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(54) **METHODS AND MATERIALS FOR CANINE BREED IDENTIFICATION**

(71) Applicant: **Fred Hutchinson Cancer Center**, Seattle, WA (US)

(72) Inventors: **Elaine Ostrander**, Potomac, MD (US); **Leonid Kruglyak**, Princeton, NJ (US); **Heidi G. Parker**, Germantown, MD (US); **Lisa V. Kim**, Seattle, WA (US); **Matthew Stephens**, Seattle, WA (US); **Tiffany B. Malek**, La Mesa, CA (US); **Nathan B. Sutter**, Rockville, MD (US); **Scott Carlson**, Seattle, WA (US)

(73) Assignee: **Fred Hutchinson Cancer Center**, Seattle, WA (US)

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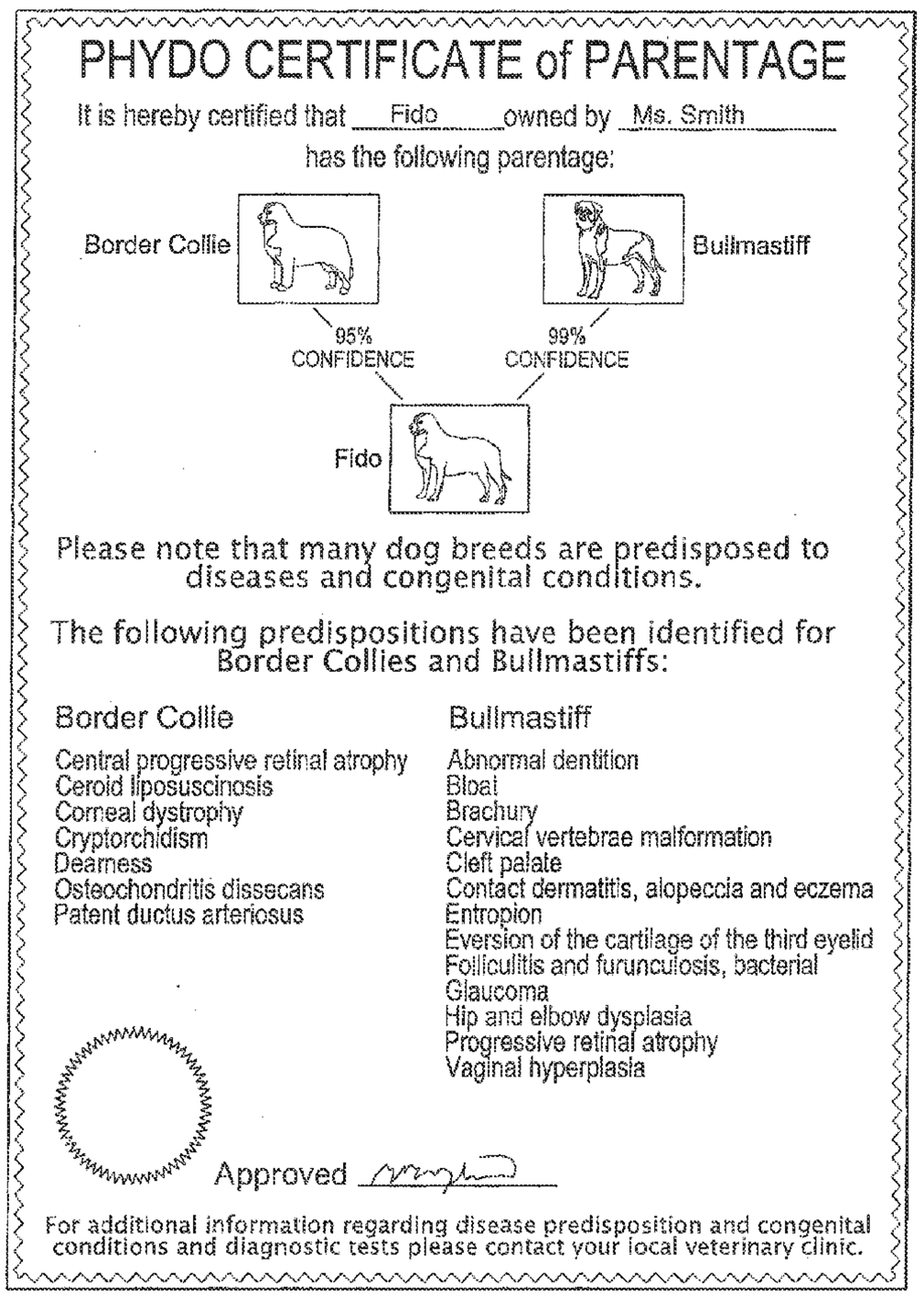
(57) **ABSTRACT**

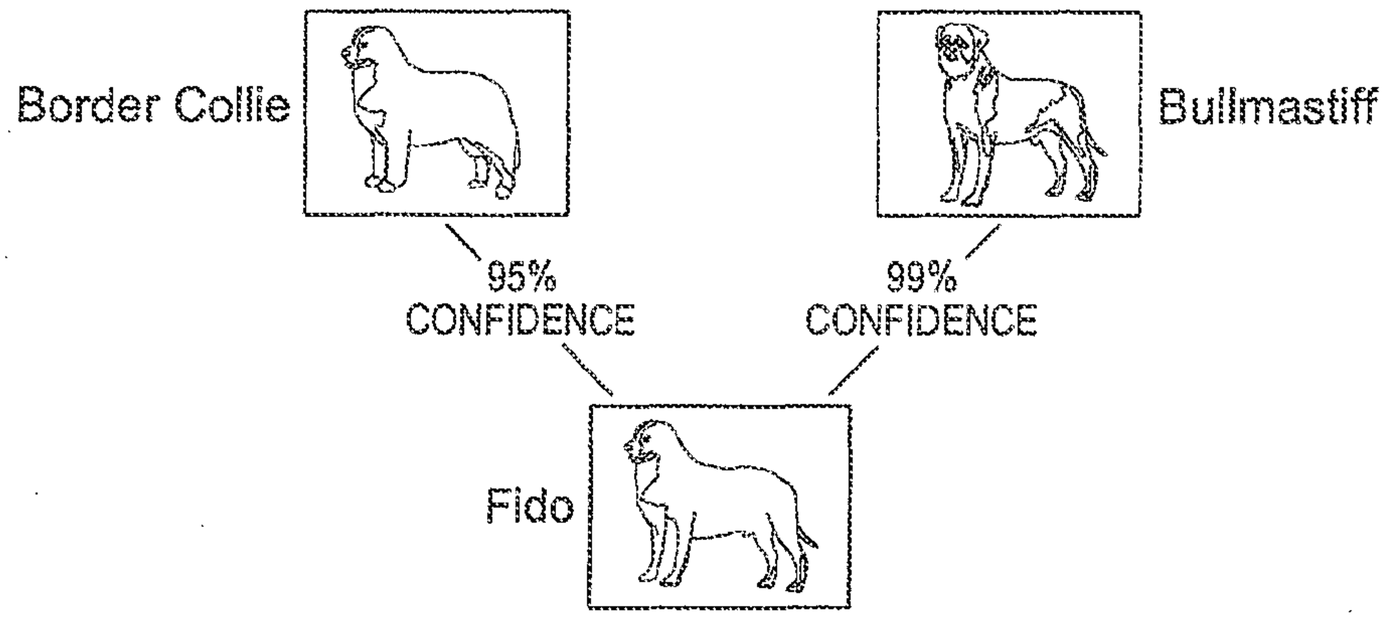
In one aspect, the invention provides methods for determining the contributions of canid populations to a canid genome. The methods comprise the steps of: (a) obtaining the identity of one or both alleles in a test canid genome for each of a set of markers; and (b) determining the contributions of canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid populations.

Specification includes a Sequence Listing.



PHYDO CERTIFICATE of PARENTAGE

It is hereby certified that Fido owned by Ms. Smith
has the following parentage:



Please note that many dog breeds are predisposed to diseases and congenital conditions.

The following predispositions have been identified for Border Collies and Bullmastiffs:

Border Collie

Central progressive retinal atrophy
Ceroid liposuscinosis
Corneal dystrophy
Cryptorchidism
Dearness
Osteochondritis dissecans
Patent ductus arteriosus

Bullmastiff

Abnormal dentition
Bloat
Brachury
Cervical vertebrae malformation
Cleft palate
Contact dermatitis, alopeccia and eczema
Entropion
Eversion of the cartilage of the third eyelid
Folliculitis and furunculosis, bacterial
Glaucoma
Hip and elbow dysplasia
Progressive retinal atrophy
Vaginal hyperplasia

Approved

For additional information regarding disease predisposition and congenital conditions and diagnostic tests please contact your local veterinary clinic.

Fig. 1.

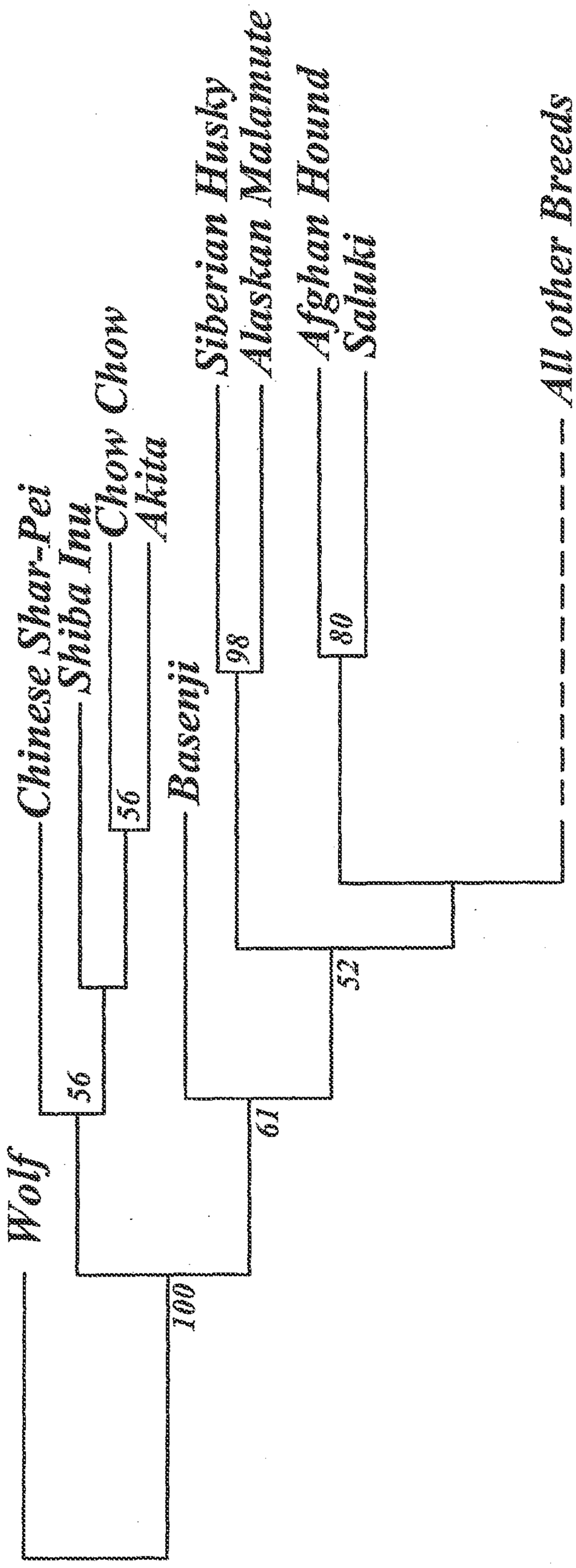

Wolf
Chinese Shar-Pei
Shiba Inu
Chow Chow
Akita
Basenji
Siberian Husky
Alaskan Malamute
Afghan Hound
Saluki
All other Breeds
100
56
56
61
52
98
80

Fig. 2.

METHODS AND MATERIALS FOR CANINE BREED IDENTIFICATION

CROSS-REFERENCES TO RELATED APPLICATIONS

[0001] This application is a continuation of U.S. application Ser. No. 13/039,240, filed Mar. 2, 2011, now abandoned, which is a continuation of U.S. application Ser. No. 12/768,427, filed Apr. 27, 2010, now abandoned, which is a continuation of U.S. application Ser. No. 10/536,369, filed Feb. 1, 2006, now U.S. Pat. No. 7,729,863, issued Jun. 1, 2010, which is a national stage of International Application No. PCT/US04/42267, filed Dec. 15, 2004, which claims the benefit of U.S. Provisional Application No. 60/530,464, filed Dec. 17, 2003, the disclosures of which are hereby expressly incorporated by reference.

STATEMENT OF GOVERNMENT LICENSE RIGHTS

[0002] This invention was made with government support under grant number HG000035 awarded by the National Institutes of Health. The government has certain rights in the invention.

STATEMENT REGARDING SEQUENCE LISTING

[0003] The sequence listing XML associated with this application is provided in XML format in lieu of a paper copy and is hereby incorporated by reference into the specification. The name of the XML file containing the sequence listing is 1894-P4USCON2_Seq_List_20221208.xml. The XML file is 482,945 bytes; was created on Dec. 8, 2022; and was submitted electronically via Patent Center with the filing of the specification.

REFERENCE TO TABLES SUBMITTED ELECTRONICALLY

[0004] Submitted herewith in ASCII text file format are large Tables 3 and 4. Table 3 (Table3.txt, 424 kb, created Feb. 25, 2010) and Table 4 (Table4.txt, 55 kb, created Feb. 25, 2010) are both incorporated herein by reference in their entireties.

FIELD OF THE INVENTION

[0005] The invention relates to determining the contribution of one or more canid populations to the genome of a canid using polymorphic markers.

LENGTHY TABLES

The patent application contains a lengthy table section. A copy of the table is available in electronic form from the USPTO web site (https://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20230279505A1). An electronic copy of the table will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

BACKGROUND OF THE INVENTION

[0006] *Canis familiaris*, the domestic dog, is a single species divided into more than 400 phenotypically divergent genetic isolates termed breeds, 152 of which are recognized by the American Kennel Club in the United States (American Kennel Club (1998) *The Complete Dog Book,* eds. Crowley & Adelman, Howell Book Hues, New York, NY). Distinct breeds of dog are characterized by unique constellations of morphology, behavior, and disease susceptibility (Ostrander et al. (2000) *Trends in Genetics* 16:117-23). A variety of dog morphologies have existed for millennia, and reproductive isolation between them was formalized with the advent of breed clubs and breed standards in the mid 19th century. Since that time, the promulgation of the "breed barrier" rule—no dog may become a registered member of a breed unless both its dam and sire are registered members—has ensured a relatively closed genetic pool among dogs of each breed.

[0007] Over 350 inherited disorders segregate in the purebred dog population (Patterson et al. (1988) *J. Am. Vet. Med. Assoc.* 193:1131.) Many of these mimic common human disorders and are restricted to particular breeds or groups of breeds as a result of 20 aggressive inbreeding programs used to generate specific morphologies.

[0008] There are many potential uses for objectively determining the breed of an individual dog, such as the certification of dogs as belonging to a particular breed. Because historical records vary in reliability from breed to breed, a genetic analysis that does not rely on prior population information is the most direct and accurate method for determining population structure. Over the past decade, molecular methods have been used to enhance our understanding of wild canid species and to determine their relationships to the domestic dog. Mitochondrial DNA sequence analyses describe the relationship between the domestic dog and the wolf, elucidating the multiple domestication events that occurred 40,000-100,000 years ago (Vila et al. (1997) *Science* 276:1687-9; Savolainen et al. (2002) *Science* 298:1610-3, Leonard et al. (2002) *Science* 298:1613-6). However, the evolution of mitochondrial DNA is too slow to allow inference of relationships among modern dog breeds, most of which have existed for fewer than 400 years. In addition, phylogenetic distances measures and tree building programs are not equipped to deal with reticulate evolution as is commonly observed in dog populations (Zajc et al. (1997) *Mamm. Genome* 8(3):182-5; Koskinen & Bredbacka (2000) *Animal Genetics* 31:310-17; Irion et al. (2003) *J. Hered.* 94(1):81-7). One previous study showed that nuclear microsatellite loci could be used to assign dogs from five breeds to their breed of origin, demonstrating large genetic distances among these breeds (Koskinen (2003) *Anim. Genet.* 34:297). Another study used microsatellites to detect relatedness of two breed pairs in a collection of 28 breeds but could not establish broader phylogenetic relationships among the breeds (Irion et al. (2003) *J. Hered.* 94(1):81-7). The failure to find such relationships could reflect the properties of microsatellite loci (Irion et al. (2003) *J. Hered.*

94(1):81-7), the limited number of breeds examined, or the analytical methods used in the study. Alternatively, it may reflect the complex structure in purebred dog populations, due to the recent origin of most breeds and the mixing of ancestral types in their creation.

[0009] There is a need for methods for defining related groups of breeds and for unambiguously identifying breed contributions to the genome of an individual dog. The present invention addresses this and other needs.

SUMMARY OF THE INVENTION

[0010] In one aspect, the invention provides methods for determining the contributions of canid populations to a canid genome. The methods comprise the steps of: (a) obtaining the identity of one or both alleles in a test canid genome for each of a set of markers; and (b) determining the contributions of canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population. The set of markers may comprise at least about five markers, for example, at least about five markers set forth on the map of the canine genome. Exemplary markers suitable for use in the methods of the invention include, for example, microsatellite markers, single nucleotide polymorphisms (SNPs), mitochondrial markers, and restriction fragment length polymorphisms. For example, the set of markers may comprise at least 5 of the SNP markers set forth in Table 2, and/or at least 5 microsatellite markers set forth in Table 1. The set of markers may comprise one or more population-specific markers, such as one or more population-specific SNP markers or one or more population-specific microsatellite markers. For example, one or more SNP markers may be selected from the group consisting of 372c5t-82, 372e13t-57, 372m6t-88, 372m23t-76, 373a15t-112, 373e1t-50, 373e1t-130, 373g19t-246, 373i8s-224, 373k8s-181, 372c5s-168, 372C155-196, 372e15s-71, and 373a21t-93.

[0011] The identity of one or both alleles in a test canid genome for each of the set of markers may be obtained using methods standard in the art, such as hybridization, Polymerase Chain Reaction, size fractionation, DNA sequencing, etc. For example, step (a) of the methods may comprise amplifying genomic DNA of the test canid using primers specific for each of the set markers and determining the size of the amplification product. Step (a) may also comprise amplifying genomic DNA of the test canid using primers specific for each of the set of markers and determining the nucleotide sequence of the amplification product. In some embodiments, the primers are selected from the group consisting of SEQ ID NOs:1-200. In some embodiments, the primers are selected from the group consisting of SEQ ID NOs:1-244-327.

[0012] The genotype information in a canid population profile may comprise information such as the identity of one or both alleles of most or all the markers in the set of markers in one or more canids that are members of that canid population, and/or estimated allele frequencies for at least one allele of most or all of the markers in the set of markers in that canid population. Each estimated allele frequency in a canid population profile is typically based on the identities of one or both alleles in at least two genomes of canids that are members of the canid population. The database of canid population profiles may comprise between about five and several hundreds of canid population profiles, such as at least about 100 canid population profiles. In some embodiments, the canid population profiles comprise profiles of registered breeds, such as breeds registered by the American Kennel Club.

[0013] In some embodiments, the set of markers comprises fewer than about 1500 SNP markers and wherein the method determines the contributions of at least 87 canid populations to the test canid genome. In some embodiments, the set of markers comprises fewer than about 200 SNP markers (such as about 100 SNP markers, or about 50 SNP markers) and wherein the method determines the contributions of at least 87 canid populations to the test canid genome.

[0014] In step (b) of the method, the likelihood that one or more canid populations contributed to the test canid genome may be determined using any suitable algorithm, such as Bayesian model-based clustering algorithms or assignment algorithms. In some embodiments, step (b) comprises determining the probability that a specific canid population contributed to the genome of the test canid by determining the conditional probability that the alleles in the test canid genome would occur in the specific canid population divided by the sum of conditional probabilities that the alleles in the test canid genome would occur in each canid population in the database. In some embodiments, step (b) comprises discriminating between the contributions of two or more genetically related canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising profiles of the two or more genetically related canid populations. Exemplary genetically related canid populations include, but are not limited to, Belgian Sheep Dog and Belgian Tervuren; Collie and Shetland Sheep Dog; Whippet and Greyhound; Siberian Husky and Alaskan Malamute; Mastiff and Bullmastiff; Greater Swiss Mountain Dog and Bemese Mountain Dog; West Highland White Terrier and Cairn Terrier; and Lhasa Apso, Shih Tzu, and Pekinese.

[0015] In some embodiments, the methods of the invention further comprise the step of providing a document displaying the contributions of one or more canid populations to the genome of the test canid genome. The document may provide information regarding the one or more canid populations that contributed to the genome of the test canid or the test canid, such as health-related information (e.g., disease predispositions), insurance information, or any other kind of information. The document may also provide a certification of the contributions of one or more canid populations to the genome of the test canid genome. In some embodiments, the document provides a representation (e.g., a photograph, drawing, or other depiction) of the one or more canid populations that contributed to the genome of the test canid.

[0016] In some embodiments, the invention provides methods for defining one or more canid populations, comprising: (a) for each of a set of canid genomes, obtaining the identity of one or both alleles for each of a set of markers; and (b) defining one or more canid populations by determining the likelihood that one or more members of the set of canid genomes define distinct canid populations characterized by a set of allele frequencies for each marker using statistical modeling.

[0017] In another aspect, the invention provides substrates comprising nucleic acid sequences for obtaining the identity of one or both alleles in a canid genome for each of a set of markers.

[0018] In a further aspect, the invention provides a computer-readable medium comprising a data structure stored thereon for use in distinguishing canid populations, the data structure comprising: (a) a marker field, which is capable of storing the name of a marker or of an allele of the marker; and (b) a genotype information field, which is capable of storing genotype information for the marker in a canid population, wherein a record comprises an instantiation of the marker field and an instantiation of the genotype information field and a set of records represents a canid population profile. For example, the genotype information field may be capable of storing an estimate of the frequency of the allele of a marker (e.g., an SNP marker) in a canid population. The genotype information field may also be capable of storing the identity of one or both alleles of each of a set of markers in one or more canids that are members of that canid population. In some embodiments, the computer readable medium comprises a substrate having stored thereon: computer-readable information comprising (a) a data structure for use in distinguishing canid populations, the data structure comprising: (i) a marker field, which is capable of storing the name of a marker or of an allele of the marker; and (ii) a genotype information field, which is capable of storing genotype information for the marker in a canid population, wherein a record comprises an instantiation of the marker field and an instantiation of the genotype information field and a set of records represents a canid population profile; and, (b) computer-executable instructions for implementing a method for determining the contributions of canid populations to a canid genome, comprising: (i) obtaining the identity of one or both alleles in a test canid genome for each of a set of markers; and (ii) determining the contributions of canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population.

BRIEF DESCRIPTION OF THE DRAWINGS

[0019] The foregoing aspects and many of the attendant advantages of this invention will become more readily appreciated as the same become better understood by reference to the following detailed description, when taken in conjunction with the accompanying drawings, wherein:

[0020] FIG. **1** shows an exemplary document displaying the contributions of two canid populations (Border Collie and Bullmastiff) to the genome of a test canid (Fido), along with information about disease predispositions for the two canid populations.

[0021] FIG. **2** shows a consensus neighbor-joining tree of 85 dog breeds and the gray wolf, as described in EXAMPLE 4. Nine breeds that form branches with statistical support are shown. The remaining 76 breeds show little phylogenetic structure and have been combined into one branch labeled "All Other Breeds" for simplification. The trees that formed the consensus are based on the chord distance measure. 500 bootstrap replicates of the data were carried out, and the fraction of bootstraps supporting each branch is indicated at the corresponding node as a percentage for those branches supported in over 50% of the replicates. The wolf population at the root of the tree consists of 8 individuals, one from each of the following countries: China, Oman, Iran, Sweden, Italy, Mexico, Canada and the United States. Branch lengths are proportional to bootstrap values.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

[0022] Unless specifically defined herein, all terms used herein have the same meaning as they would to one skilled in the art of the present invention.

[0023] In a first aspect, the invention provides methods for determining the contributions of canid populations to a canid genome, comprising: (a) obtaining the identity of one or both alleles in a test canid genome for each of a set of markers; and (b) determining the contributions of canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population.

[0024] As used here, the term "determining the contributions of canid populations" refers to estimating or inferring using statistical methods the contributions of canid populations to draw conclusions regarding whether one or more canid populations contributed to the genome of a test canid.

[0025] The term "canid" as used herein refers to an animal that is a member of the family Canidae, which includes wolves, jackals, foxes, coyotes, and the domestic dog. For example, a canid may be a domestic dog, a wolf, or an animal that has some genetic contributions from more than one species of the family Canidae. The term "canid population" refers to a group of canids related by descent, such as a domestic dog breed. The term "breed" refers to an intraspecies group of animals with relatively uniform phenotypic traits that have been selected for under controlled conditions by man. For example, the American Kennel Club (AKC) recognizes 152 breeds distributed in seven breed groups (Herding, Hound, Nonsporting, Sporting, Terrier, Toy, and Working) (American Kennel Club (1998) *The Complete Dog Book,* eds. Crowley & Adelman, Howell Book Hues, New York, NY). The methods of the invention may be used to estimate the genetic contributions of any dog breed, including, but not limited to Afghan Hound, Airedale Terrier, Akita, Alaskan Malamute, American Eskimo Dog, American Foxhound, American Hairless Rat Terrier, American Staffordshire Terrier, American Water Spaniel, Australian Cattle Dog, Australian Shepherd, Australian Terrier, Basenji, Basset Hound, Beagle, Bearded Collie, Bedlington Terrier, Belgian Laekenois, Belgian Malinois, Belgian Sheepdog, Belgian Tervuren, Bernese Mountain Dog, Bichon Frise, Bloodhound, Border Collie, Border Terrier, Borzoi, Boston Terrier, Bouvier des Flandres, Boykin Spaniel, Boxer, Briard, Brittany, Bulldog, Brussels Griffon, Bullmastiff, Bull Terrier, Cairn Terrier, Cardigan Welsh Corgi, Cavalier King Charles Spaniel, Chesapeake Bay Retriever, Chihuahua, Chinese Crested, Chinese Shar-Pei, Chow Chow, Clumber Spaniel, Cocker Spaniel, Collie, Curly-Coated Retriever, Dachshund, Dalmatian, Dandie Dinmont Terrier, Doberman Pinscher, Dogo Canario, English Cocker Spaniel, English Foxhound, English Setter, English Springer Spaniel, Entlebucher Mountain Dog, Field Spaniel, Flat-Coated Retriever, French Bulldog, German Longhaired Pointer, German Shepherd Dog, German Shorthaired Pointer, German Wirehaired Pointer, Giant Schnauzer,

Golden Retriever, Gordon Setter, Great Dane, Great Pyrenees, Greater Swiss Mountain Dog, Greyhound, Harrier, Havanese, Ibizan Hound, Irish Setter, Irish Terrier, Irish Water Spaniel, Irish Wolfhound, Italian Greyhound, Jack Russell Terrier, Keeshond, Kerry Blue Terrier, Komondor, Kuvasz, Labrador Retriever, Leonberger, Lhasa Apso, Lowchen, Maltese, Manchester Terrier—Standard, Manchester Terrier—Toy, Mastiff, Miniature Bull Terrier, Miniature Pinscher, Miniature Poodle, Miniature Schnauzer, Munsterlander, Neapolitan Mastiff, Newfoundland, New Guinea Singing Dog, Norwegian Elkhound, Norwich Terrier, Old English Sheepdog, Papillon, Pekingese, Pembroke Welsh Corgi, Petit Basset Griffon Vendeen, Pharaoh Hound, Pointer, Polish Lowland Sheepdog, Pomeranian, Portuguese Water Dog, Presa Canario, Pug, Puli, Pumi, Rhodesian Ridgeback, Rottweiler, Saint Bernard, Saluki, Samoyed, Schipperke, Scottish Deerhound, Scottish Terrier, Silky Terrier, Shetland Sheepdog, Shiba Inu, Shih Tzu, Siberian Husky, Smooth Fox Terrier, Soft Coated Wheaten Terrier, Spinone Italiano, Staffordshire Bull Terrier, Standard Poodle, Standard Schnauzer, Sussex Spaniel, Tibetan Spaniel, Tibetan Terrier, Toy Fox Terrier, Toy Poodle, Vizsla, Weimaraner, Welsh Springer Spaniel, Welsh Terrier, West Highland White Terrier, Wirehaired Pointing Griffon, Whippet, Yorkshire Terrier.

[0026] The methods of the invention may also be used to determine genetic contributions from canid populations that are subsets of recognized breeds, for example, a group of Dalmatians originating from a particular breeder, or a group of canids that are not, or not yet, recognized as a breed. Similarly, the methods of the invention may be used to determine genetic contributions from canid populations that are not domestic dogs.

[0027] The first step in the methods of the invention comprises obtaining the identity of one or both alleles in a test canid genome for each of a set of markers. The term "marker" refers to any polymorphic genomic locus that is sufficiently informative across the canid populations used in the methods of the invention to be useful for estimating the genetic contribution of these canid populations to the genome of a test canid. A genomic locus is polymorphic if it has at least two alleles. The term "allele" refers to a particular form of a genomic locus that may be distinguished from other forms of the genomic locus by its nucleic acid sequence. Thus, different alleles of a genomic locus represent alternative nucleic acid sequences at that locus. In any individual canid genome, there are two alleles for each marker. If both alleles are the same, the genome is homozygous for that marker. Conversely, if the two alleles differ, the genome is heterozygous for that marker.

[0028] Population-specific alleles are alleles that are present at some frequency in one canid population but have not been observed in the sampled canids from comparison canid populations (although they may be present at a significantly lower frequency). Population-specific alleles may be used to assign an individual to a particular population. Accordingly, the difference in allele frequencies between populations can be used for determining genetic contributions.

[0029] A "set of markers" refers to a minimum number of markers that are sufficient for determining the genetic contribution of the canid populations used in the methods of the invention to the genome of a test canid. The minimum number of markers required depends on the informativeness of the markers for the particular canid populations that are being used, as further described below. The set of markers may comprise at least about 5 markers, at least about 10 markers, at least about 50 markers, or more than about 100 markers.

[0030] Representative markers that may be used according to the invention include microsatellite markers, mitochondrial markers, restriction fragment length polymorphisms, and single nucleotide polymorphisms (SNPs). Useful canine microsatellite markers include, but are not limited to, dinucleotide repeats, such as $(CA)_n$, trinucleotide repeats, and tetranucleotide repeats, such as $(GAAA)_n$ (Francisco et al. (1996) *Mamm. Genome* 7:359-62; Ostrander et al. (1993) *Genomics* 16:207-13). Exemplary markers for use in the methods of the invention include the microsatellite markers set forth in Table 1, the SNP markers set forth in Table 2, and the markers described in Guyon et al. (2003) *Proc. Natl. Acad. Sci U.S.A.* 100(9):5296-5301. The set of markers used in the methods of the invention may comprise at least about 5 markers from the microsatellite markers in Table 1 and/or at least about 5 markers from the SNP markers in Table 2. In some embodiments, the set of markers are selected from the group consisting of 372c5t-82, 372e13t-57, 372m6t-88, 372m23t-76, 373a15t-112, 373e1t-50, 373e1t-130, 373g19t-246, 373i8s-224, 373k8s-181, 372c5s-168, 372C15S-196, 372e15s-71, and 373a21t-93. In some embodiments, a set of markers comprising fewer than about 1500 SNP markers is used to determine the contributions of at least 87 canid populations to the test canid genome. In some embodiments, a set of markers comprising fewer than about 200 SNP markers is used to determine the contributions of at least 87 canid populations to the test canid genome.

[0031] According to the methods of the invention, the identities of one or both alleles of each marker may be obtained. In some embodiments, the identities of one or both alleles of a marker in a test canid may be determined experimentally using methods that are standard in the art. For example, the identities of one or both alleles of a genomic marker may be determined using any genotyping method known in the art. Exemplary genotyping methods include, but are not limited to, the use of hybridization, Polymerase Chain Reaction (PCR), size fractionation, DNA sequencing, DNA microarrays, high density fiber-optic arrays of beads (see, e.g., Jianbing et al. (2003) *Chin. Sci. Bull.* 48(18):1903-5), primer extension, mass spectrometry (see, e.g., Jurinke et al. (2002) *Meth. Mol. Biol.* 187:179-92), and whole-genome sampling analysis (see, e.g., Kennedy et al. (2003) *Nat. Biotechnol.* 21(10):1233-7). The identities of alleles of markers in a test canid may also have been previously determined and be available from sources such as published literature.

[0032] In some embodiments, the genomic DNA of the test canid may be amplified using primers specific for the markers, followed by size analysis or sequencing of the amplification product. Exemplary methods for obtaining the identities of one or both alleles of markers in canid genomes are described in EXAMPLE 1. In some embodiments, the primers used for amplifying genomic DNA containing microsatellite markers are selected from the group consisting of SEQ ID NOs:1-200, although other primers and other microsatellite markers may be used. In some embodiments, the primers used for amplifying genomic DNA containing SNP markers are selected from the group consisting of SEQ ID NOs:244 to 327, although other primers and other SNP markers may be used. The identities of alleles of 68-100

microsatellite markers in 422 canids, including 414 dogs representing 85 breeds, and 8 wolves are set forth in Table 3 (filed herewith on a compact disc). The identities of alleles of 100 SNP markers in 189 canids, including 186 dogs representing 67 breeds, two wolves, and a coyote are set forth in Table 4 (filed herewith on a compact disc).

[0033] The minimum number of markers included in the set of markers used in the first step of the methods of the invention depends on the informativeness of the markers for the particular canid populations that are being used. The informativeness of a marker is a function of the number of different alleles within and between the canid populations used in the methods of the invention, the frequency of these alleles, and the rate of mutation rate at the locus. The degree of polymorphism of a genomic locus may be evaluated by an estimation of the polymorphic information content (PIC), which is a function of the number of alleles and their frequency distribution. Exemplary PIC values for microsatellite markers suitable for use in the methods of the invention are set forth in Table 1. Suitable markers for use in the methods of the invention may have an average PIC value of about 0.65%, as shown in EXAMPLE 1.

[0034] Methods of determining the number of alleles of markers in different canid populations and their frequencies within and between canid populations are described in EXAMPLE 1. For example, the mean number of alleles per maker, the expected heterozygosity (based on Hardy-Weinberg Equilibrium assumptions), the observed heterozygosity, and the estimated inbreeding coefficients across 95 microsatellite markers in 94 canids, including 90 dogs representing 18 breeds, and 4 wolves, are described in EXAMPLE 1.

[0035] The existence of breed barriers would predict that dogs from the same breed should be more similar genetically than dogs from different breeds. To test this prediction, the proportion of genetic variation between individual dogs that could be attributed to breed membership was estimated. Analysis of molecular variance for microsatellite data including 96 markers in 328 dogs representing 68 breeds showed that variation between breeds accounts for more than 27% of total genetic variation, as described in EXAMPLE 1. Similarly, the genetic distance between breeds calculated from SNP marker data including 75 SNPs in 120 dogs representing 60 breeds was FST=0.36, as described in EXAMPLE 1. These observations are consistent with previous reports that analyzed fewer dog breeds (Koskinen (2003) *Anim. Genet.* 34:297; Trion et al. (2003) *J. Hered.* 94:81), confirming the prediction that breed barriers have led to strong genetic isolation among breeds, and are in striking contrast to the much lower genetic differentiation (typically in the range of 5-10%) found between human populations (Rosenberg et al. (2002) *Science* 298: 2381-5; Cavelli-Sforza et al. (1994) *The History and Geography of Human Genes*, Princeton University Press, Princeton). Variation among breeds in dogs is on the high end of the range reported for livestock populations (MacHugh et al. (1998) *Anim. Genet.* 29:333; Laval et al. (2000) *Gen. Sel. Evol.* 32:187). Strong genetic differentiation among dog breeds indicates that breed membership may be determined from genotype information for individual canids.

[0036] The influence of the number of distinct alleles of a marker in a dataset on the informativeness of the marker is shown in EXAMPLE 2. For example, in an analysis of 19 canid populations and 95 microsatellite markers, 86% of canids were correctly assigned to their breed using 5 markers that each had more than 10 distinct alleles, and 95% of canids were correctly assigned using 10 or more markers that each had more than 10 distinct alleles. For markers with 1-3 distinct alleles, 46% of canids were correctly assigned to their breed using 5 markers, and 62% of canids were correctly assigned using 10 or more markers.

[0037] The influence of the number of markers used on the ability to discriminate between 19 canid populations using genotype information for 95 markers for 4 or 5 canids per canid population is shown in EXAMPLE 2. For example, the minimum number of markers required to successfully assign 100% of individuals to the correct canid population ranged between 2 (Pekingese) and 52 (American Hairless Terrier) depending on the canid population. The minimum number of microsatellite markers required to successfully assign at least 90% of all 94 tested individuals across the 19 canid populations, with the chosen canid population having 100% accuracy, ranged between 8 (for Pekingese) to 95 (for Preso Canario, Chihuahua, and American Hairless Terrier).

[0038] The second step of the methods of the first aspect of the invention comprises determining the contributions of canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising canid population profiles, wherein each canid population profile comprises genotype information for alleles of the markers in the set of markers in the canid population. A "canid population profile" as used herein refers to the collection of genotype information for the set of markers in a canid population. Thus, a canid population profile may comprise genotype information for most or all alleles of most or all markers in the set of markers in the canid population. For example, a canid population profile may comprise genotype information for each allele of each marker in the set of markers in the canid population. The genotype information in a canid population profile may comprise information such as the identity of one or both alleles of most or all of the markers in the set of markers in one or more canids that are members of that canid population, and/or estimated allele frequencies for at least one allele of most or all of the markers in the set of markers in that canid population. An "allele frequency" refers to the rate of occurrence of an allele in a population. Allele frequencies are typically estimated by direct counting. Generally, allele frequencies in a canid population are estimated by obtaining the identity of one or both alleles for each of the set of markers in at least about five members of that canid population. A "database of canid population profiles" refers to the collection of canid population profiles for all of the canid populations used in an exemplary method of the invention. In some embodiments, the database of canid population profiles comprises between about five and about 500 canid population profiles, such as about 20 canid population profiles, about 50 canid population profiles, or about 100 canid population profiles.

[0039] Determining the contributions of canid populations to the test canid genome encompasses both assigning a canid genome to a particular canid population and determining the fraction of the canid genome that was derived from one or more canid populations. In some embodiments of the method, a Bayesian model-based clustering approach is used. There are two broad classes of clustering methods that are used to assign individuals to populations (Pritchard et al. (2000) *Genetics* 155:945-59). Distance based methods cal-

culate a pairwise distance matrix to provide the distance between every pair of individuals. Model-based methods proceed by assuming that observations from each cluster are random draws from some parametric model; inference for the parameters corresponding to each cluster is then done jointly with inference for the cluster membership of each individual, using standard statistical methods. Any standard statistical method may be used in the methods of the invention, including maximum likelihood, bootstrapping methodologies, Bayesian methods and any other statistical methodology that can be used to analyze genotype data. These statistical methods are well-known in the art. Many software programs for population genetics studies have been developed and may be used in the methods of the invention, including, but not limited to TFPGA, Arlequin, GDA, GENEPOP, GeneStrut, POPGENE (Labate (2000) *Crop. Sci.* 40:1521-1528), and structure (Pritchard et al. (2000) *Genetics* 155:945-59).

[0040] An exemplary Bayesian model-based clustering approach is provided by the genotype clustering program structure (Pritchard et al. (2000) *Genetics* 155:945-59), which has proven useful for defining populations within a species (Rosenburg et al. (2001) *Genetics* 159:699-713; Rosenburg et al. (2002) *Science* 298:2381-5; Falush et al. (2003) *Genetics* 164(4):1567-87). The clustering method used by structure requires no prior information about either phenotype or genetic origin to accurately place an individual or set of related individuals in a population.

[0041] Any algorithms useful for multi-locus genotype analysis may be used in the methods of the invention, for example, classic assignment algorithms. Suitable algorithms include those described in Ranala & Mountain (1997) *Proc. Natl. Acad. Sci. USA* 94:9197-9201 and Cornuet et al. (1999) *Genetics* 153:1989-2000 and variations thereof. Exemplary programs available for multi-locus genotype analysis can be found on the worldwide web and include Doh (available at the University of Alberta website) and GeneClass (available at the website of CBPG of the French National Institute for Agricultural Research (INRA)).

[0042] In some embodiments, the methods of the invention comprise determining the probability that a specific canid population contributed to the genome of the test canid by determining the conditional probability that the alleles in the test canid genome would occur in the specific canid population divided by the sum of conditional probabilities that the alleles in the test canid genome would occur in each canid population in the database.

[0043] Some embodiments of the methods of the invention comprise discriminating between the contributions of two or more genetically related canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising profiles of the two or more genetically related canid populations. The two or more genetically related canid populations may comprise Belgian Sheep Dog and Belgian Tervuren; Collie and Shetland Sheep Dog; Whippet and Greyhound; Siberian Husky and Alaskan Malamute; Mastiff and Bullmastiff; Greater Swiss Mountain Dog and Bernese Mountain Dog; West Highland White Terrier and Cairn Terrier; or Lhasa Apso, Shih Tzu, and Pekinese.

[0044] Using an assignment algorithm on genotype information for 95 microsatellite markers from 94 canids, including 90 canids representing 18 breeds and 4 wolves, the methods of the invention have been used to assign each individual canid to its breed with 99% accuracy, as described in EXAMPLE 2. A clustering algorithm used on the same genotype information predicted 20 canid populations and assigned each canid to one population with 99% accuracy, as described in EXAMPLE 3.

[0045] Using an assignment algorithm on genotype information for 68 microsatellite markers from 341 canids representing 72 breeds, the methods of the invention have been used to assign 96% of the canids to the correct breed, as described in EXAMPLE 2. Using an assignment algorithm on genotype information for 96 microsatellite markers from 414 canids representing 85 breeds, the methods of the invention have been used to assign 99% of the canids to the correct breed, as described in EXAMPLE 4. Similar results were obtained using a clustering algorithm. Using an assignment algorithm on genotype information for 100 SNP markers from 189 canids representing 67 breeds, the methods of the invention have been used to assign 80% of canids to the correct breed with a probability of 99% of greater, as described in EXAMPLE 6.

[0046] The methods of the invention are also useful for determining the contributions of canid populations to mixed-breed canids. Admixed individuals represent approximately 50% of the canine population. Models that detect an individual's admixed state can be considered to group into two classes: models that require a combinatoric set of unique alleles for each of the possible mixtures of ancestral populations (Nason & Ellstrand (1993) *J. Hered.* 84:1-12; Epifanio & Philipp (1997) *J. Hered.* 88:62-65, and Bayesian methods where ancestral populations are not required to contain a combination describing unique alleles, but instead assign individuals to admixed states probabilistically based on differences in allele frequencies between populations (Corander et al. (2003) *Genetics* 163(1):367-74; Anderson & Thompson (2002) *Genetics* 160:1217-29, Pritchard et al. (2000) *Genetics* 155:945-59, Rannala & Mountain (1997) *Proc. Natl. Acad. Sci. U.S.A.* 94:9197-9201. The latter set of models are more informative for most populations and data sets as they allow for a Bayesian posterior probabilistic assignment vector for each population/generation combination, thereby allowing for uncertainty analysis to be incorporated into the assignment vector; but existing models for the exact, recent admixture assignments of individuals from multiple ancestral populations are limited in their scope as they have been developed thus far only for two generation prediction and allow for only a few ancestral populations. For example, the methods of Anderson & Thompson (2002) are developed for a two generation, two population model with unlinked microsatellite data. A naïve Bayesian classification model that incorporates linked and unlinked microsatellite loci information, higher-dimensioned ancestral populations, and higher-ordered generation pedigrees for the probabilistic assignment of individuals to mixtures of ancestral subpopulations is described in EXAMPLE 7. This model simultaneously addresses the generation, subpopulation, and linkage limitations of previous models, and 2- and 3-generational models have been implemented for exact admixture detection and assignment, as described in EXAMPLE 7.

[0047] Using a clustering algorithm on in silico mixes of genotype information for 95 markers from 85 canids, consisting of 81 canids representing 18 breeds and 4 wolves, the methods of the invention have been used to identify in silico mixing at the parent level with 100% accuracy, as described in EXAMPLE 5. The methods of the invention were also

highly accurate at detecting in silico mixing at the grandparent level, and fairly accurate at detecting in silico mixing at the great-grandparent level, as shown in EXAMPLE 5. Thus, the methods of the invention may be used to discriminate mixes at the parent and grandparent level from purebred dogs (as well as ½ wolf and ¼ wolf mixes from dogs) and identify breed contributions in the genome of a mixed-breed dog.

[0048] Using a Bayesian classification model on in silico mixes of genotype information for 96 markers from 429 canids representing 88 breeds, the methods of the invention have been used to correctly assign more than 98% of F1 mixes and more than 94% of F2 mixes, as described in EXAMPLE 7. Using this model on genotype information for 72 markers from 160 known mixed-breed canids, the methods of the invention have been used to correctly assign more than 96% of F1 mixes and more than 91% of F2 mixes, as described in EXAMPLE 7.

[0049] The methods of the invention may further comprise the step of providing a document displaying the contributions of one or more canid populations to the genome of the test canid genome. The term "document" refers to a chart, certificate, card, or any other kind of documentation. The document may display the contributions of one or more canid populations to the test canid genome in a numeric format or in a graphic format. For example, the document may include photographs or other depictions, drawings, or representations of the one or more canid populations. The document may also provide confidence values for the determined contributions (such as 80%, 85%, 90% 95%, or 99% confidence). In some embodiments, the document provides a certification of the contributions of one or more canid populations to the genome of the test canid genome.

[0050] In some embodiments, the document additionally provides information regarding the one or more canid populations that contributed to the genome of the test canid or the test canid. The information regarding canid populations that contributed to the genome of the test canid may include information related to the characteristics and origin of the canid population or any other kind of information that would be useful to the owner of the test canid. In some embodiments, the information includes health-related information. Many canid populations have predispositions to particular diseases or conditions. For example, Afghan hounds are predisposed to glaucoma, hepatitis, and hypothyroidism; Basenji are predisposed to coliform enteritis and pyruvate kinase deficiency; Beagles are predisposed to bladder cancer and deafness; Bernese Mountain dogs are predisposed to cerebellar degeneration; Border Terriers are predisposed to oligodendroglioma; and Labrador Retrievers are predisposed to food allergies (see, e.g., Dr. Bob's All Creatures Site on the internet, Predisposition of Dog Breeds to Disease and Congenital Conditions; Patterson et al. (1988) *J. Am. Vet. Med. Assoc.* 193:1131). Of the genetic diseases discovered in dogs, 46% are believed to occur predominantly or exclusively in one or a few breeds (Patterson et al. (1988) *J. Am. Vet. Med. Assoc.* 193:1131.) Therefore, information regarding the contributions of one or more canid populations to the genome of the test canid genome is particularly valuable to mixed-breed canid owners or caretakers (both professional and non-professional) for the purpose of proactively considering health risks for individual tested animals. For example, a mixed breed dog that is found to be a mixture of Newfoundland and Bernese Mountain Dog should be actively monitored for genetic diseases that occur with rare frequency in the general population of dogs, but occur with significant frequency in these specific breeds; thus, a mixed-breed individual of this type would benefit from screens for malignant histiocytosis (disease heritability of 0.298 in Bernese Mountain dogs, Padgett et al. (1995) *J. Small Anim. Pract.* 36(3):93-8) in addition to Type I cystinuria genetic screens (nonsense mutation isolated in Newfoundlands at exon 2 of SLC3A1 gene, Henthorn et al. (2000) *Hum. Genet.* 107(4):295-303).

[0051] Health-related information may also include potential treatments, special diets or products, diagnostic information, and insurance information. An exemplary document displaying the contributions of one or more canid populations to the genome of a test canid is shown in FIG. **1**.

[0052] In some embodiments, the invention provides methods for defining one or more canid populations, comprising: (a) for each of a set of canid genomes, obtaining the identity of one or both alleles for each of a set of markers; and (b) defining one or more canid populations by determining the likelihood that one or more members of the set of canid genomes define distinct canid populations characterized by a set of allele frequencies for each marker. Exemplary methods of the invention for defining one or more canid populations are described in EXAMPLES 3 and 4.

[0053] In another aspect, the invention provides substrates comprising nucleic acid sequences for determining the identity of one or both alleles in a canid genome for each of a set of markers. The substrates may be in any form suitable for determining the identity of alleles of markers. For example, the substrate may be in the form of a microarray or a collection of beads.

[0054] In a further aspect, the invention provides a computer-readable medium comprising a data structure stored thereon for use in distinguishing canid populations, the data structure comprising: a marker field, which is capable of storing the name of a marker (for example, an SNP marker) or the name of an allele of a marker; and a genotype information field, which is capable of storing genotype information for the marker (for example, the identity of one or both alleles of the marker in a canid genome or an estimate of the frequency of an allele of the marker in a canid population), wherein a record comprises an instantiation of the marker field and an instantiation of the genotype information field and a set of records represents a canid population profile.

[0055] A "computer-readable medium" refers to any available medium that can be accessed by computer and includes both volatile and nonvolatile media, removable and non-removable media. By way of example, and not limitation, computer-readable media may comprise computer storage media and communication media. Computer storage media includes both volatile and nonvolatile, removable, and non-removable media implemented in any method or technology for storage of information, such as computer readable instructions, data structures, program modules, or other data. Computer storage media include, but are not limited to, RAM, ROM, EEPROM, flash memory or other memory technology, CD-ROM, digital versatile disks (DVD) or other optical disk storage, magnetic cassettes, magnetic tapes, magnetic disk storage or other magnetic storage devices, or any other computer storage media. Communication media typically embody computer-readable instructions, data

structures, program modules or other data in a modulated data signal, such as a carrier wave or other transport mechanism that includes any information delivery media. The term "modulated data signal" means a signal that has one or more of its characteristics set or changed in such a manner as to encode information in the signal. By way of example, and not limitation, communication media include wired media, such as a wired network or direct-wired connection, and wireless media, such as acoustic, RF infrared, and other wireless media. A combination of any of the above should also be included within the scope of computer-readable media.

[0056] A "data structure" refers to a conceptual arrangement of data and is typically characterized by rows and columns, with data occupying or potentially occupying each cell formed by a row-column intersection. The data structure in the computer-readable medium of the invention comprises a marker field and a genotype information field, as described above. The instantiation of the marker field and the genotype information field provides a record, and a set of records provides a canid population profile. Thus, the data structure may be used to create a database of canid population profiles.

[0057] In some embodiments, the computer readable medium comprises a substrate having stored thereon: (a) a data structure for use in distinguishing canid populations, the data structure comprising: (i) a marker field, which is capable of storing the name of a marker or of an allele of a marker; and (ii) a genotype information field, which is capable of storing genotype information for the marker, wherein a record comprises an instantiation of the marker field and an instantiation of the frequency field and a set of records represents a canid population profile; and (b) computer-executable instructions for implementing a method for determining the contributions of canid populations to a canid genome, comprising: (i) obtaining the identity of one or both alleles in a test canid genome for each of a set of markers; and (ii) determining the contributions of canid populations to the test canid genome by comparing the alleles in the test canid genome to a database comprising canid population profiles, wherein each canid population profile comprises genotype information for the set of markers in the canid population.

[0058] The following examples merely illustrate the best mode now contemplated for practicing the invention, but should not be construed to limit the invention.

Example 1

[0059] This example describes a representative method of the invention for obtaining the identity of one or both alleles for a set of markers and selecting markers suitable for determining the contribution of canid populations to the genome of a canid.

[0060] A. Methods

[0061] 1. Sample Collection and DNA Extraction

[0062] Canid DNA samples from 513 American Kennel Club-registered dogs representing 103 breeds and 8 gray wolves from eight countries (China, Oman, Italy, Iran, U.S.A. (Alaska), Canada (Quebec), Sweden, Mexico) were obtained by collecting buccal (cheek) swabs and/or blood samples from volunteers at dog shows and dog club specialty events, as well as by mail-in donations. American Kennel Club registration number and detailed pedigree information was requested for all dogs, as participation was limited to unrelated dogs that did not share grandparents. Pedigree information was also collected for 84% of sampled individuals. In many cases, five-generation pedigrees were obtained, and while dogs sometimes appear redundantly at the great-grandparent level or higher, inspection of the complete lineage indicates a high degree of unrelatedness among dogs of the same breed. For those individuals where a pedigree was not available, unrelatedness was verified by breed club representatives. Each individual canid was given a canid identification number. Abbreviations used for breeds and other canid populations are shown in Table 5. In addition, DNA samples from 160 mixed-breed canids comprising admixture components from 20 AKC breeds were obtained by collecting buccal swabs.

[0063] Buccal swabs were collected in a manner similar to that suggested by the American Kennel Club (AKC) website using cytology brushes (Medical Packaging Corp., Camarillo, CA). DNA was extracted from buccal swabs using QiaAmp® blood kits following manufacturers' protocol (Qiagen, Valencia, CA). DNA extraction from blood was done as described previously (Comstock et al. (2002) *Mol. Ecol.* 11:2489-98).

[0064] 2. Analysis of Microsatellite Markers

[0065] One hundred dinucleotide microsatellite markers were chosen from the 1596 microsatellites currently localized on the 3300 marker map of the dog (Guyon et al. (2003) *Proc. Natl. Acad. Sci U.S.A.* 100(9):5296-5301) (Table 1). Markers were selected based on informativeness, calculated as a PIC value, and distribution across all 38 autosomes. Selected markers had an average PIC value of 0.65% (range 36%-86%) and an average spacing of 29.5 Mb (range 21.5-50.9 Mb). Dinucleotide, rather than tetranucleotide microsatellites, were chosen to reduce the number of spurious mutations observed that could hamper breed identification.

