

## **PSC Northern Fund Final Report**

Project Number: NF-2016-I-18

Project Title: Mixed stock analysis of U.S. Districts 101, 102 and 103 sockeye salmon seine fisheries, 2016

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### **Abstract:**

Sockeye salmon are harvested by commercial fishers in the Northern Boundary Area (NBA) in U.S. Districts 101 through 104 and 106 in Southeast Alaska. In these fisheries, mixed stocks of sockeye salmon are harvested, including salmon originating from Alaska and British Columbia. Thus, the salmon fisheries in these districts are managed in accordance with the current PST Annex IV, Chapter 2 NBA provisions. The Northern Boundary Annex to the 1999 Pacific Salmon Treaty agreement requires detailed accounting of the harvests for Nass and Skeena sockeye salmon stocks. This project continues the use of genetic stock identification (GSI) of sockeye salmon harvested in Districts 101, 102, and 103 seine fisheries by screening 96 single nucleotide polymorphic genetic markers in 1,615 sockeye salmon. For the purpose of this analysis, fishery samples were proportionally allocated to four aggregate groups of collections (reporting groups) defined based on a combination of the genetic distinctions in the baseline and the resolution necessary to meet management needs: *Alaska*, *Nass*, *Skeena*, and *Other*. The *Alaska* reporting group was the largest overall contributor in all 3 districts for the 2016 season.

### **Introduction:**

Significant numbers of Canada- and Alaska-origin sockeye salmon are harvested in NBA fisheries. This includes harvests in U.S. Districts 101, 102, 103, 104, and 106 net fisheries, and Canadian Areas 1, 3, 4, and 5 net fisheries. The Northern Boundary chapter of Annex IV of the Pacific Salmon Treaty agreement requires detailed accounting of the harvests for Nass and Skeena sockeye salmon stocks. This information is used to calculate total returns to the Nass and Skeena rivers, to determine the Annual Allowable Harvest (AAH) of Nass and Skeena stocks in Alaskan fisheries, and to calculate the Alaska catch for these stocks.

Annual stock-specific run reconstructions (catch plus escapements) are required to accurately estimate relative contribution of each stock caught in NBA fisheries (English et al. 2004; Alexander et al. 2010). Estimates of origin of contributing stocks provides the most reliable information currently available to complete these run reconstructions, and are used to evaluate stock-specific productivity and revise pre-season forecasts. While the catch of Nass and Skeena sockeye salmon is only subject to treaty harvest-sharing annexes in the Alaska District 101 gillnet and Alaska District 104 purse seine fisheries, the harvest of these stocks in all fisheries,

and their escapements, is necessary in order to calculate the total run and the percentage caught in the annexed fisheries.

In the past, matched samples collected from these fisheries had been analyzed using scale pattern analysis (SPA). Since 2005, the Alaska Department of Fish and Game (ADF&G) and the NOAA Auke Bay Laboratories (ABL) have conducted GSI to determine the stock composition of NBA fishery harvests. ADF&G and the Department of Fisheries and Oceans Canada (DFO) compared SPA and GSI in limited sample sets from District 101 gillnet samples and found that although the two methods provide similar estimates, GSI analysis was slightly more accurate and was able to discriminate stocks at a finer resolution than SPA (PSC NBTC 2005). After 2010, SPA was discontinued and run reconstructions and subsequent AAH calculations were conducted using GSI only.

This project completes GSI analysis on sockeye salmon tissue samples collected from the 2016 commercial purse seine fisheries in U.S. Districts 101, 102, and 103 in Southeast Alaska. This project is a complement to the ongoing project at ABL for NBA sockeye salmon GSI in Districts 101 and 104 and continuing work by DFO in Areas 3, 4, and 5, and will allow for complete assessment of the catches of Nass and Skeena sockeye salmon in all major NBA fisheries for run reconstructions.

