSA93L[e]		410		8/2/1993	95	0	0	0
		SRUSB93	Russian River below falls (Upper Kenai River)	411	249	8/2/1993	95	0	1	94
		SSKK194L	Upper Kenai River	412	249	8/22/1994	47	0	0	47
		SSKK294L		413	249	8/22/1994	48	0	0	48
		SSKK494L		414	249	8/22/1994	48	0	0	48
		SSKK394E		415	249	1994	96	1	0	95
		SSKK394L		416	249	8/22/1994	47	0	0	47
		SSKKE93E		417	249	8/18/1993	48	1	0	47
		SSKKE93L		418	249	9/11/1993	47	1	0	46
		SSKK594L		419	249	9/9/1994	95	0	0	95
		SHIDDN08	Hidden Lake - North shore	420	250	9/23/2008	95	2	0	93
		SHIDD93	Hidden Creek	421	250	7/29/1993	95	0	0	95
		SSKIL95	Skilak Lake	422	251	1995	48	0	0	48
		SSKIL92	Skilak Lake - outlet	423	251	8/1/1992	96	0	0	96
		SSKIL94E		424	251	1994	45	2	0	43
		SSKIL94L		425	251	1994	50	3	0	47

-continued-

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Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
East of WASSIP	East of WASSIP	STUST941	Tustumena Lake (Upper)	426	252	1994	48	0	0	48
		STUST942		427	252	1994	48	0	0	48
		SSEEP94	Seepage Creek (Upper)	428	252	1994	95	0	0	95
		SGLAC94	Glacier Flats Creek (Mid)	429	253	1994	95	0	0	95
		SMOOT92	Moose Creek (Mid)	430	253	8/1/1992	96	2	0	94
		SBEAR92	Bear Creek (Lower)	431	254	8/1/1992	95	0	0	95
		SNIKO92	Nikolai Creek (Lower)	432	254	7/1/1992	95	0	0	95
		SENG92E	English Bay early	433	255	6/1/1992	95	9	0	86
		SENG92L	English Bay late	434	256	10/1/1992	95	1	0	94
		SBEARLK10	Bear Lake Resurrection	435	257	8/9/2010	190	0	1	189
		SBAIN10	Bainbridge Lake	436	258	8/6/2010	95	0	0	95
		SESHA91	Eshamy Lake	437	259	10/1/1991	96	6	0	90
		SESHAR08	Eshamy Creek	438	259	8/3/2008	95	0	0	95
		SMAIN91[g]	Main Bay	439		7/13/1991	96	0	0	0
		SCOG92HL	Upper Coghill Lake	440	260	8/27/1992	96	3	0	93
		SCOG92ES		441	260	8/27/1992	96	1	0	95
		SCOGH91	Lower Cognill Lake	442	261	9/1/1991	96	1	0	95
		SCOGH10		443	261	7/7/2010	95	0	0	95
		SMINE09	Miners Lake	444	262	7/9/2009	95	0	0	95
		SMINE91		445	262	8/9/1991	96	0	0	96
		SEYAK10	Eyak Lake - Hatchery Creek	446	263	7/24/2010	95	0	0	95
		SEYAM07	Eyak Lake - Middle Arm	447	264	8/2/2007	95	0	0	95
		SEYASB07	Eyak Lake - South beaches	448	265	8/22/2007	95	7	1	87
		SMCKI07	Upper McKinley Lake	449	266	8/20/2007	95	0	0	95
		SMCKI08	McKinley Lake	450	267	7/29/2008	95	0	0	95
		SMCKI91	McKinley Lake - Salmon Creek	451	268	7/1/1991	95	0	0	95
		SMCKSC07		452	268	7/25/2007	95	2	0	93
		STANAS09	Tanada Lake beach	453	269	9/9/2009	95	2	0	93
		STANAO09	Tanada Lake outlet	454	270	9/9/2009	95	0	0	95
		STANA05	Tanada Creek	455	271	8/21/2005	95	0	1	94
		SMENT08	Mentasta Lake	456	272	7/15/2008	95	0	0	95

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Table 3. Page 17 of 18.

Reporting Group							No. of individuals			
Regional	Subregional	ADF&G code	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
East of WASSIP	East of WASSIP	SFISHC08	Fish Creek - East Fork Gulkana River	457	273	8/1/2008	95	0	0	95
		SGULK08EF	East Fork Gulkana River	458	274	8/1/2008	75	0	0	75
		SSWEDE08	Swede Lake	459	275	8/13/2008	95	0	0	95
		SPAXSO09	Paxson Lake outlet	460	276	8/21/2009	77	0	2	75
		SMEND08	Mendeltna Creek	461	277	8/22/2008	95	0	1	94
		SMEND09		462	277	8/12/2009	94	0	0	94
		SBANA08	Banana Lake - Klutina drainage	463	278	8/18/2008	82	2	0	80
		SBEARH08	Bear Hole - Klutina tributary	464	279	8/14/2008	95	1	0	94
		SKLUTI08	Klutina Lake inlet	465	280	8/21/2008	44	0	0	44
		SKLUTI09		466	280	8/13/2009	51	0	0	51
		SSANN05	St. Anne Creek	467	281	7/15/2005	95	0	1	94
		SSTACR08		468	281	7/22/2008	95	0	3	92
		SMAHL08	Mahlo River	469	282	7/22/2008	95	0	1	94
		SKLUT08	Klutina River mainstem	470	283	8/21/2008	95	0	0	95
		STONSL09	Tonsina Lake	471	284	8/8/2009	95	0	1	94
		SLONGLK05	Long Lake	472	285	9/7/2005	95	0	0	95
		STEBA08	Tebay Outlet	473	286	8/18/2008	94	1	0	93
		SSALMC08	Salmon Creek - Bremner drainage	474	287	8/17/2008	95	2	0	93
		SSTEAM08	Steamboat Lake	475	288	8/17/2008	95	0	0	95
		SCLEAR07	Clear Creek at 40 Mile	476	289	8/24/2007	95	8	1	86
		STOKUN08	Lake Tokun	477	290	6/19/2008	95	0	0	95
		STOKUN09		478	290	6/25/2009	94	0	0	94
		SMART07	Martin Lake	479	291	7/26/2007	95	2	0	93
		SMART08		480	291	7/21/2008	95	1	0	94
		SERB91[e]		481		7/28/1991	96	0	0	0
		SMARTR08	Martin River Slough	482	292	7/11/2008	95	0	0	95
		SKUSH07	Kushtaka Lake	483	293	8/9/2007	95	1	0	94
		SKUSH08		484	293	8/8/2008	95	0	0	95
		SBERI91	Bering Lake	485	294	7/10/1991	95	0	0	95
						East of WASSIP Total	19,024	202	41	17,924
						Cape Suckling to Cape Prince of Wales Total	42,636	590	148	39,205

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[a] These collections belong to a reporting group that has too few fish to be independent and also lacks genetic distinction from river-type sockeye from the Kuskokwim River group.

[b] These collections have a sample size less than our desired minimum cut-off of 75 individuals and do not pool with other collections.

[c] These collections are samples taken from weirs that are not needed in the baseline. They have been used as escapement tests of the baseline.

[d] These collections failed to conform to Hardy-Weinberg expectations.

[e] These collections are outliers, lack reliable metadata and so are treated as unknown collections.

[f] These collections are likely a mixture of fish.

[g] This collection is a sample from a hatchery and is not needed to represent its broodstock population.

Table 4.– Escapement test number, reporting group of origin, river of origin, type of collection, year collected and final sample size for samples of escapement that served as tests of the WASSIP sockeye salmon baseline.

Number	Reporting Group	River	Type	Date	N
1	Kuskokwim River	Kuskokwim	Bethel Test Fishery	7/1-20/2008	283
2	Kuskokwim River	Kuskokwim	Bethel Test Fishery	6/1-7/14/2009	410
3	Kuskokwim River	Kuskokwim	Bethel Test Fishery	6/8-7/29/2010	373
4[a]	Kuskokwim River	Kogrukluk	Weir	7/6/2001	91
5[a]	Kuskokwim River	Kogrukluk	Weir	7/24-8/15/2007	95
6[a]	Kuskokwim River	Kwethluk	Weir	2007	141
7[a]	Kanektok	Kanektok	Weir	7/16/2002	95
8[a]	Kanektok	Kanektok	Weir	7/10-19/2007	96
9[a]	Goodnews	Goodnews	Weir	7/15/2001	96
10[a]	Goodnews	Goodnews	Weir	6/1-7/31/2007	140
11	Togiak	Togiak	Subsistence	7/11-8/1/2008	473
12	Igushik	Igushik	Tower	6/26-7/16/2005	190
13[a]	Igushik	Igushik	Tower	6/26-7/19/2007	186
14[a]	Wood	Wood	Tower	7/5-7/2003	174
15	Wood	Wood	Tower	6/19-7/13/2004	191
16	Wood	Wood	Tower	6/24-7/13/2007	190
17[a]	Nushagak	Nushagak	Sonar	6/19-7/18/2006	185
18	Nushagak	Nushagak	Radio telemetry	2005	190
19[a]	Nushagak	Nushagak	Radio telemetry	2006	164
20[a]	Nushagak	Nuyakuk	Tower	6/27-7/16/2004	189
21	Kvichak	Kvichak	Tower	7/6/2005	190
22	Kvichak	Kvichak	Tower	7/7-9/2006	190
23	Alagnak	Alagnak	Tower	7/13/2004	192
24[a]	Alagnak	Alagnak	Tower	7/1-12/2008	188
25	Naknek	Naknek	Tower	6/28/2002	190
26	Naknek	Naknek	Tower	6/29-7/9/2008	190
27	Egegik	Egegik	Tower	6/19-7/9/2004	192
28	Egegik	Egegik	Tower	6/23-7/16/2007	190
29	Ugashik	Ugashik	Tower	7/7-21/2004	192
30	Ugashik	Ugashik	Tower	7/4-6/2008	190
31	Black Lake	Chignik	Weir	6/14-21/2010	379
32	Chignik Lake	Chignik	Weir	7/23-30/2010	379

[a] These tests contain fewer than 190 individuals and results should be interpreted with caution.

Table 5.– Sum of rankings and final rank for 124 SNPs screened for 36 test populations in locus selection analyses for WASSIP.

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

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Assay	Sum of ranks	Final rank	Assay	Sum of ranks	Final rank
One_ssrd-135	1444	21	*One_U1202-1052*	1741.5	68
One_STC-410	1695	61	*One_U1203-175*	1520	33
One_STR07	1528	36	*One_U1204-53*	1626	52
One_SUMO1-6	1858	82	*One_U1205-57*	2064	95
One_sys1-230	1844.5	80	*One_U1206-108*	1824	77
One_taf12-248	1915.5	87	*One_U1207-231*[f]	N/A	N/A
One_Tf_ex11-750	1538.5	37	*One_U1208-67*	1543.5	39
One_Tf_in3-182	1410	16	*One_U1209-111*	1291.5	11
One_tshB-92	1666	59	*One_U1210-173*	1646	57
One_txnip-401	1959	90	*One_U1211-97*	1992	92
One_U1002-101	2111.5	100	*One_U1212-106*	1758.5	72
One_U1003-75	1417.5	17	*One_U1214-107*	1550	41
One_U1004-183	1123	7	*One_U1215-82*	2393.5	110
One_U1009-91	1504.5	29	*One_U1216-230*	1831	78
One_U1010-81	1500.5	28	*One_U301-92*	1888	85
One_U1012-68	1317.5	12	*One_U401-224*	1753.5	70
One_U1013-108	1876	83	*One_U404-229*	1579	46
One_U1014-74	1606.5	48	*One_U502-167*	1471	25
One_U1016-115	1334	13	*One_U503-170*	1567.5	44
One_U1017-62	2221.5	104	*One_U504-141*	1925.5	88
One_U1021-57[g]	N/A	N/A	*One_U508-533*	2286.5	106
One_U1024-197	1607	49	*One_UCA-24*[f]	N/A	N/A
One_U1101	1547	40	*One_vamp5-255*	1933	89
One_U1102-220	2241	105	*One_vatf-214*	1757.5	71
One_U1103	1579	45	*One_VIM-569*	1768.5	73
One_U1104-138	2151.5	102	*One_zn706-68*	2472	113
One_U1105	1521	35	*One_ZNF-61*	1457.5	22
One_U1201-492	1884.5	84	*One_Zp3b-49*	1777	75

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

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

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

[d] These 2 linked assays have nearly identical allele frequencies for the 36 test populations and are expected to provide similar test statistics and rankings for all measures except laboratory performance. These were exchanged to provide additional overlap among markers run by stakeholder laboratories (i.e., CDFO). See text for details.

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

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

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

Table 6.– Quality control (QC) results including the number of genotypes compared, discrepancy rates and estimated error rates of the collections genotyped for the WASSIP sockeye baseline for the 4 methods used: Old, New, 39, and Assay.

		Discrepancy rate			
QC Method	Genotypes compared	Homo-homo	Homo-het	Overall	Error Rate
Old	8,448	0.00%	0.24%	0.24%	0.12%
New	72,192	0.01%	0.22%	0.23%	0.12%
39	1,172,836	0.02%	0.34%	0.36%	0.18%
Assay	89,760	0.00%	0.13%	0.14%	0.07%
Total	1,343,236	0.02%	0.32%	0.34%	0.17%

Note: See text for descriptions of methods and QC details. Discrepancy rates include the rate due to differences of alternate homozygote genotypes (Homo-homo), of homozygote and heterozygote genotypes (Homo-het) and the total discrepancy rate. Error rate assumes that differences are the result of errors that are equally likely to have occurred in the production and QC genotyping process.

Table 7.– Quality control (QC) results including the number of genotypes compared, discrepancy rates and estimated error rates of the collections genotyped for the WASSIP sockeye escapement samples for the 3 methods used: New, 39, and Assay.

		Discrepancy rate			
QC Method	Genotypes compared	Homo-homo	Homo-het	Overall	Error Rate
New	18,240	0.00%	0.02%	0.02%	0.01%
39	157,953	0.01%	0.29%	0.31%	0.15%
Assay	25,728	0.00%	0.07%	0.07%	0.04%
Total	201,921	0.01%	0.24%	0.25%	0.12%

Note: See text for descriptions of methods and QC details. Discrepancy rates include the rate due to differences of alternate homozygote genotypes (Homo-homo), of homozygote and heterozygote genotypes (Homo-het) and the total discrepancy rate. Error rate assumes that differences are the result of errors that are equally likely to have occurred in the production and QC genotyping process.

Table 8.– Pairs of single nucleotide polymorphisms (SNPs) that exhibited significant ($P < 0.01$) linkage disequilibrium in 294 populations of sockeye salmon in the WASSIP study area, f_{ORCA} values for each locus separate as well as for combined loci, and decision for handling linkage for each locus pair based upon the Δ_{90} of 0.017.

Locus	Linkage pair	f_{ORCA}	Decision
One_GPDH-201	1	0.055	Keep
One_GPDH2-1872	1	0.051	Drop
One_GPDH-201_GPDH2-1872	1	0.064	Do not combine
One_MHC2_190	2	0.037	Drop
One_MHC2_251	2	0.053	Drop
One_MHC2_190_251	2	0.081	Combine
One_Tf_ex11-750	3	0.046	Drop
One_Tf_in3-182	3	0.048	Keep
One_Tf_ex11-750_in3-182	3	0.048	Do not combine

Note: See text for details.

Table 9.– Comparison number, collection code, number and name, population number, and regional reporting group affiliation for 127 collections included in an analysis of temporal variation.

	Collection				
Comparison	Code	Number	Name	Population Name	Regional Group
1	SNECO06	8	Necons River 2006	Necons River	Kuskokwim Bay
1	SNECO07	9	Necons River 2007	Necons River	Kuskokwim Bay
2	STELA03	10	Telaquana Lake outlet 2003	Telaquana Lake outlet	Kuskokwim Bay
3	STELA05	11	Telaquana Lake - east beach 2005	Telaquana Lake - east beach	Kuskokwim Bay
2	STELA09	12	Telaquana Lake outlet 2009	Telaquana Lake outlet	Kuskokwim Bay
3	STELAUB09	14	Telaquana Lake - east beach 2009	Telaquana Lake - east beach	Kuskokwim Bay
4	SKWETL06	25	Kwethluk River lakes 2006	Kwethluk River lakes	Kuskokwim Bay
4	SKWETR07	27	Kwethluk River lakes 2007	Kwethluk River lakes	Kuskokwim Bay
5	SGOODR10NF	40	Goodnews River - North Fork 2010	Goodnews River - North Fork	Kuskokwim Bay
5	SGOOD02	41	Goodnews River - North Fork 2002	Goodnews River - North Fork	Kuskokwim Bay
5	SGOOD06	42	Goodnews River - North Fork 2006	Goodnews River - North Fork	Kuskokwim Bay
6	STOGL00	53	Sunday Creek 2000	Sunday Creek	Bristol Bay
6	STOGT06	54	Togiak Tower 2006	Togiak Tower	Bristol Bay
7	SABEA04	80	A Beach - Little Togiak Lake 2004	A Beach - Little Togiak Lake	Bristol Bay
7	SABEA05	81	A Beach - Little Togiak Lake 2005	A Beach - Little Togiak Lake	Bristol Bay
8	SPICK01	83	Pick Creek 2001	Pick Creek	Bristol Bay
8	SPICK08	84	Pick Creek 2008	Pick Creek	Bristol Bay
9	SLYNX01	88	Lynx Creek 2001	Lynx Creek	Bristol Bay
9	SLYNXCK09	89	Lynx Creek 2009	Lynx Creek	Bristol Bay
10	STLGF99	113	Tlikakila River - Glacier Fork 1999	Tlikakila River - Glacier Fork	Bristol Bay
10	SUTLIK01	114	Upper Tlikakila River 2001	Upper Tlikakila River	Bristol Bay
11	STOMK00	123	Tomkok Creek 2000	Tomkok Creek	Bristol Bay
11	STOMK02	124	Tomkok Creek 2002	Tomkok Creek	Bristol Bay
12	SKNUT00	125	Knutson Bay 2000	Knutson Bay	Bristol Bay
12	SKNUT99L	126	Knutson Bay 1999	Knutson Bay	Bristol Bay
13	STOMM00	138	Tommy Creek 2000	Tommy Creek	Bristol Bay