[0066] DNA samples were arrayed on five 96-well plates. A positive control was included on each plate to ensure consistent allele binning PCR was performed in 10 microliter reactions containing 1 ng of genomic DNA and final concentrations of the following reagents: 16 mM ammonium sulfate, 67 mM Tris-HCl pH 8.8, 2.0 mM $MgCl_2$, 0.1 mM dNTPs, 300 nM forward primers (SEQ ID NOs:1-100), reverse primers (SEQ ID NOs:101-200), and dye-labeled M13 Primers (PE Applied Biosystems, Foster City, CA USA). Forward primers were redesigned to include a 19 base M13 forward (−29) sequence, 5'-CACGACGTTGTAAAACGAC-3' (SEQ ID NO:201), on the 5 prime end. Samples were labeled by the addition of 0.25 pmol of an M13 primer (SEQ ID NO:201) tagged with either 6FAM™, VIC™, NED™ or PET™ (ABI, Foster City, CA) dyes to each reaction. PCR incubation was carried out according to standard protocols (see, e.g., Lowe et al. (2003) *Genomics* 82:86-95). Annealing temperatures used are provided in Table 1. Four samples labeled with different dyes were multiplexed following completion of PCR by combining 3 microliters of each reaction mix into a single 96 well plate. Samples were denatured in 2 volumes Hi-Di™ formamide with 16 pmol of GeneScan™ 500LIZ™ size standard (ABI, Foster City, CA) according to manufacturers' protocols. All samples were loaded on an ABI 3730 DNA Analyzer™ (PE Applied Biosystems) capillary electrophoresis instrument for allele separation. Genotypes were called using GeneMapper™ v3.0 software (ABI, Foster City, CA). All calls were checked manually, and each subsequent run

was scanned for the appearance of new alleles outside existing bins. Four markers failed to amplify consistently and were discarded.

[0067] 3. SNP Discovery and Genotyping

[0068] Fifty canine bacterial artificial chromosomes (BACs) were chosen at random from the canine radiation hybrid map (Guyon et al. (2003) *Proc. Natl. Acad. Sci U.S.A.* 100(9):5296-5301). The Primer3 program (available on line) was used to design primers from each BAC end sequence. The resulting amplicons averaged 334 base pairs. Primers were used to amplify 19867 base pairs of non-continuous genomic sequence in 189 dogs representing 67 domestic dog breeds, coyote, and the gray wolf. The resulting PCR products were sequenced using standard methods on an ABI 3700 capillary sequencer with standard ABI dye terminator chemistry (ABI, Foster City, CA), and resequenced. All sequence reads were aligned and viewed using Phred, Phrap and Consed (Ewing & Green (1998) *Genome Res.* 8:186-94; Ewing et al. (1998) *Genome Res.* 8: 175-85). The computer program Polyphred was used to identify regions of polymorphism, both SNP and insertion/deletion, within and between sequence reads (Nickerson et al. (1997) Nucl. Acids Res. 25:2745-51). All allele calls were confirmed manually and confirmed through visual inspection of the traces.

[0069] 4. Statistical Analysis

[0070] An analysis of molecular variance (AMOVA) was performed with GDA (Lewis & Zaykin (2001) Genetic Data Analysis: Computer Program for the Analysis of Allelic Data, Version 1.0 (d16c), available on line at the University of Connecticut website) under assumption of Hardy-Weinberg equilibrium. Similar results were obtained for the fraction of genetic variation among breeds when inbreeding was allowed for in the analysis.

[0071] Expected heterozygosity for each breed was calculated from allele frequencies using Tajima's unbiased estimator (Tajima (1989) *Genetics* 123:585-95).

[0072] B. Results

[0073] 1. Informativeness of Dinucleotide Microsatellites

[0074] The identities of alleles (length of the amplified region) of 68-100 microsatellite markers in 422 canids, including 414 dogs representing 85 breeds, and 8 wolves, are set forth in Table 3 (filed herewith on a compact disc). 148 alleles were found to be unique to a specific canid population: 1 each to ACKR, AUST, BORD, BOX, BULD, DACH, GOLD, GSHP, GSMD, IBIZ, KEES, NELK, PEKE, POM, ROTT, SFXT, TERV, and WHIP, 2 each to BEAG, CAIR, HUSK, IRSE, MAST, OES, SCHP, SCWT, SPOO, and SSHP, 3 each to AMAL, BMD, KOMO, NEWF, STBD, and WSSP, 4 each to KUVZ, PNTR, and PRES, 5 each to BSJI and SHAR, 6 to AKIT, and 64 to WOLF.

[0075] Six different datasets were used for subsequent analyses, as further described in EXAMPLES 2-5 and 7. The first dataset included genotype information for microsatellite markers (microsatellite markers 1-14, 16, 18-21, 23-36, 39-100, see Table 1) in 94 canids, including 90 canids representing 18 breeds and 4 wolves (dataset 1, Table 6). The second dataset included genotype information for 68 microsatellite markers (microsatellite markers 2-8, 11, 12, 14-16, 18-21, 23, 24, 26-32, 34-36, 38, 41, 42, 44-46, 50, 51, 53, 54, 56, 60-64, 67, 68, 70-74, 78, 79, 81-83, 85, 87-91, 93-98, see Table 1) in 341 canids representing 72 breeds (dataset 2, Table 7). The third dataset included genotype information for 96 microsatellite markers (microsatellite markers 1-9, 11-38, 40-42, 44-75, 77-100, see Table 1) in 414 canids representing 85 breeds (dataset 3, Table 8). The fourth dataset included genotype information for microsatellite markers (microsatellite markers 1-9, 11-38, 40-42, 44-75, 77-100, see Table 1) in 85 canids, including 81 dogs representing 18 breeds, and 4 wolves (dataset 4, Table 9). The fifth dataset included genotype information for 96 microsatellite markers (microsatellite markers 1-9, 11-38, 40-42, 44-75, 77-100, see Table 1) in 429 canids representing 88 breeds. The sixth dataset included genotype information for 72 of the microsatellite markers in Table 1 in 160 mixed-breed canids, as set forth in Table 3 (filed herewith on a compact disc).

[0076] The proportion of polymorphic markers, the mean number of alleles per maker, the mean number of alleles per polymorphic maker, the expected heterozygosity (based on Hardy-Weinberg Equilibrium assumptions), the observed heterozygosity, and the estimated inbreeding coefficients across 95 microsatellite markers in dataset 1 are shown in Table 10. The expected heterozygosity of 85 canid populations averaged over 96 microsatellites (dataset 3) using Tajima's unbiased estimator is shown in Table 11.

[0077] The existence of breed barriers would predict that dogs from the same breed should be more similar genetically than dogs from different breeds. To test this prediction, the proportion of genetic variation between individual dogs that could be attributed to breed membership was estimated. Analysis of molecular variance in the microsatellite data for 96 microsatellites in 414 dogs representing 85 breeds (dataset 3, Table 8) showed that variation between breeds accounts for more than 27% of total genetic variation.

[0078] 2. Informativeness of SNP Markers

[0079] Using 189 canids representing 67 domestic breeds, coyote and wolf, 100 polymorphic sites in approximately 20 Kb of non-continuous canine genomic sequence were identified, as shown in Table 2. These include 92 single base substitutions and 11 insertion or deletion mutations ranging from one to eight nucleotides in length. The identities of alleles for 100 SNP markers in 189 canids, including 186 dogs representing 67 breeds, two wolves, and a coyote are set forth in Table 4 (filed herewith on a compact disc). Minor allele frequencies in 75 SNPs from 120 dogs representing 60 breeds ranged from 0.4% to 48%, as shown in Table 2. Fourteen of these SNPs were breed-specific: 372c5t-82 (English Shepherd), 372e13t-57 (Cocker Spaniel), 372m6t-88 (English Shepherd), 372m23t-76 (Alaskan Malamute), 373a15t-112 (Chesapeake Bay Retriever), 373e1t-50 (Spinoni Italiano), 373e1t-130 (Scottish Deerhound), 373g19t-246 (Borzoi), 373i8s-224 (Chesapeake Bay Retriever), 373k8s-181 (Tibetan Terrier), 372c5s-168 (Akita), 372C15S-196 (Labrador Retriever), 372e15s-71 (Field Spaniel), 373a21t-93 (Italian Greyhound).

[0080] When all dogs were considered as a single population, the observed heterozygosity (Tajima & Nei (1984) *Mol. Biol. Evol.* 1:269-85) was 8×10^{-4}, essentially the same as that seen in the human population (Sachidanandam et al. (2001) *Nature* 409:928-33; Venter et al. (2001) *Science* 291:3104-51). However, when the breeds are separated, there is a 4-fold range in heterozygosity between the least outbred (Scottish Deerhound, 2.5×10^{-4}) to most outbred (English Shepherd, 1.0×10^{-3}). The genetic distance between breeds calculated from the SNP data for 75 SNPs in 120 dogs representing 60 breeds was FST=0.36.

[0081] The expected heterozygosity of 60 canid populations based on allele frequencies at 75 SNP loci (dataset 3)

using Tajima's unbiased estimator is shown in Table 12. Each breed is represented by 2 dogs.

Example 2

[0082] This example describes a representative method of the invention for estimating the contributions of canid populations to a canid genome using an assignment test calculator on genotype information for 95 microsatellite markers from 94 canids, and on genotype information for 68 microsatellite markers from 341 canids.

[0083] A. Methods

[0084] 1. Datasets

[0085] Dataset 1 included genotype information for 95 microsatellite markers from 94 canids, including 90 dogs representing 18 breeds, and 4 wolves (AHRT, AKIT, BEAG, BMD, BOX, BULD, BULM, CHIH, DACH, GOLD, IBIZ, MAST, NEWF, PEKE, POM, PRES, PUG, ROTT, WOLF, see Table 5 for abbreviations of canid populations). The 95 microsatellite markers were microsatellite markers 1-14, 16, 18-21, 23-36, 39-100 (Table 1). The dataset contained genotype information from 5 canids for each breed and 4 wolves (Table 6). The genotype information for the canids in dataset 1 is set forth in Table 3 (filed herewith on a compact disc).

[0086] Dataset 2 included genotype information for 68 markers from 341 canids representing 72 breeds (ACKR, AFGH, AHRT, AIRT, AKIT, AMAL, AMWS, AUSS, AUST, BASS, BEAG, BEDT, BELS, BLDH, BMD, BORD, BORZ, BOX, BSJI, BULD, BULM, CAIR, CHBR, CHIH, CKCS, CLSP, COLL, DACH, DANE, DNDT, DOBP, ECKR, FCR, GOLD, GREY, GSD, GSHP, GSMD, HUSK, IBIZ, IRSE, IRTR, IWOF, KEES, KOMO, KUVZ, LAB, MAST, MBLT, MNTY, NELK, NEWF, OES, PEKE, PNTR, POM, PRES, PTWD, PUG, RHOD, ROTT, SCHP, SCWT, SFXT, SHAR, SPOO, SSHP, STBD, TERV, WHIP, WHWT, WSSP, see Table 5 for abbreviations of canid populations). The 68 microsatellite markers were microsatellite markers 2-8, 11, 12, 14-16, 18-21, 23, 24, 26-32, 34-36, 38, 41, 42, 44-46, 50, 51, 53, 54, 56, 60-64, 67, 68, 70-74, 78, 79, 81-83, 85, 87-91, 93-98 (Table 1). The dataset contained genotype information from 5 canids for each breed, except for SFXT (2 canids), ACKR, AFGH, DNDT, OES (3 canids each), AIRT, BASS, BEDT, IRTR, MNTY, SCHP, SCWT, and TERV (4 canids each) (Table 7). The genotype information for the canids in dataset 2 is set forth in Table 3 (filed herewith on a compact disc).

[0087] 2. Doh Analysis

[0088] The assignment test calculator Doh (available at the University of Alberta website) was used for an analysis of the two datasets of genotype information. All individual canids were designated with their known population except for the canid to be tested, which was then assigned by the program to the canid population with the highest probability of generating the test canid's genotype. The program repeats this procedure with each canid as the test canid.

[0089] B. Results

[0090] 1. Doh Analyses Using Dataset 1

[0091] Using Doh on the genotype information in dataset 1, including genotype information for 95 microsatellite markers in 94 canids (90 dogs representing 18 breeds, and 4 wolves), 99% of the canids were assigned to the correct canid population. 100% canids were correctly assigned for the following breeds: AHRT, AKIT, BEAG, BMD, BOX, BULD, CHIH, DACH, GOLD, IBIZ, MAST, NEWF, PEKE, POM, PUG, ROTT, WOLF The only canid that was misassigned was one dog (out of 5 dogs) of the Presa Canario breed. The misassigned Presa Canario dog was assigned to Chihuahua.

[0092] It was found that the discrimination power of the allelic patterns depended on the number of independent microsatellite loci, the allelic diversity at each locus, and the number of individuals sampled from each breed. To evaluate the effect of the number of alleles of a marker and the number of markers on informativeness of that marker, a Doh assignment analysis for the first 19 breeds was performed with 5, 10, 15, and 20 markers, binning markers with 1-3 distinct alleles found in the dataset, 4-6 distinct alleles, 7-10 distinct alleles, and more than 10 distinct alleles. For the bins that did not contain markers, the maximum number of markers was used. For markers with more than 10 distinct alleles, 86% of canids were correctly assigned to their breed using five markers, and 95% of canids were correctly assigned using 10, 15, or 20 markers. For markers with 7-10 distinct alleles, 84% of canids were correctly assigned to their breed using 5 markers and 91% of canids were correctly assigned using 10 markers, and 94% of canids were correctly assigned using 15, or 20 markers. For markers with 4-6 distinct alleles, 62% of canids were correctly assigned to their breed using 5 markers, and 71% of canids were correctly assigned using 10, 15, or 20 markers. For markers with 1-3 distinct alleles, 46% of canids were correctly assigned to their breed using 5 markers, and 62% of canids were correctly assigned using 10, 15, or 20 markers.

[0093] The minimum number of microsatellite markers found in a 2-class (0-1) directed search of the allele frequency patterns within the 95 markers required to successfully assign 100% of the individuals to the correct canid populations (incorrect assignment is to any other breed) was 2 for PEKE, 3 for BOX, POM, and WOLF, 4 for AKIT, MAST, and PUG, 5 for NEWF and ROTT, 6 for BMD, 8 for BEAG, 11 for I131Z, 12 for GOLD, 17 for DACH, 19 for BULD, 26 for BULM, 44 for PRES, 49 for CHIH, and 52 for AHRT. There is a positive correlation between the minimum number of microsatellite markers required for 100% (0-1) discrimination, and the mean number of alleles across the 95 microsatellite markers for the 94 canids tested in 19 canid populations (see Table 10).

[0094] The minimum number of microsatellite markers found in a multiclass (0, 1, 2, . . . 18) directed search of the allele frequency patterns within the 95 markers required to successfully assign at least 90% of all 94 tested individuals across the 19 canid populations, with the chosen canid population having 100% accuracy, was 8 for PEKE, BOX, POM, WOLF, AKIT, MAST, PUG, NEWF, ROTT, and BMD, 11 for BEAG, 14 for IBIZ, 14 for GOLD, 23 for DACH, 24 for BULD, 28 for BULM, and 95 for PRES, CHIH, and AHRT.

[0095] As expected, the discrimination power reflects the level of inbreeding observed in each breed. For example, certain breeds have allelic variation 3-fold less than the average breed allelic variation and those breeds have both higher discrimination power and the characteristic population dynamics of long population bottlenecks and small effective population sizes

[0096] 2. Doh Analysis Using Dataset 2

[0097] Using Doh on the genotype information in dataset 2, including genotype information for 68 markers from 341 canids representing 72 breeds, 96% of the dogs tested were

assigned to the correct breed, as shown in Table 13. If both Belgian breeds (Belgian Sheepdog and Belgian Tervuren) were counted as one breed, 98% of the dogs tested were assigned to the correct breed.

Example 3

[0098] This example describes a representative method of the invention for estimating the contributions of canid populations to a canid genome using cluster analysis on genotype information for 95 microsatellite markers from 94 canids.

[0099] A. Methods

[0100] 1. Dataset

[0101] Dataset 1 included genotype information for 95 microsatellite markers from 94 canids, including 90 dogs representing 18 breeds, and 4 wolves, as described in EXAMPLE 2.

[0102] 2. Cluster Analysis

[0103] Cluster analysis was performed using the multilocus genotype clustering program structure (Pritchard et al. (2000) *Genetics* 155:945-59; Falush et al. (2003) *Science* 299:1582-5), which employs a Bayesian model-based clustering algorithm to identify genetically distinct subpopulations based on patterns of allele frequencies. Multiple runs were completed for each value of K (number of genetic clusters) with burn-in lengths of 10,000 steps and 100,000 iterations of the Gibbs sampler. The correlated allele frequency model was used with asymmetric admixture allowed. All values of K from 2 to 80 were tested and the clustering solutions that produced the highest likelihood were retained for further verification. To choose the overall best clustering solution for the data set, an all-pairs Wilcoxon two-sample test was performed for the 5 highest likelihood values of K.

[0104] 3. Nested Set Clustering

[0105] Starting with the complete data set, all individuals were hierarchically divided into sub-clusters where each (K+1)th sub-cluster was created by splitting one of the previous K clusters based on the highest observed likelihood value across 10 runs. Employing a hierarchical method for deriving clusters of individuals may infer a reasonable methodology for ascertaining population phylogeny when genetic variability between sub-populations is reduced due to a modified amount of admixture.

[0106] B. Results

[0107] A maximum likelihood calculation using structure predicted 20 populations in dataset 1 (95 markers in 19 canid populations) and assigned each individual to one group with 99% accuracy, as shown in Table 14. The one individual that was not assigned to its breed group was a single Presa Canario, which was placed between the Bulldog and the Bullmastiff groups. The Presa Canario is a recreated breed that has been developed through admixture of various mastiff types. The misassigned dog, in particular, can trace its heritage to both a bulldog and a Bullmastiff within the last 12 generations.

[0108] The clustering assignment was not able to distinguish between the Bullmastiffs and the Mastiffs at this level of analysis, but this was solved by nested analysis, as shown in Tables 15A-D. In the nested analysis, the same clustering algorithms were applied in a stepwise fashion. First, the entire set was divided into two populations. Based on maximum likelihood, one of these two populations was then divided into two to provide a total of three populations. This process was repeated until all populations were resolved. The divisions from five to nine groups clearly show the relationships between the mastiff type breeds. This relationship and the hierarchy predicted conforms perfectly to that expected from breed accounts.

Example 4

[0109] This example describes a representative method of the invention for estimating the contributions of canid populations to a canid genome using cluster analysis on genotype information for 96 microsatellite markers in 85 canid populations.

[0110] A. Methods

[0111] 1. Dataset

[0112] Dataset 3 included genotype information for 96 markers from 414 canids representing 85 breeds (ACKR, AFGH, AHRT, AIRT, AKIT, AMAL, AMWS, AUSS, AUST, BASS, BEAG, BEDT, BELS, BICH, BLDH, BMD, BORD, BORZ, BOX, BSJI, BULD, BULM, CAIR, CHBR, CHIH, CHOW, CKCS, CLSP, COLL, DACH, DANE, DOBP, ECKR, FBLD, FCR, GOLD, GREY, GSD, GSHP, GSMD, GSNZ, HUSK, IBIZ, IRSE, IRTR, ITGR, IWOF, KEES, KERY, KOMO, KUVZ, LAB, LHSA, MAST, MBLT, MNTY, MSNZ, NELK, NEWF, OES, PEKE, PHAR, PNTR, POM, PRES, PTWD, PUG, RHOD, ROTT, SALU, SAMO, SCHP, SCWT, SHAR, SHIB, SHIH, SPOO, SSHP, SSNZ, STBD, TIBT, TERV, WHIP, WHWT, WSSP, see Table 5 for abbreviations of canid populations). The 96 microsatellite markers were microsatellite markers 1-9, 11-38, 40-42, 44-75, 77-100 (Table 1). The dataset contained genotype information for 5 canids for all breeds, except for AIRT, BASS, BEDT, BICH, FBLD, IRTR, MNTY, PHAR, SCHP, SCWT, TERV (4 canids each) (Table 8). The genotype information for the canids in this dataset is set forth in Table 3 (filed herewith on a compact disc).

[0113] 2. Statistical Analyses

[0114] Structure was run for 100,000 iterations of the Gibbs sampler after a burn-in of 20,000 iterations. The correlated allele frequency model was used with asymmetric admixture allowed. The similarity coefficient across runs of structure was computed as described (Rosenberg et al. (2002) *Science* 298:2381-5). When the program was run on a partial data set of 68 breeds, it was noted that at values of K above 40 the program created clusters to which no individuals were assigned, and the clusters were unstable from run to run. This is most likely because the algorithm, which was initially designed to separate 2-3 populations, is unable to handle such large numbers of populations simultaneously. Because structure has previously been shown to reliably separate 20 populations (Rosenberg et al. (2001) *Genetics* 159:699-713), the data were divided set into 8 subsets of 10 to 11 breeds each, and all possible pairs of these subsets were analyzed. Historically related or morphologically similar breeds were retained in the same subset.

[0115] Structure was then applied to the entire data set at K=2 to K=10, with fifteen runs at each K. As K is increased, structure first separates the most divergent groups into clusters, followed by separation of more closely related groups (Rosenberg et al. (2002) *Science* 298:2381). In the analysis, the likelihood increased with increasing values of K, reflecting additional structure found at each K, but multiple different clustering solutions were found for K>4, and therefore K=2 to 4 were used to describe the global breed structure, with phylogenetic analysis and cluster

analysis of subgroups used to define constellations of closely related breeds. Structure runs at K=2-5 were repeated under the no admixture model with similar results. In a separate analysis, eight wolves were added to the structure run at K=2. The wolves were sampled from eight countries: China, Oman, Iran, Italy, Sweden, Mexico, Canada (Ontario), and the United States (Alaska). All wolves clustered together with the first cluster of dog breeds shown in Table 16.

[0116] Each breed was assigned to one of the four groups based on breed average majority and structure was run on each group at K=2-4. No additional consistent patterns were observed within the individual groups apart from the reported breed pairs and trios. Outlier analysis was carried out using the software package fdist2. Eleven markers were identified as potential "outliers" with Fst values above the 95th percentile achieved by simulation under the infinite allele model with 85 populations assumed and an average of 10 haploid genotypes per population (Beaumont & Nichols (Dec. 22, 1996) Proceedings: Biological Sciences 263: 1619). Assignment and structure analysis performed with these markers removed did not result in significant changes.

[0117] For the phylogenetic tree analysis, individual dogs and wolves were assigned to one of 86 populations based on breed or species. Distances between the populations were computed using the program Microsat (E. Minch, A. Ruiz-Linares, D. Goldstein, M. Feldman, L. L. Cavalli-Sforza (1995, 1996)) with the chord distance measure. 500 bootstrap replicates were generated. Neighbor-joining trees were constructed for each replicate using the program Neighbor, and the program Consense was used to create a majority-rule consensus tree. Both of these programs are part of the Phylip package (Felsenstein (1989) Cladistics 5:164) available at the University of Washington website. The wolf population was designated as the outgroup in order to root the tree. Wolves from eight different countries were combined into one population for simplicity on the tree shown in FIG. **2**. When taken as individuals, all wolves split off from a single branch, which falls in the same place as the root. The splitting order in the phylogenetic analysis was not correlated with heterozygosity (Table 11), and the twelve breeds that split off first closely mirrored the first cluster identified by structure. These observations argue that the analysis identified a distinct subgroup of genetically related breeds, rather than splitting off idiosyncratic breeds that are unusually inbred or that recently mixed with wild canids.

[0118] The assignment test was carried out with the Doh assignment test calculator available from J. Brzustowski (available at the University of Alberta website). All dogs were designated with their known breed except for the one dog to be tested, which was then assigned by the program to the breed with the highest probability of generating the test dog's genotype. The program repeats this procedure with each dog as the test dog. The Belgian Sheepdog and Belgian Tervuren breeds were combined into one designation for this analysis; when they are treated as separate breeds the individual dogs are assigned to one or the other essentially at random.

[0119] B. Results

[0120] When structure was applied to overlapping subsets of 20-22 breeds at a time, it was observed that most breeds formed distinct clusters consisting solely of all the dogs from that breed, as shown in Table 17. Dogs in only four breeds failed to consistently cluster with others of the same breed: Perro de Presa Canario, German Shorthaired Pointer, Australian Shepherd, and Chihuahua. In addition, six pairs of breeds clustered together in the majority of runs: Belgian Sheepdog and Belgian Tervuren, Collie and Shetland Sheepdog, Whippet and Greyhound, Siberian Husky and Alaskan Malamute, Mastiff and Bullmastiff, and Greater Swiss Mountain Dog and Bernese Mountain Dog. These pairings are expected based on known breed history.

[0121] To test whether these closely related breed pairs were nonetheless genetically distinct, structure was applied to each of these clusters. In all but one case the clusters separated into two populations corresponding to the individual breeds, as shown in Table 18. The single exception was the cluster containing Belgian Sheepdogs and Belgian Tervurens. The European and Japanese Kennel Clubs classify them as coat color and length varieties of a single breed (Yamazaki & Yamazaki (1995) *Legacy of the Dog: The Ultimate Illustrated Guide to Over* 200 *Breeds*, Chronicle Books, San Francisco, CA; Wilcox & Walkowicz (1995) *Atlas of Dog Breeds of the World*, T.F.H. Publications, Neptune City, NJ), and while the American Kennel Club recognizes these as distinct breeds, the breed barrier is apparently too recent or insufficiently strict to have resulted in genetic differentiation. This example confirms that the algorithm only separates groups that have true genetic differences (Falush et al. (2003) *Science* 299:1582-5; Pritchard & Rosenberg (1999) *Am. J. Hum. Genet.* 65:200-8).

[0122] To test whether a dog could be assigned to its breed based on genotype data alone, the direct assignment method (Paetkau et al. (1995) *Mol. Ecol.* 4:347-54) with a leave-one-out analysis was used. 99% of individual dogs were correctly assigned to the correct breed. Only four dogs out of 414 were assigned incorrectly: one Beagle (assigned to Perro de Presa Canario), one Chihuahua (assigned to Cairn Terrier), and two German Shorthaired Pointers (assigned to Kuvasz and Standard Poodle, respectively). All four errors involved breeds that did not form single-breed clusters in the structure analysis.

[0123] Having demonstrated that modern dog breeds form distinct genetic units, it was attempted to define broader historical relationships among the breeds. First, standard neighbor-joining methods were used to build a majority-rule consensus tree of breeds (FIG. **2**), with distances calculated using the chord distance measure (Cavalli-Sforza & Edwards (1967) *Evolution* 32:550), which does not assume a particular mutation model and is thought to perform well for closely related taxa (Goldstein et al. (1995) *Genetics* 139:463). The tree was rooted using wolf samples. The deepest split in the tree separated four Asian spitz-type breeds, and within this branch the Shar-Pei split first, followed by the Shiba Inu, with the Akita and Chow Chow grouping together. The second split separated the Basenji, an ancient African breed. The third split separated two Arctic spitz-type breeds, the Alaskan Malamute and Siberian Husky, and the fourth split separated two Middle Eastern sight hounds, the Afghan and Saluki, from the remaining breeds.

[0124] The first four splits exceeded the "majority rule" criterion, appearing in more than half of the bootstrap replicates. In contrast, the remaining breeds showed few consistent phylogenetic relationships, except for close groupings of five breed pairs that also clustered together in the structure analysis, one new pairing of the closely related West Highland White Terrier and Cairn Terrier, and the significant grouping of three Asian companion breeds of

similar appearance, the Lhasa Apso, Shih Tzu, and Pekingese. A close relationship among these three breeds was also observed in the structure analysis, with at least two of the three clustering together in a majority of runs. The flat topology of the tree likely reflects a largely common founder stock and occurrence of extensive gene flow between phenotypically dissimilar dogs before the advent of breed clubs and breed barrier rules. In addition, it probably reflects the recreation of some historically older breeds that died out during the famines, depressions and wars of the 19th and 20th centuries, using stock from phenotypically similar or historically related dogs.

[0125] While the phylogenetic analysis showed separation of several breeds with ancient origins from a large group of breeds with presumed modern European origins, additional subgroups may be present within the latter group that are not detected by this approach for at least two reasons (Rosenberg et al. (2001) *Genetics* 159:699). First, the true evolutionary history of dog breeds is not well-represented by the bifurcating tree model assumed by the method, but rather involved mixing of existing breeds to create new breeds (a process that continues today). Second, methods based on genetic distance matrices lose information by collapsing all genotype data for pairs of breeds into a single number.

[0126] The clustering algorithm implemented in structure was explicitly designed to overcome these limitations (Pritchard et al. (2000) *Am. J. Hum. Genet.* 67:170-81; Falush et al. (2003) *Genetics* 164:1567; Rosenberg et al. (2001) *Genetics* 159:69-713) and has been applied to infer the genetic structure of several species (Rosenberg et al. (2002) *Science* 298:2181-5; Falush et al. (2003) *Science* 299:1582-5; Rosenberg et al. (2001) *Genetics* 159:699-713). Structure was run on the entire data set using increasing values of K (the number of subpopulations the program attempts to find) to identify ancestral source populations. In this analysis, a modern breed could closely mirror a single ancestral population or represent a mixture of two or more ancestral types.

[0127] At K=2, one cluster was anchored by the first seven breeds to split in the phylogenetic analysis, while the other cluster contained the large number of breeds with a flat phylogenetic topology (Table 19A). Five runs of the program produced nearly identical results, with a similarity coefficient (Rosenberg et al. (2002) *Science* 298:2381) of 0.99 across runs. Seven other breeds share a sizeable fraction of their ancestry with the first cluster. These fourteen breeds all date to antiquity and trace their ancestry to Asia or Africa. When a diverse set of wolves from eight different countries was included in the analysis, they fell entirely within this cluster (Table 20). The branch leading to the wolf outgroup also fell within this group of breeds in the phylogenetic analysis (FIG. **2**).

[0128] At K=3, additional structure was detected that was not readily apparent from the phylogenetic tree (Table 19B). The new third cluster consisted primarily of breeds related in heritage and appearance to the Mastiff and is anchored by the Mastiff, Bulldog and Boxer, along with their close relatives the Bullmastiff, French Bulldog, Miniature Bull Terrier and Perro de Presa Canario. Also included in the cluster are the Rottweiler, Newfoundland and Bernese Mountain Dog, large breeds that are reported to have gained their size from ancient Mastiff-type ancestors. Less expected is the inclusion of the German Shepherd Dog. The exact origins of this breed are unknown, but the results suggest that the years spent as a military and police dog in the presence of working dog types, such as the Boxer, are responsible for shaping the genetic background of this popular breed. Three other breeds showed partial and inconsistent membership in this cluster across structure runs (Table 16), which lowered the similarity coefficient to 0.84.

[0129] At K=4, a fourth cluster was observed, which included several breeds used as herding dogs: Belgian Sheepdog, Belgian Tervuren, Collie and Shetland Sheepdog (Table 19C). The Irish Wolfhound, Greyhound, Borzoi and Saint Bernard were also frequently assigned to this cluster. While historical records do not suggest that these dogs were ever used to herd livestock, the results suggest that these breeds are either progenitors to, or descendants of, herding types. The breeds in the remaining cluster are primarily of relatively recent European origins, and are mainly different types of hunting dogs: scent hounds, terriers, spaniels, pointers and retrievers. Clustering at K=4 showed a similarity coefficient of 0.61, reflecting similar cluster membership assignments for most breeds but variable assignments for other breeds across runs (Table 16). At K=5 the similarity coefficient dropped to 0.26 and no additional consistent subpopulations were inferred, suggesting lack of additional high-level substructure in the sampled purebred dog population.

[0130] The results paint the following picture of the relationships among domestic dog breeds. Different breeds are genetically distinct, and individuals can be readily assigned to breeds based on their genotypes. This level of divergence is surprising given the short time since the origin of most breeds from mixed ancestral stocks and supports strong reproductive isolation within each breed as a result of the breed barrier rule. The results support at least four distinct breed groupings representing separate "adaptive radiations." A subset of breeds with ancient Asian and African origins splits off from the rest of the breeds and shows shared patterns of allele frequencies. At first glance, the inclusion of breeds from Central Africa (Basenji), the Middle East (Saluki and Afghan), as well as Tibet (Tibetan Terrier, Lhasa Apso), China (Chow Chow, Pekingese, Sharpei, Shi Tzu), Japan (Akita, Shiba Inu), and the Arctic (Alaskan Malamute, Siberian Husky, Samoyed) in a single genetic cluster is surprising. However, it is hypothesized that early pariah dogs originated in Asia and migrated with nomadic human groups both south to Africa and north to the Arctic, with subsequent migrations occurring throughout Asia (Savolainen et al. (2002) *Science* 298:1610; Leonard et al. (2002) *Science* 298:1613; Sablin & Khlopachev (2002) *Current Anthropology* 43:795). This cluster includes Nordic breeds that phenotypically resemble the wolf, such as the Alaskan Malamute and Siberian Husky, and shows the closest genetic relationship to the wolf, which is the direct ancestor of domestic dogs. Thus, dogs from these breeds may be the best living representatives of the ancestral dog gene pool. It is notable that several breeds commonly believed to be of ancient origin are not included in this group, for example the Pharaoh Hound and Ibizan Hound. These are often thought to be the oldest of all dog breeds, descending directly from the ancient Egyptian dogs drawn on tomb walls more than 5000 years ago. The results indicate, however, that these two breeds have been recreated in more recent times from combinations of other breeds. Thus, while their appearance matches the ancient Egyptian sight hounds, their genomes do not. Similar conclusions apply to the Norwegian Elkhound, which clusters with modern European breeds rather

than with the other Arctic dogs, despite reports of direct descent from Scandinavian origins over 5000 years ago (American Kennel Club (1998) *The Complete Dog Book*, eds. Crowley & Adelman, Howell Book House, New York, NY; Wilcox & Walkowicz (1995) *Atlas of Dog Breeds of the World,* T.F.H. Publications, Neptune City, NJ).

[0131] The large majority of breeds appear to represent a more recent radiation from shared European stock. While the individual breeds are genetically differentiated, they appear to have diverged at essentially the same time. This radiation probably reflects the proliferation of distinct breeds from less codified phenotypic varieties following the introduction of the breed concept and the creation of breed clubs in Europe in the 1800s. A more sensitive cluster analysis is able to discern additional genetic structure of three subpopulations within this group. One contains Mastiff-like breeds and appears to reflect shared morphology derived from a common ancestor. Another includes Shetland Sheep Dog, the two Belgian Sheepdogs, and Collie, and may reflect shared ancestral herding behavior. The remaining population is dominated by a proliferation of breeds dedicated to various aspects of the hunt. For these breeds, historical and breed club records suggest highly intertwined bloodlines, consistent with the results obtained.

[0132] Dog breeds have traditionally been grouped on the basis of their roles in human activities, physical phenotypes, and historical records. The results described above provide an independent classification based on patterns of genetic variation. This classification supports a subset of traditional groupings and also reveals previously unrecognized connections among breeds. An accurate understanding of the genetic relationships among breeds lays the foundation for studies aimed at uncovering the complex genetic basis of breed differences in morphology, behavior, and disease susceptibility.

Example 5

[0133] This example describes an in silico method for estimating the contribution of parent, grandparent and great-grandparent canids from different canid populations to the genomes of mixed progeny canids using microsatellite markers.

[0134] A. Methods

[0135] 1. Dataset

[0136] Dataset 4 included genotype information for 95 markers from 85 canids, consisting of 81 dogs from 18 different dog breeds and 4 wolves (AHRT, AKIT, BEAG, BMD, BOX, BULD, BULM, CHIH, DACH, GOLD, IBIZ, MAST, NEWF, PEKE, POM, PRES, PUG, ROTT, WOLF, see Table 5 for abbreviations of canid populations). The 95 microsatellite markers were microsatellite markers 1-14, 16, 18-21, 23-36, 39-100 (Table 1). This dataset was chosen on the basis of the fact that greater than 90% of each of the 85 canids' genome was assigned to the correct breed. The four wolves were designated as one canid population. 12 breeds were represented by 5 dogs each, 3 breeds by 4 dogs, and 3 breeds by 3 dogs, as shown in Table 9. The genotypes for each of the microsatellite markers used in each canid are set forth in Table 3 (filed herewith on a compact disc).

[0137] 2. Cluster Analyses

[0138] In silico canid mixes were created by randomly drawing one of the two alleles from each parent at each locus and designating them as the mix's alleles at that locus. An F1 mix was produced by an in silico mixing of alleles of two of the original 81 canids. An N2 mix was then produced by in silico mixing the F1 with one of its two parents, and an N3 mix was produced by in silico mixing the N2 with that same parent.

[0139] Three types of mixes were formed, test mixes, control mixes, and grandparent mixes. In the test mixes, the two parents were selected from two different breeds, chosen at random. 100 F1, N2, and N3 mixes were formed. Note that an F1 mix has two parents from different breeds, an N2 mix has three of four grandparents from one breed and one from another, and an N3 mix has seven of eight great-grandparents from one breed and one from another.

[0140] In the control mixes, the two parents were chosen from the same breed and 100 F1, N2, and N3 mixes were formed by the same procedure. Note that these all correspond to pure-bred dogs from the chosen breed.

[0141] Several grandparent mixes were also formed by choosing the four grandparents from 4 different breeds.

[0142] All the 300 test mixes were run together in a run of structure with the 85 chosen canids. The same analysis was performed for the control mixes, and for the 4 grandparent mixes. The program was run with the following parameter settings: #define NUMINDS 395; #define NUMLOCI 95; #define LABEL 1; #define POPDATA 1; #define POPFLAG 1; #define PHENOTYPE 0; #define MARKERNAMES 0; #define MAPDISTANCES 0; #define ONEROWPERIND 1; #define PHASEINFO 0; #define PHASED 0; #define EXTRACOLS 0; #define MISSING 0; #define PLOIDY 2; #define MAXPOPS 19; #define BURNIN 5000; #define NUMREPS 5000; #define USEPOPINFO 1; #define GENSBACK 0; #define MIGRPRIOR 0.0; #define NOADMIX 0; #define LINKAGE 0; #define INFERALPHA 1; #define ALPHA 1.0; #define POPALPHAS 0; #define UNIFPRIORALPHA 1; #define ALPHAMAX 10.0; #define ALPHAPROPSD 0.025; #define FREQSCORR 1; #define ONEFST 0; #define FPRIORMEAN 0.01; #define FPRIORSD 0.05; #define INFERLAMBDA 0; #define LAMBDA 1.; #define COMPUTEPROB 1; #define PFROMPOPFLAGONLY 0; #define ANCESTDIST 1; #define NUMBOXES 1000; #define ANCESTPINT 0.95; #define STARTATPOPINFO 1; #define METROFREQ 10; #define UPDATEFREQ 1; #define PRINTQHAT 1.

[0143] Each of the 85 canids was designated as belonging to its appropriate breed, and the mixes were not assigned to any breed.

[0144] B. Results

[0145] For the control mixes, each mix was always assigned by the program to the correct breed, and the fraction of the genome assigned to that breed exceeded 95% in all 300 cases (the minimum was 95.75%), 98% in 297 cases, and 99% in 266 cases. Therefore, assignment of <95% of genome to a single breed provided unambiguous detection of mixing for the test mixes, and assignment of <98% provides strong evidence of mixing at the 0.99 confidence level.

[0146] For the F1 test mixes, all 100 mixes were correctly assigned genome contributions from the two parent breeds, with contributions of each breed ranging from 28% to 70%. In 82 of 100 cases each of the two parent breeds was assigned a contribution of >40% and <60%. This shows that mixes between two breeds can be reliably identified 100% of the time at the parent level.

[0147] For the N2 test mixes, 99 of 100 cases had <98% of the genome assigned to one breed, and 97 of 100 cases

had <95% of the genome assigned to one breed, showing highly accurate ability to detect mixing at the grandparent level. In all but one case where mixing was detected, both breeds contributing to the mix were accurately identified (in one case the breed contributing one of the 4 grandparents was not detected as contributing significantly). In 80-85% of the cases, the N2 mixes could be reliably discriminated from F1 mixes (that is, it could be determined that the mixing occurred at the level of grandparents and not parents).

[0148] For the N3 test mixes, 85 of 100 cases had <98% of the genome assigned to one breed, and 77 of 100 cases had <95% of the genome assigned to one breed, showing fairly good ability to detect mixing at the great-grandparent level. In all cases where mixing was detected, both breeds contributing to the mix were accurately identified. In all cases, the N3 mixes could be reliably discriminated from F1 mixes (that is, it could be determined that the mixing occurred at the level of great-grandparents and not parents), but there was less ability to distinguish between mixes at the grandparent and great-grandparent levels.

[0149] Finally, for mixes with four different grandparents, all four grandparent breeds were reliably identified, with contributions of each breed to the genome of the mix estimated in the 20-30% range.

[0150] These results clearly demonstrate the ability of the method to discriminate mixes at the parent and grandparent level from pure-bred dogs (as well as ½ wolf and ¼ wolf mixes from dogs), with some ability to discriminate mixes at the great-grandparent level. The method also accurately identifies breed contributions in the genome of a mixed-breed dog. Larger databases containing more dogs from each breed, as well as additional markers and optimized sets of markers chosen according to criteria described elsewhere in this application, permits more accurate discrimination of mixing at the level of great-grandparents and, by straightforward extension, mixing that occurred in more distant ancestors.

Example 6

[0151] This example describes a representative method of the invention for estimating the contribution of canid populations to the genome of test canids using SNP markers.

[0152] A. Methods

[0153] 1. Dataset

[0154] A dataset of single nucleotide polymorphisms (SNPs) in a variety of dog breeds was used to calculate the frequency of each allele in each breed. The database contained genotype information for 100 SNPs from 189 canids representing 67 breeds, with two to eleven purebred dogs per breed, as described in EXAMPLE 1. The identities of alleles in the dogs are set forth in Table 4 (filed herewith on a compact disc).

[0155] 2. Doh Analysis

[0156] Using a leave-one-out procedure each dog was temporarily removed from the database and assigned to a breed based on comparison of the dog's genotypes to allele frequencies of each breed. Bayes' Theorem was used for the assignment: the probability that a dog comes from a given breed is the conditional probability that the observed genotype would occur in a dog of that breed divided by the sum of conditional probabilities that the observed genotype would occur for every breed in the database (essentially as described in Cornuet et al. (1999) *Genetics* 153:1989-2000). Software was developed to implement this algorithm. Breeds with only two individuals were included in the database but no attempt was made to classify their members because temporarily removing one of the two members did not leave enough information to calculate reliable allele frequencies.

[0157] B. Results

[0158] The output of this analysis was, for each dog, a list of the probabilities that the dog had come from each breed in the database, as shown in Table 21. Eighty percent of dogs were assigned to the correct breed with a probability of 99% or greater. For breeds in which genotypes were obtained for five or more individuals, 88% of the dogs were assigned to the correct breed with 99 percent probability. Fourteen dogs (sixteen percent of the total tested) were not assigned to the correct breed with better than 65% probability. Of these, thirteen were assigned incorrectly with a probability of fifty percent or better, nearly three-quarters with a probability of greater than ninety percent. The remaining dog was assigned 20-45% probabilities of coming from several breeds, one of which was correct.

[0159] These results demonstrate the feasibility of breed assignment based on SNP markers. Performance may be improved by generating SNP genotype profiles for a larger number of dogs (5 or more from each breed), using a larger set of SNPs, and selecting SNPs to be maximally informative. SNPs can be selected for inclusion in the panel both based on having a high heterozygosity across breeds (i.e., both alleles occur at high frequency) and based on large differences in frequency between breeds.

Example 7

[0160] This example describes a naïve Bayesian classification model for estimating the contribution of parent and grandparent canids from different canid populations to the genomes of mixed progeny canids using microsatellite markers.

[0161] A. Methods

[0162] 1. Dataset

[0163] Dataset 5 included genotype information for 96 markers from 429 canids representing 88 breeds (ACKR, AFGH, AHRT, AIRT, AKIT, AMAL, AMWS, ASBT, AUSS, AUST, BASS, BEAG, BEDT, BELS, BICH, BLDH, BMD, BORD, BORZ, BOX, BRIA, BSJI, BULD, BULM, CAIR, CHBR, CHIH, CHOW, CKCS, CLSP, COLL, DACH, DANE, DOBP, ECKR, FBLD, FCR, GOLD, GREY, GSD, GSHP, GSMD, GSNZ, HUSK, IBIZ, IRSE, IRTR, ITGR, IWOF, KEES, KERY, KOMO, KUVZ, LAB, LHSA, MAST, MBLT, MNTY, MSNZ, NELK, NEWF, OES, PEKE, PHAR, PNTR, POM, PRES, PTWD, PUG, RHOD, ROTT, SALU, SAMO, SCHP, SCWT, SHAR, SHIB, SHIH, SPOO, SSHP, SSNZ, STBD, TIBT, TERV, TPOO, WHIP, WHWT, WSSP, see Table 5 for abbreviations of canid populations). The 96 microsatellite markers were microsatellite markers 1-9, 11-38, 40-42, 44-75, 77-100 (Table 1). The genotype information for the canids in this dataset is set forth in Table 3 (filed herewith on a compact disc).

[0164] Dataset 6 included genotype information for 72 of the markers in Table 1 from 160 mixed-breed canids with known admixture composition. The genotype information for the mixed-breed canids in this dataset is set forth in Table 3 (filed herewith on a compact disc).

[0165] 2. Analyses

[0166] A naïve Bayesian classification model was developed that incorporates linked and unlinked microsatellite

loci information, higher-dimensioned ancestral populations, and higher-ordered generation pedigrees for the probabilistic assignment of individuals to mixtures of ancestral subpopulations. Two- and three-generational models were implemented for exact admixture detection and assignment, simultaneously addressing the generation, subpopulation, and linkage limitations of previous models.

[0167] The 2-generational model closely follows the model outlined in Anderson & Thompson (2002) *Genetics* 160:1217-29, with extensions for greater than two classes of "pure" subpopulations. For the L unlinked loci, we have N subpopulations (deemed breeds), and j_l alleles at the l^{th} locus. For each individual at the L loci, we have a 20 genotype: ($g_l^{(0)}$, $g_l^{(1)}$). Aggregating subpopulation allele information provides information about the frequency of any given allele, denoted as $f_{lj}^{(i)}$. Thus, for individual, non-admixed subpopulation assignments we have:

$$P(g|\text{breed } i) = \prod_{l=1}^{L} ? \text{ and } P(\text{breed } i|g) = \frac{P(g|\text{breed } i)P(\text{breed } i)}{? P(g|\text{breed } i)P(\text{breed } i)} ?$$

? indicates text missing or illegible when filed

[0168] For a parental mixture assignment, we now have:

$$P(g|b1 \text{ paternal}, b2 \text{ maternal}) = ?$$

? indicates text missing or illegible when filed

where superscripts of (0) denote paternal relations and (1) denote maternal relations (with obvious interchangeability options).

[0169] The 3-generation model allows the extension of the model to consider 4subpopulation, 2-generation representation across the N subpopulations:

$$P(g|(b1 \times b2) \times (b3 \times b4)) = ?$$

? indicates text missing or illegible when filed

[0170] Exhaustive searches for the mixtures with the highest posterior probability are possible for 2- and 3-generation models.

[0171] For the in silico individuals, model validation was performed via a leave-one-out cross validation, where sampled alleles used in creating the in silico mixed-breed individual are removed from the ancestral population and allele frequencies are updated prior to maximum likelihood mixture proportion assignment.

[0172] B. Results

[0173] Analysis on in-silico mixed-breed individuals across all 96 dinucleotide markers show that the model at 2- and 3-generations performs exceedingly well with 98.4% of F1 mixes and 94.3% of F2 mixes correctly assigned, with no obvious patterns for breed-specific deficits. Analysis on the 160 known mixed-breed individuals genotyped at 72 of the 96 dinucleotide markers show that the model at 2- and 3-generations performs nearly as accurately with 96.2% of F1 mixes and 91.8% of F2 mixes correctly assigned.

[0174] While the preferred embodiment of the invention has been illustrated and described, it will be appreciated that various changes can be made therein without departing from the spirit and scope of the invention.

TABLE 1

Microsatellite Markers

	Marker Name	Forward Primer	Reverse Primer	Reference	Ann. Temp. (° C.)	PIC
1	REN285G14	SEQ ID NO: 1	SEQ ID NO: 101	1[a]	55	NA
2	C01.673	SEQ ID NO: 2	SEQ ID NO: 102	1	58	0.36
3	REN112I02	SEQ ID NO: 3	SEQ ID NO: 103	1	58	0.76
4	REN172C02	SEQ ID NO: 4	SEQ ID NO: 104	1	55	0.48
5	FH2793	SEQ ID NO: 5	SEQ ID NO: 105	2[b]	58	0.76
6	REN143K19	SEQ ID NO: 6	SEQ ID NO: 106	1	55	0.5
7	FH2890	SEQ ID NO: 7	SEQ ID NO: 107	2	55	0.59
8	C02.466	SEQ ID NO: 8	SEQ ID NO: 108	1	58	0.55
9	C02.894	SEQ ID NO: 9	SEQ ID NO: 109	1	58	0.72
10	C02.342	SEQ ID NO: 10	SEQ ID NO: 110	1		0.77
11	FH2895	SEQ ID NO: 11	SEQ ID NO: 111	2	58	0.7
12	REN157C08	SEQ ID NO: 12	SEQ ID NO: 112	1	55	0.72
13	C03.445	SEQ ID NO: 13	SEQ ID NO: 113	1	58	0.6
14	FH2732	SEQ ID NO: 14	SEQ ID NO: 114	2	58	0.84
15	FH2776	SEQ ID NO: 15	SEQ ID NO: 115	2	58	0.49
16	REN160J02	SEQ ID NO: 16	SEQ ID NO: 116	1	58	0.82
17	REN262N08	SEQ ID NO: 17	SEQ ID NO: 117	1	55	0.72
18	REN92G21	SEQ ID NO: 18	SEQ ID NO: 118	1	58	0.66
19	REN285I23	SEQ ID NO: 19	SEQ ID NO: 119	1	55	0.58
20	C05.414	SEQ ID NO: 20	SEQ ID NO: 120	1	58	0.47
21	FH2752	SEQ ID NO: 21	SEQ ID NO: 121	2	58	0.38
22	REN210I14	SEQ ID NO: 22	SEQ ID NO: 122	1	55	0.66
23	REN37H09	SEQ ID NO: 23	SEQ ID NO: 123	3[c]	58	0.67
24	REN97M11	SEQ ID NO: 24	SEQ ID NO: 124	1	55	NA
25	REN286L19	SEQ ID NO: 25	SEQ ID NO: 125	1	58	0.66
26	FH2860	SEQ ID NO: 26	SEQ ID NO: 126	2	55	0.62
27	REN204K13	SEQ ID NO: 27	SEQ ID NO: 127	1	55	0.48

TABLE 1-continued

Microsatellite Markers

	Marker Name	Forward Primer	Reverse Primer	Reference	Ann. Temp. (° C.)	PIC
28	C08.373	SEQ ID NO: 28	SEQ ID NO: 128	1	58	0.68
29	C08.618	SEQ ID NO: 29	SEQ ID NO: 129	1	55	0.82
30	C09.173	SEQ ID NO: 30	SEQ ID NO: 130	1	58	0.78
31	C09.474	SEQ ID NO: 31	SEQ ID NO: 131	1	55	0.78
32	FH2885	SEQ ID NO: 32	SEQ ID NO: 132	2	55	0.74
33	C10.781	SEQ ID NO: 33	SEQ ID NO: 133	1	55	0.62
34	REN73F08	SEQ ID NO: 34	SEQ ID NO: 134	1	55	0.54
35	REN154G10	SEQ ID NO: 35	SEQ ID NO: 135	1	55	0.71
36	REN164B05	SEQ ID NO: 36	SEQ ID NO: 136	1	55	0.5
37	FH2874	SEQ ID NO: 37	SEQ ID NO: 137	2	55	NA
38	C11.873	SEQ ID NO: 38	SEQ ID NO: 138	1	58	0.81
39	REN258L11	SEQ ID NO: 39	SEQ ID NO: 139	1		0.72
40	REN213F01	SEQ ID NO: 40	SEQ ID NO: 140	1	55	0.82
41	REN208M20	SEQ ID NO: 41	SEQ ID NO: 141	1	58	0.64
42	REN94K11	SEQ ID NO: 42	SEQ ID NO: 142	1	55	0.56
43	REN120P21	SEQ ID NO: 43	SEQ ID NO: 143	1		0.5
44	REN286P03	SEQ ID NO: 44	SEQ ID NO: 144	1	58	0.78
45	C13.758	SEQ ID NO: 45	SEQ ID NO: 145	1	55	0.75
46	C14.866	SEQ ID NO: 46	SEQ ID NO: 146	1	55	0.74
47	FH3072	SEQ ID NO: 47	SEQ ID NO: 147	2	55	0.63
48	FH3802	SEQ ID NO: 48	SEQ ID NO: 148	2	55	0.44
49	REN06C11	SEQ ID NO: 49	SEQ ID NO: 149	3	58	0.79
50	REN144M10	SEQ ID NO: 50	SEQ ID NO: 150	1	58	0.66
51	REN85N14	SEQ ID NO: 51	SEQ ID NO: 151	1	58	0.78
52	FH3096	SEQ ID NO: 52	SEQ ID NO: 152	2	55	0.79
53	C17.402	SEQ ID NO: 53	SEQ ID NO: 153	1	58	0.75
54	REN50B03	SEQ ID NO: 54	SEQ ID NO: 154	3	58	0.74
55	REN112G10	SEQ ID NO: 55	SEQ ID NO: 155	1	55	0.7
56	REN186N13	SEQ ID NO: 56	SEQ ID NO: 156	1	58	0.66
57	FH2795	SEQ ID NO: 57	SEQ ID NO: 157	2	58	0.71
58	C18.460	SEQ ID NO: 58	SEQ ID NO: 158	1	58	0.53
59	FH2783	SEQ ID NO: 59	SEQ ID NO: 159	2	55	NA
60	REN91I14	SEQ ID NO: 60	SEQ ID NO: 160	1	58	0.72
61	REN274F18	SEQ ID NO: 61	SEQ ID NO: 161	1	58	0.66
62	FH2887	SEQ ID NO: 62	SEQ ID NO: 162	2	55	0.77
63	FH3109	SEQ ID NO: 63	SEQ ID NO: 163	2	58	0.62
64	REN293N22	SEQ ID NO: 64	SEQ ID NO: 164	1	58	0.48
65	FH2914	SEQ ID NO: 65	SEQ ID NO: 165	2	55	0.61
66	FH3069	SEQ ID NO: 66	SEQ ID NO: 166	2	55	0.53
67	REN49F22	SEQ ID NO: 67	SEQ ID NO: 167	3	55	0.66
68	REN107H05	SEQ ID NO: 68	SEQ ID NO: 168	1	55	0.86
69	REN78I16	SEQ ID NO: 69	SEQ ID NO: 169	1	55	0.63
70	FH3078	SEQ ID NO: 70	SEQ ID NO: 170	2	55	0.67
71	C23.277	SEQ ID NO: 71	SEQ ID NO: 171	1	55	0.54
72	REN181K04	SEQ ID NO: 72	SEQ ID NO: 172	1	58	0.64
73	REN106I06	SEQ ID NO: 73	SEQ ID NO: 173	1	55	0.58
74	FH3083	SEQ ID NO: 74	SEQ ID NO: 174	2	55	0.61
75	REN54E19	SEQ ID NO: 75	SEQ ID NO: 175	1	55	0.54
76	C25.213	SEQ ID NO: 76	SEQ ID NO: 176	1		0.78
77	REN87O21	SEQ ID NO: 77	SEQ ID NO: 177	1	55	0.62
78	C26.733	SEQ ID NO: 78	SEQ ID NO: 178	1	55	0.61
79	C27.442	SEQ ID NO: 79	SEQ ID NO: 179	1	55	0.74
80	C27.436	SEQ ID NO: 80	SEQ ID NO: 180	1	55	0.51
81	REN72K15	SEQ ID NO: 81	SEQ ID NO: 181	1	55	0.66
82	FH2759	SEQ ID NO: 82	SEQ ID NO: 182	2	55	0.71
83	FH2785	SEQ ID NO: 83	SEQ ID NO: 183	2	55	0.46
84	REN239K24	SEQ ID NO: 84	SEQ ID NO: 184	1	55	0.78
85	FH3082	SEQ ID NO: 85	SEQ ID NO: 185	2	55	0.54
86	REN51C16	SEQ ID NO: 86	SEQ ID NO: 186	4[d]	55	0.8
87	FH3053	SEQ ID NO: 87	SEQ ID NO: 187	2	55	0.74
88	REN43H24	SEQ ID NO: 88	SEQ ID NO: 188	3	55	0.66
89	FH2712	SEQ ID NO: 89	SEQ ID NO: 189	2	55	0.67
90	FH2875	SEQ ID NO: 90	SEQ ID NO: 190	2	55	0.6
91	FH2790	SEQ ID NO: 91	SEQ ID NO: 190	2	55	0.58
92	REN291M20	SEQ ID NO: 92	SEQ ID NO: 192	1	58	0.76
93	REN160M18	SEQ ID NO: 93	SEQ ID NO: 193	1	58	0.76
94	FH3060	SEQ ID NO: 94	SEQ ID NO: 194	2	55	0.4
95	REN314H10	SEQ ID NO: 95	SEQ ID NO: 195	1	55	0.54
96	REN01G01	SEQ ID NO: 96	SEQ ID NO: 196	3	55	0.54

TABLE 1-continued

Microsatellite Markers

	Marker Name	Forward Primer	Reverse Primer	Reference	Ann. Temp. (° C.)	PIC
97	REN112C08	SEQ ID NO: 97	SEQ ID NO: 197	1	55	0.42
98	REN106I07	SEQ ID NO: 98	SEQ ID NO: 198	1	55	0.78
99	FH2708	SEQ ID NO: 99	SEQ ID NO: 199	2	55	0.63
100	REN86G15	SEQ ID NO: 100	SEQ ID NO: 200	1	55	0.76

[a]Breen et al. (2001) *Genome Res.* 11: 1784-95.