### **Objectives:**

The objective of this project is to estimate the stock composition of Southeast Alaska sockeye seine fisheries in U.S. Districts 101, 102, and 103 in 2016 using genetic stock identification for 4 reporting groups (*Alaska*, *Nass*, *Skeena*, and *Other*) such that the estimates are within 7% of the true value 90% of the time. This will be accomplished by estimating the stock composition of 2016 sockeye harvests for the following:

- District 101 seine: up to 3 time strata;
- District 102 seine: up to 3 time strata; and
- District 103 seine: total season.

### **Approach:**

#### *Fishery Sampling*

Landings from purse seine fisheries were sampled by ADF&G at fish processing facilities in Petersburg and Ketchikan. Sampling protocols ensured that the fish sampled were as representative of catches as possible. Axillary processes were excised and placed onto Whatman filter paper for dry preservation. Associated data for each sample including fishery and capture date were recorded, and the tissue sample for each fish was paired with age, sex, and length (ASL) information.

#### *Laboratory Analysis*

A single nucleotide polymorphism (SNP) baseline for Southeast Alaska (SEAK) and British Columbia (BC) including 45 markers was first completed in 2007. The baseline included all major sockeye salmon-producing systems in SEAK and in BC (north of and including the Skeena River) and from representative sockeye salmon producing systems in BC south of the Skeena River. A cooperative project between ADF&G and Department of Fisheries and Oceans (DFO) Canada in 2007-2009 added several collections to the baseline for transboundary rivers (Northern Fund project no. NF-2008-I-15A). In addition, these and existing collections have

been analyzed at a total of 96 SNP markers in order to further enhance the baseline for fishery applications. The current baseline includes 171 populations and 96 markers (Table 1; Rogers Olive et al. *in prep*).

Samples were analyzed for 96 SNP loci. Genomic DNA was extracted using a NucleoSpin® 96 Tissue Kit by Macherey-Nagel (Düren, Germany). All SNPs were detected using a TaqMAN SNP Genotyping Assay (Applied Biosystems). SNP assays were generally performed using the BioMark 96.96 Dynamic Array (Fluidigm). The data collected was individual genotypes for each locus. Genotype data were stored in an *Oracle* database (*LOKI*) on a network drive maintained by ADF&G computer services. Quality control measures included reanalysis of 8% of each collection for all markers to ensure that genotypes were reproducible and to identify laboratory errors and measure rates of inconsistencies during repeated analyses.

#### *Mixture Analysis*

Mixtures of fish representing catches by statistical week from the U.S. Districts 101, 102 and 103 fisheries were screened for genetic variation at 96 SNPs for a goal of 1,500 samples total. For 2016 fisheries, analysis goals were to provide estimates for 1) District 101, up to 3 time strata; 2) District 102, up to 3 time strata; 3) District 103, total season estimate. Samples were weighted by harvest by statistical week whenever possible, and samples were divided between strata to maximize the number of estimates while still staying within precision and accuracy goals.

The stock composition of fishery mixtures was estimated using the program BAYES (Pella and Masuda 2001). We used reporting groups necessary for NBA harvest sharing agreements: 1) *Alaska*, 2) *Nass*, 3) *Skeena*, and 4) *Other*. We defined prior parameters for each reporting group based on results from the 2015 analysis. We ran five independent Markov Chain Monte Carlo (MCMC) chains of 40,000 iterations with different starting values, then discarding the first 20,000 iterations to remove the influence of the initial start values. Estimates and 90% credibility intervals were tabulated from the combined set of the second half of five 40,000-iteration chains. This procedure was repeated for each fishery mixture, with the goal of estimating the proportion of the mixtures within 7% of the true value 90% of the time (Thompson 1987).

### **Results/Findings:**

#### *Fishery sampling*

In 2016, 3,430 samples were collected from sockeye salmon harvested in the seine fisheries in U.S. Districts 101, 102, and 103, of which 1,611 were selected for analysis (Table 2). In District 101, estimates were provided for 3 distinct temporal strata, in District 102 estimates for 2 distinct temporal strata were provided, and in District 103 one estimate for the entire season was provided.

