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Project Final Product¹**

Genetic Analysis of Immature Bering Sea Chum Salmon: Part I. Baseline evaluation

by:

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II. ABSTRACT:

Keywords: bycatch, chum salmon, cross validation, genetic baseline, mixed-stock analysis

Chum salmon populations from across their geographic distribution have been analyzed with a set of SNP and microsatellite markers. As is typical for chum salmon populations, more genetic divergence was observed on larger geographic scales than on smaller regional scales. Strong divergence exists within and among the three regions of Asia, western Alaska, and the northeast Pacific. However, separation of coastal western Alaskan summer-run chum salmon populations from Norton Sound to western Bristol Bay remains problematic. The degree of divergence determines the spatial scale to which stock proportions of mixtures of chum salmon can be resolved. The baseline developed in this project will be used for mixture analyses to study the marine distribution of chum salmon populations in the Bering Sea. Scale and fin samples collected in the eastern Bering Sea will be used to determine whether the stock composition of chum salmon aggregations differ across areas, seasonally, and annually. Determining the stock distributions of these mixtures will provide information on the migratory pathways of chum salmon in the Bering Sea and the potential impact of bycatch of coastal western Alaskan chum salmon in the Bering Sea pollock fishery.

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IV. INTRODUCTION:

Salmon bycatch, especially of chum salmon (*Oncorhynchus keta*) and Chinook salmon (*O. tshawytscha*), is an important issue for Alaskan trawl fisheries. Chum salmon dominate the “non-Chinook” bycatch. National Marine Fisheries Service (NMFS) catch statistics (http://www.fakr.noaa.gov/sustainablefisheries/inseason/chum_salmon_mortality.pdf) indicate that most of the chum salmon bycatch in the Bering Sea occurs in the walleye pollock (*Theragra chalcogramma*) directed fisheries. The number of chum salmon incidentally caught in the Bering Sea pollock fisheries varies widely on an annual basis, and industry and fishery managers have realized for some time that salmon bycatch is a concern (Gisclair 2009). Management of the Bering Sea pollock fisheries has evolved over the last couple of decades to reduce bycatch (e.g., Haflinger and Gruver 2009), but salmon bycatch has proven to be a difficult problem to address and new management measures on the pollock fisheries are being considered (<http://www.fakr.noaa.gov/npfmc/bycatch-controls/BSChumBycatch.html>).

Chum salmon bycatch is of general concern because it impacts a variety of societal, allocation, conservation, and international treaty issues. Societal and allocation issues arise because many intercepted salmon might have returned to western Alaskan river systems, and rural Alaskans depend on them for subsistence and commercial fisheries (Wolfe and Spaeder 2009). Precipitous declines of chum salmon returns to western Alaskan rivers in the late 1990s and early 2000s prompted numerous State of Alaska and Federal fisheries disaster declarations and led to severe restrictions on commercial and subsistence chum salmon fisheries in the region (AYK SSI 2006). Since then, the abundance of chum salmon has rebounded in many river systems (e.g., Bue et al. 2009), but incidental catches of chum salmon in the pelagic trawl fisheries has also increased in some years. The Federal Subsistence Board has the power to restrain fisheries (e.g., pollock) that interfere with subsistence catches in western Alaskan Rivers.

Conservation concerns result because migratory salmon from as far away as the Pacific Northwest move through the Bering Sea and Aleutian Islands and the Gulf of Alaska. Many chum salmon returning to the Yukon River ascend to Canadian spawning grounds and are, consequently, counted as Canadian under the U.S.-Canada Pacific Salmon Treaty (JTC 2011). The Alaskan groundfish fisheries are among the most valuable commercial fisheries in the world, but their value notwithstanding, excessive salmon bycatch can alter the way they are conducted or even close them.

Recent oceanographic and fish ecology research in the Bering Sea has begun to tease apart the connections between temperature regimes, food-web interactions, and salmon movement in the eastern Bering Sea, thus affecting the bycatch potential (Murphy and Farley 2012). Although chum salmon bycatch is closely monitored, one of the underlying questions—the origins (and destinations) of the fish—has only recently begun to be addressed (e.g., Kondzela et al. 2012), and the dynamics of the variation of their movements is little understood. This knowledge is crucial in determining the ultimate impact of the bycatch (Stram and Ianelli 2009).

The availability of genetic tools that can estimate regional contributions of chum salmon to high seas aggregations make it possible to analyze samples that have been archived from

incidental catches and from research sampling efforts in the Bering Sea and Gulf of Alaska over decades. A subset of samples has been chosen with which to address questions about the distribution in time and space of chum salmon in the eastern Bering Sea. The genetic baseline with which these samples will be analyzed expands upon earlier efforts (Gharrett et al. 2007). The evaluation of this baseline is the focus of Part I of this report. The results of the mixed-stock analyses of the bycatch and research samples will be reported in Part II.

V. OBJECTIVES:

The primary objective of our genetic work was to determine the origins of immature chum salmon caught incidentally in Bering Sea groundfish fisheries and in other surveys in which admixtures of chum salmon populations were collected. The intent of the work was to learn about the marine distributions of chum salmon populations or of regional aggregations of chum salmon populations in the Bering Sea. The specific questions we asked were: (1) What are the compositions of chum salmon aggregations in different regions of the eastern Bering Sea? (2) Do the distributions vary seasonally within a year in each area? and (3) Do the distributions vary among years? To address these questions, a second objective involved further development of a genetic baseline for chum salmon that was initiated by the University of Alaska Fairbanks (UAF) in an earlier project (Gharrett et al. 2007), and then application of that baseline to mixed-stock analyses (MSA) of the Bering Sea chum salmon samples. Although the original proposal did not explicitly state the further development of the baseline as a separate objective, the expansion of the baseline was a substantial body of work and as such we list it here as Objective 1 and focus on that objective in this part of the Final Report.

Objective 1. Further develop the chum salmon coastwide genetic baseline.

The first objective was comprised of two parts (1) develop new SNP markers and (2) expand the baseline by increasing the number of representative populations and adding genetic markers. For the first part, twenty-three SNPs representing 12 loci were developed for a temperature (T_m)-shift assay. All but four SNPs were discovered and developed during this project. For the second part, the coastwide chum salmon genetic baseline was expanded to increase geographic coverage and add markers that might better delineate western Alaskan stocks. Markers were added to the 73 populations from an earlier study (Gharrett et al. 2007)—the 12 SNP loci that were developed and three additional microsatellite loci, for a total of 12 microsatellite loci. Data for this marker set were also obtained from an additional 53 populations, for a total of 126 populations. The additional populations were a substantial increase in coverage for some geographic areas, as well as coverage of several areas previously unrepresented. Nearly half of the additional populations were from the western Alaskan region. We added more baseline populations than originally planned, and in doing so, took longer to complete both the laboratory and data analyses than anticipated.

We successfully converted the laboratory analyses of microsatellite loci from one platform to another, that is, from the gel-based LI-COR to the capillary-based ABI 3130xl.

Results were standardized across platforms and among the UAF, Auke Bay Laboratories (ABL), and Fisheries and Oceans Canada, Nanaimo, British Columbia (DFO) laboratories. By having compatible microsatellite data across laboratories, we could focus on obtaining SNP data from populations in the DFO microsatellite dataset (allele frequencies), which became publically available during the course of our study, and thereby increase the number of populations in the baseline with the rationale that greater geographic coverage will improve stock composition estimates. For our project, the locus *Oke3* was not used because differences in allele sizes could not be resolved in a previous study (Gharrett et al. 2007), and the locus *Oki2* was not included because more than two alleles amplify in some samples. For technical reasons detailed below, standardization of two loci (*One111* and *Ots3*) between the ABL and DFO datasets had some limitations. The problem with *One111* might be resolved with additional sample sharing from DFO with the specific alleles in question.

We evaluated the baseline data in several ways and then applied it to the Bering Sea immature chum salmon samples with mixed-stock analyses for Objective 2. The performance measure for Part I of the project was the cross validation analysis of the genetic baseline.

Objective 2. Estimate origin of immature chum salmon in the eastern Bering Sea.

The second objective is addressed more fully in Part II of the Final Report. Briefly, nearly 6,000 immature chum salmon samples from the eastern Bering Sea, and small collections from the western Bering Sea and Gulf of Alaska for contrast, were analyzed with the combined SNP and microsatellite coastwide baseline developed in Objective 1. The origin of fish was determined in different regions of the eastern Bering Sea, seasonal variation in the distribution of chum salmon within regions was examined, and variation in distributions was compared across years.

VI. METHODS:

Approach

Our ability to estimate the composition of mixtures accurately depends largely on the extent of genetic divergence that exists among populations. Previous population genetics descriptions have documented similarities among chum salmon populations within locales and increasing divergence at broader geographic scales (Olsen et al. 2008; Beacham et al. 2009a,b; Seeb et al. 2011). This concept underlies our approach because it is unlikely that the thousands of chum salmon populations throughout their natural range will ever be exhaustively sampled, so the patterns of divergence among populations and reporting groups will determine the efficacy of applying genetic markers to mixture analyses. Genetic similarities among populations within a region may also preclude attribution to specific populations.

We conducted population genetics analyses to describe the population structure. From those results and with consideration of population structure from other recent studies, we evaluated the strengths and weaknesses of applying the genetic variability to stock identification

analyses. For some analyses, we combined our data with other available data (i.e., microsatellite allele frequencies from DFO) to analyze more populations.

Samples

The genetic baseline was expanded from nine microsatellite loci and 73 populations (Gharrett et al. 2007) to 12 microsatellite and 12 SNP loci from 126 populations (Table 1; Figure 1). The chum salmon samples from the additional 53 populations had been collected and archived from agencies around the Pacific Rim. These collections increased the number of populations within most geographic regions and added populations from previously unrepresented geographic regions or run-times. New or substantially increased geographic representation included collections from Hokkaido; Norton Sound; Koyukuk River (a Yukon River tributary); summer-run Kuskokwim; fall-run Kuskokwim; southern Alaska Peninsula; northern SE Alaska; Prince of Wales Island; and southern British Columbia. DNA was extracted from the samples with DNeasy Blood and Tissue Kits¹ as described by the manufacturer (QIAGEN, Inc., Germantown, Maryland), resulting in approximately 10-20 µg total DNA per sample.

Single nucleotide polymorphism assays

For 126 populations, a total of 23 SNPs were genotyped that represented 12 loci. In the text abbreviations are used for the loci, the sources of which are in Table 2. Seven loci were comprised of single SNPs: vasotocin I (VT), RH-opsin (RH), serpin (SP), estrogen receptor (ER), clock (CL), period (PER), and RFC2 (RF) (Garvin and Gharrett 2010; Smith et al. 2005a). Prolactin (PL) had a 21 base pair (bp) insert/deletion (INDEL). Three loci were comprised of multiple, linked SNPs: the insulin (IN) and isotocin II (IS) loci each had two SNPs, and the vitellogenin receptor (VR) locus had three SNPs. Genotypes of linked genomic SNPs were combined after the linkage phase was resolved (Garvin and Gharrett 2010; Garvin et al. 2010a). The linkage phase of the VR and IN double-heterozygotes were assumed to be in the repulsion form because there were no ‘ab’ or ‘abc’ types present in any baseline population (e.g., Table V in Garvin and Gharrett 2010). Because ‘ab’ types of the two isotocin II SNPs were found in some baseline populations, the linkage phase of double-heterozygotes was determined with four primer sets (Table 3). The mitochondrial locus was comprised of eight SNPs: Oke_Cr30, Oke_Cr231, Oke_Cr386, MT5, MT12, MT18, MT21, and MT27 (Garvin et al. 2010b; Sato et al. 2001). Previously unpublished sequence information for the period locus was deposited in GenBank (accession number JQ606803). For ease of interpretation, “allele” is used generically throughout this report to include “haplotype”, the technically correct term for the linked SNPs.

Early in the project, *Taqman* assays (e.g., Smith et al. 2005b) were converted to “ T_m -shift” assays, which require less expensive reagents (see Garvin et al. 2011 for details). The T_m -shift assay detects sequence differences from DNA melting temperature differences of PCR products. The reaction conditions differed from the original publication in the use of a generic *Taq* polymerase, a lower MgCl₂ concentration and the omission of ROX dye. The T_m -shift

¹ Reference to trade names does not imply endorsement by the National Marine Fisheries Service, NOAA.

primers were designed as described by Wang et al. (2005) but further modified by incorporating locked nucleic acids (LNAs; Exiqon; www.exiqon.com) (You et al. 2006) at the 3'-end to increase base-pairing specificity at the SNP site (Garvin et al. 2010a). Allele specific primers included tails with a high GC content: a short tail for one allele and a long tail for the other allele at the 5'-end to improve detection of sequence differences.

Each SNP was PCR amplified separately in a 6 μ L reaction that included 10 mM Tris pH 9.0, 50 mM KCl, 0.1% Triton X-100, 1.5 or 3.0 mM MgCl₂, 0.2 mM dNTPs, 200 nM primers, ~0.5 unit *Taq* polymerase, 5% DMSO, 4X SYBR™ green dye (Sigma Aldrich; www.sigmaaldrich.com), and ~10 ng of DNA. Three of the assays required 3 mM MgCl₂: one of the three sites discovered in the vitellogenin receptor locus (VR3), one of the restriction fragment length polymorphism (RFLP) sites in the mitochondrial locus (MT5) (Garvin et al. 2010b), and the INDEL in the prolactin locus (PL). The assay for PL did not use LNA-modified or tailed primers. Instead, the PL assay used normal, untailed primers that flanked a 21 bp INDEL and amplified two PCR fragments that had different sizes, which resulted in a large delineating T_m -shift. Thermocycling conditions (Table 4) for PCR amplification were the same for most of the primer pairs except for the annealing temperature, which was determined empirically for each assay (Table 2). Thermocycling included an initial 2 min dissociation at 94°C, followed by 45 cycles at 94°C for 20 s, at the appropriate annealing temperature for 1 min, and at 72°C for 30 s.

The PER, IS (linkage phase), and CLOCK assays differed from the other SNP reaction assays. The PER annealing temperature was held longer (1 min) and there was no elongation step. The IS (linkage phase) elongation temperature was held longer (1 min) than for the other assays with the assay resulting in the presence or absence of PCR product. The CLOCK assay required the use of nested primers, which included the primer set used for the original SNP discovery (Garvin and Gharrett 2007) and the assay-specific primers. This was because the assay-specific primers appeared to amplify a paralog of the CLOCK gene, but the SNP discovery primer set did not. We took advantage of this and used a limited amount of the original SNP discovery primer set (which had a higher annealing temperature) for the first five cycles of the PCR. The assay-specific primers had a lower annealing temperature and were internal to the first set; the lower annealing temperature of the assay specific primer set was then used for the remaining 40 cycles of the PCR. This eliminated the amplification of the paralog by the assay specific primers.

Dissociation curves were generated with the LightScanner™ from Idaho Technologies and their software was used to identify the genotypes (Idaho Technology Inc., Salt lake City, Utah).

Microsatellite assays

Genotypes were obtained from 3-12 microsatellite loci per collection (Table 5). Allele frequencies from the DFO web portal (<http://www.pac.dfo-mpo.gc.ca/science/facilities-installations/pbs-sbp/mgl-lgm/data-donnees/index-eng.htm>, accessed January 6, 2009) were used to fill in microsatellite data for some populations. For 67 collections in which nine microsatellite loci had been genotyped previously (Gharrett et al. 2007), we obtained genotypes for three

additional loci: *One111*, *Ots3*, and *Omm1070*. Microsatellite allele frequencies available from DFO for these three loci were used for the other six populations genotyped previously. Thirty-five of the 53 new populations were genotyped for 12 microsatellite loci: *Oki100*, *Omm1070*, *Omy1011*, *One101*, *One102*, *One104*, *One111*, *One114*, *Ots3*, *Ots103*, *OtsG68*, and *Ssa419*. Allele frequencies available from DFO were used for the other 18 populations. With the exception of *Ots3*, we used the same primer sequences used by DFO with a fluorescent dye on the 5'-end of the forward primer and GTT added to the 5'-end of each reverse primer. The *Ots3* primers in Greig and Banks (1999) were used because they produced higher quality amplification than the primers used by DFO (Banks et al. 1999). The microsatellite loci were PCR amplified in multiplexed panels (Table 5). Initially, the 12 loci were multiplexed on four panels (1b, 2d, 3c, and 4). During the project they were reorganized into three more efficient panels (A, B, C). The three loci, *One111*, *Ots3*, and *Omm1070* amplified to complete data for some populations, were multiplexed in panel 5. Each PCR reaction was conducted in a 5 μ L volume containing \sim 10 ng of DNA, 2.5 μ L QIAGEN Multiplex PCR Master Mix, 0.2 μ M of each primer, and RNase-free water. Thermal cycling for the PCR amplification of DNA fragments (Table 6) was performed on a dual 384-well GeneAmp PCR System 9700 (Life Technologies, Inc., Carlsbad, CA). Samples from the PCR reactions were diluted into 96-well plates for analysis with a 16-capillary, 36 cm array on the Applied Biosystems (ABI) 3130xl Genetic Analyzer as follows: 1 μ L diluted (1:25) PCR product, 4.4 μ L Hi-Di™ formamide, 4.4 μ L de-ionized water, 0.2 μ L GeneScan™ 600 LIZ® size standard (Life Technologies, Inc., Carlsbad, CA). Samples were denatured at 95°C for 3 min, then cooled to 4°C and stored until analysis on the ABI 3130xl. Genotypes were identified with GeneMapper® 4.0 software (Life Technologies, Inc., Carlsbad, CA) and exported to Excel spreadsheets (Microsoft, Inc.) for further analysis.

Data compatibility

During our project, the laboratory platform on which the microsatellite loci were analyzed was converted from the LI-COR automated DNA sequencer (LI-COR Biosciences, Lincoln, NE) to the ABI 3130xl Genetic Analyzer. Samples from the 1998 Grant, Washington collection were used in this conversion to set up consistent genotyping for nine loci (*Oki100*, *Omy1011*, *One101*, *One102*, *One104*, *One114*, *Ots103*, *OtsG68*, and *Ssa419*). After conversion to the ABI 3130xl, data for an additional three microsatellite loci were added to the baseline (*One111*, *Omm1070*, and *Ots3*). Then, as in an earlier baseline analysis (Gharrett et al. 2007), we compared the results of the microsatellite analysis conducted in our laboratories sample-by-sample for one collection (Unalakleet) with results obtained in the DFO Molecular Genetics Laboratory (courtesy of T. D. Beacham). Ensuring that the microsatellite data were compatible across laboratories allowed us to use existing microsatellite data from DFO (allele frequencies) for some of the populations to complete the baseline where samples were unavailable or monetary resources were limited.

Genetic analysis

Variation within populations – Variation at SNP and microsatellite loci within populations was characterized by 1) allele frequencies, 2) total number of distinct types of alleles (n_a), 3) the effective number of alleles (n_{eff}), 4) allele richness (a), 5) observed proportion of heterozygosity (H_O), and 6) unbiased expected heterozygosity (H_E). Direct calculations and the programs GENEPOP 4.0 (Rousset 2008), FSTAT version 2.9.3.2 (Goudet 1995), and GDA version 1.1 (Lewis and Zaykin 2001) were used to estimate these values.

We tested each locus in each population for conformance to Hardy-Weinberg equilibrium expectations by using GENEPOP 4.0. An index of departure from Hardy-Weinberg expectations (inbreeding coefficient F_{IS}) was estimated from the observed (H_O) and expected (H_E) heterozygosities in FSTAT. The assumption that loci are unlinked was tested with GENETIX version 4.05 (Belkhir et al. 2004) for each locus-pair in each population for which genotype data were available. Sequential Bonferroni corrections were used to adjust for multiple testing (Rice 1989).

Several populations were represented by two or more collections that were sampled in different years, at different times within years, or in slightly different locations. Collections were pooled if testing for homogeneity between them indicated no significant differences. The tests of homogeneity were exact tests in GenAIEx version 6.4 (Peakall and Smouse 2006).

Variation among populations – Divergence among populations and geographic regions was graphically examined with principle components analysis (PCA) conducted with Minitab version 15.1.30.0 (Minitab Inc. 2006). This analysis converts the multi-dimensional allele frequency space to linear combinations called principal components (PCs) that account for the most, second most, third most, and so on variation. Typically, much of the population divergence can be viewed with a plot of the first two PCs. In addition, the analysis provides the component loadings for each allele, i.e., the weight of each individual allele that is used to determine each PC. The analysis included alleles with a frequency not less than 0.06 in at least one population to evaluate the influence of the more abundant alleles. Only the most common allele was included for di-allelic SNP loci. Allele frequencies were arcsine-square root-transformed to “normalize” the frequency data (Sokal and Rohlf 1995). Populations were plotted on the first two PCs from the sum of the products of the transformed allele frequencies and loadings for each component.

A neighbor-joining tree was constructed from unitized chord distances (Cavalli-Sforza and Edwards 1967). This descriptive analysis of the genetic data provides a view of the population structure with a different methodology and provides another means to examine the strength of population structure.

Baseline evaluation

The baseline was evaluated with an approach recently suggested by Anderson (2010) that may provide a more realistic measure of the accuracy and precision a baseline yields to stock composition estimates than does the typical evaluation of simulations based on mixtures composed of 100% of the samples from one region. We used a leave-ten-percent-out (LTO) cross validation approach (Garvin et al. submitted), in which the baseline was split into ten parts,

with one part (the mixture) including samples from 10% of each of the baseline populations and the other part (the baseline) including the remaining 90%. Mixtures that include fish from across the geographic range from all populations better represents the actual composition of immature chum salmon found in the Bering Sea than simulated mixtures in which 100% of the samples are from a single region (e.g. Wilmot et al. 1998; Gray et al. 2011). Moreover, it is a more rigorous test of the baseline. The advantages of the LTO method are that Hardy-Weinberg assumptions do not need to be met and the baseline does not include any of the mixture samples (no replacement).

Each mixture was subjected to a mixed-stock analysis with maximum-likelihood (SPAM; Debevec et al. 2000) and Bayesian (BAYES; Pella and Masuda 2001) methods to reallocate each mixture back to the remaining 90% of the baseline. For each Bayesian analysis, three Monte Carlo chains with 100,000 MCMC samples, starting at disparate values of stock proportions were configured such that 95% of the stocks came from one designated region with weights distributed equally among the stocks of that region. The remaining 5% was distributed as 2.5% to each of the two other regions; within each of those regions, the 2.5% was distributed equally among the stocks. The first chain had 95% contributions set to Asian populations (populations coded within 1-36), the second chain had 95% contributions set to western Alaska populations (37-80), and the third chain had 95% contributions set to northeastern Pacific populations (81-126). For all BAYES estimates, a flat prior (calculated as $1/n$ populations) was used. Convergence of the chains to posterior distributions of stock proportions was determined with Gelman and Rubin shrink statistics, most of which were 1.00 and all were less than 1.03, conveying strong convergence to a single posterior distribution.

We also ran SPAM in simulation mode for each of the ten baseline files with population contribution set at the same proportions used with the LTO method. Analyses of the ten datasets were summarized to determine mean stock composition estimates, and the bias and precision of those estimates.

List of individuals and organizations that performed the work

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VII. RESULTS:

Variation within populations

We surveyed collections from 126 populations for variation at 23 single nucleotide polymorphisms (SNPs) developed in this project that represent 12 loci and for a portion of these populations at 12 microsatellite loci. The genetic variation characterized for each population is in Appendices I and II. The populations were distributed along the Pacific Rim from Puget Sound in Washington State to northeastern Honshu Island of the Japan Archipelago (Table 1 and Fig.

1). Sample sizes ranged from 11 to 186; nearly all of the small samples were Asian. The harmonic mean of sample sizes was 56 for SNP and 58 for microsatellite loci. The eight mitochondrial SNPs resolved 20 composite haplotypes (Table 7); the nuclear SNPs resolved 2-4 alleles per gene (Table 8). The number of alleles per locus per population ranged from 1-10 for the SNP loci and 4-79 for the microsatellite loci.

Of the 1241 possible probability tests for Hardy-Weinberg equilibrium for SNP loci, less than 3% had $P < 0.05$, and no tests were significant after adjustment for sequential Bonferroni multiple testing. Nearly 8% of the 1278 probability tests for microsatellite loci had $P < 0.05$, but only four were significant after multiple testing was taken into account. There was no evidence of linkage disequilibrium between pairs of loci, so each locus can be considered to provide independent information. The proportion of linkage disequilibrium tests with $P < 0.05$ was 5.6%, about what is expected by chance. There was no particular pattern as to population or locus-pairs and after multiple testing was taken into account the fraction of tests was nearly 0%.

Where several populations were represented by two or more collections that were sampled in different years, different times within years, or slightly different locations, no significant differences in allele frequencies were observed. Collections were pooled from Amur 2003 early and late, Olsen 1992 and 1997, and Stony 1994 early and late.

Data compatibility

With samples from the Unalakleet River, we compared microsatellite allele designations 1) between the LI-COR and ABI instrumentation platforms in our laboratory, and 2) with results obtained by the DFO laboratory (Table 9). Concordance with the blind test was high both between the LI-COR and ABI instrumentation within our lab, and between our instrumentation and that at DFO; most of the differences in assigning the alleles were resolved. *One111* is a dinucleotide repeat with a large number of alleles (166 alleles in the ABL dataset), which posed several challenges. The ABL dataset had excellent concordance with DFO for alleles up to 378 base pairs (bp) in size. When data were combined from the ABL and DFO datasets, we pooled *One111* alleles in our dataset that were larger than 376 bp (and concordantly, >378 bp for the DFO dataset) because assigning the alleles differed slightly, typically by two base pairs, due to differences in instrumentation, PCR amplification, or size standard reagents or a combination of these factors. Another challenge was the limitation of several analytical programs that handle fewer than 100 alleles per locus, so at *One111* we also pooled alleles 162-178 at the lower size range of the alleles and 206 with 208 due to its presence in only one population. The program OPTIBIN (Bromaghin 2006) was used to test that this pattern of pooling did not change our ability to detect population divergence. We observed eight alleles at *Ots3* in the upper size range (181-197), all at low frequency, that are not present in the 381-population DFO dataset, so these alleles were pooled with the 179 allele when data were combined from the ABL and DFO datasets. The presence of larger alleles at *Ots3* in the ABL dataset may be due to the use of different primer sets by the two laboratories. To improve scoring this locus, we used the primer set applied by the Chinook GAPS forum (Greig and Banks 1999), rather than the primer set used by DFO (Banks et al. 1999).

We also compared our microsatellite allele frequencies with those reported by the DFO laboratory for the same populations by using a chi-square test (likelihood ratio). Twelve collections (Table 10) included nearly the same set of individual fish; samples from 28 other collections broadly overlapped in the sets of individuals that were analyzed; and samples from 23 collections were non-overlapping. The chi-square probabilities in comparisons of loci for the 12 most overlapping samples were very close to one at all 12 loci. Only Suifen, Atchuelinguk, and Sturgeon had somewhat lower probabilities at several loci.

Comparisons of overlapping samples showed high concordance in allele frequencies, but not as high as those seen in the nearly identical samples. Combined probabilities for 20 of the 28 populations with overlapping samples were one; all combined probabilities across loci for a population exceeded 0.70 (except Olsen). Further examination of Olsen indicated no significant difference between our 1992 and 1997 samples (combined $P = 0.1044$, exact G -tests run in Genepop); a mixed-stock analysis treating our Olsen collection as a mixture, with the DFO 381-population baseline, resulted in our samples allocating primarily to Prince William Sound, the region it is from (not shown). Combined probabilities at a locus across overlapping samples were 1.0 at eight loci; combined probabilities were lower for *One111* (0.770), *One104* (0.896), *Ots3* (0.947), and *Omm1070* (0.967).

The non-overlapping samples from 23 collections were clearly independent sample sets because there was higher divergence in allele frequencies across loci except for the Grant, WA collection, which indicated that samples from this collection were nearly identical (possible mislabeling of year by DFO, UAF, or WDFW). Three of the collections (Narva, Amur early, and Amur late) did not differ significantly between the two datasets. For the remaining 19 collections the range of combined probabilities of G -tests across loci was 0-0.062, which suggests that either temporal structure (within or among years) or additional geographic structure of populations, or both, contributed to the genetic differences. Another possibility, which cannot be confirmed, is that samples were mislabeled somewhere in the field or laboratory processes. Although comparisons of genotypes across labs from identical and overlapping samples indicated that genotyping was consistent across datasets obtained by different laboratories and equipment, we evaluated whether the statistical differences (G -tests) observed between the non-overlapping samples would impact the application of mixed-stock analyses (MSA). For this evaluation, two MSAs were done with the program BAYES. The baseline for both analyses was a subset of data from the 381-population DFO baseline and the mixtures were made from the corresponding UAF-ABL baseline dataset. Two mixtures were used because data were not available for all loci and all populations: one mixture contained data for all 19 populations and 9 loci, the other mixture contained data for 15 populations and 12 loci. The allocation of the UAF-ABL baseline data (treated as a mixture) to the DFO baseline populations was determined for each population by taking the proportion of the summed probabilities of assignment for each individual sample (Appendix III). Most of the UAF-ABL samples allocated to either the corresponding DFO baseline population or to populations in the same reporting group.

All of these comparisons of UAF-ABL and DFO collections indicate that the data scored at the 12 microsatellite loci were nearly identical for the three laboratories. Statistical differences in the allele frequencies of collections from populations sampled at either different times or locations appear to have limited effect on the results of mixed-stock analyses.

Variation among populations

One of the primary objectives of our project was to expand an earlier version of the chum salmon baseline (Gharrett et al. 2007) to use in the estimation of the origins of chum salmon captured in the Bering Sea. Our project resulted in a combined SNP and microsatellite baseline for 126 populations (with microsatellite data for some populations and loci from DFO). The ability to make accurate stock composition estimates depends on the extent of divergence that exists among populations. We examined the divergence in a number of ways. Genetic diversity measures for the 126 populations varied by locus (Table 11). As expected for highly variable loci, the θ and G_{ST} (the multi-allelic extension of F_{ST}) parameters were much lower than the D_{est} and G''_{ST-est} parameters for microsatellite loci (Jost 2008; Meirmans and Hedrick 2011). Although F_{ST} -like indices are the most commonly used parameters in the population genetic literature and are valuable in evolutionary research (Whitlock 2011), D_{est} and G''_{ST} parameters are better at measuring population allele differences, regardless of evolutionary processes (Heller and Siegismund 2009; Gerlach et al. 2010). The *One111* and *One101* microsatellite loci had the highest D_{est} and G''_{ST-est} values. For the SNP loci, the four diversity measures were highly variable across loci, but within loci tended to be similar to each other. Of the nuclear SNPs, the ER, RF, and VR loci had the highest diversity across populations. The mtDNA locus had nearly uniformly higher values at all genetic diversity indices than any other locus. The diversity measures at the mtDNA locus were roughly three times higher than the average diversity of the nuclear SNP loci, likely due to its smaller effective population size. Among the coastal western Alaskan populations, there was about an order of magnitude less diversity (Table 12) than that observed in the entire dataset. Of the SNP loci, IS, VR, and MT had the highest diversity. The average D_{est} and G''_{ST-est} values of microsatellite loci were somewhat higher (1.3-2.5 times) than those of the SNP loci for all 126 populations; however, the average diversity of microsatellite loci was 3-7 times higher than the average diversity of the SNP loci for the 34 coastal western Alaskan populations.

Principal components analysis

Plots of the first two principal components (Fig. 2) for the 366 alleles that had frequencies of at least 0.06 in at least one population clearly delineated three major regions—Asia, western Alaska, and the northeastern Pacific. The plot of these principal components also displayed much of the divergence among geographic locales within these regions, but plots of other components may resolve other differences. Northeast Russia (Anadyr and Kanchalan) and Little Susitna from Cook Inlet more closely align with the western Alaskan region than with the Asian and northeastern Pacific regions. The separation of populations in western Alaska from

other populations in North America occurred between Meshik and Frosty on the northern Alaska Peninsula as has been observed previously (e.g., Seeb and Crane 1999).

As with the earlier (Gharrett et al. 2007) study, we conducted separate analyses for individual regions. Our analysis of the Asian populations was based on 304 alleles and 36 populations, and showed strong separation of three major areas on the first two principal components: 1) the more western and southern locales of Honshu, Hokkaido, Primorye, and the Kuril Islands, 2) southern Sakhalin Island, and 3) northern Sakhalin Island, Magadan–Sea of Okhotsk, Kamchatka Peninsula, and the Amur River (Fig. 3). The third principal component separated the Amur River from other locales (not shown).

The principal component analysis of the western Alaskan region with 227 alleles and 44 populations separated those populations into three major groups based in part on geography and in part on run-timing: 1) upper-middle Yukon River, 2) fall-run Kuskokwim River, and 3) coastal western Alaska from Kotzebue Sound to the northern Alaska Peninsula (Fig. 4). The coastal western Alaskan group included a mix of tightly clustered populations from the lower Yukon River, summer-run Kuskokwim River, and S. Seward Peninsula–Norton Sound, along with a more diffuse group of populations from Kotzebue Sound (the Kobuk clustered more closely with the S. Seward Peninsula–Norton Sound populations). The late-run Inmachuk population in Kotzebue Sound was distinct from all other populations. An analysis of the coastal western Alaska area based on 191 alleles and 30 populations, excluding Kotzebue Sound, separated the east Bristol Bay–northern Alaska Peninsula populations on PC1, and slightly separated the S. Seward Peninsula–Norton Sound populations from the Kuskokwim summer and lower Yukon on PC2 (Fig. 5). The Agiapuk (late-run timing) and Koyuk (early-run timing) populations were distinct from all other coastal western Alaskan populations.

The principal component analysis of the northeastern Pacific populations was based on 265 alleles and 45 populations (excluding Little Susitna, which clusters more closely with western Alaska) and clearly delineated the Alek–East Alek rivers and Kodiak Island–Alaska Peninsula (Fig. 6). The rest of the populations between northern SE Alaska and Washington were not separated as strongly, although there was little overlap among sub-groupings.

Component loadings are the weighted contribution of each allele to each principal component; the loadings with the largest absolute values explain the majority of the variation among populations observed graphically with principal components (Figs. 7A-E). Overall, the SNPs contributed about one-third of the highest loadings and the microsatellite alleles the other two-thirds. For the PCA with all 126 populations, more than half (22 of 35) of the SNP alleles were in the top 50 loadings for the first two PCs, whereas about one-sixth (55 of 331) of the microsatellite alleles were in the top 50 loadings. *Ots3* had fewer alleles than other microsatellite loci but they were proportionately more frequent in the top 50 loadings than alleles of other microsatellite loci. The genetic markers (loci and alleles) that explain the most variation in the first two PCs may differ among regions. Knowledge of these differences can help to identify the markers that would be the most useful for mixed-stock analyses for a particular mixture. For example, most of the mitochondrial SNP alleles contributed to the highest loadings in the Asian

region (Fig. 7B), so this marker is important for separating the population sub-groupings within Asia to a greater extent than in other regions. The CL locus was in the top 50 component loadings in only the NE Pacific region, contributing little to the variation observed in the other regions; on the other hand, the PER locus contributed variation to all regions except the NE Pacific (Fig. 7E). The two ER alleles exhibited a strong frequency cline in North American populations and more variable frequencies within Asia. Differences in allele frequencies were also observed within regions, e.g., the “33” allele (see Tables 7 and 8 for allele and haplotype designations) at the VT locus was at low frequency in the middle-upper Yukon River populations relative to the other western Alaskan populations.

The importance of determining the linkage phase of nuclear SNPs to combine haplotypes was evident in the large allele frequency differences among and within the three major geographic regions (Fig. 8). At the VR locus, the “53” allele was the most abundant allele in the Asian populations, with the exception of the Amur River populations, and it occurred at much lower frequency in western Alaska and at moderate frequencies in the NE Pacific region. The “51” allele was the most abundant allele in western Alaska, but it occurred at very low frequency in the NE Pacific populations, with the exception of Little Susitna in Cook Inlet, and the Alesk River, north of SE Alaska. For most NE Pacific populations, the “54” allele was the abundant allele. Another example of large regional differences in allele frequencies with linked SNPs is the IS locus, in which the “25 and 45” alleles were the most abundant alleles in Asia and western Alaska, but in the NE Pacific region, the “25, 35, and 45” alleles had relatively equal frequencies. These results show that the combined, linked SNPs increase power to detect population differences more than the individual SNPs alone.

Neighbor-joining tree

The topology of the neighbor-joining (NJ) tree (Fig. 9) was similar to the population clustering in the principal component analyses and to trees in other chum salmon baseline studies (Gharrett et al. 2007; Beacham et al. 2009a). The NJ tree was divided into the same three major regions of Asia, western Alaska, and the northeastern Pacific and corroborates the population structure observed in the PCA. The finer-scale geographic resolution observed was similar to that in the PCA with distinct clustering of branches in the Asian region for the areas of Honshu, Hokkaido, Primorye–Kuril, S. Sakhalin, Amur River, and the Sea of Okhotsk–Kamchatka Peninsula. The two NE Russian populations, Anadyr and Kanchalan, form a distinct cluster that is more closely aligned with western Alaska than the other Asian populations. The fall-run Kuskokwim populations cluster most closely with the upper and middle Yukon River populations. The coastal western Alaskan populations from Norton Sound to Bristol Bay have shallow branching and do not always cluster on a latitudinal basis or by watershed. The Little Susitna River population in Cook Inlet is an outlier more closely aligned with populations in western Alaska than the northeastern Pacific. The Frosty Creek and Meshik River populations on the northern Alaska Peninsula demark the genetic separation of populations in western Alaska from those in the Pacific region. Populations between the southern Alaska Peninsula and northern SE Alaska clustered separately from the other Pacific populations. Some additional

finer-scale structure was observed in the northeastern Pacific region, particularly the areas of (1) northern SE Alaska, (2) Prince of Wales and Haida Gwaii island archipelagos, (3) southern SE Alaska mainland and north-central British Columbia mainland, and (4) southern British Columbia and Washington State.

Baseline evaluation

Results of the principal component and neighbor-joining analyses, and groupings used by other agencies helped guide the grouping of populations used for baseline evaluation (Gharrett et al. 2007; Seeb et al 2011; Garvin et al. submitted; W. D. Templin, Alaska Department of Fish and Game, personal communication). The 18 reporting groups we chose to evaluate balance the desires for finer scale geographic resolution and minimal error in stock composition estimates. Because our project has a western Alaska focus, we pooled populations to a greater extent at the ends of the geographic range, and retained groupings with greater detail in western Alaska. These 18 reporting groups were used for the LTO cross validation evaluation of the baseline (Garvin et al. submitted). Pairwise F_{ST} estimates of the 18 reporting groups are in Table 13; all pairwise tests of homogeneity of the 18 reporting groups were highly significant, $P < 10^{-8}$.

The LTO cross validation approach provides a means to examine how well mixture samples correctly allocate to the baseline. We were constrained to use a somewhat smaller baseline for this analysis, i.e., the 101 populations (Table 1) for which genotype data were available (genotypes were not available for the online DFO microsatellite dataset). Although the DFO data used in our project were from populations throughout the geographic distribution of chum salmon, one of the biggest differences between the 101- and 126-population datasets was with the S. Seward Peninsula–Norton Sound region, which lacked data for five populations in the 101-population dataset (see Appendix IV for sample sizes and number of populations per reporting group for the two baseline datasets).

For clarification the LTO cross validation results are shown in two formats. The first format presents the means of stock mixture estimates for all three analyses (BAYES LTO, SPAM LTO, and SPAM simulation) with the true, known contribution (Fig. 10A). The second format presents the mean estimated proportions with the true proportions separately for each analysis (Figs. 10B-D). The highest overestimation occurred with two reporting groups—Kuskokwim summer–west Bristol Bay and southern SE Alaska–north British Columbia—by both the SPAM and BAYES programs. East Bristol Bay and Haida Gwaii–central British Columbia were underestimated to a greater extent than other reporting groups. The BAYES estimates were generally more accurate than the SPAM estimates; the SPAM simulation mode substantially underestimated the bias (Fig. 11). The variance of the estimates was generally higher for BAYES than SPAM; the variance of SPAM simulations was low, near zero (Fig. 12). The combination of bias and variance summarized in the mean square error was higher for the BAYES estimates for some reporting groups and higher for the SPAM estimates for other reporting groups. The largest differences in mean square error between the two programs was the larger error for the BAYES estimate of the Norton Sound and the lower Yukon River reporting groups and the larger error for the SPAM estimate of the Kuskokwim summer–west Bristol Bay

reporting group (Fig. 13). Overall mean square error summed across the 18 reporting groups was less for the BAYES estimates (0.0039) than the SPAM estimates (0.0044). As with the bias and variance, the error associated with the SPAM simulations of the baseline was very low and indicates overly-optimistic allocations. With the exception of the Japan–Kuril group, the number of baseline samples in the reporting groups corresponded to the fluctuations in bias, variance, and mean square error.

The LTO analysis indicated that several reporting groups over- or under-estimate stock contributions, but it did not indicate where misallocation occurred among reporting groups or the extent to which it occurred. To further examine the misallocation among reporting groups, the BAYES analyses of the ten LTO mixtures and baselines were repeated to determine the probability of assignment of known individual samples to 18 reporting groups. Those probabilities were summarized, resulting in a region-by-region table of assignments (Table 14). Analysis of individual assignment takes considerably more computing resources than estimating regional stock contributions of the same mixtures. Only the Japan–Kuril group had >90% correct assignment of individuals back to the baseline. Thirteen of the groups had >50% correct assignment and four groups had <50% correct assignment. Misallocation was primarily to geographically proximate reporting groups, but it was not always symmetric in proportion, e.g., reporting groups 16 and 17 (southern SE Alaska–N. British Columbia and Haida Gwaii–N. British Columbia). The coastal, lower river, summer-run individuals from Norton Sound to E. Bristol Bay–N. Alaska Peninsula were similar and form a large coastal western Alaska group (reporting groups 5, 6, 9, and 11) that has been observed in other studies (Seeb et al. 2011; DeCovich et al. 2012). Two reporting groups stand out as being significant contributors to other reporting groups. The first was the Kuskokwim summer–W. Bristol Bay (9) group, to which a large proportion of chum salmon misallocated from the Norton Sound (5) and Lower Yukon (6) groups, and to a lesser extent from the E. Bristol Bay–N. Alaska Peninsula group (11). The second was the southern SE Alaska–N. British Columbia (16) group, to which approximately one-third of the chum salmon from northern SE Alaska (15) and Haida Gwaii–central British Columbia (17) misallocated. This analysis indicated that additional pooling of some reporting groups should be considered for mixed-stock analysis of the Bering Sea immature chum salmon in Part II.

We examined one version of additional population pooling to increase correct allocation to reporting groups (Table 15). Reporting groups pooled included: 5, 6, 9, and 11, coastal western Alaska; 7 and 8, Upper and Middle Yukon River; 12 and 13, Alaska Peninsula and Kodiak; and 16 and 17, southern SE Alaska to central British Columbia. Reporting groups 12 and 13 were pooled to increase the sample sizes of these two geographically adjacent, albeit genetically distinct areas. This pooling to 12 reporting groups resulted in a narrower and higher range of correct allocations, 58 to 97%, with an average of 77%.

VIII. DISCUSSION:

Objectives

Our objectives were 1) to develop an enhanced coastwide genetic baseline, and 2) to estimate the origin of immature chum salmon in the eastern Bering Sea. Part I of the Final Product (this report) focused on the first objective, which is necessary for completion of the second objective. The activities of the first objective resulted in a more fully developed coastwide genetic baseline that contains data for 12 microsatellite loci, compatible with and complemented by the baseline developed by DFO, and 12 loci generated from 23 SNPs for 126 populations of chum salmon populations throughout the geographic range of this species. This baseline builds on prior baseline development research supported by the Bering Sea Fishermen's Association and the Pollock Conservation Cooperative Research Center (Gharrett et al. 2007). It will be used to complete the second objective to determine the stock compositions of immature chum salmon aggregations in different regions of the eastern Bering Sea, and the seasonal and yearly variation of stocks present. The stock compositions are expected to shed light on the ocean migration patterns and abundances of chum salmon in the Bering Sea and to help determine the impact of chum salmon bycatch in the Bering Sea groundfish fisheries on western Alaskan chum salmon returns.

Data compatibility

Substantial effort was made to produce compatible microsatellite datasets for different laboratory equipment platforms at UAF and ABL, as well as between the UAF, ABL, and DFO laboratories. Standardization among laboratories gave us the option of incorporating microsatellite data from the DFO laboratory, which in turn allowed us to focus more effort on obtaining SNP data, thus maximizing the number of populations in the baseline with data for both marker types. New methodologies were created to develop and analyze SNP loci over the course of our project (Garvin and Gharrett 2010; Garvin et al. 2010a,b), as was a new approach for baseline evaluation in mixed-stock analyses (Garvin et al. submitted). Evaluation of statistical differences in allele frequencies of baseline data from UAF, ABL, and DFO collections indicated that there may be additional temporal or spatial population structure beyond that described in this report or in Beacham et al. (2009a,b); however, the effect of these differences in mixed-stock analyses is nominal. We expect that mixed-stock analyses with baseline data from either dataset would produce similar results. Because of the uncertainty of allele frequency estimates between the UAF-ABL and DFO non-overlapping samples (Table 10), we recommend re-sampling those populations.

Population structure

The population genetic structure observed in our project was similar to that described in other studies. The populations separated into three large regions (Figs. 2 and 9), Asia, western Alaska, and the northeastern Pacific, similar to that observed in the earlier study (Gharrett et al. 2007), and in other studies, e.g., Seeb et al. (2011), Beacham et al. (2009a,b), and Olsen et al. (2006). Finer-scale structure was observed within each of these three large regions (Figs. 3-6, 9).

With the focus of this project on impacts to western Alaskan populations, we note that as in other studies, the upper-middle Yukon River, fall-run Kuskokwim, and east Bristol Bay stocks are genetically distinct from the genetically shallow-structured, coastal stocks from west Bristol Bay to Norton Sound. Resolution of the coastal stocks to individual river systems or small-scale areas within western Alaska was limited.

Baseline evaluation

One of the goals of mixed-stock analyses is to choose geographically useful and biologically meaningful reporting groups that optimize correct allocation of mixtures to the baseline. The choice of groupings has typically been evaluated with simulations of mixtures derived from baseline samples that contain 100% of the samples from single reporting groups (e.g., Seeb et al. 2011). This approach is most useful where aggregations of fish are known to originate primarily from one region (e.g., coastal juvenile chum salmon; Kondzela et al. 2009). However, past studies have shown that immature chum salmon from the Bering Sea originate from multiple regions (Kondzela et al. 2012; Wilmot et al. 1998). Mixed-stock analyses of 100% simulated mixtures will underestimate the actual contribution due to boundary constraints (Pella and Milner 1987) and additionally, will underestimate the actual uncertainty associated with the stock composition estimates (e.g., Table 3 in Pella and Masuda (2001)). Underestimation of stock composition variance will also occur if simulated mixtures are made *with* replacement (e.g., the SPAM program). Due to the use of equal proportions of baseline samples to create the mixtures and the removal of mixture samples from the baseline, the LTO analysis provides a more maximal measure of error a baseline contributes to stock estimation in situations where mixtures would be expected to contain chum salmon from many parts of their geographic distribution. We acknowledge that some of the increased uncertainty in the LTO approach is due to the use of slightly smaller baselines (90% of the original) inherent to this method, but this method has the advantage of separating the mixture samples from the baseline. A complication of using the LTO approach in our project was the lack of genotype data for the populations we used to fill in the microsatellite data. Allele frequencies rather than genotypes were available from DFO; due to this constraint, evaluation of the 126-population baseline would require the use of constructed genotypes from allele frequencies for the DFO data under the assumption that the populations are in Hardy-Weinberg equilibrium. The largest gap between the 101- and 126-population datasets was the lack of information from the coastal western Alaskan populations in the Norton Sound–S. Seward Peninsula reporting group in the smaller dataset. This was one of the four reporting groups with the highest mean square error (along with the lower Yukon, Kuskokwim summer–west Bristol Bay, and southern SE Alaska–N. British Columbia).

The examination of how individual samples in a mixture allocated to the reporting groups confirmed the difficulty of separating the coastal western Alaska populations into finer-scale geographic groupings (Table 14). Most of the Norton Sound and lower Yukon River chum salmon misallocated to the Kuskokwim summer–west Bristol Bay reporting group. One-quarter of the Kuskokwim summer–west Bristol Bay chum salmon misallocated to the combined Norton Sound and lower Yukon River reporting groups. The east Bristol Bay–N. Alaska Peninsula

reporting group also had substantial misallocation to the Kuskokwim summer–west Bristol Bay reporting group. About half of the middle Yukon chum salmon misallocated to other reporting groups, primarily to the upper Yukon and Kuskokwim summer–west Bristol Bay groups. As the PCA indicated, the population genetic structure of chum salmon is not strong in the region that includes Southeast Alaska to north-central British Columbia, and this was evident from the frequent misallocation of individuals among the reporting groups within this area. By pooling some of the problematic reporting groups, correct allocation of individual samples to broader-scale reporting groups increased (Table 15). Another benefit of the use of fewer reporting groups is that stock composition estimates of mixture samples improves, particularly for smaller datasets, in part through the reduction of bias and variance achieved by eliminating the cumulative effect of small allocations to populations that have little or no contribution.

Others have observed that with weak stock structure, such as the situation in coastal western Alaska, one component to misallocation can be related to the number of populations within regions (Jasper et al. 2010), i.e., regions with more populations acquire more allocation. This may explain some of the overestimation in the Kuskokwim summer–west Bristol and southern SE Alaska–N. British Columbia reporting groups (Fig. 10A), two groups with the largest number of populations (and samples) in their respective broader regions of western Alaska and the northeastern Pacific (Table 1; Appendix IV). The shallow genetic structure of the coastal western Alaskan populations contributes to the higher mean square error of stock estimates for this area and suggests that coastal western Alaska remains a challenge to the use of fine-scale resolution for mixed-stock analyses. Development of additional genetic markers, perhaps those under selection, and larger sample sizes for the microsatellite loci would be the next logical direction to pursue, although separation of these coastal populations may never be clearly resolved given their recent shared history since the last ice age.

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X. DELIVERABLES:

Allele frequencies of 12 SNP and 12 microsatellite loci for 126 chum salmon populations are appended to this report. Project results will be useful for agencies (e.g., NMFS and ADFG) involved in chum salmon management and mixed-stock analyses, e.g. Bering Sea bycatch. A manuscript will be submitted to a peer-reviewed journal upon completion of Part II of this report.

Publications:

Several publications were an outgrowth of this project:

- Garvin, M. R., K. Saitoh, and A. J. Gharrett. 2010. Application of single nucleotide polymorphisms to non-model species: a technical review. *Molecular Ecology Resources* 10:915-934.
- Garvin, M. R., K. Saitoh, D. Y. Churikov, V. A. Brykov, and A. J. Gharrett. 2010. Single nucleotide polymorphisms in chum salmon (*Oncorhynchus keta*) mitochondrial DNA derived from restriction site haplotype information. *Genome* 53:501-507.
- Garvin, M. R. and A. J. Gharrett. 2010. Application of single nucleotide polymorphism markers to chum salmon *Oncorhynchus keta*: discovery, genotyping and linkage phase resolution. *Journal of Fish Biology* 77:2137-2162.
- Garvin, M. R., M. M. Masuda, J. J. Pella, S. A. Fuller, R. J. Riley, R. L. Wilmot, V. Brykov, and A. J. Gharrett. Submitted. A cross-validation approach to evaluate genetic baselines and approximate the number of informative SNP loci needed for mixed-stock analysis.

Reports:

- Guyon, J. R., C. Kondzela, T. McCraney, C. Marvin, and E. Martinson. 2010. Genetic stock composition analysis of chum salmon bycatch samples from the 2005 Bering Sea groundfish fishery. Report to the North Pacific Fishery Management Council, submitted February 2, 2010. Genetic Stock Identification Auke Bay Laboratories, Alaska Fisheries Science Center, NMFS, NOAA, Ted Stevens Marine Research Institute, 17109 Pt. Lena Loop Road, Juneau, AK 99801.
- Kondzela, C. M., M. R. Garvin, R. L. Wilmot, V. Brykov, S. Sato, S. Abe, and A. J. Gharrett. In prep. Population genetic structure of chum salmon (*Oncorhynchus keta*) across the Pacific Rim based on single-nucleotide-polymorphisms and microsatellites. U.S. Department of Commerce, NOAA Technical Memorandum NMFS-AFSC-xxx, xx p.

Oral presentations:

- Guyon, J.R. 2010. Genetic stock composition analysis of chum salmon bycatch samples from the 2005 Bering Sea groundfish fishery. Oral presentation at the North Pacific Fishery Management Council Science and Statistical Committee, February 8, 2010.
- Gharrett, A. J., M. Garvin, S. Hall, C.M. Kondzela, R.L. Wilmot, J. Guyon, E. Martinson, T. McCraney, C. Marvin, J. Murphy, E. Farley. 2010. Genetic Analysis of Immature Chum Salmon. Oral presentation at the Arctic-Yukon-Kuskokwim Sustainable Salmon Initiative Mini-Symposium, Nome, Alaska, March 11, 2010.

Poster presentations:

- Kondzela et al. 2010. Genetic analysis of immature Bering Sea chum salmon. Presented at the 2010 Coastwide Genetics Workshop in Boise, ID by T. McCraney.

XI. PROJECT DATA:

1. Metadata description in FGDC format:

- [Identification Information](#)
- [Data Quality Information](#)
- [Distribution Information](#)
- [Metadata Reference Information](#)

*Identification_Information:**Citation:**Citation_Information:**Originator:*

C. Kondzela

Originator:

A.J. Gharrett

Originator:

AFSC

Publication_Date:

Unknown

Title:

AFSC/ABL: Genetic Analysis of Immature Bering Sea Chum Salmon: Part I. Baseline Evaluation

Geospatial_Data_Presentation_Form:

maps and data

*Description:**Abstract:*

Chum salmon populations from across their geographic distribution have been analyzed with a set of SNP and microsatellite markers. As is typical for chum salmon populations, more genetic divergence was observed on larger geographic scales than on smaller regional scales. Strong divergence exists within and among the three regions of Asia, western Alaska, and the northeast Pacific. However, separation of coastal western

Alaskan summer-run chum salmon populations, from Norton Sound to western Bristol Bay remains problematic. The degree of divergence determines the spatial scale to which stock proportions of mixtures of chum salmon can be resolved. The baseline developed in this project will be used for mixture analyses to study the marine distribution of chum salmon populations in the Bering Sea. Scale and fin samples collected in the eastern Bering Sea will be used to determine whether the stock composition of chum salmon aggregations differ across areas, seasonally, and annually. Determining the stock distributions of these mixtures will provide information on the migratory pathways of chum salmon in the Bering Sea and the potential impact of bycatch of coastal western Alaskan chum salmon in the Bering Sea pollock fishery.

Purpose:

This dataset contains SNP and microsatellite marker information.

Time_Period_of_Content:

Time_Period_Information:

Range_of_Dates/Times:

Beginning_Date:

1986

Ending_Date:

2006

Currentness_Reference:

ground condition

Status:

Progress:

Complete

Maintenance_and_Update_Frequency:

None Planned

Spatial_Domain:

Description_of_Geographic_Extent:

Bering Sea

Bounding_Coordinates:

West_Bounding_Coordinate:

-131

East_Bounding_Coordinate:

-134.6310

North_Bounding_Coordinate:

58.3835

South_Bounding_Coordinate:

58.3546

Keywords:

Theme:

Theme_Keyword_Thesaurus:

ISO 19115 Topic Categories

Theme_Keyword:

Biota

Theme_Keyword:

002

Theme_Keyword:

Oceans

Theme_Keyword:

014

Theme:

Theme_Keyword_Thesaurus:

None

Theme_Keyword:

Chum salmon

Theme_Keyword:

Genetic baseline

Theme_Keyword:

microsatellites

Theme_Keyword:

single nucleotide polymorphisms

Theme_Keyword:

mixed-stock analysis

Theme_Keyword:

cross validation

Theme:

Theme_Keyword_Thesaurus:

ITIS

Theme_Keyword:

Oncorhynchus keta

Place:

Place_Keyword_Thesaurus:

Geographic Names Information System

Place_Keyword:

Alaska

Place_Keyword:

Bering Sea

Taxonomy:

Keywords/Taxon:

Taxonomic_Keyword_Thesaurus:

None

Taxonomic_Keywords:

single species

Taxonomic_Keywords:

vertebrates

Taxonomic_Classification:

Taxon_Rank_Name:

Empire

Taxon_Rank_Value:

Biovitae

Applicable_Common_Name:

Carbon-based lifeforms

Taxonomic_Classification:
Taxon_Rank_Name:
 Kingdom
Taxon_Rank_Value:
 Animalia
Taxonomic_Classification:
Taxon_Rank_Name:
 Phylum
Taxon_Rank_Value:
 Chordata
Taxonomic_Classification:
Taxon_Rank_Name:
 Subphylum
Taxon_Rank_Value:
 Vertebrata
Taxonomic_Classification:
Taxon_Rank_Name:
 Superclass
Taxon_Rank_Value:
 Osteichthyes
Taxonomic_Classification:
Taxon_Rank_Name:
 Class
Taxon_Rank_Value:
 Actinopterygii
Taxonomic_Classification:
Taxon_Rank_Name:
 Subclass
Taxon_Rank_Value:
 Neopterygii
Taxonomic_Classification:
Taxon_Rank_Name:
 Infraclass
Taxon_Rank_Value:
 Teleostei
Taxonomic_Classification:
Taxon_Rank_Name:
 Superorder
Taxon_Rank_Value:
 Protacanthopterygii
Taxonomic_Classification:
Taxon_Rank_Name:
 Order
Taxon_Rank_Value:
 Salmoniformes
Taxonomic_Classification:

Taxon_Rank_Name:

Family

Taxon_Rank_Value:

Salmonidae

Taxonomic_Classification:

Taxon_Rank_Name:

Subfamily

Taxon_Rank_Value:

Salmoninae

Taxonomic_Classification:

Taxon_Rank_Name:

Genus

Taxon_Rank_Value:

Oncorhynchus

Taxonomic_Classification:

Taxon_Rank_Name:

Species

Taxon_Rank_Value:

keta

Applicable_Common_Name:

chum salmon

Access_Constraints:

Contact the Point of Contact for access constraints if none are provided.

Use_Constraints:

User must read and fully comprehend the metadata prior to use. User must acknowledge the Originator when using the data set as a source. User must share data products developed using the source data set with the Originator. Data should not be used beyond the limits of the source scale.

Point_of_Contact:

Contact_Information:

Contact_Person_Primary:

Contact_Person:

Chris Kondzela

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Contact_Instructions:

The e-mail address directs you to the person most knowledgeable about this data. If an alternative contact person becomes necessary, use the voice phone number for referral.

Data_Set_Credit:

Arctic-Yukon-Kuskokwim Sustainable Salmon Initiative (AYK SSI) University of Alaska Fairbanks

Native_Data_Set_Environment:

Microsoft Excel

Program_Affiliation:

Program_Name:

National Marine Fisheries Service - Alaska Fisheries Science Center

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Data_Quality_Information:

Logical_Consistency_Report:

No logical consistency test were run.

Completeness_Report:

None

Lineage:

Process_Step:

Process_Description:

No process steps have been described for this data set

Process_Date:

Unknown

[Back To Index](#)

Distribution_Information:

Distributor:

Contact_Information:

Contact_Person_Primary:

Contact_Person:

Chris Kondzela

Contact_Organization:

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Contact_Instructions:

The e-mail address directs you to the person most knowledgeable about this data. If an alternative contact person becomes necessary, use the voice phone number for referral.

Resource_Description:

Offline data

Distribution_Liability:

The user is responsible for the results of any application of this data for other than its intended purpose

[Back To Index](#)

Metadata_Reference_Information:

Metadata_Date:

20121212

Metadata_Contact:

Contact_Information:

Contact_Person_Primary:

Contact_Person:

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 99801
Country:
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 907-789-6613
Contact_Facsimile_Telephone:
 907-789-6094
Contact_Electronic_Mail_Address:
 emily.fergusson@noaa.gov
Hours_of_Service:
 8:00 a.m. - 4:30 p.m. AK time Monday-Friday
Contact_Instructions:
 Contact during business hours only.
Metadata_Standard_Name:
 FGDC Biological Data Profile of the Content Standard for Digital Geospatial Metadata
Metadata_Standard_Version:
 FGDC-STD-001.1-1999
Metadata_Extensions:
Online_Linkage:
http://www.ncddc.noaa.gov/metadatarresource/metadatarreferences/files/ncddcmdprofile_v2.pdf
Profile_Name:
 Content Specification for Metadata in the National Coastal Data Development Center's
 Data Catalog Version 2.0
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2. The available data is sample information (e.g., population names, latitude, longitude, collector, etc.) and allele frequencies in Excel spreadsheets and PDF files.
3. Archive or custodian of data:
 Christine Kondzela
 NOAA Fisheries, Alaska Fisheries Science Center
 Auke Bay Laboratories, Ted Stevens Marine Research Institute
 17109 Pt. Lena Loop Road, Juneau, Alaska 99801
 (907) 789-6084 phone, (907) 789-6094 fax
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4. An electronic copy and two paper copies of data are provided with the Final Product.

XII. ACKNOWLEDGEMENTS:

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 Lev Zhivotovsky, Russian Academy of Sciences, Moscow, Russia

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 Natalya Varnavskaya, Kamchatka Research Institute of Fisheries and Oceanography,
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 William Templin, Alaska Department of Fish and Game, Anchorage, Alaska
 Terry Beacham and others, Canada Fisheries and Oceans, Nanaimo, Canada
 John Wenburg, Blair Flannery, U.S. Fish and Wildlife Service, Anchorage, Alaska
 Washington Department of Fish and Wildlife

We also thank Jeff Guyon for the use of his C++ program to calculate chord distances used for the neighbor-joining tree.

Publically available microsatellite data from Canada Fisheries and Oceans was incorporated into the genetic baseline analyzed for our project (<http://www.pac.dfo-mpo.gc.ca/science/facilities-installations/pbs-sbp/mgl-lgm/data-donnees/index-eng.htm>).

XIII. PRESS RELEASE:



Contact: [Julie Speegle](mailto:Julie.Speegle@noaa.gov)
 907-586-7032 w.
 907-321-7032 c.

NEWS RELEASE:
 Date

UAF and NOAA scientists team up to unravel chum salmon origin with genetic tools

Scientists from the University of Alaska Fairbanks and National Marine Fisheries Service are seeking to understand the causes of periodic declines in chum salmon abundance in many western Alaskan river systems over the last decade.

As part of a project sponsored by the Arctic-Yukon-Kuskokwim Sustainable Salmon Initiative, UAF and NMFS fisheries geneticists have developed genetic data for chum salmon that can be used to determine where chum salmon caught on the high seas originate.

Chum salmon abundance in many western Alaskan river systems has varied over the last decade, with very low returns in some years. That affects rural Alaskans along those rivers who depend on chum salmon for subsistence and commercial fisheries.

Contributing factors could be changes in climate and oceanographic conditions during the last decade, as well as chum salmon being intercepted in Bering Sea commercial fisheries that target other marine species.

To understand the influences of changes in the marine environment and to avoid incidental catches, scientists need to know how chum salmon from different rivers are distributed in the Bering Sea. Specifically, research is focused on whether fish from different rivers and geographic areas are found in different areas of the Bering Sea; if the locations of fish from a stream change seasonally; and whether their locations change from year to year.

The genetic data will go a long way towards finding answers. Scientists expanded the existing dataset from a previous study to include more baseline populations and additional genetic markers. Their work provides a foundation that current baseline projects can continue to build upon with multi-agency collaboration.

With the data provided by this project, a large set of archived chum salmon samples collected between 1988 and 2005 from different sites in the Bering Sea will be analyzed to trace the marine movements of chum salmon and to learn about how environmental changes may alter their movements, and ultimately, their productivity.

NOAA's mission is to understand and predict changes in the Earth's environment, from the depths of the ocean to the surface of the sun, and to conserve and manage our coastal and marine resources. Join us on [Facebook](#), [Twitter](#) and our other [social media channels](#).

*Keep up with NOAA Fisheries in Alaska on the web:
alaskafisheries.noaa.gov or www.afsc.noaa.gov, and on [Facebook](#) and [Twitter](#).*

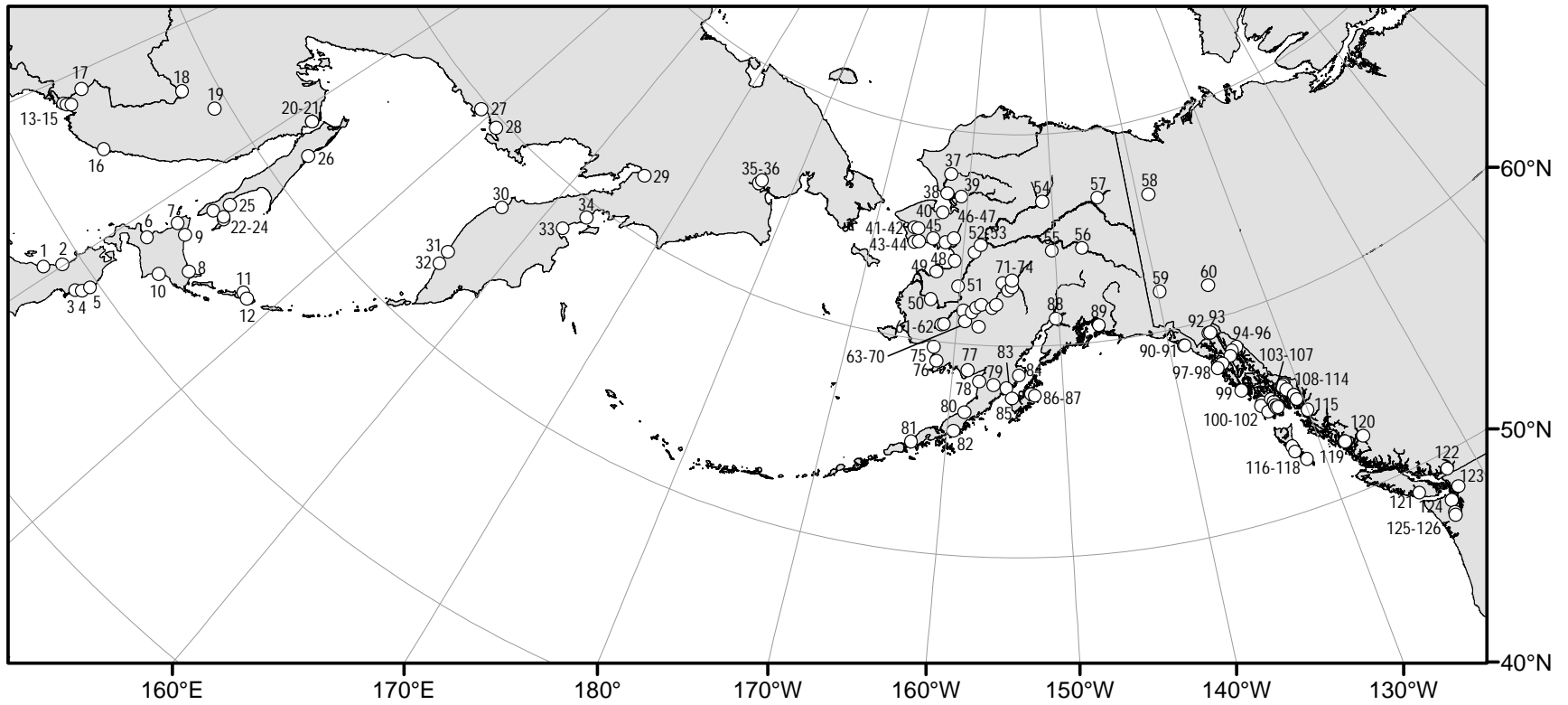


Figure 1. Chum salmon populations sampled to develop a microsatellite and SNP baseline. The numbers correspond to the code in Table 1.

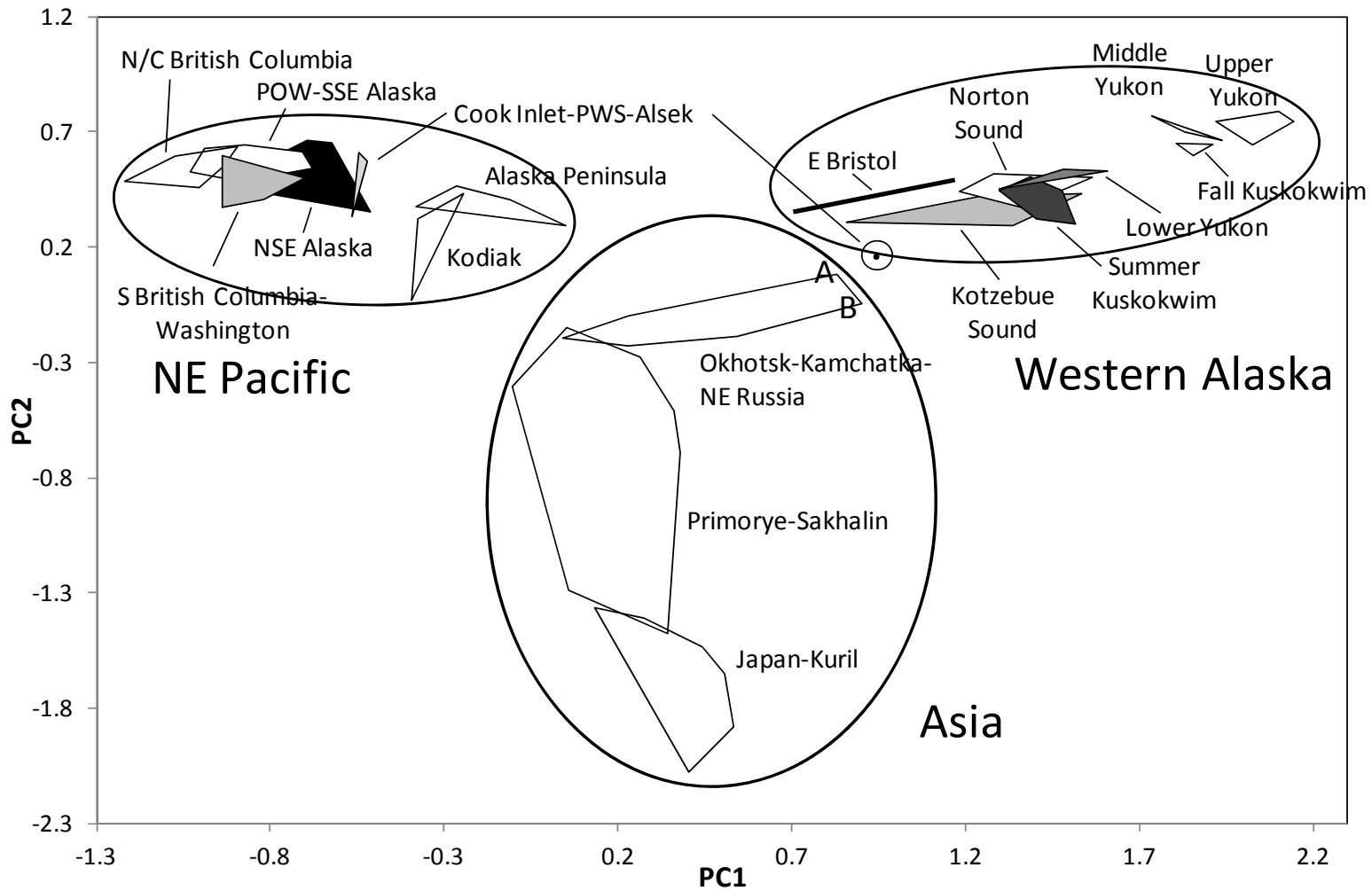


Figure 2. Plot of populations on the first two principal components (PC1 and PC2) of arcsine-squareroot-transformed microsatellite and SNP allele frequencies of all 126 chum salmon populations. A is Kanchalan (36) and B is Anadyr (35).

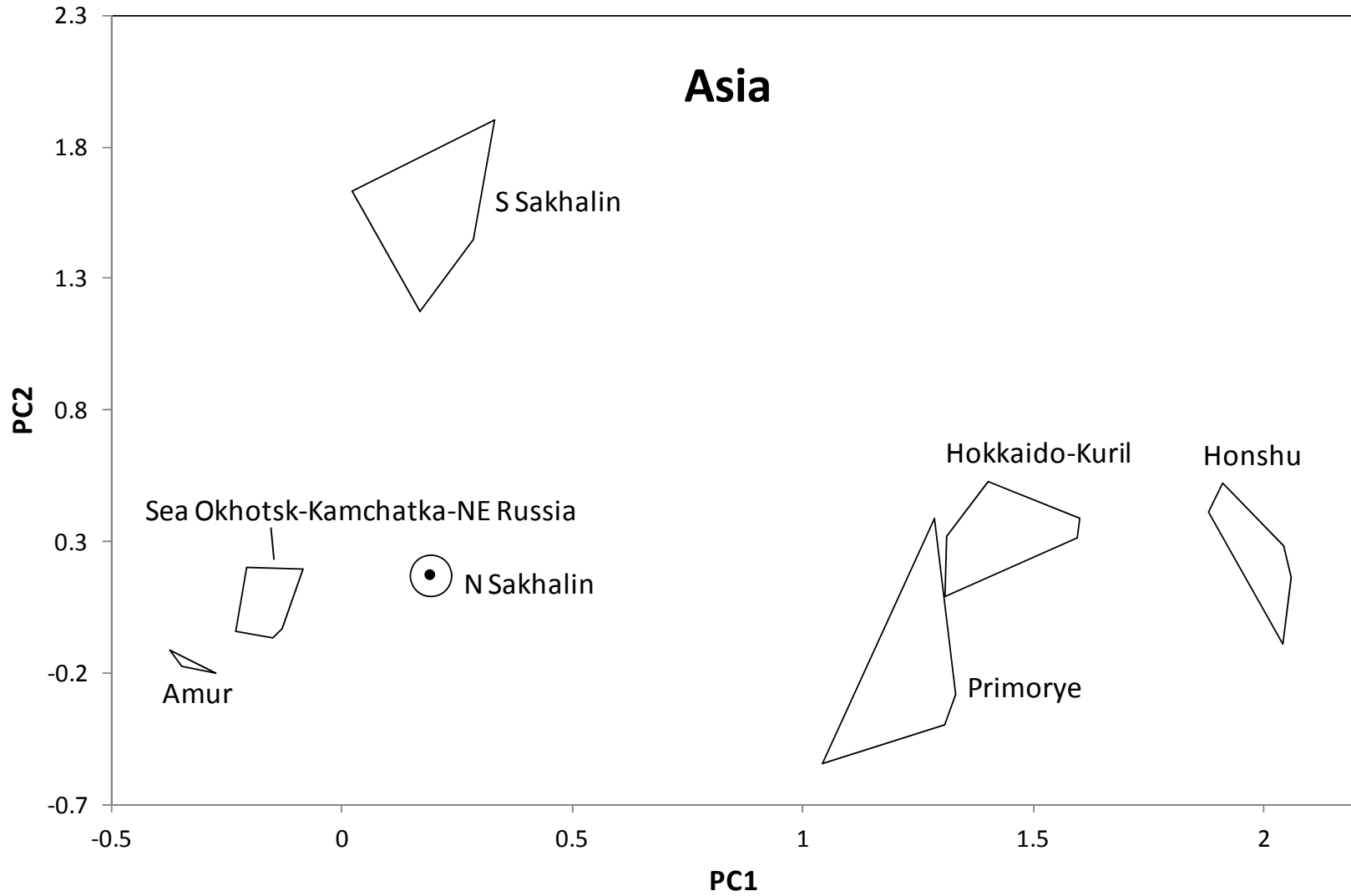


Figure 3. Plot of populations on the first two principal components (PC1 and PC2) of arcsine-squareroot-transformed microsatellite and SNP allele frequencies of Asian chum salmon populations. Tym (26) represents N. Sakhalin (circled).

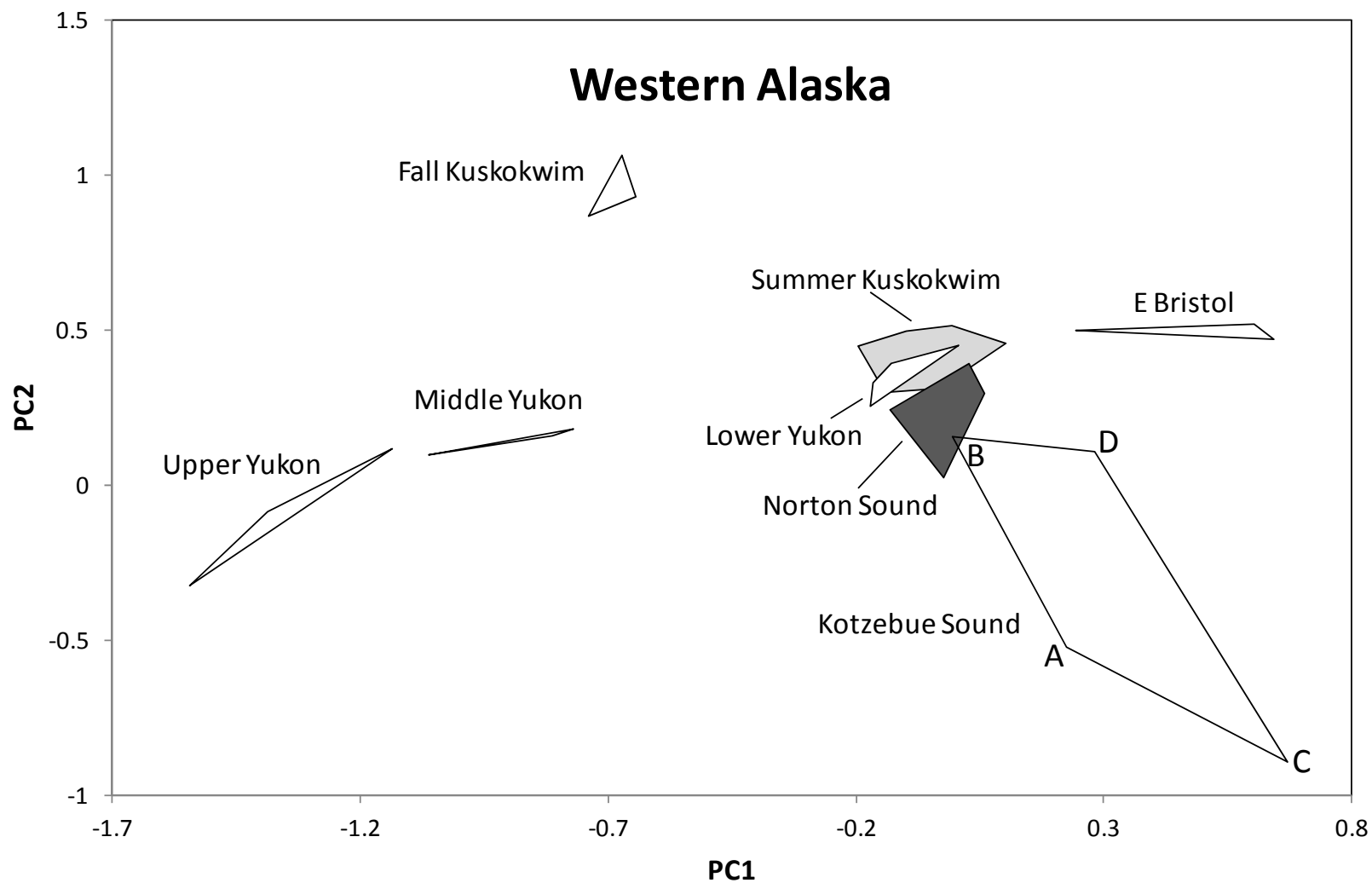


Figure 4. Plot of populations on the first two principal components (PC1 and PC2) of arcsine-squareroot-transformed microsatellite and SNP allele frequencies of western Alaskan chum salmon populations. A is Kelly Lake (37), B is Kobuk (39), C is Innachuk (40), and D is Agiapuk (41).

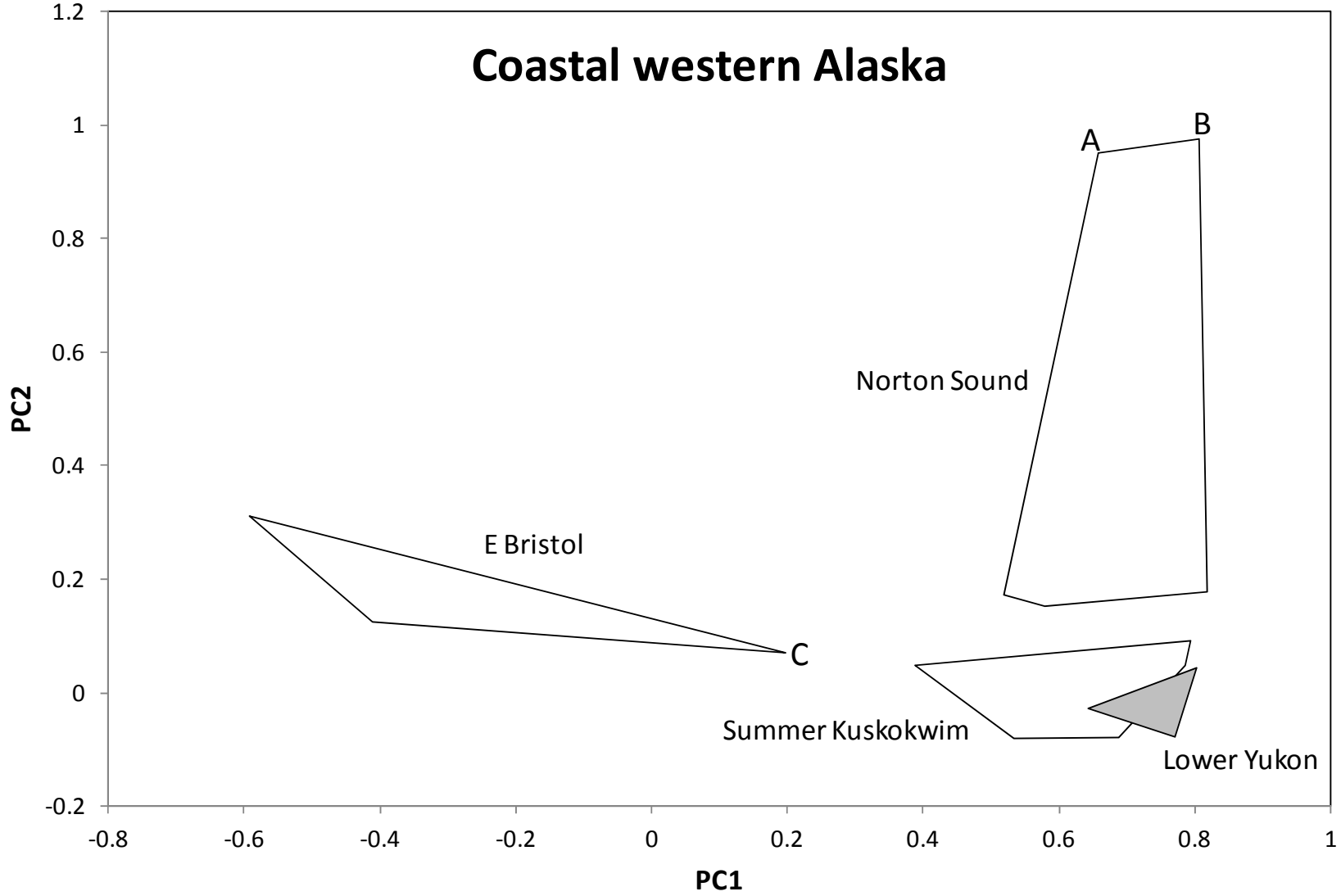


Figure 5. Plot of populations on the first two principal components (PC1 and PC2) of arcsine-squareroot-transformed microsatellite and SNP allele frequencies of coastal western Alaskan (excluding Kotzebue Sound) chum salmon populations. A is Agiapuk (41), B is Koyuk (47), and C is Big Creek (78).

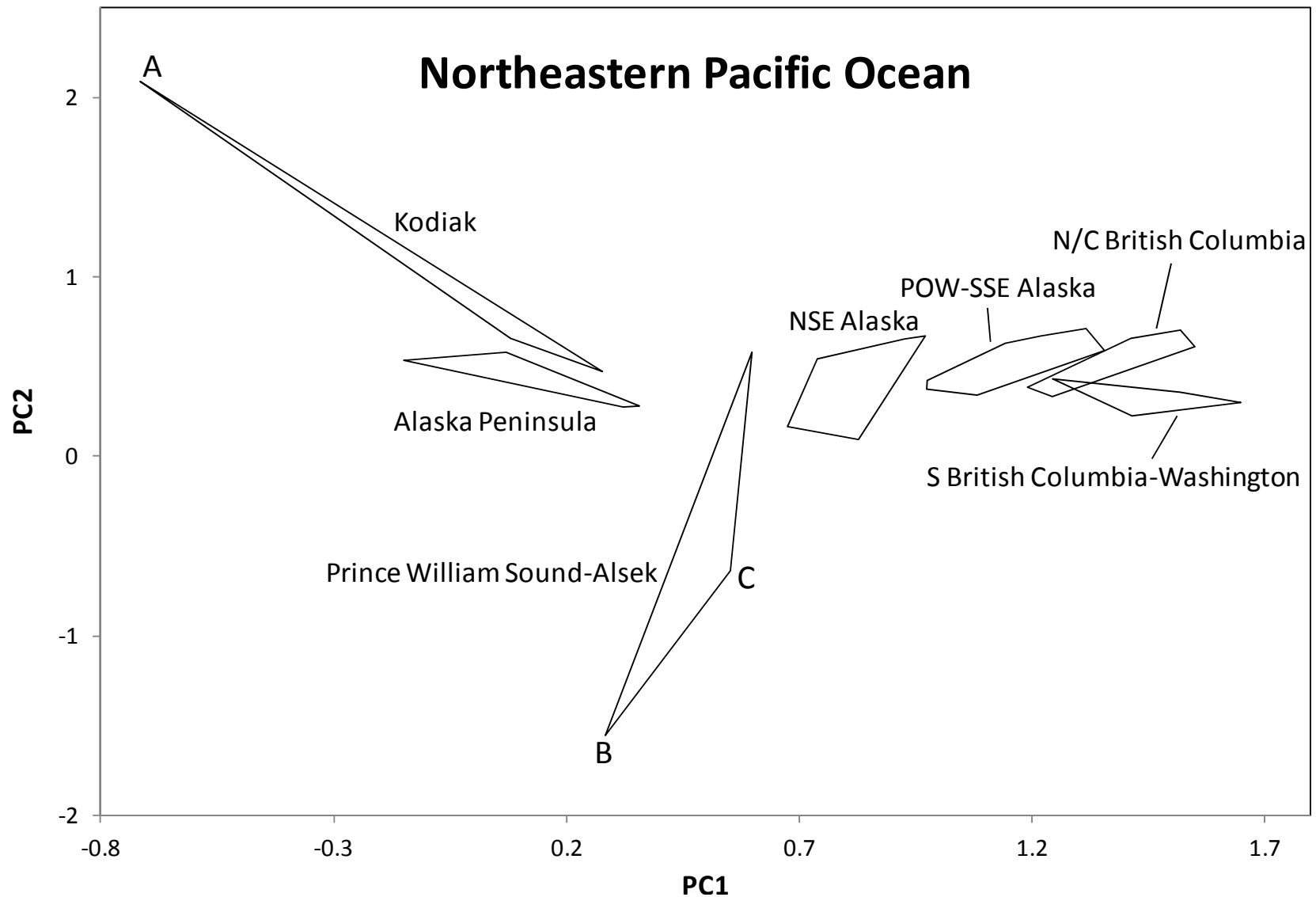


Figure 6. Plot of populations on the first two principal components (PC1 and PC2) of arcsine-squareroot-transformed microsatellite and SNP allele frequencies of northeastern Pacific Ocean (excluding Cook Inlet) chum salmon populations. A is Sturgeon (85), B is Alsek (90), and C is East Alsek (91).

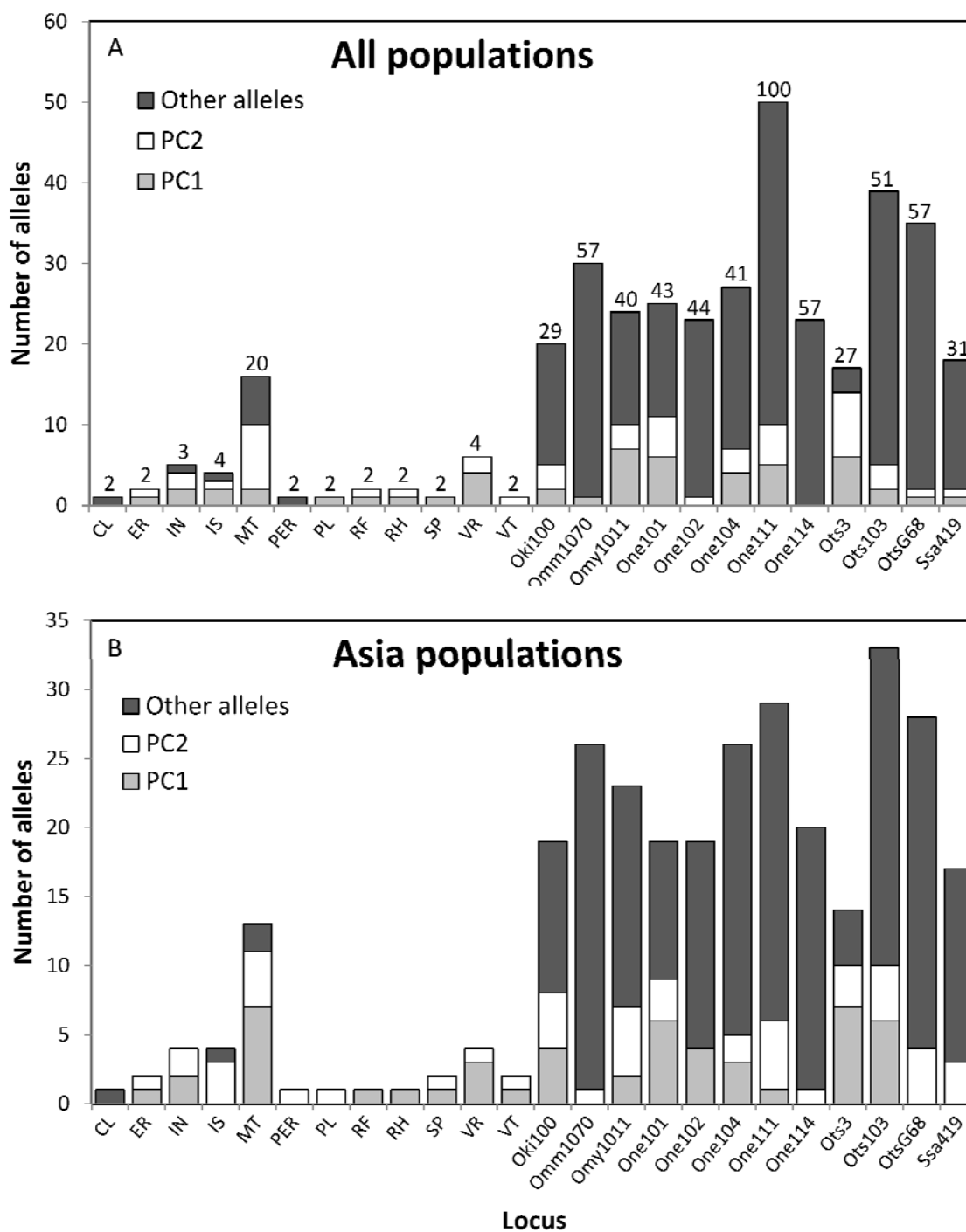


Figure 7. Number of alleles at each locus (with a frequency of ≥ 0.06 in at least one population) with the 50 largest absolute component loadings in each of the first two principal components. The value at the top of the first histogram is the number of alleles that we observed at that locus. (A) All populations (126) and 366 alleles; (B) Asian populations (36) and 304 alleles; (C) western Alaskan populations (44) and 227 alleles; (D) coastal western Alaskan populations (30) and 191 alleles; and (E) northeastern Pacific Ocean populations (45) and 265 alleles.

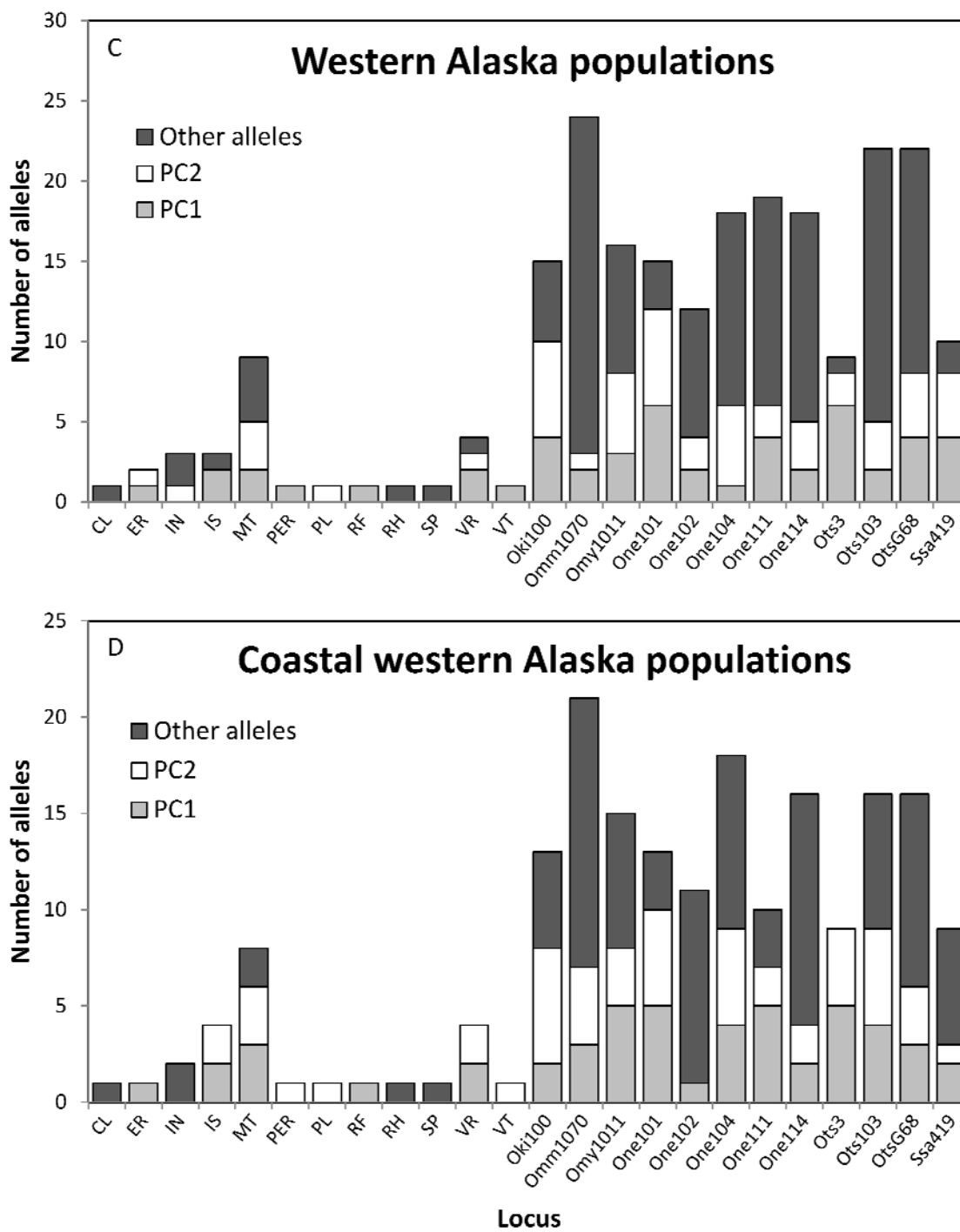


Figure 7. Continued.

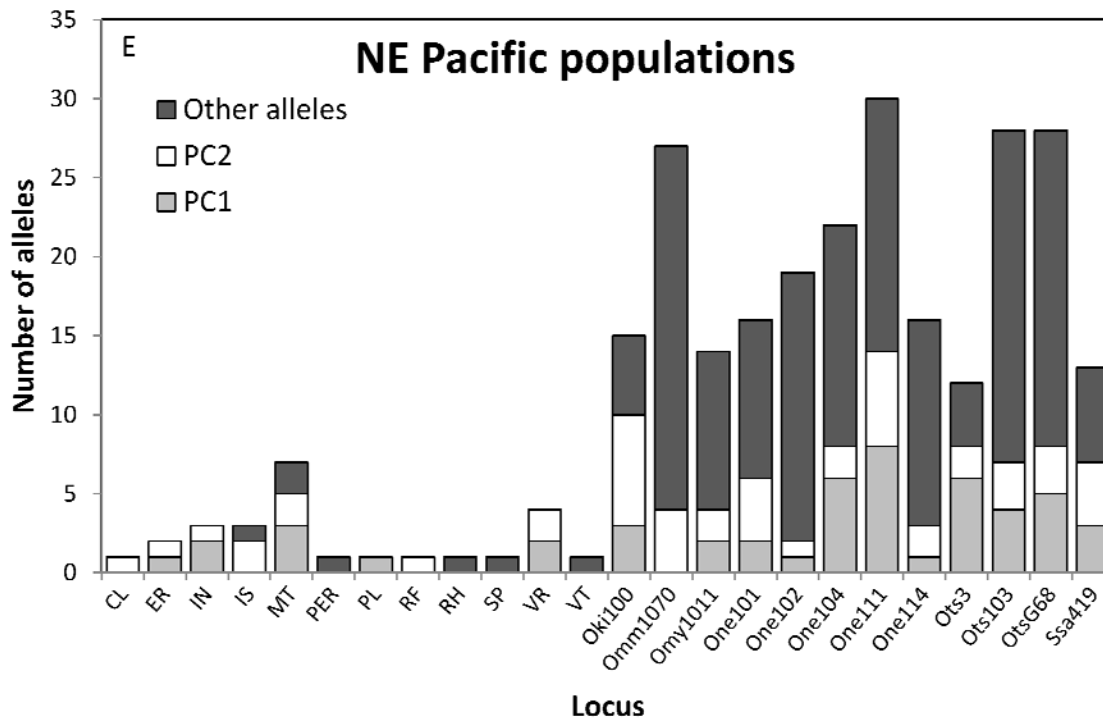


Figure 7. Continued.

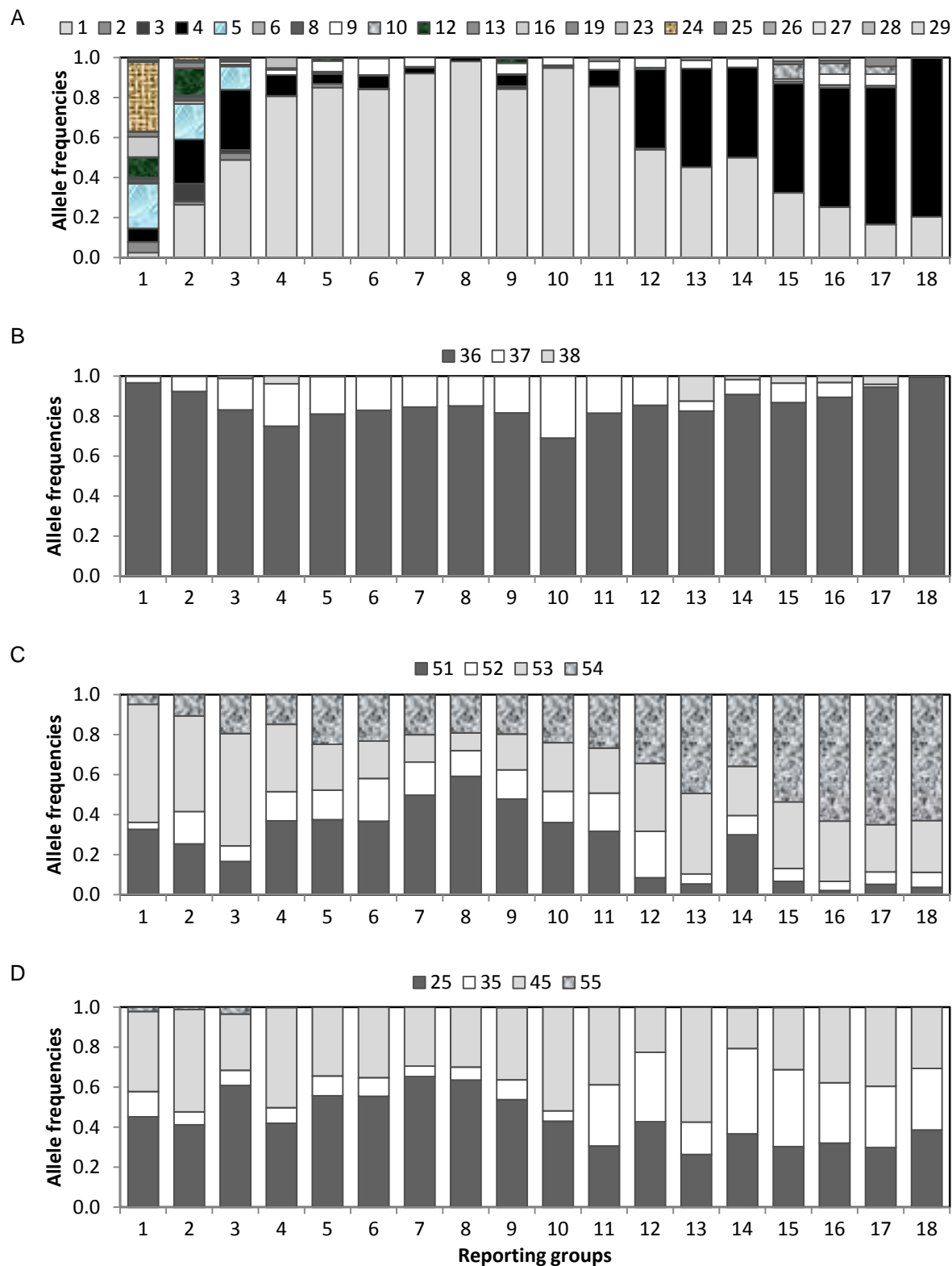


Figure 8. Allele (haplotype) frequencies of linked SNPs for 18 reporting groups listed in Table 1: A) mtDNA, B) IN, C) VR, and D) IS. The three major geographic regions are comprised of reporting groups 1-3 (Asia), 4-11 (western Alaska), and 12-18 (NE Pacific). The allele designations are at the top of each figure (Tables 7 and 8).

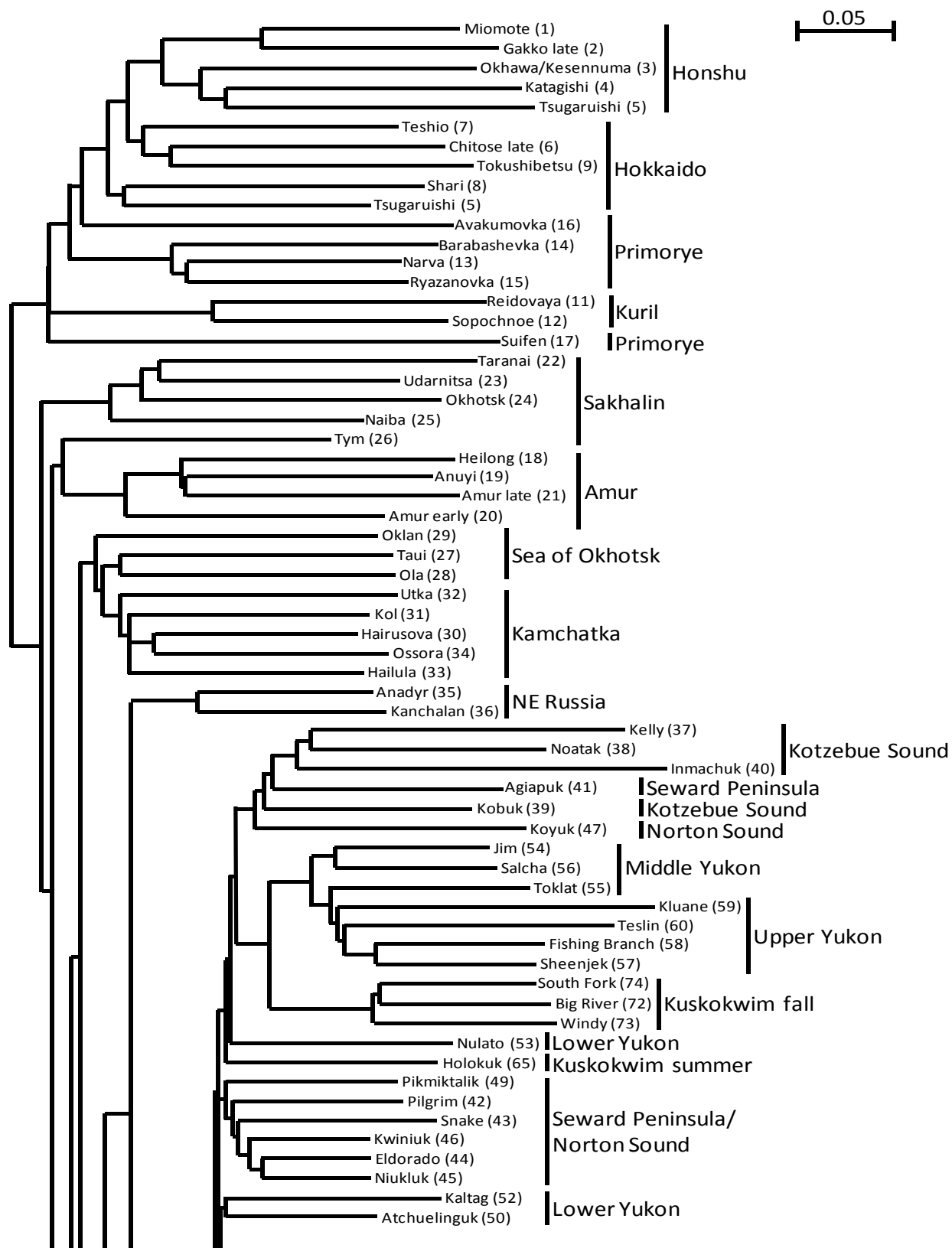


Figure 9. Neighbor-joining tree for 126 chum salmon populations based on unitized chord distances (Cavalli-Sforza and Edwards 1967) from 12 microsatellite and 12 SNP loci.

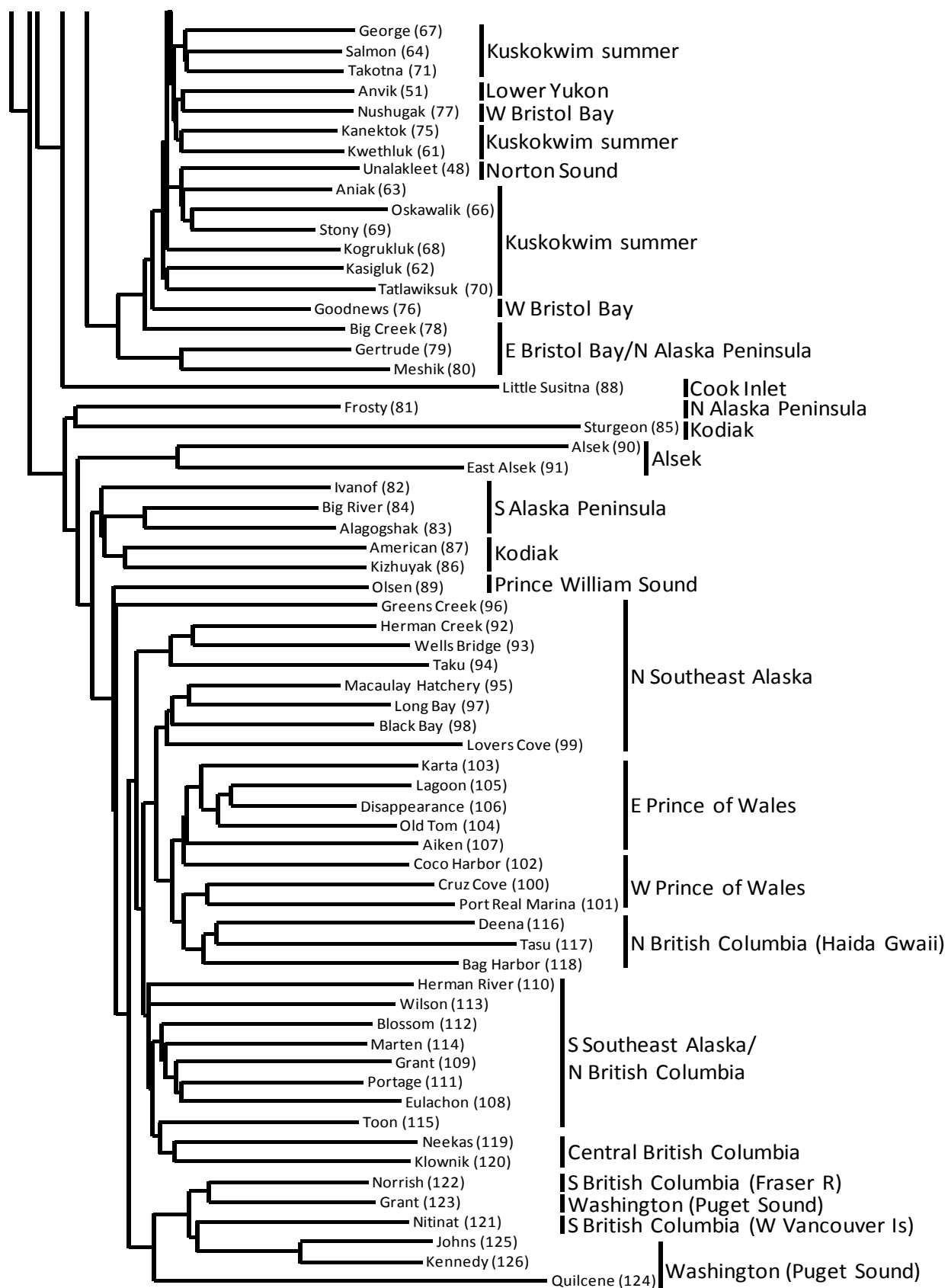


Figure 9. Continued.