[b]Guyon et al. (2003) *Proc. Natl. Acad. Sci. U.S.A.* 100(9): 5296-301.

[c]Jouquand et al. (2000) *Animal Genetics* 31: 266-72.

[d]Mellersh et al. (2000) *Mamm. Genome* 11: 120-30.

TABLE 2

SNP Markers

BAC	Forward Primer	Reverse Primer	SNP*	Major Allele	Minor Allele	Minor Allele Frequency**	Heterozygosity**
372-c5t (SEQ ID NO: 202)	SEQ ID NO: 244	SEQ ID NO: 286	82	C	T	0.004	0.009
			133	T	C	ND	ND
372-c15t (SEQ ID NO: 203)	SEQ ID NO: 245	SEQ ID NO: 287	285	G	A	0.013	0.025
372-e2s (SEQ ID NO: 204)	SEQ ID NO: 246	SEQ ID NO: 288	271	G	T	0.029	0.057
			257	C	T	0.071	0.132
			128	C	G	0.046	0.087
			93	C	G	0.021	0.041
			50	A	—	ND	ND
372-e13t (SEQ ID NO: 205)	SEQ ID NO: 247	SEQ ID NO: 289	57	T	C	0.004	0.008
372-e15t(SEQ ID NO: 206)	SEQ ID NO: 248	SEQ ID NO: 290	312	—	A	ND	ND
			301	C	T	ND	ND
			258	C	T	0.009	0.018
			156	—	T	ND	ND
372-e16s (SEQ ID NO: 207)	SEQ ID NO: 249	SEQ ID NO: 291	254	G	A	ND	ND
372-e18t (SEQ ID NO: 208)	SEQ ID NO: 250	SEQ ID NO: 292	165	G	C	0.254	0.379
372-g17t (SEQ ID NO: 209)	SEQ ID NO: 251	SEQ ID NO: 293	66	T	A	0.134	0.232
372-i23s (SEQ ID NO: 210)	SEQ ID NO: 252	SEQ ID NO: 294	384	A	G	0.312	0.429
372-m6t (SEQ ID NO: 211)	SEQ ID NO: 253	SEQ ID NO: 295	138	C	A	0.275	0.399
			88	T	C	0.004	0.009
			266	T	G	ND	ND
372-m7s (SEQ ID NO: 212)	SEQ ID NO: 254	SEQ ID NO: 296	317	T	A	ND	ND
372-m9t (SEQ ID NO: 213)	SEQ ID NO: 255	SEQ ID NO: 297	108	A	T	0.368	0.465
			58	G	C	0.362	0.462
372-m18t (SEQ ID NO: 214)	SEQ ID NO: 256	SEQ ID NO: 298	170	—	T	ND	ND
			129	G	A	0.159	0.267
372-m23t (SEQ ID NO: 215)	SEQ ID NO: 257	SEQ ID NO: 299	76	C	T	0.017	0.034
			108	G	A	0.081	0.149
			229	G	A	0.078	0.143
			238	T	C	0.078	0.143
			263	A	G	0.157	0.265
372-o13s (SEQ ID NO: 216)	SEQ ID NO: 258	SEQ ID NO: 300	212	T	C	0.316	0.433
373-a10s (SEQ ID NO: 217)	SEQ ID NO: 259	SEQ ID NO: 301	274	T	C	0.131	0.228
373-a15t (SEQ ID NO: 218)	SEQ ID NO: 260	SEQ ID NO: 302	112	G	A	0.004	0.008
373-a17t (SEQ ID NO: 219)	SEQ ID NO: 261	SEQ ID NO: 303	73	G	A	ND	ND
			136	A	G	0.394	0.477
373-a21s (SEQ ID NO: 220)	SEQ ID NO: 262	SEQ ID NO: 304	89	C	T	0.017	0.034
373-c13s (SEQ ID NO: 221)	SEQ ID NO: 263	SEQ ID NO: 305	93	C	T	0.028	0.054
373-c15t (SEQ ID NO: 222)	SEQ ID NO: 264	SEQ ID NO: 306	242	C	T	0.209	0.331
			202	C	T	0.174	0.288
			131	—	AA	ND	ND
373-e1t (SEQ ID NO: 223)	SEQ ID NO: 265	SEQ ID NO: 307	50	T	C	0.009	0.019
			102		Del. 8 bp	ND	ND
			130	G	A	0.01	0.02
373-e21t (SEQ ID NO: 224)	SEQ ID NO: 266	SEQ ID NO: 308	282	A	G	0.049	0.093
			116	C	T	0.215	0.338
373-g7t (SEQ ID NO: 225)	SEQ ID NO: 267	SEQ ID NO: 309	243	C	T	0.014	0.028
			242	G	A	ND	ND
			84	T	—	ND	ND
373-g19t (SEQ ID NO: 226)	SEQ ID NO: 268	SEQ ID NO: 310	249	—	A	ND	ND
			251	A	—	ND	ND
			246	G	A	0.004	0.008
			224	T	C	ND	ND
			378	A	C	0.082	0.15

TABLE 2-continued

SNP Markers							
BAC	Forward Primer	Reverse Primer	SNP*	Major Allele	Minor Allele	Minor Allele Frequency**	Heterozygosity**
373-i8s (SEQ ID NO: 227)	SEQ ID NO: 269	SEQ ID NO: 311	199	A	C	0.073	0.136
			224	G	A	0.004	0.009
373-i16s (SEQ ID NO: 228)	SEQ ID NO: 270	SEQ ID NO: 312	312	A	G	0.078	0.144
			254	G	A	0.24	0.365
			250	C	T	0.079	0.146
			249	C	T	0.031	0.06
373-k8s (SEQ ID NO: 229)	SEQ ID NO: 271	SEQ ID NO: 313	181	C	T	0.005	0.009
			224		Del. 2 bp	ND	ND
373-k10t (SEQ ID NO: 230)	SEQ ID NO: 272	SEQ ID NO: 314	261	A	C	0.353	0.457
			264	T	C	0.008	0.017
372-c5s (SEQ ID NO: 231)	SEQ ID NO: 273	SEQ ID NO: 315	112	A	G	0.357	0.459
			168	A	G	0.01	0.02
372-c15s (SEQ ID NO: 232)	SEQ ID NO: 274	SEQ ID NO: 316	121	T	C	0.017	0.034
			196	G	A	0.004	0.009
372-e15s (SEQ ID NO: 233)	SEQ ID NO: 275	SEQ ID NO: 317	67	A	G	0.186	0.303
			71	A	C	0.013	0.026
			165	G	A	0.105	0.188
			221	C	A	0.189	0.307
372-i23t (SEQ ID NO: 234)	SEQ ID NO: 276	SEQ ID NO: 318	97	A	G	0.119	0.21
			224	—	T	ND	ND
372-m6s (SEQ ID NO: 235)	SEQ ID NO: 277	SEQ ID NO: 319	67	A	G	0.323	0.437
			73	A	C	0.042	0.081
			100	T	C	0.042	0.081
			108	C	T	ND	ND
			127	T	A	ND	ND
			147	T	G	0.349	0.454
			186	A	G	0.008	0.017
372-m7t (SEQ ID NO: 236)	SEQ ID NO: 278	SEQ ID NO: 320	100	C	A	0.101	0.181
			273	A	G	0.051	0.097
372-m18s (SEQ ID NO: 237)	SEQ ID NO: 279	SEQ ID NO: 321	131	T	C	0.339	0.448
373-a14t (SEQ ID NO: 238)	SEQ ID NO: 280	SEQ ID NO: 322	290	T	C	0.224	0.347
			197	C	T	0.225	0.349
			160	A	T	0.441	0.493
			55	T	—	ND	ND
373-a21t (SEQ ID NO: 239)	SEQ ID NO: 281	SEQ ID NO: 323	93	A	G	0.008	0.017
373-e21s (SEQ ID NO: 240)	SEQ ID NO: 282	SEQ ID NO: 324	136	C	T	0.332	0.443
			175	C	T	0.332	0.443
			191	G	C	0.33	0.442
373-g7s (SEQ ID NO: 241)	SEQ ID NO: 283	SEQ ID NO: 325	263	C	T	0.204	0.325
			266	T	C	0.201	0.321
373-i16t (SEQ ID NO: 242)	SEQ ID NO: 284	SEQ ID NO: 326	47	G	A	0.457	0.496
			133	C	T	ND	ND
			173	G	A	ND	ND
			210	G	A	ND	ND
			302	C	T	0.476	0.499
			319	C	A	0.381	0.472
373-k16t (SEQ ID NO: 243)	SEQ ID NO: 285	SEQ ID NO: 327	54	—	A	ND	ND

*Position from 5' Forward Primer.

**Based on 120 canids representing 60 breeds.

ND = Not done.

TABLE 5

Abbreviations for Canid Populations	
ACKR	American Cocker Spaniel
AFGH	Afghan Hound
AHRT	American Hairless Terrier
AIRT	Airedale Terrier
AKAB	Akabash
AKIT	Akita
AMAL	Alaskan Malamute
AMWS	American Water Spaniel
ASBT	American Staffordshire Bull Terrier
AUSS	Australian Shepherd
AUST	Australian Terrier
BASS	Basset Hound
BEAC	Bearded Collie
BEAG	Beagle

TABLE 5-continued

Abbreviations for Canid Populations	
BEDT	Bedlington Terrier
BELS	Belgian Sheepdog
BICH	Bichon Frise
BLDH	Bloodhound
BMD	Bernese Mountain Dog
BORD	Border Collie
BORZ	Borzoi
BOST	Boston Terrier
BOX	Boxer
BOYK	Boykin Spaniel
BRIA	Briard
BSJI	Basenji
BULD	Bulldog
BULM	Bullmastiff

TABLE 5-continued

Abbreviations for Canid Populations	
BULT	Bull Terrier
CAIR	Cairn Terrier
CHBR	Chesapeak Bay Retriever
CHIH	Chihuahua
CHOW	Chow Chow
CKCS	Cavalier King Charles Spaniel
CLSP	Clumber Spaniel
COLL	Collie
COY	Coyote
DACH	Dachshund
DALM	Dalmatian
DANE	Great Dane
DNDT	Dandie Dinmont Terrier
DOBP	Doberman Pinscher
ECKR	English Cocker Spaniel
ESHP	English Shepherd
ESPR	English Springer Spaniel
EFOX	English Foxhound
FCR	Flat-Coated Retriever
FBLD	French Bulldog
FSP	Field Spaniel
GOLD	Golden Retriever
GREY	Greyhound
GPIN	German Pincher
GSD	German Shepherd Dog
GSHP	German Short-haired Pointer
GSMD	Greater Swiss Mountain Dog
GSNZ	Giant Schnauzer
HUSK	Siberian Husky
IBIZ	Ibizan Hound
IRSE	Irish Setter
IRTR	Irish Terrier
IRWS	Irish Water Spaniel
IWOF	Irish Wolfhound
ITGR	Italian Greyhound
KEES	Keeshond
KERY	Kerry Blue Terrier
KOMO	Komondor
KUVZ	Kuvasz
LAB	Labrador Retriever
LHSA	Lhasa Apso
MAST	Mastiff
MBLT	Miniature Bull Terrier
MNTY	Manchester Terrier-toy
MSNZ	Miniature Schnauzer
NELK	Norwegian Elkhound
NEWF	Newfoundland
OES	Old English Sheepdog
PAPI	Papillon
PEKE	Pekingese
PBGV	Petit Basset Griffon Vendeen
PHAR	Pharaoh Hound
PNTR	Pointer
POM	Pomeranian
PRES	Presa Canario
PTWD	Portuguese Water Dog
PUG	Pug
RHOD	Rhodesian Ridgeback
ROTT	Rottweiler
SALU	Saluki
SAMO	Samoyed
SCHP	Schiperke
SCDH	Scottish Deerhound
SCWT	Soft-coated Wheaten Terrier
SFXT	Smooth Fox Terrier
SHAR	Shar-Pei
SHIB	Shiba Ina
SHIH	Shih Tzu
SPIN	Spinoni Italiano
SPIX	Springer Mix
SCOL	Standard Collie
SPOO	Standard Poodle
SSNZ	Standard Schnauzer
SSHP	Shetland Sheepdog
STBD	Saint Bernard

TABLE 5-continued

Abbreviations for Canid Populations	
SUSP	Sussex Spaniel
TERV	Belgian Tervuren
TIBT	Tibetan Terrier
TPOO	Toy Poodle
WEIM	Weimaraner
WHIP	Whippet
WHWT	West Highland White Terrier
WOLF	Wolf
WSSP	Welsh Springer Spaniel
WST	Welsh Terrier

TABLE 6

94 Canids in Dataset 1					
Population*	Canid Identification Number				
AHRT	1120	1121	1122	1123	1124
AKIT	1130	1131	1132	1133	1134
BEAG	994	995	1323	1324	1327
BMD	941	943	968	970	971
BOX	1176	1177	1178	1179	1304
BULD	1193	1194	1195	1197	1198
BULM	1105	1106	1107	1108	1109
CHIH	1202	1203	1204	1205	1206
DACH	1051	1052	1053	1054	1055
GOLD	591	592	593	603	604
IBIZ	1147	1148	1162	1172	1280
MAST	991	1015	1016	1017	1066
NEWF	271	274	275	277	278
PEKE	1143	1145	1211	1212	1213
POM	1190	1191	1210	1238	1239
PRES	1082	1093	1096	1115	1127
PUG	1077	1104	1183	1184	1192
ROTT	1014	1028	1029	1033	1034
WOLF	282135	492-8	930121	Iran-1	

*See Table 5 for abbreviations of canid populations.

TABLE 7

341 Canids in Dataset 2						
Population*	Canid Identification Number					
ACKR	1035	2261	2310			
AFGH	1812	1939	2264			
AHRT	1120	1121	1122	1123	1124	
AIRT	1603	1604	1788	1875		
AKIT	1130	1131	1132	1133	1134	
AMAL	1629	1779	1845	2132	2214	
AMWS	2168	2279	2327	987	988	
AUSS	1336	1337	1500	1521	1683	
AUST	1387	1531	1533	1564	1870	1871
BASS	1341	1342	1506	1917		
BEAG	1323	1324	1327	994	995	
BEDT	1422	1423	1424	1426		
BELS	1351	2111	2153	2209	2210	
BLDH	1186	1223	1410	1942	1957	
BMD	941	943	968	1763	969	
BORD	1648	1828	1829	2002	2003	
BORZ	1378	1401	1808	2268	978	
BOX	1176	1177	1178	1179	1304	
BSJI	1338	1339	1645	1675	1717	
BULD	1193	1194	1195	1197	1198	
BULM	1105	1106	1107	1108	1109	
CAIR	1405	2096	2113	2125	2131	
CHBR	1546	1549	1813	2091	888	
CHIH	1202	1203	1204	1205	1206	
CKCS	1513	1639	1640	1642	2054	
CLSP	1008	1009	1802	2312	2314	

TABLE 7-continued

341 Canids in Dataset 2					
Population*	Canid Identification Number				
COLL	1692	1701	2284	373	379
DACH	1051	1052	1053	1054	1055
DANE	1574	1575	1580	1700	1748
DNDT	2204	2219	2221		
DOBP	1031	1749	2162	2245	
ECKR	1376	1377	1400	1404	1511
FCR	1188	2020	2042	2044	2259
GOLD	591	592	593	603	604
GREY	2477	2478	2479	2480	2481
GSD	1666	1776	2011	2060	2086
GSHP	1628	1708	1710	1833	1892
GSMD	1547	1659	1660	1662	1663
HUSK	1469	1883	2115	2117	2118
IBIZ	1147	1148	1162	1172	1280
IRSE	1540	1617	1896	2084	2085
IRTR	2152	2189	2238	2242	
IWOF	1581	1761	1792	1906	1993
KEES	1501	1589	1818	1819	2072
KOMO	1484	1964	2321	2323	2334
KUVZ	1482	1551	1672	1913	1994
LAB	1310	1465	1468	1754	1830
MAST	1015	1016	1017	1066	991
MBLT	1915	2253	2254	2255	2256
MNTY	1539	1732	2145	2149	
NELK	2216	2239	2240	2281	2295
NEWF	271	274	275	277	278
OES	1984	2171	2179		
PEKE	1143	1145	1211	1212	1213
PNTR	1382	1383	1869	1938	1948
POM	1190	1191	1210	1238	1239
PRES	1082	1096	1115	1127	1095
PTWD	P142	P1	P238	P25	P67
PUG	1077	1104	1183	1184	1192
RHOD	1444	1454	1505	1592	1609
ROTT	1014	1028	1029	1033	1034
SCHP	1386	1471	1814	1852	
SCWT	1624	1770	2250	2301	
SFXT	1550	2167			
SHAR	1573	1593	1619	1998	1999
SPOO	1530	1582	1876	1877	2337
SSHP	1379	1523	1824	1921	2040
STBD	1075	1714	1750	2403	2404
TERV	1622	2194	2200	2222	
WHIP	1355	1395	1407	1409	1518
WHWT	1388	1420	1992	2100	2128
WSSP	1955	2139	2143	2195	2286

*See Table 5 for abbreviations of canid populations.

TABLE 8

414 Canids in Dataset 3					
Population*	Canid Identification Number				
ACKR	1035	2261	2310	1956	2260
AFGH	1812	1939	2264	1936	1937
AHRT	1120	1121	1122	1123	1124
AIRT	1603	1604	1788	1875	
AKIT	1130	1131	1132	1133	1134
AMAL	1629	1779	1845	2132	2214
AMWS	2168	2279	2327	987	988
AUSS	1336	1337	1500	1521	1683
AUST	1387	1531	1564	1870	1871
BASS	1341	1342	1506	1917	
BEAG	1323	1324	1327	994	995
BEDT	1422	1423	1424	1426	
BELS	1351	2111	2153	2209	2210
BICH	1943	1954	933	974	
BLDH	1186	1223	1410	1942	1957
BMD	941	943	968	1763	969

TABLE 8-continued

414 Canids in Dataset 3					
Population*	Canid Identification Number				
BORD	1648	1828	1829	2002	2003
BORZ	1378	1401	1808	2268	978
BOX	1176	1177	1178	1179	1304
BSJI	1338	1339	1645	1675	1717
BULD	1193	1194	1195	1197	1198
BULM	1105	1106	1107	1108	1109
CAIR	1405	2096	2113	2125	2131
CHBR	1546	1549	1813	2091	888
CHIH	1202	1203	1204	1205	1206
CHOW	1633	1835	1837	1838	1839
CKCS	1513	1639	1640	1642	2054
CLSP	1008	1009	1802	2312	2314
COLL	1692	1701	2284	373	379
DACH	1051	1052	1053	1054	1055
DANE	1574	1575	1580	1700	1748
DOBP	1031	1032	1749	2162	2245
ECKR	1376	1377	1400	1404	1511
FBLD	1507	1508	1509	2671	
FCR	1188	2020	2042	2044	2259
GOLD	591	592	593	603	604
GREY	2477	2478	2479	2480	2481
GSD	1666	1776	2011	2060	2086
GSHP	1628	1708	1710	1833	1892
GSMD	1547	1659	1660	1662	1663
GSNZ	1868	22739	27093	27106	33390
HUSK	1469	1883	2115	2117	2118
IBIZ	1147	1148	1162	1172	1280
IRSE	1540	1617	1896	2084	2085
IRTR	2152	2189	2238	2242	
ITGR	1568	1570	1862	1881	1882
IWOF	1581	1761	1792	1906	1993
KEES	1501	1589	1818	1819	2072
KERY	13878	1483	1579	2014	24255
KOMO	1484	1964	2321	2323	2334
KUVZ	1482	1551	1672	1913	1994
LAB	1310	1465	1468	1754	1830
LHSA	1524	1525	1526	1528	2074
MAST	1015	1016	1017	1066	991
MBLT	1915	2253	2254	2255	2256
MNTY	1539	1732	2145	2149	
MSNZ	1587	1756	1851	2034	2613
NELK	2216	2239	2240	2281	2295
NEWF	271	274	275	277	278
OES	1984	2171	2179	1914	1626
PEKE	1143	1145	1211	1212	1213
PHAR	1292	1947	1962	1963	
PNTR	1382	1383	1869	1938	1948
POM	1190	1191	1210	1238	1239
PRES	1082	1096	1115	1127	1095
PTWD	P142	P1	P238	P25	P67
PUG	1077	1104	1183	1184	1192
RHOD	1444	1454	1505	1592	1609
ROTT	1014	1028	1029	1033	1034
SALU	1491	1535	1607	1873	2610
SAMO	1375	1532	1560	169	239
SCHP	1386	1471	1814	1852	
SCWT	1624	1770	2250	2301	
SHAR	1573	1593	1619	1998	1999
SHIB	1769	1854	1856	1860	1981
SHIH	1393	1783	2068	2859	2860
SPOO	1530	1582	1876	1877	2337
SSHP	1379	1523	1824	1921	2040
SSNZ	13352	1360	1827	20457	22647
STBD	1075	1714	1750	2403	2404
TIBT	1466	1562	1707	26078	28086
TERV	1622	2194	2200	2222	
WHIP	1355	1395	1407	1409	1518
WHWT	1388	1420	1992	2100	2128
WSSP	1955	2139	2143	2195	2286

*See Table 5 for abbreviations of canid populations.

TABLE 9

85 Canids in Dataset 5

Population*	Canid Identification Number				
AHRT	1120	1121	1124		
AKIT	1130	1131	1132	1133	1134
BEAG	1323	1327	994	995	
BMD	941	943	968	970	971
BOX	1176	1177	1178	1179	1304
BULD	1193	1194	1195	1197	1198
BULM	1105	1106	1107	1108	1109
CHIN	1202	1203	1204		
DACH	1051	1052	1053	1054	1055
GOLD	591	593	603	604	
IBIZ	1147	1148	1162	1172	1280
MAST	1015	1016	1017	1066	991
NEWF	271	274	275	277	278
PEKE	1143	1145	1211	1212	1213
POM	1190	1191	1210	1238	
PRES	1093	1096	1115		
PUG	1077	1104	1183	1184	1192
ROTT	1014	1028	1029	1033	1034
WOLF	282135	492-8	930121	Iran-1	

*See Table 5 for abbreviations of canid populations.

TABLE 10

Microsatellite Marker Alleles and Heterozygosities in 19 Canid Populations

Population*	n	P	A	Ap	He	Ho	f
AHRT	4.882353	0.835294	2.576471	2.887324	0.439286	0.432549	0.017577
AKIT	4.8	0.917647	3.035294	3.217949	0.550509	0.522157	0.058242
BEAG	4.941176	0.929412	2.952941	3.101266	0.560938	0.482941	0.153823
BMD	3.938272	0.82716	2.296296	2.552239	0.396752	0.38642	0.095341
BOX	4.905882	0.764706	2.141176	2.492308	0.348287	0.308235	0.13062
BULD	4.8	0.870588	2.6	2.837838	0.47183	0.42902	0.104385
BULM	4.952941	0.917647	2.752941	2.910256	0.518151	0.488235	0.064621
CHIH	4.811765	0.976471	3.447059	3.506024	0.611858	0.556667	0.101951
DACH	4.847059	0.882353	2.658824	2.853333	0.487712	0.482941	0.016864
GOLD	4.905882	0.905882	2.905882	3.103896	0.529542	0.520784	0.018744
IBIZ	4.682353	0.905882	2.847059	3.038961	0.517372	0.462745	0.118169
MAST	4.576471	0.905882	2.541176	2.701299	0.488389	0.466667	0.051889
NEWF	4.882353	0.941176	2.905882	3.025	0.516111	0.49	0.05822
PEKE	4.917647	0.858824	2.552941	2.808219	0.453319	0.428824	0.062983
POM	4.717647	0.929412	3.176471	3.341772	0.576965	0.482941	0.17924
PRES	4.717647	0.964706	3.435294	3.52439	0.616111	0.558824	0.103943
PUG	4.870588	0.776471	2.223529	2.575758	0.397302	0.315882	0.224817
ROTT	4.882353	0.882353	2.670588	2.893333	0.475864	0.44902	0.063943
WOLF	3.847059	0.964706	3.870588	3.97561	0.712773	0.492157	0.345081
Mean	4.730497	0.892451	2.820548	3.018251	0.508899	0.460895	0.108623

*See Table 5 for abbreviations of canid populations.

a = Effective number of individuals sampled from the population (n is smaller than the number of individuals tested due to missing marker data);
P = Proportion of polymorphic loci across all 95 markers for individuals in a population;

A = mean number of alleles per locus;

Ap = mean number of alleles per polymorphic locus;

He = expected heterozygosity;

Ho = observed heterozygosity;

f = estimate of inbreeding coefficient for the population.

TABLE 11

Heterozygosity of 85 Dog Breeds

Population	Heterozygosity
Bedlington Terrier	0.312842
Miniature Bull Terrier	0.321619
Boxer	0.343151
Clumber Spaniel	0.363595
Greater Swiss Mountain Dog	0.364943
Airedale Terrier	0.372793

TABLE 11-continued

Heterozygosity of 85 Dog Breeds

Population	Heterozygosity
Soft Coated Wheaten Terrier	0.37376
Collie	0.383453
Doberman Pinscher	0.383763
Irish Terrier	0.390427
Bloodhound	0.391559
German Shepherd Dog	0.397957
Pug Dog	0.398442
Bernese Mountain Dog	0.399599
Flat-coated Retriever	0.402832
Miniature Schnauzer	0.414528
Irish Wolfhound	0.418039
Pharaoh Hound	0.420188
Cavalier King Charles Spaniel	0.427633
Shetland Sheepdog	0.43244
Manchester Terrier Toy	0.432937
French Bulldog	0.439855
Basset Hound	0.441171
American Cocker Spaniel	0.443841
Schipperke	0.445437
Irish Setter	0.446656
Basenji	0.447739

TABLE 11-continued

Heterozygosity of 85 Dog Breeds

Population	Heterozygosity
Bulldog	0.449549
Standard Schnauzer	0.450041
Whippet	0.450959
American Hairless Terrier	0.454113
Mastiff	0.455126
Rottweiler	0.45651

TABLE 11-continued

Heterozygosity of 85 Dog Breeds

Population	Heterozygosity
Pekingese	0.459983
English Cocker Spaniel	0.46565
Saint Bernard	0.465724
Italian Greyhound	0.468797
Afghan Hound	0.468924
Pointer	0.469444
Shih Tzu	0.472193
Welsh Springer Spaniel	0.473917
Kerry Blue Terrier	0.477836
Dachshund	0.483817
Borzoi	0.487909
Great Dane	0.488697
Alaskan Malamute	0.489877
Newfoundland	0.490617
West Highland White Terrier	0.493936
Belgian Sheepdog	0.495114
Australian Terrier	0.499343
Ibizan Hound	0.503981
Keeshond	0.505126
Bullmastiff	0.509243
Akita	0.510396
Greyhound	0.513409
Chesapeake Bay Retriever	0.514166
Golden Retriever	0.517779
Tibetan Terrier	0.519535
Chow Chow	0.52043
Rhodesian Ridgeback	0.520493
Siberian Husky	0.527344
Bichon Frise	0.528271
Standard Poodle	0.529948
Old English Sheepdog	0.530192
Norwegian Elkhound	0.532854
German Shorthaired Pointer	0.538761
American Water Spaniel	0.540183
Lhasa Apso	0.541245
Samoyed	0.542932
Pomeranian	0.546007
Beagle	0.549119
Border Collie	0.549583
Belgian Tervuren	0.551091
Kuvasz	0.553538
Shiba Inu	0.560543
Labrador Retriever	0.56059
Giant Schnauzer	0.56131
Saluki	0.563037
Portugurese Water Dog	0.568882
Komondor	0.57321
Cairn Terrier	0.575823
Chinese Shar-Pei	0.584412
Perro de Presa Canario	0.589397
Chihuahua	0.592353
Australian Shepherd	0.609668

TABLE 12

Expected Heterozygosity of 60 Breeds Based on Allele Frequencies at 75 SNP Loci

Breed	Heterozygosity ($\times 10^{-4}$)
Scottish Deerhound	2.0683
Field Spaniel	2.3165
Flat-coated Retriever	2.6474
Bernese Mountain Dog	2.8129
Standard Schnauzer	2.8129
Boxer	3.0611
Collie	3.0611
Bearded Collie	3.1438
Miniature Bull Terrier	3.2266

TABLE 12-continued

Expected Heterozygosity of 60 Breeds Based on Allele Frequencies at 75 SNP Loci

Breed	Heterozygosity ($\times 10^{-4}$)
Perro de Presa Canario	3.392
Bull Terrier	3.8057
Mastiff	3.8057
Petite Basset Griffon Vendeen	3.8884
Bedlington Terrier	3.9712
Saluki	4.1366
Standard Poodle	4.1366
Cavalier King Charles Spaniel	4.2194
Sussex Spaniel	4.2194
American Water Spaniel	4.5503
Ibizan Hound	4.7158
Beagle	4.7985
Boston Terrier	4.7985
German Pinscher	4.8812
Basset Hound	4.964
Bichon Frise	4.964
Rottweiler	4.964
Bullmastiff	5.1294
English Springer Spaniel	5.1294
Greater Swiss Mountain Dog	5.3776
Pug Dog	5.3776
Boykin Spaniel	5.5431
Italian Greyhound	5.5431
Newfoundland	5.5431
American Hairless Terrier	5.7086
Borzoi	5.7913
German Shepherd Dog	5.7913
Saint Bernard	5.7913
Dachshund	5.874
Akita	5.9568
Cocker Spaniel	6.0395
French Bulldog	6.0395
Greyhound	6.0395
Irish Water Spaniel	6.0395
Shetland Sheepdog	6.205
Papillon	6.2877
Foxhound (English)	6.3704
Tibetan Terrier	6.4532
Welsh Springer Spaniel	6.4532
German Shorthaired Pointer	6.6186
Welsh Terrier	6.6186
Dalmatian	6.7014
Irish Setter	6.7014
Alaskan Malamute	6.8668
Golden Retriever	7.0323
Portugese Water Dog	7.115
Weimaraner	7.6942
Labrador Retriever	8.4388
Spinoni Italiano	8.9352
Chesapeak Bay Retriever	9.1006
English Shepherd	9.2661

TABLE 13

Assignments of 346 Canids to 72 Breeds Using Doh

Breed*	Correct	Incorrect
ACKR	3	0
AFGH	3	0
AHRT	5	0
AIRT	4	0
AKIT	5	0
AMAL	5	0
AMWS	5	0
AUSS	5	0
AUST	5	0
BASS	4	0

TABLE 13-continued

Assignments of 346 Canids to 72 Breeds Using Doh

Breed*	Correct	Incorrect
BEAG	4	1[a]
BEDT	4	0
BELS	3	2[b]
BLDH	5	0
BMD	5	0
BORD	5	0
BORZ	5	0
BOX	5	0
BSJI	5	0
BULD	5	0
BULM	5	0
CAIR	5	0
CHBR	5	0
CHIH	4	1[c]
CKCS	5	0
CLSP	5	0
COLL	5	0
DACH	5	0
DANE	5	0
DNDT	3	0
DOBP	5	0
ECKR	5	0
FCR	5	0
GOLD	5	0
GREY	5	0
GSD	5	0
GSHP	3	2[d]
GSMD	5	0
HUSK	5	0
IBIZ	5	0
IRSE	5	0
IRTR	4	0
IWOF	5	0
KEES	5	0
KOMO	5	0

TABLE 13-continued

Assignments of 346 Canids to 72 Breeds Using Doh

Breed*	Correct	Incorrect
KUVZ	5	0
LAB	5	0
MAST	5	0
MBLT	5	0
MNTY	4	0
NELK	5	0
NEWF	5	0
OES	3	0
PEKE	5	0
PNTR	5	0
POM	5	0
PRES	5	0
PTWD	5	0
PUG	5	0
RHOD	5	0
ROTT	5	0
SCHP	4	0
SCWT	4	0
SFXT	2	0
SHAR	5	0
SPOO	5	0
SSHP	5	0
STBD	5	0
TERV	1	3[e]
WHIP	5	0
WHWT	5	0
WSSP	5	0

*See Table 5 for abbreviations of canid populations.

[a]1 dog was misassigned to Presa Canario.

[b]2 dogs were misassigned to Belgian Tervuren.

[c]1 dog was misassigned to Cairn Terrier.

[d]1 dog was misassigned to Kuvasz and 1 dog was misassigned to Standard Poodle.

[e]3 dogs were misassigned to Belgian Sheepdog.

TABLE 14

Canid	Canid	Missing	Groups									
Population[a]	ID No.	Data	1	2	3	4	5	6	7	8	9	10
AHRT	1124	−2	0.001	0.001	0.001	0.001	0.002	0.001	0.003	0.001	0.002	0.001
AHRT	1120	−1	0.001	0.002	0.002	0.001	0.001	0.001	0.005	0.001	0.001	0.002
AHRT	1121	−4	0.002	0.002	0.003	0.001	0.004	0.001	0.006	0.001	0.001	0.002
AHRT	1123	−2	0.004	0.009	0.038	0.002	0.004	0.005	0.004	0.005	0.003	0.018
AHRT	1122	0	0.008	0.002	0.001	0.008	0.002	0.003	0.002	0.003	0.002	0.002
AKIT	1132	−3	0.001	0.001	0.001	0.975	0.001	0.002	0.001	0.001	0.001	0.001
AKIT	1131	0	0.002	0.003	0.001	0.962	0.002	0.003	0.002	0.006	0.002	0.001
AKIT	1130	−4	0.003	0.001	0.003	0.961	0.001	0.002	0.001	0.001	0.003	0.001
AKIT	1134	−4	0.002	0.001	0.001	0.953	0.002	0.003	0.001	0.014	0.002	0.002
AKIT	1133	−5	0.002	0.001	0.001	0.949	0.001	0.003	0.001	0.001	0.002	0.002
BEAG	995	−1	0.001	0.002	0.003	0.001	0.002	0.001	0.002	0.006	0.001	0.96
BEAG	994	−2	0.001	0.001	0.002	0.001	0.001	0.001	0.014	0.003	0.001	0.939
BEAG	1323	−1	0.005	0.003	0.007	0.003	0.004	0.002	0.004	0.002	0.004	0.909
BEAG	1327	0	0.007	0.002	0.005	0.002	0.002	0.002	0.002	0.001	0.003	0.892
BEAG	1324	0	0.015	0.014	0.002	0.002	0.065	0.016	0.057	0.004	0.015	0.42
BMD	968	−17	0.002	0.002	0.003	0.001	0.001	0.001	0.002	0.001	0.001	0.001
BMD	970	−31	0.002	0.002	0.001	0.003	0.004	0.002	0.003	0.002	0.002	0.002
BMD	941	−11	0.005	0.002	0.002	0.001	0.006	0.002	0.006	0.004	0.002	0.006
BMD	943	−10	0.006	0.007	0.003	0.002	0.003	0.002	0.002	0.003	0.001	0.01
BMD	971	−51	0.017	0.004	0.004	0.002	0.002	0.002	0.002	0.002	0.004	0.002
BOX	1304	−1	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
BOX	1179	−3	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
BOX	1178	−1	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001
BOX	1176	−1	0.002	0.001	0.002	0.001	0.004	0.001	0.002	0.001	0.002	0.002
BOX	1177	0	0.002	0.007	0.008	0.001	0.002	0.003	0.01	0.002	0.004	0.004
BULD	1195	−9	0.002	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.002	0.001
BULD	1193	−1	0.004	0.003	0.002	0.001	0.001	0.002	0.001	0.001	0.004	0.002
BULD	1197	−3	0.002	0.003	0.002	0.002	0.002	0.002	0.01	0.002	0.001	0.002
BULD	1194	−2	0.004	0.007	0.004	0.002	0.001	0.003	0.006	0.002	0.004	0.003

TABLE 14-continued

BULD	1198	0	0.003	0.003	0.001	0.001	0.001	0.001	0.004	0.001	0.004	0.002
PRES	1082	−3	0.008	0.01	0.003	0.002	0.002	0.033	0.002	0.001	0.015	0.025
BULM	1107	−1	0.005	0.004	0.001	0.003	0.003	0.002	0.002	0.006	0.002	0.002
BULM	1109	0	0.002	0.004	0.003	0.004	0.006	0.002	0.003	0.002	0.01	0.002
BULM	1108	0	0.006	0.011	0.006	0.006	0.002	0.006	0.004	0.003	0.013	0.002
BULM	1105	0	0.028	0.006	0.016	0.001	0.004	0.002	0.001	0.001	0.008	0.004
BULM	1106	−3	0.008	0.002	0.04	0.004	0.003	0.005	0.002	0.003	0.031	0.024
MAST	991	−14	0.002	0.001	0.001	0.004	0.002	0.001	0.001	0.001	0.002	0.003
MAST	1066	−2	0.003	0.002	0.002	0.002	0.001	0.002	0.004	0.003	0.003	0.003
MAST	1016	−1	0.003	0.003	0.003	0.001	0.005	0.002	0.002	0.002	0.002	0.001
MAST	1015	0	0.002	0.005	0.008	0.001	0.001	0.002	0.003	0.001	0.002	0.004
MAST	1017	−22	0.002	0.002	0.004	0.001	0.002	0.002	0.001	0.001	0.059	0.001
CHIH	1203	−3	0.002	0.002	0.002	0.002	0.005	0.002	0.003	0.002	0.003	0.002
CHIH	1202	−10	0.006	0.007	0.004	0.001	0.005	0.002	0.005	0.003	0.006	0.012
CHIH	1204	0	0.023	0.037	0.003	0.001	0.004	0.003	0.004	0.004	0.004	0.008
CHIH	1205	−3	0.002	0.028	0.008	0.002	0.004	0.09	0.014	0.065	0.116	0.104
CHIH	1206	−1	0.059	0.125	0.015	0.004	0.012	0.029	0.003	0.025	0.006	0.024
DACH	1052	−2	0.002	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
DACH	1055	−1	0.003	0.001	0.002	0.002	0.001	0.001	0.002	0.001	0.004	0.002
DACH	1054	0	0.002	0.002	0.002	0.002	0.001	0.002	0.002	0.001	0.005	0.002
DACH	1051	−5	0.001	0.002	0.003	0.001	0.006	0.002	0.003	0.004	0.003	0.002
DACH	1053	−1	0.004	0.01	0.01	0.001	0.016	0.004	0.003	0.004	0.004	0.012
GOLD	603	0	0.003	0.001	0.967	0.001	0.001	0.001	0.001	0.001	0.001	0.002
GOLD	591	−4	0.009	0.004	0.925	0.002	0.007	0.003	0.004	0.002	0.005	0.005
GOLD	593	0	0.022	0.005	0.885	0.001	0.005	0.003	0.018	0.001	0.006	0.004
GOLD	604	0	0.004	0.003	0.875	0.001	0.009	0.002	0.005	0.001	0.002	0.002
GOLD	592	−4	0.006	0.006	0.733	0.006	0.009	0.016	0.003	0.002	0.04	0.098
IBIZ	1148	−20	0.001	0.004	0.004	0.001	0.002	0.003	0.002	0.002	0.025	0.002
IBIZ	1172	0	0.021	0.002	0.002	0.002	0.003	0.002	0.002	0.002	0.004	0.002
IBIZ	1162	0	0.003	0.005	0.013	0.002	0.003	0.003	0.002	0.003	0.002	0.002
IBIZ	1280	−1	0.008	0.005	0.004	0.001	0.006	0.002	0.006	0.003	0.004	0.004
IBIZ	1147	−8	0.002	0.001	0.001	0.001	0.003	0.001	0.003	0.003	0.003	0.086
NEWF	275	−3	0.963	0.001	0.002	0.001	0.002	0.001	0.005	0.001	0.002	0.002
NEWF	274	−1	0.953	0.002	0.006	0.001	0.001	0.001	0.002	0.001	0.003	0.003
NEWF	277	0	0.855	0.003	0.002	0.001	0.001	0.002	0.008	0.003	0.002	0.003
NEWF	271	−3	0.848	0.005	0.023	0.002	0.005	0.003	0.027	0.001	0.007	0.002
NEWF	278	−1	0.744	0.007	0.009	0.003	0.002	0.016	0.005	0.004	0.113	0.008
PEKE	1143	0	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.985	0.001	0.001
PEKE	1145	−1	0.001	0.004	0.002	0.001	0.003	0.002	0.001	0.964	0.001	0.002
PEKE	1211	0	0.001	0.001	0.001	0.004	0.001	0.002	0.003	0.955	0.001	0.002
PEKE	1213	−4	0.001	0.003	0.001	0.001	0.026	0.002	0.003	0.946	0.001	0.001
PEKE	1212	0	0.003	0.005	0.017	0.001	0.001	0.002	0.001	0.932	0.002	0.003
POM	1238	0	0.001	0.964	0.003	0.001	0.004	0.001	0.002	0.003	0.001	0.002
POM	1190	0	0.004	0.794	0.087	0.002	0.003	0.003	0.004	0.005	0.004	0.004
POM	1191	−2	0.051	0.785	0.003	0.002	0.001	0.002	0.005	0.001	0.003	0.003
POM	1210	−7	0.036	0.77	0.013	0.002	0.054	0.004	0.009	0.002	0.012	0.012
POM	1239	−14	0.002	0.598	0.005	0.007	0.006	0.069	0.003	0.014	0.009	0.009
PRES	1093	−14	0.02	0.004	0.002	0.004	0.002	0.005	0.002	0.001	0.865	0.002
PRES	1115	−1	0.008	0.002	0.022	0.001	0.001	0.005	0.003	0.001	0.838	0.002
PRES	1127	−7	0.004	0.008	0.007	0.004	0.002	0.025	0.008	0.002	0.68	0.005
PRES	1096	0	0.007	0.003	0.002	0.001	0.002	0.004	0.003	0.002	0.653	0.004
PUG	1184	−1	0.001	0.001	0.001	0.001	0.988	0.001	0.001	0.001	0.001	0.001
PUG	1077	−4	0.001	0.002	0.002	0.001	0.973	0.001	0.001	0.003	0.001	0.001
PUG	1104	−1	0.001	0.002	0.004	0.001	0.962	0.001	0.001	0.007	0.001	0.002
PUG	1183	−1	0.003	0.001	0.003	0.004	0.96	0.001	0.002	0.002	0.001	0.002
PUG	1192	−3	0.002	0.002	0.001	0.001	0.96	0.001	0.002	0.001	0.003	0.002
ROTT	1034	0	0.002	0.002	0.003	0.001	0.001	0.001	0.952	0.002	0.002	0.003
ROTT	1033	−1	0.004	0.002	0.002	0.001	0.001	0.002	0.951	0.001	0.003	0.002
ROTT	1028	−3	0.002	0.002	0.003	0.001	0.002	0.001	0.95	0.001	0.002	0.016
ROTT	1029	−1	0.015	0.002	0.006	0.002	0.001	0.001	0.917	0.001	0.001	0.005
ROTT	1236	0	0.004	0.022	0.002	0.001	0.002	0.003	0.901	0.002	0.007	0.007
ROTT	1014	−2	0.048	0.002	0.004	0.002	0.004	0.002	0.898	0.002	0.002	0.006
WOLF	282135	−1	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.002	0.001	0.001
WOLF	930121	−3	0.001	0.002	0.001	0.008	0.001	0.002	0.001	0.003	0.001	0.001
WOLF	492	−1	0.001	0.002	0.001	0.002	0.002	0.559	0.001	0.002	0.005	0.001
WOLF	Iran	−7	0.001	0.001	0.002	0.002	0.002	0.741	0.001	0.003	0.002	0.002

Canid	Canid	Missing	Groups									
Population[a]	ID No.	Data	11	12	13	14	15	16	17	18	19	20
AHRT	1124	−2	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.972
AHRT	1120	−1	0.002	0.001	0.001	0.004	0.002	0.001	0.001	0.002	0.002	0.966
AHRT	1121	−4	0.002	0.001	0.003	0.001	0.002	0.001	0.001	0.001	0.002	0.963
AHRT	1123	−2	0.007	0.003	0.019	0.004	0.012	0.015	0.003	0.002	0.004	0.84
AHRT	1122	0	0.048	0.002	0.009	0.016	0.003	0.002	0.002	0.002	0.059	0.825
AKIT	1132	−3	0.002	0.001	0.002	0.001	0.002	0.001	0.002	0.001	0.001	0.002

TABLE 14-continued

AKIT	1131	0	0.002	0.002	0.001	0.001	0.001	0.001	0.002	0.001	0.002	0.003
AKIT	1130	−4	0.003	0.002	0.002	0.002	0.003	0.001	0.005	0.002	0.002	0.001
AKIT	1134	−4	0.002	0.001	0.003	0.001	0.001	0.001	0.003	0.001	0.001	0.004
AKIT	1133	−5	0.001	0.025	0.001	0.001	0.002	0.001	0.001	0.001	0.002	0.001
BEAG	995	−1	0.002	0.001	0.002	0.002	0.001	0.001	0.001	0.001	0.002	0.005
BEAG	994	−2	0.002	0.001	0.001	0.022	0.001	0.001	0.001	0.002	0.001	0.002
BEAG	1323	−1	0.007	0.001	0.005	0.003	0.006	0.008	0.002	0.006	0.007	0.013
BEAG	1327	0	0.004	0.002	0.002	0.005	0.002	0.048	0.002	0.008	0.006	0.002
BEAG	1324	0	0.01	0.005	0.003	0.002	0.002	0.001	0.086	0.005	0.002	0.274
BMD	968	−17	0.001	0.001	0.001	0.002	0.002	0.001	0.001	0.002	0.972	0.001
BMD	970	−31	0.003	0.005	0.002	0.003	0.002	0.001	0.002	0.002	0.956	0.002
BMD	941	−11	0.003	0.002	0.002	0.001	0.002	0.009	0.002	0.004	0.937	0.001
BMD	943	−10	0.004	0.001	0.005	0.007	0.002	0.002	0.001	0.002	0.934	0.003
BMD	971	−51	0.003	0.003	0.003	0.003	0.002	0.003	0.002	0.003	0.933	0.006
BOX	1304	−1	0.001	0.001	0.001	0.001	0.001	0.983	0.001	0.001	0.001	0.001
BOX	1179	−3	0.001	0.001	0.001	0.001	0.001	0.982	0.001	0.001	0.001	0.001
BOX	1178	−1	0.001	0.001	0.001	0.001	0.002	0.978	0.001	0.002	0.001	0.001
BOX	1176	−1	0.001	0.001	0.002	0.001	0.001	0.972	0.001	0.001	0.001	0.002
BOX	1177	0	0.012	0.001	0.003	0.037	0.004	0.889	0.001	0.003	0.003	0.004
BULD	1195	−9	0.001	0.001	0.002	0.001	0.004	0.003	0.001	0.974	0.001	0.001
BULD	1193	−1	0.002	0.002	0.002	0.002	0.006	0.002	0.001	0.96	0.001	0.001
BULD	1197	−3	0.002	0.004	0.005	0.001	0.002	0.003	0.004	0.948	0.002	0.002
BULD	1194	−2	0.002	0.001	0.002	0.01	0.006	0.004	0.002	0.935	0.001	0.002
BULD	1198	0	0.005	0.001	0.003	0.002	0.005	0.004	0.001	0.912	0.043	0.002
PRES	1082	−3	0.151	0.206	0.002	0.023	0.293	0.008	0.003	0.199	0.004	0.009
BULM	1107	−1	0.005	0.001	0.005	0.001	0.95	0.002	0.001	0.002	0.002	0.001
BULM	1109	0	0.002	0.001	0.004	0.001	0.932	0.013	0.002	0.005	0.001	0.002
BULM	1108	0	0.003	0.001	0.005	0.002	0.894	0.002	0.01	0.009	0.007	0.009
BULM	1105	0	0.011	0.002	0.002	0.008	0.87	0.012	0.002	0.012	0.004	0.004
BULM	1106	−3	0.002	0.003	0.004	0.002	0.823	0.004	0.017	0.017	0.003	0.004
MAST	991	−14	0.002	0.001	0.002	0.006	0.963	0.001	0.001	0.001	0.002	0.002
MAST	1066	−2	0.003	0.001	0.002	0.003	0.948	0.003	0.001	0.007	0.003	0.005
MAST	1016	−1	0.004	0.002	0.003	0.003	0.93	0.001	0.002	0.025	0.006	0.001
MAST	1015	0	0.002	0.001	0.002	0.019	0.929	0.002	0.001	0.003	0.006	0.004
MAST	1017	−22	0.002	0.001	0.025	0.001	0.885	0.001	0.001	0.002	0.003	0.003
CHIH	1203	−3	0.932	0.003	0.009	0.003	0.002	0.003	0.003	0.003	0.014	0.003
CHIH	1202	−10	0.916	0.001	0.003	0.005	0.005	0.003	0.002	0.004	0.001	0.007
CHIH	1204	0	0.868	0.002	0.004	0.002	0.003	0.002	0.002	0.003	0.018	0.005
CHIH	1205	−3	0.455	0.008	0.032	0.004	0.012	0.003	0.023	0.022	0.001	0.006
CHIH	1206	−1	0.436	0.003	0.016	0.008	0.033	0.152	0.006	0.006	0.006	0.031
DACH	1052	−2	0.001	0.001	0.001	0.976	0.003	0.001	0.001	0.002	0.001	0.001
DACH	1055	−1	0.003	0.001	0.002	0.958	0.002	0.005	0.002	0.002	0.004	0.002
DACH	1054	0	0.002	0.002	0.002	0.951	0.002	0.014	0.001	0.003	0.002	0.002
DACH	1051	−5	0.003	0.001	0.004	0.949	0.004	0.002	0.002	0.002	0.002	0.005
DACH	1053	−1	0.011	0.002	0.005	0.892	0.002	0.004	0.002	0.01	0.002	0.003
GOLD	603	0	0.001	0.001	0.002	0.001	0.002	0.002	0.001	0.002	0.006	0.001
GOLD	591	−4	0.002	0.001	0.003	0.004	0.011	0.004	0.004	0.004	0.001	0.003
GOLD	593	0	0.002	0.001	0.003	0.027	0.002	0.004	0.001	0.003	0.003	0.005
GOLD	604	0	0.002	0.001	0.002	0.003	0.003	0.072	0.001	0.004	0.002	0.004
GOLD	592	−4	0.002	0.003	0.003	0.021	0.012	0.004	0.006	0.002	0.003	0.022
IBIZ	1148	−20	0.002	0.002	0.929	0.001	0.004	0.001	0.009	0.002	0.001	0.003
IBIZ	1172	0	0.004	0.001	0.917	0.016	0.003	0.002	0.001	0.003	0.009	0.004
IBIZ	1162	0	0.03	0.001	0.913	0.001	0.004	0.003	0.001	0.003	0.002	0.003
IBIZ	1280	−1	0.002	0.001	0.888	0.002	0.006	0.036	0.004	0.005	0.007	0.003
IBIZ	1147	−8	0.007	0.001	0.871	0.001	0.003	0.002	0.001	0.005	0.002	0.002
NEWF	275	−3	0.002	0.001	0.002	0.002	0.002	0.004	0.001	0.002	0.004	0.001
NEWF	274	−1	0.002	0.001	0.007	0.001	0.003	0.003	0.001	0.003	0.001	0.003
NEWF	277	0	0.002	0.002	0.001	0.002	0.076	0.028	0.001	0.002	0.002	0.003
NEWF	271	−3	0.034	0.002	0.004	0.003	0.002	0.003	0.001	0.016	0.008	0.003
NEWF	278	−1	0.011	0.002	0.011	0.018	0.029	0.003	0.004	0.004	0.006	0.001
PEKE	1143	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
PEKE	1145	−1	0.003	0.002	0.002	0.002	0.001	0.001	0.002	0.001	0.001	0.003
PEKE	1211	0	0.007	0.004	0.002	0.002	0.002	0.004	0.001	0.002	0.002	0.003
PEKE	1213	−4	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.002	0.003
PEKE	1212	0	0.003	0.001	0.003	0.002	0.005	0.011	0.002	0.002	0.002	0.001
POM	1238	0	0.002	0.001	0.001	0.002	0.002	0.001	0.002	0.001	0.002	0.001
POM	1190	0	0.018	0.003	0.003	0.001	0.003	0.004	0.003	0.005	0.034	0.015
POM	1191	−2	0.006	0.001	0.002	0.004	0.097	0.006	0.002	0.022	0.002	0.001
POM	1210	−7	0.003	0.01	0.006	0.007	0.002	0.012	0.004	0.035	0.005	0.002
POM	1239	−14	0.004	0.002	0.232	0.007	0.004	0.003	0.004	0.007	0.005	0.01
PRES	1093	−14	0.004	0.008	0.01	0.002	0.028	0.022	0.003	0.01	0.002	0.004
PRES	1115	−1	0.003	0.002	0.002	0.003	0.01	0.066	0.009	0.01	0.001	0.01
PRES	1127	−7	0.008	0.002	0.067	0.016	0.008	0.012	0.006	0.123	0.003	0.01
PRES	1096	0	0.003	0.002	0.004	0.105	0.019	0.019	0.006	0.145	0.008	0.007
PUG	1184	−1	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
PUG	1077	−4	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.004
PUG	1104	−1	0.001	0.001	0.002	0.001	0.003	0.002	0.001	0.001	0.002	0.002

TABLE 14-continued

PUG	1183	−1	0.001	0.001	0.008	0.001	0.002	0.001	0.001	0.001	0.002	0.002
PUG	1192	−3	0.002	0.001	0.003	0.001	0.001	0.006	0.002	0.003	0.003	0.002
ROTT	1034	0	0.003	0.001	0.003	0.004	0.001	0.006	0.001	0.003	0.005	0.002
ROTT	1033	−1	0.002	0.001	0.002	0.003	0.003	0.003	0.002	0.007	0.001	0.008
ROTT	1028	−3	0.001	0.001	0.001	0.007	0.001	0.005	0.001	0.001	0.001	0.001
ROTT	1029	−1	0.002	0.001	0.001	0.004	0.002	0.001	0.001	0.001	0.034	0.002
ROTT	1236	0	0.003	0.003	0.004	0.01	0.002	0.006	0.003	0.016	0.001	0.001
ROTT	1014	−2	0.004	0.002	0.004	0.001	0.004	0.001	0.002	0.003	0.006	0.003
WOLF	282135	−1	0.001	0.979	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001
WOLF	930121	−3	0.001	0.032	0.001	0.001	0.001	0.001	0.938	0.001	0.001	0.001
WOLF	492	−1	0.001	0.044	0.001	0.001	0.001	0.001	0.371	0.001	0.001	0.001
WOLF	Iran	−7	0.002	0.022	0.002	0.004	0.003	0.001	0.203	0.001	0.001	0.002

[a]See Table 5 for abbreviations of canid populations.