#### *Laboratory analyses*

Of the samples collected in District 101, 794 samples were genotyped at 96 SNP genetic markers. During quality control procedures a total of 66 fish were reanalyzed at all 96 markers for a total of 6,336 comparisons. The average failure rate for District 101 was 2%. Few inconsistencies were found (1% across all comparisons).

Of the samples collected in District 102, 488 samples were genotyped at 96 SNP genetic markers. During quality control procedures a total of 40 fish were reanalyzed at all 96 markers for a total of 3,840 comparisons. The average failure rate for District 102 was 1%. Few inconsistencies were found (0.4% across all comparisons).

Of the samples collected in District 103, 329 samples were genotyped at 96 SNP genetic markers. During quality control procedures a total of 28 fish were reanalyzed at all 96 markers for a total of 2,688 comparisons. The average failure rate for District 103 was 2%. No inconsistencies were found.

### *Mixture analysis*

Priors for stock composition estimates in BAYES were selected following the methods of Jasper et al. (2012). For U.S. Districts 101 and 102 the results for the first temporal stratum from the respective district harvest in 2015 were used as prior information for the corresponding stratum in 2016. The resulting estimates from each temporal stratum were then used as the prior for the following temporal stratum. The estimated stock composition of the harvest in District 103 for the entire 2015 season was used as prior information for the estimate in 2016.

Mixtures of fish representing catches by statistical week from the Districts 101, 102 and 103 seine fisheries were analyzed. Of the samples extracted and genotyped, genotypes from 1,557 fish were used for GSI. We used the 80% rule (Dann et al. 2009) to exclude individuals missing genotypes for 20% or more of loci to avoid using individuals with poor quality DNA. Stock composition estimates can be found in Figures 1–3.

In District 101, 767 samples were available for analysis after quality control (Table 2). These samples were divided into 3 temporal strata that included: statistical weeks 28-30, weeks 31-31, and weeks 33-34 (Figure 1, Table 3). The *Alaska* reporting group contributed between 31% and 63% to the sample mixtures throughout the 2016 season, followed by the *Skeena* reporting group (18% to 54%). The *Nass* reporting group contributed between 9% and 15% over the course of the entire season, while the *Other* reporting group contributed 7% or in the first 2 strata before decreasing to 2%.

In District 102, 476 samples were available for analysis after quality control (Table 2). These samples were divided into 2 temporal strata that included: statistical weeks 26-30 and statistical weeks 32-33 (Figure 2, Table 4). The *Alaska* reporting group contributed between 69% and 85% to the sample mixtures throughout the 2016 season. The *Nass* reporting group contribution to the sample mixtures was between 2% and 4% throughout the season. The *Skeena* reporting group contributed 12% in both strata while the *Other* reporting group contributed 14% in stratum 1 before decreasing to 2%.

In District 103, 314 were available for analysis after quality control (Table 2). These samples were used to estimate the stock composition of the harvest for the entire season (Figure 3, Table 5). The *Alaska* and *Skeena* reporting groups were the only groups to contribute greater than 5% to the mixture (83% and 12% respectively).

**Evaluation:**

We accomplished the following:

- A total of 3,430 sockeye salmon were sampled from U.S. Districts 101, 102, and 103 seine fisheries during the 2016 season.
- A total of 1,611 samples were assayed for genotypes for the 96 SNP loci in the sockeye salmon baseline, and quality control procedures revealed a low rate of inconsistencies. The genotypes for 767 samples were used for analysis of U.S. District 101, 476 samples for District 102, and 314 for District 103.
- Mixture analyses estimated the contributions of 4 reporting groups to 3 temporal strata in U.S. District 101, 2 temporal strata in District 102, and a full season estimate for District 103.
- Results were provided to the NBTC by mid-December to facilitate run reconstructions.