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Comparison	Collection Code	Collection Number	Collection Name	Population Name	Regional Group
13	STOMM02	139	Tommy Creek 2002	Tommy Creek	Bristol Bay
14	SCOPP00	140	Copper River 2000	Copper River	Bristol Bay
14	SCOPP99	141	Copper River 1999	Copper River	Bristol Bay
15	SGIBR00	146	Gibralter River 2000	Gibralter River	Bristol Bay
15	SGIBR99	147	Gibralter River 1999	Gibralter River	Bristol Bay
16	SUTAL04	150	Upper Talarik Creek 2004	Upper Talarik Creek	Bristol Bay
16	SUTAL06	151	Upper Talarik Creek 2006	Upper Talarik Creek	Bristol Bay
17	SLTAL00	152	Lower Talarik Creek 2000	Lower Talarik Creek	Bristol Bay
17	SLTAL01	153	Lower Talarik Creek 2001	Lower Talarik Creek	Bristol Bay
18	SKULI01	161	Kulik River 2001	Kulik River	Bristol Bay
18	SKULI04	162	Kulik River 2004	Kulik River	Bristol Bay
19	SAMER00	163	American River 2000	American River	Bristol Bay
19	SAMER01	164	American River 2001	American River	Bristol Bay
20	SIDAV00	174	Idavain Creek 2000	Idavain Creek	Bristol Bay
20	SIDAV06	175	Idavain Creek 2006	Idavain Creek	Bristol Bay
21	SKEJU00	184	Upper Kejulik River 2000	Upper Kejulik River	Bristol Bay
21	SKEJU01	185	Kejulik River 2001	Kejulik River	Bristol Bay
22	SCHIA08	249	Chiaktuak Creek 2008	Chiaktuak Creek	Chignik
22	SCHIA97E	250	Chiaktuak Creek 1997	Chiaktuak Creek	Chignik
22	SCHIA97M	251	Chiaktuak Creek 1997	Chiaktuak Creek	Chignik
23	SHAT08E	255	Hatchery Beach 2008	Hatchery Beach	Chignik
23	SHAT97E	257	Hatchery Beach 1997	Hatchery Beach	Chignik
24	SCLARK08	258	Clark River 2008	Clark River	Chignik
24	SCLRK97E	260	Clark River 1997	Clark River	Chignik
25	SCHIG08	261	Chignik River 2008	Chignik River	Chignik
25	SCHIG98	262	Chignik River 1998	Chignik River	Chignik

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	Collection				
Comparison	Code	Number	Name	Population Name	Regional Group
26	SAYAK00	280	Ayakulik River 2000	Ayakulik River	East of WASSIP
26	SAYAK08L	281	Ayakulik River 2008	Ayakulik River	East of WASSIP
27	SBUSK05	287	Buskin Lake 2005	Buskin Lake	East of WASSIP
27	SBUSKL10	288	Buskin Lake 2010	Buskin Lake	East of WASSIP
28	SLKLOU05	289	Lake Louise - Buskin River 2005	Lake Louise - Buskin River	East of WASSIP
28	SLKLOU10	290	Lake Louise - Buskin River 2010	Lake Louise - Buskin River	East of WASSIP
29	SSALT94	293	Saltery Lake 1994	Saltery Lake	East of WASSIP
29	SSALT99	294	Saltery Lake 1999	Saltery Lake	East of WASSIP
30	SCHIL92	314	Chilligan River 1992	Chilligan River	East of WASSIP
30	SCHIL94	315	Chilligan River 1994	Chilligan River	East of WASSIP
31	STRIM207	324	Trimble River 2007	Trimble River	East of WASSIP
31	STRIM209	325	Trimble River 2009	Trimble River	East of WASSIP
32	SHAYT08	326	Hayes River tributary 2008	Hayes River tributary	East of WASSIP
32	SHAYT09	327	Hayes River tributary 2009	Hayes River tributary	East of WASSIP
33	SJUDD06	330	Judd Lake 2006	Judd Lake	East of WASSIP
33	SJUDD09	331	Judd Lake 2009	Judd Lake	East of WASSIP
33	SJUDD93	332	Judd Lake 1993	Judd Lake	East of WASSIP
34	STRIN09	333	Trinity Lake - inlet 2009	Trinity Lake - inlet	East of WASSIP
34	STRIN92	334	Trinity Lake 1992	Trinity Lake	East of WASSIP
35	SSHEL06	335	Shell Lake 2006	Shell Lake	East of WASSIP
35	SSHEL09	336	Shell Lake 2009	Shell Lake	East of WASSIP
35	SSHEL93	337	Shell Lake 1993	Shell Lake	East of WASSIP
36	SWHISK06	338	Whiskey Lake Outlet 2006	Whiskey Lake Outlet	East of WASSIP
36	SWHISK09	339	Whiskey Lake Outlet 2009	Whiskey Lake Outlet	East of WASSIP
37	SYENW92	344	West Fork Yentna River 1992	West Fork Yentna River	East of WASSIP
37	SYENW93	345	West Fork Yentna River 1993	West Fork Yentna River	East of WASSIP

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	Collection				
Comparison	Code	Number	Name	Population Name	Regional Group
38	SCHEL06	346	Chelatna Lake 2006	Chelatna Lake	East of WASSIP
38	SCHEL09	347	Chelatna Lake 2009	Chelatna Lake	East of WASSIP
38	SCHEL93	348	Chelatna Lake 1993	Chelatna Lake	East of WASSIP
39	SBYER07	349	Byers Lake 2007	Byers Lake	East of WASSIP
39	SBYER93	350	Byers Lake 1993	Byers Lake	East of WASSIP
40	SSWALK06	352	Swan Lake 2006	Swan Lake	East of WASSIP
40	SSWALK09	353	Swan Lake 2009	Swan Lake	East of WASSIP
40	SSWLK07	354	Swan Lake 2007	Swan Lake	East of WASSIP
41	SSTEP07	358	Stephan Lake 2007	Stephan Lake	East of WASSIP
41	SSTEP93	359	Stephan Lake 1993	Stephan Lake	East of WASSIP
42	SMAMA97	364	Mama and Papa Bear Lakes 1997	Mama and Papa Bear Lakes	East of WASSIP
42	SPAPA07	365	Mama and Papa Bear Lakes 2007	Mama and Papa Bear Lakes	East of WASSIP
43	SNANC10	370	Nancy Lake 2010	Nancy Lake	East of WASSIP
43	SNANC93	371	Nancy Lake 1993	Nancy Lake	East of WASSIP
44	SWILLIW06	386	Williwaw Creek 2006	Williwaw Creek	East of WASSIP
44	SWILLIW07	387	Williwaw Creek 2007	Williwaw Creek	East of WASSIP
45	SMOOK93	394	Moose Creek 1993	Moose Creek	East of WASSIP
45	SMOOK94	395	Moose Creek 1994	Moose Creek	East of WASSIP
46	SPTAR92	396	Ptarmigan Creek 1992	Ptarmigan Creek	East of WASSIP
46	SPTAR93	397	Ptarmigan Creek 1993	Ptarmigan Creek	East of WASSIP
47	STERN92	398	Tern Lake 1992	Tern Lake	East of WASSIP
47	STERN93	399	Tern Lake 1993	Tern Lake	East of WASSIP
48	SURGOAT09E	401	Upper Russian Lake - Goat Creek 2009	Upper Russian Lake - Goat Creek	East of WASSIP
48	SURUS97	403	Upper Russian Lake - Goat Creek 1997	Upper Russian Lake - Goat Creek	East of WASSIP
49	SURSHOAL09	405	Upper Russian Lake beach 2009	Upper Russian Lake beach	East of WASSIP
49	SUPRUS99	406	Upper Russian Lake South beach 1999	Upper Russian Lake South beach	East of WASSIP

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Table 9. Page 5 of 5.

	Collection				
Comparison	Code	Number	Name	Population Name	Regional Group
50	SURUSA99	407	Upper Russian Lake outlet 1999	Upper Russian Lake outlet	East of WASSIP
50	SUROUT09	408	Upper Russian Lake outlet 2009	Upper Russian Lake outlet	East of WASSIP
48	SRUSA92E	409	Russian River above falls 1992	Russian River above falls	East of WASSIP
51	SHIDDN08	420	Hidden Lake - North shore 2008	Hidden Lake - North shore	East of WASSIP
51	SHIDD93	421	Hidden Creek 1993	Hidden Creek	East of WASSIP
52	SSKIL95	422	Skilak Lake 1995	Skilak Lake	East of WASSIP
52	SSKIL92	423	Skilak Lake - outlet 1992	Skilak Lake - outlet	East of WASSIP
53	SESHA91	437	Eshamy Lake 1991	Eshamy Lake	East of WASSIP
53	SESHAR08	438	Eshamy Creek 2008	Eshamy Creek	East of WASSIP
54	SMINE09	444	Miners Lake 2009	Miners Lake	East of WASSIP
54	SMINE91	445	Miners Lake 1991	Miners Lake	East of WASSIP
55	SMEND08	461	Mendeltna Creek 2008	Mendeltna Creek	East of WASSIP
55	SMEND09	462	Mendeltna Creek 2009	Mendeltna Creek	East of WASSIP
56	SKLUTI08	465	Klutina Lake inlet 2008	Klutina Lake inlet	East of WASSIP
56	SKLUTI09	466	Klutina Lake inlet 2009	Klutina Lake inlet	East of WASSIP
57	SSANN05	467	St. Anne Creek 2005	St. Anne Creek	East of WASSIP
57	SSTACR08	468	St. Anne Creek 2008	St. Anne Creek	East of WASSIP
58	STOKUN08	477	Lake Tokun 2008	Lake Tokun	East of WASSIP
58	STOKUN09	478	Lake Tokun 2009	Lake Tokun	East of WASSIP
59	SMART07	479	Martin Lake 2007	Martin Lake	East of WASSIP
59	SMART08	480	Martin Lake 2008	Martin Lake	East of WASSIP
60	SKUSH07	483	Kushtaka Lake 2007	Kushtaka Lake	East of WASSIP
60	SKUSH08	484	Kushtaka Lake 2008	Kushtaka Lake	East of WASSIP

Table 10.– Variance components and associated *F* statistics for the ANOVA among temporal collections (P) within populations (R) nested within regional reporting groups (S). Variance component and *F* statistic notation follows Weir (1996): individual (I), sub-subpopulation (temporal collection in this analysis; P), subpopulation (population in this analysis; R), population (region in this analysis; S) and total (T).

	Between Genes within Individuals	Among Individuals within Temporal Collections	Among Temporal Collections within Populations	Among Populations within Regions	Among Regions
Variance Component	σ^2_G	σ^2_I	σ^2_{SS}	σ^2_S	σ^2_P
	23.97	0.10	-0.89	3.26	1.18
F Statistic	F_{IT}	F_{IP}	F_{PR}	F_{RS}	F_{ST}
	0.87	0.00	-0.03	0.12	0.04

Note: See text for details.

Table 11.– Estimates of stock composition, upper and lower 90% credibility interval bounds, and standard deviations for mixtures of known-origin fish removed from the WASSIP baseline populations of sockeye salmon that comprise the regional reporting groups that are not sub-divided into smaller subregional reporting groups (Norton Sound, South Peninsula and East of WASSIP; i.e., 100% proof tests) using the program BAYES with a flat prior. One hundred fish were removed from the Norton Sound group while 200 fish were removed from the South Peninsula and East of WASSIP groups. Correct allocations are in bold.

	Norton Sound				South Peninsula				East of WASSIP			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Norton Sound	**0.93**	0.88	0.97	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay	0.06	0.02	0.11	0.03	0.00	0.00	0.01	0.01	0.01	0.00	0.03	0.01
North Peninsula	0.00	0.00	0.01	0.01	0.00	0.00	0.02	0.01	0.01	0.00	0.03	0.01
South Peninsula	0.00	0.00	0.00	0.00	**0.98**	0.96	1.00	0.01	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.01	**0.97**	0.95	0.99	0.01

Table 12.– Estimates of stock composition, upper and lower 90% credibility intervals, and standard deviations for mixtures of 200 known-origin fish removed from the WASSIP baseline populations of sockeye salmon that comprise the Kuskokwim Bay reporting groups (i.e., 100% proof tests) using the program BAYES with a flat prior. Correct allocations are in bold.

	Kuskokwim River				Kanektok				Goodnews			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay	**0.98**	0.94	1.00	0.02	**0.99**	0.96	1.00	0.02	**0.89**	0.83	0.95	0.03
Bristol Bay	0.02	0.00	0.06	0.02	0.01	0.00	0.04	0.01	0.10	0.05	0.16	0.03
North Peninsula	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim River	**0.98**	0.94	1.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Kanektok	0.00	0.00	0.00	0.00	**0.93**	0.89	0.98	0.03	0.00	0.00	0.01	0.00
Goodnews	0.00	0.00	0.00	0.00	0.06	0.00	0.10	0.03	**0.89**	0.83	0.94	0.04

Table 13.– Estimates of stock composition, upper and lower 90% credibility intervals, and standard deviations for mixtures of 200 known-origin fish removed from the WASSIP baseline populations of sockeye salmon that comprise the Bristol Bay reporting groups (i.e., 100% proof tests) using the program BAYES with a flat prior. Correct allocations are in bold.

	Togiak				Igushik				Wood			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.01	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.18	0.09	0.27	0.06	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00
Bristol Bay	**0.82**	0.72	0.91	0.06	**0.99**	0.97	1.00	0.01	**1.00**	0.99	1.00	0.00
North Peninsula	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	**0.81**	0.72	0.91	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	**0.97**	0.89	1.00	0.03	0.00	0.00	0.03	0.01
Wood	0.00	0.00	0.00	0.00	0.02	0.00	0.09	0.03	**0.99**	0.96	1.00	0.01
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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Table 13. Page 2 of 3.

	Nushagak				Kvichak				Alagnak			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.01	0.00	0.02	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Bristol Bay	**0.99**	0.97	1.00	0.01	**1.00**	0.99	1.00	0.01	**1.00**	0.98	1.00	0.01
North Peninsula	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nushagak	**0.98**	0.94	1.00	0.02	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.00	0.00	**0.99**	0.98	1.00	0.01	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.99**	0.98	1.00	0.01
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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Table 13. Page 3 of 3.

	Naknek				Egegik				Ugashik			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay	**0.99**	0.98	1.00	0.01	**1.00**	0.98	1.00	0.01	**0.97**	0.92	1.00	0.03
North Peninsula	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00	0.03	0.00	0.08	0.03
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	**0.99**	0.97	1.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.01	0.00	**0.89**	0.81	0.99	0.05	0.01	0.00	0.03	0.02
Ugashik	0.00	0.00	0.00	0.00	0.10	0.00	0.18	0.05	**0.96**	0.90	1.00	0.03

Table 14.– Estimates of stock composition, upper and lower 90% credibility intervals, and standard deviations for mixtures of known-origin fish removed from the WASSIP baseline populations of sockeye salmon that comprise the North Peninsula reporting groups (i.e., 100% proof tests) using the program BAYES with a flat prior. One hundred fish were removed from the Cinder, Sandy and Nelson River groups while 200 fish were removed from the Meshik, Ilnik, Bear, and NW District-Black Hills groups. Correct allocations are in bold.

	Cinder				Meshik				Ilnik			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Kuskokwim Bay	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Bristol Bay	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01
North Peninsula	**0.99**	0.97	1.00	0.01	**0.99**	0.96	1.00	0.01	**0.99**	0.98	1.00	0.01
South Peninsula	0.00	0.00	0.00	0.00	0.01	0.00	0.03	0.01	0.00	0.00	0.01	0.00
Chignik	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	**0.98**	0.91	1.00	0.03	0.01	0.00	0.05	0.02	0.03	0.00	0.07	0.02
Meshik	0.01	0.00	0.07	0.03	**0.98**	0.94	1.00	0.02	0.00	0.00	0.01	0.00
Ilnik	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	**0.96**	0.91	1.00	0.03
Sandy	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW District-Black Hills	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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Table 14. Page 2 of 3.

	Sandy				Bear				Nelson River			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Bristol Bay	0.01	0.00	0.03	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01
North Peninsula	**0.98**	0.93	1.00	0.02	**0.99**	0.98	1.00	0.01	**0.99**	0.97	1.00	0.01
South Peninsula	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik	0.01	0.00	0.04	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Meshik	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.02	0.00	0.05	0.02
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Sandy	**0.94**	0.89	0.98	0.03	0.00	0.00	0.00	0.00	0.02	0.00	0.06	0.02
Bear	0.03	0.00	0.06	0.02	**0.99**	0.98	1.00	0.01	0.00	0.00	0.01	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.95**	0.90	0.98	0.02
NW District-Black Hills	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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Table 14. Page 3 of 3.

	NW District/Black Hills			
Reporting Group	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.00	0.00	0.00	0.00
Bristol Bay	0.00	0.00	0.01	0.00
North Peninsula	**1.00**	0.98	1.00	0.01
South Peninsula	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00
North Peninsula				
Cinder	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.00	0.00
Ilnik	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00
NW District-Black Hills	**0.99**	0.98	1.00	0.01

Table 15.– Estimates of stock composition, upper and lower 90% credibility intervals, and standard deviations for mixtures of 200 known-origin fish removed from the WASSIP baseline populations of sockeye salmon that comprise the Chignik reporting groups (i.e., 100% proof tests) using the program BAYES with a flat prior. Correct allocations are in bold.

	Black Lake				Chignik Lake			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Bristol Bay	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
North Peninsula	0.00	0.00	0.01	0.00	0.01	0.00	0.03	0.01
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Chignik	**0.99**	0.98	1.00	0.01	**0.99**	0.97	1.00	0.01
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik								
Black Lake	**0.99**	0.98	1.00	0.01	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.01	0.01	**0.99**	0.96	1.00	0.01

Table 16.– Estimates of stock composition, upper and lower 90% credibility intervals, and standard deviations for samples of escapement to rivers within the Kuskokwim Bay reporting groups (i.e., escapement tests) using the program BAYES with a flat prior. Correct allocations are in bold.