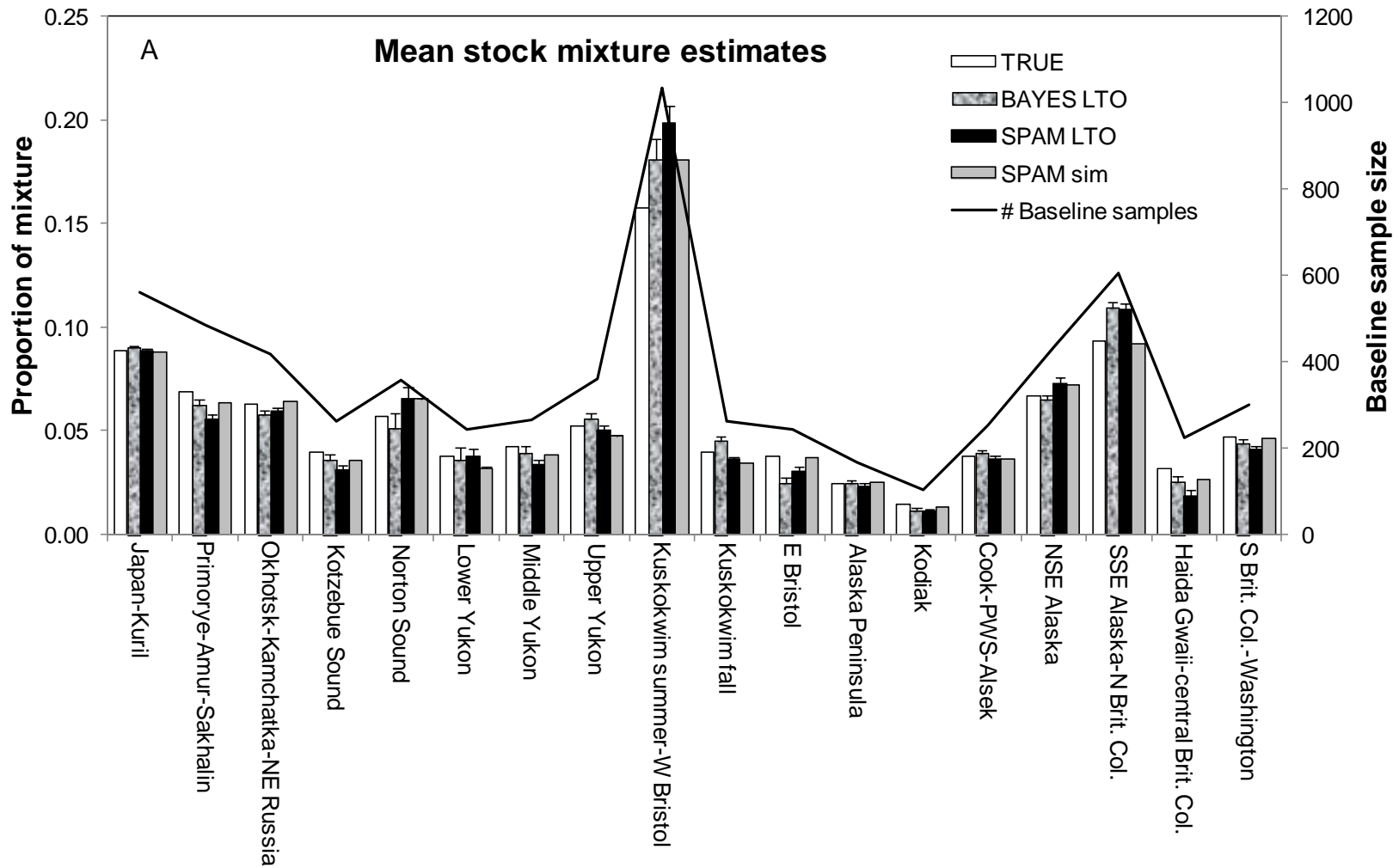


Figure 10. Baseline evaluation of chum salmon populations with 18 reporting groups in a “leave-ten-percent-out” (LTO) cross-validation analysis. Baseline sample sizes are given for each reporting group (black line). (A) Mean stock estimates of 10 datasets for the BAYES LTO, SPAM LTO, and SPAM simulation. The expected versus true stock proportions for the (B) BAYES LTO analysis; (C) SPAM LTO analysis; and (D) SPAM simulation analysis.

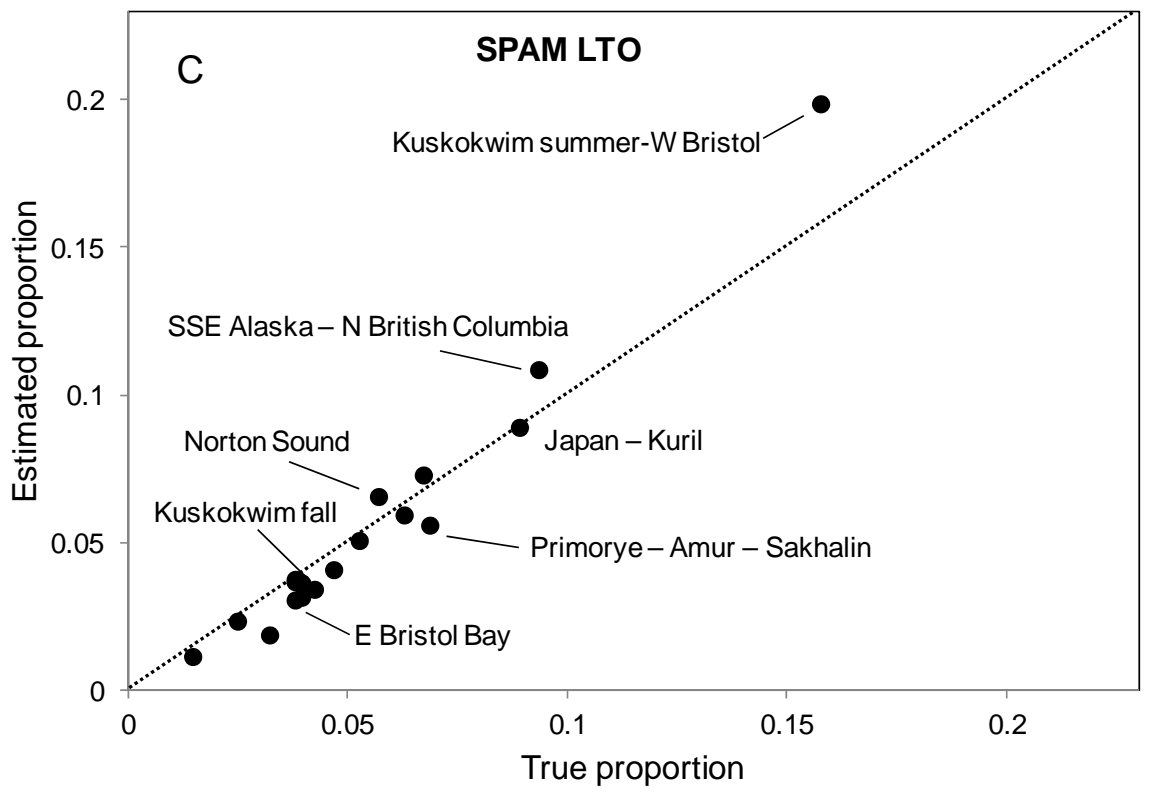
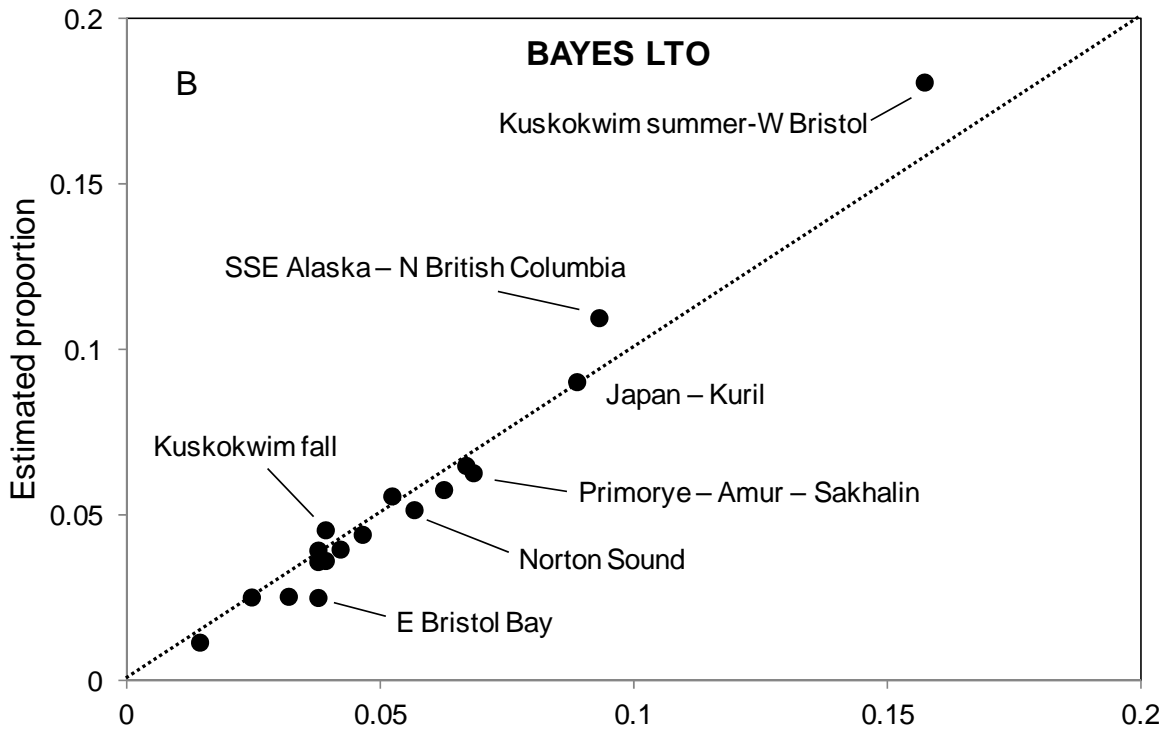


Figure 10. Continued.

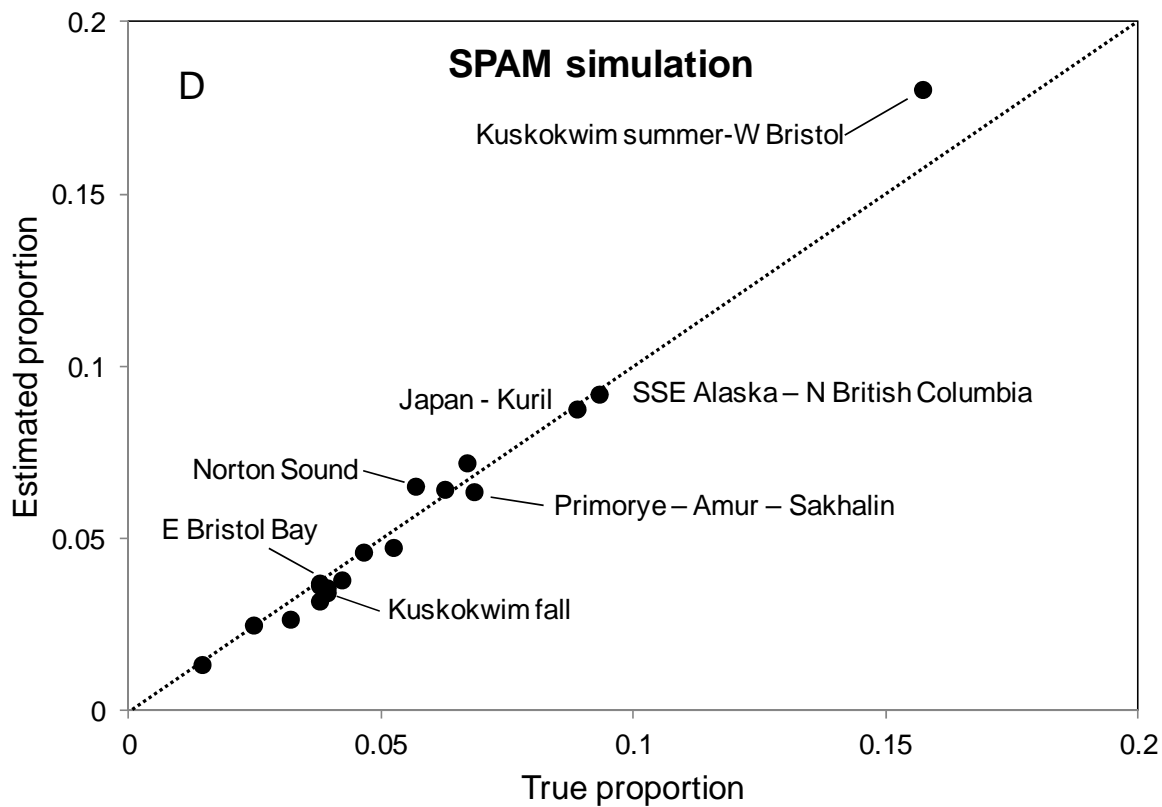


Figure 10. Continued.

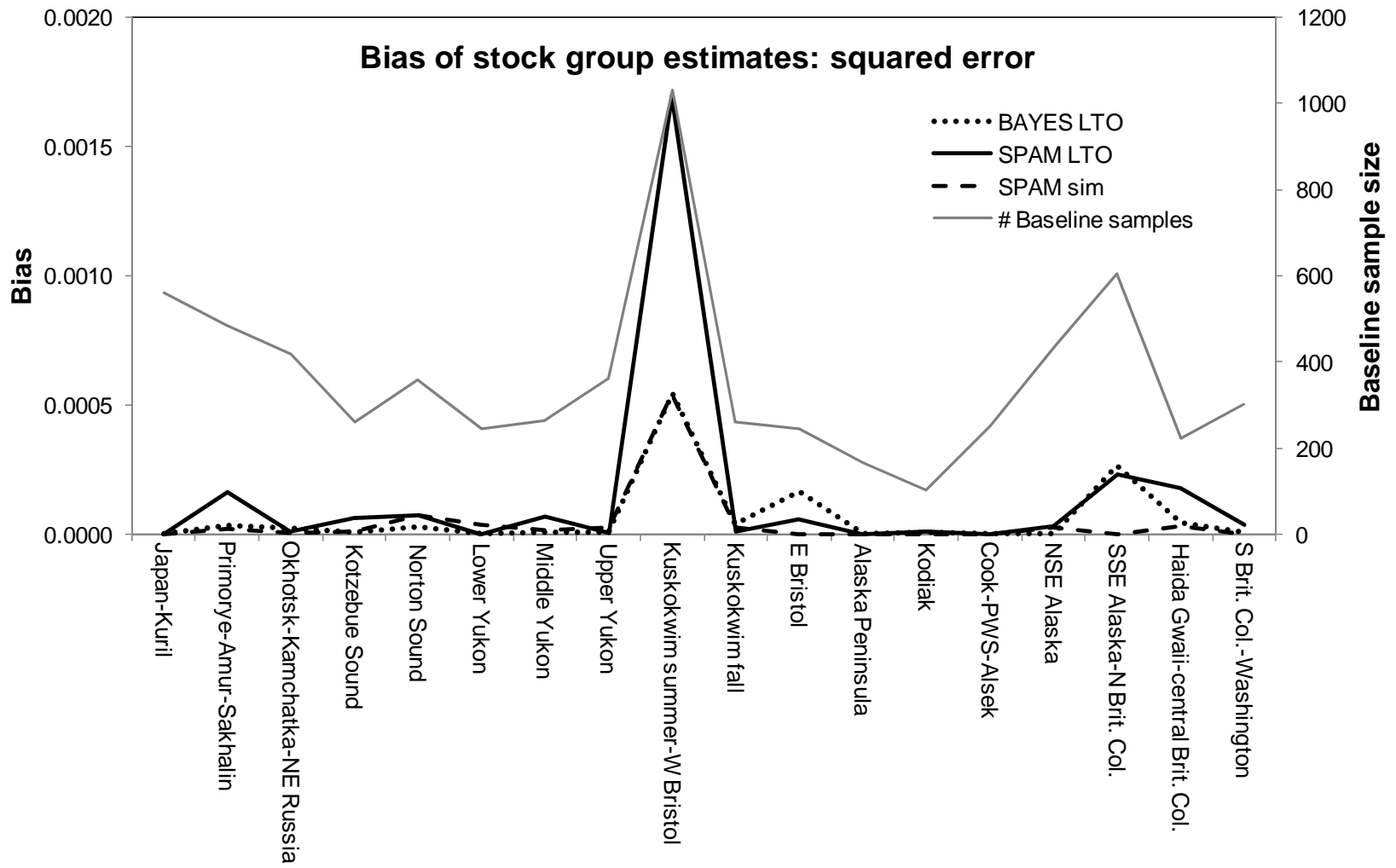


Figure 11. Bias of stock proportion estimates from the LTO cross-validation analysis, calculated as the squared difference of the mean of 10 datasets from the true value for each of the 18 reporting groups for the BAYES LTO, SPAM LTO, and SPAM simulation analyses. Baseline sample sizes are given for each reporting group (gray line).

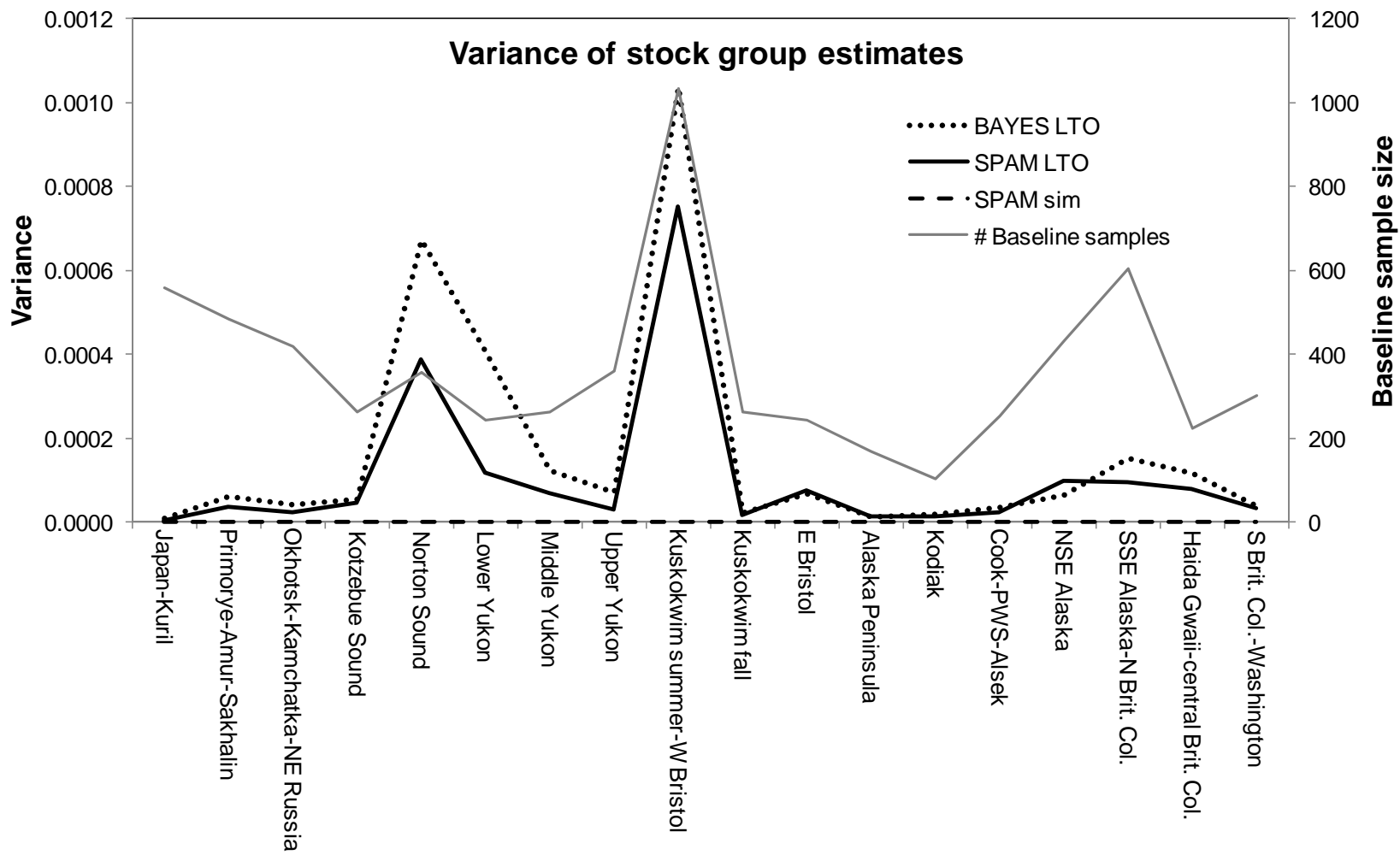


Figure 12. Variance of stock proportion estimates of the 10 datasets from the LTO cross-validation analysis for each of the 18 reporting groups for the BAYES LTO, SPAM LTO, and SPAM simulation analyses. Baseline sample sizes are given for each reporting group (gray line).

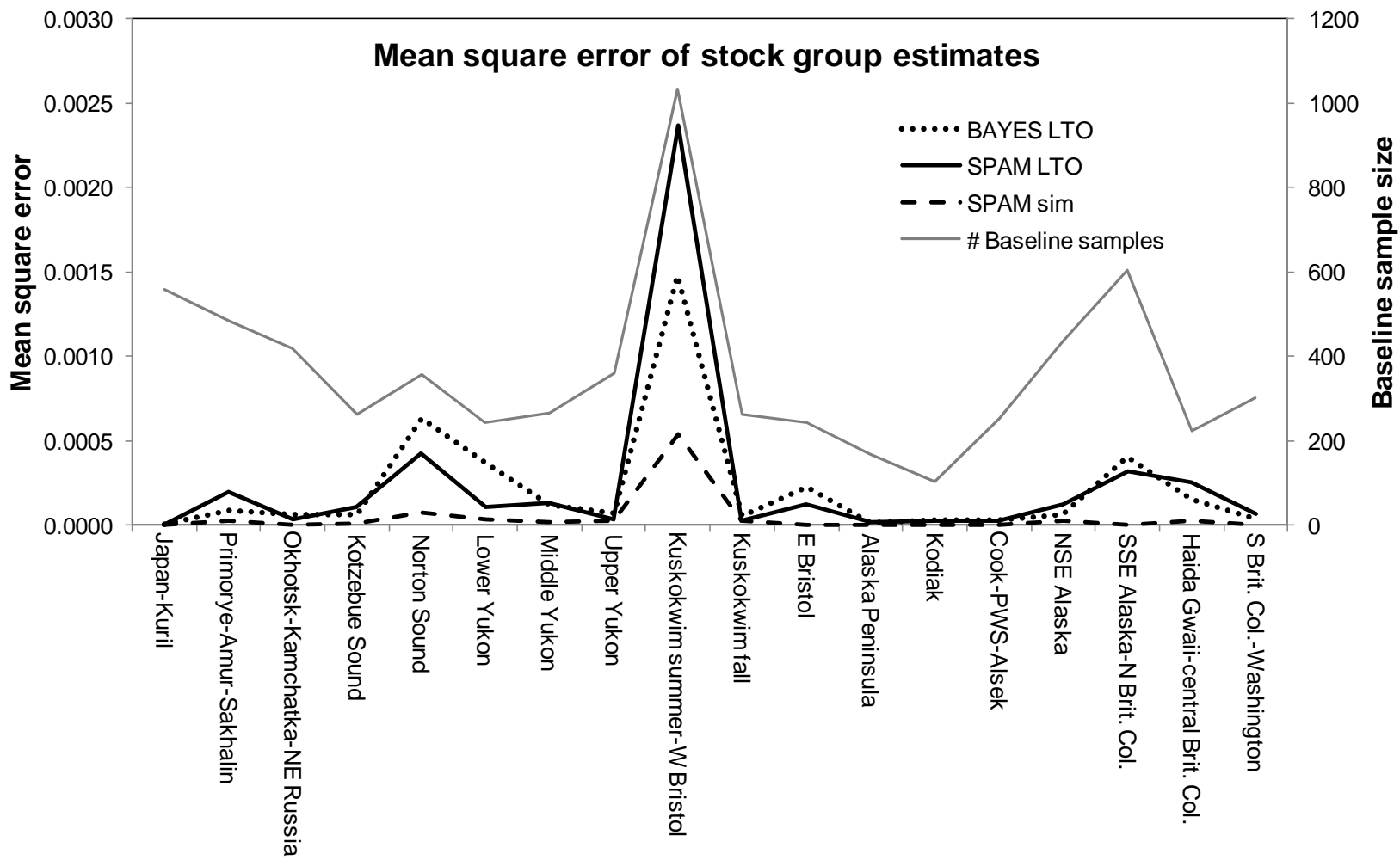


Figure 13. Mean square error of stock proportion estimates of the 10 datasets from the LTO cross-validation analysis for each of the 18 reporting groups for the BAYES LTO, SPAM LTO, and SPAM simulation analyses. Baseline sample sizes are given for each reporting group (gray line).

Table 1. Chum salmon populations analyzed for microsatellite and SNP variation, regional reporting group, geographic location, number of individuals (n), year sampled, and sources of the samples. The geographical coordinates locate the mouth of the stream or, for tributaries in larger systems, the mouth within the main system.

Populations in the earlier, 73-population baseline (Gharrett et al. (2007) are indicated with "*"; the 101 populations used for the LTO analysis are indicated with "#".

Population Reporting			Geographic location	Country		Collection year(s)	Latitude	Longitude	Source ^c
code	group	Population ^{a,b}		of origin	n				
1	1	Miomote#	Honshu (Sea of Japan)	Japan	95	2006	38.242	139.449	HNFRI
2	1	Gakko late#	Honshu (Sea of Japan)	Japan	70	2003	39.076	139.911	NSRC
3	1	Kesenuma/Ohkawa#	Honshu (Pacific coast)	Japan	95	2006	38.909	141.585	HNFRI
4	1	Katagishi*#	Honshu (Pacific coast)	Japan	40	1991	39.150	141.842	Kitasato
5	1	Tsugaruishi*#	Honshu (Pacific coast)	Japan	40	1991	39.589	141.952	Kitasato
6	1	Chitose late#	Hokkaido (Sea of Japan)	Japan	80	2003	43.267	141.372	NSRC
7	1	Teshio#	Hokkaido (Sea of Japan)	Japan	80	2001	44.883	141.733	NSRC
8	1	Shari ^b	Hokkaido (Sea of Okhotsk)	Japan	78	2001	43.933	144.683	NSRC
9	1	Tokushibetsu#	Hokkaido (Sea of Okhotsk)	Japan	40	2004	44.842	142.656	NSRC
10	1	Tokachi ^b	Hokkaido (Pacific coast)	Japan	79	1990	42.695	143.665	NSRC
11	1	Reidovaya*#	Kuril Islands	Russia	30	2004	45.383	147.983	RAS
12	1	Sopochnoe Lake*#	Kuril Islands	Russia	50	2004	45.317	148.414	RAS
13	2	Narva*#	Primorye	Russia	68	1995, 2005	42.991	131.487	RAS
14	2	Barabashevka*#	Primorye	Russia	54	1994, 1995	43.112	131.635	RAS
15	2	Ryazanovka* ^a	Primorye	Russia	63	1994, 1995	43.316	131.767	RAS
16	2	Avakumovka ^b	Primorye	Russia	34	1994	43.727	135.211	RAS
17	2	Suifen*#	Primorye	China	23	1994	44.075	131.121	HRFRI
18	2	Amur (Heilong)*#	Amur River	China	44	1994	48.370	134.290	HRFRI
19	2	Anuyi*#	Amur River	Russia	46	2002	49.317	136.467	RAS
20	2	Amur early*#	Amur River	Russia	51	2003	52.933	141.167	RAS
21	2	Amur late*#	Amur River	Russia	27	2003	52.933	141.167	RAS
22	2	Taranai*#	S. Sakhalin Island	Russia	25	2003	46.625	142.433	RAS
23	2	Udarnitsa*#	S. Sakhalin Island	Russia	49	1994	46.800	143.300	RAS
24	2	Okhotsk*#	S. Sakhalin Island	Russia	25	2003	46.867	143.167	RAS
25	2	Naiiba*#	S. Sakhalin Island	Russia	46	1995, 1996	47.447	142.756	RAS
26	2	Tym*#	N. Sakhalin Island	Russia	72	1995, 2003	51.830	143.190	RAS
27	3	Tau ^a	Sea of Okhotsk (Magadan)	Russia	40	1999	59.632	149.099	RAS
28	3	Ola* ^a	Sea of Okhotsk (Magadan)	Russia	45	1999	59.561	151.270	RAS
29	3	Oklan#	Sea of Okhotsk (NE)	Russia	77	1993	62.460	165.330	KNIRO
30	3	Hairusova*#	W. Kamchatka	Russia	100	1990, 1993	57.083	156.750	KNIRO

Table 1. Continued.

Population Reporting				Country						
code	group	Population ^{a,b}	Geographic location	of origin	n	Collection year(s)	Latitude	Longitude	Source ^c	
31	3	Kol* ^a	W. Kamchatka	Russia	48	2003	53.810	155.950	KNIRO	
32	3	Utka* ^a	W. Kamchatka	Russia	35	2002	53.154	156.083	KNIRO	
33	3	Hailula*#	E. Kamchatka	Russia	49	2003	58.200	162.030	KNIRO	
34	3	Ossora*#	E. Kamchatka	Russia	47	1996	59.269	163.142	KNIRO	
35	3	Anadyr*#	N.E. Russia	Russia	112	1991, 2000	64.900	176.217	KNIRO, RAS	
36	3	Kanchalan#	N.E. Russia	Russia	77	1991	65.083	176.400	KIRO	
37	4	Kelly Lake#	Kotzebue Sound	US	94	1991	67.919	-162.350	ADFG	
38	4	Noatak#	Kotzebue Sound	US	95	1991	66.981	-162.506	ADFG	
39	4	Kobuk*#	Kotzebue Sound	US	99	2000	66.921	-160.813	USFWS	
40	4	Inmachuk ^b	Kotzebue Sound	US	99	2005	66.075	-162.713	Kawerak	
41	4	Agiapuk* ^a	S.W. Seward Peninsula	US	100	2005	65.166	-165.684	Kawerak	
42	5	Pilgrim*#	S.W. Seward Peninsula	US	100	2004	65.156	-165.223	Kawerak	
43	5	Snake*#	Norton Sound (S. Seward Peninsula)	US	100	2004	64.499	-165.413	Kawerak	
44	5	Eldorado ^b	Norton Sound (S. Seward Peninsula)	US	96	2004	64.582	-164.949	Kawerak	
45	5	Niukluk ^b	Norton Sound (S. Seward Peninsula)	US	95	2005	64.809	-163.443	Kawerak	
46	5	Kwiniuk ^b	Norton Sound (S. Seward Peninsula)	US	95	2004	64.698	-162.036	Kawerak	
47	5	Koyuk ^b	Norton Sound (S. Seward Peninsula)	US	46	2005	64.927	-161.153	Kawerak	
48	5	Unalakleet*#	Norton Sound	US	96	2005	63.869	-160.788	Kawerak	
49	5	Pikmiktalik*#	Norton Sound	US	100	2004	63.270	-162.601	Kawerak	
50	6	Atchuelinguk*#	Lower Yukon	US	96	1989	61.958	-162.827	USFWS	
51	6	Anvik*#	Lower Yukon	US	74	1989	62.681	-160.203	USFWS	
52	6	Kaltag*#	Lower Yukon	US	50	1992	64.334	-158.724	USFWS	
53	6	Nulato*#	Lower Yukon	US	50	2003	64.707	-158.139	USFWS	
54	7	Jim#	Middle Yukon (Koyukuk)	US	93	2002	66.790	-151.190	USFWS	
55	7	Toklat*#	Middle Yukon (fall)	US	100	1994	64.454	-150.312	USFWS	
56	7	Salcha*#	Middle Yukon (summer)	US	100	1994	64.467	-146.979	USFWS	
57	8	Sheenjek*#	Upper Yukon (Porcupine)	US	99	1988, 1989	66.740	-144.567	USFWS	
58	8	Fishing Branch*#	Upper Yukon (Porcupine)	Canada	99	1992	66.450	-138.583	USFWS	
59	8	Kluane*#	Upper Yukon (White River)	Canada	99	1992	61.876	-139.718	USFWS	
60	8	Teslin*#	Upper Yukon	Canada	99	1992	61.574	-134.900	USFWS	
61	9	Kwethluk*#	Kuskokwim (summer)	US	76	1989	60.814	-161.448	USFWS	
62	9	Kasigluk*#	Kuskokwim (summer)	US	73	1990	60.846	-161.234	USFWS	

Table 1. Continued.

Population Reporting				Country						
code	group	Population ^{a,b}	Geographic location	of origin	n	Collection year(s)	Latitude	Longitude	Source ^c	
63	9	Aniak#	Kuskokwim (summer)	US	94	1992	61.574	-159.490	ADFG	
64	9	Salmon#	Kuskokwim (summer)	US	96	2007	61.063	-159.195	USFWS	
65	9	Holokuk#	Kuskokwim (summer)	US	42	2007	61.537	-158.594	USFWS	
66	9	Oskawalik#	Kuskokwim (summer)	US	58	1994	61.746	-158.180	ADFG	
67	9	George#	Kuskokwim (summer)	US	93	2007	61.898	-157.709	USFWS	
68	9	Kogruklu#	Kuskokwim (summer)	US	59	2007	60.850	-157.850	USFWS	
69	9	Stony (early/late)#	Kuskokwim (summer)	US	151	1994	61.769	-156.593	ADFG	
70	9	Tatlawiksuk#	Kuskokwim (summer)	US	57	2007	61.918	-156.243	USFWS	
71	9	Takotna#	Kuskokwim (summer)	US	92	2007	62.963	-155.598	USFWS	
72	10	Big River#	Kuskokwim (fall)	US	96	2008	62.606	-155.013	ADFG	
73	10	Windy Fork#	Kuskokwim (fall)	US	96	2008	62.760	-154.631	ADFG	
74	10	South Fork#	Kuskokwim (fall)	US	96	2008	63.088	-154.642	ADFG	
75	9	Kanektok*#	Kuskokwim Bay	US	75	1989	59.746	-161.931	USFWS	
76	9	Goodnews*#	W. Bristol Bay	US	100	1989	59.103	-161.561	USFWS	
77	9	Nushagak*#	W. Bristol Bay	US	74	1988	58.799	-158.633	USFWS	
78	11	Big Creek*#	E. Bristol Bay/N. Alaska Peninsula	US	95	1988, 2000	58.292	-157.532	USFWS	
79	11	Gertrude*#	E. Bristol Bay/N. Alaska Peninsula	US	100	1987, 1999	58.172	-156.211	USFWS	
80	11	Meshik*#	E. Bristol Bay/N. Alaska Peninsula	US	75	1989	56.809	-158.663	USFWS	
81	12	Frosty*#	N. Alaska Peninsula	US	97	2000	55.193	-162.860	USFWS	
82	12	Ivanof#	S.W. Alaska Peninsula	US	87	1993	55.897	-159.461	ADFG	
83	12	Alagogshak ^b	S.E. Alaska Peninsula	US	93	1993	58.018	-155.042	ADFG	
84	12	Big River ^b	S.E. Alaska Peninsula	US	84	1993	58.610	-153.903	ADFG	
85	13	Sturgeon#	Kodiak Island	US	66	1992	57.541	-154.527	ADFG	
86	13	Kizhuyak*#	Kodiak Island	US	48	1989	57.738	-152.874	ADFG	
87	13	American ^b	Kodiak Island	US	45	1995	57.648	-152.510	ADFG	
88	14	Little Susitna*#	Cook Inlet	US	39	1990	61.251	-150.288	ABL	
89	14	Olsen*#	Prince William Sound	US	92	1992, 1997	60.760	-146.174	ABL	
90	14	Alsek*#	Alsek River	US	100	2000	59.128	-138.621	ABL	
91	14	East Alsek*#	Alsek River	US	47	2006	59.106	-138.518	UAF	
92	15	Herman Creek*#	N. Southeast Alaska	US	191	1987, 1990, 2008	59.415	-136.100	ABL	
93	15	Wells Bridge ^b	N. Southeast Alaska	US	90	2008	59.415	-135.931	ABL	
94	15	Taku*#	N. Southeast Alaska	US	45	2000	58.426	-133.977	ABL	
95	15	Macaulay Hatchery ^b	N. Southeast Alaska	US	78	1998	58.326	-134.464	ABL	

Table 1. Continued.

Population Reporting				Country						
code	group	Population ^{a,b}	Geographic location	of origin	n	Collection year(s)	Latitude	Longitude	Source ^c	
96	15	Greens Creek*#	N. Southeast Alaska (Admiralty Is.)	US	100	1995	58.099	-134.760	ABL	
97	15	Long Bay#	N. Southeast Alaska (Chichagof Is.)	US	96	1992	57.856	-135.656	ABL	
98	15	Black Bay#	N. Southeast Alaska (Chichagof Is.)	US	90	1992	57.717	-136.120	ABL	
99	15	Lovers Cove#	N. Southeast Alaska (Baranof Is.)	US	48	1987	56.393	-134.716	ABL	
100	16	Cruz Cove#	W. Prince of Wales Island	US	50	1998	55.541	-133.324	ABL	
101	16	Port Real Marina#	W. Prince of Wales Island	US	45	1988	55.412	-133.521	ABL	
102	16	Coco Harbor	W. Prince of Wales Island	US	48	1998	55.046	-133.084	ABL	
103	16	Karta*#	E. Prince of Wales Island	US	48	1986	55.564	-132.573	ABL	
104	16	Old Tom*#	E. Prince of Wales Island	US	99	1986, 1988	55.397	-132.404	ABL	
105	16	Lagoon ^b	E. Prince of Wales Island	US	48	1986	55.231	-132.399	ABL	
106	16	Disappearance ^b	E. Prince of Wales Island	US	96	1998	55.131	-132.333	ABL	
107	16	Aiken#	E. Prince of Wales Island	US	46	1986	55.120	-132.204	ABL	
108	16	Eulachon#	S. Southeast Alaska	US	50	1986	56.086	-131.093	ABL	
109	16	Grant#	S. Southeast Alaska	US	50	1986	56.039	-131.213	ABL	
110	16	Herman River*#	S. Southeast Alaska	US	40	1986	55.997	-131.299	ABL	
111	16	Portage*#	S. Southeast Alaska	US	100	1986, 1988	55.765	-131.070	ABL	
112	16	Blossom*#	S. Southeast Alaska	US	50	1986	55.403	-130.607	ABL	
113	16	Wilson*#	S. Southeast Alaska	US	40	1986	55.396	-130.609	ABL	
114	16	Marten*#	S. Southeast Alaska	US	50	1986	55.158	-130.532	ABL	
115	16	Toon ^b	N. British Columbia (North Coast)	Canada	49	1988	54.517	-129.983	DFO	
116	17	Deena#	N. British Columbia (Skidgate Channel, Haida Gwaii)	Canada	48	1989	53.150	-132.133	DFO	
117	17	Tasu*#	N. British Columbia (W. Haida Gwaii)	Canada	48	1989	52.867	-132.083	DFO	
118	17	Bag Harbour*#	N. British Columbia (E. Haida Gwaii)	Canada	50	1989	52.343	-131.372	DFO	
119	17	Neekas*#	Central British Columbia	Canada	50	1989	52.467	-128.167	DFO	
120	17	Klownik*#	Central British Columbia (Bella Coola River)	Canada	49	1989	52.383	-126.750	DFO	
121	18	Nitinat ^b	S. British Columbia (W. Vancouver Is.)	Canada	94	2006	48.821	-124.682	DFO	
122	18	Norrish ^b	S. British Columbia (Fraser River)	Canada	95	2006	49.233	-122.133	DFO	
123	18	Grant*#	Washington (N. Puget Sound, Stillaguamish River, fall)	US	99	1998	48.271	-122.018	WDFW	
124	18	Quilcene*#	Washington (Puget Sound, Hood Canal, summer)	US	40	1997	47.819	-122.863	WDFW	
125	18	Johns*#	Washington (S. Puget Sound, summer)	US	100	2003	47.243	-123.042	WDFW	
126	18	Kennedy*#	Washington (S. Puget Sound, fall)	US	93	1996	47.095	-123.090	WDFW	

^aMicrosatellite data for 3 loci (*Omm1070*, *One111*, *Ots3*) were used from the DFO baseline.

^bMicrosatellite data for 12 loci (*Oki100*, *Omm1070*, *Omy1011*, *One101*, *One102*, *One104*, *One111*, *One114*, *Ots3*, *Ots103*, *Ots68*, *Ssa419*) were used from the DFO baseline.

^cABL=Auke Bay Laboratories, NOAA; ADFG=Alaska Department of Fish and Game; DFO=Fisheries and Oceans Canada; HNFRI=Hokkaido National Fisheries Research Institute; HRFRI=Heilongjiang River Fisheries Research Institute, Chinese Academy of Fishery Sciences; KNIRO=Kamchatka Research Institute of Fisheries and Oceanography; Kawerak=Kawerak Inc., Nome, Alaska; Kitasato=Kitasato University; NSRC=National Salmon Research Center; RAS=Russian Academy of Sciences; UAF=University of Alaska Fairbanks; USFWS=U.S. Fish and Wildlife Service; WDFW=Washington Department of Fish and Wildlife.

Table 2. SNPs surveyed in chum salmon samples, GenBank accession numbers, primer sequences for the T_m -shift assay, PCR annealing temperature, MgCl₂ concentration, and original SNP reference. Bold sequences are the GC-rich tails added to the 5'-ends that generate differentiating melting curves for each allele. The +N at the 3'-ends are the locked nucleic acids. To eliminate a paralog amplicon that forms with the CLOCK T_m -shift primers alone, a low concentration of the TILLING primers external of the T_m -shift primers was used in the PCR process.

SNP site	Gene name	Accession number	Primer specificity	Primer sequence, 5' to 3'	Anneal temperature (°C)	MgCl ₂ (mM)	Reference ^a
Oke_Cr30	Mitochondrial, control region	AP010773	Haplotype 1	GCGGGCCGCACATTTGTAAATGC +T	62	1.5	1
			Haplotype 2	GCGGGCAGGGCGGCCGCACATTTGTAAATGC +C			
			Reverse primer	ACATAATATGTAATATTATAATAGTGTAGTATAACATTGG			
Oke_Cr231	Mitochondrial, control region	AP010773	Haplotype 1	GCGGGCCAACTAAGTTGTCTGCAAC +T	66	1.5	1
			Haplotype 2	GCGGGCAGGGCGGCCAACTAAGTTGTCTGCAAC +C			
			Reverse primer	CCCGTGTAGTTGGAGGTTTATTG			
Oke_Cr386	Mitochondrial, control region	AP010773	Haplotype 1	GCGGGCAGGGACAGAAATCGTATTAG +T	68	1.5	1
			Haplotype 2	GCGGGCAGGGCGGCCGGACAGAAATCGTATTAG +G			
			Reverse primer	ACTTAGGAACCAAATGCCAGGAAT			
MT5	Mitochondrial, ATPase	AP010773	Haplotype 1	GCGGGCAGGGCGGCCGTCATCTCTTGCCTGA +G	66	3	2
			Haplotype 2	GCGGGCGGTCATCTCTTGCCTGA +A			
			Reverse primer	GTTTCGATGATAATCAGTACAGGGATTAGT			
MT12	Mitochondrial, COX2	AP010773	Haplotype 1	GCGGGCAGGGCGGCCCCCTCCCTCCGGAT +C	66	1.5	2
			Haplotype 2	GCGGGCCCCCTCCCTCCGAAT +T			
			Reverse primer	TAATAGTAAGGTGCGGGTCGTTAATTTCA			
MT18	Mitochondrial, ND4	AP010773	Haplotype 1	GCGGGCAGGGCGGCCCTGATTACTCCCCCTTAT +G	65	1.5	2
			Haplotype 2	GCGGGCGCTGATTACTCCCCCTTAT +A			
			Reverse primer	TTAATGGTTCAGGGGATAGGTGATT			
MT21	Mitochondrial, ND4	AP010773	Haplotype 1	GCGGGCACTAATCGCCTACTCTTCAGT +A	65	1.5	2
			Haplotype 2	GCGGGCAGGGCGGCCAATCGCCTACTCTTCAGT +G			
			Reverse primer	AATTAAAATACCCCTGCAACCA			
MT27	Mitochondrial, ND5	AP010773	Haplotype 1	GCGGGCAGGGCGGCCGCGGGCATCTTCCT +G	65	1.5	2
			Haplotype 2	GCGGGCGCGGGCATCTTCCT +A			
			Reverse primer	GGCTGCTTGGTTATTTTCTATAAGAGG			
VTI	Vasotocin I	AB164428	Haplotype 1	GCGGGCAGGGCGGCTGCTGCTGGCCAC +G	61	1.5	3
			Haplotype 2	GCGGGCCCGTCTGCTGGCCAC +T			
			Reverse primer	GAAATGAAAGCATCCATTGTTAATCC			
RH1OP	RH-Opisin	DQ025627	Haplotype 1	GCGGGCAGGGCGGCTGGTAATCGGAGGCTT +C	62	1.5	3
			Haplotype 2	GCGGGCATGGTAATCGGAGGCTT +T			
			Reverse primer	CGAAATAGCCATGCATGGAGGT			
SP	Serpins	DQ025636	Haplotype 1	GCGGGCGTTAATCCAAGAAGTACCTT +A	64	1.5	3
			Haplotype 2	GCGGGCAGGGCGGCTTAATCCAAGAAGTACCTT +T			
			Reverse primer	CTAACCTACTAAATTGAGCAAAGACCTA			

Table 2. Continued.

SNP site	Gene name	Accession number	Primer specificity	Primer sequence, 5' to 3'	Anneal temperature (°C)	MgCl ₂ (mM)	Reference ^a
IN1	Insulin	X13559	Haplotype 1	GCGGGCTGTTCAACAAAAACGATAA+G	60	1.5	5
			Haplotype 2	GCGGGCAGGGCGGCTGTTCAACAAAAACGATAA+C			
			Reverse primer	GATGTAAACTGCAACTAGAATATGA			
IN2	Insulin	X13559	Haplotype 1	GCGGGCGGATATGGTTTATTTAGAACATA+C	63	1.5	5
			Haplotype 2	GCGGGCAGGGCGGCGGATATGGTTTATTTAGAACATA+G			
			Reverse primer	CTGACGACCCATATCCTGTTGA			
ISO1	Isotocin II	AB164431	Haplotype 1	GCGGGCAGGGCGGCAGAATTGACAATGAACCATT+G	64	1.5	3
			Haplotype 2	GCGGGCGAGAATTGACAATGAACCATT+A			
			Reverse primer	CTTATCGACATTCTTGCTCCCTTT			
ISOP	Isotocin II	AB164431	Haplotype 1	GCGGGCTCTCCGAGAGTGACACG+T	61	1.5	3
			Haplotype 2	GCGGGCAGGGCGGCCTCCGAGAGTGACACG+G			
			Reverse primer	TAAGCGAGGCTCATTAAATACACACCT			
VR1	Vitellogenin receptor	DQ924528	Haplotype 1	GCGGGCGTGATTGTGTGAACCTCCAAT+T	62	1.5	3
			Haplotype 2	GCGGGCAGGGCGGCTGATTGTGTGAACCTCCAAT+G			
			Reverse primer	ACAGTCTGCAAGTAAACGTAAGGTGATA			
VR2	Vitellogenin receptor	DQ924528	Haplotype 1	GCGGGCAGGGCGGCTTTGGACACACTGTGTGA+G	61	1.5	3
			Haplotype 2	GCGGGCACTTTGGACACACTGTGAGT+A			
			Reverse primer	TGTTTGTCAATTAGTTGTGTGAATGATG			
VR3	Vitellogenin receptor	DQ924528	Haplotype 1	GCGGGCTTAGGCAGTACTGTCTTAAAAT+A	66	3	3
			Haplotype 2	GCGGGCAGGGCGGCTTAGGCAGTACTGTCTTAAAAT+G			
			Reverse primer	AAGAATGTGCTTCTGGAGATAATGTTC			
ER	Estrogen receptor	EU414520	Haplotype 1	GCGGGCGCCAAGCTCATGCAAA+A	63	1.5	3
			Haplotype 2	GCGGGCAGGGCGGCCCAAGCTCATGCAAA+G			
			Reverse primer	TAACACCCAAAGCCAGCGCTA			
PL	Prolactin	EU414521	Forward primer	CCAGTGTTTAGAACGCTACGCC	59	3	3
			Reverse primer	ACCAATGTTACAGCATTGCTAAA			
CLOCK	Clock	AF494062	Forward TILLING primer	CCCAAAGAGCCTCCTGTGTA	66	1.5	4
			Reverse TILLING primer	GAACCTCAAACGGCAGGTAA			
			Haplotype 1	GCGGGCGTTAATACAATGCTTTGTAT+T	64		5
			Haplotype 2	GCGGGCAGGGCGGCTTAATACAATGCTTTGTAT+G			
			Reverse primer	CAGCCTTTAAGCAGTAATAACAC			
PER	Period	JQ606803	Haplotype 1	GCGGGCAGGGCGGCCAGTTCAGGGCGTACTG+G	66	1.5	5
			Haplotype 2	GCGGGCCAGTTCAGGGCGTACTG+A			
			Reverse primer	AAGGGCAAAGGTCGCTCCAGCA			
RFC2	Genomic sequence	DQ025649.1	Haplotype 1	GCGGGCAGGGCGGCTCAAAATGCAGCTCCT+G	63	1.5	6
			Haplotype 2	GCGGGCTCTCAAAATGCAGCTCCT+A			
			Reverse primer	AATGTTACACTGGAATACTTAAGTGC			

^aSources are as follows: (1) Sato et al. (2001), (2) Garvin et al. (2010b), (3) Garvin and Gharrett (2010), (4) Garvin and Gharrett (2007), (5) this report, and (6) Smith et al. (2005a).

Table 3. Primer sequences used to determine the linkage phase of the isotocin II double-heterozygote haplotypes. The +N at the 3'-ends are the locked nucleic acids. Annealing temperature is 62°C, MgCl₂ concentration is 3.0 mM.

Haplotype	Primer	
	specificity	Primer sequence, 5' to 3'
AB	Forward	TTAAGTGGTTGTCAGGGGT+A
	Reverse	TCCCTTTTACAGGAGGAAGA+T
Ab	Forward	TTAAGTGGTTGTCAGGGGT+A
	Reverse	CCCTTTTACAGGAGGAAGA+C
aB	Forward	TTAAGTGGTTGTCAGGGGT+C
	Reverse	TCCCTTTTACAGGAGGAAGA+T
ab	Forward	TTAAGTGGTTGTCAGGGGT+C
	Reverse	CCCTTTTACAGGAGGAAGA+C

Table 4. PCR thermocycling protocols used for SNPs surveyed in chum salmon.

	Annealing temperature (°C)	Time	Number of cycles
PER			
initial denaturation	94	2 min	1
denature	94	20 sec	45
anneal	66	1 min	
IS (linkage phase protocol)			
initial denaturation	94	2 min	1
denature	94	20 sec	45
anneal	62	1 min	
elongate	72	1 min	
CLOCK			
initial denaturation	94	2 min	1
denature	94	30 sec	5
anneal	66	1 min	
elongate	72	2 min	
denature	94	20 sec	40
anneal	64	1 min	
elongate	72	30 sec	
All other SNPs			
initial denaturation	94	2 min	1
denature	94	20 sec	45
anneal	see Table 2	1 min	
elongate	72	30 sec	

Table 5. PCR multiplex panels and primer sequences used for microsatellite loci surveyed in chum salmon.

Locus	Panels (fluorescent dye on 5'-end of forward primer)	Primer specificity	Primer sequence, 5' to 3' ^a	Primer reference
<i>Oki100</i> ^b	4 (NED)	Forward	GGTGTTTTAATGTTGTTTCCT	Beacham et al. (2008)
	B (NED)	Reverse	GTTTCCAGAGTAGTCATCTCTG	
<i>Omm1070</i>	1b (PET), 5 (VIC)	Forward	GACAGGTTGTGTCGAATGGA	Rexroad et al. 2001
	A (VIC)	Reverse	GTTTGGTGGGATTTCAGTGTGTAAAC	
<i>Omy1011</i>	3c (PET)	Forward	AACTTGCTATGTGAATGTGC	Spies et al. 2005
	A (PET)	Reverse	GTTTGACAAAAGTGACTGGTTGGT	
<i>One101</i>	1b (VIC)	Forward	AAATGACTGAAATGTTGAGAGC	Olsen et al. (2000)
	B (VIC)	Reverse	GTTTGGATGGATTGATGAATGG	
<i>One102</i>	1b (NED)	Forward	CATGGAGAAAAGACCAATCA	Olsen et al. (2000)
	A (NED)	Reverse	GTTTCACTGCCCTACAACAGAAG	
<i>One104</i>	2d (PET)	Forward	GCTACTACAATCCTAGTCTGTGAT	Olsen et al. (2000)
	C (PET)	Reverse	GTTTGCCATCTTCTTCAGTGGCTGTA	
<i>One111</i>	1b (FAM), 5 (FAM)	Forward	ATGACCAAGGAGCTTCTGC	Olsen et al. (2000)
	B (FAM)	Reverse	GTTTATCCAGGTAAGACAAGGTATCC	
<i>One114</i>	3c (NED)	Forward	TCATTAATCTAGGCTTGTGAGC	Olsen et al. (2000)
	C (NED)	Reverse	GTTTGCAGGTAAGACAAGGTATCC	
<i>Ots3</i>	4 (PET), 5 (PET)	Forward	TGTCACTCACACTCTTTCAGGAG	Greig and Banks (1999)
	B (PET)	Reverse	GAGAGTGCTGTCCAAAGGTGA	
<i>Ots103</i> ^c	2d (VIC)	Forward	AGGCTCTGGGTCCGTG	Beacham et al. (1998); Small et al. (1998)
	C (VIC)	Reverse	GTTTGATATGGTGTGATAGCTGG	
<i>OtsG68</i>	3c (FAM)	Forward	TATGAACTGCAGCTTGTATGTTAGT	Williamson et al. (2002)
	C (FAM)	Reverse	GTTTCATGTCGGCTGCTCAATGTA	
<i>Ssa419</i>	2d (FAM)	Forward	GGTCGTATCGCGTTTCAGGA	Cairney et al. (2000)
	B (PET)	Reverse	GTTTGCTGCAATAAAGAGATGCTTGTT	

^aWe followed the DFO laboratory protocol by adding GTT to the 5'-end of the reverse primers, except for *Ots3*.

^bLocus amplified separately for Panel B, then combined post-PCR with Panel B multiplex.

^cForward primer in both references; reverse primer in Beacham et al. (1998).

Table 6. PCR thermocycling protocols used for microsatellite loci surveyed in chum salmon.

	Annealing temperature (°C)	Time	Number of cycles
Panels 1b, 2d, 5, B, C, <i>Oki100</i>			
initial denaturation	95	15 min	1
denature	94	30 sec	34
anneal	60	1.5 min	
elongate	72	1 min	
final elongate	60	30 min	1
Panels 3c, 4			
initial denaturation	95	15 min	1
denature	94	30 sec	35
anneal	60	1.5 min	
elongate	72	1 min	
final elongate	60	30 min	1
Panel A			
initial denaturation	95	15 min	1
denature	94	30 sec	16
anneal	60 (-0.5 per cycle)	1.5 min	
elongate	72	1 min	
denature	94	30 sec	24
anneal	52	1.5 min	
elongate	72	1 min	
final elongate	60	30 min	1

Table 7. Mitochondrial SNP haplotypes; nucleotide at 3'-end of primer (SNP site) and haplotype letter designation in parentheses. Composite haplotypes with (*) seen only in high seas samples.

Primer tail	Oke_Cr30	Oke_Cr231	Oke_Cr386	MT5	MT12	MT18	MT21	MT27
Short	T (A)	T (A)	del (A)	A (B)	AT (B)	A (B)	A (A)	A (B)
Long	C (B)	C (B)	G (B)	G (A)	GC (A)	G (A)	G (B)	G (A)
mtDNA region	control	control	control	A8/A6/ COIII/ ND3	COI/COII/ A8	ND3/ND4	ND3/ND4	ND5/ND6
Restriction endonuclease				Dde I	Mbo I	Mbo I	Sau 96I	Ase I
Haplotype "A"				Cut	Cut	Cut	No Cut	No Cut
Composite haplotype								
1	A	A	A	A	A	A	A	A
2	B	B	B	B	B	B	A	B
3	A	A	A	B	A	A	A	A
4	A	A	A	A	B	A	A	A
5	B	A	B	B	B	B	A	B
6	A	A	A	B	B	A	A	A
8	A	A	A	A	B	A	A	B
9	A	A	A	B	B	A	A	B
10	A	A	A	A	B	A	B	A
12	A	A	B	B	B	A	A	B
13	A	B	A	B	B	A	A	B
16	A	B	B	B	B	B	A	B
19	A	A	A	A	B	A	B	B
23	A	B	A	A	A	A	A	A
24	A	A	B	B	B	B	A	B
25	B	B	B	B	B	B	A	A
26	A	A	B	B	B	B	B	B
27	A	B	A	A	B	A	A	A
28	A	B	B	B	B	A	A	B
29	A	B	A	B	B	A	A	A
30*	A	A	A	A	B	B	B	A
31*	A	A	A	A	B	B	A	A
41*	A	A	A	B	B	B	A	B
43*	B	A	A	B	B	B	A	B

Table 8. Nuclear SNP haplotypes and allele designations. The nucleotide at the SNP site on the 3'-end of the primer is followed by the haplotype or allele designation in parentheses. The haplotypes of linked SNPs are shown in letter and numeric allele designations.

SNP	Primer tails		Linked
	Short	Long	
CL	T (78)	del (79)	
ER	A (50)	G (60)	
IN1	C (a)	G (A)	
IN2	C (B)	G (b)	
IN linked			AB (36) aB (37) Ab (38)
ISOP	T (A)	G (a)	
ISO1	A (B)	G (b)	
IS linked			Ab (25) aB (35) AB (45) ab (55)
PER	A (82)	G (83)	
PL	del (70)	in (80)	
RF	G (51)	A (52)	
RH	T (43)	C (44)	
SP	A (41)	T (42)	
VR1	T (A)	G (a)	
VR2	A (b)	G (B)	
VR3	A (C)	G (c)	
VR linked			ABC (51) AbC (52) aBC (53) ABc (54)
VT	T (33)	G (34)	

Table 9. Concordance of microsatellite allele designations between the ABL laboratory and the UAF and DFO laboratories (A.) in a preliminary blind comparison and (B.) after resolving differences. Net alleles is the sample size (i.e., 2n), discrepancies indicates the number of differences between allele designations, and concordance is the proportion of identical allele designations. Instrumentation: ABL from ABI 3130xl, UAF from LI-COR, and DFO from ABI 3730.

Locus	A. Blind test						B. After differences resolved			
	ABL net alleles		Disagree		Concordance		Disagree		Concordance	
	Scored with:		Allele designation		UAF	DFO	Allele designation		UAF	DFO
<i>Oki100</i>	UAF	DFO	UAF	DFO	UAF	DFO	UAF	DFO	UAF	DFO
<i>Oki100</i>	168	170	8	6	0.952	0.965	0	0	1	1
<i>Omm1070</i>	n/a	184	n/a	0	n/a	1	n/a	0	n/a	1
<i>Omy1011</i>	182	178	7	0	0.962	1	0	0	1	1
<i>One101</i>	185	183	1	0	0.995	1	0	0	1	1
<i>One102</i>	180	180	8	12	0.956	0.933	1	2	0.994	0.989
<i>One104</i>	177	166	7	0	0.960	1	0	0	1	1
<i>One111^a</i>	n/a	180	n/a	n/a	n/a	n/a ^b	n/a	0	n/a	1
<i>One114</i>	176	182	1	0	0.994	1	0	0	1	1
<i>Ots3</i>	n/a	180	n/a	0	n/a	1	n/a	0	n/a	1
<i>Ots103</i>	184	184	6	2	0.967	0.989	0	0	1	1
<i>OtsG68</i>	180	178	2	0	0.989	1	0	0	1	1
<i>Ssa419</i>	184	184	0	0	1	1	0	0	1	1

^aThe DFO and ABL datasets differ by one allele for alleles larger than 378 bp (ABL designation), likely a result of differences in size standards, instrumentation, or both. Ten such alleles were observed, but when alleles >378 bp were pooled, concordance was very high.

^bDFO genotypes for *One111* were used to set up compatible scoring on ABL's instrument, thus there is no blind test for *One111*.

Table 10. Comparison of allele frequency estimates between the UAF-ABL laboratories and the DFO Molecular Genetics Laboratory for 9-12 microsatellite loci. *n* UAF-ABL is the sample size examined in the UAF-ABL laboratories, *n* DFO is the sample size analyzed in the DFO laboratory. *G* is the log-likelihood ratio statistic for the test of homogeneity, *df* is the degrees of freedom for the test, and *P* is the probability of homogeneity. Probabilities are also combined across loci for each population and across overlapping, but not mostly coincident samples for each locus.

Population (code)		Locus											Combined probability	
		<i>Oki100</i>	<i>Omm1070</i>	<i>Omy1011</i>	<i>One101</i>	<i>One102</i>	<i>One104</i>	<i>One111</i>	<i>One114</i>	<i>Ots3</i>	<i>Ots103</i>	<i>OtsG68</i>		<i>Ssa419</i>
Mostly coincident samples														
Suifen (17)	n UAF-ABL	22	23	22	22	23	22	23	23	23	23	23	23	23
	<i>n</i> DFO	23	23	23	23	23	21	23	23	23	23	23	23	23
	<i>G</i>	9.80	0.00	7.46	12.94	8.86	19.12	4.20	9.86	0.00	15.02	18.30	7.88	
	<i>df</i>	12	16	17	14	14	24	20	15	8	17	20	10	
	<i>P</i>	0.633	1.000	0.977	0.531	0.840	0.746	1.000	0.828	1.000	0.594	0.567	0.640	1.000
Udarnitsa (23)	n UAF-ABL	48	36	48	48	48	48	36	48	34	48	48	48	
	<i>n</i> DFO	50	50	50	50	50	49	47	48	50	50	49	49	
	<i>G</i>	0.16	6.28	3.02	1.90	1.06	0.68	18.33	0.81	3.03	0.56	2.78	0.39	
	<i>df</i>	20	25	19	14	18	19	37	21	13	35	32	14	
	<i>P</i>	1.000	1.000	1.000	1.000	1.000	1.000	0.996	1.000	0.998	1.000	1.000	1.000	1.000
Oklan (29)	n UAF-ABL	76	76	76	76	76	76	76	76	76	76	76	76	
	<i>n</i> DFO	74	73	72	76	76	76	76	76	76	76	74	76	
	<i>G</i>	0.37	0.98	0.60	0.26	0.00	0.00	5.04	0.00	0.00	0.00	0.11	0.00	
	<i>df</i>	17	28	25	14	16	23	59	19	7	24	26	13	
	<i>P</i>	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Kanchalan (36)	n UAF-ABL	77	76	77	77	77	77	77	77	77	77	77	77	
	<i>n</i> DFO	77	79	77	79	79	79	79	78	79	79	78	78	
	<i>G</i>	0.36	1.05	2.95	5.95	0.35	0.93	8.69	0.81	0.25	0.90	0.75	0.15	
	<i>df</i>	19	29	24	26	14	20	59	25	12	28	30	11	
	<i>P</i>	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Kelly Lake (37)	n UAF-ABL	93	92	93	93	93	93	93	93	93	92	93	93	
	<i>n</i> DFO	93	95	94	93	94	92	92	94	93	92	93	91	
	<i>G</i>	1.65	0.29	0.22	0.27	0.16	0.32	4.20	0.16	0.10	0.39	0.69	0.63	
	<i>df</i>	11	24	18	18	13	16	39	18	9	21	26	11	
	<i>P</i>	0.999	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

Table 10. Continued.

Population		Locus											Combined probability	
		<i>Oki100</i>	<i>Omm1070</i>	<i>Omy1011</i>	<i>One101</i>	<i>One102</i>	<i>One104</i>	<i>One111</i>	<i>One114</i>	<i>Ots3</i>	<i>Ots103</i>	<i>OtsG68</i>		<i>Ssa419</i>
Atchuelinguk (50)	n UAF-ABL	94	89	94	94	93	94	88	94	93	94	94	94	1.000
	n DFO	70	28	58	94	98	88	91	83	96	33	87	84	
	<i>G</i>	10.59	27.79	8.61	5.02	2.41	1.51	26.00	8.33	10.45	25.39	6.41	4.22	
	df	18	31	22	23	13	19	58	23	12	29	31	12	
	<i>P</i>	0.911	0.632	0.995	1.000	0.999	1.000	1.000	0.998	0.577	0.658	1.000	0.979	
Kwethluk (61)	n UAF-ABL	76	75	73	76	76	76	74	76	75	76	76	76	1.000
	n DFO	75	74	74	75	75	74	74	75	74	74	69	74	
	<i>G</i>	2.06	5.03	3.93	0.09	0.24	0.19	2.93	1.64	0.41	0.29	2.32	0.49	
	df	18	32	23	24	13	21	49	20	10	30	25	11	
	<i>P</i>	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
Kasigluk (62)	n UAF-ABL	73	73	73	72	73	73	72	73	73	73	73	73	1.000
	n DFO	72	67	70	68	69	67	68	69	70	72	69	67	
	<i>G</i>	0.12	2.08	0.44	2.95	0.51	1.49	3.40	0.68	0.18	0.12	0.53	0.27	
	df	18	30	20	22	16	20	55	21	10	28	27	10	
	<i>P</i>	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
Aniak (63)	n UAF-ABL	88	94	94	94	93	93	94	93	94	93	93	94	1.000
	n DFO	89	84	86	85	87	86	81	82	88	86	86	76	
	<i>G</i>	2.61	4.88	5.25	2.87	3.36	2.61	20.16	2.57	1.08	7.47	3.32	3.73	
	df	20	29	21	24	16	23	65	24	12	34	32	12	
	<i>P</i>	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.988	
Gertrude (79)	n UAF-ABL	100	94	99	99	99	100	92	99	92	99	100	100	1.000
	n DFO	99	96	99	97	97	99	96	98	98	99	87	98	
	<i>G</i>	0.06	1.26	2.52	0.43	0.17	0.07	18.89	0.57	0.45	1.91	4.02	0.28	
	df	16	31	21	21	17	23	58	21	14	30	35	9	
	<i>P</i>	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	

Table 10. Continued.

Population		Locus												Combined probability
		<i>Oki100</i>	<i>Omm1070</i>	<i>Omy1011</i>	<i>One101</i>	<i>One102</i>	<i>One104</i>	<i>One111</i>	<i>One114</i>	<i>Ots3</i>	<i>Ots103</i>	<i>OtsG68</i>	<i>Ssa419</i>	
Meshik (80)	n UAF-ABL	75	74	74	74	73	75	74	75	72	75	75	75	1.000
	n DFO	72	67	69	59	69	46	54	54	70	74	67	53	
	<i>G</i>	1.13	3.66	2.08	2.15	0.91	8.78	16.23	8.75	2.99	0.37	7.74	3.05	
	df	16	29	20	19	16	23	43	19	11	29	29	9	
	<i>P</i>	1.000	1.000	1.000	1.000	1.000	0.997	1.000	0.977	0.991	1.000	1.000	0.962	
Sturgeon (85)	n UAF-ABL	65	65	64	62	65	64	65	63	64	65	65	65	1.000
	n DFO	71	55	69	70	63	41	71	70	70	69	70	70	
	<i>G</i>	4.28	4.84	0.20	2.99	3.43	11.39	3.79	1.97	1.65	2.70	2.36	9.90	
	df	12	21	13	8	16	29	24	15	7	25	21	11	
	<i>P</i>	0.978	1.000	1.000	0.935	1.000	0.999	1.000	1.000	0.977	1.000	1.000	0.540	
Overlapping samples														
Teshio (7)	n UAF-ABL	75	74	74	79	73	78	79	78	79	78	78	79	1.000
	n DFO	98	35	82	99	99	96	99	99	98	86	100	97	
	<i>G</i>	2.47	25.28	4.89	7.37	6.90	8.44	44.19	6.01	18.72	8.31	7.04	3.24	
	df	18	32	24	18	26	27	63	26	21	37	37	18	
	<i>P</i>	1.000	0.794	1.000	0.987	1.000	1.000	0.965	1.000	0.603	1.000	1.000	1.000	
Tokushibetsu (9)	n UAF-ABL	37	38	39	40	40	40	40	40	40	40	40	40	1.000
	n DFO	148	147	150	144	158	136	149	158	156	147	158	158	
	<i>G</i>	18.17	22.90	38.28	16.55	10.66	14.03	71.96	13.86	11.90	33.30	29.39	12.31	
	df	20	34	34	24	27	26	76	24	15	39	38	19	
	<i>P</i>	0.576	0.926	0.281	0.867	0.998	0.973	0.610	0.950	0.686	0.727	0.840	0.872	
Ryazanovka (15)	n UAF-ABL	63	---	62	62	63	63	---	62	---	62	62	63	0.995
	n DFO	49	---	49	46	48	49	---	48	---	50	48	49	
	<i>G</i>	7.91	---	10.55	8.06	6.60	12.90	---	27.73	---	15.45	16.10	24.63	
	df	15	---	21	16	21	23	---	25	---	27	28	19	
	<i>P</i>	0.927	---	0.971	0.947	0.999	0.954	---	0.321	---	0.963	0.964	0.173	

Table 10. Continued.

Population		Locus											Combined probability	
		<i>Oki100</i>	<i>Omm1070</i>	<i>Omy1011</i>	<i>One101</i>	<i>One102</i>	<i>One104</i>	<i>One111</i>	<i>One114</i>	<i>Ots3</i>	<i>Ots103</i>	<i>OtsG68</i>		<i>Ssa419</i>
Tym (26)	n UAF-ABL	71	53	71	71	71	69	53	71	53	70	71	71	1.000
	n DFO	55	52	55	54	54	53	54	55	55	51	55	54	
	<i>G</i>	6.52	23.26	11.24	9.78	6.73	7.22	48.54	7.46	9.11	12.06	12.89	6.56	
	df	22	32	22	23	18	24	67	27	15	35	33	15	
	<i>P</i>	0.999	0.870	0.971	0.993	0.992	1.000	0.956	1.000	0.872	1.000	0.999	0.969	
Hairusova (30)	n UAF-ABL	100	90	99	100	100	100	91	100	91	99	100	100	1.000
	n DFO	180	154	172	173	156	173	158	170	182	181	154	158	
	<i>G</i>	8.41	10.17	6.31	9.87	8.56	13.18	65.71	9.80	12.31	16.74	16.09	14.41	
	df	20	34	26	25	19	25	102	26	18	35	36	20	
	<i>P</i>	0.989	1.000	1.000	0.997	0.980	0.974	0.998	0.998	0.831	0.996	0.998	0.809	
Ossora (34)	n UAF-ABL	46	47	46	46	46	46	47	46	47	46	46	46	1.000
	n DFO	137	135	134	134	131	135	129	133	132	134	132	132	
	<i>G</i>	13.06	17.82	18.67	14.58	8.29	22.42	88.59	24.83	10.21	26.38	17.46	14.01	
	df	23	35	19	29	20	25	96	29	16	38	38	15	
	<i>P</i>	0.951	0.993	0.478	0.988	0.990	0.612	0.692	0.687	0.855	0.922	0.998	0.525	
Anadyr (35)	n UAF-ABL	112	79	111	111	112	111	77	112	78	112	112	112	1.000
	n DFO	93	91	91	90	91	90	90	92	93	93	92	90	
	<i>G</i>	12.57	4.15	5.23	7.03	5.62	9.83	18.70	6.29	2.86	5.80	12.39	4.33	
	df	19	28	21	24	15	25	65	24	13	31	33	12	
	<i>P</i>	0.860	1.000	1.000	1.000	0.985	0.997	1.000	1.000	0.998	1.000	1.000	0.977	
Noatak (38)	n UAF-ABL	87	93	91	94	93	93	94	91	94	92	91	94	1.000
	n DFO	47	46	47	45	46	46	43	44	46	47	46	47	
	<i>G</i>	7.47	10.87	10.39	9.49	7.52	9.79	36.99	9.53	8.68	9.77	15.47	4.10	
	df	16	27	18	19	14	19	51	22	13	23	29	11	
	<i>P</i>	0.963	0.998	0.918	0.964	0.913	0.958	0.929	0.990	0.797	0.993	0.981	0.967	

Table 10. Continued.

Population		Locus												Combined probability
		<i>Oki100</i>	<i>Omm1070</i>	<i>Omy1011</i>	<i>One101</i>	<i>One102</i>	<i>One104</i>	<i>One111</i>	<i>One114</i>	<i>Ots3</i>	<i>Ots103</i>	<i>OtsG68</i>	<i>Ssa419</i>	
Kobuk (39)	n UAF-ABL	99	94	99	99	99	99	94	99	94	99	99	99	
	<i>n</i> DFO	379	377	379	372	379	374	365	371	378	376	375	372	
	<i>G</i>	17.14	24.11	13.84	22.28	8.71	23.88	66.25	16.56	15.22	30.81	22.63	6.48	
	df	21	32	23	28	15	21	75	28	13	35	37	15	
	<i>P</i>	0.703	0.841	0.931	0.768	0.892	0.299	0.755	0.957	0.294	0.670	0.970	0.971	0.999
Agiapuk (41)	n UAF-ABL	97	---	98	98	98	94	---	95	---	93	99	94	
	<i>n</i> DFO	179	---	179	179	181	182	---	179	---	176	178	181	
	<i>G</i>	6.66	---	10.05	11.58	2.13	7.11	---	10.65	---	17.62	10.38	8.66	
	df	18	---	21	25	14	23	---	24	---	36	32	15	
	<i>P</i>	0.993	---	0.978	0.990	1.000	0.999	---	0.991	---	0.996	1.000	0.895	1.000
Pilgrim (42)	n UAF-ABL	100	94	100	100	100	100	95	100	94	100	100	100	
	<i>n</i> DFO	460	473	471	472	477	471	477	471	478	477	475	474	
	<i>G</i>	16.32	51.60	11.19	17.34	9.94	16.71	78.91	33.11	8.42	26.99	38.83	6.62	
	df	21	32	23	29	18	26	95	36	15	38	39	13	
	<i>P</i>	0.751	0.016	0.981	0.957	0.934	0.918	0.883	0.607	0.906	0.909	0.477	0.921	0.972
Snake (43)	n UAF-ABL	100	96	100	100	100	100	96	100	96	100	100	100	
	<i>n</i> DFO	390	394	393	391	399	391	391	390	399	393	393	394	
	<i>G</i>	24.27	19.74	11.76	19.41	10.91	10.40	57.38	11.78	12.36	42.34	25.53	3.00	
	df	22	30	24	28	18	24	86	24	16	36	33	13	
	<i>P</i>	0.333	0.923	0.982	0.885	0.898	0.993	0.993	0.982	0.719	0.216	0.820	0.998	1.000
Unalakleet (48)	n UAF-ABL	94	94	94	94	94	94	93	94	94	94	94	94	
	<i>n</i> DFO	192	191	189	190	187	179	190	191	189	192	190	190	
	<i>G</i>	13.45	10.12	11.91	10.14	7.70	7.56	55.90	12.15	8.80	15.85	14.76	6.38	
	df	21	32	21	28	18	22	83	27	15	35	36	13	
	<i>P</i>	0.892	1.000	0.942	0.999	0.983	0.998	0.990	0.994	0.888	0.998	0.999	0.931	1.000

Table 10. Continued.

Population		Locus												Combined probability
		<i>Oki100</i>	<i>Omm1070</i>	<i>Omy1011</i>	<i>One101</i>	<i>One102</i>	<i>One104</i>	<i>One111</i>	<i>One114</i>	<i>Ots3</i>	<i>Ots103</i>	<i>OtsG68</i>	<i>Ssa419</i>	
Pikmiktalik (49)	n UAF-ABL	99	92	99	99	100	100	92	100	93	100	99	100	1.000
	n DFO	383	391	386	389	393	392	388	384	394	387	389	393	
	<i>G</i>	13.32	19.43	14.30	16.99	10.88	16.60	85.58	16.08	9.43	30.79	21.90	5.26	
	df	24	33	23	31	17	24	87	28	14	37	38	13	
	<i>P</i>	0.961	0.971	0.918	0.981	0.863	0.865	0.523	0.965	0.802	0.754	0.983	0.969	
Nulato (53)	n UAF-ABL	50	47	50	50	50	50	48	50	48	50	50	50	1.000
	n DFO	117	103	146	112	105	117	118	137	118	163	163	129	
	<i>G</i>	7.80	22.35	13.87	14.46	5.91	15.86	32.45	13.76	8.12	21.11	26.78	2.63	
	df	20	28	22	25	13	22	64	22	12	31	32	12	
	<i>P</i>	0.993	0.765	0.906	0.953	0.949	0.823	1.000	0.910	0.776	0.909	0.728	0.998	
Jim River (54)	n UAF-ABL	92	93	92	90	92	92	92	93	92	91	93	90	0.937
	n DFO	149	153	157	153	155	147	157	151	136	153	157	152	
	<i>G</i>	13.54	8.31	8.24	21.82	5.08	6.40	63.49	8.58	38.21	13.15	9.90	4.06	
	df	16	30	24	25	15	22	65	21	18	27	28	12	
	<i>P</i>	0.633	1.000	0.999	0.646	0.991	1.000	0.530	0.992	0.004	0.988	0.999	0.982	
Toklat (55)	n UAF-ABL	100	94	100	100	100	100	93	100	94	100	100	100	1.000
	n DFO	235	236	236	236	244	244	241	243	244	245	237	241	
	<i>G</i>	9.02	20.22	21.39	15.55	8.16	7.31	37.88	13.39	4.68	13.10	17.97	1.84	
	df	17	30	24	21	14	18	62	21	9	28	26	9	
	<i>P</i>	0.940	0.911	0.616	0.794	0.881	0.987	0.993	0.894	0.861	0.992	0.877	0.994	
Salcha (56)	n UAF-ABL	100	96	100	100	100	100	96	100	96	100	100	100	1.000
	n DFO	170	162	174	173	179	173	167	171	181	182	171	175	
	<i>G</i>	3.57	12.70	12.36	9.48	4.35	9.11	29.99	12.20	4.78	11.43	8.62	4.78	
	df	18	29	23	22	14	22	59	22	10	28	25	10	
	<i>P</i>	1.000	0.996	0.964	0.990	0.993	0.993	0.999	0.953	0.906	0.998	0.999	0.906	

Table 10. Continued.

Population		Locus												Combined probability
		<i>Oki100</i>	<i>Omm1070</i>	<i>Omy1011</i>	<i>One101</i>	<i>One102</i>	<i>One104</i>	<i>One111</i>	<i>One114</i>	<i>Ots3</i>	<i>Ots103</i>	<i>OtsG68</i>	<i>Ssa419</i>	
Sheenjek (57)	n UAF-ABL	99	94	99	99	99	99	94	99	94	99	99	99	0.996
	n DFO	256	165	186	245	241	226	238	238	238	242	242	241	
	G	8.15	14.02	13.06	26.13	8.84	18.12	76.00	18.90	12.28	15.26	14.31	7.88	
	df	16	33	21	28	14	21	64	23	14	29	25	9	
	P	0.944	0.998	0.907	0.566	0.841	0.641	0.145	0.707	0.584	0.983	0.956	0.546	
Fishing Branch (58)	n UAF-ABL	99	91	99	99	99	99	91	99	91	99	99	99	0.998
	n DFO	643	484	568	596	595	599	636	639	580	526	665	590	
	G	11.37	27.84	13.87	18.82	13.34	22.67	73.01	27.28	13.07	18.45	26.11	7.21	
	df	17	32	23	28	22	21	76	27	16	29	27	12	
	P	0.836	0.677	0.930	0.904	0.923	0.362	0.576	0.449	0.668	0.935	0.512	0.844	
Teslin (60)	n UAF-ABL	98	94	99	99	99	99	94	99	94	99	99	99	0.706
	n DFO	126	110	131	126	137	116	136	142	136	141	139	135	
	G	7.51	4.99	13.72	18.19	9.16	20.63	76.14	3.49	15.36	4.14	4.47	2.43	
	df	15	27	18	18	10	20	47	11	11	21	16	9	
	P	0.942	1.000	0.747	0.443	0.517	0.419	0.005	0.982	0.166	1.000	0.998	0.983	
Kanektok (75)	n UAF-ABL	75	75	75	75	75	74	74	75	75	75	75	75	1.000
	n DFO	173	169	170	167	172	173	169	171	173	170	165	173	
	G	8.56	15.02	8.24	8.16	7.12	12.52	37.92	12.15	8.57	14.26	19.40	5.32	
	df	20	34	21	24	17	23	76	28	15	35	34	11	
	P	0.987	0.998	0.994	0.999	0.982	0.962	1.000	0.996	0.899	0.999	0.979	0.914	
Frosty (81)	n UAF-ABL	95	83	97	96	96	96	83	97	84	94	97	97	1.000
	n DFO	173	177	173	178	177	173	176	177	178	171	177	176	
	G	13.33	15.73	9.82	10.29	7.28	15.34	43.60	11.69	7.71	18.62	17.94	10.69	
	df	19	31	21	25	17	25	62	21	12	32	29	12	
	P	0.821	0.990	0.981	0.996	0.980	0.933	0.963	0.948	0.807	0.971	0.945	0.556	

Table 10. Continued.

Population		Locus											Combined probability	
		<i>Oki100</i>	<i>Omm1070</i>	<i>Omy1011</i>	<i>One101</i>	<i>One102</i>	<i>One104</i>	<i>One111</i>	<i>One114</i>	<i>Ots3</i>	<i>Ots103</i>	<i>OtsG68</i>		<i>Ssa419</i>
Olsen (89)	n UAF-ABL	92	85	92	92	92	92	85	92	83	92	92	92	0.000
	n DFO	84	81	80	88	85	86	85	78	85	75	84	77	
	G	38.69	77.23	38.62	41.54	59.99	76.97	116.80	53.64	26.13	70.60	79.37	23.33	
	df	17	31	20	19	25	22	59	21	12	34	35	12	
	P	0.002	0.000	0.007	0.002	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.025	
Herman Creek (92)	n UAF-ABL	100	91	99	100	100	100	91	100	88	100	100	100	1.000
	n DFO	58	57	57	59	58	59	58	56	59	58	54	58	
	G	4.56	14.58	15.20	17.05	7.97	10.07	34.89	12.10	3.65	17.01	12.72	11.03	
	df	11	35	19	25	22	22	58	24	9	34	33	12	
	P	0.951	0.999	0.710	0.880	0.997	0.986	0.993	0.979	0.933	0.993	0.999	0.527	
Taku (94)	n UAF-ABL	45	45	45	45	45	45	45	45	45	45	45	45	1.000
	n DFO	57	58	57	61	63	60	61	60	60	58	58	61	
	G	2.24	5.76	2.46	9.45	5.45	10.20	13.67	7.78	0.40	5.41	6.57	2.57	
	df	10	26	15	20	16	23	46	18	8	32	24	14	
	P	0.994	1.000	1.000	0.977	0.993	0.990	1.000	0.982	1.000	1.000	1.000	1.000	
Greens Creek (96)	n UAF-ABL	100	88	100	100	100	100	88	100	88	100	100	100	1.000
	n DFO	50	50	50	50	50	50	50	50	50	50	50	50	
	G	9.85	12.68	6.04	17.94	6.50	7.74	34.85	14.16	6.49	16.20	14.11	7.42	
	df	15	31	21	26	23	20	54	22	11	28	31	16	
	P	0.829	0.999	0.999	0.878	1.000	0.993	0.980	0.896	0.839	0.963	0.996	0.964	
Bag Harbour (118)	n UAF-ABL	50	32	50	50	50	50	31	50	32	50	50	50	1.000
	n DFO	107	70	89	88	89	105	85	91	118	80	96	91	
	G	9.98	17.02	7.70	13.61	11.60	6.71	22.66	6.44	9.67	9.72	17.00	8.12	
	df	14	30	17	28	19	18	37	20	10	27	34	15	
	P	0.763	0.972	0.973	0.990	0.902	0.992	0.969	0.998	0.470	0.999	0.993	0.919	
Chi-square		21.104	34.863	17.614	18.859	22.046	43.154	44.224	25.862	36.672	22.845	25.991	18.417	
df		56	52	56	56	56	56	52	56	52	56	56	56	
Combined probability across overlapping samples		1.000	0.967	1.000	1.000	1.000	0.896	0.770	1.000	0.947	1.000	1.000	1.000	

Table 10. Continued.

Population		Locus											Combined probability	
		<i>Oki100</i>	<i>Omm1070</i>	<i>Omy1011</i>	<i>One101</i>	<i>One102</i>	<i>One104</i>	<i>One111</i>	<i>One114</i>	<i>Ots3</i>	<i>Ots103</i>	<i>OtsG68</i>		<i>Ssa419</i>
Non-overlapping samples														
Miomote (1)	n UAF-ABL	95	95	95	93	91	95	94	94	92	92	94	94	0.000
	n DFO	91	77	79	94	95	91	95	92	91	79	93	94	
	<i>G</i>	30.20	85.68	58.43	63.28	63.18	62.22	116.96	55.00	51.10	89.06	82.52	39.92	
	df	16	44	28	23	33	30	71	26	19	42	38	22	
	<i>P</i>	0.017	0.000	0.001	0.000	0.001	0.000	0.000	0.001	0.000	0.000	0.000	0.011	
Gakko late (2)	n UAF-ABL	56	63	63	65	60	66	67	65	66	66	66	65	0.000
	n DFO	158	124	155	158	157	159	158	158	156	147	159	154	
	<i>G</i>	28.48	72.35	47.23	53.33	23.64	21.99	86.57	23.52	17.17	34.51	45.54	25.05	
	df	17	37	30	19	23	27	66	28	20	40	45	20	
	<i>P</i>	0.040	0.000	0.024	0.000	0.424	0.738	0.046	0.706	0.642	0.715	0.449	0.200	
Kesenuma (3) (Okhawa R.)	n UAF-ABL	95	93	93	95	94	94	95	95	92	95	92	95	0.000
	n DFO	19	17	19	19	19	19	19	17	19	19	18	18	
	<i>G</i>	35.84	43.30	43.79	15.06	48.21	33.26	70.09	34.36	10.71	54.34	23.98	37.89	
	df	18	38	24	16	23	23	54	27	14	38	25	19	
	<i>P</i>	0.007	0.256	0.008	0.520	0.002	0.077	0.069	0.156	0.709	0.042	0.521	0.006	
Tsugaruishi (5)	n UAF-ABL	40	40	40	40	40	40	40	40	40	40	40	40	0.001
	n DFO	79	59	80	77	77	78	77	80	74	80	80	79	
	<i>G</i>	27.07	41.03	38.97	21.58	32.22	28.37	95.17	27.25	18.32	41.11	30.84	26.84	
	df	16	38	25	15	25	26	56	28	15	34	29	21	
	<i>P</i>	0.041	0.339	0.037	0.119	0.152	0.340	0.001	0.505	0.246	0.187	0.373	0.176	
Chitose late (6)	n UAF-ABL	61	67	66	68	66	68	66	68	67	68	68	66	0.008
	n DFO	266	169	247	263	248	258	250	266	261	247	268	235	
	<i>G</i>	28.57	41.34	58.44	18.97	27.95	28.86	115.47	23.95	11.55	62.80	61.16	11.23	
	df	20	39	34	25	31	33	84	28	19	42	42	20	
	<i>P</i>	0.097	0.369	0.006	0.799	0.624	0.673	0.013	0.684	0.904	0.020	0.028	0.940	

Table 10. Continued.

Population		Locus												Combined probability
		<i>Oki100</i>	<i>Omm1070</i>	<i>Omy1011</i>	<i>One101</i>	<i>One102</i>	<i>One104</i>	<i>One111</i>	<i>One114</i>	<i>Ots3</i>	<i>Ots103</i>	<i>OtsG68</i>	<i>Ssa419</i>	
Narva (13)	n UAF-ABL	67	55	67	67	67	67	56	66	54	67	67	67	0.339
	n DFO	17	17	17	16	17	17	17	17	17	16	17	17	
	<i>G</i>	10.17	33.48	30.87	24.63	25.26	20.73	44.72	16.72	12.89	28.55	31.10	4.43	
	df	15	28	20	21	21	21	39	22	11	28	27	14	
	<i>P</i>	0.809	0.219	0.057	0.264	0.236	0.476	0.244	0.779	0.301	0.436	0.267	0.992	
Amur early (20) ^a	n UAF-ABL	49	33	43	43	43	48	34	42	33	48	43	42	0.531
	n DFO	329	336	338	332	335	294	336	337	339	333	310	332	
	<i>G</i>	27.71	24.41	17.79	21.85	16.97	17.38	78.45	39.46	30.62	37.43	41.55	15.52	
	df	21	33	25	35	21	32	84	32	16	42	37	16	
	<i>P</i>	0.149	0.860	0.851	0.960	0.713	0.983	0.650	0.171	0.015	0.672	0.279	0.487	
Amur late (21) ^a	n UAF-ABL	27	27	27	27	27	27	27	27	27	27	27	27	0.611
	n DFO	329	336	338	332	335	294	336	337	339	333	310	332	
	<i>G</i>	17.120	32.911	22.621	38.581	18.111	39.760	75.645	19.775	21.709	43.109	46.852	15.954	
	df	21	33	25	35	21	32	86	32	16	42	38	16	
	<i>P</i>	0.704	0.472	0.600	0.311	0.642	0.163	0.780	0.955	0.153	0.424	0.154	0.456	
Naiba (25)	n UAF-ABL	46	32	46	46	46	46	31	46	32	46	46	46	0.026
	n DFO	146	144	145	143	138	146	147	146	146	147	140	146	
	<i>G</i>	45.36	33.94	32.26	16.87	20.04	12.38	80.19	27.93	9.16	52.26	53.53	24.07	
	df	21	31	25	27	21	24	72	24	13	40	43	18	
	<i>P</i>	0.002	0.327	0.151	0.934	0.519	0.975	0.238	0.263	0.761	0.093	0.130	0.153	
Tauí (27)	n UAF-ABL	36	---	32	34	34	36	---	28	---	35	36	26	0.023
	n DFO	55	---	53	54	55	55	---	55	---	55	55	53	
	<i>G</i>	24.22	---	22.65	37.06	9.19	26.67	---	24.44	---	59.33	49.48	18.53	
	df	22	---	22	24	16	25	---	25	---	35	37	15	
	<i>P</i>	0.336	---	0.422	0.043	0.906	0.372	---	0.494	---	0.006	0.082	0.236	

Table 10. Continued.

Population		Locus											Combined probability	
		<i>Oki100</i>	<i>Omm1070</i>	<i>Omy1011</i>	<i>One101</i>	<i>One102</i>	<i>One104</i>	<i>One111</i>	<i>One114</i>	<i>Ots3</i>	<i>Ots103</i>	<i>OtsG68</i>		<i>Ssa419</i>
Ola (28)	n UAF-ABL	45	---	45	45	45	45	---	45	---	45	45	44	0.000
	<i>n</i> DFO	117	---	119	118	117	117	---	119	---	118	119	117	
	<i>G</i>	29.73	---	24.00	45.34	41.84	56.86	---	36.33	---	37.78	52.31	26.65	
	df	23	---	23	28	19	25	---	28	---	35	42	18	
	<i>P</i>	0.157	---	0.404	0.020	0.002	0.000	---	0.134	---	0.343	0.132	0.086	
Kol (31)	n UAF-ABL	48	---	48	48	48	48	---	48	---	48	48	48	0.023
	<i>n</i> DFO	77	---	79	79	77	79	---	79	---	78	79	75	
	<i>G</i>	20.79	---	30.11	26.28	26.24	24.11	---	24.87	---	44.46	52.97	35.00	
	df	22	---	23	27	18	24	---	28	---	37	39	18	
	<i>P</i>	0.534	---	0.146	0.503	0.094	0.456	---	0.635	---	0.186	0.067	0.009	
Utka (32)	n UAF-ABL	35	---	35	35	35	35	---	35	---	35	35	35	0.000
	<i>n</i> DFO	39	---	39	40	37	39	---	39	---	40	39	38	
	<i>G</i>	46.95	---	36.87	43.75	24.94	53.18	---	37.33	---	55.85	35.75	12.94	
	df	21	---	22	23	16	22	---	25	---	33	32	14	
	<i>P</i>	0.001	---	0.024	0.006	0.071	0.000	---	0.054	---	0.008	0.296	0.531	
Anvik (51)	n UAF-ABL	74	72	74	74	74	73	71	74	73	74	74	74	0.000
	<i>n</i> DFO	183	183	186	186	183	185	183	182	185	184	185	176	
	<i>G</i>	29.23	51.12	27.59	39.71	17.15	33.52	105.34	54.80	18.68	43.88	57.11	12.98	
	df	20	34	26	28	15	22	94	32	16	35	36	14	
	<i>P</i>	0.083	0.030	0.379	0.070	0.310	0.055	0.199	0.007	0.286	0.144	0.014	0.528	
Kluane (59) (river for DFO)	n UAF-ABL	99	94	98	98	98	99	94	99	94	99	98	99	0.000
	<i>n</i> DFO	535	393	444	478	514	475	497	471	529	418	480	493	
	<i>G</i>	20.51	20.83	25.56	64.02	34.91	29.27	139.00	6.99	20.04	21.35	18.22	13.24	
	df	18	29	20	35	29	18	77	14	15	25	22	12	
	<i>P</i>	0.305	0.865	0.181	0.002	0.207	0.045	0.000	0.935	0.171	0.673	0.693	0.352	

Table 10. Continued.

Population		Locus												Combined probability
		<i>Oki100</i>	<i>Omm1070</i>	<i>Omy1011</i>	<i>One101</i>	<i>One102</i>	<i>One104</i>	<i>One111</i>	<i>One114</i>	<i>Ots3</i>	<i>Ots103</i>	<i>OtsG68</i>	<i>Ssa419</i>	
George (67)	n UAF-ABL	78	77	78	78	77	78	77	76	75	77	78	78	0.027
	n DFO	84	84	83	80	87	87	74	76	86	83	82	78	
	<i>G</i>	9.71	46.74	25.60	37.54	19.01	21.83	88.16	27.33	15.82	47.71	32.22	17.03	
	df	17	33	22	29	16	25	71	22	12	31	32	14	
	<i>P</i>	0.915	0.057	0.269	0.133	0.268	0.645	0.082	0.199	0.200	0.028	0.456	0.255	
Goodnews (76)	n UAF-ABL	100	95	100	100	100	100	92	100	95	100	100	100	0.006
	n DFO	97	76	96	65	97	94	96	94	96	89	96	97	
	<i>G</i>	11.97	48.39	46.14	27.55	20.98	19.65	106.06	35.25	11.57	42.94	42.24	14.61	
	df	19	34	25	26	17	22	81	28	13	32	35	12	
	<i>P</i>	0.887	0.052	0.006	0.381	0.227	0.605	0.032	0.163	0.563	0.094	0.187	0.264	
Deena (116)	n UAF-ABL	36	48	48	48	48	47	48	48	48	48	48	48	0.009
	n DFO	210	209	196	211	210	209	207	209	207	206	208	210	
	<i>G</i>	26.63	39.67	20.32	28.70	30.23	29.94	52.97	20.15	3.43	53.41	35.46	11.89	
	df	15	35	15	26	22	19	44	17	7	35	36	10	
	<i>P</i>	0.032	0.270	0.160	0.325	0.113	0.053	0.167	0.267	0.843	0.024	0.494	0.293	
Neekas (119)	n UAF-ABL	50	48	50	50	50	50	48	50	48	50	50	50	0.001
	n DFO	161	117	167	178	180	152	176	158	173	167	156	144	
	<i>G</i>	16.34	54.07	15.54	40.19	18.35	27.15	60.28	35.85	51.08	34.11	45.53	29.11	
	df	15	34	20	35	18	22	63	27	21	31	39	16	
	<i>P</i>	0.360	0.016	0.745	0.251	0.433	0.206	0.574	0.119	0.000	0.320	0.219	0.023	
Klownik (120)	n UAF-ABL	49	47	49	49	49	49	47	49	47	49	49	49	0.062
	n DFO	175	202	193	199	200	192	200	177	194	198	181	190	
	<i>G</i>	12.99	43.16	27.64	33.92	20.72	30.72	61.29	30.20	10.49	49.73	48.51	20.69	
	df	17	34	21	32	22	23	60	23	14	34	38	17	
	<i>P</i>	0.737	0.135	0.151	0.375	0.538	0.130	0.429	0.144	0.726	0.040	0.118	0.240	

Table 10. Continued.

Population		Locus												Combined probability
		<i>Oki100</i>	<i>Omm1070</i>	<i>Omy1011</i>	<i>One101</i>	<i>One102</i>	<i>One104</i>	<i>One111</i>	<i>One114</i>	<i>Ots3</i>	<i>Ots103</i>	<i>OtsG68</i>	<i>Ssa419</i>	
Grant (WA) (123)	n UAF-ABL	88	87	88	88	96	91	88	90	90	91	95	90	1.000
	n DFO	48	40	40	37	38	34	38	46	49	41	49	26	
	<i>G</i>	7.79	18.17	8.80	18.08	10.48	6.92	32.68	21.83	5.96	15.12	28.45	7.23	
	df	13	30	14	26	19	22	46	28	11	32	39	9	
	<i>P</i>	0.857	0.956	0.844	0.873	0.940	0.999	0.931	0.789	0.876	0.995	0.893	0.613	
Quilcene (124)	n UAF-ABL	40	35	40	40	40	38	35	40	35	40	40	40	0.005
	n DFO	86	84	88	82	82	87	85	83	88	83	82	80	
	<i>G</i>	13.98	32.46	21.73	33.44	24.18	18.31	40.25	16.08	1.04	28.34	24.03	11.71	
	df	12	21	13	22	14	19	27	14	4	23	23	7	
	<i>P</i>	0.302	0.053	0.060	0.056	0.044	0.502	0.049	0.309	0.903	0.203	0.402	0.111	
Kennedy (126)	n UAF-ABL	82	86	79	81	85	87	85	84	86	87	83	84	0.000
	n DFO	95	88	94	83	85	88	87	97	96	88	94	95	
	<i>G</i>	41.70	45.72	48.86	80.43	77.27	77.39	56.07	96.87	5.36	164.82	79.99	32.59	
	df	12	29	16	30	19	22	35	28	8	34	32	10	
	<i>P</i>	0.000	0.025	0.000	0.000	0.000	0.000	0.013	0.000	0.719	0.000	0.000	0.000	

^aThe run-timing of the DFO Amur collections is unknown.

Table 11. Genetic diversity measures among 126 chum salmon populations. ϑ (F_{ST}) estimated from Weir and Cockerham (1984); G_{ST-est} from Nei and Chesser (1983); G''_{ST-est} from Meirmans and Hedrick (2011); D_{est} from Jost (2008); H_S is the average expected heterozygosity within populations under Hardy-Weinberg equilibrium.

Locus	Type	ϑ	G_{ST-est}	G''_{ST-est}	D_{est}	H_S
CLOCK	SNP	0.0150	0.0275	0.0455	0.0183	0.3868
ER	SNP	0.3884	0.3558	0.4985	0.2192	0.2799
IN	SNP	0.0520	0.1106	0.1418	0.0343	0.2130
IS	SNP	0.0734	0.0735	0.1784	0.1127	0.5797
MT	SNP	0.3558	0.2897	0.5296	0.3362	0.4419
PER	SNP	0.0294	0.0330	0.0355	0.0024	0.0645
PL	SNP	0.0945	0.0351	0.0468	0.0118	0.2413
RF	SNP	0.2115	0.3170	0.3957	0.1129	0.1927
RH	SNP	0.0888	0.0727	0.0835	0.0111	0.1219
SP	SNP	0.0582	0.0774	0.1434	0.0710	0.4527
VR	SNP	0.1453	0.1662	0.4226	0.3066	0.5983
VT	SNP	0.1062	0.1196	0.2136	0.1058	0.4321
<i>Oki100</i>	mSAT	0.0341	0.0378	0.2846	0.2563	0.8591
<i>Omm1070</i>	mSAT	0.0031	0.0102	0.2200	0.2119	0.9450
<i>Omy1011</i>	mSAT	0.0201	0.0258	0.3005	0.2818	0.9059
<i>One101</i>	mSAT	0.0549	0.0692	0.4570	0.4163	0.8407
<i>One102</i>	mSAT	0.0051	0.0093	0.1108	0.1023	0.9076
<i>One104</i>	mSAT	0.0223	0.0265	0.3566	0.3390	0.9176
<i>One111</i>	mSAT	0.0349	0.0364	0.5344	0.5167	0.9234
<i>One114</i>	mSAT	0.0081	0.0142	0.1765	0.1646	0.9115
<i>Ots3</i>	mSAT	0.0808	0.0754	0.3342	0.2794	0.7661
<i>Ots103</i>	mSAT	0.0155	0.0191	0.3552	0.3426	0.9383
<i>OtsG68</i>	mSAT	0.0116	0.0162	0.2837	0.2718	0.9349
<i>Ssa419</i>	mSAT	0.0209	0.0229	0.1544	0.1344	0.8435
Average SNPs only		0.1349	0.1398	0.2279	0.1119	0.3337
Average mSAT only		0.0259	0.0303	0.2973	0.2764	0.8911
Average overall		0.0804	0.0851	0.2626	0.1941	0.6124

Table 12. Genetic diversity measures among 34 coastal western Alaskan chum salmon populations (population code numbers 37-53, 61-71, 75-80). ϑ (F_{ST}) estimated from Weir and Cockerham (1984); G_{ST-est} from Nei and Chesser (1983); G''_{ST-est} from Meirmans and Hedrick (2011); D_{est} from Jost (2008); H_S is the average expected heterozygosity within populations under Hardy-Weinberg equilibrium.

Locus	Type	ϑ	G_{ST-est}	G''_{ST-est}	D_{est}	H_S
CLOCK	SNP	-0.0042	0.0013	0.0023	0.0009	0.4034
ER	SNP	0.0140	0.0221	0.0271	0.0045	0.1599
IN	SNP	0.0091	0.0138	0.0206	0.0065	0.3087
IS	SNP	0.0339	0.0334	0.0795	0.0467	0.5633
MT	SNP	0.0423	0.0402	0.0571	0.0164	0.2718
PER	SNP	0.0078	0.0149	0.0164	0.0011	0.0667
PL	SNP	0.0258	0.0313	0.0381	0.0061	0.1539
RF	SNP	0.0079	0.0143	0.0251	0.0105	0.4106
RH	SNP	0.0012	0.0075	0.0082	0.0005	0.0543
SP	SNP	-0.0024	0.0040	0.0081	0.0040	0.4927
VR	SNP	0.0176	0.0216	0.0740	0.0529	0.6942
VT	SNP	-0.0030	0.0024	0.0048	0.0024	0.4819
<i>Oki100</i>	mSAT	0.0076	0.0101	0.1019	0.0924	0.8922
<i>Omm1070</i>	mSAT	0.0000	0.0037	0.0903	0.0868	0.9518
<i>Omy1011</i>	mSAT	0.0028	0.0072	0.0939	0.0871	0.9150
<i>One101</i>	mSAT	0.0088	0.0124	0.1144	0.1030	0.8832
<i>One102</i>	mSAT	0.0004	0.0043	0.0483	0.0440	0.9021
<i>One104</i>	mSAT	0.0026	0.0071	0.1058	0.0992	0.9249
<i>One111</i>	mSAT	0.0042	0.0074	0.1165	0.1097	0.9286
<i>One114</i>	mSAT	0.0038	0.0068	0.0889	0.0824	0.9155
<i>Ots3</i>	mSAT	0.0132	0.0171	0.0709	0.0543	0.7476
<i>Ots103</i>	mSAT	0.0076	0.0090	0.1584	0.1505	0.9354
<i>OtsG68</i>	mSAT	0.0043	0.0069	0.1143	0.1080	0.9325
<i>Ssa419</i>	mSAT	0.0074	0.0082	0.0579	0.0499	0.8486
Average SNPs only		0.0125	0.0172	0.0301	0.0127	0.3384
Average mSAT only		0.0052	0.0084	0.0968	0.0889	0.8981
Average overall		0.0089	0.0128	0.0634	0.0508	0.6183

Table 13. Pairwise F_{ST} estimates for 18 reporting groups from the 101-population dataset used for the LTO baseline evaluation. All pairwise tests of homogeneity across all loci (G tests in program GENEPOP 4.0) for the 18 reporting groups had $P < 10^{-8}$.

Code	Reporting group	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	Japan-Kuril																	
2	Primorye-Amur-Sakhalin	0.029																
3	Okhotsk-Kam.-NE Russia	0.052	0.018															
4	Kotzebue Sound	0.072	0.042	0.031														
5	Norton Sound	0.071	0.040	0.026	0.007													
6	Lower Yukon	0.079	0.045	0.031	0.010	0.002												
7	Middle Yukon	0.118	0.077	0.058	0.027	0.018	0.013											
8	Upper Yukon	0.126	0.090	0.072	0.034	0.024	0.021	0.008										
9	Kusk. summer-W Bristol Bay	0.071	0.041	0.029	0.010	0.001	0.001	0.017	0.022									
10	Kuskokwim fall	0.110	0.070	0.058	0.031	0.019	0.019	0.024	0.028	0.020								
11	E Bristol-N Alaska Peninsula	0.065	0.031	0.026	0.016	0.011	0.014	0.042	0.051	0.011	0.037							
12	Alaska Peninsula	0.082	0.033	0.024	0.050	0.044	0.047	0.076	0.092	0.047	0.078	0.031						
13	Kodiak	0.089	0.048	0.048	0.078	0.079	0.084	0.121	0.137	0.082	0.113	0.064	0.036					
14	Cook Inlet-PWS-Alsek	0.093	0.045	0.041	0.069	0.064	0.068	0.097	0.110	0.065	0.097	0.049	0.026	0.055				
15	NSE Alaska	0.096	0.051	0.050	0.083	0.080	0.085	0.117	0.133	0.085	0.114	0.063	0.029	0.048	0.021			
16	SSE Alaska-N Brit. Columbia	0.096	0.047	0.048	0.084	0.080	0.086	0.117	0.132	0.084	0.113	0.063	0.032	0.052	0.024	0.005		
17	Haida Gwaii-central Brit. Col.	0.105	0.056	0.059	0.100	0.096	0.103	0.135	0.152	0.099	0.132	0.078	0.042	0.057	0.030	0.010	0.005	
18	S Brit. Columbia-Washington	0.111	0.059	0.064	0.101	0.095	0.103	0.132	0.146	0.099	0.128	0.080	0.050	0.075	0.039	0.024	0.015	0.015

Table 14. Mean individual assignments by 18 reporting groups from BAYES analysis (read down) for chum salmon from the 101-population, LTO baseline evaluation datasets. Proportion of correct assignments to reporting group are on the diagonal in bold font. The difference of one from the summary across rows indicates whether a region is a sink (-) or contributor (+) to other regions.