**Project Products:**

Results from this project have been presented both to ADF&G Commercial Fisheries management staff and to the bilateral PSC Transboundary Technical Committee. A report published in the ADF&G Fishery Data Series is expected in 2017.

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Table 1. Reporting groups and collection locations defined for use in genetic stock identification of sockeye salmon caught in seine fisheries in U.S. Districts 101, 102, and 103 in 2016

Reporting Group	Collection Location	Population	Reporting Group	Collection Location	Population	
<i>Alaska</i>	Bainbridge Lake	1	<i>Alaska</i> (cont.)	Tanada Lake		
	Coghill Lake	2		lower outlet	33	
	Eshamy Lake	3		shore	34	
	Main Bay	4		Tebay River - Outlet	35	
	Miners Lake	5		Tokun Lake	36	
	Bering Lake	6		Tonsina Lake	37	
	Clear Creek at 40 Mile	7		Ahrnklin River	38	
	Eyak Lake			Akwe River	39	
	Hatchery Creek	8		Dangerous River	40	
	Middle Arm	9		East Alsek River	41	
	South beaches	10		Lost/Tahwah Rivers	42	
	Gulkana River			Old Situk River	43	
	Fish Creek	11		Mountain Stream	44	
	East Fork	12		Situk Lake	45	
	Klutina Lake Inlet	13		<i>Other</i>	Blanchard River	46
	Klutina River				Border Slough	47
	Mainstem	14			Klukshu River	48
	Banana Lake	15			Upper Tatshenshini River	49
	Bear Hole	16			Kwatini River	50
Kushtaka Lake	17	Neskataheen Lake	51			
Long Lake weir	18	Tweedsmuir River	52			
Mahlo River	19	Vern Ritchie	53			
Martin Lake	20	<i>Alaska</i> (cont.)	Chilkat Lake		54	
Martin River Slough	21		Chilkat River			
McKinley Lake	22		Mosquito Lake	55		
	23		Bear Flats	56		
	24		Mule Meadows	57		
Salmon Creek - Bremner	25		Chilkoot Lake			
Mendeltna Creek	26		Beaches	58		
Mentasta Lake	27		Bear Creek	59		
Paxson Lake Outlet	28		Chilkoot River	60		
St. Anne Creek	29		Berners Bay	61		
Steamboat Lake - Bremner	30	Lace River	62			
Swede Lake	31	Steep Creek	63			
Tanada Creek weir	32	Windfall Lake	64			

Table 1 (cont.)

Reporting Group	Collection Location	Population	Reporting Group	Collection Location	Population
<i>Alaska</i> (cont.)	Lake Creek	65	<i>Other</i> (cont.)	Fish Creek	101
	Crescent Lake	66		Yehring Creek	102
	Speel Lake	67		Shakes Slough	103
	Snettisham Hatchery	68		Iskut River	104
	Vivid Lake	69		Verrett River	105
	Bartlett River	70		Scud River	106
	North Berg Bay Inlet	71		Andy Smith Slough	107
	Neva Lake	72		Devil's Elbow	108
	Sitkoh Lake	73		Chutine River	109
	Lake Eva	74		Chutine Lake	110
	Kook Lake	75		Christina Lake	111
	Pavlof Lake	76		Tahltan Lake (1990)	112
	Hasselborg Lake	77		Tahltan Lake (2006)	113
		78	<i>Alaska</i> (cont.)	Hugh Smith Lake	114
	Kanalku Lake	79		McDonald Lake	115
	Kutlaku Lake	80		Hatchery Creek	116
	Hoktaheen Lake	81		Kah Sheets Lake	117
	Falls Lake	82		Kunk Lake	118
	Ford Arm Creek	83		Luck Lake	119
	Klag Bay	84		Big Lake	120
	Redfish Lake	85		Mill Creek Weir	121
	Salmon Lake weir	86		Petersburg Lake	122
	Redoubt Lake	87		Red Bay Lake	123
<i>Other</i> (cont.)	Benzeman Lake	88		Salmon Bay Lake	124
	King Salmon Lake	89		Shiple Lake	125
	Little Tatsamenie	90		Thoms Lake	126
	Little Trapper Lake	91		Sarkar Lakes	127
	Kuthai Lake	92		Heckman Lake	128
	Tatsamenie Lake	93		Helm Lake	129
	Hackett River	94		Karta River	130
	Nahlin River	95		Kegan Lake	131
	Tulsequah River	96		Mahoney Creek	132
	Yellow Bluff Slough	97		Unuk River	133
	Sustahine Slough	98		Fillmore Lake	134
	Taku River	99		Klakas Lake	135
	Takwahoni/Sinwa Creek	100		Essowah Lake	136
	Tuskwa/Chunk Slough	100			



