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Love the one you're with: Genomic evidence of panmixia in the sablefish
(*Anoplopoma fimbria*)

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Abstract

Understanding the genetic structure of a fishery may help delineate stocks and is directly applicable to resource management. To date, studies have not found clear population genetic structure across the range of the sablefish (*Anoplopoma fimbria*), yet significant biological differences are recognized. Here we use restriction site associated DNA (RAD) sequencing to develop thousands of single nucleotide polymorphisms (SNPs) throughout the sablefish genome and assess population genetic structure and examine the genome for SNPs under natural selection. Our study was unable to target spawning groups, having the potential to bias analyses that require *a priori* hypotheses of population structure. Low and insignificant levels of differentiation ($F_{ST} = 0.0002$) were observed among survey areas and analyses of population structure suggested a single population. Only two SNPs were significantly associated with environmental variables. These results are likely due to considerable population mixing and suggest a single panmictic group of sablefish off the West Coast of the United States and Alaska that is likely a consequence of a complex juvenile life history and long range movements as adults.

55 Introduction

56 The concept of a stock is central to the conservation and management of marine
57 fisheries (Begg and Waldman 1999). Under the stock concept, managers define semi-
58 discrete boundaries to fish populations in order to make decisions regarding those
59 management units (Begg et al. 1999). Knowledge of genetic structure or an
60 understanding of localized adaptation may help delineate fish stocks and can be
61 extremely relevant in the management of a fishery (Hauser and Carvalho 2008). Many
62 commercially important marine species fall into the category of “classical marine
63 species”, characterized by large geographic distributions and population sizes, high
64 fecundity, and pelagic larvae (Nielsen and Kenchington 2001). Many of these species
65 typically display relatively low levels of genetic differentiation among population
66 groupings; however, significant genetic differentiation has been observed in a number of
67 these species, even at relatively small spatial scales (Nielsen and Kenchington 2001,
68 Nielsen et al. 2009).

69 The sablefish (*Anoplopoma fimbria*) could be considered a “classical marine
70 species” (see Nielsen and Kenchington 2001). It is a long-lived, demersal species found
71 in the northern Pacific Ocean, where it inhabits deep water along the continental slope
72 (Sasaki 1985, Beamish and McFarlane 1988, Beamish et al. 2006). It is found along the
73 west coast of North America from Baja California to the Bering Sea, throughout the
74 Aleutian Islands into waters off the Kamchatka Peninsula, Russia and northern Japan
75 (Sasaki 1985). It is generally accepted that two sablefish stocks exist in the Northeast
76 Pacific Ocean (Hanselman et al. 2012). A northern stock inhabits waters off of the
77 Alaskan Coast and northern British Columbia while a southern stock is found off

southern British Columbia and the West Coast of the contiguous United States (Hanselman et al. 2012). The division of these stocks is primarily based on tagging studies and differences in growth and maturity between fish in these areas (Kimura et al. 1998, Hanselman et al. 2012, Head et al. 2014). Sablefish in the northern stock generally grow to and mature at larger sizes than the fish in the southern stock (Sasaki 1985, Kimura et al. 1993, Head et al. 2014).

The sablefish is a highly mobile species, and there is little known about the timing or location of spawning. It is thought that spawning occurs at depth along the continental slope (Mason et al. 1983) though no specific spawning sites have been documented in the literature. The eggs are pelagic and believed to incubate at depths of about 400 m and descend to depths of 1 000 m or more after hatching (Alderdice et al. 1988, McFarlane and Beamish 1992). During yolk sac absorption the larvae ascend to the surface where they are very abundant in the neuston (Doyle 1992). The development of eggs to 40 mm larvae is estimated to take about 10 weeks in the wild (Boehlert & Yoklavich 1985; Kendall & Matarese 1987). Juvenile sablefish utilize nearshore areas (1-2 years) before they begin to gradually move back out to the slope as they reach maturity (Maloney and Sigler 2008).

While the current paradigm suggests that there are two biological stocks of sablefish in the northeast Pacific Ocean, studies have found evidence of biological differences on a finer geographic scale (Hanselman et al. 2012). For example, stable isotope analysis of otoliths from juvenile sablefish suggests that three spawning stocks may exist from Oregon to Vancouver Island, British Columbia (Gao et al. 2004).

Differences in maturity and growth parameters observed between groups of sablefish

collected off the West Coast of the United States might suggest population differences occur within the southern stock (Head et al. 2014). It has also been suggested that genetic differences may be responsible for the so called “soft flesh problem” observed in sablefish; where fish caught in deeper water generally have softer flesh, less protein content, increased lipid levels and have a less desirable flesh quality when compared to fish harvested from shallower water (Norris et al. 1987, Karinen et al. 2010).

Previous genetic studies have attempted to characterize the population structure of this species (Tsuyuki and Roberts 1969, Gharrett et al. 1982, Tripp-Valdez et al. 2012). These studies suggest that there is little or no genetic structure across large geographic scales; however, they have only examined variation at genetic markers that are presumed to be neutral to the effects of natural selection, such as microsatellites. While useful in examining demographic processes, care should be taken when interpreting low or insignificant values of genetic differentiation derived from neutral markers in marine populations as these estimates may not accurately represent contemporary patterns of stock structure in such large populations (Allendorf and Phelps 1981, Conover et al. 2006). Large population sizes typical of many marine species make them less susceptible to the effects of genetic drift; therefore, apparent genetic homogeneity may persist at neutral genes even at low levels of migration (Allendorf and Phelps 1981, Nielsen et al. 2009). Given that large populations are less susceptible to drift, beneficial alleles are less likely to be lost though drift and may respond to relatively weak selection pressure in marine fish species (Nielsen et al. 2009). Also, many more migrants are needed to effectively counteract the effects of natural selection than are required to maintain genetic homogeneity in the face of genetic drift (Conover et al. 2006). So, while neutral markers

may fail to show any patterns of significant differentiation, significant adaptive variation may persist (Conover et al. 2006, Larsen et al. 2007, Hauser and Carvalho 2008). In species such as the sablefish that have large geographic ranges and large population sizes, apparent genetic homogeneity may be observed as a result of low levels of genetic drift even when migration rates are low. In this scenario, genes subject to natural selection may offer more power to distinguish stocks over loci that are presumed to be selectively neutral and by incorporating non-neutral genes it may be possible to more accurately assess the genetic structure of sablefish stocks.

The emerging field of landscape genomics provides a framework to examine the association between environmental variables and genomic variation in wild populations. Schwartz *et al.* (2010) refers to landscape genomics as "...the simultaneous study of tens-to-hundreds of markers, ideally including markers in candidate adaptive genes (genes under selection), with georeferenced samples collected across a landscape". While approaches like this are not particularly abundant in the literature on classical marine fishes, they have been successfully applied to analyses of local adaptation and population structure in other fishes such as salmon (Zueva et al. 2014), and other organisms such as trees (Bashalkhanov et al. 2013, Frichot et al. 2013, Sork et al. 2013), plants (Bothwell *et al.* 2013; Jones *et al.* 2013) goats (Pariset et al. 2009) and humans (Frichot et al. 2013).

Here, restriction site associated DNA sequencing (RAD-seq) was used to obtain single nucleotide polymorphism (SNP) markers that were used to 1) test the null hypothesis of genetic homogeneity of sablefish collections from the Bering Sea, Gulf of Alaska, and the West Coast of the U.S., using traditional population genetic analyses, 2) investigate the possibility of cryptic population structure using individual based genetic

methods; and 3) test for signatures of natural selection in the sablefish genome by associating SNP genotypes with environmental conditions. Lack of information on the location and timing of sablefish spawning meant that groups of spawning fish were not specifically targeted during sampling, posing limitations on *a priori* hypotheses regarding population boundaries. Therefore, this should be considered when interpreting the results.

Materials and Methods

Sample Collection

Fin clips were collected and stored in 95% ethanol as a part of the National Oceanic and Atmospheric Administration's National Marine Fisheries Service (NOAA, NMFS) surveys in the summer of 2012. The Fishery Resource Analysis and Monitoring (FRAM) Division at NOAA's Northwest Fisheries Science Center (NWFSC) collected fin clips (n=600) during their annual U.S West Coast Groundfish Bottom Trawl Survey. As part of their annual longline survey, the Marine Ecology and Stock Assessment (MESA) Division of NOAA's Alaska Fisheries Science Center (AFSC) collected fin clips (n=1 929) from the Gulf of Alaska. The Resource Assessment and Conservation Engineering Division (RACE) at AFSC collected fin clips (n=140) from sablefish opportunistically encountered as part of their trawl survey of the Bering Sea Slope. In addition to fin clips, biological data were collected for each sample as well including length, weight, sex, and maturity (FRAM and MESA). The three major regions (West Coast, Gulf of Alaska, Bering Sea) covered by the surveys, were further divided into eleven sub-regions to provide a means to choose samples evenly across the study area (Figure 1).

In order to restrict the genetic analysis to fish at a similar life stage we used maturity data to select individuals that were likely to be adults. The data from the macroscopic assessment of maturity status at the time of sampling could not be used because maturity data were not collected on fish caught in the Bering Sea. While a number of studies have been conducted on size at maturity in sablefish, the results are variable and nearly all of the data are over 25 years old and focus on localized groups of fish off the West Coast of the U.S (Parks and Shaw 1987, Fujiwara and Hankin 1988, Hunter et al. 1989) and British Columbia (Mason et al. 1983, McFarlane and Beamish 1990). While more current estimates of size at maturity are available for females off the West Coast of the U.S., no estimates are available for males (Head et al. 2014). Therefore, to generate a criterion by which mature fish could be subsampled with reasonable confidence over this study area, data on maturity status for the fish collected in the Gulf of Alaska and West Coast were pooled and logistic regressions were fit separately for males and females to determine the length at 50% probability of maturity (L_{50}) (Figure S1). Only fish above the size thresholds set by L_{50} were considered for genetic analysis. A logistic regression model (GLM, R version 3.1.2) was fit to the data to estimate the parameters of the equation where the probability of being mature (P) was calculated by:

$$(1) \quad P = \frac{e^{\beta_0 + \beta_1 X}}{1 + e^{\beta_0 + \beta_1 X}}$$

where X is length and β_0 and β_1 are regression coefficients (Quinn and Deriso 1999). The inflection point of the L_{50} was calculated by:

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200 *Genomic Library Construction*

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Q800R DNA Sonicator (QSonica, LLC, Newtown, CT). Gel electrophoresis was used to identify and cut out DNA fragments that were 300-500 bp in length for single end libraries and 200-400, 400-600, 600-900 bp for paired end. Illumina P2 adapters were then blunt-end ligated to the other end of the DNA fragments. Libraries were quantified via qPCR using Kapa Biosystems, Kapa Illumina library quantification kit (Kapa Biosystems Inc, Woburn, MA, USA) on an ABI 7900 real time PCR system (Life Technologies, Carlsbad, CA). Four libraries were pooled in equimolar concentrations prior to sequencing.

Single end sequencing libraries consisting of samples digested with the restriction endonuclease *SbfI* were sequenced on an Illumina HiSeq 2500 (Illumina, San Diego, CA) for read lengths of 100 bp. Individuals were pooled into a single lane of 48 samples for the single end runs. Paired end sequencing was done on a library of 4 individuals digested with *PstI* on the Illumina HiSeq 2500 for read lengths of 100 bp in a single lane and a single library of 10 individuals digested with *PstI* on an Illumina MiSeq for read lengths of 250 bp.

Processing Sequence Reads

FastQC (Andrews 2012) was used to assess the quality of each Illumina sequencing run. The raw sequence reads were de-multiplexed, quality filtered and trimmed using *process_radtags* in *Stacks* (version 1.21) (Catchen et al. 2011, 2013). The sequence reads were trimmed to 75 bp (-t 75) during de-multiplexing to remove poor quality base calls at the end of each sequence read. Reads with low quality scores (-q) and any uncalled bases were removed (-c). The default sliding window parameter (-w) of 0.15 was used in *process_radtags* when evaluating read quality scores. Bowtie (version

1.0.0) (Langmead et al. 2009) was used to align sequence reads from each individual to the sablefish draft genome (GenBank: AWGY000000000.1) and mitogenome (NCBI RefSeq: NC_018119.1) (Rondeau et al. 2013). Up to three mismatches were allowed when aligning reads to the genome and reads with more than one valid alignment were discarded. The *Stacks* program *pstacks* was used to form loci from stacks of sequence reads within individuals. A minimum of five reads was required to form a stack at a locus. The bounded SNP calling model implemented in *pstacks* was used (upper bound: 0.1, lower bound: 0.001, α : 0.05). Eleven individuals were then selected at random from each of the 11 geographic sub-regions (Figure 1) to create a catalog of reference loci in the *Stacks* program *cstacks*. The *Stacks* program *sstacks* was then used to match loci in each individual back to the catalog of reference loci. The program *populations* was used to export a Variant Call Format (VCF) file (Danecek et al. 2011) containing the genotype information for all individuals. *populations* was used to process and export RAD tags within individuals that have minimum stack depth of eight reads for further analyses.

SNP Quality Filtering

First, to restrict the analyses to nuclear SNPs, all RAD loci in the mitochondrial genome were removed from further analysis. Next, RAD tags were culled from further filtering if they contained more than three SNPs. The program *VCFTools* (v0.1.12) (Danecek et al. 2011) was then used to filter out loci with a global minor allele frequency (MAF) less than 0.05 and with more than 20% missing data. Individuals were then removed from further analyses if they were missing genotypes at more than 40% of the filtered loci. For tags that contained more than one SNP, only the SNP with the highest minor allele frequency was retained. Linkage disequilibrium was assessed by calculating

the r^2 statistic between each pair of SNPs using the program *Plink* (v1.07) (Purcell et al. 2007). In cases where $r^2 > 0.8$, the SNP with more missing data was culled from the dataset. Exact tests for Hardy-Weinberg equilibrium (HWE) were conducted in *VCFTools* and SNPs that were out of HWE in any one population (West Coast, Bering Sea, Gulf of Alaska) were removed in all populations prior to conducting analyses that required population groups to be defined *a priori*.