	Bethel Test Fish 2008				Bethel Test Fish 2009				Bethel Test Fish 2010			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Kuskokwim Bay	0.94	0.90	0.99	0.03	0.94	0.90	0.98	0.03	0.91	0.87	0.94	0.02
Bristol Bay	0.05	0.00	0.09	0.03	0.06	0.02	0.10	0.03	0.09	0.05	0.12	0.02
North Peninsula	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.01	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim River	**0.94**	0.90	0.99	0.03	**0.94**	0.90	0.98	0.03	**0.91**	0.87	0.94	0.02
Kanektok	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

	Kogrukluk Weir 2001				Kogrukluk Weir 2007				Kwethluk Weir 2007			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Kuskokwim Bay	0.99	0.97	1.00	0.01	0.94	0.89	0.98	0.03	0.50	0.38	0.66	0.09
Bristol Bay	0.00	0.00	0.02	0.01	0.05	0.02	0.10	0.03	0.48	0.33	0.59	0.08
North Peninsula	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.01	0.02	0.00	0.05	0.02
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim River	**0.99**	0.97	1.00	0.01	**0.94**	0.89	0.98	0.03	**0.49**	0.38	0.65	0.09
Kanektok	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01

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Table 16. Page 2 of 2.

	Kanektok Weir 2002				Kanektok Weir 2007				Goodnews Weir 2001			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.98	0.95	1.00	0.01	0.98	0.94	1.00	0.02	0.96	0.86	1.00	0.05
Bristol Bay	0.01	0.00	0.04	0.01	0.01	0.00	0.03	0.01	0.03	0.00	0.12	0.04
North Peninsula	0.00	0.00	0.01	0.01	0.01	0.00	0.02	0.01	0.01	0.00	0.03	0.01
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Chignik	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kanektok	**0.98**	0.95	1.00	0.02	**0.98**	0.93	1.00	0.02	0.00	0.00	0.01	0.01
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	**0.96**	0.86	1.00	0.05

	Goodnews Weir 2007			
Reporting Group	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.83	0.74	0.92	0.05
Bristol Bay	0.15	0.07	0.24	0.05
North Peninsula	0.01	0.00	0.04	0.01
South Peninsula	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00
Kuskokwim Bay				
Kuskokwim River	0.00	0.00	0.00	0.00
Kanektok	0.00	0.00	0.02	0.01
Goodnews	**0.83**	0.73	0.91	0.05

Table 17.– Estimates of stock composition, upper and lower 90% credibility intervals, and standard deviations for samples of escapement to rivers within the Bristol Bay reporting groups (i.e., escapement tests) using the program BAYES with a flat prior. Correct allocations are in bold.

	Togiak 2008 Subsistence				Igushik Tower 2005				Igushik Tower 2007			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.18	0.07	0.31	0.07	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01
Bristol Bay	0.81	0.69	0.93	0.07	1.00	0.98	1.00	0.01	0.99	0.98	1.00	0.01
North Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	**0.81**	0.69	0.93	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	**0.90**	0.80	0.99	0.06	**0.90**	0.75	1.00	0.08
Wood	0.00	0.00	0.00	0.00	0.10	0.00	0.19	0.06	0.09	0.00	0.24	0.09
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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Table 17. Page 2 of 7.

	Wood Tower 2003				Wood Tower 2004				Wood Tower 2007			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01
Bristol Bay	0.99	0.98	1.00	0.01	0.99	0.98	1.00	0.01	0.99	0.98	1.00	0.01
North Peninsula	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.02	0.00	0.09	0.03	0.00	0.00	0.03	0.01	0.02	0.00	0.08	0.03
Wood	**0.93**	0.85	0.97	0.04	**0.98**	0.93	1.00	0.02	**0.97**	0.91	1.00	0.03
Nushagak	0.05	0.02	0.08	0.02	0.01	0.00	0.05	0.02	0.00	0.00	0.01	0.01
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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Table 17. Page 3 of 7.

	Nushagak Sonar 2006				Nushagak Radio Telemetry 2005				Nushagak Radio Telemetry 2006			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.01	0.00	0.03	0.01	0.12	0.04	0.21	0.05	0.00	0.00	0.02	0.01
Bristol Bay	0.99	0.96	1.00	0.01	0.87	0.79	0.95	0.05	0.99	0.97	1.00	0.01
North Peninsula	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Igushik	0.01	0.00	0.03	0.01	0.01	0.00	0.05	0.02	0.01	0.00	0.04	0.02
Wood	0.02	0.00	0.04	0.01	0.01	0.00	0.04	0.01	0.00	0.00	0.03	0.01
Nushagak	**0.97**	0.93	0.99	0.02	**0.84**	0.75	0.92	0.05	**0.98**	0.94	1.00	0.02
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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Table 17. Page 4 of 7.

	Nuyakuk Tower 2004				Kvichak Tower 2005				Kvichak Tower 2006			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.06	0.01	0.12	0.03	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Bristol Bay	0.93	0.87	0.99	0.03	0.99	0.98	1.00	0.01	1.00	0.99	1.00	0.00
North Peninsula	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nushagak	**0.92**	0.86	0.98	0.03	0.04	0.01	0.08	0.02	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.00	0.00	**0.95**	0.91	0.98	0.02	**0.99**	0.98	1.00	0.01
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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Table 17. Page 5 of 7.

	Alagnak Tower 2004				Alagnak Tower 2008				Naknek Tower 2002			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay	1.00	0.99	1.00	0.00	0.99	0.98	1.00	0.01	1.00	0.99	1.00	0.00
North Peninsula	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Alagnak	**0.99**	0.98	1.00	0.01	**0.99**	0.97	1.00	0.01	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	**0.99**	0.98	1.00	0.01
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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Table 17. Page 6 of 7.

Reporting Group	Naknek Tower 2008				Egegik Tower 2004				Egegik Tower 2007			
	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Bristol Bay	1.00	0.99	1.00	0.01	1.00	0.98	1.00	0.01	0.99	0.98	1.00	0.01
North Peninsula	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.01	0.00	0.00	0.00	0.00
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Alagnak	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	**0.99**	0.97	1.00	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.01	0.00	**0.97**	0.91	1.00	0.03	**0.99**	0.97	1.00	0.01
Ugashik	0.00	0.00	0.00	0.00	0.01	0.00	0.07	0.03	0.00	0.00	0.01	0.01

-continued-

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	Ugashik Tower 2004				Ugashik Tower 2008			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay	0.99	0.98	1.00	0.01	1.00	0.98	1.00	0.01
North Peninsula	0.01	0.00	0.02	0.01	0.00	0.00	0.01	0.01
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay								
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.03	0.02	0.05	0.00	0.20	0.07
Ugashik	**0.99**	0.95	1.00	0.02	**0.94**	0.79	1.00	0.07

Table 18.– Estimates of stock composition, upper and lower 90% credibility intervals, and standard deviations for samples of escapement to rivers within the Chignik reporting groups (i.e., escapement tests) using the program BAYES with a flat prior. Correct allocations are in bold.

	Chignik 2010 Early Run				Chignik 2010 Late Run			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
North Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik	1.00	0.99	1.00	0.00	0.99	0.98	1.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik								
Black Lake	**0.98**	0.94	1.00	0.02	0.08	0.04	0.12	0.02
Chignik Lake	0.02	0.00	0.06	0.02	**0.92**	0.88	0.96	0.02

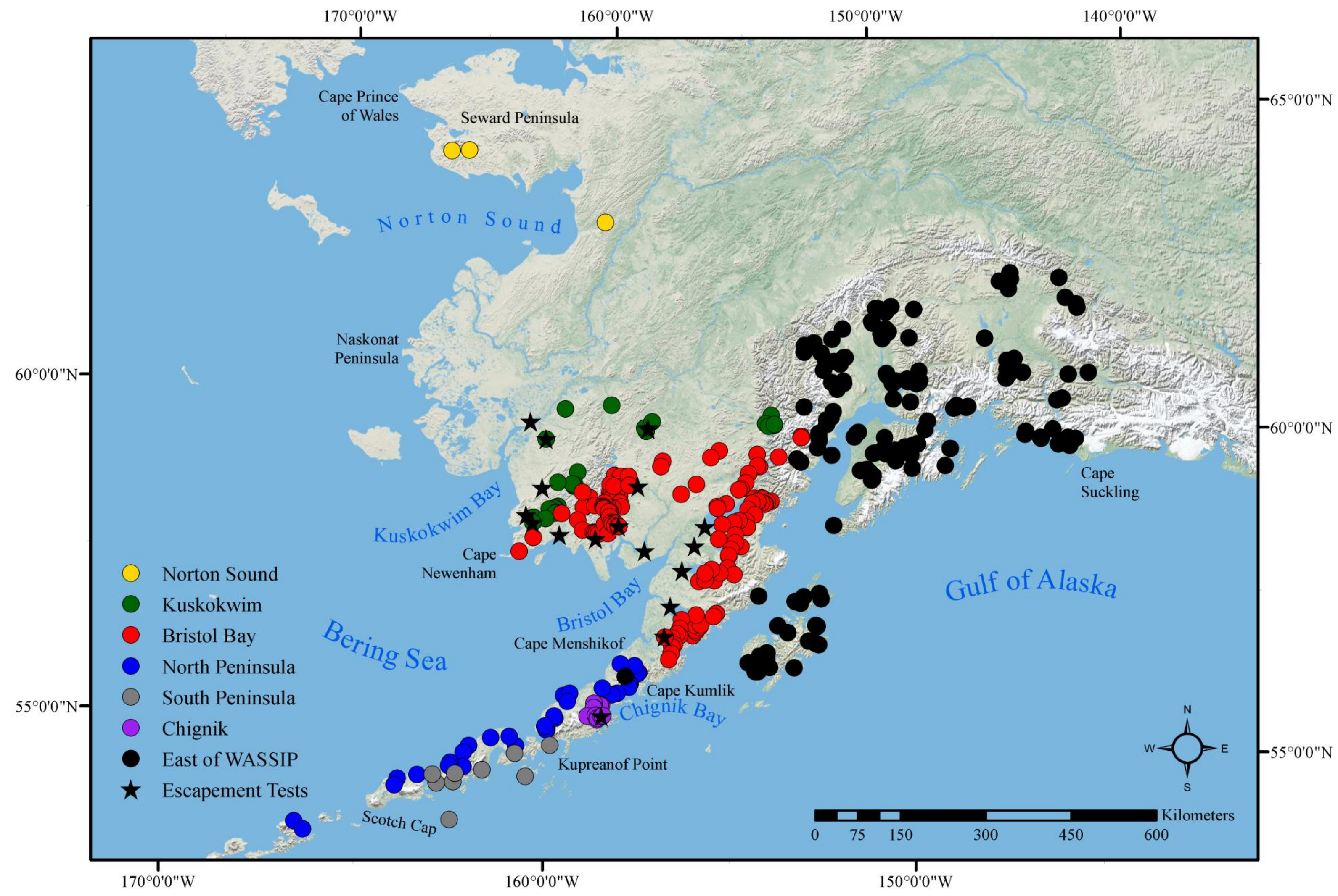


Figure 1.– The location and regional reporting group affiliation of 450 collections of sockeye salmon included in final baseline analyses for WASSIP and location of escapement samples used as tests of the baseline.

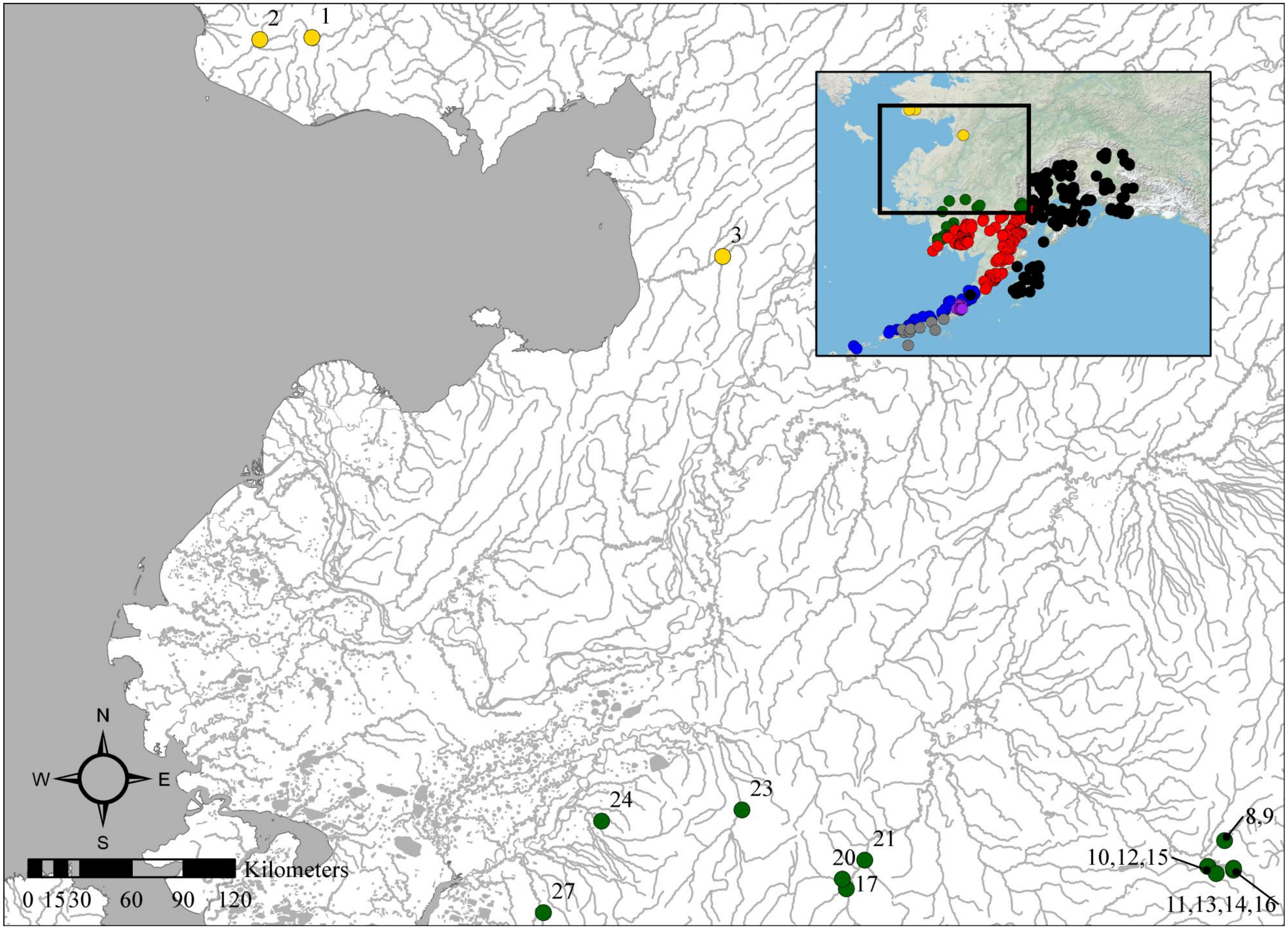


Figure 2.– The location of collections of sockeye salmon from the Norton Sound and Kuskokwim River subregional reporting groups included in final baseline analyses for WASSIP.

Note: Numbers correspond to collection numbers listed in Table 3.

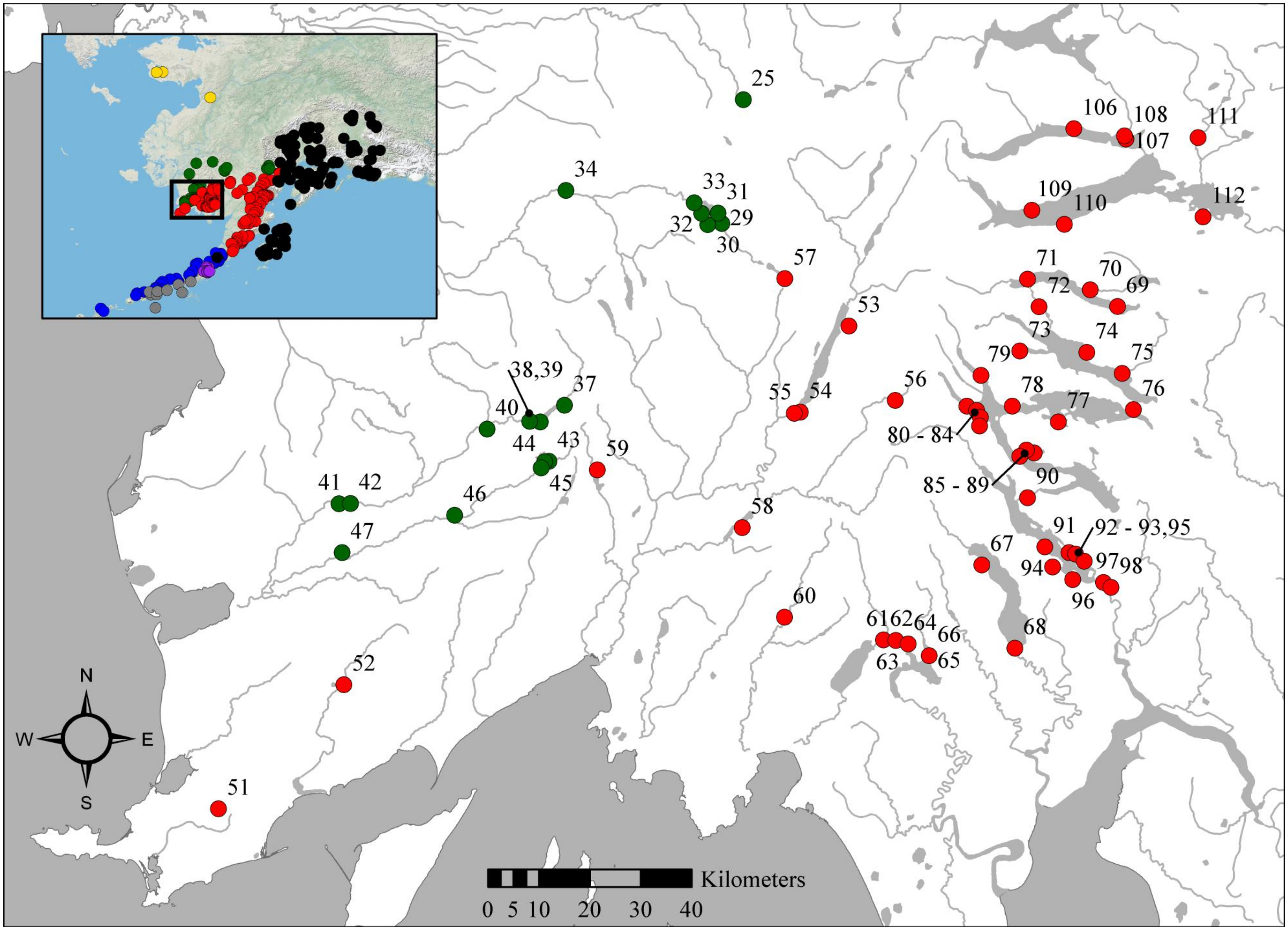


Figure 3.– The location of collections of sockeye salmon from the Kuskokwim River, Kanektok, Goodnews, Togiak, Igushik, Wood and Nushagak subregional reporting groups included in final baseline analyses for WASSIP.

