INTERANNUAL AND SPATIAL VARIATION IN THE POPULATION GENETIC COMPOSITION OF YOUNG-OF-THE-YEAR PACIFIC OCEAN PERCH (*Sebastes alutus*) IN ALASKAN WATERS

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A

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Abstract

We know little about the population structure of Gulf of Alaska (GOA) and Bering Sea rockfish, including Pacific ocean perch (POP, *Sebastes alutus*), and early life history information is sparse for many rockfish species. Young-of-the-year (YOY) POP were collected with surface trawls during surveys of juvenile salmon in the GOA and Bering Sea. These samples presented a unique opportunity to study POP genetics and life history. Fourteen microsatellite loci were used to characterize the genetic variation in POP collected in a total of 45 hauls over five years. The coincidence in timing and location of several collections between years allowed examination of both fine- and broad-scale geographic variation (within cohorts) as well as interannual (between cohorts) genetic variation. The geographic genetic structure of these collections was also compared to geographic structure of adult POP described in a previous study (Palof, 2008). As in the adult study, significant broad-scale geographic divergence was observed in YOY POP in the GOA. Fine-scale geographic divergence was also observed and may be the result of variable current regimes and oceanographic features at several locations. The limited amount of temporal variation observed seems to be the result of variable oceanography and fine-scale population structure rather than the influence of a sweepstakes effect. The relationship between genetic divergence and geographic separation is virtually identical in YOY and adult POP, which confirms that dispersal of POP is limited in all life stages and also demonstrates that most YOY are produced by adults that are located nearby.

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Introduction

Pacific ocean perch (POP, *Sebastes alutus*) and other rockfish species are valuable contributors to Alaska's groundfish fisheries and are important components of the marine ecosystem. However, surprisingly little is known about their early life histories and the factors that influence their dispersal and recruitment in Alaskan waters. For marine species, the physical features (i.e., oceanographic and geographic) that restrict population sizes are not always obvious to scientists and the contributing biological and ecological factors may be difficult or impossible to observe. Many species of rockfish are strongly associated with a particular location or physical structure as adults (Mathews and Barker, 1983; Hartmann, 1987; Matthews, 1990). As a result, the pelagic larval stage may account for much of the lifetime dispersal of these species (Buonaccorsi *et al.*, 2004).

Many marine species have the potential to disperse over long distances, both as juveniles and adults, and there are often few evident barriers to dispersal. Thus, marine species with extensive pelagic larval periods are generally assumed to also have widespread larval dispersal (Doherty *et al.*, 1995; Cowen *et al.*, 2000; Palumbi, 2003). Oceanographic features, especially strong currents, may entrain larvae and sweep them far from their natal grounds (Bailey, 1981; Ainley *et al.*, 1993; Fisher 2005). However, recent studies suggest that larval dispersal of many marine species may be more limited than the long pelagic duration of the larval stage would suggest (Marliave, 1986; Withler *et al.*, 2001; Sponaugle *et al.*, 2002; Swearer *et al.*, 2002; Miller and Shanks, 2004). Although some types of oceanographic features may contribute to dispersal, others may act as barriers. Recirculating currents and mesoscale eddies may entrain and limit alongshore transport of larvae (Morgan and Botsford, 1998; Wing *et al*., 1998). Several studies have noted the high densities of juvenile (Larson *et al*., 1994; Wing *et al*., 1998) and larval rockfish (Bjorkstedt *et al*., 2002) at upwelling fronts, which concentrate and retain plankton.

Rockfishes (genus *Sebastes*) are an abundant and widely distributed taxon and there are more than 100 known species. The majority (about 96 species) of these species are located in the North Pacific Ocean and Gulf of California (Love *et al*., 2002). Approximately 30 species occur in Alaskan waters, and some of those species are targeted by commercial fisheries and others are harvested as incidental catch in fisheries for other species and by recreational anglers. In addition to being commercially important, rockfishes play important roles in Gulf of Alaska (GOA) ecosystems (Love *et al*., 2002). Rockfishes are extremely diverse, inhabiting a wide range of depths and acting in a variety of food-chain capacities. In Alaska, POP are especially important because they are the most abundant rockfish in these waters, in some years constituting as much as nearly three-quarters of the rockfish biomass of the GOA (Love *et al*., 2002). They are planktivorous and compete for food with other commercially important species such as walleye pollock. Additionally, POP themselves are commercially valuable, in part due to their bright red coloration.

Given the importance of *Sebastes* in general, and POP in particular, both in the GOA and along the Pacific Rim, it is surprising that so little is known about their early life histories. We do not know the locations of mating and parturition (Gunderson, 1972; Gray *et al*., 2006), the extent of dispersal of young and adult fish (Moser and Boehlert, 1991), or the locations of or habitat requirements for larval and juvenile fish (Carlson and Haight, 1976; Love *et al.*, 1991; Rooper and Boldt, 2005). The pelagic larvae are subject to oceanographic variability such as currents, eddies, cross-sectional structure, and upwelling fronts, all of which may influence their dispersal and recruitment (Bailey, 1981; Ainley *et al.*, 1993; Morgan and Botsford, 1998; Wing *et al.*, 1998). Larval POP are not frequently encountered, but it is thought that the larvae settle and transform to a demersal existence during the first year of life (Carlson and Haight, 1976).

One reason that larval and juvenile rockfish are so poorly understood is that early life history studies are hampered by difficulties in identifying young rockfish to a species level from morphological characteristics. Identification of larval rockfishes is particularly difficult because they lack diagnostic characteristics (Kendall, 1991; Gray *et al.*, 2006; Kendall *et al.*, 2007; Kondzela *et al.*, 2007). In addition, rockfish are not fully developed at the time of parturition and subsequently undergo a series of morphological changes as they develop into juveniles and then adults, which further complicates identification (Kendall, 1991). Intraspecific variability in the pigmentation also contributes to the dilemma (Westrheim, 1975; Gray *et al.*, 2006).

Careful management of rockfishes is important because their life histories are characterized by slow growth, late age at maturity, and longevity (Gunderson, 1977; Lunsford, 1999), all of which make them especially vulnerable to overfishing. In Alaska, POP are managed by using a species-specific acceptable biological catch (ABC) and total allowable catch (TAC). The ABC's and TAC's are further divided into several large, geographically-defined management areas (Hanselman *et al.*, 2008).

Definition of the spatial dimensions, or geographic scale of production units, is a fundamental piece of information needed to optimize conservation and management of species that have limited dispersal over their lifetimes. Overestimating the sizes and boundaries of production units can reduce the productivity of species, especially if individuals do not range far from their natal sites. If management areas greatly exceed the dispersal range, reproductive potential may be compromised by uneven fishing effort.

There is evidence that population structure exists within the distribution range of POP. Results of a study on adult POP in the GOA and Bering Sea indicated that this species has a strong, geographically-based genetic structure (Palof, 2008). Withler *et al.* (2001) reported fine-scale genetic structure in POP in Queen Charlotte Sound, British Columbia. Highly localized responses to fishing pressure (Gunderson, 1997) also indicated that POP have some degree of population structure. Distinguishing stocks is necessary for effective conservation and management and often phenotypic or morphological differences are insufficient to separate stocks (Carvalho and Hauser, 1994). Because the genetic structure of a species mirrors its distribution and scale of productivity units, an understanding of this structure can play a critical role in developing effective management strategies.

One concern in the interpretation of data from adult POP was that the genetic structure apparent in the adult collections, which were sampled at particular times and places from complex mixtures of age classes, might be biased or suggest structure that is not really present if there are large differences in the genetic compositions of different cohorts (Palof, 2008). This concern arose because of the potential occurrence of a "sweepstakes" effect (Hedgecock, 1994), which is characterized by large differences in the genetic compositions of different cohorts because of disproportionate successes of offspring from a few females. Like many other rockfish species, POP are long lived, iteroparous, and highly fecund; females produce tens to hundreds of thousands of larvae during each reproduction cycle (Love *et al.*, 2002). Because present populations of POP in Alaska do not seem to be expanding substantially, we can assume that reproduction is occurring at approximately a replacement level. Consequently, the lifetime average contribution of a female is two offspring out of a potential lifetime production in the millions. Although offspring are produced at roughly a replacement level, environmental patchiness within an area and differences among years may subject larvae to variable conditions, which may influence recruitment levels and could cause large variance in the numbers of offspring contributed by each female. Recruitment in POP is highly variable, possibly due in part to dependence on the timing of the spring plankton bloom (Hanselman *et al.*, 2003). A consequence of this "sweepstakes" effect (Hedgecock, 1994) is that, potentially, each cohort could differ genetically and that the genetic composition of different collections could reflect the contributing cohorts. If this occurred, genetic differences among collections might not be of geographic relevance.

Unlike the adult samples, which are composed of a variety of age classes, a collection of young-of-the-year (YOY) samples from the GOA and Bering Sea captures distinct cohorts. Palof (2008) observed strong genetic structure in adult POP in the GOA which followed an isolation-by-distance pattern. She observed that the demographic scale of productivity, or the neighborhood size, is much less than 400 km. These results indicate that the lifetime dispersal of this species is limited, and consequently, juveniles and adults should both have similar distributions. In my study, temporal (between cohort) and geographic (within cohort) variation in YOY POP, both on a broad- (across the GOA) and fine- (within transect) scale, will be assessed and compared with the adult structure described by Palof (2008).

My study addresses four specific questions about the broad- and fine-scale geographic distributions and the temporal variation in YOY POP: (1) do the collections taken within a year vary across the GOA?; (2) do collections vary along sampling transects within a year?; (3) does the genetic composition of collections vary interannually at a particular geographic location?; and (4) by using population genetic data of adults (Palof, 2008) as a framework for interpreting data from YOY collections, is it reasonable to conclude that the YOY collections originated from geographically proximal adults rather than from a broad mixture of GOA sources? These questions are critical for the interpretation of genetic variation observed in population genetics surveys of not just POP, but also other species of rockfish, and in turn to their conservation and management.

Materials and Methods

Sample Collection

Young-of-the-year (YOY) rockfish samples were collected by NOAA personnel during juvenile salmonid survey cruises in the Gulf of Alaska (GOA) during 1998 and 2003 and in the Bering Sea in 2002 (Kondzela *et al.*, 2007). Collections were made with a rope trawl towed at or near the surface. The trawl was towed at a speed between 6.48 and 9.26 km/hr for 30 to 60 minutes and covered a distance of 2.5 to 5.0 km. Mixed YOY rockfish species from each haul were frozen together at -70°C onboard the vessel. In the lab, the fish were partially thawed to facilitate separation of individuals and a sample of muscle tissue was excised from each fish and stored in a tissue sample DNA preservative solution, prepared as described by Seutin *et al.* (1991), at -20°C. A total of 2208 fish were analyzed in this study. Samples were collected throughout the GOA and Bering Sea along transects consisting of one or more hauls (Figures 1, 2 and Table 1).

Species Identification

The entirety of each collection of YOY fish was examined and visual identification features were used to remove specimens that were clearly not POP (Kendall et al. 2007). The majority of specimens that were collected visually resembled young POP. All of the 2208 samples selected for this study were analyzed at a SNP site developed by Garvin *et al.* (unpublished, based on a mitochondrial DNA key by Li *et al.*, 2006) that distinguishes POP from other northern Pacific Ocean rockfishes. Only the samples that were positively identified as POP were used in subsequent data analyses.

Microsatellite Analysis

Total cellular DNA was isolated with Qiagen DNeasy kits (Qiagen, Valencia, CA) and stored at -20°C. The same suite of fourteen microsatellite loci that was used in an adult POP survey (Palof, 2008) was applied in this YOY study: µSal1, µSal2, µSal3, µSal4,

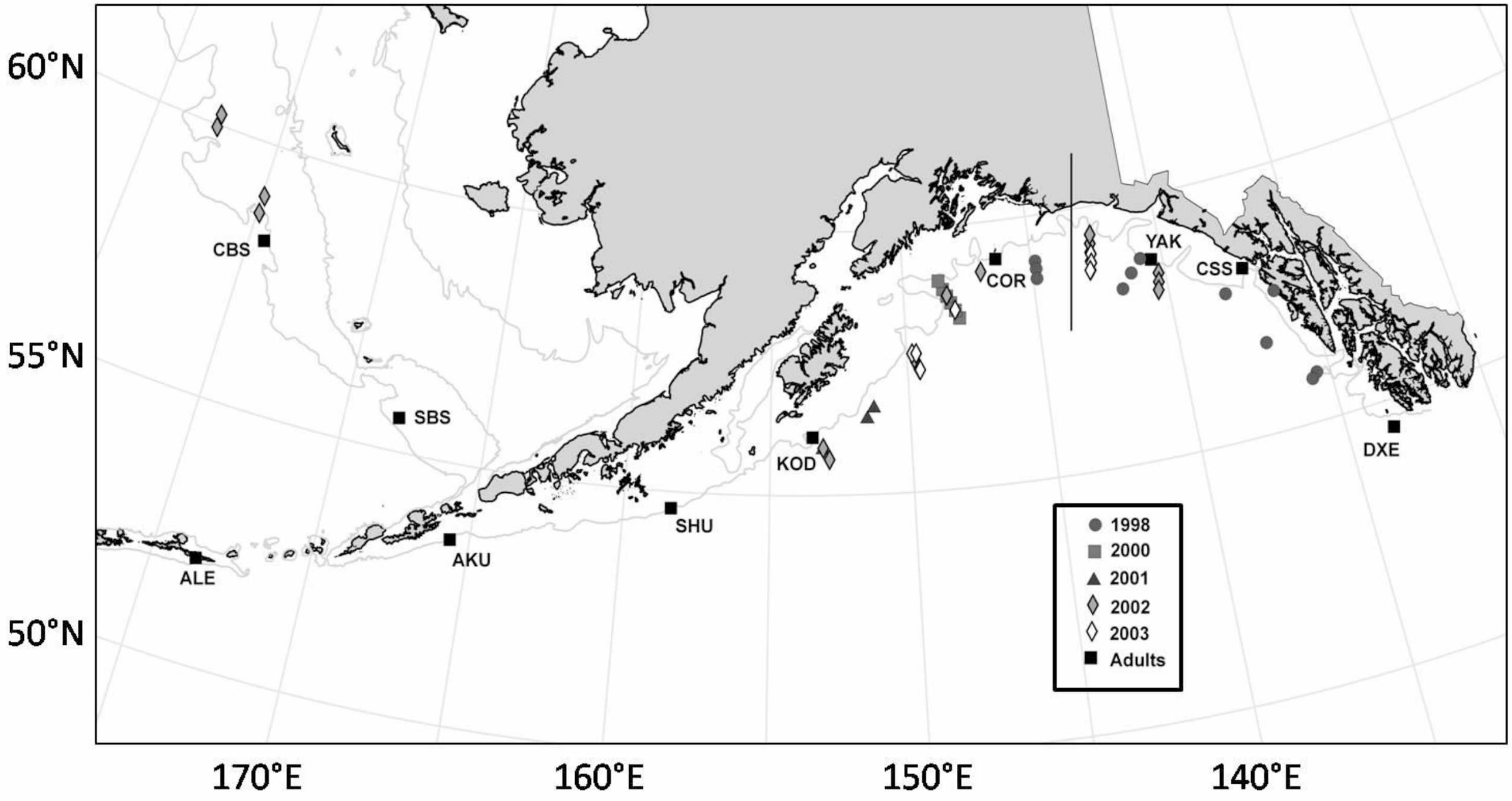

Figure 1. Map of adult and YOY POP collection locations. Refer to Table 1 for details regarding YOY sample collection and locations. Three letter acronyms indicate adult collections (Palof, 2008). The solid black line indicates the approximate location of the break between eastern and western adult collections (Palof, 2008). The light gray bathymetry line represents a depth of 200m, which approximates the continental shelf break. Refer to Figure 2 for finer detail.

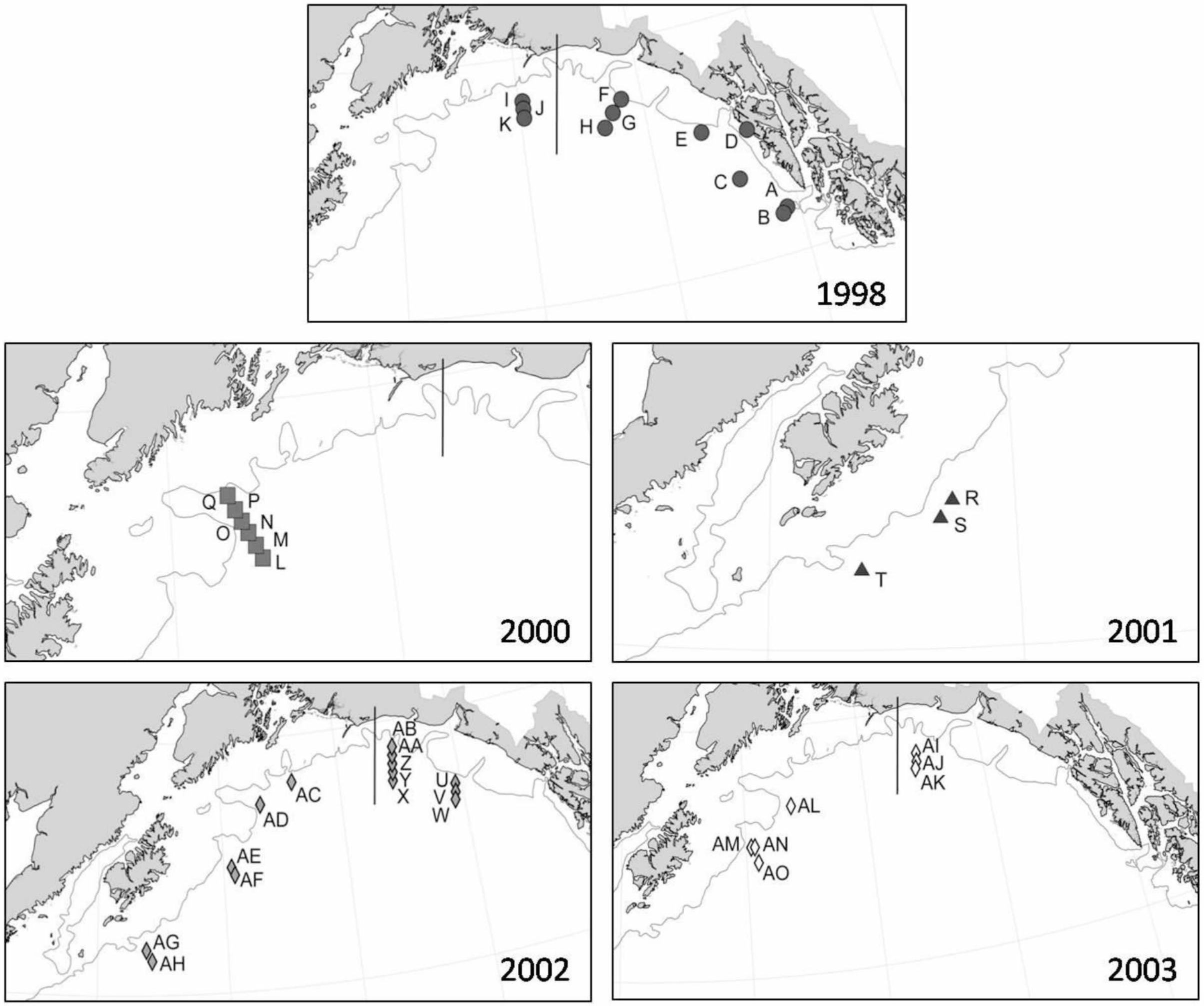

Figure 2. Maps of YOY POP sampling locations, by year. Refer to Table 1 for detailed sample collection information and locations. The solid black lines indicate the approximate location of the break between eastern and western adult collections (Palof, 2008).

Table 1. Location and dates of YOY POP sample collection. Sample designations, locations, dates of capture, and number used in POP YOY analysis. The number of samples not confirmed as POP is shown. Sample locations are depicted in Figures 1 and 2.

Sample designation	Date sampled	Location	Haul #	Latitude	Longitude	Samples POP	Samples Other spp.
	1998						
A	25-Jul	Cape Ommaney	75	55.92	-135.47	62	3
B	26-Jul	Cape Ommaney	76	55.82	-135.67	57	
C	26-Jul	Cape Ommaney	77	56.72	-136.93	55	
D	26-Jul	Cape Ommaney	78	57.63	-136.20	64	
E	27-Jul	Cape Spencer	82	57.82	-137.97	81	
F	29-Jul	Ocean Cape	86	58.83	-140.83	56	1
G	29-Jul	Ocean Cape	87	58.60	-141.27	51	3
H	29-Jul	Ocean Cape	88	58.33	-141.68	66	1
I	31-Jul	Cape St. Elias	94	59.13	-144.83	50	
J	31-Jul	Cape St. Elias	95	58.98	-144.83	53	
K	31-Jul	Cape St. Elias	96	58.80	-144.85	55	
						650	8
	1999						
		no samples retained					
	2000						
L	11-Aug	Seward Line	1	58.23	-147.93	46	18
M	11-Aug	Seward Line	2	58.38	-148.07	39	11
N	11-Aug	Seward Line	3	58.53	-148.22	43	11
O	11-Aug	Seward Line	4	58.67	-148.35	49	3
P	12-Aug	Seward Line	5	58.80	-148.48	49	11
Q	12-Aug	Seward Line	6	58.97	-148.63	31	14
						257	68
	2001						
R	1-Aug	Cape Chiniak	58	56.48	-151.53	49	
S	1-Aug	Cape Chiniak	59	56.68	-151.28	55	
T	5-Aug	Cape Kaguyak	74	55.92	-153.15	43	
						147	
	2002						
U	18-Jul	Ocean Cape	7	58.50	-140.25	50	
V	18-Jul	Ocean Cape	8	58.33	-140.30	52	
W	18-Jul	Ocean Cape	9	58.18	-140.37	43	
X	19-Jul	Cape Yakutaga	11	58.80	-142.77	32	
Y	19-Jul	Cape Yakutaga	12	58.97	-142.72	53	
Z	19-Jul	Cape Yakutaga	13	59.13	-142.68	55	
AA	19-Jul	Cape Yakutaga	14	59.30	-142.63	56	
AB	19-Jul	Cape Yakutaga	15	59.47	-142.58	21	
AC	23-Jul	Cape Clear	31	59.07	-146.97	50	
AD	24-Jul	Seward Line	37	58.68	-148.35	53	
AE	31-Jul	Gore Point	62	57.48	-149.68	30	
AF	31-Jul	Gore Point	63	57.33	-149.57	55	
AG	5-Aug	Cape Kaguyak	82	55.90	-153.13	65	
AH	5-Aug	Cape Kaguyak	83	55.68	-152.92	17	
						632	
BC	29-Sep	Bering Sea	B34	59.02	-174.92	49	
BD	29-Sep	Bering Sea	B34a	58.68	-174.92	49	3
BA	30-Sep	Bering Sea	B27	59.95	-177.52	52	
BB	30-Sep	Bering Sea	B28	60.20	-177.52	50	
						200	3
	2003						
AM	26-Jul	Gore Point	30	57.63	-149.80	30	
AN	26-Jul	Gore Point	31	57.63	-149.65	50	
AO	26-Jul	Gore Point	32, 33	57.32	-149.53	58	
AL	27-28-Jul	Seward Line	34-36, 38, 40	58.39	-148.07	45	
AI	5-Aug	Cape Yakutaga	74	59.10	-142.67	14	5
AJ	5-Aug	Cape Yakutaga	75	58.93	-142.70	19	
AK	5-Aug	Cape Yakutaga	76	58.80	-142.78	22	
						238	5
Total						2124	84

µSal6 (Miller *et al.*, 2000), µSR7-2, µSR7-7 (Westerman *et al.*, 2005), µSma5, µSma7 (Wimberger *et al.*, 1999), µSpi4, µSpi6, µSpi10, µSpi12 (Gomez-Uchida *et al.*, 2003), and µSth3B (Sekino *et al.*, 2000). All PCR reactions had a total volume of 10 µl and included approximately 1 unit of Taq polymerase and final concentrations of: 1X PCR buffer (50 mM KCl, 10 mM Tris-HCl pH 9.0, 0.1% Triton x 100; Promega, Madison, WI), 0.5 µM deoxyribonucleotide triphosphates, and approximately 0.05 to 0.1 µg DNA template. The concentrations of $MgCl_2$ and primer were adjusted for optimal amplification of each locus (Table A-1). Reactions included a fluorescently labeled primer with an IRDye® infrared dye (LI-COR, Lincoln, NE). Amplification profiles varied by locus (Table A-1), but followed the general pattern of 95°C for 5 min, 21-30 cycles of 0.5-0.75 min at 95°C, 0.5-0.75 min at a locus-specific annealing temperature, and 0.5-0.75 min at 72°C, followed by an elongation period of 3 min at 72°C.

Approximately 0.5 µl of amplified product from each PCR reaction was loaded, along with a LI-COR DNA standard (50-300 bp), onto a 0.25 mm thick 6% polyacrylamide gel (19:1 acrylamide/bisacrylamide) and run in 1X TBE (0.09M Tris-Borate, 2mM EDTA, pH 8.3) buffer at 1500 V and 45°C for 1.5 hours. A LI-COR 4300 DNA Analyzer was used to visualize the PCR product. Gel images were analyzed with the allele scoring program SAGA^{TM} v3.2 (LI-COR, Lincoln, NE).

Data Analysis

Allele frequencies were estimated with the program GENEPOP v.4 (Rousset 2008), which was also used to perform pseudo-exact tests of conformance to Hardy-

Weinberg expectations (HWE). The results of the Hardy-Weinberg tests were corrected for multiple testing by a sequential Bonferroni adjustment (Rice, 1989) and a Benjamini and Hochberg (1995) false discovery rate (B-H FDR) procedure. Since the results for the Bonferroni and B-H FDR were identical, only the results of the B-H FDR procedures are reported.

Tests for linkage disequilibrium within a transect were conducted by permutation tests with 10,000 permutations with the program GENETIX v.4.05 (Belkhir, 2004). The results were corrected for multiple testing by a sequential Bonferroni adjustment and a B-H FDR, which were identical; the results of the B-H FDR procedures are reported.

Tests of homogeneity of allelic frequencies, which were conducted by performing pseudo-exact tests in GENEPOP v.4 (Rousset, 2008), were used to examine both fine- and broad-scale divergence, as well as spatial and temporal homogeneity. Tests were conducted between hauls within transects, among transects within each year, and among transects collected in the same location in different years.

The program Arlequin v.3.1 (Excoffier *et al.*, 2005) was used to estimate the coefficient of inbreeding (F_{IS}) within transects and the fixation index, F_{ST}, which is the same as Weir and Cockerham's θ (1984), among transects within each sampling year and also within the entire data set. Permutations were conducted in Arlequin v.3.1 (Excoffier *et al.*, 2005) to estimate significance levels for the HWE probabilities and F_{ST} values.

The data from transects collected in the Gulf of Alaska were examined for evidence of an isolation-by-distance pattern (Wright, 1943; Mantel, 1967), which is interpreted from correlations between geographic distance and genetic divergence estimates. Hauls collected along the same transect were pooled together for this analysis. Pairwise F_{ST} values between transects were calculated in GENEPOP v.3.4 (Raymond and Rousset, 1995). The relationship was plotted as $F_{ST}/(1-F_{ST})$ against the corresponding great circle distances (in km) and examined for evidence of a linear relationship (Rousset, 1997). Great circle distances were corrected to approximate continental shelf-break distances because it is likely that dispersal occurs along the shelf rather than in a trans-basin pattern. A Mantel test was conducted to estimate the slope and the significance of the relationship. These analyses were conducted for both the YOY transects and the adult collections from the GOA (Palof, 2008) to compare the results of regression analyses from the two data sets.

Principal-components analyses (PCA) is a multivariate approach to clustering collections that is based on their allele-frequency distributions. Allelic frequencies for each collection were arcsine-square-root transformed and analyzed by SYSTAT v.11 (Systat Software Inc., Richmond, CA) to obtain loadings of the components. The sum of the products of the component loadings and the arcsine-square-root-transformed allele frequencies were used to plot the first and second principal components for each collection. Principle-components analysis was conducted on the five locations from which samples were taken in multiple years. The samples from Cape Ommaney (hauls A, B, C, and D) and the Bering Sea were also included in the PCA for scaling purposes. A second PCA was conducted on transects which were composed of more than one haul.

A maximum-likelihood tree was constructed to explore the relationship between the YOY transects and adult samples. The CONTML routine in the program PHYLIP

(Felsenstein, 1993) was used to estimate trees that were based on chord distances (Cavalli-Sforza and Edwards, 1967). Only collections from the GOA were used in this analysis because this is the area where there is overlap in the geographic locations of the adult and YOY samples. For the adult references, the collections included were: Dixon Entrance, Cross Sound, Yakutat, Cordova, and Kodiak (Palof, 2008).

The relationships between the adult collections from the GOA and YOY transects were also examined by performing assignment tests. These tests were conducted with the program GeneClass v.2.0.h (Piry *et al.*, 2004). The assignment criterion was based on a Bayesian method developed by Rannala and Mountain (1997). The adult collections served as a baseline to which the YOY samples were assigned. As in the maximum likelihood-tree, only collections from the GOA were included.

The two transects that were composed of more than four hauls (L·M·N·O·P·Q from the Seward Line and X·Y·Z·AA·AB from Cape Yakutaga, Figure 2) were each examined for spatial autocorrelation with the program GenAlEx v.6.1 (Peakall and Smouse, 2006). This program generates an autocorrelation coefficient, r, as well as 95% confidence intervals based on 10,000 random permutations of the data.

Contemporary effective population sizes (N_e) of each haul and each transect were estimated with the program LDNe (Waples and Do, 2008), which used linkage disequilibria between loci to estimate the effective number of breeders. This program also corrects for bias in sampling size (Waples, 2006). A jackknifing procedure was used to obtain 95% confidence intervals for these estimates.