KBB: pbe

TABLE 15A

	Canid ID	Missing	Groups					
Canid Population[a]	No.	Data	1	2	3	4	5	6
WOLF	4928	−1	0	0.999	0	0.001	0	0
WOLF	282135	−1	0	0.998	0	0.002	0	0
WOLF	930121	−3	0	0.997	0	0.003	0	0
WOLF	Iran1	−7	0	0.999	0	0.001	0	0
AKIT	1130	−4	0	0.005	0	0.995	0	0
AKIT	1131	0	0	0.013	0	0.987	0	0
AKIT	1132	−3	0	0.004	0	0.996	0	0
AKIT	1133	−5	0	0.005	0	0.995	0	0
AKIT	1134	−4	0	0.007	0	0.993	0	0
PEKE	1143	0	0	0	0.999	0.001	0	0
PEKE	1145	−1	0	0	0.992048	0.007952	0	0
PEKE	1211	0	0	0	0.947818	0.052182	0	0
PEKE	1212	0	0	0	0.961501	0.038499	0	0
PEKE	1213	−4	0	0	0.997994	0.002006	0	0
PUG	1077	−4	0	0	0	0.002	0.998	0
PUG	1104	−1	0	0	0	0.006	0.994	0
PUG	1183	−1	0	0	0	0.002	0.998	0
PUG	1184	−1	0	0	0	0.001	0.999	0
PUG	1192	−3	0	0	0	0.001	0.999	0
GOLD	591	−4	0.021339	0	0	0.030068	0	0.948594
GOLD	592	−4	0.004314	0	0	0.137187	0	0.858499
GOLD	593	0	0.005935	0	0	0.01088	0	0.983185
GOLD	603	0	0.008929	0	0	0.007937	0	0.983135
GOLD	604	0	0.037624	0	0	0.009901	0	0.952475
AHRT	1120	−1	0.006289	0	0	0.213836	0	0.779874
AHRT	1121	−4	0.003885	0	0	0.222999	0	0.773116
AHRT	1122	0	0.003079	0	0	0.230177	0	0.766744
AHRT	1123	−2	0.016419	0	0	0.218139	0	0.765442
AHRT	1124	−2	0.004594	0	0	0.234303	0	0.761103
CHIH	1202	−10	0.008326	0	0	0.074931	0	0.916744
CHIH	1203	−3	0.005578	0	0	0.203187	0	0.791235
CHIH	1204	0	0.004184	0	0	0.16318	0	0.832636
CHIH	1205	−3	0.021598	0	0	0.280058	0	0.698344
CHIH	1206	−1	0.097854	0	0	0.141631	0	0.760515
POM	1190	0	0.038938	0	0	0.115044	0	0.846018
POM	1191	−2	0.480901	0	0	0.020568	0	0.498531
POM	1210	−7	0.020236	0	0	0.15683	0	0.822934
POM	1238	0	0.006961	0	0	0.226605	0	0.766435
POM	1239	−14	0.006266	0	0	0.373434	0	0.620301
DACH	1051	−5	0.008145	0	0	0.095023	0	0.896833
DACH	1052	−2	0.013889	0	0	0.007937	0	0.978175
DACH	1053	−1	0.009747	0	0	0.025341	0	0.964912
DACH	1054	0	0.006917	0	0	0.011858	0	0.981225
DACH	1055	−1	0.010848	0	0	0.013807	0	0.975345
BEAG	994	−2	0.004869	0	0	0.02629	0	0.968841
BEAG	995	−1	0.002681	0	0	0.106345	0	0.890974
BEAG	1323	−1	0.009747	0	0	0.025341	0	0.964912
BEAG	1324	0	0.002839	0	0	0.290277	0	0.706884
BEAG	1327	0	0.01256	0	0	0.033816	0	0.953623
IBIZ	1147	−8	0.011867	0	0	0.208861	0	0.779272
IBIZ	1148	−20	0.01225	0	0	0.355255	0	0.632495
IBIZ	1162	0	0.019639	0	0	0.214454	0	0.765907
IBIZ	1172	0	0.00639	0	0	0.201278	0	0.792332

TABLE 15A-continued

Canid Population[a]	Canid ID No.	Missing Data	Groups 1	2	3	4	5	6
IBIZ	1280	−1	0.023682	0	0	0.236058	0	0.74026
BMD	941	−11	0.009709	0	0	0.029126	0	0.961165
BMD	943	−10	0.006686	0	0	0.04489	0	0.948424
BMD	968	−17	0.005831	0	0	0.028183	0	0.965986
BMD	970	−31	0.011354	0	0	0.18897	0	0.799676
BMD	971	−51	0.020568	0	0	0.020568	0	0.958864
NEWF	271	−3	0.010913	0	0	0.007937	0	0.981151
NEWF	274	−1	0.019881	0	0	0.005964	0	0.974155
NEWF	275	−3	0.010934	0	0	0.005964	0	0.983101
NEWF	277	0	0.05859	0	0	0.006951	0	0.934459
NEWF	278	−1	0.034213	0	0	0.022483	0	0.943304
ROTT	1014	−2	0.0059	0	0	0.016716	0	0.977384
ROTT	1028	−3	0.005946	0	0	0.00892	0	0.985134
ROTT	1029	−1	0.004955	0	0	0.00892	0	0.986125
ROTT	1033	−1	0.009728	0	0	0.027237	0	0.963035
ROTT	1034	0	0.021782	0	0	0.009901	0	0.968317
PRES	1082	−3	0.419635	0	0	0.13119	0	0.449175
PRES	1093	−14	0.430979	0	0	0.197432	0	0.371589
PRES	1096	0	0.705253	0	0	0.027237	0	0.26751
PRES	1115	−1	0.572519	0	0	0.045802	0	0.381679
PRES	1127	−7	0.418004	0	0	0.108734	0	0.473262
BOX	1176	−1	0.98806	0	0	0.004975	0	0.006965
BOX	1177	0	0.964108	0	0	0.002991	0	0.032901
BOX	1178	−1	0.993028	0	0	0.003984	0	0.002988
BOX	1179	−3	0.993028	0	0	0.003984	0	0.002988
BOX	1304	−1	0.989066	0	0	0.005964	0	0.00497
BULD	1193	−1	0.971202	0	0	0.006951	0	0.021847
BULD	1194	−2	0.989044	0	0	0.003984	0	0.006972
BULD	1195	−9	0.99005	0	0	0.004975	0	0.004975
BULD	1197	−3	0.879648	0	0	0.021526	0	0.098826
BULD	1198	0	0.983051	0	0	0.002991	0	0.013958
MAST	991	−14	0.97931	0	0	0.014778	0	0.005911
MAST	1015	0	0.983085	0	0	0.004975	0	0.01194
MAST	1016	−1	0.981188	0	0	0.009901	0	0.008911
MAST	1017	−22	0.94294	0	0	0.032882	0	0.024178
MAST	1066	−2	0.983168	0	0	0.009901	0	0.006931
BULM	1105	0	0.985075	0	0	0.004975	0	0.00995
BULM	1106	−3	0.971429	0	0	0.014778	0	0.013793
BULM	1107	−1	0.973529	0	0	0.019608	0	0.006863
BULM	1108	0	0.970559	0	0	0.018646	0	0.010795
BULM	1109	0	0.974535	0	0	0.020568	0	0.004897

TABLE 15B

Canid Population[a]	Canid ID No.	Missing Data	Groups 1	2	3	4	5	6
WOLF	4928	−1	0	0.999	0	0.001	0	0
WOLF	282135	−1	0	0.998	0	0.002	0	0
WOLF	930121	−3	0	0.997	0	0.003	0	0
WOLF	Iran1	−7	0	0.999	0	0.001	0	0
AKIT	1130	−4	0	0.005	0	0.995	0	0
AKIT	1131	0	0	0.013	0	0.987	0	0
AKIT	1132	−3	0	0.004	0	0.996	0	0
AKIT	1133	−5	0	0.005	0	0.995	0	0
AKIT	1134	−4	0	0.007	0	0.993	0	0
PEKE	1143	0	0	0	0.999	0.001	0	0
PEKE	1145	−1	0	0	0.992048	0.007952	0	0
PEKE	1211	0	0	0	0.947818	0.052182	0	0
PEKE	1212	0	0	0	0.961501	0.038499	0	0
PEKE	1213	−4	0	0	0.997994	0.002006	0	0
PUG	1077	−4	0	0	0	0.002	0.998	0
PUG	1104	−1	0	0	0	0.006	0.994	0
PUG	1183	−1	0	0	0	0.002	0.998	0
PUG	1184	−1	0	0	0	0.001	0.999	0
PUG	1192	−3	0	0	0	0.001	0.999	0
GOLD	591	−4	0.021339	0	0	0.030068	0	0.948594
GOLD	592	−4	0.004314	0	0	0.137187	0	0.858499
GOLD	593	0	0.005935	0	0	0.01088	0	0.983185

TABLE 15B-continued

Canid Population[a]	Canid ID No.	Missing Data	Groups 1	2	3	4	5	6
GOLD	603	0	0.008929	0	0	0.007937	0	0.983135
GOLD	604	0	0.037624	0	0	0.009901	0	0.952475
AHRT	1120	−1	0.006289	0	0	0.213836	0	0.779874
AHRT	1121	−4	0.003885	0	0	0.222999	0	0.773116
AHRT	1122	0	0.003079	0	0	0.230177	0	0.766744
AHRT	1123	−2	0.016419	0	0	0.218139	0	0.765442
AHRT	1124	−2	0.004594	0	0	0.234303	0	0.761103
CHIH	1202	−10	0.008326	0	0	0.074931	0	0.916744
CHIH	1203	−3	0.005578	0	0	0.203187	0	0.791235
CHIH	1204	0	0.004184	0	0	0.16318	0	0.832636
CHIH	1205	−3	0.021598	0	0	0.280058	0	0.698344
CHIH	1206	−1	0.097854	0	0	0.141631	0	0.760515
POM	1190	0	0.038938	0	0	0.115044	0	0.846018
POM	1191	−2	0.480901	0	0	0.020568	0	0.498531
POM	1210	−7	0.020236	0	0	0.15683	0	0.822934
POM	1238	0	0.006961	0	0	0.226605	0	0.766435
POM	1239	−14	0.006266	0	0	0.373434	0	0.620301
DACH	1051	−5	0.008145	0	0	0.095023	0	0.896833
DACH	1052	−2	0.013889	0	0	0.007937	0	0.978175
DACH	1053	−1	0.009747	0	0	0.025341	0	0.964912
DACH	1054	0	0.006917	0	0	0.011858	0	0.981225
DACH	1055	−1	0.010848	0	0	0.013807	0	0.975345
BEAG	994	−2	0.004869	0	0	0.02629	0	0.968841
BEAG	995	−1	0.002681	0	0	0.106345	0	0.890974
BEAG	1323	−1	0.009747	0	0	0.025341	0	0.964912
BEAG	1324	0	0.002839	0	0	0.290277	0	0.706884
BEAG	1327	0	0.01256	0	0	0.033816	0	0.953623
IBIZ	1147	−8	0.011867	0	0	0.208861	0	0.779272
IBIZ	1148	−20	0.01225	0	0	0.355255	0	0.632495
IBIZ	1162	0	0.019639	0	0	0.214454	0	0.765907
IBIZ	1172	0	0.00639	0	0	0.201278	0	0.792332
IBIZ	1280	−1	0.023682	0	0	0.236058	0	0.74026
BMD	941	−11	0.009709	0	0	0.029126	0	0.961165
BMD	943	−10	0.006686	0	0	0.04489	0	0.948424
BMD	968	−17	0.005831	0	0	0.028183	0	0.965986
BMD	970	−31	0.011354	0	0	0.18897	0	0.799676
BMD	971	−51	0.020568	0	0	0.020568	0	0.958864
NEWF	271	−3	0.010913	0	0	0.007937	0	0.981151
NEWF	274	−1	0.019881	0	0	0.005964	0	0.974155
NEWF	275	−3	0.010934	0	0	0.005964	0	0.983101
NEWF	277	0	0.05859	0	0	0.006951	0	0.934459
NEWF	278	−1	0.034213	0	0	0.022483	0	0.943304
ROTT	1014	−2	0.0059	0	0	0.016716	0	0.977384
ROTT	1028	−3	0.005946	0	0	0.00892	0	0.985134
ROTT	1029	−1	0.004955	0	0	0.00892	0	0.986125
ROTT	1033	−1	0.009728	0	0	0.027237	0	0.963035
ROTT	1034	0	0.021782	0	0	0.009901	0	0.968317
PRES	1082	−3	0.419635	0	0	0.13119	0	0.449175
PRES	1093	−14	0.430979	0	0	0.197432	0	0.371589
PRES	1096	0	0.705253	0	0	0.027237	0	0.26751
PRES	1115	−1	0.572519	0	0	0.045802	0	0.381679
PRES	1127	−7	0.418004	0	0	0.108734	0	0.473262
BOX	1176	−1	0.002964	0	0	0.004941	0	0.006917
BOX	1177	0	0.046332	0	0	0.002896	0	0.031853
BOX	1178	−1	0.002979	0	0	0.003972	0	0.002979
BOX	1179	−3	0.000993	0	0	0.003972	0	0.002979
BOX	1304	−1	0.001978	0	0	0.005935	0	0.004946
BULD	1193	−1	0.968902	0	0	0.006803	0	0.02138
BULD	1194	−2	0.986152	0	0	0.003956	0	0.006924
BULD	1195	−9	0.988119	0	0	0.00495	0	0.00495
BULD	1197	−3	0.887801	0	0	0.01959	0	0.089938
BULD	1198	0	0.979351	0	0	0.00295	0	0.013766
MAST	991	−14	0.978452	0	0	0.014691	0	0.005877
MAST	1015	0	0.981318	0	0	0.004916	0	0.011799
MAST	1016	−1	0.980373	0	0	0.009814	0	0.008832
MAST	1017	−22	0.943343	0	0	0.032106	0	0.023607
MAST	1066	−2	0.981318	0	0	0.009833	0	0.006883
BULM	1105	0	0.981281	0	0	0.004926	0	0.009852
BULM	1106	−3	0.969874	0	0	0.014577	0	0.013605
BULM	1107	−1	0.971762	0	0	0.019474	0	0.006816
BULM	1108	0	0.969903	0	0	0.018447	0	0.01068
BULM	1109	0	0.971735	0	0	0.020468	0	0.004873

TABLE 15C

Canid Population[a]	Canid ID No.	Missing Data	Groups 1	2	3	4	5	6
WOLF	4928	−1	0	0.999	0	0.001	0	0
WOLF	282135	−1	0	0.998	0	0.002	0	0
WOLF	930121	−3	0	0.997	0	0.003	0	0
WOLF	Iran1	−7	0	0.999	0	0.001	0	0
AKIT	1130	−4	0	0.005	0	0.995	0	0
AKIT	1131	0	0	0.013	0	0.987	0	0
AKIT	1132	−3	0	0.004	0	0.996	0	0
AKIT	1133	−5	0	0.005	0	0.995	0	0
AKIT	1134	−4	0	0.007	0	0.993	0	0
PEKE	1143	0	0	0	0.999	0.001	0	0
PEKE	1145	−1	0	0	0.992048	0.007952	0	0
PEKE	1211	0	0	0	0.947818	0.052182	0	0
PEKE	1212	0	0	0	0.961501	0.038499	0	0
PEKE	1213	−4	0	0	0.997994	0.002006	0	0
PUG	1077	−4	0	0	0	0.002	0.998	0
PUG	1104	−1	0	0	0	0.006	0.994	0
PUG	1183	−1	0	0	0	0.002	0.998	0
PUG	1184	−1	0	0	0	0.001	0.999	0
PUG	1192	−3	0	0	0	0.001	0.999	0
GOLD	591	−4	0.021339	0	0	0.030068	0	0.948594
GOLD	592	−4	0.004314	0	0	0.137187	0	0.858499
GOLD	593	0	0.005935	0	0	0.01088	0	0.983185
GOLD	603	0	0.008929	0	0	0.007937	0	0.983135
GOLD	604	0	0.037624	0	0	0.009901	0	0.952475
AHRT	1120	−1	0.006289	0	0	0.213836	0	0.779874
AHRT	1121	−4	0.003885	0	0	0.222999	0	0.773116
AHRT	1122	0	0.003079	0	0	0.230177	0	0.766744
AHRT	1123	−2	0.016419	0	0	0.218139	0	0.765442
AHRT	1124	−2	0.004594	0	0	0.234303	0	0.761103
CHIH	1202	−10	0.008326	0	0	0.074931	0	0.916744
CHIH	1203	−3	0.005578	0	0	0.203187	0	0.791235
CHIH	1204	0	0.004184	0	0	0.16318	0	0.832636
CHIH	1205	−3	0.021598	0	0	0.280058	0	0.698344
CHIH	1206	−1	0.097854	0	0	0.141631	0	0.760515
POM	1190	0	0.038938	0	0	0.115044	0	0.846018
POM	1191	−2	0.480901	0	0	0.020568	0	0.498531
POM	1210	−7	0.020236	0	0	0.15683	0	0.822934
POM	1238	0	0.006961	0	0	0.226605	0	0.766435
POM	1239	−14	0.006266	0	0	0.373434	0	0.620301
DACH	1051	−5	0.008145	0	0	0.095023	0	0.896833
DACH	1052	−2	0.013889	0	0	0.007937	0	0.978175
DACH	1053	−1	0.009747	0	0	0.025341	0	0.964912
DACH	1054	0	0.006917	0	0	0.011858	0	0.981225
DACH	1055	−1	0.010848	0	0	0.013807	0	0.975345
BEAG	994	−2	0.004869	0	0	0.02629	0	0.968841
BEAG	995	−1	0.002681	0	0	0.106345	0	0.890974
BEAG	1323	−1	0.009747	0	0	0.025341	0	0.964912
BEAG	1324	0	0.002839	0	0	0.290277	0	0.706884
BEAG	1327	0	0.01256	0	0	0.033816	0	0.953623
IBIZ	1147	−8	0.011867	0	0	0.208861	0	0.779272
IBIZ	1148	−20	0.01225	0	0	0.355255	0	0.632495
IBIZ	1162	0	0.019639	0	0	0.214454	0	0.765907
IBIZ	1172	0	0.00639	0	0	0.201278	0	0.792332
IBIZ	1280	−1	0.023682	0	0	0.236058	0	0.74026
BMD	941	−11	0.009709	0	0	0.029126	0	0.961165
BMD	943	−10	0.006686	0	0	0.04489	0	0.948424
BMD	968	−17	0.005831	0	0	0.028183	0	0.965986
BMD	970	−31	0.011354	0	0	0.18897	0	0.799676
BMD	971	−51	0.020568	0	0	0.020568	0	0.958864
NEWF	271	−3	0.010913	0	0	0.007937	0	0.981151
NEWF	274	−1	0.019881	0	0	0.005964	0	0.974155
NEWF	275	−3	0.010934	0	0	0.005964	0	0.983101
NEWF	277	0	0.05859	0	0	0.006951	0	0.934459
NEWF	278	−1	0.034213	0	0	0.022483	0	0.943304
ROTT	1014	−2	0.0059	0	0	0.016716	0	0.977384
ROTT	1028	−3	0.005946	0	0	0.00892	0	0.985134
ROTT	1029	−1	0.004955	0	0	0.00892	0	0.986125
ROTT	1033	−1	0.009728	0	0	0.027237	0	0.963035
ROTT	1034	0	0.021782	0	0	0.009901	0	0.968317
PRES	1082	−3	0.419635	0	0	0.13119	0	0.449175
PRES	1093	−14	0.430979	0	0	0.197432	0	0.371589
PRES	1096	0	0.705253	0	0	0.027237	0	0.26751
PRES	1115	−1	0.572519	0	0	0.045802	0	0.381679

TABLE 15C-continued

Canid Population[a]	Canid ID No.	Missing Data	Groups 1	2	3	4	5	6
PRES	1127	−7	0.418004	0	0	0.108734	0	0.473262
BOX	1176	−1	0.002964	0	0	0.004941	0	0.006917
BOX	1177	0	0.046332	0	0	0.002896	0	0.031853
BOX	1178	−1	0.002979	0	0	0.003972	0	0.002979
BOX	1179	−3	0.000993	0	0	0.003972	0	0.002979
BOX	1304	−1	0.001978	0	0	0.005935	0	0.004946
BULD	1193	−1	0.001938	0	0	0.006783	0	0.021318
BULD	1194	−2	0.004931	0	0	0.003945	0	0.006903
BULD	1195	−9	0.000988	0	0	0.004941	0	0.004941
BULD	1197	−3	0.003552	0	0	0.019538	0	0.089698
BULD	1198	0	0.003918	0	0	0.002938	0	0.013712
MAST	991	−14	0.976517	0	0	0.014677	0	0.005871
MAST	1015	0	0.979392	0	0	0.004907	0	0.011776
MAST	1016	−1	0.972549	0	0	0.009804	0	0.008824
MAST	1017	−22	0.941509	0	0	0.032075	0	0.023585
MAST	1066	−2	0.975466	0	0	0.009814	0	0.006869
BULM	1105	0	0.976447	0	0	0.004907	0	0.009814
BULM	1106	−3	0.964113	0	0	0.014549	0	0.013579
BULM	1107	−1	0.969874	0	0	0.019436	0	0.006803
BULM	1108	0	0.967022	0	0	0.018429	0	0.010669
BULM	1109	0	0.968902	0	0	0.020408	0	0.004859

TABLE 15D

Canid Population[a]	Canid ID No.	Missing Data	Groups 1	2	3	4	5	6	7	8	9
WOLF	4928	−1	0	0.999	0	0.001	0	0	0	0	0
WOLF	282135	−1	0	0.998	0	0.002	0	0	0	0	0
WOLF	930121	−3	0	0.997	0	0.003	0	0	0	0	0
WOLF	Iran1	−7	0	0.999	0	0.001	0	0	0	0	0
AKIT	1130	−4	0	0.005	0	0.995	0	0	0	0	0
AKIT	1131	0	0	0.013	0	0.987	0	0	0	0	0
AKIT	1132	−3	0	0.004	0	0.996	0	0	0	0	0
AKIT	1133	−5	0	0.005	0	0.995	0	0	0	0	0
AKIT	1134	−4	0	0.007	0	0.993	0	0	0	0	0
PEKE	1143	0	0	0	0.999	0.001	0	0	0	0	0
PEKE	1145	−1	0	0	0.992048	0.007952	0	0	0	0	0
PEKE	1211	0	0	0	0.947818	0.052182	0	0	0	0	0
PEKE	1212	0	0	0	0.961501	0.038499	0	0	0	0	0
PEKE	1213	−4	0	0	0.997994	0.002006	0	0	0	0	0
PUG	1077	−4	0	0	0	0.002	0.998	0	0	0	0
PUG	1104	−1	0	0	0	0.006	0.994	0	0	0	0
PUG	1183	−1	0	0	0	0.002	0.998	0	0	0	0
PUG	1184	−1	0	0	0	0.001	0.999	0	0	0	0
PUG	1192	−3	0	0	0	0.001	0.999	0	0	0	0
GOLD	591	−4	0.021339	0	0	0.030068	0	0.948594	0	0	0
GOLD	592	−4	0.004314	0	0	0.137187	0	0.858499	0	0	0
GOLD	593	0	0.005935	0	0	0.01088	0	0.983185	0	0	0
GOLD	603	0	0.008929	0	0	0.007937	0	0.983135	0	0	0
GOLD	604	0	0.037624	0	0	0.009901	0	0.952475	0	0	0
AHRT	1120	−1	0.006289	0	0	0.213836	0	0.779874	0	0	0
AHRT	1121	−4	0.003885	0	0	0.222999	0	0.773116	0	0	0
AHRT	1122	0	0.003079	0	0	0.230177	0	0.766744	0	0	0
AHRT	1123	−2	0.016419	0	0	0.218139	0	0.765442	0	0	0
AHRT	1124	−2	0.004594	0	0	0.234303	0	0.761103	0	0	0
CHIH	1202	−10	0.008326	0	0	0.074931	0	0.916744	0	0	0
CHIH	1203	−3	0.005578	0	0	0.203187	0	0.791235	0	0	0
CHIH	1204	0	0.004184	0	0	0.16318	0	0.832636	0	0	0
CHIH	1205	−3	0.021598	0	0	0.280058	0	0.698344	0	0	0
CHIH	1206	−1	0.097854	0	0	0.141631	0	0.760515	0	0	0
POM	1190	0	0.038938	0	0	0.115044	0	0.846018	0	0	0
POM	1191	−2	0.480901	0	0	0.020568	0	0.498531	0	0	0
POM	1210	−7	0.020236	0	0	0.15683	0	0.822934	0	0	0
POM	1238	0	0.006961	0	0	0.226605	0	0.766435	0	0	0
POM	1239	−14	0.006266	0	0	0.373434	0	0.620301	0	0	0
DACH	1051	−5	0.008145	0	0	0.095023	0	0.896833	0	0	0
DACH	1052	−2	0.013889	0	0	0.007937	0	0.978175	0	0	0
DACH	1053	−1	0.009747	0	0	0.025341	0	0.964912	0	0	0

TABLE 15D-continued

Canid Population[a]	Canid ID No.	Missing Data	Groups 1	2	3	4	5	6	7	8	9
DACH	1054	0	0.006917	0	0	0.011858	0	0.981225	0	0	0
DACH	1055	−1	0.010848	0	0	0.013807	0	0.975345	0	0	0
BEAG	994	−2	0.004869	0	0	0.02629	0	0.968841	0	0	0
BEAG	995	−1	0.002681	0	0	0.106345	0	0.890974	0	0	0
BEAG	1323	−1	0.009747	0	0	0.025341	0	0.964912	0	0	0
BEAG	1324	0	0.002839	0	0	0.290277	0	0.706884	0	0	0
BEAG	1327	0	0.01256	0	0	0.033816	0	0.953623	0	0	0
IBIZ	1147	−8	0.011867	0	0	0.208861	0	0.779272	0	0	0
IBIZ	1148	−20	0.01225	0	0	0.355255	0	0.632495	0	0	0
IBIZ	1162	0	0.019639	0	0	0.214454	0	0.765907	0	0	0
IBIZ	1172	0	0.00639	0	0	0.201278	0	0.792332	0	0	0
IBIZ	1280	−1	0.023682	0	0	0.236058	0	0.74026	0	0	0
BMD	941	−11	0.009709	0	0	0.029126	0	0.961165	0	0	0
BMD	943	−10	0.006686	0	0	0.04489	0	0.948424	0	0	0
BMD	968	−17	0.005831	0	0	0.028183	0	0.965986	0	0	0
BMD	970	−31	0.011354	0	0	0.18897	0	0.799676	0	0	0
BMD	971	−51	0.020568	0	0	0.020568	0	0.958864	0	0	0
NEWF	271	−3	0.010913	0	0	0.007937	0	0.981151	0	0	0
NEWF	274	−1	0.019881	0	0	0.005964	0	0.974155	0	0	0
NEWF	275	−3	0.010934	0	0	0.005964	0	0.983101	0	0	0
NEWF	277	0	0.05859	0	0	0.006951	0	0.934459	0	0	0
NEWF	278	−1	0.034213	0	0	0.022483	0	0.943304	0	0	0
ROTT	1014	−2	0.0059	0	0	0.016716	0	0.977384	0	0	0
ROTT	1028	−3	0.005946	0	0	0.00892	0	0.985134	0	0	0
ROTT	1029	−1	0.004955	0	0	0.00892	0	0.986125	0	0	0
ROTT	1033	−1	0.009728	0	0	0.027237	0	0.963035	0	0	0
ROTT	1034	0	0.021782	0	0	0.009901	0	0.968317	0	0	0
PRES	1082	−3	0.419635	0	0	0.13119	0	0.449175	0	0	0
PRES	1093	−14	0.430979	0	0	0.197432	0	0.371589	0	0	0
PRES	1096	0	0.705253	0	0	0.027237	0	0.26751	0	0	0
PRES	1115	−1	0.572519	0	0	0.045802	0	0.381679	0	0	0
PRES	1127	−7	0.418004	0	0	0.108734	0	0.473262	0	0	0
BOX	1176	−1	0.002964	0	0	0.004941	0	0.006917	0.985178	0	0
BOX	1177	0	0.046332	0	0	0.002896	0	0.031853	0.918919	0	0
BOX	1178	−1	0.002979	0	0	0.003972	0	0.002979	0.99007	0	0
BOX	1179	−3	0.000993	0	0	0.003972	0	0.002979	0.992056	0	0
BOX	1304	−1	0.001978	0	0	0.005935	0	0.004946	0.987141	0	0
BULD	1193	−1	0.001938	0	0	0.006783	0	0.021318	0.002907	0.967054	0
BULD	1194	−2	0.004931	0	0	0.003945	0	0.006903	0.002959	0.981262	0
BULD	1195	−9	0.000988	0	0	0.004941	0	0.004941	0.001976	0.987154	0
BULD	1197	−3	0.003552	0	0	0.019538	0	0.089698	0.002664	0.884547	0
BULD	1198	0	0.003918	0	0	0.002938	0	0.013712	0.003918	0.975514	0
MAST	991	−14	0.984143	0	0	0	0	0.005946	0.000991	0.001982	0.006938
MAST	1015	0	0.979331	0	0	0	0	0.011811	0.001969	0.001969	0.004921
MAST	1016	−1	0.978389	0	0	0	0	0.008841	0.000982	0.007859	0.003929
MAST	1017	−22	0.966926	0	0	0	0	0.024319	0.000973	0.001946	0.005837
MAST	1066	−2	0.982266	0	0	0	0	0.006897	0.00197	0.005911	0.002956
BULM	1105	0	0.003925	0	0	0	0	0.009814	0.003925	0.004907	0.977429
BULM	1106	−3	0.002935	0	0	0	0	0.013699	0.001957	0.005871	0.975538
BULM	1107	−1	0.003956	0	0	0	0	0.006924	0.001978	0.001978	0.985163
BULM	1108	0	0.009852	0	0	0	0	0.010837	0.000985	0.002956	0.975369
BULM	1109	0	0.003956	0	0	0	0	0.004946	0.002967	0.002967	0.985163

[a]See Table 5 for abbreviations of canid populations.

KBB: pbe

TABLE 16

Average Membership Coefficient for Each Breed From the K = 4 Cluster Results

Breed	Number of Individuals	Inferred Clusters 1	2	3	4
Shiba Inu	5	0.974	0.007	0.010	0.009
Chow Chow	5	0.983	0.006	0.005	0.006
Akita	5	0.977	0.005	0.013	0.006
Alaskan Malamute	5	0.884	0.029	0.023	0.064
Basenji	5	0.925	0.030	0.012	0.033
Chinese Shar-Pei	5	0.894	0.050	0.029	0.027
Siberian Husky	5	0.828	0.021	0.071	0.080

TABLE 16-continued

Average Membership Coefficient for Each Breed From the K = 4 Cluster Results

	Number of	Inferred Clusters			
Breed	Individuals	1	2	3	4
Afghan Hound	5	0.634	0.041	0.068	0.256
Saluki	5	0.392	0.041	0.058	0.509
Tibetan Terrier	5	0.368	0.120	0.141	0.371
Lhasa Apso	5	0.402	0.030	0.444	0.125
Samoyed	5	0.404	0.017	0.501	0.078
Pekingese	5	0.210	0.026	0.603	0.161
Shih Tzu	5	0.199	0.026	0.616	0.159
Irish Wolfhound	5	0.011	0.165	0.650	0.173
Saint Bernard	5	0.016	0.201	0.557	0.226
Greyhound	5	0.017	0.091	0.740	0.152
Belgian Sheepdog	5	0.013	0.009	0.962	0.016
Belgian Tervuren	4	0.018	0.022	0.856	0.103
Borzoi	5	0.041	0.024	0.720	0.215
Collie	5	0.007	0.019	0.766	0.208
Shetland Sheepdog	5	0.017	0.105	0.684	0.193
Pug Dog	5	0.022	0.017	0.466	0.494
Komondor	5	0.039	0.101	0.206	0.653
Whippet	5	0.007	0.087	0.480	0.426
Standard Poodle	5	0.032	0.144	0.370	0.454
Bichon Frise	4	0.074	0.087	0.362	0.477
Keeshond	5	0.016	0.043	0.479	0.462
Manchester Terrier, Toy	4	0.024	0.161	0.303	0.513
Norwegian Elkhound	5	0.104	0.090	0.329	0.477
Kuvasz	5	0.077	0.043	0.378	0.502
Great Dane	5	0.067	0.085	0.240	0.608
Welsh Springer Spaniel	5	0.007	0.083	0.255	0.654
Doberman Pinscher	5	0.015	0.103	0.194	0.688
Standard Schnauzer	5	0.006	0.149	0.165	0.681
Italian Greyhound	5	0.074	0.068	0.096	0.762
Old English Sheepdog	5	0.024	0.086	0.122	0.768
American Water Spaniel	5	0.023	0.127	0.131	0.719
Miniature Schnauzer	5	0.009	0.136	0.129	0.726
Australian Terrier	5	0.022	0.107	0.104	0.767
English Cocker Spaniel	5	0.004	0.088	0.182	0.725
Irish Setter	5	0.005	0.074	0.117	0.804
West Highland White Terrier	5	0.019	0.079	0.058	0.844
Pointer	5	0.019	0.067	0.105	0.809
Basset Hound	4	0.020	0.086	0.077	0.818
Cavalier King Charles Spaniel	5	0.013	0.078	0.122	0.787
Giant Schnauzer	5	0.106	0.082	0.060	0.752
Pharaoh Hound	4	0.102	0.081	0.025	0.792
Golden Retriever	5	0.009	0.184	0.019	0.789
Beagle	5	0.016	0.175	0.058	0.751
Bloodhound	5	0.009	0.203	0.014	0.775
Airedale Terrier	4	0.016	0.127	0.109	0.748
American Cocker Spaniel	5	0.010	0.103	0.053	0.834
American Hairless Rat Terrier	5	0.009	0.149	0.064	0.778
Chesapeake Bay Retriever	5	0.019	0.173	0.032	0.776
Cairn Terrier	5	0.015	0.123	0.073	0.790
Portuguese Water Dog	5	0.007	0.134	0.139	0.720
German Shorthaired Pointer	5	0.015	0.172	0.094	0.719
Border Collie	5	0.037	0.116	0.101	0.746
Bedlington Terrier	4	0.010	0.233	0.145	0.613
Clumber Spaniel	5	0.005	0.355	0.066	0.573
Ibizan Hound	5	0.015	0.149	0.120	0.716
Rhodesian Ridgeback	5	0.010	0.215	0.150	0.625
Dachshund	5	0.015	0.315	0.192	0.479
Australian Shepherd	5	0.068	0.221	0.170	0.540
Chihuahua	5	0.028	0.229	0.161	0.582
Kerry Blue Terrier	5	0.008	0.257	0.147	0.588
Schipperke	4	0.011	0.195	0.078	0.717
Irish Terrier	4	0.009	0.277	0.070	0.644
Flat-coated Retriever	5	0.005	0.207	0.084	0.704
Soft Coated Wheaten Terrier	4	0.035	0.329	0.163	0.473
Pomeranian	5	0.055	0.340	0.203	0.402
Labrador Retriever	5	0.033	0.488	0.075	0.404
Presa Canario	5	0.036	0.762	0.044	0.158
Rottweiler	5	0.006	0.798	0.098	0.098
Bullmastiff	5	0.008	0.873	0.032	0.087

TABLE 16-continued

Average Membership Coefficient for Each Breed From the K = 4 Cluster Results

Breed	Number of Individuals	Inferred Clusters 1	2	3	4
Newfoundland	5	0.020	0.923	0.018	0.040
German Shepherd Dog	5	0.006	0.858	0.090	0.046
French Bulldog	4	0.009	0.945	0.012	0.034
Miniature Bull Terrier	5	0.013	0.921	0.020	0.047
Bulldog	5	0.008	0.962	0.019	0.011
Boxer	5	0.003	0.923	0.065	0.008
Mastiff	5	0.010	0.934	0.032	0.024
Bernese Mountain Dog	5	0.006	0.708	0.229	0.057
Greater Swiss Mountain Dog	5	0.015	0.488	0.373	0.124

TABLE 17A

Canid Population[a]	Canid ID No.	Missing Data	Populations* 1	2	3	4	5	6	7	8	9	10	11
CHOW	1633	−10	0.006	0.001	0.001	0.002	0.001	0.023	0.003	0.002	0.001	0.001	0.001
CHOW	1835	−9	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001
CHOW	1837	−18	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.001
CHOW	1838	−19	0.001	0.001	0.005	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
CHOW	1839	−1	0.002	0.001	0.001	0.001	0.003	0.013	0.016	0.001	0.001	0.001	0.001
SHAR	1573	−5	0.001	0.001	0.001	0.002	0.002	0.964	0.001	0.001	0.001	0.001	0.001
SHAR	1593	−11	0.011	0.001	0.001	0.002	0.003	0.935	0.002	0.001	0.002	0.001	0.008
SHAR	1619	−6	0.001	0.001	0.001	0.001	0.001	0.982	0.001	0.001	0.001	0.001	0.001
SHAR	1998	−2	0.016	0.025	0.001	0.002	0.043	0.72	0.003	0.002	0.005	0.01	0.006
SHAR	1999	−4	0.031	0	0.002	0.004	0.098	0.713	0.062	0.003	0.002	0.003	0.001
SHIB	1769	−22	0.001	0.001	0.001	0.001	0.003	0.001	0.002	0.001	0.001	0.001	0.001
SHIB	1854	−11	0.002	0.001	0.001	0.001	0.008	0.002	0.001	0.001	0.001	0.001	0.001
SHIB	1856	−6	0.003	0.001	0.001	0.003	0.001	0.035	0.002	0.002	0.004	0.002	0.001
SHIB	1860	−7	0.002	0.001	0.001	0.001	0.01	0.008	0.001	0.001	0.002	0.001	0.001
SHIB	1981	−1	0.004	0.001	0.002	0.001	0.026	0.01	0.001	0.002	0.001	0.002	0.005
AKIT	1130	−5	0.002	0.001	0.001	0.001	0.969	0.001	0.002	0.001	0.001	0.001	0.007
AKIT	1131	0	0.003	0.001	0.001	0.002	0.97	0.001	0.001	0.003	0.003	0.001	0.001
AKIT	1132	−3	0.001	0	0.001	0.001	0.981	0.002	0.003	0.001	0.001	0.001	0
AKIT	1133	−5	0.002	0.001	0.001	0	0.974	0.003	0.001	0.001	0.001	0.001	0.001
AKIT	1134	−3	0.001	0.001	0.004	0.001	0.976	0.002	0.001	0.001	0.002	0.001	0.001
AMAL	1629	−3	0.003	0.002	0.001	0.015	0	0.002	0.952	0.001	0.001	0.002	0.002
AMAL	1779	−3	0.002	0.005	0.003	0.004	0.001	0.002	0.938	0.001	0.002	0.003	0.012
AMAL	1845	−3	0.003	0.003	0.003	0.001	0.003	0.002	0.964	0.001	0.001	0.002	0.004
AMAL	2132	−6	0.005	0.004	0.002	0.001	0.003	0.001	0.925	0.01	0.002	0.008	0.013
AMAL	2214	−1	0.003	0.002	0.01	0.004	0.004	0.001	0.943	0.004	0.001	0.002	0.001
HUSK	1469	−12	0.002	0.001	0.001	0.001	0.001	0.001	0.96	0.001	0.008	0.002	0.001
HUSK	1883	−2	0.002	0.001	0.011	0.001	0.001	0.001	0.956	0.003	0.003	0.001	0.001
HUSK	2115	−6	0.003	0.001	0.001	0.006	0.001	0.002	0.947	0.004	0.002	0.003	0.004
HUSK	2117	−1	0.019	0.041	0.002	0.001	0.002	0.002	0.778	0.007	0.003	0.003	0.002
HUSK	2118	−3	0.013	0.001	0.004	0.031	0.001	0.003	0.838	0.025	0.001	0.003	0.004
SAMO	1375	0	0.001	0.001	0.961	0.002	0.001	0.001	0.001	0.001	0.008	0.001	0.001
SAMO	1532	−5	0.001	0.001	0.973	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001
SAMO	1560	−1	0.002	0.007	0.928	0.001	0.001	0.003	0.001	0.017	0.003	0.011	0.002
SAMO	169	0	0.001	0.001	0.981	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002
SAMO	239	0	0.002	0.002	0.97	0.002	0.002	0.001	0.001	0.001	0.002	0.001	0.003
AFGH	1812	−3	0.002	0.001	0.001	0.002	0.001	0.001	0.003	0.001	0.001	0.001	0.001
AFGH	1939	−3	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
AFGH	2264	−7	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.002
AFGH	1936	−9	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001
AFGH	1937	−13	0.002	0.001	0.006	0.005	0.001	0.001	0.007	0.002	0.002	0.002	0.002
SALU	1491	0	0.004	0.001	0.001	0.002	0.001	0.001	0.001	0.01	0.002	0.001	0.003
SALU	1535	−5	0.002	0.002	0.002	0.001	0.001	0.001	0.019	0.001	0.002	0.002	0.003
SALU	1607	−14	0.001	0.001	0.002	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.002
SALU	1873	−2	0.001	0.001	0.001	0.002	0.001	0.006	0.002	0.002	0.001	0.007	0.005
SALU	2610	−20	0.078	0.004	0.001	0.011	0.003	0.005	0.005	0.1	0.002	0.007	0.004
BSJI	1338	−9	0.281	0.001	0.001	0.002	0.005	0.003	0.001	0.002	0.001	0.026	0.002
BSJI	1339	−3	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0	0	0.001
BSJI	1645	−12	0	0	0	0	0	0	0	0	0	0	0
BSJI	1675	0	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0	0.001
BSJI	1717	−2	0.002	0	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001
TIBT	1466	−8	0.006	0.003	0.005	0.003	0.005	0.002	0.003	0.014	0.002	0.009	0.007
TIBT	1562	−9	0.001	0.001	0.001	0.001	0	0	0.001	0.001	0.001	0.001	0.001

TABLE 17A-continued

TIBT	1707	−12	0.001	0.01	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001
TIBT	26078	−2	0.012	0.004	0.004	0.003	0.005	0.002	0.006	0.008	0.023	0.076	0.009
TIBT	28086	0	0.001	0.001	0.001	0.001	0	0.001	0.001	0.004	0	0.001	0.001
LHSA	1524	−1	0.002	0.002	0.002	0.086	0.001	0.001	0.002	0.001	0.081	0.005	0.002
LHSA	1525	−41	0.003	0.002	0.004	0.043	0.001	0.002	0.002	0.002	0.245	0.003	0.002
LHSA	1526	−18	0.006	0.001	0.005	0.085	0.001	0.002	0.001	0.002	0.007	0.003	0.004
LHSA	1528	−2	0.003	0.002	0.004	0.051	0.001	0.001	0.004	0.238	0.166	0.004	0.001
LHSA	2074	−3	0.004	0.002	0.001	0.079	0.001	0.001	0.004	0.004	0.009	0.001	0.001
PEKE	1143	0	0	0.001	0	0.001	0	0	0.001	0	0.99	0.001	0
PEKE	1145	−2	0.001	0.002	0.001	0.004	0.001	0.001	0.001	0.001	0.974	0.001	0.001
PEKE	1211	0	0.001	0.001	0.001	0.005	0.001	0.002	0.001	0.002	0.951	0.001	0.003
PEKE	1212	−1	0.003	0.012	0.002	0.008	0.001	0.001	0.001	0.002	0.919	0.001	0.004
PEKE	1213	−3	0.001	0.014	0.001	0.001	0.001	0.001	0.001	0.001	0.963	0.002	0.002
SHIH	1393	0	0.001	0.001	0.001	0.166	0.001	0.002	0.001	0.001	0.106	0.001	0.001
SHIH	1783	−11	0.001	0.002	0.001	0.186	0.001	0.001	0.001	0.006	0.018	0.001	0.001
SHIH	2068	−3	0.001	0.001	0.001	0.188	0.001	0.001	0.001	0.001	0.021	0.001	0.001
SHIH	2859	−44	0.001	0.001	0.001	0.198	0.002	0.002	0.001	0.001	0.002	0.001	0.002
SHIH	2860	−12	0.002	0.002	0.001	0.151	0.007	0.001	0.001	0.002	0.124	0.001	0.001
PUG	1077	−5	0.001	0.986	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
PUG	1104	0	0.001	0.954	0.001	0.004	0.001	0.001	0.002	0.001	0.005	0.004	0.001
PUG	1183	−2	0.001	0.986	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001
PUG	1184	−1	0	0.993	0	0	0	0	0	0	0	0	0
PUG	1192	−3	0.001	0.986	0.001	0.001	0.001	0	0.001	0.001	0	0.001	0.001
BICH	1943	−17	0.002	0.002	0.007	0.003	0.007	0.002	0.002	0.917	0.002	0.007	0.003
BICH	1954	−7	0.002	0.001	0.001	0.004	0	0.001	0.001	0.963	0.001	0.001	0.001
BICH	933	−4	0.002	0.002	0.003	0.001	0.001	0.002	0.001	0.954	0.001	0.003	0.001
BICH	974	−2	0.002	0.091	0.002	0.001	0.001	0.002	0.003	0.87	0.002	0.001	0.005
SPOO	1530	−3	0.004	0.001	0.003	0.003	0.001	0.002	0.005	0.006	0.001	0.003	0.002
SPOO	1582	−1	0.002	0.001	0.002	0.004	0.001	0.002	0.001	0.003	0.001	0.003	0.001
SPOO	1876	−18	0.01	0.001	0.003	0.054	0.001	0.002	0.002	0.005	0.001	0.012	0.003
SPOO	1877	−5	0.002	0.001	0.002	0.002	0.001	0.001	0.001	0.002	0.002	0.009	0.001
SPOO	2337	−13	0.001	0.002	0.001	0.003	0.001	0.001	0.001	0.002	0.001	0.002	0.002
KOMO	1484	−13	0.001	0.001	0.003	0.001	0.001	0.001	0.003	0.001	0.002	0.967	0.002
KOMO	1964	−17	0.014	0.001	0.001	0.003	0.001	0.001	0.001	0.003	0.001	0.851	0.025
KOMO	2321	−1	0.002	0.017	0.002	0.012	0.001	0.001	0.003	0.019	0.001	0.899	0.001
KOMO	2323	−1	0.004	0.014	0.003	0.003	0.001	0.002	0.001	0.002	0.009	0.859	0.002
KOMO	2334	−2	0.001	0.004	0.002	0.002	0.002	0.001	0.001	0.002	0.003	0.968	0.002
KUVZ	1482	−3	0.002	0.009	0.013	0.047	0.001	0.001	0.006	0.009	0.001	0.002	0.001
KUVZ	1551	0	0.004	0.001	0.002	0.002	0.001	0.003	0.002	0.015	0.001	0.001	0.013
KUVZ	1672	−23	0.002	0.004	0.001	0.005	0.011	0.001	0.002	0.001	0.001	0.007	0.001
KUVZ	1913	−2	0.004	0.001	0.006	0.007	0.001	0.003	0.002	0.007	0.004	0.01	0.012
KUVZ	1994	−2	0.005	0.002	0.006	0.003	0.001	0.003	0.001	0.006	0.003	0.008	0.005
KEES	1501	0	0.001	0.003	0.188	0.771	0.001	0.001	0.003	0.002	0.001	0.001	0.008
KEES	1589	−2	0.002	0.008	0.155	0.77	0.001	0.002	0.001	0.002	0.002	0.004	0.017
KEES	1818	−41	0.001	0.001	0.19	0.778	0.001	0.001	0.001	0.001	0.001	0.002	0.004
KEES	1819	−1	0.002	0.002	0.174	0.767	0.002	0.001	0.001	0.02	0.001	0.002	0.002
KEES	2072	−4	0.003	0.003	0.168	0.749	0.001	0.001	0.002	0.035	0.005	0.003	0.001
NELK	2216	−4	0.039	0.003	0.018	0.017	0.001	0.002	0.005	0.004	0.003	0.008	0.846
NELK	2239	−2	0.001	0.001	0.001	0.002	0	0.001	0.001	0.001	0.001	0.001	0.984
NELK	2240	−2	0.002	0.001	0.005	0.008	0.001	0.001	0.002	0.002	0.007	0.003	0.948
NELK	2281	−1	0.001	0.003	0.002	0.008	0.001	0.001	0.002	0.002	0.001	0.001	0.949
NELK	2295	−15	0.001	0.002	0.002	0.002	0.002	0.001	0.002	0.002	0.001	0.001	0.957