Code	Reporting group	Sum across rows	Japan-Kuril	Primorye-Amur-Sakhalin	Okhotsk-Kam.-NE Russia	Kotzebue Sound	Norton Sound	Lower Yukon	Middle Yukon	Upper Yukon	Kusk. summer-W Bristol Bay	Kuskokwim fall	E Bristol-N Alaska Pen.	Alaska Peninsula	Kodiak	Cook Inlet-PWS-Alsek	NSE Alaska	SSE Alaska-N Brit Columbia	Haida Gwaii-central Brit. Col.	S Brit. Columbia-Washington	
1	Japan-Kuril	0.02	0.97	0.03	0.01	0.00	0.00	0.00	0	0	0.00	0	0.00	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00
2	Primorye-Amur-Sakhalin	-0.02	0.02	0.82	0.06	0.01	0.00	0.00	0.00	0	0.01	0	0.01	0.01	0.01	0.01	0.01	0.00	0.01	0.01	0.01
3	Okhotsk-Kam.-NE Russia	-0.10	0.00	0.06	0.65	0.02	0.02	0.02	0.00	0.00	0.02	0.00	0.02	0.01	0.03	0.01	0.01	0.01	0.01	0.01	0.01
4	Kotzebue Sound	-0.20	0.00	0.00	0.02	0.64	0.05	0.03	0.01	0.00	0.02	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
5	Norton Sound	-0.23	0.00	0.01	0.03	0.07	0.22	0.14	0.04	0.01	0.14	0.02	0.08	0.01	0.00	0.00	0.00	0.00	0	0	0.00
6	Lower Yukon	-0.48	0.00	0.00	0.02	0.04	0.09	0.13	0.05	0.01	0.11	0.01	0.05	0.00	0.00	0.00	0.00	0.00	0	0	0.00
7	Middle Yukon	-0.20	0.00	0.00	0.00	0.01	0.03	0.05	0.51	0.11	0.04	0.03	0.01	0.00	0.01	0.01	0.00	0	0	0	0.00
8	Upper Yukon	0.06	0.00	0.00	0.00	0.01	0.03	0.02	0.16	0.79	0.02	0.03	0.00	0	0.00	0.00	0	0.00	0	0	0.00
9	Kusk. summer-W Bristol Bay	1.52	0.00	0.02	0.10	0.17	0.48	0.54	0.16	0.05	0.57	0.07	0.33	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
10	Kuskokwim fall	0.03	0.00	0.00	0.00	0.02	0.03	0.03	0.05	0.02	0.03	0.83	0.01	0	0	0	0	0.00	0	0	0.00
11	E Bristol-N Alaska Peninsula	-0.44	0.00	0.01	0.02	0.01	0.02	0.02	0.00	0.00	0.03	0.00	0.41	0.02	0.02	0.00	0.00	0.01	0.00	0.00	0.00
12	Alaska Peninsula	-0.06	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0	0.00	0	0.01	0.74	0.10	0.01	0.01	0.01	0.01	0.01	0.01
13	Kodiak	-0.38	0.00	0.00	0.00	0	0.00	0.00	0.00	0	0.00	0	0.00	0.02	0.58	0.00	0.01	0.00	0.00	0.00	0.00
14	Cook Inlet-PWS-Alsek	0.03	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0	0.00	0	0.01	0.03	0.05	0.81	0.03	0.03	0.04	0.01	0.01
15	NSE Alaska	0.11	0.00	0.00	0.01	0.00	0.00	0.00	0	0	0.00	0	0.01	0.06	0.07	0.05	0.58	0.16	0.14	0.03	0.03
16	SSE Alaska-N Brit. Columbia	0.69	0.00	0.01	0.03	0.00	0.00	0.00	0	0	0.00	0	0.02	0.06	0.10	0.07	0.29	0.67	0.34	0.10	0.10
17	Haida Gwaii-central Brit. Col.	-0.42	0.00	0.00	0.00	0.00	0.00	0	0.00	0	0.00	0	0.00	0.01	0.01	0.02	0.04	0.08	0.38	0.03	0.03
18	S Brit. Columbia-Washington	-0.04	0.00	0.01	0.01	0.00	0.00	0	0.00	0.00	0.00	0	0.00	0.02	0.01	0.01	0.02	0.03	0.07	0.79	0.03

Table 15. Mean individual assignments by 12 reporting groups from BAYES analysis (read down) for chum salmon from the 101-population, LTO baseline evaluation datasets. Proportion of correct assignments to reporting group are on the diagonal in bold font. The difference of one from the summary across rows indicates whether a region is a sink (-) or contributor (+) to other regions.

Code	Reporting group	Sum across rows	Japan-Kuril	Primorye-Amur-Sakhalin	Okhotsk-Kam.-NE Russia	Kotzebue Sound	Coastal western Alaska	Upper-Middle Yukon	Kuskowkwim fall	AK Peninsula-Kodiak	Cook Inlet-PWS-Alsek	NSE Alaska	SSE AK-central BC	S Brit. Columbia-Washington
1	Japan-Kuril	0.02	0.97	0.03	0.01	0.00	0.00	0	0	0.00	0.00	0.00	0.00	0.00
2	Primorye-Amur-Sakhalin	-0.06	0.02	0.82	0.06	0.01	0.01	0.00	0	0.01	0.01	0.01	0.00	0.01
3	Okhotsk-Kam-NE Russia	-0.19	0.00	0.06	0.65	0.02	0.02	0.00	0.00	0.02	0.01	0.01	0.01	0.01
4	Kotzebue Sound	-0.30	0.00	0.00	0.02	0.64	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
5,6,9,11	Coastal western Alaska	0.65	0.00	0.05	0.16	0.28	0.84	0.15	0.11	0.03	0.01	0.01	0.01	0.01
7,8	Upper-Middle Yukon	-0.05	0.00	0.00	0.00	0.02	0.06	0.80	0.06	0.00	0.01	0.00	0.00	0.00
10	Kuskowkwim fall	-0.09	0.00	0.00	0.00	0.02	0.03	0.03	0.83	0	0	0	0.00	0.00
12,13	AK Peninsula-Kodiak	-0.19	0.00	0.01	0.02	0.00	0.00	0.00	0	0.72	0.01	0.01	0.01	0.01
14	Cook Inlet-PWS-Alsek	-0.06	0.00	0.00	0.01	0.00	0.00	0.00	0	0.04	0.81	0.03	0.03	0.01
15	NSE Alaska	-0.10	0.00	0.00	0.01	0.00	0.00	0	0	0.06	0.05	0.58	0.15	0.03
16,17	SSE AK-central BC	0.42	0.00	0.01	0.03	0.00	0.00	0.00	0	0.09	0.09	0.32	0.74	0.13
18	S Brit. Columbia-Washington	-0.12	0.00	0.01	0.01	0.00	0.00	0.00	0	0.01	0.01	0.02	0.04	0.79

XIV. APPENDICES:

Appendix I. Single nucleotide polymorphism (SNP) allele frequencies, collection sizes (n), number of alleles (n_a), effective number of alleles (n_{eff}), allele richness (a ; based on 11 individuals), expected heterozygosity (H_E), observed heterozygosity (H_O), and estimated inbreeding coefficient (F_{IS}) for 126 chum salmon populations. Totals for all populations appear in right hand column. Significant tests of Hardy-Weinberg equilibrium before Bonferroni multiple testing are indicated at the F_{IS} values as: * $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$.

VT	Allele name	Population															
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	33	0.918	0.813	0.904	0.813	0.9	0.922	0.747	0.671	0.795	0.909	0.95	0.927	0.545	0.563	0.664	0.922
2	34	0.082	0.187	0.096	0.188	0.1	0.078	0.253	0.329	0.205	0.091	0.05	0.073	0.455	0.438	0.336	0.078
n		92	67	94	40	40	77	79	76	39	77	30	48	55	48	61	32
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
n_{eff}		1.18	1.44	1.21	1.45	1.22	1.17	1.61	1.80	1.49	1.20	1.11	1.16	2.00	1.99	1.82	1.17
a		1.9	2.0	1.9	2.0	1.9	1.9	2.0	2.0	2.0	1.9	1.8	1.8	2.0	2.0	2.0	1.9
H_E		0.151	0.306	0.174	0.309	0.182	0.145	0.381	0.444	0.330	0.166	0.097	0.137	0.500	0.497	0.450	0.146
H_O		0.141	0.313	0.191	0.225	0.150	0.130	0.456	0.526	0.359	0.182	0.100	0.146	0.400	0.458	0.443	0.156
F_{IS}		0.062	-0.025	-0.101	0.273	0.179	0.103	-0.199	-0.186	-0.088	-0.094	-0.036	-0.068	0.202	0.079	0.016	-0.069
IN																	
1	36	0.989	0.975	0.925	0.938	0.975	0.972	0.948	0.984	0.971	0.958	0.983	1	0.954	0.97	0.958	0.859
2	37	0.011	0.025	0.075	0.063	0.025	0.028	0.052	0.016	0.029	0.042	0	0	0.046	0.03	0.042	0.141
3	38	0	0	0	0	0	0	0	0	0	0	0.017	0	0	0	0	0
n		94	59	93	40	40	72	77	62	34	72	30	47	65	50	60	32
n_a		2	2	2	2	2	2	2	2	2	2	2	1	2	2	2	2
n_{eff}		1.02	1.05	1.16	1.13	1.05	1.06	1.11	1.03	1.06	1.09	1.03	1.00	1.10	1.06	1.09	1.33
a		1.2	1.5	1.8	1.8	1.5	1.5	1.7	1.3	1.5	1.6	1.4	1.0	1.7	1.5	1.6	2.0
H_E		0.021	0.050	0.140	0.119	0.049	0.054	0.099	0.032	0.058	0.080	0.033	0	0.089	0.059	0.081	0.246
H_O		0.021	0.051	0.151	0.125	0.050	0.056	0.104	0.032	0.059	0.083	0.033	0	0.092	0.060	0.083	0.281
F_{IS}		-0.005	-0.018	-0.076	-0.054	-0.013	-0.022	-0.048	-0.008	-0.015	-0.036	0	0	-0.041	-0.021	-0.035	-0.148
SP																	
1	41	0.67	0.648	0.758	0.688	0.7	0.532	0.426	0.628	0.459	0.546	0.589	0.511	0.508	0.511	0.34	0.567
2	42	0.33	0.352	0.242	0.313	0.3	0.468	0.574	0.372	0.541	0.454	0.411	0.489	0.492	0.489	0.66	0.433
n		94	64	93	40	40	78	74	78	37	76	28	44	61	44	50	30
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
n_{eff}		1.80	1.85	1.58	1.77	1.74	2.00	1.97	1.89	2.01	2.00	1.97	2.02	2.02	2.02	1.83	2.00
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
H_E		0.444	0.460	0.369	0.435	0.425	0.501	0.492	0.470	0.504	0.499	0.493	0.505	0.504	0.505	0.453	0.499
H_O		0.404	0.578	0.376	0.375	0.300	0.551	0.500	0.564	0.541	0.592	0.464	0.432	0.361	0.523	0.480	0.600
F_{IS}		0.091	-0.261	-0.021	0.140	0.297	-0.101	-0.016	-0.201	-0.075	-0.188	0.059	0.147	0.286*	-0.035	-0.059	-0.206
RH																	
1	43	0.005	0	0	0	0	0	0	0	0	0	0	0	0.016	0.053	0.035	0
2	44	0.995	1	1	1	1	1	1	1	1	1	1	1	0.984	0.947	0.965	1
n		94	69	93	40	40	79	79	74	40	79	29	46	61	47	57	31
n_a		2	1	1	1	1	1	1	1	1	1	1	1	2	2	2	1
n_{eff}		1.01	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.03	1.11	1.07	1.00
a		1.1	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.3	1.7	1.6	1.0
H_E		0.011	0	0	0	0	0	0	0	0	0	0	0	0.033	0.102	0.068	0
H_O		0.011	0	0	0	0	0	0	0	0	0	0	0	0.033	0.106	0.035	0
F_{IS}		0	0	0	0	0	0	0	0	0	0	0	0	-0.008	-0.045	0.489	0
VR																	
1	51	0.367	0.455	0.326	0.213	0.282	0.25	0.159	0.406	0.321	0.306	0.571	0.407	0.214	0.048	0.318	0.352
2	52	0.042	0.063	0.017	0.025	0.064	0.023	0.038	0.014	0.036	0.049	0.048	0.023	0.107	0.048	0.068	0
3	53	0.572	0.455	0.599	0.7	0.615	0.705	0.742	0.529	0.554	0.597	0.31	0.488	0.619	0.679	0.545	0.63
4	54	0.018	0.027	0.058	0.063	0.038	0.023	0.061	0.051	0.089	0.049	0.071	0.081	0.06	0.226	0.068	0.019
n		83	56	86	40	39	66	66	69	28	72	21	43	42	42	44	27
n_a		4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	3
n_{eff}		2.17	2.41	2.15	1.87	2.19	1.80	1.73	2.26	2.45	2.22	2.41	2.47	2.29	1.96	2.49	1.95
a		3.0	3.3	3.1	3.3	3.5	2.8	3.4	3.0	3.6	3.4	3.7	3.3	3.7	3.4	3.7	2.4
H_E		0.539	0.586	0.535	0.466	0.543	0.443	0.422	0.557	0.592	0.549	0.584	0.596	0.563	0.490	0.599	0.488
H_O		0.566	0.625	0.523	0.425	0.615	0.439	0.333	0.536	0.464	0.500	0.667	0.488	0.548	0.548	0.568	0.481
F_{IS}		-0.052	-0.067	0.022	0.089	-0.135	0.009	0.211	0.037	0.218	0.090	-0.145	0.182	0.027	-0.120**	0.052	0.015

Appendix I. Continued.

IS	Allele		Population															
	Allele name		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
	1	25	0.432	0.491	0.546	0.513	0.4	0.363	0.395	0.521	0.324	0.547	0.138	0.576	0.454	0.57	0.42	0.364
	2	35	0.147	0.089	0.069	0.1	0.025	0.089	0.158	0.129	0.176	0.095	0.397	0.163	0.019	0	0.018	0.136
	3	45	0.421	0.42	0.385	0.338	0.513	0.521	0.414	0.336	0.412	0.351	0.448	0.239	0.509	0.43	0.563	0.5
	4	55	0	0	0	0.05	0.063	0.027	0.033	0.014	0.088	0.007	0.017	0.022	0.019	0	0	0
	<i>n</i>		95	56	65	40	40	73	76	70	34	74	29	46	54	43	56	33
	<i>n_a</i>		3	3	3	4	4	4	4	4	4	4	4	4	4	2	3	3
	<i>n_{eff}</i>		2.62	2.38	2.24	2.62	2.38	2.45	2.86	2.52	3.30	2.34	2.73	2.44	2.17	1.98	2.05	2.55
	<i>a</i>		3.0	2.9	2.8	3.7	3.3	3.4	3.5	3.3	3.9	3.1	3.4	3.4	2.7	2.0	2.4	3.0
	<i>H_E</i>		0.618	0.580	0.553	0.619	0.580	0.593	0.651	0.603	0.697	0.572	0.633	0.590	0.539	0.496	0.512	0.608
	<i>H_O</i>		0.558	0.589	0.538	0.500	0.475	0.575	0.711	0.543	0.647	0.608	0.517	0.652	0.481	0.535	0.482	0.515
	<i>F_{IS}</i>		0.098	-0.016	0.027	0.194	0.183	0.029	-0.093	0.100	0.073	-0.064	0.186	-0.106	0.108	-0.079	0.058	0.155
ER																		
	1	50	0.069	0.01	0.043	0.064	0.138	0.01	0.007	0.52	0	0.455	0.268	0.344	0.2	0.213	0.193	0.227
	2	60	0.931	0.99	0.957	0.936	0.863	0.99	0.993	0.48	1	0.545	0.732	0.656	0.8	0.787	0.807	0.773
	<i>n</i>		87	52	93	39	40	48	70	75	25	77	28	48	50	47	57	33
	<i>n_a</i>		2	2	2	2	2	2	2	2	1	2	2	2	2	2	2	2
	<i>n_{eff}</i>		1.15	1.02	1.09	1.14	1.32	1.02	1.01	2.01	1.00	2.00	1.66	1.84	1.48	1.51	1.46	1.55
	<i>a</i>		1.8	1.2	1.6	1.8	2.0	1.2	1.2	2.0	1.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
	<i>H_E</i>		0.129	0.019	0.083	0.122	0.240	0.021	0.014	0.503	0	0.499	0.399	0.456	0.323	0.339	0.314	0.357
	<i>H_O</i>		0.138	0.019	0.086	0.128	0.175	0.021	0.014	0.507	0	0.597	0.536	0.521	0.240	0.298	0.246	0.394
	<i>F_{IS}</i>		-0.068	0	-0.040	-0.056	0.274	0	0	-0.008	0	-0.198	-0.350	-0.144	0.259	0.121	0.220	-0.106
PL																		
	1	70	0.135	0.093	0.077	0.15	0.218	0.074	0.169	0.014	0.059	0.117	0.033	0.042	0.23	0.125	0.17	0.226
	2	80	0.865	0.907	0.923	0.85	0.782	0.926	0.831	0.986	0.941	0.883	0.967	0.958	0.77	0.875	0.83	0.774
	<i>n</i>		89	43	91	40	39	68	74	73	34	77	30	48	61	44	56	31
	<i>n_a</i>		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
	<i>n_{eff}</i>		1.31	1.21	1.17	1.35	1.53	1.16	1.39	1.03	1.13	1.26	1.07	1.09	1.55	1.28	1.40	1.55
	<i>a</i>		2.0	1.9	1.8	2.0	2.0	1.8	2.0	1.3	1.8	1.9	1.6	1.7	2.0	2.0	2.0	2.0
	<i>H_E</i>		0.235	0.171	0.143	0.258	0.345	0.137	0.283	0.027	0.112	0.208	0.066	0.081	0.357	0.221	0.284	0.355
	<i>H_O</i>		0.270	0.186	0.132	0.250	0.333	0.147	0.311	0.027	0.118	0.234	0.067	0.042	0.295	0.250	0.304	0.452
	<i>F_{IS}</i>		-0.150	-0.091	0.077	0.032	0.035	-0.072	-0.100	-0.007	-0.048	-0.126	-0.018	0.486	0.174	-0.132	-0.069	-0.277
RF																		
	1	51	0.005	0	0	0.026	0.026	0.032	0	0.019	0	0.006	0	0	0.016	0.01	0.016	0
	2	52	0.995	1	1	0.974	0.974	0.968	1	0.981	1	0.994	1	1	0.984	0.99	0.984	1
	<i>n</i>		94	68	95	38	39	79	80	78	39	79	25	43	64	50	61	33
	<i>n_a</i>		2	1	1	2	2	2	1	2	1	2	1	1	2	2	2	1
	<i>n_{eff}</i>		1.01	1.00	1.00	1.05	1.05	1.07	1.00	1.04	1.00	1.01	1.00	1.00	1.03	1.02	1.03	1.00
	<i>a</i>		1.1	1.0	1.0	1.5	1.5	1.5	1.0	1.4	1.0	1.1	1.0	1.0	1.3	1.2	1.3	1.0
	<i>H_E</i>		0.011	0	0	0.052	0.051	0.062	0	0.038	0	0.013	0	0	0.031	0.020	0.033	0
	<i>H_O</i>		0.011	0	0	0.053	0.051	0.038	0	0.038	0	0.013	0	0	0.031	0.020	0.033	0
	<i>F_{IS}</i>		0	0	0	-0.014	-0.013	0.386	0	-0.013	0	0	0	0	-0.008	0	-0.008	0
CLOCK																		
	1	78	0.181	0.312	0.301	0.329	0.236	0.236	0.289	0.128	0.25	0.185	0.172	0.141	0.086	0.125	0.173	0.21
	2	79	0.819	0.688	0.699	0.671	0.764	0.764	0.711	0.872	0.75	0.815	0.828	0.859	0.914	0.875	0.827	0.79
	<i>n</i>		94	69	93	38	36	72	71	47	36	73	29	46	64	40	49	31
	<i>n_a</i>		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
	<i>n_{eff}</i>		1.42	1.76	1.73	1.81	1.58	1.57	1.71	1.29	1.61	1.44	1.41	1.33	1.19	1.28	1.41	1.51
	<i>a</i>		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	1.9	2.0	2.0	2.0
	<i>H_E</i>		0.298	0.432	0.423	0.447	0.366	0.363	0.414	0.225	0.380	0.304	0.290	0.245	0.158	0.222	0.290	0.337
	<i>H_O</i>		0.255	0.420	0.430	0.395	0.361	0.389	0.352	0.255	0.389	0.342	0.276	0.283	0.172	0.250	0.306	0.226
	<i>F_{IS}</i>		0.144	0.028	-0.017	0.119	0.013	-0.071	0.150	-0.136	-0.023	-0.129	0.051	-0.154	-0.086	-0.130	-0.057	0.333

Appendix I. Continued.

VT	Allele name	Population															
		17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
1	33	0.921	0.568	0.581	0.295	0.462	0.773	0.729	0.717	0.573	0.507	0.385	0.243	0.453	0.642	0.489	0.433
2	34	0.079	0.432	0.419	0.705	0.538	0.227	0.271	0.283	0.427	0.493	0.615	0.757	0.547	0.358	0.511	0.567
n		19	44	43	44	26	22	48	23	41	70	26	37	75	95	44	30
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
n_{eff}		1.18	1.99	1.97	1.73	2.03	1.56	1.66	1.71	1.98	2.01	1.93	1.60	2.00	1.86	2.02	2.00
a		1.9	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
H_E		0.149	0.496	0.492	0.421	0.507	0.359	0.399	0.414	0.495	0.503	0.483	0.373	0.499	0.462	0.505	0.499
H_O		0.053	0.500	0.512	0.364	0.538	0.273	0.292	0.304	0.366	0.500	0.308	0.486	0.533	0.463	0.477	0.600
F_{IS}		0.654	-0.007	-0.039	0.138	-0.064	0.246	0.271	0.270	0.264	0.007	0.367	-0.309	-0.069	-0.002	0.056	-0.206
IN																	
1	36	1	1	0.86	1	0.88	0.891	0.837	0.857	0.814	0.955	0.839	0.863	0.768	0.719	0.86	0.867
2	37	0	0	0.14	0	0.12	0.109	0.163	0.143	0.186	0.038	0.161	0.125	0.21	0.276	0.128	0.133
3	38	0	0	0	0	0	0	0	0	0	0.008	0	0.013	0.022	0.005	0.012	0
n		21	44	43	43	25	23	49	21	43	66	28	40	69	96	43	30
n_a		1	1	2	1	2	2	2	2	2	3	2	3	3	3	3	2
n_{eff}		1.00	1.00	1.32	1.00	1.27	1.25	1.38	1.33	1.44	1.10	1.38	1.32	1.58	1.69	1.33	1.31
a		1.0	1.0	2.0	1.0	2.0	2.0	2.0	2.0	2.0	1.8	2.0	2.2	2.4	2.1	2.2	2.0
H_E		0	0	0.243	0	0.216	0.198	0.276	0.251	0.306	0.088	0.275	0.243	0.368	0.409	0.246	0.235
H_O		0	0	0.233	0	0.160	0.217	0.286	0.286	0.233	0.091	0.321	0.250	0.333	0.417	0.256	0.267
F_{IS}		0	0	0.043	0	0.262	-0.100	-0.035	-0.143	0.243	-0.033	-0.174	-0.028	0.095	-0.018	-0.041	-0.137
SP																	
1	41	0.429	0.114	0.167	0.089	0.192	0.48	0.439	0.476	0.553	0.21	0.224	0.188	0.267	0.201	0.196	0.191
2	42	0.571	0.886	0.833	0.911	0.808	0.52	0.561	0.524	0.447	0.79	0.776	0.813	0.733	0.799	0.804	0.809
n		14	44	42	45	26	25	49	21	38	69	38	40	73	92	46	34
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
n_{eff}		2.03	1.26	1.39	1.20	1.46	2.04	1.99	2.05	2.00	1.50	1.54	1.45	1.65	1.48	1.47	1.46
a		2.0	2.0	2.0	1.9	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
H_E		0.508	0.204	0.281	0.164	0.317	0.509	0.498	0.511	0.501	0.334	0.352	0.309	0.394	0.323	0.318	0.314
H_O		0.429	0.227	0.286	0.178	0.231	0.560	0.592	0.286	0.316	0.333	0.342	0.275	0.425	0.359	0.304	0.324
F_{IS}		0.161	-0.117	-0.017	-0.086	0.275	-0.102	-0.192	0.447	0.373*	0.003	0.028	0.110	-0.078	-0.111	0.044	-0.031
RH																	
1	43	0.079	0	0.011	0.012	0.019	0	0.02	0.083	0.041	0.09	0.125	0.024	0	0.134	0.076	0.1
2	44	0.921	1	0.989	0.988	0.981	1	0.98	0.917	0.959	0.91	0.875	0.976	1	0.866	0.924	0.9
n		19	44	46	43	26	25	49	24	37	72	36	41	74	93	46	35
n_a		2	1	2	2	2	1	2	2	2	2	2	2	1	2	2	2
n_{eff}		1.18	1.00	1.02	1.02	1.04	1.00	1.04	1.18	1.09	1.20	1.29	1.05	1.00	1.31	1.17	1.22
a		1.9	1.0	1.2	1.3	1.4	1.0	1.4	1.9	1.7	1.9	2.0	1.5	1.0	2.0	1.9	1.9
H_E		0.149	0	0.022	0.023	0.038	0	0.040	0.156	0.079	0.165	0.222	0.048	0	0.234	0.142	0.183
H_O		0.158	0	0.022	0.023	0.038	0	0.041	0.167	0.081	0.153	0.250	0.049	0	0.247	0.152	0.143
F_{IS}		-0.059	0	0	0	0	0	-0.011	-0.070	-0.029	0.077	-0.129	-0.013	0	-0.057	-0.071	0.220
VR																	
1	51	0.118	0.128	0.3	0.459	0.25	0.438	0.311	0.267	0.204	0.225	0.293	0.182	0.055	0.058	0.163	0.077
2	52	0	0.384	0.52	0.216	0.442	0.083	0.1	0.233	0.167	0.077	0.052	0.091	0.117	0.053	0.033	0.058
3	53	0.765	0.465	0.18	0.176	0.25	0.396	0.433	0.333	0.463	0.556	0.569	0.591	0.523	0.726	0.63	0.692
4	54	0.118	0.023	0	0.149	0.058	0.083	0.156	0.167	0.167	0.141	0.086	0.136	0.305	0.163	0.174	0.173
n		17	43	25	37	26	24	45	15	27	71	29	33	64	95	46	26
n_a		3	4	3	4	4	4	4	4	4	4	4	4	4	4	4	4
n_{eff}		1.66	2.68	2.63	3.32	3.22	2.87	3.21	4.18	3.35	2.62	2.44	2.50	2.64	1.79	2.23	1.96
a		3.0	3.4	3.0	4.0	3.8	3.8	3.9	4.0	4.0	3.8	3.7	3.9	3.7	3.5	3.5	3.7
H_E		0.399	0.627	0.620	0.699	0.689	0.652	0.689	0.761	0.702	0.618	0.590	0.600	0.621	0.442	0.551	0.491
H_O		0.294	0.721	0.600	0.595	0.654	0.625	0.667	0.667	0.667	0.667	0.621	0.545	0.594	0.400	0.522	0.577
F_{IS}		0.269	-0.152	0.032	0.151	0.052	0.042	0.033	0.128*	0.051	0.066	-0.052	0.092	0.045	0.096	0.053	-0.179

Appendix I. Continued.

IS	Allele		Population															
	Allele name		17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
1	25	0.5	0.316	0.528	0.4	0.563	0.26	0.289	0.25	0.392	0.417	0.294	0.679	0.736	0.511	0.478	0.55	
2	35	0.059	0.145	0.028	0.1	0.021	0.1	0.044	0.205	0.135	0.042	0.25	0.018	0.027	0.133	0.13	0.133	
3	45	0.441	0.539	0.444	0.5	0.417	0.64	0.633	0.545	0.419	0.521	0.426	0.286	0.209	0.346	0.391	0.317	
4	55	0	0	0	0	0	0	0.033	0	0.054	0.021	0.029	0.018	0.027	0.011	0	0	
n		17	38	36	35	24	25	45	22	37	72	34	28	74	94	46	30	
n_a		3	3	3	3	3	3	4	3	4	4	4	4	4	4	3	3	
n_{eff}		2.32	2.48	2.13	2.43	2.09	2.10	2.08	2.58	2.93	2.26	3.11	1.87	1.71	2.53	2.55	2.43	
a		2.9	3.0	2.5	2.9	2.5	3.0	3.3	3.0	3.7	3.0	3.5	2.8	3.0	3.2	3.0	3.0	
H_E		0.569	0.596	0.531	0.588	0.520	0.523	0.518	0.612	0.659	0.557	0.678	0.466	0.415	0.605	0.608	0.589	
H_O		0.824	0.500	0.278	0.714	0.375	0.400	0.578	0.773	0.649	0.444	0.441	0.429	0.446	0.596	0.630	0.567	
F_{IS}		-0.469	0.163	0.480***	-0.218	0.284	0.239	-0.117	-0.270	0.015	0.203	0.353**	0.081	-0.075	0.016	-0.038	0.039	
ER																		
1	50	0.533	0.351	0.467	0.267	0.389	0.14	0.163	0.175	0.132	0.148	0.167	0.279	0.278	0.347	0.326	0.397	
2	60	0.467	0.649	0.533	0.733	0.611	0.86	0.837	0.825	0.868	0.852	0.833	0.721	0.722	0.653	0.674	0.603	
n		15	37	45	30	27	25	49	20	34	71	27	34	72	95	46	34	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		2.06	1.86	2.01	1.66	1.94	1.33	1.38	1.42	1.30	1.34	1.39	1.69	1.68	1.84	1.80	1.95	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.515	0.462	0.503	0.398	0.484	0.246	0.276	0.296	0.233	0.254	0.283	0.409	0.404	0.456	0.444	0.486	
H_O		0.533	0.649	0.489	0.267	0.556	0.280	0.245	0.350	0.265	0.268	0.259	0.382	0.444	0.421	0.435	0.324	
F_{IS}		-0.037	-0.412*	0.029	0.333	-0.150	-0.143	0.114	-0.188	-0.138	-0.055	0.085	0.065	-0.101	0.077	0.022	0.338	
PL																		
1	70	0.143	0.284	0.134	0.129	0.278	0.08	0.106	0.091	0.1	0.181	0.461	0.429	0.162	0.182	0.175	0.339	
2	80	0.857	0.716	0.866	0.871	0.722	0.92	0.894	0.909	0.9	0.819	0.539	0.571	0.838	0.818	0.825	0.661	
n		14	44	41	35	27	25	47	22	30	69	38	42	65	88	40	31	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.34	1.70	1.31	1.29	1.69	1.18	1.24	1.20	1.22	1.43	2.01	1.98	1.38	1.43	1.41	1.84	
a		2.0	2.0	2.0	2.0	2.0	1.9	1.9	1.9	1.9	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.254	0.411	0.235	0.227	0.409	0.150	0.192	0.169	0.183	0.299	0.504	0.496	0.273	0.299	0.292	0.455	
H_O		0.286	0.341	0.220	0.200	0.333	0.160	0.170	0.182	0.200	0.275	0.395	0.476	0.292	0.273	0.350	0.290	
F_{IS}		-0.130	0.173	0.067	0.122	0.188	-0.067	0.115	-0.077	-0.094	0.079	0.218	0.040	-0.071	0.089	-0.200	0.366	
RF																		
1	51	0	0.029	0.043	0.131	0.038	0	0.012	0.15	0.025	0.014	0.188	0.149	0.14	0.069	0.013	0.017	
2	52	1	0.971	0.957	0.869	0.962	1	0.988	0.85	0.975	0.986	0.813	0.851	0.86	0.931	0.987	0.983	
n		16	34	46	42	26	23	43	20	40	70	32	37	75	80	39	30	
n_a		1	2	2	2	2	1	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.00	1.06	1.09	1.30	1.08	1.00	1.02	1.35	1.05	1.03	1.45	1.35	1.32	1.15	1.03	1.03	
a		1.0	1.5	1.7	2.0	1.7	1.0	1.3	2.0	1.5	1.3	2.0	2.0	2.0	1.8	1.3	1.4	
H_E		0	0.058	0.084	0.230	0.075	0	0.023	0.262	0.049	0.028	0.310	0.257	0.242	0.129	0.026	0.033	
H_O		0	0.059	0.087	0.262	0.077	0	0.023	0.200	0.050	0.029	0.188	0.189	0.227	0.138	0.026	0.033	
F_{IS}		0	-0.015	-0.034	-0.139	-0.020	0	0	0.240	-0.013	-0.007	0.398*	0.265	0.065	-0.068	0	0	
CLOCK																		
1	78	0.455	0.347	0.449	0.218	0.318	0.16	0.128	0.25	0.189	0.229	0.314	0.284	0.073	0.263	0.287	0.279	
2	79	0.545	0.653	0.551	0.782	0.682	0.84	0.872	0.75	0.811	0.771	0.686	0.716	0.927	0.737	0.713	0.721	
n		11	36	39	39	22	25	47	18	45	72	35	37	75	93	47	34	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		2.08	1.85	2.00	1.53	1.80	1.38	1.29	1.63	1.45	1.55	1.78	1.70	1.16	1.64	1.71	1.69	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	1.8	2.0	2.0	2.0	
H_E		0.519	0.460	0.501	0.345	0.444	0.274	0.225	0.386	0.310	0.356	0.437	0.412	0.137	0.390	0.414	0.409	
H_O		0.364	0.472	0.641	0.282	0.455	0.240	0.213	0.278	0.333	0.292	0.400	0.459	0.120	0.419	0.447	0.265	
F_{IS}		0.310	-0.028	-0.284	0.185	-0.024	0.127	0.055	0.286	-0.077	0.181	0.086	-0.117	0.124	-0.075	-0.081	0.356	

Appendix I. Continued.

VT	Allele name	Population															
		33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48
1	33	0.63	0.681	0.477	0.41	0.422	0.44	0.479	0.361	0.55	0.396	0.443	0.464	0.371	0.511	0.393	0.424
2	34	0.37	0.319	0.523	0.59	0.578	0.56	0.521	0.639	0.45	0.604	0.557	0.536	0.629	0.489	0.607	0.576
<i>n</i>		46	47	107	72	90	83	94	90	90	96	96	96	93	91	28	92
<i>n_a</i>		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
<i>n_{eff}</i>		1.89	1.78	2.01	1.95	1.96	1.98	2.01	1.87	1.99	1.93	1.98	2.00	1.88	2.01	1.94	1.96
<i>a</i>		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
<i>H_E</i>		0.471	0.439	0.501	0.487	0.491	0.496	0.502	0.464	0.498	0.481	0.496	0.500	0.469	0.503	0.486	0.491
<i>H_O</i>		0.565	0.511	0.449	0.458	0.533	0.470	0.553	0.456	0.411	0.500	0.448	0.552	0.419	0.429	0.571	0.543
<i>F_{IS}</i>		-0.202	-0.165	0.105	0.059	-0.088	0.052	-0.103	0.018	0.175	-0.040	0.097	-0.105	0.107	0.148	-0.180	-0.107
IN																	
1	36	0.75	0.691	0.936	0.974	0.778	0.81	0.863	0.612	0.701	0.76	0.771	0.849	0.853	0.811	0.856	0.803
2	37	0.25	0.298	0.054	0	0.103	0.13	0.121	0.383	0.278	0.24	0.229	0.151	0.147	0.189	0.144	0.176
3	38	0	0.011	0.01	0.026	0.119	0.06	0.016	0.005	0.021	0	0	0	0	0	0	0.021
<i>n</i>		48	47	102	76	63	92	95	98	97	96	96	96	95	95	45	94
<i>n_a</i>		2	3	3	2	3	3	3	3	3	2	2	2	2	2	2	3
<i>n_{eff}</i>		1.61	1.78	1.14	1.05	1.60	1.48	1.32	1.93	1.76	1.58	1.55	1.35	1.34	1.45	1.33	1.48
<i>a</i>		2.0	2.2	1.9	1.5	2.9	2.7	2.3	2.1	2.4	2.0	2.0	2.0	2.0	2.0	2.0	2.4
<i>H_E</i>		0.379	0.438	0.121	0.052	0.373	0.325	0.241	0.481	0.433	0.366	0.355	0.258	0.253	0.309	0.250	0.325
<i>H_O</i>		0.375	0.426	0.127	0.026	0.333	0.326	0.221	0.439	0.433	0.313	0.333	0.219	0.211	0.253	0.200	0.351
<i>F_{IS}</i>		0.011	0.028	-0.054	0.492*	0.108	-0.002	0.084	0.089	0	0.147	0.062	0.152	0.167	0.183	0.202	-0.079
SP																	
1	41	0.25	0.266	0.287	0.314	0.576	0.593	0.425	0.505	0.546	0.463	0.51	0.516	0.565	0.532	0.488	0.565
2	42	0.75	0.734	0.713	0.686	0.424	0.407	0.575	0.495	0.454	0.537	0.49	0.484	0.435	0.468	0.512	0.435
<i>n</i>		42	47	101	70	92	86	93	94	97	95	96	94	93	94	43	92
<i>n_a</i>		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
<i>n_{eff}</i>		1.61	1.65	1.70	1.77	1.96	1.94	1.97	2.01	1.99	2.00	2.01	2.01	1.98	2.00	2.02	1.98
<i>a</i>		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
<i>H_E</i>		0.380	0.395	0.411	0.434	0.491	0.486	0.491	0.503	0.498	0.500	0.502	0.502	0.494	0.501	0.506	0.494
<i>H_O</i>		0.357	0.362	0.455	0.486	0.522	0.581	0.570	0.500	0.515	0.568	0.563	0.457	0.484	0.511	0.465	0.522
<i>F_{IS}</i>		0.060	0.084	-0.108	-0.120	-0.063	-0.199	-0.161	0.005	-0.035	-0.138	-0.120	0.089	0.021	-0.020	0.081	-0.056
RH																	
1	43	0.149	0.074	0.041	0.045	0.043	0.056	0.032	0.01	0.04	0.016	0.026	0.043	0.026	0.017	0.012	0.016
2	44	0.851	0.926	0.959	0.955	0.957	0.944	0.968	0.99	0.96	0.984	0.974	0.957	0.974	0.983	0.988	0.984
<i>n</i>		47	47	109	77	93	89	93	98	99	95	95	94	95	90	42	93
<i>n_a</i>		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
<i>n_{eff}</i>		1.34	1.16	1.09	1.10	1.09	1.12	1.07	1.02	1.08	1.03	1.05	1.09	1.05	1.03	1.02	1.03
<i>a</i>		2.0	1.9	1.6	1.7	1.6	1.7	1.5	1.2	1.6	1.3	1.5	1.6	1.5	1.3	1.3	1.3
<i>H_E</i>		0.256	0.139	0.080	0.087	0.083	0.107	0.063	0.020	0.078	0.031	0.052	0.082	0.052	0.033	0.024	0.032
<i>H_O</i>		0.255	0.106	0.083	0.091	0.086	0.090	0.065	0.020	0.081	0.032	0.053	0.064	0.053	0.011	0.024	0.032
<i>F_{IS}</i>		0.004	0.238	-0.038	-0.041	-0.040	0.158	-0.028	-0.005	-0.037	-0.011	-0.022	0.222	-0.022	0.664*	0	-0.011
VR																	
1	51	0.136	0.05	0.269	0.326	0.371	0.282	0.388	0.374	0.426	0.361	0.354	0.359	0.376	0.362	0.43	0.412
2	52	0.061	0.063	0.101	0.106	0.171	0.167	0.144	0.047	0.205	0.167	0.141	0.125	0.134	0.17	0.047	0.159
3	53	0.697	0.738	0.404	0.318	0.3	0.42	0.266	0.442	0.258	0.222	0.224	0.245	0.22	0.277	0.221	0.198
4	54	0.106	0.15	0.226	0.25	0.159	0.132	0.202	0.137	0.111	0.25	0.281	0.271	0.269	0.191	0.302	0.231
<i>n</i>		33	40	104	66	85	87	94	95	95	90	96	96	93	94	43	91
<i>n_a</i>		4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
<i>n_{eff}</i>		1.95	1.76	3.41	3.63	3.60	3.37	3.58	2.84	3.35	3.76	3.69	3.65	3.61	3.72	3.13	3.53
<i>a</i>		3.7	3.5	3.9	3.9	4.0	4.0	4.0	3.6	3.9	4.0	4.0	4.0	4.0	4.0	3.7	4.0
<i>H_E</i>		0.488	0.433	0.707	0.724	0.723	0.703	0.721	0.647	0.701	0.734	0.729	0.726	0.723	0.731	0.680	0.716
<i>H_O</i>		0.455	0.375	0.721	0.818	0.765	0.747	0.691	0.653	0.663	0.689	0.625	0.760	0.796	0.713	0.674	0.714
<i>F_{IS}</i>		0.070	0.135	-0.021	-0.131	-0.059	-0.062	0.041	-0.008	0.054	0.062	0.144	-0.048	-0.101	0.025	0.009	0.003

Appendix I. Continued.

IS	Allele		Population															
	Allele name		33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48
1	25	0.561	0.634	0.757	0.623	0.431	0.475	0.505	0.283	0.423	0.447	0.609	0.646	0.511	0.605	0.486	0.674	
2	35	0.085	0.037	0.023	0.032	0.138	0.031	0.038	0.131	0.046	0.089	0.047	0.047	0.157	0.093	0.068	0.157	
3	45	0.354	0.317	0.144	0.266	0.431	0.494	0.457	0.586	0.526	0.463	0.344	0.307	0.331	0.302	0.446	0.169	
4	55	0	0.012	0.077	0.078	0	0	0	0	0.005	0	0	0	0	0	0	0	
n		41	41	111	77	87	80	93	99	98	95	96	96	89	86	37	89	
n_a		3	4	4	4	3	3	3	3	4	3	3	3	3	3	3	3	
n_{eff}		2.27	2.01	1.67	2.16	2.58	2.14	2.16	2.29	2.20	2.38	2.04	1.96	2.55	2.16	2.31	1.98	
a		2.9	2.9	3.2	3.4	3.0	2.5	2.6	3.0	2.8	2.9	2.7	2.7	3.0	2.9	2.8	3.0	
H_E		0.560	0.502	0.402	0.537	0.613	0.533	0.537	0.562	0.545	0.580	0.511	0.489	0.607	0.537	0.568	0.495	
H_O		0.634	0.439	0.441	0.429	0.701	0.538	0.505	0.566	0.622	0.632	0.552	0.448	0.618	0.570	0.595	0.596	
F_{IS}		-0.135	0.127	-0.099	0.203*	-0.145	-0.009	0.060	-0.006	-0.143	-0.089	-0.081	0.084	-0.017	-0.060	-0.048	-0.204	
ER																		
1	50	0.25	0.231	0.207	0.196	0.098	0.203	0.074	0.06	0.046	0.038	0.057	0.083	0.105	0.087	0.033	0.214	
2	60	0.75	0.769	0.793	0.804	0.902	0.797	0.926	0.94	0.954	0.962	0.943	0.917	0.895	0.913	0.967	0.786	
n		46	39	111	74	87	91	95	67	76	92	96	96	95	92	30	56	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.61	1.56	1.49	1.46	1.22	1.48	1.16	1.13	1.10	1.08	1.12	1.18	1.23	1.19	1.07	1.51	
a		2.0	2.0	2.0	2.0	1.9	2.0	1.8	1.8	1.7	1.6	1.7	1.9	1.9	1.9	1.6	2.0	
H_E		0.379	0.360	0.330	0.317	0.177	0.326	0.137	0.113	0.088	0.074	0.109	0.154	0.189	0.160	0.066	0.340	
H_O		0.326	0.462	0.324	0.392	0.149	0.385	0.126	0.119	0.092	0.054	0.115	0.167	0.211	0.152	0.067	0.357	
F_{IS}		0.141	-0.288	0.017	-0.237	0.158	-0.182	0.080	-0.056	-0.042	0.263	-0.056	-0.086	-0.112	0.047	-0.018	-0.052	
PL																		
1	70	0.151	0.25	0.106	0.075	0.054	0	0.038	0.052	0.015	0.084	0.068	0.073	0.064	0.115	0.065	0.027	
2	80	0.849	0.75	0.894	0.925	0.946	1	0.962	0.948	0.985	0.916	0.932	0.927	0.936	0.885	0.935	0.973	
n		43	42	104	67	84	76	92	97	98	95	96	96	78	87	46	91	
n_a		2	2	2	2	2	1	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.35	1.61	1.23	1.16	1.11	1.00	1.08	1.11	1.03	1.18	1.15	1.16	1.14	1.26	1.14	1.06	
a		2.0	2.0	1.9	1.8	1.7	1.0	1.6	1.7	1.3	1.9	1.8	1.8	1.8	1.9	1.8	1.5	
H_E		0.260	0.380	0.190	0.139	0.102	0	0.074	0.098	0.030	0.155	0.127	0.136	0.121	0.205	0.123	0.054	
H_O		0.209	0.310	0.212	0.149	0.107	0	0.076	0.103	0.031	0.126	0.135	0.146	0.128	0.138	0.130	0.055	
F_{IS}		0.196	0.186	-0.114	-0.073	-0.051	0	-0.034	-0.049	-0.010	0.186	-0.067	-0.073	-0.062	0.327*	-0.059	-0.023	
RF																		
1	51	0.076	0.106	0.189	0.242	0.275	0.451	0.353	0.288	0.242	0.356	0.314	0.306	0.31	0.278	0.33	0.261	
2	52	0.924	0.894	0.811	0.758	0.725	0.549	0.647	0.712	0.758	0.644	0.686	0.694	0.69	0.722	0.67	0.739	
n		46	47	106	64	91	91	85	85	95	94	94	93	79	90	44	94	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.17	1.24	1.44	1.59	1.67	1.99	1.85	1.70	1.58	1.86	1.76	1.75	1.76	1.68	1.81	1.63	
a		1.9	1.9	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.142	0.192	0.308	0.370	0.401	0.498	0.459	0.413	0.369	0.461	0.433	0.427	0.431	0.403	0.447	0.387	
H_O		0.152	0.170	0.283	0.391	0.352	0.571	0.494	0.341	0.442	0.500	0.394	0.398	0.494	0.489	0.477	0.372	
F_{IS}		-0.071	0.115	0.080	-0.056	0.123	-0.149	-0.076	0.174	-0.200	-0.085	0.091	0.069	-0.147	-0.213	-0.069	0.039	
CLOCK																		
1	78	0.34	0.3	0.267	0.304	0.261	0.332	0.247	0.201	0.27	0.269	0.197	0.25	0.344	0.277	0.289	0.253	
2	79	0.66	0.7	0.733	0.696	0.739	0.668	0.753	0.799	0.73	0.731	0.803	0.75	0.656	0.723	0.711	0.747	
n		47	45	103	74	90	92	93	97	87	93	94	96	93	92	45	89	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.83	1.74	1.65	1.74	1.63	1.80	1.60	1.48	1.66	1.65	1.47	1.61	1.83	1.67	1.71	1.61	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.454	0.425	0.393	0.426	0.388	0.446	0.374	0.323	0.397	0.395	0.318	0.377	0.454	0.403	0.415	0.380	
H_O		0.468	0.467	0.359	0.392	0.389	0.533	0.366	0.340	0.448	0.387	0.309	0.396	0.366	0.380	0.444	0.371	
F_{IS}		-0.032	-0.100	0.087	0.081	-0.002	-0.196	0.023	-0.054	-0.131	0.021	0.030	-0.050	0.195	0.056	-0.071	0.024	

Appendix I. Continued.

VT		Population															
Allele	Allele name	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
1	33	0.474	0.385	0.372	0.323	0.406	0.165	0.203	0.24	0.258	0.247	0.205	0.184	0.431	0.438	0.419	0.449
2	34	0.526	0.615	0.628	0.677	0.594	0.835	0.797	0.76	0.742	0.753	0.795	0.816	0.569	0.562	0.581	0.551
n		96	96	74	48	48	82	96	96	95	95	95	95	65	73	93	89
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
n_{eff}		2.01	1.91	1.89	1.79	1.95	1.38	1.48	1.58	1.63	1.60	1.49	1.43	1.98	1.98	1.96	1.99
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
H_E		0.501	0.476	0.470	0.442	0.488	0.277	0.325	0.366	0.385	0.374	0.328	0.302	0.494	0.496	0.490	0.498
H_O		0.531	0.479	0.554	0.354	0.479	0.280	0.344	0.417	0.432	0.411	0.305	0.284	0.615	0.438	0.409	0.427
F_{IS}		-0.060	-0.006	-0.180	0.200	0.017	-0.014	-0.057	-0.138	-0.122	-0.097	0.070	0.060	-0.248	0.117	0.166	0.143
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IN																	
1	36	0.802	0.87	0.851	0.823	0.719	0.8	0.891	0.828	0.789	0.816	0.878	0.921	0.809	0.764	0.835	0.815
2	37	0.198	0.13	0.142	0.177	0.281	0.2	0.109	0.172	0.211	0.184	0.122	0.079	0.184	0.236	0.165	0.185
3	38	0	0	0.007	0	0	0	0	0	0	0	0	0	0.007	0	0	0
n		96	96	74	48	48	60	96	96	95	95	94	95	76	72	88	81
n_a		2	2	3	2	2	2	2	2	2	2	2	2	3	2	2	2
n_{eff}		1.47	1.29	1.35	1.42	1.69	1.48	1.24	1.40	1.50	1.43	1.28	1.17	1.46	1.57	1.38	1.44
a		2.0	2.0	2.1	2.0	2.0	2.0	1.9	2.0	2.0	2.0	2.0	1.9	2.1	2.0	2.0	2.0
H_E		0.319	0.228	0.257	0.295	0.409	0.323	0.196	0.286	0.334	0.302	0.216	0.146	0.313	0.363	0.277	0.304
H_O		0.271	0.219	0.216	0.313	0.313	0.300	0.219	0.240	0.337	0.368	0.245	0.158	0.250	0.278	0.284	0.272
F_{IS}		0.152	0.039	0.159	-0.062	0.237	0.071	-0.118	0.163	-0.008	-0.221*	-0.134	-0.080	0.203	0.237	-0.026	0.106
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SP																	
1	41	0.563	0.571	0.534	0.573	0.583	0.5	0.474	0.464	0.468	0.5	0.628	0.658	0.527	0.603	0.586	0.552
2	42	0.437	0.429	0.466	0.427	0.417	0.5	0.526	0.536	0.532	0.5	0.372	0.342	0.473	0.397	0.414	0.448
n		95	92	74	48	48	76	96	96	95	94	92	75	73	93	96	96
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
n_{eff}		1.98	1.97	2.00	1.98	1.97	2.01	2.01	2.00	2.00	2.01	1.89	1.83	2.01	1.93	1.95	1.99
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
H_E		0.495	0.493	0.501	0.495	0.491	0.503	0.501	0.500	0.501	0.503	0.470	0.453	0.502	0.482	0.488	0.497
H_O		0.474	0.554	0.446	0.396	0.458	0.526	0.573	0.469	0.495	0.532	0.511	0.467	0.493	0.493	0.484	0.458
F_{IS}		0.043	-0.126	0.111	0.201	0.068	-0.046	-0.144	0.063	0.012	-0.059	-0.087	-0.032	0.017	-0.023	0.008	0.078
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RH																	
1	43	0.068	0.011	0.014	0	0.063	0.029	0.021	0.005	0.016	0.005	0	0.027	0.007	0.021	0.037	0
2	44	0.932	0.989	0.986	1	0.938	0.971	0.979	0.995	0.984	0.995	1	0.973	0.993	0.979	0.963	1
n		96	95	74	48	48	87	96	96	94	95	95	93	76	73	94	96
n_a		2	2	2	1	2	2	2	2	2	2	1	2	2	2	2	1
n_{eff}		1.15	1.02	1.03	1.00	1.13	1.06	1.04	1.01	1.03	1.01	1.00	1.06	1.01	1.04	1.08	1.00
a		1.8	1.2	1.3	1.0	1.8	1.5	1.4	1.1	1.3	1.1	1.0	1.5	1.1	1.4	1.6	1.0
H_E		0.127	0.021	0.027	0	0.118	0.056	0.041	0.010	0.032	0.011	0	0.053	0.013	0.041	0.072	0
H_O		0.135	0.021	0.027	0	0.125	0.034	0.042	0.010	0.032	0.011	0	0.054	0.013	0.041	0.074	0
F_{IS}		-0.067	-0.005	-0.007	0	-0.056	0.387	-0.016	0	-0.011	0	0	-0.022	0	-0.014	-0.033	0
<hr/>																	
VR																	
1	51	0.375	0.384	0.365	0.378	0.326	0.463	0.526	0.5	0.543	0.505	0.774	0.541	0.441	0.387	0.424	0.592
2	52	0.188	0.2	0.196	0.233	0.256	0.177	0.135	0.184	0.149	0.179	0.042	0.145	0.184	0.12	0.168	0.121
3	53	0.219	0.174	0.243	0.167	0.14	0.098	0.193	0.116	0.096	0.147	0.047	0.064	0.151	0.155	0.163	0.27
4	54	0.219	0.242	0.196	0.222	0.279	0.262	0.146	0.2	0.213	0.168	0.137	0.25	0.224	0.338	0.245	0.017
n		96	95	74	45	43	82	96	95	94	95	95	86	76	71	92	87
n_a		4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
n_{eff}		3.74	3.67	3.79	3.76	3.84	3.12	2.86	3.00	2.72	2.99	1.61	2.66	3.37	3.36	3.44	2.30
a		4.0	4.0	4.0	4.0	4.0	3.9	3.9	3.9	3.9	4.0	3.3	3.8	4.0	3.9	4.0	3.3
H_E		0.732	0.727	0.736	0.734	0.740	0.680	0.650	0.666	0.632	0.666	0.381	0.624	0.703	0.702	0.709	0.565
H_O		0.698	0.832	0.730	0.844	0.651	0.671	0.656	0.642	0.617	0.674	0.389	0.593	0.684	0.704	0.772	0.598
F_{IS}		0.047	-0.144	0.008	-0.153	0.121	0.014	-0.010	0.036	0.024	-0.011	-0.023	0.049	0.028	-0.003	-0.088	-0.058

Appendix I. Continued.

IS	Allele		Population															
	Allele name		49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
1	25	0.448	0.577	0.534	0.535	0.564	0.644	0.758	0.558	0.517	0.564	0.663	0.803	0.563	0.5	0.505	0.601	
2	35	0.12	0.054	0.089	0.14	0.128	0.098	0.011	0.053	0.078	0.085	0.032	0.067	0.063	0.063	0.112	0.08	
3	45	0.432	0.369	0.377	0.326	0.309	0.259	0.232	0.389	0.406	0.351	0.305	0.129	0.373	0.43	0.383	0.314	
4	55	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0	0.005	
n		96	84	73	43	47	87	95	95	90	94	95	89	71	71	94	94	
n_a		3	3	3	3	3	3	3	3	3	3	3	3	3	4	3	4	
n_{eff}		2.51	2.13	2.32	2.47	2.36	2.05	1.60	2.16	2.30	2.24	1.88	1.50	2.19	2.30	2.43	2.16	
a		2.9	2.7	2.9	3.0	3.0	2.9	2.2	2.7	2.9	2.9	2.5	2.8	2.8	2.9	2.9	3.0	
H_E		0.601	0.531	0.569	0.595	0.577	0.512	0.374	0.537	0.566	0.555	0.469	0.335	0.543	0.565	0.589	0.537	
H_O		0.615	0.488	0.671	0.535	0.553	0.529	0.411	0.495	0.533	0.574	0.463	0.337	0.606	0.592	0.574	0.543	
F_{IS}		-0.022	0.081	-0.182	0.103	0.041	-0.032	-0.099	0.079	0.057	-0.036	0.011	-0.006	-0.116	-0.047	0.024	-0.011	
ER																		
1	50	0.078	0.047	0.092	0.073	0.021	0.063	0.052	0.016	0.011	0	0	0	0.069	0.06	0.071	0.068	
2	60	0.922	0.953	0.908	0.927	0.979	0.937	0.948	0.984	0.989	1	1	1	0.931	0.94	0.929	0.932	
n		90	86	71	48	48	87	96	95	95	95	78	86	72	67	85	95	
n_a		2	2	2	2	2	2	2	2	2	1	1	1	2	2	2	2	
n_{eff}		1.17	1.10	1.20	1.16	1.04	1.14	1.11	1.03	1.02	1.00	1.00	1.00	1.15	1.13	1.15	1.15	
a		1.9	1.7	1.9	1.8	1.4	1.8	1.7	1.3	1.2	1.0	1.0	1.0	1.8	1.8	1.8	1.8	
H_E		0.144	0.089	0.168	0.137	0.041	0.119	0.099	0.031	0.021	0	0	0	0.130	0.113	0.132	0.128	
H_O		0.156	0.093	0.155	0.146	0.042	0.126	0.104	0.032	0.021	0	0	0	0.139	0.119	0.141	0.137	
F_{IS}		-0.079	-0.043	0.076	-0.068	-0.011	-0.062	-0.050	-0.011	-0.005	0	0	0	-0.068	-0.056	-0.070	-0.068	
PL																		
1	70	0.085	0.16	0.195	0.125	0.096	0.066	0.07	0.13	0.023	0.044	0.016	0.006	0.101	0.196	0.023	0.116	
2	80	0.915	0.84	0.805	0.875	0.904	0.934	0.93	0.87	0.977	0.956	0.984	0.994	0.899	0.804	0.977	0.884	
n		94	78	64	44	47	91	86	96	87	91	91	87	74	69	86	95	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.19	1.37	1.46	1.28	1.21	1.14	1.15	1.29	1.05	1.09	1.03	1.01	1.22	1.46	1.05	1.26	
a		1.9	2.0	2.0	2.0	1.9	1.8	1.8	2.0	1.4	1.7	1.3	1.1	1.9	2.0	1.4	1.9	
H_E		0.157	0.271	0.317	0.221	0.175	0.124	0.131	0.228	0.045	0.085	0.033	0.011	0.183	0.317	0.046	0.206	
H_O		0.170	0.218	0.266	0.205	0.191	0.110	0.140	0.260	0.046	0.088	0.033	0.011	0.203	0.246	0.047	0.211	
F_{IS}		-0.088	0.196	0.163	0.076	-0.095	0.113	-0.069	-0.145	-0.018	-0.040	-0.011	0	-0.106	0.224	-0.018	-0.023	
RF																		
1	51	0.321	0.37	0.397	0.352	0.385	0.557	0.625	0.516	0.571	0.608	0.384	0.596	0.281	0.288	0.3	0.302	
2	52	0.679	0.63	0.603	0.648	0.615	0.443	0.375	0.484	0.429	0.392	0.616	0.404	0.719	0.712	0.7	0.698	
n		92	81	63	44	48	88	92	94	92	83	95	83	73	73	90	96	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.78	1.88	1.93	1.86	1.92	1.99	1.89	2.01	1.97	1.92	1.91	1.94	1.69	1.70	1.73	1.74	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.438	0.469	0.483	0.462	0.479	0.496	0.471	0.502	0.493	0.479	0.476	0.484	0.407	0.413	0.422	0.424	
H_O		0.467	0.395	0.476	0.432	0.563	0.386	0.380	0.479	0.424	0.422	0.432	0.518	0.452	0.466	0.422	0.438	
F_{IS}		-0.067	0.159	0.013	0.065	-0.177	0.223	0.194	0.047	0.140	0.121	0.093	-0.070	-0.112	-0.130	0.000	-0.032	
CLOCK																		
1	78	0.277	0.297	0.261	0.305	0.25	0.185	0.351	0.293	0.375	0.339	0.433	0.37	0.323	0.325	0.37	0.32	
2	79	0.723	0.703	0.739	0.695	0.75	0.815	0.649	0.707	0.625	0.661	0.567	0.63	0.677	0.675	0.63	0.68	
n		94	91	69	41	48	81	94	94	88	93	90	73	65	63	92	89	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.67	1.72	1.64	1.75	1.61	1.44	1.85	1.71	1.89	1.82	1.98	1.88	1.79	1.79	1.88	1.78	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.402	0.420	0.388	0.429	0.379	0.304	0.458	0.416	0.471	0.450	0.494	0.469	0.441	0.443	0.469	0.438	
H_O		0.447	0.418	0.319	0.317	0.333	0.272	0.468	0.394	0.500	0.548	0.444	0.438	0.523	0.333	0.543	0.438	
F_{IS}		-0.111	0.005	0.180	0.263	0.121	0.106	-0.022	0.054	-0.061	-0.219*	0.101	0.066	-0.188	0.248	-0.161	-0.001	

Appendix I. Continued.

VT		Population																
Allele	Allele name	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	
1	33	0.39	0.371	0.434	0.407	0.392	0.37	0.401	0.287	0.302	0.286	0.4	0.387	0.361	0.415	0.5	0.407	
2	34	0.61	0.629	0.566	0.593	0.608	0.63	0.599	0.713	0.698	0.714	0.6	0.613	0.639	0.585	0.5	0.593	
<i>n</i>		41	58	76	59	148	50	91	94	96	96	75	93	72	94	96	75	
<i>n_a</i>		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
<i>n_{eff}</i>		1.93	1.89	1.98	1.95	1.92	1.89	1.93	1.70	1.74	1.70	1.94	1.91	1.87	1.95	2.01	1.94	
<i>a</i>		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
<i>H_E</i>		0.482	0.471	0.495	0.487	0.478	0.471	0.483	0.412	0.424	0.411	0.483	0.477	0.465	0.488	0.503	0.486	
<i>H_O</i>		0.390	0.500	0.474	0.542	0.459	0.460	0.385	0.319	0.396	0.385	0.480	0.452	0.556	0.383	0.542	0.520	
<i>F_{IS}</i>		0.192	-0.063	0.043	-0.115	0.039	0.023	0.205	0.226*	0.066	0.062	0.007	0.054	-0.197	0.216	-0.078	-0.071	
IN																		
1	36	0.845	0.819	0.85	0.741	0.789	0.844	0.815	0.66	0.703	0.707	0.88	0.835	0.804	0.83	0.818	0.793	
2	37	0.155	0.181	0.15	0.259	0.211	0.156	0.179	0.34	0.297	0.293	0.12	0.165	0.196	0.17	0.182	0.207	
3	38	0	0	0	0	0	0	0.006	0	0	0	0	0	0	0	0	0	
<i>n</i>		42	58	80	58	149	48	81	94	96	92	75	94	74	94	96	75	
<i>n_a</i>		2	2	2	2	2	2	3	2	2	2	2	2	2	2	2	2	
<i>n_{eff}</i>		1.36	1.43	1.35	1.63	1.50	1.36	1.44	1.82	1.72	1.72	1.27	1.38	1.46	1.40	1.43	1.49	
<i>a</i>		2.0	2.0	2.0	2.0	2.0	2.0	2.1	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
<i>H_E</i>		0.265	0.299	0.257	0.387	0.335	0.266	0.306	0.451	0.420	0.417	0.213	0.277	0.317	0.284	0.300	0.330	
<i>H_O</i>		0.214	0.259	0.200	0.448	0.329	0.271	0.321	0.468	0.469	0.478	0.240	0.245	0.311	0.255	0.323	0.307	
<i>F_{IS}</i>		0.193	0.136	0.222	-0.161	0.017	-0.017	-0.050	-0.037	-0.118	-0.148	-0.130	0.117	0.020	0.101	-0.078	0.071	
SP																		
1	41	0.464	0.543	0.549	0.586	0.521	0.632	0.549	0.49	0.521	0.511	0.507	0.531	0.399	0.468	0.51	0.48	
2	42	0.536	0.457	0.451	0.414	0.479	0.368	0.451	0.51	0.479	0.489	0.493	0.469	0.601	0.532	0.49	0.52	
<i>n</i>		42	58	92	58	146	57	92	96	96	95	75	96	74	94	96	75	
<i>n_a</i>		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
<i>n_{eff}</i>		2.01	2.00	1.99	1.96	2.00	1.88	1.99	2.01	2.01	2.01	2.01	2.00	1.93	2.00	2.01	2.01	
<i>a</i>		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
<i>H_E</i>		0.503	0.501	0.498	0.489	0.501	0.469	0.498	0.502	0.502	0.502	0.503	0.501	0.483	0.501	0.502	0.503	
<i>H_O</i>		0.452	0.569	0.511	0.655	0.493	0.351	0.489	0.500	0.375	0.537	0.640	0.521	0.392	0.447	0.542	0.453	
<i>F_{IS}</i>		0.103	-0.138	-0.026	-0.343**	0.015	0.254	0.018	0.005	0.254*	-0.069	-0.274*	-0.041	0.189	0.108	-0.079	0.099	
RH																		
1	43	0.048	0.009	0.049	0.034	0.02	0	0.049	0.016	0.036	0.057	0.033	0.031	0.007	0.011	0.063	0.053	
2	44	0.952	0.991	0.951	0.966	0.98	1	0.951	0.984	0.964	0.943	0.967	0.969	0.993	0.989	0.938	0.947	
<i>n</i>		42	58	92	58	151	57	92	96	96	96	75	96	74	94	96	75	
<i>n_a</i>		2	2	2	2	2	1	2	2	2	2	2	2	2	2	2	2	
<i>n_{eff}</i>		1.10	1.02	1.10	1.07	1.04	1.00	1.10	1.03	1.08	1.12	1.07	1.06	1.01	1.02	1.13	1.11	
<i>a</i>		1.7	1.2	1.7	1.6	1.4	1.0	1.7	1.3	1.6	1.7	1.6	1.5	1.1	1.2	1.8	1.7	
<i>H_E</i>		0.092	0.017	0.094	0.067	0.039	0	0.094	0.031	0.071	0.109	0.065	0.061	0.014	0.021	0.118	0.102	
<i>H_O</i>		0.095	0.017	0.098	0.034	0.026	0	0.098	0.031	0.073	0.115	0.067	0.063	0.014	0.021	0.104	0.107	
<i>F_{IS}</i>		-0.038	0	-0.046	0.489	0.323	0	-0.046	-0.011	-0.033	-0.056	-0.028	-0.027	0	-0.005	0.116	-0.050	
VR																		
1	51	0.427	0.457	0.687	0.444	0.453	0.378	0.647	0.383	0.386	0.31	0.405	0.41	0.452	0.324	0.296	0.336	
2	52	0.122	0.138	0.066	0.185	0.126	0.156	0.147	0.167	0.152	0.149	0.182	0.144	0.212	0.154	0.253	0.157	
3	53	0.22	0.198	0.211	0.167	0.147	0.233	0.182	0.2	0.272	0.259	0.176	0.197	0.075	0.231	0.22	0.224	
4	54	0.232	0.207	0.036	0.204	0.273	0.233	0.024	0.25	0.19	0.282	0.236	0.25	0.26	0.291	0.231	0.284	
<i>n</i>		41	58	83	54	139	45	85	90	92	87	74	94	73	91	93	67	
<i>n_a</i>		4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	
<i>n_{eff}</i>		3.45	3.29	1.93	3.39	3.17	3.74	2.12	3.66	3.60	3.84	3.58	3.50	3.14	3.81	4.01	3.81	
<i>a</i>		4.0	4.0	3.4	4.0	3.9	4.0	3.4	4.0	4.0	4.0	4.0	4.0	3.8	4.0	4.0	4.0	
<i>H_E</i>		0.710	0.696	0.481	0.705	0.685	0.732	0.529	0.727	0.722	0.739	0.720	0.714	0.682	0.737	0.751	0.738	
<i>H_O</i>		0.707	0.690	0.494	0.630	0.698	0.756	0.588	0.722	0.717	0.782	0.716	0.702	0.685	0.714	0.710	0.612	
<i>F_{IS}</i>		0.003	0.009	-0.027	0.108	-0.019	-0.032	-0.113	0.006	0.006	-0.057	0.006	0.017	-0.005	0.031	0.055	0.171	

Appendix I. Continued.

IS	Allele		Population															
	Allele name		65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
1	25	0.571	0.448	0.546	0.509	0.57	0.547	0.494	0.468	0.339	0.484	0.547	0.537	0.549	0.097	0.418	0.453	
2	35	0.119	0.172	0.098	0.089	0.096	0.123	0.133	0.059	0.065	0.033	0.093	0.1	0.07	0.548	0.187	0.125	
3	45	0.31	0.379	0.351	0.402	0.331	0.33	0.372	0.473	0.597	0.484	0.36	0.363	0.38	0.355	0.396	0.422	
4	55	0	0	0.006	0	0.003	0	0	0	0	0	0	0	0	0	0	0	
n		42	58	87	56	151	53	90	94	93	92	75	95	71	93	91	64	
n_a		3	3	4	3	4	3	3	3	3	3	3	3	3	3	3	3	
n_{eff}		2.33	2.71	2.34	2.36	2.27	2.39	2.52	2.25	2.12	2.15	2.31	2.34	2.24	2.31	2.76	2.54	
a		3.0	3.0	3.0	2.9	3.0	3.0	3.0	2.8	2.8	2.5	2.9	2.9	2.8	2.9	3.0	3.0	
H_E		0.570	0.631	0.573	0.577	0.559	0.582	0.603	0.556	0.528	0.534	0.567	0.573	0.553	0.567	0.638	0.606	
H_O		0.548	0.483	0.598	0.536	0.483	0.604	0.589	0.543	0.516	0.467	0.613	0.537	0.563	0.570	0.582	0.672	
F_{IS}		0.040	0.236	-0.044	0.072	0.135	-0.038*	0.023	0.025*	0.022	0.125	-0.083	0.063	-0.020	-0.005	0.087	-0.110	
ER																		
1	50	0.048	0.055	0.079	0.061	0.107	0.176	0.087	0.179	0.06	0.105	0.107	0.161	0.079	0.09	0.197	0.153	
2	60	0.952	0.945	0.921	0.939	0.893	0.824	0.913	0.821	0.94	0.895	0.893	0.839	0.921	0.91	0.803	0.847	
n		42	55	89	57	150	51	92	95	91	95	75	96	70	94	94	75	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.10	1.12	1.17	1.13	1.24	1.42	1.19	1.42	1.13	1.23	1.24	1.37	1.17	1.20	1.47	1.35	
a		1.7	1.7	1.9	1.8	1.9	2.0	1.9	2.0	1.8	1.9	1.9	2.0	1.9	1.9	2.0	2.0	
H_E		0.092	0.104	0.146	0.116	0.191	0.294	0.160	0.295	0.114	0.189	0.192	0.272	0.146	0.165	0.318	0.261	
H_O		0.095	0.109	0.135	0.123	0.160	0.275	0.174	0.274	0.121	0.211	0.160	0.219	0.157	0.160	0.330	0.280	
F_{IS}		-0.038	-0.049	0.075	-0.057	0.164	0.065	-0.090	0.074	-0.059	-0.112	0.167	0.197	-0.078	0.035	-0.038	-0.072	
PL																		
1	70	0.064	0	0.111	0.115	0.007	0.223	0.1	0.053	0.063	0.057	0.107	0.133	0.125	0.134	0.073	0.036	
2	80	0.936	1	0.889	0.885	0.993	0.777	0.9	0.947	0.938	0.943	0.893	0.867	0.875	0.866	0.927	0.964	
n		39	58	90	52	145	47	90	95	96	96	75	94	72	93	96	69	
n_a		2	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.14	1.00	1.25	1.26	1.01	1.54	1.22	1.11	1.13	1.12	1.24	1.30	1.28	1.31	1.16	1.08	
a		1.8	1.0	1.9	2.0	1.1	2.0	1.9	1.7	1.8	1.7	1.9	2.0	2.0	2.0	1.8	1.6	
H_E		0.122	0	0.199	0.206	0.014	0.351	0.181	0.100	0.118	0.109	0.192	0.232	0.220	0.234	0.136	0.070	
H_O		0.128	0	0.222	0.231	0.014	0.404	0.200	0.105	0.104	0.094	0.213	0.245	0.250	0.204	0.146	0.072	
F_{IS}		-0.056	0	-0.119	-0.121	-0.003	-0.155	-0.106	-0.050	0.116	0.137	-0.113	-0.056	-0.136	0.127	-0.073	-0.030	
RF																		
1	51	0.207	0.281	0.339	0.313	0.339	0.255	0.286	0.413	0.399	0.368	0.321	0.262	0.257	0.313	0.165	0.075	
2	52	0.793	0.719	0.661	0.688	0.661	0.745	0.714	0.587	0.601	0.632	0.679	0.738	0.743	0.687	0.835	0.925	
n		41	57	87	56	149	49	91	92	94	95	67	84	72	75	85	73	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.50	1.69	1.82	1.77	1.82	1.62	1.70	1.95	1.93	1.88	1.78	1.64	1.62	1.76	1.38	1.16	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	1.8	
H_E		0.333	0.407	0.451	0.434	0.450	0.384	0.410	0.488	0.482	0.468	0.439	0.389	0.385	0.433	0.277	0.140	
H_O		0.317	0.456	0.425	0.375	0.436	0.429	0.396	0.543	0.479	0.484	0.522	0.381	0.403	0.360	0.282	0.151	
F_{IS}		0.048	-0.121	0.057	0.136	0.030	-0.118	0.036	-0.115	0.007	-0.035	-0.191	0.021	-0.048	0.170	-0.020	-0.075	
CLOCK																		
1	78	0.232	0.302	0.301	0.333	0.283	0.333	0.25	0.223	0.276	0.195	0.295	0.333	0.235	0.298	0.291	0.25	
2	79	0.768	0.698	0.699	0.667	0.717	0.667	0.75	0.777	0.724	0.805	0.705	0.667	0.765	0.702	0.709	0.75	
n		41	58	88	57	150	54	90	94	96	95	73	93	66	84	91	54	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.56	1.74	1.73	1.81	1.69	1.81	1.61	1.54	1.67	1.46	1.72	1.81	1.57	1.73	1.71	1.61	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.360	0.425	0.423	0.448	0.407	0.449	0.377	0.349	0.402	0.315	0.418	0.447	0.362	0.421	0.415	0.379	
H_O		0.317	0.466	0.375	0.456	0.420	0.519	0.367	0.340	0.406	0.263	0.452	0.473	0.409	0.452	0.451	0.352	
F_{IS}		0.122	-0.096	0.115	-0.017	-0.031	-0.158	0.028	0.024	-0.011	0.166	-0.081	-0.059	-0.131	-0.076	-0.086	0.071	

Appendix I. Continued.

VT		Population																
Allele	Allele name	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	
1	33	0.355	0.283	0.41	0.357	0.785	0.25	0.69	0.447	0.273	0.458	0.489	0.372	0.306	0.433	0.41	0.406	
2	34	0.645	0.717	0.59	0.643	0.215	0.75	0.31	0.553	0.727	0.542	0.511	0.628	0.694	0.567	0.59	0.594	
n		93	76	89	84	65	48	42	38	86	95	47	179	80	45	78	96	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.85	1.69	1.95	1.86	1.52	1.61	1.76	2.00	1.67	2.00	2.02	1.88	1.75	1.99	1.95	1.94	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.460	0.408	0.487	0.462	0.341	0.379	0.433	0.501	0.399	0.499	0.505	0.468	0.428	0.497	0.487	0.485	
H_O		0.430	0.434	0.461	0.429	0.277	0.375	0.429	0.632	0.360	0.432	0.468	0.464	0.413	0.600	0.436	0.479	
F_{IS}		0.066	-0.064	0.054	0.073	0.188	0.011	0.009	-0.265	0.098	0.136	0.074	0.010	0.036	-0.211	0.106	0.012	

IN																		
1	36	0.828	0.822	0.86	0.921	0.731	0.95	0.857	0.949	0.875	0.926	0.9	0.831	0.86	0.789	0.877	0.911	
2	37	0.172	0.169	0.14	0.079	0.008	0.05	0.129	0.051	0.085	0.074	0.078	0.13	0.118	0.156	0.104	0.052	
3	38	0	0.008	0	0	0.262	0	0.014	0	0.04	0	0.022	0.04	0.022	0.056	0.019	0.036	
n		93	59	75	57	65	40	35	39	88	95	45	177	68	45	77	96	
n_a		2	3	2	2	3	2	3	2	3	2	3	3	3	3	3	3	
n_{eff}		1.40	1.42	1.32	1.17	1.67	1.11	1.34	1.11	1.29	1.16	1.23	1.41	1.33	1.55	1.29	1.20	
a		2.0	2.2	2.0	1.9	2.2	1.7	2.3	1.7	2.5	1.8	2.3	2.6	2.4	2.7	2.3	2.3	
H_E		0.286	0.298	0.242	0.147	0.401	0.096	0.252	0.099	0.227	0.137	0.186	0.293	0.247	0.354	0.222	0.166	
H_O		0.301	0.322	0.280	0.158	0.415	0.100	0.286	0.103	0.227	0.147	0.200	0.305	0.221	0.356	0.247	0.167	
F_{IS}		-0.051	-0.081	-0.156	-0.077	-0.037	-0.040	-0.135	-0.041	-0.002	-0.074	-0.079	-0.043	0.109	-0.004	-0.113	-0.004	

SP																		
1	41	0.25	0.257	0.362	0.344	0.254	0.271	0.41	0.231	0.403	0.37	0.245	0.379	0.36	0.433	0.545	0.49	
2	42	0.75	0.743	0.638	0.656	0.746	0.729	0.59	0.769	0.597	0.63	0.755	0.621	0.64	0.567	0.455	0.51	
n		92	74	76	77	65	48	39	39	88	96	47	177	82	45	78	96	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.61	1.62	1.87	1.83	1.62	1.66	1.96	1.56	1.94	1.88	1.60	1.89	1.86	1.99	2.00	2.01	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.377	0.384	0.465	0.454	0.382	0.399	0.490	0.360	0.484	0.469	0.374	0.472	0.463	0.497	0.499	0.502	
H_O		0.370	0.405	0.513	0.403	0.385	0.375	0.513	0.359	0.580	0.510	0.319	0.531	0.427	0.511	0.500	0.438	
F_{IS}		0.020	-0.055	-0.105	0.115	-0.008	0.061	-0.047	0.002	-0.199	-0.090	0.147	-0.126	0.080	-0.030	-0.002	0.130	

RH																		
1	43	0.189	0.127	0.152	0.203	0.162	0.188	0.125	0	0.273	0.138	0.106	0.177	0.167	0.156	0.192	0.005	
2	44	0.811	0.873	0.848	0.797	0.838	0.813	0.875	1	0.727	0.862	0.894	0.823	0.833	0.844	0.808	0.995	
n		90	79	89	79	65	48	44	39	88	94	47	184	90	45	78	93	
n_a		2	2	2	2	2	2	2	1	2	2	2	2	2	2	2	2	
n_{eff}		1.45	1.29	1.35	1.48	1.38	1.44	1.28	1.00	1.66	1.32	1.24	1.41	1.39	1.36	1.45	1.01	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	1.0	2.0	2.0	1.9	2.0	2.0	2.0	2.0	1.1	
H_E		0.308	0.223	0.259	0.325	0.273	0.308	0.221	0	0.399	0.240	0.192	0.292	0.279	0.266	0.313	0.011	
H_O		0.356	0.203	0.303	0.405	0.292	0.292	0.250	0	0.341	0.255	0.213	0.332	0.267	0.311	0.359	0.011	
F_{IS}		-0.155	0.090	-0.173	-0.248*	-0.071	0.053	-0.132	0	0.146	-0.066	-0.108	-0.137	0.046	-0.173	-0.149	0	

VR																		
1	51	0.083	0.065	0.112	0.075	0.008	0.085	0.103	0.446	0	0.643	0.067	0.073	0.212	0.044	0.035	0.054	
2	52	0.456	0.097	0.171	0.171	0	0.11	0.074	0.014	0.167	0.022	0.178	0.056	0.064	0.067	0.063	0.091	
3	53	0.217	0.416	0.365	0.384	0.586	0.244	0.25	0.351	0.144	0.236	0.378	0.317	0.192	0.333	0.431	0.371	
4	54	0.244	0.422	0.353	0.37	0.406	0.561	0.574	0.189	0.69	0.099	0.378	0.553	0.532	0.556	0.472	0.484	
n		90	77	85	73	64	41	34	37	87	91	45	178	78	45	72	93	
n_a		4	4	4	4	3	4	4	4	3	4	4	4	4	4	4	4	
n_{eff}		3.15	2.77	3.39	3.18	1.98	2.59	2.51	2.86	1.92	2.10	3.19	2.42	2.74	2.38	2.44	2.63	
a		3.9	3.7	3.9	3.8	2.2	3.8	3.8	3.3	3.0	3.3	3.8	3.6	3.8	3.5	3.4	3.6	
H_E		0.683	0.640	0.705	0.686	0.495	0.614	0.601	0.651	0.479	0.524	0.686	0.586	0.635	0.580	0.591	0.620	
H_O		0.689	0.662	0.741	0.712	0.438	0.683	0.647	0.568	0.494	0.527	0.667	0.567	0.679	0.556	0.611	0.613	
F_{IS}		-0.009	-0.036	-0.052	-0.039	0.118	-0.114	-0.077	0.129	-0.033	-0.008*	0.029	0.032	-0.070	0.043	-0.035	0.012	

Appendix I. Continued.

IS	Allele		Population															
	Allele name		81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96
1	25	0.44	0.446	0.4	0.424	0.063	0.393	0.398	0.789	0.215	0.37	0.295	0.24	0.204	0.43	0.424	0.301	
2	35	0.398	0.337	0.367	0.273	0.036	0.286	0.205	0.066	0.471	0.478	0.545	0.407	0.407	0.174	0.396	0.344	
3	45	0.163	0.217	0.233	0.303	0.902	0.321	0.398	0.118	0.314	0.152	0.159	0.35	0.383	0.395	0.181	0.355	
4	55	0	0	0	0	0	0	0	0.026	0	0	0	0.003	0.006	0	0	0	
n		83	83	75	66	56	42	44	38	86	92	44	177	81	43	72	93	
n_a		3	3	3	3	3	3	3	4	3	3	3	4	4	3	3	3	
n_{eff}		2.67	2.81	2.90	2.93	1.22	3.02	2.85	1.57	2.76	2.60	2.48	2.91	2.86	2.74	2.74	3.02	
a		3.0	3.0	3.0	3.0	2.4	3.0	3.0	3.3	3.0	3.0	3.0	3.1	3.1	3.0	3.0	3.0	
H_E		0.626	0.644	0.655	0.659	0.183	0.669	0.649	0.362	0.637	0.615	0.597	0.656	0.650	0.636	0.636	0.669	
H_O		0.554	0.747	0.667	0.652	0.196	0.595	0.659	0.316	0.570	0.663	0.614	0.661	0.704	0.651	0.722	0.710	
F_{IS}		0.115	-0.160*	-0.017	0.011	-0.073	0.111	-0.015	0.130*	0.106	-0.079	-0.029	-0.008	-0.083*	-0.025	-0.137	-0.062	
ER																		
1	50	0.311	0.426	0.546	0.662	0.092	0.542	0.467	0.115	0.661	0.766	0.819	0.79	0.828	0.711	0.769	0.74	
2	60	0.689	0.574	0.454	0.338	0.908	0.458	0.533	0.885	0.339	0.234	0.181	0.21	0.172	0.289	0.231	0.26	
n		90	81	76	71	65	48	45	39	84	96	47	186	90	45	78	96	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.76	1.97	2.00	1.82	1.20	2.01	2.01	1.26	1.82	1.56	1.43	1.50	1.40	1.71	1.56	1.63	
a		2.0	2.0	2.0	2.0	1.9	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.431	0.492	0.499	0.451	0.169	0.502	0.503	0.207	0.451	0.361	0.299	0.332	0.287	0.415	0.357	0.387	
H_O		0.444	0.506	0.434	0.479	0.185	0.583	0.533	0.179	0.488	0.344	0.277	0.344	0.278	0.444	0.359	0.396	
F_{IS}		-0.031	-0.029	0.131	-0.063	-0.094	-0.165	-0.060	0.134	-0.083	0.047	0.077	-0.036	0.031	-0.071	-0.005	-0.022	
PL																		
1	70	0.451	0.071	0.178	0.075	0.68	0.266	0.213	0.321	0.19	0.39	0.213	0.395	0.301	0.432	0.281	0.339	
2	80	0.549	0.929	0.822	0.925	0.32	0.734	0.788	0.679	0.81	0.61	0.787	0.605	0.699	0.568	0.719	0.661	
n		91	56	73	67	50	47	40	39	84	91	47	167	78	44	73	96	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.99	1.15	1.42	1.16	1.78	1.65	1.51	1.79	1.45	1.92	1.51	1.92	1.74	1.99	1.69	1.82	
a		2.0	1.8	2.0	1.8	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.498	0.134	0.295	0.139	0.440	0.395	0.339	0.441	0.310	0.478	0.339	0.479	0.424	0.496	0.407	0.450	
H_O		0.527	0.143	0.329	0.149	0.440	0.362	0.425	0.385	0.333	0.473	0.298	0.515	0.474	0.409	0.315	0.427	
F_{IS}		-0.060	-0.068	-0.116	-0.073	-0.001	0.084	-0.258	0.130	-0.075	0.013	0.121	-0.074	-0.120	0.177	0.227	0.052	
RF																		
1	51	0.079	0.012	0.024	0.024	0	0.01	0	0.269	0.012	0.107	0.125	0	0	0.023	0.017	0.034	
2	52	0.921	0.988	0.976	0.976	1	0.99	1	0.731	0.988	0.893	0.875	1	1	0.977	0.983	0.966	
n		57	81	83	82	62	48	45	39	83	75	40	183	88	43	59	89	
n_a		2	2	2	2	1	2	1	2	2	2	2	1	1	2	2	2	
n_{eff}		1.17	1.03	1.05	1.05	1.00	1.02	1.00	1.66	1.02	1.24	1.28	1.00	1.00	1.05	1.03	1.07	
a		1.9	1.3	1.4	1.4	1.0	1.2	1.0	2.0	1.2	1.9	2.0	1.0	1.0	1.4	1.3	1.6	
H_E		0.147	0.025	0.047	0.048	0	0.021	0	0.399	0.024	0.192	0.222	0	0	0.046	0.034	0.066	
H_O		0.123	0.025	0.048	0.049	0	0.021	0	0.487	0.024	0.160	0.250	0	0	0.047	0.034	0.045	
F_{IS}		0.164	-0.006	-0.019	-0.019	0	0	0	-0.226	-0.006	0.167	-0.130	0	0	-0.012	-0.009	0.315	
CLOCK																		
1	78	0.227	0.266	0.245	0.296	0.262	0.348	0.256	0.565	0.236	0.621	0.415	0.398	0.324	0.307	0.303	0.271	
2	79	0.773	0.734	0.755	0.704	0.738	0.652	0.744	0.435	0.764	0.379	0.585	0.602	0.676	0.693	0.697	0.729	
n		86	79	92	81	61	46	45	31	74	95	47	177	74	44	76	96	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.54	1.65	1.59	1.72	1.64	1.85	1.63	2.00	1.57	1.90	1.96	1.93	1.79	1.76	1.74	1.66	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.353	0.393	0.372	0.420	0.390	0.459	0.385	0.500	0.364	0.473	0.491	0.481	0.441	0.430	0.425	0.397	
H_O		0.314	0.354	0.315	0.420	0.426	0.478	0.333	0.613	0.365	0.505	0.447	0.492	0.351	0.477	0.447	0.375	
F_{IS}		0.110	0.098	0.152	0	-0.093	-0.043	0.135	-0.231	-0.004	-0.068	0.090	-0.023	0.205	-0.111	-0.053	0.056	

Appendix I. Continued.

VT	Allele name	Population															
		97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112
1	33	0.283	0.456	0.359	0.314	0.455	0.398	0.432	0.379	0.398	0.381	0.465	0.429	0.367	0.382	0.396	0.348
2	34	0.717	0.544	0.641	0.686	0.545	0.602	0.568	0.621	0.602	0.619	0.535	0.571	0.633	0.618	0.604	0.652
n		90	90	46	43	44	44	44	95	44	80	43	49	49	38	96	46
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
n_{eff}		1.69	2.00	1.87	1.77	2.01	1.94	1.99	1.90	1.94	1.90	2.01	1.98	1.89	1.92	1.93	1.85
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
H_E		0.408	0.499	0.465	0.436	0.502	0.485	0.496	0.473	0.485	0.475	0.503	0.495	0.470	0.478	0.481	0.459
H_O		0.433	0.489	0.587	0.442	0.500	0.432	0.500	0.484	0.568	0.538	0.465	0.531	0.490	0.553	0.458	0.304
F_{IS}		-0.061	0.020	-0.266	-0.014	0.003	0.110	-0.007	-0.023	-0.175	-0.133	0.077	-0.073	-0.043	-0.158	0.047	0.339*

IN																	
1	36	0.899	0.865	0.927	0.857	0.934	0.894	0.88	0.823	0.837	0.88	0.833	0.9	0.918	0.95	0.922	0.938
2	37	0.064	0.09	0.052	0.107	0.039	0.043	0.054	0.125	0.14	0.082	0.131	0.08	0.071	0.038	0.036	0.052
3	38	0.037	0.045	0.021	0.036	0.026	0.064	0.065	0.052	0.023	0.038	0.036	0.02	0.01	0.013	0.042	0.01
n		94	89	48	42	38	47	46	96	43	92	42	50	49	40	96	48
n_a		3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
n_{eff}		1.23	1.32	1.16	1.34	1.15	1.25	1.28	1.44	1.39	1.28	1.41	1.23	1.18	1.11	1.17	1.14
a		2.4	2.6	2.1	2.5	2.1	2.5	2.6	2.7	2.4	2.5	2.6	2.3	2.1	1.9	2.2	2.0
H_E		0.187	0.243	0.139	0.256	0.127	0.198	0.220	0.306	0.282	0.218	0.291	0.185	0.153	0.097	0.148	0.120
H_O		0.181	0.247	0.146	0.262	0.105	0.213	0.174	0.313	0.326	0.217	0.286	0.200	0.163	0.100	0.146	0.125
F_{IS}		0.035	-0.018	-0.051	-0.025	0.171	-0.077	0.211	-0.021	-0.155	0.002	0.017	-0.082	-0.068	-0.030	0.014	-0.046

SP																	
1	41	0.506	0.545	0.5	0.439	0.366	0.478	0.33	0.375	0.404	0.344	0.321	0.44	0.296	0.5	0.396	0.396
2	42	0.494	0.455	0.5	0.561	0.634	0.522	0.67	0.625	0.596	0.656	0.679	0.56	0.704	0.5	0.604	0.604
n		89	89	46	41	41	46	44	96	47	90	42	50	49	37	96	48
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
n_{eff}		2.01	2.00	2.02	1.99	1.89	2.02	1.81	1.89	1.95	1.83	1.79	1.99	1.73	2.03	1.93	1.94
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
H_E		0.503	0.499	0.505	0.499	0.470	0.505	0.447	0.471	0.487	0.454	0.441	0.498	0.421	0.507	0.481	0.483
H_O		0.382	0.438	0.435	0.634	0.439	0.565	0.386	0.500	0.553	0.489	0.357	0.560	0.429	0.297	0.417	0.583
F_{IS}		0.241*	0.122	0.141	-0.276	0.066	-0.122	0.137	-0.061	-0.138	-0.077	0.193	-0.126	-0.018	0.417*	0.134	-0.210

RH																	
1	43	0.305	0.287	0.188	0.151	0.116	0.287	0.109	0.161	0.01	0.021	0.081	0.14	0.092	0.125	0.121	0.125
2	44	0.695	0.713	0.813	0.849	0.884	0.713	0.891	0.839	0.99	0.979	0.919	0.86	0.908	0.875	0.879	0.875
n		95	89	48	43	43	47	46	96	48	95	43	50	49	40	95	48
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
n_{eff}		1.74	1.70	1.44	1.35	1.26	1.71	1.24	1.37	1.02	1.04	1.18	1.32	1.20	1.28	1.27	1.28
a		2.0	2.0	2.0	2.0	2.0	2.0	1.9	2.0	1.2	1.4	1.9	2.0	1.9	2.0	2.0	2.0
H_E		0.426	0.411	0.308	0.260	0.208	0.414	0.196	0.272	0.021	0.041	0.151	0.243	0.169	0.222	0.214	0.221
H_O		0.400	0.348	0.292	0.302	0.233	0.362	0.217	0.240	0.021	0.042	0.163	0.200	0.143	0.250	0.221	0.250
F_{IS}		0.062	0.154	0.053	-0.167	-0.120	0.127	-0.111	0.120	0	-0.016	-0.077	0.179	0.154	-0.130	-0.034	-0.133

VR																	
1	51	0.048	0.034	0	0.013	0.064	0.011	0.054	0.005	0	0	0	0.021	0.011	0.027	0.021	0.011
2	52	0.075	0.063	0.021	0.066	0.051	0.067	0.065	0.049	0.05	0.032	0.024	0.043	0.074	0.041	0.032	0.032
3	53	0.414	0.328	0.255	0.25	0.282	0.311	0.457	0.33	0.288	0.316	0.341	0.287	0.234	0.338	0.298	0.309
4	54	0.462	0.575	0.723	0.671	0.603	0.611	0.424	0.615	0.663	0.652	0.634	0.649	0.681	0.595	0.649	0.649
n		93	87	47	38	39	45	46	91	40	79	41	47	47	37	94	47
n_a		4	4	3	4	4	4	4	4	3	3	3	4	4	4	4	4
n_{eff}		2.56	2.27	1.71	1.96	2.26	2.13	2.57	2.05	1.93	1.91	1.95	2.00	1.93	2.16	1.97	1.95
a		3.5	3.3	2.4	3.1	3.6	3.1	3.6	2.8	2.7	2.5	2.5	3.1	3.1	3.2	2.9	2.8
H_E		0.610	0.560	0.415	0.489	0.558	0.531	0.611	0.513	0.482	0.477	0.487	0.499	0.481	0.537	0.491	0.488
H_O		0.656	0.598	0.340	0.579	0.410	0.556	0.522	0.615	0.400	0.582	0.390	0.447	0.362	0.568	0.436	0.468
F_{IS}		-0.076	-0.067	0.182	-0.187	0.267	-0.047	0.148*	-0.201	0.172	-0.223	0.200	0.106	0.250	-0.057	0.113	0.041*

Appendix I. Continued.

IS	Allele		Population															
	Allele name		97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112
1	25	0.261	0.382	0.355	0.279	0.378	0.39	0.333	0.332	0.479	0.253	0.384	0.333	0.255	0.135	0.337	0.38	
2	35	0.549	0.264	0.434	0.233	0.195	0.232	0.269	0.266	0.24	0.332	0.302	0.313	0.378	0.405	0.382	0.13	
3	45	0.19	0.354	0.211	0.488	0.427	0.378	0.397	0.402	0.281	0.416	0.314	0.354	0.367	0.459	0.281	0.489	
4	55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
n		92	89	38	43	41	41	39	92	48	95	43	48	49	37	89	46	
n_a		3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	
n_{eff}		2.49	2.97	2.85	2.75	2.81	2.93	3.00	2.95	2.78	2.91	3.04	3.06	2.98	2.59	2.99	2.54	
a		3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	
H_E		0.598	0.663	0.649	0.637	0.645	0.659	0.667	0.661	0.641	0.657	0.671	0.673	0.664	0.615	0.665	0.606	
H_O		0.620	0.629	0.658	0.674	0.585	0.683	0.667	0.739	0.688	0.653	0.721	0.646	0.633	0.514	0.607	0.587	
F_{IS}		-0.037	0.051	-0.013	-0.060	0.093	-0.037	0.001	-0.119	-0.074	0.006	-0.076	0.041	0.048	0.166	0.088	0.031	

ER																		
1	50	0.819	0.711	0.728	0.767	0.857	0.641	0.744	0.794	0.648	0.671	0.386	0.76	0.643	0.756	0.768	0.716	
2	60	0.181	0.289	0.272	0.233	0.143	0.359	0.256	0.206	0.352	0.329	0.614	0.24	0.357	0.244	0.232	0.284	
n		94	90	46	43	42	46	41	85	44	85	35	50	49	39	95	44	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.42	1.70	1.67	1.57	1.33	1.87	1.63	1.49	1.86	1.80	1.93	1.58	1.87	1.60	1.56	1.70	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.298	0.413	0.400	0.361	0.248	0.465	0.386	0.329	0.462	0.444	0.481	0.368	0.464	0.373	0.358	0.411	
H_O		0.298	0.444	0.413	0.372	0.190	0.500	0.415	0.271	0.477	0.518	0.486	0.320	0.265	0.385	0.358	0.250	
F_{IS}		0	-0.076	-0.033	-0.031	0.234	-0.076	-0.076	0.178	-0.034	-0.166	-0.010	0.133	0.431**	-0.031	0	0.395*	

PL																		
1	70	0.276	0.27	0.208	0.209	0.233	0.181	0.307	0.247	0.25	0.214	0.135	0.177	0.173	0.284	0.229	0.283	
2	80	0.724	0.73	0.792	0.791	0.767	0.819	0.693	0.753	0.75	0.786	0.865	0.823	0.827	0.716	0.771	0.717	
n		96	89	48	43	43	47	44	95	42	77	37	48	49	37	94	46	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.67	1.66	1.50	1.50	1.57	1.43	1.76	1.60	1.61	1.51	1.31	1.42	1.41	1.70	1.55	1.69	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.402	0.396	0.333	0.335	0.361	0.299	0.430	0.374	0.380	0.339	0.237	0.295	0.290	0.412	0.355	0.410	
H_O		0.490	0.539	0.417	0.419	0.419	0.362	0.386	0.389	0.405	0.325	0.270	0.313	0.347	0.351	0.372	0.435	
F_{IS}		-0.229*	-0.364***	-0.253	-0.254	-0.161	-0.211	0.103	-0.041	-0.067	0.042	-0.143	-0.062	-0.200	0.149	-0.050	-0.061	

RF																		
1	51	0.038	0.006	0	0	0	0	0.011	0.032	0	0.005	0.011	0.01	0.02	0.03	0.027	0.152	
2	52	0.962	0.994	1	1	1	1	0.989	0.968	1	0.995	0.989	0.99	0.98	0.97	0.973	0.848	
n		91	90	48	42	44	47	44	78	47	91	45	50	49	33	92	46	
n_a		2	2	1	1	1	1	2	2	1	2	2	2	2	2	2	2	
n_{eff}		1.08	1.01	1.00	1.00	1.00	1.00	1.02	1.07	1.00	1.01	1.02	1.02	1.04	1.06	1.06	1.35	
a		1.6	1.1	1.0	1.0	1.0	1.0	1.3	1.5	1.0	1.1	1.2	1.2	1.4	1.6	1.5	2.0	
H_E		0.074	0.011	0	0	0	0	0.023	0.062	0	0.011	0.022	0.020	0.040	0.060	0.053	0.261	
H_O		0.077	0.011	0	0	0	0	0.023	0.038	0	0.011	0.022	0.020	0.041	0.061	0.033	0.261	
F_{IS}		-0.034	0	0	0	0	0	0	0.386	0	0	0	0	-0.011	-0.016	0.388	0	

CLOCK																		
1	78	0.205	0.311	0.244	0.195	0.256	0.319	0.315	0.322	0.25	0.3	0.273	0.24	0.214	0.221	0.314	0.226	
2	79	0.795	0.689	0.756	0.805	0.744	0.681	0.685	0.678	0.75	0.7	0.727	0.76	0.786	0.779	0.686	0.774	
n		95	90	45	41	43	47	46	87	48	95	44	50	49	34	94	42	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.49	1.76	1.60	1.47	1.63	1.78	1.77	1.78	1.61	1.73	1.67	1.58	1.52	1.54	1.76	1.55	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.328	0.431	0.374	0.318	0.385	0.439	0.436	0.439	0.379	0.422	0.401	0.368	0.340	0.349	0.433	0.354	
H_O		0.326	0.467	0.400	0.293	0.326	0.383	0.326	0.391	0.417	0.432	0.364	0.440	0.306	0.324	0.479	0.405	
F_{IS}		0.005	-0.083	-0.072	0.080	0.156	0.129	0.255	0.110	-0.101	-0.022	0.095	-0.196	0.101	0.074	-0.106	-0.144	

Appendix I. Continued.

VT	Allele name	Population														Total
		113	114	115	116	117	118	119	120	121	122	123	124	125	126	
1	33	0.444	0.333	0.522	0.565	0.372	0.427	0.521	0.489	0.385	0.522	0.468	0.175	0.29	0.391	0.451
2	34	0.556	0.667	0.478	0.435	0.628	0.573	0.479	0.511	0.615	0.478	0.532	0.825	0.71	0.609	0.549
n		36	48	46	46	47	48	48	47	91	91	78	40	93	87	8631
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
n_{eff}		2.00	1.82	2.02	1.99	1.90	1.98	2.02	2.02	1.91	2.01	2.00	1.41	1.71	1.92	1.77
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
H_E		0.501	0.449	0.505	0.497	0.472	0.495	0.504	0.505	0.476	0.502	0.501	0.292	0.414	0.479	0.436
H_O		0.500	0.417	0.565	0.522	0.574	0.396	0.542	0.553	0.571	0.538	0.526	0.300	0.452	0.483	
F_{IS}		0.002	0.073	-0.122	-0.051	-0.219	0.201	-0.075	-0.096	-0.202	-0.074	-0.049	-0.026	-0.091	-0.008	

IN																
1	36	0.913	0.927	0.956	0.947	0.99	1	0.875	0.917	1	1	0.995	0.938	1	1	0.862
2	37	0.05	0.063	0.044	0.011	0	0	0.031	0.033	0	0	0.005	0.063	0	0	0.125
3	38	0.038	0.01	0	0.043	0.01	0	0.094	0.05	0	0	0	0	0	0	0.013
n		40	48	45	47	48	35	48	30	91	92	93	40	96	93	8522
n_a		3	3	2	3	2	1	3	3	1	1	2	2	1	1	3
n_{eff}		1.20	1.16	1.09	1.11	1.02	1.00	1.29	1.19	1.00	1.00	1.01	1.13	1.00	1.00	1.27
a		2.4	2.0	1.7	1.9	1.2	1.0	2.5	2.4	1.0	1.0	1.1	1.8	1.0	1.0	2.2
H_E		0.166	0.138	0.086	0.103	0.021	0	0.227	0.159	0	0	0.011	0.119	0	0	0.215
H_O		0.175	0.146	0.089	0.085	0.021	0	0.229	0.133	0	0	0.011	0.075	0	0	
F_{IS}		-0.058	-0.058	-0.035	0.173*	0	0	-0.010	0.162	0	0	0	0.371	0	0	

SP																
1	41	0.275	0.34	0.545	0.333	0.177	0.281	0.33	0.319	0.386	0.406	0.21	0.663	0.25	0.344	0.45
2	42	0.725	0.66	0.455	0.667	0.823	0.719	0.67	0.681	0.614	0.594	0.79	0.338	0.75	0.656	0.55
n		40	47	44	45	48	48	44	47	88	90	93	40	90	90	8659
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
n_{eff}		1.68	1.83	2.01	1.82	1.42	1.69	1.81	1.78	1.91	1.94	1.50	1.83	1.61	1.83	1.84
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
H_E		0.404	0.454	0.502	0.449	0.295	0.409	0.447	0.439	0.477	0.485	0.333	0.453	0.377	0.454	0.457
H_O		0.350	0.468	0.591	0.489	0.354	0.438	0.432	0.426	0.545	0.522	0.355	0.475	0.322	0.378	
F_{IS}		0.135	-0.032	-0.181	-0.089	-0.205	-0.072	0.034	0.032	-0.145	-0.078	-0.065	-0.050	0.146	0.169	

RH																
1	43	0.188	0.104	0	0.436	0.33	0.375	0.141	0.085	0.043	0.128	0.11	0.063	0.092	0.092	0.071
2	44	0.813	0.896	1	0.564	0.67	0.625	0.859	0.915	0.957	0.872	0.89	0.938	0.908	0.908	0.929
n		40	48	39	47	47	48	46	47	93	94	91	40	92	92	8819
n_a		2	2	1	2	2	2	2	2	2	2	2	2	2	2	2
n_{eff}		1.45	1.23	1.00	1.99	1.81	1.90	1.33	1.19	1.09	1.29	1.24	1.13	1.20	1.20	1.14
a		2.0	1.9	1.0	2.0	2.0	2.0	2.0	1.9	1.6	2.0	1.9	1.8	1.9	1.9	1.8
H_E		0.309	0.189	0	0.497	0.447	0.474	0.245	0.157	0.083	0.224	0.197	0.119	0.169	0.169	0.123
H_O		0.325	0.208	0	0.532	0.532	0.458	0.283	0.170	0.065	0.234	0.220	0.125	0.185	0.163	
F_{IS}		-0.054	-0.106	0	-0.071	-0.193	0.033	-0.154	-0.082	0.221	-0.045	-0.118	-0.054	-0.096	0.033	

VR																
1	51	0.054	0.063	0.026	0.08	0.068	0.088	0.012	0.014	0.029	0.024	0.021	0	0.073	0.056	0.267
2	52	0.014	0.042	0.079	0.045	0.027	0.05	0.116	0.068	0.064	0.048	0.106	0.088	0.017	0.128	0.115
3	53	0.243	0.219	0.263	0.295	0.324	0.113	0.186	0.27	0.326	0.327	0.261	0.25	0.197	0.194	0.309
4	54	0.689	0.677	0.632	0.58	0.581	0.75	0.686	0.649	0.581	0.601	0.612	0.663	0.713	0.622	0.309
n		37	48	38	44	37	40	43	37	86	84	94	40	89	90	8252
n_a		4	4	4	4	4	4	4	4	4	4	4	3	4	4	4
n_{eff}		1.88	1.97	2.14	2.35	2.27	1.72	1.95	2.03	2.24	2.14	2.22	1.99	1.82	2.27	2.52
a		3.1	3.5	3.4	3.6	3.3	3.6	3.2	3.1	3.3	3.1	3.3	2.9	3.2	3.7	3.9
H_E		0.469	0.493	0.532	0.575	0.559	0.420	0.487	0.508	0.554	0.532	0.549	0.497	0.449	0.559	0.604
H_O		0.514	0.500	0.500	0.636	0.405	0.375	0.512	0.568	0.512	0.548	0.521	0.450	0.494	0.533	
F_{IS}		-0.096	-0.014	0.061	-0.108	0.278	0.108	-0.052	-0.118	0.077	-0.030	0.051	0.096	-0.101	0.046	

Appendix I. Continued.

IS	Allele		Population														
	Allele name		113	114	115	116	117	118	119	120	121	122	123	124	125	126	Total
1	25	0.219	0.344	0.292	0.293	0.293	0.5	0.156	0.257	0.56	0.335	0.348	0.313	0.372	0.35	0.451	
2	35	0.344	0.26	0.469	0.337	0.28	0.119	0.411	0.386	0.261	0.372	0.247	0.45	0.25	0.344	0.179	
3	45	0.438	0.396	0.24	0.37	0.427	0.381	0.433	0.357	0.179	0.293	0.404	0.238	0.378	0.306	0.364	
4	55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005	
n		32	48	48	46	41	42	45	35	92	94	89	40	94	90	8420	
n_a		3	3	3	3	3	3	3	3	3	3	3	3	3	3	4	
n_{eff}		2.88	2.98	2.81	3.04	2.95	2.49	2.67	3.00	2.44	3.00	2.92	2.87	2.94	3.02	2.41	
a		3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.1	
H_E		0.653	0.664	0.645	0.671	0.662	0.598	0.626	0.667	0.590	0.667	0.658	0.652	0.660	0.669	0.585	
H_O		0.656	0.604	0.625	0.717	0.561	0.690	0.600	0.686	0.489	0.723	0.551	0.650	0.681	0.678		
F_{IS}		-0.005	0.091	0.031	-0.070	0.154	-0.157	0.042	-0.028	0.171	-0.085	0.164	0.002	-0.032	-0.013		
ER																	
1	50	0.635	0.656	0.7	0.486	0.833	0.81	0.688	0.878	0.764	0.622	0.691	0.808	0.615	0.771	0.325	
2	60	0.365	0.344	0.3	0.514	0.167	0.19	0.313	0.122	0.236	0.378	0.309	0.192	0.385	0.229	0.675	
n		37	48	45	37	48	50	48	45	91	90	89	39	91	83	8394	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.89	1.84	1.74	2.03	1.39	1.45	1.77	1.28	1.57	1.90	1.75	1.46	1.91	1.55	1.39	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.470	0.456	0.425	0.506	0.281	0.311	0.434	0.217	0.363	0.473	0.429	0.315	0.476	0.355	0.283	
H_O		0.514	0.438	0.511	0.378	0.292	0.380	0.375	0.200	0.363	0.422	0.393	0.333	0.505	0.337		
F_{IS}		-0.094	0.041	-0.206	0.256	-0.039	-0.225	0.138	0.079	0.001	0.107	0.085	-0.060	-0.062	0.050		
PL																	
1	70	0.279	0.287	0.15	0.192	0.323	0.22	0.323	0.191	0.051	0.056	0.078	0.115	0.04	0.028	0.148	
2	80	0.721	0.713	0.85	0.808	0.677	0.78	0.677	0.809	0.949	0.944	0.922	0.885	0.96	0.972	0.852	
n		34	47	40	39	48	50	48	47	88	80	83	39	88	90	8334	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.69	1.71	1.35	1.46	1.79	1.53	1.79	1.46	1.11	1.12	1.17	1.26	1.08	1.06	1.32	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	1.7	1.7	1.9	2.0	1.6	1.5	2.0	
H_E		0.409	0.414	0.258	0.315	0.442	0.347	0.442	0.313	0.098	0.107	0.145	0.207	0.077	0.054	0.244	
H_O		0.324	0.404	0.300	0.179	0.396	0.360	0.438	0.298	0.102	0.088	0.108	0.231	0.080	0.056		
F_{IS}		0.211	0.023	-0.164	0.433*	0.105	-0.039	0.010	0.049	-0.048	0.182	0.255	-0.118	-0.036	-0.023		
RF																	
1	51	0.013	0.071	0.011	0	0.011	0	0.011	0.012	0	0	0.09	0	0.034	0.032	0.172	
2	52	0.988	0.929	0.989	1	0.989	1	0.989	0.988	1	1	0.91	1	0.966	0.968	0.828	
n		40	42	46	48	47	40	45	41	68	75	83	37	89	79	8344	
n_a		2	2	2	1	2	1	2	2	1	1	2	1	2	2	2	
n_{eff}		1.03	1.16	1.02	1.00	1.02	1.00	1.02	1.02	1.00	1.00	1.20	1.00	1.07	1.07	1.24	
a		1.3	1.8	1.2	1.0	1.2	1.0	1.2	1.3	1.0	1.0	1.9	1.0	1.6	1.5	2.0	
H_E		0.025	0.134	0.022	0	0.021	0	0.022	0.024	0	0	0.165	0	0.066	0.062	0.194	
H_O		0.025	0.143	0.022	0	0.021	0	0.022	0.024	0	0	0.181	0	0.045	0.038		
F_{IS}		0	-0.065	0	0	0	0	0	0	0	0	-0.093	0	0.315	0.386		
CLOCK																	
1	78	0.203	0.359	0.265	0.375	0.263	0.267	0.239	0.24	0.226	0.263	0.182	0.385	0.238	0.181	0.278	
2	79	0.797	0.641	0.735	0.625	0.738	0.733	0.761	0.76	0.774	0.737	0.818	0.615	0.762	0.819	0.722	
n		32	46	49	48	40	43	44	48	93	93	88	39	86	83	8428	
n_a		2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	
n_{eff}		1.49	1.87	1.65	1.90	1.64	1.66	1.58	1.58	1.54	1.64	1.43	1.92	1.58	1.42	1.64	
a		2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	
H_E		0.329	0.465	0.394	0.474	0.392	0.396	0.368	0.368	0.352	0.390	0.299	0.480	0.365	0.298	0.390	
H_O		0.406	0.413	0.286	0.375	0.275	0.442	0.432	0.354	0.344	0.419	0.295	0.359	0.384	0.265		
F_{IS}		-0.240	0.113	0.277	0.210	0.301	-0.116	-0.177	0.039	0.021	-0.075	0.013	0.254	-0.051	0.111		

Appendix II. Microsatellite allele frequencies, collection sizes (n), number of alleles (n_a), effective number of alleles (n_{eff}), allele richness (a ; based on 16 individuals), expected heterozygosity (H_E), observed heterozygosity (H_O), and estimated inbreeding coefficient (F_{IS}) for chum salmon populations genotyped by UAF or ABL (grayed-out alleles not observed). "*" allele not observed in DFO dataset. Totals for all populations appear in right hand column. Grayed-out populations are allele frequencies from DFO dataset; DFO allele frequencies are pooled for alleles 380 and larger at *One111*. Significant tests of Hardy-Weinberg equilibrium before Bonferroni multiple testing are indicated at the F_{IS} values as: * $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$.