The degree of relatedness between individuals within each haul and each transect was estimated with the program Identix v1.1 (Belkhir *et al.*, 2002), which estimates the average pairwise relatedness as well as its variance. Two different estimators were used, one based on an estimator developed by Lynch and Ritland (1999) and Identity (Belkhir *et al.*, 2002). One-thousand permutations were conducted to determine the significance of the estimates.

Results

Species Identification

Analysis of a diagnostic SNP site (Garvin *et al.*, unpublished data) confirmed that samples visually identified as POP were mostly POP. Approximately 4% (84 fish) of the YOY samples selected for this study were not confirmed as POP (Table 1). Those fish were removed from subsequent analyses. A total of 2124 samples were confirmed as YOY POP and these samples were used in further data analyses.

Microsatellite Data Analysis

The samples of POP were genotyped at 14 microsatellite loci. Descriptive statistics of the data are reported in Table A-2 and allele frequencies in Table A-3. Previously, Palof (2008) observed little evidence for null alleles, large allele dropout, linkage disequilibrium, or deviation from Hardy-Weinberg expectations in collections of adult POP. Analysis of the YOY samples showed that 43 of the 630 locus-by-population combinations differed significantly from Hardy-Weinberg expectations (HWE). After a

Benjamini and Hochberg (1995) false discovery rate (B-H FDR) adjustment, only one test (µSal1 for haul F, $p = 0.0007$) remained significant. Analysis of linkage-disequilibrium in the YOY transects was significant for one (µSal1-µSal6 for transect UVW, $p = 0.0005$) of the 1820 tests after a B-H FDR adjustment.

Pseudo-exact tests showed that there was significant, broad-scale geographic divergence among transects within a year for two of the four years that included more than one transect (Table 2; $p < 0.001$ in 1998 and $p = 0.002$ in 2002).

There was a significant difference among the allele-frequency distributions of hauls within three of the 13 transects that included multiple hauls (Table 2). Two were weakly significant, but the divergence within the 2002 Cape Yakutaga transect (X·Y·Z·AA·AB) was strong ($p < 0.001$). Scrutiny of the collections showed that this transect breaks linearly into two clear groups. Hauls X, Y, and Z all differed significantly from hauls AA ($p = 0.003$, 0.017, and 0.005 respectively) and AB ($p = 0.001$, 0.001, and 0.005 respectively), but did not differ from each other (X·Y: $p = 0.081$, X·Z: $p = 0.516$, Y·Z: $p = 0.318$). Hauls AA and AB did not differ from each other ($p = 0.135$).

There were also interannual differences among transects at three of the five locations sampled in multiple years (Table 3). At Cape Yakutaga, AI·AJ·AK from 2003 was homogenous with the X·Y·Z portion of the 2002 transect ($p = 0.158$), but differed significantly from the AA·AB portion of the 2002 transect ($p = 0.001$). The Seward Line was sampled in three different years (transects: L·M·N·O·P·Q in 2000, AD in 2002, and AL in 2003). Homogeneity tests show that AD and AL did not differ from each other ($p = 0.136$), but both differed significantly from L·M·N·O·P·Q ($p = 0.006$ and 0.003,

Table 2. Results of tests of geographic homogeneity. Tests of homogeneity of allelic frequencies within hauls and transects from each sampling year were conducted and results are reported as p-values. Analyses were conducted by performing pseudo-exact tests in GENEPOP v.4 (Rousset, 2008). Results are shown for both fine-scale (within transect) tests and for broad-scale (among transects within a year) geographic tests.

Location	Hauls	Within Transect	Among Transects
Cape Ommaney	A•B	0.286	
Cape Ommaney	C		
Cape Ommaney	D		
Cape Spencer	E		
Ocean Cape	F•G•H	**0.048**	
Cape St. Elias	I•J•K	0.062	
			< 0.001
Seward Line	L•M•N•O•P•Q	0.077	
Cape Chiniak	R•S	0.437	
Cape Kaguyak	T		
			0.914
Ocean Cape	U•V•W	0.654	
Cape Yakutaga	X•Y•Z•AA•AB	**< 0.001**	
Cape Clear	AC		
Seward Line	AD		
Gore Point	AE•AF	0.955	
Cape Kaguyak	AG•AH	**0.047**	
			0.002
Bering Sea	BA•BB	0.086	
Bering Sea	BC•BD	0.209	
			0.793
Cape Yakutaga	AI•AJ•AK	0.687	
Seward Line	AL		
Gore Point	AM•AN•AO	0.053	
			0.070

Table 3. Results of tests of temporal homogeneity. Tests of homogeneity of allelic frequencies within transects were conducted with results reported as *p*-values. Analyses were conducted by performing pseudo-exact tests in GENEPOP v.4 (Rousset, 2008). Results are shown for both fine-scale spatial (within transect) tests and for temporal (between year) tests.

Location	Year	Transect	Within Transect	Between Years
Ocean Cape	1998	F•G•H	**0.048**	
	2002	U•V•W	0.654	
				0.028
Cape Yakutaga	2002	X•Y•Z•AA•AB	**< 0.001**	
	2003	AI•AJ•AK	0.687	
				0.010
Seward Line	2000	L•M•N•O•P•Q	0.077	
	2002	AD		
	2003	AL		
				< 0.001
Gore Point	2002	AE•AF	0.955	
	2003	AM•AN•AO	0.053	
				0.053
Cape Kaguyak	2001	T		
	2002	AG•AH	**0.047**	
				0.624

respectively).

The variation among transects was partitioned into components that estimated the relative divergence among collections (F_{ST}). The F_{ST} over the entire data set was significant ($F_{ST}=0.005$, $p<10^{-4}$) as were F_{ST} values over all loci except µSma5, the least variable locus. The F_{ST} was also significant over all loci in 1998 and in the GOA in 2002 (Table 4). These results are consistent with the homogeneity tests. Among the 1998 collections, every locus except µSma5 was significant; and among the GOA 2002 collections, five of the 14 loci showed significant divergence. None of the loci exhibited significant F_{ST} values for samples collected in 2001 or in the Bering Sea in 2002. Only one locus, µSpi12, had a significant F_{ST} value for the 2003 samples. These statistics could not be calculated for the 2000 samples because only one transect was sampled that year.

Principle-components analysis (PCA) showed a general east to west geographic trend among locations that were sampled in multiple years as well as the hauls from Cape Ommaney (A, B, C, D) and the Bering Sea (Figure 3). Cape Ommaney and the Bering Sea provided the extreme east and west values for principle component 1, while locations in the middle to western GOA overlapped and were not clearly delineated on this PCA plot. In particular, the hauls from Cape Yakutaga, in the northeastern GOA, formed a fairly large polygon while the other transects clustered more tightly. Improved resolution among transects was not observed in plots that used the other principle components. The loadings of the PCA show that most of the loci contribute to this pattern. Principle component 1 explains 9.023% of the total variance and principle component 2 explains 5.863%.

Table 4. Estimates of F_{ST} among transects within a year over all loci. Weir and Cockerham (1984) estimates of F_{ST} and significance levels reported as p-values. Significant results are in bold. Values and significance levels were calculated by permutation tests in Arlequin v.3.1 (Excoffier *et al.*, 2005). There was too few transects in 2000 to calculate these statistics.

Year	F_{ST}	p
1998	0.008	**$<10^{-4}$**
2001	-0.001	0.820
2002 GOA	0.001	**0.003**
2002 BS	0.000	0.720
2003	0.001	0.111
Overall	0.005	**$<10^{-4}$**

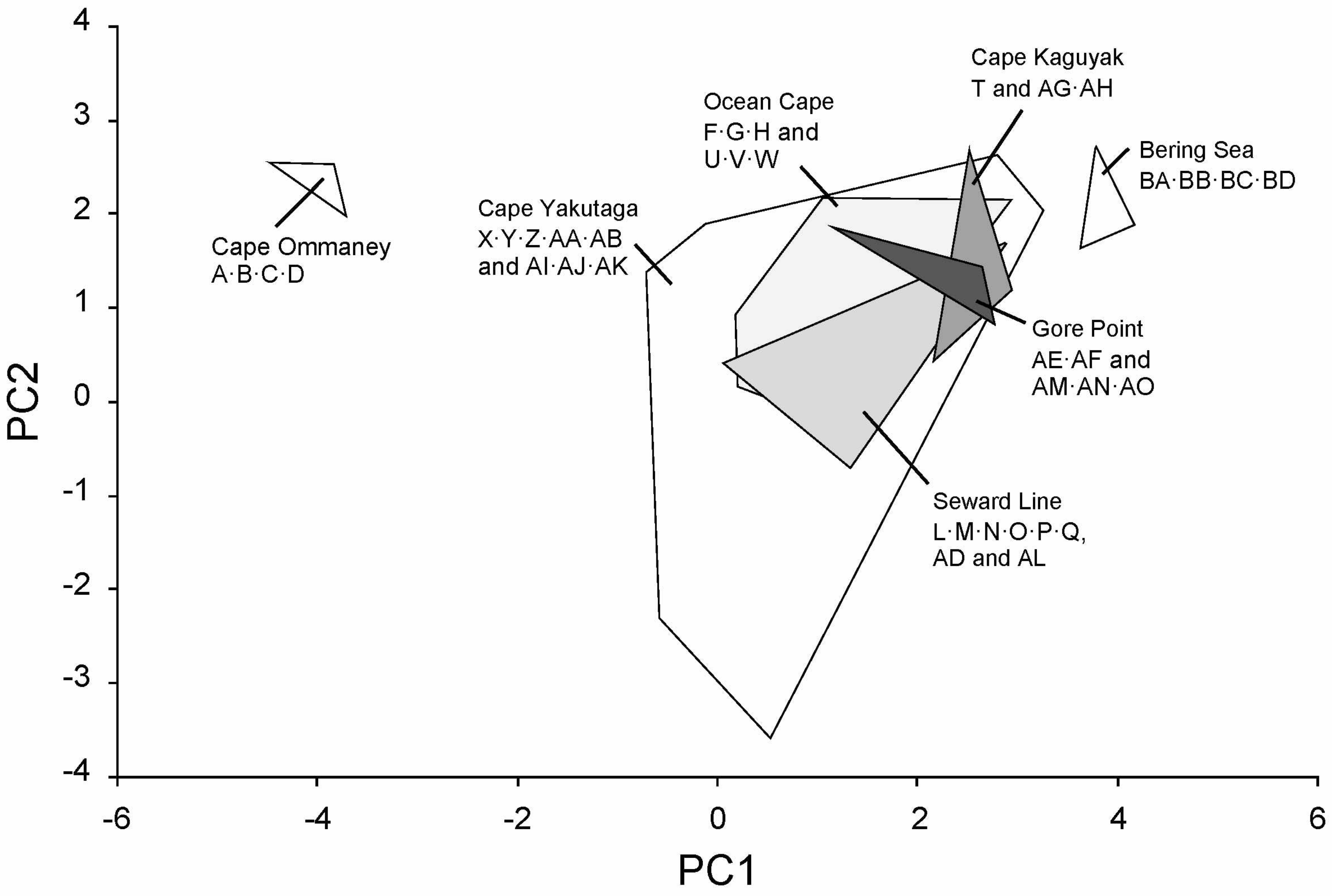

Figure 3. Principle component analysis conducted on locations with samples from multiple years. Polygons are defined by transect location. Although samples from Southeast Alaska (Cape Ommaney) and the Bering Sea were not taken in multiple years, these hauls were included for geographic scaling purposes.

A second PCA revealed that most transects composed of multiple hauls formed relatively tight clusters (Figure 4). The two exceptions included a transect from Cape Yakutaga (X·Y·Z·AA·AB in 2002) and a transect from Cape Kaguyak (AG·AH in 2002). As in the first PCA, most of the loci contribute to this pattern. Principle component 1 explains 6.865% of the total variance and principle component 2 explains 6.493%.

Previous analysis of the relationship between genetic and geographic distances in the adult POP collections, using the same method described in my study, showed a strong correlation and an isolation-by-distance (IBD) pattern (Palof, 2008). The IBD pattern observed in the GOA for both the YOY and the adult POP was similar (Figure 5). The relationships were significant for both groups (adults: $p < 0.05$ and YOY: $p < 0.002$) and had similar slopes.

The maximum-likelihood tree showed that clustering of the adult and YOY collections has a strong geographic component (Figure 6). The easternmost YOY collections (A, B, C, and D) clustered with the eastern adult collections (DXE, CSS, and YAK). Haul E appears to more resemble the western group despite its geographic location. The remaining YOY collections are interspersed roughly from east to west and group with the western GOA adult collections (COR and KOD).

Assignment tests that were used to investigate the relationship between the adult and YOY samples showed that the easternmost YOY collections were generally most similar to the eastern adult collections, whereas the western YOY collections assigned predominately to the western adult collections (Table 5). There are exceptions, such as

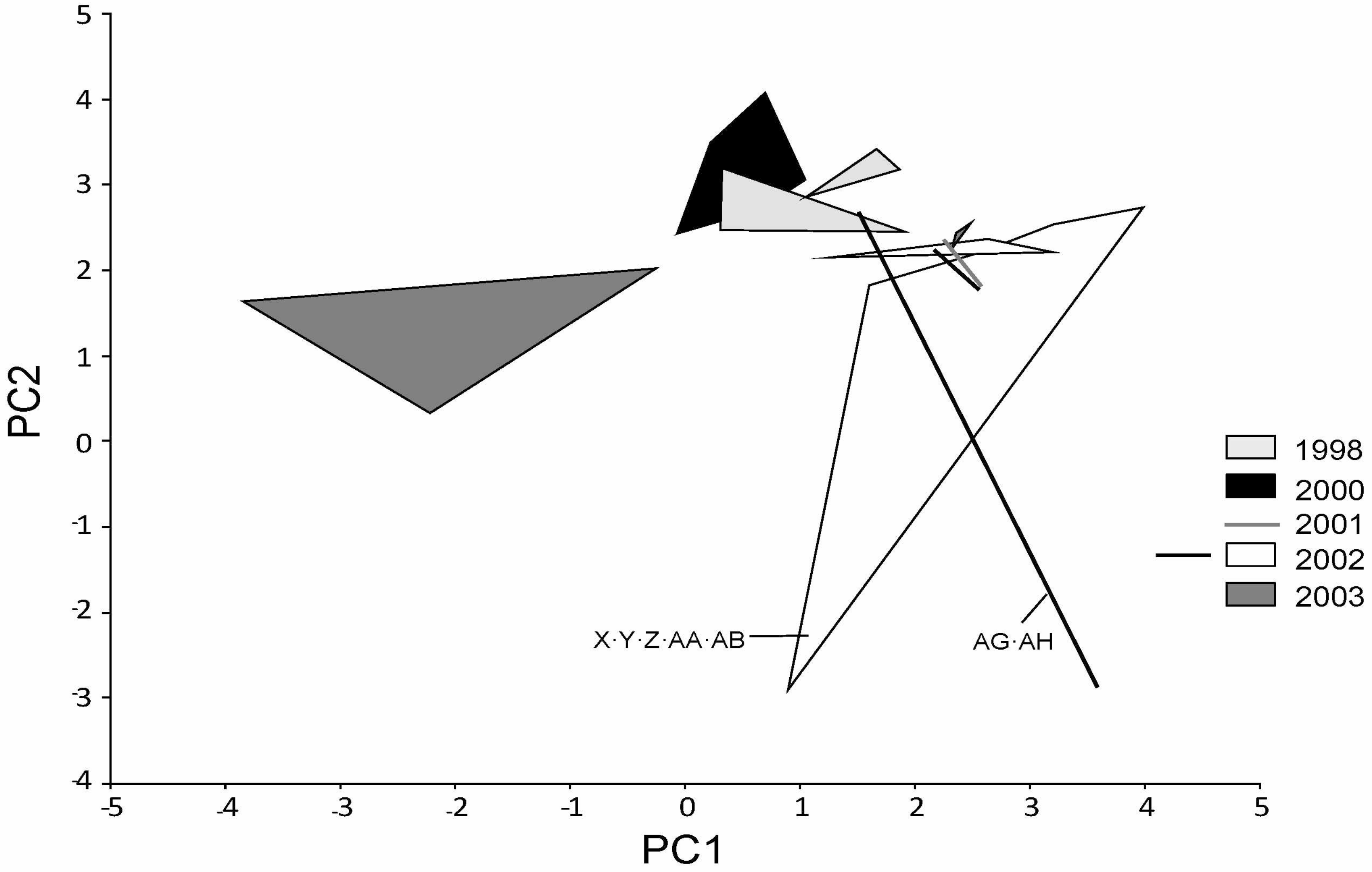

Figure 4. Principle component analysis conducted of transects with multiple hauls. Samples were grouped by transects and shadings indicate different years.

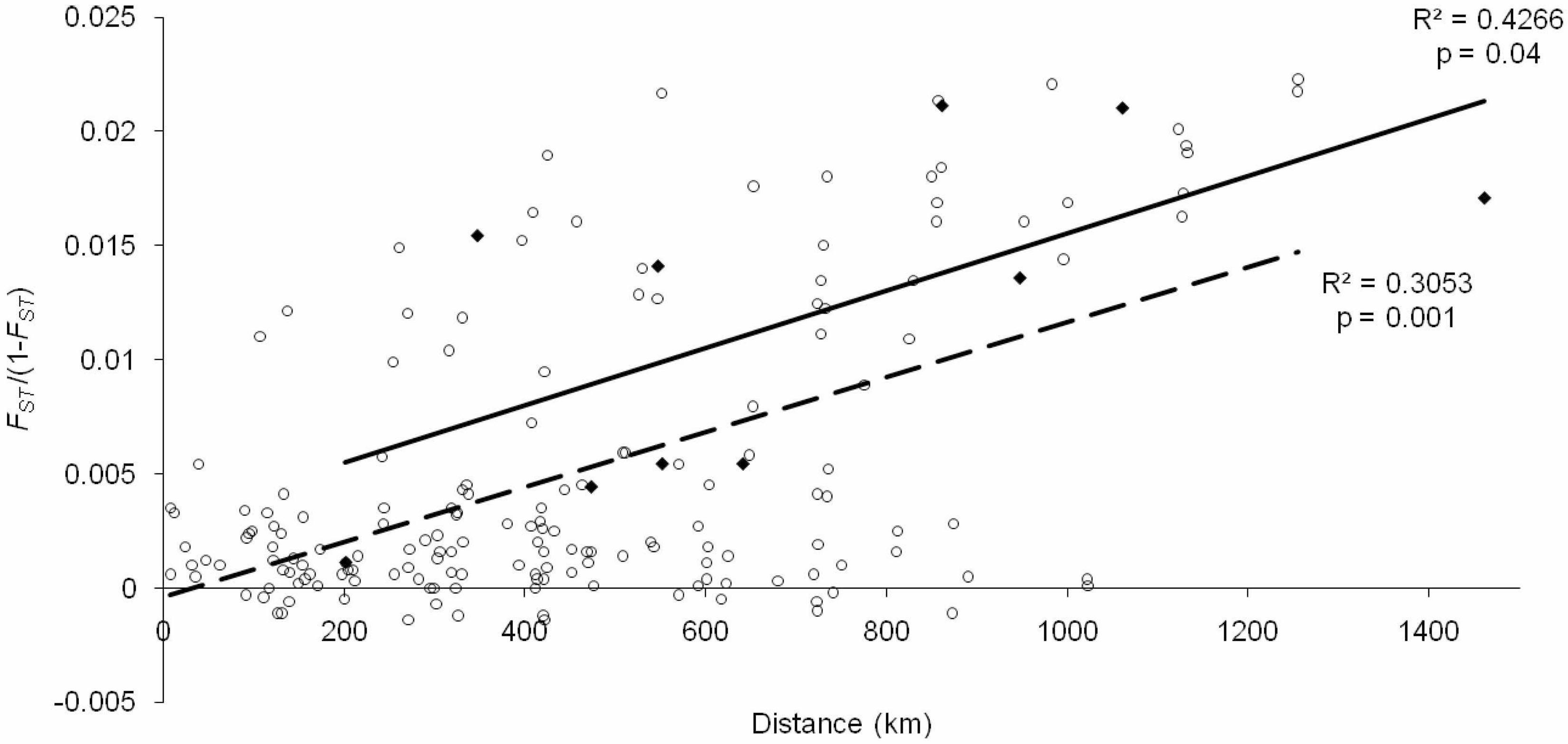

Figure 5. Regression of geographic distance on genetic distance. Geographic shelf break distance (km) regressed on standardized pairwise F_{ST} ($F_{ST}/(1- F_{ST})$) values shows an isolation by distance pattern. Genetic distances were calculated with GENEPOP v.3.4 (Raymond and Rousset, 1995). Similar patterns were observed for both the adult collections (diamonds, solid line) from the Gulf of Alaska (DXE, CSS, YAK, COR, KOD; Palof, 2008) and the Gulf of Alaska YOY transects (circles, dashed line). A Mantel test indicated that both had significant correlations between geographic and genetic distance: Adults: $y = 1.26\times10^{-5}x + 0.0029$, YOY: $y = 1.21\times10^{-5}x - 0.0004$.

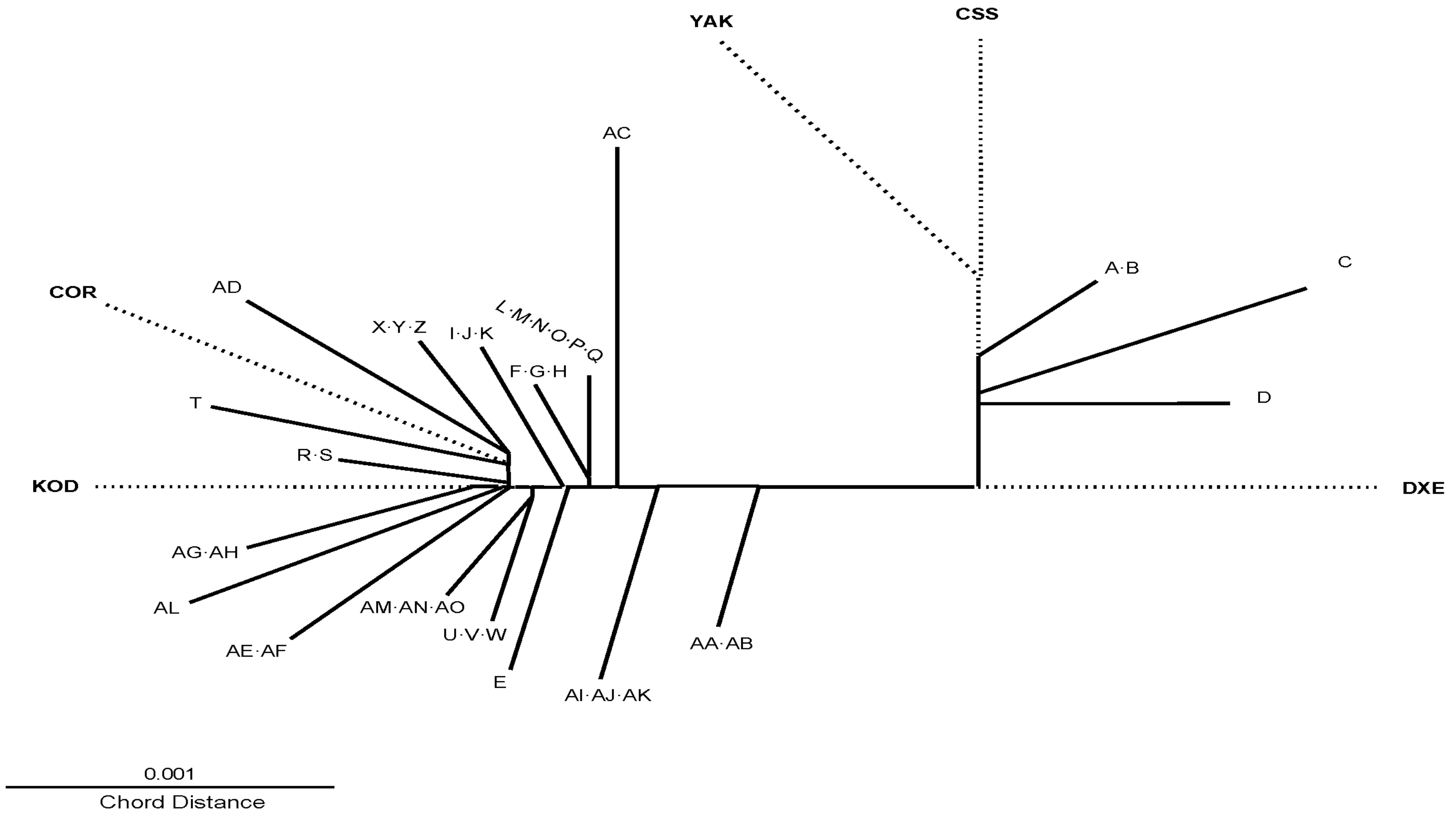

Figure 6. Tree of genetic distances among YOY and adult collections. Maximum-likelihood tree based on Cavalli-Sforza and Edwards (1967) chord distances between Gulf of Alaska (GOA) YOY transects and adult collections from the GOA (Palof, 2008). Chord distances were calculated and the tree estimated with CONTML in PHYLIP v.3.5 (Felsenstein, 1993). Adult collections are marked in bold with dashed lines. Adult collections are designated by three-letter acronyms found in Palof (2008).

Table 5. Assignment of YOY hauls and transects to adult collections located in the GOA. Assignments conducted with GeneClass v.2.0.h (Piry *et al.*, 2004). The percentage of samples assigned to each adult collection (Palof, 2008) is reported with the highest assignment for each transect in bold. Dotted lines indicate the position of these samples relative to the geographic location of the break found between eastern and western collections of adults.

		Adult Collection						Adult Collection				
Year	**Haul**	**DXE**	**CSS**	**YAK**	**COR**	**KOD**	**Transect**	**DXE**	**CSS**	**YAK**	**COR**	**KOD**
1998												
East	**A**	20.77	28.70	**38.63**	7.84	4.07	**A•B**	19.16	**34.13**	33.02	7.07	6.62
	B	17.42	**40.04**	26.92	6.23	9.38						
	C	17.65	26.26	**30.93**	17.67	7.48	**C**	17.65	26.26	**30.93**	17.67	7.48
	D	21.63	26.36	**31.20**	13.22	7.60	**D**	21.63	26.36	**31.20**	13.22	7.60
	E	11.72	9.38	11.28	**41.33**	26.29	**E**	11.72	9.38	11.28	**41.33**	26.29
West	**F**	19.40	19.27	15.47	**25.75**	20.11	**F•G•H**	18.47	11.73	9.29	**35.46**	25.05
	G	18.77	9.31	6.99	**37.57**	27.37						
	H	17.45	7.22	5.83	**42.07**	27.44						
	I	17.33	10.53	11.75	27.11	**33.28**	**I•J•K**	18.80	10.34	11.82	**31.50**	27.54
	J	19.67	7.02	16.84	**29.03**	27.43						
	K	19.29	13.36	7.05	**37.87**	22.43						
2000												
West	**L**	13.24	9.51	10.06	**41.57**	25.62	**L•M•N•O•P•Q**	16.08	12.67	10.08	**32.93**	28.24
	M	11.58	14.59	13.78	25.52	**34.53**						
	N	13.25	9.06	9.21	30.45	**38.03**						
	O	23.92	21.33	11.43	**28.60**	14.72						
	P	19.04	12.98	7.08	**35.36**	25.54						
	Q	12.77	5.82	9.24	35.88	**36.29**						
2001												
West	**R**	8.73	8.57	6.92	**52.52**	23.25	**R•S**	11.02	6.18	7.32	**46.40**	29.10
	S	13.05	4.04	7.66	**40.94**	34.31						
	T	4.49	11.60	3.41	**49.92**	30.58	**T**	4.49	11.60	3.41	**49.92**	30.58
2002												
West	**U**	13.42	7.48	5.83	**46.22**	27.05	**U•V•W**	10.83	10.98	12.60	**44.13**	21.46
	V	7.44	11.73	13.19	**47.51**	20.13						
	W	11.91	14.14	19.76	**37.62**	16.57						
	X	6.47	4.83	13.37	**46.00**	29.32	**X•Y•Z**	9.88	5.58	6.83	**50.22**	27.50
	Y	8.89	7.37	4.43	**51.36**	27.95						
	Z	12.81	4.27	5.34	**51.59**	25.99						
	AA	20.21	10.90	19.95	24.35	**24.58**	**AA•AB**	20.20	11.68	19.58	**26.22**	22.33
	AB	20.15	13.74	18.60	**31.19**	16.32						
	AC	9.23	13.09	22.20	**36.19**	19.28	**AC**	9.23	13.09	22.20	**36.19**	19.28
	AD	6.34	6.03	7.08	**54.58**	25.96	**AD**	6.34	6.03	7.08	**54.58**	25.96
	AE	11.18	8.67	7.88	**38.59**	33.69	**AE•AF**	11.18	10.07	9.58	**35.58**	33.60
	AF	11.18	10.83	10.50	**33.94**	33.55						
	AG	8.47	8.73	7.37	37.70	**37.72**	**AG•AH**	7.19	7.36	8.03	**41.73**	36.93
	AH	1.88	1.67	10.06	**54.68**	31.71						
2003												
West	**AI**	18.84	16.38	14.65	18.80	**31.34**	**AI•AJ•AK**	20.26	10.65	11.38	27.31	**30.39**
	AJ	20.96	12.59	8.28	23.29	**34.88**						
	AK	20.56	5.34	11.98	**36.21**	25.91						
	AL	9.37	8.06	6.21	35.10	**41.26**	**AL**	9.37	8.06	6.21	35.10	**41.26**
	AM	14.17	8.55	12.79	**42.45**	22.04	**AM•AN•AO**	14.28	10.31	10.14	**37.15**	27.40
	AN	9.42	11.95	6.27	**43.31**	29.05						
	AO	18.77	9.98	12.29	**29.74**	29.23						

haul E, which assigns predominantly to western collections despite its geographically more eastern location.

Analysis of spatial autocorrelation was conducted on the two transects that included more than five hauls. Significant autocorrelation was observed among hauls less than 21 km apart in Cape Yakutaga (2002, X·Y·Z·AA·AB), but no autocorrelation was detected in a transect along the Seward Line (2000, L·M·N·O·P·Q) (Figure 7).