Canid Population[a]	Canid ID No.	Missing Data	Populations* 12	13	14	15	16	17	18	19	20	21
CHOW	1633	−10	0.001	0.001	0.915	0.002	0.004	0.002	0.021	0.006	0.002	0.003
CHOW	1835	−9	0.001	0.001	0.981	0.001	0.001	0.003	0.001	0.001	0.001	0.001
CHOW	1837	−18	0.001	0	0.981	0.001	0.001	0.001	0.001	0	0.001	0.001
CHOW	1838	−19	0	0.001	0.978	0.001	0.001	0	0.002	0.001	0.001	0.001
CHOW	1839	−1	0.001	0.002	0.936	0.004	0.001	0.001	0.009	0.003	0.001	0.002
SHAR	1573	−5	0.001	0.001	0.002	0.001	0.003	0.012	0.001	0.002	0.001	0.001
SHAR	1593	−11	0.002	0.001	0.009	0.002	0.003	0.002	0.006	0.001	0.005	0.006
SHAR	1619	−6	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001
SHAR	1998	−2	0.004	0.003	0.049	0.003	0.003	0.002	0.003	0.001	0.094	0.005
SHAR	1999	−4	0.004	0.004	0.025	0.001	0.01	0.004	0.002	0.001	0.001	0.026
SHIB	1769	−22	0.001	0.001	0.002	0.001	0.001	0.98	0.001	0	0.001	0.001
SHIB	1854	−11	0.001	0.001	0.006	0.002	0.001	0.958	0.001	0.011	0.001	0.001
SHIB	1856	−6	0.005	0.001	0.021	0.001	0.013	0.837	0.002	0.001	0.001	0.064
SHIB	1860	−7	0.001	0.001	0.005	0.001	0.002	0.958	0.001	0.001	0.001	0.002
SHIB	1981	−1	0.006	0.001	0.053	0.001	0.003	0.875	0.001	0.002	0.001	0.003
AKIT	1130	−5	0.001	0	0.001	0.001	0.001	0.005	0.001	0.001	0.001	0.001
AKIT	1131	0	0	0.001	0.005	0.001	0.001	0.002	0.001	0	0.001	0.001
AKIT	1132	−3	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0	0.001	0.001
AKIT	1133	−5	0.001	0.001	0.003	0.001	0.001	0.003	0.002	0	0.002	0.001
AKIT	1134	−3	0.001	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.001

TABLE 17A-continued

AMAL	1629	−3	0.003	0.001	0.003	0.001	0.002	0.002	0.002	0.001	0.001	0.002
AMAL	1779	−3	0.001	0.002	0.001	0.002	0.004	0.001	0.001	0.001	0.004	0.008
AMAL	1845	−3	0.001	0.004	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001
AMAL	2132	−6	0.001	0.003	0.001	0.001	0.001	0.002	0.002	0.001	0.011	0.004
AMAL	2214	−1	0.007	0.001	0.001	0.001	0.002	0.004	0.001	0.001	0.003	0.002
HUSK	1469	−12	0.001	0.001	0.013	0.001	0.001	0.001	0.001	0.001	0.001	0.002
HUSK	1883	−2	0.001	0.001	0.003	0.002	0.001	0.001	0.002	0.001	0.005	0.002
HUSK	2115	−6	0.004	0.002	0.001	0.005	0.003	0.001	0.001	0.001	0.002	0.007
HUSK	2117	−1	0.001	0.002	0.009	0.002	0.004	0.002	0.003	0.001	0.11	0.006
HUSK	2118	−3	0.003	0.002	0.003	0.001	0.016	0.002	0.004	0.014	0.027	0.005
SAMO	1375	0	0.008	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.004	0.001
SAMO	1532	−5	0.001	0.003	0.001	0.001	0.002	0.002	0.001	0.001	0.003	0.001
SAMO	1560	−1	0.001	0.001	0.001	0.001	0.009	0.001	0.002	0.002	0.002	0.007
SAMO	169	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
SAMO	239	0	0.003	0	0.001	0.001	0.002	0.001	0.002	0.002	0.001	0.001
AFGH	1812	−3	0.001	0.976	0.001	0.002	0.001	0.001	0.001	0.002	0.001	0.001
AFGH	1939	−3	0.001	0.981	0	0.002	0.001	0.001	0.001	0.001	0.001	0.001
AFGH	2264	−7	0.001	0.983	0	0.001	0.001	0	0.001	0.001	0.001	0.001
AFGH	1936	−9	0	0.983	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001
AFGH	1937	−13	0.002	0.948	0.001	0.004	0.003	0	0.001	0	0.001	0.009
SALU	1491	0	0.001	0.02	0.001	0.922	0.002	0.004	0.009	0.001	0.009	0.002
SALU	1535	−5	0.001	0.02	0.002	0.931	0.001	0.001	0.002	0.002	0.001	0.002
SALU	1607	−14	0.002	0.017	0.001	0.961	0.001	0.001	0.001	0.001	0.002	0.001
SALU	1873	−2	0.004	0.019	0.001	0.939	0.002	0.001	0.001	0.001	0.001	0.002
SALU	2610	−20	0.004	0.075	0.005	0.579	0.032	0.001	0.001	0.032	0.006	0.046
BSJI	1338	−9	0.003	0.002	0.001	0.017	0.03	0.004	0.002	0.548	0.003	0.064
BSJI	1339	−3	0.001	0.001	0.001	0	0.001	0	0.001	0.986	0.001	0.001
BSJI	1645	−12	0	0	0	0	0	0	0	0.992	0	0
BSJI	1675	0	0	0	0	0.001	0.001	0.001	0.001	0.988	0	0.001
BSJI	1717	−2	0.001	0.004	0.001	0.001	0	0.005	0.001	0.976	0.001	0.001
TIBT	1466	−8	0.008	0.004	0.002	0.004	0.003	0.004	0.904	0.002	0.005	0.005
TIBT	1562	−9	0.001	0	0.001	0	0.002	0.001	0.985	0.001	0.001	0.001
TIBT	1707	−12	0.002	0.001	0.001	0.001	0.001	0	0.974	0	0.001	0.001
TIBT	26078	−2	0.004	0.003	0.002	0.031	0.009	0.015	0.756	0.001	0.001	0.027
TIBT	28086	0	0.002	0.001	0.001	0.001	0.001	0.001	0.967	0.001	0.012	0.001
LHSA	1524	−1	0.001	0.001	0.001	0.001	0.269	0.003	0.001	0.001	0.003	0.537
LHSA	1525	−41	0.001	0.003	0.002	0.002	0.138	0.002	0.001	0.003	0.004	0.535
LHSA	1526	−18	0.005	0.004	0.001	0.002	0.22	0.001	0.001	0.001	0.002	0.647
LHSA	1528	−2	0.009	0.001	0.006	0.01	0.157	0.001	0.009	0.002	0.003	0.325
LHSA	2074	−3	0.002	0.001	0.001	0.005	0.203	0.002	0.003	0.002	0.001	0.672
PEKE	1143	0	0	0	0.001	0	0.001	0	0	0	0	0.001
PEKE	1145	−2	0.001	0.001	0.002	0.002	0.002	0.001	0.001	0.001	0.001	0.001
PEKE	1211	0	0.002	0.001	0.001	0.001	0.023	0	0.001	0.001	0.001	0.002
PEKE	1212	−1	0.001	0.002	0.001	0.006	0.026	0.001	0.001	0.004	0.002	0.003
PEKE	1213	−3	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.003
SHIH	1393	0	0.002	0	0.001	0.001	0.71	0.001	0.001	0	0.001	0.001
SHIH	1783	−11	0.002	0.001	0.001	0.001	0.769	0.001	0.001	0.001	0.002	0.005
SHIH	2068	−3	0.001	0.001	0.001	0.001	0.772	0.001	0.001	0	0.001	0.005
SHIH	2859	−44	0.001	0.001	0.002	0.001	0.777	0.002	0.001	0.001	0.001	0.001
SHIH	2860	−12	0.003	0.001	0.005	0.001	0.624	0.005	0.001	0.001	0.001	0.068
PUG	1077	−5	0.001	0	0	0.001	0.001	0.001	0.001	0	0.001	0.001
PUG	1104	0	0.001	0.001	0.001	0.001	0.014	0.001	0.003	0.001	0.001	0.002
PUG	1183	−2	0.001	0	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001
PUG	1184	−1	0	0	0	0	0	0	0	0	0	0
PUG	1192	−3	0.001	0.001	0.001	0.001	0	0	0.001	0	0.001	0.001
BICH	1943	−17	0.003	0.001	0.003	0.001	0.003	0.001	0.023	0.001	0.008	0.004
BICH	1954	−7	0.003	0.002	0.001	0.005	0.004	0.003	0.003	0.001	0.002	0.001
BICH	933	−4	0.004	0.004	0.001	0.003	0.003	0.001	0.006	0.001	0.002	0.005
BICH	974	−2	0.002	0.001	0.001	0.001	0.004	0.001	0.001	0.002	0.005	0.002
SPOO	1530	−3	0.942	0.001	0.002	0.004	0.002	0.002	0.011	0.001	0.003	0.003
SPOO	1582	−1	0.954	0.001	0.001	0.001	0.003	0.001	0.001	0.004	0.005	0.006
SPOO	1876	−18	0.818	0.003	0.001	0.004	0.047	0.001	0.002	0.003	0.022	0.006
SPOO	1877	−5	0.964	0.002	0.001	0.004	0.001	0.002	0.001	0.001	0.001	0.002
SPOO	2337	−13	0.961	0.004	0.001	0.001	0.002	0.001	0.007	0.001	0.002	0.001
KOMO	1484	−13	0.002	0.001	0.001	0.002	0.001	0.001	0.004	0.001	0.003	0.002
KOMO	1964	−17	0.007	0.011	0.002	0.047	0.002	0.002	0.003	0.003	0.014	0.007
KOMO	2321	−1	0.003	0.002	0.001	0.001	0.005	0.001	0.008	0.001	0.021	0.002
KOMO	2323	−1	0.083	0.004	0.001	0.001	0.004	0.001	0.002	0.001	0.001	0.003
KOMO	2334	−2	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001
KUVZ	1482	−3	0.006	0.001	0.001	0.004	0.004	0	0.001	0.001	0.889	0.001
KUVZ	1551	0	0.027	0.001	0.001	0.005	0.002	0.002	0.007	0.002	0.905	0.003
KUVZ	1672	−23	0.007	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.942	0.003
KUVZ	1913	−2	0.003	0.026	0.001	0.003	0.005	0.001	0.003	0.001	0.896	0.003
KUVZ	1994	−2	0.014	0.002	0.002	0.002	0.003	0.001	0.003	0.006	0.916	0.006
KEES	1501	0	0.003	0.002	0.001	0.002	0.004	0.001	0.002	0.004	0.002	0.001
KEES	1589	−2	0.003	0.003	0.001	0.021	0.002	0.001	0.001	0.001	0.002	0.002
KEES	1818	−41	0.006	0.001	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.001

TABLE 17A-continued

KEES	1819	−1	0.009	0.001	0.001	0.001	0.002	0.001	0.003	0.002	0.004	0.002
KEES	2072	−4	0.008	0.002	0.001	0.002	0.002	0.001	0.001	0.002	0.006	0.004
NELK	2216	−4	0.005	0.002	0.01	0.002	0.006	0.001	0.011	0.004	0.004	0.01
NELK	2239	−2	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
NELK	2240	−2	0.002	0.001	0.001	0.003	0.002	0.001	0.002	0.001	0.008	0.001
NELK	2281	−1	0.001	0.005	0.001	0.008	0.001	0.001	0.01	0.001	0.001	0.001
NELK	2295	−15	0.001	0.001	0.001	0.004	0.004	0.001	0.007	0.001	0.003	0.002

TABLE 17B

Canid	Canid	Missing	Populations*										
Population[a]	ID No.	Data	44	45	46	47	48	49	50	51	52	53	54
ECKR	1376	−1	0.002	0.001	0.01	0.002	0.003	0.001	0.863	0.007	0.001	0.001	0.002
ECKR	1377	−2	0.001	0.056	0.012	0.003	0.003	0.002	0.859	0.001	0.007	0.001	0.004
ECKR	1400	−2	0.001	0.001	0	0.001	0.001	0.001	0.983	0.002	0.001	0.001	0.001
ECKR	1404	−7	0.001	0.001	0.002	0.001	0.001	0.001	0.977	0.001	0.001	0.001	0.001
ECKR	1511	−6	0.002	0.004	0.003	0.001	0.001	0.001	0.959	0.001	0.001	0.002	0.004
ACKR	1035	−2	0.002	0.001	0.001	0.739	0.003	0.186	0.009	0.001	0.003	0.002	0.001
ACKR	2261	−2	0.003	0.001	0.001	0.961	0.001	0.001	0.006	0.003	0.001	0.001	0.001
ACKR	2310	−1	0.004	0.001	0.001	0.949	0.019	0.003	0.002	0.004	0.001	0.001	0.001
ACKR	1956	−18	0.001	0.001	0.001	0.981	0.001	0.001	0.002	0.001	0.001	0.001	0.001
ACKR	2260	−2	0.001	0.001	0.001	0.983	0.001	0.001	0.002	0	0.001	0.001	0.001
CKCS	1513	−6	0.001	0.004	0.001	0.001	0.002	0.002	0.002	0.965	0.001	0.001	0.002
CKCS	1639	−2	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.98	0.001	0.001	0.001
CKCS	1640	−15	0.001	0.001	0.034	0	0.001	0.001	0.001	0.941	0.002	0.001	0.006
CKCS	1642	−4	0.005	0.001	0.001	0.003	0.001	0.001	0.002	0.975	0.001	0.001	0.001
CKCS	2054	−5	0.001	0.001	0	0	0	0	0	0.991	0	0	0
DOBP	1031	−1	0.002	0.001	0.004	0.002	0.001	0.001	0.001	0.002	0.001	0.003	0.002
DOBP	1032	−3	0.001	0.001	0.001	0.002	0.004	0.011	0.004	0.001	0.026	0.002	0.001
DOBP	1749	−2	0.001	0.001	0.001	0.002	0.001	0.001	0	0	0.002	0.001	0.002
DOBP	2162	−5	0.009	0.001	0.004	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002
DOBP	2245	−2	0.001	0	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0
MNTY	1539	−1	0.924	0.003	0.001	0.013	0.001	0.007	0.002	0.003	0.002	0.003	0.008
MNTY	1732	−15	0.978	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001
MNTY	2145	−19	0.983	0.001	0.002	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.001
MNTY	2149	−47	0.945	0.002	0.002	0.003	0.001	0.001	0.014	0.001	0.002	0.001	0.002
IRSE	1540	−5	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
IRSE	1617	−4	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.002	0.001
IRSE	1896	0	0.002	0.003	0.004	0.008	0.002	0.001	0.003	0.001	0.002	0.002	0.002
IRSE	2084	−6	0.017	0.002	0.008	0.003	0.002	0.001	0.002	0.001	0.003	0.001	0.001
IRSE	2085	−17	0.002	0.001	0.001	0.002	0.001	0.002	0.015	0.006	0.005	0.002	0.001
PNTR	1382	0	0.001	0.002	0.001	0.001	0.002	0.008	0.001	0.001	0.004	0.002	0.001
PNTR	1383	−2	0.002	0.003	0.002	0.001	0.001	0.002	0.001	0.003	0.001	0.001	0.002
PNTR	1869	−2	0.001	0.003	0.003	0.005	0.006	0.002	0.001	0.001	0.001	0.001	0.008
PNTR	1938	−6	0.001	0.001	0.001	0.003	0.001	0.002	0.001	0.001	0.004	0.001	0.002
PNTR	1948	−31	0.004	0.001	0.005	0.002	0.001	0.002	0.003	0.027	0.002	0.001	0.001
GSHP	1628	−5	0.025	0.002	0.009	0.002	0.005	0.808	0.002	0.002	0.003	0.003	0.011
GSHP	1708	−22	0.001	0.001	0.002	0.002	0.002	0.929	0.001	0.001	0.002	0.001	0.002
GSHP	1710	−28	0.001	0.001	0.002	0.002	0.002	0.959	0.002	0.001	0.002	0.001	0.002
GSHP	1833	−26	0.335	0.013	0.008	0.155	0.003	0.146	0.003	0.002	0.013	0.002	0.001
GSHP	1892	−4	0.012	0.001	0.003	0.004	0.104	0.398	0.002	0.004	0.016	0.002	0.001
MSNZ	1587	−9	0.001	0.001	0.984	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001
MSNZ	1756	−6	0.001	0.001	0.982	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001
MSNZ	1851	−7	0.001	0.001	0.976	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001
MSNZ	2034	−1	0.001	0.001	0.919	0.001	0.002	0.003	0.001	0.001	0.005	0.002	0.001
MSNZ	2613	−16	0.001	0.001	0.912	0.006	0.001	0.002	0.028	0.001	0.002	0.003	0.001
SSNZ	13352	0	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.001	0.001	0.001
SSNZ	1360	−3	0.008	0.003	0.075	0.004	0.001	0.002	0.005	0.009	0.01	0.001	0.003
SSNZ	1827	−9	0.001	0	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001
SSNZ	20457	−1	0.001	0.001	0.001	0.002	0.001	0.002	0.001	0.001	0.001	0.002	0.001
SSNZ	22647	−3	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.005	0.001	0.001	0.001
GSNZ	1868	−6	0.009	0.003	0.002	0.01	0.14	0.006	0.002	0.006	0.597	0.01	0.003
GSNZ	22739	0	0.001	0.001	0.006	0.002	0.042	0.002	0.001	0.003	0.928	0.001	0.001
GSNZ	27093	0	0.003	0.005	0.002	0.001	0.002	0.002	0.003	0.003	0.948	0.002	0.006
GSNZ	27106	−1	0.001	0.009	0.001	0.002	0.002	0.001	0.008	0.001	0.863	0.002	0.001
GSNZ	33390	0	0.007	0.003	0.007	0.003	0.002	0.004	0.004	0.002	0.775	0.004	0.04
AHRT	1120	−1	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001
AHRT	1121	−3	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
AHRT	1122	0	0.004	0.004	0.002	0.006	0.061	0.004	0.002	0.002	0.003	0.002	0.001
AHRT	1123	−1	0.001	0.001	0.002	0.003	0.003	0.03	0.002	0.003	0.004	0.001	0.023
AHRT	1124	−2	0.001	0	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001
AIRT	1603	−3	0.001	0	0.001	0.001	0.001	0.001	0.001	0	0.001	0	0.99

TABLE 17B-continued

AIRT	1604	−7	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.975
AIRT	1788	−2	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.981
AIRT	1875	−1	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.982
BASS	1341	0	0.001	0.003	0.001	0.001	0.981	0.001	0.001	0.001	0.001	0.001	0.001
BASS	1342	−5	0.001	0.001	0.003	0.001	0.966	0.002	0.006	0.001	0.002	0.001	0.001
BASS	1506	0	0.001	0.002	0.001	0.001	0.951	0.001	0.004	0.002	0.001	0.004	0.001
BASS	1917	−4	0.001	0.003	0.001	0.001	0.971	0.007	0.002	0.001	0.002	0.001	0.001
BEAG	1323	−2	0.001	0.059	0.011	0.019	0.002	0.002	0.002	0.001	0.002	0.002	0.001
BEAG	1324	−1	0.003	0.001	0.004	0.002	0.005	0.04	0.001	0.012	0.004	0.003	0.001
BEAG	1327	−2	0.003	0.017	0.002	0.002	0.003	0.006	0.002	0.001	0.003	0.002	0.002
BEAG	994	−3	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
BEAG	995	−2	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.002	0.001
BLDH	1186	0	0.001	0.989	0	0.001	0.001	0.001	0.001	0	0	0	0
BLDH	1223	−2	0.01	0.945	0.001	0.002	0.001	0.002	0.003	0.006	0.001	0.001	0.001
BLDH	1410	−8	0.001	0.978	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001
BLDH	1942	−6	0.001	0.981	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001
BLDH	1957	0	0.001	0.973	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.002	0.001
IBIZ	1147	−8	0.001	0.002	0.003	0.001	0.001	0.001	0.017	0.001	0.002	0.097	0.002
IBIZ	1148	−19	0.002	0.001	0.011	0.001	0.003	0.002	0.002	0.001	0.002	0.109	0.004
IBIZ	1162	0	0.001	0.002	0.002	0.002	0.001	0.001	0.003	0.001	0.002	0.247	0.001
IBIZ	1172	0	0.002	0.075	0.001	0.007	0.001	0.001	0.001	0.001	0.003	0.098	0.001
IBIZ	1280	0	0.002	0.001	0.001	0.003	0.004	0.005	0.004	0.001	0.001	0.102	0.007
PHAR	1292	−3	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.977	0.001
PHAR	1947	−14	0.001	0	0.002	0.001	0.001	0.009	0.001	0.001	0.006	0.968	0.001
PHAR	1962	−14	0.001	0.001	0.001	0.002	0.001	0.002	0.001	0.001	0.001	0.969	0
PHAR	1963	−10	0.002	0.001	0.001	0.001	0.008	0.001	0.002	0.001	0.001	0.956	0.001
PTWD	P142	−3	0.002	0.001	0.009	0.001	0.001	0.001	0.002	0.001	0.002	0.002	0.007
PTWD	P1	−6	0.001	0.008	0.003	0.001	0.002	0.002	0.001	0.001	0.002	0.001	0.001
PTWD	P238	−3	0.003	0.002	0.005	0.005	0.004	0.025	0.002	0.021	0.035	0.024	0.008
PTWD	P25	−2	0.006	0.002	0.016	0.005	0.002	0.031	0.028	0.005	0.004	0.003	0.003
PTWD	P67	0	0.002	0.001	0.001	0.001	0.003	0.003	0.001	0.001	0.002	0.009	0.001
AMWS	2168	0	0.004	0.001	0.09	0.007	0.002	0.005	0.002	0.204	0.002	0.001	0.002
AMWS	2279	−4	0.005	0.016	0.001	0.025	0.003	0.01	0.039	0.009	0.012	0.004	0.002
AMWS	2327	−36	0.002	0.001	0.001	0.001	0.001	0.001	0.003	0.003	0.001	0.001	0.001
AMWS	987	−1	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001
AMWS	988	0	0.004	0.001	0.019	0.002	0.004	0.003	0.002	0.007	0.006	0.007	0.002
WSSP	1955	−14	0.001	0.001	0.001	0.001	0.004	0.001	0.001	0.001	0.001	0.001	0.001
WSSP	2139	−1	0.002	0.002	0.001	0.001	0.001	0.002	0.01	0.017	0.002	0.001	0.001
WSSP	2143	0	0.001	0.001	0.001	0.002	0.001	0.002	0.001	0.001	0.002	0.001	0.001
WSSP	2195	−27	0.003	0.002	0.003	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.004
WSSP	2286	−5	0.002	0.02	0.001	0.005	0.002	0.001	0.004	0.002	0.001	0.002	0.002

Canid	Canid	Missing	Populations*									
Population[a]	ID No.	Data	55	56	57	58	59	60	61	62	63	64
ECKR	1376	−1	0.008	0.001	0.001	0.001	0.006	0.003	0.004	0.002	0.072	0.009
ECKR	1377	−2	0.003	0.003	0.002	0.002	0.003	0.003	0.005	0.003	0.023	0.002
ECKR	1400	−2	0.001	0.001	0	0.001	0.001	0.001	0	0.001	0.002	0
ECKR	1404	−7	0.001	0.002	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.001
ECKR	1511	−6	0.001	0.001	0.005	0.003	0.001	0.002	0.002	0.004	0.002	0.001
ACKR	1035	−2	0.007	0.003	0.023	0.001	0.001	0.007	0.002	0.003	0.004	0.001
ACKR	2261	−2	0.001	0.003	0.001	0.001	0.003	0.001	0.001	0.001	0.006	0.001
ACKR	2310	−1	0.002	0.001	0.001	0.002	0.001	0.002	0.001	0.002	0.001	0.001
ACKR	1956	−18	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.002
ACKR	2260	−2	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0	0.001
CKCS	1513	−6	0.004	0.003	0.001	0.001	0.001	0.001	0.003	0.002	0.001	0.001
CKCS	1639	−2	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.002	0.001	0.001
CKCS	1640	−15	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.001
CKCS	1642	−4	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
CKCS	2054	−5	0	0	0.001	0.001	0	0	0	0	0	0
DOBP	1031	−1	0.003	0.001	0.966	0.001	0.001	0.001	0.002	0.003	0.001	0.001
DOBP	1032	−3	0.001	0.001	0.929	0.001	0.001	0.005	0.001	0.002	0.003	0.002
DOBP	1749	−2	0.001	0.001	0.979	0.002	0.001	0.001	0.001	0.001	0	0.002
DOBP	2162	−5	0.001	0.002	0.964	0.001	0.001	0.003	0.001	0.001	0.001	0.001
DOBP	2245	−2	0	0.001	0.989	0.001	0	0	0	0	0.001	0.001
MNTY	1539	−1	0.001	0.001	0.006	0.007	0.001	0.005	0.001	0.001	0.007	0.003
MNTY	1732	−15	0.001	0.001	0.004	0.002	0.001	0.001	0.001	0.001	0.001	0.001
MNTY	2145	−19	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
MNTY	2149	−47	0.003	0.008	0.002	0.001	0.001	0.001	0.001	0.001	0.004	0.003
IRSE	1540	−5	0.006	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.978
IRSE	1617	−4	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.983
IRSE	1896	0	0.015	0.001	0.001	0.002	0.002	0.004	0.001	0.002	0.002	0.94
IRSE	2084	−6	0.001	0.001	0.001	0.004	0.001	0.002	0.014	0.008	0.001	0.927
IRSE	2085	−17	0.001	0.003	0.001	0.005	0.004	0.002	0.003	0.001	0.005	0.936
PNTR	1382	0	0.965	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.003
PNTR	1383	−2	0.967	0.003	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.002

TABLE 17B-continued

PNTR	1869	−2	0.942	0.003	0.001	0.002	0.004	0.001	0.011	0.001	0.001	0.002
PNTR	1938	−6	0.965	0.001	0.001	0.002	0.001	0.002	0.002	0.001	0.006	0.003
PNTR	1948	−31	0.933	0.003	0.002	0.001	0.003	0.002	0.002	0.002	0.003	0.002
GSHP	1628	−5	0.015	0.001	0.087	0.002	0.002	0.003	0.002	0.012	0.002	0.003
GSHP	1708	−22	0.005	0.003	0.001	0.042	0.001	0.001	0.001	0.002	0.001	0.001
GSHP	1710	−28	0.001	0.002	0.001	0.001	0.005	0.003	0.005	0.001	0.006	0.001
GSHP	1833	−26	0.072	0.001	0.001	0.01	0.044	0.025	0.067	0.095	0.001	0.003
GSHP	1892	−4	0.012	0.002	0.002	0.004	0.182	0.011	0.004	0.028	0.003	0.203
MSNZ	1587	−9	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001
MSNZ	1756	−6	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.002	0.001
MSNZ	1851	−7	0.001	0.001	0.001	0.002	0.002	0.003	0.001	0.001	0.001	0.001
MSNZ	2034	−1	0.002	0.003	0.001	0.027	0.001	0.011	0.01	0.004	0.001	0.001
MSNZ	2613	−16	0.002	0.023	0.003	0.003	0.001	0.001	0.002	0.001	0.003	0.002
SSNZ	13352	0	0.002	0.002	0.001	0.968	0.004	0.002	0.002	0.001	0.001	0.003
SSNZ	1360	−3	0.001	0.002	0.002	0.855	0.002	0.006	0.001	0.004	0.005	0.001
SSNZ	1827	−9	0.001	0.001	0.001	0.988	0.001	0.001	0	0.001	0	0.001
SSNZ	20457	−1	0.002	0.002	0	0.97	0.001	0.002	0.001	0.001	0.001	0.004
SSNZ	22647	−3	0.001	0.001	0.001	0.976	0.001	0.001	0.001	0.001	0.001	0.001
GSNZ	1868	−6	0.015	0.012	0.005	0.035	0.012	0.007	0.008	0.106	0.004	0.008
GSNZ	22739	0	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.003
GSNZ	27093	0	0.002	0.001	0.001	0.002	0.001	0.004	0.008	0.001	0.002	0.002
GSNZ	27106	−1	0.004	0.001	0.002	0.093	0.002	0.002	0.001	0.001	0.001	0.003
GSNZ	33390	0	0.001	0.104	0.002	0.016	0.012	0.004	0.002	0.005	0.001	0.001
AHRT	1120	−1	0.002	0.001	0.001	0.002	0.977	0.001	0.002	0.001	0.001	0.001
AHRT	1121	−3	0.002	0.001	0	0.001	0.979	0.001	0.002	0.002	0.001	0.001
AHRT	1122	0	0.001	0.016	0.003	0.001	0.854	0.009	0.002	0.008	0.008	0.005
AHRT	1123	−1	0.001	0.004	0.003	0.003	0.888	0.004	0.011	0.004	0.007	0.002
AHRT	1124	−2	0.001	0.001	0.001	0.001	0.984	0.001	0.001	0.001	0.001	0.001
AIRT	1603	−3	0.001	0.001	0	0	0.001	0.001	0.001	0	0.001	0
AIRT	1604	−7	0.001	0.005	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001
AIRT	1788	−2	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002
AIRT	1875	−1	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
BASS	1341	0	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
BASS	1342	−5	0.001	0.001	0.001	0.001	0.004	0.001	0.001	0.001	0.003	0.001
BASS	1506	0	0.001	0.001	0.002	0.001	0.001	0.002	0.002	0.005	0.011	0.005
BASS	1917	−4	0.001	0.002	0.001	0	0.001	0.001	0.003	0.001	0.001	0.001
BEAG	1323	−2	0.001	0.017	0.001	0.001	0.007	0.004	0.859	0.003	0.002	0.002
BEAG	1324	−1	0.001	0.001	0.231	0.001	0.244	0.008	0.421	0.012	0.002	0.001
BEAG	1327	−2	0.002	0.011	0.001	0.001	0.002	0.007	0.928	0.002	0.001	0.001
BEAG	994	−3	0.002	0.001	0.001	0.001	0.001	0.001	0.98	0.001	0.001	0.001
BEAG	995	−2	0.001	0.002	0.001	0.002	0.001	0.001	0.972	0.001	0.001	0.002
BLDH	1186	0	0	0.001	0.001	0	0	0.001	0.001	0	0.001	0
BLDH	1223	−2	0.001	0.002	0.001	0.001	0.001	0.001	0.006	0.001	0.006	0.007
BLDH	1410	−8	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001
BLDH	1942	−6	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
BLDH	1957	0	0.001	0.003	0.001	0.001	0.001	0.001	0.002	0.003	0.001	0.001
IBIZ	1147	−8	0.001	0.01	0.001	0.003	0.001	0.002	0.008	0.84	0.002	0.002
IBIZ	1148	−19	0.001	0.002	0.001	0.001	0.002	0.002	0.001	0.852	0.001	0.001
IBIZ	1162	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.725	0.001	0.003
IBIZ	1172	0	0.001	0.002	0.001	0.002	0.002	0.002	0.002	0.795	0.001	0.002
IBIZ	1280	0	0.005	0.001	0.001	0.001	0.003	0.004	0.001	0.85	0.002	0.002
PHAR	1292	−3	0.001	0.001	0.001	0.001	0.001	0.004	0.001	0.002	0.001	0.002
PHAR	1947	−14	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.001
PHAR	1962	−14	0.001	0.001	0.001	0.002	0.001	0.005	0.001	0.003	0.003	0.001
PHAR	1963	−10	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.016
PTWD	P142	−3	0.003	0.005	0.002	0.002	0.005	0.942	0.002	0.003	0.005	0.002
PTWD	P1	−6	0.001	0.001	0.001	0.023	0.002	0.929	0.002	0.002	0.015	0.002
PTWD	P238	−3	0.007	0.002	0.002	0.003	0.003	0.503	0.301	0.018	0.022	0.005
PTWD	P25	−2	0.007	0.005	0.054	0.004	0.01	0.767	0.008	0.014	0.025	0.003
PTWD	P67	0	0.001	0.001	0.001	0.001	0.005	0.957	0.003	0.002	0.002	0.002
AMWS	2168	0	0.001	0.626	0.001	0.002	0.004	0.002	0.005	0.002	0.036	0.003
AMWS	2279	−4	0.013	0.706	0.069	0.005	0.042	0.005	0.014	0.009	0.002	0.011
AMWS	2327	−36	0.001	0.975	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.001
AMWS	987	−1	0.001	0.974	0.001	0.001	0.001	0.001	0.003	0.003	0.003	0.001
AMWS	988	0	0.002	0.897	0.001	0.003	0.025	0.007	0.002	0.004	0.002	0.001
WSSP	1955	−14	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.002	0.977	0.001
WSSP	2139	−1	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.948	0.001
WSSP	2143	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.977	0.002
WSSP	2195	−27	0.002	0.004	0.002	0.002	0.001	0.003	0.002	0.001	0.962	0.001
WSSP	2286	−5	0.001	0.002	0.002	0.002	0.002	0.003	0.002	0.001	0.943	0.001

TABLE 17C

Canid Population[a]	Canid ID No.	Missing Data	Populations* 22	23	24	25	26	27	28	29	30	31	32	33	34
TURV	1622	−1	0.001	0.002	0.001	0.002	0.004	0.003	0.002	0.001	0.003	0.002	0.001	0.002	0.001
TURV	2194	−1	0.003	0.001	0.001	0.008	0.001	0.002	0.005	0.001	0.005	0.002	0.001	0.005	0.002
TURV	2200	0	0.003	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.004	0.005	0.005	0.002	0.002
TURV	2222	0	0.003	0.003	0.008	0.004	0.009	0.006	0.006	0.001	0.003	0.004	0.003	0.002	0.002
BELS	1351	−1	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.003	0.002	0.005	0.001	0.001	0.001
BELS	2111	−6	0.001	0.004	0.006	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.002	0.001	0.002
BELS	2153	0	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.003	0.001	0.001	0.001
BELS	2209	−1	0.001	0.001	0.001	0.001	0.001	0.001	0.011	0.001	0.001	0.001	0.002	0.001	0.001
BELS	2210	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001
OES	1984	−1	0.905	0.004	0.006	0.002	0.006	0.002	0.004	0.002	0.004	0.001	0.001	0.004	0.003
OES	2171	−4	0.85	0.004	0.002	0.004	0.003	0.001	0.001	0.002	0.003	0.002	0.003	0.019	0.001
OES	2179	−9	0.881	0.025	0.004	0.002	0.002	0.001	0.001	0.007	0.001	0.007	0.012	0.008	0.006
OES	1914	−5	0.966	0.001	0.001	0.004	0.002	0.001	0.003	0.001	0.002	0.003	0.001	0.001	0.001
OES	2626	−38	0.965	0.001	0.001	0.001	0.003	0.002	0.002	0.001	0.001	0.002	0.002	0.002	0.001
BORD	1648	−26	0.003	0.001	0.003	0.003	0.001	0.001	0.001	0.001	0.002	0.004	0.003	0.002	0.002
BORD	1828	−17	0.002	0.005	0.023	0.002	0.001	0.01	0.003	0.001	0.001	0.001	0.003	0.002	0.001
BORD	1829	−1	0.009	0.003	0.012	0.012	0.021	0.002	0.004	0.003	0.005	0.017	0.001	0.002	0.008
BORD	2002	−3	0.006	0.002	0.002	0.003	0.001	0.001	0.001	0.001	0.002	0.005	0.002	0.002	0.001
BORD	2003	−3	0.008	0.021	0.002	0.004	0.002	0.004	0.002	0.008	0.002	0.001	0.003	0.005	0.007
AUSS	1336	−2	0.011	0.003	0.002	0.009	0.039	0.008	0.003	0.002	0.004	0.01	0.015	0.002	0.003
AUSS	1337	−2	0.005	0.006	0.001	0.005	0.013	0.004	0.001	0.001	0.096	0.003	0.002	0.032	0.003
AUSS	1500	−15	0.002	0.001	0.003	0.003	0.015	0.002	0.002	0.003	0.004	0.009	0.001	0.001	0.001
AUSS	1521	−3	0.128	0.003	0.002	0.08	0.074	0.001	0.002	0.001	0.007	0.002	0.001	0.003	0.002
AUSS	1683	−4	0.031	0.004	0.002	0.013	0.005	0.001	0.002	0.001	0.003	0.006	0.002	0.014	0.001
COLL	1692	−2	0.001	0.001	0.001	0.002	0.973	0.001	0.001	0.001	0.001	0.001	0.001	0.004	0.002
COLL	1701	−11	0.001	0.001	0.001	0.002	0.958	0	0.003	0.002	0.001	0.001	0.003	0.002	0.002
COLL	2284	−16	0.001	0.001	0.001	0.001	0.978	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
COLL	373	−2	0.001	0	0.001	0.001	0.983	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
COLL	379	−3	0.001	0.001	0.001	0.001	0.978	0	0.001	0.001	0.002	0.001	0.001	0.001	0.001
SSHP	1379	0	0.005	0.002	0.002	0.01	0.878	0.003	0.006	0.002	0.002	0.012	0.001	0.018	0.003
SSHP	1523	−1	0.001	0.008	0.002	0.002	0.868	0.035	0.001	0.003	0.001	0.003	0.008	0.002	0.004
SSHP	1824	−6	0.004	0.001	0.006	0.003	0.869	0.001	0.001	0.001	0.001	0.004	0.001	0.011	0.001
SSHP	1921	−30	0.002	0.002	0.004	0.001	0.971	0.001	0.001	0.001	0.002	0.002	0.001	0.001	0.001
SSHP	2040	−19	0.004	0.002	0.001	0.001	0.907	0.002	0.006	0.003	0.002	0.004	0.001	0.003	0.001
DACH	1051	−5	0.002	0.001	0.001	0.002	0.001	0.001	0.001	0.003	0.002	0.001	0.002	0.002	0.002
DACH	1052	−2	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001
DACH	1053	−2	0.012	0.005	0.002	0.002	0.002	0.002	0.002	0.016	0.001	0.002	0.001	0.002	0.004
DACH	1054	0	0.001	0.001	0.001	0.002	0.001	0.014	0.001	0.002	0.001	0.002	0.001	0.001	0.001
DACH	1055	−1	0.001	0.001	0.002	0.001	0.002	0.001	0.002	0.001	0.001	0.002	0.003	0.001	0.001
DANE	1574	−5	0.004	0.922	0.002	0.002	0.003	0.002	0.001	0.002	0.001	0.001	0.003	0.002	0.001
DANE	1575	−11	0.004	0.9	0.002	0.002	0.001	0.032	0.001	0.001	0.002	0.001	0.002	0.002	0.003
DANE	1580	−2	0.002	0.977	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002
DANE	1700	−7	0.002	0.934	0.003	0.002	0.004	0.001	0.002	0.004	0.002	0.012	0.001	0.001	0.002
DANE	1748	−3	0.001	0.973	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.004	0.001	0.001
IWOF	1581	−21	0.001	0.001	0.001	0.001	0	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001
IWOF	1761	−12	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
IWOF	1792	−4	0.001	0.001	0.003	0.002	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001
IWOF	1906	−6	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001

TABLE 17C-continued

IWOF	1993	−3	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.002	0.001	0.001	0.001
BORZ	1378	0	0.004	0.001	0.001	0.002	0.004	0.001	0.944	0.007	0.001	0.003	0.002	0.007	0.003
BORZ	1401	−4	0.001	0.001	0.002	0.001	0.001	0.001	0.979	0.001	0	0.001	0.001	0.001	0.002
BORZ	1808	−2	0.001	0.004	0.001	0.003	0.001	0.002	0.959	0.001	0.001	0.001	0.004	0.001	0.002
BORZ	2268	0	0.003	0.003	0.002	0.002	0.008	0.004	0.858	0.004	0.002	0.012	0.005	0.002	0.002
BORZ	978	−1	0.003	0.008	0.001	0.004	0.002	0.001	0.936	0.001	0.011	0.006	0.006	0.003	0.003
GREY	2477	−1	0.002	0.001	0.001	0.001	0.001	0.001	0.019	0.023	0.001	0.864	0.008	0.002	0.001
GREY	2478	0	0.001	0.004	0.01	0.002	0.002	0.002	0.001	0.002	0.006	0.951	0.001	0.001	0.003
GREY	2479	0	0.004	0.002	0.001	0.007	0.003	0.001	0.005	0.001	0.004	0.932	0.009	0.002	0.003
GREY	2480	−3	0.002	0.001	0.001	0.004	0.004	0.011	0.004	0.001	0.001	0.929	0.002	0.001	0.002
GREY	2481	−3	0.001	0.004	0.002	0.013	0.002	0.004	0.012	0.045	0.006	0.829	0.004	0.001	0.002
WHIP	1355	−1	0.003	0.001	0.002	0.001	0.001	0.001	0.002	0.001	0.002	0.96	0.004	0.008	0.002
WHIP	1395	−42	0.003	0.002	0.004	0.006	0.001	0.004	0.022	0.005	0.003	0.61	0.001	0.002	0.002
WHIP	1407	−2	0.001	0.001	0.001	0.002	0.001	0.002	0.002	0.002	0.002	0.881	0.002	0.005	0.002
WHIP	1409	−2	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002	0.001	0.97	0.001	0.002	0.001
WHIP	1518	−14	0.001	0.001	0.001	0.003	0.003	0.001	0.001	0.002	0.001	0.942	0.006	0.012	0.001
ITGR	1568	−1	0.001	0.004	0.008	0.002	0.001	0.004	0.001	0.001	0.008	0.002	0.95	0.001	0.002
ITGR	1570	−25	0.001	0.001	0.001	0.001	0.001	0.004	0.002	0.001	0.001	0.001	0.975	0.002	0.001
ITGR	1862	−5	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.978	0.002	0.001
ITGR	1881	−12	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.006	0.002	0.949	0.004	0.001
ITGR	1882	−3	0.001	0.002	0.001	0.001	0.001	0.001	0.004	0.002	0.001	0.002	0.972	0.002	0.001
RHOD	1444	−16	0.002	0.001	0.006	0.003	0.043	0.002	0.001	0.001	0.002	0.001	0.002	0.004	0.002
RHOD	1454	−2	0.035	0.003	0.01	0.014	0.004	0.001	0.002	0.002	0.002	0.015	0.014	0.004	0.01
RHOD	1505	−3	0.03	0.023	0.003	0.036	0.002	0.014	0.002	0.001	0.03	0.003	0.002	0.008	0.005
RHOD	1592	−14	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001
RHOD	1609	−50	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.001
STBD	1075	−1	0.006	0.005	0.005	0.026	0.003	0.005	0.002	0.838	0.017	0.005	0.001	0.002	0.012
STBD	1714	−5	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.98	0.001	0.001	0	0.001	0.001
STBD	1750	−22	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.982	0.001	0.001	0.001	0.001	0.001
STBD	2403	−17	0.001	0.002	0.001	0.001	0.003	0.001	0.005	0.967	0.001	0.001	0.001	0.005	0.001
STBD	2404	−2	0.001	0.001	0.002	0.001	0.002	0	0.001	0.975	0.001	0.001	0.001	0.001	0.001
CLSP	1008	−1	0.001	0.003	0.003	0.001	0.001	0.976	0	0.001	0.001	0.001	0.001	0.001	0.001
CLSP	1009	0	0	0.001	0	0.001	0.001	0.988	0	0.001	0.001	0.001	0.001	0	0
CLSP	1802	−2	0	0.001	0	0	0	0.992	0	0	0	0	0	0	0
CLSP	2312	−1	0.001	0.001	0.001	0.002	0.001	0.978	0.001	0.001	0.001	0.001	0.001	0.001	0.001
CLSP	2314	0	0	0	0.001	0.001	0.001	0.988	0	0.001	0	0.001	0.001	0	0
AUST	1387	−3	0.006	0.006	0.002	0.003	0.006	0.001	0.003	0.001	0.002	0.004	0.011	0.91	0.004
AUST	1531	−1	0.003	0.004	0.002	0.002	0.004	0.007	0.005	0.002	0.018	0.002	0.001	0.899	0.004
AUST	1564	−7	0.001	0.001	0.001	0.002	0.003	0	0.001	0.001	0.001	0.001	0.003	0.973	0.002
AUST	1870	−5	0.001	0.001	0.002	0.002	0.003	0.003	0.011	0.001	0.001	0.001	0.001	0.95	0.001
AUST	1871	0	0.012	0.009	0.005	0.016	0.002	0.002	0.002	0.003	0.002	0.014	0.001	0.806	0.007
WHWT	1388	−13	0.002	0.001	0.001	0.001	0.002	0.007	0.004	0.001	0.954	0.002	0.007	0.002	0.002
WHWT	1420	−7	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.113	0.856	0.003	0.001	0.002	0.001
WHWT	1992	−5	0.002	0.001	0.001	0.003	0.001	0.006	0.001	0.001	0.968	0.001	0.001	0.001	0.001
WHWT	2100	−4	0.002	0.003	0.005	0.003	0.006	0.001	0.001	0.003	0.948	0.002	0.002	0.001	0.001
WHWT	2128	0	0.002	0.001	0.001	0.002	0.001	0	0.001	0.001	0.979	0.001	0.001	0.001	0.001
CAIR	1405	−1	0.002	0.002	0.002	0.638	0.002	0.007	0.001	0.004	0.28	0.006	0.001	0.002	0.011
CAIR	2096	−28	0.001	0.001	0.003	0.857	0.002	0.002	0.002	0.001	0.076	0.005	0.011	0.002	0.003
CAIR	2113	−4	0.003	0.003	0.003	0.693	0.001	0.001	0.004	0.001	0.242	0.004	0.004	0.002	0.004
CAIR	2125	−1	0.005	0.001	0.005	0.619	0.001	0.001	0.001	0.001	0.332	0.004	0.002	0.002	0.002
CAIR	2131	−8	0.009	0.003	0.002	0.917	0.005	0.003	0.003	0.002	0.007	0.005	0.002	0.004	0.003
BEDT	1422	−5	0.001	0	0.987	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001
BEDT	1423	−8	0	0.001	0.986	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001

TABLE 17C-continued

BEDT	1424	−21	0.001	0.001	0.982	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
BEDT	1426	−30	0.001	0.001	0.981	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
CHIH	1202	−8	0.002	0.002	0.002	0.002	0.003	0.001	0.001	0.003	0.001	0.001	0.002	0.002	0.963
CHIH	1203	−4	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002	0.969
CHIH	1204	0	0.003	0.002	0.002	0.005	0.001	0.002	0.009	0.002	0.002	0.013	0.001	0.006	0.921
CHIH	1205	−2	0.013	0.003	0.001	0.007	0.003	0.004	0.001	0.001	0.002	0.002	0.001	0.001	0.417
CHIH	1206	−1	0.001	0.001	0.003	0.409	0.002	0.007	0.001	0.003	0.002	0.018	0.005	0.029	0.405

	Canid	Canid	Missing	Populations*								
	Population[a]	ID No.	Data	35	36	37	38	39	40	41	42	43
	TURV	1622	−1	0.002	0.002	0.002	0.001	0.002	0.002	0.958	0.004	0.00?
	TURV	2194	−1	0.009	0.005	0.016	0.002	0.01	0.004	0.881	0.019	0.01?
	TURV	2200	0	0.003	0.001	0.008	0.001	0.003	0.001	0.951	0.002	0.00?
	TURV	2222	0	0.005	0.013	0.001	0.001	0.005	0.007	0.907	0.004	0.00?
	BELS	1351	−1	0.001	0.001	0.001	0.002	0.001	0.001	0.967	0.002	0.00?
	BELS	2111	−6	0.002	0.002	0.001	0.008	0.002	0.001	0.954	0.002	0.00?
	BELS	2153	0	0.001	0.001	0.001	0.001	0.001	0.001	0.981	0.001	0.00?
	BELS	2209	−1	0.001	0.001	0.001	0.001	0.001	0	0.973	0.001	0.00?
	BELS	2210	0	0.001	0.001	0.001	0.004	0.001	0.001	0.976	0.001	0.00?
	OES	1984	−1	0.006	0.002	0.001	0.003	0.021	0.001	0.002	0.0?	? .01?
	OES	2171	−4	0.018	0.019	0.002	0.004	0.023	0.002	0.001	0.0?	? .01?
	OES	2179	−9	0.004	0.01	0.005	0.006	0.004	0.002	0.005	0.004	0.00?
	OES	1914	−5	0.002	0.001	0.001	0.002	0.002	0.001	0.001	0.002	0.00?
	OES	2626	−38	0.002	0.002	0.002	0.001	0.002	0.002	0.002	0.002	0.00?
	BORD	1648	−26	0.002	0.958	0.003	0.001	0.002	0.001	0.001	0.002	0.00?
	BORD	1828	−17	0.003	0.749	0.006	0.168	0.003	0.006	0.001	0.004	0.00?
	BORD	1829	−1	0.018	0.823	0.001	0.002	0.02	0.002	0.005	0.014	0.01?
	BORD	2002	−3	0.002	0.955	0.002	0.001	0.003	0.001	0.001	0.003	0.00?
	BORD	2003	−3	0.006	0.886	0.002	0.005	0.005	0.003	0.008	0.011	0.00?
	AUSS	1336	−2	0.26	0.034	0.002	0.005	0.347	0.016	0.005	0.064	0.155
	AUSS	1337	−2	0.015	0.022	0.001	0.002	0.342	0.002	0.003	0.2	0.239
	AUSS	1500	−15	0.003	0.005	0.001	0.001	0.003	0.003	0.001	0.472	0.463
	AUSS	1521	−3	0.073	0.004	0.003	0.002	0.382	0.002	0.001	0.085	0.141
	AUSS	1683	−4	0.128	0.078	0.002	0.002	0.06	0.003	0.002	0.344	0.297
	COLL	1692	−2	0.001	0.003	0.001	0.002	0.001	0.002	0.001	0.001	0.001
	COLL	1701	−11	0.003	0.002	0.001	0.001	0.004	0.005	0.002	0.00?	? .003
	COLL	2284	−16	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.0?	? .002
	COLL	373	−2	0.001	0.001	0.001	0.001	0.001	0	0.001	0.001	0.001
	COLL	379	−3	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001
	SSHP	1379	0	0.006	0.005	0.002	0.013	0.004	0.001	0.001	0.012	0.011
	SSHP	1523	−1	0.006	0.001	0.029	0.005	0.004	0.003	0.003	0.006	0.005
	SSHP	1824	−6	0.002	0.004	0.005	0.004	0.003	0.008	0.066	0.003	0.003
	SSHP	1921	−30	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002	0.002
	SSHP	2040	−19	0.013	0.004	0.002	0.002	0.009	0.001	0.018	0.007	0.008
	DACH	1051	−5	0.002	0.002	0.001	0.001	0.002	0.968	0.001	0.001	0.001
	DACH	1052	−2	0.001	0.001	0.001	0.001	0.001	0.984	0.001	0.001	0.001
	DACH	1053	−2	0.005	0.002	0.007	0.004	0.003	0.915	0.002	0.005	0.004
	DACH	1054	0	0.002	0.001	0.001	0.001	0.001	0.961	0.001	0.001	0.002
	DACH	1055	−1	0.002	0.001	0.001	0.001	0.002	0.971	0.002	0.001	0.002
	DANE	1574	−5	0.002	0.001	0.005	0.037	0.001	0.002	0.004	0.00?	?002
	DANE	1575	−11	0.006	0.002	0.001	0.02	0.005	0.006	0.002	0.0?	? .00?