One104 Allele	Size		Population													
	ABL	DFO	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	109	112	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	113	115	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	117	119	0	0	0	0.013	0	0	0	0	0	0	0	0	0	0
4	121	123	0	0	0	0	0	0.007	0.013	0	0	0.004	0	0	0	0.01
5	125	127	0	0.008	0	0	0	0.015	0.013	0	0.013	0.008	0	0	0	0
6	129	132	0.005	0	0	0	0	0	0.013	0	0	0.008	0	0	0.007	0.01
7	133	136	0.026	0.03	0.059	0.075	0.025	0.022	0.032	0.007	0.025	0.012	0.033	0.01	0.052	0.067
8	137	140	0.026	0.061	0.011	0.013	0.013	0.074	0.083	0.020	0.037	0.012	0	0.01	0.134	0.106
9	141	145	0.026	0.008	0.005	0	0	0.022	0.032	0.072	0.037	0.016	0	0	0.045	0.01
10	145	149	0.016	0	0.016	0	0.037	0	0.013	0.020	0.013	0.008	0	0.01	0.03	0.01
11	149	153	0.011	0	0	0	0.013	0	0	0.013	0.037	0.019	0.033	0.04	0.06	0.019
12	153	157	0.005	0.023	0.059	0.013	0	0.022	0.006	0	0.025	0.031	0.033	0.02	0.03	0.058
13	157	161	0.058	0.045	0.064	0.125	0	0.096	0.064	0.086	0.05	0.043	0.067	0.04	0.052	0.019
14	161	165	0.047	0.068	0.037	0.013	0.063	0.037	0.045	0.046	0.05	0.101	0.1	0.12	0.097	0.048
15	165	169	0.068	0.091	0.027	0.05	0.087	0.081	0.071	0.039	0.063	0.066	0.033	0.02	0.104	0.029
16	169	173	0.074	0.098	0.144	0.175	0.275	0.074	0.122	0.072	0.087	0.058	0.117	0.05	0.06	0.096
17	173	177	0.037	0.045	0.096	0.063	0.1	0.125	0.064	0.079	0.063	0.136	0.15	0.15	0.06	0.048
18	175	*	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	177	181	0.116	0.167	0.085	0.087	0.037	0.074	0.083	0.039	0.075	0.078	0.05	0.06	0.03	0.144
20	181	185	0.063	0.076	0.101	0.113	0.037	0.066	0.103	0.132	0.063	0.089	0.083	0.13	0.06	0.077
21	185	190	0.074	0.03	0.059	0.037	0.063	0.037	0.045	0.132	0.05	0.066	0.117	0.06	0.06	0.029
22	189	194	0.053	0.023	0.037	0.025	0.013	0.051	0.051	0.066	0.087	0.035	0.033	0.12	0.015	0.106
23	193	198	0.026	0.015	0.027	0.025	0.063	0	0.019	0.020	0.013	0.023	0.017	0.02	0.03	0.019
24	197	202	0.042	0.008	0.011	0	0	0.029	0.032	0.033	0.05	0.027	0.05	0.07	0.022	0
25	201	206	0.089	0.106	0.011	0	0	0.051	0.019	0.039	0.025	0.050	0.033	0.01	0.037	0.029
26	205	210	0.042	0	0.005	0	0.013	0.015	0.006	0	0.037	0.027	0.017	0.02	0	0.038
27	209	214	0.016	0.038	0.037	0.075	0.037	0.007	0	0.039	0	0.016	0	0	0.015	0
28	213	218	0.021	0.023	0.021	0.025	0.063	0.037	0.026	0.026	0.037	0.004	0	0.01	0	0
29	217	222	0.016	0	0.011	0	0.013	0.022	0.019	0.013	0.025	0.012	0.017	0.02	0	0.029
30	221	226	0.016	0	0	0	0.013	0.007	0.013	0	0.025	0	0	0	0	0
31	225	230	0.016	0.023	0.043	0.063	0.025	0.007	0	0	0	0.035	0	0.01	0	0
32	229	234	0	0	0.027	0	0.013	0.007	0	0	0	0.004	0.017	0	0	0
33	233	238	0.005	0	0	0.013	0	0	0.006	0	0.013	0.004	0	0	0	0
34	237	242	0	0	0	0	0	0	0	0.007	0	0.004	0	0	0	0
35	241	246	0	0	0.011	0	0	0.007	0.006	0	0	0.004	0	0	0	0
36	245	250	0	0	0	0	0	0	0	0	0	0.004	0	0	0	0
37	249	254	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	253	258	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0
39	257	262	0	0.015	0	0	0	0	0	0	0	0	0	0	0	0
40	269	274	0	0	0	0	0	0.007	0	0	0	0	0	0	0	0
41	273	278	0	0	0	0	0	0	0	0	0	0	0	0	0	0
n			95	66	94	40	40	68	78	76	40	129	30	50	67	52
n_a			27	21	24	18	20	26	26	21	24	31	18	21	20	21
n_{eff}			18.55	13.49	15.14	12.39	9.46	17.26	16.98	N/A	24.12	N/A	14.63	12.60	15.97	14.67
a			16.53	14.30	15.12	13.34	13.92	15.96	15.92	N/A	17.97	N/A	14.59	13.80	15.03	14.69
H_E			0.946	0.926	0.934	0.919	0.894	0.942	0.941	N/A	0.959	N/A	0.932	0.921	0.937	0.932
H_O			0.916	0.894	0.915	0.850	0.875	0.912	0.949	N/A	0.975	N/A	0.933	0.940	0.970	0.981
F_{IS}			0.032	0.035	0.021	0.076	0.022	0.032	-0.008	N/A	-0.017	N/A	-0.002	-0.021	-0.035	-0.053

Appendix II. Continued.

Allele	Population															
	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0.011	0	0	0	0	0	0	0	0.014	0	0	0
3	0	0	0	0	0	0	0	0	0	0.021	0.022	0	0.014	0	0.013	0.025
4	0	0	0.023	0.045	0.011	0.01	0.019	0	0	0	0	0	0	0	0.033	0.005
5	0	0	0	0	0.011	0	0	0	0	0	0	0.007	0.014	0.022	0.145	0.005
6	0	0.014	0	0	0.011	0	0.037	0.02	0.063	0.042	0.033	0	0.056	0.033	0.039	0.005
7	0.063	0.057	0.023	0.023	0.011	0.031	0	0	0	0	0.022	0.029	0.028	0.033	0.02	0.02
8	0.119	0.043	0.045	0	0.022	0.031	0	0.02	0	0	0.065	0.014	0.028	0.044	0.039	0.045
9	0.032	0.043	0	0.045	0.022	0.031	0.056	0	0.042	0.042	0.033	0.051	0.042	0.067	0.072	0.025
10	0.024	0.043	0.045	0.08	0.033	0.073	0	0.1	0.115	0.042	0.076	0.036	0.042	0.122	0.039	0.075
11	0.032	0.043	0.023	0.045	0.022	0.042	0.056	0.06	0.01	0.042	0.043	0.072	0.125	0.011	0.039	0.09
12	0.024	0.029	0	0.011	0.065	0.021	0.019	0	0.021	0	0.011	0.014	0.139	0	0.039	0.085
13	0.032	0.014	0.023	0.034	0.011	0.042	0.019	0.14	0.115	0.104	0.065	0.109	0.056	0.044	0.059	0.03
14	0.048	0.214	0.023	0.045	0.022	0.052	0.037	0.14	0.083	0.042	0.12	0.036	0.069	0.111	0.079	0.065
15	0.087	0.057	0.023	0.034	0.033	0.031	0.037	0.1	0.094	0.104	0.065	0.065	0.083	0.133	0.02	0.025
16	0.04	0.014	0.023	0.045	0.076	0.063	0.074	0.12	0.073	0.083	0.13	0.043	0.042	0.033	0.053	0.07
17	0.048	0.086	0.045	0.057	0.054	0.052	0.037	0.08	0.052	0.083	0.087	0.036	0	0.011	0.033	0.04
18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	0.143	0.143	0.045	0.045	0.087	0.052	0	0.04	0.052	0.021	0.011	0.036	0.069	0.022	0.053	0.07
20	0.071	0.043	0.045	0.068	0.054	0.042	0.074	0.08	0.094	0.063	0.054	0.051	0.042	0.033	0.046	0.05
21	0.063	0.029	0.045	0.023	0.033	0.031	0.056	0.02	0.042	0.063	0.022	0.043	0.042	0.067	0.033	0.075
22	0.079	0.043	0.136	0.023	0.109	0.031	0.037	0.06	0.01	0.021	0.065	0.094	0.014	0.022	0.072	0.04
23	0.016	0	0.023	0.045	0.076	0.063	0.093	0	0.031	0.063	0.022	0.065	0.042	0.011	0.026	0.065
24	0	0	0	0.023	0.033	0.031	0.019	0	0.031	0	0.022	0.014	0.014	0.033	0.013	0.02
25	0.024	0.029	0.091	0.125	0.022	0.063	0.056	0	0.021	0.021	0.011	0.029	0.014	0.056	0.013	0.03
26	0.008	0	0.023	0.08	0.054	0.094	0.111	0.02	0.031	0.146	0.011	0.058	0.014	0.033	0.013	0.01
27	0.008	0	0.045	0.045	0.022	0.052	0.093	0	0.01	0	0	0.051	0	0	0.007	0.01
28	0	0.043	0.023	0.057	0.033	0.031	0.037	0	0	0	0.011	0.022	0	0.033	0	0.015
29	0.024	0	0	0.011	0.033	0.01	0	0	0.01	0	0	0.007	0	0.011	0	0.005
30	0	0	0.023	0.023	0.011	0	0.037	0	0	0	0	0.007	0	0.011	0	0
31	0.008	0.014	0.023	0.011	0.022	0.021	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0.007	0	0	0	0
33	0	0	0.045	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0.023	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0.114	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0.008	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	63	35	22	44	46	48	27	25	48	24	46	69	36	45	76	100
<i>n_a</i>	22	19	24	23	28	24	20	14	20	17	22	25	22	23	24	26
<i>n_{eff}</i>	15.12	N/A	24.26	20.69	22.63	24.52	21.68	12.76	15.78	16.84	16.29	19.73	17.27	16.55	17.90	18.93
<i>a</i>	15.01	N/A	19.89	17.14	18.31	18.06	16.93	12.32	14.72	15.01	15.43	16.74	16.21	16.12	16.51	16.30
<i>H_E</i>	0.934	N/A	0.959	0.952	0.956	0.959	0.954	0.922	0.937	0.941	0.939	0.949	0.942	0.940	0.944	0.947
<i>H_O</i>	0.952	N/A	0.955	0.932	0.957	0.958	1.000	0.840	0.917	0.917	0.891	0.971	0.889	1.000	0.947	0.950
<i>F_{IS}</i>	-0.020	N/A	0.005	0.021	-0.001	0.001	-0.049	0.090	0.022	0.026	0.051*	-0.023	0.057	-0.065	-0.003	-0.003

Appendix II. Continued.

Allele	Population															
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0.014	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0.005	0.006	0	0	0	0.003	0	0	0.02	0.016	0.007	0.013
4	0	0.014	0	0	0.063	0.091	0.016	0	0	0.003	0	0.025	0.1	0.015	0.033	0.039
5	0.01	0	0.01	0.011	0.144	0.149	0.151	0.118	0.051	0.158	0.133	0.115	0.12	0.107	0.149	0.100
6	0.031	0.029	0.01	0.011	0.099	0.104	0.065	0.151	0.131	0.181	0.069	0.135	0.165	0.143	0.153	0.105
7	0.031	0.014	0.02	0.011	0.041	0.032	0.032	0.027	0.096	0.036	0.027	0.04	0.04	0.049	0.058	0.113
8	0.073	0.043	0.02	0.011	0.09	0.058	0.059	0.016	0.015	0.003	0.005	0.02	0.025	0.024	0.042	0.053
9	0.073	0.071	0.031	0.043	0.072	0.091	0.005	0.027	0.02	0.008	0.027	0.05	0.01	0.028	0.029	0.019
10	0.031	0.057	0.092	0.043	0.032	0.039	0.183	0.07	0.051	0.049	0.096	0.05	0.03	0.037	0.033	0.032
11	0.104	0.071	0.092	0.087	0.063	0.026	0.027	0.032	0.045	0.075	0.027	0.05	0.005	0.030	0.022	0.015
12	0.094	0.071	0.112	0.12	0.014	0.039	0.016	0.108	0.04	0.176	0.074	0.065	0.02	0.039	0.022	0.028
13	0.01	0.071	0.02	0.043	0.036	0.052	0.091	0.016	0.061	0.018	0.048	0.035	0.04	0.037	0.033	0.034
14	0.063	0.029	0.082	0.033	0.081	0.071	0.075	0.027	0.035	0.008	0.027	0.04	0.035	0.066	0.056	0.088
15	0.104	0.057	0.092	0.065	0.036	0.058	0.081	0.022	0.015	0.031	0.021	0.02	0.035	0.035	0.033	0.034
16	0.073	0.071	0.082	0.076	0.077	0.071	0.005	0.032	0.116	0.026	0.048	0.05	0.07	0.038	0.047	0.041
17	0.031	0.086	0.071	0.12	0.018	0.019	0.102	0.124	0.066	0.075	0.122	0.055	0.06	0.090	0.082	0.079
18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	0.052	0.029	0.051	0.076	0.014	0.006	0.011	0.043	0.071	0.060	0.021	0.075	0.05	0.062	0.060	0.068
20	0.042	0.1	0.061	0.022	0	0.013	0.059	0.027	0.096	0.010	0.096	0.05	0.065	0.062	0.044	0.038
21	0.094	0	0.041	0.033	0.023	0.013	0.022	0.048	0.04	0.070	0.032	0.03	0.045	0.045	0.024	0.045
22	0.031	0.071	0.041	0	0.027	0.006	0	0.032	0.015	0	0.064	0.02	0.025	0.018	0.020	0.032
23	0.01	0.029	0.02	0.011	0.023	0.019	0	0.032	0.03	0.005	0.027	0.015	0.01	0.019	0.022	0.015
24	0.031	0.029	0.01	0.022	0.005	0.032	0	0	0.005	0.003	0.011	0.03	0.015	0.008	0.009	0.008
25	0.01	0.014	0.01	0.098	0.014	0	0	0.027	0	0	0.016	0.015	0.015	0.021	0.013	0.002
26	0	0.014	0.01	0.033	0	0	0	0.022	0	0	0	0.01	0	0.005	0.002	0
27	0	0	0	0.022	0.005	0	0	0	0	0.003	0.005	0	0	0.004	0	0
28	0	0	0.02	0	0.005	0	0	0	0	0	0.005	0	0	0.001	0.002	0
29	0	0.014	0	0	0.009	0	0	0	0	0	0	0	0	0.001	0.002	0
30	0	0	0	0.011	0	0	0	0	0	0	0	0.005	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	48	35	49	46	111	77	93	93	99	193	94	100	100	396	225	266
<i>n_a</i>	20	22	22	22	26	21	17	20	19	21	22	23	22	26	25	22
<i>n_{eff}</i>	16.64	20.82	16.68	16.04	14.67	14.21	10.39	13.01	14.05	N/A	14.10	16.46	13.60	N/A	N/A	N/A
<i>a</i>	14.96	16.69	15.25	15.26	14.82	14.29	11.85	14.24	13.92	N/A	14.37	15.75	14.65	N/A	N/A	N/A
<i>H_E</i>	0.940	0.952	0.940	0.938	0.932	0.930	0.904	0.923	0.929	N/A	0.929	0.939	0.926	N/A	N/A	N/A
<i>H_O</i>	0.979	0.943	0.959	0.978	0.847	0.935	0.914	0.925	0.970	N/A	0.904	0.970	0.930	N/A	N/A	N/A
<i>F_{IS}</i>	-0.042	0.010	-0.021	-0.044	0.092**	-0.006	-0.011	-0.002	-0.044	N/A	0.027	-0.033	-0.004	N/A	N/A	N/A

Appendix II. Continued.

Allele	Population															
	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0.011	0	0.01	0.01	0	0	0	0	0
3	0	0.005	0	0	0	0.01	0.01	0	0	0	0	0	0	0	0.007	0
4	0.014	0.064	0.04	0.037	0.021	0.03	0.01	0	0.01	0	0.005	0.025	0.005	0.01	0.013	0.014
5	0.083	0.09	0.165	0.122	0.164	0.06	0.07	0.06	0.115	0.12	0.192	0.207	0.131	0.116	0.099	0.096
6	0.097	0.128	0.12	0.133	0.151	0.19	0.12	0.174	0.265	0.18	0.136	0.182	0.146	0.303	0.092	0.158
7	0.056	0.064	0.085	0.08	0.062	0.12	0.06	0.12	0.19	0.175	0.076	0.086	0.121	0.096	0.099	0.062
8	0.028	0.037	0.02	0.037	0.068	0.05	0.05	0.038	0.085	0.03	0.051	0.025	0.167	0	0.046	0.062
9	0.042	0.032	0.035	0.059	0.034	0.02	0.03	0.043	0.055	0.1	0.071	0.015	0.025	0.005	0.066	0.041
10	0.069	0.037	0.02	0.021	0.014	0.04	0	0.054	0.02	0.04	0.02	0.005	0.02	0.025	0.039	0.062
11	0.014	0.032	0.015	0.016	0.041	0.01	0.02	0.033	0.015	0.025	0.015	0	0.005	0.02	0.046	0.021
12	0.139	0.059	0.02	0.043	0.007	0.02	0.05	0.038	0.04	0.015	0.04	0.035	0.081	0.04	0.039	0.027
13	0.028	0.032	0.06	0.027	0.027	0.05	0.03	0.016	0.02	0.02	0.025	0.035	0.096	0.035	0.026	0.027
14	0.014	0.09	0.035	0.027	0.034	0.03	0	0.016	0.01	0.005	0.025	0.015	0.025	0.02	0.059	0.048
15	0.042	0.032	0.045	0.053	0.048	0.06	0.08	0.027	0.015	0.02	0.035	0.03	0.03	0.056	0.046	0.048
16	0.028	0.059	0.06	0.059	0.089	0.02	0.08	0.06	0.025	0.02	0.03	0.04	0.005	0.035	0.02	0.068
17	0.222	0.037	0.075	0.048	0.048	0.07	0.11	0.038	0.04	0.05	0.025	0.01	0.03	0.091	0.059	0.021
18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	0.042	0.069	0.065	0.074	0.034	0.03	0.08	0.054	0.03	0.035	0.045	0.035	0.056	0.025	0.033	0.089
20	0.014	0.048	0.055	0.053	0.062	0.05	0.04	0.049	0.02	0.03	0.056	0.101	0.02	0.04	0.059	0.041
21	0.014	0.016	0.02	0.032	0.041	0.01	0.03	0.06	0.02	0.045	0.04	0.04	0	0.015	0.059	0.062
22	0.028	0.043	0.02	0.027	0.041	0.04	0.02	0.065	0.02	0.05	0.081	0.096	0.015	0.04	0.053	0.034
23	0.028	0.016	0.025	0.032	0	0.04	0.05	0.005	0.005	0	0.015	0.015	0.005	0.025	0.02	0.007
24	0	0.005	0	0.021	0.007	0.02	0.02	0.016	0	0.01	0	0	0.015	0	0	0.007
25	0	0.005	0.015	0	0	0.02	0.03	0	0	0.005	0	0	0	0	0.013	0
26	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0.007
27	0	0	0	0	0	0	0	0.011	0	0.005	0	0	0	0	0	0
28	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0.007	0	0	0.011	0	0.01	0.005	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0
32	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	36	94	100	94	73	50	50	92	100	100	99	99	99	99	76	73
<i>n_a</i>	19	22	21	20	20	23	21	22	19	22	21	18	19	18	22	21
<i>n_{eff}</i>	N/A	16.57	13.61	15.56	12.77	14.14	16.95	13.89	7.53	10.31	11.88	9.24	10.01	7.58	18.07	14.87
<i>a</i>	N/A	15.30	14.48	15.08	14.04	15.76	15.43	14.87	11.65	13.08	13.93	12.11	11.74	12.16	15.74	14.76
<i>H_E</i>	N/A	0.940	0.927	0.936	0.922	0.929	0.941	0.928	0.867	0.903	0.916	0.892	0.900	0.868	0.945	0.933
<i>H_O</i>	N/A	0.968	0.930	0.968	0.890	0.940	0.940	0.957	0.880	0.930	0.889	0.889	0.909	0.828	0.974	0.945
<i>F_{IS}</i>	N/A	-0.030	-0.004	-0.035	0.034	-0.012	0.001	-0.031	-0.015*	-0.030	0.030	0.003	-0.010	0.046	-0.031	-0.013*

Appendix II. Continued.

Allele	Population															
	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0.006	0	0	0	0	0	0	0	0.014	0.01	0.007	0.016
3	0.005	0.006	0	0	0	0	0	0.011	0.006	0.005	0	0.011	0.007	0	0.02	0.005
4	0.005	0.044	0.024	0.026	0.038	0.051	0.017	0.011	0.023	0.073	0.074	0.086	0.034	0.02	0.02	0.032
5	0.134	0.139	0.155	0.088	0.122	0.102	0.116	0.149	0.091	0.229	0.237	0.247	0.142	0.13	0.101	0.047
6	0.124	0.156	0.107	0.105	0.147	0.136	0.146	0.106	0.165	0.396	0.4	0.392	0.142	0.165	0.149	0.068
7	0.043	0.039	0.06	0.088	0.096	0.059	0.076	0.053	0.08	0.073	0.037	0.059	0.081	0.055	0.054	0.037
8	0.043	0.028	0.048	0.053	0.026	0.042	0.043	0.053	0.045	0.005	0.026	0.005	0.068	0.04	0.081	0.016
9	0.054	0.061	0.06	0.044	0.032	0.042	0.06	0.032	0.04	0.01	0.068	0.032	0.027	0.06	0.027	0.079
10	0.016	0.05	0.024	0.018	0.045	0.051	0.03	0.032	0.028	0.031	0.026	0.011	0.014	0.05	0.02	0.021
11	0.038	0.011	0.012	0.026	0.026	0.025	0.017	0.021	0.011	0.01	0.005	0.005	0.034	0.045	0.054	0.042
12	0.043	0.033	0.036	0.026	0.045	0.025	0.023	0.064	0.017	0.052	0.032	0.011	0.02	0.025	0.027	0.021
13	0.032	0.022	0.024	0.026	0.019	0.025	0.036	0.032	0.051	0.005	0	0	0.041	0.035	0.047	0.063
14	0.038	0.028	0.048	0.07	0.019	0.059	0.04	0.043	0.034	0.01	0	0	0.041	0.025	0.02	0.058
15	0.038	0.039	0.048	0.018	0.038	0.076	0.04	0.128	0.057	0.016	0.011	0.016	0.027	0.04	0.074	0.079
16	0.081	0.061	0.06	0.053	0.096	0.059	0.05	0.085	0.068	0.005	0.026	0.027	0.041	0.075	0.061	0.1
17	0.059	0.056	0.095	0.061	0.045	0.042	0.076	0.053	0.057	0.042	0.021	0.022	0.047	0.02	0.054	0.074
18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	0.075	0.072	0.06	0.07	0.058	0.068	0.073	0.032	0.034	0	0	0.022	0.061	0.07	0.027	0.084
20	0.043	0.078	0.024	0.079	0.045	0.042	0.066	0.032	0.074	0.016	0.011	0.027	0.068	0.055	0.041	0.042
21	0.048	0.033	0.012	0.044	0.019	0.042	0.033	0.032	0.045	0.01	0.011	0.022	0.034	0.03	0.074	0.047
22	0.038	0.006	0.036	0.061	0.026	0.008	0.033	0.011	0.011	0.005	0.016	0	0.02	0.01	0.02	0.026
23	0.016	0.011	0.012	0.009	0.006	0.017	0.01	0.011	0.034	0	0	0	0.027	0.015	0.014	0.021
24	0.005	0.011	0.024	0.018	0.019	0.008	0.01	0.011	0.017	0.005	0	0.005	0.007	0.01	0	0.016
25	0.016	0.011	0.012	0	0.006	0.008	0.007	0	0.011	0	0	0	0	0.005	0.007	0.005
26	0.005	0	0	0.009	0.006	0	0	0	0	0	0	0	0	0.01	0	0
27	0	0.006	0.012	0	0.006	0.008	0	0	0	0	0	0	0	0	0	0
28	0	0	0.012	0	0	0	0	0	0	0	0	0	0.007	0	0	0
29	0	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0.009	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
n	93	90	42	57	78	59	151	47	88	96	95	93	74	100	74	95
n_a	23	23	23	22	25	22	21	21	22	19	15	17	23	23	22	23
n_{eff}	15.57	13.79	16.52	18.14	14.67	17.13	14.36	14.57	14.89	4.50	4.39	4.41	14.82	13.85	15.50	18.10
a	15.21	14.68	16.13	15.75	15.28	15.67	14.53	14.92	15.12	9.22	9.12	9.25	15.31	14.90	15.20	15.84
H_E	0.936	0.927	0.939	0.945	0.932	0.942	0.930	0.931	0.933	0.778	0.772	0.773	0.933	0.928	0.935	0.945
H_O	0.903	0.933	0.976	0.965	0.897	0.983	0.967	0.915	0.943	0.844	0.811	0.699	0.959	0.880	0.919	0.979
F_{IS}	0.035*	-0.006	-0.040	-0.021	0.037	-0.044	-0.039	0.018	-0.011	-0.085	-0.050	0.097	-0.029	0.052	0.018	-0.036

Appendix II. Continued.

Allele	Population															
	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94
1	0	0	0	0	0	0	0.047	0	0.005	0	0	0	0	0	0	0
2	0.045	0	0.036	0.081	0.067	0.036	0.008	0.053	0.097	0.068	0.016	0.165	0.138	0.03	0.020	0.111
3	0.02	0.033	0.016	0.012	0.022	0.030	0	0.021	0.016	0.014	0.011	0	0	0.01	0.010	0.011
4	0.03	0.02	0.016	0.087	0.022	0.024	0	0.021	0.022	0.041	0	0	0	0	0	0
5	0.04	0.027	0.021	0.023	0.011	0.018	0.016	0.011	0.054	0.081	0.005	0	0	0.01	0.010	0
6	0.09	0.047	0.042	0.012	0.079	0.048	0.016	0.043	0.022	0.041	0.005	0.01	0.074	0.02	0.050	0.022
7	0.065	0.033	0.01	0	0.062	0.048	0	0	0	0	0.06	0	0.021	0.045	0.090	0.022
8	0.075	0.207	0.021	0.012	0.051	0.030	0.008	0.032	0.038	0	0.065	0.055	0	0.06	0.040	0.056
9	0.075	0.06	0.01	0.128	0.051	0.096	0.039	0.053	0.038	0.027	0.054	0.04	0.106	0.1	0.070	0.111
10	0.02	0.02	0.01	0.041	0.062	0.030	0.016	0.085	0.075	0.041	0.043	0.05	0.085	0.135	0.160	0.133
11	0.065	0.04	0.021	0.029	0.084	0.078	0	0.021	0.043	0	0.13	0.345	0.138	0.095	0.090	0.122
12	0.06	0.067	0.063	0.041	0.045	0.036	0.039	0.096	0.065	0.014	0.098	0.05	0.021	0.08	0.080	0.033
13	0.035	0.02	0.01	0.064	0.045	0.042	0.055	0.043	0.016	0.054	0.038	0.035	0.128	0.03	0.030	0
14	0.03	0.06	0.052	0.023	0.051	0.054	0.016	0.011	0.016	0.149	0.141	0.005	0.085	0.02	0.030	0.011
15	0.07	0.06	0.094	0.023	0.039	0.024	0.023	0.064	0.075	0.108	0.065	0.075	0.021	0.045	0.020	0.067
16	0.035	0.047	0.094	0.058	0.045	0.024	0.016	0.043	0.038	0.054	0.082	0.005	0.011	0.08	0.050	0.044
17	0.03	0.04	0.104	0.023	0.034	0.030	0.008	0.074	0.102	0.149	0.087	0.04	0.106	0.04	0.030	0.1
18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	0.065	0.033	0.094	0.099	0.022	0.054	0.07	0.106	0.048	0	0.038	0.005	0.011	0.035	0.020	0.011
20	0.04	0.073	0.13	0.023	0.073	0.042	0.047	0.032	0.022	0.095	0.027	0	0.021	0.06	0.030	0.011
21	0.045	0.033	0.036	0.058	0.062	0.060	0.008	0.032	0.027	0	0.016	0.01	0.011	0.055	0.050	0.022
22	0.02	0.047	0.047	0.023	0.028	0.048	0.016	0.021	0.065	0.041	0.005	0	0.021	0.04	0.080	0.067
23	0.015	0.007	0.01	0.047	0.017	0.030	0.055	0.043	0.075	0	0	0.1	0	0.005	0.010	0
24	0.02	0.007	0.031	0.035	0.006	0.078	0.086	0.021	0.016	0	0.011	0	0	0	0.030	0.022
25	0	0.007	0.021	0.041	0.011	0.024	0.094	0.043	0.011	0	0	0	0	0.005	0	0
26	0	0	0.005	0	0.006	0.012	0.047	0.021	0	0	0	0.005	0	0	0	0.011
27	0.005	0.007	0	0	0.006	0	0.031	0	0	0	0	0	0	0	0	0
28	0	0.007	0.005	0	0	0	0.086	0.011	0.005	0	0	0.005	0	0	0	0
29	0.005	0	0	0	0	0	0.023	0	0.011	0	0	0	0	0	0	0.011
30	0	0	0	0	0	0	0.023	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0.016	0	0	0	0	0	0	0	0	0
32	0	0	0	0.006	0	0	0.023	0	0	0	0	0	0	0	0	0
33	0	0	0	0.006	0	0	0.039	0	0	0.027	0	0	0	0	0	0
34	0	0	0	0.006	0	0	0.023	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0.008	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
n	100	75	96	86	89	83	64	47	93	37	92	100	47	100	50	45
n_a	24	24	25	25	25	24	30	24	25	16	20	17	16	21	21	20
n_{eff}	19.98	13.61	15.08	17.04	N/A	N/A	22.77	20.81	N/A	12.86	12.96	5.86	11.09	14.94	N/A	13.35
a	16.60	15.58	15.13	15.99	N/A	N/A	18.29	17.24	N/A	13.22	13.36	10.05	11.72	14.51	N/A	13.78
H_E	0.950	0.927	0.934	0.941	N/A	N/A	0.956	0.952	N/A	0.922	0.923	0.829	0.910	0.933	N/A	0.925
H_O	0.950	0.893	0.969	0.977	N/A	N/A	0.953	1.000	N/A	0.919	0.880	0.860	0.872	0.930	N/A	0.933
F_{IS}	0.000	0.036	-0.038	-0.038	N/A	N/A	0.003	-0.051	N/A	0.004	0.046	-0.037	0.042	0.003	N/A	-0.009

Appendix II. Continued.

Allele	Population															
	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110
1	0.003	0.025	0.026	0	0	0	0	0	0	0.005	0.007	0.005	0	0	0	0
2	0.028	0.02	0.021	0.067	0.032	0.02	0.058	0.021	0.021	0.061	0.014	0.074	0.022	0.031	0.01	0.013
3	0.003	0.005	0.005	0.017	0.011	0	0	0	0.011	0.015	0	0.015	0	0	0.04	0.013
4	0.003	0	0	0	0	0	0	0.01	0	0	0	0.002	0	0	0	0.025
5	0	0	0	0.006	0	0.03	0	0	0	0	0	0.002	0.011	0	0	0.013
6	0.020	0.035	0.032	0.006	0.021	0.04	0.047	0.052	0.021	0.031	0.007	0.015	0	0.021	0	0.013
7	0.013	0.035	0.042	0.067	0	0.02	0.012	0.01	0.021	0	0.014	0.020	0.043	0	0.03	0.025
8	0.068	0.125	0.042	0.089	0.064	0.04	0.047	0.042	0.053	0.071	0.082	0.069	0.109	0.115	0.05	0.1
9	0.116	0.07	0.068	0.167	0.245	0.11	0.198	0.042	0.106	0.117	0.158	0.092	0.065	0.115	0.11	0.087
10	0.088	0.075	0.111	0.078	0.043	0.14	0.116	0.177	0.128	0.082	0.144	0.097	0.087	0.052	0.09	0.087
11	0.066	0.085	0.047	0.133	0.074	0.14	0.093	0.156	0.096	0.163	0.075	0.108	0.13	0.198	0.16	0.113
12	0.088	0.07	0.1	0.1	0.053	0.1	0.163	0.115	0.149	0.112	0.144	0.125	0.109	0.042	0.13	0.05
13	0.083	0.08	0.1	0.083	0.053	0.04	0.07	0.052	0.17	0.061	0.075	0.070	0.076	0.063	0.07	0.087
14	0.121	0.085	0.132	0.022	0.17	0.05	0.047	0.052	0.032	0.066	0.068	0.051	0.098	0.073	0.05	0.025
15	0.058	0.06	0.058	0.028	0.053	0.07	0.07	0.073	0.053	0.031	0.021	0.056	0.033	0.042	0.04	0.037
16	0.091	0.075	0.121	0.022	0.032	0.05	0.035	0.042	0.021	0.036	0.048	0.051	0.054	0.042	0.01	0.1
17	0.038	0.045	0.032	0.017	0.064	0.05	0.023	0.021	0.021	0.046	0.014	0.048	0.076	0.052	0.02	0
18	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0	0	0
19	0.025	0.04	0.005	0.017	0	0.05	0	0.052	0.032	0.046	0.055	0.033	0.011	0.094	0.03	0.087
20	0.028	0.02	0.005	0.028	0.021	0.03	0.012	0.042	0.064	0.036	0.041	0.038	0.076	0.021	0.03	0.037
21	0.030	0.025	0.026	0.006	0.011	0.01	0	0.01	0	0.005	0.014	0.007	0	0	0.02	0.037
22	0.018	0.015	0.011	0.022	0.021	0.01	0	0	0	0.005	0.007	0.013	0	0.021	0.01	0.013
23	0.003	0	0.005	0.011	0	0	0	0	0	0	0	0.002	0	0.01	0.04	0.025
24	0	0.005	0	0	0.032	0	0.012	0.01	0	0	0.007	0.005	0	0.01	0.01	0.013
25	0.010	0.005	0	0.017	0	0	0	0	0	0.01	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0.002	0	0	0.02	0
27	0	0	0	0	0	0	0	0	0	0	0.007	0	0	0	0.02	0
28	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0.01	0
29	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0.002	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0.003	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
n	198	100	95	90	47	50	43	48	47	98	73	305	46	48	50	40
n_a	22	21	21	21	17	18	15	20	16	19	20	26	15	17	22	21
n_{eff}	N/A	15.41	12.94	11.82	9.26	13.41	10.10	11.91	10.82	12.34	N/A	N/A	13.16	11.49	13.71	16.21
a	N/A	14.49	13.46	13.19	12.80	13.83	11.81	13.79	12.26	13.11	N/A	N/A	12.44	13.05	14.83	15.09
H_E	N/A	0.935	0.923	0.915	0.892	0.925	0.901	0.916	0.908	0.919	N/A	N/A	0.924	0.913	0.927	0.938
H_O	N/A	0.870	0.926	0.911	0.851	0.920	0.884	0.958	0.957	0.918	N/A	N/A	0.891	0.896	0.920	0.900
F_{IS}	N/A	0.070*	-0.004	0.005	0.046	0.006	0.019	-0.047	-0.056	0.001	N/A	N/A	0.036	0.019	0.008	0.041

Appendix II. Continued.

Allele	Population																Total
	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0.07	0.04	0.037	0.04	0.044	0	0.042	0	0.03	0.051	0	0.008	0	0	0	0	0
3	0.035	0	0.025	0.02	0.007	0	0.021	0	0.02	0.01	0	0	0	0	0.005	0.006	0
4	0.005	0	0	0	0.004	0	0	0	0	0	0	0.010	0.011	0	0	0	0
5	0.005	0.01	0	0	0.026	0.011	0	0	0	0.01	0.011	0.035	0.027	0	0.011	0.011	0
6	0.01	0.01	0.013	0.02	0.015	0.011	0	0	0.02	0.01	0.009	0.038	0.038	0.184	0.054	0.052	0
7	0.025	0.01	0.025	0.01	0.004	0.011	0.01	0.05	0.01	0.031	0.049	0.056	0.038	0.026	0.081	0.075	0
8	0.085	0.08	0.05	0.09	0.115	0.053	0.063	0.04	0.04	0.051	0.064	0.040	0.027	0	0.027	0.029	0
9	0.055	0.06	0.075	0.09	0.048	0.096	0.021	0.1	0.1	0.071	0.118	0.038	0.044	0	0.022	0.023	0
10	0.105	0.12	0.075	0.09	0.096	0.106	0.104	0.16	0.1	0.092	0.109	0.063	0.038	0.013	0.07	0.075	0
11	0.12	0.12	0.1	0.07	0.111	0.096	0.208	0.17	0.1	0.143	0.105	0.086	0.055	0.013	0.038	0.04	0
12	0.095	0.06	0.138	0.13	0.107	0.202	0.125	0.1	0.08	0.082	0.047	0.114	0.082	0.105	0.07	0.069	0
13	0.065	0.08	0.063	0.14	0.137	0.043	0.063	0.19	0.05	0.092	0.062	0.088	0.071	0.013	0.043	0.04	0
14	0.08	0.05	0.025	0.04	0.067	0.064	0.167	0.06	0.01	0.092	0.039	0.043	0.049	0.039	0.054	0.057	0
15	0.04	0.03	0.025	0.06	0.030	0.085	0.063	0.06	0.06	0.051	0.032	0.038	0.044	0.079	0.022	0.023	0
16	0.035	0.08	0.087	0.04	0.048	0.096	0.01	0.01	0.07	0.041	0.017	0.033	0.055	0.132	0.032	0.029	0
17	0.025	0.08	0.05	0.04	0.033	0.032	0.073	0	0.06	0	0.054	0.063	0.077	0.066	0.081	0.08	0
18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	0.045	0.03	0.025	0.04	0.022	0.043	0	0.03	0.02	0.041	0.039	0.061	0.055	0.026	0.172	0.184	0
20	0.025	0.02	0.05	0.01	0.026	0.011	0.021	0.01	0.01	0.041	0.058	0.048	0.088	0.066	0.065	0.063	0
21	0.05	0.05	0.013	0.02	0.019	0	0	0	0.06	0.031	0.077	0.020	0.049	0.053	0.065	0.057	0
22	0.005	0.03	0.025	0.03	0.007	0.043	0.01	0	0.05	0.031	0.041	0.038	0.033	0	0.016	0.017	0
23	0.015	0.02	0.013	0.01	0.011	0	0	0	0.04	0	0.043	0.020	0.027	0	0.038	0.04	0
24	0	0.01	0.037	0	0.015	0	0	0	0.05	0.02	0.006	0.018	0.027	0	0.027	0.023	0
25	0.005	0.01	0	0	0.004	0	0	0	0	0.01	0	0.015	0.033	0.026	0	0	0
26	0	0	0	0	0	0	0	0	0.02	0	0.006	0.020	0.022	0.013	0.005	0.006	0
27	0	0	0.013	0.01	0	0	0	0.01	0	0	0.002	0	0	0.039	0	0	0
28	0	0	0.037	0	0	0	0	0	0	0	0	0.003	0	0.105	0.005	0	0
29	0	0	0	0	0.004	0	0	0.01	0	0	0.011	0.003	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0.003	0.005	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	100	50	40	50	135	47	48	50	50	49	233	198	91	38	93	87	10311
<i>n_a</i>	22	21	22	20	24	16	15	14	21	20	22	26	23	17	22	21	40
<i>n_{eff}</i>	15.05	15.92	17.85	14.18	N/A	10.98	9.19	8.75	17.81	15.53	N/A	N/A	20.67	11.78	14.28	13.75	
<i>a</i>	14.44	14.91	16.27	14.31	N/A	12.24	11.17	10.41	15.55	14.79	N/A	N/A	16.79	13.03	14.77	14.67	
<i>H_E</i>	0.934	0.937	0.944	0.929	N/A	0.909	0.891	0.886	0.944	0.936	N/A	N/A	0.952	0.915	0.930	0.927	
<i>H_O</i>	0.950	0.860	0.925	0.860	N/A	0.809	0.938	0.920	0.960	0.959	N/A	N/A	0.945	0.842	0.946	0.943	
<i>F_{IS}</i>	-0.018	0.083	0.020	0.075	N/A	0.112	-0.053	-0.039	-0.017	-0.025	N/A	N/A	0.007	0.081*	-0.018	-0.017	

Appendix II. Continued.

One102 Allele	Size		Population													
	ABL	DFO	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	204	200	0	0	0	0	0	0	0	0.006	0	0	0	0.01	0	0
2	208	204	0.005	0	0	0	0	0.008	0.007	0	0.05	0.008	0.033	0.02	0	0
3	212	208	0	0	0	0	0.013	0	0.007	0	0.025	0.012	0.033	0.03	0	0
4	216	212	0	0	0	0	0.013	0	0	0	0	0	0	0	0	0
5	220	216	0.005	0	0.005	0	0.013	0.015	0.007	0	0.037	0.004	0	0	0	0
6	224	220	0.011	0.017	0.048	0.075	0.037	0.015	0.014	0	0.013	0.012	0	0.01	0.022	0
7	228	224	0.016	0.042	0.043	0.125	0.025	0	0.007	0.038	0.013	0.016	0.1	0.16	0.03	0.02
8	232	228	0.016	0	0.021	0.013	0.013	0.03	0.041	0.013	0.1	0.056	0.1	0.06	0	0
9	236	232	0.005	0.008	0.016	0.013	0.05	0.03	0.027	0.006	0.063	0.052	0.017	0.05	0.052	0.118
10	240	236	0.082	0.117	0	0	0.037	0.023	0.041	0.051	0.013	0.016	0.05	0.06	0.03	0.078
11	244	240	0.066	0.117	0.005	0	0	0.061	0.041	0.064	0.013	0.056	0.017	0.01	0.104	0.108
12	248	244	0.027	0.033	0.048	0.05	0.025	0.098	0.082	0.077	0.05	0.052	0.117	0.06	0.149	0.127
13	252	248	0.088	0.05	0.048	0.113	0.013	0.076	0.068	0.096	0.1	0.032	0.017	0.04	0.112	0.059
14	256	252	0.055	0.058	0.144	0.075	0.075	0.159	0.13	0.160	0.087	0.067	0.15	0.06	0.09	0.098
15	260	256	0.066	0.05	0.048	0	0.075	0.076	0.075	0.109	0.025	0.075	0.033	0.05	0.112	0.078
16	264	260	0.115	0.042	0.112	0.113	0.05	0.038	0.041	0.103	0.075	0.075	0.033	0.07	0.052	0.098
17	268	265	0.082	0.05	0.117	0.075	0.037	0.053	0.075	0.051	0.063	0.115	0.05	0.04	0.037	0.01
18	272	269	0.06	0.017	0.08	0.1	0.063	0.015	0.027	0.026	0.05	0.067	0.033	0.04	0.03	0.01
19	276	273	0.077	0.042	0.016	0.013	0.05	0.053	0.055	0.032	0.013	0.060	0	0.01	0	0.02
20	280	277	0.027	0.033	0.048	0.037	0.075	0.023	0	0.032	0.05	0.052	0.05	0.06	0.045	0.039
21	284	281	0.033	0.042	0.021	0.025	0.037	0.015	0.027	0.013	0.037	0.056	0.067	0.03	0.007	0.01
22	288	285	0.016	0.075	0.048	0.025	0.1	0.023	0.034	0.013	0.013	0.020	0.067	0.03	0.037	0.01
23	292	289	0.033	0.017	0.064	0.05	0.075	0.03	0.055	0.006	0.05	0.016	0	0.03	0	0.01
24	296	293	0.016	0.033	0.027	0.037	0.037	0.038	0.021	0.026	0.025	0.020	0	0.02	0	0
25	300	297	0.027	0.058	0.016	0.013	0.025	0.03	0.027	0	0	0.008	0.017	0.02	0	0
26	304	301	0.022	0.075	0	0.025	0.037	0.03	0.027	0.026	0.037	0.016	0	0.01	0.015	0.01
27	308	305	0.011	0	0.021	0	0	0	0.021	0.019	0	0.008	0	0	0.022	0.029
28	312	309	0.005	0	0	0	0	0.008	0	0	0	0.008	0	0	0.007	0
29	316	314	0.011	0.025	0	0	0.025	0.015	0	0	0	0.008	0	0	0.007	0
30	320	318	0.011	0	0	0	0	0.023	0.021	0	0	0.008	0	0	0.037	0.049
31	324	322	0	0	0	0	0	0.008	0	0	0	0	0	0	0	0
32	328	326	0	0	0	0	0	0.008	0	0	0	0	0	0	0	0
33	332	330	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	340	338	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	352	350	0	0	0	0	0	0	0	0	0	0.004	0	0	0	0
36	356	354	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0
37	360	358	0	0	0	0.025	0	0	0	0	0	0	0	0	0	0
38	364	362	0.005	0	0	0	0	0	0	0	0	0	0.017	0	0	0
39	368	366	0	0	0	0	0	0	0	0	0	0	0	0.01	0	0
40	372	370	0	0	0	0	0	0	0.021	0.006	0	0	0	0.01	0	0
41	376	374	0	0	0	0	0	0	0	0.006	0	0	0	0	0	0
42	380	378	0	0	0	0	0	0	0	0.013	0	0	0	0	0	0.02
43	384	382	0	0	0	0	0	0	0	0.006	0	0	0	0	0	0
44	392	390	0	0	0	0	0	0	0	0	0	0.004	0	0	0	0
<i>n</i>			91	60	94	40	40	66	73	78	40	126	30	50	67	51
<i>n_a</i>			28	21	22	19	24	27	26	25	23	30	19	26	20	20
<i>n_{eff}</i>			17.43	17.63	14.13	14.91	22.90	16.79	18.87	N/A	20.52	N/A	15.66	18.40	13.32	13.48
<i>a</i>			16.10	15.81	14.52	14.35	17.69	16.76	16.87	N/A	16.85	N/A	15.21	17.20	13.98	13.55
<i>H_E</i>			0.943	0.943	0.929	0.933	0.956	0.940	0.947	N/A	0.951	N/A	0.936	0.946	0.925	0.926
<i>H_O</i>			0.835	0.817	0.883	0.975	0.950	0.924	0.945	N/A	0.950	N/A	0.967	0.880	0.925	0.902
<i>F_{IS}</i>			0.115**	0.135**	0.050	-0.046	0.007	0.017	0.002	N/A	0.001	N/A	-0.033	0.070	0.000	0.026

Appendix II. Continued.

One102 Allele	Population															
	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0.04	0.042	0.022	0.022	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0.011	0	0.005
5	0	0	0	0	0.011	0	0	0	0	0	0	0.007	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0	0.007	0	0	0	0
7	0.032	0.014	0	0	0	0.012	0.019	0	0.042	0.022	0	0.007	0	0.033	0.026	0.005
8	0.016	0	0.043	0.023	0	0.035	0.019	0.02	0.083	0.043	0.065	0.035	0.015	0.022	0.046	0.025
9	0.048	0.057	0	0.045	0.12	0.07	0.093	0.04	0.01	0.065	0.043	0.042	0.059	0.067	0.066	0.045
10	0.056	0.071	0.065	0.193	0.076	0.058	0.111	0.16	0.125	0.196	0.13	0.063	0.088	0.122	0.066	0.065
11	0.063	0.100	0.087	0.08	0.087	0.116	0.111	0.16	0.177	0.109	0.163	0.141	0.162	0.211	0.112	0.115
12	0.111	0.100	0.109	0.08	0.087	0.116	0.093	0.1	0.083	0	0.054	0.197	0.118	0.111	0.118	0.105
13	0.127	0.129	0.174	0.227	0.13	0.128	0.111	0.04	0.063	0.065	0.141	0.077	0.103	0.044	0.132	0.13
14	0.079	0.071	0.196	0.045	0.054	0.128	0.056	0.1	0.063	0.065	0.043	0.099	0.103	0.067	0.132	0.1
15	0.087	0.043	0	0.068	0.054	0.058	0.148	0.1	0.042	0.109	0.076	0.042	0.088	0.056	0.092	0.12
16	0.071	0.043	0.13	0.045	0.076	0.093	0.056	0.02	0.021	0.087	0.033	0.063	0.059	0.067	0.039	0.055
17	0.04	0.057	0.022	0.102	0.109	0.047	0.074	0.02	0.01	0.043	0.011	0.049	0.059	0.011	0.066	0.09
18	0.024	0.029	0.043	0.057	0.076	0.047	0.037	0.08	0.083	0.065	0.087	0.099	0.044	0.022	0.02	0.035
19	0.032	0.100	0.022	0.011	0.033	0.023	0.037	0.1	0.083	0.043	0.076	0.021	0.015	0.044	0.013	0.04
20	0.008	0.014	0	0.011	0.022	0.035	0	0	0.021	0.022	0.011	0.021	0.044	0.033	0.02	0.035
21	0.008	0	0	0.011	0.022	0	0	0	0.01	0	0	0.014	0.015	0.044	0.013	0.005
22	0.048	0.014	0	0	0.022	0	0	0	0.01	0	0.011	0.007	0	0.022	0.026	0.01
23	0.04	0	0	0	0	0.012	0	0	0.01	0.022	0.022	0	0.029	0.011	0.013	0.01
24	0	0.029	0.043	0	0	0.012	0	0	0.021	0.022	0	0.007	0	0	0	0
25	0.056	0	0.022	0	0	0.012	0.037	0.02	0	0	0	0	0	0	0	0
26	0	0.057	0.022	0	0.011	0	0	0	0	0	0	0	0	0	0	0
27	0.016	0.029	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0.005
28	0.008	0.043	0.022	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0.008	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0.024	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0.011	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	63	35	23	44	46	43	27	25	48	23	46	71	34	45	76	100
<i>n_a</i>	22	18	14	14	17	17	14	14	19	16	17	19	15	18	17	19
<i>n_{eff}</i>		N/A	10.25	8.54	13.46	12.96	13.25	11.67	12.49	13.44	11.60	10.59	12.66	11.35	12.05	12.00
<i>a</i>	15.20	N/A	12.18	10.97	13.07	13.04	12.53	12.16	13.47	14.11	12.62	12.46	12.58	13.49	12.64	12.45
<i>H_E</i>	0.938	N/A	0.902	0.883	0.926	0.923	0.925	0.914	0.920	0.926	0.914	0.906	0.921	0.912	0.917	0.917
<i>H_O</i>	1.000	N/A	0.913	0.909	0.913	0.884	0.926	0.880	0.896	0.870	0.891	0.887	0.853	0.889	0.921	0.920
<i>F_{IS}</i>	-0.066	N/A	-0.012	-0.030	0.014	0.043	-0.002	0.038	0.026	0.062	0.025	0.020	0.075	0.025	-0.004	-0.004

Appendix II. Continued.

One102 Allele	Population															
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0.014	0	0	0	0	0	0	0	0	0	0.005	0	0	0.004	0
6	0.01	0	0	0	0.004	0	0	0	0	0	0	0	0	0	0	0
7	0.021	0.029	0	0.022	0.027	0.013	0.038	0.016	0	0.003	0.005	0.005	0	0.004	0.006	0
8	0.01	0.071	0	0.011	0.004	0	0.027	0.075	0.03	0.177	0.026	0.015	0.015	0.012	0.009	0.016
9	0.021	0.029	0.041	0.098	0.054	0.045	0.005	0.027	0.061	0.060	0.051	0.08	0.025	0.057	0.041	0.021
10	0.042	0.043	0.082	0.076	0.071	0.084	0.081	0.167	0.091	0.198	0.158	0.085	0.13	0.113	0.078	0.101
11	0.083	0.086	0.194	0.141	0.103	0.201	0.151	0.194	0.157	0.133	0.189	0.125	0.11	0.134	0.125	0.163
12	0.104	0.086	0.122	0.065	0.134	0.078	0.075	0.075	0.071	0.107	0.087	0.09	0.085	0.082	0.140	0.112
13	0.104	0.129	0.061	0.12	0.085	0.149	0.059	0.054	0.121	0.029	0.041	0.14	0.14	0.091	0.080	0.087
14	0.115	0.1	0.051	0.098	0.107	0.117	0.075	0.065	0.106	0.117	0.097	0.085	0.095	0.122	0.112	0.093
15	0.146	0.114	0.082	0.163	0.067	0.065	0.183	0.129	0.146	0.026	0.097	0.105	0.115	0.099	0.097	0.109
16	0.125	0.114	0.071	0.065	0.063	0.065	0.086	0.048	0.096	0.070	0.071	0.085	0.1	0.110	0.108	0.109
17	0.073	0.043	0.102	0.033	0.152	0.084	0.14	0.065	0.066	0.029	0.071	0.075	0.075	0.045	0.075	0.052
18	0.073	0.043	0.061	0.033	0.045	0.006	0.048	0.059	0.035	0.036	0.051	0.045	0.075	0.066	0.073	0.066
19	0.021	0.043	0.031	0.022	0.045	0.052	0.016	0.005	0.015	0.005	0.026	0.025	0.02	0.034	0.028	0.041
20	0.01	0.014	0.051	0.022	0.027	0.026	0.016	0.016	0.005	0.008	0.026	0.02	0.015	0.025	0.013	0.021
21	0.01	0.029	0.031	0.022	0.013	0.013	0	0	0	0	0.005	0.005	0	0.005	0.006	0.002
22	0	0.014	0.01	0	0	0	0	0.005	0	0	0	0	0	0	0.002	0
23	0.031	0	0	0	0	0	0	0	0	0.003	0	0.005	0	0.001	0.002	0
24	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0.006
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	48	35	49	46	112	77	93	93	99	192	98	100	100	385	232	258
<i>n_a</i>	17	17	15	16	16	14	14	15	13	15	15	18	13	16	18	16
<i>n_{eff}</i>	11.87	14.38	11.29	11.28	11.35	9.50	9.56	9.37	9.98	N/A	9.86	11.51	10.39	N/A	N/A	N/A
<i>a</i>	12.34	13.78	12.27	12.23	11.93	10.90	10.87	11.06	10.56	N/A	11.30	11.77	10.63	N/A	N/A	N/A
<i>H_E</i>	0.916	0.930	0.911	0.911	0.912	0.895	0.895	0.893	0.900	N/A	0.899	0.913	0.904	N/A	N/A	N/A
<i>H_O</i>	0.958	0.857	0.959	0.891	0.911	0.935	0.914	0.817	0.899	N/A	0.867	0.870	0.860	N/A	N/A	N/A
<i>F_{IS}</i>	-0.047	0.080	-0.053	0.022	0.001	-0.045	-0.021	0.086	0.001	N/A	0.035	0.047	0.049	N/A	N/A	N/A

Appendix II. Continued.

One102 Allele	Population															
	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007
7	0	0.005	0.01	0	0	0	0	0	0	0.005	0	0	0	0	0	0.007
8	0.012	0.032	0.02	0.011	0.027	0.02	0.02	0.011	0	0.02	0	0	0.005	0	0.026	0.007
9	0.035	0.037	0.045	0.065	0.061	0.02	0.07	0.043	0.075	0.01	0.03	0.02	0.026	0.035	0.053	0.062
10	0.047	0.08	0.1	0.086	0.047	0.05	0.1	0.033	0.035	0.045	0.005	0.025	0.036	0.025	0.112	0.055
11	0.093	0.101	0.14	0.097	0.095	0.15	0.12	0.125	0.13	0.14	0.121	0.202	0.117	0.162	0.099	0.137
12	0.116	0.08	0.085	0.129	0.101	0.12	0.13	0.087	0.085	0.095	0.111	0.091	0.031	0.227	0.099	0.075
13	0.128	0.101	0.095	0.129	0.155	0.17	0.13	0.163	0.135	0.195	0.141	0.106	0	0.131	0.086	0.103
14	0.058	0.101	0.085	0.097	0.128	0.13	0.09	0.141	0.145	0.085	0.106	0.061	0.128	0.066	0.118	0.144
15	0.105	0.106	0.12	0.097	0.108	0.14	0.09	0.087	0.105	0.11	0.106	0.101	0.173	0.035	0.105	0.103
16	0.047	0.128	0.105	0.113	0.095	0.08	0.05	0.098	0.07	0.09	0.061	0.091	0.036	0.035	0.112	0.055
17	0.058	0.08	0.035	0.054	0.061	0.04	0.08	0.092	0.095	0.085	0.131	0.126	0.092	0.136	0.072	0.068
18	0.047	0.096	0.075	0.054	0.034	0.03	0.03	0.038	0.075	0.04	0.136	0.101	0.224	0.126	0.039	0.055
19	0.151	0.021	0.04	0.043	0.027	0.02	0.07	0.06	0.025	0.04	0.02	0.066	0.082	0.02	0.046	0.048
20	0.035	0.011	0.02	0.022	0.027	0.01	0	0.005	0.02	0.015	0.015	0.005	0.046	0	0.026	0.048
21	0.047	0.005	0.005	0.005	0.027	0.01	0.02	0.005	0.005	0.025	0.005	0	0.005	0	0.007	0
22	0.023	0.005	0.015	0	0.007	0	0	0.005	0	0	0.005	0.005	0	0	0	0
23	0	0.011	0	0	0	0.01	0	0.005	0	0	0.005	0	0	0	0	0.021
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	43	94	100	93	74	50	50	92	100	100	99	99	98	99	76	73
<i>n_a</i>	15	17	17	14	15	15	13	16	13	15	15	13	13	11	14	17
<i>n_{eff}</i>	N/A	11.79	11.69	11.23	11.35	9.41	11.67	10.13	10.27	9.67	9.42	9.13	7.84	7.45	11.90	12.10
<i>a</i>	N/A	11.79	12.05	11.27	11.95	10.87	11.39	10.97	10.64	11.09	10.03	10.07	9.72	9.13	11.67	12.39
<i>H_E</i>	N/A	0.915	0.914	0.911	0.912	0.894	0.914	0.901	0.903	0.897	0.894	0.890	0.873	0.866	0.916	0.917
<i>H_O</i>	N/A	0.883	0.880	0.892	0.824	0.900	0.920	0.870	0.850	0.990	0.859	0.960	0.888	0.869	0.947	0.959
<i>F_{IS}</i>	N/A	0.035*	0.038	0.020	0.097	-0.007	-0.006	0.035	0.059	-0.105	0.040	-0.078	-0.018	-0.003	-0.034	-0.046

Appendix II. Continued.

One102 Allele	Population															
	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0.011
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.014	0
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0
7	0	0.006	0	0	0.006	0	0.003	0.01	0	0	0	0	0.013	0	0	0
8	0.011	0.006	0	0.017	0.039	0.009	0.017	0	0.006	0.017	0.016	0.011	0.007	0.015	0.041	0.005
9	0.038	0.039	0.024	0.069	0.045	0.018	0.040	0.02	0.028	0.108	0.074	0.07	0.06	0.03	0.054	0.053
10	0.134	0.089	0.071	0.112	0.058	0.088	0.090	0.112	0.074	0.023	0.037	0.048	0.093	0.12	0.088	0.142
11	0.134	0.122	0.083	0.103	0.156	0.105	0.130	0.112	0.142	0.068	0.053	0.065	0.107	0.07	0.095	0.105
12	0.075	0.1	0.083	0.112	0.13	0.088	0.120	0.133	0.057	0.159	0.132	0.113	0.107	0.115	0.115	0.084
13	0.091	0.111	0.131	0.103	0.084	0.149	0.113	0.051	0.136	0.097	0.153	0.118	0.08	0.145	0.108	0.095
14	0.108	0.089	0.131	0.138	0.097	0.044	0.110	0.184	0.119	0.068	0.116	0.14	0.107	0.08	0.128	0.089
15	0.091	0.083	0.155	0.069	0.13	0.132	0.110	0.092	0.097	0.159	0.095	0.129	0.073	0.115	0.074	0.079
16	0.102	0.089	0.131	0.069	0.052	0.088	0.060	0.082	0.074	0.085	0.047	0.102	0.093	0.1	0.101	0.1
17	0.059	0.094	0.083	0.069	0.058	0.14	0.080	0.112	0.091	0.148	0.147	0.145	0.06	0.105	0.081	0.105
18	0.081	0.083	0.036	0.034	0.078	0.088	0.043	0.02	0.057	0.034	0.068	0.032	0.107	0.05	0.041	0.074
19	0.032	0.044	0.036	0.052	0.032	0.044	0.043	0.051	0.028	0.011	0.026	0.022	0.047	0.03	0.007	0.037
20	0.022	0.033	0.024	0.034	0.013	0.009	0.027	0.01	0.04	0.023	0.026	0.005	0.027	0.01	0.02	0.005
21	0.011	0.006	0.012	0	0.013	0	0.007	0	0.017	0	0.005	0	0.007	0.005	0.02	0.016
22	0.005	0.006	0	0.017	0	0	0.007	0	0.011	0	0.005	0	0.013	0	0.014	0
23	0.005	0	0	0	0.006	0	0	0	0.023	0	0	0	0	0.005	0	0
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	93	90	42	58	77	57	150	49	88	88	95	93	75	100	74	95
<i>n_a</i>	16	16	13	14	16	13	16	14	16	13	15	13	16	16	16	15
<i>n_{eff}</i>	11.26	11.99	10.60	12.15	11.19	10.26	11.13	9.86	11.50	9.30	10.19	9.74	12.64	10.60	12.25	11.39
<i>a</i>	11.58	11.67	11.01	11.95	11.91	10.52	11.54	10.72	12.09	10.34	11.17	10.29	12.18	11.10	12.22	11.35
<i>H_E</i>	0.911	0.917	0.906	0.918	0.911	0.903	0.910	0.899	0.913	0.892	0.902	0.897	0.921	0.906	0.918	0.912
<i>H_O</i>	0.892	0.889	0.905	0.914	0.870	0.860	0.893	0.837	0.886	0.841	0.895	0.849	0.973	0.880	0.932	0.905
<i>F_{IS}</i>	0.021	0.030*	0.001	0.004	0.045	0.048	0.019	0.070	0.029	0.058	0.008	0.054	-0.057	0.028	-0.015	0.008

Appendix II. Continued.

One102 Allele	Population															
	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0.007	0	0.006	0	0	0	0	0	0	0.011	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0.005	0	0
6	0.005	0	0	0	0	0.006	0.008	0	0	0	0	0.005	0	0	0	0
7	0	0	0	0	0.016	0	0	0.011	0.016	0	0.027	0	0	0	0	0
8	0.015	0.007	0.063	0.036	0.022	0.006	0	0.011	0.048	0.026	0.016	0.005	0.053	0.005	0.070	0.067
9	0.071	0.021	0.042	0.054	0.027	0.017	0.008	0.011	0.043	0.141	0.022	0.115	0.053	0.045	0.070	0.067
10	0.111	0.13	0.073	0.066	0.070	0.052	0.092	0.076	0.048	0.218	0.06	0.155	0.096	0.03	0.100	0.122
11	0.106	0.075	0.078	0.133	0.075	0.075	0.208	0.087	0.059	0.141	0.065	0.02	0.117	0.035	0.090	0.067
12	0.086	0.178	0.109	0.127	0.124	0.109	0.077	0.141	0.176	0.038	0.076	0.125	0.223	0.145	0.080	0.033
13	0.167	0.151	0.089	0.12	0.161	0.161	0.115	0.152	0.059	0.013	0.141	0.29	0.138	0.07	0.040	0.044
14	0.131	0.103	0.052	0.06	0.118	0.092	0.123	0.152	0.101	0.051	0.049	0.045	0.096	0.07	0.120	0.167
15	0.045	0.041	0.094	0.06	0.065	0.121	0.092	0.033	0.080	0.064	0.054	0.055	0.011	0.06	0.090	0.044
16	0.066	0.096	0.109	0.06	0.032	0.092	0.008	0.054	0.053	0.077	0.033	0.005	0.043	0.09	0.060	0.011
17	0.061	0.041	0.078	0.108	0.054	0.052	0.038	0.033	0.048	0.09	0.071	0.12	0.021	0.105	0.060	0.133
18	0.066	0.068	0.068	0.054	0.059	0.075	0.023	0.076	0.048	0.013	0.065	0.02	0.021	0.1	0.080	0.078
19	0.025	0.034	0.036	0.03	0.070	0.034	0.092	0.043	0.027	0.103	0.027	0.01	0.032	0.04	0.020	0.089
20	0.02	0.007	0.016	0.018	0.032	0.017	0.015	0.033	0.037	0.013	0.054	0	0	0.025	0.010	0.011
21	0.005	0.007	0.036	0.024	0.043	0.029	0.046	0	0.021	0	0.06	0.005	0	0.04	0.070	0.044
22	0.005	0.021	0.036	0.018	0.005	0.029	0.023	0.054	0.032	0.013	0.054	0	0	0.04	0.060	0
23	0.01	0.014	0.016	0.006	0.016	0.011	0.015	0.022	0.032	0	0.022	0	0.011	0.035	0.020	0
24	0	0	0.005	0	0.011	0.006	0	0	0.011	0	0.016	0	0.011	0.015	0	0.033
25	0	0	0	0.012	0	0.006	0	0	0.027	0	0.005	0	0.043	0.015	0.010	0.044
26	0	0	0	0.006	0	0	0.015	0.011	0.021	0	0.005	0	0.032	0.005	0.010	0.011
27	0.005	0	0	0	0	0.006	0	0	0	0	0.005	0.02	0	0.01	0.010	0
28	0	0	0	0	0	0.006	0	0	0.005	0	0.005	0	0	0.005	0	0
29	0	0	0	0	0	0	0	0	0	0	0.033	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0.011	0	0.022	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	99	73	96	83	93	87	65	46	94	39	92	100	47	100	50	45
<i>n_a</i>	18	17	17	19	18	21	17	17	22	14	25	16	16	23	18	16
<i>n_{eff}</i>	10.84	9.89	14.15	12.63	N/A	N/A	9.83	11.44	N/A	9.10	17.14	6.51	9.61	14.19	N/A	11.96
<i>a</i>	11.79	11.41	13.33	13.12	N/A	N/A	11.62	12.63	N/A	10.85	15.97	9.23	11.94	14.42	N/A	12.67
<i>H_E</i>	0.908	0.899	0.929	0.921	N/A	N/A	0.898	0.913	N/A	0.890	0.942	0.846	0.896	0.930	N/A	0.916
<i>H_O</i>	0.899	0.904	0.865	0.892	N/A	N/A	0.908	0.935	N/A	0.872	0.967	0.800	0.915	0.960	N/A	0.933
<i>F_{IS}</i>	0.010	-0.006	0.070	0.032	N/A	N/A	-0.011	-0.025	N/A	0.021	-0.027	0.055	-0.021	-0.033*	N/A	-0.019

Appendix II. Continued.

Allele	Population															
	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0
5	0	0	0	0.006	0.033	0.011	0.012	0	0	0	0	0.002	0	0	0	0
6	0	0.01	0.011	0	0	0	0	0	0	0.02	0	0.002	0	0	0	0
7	0.003	0	0.011	0.023	0	0.011	0.012	0	0	0	0.014	0.003	0.011	0	0.01	0
8	0.013	0	0.006	0.017	0.011	0.011	0.036	0	0.021	0.005	0.042	0.017	0.011	0	0.04	0.05
9	0.038	0.04	0.017	0.011	0	0	0.024	0.058	0.043	0.02	0.028	0.023	0.043	0.056	0	0.075
10	0.038	0.07	0.072	0.028	0.033	0.064	0.06	0.012	0.085	0.111	0.056	0.071	0.054	0.044	0.02	0.1
11	0.083	0.08	0.083	0.074	0.087	0.064	0.024	0.07	0.053	0.086	0.035	0.073	0.033	0.067	0.04	0.1
12	0.088	0.085	0.061	0.091	0.12	0.106	0.048	0.093	0.043	0.101	0.092	0.080	0.13	0.122	0.15	0.05
13	0.090	0.115	0.117	0.097	0.196	0.032	0.012	0.058	0.096	0.096	0.092	0.087	0.087	0.078	0.11	0.013
14	0.118	0.095	0.089	0.074	0.076	0.245	0.25	0.151	0.191	0.086	0.113	0.111	0.065	0.089	0.12	0.125
15	0.138	0.08	0.139	0.159	0.065	0.128	0.06	0.105	0.16	0.131	0.106	0.116	0.087	0.078	0.05	0.15
16	0.075	0.065	0.078	0.125	0.098	0.106	0.083	0.163	0.064	0.071	0.141	0.080	0.13	0.133	0.08	0.063
17	0.070	0.08	0.067	0.063	0.054	0.053	0.06	0.035	0.043	0.051	0.063	0.043	0.087	0.022	0.07	0.1
18	0.028	0.075	0.044	0.034	0.033	0.021	0.048	0.058	0.032	0.025	0.049	0.054	0.109	0.122	0.09	0.075
19	0.018	0.015	0.033	0.045	0	0.032	0.012	0.047	0.021	0.061	0.007	0.057	0.054	0.044	0.07	0
20	0.033	0.04	0.011	0.034	0.022	0.021	0	0.012	0.011	0.015	0.028	0.040	0	0.011	0.03	0
21	0.023	0.04	0.094	0.04	0.043	0.021	0.012	0.047	0.011	0.03	0.035	0.021	0.022	0.044	0.02	0
22	0.033	0.02	0.05	0.017	0.043	0	0.095	0	0.032	0.01	0.021	0.026	0.011	0.011	0.03	0.025
23	0.030	0.015	0	0.017	0.011	0.021	0.012	0.023	0.032	0.005	0.014	0.019	0	0.033	0	0
24	0.038	0.025	0	0.017	0.065	0.021	0.036	0.035	0.011	0.03	0.021	0.014	0.022	0.011	0	0.013
25	0.015	0.02	0.006	0	0	0.011	0.036	0	0	0.035	0.007	0.028	0.011	0	0.03	0
26	0.015	0.005	0.006	0.011	0.011	0.011	0.012	0.012	0.011	0.005	0	0.009	0	0	0.01	0.013
27	0.010	0.005	0.006	0.011	0	0	0.06	0	0.021	0.005	0.007	0.003	0	0.033	0	0.013
28	0	0.005	0	0.006	0	0.011	0	0	0.011	0	0.021	0.009	0	0	0	0
29	0.003	0	0	0	0	0	0	0.012	0.011	0	0	0.002	0.011	0	0.01	0.013
30	0	0.005	0	0	0	0	0	0	0	0	0.007	0.009	0	0	0	0.013
31	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0.003	0	0	0	0	0	0	0	0	0	0	0.002	0	0	0	0.013
33	0	0	0	0	0	0	0	0	0	0	0	0	0.022	0	0.01	0
34	0	0	0	0	0	0	0	0.012	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	199	100	90	88	46	47	42	43	47	99	71	288	46	45	50	40
<i>n_a</i>	23	24	20	22	17	20	21	18	21	21	22	27	19	17	20	18
<i>n_{eff}</i>	N/A	15.23	12.93	12.98	11.79	9.50	10.83	12.31	11.59	13.29	N/A	N/A	13.59	13.53	13.56	12.74
<i>a</i>	N/A	14.45	13.01	14.04	13.11	13.02	14.55	13.33	14.11	13.48	N/A	N/A	13.63	13.34	13.99	13.00
<i>H_E</i>	N/A	0.934	0.923	0.923	0.915	0.895	0.908	0.919	0.914	0.925	N/A	N/A	0.926	0.926	0.926	0.922
<i>H_O</i>	N/A	0.960	0.844	0.920	0.783	0.745	0.762	0.791	0.872	0.919	N/A	N/A	0.913	0.933	0.900	0.900
<i>F_{IS}</i>	N/A	-0.028	0.085**	0.003	0.146*	0.169**	0.162*	0.141	0.046	0.006	N/A	N/A	0.015	-0.008	0.029	0.024

Appendix II. Continued.

Allele	Population																Total
	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0.005	0	0	0.01	0	0.01	0.138	0	0	0	0	0.002	0.005	0	0	0	0
5	0	0	0.013	0	0	0.01	0	0.06	0	0.01	0.005	0	0	0	0	0	0
6	0	0	0	0	0.004	0	0	0	0	0	0.029	0	0	0	0	0	0
7	0	0	0	0	0.032	0	0	0	0	0	0.005	0.010	0	0	0.016	0.018	0
8	0.01	0.02	0.025	0.01	0.004	0.031	0.032	0	0.03	0.02	0.018	0.010	0.021	0.013	0.027	0.024	0
9	0.005	0.06	0.037	0.04	0.032	0.042	0	0.04	0.01	0.082	0.032	0.027	0.021	0.013	0.011	0.012	0
10	0.035	0.07	0.025	0.04	0.067	0.042	0.032	0.05	0.11	0.051	0.009	0.055	0.073	0	0.044	0.041	0
11	0.08	0.1	0.087	0.11	0.074	0.042	0.053	0.07	0.12	0.071	0.070	0.060	0.047	0	0.121	0.118	0
12	0.05	0.11	0.063	0.06	0.064	0.104	0.117	0.13	0.14	0.092	0.072	0.112	0.063	0.087	0.154	0.147	0
13	0.085	0.1	0.087	0.11	0.145	0.167	0.117	0.11	0.14	0.082	0.109	0.097	0.141	0.1	0.137	0.135	0
14	0.1	0.09	0.087	0.09	0.149	0.094	0.149	0.08	0.07	0.133	0.120	0.152	0.172	0.075	0.104	0.112	0
15	0.13	0.06	0.1	0.09	0.053	0.125	0.043	0.2	0.05	0.071	0.086	0.112	0.104	0.037	0.093	0.106	0
16	0.065	0.08	0.063	0.11	0.046	0.177	0.085	0.08	0.07	0.143	0.075	0.070	0.089	0.212	0.06	0.065	0
17	0.05	0.08	0.113	0.06	0.071	0.052	0.096	0.07	0.06	0.051	0.106	0.085	0.109	0.113	0.093	0.088	0
18	0.075	0.07	0.063	0.07	0.067	0.01	0.053	0.04	0.05	0.051	0.133	0.065	0.042	0.075	0.033	0.035	0
19	0.085	0.07	0.05	0.05	0.028	0.052	0.074	0.01	0.06	0.031	0.084	0.032	0.031	0.063	0.027	0.024	0
20	0.02	0.01	0.037	0.01	0.043	0.01	0	0.01	0.02	0.041	0.029	0.060	0.036	0.075	0.005	0.006	0
21	0.025	0	0.05	0.01	0.035	0	0	0	0.04	0.041	0.011	0.020	0.026	0.1	0.044	0.041	0
22	0.05	0.01	0.013	0.05	0.028	0.021	0	0	0.01	0.02	0.005	0.010	0.01	0.025	0.016	0.018	0
23	0.05	0	0.013	0	0.014	0	0.011	0.03	0.01	0	0.002	0.007	0.005	0	0.005	0.006	0
24	0.02	0	0.025	0.01	0.007	0	0	0.02	0.01	0	0	0.010	0.005	0	0	0	0
25	0.015	0.03	0	0.02	0.025	0	0	0	0	0	0	0.002	0.005	0	0.005	0.006	0
26	0.015	0	0.025	0.02	0.007	0.01	0	0	0	0.01	0	0	0.005	0	0	0	0
27	0.01	0.01	0.013	0	0.004	0	0	0	0	0	0	0	0	0	0	0	0
28	0.005	0.02	0	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0.01	0	0	0	0	0	0	0	0	0	0	0.002	0	0	0	0	0
30	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0.013	0	0	0
32	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0.013	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	100	50	40	50	141	48	47	50	50	49	221	201	96	40	91	85	10245
<i>n_a</i>	24	18	21	21	22	17	13	15	17	17	19	21	20	14	18	18	40
<i>n_{eff}</i>	15.05	14.78	17.65	15.32	N/A	10.25	11.04	10.71	12.22	13.58	N/A	N/A	10.85	10.26	10.94	11.02	
<i>a</i>	14.64	13.54	15.60	14.52	N/A	12.07	11.24	12.01	12.70	13.44	N/A	N/A	12.30	11.38	12.05	12.06	
<i>H_E</i>	0.934	0.932	0.943	0.935	N/A	0.902	0.909	0.907	0.918	0.926	N/A	N/A	0.908	0.903	0.909	0.909	
<i>H_O</i>	0.910	0.920	0.925	1.000	N/A	0.958	0.894	0.920	0.860	0.918	N/A	N/A	0.938	0.900	0.934	0.953	
<i>F_{IS}</i>	0.025	0.013*	0.020	-0.071	N/A	-0.063	0.018	-0.015	0.064	0.009	N/A	N/A	-0.033	0.003	-0.028	-0.048	

Appendix II. Continued

<i>OtsG68</i>	Size	Size	Population															
			Allele	ABL	DFO	1	2	3	4	5	6	7	8	9	10	11	12	13
1	139	134	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	143	139	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	147	143	0	0	0	0	0	0	0	0	0.038	0.037	0.004	0	0	0	0	0
4	151	148	0.005	0	0	0	0	0.029	0.026	0.032	0.013	0.040	0.017	0.03	0	0	0	
5	155	152	0.016	0.008	0.027	0.013	0.013	0	0	0	0.025	0	0	0.01	0	0	0	
6	159	156	0.016	0.03	0.005	0.025	0.037	0.007	0	0.006	0.013	0.028	0	0	0	0	0	
7	163	160	0.037	0.015	0.027	0.013	0	0.037	0.013	0.013	0.037	0.024	0	0	0	0	0	
8	167	164	0.059	0.03	0.049	0.025	0.037	0.066	0.058	0.045	0.087	0.052	0.05	0.06	0.06	0.06	0.069	
9	171	168	0.053	0.083	0.076	0.113	0.013	0.037	0.064	0.051	0.075	0.067	0	0.03	0.112	0.137	0.137	
10	175	172	0.048	0.008	0.054	0.05	0.037	0.037	0.064	0.051	0.025	0.048	0.1	0.11	0.06	0.069	0.069	
11	179	176	0.021	0.038	0.092	0.025	0.075	0.037	0.032	0.013	0.013	0.067	0.167	0.14	0.015	0.01	0.01	
12	183	179	0.048	0.03	0.092	0.037	0.05	0.147	0.096	0.115	0.075	0.071	0.033	0.03	0.037	0.049	0.049	
13	187	183	0.027	0.023	0.022	0.087	0.025	0.051	0.019	0.045	0.037	0.079	0.017	0.07	0.172	0.157	0.157	
14	191	187	0.016	0	0.027	0.025	0.025	0.044	0.064	0.103	0.05	0.040	0.117	0.03	0.06	0.02	0.02	
15	195	191	0.064	0.045	0.027	0	0	0.022	0.026	0.109	0.013	0.020	0.1	0.08	0.075	0.059	0.059	
16	199	195	0.059	0.083	0.054	0.063	0.1	0.044	0.051	0.038	0.025	0.020	0.033	0.11	0.052	0.029	0.029	
17	203	199	0.043	0.008	0.022	0.025	0.1	0.029	0.019	0.013	0.087	0.028	0	0.03	0.082	0.118	0.118	
18	207	203	0.059	0.136	0.13	0.138	0.138	0.051	0.032	0.019	0	0.020	0	0	0.045	0.059	0.059	
19	211	207	0.027	0.045	0.103	0.138	0.125	0.066	0.013	0	0.013	0.036	0.017	0.02	0.015	0	0	
20	215	211	0.048	0.068	0.022	0.025	0.063	0.007	0.019	0	0.087	0.036	0.017	0.02	0.022	0	0	
21	219	215	0.021	0.008	0.043	0.025	0.025	0	0.006	0.026	0.013	0.016	0	0.01	0	0	0	
22	223	219	0.011	0.008	0.016	0	0.013	0.022	0.019	0	0	0.024	0	0	0.022	0.059	0.059	
23	227	223	0.059	0.045	0.038	0.075	0	0.022	0.013	0	0	0.016	0	0.01	0	0	0	
24	231	227	0.016	0.023	0	0	0	0.022	0.019	0.006	0.013	0	0	0.01	0.007	0	0	
25	235	231	0	0	0	0	0	0.015	0.032	0	0.037	0.016	0.05	0.03	0	0	0	
26	239	235	0	0	0	0	0	0.007	0.019	0	0.013	0.020	0.017	0	0.022	0	0	
27	243	238	0	0	0.005	0	0	0	0.006	0.006	0	0.008	0	0.01	0.007	0.01	0.01	
28	247	242	0	0	0	0	0	0.007	0	0	0	0.004	0	0	0.015	0	0	
29	251	247	0	0	0	0	0	0.007	0	0.013	0.037	0.012	0	0	0	0	0	
30	255	251	0.005	0	0	0	0	0.007	0.032	0.045	0.025	0.012	0	0.01	0.015	0.02	0.02	
31	259	255	0.005	0.008	0	0	0	0	0.006	0.006	0	0.032	0	0	0.03	0.029	0.029	
32	263	259	0	0.015	0.005	0.025	0.013	0	0.013	0.013	0	0.008	0.033	0	0	0	0	
33	267	263	0	0	0	0	0.013	0.029	0.026	0.006	0	0.004	0	0.01	0	0	0	
34	271	267	0.005	0.015	0	0.013	0	0.037	0.006	0	0.013	0.020	0.05	0.04	0.007	0.01	0.01	
35	275	271	0.005	0	0.011	0	0	0.059	0.051	0.019	0.037	0.016	0.017	0.02	0.03	0.029	0.029	
36	279	275	0.011	0.015	0	0	0	0.007	0.032	0.006	0.013	0.012	0.05	0	0	0	0	
37	283	279	0.043	0.023	0	0	0	0.022	0.045	0.058	0	0.024	0.033	0.01	0	0	0	
38	287	283	0.016	0	0	0	0.013	0.007	0.026	0	0	0.016	0.033	0.03	0.015	0.01	0.01	
39	291	287	0.016	0.015	0.005	0	0.013	0	0.006	0.013	0	0.012	0.033	0	0	0	0	
40	295	291	0.027	0.023	0.016	0.013	0.037	0	0.019	0	0	0.012	0	0.01	0	0	0	
41	299	295	0	0.015	0.016	0.025	0.025	0	0	0	0	0	0	0.01	0	0	0	
42	303	299	0	0.008	0	0	0	0	0.006	0.006	0	0.012	0	0	0	0	0	
43	307	303	0	0.008	0	0	0	0.007	0	0.019	0.013	0.020	0	0	0.007	0.01	0.01	
44	311	307	0	0	0	0	0	0	0.006	0	0.025	0	0	0.01	0	0	0	
45	315	312	0	0	0	0.013	0	0	0	0	0	0	0	0	0	0	0	
46	319	316	0	0.008	0	0	0.013	0.007	0	0	0	0	0.017	0	0.007	0.049	0.049	
47	323	320	0.016	0.015	0	0	0	0	0	0	0.025	0	0	0.01	0	0	0	
48	327	324	0.09	0.076	0	0	0	0	0.006	0.019	0	0	0	0	0	0	0	
49	331	328	0.011	0.008	0.011	0.013	0	0	0	0.013	0	0.008	0	0	0	0	0	
50	335	332	0	0	0	0	0	0	0	0.006	0	0	0	0	0.007	0	0	
51	339	336	0	0.015	0	0	0	0	0.006	0.013	0	0	0	0	0	0	0	
52	343	340	0	0	0	0	0	0	0	0.006	0	0	0	0	0	0	0	
53	347	344	0	0	0	0	0	0	0	0	0.025	0	0	0	0	0	0	
54	351	348	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
55	423	420	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
56	431	428	0	0	0	0	0	0	0	0.006	0	0	0	0	0	0	0	
57	443	440	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>n</i>			94	66	92	40	40	68	78	78	40	126	30	50	67	51	51	
<i>n_a</i>			33	34	26	23	23	32	37	35	30	39	21	29	26	20	20	
<i>n_{eff}</i>			24.48	19.78	15.97	15.05	15.57	20.58	26.75	N/A	25.48	N/A	15.53	16.78	14.51	13.04	13.04	
<i>a</i>			18.69	18.14	15.66	15.71	15.66	18.31	19.76	N/A	19.36	N/A	16.05	16.87	15.56	13.95	13.95	
<i>H_E</i>			0.959	0.949	0.937	0.934	0.936	0.951	0.963	N/A	0.961	N/A	0.936	0.940	0.931	0.923	0.923	
<i>H_O</i>			0.957	0.909	0.913	0.950	1.000	0.985	0.962	N/A	0.950	N/A	0.900	0.880	0.925	0.922	0.922	
<i>F_{IS}</i>			0.002	0.043*	0.026	-0.018	-0.070	-0.036	0.001	N/A	0.011	N/A	0.039	0.065	0.006	0.002*	0.002*	

Appendix II. Continued

Allele	Population															
	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.011	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0.011	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0.015	0	0	0	0	0	0.1	0.063	0.063	0.054	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0.016	0	0	0	0	0	0	0	0	0	0	0.007	0	0.011	0	0.005
7	0.016	0	0	0	0	0	0	0	0.021	0	0	0.014	0	0	0	0
8	0.016	0.029	0.065	0.034	0.033	0.023	0.037	0.02	0.01	0	0.022	0	0	0.022	0	0.025
9	0.073	0.029	0.087	0.08	0.065	0	0.074	0	0	0	0	0.035	0.056	0.011	0.007	0.04
10	0.04	0.074	0	0	0.033	0.035	0.074	0.02	0.021	0.021	0.087	0.099	0.014	0.044	0.112	0.1
11	0.024	0.029	0.043	0.034	0.022	0.023	0	0.02	0.042	0.021	0.054	0.085	0.042	0.078	0.112	0.075
12	0.048	0.162	0.217	0.023	0.011	0.116	0.074	0.08	0.042	0.021	0.011	0.085	0.069	0.033	0.197	0.03
13	0.081	0.059	0.065	0.023	0.065	0.07	0.056	0.02	0.052	0.063	0.054	0.077	0.056	0.044	0.079	0.035
14	0.048	0.044	0.022	0.057	0.054	0.116	0.037	0.12	0.052	0.125	0.033	0.014	0.042	0.067	0.079	0.035
15	0.089	0.029	0.022	0.023	0.033	0.058	0.019	0	0.021	0.021	0.011	0.028	0.056	0.011	0.033	0.035
16	0.065	0.029	0.022	0.023	0.011	0.012	0.111	0	0.021	0.042	0.022	0.021	0.069	0.033	0.02	0.045
17	0.113	0.044	0	0.034	0.033	0.012	0.019	0.06	0.063	0.042	0.054	0.007	0.014	0.111	0.013	0.07
18	0.065	0.059	0	0	0.065	0.035	0.019	0.06	0.083	0.104	0.065	0.028	0.042	0.044	0.039	0.04
19	0.016	0.059	0.022	0.023	0.011	0.035	0.019	0.16	0.094	0.104	0.076	0.007	0.014	0.044	0.046	0.01
20	0.008	0.029	0	0.057	0.043	0.035	0.019	0.02	0.073	0	0.043	0	0.028	0.022	0.046	0.01
21	0	0	0.065	0.057	0.054	0.023	0.019	0.02	0.01	0	0.022	0.049	0.014	0	0.013	0.02
22	0.065	0.015	0	0.011	0.011	0.035	0.019	0.02	0.031	0.021	0.011	0.021	0.028	0.011	0.026	0.015
23	0.016	0	0	0.023	0.022	0.047	0.056	0	0	0	0.033	0.007	0	0.011	0.013	0.015
24	0	0	0	0.011	0.043	0.012	0	0	0	0.021	0.011	0.049	0.056	0	0.026	0.03
25	0	0	0.065	0.08	0.022	0	0.019	0.06	0.042	0.021	0.043	0.007	0.042	0.022	0	0.03
26	0.008	0	0.022	0.034	0.043	0.023	0.037	0	0.01	0	0	0.056	0.056	0.022	0.026	0.02
27	0.016	0	0	0.034	0	0.023	0	0.04	0.01	0.083	0.076	0.014	0.042	0.011	0.02	0.01
28	0	0	0	0.045	0.022	0.012	0.037	0.02	0.031	0	0.033	0.014	0.056	0.033	0.007	0.025
29	0	0	0	0.011	0.011	0.012	0	0.02	0.01	0.021	0.011	0.056	0.028	0	0	0.025
30	0.04	0.015	0	0.034	0.033	0.012	0.037	0	0	0	0	0	0	0.022	0.007	0.015
31	0.032	0.015	0	0.011	0.011	0	0.019	0	0.021	0	0	0.014	0.028	0	0	0.01
32	0	0	0	0.023	0.033	0.012	0.019	0	0.01	0.021	0	0.007	0.014	0.022	0	0.035
33	0	0.015	0.109	0.011	0.011	0.023	0	0.04	0	0	0.033	0.014	0.028	0.033	0.007	0.025
34	0.04	0	0.043	0.011	0.033	0.012	0	0	0.052	0.021	0.033	0.035	0.014	0.044	0.013	0.015
35	0.016	0.029	0	0.011	0.065	0.023	0.019	0	0	0	0.011	0.028	0.042	0.067	0.02	0.045
36	0.008	0	0.022	0.08	0.043	0.081	0.019	0	0	0	0.011	0.021	0	0.022	0.007	0.015
37	0.008	0.029	0	0.034	0.011	0.047	0	0	0	0.042	0.011	0.042	0.028	0.022	0.013	0.035
38	0.016	0.015	0.022	0.011	0.011	0	0.056	0	0	0	0	0.014	0	0	0	0.025
39	0	0	0.022	0.011	0.033	0	0.074	0	0	0	0.011	0.007	0	0.022	0.007	0
40	0	0.015	0	0	0.011	0.035	0	0	0	0	0	0.014	0	0.011	0	0.015
41	0	0.044	0	0.023	0	0	0	0	0	0	0	0.014	0	0	0.013	0.005
42	0.008	0	0	0	0	0	0	0	0	0	0	0.022	0.007	0	0	0.005
43	0	0.029	0	0	0	0	0	0	0	0.063	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0.021	0	0	0.014	0.011	0	0.01
45	0	0	0.022	0	0	0	0	0	0.01	0	0.011	0	0	0	0	0
46	0.008	0.015	0	0	0	0	0	0	0.01	0.021	0	0	0.014	0	0	0
47	0	0.044	0	0	0	0	0	0.08	0.021	0	0.011	0	0	0.011	0	0
48	0	0	0	0	0	0	0	0	0.021	0	0.022	0	0	0	0	0
49	0	0.029	0.043	0	0	0	0	0	0.01	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0.021	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0.021	0	0	0	0	0	0	0
52	0	0	0	0.023	0	0	0	0	0.01	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0.02	0.01	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0.019	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	62	34	23	44	46	43	27	25	48	24	46	71	36	45	76	100
<i>n_a</i>	28	27	19	32	32	28	26	20	32	23	31	34	28	33	27	36
<i>n_{eff}</i>	19.65	N/A	13.62	29.67	31.71	21.13	27.00	16.12	25.76	21.28	26.66	22.40	31.95	27.24	12.22	26.57
<i>a</i>	17.08	N/A	15.89	20.32	20.41	18.29	19.62	15.99	19.33	18.24	19.37	18.48	20.10	20.14	14.87	19.81
<i>H_E</i>	0.949	N/A	0.927	0.966	0.968	0.953	0.963	0.938	0.961	0.953	0.962	0.955	0.969	0.963	0.918	0.962
<i>H_O</i>	0.952	N/A	0.957	0.909	0.978	0.884	1.000	0.760	0.979	1.000	1.000	0.972	0.861	1.000	0.895	0.930
<i>F_{IS}</i>	-0.003	N/A	-0.033	0.060*	-0.010	0.073	-0.039	0.193*	-0.019	-0.050	-0.039	-0.017	0.112	-0.039	0.026	0.034

Appendix II. Continued

Allele	Population															
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
1	0	0	0	0	0	0	0	0	0	0.008	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0.003	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0.014	0.01	0	0.009	0.006	0	0	0.015	0.003	0	0	0.01	0.004	0.011	0
7	0.01	0.029	0	0	0.004	0	0	0	0	0.003	0	0	0	0.004	0.007	0.006
8	0.01	0.014	0.02	0.011	0	0.019	0.011	0.038	0.015	0.003	0.005	0.01	0.005	0.010	0.011	0.004
9	0.031	0	0.041	0.054	0.013	0.013	0.011	0.104	0.04	0.008	0.015	0	0.005	0.033	0.016	0.028
10	0.042	0.114	0.071	0.076	0.067	0.065	0.027	0.033	0.035	0.023	0.015	0.06	0.105	0.080	0.068	0.059
11	0.115	0.029	0.02	0.065	0.089	0.084	0.048	0.055	0.146	0.049	0.177	0.12	0.055	0.059	0.100	0.106
12	0.042	0.057	0.102	0.098	0.121	0.104	0.14	0.104	0.121	0.124	0.167	0.085	0.19	0.103	0.127	0.121
13	0.094	0.057	0.071	0.054	0.063	0.071	0.07	0.049	0.061	0.028	0.096	0.11	0.11	0.087	0.116	0.087
14	0.073	0.086	0.082	0.065	0.08	0.078	0.086	0.049	0.035	0.031	0.066	0.045	0.085	0.061	0.068	0.047
15	0.042	0.071	0.041	0.054	0.031	0.039	0.005	0.011	0.03	0.008	0.02	0.03	0.025	0.028	0.027	0.015
16	0.042	0.029	0.02	0.043	0.04	0.071	0.016	0.038	0.04	0.288	0.025	0.015	0.015	0.019	0.011	0.015
17	0.052	0.029	0.031	0.011	0.022	0.032	0.161	0.044	0.04	0.021	0.066	0.02	0.035	0.017	0.011	0.025
18	0.01	0.014	0.02	0.043	0.027	0	0.011	0.011	0.03	0.049	0.005	0.035	0.015	0.036	0.030	0.040
19	0	0.057	0.031	0.011	0.027	0.019	0.016	0.011	0.005	0.005	0	0.005	0.005	0.014	0.009	0.013
20	0.01	0.029	0.031	0.022	0.022	0.032	0	0.005	0.005	0.036	0	0.015	0	0.006	0.005	0
21	0.021	0.029	0.051	0.022	0.022	0.045	0	0.005	0.005	0.005	0.025	0.01	0.01	0.004	0.005	0.017
22	0	0	0.02	0.011	0.009	0.006	0.005	0.027	0.005	0.065	0.01	0	0	0.001	0.009	0.006
23	0.01	0	0	0.011	0.013	0	0	0.005	0.01	0.003	0.015	0.01	0.005	0.019	0.005	0.008
24	0.021	0.057	0.02	0	0.027	0.026	0	0	0.015	0.005	0.025	0.015	0.02	0.029	0.025	0.032
25	0.031	0	0.01	0.033	0.022	0.019	0.005	0.033	0.015	0.026	0.005	0.03	0.015	0.014	0.023	0.008
26	0.01	0	0.01	0	0.08	0.032	0.016	0.022	0.045	0.013	0.02	0.02	0.01	0.050	0.020	0.042
27	0	0	0.01	0.033	0.013	0.013	0.032	0.005	0.015	0.008	0.015	0.02	0.03	0.031	0.030	0.023
28	0.01	0.029	0	0.033	0.013	0.013	0.027	0.022	0.005	0.018	0.035	0.02	0.07	0.017	0.016	0.021
29	0	0.014	0.02	0.011	0.027	0	0.027	0.049	0.045	0.016	0.01	0.06	0.03	0.061	0.050	0.057
30	0.021	0	0	0.011	0.009	0.006	0.032	0.082	0.056	0.016	0.061	0.025	0.035	0.042	0.034	0.053
31	0.01	0.014	0.02	0.011	0.022	0.019	0.075	0.137	0.056	0.008	0.04	0.05	0.045	0.069	0.050	0.038
32	0	0.029	0.01	0.022	0.022	0.026	0.097	0.005	0.005	0	0.005	0.04	0.015	0.015	0.034	0.021
33	0.073	0.057	0.031	0.022	0.045	0.052	0	0.005	0.005	0.003	0.005	0.005	0.01	0.017	0.025	0.042
34	0.031	0.014	0.051	0.043	0.013	0.026	0.005	0.011	0	0.010	0	0.035	0.01	0.009	0.011	0.015
35	0	0.014	0.01	0.033	0.004	0.006	0.011	0	0.005	0	0.005	0.005	0	0.005	0.009	0.017
36	0.042	0.029	0.031	0.011	0.004	0.019	0	0.011	0.005	0.005	0.005	0.01	0.02	0.004	0.011	0.011
37	0.063	0.043	0.061	0.011	0	0.006	0.027	0.011	0	0.021	0	0.01	0.005	0.008	0.005	0.004
38	0.042	0.029	0.031	0.011	0.013	0.013	0.005	0	0.02	0	0.02	0.015	0.005	0.009	0.002	0.002
39	0.021	0.014	0.01	0.011	0	0.026	0	0.005	0.015	0.008	0.005	0.005	0	0.006	0.002	0.009
40	0	0	0.01	0.022	0.009	0.006	0.005	0	0.01	0.010	0.02	0.015	0	0.005	0	0.002
41	0.01	0	0	0.011	0.013	0	0	0	0.02	0.005	0.005	0.02	0	0.011	0.014	0.006
42	0	0	0	0.011	0	0	0	0	0	0.005	0	0.005	0	0.001	0	0
43	0	0	0	0	0	0	0.027	0.005	0.02	0.052	0	0.005	0.005	0.009	0	0
44	0	0	0	0.011	0	0	0	0	0	0.010	0.01	0.02	0	0.003	0	0.002
45	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	48	35	49	46	112	77	93	91	99	193	99	100	100	392	220	264
<i>n_a</i>	29	27	31	34	33	31	27	30	34	38	31	35	30	39	36	35
<i>n_{eff}</i>	22.03	25.16	25.28	27.54	19.36	21.19	12.93	16.02	17.35	N/A	11.94	19.47	12.65	N/A	N/A	N/A
<i>a</i>	18.20	19.12	19.28	19.96	17.63	17.87	14.65	15.98	17.29	N/A	14.95	17.91	15.05	N/A	N/A	N/A
<i>H_E</i>	0.955	0.960	0.960	0.964	0.948	0.953	0.923	0.938	0.942	N/A	0.916	0.949	0.921	N/A	N/A	N/A
<i>H_O</i>	0.979	0.914	0.959	0.935	0.946	1.000	0.946	0.934	0.960	N/A	0.909	0.900	0.910	N/A	N/A	N/A
<i>F_{IS}</i>	-0.026	0.049	0.001	0.030	0.002	-0.050	-0.026	0.004	-0.018	N/A	0.008	0.052*	0.012	N/A	N/A	N/A

Appendix II. Continued

Allele	Population															
	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0.022	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0.007	0	0	0.011	0	0	0	0	0	0	0	0
7	0.011	0.011	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	0	0.005	0.01	0.005	0.027	0	0	0.005	0	0.005	0	0	0	0	0.026	0.007
9	0.022	0.037	0.02	0.011	0.007	0.02	0.02	0	0.015	0.02	0.005	0.005	0	0.005	0.039	0.034
10	0.044	0.032	0.091	0.106	0.095	0.11	0.08	0.086	0.065	0.1	0.045	0.076	0.015	0.172	0.059	0.062
11	0.100	0.106	0.121	0.08	0.081	0.09	0.11	0.043	0.075	0.03	0.035	0.066	0.061	0.157	0.145	0.116
12	0.089	0.165	0.146	0.106	0.101	0.1	0.09	0.108	0.1	0.095	0.121	0.202	0.224	0.167	0.072	0.096
13	0.033	0.069	0.081	0.101	0.074	0.07	0.08	0.113	0.135	0.09	0.146	0.152	0.092	0.182	0.105	0.13
14	0.133	0.064	0.02	0.069	0.068	0.07	0.01	0.038	0.08	0.035	0.106	0.045	0.056	0.056	0.066	0.034
15	0.022	0.011	0.015	0.016	0.041	0.02	0.03	0.005	0.015	0.01	0.04	0.015	0	0.005	0.039	0.027
16	0.011	0.011	0.01	0.016	0.027	0.03	0.04	0.054	0.04	0.05	0.005	0.01	0	0	0.046	0.055
17	0.022	0.021	0.015	0.011	0.027	0.03	0.02	0.038	0.015	0.015	0.015	0	0	0.01	0.007	0.021
18	0.022	0.021	0.015	0.037	0	0.03	0	0.005	0.005	0	0.01	0.005	0	0.03	0.046	0
19	0.011	0.011	0.005	0.011	0.014	0.01	0	0.011	0.04	0.035	0.061	0.061	0.092	0.01	0.013	0.007
20	0	0.011	0.005	0.005	0.014	0.04	0.01	0	0	0	0	0.005	0.02	0	0	0.034
21	0.022	0.011	0.005	0.005	0	0.01	0.01	0.005	0	0	0	0.005	0	0	0	0
22	0.044	0.021	0.01	0.011	0.014	0	0.01	0	0	0	0.005	0	0	0	0	0.014
23	0	0.005	0.015	0.016	0.027	0	0.01	0.016	0.015	0	0.005	0.005	0	0	0.007	0.007
24	0.033	0.032	0.015	0.021	0.02	0.03	0.04	0.065	0.115	0.055	0.076	0.101	0.02	0.04	0.013	0.027
25	0.022	0.011	0.02	0.032	0.014	0.03	0	0.022	0.015	0.02	0.025	0.015	0.005	0.02	0.02	0
26	0.022	0.032	0.025	0.011	0.047	0.01	0.06	0.022	0.015	0.005	0	0	0	0	0.013	0.007
27	0.011	0.021	0.015	0.027	0.014	0	0.06	0.011	0	0.005	0	0.005	0	0	0.02	0.027
28	0.022	0.011	0.035	0.005	0.007	0	0	0.005	0	0	0.035	0.01	0	0	0.013	0.007
29	0.067	0.016	0.035	0.037	0.02	0.03	0.06	0.027	0.02	0.005	0.02	0.02	0.036	0	0.039	0.027
30	0.033	0.074	0.035	0.074	0.014	0.02	0.02	0.016	0.005	0.04	0.025	0.025	0.01	0.01	0.026	0.021
31	0.067	0.069	0.096	0.059	0.041	0.06	0.08	0.183	0.075	0.215	0.086	0.061	0.179	0.035	0.066	0.068
32	0.033	0.037	0.045	0.053	0.074	0.06	0.02	0.032	0.015	0.06	0.015	0.04	0	0	0.046	0.062
33	0.011	0.027	0.005	0.021	0.041	0.03	0.07	0.07	0.125	0.06	0.091	0.061	0.184	0.086	0.026	0.021
34	0	0.011	0.01	0.011	0.014	0.04	0.02	0	0.01	0.045	0.02	0.005	0	0	0	0.034
35	0	0.011	0.01	0.016	0.034	0	0.03	0	0	0	0.005	0.005	0	0	0.013	0.021
36	0	0	0.02	0.005	0.007	0.01	0	0.005	0.005	0	0	0	0	0	0.007	0.014
37	0.044	0.021	0.02	0.011	0.02	0.01	0.01	0	0	0	0	0	0	0	0.026	0
38	0.022	0.011	0.01	0.005	0.007	0	0	0	0	0	0	0	0	0	0	0.014
39	0	0	0	0	0	0.02	0	0	0	0	0	0	0.005	0	0	0.007
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0.015	0	0
41	0	0	0	0	0.007	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0.005	0.005	0	0.01	0	0	0	0	0	0	0	0	0	0
43	0	0.005	0.01	0	0	0	0.01	0	0	0.005	0	0	0	0	0	0
44	0	0	0	0	0	0.01	0	0.005	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	45	94	99	94	74	50	50	93	100	100	99	99	98	99	76	73
<i>n_a</i>	27	32	33	32	31	27	25	26	22	22	23	24	14	16	26	28
<i>n_{eff}</i>	N/A	15.85	15.12	17.18	20.41	20.20	18.75	12.41	12.55	11.14	13.03	10.41	7.25	7.96	17.00	17.02
<i>a</i>	N/A	16.79	16.32	16.39	17.64	17.46	16.41	14.26	13.32	13.52	13.83	12.85	9.47	10.09	16.37	16.54
<i>H_E</i>	N/A	0.937	0.934	0.942	0.951	0.951	0.947	0.919	0.920	0.910	0.923	0.904	0.862	0.874	0.941	0.941
<i>H_O</i>	N/A	0.926	0.909	0.968	0.986	0.940	0.980	0.914	0.870	0.940	0.889	0.899	0.918	0.869	0.921	0.973
<i>F_{IS}</i>	N/A	0.012	0.027	-0.028	-0.038	0.011	-0.036	0.006	0.055	-0.033	0.037	0.005	-0.066	0.006	0.022	-0.034

Appendix II. Continued

Allele	Population															
	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0
7	0.005	0.006	0.012	0	0	0.009	0.003	0	0	0.005	0	0	0	0	0.007	0
8	0.005	0.006	0	0	0	0.009	0.007	0.01	0.011	0.053	0.026	0.037	0	0.01	0	0.011
9	0.022	0.011	0.024	0.018	0.038	0.034	0.023	0.02	0.011	0.132	0.146	0.138	0.013	0.01	0.027	0.026
10	0.075	0.056	0.083	0.044	0.064	0.086	0.073	0.071	0.098	0.153	0.151	0.154	0.067	0.06	0.095	0.053
11	0.129	0.135	0.119	0.096	0.064	0.069	0.132	0.102	0.132	0.105	0.047	0.08	0.067	0.115	0.081	0.095
12	0.108	0.163	0.19	0.149	0.09	0.181	0.129	0.133	0.092	0.089	0.068	0.08	0.147	0.12	0.061	0.147
13	0.065	0.112	0.06	0.105	0.096	0.043	0.093	0.071	0.075	0.074	0.115	0.101	0.1	0.13	0.108	0.1
14	0.091	0.056	0.06	0.044	0.103	0.052	0.04	0.071	0.023	0.058	0.099	0.048	0.06	0.04	0.088	0.089
15	0.032	0.034	0.012	0.053	0.032	0.026	0.03	0.02	0.017	0.011	0.047	0.043	0.04	0.05	0.02	0.037
16	0.032	0.022	0.012	0	0.038	0.009	0.02	0.041	0.046	0.037	0.005	0.005	0.04	0.025	0.014	0.037
17	0.016	0.028	0.024	0.044	0.019	0.026	0.036	0.041	0.011	0.026	0.01	0.011	0.013	0.03	0.047	0.021
18	0.022	0.028	0.048	0.009	0.019	0.017	0.017	0.031	0.006	0	0	0	0.033	0.02	0.034	0.026
19	0.032	0.017	0	0	0.013	0.009	0.003	0	0.029	0	0	0	0.02	0	0.027	0.016
20	0.005	0.011	0.012	0	0.006	0.009	0.01	0	0.006	0	0.016	0.005	0	0.015	0.007	0
21	0.005	0.006	0	0	0.006	0.009	0.007	0	0.011	0.005	0.01	0	0	0.005	0.014	0.011
22	0.005	0	0	0.009	0.006	0.017	0	0.01	0.006	0.005	0.016	0.027	0	0.005	0	0.005
23	0.027	0.006	0.036	0.009	0.006	0	0.013	0.02	0.011	0	0.089	0.032	0.02	0	0.007	0
24	0.027	0.022	0.012	0.035	0.045	0.017	0.007	0.051	0.052	0.042	0.052	0.032	0.033	0.02	0.02	0.016
25	0.011	0.006	0.012	0.044	0.019	0.06	0.026	0.02	0.011	0.032	0.021	0.048	0.013	0.005	0.014	0.021
26	0.011	0.022	0.012	0.018	0.019	0.026	0.003	0	0.017	0	0	0	0.007	0.01	0.014	0.005
27	0.022	0.034	0	0.009	0.032	0.069	0.017	0.061	0.006	0	0.005	0	0.02	0.04	0.027	0.011
28	0.027	0.017	0.012	0.018	0.006	0.034	0.01	0.01	0.034	0.026	0.026	0.005	0.027	0.035	0.02	0.026
29	0.043	0.022	0	0.044	0.032	0.017	0.046	0.02	0.075	0.021	0.016	0	0.04	0.015	0.041	0.021
30	0.011	0.022	0.012	0.044	0.026	0.017	0.043	0.061	0.017	0.042	0.021	0.053	0.053	0.05	0.014	0.053
31	0.043	0.056	0.083	0.044	0.038	0.052	0.06	0.02	0.075	0.026	0.01	0.053	0.053	0.06	0.061	0.063
32	0.043	0.028	0.071	0.07	0.09	0.026	0.033	0.01	0.029	0.016	0	0.021	0.033	0.03	0.041	0.074
33	0.027	0.011	0.036	0.035	0.013	0.034	0.04	0.01	0.04	0.021	0	0.016	0.013	0.02	0.047	0.005
34	0.016	0.028	0.036	0.009	0.026	0.017	0.02	0.01	0.017	0	0	0	0.013	0	0.034	0.011
35	0.011	0	0.012	0.026	0.013	0.009	0.01	0.01	0.023	0	0	0.005	0.02	0.01	0	0
36	0.011	0.011	0	0.009	0.013	0	0.017	0.02	0	0.021	0	0.005	0.013	0.015	0.014	0
37	0.005	0.011	0.012	0.009	0.013	0	0.01	0.01	0.006	0	0.005	0	0.02	0.005	0.007	0
38	0.005	0	0	0.009	0.013	0	0.01	0.02	0	0	0	0	0	0	0	0.011
39	0.011	0	0	0	0	0.009	0	0	0.006	0	0	0	0.007	0.025	0	0
40	0	0	0	0	0	0	0.007	0	0	0	0	0	0	0.005	0	0.005
41	0	0	0	0	0	0	0.003	0	0	0	0	0	0.007	0.005	0.014	0
42	0	0.006	0	0	0	0	0	0.01	0.006	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0.01	0	0.005
44	0	0.006	0	0	0	0.009	0.003	0	0	0	0	0	0.007	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	93	89	42	57	78	58	151	49	87	95	96	94	75	100	74	95
<i>n_a</i>	33	31	24	26	30	30	34	29	31	22	22	22	29	32	29	28
<i>n_{eff}</i>	17.96	14.09	13.46	16.60	19.41	16.35	15.93	19.09	16.85	13.13	11.75	12.80	18.02	16.11	19.67	15.14
<i>a</i>	17.21	16.08	15.31	16.27	17.28	17.30	16.39	17.46	16.41	14.19	13.24	13.82	17.19	16.45	17.30	15.53
<i>H_E</i>	0.944	0.929	0.926	0.940	0.948	0.939	0.937	0.948	0.941	0.924	0.915	0.922	0.945	0.938	0.949	0.934
<i>H_O</i>	0.903	0.899	0.929	0.912	0.987	0.931	0.914	1.000	0.897	0.905	0.906	0.915	0.933	0.940	0.946	0.905
<i>F_{IS}</i>	0.044**	0.033	-0.003	0.029	-0.041	0.008	0.025	-0.056	0.047	0.020	0.009	0.008*	0.012	-0.002	0.003	0.031