Effective population sizes (N_e) were estimated for each transect as well as individually for each haul (Table A-4). The majority of the transects and hauls had finite point estimates for N_e, but the 95% confidence intervals included infinity for all but one transect and for all but three hauls. The non-infinite point estimates ranged from 112 to 8937. Although LDNe (Waples and Do, 2008) has some capacity to correct for the bias introduced by a sample size much smaller than the actual N_e, there is still substantial uncertainty in the estimates; however, none of the collections had a point estimate of less than 100 individuals.

The mean pairwise relatedness and the variance in relatedness of the samples within each haul were estimated with two different estimators (Table A-5). The relatedness estimator based on Lynch and Ritland (1999) showed that only three of the 45 hauls included individuals that appeared to be significantly more related than expected at random and only four of the hauls had significantly higher than expected variance in pairwise relatedness. Analysis under the Identity estimator (Belkhir *et al.*, 2002) indicated that just one haul was significantly more related than expected and five of the 45 hauls showed significantly higher than expected variance. The two estimators showed sporadic

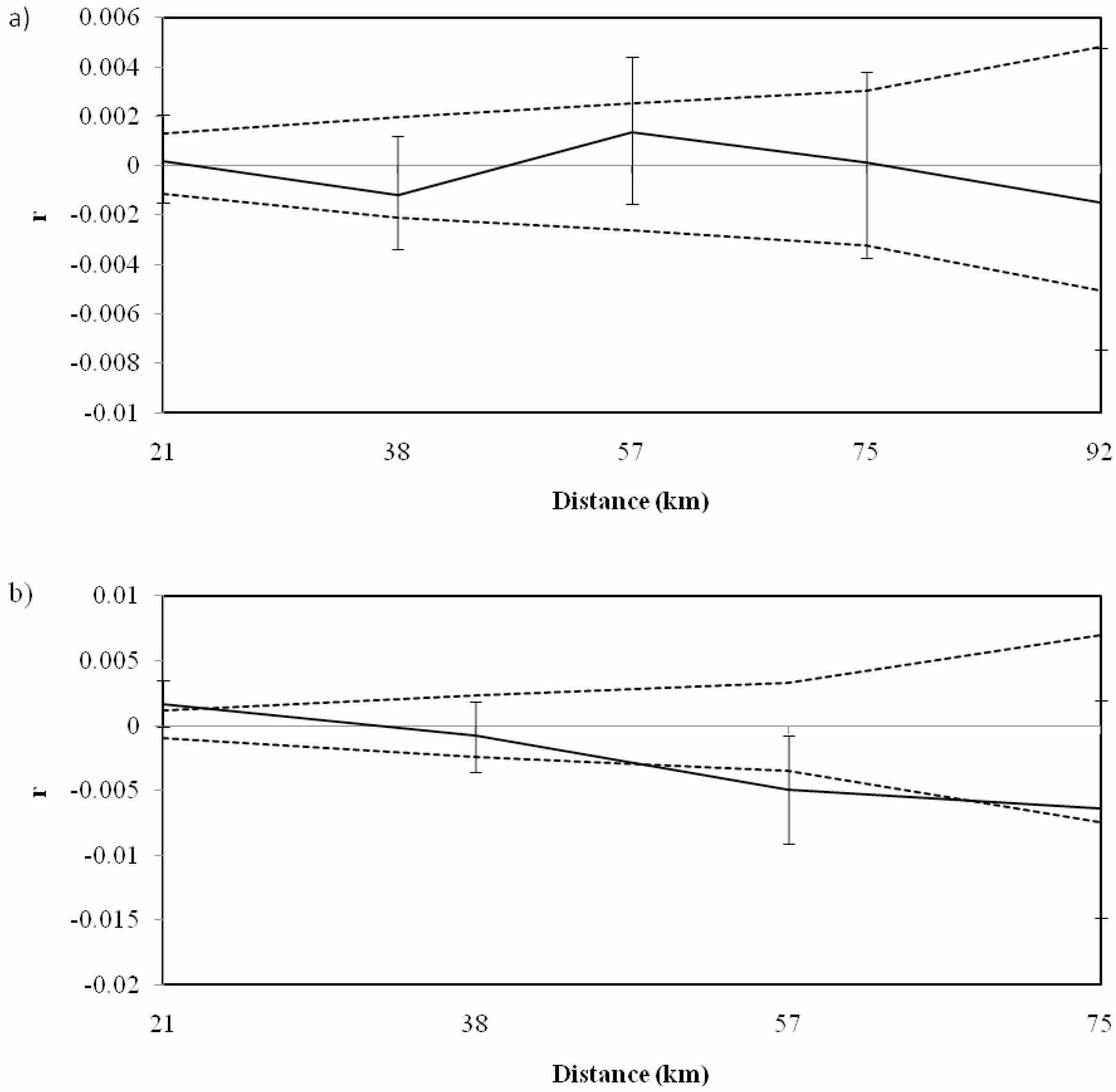

Figure 7. Spatial autocorrelation within transects composed of five or more hauls. Transects a) L·M·N·O·P·Q from the Seward Line and b) X·Y·Z·AA·AB from Cape Yakutaga. Dashed lines represent the upper and lower 95% confidence interval about the null hypothesis of no spatial structure. Error bars bound the 95% confidence interval about r as determined by bootstrap resampling.

significance but there was little correspondence in the significant hauls between the two estimators.

Discussion and Conclusions

The results of my analysis of the genetic structure of juvenile POP and the previous survey of adults (Palof, 2008) indicate that this species has limited lifetime dispersal and that genetic structure exists within the distribution range of the species. Four specific questions regarding the nature of this structure were addressed in this study. These questions were designed to characterize the broad- and fine-scale geographic structure, the temporal structure, and the relationship between the structure found in adult POP and that found in the YOY POP.

Do the collections taken within a year vary across the GOA?

As in the adult POP study (Palof, 2008), broad-scale geographic divergence was detected in the GOA YOY samples. Tests for genetic homogeneity indicated significant divergence among transects in the two years in which transects were sampled across a large geographic area (1998 and 2002). Significant F_{ST} values for these same years are consistent with this divergence. In addition, an isolation-by-distance (IBD) pattern, which echoed the pattern detected in adult POP, was observed among the YOY samples. These analyses demonstrated that the observed wide-scale divergence has a geographic basis.

Dispersal of all life stages must be limited in order to produce such a strong IBD pattern of geographic divergence in both the YOY and adults (Slatkin, 1993).

Do collections vary along sampling transects within a year?

Fine-scale geographic variation was also apparent in some of the YOY samples. Tests of genetic homogeneity indicated divergence among hauls along a transect in three of the thirteen transects that were composed of multiple hauls: transects F·G·H (1998, Ocean Cape), AG·AH (2002, Cape Kaguyak), and X·Y·Z·AA·AB (2002, Cape Yakutaga). Principle-components analysis also suggested divergence within two of these transects, X·Y·Z·AA·AB and AG·AH. Fine-scale geographic heterogeneity could result from differences in current patterns along the continental shelf and slope as compared to currents further offshore.

Assignment tests showed a decreasing influence of the eastern adult collections (DXE, CSS, and YAK) along each of these three divergent transects as the transect extended from nearshore to offshore. These results may be evidence for different larval transportation regimes between the continental shelf and slope and the deeper basin. Fine-scale genetic structure was previously reported in POP in Queen Charlotte Sound, British Columbia (Withler *et al.*, 2001). Withler *et al.* (2001) proposed that the structure they observed could be the result of selection of different current environments by the pelagic larvae. However, the oceanography of that system is heavily influenced by land masses, unlike the system involved in this study.

Of the three divergent transects, only the transect from Cape Yakutaga in 2002 (X·Y·Z·AA·AB) showed strong divergence. Homogeneity tests showed that this transect breaks into two clear groups (X·Y·Z and AA·AB). This transect is located in the area where Palof (2008) observed a discontinuity between the eastern and western adult POP. Her study indicated that the break occurred somewhere between Yakutat and Cordova. The shelf distance between these two sites is nearly 350 km; so the exact location of the break is unknown and other characteristics of the break, which include its spatial dimensions, temporal longevity, and temporal variability, are poorly understood.

Spatial autocorrelation was observed in transect X·Y·Z·AA·AB from Cape Yakutaga, but not in the other transect that consisted of more than five hauls, L·M·N·O·P·Q from the Seward Line. The spatial autocorrelation detected at Cape Yakutaga (X·Y·Z·AA·AB) may be due to variable current patterns that result from its location in the break region observed in the adult study (Palof, 2008). Another possibility is that the Seward Line transect (L·M·N·O·P·Q) does not exhibit autocorrelation because the Line was sampled entirely offshore and may not be subject to the potentially different current patterns that occur nearshore, whereas the Cape Yakutaga transect (X·Y·Z·AA·AB) is composed of hauls that were collected on both the shelf break/slope and further offshore. The Seward Line transect (L·M·N·O·P·Q) does not exhibit a trend in the assignment of individuals to hauls like that observed in the three transects which showed fine-scale divergence.

Do the genetic compositions of collections vary interannually at a particular geographic location?

Tests of genetic homogeneity also showed significant interannual divergence among transects collected from three of the five locations that were sampled in multiple years. The three locations were: Ocean Cape (transects F·G·H and U·V·W), Cape Yakutaga (X·Y·Z·AA·AB and AI·AJ·AK), and the Seward Line (L·M·N·O·P·Q, AD and AL). However, there is little support for the presence of a sweepstakes effect. The expected signature of a sweepstakes effect would be small effective population sizes (N_e) and higher average pairwise relatedness than would be predicted for random mating. All of the point estimates of N_e for the hauls exceeded 100 and many were much higher. Even the lower confidence intervals rarely fell to 50. If indeed there was an important sweepstakes effect, we would expect smaller values. In addition, relatedness indices suggested that the individuals comprising the YOY collection were no more closely related than would be expected at random. If a sweepstakes effect is occurring, it is not the driving influence on the structure observed in POP; otherwise, the similarity in the IBD patterns between the adult (Palof, 2008) and YOY POP would not have been observed. These results indicate that a sweepstakes effect probably does not substantially bias estimates of population genetic structure in adult collections.

Besides a sweepstakes effect, there are several possible explanations for the interannual divergence detected by homogeneity tests. Two of the three divergent locations, Ocean Cape and Cape Yakutaga, involve transects that were not homogenous, which indicates that variable current transportation regimes may be acting in these areas.

Transect F·G·H and U·V·W are located at Ocean Cape, a region that is oceanographically complex and distinguished by unpredictable seasonal eddy formation (Stabeno *et al.*, 2004). This region also includes the discontinuity noted in the adult study (Palof, 2008). Transect F·G·H is one of the three transects that exhibits fine-scale structure, and it includes the one haul with significant deviation from HWE after B-H FDR. This haul, F, also had a significant and positive F_{IS} value for the locus that does not meet Hardy-Weinberg expectations, which may indicate that this haul is a mixture of individuals from different sources. Transect U·V·W showed significant linkage disequilibrium between loci μSal1 and μSal6 after B-H FDR. These results indicate that there may be mixing of offspring from distinct adult populations near this area. However, if all of the collections are mixtures, they are likely mixtures from relatively discretely distributed and nearby parental sources and not sampled broadly across the geographic range. Otherwise, the IBD relationship would not be strong and would not be so similar in slope to the one observed in the adult study. One of the transects from Cape Yakutaga, X·Y·Z·AA·AB from 2002, also showed significant fine-scale variation. This transect broke into two sections, an onshore group (AA·AB) and an offshore group (X·Y·Z). In concordance with its offshore position, transect AI·AJ·AK, from this location in 2003, is homogenous with the group X·Y·Z but differed significantly from the group AA·AB.

While there is no evidence for fine-scale structure at the third location, the Seward Line, which showed interannual divergence, the date of sample collection may have influenced the results. Samples were collected from this location in three different years. Two of the samples (AD and AL) were taken at the end of July 2002 and 2003, respectively; whereas transect L·M·N·O·P·Q was collected in mid-August 2000, approximately two weeks later than the sampling dates of AD and AL, which could explain why AD and AL are homogenous and both differed from L·M·N·O·P·Q.

Is it reasonable to conclude that the YOY collections originated from geographically proximal adults?

This study indicated that most YOY fish in a sampling area are likely derived from adults in close geographic proximity. The isolation-by-distance patterns observed in both the YOY and the adults (Palof, 2008) are nearly identical. The correspondence in slopes indicates that the geographic basis of divergence that was detected in the YOY mirrors the results of the adult study (Palof, 2008). Dispersal of all life stages must be limited in order to produce such a strong IBD pattern in both YOY and adults.

In addition, both the adult study (Palof, 2008) and my study noted a distinct break between samples collected in the eastern and western GOA. Palof (2008) observed that the break was located between the adult samples from Yakutat and Cordova. The YOY study indicated a break east of Yakutat, between hauls D and E. Despite its eastern geographic location, the genetic makeup of haul E is more like the western adults than the eastern adults as indicated by the assignment tests and its position on the maximum-likelihood tree. There are several potential explanations for this result. Haul E is located offshore, and as previously discussed, offshore hauls tended to reflect the western adult collections more than hauls located on the shelf or slope. While the nearby transect F·G·H assigns to the western adult collections when the hauls are pooled, haul F, the closest to shore, assigns predominately to the eastern adult collections (DXE, CSS, and YAK). The oceanographic processes underlying the biogeographic break are poorly understood and it is possible that the location may shift from year to year. It is also evident from this study that the genetic structure has a much finer scale than was observed in the adult study (Palof, 2008). More intensive sampling of adult POP could help to clarify the origins and dispersal path of the samples from haul E.

The adult samples (Palof, 2008) do not represent a true baseline. The gaps between the samples are large, and many areas were not sampled. This may help to explain why YOY collections do not assign completely to one adult collection, even if they are located in close geographic proximity. In addition, although the adult collections all differ significantly (Palof, 2008), the divergence, as measured by F_{ST}, is rather weak, as it is for many marine species (Palumbi, 1994; Waples, 1998). Even though dispersal of all life stages is sufficiently limited to create divergence, collections are still similar in their genetic compositions. In particular, the YOY samples from the middle and western GOA show substantial similarity. This overlap can be seen both in the PCA and in the grouping of these transects on the maximum-likelihood tree. The lack of definition in these samples could be attributed to a high degree of mixing as a result of the widening of the continental shelf. The east side of the tree may exhibit better separation because the continental shelf is much narrower in that region.

Given the high mortality rates incurred by juvenile POP (Leaman, 1991), it is also likely that many of the YOY sampled in this study would neither have survived nor recruited to the adult populations. The fish in these collections may have been entrained in a current and swept away from their source populations. This study may have captured few individuals that would have entered the breeding adult populations. Fish sampled nearer to shore might be representatives of the few fish that would have eventually recruited to an adult population.

In summary, the purpose of this research was to survey genetic variation in YOY POP to gain a better understanding of the dispersal of the species. The relationship between genetic divergence and geographic separation is virtually identical in YOY and adult POP, which confirms that dispersal of POP is limited for all life stages and also demonstrates that most YOY are produced by adults in close geographic proximity. Fine-scale structure was detected and genetic differences among hauls along a transect appear to be related to the distance from shore of collection sites and thus to the differences in prevailing currents on the GOA shelf and slope. Finally, there is little evidence for an influential sweepstakes effect (Hedgecock, 1994) on the genetic structure this species, and the differences observed between years at the same sampling area may result from different dates of capture or variations in the oceanographic conditions of these areas.

The results of this study and the adult study (Palof, 2008) clearly show that there is population structure within the Alaskan range of POP. Although they are not physically constrained in the marine environment, most individuals that recruit to adult populations apparently do not travel far during the course of their lives. Moreover, although they have the opportunity and ability to disperse long distances during their lifetimes, they do not, which means that harvested fish originate close to where they are caught. Although this study gave us some insight into the dispersal patterns of this species, more research will be necessary to fully describe this complex process. Effective management and conservation of POP must take these insights into their life histories into account.

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Appendix

Table A-1. PCR amplification reaction conditions. Reaction components are reported as final concentrations in a 10-µL reaction.

	Primer Concentrations, µM					
Locus	**Forward**	**Reverse**	**Labeled**	**$MgCl_2$ (mM)**	**Temp (°C)**	**Cycles**
Sal1	0.35	0.40	0.040	3.000	50	28
Sal2	0.35	0.40	0.040	1.875	48	25
Sal3	0.35	0.40	0.040	1.875	48	25
Sal4	0.35	0.40	0.040	1.875	52	24
Sal6	0.35	0.40	0.040	1.875	55	22
SR7-2	0.30	0.35	0.035	1.250	54	21
SR7-7	0.30	0.35	0.035	1.250	56	25
Sma5	0.35	0.40	0.040	1.875	52	25
Sma7	0.35	0.40	0.040	1.875	54	28
Spi4	0.20	0.25	0.025	1.875	56	28
Spi6	0.20	0.25	0.025	1.250	58	30
Spi10	0.20	0.25	0.025	1.250	60	30
Spi12	0.20	0.25	0.025	1.875	54	30
Sth3B	0.20	0.25	0.025	1.875	60	30

Table A-2. Descriptive statistics of YOY POP microsatellite data. Includes sample size (n), number of alleles (n_a), unbiased expected heterozygosity (H_E), effective number of alleles (n_{eff}), and observed inbreeding coefficient (F_{is}) for each of the 45 hauls (Figure 1). Summary over populations includes an estimate of total subpopulation heterozygosity (H_T) and fixation indices (F_{ST}).

		Locus													
Haul	**Value**	**Sal1**	**Sal2**	**Sal3**	**Sal4**	**Sal6**	**Spi4**	**Spi6**	**Spi10**	**Spi12**	**Sth3B**	**Sma5**	**Sma7**	**SR7-2**	**SR7-7**
A	n	61	62	62	62	62	61	62	62	62	62	62	62	62	62
	n_a	22	12	13	14	9	14	12	9	8	12	4	21	37	23
	H_E	0.911	0.810	0.861	0.785	0.653	0.854	0.809	0.744	0.560	0.795	0.182	0.909	0.968	0.901
	n_{eff}	10.251	5.078	6.840	4.509	2.838	6.500	5.068	3.806	2.251	4.714	1.220	10.156	25.290	9.353
	F_{is}	0.100	0.004	-0.012	0.055	0.087	0.059	0.003	0.089	-0.008	0.087	0.023	0.024	-0.033	0.033
B	n	57	57	57	57	57	55	57	57	57	57	57	57	57	57
	n_a	22	14	11	13	7	13	15	9	8	11	4	22	37	26
	H_E	0.912	0.795	0.839	0.810	0.606	0.809	0.807	0.818	0.610	0.835	0.298	0.911	0.973	0.906
	n_{eff}	10.298	4.740	5.940	5.061	2.503	5.050	5.010	5.262	2.531	5.807	1.418	10.282	27.888	9.875
	F_{is}	0.134	-0.103	-0.004	0.025	-0.014	0.012	-0.087	0.056	0.023	-0.030	0.116	-0.002	-0.010	-0.045
C	n	55	55	55	55	55	53	55	55	55	55	55	55	55	55
	n_a	21	12	15	14	7	16	15	8	9	11	3	24	34	25
	H_E	0.894	0.814	0.850	0.779	0.656	0.839	0.862	0.788	0.628	0.795	0.216	0.920	0.964	0.905
	n_{eff}	8.730	5.158	6.335	4.390	2.850	5.901	6.813	4.549	2.648	4.697	1.271	11.372	22.325	9.727
	F_{is}	0.085	0.084	0.038	-0.027	0.113	0.033	0.178	0.077	-0.013	0.039	0.242	-0.027	-0.019	-0.004
D	n	64	64	64	64	61	64	64	64	64	64	64	64	64	64
	n_a	20	12	13	15	9	16	17	10	9	12	4	24	39	25
	H_E	0.922	0.812	0.853	0.813	0.685	0.854	0.805	0.794	0.562	0.786	0.214	0.898	0.968	0.890
	n_{eff}	11.736	5.143	6.517	5.175	3.111	6.507	4.947	4.714	2.260	4.536	1.270	9.143	25.362	8.569
	F_{is}	0.017	0.038	-0.026	0.059	0.114	0.085	0.087	-0.063	0.055	0.086	0.053	0.096	0.016	-0.054
E	n	80	81	81	81	81	79	81	81	81	81	81	81	81	81
	n_a	23	16	12	15	11	15	15	10	12	11	5	23	41	30
	H_E	0.927	0.711	0.813	0.869	0.789	0.781	0.885	0.800	0.716	0.820	0.257	0.900	0.964	0.902
	n_{eff}	12.673	3.404	5.209	7.323	4.612	4.464	8.300	4.882	3.471	5.422	1.342	9.481	23.858	9.677
	F_{is}	0.029	0.027	0.044	-0.038	0.139	0.044	-0.004	0.044	0.000	-0.038	-0.011	0.013	-0.038	0.015
F	n	55	56	56	56	56	55	56	56	56	56	56	56	56	56
	n_a	21	13	13	12	8	16	12	9	13	13	4	24	34	30
	H_E	0.932	0.786	0.800	0.830	0.739	0.862	0.866	0.798	0.647	0.857	0.185	0.896	0.965	0.932
	n_{eff}	13.011	4.522	4.840	5.640	3.733	6.859	7.024	4.770	2.784	6.588	1.225	8.859	22.807	13.012
	F_{is}	0.064	0.069	-0.004	0.032	0.082	0.051	0.072	0.083	0.034	0.125	-0.061	0.063	0.038	0.042
G	n	51	51	51	51	50	50	51	51	51	51	51	49	51	51
	n_a	18	13	10	11	8	16	13	10	13	10	4	17	37	21
	H_E	0.917	0.676	0.815	0.838	0.751	0.843	0.900	0.810	0.682	0.816	0.218	0.883	0.969	0.901
	n_{eff}	10.770	3.030	5.176	5.858	3.885	6.068	9.207	5.055	3.087	5.239	1.275	7.872	24.195	9.306
	F_{is}	0.124	-0.073	0.013	0.017	0.175	-0.044	-0.046	0.032	-0.063	-0.081	0.100	0.098	0.049	-0.023
H	n	66	66	66	66	66	62	66	66	66	66	66	66	66	66
	n_a	23	11	13	11	8	15	16	8	11	10	6	22	37	28
	H_E	0.940	0.659	0.835	0.850	0.751	0.835	0.886	0.801	0.714	0.824	0.212	0.885	0.963	0.888
	n_{eff}	14.842	2.887	5.824	6.382	3.928	5.802	8.289	4.878	3.431	5.486	1.267	8.211	22.396	8.401
	F_{is}	0.033	0.057	0.002	0.091	0.012	0.053	0.008	-0.041	-0.040	-0.067	0.002	-0.028	-0.007	0.062

		Locus													
Haul	**Value**	**Sal1**	**Sal2**	**Sal3**	**Sal4**	**Sal6**	**Spi4**	**Spi6**	**Spi10**	**Spi12**	**Sth3B**	**Sma5**	**Sma7**	**SR7-2**	**SR7-7**
I	n	50	50	50	50	50	50	50	50	50	50	50	50	48	50
	n_a	21	12	11	10	8	18	13	9	13	12	4	19	32	23
	H_E	0.916	0.673	0.790	0.841	0.766	0.875	0.845	0.811	0.756	0.813	0.151	0.899	0.960	0.904
	n_{eff}	10.707	3.001	4.591	6.024	4.153	7.452	6.098	5.025	3.971	5.113	1.176	9.141	20.035	9.488
	F_{is}	0.017	-0.070	0.013	-0.117	-0.070	0.017	0.029	0.186	0.021	0.065	-0.058	-0.023	0.002	0.026
J	n	51	53	52	53	53	53	53	53	53	53	53	52	53	53
	n_a	22	12	13	14	7	14	15	10	13	12	6	20	33	25
	H_E	0.916	0.726	0.849	0.863	0.780	0.744	0.862	0.784	0.674	0.825	0.128	0.882	0.966	0.913
	n_{eff}	10.704	3.560	6.296	6.885	4.389	3.786	6.818	4.469	3.011	5.470	1.145	7.906	23.215	10.462
	F_{is}	0.037	0.065	-0.065	0.016	0.105	0.112	0.059	-0.011	0.021	0.063	-0.033	-0.047	-0.016	-0.034
K	n	55	55	55	55	55	55	55	55	55	55	55	55	55	55
	n_a	23	13	11	12	10	14	12	9	13	10	4	22	33	26
	H_E	0.927	0.715	0.831	0.860	0.780	0.785	0.885	0.785	0.729	0.836	0.319	0.863	0.958	0.926
	n_{eff}	12.149	3.432	5.638	6.783	4.410	4.495	8.077	4.482	3.595	5.829	1.462	6.930	19.771	12.149
	F_{is}	0.058	0.034	0.081	-0.057	-0.049	0.027	0.034	0.073	0.127	0.000	-0.027	-0.032	-0.006	-0.001
L	n	46	46	44	46	46	46	45	46	46	46	46	46	45	46
	n_a	20	13	9	11	8	15	14	10	10	13	5	22	32	27
	H_E	0.927	0.741	0.809	0.846	0.750	0.844	0.887	0.780	0.664	0.846	0.222	0.898	0.965	0.933
	n_{eff}	11.921	3.752	4.958	6.089	3.883	6.011	8.084	4.372	2.915	6.107	1.282	8.947	22.011	12.942
	F_{is}	0.109	-0.115	0.214	0.075	-0.014	0.098	0.073	0.053	-0.015	0.023	-0.075	0.032	0.010	-0.026
M	n	39	39	36	39	39	37	39	39	39	39	39	39	39	38
	n_a	21	12	8	11	7	16	14	10	10	12	4	18	35	21
	H_E	0.920	0.737	0.796	0.870	0.738	0.819	0.901	0.788	0.651	0.836	0.147	0.874	0.974	0.880
	n_{eff}	10.942	3.670	4.645	7.108	3.705	5.186	9.135	4.527	2.809	5.729	1.171	7.313	25.780	7.600
	F_{is}	-0.031	0.026	-0.012	-0.002	-0.182	0.109	-0.052	-0.106	-0.142	-0.012	-0.043	0.003	-0.001	-0.017
N	n	43	43	43	43	43	43	43	43	43	43	43	43	43	43
	n_a	19	9	12	12	9	14	14	10	12	13	4	16	29	24
	H_E	0.916	0.806	0.837	0.877	0.796	0.812	0.843	0.823	0.673	0.861	0.236	0.877	0.951	0.891
	n_{eff}	10.506	4.918	5.796	7.486	4.663	5.052	5.974	5.375	2.987	6.724	1.304	7.516	16.658	8.386
	F_{is}	0.009	-0.010	0.000	0.072	0.094	0.026	0.034	-0.017	0.033	0.001	0.015	-0.061	-0.027	0.035
O	n	49	49	49	49	49	45	49	49	49	49	49	49	49	49
	n_a	20	12	12	11	9	13	14	10	8	13	4	21	37	27
	H_E	0.918	0.753	0.784	0.844	0.773	0.818	0.901	0.787	0.698	0.850	0.259	0.895	0.971	0.905
	n_{eff}	10.791	3.923	4.455	6.109	4.276	5.239	9.235	4.526	3.240	6.285	1.345	8.795	25.407	9.509
	F_{is}	0.088	-0.003	0.010	-0.088	-0.082	-0.032	0.049	-0.011	-0.082	0.040	-0.103	-0.003	0.012	0.098
P	n	49	49	49	49	49	48	49	49	49	49	49	49	49	49
	n_a	21	12	11	12	8	16	13	9	10	10	4	20	36	24
	H_E	0.919	0.663	0.795	0.866	0.789	0.797	0.892	0.774	0.722	0.822	0.336	0.883	0.967	0.906
	n_{eff}	11.065	2.916	4.717	6.959	4.556	4.731	8.606	4.284	3.508	5.365	1.498	7.924	23.424	9.721
	F_{is}	0.023	-0.046	-0.077	0.057	0.069	0.059	-0.052	-0.001	-0.017	0.032	0.089	0.053	0.008	-0.059
Q	n	31	31	30	31	31	30	31	31	31	31	31	31	31	30
	n_a	19	10	7	11	6	15	11	9	11	11	4	17	31	24
	H_E	0.934	0.658	0.789	0.876	0.758	0.781	0.888	0.787	0.763	0.883	0.184	0.903	0.974	0.925
	n_{eff}	12.321	2.831	4.467	7.308	3.922	4.276	7.877	4.439	4.013	7.537	1.220	8.940	24.329	11.043
	F_{is}	-0.002	0.069	-0.057	-0.067	0.021	0.146	0.056	-0.066	0.028	0.124	0.123	-0.001	-0.026	-0.009