TABLE 17C-continued

−2	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.00?	1580	DANE
−7	0.002	0.002	0.013	0.001	0.002	0.002	0.002	0.00?	1700	DANE
−3	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.00?	1748	DANE
−21	0.001	0.001	0.985	0.001	0.001	0.001	0.001	0.00?	1581	IWOF
−12	0.001	0.001	0.981	0.001	0.001	0.001	0.001	0.00?	1761	IWOF
−4	0.001	0.001	0.972	0.003	0.001	0.001	0.001	0.00?	1792	IWOF
−6	0.001	0.001	0.982	0.002	0.001	0.001	0.001	0.00?	1906	IWOF
−3	0.001	0	0.972	0.001	0.001	0.001	0.001	0.00?	1993	IWOF
0	0.003	0.002	0.001	0.001	0.004	0.004	0.004	0.00?	1378	BORZ
−4	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.00?	1401	BORZ
−2	0.002	0.001	0.001	0.003	0.003	0.003	0.003	0.00?	1808	BORZ
0	0.007	0.002	0.058	0.002	0.005	0.005	0.005	0.00?	2268	BORZ
−1	0.002	0.001	0.001	0.001	0.001	0.002	0.002	0.00?	978	BORZ
−1	0.012	0.001	0.018	0.005	0.011	0.011	0.011	0.00?	2477	GREY
0	0.002	0.001	0.001	0.001	0.002	0.002	0.002	0.00?	2478	GREY
0	0.004	0.002	0.004	0.002	0.005	0.005	0.005	0.00?	2479	GREY
−3	0.006	0.001	0.012	0.002	0.005	0.005	0.005	0.00?	2480	GREY
−3	0.011	0.005	0.017	0.001	0.006	0.006	0.006	0.00?	2481	GREY
−1	0.002	0.001	0.002	0.001	0.002	0.002	0.002	0.00?	1355	WHIP
−42	0.006	0.02	0.148	0.004	0.02	0.02	0.02	0.00?	1395	WHIP
−2	0.003	0.002	0.083	0.001	0.002	0.002	0.002	0.00?	1407	WHIP
−2	0.001	0.001	0.007	0.001	0.001	0.001	0.001	0.00?	1409	WHIP
−14	0.003	0.002	0.001	0.001	0.003	0.003	0.003	0.00?	1518	WHIP
−1	0.002	0.001	0.003	0.001	0.002	0.002	0.002	0.00?	1568	ITGR
−25	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.00?	1570	ITGR
−5	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.00?	1862	ITGR
−12	0.003	0.003	0.001	0.005	0.002	0.002	0.002	0.00?	1881	ITGR
−3	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.00?	1882	ITGR
−16	0.002	0.004	0.001	0.908	0.003	0.003	0.003	0.00?	1444	RHOD
−2	0.011	0.002	0.009	0.695	0.008	0.008	0.008	0.00?	1454	RHOD
−3	0.01	0.003	0.009	0.774	0.023	0.023	0.023	0.00?	1505	RHOD
−14	0.001	0.001	0.001	0.979	0.001	0.001	0.001	0.00?	1592	RHOD
−50	0.001	0.001	0.001	0.977	0.001	0.001	0.001	0.00?	1609	RHOD
−1	0.02	0.004	0.002	0.001	0.011	0.011	0.011	0.00?	1075	STBD
−5	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.00?	1714	STBD
−22	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.00?	1750	STBD

TABLE 17C-continued

STBD	2403	−17	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.00?
STBD	2404	−2	0.001	0.001	0.003	0.002	0.001	0.002	0.001	0.001	0.00?
CLSP	1008	−1	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.001
CLSP	1009	0	0.001	0.001	0.001	0	0.001	0.001	0	0.001	0.001
CLSP	1802	−2	0	0	0	0	0	0	0	0	0
CLSP	2312	−1	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
CLSP	2314	0	0.001	0.001	0	0.001	0.001	0	0	0.001	0.001
AUST	1387	−3	0.003	0.002	0.015	0.002	0.005	0.003	0.002	0.005	0.004
AUST	1531	−1	0.005	0.017	0.003	0.002	0.005	0.005	0.002	0.00?	? .004
AUST	1564	−7	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.0?	? .001
AUST	1870	−5	0.003	0.002	0.001	0.001	0.004	0.003	0.001	0.003	0.00?
AUST	1871	0	0.006	0.004	0.002	0.083	0.007	0.001	0.003	0.007	0.00?
WHWT	1388	−13	0.002	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.00?
WHWT	1420	−7	0.002	0.002	0.001	0.001	0.002	0.001	0.001	0.002	0.00?
WHWT	1992	−5	0.001	0.001	0.003	0.001	0.001	0.001	0.002	0.001	0.00?
WHWT	2100	−4	0.003	0.002	0.001	0.001	0.003	0.005	0.003	0.002	0.00?
WHWT	2128	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.00?
CAIR	1405	−1	0.008	0.004	0.003	0.002	0.008	0.002	0.004	0.004	0.00?
CAIR	2096	−28	0.004	0.001	0.001	0.002	0.005	0.003	0.001	0.007	0.00?
CAIR	2113	−4	0.005	0.002	0.001	0.002	0.006	0.003	0.003	0.006	0.00?
CAIR	2125	−1	0.004	0.001	0.001	0.004	0.003	0.001	0.005	0.003	0.00?
CAIR	2131	−8	0.004	0.01	0.001	0.001	0.005	0.001	0.002	0.006	0.00?
BEDT	1422	−5	0.001	0.001	0.001	0.001	0.001	0.001	0	0.00?	?00?
BEDT	1423	−8	0.001	0	0.001	0.001	0.001	0.001	0	0.00?	? .00?
BEDT	1424	−21	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.00?
BEDT	1426	−30	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.00?
CHIH	1202	−8	0.002	0.001	0.002	0.003	0.002	0.002	0.002	0.001	0.00?
CHIH	1203	−4	0.002	0.001	0.001	0.001	0.002	0.002	0.002	0.001	0.00?
CHIH	1204	0	0.006	0.003	0.002	0.001	0.007	0.001	0.001	0.005	0.00?
CHIH	1205	−2	0.176	0.003	0.001	0.005	0.113	0.004	0.005	0.118	0.11?
CHIH	1206	−1	0.013	0.018	0.012	0.006	0.011	0.005	0.007	0.021	0.01?

? indicates text missing or illegible when filed

TABLE 17D

Canid Population[a]	Canid ID No.	Missing Data	Populations* 65	66	67	68	69	70	71	72	73	74
CHBR	1546	−4	0.002	0.832	0.008	0.001	0.006	0.003	0.002	0.004	0.004	0.006
CHBR	1549	−4	0.001	0.955	0.001	0.002	0.001	0.001	0.004	0.003	0.004	0.003
CHBR	1813	−3	0.001	0.951	0.002	0.001	0.003	0.003	0.002	0.003	0.002	0.002
CHBR	2091	−1	0.003	0.868	0.005	0.001	0.003	0.003	0.001	0.004	0.022	0.021
CHBR	888	−12	0.002	0.959	0.001	0.009	0.001	0.001	0.001	0.001	0.002	0.001
FCR	1188	−1	0.002	0.001	0.001	0.001	0.221	0.001	0.001	0.001	0.001	0.001
FCR	2020	−11	0.001	0.005	0.001	0.001	0.215	0.001	0.001	0.001	0.002	0.001
FCR	2042	−7	0.002	0.001	0.001	0.001	0.221	0.001	0.001	0.001	0.001	0.001
FCR	2044	0	0.002	0.009	0.001	0.001	0.193	0.002	0.007	0.001	0.001	0.001
FCR	2259	0	0.005	0.001	0.001	0.001	0.213	0.008	0.002	0.002	0.001	0.001
GOLD	591	−3	0.003	0.002	0.003	0.002	0.001	0.002	0.004	0.004	0.001	0.005
GOLD	592	−3	0.001	0.009	0.001	0.003	0.01	0.001	0.002	0.005	0.004	0.01
GOLD	593	−1	0.002	0.003	0.001	0.001	0.001	0.007	0.003	0.001	0.002	0.003
GOLD	603	0	0.001	0.002	0.001	0.002	0.001	0.001	0.001	0.002	0.001	0.001
GOLD	604	0	0.001	0.002	0.001	0.001	0.009	0.002	0.002	0.004	0.002	0.001
LAB	1310	−2	0.008	0.002	0.005	0.102	0.003	0.016	0.002	0.019	0.01	0.012
LAB	1465	−2	0.001	0.003	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001
LAB	1468	−12	0.001	0.004	0.001	0.001	0.005	0.005	0.005	0.001	0.004	0.002
LAB	1754	−12	0.023	0.002	0.002	0.001	0.001	0.002	0.001	0.009	0.005	0.004
LAB	1830	−17	0.001	0.003	0.005	0.021	0.001	0.009	0.003	0.013	0.003	0.002
GSD	1666	−23	0.002	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001
GSD	1776	−9	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001
GSD	2011	−2	0.001	0.001	0.001	0.003	0.001	0.002	0.001	0.001	0.001	0.001
GSD	2060	−2	0.001	0.001	0.001	0.001	0.003	0.001	0.002	0.001	0.001	0.002
GSD	2086	−6	0.003	0.003	0.005	0.001	0.001	0.002	0.001	0.002	0.002	0.001
IRTR	2152	−4	0.75	0.055	0.008	0.053	0.007	0.001	0.001	0.013	0.004	0.003
IRTR	2189	−4	0.987	0.001	0.001	0.001	0.001	0	0	0	0.001	0.001
IRTR	2238	−1	0.973	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
IRTR	2242	−1	0.984	0.001	0.001	0.001	0.001	0	0.001	0.002	0.001	0.001
KERY	13878	0	0.007	0.042	0.006	0.003	0.001	0.001	0.002	0.002	0.91	0.002
KERY	1483	−11	0.001	0.002	0.001	0.002	0.001	0.001	0.001	0.001	0.975	0.001
KERY	1579	−2	0.002	0.001	0.001	0.004	0.001	0.001	0.001	0.002	0.968	0.001
KERY	2014	0	0.003	0.058	0.003	0.002	0.001	0.004	0.001	0.009	0.852	0.006
KERY	24255	−1	0.001	0.001	0.001	0.134	0.002	0.001	0.001	0.001	0.826	0.001
SCWT	1624	−30	0.001	0.001	0.001	0.978	0.001	0.001	0.001	0.001	0.001	0.001
SCWT	1770	−4	0.004	0.001	0.001	0.973	0.001	0.001	0.001	0.001	0.005	0.001
SCWT	2250	−6	0.003	0.001	0.001	0.982	0.001	0.001	0	0.001	0.001	0.001
SCWT	2301	−15	0.001	0.002	0.001	0.975	0.001	0.001	0.001	0.001	0.001	0.001
POM	1190	−2	0.001	0.002	0.001	0.003	0.004	0.001	0.004	0.002	0.004	0.002
POM	1191	−2	0.001	0.002	0.003	0.005	0.005	0.009	0.004	0.02	0.004	0.002
POM	1210	−8	0.007	0.003	0.003	0.007	0.004	0.007	0.007	0.001	0.003	0.007
POM	1238	0	0.003	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.002
POM	1239	−14	0.004	0.005	0.002	0.003	0.001	0.001	0.001	0.002	0.003	0.002
SCHP	1386	−9	0.008	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.002
SCHP	1471	−13	0.002	0.001	0.001	0.001	0.002	0.002	0.001	0.001	0.001	0.002
SCHP	1814	−1	0.001	0.001	0.001	0.001	0.001	0.002	0.028	0.002	0.001	0.001
SCHP	1852	0	0.001	0.001	0.001	0.004	0.001	0.001	0.001	0.001	0.001	0.003
BMD	941	−11	0.001	0.003	0.001	0.002	0.004	0.014	0.007	0.002	0.002	0.002
BMD	943	−10	0.002	0.002	0.001	0.002	0.002	0.005	0.002	0.001	0.002	0.002
BMD	968	−15	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.002	0.001	0.001
BMD	1763	−10	0.012	0.003	0.002	0.002	0.005	0.003	0.003	0.002	0.012	0.002
BMD	969	−2	0.001	0.001	0.001	0.001	0.013	0.002	0.001	0.003	0.004	0.001
GSMD	1547	−4	0.001	0.001	0.001	0.001	0	0.001	0.001	0	0.001	0.001
GSMD	1659	0	0.002	0.001	0.001	0.001	0.001	0.001	0.003	0.001	0.002	0.001
GSMD	1660	−4	0.003	0.003	0.007	0.005	0.001	0.002	0.002	0.002	0.002	0.002
GSMD	1662	−42	0.001	0.004	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
GSMD	1663	−5	0.001	0.001	0	0.001	0	0.001	0	0.001	0.001	0
BOX	1176	0	0.001	0.001	0	0	0.981	0.001	0.001	0.001	0.001	0.002
BOX	1177	−1	0.004	0.021	0.002	0.002	0.912	0.001	0.006	0.002	0.002	0.003
BOX	1178	0	0.001	0.001	0.003	0.001	0.978	0.001	0.001	0.002	0.002	0.001
BOX	1179	−3	0.001	0	0.001	0	0.988	0.001	0.001	0.001	0	0.001
BOX	1304	−1	0.001	0.001	0.001	0.001	0.984	0.001	0.001	0.001	0.001	0.002
MBLT	1915	−5	0.003	0.001	0.956	0.001	0.002	0.001	0.001	0.002	0.003	0.002
MBLT	2253	−12	0.001	0.001	0.979	0.002	0.001	0.001	0.001	0.001	0.001	0.001
MBLT	2254	−33	0.001	0.001	0.989	0.001	0.001	0.001	0.001	0.001	0	0.001
MBLT	2255	−23	0.002	0.001	0.98	0.001	0.001	0.001	0.001	0.001	0.001	0.001
MBLT	2256	−34	0.001	0.001	0.981	0.001	0.002	0.002	0.001	0.001	0.001	0.001
BULD	1193	−1	0.001	0.002	0.003	0.001	0.002	0.002	0.001	0.003	0.009	0.003
BULD	1194	−2	0.001	0.001	0.001	0.009	0.001	0.002	0.002	0.003	0.002	0.002
BULD	1195	−8	0.005	0.001	0.001	0.002	0.001	0.001	0.001	0.003	0.001	0.002
BULD	1197	−3	0.001	0.001	0.002	0.001	0.001	0.001	0.005	0.001	0.001	0.001
BULD	1198	0	0.001	0.004	0.002	0.001	0.002	0.002	0.001	0.005	0.003	0.003
FBLD	1507	−9	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001

TABLE 17D-continued

FBLD	1508	−7	0.001	0.003	0.003	0.004	0.004	0.002	0.001	0.003	0.008	0.003
FBLD	1509	−5	0.001	0.001	0.002	0.002	0.002	0.001	0.002	0.001	0.001	0.001
FBLD	2671	−15	0.017	0.001	0.05	0.003	0.001	0.001	0.001	0.003	0.001	0.002
PRES	1082	−4	0.002	0.003	0.12	0.001	0.012	0.002	0.001	0.016	0.002	0.002
PRES	1096	0	0.003	0.018	0.003	0.001	0.007	0.006	0.002	0.007	0.05	0.748
PRES	1115	0	0.001	0.002	0.015	0.002	0.016	0.002	0.001	0.003	0.002	0.926
PRES	1127	−7	0.002	0.021	0.003	0.001	0.011	0.002	0.006	0.002	0.001	0.817
PRES	1095	−5	0.005	0.003	0.009	0.013	0.006	0.002	0.002	0.014	0.007	0.909
BULM	1105	0	0.008	0.003	0.003	0.002	0.008	0.011	0.001	0.922	0.001	0.005
BULM	1106	−3	0.002	0.009	0.003	0.002	0.001	0.004	0.001	0.902	0.002	0.007
BULM	1107	−1	0.002	0.002	0.001	0.001	0.003	0.001	0.001	0.972	0.001	0.001
BULM	1108	0	0.016	0.01	0.065	0.005	0.001	0.002	0.001	0.844	0.004	0.015
BULM	1109	0	0.005	0.001	0.007	0.004	0.007	0.001	0.002	0.915	0.002	0.01
MAST	1015	0	0.001	0.001	0.004	0.002	0.001	0.001	0.001	0.968	0.004	0.001
MAST	1016	0	0.002	0.002	0.001	0.001	0.001	0.001	0.001	0.911	0.003	0.002
MAST	1017	−25	0.002	0.001	0.001	0.002	0.002	0.002	0.001	0.964	0.002	0.002
MAST	1066	−3	0.001	0.002	0.002	0.001	0.001	0.001	0.002	0.962	0.002	0.001
MAST	991	−18	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.977	0.003	0.001
NEWF	271	−2	0.002	0.004	0.001	0.001	0.005	0.874	0.01	0.002	0.002	0.016
NEWF	274	−1	0.001	0.001	0.002	0.001	0.001	0.968	0.001	0.002	0.001	0.001
NEWF	275	−2	0.002	0.002	0.001	0.001	0.001	0.979	0.002	0.001	0.001	0.001
NEWF	277	0	0.002	0.001	0.001	0.001	0.006	0.904	0.005	0.02	0.001	0.002
NEWF	278	−2	0.002	0.003	0.001	0.001	0.002	0.667	0.003	0.005	0.002	0.203
ROTT	1014	−2	0.003	0.005	0.001	0.004	0.001	0.011	0.933	0.002	0.001	0.001
ROTT	1028	−3	0.001	0.001	0	0	0.001	0.003	0.981	0	0	0.001
ROTT	1029	−1	0.001	0.002	0.002	0.006	0.001	0.007	0.939	0.001	0.001	0.001
ROTT	1033	−4	0.002	0.002	0.003	0.001	0.001	0.003	0.963	0.002	0.001	0.003
ROTT	1034	0	0.001	0.002	0.001	0.001	0.004	0.001	0.967	0.001	0.002	0.001

Canid	Populations*										
Population[a]	75	76	77	78	79	80	81	82	83	84	85
CHBR	0.031	0.008	0.003	0.007	0.044	0.005	0.014	0.009	0.002	0.002	0.006
CHBR	0.002	0.004	0.001	0.002	0.003	0.001	0.002	0.004	0.001	0.003	0.001
CHBR	0.002	0.002	0.005	0.003	0.006	0.002	0.002	0.001	0.003	0.003	0.001
CHBR	0.002	0.007	0.002	0.002	0.007	0.007	0.004	0.027	0.001	0.002	0.009
CHBR	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.002	0.001	0.01
FCR	0.005	0.002	0.002	0.001	0.001	0.002	0.002	0.748	0.001	0.001	0.004
FCR	0.002	0.001	0.001	0.001	0.003	0.001	0.002	0.759	0.001	0.001	0.001
FCR	0.001	0.001	0.001	0	0.001	0.001	0.001	0.759	0.001	0.004	0.001
FCR	0.003	0.004	0.004	0.002	0.002	0.001	0.002	0.746	0.001	0.011	0.004
FCR	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.754	0.001	0.001	0.002
GOLD	0.027	0.003	0.001	0.001	0.925	0.002	0.003	0.01	0.001	0.001	0.001
GOLD	0.144	0.07	0.003	0.001	0.642	0.005	0.019	0.063	0.001	0.002	0.003
GOLD	0.006	0.003	0.004	0.001	0.95	0.002	0.003	0.002	0.002	0.001	0.003
GOLD	0.001	0.001	0.002	0.001	0.979	0.001	0.001	0.001	0.001	0.001	0
GOLD	0.001	0.002	0.004	0.011	0.939	0.003	0.002	0.005	0.002	0.001	0.003
LAB	0.547	0.045	0.001	0.008	0.002	0.004	0.029	0.179	0.003	0.003	0.002
LAB	0.745	0.001	0.003	0.002	0.002	0.001	0.001	0.23	0.001	0.001	0.001
LAB	0.728	0.004	0.002	0.001	0.001	0.001	0.002	0.222	0.001	0.005	0.001
LAB	0.703	0.004	0.002	0.003	0.006	0.002	0.007	0.214	0.006	0.001	0.001
LAB	0.359	0.082	0.001	0.006	0.027	0.001	0.363	0.095	0.002	0.001	0.002
GSD	0.001	0.001	0.006	0.977	0.001	0.001	0.001	0.001	0.001	0.001	0.001
GSD	0.001	0.001	0.003	0.98	0.001	0.001	0.001	0.001	0.001	0.002	0.001
GSD	0.001	0.001	0.002	0.975	0.001	0.001	0.002	0.001	0.001	0.001	0.001
GSD	0.001	0.001	0.001	0.977	0.001	0.001	0.001	0.001	0.001	0.001	0.001
GSD	0.003	0.002	0.003	0.961	0.002	0.001	0.003	0.002	0.001	0.001	0.002
IRTR	0.008	0.034	0.002	0.002	0.005	0.003	0.009	0.036	0.001	0.002	0.002
IRTR	0.001	0.001	0.001	0	0	0.001	0	0.001	0.001	0	0.001
IRTR	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.003	0.001	0.001	0.004
IRTR	0.001	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001
KERY	0.003	0.003	0.005	0.001	0.001	0.001	0.001	0.002	0.003	0.001	0.001
KERY	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.003
KERY	0.003	0.001	0.001	0.001	0.004	0.001	0.002	0.002	0.001	0.001	0.001
KERY	0.006	0.005	0.002	0.002	0.002	0.028	0.004	0.002	0.002	0.001	0.007
KERY	0.001	0.001	0.001	0.001	0.001	0.003	0.002	0.001	0.002	0.013	0.005
SCWT	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.003	0.001
SCWT	0.001	0.001	0.001	0	0.001	0.001	0.002	0.001	0.004	0.001	0.001
SCWT	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001
SCWT	0.001	0.001	0.001	0.002	0.001	0	0.001	0.003	0.001	0.001	0.002
POM	0.004	0.005	0.026	0.001	0.008	0.895	0.022	0.003	0.003	0.003	0.006
POM	0.005	0.004	0.003	0.009	0.002	0.892	0.003	0.007	0.011	0.008	0.002
POM	0.004	0.007	0.007	0.002	0.003	0.908	0.003	0.002	0.001	0.008	0.005
POM	0.001	0.002	0.001	0.001	0.001	0.975	0.001	0.001	0.001	0.001	0.001
POM	0.03	0.352	0.002	0.001	0.005	0.553	0.025	0.001	0.002	0.002	0.002
SCHP	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.969

TABLE 17D-continued

SCHP	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.003	0.001	0.001	0.972
SCHP	0.001	0.002	0.006	0.002	0.004	0.002	0.001	0.001	0.001	0.001	0.941
SCHP	0.002	0.001	0.002	0.001	0.001	0.002	0.001	0.004	0.001	0.002	0.966
BMD	0.001	0.002	0.94	0.001	0.003	0.003	0.004	0.001	0.001	0.005	0.001
BMD	0.005	0.005	0.869	0.002	0.002	0.087	0.004	0.002	0.001	0.002	0.001
BMD	0.001	0.002	0.973	0.001	0.004	0.001	0.001	0.001	0.001	0.001	0.001
BMD	0.001	0.002	0.916	0.005	0.007	0.005	0.002	0.002	0.01	0.001	0.003
BMD	0.002	0.001	0.954	0.002	0.002	0.001	0.002	0.002	0.002	0.003	0.001
GSMD	0.001	0.001	0.986	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
GSMD	0.001	0.001	0.976	0.001	0.002	0.002	0.001	0.001	0.001	0.001	0.001
GSMD	0.002	0.002	0.932	0.023	0.001	0.002	0.002	0.001	0.001	0.001	0.001
GSMD	0.001	0.002	0.97	0.001	0.002	0.001	0.004	0.001	0.002	0.001	0.001
GSMD	0.001	0.001	0.988	0.001	0	0.001	0	0.001	0.001	0	0.001
BOX	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001
BOX	0.002	0.003	0.002	0.002	0.006	0.014	0.003	0.005	0.002	0.002	0.003
BOX	0.001	0.001	0	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001
BOX	0.001	0.001	0.001	0	0	0.001	0.001	0	0.001	0.001	0.001
BOX	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
MBLT	0.002	0.002	0.001	0.001	0.001	0.001	0.002	0.004	0.002	0.004	0.01
MBLT	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001
MBLT	0.001	0.001	0	0	0.001	0.001	0.001	0.001	0.001	0.001	0.001
MBLT	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.004	0.001	0.001	0.001
MBLT	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001
BULD	0.005	0.002	0.002	0.001	0.001	0.002	0.006	0.002	0.001	0.952	0.001
BULD	0.002	0.002	0.001	0	0.001	0.003	0.001	0.001	0.009	0.952	0.002
BULD	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.974	0.001
BULD	0.003	0.002	0.001	0.001	0.001	0.001	0.002	0.002	0.001	0.97	0.001
BULD	0.002	0.002	0.005	0.001	0.001	0.003	0.002	0.002	0.013	0.944	0.001
FBLD	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.984	0.001	0.001
FBLD	0.002	0.002	0.001	0.001	0.002	0.01	0.002	0.001	0.939	0.002	0.004
FBLD	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.95	0.029	0.001
FBLD	0.001	0.002	0.002	0.001	0.002	0.001	0.004	0.001	0.9	0.001	0.004
PRES	0.043	0.015	0.002	0.001	0.001	0.003	0.757	0.002	0.002	0.013	0.002
PRES	0.002	0.008	0.002	0.032	0.001	0.002	0.014	0.005	0.001	0.082	0.008
PRES	0.002	0.003	0.001	0.001	0.009	0.001	0.003	0.002	0.003	0.003	0.001
PRES	0.01	0.017	0.004	0.002	0.004	0.006	0.004	0.003	0.02	0.059	0.005
PRES	0.003	0.004	0.002	0.002	0.002	0.002	0.003	0.001	0.005	0.003	0.002
BULM	0.002	0.003	0.003	0.001	0.005	0.002	0.004	0.002	0.004	0.006	0.002
BULM	0.007	0.004	0.002	0.001	0.024	0.002	0.006	0.002	0.003	0.006	0.007
BULM	0.001	0.002	0.001	0.001	0.001	0.002	0.002	0.002	0.001	0.001	0.001
BULM	0.003	0.004	0.002	0.008	0.002	0.003	0.003	0.003	0.002	0.003	0.004
BULM	0.003	0.003	0.001	0.005	0.002	0.003	0.003	0.006	0.001	0.018	0.001
MAST	0.001	0.002	0.002	0.001	0.003	0.002	0.001	0.001	0.002	0.001	0.001
MAST	0.002	0.002	0.003	0.001	0.001	0.002	0.004	0.001	0.002	0.055	0.001
MAST	0.001	0.002	0.002	0.003	0.002	0.001	0.002	0.002	0.001	0.002	0.003
MAST	0.002	0.003	0.001	0.001	0.002	0.001	0.007	0.001	0.003	0.003	0.001
MAST	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001
NEWF	0.006	0.009	0.006	0.002	0.01	0.015	0.006	0.014	0.005	0.005	0.004
NEWF	0.005	0.002	0.002	0.002	0.002	0.001	0.002	0.002	0.001	0.001	0.001
NEWF	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.001	0
NEWF	0.034	0.002	0.001	0.004	0.001	0.001	0.003	0.011	0.001	0.001	0.001
NEWF	0.013	0.057	0.001	0.015	0.003	0.004	0.01	0.004	0.002	0.002	0.001
ROTT	0.002	0.004	0.008	0.004	0.002	0.004	0.005	0.001	0.004	0.002	0.002
ROTT	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001
ROTT	0.004	0.003	0.007	0.008	0.004	0.001	0.002	0.003	0.002	0.002	0.001
ROTT	0.002	0.003	0.001	0.001	0.002	0.001	0.004	0.001	0.001	0.002	0.002
ROTT	0.001	0.001	0.004	0.003	0.001	0.001	0.001	0.001	0.004	0.001	0.001

[a]See Table 5 for abbreviations of canid populations.

*All values for the populations that are not shown are zero.

KBB:pbe

TABLE 18A-F

Population	Canid ID No.		
AMAL	1629	0.998	0.002
AMAL	1779	0.997	0.003
AMAL	1845	0.997	0.003
AMAL	2132	0.987	0.013
AMAL	2214	0.997	0.003
HUSK	1469	0.003	0.997
HUSK	1883	0.001	0.999
HUSK	2115	0.003	0.997
HUSK	2117	0.006	0.994

TABLE 18A-F-continued

Population	Canid ID No.		
HUSK	2118	0.005	0.995
BULM	1105	0.003	0.997
BULM	1106	0.002	0.998
BULM	1107	0.002	0.998
BULM	1108	0.006	0.994
BULM	1109	0.003	0.997
MAST	1015	0.998	0.002
MAST	1016	0.997	0.003
MAST	1017	0.995	0.005

TABLE 18A-F-continued

Population	Canid ID No.		
MAST	1066	0.997	0.003
MAST	991	0.995	0.005
BMD	941	0.002	0.998
BMD	943	0.003	0.997
BMD	968	0.001	0.999
BMD	1763	0.002	0.998
BMD	969	0.002	0.998
GSMD	1547	0.998	0.002
GSMD	1659	0.997	0.003
GSMD	1660	0.999	0.001
GSMD	1662	0.997	0.003
GSMD	1663	0.998	0.002
GREY	2477	0.005	0.995
GREY	2478	0.007	0.993
GREY	2479	0.003	0.997
GREY	2480	0.003	0.997
GREY	2481	0.005	0.995
WHIP	1355	0.993	0.007
WHIP	1395	0.992	0.008
WHIP	1407	0.919	0.081
WHIP	1409	0.997	0.003
WHIP	1518	0.976	0.024

TABLE 18A-F-continued

Population	Canid ID No.		
BELS	1351	0.515	0.485
BELS	2111	0.515	0.485
BELS	22153	0.504	0.496
BELS	2209	0.504	0.496
BELS	2210	0.522	0.478
TURV	1622	0.517	0.483
TURV	2194	0.521	0.479
TURV	2200	0.527	0.473
TURV	2222	0.514	0.486
COLL	1692	0.003	0.997
COLL	1701	0.005	0.995
COLL	2284	0.002	0.998
COLL	373	0.003	0.997
COLL	379	0.003	0.997
SSHP	1379	0.996	0.004
SSHP	1523	0.998	0.002
SSHP	1824	0.998	0.002
SSHP	1921	0.998	0.002
SSHP	2040	0.997	0.003

* See Table 5 for abbreviations of canid populations.

TABLE 19A

Canid Population[a]	Canid ID No.	k = 4, 15 Run Average Pop1	Pop2	Pop3	Pop4
SHIB	1769	0.9862	0.00393333	0.00473333	0.00493333
SHIB	1854	0.9806	0.0052	0.00626667	0.00793333
SHIB	1856	0.94133333	0.01373333	0.02513333	0.02
SHIB	1860	0.98093333	0.0056	0.00733333	0.00653333
SHIB	1981	0.98026667	0.00573333	0.00753333	0.00653333
CHOW	1633	0.98393333	0.00593333	0.0052	0.005
CHOW	1835	0.986	0.00473333	0.00366667	0.00546667
CHOW	1837	0.9802	0.00813333	0.00606667	0.00553333
CHOW	1838	0.98626667	0.0044	0.0048	0.0048
CHOW	1839	0.97853333	0.0088	0.00573333	0.0068
AKIT	1130	0.94546667	0.0058	0.0374	0.01133333
AKIT	1131	0.97693333	0.00486667	0.0144	0.0038
AKIT	1132	0.9882	0.00453333	0.00333333	0.00393333
AKIT	1133	0.98713333	0.00546667	0.00393333	0.00366667
AKIT	1134	0.98873333	0.00266667	0.00353333	0.00526667
AMAL	1629	0.87893333	0.06	0.0244	0.03693333
AMAL	1779	0.7818	0.01673333	0.01706667	0.1842
AMAL	1845	0.9252	0.02833333	0.02626667	0.0202
AMAL	2132	0.91766667	0.02413333	0.01786667	0.04006667
AMAL	2214	0.91493333	0.01646667	0.03	0.0388
BSJI	1338	0.7572	0.0864	0.02133333	0.1354
BSJI	1339	0.96393333	0.01353333	0.0158	0.00686667
BSJI	1645	0.97746667	0.00886667	0.00626667	0.00733333
BSJI	1675	0.95526667	0.02933333	0.00886667	0.00673333
BSJI	1717	0.97253333	0.00953333	0.00733333	0.01033333
SHAR	1573	0.95946667	0.0204	0.00653333	0.01366667
SHAR	1593	0.85086667	0.111	0.02073333	0.0172
SHAR	1619	0.90013333	0.0718	0.01546667	0.0128
SHAR	1998	0.8014	0.02793333	0.09453333	0.07633333
SHAR	1999	0.956	0.01933333	0.0078	0.01686667
HUSK	1469	0.90333333	0.02393333	0.0232	0.04973333
HUSK	1883	0.8904	0.00786667	0.07193333	0.02953333
HUSK	2115	0.77413333	0.0192	0.09933333	0.1074
HUSK	2117	0.67213333	0.027	0.1188	0.18193333
HUSK	2118	0.90086667	0.02786667	0.04093333	0.03006667
AFGH	1812	0.56573333	0.02113333	0.06673333	0.3464
AFGH	1939	0.6262	0.03553333	0.1018	0.23666667
AFGH	2264	0.55926667	0.05073333	0.0692	0.3208
AFGH	1936	0.74713333	0.05586667	0.05413333	0.14273333
AFGH	1937	0.67166667	0.0436	0.04986667	0.23486667
SALU	1491	0.4006	0.04506667	0.06466667	0.4898
SALU	1535	0.49886667	0.01166667	0.05393333	0.4354
SALU	1607	0.45526667	0.02433333	0.04333333	0.477
SALU	1873	0.2272	0.06186667	0.08613333	0.62433333

TABLE 19A-continued

Canid	Canid	k = 4, 15 Run Average			
Population[a]	ID No.	Pop1	Pop2	Pop3	Pop4
SALU	2610	0.37806667	0.0618	0.0416	0.5184
TIBT	1466	0.49693333	0.0552	0.18146667	0.26653333
TIBT	1562	0.36673333	0.1172	0.24446667	0.27173333
TIBT	1707	0.38166667	0.2034	0.04906667	0.36593333
TIBT	26078	0.43486667	0.0804	0.101	0.38373333
TIBT	28086	0.16093333	0.14593333	0.12653333	0.56666667
LHSA	1524	0.35406667	0.01493333	0.55546667	0.0756
LHSA	1525	0.44253333	0.01693333	0.4188	0.12166667
LHSA	1526	0.331	0.03193333	0.42106667	0.21606667
LHSA	1528	0.28613333	0.07026667	0.5356	0.10806667
LHSA	2074	0.59526667	0.01573333	0.28666667	0.1024
SAMO	1375	0.23546667	0.01233333	0.6444	0.1078
SAMO	1532	0.46653333	0.0064	0.48693333	0.04046667
SAMO	1560	0.51173333	0.02726667	0.37386667	0.08686667
SAMO	169	0.3968	0.0122	0.50726667	0.0838
SAMO	239	0.40986667	0.02673333	0.49193333	0.07133333
PEKE	1143	0.30666667	0.0062	0.5552	0.13173333
PEKE	1145	0.1708	0.00693333	0.60313333	0.2192
PEKE	1211	0.1872	0.0086	0.65013333	0.15393333
PEKE	1212	0.14846667	0.1002	0.59466667	0.15693333
PEKE	1213	0.23773333	0.0056	0.6136	0.14306667
SHIH	1393	0.15306667	0.08493333	0.61986667	0.14206667
SHIH	1783	0.14486667	0.00826667	0.70373333	0.14333333
SHIH	2068	0.15553333	0.0106	0.66613333	0.16773333
SHIH	2859	0.20993333	0.01053333	0.69053333	0.08913333
SHIH	2860	0.3304	0.01586667	0.40086667	0.2528
IWOF	1581	0.0168	0.3314	0.57773333	0.0742
IWOF	1761	0.00506667	0.11346667	0.66893333	0.2124
IWOF	1792	0.01426667	0.1258	0.641	0.21893333
IWOF	1906	0.01446667	0.13733333	0.70666667	0.14166667
IWOF	1993	0.00586667	0.11806667	0.65613333	0.22006667
STBD	1075	0.0306	0.2296	0.40906667	0.33073333
STBD	1714	0.01853333	0.08833333	0.6668	0.2266
STBD	1750	0.01566667	0.22233333	0.48973333	0.27226667
STBD	2403	0.00846667	0.0614	0.69553333	0.23453333
STBD	2404	0.0078	0.40166667	0.524	0.0666
GREY	2477	0.0444	0.09686667	0.765	0.0938
GREY	2478	0.01273333	0.05146667	0.75186667	0.18393333
GREY	2479	0.0094	0.17826667	0.6994	0.11306667
GREY	2480	0.01386667	0.04133333	0.8324	0.1126
GREY	2481	0.00573333	0.0872	0.65273333	0.2544
BELS	1351	0.00686667	0.0086	0.96793333	0.0168
BELS	2111	0.0314	0.00953333	0.94333333	0.0158
BELS	2153	0.00373333	0.00453333	0.98086667	0.0108
BELS	2209	0.01126667	0.0056	0.9696	0.01353333
BELS	2210	0.01166667	0.01566667	0.94853333	0.02413333
TURV	1622	0.00333333	0.0054	0.97573333	0.01573333
TURV	2194	0.01046667	0.05633333	0.799	0.13413333
TURV	2200	0.01726667	0.01913333	0.90673333	0.05713333
TURV	2222	0.00473333	0.01653333	0.84253333	0.13633333
BORZ	1378	0.05593333	0.01486667	0.7554	0.17386667
BORZ	1401	0.0358	0.03173333	0.68146667	0.25066667
BORZ	1808	0.064	0.0278	0.66526667	0.2428
BORZ	2268	0.02186667	0.0252	0.81853333	0.13446667
BORZ	978	0.0262	0.02046667	0.68133333	0.2722
COLL	1692	0.00513333	0.0512	0.718	0.22553333
COLL	1701	0.01646667	0.01206667	0.76006667	0.21133333
COLL	2284	0.0048	0.01013333	0.786	0.19926667
COLL	373	0.00393333	0.01066667	0.78246667	0.2028
COLL	379	0.00393333	0.0094	0.7856	0.20113333
SSHP	1379	0.02233333	0.19673333	0.5936	0.18726667
SSHP	1523	0.02086667	0.04446667	0.73086667	0.20373333
SSHP	1824	0.0084	0.168	0.65733333	0.16646667
SSHP	1921	0.00573333	0.08706667	0.6808	0.22633333
SSHP	2040	0.0296	0.03046667	0.7582	0.18166667
PUG	1077	0.00746667	0.0072	0.4794	0.50606667
PUG	1104	0.0188	0.0076	0.49706667	0.47646667
PUG	1183	0.07146667	0.01226667	0.4226	0.49393333
PUG	1184	0.0082	0.00713333	0.495	0.48966667
PUG	1192	0.006	0.05273333	0.438	0.50326667
KOMO	1484	0.02893333	0.08226667	0.29953333	0.5892
KOMO	1964	0.03166667	0.1022	0.2362	0.63
KOMO	2321	0.04006667	0.13546667	0.2222	0.6022

TABLE 19A-continued

Canid	Canid	k = 4, 15 Run Average			
Population[a]	ID No.	Pop1	Pop2	Pop3	Pop4
KOMO	2323	0.08526667	0.10286667	0.14026667	0.67173333
KOMO	2334	0.00913333	0.08426667	0.1342	0.77246667
WHIP	1355	0.0062	0.05526667	0.4162	0.52246667
WHIP	1395	0.00873333	0.09993333	0.4982	0.39313333
WHIP	1407	0.00713333	0.12913333	0.30046667	0.56313333
WHIP	1409	0.00566667	0.05026667	0.72593333	0.218
WHIP	1518	0.0056	0.10146667	0.45786667	0.435
SPOO	1530	0.05693333	0.25666667	0.36106667	0.3252
SPOO	1582	0.07346667	0.11826667	0.38393333	0.42473333
SPOO	1876	0.0106	0.12953333	0.50726667	0.35246667
SPOO	1877	0.0136	0.16693333	0.37186667	0.44753333
SPOO	2337	0.00593333	0.0468	0.2268	0.7206
BICH	1943	0.0758	0.0702	0.35546667	0.4986
BICH	1954	0.14973333	0.05386667	0.31746667	0.47873333
BICH	933	0.03653333	0.1844	0.31173333	0.46746667
BICH	974	0.07046667	0.0902	0.29946667	0.53993333
KEES	1501	0.03973333	0.03486667	0.5276	0.39786667
KEES	1589	0.00533333	0.03853333	0.44706667	0.5092
KEES	1818	0.02126667	0.0422	0.4594	0.47733333
KEES	1819	0.00526667	0.0386	0.54426667	0.41153333
KEES	2072	0.0064	0.06153333	0.4162	0.51586667
MNTY	1539	0.01293333	0.2696	0.13173333	0.5856
MNTY	1732	0.0262	0.15633333	0.1496	0.66773333
MNTY	2145	0.01133333	0.20213333	0.35033333	0.4362
MNTY	2149	0.01066667	0.06813333	0.57466667	0.34666667
NELK	2216	0.05673333	0.1076	0.30873333	0.52693333
NELK	2239	0.18626667	0.03333333	0.4914	0.289
NELK	2240	0.02666667	0.1904	0.44286667	0.34013333
NELK	2281	0.012	0.0752	0.10806667	0.80493333
NELK	2295	0.24066667	0.04506667	0.29186667	0.42233333
KUVZ	1482	0.0566	0.0156	0.52573333	0.4018
KUVZ	1551	0.18713333	0.02206667	0.41506667	0.3758
KUVZ	1672	0.07186667	0.05426667	0.20386667	0.66993333
KUVZ	1913	0.02453333	0.06113333	0.34526667	0.56926667
KUVZ	1994	0.04446667	0.06193333	0.40193333	0.49186667
DANE	1574	0.01126667	0.086	0.17386667	0.72873333
DANE	1575	0.1096	0.12853333	0.19233333	0.5696
DANE	1580	0.0112	0.0698	0.21413333	0.705
DANE	1700	0.00773333	0.06426667	0.41106667	0.51706667
DANE	1748	0.19526667	0.07813333	0.20826667	0.51826667
WSSP	1955	0.00506667	0.0726	0.3252	0.59726667
WSSP	2139	0.01333333	0.0658	0.24086667	0.67993333
WSSP	2143	0.00386667	0.07613333	0.20346667	0.71646667
WSSP	2195	0.0078	0.10353333	0.29773333	0.59093333
WSSP	2286	0.0054	0.09933333	0.20973333	0.68546667
DOBP	1031	0.007	0.08406667	0.18426667	0.7248
DOBP	1032	0.03506667	0.09113333	0.1938	0.68006667
DOBP	1749	0.01766667	0.17506667	0.19726667	0.60986667
DOBP	2162	0.00786667	0.08273333	0.19973333	0.70986667
DOBP	2245	0.0054	0.0814	0.1972	0.71593333
SSNZ	13352	0.00353333	0.26246667	0.1206	0.61326667
SSNZ	1360	0.00353333	0.12506667	0.1222	0.74906667
SSNZ	1827	0.00653333	0.092	0.19446667	0.70726667
SSNZ	20457	0.0084	0.07666667	0.22706667	0.6882
SSNZ	22647	0.00753333	0.18713333	0.16033333	0.64526667
ITGY	1568	0.03193333	0.076	0.1174	0.77473333
ITGY	1570	0.01333333	0.0768	0.0818	0.82806667
ITGY	1862	0.10826667	0.06413333	0.08133333	0.74633333
ITGY	1881	0.042	0.06533333	0.0726	0.82
ITGY	1882	0.172	0.05926667	0.12893333	0.6398
OES	1984	0.0208	0.0792	0.06466667	0.83533333
OES	2171	0.0094	0.07693333	0.17926667	0.7344
OES	2179	0.01033333	0.08166667	0.1854	0.72273333
OES	1914	0.02013333	0.12153333	0.10093333	0.75773333
OES	2626	0.05893333	0.0684	0.0808	0.79173333
AMWS	2168	0.01106667	0.07626667	0.16186667	0.7508
AMWS	2279	0.01213333	0.13833333	0.1118	0.73766667
AMWS	2327	0.06306667	0.14373333	0.07946667	0.71366667
AMWS	987	0.0132	0.09766667	0.17166667	0.71766667
AMWS	988	0.0164	0.17813333	0.12913333	0.6764
MSNZ	1587	0.00553333	0.15366667	0.11553333	0.72533333
MSNZ	1756	0.00593333	0.07446667	0.16326667	0.75586667
MSNZ	1851	0.00406667	0.09013333	0.1284	0.77753333

TABLE 19A-continued

Canid Population[a]	Canid ID No.	k = 4, 15 Run Average Pop1	Pop2	Pop3	Pop4
MSNZ	2034	0.026	0.2376	0.1144	0.62193333
MSNZ	2613	0.00513333	0.12266667	0.12486667	0.74726667
AUST	1387	0.04046667	0.11066667	0.20053333	0.6482
AUST	1531	0.0178	0.139	0.06606667	0.77713333
AUST	1564	0.00726667	0.0902	0.0582	0.8444
AUST	1870	0.0388	0.1046	0.13213333	0.7246
AUST	1871	0.00673333	0.0902	0.06326667	0.84006667
ECKR	1376	0.004	0.11126667	0.0808	0.8038
ECKR	1377	0.00406667	0.08373333	0.14606667	0.76593333
ECKR	1400	0.0034	0.06993333	0.26133333	0.66546667
ECKR	1404	0.0034	0.09186667	0.23986667	0.66486667
ECKR	1511	0.0068	0.08413333	0.18326667	0.72573333
IRSE	1540	0.00333333	0.0736	0.08586667	0.83726667
IRSE	1617	0.0038	0.072	0.07486667	0.8494
IRSE	1896	0.00906667	0.07533333	0.11866667	0.79666667
IRSE	2084	0.00406667	0.06606667	0.2228	0.70706667
IRSE	2085	0.00326667	0.0842	0.0818	0.831
WHWT	1388	0.0142	0.0704	0.05473333	0.86053333
WHWT	1420	0.0452	0.0842	0.08166667	0.7888
WHWT	1992	0.0108	0.08613333	0.07613333	0.82693333
WHWT	2100	0.01053333	0.0824	0.04333333	0.86353333
WHWT	2128	0.0158	0.0728	0.03166667	0.87973333
PNTR	1382	0.00826667	0.07166667	0.07566667	0.8442
PNTR	1383	0.01426667	0.07086667	0.0714	0.84353333
PNTR	1869	0.00726667	0.0582	0.12293333	0.81146667
PNTR	1938	0.0098	0.07566667	0.15733333	0.75693333
PNTR	1948	0.05646667	0.0598	0.0958	0.78773333
BASS	1341	0.02966667	0.1016	0.04426667	0.82446667
BASS	1342	0.01053333	0.0758	0.09866667	0.81473333
BASS	1506	0.0078	0.08493333	0.0752	0.8318
BASS	1917	0.00926667	0.10106667	0.04406667	0.84593333
CKCS	1513	0.0408	0.0656	0.12133333	0.77233333
CKCS	1639	0.00753333	0.07806667	0.12053333	0.794
CKCS	1640	0.00806667	0.0998	0.1152	0.77686667
CKCS	1642	0.0048	0.07466667	0.13413333	0.78653333
CKCS	2054	0.00553333	0.07133333	0.1202	0.80293333
GSNZ	1868	0.27746667	0.06873333	0.06233333	0.5912
GSNZ	22739	0.1848	0.06566667	0.06806667	0.68133333
GSNZ	27093	0.05206667	0.08053333	0.06046667	0.807
GSNZ	27106	0.0098	0.10226667	0.0224	0.8656
GSNZ	33390	0.0082	0.09093333	0.0874	0.81346667
PHAR	1292	0.12533333	0.05726667	0.0088	0.80886667
PHAR	1947	0.1386	0.05446667	0.01913333	0.78773333
PHAR	1962	0.13706667	0.0674	0.06313333	0.7326
PHAR	1963	0.10473333	0.0708	0.012	0.81246667
GOLD	591	0.00453333	0.15633333	0.02266667	0.8164
GOLD	592	0.02186667	0.2448	0.0112	0.72213333
GOLD	593	0.00693333	0.1734	0.01473333	0.80526667
GOLD	603	0.0058	0.148	0.009	0.83726667
GOLD	604	0.00386667	0.19653333	0.03653333	0.76313333
BEAG	1323	0.012	0.169	0.01126667	0.80753333
BEAG	1324	0.01733333	0.09226667	0.126	0.7644
BEAG	1327	0.00813333	0.2708	0.0204	0.70093333
BEAG	994	0.029	0.25213333	0.06993333	0.64906667
BEAG	995	0.01573333	0.0918	0.06013333	0.83213333
BLDH	1186	0.0088	0.224	0.02646667	0.7406
BLDH	1223	0.0126	0.15126667	0.01466667	0.82126667
BLDH	1410	0.0056	0.3068	0.00726667	0.68026667
BLDH	1942	0.00893333	0.17273333	0.00906667	0.80933333
BLDH	1957	0.00693333	0.16	0.01146667	0.82153333
AIRT	1603	0.03993333	0.15466667	0.11033333	0.69526667
AIRT	1604	0.00613333	0.08966667	0.12693333	0.7772
AIRT	1788	0.00466667	0.20253333	0.09266667	0.70013333
AIRT	1875	0.01793333	0.09733333	0.13313333	0.7516
ACKR	1035	0.0102	0.09006667	0.08406667	0.8156
ACKR	2261	0.02313333	0.0972	0.1014	0.77833333
ACKR	2310	0.0038	0.09926667	0.026	0.87086667
ACKR	1956	0.00913333	0.1278	0.02146667	0.84173333
ACKR	2260	0.00533333	0.10193333	0.03026667	0.86233333
AHRT	1120	0.00986667	0.12326667	0.0524	0.8144
AHRT	1121	0.0104	0.18726667	0.04926667	0.753
AHRT	1122	0.00853333	0.1532	0.089	0.74886667
AHRT	1123	0.00866667	0.14433333	0.07606667	0.77093333

TABLE 19A-continued

Canid	Canid	k = 4, 15 Run Average			
Population[a]	ID No.	Pop1	Pop2	Pop3	Pop4
AHRT	1124	0.0076	0.1374	0.05166667	0.80346667
CHBR	1546	0.01113333	0.13993333	0.05573333	0.7932
CHBR	1549	0.06426667	0.33173333	0.01326667	0.5908
CHBR	1813	0.00446667	0.17893333	0.02786667	0.7888
CHBR	2091	0.0086	0.1008	0.038	0.85266667
CHBR	888	0.00506667	0.11486667	0.02473333	0.8552
CAIR	1405	0.00846667	0.277	0.0828	0.6316
CAIR	2096	0.0146	0.07973333	0.03353333	0.87213333
CAIR	2113	0.01413333	0.1012	0.10746667	0.77733333
CAIR	2125	0.0062	0.0752	0.07646667	0.8422
CAIR	2131	0.0292	0.08106667	0.0632	0.82666667
PTWD	P142	0.0074	0.1588	0.11633333	0.71733333
PTWD	P1	0.00453333	0.192	0.1194	0.68413333
PTWD	P238	0.01333333	0.1686	0.17253333	0.64566667
PTWD	P25	0.00413333	0.07453333	0.1428	0.77853333
PTWD	P67	0.00613333	0.07766667	0.1434	0.77266667
GSHP	1628	0.00506667	0.13306667	0.08306667	0.77886667
GSHP	1708	0.02013333	0.08246667	0.20713333	0.69033333
GSHP	1710	0.02533333	0.08533333	0.072	0.8172
GSHP	1833	0.00806667	0.44793333	0.03073333	0.5134
GSHP	1892	0.01533333	0.1122	0.07586667	0.79673333
BORD	1648	0.11253333	0.07173333	0.0404	0.77573333
BORD	1828	0.01326667	0.07473333	0.09166667	0.82006667
BORD	1829	0.00546667	0.24266667	0.13626667	0.61566667
BORD	2002	0.01993333	0.10706667	0.12306667	0.75
BORD	2003	0.03286667	0.08433333	0.11186667	0.77086667
BEDT	1422	0.00793333	0.32966667	0.12893333	0.5334
BEDT	1423	0.00626667	0.1544	0.15853333	0.68086667
BEDT	1424	0.01353333	0.12806667	0.2118	0.64666667
BEDT	1426	0.0142	0.2006	0.16206667	0.62333333
CLSP	1008	0.00746667	0.3506	0.06153333	0.5802
CLSP	1009	0.00386667	0.316	0.075	0.60473333
CLSP	1802	0.00646667	0.32126667	0.07473333	0.59733333
CLSP	2312	0.00413333	0.3918	0.06026667	0.5438
CLSP	2314	0.00473333	0.395	0.06026667	0.53973333
IBIZ	1147	0.0094	0.09326667	0.0498	0.84746667
IBIZ	1148	0.0076	0.2762	0.12373333	0.59233333
IBIZ	1162	0.00813333	0.07513333	0.0816	0.8354
IBIZ	1172	0.02393333	0.09233333	0.1424	0.7416
IBIZ	1280	0.027	0.20926667	0.20173333	0.56186667
RHOD	1444	0.0056	0.13373333	0.17626667	0.68426667
RHOD	1454	0.02113333	0.17686667	0.17033333	0.63213333
RHOD	1505	0.01006667	0.11066667	0.0728	0.80653333
RHOD	1592	0.00833333	0.4782	0.06833333	0.44506667
RHOD	1609	0.00606667	0.1752	0.2602	0.55853333
DACH	1051	0.01053333	0.25333333	0.23673333	0.49933333
DACH	1052	0.00893333	0.2756	0.21553333	0.49993333
DACH	1053	0.0174	0.33433333	0.12966667	0.5186
DACH	1054	0.02753333	0.43573333	0.13406667	0.40273333
DACH	1055	0.00966667	0.27553333	0.24213333	0.47253333
AUSS	1336	0.19213333	0.16606667	0.19266667	0.449
AUSS	1337	0.01626667	0.218	0.16453333	0.60106667
AUSS	1500	0.00893333	0.06726667	0.2208	0.70266667
AUSS	1521	0.11106667	0.43073333	0.18213333	0.27613333
AUSS	1683	0.01366667	0.2222	0.091	0.67313333
CHIH	1202	0.0064	0.22773333	0.1	0.66586667
CHIH	1203	0.0148	0.09106667	0.30626667	0.58766667
CHIH	1204	0.01226667	0.12713333	0.14806667	0.71253333
CHIH	1205	0.0992	0.32273333	0.15366667	0.42466667
CHIN	1206	0.0062	0.37573333	0.09806667	0.51986667
KERY	13878	0.00706667	0.22393333	0.15313333	0.61586667
KERY	1483	0.00713333	0.2578	0.16	0.57506667
KERY	1579	0.0126	0.10493333	0.18953333	0.69286667
KERY	2014	0.0036	0.342	0.07906667	0.5752
KERY	24255	0.00853333	0.35613333	0.15386667	0.48133333
SCHP	1386	0.0076	0.19293333	0.036	0.76353333
SCHP	1471	0.00766667	0.20733333	0.02273333	0.76213333
SCHP	1814	0.01046667	0.289	0.0824	0.6182
SCHP	1852	0.0162	0.13586667	0.15466667	0.69326667
IRTR	2152	0.01113333	0.14993333	0.093	0.746
IRTR	2189	0.01146667	0.36666667	0.08746667	0.53433333
IRTR	2238	0.0052	0.36626667	0.043	0.58546667
IRTR	2242	0.00893333	0.27573333	0.06926667	0.64613333