Note: Numbers correspond to collection numbers listed in Table 3.

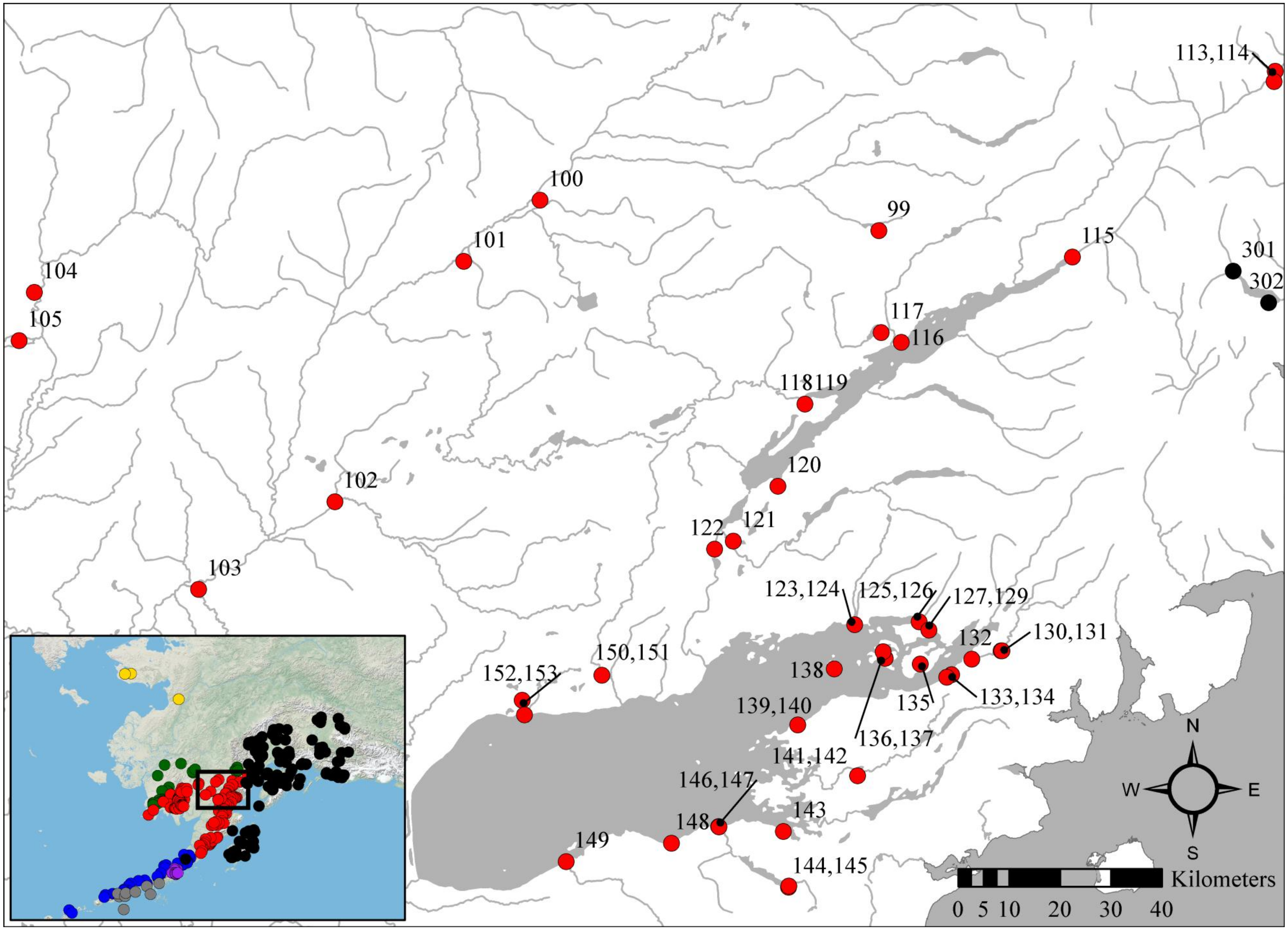


Figure 4.– The location of collections of sockeye salmon from the Nushagak and Kvichak subregional reporting groups included in final baseline analyses for WASSIP.

Note: Numbers correspond to collection numbers listed in Table 3.

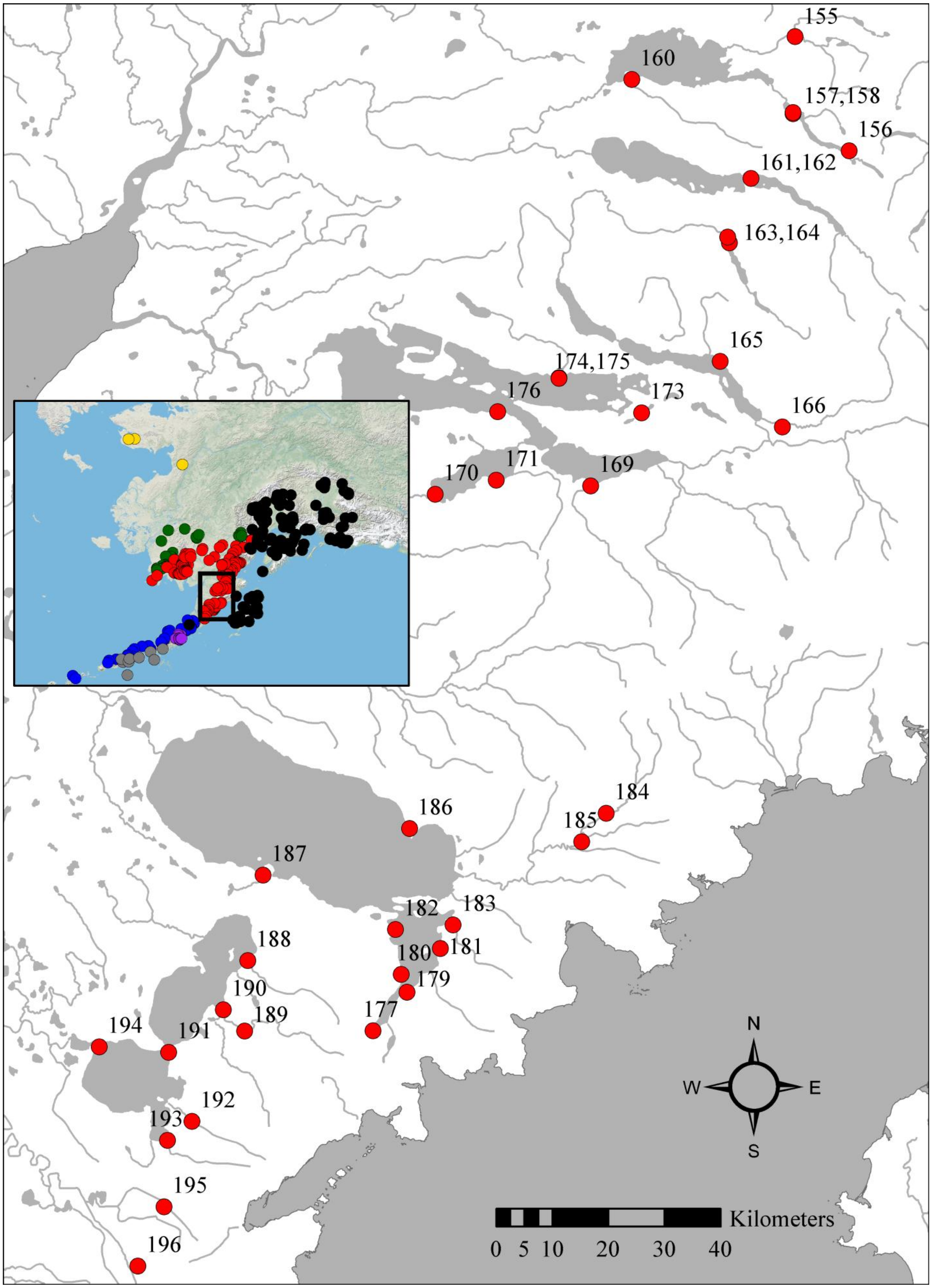


Figure 5.– The location of collections of sockeye salmon from the Alagnak, Naknek, Egegik and Ugashik subregional reporting groups included in final baseline analyses for WASSIP.
Note: Numbers correspond to collection numbers listed in Table 3.

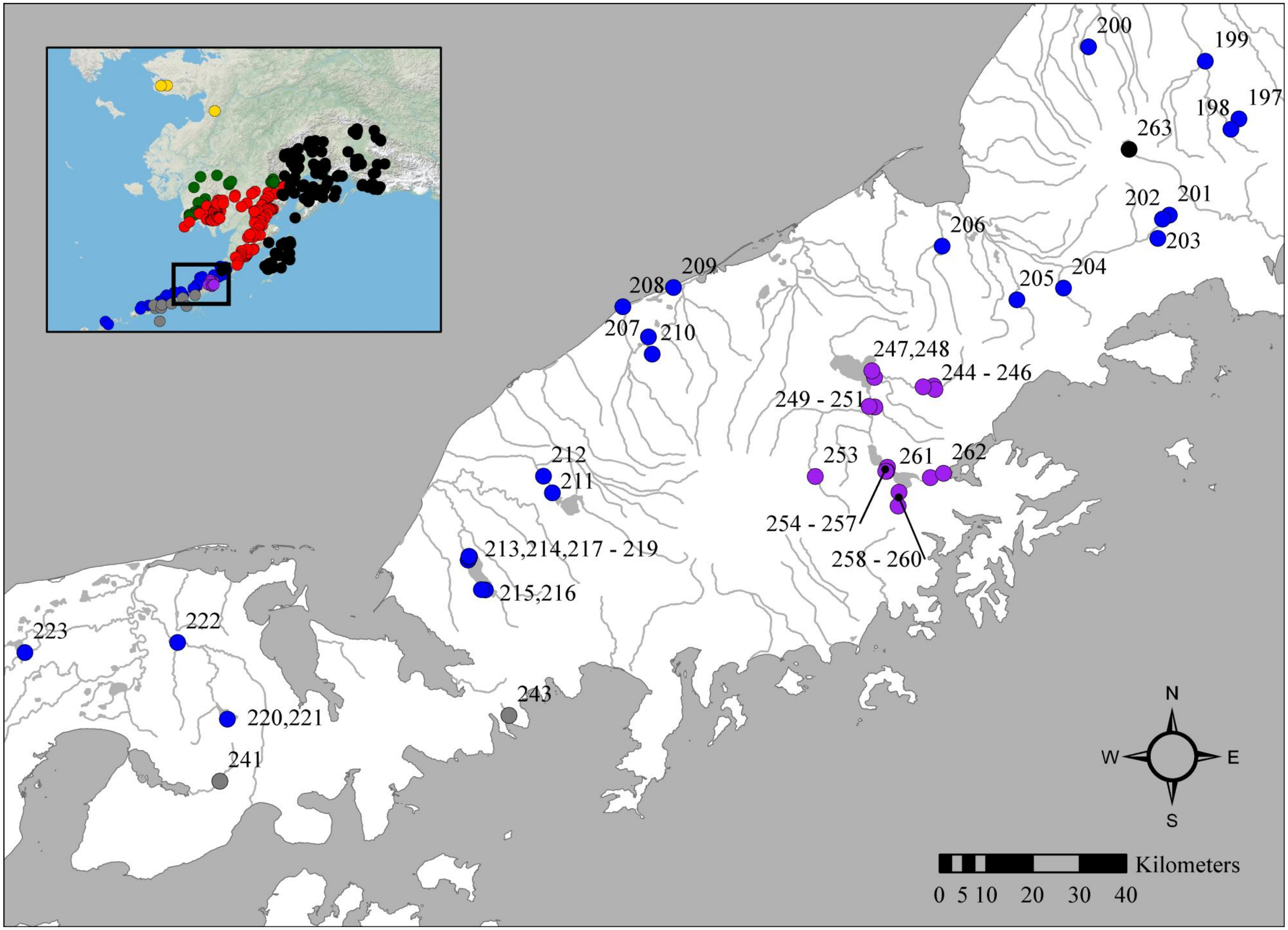


Figure 6.– The location of collections of sockeye salmon from the Cinder, Meshik, Ilnik, Sandy, Bear, Nelson, South Peninsula, Black Lake, Chignik Lake, and East of WASSIP subregional reporting groups included in final baseline analyses for WASSIP.

Note: Numbers correspond to collection numbers listed in Table 3.

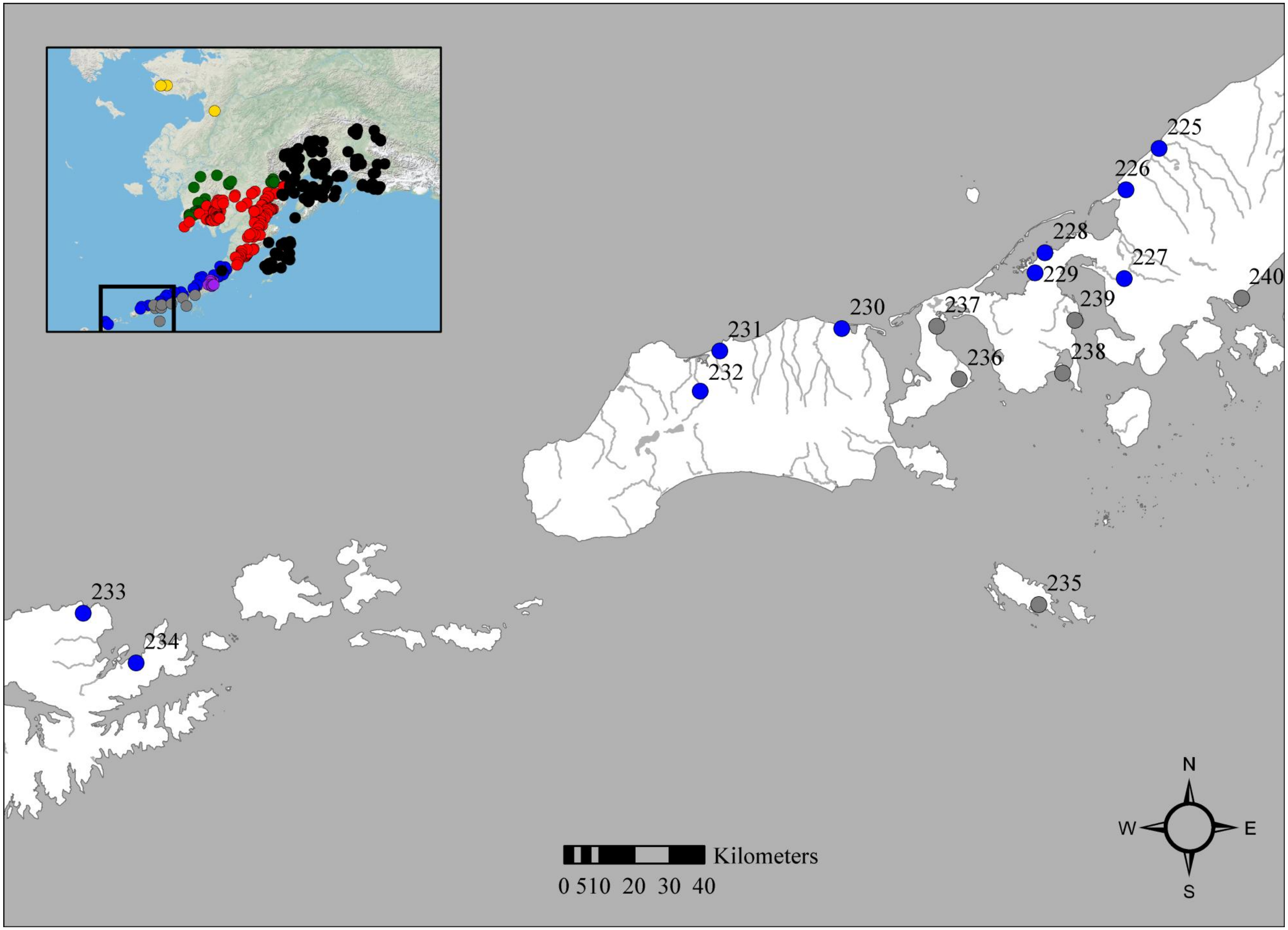


Figure 7.– The location of collections of sockeye salmon from the NW District-Black Hills and South Peninsula subregional reporting groups included in final baseline analyses for WASSIP. Numbers correspond to collection numbers listed in Table 3.