Table 1 (cont.)

Reporting Group	Collection Location	Population
<i>Alaska</i> (cont.)	Eek Creek	137
	Middle run	138
	Early run	139
	Hetta Lake	140
	Klawock River	141
<i>Nass</i>	Bowser Lake	142
	Damdochax Creek	143
	Meziadin Lake	144
	Tintina Creek	145
<i>Skeena</i>	Alastair Lake	146
	Four Mile Creek	147
	Fulton River	148
	Kitsumkalum Lake	149
	Lower Tahlo River	150
	McDonell Lake	151
	Nangeese River	152
	Nanika River	153
	Slamgeesh River	154
	Johanson Lake	155
	Swan Lake	156
	Upper Babine River	157
<i>Other</i> (cont.)	Naden River	158
	Kitlope Lake	159
	Baker Lake	160
	Issaquah Creek	161
	Cedar River	162
	Adams River	163
	Birkenhead River	164
	Chilko Lake	165
	Gates Creek	166
	Harrison River	167
	Horsefly River	168
	Raft River	169
	Stellako River	170
	Weaver Creek	171

Table 2. The total number of sockeye salmon harvested from the purse seine fisheries in districts 101, 102, 103 in 2016, the total number of sockeye salmon sampled per statistical week, and the total number genotyped and analyzed for GSI. Note: 3 District 103 samples were missing and were therefore not genotyped.

District	Statistical Weeks	Harvest	Samples	Genotyped	Analyzed
101	28	3,516	260		
	29	5,800	213	200	199
	30	7,211	185		
	31	34,478	260	378	370
	32	21,230	261		
	33	14,366	260	216	198
	34	7,151	260		
102	26	448	135		
	27	725	195		
	28	1,562	269	200	196
	29	3,126	177		
	30	7,898	260		
	31	3,565	0		
	32	27,662	280	288	280
	33	6,816	83		
	34	1,993	0		
	35	102	0		
	36	100	0		
	37	4	0		
	103	30	3,541	80	
31		780	53		
32		7,544	117	329	314
33		4,410	60		
34		363	22		
Total		164,391	3,430	1,611	1,557

Table 3. Estimated stock composition (Proportion), upper and lower bounds of the 90% credibility intervals, the number of fish analyzed for each stratum (n), and standard deviations (SD) for District 101 seine fishery samples collected in 2016.

Reporting Group	Statistical Weeks 28-30 (n = 199) <sup>a</sup>				Statistical Weeks 31-32 (n = 370) <sup>b</sup>				Statistical Weeks 32-33 (n = 198) <sup>c</sup>			
	Proportion	90% CI		SD	Proportion	90% CI		SD	Proportion	90% CI		SD
		Lower	Upper			Lower	Upper			Lower	Upper	
Alaska	0.586	0.525	0.646	0.037	0.598	0.553	0.643	0.027	0.312	0.259	0.368	0.033
Nass	0.158	0.116	0.205	0.027	0.089	0.064	0.116	0.016	0.124	0.087	0.165	0.024
Skeena	0.184	0.138	0.234	0.029	0.247	0.209	0.287	0.023	0.541	0.483	0.599	0.035
Other	0.072	0.038	0.111	0.022	0.066	0.040	0.096	0.017	0.023	0.008	0.045	0.012

<sup>a</sup> Estimated stock proportions from the 2015 District 101 early stratum were used as the prior for this mixture.