TABLE 19A-continued

Canid	Canid	k = 4, 15 Run Average			
Population[a]	ID No.	Pop1	Pop2	Pop3	Pop4
FCR	1188	0.0062	0.22606667	0.05746667	0.7102
FCR	2020	0.00506667	0.1566	0.08913333	0.749
FCR	2042	0.0048	0.23086667	0.0638	0.70053333
FCR	2044	0.00613333	0.17806667	0.16073333	0.65506667
FCR	2259	0.0036	0.24293333	0.048	0.70526667
SCWT	1624	0.0506	0.4248	0.08933333	0.4352
SCWT	1770	0.00433333	0.2824	0.31153333	0.40166667
SCWT	2250	0.00513333	0.22033333	0.04646667	0.7282
SCWT	2301	0.0162	0.36513333	0.03973333	0.57913333
POM	1190	0.09806667	0.35386667	0.32793333	0.22
POM	1191	0.00926667	0.7472	0.04853333	0.19473333
POM	1210	0.04093333	0.3494	0.1288	0.48053333
POM	1238	0.00613333	0.16306667	0.26906667	0.56173333
POM	1239	0.1202	0.08513333	0.2394	0.555
LAB	1310	0.11153333	0.54806667	0.0612	0.2794
LAB	1465	0.01346667	0.33846667	0.05966667	0.5884
LAB	1468	0.02113333	0.40553333	0.09626667	0.477
LAB	1754	0.01206667	0.6368	0.01	0.34093333
LAB	1830	0.00533333	0.5134	0.14593333	0.33526667
PRES	1082	0.00793333	0.73346667	0.0294	0.22913333
PRES	1096	0.00493333	0.7488	0.05413333	0.19193333
PRES	1115	0.00993333	0.64406667	0.086	0.2604
PRES	1127	0.10286667	0.85446667	0.01946667	0.0234
PRES	1095	0.05353333	0.82886667	0.03246667	0.08533333
ROTT	1014	0.01153333	0.72453333	0.13553333	0.12833333
ROTT	1028	0.00553333	0.712	0.13746667	0.1448
ROTT	1029	0.0042	0.8398	0.05386667	0.10193333
ROTT	1033	0.006	0.85826667	0.04853333	0.08746667
ROTT	1034	0.00453333	0.85426667	0.11393333	0.02726667
BULM	1105	0.0056	0.94446667	0.01333333	0.03626667
BULM	1106	0.00486667	0.61486667	0.0896	0.2908
BULM	1107	0.01853333	0.90133333	0.026	0.05413333
BULM	1108	0.00653333	0.93873333	0.02386667	0.03073333
BULM	1109	0.00513333	0.96613333	0.00746667	0.0212
NEWF	271	0.0132	0.866	0.0532	0.0676
NEWF	274	0.00526667	0.94806667	0.00966667	0.03706667
NEWF	275	0.00733333	0.97226667	0.0052	0.01533333
NEWF	277	0.00586667	0.97893333	0.00673333	0.00833333
NEWF	278	0.06706667	0.8476	0.01493333	0.07053333
GSD	1666	0.00613333	0.88413333	0.08013333	0.02946667
GSD	1776	0.00306667	0.89873333	0.07173333	0.0264
GSD	2011	0.00773333	0.853	0.0962	0.04313333
GSD	2060	0.00613333	0.81526667	0.10273333	0.07626667
GSD	2086	0.00573333	0.84086667	0.10013333	0.05313333
FBUL	1507	0.0104	0.96366667	0.0158	0.00986667
FBUL	1508	0.00626667	0.96013333	0.01466667	0.0188
FBUL	1509	0.00493333	0.97453333	0.0106	0.01006667
FBUL	2671	0.01693333	0.91053333	0.01173333	0.0608
MBLT	1915	0.00553333	0.9154	0.008	0.071
MBLT	2253	0.0068	0.89166667	0.045	0.0564
MBLT	2254	0.036	0.9132	0.03073333	0.02006667
MBLT	2255	0.0098	0.90326667	0.00946667	0.0772
MBLT	2256	0.0062	0.97946667	0.00573333	0.0086
BULD	1193	0.01906667	0.95466667	0.01473333	0.01153333
BULD	1194	0.00513333	0.9824	0.00626667	0.00593333
BULD	1195	0.0036	0.98433333	0.00473333	0.00726667
BULD	1197	0.0052	0.92026667	0.05506667	0.0194
BULD	1198	0.00553333	0.96853333	0.0138	0.01206667
BOX	1176	0.00313333	0.91446667	0.07333333	0.009
BOX	1177	0.00366667	0.92693333	0.05286667	0.01653333
BOX	1178	0.00446667	0.93326667	0.05726667	0.00513333
BOX	1179	0.00233333	0.92526667	0.06886667	0.0036
BOX	1304	0.00266667	0.9162	0.07473333	0.00593333
MAST	1015	0.004	0.9386	0.0162	0.04126667
MAST	1016	0.009	0.90766667	0.06406667	0.01933333
MAST	1017	0.0046	0.9216	0.0498	0.024
MAST	1066	0.0158	0.94853333	0.018	0.01753333
MAST	991	0.01866667	0.95213333	0.0108	0.0186
BMD	941	0.00406667	0.76213333	0.21013333	0.02386667
BMD	943	0.0094	0.58306667	0.2496	0.1578
BMD	968	0.0062	0.74973333	0.21286667	0.03113333
BMD	1763	0.0046	0.74813333	0.20066667	0.04646667
BMD	969	0.00373333	0.69866667	0.2714	0.02653333

TABLE 19A-continued

Canid Population[a]	Canid ID No.	k = 4, 15 Run Average Pop1	Pop2	Pop3	Pop4
GSMD	1547	0.0066	0.41546667	0.36546667	0.21266667
GSMD	1659	0.0052	0.5908	0.34013333	0.0638
GSMD	1660	0.013	0.41086667	0.435	0.14126667
GSMD	1662	0.04386667	0.51266667	0.304	0.13973333
GSMD	1663	0.00653333	0.50973333	0.42086667	0.063

TABLE 19B

Canid Population[a]	Canid ID No.	k = 3, 15 Run Average Pop1	Pop2	Pop3
SHIB	1769	0.989667	0.004667	0.005667
SHIB	1854	0.982933	0.006867	0.0102
SHIB	1856	0.9584	0.016067	0.025667
SHIB	1860	0.9852	0.0066	0.008267
SHIB	1981	0.983733	0.0078	0.008133
CHOW	1633	0.985533	0.008133	0.0064
CHOW	1835	0.988133	0.006133	0.0058
CHOW	1837	0.982067	0.0094	0.0084
CHOW	1838	0.9884	0.0056	0.006
CHOW	1839	0.978667	0.0116	0.009867
AKIT	1130	0.9576	0.007467	0.035
AKIT	1131	0.988933	0.0052	0.005733
AKIT	1132	0.989133	0.005867	0.004933
AKIT	1133	0.988133	0.0072	0.004667
AKIT	1134	0.991	0.003667	0.005467
AMAL	1629	0.8604	0.083867	0.055733
AMAL	1779	0.7986	0.020667	0.1806
AMAL	1845	0.9078	0.047	0.045067
AMAL	2132	0.920333	0.0362	0.043533
AMAL	2214	0.908333	0.0218	0.069733
BSJI	1338	0.762067	0.122333	0.1156
BSJI	1339	0.973267	0.018	0.0088
BSJI	1645	0.977733	0.012933	0.009467
BSJI	1675	0.945333	0.0468	0.007933
BSJI	1717	0.972533	0.013667	0.013867
SHAR	1573	0.9602	0.028267	0.0116
SHAR	1593	0.845667	0.138	0.016533
SHAR	1619	0.870933	0.1136	0.015467
SHAR	1998	0.7902	0.031533	0.178267
SHAR	1999	0.957	0.029067	0.014
HUSK	1469	0.915533	0.037133	0.0474
HUSK	1883	0.907867	0.0104	0.0818
HUSK	2115	0.748733	0.013533	0.237867
HUSK	2117	0.632333	0.013333	0.3544
HUSK	2118	0.905133	0.042133	0.052533
AFGH	1812	0.601933	0.0432	0.3548
AFGH	1939	0.6604	0.084067	0.255467
AFGH	2264	0.6198	0.122933	0.2574
AFGH	1936	0.785067	0.0934	0.121467
AFGH	1937	0.717867	0.070933	0.2112
SALU	1491	0.4102	0.017667	0.5722
SALU	1535	0.542067	0.007067	0.450867
SALU	1607	0.500067	0.020533	0.479467
SALU	1873	0.292667	0.031667	0.675733
SALU	2610	0.4434	0.055533	0.501
TIBT	1466	0.479867	0.027867	0.492333
TIBT	1562	0.355667	0.0502	0.594
TIBT	1707	0.397133	0.240333	0.362333
TIBT	26078	0.431867	0.0466	0.521533
TIBT	28086	0.163267	0.103733	0.733067
LHSA	1524	0.558933	0.034333	0.4066
LHSA	1525	0.5262	0.023	0.451
LHSA	1526	0.463467	0.020533	0.5162
LHSA	1528	0.3624	0.0748	0.562667
LHSA	2074	0.705	0.023	0.272067
SAMO	1375	0.271267	0.011733	0.716867
SAMO	1532	0.553067	0.0086	0.438267
SAMO	1560	0.5902	0.0374	0.372533

TABLE 19B-continued

Canid Population[a]	Canid ID No.	k = 3, 15 Run Average Pop1	Pop2	Pop3
SAMO	169	0.436867	0.016867	0.546267
SAMO	239	0.458933	0.038267	0.502867
PEKE	1143	0.696267	0.013267	0.2904
PEKE	1145	0.445133	0.011533	0.543333
PEKE	1211	0.457267	0.010667	0.532133
PEKE	1212	0.380333	0.2828	0.336733
PEKE	1213	0.61	0.012933	0.377067
SHIH	1393	0.390067	0.1362	0.473867
SHIN	1783	0.3624	0.011267	0.626333
SHIH	2068	0.379533	0.009533	0.610867
SHIH	2859	0.4456	0.0228	0.531667
SHIH	2860	0.5422	0.0238	0.433933
IWOF	1581	0.0226	0.2552	0.7222
IWOF	1761	0.0088	0.020333	0.970733
IWOF	1792	0.026267	0.069467	0.904467
IWOF	1906	0.052267	0.033933	0.914
IWOF	1993	0.007267	0.026733	0.966067
STBD	1075	0.0464	0.139933	0.813733
STBD	1714	0.059	0.030333	0.910733
STBD	1750	0.047733	0.2466	0.705533
STBD	2403	0.013333	0.0294	0.9572
STBD	2404	0.0206	0.376867	0.602533
GREY	2477	0.1562	0.0356	0.808267
GREY	2478	0.017867	0.018267	0.963733
GREY	2479	0.0112	0.063333	0.925333
GREY	2480	0.059467	0.011467	0.929067
GREY	2481	0.009133	0.02	0.970867
BELS	1351	0.0132	0.007333	0.979467
BELS	2111	0.0744	0.013133	0.912267
BELS	2153	0.0058	0.006067	0.988
BELS	2209	0.031467	0.005733	0.962933
BELS	2210	0.034733	0.026267	0.938867
TURV	1622	0.009067	0.010133	0.980667
TURV	2194	0.013067	0.057467	0.929333
TURV	2200	0.020267	0.010467	0.969133
TURV	2222	0.0056	0.009133	0.985133
BORZ	1378	0.136	0.007733	0.856333
BORZ	1401	0.114733	0.024133	0.861133
BORZ	1808	0.1772	0.014467	0.8084
BORZ	2268	0.063467	0.015867	0.920867
BORZ	978	0.042	0.014733	0.9434
COLL	1692	0.011933	0.020667	0.9674
COLL	1701	0.0218	0.011	0.967
COLL	2284	0.0116	0.021867	0.9666
COLL	373	0.008933	0.013	0.977933
COLL	379	0.0058	0.011267	0.9828
SSHP	1379	0.032667	0.1834	0.783933
SSHP	1523	0.050067	0.043333	0.9064
SSHP	1824	0.016067	0.141133	0.842867
SSHP	1921	0.0062	0.118733	0.875
SSHP	2040	0.08	0.152	0.768133
PUG	1077	0.010667	0.008933	0.9804
PUG	1104	0.048267	0.017733	0.933933
PUG	1183	0.121733	0.0116	0.866667
PUG	1184	0.013467	0.011733	0.975
PUG	1192	0.009333	0.098867	0.8916
KOMO	1484	0.035	0.041867	0.923067
KOMO	1964	0.036133	0.055333	0.908333

TABLE 19B-continued

Canid Population[a]	Canid ID No.	k = 3, 15 Run Average Pop1	Pop2	Pop3
KOMO	2321	0.036	0.099533	0.8644
KOMO	2323	0.086267	0.096333	0.817467
KOMO	2334	0.0092	0.036467	0.9544
WHIP	1355	0.006867	0.0162	0.9768
WHIP	1395	0.010667	0.0362	0.953067
WHIP	1407	0.0076	0.073267	0.9192
WHIP	1409	0.006333	0.014267	0.9794
WHIP	1518	0.005933	0.039267	0.9546
SPOO	1530	0.0676	0.185267	0.747067
SPOO	1582	0.0744	0.064333	0.8612
SPOO	1876	0.015	0.155	0.830067
SPOO	1877	0.018467	0.190133	0.791333
SPOO	2337	0.006867	0.016533	0.976667
BICH	1943	0.0654	0.019933	0.9146
BICH	1954	0.239867	0.018	0.741933
BICH	933	0.050933	0.159467	0.789467
BICH	974	0.109533	0.092333	0.798067
KEES	1501	0.060867	0.013067	0.925933
KEES	1589	0.006467	0.007267	0.986267
KEES	1818	0.015467	0.027133	0.9572
KEES	1819	0.007133	0.012733	0.980067
KEES	2072	0.008	0.0212	0.970667
MNTY	1539	0.0138	0.264733	0.7214
MNTY	1732	0.0298	0.1218	0.8486
MNTY	2145	0.014333	0.155133	0.830333
MNTY	2149	0.010533	0.014533	0.974933
NELK	2216	0.0872	0.0802	0.832467
NELK	2239	0.214533	0.02	0.765467
NELK	2240	0.0426	0.1888	0.768667
NELK	2281	0.0142	0.027533	0.958333
NELK	2295	0.293	0.025867	0.681467
KUVZ	1482	0.0854	0.0086	0.906
KUVZ	1551	0.198533	0.008533	0.793
KUVZ	1672	0.075467	0.032267	0.8924
KUVZ	1913	0.033333	0.073267	0.8936
KUVZ	1994	0.0498	0.042467	0.907867
DANE	1574	0.016533	0.026467	0.957
DANE	1575	0.1558	0.1312	0.713
DANE	1580	0.011	0.007067	0.982
DANE	1700	0.0088	0.016933	0.9742
DANE	1748	0.1982	0.034533	0.767333
WSSP	1955	0.0066	0.015867	0.977533
WSSP	2139	0.018667	0.028867	0.952533
WSSP	2143	0.0056	0.033333	0.961133
WSSP	2195	0.014467	0.065667	0.920133
WSSP	2286	0.007133	0.102133	0.890867
DOBP	1031	0.012667	0.102067	0.8852
DOBP	1032	0.047733	0.092733	0.859267
DOBP	1749	0.0394	0.2362	0.724467
DOBP	2162	0.013133	0.0862	0.9008
DOBP	2245	0.008467	0.085933	0.9056
SSNZ	13352	0.004733	0.290333	0.705133
SSNZ	1360	0.004267	0.093667	0.902133
SSNZ	1827	0.007067	0.034467	0.958533
SSNZ	20457	0.009267	0.021267	0.969267
SSNZ	22647	0.0088	0.203333	0.7878
ITGY	1568	0.022933	0.012267	0.965067
ITGY	1570	0.019333	0.061067	0.919533
ITGY	1862	0.1134	0.021067	0.865533
ITGY	1881	0.0564	0.017467	0.9262
ITGY	1882	0.1768	0.014467	0.808667
OES	1984	0.022133	0.022067	0.955667
OES	2171	0.009	0.028867	0.962067
OES	2179	0.011267	0.022	0.966867
OES	1914	0.020467	0.0566	0.9232
OES	2626	0.062467	0.013267	0.924333
AMWS	2168	0.012	0.020333	0.967667
AMWS	2279	0.012	0.195533	0.792467
AMWS	2327	0.0978	0.257667	0.6446
AMWS	987	0.018933	0.108533	0.8722
AMWS	988	0.019667	0.155133	0.825333
MSNZ	1587	0.0078	0.129067	0.8634
MSNZ	1756	0.006733	0.011	0.9824

TABLE 19B-continued

Canid Population[a]	Canid ID No.	k = 3, 15 Run Average Pop1	Pop2	Pop3
MSNZ	1851	0.005067	0.029733	0.9652
MSNZ	2034	0.0352	0.1964	0.7686
MSNZ	2613	0.0062	0.0746	0.919333
AUST	1387	0.046333	0.052533	0.9012
AUST	1531	0.0178	0.145467	0.836933
AUST	1564	0.008067	0.045867	0.946
AUST	1870	0.051933	0.069333	0.878667
AUST	1871	0.008533	0.072	0.9196
ECKR	1376	0.005467	0.0664	0.928
ECKR	1377	0.005133	0.032267	0.962333
ECKR	1400	0.003867	0.036667	0.9594
ECKR	1404	0.004067	0.042933	0.952867
ECKR	1511	0.008333	0.081333	0.910267
IRSE	1540	0.0042	0.0116	0.984133
IRSE	1617	0.005267	0.010867	0.9838
IRSE	1896	0.009267	0.017133	0.9736
IRSE	2084	0.004333	0.008133	0.9876
IRSE	2085	0.004267	0.029467	0.966067
WHWT	1388	0.013	0.013667	0.973533
WHWT	1420	0.037133	0.0254	0.937267
WHWT	1992	0.0094	0.02	0.970867
WHWT	2100	0.009933	0.033333	0.956667
WHWT	2128	0.011533	0.009467	0.979
PNTR	1382	0.0116	0.0096	0.978867
PNTR	1383	0.025867	0.019933	0.9542
PNTR	1869	0.011667	0.007867	0.980533
PNTR	1938	0.010867	0.015533	0.973667
PNTR	1948	0.066533	0.008533	0.925
BASS	1341	0.035333	0.0746	0.890067
BASS	1342	0.014067	0.015467	0.970533
BASS	1506	0.008467	0.045133	0.946533
BASS	1917	0.0118	0.065067	0.923133
CKCS	1513	0.039067	0.011467	0.949533
CKCS	1639	0.0096	0.034067	0.956267
CKCS	1640	0.011467	0.1124	0.875867
CKCS	1642	0.008133	0.017133	0.9748
CKCS	2054	0.0076	0.014533	0.977733
GSNZ	1868	0.2806	0.028467	0.691
GSNZ	22739	0.187	0.026133	0.787
GSNZ	27093	0.064533	0.027667	0.9078
GSNZ	27106	0.0126	0.0828	0.9048
GSNZ	33390	0.011667	0.053533	0.9348
PHAR	1292	0.152867	0.015267	0.831867
PHAR	1947	0.207067	0.007933	0.785067
PHAR	1962	0.1676	0.0442	0.788333
PHAR	1963	0.142533	0.021667	0.8358
GOLD	591	0.006467	0.268667	0.724933
GOLD	592	0.0284	0.465467	0.506067
GOLD	593	0.007867	0.295733	0.696533
GOLD	603	0.0082	0.3306	0.6614
GOLD	604	0.004533	0.283333	0.712267
BEAG	1323	0.012467	0.292	0.695667
BEAG	1324	0.019267	0.052133	0.928667
BEAG	1327	0.008867	0.3602	0.630667
BEAG	994	0.0326	0.3418	0.625467
BEAG	995	0.026333	0.1152	0.858467
BLDH	1186	0.014133	0.626733	0.358933
BLDH	1223	0.017133	0.404467	0.578267
BLDH	1410	0.006467	0.772733	0.2208
BLDH	1942	0.013	0.5678	0.419333
BLDH	1957	0.008933	0.458133	0.532733
AIRT	1603	0.059733	0.2394	0.701067
AIRT	1604	0.008533	0.090133	0.901467
AIRT	1788	0.006533	0.4282	0.5652
AIRT	1875	0.022733	0.1192	0.857867
ACKR	1035	0.014333	0.040733	0.944933
ACKR	2261	0.0278	0.050867	0.921333
ACKR	2310	0.004867	0.061133	0.9338
ACKR	1956	0.0142	0.155667	0.830267
ACKR	2260	0.006867	0.077	0.915867
AHRT	1120	0.016333	0.104	0.879467
AHRT	1121	0.013733	0.185067	0.801267
AHRT	1122	0.0096	0.190467	0.8002

TABLE 19B-continued

Canid Population[a]	Canid ID No.	k = 3, 15 Run Average Pop1	Pop2	Pop3
AHRT	1123	0.0118	0.097333	0.891
AHRT	1124	0.0106	0.091933	0.8974
CHBR	1546	0.013133	0.096333	0.890667
CHBR	1549	0.0814	0.445533	0.473
CHBR	1813	0.0054	0.23	0.7646
CHBR	2091	0.0118	0.073267	0.915
CHBR	888	0.0056	0.118533	0.876
CAIR	1405	0.01	0.289333	0.7004
CAIR	2096	0.022667	0.041733	0.935533
CAIR	2113	0.0158	0.050867	0.933333
CAIR	2125	0.006333	0.0114	0.9824
CAIR	2131	0.0202	0.027533	0.952333
PTWD	P142	0.007067	0.1418	0.8512
PTWD	P1	0.005067	0.2378	0.757
PTWD	P238	0.0172	0.209333	0.773467
PTWD	P25	0.005133	0.021667	0.9732
PTWD	P67	0.007067	0.023	0.97
GSHP	1628	0.006533	0.155933	0.837533
GSHP	1708	0.042867	0.041333	0.915867
GSHP	1710	0.0406	0.0372	0.922133
GSHP	1833	0.012533	0.549533	0.438133
GSHP	1892	0.0154	0.0414	0.943267
BORD	1648	0.1348	0.036733	0.8286
BORD	1828	0.017867	0.032733	0.949467
BORD	1829	0.006667	0.211667	0.781733
BORD	2002	0.026467	0.061533	0.911933
BORD	2003	0.044533	0.055467	0.9
BEDT	1422	0.009067	0.3274	0.6634
BEDT	1423	0.007933	0.189867	0.802333
BEDT	1424	0.017533	0.1126	0.870133
BEDT	1426	0.014933	0.238867	0.7462
CLSP	1008	0.01	0.7082	0.281667
CLSP	1009	0.005333	0.637667	0.3572
CLSP	1802	0.010467	0.666267	0.323267
CLSP	2312	0.005	0.752	0.242867
CLSP	2314	0.006067	0.7524	0.2416
IBIZ	1147	0.011533	0.1148	0.8738
IBIZ	1148	0.0164	0.235267	0.7482
IBIZ	1162	0.013	0.055133	0.932
IBIZ	1172	0.0232	0.1398	0.837
IBIZ	1280	0.022333	0.175667	0.801867
RHOD	1444	0.007267	0.143733	0.848733
RHOD	1454	0.027467	0.127333	0.845067
RHOD	1505	0.011	0.135467	0.853467
RHOD	1592	0.010067	0.5242	0.4658
RHOD	1609	0.008133	0.110267	0.881467
DACH	1051	0.0216	0.564	0.414467
DACH	1052	0.015267	0.618867	0.365733
DACH	1053	0.015533	0.563867	0.420667
DACH	1054	0.0254	0.728467	0.246133
DACH	1055	0.016667	0.6114	0.3718
AUSS	1336	0.17	0.2254	0.6046
AUSS	1337	0.016133	0.237267	0.7464
AUSS	1500	0.012067	0.026	0.962133
AUSS	1521	0.1014	0.3078	0.590867
AUSS	1683	0.0128	0.210267	0.776933
CHIH	1202	0.007267	0.219867	0.7728
CHIH	1203	0.022	0.0794	0.898667
CHIH	1204	0.014467	0.104733	0.880667
CHIN	1205	0.1532	0.3324	0.514333
CHIH	1206	0.0068	0.388867	0.6042
KERY	13878	0.007533	0.159533	0.833067
KERY	1483	0.0064	0.175733	0.817867
KERY	1579	0.012133	0.034067	0.953533
KERY	2014	0.004333	0.339933	0.655933
KERY	24255	0.009733	0.294667	0.695467
SCHP	1386	0.0092	0.0818	0.9088
SCHP	1471	0.013867	0.077267	0.908933
SCHP	1814	0.0104	0.090933	0.898667
SCHP	1852	0.013067	0.013733	0.973333
IRTR	2152	0.011533	0.1228	0.865533
IRTR	2189	0.0128	0.413133	0.5742
IRTR	2238	0.006667	0.4018	0.591467

TABLE 19B-continued

Canid Population[a]	Canid ID No.	k = 3, 15 Run Average Pop1	Pop2	Pop3
IRTR	2242	0.009667	0.282267	0.7082
FCR	1188	0.0058	0.172933	0.821267
FCR	2020	0.006267	0.020467	0.973267
FCR	2042	0.006067	0.123533	0.870267
FCR	2044	0.006533	0.0468	0.946733
FCR	2259	0.004667	0.199467	0.796
SCWT	1624	0.081533	0.640867	0.2776
SCWT	1770	0.005933	0.3122	0.682
SCWT	2250	0.006867	0.422133	0.571
SCWT	2301	0.021667	0.636533	0.3418
POM	1190	0.155933	0.333533	0.5108
POM	1191	0.010667	0.731067	0.258267
POM	1210	0.050933	0.3128	0.636333
POM	1238	0.007867	0.163933	0.827933
POM	1239	0.203467	0.0754	0.721
LAB	1310	0.119267	0.587867	0.292733
LAB	1465	0.016267	0.392	0.591933
LAB	1468	0.022733	0.3696	0.6078
LAB	1754	0.0192	0.791933	0.188867
LAB	1830	0.006333	0.538667	0.454867
PRES	1082	0.009467	0.803133	0.187667
PRES	1096	0.0064	0.797133	0.1968
PRES	1115	0.012333	0.656733	0.330733
PRES	1127	0.0976	0.877933	0.024533
PRES	1095	0.083267	0.823733	0.0932
ROTT	1014	0.015867	0.725267	0.258933
ROTT	1028	0.006667	0.7466	0.246533
ROTT	1029	0.004867	0.9082	0.086867
ROTT	1033	0.007133	0.946867	0.045933
ROTT	1034	0.006467	0.921933	0.071733
BULM	1105	0.0064.	0.954333	0.0392
BULM	1106	0.005667	0.552933	0.4414
BULM	1107	0.0256	0.9174	0.057267
BULM	1108	0.0084	0.9536	0.038
BULM	1109	0.0064	0.9706	0.023267
NEWF	271	0.0176	0.865867	0.116467
NEWF	274	0.006533	0.9628	0.030333
NEWF	275	0.006467	0.983733	0.009867
NEWF	277	0.0074	0.983867	0.008667
NEWF	278	0.086	0.862667	0.051467
GSD	1666	0.007	0.954733	0.038133
GSD	1776	0.003733	0.958067	0.0382
GSD	2011	0.009867	0.893933	0.096067
GSD	2060	0.0064	0.8242	0.169467
GSD	2086	0.006933	0.917267	0.075733
FBUL	1507	0.0122	0.975067	0.012933
FBUL	1508	0.0082	0.970733	0.0212
FBUL	1509	0.005	0.986333	0.008933
FBUL	2671	0.023467	0.918267	0.0582
MBLT	1915	0.007	0.936867	0.055933
MBLT	2253	0.008133	0.953533	0.038467
MBLT	2254	0.060133	0.904933	0.034933
MBLT	2255	0.010533	0.957533	0.031867
MBLT	2256	0.0066	0.985667	0.0078
BULD	1193	0.021133	0.964667	0.0142
BULD	1194	0.0056	0.9872	0.007067
BULD	1195	0.003933	0.988533	0.0074
BULD	1197	0.007133	0.9042	0.0888
BULD	1198	0.006733	0.9778	0.0154
BOX	1176	0.0038	0.982933	0.0132
BOX	1177	0.0044	0.9746	0.020933
BOX	1178	0.005733	0.9872	0.007133
BOX	1179	0.002933	0.9922	0.004733
BOX	1304	0.003733	0.9868	0.009667
MAST	1015	0.0052	0.943267	0.0516
MAST	1016	0.0114	0.9228	0.065867
MAST	1017	0.006133	0.913733	0.08
MAST	1066	0.0174	0.9588	0.023733
MAST	991	0.017933	0.965933	0.016067
BMD	941	0.004867	0.9596	0.035667
BMD	943	0.013133	0.7552	0.231733
BMD	968	0.010467	0.949133	0.040333
BMD	1763	0.005733	0.938867	0.055267

TABLE 19B-continued

Canid Population[a]	Canid ID No.	k = 3, 15 Run Average Pop1	Pop2	Pop3
BMD	969	0.005067	0.902933	0.092067
GSMD	1547	0.007533	0.4592	0.533067
GSMD	1659	0.006133	0.687133	0.3066
GSMD	1660	0.017067	0.4854	0.4974
GSMD	1662	0.063933	0.632667	0.303133
GSMD	1663	0.009933	0.5714	2.93

TABLE 19C

Canid Population[a]	Canid ID No.	k = 2, 15 Run Average Pop1	Pop2
SHIB	1769	0.9954	0.0046
SHIB	1854	0.991133	0.008867
SHIB	1856	0.9642	0.0358
SHIB	1860	0.992133	0.007867
SHIB	1981	0.989467	0.010533
CHOW	1633	0.993733	0.006267
CHOW	1835	0.994867	0.005133
CHOW	1837	0.991533	0.008467
CHOW	1838	0.995	0.005
CHOW	1839	0.988	0.012
AKIT	1130	0.9788	0.0212
AKIT	1131	0.995067	0.004933
AKIT	1132	0.995267	0.004733
AKIT	1133	0.994933	0.005067
AKIT	1134	0.996	0.004
AMAL	1629	0.8468	0.1532
AMAL	1779	0.816733	0.183267
AMAL	1845	0.913667	0.086333
AMAL	2132	0.934867	0.065133
AMAL	2214	0.9108	0.0892
BSJI	1338	0.735267	0.264733
BSJI	1339	0.986933	0.013067
BSJI	1645	0.989667	0.010333
BSJI	1675	0.9814	0.0186
BSJI	1717	0.984867	0.015133
SHAR	1573	0.9826	0.0174
SHAR	1593	0.932	0.068
SHAR	1619	0.931133	0.068867
SHAR	1998	0.7944	0.2056
SHAR	1999	0.9768	0.0232
HUSK	1469	0.916333	0.083667
HUSK	1883	0.939	0.061
HUSK	2115	0.797333	0.202667
HUSK	2117	0.642933	0.357067
HUSK	2118	0.889267	0.110733
AFGH	1812	0.582533	0.417467
AFGH	1939	0.6042	0.3958
AFGH	2264	0.572067	0.427933
AFGH	1936	0.7372	0.2628
AFGH	1937	0.666533	0.333467
SALU	1491	0.427467	0.572533
SALU	1535	0.6256	0.3744
SALU	1607	0.548533	0.451467
SALU	1873	0.323	0.677
SALU	2610	0.452133	0.547867
TIBT	1466	0.463867	0.536133
TIBT	1562	0.334267	0.665733
TIBT	1707	0.369133	0.630867
TIBT	26078	0.402067	0.597933
TIBT	28086	0.160333	0.839667
LHSA	1524	0.547533	0.452467
LHSA	1525	0.5422	0.4578
LHSA	1526	0.453533	0.546467
LHSA	1528	0.339	0.661
LHSA	2074	0.688267	0.311733
SAMO	1375	0.303933	0.696067
SAMO	1532	0.592467	0.407533

TABLE 19C-continued

Canid Population[a]	Canid ID No.	k = 2, 15 Run Average Pop1	Pop2
SAMO	1560	0.5672	0.4328
SAMO	169	0.461933	0.538067
SAMO	239	0.4442	0.5558
PEKE	1143	0.7292	0.2708
PEKE	1145	0.4824	0.5176
PEKE	1211	0.4778	0.5222
PEKE	1212	0.351067	0.648933
PEKE	1213	0.638467	0.361533
SHIH	1393	0.385467	0.614533
SHIH	1783	0.4202	0.5798
SHIH	2068	0.433667	0.566333
SHIH	2859	0.481267	0.518733
SHIH	2860	0.542	0.458
IWOF	1581	0.018867	0.981133
IWOF	1761	0.0092	0.9908
IWOF	1792	0.017467	0.982533
IWOF	1906	0.061533	0.938467
IWOF	1993	0.0062	0.9938
STBD	1075	0.035	0.965
STBD	1714	0.056733	0.943267
STBD	1750	0.045267	0.954733
STBD	2403	0.019667	0.980333
STBD	2404	0.021467	0.978533
GREY	2477	0.155267	0.844733
GREY	2478	0.0156	0.9844
GREY	2479	0.0088	0.9912
GREY	2480	0.1108	0.8892
GREY	2481	0.0092	0.9908
BELS	1351	0.030333	0.969667
BELS	2111	0.1014	0.8986
BELS	2153	0.0072	0.9928
BELS	2209	0.053933	0.946067
BELS	2210	0.0352	0.9648
TURV	1622	0.0158	0.9842
TURV	2194	0.0078	0.9922
TURV	2200	0.030867	0.969133
TURV	2222	0.006133	0.993867
BORZ	1378	0.2322	0.7678
BORZ	1401	0.170933	0.829067
BORZ	1808	0.229267	0.770733
BORZ	2268	0.1112	0.8888
BORZ	978	0.102267	0.897733
COLL	1692	0.011133	0.988867
COLL	1701	0.0226	0.9774
COLL	2284	0.015333	0.984667
COLL	373	0.009267	0.990733
COLL	379	0.006133	0.993867
SSHP	1379	0.027867	0.972133
SSHP	1523	0.054133	0.945867
SSHP	1824	0.008133	0.991867
SSHP	1921	0.0048	0.9952
SSHP	2040	0.0838	0.9162
PUG	1077	0.028133	0.971867
PUG	1104	0.104933	0.895067
PUG	1183	0.159933	0.840067
PUG	1184	0.027533	0.972467
PUG	1192	0.009467	0.990533
KOMO	1484	0.025667	0.974333
KOMO	1964	0.0836	0.9164
KOMO	2321	0.035333	0.964667
KOMO	2323	0.091133	0.908867
KOMO	2334	0.0158	0.9842
WHIP	1355	0.0084	0.9916
WHIP	1395	0.008133	0.991867
WHIP	1407	0.005533	0.994467
WHIP	1409	0.006	0.994
WHIP	1518	0.005267	0.994733
SPOO	1530	0.044667	0.955333
SPOO	1582	0.050467	0.949533
SPOO	1876	0.022133	0.977867
SPOO	1877	0.011933	0.988067
SPOO	2337	0.0062	0.9938
BICH	1943	0.131	0.869

TABLE 19C-continued

Canid Population[a]	Canid ID No.	k = 2, 15 Run Average Pop1	Pop2
BICH	1954	0.286533	0.713467
BICH	933	0.056867	0.943133
BICH	974	0.142267	0.857733
KEES	1501	0.059533	0.940467
KEES	1589	0.009067	0.990933
KEES	1818	0.018533	0.981467
KEES	1819	0.007	0.993
KEES	2072	0.0066	0.9934
MNTY	1539	0.010933	0.989067
MNTY	1732	0.022533	0.977467
MNTY	2145	0.012533	0.987467
MNTY	2149	0.011333	0.988667
NELK	2216	0.107867	0.892133
NELK	2239	0.220267	0.779733
NELK	2240	0.037333	0.962667
NELK	2281	0.0152	0.9848
NELK	2295	0.2866	0.7134
KUVZ	1482	0.1712	0.8288
KUVZ	1551	0.2862	0.7138
KUVZ	1672	0.110333	0.889667
KUVZ	1913	0.041067	0.958933
KUVZ	1994	0.104667	0.895333
DANE	1574	0.018667	0.981333
DANE	1575	0.153333	0.846667
DANE	1580	0.0202	0.9798
DANE	1700	0.007333	0.992667
DANE	1748	0.1858	0.8142
WSSP	1955	0.006133	0.993867
WSSP	2139	0.015867	0.984133
WSSP	2143	0.005067	0.994933
WSSP	2195	0.020133	0.979867
WSSP	2286	0.005333	0.994667
DOBP	1031	0.014467	0.985533
DOBP	1032	0.062467	0.937533
DOBP	1749	0.052933	0.947067
DOBP	2162	0.0146	0.9854
DOBP	2245	0.0092	0.9908
SSNZ	13352	0.003467	0.996533
SSNZ	1360	0.003	0.997
SSNZ	1827	0.004867	0.995133
SSNZ	20457	0.010667	0.989333
SSNZ	22647	0.006267	0.993733
ITGY	1568	0.025333	0.974667
ITGY	1570	0.016533	0.983467
ITGY	1862	0.137667	0.862333
ITGY	1881	0.0804	0.9196
ITGY	1882	0.159933	0.840067
OES	1984	0.0414	0.9586
OES	2171	0.009067	0.990933
OES	2179	0.008133	0.991867
OES	1914	0.0212	0.9788
OES	2626	0.142733	0.857267
AMWS	2168	0.010867	0.989133
AMWS	2279	0.007733	0.992267
AMWS	2327	0.080333	0.919667
AMWS	987	0.014133	0.985867
AMWS	988	0.015467	0.984533
MSNZ	1587	0.005	0.995
MSNZ	1756	0.008267	0.991733
MSNZ	1851	0.004667	0.995333
MSNZ	2034	0.039	0.961
MSNZ	2613	0.004867	0.995133
AUST	1387	0.036867	0.963133
AUST	1531	0.009	0.991
AUST	1564	0.006133	0.993867
AUST	1870	0.051467	0.948533
AUST	1871	0.0066	0.9934
ECKR	1376	0.004133	0.995867
ECKR	1377	0.003933	0.996067
ECKR	1400	0.002933	0.997067
ECKR	1404	0.003133	0.996867
ECKR	1511	0.0066	0.9934
IRSE	1540	0.003267	0.996733

TABLE 19C-continued

Canid Population[a]	Canid ID No.	k = 2, 15 Run Average Pop1	Pop2
IRSE	1617	0.004133	0.995867
IRSE	1896	0.0136	0.9864
IRSE	2084	0.004533	0.995467
IRSE	2085	0.003533	0.996467
WHWT	1388	0.016133	0.983867
WHWT	1420	0.031467	0.968533
WHWT	1992	0.0064	0.9936
WHWT	2100	0.0078	0.9922
WHWT	2128	0.010867	0.989133
PNTR	1382	0.015	0.985
PNTR	1383	0.0574	0.9426
PNTR	1869	0.0322	0.9678
PNTR	1938	0.009867	0.990133
PNTR	1948	0.2778	0.7222
BASS	1341	0.024267	0.975733
BASS	1342	0.012733	0.987267
BASS	1506	0.006667	0.993333
BASS	1917	0.0066	0.9934
CKCS	1513	0.070867	0.929133
CKCS	1639	0.0084	0.9916
CKCS	1640	0.0086	0.9914
CKCS	1642	0.007267	0.992733
CKCS	2054	0.007067	0.992933
GSNZ	1868	0.274133	0.725867
GSNZ	22739	0.177133	0.822867
GSNZ	27093	0.087533	0.912467
GSNZ	27106	0.0126	0.9874
GSNZ	33390	0.008333	0.991667
PHAR	1292	0.1702	0.8298
PHAR	1947	0.275533	0.724467
PHAR	1962	0.1786	0.8214
PHAR	1963	0.158467	0.841533
GOLD	591	0.0048	0.9952
GOLD	592	0.029667	0.970333
GOLD	593	0.005933	0.994067
GOLD	603	0.007267	0.992733
GOLD	604	0.003333	0.996667
BEAG	1323	0.0084	0.9916
BEAG	1324	0.037133	0.962867
BEAG	1327	0.006667	0.993333
BEAG	994	0.0264	0.9736
BEAG	995	0.030333	0.969667
BLDH	1186	0.007733	0.992267
BLDH	1223	0.011667	0.988333
BLDH	1410	0.005267	0.994733
BLDH	1942	0.008933	0.991067
BLDH	1957	0.0058	0.9942
AIRT	1603	0.072867	0.927133
AIRT	1604	0.007	0.993
AIRT	1788	0.005667	0.994333
AIRT	1875	0.029867	0.970133
ACKR	1035	0.0096	0.9904
ACKR	2261	0.023267	0.976733
ACKR	2310	0.003667	0.996333
ACKR	1956	0.012333	0.987667
ACKR	2260	0.0052	0.9948
AHRT	1120	0.011133	0.988867
AHRT	1121	0.010067	0.989933
AHRT	1122	0.007533	0.992467
AHRT	1123	0.0102	0.9898
AHRT	1124	0.006467	0.993533
CHBR	1546	0.009667	0.990333
CHBR	1549	0.088867	0.911133
CHBR	1813	0.0042	0.9958
CHBR	2091	0.011	0.989
CHBR	888	0.004267	0.995733
CAIR	1405	0.009	0.991
CAIR	2096	0.029667	0.970333
CAIR	2113	0.0138	0.9862
CAIR	2125	0.006333	0.993667
CAIR	2131	0.020467	0.979533
PTWD	P142	0.005333	0.994667
PTWD	P1	0.0038	0.9962

TABLE 19C-continued

Canid Population[a]	Canid ID No.	k = 2, 15 Run Average Pop1	Pop2
PTWD	P238	0.011533	0.988467
PTWD	P25	0.0044	0.9956
PTWD	P67	0.006933	0.993067
GSHP	1628	0.004733	0.995267
GSHP	1708	0.048067	0.951933
GSHP	1710	0.040933	0.959067
GSHP	1833	0.007667	0.992333
GSHP	1892	0.008733	0.991267
BORD	1648	0.164267	0.835733
BORD	1828	0.0184	0.9816
BORD	1829	0.0054	0.9946
BORD	2002	0.033	0.967
BORD	2003	0.045267	0.954733
BEDT	1422	0.006933	0.993067
BEDT	1423	0.0062	0.9938
BEDT	1424	0.018133	0.981867
BEDT	1426	0.01	0.99
CLSP	1008	0.0074	0.9926
CLSP	1009	0.004067	0.995933
CLSP	1802	0.006667	0.993333
CLSP	2312	0.004133	0.995867
CLSP	2314	0.005067	0.994933
IBIZ	1147	0.011467	0.988533
IBIZ	1148	0.030933	0.969067
IBIZ	1162	0.0162	0.9838
IBIZ	1172	0.017867	0.982133
IBIZ	1280	0.018733	0.981267
RHOD	1444	0.004333	0.995667
RHOD	1454	0.018	0.982
RHOD	1505	0.008	0.992
RHOD	1592	0.006733	0.993267
RHOD	1609	0.005067	0.994933
DACH	1051	0.0188	0.9812
DACH	1052	0.009067	0.990933
DACH	1053	0.016733	0.983267
DACH	1054	0.028867	0.971133
DACH	1055	0.009933	0.990067
AUSS	1336	0.1524	0.8476
AUSS	1337	0.013133	0.986867
AUSS	1500	0.010667	0.989333
AUSS	1521	0.102067	0.897933
AUSS	1683	0.008467	0.991533
CHIH	1202	0.005267	0.994733
CHIH	1203	0.03	0.97
CHIH	1204	0.013333	0.986667
CHIH	1205	0.166867	0.833133
CHIH	1206	0.004867	0.995133
KERY	13878	0.0066	0.9934
KERY	1483	0.005867	0.994133
KERY	1579	0.011133	0.988867
KERY	2014	0.0034	0.9966
KERY	24255	0.007267	0.992733
SCHP	1386	0.0082	0.9918
SCHP	1471	0.020933	0.979067
SCHP	1814	0.007667	0.992333
SCHP	1852	0.0184	0.9816
IRTR	2152	0.009333	0.990667
IRTR	2189	0.008333	0.991667
IRTR	2238	0.005467	0.994533
IRTR	2242	0.0076	0.9924
FCR	1188	0.004267	0.995733
FCR	2020	0.0052	0.9948
FCR	2042	0.004333	0.995667
FCR	2044	0.005133	0.994867
FCR	2259	0.003733	0.996267
SCWT	1624	0.051067	0.948933
SCWT	1770	0.004467	0.995533
SCWT	2250	0.005533	0.994467
SCWT	2301	0.0124	0.9876
POM	1190	0.181067	0.818933
POM	1191	0.006067	0.993933
POM	1210	0.049267	0.950733
POM	1238	0.010067	0.989933

TABLE 19C-continued

Canid Population[a]	Canid ID No.	k = 2, 15 Run Average Pop1	Pop2
POM	1239	0.298467	0.701533
LAB	1310	0.0756	0.9244
LAB	1465	0.011	0.989
LAB	1468	0.013533	0.986467
LAB	1754	0.007067	0.992933
LAB	1830	0.0052	0.9948
PRES	1082	0.009	0.991
PRES	1096	0.004667	0.995333
PRES	1115	0.008667	0.991333
PRES	1127	0.147867	0.852133
PRES	1095	0.115533	0.884467
ROTT	1014	0.016467	0.983533
ROTT	1028	0.005333	0.994667
ROTT	1029	0.003733	0.996267
ROTT	1033	0.006933	0.993067
ROTT	1034	0.003867	0.996133
BULM	1105	0.004067	0.995933
BULM	1106	0.004467	0.995533
BULM	1107	0.007933	0.992067
BULM	1108	0.005533	0.994467
BULM	1109	0.004533	0.995467
NEWF	271	0.014333	0.985667
NEWF	274	0.005867	0.994133
NEWF	275	0.006467	0.993533
NEWF	277	0.008933	0.991067
NEWF	278	0.106	0.894
GSD	1666	0.005467	0.994533
GSD	1776	0.003	0.997
GSD	2011	0.004267	0.995733
GSD	2060	0.004467	0.995533
GSD	2086	0.005867	0.994133
FBUL	1507	0.016867	0.983133
FBUL	1508	0.0084	0.9916
FBUL	1509	0.0066	0.9934
FBUL	2671	0.032867	0.967133
MBLT	1915	0.005467	0.994533
MBLT	2253	0.007467	0.992533
MBLT	2254	0.063667	0.936333
MBLT	2255	0.006333	0.993667
MBLT	2256	0.0102	0.9898
BULD	1193	0.035	0.965
BULD	1194	0.010067	0.989933
BULD	1195	0.010867	0.989133
BULD	1197	0.0042	0.9958
BULD	1198	0.005133	0.994867
BOX	1176	0.003133	0.996867
BOX	1177	0.003467	0.996533
BOX	1178	0.005533	0.994467
BOX	1179	0.004467	0.995533
BOX	1304	0.0046	0.9954
MAST	1015	0.003533	0.996467
MAST	1016	0.012467	0.987533
MAST	1017	0.006933	0.993067
MAST	1066	0.011333	0.988667
MAST	991	0.0132	0.9868
BMD	941	0.0054	0.9946
BMD	943	0.0054	0.9946
BMD	968	0.005933	0.994067
BMD	1763	0.004133	0.995867
BMD	969	0.0034	0.9966
GSMD	1547	0.004867	0.995133
GSMD	1659	0.004467	0.995533
GSMD	1660	0.010933	0.989067
GSMD	1662	0.0276	0.9724
GSMD	1663	0.009267	0.990733

[a]See Table 5 for abbreviations of canid populations.