		Locus													
Haul	**Value**	**Sal1**	**Sal2**	**Sal3**	**Sal4**	**Sal6**	**Spi4**	**Spi6**	**Spi10**	**Spi12**	**Sth3B**	**Sma5**	**Sma7**	**SR7-2**	**SR7-7**
R	n	49	46	49	49	49	48	48	49	49	49	49	49	49	49
	n_a	21	14	13	13	8	14	13	9	9	10	5	16	36	24
	H_E	0.921	0.678	0.858	0.858	0.751	0.796	0.886	0.803	0.619	0.821	0.156	0.897	0.962	0.936
	n_{eff}	11.379	3.042	6.651	6.660	3.904	4.721	8.084	4.855	2.579	5.330	1.183	8.811	20.609	13.642
	F_{is}	-0.019	-0.058	-0.023	-0.046	-0.005	-0.020	0.060	0.111	0.077	0.031	-0.048	0.135	0.024	-0.003
S	n	55	55	55	55	55	53	54	55	55	55	55	55	55	55
	n_a	20	11	11	11	7	16	12	8	11	13	3	19	31	21
	H_E	0.923	0.661	0.866	0.875	0.760	0.784	0.865	0.782	0.711	0.861	0.155	0.879	0.961	0.917
	n_{eff}	11.590	2.899	7.060	7.544	4.050	4.487	6.984	4.458	3.384	6.844	1.181	7.766	21.303	10.940
	F_{is}	0.054	-0.046	-0.029	-0.018	0.043	-0.059	0.015	-0.046	0.028	-0.056	-0.057	-0.013	-0.040	-0.031
T	n	43	42	43	43	43	43	43	43	43	43	43	43	43	42
	n_a	20	15	9	11	8	15	14	9	10	12	4	25	33	28
	H_E	0.935	0.690	0.857	0.866	0.791	0.801	0.881	0.778	0.610	0.820	0.236	0.914	0.958	0.939
	n_{eff}	12.975	3.139	6.534	6.938	4.582	4.796	7.672	4.351	2.517	5.260	1.305	10.359	18.772	13.890
	F_{is}	0.130	-0.001	-0.004	-0.021	0.000	-0.017	0.102	-0.106	0.047	0.064	0.016	-0.044	-0.020	-0.040
U	n	50	50	50	50	50	47	50	50	50	50	50	50	50	49
	n_a	22	10	13	15	8	16	15	9	12	11	3	21	29	25
	H_E	0.931	0.692	0.859	0.877	0.778	0.776	0.881	0.808	0.696	0.831	0.216	0.915	0.946	0.917
	n_{eff}	12.690	3.177	6.685	7.599	4.344	4.294	7.825	4.985	3.211	5.656	1.271	10.571	15.723	10.695
	F_{is}	0.011	0.018	0.022	0.020	0.049	0.068	0.047	0.034	0.023	-0.035	0.166	0.038	0.006	0.087
V	n	52	52	52	52	52	51	52	52	52	52	52	52	52	52
	n_a	23	11	14	12	8	16	14	10	9	11	5	24	36	23
	H_E	0.929	0.704	0.864	0.886	0.785	0.791	0.867	0.826	0.595	0.811	0.335	0.931	0.963	0.919
	n_{eff}	12.404	3.296	6.925	8.145	4.488	4.620	7.088	5.474	2.438	5.078	1.497	12.695	21.460	11.151
	F_{is}	0.048	0.126	0.021	0.023	0.069	0.009	-0.043	0.092	-0.034	-0.020	0.083	0.049	0.021	-0.025
W	n	42	43	43	43	43	43	43	43	43	43	43	43	43	43
	n_a	17	12	11	10	7	16	12	8	9	11	3	17	30	23
	H_E	0.930	0.786	0.847	0.826	0.740	0.756	0.880	0.811	0.643	0.796	0.091	0.875	0.965	0.899
	n_{eff}	12.124	4.477	6.123	5.430	3.713	3.955	7.593	5.038	2.749	4.693	1.098	7.396	21.626	8.954
	F_{is}	0.130	0.054	0.067	0.071	0.120	0.047	0.128	0.054	-0.048	-0.023	-0.028	-0.037	0.012	0.017
X	n	32	32	32	32	32	32	32	32	32	32	32	32	32	32
	n_a	22	9	12	13	7	15	11	8	10	10	5	17	28	19
	H_E	0.932	0.680	0.872	0.881	0.780	0.766	0.845	0.819	0.609	0.827	0.206	0.909	0.958	0.894
	n_{eff}	11.907	3.043	7.038	7.447	4.285	4.064	5.936	5.172	2.495	5.390	1.255	9.526	17.504	8.292
	F_{is}	0.095	-0.195	0.032	0.077	0.078	-0.020	0.039	-0.069	0.077	-0.020	-0.061	-0.032	-0.012	0.021
Y	n	52	53	53	53	53	53	53	53	53	53	53	53	53	53
	n_a	24	10	11	10	7	14	13	9	12	14	4	24	33	25
	H_E	0.931	0.704	0.853	0.849	0.792	0.761	0.843	0.776	0.689	0.847	0.272	0.911	0.950	0.932
	n_{eff}	12.846	3.305	6.413	6.334	4.647	4.059	6.054	4.325	3.149	6.222	1.368	10.308	16.871	13.065
	F_{is}	0.009	-0.073	0.071	-0.088	0.000	-0.042	-0.030	0.028	-0.013	-0.092	0.027	-0.014	0.007	-0.053
Z	n	55	55	55	55	55	53	55	55	55	55	55	55	55	55
	n_a	25	12	9	12	8	19	14	9	10	11	6	18	36	28
	H_E	0.913	0.676	0.832	0.866	0.764	0.834	0.868	0.818	0.695	0.867	0.156	0.885	0.957	0.928
	n_{eff}	10.504	3.025	5.702	7.068	4.116	5.744	7.126	5.247	3.218	7.051	1.184	8.132	19.268	12.398
	F_{is}	-0.016	0.004	-0.027	-0.007	-0.048	-0.018	0.036	0.155	-0.125	0.119	-0.046	-0.007	-0.026	0.020

		Locus													
Haul	**Value**	**Sal1**	**Sal2**	**Sal3**	**Sal4**	**Sal6**	**Spi4**	**Spi6**	**Spi10**	**Spi12**	**Sth3B**	**Sma5**	**Sma7**	**SR7-2**	**SR7-7**
AA	n	56	56	56	56	56	56	56	56	56	56	56	56	55	56
	n_a	18	12	10	13	9	15	15	10	12	12	4	25	37	26
	H_E	0.913	0.790	0.839	0.840	0.699	0.803	0.836	0.783	0.658	0.792	0.225	0.919	0.959	0.925
	n_{eff}	10.384	4.588	5.939	5.956	3.250	4.885	5.824	4.464	2.878	4.643	1.287	11.200	20.167	12.062
	F_{is}	0.120	0.096	-0.065	0.022	0.080	0.043	0.017	0.042	-0.113	0.099	-0.033	0.048	0.034	0.016
AB	n	21	21	21	21	21	21	21	21	21	21	21	21	21	21
	n_a	12	9	8	13	6	12	12	7	7	11	5	15	22	19
	H_E	0.907	0.781	0.848	0.886	0.614	0.706	0.837	0.824	0.656	0.814	0.376	0.913	0.964	0.921
	n_{eff}	8.563	4.180	5.690	7.350	2.492	3.219	5.444	5.098	2.765	4.794	1.584	9.000	16.962	10.023
	F_{is}	0.108	0.085	0.157	0.032	0.070	-0.012	0.033	0.017	0.129	0.181	-0.139	0.113	0.012	-0.034
AC	n	50	50	50	50	50	50	50	50	50	50	50	50	50	50
	n_a	25	11	10	14	8	15	13	9	11	10	5	21	35	25
	H_E	0.916	0.772	0.826	0.872	0.726	0.789	0.829	0.796	0.651	0.831	0.256	0.890	0.964	0.883
	n_{eff}	10.730	4.263	5.489	7.342	3.551	4.533	5.562	4.726	2.820	5.612	1.339	8.418	22.222	7.924
	F_{is}	0.040	-0.140	-0.066	-0.055	0.091	0.163	0.035	-0.005	-0.137	0.085	-0.095	0.034	-0.016	0.003
AD	n	53	53	53	53	53	50	53	53	53	53	53	53	53	53
	n_a	24	9	11	13	7	17	11	7	12	12	5	22	32	24
	H_E	0.917	0.723	0.867	0.869	0.796	0.774	0.851	0.811	0.668	0.835	0.128	0.886	0.955	0.874
	n_{eff}	10.867	3.527	7.058	7.193	4.733	4.270	6.377	5.075	2.944	5.798	1.145	8.084	18.727	7.402
	F_{is}	0.033	-0.018	0.042	0.001	0.029	0.070	0.003	0.046	0.152	0.006	-0.036	0.105	-0.047	0.050
AE	n	30	30	30	30	30	29	30	30	30	30	30	30	30	30
	n_a	20	9	9	12	7	11	10	9	11	11	4	18	32	21
	H_E	0.944	0.705	0.774	0.856	0.790	0.792	0.886	0.823	0.714	0.819	0.299	0.913	0.967	0.945
	n_{eff}	13.954	3.279	4.186	6.228	4.500	4.462	7.725	5.202	3.352	5.172	1.418	9.730	20.455	13.954
	F_{is}	0.012	-0.134	-0.034	0.183	-0.055	0.173	0.060	0.109	0.067	-0.099	-0.113	0.051	0.001	0.083
AF	n	55	55	55	55	54	55	55	55	55	54	55	55	54	54
	n_a	23	11	10	16	8	17	15	10	11	10	4	22	35	28
	H_E	0.929	0.672	0.839	0.888	0.803	0.776	0.894	0.796	0.560	0.815	0.245	0.900	0.965	0.937
	n_{eff}	12.578	2.994	5.914	8.322	4.876	4.318	8.806	4.734	2.247	5.203	1.322	9.209	22.605	13.853
	F_{is}	0.022	-0.001	0.068	-0.003	0.101	0.134	-0.057	-0.005	-0.006	-0.022	-0.112	0.010	0.021	0.051
AG	n	65	65	65	65	65	65	65	65	65	65	65	65	65	65
	n_a	21	12	9	11	9	15	12	10	11	12	5	20	39	28
	H_E	0.902	0.654	0.823	0.830	0.777	0.786	0.875	0.761	0.757	0.844	0.289	0.875	0.972	0.919
	n_{eff}	9.548	2.846	5.441	5.664	4.367	4.538	7.620	4.070	4.005	6.154	1.401	7.579	27.524	11.327
	F_{is}	0.011	0.035	0.065	-0.001	-0.030	0.041	-0.037	0.090	0.085	-0.058	0.094	0.033	0.066	0.012
AH	n	17	17	17	17	17	17	17	17	17	17	17	17	17	17
	n_a	12	7	10	11	7	8	11	7	8	10	4	15	18	17
	H_E	0.836	0.658	0.860	0.888	0.820	0.792	0.849	0.783	0.568	0.871	0.222	0.893	0.926	0.941
	n_{eff}	5.352	2.779	6.084	7.225	4.898	4.250	5.612	4.188	2.249	6.568	1.276	7.410	9.966	11.115
	F_{is}	-0.055	-0.073	-0.026	0.006	-0.004	0.183	0.100	-0.052	-0.243	-0.080	-0.058	0.078	-0.016	0.125
AM	n	30	30	30	30	30	29	30	30	30	30	30	30	30	30
	n_a	22	13	9	10	7	12	14	7	10	11	4	16	25	20
	H_E	0.937	0.720	0.834	0.875	0.778	0.794	0.870	0.785	0.603	0.850	0.219	0.882	0.949	0.907
	n_{eff}	12.500	3.429	5.539	7.171	4.245	4.522	6.923	4.369	2.456	6.164	1.274	7.531	14.754	9.278
	F_{is}	0.075	-0.018	0.081	-0.029	0.058	0.132	0.004	0.066	0.005	-0.137	0.087	-0.021	0.016	-0.029

		Locus													
Haul	**Value**	**Sal1**	**Sal2**	**Sal3**	**Sal4**	**Sal6**	**Spi4**	**Spi6**	**Spi10**	**Spi12**	**Sth3B**	**Sma5**	**Sma7**	**SR7-2**	**SR7-7**
AN	n	50	50	50	50	50	48	50	50	50	50	50	50	50	50
	n_a	20	10	13	11	8	16	12	10	10	8	3	17	32	25
	H_E	0.913	0.635	0.854	0.878	0.800	0.757	0.829	0.805	0.671	0.813	0.133	0.902	0.961	0.912
	n_{eff}	10.267	2.687	6.485	7.599	4.803	3.993	5.549	4.931	2.978	5.144	1.151	9.363	20.921	10.225
	F_{is}	0.102	0.118	-0.030	0.089	0.000	-0.073	0.059	0.007	-0.014	-0.107	0.248	0.025	-0.040	0.079
AO	n	58	58	58	58	58	58	58	58	58	58	58	58	58	58
	n_a	22	12	12	12	7	16	14	8	10	13	5	23	34	26
	H_E	0.918	0.716	0.863	0.833	0.740	0.819	0.795	0.780	0.647	0.794	0.148	0.923	0.959	0.919
	n_{eff}	11.121	3.443	6.901	5.755	3.738	5.294	4.731	4.392	2.792	4.705	1.172	11.742	20.204	11.289
	F_{is}	0.024	0.061	0.021	-0.035	0.114	0.116	-0.063	0.138	-0.039	0.002	-0.048	0.010	-0.025	0.006
AL	n	45	45	45	45	45	45	44	45	45	45	45	45	45	45
	n_a	18	12	9	15	8	15	13	8	13	9	4	21	33	23
	H_E	0.906	0.663	0.847	0.876	0.802	0.744	0.842	0.784	0.739	0.848	0.206	0.899	0.964	0.912
	n_{eff}	9.529	2.899	6.127	7.472	4.810	3.782	5.957	4.446	3.692	6.193	1.255	8.940	21.204	10.202
	F_{is}	0.093	0.027	0.108	-0.015	0.057	0.044	0.001	0.008	0.188	0.031	0.027	0.060	0.008	0.026
AI	n	14	14	14	14	14	14	14	14	14	14	14	14	14	14
	n_a	12	8	7	9	6	10	11	6	6	9	3	10	21	13
	H_E	0.898	0.736	0.783	0.852	0.797	0.876	0.909	0.725	0.571	0.857	0.140	0.887	0.978	0.890
	n_{eff}	7.686	3.409	4.083	5.521	4.405	6.644	8.000	3.409	2.227	5.765	1.156	7.000	17.818	7.259
	F_{is}	-0.113	0.127	-0.004	0.077	-0.166	-0.141	0.057	-0.280	0.000	0.000	-0.020	-0.046	-0.022	-0.123
AJ	n	19	19	19	19	19	19	19	19	19	17	19	18	19	19
	n_a	14	9	8	9	6	12	11	7	5	8	4	10	23	18
	H_E	0.92	0.78	0.76	0.85	0.77	0.78	0.80	0.82	0.54	0.81	0.32	0.84	0.97	0.93
	n_{eff}	9.26	4.13	3.78	5.73	3.99	4.10	4.46	4.88	2.12	4.86	1.46	5.31	17.19	10.03
	F_{is}	0.14	-0.09	0.10	-0.06	0.04	0.19	0.01	-0.03	0.13	-0.16	-0.14	0.07	-0.04	0.15
AK	n	21	22	22	22	22	22	22	22	22	22	22	22	22	22
	n_a	19	11	7	9	7	15	12	7	7	10	3	15	24	19
	H_E	0.958	0.719	0.824	0.803	0.718	0.799	0.902	0.764	0.556	0.834	0.172	0.886	0.960	0.932
	n_{eff}	14.949	3.373	5.042	4.699	3.327	4.502	8.417	3.919	2.205	5.469	1.203	7.389	16.133	11.388
	F_{is}	0.106	-0.075	0.172	-0.132	0.113	0.146	-0.008	0.108	-0.226	-0.089	-0.057	0.077	0.006	-0.073
BA	n	51	52	52	48	51	51	51	51	48	48	52	52	31	45
	n_a	23	13	10	14	9	17	14	8	12	11	3	23	21	24
	H_E	0.891	0.594	0.811	0.842	0.831	0.756	0.871	0.789	0.628	0.849	0.161	0.929	0.945	0.932
	n_{eff}	8.500	2.427	5.097	6.016	5.667	3.989	7.255	4.555	2.641	6.236	1.190	12.548	14.343	12.656
	F_{is}	-0.057	0.029	-0.115	-0.039	-0.038	-0.037	-0.014	0.055	0.072	0.018	-0.075	-0.014	-0.059	0.046
BB	n	47	50	50	48	50	40	45	47	48	43	47	50	40	44
	n_a	22	11	11	11	9	15	13	10	10	12	5	20	23	25
	H_E	0.912	0.681	0.857	0.891	0.802	0.797	0.888	0.793	0.642	0.778	0.123	0.919	0.937	0.935
	n_{eff}	10.156	3.075	6.527	8.424	4.845	4.665	8.198	4.626	2.740	4.335	1.139	11.062	13.169	13.170
	F_{is}	0.043	-0.027	0.136	0.089	0.002	0.121	0.024	0.034	-0.007	-0.046	-0.034	0.043	0.093	0.028
BC	n	38	45	49	41	48	43	46	45	48	45	48	49	43	42
	n_a	17	11	9	12	7	14	13	9	10	11	6	22	24	21
	H_E	0.872	0.731	0.854	0.874	0.781	0.733	0.860	0.788	0.642	0.827	0.195	0.911	0.927	0.894
	n_{eff}	7.238	3.619	6.463	7.309	4.393	3.622	6.718	4.535	2.746	5.429	1.239	10.131	11.968	8.584
	F_{is}	-0.086	-0.094	-0.004	0.052	0.039	0.016	-0.011	-0.072	-0.038	0.167	-0.068	0.059	0.022	-0.012

		Locus													
Haul	**Value**	**Sal1**	**Sal2**	**Sal3**	**Sal4**	**Sal6**	**Spi4**	**Spi6**	**Spi10**	**Spi12**	**Sth3B**	**Sma5**	**Sma7**	**SR7-2**	**SR7-7**
BD	n	45	46	49	48	49	41	47	44	49	46	48	49	37	43
	n_a	18	11	11	11	7	13	14	9	14	10	4	21	24	24
	H_E	0.897	0.626	0.848	0.863	0.809	0.685	0.885	0.815	0.679	0.847	0.212	0.914	0.945	0.929
	n_{eff}	8.921	2.625	6.253	6.867	5.002	3.079	8.077	5.156	3.049	6.160	1.265	10.485	14.800	12.368
	F_{is}	-0.065	-0.042	-0.059	0.011	0.066	0.217	-0.082	-0.060	0.069	-0.001	-0.083	-0.005	-0.030	-0.051
Total	n	2097	2113	2117	2109	2117	2062	2109	2111	2117	2103	2119	2120	2070	2093
	n_a	32	21	20	18	13	22	20	15	19	21	10	34	66	44
	H_T	0.917	0.715	0.832	0.855	0.759	0.795	0.863	0.794	0.655	0.829	0.215	0.897	0.960	0.914
	F_{is}	0.044	-0.001	0.014	0.006	0.038	0.047	0.017	0.028	0.005	0.009	0.004	0.020	-0.001	0.009
	F_{ST}	0.005	0.015	0.006	0.007	0.007	0.004	0.006	0.004	0.003	0.002	0.003	0.004	0.003	0.002

Table A-3. Allele frequencies and sample sizes. Data for each of 45 YOY POP collections at 14 microsatellite loci and the number of samples analyzed (*n*).

μSal1

	Collection											
Allele	A	B	C	D	E	F	G	H	I	J	K	L
107	0.000	0.009	0.036	0.008	0.031	0.036	0.010	0.015	0.020	0.029	0.018	0.044
111	0.008	0.026	0.018	0.008	0.006	0.000	0.000	0.015	0.020	0.010	0.009	0.000
115	0.008	0.009	0.009	0.008	0.013	0.000	0.010	0.023	0.010	0.010	0.009	0.011
119	0.025	0.026	0.009	0.016	0.019	0.027	0.049	0.046	0.010	0.020	0.018	0.022
123	0.016	0.009	0.018	0.031	0.044	0.064	0.069	0.083	0.080	0.049	0.055	0.076
127	0.025	0.026	0.000	0.000	0.031	0.018	0.020	0.023	0.030	0.000	0.009	0.044
131	0.000	0.018	0.009	0.000	0.019	0.027	0.000	0.023	0.000	0.039	0.000	0.022
135	0.123	0.175	0.146	0.133	0.194	0.136	0.196	0.136	0.220	0.226	0.191	0.152
139	0.098	0.070	0.091	0.117	0.094	0.118	0.059	0.099	0.120	0.069	0.064	0.098
143	0.049	0.026	0.046	0.078	0.069	0.055	0.069	0.030	0.060	0.078	0.091	0.054
147	0.090	0.132	0.027	0.078	0.050	0.064	0.039	0.061	0.040	0.020	0.064	0.087
151	0.033	0.035	0.027	0.078	0.044	0.073	0.039	0.046	0.030	0.098	0.027	0.022
155	0.057	0.070	0.018	0.047	0.050	0.018	0.029	0.023	0.010	0.020	0.036	0.011
159	0.074	0.053	0.046	0.023	0.038	0.046	0.039	0.030	0.010	0.069	0.073	0.011
163	0.008	0.009	0.046	0.039	0.006	0.000	0.000	0.038	0.040	0.020	0.036	0.000
167	0.008	0.000	0.009	0.016	0.013	0.027	0.020	0.015	0.030	0.020	0.018	0.033
171	0.025	0.026	0.073	0.031	0.063	0.118	0.128	0.099	0.070	0.049	0.091	0.130
175	0.041	0.018	0.009	0.008	0.031	0.009	0.049	0.015	0.030	0.020	0.009	0.022
179	0.033	0.018	0.055	0.055	0.056	0.055	0.088	0.061	0.040	0.069	0.027	0.054
183	0.213	0.167	0.255	0.148	0.069	0.064	0.078	0.046	0.040	0.049	0.055	0.087
187	0.041	0.026	0.018	0.055	0.038	0.018	0.000	0.023	0.060	0.010	0.064	0.011
191	0.008	0.044	0.036	0.023	0.019	0.009	0.010	0.046	0.030	0.020	0.018	0.000
195	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.009	0.000
199	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
207	0.000	0.009	0.000	0.000	0.006	0.000	0.000	0.008	0.000	0.000	0.009	0.000
211	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
215	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
219	0.008	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000
223	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000
227	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
231	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011
251	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	61	57	55	64	80	55	51	66	50	51	55	46

µSal1

	Collection											
Allele	M	N	O	P	Q	R	S	T	U	V	W	X
107	0.039	0.023	0.041	0.020	0.000	0.020	0.027	0.058	0.040	0.010	0.048	0.016
111	0.013	0.000	0.041	0.010	0.000	0.000	0.018	0.023	0.010	0.010	0.000	0.031
115	0.000	0.023	0.031	0.000	0.016	0.000	0.000	0.023	0.030	0.019	0.000	0.031
119	0.013	0.035	0.020	0.031	0.032	0.031	0.009	0.023	0.010	0.010	0.012	0.000
123	0.115	0.047	0.031	0.031	0.097	0.051	0.018	0.047	0.020	0.019	0.048	0.063
127	0.000	0.058	0.000	0.020	0.000	0.031	0.009	0.035	0.030	0.000	0.024	0.000
131	0.039	0.023	0.000	0.010	0.000	0.020	0.036	0.023	0.010	0.029	0.000	0.047
135	0.180	0.198	0.143	0.204	0.177	0.174	0.182	0.151	0.150	0.154	0.119	0.203
139	0.103	0.116	0.184	0.061	0.081	0.071	0.091	0.081	0.110	0.058	0.143	0.094
143	0.103	0.116	0.031	0.071	0.048	0.071	0.073	0.128	0.120	0.135	0.083	0.031
147	0.026	0.000	0.020	0.051	0.016	0.061	0.091	0.058	0.080	0.096	0.036	0.031
151	0.039	0.023	0.020	0.071	0.032	0.051	0.073	0.058	0.040	0.048	0.000	0.078
155	0.013	0.023	0.061	0.071	0.032	0.020	0.000	0.012	0.020	0.029	0.048	0.031
159	0.013	0.081	0.031	0.051	0.065	0.020	0.064	0.058	0.030	0.039	0.083	0.031
163	0.000	0.035	0.031	0.031	0.000	0.020	0.027	0.023	0.020	0.019	0.000	0.031
167	0.013	0.012	0.010	0.010	0.016	0.020	0.009	0.035	0.040	0.029	0.024	0.047
171	0.090	0.093	0.122	0.082	0.081	0.153	0.109	0.093	0.090	0.087	0.107	0.047
175	0.026	0.023	0.031	0.010	0.048	0.020	0.018	0.023	0.010	0.010	0.060	0.016
179	0.013	0.000	0.051	0.031	0.048	0.041	0.027	0.000	0.030	0.058	0.036	0.016
183	0.090	0.012	0.082	0.112	0.081	0.092	0.055	0.023	0.040	0.077	0.083	0.094
187	0.039	0.047	0.010	0.000	0.032	0.010	0.046	0.023	0.060	0.039	0.036	0.016
191	0.000	0.012	0.000	0.010	0.065	0.000	0.018	0.000	0.000	0.010	0.012	0.000
195	0.013	0.000	0.010	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.016
199	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
207	0.000	0.000	0.000	0.000	0.016	0.000	0.000	0.000	0.010	0.010	0.000	0.000
211	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.016
215	0.013	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.010	0.000	0.016
219	0.013	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
223	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
227	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
231	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
251	0.000	0.000	0.000	0.000	0.016	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	39	43	49	49	31	49	55	43	50	52	42	32

µSal1

	Collection											
Allele	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AM	AN
107	0.039	0.027	0.018	0.000	0.020	0.019	0.100	0.027	0.039	0.000	0.017	0.000
111	0.010	0.018	0.000	0.000	0.030	0.009	0.017	0.018	0.008	0.000	0.017	0.020
115	0.019	0.009	0.000	0.000	0.010	0.009	0.000	0.018	0.000	0.000	0.017	0.000
119	0.029	0.009	0.000	0.048	0.010	0.019	0.017	0.018	0.039	0.000	0.017	0.010
123	0.019	0.046	0.054	0.048	0.010	0.047	0.033	0.100	0.031	0.000	0.067	0.010
127	0.039	0.064	0.000	0.000	0.010	0.076	0.067	0.018	0.062	0.059	0.000	0.030
131	0.029	0.018	0.009	0.000	0.010	0.009	0.033	0.009	0.000	0.029	0.033	0.010
135	0.154	0.209	0.205	0.167	0.200	0.217	0.133	0.173	0.254	0.382	0.183	0.200
139	0.096	0.091	0.089	0.000	0.120	0.057	0.033	0.046	0.108	0.059	0.017	0.050
143	0.087	0.036	0.116	0.119	0.040	0.123	0.050	0.100	0.054	0.059	0.100	0.120
147	0.125	0.082	0.071	0.071	0.050	0.038	0.083	0.082	0.054	0.088	0.000	0.120
151	0.019	0.009	0.027	0.000	0.040	0.076	0.083	0.055	0.015	0.000	0.017	0.040
155	0.010	0.009	0.036	0.071	0.020	0.009	0.017	0.009	0.039	0.029	0.017	0.030
159	0.010	0.027	0.036	0.048	0.050	0.009	0.000	0.027	0.046	0.059	0.017	0.040
163	0.019	0.027	0.027	0.000	0.020	0.019	0.017	0.009	0.023	0.000	0.033	0.020
167	0.048	0.009	0.009	0.000	0.030	0.028	0.033	0.009	0.008	0.000	0.067	0.030
171	0.087	0.146	0.063	0.214	0.090	0.047	0.067	0.073	0.054	0.088	0.050	0.100
175	0.010	0.009	0.036	0.048	0.010	0.019	0.017	0.018	0.000	0.000	0.033	0.030
179	0.048	0.036	0.045	0.048	0.020	0.057	0.067	0.036	0.046	0.088	0.067	0.010
183	0.048	0.018	0.107	0.071	0.130	0.047	0.083	0.055	0.069	0.029	0.100	0.080
187	0.010	0.036	0.018	0.048	0.010	0.028	0.033	0.064	0.023	0.000	0.033	0.040
191	0.019	0.036	0.036	0.000	0.020	0.019	0.000	0.027	0.015	0.029	0.050	0.010
195	0.019	0.009	0.000	0.000	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000
199	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000
207	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.008	0.000	0.017	0.000
211	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
215	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.000	0.008	0.000	0.033	0.000
219	0.000	0.009	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000
223	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
227	0.000	0.009	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000
231	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
251	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	52	55	56	21	50	53	30	55	65	17	30	50

µSal1

	Collection									
Allele	AO	AL	AI	AJ	AK	BA	BB	BC	BD	Overall
107	0.043	0.044	0.000	0.026	0.000	0.020	0.021	0.000	0.033	0.025
111	0.009	0.000	0.000	0.000	0.000	0.020	0.000	0.026	0.000	0.011
115	0.000	0.011	0.036	0.000	0.048	0.010	0.011	0.013	0.000	0.011
119	0.017	0.011	0.036	0.026	0.024	0.020	0.000	0.026	0.000	0.020
123	0.043	0.033	0.143	0.079	0.071	0.020	0.075	0.053	0.044	0.046
127	0.026	0.044	0.036	0.000	0.024	0.010	0.021	0.000	0.000	0.023
131	0.009	0.022	0.000	0.000	0.048	0.039	0.021	0.026	0.022	0.017
135	0.216	0.233	0.179	0.211	0.095	0.284	0.223	0.290	0.256	0.187
139	0.095	0.056	0.214	0.105	0.095	0.069	0.064	0.066	0.100	0.088
143	0.078	0.078	0.107	0.105	0.071	0.059	0.096	0.040	0.100	0.075
147	0.069	0.056	0.036	0.053	0.024	0.098	0.128	0.132	0.089	0.066
151	0.035	0.089	0.036	0.079	0.024	0.049	0.032	0.013	0.067	0.043
155	0.017	0.022	0.036	0.026	0.048	0.000	0.021	0.026	0.033	0.028
159	0.017	0.000	0.000	0.053	0.048	0.020	0.021	0.000	0.000	0.036
163	0.000	0.000	0.000	0.000	0.000	0.029	0.011	0.026	0.011	0.019
167	0.035	0.022	0.000	0.000	0.024	0.059	0.021	0.040	0.033	0.022
171	0.078	0.089	0.107	0.132	0.095	0.029	0.064	0.145	0.033	0.083
175	0.026	0.011	0.000	0.000	0.048	0.029	0.043	0.026	0.044	0.022
179	0.043	0.056	0.000	0.026	0.095	0.010	0.043	0.026	0.011	0.041
183	0.078	0.111	0.036	0.026	0.071	0.078	0.032	0.026	0.056	0.081
187	0.026	0.000	0.000	0.053	0.024	0.010	0.011	0.000	0.044	0.028
191	0.017	0.000	0.000	0.000	0.000	0.020	0.011	0.000	0.011	0.017
195	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.003
199	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
207	0.017	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.003
211	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
215	0.009	0.000	0.000	0.000	0.000	0.010	0.021	0.000	0.011	0.003
219	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
223	0.000	0.000	0.000	0.000	0.024	0.000	0.000	0.000	0.000	0.001
227	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
231	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
251	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	58	45	14	19	21	51	47	38	45	2097