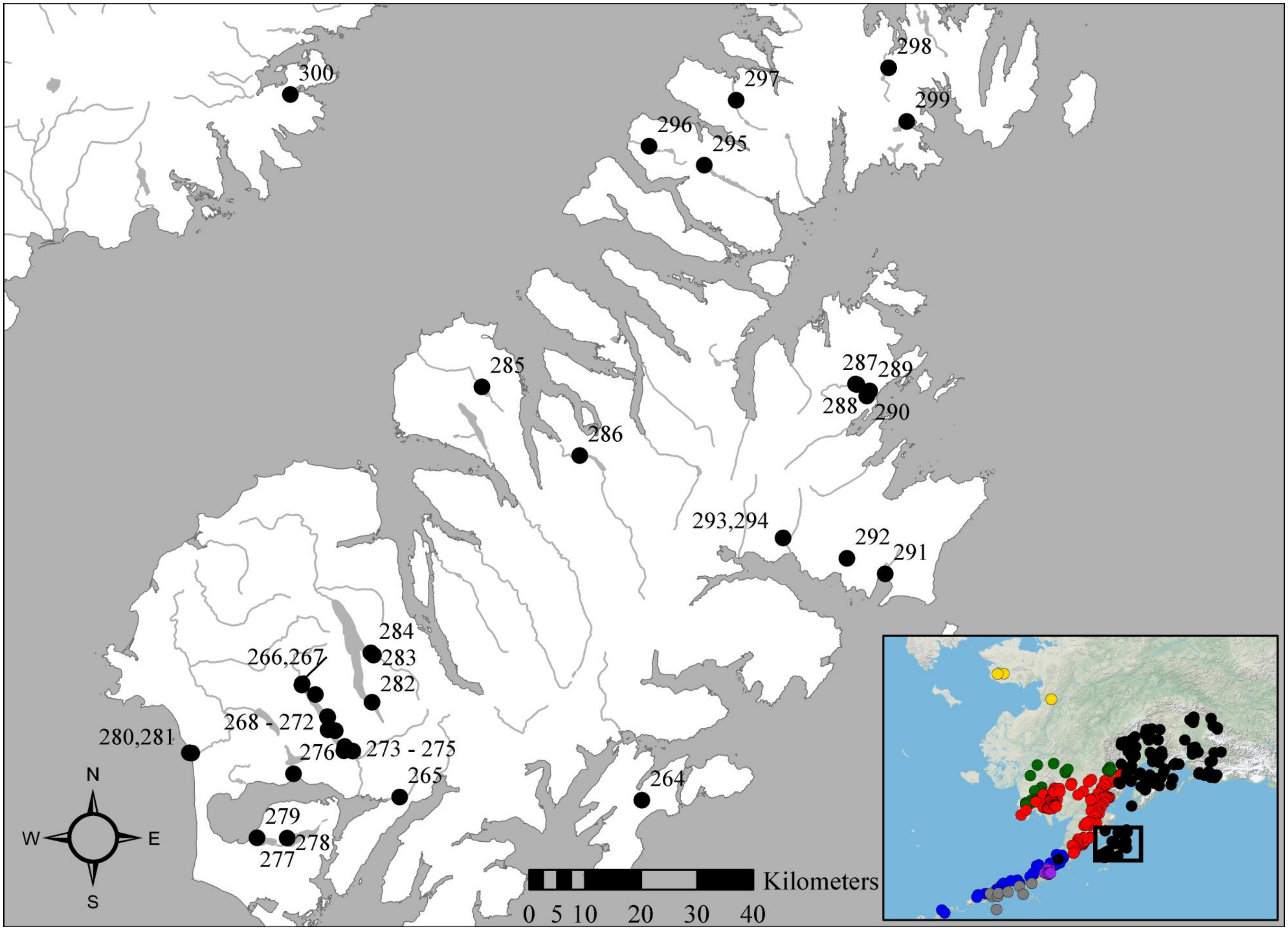


Figure 8.– The location of collections of sockeye salmon from the East of WASSIP reporting group included in final baseline analyses for WASSIP.

Note: Numbers correspond to collection numbers listed in Table 3.

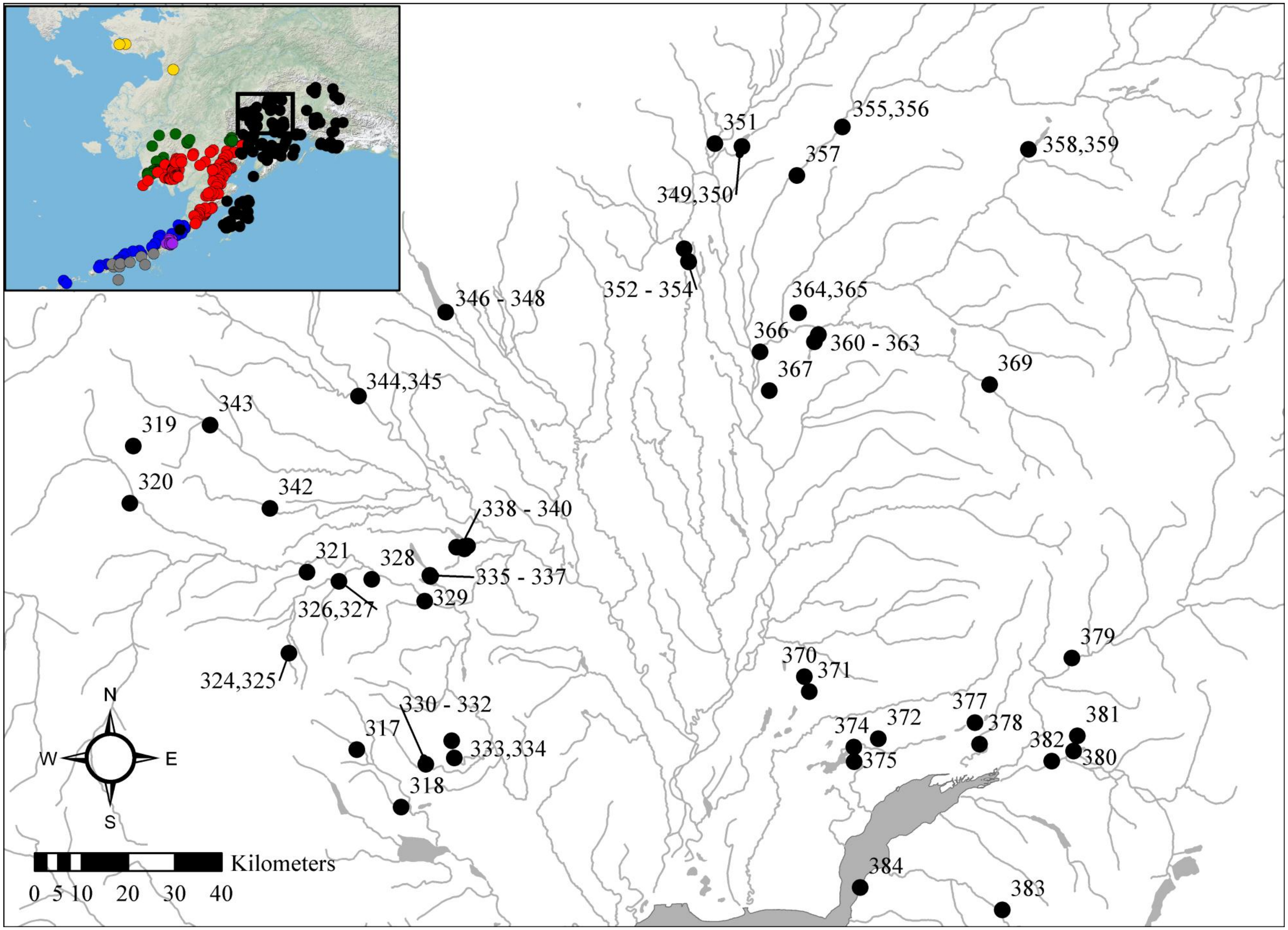


Figure 9.– The location of collections of sockeye salmon from the East of WASSIP reporting group included in final baseline analyses for WASSIP.

Note: Numbers correspond to collection numbers listed in Table 3.

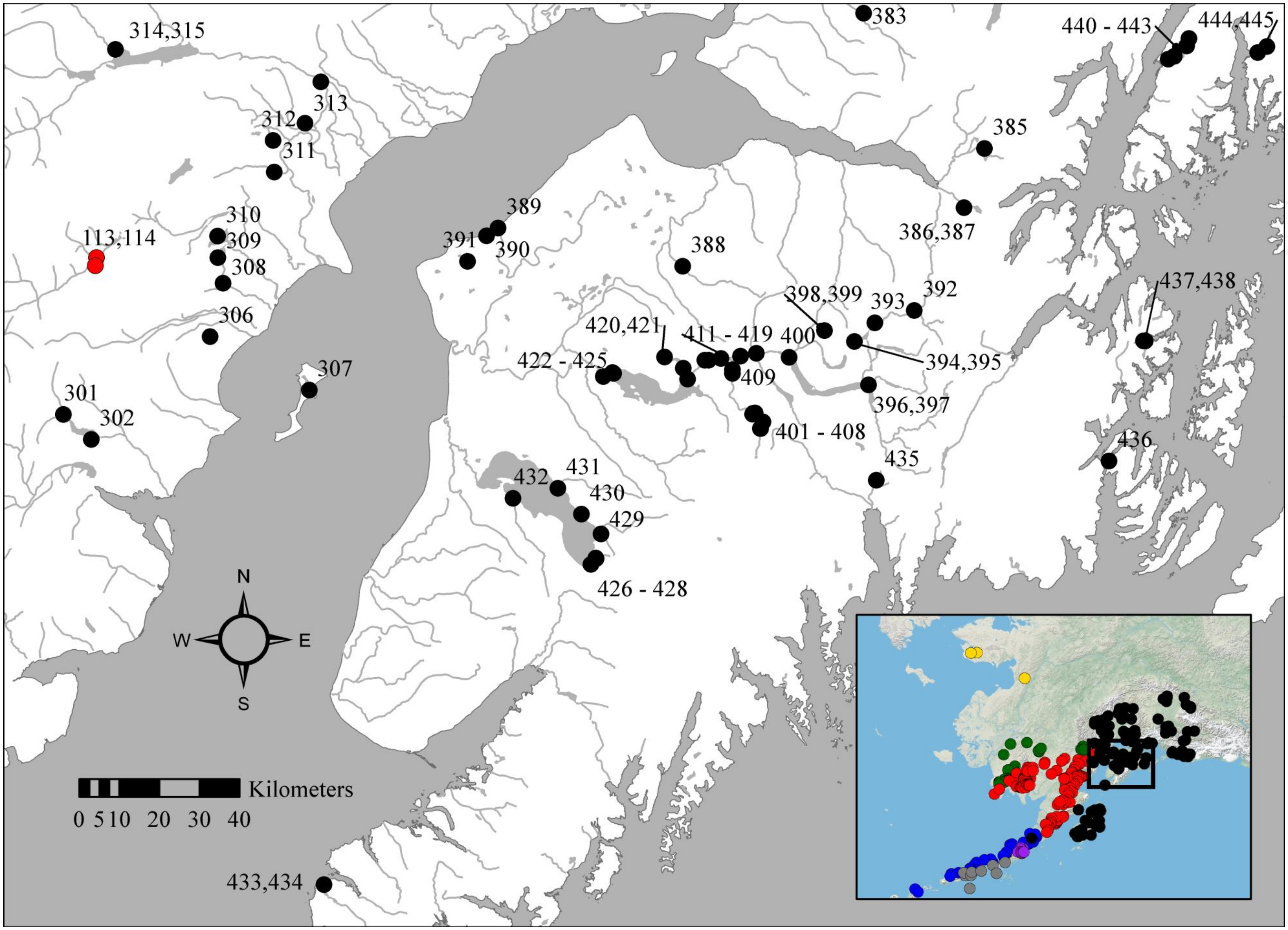


Figure 10.– The location of collections of sockeye salmon from the Kvichak and East of WASSIP reporting groups included in final baseline analyses for WASSIP.

Note: Numbers correspond to collection numbers listed in Table 3.

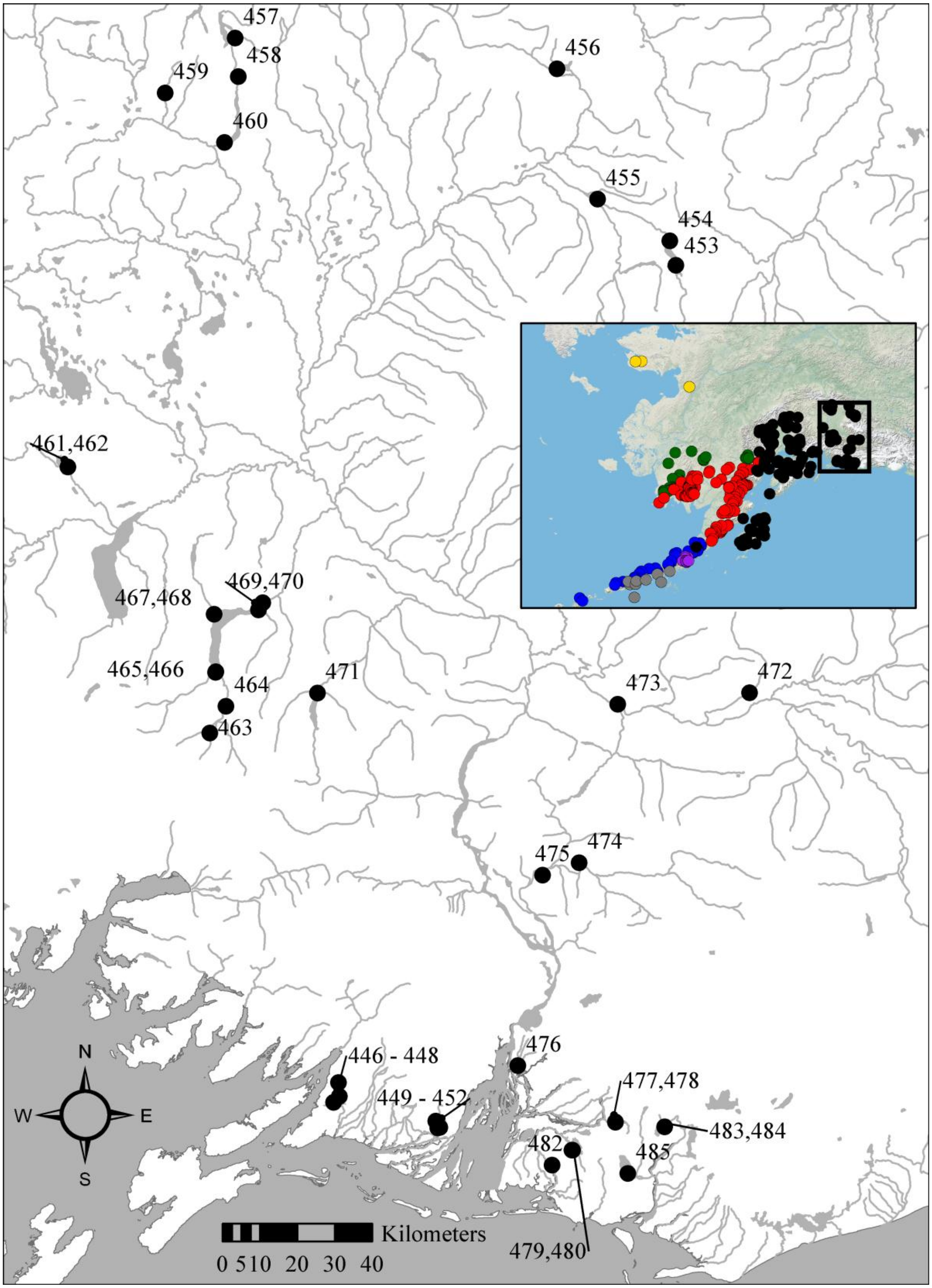


Figure 11.– The location of collections of sockeye salmon from the East of WASSIP reporting group included in final baseline analyses for WASSIP.
Note: Numbers correspond to collection numbers listed in Table 3.

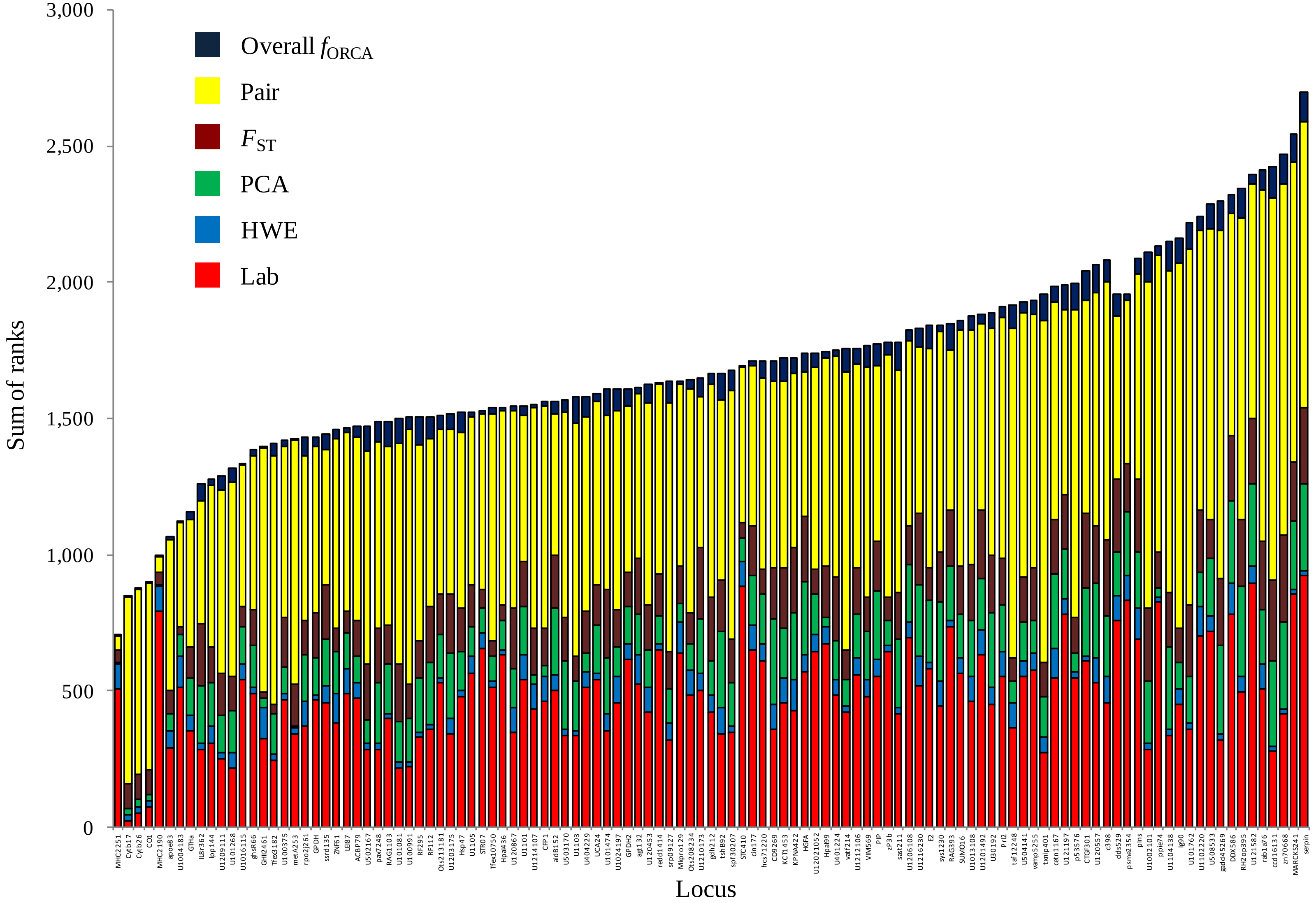


Figure 12.– The sum of rankings for the 115 SNPs that were not removed from consideration in locus selection color-coded by category of judge: Overall f_{ORCA} = Overall f_{ORCA} measure; Pair = 14 measures of differentiation between pairs of populations; F_{ST} = 3 measures of F_{ST}; PCA = 3 measures from principal component analysis; HWE = Hardy-Weinberg Equilibrium measure; and Lab = 8 measures of laboratory performance.