Population Structure

To assess the genetic structure of sablefish across their sampled range, we combined the use of traditional population genetic techniques with individual based analyses that may be better suited when individuals are sampled across a landscape (Jones et al. 2013). We pooled individuals into population groups defined by the survey on which they were collected (West Coast: FRAM, Gulf of Alaska: MESA, Bering Sea: RACE). Levels of expected heterozygosity were calculated in *VCFTools* for each population and F_{IS} was calculated for each SNP both globally and in each survey area. Fisher's exact test as implemented in *Genepop* v4.2.2 (Rousset 2008) was used to test for differences in allele frequency between survey areas. Markov chain parameters of 10 000 dememorization steps, 100 batches and 5 000 iterations per batch were used for the exact test in *Genepop*. *POWSIM* (Ryman and Palm 2006) was used to assess the statistical power of this dataset to detect differences in allele frequency between survey areas at known levels of genetic divergence or F_{ST} for both the global and pairwise tests. Twenty five replicate runs were used with the same Markov chain parameters as *Genepop*. The number of samples selected from each population at the end of the drift simulations was defined by the sample sizes of each area in the filtered SNP dataset used

for this study. A version of *POWSIM* was specifically compiled to accommodate the size of this dataset (Ryman and Palm 2006). *Genepop* was also used to test for differences in genotype frequency between the survey areas using the same Markov chain parameters used to test for differences in allele frequency. F_{ST} (Weir and Cockerham 1984) was estimated globally and between all group pairs using *Genepop*. The R package *StAMPP* (Pembleton et al. 2013) was used to test for significance of the pairwise F_{ST} values obtained in *Genepop*. *StAMPP* was chosen because it also estimates F_{ST} using the method of Weir & Cockerham (1984) and is comparable to *Genepop*. Individuals were randomized among groups for 1 000 permutations and a p value was obtained by converting the simulated values to an object of the class *randtest* in the R package *ade4* (Chessel et al. 2004).

Isolation by distance (IBD) was evaluated by calculating Rousset's $\hat{a}$ (Rousset 2000) between individuals in *SPAGeDi* v1.4 (Hardy and Vekemans 2002). Geographic distance between individuals was calculated as great-circle distance in the *fields* package in R (Nychka et al. 2014). Distance between individuals along the 500 m isobath was also estimated using the R package *gdistance* to route individuals between sample locations along the 500 m isobath (van Etten 2014). Significance of IBD relationships were assessed by Mantel's test with 1 000 permutations implemented in R using the *vegan* package (Oksanen et al. 2013). Values of great circle distance were log transformed prior to analysis to account for the possibility of dispersal in two dimensions, while distances along the 500 m isobath were not because under that dispersal scenario, it is assumed to take place in one dimension (Rousset 1997).

To investigate the possibility of cryptic population genetic structure we used a

combination of methods that do not rely on predefined population groupings. First, the program *SmartPCA* in the software package *Eigensoft* v5.0.2 was used to perform principal components analysis of the genotype data (Patterson et al. 2006). Default outlier removal parameters were used in *SmartPCA* ($> |6\sigma|$ on one of the top 10 PCs, 10 iterations). Principal components analysis (PCA) was used because it does not rely on any underlying population genetic models and does not attempt to group individuals into discrete populations (Patterson et al. 2006). Individuals are placed along axes of variation (principal components) and once plotted, a decomposition of the genetic structure from the entire set of SNPs can be visualized (Patterson et al. 2006). The spatial clustering algorithm implemented in *BAPS* v6 was also used to examine population genetic structure (Corander et al. 2008). Unlike PCA, *BAPS* uses a model that attempts to minimize linkage and Hardy-Weinberg disequilibrium within groups of samples while also incorporating spatial information to improve the partitioning of individuals into biologically meaningful groups (Latch et al. 2006, Corander et al. 2008). Partitions of one to 30 groups were tested in *BAPS*.

Landscape Genomics

Environmental Variables

The samples obtained for this study were collected using bottom contact fishing methods; thus, depth of capture for each individual was extracted from the gebco_08 30 arc second grid bathymetry data (IOC, IHO & BDOC 2003) using the GPS location of each individual in *QGIS* (QGIS Development Team 2009). Environmental conditions at the sampling location of each individual were estimated using salinity and temperature profiles collected by the Argo profiling float network. These data were collected and are

made freely available by the International Argo Program and the national programs that contribute to it (<http://www.argo.ucsd.edu>, <http://argo.jcommops.org>). The Argo Program is part of the Global Ocean Observing System. Argo data from the time period that the samples were collected (03/01/2012 – 10/31/2012) were obtained from the Coriolis project's webserver (<http://www.coriolis.eu.org>). Temperature and salinity were estimated using the sampling location and bottom depth for each individual using the computer program *Ocean Data View* v4.6.2 (Schlitzer 2014). To reduce collinearity among the environmental variables, Pearson's correlation coefficient (r) was calculated between each pair of variables in *R* (R Development Core Team 2013) and if a pair of variables were correlated with an $|r| > 0.8$, one variable was removed from the association analyses.

Association Analyses

Latent factor mixed models implemented in *LFMM* (Frichot et al. 2013) were used to test for genotype – environment associations. *LFMM* has been shown to reduce the number of false positives in association studies by accounting for population history including patterns of isolation by distance (Jones et al. 2013). Population structure is modeled using unobserved variables or “latent factors” (Frichot et al. 2013). We chose to use a single latent factor (k) because our analyses suggested the existence of a single cluster. *LFMM*'s Gibbs sampler was set to estimate model parameters using 10 000 sampling iterations with 1 000 iterations discarded as burn-in. The *LFMM* results did not change over replicate runs for the same variable so we determined that the Gibbs sampler was run long enough. P values obtained in *LFMM* were adjusted for a false discovery rate (FDR) of 0.05 by calculating q values (Storey and Tibshirani 2003) in the *R* package

q-value (Dabney and Storey 2014).

Gene Annotation

Single nucleotide polymorphisms with a significant association to an environmental variable were annotated by using Ensembl's BLASTN search tool (http://www.ensembl.org/Gasterosteus_aculeatus/Tools/Blast?db=core) to align the full contig sequence from the sablefish genome assembly (Rondeau et al. 2013) containing the SNP/RAD tag of interest to release 78 of the stickleback (*Gasterosteus aculeatus*) BROAD S1 genome (Kersey et al. 2014). An E-value of $< 1e^{-03}$ was used as a cutoff to identify valid alignments. The alignments were then viewed using the BROAD S1 genome browser in Ensembl (Kersey et al. 2014). While the raw sequence reads were aligned to contigs from the sablefish draft genome, those contigs are not annotated. The stickleback genome was chosen because it is fully annotated and stickleback are the most closely related species to the sablefish for which a complete genome is available (Rondeau et al. 2013). It is thought that the divergence of sablefish and stickleback lineages occurred less than 150 mya and possibly as recent as 50 mya (Rondeau et al. 2013). A high degree of synteny between stickleback and sablefish chromosomes is also observed (Rondeau et al. 2013).

Results

Sequencing

There were on average 145 960 310 reads per lane for the Illumina HiSeq runs. On average we were able to recover 80% of the barcoded reads per lane with 3 274 890 reads per individual. On average, 65% of the reads for each individual aligned to the draft genome unambiguously, 16% of the reads had more than 1 valid alignment and

were discarded, and 19% failed to align altogether. The *Stacks* pipeline produced 100 317 SNPs in 29 242 tags and after SNP quality filtering (see Methods) in *VCFtools* and *Plink*, the final dataset consisted of 2 661 SNPs in 404 individuals (West Coast: 117, Gulf of Alaska: 217, Bering Sea: 70). While 441 individuals were submitted for sequencing, 37 were removed due to missing data, leaving 404 individuals for subsequent analyses.

Population Structure

For analyses that required *a priori* population groupings (West Coast, Gulf of Alaska, Bering Sea), a number of SNP loci (624) were found to be out of HWE and were filtered prior to any population genetic analyses, for a total of 2 037 SNPs. The removal of SNPs from the data set that were out of HWE brought the mean F_{IS} across loci closer to 0 both globally and for all population groups (Table S1, Figure S2). Differentiation among groups was very low (global $F_{ST} = 0.0002$). Pairwise estimates of F_{ST} between the three survey areas were all 0.0002 (Table 1) and non-significant. No significant differences in genotype frequencies were detected between any population pairs (BS – GOA; $P = 1.0$, GOA – WC: $P = 0.999$, BS – WC: $P = 0.889$). The simulations conducted in *POWSIM* revealed that statistical power was not sufficient at the levels of differentiation (F_{ST}) observed to identify differences in allele frequency between population pairs using Fisher's exact test (Table 2).

A small number of individuals had very low estimates of genetic distance ($\hat{a} < 0.4$) between them (Figure 2 a & b). These were considered to be outliers and all comparisons with those samples were removed from the analysis. A number of samples were collected within 1 km from another sample and multiple samples were collected at many of the sampling stations yielding a distance of 0 km for those comparisons. To

successfully log transform distance measures of 0 km and produce positive values for comparisons of samples collected within 1 km of each other, a constant of 1 km was added to each measurement of great circle distance. The relationship between genetic ($\hat{a}$) and geographic distance between individuals was non-significant for all tests prior to outlier removal ($\log(\text{great circle} + 1 \text{ km})$; Mantel's $R = 0.007$, $P = 0.181$, distance along 500 m isobath; Mantel's $R = -0.016$, $P = 0.846$) and after ($\log(\text{great circle} + 1 \text{ km})$; Mantel's $R = 0.005$, $P = 0.293$, distance along 500 m isobath; Mantel's $R = -0.016$, $P = 0.847$), suggesting that there is no pattern of isolation by distance in sablefish (Figure 2).

Results from the Bayesian clustering analysis and PCA did not identify genetic groups defined by geographic region or reveal any cryptic patterns of population genetic structure. Seven samples were more than six standard deviations along one of the first 10 principal components and flagged as outliers by *SmartPCA*. These samples were excluded from the PCA as a result. The first principal component explains a very small proportion of the total variation (0.73 %). When individuals were plotted on the first two principal component axes calculated from the SNP dataset in *SmartPCA*, there was considerable overlap amongst the sampling regions suggestive of little to no differentiation between the survey areas (Figure 3). There was no clear geographic pattern to the placement of individuals along the PCA axes. Similarly, a single group was also identified by *BAPS*.

Environmental Associations

Of the five environmental variables selected for this analysis, salinity and depth were correlated with one another (Pearson's $r > |0.8|$). Salinity was subsequently excluded from further analyses because it was estimated from the Argo float profile data

and not directly measured. After p values were adjusted for multiple testing, the latent factor mixed models implemented in *LFMM* detected two significant SNP associations with depth (Table 3). These SNPs were contained in RAD tags 9124 and 12048 (Table 3).

Gene Annotation

Each of the sablefish genome contigs containing the SNPs associated with depth in this study were successfully aligned to the stickleback genome. The sablefish contig 152341 (GenBank: AWGY01151885.1) containing the SNP in RAD tag 9124, aligned to the stickleback linkage group XX (Table S2). The contig did not align continuously to this region but many fragments aligned in order with gaps between them. While the portion of the contig containing the SNP (bp 11 333) did not align directly to the stickleback genome, based on the order of the contig segments that did align, the SNP is presumably part of an intron of the ETS translocation variant 1 (*etv1*) gene (Ensembl ID: ENSGACG00000012802.1). The alignment was similar for sablefish contig 133848 (GenBank: AWGY01133477.1). A number of fragments aligned in order to stickleback linkage group VI (Table S3). Based on the alignment order of the fragments, this SNP (bp 4 995) occurs in an intron of the gene that codes for the FAM196ab protein (*fam196ab-201*) (Ensembl ID: ENSGACG00000009611.1).

Discussion

Using thousands of SNP markers throughout the sablefish genome, we were unable to find evidence that would suggest there are genetically distinct populations of sablefish within their North American range. While the current paradigm for sablefish

stock structure suggests the existence of northern and southern biological stocks, results from population genetic and individual based genetic analyses in this study are suggestive of a single genetic group across the North American range of the sablefish. This suggests random mating of individuals across the sablefish range and this pattern of population genetic structure is often referred to as panmixia. The estimates of F_{ST} observed in this study are well below the level required to maintain similar allele frequencies between populations ($F_{ST} < 0.02$) (Lowe and Allendorf 2010). Further results from our analysis of isolation by distance and individual based genetic analyses were also suggestive of panmixia. A non-significant relationship was observed between genetic and geographic distance and genetic groupings were not identified by the PCA or *BAPS* suggesting that dispersal may occur over large spatial scales or gene flow occurs between distant areas. Also, very few SNPs were associated with the environmental variables examined in this study. While this suggests that there is essentially no selective pressure associated with geography or the environmental conditions used in this study, it could also be an artifact of high levels of gene flow throughout the northeast Pacific that homogenizes adaptive variation brought about by selection at earlier life stages.