Appendix II. Continued

Allele	Population															
	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0.021	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	0.005	0	0	0.012	0.011	0	0	0.022	0.016	0.077	0.011	0	0.053	0.005	0	0.011
9	0.025	0.047	0	0.017	0.027	0.023	0	0.011	0	0	0.022	0	0	0.015	0.020	0
10	0.06	0.007	0.031	0.116	0.060	0.068	0.054	0.043	0.043	0	0.065	0	0	0.015	0.050	0.056
11	0.125	0.06	0.005	0.029	0.060	0.051	0.015	0.043	0.032	0.128	0.071	0.065	0.149	0.045	0.050	0.044
12	0.145	0.14	0.057	0.064	0.126	0.125	0.015	0.043	0.080	0	0.087	0.045	0.021	0.03	0.110	0.056
13	0.09	0.073	0.036	0.076	0.143	0.097	0.131	0.076	0.064	0.013	0.114	0.065	0	0.06	0.040	0.1
14	0.03	0.027	0.026	0.064	0.071	0.102	0.046	0.076	0.048	0.013	0.076	0.11	0.074	0.075	0.100	0.067
15	0.035	0.1	0.041	0.076	0.044	0.057	0.177	0.109	0.027	0.051	0.152	0	0.074	0.12	0.120	0.067
16	0.035	0.033	0.041	0.012	0.088	0.102	0.023	0.033	0.021	0	0.049	0.155	0.011	0.115	0.160	0.167
17	0.04	0.02	0.124	0.023	0.027	0.017	0.054	0	0.021	0.154	0.033	0.275	0.064	0.05	0.060	0.033
18	0.03	0.027	0.072	0	0.049	0.040	0.015	0.022	0.016	0.09	0.022	0.015	0.032	0.03	0.030	0.044
19	0.03	0.013	0.015	0.006	0.038	0.028	0.015	0.011	0.011	0.077	0.016	0.06	0.032	0.055	0.020	0.089
20	0.005	0.013	0	0.006	0.033	0.011	0	0.033	0.059	0	0.038	0.005	0.128	0.025	0.020	0.011
21	0.005	0.027	0.005	0.006	0.016	0.006	0	0	0.069	0	0	0.02	0.032	0.025	0.010	0.011
22	0.005	0	0	0.006	0	0.006	0	0	0.016	0.013	0	0	0.043	0.04	0	0.011
23	0.01	0	0	0	0	0	0	0.011	0.021	0.064	0.016	0	0.043	0.025	0.010	0.022
24	0.025	0.027	0.01	0	0	0	0.031	0	0.011	0.09	0	0	0	0.025	0.010	0.011
25	0.015	0.067	0	0	0.011	0	0	0	0.005	0	0	0.03	0.032	0.015	0.020	0
26	0.02	0.007	0.005	0.017	0.005	0.017	0	0.011	0.021	0.077	0.005	0	0.011	0.005	0.020	0
27	0.025	0.007	0.021	0.047	0.016	0.011	0.015	0.033	0.064	0.026	0	0	0	0	0	0
28	0.03	0.007	0.01	0.052	0.005	0.034	0.108	0.011	0.027	0	0	0	0.011	0.01	0.010	0
29	0.01	0.027	0.026	0.017	0.005	0.011	0.046	0.011	0.027	0	0.005	0	0	0.015	0.010	0
30	0.045	0.093	0.088	0.017	0.005	0.011	0.046	0.033	0.043	0.013	0.011	0	0	0	0.010	0.011
31	0.03	0.02	0.093	0.023	0.022	0.011	0.015	0.033	0.011	0.038	0.027	0	0	0.05	0	0.067
32	0.03	0.053	0.088	0.041	0.016	0.017	0.1	0.087	0.053	0	0.027	0.005	0.053	0	0.010	0
33	0.005	0.033	0.098	0.012	0.038	0.040	0.054	0.033	0.037	0	0	0	0	0.005	0.010	0
34	0	0.02	0.057	0.017	0.016	0.011	0.015	0.076	0.005	0	0.033	0.015	0	0.005	0	0
35	0.01	0.007	0.021	0.041	0.022	0.006	0	0.033	0	0.038	0.005	0	0	0.005	0	0.033
36	0.005	0.007	0.015	0.006	0.005	0.017	0.015	0.033	0.005	0	0.011	0.005	0	0.03	0	0.044
37	0	0	0.005	0	0	0.006	0	0.011	0.005	0	0.011	0	0.096	0.005	0	0
38	0.005	0	0.005	0.006	0.022	0.023	0	0	0.005	0	0.005	0	0	0	0	0.011
39	0.01	0.007	0	0.006	0.005	0.017	0	0.011	0.011	0.038	0	0.13	0	0.03	0.040	0
40	0.015	0	0	0.006	0	0.011	0.008	0.022	0.048	0	0.005	0	0	0.02	0.020	0
41	0	0.013	0	0.023	0.005	0.017	0	0.011	0.043	0	0.033	0	0	0.005	0	0.022
42	0.005	0.013	0	0.041	0	0.006	0	0.022	0.011	0	0.011	0	0.021	0.01	0	0
43	0.005	0	0.005	0.099	0	0	0	0	0.021	0	0.022	0	0	0.005	0.010	0
44	0.02	0	0	0.012	0	0	0	0	0	0	0.011	0	0	0.025	0.020	0
45	0.01	0.007	0	0.006	0	0	0	0	0	0	0.005	0	0	0.005	0.010	0.011
46	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	100	75	97	86	91	88	65	46	94	39	92	100	47	100	50	45
<i>n_a</i>	36	30	26	33	29	31	21	29	35	17	30	15	20	34	27	23
<i>n_{eff}</i>	16.95	17.09	15.54		N/A	N/A	12.28	23.00	N/A	13.41	15.38	7.13	14.72	19.15	N/A	15.40
<i>a</i>	17.40	16.67	15.11	17.31	N/A	N/A	14.00	18.57	N/A	13.36	16.03	9.92	14.80	17.59	N/A	15.55
<i>H_E</i>	0.941	0.941	0.936	0.948	N/A	N/A	0.919	0.957	N/A	0.925	0.935	0.860	0.932	0.948	N/A	0.935
<i>H_O</i>	0.960	0.933	0.918	0.942	N/A	N/A	0.954	0.935	N/A	0.974	0.924	0.930	0.915	0.940	N/A	0.911
<i>F_{IS}</i>	-0.020	0.009	0.019	0.006	N/A	N/A	-0.039	0.023	N/A	-0.054	0.012	-0.082	0.019	0.008	N/A	0.026

Appendix II. Continued

Allele	Population															
	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0.011	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	0.013	0	0	0	0.021	0	0.024	0.01	0	0	0	0.003	0	0	0.01	0
8	0.020	0.01	0	0.006	0	0	0	0	0	0.015	0	0.008	0.011	0	0.01	0
9	0.020	0.045	0.032	0.028	0.021	0.03	0	0	0	0.01	0.021	0.018	0	0.013	0.01	0
10	0.073	0.04	0.026	0.006	0.052	0.04	0	0.021	0	0.025	0.028	0.016	0.022	0	0.041	0.075
11	0.035	0.055	0.058	0.072	0.125	0.06	0.122	0.021	0.031	0.061	0.035	0.018	0	0.013	0.041	0.063
12	0.098	0.055	0.074	0.056	0.167	0.09	0.122	0.052	0.063	0.051	0.077	0.067	0.065	0.115	0.092	0.087
13	0.063	0.055	0.068	0.083	0.063	0.01	0.085	0.125	0.052	0.076	0.035	0.050	0.076	0.115	0.092	0.063
14	0.080	0.14	0.068	0.044	0.167	0.12	0.049	0.052	0.042	0.056	0.056	0.059	0.065	0.064	0.092	0.1
15	0.065	0.09	0.121	0.061	0.01	0.04	0.037	0.094	0.073	0.061	0.063	0.055	0.054	0.09	0.041	0.05
16	0.060	0.065	0.053	0.044	0.052	0.07	0.024	0.052	0.052	0.03	0.063	0.054	0.033	0.051	0	0.087
17	0.068	0.055	0.047	0.028	0	0.01	0	0.031	0.042	0.035	0.085	0.049	0.076	0.077	0.092	0.037
18	0.060	0.05	0.042	0.056	0.031	0.04	0.037	0.021	0.146	0.061	0.056	0.042	0.065	0.038	0.01	0.025
19	0.030	0.025	0.079	0.028	0	0.04	0.012	0.031	0.042	0.03	0.049	0.059	0.022	0.038	0.02	0.025
20	0.023	0.025	0.021	0.011	0.01	0.02	0.085	0.042	0.021	0.025	0.007	0.036	0.043	0.064	0.051	0.05
21	0.015	0.01	0.042	0.028	0.01	0.06	0	0.01	0.01	0.045	0.007	0.020	0.022	0.013	0.071	0.075
22	0.018	0.005	0.021	0.022	0	0.01	0.037	0.01	0.021	0.01	0.021	0.018	0	0.038	0.041	0.013
23	0.010	0	0.011	0.022	0.01	0.02	0.024	0.01	0	0.03	0.007	0.010	0.011	0.026	0.02	0.013
24	0.015	0.02	0.021	0.05	0	0.03	0.012	0.01	0.031	0.035	0.035	0.018	0.011	0.038	0.01	0.013
25	0.025	0.04	0.026	0.056	0.01	0	0.037	0.042	0.021	0.02	0.042	0.054	0.087	0.013	0.01	0.037
26	0.010	0.01	0.005	0.022	0	0.01	0.012	0.01	0.01	0	0.021	0.010	0.011	0.026	0	0.013
27	0	0	0	0.006	0	0	0.049	0.021	0	0	0.007	0.016	0.011	0	0	0
28	0.005	0.01	0.005	0.028	0	0.04	0	0.01	0.063	0.051	0.028	0.052	0.033	0.013	0.031	0
29	0.013	0	0.026	0.022	0.063	0.01	0	0.01	0	0.005	0.014	0.013	0.054	0.026	0.01	0.013
30	0.008	0.025	0.011	0.011	0.031	0.02	0.024	0.01	0.021	0	0.007	0.034	0	0.013	0	0.025
31	0.008	0.005	0.021	0.011	0	0.01	0	0.031	0.01	0.01	0.021	0.015	0	0.013	0.031	0.013
32	0.015	0.02	0.011	0	0	0.01	0.049	0.031	0.042	0.03	0.021	0.034	0.022	0	0.01	0.013
33	0.015	0	0.005	0.006	0.031	0.04	0.024	0.021	0.021	0.025	0	0.011	0.011	0	0	0.013
34	0.038	0.02	0.016	0.022	0	0	0.024	0.021	0.01	0.02	0.007	0.026	0.011	0.026	0.01	0.013
35	0.015	0.005	0.032	0.006	0	0.06	0	0.021	0.021	0.02	0.014	0.015	0.065	0.026	0	0.025
36	0.018	0.025	0.011	0.078	0.021	0.02	0.037	0	0.031	0.025	0.021	0.018	0.022	0	0.041	0.013
37	0.018	0.04	0	0.033	0.021	0.01	0.037	0.073	0.01	0.035	0.028	0.016	0	0.013	0.02	0
38	0.005	0.025	0.005	0.022	0	0.01	0	0.01	0.021	0.005	0.021	0.015	0.022	0	0.01	0.025
39	0.008	0.005	0	0.006	0.031	0.02	0.024	0.021	0	0.005	0.014	0.013	0.011	0	0.02	0
40	0.015	0.005	0.021	0.006	0	0	0	0.021	0.031	0.025	0.021	0.011	0.011	0.013	0	0.013
41	0.008	0.01	0.011	0	0.052	0	0	0	0.021	0.03	0.028	0.016	0.011	0	0.031	0.013
42	0.008	0	0	0.011	0	0.05	0.012	0.031	0.031	0.035	0.014	0.016	0.033	0.013	0	0
43	0	0.005	0	0.006	0	0	0	0	0.01	0	0	0.005	0	0	0.01	0
44	0.003	0.005	0	0	0	0	0	0.01	0	0	0	0.005	0	0	0	0
45	0.003	0	0.011	0.006	0	0	0	0.01	0	0	0	0.002	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0.007	0	0	0.013	0.02	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0.014	0.003	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	199	100	95	90	48	50	41	48	48	99	71	307	46	39	49	40
<i>n_a</i>	37	32	31	35	21	29	24	34	29	32	35	40	30	27	30	28
<i>n_{eff}</i>	N/A	18.65	20.04	24.37	11.94	22.00	18.98	24.13	21.82	27.20	N/A	N/A	24.48	19.89	21.70	22.10
<i>a</i>	N/A	17.25	17.55	18.77	14.19	18.21	17.19	19.73	18.78	19.35	N/A	N/A	18.68	17.68	18.15	18.07
<i>H_E</i>	N/A	0.946	0.950	0.959	0.916	0.955	0.947	0.959	0.954	0.963	N/A	N/A	0.959	0.950	0.954	0.955
<i>H_O</i>	N/A	0.960	0.958	0.944	0.854	0.960	0.951	0.958	0.938	0.990	N/A	N/A	0.848	0.872	0.918	0.900
<i>F_{IS}</i>	N/A	-0.014	-0.008	0.015*	0.068	-0.006	-0.004	0.000	0.018*	-0.028	N/A	N/A	0.117*	0.083	0.038	0.058*

Appendix II. Continued

Allele	Population																Total
	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0.01	0	0	0.002	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0.007	0	0	0	0.006	0.006	0
7	0.005	0	0.013	0	0	0	0	0	0	0	0	0.007	0	0	0	0	0
8	0.005	0	0.013	0	0.008	0	0	0	0	0	0	0.005	0.011	0	0	0	0
9	0.015	0.02	0	0.03	0.011	0.01	0.011	0.01	0.02	0	0	0.005	0.005	0	0	0	0
10	0.035	0.03	0.075	0.01	0.076	0.01	0.011	0.01	0.1	0.02	0.007	0.022	0.021	0	0.022	0.024	0
11	0.045	0.06	0.063	0.05	0.045	0.083	0.074	0.08	0.07	0.061	0.058	0.037	0.037	0.087	0.096	0.102	0
12	0.04	0.09	0.063	0.11	0.106	0.073	0.138	0.11	0.07	0.061	0.009	0.092	0.047	0.013	0.079	0.072	0
13	0.07	0.1	0.138	0.03	0.110	0.135	0.064	0.06	0.05	0.061	0.029	0.060	0.026	0.075	0.096	0.102	0
14	0.055	0.02	0.037	0.07	0.034	0.021	0.011	0.04	0.05	0.061	0.038	0.032	0.021	0.075	0.045	0.048	0
15	0.05	0.03	0.075	0.04	0.042	0.021	0.011	0.06	0	0.051	0.027	0.040	0.032	0.163	0.039	0.036	0
16	0.055	0.05	0.087	0.06	0.042	0.01	0.043	0	0.01	0.082	0.029	0.032	0.063	0.125	0.096	0.09	0
17	0.05	0.07	0.063	0.09	0.034	0.052	0.053	0.01	0.08	0.051	0.045	0.047	0.026	0.087	0.073	0.078	0
18	0.06	0.02	0.05	0.02	0.042	0.125	0.021	0.04	0.01	0.061	0.092	0.055	0.111	0	0.096	0.084	0
19	0.015	0.05	0.025	0.01	0.019	0.021	0.064	0.05	0.01	0.01	0.049	0.057	0.021	0.013	0.017	0.018	0
20	0.06	0.07	0.025	0.05	0.042	0.052	0	0.05	0.04	0.051	0.080	0.057	0.079	0	0.039	0.042	0
21	0.055	0.03	0.025	0.02	0.038	0.073	0.021	0.04	0.04	0.041	0.074	0.032	0.053	0	0.039	0.036	0
22	0.055	0.03	0	0.03	0.038	0.01	0.043	0.03	0.03	0.061	0.083	0.055	0.011	0	0.017	0.012	0
23	0.02	0.02	0.013	0.02	0.038	0.01	0.128	0.02	0.06	0.051	0.060	0.017	0.026	0.013	0.017	0.018	0
24	0.03	0.01	0.037	0.02	0.015	0	0.021	0.03	0.05	0	0.036	0.037	0.053	0	0.039	0.042	0
25	0.02	0.04	0.037	0.07	0.011	0.031	0	0	0.03	0.061	0.018	0.025	0.005	0.013	0.011	0.012	0
26	0.015	0.01	0	0.03	0.004	0	0	0.01	0.02	0.02	0.011	0.005	0.005	0	0	0	0
27	0.01	0	0	0.02	0.004	0.01	0.032	0	0	0	0.002	0.012	0.016	0.013	0	0	0
28	0	0.04	0.025	0.01	0.011	0.01	0.043	0.01	0.01	0	0.002	0.012	0.005	0	0	0	0
29	0.03	0.06	0	0.02	0.011	0	0	0.01	0	0.01	0.007	0.005	0	0	0	0	0
30	0	0	0.037	0.03	0.019	0	0	0	0.04	0	0	0.005	0	0	0	0	0
31	0.015	0.02	0	0.02	0.027	0.01	0	0	0.02	0.041	0.011	0.012	0.011	0.025	0.011	0.012	0
32	0.03	0.01	0.013	0.02	0.015	0.01	0.011	0.01	0.02	0.01	0.022	0.002	0.016	0.013	0.006	0.006	0
33	0	0.01	0	0.02	0.015	0.042	0.074	0.02	0.01	0	0.016	0.005	0.026	0.125	0.011	0.012	0
34	0.02	0.02	0.013	0.02	0.004	0.042	0.021	0.04	0.03	0.02	0.078	0.012	0.021	0.037	0.011	0.012	0
35	0.03	0.03	0.013	0.01	0.015	0.042	0.021	0.01	0.01	0.01	0.033	0	0.021	0.013	0.006	0.006	0
36	0.025	0	0	0.01	0.019	0.01	0	0.06	0.01	0.01	0.002	0.012	0.026	0.037	0.011	0.012	0
37	0.005	0	0	0.01	0.023	0.01	0.032	0.02	0	0	0.016	0.017	0.021	0	0.034	0.03	0
38	0.005	0	0.013	0	0.011	0	0	0	0.02	0	0.025	0.017	0.016	0	0.011	0.012	0
39	0.005	0.02	0	0.01	0.008	0	0.021	0.01	0	0.01	0.007	0.012	0.016	0	0.011	0.012	0
40	0.025	0	0	0.02	0.023	0.01	0	0.01	0.03	0.041	0.007	0.015	0	0	0.017	0.018	0
41	0.02	0.01	0.037	0	0	0.01	0	0.03	0.01	0.01	0.007	0.015	0.011	0.025	0.006	0.006	0
42	0.005	0.01	0	0	0.011	0.01	0.011	0.04	0.01	0.01	0.007	0.010	0.016	0.037	0.011	0.012	0
43	0.015	0.01	0	0	0.008	0.01	0.021	0.04	0.01	0.01	0	0.022	0.037	0.013	0.006	0.006	0
44	0.005	0	0.013	0	0.019	0.01	0	0.03	0.02	0.01	0.004	0.035	0.011	0	0.011	0.012	0
45	0	0.01	0	0.02	0	0.021	0	0	0	0	0	0.015	0.026	0	0.006	0	0
46	0	0	0	0	0.004	0	0	0.01	0	0	0	0.007	0.011	0	0.006	0.006	0
47	0	0	0	0	0	0	0	0	0	0	0.002	0.007	0.011	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0.002	0.010	0.026	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0.002	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0.002	0	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0.002	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0
<i>n</i>	100	50	40	50	132	48	47	50	50	49	224	201	95	40	89	83	10297
<i>n_a</i>	35	30	25	32	37	31	25	31	32	28	36	46	39	20	33	32	55
<i>n_{eff}</i>	26.97	23.91	19.63	24.63	N/A	17.61	17.01	24.87	25.26	24.50	N/A	N/A	25.95	12.59	18.17	18.33	
<i>a</i>	19.33	18.75	17.28	19.43	N/A	17.30	16.53	19.05	19.21	18.15	N/A	N/A	20.02	13.72	16.85	16.93	
<i>H_E</i>	0.963	0.958	0.949	0.959	N/A	0.943	0.941	0.960	0.960	0.959	N/A	N/A	0.961	0.921	0.945	0.945	
<i>H_O</i>	0.950	0.920	0.900	0.960	N/A	0.896	0.915	0.960	0.980	0.939	N/A	N/A	0.905	0.875	0.989	0.988	
<i>F_{IS}</i>	0.013	0.040*	0.052	-0.001	N/A	0.051*	0.028	0.000	-0.021	0.021	N/A	N/A	0.059***	0.050	-0.047*	-0.045*	

Appendix II. Continued.

<i>Ssa419</i>	Size	Size	Population															
			Allele	ABL	DFO	1	2	3	4	5	6	7	8	9	10	11	12	13
1	179	178	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	242	241	0	0	0	0	0	0	0	0	0	0	0	0.004	0	0	0	0.01
3	250	249	0.011	0	0.053	0.037	0.063	0.023	0.044	0.013	0.025	0.008	0	0	0	0	0	
4	254	252	0.016	0	0	0.037	0.075	0.008	0.006	0.026	0.013	0.013	0	0	0	0	0	
5	258	256	0.016	0.008	0.016	0.013	0.025	0.015	0.006	0.006	0.025	0.017	0	0	0.052	0	0	
6	262	260	0.08	0.077	0.068	0.05	0.063	0.129	0.114	0.065	0.087	0.113	0.083	0.04	0.09	0.06	0.06	
7	266	264	0.128	0.092	0.116	0.1	0.113	0.189	0.127	0.182	0.212	0.097	0.183	0.26	0.067	0.01	0.01	
8	270	268	0.064	0.062	0.116	0.212	0.175	0.106	0.177	0.156	0.163	0.139	0.267	0.22	0.127	0.1	0.1	
9	274	272	0.122	0.169	0.047	0.05	0.013	0.098	0.063	0.130	0.1	0.084	0.15	0.14	0.127	0.06	0.06	
10	278	276	0.043	0.038	0.142	0.1	0.037	0.038	0.057	0.032	0.075	0.055	0.05	0.12	0.134	0.2	0.2	
11	282	280	0.085	0.062	0.053	0.063	0.05	0.038	0.057	0.039	0.1	0.046	0.017	0.02	0.06	0.08	0.08	
12	286	284	0.101	0.092	0.074	0.05	0.063	0.061	0.051	0.026	0.037	0.046	0.017	0.07	0.097	0.16	0.16	
13	290	288	0.027	0.046	0.037	0.025	0.05	0.061	0.089	0.039	0.025	0.046	0.033	0.02	0.037	0.08	0.08	
14	294	291	0.059	0.115	0.137	0.075	0.125	0.023	0.063	0.039	0.037	0.067	0.033	0.01	0.045	0.11	0.11	
15	298	295	0.085	0.069	0.053	0.025	0.05	0.045	0.057	0.045	0.075	0.071	0.017	0	0.037	0.06	0.06	
16	302	299	0.048	0.015	0.011	0.063	0.025	0.083	0.025	0.091	0.013	0.059	0.033	0.07	0.09	0.05	0.05	
17	306	303	0.016	0.023	0	0	0.013	0.03	0.013	0.058	0	0.029	0.067	0.02	0.022	0	0	
18	310	307	0.011	0.031	0.005	0.013	0	0.015	0.019	0.019	0.013	0.050	0.017	0	0.007	0.01	0.01	
19	314	311	0.011	0.008	0.016	0	0	0.015	0.025	0.019	0	0.017	0	0.01	0	0	0	
20	318	315	0.005	0	0	0	0	0.015	0	0	0	0	0	0	0	0	0	
21	322	319	0	0	0.005	0	0.037	0.008	0	0	0	0.013	0.033	0	0	0.01	0.01	
22	326	323	0.059	0.092	0.011	0.037	0	0	0.006	0	0	0.004	0	0	0	0	0	
23	330	327	0	0	0.016	0.05	0.013	0	0	0.013	0	0.004	0	0	0	0	0	
24	334	331	0	0	0	0	0	0	0	0	0	0.017	0	0	0	0	0	
25	338	336	0.016	0	0.005	0	0	0	0	0	0	0	0	0	0.007	0	0	
26	342	340	0	0	0.021	0	0.013	0	0	0	0	0	0	0	0	0	0	
27	346	344	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
28	350	348	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
29	394	392	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
30	406	404	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
31	426	424	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>n</i>			94	65	95	40	40	66	79	77	40	119	30	50	67	50	50	
<i>n_a</i>			20	16	20	17	18	19	18	18	15	22	14	12	15	14	14	
<i>n_{eff}</i>			13.42	11.88	11.84	12.06	13.00	11.27	11.54	N/A	9.58	N/A	7.56	6.48	11.76	9.50	9.50	
<i>a</i>			13.52	12.35	12.84	13.75	13.83	13.05	12.69	N/A	11.58	N/A	11.12	8.92	11.92	10.76	10.76	
<i>H_E</i>			0.925	0.916	0.916	0.917	0.923	0.911	0.913	N/A	0.896	N/A	0.868	0.846	0.915	0.895	0.895	
<i>H_O</i>			0.968	0.938	0.905	0.950	0.825	0.955	0.924	N/A	0.925	N/A	0.867	0.820	0.925	0.920	0.920	
<i>F_{IS}</i>			-0.046	-0.025	0.011	-0.036	0.107*	-0.048	-0.012	N/A	-0.033	N/A	0.001	0.031	-0.011	-0.029	-0.029	

Appendix II. Continued.

Allele	Population															
	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0.016	0	0	0	0	0	0	0	0.063	0	0.022	0.007	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0.011	0	0	0	0	0	0.024	0	0.007	0.019	0	0.013	0.01
5	0.087	0.014	0	0	0	0	0	0.06	0.042	0.024	0.043	0.007	0.019	0.011	0.007	0.005
6	0.111	0.086	0.043	0.011	0.022	0.024	0.037	0.22	0.281	0.238	0.272	0.028	0.019	0.114	0.039	0.055
7	0.111	0.057	0.109	0.159	0.152	0.107	0.185	0.22	0.073	0.095	0.033	0.148	0.269	0.045	0.178	0.145
8	0.119	0.214	0.109	0.136	0.217	0.226	0.241	0.1	0.083	0.19	0.152	0.19	0.173	0.136	0.303	0.21
9	0.103	0.200	0.13	0.102	0.13	0.19	0.204	0.12	0.208	0.143	0.25	0.183	0.135	0.159	0.171	0.14
10	0.095	0.129	0.239	0.227	0.109	0.143	0.074	0.1	0.063	0.048	0.109	0.12	0.058	0.057	0.112	0.125
11	0.087	0.057	0.13	0.08	0.022	0.024	0	0.02	0.01	0.048	0.043	0.077	0.019	0.068	0.02	0.05
12	0.111	0	0.109	0.034	0.054	0.036	0.037	0.02	0.01	0.024	0	0.063	0.038	0.034	0.026	0.06
13	0.04	0.029	0.043	0.034	0.054	0.083	0	0.04	0.031	0	0.011	0.028	0.038	0.159	0.059	0.075
14	0.016	0.029	0.043	0.057	0.087	0.083	0.074	0.08	0.073	0.071	0.033	0.049	0.135	0.057	0.026	0.045
15	0.024	0.086	0	0.057	0.054	0.048	0.056	0	0.01	0.024	0.022	0.035	0.038	0.091	0.02	0.03
16	0.048	0.043	0.022	0.034	0.033	0.012	0.037	0	0.01	0	0	0.035	0	0.023	0.02	0.01
17	0.008	0.029	0	0.034	0.033	0.012	0.037	0.02	0.021	0.071	0.011	0.014	0.019	0	0	0.01
18	0	0.029	0	0.023	0.022	0.012	0.019	0	0	0	0	0	0	0.011	0	0.005
19	0.008	0	0	0	0.011	0	0	0	0.021	0	0	0	0	0.011	0	0.01
20	0.016	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0.005
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01
22	0	0	0.022	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0	0	0.007	0	0	0	0
25	0	0	0	0	0	0	0	0	0	0	0	0	0.019	0.011	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0.011	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	63	35	23	44	46	42	27	25	48	21	46	71	26	44	76	100
<i>n_a</i>	16	13	11	14	14	13	11	11	15	12	12	16	14	16	14	18
<i>n_{eff}</i>	11.88	N/A	8.77	8.76	9.12	7.82	7.26	7.90	6.99	8.44	5.90	8.58	7.58	10.46	5.98	8.76
<i>a</i>	11.88	N/A	10.12	11.07	11.16	9.94	9.84	9.73	10.67	10.92	8.94	10.73	11.21	11.72	9.20	10.90
<i>H_E</i>	0.916	N/A	0.886	0.886	0.890	0.872	0.862	0.873	0.857	0.882	0.831	0.883	0.868	0.904	0.833	0.886
<i>H_O</i>	0.857	N/A	0.913	0.886	0.935	0.881	0.926	0.880	0.854	0.952	0.804	0.817	0.769	0.909	0.776	0.830
<i>F_{IS}</i>	0.065	N/A	-0.031	-0.001	-0.050	-0.010	-0.075	-0.008	0.003	-0.083	0.032	0.076	0.116	-0.005	0.068	0.063

Appendix II. Continued.

Allele	Population															
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002	0.011
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002	0
4	0	0	0	0	0	0	0	0	0	0.003	0	0	0	0.003	0.004	0
5	0.01	0.029	0.01	0.011	0.027	0.013	0	0.021	0.005	0	0	0.015	0.03	0.010	0.015	0.008
6	0.063	0.043	0.082	0.033	0.076	0.065	0.032	0.059	0.056	0.180	0.027	0.05	0.075	0.064	0.046	0.076
7	0.208	0.257	0.122	0.141	0.188	0.201	0.301	0.218	0.232	0.094	0.202	0.245	0.245	0.292	0.261	0.239
8	0.125	0.171	0.214	0.261	0.263	0.24	0.108	0.176	0.172	0.130	0.255	0.15	0.125	0.144	0.184	0.123
9	0.156	0.171	0.163	0.283	0.192	0.175	0.022	0.021	0.146	0.109	0.112	0.165	0.15	0.126	0.144	0.125
10	0.063	0.071	0.112	0.022	0.063	0.071	0.097	0.09	0.066	0.026	0.101	0.095	0.12	0.091	0.088	0.125
11	0.042	0.043	0.031	0.011	0.027	0.065	0.054	0.128	0.091	0.029	0.085	0.08	0.09	0.105	0.106	0.121
12	0.042	0.043	0.071	0.076	0.063	0.039	0.113	0.181	0.141	0.065	0.09	0.055	0.06	0.064	0.069	0.070
13	0.042	0.043	0.041	0.043	0.036	0.032	0.156	0.053	0.066	0.320	0.027	0.07	0.045	0.054	0.053	0.032
14	0.135	0.029	0.041	0.033	0.04	0.039	0	0.005	0.015	0.036	0.016	0.04	0.035	0.025	0.018	0.034
15	0.042	0.014	0.051	0.033	0.013	0.039	0.016	0.037	0.005	0.008	0.064	0.03	0.02	0.018	0.004	0.015
16	0	0.029	0.041	0.033	0.004	0.019	0	0	0	0	0.005	0	0.005	0.004	0.002	0.011
17	0.01	0	0.01	0.011	0.009	0	0	0	0	0	0	0	0	0	0	0
18	0	0.014	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0
19	0.01	0	0	0.011	0	0	0.032	0.011	0.005	0	0.011	0.005	0	0	0	0
20	0	0	0.01	0	0	0	0.065	0	0	0	0	0	0	0	0	0.006
21	0.021	0	0	0	0	0	0.005	0	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	0	0.029	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0.021	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0.014	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	48	35	49	46	112	77	93	94	99	192	94	100	100	396	226	264
<i>n_a</i>	16	15	14	14	13	12	12	12	12	11	13	12	12	13	15	16
<i>n_{eff}</i>	9.21	7.77	8.95	5.82	6.42	6.99	6.49	7.16	7.10	N/A	6.87	7.46	7.69	N/A	N/A	N/A
<i>a</i>	11.51	11.55	10.84	9.66	9.19	9.60	9.20	8.96	8.53	N/A	9.09	9.51	9.59	N/A	N/A	N/A
<i>H_E</i>	0.891	0.871	0.888	0.828	0.844	0.857	0.846	0.860	0.859	N/A	0.854	0.866	0.870	N/A	N/A	N/A
<i>H_O</i>	0.938	0.886	0.878	0.696	0.795	0.883	0.849	0.883	0.859	N/A	0.862	0.850	0.870	N/A	N/A	N/A
<i>F_{IS}</i>	-0.052	-0.017	0.012	0.162	0.059	-0.031	-0.004	-0.026	0.001*	N/A	-0.009	0.019	0.000	N/A	N/A	N/A

Appendix II. Continued.

<i>Ssa419</i> Allele	Population															
	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0.007	0	0	0	0	0	0	0	0	0	0	0
4	0	0.005	0	0.011	0.007	0	0	0	0	0	0	0	0.005	0	0	0
5	0	0.005	0.035	0.016	0.02	0.03	0.02	0.006	0	0.01	0	0	0	0	0.013	0
6	0.057	0.048	0.065	0.069	0.054	0.07	0.06	0.061	0.07	0.065	0.025	0.04	0.015	0.005	0.039	0.082
7	0.250	0.266	0.27	0.282	0.284	0.21	0.22	0.217	0.275	0.3	0.197	0.258	0.278	0.131	0.25	0.281
8	0.114	0.16	0.17	0.186	0.182	0.17	0.19	0.1	0.04	0.1	0.045	0.101	0.056	0.111	0.217	0.151
9	0.148	0.181	0.12	0.149	0.135	0.1	0.15	0.122	0.09	0.085	0.192	0.116	0.197	0.152	0.112	0.13
10	0.080	0.138	0.08	0.096	0.101	0.09	0.09	0.15	0.185	0.085	0.167	0.111	0.136	0.136	0.105	0.096
11	0.125	0.096	0.085	0.059	0.061	0.07	0.06	0.111	0.125	0.1	0.146	0.157	0.232	0.167	0.053	0.055
12	0.114	0.043	0.07	0.059	0.054	0.09	0.09	0.1	0.055	0.105	0.121	0.152	0.03	0.167	0.079	0.103
13	0.068	0.021	0.04	0.053	0.041	0.08	0.05	0.083	0.12	0.09	0.071	0.056	0.03	0.116	0.053	0.034
14	0.023	0.021	0.035	0	0.02	0.04	0.02	0.028	0.025	0.03	0.01	0.005	0	0	0.059	0.041
15	0.023	0.011	0.01	0.011	0.007	0.04	0.04	0.011	0.015	0.03	0.025	0.005	0.02	0.015	0.013	0.021
16	0	0	0.005	0.005	0.02	0.01	0.01	0.011	0	0	0	0	0	0	0.007	0.007
17	0	0	0.01	0	0.007	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	0	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	44	94	100	94	74	50	50	90	100	100	99	99	99	99	76	73
<i>n_a</i>	10	13	14	13	15	12	12	12	10	11	10	10	10	9	12	11
<i>n_{eff}</i>	N/A	6.33	7.20	6.41	6.70	9.03	7.89	8.09	6.49	6.88	6.96	6.65	5.26	7.35	6.90	6.87
<i>a</i>	N/A	8.45	9.80	8.89	9.80	10.36	9.82	9.22	8.48	9.31	8.19	7.89	7.26	7.53	9.25	9.01
<i>H_E</i>	N/A	0.842	0.861	0.844	0.851	0.889	0.873	0.876	0.846	0.855	0.856	0.850	0.810	0.864	0.855	0.855
<i>H_O</i>	N/A	0.809	0.870	0.894	0.892	0.880	0.860	0.878	0.770	0.870	0.889	0.808	0.919	0.859	0.921	0.795
<i>F_{IS}</i>	N/A	0.040	-0.010	-0.059	-0.049	0.011	0.015	-0.002	0.090*	-0.018	-0.038	0.049	-0.136	0.006	-0.078	0.071

Appendix II. Continued.

<i>Ssa419</i> Allele	Population															
	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0.007
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0.005	0	0	0	0	0	0	0	0.006	0	0	0	0	0	0.007	0
5	0.032	0.022	0.036	0.026	0.019	0	0.026	0.021	0.034	0.016	0	0.011	0.02	0.015	0.047	0.042
6	0.059	0.067	0.06	0.06	0.026	0.034	0.086	0.064	0.086	0	0	0	0.073	0.06	0.074	0.053
7	0.287	0.244	0.143	0.25	0.218	0.297	0.278	0.234	0.247	0.198	0.158	0.128	0.28	0.225	0.264	0.205
8	0.207	0.156	0.155	0.198	0.199	0.153	0.189	0.245	0.167	0.13	0.147	0.09	0.207	0.205	0.209	0.316
9	0.144	0.122	0.143	0.121	0.167	0.136	0.123	0.085	0.098	0.245	0.158	0.213	0.107	0.13	0.081	0.095
10	0.08	0.089	0.143	0.121	0.064	0.059	0.113	0.074	0.092	0.151	0.174	0.17	0.087	0.09	0.068	0.074
11	0.021	0.1	0.071	0.069	0.058	0.11	0.06	0.053	0.069	0.151	0.221	0.207	0.053	0.05	0.081	0.074
12	0.069	0.078	0.107	0.06	0.122	0.119	0.066	0.106	0.103	0.026	0.026	0.032	0.047	0.095	0.088	0.079
13	0.064	0.056	0.083	0.034	0.064	0.042	0.033	0.032	0.023	0.068	0.063	0.09	0.053	0.075	0.02	0.016
14	0.016	0.039	0.048	0.043	0.038	0.017	0.01	0.021	0.034	0.005	0.005	0.048	0.033	0.025	0.034	0.032
15	0.005	0.022	0	0	0.019	0.025	0.01	0.043	0.029	0.01	0.016	0	0.04	0.01	0.014	0.016
16	0.011	0.006	0.012	0.017	0.006	0	0.007	0.021	0.011	0	0.011	0	0	0.01	0.007	0
17	0	0	0	0	0	0.008	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0	0	0	0.021	0.005	0	0	0	0
23	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31																
<i>n</i>	94	90	42	58	78	59	151	47	87	96	95	94	75	100	74	95
<i>n_a</i>	13	12	11	11	12	11	12	12	13	10	11	11	11	13	14	11
<i>n_{eff}</i>	6.16	7.81	9.50	7.16	7.22	6.40	6.44	7.11	7.77	6.14	6.59	6.72	6.64	7.40	7.01	5.90
<i>a</i>	8.93	9.67	9.83	9.36	9.25	8.75	8.75	9.95	9.94	7.40	7.93	8.07	9.41	9.46	9.82	8.93
<i>H_E</i>	0.838	0.872	0.895	0.860	0.861	0.844	0.845	0.859	0.871	0.837	0.848	0.851	0.849	0.865	0.857	0.830
<i>H_O</i>	0.872	0.811	0.929	0.879	0.897	0.864	0.868	0.936	0.897	0.813	0.811	0.851	0.813	0.910	0.797	0.832
<i>F_{IS}</i>	-0.042	0.070	-0.038	-0.022	-0.042	-0.025	-0.027	-0.091	-0.029	0.029	0.045*	0.000	0.043	-0.053	0.071	-0.001

Appendix II. Continued.

<i>Ssa419</i>	Population																
	Allele	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0.011	0.079	0	0.075	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0.013	0	0.015	0	0	0	0
5	0.05	0.02	0.005	0.058	0.005	0	0	0	0	0	0.079	0	0	0.011	0	0	0.011
6	0.075	0.06	0.129	0.047	0.114	0.110	0	0.138	0.033	0.039	0.005	0.12	0.087	0.07	0.040	0.044	0.044
7	0.275	0.253	0.294	0.198	0.136	0.262	0.362	0.266	0.170	0.118	0.207	0.15	0.207	0.235	0.150	0.256	0.256
8	0.29	0.347	0.222	0.349	0.337	0.250	0.092	0.234	0.231	0.184	0.288	0.05	0.141	0.265	0.310	0.189	0.189
9	0.115	0.153	0.113	0.122	0.152	0.134	0.008	0.085	0.220	0.053	0.19	0.465	0.293	0.155	0.200	0.156	0.156
10	0.055	0.047	0.098	0.093	0.082	0.052	0.385	0.128	0.110	0.145	0.12	0.045	0.087	0.095	0.140	0.133	0.133
11	0.06	0.04	0.015	0.029	0.033	0.035	0.015	0.021	0.011	0.092	0.011	0.01	0.141	0.07	0.040	0.033	0.033
12	0.035	0.053	0.036	0.012	0.022	0.017	0.015	0	0.011	0.092	0.043	0	0	0.05	0.010	0.056	0.056
13	0.025	0.02	0.01	0	0.011	0.012	0.038	0.032	0.005	0.079	0.027	0	0.033	0.015	0.070	0.011	0.011
14	0.02	0.007	0.005	0.023	0.022	0.029	0	0.011	0.033	0	0.071	0	0	0.02	0.010	0.011	0.011
15	0	0	0	0.017	0.016	0.023	0.015	0	0.016	0.026	0.011	0.07	0	0.005	0	0.033	0.033
16	0	0	0.026	0.035	0.038	0.017	0	0.021	0.049	0	0.022	0	0	0.01	0	0	0
17	0	0	0.046	0	0	0.017	0.031	0.053	0.071	0	0	0	0	0	0	0	0
18	0	0	0	0.006	0.022	0.012	0.031	0.011	0.016	0	0.005	0	0	0	0.010	0.011	0.011
19	0	0	0	0	0	0	0.008	0	0.005	0	0	0	0	0.01	0	0.011	0.011
20	0	0	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0.044	0.044
21	0	0	0	0	0.011	0.012	0	0	0	0	0	0	0	0	0.020	0	0
22	0	0	0	0.012	0	0	0	0	0.005	0	0	0	0	0	0	0	0
23	0	0	0	0	0	0.012	0	0	0	0	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	100	75	97	86	92	86	65	47	91	38	92	100	46	100	50	45	45
<i>n_a</i>	10	10	12	13	14	16	11	11	16	12	12	9	8	12	11	14	14
<i>n_{eff}</i>	5.38	4.68	5.72	5.31	N/A	N/A	3.50	6.09	N/A	10.22	5.55	3.78	5.68	5.97	N/A	6.98	6.98
<i>a</i>	8.30	7.59	8.13	8.91	N/A	N/A	6.89	8.38	N/A	10.66	7.84	7.18	7.02	8.30	N/A	9.81	9.81
<i>H_E</i>	0.814	0.786	0.825	0.812	N/A	N/A	0.714	0.836	N/A	0.902	0.820	0.735	0.824	0.833	N/A	0.857	0.857
<i>H_O</i>	0.880	0.760	0.804	0.860	N/A	N/A	0.585	0.851	N/A	0.895	0.783	0.800	0.848	0.820	N/A	0.800	0.800
<i>F_{IS}</i>	-0.081	0.034	0.026	-0.061	N/A	N/A	0.183	-0.019	N/A	0.008	0.046*	-0.089	-0.029	0.015*	N/A	0.067	0.067

Appendix II. Continued.

Allele	Population															
	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0.072	0	0	0	0.01	0	0	0	0.002	0.011	0	0	0
5	0.010	0.025	0.016	0.006	0	0	0	0.01	0	0	0.013	0.008	0.033	0.021	0.01	0.025
6	0.056	0.085	0.147	0.033	0.085	0.08	0.023	0.031	0.096	0.071	0.052	0.066	0.022	0.052	0.03	0.05
7	0.131	0.155	0.158	0.244	0.223	0.1	0.193	0.146	0.064	0.136	0.084	0.136	0.12	0.073	0.16	0.15
8	0.207	0.21	0.274	0.267	0.245	0.39	0.341	0.365	0.319	0.348	0.377	0.347	0.424	0.354	0.26	0.225
9	0.318	0.18	0.116	0.117	0.128	0.23	0.17	0.24	0.191	0.182	0.227	0.175	0.152	0.188	0.16	0.212
10	0.088	0.11	0.095	0.094	0.181	0.04	0.08	0.104	0.138	0.111	0.097	0.094	0.098	0.083	0.13	0.075
11	0.058	0.05	0.016	0.056	0.043	0.07	0.045	0.01	0.064	0.061	0.026	0.039	0.043	0.073	0.01	0.037
12	0.033	0.03	0.021	0.028	0.053	0.03	0.08	0.042	0.043	0.03	0.039	0.061	0.076	0.01	0.03	0.037
13	0.028	0.04	0.026	0.028	0	0.02	0.045	0	0.053	0.035	0.052	0.035	0.011	0.01	0.07	0.05
14	0.015	0.015	0.021	0.033	0.032	0	0	0	0	0.015	0.013	0.008	0	0.042	0.03	0.087
15	0.018	0.02	0.026	0.017	0	0.01	0	0.01	0	0	0	0.005	0	0.021	0.04	0.05
16	0.005	0.035	0.021	0	0	0	0	0	0	0.005	0.013	0.008	0	0.01	0.03	0
17	0.010	0.005	0.021	0	0	0	0	0	0.011	0	0.006	0.002	0	0.01	0	0
18	0.013	0.025	0.005	0	0.011	0	0	0.01	0	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0.011	0	0	0	0	0	0	0	0	0
20	0	0	0	0.006	0	0.03	0.011	0	0.011	0	0	0.003	0	0	0	0
21	0	0	0.005	0	0	0	0	0	0	0.005	0	0	0	0.01	0	0
22	0	0	0	0	0	0	0	0	0.011	0	0	0.003	0.011	0.01	0	0
23	0.003	0	0	0	0	0	0	0.01	0	0	0	0.002	0	0.01	0.01	0
24	0.005	0.01	0	0	0	0	0	0	0	0	0	0.003	0	0.021	0.02	0
25	0.003	0	0.011	0	0	0	0	0.01	0	0	0	0	0	0	0.01	0
26	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0.002	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	198	100	95	90	47	50	44	48	47	99	77	297	46	48	50	40
<i>n_a</i>	17	16	19	13	9	10	10	13	11	11	12	19	11	17	15	11
<i>n_{eff}</i>	N/A	8.08	6.97	6.21	6.14	4.50	5.24	4.59	5.84	5.20	N/A	N/A	4.39	5.68	7.25	7.60
<i>a</i>	N/A	10.59	10.41	9.21	7.72	7.92	7.94	7.84	8.55	7.90	N/A	N/A	8.11	10.55	10.31	9.79
<i>H_E</i>	N/A	0.876	0.857	0.839	0.837	0.778	0.809	0.782	0.829	0.808	N/A	N/A	0.772	0.824	0.862	0.868
<i>H_O</i>	N/A	0.930	0.842	0.867	0.872	0.780	0.864	0.813	0.851	0.798	N/A	N/A	0.783	0.771	0.840	0.900
<i>F_{IS}</i>	N/A	-0.062	0.017	-0.033	-0.043	-0.003	-0.068	-0.039	-0.027	0.012	N/A	N/A	-0.014	0.065	0.026	-0.037

Appendix II. Continued.

Allele	Population																Total
	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0.031	0	0	0	0	0	0	0	0	0	0
5	0	0.02	0	0.01	0.007	0	0	0	0	0	0.014	0	0	0	0.006	0.006	0
6	0.02	0.05	0.075	0.08	0.056	0.052	0.073	0.1	0.08	0.041	0.044	0.038	0.022	0.025	0.061	0.065	0
7	0.145	0.13	0.138	0.24	0.194	0.156	0.302	0.24	0.11	0.184	0.182	0.136	0.139	0.125	0.061	0.065	0
8	0.245	0.41	0.237	0.24	0.253	0.323	0.208	0.31	0.22	0.245	0.215	0.274	0.306	0.275	0.233	0.232	0
9	0.21	0.16	0.225	0.2	0.167	0.208	0.063	0.14	0.33	0.163	0.269	0.272	0.289	0.287	0.289	0.292	0
10	0.065	0.04	0.063	0.07	0.097	0.167	0.125	0.03	0.06	0.173	0.093	0.126	0.1	0.237	0.283	0.274	0
11	0.085	0.03	0.05	0.05	0.042	0.083	0.063	0.03	0.02	0.071	0.072	0.049	0.067	0	0.033	0.036	0
12	0.05	0.01	0.025	0.02	0.063	0.01	0.063	0.03	0.05	0.02	0.061	0.026	0.017	0.037	0.011	0.012	0
13	0.045	0.04	0.013	0.02	0.014	0	0.031	0.03	0.06	0.041	0.030	0.031	0.05	0	0.006	0.006	0
14	0.04	0.03	0.05	0.03	0.031	0	0.01	0.03	0.01	0.02	0.016	0.023	0.006	0.013	0	0	0
15	0.04	0.03	0.037	0.03	0.042	0	0	0.02	0.02	0	0.002	0.021	0	0	0.006	0	0
16	0.015	0.02	0	0.01	0.014	0	0	0.01	0.03	0.01	0	0	0	0	0	0	0
17	0.01	0	0.013	0	0	0	0.031	0.01	0.01	0	0	0.005	0	0	0.011	0.012	0
18	0	0.01	0	0	0	0	0	0	0	0	0	0	0.006	0	0	0	0
19	0	0	0.013	0	0.003	0	0	0	0	0.01	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	0.01	0.025	0	0.007	0	0	0	0	0	0	0	0	0	0	0	0
23	0.01	0	0.025	0	0.003	0	0	0	0	0	0	0	0	0	0	0	0
24	0.01	0.01	0.013	0	0.003	0	0	0.02	0	0.01	0	0	0	0	0	0	0
25	0.01	0	0	0	0.003	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	100	50	40	50	144	48	48	50	50	49	214	195	90	40	90	84	10278
<i>n_a</i>	15	15	15	12	17	7	11	13	12	13	11	11	10	7	11	10	28
<i>n_{eff}</i>	7.09	4.71	7.49	6.12	N/A	4.97	6.19	5.54	5.58	6.60	N/A	N/A	4.77	4.49	4.49	4.56	
<i>a</i>	10.10	9.87	10.96	8.86	N/A	6.17	9.16	9.15	9.04	8.95	N/A	N/A	7.07	5.83	6.66	6.62	
<i>H_E</i>	0.859	0.788	0.866	0.837	N/A	0.799	0.838	0.819	0.821	0.849	N/A	N/A	0.791	0.777	0.777	0.781	
<i>H_O</i>	0.880	0.860	0.800	0.780	N/A	0.771	0.854	0.740	0.820	0.816	N/A	N/A	0.789	0.775	0.767	0.762	
<i>F_{IS}</i>	-0.025	-0.093	0.078*	0.068	N/A	0.035	-0.019	0.098	0.001	0.038	N/A	N/A	0.002	0.003	0.014	0.024	

Appendix II. Continued.

One114	Size		Population														
	Allele	ABL	DFO	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	171	171		0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	175	175		0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	179	179		0.005	0.008	0.005	0.013	0	0	0.006	0	0	0.004	0	0	0.045	0.04
4	183	183		0	0	0	0.013	0	0	0.013	0	0.013	0	0	0	0	0
5	187	187		0	0	0	0	0	0	0	0.006	0	0.008	0	0.03	0	0
6	191	191		0	0	0.053	0	0.013	0.007	0	0	0	0.049	0.017	0.03	0	0
7	195	194		0.064	0.085	0.016	0.025	0.025	0.007	0	0.218	0.037	0.012	0	0.07	0.03	0.02
8	199	198		0.021	0.038	0.089	0.025	0.063	0.059	0.083	0.051	0.1	0.057	0.183	0.15	0.068	0.02
9	203	202		0.037	0.1	0.026	0.075	0.025	0.081	0.064	0.103	0.125	0.065	0.133	0.09	0.03	0.03
10	207	206		0.149	0.108	0.047	0.05	0.025	0.088	0.115	0.083	0.05	0.110	0.1	0.07	0.076	0.04
11	211	210		0.154	0.169	0.042	0.125	0.1	0.11	0.096	0.019	0.013	0.065	0.133	0.08	0.083	0.15
12	215	214		0.069	0.023	0.089	0.025	0.025	0.081	0.103	0.026	0.05	0.089	0.117	0.21	0.144	0.12
13	219	218		0.085	0.031	0.021	0.037	0	0.037	0.058	0.019	0.063	0.045	0.15	0.07	0.106	0.12
14	223	222		0.037	0.077	0.042	0.087	0.05	0.066	0.019	0.058	0.087	0.069	0.033	0.03	0.114	0.1
15	227	226		0.064	0.054	0.079	0.1	0.05	0.074	0.032	0.051	0.087	0.073	0.017	0.04	0.076	0.04
16	231	230		0.048	0.023	0.063	0.05	0.025	0.022	0.051	0.038	0.025	0.049	0.033	0.04	0.015	0.05
17	235	234		0.032	0.008	0.063	0.1	0.025	0.081	0.083	0.013	0.025	0.057	0	0	0.038	0.03
18	239	238		0.048	0.038	0.037	0.075	0.063	0.051	0.026	0.006	0.05	0.020	0.033	0.01	0.015	0.04
19	243	242		0.043	0.046	0.026	0.05	0.05	0.051	0.051	0.058	0.013	0.045	0	0.01	0.023	0.06
20	247	246		0.053	0.054	0.111	0.063	0.113	0.029	0.019	0.026	0.025	0.012	0.017	0.02	0.015	0.02
21	251	250		0	0	0.058	0.037	0.1	0.015	0.026	0.013	0.075	0.041	0.033	0.03	0.015	0.04
22	255	254		0.011	0	0.026	0.013	0.037	0.051	0.032	0.051	0.075	0.028	0	0.01	0	0.01
23	259	258		0.011	0.023	0	0	0.025	0.007	0.032	0.026	0.037	0.033	0	0.01	0.015	0.01
24	263	262		0.016	0.038	0	0	0.013	0.015	0.019	0.019	0.013	0.012	0	0	0.03	0.01
25	267	266		0.005	0.015	0.005	0	0.013	0.007	0.019	0.013	0.025	0.012	0	0	0.008	0
26	271	270		0.016	0.008	0.032	0.013	0.037	0.022	0.026	0.058	0	0	0	0	0	0.01
27	275	274		0.005	0.008	0.011	0	0.013	0	0	0.032	0	0.008	0	0	0	0
28	279	278		0	0.008	0.021	0	0.013	0	0	0	0	0.016	0	0	0.03	0
29	283	282		0	0	0.016	0.013	0.013	0.015	0.013	0	0	0.004	0	0	0	0
30	287	286		0.011	0	0	0	0.013	0	0	0	0	0.008	0	0	0.008	0.01
31	291	290		0.011	0.038	0	0	0.013	0.007	0	0	0	0.004	0	0	0.008	0.01
32	295	294		0	0	0.005	0	0.05	0	0.006	0	0	0	0	0	0	0
33	299	298		0	0	0.016	0.013	0.013	0.015	0.006	0	0	0	0	0	0	0
34	303	302		0	0	0	0	0	0	0	0.013	0.013	0	0	0	0	0
35	307	306		0	0	0	0	0	0	0	0	0	0.004	0	0	0	0
36	311	310		0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	315	314		0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	319	318		0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	323	322		0.005	0	0	0	0	0	0	0	0	0	0	0	0	0
40	327	326		0	0	0	0	0	0	0	0	0	0	0	0	0	0.02
41	331	330		0	0	0	0	0	0	0	0	0	0	0	0	0.008	0
42	335	334		0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	339	338		0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	343	342		0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	347	346		0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	351	350		0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	355	354		0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	359	358		0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	363	362		0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	367	366		0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	371	370		0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	375	374		0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	379	378		0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	383	382		0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	387	385		0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	391	389		0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	399	397		0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>				94	65	95	40	40	68	78	78	40	123	30	50	66	50
<i>n_a</i>				24	22	25	21	27	24	24	23	21	28	13	18	23	23
<i>n_{eff}</i>				13.20	13.68	17.97	16.72	21.21	17.19	16.49	N/A	17.27	N/A	9.47	10.60	14.29	14.27
<i>a</i>				14.42	14.56	16.12	15.33	18.01	15.49	15.57	N/A	15.57	N/A	10.73	12.92	14.69	15.16
<i>H_E</i>				0.924	0.927	0.944	0.940	0.953	0.942	0.939	N/A	0.942	N/A	0.894	0.906	0.930	0.930
<i>H_O</i>				0.957	0.908	0.958	0.900	0.975	0.926	0.987	N/A	0.900	N/A	0.900	0.920	0.939	0.980
<i>F_{IS}</i>				-0.036	0.021	-0.014	0.043*	-0.024	0.016	-0.051	N/A	0.045	N/A	-0.006	-0.016	-0.010	-0.054

Appendix II. Continued.

Allele	Population															
	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.022	0	0
2	0	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0
3	0.04	0	0.043	0.057	0.109	0.06	0.093	0	0.01	0.024	0.022	0	0.018	0.022	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0.014	0	0	0.013	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01
6	0	0	0	0	0	0	0.019	0	0.031	0	0.011	0.014	0	0	0	0.005
7	0.048	0	0.087	0.011	0.011	0	0	0.04	0.083	0.048	0.054	0.049	0.036	0.033	0.059	0.035
8	0.056	0.029	0	0.011	0	0.012	0.037	0.08	0.021	0.048	0.043	0.042	0.018	0.033	0.118	0.185
9	0.056	0.100	0.065	0.034	0.076	0.012	0.074	0.08	0.052	0.071	0.076	0.077	0.071	0.056	0.105	0.135
10	0.113	0.057	0.043	0.148	0.065	0.119	0.056	0.18	0.125	0.095	0.098	0.099	0.196	0.1	0.105	0.115
11	0.073	0	0.109	0.159	0.185	0.202	0.093	0.24	0.198	0.238	0.109	0.169	0.107	0.122	0.099	0.085
12	0.065	0.057	0.196	0.227	0.076	0.119	0.13	0.04	0.125	0.024	0.12	0.077	0.089	0.144	0.072	0.1
13	0.089	0.286	0.13	0.102	0.141	0.179	0.148	0.02	0.031	0.024	0.076	0.063	0.036	0.089	0.039	0.045
14	0.113	0.257	0.065	0.045	0.098	0.083	0.093	0	0.031	0.095	0.033	0.07	0.036	0.067	0.086	0.04
15	0.089	0.057	0.022	0.034	0.033	0.048	0.056	0	0.031	0.048	0.054	0.042	0.125	0.056	0.079	0.04
16	0.024	0.014	0.087	0.034	0.043	0.048	0.037	0.06	0.031	0.048	0.087	0.042	0.054	0.056	0.092	0.025
17	0.048	0.057	0	0.023	0.022	0	0.019	0.04	0.021	0	0	0.021	0.036	0.022	0.053	0.025
18	0.016	0.014	0.043	0	0.022	0.036	0.019	0	0.01	0	0	0.014	0.036	0.033	0.013	0.01
19	0.008	0	0.043	0	0	0.012	0	0	0	0.048	0	0.007	0	0	0.02	0.005
20	0.04	0.014	0	0.023	0.011	0	0	0	0.01	0	0.011	0.007	0.018	0.011	0	0.015
21	0.008	0	0	0.011	0.022	0.012	0.019	0	0.031	0.048	0.022	0.035	0	0.011	0	0.01
22	0	0.029	0	0	0.022	0	0.037	0.02	0.031	0.048	0.033	0.042	0.054	0	0	0.015
23	0.008	0.014	0	0.023	0	0.012	0.019	0.06	0.052	0.048	0.033	0.014	0.018	0.033	0.007	0.025
24	0	0	0	0	0	0.012	0.019	0	0.01	0	0.011	0.007	0	0.033	0	0.01
25	0	0	0	0	0	0	0	0	0.01	0.024	0.076	0.007	0.036	0	0.007	0.03
26	0.008	0	0.022	0.011	0.011	0.012	0	0.08	0.042	0	0.011	0.021	0	0.011	0.007	0
27	0.016	0	0	0	0.011	0	0	0.04	0	0	0.011	0.014	0.018	0.022	0.007	0.015
28	0.016	0	0.022	0.034	0	0	0.019	0	0.01	0.024	0	0.021	0	0.011	0	0.015
29	0.008	0	0	0.011	0.022	0.012	0.019	0.02	0	0	0	0.007	0	0.011	0	0
30	0.024	0.014	0	0	0	0	0	0	0	0	0	0.007	0	0	0	0.005
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0.032	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0.022	0	0	0.012	0	0	0	0	0	0.007	0	0	0	0
34	0	0	0	0	0.011	0	0	0	0	0	0	0.007	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0.011	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.013	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	62	35	23	44	46	42	27	25	48	21	46	71	28	45	76	100
<i>n_a</i>	23	14	15	18	20	18	19	14	22	17	21	28	18	22	20	24
<i>n_{eff}</i>	16.47	N/A	12.47	8.99	11.44	9.25	15.22	9.42	12.00	12.66	15.86	15.10	12.94	15.34	13.15	11.24
<i>a</i>	15.31	N/A	13.37	12.33	13.34	11.79	15.08	12.30	14.59	15.38	14.83	15.86	14.59	15.39	12.95	13.64
<i>H_E</i>	0.939	N/A	0.920	0.889	0.913	0.892	0.934	0.894	0.917	0.921	0.937	0.934	0.923	0.935	0.924	0.911
<i>H_O</i>	0.935	N/A	1.000	0.864	0.913	0.857	0.963	0.880	0.896	0.905	0.935	0.930	0.929	0.911	0.882	0.860
<i>F_{IS}</i>	0.004	N/A	-0.089	0.029	-0.001	0.039	-0.031	0.016	0.023	0.018	0.002	0.005	-0.006	0.026	0.046	0.056

Appendix II. Continued.

Allele	Population															
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
1	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0.01	0	0.01	0.011	0.022	0.013	0	0	0.005	0	0	0	0.015	0.006	0.002	0.002
4	0.01	0	0	0	0.036	0.058	0.043	0.033	0.04	0.008	0.032	0.025	0.035	0.029	0.014	0.011
5	0.01	0	0.01	0	0.022	0.013	0.016	0.027	0.03	0.008	0.089	0.065	0.03	0.019	0.020	0.040
6	0.021	0.014	0.02	0.043	0	0	0	0	0	0	0.005	0.01	0	0.005	0.002	0.004
7	0.031	0	0.02	0.033	0.022	0.026	0	0	0	0.003	0	0	0	0.004	0	0
8	0.083	0.043	0.071	0.076	0.031	0.071	0	0.005	0.01	0.008	0.016	0.01	0.015	0.023	0.018	0.025
9	0.052	0.1	0.061	0.12	0.076	0.058	0.022	0.027	0.01	0.068	0.026	0.025	0.025	0.048	0.041	0.049
10	0.146	0.129	0.071	0.076	0.116	0.071	0.048	0.088	0.066	0.229	0.079	0.1	0.08	0.084	0.070	0.077
11	0.104	0.171	0.051	0.065	0.08	0.104	0.29	0.154	0.141	0.029	0.032	0.09	0.17	0.123	0.139	0.128
12	0.135	0.1	0.082	0.12	0.063	0.071	0.102	0.148	0.071	0.034	0.121	0.075	0.07	0.094	0.086	0.125
13	0.083	0.129	0.122	0.043	0.107	0.071	0.065	0.071	0.101	0.074	0.068	0.08	0.09	0.105	0.093	0.108
14	0.073	0.043	0.082	0.054	0.071	0.058	0.177	0.044	0.126	0.063	0.058	0.085	0.105	0.075	0.114	0.085
15	0.042	0.1	0.061	0.065	0.071	0.045	0.016	0.115	0.086	0.029	0.121	0.1	0.08	0.084	0.084	0.079
16	0.031	0.029	0.031	0.011	0.076	0.065	0	0.06	0.076	0.029	0.037	0.035	0.06	0.058	0.061	0.051
17	0.021	0.014	0.031	0.065	0.058	0.071	0.022	0.005	0.025	0.084	0.032	0.06	0.08	0.056	0.057	0.055
18	0	0.043	0.051	0.043	0.045	0.071	0.038	0.049	0.071	0.032	0.063	0.065	0.07	0.089	0.084	0.053
19	0.021	0	0.01	0.033	0.036	0	0.011	0.044	0.056	0.013	0.095	0.025	0.015	0.032	0.032	0.025
20	0.021	0.014	0.01	0.033	0.009	0.019	0.022	0.066	0.025	0.008	0.079	0.03	0.025	0.016	0.025	0.042
21	0.021	0.014	0.031	0	0.013	0.013	0	0.011	0.005	0.008	0.016	0.02	0.005	0.011	0.007	0.008
22	0.021	0	0.02	0.022	0.018	0.006	0	0.005	0.01	0.021	0.005	0.025	0.01	0.006	0.011	0.006
23	0.01	0.014	0.01	0.022	0	0.013	0	0	0	0.008	0	0.01	0	0.003	0.002	0
24	0.01	0.014	0	0	0.004	0.013	0.075	0	0.005	0.024	0.005	0.005	0.015	0.001	0.007	0.002
25	0	0	0.031	0.022	0.004	0.026	0	0.005	0	0.200	0.011	0	0	0.005	0.007	0.006
26	0	0.014	0.041	0	0.009	0	0	0.005	0.005	0.013	0	0.005	0	0.004	0	0.002
27	0.01	0.014	0.01	0	0	0	0.005	0	0.02	0.003	0	0.015	0.005	0.004	0	0.009
28	0.01	0	0.02	0.011	0	0	0.011	0.011	0.01	0.003	0.011	0.015	0	0.005	0.009	0.002
29	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0.01	0.022	0.004	0.006	0	0	0.005	0	0	0	0	0	0.002	0
31	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0.002
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0.005	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0.001	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0.009	0.002	0
43	0	0	0	0	0	0	0	0.011	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0.027	0	0	0	0	0	0	0	0	0.006
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0.011	0	0	0	0.005	0	0	0	0	0	0	0.005	0
47	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0.002
48	0	0	0.01	0	0	0	0	0.005	0	0.003	0	0	0	0	0	0
49	0	0	0	0	0	0	0.005	0	0	0.003	0	0.005	0	0	0.002	0
50	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0.004	0.013	0	0	0	0	0	0	0	0.001	0.002	0
53	0	0	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0.001	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	48	35	49	46	112	77	93	91	99	190	95	100	100	395	220	265
<i>n_a</i>	25	18	28	22	24	26	19	23	23	25	21	28	20	30	28	27
<i>n_{eff}</i>	14.29	11.45	20.14	17.59	15.63	18.27	7.14	11.87	13.03	N/A	13.94	16.49	12.43	N/A	N/A	N/A
<i>a</i>	15.31	12.87	17.43	15.94	14.84	15.94	11.40	13.22	13.58	N/A	13.83	15.48	13.29	N/A	N/A	N/A
<i>H_E</i>	0.930	0.913	0.950	0.943	0.936	0.945	0.860	0.916	0.923	N/A	0.928	0.939	0.920	N/A	N/A	N/A
<i>H_O</i>	0.958	0.943	0.939	0.978	0.920	0.948	0.871	0.934	0.929	N/A	0.884	0.950	0.860	N/A	N/A	N/A
<i>F_{IS}</i>	-0.031	-0.034	0.012	-0.038	0.018	-0.003	-0.013	-0.020	-0.007	N/A	0.048*	-0.011	0.065	N/A	N/A	N/A

Appendix II. Continued.

Allele	Population															
	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0.011	0	0.01	0	0.007	0	0	0	0	0	0	0	0	0	0	0
4	0.011	0.027	0.025	0.011	0.034	0.01	0.01	0	0	0.005	0	0	0	0	0.007	0.021
5	0.057	0.032	0.035	0.011	0	0.01	0.02	0.016	0.04	0.04	0.03	0.015	0.005	0	0.007	0.062
6	0	0	0.015	0.005	0.014	0.01	0.01	0.005	0	0.015	0	0	0	0	0	0
7	0	0.005	0.015	0.005	0.014	0.01	0	0.011	0.005	0.015	0	0.005	0.015	0	0.007	0.007
8	0.034	0.027	0.03	0.032	0.034	0.03	0.07	0.005	0.04	0.015	0.005	0.035	0	0	0.026	0.021
9	0.023	0.08	0.07	0.064	0.014	0.05	0.03	0.065	0.02	0.02	0.045	0.03	0.005	0	0.033	0.041
10	0.080	0.037	0.095	0.08	0.061	0.1	0.09	0.172	0.215	0.145	0.121	0.131	0.177	0.146	0.092	0.048
11	0.148	0.096	0.07	0.149	0.081	0.12	0.14	0.188	0.255	0.165	0.177	0.141	0.157	0.207	0.099	0.164
12	0.125	0.133	0.135	0.138	0.182	0.08	0.09	0.07	0.07	0.11	0.136	0.116	0.02	0.172	0.138	0.144
13	0.125	0.085	0.09	0.069	0.128	0.05	0.14	0.118	0.085	0.12	0.126	0.086	0.086	0.126	0.105	0.089
14	0.045	0.128	0.07	0.074	0.081	0.14	0.12	0.07	0.1	0.08	0.096	0.162	0.096	0.202	0.099	0.096
15	0.034	0.059	0.055	0.08	0.115	0.08	0.04	0.086	0.055	0.105	0.106	0.106	0.258	0.071	0.092	0.068
16	0.091	0.032	0.05	0.064	0.047	0.04	0.11	0.043	0.03	0.045	0.035	0.03	0.146	0.025	0.046	0.048
17	0.023	0.053	0.065	0.059	0.041	0.04	0.02	0.005	0.025	0.025	0.03	0.051	0.005	0.02	0.053	0.062
18	0.102	0.09	0.07	0.032	0.074	0.07	0.02	0.038	0.015	0.03	0.025	0.025	0.02	0.005	0.053	0.034
19	0.011	0.043	0.035	0.064	0.02	0.04	0.04	0.011	0	0.025	0	0.015	0	0.005	0.066	0.021
20	0.011	0.016	0.02	0.005	0.014	0.01	0.02	0.054	0.01	0.03	0.01	0	0.005	0	0.026	0.014
21	0	0.011	0.005	0.011	0.007	0.05	0	0.005	0.01	0.005	0	0	0	0	0.026	0.014
22	0.011	0.005	0.005	0.005	0	0.03	0.02	0	0.005	0	0	0.005	0	0.005	0.013	0.007
23	0	0.011	0.005	0.021	0.02	0.01	0	0	0.005	0	0.015	0	0	0	0.007	0.014
24	0	0.016	0.005	0.005	0	0.01	0	0.016	0	0	0.03	0.015	0	0.02	0	0.007
25	0.011	0	0.005	0	0.014	0	0.01	0	0	0	0	0	0	0	0	0.007
26	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0	0
27	0.023	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0
28	0.023	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0
29	0	0.005	0.005	0	0	0.01	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0.005	0	0	0	0	0	0	0	0
49	0	0.005	0	0	0	0	0	0.005	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0.01	0	0	0.005	0	0	0	0
51	0	0	0	0	0	0	0	0	0.005	0	0.01	0.015	0	0	0	0
52	0	0	0	0	0	0	0	0.011	0	0.005	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0	0	0.01	0	0	0	0	0	0	0	0	0.005	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0.01	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.014
<i>n</i>	44	94	100	94	74	50	50	93	100	100	99	99	99	99	76	73
<i>n_a</i>	20	23	26	23	20	22	18	21	19	19	16	19	14	11	20	22
<i>n_{eff}</i>	N/A	13.55	15.33	12.78	11.47	14.86	11.90	9.74	7.25	10.47	9.65	10.17	6.37	6.54	13.15	12.42
<i>a</i>	N/A	13.99	14.90	13.48	13.15	14.74	12.80	11.92	10.91	12.14	11.18	11.80	8.16	7.84	13.29	13.84
<i>H_E</i>	N/A	0.926	0.935	0.922	0.913	0.933	0.916	0.897	0.862	0.905	0.896	0.902	0.843	0.847	0.924	0.920
<i>H_O</i>	N/A	0.957	0.910	0.947	0.932	0.880	0.940	0.903	0.840	0.950	0.848	0.889	0.838	0.798	0.908	0.945
<i>F_{IS}</i>	N/A	-0.034	0.027	-0.027	-0.022	0.057	-0.027	-0.007	0.026	-0.051	0.054	0.014	0.005	0.058*	0.017	-0.028

Appendix II. Continued.

Allele	Population															
	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0.005	0	0	0	0	0	0	0	0	0	0	0	0.007	0.02	0.007	0.016
4	0.016	0.006	0.024	0	0.007	0.008	0.01	0	0.017	0	0	0	0.007	0.02	0.007	0.016
5	0.022	0.022	0.012	0.009	0.02	0.034	0.013	0.041	0.023	0.064	0.115	0.021	0.027	0.025	0.027	0.027
6	0	0.011	0	0.009	0	0.017	0.003	0	0	0	0	0.005	0.027	0.015	0.014	0.011
7	0.005	0.011	0.012	0.018	0.02	0	0.007	0.02	0.006	0.016	0.031	0.032	0	0.01	0.007	0.022
8	0.016	0.056	0.036	0.044	0.013	0.025	0.027	0.01	0.023	0.016	0.016	0.005	0.04	0.015	0.047	0.022
9	0.027	0.051	0.036	0.035	0.026	0.025	0.037	0.01	0.023	0.048	0.026	0.021	0.047	0.02	0.041	0.027
10	0.065	0.056	0.095	0.079	0.086	0.068	0.114	0.122	0.131	0.112	0.078	0.053	0.073	0.09	0.068	0.066
11	0.129	0.135	0.107	0.132	0.191	0.136	0.101	0.143	0.159	0.17	0.161	0.163	0.093	0.075	0.081	0.11
12	0.118	0.14	0.107	0.105	0.138	0.144	0.134	0.143	0.142	0.181	0.099	0.126	0.087	0.095	0.135	0.11
13	0.113	0.107	0.143	0.14	0.118	0.085	0.077	0.071	0.057	0.101	0.135	0.184	0.107	0.115	0.115	0.077
14	0.07	0.101	0.095	0.088	0.039	0.136	0.077	0.092	0.068	0.074	0.057	0.105	0.093	0.05	0.081	0.093
15	0.059	0.062	0.06	0.053	0.066	0.042	0.081	0.092	0.085	0.053	0.042	0.047	0.087	0.065	0.054	0.11
16	0.091	0.051	0.071	0.07	0.013	0.017	0.077	0.051	0.028	0.027	0.089	0.037	0.04	0.065	0.061	0.044
17	0.038	0.056	0.107	0.061	0.066	0.034	0.057	0.051	0.074	0.021	0.036	0.016	0.107	0.1	0.061	0.06
18	0.091	0.056	0.012	0.061	0.092	0.093	0.081	0.082	0.051	0.053	0.021	0.074	0.04	0.075	0.054	0.055
19	0.043	0.034	0.012	0.026	0.066	0.042	0.03	0.051	0.034	0.043	0.068	0.032	0.053	0.035	0.041	0.016
20	0.022	0.022	0.036	0.009	0.02	0.025	0.027	0.02	0.028	0.005	0.005	0.068	0.02	0.025	0.007	0.049
21	0.011	0	0.012	0.018	0.007	0.017	0.007	0	0.017	0.016	0.01	0.011	0.02	0.015	0.061	0.022
22	0.016	0	0.012	0	0.007	0.034	0.02	0	0.017	0	0.01	0	0.013	0.015	0	0
23	0.011	0	0	0.009	0	0.017	0	0	0.006	0	0	0	0.007	0.015	0.014	0.005
24	0	0.006	0	0.018	0	0	0.007	0	0.006	0	0	0	0	0	0.007	0.005
25	0.005	0	0	0	0	0	0.007	0	0	0	0	0	0	0	0	0.011
26	0.005	0.006	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0
27	0	0	0	0.009	0	0	0	0	0.006	0	0	0	0	0	0.014	0.005
28	0	0	0	0	0.007	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0.003	0	0	0	0	0	0	0	0	0.005
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0.003	0	0	0	0	0	0	0.005	0	0
48	0.011	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0	0	0
50	0	0.006	0	0.009	0	0	0	0	0	0	0	0	0	0.015	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0.012	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0.006	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	93	89	42	57	76	59	149	49	88	94	96	95	75	100	74	91
<i>n_a</i>	25	21	19	21	19	19	23	15	21	16	17	17	21	26	22	26
<i>n_{eff}</i>	13.54	12.75	13.15	13.45	10.39	12.44	13.02	11.68	11.64	9.91	11.11	9.74	14.98	15.83	14.96	15.31
<i>a</i>	14.09	13.36	13.39	13.84	12.16	13.63	13.36	12.01	13.25	11.71	12.14	11.69	14.27	15.32	14.47	15.05
<i>H_E</i>	0.926	0.922	0.924	0.926	0.904	0.920	0.923	0.914	0.914	0.899	0.910	0.897	0.933	0.937	0.933	0.935
<i>H_O</i>	0.925	0.944	0.905	0.930	0.921	0.949	0.919	0.898	0.909	0.872	0.948	0.853	0.933	0.960	0.932	0.934
<i>F_{IS}</i>	0.002	-0.024	0.021	-0.005	-0.019	-0.032	0.004	0.018	0.006	0.030	-0.042	0.050	0.000	-0.025***	0.001*	0.001

Appendix II. Continued.

Allele	Population															
	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0.007	0	0	0	0	0	0	0	0	0.016	0	0	0	0	0
3	0.025	0.027	0.088	0.046	0.011	0.024	0	0.043	0	0.079	0	0.005	0	0.015	0	0.022
4	0	0	0	0	0	0.012	0	0	0	0.013	0	0.005	0	0.02	0.010	0.022
5	0.01	0.007	0	0.006	0	0	0.008	0	0	0.013	0.011	0	0	0.02	0	0
6	0.061	0.06	0.015	0.046	0	0.012	0.246	0.021	0.022	0	0.022	0	0	0.005	0	0
7	0.02	0.04	0.057	0.023	0.043	0.012	0.032	0.064	0.027	0.013	0.027	0.025	0.053	0.04	0.010	0.033
8	0.116	0.033	0.005	0	0.043	0.024	0	0.011	0.016	0.039	0.071	0.095	0.074	0.05	0.110	0.078
9	0.04	0.073	0.041	0.034	0.130	0.119	0.024	0.053	0.143	0.079	0.049	0.025	0.043	0.12	0.140	0.1
10	0.086	0.053	0.057	0.08	0.092	0.101	0	0.106	0.143	0.118	0.103	0.01	0.074	0.12	0.090	0.133
11	0.116	0.06	0.149	0.069	0.071	0.077	0.032	0.085	0.143	0.171	0.06	0.055	0.032	0.145	0.100	0.2
12	0.081	0.147	0.098	0.08	0.060	0.083	0.016	0.106	0.060	0.079	0.049	0.1	0.138	0.125	0.130	0.044
13	0.101	0.113	0.098	0.092	0.043	0.077	0.048	0.043	0.044	0.079	0.125	0.025	0.096	0.12	0.130	0.189
14	0.081	0.1	0.057	0.063	0.043	0.071	0.087	0.053	0.077	0.079	0.06	0.305	0.064	0.085	0.120	0.056
15	0.04	0.08	0.067	0.08	0.065	0.083	0.23	0.085	0.033	0.066	0.043	0.01	0	0.025	0.060	0.011
16	0.071	0.053	0.052	0.057	0.043	0.042	0.056	0.032	0.099	0.092	0.174	0.245	0.053	0.015	0.050	0.033
17	0.045	0.027	0.046	0.086	0.049	0.071	0.087	0.064	0.104	0.053	0.065	0.065	0.234	0.025	0.010	0
18	0.04	0.073	0.041	0.052	0.076	0.048	0.079	0.106	0.016	0	0.076	0.02	0.085	0.005	0	0.011
19	0.01	0	0.01	0.057	0.054	0.071	0.032	0.043	0.033	0	0.027	0	0.011	0.02	0.010	0.056
20	0.005	0	0.01	0.034	0.022	0.030	0.016	0.011	0.005	0	0.005	0	0.021	0.01	0	0
21	0.015	0.013	0.021	0.017	0.016	0.012	0.008	0.021	0.011	0.026	0	0.005	0	0	0	0
22	0.01	0.02	0.015	0.006	0.043	0.006	0	0	0	0	0	0	0	0	0	0
23	0.005	0	0.026	0.029	0	0	0	0.011	0	0	0.005	0	0	0	0	0
24	0.005	0.007	0.046	0.023	0.033	0.006	0	0	0.011	0	0.005	0	0.011	0.005	0.010	0
25	0.015	0.007	0	0	0.005	0	0	0	0	0	0	0	0	0.01	0	0
26	0	0	0	0	0.016	0.006	0	0	0	0	0	0	0	0.005	0	0.011
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0.005	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0.016	0.006	0	0	0	0	0.005	0	0	0	0.010	0
32	0	0	0	0	0.011	0.006	0	0	0	0	0	0	0	0.005	0	0
33	0	0	0	0	0	0	0	0.032	0	0	0	0	0	0	0.010	0
34	0	0	0	0	0	0	0	0.011	0	0	0	0	0.011	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0.011	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	99	75	97	87	92	84	63	47	91	38	92	100	47	100	50	45
<i>n_a</i>	22	20	20	23	23	23	15	20	18	15	20	16	15	24	16	15
<i>n_{eff}</i>	14.19	13.68	14.14	17.58	N/A	N/A	7.26	16.37	N/A	12.39	12.07	5.62	9.50	11.12	N/A	8.98
<i>a</i>	14.00	13.76	14.15	15.38	N/A	N/A	10.67	14.90	N/A	12.39	13.19	9.20	11.66	12.71	N/A	11.28
<i>H_E</i>	0.930	0.927	0.929	0.943	N/A	N/A	0.862	0.939	N/A	0.919	0.917	0.822	0.895	0.910	N/A	0.889
<i>H_O</i>	0.960	0.920	0.948	0.943	N/A	N/A	0.810	0.915	N/A	0.974	0.891	0.850	0.894	0.860	N/A	0.911
<i>F_{IS}</i>	-0.032	0.007	-0.021	0.001	N/A	N/A	0.062	0.026	N/A	-0.060	0.028	-0.034	0.001*	0.055*	N/A	-0.026

Appendix II. Continued.

Allele	Population															
	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0.003	0	0	0	0.011	0	0	0	0	0	0	0.002	0	0.013	0	0
3	0.043	0.03	0	0.006	0.011	0.03	0.012	0	0	0.01	0.014	0.006	0.033	0.077	0.051	0.075
4	0.010	0.015	0.011	0	0.021	0	0.024	0	0	0.005	0.007	0.003	0	0.013	0.051	0.025
5	0.005	0.015	0.005	0	0	0.02	0	0	0	0	0	0.002	0	0	0	0
6	0.015	0.015	0.026	0.044	0.021	0.03	0.012	0.031	0.022	0.03	0.042	0.027	0.011	0.013	0	0.025
7	0.061	0.045	0.063	0.083	0.032	0.07	0.071	0.052	0.011	0.056	0.042	0.032	0.065	0.026	0.02	0.025
8	0.051	0.065	0.068	0.033	0.011	0.04	0.095	0.021	0.065	0.061	0.056	0.041	0.076	0.064	0.051	0.025
9	0.071	0.08	0.084	0.078	0.021	0.12	0.107	0.115	0.098	0.111	0.063	0.076	0.065	0.077	0.041	0.087
10	0.117	0.12	0.079	0.111	0.181	0.05	0.155	0.104	0.098	0.141	0.077	0.078	0.076	0.128	0.061	0.013
11	0.094	0.135	0.068	0.089	0.096	0.07	0.024	0.073	0.076	0.126	0.049	0.105	0.098	0.09	0.112	0.1
12	0.117	0.1	0.1	0.078	0.064	0.09	0.071	0.125	0.098	0.086	0.070	0.094	0.098	0.141	0.102	0.138
13	0.079	0.06	0.095	0.1	0.064	0.1	0.083	0.104	0.12	0.061	0.099	0.113	0.109	0.051	0.122	0.113
14	0.038	0.08	0.089	0.067	0.128	0.08	0.083	0.115	0.087	0.076	0.106	0.092	0.054	0.064	0.061	0.087
15	0.058	0.04	0.074	0.067	0.011	0.07	0.048	0.063	0.109	0.081	0.063	0.097	0.087	0.09	0.082	0.063
16	0.051	0.045	0.053	0.072	0.106	0.06	0.083	0.031	0.022	0.025	0.092	0.048	0.076	0.013	0.112	0.05
17	0.046	0.015	0.095	0.028	0.106	0.03	0.024	0.031	0.043	0.056	0.028	0.048	0.098	0.064	0.041	0.05
18	0.046	0.055	0.021	0.078	0.043	0.02	0.024	0.063	0.033	0.02	0.113	0.065	0.033	0.026	0.041	0.075
19	0.018	0.025	0.016	0.033	0.043	0.08	0.06	0.042	0.022	0.025	0.028	0.040	0	0.038	0.02	0.013
20	0.003	0.015	0.026	0.011	0	0.01	0.012	0.021	0.076	0.01	0.021	0.013	0.011	0	0.02	0
21	0.023	0.02	0	0.011	0.021	0.01	0.012	0.01	0.011	0	0.021	0.008	0.011	0	0	0
22	0.013	0	0.021	0	0	0.01	0	0	0	0	0	0.002	0	0.013	0	0
23	0.003	0.005	0.005	0.006	0	0.01	0	0	0	0	0	0.002	0	0	0	0
24	0	0.005	0	0	0	0	0	0	0	0	0	0.003	0	0	0	0.037
25	0.003	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0.003	0.01	0	0	0	0	0	0	0	0.02	0	0.003	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0.003	0	0	0	0	0	0	0	0.011	0	0.007	0	0	0	0.01	0
29	0.010	0	0	0	0.011	0	0	0	0	0	0	0.002	0	0	0	0
30	0.003	0	0	0	0	0	0	0	0	0	0	0.002	0	0	0	0
31	0.003	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0.003	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0.008	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	197	100	95	90	47	50	42	48	46	99	71	315	46	39	49	40
<i>n_a</i>	31	23	19	19	19	20	18	16	17	18	19	26	16	18	17	17
<i>n_{eff}</i>	N/A	14.18	14.57	14.37	11.59	16.07	13.67	13.26	13.72	12.49	N/A	N/A	14.43	14.10	14.40	14.36
<i>a</i>	N/A	14.42	13.63	13.46	13.13	14.68	13.56	13.00	13.07	12.93	N/A	N/A	13.03	13.74	13.73	13.69
<i>H_E</i>	N/A	0.929	0.931	0.930	0.914	0.938	0.927	0.925	0.927	0.920	N/A	N/A	0.931	0.929	0.931	0.930
<i>H_O</i>	N/A	0.930	0.958	0.922	1.000	0.960	0.905	0.938	0.870	0.899	N/A	N/A	0.848	0.923	0.837	0.975
<i>F_{IS}</i>	N/A	-0.001	-0.029	0.009	-0.096	-0.024	0.024**	-0.014	0.063	0.023	N/A	N/A	0.090*	0.007	0.102*	-0.049

Appendix II. Continued.

Allele	Population																Total
	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0.025	0	0	0	0	0	0.01	0	0	0	0.006	0	0	0	0
3	0.035	0.03	0.013	0.03	0.053	0.021	0	0.01	0.04	0.041	0.007	0.070	0.106	0.063	0.044	0.042	0.042
4	0.02	0	0.013	0.03	0.015	0	0	0.01	0	0.031	0	0.010	0.017	0.013	0.033	0.036	0.036
5	0.005	0	0.013	0	0	0	0.01	0	0	0	0.005	0.022	0.011	0	0.006	0.006	0.006
6	0.025	0.03	0.013	0.01	0.008	0.073	0.052	0.02	0	0.051	0	0.015	0.006	0	0	0	0
7	0.035	0.05	0.013	0.03	0.046	0.052	0.073	0.05	0.04	0.031	0.045	0.017	0.028	0	0.083	0.083	0.083
8	0.05	0.1	0.025	0.13	0.080	0.146	0.031	0.09	0.02	0.112	0.029	0.052	0.028	0.025	0.017	0.018	0.018
9	0.07	0.11	0.113	0.06	0.073	0.104	0.104	0.1	0.04	0.031	0.079	0.067	0.028	0.013	0.022	0.024	0.024
10	0.1	0.05	0.075	0.06	0.111	0.083	0.135	0.16	0.12	0.061	0.061	0.080	0.078	0.087	0.1	0.101	0.101
11	0.11	0.09	0.113	0.07	0.095	0.083	0.063	0.08	0.09	0.071	0.158	0.122	0.1	0.087	0.1	0.089	0.089
12	0.09	0.11	0.063	0.1	0.061	0.052	0.135	0.05	0.12	0.071	0.165	0.097	0.067	0.163	0.033	0.03	0.03
13	0.085	0.11	0.1	0.08	0.118	0.063	0.031	0.06	0.07	0.082	0.038	0.097	0.094	0.362	0.111	0.113	0.113
14	0.08	0.05	0.075	0.09	0.080	0.115	0.073	0.03	0.08	0.143	0.081	0.080	0.111	0.1	0.156	0.161	0.161
15	0.045	0.05	0.063	0.06	0.069	0.094	0.083	0.03	0.11	0.041	0.084	0.057	0.078	0.013	0.056	0.054	0.054
16	0.09	0.04	0.087	0.06	0.034	0.052	0.073	0.09	0.07	0.061	0.072	0.035	0.061	0.063	0.078	0.083	0.083
17	0.03	0.03	0.037	0.06	0.053	0.021	0.052	0.04	0.09	0.041	0.025	0.045	0.017	0	0.028	0.024	0.024
18	0.055	0.07	0.025	0.05	0.031	0.021	0.063	0.08	0.02	0.051	0.032	0.022	0.022	0	0.006	0.006	0.006
19	0.035	0.03	0.05	0.02	0.023	0	0.01	0.05	0	0.031	0.041	0.012	0.006	0	0.022	0.024	0.024
20	0.02	0.02	0.05	0.03	0.004	0.01	0	0.02	0.01	0.02	0.009	0.010	0.011	0.013	0.011	0.012	0.012
21	0	0	0	0	0.004	0.01	0.01	0.02	0.01	0	0.009	0.002	0.006	0	0	0	0
22	0.005	0.01	0	0	0.004	0	0	0	0.01	0	0.002	0.017	0.017	0	0.011	0.006	0.006
23	0	0	0	0	0.015	0	0	0	0.01	0	0.007	0.007	0.039	0	0	0	0
24	0.005	0	0	0	0.004	0	0	0	0.02	0.01	0.002	0.010	0.011	0	0.022	0.03	0.03
25	0.005	0.01	0.013	0.01	0.004	0	0	0.01	0	0	0.016	0.017	0.017	0	0.006	0.006	0.006
26	0	0	0	0	0.004	0	0	0	0	0.01	0.007	0.010	0.017	0	0.006	0.006	0.006
27	0	0	0	0	0	0	0	0	0	0	0.016	0.005	0.006	0	0.028	0.024	0.024
28	0	0	0	0	0	0	0	0	0	0.01	0.009	0.002	0.006	0	0.006	0.006	0.006
29	0	0	0	0	0	0	0	0	0	0	0	0	0.006	0	0.011	0.012	0.012
30	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0
31	0	0.01	0.013	0.01	0	0	0	0	0	0	0	0.005	0.006	0	0	0	0
32	0	0	0	0.01	0	0	0	0	0	0	0	0.002	0	0	0.006	0.006	0.006
33	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0.005	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0
39	0	0	0.013	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	100	50	40	50	131	48	48	50	50	49	221	201	90	40	90	84	10265
<i>n_a</i>	22	19	22	20	24	16	16	19	21	20	24	30	29	12	25	25	57
<i>n_{eff}</i>	15.19	15.18	16.72	16.18	N/A	12.95	13.10	14.02	14.14	16.00	N/A	N/A	15.67	5.50	13.24	13.16	
<i>a</i>	14.38	14.36	15.40	14.84	N/A	12.72	12.80	14.10	14.00	15.13	N/A	N/A	15.41	9.04	14.27	14.31	
<i>H_E</i>	0.934	0.934	0.940	0.938	N/A	0.923	0.924	0.929	0.929	0.938	N/A	N/A	0.936	0.818	0.924	0.924	
<i>H_O</i>	0.950	0.940	0.925	0.940	N/A	0.896	0.958	0.880	0.960	0.918	N/A	N/A	0.856	0.875	0.922	0.917	
<i>F_{IS}</i>	-0.017	-0.006	0.016	-0.002	N/A	0.030	-0.038	0.053	-0.033	0.021*	N/A	N/A	0.087***	-0.071	0.002	0.008	

Appendix II. Continued.

Omy1011 Allele	Size ABL	Size DFO	Population														
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	
1	167	172	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	183	188	0	0	0	0	0	0	0	0	0	0	0.011	0	0	0	0.01
3	187	192	0	0	0.022	0.025	0.013	0.038	0.041	0.026	0	0.044	0.1	0.03	0.067	0.049	
4	191	196	0	0	0.005	0.025	0	0	0	0.013	0	0	0	0	0.007	0	
5	195	199	0.016	0	0.108	0.037	0.113	0.023	0	0.019	0	0.011	0.033	0.02	0.09	0.196	
6	199	203	0.026	0.016	0.011	0.025	0.075	0	0	0	0.026	0	0.017	0	0.075	0.078	
7	203	207	0.063	0.087	0.081	0.05	0.087	0.076	0.047	0.096	0.051	0.055	0.1	0.02	0.06	0.039	
8	207	211	0.005	0.016	0.011	0	0.013	0	0.02	0.026	0.026	0.022	0.033	0.03	0.022	0.029	
9	211	214	0	0	0.016	0.013	0.013	0.038	0.027	0.013	0.013	0.033	0	0	0.03	0	
10	215	218	0.047	0.016	0.043	0.025	0.05	0.023	0.068	0.077	0.038	0.044	0.017	0.02	0.075	0.137	
11	219	222	0.105	0.056	0.075	0.05	0.05	0.076	0.061	0.058	0.103	0.077	0.017	0.03	0.075	0.069	
12	223	226	0.184	0.294	0.097	0.175	0.1	0.091	0.068	0.160	0.064	0.082	0.083	0.07	0.112	0.059	
13	227	230	0.021	0.103	0.032	0.1	0.037	0.03	0.068	0.026	0.051	0.033	0.05	0.05	0.022	0.049	
14	231	233	0.074	0.056	0.043	0.063	0.013	0.098	0.047	0.109	0.128	0.066	0.133	0.1	0.03	0.069	
15	235	237	0.037	0.04	0.075	0.063	0.037	0.098	0.108	0.064	0.038	0.044	0.15	0.11	0.052	0.01	
16	239	241	0.047	0.048	0.038	0.075	0.05	0.03	0.081	0.083	0.103	0.132	0.033	0.06	0.03	0.039	
17	243	245	0.037	0	0.081	0.075	0.025	0.038	0.027	0.019	0.051	0.038	0.017	0.05	0.052	0.02	
18	247	249	0.079	0.079	0.102	0.075	0.075	0.015	0.02	0.026	0.038	0.060	0.033	0.09	0.037	0	
19	251	253	0.026	0.048	0.011	0	0.063	0.053	0.014	0.045	0.013	0.055	0.017	0.08	0.022	0.01	
20	255	257	0.032	0.008	0.016	0	0	0.023	0.047	0.026	0.026	0.044	0	0.04	0.03	0.039	
21	259	261	0.037	0	0.005	0.05	0.013	0.03	0.034	0.026	0	0.038	0.033	0	0.037	0.039	
22	263	265	0.021	0.008	0.043	0.025	0.05	0.061	0.027	0.006	0.026	0.033	0.05	0.04	0.067	0.049	
23	267	269	0.021	0	0.011	0.013	0	0	0	0	0.064	0.005	0	0.02	0	0	
24	271	273	0.021	0.008	0.038	0	0.05	0.015	0	0.006	0	0.011	0.017	0.02	0.007	0.01	
25	275	277	0.021	0.024	0.005	0	0.013	0.068	0.041	0	0	0.016	0.033	0.03	0	0	
26	277	*	0	0	0	0	0	0	0	0	0.013	0	0	0	0	0	
27	279	281	0	0.016	0	0	0	0	0.007	0	0	0.011	0.017	0.04	0	0	
28	283	285	0.005	0	0	0	0.013	0	0	0	0	0	0	0.03	0	0	
29	287	289	0	0	0	0	0.025	0.015	0.027	0.019	0	0.011	0	0	0	0	
30	291	293	0	0	0	0	0	0	0.02	0.006	0	0.005	0	0	0	0	
31	295	296	0	0	0	0	0	0	0.061	0.013	0.013	0	0.017	0.01	0	0	
32	299	300	0	0	0	0	0	0	0	0	0	0	0	0.01	0	0	
33	303	304	0	0	0	0	0	0.023	0	0	0	0.005	0	0	0	0	
34	307	308	0.005	0	0	0	0	0.008	0	0	0	0	0	0	0	0	
35	311	313	0	0	0	0.013	0	0.008	0.02	0.013	0.013	0	0	0	0	0	
36	315	317	0	0	0.005	0.025	0	0	0	0	0.026	0.005	0	0	0	0	
37	319	321	0.011	0	0.027	0	0.025	0	0.007	0.019	0.013	0	0	0	0	0	
38	323	325	0.037	0.056	0	0	0	0.008	0.007	0	0.064	0	0	0	0	0	
39	327	329	0.021	0.016	0	0	0	0.015	0.007	0.006	0	0.005	0	0	0	0	
40	331	333	0	0.008	0	0	0	0	0	0	0	0	0	0	0	0	
n			95	63	93	40	40	66	74	78	39	91	30	50	67	51	
n_a			25	20	25	20	23	25	26	26	23	28	21	23	21	19	
n_{eff}			14.05	8.25	16.03	14.98	19.27	18.76	20.41	N/A	18.42	N/A	15.26	19.19	17.79	12.15	
a			15.59	12.81	15.19	15.20	16.50	16.51	17.07	N/A	16.58	N/A	15.76	16.64	15.58	13.90	
H_E			0.929	0.879	0.938	0.933	0.948	0.947	0.951	N/A	0.946	N/A	0.934	0.948	0.944	0.918	
H_O			0.905	0.937	0.871	0.950	0.975	0.970	0.973	N/A	0.974	N/A	0.867	0.960	0.910	0.922	
F_{IS}			0.025	-0.066	0.071	-0.018	-0.029*	-0.025	-0.023	N/A	-0.031	N/A	0.074	-0.013	0.036	-0.004	

Appendix II. Continued.

Allele	Population															
	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0.008	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0.04	0.100	0	0	0	0	0	0.04	0.01	0.023	0.011	0	0	0	0.007	0
4	0.024	0	0.023	0.023	0.033	0.012	0.019	0.02	0.031	0.023	0.033	0	0.016	0.011	0.026	0.01
5	0.105	0.043	0.068	0.205	0.12	0.093	0.204	0.02	0.031	0.023	0.022	0.056	0.047	0.011	0	0.025
6	0.089	0.186	0.023	0	0	0.035	0.037	0.18	0.125	0.159	0.12	0.028	0	0.033	0.02	0.005
7	0.081	0.014	0.136	0.011	0.011	0.023	0.037	0.02	0.021	0.023	0.043	0.007	0.031	0.011	0.007	0.01
8	0.008	0	0.068	0	0.087	0.093	0.111	0.1	0.104	0.023	0.076	0.056	0.047	0.033	0.013	0.02
9	0.073	0.014	0.023	0.057	0.13	0.058	0.111	0.08	0.083	0.205	0.12	0.085	0.078	0.033	0.039	0.111
10	0.073	0.129	0.091	0.136	0.033	0.07	0.037	0.06	0.135	0.068	0.043	0.134	0.141	0.033	0.105	0.121
11	0.105	0.029	0.136	0.057	0.174	0.081	0.019	0.1	0.094	0.045	0.13	0.092	0.047	0.067	0.145	0.126
12	0.056	0.043	0.068	0.136	0.163	0.174	0.093	0	0.01	0.068	0.043	0.07	0.078	0.1	0.105	0.071
13	0.024	0.043	0.023	0.068	0.033	0.105	0.074	0.02	0.031	0.023	0.033	0.049	0.047	0.111	0.086	0.076
14	0.04	0.114	0.068	0.091	0.033	0.14	0.074	0	0.042	0	0.011	0.056	0.109	0.056	0.033	0.045
15	0.073	0.043	0.091	0.08	0.054	0.047	0.111	0.04	0.042	0.023	0.022	0.092	0.063	0.167	0.066	0.051
16	0.032	0.043	0	0	0.022	0.035	0	0.04	0.031	0.068	0.087	0.014	0.078	0.078	0.026	0.086
17	0.048	0.014	0.023	0.057	0.011	0	0.019	0.04	0.073	0.068	0.065	0.092	0.063	0.033	0.013	0.025
18	0.016	0	0.045	0.034	0.011	0.023	0.019	0	0.042	0.023	0.043	0.035	0.016	0.056	0.046	0.035
19	0.016	0	0.045	0.011	0.033	0	0	0.04	0.031	0	0.033	0.042	0.031	0.067	0.033	0.035
20	0.032	0.014	0	0.023	0.033	0.012	0	0.14	0.021	0.114	0.033	0.021	0.031	0.033	0.053	0.025
21	0.016	0	0	0.011	0.022	0	0.019	0.06	0.031	0.023	0	0.021	0.016	0.022	0.026	0.035
22	0.032	0.100	0.023	0	0	0	0	0	0	0	0	0.007	0.016	0.022	0.039	0.025
23	0	0.071	0	0	0	0	0	0	0	0	0.011	0.014	0	0	0.007	0.01
24	0	0	0.045	0	0	0	0	0	0	0	0.011	0.007	0.016	0	0.013	0.015
25	0	0	0	0	0	0	0	0	0	0	0.011	0	0	0	0.026	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0.007	0.016	0.011	0.02	0.005
28	0	0	0	0	0	0	0	0	0.01	0	0	0.007	0	0.011	0.007	0.015
29	0	0	0	0	0	0	0.019	0	0	0	0	0.007	0.016	0	0.026	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.013	0.005
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0.008	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	62	35	22	44	46	43	27	25	48	22	46	71	32	45	76	99
<i>n_a</i>	22	16	17	15	17	15	16	16	20	17	21	23	21	21	26	26
<i>n_{eff}</i>	17.06	N/A	16.60	9.97	10.36	11.32	11.45	13.03	14.62	11.82	15.06	15.17	17.68	14.46	15.66	14.58
<i>a</i>	15.42	N/A	15.08	11.62	12.41	12.10	13.01	13.83	14.66	14.41	14.95	14.66	16.09	14.97	15.89	14.96
<i>H_E</i>	0.941	N/A	0.940	0.900	0.903	0.912	0.913	0.923	0.932	0.915	0.934	0.934	0.943	0.931	0.936	0.931
<i>H_O</i>	0.919	N/A	0.955	0.864	0.913	0.837	0.963	0.760	0.938	0.909	0.913	0.958	0.969	0.867	0.974	0.919
<i>F_{IS}</i>	0.024	N/A	-0.016	0.041	-0.011	0.083	-0.056	0.180**	-0.006	0.007	0.022	-0.026	-0.027	0.070	-0.040	0.013

Appendix II. Continued.

Allele	Population															
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.004
3	0	0	0	0	0.009	0	0	0	0	0	0	0	0	0	0	0
4	0.01	0.014	0	0	0.018	0	0	0.005	0.005	0	0	0	0	0	0	0
5	0.01	0.029	0.051	0.011	0	0	0	0	0.005	0.003	0	0.02	0.01	0.009	0.018	0.009
6	0	0.014	0.031	0.011	0.009	0.026	0.032	0.011	0.03	0	0.005	0.025	0.03	0.020	0.025	0.022
7	0.021	0.057	0.02	0	0.023	0.013	0.048	0.06	0.03	0.010	0.02	0.025	0.035	0.026	0.029	0.022
8	0.073	0.014	0.02	0.033	0.059	0.091	0.129	0.231	0.101	0.065	0.23	0.15	0.105	0.115	0.138	0.110
9	0.083	0.029	0.082	0.13	0.171	0.117	0.081	0.088	0.172	0.086	0.194	0.18	0.17	0.160	0.179	0.139
10	0.083	0.114	0.153	0.12	0.086	0.091	0.043	0.066	0.045	0.065	0.097	0.065	0.05	0.056	0.072	0.054
11	0.146	0.129	0.092	0.12	0.104	0.065	0.022	0.077	0.076	0.010	0.041	0.025	0.015	0.051	0.052	0.056
12	0.125	0.114	0.092	0.12	0.117	0.065	0.032	0.11	0.091	0.018	0.041	0.07	0.07	0.064	0.063	0.071
13	0.042	0.086	0.061	0.011	0.063	0.078	0.043	0.016	0.045	0.021	0.066	0.065	0.075	0.077	0.075	0.080
14	0.042	0.043	0.092	0.098	0.068	0.065	0.075	0.027	0.051	0.045	0.036	0.045	0.03	0.031	0.025	0.037
15	0.094	0.071	0.112	0.076	0.036	0.039	0.011	0.066	0.04	0.092	0.046	0.035	0.03	0.028	0.016	0.035
16	0.063	0.014	0.041	0.076	0.045	0.058	0.005	0.027	0.061	0.034	0.015	0.055	0.06	0.049	0.041	0.052
17	0.083	0.086	0.02	0.011	0.041	0.052	0.118	0.038	0.076	0.154	0.026	0.055	0.055	0.046	0.048	0.054
18	0.021	0	0.01	0.022	0.036	0.045	0.043	0.049	0.035	0.018	0.041	0.03	0.055	0.041	0.032	0.052
19	0.052	0.071	0.061	0.043	0.054	0.071	0	0.027	0.04	0.042	0.077	0.045	0.08	0.064	0.054	0.035
20	0.01	0.014	0.01	0.054	0.009	0.026	0.151	0.049	0.035	0.060	0.036	0.04	0.03	0.032	0.045	0.056
21	0.021	0.029	0.02	0.043	0.014	0.013	0.011	0.033	0.03	0.013	0	0.025	0.05	0.036	0.036	0.035
22	0	0.029	0.02	0	0.023	0.013	0.091	0.011	0.02	0.144	0.02	0.015	0	0.026	0.018	0.019
23	0.01	0	0.01	0	0.005	0.006	0	0	0.005	0.047	0.005	0.015	0.04	0.052	0.020	0.024
24	0	0.014	0	0.022	0	0.013	0	0	0	0	0	0.01	0.005	0.003	0.007	0.009
25	0	0	0	0	0	0	0.022	0	0	0	0	0.005	0.005	0.008	0	0.004
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0.01	0	0	0	0	0.006	0	0	0.005	0.003	0	0	0	0.001	0.002	0.009
28	0	0.014	0	0	0	0.006	0	0.005	0	0.024	0	0	0	0.003	0.002	0
29	0	0	0	0	0	0.006	0.038	0	0	0.029	0.005	0	0	0.001	0	0.004
30	0	0	0	0	0.009	0.013	0.005	0	0	0.010	0	0	0	0	0	0.006
31	0	0	0	0	0	0.013	0	0	0	0.005	0	0	0	0	0.002	0.002
32	0	0.014	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0.005	0	0	0	0	0	0	0	0	0.003	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	48	35	49	46	111	77	93	91	99	191	98	100	100	391	221	269
<i>n_a</i>	19	21	19	17	22	25	19	19	21	23	18	21	20	25	23	26
<i>n_{eff}</i>	13.49	15.58	13.58	12.46	12.50	16.62	12.27	10.35	13.49	N/A	8.55	12.35	13.57	N/A	N/A	N/A
<i>a</i>	13.57	15.12	13.80	12.69	13.74	15.34	13.16	13.01	14.22	N/A	11.89	14.29	14.16	N/A	N/A	N/A
<i>H_E</i>	0.926	0.936	0.926	0.920	0.920	0.940	0.919	0.903	0.926	N/A	0.883	0.919	0.926	N/A	N/A	N/A
<i>H_O</i>	0.917	0.971	0.959	0.957	0.919	0.922	0.914	0.901	0.929	N/A	0.867	0.910	0.930	N/A	N/A	N/A
<i>F_{IS}</i>	0.010	-0.039	-0.036	-0.040	0.001	0.019	0.005	0.003	-0.004	N/A	0.018	0.010	-0.004	N/A	N/A	N/A

Appendix II. Continued.