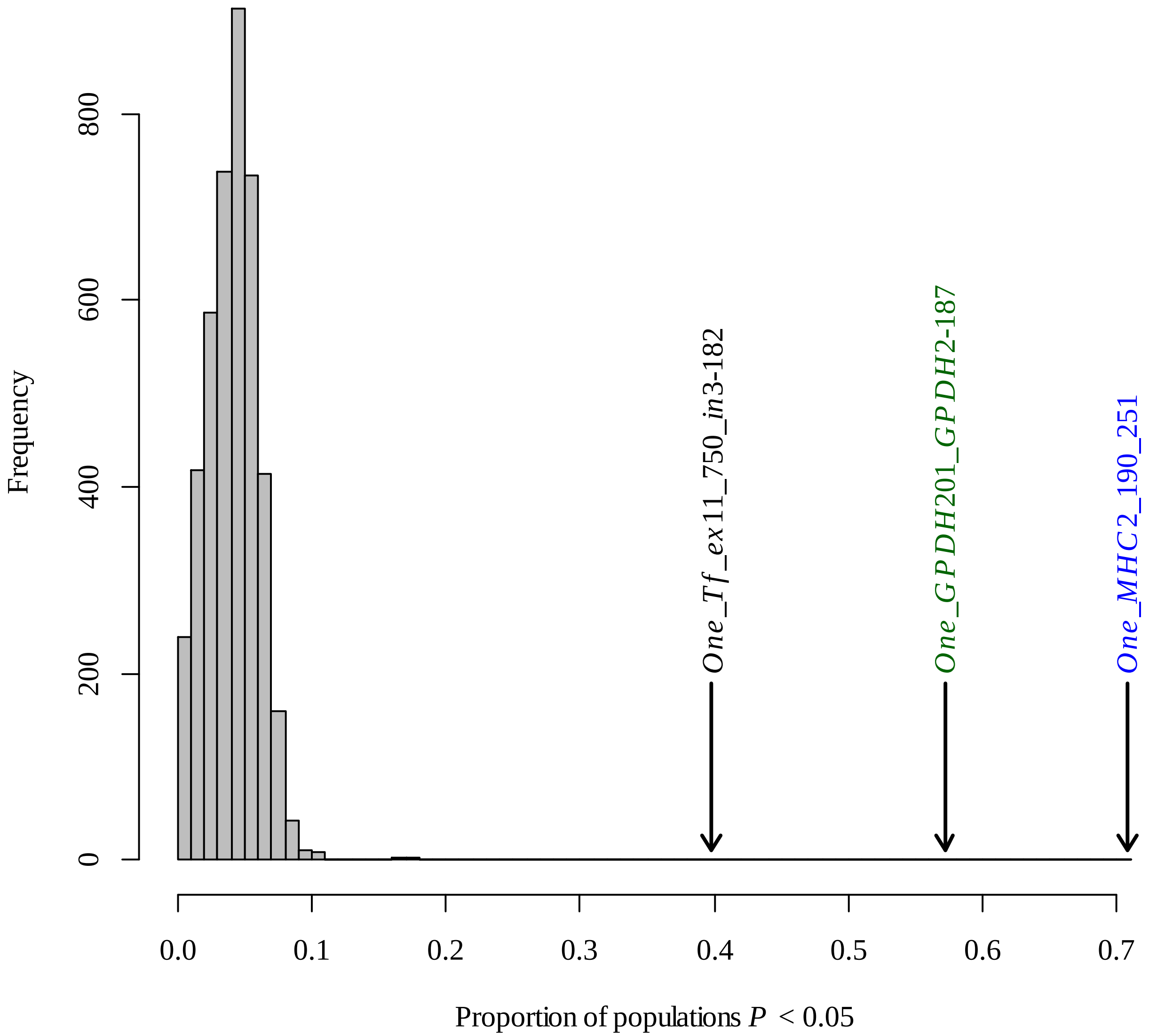


Figure 13.– Histogram of the proportion of populations with significant (P < 0.05) linkage disequilibrium between the 4,278 pairs of the 93 nuclear SNPs tested in 294 WASSIP area populations.

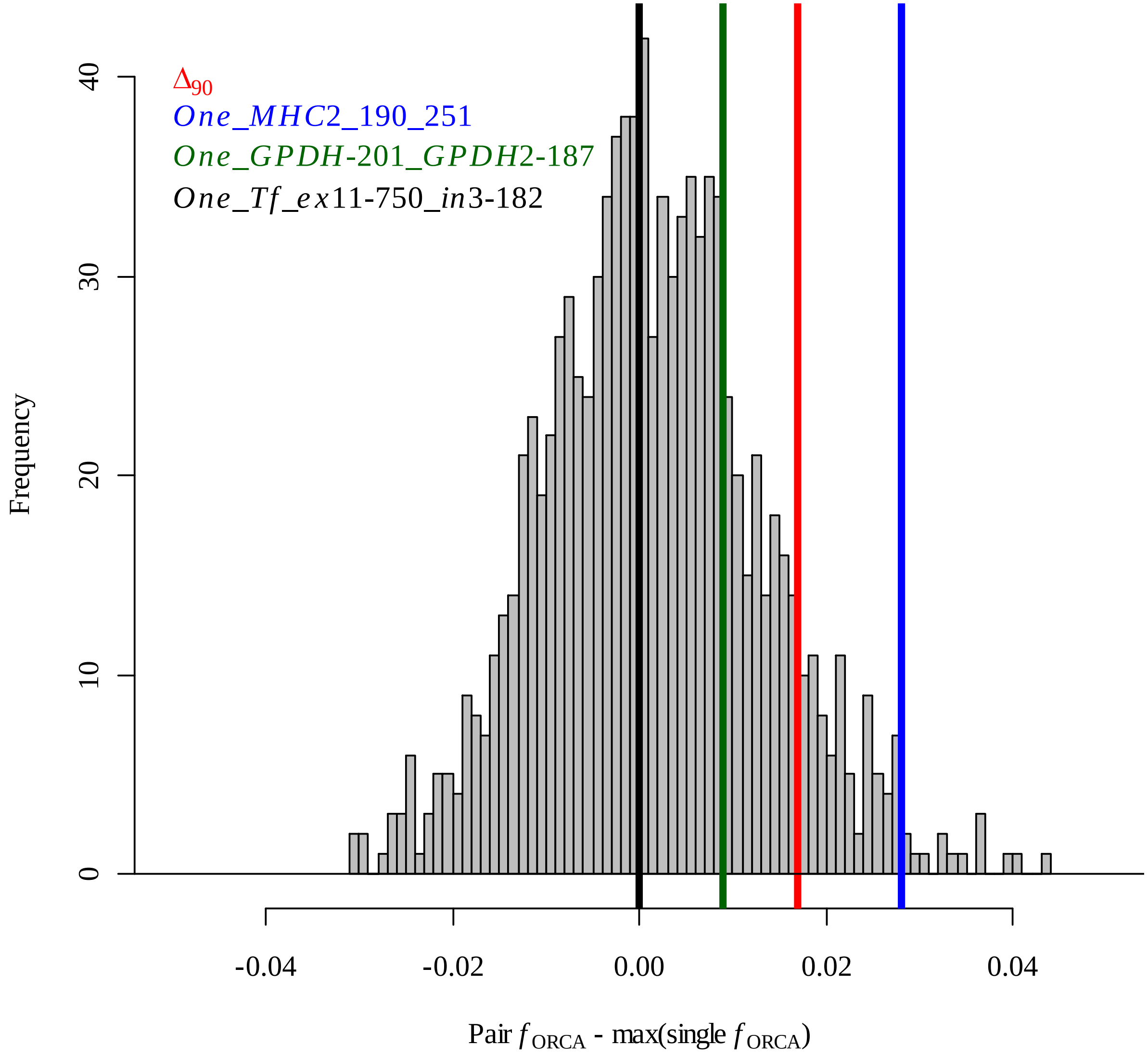
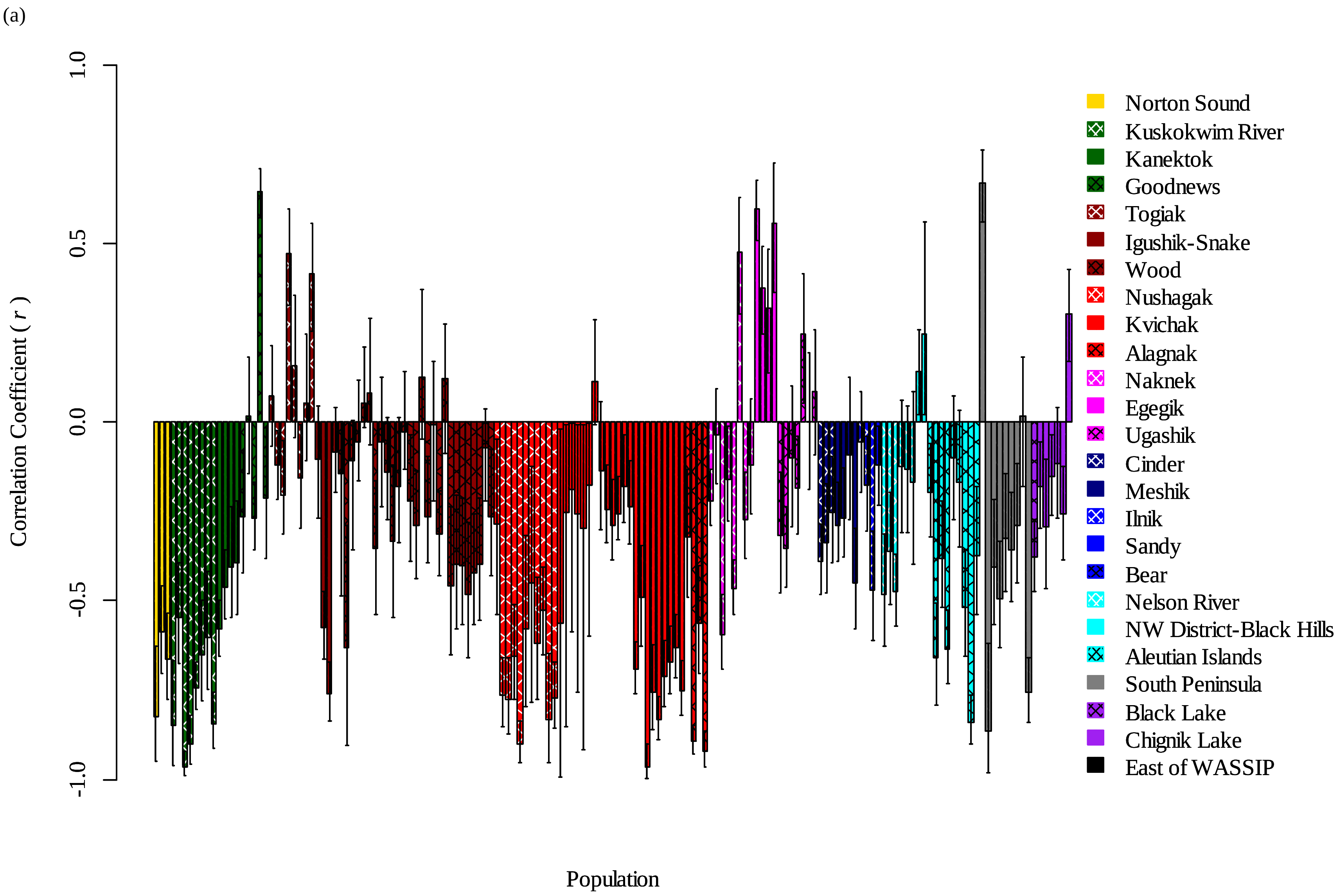


Figure 14.– The distribution of Δ for 1,000 random SNP pairs with Δ_{90} in red and the Δ values for *One_MHC*2190_251 in blue, *One_GPDH*-201_*GPDH*2-187 in green, and *One_Tf_ex*11-750_*in*3-182 in black.
Note: See text for details.


(a)
Correlation Coefficient (r)
1.0
0.5
0.0
-0.5
-1.0
Population
Norton Sound
Kuskokwim River
Kanektok
Goodnews
Togiak
Igushik-Snake
Wood
Nushagak
Kvichak
Alagnak
Naknek
Egegik
Ugashik
Cinder
Meshik
Ilnik
Sandy
Bear
Nelson River
NW District-Black Hills
Aleutian Islands
South Peninsula
Black Lake
Chignik Lake
East of WASSIP

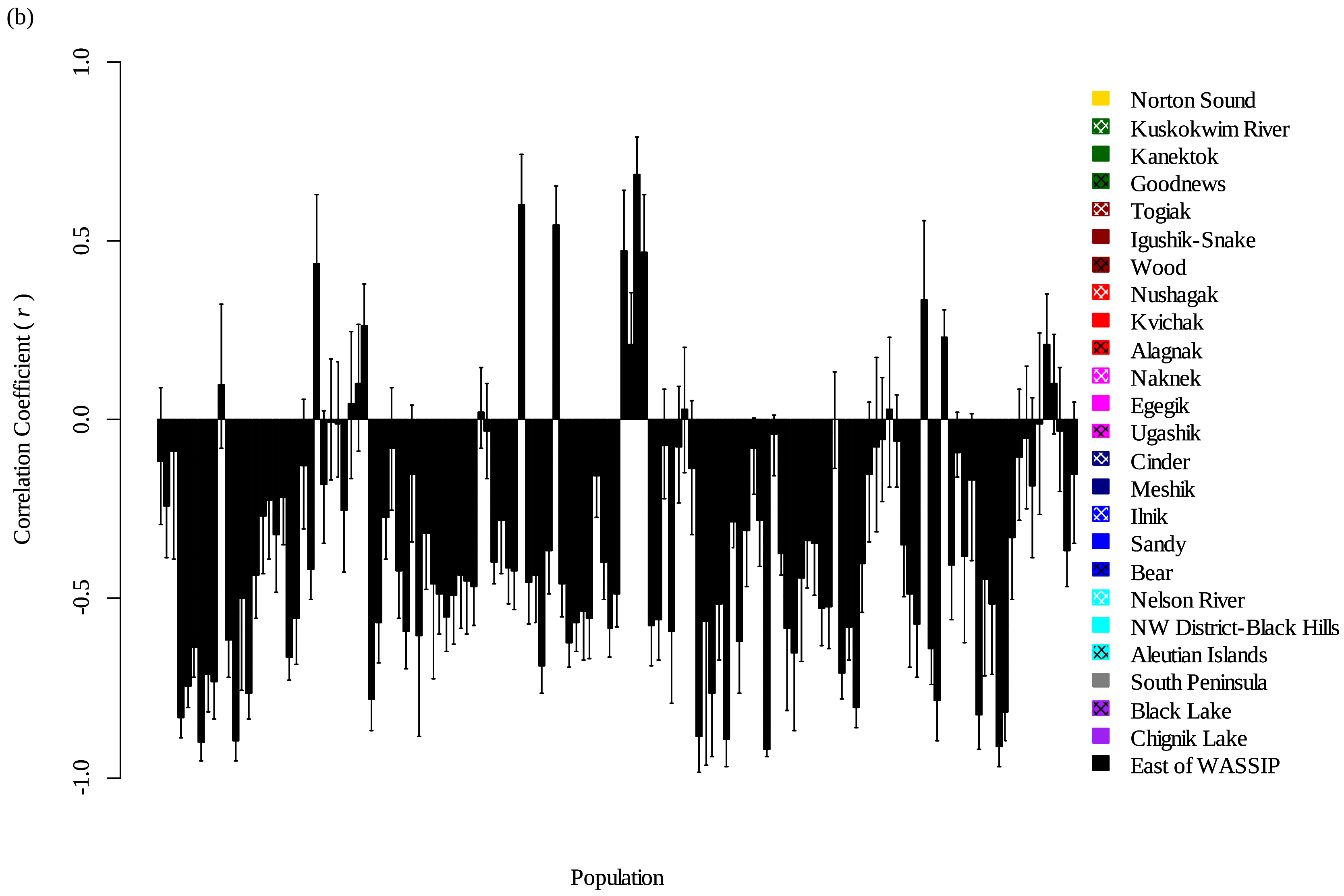


Figure 15.–(a) Correlation coefficient *r* between the first alphabetical allele in the pair of MHC SNPs in each population within the WASSIP study area ranging from Salmon Lake (left) in the north to the Chignik River (right) to the south; (b) Correlation coefficient *r* between the first alphabetical allele in the pair of MHC SNPs in each population in the East of WASSIP reporting group ranging from Surprise Lake (left) in the west to Bering Lake (right) to the east.