The extensive movements that characterize sablefish life history offer one explanation for the apparent genetic homogeneity and lack of adaptive variation observed in this study. Sablefish undergo a pelagic larval period and utilize nearshore areas as juveniles for a number of years before they move back to deep water habitat on the continental slope (Sasaki 1985, Maloney and Sigler 2008). To our knowledge there are no studies that have examined the capacity for natal homing in this species, so the location where an individual migrates back to the slope could be very far from where it

was conceived. Tagging data also demonstrates that both juvenile and adult sablefish (McFarlane and Saunders 1993, Maloney and Sigler 2008) have the capacity for frequent long distance movements, often moving over 200 km in a single year (Kimura et al. 1998, Morita et al. 2012, Hanselman et al. 2015). This, coupled with relatively long lifespans where individuals can exceed 40 years old (Kimura et al. 1993, Maloney 2004, Head et al. 2014) provide ample opportunities for gene flow to occur.

While the lack of significant SNP-environment associations could indicate that the environmental conditions examined in this study have little selective influence on the genome in adult sablefish, it may also provide further support for the idea that extensive gene flow is occurring. As migration and subsequent gene flow occur, potentially adaptive alleles are transferred among populations or geographically distant areas. In cases where migration rate is large relative to the strength of selection and the strength of selection for alternate alleles varies spatially, locally adaptive alleles are easily lost. Often, alleles with the best average reproductive success become fixed in the metapopulation, preventing local adaptation (Lenormand 2002). This phenomenon is termed gene-swamping (Lenormand 2002) or patch-swamping (Felsenstein 2015). Movement throughout the entire lifecycle of the sablefish must be considered when interpreting these results. For example, if the environment imposes natural selection at earlier life stages (e.g. during larval development, recruitment, or when juvenile sablefish are in nearshore areas), environmental conditions associated with the sampling location of adult fish may not capture this selective signal, especially if migration and dispersal distances are long.

In the case of the sablefish, regional differences in life history (growth and maturity) have been clearly demonstrated by a number of studies (Kimura et al. 1993, 1998, Echave et al. 2012, Head et al. 2014). While previous genetics studies including the data presented here, suggest a lack a genetic structure (Gharrett et al. 1982, Tripp-Valdez et al. 2012, Orlova et al. 2014), an interesting question that arises is how can regional biological differences be observed when migration rates are high enough that genetic variation is effectively homogenized? Phenotypic plasticity offers one explanation for this phenomenon. Phenotypic plasticity is the ability for similar genotypes to display different phenotypes in response to variable environmental conditions. Latitudinal variation in growth and size at first sexual maturity has been documented in other marine fish species in the northeast Pacific Ocean as well. Pacific cod (*Gadus macrocephalus*) (Ormseth and Norcross 2009), dover sole (*Microstomus pacificus*) (Abookire and Macewicz 2003) and a number of rockfish species (*Sebastes spp.*) (Haldorson and Love 1991, Gertseva et al. 2010), all exhibit some degree of latitudinal variation in growth and size at maturity. While, some of these species are not necessarily considered panmictic (Stepien 1999, Cunningham et al. 2009, Spies 2012), the observation of geographic variation in life history parameters when genetic evidence supports panmixia is not unique to sablefish. Genetic evidence suggests a single coastal population of yelloweye rockfish (*Sebastes ruberrimus*) from Alaska to Oregon (Siegle et al. 2013) yet growth and maturity parameters vary within this area (Wallace 2001, O'Connell et al. 2003). This pattern has been observed in commercially important marine fishes in other oceans as well including Greenland halibut (*Reinhardtius hippoglossoides*) in the northwest Atlantic (Bowering 1983, Morgan and Bowering 1997,

Roy et al. 2014), orange roughy (*Hoplostethus atlanticus*) within different ocean basins though out their range (Branch 2001, White et al. 2009, Varela et al. 2013), and the red snapper (*Lutjanus campechanus*) in the Gulf of Mexico (Gold et al. 2001, Fischer et al. 2004, Saari et al. 2014).

Phenotypic plasticity may help explain the differences in growth and maturity observed in sablefish stocks across their range. In the absence of data that would suggest there is a genetic component to the regional differences in life history parameters observed in sablefish, it is certainly possible that environmental conditions cause these differences. Laboratory studies suggest that sablefish growth is tightly coupled to environmental conditions where physiological limits to maximum growth are often imposed by temperature or available food sources (Sogard and Olla 2001, 2002, Sogard and Spencer 2004). The differences in oceanographic conditions between the West Coast of the U.S. and Alaska (Huyer 1983, Ware and Thomson 2005), may influence ecosystem productivity and the quantity and quality of the food that is available to young sablefish in different regions (Hooff and Peterson 2006, Kudela et al. 2008). In the wild, Sogard (2011) found that growth is negatively correlated with the Pacific Decadal Oscillation (PDO) index, suggesting that cooler conditions actually improve growth. After adjusting growth rate for temperature and size, juvenile sablefish actually tended to grow better during cooler years (Sogard 2011). This is likely a function of better quality food sources and improved foraging opportunities provided by cooler conditions during negative PDO regimes (Hooff and Peterson 2006, Sogard 2011). While these studies focus on the southern sablefish stock, Alaskan waters (Stabeno et al. 2004, Ware and Thomson 2005) and those off Washington and Oregon (Hooff and Peterson 2006, Kudela et al. 2008) may

be more productive in general and support the high levels of consumption required for the fast growth of juvenile sablefish. Juvenile sablefish in St. John Baptist Bay, Alaska have been observed foraging on salmon carcasses and this seasonally abundant and high-energy food source may improve sablefish growth in these areas (Coutr et al. 2015). The regional differences in environmental conditions experienced by sablefish especially at early life stages may alter the rate of adult growth and timing of first maturation (Berrigan and Charnov 1994). More surplus energy may be available for growth at higher latitudes and this could be why the regional differences in sablefish growth and maturity exist in the absence of genetic differentiation.

In summary, the lack of genetic structure observed in this study supports past genetic work and is not surprising when viewed in light of tagging data that suggests that these fish move frequently and over long distances (Kimura et al. 1998, Maloney and Sigler 2008, Morita et al. 2012, Hanselman et al. 2015). High annual movement probabilities (Kimura et al. 1998, Morita et al. 2012, Hanselman et al. 2015) combined with a relatively long lifespan (Kimura et al. 1993, Head et al. 2014) provide ample opportunity for gene flow and the data we present here are consistent with panmixia. Interestingly the levels of differentiation observed here are similar to those described for two species known to be panmictic, the European eel (*Anguilla anguilla*) ($F_{ST} \sim 0.0007$ Als et al. 2011; Pujolar et al. 2014) and American eel (*Anguilla rostrata*) ($F_{ST} \sim 0.00009$ Ct et al. 2013). However, it is important to keep in mind that while the life history characteristics of sablefish may provide one possible explanation for the apparent genetic homogeneity we observe, the study of differentiation among known spawning populations of sablefish is difficult because there is little data available on the specific location or time of

spawning for this species. As a result, the sample collections made for this study were unable to target spawning groups of sablefish. This has the potential to influence the results of population genetic analyses in particular, as a priori hypotheses of population structure are restricted to where the fish were sampled, and not potentially where they were spawned. Although it is important to recognize that while we cannot prove that panmixia exists by simply failing to reject our null hypothesis of genetic homogeneity (discussed in Gold & Richardson 1998; Heist & Gold 2000; Gold et al. 2001), the results we present here are suggestive of considerable mixing of fish between the areas sampled for this study outside of the reproductive season. While our study failed to uncover spatial genetic structure or signals of natural selection in the genome, further studies that investigate temporal changes in these population genetic parameters or studies that examine selection at early life stages may provide a more complete understanding of the genetic structure of this species.

Data Accessibility

Sequence reads for this project have been deposited in the NCBI Sequence Read Archive (BioProject ID: PRJNA279314).

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Figure 1. Map locations of sablefish samples used for RAD sequencing in this study. Survey areas are shaded (red = Bering Sea: Northern Bering Sea, Southern Bering Sea, yellow = Gulf of Alaska: Aleutian Islands, Western Gulf of Alaska, Central Gulf of Alaska, West Yakutat, East Yakutat, green = West Coast of the U.S.: Washington, Oregon, Northern California, Southern California). Black diamonds represent female fish and white circles are males. Image reproduced from the GEBCO world map 2008, www.gebco.net.

Figure 1
129x82mm (300 x 300 DPI)

Figure 2. Patterns of isolation by distance for sablefish in the northeast Pacific Ocean. Pairwise genetic distance between individuals ($\hat{a}$) is plotted against geographic distance calculated as log of great circle distance + 1 km (a) and distance along the 500 m isobath (b) before removing individuals identified as outliers. Relationship between log of great circle distance + 1 km (c) and distance along the 500 m isobath (d) after outliers were removed.

Figure 2

215x229mm (300 x 300 DPI)

Figure 3. Plot of the first two principal component axes in a principal component analysis of 2661 RAD-seq derived SNPs. Points are colored by the area (yellow square = Bering Sea, red triangle = Gulf of Alaska, blue square = West Coast) that each individual was collected. Lines represent 95% confidence ellipses calculated using the R package, vegan (Oksanen et al. 2013) for each group

Figure 3
136x86mm (300 x 300 DPI)

- 1 Table 1. Table of F_{ST} estimates for each pair of survey groups. F_{ST} below diagonal and p-
2 values above.

	Bering Sea	Gulf of AK	West Coast
Bering Sea	-	0.1199	0.0889
Gulf of AK	0.0002	-	0.0589
West Coast	0.0002	0.0002	-

3

Draft

4 Table 2. *P* values (below diagonal) for tests of allelic differentiation between each
5 population pair and statistical power (above diagonal) of each comparison calculated in
6 POWSIM for the level of F_{ST} observed between each population pair (Table 1).

	Bering Sea	Gulf of AK	West Coast
Bering Sea	-	0.0000	0.0000
Gulf of AK	0.9997	-	0.0000
West Coast	0.9970	0.8230	-

7

Draft

- 8 Table 3. Significant SNP – environment associations found using LFMM. Q values were
9 calculated from p values using an FDR threshold of 0.05.

RAD Tag	Contig	BP Position	Variable	p value	q value
9124	gi 559591484 gb AWGY01151885.1	11333	Depth	6.35E-06	0.0338
12048	gi 559609892 gb AWGY01133477.1	4995	Depth	2.81E-08	0.0003

10

1 Supplemental Information:

2
3 Figure S1. Estimated length at 50% probability of maturity for female (614.8 mm) (a)
4 and male (573.7 mm) (b) sablefish samples collected for this study. Dashed lines
5 represent the estimated length at 50% probability of maturity.

6

7 Figure S2. Histogram of F_{IS} calculated by locus for the population groupings used for the
 8 population genetic analyses as well as globally. Top row is prior to removing SNPs on
 9 the basis of HWE and the bottom row is after.

10 Table S1. Summary of F_{IS} for the SNP loci used in this study before and after filtering
11 SNPs on the basis of Hardy - Weinberg equilibrium (HWE). Calculated for each
12 population (BS: Bering Sea, GOA: Gulf of Alaska, WC: West Coast) and globally.

	Population	Mean	Median	σ
All QC loci	BS	0.0160	-0.0152	0.1824
	GOA	0.0308	0.0234	0.1382
	WC	0.0302	0.0166	0.1591
	Global	0.0311	0.0232	0.1317
Filtered on HWE	BS	-0.0038	-0.0337	0.1106
	GOA	0.0097	0.0099	0.0655
	WC	0.0076	0.0000	0.0886
	Global	0.0096	0.0080	0.0515

Draft

- 13 Table S2. Summary of BLASTN alignments of sablefish contig 152341 (gi:559591484, gb:AWGY01151885.1) to the stickleback
- 14 BORAD S1 genome. Results are ordered by their genomic location in the stickleback genome.

Stickleback Genomic Location	Orientation	Query start	Query end	Query ori	Length	Score	E-val	%ID
groupIII:7438342-7438369	Forward	10269	10296	Forward	28	56	8.00E-05	100.00
groupIII:9945023-9945088	Forward	6492	6555	Forward	66	60	5.00E-06	89.39
groupXX:14624125-14624397	Forward	72	364	Forward	293	248	1.00E-62	85.67
groupXX:14624913-14625548	Forward	1055	1675	Forward	643	414	8.00E-113	84.14
groupXX:14625850-14625961	Forward	2053	2164	Forward	112	190	2.00E-45	96.43
groupXX:14625990-14626081	Forward	2184	2275	Forward	92	79.8	6.00E-12	85.87
groupXX:14626362-14626462	Forward	2588	2688	Forward	101	81.8	1.00E-12	85.15
groupXX:14626513-14626702	Forward	2772	2955	Forward	191	222	6.00E-55	90.58
groupXX:14626779-14626967	Forward	3001	3189	Forward	189	232	6.00E-58	90.48
groupXX:14627240-14627284	Forward	3589	3633	Forward	45	58	2.00E-05	91.11
groupXX:14627550-14627784	Forward	3941	4177	Forward	238	222	6.00E-55	87.39
groupXX:14627954-14628035	Forward	4320	4401	Forward	82	99.6	6.00E-18	90.24
groupXX:14628123-14628198	Forward	4470	4547	Forward	78	77.8	2.00E-11	88.46
groupXX:14628262-14628435	Forward	4628	4803	Forward	176	167	3.00E-38	88.07
groupXX:14628550-14628834	Forward	4897	5181	Forward	285	406	2.00E-110	92.98
groupXX:14628902-14628941	Forward	5277	5316	Forward	40	56	8.00E-05	92.50