μSal2

	Collection											
Allele	A	B	C	D	E	F	G	H	I	J	K	L
81	0.000	0.009	0.000	0.016	0.019	0.027	0.020	0.008	0.020	0.038	0.018	0.033
85	0.177	0.114	0.136	0.094	0.080	0.134	0.029	0.114	0.080	0.038	0.155	0.087
89	0.186	0.281	0.264	0.297	0.500	0.402	0.529	0.553	0.550	0.453	0.482	0.457
93	0.008	0.009	0.027	0.008	0.025	0.000	0.029	0.000	0.000	0.028	0.027	0.022
97	0.016	0.009	0.009	0.000	0.025	0.027	0.020	0.038	0.030	0.009	0.055	0.011
101	0.331	0.325	0.300	0.266	0.173	0.161	0.206	0.144	0.110	0.245	0.173	0.207
105	0.048	0.053	0.064	0.070	0.019	0.089	0.029	0.030	0.090	0.085	0.009	0.033
109	0.016	0.018	0.009	0.023	0.012	0.018	0.010	0.015	0.020	0.009	0.000	0.033
113	0.129	0.079	0.082	0.133	0.056	0.071	0.039	0.061	0.030	0.066	0.027	0.054
117	0.032	0.061	0.055	0.055	0.043	0.018	0.020	0.023	0.030	0.000	0.009	0.022
121	0.016	0.009	0.018	0.008	0.006	0.018	0.039	0.000	0.020	0.000	0.018	0.022
125	0.016	0.018	0.027	0.016	0.012	0.018	0.010	0.008	0.010	0.009	0.009	0.000
129	0.024	0.000	0.000	0.016	0.000	0.000	0.020	0.000	0.010	0.000	0.000	0.011
133	0.000	0.009	0.000	0.000	0.012	0.000	0.000	0.008	0.000	0.009	0.009	0.011
137	0.000	0.009	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000
141	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000
145	0.000	0.000	0.009	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.009	0.000
153	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
157	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000
161	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000
165	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	62	57	55	64	81	56	51	66	50	53	55	46

μSal2

	Collection											
Allele	M	N	O	P	Q	R	S	T	U	V	W	X
81	0.026	0.000	0.071	0.010	0.048	0.022	0.009	0.012	0.030	0.019	0.023	0.016
85	0.064	0.093	0.061	0.082	0.032	0.076	0.073	0.024	0.090	0.048	0.105	0.109
89	0.462	0.326	0.459	0.551	0.548	0.533	0.546	0.512	0.510	0.500	0.384	0.500
93	0.013	0.012	0.031	0.031	0.000	0.011	0.009	0.012	0.000	0.010	0.023	0.016
97	0.026	0.058	0.061	0.000	0.032	0.022	0.027	0.083	0.050	0.019	0.012	0.047
101	0.205	0.244	0.153	0.163	0.210	0.185	0.182	0.214	0.190	0.192	0.221	0.250
105	0.051	0.047	0.071	0.031	0.016	0.044	0.009	0.024	0.010	0.019	0.047	0.016
109	0.013	0.000	0.020	0.020	0.016	0.022	0.018	0.012	0.010	0.029	0.023	0.031
113	0.090	0.140	0.020	0.051	0.016	0.033	0.082	0.036	0.080	0.087	0.105	0.000
117	0.026	0.058	0.031	0.000	0.000	0.011	0.027	0.012	0.010	0.067	0.035	0.000
121	0.000	0.000	0.000	0.010	0.000	0.011	0.000	0.012	0.000	0.010	0.012	0.000
125	0.000	0.023	0.010	0.000	0.048	0.011	0.018	0.012	0.000	0.000	0.000	0.016
129	0.000	0.000	0.000	0.020	0.032	0.000	0.000	0.012	0.000	0.000	0.000	0.000
133	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.020	0.000	0.012	0.000
137	0.000	0.000	0.000	0.020	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000
141	0.013	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
145	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
153	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000
157	0.013	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
161	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
165	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000
n	39	43	49	49	31	46	55	42	50	52	43	32

μSal2

	Collection											
Allele	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AM	AN
81	0.028	0.018	0.036	0.024	0.000	0.028	0.000	0.046	0.008	0.029	0.017	0.030
85	0.057	0.100	0.152	0.095	0.110	0.151	0.117	0.055	0.069	0.029	0.067	0.080
89	0.481	0.536	0.393	0.214	0.360	0.472	0.500	0.546	0.569	0.529	0.500	0.570
93	0.000	0.009	0.018	0.000	0.040	0.000	0.000	0.009	0.023	0.000	0.017	0.010
97	0.047	0.046	0.027	0.024	0.010	0.076	0.017	0.055	0.092	0.000	0.067	0.050
101	0.245	0.164	0.170	0.381	0.280	0.170	0.183	0.155	0.100	0.265	0.167	0.190
105	0.038	0.046	0.045	0.000	0.100	0.038	0.050	0.027	0.023	0.000	0.033	0.020
109	0.019	0.027	0.018	0.000	0.000	0.019	0.050	0.036	0.015	0.059	0.033	0.010
113	0.038	0.018	0.071	0.191	0.040	0.019	0.033	0.046	0.031	0.059	0.033	0.020
117	0.038	0.009	0.036	0.024	0.030	0.028	0.033	0.018	0.023	0.000	0.017	0.020
121	0.009	0.018	0.027	0.000	0.010	0.000	0.000	0.000	0.031	0.000	0.000	0.000
125	0.000	0.000	0.000	0.024	0.000	0.000	0.000	0.009	0.015	0.029	0.000	0.000
129	0.000	0.000	0.009	0.024	0.010	0.000	0.017	0.000	0.000	0.000	0.017	0.000
133	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
137	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
141	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.000
145	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
153	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
157	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
161	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.000
165	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	53	55	56	21	50	53	30	55	65	17	30	50

μSal2

	Collection									
Allele	AO	AL	AI	AJ	AK	BA	BB	BC	BD	Overall
81	0.000	0.011	0.000	0.000	0.023	0.010	0.020	0.011	0.000	0.019
85	0.095	0.056	0.071	0.132	0.046	0.039	0.090	0.089	0.054	0.088
89	0.474	0.522	0.464	0.342	0.500	0.606	0.530	0.467	0.587	0.466
93	0.026	0.000	0.000	0.026	0.000	0.010	0.010	0.011	0.000	0.013
97	0.035	0.022	0.000	0.026	0.023	0.029	0.020	0.100	0.044	0.034
101	0.224	0.256	0.250	0.316	0.182	0.202	0.170	0.189	0.163	0.205
105	0.043	0.033	0.071	0.000	0.023	0.019	0.060	0.056	0.033	0.041
109	0.009	0.000	0.036	0.000	0.046	0.019	0.010	0.022	0.011	0.017
113	0.043	0.033	0.036	0.053	0.068	0.019	0.030	0.022	0.054	0.056
117	0.017	0.022	0.036	0.000	0.000	0.019	0.030	0.022	0.022	0.026
121	0.009	0.011	0.000	0.026	0.000	0.010	0.000	0.000	0.011	0.010
125	0.017	0.011	0.036	0.053	0.046	0.010	0.000	0.000	0.011	0.010
129	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.005
133	0.000	0.000	0.000	0.026	0.023	0.010	0.000	0.000	0.011	0.004
137	0.000	0.000	0.000	0.000	0.000	0.000	0.030	0.000	0.000	0.002
141	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
145	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
153	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
157	0.000	0.000	0.000	0.000	0.023	0.000	0.000	0.000	0.000	0.001
161	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
165	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
n	58	45	14	19	22	52	50	45	46	2113

µSal3

	Collection											
Allele	A	B	C	D	E	F	G	H	I	J	K	L
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
91	0.000	0.009	0.009	0.000	0.006	0.000	0.010	0.000	0.010	0.010	0.009	0.000
96	0.000	0.000	0.000	0.016	0.000	0.018	0.010	0.008	0.000	0.010	0.000	0.000
101	0.016	0.053	0.018	0.031	0.019	0.009	0.000	0.023	0.000	0.019	0.018	0.011
106	0.040	0.123	0.027	0.094	0.161	0.232	0.157	0.121	0.190	0.173	0.173	0.148
111	0.250	0.281	0.227	0.250	0.265	0.295	0.284	0.250	0.240	0.221	0.182	0.250
116	0.202	0.228	0.264	0.227	0.265	0.241	0.216	0.220	0.330	0.212	0.300	0.296
121	0.089	0.079	0.091	0.094	0.142	0.054	0.186	0.197	0.110	0.135	0.118	0.148
126	0.129	0.061	0.082	0.117	0.043	0.027	0.059	0.053	0.030	0.115	0.073	0.068
131	0.081	0.079	0.127	0.055	0.025	0.045	0.049	0.046	0.030	0.048	0.046	0.057
136	0.081	0.053	0.046	0.047	0.043	0.036	0.010	0.038	0.010	0.019	0.046	0.011
141	0.040	0.018	0.027	0.039	0.019	0.009	0.020	0.015	0.030	0.019	0.018	0.000
146	0.016	0.018	0.018	0.008	0.006	0.000	0.000	0.015	0.000	0.010	0.018	0.000
151	0.040	0.000	0.027	0.016	0.000	0.018	0.000	0.008	0.010	0.010	0.000	0.000
156	0.008	0.000	0.018	0.000	0.006	0.000	0.000	0.000	0.010	0.000	0.000	0.011
161	0.008	0.000	0.009	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
166	0.000	0.000	0.009	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000
171	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
181	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000
196	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000
n	62	57	55	64	81	56	51	66	50	52	55	44

µSal3

	Collection											
Allele	M	N	O	P	Q	R	S	T	U	V	W	X
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
91	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000
96	0.000	0.023	0.000	0.000	0.000	0.010	0.000	0.000	0.010	0.010	0.000	0.000
101	0.000	0.023	0.010	0.010	0.000	0.010	0.000	0.000	0.010	0.019	0.012	0.016
106	0.222	0.221	0.153	0.184	0.200	0.153	0.191	0.140	0.160	0.125	0.151	0.188
111	0.319	0.244	0.367	0.357	0.333	0.204	0.182	0.163	0.190	0.231	0.244	0.188
116	0.208	0.221	0.225	0.184	0.200	0.184	0.182	0.198	0.220	0.212	0.186	0.156
121	0.125	0.081	0.112	0.102	0.167	0.194	0.136	0.209	0.120	0.115	0.174	0.094
126	0.028	0.058	0.031	0.031	0.067	0.071	0.100	0.128	0.130	0.096	0.105	0.172
131	0.056	0.035	0.031	0.051	0.017	0.082	0.073	0.047	0.080	0.067	0.058	0.063
136	0.028	0.023	0.010	0.051	0.017	0.031	0.055	0.058	0.030	0.019	0.023	0.063
141	0.014	0.047	0.020	0.010	0.000	0.010	0.027	0.047	0.010	0.029	0.023	0.016
146	0.000	0.012	0.000	0.000	0.000	0.020	0.036	0.012	0.010	0.010	0.000	0.016
151	0.000	0.000	0.020	0.010	0.000	0.020	0.000	0.000	0.020	0.039	0.012	0.016
156	0.000	0.012	0.010	0.000	0.000	0.010	0.009	0.000	0.010	0.019	0.000	0.016
161	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000
166	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
171	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000
181	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
196	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	36	43	49	49	30	49	55	43	50	52	43	32

μSal3

	Collection											
Allele	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AM	AN
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010
91	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
96	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.010
101	0.009	0.000	0.027	0.000	0.030	0.028	0.017	0.000	0.000	0.029	0.000	0.000
106	0.226	0.173	0.161	0.119	0.260	0.142	0.317	0.182	0.154	0.235	0.250	0.150
111	0.113	0.146	0.214	0.191	0.260	0.104	0.133	0.164	0.239	0.059	0.217	0.160
116	0.226	0.291	0.232	0.262	0.150	0.255	0.333	0.236	0.246	0.147	0.200	0.270
121	0.113	0.155	0.170	0.191	0.110	0.123	0.067	0.191	0.162	0.235	0.050	0.130
126	0.094	0.082	0.098	0.071	0.090	0.132	0.033	0.118	0.108	0.147	0.150	0.090
131	0.123	0.046	0.054	0.119	0.040	0.076	0.033	0.027	0.069	0.059	0.067	0.070
136	0.057	0.082	0.018	0.024	0.040	0.066	0.050	0.027	0.000	0.029	0.017	0.040
141	0.009	0.018	0.018	0.000	0.000	0.047	0.000	0.036	0.008	0.029	0.000	0.030
146	0.019	0.009	0.009	0.024	0.000	0.019	0.017	0.009	0.000	0.000	0.033	0.010
151	0.000	0.000	0.000	0.000	0.010	0.009	0.000	0.000	0.000	0.029	0.000	0.020
156	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000
161	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.000
166	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
171	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.010
181	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
196	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	53	55	56	21	50	53	30	55	65	17	30	50

μSal3

	Collection									
Allele	AO	AL	AI	AJ	AK	BA	BB	BC	BD	Overall
86	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
91	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.002
96	0.017	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.010	0.005
101	0.026	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.020	0.013
106	0.172	0.211	0.214	0.184	0.068	0.240	0.160	0.174	0.245	0.168
111	0.172	0.189	0.357	0.263	0.250	0.279	0.130	0.153	0.163	0.222
116	0.190	0.211	0.250	0.395	0.273	0.202	0.190	0.194	0.204	0.228
121	0.181	0.133	0.071	0.053	0.205	0.115	0.220	0.204	0.122	0.135
126	0.095	0.111	0.036	0.026	0.091	0.058	0.110	0.102	0.102	0.085
131	0.052	0.044	0.000	0.000	0.068	0.048	0.110	0.092	0.020	0.058
136	0.060	0.078	0.000	0.026	0.000	0.019	0.040	0.051	0.051	0.038
141	0.017	0.011	0.000	0.026	0.046	0.019	0.000	0.010	0.051	0.020
146	0.009	0.000	0.036	0.000	0.000	0.010	0.000	0.020	0.010	0.010
151	0.009	0.011	0.036	0.026	0.000	0.000	0.010	0.000	0.000	0.009
156	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.004
161	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
166	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
171	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
181	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
196	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	58	45	14	19	22	52	50	49	49	2117

µSal4

	Collection											
Allele	A	B	C	D	E	F	G	H	I	J	K	L
83	0.016	0.009	0.027	0.016	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000
87	0.000	0.009	0.009	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.009	0.000
91	0.008	0.000	0.027	0.000	0.012	0.000	0.010	0.000	0.000	0.009	0.000	0.000
95	0.202	0.193	0.191	0.188	0.216	0.205	0.177	0.250	0.280	0.217	0.236	0.185
99	0.016	0.079	0.018	0.016	0.062	0.063	0.098	0.038	0.050	0.047	0.100	0.033
103	0.403	0.368	0.409	0.367	0.210	0.304	0.304	0.189	0.190	0.217	0.200	0.304
107	0.065	0.079	0.118	0.070	0.117	0.063	0.147	0.068	0.070	0.104	0.091	0.054
111	0.040	0.061	0.055	0.047	0.111	0.143	0.088	0.182	0.140	0.142	0.136	0.109
115	0.081	0.053	0.046	0.070	0.093	0.107	0.069	0.114	0.130	0.113	0.082	0.109
119	0.048	0.035	0.027	0.031	0.049	0.045	0.029	0.053	0.050	0.047	0.082	0.065
123	0.024	0.018	0.046	0.031	0.062	0.027	0.039	0.038	0.000	0.019	0.027	0.054
127	0.040	0.044	0.000	0.086	0.019	0.009	0.029	0.008	0.070	0.047	0.009	0.022
131	0.024	0.044	0.009	0.023	0.012	0.018	0.010	0.038	0.000	0.009	0.018	0.033
135	0.016	0.009	0.000	0.016	0.006	0.009	0.000	0.023	0.010	0.000	0.009	0.000
139	0.016	0.000	0.009	0.016	0.019	0.000	0.000	0.000	0.010	0.009	0.000	0.033
143	0.000	0.000	0.009	0.016	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000
147	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000
151	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000
n	62	57	55	64	81	56	51	66	50	53	55	46

µSal4

	Collection											
Allele	M	N	O	P	Q	R	S	T	U	V	W	X
83	0.000	0.000	0.000	0.010	0.000	0.010	0.000	0.000	0.000	0.010	0.000	0.000
87	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.010	0.000	0.000	0.016
91	0.000	0.012	0.000	0.000	0.016	0.000	0.000	0.000	0.010	0.000	0.012	0.016
95	0.180	0.186	0.235	0.204	0.177	0.194	0.191	0.256	0.200	0.164	0.233	0.188
99	0.077	0.105	0.082	0.051	0.097	0.031	0.100	0.070	0.050	0.048	0.047	0.125
103	0.205	0.209	0.225	0.214	0.226	0.214	0.200	0.198	0.190	0.173	0.314	0.094
107	0.128	0.081	0.082	0.153	0.113	0.061	0.082	0.070	0.110	0.087	0.105	0.063
111	0.167	0.081	0.184	0.112	0.129	0.214	0.146	0.081	0.150	0.115	0.081	0.156
115	0.103	0.140	0.092	0.082	0.081	0.071	0.100	0.105	0.110	0.164	0.058	0.203
119	0.064	0.093	0.041	0.092	0.032	0.071	0.036	0.070	0.050	0.096	0.047	0.000
123	0.026	0.035	0.010	0.010	0.016	0.061	0.064	0.058	0.050	0.029	0.035	0.031
127	0.026	0.035	0.010	0.041	0.081	0.010	0.046	0.058	0.020	0.067	0.070	0.047
131	0.013	0.012	0.020	0.010	0.032	0.041	0.027	0.023	0.010	0.039	0.000	0.031
135	0.013	0.000	0.020	0.020	0.000	0.000	0.000	0.000	0.010	0.010	0.000	0.016
139	0.000	0.000	0.000	0.000	0.000	0.010	0.009	0.012	0.010	0.000	0.000	0.000
143	0.000	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.000	0.000	0.016
147	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
151	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	39	43	49	49	31	49	55	43	50	52	43	32

µSal4

	Collection											
Allele	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AM	AN
83	0.000	0.000	0.009	0.024	0.040	0.000	0.000	0.009	0.000	0.000	0.017	0.000
87	0.000	0.009	0.000	0.000	0.010	0.000	0.000	0.009	0.000	0.000	0.000	0.000
91	0.000	0.000	0.000	0.024	0.000	0.009	0.033	0.009	0.008	0.000	0.000	0.010
95	0.226	0.264	0.170	0.214	0.180	0.198	0.133	0.200	0.215	0.177	0.233	0.190
99	0.038	0.064	0.071	0.000	0.060	0.085	0.033	0.064	0.031	0.118	0.083	0.150
103	0.208	0.109	0.330	0.214	0.210	0.189	0.300	0.164	0.292	0.088	0.150	0.190
107	0.094	0.046	0.063	0.048	0.120	0.047	0.100	0.073	0.085	0.206	0.067	0.100
111	0.198	0.127	0.071	0.048	0.170	0.142	0.083	0.118	0.115	0.000	0.167	0.100
115	0.094	0.155	0.089	0.143	0.090	0.160	0.167	0.146	0.139	0.177	0.117	0.090
119	0.038	0.091	0.054	0.024	0.030	0.085	0.017	0.064	0.039	0.029	0.050	0.060
123	0.028	0.036	0.018	0.095	0.030	0.019	0.050	0.036	0.046	0.088	0.067	0.010
127	0.038	0.046	0.036	0.071	0.030	0.019	0.050	0.046	0.015	0.029	0.050	0.050
131	0.038	0.046	0.045	0.048	0.010	0.009	0.017	0.027	0.015	0.029	0.000	0.050
135	0.000	0.000	0.036	0.024	0.010	0.028	0.000	0.009	0.000	0.029	0.000	0.000
139	0.000	0.009	0.000	0.024	0.010	0.000	0.000	0.018	0.000	0.029	0.000	0.000
143	0.000	0.000	0.000	0.000	0.000	0.009	0.017	0.009	0.000	0.000	0.000	0.000
147	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
151	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	53	55	56	21	50	53	30	55	65	17	30	50

µSal4

	Collection									
Allele	AO	AL	AI	AJ	AK	BA	BB	BC	BD	Overall
83	0.000	0.022	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.006
87	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.003
91	0.000	0.011	0.036	0.000	0.023	0.021	0.000	0.012	0.000	0.006
95	0.250	0.133	0.179	0.263	0.136	0.271	0.167	0.220	0.271	0.207
99	0.017	0.044	0.000	0.105	0.023	0.021	0.073	0.110	0.063	0.060
103	0.267	0.256	0.321	0.263	0.386	0.125	0.125	0.171	0.156	0.235
107	0.112	0.122	0.107	0.053	0.091	0.063	0.115	0.122	0.115	0.090
111	0.078	0.067	0.143	0.079	0.091	0.219	0.177	0.146	0.115	0.120
115	0.121	0.144	0.071	0.079	0.136	0.115	0.104	0.073	0.094	0.106
119	0.060	0.056	0.071	0.000	0.091	0.104	0.031	0.049	0.042	0.053
123	0.026	0.044	0.036	0.053	0.000	0.010	0.094	0.049	0.000	0.035
127	0.043	0.022	0.036	0.079	0.023	0.010	0.052	0.000	0.063	0.036
131	0.009	0.044	0.000	0.000	0.000	0.010	0.042	0.012	0.052	0.023
135	0.009	0.011	0.000	0.000	0.000	0.010	0.000	0.024	0.021	0.009
139	0.000	0.011	0.000	0.026	0.000	0.000	0.021	0.012	0.000	0.007
143	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.010	0.003
147	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
151	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
n	58	45	14	19	22	48	48	41	48	2109

µSal6

	Collection											
Allele	A	B	C	D	E	F	G	H	I	J	K	L
122	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.009	0.000
126	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000
128	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.009	0.009	0.000
132	0.145	0.088	0.109	0.123	0.204	0.152	0.190	0.159	0.120	0.170	0.227	0.120
134	0.557	0.605	0.555	0.525	0.346	0.420	0.400	0.424	0.410	0.330	0.364	0.424
136	0.105	0.123	0.118	0.115	0.185	0.232	0.210	0.167	0.180	0.226	0.146	0.196
138	0.081	0.044	0.046	0.115	0.068	0.054	0.050	0.068	0.060	0.047	0.082	0.087
140	0.057	0.079	0.118	0.057	0.124	0.107	0.120	0.121	0.110	0.189	0.118	0.130
142	0.024	0.044	0.027	0.016	0.006	0.009	0.010	0.008	0.010	0.028	0.027	0.011
144	0.008	0.000	0.000	0.008	0.037	0.009	0.000	0.046	0.100	0.000	0.009	0.022
146	0.008	0.000	0.000	0.000	0.006	0.000	0.010	0.008	0.010	0.000	0.009	0.011
148	0.016	0.018	0.027	0.033	0.012	0.018	0.000	0.000	0.000	0.000	0.000	0.000
154	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	62	57	55	61	81	56	50	66	50	53	55	46

µSal6

	Collection											
Allele	M	N	O	P	Q	R	S	T	U	V	W	X
122	0.000	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
126	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.016
128	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000
132	0.167	0.174	0.143	0.174	0.145	0.133	0.255	0.279	0.190	0.183	0.163	0.203
134	0.423	0.314	0.357	0.347	0.355	0.429	0.373	0.302	0.390	0.356	0.442	0.375
136	0.218	0.256	0.235	0.194	0.307	0.153	0.182	0.163	0.160	0.192	0.151	0.188
138	0.026	0.035	0.061	0.041	0.081	0.041	0.036	0.070	0.080	0.058	0.116	0.078
140	0.115	0.116	0.163	0.163	0.081	0.163	0.064	0.128	0.070	0.144	0.105	0.078
142	0.013	0.000	0.010	0.020	0.000	0.020	0.027	0.012	0.050	0.029	0.012	0.000
144	0.039	0.070	0.010	0.051	0.032	0.051	0.064	0.023	0.050	0.029	0.012	0.063
146	0.000	0.012	0.010	0.000	0.000	0.000	0.000	0.023	0.010	0.010	0.000	0.000
148	0.000	0.012	0.010	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
154	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	39	43	49	49	31	49	55	43	50	52	43	32

µSal6

	Collection											
Allele	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AM	AN
122	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
126	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
128	0.000	0.009	0.009	0.000	0.010	0.000	0.000	0.000	0.015	0.000	0.000	0.010
132	0.208	0.164	0.161	0.119	0.100	0.189	0.167	0.157	0.146	0.177	0.217	0.170
134	0.349	0.400	0.500	0.595	0.470	0.340	0.367	0.333	0.369	0.265	0.383	0.330
136	0.151	0.191	0.143	0.167	0.180	0.179	0.167	0.204	0.231	0.206	0.150	0.210
138	0.094	0.036	0.045	0.048	0.080	0.057	0.083	0.083	0.046	0.059	0.000	0.100
140	0.123	0.100	0.089	0.048	0.090	0.132	0.150	0.130	0.108	0.029	0.100	0.120
142	0.019	0.000	0.009	0.000	0.010	0.019	0.000	0.028	0.015	0.029	0.083	0.030
144	0.057	0.091	0.036	0.024	0.060	0.085	0.050	0.056	0.062	0.235	0.033	0.030
146	0.000	0.009	0.009	0.000	0.000	0.000	0.017	0.009	0.008	0.000	0.033	0.000
148	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
154	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	53	55	56	21	50	53	30	54	65	17	30	50

μSal6

	Collection									
Allele	AO	AL	AI	AJ	AK	BA	BB	BC	BD	Overall
122	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
126	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
128	0.000	0.011	0.000	0.000	0.000	0.010	0.000	0.021	0.000	0.003
132	0.138	0.233	0.286	0.158	0.250	0.157	0.160	0.188	0.194	0.169
134	0.422	0.322	0.321	0.368	0.455	0.294	0.370	0.344	0.296	0.397
136	0.216	0.133	0.107	0.263	0.159	0.128	0.110	0.240	0.194	0.179
138	0.026	0.044	0.071	0.053	0.023	0.118	0.110	0.104	0.122	0.066
140	0.147	0.156	0.143	0.132	0.068	0.157	0.120	0.063	0.143	0.114
142	0.017	0.033	0.000	0.000	0.023	0.029	0.020	0.000	0.010	0.018
144	0.035	0.067	0.000	0.026	0.023	0.098	0.060	0.042	0.041	0.041
146	0.000	0.000	0.000	0.000	0.000	0.010	0.020	0.000	0.000	0.005
148	0.000	0.000	0.071	0.000	0.000	0.000	0.030	0.000	0.000	0.005
154	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	58	45	14	19	22	51	50	48	49	2117

μSpi4

	Collection											
Allele	A	B	C	D	E	F	G	H	I	J	K	L
150	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
154	0.025	0.027	0.019	0.016	0.013	0.000	0.000	0.000	0.020	0.009	0.000	0.011
158	0.295	0.346	0.330	0.297	0.430	0.309	0.350	0.363	0.300	0.481	0.436	0.337
162	0.000	0.000	0.000	0.000	0.006	0.000	0.010	0.000	0.020	0.000	0.027	0.011
166	0.115	0.046	0.047	0.039	0.051	0.036	0.050	0.073	0.050	0.057	0.055	0.054
170	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.010	0.000	0.000	0.000
174	0.000	0.000	0.000	0.008	0.000	0.018	0.010	0.016	0.010	0.000	0.000	0.000
178	0.000	0.000	0.009	0.000	0.000	0.018	0.030	0.008	0.000	0.019	0.009	0.022
182	0.049	0.027	0.028	0.078	0.070	0.091	0.100	0.065	0.120	0.085	0.073	0.152
186	0.033	0.118	0.076	0.039	0.051	0.064	0.070	0.105	0.040	0.038	0.036	0.087
190	0.008	0.009	0.028	0.023	0.051	0.027	0.040	0.065	0.050	0.028	0.027	0.044
194	0.090	0.055	0.085	0.055	0.013	0.091	0.100	0.057	0.060	0.019	0.091	0.054
198	0.180	0.227	0.179	0.203	0.139	0.127	0.080	0.057	0.080	0.113	0.064	0.033
202	0.066	0.055	0.094	0.039	0.038	0.082	0.030	0.081	0.070	0.057	0.073	0.065
206	0.041	0.055	0.009	0.070	0.051	0.046	0.020	0.008	0.030	0.000	0.036	0.087
210	0.025	0.009	0.028	0.008	0.038	0.027	0.060	0.024	0.050	0.028	0.036	0.011
214	0.041	0.009	0.000	0.047	0.019	0.027	0.020	0.032	0.060	0.047	0.018	0.022
218	0.016	0.018	0.028	0.031	0.025	0.018	0.020	0.024	0.010	0.009	0.018	0.000
222	0.000	0.000	0.009	0.039	0.006	0.009	0.000	0.024	0.010	0.009	0.000	0.011
226	0.016	0.000	0.019	0.008	0.000	0.009	0.000	0.000	0.010	0.000	0.000	0.000
230	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
234	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	61	55	53	64	79	55	50	62	50	53	55	46