<sup>b</sup> Estimated stock proportions from the 2016 District 101 early stratum were used as the prior for this mixture.

<sup>c</sup> Estimated stock proportions from the 2016 District 101 middle stratum were used as the prior for this mixture.

Table 4. Estimated stock composition (Proportion), upper and lower bounds of the 90% credibility intervals, the number of fish analyzed for each stratum (n), and standard deviations (SD) for District 102 seine fishery samples collected in 2016.

Reporting Group	Statistical Weeks 26-30 (n = 196) <sup>a</sup>				Statistical Weeks 32-33 (n = 280) <sup>b</sup>			
	Proportion	90% CI		SD	Proportion	90% CI		SD
		Lower	Upper			Lower	Upper	
Alaska	0.692	0.630	0.752	0.037	0.846	0.807	0.882	0.023
Nass	0.044	0.020	0.073	0.016	0.016	0.005	0.030	0.008
Skeena	0.124	0.086	0.168	0.025	0.120	0.089	0.153	0.020
Other	0.140	0.091	0.194	0.031	0.019	0.002	0.041	0.012

<sup>a</sup> Estimated stock proportions from the 2015 District 102 early stratum were used as the prior for this mixture.

<sup>b</sup> Estimated stock proportions from the 2016 District 102 early stratum were used as the prior for this mixture.

Table 5. Estimated stock composition (Proportion), upper and lower bounds of the 90% credibility intervals, the number of fish analyzed (n), and standard deviations (SD) for District 103 seine fishery samples collected in 2016.

Season Total (n = 314) <sup>a</sup>				
Reporting Group	Proportion	90% CI		SD
		Lower	Upper	
Alaska	0.832	0.796	0.866	0.021
Nass	0.015	0.005	0.028	0.007
Skeena	0.119	0.090	0.151	0.018
Other	0.034	0.018	0.053	0.011

<sup>a</sup> Estimated stock proportions from the 2015 District 103 early stratum were used as the prior for this mixture.