15

16 Table S2. continued
17

Stickleback Genomic Location	Orientation	Query start	Query end	Query ori	Length	Score	E-val	%ID
groupXX:14629253-14629480	Forward	5776	6015	Forward	240	289	3.00E-75	90.00
groupXX:14630385-14630912	Forward	7536	8060	Forward	534	442	4.00E-121	86.14
groupXX:14630969-14631303	Forward	8133	8477	Forward	345	375	7.00E-101	88.70
groupXX:14631484-14631784	Forward	8691	8982	Forward	301	254	2.00E-64	87.38
groupXX:14632072-14632221	Forward	9319	9467	Forward	150	210	2.00E-51	93.33
groupXX:14632278-14632325	Forward	9512	9559	Forward	48	63.9	3.00E-07	91.67
groupXX:14632661-14632803	Forward	10300	10442	Forward	143	244	2.00E-61	96.50
groupXX:14633048-14633097	Forward	10810	10859	Forward	50	67.9	2.00E-08	92.00
groupXX:14633459-14633606	Forward	11118	11265	Forward	148	135	1.00E-28	86.49
groupXX:14633693-14633896	Forward	11357	11560	Forward	204	325	6.00E-86	95.10
groupXX:14634494-14634561	Forward	12751	12818	Forward	68	95.6	1.00E-16	92.65

18

- 19 Table S3. Summary of BLASTN alignments of sablefish contig 133848 (gi: 559609892, gb: AWGY01133477.1) to the stickleback
- 20 BORAD S1 genome. Results are ordered by their genomic location in the stickleback genome

Stickleback Genomic Location	Orientation	Query start	Query end	Query ori	Length	Score	E-val	%ID
groupV:10115094-10115124	Forward	1000	1030	Forward	31	61.9	7.00E-07	100.00
groupVI:11485733-11485859	Reverse	6059	6186	Forward	128	151	9.00E-34	90.62
groupVI:11486211-11486456	Reverse	5371	5611	Forward	246	192	3.00E-46	85.37
groupVI:11486517-11486632	Reverse	5166	5285	Forward	122	77.8	1.00E-11	84.43
groupVI:11486658-11486734	Reverse	5051	5127	Forward	77	73.8	2.00E-10	87.01
groupVI:11487005-11487307	Reverse	4417	4721	Forward	305	224	8.00E-56	84.92
groupVI:11487498-11488004	Reverse	3667	4185	Forward	520	392	1.00E-106	84.81
groupVI:11488131-11488370	Reverse	3257	3497	Forward	241	343	1.00E-91	93.36
groupVI:11488704-11489211	Reverse	2403	2925	Forward	533	274	9.00E-71	81.24
groupVI:11489604-11490064	Reverse	1489	1944	Forward	467	283	1.00E-73	83.08
groupVI:11490265-11490335	Reverse	542	612	Forward	71	54	2.00E-04	84.51
groupVI:11490427-11490562	Reverse	308	443	Forward	136	63.9	2.00E-07	80.88
groupXI:16431271-16431298	Forward	1003	1030	Forward	28	56	4.00E-05	100.00
groupXIV:1140798-1140831	Reverse	1006	1039	Forward	34	52	6.00E-04	94.12

21

LaneName	Library ID	Enzyme	Survey
Anofim_Test_1	Krista_Sbf1	SBFI	FRAM
Anofim_Test_1	Krista_Sbf1	SBFI	FRAM
Anofim_Test_1	Krista_Sbf1	SBFI	FRAM
Anofim_Test_1	Krista_Pst1	PSTI	FRAM
Anofim_Test_1	Krista_Pst1	PSTI	FRAM
Anofim_Test_1	Krista_Pst1	PSTI	FRAM
Anofim_Test_1	Andy_Sbfl	SBFI	FRAM
Anofim_Test_1	Krista_Sbf1	SBFI	FRAM
Anofim_Test_1	Krista_Sbf1	SBFI	FRAM
Anofim_Test_1	Krista_Pst1	PSTI	FRAM
Anofim_Test_1	Krista_Pst1	PSTI	FRAM
Anofim_Test_1	Krista_Pst1	PSTI	FRAM
Anofim_Test_1	Andy_Sbfl	SBFI	FRAM
Anofim_Test_1	Andy_Sbfl	SBFI	MESA
Anofim_Test_1	Krista_Pst1	PSTI	MESA
Anofim_Test_1	Andy_Sbfl	SBFI	MESA
Anofim_Test_1	Krista_Sbf1	SBFI	MESA
Anofim_Test_1	Krista_Sbf1	SBFI	MESA
Anofim_Test_1	Krista_Sbf1	SBFI	MESA
Anofim_Test_1	Krista_Pst1	PSTI	MESA
Anofim_Test_1	Krista_Pst1	PSTI	MESA
Anofim_Test_1	Andy_Sbfl	SBFI	MESA
Anofim_Test_1	Krista_Pst1	PSTI	RACE
Anofim_Test_1	Krista_Pst1	PSTI	RACE
Anofim_Test_1	Krista_Pst1	PSTI	RACE
Anofim_Test_1	Andy_Sbfl	SBFI	RACE
Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM

Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM
Anofim_Test_2	anofim_test2	PSTI	FRAM
anofimSBFI_1.2.3.4	1	SBFI	FRAM
anofimSBFI_1.2.3.4	2	SBFI	FRAM
anofimSBFI_1.2.3.4	3	SBFI	FRAM
anofimSBFI_1.2.3.4	4	SBFI	FRAM
anofimSBFI_1.2.3.4	3	SBFI	FRAM
anofimSBFI_1.2.3.4	1	SBFI	FRAM
anofimSBFI_1.2.3.4	2	SBFI	FRAM
anofimSBFI_1.2.3.4	3	SBFI	FRAM
anofimSBFI_1.2.3.4	4	SBFI	FRAM
anofimSBFI_1.2.3.4	2	SBFI	FRAM
anofimSBFI_1.2.3.4	3	SBFI	FRAM
anofimSBFI_1.2.3.4	4	SBFI	FRAM
anofimSBFI_1.2.3.4	1	SBFI	FRAM
anofimSBFI_1.2.3.4	2	SBFI	FRAM
anofimSBFI_1.2.3.4	3	SBFI	FRAM
anofimSBFI_1.2.3.4	4	SBFI	FRAM
anofimSBFI_1.2.3.4	2	SBFI	FRAM
anofimSBFI_1.2.3.4	1	SBFI	FRAM
anofimSBFI_1.2.3.4	2	SBFI	FRAM
anofimSBFI_1.2.3.4	3	SBFI	FRAM
anofimSBFI_1.2.3.4	4	SBFI	FRAM
anofimSBFI_1.2.3.4	1	SBFI	FRAM
anofimSBFI_1.2.3.4	2	SBFI	FRAM
anofimSBFI_1.2.3.4	3	SBFI	FRAM
anofimSBFI_1.2.3.4	4	SBFI	FRAM
anofimSBFI_1.2.3.4	1	SBFI	FRAM
anofimSBFI_1.2.3.4	2	SBFI	FRAM

anofimSBFI_1.2.3.4	3	SBFI	FRAM
anofimSBFI_1.2.3.4	4	SBFI	FRAM
anofimSBFI_1.2.3.4	1	SBFI	MESA
anofimSBFI_1.2.3.4	2	SBFI	MESA
anofimSBFI_1.2.3.4	3	SBFI	MESA
anofimSBFI_1.2.3.4	4	SBFI	MESA
anofimSBFI_1.2.3.4	1	SBFI	MESA
anofimSBFI_1.2.3.4	2	SBFI	MESA
anofimSBFI_1.2.3.4	3	SBFI	MESA
anofimSBFI_1.2.3.4	4	SBFI	MESA
anofimSBFI_1.2.3.4	1	SBFI	MESA
anofimSBFI_1.2.3.4	2	SBFI	MESA
anofimSBFI_1.2.3.4	3	SBFI	MESA
anofimSBFI_1.2.3.4	4	SBFI	MESA
anofimSBFI_1.2.3.4	1	SBFI	MESA
anofimSBFI_1.2.3.4	2	SBFI	MESA
anofimSBFI_1.2.3.4	3	SBFI	MESA
anofimSBFI_1.2.3.4	1	SBFI	RACE
BGI-1	6	SBFI	FRAM
BGI-1	7	SBFI	FRAM
BGI-1	5	SBFI	FRAM
BGI-1	5	SBFI	FRAM
BGI-1	7	SBFI	FRAM
BGI-1	8	SBFI	FRAM
BGI-1	5	SBFI	FRAM
BGI-1	6	SBFI	FRAM
BGI-1	7	SBFI	FRAM
BGI-1	8	SBFI	FRAM
BGI-1	5	SBFI	FRAM
BGI-1	6	SBFI	FRAM
BGI-1	8	SBFI	FRAM
BGI-1	5	SBFI	FRAM
BGI-1	6	SBFI	FRAM

BGI-1	7	SBFI	FRAM
BGI-1	8	SBFI	FRAM
BGI-1	5	SBFI	FRAM
BGI-1	6	SBFI	FRAM
BGI-1	7	SBFI	FRAM
BGI-1	8	SBFI	FRAM
BGI-1	5	SBFI	FRAM
BGI-1	6	SBFI	FRAM
BGI-1	7	SBFI	FRAM
BGI-1	8	SBFI	FRAM
BGI-1	5	SBFI	FRAM
BGI-1	6	SBFI	FRAM
BGI-1	7	SBFI	FRAM
BGI-1	5	SBFI	MESA
BGI-1	6	SBFI	MESA
BGI-1	7	SBFI	MESA
BGI-1	8	SBFI	MESA
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BGI-7	32	SBFI	RACE
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[illegible]

Reads Combined from Multiple Lanes	Reads Combined from Multiple Lanes	SBFI	MESA
Reads Combined from Multiple Lanes	Reads Combined from Multiple Lanes	PSTI	RACE
Reads Combined from Multiple Lanes	Reads Combined from Multiple Lanes	SBFI	RACE
Reads Combined from Multiple Lanes	Reads Combined from Multiple Lanes	SBFI	RACE
Reads Combined from Multiple Lanes	Reads Combined from Multiple Lanes	SBFI	RACE

Draft

Sample ID	LENGTH mm	WEIGHT g	Barcode
FRAM_100233470	400	520	TTTAAT
FRAM_100233471	410	540	TAATTC
FRAM_100233473	390	520	AACGTT
FRAM_100233477	550	1680	TACGGG
FRAM_100233478	590	2140	GGTACA
FRAM_100233479	530	1440	AGGTGT
FRAM_100233480	510	1620	CAATCG
FRAM_100296701	600	2000	CGAGGC
FRAM_100296703	590	1960	GGGGCG
FRAM_100296708	610	2320	CCTAAC
FRAM_100296709	530	1440	TCTTCT
FRAM_100296710	590	1800	ATGTTG
FRAM_100296712	540	1520	AGCCAT
MESA_101	670	2980	TGCTTA
MESA_1290	770	6450	CTGGTT
MESA_1299	640	2480	GAACCA
MESA_1306	740	4405	ATTCCG
MESA_1309	660	2930	ACTCTT
MESA_1339	620	2410	AAACGG
MESA_1342	770	5145	GTGTAA
MESA_1345	710	3490	TCGGAC
MESA_1346	710	3620	TCTCGG
RACE_91	680	3560	TAAGCT
RACE_92	630	2720	ACATAC
RACE_93	660	3698	CTTTGC
RACE_94	600	2578	GTTGGA
FRAM_100228848	650	2480	CCGAGG
FRAM_100228851	670	3020	CGTCTA
FRAM_100228853	660	2600	CTCGCC
FRAM_100228864	620	2120	GAGAGA
FRAM_100228869	610	2180	GATCGT
FRAM_100228874	620	2380	GCAGAT
FRAM_100228878	650	2800	GCCGTA
FRAM_100228881	780	5120	GCTCAA
FRAM_100228889	600	2060	GGACTT

FRAM_100228955	680	3180	GGTTTG
FRAM_100228960	610	2160	TAGTAT
FRAM_100228962	630	2540	TCGATT
FRAM_100228967	590	1800	TCTTCT
FRAM_100228972	610	2000	TGCTTA
FRAM_100228974	620	2460	TTATGA
FRAM_100228978	650	3320	TTCTAG
FRAM_100232477	820	6700	TTTGTC
FRAM_100232482	620	2340	TTTAAT
FRAM_100232528	670	3300	AAACGG
FRAM_100232534	660	2800	GAACCA
FRAM_100232539	620	2260	AAGACG
FRAM_100232540	600	2120	GAGAGA
FRAM_100232541	670	3300	GACTCT
FRAM_100234921	630	2760	ACTCTT
FRAM_100247265	640	4040	GGCAAG
FRAM_100262657	590	2220	AGCGCA
FRAM_100262663	700	4000	GGTACA
FRAM_100267295	680	3320	TAATTC
FRAM_100267296	660	3240	CACCTC
FRAM_100293493	860	7100	TAGTAT
FRAM_100293501	640	2680	CGAGGC
FRAM_100293502	650	2980	TGAACC
FRAM_100293506	590	1940	CGGTCC
FRAM_100293507	580	2080	TGCTTA
FRAM_100296707	630	2680	AACTGA
FRAM_100296739	670	3020	GGACTT
FRAM_100296740	630	2280	AGCCAT
FRAM_100296741	630	2120	GGGGCG
FRAM_100296745	600	1880	AGGTGT
FRAM_100296771	660	2880	TAAGCT
FRAM_100296778	620	2260	CAATCG
FRAM_100296793	620	2720	TACGGG
FRAM_100296802	620	2520	CATACT
FRAM_100296818	610	2380	TCTTCT
FRAM_100296819	630	2600	CGCGTG