μSpi4

	Collection											
Allele	M	N	O	P	Q	R	S	T	U	V	W	X
150	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
154	0.000	0.000	0.000	0.010	0.017	0.000	0.000	0.000	0.000	0.020	0.012	0.016
158	0.392	0.395	0.389	0.427	0.450	0.417	0.443	0.419	0.447	0.431	0.477	0.469
162	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.011	0.010	0.012	0.016
166	0.027	0.058	0.056	0.052	0.050	0.031	0.047	0.035	0.000	0.020	0.035	0.031
170	0.014	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.011	0.010	0.000	0.000
174	0.014	0.023	0.000	0.010	0.000	0.000	0.000	0.023	0.011	0.000	0.000	0.031
178	0.014	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.021	0.010	0.000	0.000
182	0.122	0.093	0.067	0.063	0.033	0.063	0.047	0.070	0.085	0.059	0.035	0.031
186	0.068	0.058	0.056	0.042	0.033	0.021	0.038	0.047	0.043	0.078	0.058	0.094
190	0.041	0.035	0.078	0.052	0.050	0.063	0.057	0.035	0.032	0.020	0.035	0.047
194	0.014	0.093	0.044	0.031	0.017	0.042	0.057	0.070	0.064	0.059	0.070	0.063
198	0.054	0.105	0.111	0.063	0.117	0.135	0.076	0.105	0.106	0.088	0.070	0.047
202	0.081	0.023	0.067	0.083	0.067	0.052	0.047	0.023	0.053	0.049	0.047	0.047
206	0.068	0.058	0.033	0.042	0.033	0.042	0.019	0.047	0.053	0.039	0.023	0.047
210	0.041	0.012	0.011	0.010	0.017	0.042	0.038	0.058	0.032	0.049	0.070	0.000
214	0.014	0.012	0.044	0.042	0.050	0.021	0.038	0.023	0.011	0.029	0.012	0.016
218	0.027	0.023	0.022	0.042	0.017	0.042	0.019	0.023	0.011	0.029	0.023	0.016
222	0.000	0.012	0.022	0.021	0.033	0.021	0.047	0.000	0.011	0.000	0.012	0.031
226	0.014	0.000	0.000	0.000	0.000	0.000	0.009	0.012	0.000	0.000	0.012	0.000
230	0.000	0.000	0.000	0.000	0.017	0.010	0.000	0.000	0.000	0.000	0.000	0.000
234	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	37	43	45	48	30	48	53	43	47	51	43	32

μSpi4

	Collection											
Allele	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AM	AN
150	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
154	0.000	0.009	0.018	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
158	0.462	0.377	0.411	0.524	0.430	0.450	0.431	0.446	0.431	0.412	0.431	0.469
162	0.009	0.009	0.000	0.000	0.010	0.000	0.000	0.009	0.008	0.000	0.000	0.000
166	0.009	0.028	0.054	0.000	0.010	0.050	0.086	0.027	0.054	0.059	0.017	0.031
170	0.000	0.009	0.000	0.024	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.010
174	0.009	0.009	0.000	0.000	0.000	0.010	0.000	0.009	0.008	0.000	0.000	0.000
178	0.000	0.009	0.027	0.024	0.000	0.010	0.000	0.009	0.000	0.000	0.000	0.010
182	0.085	0.057	0.063	0.000	0.050	0.090	0.069	0.046	0.115	0.000	0.069	0.115
186	0.066	0.085	0.045	0.048	0.040	0.020	0.000	0.055	0.062	0.000	0.086	0.031
190	0.000	0.057	0.018	0.024	0.050	0.010	0.086	0.018	0.031	0.029	0.052	0.052
194	0.066	0.066	0.116	0.095	0.060	0.050	0.052	0.073	0.054	0.118	0.086	0.063
198	0.038	0.076	0.080	0.143	0.120	0.090	0.052	0.082	0.062	0.177	0.035	0.063
202	0.066	0.038	0.054	0.024	0.060	0.030	0.086	0.109	0.046	0.000	0.035	0.052
206	0.085	0.028	0.027	0.024	0.030	0.080	0.052	0.036	0.008	0.029	0.052	0.010
210	0.047	0.038	0.027	0.024	0.070	0.030	0.052	0.027	0.046	0.088	0.017	0.021
214	0.028	0.038	0.018	0.000	0.020	0.030	0.000	0.009	0.023	0.000	0.069	0.010
218	0.019	0.028	0.036	0.024	0.000	0.010	0.017	0.009	0.046	0.088	0.052	0.031
222	0.009	0.028	0.009	0.000	0.010	0.020	0.000	0.018	0.008	0.000	0.000	0.021
226	0.000	0.009	0.000	0.024	0.000	0.010	0.017	0.018	0.000	0.000	0.000	0.000
230	0.000	0.000	0.000	0.000	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.010
234	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	53	53	56	21	50	50	29	55	65	17	29	48

μSpi4

Allele	**Collection** AO	AL	AI	AJ	AK	BA	BB	BC	BD	Overall
150	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
154	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007
158	0.388	0.489	0.286	0.447	0.432	0.471	0.425	0.500	0.549	0.412
162	0.026	0.078	0.000	0.000	0.023	0.020	0.013	0.023	0.000	0.008
166	0.026	0.000	0.071	0.026	0.023	0.029	0.025	0.012	0.098	0.042
170	0.000	0.000	0.000	0.026	0.000	0.010	0.000	0.000	0.000	0.003
174	0.009	0.022	0.000	0.000	0.023	0.010	0.013	0.012	0.012	0.007
178	0.052	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008
182	0.078	0.044	0.143	0.079	0.046	0.098	0.063	0.058	0.049	0.071
186	0.052	0.022	0.143	0.026	0.023	0.049	0.050	0.093	0.049	0.055
190	0.035	0.033	0.000	0.053	0.023	0.029	0.038	0.035	0.000	0.036
194	0.103	0.044	0.071	0.053	0.136	0.029	0.075	0.035	0.049	0.062
198	0.095	0.089	0.036	0.158	0.046	0.098	0.075	0.058	0.049	0.098
202	0.026	0.044	0.071	0.000	0.068	0.039	0.038	0.058	0.049	0.054
206	0.052	0.022	0.000	0.026	0.046	0.029	0.100	0.047	0.024	0.040
210	0.009	0.033	0.071	0.000	0.046	0.029	0.025	0.023	0.000	0.031
214	0.035	0.033	0.071	0.026	0.023	0.010	0.038	0.000	0.024	0.026
218	0.000	0.000	0.000	0.053	0.023	0.029	0.013	0.012	0.012	0.022
222	0.009	0.011	0.036	0.000	0.023	0.010	0.000	0.035	0.024	0.013
226	0.000	0.022	0.000	0.026	0.000	0.000	0.013	0.000	0.000	0.005
230	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.002
234	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000
n	58	45	14	19	22	51	40	43	41	2062

μSpi6

Allele	**Collection** A	B	C	D	E	F	G	H	I	J	K	L
95	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
99	0.000	0.000	0.018	0.000	0.006	0.000	0.000	0.000	0.000	0.009	0.000	0.000
103	0.008	0.018	0.000	0.016	0.019	0.000	0.000	0.015	0.010	0.000	0.000	0.000
107	0.000	0.018	0.018	0.000	0.012	0.018	0.020	0.015	0.000	0.009	0.000	0.056
111	0.387	0.386	0.300	0.391	0.235	0.277	0.167	0.242	0.330	0.255	0.173	0.244
115	0.145	0.097	0.164	0.180	0.167	0.089	0.137	0.167	0.140	0.226	0.209	0.156
119	0.040	0.035	0.036	0.031	0.068	0.063	0.078	0.076	0.080	0.085	0.109	0.089
123	0.040	0.000	0.036	0.039	0.068	0.054	0.147	0.076	0.050	0.066	0.109	0.089
127	0.000	0.009	0.018	0.039	0.049	0.063	0.078	0.061	0.050	0.038	0.027	0.056
131	0.065	0.026	0.064	0.039	0.093	0.098	0.049	0.053	0.080	0.028	0.082	0.089
135	0.040	0.026	0.073	0.047	0.074	0.170	0.078	0.083	0.080	0.076	0.091	0.056
139	0.073	0.149	0.073	0.023	0.074	0.071	0.108	0.068	0.090	0.057	0.055	0.067
143	0.065	0.105	0.073	0.078	0.012	0.036	0.029	0.023	0.020	0.076	0.073	0.033
147	0.073	0.053	0.073	0.031	0.062	0.000	0.078	0.038	0.050	0.038	0.046	0.022
151	0.048	0.018	0.027	0.031	0.037	0.036	0.000	0.030	0.010	0.009	0.009	0.022
155	0.000	0.035	0.018	0.016	0.025	0.027	0.000	0.030	0.000	0.019	0.018	0.011
159	0.000	0.018	0.009	0.008	0.000	0.000	0.020	0.015	0.010	0.009	0.000	0.000
163	0.000	0.009	0.000	0.016	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
167	0.016	0.000	0.000	0.008	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000
171	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.011
n	62	57	55	64	81	56	51	66	50	53	55	45

μSpi6

	Collection										
Allele	M	N	O	P	Q	R	S	T	U	V	W	X
95	0.000	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
99	0.026	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000
103	0.000	0.012	0.000	0.000	0.032	0.031	0.000	0.012	0.010	0.029	0.000	0.031
107	0.026	0.012	0.010	0.000	0.032	0.000	0.000	0.035	0.000	0.019	0.023	0.000
111	0.180	0.326	0.163	0.214	0.242	0.208	0.269	0.244	0.250	0.289	0.256	0.281
115	0.115	0.128	0.163	0.133	0.129	0.156	0.167	0.105	0.150	0.164	0.128	0.234
119	0.051	0.128	0.082	0.082	0.065	0.125	0.083	0.105	0.060	0.077	0.081	0.109
123	0.103	0.093	0.102	0.092	0.129	0.135	0.120	0.081	0.110	0.096	0.151	0.078
127	0.064	0.105	0.061	0.051	0.081	0.073	0.056	0.035	0.080	0.048	0.047	0.000
131	0.167	0.035	0.061	0.122	0.081	0.073	0.065	0.140	0.090	0.058	0.047	0.078
135	0.090	0.070	0.082	0.082	0.065	0.042	0.074	0.105	0.080	0.029	0.058	0.063
139	0.051	0.012	0.122	0.082	0.000	0.083	0.074	0.093	0.020	0.058	0.058	0.031
143	0.077	0.047	0.082	0.071	0.097	0.021	0.056	0.012	0.060	0.048	0.070	0.063
147	0.000	0.012	0.010	0.031	0.048	0.031	0.009	0.012	0.030	0.039	0.058	0.016
151	0.013	0.012	0.041	0.020	0.000	0.000	0.009	0.012	0.030	0.029	0.023	0.000
155	0.026	0.000	0.000	0.010	0.000	0.010	0.019	0.012	0.010	0.019	0.000	0.016
159	0.013	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000
163	0.000	0.000	0.010	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000
167	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
171	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	39	43	49	49	31	48	54	43	50	52	43	32

μSpi6

	Collection										
Allele	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AM	AN
95	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
99	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
103	0.000	0.027	0.009	0.024	0.000	0.000	0.033	0.009	0.000	0.000	0.000	0.000
107	0.000	0.000	0.018	0.000	0.020	0.028	0.000	0.009	0.015	0.000	0.017	0.010
111	0.321	0.209	0.348	0.333	0.360	0.302	0.217	0.200	0.185	0.353	0.250	0.360
115	0.123	0.255	0.116	0.191	0.140	0.170	0.150	0.100	0.223	0.118	0.217	0.120
119	0.076	0.082	0.009	0.024	0.050	0.104	0.083	0.073	0.100	0.029	0.050	0.060
123	0.132	0.046	0.089	0.048	0.100	0.057	0.083	0.118	0.069	0.088	0.117	0.060
127	0.085	0.082	0.045	0.048	0.050	0.057	0.033	0.064	0.062	0.059	0.050	0.090
131	0.113	0.082	0.071	0.024	0.060	0.066	0.050	0.055	0.077	0.118	0.067	0.060
135	0.028	0.055	0.089	0.119	0.060	0.085	0.117	0.146	0.077	0.029	0.050	0.110
139	0.038	0.055	0.098	0.119	0.070	0.076	0.133	0.091	0.123	0.088	0.083	0.050
143	0.028	0.027	0.054	0.024	0.010	0.028	0.100	0.082	0.023	0.029	0.033	0.030
147	0.028	0.036	0.027	0.024	0.010	0.028	0.000	0.027	0.023	0.059	0.017	0.040
151	0.009	0.027	0.009	0.000	0.050	0.000	0.000	0.009	0.023	0.029	0.017	0.010
155	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.017	0.000
159	0.000	0.000	0.009	0.000	0.020	0.000	0.000	0.009	0.000	0.000	0.017	0.000
163	0.000	0.000	0.009	0.024	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
167	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
171	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	53	55	56	21	50	53	30	55	65	17	30	50

µSpi6

	Collection									
Allele	AO	AL	AI	AJ	AK	BA	BB	BC	BD	Overall
95	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
99	0.000	0.000	0.000	0.026	0.000	0.000	0.000	0.000	0.000	0.002
103	0.009	0.000	0.036	0.000	0.023	0.029	0.000	0.044	0.000	0.010
107	0.009	0.011	0.036	0.000	0.000	0.010	0.011	0.011	0.011	0.012
111	0.405	0.296	0.214	0.421	0.205	0.245	0.167	0.294	0.160	0.270
115	0.155	0.227	0.143	0.105	0.114	0.216	0.189	0.174	0.234	0.160
119	0.086	0.102	0.000	0.026	0.114	0.069	0.122	0.065	0.106	0.074
123	0.060	0.057	0.107	0.053	0.159	0.069	0.111	0.065	0.096	0.083
127	0.035	0.057	0.071	0.026	0.046	0.078	0.133	0.065	0.053	0.055
131	0.052	0.057	0.071	0.079	0.068	0.049	0.056	0.054	0.075	0.070
135	0.060	0.068	0.143	0.132	0.068	0.069	0.067	0.076	0.053	0.074
139	0.052	0.034	0.107	0.079	0.091	0.069	0.056	0.087	0.085	0.072
143	0.026	0.046	0.036	0.026	0.068	0.029	0.044	0.022	0.053	0.047
147	0.026	0.000	0.036	0.026	0.023	0.039	0.022	0.000	0.011	0.032
151	0.009	0.023	0.000	0.000	0.023	0.020	0.011	0.022	0.021	0.019
155	0.017	0.011	0.000	0.000	0.000	0.000	0.011	0.022	0.032	0.011
159	0.000	0.011	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.005
163	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002
167	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
171	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.001
n	58	44	14	19	22	51	45	46	47	2109

µSpi10

	Collection											
Allele	A	B	C	D	E	F	G	H	I	J	K	L
103	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
107	0.097	0.123	0.136	0.109	0.210	0.205	0.235	0.227	0.210	0.283	0.227	0.109
111	0.040	0.070	0.018	0.070	0.037	0.045	0.029	0.046	0.010	0.009	0.009	0.022
115	0.186	0.246	0.264	0.195	0.222	0.295	0.284	0.258	0.260	0.208	0.318	0.304
119	0.024	0.026	0.000	0.000	0.043	0.009	0.039	0.053	0.030	0.009	0.009	0.033
123	0.444	0.298	0.327	0.367	0.315	0.232	0.206	0.265	0.260	0.293	0.227	0.326
127	0.121	0.105	0.127	0.125	0.062	0.152	0.118	0.099	0.110	0.094	0.100	0.109
131	0.073	0.088	0.082	0.070	0.068	0.036	0.049	0.046	0.070	0.076	0.091	0.065
135	0.008	0.035	0.036	0.039	0.019	0.018	0.010	0.000	0.040	0.009	0.009	0.011
139	0.008	0.009	0.009	0.008	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.011
143	0.000	0.000	0.000	0.000	0.012	0.009	0.010	0.000	0.000	0.009	0.000	0.000
147	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000
151	0.000	0.000	0.000	0.008	0.012	0.000	0.020	0.000	0.000	0.009	0.000	0.011
155	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
163	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000
n	62	57	55	64	81	56	51	66	50	53	55	46

µSpi10

	Collection											
Allele	M	N	O	P	Q	R	S	T	U	V	W	X
103	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
107	0.231	0.151	0.092	0.184	0.177	0.276	0.182	0.186	0.240	0.240	0.186	0.203
111	0.013	0.047	0.041	0.010	0.032	0.020	0.027	0.023	0.030	0.019	0.058	0.063
115	0.269	0.279	0.388	0.337	0.258	0.235	0.255	0.361	0.300	0.231	0.291	0.266
119	0.026	0.000	0.031	0.010	0.016	0.071	0.036	0.058	0.070	0.058	0.023	0.094
123	0.295	0.221	0.194	0.265	0.323	0.245	0.327	0.233	0.180	0.221	0.233	0.250
127	0.064	0.105	0.112	0.102	0.145	0.082	0.127	0.070	0.110	0.096	0.128	0.047
131	0.039	0.151	0.092	0.071	0.016	0.051	0.027	0.047	0.050	0.096	0.070	0.063
135	0.039	0.012	0.020	0.000	0.000	0.010	0.018	0.012	0.010	0.019	0.012	0.016
139	0.013	0.012	0.020	0.010	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000
143	0.013	0.000	0.000	0.010	0.016	0.000	0.000	0.000	0.010	0.000	0.000	0.000
147	0.000	0.000	0.010	0.000	0.016	0.010	0.000	0.012	0.000	0.010	0.000	0.000
151	0.000	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
155	0.000	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
163	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	39	43	49	49	31	49	55	43	50	52	43	32

µSpi10

	Collection											
Allele	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AM	AN
103	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
107	0.170	0.246	0.196	0.214	0.250	0.226	0.217	0.246	0.162	0.206	0.250	0.200
111	0.066	0.055	0.009	0.071	0.010	0.047	0.017	0.064	0.008	0.029	0.017	0.020
115	0.349	0.291	0.277	0.214	0.220	0.283	0.233	0.309	0.300	0.177	0.250	0.290
119	0.047	0.082	0.036	0.048	0.030	0.066	0.067	0.046	0.023	0.118	0.050	0.030
123	0.264	0.155	0.313	0.262	0.280	0.208	0.267	0.209	0.346	0.382	0.300	0.230
127	0.028	0.082	0.054	0.167	0.140	0.113	0.067	0.036	0.054	0.029	0.100	0.150
131	0.057	0.073	0.080	0.024	0.030	0.057	0.100	0.064	0.077	0.059	0.033	0.030
135	0.009	0.009	0.018	0.000	0.020	0.000	0.017	0.009	0.015	0.000	0.000	0.030
139	0.000	0.000	0.009	0.000	0.020	0.000	0.000	0.000	0.000	0.000	0.000	0.010
143	0.009	0.000	0.009	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000
147	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000
151	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000
155	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
163	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.009	0.000	0.000	0.000	0.010
n	53	55	56	21	50	53	30	55	65	17	30	50

μSpi10

	Collection									
Allele	AO	AL	AI	AJ	AK	BA	BB	BC	BD	Overall
103	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.000
107	0.164	0.189	0.143	0.184	0.136	0.226	0.245	0.300	0.239	0.198
111	0.017	0.000	0.000	0.053	0.046	0.029	0.021	0.022	0.011	0.031
115	0.302	0.278	0.429	0.237	0.432	0.294	0.340	0.256	0.273	0.276
119	0.035	0.044	0.036	0.000	0.046	0.039	0.085	0.033	0.068	0.038
123	0.302	0.311	0.286	0.290	0.182	0.265	0.160	0.233	0.216	0.268
127	0.121	0.100	0.071	0.158	0.068	0.078	0.021	0.067	0.057	0.095
131	0.052	0.056	0.000	0.053	0.091	0.059	0.075	0.067	0.080	0.064
135	0.009	0.011	0.000	0.026	0.000	0.010	0.032	0.011	0.034	0.016
139	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.023	0.005
143	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.003
147	0.000	0.011	0.036	0.000	0.000	0.000	0.000	0.000	0.000	0.002
151	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002
155	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
163	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
n	58	45	14	19	22	51	47	45	44	2111

μSpi12

	Collection											
Allele	A	B	C	D	E	F	G	H	I	J	K	L
75	0.274	0.272	0.273	0.219	0.191	0.179	0.216	0.220	0.170	0.179	0.246	0.196
77	0.016	0.009	0.027	0.016	0.062	0.036	0.029	0.046	0.070	0.057	0.055	0.033
79	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000
81	0.032	0.018	0.036	0.039	0.056	0.080	0.039	0.076	0.070	0.047	0.027	0.044
83	0.008	0.000	0.000	0.000	0.019	0.000	0.020	0.008	0.010	0.019	0.009	0.044
85	0.000	0.000	0.027	0.000	0.019	0.009	0.020	0.008	0.010	0.009	0.009	0.011
87	0.008	0.018	0.009	0.016	0.031	0.027	0.020	0.068	0.010	0.019	0.046	0.033
89	0.000	0.035	0.000	0.016	0.012	0.009	0.029	0.015	0.030	0.019	0.027	0.000
91	0.000	0.000	0.000	0.000	0.000	0.009	0.010	0.000	0.020	0.009	0.009	0.000
93	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
97	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
99	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000
101	0.000	0.000	0.027	0.023	0.025	0.000	0.020	0.030	0.030	0.028	0.027	0.033
103	0.016	0.035	0.009	0.016	0.043	0.027	0.039	0.038	0.080	0.009	0.055	0.022
105	0.605	0.561	0.546	0.625	0.488	0.563	0.520	0.477	0.450	0.538	0.455	0.544
107	0.040	0.053	0.046	0.031	0.049	0.036	0.029	0.015	0.040	0.057	0.027	0.044
109	0.000	0.000	0.000	0.000	0.006	0.009	0.010	0.000	0.010	0.000	0.009	0.000
111	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
113	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000
n	62	57	55	64	81	56	51	66	50	53	55	46

μSpi12

	Collection											
Allele	M	N	O	P	Q	R	S	T	U	V	W	X
75	0.295	0.256	0.235	0.214	0.290	0.153	0.173	0.151	0.160	0.221	0.163	0.141
77	0.000	0.035	0.051	0.061	0.032	0.020	0.046	0.035	0.090	0.039	0.047	0.047
79	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.010	0.010	0.000	0.000
81	0.026	0.047	0.071	0.102	0.048	0.061	0.046	0.047	0.040	0.039	0.058	0.063
83	0.000	0.000	0.000	0.000	0.000	0.020	0.018	0.023	0.010	0.000	0.000	0.000
85	0.013	0.000	0.000	0.041	0.016	0.000	0.000	0.000	0.000	0.010	0.012	0.000
87	0.051	0.012	0.041	0.031	0.032	0.000	0.073	0.035	0.030	0.019	0.058	0.016
89	0.000	0.012	0.000	0.031	0.032	0.000	0.027	0.012	0.020	0.000	0.000	0.031
91	0.026	0.012	0.000	0.000	0.000	0.010	0.000	0.012	0.000	0.000	0.000	0.016
93	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
97	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
99	0.000	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000
101	0.013	0.012	0.041	0.010	0.016	0.010	0.046	0.000	0.040	0.000	0.000	0.016
103	0.013	0.035	0.041	0.010	0.081	0.082	0.055	0.035	0.040	0.029	0.047	0.031
105	0.513	0.512	0.490	0.469	0.387	0.592	0.500	0.605	0.520	0.596	0.570	0.609
107	0.039	0.047	0.031	0.031	0.048	0.051	0.009	0.047	0.030	0.039	0.035	0.031
109	0.013	0.012	0.000	0.000	0.016	0.000	0.000	0.000	0.000	0.000	0.000	0.000
111	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000
113	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	39	43	49	49	31	49	55	43	50	52	43	32

μSpi12

	Collection											
Allele	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AM	AN
75	0.217	0.218	0.268	0.214	0.210	0.226	0.183	0.182	0.246	0.118	0.133	0.190
77	0.028	0.036	0.018	0.000	0.050	0.047	0.067	0.018	0.039	0.088	0.050	0.100
79	0.019	0.000	0.000	0.024	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010
81	0.019	0.046	0.009	0.000	0.040	0.047	0.033	0.009	0.062	0.000	0.033	0.080
83	0.019	0.027	0.009	0.024	0.000	0.009	0.017	0.018	0.008	0.000	0.000	0.000
85	0.009	0.000	0.009	0.000	0.010	0.009	0.050	0.009	0.031	0.029	0.033	0.000
87	0.066	0.064	0.054	0.095	0.030	0.019	0.067	0.073	0.069	0.029	0.017	0.020
89	0.009	0.009	0.018	0.000	0.020	0.009	0.000	0.018	0.031	0.029	0.000	0.010
91	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010
93	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
97	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
99	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
101	0.009	0.009	0.009	0.071	0.020	0.009	0.017	0.009	0.015	0.000	0.017	0.010
103	0.047	0.064	0.054	0.024	0.020	0.057	0.017	0.018	0.062	0.029	0.050	0.040
105	0.509	0.500	0.518	0.548	0.550	0.528	0.500	0.636	0.415	0.647	0.617	0.530
107	0.047	0.027	0.027	0.000	0.040	0.028	0.033	0.009	0.023	0.029	0.033	0.000
109	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.000	0.000	0.000	0.000	0.000
111	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000
113	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.000
n	53	55	56	21	50	53	30	55	65	17	30	50

µSpi12

	Collection								
Allele	AO	AL	AI	AJ	AK	BA	BB	BC	BD	Overall
75	0.147	0.222	0.143	0.263	0.205	0.094	0.188	0.135	0.174	0.204
77	0.035	0.033	0.036	0.000	0.000	0.042	0.042	0.063	0.031	0.040
79	0.000	0.011	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.002
81	0.078	0.033	0.000	0.053	0.068	0.021	0.010	0.010	0.031	0.044
83	0.035	0.033	0.000	0.000	0.000	0.021	0.021	0.000	0.020	0.011
85	0.000	0.011	0.036	0.000	0.000	0.021	0.000	0.010	0.010	0.010
87	0.052	0.067	0.036	0.026	0.023	0.021	0.042	0.094	0.112	0.039
89	0.017	0.011	0.000	0.000	0.023	0.010	0.021	0.010	0.020	0.014
91	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.003
93	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.001
97	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000
99	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
101	0.017	0.011	0.000	0.000	0.023	0.010	0.000	0.010	0.010	0.016
103	0.026	0.067	0.000	0.000	0.000	0.104	0.094	0.042	0.010	0.040
105	0.569	0.456	0.643	0.632	0.636	0.594	0.563	0.573	0.531	0.536
107	0.026	0.033	0.107	0.026	0.023	0.052	0.010	0.052	0.020	0.034
109	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.003
111	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.001
113	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
n	58	45	14	19	22	48	48	48	49	2117

µSth3B

	Collection											
Allele	A	B	C	D	E	F	G	H	I	J	K	L
136	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
138	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
140	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
142	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011
144	0.000	0.000	0.000	0.008	0.000	0.027	0.000	0.000	0.000	0.000	0.000	0.000
146	0.250	0.193	0.300	0.297	0.124	0.214	0.196	0.205	0.140	0.217	0.136	0.196
148	0.194	0.219	0.200	0.203	0.235	0.188	0.137	0.182	0.170	0.179	0.182	0.163
150	0.040	0.088	0.046	0.039	0.093	0.089	0.059	0.046	0.070	0.066	0.082	0.120
152	0.323	0.263	0.273	0.289	0.303	0.223	0.333	0.303	0.360	0.293	0.309	0.272
154	0.032	0.018	0.046	0.055	0.080	0.071	0.088	0.068	0.070	0.094	0.073	0.054
156	0.040	0.070	0.018	0.016	0.068	0.063	0.088	0.061	0.070	0.038	0.082	0.065
158	0.008	0.035	0.055	0.031	0.031	0.027	0.029	0.030	0.030	0.047	0.036	0.044
160	0.032	0.035	0.018	0.008	0.043	0.027	0.049	0.053	0.020	0.028	0.055	0.033
162	0.008	0.018	0.009	0.008	0.006	0.036	0.010	0.030	0.020	0.009	0.036	0.011
164	0.016	0.026	0.018	0.039	0.006	0.018	0.000	0.023	0.010	0.000	0.000	0.000
166	0.048	0.035	0.018	0.008	0.012	0.009	0.010	0.000	0.030	0.000	0.009	0.000
168	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.009	0.000	0.011
170	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.011
172	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.011
174	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000
176	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	62	57	55	64	81	56	51	66	50	53	55	46

μSth3B

	Collection											
Allele	M	N	O	P	Q	R	S	T	U	V	W	X
136	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000
138	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.016
140	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
142	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
144	0.000	0.000	0.000	0.010	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000
146	0.141	0.221	0.214	0.194	0.161	0.143	0.118	0.093	0.150	0.115	0.198	0.094
148	0.180	0.105	0.143	0.204	0.129	0.122	0.164	0.163	0.230	0.154	0.128	0.203
150	0.064	0.105	0.082	0.061	0.113	0.082	0.073	0.070	0.070	0.096	0.105	0.063
152	0.308	0.233	0.265	0.296	0.210	0.347	0.273	0.361	0.290	0.365	0.372	0.328
154	0.115	0.116	0.092	0.071	0.145	0.122	0.091	0.070	0.080	0.096	0.058	0.125
156	0.090	0.081	0.051	0.092	0.065	0.082	0.091	0.105	0.030	0.077	0.058	0.000
158	0.013	0.023	0.051	0.041	0.032	0.041	0.064	0.023	0.050	0.029	0.023	0.047
160	0.000	0.023	0.031	0.000	0.065	0.041	0.064	0.047	0.030	0.019	0.012	0.031
162	0.013	0.012	0.020	0.020	0.048	0.000	0.027	0.035	0.020	0.019	0.023	0.063
164	0.039	0.012	0.010	0.000	0.016	0.000	0.009	0.012	0.030	0.019	0.012	0.000
166	0.013	0.047	0.020	0.010	0.016	0.010	0.009	0.012	0.020	0.010	0.012	0.031
168	0.013	0.012	0.000	0.000	0.000	0.010	0.000	0.012	0.000	0.000	0.000	0.000
170	0.013	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
172	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
174	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
176	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	39	43	49	49	31	49	55	43	50	52	43	32