Allele	Population															
	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0.007	0
5	0	0.011	0.03	0.011	0.007	0	0.01	0	0	0.015	0	0.005	0	0	0.007	0.014
6	0.011	0.005	0.025	0.027	0.007	0.02	0.02	0	0.015	0.005	0.005	0.015	0	0.015	0.007	0
7	0.045	0.048	0.071	0.064	0.047	0.08	0.08	0.033	0.03	0.03	0.045	0.081	0.026	0.025	0.041	0.055
8	0.114	0.074	0.086	0.154	0.128	0.12	0.12	0.109	0.105	0.125	0.101	0.106	0.026	0.025	0.151	0.075
9	0.273	0.186	0.141	0.154	0.25	0.15	0.22	0.228	0.115	0.24	0.172	0.126	0.214	0.02	0.185	0.233
10	0.034	0.074	0.051	0.053	0.074	0.03	0.03	0.027	0.04	0.015	0.03	0.035	0	0.035	0.055	0.082
11	0.068	0.074	0.076	0.037	0.068	0.07	0.04	0.06	0.015	0.025	0.01	0.056	0.015	0.04	0.068	0.021
12	0.011	0.027	0.066	0.074	0.034	0.04	0.09	0.043	0.02	0.005	0.015	0.01	0.036	0.086	0.041	0.041
13	0.114	0.096	0.051	0.048	0.027	0.04	0.02	0.043	0.04	0.08	0.02	0.005	0.01	0.111	0.055	0.075
14	0.011	0.043	0.056	0.053	0.054	0.06	0.02	0.027	0.015	0.055	0.03	0.04	0	0.02	0.068	0.034
15	0.023	0.069	0.02	0.037	0.041	0.04	0.03	0.06	0.055	0.045	0.081	0.02	0	0.01	0.041	0.041
16	0.023	0.059	0.051	0.027	0.027	0.06	0.02	0.049	0.07	0.035	0.01	0.066	0.071	0.051	0.034	0.034
17	0.148	0.037	0.056	0.064	0.02	0.05	0.08	0.098	0.12	0.125	0.162	0.172	0.107	0.227	0.027	0.034
18	0	0.043	0.045	0.043	0.027	0.03	0.05	0.082	0.11	0.065	0.076	0.071	0.041	0.101	0.048	0.055
19	0.011	0.043	0.056	0.048	0.041	0.07	0.08	0.022	0.07	0.025	0.111	0.076	0.051	0.086	0.027	0.062
20	0.023	0.021	0.035	0.027	0.041	0.03	0.03	0.043	0.055	0.03	0.091	0.076	0.306	0.076	0.034	0.041
21	0.011	0.032	0.025	0.011	0.034	0.07	0.01	0.027	0.045	0.05	0.015	0.015	0.015	0.04	0.021	0.021
22	0.034	0.021	0.005	0.027	0.007	0	0.03	0.005	0	0	0	0.005	0.031	0	0.027	0.027
23	0.023	0.005	0.015	0.011	0.02	0	0.01	0	0	0	0	0.005	0.036	0	0.007	0.027
24	0	0.021	0.015	0.016	0.034	0.04	0	0.005	0.005	0.015	0	0	0	0	0.027	0.014
25	0.011	0.005	0.005	0.005	0.014	0	0.01	0.005	0.01	0	0	0	0	0	0.007	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0.011	0	0.01	0.005	0	0	0	0.005	0.01	0	0	0.015	0	0	0	0
28	0	0.005	0.005	0	0	0	0	0.011	0.025	0.01	0.015	0	0.015	0	0	0
29	0	0	0	0.005	0	0	0	0.011	0.02	0.005	0.005	0	0	0	0	0.007
30	0	0	0.005	0	0	0	0	0	0.01	0	0	0	0	0.015	0.007	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0.007	0
32	0	0	0	0	0	0	0	0.005	0	0	0	0	0	0.005	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
n	44	94	99	94	74	50	50	92	100	100	99	99	98	99	73	73
n_a	19	22	24	23	21	17	20	22	22	20	19	20	15	19	24	21
n_{eff}	N/A	13.13	16.35	13.39	10.02	14.73	11.02	10.58	14.18	9.29	10.06	11.54	6.18	10.00	12.59	11.46
a	N/A	14.34	15.45	14.65	13.95	14.23	13.70	13.47	14.34	12.52	11.75	12.65	10.35	12.67	14.77	14.50
H_E	N/A	0.924	0.939	0.925	0.900	0.932	0.909	0.905	0.929	0.892	0.901	0.913	0.838	0.900	0.921	0.913
H_O	N/A	0.904	0.970	0.957	0.865	0.940	0.960	0.924	0.930	0.900	0.869	0.889	0.816	0.909	0.918	0.932
F_{IS}	N/A	0.021	-0.033	-0.035	0.039	-0.009	-0.056	-0.021	-0.001	-0.009***	0.036	0.027	0.026	-0.010	0.003	-0.021

Appendix II. Continued.

Allele	Population															
	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0.011	0.006	0	0.009	0.013	0	0.02	0.021	0	0.016	0.021	0.011	0	0.01	0	0.005
6	0.005	0.044	0.024	0	0.019	0.017	0.017	0.01	0.04	0	0	0.011	0.027	0.01	0	0.011
7	0.037	0.05	0.06	0.026	0.013	0.034	0.033	0.031	0.011	0.043	0.005	0.027	0.047	0.045	0.041	0.005
8	0.106	0.111	0.143	0.138	0.147	0.127	0.119	0.073	0.148	0.027	0.078	0.09	0.087	0.1	0.122	0.079
9	0.165	0.206	0.143	0.198	0.231	0.119	0.212	0.104	0.142	0.314	0.365	0.298	0.14	0.095	0.149	0.184
10	0.064	0.039	0.024	0.034	0.09	0.034	0.046	0.073	0.057	0.09	0.161	0.085	0.06	0.035	0.081	0.053
11	0.053	0.05	0.071	0.052	0.071	0.085	0.063	0.063	0.057	0.016	0.021	0.011	0.073	0.075	0.041	0.079
12	0.053	0.056	0.071	0.052	0.013	0.034	0.056	0.073	0.034	0.037	0.021	0.021	0.053	0.03	0.101	0.037
13	0.048	0.067	0.071	0.043	0.038	0.051	0.036	0.063	0.045	0.037	0.036	0.037	0.04	0.065	0.108	0.068
14	0.059	0.017	0.012	0.026	0.064	0.034	0.036	0.104	0.04	0.037	0.052	0.043	0.027	0.06	0.068	0.047
15	0.027	0.028	0.036	0.043	0.026	0.042	0.04	0.021	0.045	0.032	0.031	0	0.04	0.035	0.027	0.063
16	0.032	0.044	0.036	0.052	0.064	0.059	0.043	0.063	0.051	0.069	0.031	0.085	0.047	0.1	0.034	0.042
17	0.074	0.028	0.06	0.078	0.038	0.034	0.043	0.052	0.074	0.085	0.016	0.059	0.04	0.055	0.054	0.063
18	0.08	0.033	0.048	0.034	0.026	0.093	0.036	0.031	0.057	0.032	0.036	0.027	0.087	0.065	0.014	0.047
19	0.053	0.056	0.095	0.06	0.019	0.068	0.043	0.052	0.085	0.037	0.021	0.059	0.047	0.075	0.041	0.021
20	0.048	0.056	0.048	0.043	0.045	0.042	0.026	0.021	0.045	0.074	0.026	0.048	0.06	0.02	0.054	0.053
21	0.037	0.039	0.012	0.026	0.019	0.017	0.046	0.042	0.017	0.027	0.016	0.043	0.053	0.04	0.014	0.047
22	0.011	0.011	0	0.009	0.026	0.034	0.033	0.031	0.011	0.005	0.005	0.011	0.027	0.01	0.014	0.032
23	0.011	0.028	0.012	0.026	0.013	0.034	0.023	0.052	0.011	0	0.005	0.011	0.007	0.025	0.02	0.032
24	0.011	0.017	0.012	0.026	0.019	0.008	0.01	0	0.017	0	0.005	0	0.013	0.015	0.014	0.026
25	0	0.006	0.012	0.017	0	0.008	0.007	0	0.006	0.005	0.036	0.016	0.013	0.015	0.007	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0.011	0.011	0	0	0.006	0	0	0.01	0	0	0	0	0.013	0	0	0
28	0	0	0	0	0	0.017	0.007	0	0	0.016	0	0.011	0	0.005	0	0
29	0.005	0	0.012	0	0	0	0	0.01	0.006	0	0	0	0	0.005	0	0
30	0	0	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0.005
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0
33	0	0	0	0.009	0	0	0.003	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0.008	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
n	94	90	42	58	78	59	151	48	88	94	96	94	75	100	74	95
n_a	22	22	20	21	21	22	23	21	21	19	21	20	21	25	19	21
n_{eff}	14.05	12.59	14.23	12.51	10.04	16.24	12.06	18.54	13.64	7.62	5.80	8.09	16.48	16.81	12.89	13.72
a	14.50	14.75	14.44	14.75	13.52	15.50	14.77	15.81	14.26	12.71	11.81	12.81	15.36	15.41	13.50	14.56
H_E	0.929	0.921	0.930	0.920	0.900	0.938	0.917	0.946	0.927	0.869	0.827	0.876	0.939	0.941	0.922	0.927
H_O	0.989	0.922	1.000	0.948	0.910	0.881	0.901	1.000	0.943	0.894	0.823	0.926	0.920	0.940	0.946	0.937
F_{IS}	-0.066	-0.002	-0.077	-0.031	-0.011	0.061	0.018	-0.058	-0.018	-0.029	0.005	-0.056	0.021	0.001	-0.026	-0.011

Appendix II. Continued.

Allele	Population															
	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0.014	0.057	0.012	0.011	0	0.023	0.054	0.011	0.09	0.011	0	0	0.005	0	0.011
5	0.015	0.034	0.253	0.134	0.108	0.098	0.016	0.076	0.112	0	0.087	0	0.033	0.045	0.040	0.056
6	0.015	0.014	0.067	0.041	0.118	0.069	0.023	0.076	0.101	0.115	0.043	0	0.011	0.015	0.030	0.011
7	0.03	0.007	0.01	0.041	0.081	0.086	0.008	0.011	0.032	0.026	0.049	0	0.065	0.015	0.040	0.033
8	0.051	0.061	0.015	0.041	0.011	0.052	0	0.043	0.016	0.167	0.033	0.015	0.261	0.04	0.070	0.078
9	0.071	0.149	0.021	0.023	0.011	0.023	0.063	0.033	0.037	0.038	0.065	0.06	0.011	0.071	0.050	0.033
10	0.126	0.169	0.093	0.047	0.032	0.046	0.227	0.109	0.074	0.051	0.179	0.27	0.13	0.091	0.050	0.078
11	0.172	0.149	0.057	0.035	0.091	0.103	0.148	0.098	0.053	0.013	0.114	0.25	0.141	0.136	0.170	0.111
12	0.076	0.074	0.103	0.076	0.145	0.121	0.242	0.065	0.043	0	0.13	0.01	0	0.096	0.100	0.111
13	0.066	0.027	0.01	0.081	0.102	0.069	0.109	0.054	0.027	0.128	0.082	0.015	0.033	0.086	0.130	0.022
14	0.091	0.047	0.046	0.099	0.140	0.075	0.102	0.098	0.059	0.051	0.06	0.19	0.098	0.086	0.040	0.111
15	0.045	0.034	0.057	0.076	0.022	0.046	0.008	0.098	0.117	0.218	0.022	0.06	0.043	0.076	0.060	0.111
16	0.015	0.074	0.072	0.128	0.027	0.086	0.008	0.065	0.122	0.013	0.033	0.02	0.054	0.045	0.100	0.156
17	0.045	0.047	0.046	0.058	0.032	0.069	0	0.054	0.096	0.026	0	0.09	0.065	0.045	0.070	0.044
18	0.015	0.041	0.052	0.023	0.032	0.034	0.016	0.054	0.090	0	0.027	0.005	0	0.056	0.020	0.011
19	0.025	0.014	0	0.012	0	0.017	0	0.011	0.011	0.013	0.016	0	0.043	0.02	0	0.022
20	0.045	0.02	0.005	0.017	0.038	0	0	0	0	0.038	0.011	0	0.011	0.015	0	0
21	0.051	0	0.021	0	0	0.006	0.008	0	0	0	0.011	0	0	0.005	0	0
22	0.025	0.007	0.005	0.012	0	0	0	0	0	0.013	0.011	0	0	0.02	0.020	0
23	0.005	0.007	0.005	0	0	0	0	0	0	0	0.011	0.01	0	0.03	0.010	0
24	0	0	0	0.012	0	0	0	0	0	0	0.005	0	0	0	0	0
25	0.005	0.007	0.005	0.035	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0.007	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	99	74	97	86	93	87	64	46	94	39	92	100	46	99	50	45
<i>n_a</i>	21	21	20	20	16	16	14	16	16	15	20	13	14	20	16	16
<i>n_{eff}</i>	12.71	10.91	9.42	13.98	N/A	N/A	6.52	15.28	N/A	8.94	11.39	5.44	8.14	14.24	N/A	
<i>a</i>	13.91	13.00	12.58	14.17	N/A	N/A	8.91	13.51	N/A	11.29	13.04	7.96	10.88	13.97	N/A	12.33
<i>H_E</i>	0.921	0.908	0.894	0.928	N/A	N/A	0.847	0.935	N/A	0.888	0.912	0.816	0.877	0.930	N/A	0.916
<i>H_O</i>	0.909	0.892	0.876	0.930	N/A	N/A	0.875	0.935	N/A	0.897	0.913	0.890	0.870	0.909	N/A	0.889
<i>F_{IS}</i>	0.013	0.018	0.020	-0.002*	N/A	N/A	-0.034	0.000	N/A	-0.011	-0.001	-0.091	0.009	0.022	N/A	0.030

Appendix II. Continued.

Allele	Population															
	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0
2	0	0	0	0	0	0	0	0	0	0	0	0.002	0	0	0	0
3	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0.015	0.025	0.011	0.046	0	0	0	0	0.032	0.01	0	0.028	0.011	0	0.02	0.013
5	0.071	0.06	0.047	0.029	0.083	0.082	0.049	0.043	0.085	0.066	0.049	0.062	0.067	0.026	0.051	0.09
6	0.018	0.03	0.032	0.063	0	0.112	0.122	0.065	0.064	0.081	0.070	0.047	0.089	0.026	0.02	0.051
7	0.043	0.015	0.037	0.011	0.042	0.051	0.037	0.033	0.021	0.025	0.049	0.021	0.011	0.038	0	0.09
8	0.068	0.045	0.053	0.069	0.021	0.031	0.061	0.033	0.053	0.056	0.028	0.062	0.056	0.026	0.051	0.026
9	0.043	0.1	0.058	0.075	0.063	0.031	0.012	0.054	0.085	0.071	0.035	0.059	0.056	0.103	0.102	0.013
10	0.061	0.11	0.111	0.109	0.073	0.102	0.073	0.087	0.074	0.096	0.106	0.092	0.089	0.167	0.163	0.231
11	0.121	0.085	0.105	0.121	0.188	0.092	0.268	0.13	0.17	0.182	0.120	0.127	0.067	0.167	0.163	0.115
12	0.096	0.085	0.037	0.092	0.135	0.194	0.11	0.141	0.085	0.096	0.169	0.125	0.089	0.141	0.112	0.077
13	0.076	0.08	0.111	0.086	0.063	0.102	0.012	0.109	0.106	0.081	0.134	0.112	0.133	0.077	0.051	0.103
14	0.098	0.1	0.137	0.121	0.135	0.031	0.037	0.152	0.16	0.106	0.127	0.155	0.2	0.077	0.133	0.115
15	0.096	0.095	0.095	0.04	0.031	0.061	0.122	0.054	0.043	0.091	0.042	0.059	0.033	0.09	0.031	0
16	0.048	0.02	0.032	0.052	0.063	0.041	0	0.011	0	0.02	0.014	0.021	0.011	0.038	0.031	0
17	0.035	0.06	0.011	0.011	0.083	0.051	0.037	0.011	0	0.005	0.014	0.005	0	0.013	0.01	0.013
18	0.030	0.03	0.032	0.04	0	0	0.037	0	0.021	0.01	0.014	0.005	0.056	0.013	0.031	0
19	0.023	0.005	0.005	0.029	0.01	0.01	0.024	0.033	0	0	0.007	0.011	0.011	0	0.01	0.013
20	0.013	0.015	0.032	0.006	0.01	0	0	0.022	0	0	0.007	0.003	0	0	0	0
21	0	0.005	0	0	0	0	0	0.022	0	0	0.007	0.003	0	0	0	0.013
22	0.018	0.01	0.005	0	0	0	0	0	0	0.005	0	0.002	0.011	0	0.01	0.026
23	0.023	0.015	0.042	0	0	0	0	0	0	0	0	0	0	0	0	0.013
24	0.005	0.005	0	0	0	0	0	0	0	0	0	0	0.011	0	0	0
25	0	0	0.011	0	0	0	0	0	0	0	0	0.002	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0.007	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	198	100	95	87	48	49	41	46	47	99	71	316	45	39	49	39
<i>n_a</i>	20	22	20	17	14	15	14	16	13	16	18	21	17	14	17	16
<i>n_{eff}</i>	N/A	14.23	13.23	13.17	10.34	11.05	8.28	11.63	10.64	10.73	N/A	N/A	10.94	10.04	10.36	9.44
<i>a</i>	N/A	13.89	13.66	12.97	11.37	12.10	11.25	12.52	11.32	11.49	N/A	N/A	12.35	11.28	12.08	11.56
<i>H_E</i>	N/A	0.930	0.924	0.924	0.903	0.910	0.879	0.914	0.906	0.907	N/A	N/A	0.909	0.900	0.903	0.894
<i>H_O</i>	N/A	0.930	0.937	0.920	0.896	0.918	0.854	0.978	0.979	0.929	N/A	N/A	0.889	0.897	0.918	0.923
<i>F_{IS}</i>	N/A	0.000	-0.014	0.005	0.008	-0.010	0.029	-0.071	-0.081	-0.025	N/A	N/A	0.022	0.003	-0.017	-0.033

Appendix II. Continued.

Allele	Population																Total
	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0.004	0	0	0	0.02	0	0	0	0	0	0	0	0
4	0.02	0.02	0.013	0	0.029	0	0	0.01	0.02	0.041	0.003	0	0	0	0	0	0
5	0.07	0.05	0.038	0.04	0.033	0.042	0.076	0.06	0.05	0.031	0.103	0.007	0.023	0	0.012	0.013	0
6	0.025	0.03	0.038	0.03	0.036	0.104	0.011	0.02	0.01	0.061	0.032	0.015	0.023	0	0.006	0.006	0
7	0.04	0.03	0.013	0.01	0.018	0.125	0.033	0.06	0.04	0	0.050	0.039	0	0.013	0.035	0.038	0
8	0.035	0.04	0.026	0.06	0.076	0	0.054	0.06	0.07	0.041	0.029	0.099	0.063	0	0.029	0.025	0
9	0.045	0.15	0.179	0.11	0.083	0.073	0.174	0.12	0.06	0.092	0.061	0.081	0.125	0.013	0.035	0.032	0
10	0.17	0.1	0.154	0.17	0.156	0.125	0.141	0.07	0.06	0.153	0.116	0.153	0.131	0	0.124	0.12	0
11	0.145	0.14	0.192	0.13	0.145	0.198	0.217	0.18	0.16	0.122	0.201	0.172	0.216	0.138	0.188	0.196	0
12	0.13	0.1	0.051	0.09	0.105	0.156	0.043	0.11	0.13	0.061	0.111	0.170	0.148	0.287	0.165	0.165	0
13	0.075	0.1	0.038	0.12	0.058	0.052	0.076	0.12	0.17	0.122	0.087	0.103	0.074	0.163	0.153	0.152	0
14	0.08	0.11	0.09	0.08	0.130	0.083	0.141	0.09	0.09	0.092	0.056	0.059	0.057	0.075	0.106	0.101	0
15	0.07	0.02	0.077	0.07	0.051	0.021	0.011	0.03	0.05	0.051	0.074	0.042	0.057	0.175	0.029	0.032	0
16	0.015	0.04	0.038	0.04	0.040	0.01	0	0	0.02	0.041	0.013	0.022	0.023	0.075	0.029	0.032	0
17	0.015	0.02	0	0.03	0.004	0	0	0.01	0.01	0.031	0.021	0.010	0.028	0.025	0.029	0.032	0
18	0.02	0.02	0.026	0	0.014	0	0	0.02	0.01	0	0	0.012	0.023	0.025	0.035	0.032	0
19	0.015	0.02	0	0	0.011	0	0.011	0.02	0	0	0.003	0.005	0.011	0.013	0.012	0.013	0
20	0	0	0.013	0	0	0	0	0.01	0	0	0.032	0	0	0	0	0	0
21	0.01	0.01	0	0	0	0	0.011	0	0	0.01	0.003	0.002	0	0	0	0	0
22	0.005	0	0.013	0	0	0.01	0	0	0	0.01	0.005	0	0	0	0	0	0
23	0.005	0	0	0	0.007	0	0	0	0	0.01	0	0.002	0	0	0	0	0
24	0.01	0	0	0.02	0	0	0	0	0	0	0	0	0	0	0.012	0.013	0
25	0	0	0	0	0	0	0	0	0.01	0.031	0	0.005	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	100	50	39	50	138	48	46	50	50	49	189	203	88	40	85	79	10197
<i>n_a</i>	20	17	16	14	18	12	13	17	19	17	18	18	14	11	16	16	40
<i>n_{eff}</i>	10.95	11.81	9.44	10.90	N/A	8.79	7.94	11.05	11.00	12.64	N/A	N/A	8.70	6.21	8.71	8.67	
<i>a</i>	12.71	12.78	11.98	11.58	N/A	9.80	9.74	12.20	12.78	13.11	N/A	N/A	10.75	8.40	10.95	11.02	
<i>H_E</i>	0.909	0.915	0.894	0.908	N/A	0.886	0.874	0.909	0.909	0.921	N/A	N/A	0.885	0.839	0.885	0.885	
<i>H_O</i>	0.910	0.920	0.923	0.980	N/A	0.833	0.848	0.860	0.880	0.918	N/A	N/A	0.864	0.875	0.859	0.848	
<i>F_{IS}</i>	-0.001	-0.005	-0.033	-0.080	N/A	0.060	0.030	0.055	0.032	0.003	N/A	N/A	0.024	-0.044	0.030	0.042	

Appendix II. Continued.

One101 Allele	Size ABL	Size DFO	Population															
			1	2	3	4	5	6	7	8	9	10	11	12	13	14		
1	118	113	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	122	117	0	0	0	0	0	0	0	0	0	0	0	0.004	0	0	0	0
3	130	125	0	0	0	0	0	0	0	0	0	0	0	0.004	0	0.01	0	0
4	134	129	0.484	0.308	0.489	0.463	0.588	0.301	0.43	0.378	0.35	0.387	0.367	0.45	0.321	0.373		
5	138	133	0.075	0.115	0.011	0.037	0.063	0.059	0.057	0.083	0.138	0.073	0.1	0.06	0.067	0.039		
6	142	137	0.011	0	0.026	0.025	0.037	0.088	0.07	0.026	0.05	0.044	0.05	0.04	0.015	0		
7	146	141	0.113	0.215	0.1	0.075	0.063	0.066	0.089	0.019	0.025	0.060	0	0	0.097	0.108		
8	150	146	0	0.008	0	0.013	0.013	0.015	0	0	0	0.044	0	0	0	0		
9	154	150	0.016	0.031	0.026	0.013	0.025	0.103	0.044	0.006	0.025	0.024	0.033	0.04	0.045	0.069		
10	158	154	0.183	0.238	0.174	0.188	0.138	0.14	0.139	0.167	0.25	0.097	0.05	0.03	0.067	0.127		
11	162	158	0.011	0.008	0.047	0.1	0	0.096	0.032	0.135	0.05	0.065	0.1	0.09	0.03	0.039		
12	166	162	0.032	0.031	0.037	0.013	0.037	0.007	0.006	0.013	0.013	0.077	0.067	0.03	0.06	0.049		
13	170	166	0	0.008	0.016	0	0.013	0.007	0	0.006	0	0.036	0	0.01	0.015	0		
14	174	170	0.016	0.031	0.005	0	0	0	0	0.013	0	0.032	0.067	0.04	0.022	0.039		
15	178	174	0	0	0	0.013	0	0	0	0	0.013	0.012	0.083	0.15	0.015	0.069		
16	182	178	0	0	0.016	0.013	0	0.015	0.032	0.032	0.013	0.012	0.067	0.04	0.007	0.01		
17	186	183	0	0	0.016	0	0	0.007	0.013	0.071	0	0.016	0.017	0	0.037	0.01		
18	190	187	0	0	0	0	0	0.007	0	0	0	0	0	0	0.015	0		
19	194	191	0	0	0	0.013	0.025	0.022	0	0	0	0.004	0	0	0.015	0.02		
20	198	195	0.011	0	0	0	0	0	0.006	0.013	0	0	0	0	0.015	0		
21	202	199	0	0	0.005	0	0	0	0	0	0	0	0	0	0.06	0.02		
22	206	203	0	0	0.005	0.013	0	0	0	0.006	0	0	0	0	0	0.01		
23	210	207	0.016	0	0.005	0	0	0	0	0	0	0	0	0	0	0		
24	214	211	0.011	0.008	0	0	0	0.007	0.006	0	0	0	0	0	0.015	0.01		
25	218	215	0.005	0	0	0	0	0.007	0	0	0	0	0	0	0.045	0		
26	222	219	0	0	0	0	0	0.015	0.044	0	0	0	0	0	0	0		
27	226	223	0	0	0	0	0	0.007	0	0.006	0	0	0	0	0	0		
28	230	227	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0		
29	234	231	0	0	0	0	0	0	0.006	0	0.013	0	0	0.01	0	0		
30	238	235	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0		
31	242	239	0	0	0	0	0	0.007	0.019	0	0.025	0	0	0	0	0		
32	246	243	0	0	0.011	0.013	0	0.007	0.006	0	0.025	0.004	0	0	0	0		
33	250	247	0	0	0	0	0	0.015	0	0	0	0	0	0	0	0		
34	254	251	0.005	0	0	0	0	0	0	0	0	0	0	0	0.022	0		
35	258	255	0.005	0	0	0.013	0	0	0	0.026	0.013	0.004	0	0	0	0		
36	262	259	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01	
37	266	263	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0		
38	270	268	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0		
39	274	272	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
40	278	276	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
41	282	280	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
42	286	284	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
43	342	339	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
<i>n</i>			93	65	95	40	40	68	79	78	40	124	30	50	67	51		
<i>n_a</i>			16	11	17	15	10	21	16	16	14	19	11	13	22	16		
<i>n_{eff}</i>			3.51	4.80	3.54	3.86	2.71	7.08	4.50	N/A	4.95	N/A	5.98	4.21	7.63	5.67		
<i>a</i>			7.86	7.02	8.62	8.98	7.52	11.07	9.60	N/A	9.32	N/A	9.97	9.39	13.45	10.69		
<i>H_E</i>			0.715	0.792	0.718	0.741	0.632	0.859	0.778	N/A	0.798	N/A	0.833	0.762	0.869	0.824		
<i>H_O</i>			0.710	0.831	0.642	0.700	0.625	0.882	0.823	N/A	0.775	N/A	0.900	0.740	0.896	0.843		
<i>F_{IS}</i>			0.008	-0.050	0.106	0.056	0.011	-0.028	-0.058	N/A	0.029	N/A	-0.082	0.030	-0.031	-0.024		

Appendix II. Continued.

Allele	Population															
	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0.274	0.486	0.227	0	0	0.012	0.019	0.44	0.479	0.386	0.37	0.38	0.059	0.011	0.086	0.195
5	0.065	0.057	0.136	0.364	0.326	0.233	0.333	0.26	0.135	0.273	0.12	0.092	0.074	0.056	0.046	0.12
6	0	0	0.023	0.011	0.011	0	0	0	0.063	0.045	0.043	0	0	0.011	0.007	0.025
7	0.137	0.071	0.205	0	0	0	0	0	0	0	0	0	0	0.011	0	0
8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
9	0.016	0.029	0.045	0	0	0	0	0.02	0.031	0.045	0	0	0	0	0.026	0
10	0.121	0.100	0	0.011	0.011	0.047	0	0.02	0	0	0.011	0.035	0.147	0.144	0.151	0.12
11	0.056	0.029	0.023	0.045	0.054	0.198	0.074	0	0.021	0.045	0.065	0.113	0.309	0.244	0.322	0.265
12	0.081	0	0	0.023	0.054	0.035	0.037	0.06	0.104	0.091	0.109	0.035	0.029	0.1	0.079	0.04
13	0.008	0	0.136	0.102	0.087	0.081	0.037	0	0	0.023	0.054	0	0.147	0.133	0.171	0.04
14	0	0	0	0.023	0.022	0.047	0.037	0	0.031	0.023	0.022	0.028	0	0.022	0.007	0.04
15	0	0	0	0	0	0.023	0	0	0	0	0.022	0.014	0.029	0	0.059	0.02
16	0	0.014	0	0	0	0.023	0	0	0	0	0	0.014	0.029	0.011	0.013	0.005
17	0.065	0.029	0.023	0	0.011	0.023	0	0	0.01	0	0	0.007	0	0	0.007	0.015
18	0	0.029	0	0	0	0.023	0	0	0	0	0	0	0	0.022	0	0.005
19	0.016	0	0.023	0	0	0	0	0.02	0.021	0.023	0	0	0	0	0	0.005
20	0.008	0.043	0	0	0	0	0	0	0	0	0	0	0	0	0	0.025
21	0.089	0.071	0	0	0	0	0	0.04	0	0	0.011	0.021	0.015	0.022	0	0.005
22	0.008	0	0	0	0.011	0.012	0	0	0	0	0.011	0.035	0.029	0.022	0	0.015
23	0	0	0	0.023	0.043	0.035	0	0	0.021	0	0.011	0.028	0	0	0.013	0.015
24	0.024	0.014	0	0.057	0.022	0.023	0.037	0	0	0	0.033	0.056	0.044	0.033	0.007	0.005
25	0.024	0	0.068	0.045	0.043	0.023	0.074	0.04	0.021	0	0.033	0.021	0	0	0.007	0.015
26	0	0	0	0.045	0.076	0.023	0.074	0	0.01	0	0	0.021	0	0.033	0	0.005
27	0	0	0	0.045	0.033	0.035	0.037	0.02	0.01	0	0.033	0.021	0.015	0.011	0	0.005
28	0	0.014	0.023	0.068	0.022	0.012	0	0.08	0.021	0.045	0.022	0.021	0.015	0.022	0	0.01
29	0	0	0.023	0.045	0.022	0.023	0.074	0	0	0	0.011	0.021	0.015	0.011	0	0
30	0	0	0	0	0	0.023	0.019	0	0.021	0	0.022	0.007	0.029	0.022	0	0
31	0	0.014	0	0.011	0.033	0.012	0.019	0	0	0	0	0	0	0.011	0	0
32	0	0	0	0.023	0	0	0.019	0	0	0	0	0.007	0.015	0	0	0
33	0	0	0.023	0.011	0	0.023	0.037	0	0	0	0	0	0	0	0	0
34	0	0	0	0.011	0.033	0	0	0	0	0	0	0.007	0	0.044	0	0
35	0	0	0	0.011	0	0	0.037	0	0	0	0	0	0	0	0	0.005
36	0	0	0	0	0.054	0	0.019	0	0	0	0	0.007	0	0	0	0
37	0	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0.023	0.023	0	0.012	0	0	0	0	0	0.007	0	0	0	0
39	0	0	0	0	0.022	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0.019	0	0	0	0	0	0	0	0	0
41	0.008	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	62	35	22	44	46	43	27	25	48	22	46	71	34	45	76	100
<i>n_a</i>	16	14	14	20	21	23	18	10	15	10	18	23	16	21	15	23
<i>n_{eff}</i>	7.73	N/A	8.23	6.47	7.75	9.67	7.78	3.83	3.85	4.46	5.94	5.82	7.03	9.12	5.85	7.12
<i>a</i>	10.75	N/A	11.73	13.21	14.05	14.89	14.33	8.26	9.67	8.90	11.86	12.69	11.72	13.20	9.03	11.14
<i>H_E</i>	0.871	N/A	0.878	0.845	0.871	0.897	0.871	0.739	0.740	0.776	0.832	0.828	0.858	0.890	0.829	0.860
<i>H_O</i>	0.887	N/A	0.864	0.795	0.870	0.930	0.926	0.760	0.771	0.818	0.804	0.817	0.824	0.933	0.868	0.890
<i>F_{IS}</i>	-0.019	N/A	0.017	0.060	0.002	-0.038	-0.064	-0.029	-0.042	-0.056	0.033	0.014	0.040	-0.049	-0.048	-0.036

Appendix II. Continued.

One101 Allele	Population															
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0.033	0	0	0	0	0	0	0	0	0	0	0.002	0
4	0.281	0.314	0.255	0.141	0.131	0.117	0.081	0.202	0.212	0.068	0.179	0.185	0.18	0.229	0.191	0.205
5	0.094	0.114	0.102	0.109	0.045	0.052	0.011	0.011	0.015	0.139	0.005	0.03	0.04	0.031	0.018	0.015
6	0.01	0	0	0.011	0.032	0.019	0	0	0	0	0	0	0	0	0	0
7	0.01	0	0.01	0	0.009	0	0	0	0	0	0	0	0	0	0	0
8	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0.001	0	0
9	0	0	0.02	0.022	0.005	0.006	0.016	0	0	0.003	0	0.005	0	0.001	0.002	0.002
10	0.104	0.129	0.082	0.054	0.153	0.104	0.151	0.122	0.192	0.196	0.224	0.215	0.16	0.141	0.160	0.206
11	0.229	0.186	0.194	0.304	0.225	0.266	0.07	0.09	0.086	0.073	0.138	0.045	0.05	0.063	0.072	0.063
12	0.021	0.057	0.041	0.065	0.126	0.136	0.258	0.261	0.162	0.018	0.112	0.14	0.2	0.144	0.173	0.100
13	0.031	0.043	0.071	0.033	0.099	0.117	0.113	0.059	0.111	0.045	0.077	0.055	0.12	0.076	0.070	0.064
14	0.073	0.057	0.031	0.043	0.027	0.039	0	0	0	0	0	0.015	0.015	0	0.011	0.011
15	0.01	0	0.01	0.043	0.009	0.006	0.016	0.027	0.02	0.084	0.01	0	0.035	0.013	0.014	0.032
16	0.01	0	0	0	0.027	0.019	0.043	0.037	0.03	0.079	0.005	0.03	0.025	0.028	0.029	0.023
17	0.01	0	0	0	0.027	0.006	0	0.021	0	0.003	0.01	0.015	0.04	0.021	0.023	0.025
18	0	0	0	0	0.014	0.006	0.038	0	0.01	0	0.005	0.01	0.025	0.013	0.009	0.019
19	0	0	0	0.011	0	0.006	0	0	0.005	0	0.015	0.02	0	0.008	0.007	0.015
20	0	0	0	0.011	0	0.013	0.032	0.021	0.02	0.003	0.01	0.035	0.005	0.024	0.014	0.019
21	0.01	0.014	0	0.011	0.018	0.013	0.005	0.027	0.015	0.003	0.036	0.025	0.01	0.014	0.018	0.025
22	0.021	0.014	0.02	0.033	0	0	0	0.005	0.01	0	0.005	0.015	0	0.013	0.027	0.027
23	0.01	0	0.092	0.011	0	0.013	0	0.005	0	0	0	0.02	0	0.018	0.016	0.017
24	0.01	0.014	0.02	0.011	0.005	0	0	0.021	0.01	0.003	0.005	0.025	0	0.006	0.002	0.006
25	0	0.014	0.01	0.011	0.005	0.006	0.005	0.005	0.04	0.003	0.102	0.02	0.01	0.018	0.018	0.015
26	0.01	0	0	0	0.005	0.006	0.016	0.005	0	0.003	0	0.01	0.005	0.023	0.014	0.009
27	0.01	0	0	0.011	0.014	0.019	0.038	0.021	0.015	0.021	0	0.015	0.02	0.012	0.009	0.015
28	0.021	0.014	0	0	0.005	0.006	0.011	0	0	0.204	0.005	0.02	0.025	0.018	0.018	0.025
29	0.01	0.029	0	0	0	0.006	0.027	0.021	0	0.003	0.015	0.02	0.015	0.018	0.018	0.008
30	0	0	0	0	0	0	0.032	0.027	0.01	0.003	0.015	0.01	0	0.010	0.007	0.004
31	0	0	0.02	0	0.009	0	0	0	0.015	0.003	0.01	0.01	0.01	0.028	0.038	0.036
32	0.01	0	0.02	0	0.005	0.006	0	0	0.005	0.031	0.005	0.005	0.01	0.012	0.011	0.006
33	0	0	0	0.011	0.005	0	0	0	0.01	0.003	0	0	0	0.005	0.005	0
34	0	0	0	0.011	0.005	0	0	0.011	0	0.008	0.01	0	0	0.008	0	0.002
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002
36	0	0	0	0	0	0.006	0.038	0	0	0.003	0	0	0	0.003	0.002	0
37	0	0	0	0	0	0	0	0	0.005	0.003	0	0	0	0	0	0.002
38	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0.001	0.002	0.004
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	48	35	49	46	111	77	93	94	99	191	98	100	100	389	222	264
<i>n_a</i>	21	13	16	22	24	24	19	20	21	25	22	26	20	30	30	30
<i>n_{eff}</i>	6.61	6.21	7.73	7.64	8.38	7.80	8.43	7.31	7.80	N/A	7.79	9.23	8.47	N/A	N/A	N/A
<i>a</i>	11.30	9.67	11.09	13.04	11.43	11.49	12.12	11.35	11.00	N/A	10.51	13.67	11.63	N/A	N/A	N/A
<i>H_E</i>	0.849	0.839	0.871	0.869	0.881	0.872	0.881	0.863	0.872	N/A	0.872	0.892	0.882	N/A	N/A	N/A
<i>H_O</i>	0.875	0.829	0.837	0.870	0.901	0.844	0.935	0.787	0.859	N/A	0.888	0.950	0.870	N/A	N/A	N/A
<i>F_{IS}</i>	-0.031	0.013	0.039	-0.001	-0.023	0.032	-0.062	0.088	0.015	N/A	-0.019	-0.066	0.014	N/A	N/A	N/A

Appendix II. Continued.

Allele	Population															
	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.014
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0.128	0.223	0.187	0.181	0.25	0.13	0.16	0.133	0.145	0.105	0.157	0.101	0.077	0.061	0.184	0.222
5	0.035	0.011	0.02	0	0	0.02	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	0	0	0	0	0.007	0.01	0	0	0	0	0	0	0	0	0	0
9	0	0.005	0	0	0	0	0.01	0	0	0	0.005	0	0	0	0	0.007
10	0.337	0.197	0.131	0.25	0.162	0.17	0.2	0.194	0.245	0.195	0.273	0.197	0.112	0.515	0.125	0.132
11	0.047	0.101	0.091	0.059	0.081	0.07	0.08	0.117	0.15	0.1	0.126	0.101	0.133	0.056	0.066	0.035
12	0.151	0.08	0.126	0.09	0.081	0.08	0.15	0.244	0.205	0.29	0.202	0.293	0.173	0.212	0.132	0.125
13	0.047	0.053	0.076	0.064	0.047	0.11	0.1	0.056	0.01	0.075	0.02	0.02	0.005	0.005	0.059	0.132
14	0.012	0.027	0.01	0.011	0.014	0.03	0	0	0	0	0.005	0	0	0	0	0.042
15	0.023	0.021	0.015	0.016	0.02	0.03	0.01	0.011	0.005	0.005	0	0	0.005	0	0.02	0.021
16	0.012	0.021	0.04	0.032	0.02	0.01	0.04	0.006	0	0.005	0.005	0.005	0	0	0.02	0.028
17	0.012	0.005	0.051	0.021	0.014	0.03	0.01	0.033	0.01	0.04	0.01	0	0	0.04	0.046	0.035
18	0.023	0.021	0.005	0.016	0.007	0.02	0.02	0.011	0	0	0.005	0.01	0	0	0.007	0.014
19	0	0.011	0.02	0.005	0.02	0	0.01	0.011	0.01	0.005	0.005	0	0	0	0.02	0.007
20	0.012	0.027	0.045	0.037	0.007	0.04	0.01	0.006	0	0	0.005	0.01	0.02	0	0.039	0.035
21	0.012	0.037	0.03	0.069	0.034	0.05	0.01	0.067	0.035	0.04	0.015	0.03	0.061	0.005	0.02	0.028
22	0	0.016	0.03	0.037	0.047	0.01	0.02	0.028	0.005	0.025	0.015	0.005	0.005	0.076	0.026	0.035
23	0	0.032	0.005	0.016	0.027	0.01	0.01	0.011	0.015	0.02	0.01	0.025	0.031	0.005	0.026	0
24	0.023	0.021	0	0.005	0.014	0.01	0.02	0	0.02	0.035	0.025	0.005	0.02	0.01	0.066	0.007
25	0	0.037	0.015	0.016	0.027	0.03	0.02	0.028	0.06	0.035	0.066	0.066	0.224	0	0.007	0.021
26	0	0.005	0.02	0	0.027	0	0.02	0.017	0.005	0.005	0	0.035	0.056	0.01	0.013	0.021
27	0.035	0	0.01	0.016	0.007	0.02	0.03	0.006	0.04	0.005	0.025	0.076	0.046	0.005	0.02	0
28	0.012	0.016	0.02	0.011	0.027	0.05	0	0.035	0.005	0.01	0.01	0	0	0	0.026	0.014
29	0.047	0.005	0.015	0.011	0.014	0.03	0.02	0	0	0	0.01	0.005	0.031	0	0.046	0.007
30	0	0.005	0.005	0.005	0	0	0.03	0	0	0.005	0.005	0	0	0	0.007	0
31	0	0	0.01	0.021	0.034	0.01	0.01	0.011	0	0	0	0.005	0	0	0.007	0.014
32	0.012	0	0.005	0.011	0.007	0.02	0.01	0.006	0	0.005	0	0	0	0	0	0
33	0	0.011	0	0	0.007	0	0	0.006	0.005	0	0	0	0	0	0	0.007
34	0	0.005	0	0	0	0.01	0	0	0	0	0	0	0	0	0.007	0
35	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0.007	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0
39	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0.007	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0.012	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0.012	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	43	94	99	94	74	50	50	90	100	100	99	99	98	99	76	72
<i>n_a</i>	20	26	27	23	25	24	23	20	17	19	21	18	15	12	25	23
<i>n_{eff}</i>	N/A	8.98	11.31	8.51	9.27	13.64	9.78	7.39	6.67	6.60	6.31	6.48	8.07	3.11	12.00	9.61
<i>a</i>	N/A	13.25	13.90	12.78	13.89	15.25	13.23	10.67	9.50	10.20	9.73	9.97	10.32	6.69	14.35	13.22
<i>H_E</i>	N/A	0.889	0.912	0.883	0.892	0.927	0.898	0.865	0.850	0.849	0.842	0.846	0.876	0.679	0.917	0.896
<i>H_O</i>	N/A	0.894	0.899	0.894	0.973	0.940	0.840	0.878	0.850	0.870	0.848	0.768	0.878	0.677	0.921	0.931
<i>F_{IS}</i>	N/A	-0.006	0.014	-0.013	-0.091	-0.015	0.065	-0.015	0.000	-0.025*	-0.008	0.093	-0.002	0.003	-0.005	-0.039

Appendix II. Continued.

Allele	Population																
	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0	
4	0.223	0.219	0.298	0.284	0.256	0.293	0.193	0.277	0.192	0.332	0.313	0.274	0.233	0.215	0.284	0.321	
5	0.005	0	0.012	0.017	0.006	0	0	0.011	0	0	0	0	0	0.005	0	0.011	
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
8	0	0	0	0	0.006	0	0.003	0	0	0	0	0	0	0.005	0	0	
9	0	0.011	0	0	0	0.009	0	0	0	0	0	0	0.007	0.015	0	0.011	
10	0.138	0.129	0.155	0.103	0.147	0.103	0.13	0.117	0.151	0.136	0.083	0.126	0.1	0.09	0.108	0.058	
11	0.064	0.079	0.036	0.052	0.071	0.069	0.083	0.064	0.099	0.027	0.042	0.063	0.113	0.065	0.041	0.047	
12	0.101	0.129	0.071	0.095	0.115	0.103	0.093	0.117	0.105	0.125	0.094	0.079	0.08	0.06	0.095	0.058	
13	0.08	0.051	0.071	0.069	0.083	0.078	0.093	0.074	0.087	0.016	0.026	0.011	0.087	0.09	0.088	0.068	
14	0.016	0.011	0.024	0.052	0	0.009	0.017	0.011	0.017	0	0	0	0.013	0.025	0.027	0.042	
15	0.032	0.006	0.012	0.06	0.006	0.017	0.017	0.021	0.017	0.005	0.01	0.021	0.013	0.05	0.034	0.016	
16	0.048	0.034	0.071	0.026	0.038	0.043	0.04	0.011	0.052	0.033	0.089	0.063	0.067	0.045	0.014	0.037	
17	0.032	0.039	0.024	0	0.026	0.017	0.04	0.032	0.012	0.011	0	0.011	0.053	0.05	0.061	0.063	
18	0.011	0.006	0.012	0.009	0.032	0.043	0.03	0.032	0.012	0.005	0	0.011	0.04	0.025	0.034	0.021	
19	0.027	0.028	0	0.009	0	0.009	0.023	0.043	0	0.016	0.016	0.021	0.013	0.02	0.02	0.016	
20	0.021	0.056	0.012	0.017	0.032	0.034	0.02	0.032	0.035	0.027	0.005	0.016	0.007	0.01	0.02	0.011	
21	0.032	0.022	0.012	0.026	0.026	0.026	0.04	0	0.052	0.098	0.099	0.126	0.02	0.045	0.02	0.079	
22	0.021	0.022	0.024	0.043	0.019	0.009	0.03	0.064	0.017	0.027	0.052	0.037	0.02	0.045	0.02	0.037	
23	0.027	0.022	0.012	0.017	0.006	0.017	0.01	0.011	0.006	0.033	0.031	0.021	0.013	0.03	0.014	0.021	
24	0.005	0.011	0.024	0.026	0.019	0.017	0.02	0.021	0.006	0.022	0.005	0.016	0.007	0.01	0.007	0.021	
25	0.016	0.022	0.036	0.026	0.032	0.017	0.01	0.011	0.017	0.027	0.031	0.016	0.027	0.02	0.041	0.026	
26	0.021	0.011	0.012	0	0.006	0.009	0.007	0	0.035	0.011	0.047	0	0.027	0.015	0.014	0	
27	0.016	0.022	0.036	0.017	0.013	0.017	0.003	0	0.029	0.027	0.036	0.042	0.02	0.005	0.007	0	
28	0.027	0.017	0.012	0.026	0.019	0.017	0.037	0	0.006	0	0.01	0.042	0.013	0.035	0.007	0.021	
29	0.011	0.022	0.012	0	0.013	0.017	0.013	0.043	0.017	0.011	0	0.005	0.013	0.005	0.014	0.005	
30	0.011	0.022	0.024	0.017	0.013	0.026	0.017	0	0.017	0	0.005	0	0	0.01	0.007	0.005	
31	0.011	0	0	0	0	0	0.01	0.011	0.006	0.005	0	0	0.007	0	0.014	0	
32	0	0	0	0	0	0	0.01	0	0.006	0	0	0	0.007	0.005	0.007	0.005	
33	0	0	0	0.009	0.006	0	0.01	0	0	0	0	0	0	0	0.007	0	
34	0	0	0	0	0	0	0	0	0.006	0	0	0	0	0	0	0	
35	0	0.006	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0	
36	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0	0	
37	0.005	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0	
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>n</i>	94	89	42	58	78	58	150	47	86	92	96	95	75	100	74	95	
<i>n_a</i>	25	24	22	21	24	23	26	19	24	21	19	19	24	27	25	23	
<i>n_{eff}</i>	10.53	10.40	7.98	8.80	8.71	8.37	11.57	8.59	10.66	6.40	7.26	8.08	10.21	12.22	8.64	7.68	
<i>a</i>	14.15	13.89	13.68	13.66	12.94	13.64	14.17	12.75	13.26	11.50	11.66	11.96	13.58	14.99	13.73	13.56	
<i>H_E</i>	0.905	0.904	0.875	0.886	0.885	0.881	0.914	0.884	0.906	0.844	0.862	0.876	0.902	0.918	0.884	0.870	
<i>H_O</i>	0.947	0.854	0.857	0.931	0.859	0.845	0.920	0.915	0.884	0.880	0.875	0.863	0.920	0.920	0.905	0.916	
<i>F_{IS}</i>	-0.046	0.056	0.020	-0.051	0.030	0.041	-0.007	-0.036	0.025	-0.044	-0.015	-0.020	-0.020	-0.002	-0.024	-0.053	

Appendix II. Continued.

Allele	Population															
	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0.021	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0.283	0.345	0.115	0.012	0.016	0.045	0.032	0.033	0.032	0.128	0.082	0.09	0.043	0.085	0.120	0.067
5	0.071	0.068	0.115	0.134	0.188	0.193	0.016	0.163	0.144	0.038	0.277	0.355	0.223	0.085	0.080	0.056
6	0	0	0.005	0	0	0	0	0	0	0.013	0	0	0	0	0	0.011
7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
9	0.01	0.007	0	0	0.005	0	0	0	0.005	0	0	0	0	0.035	0	0
10	0.056	0.02	0.073	0.105	0.059	0.097	0	0.011	0.027	0.038	0.054	0.05	0.085	0.01	0.020	0
11	0.056	0.135	0.411	0.343	0.382	0.364	0.694	0.37	0.378	0.321	0.326	0.17	0.34	0.48	0.450	0.489
12	0.02	0.061	0.01	0.052	0.032	0.023	0.185	0.033	0.027	0.064	0.038	0.03	0.021	0.03	0.080	0
13	0.096	0.088	0.047	0.052	0.048	0.045	0	0.054	0.005	0.167	0.005	0.08	0.011	0.055	0.020	0.044
14	0.035	0	0.021	0.029	0.038	0.006	0	0.011	0.064	0.013	0.065	0.04	0.117	0.015	0.010	0.056
15	0.061	0.014	0.047	0.023	0.059	0.034	0	0	0.027	0.103	0.016	0.09	0.053	0.045	0.040	0.011
16	0.03	0.007	0.01	0.017	0.032	0.034	0	0.033	0.021	0.051	0.011	0	0.011	0.025	0.010	0.056
17	0.045	0.074	0.01	0	0.022	0.011	0	0.011	0.016	0.013	0.005	0	0	0.005	0.010	0.022
18	0.005	0	0.016	0.012	0.016	0.006	0	0	0.016	0.013	0	0	0.021	0	0	0
19	0.025	0	0.005	0.017	0	0.023	0	0.011	0.005	0	0	0	0	0	0	0.011
20	0.02	0.014	0.005	0.006	0	0	0	0.033	0.027	0	0.005	0	0	0.005	0.010	0
21	0.01	0.014	0.01	0.041	0.016	0	0.008	0.011	0.011	0.038	0	0	0.021	0.015	0.020	0.044
22	0.045	0.054	0.01	0.006	0.005	0.023	0	0.022	0.011	0	0	0.025	0	0.005	0.030	0
23	0.035	0.007	0	0.047	0	0	0	0.011	0.016	0	0.005	0.005	0	0.01	0	0
24	0.02	0	0	0.029	0.005	0.006	0	0.011	0.021	0	0.011	0	0	0.005	0.010	0
25	0.02	0.014	0.021	0	0.022	0.040	0.008	0.087	0.043	0	0.005	0.025	0.032	0.025	0.040	0.022
26	0.015	0.007	0	0.012	0.011	0.011	0.008	0.022	0.037	0	0.027	0	0	0.02	0.030	0.033
27	0.025	0.047	0	0.017	0.016	0.011	0.048	0.043	0.027	0	0.022	0	0	0.01	0	0.022
28	0.015	0.007	0.021	0.035	0.016	0.011	0	0	0.011	0	0.005	0	0	0.005	0	0
29	0	0	0.005	0.006	0	0.006	0	0.011	0.005	0	0	0	0	0.005	0.020	0
30	0	0	0.005	0	0.011	0.006	0	0.022	0.016	0	0	0	0	0.005	0	0.022
31	0	0	0.01	0	0	0.006	0	0	0	0	0.005	0	0	0.005	0	0
32	0	0.007	0.005	0	0	0	0	0	0	0	0.027	0.04	0	0.005	0	0
33	0	0.014	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0
34	0	0	0	0.006	0	0	0	0	0.011	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0.021	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.033
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	99	74	96	86	93	88	62	46	94	39	92	100	47	100	50	45
<i>n_a</i>	22	20	23	21	20	21	8	20	25	13	20	12	13	25	17	16
<i>n_{eff}</i>	9.03	6.27	4.90	6.42	N/A	N/A	1.94	5.77	N/A	6.31	5.08	5.52	5.38	3.98	N/A	3.95
<i>a</i>	14.00	11.16	10.87	11.98	N/A	N/A	4.77	12.11	N/A	9.85	9.70	9.21	9.33	11.05	N/A	11.18
<i>H_E</i>	0.889	0.840	0.796	0.844	N/A	N/A	0.485	0.827	N/A	0.841	0.803	0.819	0.814	0.749	N/A	0.747
<i>H_O</i>	0.879	0.838	0.854	0.872	N/A	N/A	0.452	0.913	N/A	0.821	0.826	0.790	0.830	0.750	N/A	0.822
<i>F_{IS}</i>	0.012	0.003	-0.073	-0.033	N/A	N/A	0.069	-0.106	N/A	0.025	-0.029	0.035	-0.019	-0.001	N/A	-0.102

Appendix II. Continued.

Allele	Population															
	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0.023	0.06	0.106	0.102	0.021	0.031	0.049	0.052	0.146	0.02	0.056	0.049	0.067	0.056	0.06	0.077
5	0.184	0.18	0.218	0.125	0.085	0.071	0.195	0.052	0.052	0.045	0.070	0.080	0.067	0.178	0.1	0.077
6	0.010	0.02	0.021	0.006	0.021	0	0	0	0	0	0	0.002	0	0.011	0.02	0
7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0	0.01	0.01	0	0	0.002	0	0	0	0
9	0.013	0.015	0.005	0.028	0.011	0	0.012	0.01	0.01	0.005	0	0.003	0	0.011	0.01	0
10	0.030	0.005	0.016	0	0.011	0.01	0.024	0.073	0.063	0.045	0.063	0.059	0.111	0.044	0.03	0.013
11	0.437	0.39	0.282	0.415	0.362	0.296	0.39	0.229	0.333	0.328	0.338	0.269	0.178	0.367	0.34	0.41
12	0.045	0.045	0.027	0.028	0.043	0.173	0.037	0.042	0.063	0.025	0.014	0.046	0.033	0.056	0.02	0.026
13	0.040	0.055	0.032	0.051	0.085	0.01	0.049	0.083	0.052	0.056	0.049	0.054	0.033	0.011	0.03	0.077
14	0.051	0.045	0.053	0.04	0.149	0.051	0.012	0.104	0.021	0.045	0.077	0.081	0.089	0.056	0.06	0.077
15	0.005	0.01	0	0.006	0	0.02	0	0.031	0.01	0.005	0.007	0.015	0	0	0.01	0.038
16	0.008	0	0.027	0.006	0	0.02	0.024	0	0	0	0.014	0.007	0	0.033	0.03	0
17	0.003	0.02	0.005	0	0	0	0.024	0	0	0.01	0	0.003	0	0	0.01	0
18	0	0	0	0	0	0	0	0	0	0	0	0.007	0	0	0.02	0
19	0	0	0	0.011	0	0.02	0	0.01	0.01	0.045	0.021	0.021	0.011	0.022	0.01	0
20	0.003	0.005	0.005	0	0.043	0.051	0	0.031	0	0.03	0.021	0.026	0.078	0	0.01	0
21	0.005	0.015	0.011	0.006	0.043	0.051	0.049	0.021	0	0.025	0.014	0.011	0.011	0	0.02	0.013
22	0.010	0.01	0	0.017	0	0.02	0.037	0.042	0.031	0.02	0.007	0.033	0.022	0	0.02	0.038
23	0.010	0.03	0.005	0	0.011	0	0.012	0.01	0.01	0.005	0.014	0.015	0.044	0	0	0.013
24	0.013	0.005	0.016	0.023	0.043	0.02	0.037	0.021	0	0.051	0.014	0.028	0.022	0.011	0	0
25	0.020	0	0.005	0	0	0	0	0.073	0.021	0.04	0.028	0.023	0.078	0	0.02	0.013
26	0.015	0.01	0.005	0.023	0	0.031	0	0	0	0.025	0.007	0.026	0.011	0.033	0.02	0.026
27	0.018	0.005	0.005	0.011	0	0.031	0	0.021	0.021	0.035	0.028	0.020	0.022	0	0.03	0.026
28	0.008	0.01	0.021	0	0	0	0.024	0.01	0	0.035	0.035	0.034	0.044	0.044	0.04	0.013
29	0.010	0.01	0	0.006	0	0.041	0	0.021	0.052	0.02	0.014	0.021	0.033	0	0.02	0
30	0.010	0.015	0.005	0.028	0.021	0.02	0.012	0	0	0.005	0	0.010	0.011	0	0.02	0.013
31	0.018	0.015	0.016	0.017	0.011	0.01	0	0.021	0.01	0.01	0.021	0.005	0	0.011	0	0
32	0.005	0	0.085	0.011	0	0.02	0.012	0	0	0.01	0.014	0.013	0.011	0.033	0.03	0.013
33	0	0.005	0.005	0.006	0	0	0	0.01	0	0	0.007	0.008	0	0	0.01	0
34	0	0.005	0	0	0	0	0	0	0.01	0.02	0.014	0.003	0	0	0	0.013
35	0	0.005	0.005	0.006	0.011	0	0	0	0.042	0	0.014	0.003	0.011	0.022	0.01	0
36	0.003	0	0	0.028	0.032	0	0	0	0	0.01	0.028	0.010	0	0	0	0
37	0	0	0.005	0	0	0	0	0.01	0.01	0	0.007	0.008	0.011	0	0	0.013
38	0	0	0.011	0	0	0	0	0	0	0	0	0.002	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0.025	0	0.003	0	0	0	0.013
40	0.005	0	0	0	0	0	0	0.01	0	0	0	0.003	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0.021	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	198	100	94	88	47	49	41	48	48	99	71	307	45	45	50	39
<i>n_a</i>	27	26	26	23	17	20	17	24	21	27	27	36	22	17	26	20
<i>n_{eff}</i>	N/A	5.14	6.73	4.92	5.92	7.73	5.13	11.72	6.91	7.87	N/A	N/A	13.86	5.71	7.43	5.32
<i>a</i>	N/A	11.53	11.54	11.41	11.33	13.27	11.42	15.09	12.88	14.99	N/A	N/A	14.89	11.52	15.14	12.52
<i>H_E</i>	N/A	0.805	0.851	0.797	0.831	0.871	0.805	0.915	0.855	0.873	N/A	N/A	0.928	0.825	0.865	0.812
<i>H_O</i>	N/A	0.730	0.840	0.864	0.830	0.878	0.854	0.875	0.833	0.889	N/A	N/A	0.956	0.778	0.940	0.821
<i>F_{IS}</i>	N/A	0.094*	0.013	-0.084	0.002	-0.008	-0.061	0.044	0.026	-0.018	N/A	N/A	-0.030	0.058	-0.087	-0.011

Appendix II. Continued.

Allele	Population																Total
	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0.08	0.06	0.026	0.08	0.025	0.167	0.056	0.1	0.09	0.163	0.095	0.021	0.04	0.1	0.159	0.16	0.16
5	0.175	0.14	0.141	0.17	0.174	0.115	0.056	0.12	0.21	0.173	0.130	0.187	0.142	0.05	0.182	0.185	0.185
6	0	0	0	0.01	0.007	0	0	0	0	0	0.009	0.010	0	0	0	0	0
7	0	0	0	0	0	0	0	0	0	0	0	0.005	0.006	0	0	0	0
8	0	0	0	0	0	0	0	0	0	0	0	0.015	0.034	0.037	0.074	0.068	0.068
9	0	0	0	0	0.007	0	0	0	0.01	0.01	0.002	0.072	0.04	0	0.006	0.006	0.006
10	0.05	0.02	0.013	0.03	0.007	0.042	0	0.01	0.05	0.041	0.030	0.044	0.023	0	0.051	0.049	0.049
11	0.285	0.36	0.333	0.24	0.301	0.292	0.378	0.23	0.21	0.214	0.060	0.105	0.136	0.113	0.051	0.049	0.049
12	0.05	0.02	0.051	0.05	0.054	0.208	0.067	0.04	0.04	0.102	0.100	0.056	0.097	0	0.045	0.043	0.043
13	0.045	0.04	0.064	0.03	0.029	0	0	0.05	0.06	0.041	0.056	0.067	0.085	0.188	0.085	0.086	0.086
14	0.03	0.09	0.026	0.04	0.076	0	0.056	0.07	0.05	0.02	0.130	0.059	0.08	0.163	0.04	0.043	0.043
15	0.045	0.03	0.026	0.03	0.062	0	0.033	0.02	0	0.031	0.053	0.044	0.023	0.087	0.011	0.012	0.012
16	0.01	0.01	0.026	0.02	0.004	0	0.022	0.02	0.03	0.02	0.014	0.041	0.028	0	0.017	0.019	0.019
17	0.03	0	0.013	0.03	0.011	0.01	0.022	0.01	0	0.01	0.014	0.015	0.011	0	0	0	0
18	0.005	0	0.013	0.01	0.004	0	0	0	0	0.02	0.007	0.013	0.011	0	0.011	0.012	0.012
19	0.02	0.03	0	0.02	0.007	0	0	0.02	0	0	0.012	0	0	0.013	0	0	0
20	0	0.01	0.051	0.03	0.007	0.01	0.011	0.01	0.01	0.01	0.002	0.003	0.011	0	0	0	0
21	0.005	0.01	0	0.01	0.014	0.083	0.133	0.08	0.01	0	0.005	0.015	0	0.013	0.017	0.019	0.019
22	0.01	0.02	0	0.01	0.004	0.042	0.044	0.06	0.02	0	0.037	0.003	0.011	0	0.006	0.006	0.006
23	0.01	0	0.038	0.01	0.022	0.021	0.033	0.04	0.02	0.031	0.026	0.010	0.006	0.05	0.017	0.019	0.019
24	0.005	0.01	0.013	0.02	0.014	0.01	0	0.01	0	0	0.040	0.010	0.006	0	0.006	0.006	0.006
25	0	0.02	0	0.01	0.011	0	0	0.01	0.02	0.031	0.030	0.010	0.023	0	0.017	0.012	0.012
26	0.01	0.02	0.026	0.04	0.029	0	0.033	0	0.01	0	0.021	0.013	0.045	0.037	0.006	0.006	0.006
27	0.03	0.02	0.013	0.01	0.033	0	0	0.01	0.03	0.031	0.002	0.018	0.017	0.013	0.023	0.025	0.025
28	0.01	0.03	0.026	0	0.036	0	0.011	0.02	0.02	0.02	0.012	0.021	0.034	0	0.011	0.012	0.012
29	0.025	0	0.013	0	0.029	0	0.011	0.02	0.01	0	0.014	0.026	0.034	0.1	0.017	0.019	0.019
30	0.015	0.01	0.013	0.01	0.007	0	0	0.01	0	0.01	0.012	0.041	0.011	0.013	0.017	0.012	0.012
31	0.015	0	0.013	0.01	0.011	0	0	0	0.01	0	0.014	0.013	0.028	0	0.023	0.025	0.025
32	0.005	0.02	0.013	0.04	0.004	0	0	0	0.02	0.01	0.009	0.021	0.006	0.013	0.017	0.019	0.019
33	0.01	0.01	0	0.01	0	0	0.022	0.02	0.02	0.01	0.005	0.015	0	0	0.04	0.037	0.037
34	0.01	0.01	0	0.02	0	0	0	0	0	0	0.002	0.013	0.011	0	0.006	0.006	0.006
35	0.005	0.01	0	0	0.007	0	0.011	0.01	0.02	0	0.012	0	0	0	0.017	0.012	0.012
36	0	0	0.013	0.01	0	0	0	0	0	0	0.012	0	0	0.013	0.017	0.019	0.019
37	0.01	0	0	0	0	0	0	0.01	0	0	0.009	0	0	0	0.011	0.012	0.012
38	0	0	0.038	0	0	0	0	0	0.02	0	0.014	0.005	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0.009	0.005	0	0	0	0	0
40	0	0	0	0	0.004	0	0	0	0.01	0	0	0.003	0	0	0	0	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0.003	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	100	50	39	50	138	48	45	50	50	49	215	195	88	40	88	81	10254
<i>n_a</i>	27	23	23	27	29	11	17	24	24	20	34	34	27	16	29	29	41
<i>n_{eff}</i>	7.81	6.23	7.25	10.16	N/A	5.82	5.80	10.86	9.69	8.82	N/A	N/A	14.39	10.06	12.40	12.35	
<i>a</i>	13.24	13.08	14.34	15.33	N/A	8.13	11.85	14.35	14.34	12.54	N/A	N/A	15.43	11.68	15.34	15.45	
<i>H_E</i>	0.872	0.840	0.862	0.902	N/A	0.828	0.828	0.908	0.897	0.887	N/A	N/A	0.931	0.901	0.919	0.919	
<i>H_O</i>	0.910	0.880	0.897	0.880	N/A	0.896	0.911	0.960	0.880	0.857	N/A	N/A	0.920	0.900	0.955	0.951	
<i>F_{IS}</i>	-0.044	-0.049	-0.042	0.024	N/A	-0.083	-0.102	-0.058	0.019	0.034	N/A	N/A	0.011	0.001	-0.039	-0.035	

Appendix II. Continued.

<i>Ok100</i>	Size	Size	Population															
			Allele	ABL	DFO	1	2	3	4	5	6	7	8	9	10	11	12	13
1	69	65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	77	73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	81	77	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	85	81	0	0	0.011	0	0	0	0	0.006	0	0.016	0.033	0.03	0	0	0	0
5	89	85	0	0	0.005	0.025	0	0	0.013	0.006	0.014	0.016	0.1	0.08	0	0.057	0	0
6	93	89	0.005	0	0.095	0.025	0.037	0	0.047	0.084	0.027	0.036	0.033	0.05	0.037	0.038	0	0
7	97	93	0.021	0	0.063	0.087	0.05	0.008	0.033	0.006	0.041	0.016	0.067	0.02	0.037	0.038	0	0
8	101	97	0.011	0.027	0.021	0	0	0.107	0.02	0.058	0	0.040	0.1	0.08	0.022	0.038	0	0
9	105	101	0.068	0.196	0.089	0.087	0.15	0.074	0.08	0.058	0.135	0.085	0	0.02	0.134	0.123	0	0
10	109	105	0.058	0.036	0.074	0.15	0.113	0.066	0.113	0.019	0.041	0.040	0.05	0.04	0.06	0.047	0	0
11	113	109	0.232	0.25	0.068	0.05	0.037	0.082	0.087	0.039	0.054	0.089	0.033	0.01	0.052	0.028	0	0
12	117	113	0.137	0.116	0.016	0.013	0.05	0.164	0.107	0.130	0.095	0.153	0.067	0.12	0.134	0.132	0	0
13	121	117	0.121	0.143	0.158	0.15	0.188	0.139	0.153	0.065	0.216	0.085	0.117	0.05	0.097	0.113	0	0
14	125	121	0.068	0.08	0.137	0.075	0.013	0.09	0.12	0.058	0.081	0.069	0.067	0.02	0.149	0.123	0	0
15	129	125	0.063	0.063	0.016	0	0.1	0.082	0.087	0.071	0.027	0.089	0.017	0.02	0.022	0.028	0	0
16	133	129	0.063	0.018	0.037	0.075	0.1	0.033	0.02	0.058	0.068	0.073	0	0.03	0.104	0.113	0	0
17	137	133	0.037	0	0.011	0.113	0.025	0.066	0.02	0.156	0.068	0.097	0.033	0.07	0.037	0.028	0	0
18	141	137	0.026	0	0.053	0.025	0.013	0.049	0.033	0.065	0.054	0.065	0.083	0.12	0.067	0.057	0	0
19	145	142	0.053	0.027	0.079	0.05	0.037	0.016	0.007	0.013	0.054	0.012	0.033	0.08	0.015	0	0	0
20	149	146	0.016	0.009	0.053	0.075	0.075	0.008	0.02	0	0.014	0.004	0.017	0.01	0	0.009	0	0
21	153	150	0.021	0.036	0.011	0	0	0.008	0.02	0.097	0	0.012	0.117	0.04	0.03	0.028	0	0
22	157	154	0	0	0	0	0.013	0.008	0.013	0.006	0	0	0.033	0.05	0	0	0	0
23	161	158	0	0	0	0	0	0	0	0	0.014	0.004	0	0.01	0	0	0	0
24	165	162	0	0	0	0	0	0	0	0	0	0	0	0.05	0	0	0	0
25	169	166	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0
26	173	170	0	0	0	0	0	0	0.007	0	0	0	0	0	0	0	0	0
27	177	174	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	181	178	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	185	182	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>			95	56	95	40	40	61	75	77	37	124	30	50	67	53		
<i>n_a</i>			16	12	19	14	15	16	19	18	16	19	17	21	15	16		
<i>n_{eff}</i>			9.17	7.04	11.85	11.70	10.53	11.13	11.86	N/A	10.94	N/A	16.24	16.56	11.24	12.39		
<i>a</i>			11.63	9.41	12.69	11.91	11.89	11.71	12.83	N/A	12.86	N/A	14.52	15.34	12.09	12.85		
<i>H_E</i>			0.891	0.858	0.916	0.915	0.905	0.910	0.916	N/A	0.909	N/A	0.938	0.940	0.911	0.919		
<i>H_O</i>			0.905	0.839	0.926	0.875	0.975	0.918	0.893	N/A	1.000	N/A	0.967	0.980	0.910	0.962		
<i>F_{IS}</i>			-0.016	0.022	-0.012	0.044	-0.078	-0.009	0.025	N/A	-0.102*	N/A	-0.031	-0.043	0.001	-0.047		

Appendix II. Continued.

<i>Oki100</i>	Population																
	Allele	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0.014	0	0	0.005
4	0	0	0.068	0.17	0.109	0.01	0.056	0	0	0	0.011	0.063	0.125	0.1	0.066	0.105	
5	0	0.029	0	0.091	0.12	0.122	0.056	0.2	0.25	0.208	0.196	0.162	0.014	0.044	0.039	0.145	
6	0.04	0.043	0.068	0.068	0.022	0.02	0	0	0.01	0	0.011	0.063	0.042	0.011	0.007	0.03	
7	0.032	0.014	0.068	0.091	0.043	0.02	0.019	0.04	0.063	0.042	0.043	0.042	0.028	0	0.026	0.02	
8	0.056	0.029	0.045	0.091	0.054	0.071	0.074	0.06	0.104	0.063	0.022	0.127	0.042	0.1	0.079	0.11	
9	0.167	0.057	0.114	0.159	0.207	0.102	0.222	0.14	0.042	0.083	0.054	0.162	0.097	0.156	0.118	0.105	
10	0.063	0.043	0	0.034	0.065	0.194	0.074	0.06	0.042	0.083	0.054	0.063	0.111	0.133	0.092	0.06	
11	0.016	0.200	0.023	0.011	0.065	0.041	0.074	0.06	0	0.021	0.033	0.028	0.042	0.044	0.079	0.07	
12	0.175	0.043	0.182	0.011	0.087	0.122	0.13	0.06	0.063	0.104	0.13	0.014	0.111	0.067	0.138	0.065	
13	0.111	0.071	0.205	0.034	0.054	0.071	0.074	0.1	0.063	0.188	0.076	0.014	0.139	0.033	0.033	0.04	
14	0.135	0.043	0.068	0.045	0.022	0.051	0.019	0.08	0.125	0.042	0.076	0.028	0.042	0.033	0.026	0.035	
15	0.032	0.071	0.045	0.034	0.043	0.061	0.056	0.04	0.021	0	0.065	0.007	0.056	0.056	0.02	0.05	
16	0.04	0.029	0	0.102	0.033	0.051	0.056	0	0.01	0	0	0.042	0	0.022	0.033	0.02	
17	0.056	0	0.068	0.034	0.022	0.02	0.074	0	0.042	0.021	0.022	0.035	0	0.056	0.112	0.03	
18	0.04	0.157	0.045	0.011	0.043	0.01	0.019	0	0.021	0	0	0.021	0.028	0.022	0.053	0.05	
19	0.016	0.129	0	0	0	0.01	0	0.02	0.01	0	0.022	0.028	0.028	0.067	0.026	0.025	
20	0.008	0	0	0	0.011	0	0	0.02	0.031	0.083	0	0.007	0.014	0.011	0.026	0.02	
21	0.016	0.043	0	0	0	0	0	0	0.021	0	0.054	0.014	0	0	0.026	0.01	
22	0	0	0	0	0	0.02	0	0.06	0.042	0.063	0.076	0	0.028	0	0	0	
23	0	0	0	0.011	0	0	0	0.02	0.021	0	0.011	0	0	0.022	0	0	
24	0	0	0	0	0	0	0	0.04	0.01	0	0.033	0.021	0.014	0	0	0	
25	0	0	0	0	0	0	0	0	0	0	0.011	0.007	0	0.011	0	0	
26	0	0	0	0	0	0	0	0	0.01	0	0	0.028	0	0.011	0	0	
27	0	0	0	0	0	0	0	0	0	0	0	0.014	0	0	0	0	
28	0	0	0	0	0	0	0	0	0	0	0	0.007	0.014	0	0	0	
29	0	0	0	0	0	0	0	0	0	0	0	0	0.014	0	0	0	
<i>n</i>	63	35	22	44	46	49	27	25	48	24	46	71	36	45	76	100	
<i>n_a</i>	16	15	12	16	16	17	14	15	20	12	19	23	20	19	18	20	
<i>n_{eff}</i>	10.06	N/A	10.28	10.97	11.22	10.93	11.09	12.25	9.85	9.64	12.24	11.90	14.20	13.35	13.30	13.36	
<i>a</i>	11.96	N/A	11.43	12.15	12.88	12.49	12.41	13.32	13.58	11.03	13.86	14.18	14.66	13.95	13.57	13.81	
<i>H_E</i>	0.901	N/A	0.903	0.909	0.911	0.908	0.910	0.918	0.898	0.896	0.918	0.916	0.930	0.925	0.925	0.925	
<i>H_O</i>	0.968	N/A	0.909	0.977	0.870	0.898	0.852	0.880	0.917	0.875	0.978	0.901	0.944	0.889	0.921	0.910	
<i>F_{IS}</i>	-0.076	N/A	-0.007	-0.076	0.046	0.012	0.065	0.043	-0.020	0.024	-0.066	0.016	-0.016	0.040	0.004	0.016	

Appendix II. Continued.

Allele	Population															
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0.022	0	0	0	0	0	0	0	0	0	0	0	0
4	0.073	0.014	0.061	0.109	0.009	0.019	0.059	0.046	0.03	0.013	0.005	0.075	0.075	0.086	0.080	0.076
5	0.208	0.143	0.112	0.076	0.125	0.136	0.161	0.287	0.146	0.334	0.175	0.175	0.095	0.185	0.209	0.159
6	0	0.086	0.031	0	0	0	0	0	0.005	0.003	0	0.005	0.005	0.011	0.016	0.013
7	0.021	0.029	0.061	0.022	0.031	0.052	0	0.006	0.056	0	0.026	0.01	0.04	0.023	0.027	0.021
8	0.125	0.1	0.102	0.13	0.201	0.136	0.065	0.017	0.03	0.016	0.005	0.115	0.07	0.059	0.066	0.064
9	0.115	0.114	0.122	0.12	0.058	0.058	0	0.052	0.086	0.013	0.041	0.05	0.09	0.074	0.052	0.057
10	0.083	0.1	0.102	0.065	0.058	0.039	0.113	0.098	0.217	0.039	0.113	0.11	0.065	0.101	0.107	0.093
11	0.052	0	0.071	0.033	0.045	0.084	0.172	0.121	0.051	0.189	0.062	0.11	0.165	0.113	0.093	0.114
12	0.052	0.114	0.071	0.098	0.156	0.253	0.124	0.149	0.141	0.332	0.206	0.07	0.065	0.099	0.064	0.106
13	0.042	0.071	0.02	0.065	0.045	0.032	0.005	0.04	0.04	0.003	0.077	0.04	0.045	0.033	0.045	0.045
14	0.042	0.086	0.071	0.011	0.045	0.006	0.011	0.052	0.076	0.016	0.067	0.065	0.025	0.033	0.034	0.051
15	0.01	0.029	0.051	0.076	0.036	0.026	0.226	0.011	0.045	0.005	0.093	0.04	0.055	0.044	0.045	0.042
16	0.052	0.029	0.031	0.033	0.031	0.006	0.022	0.04	0.015	0.016	0.005	0.04	0.025	0.037	0.039	0.057
17	0.031	0.014	0.01	0.022	0.076	0.058	0.038	0.023	0.025	0.003	0.01	0.02	0.11	0.030	0.050	0.038
18	0.021	0.014	0	0.033	0.031	0.026	0.005	0.023	0.01	0.005	0.036	0.015	0.025	0.019	0.016	0.025
19	0.031	0.014	0.02	0.054	0.027	0.032	0	0.006	0.005	0.003	0	0.015	0.01	0.006	0.002	0.004
20	0.021	0.014	0.031	0.011	0	0	0	0	0	0.008	0.026	0.015	0.02	0.010	0.009	0.006
21	0.01	0	0	0.011	0.009	0.006	0	0	0	0	0.021	0.01	0.005	0.013	0.014	0.008
22	0	0	0.031	0	0.009	0.006	0	0	0	0	0.026	0.01	0	0.004	0.002	0.011
23	0	0	0	0	0	0.006	0	0	0.005	0.003	0	0	0.01	0.011	0.007	0.004
24	0	0.014	0	0	0.004	0.006	0	0.006	0.01	0	0	0.01	0	0.009	0.005	0.004
25	0	0.014	0	0.011	0.004	0.006	0	0.023	0.005	0.003	0	0	0	0	0.016	0.004
26	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002	0
28	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	48	35	49	46	112	77	93	87	99	193	97	100	100	397	220	264
<i>n_a</i>	18	18	17	19	19	20	12	17	19	18	18	20	19	21	23	22
<i>n_{eff}</i>	11.09	12.98	14.49	14.14	9.99	8.48	7.16	7.31	9.13	N/A	9.09	11.49	12.50	N/A	N/A	N/A
<i>a</i>	13.23	13.21	13.70	13.93	12.45	11.90	8.69	11.02	11.71	N/A	11.46	12.89	13.17	N/A	N/A	N/A
<i>H_E</i>	0.910	0.923	0.931	0.929	0.900	0.882	0.860	0.863	0.890	N/A	0.890	0.913	0.920	N/A	N/A	N/A
<i>H_O</i>	0.875	0.943	0.939	1.000	0.893	0.922	0.946	0.851	0.838	N/A	0.918	0.920	0.960	N/A	N/A	N/A
<i>F_{IS}</i>	0.039	-0.022	-0.008	-0.077	0.008	-0.046	-0.101	0.015	0.059	N/A	-0.031	-0.008	-0.044	N/A	N/A	N/A

Appendix II. Continued.

Allele	Population															
	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0.023	0.032	0.025	0.037	0.041	0.05	0.06	0	0.005	0.02	0.01	0	0	0.02	0.033	0.041
5	0.193	0.245	0.202	0.202	0.155	0.27	0.25	0.413	0.3	0.41	0.419	0.293	0.51	0.26	0.164	0.164
6	0.011	0.021	0.035	0.032	0.02	0.02	0.02	0.016	0.045	0.015	0.015	0.01	0	0.026	0.033	0.027
7	0	0.011	0.01	0.011	0.014	0.01	0.01	0.038	0.01	0.01	0.005	0.02	0.005	0.005	0	0.007
8	0.011	0.037	0.076	0.106	0.135	0.1	0.06	0.022	0.055	0.025	0.081	0.116	0.03	0.01	0.099	0.082
9	0.102	0.053	0.056	0.048	0.101	0.04	0.01	0.054	0.07	0.025	0.076	0.086	0.025	0.163	0.059	0.068
10	0.159	0.09	0.091	0.122	0.122	0.1	0.08	0.147	0.07	0.08	0.136	0.091	0.056	0.143	0.053	0.048
11	0.068	0.096	0.152	0.133	0.101	0.09	0.12	0.152	0.175	0.095	0.136	0.192	0.263	0.117	0.151	0.164
12	0.193	0.101	0.061	0.08	0.074	0.05	0.04	0.027	0.035	0.05	0.005	0	0.02	0	0.086	0.075
13	0.034	0.043	0.03	0.032	0.02	0.02	0.02	0	0.005	0.005	0.005	0.01	0	0.01	0.046	0.041
14	0.045	0.096	0.061	0.043	0.041	0.04	0.02	0.043	0.095	0.055	0.04	0.101	0.056	0.112	0.046	0.075
15	0.034	0.011	0.02	0.032	0.034	0.04	0.09	0.005	0.055	0.02	0.015	0.02	0	0.02	0.033	0.062
16	0.023	0.037	0.056	0.021	0.047	0.05	0.04	0.027	0.025	0.025	0.015	0.02	0.02	0.051	0.059	0.048
17	0	0.048	0.035	0.027	0.041	0.05	0.06	0.016	0.035	0.055	0.015	0.02	0	0.031	0.059	0.041
18	0.023	0.021	0.005	0.011	0.034	0.01	0.02	0.011	0.005	0.015	0.015	0.015	0.005	0.031	0.02	0.021
19	0.011	0	0.03	0.016	0.007	0.01	0.02	0.005	0	0.005	0.005	0.005	0	0	0.013	0.007
20	0	0.005	0.005	0.016	0.007	0.01	0.01	0	0.01	0.015	0	0	0.01	0	0.02	0.007
21	0.011	0	0.02	0.027	0	0	0.05	0.016	0.005	0.06	0.005	0	0	0	0.013	0.014
22	0.011	0.016	0.02	0	0.007	0.03	0.01	0	0	0.015	0	0	0	0	0	0.007
23	0	0	0	0	0	0.01	0.01	0	0	0	0	0	0	0	0.013	0
24	0.023	0.011	0	0	0	0	0	0.005	0	0	0	0	0	0	0	0
25	0	0.027	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0
26	0.011	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0.011	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	44	94	99	94	74	50	50	92	100	100	99	99	99	98	76	73
<i>n_a</i>	19	19	21	19	18	19	20	16	17	19	17	14	11	14	18	19
<i>n_{eff}</i>	N/A	9.54	10.74	10.25	11.40	9.17	9.86	4.54	6.82	5.12	4.46	6.26	2.99	6.99	12.04	11.68
<i>a</i>	N/A	12.70	13.21	12.69	12.53	13.13	13.40	9.32	10.57	11.37	8.80	9.09	6.61	9.51	13.34	13.09
<i>H_E</i>	N/A	0.895	0.907	0.902	0.912	0.891	0.899	0.780	0.853	0.805	0.776	0.840	0.665	0.857	0.917	0.914
<i>H_O</i>	N/A	0.894	0.909	0.862	0.919	0.940	0.860	0.793	0.830	0.800	0.778	0.808	0.636	0.918	0.882	0.945
<i>F_{IS}</i>	N/A	0.002	-0.002	0.045	-0.007	-0.056	0.043	-0.018	0.028	0.006	-0.003	0.038	0.044	-0.072	0.039	-0.034

Appendix II. Continued.

<i>Oki100</i>	Population																
	Allele	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0.003	0	0	0	0	0	0	0	0	0	0
4	0.023	0.063	0.024	0.034	0.071	0.034	0.043	0.043	0.068	0.011	0	0	0.033	0.035	0.027	0.047	
5	0.193	0.216	0.119	0.233	0.199	0.22	0.233	0.174	0.239	0.226	0.208	0.295	0.18	0.155	0.149	0.232	
6	0.051	0.011	0.06	0.026	0.019	0.017	0.01	0.033	0.028	0	0.01	0	0.053	0.025	0.034	0.021	
7	0.023	0.028	0.024	0.009	0.006	0.017	0.007	0.043	0.017	0.074	0.13	0.063	0.007	0.015	0.02	0.011	
8	0.108	0.068	0.131	0.095	0.122	0.093	0.07	0.065	0.074	0.058	0.052	0.058	0.1	0.125	0.095	0.032	
9	0.063	0.045	0.048	0.06	0.083	0.085	0.077	0.065	0.063	0.026	0.052	0.032	0.067	0.07	0.068	0.084	
10	0.108	0.085	0.131	0.121	0.096	0.059	0.097	0.087	0.114	0.053	0.057	0.032	0.107	0.085	0.101	0.142	
11	0.102	0.136	0.155	0.043	0.115	0.136	0.143	0.185	0.125	0.184	0.182	0.221	0.107	0.165	0.169	0.137	
12	0.063	0.074	0.048	0.069	0.051	0.076	0.06	0.065	0.045	0.053	0.01	0.037	0.087	0.1	0.081	0.042	
13	0.011	0.017	0.036	0.017	0.019	0.034	0.04	0.022	0.034	0.042	0.047	0.058	0.047	0.065	0.034	0.053	
14	0.045	0.068	0.071	0.043	0.045	0.076	0.03	0.043	0.063	0.042	0.021	0.026	0.02	0.02	0.041	0.047	
15	0.034	0.028	0.06	0.052	0.051	0.025	0.037	0.054	0.034	0.005	0.021	0	0.027	0.035	0.027	0.058	
16	0.057	0.063	0.048	0.052	0.026	0.025	0.037	0.076	0.017	0.047	0.042	0.053	0.04	0.02	0.061	0.032	
17	0.04	0.057	0.012	0.06	0.051	0.034	0.043	0.022	0.034	0.032	0.031	0.011	0.033	0.03	0.047	0.021	
18	0.017	0.006	0	0.043	0.013	0.008	0.027	0.022	0.011	0.026	0.01	0.042	0.027	0.03	0.027	0.021	
19	0.006	0	0	0.009	0.013	0.017	0.007	0	0.011	0.011	0	0.011	0.013	0.005	0.014	0.011	
20	0.017	0.006	0	0.017	0	0.008	0.02	0	0.017	0.005	0.005	0	0.02	0	0	0.005	
21	0.017	0.011	0.012	0.017	0.006	0.025	0.007	0	0.006	0.079	0.089	0.042	0	0.01	0	0	
22	0.011	0.006	0.024	0	0.013	0	0.003	0	0	0.026	0.021	0.021	0.027	0.01	0.007	0	
23	0.006	0.011	0	0	0	0	0.003	0	0	0	0.01	0	0	0	0	0.005	
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
25	0.006	0	0	0	0	0.008	0.003	0	0	0	0	0	0.007	0	0	0	
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>n</i>	88	88	42	58	78	59	150	46	88	95	96	95	75	100	74	95	
<i>n_a</i>	21	19	16	18	18	19	22	15	18	18	18	15	19	18	17	18	
<i>n_{eff}</i>	11.54	10.25	11.94	10.44	10.54	10.33	9.43	10.90	9.45	9.08	8.91	6.54	12.04	10.55	11.43	9.01	
<i>a</i>	13.41	12.47	12.74	13.19	12.31	12.97	12.48	12.54	12.39	12.27	11.73	10.89	13.39	12.23	12.74	11.96	
<i>H_E</i>	0.913	0.902	0.916	0.904	0.905	0.903	0.894	0.908	0.894	0.890	0.888	0.847	0.917	0.905	0.912	0.889	
<i>H_O</i>	0.898	0.886	0.929	0.879	0.808	0.847	0.847	0.957	0.875	0.874	0.833	0.832	0.880	0.860	0.919	0.842	
<i>F_{IS}</i>	0.017	0.018	-0.014	0.028	0.108*	0.062	0.053	-0.054	0.022	0.018	0.062	0.018	0.041	0.050	-0.007	0.053**	

Appendix II. Continued.

Allele	Population															
	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0.04	0.08	0.011	0.047	0.032	0.074	0	0	0	0	0.054	0.43	0.207	0.15	0.240	0.189
5	0.13	0.18	0.147	0.171	0.223	0.261	0.023	0.087	0.282	0.013	0.196	0.08	0.174	0.455	0.380	0.5
6	0.025	0.033	0.011	0.029	0.032	0.023	0	0.033	0.048	0.077	0.065	0.015	0	0.075	0.010	0.111
7	0.005	0.027	0.011	0.047	0.011	0.006	0	0.022	0.011	0	0.016	0	0	0.015	0.010	0.022
8	0.03	0.027	0.021	0.012	0.016	0.023	0	0.011	0	0	0.071	0	0.033	0.05	0.040	0.044
9	0.15	0.147	0.089	0.1	0.048	0.051	0.077	0.065	0.027	0.013	0.082	0	0.065	0.025	0.030	0.011
10	0.145	0.1	0.179	0.1	0.122	0.068	0.231	0.217	0.154	0.167	0.158	0	0.054	0.09	0.100	0.022
11	0.055	0.1	0.063	0.094	0.144	0.063	0.138	0.196	0.069	0.115	0.087	0	0.011	0.025	0.010	0.056
12	0.08	0.053	0.042	0.124	0.085	0.080	0.3	0.13	0.160	0.269	0.082	0.045	0.054	0.03	0.040	0.011
13	0.065	0.06	0.105	0.118	0.122	0.114	0.046	0.13	0.128	0.282	0.049	0.37	0.315	0.06	0.120	0.033
14	0.04	0.04	0.079	0.018	0.011	0.119	0.015	0.011	0.005	0.038	0.027	0	0	0.015	0.010	0
15	0.095	0.073	0.116	0.029	0.064	0.028	0.146	0	0	0.026	0.054	0	0	0.01	0	0
16	0.095	0.033	0.042	0.018	0.011	0.034	0.008	0.011	0	0	0.033	0	0.033	0	0.010	0
17	0.01	0.013	0.011	0.012	0.037	0.023	0	0.022	0.037	0	0.011	0.06	0.022	0	0	0
18	0.01	0	0.011	0.006	0	0.017	0	0.022	0.016	0	0.005	0	0.033	0	0	0
19	0.01	0.007	0.026	0.041	0.005	0	0.008	0	0.016	0	0.005	0	0	0	0	0
20	0	0.013	0.032	0.012	0.005	0.006	0.008	0.022	0.005	0	0	0	0	0	0	0
21	0	0	0	0.012	0.005	0.006	0	0	0.005	0	0.005	0	0	0	0	0
22	0.015	0	0	0.012	0	0	0	0.022	0.005	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	0	0.013	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0.016	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0.027	0	0	0	0	0	0	0
29	0	0	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0
<i>n</i>	100	75	95	85	94	88	65	46	94	39	92	100	46	100	50	45
<i>n_a</i>	17	17	18	19	19	18	11	15	17	9	17	6	11	12	12	10
<i>n_{eff}</i>	10.77	10.88	10.21	11.00	N/A	N/A	5.36	7.96	N/A	5.23	10.11	3.02	5.64	4.03	N/A	3.36
<i>a</i>	11.85	12.37	11.85	12.45	N/A	N/A	7.51	10.55	N/A	7.23	11.82	5.04	8.82	8.55	N/A	7.34
<i>H_E</i>	0.907	0.908	0.902	0.909	N/A	N/A	0.813	0.874	N/A	0.809	0.901	0.669	0.823	0.752	N/A	0.702
<i>H_O</i>	0.890	0.840	0.937	0.882	N/A	N/A	0.831	0.957	N/A	0.744	0.913	0.690	0.804	0.780	N/A	0.733
<i>F_{IS}</i>	0.019	0.075	-0.039**	0.030	N/A	N/A	-0.021	-0.095	N/A	0.082	-0.013	-0.031	0.023	-0.038	N/A	-0.045

Appendix II. Continued.

Allele	Population															
	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110
1	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0.01	0.007	0.002	0	0	0
3	0	0	0	0.018	0.01	0	0.023	0.021	0	0.01	0.014	0.025	0.068	0.013	0	0.013
4	0.065	0.035	0.016	0.106	0.052	0.05	0.128	0.053	0.052	0.091	0.028	0.055	0.081	0.145	0.11	0.087
5	0.254	0.26	0.277	0.288	0.188	0.42	0.453	0.479	0.604	0.455	0.479	0.441	0.432	0.289	0.3	0.4
6	0.020	0.095	0.043	0.035	0.01	0	0	0.043	0.052	0.035	0.035	0.048	0.081	0.039	0.07	0.025
7	0.028	0.02	0.016	0.012	0	0	0.047	0.021	0	0.01	0.042	0.017	0	0.026	0.03	0.037
8	0.053	0.05	0.037	0.029	0.094	0.08	0.047	0.043	0.031	0.015	0.028	0.028	0.041	0.026	0.02	0.013
9	0.095	0.07	0.032	0.094	0.052	0.06	0.07	0.021	0.063	0.056	0.056	0.053	0.041	0.092	0.07	0.063
10	0.181	0.135	0.128	0.147	0.177	0.08	0.047	0.043	0.042	0.096	0.077	0.111	0.108	0.053	0.07	0.113
11	0.098	0.115	0.096	0.076	0.104	0.13	0.093	0.074	0.052	0.066	0.134	0.097	0.068	0.066	0.06	0.025
12	0.083	0.09	0.138	0.065	0.125	0.09	0.07	0.117	0.042	0.035	0.063	0.039	0.054	0.066	0.13	0.025
13	0.048	0.045	0.112	0.018	0.063	0.08	0.012	0.043	0.021	0.02	0.007	0.027	0.014	0.039	0.03	0.113
14	0.038	0.04	0.027	0.076	0.01	0.01	0	0.032	0.021	0.066	0.014	0.038	0.014	0.039	0.03	0.05
15	0.003	0.005	0.011	0.018	0.021	0	0.012	0.011	0.021	0.02	0.014	0.013	0	0.039	0.05	0
16	0.005	0.015	0.011	0	0.094	0	0	0	0	0	0	0.005	0	0.026	0.01	0.025
17	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.013
18	0	0.005	0.011	0	0	0	0	0	0	0	0	0.002	0	0.013	0	0
19	0.005	0.01	0	0	0	0	0	0	0	0.015	0	0.002	0	0.013	0.01	0
20	0.013	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0
21	0.008	0.01	0.048	0.012	0	0	0	0	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0.013	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	199	100	94	85	48	50	43	47	48	99	71	320	37	38	50	40
<i>n_a</i>	17	16	15	15	13	9	11	13	11	15	14	17	11	17	15	14
<i>n_{eff}</i>	N/A	8.00	7.30	7.20	8.98	4.57	4.19	3.95	2.66	4.24	N/A	N/A	4.61	8.19	7.43	5.16
<i>a</i>	N/A	10.76	10.37	10.38	10.17	7.94	8.77	9.86	8.54	9.78	N/A	N/A	9.24	12.69	11.14	10.33
<i>H_E</i>	N/A	0.875	0.863	0.861	0.889	0.781	0.761	0.747	0.624	0.764	N/A	N/A	0.783	0.878	0.865	0.806
<i>H_O</i>	N/A	0.860	0.851	0.894	0.917	0.780	0.814	0.723	0.604	0.778	N/A	N/A	0.811	0.842	0.920	0.800
<i>F_{IS}</i>	N/A	0.017	0.014	-0.039	-0.032	0.001	-0.070	0.032	0.032	-0.018	N/A	N/A	-0.036	0.041	-0.064	0.008

Appendix II. Continued.

Allele	Population																Total
	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0.01	0.05	0	0	0	0	0	0	0	0
3	0.015	0.02	0	0.01	0.004	0	0.01	0	0	0.02	0	0	0	0	0	0	0
4	0.07	0.13	0.138	0.12	0.061	0.028	0.052	0.06	0.08	0.112	0.004	0.039	0.068	0.025	0.017	0.018	0.018
5	0.295	0.35	0.237	0.32	0.414	0.5	0.385	0.4	0.5	0.296	0.291	0.249	0.267	0.275	0.375	0.372	0.372
6	0.065	0.01	0.1	0	0.043	0.014	0.031	0	0	0.031	0.066	0.037	0.023	0	0.091	0.098	0.098
7	0.015	0.05	0.037	0	0.043	0.028	0.052	0.03	0	0.01	0.026	0.012	0.023	0	0.034	0.03	0.03
8	0.02	0.04	0.013	0.06	0.029	0.028	0.01	0.02	0.02	0.02	0.212	0.032	0.091	0.063	0.04	0.037	0.037
9	0.09	0.06	0.037	0.11	0.083	0.083	0.021	0.08	0.07	0.173	0.064	0.081	0.028	0.05	0.034	0.03	0.03
10	0.115	0.08	0.113	0.05	0.061	0.181	0.219	0.09	0.07	0.061	0.079	0.167	0.119	0.05	0.045	0.037	0.037
11	0.085	0.07	0.087	0.06	0.086	0	0.052	0.12	0.04	0.051	0.060	0.084	0.045	0.025	0.028	0.024	0.024
12	0.02	0.04	0.075	0.08	0.058	0.028	0.104	0.07	0.06	0.061	0.019	0.163	0.153	0.35	0.097	0.104	0.104
13	0.125	0.05	0.063	0.07	0.061	0.097	0.01	0.02	0.05	0.01	0.118	0.059	0.08	0.037	0.119	0.116	0.116
14	0.03	0.04	0.025	0.02	0.018	0	0.052	0.05	0.01	0.01	0.041	0.015	0.057	0.037	0.068	0.079	0.079
15	0.01	0.02	0.037	0.03	0	0	0	0.03	0.04	0.061	0.013	0.025	0.028	0	0.023	0.024	0.024
16	0.035	0.03	0.013	0.03	0.032	0	0	0.01	0.01	0.061	0.009	0.032	0	0	0	0	0
17	0	0.01	0	0	0.007	0.014	0	0.01	0	0.01	0	0.005	0	0	0	0	0
18	0	0	0.013	0.01	0	0	0	0	0	0.01	0	0	0.006	0.013	0	0	0
19	0.005	0	0.013	0.01	0	0	0	0	0	0	0	0	0.011	0.075	0.028	0.03	0.03
20	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	100	50	40	50	139	36	48	50	50	49	234	203	88	40	88	82	10272
<i>n_a</i>	16	15	15	16	14	10	12	14	12	16	13	14	14	11	13	13	29
<i>n_{eff}</i>	7.17	6.35	9.13	6.94	N/A	3.42	4.73	5.13	3.69	7.07	N/A	N/A	7.60	4.83	5.53	5.55	
<i>a</i>	10.53	11.31	11.45	11.08	N/A	7.63	8.75	10.06	9.24	10.94	N/A	N/A	10.40	8.91	10.11	10.01	
<i>H_E</i>	0.860	0.842	0.891	0.856	N/A	0.707	0.788	0.805	0.729	0.859	N/A	N/A	0.869	0.793	0.819	0.820	
<i>H_O</i>	0.920	0.920	0.825	0.900	N/A	0.611	0.688	0.840	0.780	0.796	N/A	N/A	0.898	0.675	0.773	0.768	
<i>F_{IS}</i>	-0.070	-0.093	0.074	-0.052	N/A	0.138	0.129*	-0.044	-0.071	0.074	N/A	N/A	-0.034	0.150*	0.057	0.063	

Appendix II. Continued.

<i>Ots103</i>	Size		Population														
	Allele	ABL	DFO	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	68	68		0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	84	84		0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	88	88		0	0	0	0	0	0.007	0.006	0	0	0	0	0	0	0
4	92	92	0.005	0.015	0.042	0.025	0.025	0.007	0	0	0.025	0	0	0	0	0	0.03
5	96	96	0	0.008	0.021	0.013	0	0.007	0.006	0.019	0.037	0.013	0.033	0.03	0	0	0
6	100	100	0.011	0.015	0.021	0.037	0.025	0.074	0.051	0.009	0.037	0.025	0.033	0.06	0.007	0	0
7	104	103	0.005	0.008	0.026	0	0	0.051	0.045	0.074	0.087	0.021	0.067	0.03	0.007	0.01	0
8	108	107	0.033	0.03	0.016	0	0.013	0.051	0.071	0.120	0.075	0.059	0.017	0	0	0	0
9	112	111	0.016	0.015	0.011	0.013	0.013	0.029	0.032	0.056	0.025	0.017	0	0.05	0.037	0	0
10	116	115	0.054	0.114	0.068	0.025	0.05	0.015	0.013	0.019	0.025	0.101	0.05	0.12	0.104	0.08	0
11	120	119	0.027	0.015	0.063	0.037	0.063	0.029	0.077	0.019	0.05	0.109	0.05	0.06	0.09	0.09	0
12	124	123	0.038	0.045	0.032	0.063	0.087	0.022	0.032	0.028	0.063	0.046	0.017	0.03	0.09	0.07	0
13	128	127	0.06	0.061	0.074	0.125	0.063	0.029	0.051	0	0.063	0.034	0.033	0.01	0.097	0.16	0
14	132	131	0.022	0.083	0.042	0.087	0.063	0.051	0.038	0.056	0.05	0.122	0	0.05	0.037	0.03	0
15	136	135	0.049	0.023	0.011	0.013	0.025	0.022	0.006	0.019	0	0.029	0.067	0.07	0.022	0.01	0
16	140	140	0.033	0.03	0.032	0	0	0.029	0.051	0.028	0	0.025	0.017	0.06	0	0	0
17	144	144	0.005	0.023	0.005	0	0	0.029	0	0.009	0.013	0.008	0.017	0	0	0	0
18	148	148	0.016	0.008	0.005	0	0	0	0.006	0.009	0	0.013	0.017	0.03	0.037	0.01	0
19	152	152	0.103	0.091	0.011	0	0	0	0.038	0	0.013	0.004	0.033	0.02	0.03	0.01	0
20	156	156	0	0.015	0.042	0.025	0.013	0.007	0.013	0	0.037	0	0.017	0.02	0	0.02	0
21	160	160	0	0	0	0.013	0	0.059	0.019	0.037	0	0.013	0.017	0.01	0.037	0.06	0
22	164	165	0.011	0.008	0.058	0.013	0.025	0.037	0.045	0.019	0	0.013	0	0	0.067	0.03	0
23	168	169	0.087	0.098	0.032	0.037	0.037	0.029	0.077	0.046	0.025	0.013	0	0	0.03	0.04	0
24	172	173	0.071	0.03	0.016	0.025	0.075	0.044	0.006	0.065	0.025	0.013	0	0	0.007	0.01	0
25	176	177	0.071	0.015	0	0	0.013	0.022	0.013	0	0.037	0.004	0	0	0	0	0
26	180	181	0.043	0.015	0.026	0	0.025	0.007	0.006	0.037	0.025	0	0	0	0	0.01	0
27	184	184	0.005	0	0.053	0.05	0.037	0.007	0.019	0.028	0	0.008	0	0	0	0	0
28	188	188	0	0.038	0.037	0.05	0.075	0.015	0.019	0.009	0.025	0	0	0	0.015	0.04	0
29	192	192	0.022	0.038	0.011	0.013	0.013	0.015	0.019	0	0	0.017	0	0	0	0	0
30	196	196	0	0.008	0	0	0	0.007	0	0	0	0.004	0	0	0	0	0
31	200	200	0	0	0	0	0	0.022	0.032	0.009	0.025	0.004	0.033	0	0	0	0
32	204	203	0	0	0.005	0	0.013	0	0	0.009	0	0.008	0	0	0.007	0.02	0
33	208	207	0	0.008	0.037	0	0.113	0.007	0.006	0	0	0.013	0	0.02	0	0.01	0
34	212	212	0.005	0.008	0.011	0.075	0	0	0	0	0.025	0.008	0	0.03	0.015	0.04	0
35	216	216	0.011	0.015	0	0	0	0	0.006	0.046	0.025	0.021	0	0.02	0	0	0
36	220	220	0.033	0.015	0.016	0.037	0.025	0.022	0.026	0.028	0	0.046	0.017	0.03	0	0	0
37	224	224	0.011	0.008	0	0	0	0.059	0.058	0.046	0.025	0.029	0.083	0.06	0.007	0.04	0
38	228	228	0.011	0.015	0.026	0.025	0	0	0.006	0.074	0.025	0.050	0.033	0.01	0.022	0.02	0
39	232	231	0.011	0.015	0.005	0.025	0	0.066	0.032	0.009	0.063	0.029	0.133	0.07	0.015	0.03	0
40	236	235	0.043	0.015	0.042	0.075	0.037	0.015	0.019	0.028	0	0.034	0.1	0.04	0.052	0.02	0
41	240	239	0.022	0.038	0	0	0.013	0.022	0.013	0.009	0.037	0.021	0.017	0.02	0.03	0.01	0
42	244	243	0.016	0	0.042	0.013	0.025	0.007	0	0.019	0.025	0	0	0.02	0.015	0.02	0
43	248	247	0	0	0.011	0.05	0.013	0.015	0	0	0	0.013	0.033	0.01	0.06	0.03	0
44	252	251	0.016	0.015	0.026	0.013	0	0.007	0.006	0	0	0	0.017	0.01	0.022	0	0
45	256	255	0.016	0	0.005	0	0	0.044	0.013	0	0	0.004	0.033	0.01	0.037	0.05	0
46	260	259	0.011	0	0.016	0	0	0.007	0.013	0	0.013	0	0.017	0	0	0	0
47	264	263	0	0	0	0	0	0	0.006	0.019	0	0.004	0	0	0	0	0
48	268	267	0.005	0	0	0	0	0	0	0	0	0.004	0	0	0	0	0
49	272	271	0	0	0	0.025	0.025	0	0	0	0	0	0	0	0	0	0
50	276	275	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0
51	280	279	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>			92	66	95	40	40	68	78	54	40	119	30	50	67	50	
<i>n_a</i>			35	35	37	27	27	38	38	31	28	38	26	28	27	28	
<i>n_{eff}</i>			22.30	20.88	28.41	22.10	22.57	30.70	27.11	N/A	29.81	N/A	22.40	22.71	19.08	18.07	
<i>a</i>			18.44	18.54	19.90	18.31	18.26	20.54	19.69	N/A	19.98	N/A	18.86	18.32	16.90	17.52	
<i>H_E</i>			0.955	0.952	0.965	0.955	0.956	0.967	0.963	N/A	0.966	N/A	0.955	0.956	0.948	0.945	
<i>H_O</i>			0.978	0.955	0.989	0.925	0.925	0.941	1.000	N/A	0.875	N/A	0.833	0.940	0.925	1.000	
<i>F_{IS}</i>			-0.024	-0.003	-0.026	0.032	0.033	0.027	-0.039	N/A	0.096	N/A	0.130	0.017	0.024	-0.059	

Appendix II. Continued.