FRAM_100296820	610	2540	TGCCCCG
FRAM_100296821	610	2600	CGTGAT
MESA_185	660	3595	CAAAAA
MESA_197	640	2710	TACACA
MESA_215	580	1825	CAGGCA
MESA_216	660	3040	TATCAC
MESA_240	600	2330	CGCAGA
MESA_283	640	2700	TGACAA
MESA_288	660	3125	CGTCTA
MESA_291	960	9720	TGGGGA
MESA_47	580	1865	AACGTT
MESA_52	640	2836	GACGAC
MESA_57	630	2930	AAGCTA
MESA_68	630	2446	GATCGT
MESA_92	590	1845	ACTGGC
MESA_94	700	4280	GGGCGC
MESA_97	680	4250	AGGGTC
RACE_47	620	2118	ATTCCG
FRAM_100232493	630	2540	CTTATG
FRAM_100232513	630	2380	GTTGGA
FRAM_100262670	750	4520	AATGAG
FRAM_100262671	580	2020	ATGTTG
FRAM_100262674	720	3560	GCAGAT
FRAM_100262675	650	2580	TCCTGC
FRAM_100293496	730	4940	ACAAGA
FRAM_100293498	590	1980	CCATTT
FRAM_100293499	630	2580	GCATGG
FRAM_100293500	650	2680	TCGATT
FRAM_100296394	590	2340	ACAGCG
FRAM_100296397	590	1920	CCCGGT
FRAM_100296704	590	2040	TCGCCA
FRAM_100296715	680	3000	ACATAC
FRAM_100296716	610	2100	CCCTAA

FRAM_100296717	600	2060	GCGACC
FRAM_100296719	630	2360	TCGGAC
FRAM_100296747	590	1760	ACCATG
FRAM_100296752	590	2000	CCGAGG
FRAM_100296753	600	2340	GCGCTG
FRAM_100296755	750	4640	TCTCGG
FRAM_100296808	680	3400	ACCCCC
FRAM_100296812	660	3000	CCGCAT
FRAM_100296815	620	2420	GCTCAA
FRAM_100296817	590	2180	TTATGA
FRAM_100296832	670	3100	AGTAGG
FRAM_100296834	640	2780	CCTAAC
FRAM_100296835	640	2560	GTAAGT
MESA_106	740	4445	ATAGTA
MESA_162	630	2525	CTCGCC
MESA_181	690	4250	GTCATC
MESA_184	670	2955	TTGAGC
MESA_223	720	3255	ATCAAA
MESA_229	750	4632	CTGCGA
MESA_232	580	2165	GTGCCT
MESA_238	860	7610	TTTAAT
MESA_297	730	4290	ATGCAC
MESA_322	650	2630	CTGGTT
MESA_34	670	2032	TTCCGT
MESA_342	690	3965	GTGTAA
MESA_346	700	3425	TTTGTC
MESA_70	630	2634	AGTTAA
MESA_76	640	2772	CTACAG
MESA_86	590	2145	GTATCC
MESA_90	590	1980	TTCTAG
MESA_1007	775	4440	AGGTGT
MESA_1033	850	5775	CATACT
MESA_1043	770	5185	CGTGAT
MESA_1080	720	4112	GATCGT
MESA_1082	680	3108	GGTTTG
MESA_1092	600	2285	TATCAC

MESA_1103	833	5575	TGGGGA
MESA_347	790	5075	AAACGG
MESA_352	670	2944	ACTCTT
MESA_353	660	3288	ATTCCG
MESA_355	630	2812	CGAGGC
MESA_396	810	5214	GAAATG
MESA_412	580	1760	GGACTT
MESA_417	630	2710	TAAGCT
MESA_427	580	1965	TCTTCT
MESA_434	690	2860	AACGTT
MESA_438	780	5520	ACTGGC
MESA_442	710	3505	CAAAAA
MESA_445	690	3475	CGCAGA
MESA_446	650	2775	GAACCA
MESA_466	600	2000	GGCAAG
MESA_493	690	2895	TAATTC
MESA_560	650	2540	TGAACC
MESA_570	640	2410	AACTGA
MESA_589	740	3785	AGCCAT
MESA_634	625	2615	CAATCG
MESA_649	655	2828	CGCGTG
MESA_658	605	2290	GACGAC
MESA_678	620	2375	GGGCGC
MESA_681	710	3580	TACACA
MESA_683	680	3128	TGACAA
MESA_712	645	2645	AAGACG
MESA_717	630	2260	AGCGCA
MESA_720	600	2328	CACCTC

MESA_727	605	2314	CGGTCC
MESA_779	845	5460	GACTCT
MESA_801	880	7100	GGGGCG
MESA_813	655	3255	TACGGG
MESA_822	720	4075	TGCCCC
MESA_827	810	5760	AAGCTA
MESA_850	690	3570	AGGGTC
MESA_928	660	2984	CAGGCA
MESA_938	640	3206	CGTCTA
MESA_948	590	2144	GAGAGA
MESA_969	600	2330	GGTACA
MESA_974	580	1955	TAGTAT
MESA_978	610	2440	TGCTTA
RACE_116	690	3022	AATATC
MESA_1109	720	4000	AAACGG
MESA_1114	730	4166	ATTCCG
MESA_1139	850	7055	GAAATG
MESA_1142	810	6285	TAAGCT
MESA_1234	820	6260	AACGTT
MESA_1235	690	3065	CAAAAA
MESA_1236	730	3545	GAACCA
MESA_1245	580	2210	TAATTC
MESA_1282	600	2440	AACTGA
MESA_1283	620	2670	CAATCG
MESA_1287	690	3214	GACGAC
MESA_1288	640	2848	TACACA
MESA_1404	600	2230	AAGACG
MESA_1418	590	2220	CACCTC
MESA_1439	600	2480	GACTCT
MESA_1456	630	2540	TACGGG
MESA_1521	780	4615	AAGCTA
MESA_1539	630	2230	CAGGCA
MESA_1541	760	4090	GAGAGA
MESA_1544	600	2380	TAGTAT
MESA_1803	670	3170	AATATC
MESA_1858	590	2410	CATACT
MESA_1869	620	2600	GATCGT
MESA_1907	600	2610	TATCAC
RACE_101	730	3978	AGGGTC
RACE_105	720	4456	CGTCTA
RACE_109	700	3878	GGTACA

RACE_11	640	2854	CGAGGC
RACE_113	710	3812	TGCTTA
RACE_120	760	4606	AGGTGT
RACE_121	760	4700	CGTGAT
RACE_124	630	2620	GGTTTG
RACE_125	680	3370	TGGGGA
RACE_14	730	3272	GGACTT
RACE_19	670	3334	TCTTCT
RACE_32	680	3456	ACTGGC
RACE_33	670	3100	CGCAGA
RACE_37	690	3584	GGCAAG
RACE_51	630	2304	TGAACC
RACE_6	690	3382	ACTCTT
RACE_68	700	3924	AGCCAT
RACE_69	720	4212	CGCGTG
RACE_70	590	2224	GGGCGC
RACE_71	750	4588	TGACAA
RACE_86	890	6845	AGCGCA
RACE_88	790	5220	GGGGCG
RACE_89	720	3030	TGCCCCG
FRAM_100227933	540	1520	CTCGCC
FRAM_100227934	530	1480	TTCTAG
MESA_1163	630	2325	AATGAG
MESA_1175	610	2420	GCATGG
MESA_1205	730	4600	ACATAC
MESA_1216	750	4150	GCGCTG
MESA_1261	900	7965	AGTAGG
MESA_1273	660	2520	GTATCC
MESA_1275	680	3485	ATCAAA
MESA_1276	630	2500	GTGTAA
MESA_1300	700	3755	CCATTT
MESA_1341	750	4142	CCGAGG
MESA_1351	720	3709	TCGGAC
MESA_1464	690	3265	CTACAG
MESA_1490	710	3940	TTCCGT
MESA_1493	700	3190	CTGGTT
MESA_1520	700	3145	TTTAAT
MESA_1587	620	2505	GCAGAT
MESA_1609	660	2860	ACAGCG
MESA_1697	650	2640	GCGACC

MESA_1776	760	3920	ACCCCC
RACE_1	770	4142	GTAAGT
RACE_114	730	3808	AGTTAA
RACE_115	730	4534	GTCATC
RACE_118	710	3540	CCGCAT
RACE_126	650	2944	CCCGGT
RACE_128	700	3970	TCGATT
RACE_130	630	2684	CTTATG
RACE_131	650	2926	TTTGTC
RACE_2	650	2818	ATAGTA
RACE_20	620	2182	TCAAAG
RACE_28	730	3578	CCCTAA
RACE_29	640	2606	TCGCCA
RACE_3	700	3628	GTGCCT
RACE_31	690	3606	CCTAAC
RACE_5	710	3104	ATGTTG
RACE_58	670	3128	TTATGA
RACE_61	660	2734	CTGCGA
RACE_62	760	4872	TTGAGC
RACE_64	610	2284	CTTTGC
RACE_72	720	4650	ACAAGA
RACE_74	590	2104	GCCGTA
RACE_95	630	2692	ATGCAC
RACE_99	650	3036	GTTGGA
FRAM_100200267	550	1860	AAACGG
FRAM_100200269	550	1940	ATTCCG
FRAM_100208124	610	2420	GAAATG
FRAM_100227930	640	2540	TAAGCT
FRAM_100227946	570	1940	AACGTT
FRAM_100227949	540	1940	CAAAAA
FRAM_100228846	660	2780	GAACCA
FRAM_100228890	570	1740	TAATTC
FRAM_100228964	560	1920	AACTGA
FRAM_100228968	560	1620	CAATCG
FRAM_100228969	570	1840	GACGAC
FRAM_100228970	570	1940	TACACA
FRAM_100232526	620	2740	AAGACG
FRAM_100232536	710	3780	CACCTC
FRAM_100262655	600	2220	AAGCTA
FRAM_100293503	570	1840	CAGGCA
FRAM_100296718	570	1700	GAGAGA

FRAM_100296744	580	1860	TAGTAT
FRAM_100296822	610	2300	AATATC
MESA_1	580	1935	CATACT
MESA_1010	640	2705	CGTGAT
MESA_1012	840	5570	GGTTTG
MESA_102	770	5655	CGAGGC
MESA_1020	810	5240	TGGGGA
MESA_117	700	3845	GGACTT
MESA_1193	780	5375	TACGGG
MESA_122	620	2265	TCTTCT
MESA_155	670	3550	ACTGGC
MESA_168	580	2015	CGCAGA
MESA_169	620	2460	GGCAAG
MESA_172	830	4195	TGAACC
MESA_222	660	2930	AGCCAT
MESA_38	650	2910	GATCGT
MESA_476	620	2325	CGCGTG
MESA_51	670	3404	TATCAC
MESA_528	710	3380	GGGCGC
MESA_569	620	2235	TGACAA
MESA_666	800	4810	AGCGCA
MESA_689	680	2970	CGGTCC
MESA_707	690	3730	GGGGCG
MESA_739	630	2465	TGCCCCG
MESA_832	680	4195	AGGGTC
MESA_878	690	3728	CGTCTA
MESA_892	680	3325	GGTACA
MESA_896	725	4435	TGCTTA
MESA_98	680	3580	ACTCTT
RACE_127	740	5200	GACTCT
RACE_57	860	7020	AGGTGT
FRAM_100227938	570	1960	GCAGAT
FRAM_100227941	590	2160	TCAAAG
FRAM_100228954	570	1920	AATGAG
FRAM_100228956	580	2060	CCATTT
FRAM_100228958	600	2180	GCATGG
FRAM_100228963	560	1660	TCCTGC
FRAM_100228973	560	1720	ACAAGA
FRAM_100232389	560	1840	CCCGGT
FRAM_100232511	580	1940	GCCGTA

FRAM_100232518	570	1940	TCGATT
FRAM_100247184	580	2240	ACAGCG
FRAM_100247185	610	2460	CCCTAA
FRAM_100247186	560	1900	GCGACC
FRAM_100247262	540	1780	TCGCCA
FRAM_100296763	570	1660	ACATAC
FRAM_100296768	570	2080	CCGAGG
FRAM_100296774	610	2380	GCGCTG
FRAM_100296791	660	3340	TCGGAC
MESA_1072	900	8065	ATGCAC
MESA_1086	650	2748	CTTATG
MESA_1097	850	6230	GTTGGA
MESA_1104	770	4500	TTTGTC
MESA_1167	700	3445	ATGTTG
MESA_1168	800	5650	CTTTGC
MESA_137	580	1665	ACCCCC
MESA_144	650	2435	CCTAAC
MESA_151	600	2495	GTAAGT
MESA_154	660	3360	TTATGA
MESA_182	720	4240	AGTAGG
MESA_187	690	3925	CTACAG
MESA_200	660	2915	GTATCC
MESA_218	600	2585	TTCCGT
MESA_587	650	2650	AGTTAA
MESA_629	790	4785	CTCGCC
MESA_636	590	2070	GTCATC
MESA_639	640	2350	TTCTAG
MESA_64	600	2766	ACCATG
MESA_79	740	5200	CCGCAT
MESA_795	710	3285	ATAGTA
MESA_796	795	5425	CTGCGA
MESA_800	800	5945	GTGCCT
MESA_826	870	7410	TTGAGC
MESA_87	580	2305	GCTCAA
MESA_89	650	2695	TCTCGG
MESA_924	610	2796	ATCAAA
MESA_936	690	3282	CTGGTT
MESA_953	625	2466	GTGTAA
MESA_961	670	3125	TTTAAT
MESA_1113	720	4172	AATGAG