μSth3B

	Collection											
Allele	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AM	AN
136	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
138	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
140	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000
142	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
144	0.009	0.000	0.000	0.024	0.000	0.000	0.000	0.000	0.015	0.000	0.000	0.000
146	0.151	0.109	0.143	0.262	0.140	0.123	0.183	0.148	0.092	0.118	0.233	0.120
148	0.189	0.155	0.196	0.191	0.220	0.132	0.233	0.157	0.162	0.088	0.200	0.200
150	0.038	0.091	0.027	0.048	0.140	0.113	0.100	0.074	0.077	0.029	0.100	0.090
152	0.283	0.255	0.375	0.310	0.280	0.330	0.300	0.352	0.315	0.294	0.217	0.330
154	0.085	0.118	0.054	0.024	0.080	0.076	0.033	0.074	0.062	0.059	0.033	0.060
156	0.094	0.109	0.098	0.024	0.060	0.094	0.033	0.083	0.100	0.118	0.017	0.120
158	0.019	0.018	0.009	0.048	0.010	0.028	0.033	0.046	0.039	0.118	0.067	0.000
160	0.019	0.055	0.018	0.024	0.040	0.019	0.017	0.028	0.062	0.088	0.033	0.070
162	0.038	0.009	0.027	0.000	0.000	0.038	0.000	0.000	0.054	0.059	0.033	0.010
164	0.000	0.055	0.036	0.024	0.010	0.028	0.033	0.028	0.015	0.029	0.017	0.000
166	0.047	0.027	0.009	0.000	0.020	0.009	0.000	0.000	0.000	0.000	0.050	0.000
168	0.009	0.000	0.000	0.024	0.000	0.009	0.017	0.009	0.000	0.000	0.000	0.000
170	0.009	0.000	0.000	0.000	0.000	0.000	0.017	0.000	0.000	0.000	0.000	0.000
172	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
174	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
176	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	53	55	56	21	50	53	30	54	65	17	30	50

µSth3B

	Collection									
Allele	AO	AL	AI	AJ	AK	BA	BB	BC	BD	Overall
136	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
138	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
140	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
142	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
144	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002
146	0.172	0.189	0.107	0.235	0.159	0.156	0.151	0.133	0.130	0.168
148	0.172	0.144	0.143	0.088	0.250	0.146	0.140	0.167	0.163	0.175
150	0.026	0.067	0.286	0.029	0.023	0.042	0.058	0.078	0.076	0.074
152	0.371	0.244	0.214	0.324	0.273	0.281	0.419	0.322	0.294	0.304
154	0.086	0.167	0.071	0.118	0.091	0.135	0.070	0.156	0.098	0.081
156	0.078	0.067	0.036	0.147	0.046	0.083	0.035	0.033	0.109	0.069
158	0.017	0.022	0.071	0.029	0.023	0.031	0.047	0.033	0.044	0.033
160	0.026	0.089	0.036	0.000	0.091	0.083	0.023	0.011	0.054	0.036
162	0.017	0.000	0.000	0.029	0.000	0.010	0.023	0.044	0.022	0.020
164	0.009	0.000	0.036	0.000	0.023	0.010	0.000	0.011	0.011	0.015
166	0.000	0.011	0.000	0.000	0.023	0.021	0.012	0.011	0.000	0.014
168	0.009	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.004
170	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.002
172	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
174	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
176	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	58	45	14	17	22	48	43	45	46	2103

µSma5

	Collection											
Allele	A	B	C	D	E	F	G	H	I	J	K	L
98	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000
100	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000
108	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000
110	0.903	0.833	0.882	0.883	0.858	0.902	0.882	0.886	0.920	0.934	0.818	0.880
112	0.057	0.088	0.091	0.086	0.086	0.036	0.069	0.023	0.060	0.019	0.109	0.054
114	0.016	0.044	0.000	0.000	0.019	0.036	0.029	0.038	0.010	0.009	0.046	0.033
116	0.024	0.035	0.027	0.023	0.031	0.027	0.020	0.038	0.010	0.019	0.027	0.022
118	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011
120	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000
122	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000
n	62	57	55	64	81	56	51	66	50	53	55	46

µSma5

	Collection											
Allele	M	N	O	P	Q	R	S	T	U	V	W	X
98	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
108	0.000	0.000	0.020	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
110	0.923	0.872	0.857	0.806	0.903	0.918	0.918	0.872	0.880	0.808	0.954	0.891
112	0.039	0.047	0.082	0.112	0.048	0.041	0.046	0.058	0.110	0.115	0.012	0.047
114	0.026	0.058	0.041	0.071	0.032	0.010	0.036	0.035	0.010	0.039	0.000	0.000
116	0.013	0.023	0.000	0.010	0.016	0.010	0.000	0.035	0.000	0.029	0.035	0.031
118	0.000	0.000	0.000	0.000	0.000	0.020	0.000	0.000	0.000	0.000	0.000	0.016
120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.016
122	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000
n	39	43	49	49	31	49	55	43	50	52	43	32

µSma5

	Collection											
Allele	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AM	AN
98	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
108	0.000	0.009	0.000	0.024	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
110	0.849	0.918	0.875	0.786	0.860	0.934	0.833	0.864	0.839	0.882	0.883	0.930
112	0.076	0.036	0.107	0.048	0.070	0.028	0.083	0.100	0.092	0.059	0.050	0.060
114	0.066	0.018	0.009	0.095	0.040	0.019	0.033	0.027	0.039	0.029	0.033	0.010
116	0.000	0.009	0.009	0.048	0.020	0.009	0.050	0.009	0.023	0.029	0.033	0.000
118	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000
120	0.000	0.009	0.000	0.000	0.010	0.000	0.000	0.000	0.008	0.000	0.000	0.000
122	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	53	55	56	21	50	53	30	55	65	17	30	50

µSma5

	Collection									
Allele	AO	AL	AI	AJ	AK	BA	BB	BC	BD	Overall
98	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
100	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
108	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
110	0.922	0.889	0.929	0.816	0.909	0.914	0.936	0.896	0.885	0.883
112	0.043	0.078	0.036	0.132	0.068	0.077	0.032	0.063	0.073	0.066
114	0.000	0.022	0.036	0.026	0.000	0.000	0.011	0.010	0.031	0.026
116	0.017	0.011	0.000	0.026	0.023	0.000	0.011	0.010	0.010	0.018
118	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
120	0.000	0.000	0.000	0.000	0.000	0.010	0.011	0.010	0.000	0.002
122	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.001
n	58	45	14	19	22	52	47	48	48	2119

μSma7

	Collection											
Allele	A	B	C	D	E	F	G	H	I	J	K	L
104	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
110	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011
112	0.008	0.009	0.009	0.008	0.006	0.009	0.010	0.000	0.000	0.000	0.027	0.000
114	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000
116	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
118	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
120	0.000	0.000	0.009	0.008	0.000	0.009	0.000	0.000	0.000	0.000	0.018	0.000
122	0.073	0.097	0.109	0.219	0.136	0.232	0.230	0.273	0.170	0.212	0.118	0.196
124	0.153	0.175	0.118	0.141	0.204	0.152	0.180	0.144	0.180	0.212	0.327	0.207
126	0.048	0.018	0.046	0.016	0.056	0.045	0.020	0.053	0.020	0.029	0.018	0.000
128	0.000	0.009	0.027	0.008	0.037	0.027	0.050	0.061	0.020	0.039	0.046	0.044
130	0.032	0.018	0.036	0.039	0.031	0.018	0.030	0.030	0.040	0.029	0.027	0.022
132	0.000	0.000	0.018	0.016	0.012	0.018	0.000	0.015	0.010	0.019	0.000	0.011
134	0.000	0.000	0.000	0.008	0.012	0.009	0.000	0.023	0.000	0.010	0.027	0.022
136	0.000	0.009	0.009	0.008	0.006	0.009	0.000	0.030	0.050	0.019	0.009	0.022
138	0.048	0.026	0.027	0.016	0.019	0.009	0.000	0.023	0.010	0.000	0.009	0.011
140	0.016	0.026	0.009	0.023	0.025	0.018	0.020	0.008	0.020	0.019	0.027	0.022
142	0.210	0.158	0.191	0.125	0.142	0.116	0.140	0.068	0.150	0.125	0.055	0.098
144	0.081	0.140	0.100	0.125	0.111	0.098	0.050	0.076	0.110	0.106	0.091	0.054
146	0.048	0.018	0.027	0.031	0.056	0.071	0.070	0.053	0.060	0.010	0.046	0.098
148	0.008	0.035	0.036	0.008	0.025	0.027	0.030	0.008	0.030	0.019	0.027	0.022
150	0.024	0.044	0.018	0.039	0.037	0.036	0.070	0.046	0.040	0.058	0.046	0.044
152	0.016	0.018	0.009	0.039	0.012	0.018	0.040	0.008	0.000	0.000	0.018	0.022
154	0.040	0.026	0.046	0.023	0.019	0.000	0.010	0.023	0.030	0.029	0.000	0.011
156	0.048	0.026	0.018	0.023	0.006	0.009	0.000	0.000	0.000	0.010	0.000	0.022
158	0.008	0.035	0.000	0.008	0.000	0.018	0.010	0.008	0.020	0.029	0.018	0.022
160	0.008	0.000	0.009	0.000	0.012	0.009	0.000	0.000	0.010	0.010	0.000	0.000
162	0.032	0.044	0.055	0.023	0.019	0.027	0.010	0.008	0.020	0.000	0.018	0.000
164	0.024	0.035	0.036	0.008	0.012	0.009	0.000	0.030	0.000	0.010	0.000	0.011
166	0.065	0.026	0.027	0.039	0.000	0.009	0.020	0.008	0.000	0.010	0.009	0.022
168	0.000	0.009	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000
170	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000
172	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.009	0.000
174	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011
194	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000
n	62	57	55	64	81	56	50	66	50	52	55	46

µSma7

	Collection											
Allele	M	N	O	P	Q	R	S	**T**	U	V	W	X
104	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
110	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000
112	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000
114	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.016
116	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000
118	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000
120	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.012	0.000	0.000	0.000	0.000
122	0.218	0.256	0.174	0.235	0.242	0.184	0.282	0.209	0.220	0.115	0.267	0.203
124	0.218	0.174	0.204	0.174	0.113	0.163	0.127	0.151	0.100	0.144	0.186	0.156
126	0.026	0.012	0.051	0.061	0.000	0.061	0.055	0.070	0.080	0.067	0.035	0.047
128	0.026	0.070	0.020	0.031	0.065	0.102	0.073	0.047	0.040	0.039	0.035	0.063
130	0.000	0.000	0.071	0.010	0.016	0.020	0.009	0.023	0.040	0.029	0.023	0.016
132	0.013	0.023	0.010	0.010	0.000	0.000	0.000	0.012	0.000	0.010	0.000	0.000
134	0.013	0.012	0.010	0.020	0.000	0.000	0.009	0.023	0.020	0.010	0.000	0.000
136	0.013	0.012	0.031	0.000	0.016	0.051	0.036	0.023	0.030	0.029	0.023	0.047
138	0.000	0.000	0.010	0.010	0.016	0.000	0.000	0.012	0.020	0.010	0.023	0.000
140	0.013	0.012	0.000	0.000	0.016	0.010	0.018	0.012	0.020	0.010	0.012	0.016
142	0.103	0.116	0.102	0.122	0.097	0.153	0.073	0.093	0.080	0.115	0.070	0.047
144	0.141	0.070	0.133	0.122	0.081	0.082	0.082	0.081	0.040	0.058	0.093	0.094
146	0.000	0.070	0.041	0.051	0.081	0.041	0.073	0.023	0.080	0.087	0.035	0.109
148	0.013	0.035	0.010	0.020	0.081	0.000	0.018	0.035	0.020	0.039	0.047	0.063
150	0.077	0.070	0.031	0.020	0.048	0.041	0.064	0.023	0.070	0.087	0.023	0.031
152	0.026	0.023	0.020	0.020	0.032	0.041	0.027	0.035	0.020	0.010	0.000	0.031
154	0.026	0.035	0.031	0.010	0.016	0.020	0.018	0.012	0.060	0.039	0.081	0.016
156	0.000	0.000	0.010	0.020	0.016	0.000	0.009	0.012	0.010	0.010	0.023	0.000
158	0.013	0.012	0.010	0.000	0.016	0.000	0.000	0.023	0.010	0.010	0.000	0.000
160	0.013	0.000	0.000	0.010	0.000	0.000	0.009	0.023	0.000	0.010	0.012	0.000
162	0.039	0.000	0.000	0.010	0.048	0.010	0.000	0.000	0.020	0.019	0.000	0.000
164	0.013	0.000	0.010	0.031	0.000	0.000	0.009	0.000	0.000	0.029	0.000	0.031
166	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.010	0.019	0.012	0.000
168	0.000	0.000	0.010	0.010	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.016
170	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
172	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000
174	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000
194	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	39	43	49	49	31	49	55	43	50	52	43	32

µSma7

	Collection											
Allele	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AM	AN
104	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
110	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
112	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
114	0.009	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
116	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
118	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.029	0.000	0.000
120	0.000	0.000	0.000	0.000	0.000	0.019	0.000	0.000	0.000	0.000	0.000	0.000
122	0.179	0.255	0.179	0.214	0.230	0.274	0.200	0.164	0.269	0.235	0.217	0.190
124	0.170	0.164	0.116	0.119	0.150	0.151	0.183	0.236	0.177	0.206	0.233	0.140
126	0.057	0.091	0.045	0.024	0.010	0.057	0.067	0.055	0.046	0.059	0.017	0.070
128	0.038	0.036	0.018	0.048	0.000	0.076	0.067	0.055	0.085	0.029	0.083	0.080
130	0.019	0.027	0.063	0.024	0.020	0.019	0.033	0.009	0.031	0.000	0.050	0.030
132	0.019	0.000	0.018	0.000	0.010	0.009	0.033	0.000	0.015	0.000	0.000	0.000
134	0.019	0.000	0.009	0.000	0.010	0.009	0.000	0.009	0.031	0.000	0.000	0.020
136	0.019	0.018	0.009	0.000	0.010	0.009	0.050	0.018	0.000	0.029	0.017	0.010
138	0.009	0.009	0.009	0.048	0.030	0.028	0.000	0.027	0.008	0.029	0.000	0.000
140	0.019	0.018	0.018	0.000	0.000	0.009	0.017	0.018	0.000	0.029	0.033	0.020
142	0.104	0.082	0.116	0.095	0.130	0.057	0.050	0.082	0.077	0.147	0.067	0.140
144	0.028	0.046	0.125	0.095	0.100	0.066	0.017	0.046	0.054	0.029	0.100	0.040
146	0.057	0.064	0.027	0.048	0.090	0.066	0.050	0.046	0.062	0.029	0.050	0.110
148	0.028	0.055	0.018	0.000	0.020	0.028	0.050	0.018	0.015	0.000	0.033	0.020
150	0.104	0.055	0.027	0.143	0.060	0.019	0.067	0.055	0.054	0.029	0.033	0.050
152	0.047	0.027	0.000	0.048	0.000	0.028	0.033	0.036	0.015	0.029	0.017	0.020
154	0.000	0.018	0.036	0.024	0.030	0.019	0.000	0.027	0.008	0.059	0.017	0.010
156	0.009	0.009	0.045	0.024	0.030	0.009	0.017	0.018	0.015	0.029	0.017	0.030
158	0.000	0.000	0.009	0.000	0.010	0.000	0.017	0.018	0.008	0.000	0.000	0.000
160	0.000	0.009	0.009	0.000	0.010	0.000	0.000	0.009	0.000	0.000	0.000	0.000
162	0.009	0.000	0.036	0.000	0.000	0.028	0.017	0.036	0.000	0.000	0.000	0.000
164	0.009	0.000	0.027	0.024	0.020	0.009	0.033	0.009	0.000	0.000	0.000	0.020
166	0.019	0.018	0.018	0.024	0.010	0.009	0.000	0.000	0.008	0.000	0.000	0.000
168	0.009	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.015	0.000	0.000	0.000
170	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.009	0.008	0.000	0.017	0.000
172	0.009	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
174	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
194	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	53	55	56	21	50	53	30	55	65	17	30	50

µSma7

	Collection									
Allele	AO	AL	AI	AJ	AK	BA	BB	BC	BD	Overall
104	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
110	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
112	0.009	0.022	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.004
114	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
116	0.000	0.000	0.000	0.000	0.000	0.010	0.010	0.000	0.000	0.001
118	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
120	0.017	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.003
122	0.121	0.167	0.214	0.278	0.273	0.183	0.150	0.214	0.194	0.196
124	0.181	0.233	0.179	0.278	0.159	0.067	0.160	0.082	0.153	0.168
126	0.043	0.033	0.000	0.028	0.023	0.096	0.030	0.020	0.051	0.043
128	0.060	0.033	0.000	0.000	0.023	0.058	0.060	0.102	0.041	0.044
130	0.017	0.022	0.000	0.000	0.023	0.048	0.020	0.000	0.031	0.026
132	0.026	0.022	0.107	0.056	0.046	0.010	0.000	0.010	0.000	0.011
134	0.009	0.000	0.000	0.000	0.000	0.010	0.000	0.010	0.020	0.010
136	0.052	0.022	0.000	0.000	0.000	0.087	0.070	0.122	0.071	0.025
138	0.017	0.022	0.000	0.000	0.023	0.010	0.010	0.020	0.000	0.014
140	0.026	0.011	0.000	0.000	0.000	0.039	0.040	0.010	0.010	0.016
142	0.112	0.111	0.107	0.111	0.091	0.077	0.080	0.082	0.092	0.108
144	0.078	0.067	0.179	0.111	0.114	0.019	0.050	0.061	0.051	0.081
146	0.052	0.044	0.071	0.056	0.046	0.067	0.080	0.051	0.061	0.055
148	0.017	0.022	0.036	0.000	0.046	0.048	0.020	0.041	0.041	0.026
150	0.060	0.033	0.036	0.028	0.068	0.029	0.080	0.051	0.071	0.049
152	0.026	0.056	0.000	0.000	0.000	0.019	0.010	0.031	0.000	0.021
154	0.000	0.011	0.000	0.000	0.000	0.039	0.090	0.010	0.010	0.023
156	0.009	0.022	0.000	0.000	0.000	0.019	0.010	0.020	0.031	0.015
158	0.017	0.022	0.000	0.000	0.023	0.000	0.000	0.010	0.020	0.010
160	0.000	0.011	0.000	0.000	0.000	0.019	0.000	0.010	0.000	0.005
162	0.017	0.000	0.000	0.000	0.000	0.029	0.010	0.020	0.010	0.015
164	0.026	0.011	0.000	0.028	0.000	0.010	0.010	0.000	0.010	0.013
166	0.009	0.000	0.036	0.028	0.023	0.010	0.010	0.010	0.000	0.012
168	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.003
170	0.000	0.000	0.036	0.000	0.000	0.000	0.000	0.010	0.010	0.002
172	0.000	0.000	0.000	0.000	0.023	0.000	0.000	0.000	0.000	0.001
174	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
194	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	58	45	14	18	22	52	50	49	49	2121

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	Collection											
Allele	A	B	C	D	E	F	G	H	I	J	K	L
139	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
141	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011
143	0.008	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000
145	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
147	0.000	0.000	0.000	0.008	0.006	0.000	0.000	0.000	0.000	0.019	0.000	0.000
149	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.009	0.000
151	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
153	0.000	0.009	0.009	0.000	0.000	0.000	0.000	0.015	0.000	0.009	0.000	0.000
155	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.015	0.000	0.000	0.000	0.000
157	0.000	0.009	0.009	0.008	0.049	0.054	0.020	0.023	0.031	0.047	0.027	0.022
159	0.032	0.000	0.000	0.008	0.074	0.063	0.069	0.046	0.073	0.066	0.018	0.022
161	0.000	0.018	0.000	0.000	0.025	0.009	0.029	0.023	0.000	0.019	0.009	0.000
163	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.023	0.000	0.009	0.009	0.033
165	0.008	0.000	0.009	0.000	0.012	0.009	0.010	0.015	0.010	0.009	0.000	0.000
167	0.000	0.000	0.009	0.000	0.025	0.009	0.029	0.000	0.042	0.038	0.009	0.011
169	0.016	0.018	0.018	0.031	0.025	0.027	0.020	0.008	0.000	0.028	0.027	0.011
171	0.016	0.018	0.000	0.008	0.037	0.027	0.000	0.030	0.000	0.019	0.046	0.056
173	0.024	0.018	0.009	0.023	0.006	0.009	0.020	0.030	0.021	0.028	0.009	0.011
175	0.024	0.026	0.018	0.016	0.025	0.045	0.010	0.008	0.052	0.047	0.027	0.044
177	0.008	0.009	0.027	0.023	0.006	0.045	0.029	0.015	0.021	0.009	0.046	0.033
179	0.000	0.000	0.000	0.008	0.025	0.000	0.029	0.030	0.031	0.028	0.018	0.044
181	0.016	0.044	0.082	0.047	0.062	0.018	0.029	0.046	0.010	0.028	0.036	0.000
183	0.024	0.000	0.000	0.016	0.031	0.045	0.049	0.061	0.021	0.057	0.036	0.033
185	0.024	0.035	0.009	0.023	0.068	0.063	0.059	0.030	0.063	0.028	0.073	0.044
187	0.073	0.026	0.055	0.039	0.049	0.036	0.029	0.076	0.094	0.066	0.118	0.100
189	0.032	0.044	0.055	0.039	0.074	0.080	0.029	0.076	0.052	0.076	0.073	0.078
191	0.024	0.035	0.000	0.023	0.049	0.027	0.059	0.091	0.063	0.019	0.046	0.044
193	0.032	0.035	0.082	0.023	0.031	0.018	0.069	0.046	0.094	0.038	0.082	0.044
195	0.040	0.026	0.046	0.055	0.062	0.080	0.029	0.053	0.042	0.000	0.036	0.033
197	0.008	0.053	0.027	0.023	0.031	0.036	0.059	0.053	0.052	0.076	0.027	0.000
199	0.032	0.026	0.064	0.039	0.025	0.045	0.078	0.008	0.021	0.028	0.036	0.011
201	0.073	0.018	0.055	0.047	0.037	0.045	0.020	0.008	0.031	0.009	0.000	0.044
203	0.016	0.026	0.027	0.039	0.012	0.027	0.039	0.008	0.000	0.000	0.009	0.044
205	0.040	0.009	0.009	0.023	0.019	0.009	0.020	0.023	0.010	0.019	0.027	0.033
207	0.065	0.044	0.018	0.016	0.006	0.000	0.020	0.023	0.010	0.009	0.018	0.000
209	0.040	0.026	0.055	0.023	0.012	0.009	0.010	0.000	0.021	0.038	0.000	0.011
211	0.016	0.035	0.009	0.008	0.012	0.009	0.010	0.000	0.010	0.019	0.000	0.011
213	0.057	0.053	0.036	0.063	0.019	0.027	0.010	0.015	0.010	0.047	0.009	0.022
215	0.057	0.044	0.000	0.070	0.012	0.000	0.010	0.015	0.021	0.019	0.036	0.000
217	0.024	0.018	0.018	0.016	0.006	0.036	0.020	0.008	0.010	0.028	0.000	0.000
219	0.024	0.035	0.027	0.023	0.006	0.009	0.010	0.030	0.021	0.009	0.009	0.011
221	0.008	0.070	0.055	0.016	0.006	0.018	0.000	0.000	0.000	0.000	0.018	0.022
223	0.048	0.044	0.018	0.086	0.012	0.018	0.000	0.015	0.021	0.009	0.018	0.056
225	0.008	0.044	0.000	0.016	0.006	0.027	0.010	0.000	0.000	0.000	0.000	0.011
227	0.016	0.009	0.027	0.031	0.006	0.009	0.020	0.000	0.010	0.000	0.000	0.000
229	0.000	0.026	0.027	0.023	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.022
231	0.016	0.009	0.027	0.000	0.000	0.009	0.000	0.008	0.010	0.000	0.000	0.011
233	0.008	0.009	0.036	0.008	0.006	0.000	0.010	0.008	0.000	0.000	0.018	0.000
235	0.024	0.009	0.009	0.008	0.006	0.000	0.000	0.008	0.000	0.000	0.009	0.011
237	0.000	0.000	0.009	0.000	0.006	0.000	0.010	0.008	0.000	0.000	0.000	0.000
239	0.008	0.018	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

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	Collection											
Allele	A	B	C	D	E	F	G	H	I	J	K	L
241	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
243	0.000	0.009	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000
245	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000
247	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
249	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000
251	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000
253	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
255	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
257	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000
259	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000
261	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
263	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
265	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000
267	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
275	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	62	57	55	64	81	56	51	66	48	53	55	45

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Allele	Collection M	N	O	P	Q	R	S	T	U	V	W	X
139	0.000	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
141	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000
143	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
145	0.026	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
147	0.000	0.012	0.000	0.010	0.000	0.000	0.000	0.012	0.000	0.000	0.012	0.000
149	0.013	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000
151	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
153	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.012	0.010	0.000	0.000	0.000
155	0.000	0.000	0.020	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
157	0.013	0.000	0.000	0.020	0.032	0.031	0.027	0.012	0.040	0.048	0.035	0.047
159	0.026	0.093	0.020	0.010	0.000	0.020	0.027	0.047	0.020	0.019	0.035	0.016
161	0.026	0.047	0.020	0.020	0.032	0.020	0.027	0.012	0.020	0.019	0.000	0.000
163	0.039	0.000	0.010	0.020	0.000	0.010	0.018	0.035	0.010	0.019	0.012	0.000
165	0.026	0.012	0.000	0.010	0.016	0.010	0.000	0.023	0.020	0.029	0.000	0.016
167	0.026	0.023	0.041	0.031	0.048	0.061	0.027	0.023	0.030	0.019	0.000	0.000
169	0.013	0.081	0.020	0.041	0.016	0.010	0.027	0.012	0.000	0.019	0.035	0.000
171	0.013	0.058	0.031	0.010	0.032	0.041	0.036	0.023	0.010	0.010	0.023	0.031
173	0.026	0.000	0.020	0.031	0.081	0.010	0.018	0.012	0.020	0.019	0.000	0.031
175	0.026	0.000	0.071	0.071	0.048	0.020	0.027	0.023	0.040	0.039	0.035	0.016
177	0.026	0.023	0.041	0.020	0.016	0.010	0.036	0.012	0.030	0.010	0.023	0.016
179	0.000	0.035	0.010	0.010	0.016	0.051	0.009	0.047	0.060	0.019	0.012	0.016
181	0.064	0.035	0.051	0.041	0.065	0.010	0.036	0.012	0.010	0.010	0.012	0.031
183	0.039	0.023	0.020	0.031	0.032	0.051	0.073	0.058	0.010	0.010	0.035	0.031
185	0.039	0.012	0.061	0.031	0.065	0.061	0.082	0.058	0.040	0.067	0.070	0.094
187	0.039	0.058	0.071	0.082	0.032	0.051	0.073	0.105	0.150	0.087	0.081	0.125
189	0.090	0.140	0.020	0.082	0.032	0.031	0.055	0.116	0.090	0.096	0.070	0.094
191	0.026	0.058	0.020	0.041	0.048	0.122	0.064	0.058	0.100	0.087	0.023	0.031
193	0.026	0.058	0.061	0.041	0.016	0.031	0.073	0.000	0.030	0.039	0.035	0.031
195	0.051	0.012	0.020	0.051	0.048	0.051	0.018	0.047	0.050	0.039	0.047	0.078
197	0.039	0.012	0.031	0.010	0.032	0.061	0.036	0.047	0.040	0.019	0.035	0.031
199	0.039	0.035	0.031	0.041	0.032	0.051	0.018	0.058	0.030	0.019	0.012	0.047
201	0.064	0.035	0.051	0.010	0.048	0.010	0.064	0.012	0.060	0.048	0.023	0.031
203	0.026	0.023	0.010	0.051	0.016	0.020	0.000	0.000	0.020	0.000	0.023	0.000
205	0.000	0.012	0.020	0.020	0.016	0.000	0.027	0.000	0.010	0.010	0.035	0.000
207	0.013	0.012	0.020	0.051	0.000	0.010	0.018	0.023	0.010	0.010	0.012	0.031
209	0.026	0.012	0.010	0.000	0.000	0.000	0.018	0.012	0.020	0.029	0.047	0.016
211	0.013	0.012	0.000	0.010	0.032	0.010	0.000	0.000	0.000	0.029	0.035	0.031
213	0.026	0.012	0.020	0.000	0.016	0.010	0.000	0.000	0.000	0.019	0.093	0.031
215	0.000	0.023	0.010	0.010	0.016	0.031	0.009	0.012	0.000	0.010	0.035	0.000
217	0.026	0.000	0.051	0.020	0.000	0.000	0.000	0.012	0.010	0.010	0.000	0.000
219	0.013	0.000	0.000	0.010	0.000	0.010	0.009	0.012	0.000	0.029	0.000	0.000
221	0.000	0.000	0.020	0.010	0.032	0.020	0.009	0.000	0.000	0.000	0.000	0.000
223	0.000	0.000	0.010	0.020	0.032	0.010	0.000	0.012	0.000	0.019	0.023	0.016
225	0.000	0.023	0.010	0.000	0.000	0.010	0.000	0.000	0.010	0.010	0.012	0.000
227	0.013	0.000	0.020	0.010	0.000	0.000	0.018	0.023	0.000	0.010	0.000	0.000
229	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
231	0.013	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.023	0.016
233	0.013	0.000	0.010	0.010	0.000	0.010	0.000	0.000	0.000	0.019	0.000	0.016
235	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.016
237	0.000	0.000	0.010	0.000	0.016	0.010	0.000	0.000	0.000	0.000	0.000	0.000
239	0.000	0.000	0.000	0.000	0.016	0.000	0.000	0.012	0.000	0.000	0.000	0.000

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	Collection											
Allele	M	N	O	P	Q	R	S	T	U	V	W	X
241	0.000	0.000	0.020	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
243	0.013	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000
245	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
247	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
249	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
251	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000
253	0.000	0.000	0.000	0.000	0.016	0.000	0.000	0.000	0.000	0.000	0.000	0.000
255	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
257	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
259	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
261	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
263	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
265	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
267	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.016
275	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	39	43	49	49	31	49	55	43	50	52	43	32