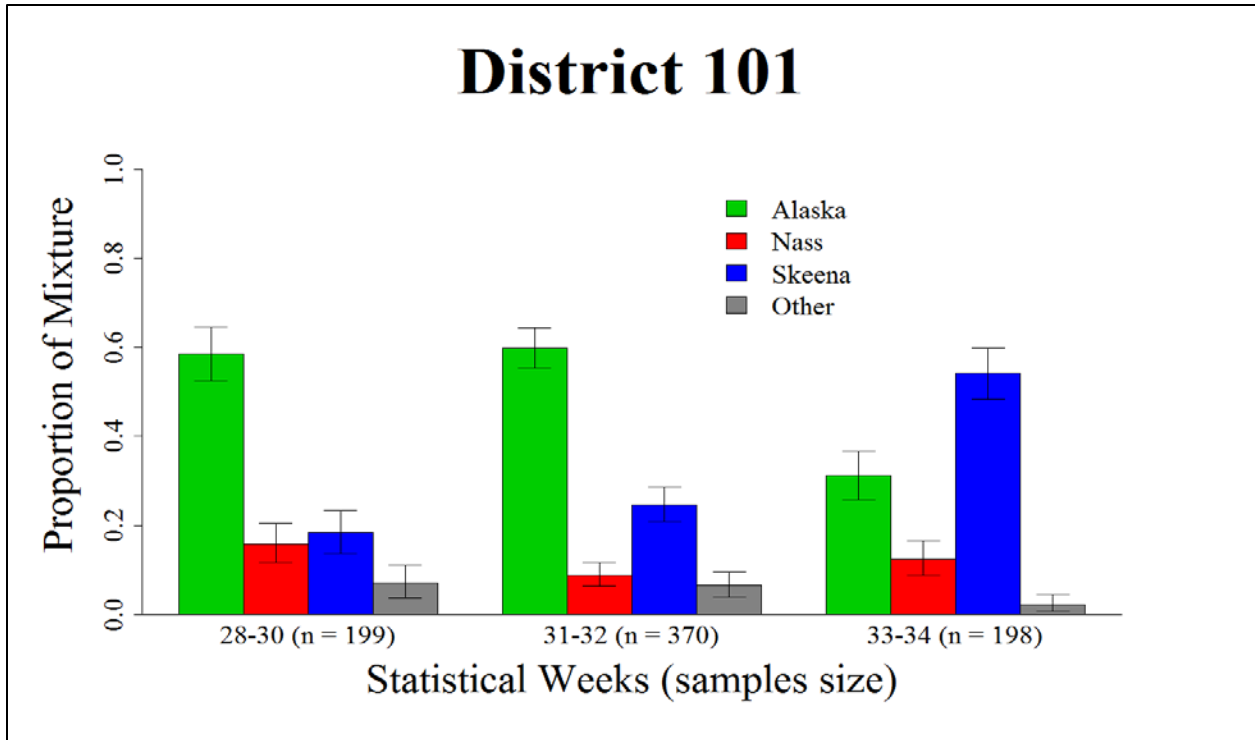


Figure 1. Stock composition estimates of sockeye salmon caught in the District 101 seine fishery in 2016. Error bars are upper and lower bounds of the 90% credibility intervals.