MESA_1145	660	3025	ATAGTA
MESA_1147	780	4350	CCGCAT
MESA_1153	830	6030	GCAGAT
MESA_1185	620	2260	TTCCGT
MESA_1208	770	5035	ACAAGA
MESA_1210	680	3415	ATCAAA
MESA_1213	660	3120	CCTAAC
MESA_1215	770	5310	GCATGG
MESA_1217	690	3790	GTATCC
MESA_1222	720	4860	TCCTGC
MESA_1233	940	9560	TTCTAG
MESA_1244	710	4045	ACAGCG
MESA_1249	620	2414	ATGCAC
MESA_1260	710	3275	CTACAG
MESA_1268	620	2710	GCCGTA
MESA_1399	750	4360	GTCATC
MESA_1436	660	2790	TCGATT
MESA_1519	700	3680	TTGAGC
MESA_1530	780	5875	ACATAC
MESA_1561	660	2400	ATGTTG
MESA_1566	670	2684	CTCGCC
MESA_1586	650	2640	GCGACC
MESA_1590	650	2645	GTGCCT
MESA_1592	600	2285	TCGCCA
MESA_1620	760	4430	TTTAAT
MESA_1647	640	2715	ACCATG
MESA_1682	780	4775	CCATTT
MESA_1720	590	1990	CTGCGA
MESA_1729	650	2584	GCGCTG
MESA_1759	700	3640	GTGTAA
MESA_1800	820	6330	TCGGAC
MESA_1871	670	2755	TTTGTC
RACE_106	690	3142	TTATGA
RACE_134	630	2654	AGTTAA
RACE_136	590	2074	CCGAGG
RACE_137	580	1900	CTTTGC
RACE_35	740	4850	GCTCAA
RACE_36	640	3244	GTTGGA
RACE_38	620	2344	TCTCGG
RACE_4	670	2680	ACCCCC
RACE_65	660	3074	AGTAGG

RACE_67	650	3948	CCCTAA
RACE_8	690	3058	CCCGGT
RACE_82	660	2798	CTTATG
RACE_83	630	2562	GTAAGT
RACE_84	670	3774	TCAAAG
RACE_9	670	2932	CTGGTT
MESA_661	600	2260	AATATC
FRAM_100200268	580	2060	Reads Combined from Multiple Lanes
FRAM_100200274	580	2240	Reads Combined from Multiple Lanes
FRAM_100208122	680	4020	Reads Combined from Multiple Lanes
FRAM_100208123	650	3280	Reads Combined from Multiple Lanes
FRAM_100208125	650	3720	Reads Combined from Multiple Lanes
FRAM_100219749	610	2380	Reads Combined from Multiple Lanes
FRAM_100227927	670	3240	Reads Combined from Multiple Lanes
FRAM_100227929	660	3460	Reads Combined from Multiple Lanes
FRAM_100227947	580	2120	Reads Combined from Multiple Lanes
FRAM_100228845	690	2700	Reads Combined from Multiple Lanes
FRAM_100228849	630	2480	Reads Combined from Multiple Lanes
FRAM_100228959	600	2300	Reads Combined from Multiple Lanes
FRAM_100233481	670	3260	Reads Combined from Multiple Lanes
FRAM_100233482	640	2840	Reads Combined from Multiple Lanes
FRAM_100296702	640	2500	Reads Combined from Multiple Lanes
FRAM_100296705	580	1780	Reads Combined from Multiple Lanes
FRAM_100296711	670	2520	Reads Combined from Multiple Lanes
MESA_100	740	4545	Reads Combined from Multiple Lanes

MESA_1303	660	3050	Reads Combined from Multiple Lanes
RACE_119	640	2922	Reads Combined from Multiple Lanes
RACE_81	770	5524	Reads Combined from Multiple Lanes
RACE_85	710	3534	Reads Combined from Multiple Lanes
RACE_87	680	3072	Reads Combined from Multiple Lanes

Draft

Sub Region	Sex	Latitude	Longitude	Depth M	Temp C	Salinity PSU
Southern California	Male	35.194	-121.0205	338	6.93131	34.0242
Southern California	Male	35.194	-121.0205	338	6.93131	34.0242
Southern California	Female	35.194	-121.0205	338	6.93131	34.0242
Southern California	Male	33.9267	-120.5337	1078	3.57457	34.4567
Southern California	Male	33.9267	-120.5337	1078	3.57457	34.4567
Southern California	Male	33.9267	-120.5337	1078	3.57457	34.4567
Southern California	Male	33.9267	-120.5337	1078	3.57457	34.4567
Washington	Female	46.6649	-125.0219	1054	3.45425	34.3951
Washington	Female	46.6649	-125.0219	1054	3.45425	34.3951
Washington	Female	46.6625	-125.0916	946	3.84831	34.3565
Washington	Male	46.6625	-125.0916	946	3.84831	34.3565
Washington	Male	46.6625	-125.0916	946	3.84831	34.3565
Washington	Male	46.7043	-125.2008	1029	3.54234	34.3844
Aleutian Islands	Male	51.7733	-178.9633	250	3.73055	33.6127
Western Yakutat	Female	59.2633	-146.8517	190	5.27835	33.4576
Western Yakutat	Male	59.2633	-146.8517	190	5.27835	33.4576
Western Yakutat	Female	59.2633	-146.8517	190	5.27835	33.4576
Western Yakutat	Male	59.2633	-146.8517	190	5.27835	33.4576
Central Gulf of Alaska	Male	59.155	-147.6033	306	4.80215	33.8565
Central Gulf of Alaska	Female	59.155	-147.6033	306	4.80215	33.8565
Central Gulf of Alaska	Female	59.155	-147.6033	306	4.80215	33.8565
Central Gulf of Alaska	Female	59.155	-147.6033	306	4.80215	33.8565
Southern Bering Sea	Male	55.8004	-168.8584	506	3.56862	33.9809
Southern Bering Sea	Male	55.8004	-168.8584	506	3.56862	33.9809
Southern Bering Sea	Male	55.8004	-168.8584	506	3.56862	33.9809
Southern Bering Sea	Male	55.8004	-168.8584	506	3.56862	33.9809
Washington	Female	46.361	-124.9454	1061	3.46496	34.4017
Oregon	Female	46.0865	-124.8225	488	5.28336	34.1029
Oregon	Female	45.5073	-124.5302	469	5.341	34.0862
Oregon	Male	44.5455	-124.7219	368	5.96064	34.0269
Oregon	Male	43.8867	-124.9067	475	5.45194	34.0885
Oregon	Female	43.6866	-124.8798	923	3.91996	34.3638
Oregon	Male	42.6146	-124.8676	894	4.07891	34.3668
Oregon	Female	42.5346	-124.7565	338	6.42333	34.0481
Northern California	Male	41.5693	-124.6063	781	4.37385	34.3174

Southern California	Female	36.4784	-122.0892	947	4.40155	34.3924
Southern California	Male	36.4784	-122.0892	947	4.40155	34.3924
Southern California	Male	36.4784	-122.0892	947	4.40155	34.3924
Southern California	Male	36.4784	-122.0892	947	4.40155	34.3924
Southern California	Male	36.4784	-122.0892	947	4.40155	34.3924
Southern California	Male	36.4784	-122.0892	947	4.40155	34.3924
Southern California	Male	35.934	-121.5741	434	6.3332	34.1286
Oregon	Female	44.9354	-124.4409	241	6.87432	33.9239
Oregon	Male	44.8933	-124.5903	396	5.75501	34.0411
Northern California	Female	41.4023	-124.7236	1100	3.52416	34.4413
Northern California	Female	40.3082	-124.9028	876	4.05987	34.3755
Northern California	Male	40.1823	-125.0096	1083	3.54131	34.4474
Northern California	Male	40.1823	-125.0096	1083	3.54131	34.4474
Northern California	Female	40.1823	-125.0096	1083	3.54131	34.4474
Oregon	Female	45.3305	-124.7288	526	5.09685	34.1247
Southern California	Female	32.8117	-118.2654	1048	4.00974	34.474
Oregon	Male	45.4043	-124.5312	419	5.59118	34.0539
Oregon	Female	45.4043	-124.5312	419	5.59118	34.0539
Southern California	Female	35.4532	-121.257	413	6.40929	34.0749
Southern California	Female	35.4532	-121.257	413	6.40929	34.0749
Washington	Female	46.434	-124.5414	209	7.9581	32.6523
Washington	Female	47.7061	-125.5211	1053	3.28788	34.3923
Washington	Male	47.7061	-125.5211	1053	3.28788	34.3923
Washington	Male	48.0324	-125.765	1038	3.29741	34.3864
Washington	Male	47.296	-125.1275	1011	3.56304	34.3749
Washington	Female	46.6625	-125.0916	946	3.84831	34.3565
Oregon	Female	45.299	-124.3936	359	5.94497	34.0178
Oregon	Female	45.299	-124.3936	359	5.94497	34.0178
Oregon	Female	45.299	-124.3936	359	5.94497	34.0178
Oregon	Male	45.2376	-124.6449	437	5.50963	34.0649
Northern California	Female	41.2391	-124.5527	1011	3.74808	34.4139
Northern California	Female	41.2391	-124.5527	1011	3.74808	34.4139
Northern California	Female	40.9967	-124.5558	603	4.96905	34.2042
Northern California	Male	40.9967	-124.5558	603	4.96905	34.2042
Northern California	Male	40.0623	-124.6971	971	3.80545	34.4186
Northern California	Male	40.0623	-124.6971	971	3.80545	34.4186

Northern California	Male	40.0623	-124.6971	971	3.80545	34.4186
Northern California	Male	40.0623	-124.6971	971	3.80545	34.4186
Aleutian Islands	Male	51.5917	-177.6167	149	3.60562	33.3681
Aleutian Islands	Female	51.5917	-177.6167	149	3.60562	33.3681
Aleutian Islands	Male	51.7333	-175.9933	185	3.57426	33.4537
Aleutian Islands	Male	51.7333	-175.9933	185	3.57426	33.4537
Aleutian Islands	Male	51.92	-173.5017	102	3.74783	33.1019
Western Gulf Of Alaska	Male	52.965	-168.135	123	3.64277	33.2665
Western Gulf Of Alaska	Female	52.965	-168.135	123	3.64277	33.2665
Western Gulf Of Alaska	Female	52.965	-168.135	123	3.64277	33.2665
Aleutian Islands	Male	52.2517	-174.8433	330	3.77584	33.7472
Aleutian Islands	Female	52.1467	-175.6017	148	3.49514	33.2966
Aleutian Islands	Male	52.1467	-175.6017	148	3.49514	33.2966
Aleutian Islands	Female	51.97	-176.45	120	3.63731	33.2539
Aleutian Islands	Male	51.97	-176.45	120	3.63731	33.2539
Aleutian Islands	Female	51.97	-176.45	120	3.63731	33.2539
Aleutian Islands	Female	51.7733	-178.9633	250	3.73055	33.6127
Northern Bering Sea	Female	59.3573	-177.9838	561	3.58142	34.041
Oregon	Male	44.4322	-124.7939	313	6.34276	33.9967
Oregon	Female	42.1202	-124.8597	862	4.17663	34.3565
Oregon	Female	45.5717	-124.5035	274	6.55485	33.9577
Washington	Male	47.7954	-125.5335	1018	3.40534	34.3785
Washington	Female	47.2087	-125.0651	704	4.4661	34.2399
Washington	Female	47.2087	-125.0651	704	4.4661	34.2399
Washington	Female	46.434	-124.5414	209	7.9581	32.6523
Washington	Male	46.4966	-124.7575	760	4.33844	34.2757
Washington	Female	47.7061	-125.5211	1053	3.28788	34.3923
Washington	Female	47.7061	-125.5211	1053	3.28788	34.3923
Oregon	Male	45.3305	-124.7288	526	5.09685	34.1247
Oregon	Male	45.3305	-124.7288	526	5.09685	34.1247
Washington	Male	46.6649	-125.0219	1054	3.45425	34.3951
Washington	Female	47.4312	-125.0182	1015	3.54112	34.3762
Washington	Male	47.4312	-125.0182	1015	3.54112	34.3762

Washington	Male	47.4312	-125.0182	1015	3.54112	34.3762
Washington	Male	47.4312	-125.0182	1015	3.54112	34.3762
Oregon	Male	45.2376	-124.6449	437	5.50963	34.0649
Oregon	Male	45.1647	-124.4096	368	5.89643	34.0237
Oregon	Male	45.1647	-124.4096	368	5.89643	34.0237
Oregon	Female	45.1647	-124.4096	368	5.89643	34.0237
Northern California	Female	40.2534	-124.609	449	5.59778	34.1338
Northern California	Female	40.2534	-124.609	449	5.59778	34.1338
Northern California	Male	40.0623	-124.6971	971	3.80545	34.4186
Northern California	Male	40.0623	-124.6971	971	3.80545	34.4186
Northern California	Male	39.5356	-124.0048	591	5.07365	34.2331
Northern California	Male	39.5356	-124.0048	591	5.07365	34.2331
Northern California	Male	39.5356	-124.0048	591	5.07365	34.2331
Aleutian Islands	Male	51.7733	-178.9633	250	3.73055	33.6127
Aleutian Islands	Male	51.4033	-178.6183	197	3.72093	33.5223
Aleutian Islands	Female	51.4033	-178.6183	197	3.72093	33.5223
Aleutian Islands	Female	51.5917	-177.6167	149	3.60562	33.3681
Aleutian Islands	Female	51.8817	-174.3383	112	3.69892	33.1518
Aleutian Islands	Female	51.92	-173.5017	102	3.74783	33.1019
Aleutian Islands	Male	51.92	-173.5017	102	3.74783	33.1019
Aleutian Islands	Female	51.92	-173.5017	102	3.74783	33.1019
Western Gulf Of Alaska	Female	53.1917	-166.855	204	3.7337	33.5532
Western Gulf Of Alaska	Female	53.7367	-164.4683	135	3.89196	33.5025
Aleutian Islands	Male	52.2517	-174.8433	330	3.77584	33.7472
Western Gulf Of Alaska	Male	53.7367	-164.4683	135	3.89196	33.5025
Western Gulf Of Alaska	Male	53.7367	-164.4683	135	3.89196	33.5025
Aleutian Islands	Female	51.97	-176.45	120	3.63731	33.2539
Aleutian Islands	Female	51.97	-176.45	120	3.63731	33.2539
Aleutian Islands	Male	51.97	-176.45	120	3.63731	33.2539
Aleutian Islands	Male	51.97	-176.45	120	3.63731	33.2539
Southeast Alaska	Female	57.8783	-137.3783	212	5.66247	33.7572
Southeast Alaska	Female	58.14	-138.73	271	4.9865	33.8869
Southeast Alaska	Female	58.14	-138.73	271	4.9865	33.8869
Western Yakutat	Female	59.4133	-141.1683	319	4.52034	33.9529
Western Yakutat	Female	59.4133	-141.1683	319	4.52034	33.9529
Western Yakutat	Male	59.4133	-141.1683	319	4.52034	33.9529