μSR7-2

	Collection											
Allele	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AM	AN
139	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.000	0.000	0.000	0.000	0.000
141	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
143	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
145	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
147	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.008	0.000	0.000	0.010
149	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
151	0.000	0.009	0.000	0.000	0.000	0.000	0.017	0.000	0.000	0.000	0.000	0.000
153	0.019	0.009	0.018	0.000	0.020	0.009	0.000	0.019	0.008	0.000	0.000	0.000
155	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.017	0.000
157	0.066	0.036	0.018	0.000	0.010	0.047	0.067	0.046	0.039	0.000	0.067	0.050
159	0.038	0.046	0.018	0.071	0.020	0.047	0.033	0.028	0.046	0.088	0.017	0.000
161	0.019	0.009	0.018	0.000	0.010	0.009	0.000	0.009	0.046	0.000	0.000	0.000
163	0.009	0.018	0.009	0.000	0.000	0.000	0.017	0.009	0.008	0.000	0.033	0.030
165	0.009	0.000	0.000	0.000	0.030	0.019	0.033	0.000	0.023	0.029	0.000	0.000
167	0.019	0.027	0.009	0.024	0.000	0.019	0.017	0.065	0.023	0.000	0.017	0.020
169	0.009	0.036	0.018	0.000	0.040	0.019	0.017	0.019	0.031	0.000	0.000	0.010
171	0.009	0.009	0.018	0.024	0.000	0.009	0.017	0.037	0.023	0.000	0.000	0.040
173	0.009	0.027	0.027	0.095	0.010	0.009	0.050	0.009	0.046	0.000	0.033	0.030
175	0.047	0.009	0.027	0.000	0.020	0.028	0.017	0.046	0.015	0.029	0.017	0.030
177	0.009	0.018	0.018	0.024	0.000	0.028	0.017	0.000	0.015	0.000	0.000	0.020
179	0.009	0.046	0.018	0.024	0.010	0.009	0.033	0.019	0.023	0.029	0.000	0.010
181	0.000	0.018	0.018	0.048	0.010	0.038	0.067	0.019	0.031	0.059	0.017	0.030
183	0.047	0.027	0.055	0.024	0.020	0.076	0.050	0.074	0.039	0.029	0.000	0.070
185	0.123	0.082	0.046	0.000	0.040	0.066	0.050	0.056	0.054	0.059	0.050	0.060
187	0.113	0.036	0.091	0.095	0.100	0.104	0.117	0.083	0.077	0.059	0.167	0.100
189	0.066	0.136	0.127	0.095	0.090	0.085	0.083	0.074	0.062	0.235	0.050	0.070
191	0.066	0.027	0.036	0.048	0.050	0.066	0.017	0.046	0.039	0.118	0.067	0.080
193	0.066	0.027	0.036	0.024	0.060	0.057	0.033	0.037	0.031	0.000	0.067	0.050
195	0.038	0.082	0.073	0.000	0.030	0.066	0.017	0.046	0.031	0.029	0.083	0.030
197	0.047	0.055	0.009	0.048	0.040	0.028	0.033	0.037	0.031	0.059	0.017	0.030
199	0.019	0.027	0.009	0.048	0.070	0.038	0.017	0.028	0.015	0.029	0.033	0.030
201	0.028	0.018	0.027	0.048	0.020	0.038	0.017	0.028	0.039	0.029	0.000	0.020
203	0.009	0.018	0.009	0.024	0.020	0.009	0.000	0.019	0.015	0.000	0.067	0.000
205	0.009	0.009	0.027	0.024	0.010	0.000	0.033	0.009	0.008	0.000	0.033	0.020
207	0.000	0.009	0.027	0.000	0.030	0.009	0.017	0.019	0.000	0.000	0.000	0.010
209	0.019	0.000	0.027	0.071	0.010	0.009	0.000	0.019	0.015	0.000	0.033	0.020
211	0.000	0.027	0.009	0.048	0.020	0.009	0.000	0.009	0.015	0.000	0.017	0.020
213	0.000	0.018	0.009	0.000	0.030	0.000	0.000	0.019	0.015	0.000	0.033	0.030
215	0.000	0.018	0.046	0.048	0.020	0.009	0.017	0.009	0.015	0.029	0.017	0.030
217	0.009	0.018	0.036	0.024	0.020	0.009	0.017	0.009	0.015	0.000	0.017	0.010
219	0.000	0.009	0.009	0.000	0.000	0.000	0.000	0.000	0.008	0.029	0.000	0.000
221	0.019	0.009	0.009	0.000	0.020	0.000	0.000	0.000	0.008	0.000	0.000	0.000
223	0.009	0.009	0.000	0.000	0.030	0.000	0.000	0.019	0.031	0.029	0.000	0.010
225	0.000	0.000	0.018	0.000	0.030	0.000	0.000	0.000	0.008	0.000	0.000	0.000
227	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.010
229	0.000	0.009	0.009	0.000	0.000	0.009	0.000	0.000	0.031	0.000	0.000	0.010
231	0.000	0.000	0.000	0.000	0.020	0.009	0.017	0.009	0.000	0.029	0.000	0.000
233	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010
235	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
237	0.009	0.000	0.000	0.000	0.000	0.000	0.017	0.000	0.008	0.000	0.000	0.000
239	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.000	0.000	0.000	0.000	0.000

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	Collection											
Allele	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AM	AN
241	0.000	0.000	0.000	0.000	0.020	0.000	0.000	0.000	0.000	0.000	0.000	0.000
243	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
245	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000
247	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
249	0.009	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
251	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
253	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
255	0.000	0.000	0.000	0.024	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
257	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
259	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.000
261	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000
263	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000
265	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
267	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.000	0.000	0.000	0.000	0.000
275	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.000
n	53	55	55	21	50	53	30	54	65	17	30	50

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	Collection									
Allele	AO	AL	AI	AJ	AK	BA	BB	BC	BD	Overall
139	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
141	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
143	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
145	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
147	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.003
149	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
151	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
153	0.009	0.000	0.000	0.000	0.000	0.048	0.013	0.012	0.014	0.006
155	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002
157	0.052	0.056	0.036	0.026	0.046	0.065	0.025	0.047	0.095	0.033
159	0.026	0.044	0.071	0.053	0.046	0.048	0.000	0.012	0.041	0.034
161	0.009	0.011	0.000	0.053	0.000	0.000	0.013	0.012	0.027	0.015
163	0.000	0.000	0.036	0.026	0.023	0.016	0.000	0.000	0.000	0.010
165	0.000	0.011	0.000	0.000	0.000	0.016	0.013	0.023	0.014	0.010
167	0.017	0.022	0.071	0.000	0.023	0.032	0.038	0.023	0.027	0.021
169	0.043	0.022	0.071	0.053	0.000	0.016	0.025	0.023	0.027	0.022
171	0.026	0.011	0.036	0.079	0.068	0.065	0.013	0.058	0.014	0.024
173	0.009	0.078	0.036	0.026	0.046	0.048	0.038	0.023	0.027	0.023
175	0.035	0.033	0.000	0.026	0.000	0.000	0.025	0.023	0.000	0.028
177	0.009	0.000	0.036	0.026	0.023	0.048	0.038	0.047	0.000	0.020
179	0.035	0.000	0.071	0.000	0.046	0.081	0.000	0.035	0.027	0.021
181	0.035	0.022	0.000	0.026	0.046	0.000	0.013	0.012	0.000	0.029
183	0.043	0.044	0.000	0.079	0.046	0.032	0.038	0.012	0.135	0.038
185	0.052	0.044	0.000	0.053	0.023	0.016	0.100	0.151	0.027	0.054
187	0.103	0.078	0.036	0.000	0.136	0.113	0.125	0.140	0.095	0.080
189	0.112	0.100	0.107	0.132	0.114	0.032	0.100	0.140	0.095	0.078
191	0.060	0.056	0.036	0.053	0.000	0.145	0.138	0.058	0.054	0.053
193	0.026	0.033	0.036	0.026	0.046	0.048	0.075	0.047	0.054	0.044
195	0.026	0.033	0.000	0.026	0.023	0.000	0.063	0.058	0.081	0.043
197	0.043	0.033	0.036	0.000	0.023	0.048	0.050	0.012	0.027	0.035
199	0.035	0.044	0.036	0.053	0.023	0.000	0.013	0.000	0.027	0.031
201	0.035	0.000	0.000	0.000	0.000	0.048	0.025	0.012	0.027	0.030
203	0.009	0.044	0.036	0.026	0.068	0.000	0.000	0.012	0.000	0.017
205	0.017	0.011	0.000	0.026	0.023	0.016	0.000	0.000	0.000	0.015
207	0.017	0.011	0.071	0.000	0.023	0.000	0.013	0.000	0.027	0.016
209	0.017	0.011	0.000	0.000	0.023	0.016	0.000	0.000	0.014	0.017
211	0.009	0.011	0.000	0.000	0.023	0.000	0.013	0.000	0.014	0.012
213	0.009	0.022	0.036	0.026	0.000	0.000	0.000	0.000	0.000	0.020
215	0.017	0.000	0.036	0.053	0.000	0.000	0.000	0.012	0.000	0.018
217	0.017	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.013
219	0.017	0.011	0.036	0.000	0.000	0.000	0.000	0.000	0.014	0.010
221	0.000	0.022	0.036	0.000	0.000	0.000	0.000	0.000	0.000	0.010
223	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.016
225	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007
227	0.017	0.022	0.000	0.000	0.023	0.000	0.000	0.000	0.000	0.008
229	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005
231	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005
233	0.000	0.000	0.000	0.026	0.000	0.000	0.000	0.000	0.000	0.005
235	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.003
237	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002
239	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001

µSR7-2

	Collection								
Allele	AO	AL	AI	AJ	AK	BA	BB	BC	BD	Overall
241	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
243	0.000	0.000	0.000	0.000	0.023	0.000	0.000	0.000	0.000	0.001
245	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
247	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
249	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
251	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
253	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
255	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
257	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
259	0.000	0.000	0.000	0.026	0.000	0.000	0.000	0.000	0.000	0.001
261	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
263	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
265	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
267	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
275	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	58	45	14	19	22	31	40	43	37	2070

μSR7-7

	Collection											
Allele	A	B	C	D	E	F	G	H	I	J	K	L
182	0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000	0.009	0.000	0.000
184	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000
186	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000
188	0.000	0.000	0.009	0.000	0.006	0.018	0.010	0.015	0.000	0.000	0.000	0.000
190	0.250	0.254	0.255	0.289	0.284	0.223	0.245	0.303	0.270	0.236	0.209	0.207
192	0.048	0.035	0.055	0.039	0.031	0.045	0.069	0.046	0.050	0.019	0.018	0.033
194	0.024	0.026	0.018	0.016	0.037	0.036	0.088	0.023	0.040	0.009	0.036	0.033
196	0.145	0.123	0.082	0.102	0.031	0.063	0.000	0.000	0.050	0.038	0.027	0.022
198	0.008	0.009	0.018	0.008	0.025	0.018	0.010	0.015	0.050	0.019	0.018	0.033
200	0.024	0.018	0.027	0.039	0.031	0.027	0.010	0.046	0.010	0.057	0.046	0.022
202	0.008	0.009	0.000	0.055	0.031	0.045	0.069	0.046	0.040	0.028	0.055	0.044
204	0.032	0.044	0.055	0.031	0.056	0.027	0.078	0.053	0.050	0.123	0.109	0.065
206	0.057	0.044	0.027	0.039	0.037	0.036	0.049	0.038	0.050	0.057	0.064	0.033
208	0.024	0.009	0.009	0.016	0.037	0.036	0.010	0.030	0.000	0.000	0.009	0.044
210	0.024	0.018	0.027	0.031	0.031	0.027	0.039	0.068	0.090	0.057	0.046	0.022
212	0.000	0.035	0.036	0.023	0.031	0.027	0.088	0.023	0.040	0.047	0.018	0.044
214	0.024	0.026	0.018	0.000	0.049	0.036	0.029	0.061	0.020	0.000	0.064	0.087
216	0.040	0.035	0.027	0.039	0.037	0.027	0.088	0.008	0.010	0.047	0.036	0.076
218	0.024	0.018	0.009	0.000	0.025	0.036	0.049	0.053	0.030	0.057	0.018	0.033
220	0.057	0.035	0.064	0.047	0.037	0.063	0.000	0.030	0.030	0.028	0.036	0.011
222	0.000	0.053	0.018	0.016	0.019	0.027	0.000	0.008	0.040	0.028	0.027	0.011
224	0.048	0.053	0.027	0.039	0.031	0.027	0.020	0.030	0.030	0.019	0.027	0.022
226	0.065	0.053	0.100	0.070	0.019	0.036	0.010	0.015	0.030	0.038	0.036	0.022
228	0.024	0.018	0.064	0.031	0.025	0.000	0.010	0.015	0.000	0.000	0.009	0.044
230	0.000	0.026	0.000	0.016	0.000	0.009	0.000	0.000	0.000	0.019	0.009	0.011
232	0.016	0.000	0.009	0.000	0.012	0.009	0.000	0.015	0.000	0.000	0.046	0.000
234	0.000	0.009	0.009	0.000	0.012	0.009	0.010	0.008	0.000	0.000	0.000	0.000
236	0.008	0.000	0.000	0.008	0.000	0.009	0.000	0.008	0.000	0.000	0.000	0.000
238	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000
240	0.000	0.000	0.009	0.008	0.019	0.027	0.000	0.008	0.010	0.009	0.000	0.011
242	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.008	0.000	0.000	0.000	0.000
244	0.000	0.009	0.018	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000
246	0.008	0.018	0.000	0.016	0.006	0.018	0.010	0.015	0.010	0.000	0.009	0.022
248	0.016	0.009	0.000	0.008	0.006	0.009	0.000	0.008	0.030	0.019	0.000	0.000
250	0.024	0.018	0.009	0.000	0.000	0.018	0.010	0.000	0.000	0.009	0.009	0.022
252	0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000	0.009	0.009	0.011
254	0.000	0.000	0.000	0.008	0.000	0.009	0.000	0.000	0.010	0.000	0.000	0.011
256	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011
258	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000
260	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
262	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000
268	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
270	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
272	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	62	57	55	64	81	56	51	66	50	53	55	46

µSR7-7

	Collection											
Allele	M	N	O	P	Q	R	S	T	U	V	W	X
182	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
184	0.013	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
186	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
188	0.000	0.000	0.000	0.010	0.000	0.020	0.000	0.000	0.000	0.000	0.000	0.000
190	0.316	0.302	0.265	0.265	0.233	0.184	0.227	0.179	0.245	0.231	0.279	0.297
192	0.040	0.047	0.082	0.031	0.033	0.071	0.027	0.060	0.061	0.048	0.035	0.063
194	0.092	0.058	0.031	0.082	0.083	0.071	0.036	0.012	0.031	0.067	0.047	0.000
196	0.026	0.035	0.041	0.031	0.033	0.010	0.027	0.024	0.020	0.029	0.081	0.063
198	0.026	0.012	0.041	0.000	0.000	0.041	0.036	0.036	0.031	0.000	0.023	0.063
200	0.053	0.012	0.051	0.031	0.067	0.041	0.000	0.024	0.051	0.029	0.023	0.031
202	0.013	0.035	0.020	0.031	0.017	0.071	0.073	0.107	0.071	0.058	0.012	0.047
204	0.013	0.047	0.092	0.031	0.017	0.041	0.046	0.048	0.061	0.087	0.070	0.031
206	0.040	0.047	0.041	0.041	0.050	0.020	0.027	0.060	0.031	0.010	0.012	0.031
208	0.026	0.023	0.020	0.020	0.017	0.020	0.046	0.036	0.031	0.029	0.035	0.063
210	0.013	0.047	0.010	0.071	0.017	0.061	0.055	0.060	0.031	0.048	0.023	0.031
212	0.013	0.058	0.061	0.031	0.050	0.031	0.018	0.024	0.020	0.039	0.035	0.031
214	0.000	0.058	0.051	0.020	0.050	0.061	0.100	0.071	0.071	0.067	0.081	0.063
216	0.026	0.035	0.041	0.041	0.067	0.010	0.055	0.012	0.020	0.039	0.012	0.047
218	0.066	0.047	0.010	0.031	0.050	0.051	0.036	0.024	0.031	0.010	0.058	0.031
220	0.026	0.012	0.010	0.071	0.067	0.051	0.027	0.048	0.061	0.039	0.035	0.016
222	0.053	0.023	0.010	0.020	0.017	0.020	0.000	0.012	0.031	0.019	0.012	0.000
224	0.053	0.023	0.010	0.031	0.017	0.020	0.073	0.012	0.010	0.019	0.035	0.016
226	0.000	0.023	0.031	0.051	0.000	0.000	0.018	0.036	0.031	0.029	0.023	0.000
228	0.000	0.000	0.010	0.010	0.017	0.051	0.018	0.012	0.010	0.039	0.023	0.031
230	0.040	0.012	0.010	0.010	0.017	0.020	0.009	0.012	0.010	0.039	0.023	0.031
232	0.000	0.000	0.000	0.000	0.017	0.010	0.000	0.012	0.010	0.000	0.000	0.000
234	0.000	0.000	0.010	0.000	0.017	0.010	0.000	0.012	0.010	0.000	0.000	0.000
236	0.000	0.000	0.000	0.010	0.000	0.010	0.027	0.000	0.000	0.010	0.000	0.000
238	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.010	0.000	0.000	0.000
240	0.013	0.012	0.010	0.020	0.017	0.000	0.000	0.000	0.000	0.000	0.012	0.000
242	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
244	0.000	0.000	0.010	0.010	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000
246	0.040	0.000	0.010	0.000	0.000	0.000	0.018	0.012	0.000	0.010	0.000	0.000
248	0.000	0.000	0.010	0.000	0.017	0.000	0.000	0.000	0.000	0.010	0.000	0.000
250	0.000	0.012	0.010	0.000	0.000	0.000	0.000	0.024	0.000	0.000	0.012	0.000
252	0.000	0.012	0.000	0.000	0.017	0.000	0.000	0.000	0.000	0.000	0.000	0.016
254	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.010	0.000	0.000	0.000
256	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
258	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
260	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
262	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
268	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
270	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
272	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	38	43	49	49	30	49	55	42	49	52	43	32

μSR7-7

	Collection											
Allele	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AM	AN
182	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
184	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.000	0.000	0.000	0.000	0.000
186	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
188	0.000	0.009	0.009	0.000	0.010	0.000	0.000	0.009	0.000	0.029	0.000	0.000
190	0.189	0.218	0.223	0.238	0.310	0.321	0.150	0.176	0.231	0.147	0.267	0.260
192	0.019	0.082	0.009	0.048	0.040	0.028	0.033	0.046	0.054	0.029	0.033	0.050
194	0.028	0.027	0.018	0.000	0.020	0.019	0.067	0.046	0.069	0.000	0.017	0.040
196	0.038	0.018	0.063	0.024	0.040	0.000	0.000	0.009	0.046	0.000	0.050	0.020
198	0.028	0.027	0.027	0.024	0.010	0.019	0.033	0.028	0.008	0.000	0.017	0.050
200	0.028	0.046	0.009	0.071	0.040	0.009	0.017	0.019	0.008	0.029	0.050	0.040
202	0.047	0.073	0.045	0.119	0.030	0.038	0.050	0.028	0.054	0.029	0.050	0.040
204	0.076	0.055	0.054	0.024	0.060	0.019	0.067	0.083	0.039	0.059	0.100	0.080
206	0.076	0.046	0.054	0.048	0.050	0.047	0.017	0.046	0.039	0.059	0.017	0.050
208	0.019	0.036	0.063	0.024	0.010	0.028	0.033	0.065	0.031	0.029	0.050	0.010
210	0.066	0.018	0.054	0.048	0.080	0.038	0.017	0.102	0.031	0.147	0.067	0.030
212	0.038	0.018	0.000	0.000	0.040	0.038	0.067	0.019	0.031	0.000	0.017	0.030
214	0.085	0.027	0.027	0.048	0.040	0.113	0.083	0.065	0.092	0.147	0.050	0.010
216	0.009	0.027	0.045	0.071	0.070	0.057	0.033	0.028	0.054	0.059	0.033	0.040
218	0.000	0.018	0.036	0.000	0.010	0.000	0.050	0.037	0.015	0.000	0.000	0.020
220	0.047	0.046	0.036	0.048	0.020	0.028	0.117	0.028	0.046	0.059	0.000	0.040
222	0.038	0.036	0.063	0.000	0.010	0.009	0.033	0.009	0.031	0.029	0.017	0.040
224	0.066	0.027	0.027	0.048	0.040	0.057	0.033	0.046	0.000	0.059	0.000	0.030
226	0.028	0.055	0.045	0.024	0.020	0.038	0.017	0.009	0.015	0.029	0.033	0.030
228	0.019	0.009	0.018	0.000	0.010	0.019	0.000	0.009	0.015	0.029	0.033	0.040
230	0.009	0.018	0.018	0.024	0.010	0.019	0.000	0.009	0.008	0.000	0.050	0.010
232	0.009	0.009	0.009	0.000	0.000	0.000	0.000	0.019	0.008	0.000	0.000	0.010
234	0.009	0.000	0.018	0.000	0.010	0.019	0.033	0.019	0.015	0.000	0.000	0.000
236	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000
238	0.000	0.009	0.009	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.033	0.000
240	0.000	0.018	0.000	0.000	0.000	0.009	0.000	0.000	0.008	0.029	0.017	0.000
242	0.009	0.000	0.000	0.024	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000
244	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.010
246	0.000	0.009	0.009	0.024	0.010	0.009	0.033	0.019	0.023	0.000	0.000	0.000
248	0.000	0.000	0.000	0.024	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010
250	0.000	0.009	0.018	0.000	0.010	0.000	0.000	0.000	0.008	0.000	0.000	0.010
252	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
254	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
256	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
258	0.009	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000
260	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000
262	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
268	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000
270	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000
272	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	53	55	56	21	50	53	30	54	65	17	30	50

µSR7-7

	Collection								
Allele	AO	AL	AI	AJ	AK	BA	BB	BC	BD	Overall
182	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
184	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
186	0.000	0.000	0.000	0.000	0.000	0.000	0.023	0.000	0.000	0.001
188	0.000	0.000	0.036	0.000	0.023	0.000	0.000	0.000	0.000	0.004
190	0.233	0.244	0.286	0.184	0.205	0.200	0.193	0.286	0.198	0.243
192	0.017	0.089	0.000	0.184	0.114	0.067	0.023	0.048	0.023	0.045
194	0.017	0.033	0.036	0.026	0.023	0.056	0.011	0.012	0.035	0.036
196	0.035	0.022	0.000	0.079	0.068	0.011	0.000	0.036	0.012	0.039
198	0.026	0.000	0.000	0.026	0.023	0.022	0.034	0.048	0.035	0.023
200	0.043	0.022	0.000	0.000	0.023	0.033	0.023	0.048	0.012	0.030
202	0.026	0.089	0.036	0.000	0.046	0.022	0.046	0.048	0.070	0.043
204	0.043	0.000	0.071	0.026	0.000	0.056	0.034	0.036	0.093	0.054
206	0.009	0.011	0.036	0.026	0.068	0.033	0.080	0.048	0.047	0.041
208	0.035	0.022	0.036	0.079	0.068	0.033	0.034	0.012	0.035	0.028
210	0.103	0.022	0.143	0.079	0.000	0.089	0.057	0.083	0.070	0.048
212	0.069	0.067	0.000	0.026	0.068	0.044	0.034	0.060	0.012	0.034
214	0.052	0.022	0.000	0.026	0.000	0.056	0.091	0.083	0.047	0.050
216	0.026	0.056	0.036	0.053	0.046	0.056	0.080	0.012	0.035	0.039
218	0.035	0.056	0.000	0.053	0.023	0.033	0.034	0.024	0.023	0.028
220	0.017	0.056	0.107	0.000	0.046	0.067	0.034	0.024	0.093	0.040
222	0.035	0.022	0.071	0.000	0.000	0.011	0.011	0.000	0.035	0.022
224	0.026	0.011	0.071	0.026	0.000	0.000	0.023	0.024	0.023	0.029
226	0.043	0.044	0.000	0.000	0.046	0.011	0.034	0.024	0.035	0.031
228	0.035	0.033	0.036	0.000	0.046	0.011	0.023	0.024	0.012	0.020
230	0.009	0.000	0.000	0.000	0.000	0.033	0.023	0.000	0.023	0.013
232	0.009	0.011	0.000	0.026	0.000	0.011	0.000	0.012	0.012	0.007
234	0.000	0.000	0.000	0.000	0.023	0.022	0.011	0.000	0.000	0.007
236	0.017	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.004
238	0.017	0.000	0.000	0.000	0.023	0.000	0.011	0.000	0.012	0.003
240	0.000	0.022	0.000	0.000	0.023	0.000	0.000	0.000	0.000	0.007
242	0.000	0.011	0.000	0.026	0.000	0.011	0.000	0.000	0.000	0.002
244	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.002
246	0.017	0.022	0.000	0.000	0.000	0.000	0.023	0.000	0.000	0.010
248	0.009	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.005
250	0.000	0.000	0.000	0.026	0.000	0.000	0.000	0.000	0.000	0.006
252	0.000	0.000	0.000	0.026	0.000	0.000	0.000	0.000	0.000	0.002
254	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
256	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.001
258	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001
260	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
262	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
268	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
270	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
272	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	58	45	14	19	22	45	44	42	43	2093

Table A-4. Estimation of the effective population size of each haul and transect. Estimates from the program LDN$_e$ v.1.2 (Waples and Do, personal communication). Point estimates are reported with their upper and lower 95% confidence intervals calculated by jackknifing. The lowest allele frequency used was 0.05. Negative results in LDN$_e$ are interpreted as infinite values.

Haul	L C.I.	Estimate	U C.I.	Transect	L C.I.	Estimate	U C.I.
1998							
A	110.6	275.2	Infinite	**A•B**	215.2	593.4	Infinite
B	127.6	291.4	Infinite	**C**	141.0	358.6	Infinite
C	141.0	358.6	Infinite	**D**	116.9	300.0	Infinite
D	116.9	300.0	Infinite	**E**	221.8	678.5	Infinite
E	221.8	678.5	Infinite	**F•G•H**	357.5	2211.8	Infinite
F	155.8	532.2	Infinite	**I•J•K**	325.5	745.5	Infinite
G	185.7	768.2	Infinite				
H	254.7	1384.0	Infinite				
I	202.3	983.5	Infinite				
J	174.3	614.2	Infinite				
K	263.6	1444.0	Infinite				
2000							
L	159.5	669.5	Infinite	**L•M•N•O•P•Q**	300.3	704.7	Infinite
M	74.0	125.8	339.0				
N	227.9	-7841.8	Infinite				
O	446.8	-605.4	Infinite				
P	134.5	352.9	Infinite				
Q	86.0	180.5	45395.4				
2001							
R	178.6	766.3	Infinite	**R•S**	248.7	666.2	Infinite
S	173.0	443.0	Infinite	**T**	157.4	1111.0	Infinite
T	157.4	1111.0	Infinite				
2002							
U	353.5	-773.3	Infinite	**U•V•W**	278.7	799.0	Infinite
V	214.3	1786.4	Infinite	**X•Y•Z**	313.2	1592.8	Infinite
W	122.3	333.6	Infinite	**AA•AB**	213.1	2099.7	Infinite
X	212.5	-670.1	Infinite	**AC**	268.4	-2649.1	Infinite
Y	131.7	400.3	Infinite	**AD**	330.3	-1407.6	Infinite
Z	259.5	-4763.5	Infinite	**AE•AF**	154.7	425.6	Infinite
AA	199.3	1105.0	Infinite	**AG•AH**	180.9	392.8	Infinite
AB	40.3	111.7	Infinite	**BA•BB**	146.2	417.6	Infinite
AC	268.4	-2649.1	Infinite	**BC•BD**	310.6	-4394.7	Infinite
AD	330.3	-1407.6	Infinite				
AE	179.3	-3283.6	Infinite				
AF	168.1	647.8	Infinite				
AG	183.4	467.8	Infinite				
AH	59.0	245.1	Infinite				
BA	196.4	-680.8	Infinite				
BB	113.8	299.5	Infinite				
BC	181.7	8936.8	Infinite				
BD	220.2	-5354.5	Infinite				
2003							
AI	49.9	338.4	Infinite	**AI•AJ•AK**	151.6	575.5	Infinite
AJ	54.0	130.7	Infinite	**AL**	82.1	156.7	791.0
AK	82.9	815.2	Infinite	**AM•AN•AO**	246.7	817.7	Infinite
AL	82.0	156.7	791.0				
AM	648.5	-238.7	Infinite				
AN	129.8	379.3	Infinite				
AO	152.0	462.7	Infinite				

Table A-5. Pairwise relatedness and variance in pairwise relatedness. Probabilities that the average pairwise relatedness and the variance in pairwise relatedness within a haul would be greater than expected under a distribution of the observed allele frequencies sampled at random. Significant values are in bold. Estimates were calculated with Identix v1.1 (Belkhir et al. 2002) and are based on Lynch and Ritland's method (1999) from 1000 permutations of alleles.

Year	Haul	Mean	Variance
1998	A	0.946	**0.019**
	B	**0.009**	**0.001**
	C	0.171	0.082
	D	0.334	0.345
	E	0.915	0.114
	F	**0.036**	0.196
	G	0.550	0.625
	H	0.302	0.750
	I	0.462	0.545
	J	0.945	0.090
	K	1.000	0.553
2000	L	0.996	0.301
	M	0.830	0.470
	N	1.000	0.375
	O	0.139	0.670
	P	0.875	0.413
	Q	0.139	0.119
2001	R	0.983	0.104
	S	0.732	0.285
	T	0.024	0.627
2002	U	**0.015**	0.919
	V	0.754	0.761
	W	0.974	0.104
	X	0.900	0.663
	Y	0.598	0.246
	Z	0.268	0.691
	AA	0.243	0.056
	AB	1.000	0.087
	AC	0.900	0.616
	AD	0.674	0.087
	AE	0.298	0.249
	AF	0.332	**0.049**
	AG	1.000	0.500
	AH	1.000	0.610
	BA	0.507	0.472
	BB	0.290	**0.012**
	BC	0.394	0.207
	BD	0.395	0.290
2003	AI	0.900	0.462
	AJ	0.433	0.129
	AK	0.116	0.310
	AL	0.511	0.072
	AM	0.318	0.915
	AN	0.386	0.119
	AO	0.900	0.389