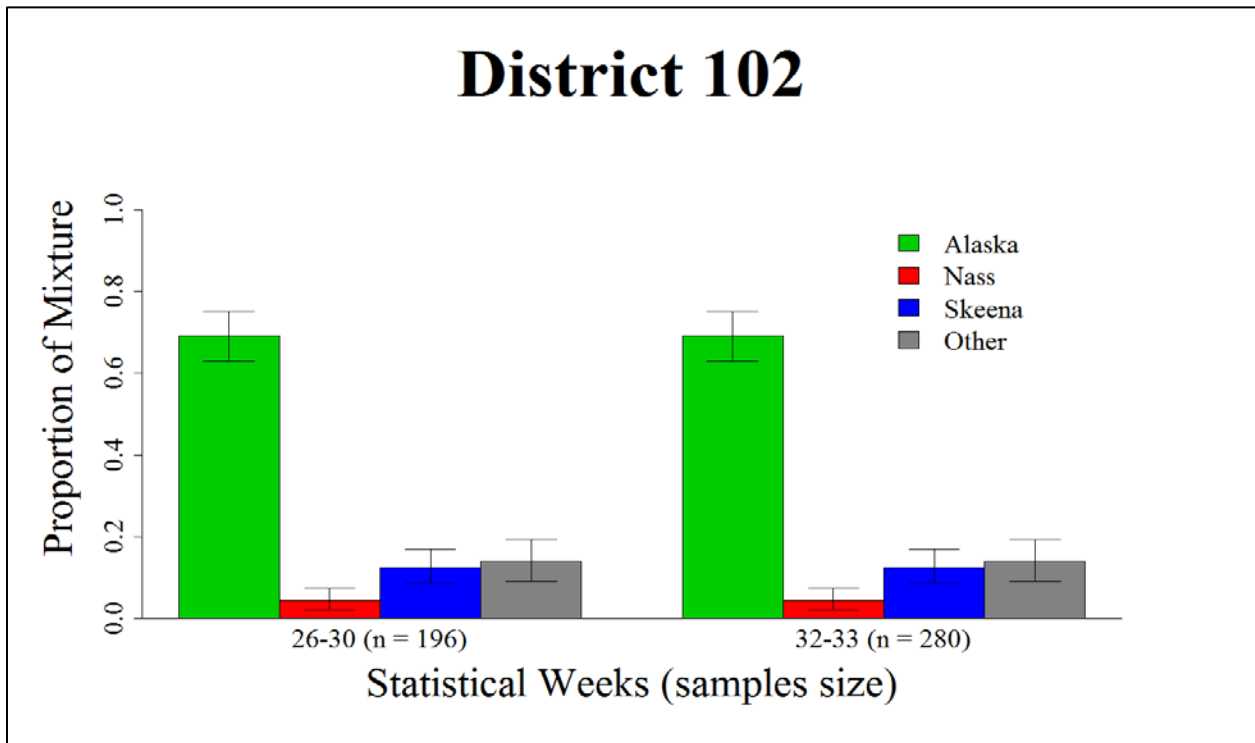


Figure 2. Stock composition estimates of sockeye salmon caught in the District 102 seine fishery in 2016. Error bars are upper and lower bounds of the 90% credibility intervals.

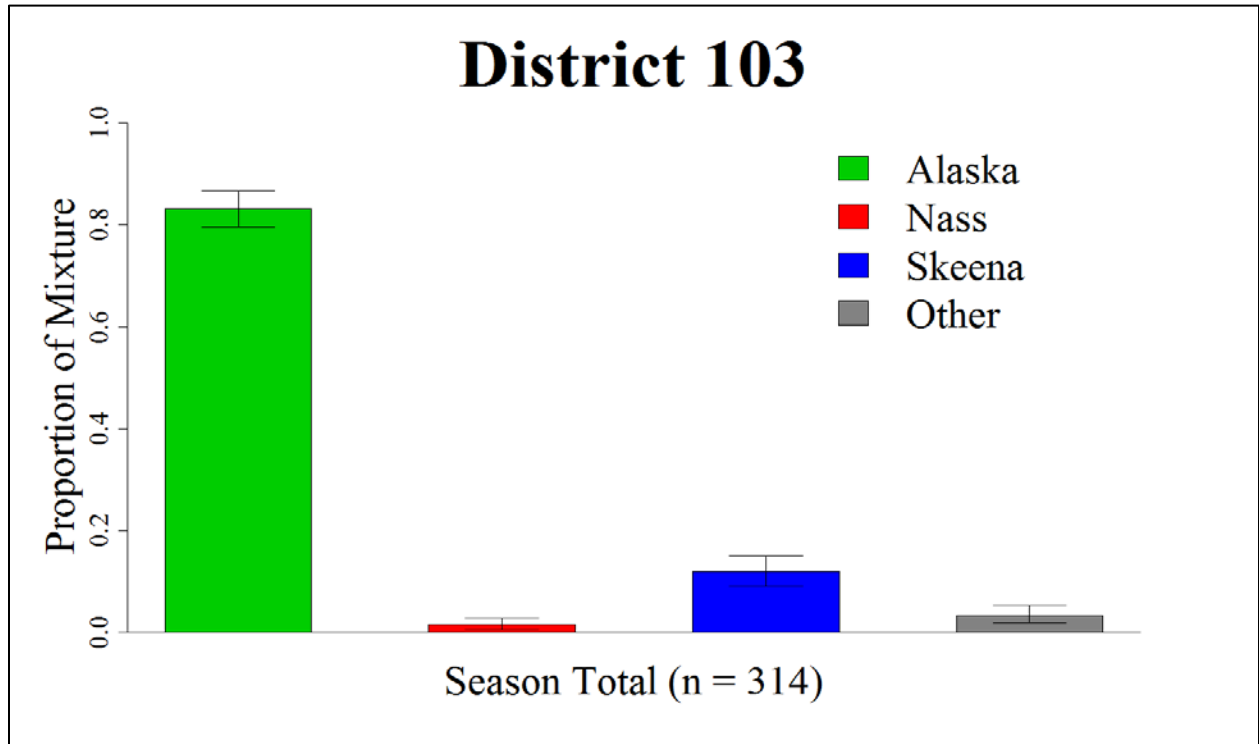


Figure 3. Stock composition estimates of sockeye salmon caught in the District 103 seine fishery in 2016. Error bars are upper and lower bounds of the 90% credibility intervals.