Western Yakutat	Female	58.685	-140.64	240	4.84441	33.8524
Western Gulf Of Alaska	Male	53.7367	-164.4683	135	3.89196	33.5025
Western Gulf Of Alaska	Female	53.97	-163.2633	115	3.99902	33.4266
Western Gulf Of Alaska	Female	53.97	-163.2633	115	3.99902	33.4266
Western Gulf Of Alaska	Male	53.97	-163.2633	115	3.99902	33.4266
Western Gulf Of Alaska	Female	54.315	-161.06	178	4.27826	33.7858
Western Gulf Of Alaska	Male	54.365	-160.235	140	4.22842	33.5793
Western Gulf Of Alaska	Female	54.365	-160.235	140	4.22842	33.5793
Western Gulf Of Alaska	Male	54.365	-160.235	140	4.22842	33.5793
Western Gulf Of Alaska	Male	54.365	-160.235	140	4.22842	33.5793
Western Gulf Of Alaska	Female	54.365	-160.235	140	4.22842	33.5793
Western Gulf Of Alaska	Female	54.51	-159.255	84	4.43837	33.1366
Western Gulf Of Alaska	Female	54.51	-159.255	84	4.43837	33.1366
Western Gulf Of Alaska	Female	54.51	-159.255	84	4.43837	33.1366
Western Gulf Of Alaska	Male	54.51	-159.255	84	4.43837	33.1366
Central Gulf of Alaska	Female	54.6333	-158.58	123	4.41308	33.3935
Central Gulf of Alaska	Female	55.24	-156.6733	128	4.91457	33.2315
Central Gulf of Alaska	Male	55.24	-156.6733	128	4.91457	33.2315
Central Gulf of Alaska	Female	55.24	-156.6733	128	4.91457	33.2315
Southeast Alaska	Female	54.648	-132.8383	139	6.80801	33.3716
Southeast Alaska	Male	54.5983	-133.0233	408	4.86955	33.9464
Southeast Alaska	Male	54.5983	-133.0233	408	4.86955	33.9464
Southeast Alaska	Male	54.45	-133.93	674	3.99677	34.1749
Southeast Alaska	Female	54.45	-133.93	674	3.99677	34.1749
Southeast Alaska	Male	54.45	-133.93	674	3.99677	34.1749
Southeast Alaska	Male	54.9	-134.2867	254	5.38896	33.8636
Southeast Alaska	Male	55.3467	-134.735	629	3.97845	34.1743
Southeast Alaska	Male	55.3467	-134.735	629	3.97845	34.1743

Southeast Alaska	Male	55.3467	-134.735	629	3.97845	34.1743
Southeast Alaska	Female	55.5583	-134.9667	221	5.50083	33.8213
Southeast Alaska	Female	55.5583	-134.9667	221	5.50083	33.8213
Southeast Alaska	Female	55.93	-134.9017	209	5.60302	33.7872
Southeast Alaska	Female	56.0333	-134.9267	360	4.78147	33.9504
Southeast Alaska	Female	55.9833	-135.4367	291	5.03727	33.9054
Southeast Alaska	Female	56.8517	-135.9967	420	4.62659	33.9863
Southeast Alaska	Male	57.6183	-136.5367	166	6.01274	33.5344
Southeast Alaska	Female	57.6183	-136.5367	166	6.01274	33.5344
Southeast Alaska	Male	57.915	-137.01	438	4.58521	33.9983
Southeast Alaska	Male	57.9667	-137.0767	414	4.67904	33.9747
Southeast Alaska	Male	57.9667	-137.0767	414	4.67904	33.9747
Southeast Alaska	Male	57.9667	-137.0767	414	4.67904	33.9747
Northern Bering Sea	Female	57.0012	-173.5462	697	3.39512	34.145
Western Yakutat	Male	58.685	-140.64	240	4.84441	33.8524
Western Yakutat	Female	59.3883	-142.1633	226	4.90313	33.8194
Western Yakutat	Female	59.3883	-142.1633	226	4.90313	33.8194
Western Yakutat	Female	59.05	-141.3433	366	4.41026	33.9807
Western Yakutat	Female	59.555	-143.6517	207	5.09404	33.729
Western Yakutat	Female	59.555	-143.6517	207	5.09404	33.729
Western Yakutat	Male	59.555	-143.6517	207	5.09404	33.729
Western Yakutat	Male	59.555	-143.6517	207	5.09404	33.729
Western Yakutat	Male	59.5	-145.525	165	5.36381	33.3943
Western Yakutat	Male	59.5	-145.525	165	5.36381	33.3943
Western Yakutat	Male	59.2633	-146.8517	190	5.27835	33.4576
Western Yakutat	Female	59.2633	-146.8517	190	5.27835	33.4576
Central Gulf of Alaska	Male	59.0833	-149.4	180	5.60433	32.7984
Central Gulf of Alaska	Male	58.95	-149.5083	241	5.09602	33.6592
Central Gulf of Alaska	Male	58.7267	-149.1967	173	5.46463	32.9714
Central Gulf of Alaska	Male	58.8017	-149.0483	249	5.00833	33.7161
Central Gulf of Alaska	Female	58.2933	-148.6167	199	5.00428	33.5712
Central Gulf of Alaska	Female	57.9717	-149.1667	160	5.01979	33.2934
Central Gulf of Alaska	Female	57.9717	-149.1667	160	5.01979	33.2934
Central Gulf of Alaska	Male	57.9717	-149.1667	160	5.01979	33.2934
Central Gulf of Alaska	Female	56.0417	-154.5667	205	4.82543	33.6639
Central Gulf of Alaska	Male	57.0017	-155.3033	250	4.76092	33.7785
Central Gulf of Alaska	Female	56.2317	-156.13	250	4.79301	33.7895
Central Gulf of Alaska	Male	55.75	-156.2017	236	4.84368	33.7449
Southern Bering Sea	Female	55.8004	-168.8584	506	3.56862	33.9809
Southern Bering Sea	Female	56.5653	-172.3317	664	3.4393	34.111
Southern Bering Sea	Male	56.4572	-172.7222	804	3.23146	34.2216

Northern Bering Sea	Male	57.8392	-173.9503	728	3.33309	34.1815
Northern Bering Sea	Female	56.9512	-173.7322	691	3.4018	34.142
Northern Bering Sea	Male	57.0012	-173.5462	697	3.39512	34.145
Northern Bering Sea	Male	57.0012	-173.5462	697	3.39512	34.145
Southern Bering Sea	Male	56.2372	-171.3864	759	3.22273	34.2093
Southern Bering Sea	Male	56.2372	-171.3864	759	3.22273	34.2093
Northern Bering Sea	Male	57.8392	-173.9503	728	3.33309	34.1815
Northern Bering Sea	Female	57.8487	-173.9051	395	3.73051	33.7622
Northern Bering Sea	Male	59.3893	-178.2569	760	3.27496	34.2076
Northern Bering Sea	Female	59.3893	-178.2569	760	3.27496	34.2076
Northern Bering Sea	Female	59.3986	-178.2134	667	3.42805	34.1407
Northern Bering Sea	Female	60.4365	-179.0462	465	3.72101	33.9174
Northern Bering Sea	Male	57.8392	-173.9503	728	3.33309	34.1815
Northern Bering Sea	Female	57.1587	-173.9649	602	3.52776	34.066
Northern Bering Sea	Female	57.1587	-173.9649	602	3.52776	34.066
Northern Bering Sea	Male	57.1528	-173.9131	407	3.71276	33.7574
Southern Bering Sea	Female	54.5222	-167.3026	571	3.48969	34.0496
Southern Bering Sea	Female	55.5895	-168.8723	1059	2.77471	34.3599
Southern Bering Sea	Female	55.5895	-168.8723	1059	2.77471	34.3599
Southern Bering Sea	Female	55.5895	-168.8723	1059	2.77471	34.3599
Southern California	Female	37.3731	-122.9308	551	5.63507	34.2155
Southern California	Female	37.3731	-122.9308	551	5.63507	34.2155
Western Yakutat	Male	59.55	-142.5633	227	4.92795	33.8155
Western Yakutat	Male	59.55	-142.5633	227	4.92795	33.8155
Western Yakutat	Female	59.7467	-143.5867	274	4.77478	33.8834
Western Yakutat	Female	59.6733	-143.3817	298	4.65806	33.9165
Western Yakutat	Female	59.5217	-144.7117	195	5.20565	33.6282
Western Yakutat	Male	59.5	-145.525	165	5.36381	33.3943
Western Yakutat	Female	59.5	-145.525	165	5.36381	33.3943
Western Yakutat	Male	59.5	-145.525	165	5.36381	33.3943
Western Yakutat	Male	59.2633	-146.8517	190	5.27835	33.4576
Central Gulf of Alaska	Female	59.155	-147.6033	306	4.80215	33.8565
Central Gulf of Alaska	Male	59.155	-147.6033	306	4.80215	33.8565
Central Gulf of Alaska	Male	58.8017	-149.0483	249	5.00833	33.7161
Central Gulf of Alaska	Female	58.6883	-148.34	267	4.88045	33.7929
Central Gulf of Alaska	Male	58.6883	-148.34	267	4.88045	33.7929
Central Gulf of Alaska	Female	58.2933	-148.6167	199	5.00428	33.5712
Central Gulf of Alaska	Male	58.0833	-149.9083	272	4.58032	33.8664
Central Gulf of Alaska	Male	57.6317	-149.9167	340	4.24955	33.9789
Central Gulf of Alaska	Female	56.485	-152.2133	167	4.66943	33.5413

Central Gulf of Alaska	Female	55.9733	-154.0217	307	4.53046	33.9102
Southern Bering Sea	Male	54.3357	-166.3667	810	3.12884	34.2443
Northern Bering Sea	Female	56.9512	-173.7322	691	3.4018	34.142
Northern Bering Sea	Female	57.0012	-173.5462	697	3.39512	34.145
Northern Bering Sea	Male	57.0012	-173.5462	697	3.39512	34.145
Southern Bering Sea	Male	56.2372	-171.3864	759	3.22273	34.2093
Southern Bering Sea	Female	56.2372	-171.3864	759	3.22273	34.2093
Southern Bering Sea	Female	55.3696	-168.1809	522	3.5503	33.9976
Southern Bering Sea	Male	55.3696	-168.1809	522	3.5503	33.9976
Southern Bering Sea	Male	54.3357	-166.3667	810	3.12884	34.2443
Northern Bering Sea	Female	57.8487	-173.9051	395	3.73051	33.7622
Northern Bering Sea	Male	58.5383	-176.8529	936	2.9857	34.305
Northern Bering Sea	Male	58.5383	-176.8529	936	2.9857	34.305
Southern Bering Sea	Male	54.3357	-166.3667	810	3.12884	34.2443
Northern Bering Sea	Male	59.3629	-178.2513	846	3.13126	34.2591
Southern Bering Sea	Male	54.3357	-166.3667	810	3.12884	34.2443
Northern Bering Sea	Female	58.536	-176.0788	424	3.75347	33.8488
Northern Bering Sea	Female	58.2695	-175.4563	591	3.52989	34.0777
Northern Bering Sea	Female	58.378	-175.0674	602	3.51676	34.0869
Northern Bering Sea	Male	57.1587	-173.9649	602	3.52776	34.066
Southern Bering Sea	Female	54.5222	-167.3026	571	3.48969	34.0496
Southern Bering Sea	Male	54.5222	-167.3026	571	3.48969	34.0496
Southern Bering Sea	Male	55.8004	-168.8584	506	3.56862	33.9809
Southern Bering Sea	Female	55.8004	-168.8584	506	3.56862	33.9809
Southern California	Female	34.3749	-120.877	842	4.30301	34.3745
Southern California	Male	32.5914	-119.8543	988	4.03417	34.4517
Northern California	Female	41.2409	-124.8164	1217	3.26017	34.4679
Northern California	Male	41.2409	-124.8164	1217	3.26017	34.4679
Southern California	Male	34.5626	-121.2512	958	3.92693	34.4181
Southern California	Female	34.5626	-121.2512	958	3.92693	34.4181
Washington	Female	46.4716	-124.616	865	4.04507	34.3308
Northern California	Male	41.5693	-124.6063	781	4.37385	34.3174
Southern California	Male	36.4784	-122.0892	947	4.40155	34.3924
Southern California	Male	36.4784	-122.0892	947	4.40155	34.3924
Southern California	Male	36.4784	-122.0892	947	4.40155	34.3924
Southern California	Male	36.4784	-122.0892	947	4.40155	34.3924
Northern California	Male	41.4023	-124.7236	1100	3.52416	34.4413
Northern California	Female	40.3082	-124.9028	876	4.05987	34.3755
Oregon	Female	45.3376	-124.8175	709	4.47384	34.2519
Washington	Male	47.7061	-125.5211	1053	3.28788	34.3923
Washington	Male	47.4312	-125.0182	1015	3.54112	34.3762