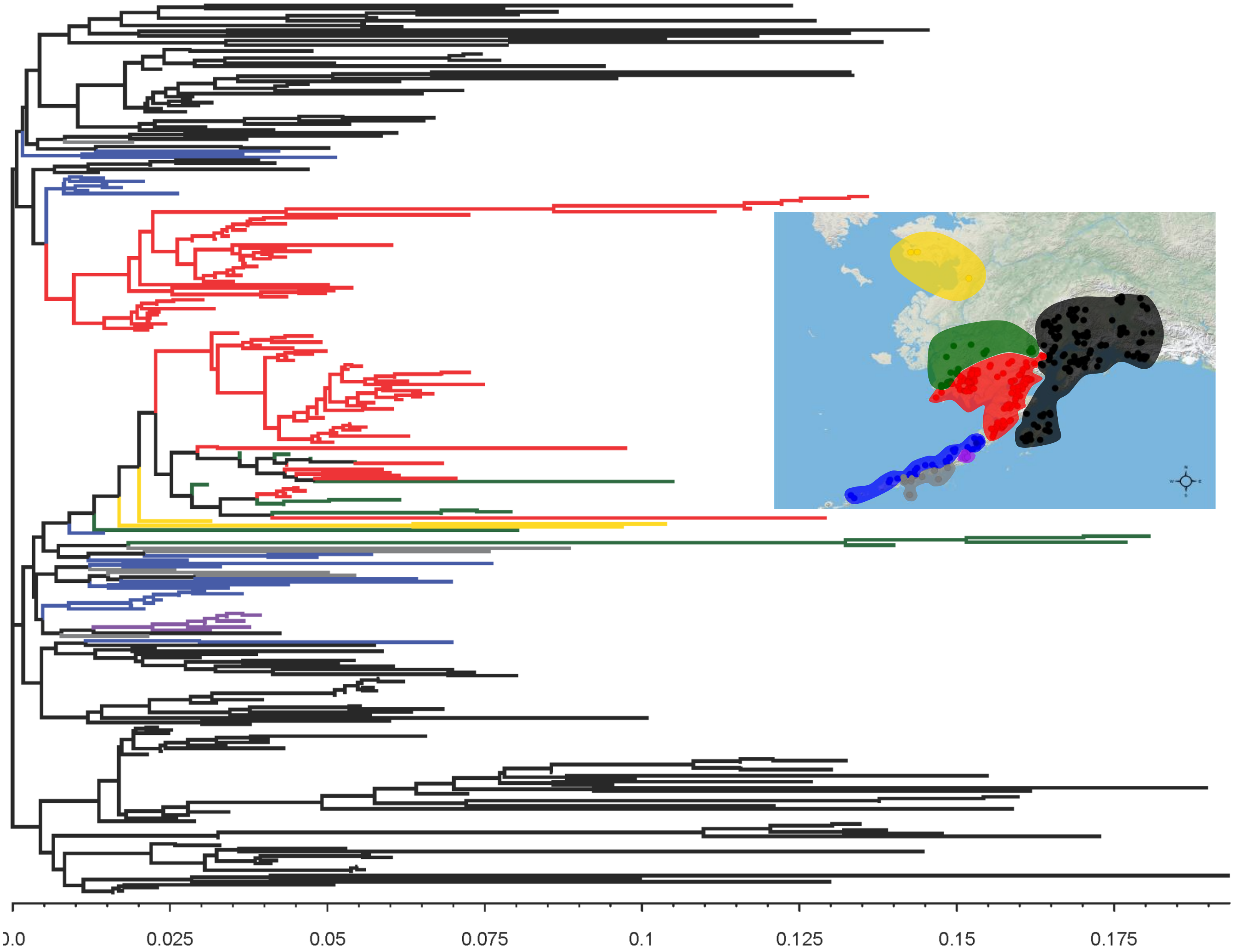


Figure 16.– Neighbor-joining tree based upon pairwise F_{ST} between 294 populations of sockeye salmon included in the WASSIP baseline and map denoting the regional reporting group colors represented on tree branches.

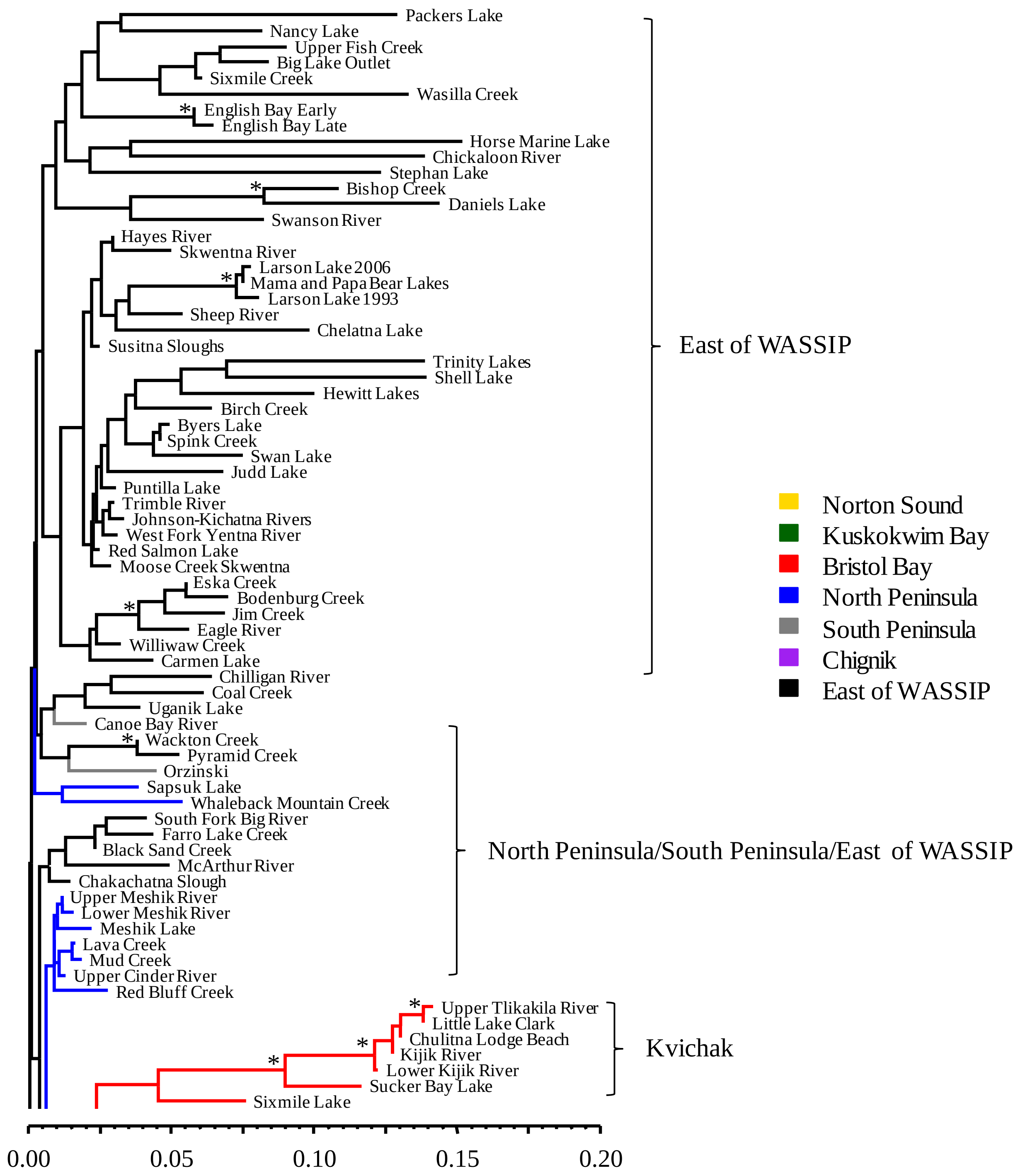


Figure 17.– Consensus neighbor-joining tree based upon pairwise F_{ST} between 294 populations of sockeye salmon included in the WASSIP baseline. Tree branch colors denote regional reporting group memberships, text brackets denote general population groupings by subregional reporting group and asterisks indicate nodes where bootstrap consensus > 90%.

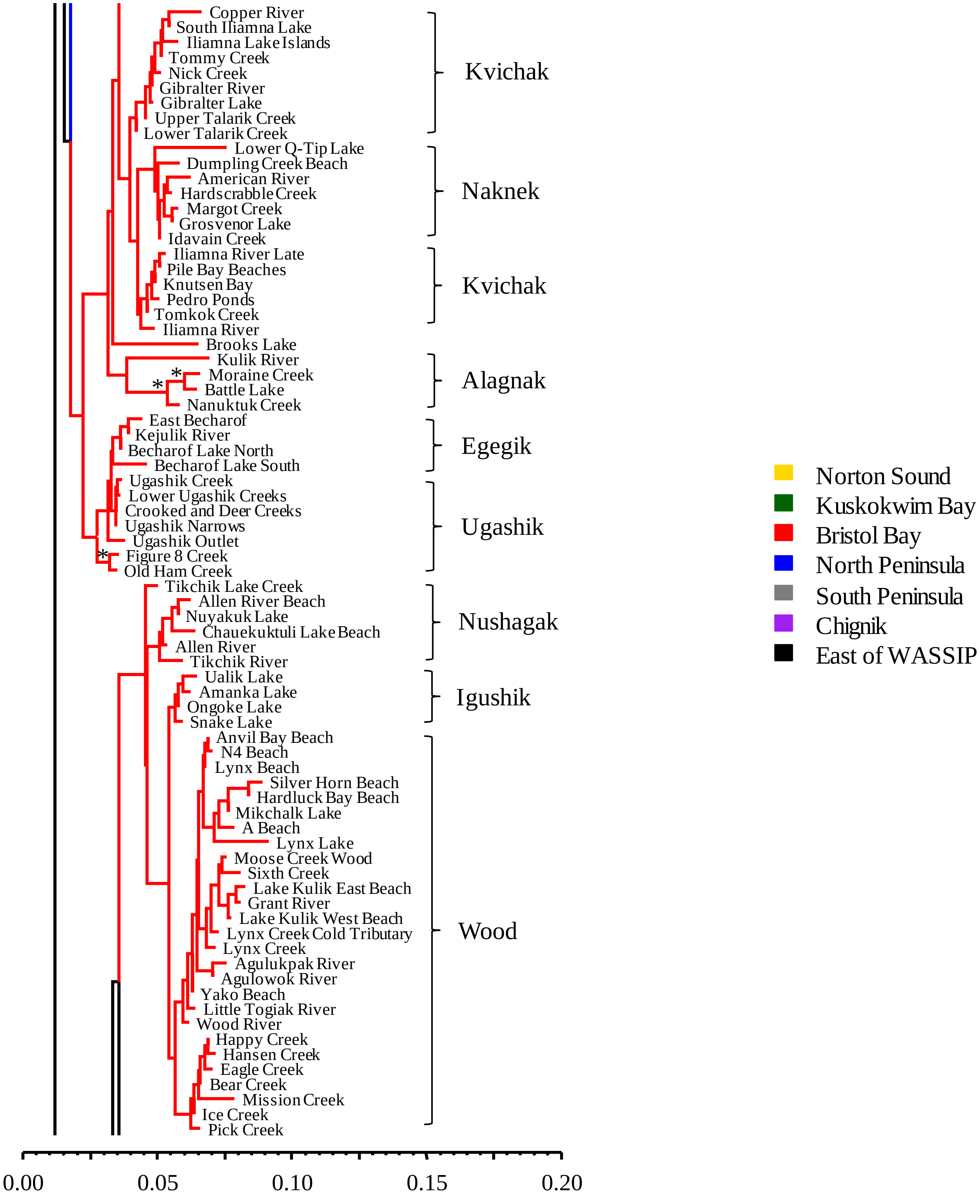


Figure 17. Page 2 of 4.

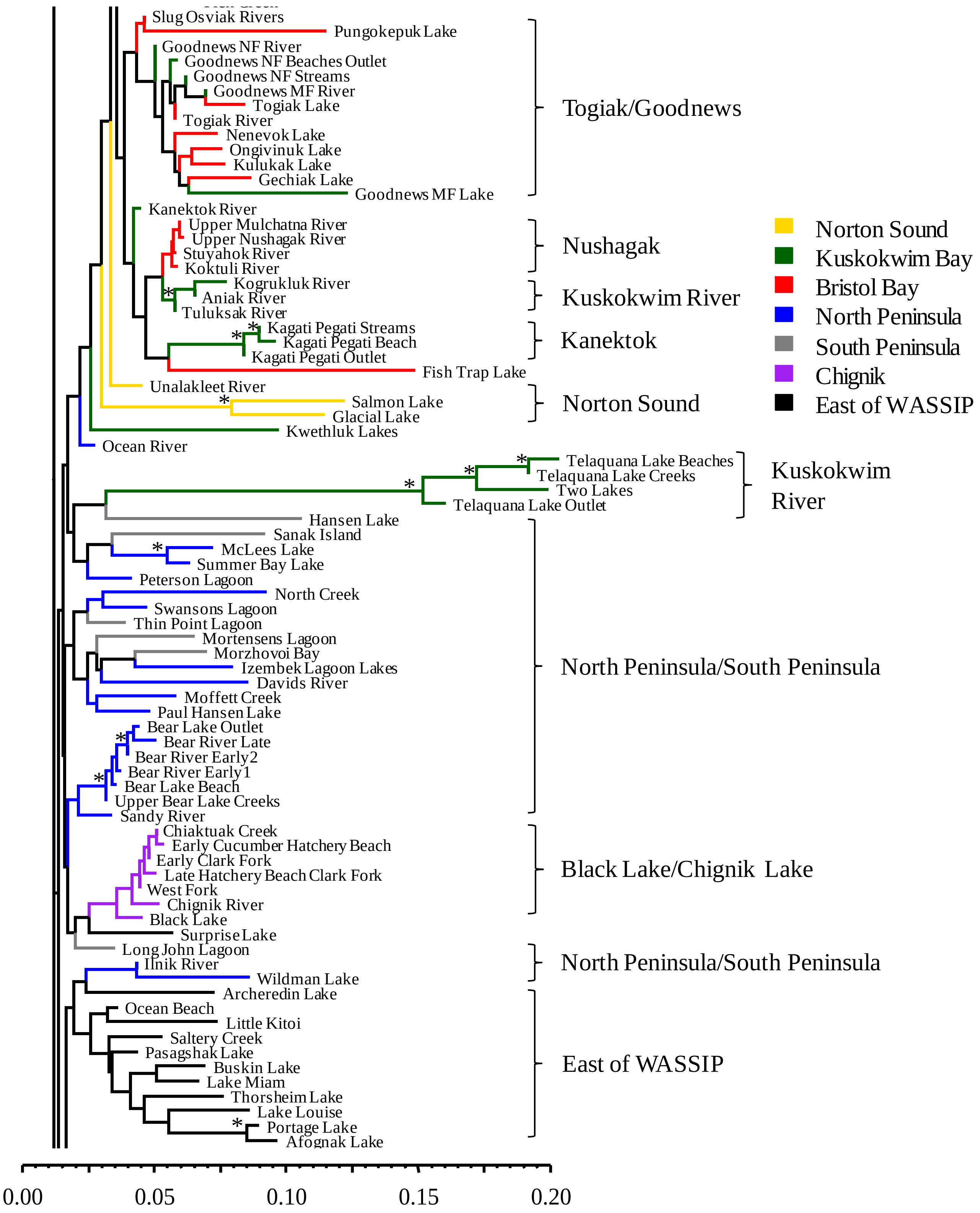


Figure 17. Page 3 of 4.

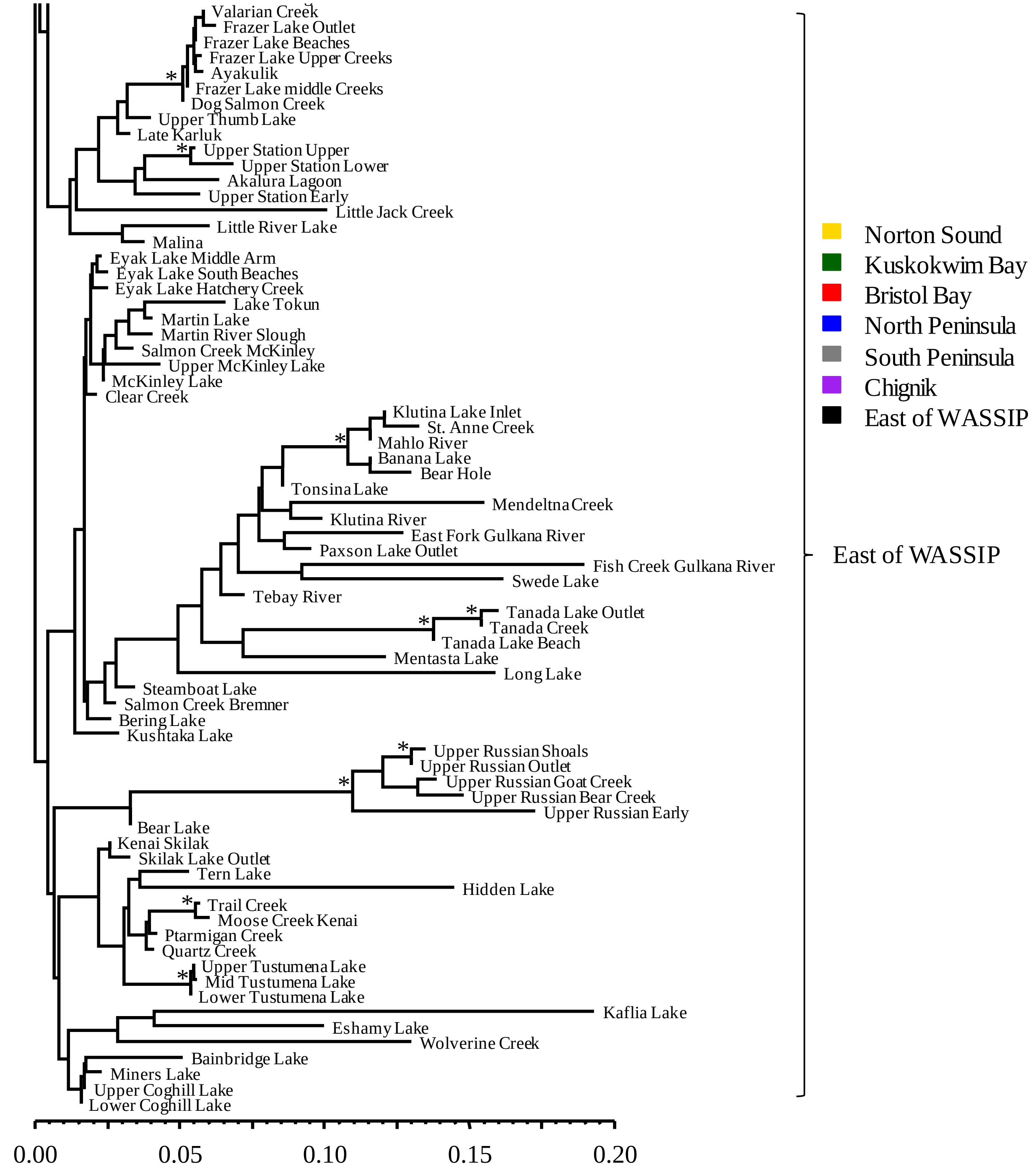


Figure 17. Page 4 of 4.