Allele	Population															
	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007
4	0.016	0	0	0.011	0	0	0	0	0	0	0	0.007	0	0.011	0.039	0.025
5	0	0	0	0.011	0.098	0.031	0.093	0.02	0.021	0.023	0.022	0.029	0.1	0	0.033	0.051
6	0	0.057	0.022	0.057	0.087	0.052	0.093	0.06	0.094	0.205	0.152	0.021	0.1	0.089	0.204	0.116
7	0.008	0.057	0.109	0.091	0.043	0.073	0.13	0.08	0.031	0.023	0	0.043	0.057	0.111	0.112	0.106
8	0	0.029	0	0.148	0.141	0.063	0.056	0.04	0.021	0.023	0.033	0.057	0.014	0.078	0.118	0.056
9	0.04	0.029	0.13	0.148	0.12	0.073	0.093	0.12	0.063	0.091	0.13	0.05	0.086	0.044	0.053	0.04
10	0.073	0.143	0.196	0.057	0.011	0.042	0.111	0	0.042	0.023	0.054	0.05	0.029	0.022	0.026	0.051
11	0.097	0.057	0.152	0.034	0.043	0.042	0.037	0.02	0.031	0.045	0.043	0.057	0.071	0.067	0.02	0.086
12	0.056	0.071	0.109	0.023	0.011	0.042	0.019	0.04	0.01	0	0.011	0.036	0.029	0.011	0.013	0.035
13	0.113	0.057	0.022	0	0	0.031	0	0	0.01	0	0	0.071	0.014	0.044	0.039	0.025
14	0.056	0	0	0	0	0.021	0.037	0	0	0	0.011	0.071	0.014	0.011	0.02	0.01
15	0.016	0.029	0.043	0	0	0	0	0.08	0.031	0.091	0.011	0.043	0	0	0.013	0
16	0	0	0	0	0	0.01	0	0.02	0.01	0	0	0.007	0.014	0	0	0
17	0	0.029	0	0	0.011	0	0	0	0.01	0	0	0.007	0	0	0	0
18	0.008	0.014	0	0	0	0	0	0	0.01	0	0	0	0	0.011	0	0
19	0.008	0	0	0	0	0	0	0.08	0.021	0	0.011	0	0.014	0.011	0	0.015
20	0.008	0	0	0	0.011	0	0	0.06	0.031	0.023	0	0	0.014	0.022	0	0
21	0.048	0.014	0	0.011	0.033	0	0	0	0	0	0	0	0	0	0	0.005
22	0.048	0.057	0.043	0.023	0	0.01	0	0	0	0	0	0.007	0.029	0.044	0	0.04
23	0.048	0.014	0	0.034	0	0	0	0.02	0.01	0.045	0.033	0.021	0	0.011	0	0.015
24	0.008	0	0	0.057	0.043	0.031	0.019	0	0.031	0.023	0.022	0.014	0.029	0.033	0.007	0.015
25	0	0	0	0.057	0.043	0.042	0.037	0	0.01	0	0.033	0.021	0.014	0.011	0	0.025
26	0	0	0	0	0.022	0.042	0.019	0	0.031	0.023	0.022	0.029	0.029	0.022	0	0.01
27	0	0	0.022	0.045	0.011	0	0.056	0.02	0.031	0.023	0.033	0.014	0.029	0.044	0.013	0.01
28	0.016	0	0	0.011	0.065	0	0.056	0	0.021	0.023	0.022	0.029	0.1	0.056	0.053	0.01
29	0.008	0	0.022	0.011	0.022	0.021	0.019	0.02	0.063	0	0.033	0.029	0.014	0.044	0.039	0.005
30	0	0	0	0	0.022	0.031	0	0.04	0.042	0.023	0.033	0.021	0.014	0.067	0.02	0.015
31	0.008	0	0	0.011	0.011	0.021	0	0.02	0.063	0.068	0.022	0.014	0.029	0.011	0.033	0.025
32	0	0.014	0.022	0.034	0.011	0.031	0	0.02	0.031	0.045	0.022	0.057	0.029	0.044	0.02	0.025
33	0.008	0	0	0.034	0.011	0.031	0	0	0	0	0.043	0.021	0.014	0.022	0.053	0.04
34	0.016	0	0	0.034	0	0.021	0	0.02	0.021	0	0	0.007	0.057	0.011	0.026	0.04
35	0	0	0	0.023	0.011	0	0.019	0.02	0.021	0.045	0.033	0.029	0.029	0	0.026	0.025
36	0	0	0	0.011	0	0.052	0	0.06	0.042	0.023	0.022	0.021	0	0	0	0.015
37	0	0	0	0	0	0.01	0	0.04	0.031	0	0.043	0.007	0.014	0.022	0.007	0.025
38	0	0.014	0.043	0	0.087	0.042	0.019	0.02	0.01	0	0.011	0	0	0.011	0	0
39	0	0.071	0.022	0	0.022	0.031	0.037	0	0.021	0.068	0.043	0.007	0	0	0	0.015
40	0.048	0.043	0	0.023	0	0.042	0.019	0.02	0.01	0	0	0.029	0	0	0	0.01
41	0.04	0.057	0	0	0	0.01	0	0	0.01	0	0.022	0.021	0	0.011	0	0.005
42	0.065	0.029	0	0	0	0	0.019	0	0	0	0.011	0.021	0.014	0	0	0.005
43	0.048	0.057	0	0	0.011	0.021	0	0	0.021	0.045	0	0.021	0	0	0	0
44	0.008	0.014	0	0	0	0.01	0	0.02	0	0	0.011	0.007	0	0	0	0
45	0.073	0.043	0.022	0	0	0.01	0.019	0	0.021	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0.022	0	0	0	0	0.04	0.021	0	0.011	0	0	0	0	0
48	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0.008	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	62	35	23	44	46	48	27	25	48	22	46	70	35	45	76	99
<i>n_a</i>	28	23	16	24	25	31	21	25	36	21	30	36	28	29	25	33
<i>n_{eff}</i>	19.16	N/A	10.89	15.37	15.45	31.45	18.11	26.06	33.53	16.03	19.03	30.22	22.16	22.50	12.26	20.11
<i>a</i>	16.68	N/A	13.30	16.10	15.67	20.31	16.47	19.53	21.45	17.61	18.68	20.37	18.61	18.28	15.10	17.96
<i>H_E</i>	0.948	N/A	0.908	0.935	0.935	0.968	0.945	0.962	0.970	0.938	0.947	0.967	0.955	0.956	0.918	0.950
<i>H_O</i>	0.903	N/A	0.870	0.932	1.000	0.958	1.000	0.960	0.979	0.909	0.870	0.943	0.914	0.933	0.947	0.949
<i>F_{IS}</i>	0.047	N/A	0.043	0.003	-0.070	0.010	-0.060	0.002	-0.009	0.031	0.083	0.025	0.043	0.024	-0.032	0.001

Appendix II. Continued.

Allele	Population															
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0.022	0	0	0	0	0	0	0	0	0	0	0	0
4	0.021	0.057	0.01	0.011	0.004	0.019	0	0	0.01	0.003	0.016	0.015	0.015	0.008	0.002	0.004
5	0.073	0.071	0.071	0.022	0.045	0.039	0.005	0.005	0.03	0.010	0.065	0.005	0.02	0.016	0.018	0.015
6	0.083	0.129	0.082	0.065	0.174	0.084	0.065	0.027	0.01	0.348	0.027	0.005	0.02	0.010	0.018	0.004
7	0.083	0.1	0.133	0.087	0.089	0.097	0.065	0.038	0.035	0.045	0.054	0.03	0.1	0.048	0.062	0.023
8	0.063	0.029	0.061	0.098	0.08	0.045	0.076	0.103	0.051	0.073	0.032	0.065	0.12	0.094	0.074	0.070
9	0.042	0.043	0.031	0.054	0.036	0.045	0.022	0.022	0.02	0.013	0.016	0.09	0.03	0.052	0.044	0.057
10	0.052	0.029	0.051	0.022	0.089	0.078	0.054	0.103	0.086	0.031	0.102	0.08	0.055	0.049	0.076	0.066
11	0.021	0.029	0.051	0.033	0.067	0.097	0.011	0	0.02	0	0	0.02	0	0.024	0.018	0.013
12	0.031	0.014	0.031	0.054	0.045	0.071	0	0	0.01	0.013	0.032	0.015	0	0.011	0.009	0.011
13	0.052	0.029	0.02	0.033	0.013	0.006	0	0.033	0	0.005	0.005	0.015	0	0.006	0.007	0.025
14	0	0.029	0.01	0.022	0.022	0.026	0.016	0.022	0.005	0.003	0.011	0.005	0.005	0.011	0.007	0.006
15	0	0	0	0.011	0	0.006	0.06	0	0.005	0	0	0	0.015	0.003	0.002	0
16	0	0	0.02	0	0.009	0.006	0	0	0	0	0.011	0.01	0	0.003	0	0.002
17	0	0	0	0	0	0	0	0.005	0.01	0	0.005	0.005	0	0.001	0.014	0.006
18	0.01	0	0	0	0.004	0	0	0	0.015	0	0.022	0.025	0	0.014	0.005	0.009
19	0.01	0	0	0	0	0.006	0	0	0.02	0.018	0.005	0.015	0.005	0.013	0.012	0.013
20	0.01	0	0	0	0.013	0	0	0.027	0.005	0.026	0	0	0.01	0.011	0.009	0.008
21	0.031	0.029	0.01	0.011	0	0	0.033	0.022	0.01	0.076	0.022	0.015	0.005	0.013	0.016	0.026
22	0.01	0.029	0.01	0.011	0.004	0.006	0	0.005	0.02	0.005	0.022	0.01	0.005	0.008	0.005	0.015
23	0	0.014	0.031	0	0.004	0	0.168	0.109	0.076	0.021	0.022	0.03	0.055	0.029	0.037	0.043
24	0.01	0.071	0.01	0.033	0.027	0.058	0.071	0.033	0.051	0.081	0.032	0.085	0.09	0.096	0.069	0.064
25	0.01	0.014	0.01	0.043	0.018	0.032	0.049	0.196	0.162	0.068	0.14	0.08	0.11	0.119	0.143	0.115
26	0.01	0.029	0.02	0.033	0.013	0.013	0.098	0.065	0.111	0.018	0.134	0.1	0.1	0.100	0.074	0.123
27	0.01	0	0.051	0.011	0.036	0.045	0.005	0.054	0.101	0.013	0.043	0.12	0.03	0.078	0.048	0.074
28	0.01	0.014	0.01	0.065	0.036	0.032	0.038	0.065	0.04	0.016	0.011	0.04	0.04	0.034	0.041	0.038
29	0.021	0.043	0.02	0	0.04	0.071	0.022	0.022	0.015	0.086	0.065	0.01	0.02	0.023	0.032	0.028
30	0.021	0.043	0.041	0.033	0.018	0.006	0.103	0	0	0.016	0.005	0.02	0.01	0.011	0.018	0.025
31	0.031	0.014	0.041	0.033	0.022	0.026	0.011	0.016	0.04	0.003	0.011	0.025	0.035	0.024	0.035	0.036
32	0.01	0.029	0.031	0.033	0.018	0.019	0	0	0	0	0.027	0.005	0.03	0.006	0.023	0.009
33	0.073	0	0.061	0.043	0.013	0.006	0	0	0.015	0.003	0.016	0.005	0.01	0.013	0.032	0.011
34	0.063	0	0.02	0	0.018	0.032	0.005	0	0	0	0.011	0.005	0	0.013	0.009	0.002
35	0.01	0	0.01	0.022	0	0	0	0	0	0	0.005	0	0.01	0.003	0.002	0.006
36	0.021	0.014	0.02	0.033	0.004	0	0.011	0.005	0	0.003	0.005	0	0.01	0.003	0.002	0.006
37	0.021	0.029	0.02	0.011	0.004	0.006	0	0	0	0.003	0.005	0.03	0.03	0.023	0.023	0.026
38	0.021	0.014	0.01	0.022	0	0.006	0	0.011	0.005	0	0.011	0	0.005	0.015	0.005	0.011
39	0.042	0.029	0	0	0	0	0	0	0	0	0.005	0.015	0.005	0.003	0.005	0.008
40	0.021	0.014	0	0.011	0.004	0.006	0.011	0.005	0	0	0.005	0.005	0	0	0	0.004
41	0	0.014	0	0.011	0.013	0	0	0	0.015	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0.001	0.002	0
43	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0.013	0	0	0	0.005	0	0	0	0.005	0	0	0
45	0	0	0	0	0	0	0	0.005	0	0	0	0	0	0.006	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	48	35	49	46	112	77	92	92	99	191	93	100	100	395	217	265
<i>n_a</i>	32	28	30	31	32	29	22	24	29	26	34	32	30	39	36	36
<i>n_{eff}</i>	25.76	23.45	21.80	26.83	14.98	18.79	13.14	11.71	14.12	N/A	15.57	16.60	15.45	N/A	N/A	N/A
<i>a</i>	19.29	19.27	18.51	19.66	16.30	16.55	13.94	13.92	15.40	N/A	16.57	16.20	15.62	N/A	N/A	N/A
<i>H_E</i>	0.961	0.957	0.954	0.963	0.933	0.947	0.924	0.915	0.929	N/A	0.936	0.940	0.935	N/A	N/A	N/A
<i>H_O</i>	0.958	1.000	0.959	0.957	0.938	0.935	0.935	0.902	0.909	N/A	0.946	0.910	0.880	N/A	N/A	N/A
<i>F_{IS}</i>	0.003	-0.045	-0.005	0.007	-0.005	0.012	-0.012	0.014	0.022	N/A	-0.011	0.032*	0.059	N/A	N/A	N/A

Appendix II. Continued.

<i>Ots103</i>	Population																
	Allele	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0.005	0.005	0	0	0	0	0	0	0	0	0	0	0	0.007	0	0
5	0.011	0.005	0.01	0.005	0.034	0	0.02	0	0	0	0	0	0	0.005	0.007	0.021	0
6	0.023	0.043	0.01	0.021	0.02	0.02	0.03	0.027	0.03	0.04	0.02	0.066	0.025	0.035	0.02	0.007	0
7	0.023	0.048	0.01	0.011	0.047	0.02	0.03	0.055	0.035	0.01	0.071	0.081	0.02	0.197	0.033	0.007	0
8	0.045	0.048	0.07	0.059	0.041	0.04	0.06	0.06	0.07	0.05	0.025	0.081	0.01	0.121	0.053	0.062	0
9	0.102	0.053	0.07	0.08	0.047	0.04	0.08	0.066	0.015	0.045	0.03	0.005	0.035	0.01	0.059	0.055	0
10	0.080	0.101	0.065	0.032	0.054	0.04	0.06	0.071	0.055	0.035	0.03	0.045	0	0.025	0.066	0.062	0
11	0	0.005	0.025	0.011	0.02	0.03	0.02	0.033	0.015	0.01	0.061	0.04	0.061	0.045	0.013	0.007	0
12	0.011	0.021	0.015	0	0.02	0	0.02	0.005	0	0	0.02	0.015	0.005	0	0.013	0.048	0
13	0.023	0.011	0.01	0.005	0.014	0	0.01	0.022	0	0.01	0.056	0.04	0	0.01	0.02	0.027	0
14	0	0	0	0.005	0.007	0	0	0	0	0.005	0	0.005	0	0	0.007	0	0
15	0.011	0.005	0.005	0	0	0	0.01	0	0	0	0.02	0.005	0	0	0	0.007	0
16	0	0	0	0.005	0.007	0	0	0.005	0.005	0.005	0.04	0.02	0.02	0	0	0	0
17	0.080	0.011	0.02	0.016	0.027	0.01	0	0.016	0.02	0.045	0.025	0.061	0.152	0.101	0.02	0	0
18	0.023	0.027	0.04	0.011	0.007	0	0.01	0.033	0.02	0.005	0.02	0.02	0.045	0.04	0.007	0	0
19	0.023	0.021	0.025	0	0.007	0	0.03	0.011	0.03	0.005	0.015	0.071	0.02	0.015	0.02	0.027	0
20	0	0.016	0	0	0.007	0	0	0	0.015	0.005	0.01	0.01	0	0	0	0.014	0
21	0	0.011	0.005	0.011	0	0.01	0	0	0.005	0.01	0	0	0	0	0.007	0	0
22	0.011	0.005	0.02	0.016	0.014	0.02	0	0	0	0	0.01	0.005	0	0	0	0.007	0
23	0.034	0.043	0.015	0.027	0.047	0.01	0.04	0.027	0.015	0.01	0.04	0.015	0.126	0.025	0.053	0.007	0
24	0.068	0.101	0.095	0.101	0.088	0.07	0.04	0.115	0.225	0.105	0.076	0.02	0.025	0.03	0.053	0.068	0
25	0.136	0.09	0.115	0.106	0.081	0.15	0.08	0.104	0.125	0.085	0.116	0.101	0.172	0.076	0.092	0.11	0
26	0.045	0.096	0.095	0.16	0.074	0.11	0.09	0.093	0.12	0.165	0.086	0.071	0.035	0.111	0.105	0.103	0
27	0.045	0.037	0.07	0.074	0.068	0.07	0.08	0.121	0.065	0.11	0.106	0.101	0.045	0.061	0.086	0.082	0
28	0.034	0.037	0.07	0.048	0.047	0.07	0.05	0.055	0.045	0.04	0.045	0.045	0.005	0.01	0.039	0.055	0
29	0.045	0.032	0.02	0.016	0.02	0.12	0.07	0.033	0.015	0.07	0.04	0.005	0	0.045	0.033	0.062	0
30	0.011	0.037	0.015	0.032	0.047	0.04	0.04	0.005	0.02	0.045	0.015	0.03	0.081	0.01	0.039	0.041	0
31	0.045	0.016	0.015	0.043	0.027	0.02	0.04	0.016	0.01	0.04	0	0.01	0.005	0.02	0.02	0.034	0
32	0	0.016	0.025	0.037	0.02	0.01	0.02	0.005	0.01	0.015	0.015	0.015	0.051	0.005	0.026	0.027	0
33	0.011	0.011	0	0	0.014	0.01	0	0.011	0.025	0.015	0.01	0.01	0.056	0	0.02	0.021	0
34	0.011	0.005	0.005	0.011	0	0.01	0	0.005	0.005	0.01	0	0	0	0	0.013	0.007	0
35	0	0.005	0	0.005	0.02	0	0	0	0.005	0	0	0	0	0	0.007	0.014	0
36	0	0.011	0.01	0.021	0.027	0.02	0.02	0	0	0.01	0	0	0	0	0.013	0.007	0
37	0.034	0.005	0.02	0.021	0.02	0.03	0.03	0	0	0	0	0	0	0	0.033	0	0
38	0	0.011	0.015	0.005	0.02	0.01	0.02	0	0	0	0	0	0	0	0	0.007	0
39	0	0.011	0.005	0.005	0.007	0.02	0	0	0	0	0.005	0	0	0	0	0	0
40	0.011	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0.02	0.007	0
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	44	94	100	94	74	50	50	91	100	100	99	99	99	99	76	73	
<i>n_a</i>	26	34	32	30	32	25	25	24	25	27	25	27	21	21	31	29	
<i>n_{eff}</i>	N/A	19.11	17.47	14.60	24.34	15.23	22.20	14.76	10.35	13.57	17.40	17.41	11.24	10.97	21.06	18.51	
<i>a</i>	N/A	17.34	16.53	15.65	18.76	15.83	17.60	14.65	13.86	14.74	16.15	15.88	13.21	13.13	17.87	16.53	
<i>H_E</i>	N/A	0.948	0.943	0.932	0.959	0.934	0.955	0.932	0.903	0.926	0.943	0.943	0.911	0.909	0.953	0.946	
<i>H_O</i>	N/A	0.926	0.960	0.979	0.946	0.940	0.940	0.945	0.920	0.910	0.929	0.939	0.919	0.889	0.974	0.959	
<i>F_{IS}</i>	N/A	0.023	-0.018	-0.051	0.014	-0.006	0.016	-0.014	-0.018	0.018	0.014	0.003	-0.009	0.022	-0.022	-0.014	

Appendix II. Continued.

Allele	Population															
	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78
1	0	0	0	0	0	0	0.003	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0.006	0	0	0	0	0	0	0
5	0.011	0.028	0.012	0	0.019	0.009	0.007	0	0.017	0	0	0	0.007	0.015	0	0.005
6	0.011	0.017	0.012	0.035	0.006	0.036	0.034	0.01	0.017	0	0	0	0.04	0.01	0.007	0.016
7	0.059	0.039	0.048	0.009	0.026	0.036	0.037	0.083	0.017	0.016	0.026	0.026	0.047	0.06	0.035	0.053
8	0.054	0.062	0.024	0.061	0.091	0.064	0.047	0.021	0.063	0.016	0.057	0.042	0.027	0.06	0.042	0.053
9	0.081	0.056	0.048	0.044	0.039	0.064	0.037	0.063	0.028	0.01	0.042	0.053	0.067	0.05	0.035	0.089
10	0.043	0.028	0.048	0.044	0.045	0.018	0.064	0.031	0.04	0.026	0.031	0.005	0.02	0.045	0.042	0.042
11	0.043	0.022	0.036	0.018	0.006	0.027	0.013	0.031	0.023	0.01	0.073	0.032	0.02	0.025	0.028	0.016
12	0.005	0.022	0	0.07	0.013	0.009	0.02	0.021	0.006	0.078	0.026	0.058	0.027	0.02	0.021	0.037
13	0.022	0.022	0.012	0.009	0.013	0.018	0.02	0.031	0.028	0.026	0.026	0.037	0.013	0.025	0.028	0.026
14	0	0.006	0.024	0	0	0	0.01	0	0.006	0.016	0.031	0.016	0.007	0.015	0	0
15	0.016	0.006	0	0.006	0	0.007	0	0	0.005	0	0	0	0.007	0	0.014	0.005
16	0	0.006	0	0	0	0.018	0.007	0.01	0.006	0	0.005	0	0	0.005	0	0
17	0.005	0.039	0.024	0.035	0.019	0.027	0.007	0.031	0.017	0.005	0.005	0.016	0	0.005	0.014	0.005
18	0.005	0.011	0.024	0	0	0.009	0.02	0.021	0.023	0	0	0.011	0	0.005	0.014	0
19	0.016	0.022	0.012	0.009	0.006	0.018	0.003	0.021	0.023	0.016	0.005	0.011	0.013	0.015	0.028	0
20	0.005	0	0	0	0	0.009	0.017	0.01	0.017	0.031	0	0	0.013	0	0.007	0
21	0.016	0.011	0	0.009	0.013	0.009	0	0	0	0	0.01	0.005	0.007	0.02	0	0.011
22	0.016	0	0.012	0.026	0.026	0.009	0.01	0.01	0	0.01	0.057	0.026	0.02	0.02	0.007	0.005
23	0.022	0.017	0	0	0.019	0.027	0.017	0.021	0.034	0.031	0.036	0.063	0.027	0.01	0.021	0.042
24	0.043	0.073	0.024	0.088	0.052	0.1	0.047	0.073	0.097	0.109	0.13	0.074	0.06	0.075	0.076	0.105
25	0.118	0.079	0.167	0.105	0.104	0.082	0.097	0.094	0.097	0.161	0.151	0.111	0.107	0.065	0.083	0.026
26	0.113	0.129	0.107	0.132	0.078	0.1	0.117	0.083	0.074	0.161	0.068	0.126	0.08	0.1	0.056	0.116
27	0.059	0.101	0.119	0.035	0.045	0.055	0.101	0.083	0.097	0.115	0.052	0.142	0.127	0.105	0.083	0.084
28	0.038	0.017	0.048	0.035	0.078	0.045	0.05	0.031	0.028	0.042	0.068	0.074	0.06	0.055	0.069	0.053
29	0.059	0.039	0.048	0.07	0.052	0.018	0.044	0.052	0.063	0.016	0.021	0.037	0.033	0.035	0.069	0.032
30	0.038	0.039	0.012	0.044	0.045	0.055	0.044	0.063	0.028	0.052	0.057	0.026	0.033	0.03	0.021	0.074
31	0.011	0.045	0.06	0.035	0.052	0.018	0.017	0.063	0.034	0.01	0.016	0.005	0.033	0.03	0.035	0.021
32	0.027	0	0.012	0.026	0.032	0.018	0.037	0	0.011	0.005	0.005	0	0.013	0.01	0.021	0.016
33	0.011	0.011	0.012	0.009	0.026	0.027	0.003	0	0.006	0.005	0	0	0.007	0.005	0.014	0.005
34	0	0.006	0	0.009	0.019	0.018	0.013	0.01	0.017	0.005	0	0.005	0.007	0.005	0.007	0.011
35	0.011	0	0.012	0.009	0.006	0	0.007	0.01	0.028	0.021	0	0	0.007	0.01	0.028	0.011
36	0.011	0.022	0	0.009	0.019	0.018	0.02	0.01	0.011	0	0	0	0.027	0.025	0.042	0.005
37	0.011	0.006	0.012	0.009	0.019	0.027	0.017	0	0.006	0	0	0	0.027	0.02	0.007	0.021
38	0.011	0.011	0.024	0	0	0.009	0.007	0	0.006	0	0	0	0.007	0.025	0.035	0.016
39	0.005	0.006	0	0	0.013	0	0	0.01	0.017	0	0	0	0	0	0	0
40	0	0	0	0.009	0.006	0	0	0	0.006	0	0	0	0.007	0	0.007	0
41	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0
42	0	0	0.012	0	0	0	0	0	0	0	0	0	0.007	0	0	0
43	0	0	0	0.009	0	0	0	0	0.006	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	93	89	42	57	77	55	149	48	88	96	96	95	75	100	72	95
<i>n_a</i>	33	31	27	28	31	31	34	27	35	26	23	23	33	32	32	29
<i>n_{eff}</i>	18.62	18.53	15.77	17.89	21.23	22.71	18.56	21.11	20.87	11.29	14.30	13.73	19.17	20.33	23.94	17.23
<i>a</i>	17.24	17.20	16.87	16.69	17.89	18.62	17.24	17.46	18.16	13.77	14.78	14.34	17.65	17.64	18.65	16.24
<i>H_E</i>	0.946	0.946	0.937	0.944	0.953	0.956	0.946	0.953	0.952	0.911	0.930	0.927	0.948	0.951	0.958	0.942
<i>H_O</i>	0.935	0.933	0.905	0.965	0.974	0.982	0.926	0.979	0.943	0.875	0.885	0.947	0.933	0.960	0.972	0.947
<i>F_{IS}</i>	0.011	0.014	0.034	-0.022	-0.022	-0.027	0.021	-0.028	0.009	0.040	0.048	-0.022	0.015	-0.010	-0.015	-0.006

Appendix II. Continued.

Allele	Population															
	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0.01	0.010	0
4	0	0	0	0.006	0	0.006	0	0.011	0.054	0	0.005	0	0	0	0.020	0.011
5	0.02	0.013	0	0	0.005	0.006	0	0.011	0.027	0	0.005	0.05	0	0.015	0.010	0.022
6	0.005	0	0	0.047	0.016	0.034	0.008	0	0.005	0.013	0.011	0.005	0.149	0.04	0.080	0.022
7	0	0	0.053	0.041	0.011	0.017	0.023	0.022	0	0.026	0.033	0	0.011	0.045	0.020	0.011
8	0.03	0.073	0.048	0.07	0.016	0.023	0	0.033	0	0.013	0.054	0	0.043	0.02	0.020	0.067
9	0.035	0.02	0.176	0.081	0.103	0.080	0.046	0.011	0.043	0.115	0.082	0.155	0.085	0.025	0.060	0.056
10	0.02	0.073	0.053	0.035	0.038	0.017	0.031	0.033	0.022	0.026	0.092	0.01	0.043	0.06	0.050	0.033
11	0.02	0.04	0.037	0.006	0.027	0.006	0	0.054	0.038	0	0.049	0	0	0.015	0.010	0.022
12	0.091	0.12	0.032	0.052	0	0.011	0.031	0.033	0.016	0.154	0.022	0.005	0.011	0.005	0	0.033
13	0.03	0.06	0.021	0.052	0	0.011	0	0.022	0.016	0.013	0.016	0	0.021	0	0.020	0
14	0.035	0.047	0.027	0.029	0.016	0.006	0	0.011	0.016	0.013	0.016	0.01	0.011	0.02	0.020	0.011
15	0.005	0	0	0	0.011	0.006	0.008	0.022	0.005	0.064	0	0	0.011	0.02	0.020	0
16	0	0.033	0	0	0.005	0.006	0.031	0.022	0	0.077	0	0	0	0	0	0
17	0.025	0.013	0.011	0	0	0	0.169	0.043	0.011	0.038	0.033	0	0	0.01	0	0.011
18	0.015	0.027	0.005	0.041	0.016	0.006	0.077	0.033	0.011	0.013	0	0.04	0	0.015	0	0.033
19	0.02	0.013	0.048	0.006	0.071	0.080	0.108	0.011	0.005	0.013	0	0.005	0	0.01	0	0
20	0	0.013	0.005	0.006	0.033	0.052	0.123	0.033	0.016	0.013	0.011	0.01	0	0.01	0.010	0.033
21	0.005	0	0.037	0.041	0.022	0.006	0.085	0.065	0.022	0.013	0.005	0.035	0.064	0.025	0.030	0.033
22	0.02	0.013	0.059	0.07	0.043	0.023	0.031	0.098	0.027	0.077	0.049	0.015	0	0.035	0.050	0.011
23	0.015	0.013	0.021	0.029	0.043	0.052	0.023	0.011	0.033	0.077	0.065	0.1	0.064	0.025	0.020	0.078
24	0.015	0.047	0	0.023	0.082	0.057	0	0.022	0.054	0.013	0.043	0.155	0.011	0.03	0.030	0.011
25	0.061	0.04	0.016	0.012	0.054	0.017	0.015	0.087	0.011	0.013	0.016	0.01	0.021	0.015	0.020	0.011
26	0.076	0.06	0	0.029	0.033	0.034	0.015	0.033	0.130	0	0.033	0.025	0	0.005	0	0.011
27	0.04	0.027	0.011	0.017	0.076	0.034	0.023	0.011	0.076	0	0.011	0.2	0.043	0.025	0.010	0.078
28	0.096	0.04	0.027	0.041	0.038	0.098	0.008	0.033	0.027	0	0.011	0.015	0.021	0.05	0.030	0.011
29	0.056	0.02	0.016	0.029	0.011	0.040	0	0.022	0.038	0	0.027	0.005	0.032	0.1	0.060	0.056
30	0.061	0.047	0.08	0.035	0.016	0.063	0.031	0.011	0	0	0.033	0	0.032	0.07	0.050	0.011
31	0.035	0.027	0.048	0.023	0.043	0.040	0.038	0.076	0.033	0.064	0.043	0.01	0	0.03	0.120	0.1
32	0.035	0.013	0.011	0.029	0.033	0.057	0	0	0.033	0	0.027	0.005	0.106	0.07	0.030	0.056
33	0	0.007	0.037	0.012	0.027	0.034	0.015	0.022	0.043	0	0.011	0.005	0.011	0.055	0.010	0.022
34	0.005	0.02	0.032	0.058	0.049	0.011	0	0.011	0.043	0	0.071	0.09	0.106	0.05	0.070	0.022
35	0.01	0.013	0	0.052	0.022	0.029	0	0.022	0.027	0.064	0.033	0.03	0.085	0.01	0.020	0.033
36	0.045	0.007	0.016	0	0.005	0	0.031	0	0.011	0.013	0.011	0	0.011	0.01	0.010	0
37	0.04	0	0.016	0.012	0.011	0.023	0.015	0	0.038	0.077	0.038	0	0	0	0	0
38	0.03	0.047	0.005	0.006	0.005	0.011	0.008	0.011	0.011	0	0.027	0	0	0.03	0.040	0.044
39	0	0.013	0.043	0.006	0.005	0	0	0.022	0.043	0	0	0	0	0.02	0.030	0.022
40	0	0	0.005	0.006	0.005	0	0.008	0	0	0	0.016	0	0	0.015	0.010	0.011
41	0	0	0.005	0	0.005	0	0	0.043	0.011	0	0	0.005	0.011	0.01	0	0.011
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.010	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	99	75	94	86	92	87	65	46	92	39	92	100	47	100	50	45
<i>n_a</i>	30	30	30	32	34	33	25	33	33	23	32	25	23	35	32	32
<i>n_{eff}</i>	21.99	21.91	16.68	25.10	N/A	N/A	13.61	27.54	N/A	15.24	23.78	9.12	14.87	24.91	N/A	26.18
<i>a</i>	17.99	18.22	17.13	18.70	N/A	N/A	15.25	20.15	N/A	15.28	18.61	12.05	15.08	19.25	N/A	19.58
<i>H_E</i>	0.955	0.954	0.940	0.960	N/A	N/A	0.927	0.964	N/A	0.934	0.958	0.890	0.933	0.960	N/A	0.962
<i>H_O</i>	0.919	0.987	0.872	0.977	N/A	N/A	0.923	0.935	N/A	1.000	0.957	0.880	0.979	0.970	N/A	0.889
<i>F_{IS}</i>	0.037	-0.034	0.072	-0.017	N/A	N/A	0.004	0.030	N/A	-0.071	0.001	0.012*	-0.050	-0.011	N/A	0.077**

Appendix II. Continued.

Allele	Population															
	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0.04	0.034	0	0	0.01	0	0.002	0	0.01	0	0
3	0	0	0	0	0	0	0	0	0	0.01	0	0.002	0	0	0.01	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0.010	0.015	0	0	0.022	0.01	0	0	0	0.005	0.021	0.003	0.011	0.031	0.02	0.026
6	0.038	0.02	0.027	0.044	0	0.03	0.011	0.052	0.033	0.04	0	0.023	0.022	0.021	0	0.013
7	0.028	0.05	0.053	0.056	0.043	0.03	0.011	0.01	0	0.051	0.021	0.026	0	0.031	0.04	0.038
8	0.018	0.02	0.027	0.044	0.033	0.04	0.068	0.115	0.109	0.051	0.092	0.069	0.109	0.021	0.03	0.013
9	0.078	0.045	0.048	0.078	0.022	0.08	0.091	0.031	0.065	0.051	0.085	0.046	0.087	0.094	0.15	0.103
10	0.053	0.05	0.037	0.106	0.141	0.04	0.045	0.042	0.043	0.04	0.063	0.048	0.043	0.01	0.03	0.038
11	0.008	0.01	0.027	0.022	0	0.06	0.125	0.01	0.033	0.03	0.028	0.034	0	0.021	0.03	0.051
12	0.020	0	0.005	0	0	0.02	0.045	0.01	0	0	0	0.008	0.011	0.042	0.03	0.013
13	0.010	0.01	0.011	0	0.033	0	0	0	0	0	0	0.007	0	0	0.01	0.013
14	0.003	0.01	0.016	0.006	0	0	0.011	0	0	0.005	0	0.003	0	0.01	0	0
15	0.003	0	0.011	0.022	0	0	0.023	0.01	0	0.01	0	0.003	0.022	0.01	0	0.013
16	0	0	0	0	0	0.01	0.011	0	0	0	0.021	0.002	0	0	0	0
17	0.005	0	0	0	0	0.02	0	0	0	0.01	0	0.015	0	0	0	0
18	0	0	0.005	0	0.011	0	0	0.01	0.011	0.005	0.007	0.002	0	0	0	0.013
19	0.025	0.015	0.021	0	0	0	0	0	0	0.005	0	0.002	0	0.021	0.02	0.013
20	0.050	0.045	0.016	0.033	0.13	0	0	0.01	0	0.005	0.014	0.018	0.011	0.031	0.03	0.051
21	0.073	0.12	0.096	0.061	0.022	0	0.023	0.031	0.022	0.03	0.042	0.038	0.043	0.031	0.04	0.077
22	0.060	0.035	0.032	0.05	0.098	0.02	0.011	0.073	0.043	0.035	0.063	0.059	0.011	0.042	0.05	0.051
23	0.028	0.03	0.043	0.017	0.022	0.11	0.08	0	0.011	0.03	0.021	0.043	0.022	0.031	0.02	0.051
24	0.033	0.04	0.032	0.039	0.043	0.05	0.034	0.031	0	0	0.014	0.016	0.022	0.01	0.01	0.026
25	0.030	0.01	0.005	0.006	0	0	0	0	0.011	0.005	0.007	0.007	0	0.031	0.01	0.051
26	0.008	0.01	0.016	0.022	0	0.01	0.011	0.021	0	0.02	0	0.018	0.022	0	0.02	0.013
27	0.058	0.035	0.027	0.05	0.011	0	0.023	0.021	0.022	0.035	0.028	0.028	0.065	0.031	0.02	0.026
28	0.040	0.06	0.043	0.028	0.022	0.02	0.023	0.052	0.022	0.035	0.014	0.048	0.033	0.073	0.04	0.013
29	0.045	0.04	0.101	0.033	0.043	0.08	0.102	0.063	0.163	0.081	0.077	0.057	0.065	0.063	0.05	0.026
30	0.040	0.085	0.053	0.028	0.033	0	0.011	0.031	0.109	0.056	0.042	0.051	0.065	0.083	0.04	0.051
31	0.055	0.07	0.043	0.072	0.043	0.05	0.023	0.031	0.011	0.015	0.028	0.044	0.054	0.063	0.1	0.026
32	0.070	0.03	0.021	0.017	0.022	0.04	0.034	0.083	0.033	0.051	0.056	0.044	0.065	0.052	0.04	0.038
33	0.038	0.075	0.074	0.056	0.043	0.06	0.057	0.073	0.022	0.03	0.049	0.031	0.033	0.031	0.02	0.038
34	0.013	0.04	0.032	0.017	0.043	0.05	0.023	0.083	0.065	0.086	0.028	0.057	0.054	0.01	0.05	0.038
35	0.023	0.005	0.011	0.044	0.033	0.05	0.023	0.01	0.011	0.03	0.085	0.038	0.043	0.052	0.03	0
36	0.010	0	0.005	0.011	0.011	0	0	0	0.065	0.02	0.028	0.031	0	0.021	0.01	0
37	0.023	0	0.016	0.017	0.065	0.03	0.034	0.021	0.022	0.04	0.028	0.020	0.065	0.021	0.01	0.038
38	0.003	0.01	0.011	0.006	0	0.02	0	0.01	0.022	0.01	0.007	0.018	0	0	0.01	0.026
39	0.003	0.005	0.027	0.011	0	0.01	0.011	0.021	0	0.015	0.014	0.013	0.011	0	0	0
40	0.003	0.01	0.011	0	0	0	0	0	0.011	0.015	0.014	0.005	0.011	0	0.01	0
41	0	0	0	0.006	0	0	0	0.031	0.033	0.02	0	0.011	0	0	0.01	0.013
42	0	0	0	0	0	0.01	0	0.01	0.011	0.005	0	0.005	0	0	0	0
43	0	0	0	0	0.011	0.01	0	0	0	0	0	0.003	0	0	0.01	0
44	0	0	0	0	0	0	0	0	0	0.005	0	0.003	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	199	100	94	90	46	50	44	48	46	99	71	305	46	48	50	39
<i>n_a</i>	34	29	33	29	24	27	27	28	25	37	28	42	25	29	32	30
<i>n_{eff}</i>	N/A	19.57	22.83	21.65	16.81	22.60	19.53	21.11	15.50	26.18	N/A	N/A	21.25	25.76	21.15	29.16
<i>a</i>	N/A	17.17	18.60	17.73	16.62	18.03	17.53	17.78	16.23	19.38	N/A	N/A	17.29	19.11	19.11	20.10
<i>H_E</i>	N/A	0.949	0.956	0.954	0.941	0.956	0.949	0.953	0.935	0.962	N/A	N/A	0.953	0.961	0.953	0.966
<i>H_O</i>	N/A	0.930	0.851	0.956	0.913	0.940	0.977	0.938	0.848	0.939	N/A	N/A	0.978	0.917	0.900	0.974
<i>F_{IS}</i>	N/A	0.020	0.110**	-0.002	0.030	0.017	-0.030	0.016	0.095*	0.023*	N/A	N/A	-0.027	0.047	0.056*	-0.009

Appendix II. Continued.

Allele	Population																Total
	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0.004	0	0	0	0.01	0.01	0	0	0	0	0	0	0
3	0.005	0	0	0	0.009	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0.01	0.009	0	0	0	0	0	0	0.017	0.011	0.013	0	0	0
5	0.045	0	0.013	0	0.013	0.021	0.032	0	0.03	0.01	0.009	0.010	0.027	0.013	0	0	0
6	0.015	0.071	0.037	0.04	0.026	0.01	0.064	0.02	0.08	0.01	0.013	0.012	0.022	0.037	0	0	0
7	0.03	0.01	0.063	0.08	0.064	0.094	0.032	0.05	0.06	0.02	0.029	0.067	0.104	0	0.086	0.086	0.086
8	0.025	0.082	0.025	0.09	0.034	0.125	0.043	0.1	0.1	0.041	0.078	0.076	0.099	0	0.027	0.029	0.029
9	0.055	0.092	0.063	0.05	0.064	0.198	0.128	0.09	0.03	0.122	0.076	0.096	0.06	0.075	0.07	0.069	0.069
10	0.035	0.01	0.025	0.05	0.051	0.083	0.096	0.07	0.04	0.112	0.114	0.111	0.071	0.075	0.124	0.115	0.115
11	0.025	0.061	0	0.01	0.047	0.063	0	0.07	0.02	0.051	0.105	0.054	0.077	0	0.075	0.063	0.063
12	0.025	0.02	0	0	0.017	0.031	0	0.05	0	0.041	0.056	0.032	0.044	0.113	0.043	0.04	0.04
13	0.01	0.01	0	0.01	0.009	0	0.043	0	0	0.01	0.002	0.015	0.022	0	0.022	0.023	0.023
14	0	0.01	0	0	0.004	0	0	0	0.02	0	0.004	0.010	0.016	0	0.005	0.006	0.006
15	0.005	0.01	0.013	0	0	0	0	0	0	0.01	0.004	0.012	0	0	0	0	0
16	0.025	0.01	0.013	0.01	0	0	0	0	0	0	0.002	0.005	0.005	0	0	0	0
17	0	0	0.025	0	0.004	0.01	0	0.02	0	0	0.007	0	0.011	0	0.048	0.046	0.046
18	0.005	0	0	0.02	0	0	0	0	0	0	0.011	0.002	0.005	0	0.038	0.046	0.046
19	0.015	0.01	0	0.01	0.026	0	0.011	0.02	0.01	0.01	0.002	0.015	0.005	0	0.016	0.017	0.017
20	0.025	0.02	0.025	0.04	0.013	0.031	0.011	0.03	0.01	0	0.004	0.020	0.016	0.087	0.011	0.011	0.011
21	0.03	0.051	0.013	0.04	0.043	0.021	0.043	0	0.01	0	0.038	0.020	0.016	0.025	0.022	0.017	0.017
22	0.06	0.041	0.063	0.03	0.026	0.021	0	0.04	0	0.02	0.002	0.020	0.033	0	0.005	0.006	0.006
23	0.035	0.041	0.025	0.04	0.009	0	0.021	0.04	0	0.01	0	0.012	0.011	0.188	0.022	0.017	0.017
24	0.015	0.01	0.037	0.02	0.009	0	0.021	0.01	0.01	0.02	0.011	0.022	0.033	0.05	0.043	0.04	0.04
25	0.015	0.041	0.025	0	0.004	0.01	0.011	0.05	0.06	0	0.013	0.022	0.022	0	0.043	0.046	0.046
26	0.015	0.031	0.013	0.01	0.004	0.01	0.032	0.02	0.01	0.01	0.009	0.012	0.011	0.075	0.016	0.017	0.017
27	0.015	0.01	0.037	0.04	0.038	0	0.064	0.02	0.04	0	0.025	0.002	0.016	0.037	0	0	0
28	0.07	0.01	0.05	0.06	0.051	0	0	0.08	0.06	0.082	0.056	0.037	0.011	0.037	0.059	0.063	0.063
29	0.035	0.051	0.05	0.05	0.051	0.073	0.064	0.03	0.09	0.02	0.040	0.032	0.044	0.013	0.011	0.011	0.011
30	0.03	0.041	0.087	0.05	0.038	0.01	0.021	0.02	0.09	0.092	0.047	0.094	0.06	0.05	0.054	0.063	0.063
31	0.05	0.02	0.037	0.01	0.047	0.01	0.117	0.01	0.04	0.112	0.067	0.049	0.055	0	0.059	0.063	0.063
32	0.06	0.051	0.063	0.03	0.064	0.031	0.021	0.01	0.03	0.061	0.098	0.037	0.022	0.025	0.038	0.04	0.04
33	0.04	0.01	0.013	0.05	0.056	0.021	0.011	0.07	0.05	0.041	0.038	0.032	0.016	0.075	0.022	0.023	0.023
34	0.04	0.031	0.075	0.03	0.068	0.031	0.021	0.03	0.01	0.02	0.016	0.010	0.011	0	0.011	0.011	0.011
35	0.05	0.041	0.013	0.01	0.017	0.042	0.032	0.02	0.01	0	0.011	0.010	0	0	0	0	0
36	0.005	0.031	0.025	0.04	0.017	0	0.021	0.02	0.03	0.02	0.002	0.007	0	0	0.005	0.006	0.006
37	0.015	0.041	0	0	0.013	0	0	0	0.01	0	0.007	0.012	0.027	0	0.011	0.006	0.006
38	0.035	0.01	0.025	0.01	0.034	0.01	0	0	0.04	0.01	0	0.012	0	0	0	0	0
39	0.015	0.01	0.013	0.01	0.013	0.01	0.032	0.01	0	0	0.002	0	0.005	0.013	0	0	0
40	0.025	0.01	0.025	0.03	0	0.01	0.011	0	0	0	0	0	0	0	0	0	0
41	0	0	0.013	0.01	0.004	0	0	0	0	0.02	0	0.002	0.005	0	0	0	0
42	0	0	0	0	0	0.021	0	0	0	0.01	0	0	0	0	0	0	0
43	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.016	0.017	0.017
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	100	49	40	50	117	48	47	50	50	49	224	203	91	40	93	87	10242
<i>n_a</i>	35	33	30	32	36	25	25	26	27	27	33	35	33	18	28	28	51
<i>n_{eff}</i>	29.53	26.70	28.99	27.65	N/A	12.67	18.14	21.43	20.80	16.39	N/A	N/A	20.61	12.90	18.99	19.60	
<i>a</i>	20.06	19.52	19.95	19.58	N/A	15.24	16.89	17.57	17.37	16.21	N/A	N/A	17.87	13.82	16.92	16.99	
<i>H_E</i>	0.966	0.963	0.966	0.964	N/A	0.921	0.945	0.953	0.952	0.939	N/A	N/A	0.951	0.922	0.947	0.949	
<i>H_O</i>	0.990	0.959	0.975	0.940	N/A	0.938	0.872	1.000	0.940	0.837	N/A	N/A	0.967	0.975	0.989	0.989	
<i>F_{IS}</i>	-0.025	0.004	-0.010	0.025	N/A	-0.018	0.078*	-0.049	0.013	0.110	N/A	N/A	-0.016	-0.058	-0.044	-0.042	

Appendix II. Continued.

Omm1070	Size		Population														
	Allele	ABL	DFO	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	188	189	0.005	0	0.059	0.014	0.013	0	0	0	0	0	0.019	0	0	0	0
2	192	193	0.005	0	0.005	0.029	0	0	0	0	0	0	0	0	0	0.009	0
3	196	197	0	0.008	0	0	0	0	0.007	0.014	0	0	0	0	0	0	0
4	200	201	0.026	0.008	0	0	0.025	0.007	0	0	0	0	0	0	0	0	0.018
5	204	204	0.047	0.032	0.065	0.114	0.138	0.015	0.007	0.009	0.013	0.019	0.111	0.031	0	0	0
6	208	208	0	0	0.027	0.057	0.037	0.015	0	0	0.013	0.019	0.037	0.094	0	0	0
7	212	212	0.016	0	0.027	0	0	0.03	0.054	0.009	0.039	0.009	0.056	0.135	0	0	0.018
8	216	216	0.011	0	0.065	0.071	0.013	0.067	0.081	0.018	0.079	0.009	0.093	0.063	0.027	0	0
9	220	220	0	0.008	0	0.014	0.013	0.052	0.041	0	0.039	0.037	0.074	0.042	0.064	0.036	0
10	224	224	0.005	0.032	0.011	0	0	0.052	0.027	0.064	0.026	0.046	0.037	0.083	0.055	0.089	0
11	228	228	0.011	0.008	0.011	0.014	0.013	0.03	0.034	0.045	0.039	0.028	0.111	0.125	0.036	0.071	0
12	232	232	0	0.024	0.038	0.014	0.025	0.06	0.027	0.018	0.039	0.046	0.056	0.073	0	0	0
13	236	236	0.079	0.048	0.043	0.043	0.087	0.015	0.061	0.018	0.053	0.056	0.019	0.031	0.1	0.161	0
14	240	240	0.047	0.095	0.065	0.043	0.087	0.045	0.047	0.018	0.013	0.028	0.13	0.083	0.045	0.018	0
15	244	244	0.068	0.063	0.027	0.029	0.013	0.015	0.007	0.055	0	0.046	0.019	0	0.009	0	0
16	248	248	0.042	0.071	0.043	0.029	0.013	0	0.034	0.145	0.039	0.074	0.037	0.01	0.036	0.018	0
17	252	252	0.026	0.04	0.016	0.029	0	0.022	0.014	0.073	0.026	0.056	0	0.01	0.018	0	0
18	256	256	0.011	0.008	0.022	0.014	0.013	0.097	0.095	0.036	0.132	0.046	0	0	0.045	0.071	0
19	260	260	0.058	0.008	0.059	0.029	0.037	0.007	0.041	0.091	0.039	0.009	0	0	0.009	0.018	0
20	264	264	0.037	0.032	0.054	0.057	0.1	0.037	0.027	0.009	0.013	0.028	0	0	0.009	0.036	0
21	268	268	0.053	0	0.054	0.071	0.025	0.037	0.014	0	0.079	0.028	0.019	0.01	0.036	0.054	0
22	272	272	0.016	0	0.027	0.014	0.025	0.03	0.014	0.018	0.026	0.037	0	0.031	0.018	0.036	0
23	276	276	0.016	0.024	0.043	0.029	0.025	0.022	0.027	0.018	0.026	0.065	0	0	0.036	0.036	0
24	280	280	0.095	0.071	0.022	0.014	0	0.045	0	0.064	0	0.037	0	0.042	0.036	0.054	0
25	284	284	0.089	0.063	0.016	0	0.013	0.022	0.034	0.009	0.026	0.065	0	0.021	0.064	0.089	0
26	288	288	0.063	0.159	0.022	0.014	0.025	0.067	0.054	0.018	0.039	0.028	0.056	0.01	0.055	0.018	0
27	292	292	0.016	0.04	0.043	0	0.05	0.022	0.02	0.027	0.079	0.037	0.037	0.021	0.073	0.089	0
28	296	296	0.016	0.008	0.016	0.014	0.025	0	0.014	0.009	0	0.009	0	0.021	0	0.018	0
29	300	300	0.005	0.024	0	0.014	0.013	0.007	0.02	0	0.026	0	0.019	0.01	0.018	0	0
30	304	304	0.016	0.032	0.005	0.029	0.013	0	0.014	0.009	0.013	0.009	0.019	0	0.009	0.018	0
31	308	308	0.011	0	0.027	0.143	0.025	0.03	0.034	0.009	0	0.046	0.056	0.031	0.018	0	0
32	312	312	0.016	0	0.005	0.014	0.025	0.022	0.054	0.027	0.013	0.019	0	0	0	0	0
33	316	316	0.011	0.008	0.011	0	0	0.052	0.02	0.036	0.026	0	0	0.021	0.045	0.018	0
34	320	320	0.005	0	0	0	0	0.022	0.014	0.055	0.039	0.009	0	0	0.018	0	0
35	324	324	0.016	0.032	0	0	0.013	0.037	0.027	0.018	0	0	0	0	0.055	0.018	0
36	328	328	0.016	0.008	0.022	0	0.013	0	0	0	0	0	0	0	0.045	0	0
37	332	333	0.021	0.024	0.011	0	0.013	0	0.007	0	0	0	0	0	0	0	0
38	336	337	0.011	0.008	0.011	0	0	0	0	0.018	0	0.009	0.019	0	0	0	0
39	340	341	0.005	0	0.005	0	0	0	0.02	0.018	0	0.019	0	0	0	0	0
40	344	345	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	348	349	0.005	0	0	0	0	0	0.007	0	0	0.009	0	0	0	0	0
42	352	353	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
43	356	357	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	360	361	0	0.008	0	0	0	0	0	0	0	0	0	0	0	0	0
45	364	365	0	0	0	0	0	0	0	0	0	0	0	0	0.009	0	0
46	368	368	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	372	372	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	376	376	0	0	0	0	0.013	0.007	0	0	0	0	0	0	0	0	0
49	380	380	0	0	0	0	0	0	0	0.027	0	0	0	0	0	0	0
50	392	393	0	0	0	0	0	0	0	0.009	0	0	0	0	0	0	0
51	396	397	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0
52	408	409	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0
53	412	413	0.005	0.008	0	0	0.013	0	0	0	0	0	0	0	0	0	0
54	416	417	0	0	0.005	0.043	0.05	0	0	0	0	0	0	0	0	0	0
55	424	425	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0	0
56	436	437	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	448	449	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>			95	63	93	35	40	67	74	55	38	54	27	48	55	28	
<i>n_a</i>			37	30	37	27	32	31	33	31	26	32	19	22	28	22	
<i>n_{eff}</i>			21.95	17.08	27.75	19.96	20.79	25.68	26.09	N/A	22.44	N/A	17.24	15.20	24.17	17.50	
<i>a</i>			18.34	16.93	19.68	18.28	19.06	19.10	19.42	N/A	18.49	N/A	15.62	15.12	18.36	16.76	
<i>H_E</i>			0.954	0.941	0.964	0.950	0.952	0.961	0.962	N/A	0.955	N/A	0.942	0.934	0.959	0.943	
<i>H_O</i>			0.989	0.937	0.946	0.943	0.950	1.000	0.959	N/A	1.000	N/A	0.963	1.000	0.927	0.964	
<i>F_{IS}</i>			-0.037	0.005	0.018	0.008	0.002	-0.041	0.002	N/A	-0.047	N/A	-0.023	-0.071	0.033**	-0.023	

Appendix II. Continued.

Allele	Population															
	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	0	0	0	0	0	0	0	0	0.014	0	0	0.009	0	0	0	0
2	0	0.043	0	0	0	0	0	0	0	0	0	0.009	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0.004	0.013	0
4	0	0	0.022	0	0	0	0	0	0	0	0	0	0	0	0.007	0.011
5	0	0	0	0	0	0	0	0	0	0	0.016	0	0.009	0.009	0.013	0
6	0	0	0	0	0	0	0	0	0	0	0	0.009	0	0.021	0.007	0.017
7	0	0	0	0	0	0.015	0	0	0.014	0	0	0	0.028	0	0.017	0.013
8	0	0.029	0	0	0.011	0.015	0.019	0.031	0.014	0	0	0.028	0.036	0.030	0.007	0.011
9	0.110	0.057	0	0	0.022	0	0	0	0.014	0	0.016	0.028	0.036	0.026	0.02	0.05
10	0.040	0.029	0.043	0.035	0.076	0.061	0.019	0.031	0.014	0	0.063	0.047	0.027	0.034	0.033	0.061
11	0.020	0.014	0.043	0.07	0.087	0.045	0.111	0.031	0.028	0.056	0.031	0.075	0.045	0.064	0.066	0.056
12	0.020	0.014	0.065	0.093	0.043	0.106	0.074	0	0.014	0.028	0.063	0.038	0.036	0.034	0.053	0.039
13	0.100	0.014	0.022	0.07	0.109	0.091	0.148	0.031	0.014	0.083	0.016	0.038	0.073	0.068	0.138	0.033
14	0.090	0.014	0.043	0.081	0.087	0.136	0.093	0.031	0.097	0.028	0	0.075	0.036	0.051	0.072	0.017
15	0.070	0.157	0.065	0.058	0.065	0.045	0.056	0.031	0.069	0	0.047	0.028	0.045	0.030	0.039	0.033
16	0.030	0.043	0.087	0.081	0.087	0.091	0.019	0.031	0.014	0.028	0.016	0.057	0.055	0.056	0.046	0.039
17	0.010	0.100	0.022	0.035	0.076	0.03	0.037	0.094	0.111	0.167	0.031	0.047	0.018	0.047	0.053	0.044
18	0.030	0.071	0	0.047	0.033	0.03	0.074	0.063	0.097	0.139	0.047	0.057	0.036	0.038	0.033	0.083
19	0.010	0.029	0.043	0.07	0.033	0.061	0.019	0.094	0.014	0.028	0.078	0.047	0.100	0.056	0.053	0.044
20	0.050	0.057	0	0.116	0.043	0.03	0.111	0.063	0.056	0.083	0.078	0.057	0.055	0.030	0.066	0.044
21	0.040	0.029	0.087	0.023	0.011	0.045	0.019	0.031	0.056	0.111	0.063	0.038	0.055	0.030	0.059	0.067
22	0	0.029	0	0.058	0.043	0.045	0.019	0.063	0.097	0.056	0.078	0.028	0.073	0.056	0.046	0.033
23	0.080	0.029	0.087	0.012	0.065	0	0.019	0.031	0.069	0.056	0.047	0.028	0.027	0.017	0.039	0.039
24	0.040	0.029	0	0	0.022	0.045	0.037	0.063	0.069	0	0.016	0.038	0.018	0.043	0.013	0.044
25	0.040	0.014	0	0.023	0.011	0.045	0.019	0.094	0.028	0.056	0.078	0.047	0.027	0.038	0.02	0.033
26	0.040	0.029	0.217	0.012	0	0.015	0.019	0.031	0.042	0.028	0.078	0.047	0.027	0.047	0.026	0.028
27	0.050	0	0	0	0	0	0.037	0	0.014	0	0.047	0.009	0.027	0.021	0.02	0.028
28	0.030	0.014	0	0.012	0.011	0.03	0	0.063	0	0.028	0.016	0.019	0.036	0.017	0.007	0.028
29	0	0	0	0.023	0.011	0	0	0.031	0	0	0.031	0.019	0.027	0.021	0.026	0.022
30	0.030	0.043	0.065	0	0	0.015	0.037	0	0	0	0.016	0.009	0	0.013	0	0.022
31	0	0.057	0	0.012	0	0	0	0	0.014	0	0	0.009	0	0	0	0.011
32	0	0	0	0.012	0.011	0	0	0	0	0	0	0.009	0	0.021	0	0.011
33	0.020	0	0	0	0	0	0	0	0	0	0.016	0.009	0	0	0	0.017
34	0.020	0	0.043	0	0	0	0	0.031	0	0	0	0	0.027	0.013	0.007	0
35	0.030	0.029	0	0	0	0	0	0.031	0.014	0	0	0	0.009	0.004	0	0
36	0	0	0	0	0	0	0	0	0.014	0.028	0	0	0.018	0.004	0	0.006
37	0	0	0.022	0	0	0	0	0	0	0	0	0	0	0.004	0	0
38	0	0.014	0	0	0	0	0	0	0	0	0	0	0.018	0.013	0.007	0.011
39	0	0.014	0.022	0	0	0	0	0	0	0	0.016	0	0	0.009	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0.004	0	0
41	0	0	0	0.012	0.011	0	0	0	0	0	0	0.009	0	0.009	0	0
42	0	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0.023	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0.012	0.011	0	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0.011	0	0.019	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.006
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	0	0	0	0.012	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	50	35	23	43	46	33	27	16	36	18	32	53	55	117	76	90
<i>n_a</i>	23	26	17	24	25	20	21	21	25	16	24	31	27	36	29	32
<i>n_{eff}</i>	N/A	N/A	13.44	18.65	18.44	17.73	16.45	35.43	18.52	15.37	24.29	28.54	N/A	N/A	19.39	26.89
<i>a</i>	N/A	N/A	14.95	16.34	16.24	15.94	16.16	21.00	16.64	15.18	17.98	19.58	N/A	N/A	17.31	19.32
<i>H_E</i>	N/A	N/A	0.926	0.946	0.946	0.944	0.939	0.972	0.946	0.935	0.959	0.965	N/A	N/A	0.948	0.963
<i>H_O</i>	N/A	N/A	1.000	0.907	0.978	0.939	0.963	0.938	0.944	0.944	0.906	0.925	N/A	N/A	0.961	0.911
<i>F_{IS}</i>	N/A	N/A	-0.082	0.042**	-0.035	0.005	-0.026	0.036	0.002	-0.010	0.056	0.042	N/A	N/A	-0.013	0.054

Appendix II. Continued.

Allele	Population															
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0.011	0.005	0.003	0.006	0	0.005	0.008	0.011	0.020
4	0	0.013	0	0.011	0.013	0.013	0	0.005	0.048	0.003	0.042	0.021	0.016	0.017	0.022	0.014
5	0	0.063	0.01	0.011	0.013	0.039	0	0	0	0.005	0.006	0	0	0.022	0.007	0.014
6	0	0	0	0.011	0.013	0.013	0.022	0.054	0.037	0.054	0.020	0.016	0.016	0.028	0.022	0.026
7	0.006	0.013	0.01	0.011	0.025	0.007	0.065	0.108	0.064	0.016	0.059	0.064	0.057	0.069	0.048	0.042
8	0.006	0.038	0.021	0	0.013	0.02	0.011	0.011	0.037	0.044	0.017	0.016	0.031	0.048	0.051	0.024
9	0.038	0.013	0.031	0.032	0.038	0.02	0.027	0.048	0.085	0.044	0.115	0.043	0.021	0.043	0.068	0.069
10	0.019	0.038	0.042	0.043	0.038	0.039	0.011	0.011	0.069	0.010	0.056	0.048	0.057	0.050	0.040	0.049
11	0.064	0.100	0.083	0.074	0.076	0.072	0.027	0.043	0.021	0.013	0.025	0.048	0.057	0.023	0.026	0.026
12	0.071	0.050	0.042	0.043	0.07	0.046	0.06	0.07	0.064	0.023	0.025	0.053	0.052	0.042	0.053	0.028
13	0.038	0.025	0.063	0.064	0.013	0.033	0.065	0.043	0.027	0.016	0.039	0.032	0.057	0.047	0.029	0.020
14	0.045	0.013	0.052	0.064	0.006	0.02	0.027	0.113	0.059	0.036	0.045	0.074	0.099	0.052	0.057	0.036
15	0.019	0.075	0.073	0.064	0.038	0.046	0.065	0.075	0.032	0.018	0.073	0.032	0.031	0.039	0.040	0.067
16	0.077	0.075	0.042	0.021	0.057	0.053	0.011	0.022	0.053	0.041	0.003	0.032	0.036	0.058	0.051	0.042
17	0.038	0.038	0.063	0.032	0.038	0.059	0.011	0.038	0.032	0.174	0.039	0.016	0.063	0.050	0.066	0.059
18	0.051	0.075	0.01	0.021	0.101	0.125	0.087	0.048	0.085	0.148	0.042	0.043	0.068	0.060	0.055	0.061
19	0.038	0.088	0.031	0.074	0.089	0.053	0.033	0.065	0.053	0.140	0.031	0.064	0.068	0.054	0.046	0.075
20	0.077	0.050	0.052	0.053	0.038	0.066	0.049	0.022	0.032	0.047	0.079	0.101	0.026	0.044	0.051	0.040
21	0.019	0.025	0.01	0.043	0.076	0.007	0.005	0.032	0.037	0.010	0.028	0.043	0.026	0.046	0.046	0.045
22	0.071	0.025	0.083	0.021	0.032	0.02	0.071	0.011	0.016	0	0.045	0.037	0.026	0.030	0.024	0.040
23	0.045	0.025	0.052	0.032	0.044	0.026	0.13	0.011	0.032	0.028	0.011	0.011	0.042	0.026	0.015	0.026
24	0.045	0	0.021	0.043	0.032	0.02	0.011	0.043	0.032	0.010	0.093	0.053	0.026	0.026	0.029	0.028
25	0.019	0.050	0.063	0.032	0.032	0.033	0.027	0.022	0.027	0.008	0.017	0.027	0.005	0.017	0.035	0.036
26	0.026	0.025	0.01	0.011	0.038	0.033	0.076	0.016	0.005	0.010	0.003	0.027	0.031	0.020	0.026	0.016
27	0.032	0	0.021	0.011	0	0.026	0.027	0.032	0.032	0.023	0.014	0.016	0.016	0.019	0.022	0.026
28	0.013	0.025	0.01	0.053	0.019	0.039	0.016	0.011	0.005	0.026	0.017	0.027	0.031	0.027	0.013	0.020
29	0.013	0.038	0.021	0.043	0.032	0.026	0.06	0.016	0.005	0.036	0.003	0.021	0.031	0.017	0.013	0.012
30	0.038	0.013	0.01	0.021	0	0.013	0	0	0	0.005	0.028	0	0	0.011	0.015	0.006
31	0.019	0	0	0	0.013	0.02	0	0.011	0	0	0	0.016	0.005	0.001	0.002	0.016
32	0.013	0	0.031	0.011	0.006	0.007	0.005	0.011	0.005	0.003	0.017	0.016	0	0	0.002	0.010
33	0.032	0	0.031	0.011	0	0	0	0	0	0.003	0	0	0	0.001	0.004	0.004
34	0.019	0	0	0	0	0	0	0	0	0	0	0	0	0.003	0	0
35	0	0	0	0.011	0	0	0	0	0	0	0.003	0	0	0.001	0	0.008
36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.004	0
37	0	0.013	0.01	0	0	0.007	0	0	0	0.003	0	0	0	0	0.002	0
38	0.006	0	0	0.011	0	0	0	0	0	0	0	0.005	0	0.001	0	0
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
41	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	78	40	48	47	79	76	92	93	94	193	178	94	96	372	227	253
<i>n_a</i>	29	25	28	32	27	30	25	28	27	30	30	28	27	33	34	32
<i>n_{eff}</i>	N/A	N/A	24.52	28.57	20.67	22.11	17.04	18.72	21.62	N/A	N/A	22.92	21.91	N/A	N/A	N/A
<i>a</i>	N/A	N/A	18.42	19.75	17.34	18.35	15.84	16.86	17.35	N/A	N/A	18.14	17.59	N/A	N/A	N/A
<i>H_E</i>	N/A	N/A	0.959	0.965	0.952	0.955	0.941	0.947	0.954	N/A	N/A	0.956	0.954	N/A	N/A	N/A
<i>H_O</i>	N/A	N/A	0.938	0.979	0.937	0.947	0.924	0.914	0.968	N/A	N/A	0.968	0.958	N/A	N/A	N/A
<i>F_{IS}</i>	N/A	N/A	0.023	-0.014	0.016	0.008	0.019	0.035*	-0.015	N/A	N/A	-0.012**	-0.004	N/A	N/A	N/A

Appendix II. Continued.

<i>Omm1070</i>	Population																
	Allele	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0.006	0	0	0.011	0.016	0.032	0.031	0.005	0	0	0	0.007	0.007	
3	0	0.005	0	0.006	0.007	0.021	0	0.005	0	0	0	0.011	0	0	0.007	0.007	
4	0	0.021	0.016	0.011	0.014	0.021	0	0.038	0.011	0.005	0.016	0.016	0.021	0.005	0.013	0.007	
5	0	0.011	0.005	0.011	0.014	0.021	0.021	0	0.005	0.01	0	0.011	0	0.011	0.02	0.014	
6	0.035	0.021	0.038	0.028	0.021	0.042	0.011	0.016	0	0.021	0.005	0.005	0	0	0.02	0.021	
7	0.035	0.053	0.054	0.056	0.076	0.021	0.032	0.027	0.037	0.036	0.011	0.033	0.005	0.021	0.047	0.048	
8	0.035	0.037	0.038	0.051	0.007	0.042	0.032	0.027	0.096	0.026	0.074	0.104	0.037	0	0.073	0.048	
9	0.035	0.043	0.071	0.062	0.049	0.01	0.043	0.027	0.016	0.026	0.016	0.005	0	0.005	0.027	0.027	
10	0.070	0.053	0.033	0.017	0.042	0.052	0.064	0.022	0.011	0.005	0.005	0	0	0	0.04	0.007	
11	0	0.037	0.038	0.034	0.049	0.031	0.043	0.027	0.037	0.021	0.011	0.011	0	0.069	0.033	0.048	
12	0.093	0.064	0.071	0.028	0.042	0.042	0.043	0.011	0.027	0.047	0.021	0.027	0.032	0.096	0.027	0.027	
13	0.070	0.048	0.054	0.034	0.014	0.01	0.011	0.048	0.069	0.036	0.011	0.016	0.053	0.032	0.047	0.021	
14	0.058	0.048	0.016	0.045	0.028	0.042	0.043	0.086	0.117	0.089	0.074	0.093	0.144	0.027	0.04	0.041	
15	0.047	0.037	0.027	0.045	0.035	0.115	0.085	0.108	0.053	0.12	0.08	0.044	0.043	0.08	0.033	0.055	
16	0.023	0.027	0.065	0.034	0.042	0.031	0.064	0.038	0.106	0.047	0.016	0.071	0.085	0.037	0.027	0.034	
17	0.047	0.074	0.049	0.051	0.035	0.073	0.043	0.048	0.011	0.036	0.048	0.044	0.005	0.021	0.033	0.089	
18	0.023	0.053	0.065	0.039	0.056	0.031	0.064	0.054	0.037	0.073	0.032	0.055	0.074	0.032	0.067	0.041	
19	0.093	0.048	0.054	0.067	0.042	0.052	0.117	0.108	0.08	0.073	0.069	0.038	0.074	0.09	0.06	0.041	
20	0.035	0.027	0.027	0.051	0.049	0.021	0.064	0.032	0.043	0.047	0.043	0.033	0.074	0.037	0.04	0.048	
21	0.116	0.053	0.054	0.039	0.035	0.042	0.043	0.032	0.021	0.042	0.043	0.044	0.053	0.005	0.02	0.034	
22	0.023	0.021	0.016	0.028	0.063	0.031	0.011	0.016	0.016	0.021	0.037	0.027	0	0.032	0.013	0.021	
23	0.012	0.027	0.022	0.039	0.076	0.042	0.043	0.027	0.037	0.01	0.021	0.033	0	0.096	0.027	0.027	
24	0.047	0.037	0.038	0.039	0.021	0.063	0.053	0.011	0.016	0.016	0.021	0.033	0.027	0.005	0.04	0.062	
25	0.023	0.032	0.022	0.039	0.007	0.042	0	0.016	0.005	0.021	0.027	0.038	0.011	0.043	0.053	0.041	
26	0.035	0.021	0.016	0.034	0.056	0.01	0	0.043	0.043	0.026	0.032	0.049	0.037	0.053	0.033	0.034	
27	0.012	0.027	0.016	0.017	0.014	0.021	0.021	0.032	0.016	0.021	0.08	0.038	0.032	0.106	0.04	0.048	
28	0.012	0.021	0.022	0.006	0.042	0.01	0.011	0.011	0.021	0.01	0.069	0.005	0.021	0.027	0.04	0.034	
29	0.012	0	0.005	0.022	0.028	0.01	0.021	0.016	0.005	0.021	0.021	0.038	0.027	0.037	0.007	0.014	
30	0	0.005	0.043	0.017	0.007	0.01	0	0.027	0.005	0.026	0.021	0.016	0.048	0.005	0.013	0.027	
31	0	0.016	0.005	0.028	0.007	0.01	0.011	0.022	0.011	0.016	0.053	0.022	0.059	0.016	0.007	0.014	
32	0	0.021	0.005	0.011	0.014	0.01	0	0.011	0.016	0.021	0.016	0.011	0.016	0.011	0.027	0.014	
33	0.012	0.005	0.005	0.006	0	0	0	0	0	0	0.011	0.011	0.021	0	0	0	
34	0	0	0	0	0	0.01	0	0	0	0	0	0.011	0	0	0	0	
35	0	0	0	0	0.007	0	0	0	0	0	0	0	0	0	0.013	0	
36	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0	
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
38	0	0	0.005	0	0	0.01	0	0	0	0	0	0	0	0	0	0	
39	0	0	0	0	0.007	0	0	0	0	0	0	0	0	0	0	0	
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
42	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0	
43	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0	
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>n</i>	43	94	92	89	72	48	47	93	94	96	94	91	94	94	75	73	
<i>n_a</i>	24	31	31	32	32	32	25	30	29	30	32	31	23	26	33	31	
<i>n_{eff}</i>	N/A	26.96	24.61	28.49	26.20	26.67	21.43	20.91	17.61	20.93	22.19	22.41	16.47	17.02	29.49	27.56	
<i>a</i>	N/A	19.15	18.47	19.53	19.01	19.79	17.44	18.11	16.59	18.03	18.01	18.29	15.66	15.82	19.93	19.42	
<i>H_E</i>	N/A	0.963	0.959	0.965	0.962	0.963	0.953	0.952	0.943	0.952	0.955	0.955	0.939	0.941	0.966	0.964	
<i>H_O</i>	N/A	0.957	0.935	0.978	0.944	0.979	0.915	0.914	0.947	0.948	0.979	0.989	0.926	0.957	0.947	0.932	
<i>F_{IS}</i>	N/A	0.006	0.026	-0.013	0.018	-0.018	0.041	0.040	-0.004	0.005	-0.025	-0.035	0.015	-0.017	0.020	0.034	

Appendix II. Continued.

Omm1070	Population																
	Allele	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78
1	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0	0	0	
2	0	0	0	0	0.006	0	0	0	0.006	0	0	0.011	0	0.016	0	0	
3	0	0	0.012	0	0.006	0	0.003	0.01	0	0.007	0.005	0	0	0.005	0	0	
4	0.016	0.006	0.024	0.026	0.006	0.026	0.017	0.01	0.017	0.041	0.031	0.053	0.013	0.005	0.029	0	
5	0	0.022	0	0	0.013	0.018	0.017	0.021	0.012	0	0.01	0	0.013	0.011	0.007	0.011	
6	0.016	0.022	0.024	0.034	0.013	0.018	0.023	0.031	0.017	0.014	0.01	0.011	0.027	0.032	0.064	0.016	
7	0.059	0.045	0.06	0.086	0.032	0.044	0.046	0.021	0.017	0.068	0.104	0.069	0.047	0.058	0.057	0.047	
8	0.059	0.062	0.024	0.026	0.078	0.053	0.043	0.083	0.052	0.034	0.036	0.048	0.067	0.042	0.029	0.032	
9	0.048	0.067	0.036	0.034	0.026	0.053	0.053	0.031	0.064	0.048	0.078	0.059	0.033	0.021	0.021	0.053	
10	0.032	0.045	0.024	0.034	0.045	0.026	0.043	0	0.035	0.021	0.078	0.037	0.013	0.058	0.05	0.053	
11	0.027	0.017	0.071	0.034	0.065	0.053	0.023	0.031	0.035	0.027	0.021	0.027	0.053	0.047	0.007	0.037	
12	0.037	0.039	0.024	0.017	0.019	0.035	0.04	0.021	0.029	0.116	0.052	0.069	0.02	0.047	0.014	0.042	
13	0.037	0.045	0.036	0.034	0.019	0.044	0.036	0.042	0.029	0.11	0.068	0.096	0.06	0.016	0.05	0.053	
14	0.032	0.039	0.048	0.043	0.065	0.07	0.04	0.042	0.047	0.11	0.104	0.112	0.06	0.037	0.014	0.063	
15	0.021	0.056	0.083	0.06	0.071	0.07	0.06	0.042	0.041	0.048	0.073	0.08	0.047	0.026	0.021	0.005	
16	0.021	0.056	0.024	0.043	0.026	0.035	0.053	0.042	0.052	0.027	0.031	0.043	0.013	0.032	0.057	0.042	
17	0.069	0.051	0.036	0.017	0.032	0.009	0.046	0.042	0.064	0.014	0.01	0.016	0.033	0.042	0.057	0.032	
18	0.043	0.039	0.036	0.069	0.045	0.044	0.053	0.063	0.047	0.027	0.047	0.016	0.047	0.068	0.021	0.053	
19	0.048	0.062	0.071	0.052	0.071	0.053	0.063	0.063	0.064	0.11	0.089	0.053	0.067	0.037	0.043	0.032	
20	0.059	0.022	0.036	0.034	0.026	0.035	0.04	0.063	0.035	0.082	0.052	0.037	0.08	0.058	0.064	0.068	
21	0.048	0.017	0.06	0.078	0.052	0.07	0.046	0.063	0.041	0.014	0.005	0.027	0.02	0.032	0.064	0.068	
22	0.037	0.045	0.024	0.017	0.039	0.044	0.023	0.021	0.035	0.007	0.016	0.032	0.027	0.042	0.043	0.032	
23	0.037	0.017	0.048	0.043	0.026	0.026	0.03	0.021	0.035	0	0	0.011	0.047	0.037	0.021	0.021	
24	0.053	0.034	0.036	0.017	0.013	0.018	0.046	0.063	0.023	0.021	0	0.016	0.007	0.026	0.029	0.016	
25	0.053	0.006	0.024	0.06	0.032	0.044	0.04	0.031	0.029	0	0.031	0.027	0.047	0.026	0.05	0.053	
26	0.043	0.045	0.048	0.026	0.013	0	0.04	0.042	0.035	0.021	0.021	0.027	0.013	0.037	0.043	0.032	
27	0.032	0.045	0.06	0.034	0.045	0.026	0.02	0.042	0.052	0.007	0.005	0	0.007	0.032	0.036	0.026	
28	0.021	0.039	0.012	0.026	0.026	0.044	0.02	0.042	0.012	0.021	0.01	0.005	0.033	0.032	0.014	0.032	
29	0.032	0.017	0.012	0.026	0.026	0.018	0.01	0.01	0.023	0	0.005	0.005	0.027	0.005	0.014	0.021	
30	0.005	0.006	0.012	0	0.026	0.018	0.013	0	0.006	0	0	0.005	0.04	0.026	0.007	0.011	
31	0	0.011	0	0.026	0.013	0.009	0.003	0.01	0.029	0.007	0.005	0.005	0.013	0.011	0.036	0.011	
32	0.005	0.011	0	0	0.006	0	0.003	0	0	0	0	0.005	0.007	0.011	0	0.016	
33	0.005	0.006	0	0	0.006	0	0	0	0.012	0	0	0	0	0.011	0.014	0.021	
34	0	0	0	0	0.006	0	0.003	0	0	0	0	0	0.007	0	0.007	0	
35	0.005	0	0	0	0	0	0	0	0.006	0	0	0	0.007	0.005	0.007	0	
36	0	0.006	0	0	0	0	0.003	0	0	0	0	0	0	0.011	0	0	
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005	
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0	
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>n</i>	94	89	42	58	77	57	151	48	86	73	96	94	75	95	70	95	
<i>n_a</i>	29	31	27	26	33	27	32	27	31	24	26	28	32	34	32	30	
<i>n_{eff}</i>	26.04	26.21	27.89	25.65	25.89	26.95	26.02	27.14	28.01	14.97	16.58	18.66	25.63	29.20	27.41	26.02	
<i>a</i>	18.69	18.83	19.29	18.71	19.15	18.89	18.79	18.99	19.41	15.03	15.42	16.60	18.88	19.84	19.30	18.86	
<i>H_E</i>	0.962	0.962	0.964	0.961	0.961	0.963	0.962	0.963	0.964	0.933	0.940	0.946	0.961	0.966	0.964	0.962	
<i>H_O</i>	0.957	0.921	0.929	1.000	0.987	0.982	0.927	0.979	0.942	0.973	0.927	0.947	0.933	0.947	0.943	1.000	
<i>F_{IS}</i>	0.004*	0.042*	0.037	-0.041	-0.027	-0.021	0.036	-0.017	0.023	-0.043	0.013	0.000	0.029	0.019	0.022	-0.040	

Appendix II. Continued.

Allele	Population															
	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0.011	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0	0.022
6	0.011	0.007	0	0	0	0	0	0	0	0.053	0.006	0.06	0	0.016	0	0
7	0.016	0.041	0.006	0.035	0.033	0.018	0	0	0.026	0.092	0.006	0	0	0	0	0.011
8	0.016	0.034	0.006	0	0.033	0.024	0	0.056	0.026	0.079	0.029	0.165	0	0.027	0.010	0
9	0.037	0	0.06	0.012	0.011	0.049	0	0.014	0.032	0.066	0.035	0.088	0.085	0.033	0.020	0.044
10	0.053	0.02	0.03	0	0.006	0.037	0.008	0.097	0.011	0.197	0.047	0.055	0	0.022	0	0.067
11	0.043	0.041	0.006	0.029	0.017	0.073	0.008	0.042	0.042	0.105	0.041	0.049	0.073	0.06	0.041	0.011
12	0.069	0.088	0.066	0.041	0.056	0.037	0	0.056	0.016	0.066	0.012	0.099	0.073	0.016	0.041	0.011
13	0.021	0.081	0.018	0.035	0.033	0.012	0.008	0.111	0.074	0.118	0.035	0	0.012	0.016	0.031	0
14	0.021	0.027	0.048	0.035	0.067	0.043	0.038	0.028	0.100	0.013	0.082	0	0.159	0.027	0.041	0.022
15	0.043	0.02	0.048	0.047	0.061	0.037	0.062	0.042	0.068	0.026	0.041	0.181	0.207	0.005	0.051	0.022
16	0.059	0.095	0.072	0.041	0.067	0.049	0.123	0.056	0.047	0	0.041	0	0.012	0.033	0	0.067
17	0.032	0.014	0.036	0.087	0.039	0.006	0.185	0.028	0.026	0	0.024	0.005	0.012	0.033	0.010	0
18	0.032	0.034	0.048	0.07	0.033	0.091	0.085	0.028	0.058	0.079	0.024	0.005	0	0.06	0.041	0.056
19	0.037	0.014	0.054	0.029	0.028	0.024	0.031	0.042	0.068	0.026	0.047	0.027	0.037	0.044	0.031	0.089
20	0.048	0.027	0.048	0.047	0.050	0.055	0.008	0.028	0.037	0	0.018	0.005	0.024	0.027	0.092	0.056
21	0.043	0.014	0.018	0.041	0.050	0.055	0.062	0.097	0.037	0	0.035	0.005	0	0.071	0.031	0.044
22	0.037	0.054	0.054	0.116	0.061	0.049	0.054	0.056	0.016	0	0.035	0.016	0.061	0.088	0.092	0.067
23	0.043	0.047	0.03	0.058	0.044	0.043	0.008	0.056	0.058	0.013	0.059	0.011	0	0.071	0.071	0.056
24	0.048	0.061	0.024	0.052	0.072	0.091	0.031	0.014	0.037	0.039	0.076	0.082	0.012	0.022	0.071	0.056
25	0.085	0.041	0.048	0.047	0.028	0.018	0.015	0.028	0.042	0.013	0.029	0	0.037	0.049	0.031	0.056
26	0.043	0.007	0.024	0.023	0.022	0.043	0.008	0.014	0.053	0.013	0.076	0	0.012	0.06	0.082	0.067
27	0.032	0.047	0.036	0.058	0.056	0.018	0.062	0.069	0.032	0	0.041	0	0.024	0.011	0.051	0.011
28	0.032	0.02	0.018	0.006	0.067	0.037	0.038	0	0.005	0	0.018	0	0.037	0.022	0.020	0.044
29	0.021	0.041	0.048	0.012	0.011	0.049	0.062	0	0.011	0	0.047	0	0.012	0.022	0	0.033
30	0.016	0.047	0.054	0.029	0.017	0.018	0.085	0.014	0	0	0.018	0	0.012	0.027	0	0.011
31	0.005	0.027	0.018	0.017	0.011	0.006	0.015	0	0.011	0	0.018	0	0.012	0.016	0.041	0
32	0.011	0.007	0.036	0.012	0.017	0	0.008	0	0.016	0	0.018	0.06	0.085	0.005	0	0
33	0.011	0.007	0.012	0	0.006	0.012	0	0	0	0	0.006	0	0	0.016	0.010	0
34	0.011	0.007	0	0.006	0.006	0	0	0.014	0.005	0	0	0	0	0	0	0
35	0.005	0.014	0.012	0	0	0.006	0	0.014	0.016	0	0.018	0	0	0	0	0
36	0.011	0	0.006	0.006	0	0	0	0	0.011	0	0.012	0	0	0.005	0.010	0.022
37	0	0	0.006	0.006	0	0	0	0	0.016	0	0	0	0	0.016	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0.011	0	0.033
39	0	0	0	0	0	0	0	0	0	0	0	0	0	0.022	0	0
40	0	0	0.006	0	0	0	0	0	0.005	0	0.006	0	0	0	0	0
41	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0.016	0.010	0
42	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0.005	0.010	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.010	0
44	0	0	0	0	0	0	0	0	0	0	0	0.077	0	0	0.020	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.011
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.020	0.011
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0.011	0.010	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	94	74	83	86	90	82	65	36	95	38	85	91	41	91	49	45
<i>n_a</i>	32	30	31	28	28	27	22	23	30	16	31	18	20	35	28	26
<i>n_{eff}</i>	26.39	22.85	25.69	20.40	N/A	N/A	12.46	20.61	N/A	11.35	25.11	10.06	10.82	25.58	N/A	24.13
<i>a</i>	19.18	18.24	18.71	17.30	N/A	N/A	13.88	17.12	N/A	12.51	18.84	11.57	13.50	19.33	N/A	18.01
<i>H_E</i>	0.962	0.956	0.961	0.951	N/A	N/A	0.920	0.951	N/A	0.912	0.960	0.901	0.908	0.961	N/A	0.959
<i>H_O</i>	0.968	1.000	0.964	0.919	N/A	N/A	0.908	1.000	N/A	0.842	0.976	0.890	0.878	0.956	N/A	0.956
<i>F_{IS}</i>	-0.006	-0.046	-0.003	0.034	N/A	N/A	0.013	-0.052*	N/A	0.078	-0.017	0.012	0.033	0.005*	N/A	0.003

Appendix II. Continued.

Allele	Population															
	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0.005	0.006	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0.008	0.006	0	0.011	0	0.01	0	0	0.011	0	0	0.003	0.011	0.011	0	0
7	0.013	0.023	0.011	0.028	0.011	0	0.012	0.033	0.032	0.011	0.014	0.019	0.022	0	0	0.029
8	0.005	0.006	0.016	0.011	0	0	0.012	0.022	0.011	0.022	0.007	0.027	0.022	0.022	0.02	0.015
9	0.013	0.023	0	0.034	0	0.02	0	0.033	0.032	0.027	0.049	0.032	0.033	0.033	0.03	0.015
10	0.046	0.051	0.069	0.045	0.067	0.01	0.012	0.022	0.011	0.011	0.035	0.032	0.011	0.022	0.01	0.029
11	0.025	0.023	0.032	0.028	0.033	0.02	0	0.044	0.053	0.07	0.063	0.054	0.033	0.022	0	0.044
12	0.043	0.063	0.016	0.045	0.122	0.06	0	0.156	0.043	0.075	0.141	0.067	0.054	0.033	0.04	0.015
13	0.030	0.017	0.043	0.09	0.011	0.02	0.06	0.067	0.053	0.027	0.014	0.054	0.076	0.067	0.06	0.029
14	0.025	0.023	0.064	0.034	0.056	0.02	0.107	0.011	0.074	0.043	0.063	0.056	0.043	0.056	0.07	0.015
15	0.033	0.063	0.048	0.011	0.011	0.11	0.024	0.011	0.064	0.059	0.049	0.033	0.065	0.011	0.03	0.015
16	0.071	0.057	0.016	0.034	0.011	0.05	0.06	0.044	0.053	0.043	0.042	0.056	0.054	0.067	0.04	0.074
17	0.041	0.045	0.027	0.073	0.122	0.09	0.048	0.033	0.043	0.07	0.070	0.045	0.043	0.011	0.03	0.059
18	0.058	0.023	0.032	0.039	0.011	0.04	0.036	0.078	0.053	0.07	0.042	0.065	0.011	0.011	0.05	0
19	0.033	0.057	0.021	0.017	0.033	0.12	0.048	0.044	0.117	0.043	0.049	0.064	0.087	0.067	0.07	0.044
20	0.056	0.057	0.09	0.039	0.033	0.03	0.06	0.044	0.043	0.07	0.049	0.041	0.011	0.022	0.05	0.103
21	0.036	0.023	0.053	0.062	0.011	0.07	0.095	0.044	0.011	0.043	0.063	0.043	0.043	0.067	0.03	0.044
22	0.069	0.04	0.09	0.045	0.067	0.03	0.048	0	0.064	0.065	0.035	0.064	0.065	0.022	0.05	0.118
23	0.079	0.074	0.043	0.045	0.089	0.1	0.06	0.056	0.043	0.032	0.014	0.030	0.054	0.033	0.05	0.059
24	0.020	0.068	0.021	0.034	0.033	0.03	0.024	0.011	0.032	0.032	0	0.025	0.054	0.022	0.07	0.015
25	0.038	0.04	0.053	0.039	0.033	0.05	0.083	0.033	0.032	0.022	0.028	0.022	0.011	0.056	0.05	0.059
26	0.051	0.068	0.037	0.051	0.067	0.04	0.048	0.056	0.032	0.027	0.014	0.025	0.033	0.067	0.02	0.059
27	0.038	0.028	0.032	0.056	0.022	0.01	0.036	0	0.043	0.011	0.042	0.032	0.043	0.044	0.05	0.029
28	0.020	0.017	0.027	0.034	0.022	0.03	0.036	0.078	0	0.005	0.007	0.018	0.011	0.033	0.03	0.029
29	0.010	0.011	0.005	0.006	0	0.02	0	0.011	0	0.016	0	0.019	0.011	0.056	0.06	0
30	0.030	0.028	0.053	0.011	0.067	0	0.012	0.011	0.011	0.016	0.042	0.011	0.022	0.033	0.02	0
31	0.020	0.011	0.005	0.011	0.011	0.01	0	0.022	0.011	0.027	0.007	0.021	0	0.022	0	0.015
32	0.025	0.011	0.021	0.011	0	0	0.036	0.022	0.021	0.016	0.021	0.006	0.022	0.022	0.01	0.029
33	0.015	0	0.032	0.017	0	0	0.024	0	0	0.005	0.007	0.010	0.033	0.011	0	0.044
34	0.008	0.006	0.005	0.028	0.011	0	0	0	0	0.005	0.007	0.005	0	0	0.03	0
35	0.003	0	0.005	0.006	0.022	0	0	0	0.011	0.005	0.007	0.006	0	0.011	0.01	0
36	0.003	0	0	0	0.011	0	0	0	0	0.005	0.007	0.003	0	0	0.01	0
37	0.008	0	0.021	0.006	0	0	0.024	0	0	0	0	0.010	0.022	0.011	0	0
38	0.010	0.011	0.005	0	0.011	0	0	0	0	0.011	0.007	0.002	0	0.022	0	0
39	0.008	0.011	0.005	0	0	0	0	0	0	0.005	0	0	0	0	0	0.015
40	0.005	0	0	0	0	0	0	0.011	0	0.011	0	0	0	0.011	0.01	0
41	0	0.011	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	197	88	94	89	45	50	42	45	47	93	71	314	46	45	50	34
<i>n_a</i>	36	32	31	31	26	24	23	25	26	33	29	33	28	31	27	25
<i>n_{eff}</i>	N/A	24.48	22.59	25.16	17.72	17.25	21.13	18.72	22.77	23.50	N/A	N/A	26.16	29.67	26.61	22.55
<i>a</i>	N/A	18.59	18.11	18.79	16.60	16.15	17.12	17.25	17.95	18.36	N/A	N/A	18.88	20.01	18.75	18.20
<i>H_E</i>	N/A	0.959	0.956	0.960	0.944	0.942	0.953	0.947	0.956	0.957	N/A	N/A	0.962	0.966	0.962	0.956
<i>H_O</i>	N/A	0.955	0.979	0.910	0.933	0.900	0.952	0.978	0.979	0.946	N/A	N/A	1.000	0.978	0.960	0.853
<i>F_{IS}</i>	N/A	0.005	-0.024	0.053*	0.011	0.045	0.000	-0.033	-0.024	0.012*	N/A	N/A	-0.040	-0.012	0.003	0.109*

Appendix II. Continued.

Allele	Population																Total
	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0.01	0.011	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.006
6	0	0	0	0	0	0	0	0	0	0.021	0.021	0	0	0	0	0	0
7	0	0	0	0	0.031	0	0	0	0	0	0	0.003	0	0	0	0	0
8	0.005	0	0.03	0	0	0.01	0	0.016	0.01	0.011	0	0.005	0.006	0	0	0	0
9	0.037	0.067	0.045	0.021	0.015	0.01	0	0.031	0.021	0.021	0.011	0.005	0.006	0	0	0	0
10	0.058	0	0.061	0	0.010	0	0	0.047	0.021	0	0.053	0.003	0.011	0.086	0	0.047	0
11	0.016	0.056	0.076	0.043	0.041	0.021	0	0.047	0.031	0.043	0.026	0.016	0.006	0.014	0.038	0.023	0
12	0.032	0.056	0.061	0.032	0.031	0.083	0.021	0.078	0	0.011	0.021	0.018	0.046	0.029	0.013	0.041	0
13	0.047	0.044	0.076	0.074	0.062	0.01	0.117	0.047	0.01	0.085	0.034	0.052	0.011	0.143	0.006	0.012	0
14	0.058	0.044	0.045	0.032	0.031	0.01	0.043	0.047	0.063	0.043	0.029	0.047	0.023	0	0.038	0.058	0
15	0.074	0.056	0.03	0.032	0.036	0.125	0.106	0.031	0.031	0.064	0.034	0.021	0.057	0	0.013	0.076	0
16	0.016	0.011	0.03	0.053	0.062	0.042	0.043	0.047	0.01	0.043	0.024	0.037	0.034	0.014	0.051	0.087	0
17	0.037	0.033	0.045	0.043	0.077	0.031	0.074	0.063	0	0.021	0.074	0.024	0.046	0.029	0.051	0.058	0
18	0.047	0.056	0.03	0.032	0.057	0.083	0.021	0.031	0.042	0.032	0.039	0.058	0.069	0.1	0.057	0.07	0
19	0.042	0.022	0.03	0.064	0.041	0.063	0.043	0.078	0.031	0.074	0.050	0.042	0.063	0.1	0.044	0.087	0
20	0.074	0.044	0.061	0.053	0.031	0.052	0.085	0.016	0.031	0.043	0.029	0.050	0.092	0.114	0.076	0.099	0
21	0.053	0.056	0.076	0.032	0.041	0.021	0.021	0.063	0.052	0.053	0.053	0.050	0.069	0.057	0.095	0.029	0
22	0.037	0.033	0.076	0.043	0.026	0.042	0.011	0	0.063	0.053	0.026	0.058	0.063	0.1	0.057	0.006	0
23	0.047	0.033	0	0.085	0.067	0.021	0.021	0.016	0.073	0.074	0.053	0.047	0.052	0.057	0.019	0.023	0
24	0.042	0.044	0.061	0.064	0.046	0.073	0.011	0	0.042	0.074	0.068	0.058	0.052	0.071	0.089	0.058	0
25	0.037	0.089	0.015	0.011	0.072	0.021	0.011	0.016	0.063	0.064	0.071	0.031	0.006	0.043	0.057	0.023	0
26	0.026	0.044	0.03	0.032	0.041	0.052	0.021	0.031	0.094	0.043	0.053	0.063	0.029	0	0.019	0.023	0
27	0.032	0.011	0	0.021	0.021	0.01	0.074	0	0.031	0.011	0.047	0.063	0.046	0	0.025	0.035	0
28	0.032	0.033	0.015	0.043	0.026	0.031	0.021	0.063	0.031	0.021	0.034	0.058	0.034	0.014	0.032	0.023	0
29	0.047	0.067	0.015	0.043	0.052	0.042	0.021	0.047	0.042	0	0.050	0.045	0.006	0	0.006	0.017	0
30	0	0.022	0.015	0.021	0.015	0	0.011	0.016	0.042	0.032	0.026	0.039	0.057	0.014	0.013	0.035	0
31	0.021	0.011	0	0.021	0.010	0.042	0.032	0	0.031	0.011	0.016	0.018	0.029	0.014	0	0.012	0
32	0.011	0.022	0.015	0.032	0.005	0.01	0.053	0.063	0	0.021	0.016	0.021	0.006	0	0.006	0.017	0
33	0.016	0.022	0.015	0	0.010	0	0.011	0	0.01	0	0.011	0.010	0.023	0	0	0.012	0
34	0.016	0	0	0.032	0.005	0	0.011	0.047	0.01	0.021	0.008	0.016	0.017	0	0.006	0	0
35	0.021	0.011	0	0.021	0	0.031	0	0.031	0.021	0	0.005	0.010	0.006	0	0.051	0.012	0
36	0	0.011	0	0	0.005	0.042	0	0.016	0	0	0.008	0.008	0.006	0	0.013	0	0
37	0.016	0	0.03	0	0	0.01	0.074	0	0.031	0	0.013	0.003	0.006	0	0.019	0	0
38	0.005	0	0	0.021	0	0	0.011	0	0	0	0.005	0.005	0.023	0	0.006	0	0
39	0	0	0	0	0.005	0	0.011	0.016	0.01	0	0.003	0.008	0	0	0.006	0.012	0
40	0	0	0.015	0	0.005	0	0.011	0	0	0	0.003	0.003	0	0	0.006	0	0
41	0	0	0	0	0.005	0	0	0	0	0	0	0	0	0	0.019	0	0
42	0	0	0	0	0	0	0	0	0.01	0.011	0	0.003	0	0	0.051	0	0
43	0	0	0	0	0	0	0	0	0	0	0.003	0.003	0	0	0.013	0	0
44	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0	0
45	0	0	0	0	0.010	0	0	0	0	0	0	0.003	0	0	0	0	0
46	0	0	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.006	0	0
<i>n</i>	95	45	33	47	97	48	47	32	48	47	190	191	87	35	79	86	9873
<i>n_a</i>	29	26	25	26	33	27	28	25	31	26	34	37	31	17	32	27	56
<i>n_{eff}</i>	25.50	26.01	26.81	27.49	N/A	20.63	19.09	28.80	27.80	23.89	N/A	N/A	22.10	13.57	21.91	19.48	
<i>a</i>	18.68	18.57	18.79	19.11	N/A	17.61	17.23	19.16	19.69	18.07	N/A	N/A	17.66	13.29	17.89	16.87	
<i>H_E</i>	0.961	0.962	0.963	0.964	N/A	0.952	0.948	0.965	0.964	0.958	N/A	N/A	0.955	0.926	0.954	0.949	
<i>H_O</i>	0.958	0.956	1.000	1.000	N/A	0.938	0.936	1.000	1.000	0.915	N/A	N/A	0.943	0.914	0.949	0.930	
<i>F_{IS}</i>	0.003	0.006	-0.039	-0.038	N/A	0.015	0.012	-0.037	-0.038	0.046	N/A	N/A	0.013	0.013	0.005	0.020	

Appendix II. Continued.

OneIII Allele	Size ABL	Size DFO	Population														
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	
1	162	163	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	168	170	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	170	172	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	172	174	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	174	176	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	176	178	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	178	180	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	180	182	0	0	0	0	0	0	0	0.013	0	0.013	0.012	0.074	0.031	0.089	0
9	182	184	0	0	0	0	0	0	0	0	0	0	0.008	0	0	0	0
10	184	186	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
11	186	188	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	188	190	0	0	0	0	0	0	0	0.013	0.019	0.013	0.020	0.056	0.031	0.009	0
13	190	192	0	0	0	0.014	0	0	0	0.013	0	0.063	0	0	0	0	0
14	192	194	0	0	0	0	0	0	0	0	0	0	0.004	0	0	0	0
15	194	196	0	0	0.005	0	0	0	0	0	0	0	0.004	0	0	0	0
16	196	198	0	0	0	0	0	0	0	0	0	0	0	0.019	0.01	0	0
17	198	200	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18	200	202	0	0	0	0	0	0	0	0	0.006	0	0	0.037	0.01	0	0
19	202	204	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	204	205	0	0.015	0	0	0	0	0	0	0	0.013	0	0.019	0.021	0	0
21	206	207	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	208	209	0	0	0	0	0	0	0	0	0.006	0	0.004	0	0.031	0	0
23	210	211	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	212	213	0	0	0	0	0	0	0	0	0.013	0	0	0.019	0.01	0	0
25	214	215	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	216	217	0.005	0.007	0	0	0	0	0	0	0	0	0	0	0	0	0
27	218	219	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	220	221	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	222	223	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	224	225	0	0	0	0	0	0	0	0	0	0	0.004	0	0	0	0
31	226	227	0.016	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	228	229	0	0	0	0	0	0	0	0	0	0	0.008	0	0	0	0
33	230	231	0.016	0.022	0	0	0	0	0	0	0	0	0	0	0	0	0
34	232	233	0	0	0	0	0	0	0	0	0	0.013	0.008	0	0	0	0
35	234	235	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0.009	0.036
36	236	237	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0.009	0
37	238	239	0.011	0.03	0	0	0	0.015	0.013	0	0	0	0	0	0	0	0
38	240	241	0	0	0.016	0	0	0.008	0.006	0	0	0.012	0	0	0	0	0
39	242	243	0	0	0	0	0	0	0.006	0	0.013	0.004	0	0	0	0	0
40	244	245	0.005	0	0	0	0	0	0.006	0	0	0.012	0	0	0	0	0.018
41	246	247	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	248	249	0.027	0	0.011	0.071	0.05	0.023	0.013	0.026	0	0.008	0	0	0.009	0	0
43	250	251	0.021	0.015	0.032	0	0	0	0.025	0	0	0	0	0	0	0	0
44	252	253	0.059	0.119	0.089	0.1	0.025	0	0	0.006	0.013	0.008	0	0.021	0.018	0.018	0
45	254	255	0	0	0	0	0	0.015	0	0	0	0.008	0	0	0	0	0
46	256	257	0.032	0.007	0.026	0.1	0	0	0.019	0.006	0.013	0.027	0	0	0	0	0
47	258	259	0.016	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0
48	260	261	0.011	0	0.005	0.029	0	0.03	0	0.019	0.037	0.004	0	0.01	0.009	0	0
49	262	263	0	0.015	0	0	0	0	0	0	0	0	0	0	0	0.018	0.018
50	264	265	0.027	0.007	0.011	0.029	0.037	0.023	0.057	0.006	0.013	0.016	0	0	0.063	0.036	0
51	266	267	0.048	0	0	0	0.013	0.008	0	0	0	0	0	0	0	0	0
52	268	269	0.005	0.015	0.032	0.043	0	0.106	0.082	0.006	0.013	0.008	0.019	0	0.009	0	0
53	270	271	0.005	0	0	0	0.013	0	0	0.006	0	0	0	0	0	0	0.054
54	272	273	0.011	0	0.042	0.014	0.013	0.045	0.019	0.038	0.05	0.016	0.019	0	0.018	0.054	0
55	274	275	0	0	0	0	0	0.015	0	0	0	0	0	0	0	0	0
56	276	277	0.005	0	0.016	0.014	0.037	0.023	0.025	0.006	0.05	0.020	0	0.031	0.009	0.018	0
57	278	279	0.005	0.015	0.011	0.014	0.025	0	0	0	0	0	0	0	0	0	0
58	280	281	0.032	0.015	0.042	0.043	0.037	0.03	0.013	0.026	0	0.012	0	0.01	0	0.054	0
59	282	283	0	0	0	0.029	0	0	0	0.006	0.037	0	0	0	0	0	0.018
60	284	285	0.027	0.045	0.005	0	0.075	0.045	0.025	0.019	0.025	0.031	0.019	0	0	0	0
61	286	287	0	0	0.011	0	0	0.045	0.013	0	0	0	0	0	0	0	0
62	288	289	0.037	0.03	0.063	0.057	0.125	0	0.019	0.006	0	0.047	0	0.031	0	0	0

Appendix II. Continued.

Allele	Population															
	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0.004	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0.012	0	0.015	0	0	0	0	0	0	0	0	0	0.011
7	0	0	0	0	0	0	0	0	0	0	0	0	0	0.009	0	0
8	0.020	0	0.022	0.128	0.13	0.103	0.111	0	0.028	0	0.048	0.057	0.045	0.068	0.086	0.055
9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	0	0	0	0.012	0	0.015	0	0	0.028	0	0.032	0	0.018	0.009	0.013	0.044
11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	0	0	0	0.023	0	0.044	0	0	0	0	0	0	0.018	0.004	0	0.022
13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0	0	0	0	0	0.009	0.009	0.013	0.007	0.005
15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
16	0	0	0	0	0.022	0.015	0	0	0	0	0	0	0.055	0.017	0.02	0.027
17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0.023	0.011	0.029	0	0	0	0	0	0	0.045	0.030	0.013	0.011
19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	0	0	0	0.012	0.033	0.044	0.019	0	0	0	0	0	0.018	0.034	0.007	0.005
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0	0	0	0.016	0.028	0.045	0.021	0.013	0
23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0	0.032	0.009	0.009	0.013	0	0.011
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0.018	0.009	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0.018	0.004	0	0.005
29	0	0	0	0	0	0.015	0.019	0	0	0	0	0	0.009	0	0	0.005
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0.013	0	0.011
31	0	0	0	0	0.011	0	0	0.029	0.042	0	0.032	0	0	0.009	0	0
32	0	0	0	0	0	0	0	0	0.014	0.056	0	0.009	0	0.004	0	0
33	0.010	0	0	0	0	0	0	0.059	0.014	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0.009	0	0
35	0	0	0	0	0.033	0	0	0.029	0	0	0	0.019	0.009	0.009	0	0.011
36	0	0.059	0	0	0	0	0	0	0	0	0	0.009	0.009	0.004	0	0
37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0.010	0	0	0	0	0	0.019	0	0	0	0	0.009	0	0.017	0.013	0.011
39	0	0	0	0	0	0	0	0	0	0	0.016	0	0	0.004	0	0.005
40	0	0	0	0	0	0	0	0	0	0	0	0.009	0	0.009	0.026	0.011
41	0	0.044	0	0	0	0	0	0	0	0	0	0	0.036	0.013	0	0.011
42	0	0	0	0	0	0	0	0.029	0.014	0	0.032	0.009	0.009	0.017	0.026	0.011
43	0	0	0	0	0	0.015	0	0	0	0	0	0	0.009	0.009	0.007	0.011
44	0.041	0	0	0	0.011	0	0	0.029	0.069	0	0	0.019	0	0.013	0	0.027
45	0	0.015	0	0.012	0.022	0	0.019	0	0	0	0	0	0.027	0.009	0.007	0
46	0.010	0.015	0.022	0.012	0	0	0.019	0.147	0.083	0.028	0.032	0.009	0.027	0.009	0.007	0.049
47	0	0.015	0	0	0.022	0.015	0	0	0	0	0	0	0.045	0.034	0.02	0.022
48	0	0.015	0	0	0.011	0.015	0	0.029	0.014	0	0	0.028	0.018	0	0.02	0.005
49	0	0	0	0.012	0.011	0.029	0.019	0	0	0	0	0.009	0.009	0.009	0.033	0.005
50	0.061	0.059	0.043	0.047	0.011	0.029	0	0	0.014	0	0	0.019	0	0.017	0	0.005
51	0	0	0	0	0.011	0	0	0	0	0	0	0	0.018	0.017	0.039	0
52	0.031	0	0.043	0.035	0	0.088	0.019	0.059	0.028	0.028	0	0.009	0	0.004	0.013	0.011
53	0	0	0	0.012	0	0.029	0	0	0.014	0.083	0	0.009	0.018	0.017	0.013	0.005
54	0.010	0	0	0.047	0.011	0	0	0	0.056	0.028	0.016	0.009	0.018	0.013	0.02	0.011
55	0	0.044	0.022	0.023	0.011	0.015	0	0	0	0	0	0	0	0.013	0	0.005
56	0	0	0.043	0.047	0.022	0.059	0.111	0	0	0	0	0.038	0	0.009	0.013	0.022
57	0	0	0	0.023	0	0	0	0	0	0	0	0.009	0	0	0.007	0
58	0.031	0.015	0.174	0.035	0.087	0.059	0.037	0	0.028	0	0.032	0.019	0.018	0.013	0.007	0.005
59	0.010	0	0	0.023	0	0	0	0	0	0	0	0	0.018	0	0.007	0
60	0.010	0.015	0.022	0.023	0.022	0.029	0.019	0.176	0.056	0.111	0.097	0	0.018	0.021	0.026	0.011
61	0	0	0	0	0.011	0	0	0	0	0	0.016	0	0.009	0.004	0	0.005
62	0	0.015	0.022	0.023	0.022	0.074	0.019	0	0.125	0.028	0.065	0.019	0.036	0.013	0.013	0.016

Appendix II. Continued.