Oregon	Male	45.2376	-124.6449	437	5.50963	34.0649
Northern California	Female	39.5356	-124.0048	591	5.07365	34.2331
Aleutian Islands	Male	53.03	-170.1033	167	3.42991	33.3228
Southeast Alaska	Male	57.8783	-137.3783	212	5.66247	33.7572
Southeast Alaska	Female	57.8783	-137.3783	212	5.66247	33.7572
Aleutian Islands	Female	51.7733	-178.9633	250	3.73055	33.6127
Southeast Alaska	Female	57.8783	-137.3783	212	5.66247	33.7572
Aleutian Islands	Female	51.7633	-178.165	104	3.65694	33.2522
Western Yakutat	Female	59.55	-142.5633	227	4.92795	33.8155
Aleutian Islands	Female	51.4033	-178.6183	197	3.72093	33.5223
Aleutian Islands	Female	51.4033	-178.6183	197	3.72093	33.5223
Aleutian Islands	Male	51.4033	-178.6183	197	3.72093	33.5223
Aleutian Islands	Female	51.4033	-178.6183	197	3.72093	33.5223
Aleutian Islands	Female	51.4033	-178.6183	197	3.72093	33.5223
Aleutian Islands	Male	51.7667	-175.1417	356	3.79577	33.8654
Aleutian Islands	Male	52.2517	-174.8433	330	3.77584	33.7472
Central Gulf of Alaska	Female	54.6333	-158.58	123	4.41308	33.3935
Aleutian Islands	Female	52.1467	-175.6017	148	3.49514	33.2966
Central Gulf of Alaska	Male	54.8517	-157.7367	165	4.61008	33.5527
Central Gulf of Alaska	Male	55.24	-156.6733	128	4.91457	33.2315
Southeast Alaska	Male	54.45	-133.93	674	3.99677	34.1749
Southeast Alaska	Male	54.9	-134.2867	254	5.38896	33.8636
Southeast Alaska	Male	54.9	-134.2867	254	5.38896	33.8636
Southeast Alaska	Male	55.3467	-134.735	629	3.97845	34.1743
Southeast Alaska	Female	55.9833	-135.4367	291	5.03727	33.9054
Southeast Alaska	Female	56.8517	-135.9967	420	4.62659	33.9863
Southeast Alaska	Female	57.1883	-136.235	292	5.1472	33.8961
Southeast Alaska	Male	57.1883	-136.235	292	5.1472	33.8961
Aleutian Islands	Male	51.7733	-178.9633	250	3.73055	33.6127
Southern Bering Sea	Female	56.2372	-171.3864	759	3.22273	34.2093
Northern Bering Sea	Female	58.6282	-177.9629	918	3.01066	34.2976
Southern California	Female	35.3638	-121.5367	951	4.13442	34.4145
Southern California	Female	34.1418	-120.8592	871	4.25147	34.3877
Southern California	Female	36.4784	-122.0892	947	4.40155	34.3924
Southern California	Female	36.4784	-122.0892	947	4.40155	34.3924
Southern California	Female	36.4784	-122.0892	947	4.40155	34.3924
Southern California	Male	36.4784	-122.0892	947	4.40155	34.3924
Southern California	Male	36.4784	-122.0892	947	4.40155	34.3924
Southern California	Female	36.3616	-122.1071	533	5.70806	34.2164
Northern California	Male	41.8702	-124.9614	899	4.07541	34.3711

Northern California	Male	41.701	-124.5509	532	5.30134	34.1576
Southern California	Female	34.3749	-120.877	842	4.30301	34.3745
Southern California	Female	34.3749	-120.877	842	4.30301	34.3745
Southern California	Female	34.3749	-120.877	842	4.30301	34.3745
Southern California	Female	32.9083	-118.1918	868	4.69697	34.4238
Northern California	Male	41.7997	-124.5921	593	5.02633	34.1941
Northern California	Male	41.3017	-124.4759	463	5.64674	34.1205
Northern California	Female	41.2391	-124.5527	1011	3.74808	34.4139
Northern California	Female	40.9967	-124.5558	603	4.96905	34.2042
Southeast Alaska	Female	58.4683	-139.4667	197	5.14521	33.7403
Western Yakutat	Female	59.4133	-141.1683	319	4.52034	33.9529
Western Yakutat	Female	58.685	-140.64	240	4.84441	33.8524
Western Yakutat	Male	58.685	-140.64	240	4.84441	33.8524
Western Yakutat	Male	59.55	-142.5633	227	4.92795	33.8155
Western Yakutat	Female	59.55	-142.5633	227	4.92795	33.8155
Aleutian Islands	Male	51.4033	-178.6183	197	3.72093	33.5223
Aleutian Islands	Female	51.4033	-178.6183	197	3.72093	33.5223
Aleutian Islands	Male	51.4033	-178.6183	197	3.72093	33.5223
Aleutian Islands	Male	51.4033	-178.6183	197	3.72093	33.5223
Aleutian Islands	Female	51.4033	-178.6183	197	3.72093	33.5223
Aleutian Islands	Male	51.5917	-177.6167	149	3.60562	33.3681
Aleutian Islands	Female	51.5917	-177.6167	149	3.60562	33.3681
Aleutian Islands	Male	51.7333	-175.9933	185	3.57426	33.4537
Central Gulf of Alaska	Female	55.24	-156.6733	128	4.91457	33.2315
Southeast Alaska	Female	54.648	-132.8383	139	6.80801	33.3716
Southeast Alaska	Male	54.648	-132.8383	139	6.80801	33.3716
Southeast Alaska	Male	54.648	-132.8383	139	6.80801	33.3716
Aleutian Islands	Male	52.1467	-175.6017	148	3.49514	33.2966
Aleutian Islands	Female	51.97	-176.45	120	3.63731	33.2539
Southeast Alaska	Female	55.5583	-134.9667	221	5.50083	33.8213
Southeast Alaska	Female	55.5583	-134.9667	221	5.50083	33.8213
Southeast Alaska	Female	55.5583	-134.9667	221	5.50083	33.8213
Southeast Alaska	Female	56.0333	-134.9267	360	4.78147	33.9504
Aleutian Islands	Male	51.97	-176.45	120	3.63731	33.2539
Aleutian Islands	Female	51.97	-176.45	120	3.63731	33.2539
Southeast Alaska	Male	57.6183	-136.5367	166	6.01274	33.5344
Southeast Alaska	Male	57.6183	-136.5367	166	6.01274	33.5344
Southeast Alaska	Male	57.915	-137.01	438	4.58521	33.9983
Southeast Alaska	Female	57.915	-137.01	438	4.58521	33.9983
Western Yakutat	Male	59.3883	-142.1633	226	4.90313	33.8194

Western Yakutat	Female	59.05	-141.3433	366	4.41026	33.9807
Western Yakutat	Female	59.05	-141.3433	366	4.41026	33.9807
Western Yakutat	Female	59.05	-141.3433	366	4.41026	33.9807
Western Yakutat	Male	59.55	-142.5633	227	4.92795	33.8155
Western Yakutat	Female	59.7467	-143.5867	274	4.77478	33.8834
Western Yakutat	Male	59.7467	-143.5867	274	4.77478	33.8834
Western Yakutat	Male	59.7467	-143.5867	274	4.77478	33.8834
Western Yakutat	Female	59.7467	-143.5867	274	4.77478	33.8834
Western Yakutat	Female	59.6733	-143.3817	298	4.65806	33.9165
Western Yakutat	Female	59.6733	-143.3817	298	4.65806	33.9165
Western Yakutat	Female	59.555	-143.6517	207	5.09404	33.729
Western Yakutat	Male	59.555	-143.6517	207	5.09404	33.729
Western Yakutat	Male	59.5217	-144.7117	195	5.20565	33.6282
Western Yakutat	Male	59.5217	-144.7117	195	5.20565	33.6282
Western Yakutat	Male	59.5	-145.525	165	5.36381	33.3943
Central Gulf of Alaska	Female	59.0833	-149.4	180	5.60433	32.7984
Central Gulf of Alaska	Male	58.7267	-149.1967	173	5.46463	32.9714
Central Gulf of Alaska	Female	58.2933	-148.6167	199	5.00428	33.5712
Central Gulf of Alaska	Female	58.2933	-148.6167	199	5.00428	33.5712
Central Gulf of Alaska	Male	58	-149.8417	229	4.68218	33.7702
Central Gulf of Alaska	Male	58	-149.8417	229	4.68218	33.7702
Central Gulf of Alaska	Male	58.0833	-149.9083	272	4.58032	33.8664
Central Gulf of Alaska	Male	58.0833	-149.9083	272	4.58032	33.8664
Central Gulf of Alaska	Male	58.0833	-149.9083	272	4.58032	33.8664
Central Gulf of Alaska	Female	57.6317	-149.9167	340	4.24955	33.9789
Central Gulf of Alaska	Male	57.4017	-150.5733	182	4.52745	33.6579
Central Gulf of Alaska	Female	57.1183	-151.2217	223	4.5149	33.769
Central Gulf of Alaska	Male	56.3033	-153.0767	289	4.55029	33.8758
Central Gulf of Alaska	Male	56.3033	-153.0767	289	4.55029	33.8758
Central Gulf of Alaska	Female	55.9733	-154.0217	307	4.53046	33.9102
Central Gulf of Alaska	Female	56.0417	-154.5667	205	4.82543	33.6639
Central Gulf of Alaska	Female	56.2317	-156.13	250	4.79301	33.7895
Southern Bering Sea	Female	56.5653	-172.3317	664	3.4393	34.111
Southern Bering Sea	Male	55.3696	-168.1809	522	3.5503	33.9976
Southern Bering Sea	Male	55.3696	-168.1809	522	3.5503	33.9976
Southern Bering Sea	Male	55.3696	-168.1809	522	3.5503	33.9976
Northern Bering Sea	Female	59.3986	-178.2134	667	3.42805	34.1407
Northern Bering Sea	Female	59.3986	-178.2134	667	3.42805	34.1407
Northern Bering Sea	Female	59.3986	-178.2134	667	3.42805	34.1407
Southern Bering Sea	Male	54.3357	-166.3667	810	3.12884	34.2443
Northern Bering Sea	Male	57.1587	-173.9649	602	3.52776	34.066

Northern Bering Sea	Female	57.1587	-173.9649	602	3.52776	34.066
Northern Bering Sea	Male	57.8392	-173.9503	728	3.33309	34.1815
Southern Bering Sea	Male	55.5755	-168.786	915	2.9755	34.2983
Southern Bering Sea	Male	55.5755	-168.786	915	2.9755	34.2983
Southern Bering Sea	Male	55.5895	-168.8723	1059	2.77471	34.3599
Northern Bering Sea	Male	57.8392	-173.9503	728	3.33309	34.1815
Southeast Alaska	Female	54.5983	-133.0233	408	4.86955	33.9464
Southern California	Male	32.5914	-119.8543	988	4.03417	34.4517
Southern California	Male	32.8117	-118.2654	1048	4.00974	34.474
Northern California	Female	41.2409	-124.8164	1217	3.26017	34.4679
Northern California	Female	41.2409	-124.8164	1217	3.26017	34.4679
Northern California	Female	41.2409	-124.8164	1217	3.26017	34.4679
Oregon	Male	43.7222	-124.6859	452	5.56963	34.0765
Northern California	Female	41.2409	-124.8164	1217	3.26017	34.4679
Northern California	Female	41.2409	-124.8164	1217	3.26017	34.4679
Southern California	Male	34.5626	-121.2512	958	3.92693	34.4181
Washington	Female	46.4716	-124.616	865	4.04507	34.3308
Washington	Female	46.361	-124.9454	1061	3.46496	34.4017
Southern California	Male	36.4784	-122.0892	947	4.40155	34.3924
Southern California	Female	33.9267	-120.5337	1078	3.57457	34.4567
Southern California	Female	33.9267	-120.5337	1078	3.57457	34.4567
Washington	Female	46.6649	-125.0219	1054	3.45425	34.3951
Washington	Male	46.6649	-125.0219	1054	3.45425	34.3951
Washington	Male	46.7043	-125.2008	1029	3.54234	34.3844
Aleutian Islands	Female	51.7733	-178.9633	250	3.73055	33.6127

Western Yakutat	Male	59.2633	-146.8517	190	5.27835	33.4576
Northern Bering Sea	Male	57.0012	-173.5462	697	3.39512	34.145
Southern Bering Sea	Female	55.5755	-168.786	915	2.9755	34.2983
Southern Bering Sea	Female	55.5895	-168.8723	1059	2.77471	34.3599
Southern Bering Sea	Female	55.5895	-168.8723	1059	2.77471	34.3599

Draft

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juvenile		No	YES
spent/post-spawning		Yes: Missing data	NO
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spawning		No	NO
spawning		No	YES
spawning		Yes: Missing data	NO
mature/developing		Yes: Missing data	NO
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spawning		No	NO
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Not Measured		No	YES
mature/developing		Yes: Missing data	NO
juvenile		Yes: Missing data	NO
juvenile		Yes: Missing data	NO
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juvenile		Yes: Missing data	NO
mature/developing		Yes: Missing data	NO
juvenile		Yes: Missing data	NO
spent/post-spawning		Yes: Missing data	NO
juvenile		Yes: Missing data	NO

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spent/post-spawning		Yes: Missing data	NO
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juvenile		No	NO
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spent/post-spawning	No	YES
spent/post-spawning	No	NO
juvenile	No	NO
spawning	No	NO
spent/post-spawning	No	YES

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