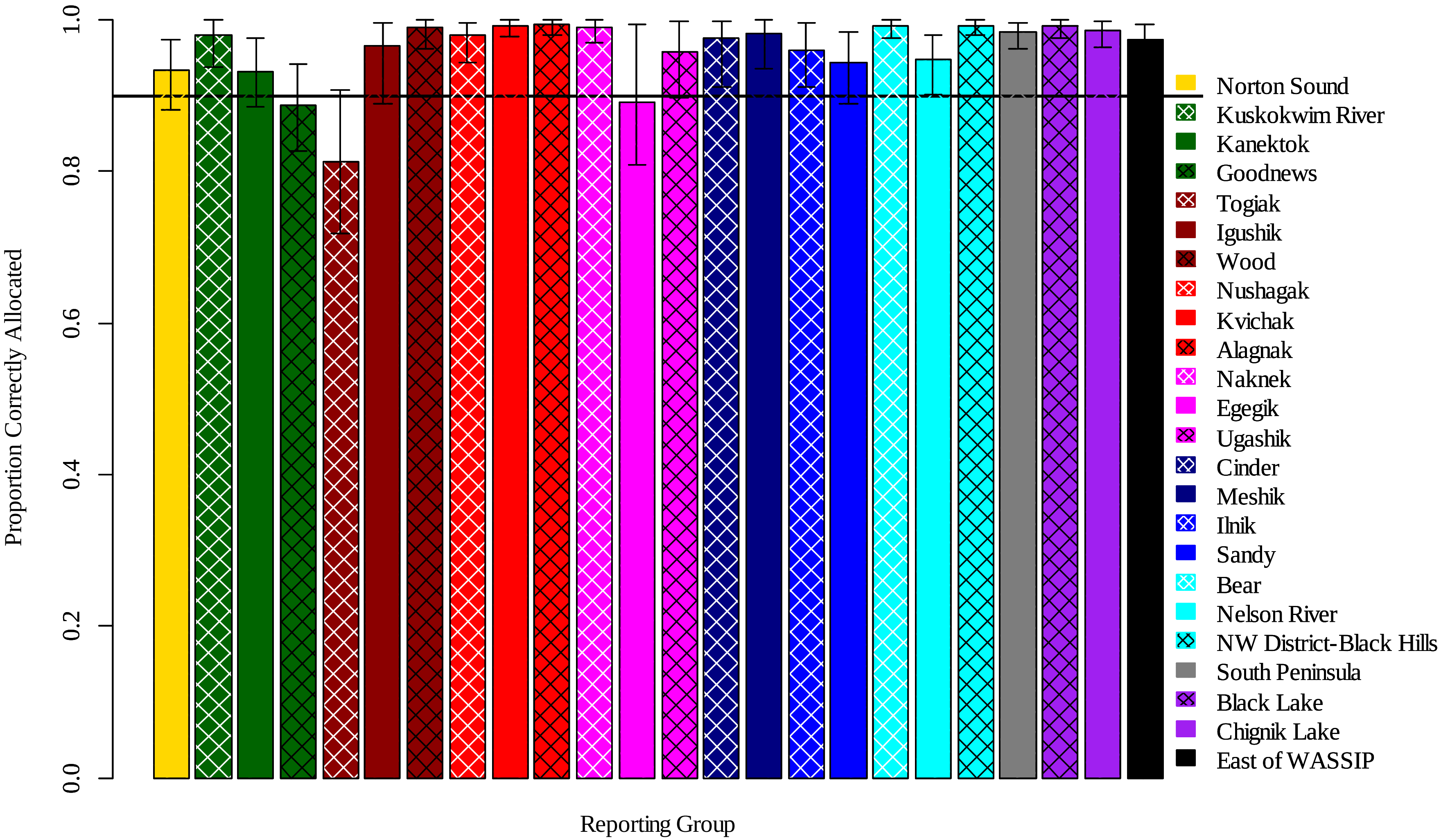


Figure 18.– Proportion of fish correctly allocated back to subregional reporting group of origin and 90% credibility intervals for mixtures of known individuals removed from the baseline population that comprise each reporting group (100% proof tests) using the program *BAYES* with a flat prior. One hundred individuals were removed from the Norton Sound, Cinder, Sandy and Nelson River groups, while 200 individuals were removed from all others.

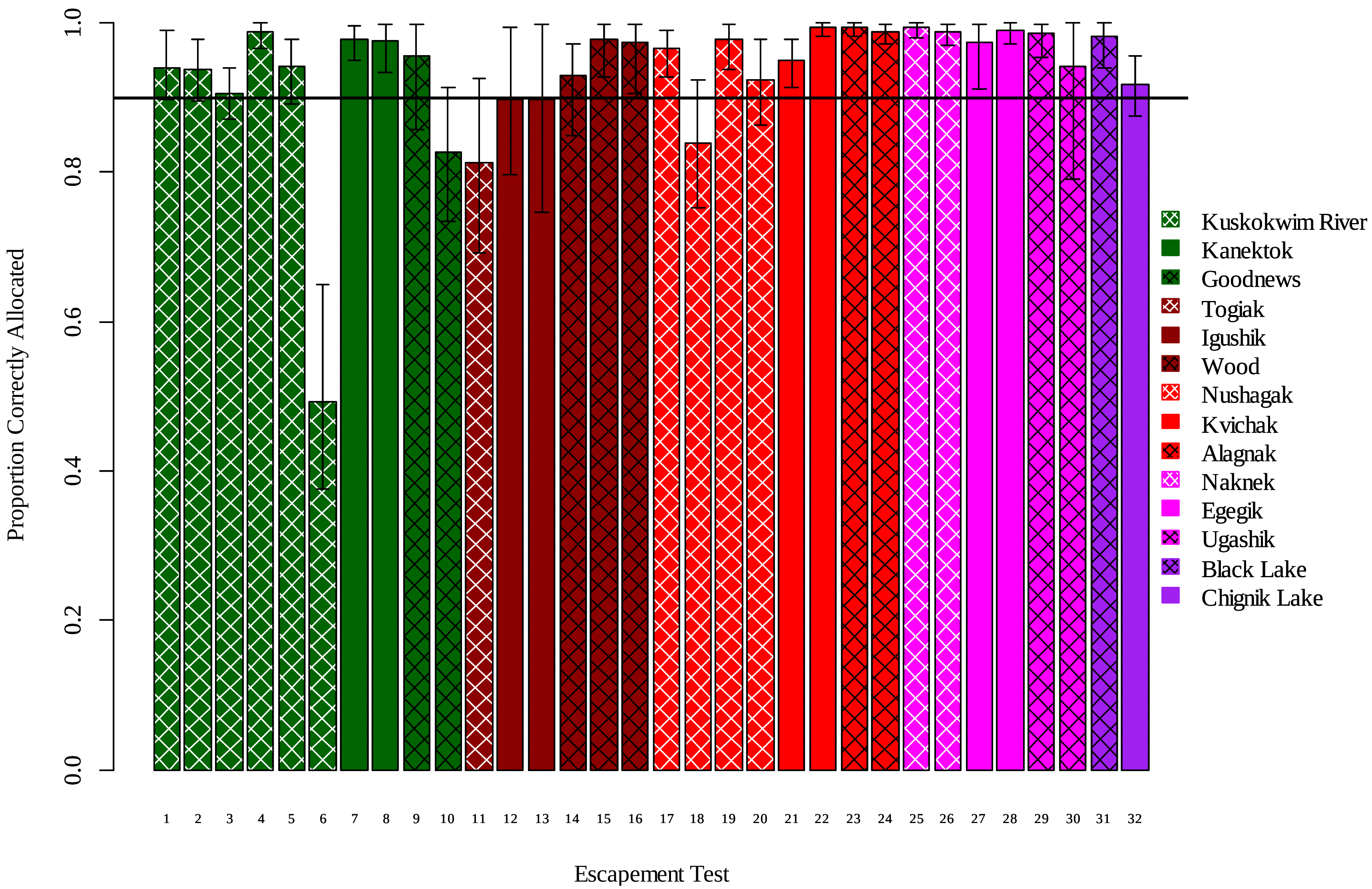


Figure 19.– Proportion of fish allocated to subregional reporting group of origin and 90% credibility intervals for samples of the escapement of sockeye salmon to rivers within 14 WASSIP area reporting groups using the program *BAYES* with a flat prior. Escapement test numbers refer to tests detailed in Table 3.

APPENDICES

Appendix A.– Differences in baseline analysis from RIR5J-19 (Dann et al. 2012c) and reviewed by the technical committee.

Method category	Difference
New collections	We incorporated 13 additional collections to better represent the Kuskokwim River, Goodnews, Togiak, and East of WASSIP reporting groups.
	We dropped some old Big Lake collections because we incorporated more representative samples from the 2011 field season.
Pooling	Our pooling results differed slightly in Frazer Lake and Kenai River populations due to the order of testing.
Reporting group definition	Aleutian Islands and NW District-Black Hills are combined.
f_{ORCA}	We previously included populations from the Aleutian Islands as a separate reporting group in f_{ORCA} analyses. This report only includes the 24 final subregional reporting groups in all f_{ORCA} analyses as opposed to the 25 groups used previously.
	The combined MHC marker was greater than Δ_{90} in this f_{ORCA} analysis.
	We dropped One_GPDH2-187 in this analysis instead of One_GPDH-201 previously.
Temporal ANOVA	We included another level in the ANOVA hierarchy to account for regional variation in allele frequency.
BAYES	We developed a new protocol for handling mixtures with non-converging chains.
	We developed a new protocol for defining initial start values.

Appendix B.– Proof test results reported to all subregional reporting groups. Estimates of stock composition, upper and lower 90% intervals, and standard deviations for proof tests of the baseline.

	Norton Sound				Kuskokwim River				Kanektok			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.93	0.88	0.97	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.02	0.01	0.98	0.94	1.00	0.02	0.00	0.00	0.00	0.00
Kanektok	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.93	0.89	0.98	0.03
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.10	0.03
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01
Igushik	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nushagak	0.05	0.01	0.10	0.03	0.01	0.00	0.06	0.02	0.00	0.00	0.02	0.01
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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Appendix B. Page 2 of 8.

	Goodnews				Togiak				Igushik			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.01
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Kanektok	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Goodnews	0.89	0.83	0.94	0.04	0.18	0.08	0.27	0.06	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.10	0.05	0.16	0.03	0.81	0.72	0.91	0.06	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.97	0.89	1.00	0.03
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.09	0.03
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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	Wood				Nushagak				Kvichak			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
Kanektok	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.99	0.96	1.00	0.01	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00
Nushagak	0.00	0.00	0.00	0.00	0.98	0.94	1.00	0.02	0.00	0.00	0.01	0.00
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.99	0.98	1.00	0.01
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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	Alagnak				Naknek				Egegik			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kanektok	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alagnak	0.99	0.98	1.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.99	0.97	1.00	0.01	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.89	0.81	0.99	0.05
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.18	0.05
North Peninsula												
Cinder	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.00
Meshik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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	Ugashik				Cinder				Meshik			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kanektok	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.01	0.00	0.03	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.96	0.90	1.00	0.03	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	0.00	0.00	0.01	0.00	0.98	0.91	1.00	0.03	0.01	0.00	0.05	0.02
Meshik	0.03	0.00	0.08	0.03	0.01	0.00	0.07	0.03	0.98	0.94	1.00	0.02
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.03	0.01
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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	Ilnik				Sandy				Bear			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kanektok	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	0.03	0.00	0.07	0.02	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Ilnik	0.96	0.91	1.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00	0.94	0.89	0.98	0.03	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.02	0.01	0.03	0.00	0.06	0.02	0.99	0.98	1.00	0.01
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.01	0.00	0.04	0.01	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00

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	Nelson				NW District-Black Hills				South Peninsula			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kanektok	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
North Peninsula												
Cinder	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Meshik	0.02	0.00	0.05	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Ilnik	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Sandy	0.02	0.00	0.06	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.95	0.90	0.98	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.99	0.98	1.00	0.01	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.98	0.96	1.00	0.01
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.01

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	Black Lake				Chignik Lake				East of WASSIP			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kanektok	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.01
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Chignik												
Black Lake	0.99	0.98	1.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.01	0.01	0.99	0.96	1.00	0.01	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.97	0.95	0.99	0.01

Appendix C.– Escapement test results reported to all subregional reporting groups. Estimates of stock composition, upper and lower 90% intervals, and standard deviations for proof tests of the baseline.

	Bethel Test Fish 2008				Bethel Test Fish 2009				Bethel Test Fish 2010			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Kuskokwim Bay												
Kuskokwim R.	0.94	0.90	0.99	0.03	0.94	0.90	0.98	0.03	0.91	0.87	0.94	0.02
Kanektok	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Nushagak	0.05	0.00	0.09	0.03	0.05	0.00	0.10	0.03	0.08	0.05	0.11	0.02
Kvichak	0.00	0.00	0.01	0.00	0.01	0.00	0.03	0.01	0.00	0.00	0.01	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.01	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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	Kogrukluk Weir 2001				Kogrukluk Weir 2007				Kwethluk Weir 2007			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Kuskokwim Bay												
Kuskokwim R.	0.99	0.97	1.00	0.01	0.94	0.89	0.98	0.03	0.49	0.38	0.65	0.09
Kanektok	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.08	0.03
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.07	0.02
Nushagak	0.00	0.00	0.00	0.00	0.05	0.01	0.09	0.02	0.42	0.27	0.54	0.08
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.05	0.01
Meshik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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	Kanektok Weir 2002				Kanektok Weir 2007				Goodnews Weir 2001			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kanektok	0.98	0.95	1.00	0.02	0.98	0.93	1.00	0.02	0.00	0.00	0.01	0.01
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.96	0.86	1.00	0.05
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.02	0.00	0.12	0.04
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Nushagak	0.01	0.00	0.03	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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	Goodnews Weir 2007				Togiak 2008 Subsistence				Igushik Tower 2005			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kanektok	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Goodnews	0.83	0.73	0.91	0.05	0.18	0.07	0.31	0.07	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.15	0.07	0.24	0.05	0.81	0.69	0.93	0.07	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.90	0.80	0.99	0.06
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.19	0.06
Nushagak	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.01	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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	Igushik Tower 2007				Wood Tower 2003				Wood Tower 2004			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Kanektok	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Goodnews	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.90	0.75	1.00	0.08	0.02	0.00	0.09	0.03	0.00	0.00	0.03	0.01
Wood	0.09	0.00	0.24	0.09	0.93	0.85	0.97	0.04	0.98	0.93	1.00	0.02
Nushagak	0.00	0.00	0.03	0.01	0.05	0.02	0.08	0.02	0.01	0.00	0.05	0.02
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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	Wood Tower 2007				Nushagak Sonar 2006				Nushagak RT 2005			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.04	0.20	0.05
Kanektok	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
Goodnews	0.00	0.00	0.00	0.00	0.01	0.00	0.03	0.01	0.00	0.00	0.01	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Igushik	0.02	0.00	0.08	0.03	0.01	0.00	0.03	0.01	0.01	0.00	0.05	0.02
Wood	0.97	0.91	1.00	0.03	0.02	0.00	0.04	0.01	0.01	0.00	0.04	0.01
Nushagak	0.00	0.00	0.01	0.01	0.97	0.93	0.99	0.02	0.84	0.75	0.92	0.05
Kvichak	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00

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	Nushagak RT 2006				Nuyakuk Tower 2004				Kvichak Tower 2005			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.00	0.00	0.01	0.00	0.06	0.02	0.00	0.00	0.01	0.00
Kanektok	0.00	0.00	0.01	0.00	0.05	0.00	0.10	0.03	0.00	0.00	0.00	0.00
Goodnews	0.00	0.00	0.01	0.01	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.01	0.00	0.04	0.02	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.03	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Nushagak	0.98	0.94	1.00	0.02	0.92	0.86	0.98	0.03	0.04	0.01	0.08	0.02
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.95	0.91	0.98	0.02
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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	Kvichak Tower 2006				Alagnak Tower 2004				Alagnak Tower 2008			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kanektok	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kvichak	0.99	0.98	1.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Alagnak	0.00	0.00	0.00	0.00	0.99	0.98	1.00	0.01	0.99	0.97	1.00	0.01
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula												
Cinder	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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	Naknek Tower 2002				Naknek Tower 2008				Egegik Tower 2004			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kanektok	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.01
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00
Naknek	0.99	0.98	1.00	0.01	0.99	0.97	1.00	0.01	0.00	0.00	0.01	0.00
Egegik	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.97	0.91	1.00	0.03
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.07	0.03
North Peninsula												
Cinder	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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	Egegik Tower 2007				Ugashik Tower 2004				Ugashik Tower 2008			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay												
Kuskokwim R.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kanektok	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay												
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.99	0.97	1.00	0.01	0.00	0.00	0.03	0.02	0.05	0.00	0.20	0.07
Ugashik	0.00	0.00	0.01	0.01	0.99	0.95	1.00	0.02	0.94	0.79	1.00	0.07
North Peninsula												
Cinder	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik												
Black Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik Lake	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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	Chignik 2010 Early Run				Chignik 2010 Late Run			
Reporting Group	Prop.	Lower	Upper	SD	Prop.	Lower	Upper	SD
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim Bay								
Kuskokwim R.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kanektok	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Goodnews	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay								
Togiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Igushik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Wood	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nushagak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kvichak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Alagnak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Naknek	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Egegik	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Ugashik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
North Peninsula								
Cinder	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Meshik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ilnik	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sandy	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bear	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Nelson River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
NW Dist.-BH	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik								
Black Lake	0.98	0.94	1.00	0.02	0.08	0.04	0.12	0.02
Chignik Lake	0.02	0.00	0.06	0.02	0.92	0.88	0.96	0.02
East of WASSIP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00