Allele	Population															
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0.003	0.004	0
7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	0.064	0.063	0.042	0.053	0.032	0.058	0.016	0.032	0	0.003	0.011	0.005	0.01	0.001	0.007	0.002
9	0.006	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	0.026	0	0.042	0.011	0.006	0	0	0.053	0.027	0.005	0.039	0.005	0.005	0.001	0.007	0.002
11	0.006	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	0.013	0.050	0	0.021	0.039	0.065	0.167	0.213	0.213	0.136	0.180	0.284	0.224	0.255	0.211	0.220
13	0	0	0	0	0	0	0	0	0	0	0	0	0	0.001	0	0.004
14	0.013	0	0.031	0.021	0	0.006	0.016	0.027	0.021	0.003	0.028	0.011	0	0.003	0.011	0.012
15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002	0
16	0.045	0.025	0.01	0.021	0	0.019	0	0.027	0.005	0.008	0.003	0	0.005	0.005	0.009	0.015
17	0	0	0	0	0	0	0	0.005	0	0	0	0	0.005	0.001	0.002	0.010
18	0.006	0.038	0.021	0.011	0.006	0.032	0.054	0.043	0.021	0.013	0.041	0.016	0.026	0.045	0.044	0.042
19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	0.019	0	0.01	0.064	0.006	0.006	0.011	0.011	0.037	0	0.006	0.026	0.016	0.021	0.031	0.035
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002
22	0.019	0	0.042	0.011	0.013	0	0	0	0	0.005	0.003	0.011	0.036	0.014	0.018	0.042
23	0.006	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0.013	0.013	0.031	0	0.013	0.013	0.005	0	0	0	0	0	0	0.001	0.004	0.006
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0.006	0	0.021	0	0	0	0	0	0.005	0	0.003	0	0	0.006	0.002	0.010
27	0	0	0	0	0	0	0.005	0.048	0	0	0.014	0.005	0	0.006	0.004	0.008
28	0	0.013	0	0	0	0	0	0.005	0	0	0	0	0.01	0.001	0	0.002
29	0	0	0	0.011	0	0	0	0	0.011	0	0.003	0	0	0.003	0.009	0.002
30	0.013	0	0.01	0.011	0	0	0	0	0.011	0	0	0	0	0.004	0.002	0
31	0.006	0	0	0	0	0	0.005	0.005	0.005	0.003	0.008	0	0	0.001	0.002	0.006
32	0	0	0	0	0	0	0	0	0	0.026	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0.003	0.006	0.005	0.005	0.005	0.009	0.012
34	0.006	0	0	0	0	0	0	0	0	0.099	0.003	0	0	0	0	0.004
35	0.006	0	0.01	0	0.013	0	0	0	0	0.003	0.003	0.011	0.026	0.008	0.004	0.010
36	0.019	0	0	0	0	0.013	0	0	0	0.003	0.003	0	0	0.003	0.002	0
37	0	0	0.01	0.011	0.006	0	0	0.032	0.005	0	0.003	0	0.021	0.008	0.020	0.006
38	0.006	0.025	0	0.021	0.026	0.019	0	0	0	0	0	0	0	0	0.009	0
39	0.013	0	0.01	0.011	0.013	0	0	0.011	0.011	0.003	0.003	0.021	0.031	0.026	0.026	0.017
40	0.013	0.025	0.01	0.032	0.026	0.052	0.022	0	0	0	0	0.005	0.005	0.010	0.007	0.010
41	0.006	0.025	0	0	0	0.013	0.005	0.016	0.037	0.005	0.052	0.005	0.01	0.018	0.022	0.023
42	0.013	0.013	0.031	0.032	0.032	0.006	0	0.011	0	0.003	0	0.011	0.005	0.023	0.020	0.012
43	0.006	0	0.01	0.021	0.006	0	0	0.005	0.005	0.003	0.003	0.016	0	0.012	0.018	0.004
44	0.013	0.025	0.01	0.011	0.039	0.039	0	0	0.016	0.003	0.011	0.021	0.005	0.013	0.026	0.008
45	0	0	0.063	0	0.019	0.006	0	0.005	0.005	0	0.028	0.005	0	0.008	0.007	0
46	0.006	0.038	0.01	0.011	0.013	0.032	0	0.011	0	0	0.019	0.016	0.016	0.008	0.015	0.019
47	0.006	0	0.052	0	0	0.006	0.043	0.027	0.005	0.060	0.006	0.005	0.005	0.001	0.011	0.006
48	0.026	0.025	0	0	0.006	0.019	0	0	0.011	0.071	0.017	0.016	0.005	0.009	0.011	0.004
49	0.006	0.013	0	0.043	0.026	0.019	0.043	0.027	0.053	0.115	0.011	0.016	0.005	0.009	0.015	0.021
50	0.006	0	0.01	0	0	0.006	0	0	0	0.018	0.003	0.011	0.005	0.009	0.015	0.008
51	0.006	0	0.01	0.011	0	0.006	0.054	0	0.043	0.029	0.006	0.011	0.021	0.019	0.022	0.015
52	0.032	0.013	0.021	0.011	0.006	0.013	0.038	0	0	0.123	0.008	0.011	0.026	0.009	0.009	0
53	0	0	0	0	0.019	0	0.011	0.021	0.005	0.005	0.006	0.005	0.021	0.009	0.007	0.010
54	0.013	0	0	0.011	0.006	0	0	0.005	0.011	0.003	0	0	0.005	0.004	0.002	0
55	0.006	0	0	0.011	0	0	0.027	0.005	0	0.003	0.028	0.005	0.01	0.003	0.002	0.002
56	0.019	0	0.01	0	0.019	0.006	0	0	0.005	0	0.008	0	0.005	0.004	0	0.002
57	0.006	0	0	0	0	0	0.011	0	0	0	0.011	0.005	0	0	0	0.002
58	0.032	0	0.031	0.043	0.006	0.013	0	0.005	0.053	0.003	0.011	0	0.01	0.009	0.013	0.010
59	0	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0
60	0.038	0	0.01	0.021	0.006	0	0	0.005	0.011	0.003	0.011	0.011	0.01	0.009	0.015	0.008
61	0	0	0.021	0	0	0	0	0	0	0	0	0	0.005	0.001	0	0.002
62	0.019	0	0.01	0	0.006	0.006	0	0.005	0.005	0.008	0.011	0.026	0	0.016	0.015	0.023

Appendix II. Continued.

Allele	Population															
	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0
8	0	0.022	0.011	0.011	0.007	0	0	0.005	0	0	0	0.005	0	0.005	0.02	0.021
9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	0	0.005	0	0.006	0.007	0	0	0.005	0.005	0.005	0.021	0.011	0.005	0	0	0.007
11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	0.221	0.231	0.25	0.29	0.232	0.191	0.25	0.353	0.355	0.333	0.452	0.434	0.42	0.612	0.27	0.264
13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14	0.012	0	0	0.017	0	0	0	0.022	0	0.01	0	0	0	0	0.007	0.007
15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
16	0	0.005	0.005	0.011	0.007	0.011	0.021	0	0	0	0.011	0	0	0	0.007	0
17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18	0.058	0.022	0.033	0.068	0.042	0.053	0.063	0.022	0.016	0	0.011	0.011	0.186	0.005	0.02	0.063
19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	0.012	0.016	0.005	0	0.021	0.011	0	0	0	0	0.011	0.005	0	0	0.014	0.021
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0.035	0.016	0.016	0.028	0.014	0.032	0.01	0.016	0	0.01	0	0.005	0	0	0.007	0
23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	0.005	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0.012	0	0.005	0	0	0	0.01	0	0	0	0	0	0	0	0.007	0
27	0.012	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0.007	0	0	0	0	0	0	0	0	0	0.007	0
29	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0.005	0	0	0	0.01	0	0	0	0	0	0	0	0.007	0
31	0	0	0.005	0.011	0	0	0	0.005	0	0	0	0	0	0	0.014	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0.016	0.022	0.006	0	0.011	0.01	0.011	0.011	0	0.005	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007
35	0	0.022	0.022	0.006	0.021	0.021	0.021	0.038	0.032	0.068	0.016	0.011	0.027	0.005	0.027	0.021
36	0	0	0.005	0	0	0.011	0	0	0	0	0	0	0	0	0	0
37	0.023	0.011	0.011	0.011	0.021	0	0.021	0.022	0.022	0.026	0.032	0.005	0	0	0	0.014
38	0	0.016	0	0	0	0	0	0	0	0	0	0	0	0	0.014	0.007
39	0	0.043	0.011	0.017	0	0.032	0.042	0.065	0.032	0.031	0.027	0.082	0	0.027	0.02	0.014
40	0.023	0.011	0.005	0.011	0.014	0.011	0.01	0	0	0.005	0	0	0	0	0.007	0
41	0.047	0.005	0.011	0.034	0.007	0	0.01	0.005	0.016	0.016	0.005	0	0	0.005	0.027	0.021
42	0.047	0.022	0	0.017	0.007	0.011	0.01	0	0	0	0	0	0	0	0.027	0.014
43	0.023	0.016	0.016	0.011	0.014	0.011	0	0.005	0.032	0.016	0	0.011	0	0	0.007	0.014
44	0	0.027	0.011	0.023	0.021	0.011	0.01	0.043	0.038	0.031	0	0.005	0.021	0	0.041	0.007
45	0	0.011	0.016	0.011	0.014	0.043	0.01	0.016	0.032	0.036	0.011	0	0	0	0.027	0.007
46	0.023	0.011	0.033	0	0.035	0	0.01	0.016	0.016	0.016	0.016	0.027	0.074	0.032	0.034	0.021
47	0.012	0.011	0.011	0.011	0.014	0.011	0.042	0	0	0	0	0	0	0	0.007	0
48	0.012	0.038	0.022	0.006	0.028	0.043	0.01	0.005	0.005	0.01	0.016	0.027	0.005	0	0	0
49	0.070	0.005	0.011	0	0.014	0.011	0	0.005	0.005	0.01	0	0	0	0	0	0.007
50	0	0	0.005	0	0	0.021	0	0	0.011	0	0	0.005	0.011	0	0	0.007
51	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0	0.007
52	0.012	0.011	0.011	0	0.014	0.021	0	0.022	0	0.01	0.016	0.011	0.005	0	0.014	0.007
53	0	0.005	0.005	0.006	0	0	0	0	0	0	0	0	0	0	0	0.014
54	0.023	0	0	0	0.014	0.021	0	0	0	0.01	0.005	0	0	0	0.02	0.014
55	0	0	0	0.006	0.007	0	0	0	0	0	0	0	0	0	0	0.007
56	0	0.005	0.022	0.006	0	0	0	0.005	0	0	0	0	0	0	0	0.007
57	0	0	0.005	0	0.014	0	0.01	0	0	0	0	0	0	0	0	0
58	0.012	0.032	0.005	0.006	0.007	0.021	0	0	0	0	0	0.005	0	0	0.02	0.021
59	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0
60	0.012	0.011	0.016	0.017	0.014	0.021	0.021	0.022	0	0.016	0	0	0	0	0.007	0.014
61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
62	0.023	0.005	0.011	0.028	0.014	0	0.021	0	0	0.016	0	0.005	0	0	0	0.014

Appendix II. Continued.

Allele	Population															
	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0.011	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0.017	0	0	0	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	0	0.006	0.012	0.009	0.006	0	0.01	0	0.028	0	0	0.016	0.02	0	0.007	0.026
9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	0	0	0.012	0	0	0.009	0.007	0	0	0.005	0	0	0	0.011	0	0
11	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0	0	0
12	0.223	0.191	0.232	0.224	0.175	0.216	0.236	0.245	0.222	0.56	0.49	0.484	0.216	0.125	0.232	0.158
13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14	0.005	0.028	0.037	0.009	0	0.026	0.01	0.01	0	0	0.005	0.021	0	0.022	0	0.021
15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
16	0.016	0.006	0	0	0.006	0	0.014	0.01	0.023	0	0	0	0	0.005	0	0.021
17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18	0.037	0.028	0.037	0.043	0.039	0.034	0.037	0.051	0.023	0	0.016	0.047	0.034	0.049	0.056	0.053
19	0	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0
20	0.005	0.011	0.012	0.034	0.006	0.009	0.01	0	0.034	0.016	0.021	0.053	0.014	0.016	0.021	0.021
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0.011	0.011	0.024	0	0.006	0.009	0.02	0.02	0.011	0	0	0.005	0.041	0.022	0.007	0.026
23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0.005	0	0	0.009	0.013	0	0.01	0.01	0	0	0	0	0.014	0	0	0.005
25	0	0	0	0	0	0.009	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0.007	0	0	0.011	0	0	0	0.005	0.007	0.011
27	0	0	0	0	0	0	0	0	0.006	0	0	0	0	0	0	0
28	0	0.006	0	0	0.006	0	0.003	0	0	0	0	0	0	0.005	0.007	0
29	0	0.006	0	0	0.006	0	0.003	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0.006	0	0	0	0	0	0	0	0.007	0.005	0	0
31	0.011	0.006	0.024	0	0.013	0	0.017	0.01	0.028	0	0	0	0.007	0.005	0.007	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0.016	0	0	0.009	0.026	0	0.01	0.031	0.006	0.016	0.021	0	0.014	0.005	0.028	0.011
34	0.005	0.006	0	0	0.006	0	0.003	0	0	0	0	0	0	0	0	0.011
35	0.027	0.028	0.024	0.026	0.032	0.009	0.02	0	0.011	0.005	0	0.021	0.014	0.022	0.021	0.005
36	0	0	0.012	0.009	0.013	0.009	0	0.01	0.011	0	0	0	0	0	0.007	0
37	0.021	0.022	0.024	0.017	0.019	0.017	0.017	0.01	0.017	0.043	0.005	0.032	0.014	0.022	0.007	0.005
38	0.005	0.006	0.012	0	0	0.009	0.01	0	0.006	0	0	0	0.014	0.011	0.007	0.005
39	0.005	0.017	0.024	0	0.032	0	0.014	0	0.023	0	0.047	0.011	0.007	0.011	0	0.026
40	0.005	0	0	0	0.006	0.026	0.007	0.031	0.017	0	0.016	0.005	0	0.011	0.014	0
41	0	0	0.024	0.043	0.019	0.009	0.03	0.01	0.017	0	0.036	0.016	0.02	0.011	0.014	0.021
42	0.011	0.022	0	0.017	0.019	0.034	0.014	0.031	0.028	0.011	0.005	0	0.02	0.005	0.035	0.005
43	0.016	0.028	0	0.017	0.006	0.026	0.02	0	0.006	0.022	0.031	0.016	0.007	0.016	0.007	0.037
44	0.037	0.017	0	0.009	0.026	0	0.017	0.01	0.011	0.027	0.016	0.005	0.014	0.022	0.007	0.021
45	0.005	0	0	0.009	0.006	0.017	0.007	0	0	0.011	0.01	0.037	0.014	0.011	0.014	0.016
46	0.027	0.006	0.012	0	0.019	0.017	0.007	0.01	0.006	0	0.005	0.005	0.027	0.005	0.007	0.011
47	0	0.006	0.012	0.009	0.019	0.017	0.014	0.01	0	0.038	0.016	0.011	0	0.005	0	0
48	0.016	0.028	0.037	0.017	0.006	0.017	0.01	0.01	0.006	0.005	0.026	0.026	0	0	0.021	0.005
49	0	0.006	0	0.009	0.019	0.009	0	0	0.017	0.005	0	0	0.007	0.022	0.021	0.005
50	0.005	0	0	0	0.006	0.009	0.003	0.01	0.023	0	0	0.005	0	0.016	0.007	0.011
51	0.016	0	0	0	0.006	0.009	0.007	0	0.011	0	0	0	0.027	0.005	0.014	0.005
52	0.016	0	0.012	0	0	0.009	0	0	0.006	0.005	0	0	0	0.005	0	0.011
53	0	0.006	0	0	0	0.009	0	0.01	0.006	0	0	0	0.007	0.011	0.007	0
54	0.005	0.011	0	0.017	0.013	0.009	0.007	0.031	0.006	0	0	0	0	0.005	0	0.011
55	0.011	0.006	0	0	0.006	0	0	0	0.006	0	0	0	0.007	0.016	0.007	0
56	0.005	0.006	0	0	0	0.009	0.01	0.01	0.006	0	0	0	0.014	0.011	0.007	0.021
57	0.005	0.006	0	0	0.013	0	0	0	0	0	0	0	0	0.005	0.007	0.005
58	0.016	0.034	0	0	0.019	0.009	0.01	0.02	0.023	0	0	0	0.014	0.016	0.014	0.005
59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0
60	0.021	0.022	0.012	0	0.006	0.017	0.027	0.031	0.028	0	0	0	0.007	0.016	0.021	0.005
61	0.005	0	0	0	0	0	0	0	0	0.005	0	0.005	0.007	0	0	0
62	0.016	0.011	0.012	0.017	0.019	0.017	0.027	0.051	0.006	0	0	0.005	0.02	0.033	0.014	0.053

Appendix II. Continued.

Allele	Population															
	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0.083	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0.016	0.020	0.033
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0.006	0	0	0	0	0	0	0	0.005	0.010	0
7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	0.054	0.027	0.193	0.065	0.109	0.071	0.238	0.054	0.022	0.25	0.065	0.111	0.097	0.115	0.071	0.067
9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	0	0	0.024	0.047	0.017	0.006	0.338	0.054	0.156	0	0.041	0.089	0.014	0.049	0.092	0.056
11	0	0	0	0	0	0	0	0.027	0	0	0	0	0	0	0	0
12	0.016	0.027	0.012	0.024	0.023	0.019	0	0.014	0.027	0	0.012	0	0	0.077	0.051	0.067
13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14	0	0	0.03	0.024	0.046	0.039	0	0	0.027	0.013	0.006	0.05	0.069	0.038	0.051	0.067
15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
16	0.005	0.007	0.12	0.082	0.063	0.065	0.015	0.027	0.075	0	0.035	0.017	0.069	0	0.051	0.022
17	0	0	0	0	0	0	0	0	0	0	0.006	0	0	0	0	0
18	0.049	0.027	0.03	0.094	0.063	0.058	0	0	0.043	0	0.041	0	0	0.011	0.082	0.033
19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	0.033	0.054	0.048	0.035	0.075	0.065	0	0.041	0.059	0	0.018	0	0.014	0.027	0.041	0
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0.033	0.041	0.072	0.112	0.052	0.071	0.008	0.068	0.048	0.039	0.024	0	0.097	0.044	0.020	0.033
23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	0.007	0	0.047	0.069	0.039	0	0.081	0.027	0	0.041	0.289	0.056	0.033	0.020	0.044
25	0.005	0.007	0	0	0	0	0	0	0	0.013	0	0	0	0	0	0
26	0	0	0.018	0	0	0.006	0	0.014	0.005	0.026	0.029	0	0	0.005	0.010	0
27	0	0.014	0	0.006	0	0	0	0	0	0	0.006	0	0	0	0	0
28	0.005	0	0.024	0	0	0	0	0	0.016	0	0.006	0.006	0	0	0	0
29	0.011	0	0.024	0	0	0	0	0.014	0	0	0	0	0	0	0	0
30	0	0	0.012	0.006	0	0	0.008	0	0	0.026	0.018	0	0	0	0	0.011
31	0.011	0	0	0	0.017	0	0	0.014	0.016	0.026	0	0	0	0.022	0.010	0
32	0.005	0	0	0	0	0	0	0	0	0	0.006	0	0	0	0	0
33	0	0	0.024	0.006	0	0.013	0	0.014	0	0	0.018	0	0	0.022	0	0.011
34	0	0	0	0	0	0	0	0	0	0.026	0	0	0	0	0	0
35	0.005	0.014	0.024	0.006	0.006	0.013	0	0.014	0	0.013	0.018	0	0.028	0.005	0	0.011
36	0	0	0	0	0	0.013	0	0.027	0.022	0.026	0.018	0.161	0.139	0	0	0
37	0.038	0.041	0.006	0.006	0	0	0	0.014	0	0.092	0.006	0	0	0.011	0.020	0.011
38	0.016	0.02	0	0	0	0	0	0	0	0.039	0	0	0	0	0	0
39	0.022	0.02	0.006	0	0	0.006	0	0.027	0	0.053	0.006	0.011	0	0.005	0.020	0.011
40	0.071	0.034	0.018	0.006	0	0	0	0	0.005	0.026	0.029	0	0	0	0	0
41	0.043	0.101	0.006	0.006	0.006	0.006	0.015	0.014	0	0.013	0.071	0	0.056	0.016	0	0
42	0	0	0.018	0	0.029	0.032	0.008	0.014	0.011	0.066	0.018	0	0	0.016	0	0
43	0.038	0.047	0	0.012	0	0.006	0.008	0	0.005	0.013	0.018	0	0.042	0.005	0.010	0
44	0.038	0.054	0.03	0.029	0.006	0.019	0.023	0.014	0.011	0	0.012	0	0	0	0	0
45	0.011	0.041	0.006	0.006	0	0	0.008	0.027	0	0.013	0.035	0.006	0	0.005	0	0
46	0.011	0.02	0.006	0.006	0.011	0.019	0	0.027	0.032	0.013	0.018	0	0	0.005	0.010	0
47	0.011	0.02	0	0.006	0	0.006	0	0	0	0.013	0.012	0	0	0	0	0
48	0	0.007	0	0.012	0.006	0.006	0	0.014	0.011	0	0.012	0.006	0	0.027	0.020	0.044
49	0	0.007	0.006	0	0	0	0	0	0	0	0	0	0	0	0.010	0.011
50	0.005	0	0.006	0.029	0.040	0.026	0.008	0.041	0.022	0	0.041	0	0.014	0.022	0.031	0.011
51	0	0	0.006	0	0	0.006	0.038	0	0	0	0.006	0	0	0.011	0	0.044
52	0.005	0	0.012	0.018	0.006	0.026	0	0.041	0.016	0.013	0.024	0	0	0.016	0.061	0.022
53	0	0	0.006	0.006	0	0	0.031	0	0.011	0	0.006	0	0	0	0	0
54	0.011	0	0.012	0	0.011	0.006	0	0.014	0.011	0	0.029	0	0.014	0.016	0.031	0.011
55	0.005	0	0	0.006	0	0.006	0.046	0	0.011	0	0.006	0	0	0	0	0
56	0	0.007	0.012	0.024	0.011	0.032	0	0.014	0	0	0.018	0.044	0	0.027	0.031	0.022
57	0	0.014	0	0.006	0.006	0	0.008	0	0	0	0	0	0	0	0	0
58	0.016	0.061	0	0.029	0.006	0.013	0	0	0.016	0.026	0.018	0.006	0	0.016	0.020	0
59	0	0	0	0.012	0	0.006	0.008	0	0	0	0	0	0	0	0	0
60	0.049	0.014	0	0.024	0	0.013	0	0	0.032	0.013	0.012	0	0	0	0	0.011
61	0	0	0	0.006	0.023	0.013	0.008	0.014	0.005	0	0.006	0	0	0.005	0	0
62	0.06	0.041	0	0.006	0	0.013	0	0.014	0	0	0.018	0	0	0.011	0	0

Appendix II. Continued.

Allele	Population															
	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0.02	0.035	0.022	0	0.021	0	0.016	0	0.011	0	0
4	0	0.011	0	0	0	0	0	0	0.011	0	0	0.002	0	0	0.02	0.029
5	0	0	0	0	0	0	0	0	0	0	0.014	0	0	0	0	0
6	0.003	0	0	0	0	0	0	0	0	0.005	0	0.008	0.011	0	0	0
7	0	0	0	0	0	0	0	0	0	0	0	0	0	0.011	0.02	0.015
8	0.159	0.131	0.168	0.131	0.281	0.13	0.128	0.087	0.011	0.069	0.086	0.092	0.144	0.1	0.09	0.103
9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	0.074	0.045	0.032	0.102	0.042	0.08	0.128	0.054	0.128	0.059	0.050	0.065	0.067	0.011	0.03	0.015
11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	0.028	0.006	0.005	0.006	0.021	0	0.012	0.011	0.021	0.011	0	0.008	0.033	0	0	0.044
13	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0	0
14	0.038	0.028	0.016	0.068	0	0.07	0.023	0.011	0	0.011	0.036	0.015	0.022	0	0.03	0.015
15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0
16	0.044	0.034	0.047	0.04	0.104	0.08	0.058	0.043	0.011	0.021	0.079	0.085	0.044	0.033	0.04	0.059
17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18	0.033	0.04	0.032	0.023	0	0.03	0.035	0.022	0.032	0.096	0.043	0.061	0.044	0.033	0.01	0
19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	0.036	0.045	0.016	0.023	0	0.05	0.012	0.033	0.011	0.011	0.014	0.006	0	0.033	0	0
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0.023	0.017	0.021	0.051	0.031	0	0	0	0	0	0	0.002	0	0	0.01	0.015
23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0.008	0.011	0.011	0.017	0	0	0	0	0	0	0	0.003	0	0	0	0
25	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0.01	0.015
26	0.003	0	0.011	0	0.01	0	0	0	0	0	0	0.003	0	0.011	0	0
27	0.008	0.006	0.005	0.006	0	0	0	0	0	0	0	0.002	0	0	0.02	0
28	0.005	0.006	0	0	0	0	0	0	0	0.005	0.007	0.003	0	0	0	0.015
29	0.005	0.006	0.005	0	0.01	0	0	0	0	0.011	0.007	0.013	0	0.022	0.01	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0.015
31	0.013	0	0.021	0	0	0.01	0	0	0	0	0.021	0.002	0	0	0.01	0
32	0	0.006	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0.010	0.04	0.016	0.006	0.021	0.01	0	0	0.021	0	0.007	0.006	0	0.011	0.02	0.029
34	0.005	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0	0
35	0.010	0.006	0	0.006	0	0	0	0	0	0.005	0.007	0.006	0.011	0.033	0.05	0.029
36	0.005	0	0.011	0.011	0	0	0	0	0	0	0	0	0	0	0	0
37	0.008	0.023	0.021	0	0	0.01	0	0.011	0	0	0.014	0.005	0	0.022	0.04	0.044
38	0.013	0.011	0	0	0	0	0.012	0.011	0	0	0	0.003	0	0	0.01	0
39	0.013	0.006	0.016	0.006	0.052	0	0	0	0	0	0.007	0.005	0.022	0.011	0.01	0
40	0.008	0.006	0	0.023	0	0.01	0	0	0.011	0.027	0.014	0.002	0	0	0	0
41	0.013	0.011	0.021	0.011	0	0.01	0.035	0.022	0.043	0.021	0.043	0.021	0.022	0.056	0	0.044
42	0.015	0.023	0.016	0.011	0.042	0	0	0.022	0.011	0.011	0.014	0.015	0.011	0.011	0.01	0
43	0.015	0.028	0	0.045	0.01	0.04	0.023	0	0.011	0.016	0	0.008	0.022	0.011	0.02	0
44	0.026	0.023	0.042	0.017	0.031	0.05	0.081	0.011	0.032	0.021	0.021	0.024	0.044	0.022	0.03	0.044
45	0.028	0.017	0	0.011	0	0.01	0.012	0.043	0	0.011	0.029	0.013	0.011	0	0.01	0.029
46	0.021	0.068	0.021	0.011	0.01	0.03	0.012	0.043	0.032	0.037	0.029	0.032	0.078	0.022	0.03	0.015
47	0.013	0.028	0	0	0	0.01	0.012	0.011	0	0.005	0	0.011	0	0.033	0.04	0.044
48	0.023	0.011	0.047	0.028	0.031	0.02	0.023	0.087	0.064	0.048	0.029	0.027	0.022	0.033	0.03	0
49	0.008	0	0.005	0.023	0	0	0	0.011	0	0.016	0	0.008	0.011	0.011	0	0.029
50	0.018	0.006	0.016	0.011	0	0.04	0.035	0.033	0.032	0.032	0.036	0.027	0.044	0.011	0.01	0
51	0.003	0.006	0	0.006	0	0.01	0	0.011	0	0.005	0	0.006	0	0	0	0.015
52	0.021	0.017	0.026	0.017	0	0.06	0.012	0.043	0.043	0.021	0.021	0.018	0.011	0.022	0.01	0
53	0	0	0.016	0	0	0	0	0	0	0.005	0	0.005	0	0	0	0
54	0.023	0.028	0.058	0.017	0.021	0.05	0.07	0.054	0.021	0.032	0.057	0.029	0.033	0.033	0.03	0.015
55	0.010	0.006	0.005	0	0	0.01	0	0	0	0	0.007	0.013	0	0.011	0	0
56	0.005	0.011	0.011	0.011	0	0.03	0.035	0.022	0.043	0.032	0.036	0.027	0.011	0.044	0.03	0
57	0.003	0	0	0	0.01	0.01	0	0	0.011	0.005	0	0	0.011	0	0	0
58	0.018	0.011	0.011	0.028	0.073	0.03	0.012	0.033	0.021	0.048	0.050	0.032	0.022	0.033	0.07	0.015
59	0	0	0	0	0	0	0	0.011	0	0.005	0	0.005	0	0	0	0.029
60	0.026	0.04	0.021	0.045	0.031	0	0.023	0.033	0.043	0.037	0.029	0.023	0.033	0.056	0.04	0.029
61	0.003	0.011	0	0	0	0	0	0	0	0	0.007	0.002	0	0	0	0
62	0.013	0.017	0.005	0.023	0.01	0	0.058	0.033	0.053	0.021	0.007	0.029	0.011	0.022	0.04	0.015

Appendix II. Continued.

Allele	Population																Total
	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	
1	0	0	0	0	0.004	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0.003	0	0	0	0	0
3	0.011	0	0	0.011	0.014	0	0	0	0	0	0	0.005	0	0	0.007	0	0
4	0.011	0.011	0	0.011	0	0	0	0	0	0	0	0	0	0	0.007	0	0
5	0.005	0	0	0	0.014	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0.002	0.003	0	0	0	0.006	0
7	0	0.022	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	0.074	0.078	0.103	0.087	0.050	0.104	0.021	0.065	0.073	0.128	0.124	0.219	0.205	0.1	0.207	0.3	0
9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0.006	0
10	0.058	0.044	0.044	0.033	0.110	0.042	0.021	0.081	0.063	0.021	0.012	0.005	0.045	0	0.04	0.012	0
11	0	0	0	0	0	0	0	0	0	0	0	0.008	0	0	0	0	0
12	0.011	0	0	0.022	0.004	0.01	0	0	0.01	0	0.010	0.005	0.028	0.014	0.027	0.018	0
13	0	0	0	0	0	0	0	0	0	0	0	0	0.006	0	0.007	0	0
14	0.016	0.044	0.015	0.022	0	0.01	0.021	0.032	0.01	0.032	0.032	0.034	0.045	0.171	0.027	0.047	0
15	0	0	0	0	0	0	0	0	0	0	0.002	0	0.011	0	0	0	0
16	0.095	0.056	0.044	0.076	0.050	0.063	0.021	0.065	0.031	0.043	0.007	0.018	0.051	0.114	0.093	0.053	0
17	0	0	0	0	0.004	0	0	0	0	0	0	0.003	0.011	0	0	0	0
18	0.053	0.033	0.029	0.043	0.053	0	0.021	0.016	0.01	0.032	0.035	0.065	0.063	0.043	0.033	0.071	0
19	0	0	0	0	0	0	0	0	0	0	0	0	0.011	0	0.007	0	0
20	0.016	0.011	0.015	0.022	0.004	0.021	0.021	0.113	0.031	0.043	0.030	0.016	0.023	0.029	0.007	0.024	0
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0.01	0.032	0.016	0.01	0.011	0.005	0.021	0.006	0.143	0.007	0.047	0
23	0	0	0	0	0.004	0	0	0	0	0	0.020	0	0	0	0	0	0
24	0.005	0	0	0	0	0.052	0.011	0	0	0	0.005	0.003	0	0	0	0.006	0
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0.016	0	0	0.011	0.004	0.021	0.021	0	0	0	0	0	0.017	0	0	0	0
27	0.005	0	0	0.011	0	0	0.043	0	0	0	0	0	0	0	0	0	0
28	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0.011	0	0	0	0.004	0.01	0.021	0	0	0	0.015	0.008	0	0	0	0	0
30	0	0.011	0.015	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0
31	0	0	0	0	0.004	0.021	0	0	0.021	0.021	0.022	0.003	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0.005	0.078	0	0.011	0.011	0.021	0	0	0.021	0.096	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0.007	0	0	0	0	0	0
35	0.042	0.011	0.015	0.054	0.032	0	0	0.016	0.021	0.011	0.030	0	0.011	0	0	0	0
36	0	0	0	0	0.004	0	0	0	0.01	0.011	0	0.005	0	0	0	0	0
37	0.047	0.033	0.029	0.033	0.018	0	0	0.032	0.01	0.011	0.015	0.008	0.006	0	0	0	0
38	0	0.011	0	0.022	0	0	0	0	0	0	0	0	0.011	0	0	0	0
39	0.011	0.022	0.029	0.022	0.011	0.042	0.043	0	0.021	0.032	0.017	0.016	0.011	0	0.033	0.035	0
40	0	0	0.029	0	0.011	0.021	0	0	0	0	0	0	0	0	0	0.006	0
41	0.037	0.033	0.015	0.043	0.025	0	0.096	0	0.052	0.021	0.020	0.016	0.028	0	0.013	0.006	0
42	0.011	0	0	0.011	0	0.01	0.011	0	0.01	0.011	0.010	0	0.017	0	0	0	0
43	0.021	0.011	0.015	0.043	0.039	0	0.074	0	0	0.021	0.025	0.016	0.034	0	0	0	0
44	0.016	0.011	0.029	0.022	0.004	0.021	0.032	0.016	0	0.011	0.005	0.018	0.017	0	0.02	0.029	0
45	0.005	0	0.015	0.011	0.028	0	0	0.032	0.021	0.032	0.007	0.021	0.017	0	0	0	0
46	0.021	0.033	0.015	0.011	0.018	0.021	0.011	0.016	0.063	0.043	0.020	0.021	0.006	0.029	0.047	0.006	0
47	0.016	0.033	0	0.043	0.018	0.01	0.021	0.016	0.042	0.021	0.017	0.026	0.006	0	0	0.024	0
48	0.042	0.1	0.044	0.033	0.028	0	0.021	0.016	0.052	0.021	0.022	0.018	0.017	0	0.02	0	0
49	0.005	0	0.029	0.011	0	0	0	0.016	0	0	0.005	0.010	0.017	0	0	0	0
50	0.005	0	0	0.011	0.039	0.031	0.043	0.113	0.031	0.011	0.054	0.021	0.006	0.014	0.04	0.012	0
51	0	0	0.015	0	0	0	0	0.016	0	0	0.027	0.013	0.011	0	0	0.012	0
52	0.011	0.011	0.015	0.011	0.032	0.083	0.021	0.032	0.031	0.053	0.057	0.036	0.011	0	0.007	0	0
53	0.005	0	0	0	0.011	0	0	0	0.01	0	0	0.008	0.011	0	0	0.006	0
54	0.053	0.022	0.059	0.033	0.050	0.063	0.064	0	0.063	0.043	0.032	0.034	0.034	0	0.093	0.024	0
55	0	0	0	0	0	0	0	0	0	0	0.007	0.026	0.006	0	0.007	0.006	0
56	0.021	0.033	0.044	0.022	0.035	0.094	0.032	0.048	0.021	0.021	0.050	0.023	0.023	0.014	0.02	0.065	0
57	0	0	0	0.022	0.004	0.021	0	0	0	0	0	0.010	0.017	0.029	0.02	0	0
58	0.037	0.056	0.059	0.022	0.032	0.052	0.064	0.097	0.01	0.011	0.059	0.029	0.04	0.043	0.04	0.053	0
59	0.005	0.011	0	0	0.011	0.01	0	0	0.01	0	0.002	0.016	0	0	0	0	0
60	0.042	0.011	0.015	0.022	0.007	0.01	0.085	0.032	0.031	0	0.042	0.052	0.017	0.071	0.06	0.029	0
61	0.005	0	0	0	0	0.021	0	0	0	0	0.005	0.008	0.017	0	0	0	0
62	0.016	0.011	0	0.011	0.021	0.031	0.053	0.016	0.01	0.011	0.040	0.039	0.028	0.057	0.04	0.053	0

Appendix II. Continued.

OneIII Allele	Size		Population													
	ABL	DFO	1	2	3	4	5	6	7	8	9	10	11	12	13	14
63	290	291	0.005	0	0	0	0.013	0.008	0	0	0	0	0	0	0.098	0.054
64	292	293	0.053	0.03	0.021	0	0.025	0.015	0.025	0.045	0	0.035	0.037	0.031	0.009	0
65	294	295	0.005	0	0	0	0.013	0	0	0.006	0	0.020	0	0	0.018	0
66	296	297	0.032	0.015	0.011	0	0	0	0	0.006	0	0.020	0	0.042	0.089	0.089
67	298	299	0.005	0	0.011	0	0	0	0	0.006	0	0.004	0	0	0	0
68	300	301	0.021	0.037	0.058	0.014	0.05	0.008	0	0.038	0.05	0.051	0.111	0.073	0.036	0.071
69	302	303	0.011	0.015	0.021	0.014	0	0	0.006	0.019	0	0.008	0	0	0	0
70	304	305	0.048	0.03	0.016	0.014	0.037	0.023	0.051	0.038	0.025	0.063	0.019	0.031	0.009	0.018
71	306	307	0	0	0	0	0	0	0	0.006	0	0.004	0	0	0	0
72	308	309	0.037	0.06	0.063	0	0	0.015	0.006	0.013	0.05	0.035	0.167	0.063	0.045	0.054
73	310	311	0	0	0.005	0	0	0	0.013	0.045	0	0	0	0	0	0
74	312	313	0.027	0.104	0.021	0	0.037	0.045	0.019	0.019	0	0.016	0.037	0.052	0.027	0.071
75	314	315	0	0	0.011	0	0	0.008	0	0	0	0.004	0	0	0	0
76	316	317	0.059	0.119	0.021	0.029	0	0.015	0.019	0.045	0.025	0.027	0.037	0.052	0	0.054
77	318	320	0	0	0	0	0	0	0	0	0	0.008	0	0	0	0
78	320	322	0.059	0.082	0.005	0	0.013	0.045	0.057	0.103	0.05	0.047	0.074	0.073	0	0
79	322	324	0.005	0	0.021	0	0	0	0.032	0.013	0	0	0	0	0	0
80	324	326	0.016	0.06	0.026	0.014	0.025	0.008	0.032	0.045	0.025	0.039	0.056	0.063	0.089	0.054
81	326	328	0	0	0	0	0	0.008	0.006	0	0.037	0	0	0	0	0
82	328	330	0.048	0.007	0.032	0.014	0.013	0.023	0.013	0.051	0.037	0.023	0.056	0.073	0.045	0.036
83	330	332	0	0	0	0	0	0.015	0.006	0	0	0.004	0	0	0	0
84	332	334	0.016	0	0.042	0.071	0.013	0.076	0.051	0.013	0.037	0.016	0.019	0.031	0.027	0
85	334	336	0	0	0	0	0	0	0	0	0	0.020	0	0	0.009	0
86	336	338	0.011	0.007	0.042	0.043	0	0.015	0.032	0.006	0.025	0.004	0	0	0.036	0.018
87	338	340	0	0	0	0	0	0	0	0	0	0.008	0	0	0	0
88	340	342	0.011	0.007	0	0.014	0.025	0.015	0.006	0.006	0	0.023	0.037	0.021	0.036	0
89	342	344	0	0	0	0	0	0	0.006	0.045	0	0	0	0	0	0
90	344	346	0	0	0.011	0.057	0.063	0.038	0.07	0	0.05	0.008	0	0.021	0.009	0.071
91	346	348	0	0	0	0	0	0	0	0	0	0.004	0	0	0	0
92	348	350	0	0.007	0.011	0	0.037	0.008	0	0	0	0	0	0	0.027	0.018
93	350	352	0	0	0	0	0	0	0	0	0	0.004	0.019	0.01	0.009	0
94	352	354	0	0	0.005	0	0.013	0	0	0.013	0	0	0	0	0	0
95	354	356	0	0	0	0	0	0	0	0	0	0	0	0	0	0
96	356	358	0	0.007	0.011	0	0.05	0.015	0	0	0	0.012	0	0.01	0.027	0
97	358	360	0	0	0	0	0	0	0	0.013	0	0	0	0	0	0
98	360	362	0.011	0.007	0	0	0	0.008	0.006	0	0.037	0.008	0	0	0.009	0.018
99	362	364	0	0	0	0	0	0	0	0	0	0	0	0.01	0	0
100	364	366	0.005	0	0	0	0	0	0.006	0	0.013	0	0	0	0.018	0
101	366	368	0	0	0	0	0	0	0	0	0	0	0	0	0	0
102	368	370	0.005	0.007	0	0	0	0	0	0.013	0	0	0	0	0	0
103	370	372	0	0	0	0	0	0	0	0	0	0	0	0	0	0
104	372	374	0	0	0.005	0	0.037	0	0.006	0.006	0	0	0	0	0	0
105	374	376	0	0	0	0	0	0	0	0.026	0	0	0	0	0	0
106	376	378	0	0	0.005	0.043	0	0.008	0.006	0.032	0	0	0	0.021	0	0
107	378	380	0	0	0	0	0	0	0.006	0.103	0	0.188	0	0	0	0
108	380	380	0	0	0.011	0	0.013	0.008	0	0	0.013	0	0.019	0	0	0
109	382	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0
110	384	380	0.032	0.007	0	0	0	0	0.006	0	0	0	0	0	0	0
111	386	380	0	0	0	0	0.013	0	0	0	0	0	0	0	0.009	0
112	388	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0
113	390	380	0	0	0.005	0	0	0	0	0	0	0	0	0	0	0
114	392	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0
115	394	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0
116	396	380	0	0	0.005	0.014	0.013	0	0	0	0.013	0	0	0	0	0
117	398	380	0	0	0.005	0.014	0	0	0.013	0	0.025	0	0	0	0	0
118	400	380	0	0	0.021	0.014	0	0	0	0	0	0	0	0.01	0	0
119	402	380	0	0	0	0	0	0	0	0	0.013	0	0	0	0	0
120	404	380	0	0	0	0	0	0.015	0.019	0	0.013	0	0	0	0	0
121	406	380	0.005	0	0	0	0	0	0	0	0.013	0	0	0	0	0
122	408	380	0.005	0.007	0	0	0	0	0	0	0.013	0	0	0	0	0
123	410	380	0.005	0.015	0	0	0	0	0	0	0	0	0	0	0	0
124	412	380	0	0	0	0	0	0	0	0	0.013	0	0	0	0.018	0.018

Appendix II. Continued.

Allele	Population															
	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62
63	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0	0.007
64	0.023	0.011	0.011	0.023	0.014	0.043	0.01	0.005	0	0.005	0	0.005	0	0	0.02	0
65	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0
66	0.012	0.022	0.038	0.034	0.035	0.021	0.021	0.016	0	0.016	0	0.005	0	0	0.02	0.028
67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
68	0	0.005	0.033	0.011	0.028	0.032	0.01	0.011	0.011	0.005	0	0.016	0	0.005	0.027	0
69	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0
70	0.035	0.022	0.011	0.023	0.021	0	0.021	0.022	0.027	0.031	0	0.022	0	0.011	0.02	0.007
71	0	0	0	0	0	0	0	0	0	0	0	0	0	0.011	0	0
72	0.023	0.022	0.005	0.017	0.042	0	0.052	0.011	0.011	0.021	0.016	0.022	0.027	0.005	0.014	0.035
73	0	0	0.005	0	0	0	0	0.011	0	0.005	0	0.011	0	0.011	0	0
74	0	0.038	0.027	0.017	0.014	0.021	0.042	0	0.011	0.01	0.005	0.005	0.011	0.027	0.027	0.049
75	0.012	0.005	0.005	0	0	0	0.01	0	0.027	0.005	0.048	0.016	0.048	0.021	0	0.007
76	0.023	0.022	0	0.034	0.021	0.032	0	0.027	0.005	0.016	0.016	0.005	0.005	0.011	0.02	0.007
77	0	0.005	0	0	0	0.011	0	0.005	0.005	0.005	0.011	0.011	0.021	0.021	0.007	0
78	0.047	0.027	0	0.023	0.035	0.011	0.01	0.005	0.022	0.01	0.027	0.027	0.016	0	0.027	0.007
79	0	0	0	0.006	0	0	0	0.005	0.054	0.005	0.048	0.049	0.053	0.021	0.014	0
80	0	0.016	0.043	0.011	0.014	0.043	0.01	0.005	0.022	0.005	0.027	0.022	0	0	0.02	0.035
81	0	0.016	0	0.006	0	0	0	0.005	0	0.005	0.032	0.027	0	0.027	0	0
82	0	0.011	0.033	0.023	0.014	0.011	0.01	0.022	0.022	0.016	0	0	0.021	0.021	0.007	0.014
83	0	0	0	0	0	0	0	0.005	0.01	0.011	0	0	0.005	0.007	0.007	0
84	0.047	0	0.016	0	0.035	0	0.031	0.005	0	0.016	0	0.005	0	0.005	0.02	0.007
85	0	0	0	0	0	0	0	0.005	0	0	0	0	0	0	0	0
86	0	0.005	0.027	0.017	0.007	0.021	0	0	0	0.01	0	0	0	0.005	0.014	0.014
87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
88	0	0.011	0	0.006	0	0.011	0.021	0	0.005	0	0.005	0	0	0	0	0
89	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90	0	0	0	0	0	0.011	0	0	0.005	0	0	0.005	0	0	0.014	0
91	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
92	0.012	0	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0
93	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
94	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0.007	0
95	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
96	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0
97	0	0.005	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0.007
98	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
99	0	0	0	0	0	0.011	0	0	0	0.005	0	0	0	0	0	0
100	0.012	0.016	0	0	0	0	0	0	0	0	0	0	0	0	0	0
101	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0
102	0	0	0	0	0.007	0.011	0.01	0	0	0	0	0	0	0	0	0
103	0	0	0.016	0.006	0	0	0	0	0	0.005	0	0	0	0	0.007	0
104	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
105	0	0.005	0.005	0	0	0	0	0	0	0.005	0	0	0	0	0	0.021
106	0	0	0	0	0	0	0	0	0.005	0	0.005	0	0	0	0	0
107	0.035	0	0	0	0.007	0	0	0	0	0	0	0.005	0	0	0	0
108	0	0	0.011	0.006	0	0	0.01	0.005	0	0	0.005	0	0	0.027	0	0
109	0	0.005	0.011	0.006	0.014	0.011	0.021	0	0	0.01	0	0	0	0	0	0.007
110	0	0	0	0	0	0	0.01	0	0.005	0.005	0.011	0	0	0.011	0	0.007
111	0	0.005	0.011	0	0	0	0.01	0	0.005	0	0	0.005	0	0	0	0.007
112	0	0	0	0.006	0	0	0	0.005	0.005	0.005	0.016	0.005	0	0.005	0	0.007
113	0	0.005	0.005	0.006	0.007	0	0	0.011	0.005	0.01	0.005	0	0	0.021	0	0.007
114	0	0.005	0	0	0	0	0	0.005	0.005	0.005	0.021	0.011	0	0.005	0.007	0.014
115	0	0.005	0.022	0.011	0.007	0.021	0	0.005	0.016	0	0	0	0.005	0	0.007	0.007
116	0	0	0	0	0.007	0	0	0.011	0.005	0	0.005	0.011	0.005	0.011	0	0.007
117	0	0.011	0.011	0	0	0	0	0.016	0.011	0.005	0.005	0	0.016	0	0	0.014
118	0	0	0.011	0.006	0.007	0	0.01	0.005	0.022	0.005	0	0.022	0	0	0	0.007
119	0	0	0	0.006	0	0	0.021	0	0.016	0.005	0	0	0	0	0.007	0
120	0	0.005	0	0	0	0	0	0.038	0.011	0.042	0.011	0.005	0.016	0.005	0	0
121	0	0	0	0	0	0.021	0	0.011	0.011	0	0	0	0	0	0.007	0.014
122	0	0.005	0.011	0	0	0.011	0	0.016	0.005	0.01	0	0	0	0.011	0	0
123	0	0	0	0	0.007	0	0	0	0	0	0	0	0	0	0	0
124	0	0	0	0.006	0	0	0	0	0	0.005	0.005	0	0	0	0	0

Appendix II. Continued.

Allele	Population															
	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78
63	0.005	0.006	0	0	0	0	0	0	0	0	0	0	0	0	0	0
64	0.032	0.034	0.012	0.026	0.019	0.009	0.02	0.01	0.006	0	0	0	0.027	0.016	0.007	0.016
65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
66	0.021	0.017	0	0.034	0.045	0.017	0.02	0.02	0.006	0	0.005	0	0.007	0.016	0.021	0.021
67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
68	0	0.034	0.012	0.009	0.013	0.026	0.003	0.01	0.017	0	0	0	0.007	0.033	0.042	0.021
69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
70	0.032	0.011	0.037	0.052	0.026	0.009	0.024	0.02	0.006	0	0.016	0	0.027	0.005	0.014	0.021
71	0.005	0	0.012	0	0	0	0	0	0	0	0	0	0	0	0	0
72	0.048	0.011	0.037	0.009	0.045	0.034	0.034	0.01	0.011	0.005	0.057	0.011	0.041	0.011	0.007	0.032
73	0	0	0	0	0	0	0.003	0	0	0	0	0	0	0	0	0
74	0.027	0.022	0.024	0.034	0.026	0.026	0.03	0.01	0.023	0	0.005	0.005	0.034	0.027	0.021	0.016
75	0	0.006	0	0	0.019	0	0.007	0	0	0	0.01	0.005	0.007	0	0	0
76	0.016	0.028	0.037	0.017	0.026	0.034	0.014	0.031	0.034	0.005	0.016	0.011	0.014	0.016	0.021	0.026
77	0	0	0	0.009	0	0	0	0	0	0	0	0	0	0	0.007	0
78	0.027	0.017	0.024	0.026	0.013	0.043	0.024	0.01	0.04	0.011	0.01	0.016	0.034	0.038	0.028	0.005
79	0	0.011	0	0	0	0.017	0	0	0	0.022	0.021	0.016	0	0	0	0
80	0.016	0.034	0	0.026	0.019	0.009	0.014	0.031	0.011	0	0	0	0.007	0.027	0.035	0.021
81	0	0	0	0	0	0.009	0.007	0	0	0	0	0	0	0	0.007	0
82	0.005	0.028	0.012	0.026	0.013	0.009	0.007	0.01	0.023	0.016	0.005	0.005	0.02	0.033	0.014	0.005
83	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0.011	0	0
84	0.016	0.017	0.049	0	0	0.017	0	0	0.011	0.005	0	0	0.034	0.016	0	0.021
85	0	0	0	0	0	0	0	0	0.017	0	0	0	0	0	0	0
86	0.005	0.011	0.024	0.043	0	0.017	0.014	0.031	0.028	0	0	0	0.007	0.016	0.007	0.016
87	0	0	0	0.009	0	0	0	0	0	0	0	0	0	0	0	0
88	0.005	0	0.037	0	0	0.009	0.01	0.01	0	0	0	0	0	0.016	0.007	0.011
89	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0	0	0
90	0.005	0	0	0	0.006	0	0	0.01	0	0	0.01	0	0.007	0.005	0	0
91	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0
92	0.005	0	0	0	0.006	0	0.017	0	0	0	0	0	0.007	0.005	0	0
93	0	0	0	0	0	0.009	0	0	0	0	0	0	0	0	0	0
94	0	0	0	0	0	0	0.003	0	0	0	0	0	0	0	0	0
95	0	0.006	0	0	0	0	0	0	0	0	0	0	0.007	0	0	0
96	0	0	0	0	0.006	0	0.003	0	0	0	0	0	0.007	0.005	0	0
97	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0
98	0.005	0	0	0	0	0	0.003	0	0	0	0	0	0	0	0	0.016
99	0	0	0	0	0	0	0	0	0.006	0	0	0	0	0.005	0	0
100	0	0	0	0.009	0	0	0.003	0	0	0	0	0	0	0.005	0	0.011
101	0.005	0	0	0.009	0	0	0	0	0	0	0	0	0.007	0.005	0	0.011
102	0.005	0	0	0.009	0	0	0	0	0	0	0	0	0	0	0.007	0
103	0.016	0.022	0	0.026	0	0	0.007	0	0	0	0	0	0.014	0	0	0
104	0	0	0	0	0.006	0	0.003	0	0	0	0	0	0	0.005	0	0
105	0	0	0	0	0	0	0.003	0.01	0.006	0	0	0	0	0	0.007	0.005
106	0.005	0	0	0	0	0.009	0	0	0	0	0	0	0	0	0.007	0
107	0	0.017	0	0	0	0	0	0.02	0.006	0.016	0	0.005	0.007	0.005	0.007	0
108	0	0	0	0.009	0	0.009	0.007	0	0	0	0	0	0	0	0	0
109	0.011	0.011	0	0.009	0	0	0.007	0.01	0.011	0.027	0.026	0.005	0	0.005	0.007	0
110	0.005	0	0	0.009	0.006	0	0	0	0	0	0	0	0.007	0	0	0
111	0.005	0.017	0	0	0	0	0.003	0.01	0.006	0	0	0.016	0.007	0.005	0	0
112	0.005	0.006	0	0	0	0	0.003	0	0	0	0	0	0	0	0	0
113	0	0	0.024	0.009	0.006	0.017	0.003	0	0.017	0.011	0.01	0.005	0	0.011	0.014	0
114	0	0	0.012	0.017	0.006	0.009	0	0.01	0	0	0	0.005	0	0	0	0
115	0	0	0.012	0	0.006	0	0.007	0	0.006	0.043	0.01	0.011	0	0.005	0.021	0
116	0.016	0.006	0	0	0.006	0	0.003	0	0.006	0	0	0	0	0.005	0	0
117	0.005	0.006	0.012	0	0	0	0.003	0	0.006	0.016	0.021	0.016	0.007	0	0	0.016
118	0	0.006	0.012	0.009	0	0	0	0	0	0.011	0	0	0.007	0.011	0	0
119	0.005	0.006	0	0	0.006	0.009	0	0	0	0	0	0.005	0.007	0	0	0
120	0	0.006	0	0	0	0.009	0	0	0	0.005	0	0	0	0.005	0	0
121	0	0.006	0	0	0	0	0	0.01	0	0	0	0	0.007	0	0	0.011
122	0	0	0	0.009	0	0	0	0	0	0	0	0	0	0	0.007	0
123	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
124	0	0	0	0.009	0	0	0	0	0	0	0.005	0.005	0.007	0.005	0	0

Appendix II. Continued.

<i>OneIII</i>	Size	Size	Population															
			Allele	ABL	DFO	1	2	3	4	5	6	7	8	9	10	11	12	13
125	414	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
126	416	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.018	0
127	418	380	0	0	0	0	0	0	0.03	0.006	0	0	0	0	0	0	0	0
128	420	380	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0.031	0	0
129	422	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
130	424	380	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
131	426	380	0.005	0	0	0	0	0	0.023	0.006	0	0.013	0	0	0	0	0	0
132	428	380	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0.01	0	0
133	430	380	0	0	0	0	0	0	0.023	0.013	0	0	0	0	0	0	0	0
134	432	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
135	434	380	0	0	0	0	0	0	0.008	0	0	0	0	0	0	0	0	0
136	436	380	0	0	0.005	0	0	0	0	0.013	0	0.013	0	0	0	0	0	0
137	438	380	0	0	0.026	0	0	0	0	0	0	0	0	0	0	0	0	0
138	440	380	0	0	0	0	0	0	0.008	0.006	0	0	0	0	0	0	0	0
139	442	380	0	0	0	0	0	0.013	0	0.013	0	0	0	0	0	0	0	0
140	444	380	0	0	0	0	0	0	0	0.006	0	0	0	0	0	0	0	0
141	448	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
142	450	380	0	0	0	0	0	0	0.015	0	0	0	0	0	0	0	0	0.018
143	452	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
144	454	380	0	0	0.005	0.029	0.013	0	0	0	0	0.013	0	0	0	0	0	0
145	456	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
146	458	380	0	0	0.011	0	0	0	0	0.006	0	0	0	0	0	0	0	0
147	460	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
148	464	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
149	466	380	0	0	0	0	0	0	0.008	0	0	0	0	0	0	0	0	0
150	468	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
151	470	380	0.011	0	0	0	0	0.013	0	0	0	0	0	0	0	0	0	0
152	472	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
153	474	380	0	0	0	0.014	0	0	0	0	0	0.013	0	0	0	0	0	0.018
154	476	380	0	0	0	0	0	0	0	0	0	0	0	0.019	0	0.009	0	0
155	478	380	0	0	0	0.014	0	0	0	0	0	0	0	0	0	0	0	0
156	480	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
157	484	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
158	488	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
159	490	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
160	494	380	0	0	0	0	0	0	0.008	0.019	0	0	0	0	0	0	0	0
161	498	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
162	500	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
163	504	380	0	0	0	0.014	0	0	0	0	0	0	0	0	0	0	0	0
164	506	380	0	0	0	0	0	0	0	0.013	0	0	0	0	0	0	0	0
165	514	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.009	0
166	518	380	0	0.007	0	0	0	0	0	0	0	0	0	0	0	0	0	0
167	532	380	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0	0
168	536	380	0	0	0	0	0	0.013	0	0	0	0	0	0	0	0.01	0	0
169	540	380	0	0	0	0	0	0	0	0	0	0	0	0.019	0	0	0	0
170	544	380	0	0	0	0	0	0	0.008	0	0	0	0	0	0	0	0	0
<i>n</i>			94	67	95	35	40	66	79	78	40	128	27	48	56	28		
<i>n_a</i>			53	35	50	31	34	46	54	46	40	54	24	34	37	26		
<i>n_{eff}</i>			35.51	17.72	31.61	26.54	27.72	31.79	35.44	N/A	45.14	N/A	18.58	30.20	23.19	29.62		
<i>a</i>			21.87	17.41	21.40	19.98	20.66	21.79	22.40	N/A	23.19	N/A	18.07	20.41	19.25	19.71		
<i>H_E</i>			0.972	0.944	0.968	0.962	0.964	0.969	0.972	N/A	0.978	N/A	0.946	0.967	0.957	0.966		
<i>H_O</i>			0.947	0.940	0.916	1.000	0.950	0.955	0.949	N/A	0.925	N/A	1.000	0.979	0.982	0.893		
<i>F_{IS}</i>			0.026	0.003	0.055	-0.040	0.015	0.015	0.023	N/A	0.055	N/A	-0.058	-0.013	-0.027	0.077		

Appendix II. Continued.

Allele	Population															
	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
125	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007	0
126	0	0	0	0	0	0	0	0	0	0	0	0.009	0	0	0.007	0
127	0	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0
128	0	0	0	0	0	0	0.019	0	0	0	0	0	0	0	0	0
129	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
130	0	0	0	0	0	0	0	0	0	0	0	0.009	0	0	0	0
131	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
132	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
133	0	0	0	0	0	0	0	0	0	0	0	0.009	0	0	0	0
134	0	0	0	0	0.011	0	0	0	0.014	0	0	0.019	0	0	0.007	0
135	0	0	0	0.012	0	0	0	0	0	0	0	0	0	0	0	0
136	0	0	0	0	0	0	0.019	0	0.014	0.083	0.016	0	0	0	0	0.005
137	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
138	0	0	0	0	0	0	0	0	0	0.028	0.016	0	0	0	0	0
139	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
140	0	0	0	0	0	0	0	0	0	0	0	0.009	0	0	0	0
141	0	0	0	0	0	0.015	0	0	0	0	0	0.009	0	0	0	0
142	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
143	0	0	0	0	0	0	0	0	0	0.028	0	0.019	0	0	0	0.005
144	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
145	0	0	0	0	0.011	0.015	0	0	0	0	0	0	0	0	0	0
146	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
147	0	0	0	0.012	0	0	0	0	0	0	0.016	0.009	0	0	0	0
148	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005
149	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005
151	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
152	0	0	0	0	0	0.015	0	0	0	0	0	0	0	0	0	0
153	0	0	0	0	0	0	0	0	0	0	0	0.009	0	0	0	0
154	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.011
155	0	0	0	0	0	0	0	0	0	0	0	0.009	0	0	0	0
156	0	0	0	0	0	0	0	0	0	0	0	0.009	0	0	0	0.011
157	0	0	0.022	0	0	0	0	0	0	0	0	0	0	0	0	0
158	0	0	0	0	0	0	0	0	0	0	0	0.009	0	0	0	0
159	0	0	0	0	0	0	0	0	0	0.028	0.016	0	0	0	0	0
160	0	0	0	0	0	0	0	0.029	0	0	0	0	0	0	0	0
161	0	0	0	0	0	0	0	0	0.028	0	0	0	0	0	0	0
162	0	0	0.022	0	0	0	0	0	0	0	0	0	0	0	0	0
163	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
164	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
165	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
166	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
167	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
169	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
170	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
n	49	34	23	43	46	34	27	17	36	18	31	53	55	117	76	91
n_a	31	28	20	34	36	31	26	17	32	21	31	55	47	63	59	79
n_{eff}	N/A	N/A	9.95	24.21	24.20	28.47	20.74	15.58	26.35	24.23	31.52	52.01	N/A	N/A	46.09	62.39
a	N/A	N/A	15.95	20.02	19.97	20.42	18.59	16.46	20.32	19.52	21.23	24.65	N/A	N/A	24.08	25.68
H_E	N/A	N/A	0.900	0.959	0.959	0.965	0.952	0.936	0.962	0.959	0.968	0.981	N/A	N/A	0.978	0.984
H_O	N/A	N/A	0.913	0.953	0.978	0.882	0.963	1.000	0.972	0.944	0.968	1.000	N/A	N/A	1.000	0.956
F_{IS}	N/A	N/A	-0.015	0.005	-0.021	0.087	-0.012	-0.071	-0.011	0.015	0.001	-0.020	N/A	N/A	-0.022	0.029

Appendix II. Continued.

Allele	Population															
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
125	0	0	0	0	0.013	0.013	0.027	0.005	0	0	0	0.016	0	0	0	0
126	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
127	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
128	0	0	0.01	0.021	0	0	0	0	0	0	0	0.011	0.005	0	0	0
129	0	0	0.01	0	0.006	0	0	0	0	0	0	0	0	0	0	0
130	0	0	0	0	0.013	0	0	0	0	0	0	0	0	0	0	0
131	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
132	0	0	0.01	0.011	0	0.006	0	0	0	0	0	0	0	0	0	0
133	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
134	0	0	0.01	0.011	0	0	0	0	0	0	0	0	0	0	0	0
135	0	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0
136	0	0	0	0.011	0	0	0	0.011	0	0	0	0	0	0	0	0
137	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
138	0	0	0.01	0.021	0	0	0	0.005	0	0	0	0	0	0	0	0
139	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
140	0	0	0.021	0	0.006	0	0	0.005	0	0	0	0	0	0	0	0
141	0	0	0	0.011	0	0	0.005	0	0	0	0	0	0	0	0	0
142	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
143	0	0	0	0	0.006	0	0	0	0	0	0	0	0.005	0	0	0
144	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
145	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
146	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
147	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0
148	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
149	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
150	0	0	0	0.021	0	0	0	0	0	0	0	0	0	0	0	0
151	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
152	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
153	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
154	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
155	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
157	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
158	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
159	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
160	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
161	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
162	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
163	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
164	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
165	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
166	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
167	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
169	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
170	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	78	40	48	47	77	77	93	94	94	191	181	95	96	387	227	259
<i>n_a</i>	61	32	58	52	59	57	39	52	47	44	59	57	52	73	69	71
<i>n_{eff}</i>	N/A	N/A	66.09	59.07	55.05	41.78	18.03	16.55	15.78	N/A	N/A	11.21	14.98	N/A	N/A	N/A
<i>a</i>	N/A	N/A	25.93	25.24	24.66	23.16	18.37	19.93	19.12	N/A	N/A	19.84	19.37	N/A	N/A	N/A
<i>H_E</i>	N/A	N/A	0.985	0.983	0.982	0.976	0.945	0.940	0.937	N/A	N/A	0.911	0.933	N/A	N/A	N/A
<i>H_O</i>	N/A	N/A	0.958	0.936	0.974	0.961	0.978	0.936	0.926	N/A	N/A	0.895	0.938	N/A	N/A	N/A
<i>F_{IS}</i>	N/A	N/A	0.027*	0.048	0.008	0.015	-0.036	0.004	0.012*	N/A	N/A	0.018**	-0.004**	N/A	N/A	N/A

Appendix II. Continued.

OneIII Allele	Population															
	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62
125	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
126	0	0	0	0	0.007	0	0.01	0	0	0	0.005	0	0	0	0	0.007
127	0	0	0	0	0	0	0	0	0.005	0	0	0.005	0	0	0	0
128	0	0	0	0	0.007	0	0	0	0	0	0	0	0	0	0	0
129	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
130	0	0	0	0	0.007	0	0	0	0	0	0	0	0	0	0	0
131	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
132	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
133	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
134	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0
135	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
136	0	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0
137	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
138	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
139	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
140	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
141	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
142	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
143	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
144	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
145	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
146	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
147	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
148	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
149	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
151	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
152	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
153	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
154	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
155	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
157	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
158	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
159	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
160	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
161	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
162	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
163	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
164	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
165	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
166	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
167	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
169	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
170	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
n	43	93	92	88	71	47	48	92	93	96	94	91	94	94	74	72
n_a	34	61	54	52	50	42	43	46	45	51	38	41	21	31	49	55
n_{eff}	N/A	15.77	13.70	10.49	15.55	20.81	13.73	7.34	7.34	8.17	4.70	4.99	4.51	2.64	12.25	12.56
a	N/A	21.03	20.21	18.91	20.71	21.41	20.18	16.90	17.02	17.67	14.62	14.57	10.35	11.17	20.03	20.14
H_E	N/A	0.937	0.927	0.905	0.936	0.952	0.927	0.864	0.864	0.878	0.787	0.800	0.778	0.622	0.918	0.920
H_O	N/A	0.925	0.946	0.909	0.901	1.000	0.938	0.815	0.903	0.906	0.819	0.813	0.734	0.660	0.905	0.875
F_{IS}	N/A	0.013	-0.020	-0.005	0.037*	-0.051	-0.011	0.057	-0.046	-0.033	-0.041	-0.017	0.057	-0.061	0.014*	0.050

Appendix II. Continued.

Allele	Population															
	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78
125	0	0.006	0	0	0	0.009	0	0	0	0	0	0	0	0	0	0
126	0	0	0	0	0	0	0.003	0	0	0	0	0	0	0	0.007	0.005
127	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0
128	0	0.006	0	0	0	0	0.003	0.01	0.006	0.005	0	0	0	0	0	0.005
129	0	0	0	0	0	0	0.003	0.01	0	0	0	0	0	0	0	0
130	0	0	0	0	0	0	0.003	0	0	0.005	0	0	0	0	0	0.005
131	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
132	0	0	0	0	0	0	0	0	0	0.005	0	0.005	0	0	0	0.005
133	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
134	0	0	0	0	0.006	0	0	0	0	0	0	0.005	0	0	0	0.005
135	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
136	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0.007	0
137	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
138	0	0	0	0	0	0	0	0	0.006	0	0	0.016	0	0.005	0	0
139	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
140	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
141	0	0	0	0	0	0	0	0	0	0	0.005	0.005	0	0	0	0.016
142	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
143	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0.005
144	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
145	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
146	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
147	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
148	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
149	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
151	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
152	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
153	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
154	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
155	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
157	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
158	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
159	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
160	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
161	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
162	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
163	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
164	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
165	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
166	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
167	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
169	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
170	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	94	89	41	58	77	58	148	49	88	92	96	95	74	92	71	95
<i>n_a</i>	61	59	37	45	58	53	70	46	57	32	32	40	57	71	57	58
<i>n_{eff}</i>	16.41	20.98	15.97	16.11	23.61	18.43	15.13	14.62	16.83	3.13	4.02	4.12	17.63	36.68	15.67	25.69
<i>a</i>	20.95	21.77	20.66	20.39	22.18	22.06	20.91	20.87	21.11	12.00	13.25	13.89	21.42	23.91	21.08	22.06
<i>H_E</i>	0.939	0.952	0.937	0.938	0.958	0.946	0.934	0.932	0.941	0.680	0.751	0.758	0.943	0.973	0.936	0.961
<i>H_O</i>	0.936	0.966	1.000	1.000	0.974	0.931	0.919	0.918	0.909	0.696	0.760	0.747	0.932	0.967	0.972	0.947
<i>F_{IS}</i>	0.003	-0.015	-0.068	-0.067	-0.017	0.016	0.016	0.014*	0.034	-0.023	-0.013	0.013	0.012*	0.006	-0.038	0.014

Appendix II. Continued.

Allele	Population															
	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94
125	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
126	0.005	0	0.006	0.006	0	0	0	0.014	0	0	0	0	0	0	0	0
127	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
128	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
129	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
130	0	0.007	0	0	0	0	0	0	0	0	0	0	0	0	0	0
131	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
132	0.011	0.007	0	0	0	0	0	0	0	0	0	0	0	0	0	0
133	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
134	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
135	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
136	0	0.014	0	0	0	0	0	0	0	0	0	0	0	0	0	0
137	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
138	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
139	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
140	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
141	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
142	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
143	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
144	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
145	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
146	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
147	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
148	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
149	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
151	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
152	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
153	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
154	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
155	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
157	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
158	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
159	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
160	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
161	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
162	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
163	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
164	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
165	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
166	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
167	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
169	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
170	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	92	74	83	85	87	77	65	37	93	38	85	90	36	91	49	45
<i>n_a</i>	53	41	49	52	41	51	24	39	45	30	54	19	24	55	39	40
<i>n_{eff}</i>	30.89	29.80	15.76	24.35	N/A	N/A	5.59	40.31	N/A	12.50	40.93	7.09	16.60	31.25	N/A	35.44
<i>a</i>	21.27	20.75	19.00	20.24	N/A	N/A	11.66	22.93	N/A	18.00	23.01	10.70	16.20	22.17	N/A	21.80
<i>H_E</i>	0.968	0.966	0.937	0.959	N/A	N/A	0.821	0.975	N/A	0.920	0.976	0.859	0.940	0.968	N/A	0.972
<i>H_O</i>	0.902	0.932	0.904	0.953	N/A	N/A	0.877	1.000	N/A	0.921	0.965	0.878	0.972	0.978	N/A	0.978
<i>F_{IS}</i>	0.068*	0.035	0.035***	0.006***	N/A	N/A	-0.069	-0.026	N/A	-0.001	0.011	-0.022	-0.035	-0.010	N/A	-0.006

Appendix II. Continued.

Allele	Population															
	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110
125	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
126	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
127	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
128	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0	0
129	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
130	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
131	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
132	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
133	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
134	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
135	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
136	0	0.006	0	0	0	0	0	0	0	0	0	0	0	0	0	0
137	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
138	0	0	0	0	0	0	0	0	0.011	0	0	0	0	0	0	0
139	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
140	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
141	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
142	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
143	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
144	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
145	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
146	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
147	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
148	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
149	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
151	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
152	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
153	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
154	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
155	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
157	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
158	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
159	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
160	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
161	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
162	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
163	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
164	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
165	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
166	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
167	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
169	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
170	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
n	195	88	95	88	48	50	43	46	47	94	70	310	45	45	50	34
n_a	72	53	54	47	27	32	28	36	34	48	45	70	34	39	44	36
n_{eff}	N/A	27.90	22.73	22.78	9.85	21.52	18.84	31.95	23.13	30.25	N/A	N/A	23.98	36.74	38.98	40.68
a	N/A	21.51	21.25	20.02	16.03	18.48	17.65	21.13	19.51	21.08	N/A	N/A	20.07	22.35	22.83	23.02
H_E	N/A	0.964	0.956	0.956	0.898	0.954	0.947	0.969	0.957	0.967	N/A	N/A	0.958	0.973	0.974	0.975
H_O	N/A	0.966	0.958	0.966	0.896	0.960	0.884	0.978	0.979	0.989	N/A	N/A	0.956	1.000	0.980	1.000
F_{IS}	N/A	-0.002	-0.002	-0.010	0.003	-0.007	0.067	-0.010	-0.023	-0.023	N/A	N/A	0.003	-0.028	-0.006	-0.026

Appendix II. Continued.

Allele	Population																Total
	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	
125	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
126	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
127	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
128	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
129	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
130	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
131	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
132	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
133	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
134	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
135	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
136	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
137	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
138	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
139	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
140	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
141	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
142	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
143	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
144	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
145	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
146	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
147	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
148	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
149	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
151	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
152	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
153	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
154	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
155	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
157	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
158	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
159	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
160	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
161	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
162	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
163	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
164	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
165	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
166	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
167	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
169	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
170	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	95	45	34	46	141	48	47	31	48	47	202	192	88	35	75	85	10048
<i>n_a</i>	50	36	38	41	59	31	29	25	42	37	51	57	46	18	30	30	166
<i>n_{eff}</i>	29.15	29.23	41.42	38.05	N/A	23.75	25.71	20.33	37.69	26.17	N/A	N/A	16.94	12.45	13.58	8.85	
<i>a</i>	20.90	20.74	23.39	22.60	N/A	18.99	19.23	17.75	22.35	20.67	N/A	N/A	19.62	13.73	16.35	15.10	
<i>H_E</i>	0.966	0.966	0.976	0.974	N/A	0.958	0.961	0.951	0.973	0.962	N/A	N/A	0.941	0.920	0.926	0.887	
<i>H_O</i>	0.937	1.000	0.971	0.978	N/A	1.000	1.000	0.968	0.938	0.957	N/A	N/A	0.875	0.943	0.920	0.894	
<i>F_{IS}</i>	0.030*	-0.036	0.005	-0.005	N/A	-0.044	-0.041	-0.018	0.037*	0.005	N/A	N/A	0.070***	-0.026	0.007	-0.008*	

Appendix II. Continued.

<i>Ots3</i>	Allele	Size ABL	Size DFO	Population													
				1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	123	72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	127	76	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	129	78	0	0	0	0	0	0	0	0	0.007	0	0	0	0	0	0
4	131	80	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	133	82	0.054	0.091	0.033	0.029	0.05	0.045	0.032	0.066	0	0.021	0.019	0.031	0	0	0
6	135	84	0.016	0.015	0.022	0.014	0.025	0.015	0	0.007	0.013	0.004	0	0	0	0	0
7	137	86	0	0	0	0	0	0	0.006	0	0	0.013	0.037	0.052	0	0	0
8	139	88	0.076	0.083	0.125	0.143	0.075	0.075	0.038	0.164	0.075	0.067	0.222	0.177	0.065	0.019	0
9	141	90	0.06	0.061	0.076	0.129	0.1	0.045	0.051	0.059	0.063	0.025	0.019	0.042	0.065	0.056	0
10	143	92	0.054	0.106	0.049	0.014	0.013	0.112	0.082	0.079	0.063	0.046	0.037	0.042	0.037	0.037	0
11	145	94	0.054	0.061	0.114	0.1	0.188	0.052	0.082	0.138	0.163	0.038	0	0	0.037	0.074	0
12	147	96	0.283	0.212	0.071	0.071	0.138	0.209	0.19	0.092	0.087	0.155	0.148	0.198	0.065	0.093	0
13	149	98	0.016	0.008	0.054	0.143	0.075	0.015	0.032	0	0.075	0.067	0	0	0.046	0.074	0
14	151	100	0.06	0.068	0.12	0.1	0.175	0.067	0.044	0.105	0.075	0.164	0.222	0.156	0.111	0.056	0
15	153	102	0.125	0.121	0.103	0.086	0.087	0.127	0.158	0.072	0.188	0.13	0.019	0.052	0.231	0.111	0
16	155	104	0.038	0.061	0.12	0.071	0.025	0.06	0.07	0.079	0.087	0.101	0.241	0.167	0.13	0.056	0
17	157	106	0.027	0.045	0.022	0.043	0.037	0.075	0.089	0.053	0.075	0.08	0.037	0.073	0.12	0.093	0
18	159	107	0.038	0.015	0.065	0.057	0.013	0.052	0.07	0.033	0.037	0.021	0	0.01	0.009	0.019	0
19	161	109	0.049	0.038	0.022	0	0	0.03	0.019	0	0	0	0	0	0	0	0
20	163	111	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	165	113	0.043	0.008	0	0	0	0	0	0	0	0.034	0	0	0	0	0
22	167	115	0	0	0	0	0	0.007	0.013	0	0	0.017	0	0	0	0	0
23	169	117	0	0	0	0	0	0	0	0	0	0.004	0	0	0.083	0.278	0
24	171	119	0	0	0	0	0	0	0	0	0	0.008	0	0	0	0.037	0
25	173	121	0	0	0	0	0	0.007	0.006	0.02	0	0.004	0	0	0	0	0
26	177	125	0	0	0	0	0	0	0	0.026	0	0	0	0	0	0	0
27	179	127	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	181	127	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	183	127	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	185	127	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	187	127	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	189	127	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	191	127	0	0	0	0	0	0	0.019	0	0	0	0	0	0	0	0
34	193	127	0	0.008	0.005	0	0	0	0	0	0	0	0	0	0	0	0
35	197	127	0	0	0	0	0	0.007	0	0	0	0	0	0	0	0	0
<i>n</i>			92	66	92	35	40	67	79	76	40	119	27	48	54	27	
<i>n_a</i>			16	16	15	13	13	17	17	15	12	19	10	11	12	13	
<i>n_{eff}</i>			8.27	10.09	11.65	11.34	9.27	10.45	10.48	N/A	10.26	N/A	5.94	7.76	8.81	8.78	
<i>a</i>			12.06	11.68	11.87	11.26	10.63	12.25	12.24	N/A	10.84	N/A	8.29	9.36	10.36	11.61	
<i>H_E</i>			0.879	0.901	0.914	0.912	0.892	0.904	0.905	N/A	0.903	N/A	0.832	0.871	0.886	0.886	
<i>H_O</i>			0.902	0.909	0.924	1.000	0.775	0.910	0.886	N/A	0.950	N/A	0.778	0.792	0.944	0.889	
<i>F_{IS}</i>			-0.027	-0.009	-0.011	-0.098	0.133	-0.007	0.021	N/A	-0.053	N/A	0.066	0.092	-0.066	-0.003	

Appendix II. Continued.

<i>Ots3</i>	Population															
	Allele	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0.011	0	0	0.056	0.015	0.053	0.031	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0.047	0.065	0.091	0.037	0	0.029	0.026	0	0.009	0.018	0.004	0	0.011
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	0	0	0	0.012	0.033	0.167	0	0	0.015	0	0.031	0.009	0.036	0.051	0	0.038
8	0.063	0	0.152	0	0.022	0.015	0	0.028	0.029	0	0.031	0.066	0.073	0.047	0	0.005
9	0.094	0.014	0	0	0	0.015	0	0	0.015	0.026	0.078	0	0	0	0	0.005
10	0.031	0.1	0	0.058	0.109	0.015	0.074	0.222	0.162	0.211	0.141	0.038	0.055	0.034	0.099	0.055
11	0.073	0.043	0.022	0.047	0	0	0.019	0.056	0.029	0.026	0.016	0	0.009	0.038	0	0.016
12	0.125	0.157	0.13	0.081	0.087	0.106	0.13	0.25	0.206	0.211	0.203	0.377	0.336	0.331	0.401	0.522
13	0.042	0	0.152	0.093	0.13	0	0.111	0.056	0.059	0.053	0.063	0.028	0.018	0.004	0.066	0.016
14	0.094	0.129	0.022	0.081	0.054	0.03	0.093	0	0.059	0	0.047	0.038	0.036	0.047	0	0.06
15	0.177	0.271	0.261	0.372	0.261	0.182	0.185	0.167	0.147	0.316	0.188	0.217	0.109	0.131	0.026	0.011
16	0.083	0.1	0.13	0	0	0.015	0	0.167	0.118	0.026	0.109	0.038	0.064	0.025	0.053	0.011
17	0.104	0.186	0.109	0.058	0.13	0.212	0.167	0	0.118	0.026	0.063	0.123	0.191	0.203	0.329	0.192
18	0.01	0	0.022	0.128	0.065	0.152	0.185	0	0	0.026	0	0.019	0.036	0.047	0.02	0.033
19	0	0	0	0.012	0	0	0	0	0	0	0	0.019	0.009	0.021	0.007	0.005
20	0	0	0	0	0.011	0	0	0	0	0	0	0.009	0.009	0.008	0	0.005
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0	0	0	0	0	0	0.004	0	0
23	0.104	0	0	0	0	0	0	0	0	0	0	0.009	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0.004	0	0
27	0	0	0	0.012	0.022	0	0	0	0	0	0	0	0	0	0	0.005
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	48	35	23	43	46	33	27	18	34	19	32	53	55	118	76	91
<i>n_a</i>	12	8	9	12	13	11	9	8	13	11	12	14	14	16	8	17
<i>n_{eff}</i>	N/A	N/A	6.99	5.60	7.96	7.30	7.99	6.49	8.69	5.67	8.80	4.82	N/A	N/A	3.54	3.16
<i>a</i>	N/A	N/A	8.09	9.55	10.28	8.66	8.40	7.86	10.43	10.01	10.50	9.13	N/A	N/A	6.08	8.10
<i>H_E</i>	N/A	N/A	0.857	0.821	0.874	0.863	0.875	0.846	0.885	0.824	0.886	0.792	N/A	N/A	0.717	0.684
<i>H_O</i>	N/A	N/A	0.870	0.884	0.891	0.818	0.926	0.944	0.882	0.895	0.906	0.849	N/A	N/A	0.776	0.725
<i>F_{IS}</i>	N/A	N/A	-0.015	-0.077	-0.020	0.053	-0.059	-0.120	0.003	-0.089	-0.023	-0.072	N/A	N/A	-0.083	-0.061

Appendix II. Continued.

Allele	Population															
	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0.011	0	0	0	0.011	0	0	0.003	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0.025	0	0.01	0.021	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0.002
7	0.013	0.025	0.021	0.053	0.006	0.013	0	0.043	0	0.063	0.022	0.032	0.078	0.029	0.029	0.021
8	0	0	0.01	0.011	0	0	0	0	0	0	0.011	0.011	0	0.008	0.004	0.004
9	0.006	0.013	0	0.011	0.013	0.013	0	0.048	0	0	0.011	0	0.01	0.004	0.007	0
10	0.063	0.088	0.052	0	0.071	0.058	0.011	0.043	0.085	0.008	0.045	0.043	0.026	0.024	0.047	0.04
11	0.013	0	0	0.032	0.006	0	0.038	0.005	0	0.047	0.034	0.016	0	0.001	0.004	0.006
12	0.5	0.288	0.333	0.457	0.218	0.253	0.441	0.505	0.505	0.419	0.349	0.362	0.297	0.363	0.36	0.334
13	0.025	0.013	0.021	0.011	0.019	0.019	0.005	0.005	0	0.029	0.131	0.053	0.01	0.039	0.038	0.034
14	0.032	0.05	0.021	0.021	0.058	0.052	0.065	0.021	0.032	0.01	0.014	0.021	0.021	0.014	0.024	0.011
15	0.051	0.088	0.115	0.085	0.115	0.065	0.054	0.149	0.154	0.224	0.17	0.096	0.146	0.121	0.113	0.088
16	0.038	0.05	0.021	0.011	0.051	0.052	0.032	0.011	0.016	0.008	0.014	0.021	0.016	0.009	0.004	0.04
17	0.171	0.338	0.313	0.202	0.397	0.37	0.199	0.096	0.197	0.154	0.184	0.298	0.292	0.34	0.32	0.355
18	0.025	0.025	0	0.043	0.013	0.032	0	0	0	0	0	0	0.042	0.01	0.002	0.013
19	0	0	0.021	0.011	0	0.006	0.145	0.053	0.005	0.018	0.003	0.005	0.01	0.008	0.011	0.006
20	0.025	0	0.021	0.011	0.026	0.019	0	0.005	0.005	0.018	0.006	0.021	0.01	0.013	0.018	0.031
21	0.006	0.025	0	0	0.006	0.045	0	0.005	0	0.003	0.003	0.021	0.036	0.018	0.018	0.015
22	0	0	0	0	0	0	0.011	0	0	0	0	0	0	0	0	0
23	0.006	0	0.01	0.011	0	0	0	0	0	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0	0	0
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0.021	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	79	40	48	47	78	77	93	94	94	192	179	94	96	394	225	262
<i>n_a</i>	15	11	15	16	13	13	10	14	8	12	15	13	14	15	15	15
<i>n_{eff}</i>	N/A	N/A	4.55	3.89	4.42	4.69	3.83	3.42	3.10	N/A	N/A	4.30	4.97	N/A	N/A	N/A
<i>a</i>	N/A	N/A	9.11	9.25	8.10	8.97	6.98	8.04	5.40	N/A	N/A	8.31	8.38	N/A	N/A	N/A
<i>H_E</i>	N/A	N/A	0.780	0.743	0.774	0.787	0.739	0.708	0.677	N/A	N/A	0.767	0.799	N/A	N/A	N/A
<i>H_O</i>	N/A	N/A	0.792	0.638	0.769	0.792	0.774	0.681	0.670	N/A	N/A	0.755	0.750	N/A	N/A	N/A
<i>F_{IS}</i>	N/A	N/A	-0.015	0.142	0.006	-0.007	-0.048	0.038	0.010	N/A	N/A	0.016	0.061	N/A	N/A	N/A

Appendix II. Continued.

<i>Ots3</i>	Population																
	Allele	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0.012	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	0.023	0.027	0.027	0	0.014	0	0	0	0	0	0	0	0	0	0	0	0
8	0	0.005	0.005	0.005	0.007	0.032	0	0.005	0.021	0.01	0.016	0.005	0	0	0.007	0.021	
9	0	0	0	0.011	0	0	0	0	0	0.005	0	0	0	0	0	0	0
10	0.093	0.048	0.054	0.038	0.048	0.053	0.073	0.098	0.101	0.146	0.16	0.264	0.223	0.138	0.007	0.062	
11	0	0.005	0	0.011	0.014	0	0	0	0	0	0	0	0	0.005	0	0.021	
12	0.372	0.356	0.339	0.387	0.288	0.309	0.406	0.266	0.191	0.224	0.117	0.121	0.191	0.298	0.333	0.274	
13	0.081	0.011	0.027	0.011	0	0.011	0.01	0.022	0.011	0.021	0.011	0	0	0	0.007	0.027	
14	0.023	0.021	0.027	0.022	0	0.011	0.01	0	0	0	0	0.005	0	0	0.047	0.014	
15	0.105	0.165	0.108	0.097	0.123	0.128	0.135	0.071	0.074	0.057	0.037	0.044	0.064	0.032	0.12	0.11	
16	0.012	0.005	0.027	0.016	0.014	0.032	0.01	0	0.043	0.026	0.005	0.016	0.016	0	0.013	0.027	
17	0.209	0.303	0.36	0.366	0.404	0.383	0.344	0.511	0.521	0.458	0.59	0.473	0.324	0.5	0.36	0.411	
18	0	0.021	0.011	0	0.014	0	0	0.005	0.011	0	0	0	0	0	0.007	0	
19	0.012	0	0	0.016	0	0.021	0	0	0.005	0.005	0.011	0	0	0.027	0	0	
20	0.012	0.016	0.005	0.005	0.034	0.011	0.01	0	0	0.005	0	0	0	0	0.04	0.021	
21	0.047	0.016	0.011	0.016	0.041	0.011	0	0.022	0.021	0.042	0.053	0.071	0.181	0	0.06	0.014	
22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>n</i>	43	94	93	93	73	47	48	92	94	96	94	91	94	94	75	73	
<i>n_a</i>	12	13	12	13	11	11	8	8	10	11	9	8	6	6	11	11	
<i>n_{eff}</i>	N/A	4.05	3.87	3.42	3.81	3.91	3.33	2.91	3.09	3.52	2.57	3.22	4.45	2.81	3.88	3.88	
<i>a</i>	N/A	7.17	7.27	6.84	7.10	7.24	5.28	5.32	6.55	6.57	5.80	5.50	5.33	4.46	6.71	7.51	
<i>H_E</i>	N/A	0.753	0.742	0.708	0.738	0.744	0.700	0.656	0.676	0.716	0.611	0.689	0.775	0.644	0.742	0.742	
<i>H_O</i>	N/A	0.713	0.731	0.677	0.781	0.809	0.688	0.576	0.660	0.708	0.617	0.736	0.702	0.553	0.720	0.781	
<i>F_{IS}</i>	N/A	0.054*	0.014	0.043	-0.059	-0.088	0.018	0.123	0.025	0.011	-0.010	-0.069	0.095	0.141	0.030	-0.052	

Appendix II. Continued.

<i>Ots3</i>	Population																
	Allele	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	0.011	0.023	0.013	0	0.027	0.009	0.013	0	0.006	0	0	0	0.02	0.016	0.02	0	0
8	0.005	0.017	0.013	0	0.013	0.009	0.007	0.01	0.011	0	0.042	0.032	0.007	0.005	0.007	0	0
9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	0.048	0.057	0.064	0.043	0.06	0.055	0.033	0.051	0.063	0.247	0.271	0.126	0.027	0.084	0.095	0.053	0
11	0	0.006	0	0.009	0	0.009	0.01	0.01	0.017	0	0	0	0.007	0.005	0	0.005	0
12	0.33	0.253	0.282	0.328	0.267	0.364	0.262	0.265	0.293	0.126	0.109	0.168	0.287	0.326	0.223	0.4	0
13	0.016	0.017	0	0.026	0.013	0.018	0.013	0.02	0.006	0.016	0	0.011	0.02	0.037	0.014	0.026	0
14	0.027	0.034	0.038	0.06	0.02	0.018	0.026	0.071	0.011	0.016	0.021	0.058	0.027	0.011	0.034	0.005	0
15	0.101	0.115	0.09	0.095	0.113	0.073	0.093	0.122	0.121	0.126	0.068	0.132	0.1	0.142	0.095	0.142	0
16	0.027	0.046	0.038	0	0.027	0.018	0.036	0.02	0.017	0.032	0.036	0.058	0.027	0.026	0.054	0.026	0
17	0.356	0.351	0.397	0.345	0.4	0.364	0.447	0.388	0.368	0.421	0.448	0.4	0.34	0.284	0.365	0.279	0
18	0.005	0.006	0.026	0	0.007	0.018	0	0.01	0.017	0	0	0	0.033	0.005	0.02	0	0
19	0.016	0.006	0.013	0	0	0	0.003	0	0.006	0.016	0.005	0.011	0	0.016	0.034	0	0
20	0.021	0.04	0.013	0.043	0.007	0.009	0.026	0	0.017	0	0	0	0.04	0.016	0.014	0.021	0
21	0.037	0.029	0.013	0.052	0.047	0.027	0.026	0.031	0.046	0	0	0.005	0.06	0.026	0.027	0.032	0
22	0	0	0	0	0	0	0.003	0	0	0	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.005	0
24	0	0	0	0	0	0.009	0	0	0	0	0	0	0.007	0	0	0.005	0
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	94	87	39	58	75	55	151	49	87	95	96	95	75	95	74	95	0
<i>n_a</i>	13	14	12	9	12	14	14	11	14	8	8	10	14	14	13	12	0
<i>n_{eff}</i>	4.03	4.86	4.09	4.18	4.05	3.72	3.58	4.21	4.18	3.73	3.44	4.43	4.72	4.67	4.94	3.85	0
<i>a</i>	7.80	8.82	8.22	7.26	7.65	7.92	7.57	7.58	7.76	5.94	6.09	7.20	8.88	7.99	8.89	6.93	0
<i>H_E</i>	0.752	0.794	0.756	0.761	0.753	0.731	0.720	0.762	0.761	0.732	0.710	0.774	0.788	0.786	0.797	0.740	0
<i>H_O</i>	0.777	0.724	0.667	0.862	0.773	0.727	0.662	0.735	0.805	0.789	0.729	0.747	0.800	0.821	0.784	0.726	0
<i>F_{IS}</i>	-0.033	0.089	0.119	-0.135	-0.027	0.006	0.081	0.037	-0.058	-0.079	-0.028	0.035	-0.015	-0.045	0.017	0.019	0

Appendix II. Continued.

<i>Ots3</i>	Population																
	Allele	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.011
5	0	0	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0.008	0	0	0	0	0	0	0	0	0
7	0.049	0.069	0.012	0.107	0.081	0.15	0.023	0.135	0.095	0.051	0.163	0.06	0.226	0.148	0.153	0.122	0
8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
9	0.005	0	0	0	0	0	0	0.014	0.005	0	0.006	0	0	0.034	0.082	0.011	0
10	0.011	0	0	0.006	0	0	0	0.014	0.005	0	0	0	0	0	0	0	0
11	0.011	0	0.012	0	0.022	0.017	0	0.014	0.016	0	0	0.076	0.012	0.04	0.071	0.044	0
12	0.418	0.424	0.25	0.44	0.333	0.422	0.156	0.473	0.468	0.141	0.392	0.223	0.369	0.449	0.449	0.522	0
13	0	0	0.125	0.024	0.005	0	0	0.014	0.005	0.218	0	0	0.036	0.006	0	0	0
14	0.082	0.042	0.113	0.03	0.016	0.022	0.047	0	0	0	0.042	0	0	0	0.01	0	0
15	0.103	0.181	0.113	0.024	0.108	0.083	0	0.068	0.042	0.128	0.072	0.234	0.226	0.125	0.082	0.156	0
16	0.016	0.028	0.012	0.06	0.048	0.033	0.617	0.027	0.011	0	0.042	0	0	0.017	0.031	0.011	0
17	0.147	0.118	0.19	0.054	0.07	0.078	0.008	0.041	0.142	0.269	0.145	0.109	0.119	0.034	0.051	0.056	0
18	0.011	0	0.101	0.107	0.194	0.1	0.133	0.081	0.089	0	0.102	0.299	0.012	0.136	0.071	0.067	0
19	0.011	0.028	0.012	0.071	0.075	0.05	0.008	0.068	0.116	0	0.012	0	0	0	0	0	0
20	0.016	0.049	0.048	0	0	0	0	0.027	0	0	0.006	0	0	0.011	0	0	0
21	0.082	0.014	0	0.071	0.005	0	0	0	0.005	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0	0.007	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0.026	0	0	0	0	0	0	0
25	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0.013	0	0	0	0	0	0	0
27	0.033	0.035	0.012	0.006	0.043	0.028	0	0.014	0	0.09	0.018	0	0	0	0	0	0
28	0	0.007	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0.014	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0.064	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	92	72	84	84	93	90	64	37	95	39	83	92	42	88	49	45	
<i>n_a</i>	15	12	12	12	12	12	8	14	12	9	11	6	7	10	9	9	
<i>n_{eff}</i>	4.53	4.30	6.75	4.33	N/A	N/A	2.37	3.97	N/A	6.20	4.63	4.75	4.08	3.88	N/A	3.18	
<i>a</i>	8.89	8.37	8.49	8.75	N/A	N/A	5.15	9.64	N/A	7.86	7.68	5.81	5.52	7.12	N/A	6.73	
<i>H_E</i>	0.779	0.767	0.852	0.769	N/A	N/A	0.579	0.748	N/A	0.839	0.784	0.789	0.755	0.742	N/A	0.686	
<i>H_O</i>	0.739	0.764	0.810	0.774	N/A	N/A	0.609	0.730	N/A	0.821	0.699	0.793	0.762	0.705	N/A	0.711	
<i>F_{IS}</i>	0.052	0.005	0.050	-0.006	N/A	N/A	-0.054	0.025	N/A	0.022	0.110	-0.005	-0.010	0.051	N/A	-0.037	

Appendix II. Continued.

Allele	Population															
	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0.003	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0.006	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0	0	0
7	0.268	0.256	0.282	0.241	0.298	0.31	0.43	0.277	0.202	0.266	0.303	0.323	0.283	0.368	0.26	0.25
8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
9	0.02	0.006	0.011	0.017	0.032	0	0.012	0.032	0	0.005	0	0.008	0.033	0.013	0	0.059
10	0.003	0	0	0.006	0	0	0	0	0.011	0	0	0	0	0.026	0.02	0.044
11	0.025	0.051	0.027	0.029	0.053	0.06	0.035	0.043	0.011	0.064	0.049	0.046	0.065	0.053	0.09	0.074
12	0.313	0.364	0.383	0.345	0.372	0.19	0.372	0.34	0.298	0.298	0.352	0.303	0.239	0.25	0.34	0.382
13	0	0.011	0	0	0	0	0	0.011	0	0.016	0	0.006	0	0	0.01	0.015
14	0.015	0.011	0.021	0.006	0.011	0.06	0.012	0.011	0.043	0.032	0.014	0.008	0.022	0.039	0.01	0
15	0.114	0.063	0.074	0.19	0.053	0.31	0.093	0.223	0.383	0.255	0.19	0.24	0.272	0.105	0.14	0.074
16	0.04	0.034	0.021	0.052	0.032	0.02	0	0.011	0.032	0.021	0.021	0.015	0.033	0.026	0	0.029
17	0.068	0.034	0.032	0.04	0.032	0.01	0.023	0.011	0.011	0.005	0	0.009	0.033	0.053	0.1	0.029
18	0.124	0.136	0.122	0.063	0.085	0.04	0.023	0.043	0.011	0.032	0.07	0.037	0.022	0.066	0.01	0.044
19	0	0	0.016	0.006	0.011	0	0	0	0	0	0	0.002	0	0	0	0
20	0	0	0	0	0.011	0	0	0	0	0	0	0	0	0	0	0
21	0.003	0.023	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0.003	0.011	0	0	0	0	0	0	0	0	0	0.003	0	0	0.02	0
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0.003	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>n</i>	198	88	94	87	47	50	43	47	47	94	71	325	46	38	50	34
<i>n_a</i>	14	12	11	12	12	8	8	10	9	11	7	12	9	10	10	10
<i>n_{eff}</i>	N/A	4.51	4.07	4.58	4.24	4.35	3.06	4.18	3.68	4.40	N/A	N/A	4.75	4.72	4.67	4.60
<i>a</i>	N/A	7.88	7.33	7.35	8.25	6.47	5.70	6.71	5.90	6.73	N/A	N/A	7.27	8.29	6.99	8.49
<i>H_E</i>	N/A	0.778	0.754	0.782	0.764	0.770	0.673	0.761	0.728	0.773	N/A	N/A	0.789	0.788	0.786	0.783
<i>H_O</i>	N/A	0.773	0.755	0.713	0.851	0.680	0.674	0.745	0.787	0.745	N/A	N/A	0.804	0.737	0.740	0.794
<i>F_{IS}</i>	N/A	0.007*	-0.001	0.089	-0.115	0.118	-0.002	0.021	-0.082	0.036	N/A	N/A	-0.019	0.066	0.059	-0.015

Appendix II. Continued.

<i>Ots3</i> Allele	Population																Total
	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	
1	0	0	0	0	0	0	0	0	0	0	0.002	0	0	0	0	0	
2	0	0	0	0	0	0	0	0	0	0	0.002	0	0	0	0	0	
3	0	0	0	0	0	0	0	0	0	0	0	0.002	0	0	0	0	
4	0	0	0	0	0	0	0	0	0	0.011	0	0	0	0	0	0	
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6	0	0	0	0	0.016	0	0	0	0	0	0.005	0	0	0	0	0	
7	0.289	0.245	0.273	0.25	0.304	0.49	0.351	0.313	0.323	0.33	0.448	0.34	0.272	0.643	0.416	0.57	
8	0	0	0	0	0.013	0	0	0	0	0	0.005	0	0	0	0	0.035	
9	0.005	0	0	0.021	0.006	0.021	0.011	0.031	0	0	0.01	0.005	0.006	0	0.006	0	
10	0.005	0.011	0.045	0.052	0	0	0	0	0	0	0.002	0.005	0.006	0	0	0	
11	0.068	0.053	0.076	0.063	0.09	0.073	0.128	0.047	0.146	0.202	0.145	0.118	0.139	0.086	0.163	0.105	
12	0.384	0.362	0.439	0.438	0.34	0.25	0.319	0.406	0.406	0.309	0.262	0.296	0.267	0.229	0.247	0.18	
13	0.005	0.011	0.015	0	0.029	0.01	0	0	0	0.011	0.002	0.002	0	0	0.006	0	
14	0.021	0.043	0	0.01	0.032	0	0	0	0	0.021	0	0.005	0.022	0	0.024	0.012	
15	0.089	0.149	0.091	0.073	0.087	0.156	0.16	0.156	0.063	0.021	0.04	0.076	0.072	0	0.006	0.035	
16	0.021	0.011	0	0.01	0.003	0	0.021	0.031	0	0	0.021	0	0.006	0	0	0	
17	0.042	0.043	0.045	0.042	0.051	0	0	0	0.021	0.043	0.021	0.103	0.117	0.043	0.012	0.035	
18	0.068	0.064	0.015	0.021	0.026	0	0.011	0.016	0.042	0.032	0.017	0.047	0.078	0	0.108	0.017	
19	0	0.011	0	0	0.003	0	0	0	0	0	0.014	0	0.011	0	0	0.012	
20	0	0	0	0	0	0	0	0	0	0.021	0	0	0.006	0	0.012	0	
21	0	0	0	0	0	0	0	0	0	0	0.002	0	0	0	0	0	
22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
23	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
27	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>n</i>	95	47	33	48	156	48	47	32	48	47	210	203	90	35	83	86	10135
<i>n_a</i>	11	11	8	12	13	6	7	7	6	10	16	11	12	4	10	9	34
<i>n_{eff}</i>	4.04	4.64	3.64	3.83	N/A	3.07	3.85	3.57	3.46	4.15	N/A	N/A	5.39	2.14	3.72	2.71	
<i>a</i>	7.13	7.80	6.66	8.00	N/A	4.84	5.24	5.89	5.28	6.92	N/A	N/A	7.44	3.83	5.84	6.26	
<i>H_E</i>	0.752	0.784	0.725	0.739	N/A	0.675	0.740	0.720	0.711	0.759	N/A	N/A	0.814	0.533	0.731	0.631	
<i>H_O</i>	0.758	0.787	0.727	0.604	N/A	0.688	0.681	0.750	0.729	0.787	N/A	N/A	0.800	0.429	0.783	0.605	
<i>F_{IS}</i>	-0.007	-0.004	-0.003*	0.184	N/A	-0.019	0.081	-0.043	-0.026*	-0.038	N/A	N/A	0.018	0.198	-0.071	0.043	

Appendix III. Results of mixed-stock analyses used to evaluate significant allele frequency differences of non-overlapping samples from the UAF-ABL and DFO baseline datasets (see Table 10): (A) 19 populations, 9 loci, (B) 15 populations, 12 loci. Read across the rows for the allocation of the UAF-ABL dataset used as mixtures, to the DFO dataset used as a baseline. Reporting groups are listed in parentheses after the population names. Proportions of mixtures allocated to the corresponding DFO population are highlighted on the diagonal.

UAF-ABL population	DFO population																			
	Miomote	Gakko	Ohkawa	Tsugaruishi	Chitose	Natba	Tauy	Ola	Kol	Utka	Anvik	Kluane River	George	Goodnews	Deena	Neekas	Bella Coala	Big Quilcene	Kennedy	
Miomote (1)	0.844	0.6933	0.0001	0.1142	0.0686	0.0034	0.0055	0.0091	0.0043	0.0002	0.0031	0	0.0013	0.0081	0.0002	0.0009	0	0.0002	0	0
Gakko late (1)	0.0052	0.8983	0	0.0518	0.0135	0.0045	0	0.0044	0.0065	0	0.0011	0	0.0003	0.0020	0.0015	0.0012	0.0009	0.0077	0	0
Keserunuma/Ohkawa (1)	0.0173	0.0869	0.0001	0.7889	0.0704	0.0009	0.0019	0.0158	0.0074	0.0002	0.0032	0	0.0004	0.0005	0.0021	0.0006	0.0004	0.0001	0	0
Tsugaruishi (1)	0.0203	0.1220	0.0003	0.8253	0.0188	0.0013	0.0003	0.0053	0.0013	0	0.0013	0	0.0010	0.0008	0.0003	0.0005	0.0013	0	0	0
Chitose late (1)	0.0535	0.2650	0.0001	0.0284	0.5293	0.0121	0.0059	0.0460	0.0285	0.0006	0.0075	0	0.0124	0.0068	0	0.0010	0.0003	0.0003	0	0
Natba (2)	0.0063	0.0046	0	0.0015	0.0248	0.6130	0.0546	0.0998	0.0502	0.0013	0.0120	0.0004	0.0096	0.0172	0.0261	0.0567	0.0167	0.0024	0	0
Tau (3)	0.0122	0.0135	0	0.0138	0.0330	0.0324	0.0970	0.2081	0.2092	0.0041	0.0584	0.0003	0.0689	0.0481	0.0346	0.0792	0.0611	0.0216	0.0003	0
Ola (3)	0.0129	0.0129	0	0.0164	0.0147	0.0460	0.1007	0.4340	0.1491	0.0193	0.0236	0	0.0433	0.0356	0.0118	0.0444	0.0282	0.0011	0	0
Kol (3)	0.0135	0.0106	0	0.0258	0.0467	0.0250	0.0877	0.1277	0.2800	0.0063	0.0485	0	0.0725	0.0221	0.0348	0.0967	0.0877	0.0092	0.0019	0
Utka (3)	0.0037	0.0303	0	0.0194	0.0503	0.0514	0.1074	0.1657	0.3046	0.0057	0.0480	0.0006	0.0554	0.0206	0.0089	0.0914	0.0277	0.0037	0.0003	0
Anvik (6)	0.0004	0.0061	0	0.0039	0.0251	0.0059	0.0120	0.0405	0.0436	0.0082	0.2450	0.0272	0.3732	0.1415	0.0070	0.0131	0.0296	0.0141	0	0
Kluane (8)	0	0	0	0	0	0	0.0003	0	0	0.0114	0.9816	0.0043	0.0012	0.0004	0.0002	0	0	0	0	0
George (9)	0.0005	0.0008	0	0.0013	0.0028	0.0237	0.0095	0.0509	0.0364	0.0031	0.3410	0.0133	0.3736	0.0946	0.0091	0.0117	0.0232	0	0	0
Goodnews (9)	0.0005	0.0026	0	0.0055	0.0043	0.0104	0.0063	0.0681	0.0423	0.0026	0.2609	0.0149	0.3080	0.2247	0.0029	0.0228	0.0184	0.0023	0.0001	0
Deena (17)	0.0008	0.0004	0	0.0029	0.0040	0.0060	0.0094	0.0329	0.0394	0.0002	0.0029	0.0004	0.0104	0.0085	0.7592	0.0763	0.0294	0.0119	0.0004	0
Neekas (17)	0	0.0032	0	0.0048	0.0002	0.0438	0.0122	0.0360	0.0754	0.0004	0.0132	0	0.0338	0.0106	0.0748	0.5728	0.1036	0.0096	0.0014	0
Klownik (17)	0.0002	0.0004	0.0002	0.0014	0.0008	0.0196	0.0161	0.0959	0.0741	0.0035	0.0390	0.0002	0.0127	0.0161	0.1069	0.1778	0.4120	0.0188	0	0
Quilcene (18)	0	0.0003	0	0	0.0003	0.0100	0.0008	0.0023	0.0030	0	0.0018	0.0003	0.0235	0.0003	0.0003	0.0023	0.0040	0.9490	0.0008	0
Kennedy (18)	0.0017	0.0222	0	0.0049	0.0170	0.0164	0.0224	0.0595	0.1178	0.0009	0.0343	0.0002	0.0298	0.0197	0.0866	0.3171	0.1288	0.1067	0.0087	0

Appendix III. Continued.

UAF/ABL population	DFO population														
	Miomote	Gakko	Ohkawa	Tsugaruishi	Chitose	Naiba	Anvik	Kluane River	George	Goodnews	Dena	Nekas	Bella Coola	Big Quilcene	Kennedy
Miomote (1)	0.0018	0.8186	0.0001	0.1032	0.0602	0.0007	0.0033	0	0.0012	0.0099	0	0	0	0	0
Gakko late (1)	0	0.9621	0	0.0259	0.0076	0.0038	0	0	0	0	0	0	0	0	0
Kesennuma/Ohkawa (1)	0.0008	0.0727	0.0005	0.8853	0.0385	0.0002	0.0006	0	0	0	0	0.0007	0	0	0
Tsugaruishi (1)	0	0.0903	0.0023	0.8975	0.0090	0.0005	0	0	0	0	0	0	0	0	0
Chitose late (1)	0.0001	0.1846	0	0.0306	0.7638	0.0181	0.0009	0	0.0001	0.0003	0	0.0001	0	0	0
Naiba (2)	0	0.0039	0	0.0004	0.0220	0.8004	0.0167	0	0.0048	0.0204	0.0222	0.0609	0.0333	0.0022	0.0117
Anvik (6)	0	0.0032	0	0.0001	0.0019	0.0012	0.3643	0.0104	0.3703	0.2124	0.0097	0.0045	0.0158	0.0043	0.0008
Kluane (8)	0	0	0	0	0	0	0.0019	0.9972	0.0005	0.0002	0	0	0	0	0
George (9)	0	0.0001	0	0.0003	0.0005	0.0150	0.4563	0.0041	0.3818	0.1327	0.0001	0.0032	0.0044	0.0004	0.0004
Goodnews (9)	0	0.0072	0	0	0.0104	0.0112	0.4003	0.0012	0.2527	0.2871	0.0014	0.0090	0.0143	0.0001	0.0054
Dena (17)	0	0	0	0	0	0	0	0	0	0.0002	0.9019	0.0292	0.0356	0.0046	0.0277
Nekas (17)	0	0.0008	0	0	0	0.0134	0.0136	0	0.0078	0.0208	0.0924	0.6132	0.2064	0.0014	0.0268
Kluwnik (17)	0	0	0	0	0.0004	0.0096	0.0014	0	0.0018	0.0041	0.1178	0.1155	0.7294	0.0076	0.0114
Quilcene (18)	0	0	0	0	0	0	0.0003	0	0.0013	0.0003	0	0	0.0008	0.9818	0.0155
Kennedy (18)	0	0.0024	0	0	0.0009	0.0019	0.0148	0	0.0048	0.0142	0.0644	0.0597	0.0959	0.1058	0.6343

Appendix IV. Total sample sizes (n) and number of populations (# pops) of reporting groups used in the Bayesian assignment of individual samples from the LTO chum salmon baseline evaluation datasets based on 101 populations. Values are provided for the 126-population baseline for comparison.

Code	Reporting group	101 populations		126 populations	
		n	# pops	n	# pops
<i>18 reporting groups</i>					
1	Japan-Kuril	620	10	777	12
2	Primorye-Amur-Sakhalin	530	12	627	14
3	Okhotsk-Kam.-NE Russia	462	6	630	10
4	Kotzebue Sound	288	3	487	5
5	Norton Sound	396	4	728	8
6	Lower Yukon	270	4	270	4
7	Middle Yukon	293	3	293	3
8	Upper Yukon	396	4	396	4
9	Kusk. summer-W Bristol	1140	14	1140	14
10	Kuskokwim fall	288	3	288	3
11	E Bristol-N Alaska Pen.	270	3	270	3
12	Alaska Peninsula	184	2	361	4
13	Kodiak	114	2	159	3
14	Cook Inlet-PWS-Alsek	278	4	278	4
15	NSE Alaska	570	6	738	8
16	SSE Alaska-N Brit Columbia	668	12	909	16
17	Haida Gwaii-central Brit. Col.	245	5	245	5
18	S Brit. Columbia-Washington	332	4	521	6
<i>12 reporting groups</i>					
1	Japan-Kuril	620	10	777	12
2	Primorye-Amur-Sakhalin	530	12	627	14
3	Okhotsk-Kam-NE Russia	462	6	630	10
4	Kotzebue	288	3	487	5
5,6,9,11	Coastal western Alaska	2076	25	2408	29
7,8	Upper-Middle Yukon	689	7	689	7
10	Kuskowkwim fall	288	3	288	3
12,13	AK Peninsula-Kodiak	298	4	520	7
14	Cook Inlet-PWS-Alsek	278	4	278	4
15	NSE Alaska	570	6	738	8
16,17	SSE AK-central BC	913	17	1154	21
18	S Brit. Columbia-Washington	332	4	521	6