KBB: pbe

TABLE 19D

Canid Population[a]	Canid ID No.	k =2 with wolf; 15 Run Average Pop1	Pop2
WOLF	W511	0.994	0.006
WOLF	W5131	0.982	0.018
WOLF	WC3	0.995	0.005
WOLF	WE10	0.995	0.005
WOLF	282135	0.9918	0.0082
WOLF	492-8	0.9968	0.0032
WOLF	930121	0.9858	0.0142
WOLF	Iran-1	0.9388	0.0612
SHIB	1769	0.993	0.007
SHIB	1854	0.98	0.02
SHIB	1856	0.938	0.062
SHIB	1860	0.99	0.01
SHIB	1981	0.987	0.013
CHOW	1633	0.9904	0.0096
CHOW	1835	0.9916	0.0084
CHOW	1837	0.9774	0.0226
CHOW	1838	0.9918	0.0082
CHOW	1839	0.9796	0.0204.
AKIT	1130	0.9724	0.0276
AKIT	1131	0.993	0.007
AKIT	1132	0.9934	0.0066
AKIT	1133	0.995	0.005
AKIT	1134	0.994	0.006
AMAL	1629	0.5876	0.4124
AMAL	1779	0.516	0.484
AMAL	1845	0.6802	0.3198
AMAL	2132	0.755	0.245
AMAL	2214	0.7298	0.2702
BSJI	1338	0.7944	0.2056
BSJI	1339	0.976	0.024
BSJI	1645	0.9792	0.0208
BSJI	1675	0.9718	0.0282
BSJI	1717	0.9672	0.0328
SHAR	1573	0.9318	0.0682
SHAR	1593	0.914	0.086
SHAR	1619	0.8048	0.1952
SHAR	1998	0.6918	0.3082
SHAR	1999	0.9372	0.0628
HUSK	1469	0.702	0.298
HUSK	1883	0.7878	0.2122
HUSK	2115	0.5934	0.4066
HUSK	2117	0.5412	0.4588
HUSK	2118	0.7718	0.2282
AFGH	1812	0.4642	0.5358
AFGH	1939	0.5172	0.4828
AFGH	2264	0.4348	0.5652
AFGH	1936	0.5942	0.4058
AFGH	1937	0.583	0.417
SALU	1491	0.3624	0.6376
SALU	1535	0.4792	0.5208
SALU	1607	0.4234	0.5766
SALU	1873	0.2304	0.7696
SALU	2610	0.4092	0.5908
TIBT	1466	0.3684	0.6316
TIBT	1562	0.2896	0.7104
TIBT	1707	0.3136	0.6864
TIBT	26078	0.3314	0.6686
TIBT	28086	0.1316	0.8684
LHSA	1524	0.4598	0.5402
LHSA	1525	0.4652	0.5348
LHSA	1526	0.4	0.6
LHSA	1528	0.2798	0.7202
LHSA	2074	0.5838	0.4162
SAMO	1375	0.1684	0.8316
SAMO	1532	0.5154	0.4846
SAMO	1560	0.4444	0.5556
SAMO	169	0.3686	0.6314
SAMO	239	0.3666	0.6334
PEKE	1143	0.5856	0.4144
PEKE	1145	0.3948	0.6052
PEKE	1211	0.416	0.584
PEKE	1212	0.2806	0.7194
PEKE	1213	0.4832	0.5168

TABLE 19D-continued

Canid Population[a]	Canid ID No.	k =2 with wolf; 15 Run Average Pop1	Pop2
SHIH	1393	0.3196	0.6804
SHIH	1783	0.3234	0.6766
SHIH	2068	0.347	0.653
SHIH	2859	0.3476	0.6524
SHIH	2860	0.4582	0.5418
IWOF	1581	0.0124	0.9876
IWOF	1761	0.0054	0.9946
IWOF	1792	0.0086	0.9914
IWOF	1906	0.026	0.974
IWOF	1993	0.0046	0.9954
STBD	1075	0.0348	0.9652
STBD	1714	0.0484	0.9516
STBD	1750	0.028	0.972
STBD	2403	0.021	0.979
STBD	2404	0.0122	0.9878
GREY	2477	0.0992	0.9008
GREY	2478	0.0146	0.9854
GREY	2479	0.0062	0.9938
GREY	2480	0.1026	0.8974
GREY	2481	0.0058	0.9942
BELS	1351	0.0142	0.9858
BELS	2111	0.0206	0.9794
BELS	2153	0.0058	0.9942
BELS	2209	0.036	0.964
BELS	2210	0.0268	0.9732
TURV	1622	0.0184	0.9816
TURV	2194	0.0062	0.9938
TURV	2200	0.0178	0.9822
TURV	2222	0.0058	0.9942
BORZ	1378	0.1582	0.8418
BORZ	1401	0.1348	0.8652
BORZ	1808	0.1496	0.8504
BORZ	2268	0.0448	0.9552
BORZ	978	0.0282	0.9718
COLL	1692	0.0102	0.9898
COLL	1701	0.0236	0.9764
COLL	2284	0.0178	0.9822
COLL	373	0.0102	0.9898
COLL	379	0.0064	0.9936
SSHP	1379	0.0186	0.9814
SSHP	1523	0.055	0.945
SSHP	1824	0.0058	0.9942
SSHP	1921	0.0048	0.9952
SSHP	2040	0.0678	0.9322
PUG	1077	0.014	0.986
PUG	1104	0.0376	0.9624
PUG	1183	0.1068	0.8932
PUG	1184	0.0102	0.9898
PUG	1192	0.0064	0.9936
KOMO	1484	0.0138	0.9862
KOMO	1964	0.1264	0.8736
KOMO	2321	0.0356	0.9644
KOMO	2323	0.072	0.928
KOMO	2334	0.0368	0.9632
WHIP	1355	0.005	0.995
WHIP	1395	0.006	0.994
WHIP	1407	0.0048	0.9952
WHIP	1409	0.0034	0.9966
WHIP	1518	0.0038	0.9962
SPOO	1530	0.0322	0.9678
SPOO	1582	0.033	0.967
SPOO	1876	0.0276	0.9724
SPOO	1877	0.0108	0.9892
SPOO	2337	0.0038	0.9962
BICH	1943	0.0252	0.9748
BICH	1954	0.2126	0.7874
BICH	933	0.0202	0.9798
BICH	974	0.09	0.91
KEES	1501	0.0352	0.9648
KEES	1589	0.012	0.988
KEES	1818	0.0182	0.9818
KEES	1819	0.005	0.995
KEES	2072	0.0054	0.9946

TABLE 19D-continued

Canid	Canid	k =2 with wolf; 15 Run Average	
Population[a]	ID No.	Pop1	Pop2
MNTY	1539	0.0104	0.9896
MNTY	1732	0.013	0.987
MNTY	2145	0.0126	0.9874
MNTY	2149	0.0068	0.9932
NELK	2216	0.0596	0.9404
NELK	2239	0.1338	0.8662
NELK	2240	0.0184	0.9816
NELK	2281	0.0078	0.9922
NELK	2295	0.1786	0.8214
KUVZ	1482	0.0726	0.9274
KUVZ	1551	0.2054	0.7946
KUVZ	1672	0.0846	0.9154
KUVZ	1913	0.012	0.988
KUVZ	1994	0.0654	0.9346
DANE	1574	0.0118	0.9882
DANE	1575	0.1232	0.8768
DANE	1580	0.0138	0.9862
DANE	1700	0.0046	0.9954
DANE	1748	0.0798	0.9202
WSSP	1955	0.004	0.996
WSSP	2139	0.0132	0.9868
WSSP	2143	0.0068	0.9932
WSSP	2195	0.0724	0.9276
WSSP	2286	0.0038	0.9962
DOBP	1031	0.0126	0.9874
DOBP	1032	0.1052	0.8948
DOBP	1749	0.0692	0.9308
DOBP	2162	0.0136	0.9864
DOBP	2245	0.0104	0.9896
SSNZ	13352	0.003	0.997
SSNZ	1360	0.0024	0.9976
SSNZ	1827	0.004	0.996
SSNZ	20457	0.0118	0.9882
SSNZ	22647	0.0048	0.9952
ITGY	1568	0.0098	0.9902
ITGY	1570	0.0132	0.9868
ITGY	1862	0.0478	0.9522
ITGY	1881	0.0746	0.9254
ITGY	1882	0.1056	0.8944
OES	1984	0.0508	0.9492
OES	2171	0.0068	0.9932
OES	2179	0.005	0.995
OES	1914	0.0148	0.9852
OES	2626	0.129	0.871
AMWS	2168	0.0194	0.9806
AMWS	2279	0.0062	0.9938
AMWS	2327	0.036	0.964
AMWS	987	0.0054	0.9946
AMWS	988	0.0116	0.9884
MSNZ	1587	0.004	0.996
MSNZ	1756	0.0076	0.9924
MSNZ	1851	0.0046	0.9954
MSNZ	2034	0.0374	0.9626
MSNZ	2613	0.0038	0.9962
AUST	1387	0.0208	0.9792
AUST	1531	0.0048	0.9952
AUST	1564	0.0038	0.9962
AUST	1870	0.026	0.974
AUST	1871	0.0038	0.9962
ECKR	1376	0.0056	0.9944
ECKR	1377	0.003	0.997
ECKR	1400	0.002	0.998
ECKR	1404	0.003	0.997
ECKR	1511	0.0048	0.9952
IRSE	1540	0.003	0.997
IRSE	1617	0.004	0.996
IRSE	1896	0.0104	0.9896
IRSE	2084	0.0046	0.9954
IRSE	2085	0.005	0.995
WHWT	1388	0.0084	0.9916
WHWT	1420	0.0328	0.9672
WHWT	1992	0.0058	0.9942
WHWT	2100	0.0054	0.9946

TABLE 19D-continued

Canid	Canid	k =2 with wolf; 15 Run Average	
Population[a]	ID No.	Pop1	Pop2
WHWT	2128	0.0074	0.9926
PNTR	1382	0.0368	0.9632
PNTR	1383	0.0748	0.9252
PNTR	1869	0.0274	0.9726
PNTR	1938	0.0166	0.9834
PNTR	1948	0.3046	0.6954
BASS	1341	0.0212	0.9788
BASS	1342	0.0078	0.9922
BASS	1506	0.005	0.995
BASS	1917	0.004	0.996
CKCS	1513	0.0502	0.9498
CKCS	1639	0.0058	0.9942
CKCS	1640	0.0068	0.9932
CKCS	1642	0.0074	0.9926
CKCS	2054	0.0064	0.9936
GSNZ	1868	0.224	0.776
GSNZ	22739	0.116	0.884
GSNZ	27093	0.0496	0.9504
GSNZ	27106	0.0094	0.9906
GSNZ	33390	0.0048	0.9952
PHAR	1292	0.1686	0.8314
PHAR	1947	0.3092	0.6908
PHAR	1962	0.1454	0.8546
PHAR	1963	0.0938	0.9062
GOLD	591	0.0058	0.9942
GOLD	592	0.0854	0.9146
GOLD	593	0.0072	0.9928
GOLD	603	0.0092	0.9908
GOLD	604	0.003	0.997
BEAG	1323	0.0048	0.9952
BEAG	1324	0.0458	0.9542
BEAG	1327	0.0068	0.9932
BEAG	994	0.0198	0.9802
BEAG	995	0.012	0.988
BLDH	1186	0.005	0.995
BLDH	1223	0.0086	0.9914
BLDH	1410	0.0038	0.9962
BLDH	1942	0.0068	0.9932
BLDH	1957	0.004	0.996
AIRT	1603	0.0658	0.9342
AIRT	1604	0.0052	0.9948
AIRT	1788	0.0046	0.9954
AIRT	1875	0.0272	0.9728
ACKR	1035	0.0066	0.9934
ACKR	2261	0.0326	0.9674
ACKR	2310	0.003	0.997
ACKR	1956	0.0108	0.9892
ACKR	2260	0.0038	0.9962
AHRT	1120	0.0084	0.9916
AHRT	1121	0.0068	0.9932
AHRT	1122	0.0054	0.9946
AHRT	1123	0.0104	0.9896
AHRT	1124	0.0058	0.9942
CHBR	1546	0.0058	0.9942
CHBR	1549	0.0746	0.9254
CHBR	1813	0.003	0.997
CHBR	2091	0.0178	0.9822
CHBR	888	0.0038	0.9962
CAIR	1405	0.0106	0.9894
CAIR	2096	0.0402	0.9598
CAIR	2113	0.0078	0.9922
CAIR	2125	0.0044	0.9956
CAIR	2131	0.0132	0.9868
PTWD	P142	0.0052	0.9948
PTWD	P1	0.0036	0.9964
PTWD	P238	0.0082	0.9918
PTWD	P25	0.004	0.996
PTWD	P67	0.0062	0.9938
GSHP	1628	0.0038	0.9962
GSHP	1708	0.0518	0.9482
GSHP	1710	0.0456	0.9544
GSHP	1833	0.0068	0.9932
GSHP	1892	0.0058	0.9942

TABLE 19D-continued

Canid Population[a]	Canid ID No.	k =2 with wolf; 15 Run Average Pop1	Pop2
BORD	1648	0.0938	0.9062
BORD	1828	0.0114	0.9886
BORD	1829	0.0034	0.9966
BORD	2002	0.0156	0.9844
BORD	2003	0.0452	0.9548
BEDT	1422	0.0048	0.9952
BEDT	1423	0.005	0.995
BEDT	1424	0.0302	0.9698
BEDT	1426	0.0072	0.9928
CLSP	1008	0.007	0.993
CLSP	1009	0.0042	0.9958
CLSP	1802	0.006	0.994
CLSP	2312	0.0038	0.9962
CLSP	2314	0.005	0.995
IBIZ	1147	0.011	0.989
IBIZ	1148	0.0974	0.9026
IBIZ	1162	0.0106	0.9894
IBIZ	1172	0.011	0.989
IBIZ	1280	0.0148	0.9852
RHOD	1444	0.0042	0.9958
RHOD	1454	0.0154	0.9846
RHOD	1505	0.006	0.994
RHOD	1592	0.0082	0.9918
RHOD	1609	0.0098	0.9902
DACH	1051	0.0166	0.9834
DACH	1052	0.0124	0.9876
DACH	1053	0.0178	0.9822
DACH	1054	0.051	0.949
DACH	1055	0.0072	0.9928
AUSS	1336	0.093	0.907
AUSS	1337	0.0182	0.9818
AUSS	1500	0.0206	0.9794
AUSS	1521	0.0788	0.9212
AUSS	1683	0.0088	0.9912
CHIH	1202	0.004	0.996
CHIH	1203	0.0298	0.9702
CHIH	1204	0.0142	0.9858
CHIH	1205	0.1506	0.8494
CHIH	1206	0.004	0.996
KERY	13878	0.0054	0.9946
KERY	1483	0.0048	0.9952
KERY	1579	0.0058	0.9942
KERY	2014	0.0028	0.9972
KERY	24255	0.0052	0.9948
SCHP	1386	0.0136	0.9864
SCHP	1471	0.0646	0.9354
SCHP	1814	0.0076	0.9924
SCHP	1852	0.0162	0.9838
IRTR	2152	0.0086	0.9914
IRTR	2189	0.0048	0.9952
IRTR	2238	0.0048	0.9952
IRTR	2242	0.0066	0.9934
FCR	1188	0.004	0.996
FCR	2020	0.004	0.996
FCR	2042	0.004	0.996
FCR	2044	0.0038	0.9962
FCR	2259	0.0028	0.9972
SCWT	1624	0.035	0.965
SCWT	1770	0.0038	0.9962
SCWT	2250	0.004	0.996
SCWT	2301	0.0084	0.9916
POM	1190	0.1668	0.8332
POM	1191	0.0042	0.9958
POM	1210	0.0374	0.9626
POM	1238	0.0078	0.9922
POM	1239	0.3112	0.6888
LAB	1310	0.063	0.937
LAB	1465	0.0172	0.9828
LAB	1468	0.0124	0.9876
LAB	1754	0.006	0.994
LAB	1830	0.0076	0.9924
PRES	1082	0.0108	0.9892
PRES	1096	0.0052	0.9948

TABLE 19D-continued

Canid Population[a]	Canid ID No.	k =2 with wolf; 15 Run Average Pop1	Pop2
PRES	1115	0.0092	0.9908
PRES	1127	0.1526	0.8474
PRES	1095	0.0906	0.9094
ROTT	1014	0.0124	0.9876
ROTT	1028	0.0068	0.9932
ROTT	1029	0.0038	0.9962
ROTT	1033	0.0204	0.9796
ROTT	1034	0.0038	0.9962
BULM	1105	0.003	0.997
BULM	1106	0.0034	0.9966
BULM	1107	0.0082	0.9918
BULM	1108	0.005	0.995
BULM	1109	0.0066	0.9934
NEWF	271	0.0114	0.9886
NEWF	274	0.0052	0.9948
NEWF	275	0.0048	0.9952
NEWF	277	0.0078	0.9922
NEWF	278	0.1024	0.8976
GSD	1666	0.0058	0.9942
GSD	1776	0.003	0.997
GSD	2011	0.004	0.996
GSD	2060	0.0042	0.9958
GSD	2086	0.0046	0.9954
FBUL	1507	0.0098	0.9902
FBUL	1508	0.0058	0.9942
FBUL	1509	0.005	0.995
FBUL	2671	0.0464	0.9536
MBLT	1915	0.0038	0.9962
MBLT	2253	0.0054	0.9946
MBLT	2254	0.0454	0.9546
MBLT	2255	0.0046	0.9954
MBLT	2256	0.0078	0.9922
BULD	1193	0.0234	0.9766
BULD	1194	0.0098	0.9902
BULD	1195	0.0162	0.9838
BULD	1197	0.0042	0.9958
BULD	1198	0.0038	0.9962
BOX	1176	0.003	0.997
BOX	1177	0.003	0.997
BOX	1178	0.0048	0.9952
BOX	1179	0.004	0.996
BOX	1304	0.0058	0.9942
MAST	1015	0.0038	0.9962
MAST	1016	0.0104	0.9896
MAST	1017	0.0096	0.9904
MAST	1066	0.0078	0.9922
MAST	991	0.012	0.988
BMD	941	0.0056	0.9944
BMD	943	0.004	0.996
BMD	968	0.0058	0.9942
BMD	1763	0.003	0.997
BMD	969	0.0028	0.9972
GSMD	1547	0.004	0.996
GSMD	1659	0.003	0.997
GSMD	1660	0.006	0.994
GSMD	1662	0.0204	0.9796
GSMD	1663	0.0072	0.9928

[a]See Table 5 for abbreviations of canid populations.

KBB: pbe

TABLE 21A

	AHRT Canid ID NO (missing genotypes)			BASS Canid ID NO (missing genotypes)			BEAG Canid ID NO (missing genotypes)					
Canid population*	1119 (8)	1081 (2)	1121 (6)	24039 (19)	930 (3)	931 (3)	18586 (51)	18424 (13)	1323 (20)	1324 (16)	1325 (8)	1327 (12)
AHTR	0.19003	0	0.2457	0	0	0	3.00E−05	0	0	0	0	0
AMWS	0.00042	0	0	0	0	0	0	0	0	0	0	0
BASS	0	0	0	2.00E−05	2.00E−05	0.36647	0	0	0	0	0	0
BEAG	0	0	0	0	0	0.00068	0.00859	0.00634	0.99969	0.99504	0.99062	0.99804
BEAC	0	0	0	0	0	0.00014	0	0	0	0	0	0
BMD	0	0	0	0	0	0	1.00E−05	0	0	0.0049	0.00893	0
BICH	0	0	0	0	0	0	0	0	0	2.00E−05	0	0
BORZ	0	0	0	9.00E−05	0.00021	0	0.00012	0.01475	0	0	0	0
BOX	0	0	0	0	0	0	0	0	0	0	0	0
BULM	0	0.00023	0	0	1.00E−05	0.58998	0.00739	0	0	0	0	0
ACKR	0.0015	0	0	0	0	0	0	0	0	0	0	0
DACH	0.00304	0.99974	0.0102	0.99988	0.9996	0.03153	0.01324	0.97888	0	0	0	0.00142
DALM	0	0	0	0	0	0	0	0	0	0	0	0
ESPR	0	0	0.00011	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0	0	0	0	0
FCR	0	0	0.2676	0	0	0	0.00017	0	0	0	0	0.00023
EFOX	0	0	0	0	0	0	7.00E−05	0	0	0	0	0
FBLD	0	0	0	0	0	0	0	0	0	0	0	0
GPIN	0	0	0.00039	0	0	0	0	0	0	0	0	0
GSHP	0.00029	0	0.00037	0	0	0	0	0	0	0	0	0
GOLD	0	1.00E−05	0.4753	0	0	0.00759	7.00E−05	0	0	0	0	0
IBIZ	0.76932	0	0.00027	0	0	0	0	0	0	0	0	0
IRSE	0	0	0	0	0	0	0	0	0	0	0	0
IRWS	0	0	0	0	0	0	0.001	0	0	0	0	0
LAB	0	0	0	0	0.00013	6.00E−05	0	0	0	0	0	0
MAST	0	0	0	0	0	0	0.92848	0	0	0	0	0
PBGV	0	0	0	0	0	0	2.00E−05	0	0	0	0	0
PAPI	0	0	0	0	0	0	3.00E−05	0	0	0	0	0
PTWD	0	0	0	0	0	0.00346	0	0	0	0	0	0
ROTT	0	0	0	0	0	0	0.04067	0	0.00029	0	0.00043	0
STBD	0.03485	0	0	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	1.00E−05	0	0	0	0	0
SPIN	0	0	0	0	0	0	0	0	0	0	0	1.00E−05
SCOL	0	0	0	0	0	0	0	0	0	0	0	0
SSCH	0	0	0	0	0	0	0	1.00E−05	0	0	0	0.00028
WSSP	0.0005	0	0	0	0	1.00E−05	0	0	0	0	0	0

TABLE 21B

	BMD Canid Identification Number (missing genotypes)										Borzoi	
Canid population*	918 (16)	883 (6)	941 (7)	943 (11)	21287 (16)	968 (45)	970 (17)	971 (7)	973 (28)	976 (9)	1655 (24)	978 (0)	979 (22)
AHTR	0	0	0	0	0	0	0	0	0	0	0	0	0
AMWS	0	0	0	0	0	0	0	0	0	0	0	0	0
BASS	0	0	0	0	0	0	0	0	0	0	0	0.8529	0.00981
BEAG	0	0	0	0	0	0	0	0	0	0	0	0.00886	0
BEAC	0	0	0	0	0	0	0	0	0	0	0	0	0
BMD	0.99999	0.99999	0.99999	0.99995	0.99999	0.99999	0.99999	0.99999	0.99999	0.99999	0	0	0
BICH	0	0	0	0	0	0	0	0	0	0	0	0	0
BORZ	0	0	0	0	0	0	0	0	0	0	0	0.06219	0
BOX	0	0	0	0	0	0	0	0	0	0	0	0	0
BULM	0	0	0	0	0	0	0	0	0	0	0	0	0.0025
ACKR	0	0	0	0	0	0	0	0	0	0	0	0	0
DACH	0	0	0	0	0	0	0	0	0	0	0.99999	0.07511	0.98767
DALM	0	0	0	0	0	0	0	0	0	0	0	1.00E−05	0
ESPR	0	0	0	0	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0	0	0	0	0	0
FCR	0	0	0	0	0	0	0	0	0	0	0	0	0
EFOX	0	0	0	0	0	0	0	0	0	0	0	4.00E−05	0
FBLD	0	0	0	0	0	0	0	0	0	0	0	0	0
GPIN	0	0	0	0	0	0	0	0	0	0	0	0	0
GSHP	0	0	0	0	0	0	0	0	0	0	0	0	0
GOLD	0	0	0	4.00E−05	0	0	0	0	0	0	0	0.0001	0
IBIZ	0	0	0	0	0	0	0	0	0	0	0	0	0
IRSE	0	0	0	0	0	0	0	0	0	0	0	0	0

TABLE 21B-continued

	BMD Canid Identification Number (missing genotypes)										Borzoi		
Canid population*	918 (16)	883 (6)	941 (7)	943 (11)	21287 (16)	968 (45)	970 (17)	971 (7)	973 (28)	976 (9)	1655 (24)	978 (0)	979 (22)
IRWS	0	0	0	0	0	0	0	0	0	0	0	0	0
LAB	0	0	0	0	0	0	0	0	0	0	0	0.00018	0
MAST	0	0	0	0	0	0	0	0	0	0	0	4.00E−05	0
PBGV	0	0	0	0	0	0	0	0	0	0	0	0	0
PAPI	0	0	0	0	0	0	0	0	0	0	0	0.0005	0
PTWD	0	0	0	0	0	0	0	0	0	0	0	0	0
ROTT	0	0	0	0	0	0	0	0	0	0	0	0	0
STBD	0	0	0	0	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	0	0	0	0	0	1.00E−05	0
SPIN	0	0	0	0	0	0	0	0	0	0	0	0	0
SCOL	0	0	0	0	0	0	0	0	0	0	0	0	0
SSCH	0	0	0	0	0	0	0	0	0	0	0	0	0
WSSP	0	0	0	0	0	0	0	0	0	0	0	0	0

TABLE 21C

	BOX Canid Identification Number (missing genotypes)										
Canid population*	584 (56)	585 (18)	583 (14)	586 (13)	587 (43)	588 (0)	589 (6)	590 (0)	997 (0)	1302 (30)	1304 (12)
AHTR	0	0	0	0	0	0	0	0	0	0	0
AMWS	0	0	0	0	0	0	0	0	0	0	0
BASS	0	0	0	0	0	0	0	0	0	0	0
BEAG	0	0	0	0	0	0	0	0	0	0	0
BEAC	0	0	0	0	0	0	0	0	0	0	0
BMD	0	0	0	0	0	0	0	0	0	0	0
BICH	0	0	0	0	0	0	0	0	0	0	0
BORZ	0	0	0	0	0	0	0	0	0	0	0
BOX	0.99999	0.99999	0.99999	0.99996	0.99996	0.99999	0.99391	0.99999	0.99999	0.99999	0.99999
BULM	0	0	0	0	0	0	0	0	0	0	0
ACKR	0	0	0	0	0	0	0	0	0	0	0
DACH	0	0	0	0	0	0	0.00153	0	0	0	0
DALM	0	0	0	0	0	0	0	0	0	0	0
ESPR	0	0	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0	0	0	0
FCR	0	0	0	0	0	0	0	0	0	0	0
EFOX	0	0	0	0	0	0	0	0	0	0	0
FBLD	0	0	0	0	0	0	0	0	0	0	0
GPIN	0	0	0	0	0	0	0	0	0	0	0
GSHP	0	0	0	0	0	0	0	0	0	0	0
GOLD	0	0	0	3.00E−05	0	0	2.00E−05	0	0	0	0
IBIZ	0	0	0	0	0	0	0	0	0	0	0
IRSE	0	0	0	0	0	0	0	0	0	0	0
IRWS	0	0	0	0	0	0	0	0	0	0	0
LAB	0	0	0	0	0	0	0	0	0	0	0
MAST	0	0	0	0	0	0	0	0	0	0	0
PBGV	0	0	0	0	0	0	0	0	0	0	0
PAPI	0	0	0	0	0	0	0	0	0	0	0
PTWD	0	0	0	0	0	0	0	0	0	0	0
ROTT	0	0	0	0	3.00E−05	0	0.00451	0	0	0	0
STBD	0	0	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	0	0	0	0	0
SPIN	0	0	0	0	0	0	0	0	0	0	0
SCOL	0	0	0	0	0	0	0	0	0	0	0
SSCH	0	0	0	0	0	0	0	0	0	0	0
WSSP	0	0	0	0	0	0	0	0	0	0	0

TABLE 21D

	BULM Canid Identification Number (missing genotypes)								FCR Canid Identification Number (missing genotypes)				
Canid population*	1098 (23)	1105 (4)	1106 (16)	1108 (24)	1109 (0)	1110 (5)	1111 (2)	1112 (11)	22417 (29)	746 (39)	752 (13)	839 (33)	791 (7)
AHTR	0	0	0	0	0	0	0	0	0	0	0	0	0
AMWS	0	0	0	0	0	0	0	0	0	0	0	0	0
BASS	0	0	0	0	0	0	0	0	0	0	0	0	0
BEAG	0	0	0	0	0	0	0	0	0	0	0	0	0
BEAC	0	0	0	0	0	0	0	0	0	0	0	0	0
BMD	0	0	0	0	0	0	0	0	0	0	0	0	0
BICH	0	0	0	0	0	0	0	0	0	0	0	0	0
BORZ	0	0	0	0	0	0	0	0	0	0	0	0	0
BOX	0	0	0	0	0	0	0	0	0	0	0	0	0
BULM	0.99999	0.99999	0.99998	0.99999	0.99999	0.99999	0.99999	0.99999	0	0	0	0	0
ACKR	0	0	0	0	0	0	0	0	0	0	0	0	0
DACH	0	0	0	0	0	0	0	0	0	0	0	0.00017	9.00E−05
DALM	0	0	0	0	0	0	0	0	0	0	0	0	0
ESPR	0	0	0	0	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0	0	0	0	0	0
FCR	0	0	0	0	0	0	0	0	0.99999	0.99999	0	0.99982	0.99986
EFOX	0	0	0	0	0	0	0	0	0	0	0	0	0
FBLD	0	0	0	0	0	0	0	0	0	0	0	0	0
GPIN	0	0	0	0	0	0	0	0	0	0	0	0	0
GSHP	0	0	0	0	0	0	0	0	0	0	0	0	0
GOLD	0	0	1.00E−05	0	0	0	0	0	0	0	0.99997	0	0
IBIZ	0	0	0	0	0	0	0	0	0	0	0	0	0
IRSE	0	0	0	0	0	0	0	0	0	0	0	0	0
IRWS	0	0	0	0	0	0	0	0	0	0	0	0	0
LAB	0	0	0	0	0	0	0	0	0	0	0	0	0
MAST	0	0	0	0	0	0	0	0	0	0	0	0	0
PBGV	0	0	0	0	0	0	0	0	0	0	0	0	0
PAPI	0	0	0	0	0	0	0	0	0	0	0	0	0
PTWD	0	0	0	0	0	0	0	0	0	0	0	0	0
ROTT	0	0	0	0	0	0	0	0	0	0	2.00E−05	0	4.00E−05
STBD	0	0	0	0	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	0	0	0	0	0	0	0
SPIN	0	0	0	0	0	0	0	0	0	0	0	0	0
SCOL	0	0	0	0	0	0	0	0	0	0	0	0	0
SSCH	0	0	0	0	0	0	0	0	0	0	0	0	0
WSSP	0	0	0	0	0	0	0	0	0	0	0	0	0

TABLE 21E

	DACH Canid Identification Number (missing genotypes)									
Canid population*	20345 (8)	20274 (14)	1036 (19)	1037 (9)	1038 (26)	1048 (15)	1049 (10)	1050 (8)	1060 (13)	1061 (28)
AHTR	0	0	0	0	0	0	0	0	0	0
AMWS	0	0	0	0	0	0	0	0	0	0
BASS	0	0	0	5.00E−05	0	0	0	0	0	0
BEAG	0	0	0	0	2.00E−05	0	0	0	0	0
BEAC	0	0	0	0	0	0	0	0	0	0
BMD	0	0	0	0	0	0	0	0	0	0
BICH	0	0	0	0	0	0	0	0	0	0
BORZ	0.00012	0	0	0	0	0	0	0	0	0
BOX	0	0	0	0	0	0	0	0	0	0
BULM	0.0001	0	0	0	0	0	0	0	0	0
ACKR	0	0	0	0	0	0	0	0	0	0
DACH	0.99971	4.00E−05	0.99837	0.99993	0.99805	0.99999	0.99689	0.99999	0.99998	0.66498
DALM	0	0	0	0	0	0	0	0	0	0
ESPR	0	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0	0	0
FCR	0	0	0	0	2.00E−05	0	0	0	0	0
EFOX	0	0	0	0	0	0	0	0	0	0
FBLD	0	0	0	0	0	0	0	0	0	0
GPIN	0	0	0	0	0	0	0	0	0	0
GSHP	0	0	0	0	0	0	0	0	0	0
GOLD	0	0	0.00162	0	0.00188	0	0.00308	0	1.00E−05	1.00E−05
IBIZ	0	0	0	0	0	0	0	0	0	0
IRSE	1.00E−05	0	0	0	0	0	0	0	0	0

TABLE 21E-continued

	DACH Canid Identification Number (missing genotypes)									
Canid population*	20345 (8)	20274 (14)	1036 (19)	1037 (9)	1038 (26)	1048 (15)	1049 (10)	1050 (8)	1060 (13)	1061 (28)
IRWS	0	0	0	0	0	0	0	0	0	0
LAB	2.00E−05	0	0	0	0	0	0	0	0	0
MAST	0	0	0	0	0	0	0	0	0	0
PBGV	0	0	0	0	0	0	0	0	0	0
PAPI	0	0	0	0	0	0	0	0	0	0
PTWD	0	0	0	0	0	0	0	0	0	0
ROTT	0	0.99994	0	0	0	0	1.00E−05	0	0	0.33498
STBD	0	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	0	0	0	0
SPIN	0	0	0	0	0	0	0	0	0	0
SCOL	0	0	0	0	0	0	0	0	0	0
SSCH	0	0	0	0	0	0	0	0	0	0
WSSP	0	0	0	0	0	0	0	0	0	0

TABLE 21F

	GOLD Canid Identification Number (missing genotypes)									
Canid population*	816 (0)	807 (1)	50 (10)	614 (16)	18477 (26)	591 (7)	592 (14)	593 (22)	603 (27)	604 (4)
AHTR	0	0	0	0	0	0	0	0	0	0
AMWS	0	0	0	0	0	0	0	0	0	0
BASS	0	0	0	0	0	0	0	0	0	0
BEAG	0	0	6.00E−05	0	0	0	0	0	0	0
BEAC	0	0	0	0	0	0	0	0	0	0
BMD	0	0	0	0.19213	0	0	0	0	0	0
BICH	0	0	0	0	0	0	0	0	0	0
BORZ	0	0	0	0	0	0	0	0	0	0
BOX	0	0	0	0	0	0	0	0	0	0
BULM	1.00E−05	0	0	0	0	0	0.00011	0	0	0
ACKR	0	0	0	0	0	0	0	0	0	0
DACH	0	0	0.7605	7.00E−05	0	0	0	0.00999	0.00015	0
DALM	0	0	0	0	0	0	0	0	0	0
ESPR	0	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0	0	0
FCR	0	0	0	0	0	0	0	0	0	0
EFOX	0	0	0	0	0	0	0	0	0	0
FBLD	0	0	0	0	0	0	0	0	0	0
GPIN	0	0	0	0	0	0	0	0	0	0
GSHP	0	0	0	0	0	0	0	0	0	0
GOLD	0.99998	0.99999	0.23937	0.80778	0.99999	0.78123	0.99987	0.99	0.99984	0.99979
IBIZ	0	0	3.00E−05	0	0	0	0	0	0	0
IRSE	0	0	0	0	0	0	0	0	0	0
IRWS	0	0	0	0	0	0	0	0	0	0
LAB	0	0	0	0	0	0	0	0	0	0
MAST	0	0	0	0	0	0	0	0	0	0
PBGV	0	0	0	0	0	0	0	0	0	0
PAPI	0	0	0	0	0	0	0	0	0	0
PTWD	0	0	0	0	0	0	0	0	0	0
ROTT	0	0	0	0	0	0.21876	0	0	0	0.0002
STBD	0	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	0	0	0	0
SPIN	0	0	0	0	0	0	0	0	0	0
SCOL	0	0	0	0	0	0	0	0	0	0
SSCH	0	0	0	0	0	0	0	0	0	0
WSSP	0	0	0	0	0	0	0	0	0	0

TABLE 21G

	ROTT Canid Identification Number (missing genotypes)									
Canid population*	817 (2)	818 (2)	886 (2)	896 (0)	22720 (15)	1014 (14)	1028 (0)	1029 (26)	1033 (79)	1034 (0)
AHTR	0	0	0	0	0	0	0	0	0	0
AMWS	0	0	0	0	0	0	0	0	0	0
BASS	0	0	0	0	0	0	0	0	0	0
BEAG	0	0	0	0	0	2.00E−05	0	0	0	0
BEAC	0	0	0	0	0	0	0	0	0	0
BMD	0	0	0	0	0	0	0	0	0	0
BICH	0	0	0	0	0	0	0	0	0	0
BORZ	0	0	0	0	0	0	0	0	0	0
BOX	0	0	0	0	0	0	0	0	0	0
BULM	0	0	0	0	0	0	0	0	0	0
ACKR	0	0	0	0	0	0	0	0	0	0
DACH	0	0	0	0	0	0.0017	0	0	0.00056	0
DALM	0	0	0	0	0	0	0	0	0	0
ESPR	0	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0	0	0
FCR	0	0	0	0	0	0	0	0	0	0
EFOX	0	0	0	0	0	0	0	0	0	0
FBLD	0	0	0	0	0	0	0	0	0	0
GPIN	0	0	0	0	0	0	0	0	0	0
GSHP	0	0	0	0	0	0	0	0	0	0
GOLD	0.02636	0	0	0	0	5.00E−05	0	0	0	0
IBIZ	0	0	0	0	0	0	0	0	0	0
IRSE	0	0	0	0	0	0	0	0	0	0
IRWS	0	0	0	0	0	0	0	0	0	0
LAB	0	0	0	0	0	0	0	0	0	0
MAST	3.00E−05	0	0	0	0	0	0	0	0	0
PBGV	0	0	0	0	0	0	0	0	0	0
PAPI	0	0	0	0	0	0	0	0	0	0
PTWD	0	0	0	0	0	0	0	0	0	0
ROTT	0.97359	0.99999	0.99999	0.99999	0.99999	0.9982	0.99999	0.99998	0.99943	0.99999
STBD	0	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	0	0	0	0
SPIN	0	0	0	0	0	0	0	0	0	0
SCOL	0	0	0	0	0	0	0	0	0	0
SSCH	0	0	0	0	0	0	0	0	0	0
WSSP	0	0	0	0	0	0	0	0	0	0

TABLE 21H

	MAST Canid ID NO (missing genotypes)					SCOL Canid ID NO (missing genotypes)			
Canid population[a]	23967 (14)	991 (6)	1015 (9)	1016 (11)	992 (1)	1013 (80)	15628 (24)	375 (12)	363 (12)
AHTR	0	0	0	0	0	0	0	0	0
AMWS	0	0	0	0	0	0	0	0	0
BASS	0	0	0	0	0	0	0	0	0
BEAG	0	0	0	0	0	0	0	0	0
BEAC	0	0	0	0	0	0	0	0	0
BMD	0	0	0	0	0	0	0	0	0
BICH	0	0	0	0	0	0	0	0	0
BORZ	0	0	0	0	0	0	0	0	0
BOX	0	0	0	0	0	0	0	0	0
BULM	0	0	0	0	0	3.00E−05	0	4.00E−05	0
ACKR	0	0	0	0	0	0	0	0	0
DACH	0	0	0	0	0	0	0.00413	0	0.00057
DALM	0	0	0	0	0	0	0	0	0
ESPR	0	0	0	0	0	0	0	0	0
FSP	0	0	0	0	0	0	0	0.00503	0
FCR	0	0	0	0	0	0	0	0	0
EFOX	0	0	0	0	0	0	0	0	0
FBLD	0	0	0	0	0	0	9.00E−05	1.00E−05	0
GPIN	0	0	0	0	0	0	0	0	0
GSHP	0	0	0	0	0	0	0	0	0
GOLD	0.00012	0	0	0	0.00146	0	4.00E−05	0.00043	0.00105
IBIZ	0	0	0	0	0	0	0	0	0
IRSE	0	0	0	0	0	0	0	0	0

TABLE 21H-continued

	MAST Canid ID NO (missing genotypes)						SCOL Canid ID NO (missing genotypes)		
Canid population[a]	23967 (14)	991 (6)	1015 (9)	1016 (11)	992 (1)	1013 (80)	15628 (24)	375 (12)	363 (12)
IRWS	0	0	0	0	0	0	0	0	0
LAB	0	0	0	0	0	0	0	0	0
MAST	0.99987	0.99999	0.99999	0.99999	0.99852	0.99995	0	0	0
PBGV	0	0	0	0	0	0	0	0	0
PAPI	0	0	0	0	0	0	0	0	0
PTWD	0	0	0	0	0	0	0	0	0
ROTT	0	0	0	0	0	0	0	0	0
STBD	0	0	0	0	0	0	0	0	0
SCDH	0	0	0	0	0	0	0	0	0
SPIN	0	0	0	0	0	0	0	0	0
SCOL	0	0	0	0	0	0	0.99572	0.99445	0.99837
SSCH	0	0	0	0	0	0	0	0	0
WSSP	0	0	0	0	0	0	0	0	0

[a]See Table 5 for abbreviations of canid populations.

KBB:pbe

SEQUENCE LISTING

Sequence total quantity: 327

SEQ ID NO: 1 moltype = DNA length = 20
FEATURE Location/Qualifiers
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 1
aacatggtga cgagaaggct 20

SEQ ID NO: 2 moltype = DNA length = 22
FEATURE Location/Qualifiers
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 2
ccaccactta cataaacatg gc 22

SEQ ID NO: 3 moltype = DNA length = 17
FEATURE Location/Qualifiers
misc_feature 1..17
note = Oligonucleotide Primer
source 1..17
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 3
atagcccatg aaatcca 17

SEQ ID NO: 4 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 4
cccttaggag gaggcaagac 20

SEQ ID NO: 5 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 5
ctatgtgcac gctgagagag 20

SEQ ID NO: 6 moltype = DNA length = 20

-continued

FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 6	
gtcagagccc cagagacaag	20
SEQ ID NO: 7	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 7	
ccagattaac caggatgagg	20
SEQ ID NO: 8	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 8	
tctggattgt ggtcacaacc	20
SEQ ID NO: 9	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 9	
tcagcatcta gaaaattagg t	21
SEQ ID NO: 10	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 10	
tctttgaaat gaaatgggcc	20
SEQ ID NO: 11	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 11	
tgcgatacac ttagaaaaca gg	22
SEQ ID NO: 12	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 12	
gcaaatggca agatttcgtt	20
SEQ ID NO: 13	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct

-continued

SEQUENCE: 13
tctttggtaa agtctccatg gg 22

SEQ ID NO: 14 moltype = DNA length = 21
FEATURE Location/Qualifiers
misc_feature 1..21
note = Oligonucleotide Primer
source 1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 14
gaaagggtgt ggataaagag c 21

SEQ ID NO: 15 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 15
ggaacagatg agaagcatgg 20

SEQ ID NO: 16 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 16
accgtgcaca agtcagtcag 20

SEQ ID NO: 17 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 17
aggattttgt ggtgattggg 20

SEQ ID NO: 18 moltype = DNA length = 21
FEATURE Location/Qualifiers
misc_feature 1..21
note = Oligonucleotide Primer
source 1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 18
tactcgttct gtgccatttc t 21

SEQ ID NO: 19 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 19
cagctgtccg gggatataaa 20

SEQ ID NO: 20 moltype = DNA length = 21
FEATURE Location/Qualifiers
misc_feature 1..21
note = Oligonucleotide Primer
source 1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 20
gcccctattt ttttttttcc c 21

SEQ ID NO: 21 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20

-continued

	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 21		
tttaggcatt tgaggaggag		20
SEQ ID NO: 22	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 22		
ctgctctctc ccccaactta		20
SEQ ID NO: 23	moltype = DNA length = 18	
FEATURE	Location/Qualifiers	
misc_feature	1..18	
	note = Oligonucleotide Primer	
source	1..18	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 23		
attcccttgt attgctca		18
SEQ ID NO: 24	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 24		
tgaggctccg tgggtatgtg		20
SEQ ID NO: 25	moltype = DNA length = 22	
FEATURE	Location/Qualifiers	
misc_feature	1..22	
	note = Oligonucleotide Primer	
source	1..22	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 25		
cagtaatgtt ttgtggcctc tg		22
SEQ ID NO: 26	moltype = DNA length = 18	
FEATURE	Location/Qualifiers	
misc_feature	1..18	
	note = Oligonucleotide Primer	
source	1..18	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 26		
tgccctcaaa caatttgc		18
SEQ ID NO: 27	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 27		
tcgggatgtt tctcttccac		20
SEQ ID NO: 28	moltype = DNA length = 22	
FEATURE	Location/Qualifiers	
misc_feature	1..22	
	note = Oligonucleotide Primer	
source	1..22	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 28		
tatttaaaaa atcccaggca ca		22

-continued

SEQ ID NO: 29	moltype = DNA length = 17
FEATURE	Location/Qualifiers
misc_feature	1..17
	note = Oligonucleotide Primer
source	1..17
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 29	
caacccaggg tggaagc	17
SEQ ID NO: 30	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 30	
atccaggtct ggaatacccc	20
SEQ ID NO: 31	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 31	
ttaagcctta ttttgtgttg gg	22
SEQ ID NO: 32	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 32	
cttttagggt gccttcaacc	20
SEQ ID NO: 33	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 33	
acctccaaga tggctcttga	20
SEQ ID NO: 34	moltype = DNA length = 17
FEATURE	Location/Qualifiers
misc_feature	1..17
	note = Oligonucleotide Primer
source	1..17
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 34	
attccccagc gatacca	17
SEQ ID NO: 35	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 35	
tggacgctaa gcctgacttt	20
SEQ ID NO: 36	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20

-continued

	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 36		
tgggatgtgt gtcatgtgtg		20
SEQ ID NO: 37	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 37		
aacttctggc tttcataccg		20
SEQ ID NO: 38	moltype = DNA length = 19	
FEATURE	Location/Qualifiers	
misc_feature	1..19	
	note = Oligonucleotide Primer	
source	1..19	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 38		
ctggcagatt acaggtagc		19
SEQ ID NO: 39	moltype = DNA length = 23	
FEATURE	Location/Qualifiers	
misc_feature	1..23	
	note = Oligonucleotide Primer	
source	1..23	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 39		
ttctctgtgt atgtgtacgc ttg		23
SEQ ID NO: 40	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 40		
cattctgggc aggtttcatt		20
SEQ ID NO: 41	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 41		
tgcatcattt gtgggtgttt		20
SEQ ID NO: 42	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
misc_feature	1..21	
	note = Oligonucleotide Primer	
source	1..21	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 42		
ataccactgt ccctcctctt a		21
SEQ ID NO: 43	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
misc_feature	1..24	
	note = Oligonucleotide Primer	
source	1..24	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 43		
ggttattgta aagtctgagt gttg		24
SEQ ID NO: 44	moltype = DNA length = 20	

-continued

FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 44	
gcacattcac aaagtggtgc	20
SEQ ID NO: 45	moltype = DNA length = 19
FEATURE	Location/Qualifiers
misc_feature	1..19
	note = Oligonucleotide Primer
source	1..19
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 45	
aagcatccag aatcctgg	19
SEQ ID NO: 46	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 46	
tgtcataata gttggaatga c	21
SEQ ID NO: 47	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 47	
cctggattaa cagttgtctg g	21
SEQ ID NO: 48	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 48	
ttttcaccag ctctgagata gc	22
SEQ ID NO: 49	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 49	
tgcagggcag aggctggagg	20
SEQ ID NO: 50	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 50	
tctcatgcaa atcttcgttc a	21
SEQ ID NO: 51	moltype = DNA length = 19
FEATURE	Location/Qualifiers
misc_feature	1..19
	note = Oligonucleotide Primer
source	1..19
	mol_type = other DNA
	organism = synthetic construct

-continued

SEQUENCE: 51
aaggcaggag gaggagcac 19

SEQ ID NO: 52 moltype = DNA length = 19
FEATURE Location/Qualifiers
misc_feature 1..19
note = Oligonucleotide Primer
source 1..19
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 52
tcagctcagg gagtgatcc 19

SEQ ID NO: 53 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 53
aaatgggtaa ttcatccagt gc 22

SEQ ID NO: 54 moltype = DNA length = 19
FEATURE Location/Qualifiers
misc_feature 1..19
note = Oligonucleotide Primer
source 1..19
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 54
atgtggggta aaataaagg 19

SEQ ID NO: 55 moltype = DNA length = 18
FEATURE Location/Qualifiers
misc_feature 1..18
note = Oligonucleotide Primer
source 1..18
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 55
gagggatggc tgtcaaga 18

SEQ ID NO: 56 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 56
aggctctccg agggtaagac 20

SEQ ID NO: 57 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 57
ggctggactt ttgtcatttg 20

SEQ ID NO: 58 moltype = DNA length = 21
FEATURE Location/Qualifiers
misc_feature 1..21
note = Oligonucleotide Primer
source 1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 58
cttcccatta tagccctgtc c 21

SEQ ID NO: 59 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20

-continued

	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 59		
tccctcctga cactgcttta		20
SEQ ID NO: 60	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
misc_feature	1..21	
	note = Oligonucleotide Primer	
source	1..21	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 60		
ccctttgca ctactgttga g		21
SEQ ID NO: 61	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 61		
ttctcgtgac ccctaaagga		20
SEQ ID NO: 62	moltype = DNA length = 23	
FEATURE	Location/Qualifiers	
misc_feature	1..23	
	note = Oligonucleotide Primer	
source	1..23	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 62		
aaacaagaca gtaggaagag agg		23
SEQ ID NO: 63	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 63		
tgggagcttc atacaaatgc		20
SEQ ID NO: 64	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 64		
aattactcgg cctctctggg		20
SEQ ID NO: 65	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
misc_feature	1..21	
	note = Oligonucleotide Primer	
source	1..21	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 65		
gtgatccact tgcttgtatc c		21
SEQ ID NO: 66	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 66		
catgcctgac tcaactgatg		20

-continued

SEQ ID NO: 67	moltype = DNA length = 19
FEATURE	Location/Qualifiers
misc_feature	1..19
	note = Oligonucleotide Primer
source	1..19
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 67	
ggggctctgt tattaggtg	19
SEQ ID NO: 68	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 68	
tgacttactc tagccacttt t	21
SEQ ID NO: 69	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 69	
ttacatttag gggctccagt	20
SEQ ID NO: 70	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 70	
gccttctttg gaaaaacacc	20
SEQ ID NO: 71	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 71	
acacatttgt gtgcttgtct tg	22
SEQ ID NO: 72	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 72	
acaagccgac tctagcgaaa	20
SEQ ID NO: 73	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 73	
ggtcccatcc tcaaaatcct c	21
SEQ ID NO: 74	moltype = DNA length = 19
FEATURE	Location/Qualifiers
misc_feature	1..19
	note = Oligonucleotide Primer
source	1..19

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	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 74	
atttgccagg taccattcc	19
SEQ ID NO: 75	moltype = DNA length = 18
FEATURE	Location/Qualifiers
misc_feature	1..18
	note = Oligonucleotide Primer
source	1..18
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 75	
gcagacgagc acaccgaa	18
SEQ ID NO: 76	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 76	
aatatgggag aggagaagag gg	22
SEQ ID NO: 77	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 77	
tggctgtggc taaggctttg t	21
SEQ ID NO: 78	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 78	
ccctctactt atgtctcggc c	21
SEQ ID NO: 79	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 79	
ccaagaacag cctaagctgg	20
SEQ ID NO: 80	moltype = DNA length = 18
FEATURE	Location/Qualifiers
misc_feature	1..18
	note = Oligonucleotide Primer
source	1..18
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 80	
cagctggatt ggggactc	18
SEQ ID NO: 81	moltype = DNA length = 18
FEATURE	Location/Qualifiers
misc_feature	1..18
	note = Oligonucleotide Primer
source	1..18
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 81	
ccgatgcctg tcctttga	18
SEQ ID NO: 82	moltype = DNA length = 22

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FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 82	
agtacttgag gcttggagtc ag	22
SEQ ID NO: 83	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 83	
atggcaggtc aagagtatgg	20
SEQ ID NO: 84	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 84	
ttcattggct ggtgactttg	20
SEQ ID NO: 85	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 85	
agtaaagggt tctcaagtgt gc	22
SEQ ID NO: 86	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 86	
cagttcatcc ttccccctct c	21
SEQ ID NO: 87	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 87	
gattaaaagg gcaagcaacc	20
SEQ ID NO: 88	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 88	
cagtgagcaa agcaaatgaa	20
SEQ ID NO: 89	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct

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SEQUENCE: 89
aaggtagtcc cacgatcctc 20

SEQ ID NO: 90 moltype = DNA length = 21
FEATURE Location/Qualifiers
misc_feature 1..21
note = Oligonucleotide Primer
source 1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 90
tgatacccat taagtccatc c 21

SEQ ID NO: 91 moltype = DNA length = 24
FEATURE Location/Qualifiers
misc_feature 1..24
note = Oligonucleotide Primer
source 1..24
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 91
ccaatattgt taagaagttc aagc 24

SEQ ID NO: 92 moltype = DNA length = 24
FEATURE Location/Qualifiers
misc_feature 1..24
note = Oligonucleotide Primer
source 1..24
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 92
cctctagatc catccatatt gtca 24

SEQ ID NO: 93 moltype = DNA length = 23
FEATURE Location/Qualifiers
misc_feature 1..23
note = Oligonucleotide Primer
source 1..23
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 93
aatggtggtg atattcacag aga 23

SEQ ID NO: 94 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 94
aggcagagct aaacctgagc 20

SEQ ID NO: 95 moltype = DNA length = 24
FEATURE Location/Qualifiers
misc_feature 1..24
note = Oligonucleotide Primer
source 1..24
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 95
gaaattgttc catttctgtg acat 24

SEQ ID NO: 96 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 96
tacatctcca catctactga 20

SEQ ID NO: 97 moltype = DNA length = 18
FEATURE Location/Qualifiers
misc_feature 1..18

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	note = Oligonucleotide Primer	
source	1..18	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 97		
atggcccacc gatacaca		18
SEQ ID NO: 98	moltype = DNA length = 16	
FEATURE	Location/Qualifiers	
misc_feature	1..16	
	note = Oligonucleotide Primer	
source	1..16	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 98		
ttccccaagc cacacc		16
SEQ ID NO: 99	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
misc_feature	1..21	
	note = Oligonucleotide Primer	
source	1..21	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 99		
cagcaattgg acaagaaaaa g		21
SEQ ID NO: 100	moltype = DNA length = 19	
FEATURE	Location/Qualifiers	
misc_feature	1..19	
	note = Oligonucleotide Primer	
source	1..19	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 100		
cagcgaattt gggcactaa		19
SEQ ID NO: 101	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 101		
ccattcgcca caagtaggtt		20
SEQ ID NO: 102	moltype = DNA length = 18	
FEATURE	Location/Qualifiers	
misc_feature	1..18	
	note = Oligonucleotide Primer	
source	1..18	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 102		
ttccagactg ctgcctcc		18
SEQ ID NO: 103	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 103		
ccccaaatac atccctacat		20
SEQ ID NO: 104	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 104		
cgtgctttgt tatggcttga		20

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SEQ ID NO: 105 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 105
tacccataaa gttgggcttg 20

SEQ ID NO: 106 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 106
ctttcttccg ccactacctg 20

SEQ ID NO: 107 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 107
aatggcaagg atgctactcc 20

SEQ ID NO: 108 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 108
actggacact tcttttcaga cg 22

SEQ ID NO: 109 moltype = DNA length = 23
FEATURE Location/Qualifiers
misc_feature 1..23
note = Oligonucleotide Primer
source 1..23
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 109
actcattttc tcttattctg cag 23

SEQ ID NO: 110 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 110
gctctcatcc ctgtgaaagc 20

SEQ ID NO: 111 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 111
aaaaacccac aacaaagtgc 20

SEQ ID NO: 112 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20

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	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 112		
caagggttag cacctgggta		20
SEQ ID NO: 113	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 113		
gggtgtgaaa acagccaact		20
SEQ ID NO: 114	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 114		
tggcatattc aacaaattgc		20
SEQ ID NO: 115	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 115		
ctgggtggtt cagtagttgg		20
SEQ ID NO: 116	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 116		
aagctgagcc attcttttcc		20
SEQ ID NO: 117	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
misc_feature	1..21	
	note = Oligonucleotide Primer	
source	1..21	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 117		
ttgcagccta ttgtggactt t		21
SEQ ID NO: 118	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
misc_feature	1..21	
	note = Oligonucleotide Primer	
source	1..21	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 118		
cacaccagct cgtcctcata a		21
SEQ ID NO: 119	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 119		
ggctgtggtt tgtccttgtt		20
SEQ ID NO: 120	moltype = DNA length = 20	

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FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 120	
ttgggtttca cactcagcag	20
SEQ ID NO: 121	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 121	
ggcacagaat ccaacttgag	20
SEQ ID NO: 122	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 122	
cagggccatt ggtctagaaa	20
SEQ ID NO: 123	moltype = DNA length = 18
FEATURE	Location/Qualifiers
misc_feature	1..18
	note = Oligonucleotide Primer
source	1..18
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 123	
ccccaaaaaa tccaacca	18
SEQ ID NO: 124	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 124	
aggccaaggg aatgatgctc	20
SEQ ID NO: 125	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 125	
gggagtgggg gaaataaatg	20
SEQ ID NO: 126	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 126	
atcatcctag cactcagaag g	21
SEQ ID NO: 127	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct

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SEQUENCE: 127
ctgcttaaat tctcccagcg 20

SEQ ID NO: 128 moltype = DNA length = 21
FEATURE Location/Qualifiers
misc_feature 1..21
note = Oligonucleotide Primer
source 1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 128
agcatcaatt agatgtcagc g 21

SEQ ID NO: 129 moltype = DNA length = 19
FEATURE Location/Qualifiers
misc_feature 1..19
note = Oligonucleotide Primer
source 1..19
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 129
tagcaagaaa atgtgccca 19

SEQ ID NO: 130 moltype = DNA length = 21
FEATURE Location/Qualifiers
misc_feature 1..21
note = Oligonucleotide Primer
source 1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 130
tcctttgaat tagcacttgg c 21

SEQ ID NO: 131 moltype = DNA length = 19
FEATURE Location/Qualifiers
misc_feature 1..19
note = Oligonucleotide Primer
source 1..19
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 131
tccaggaagt gtctgcagg 19

SEQ ID NO: 132 moltype = DNA length = 23
FEATURE Location/Qualifiers
misc_feature 1..23
note = Oligonucleotide Primer
source 1..23
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 132
tggattatta aggggaattt agc 23

SEQ ID NO: 133 moltype = DNA length = 18
FEATURE Location/Qualifiers
misc_feature 1..18
note = Oligonucleotide Primer
source 1..18
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 133
acgtcgagct cctggcat 18

SEQ ID NO: 134 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 134
aacagcattt cagacagagg 20

SEQ ID NO: 135 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20

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	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 135		
aaacggagtt ccatctctgg		20
SEQ ID NO: 136	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 136		
cctatgcagg gtaggcacat		20
SEQ ID NO: 137	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
misc_feature	1..21	
	note = Oligonucleotide Primer	
source	1..21	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 137		
tcttcaaaga aaaccaacag g		21
SEQ ID NO: 138	moltype = DNA length = 18	
FEATURE	Location/Qualifiers	
misc_feature	1..18	
	note = Oligonucleotide Primer	
source	1..18	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 138		
gttctccaaa gcactcat		18
SEQ ID NO: 139	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 139		
acaccaaatg tgtgaaggca		20
SEQ ID NO: 140	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 140		
ggggacaaat ttccactcct		20
SEQ ID NO: 141	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 141		
atggagcatg ggtgagaaat		20
SEQ ID NO: 142	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
misc_feature	1..21	
	note = Oligonucleotide Primer	
source	1..21	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 142		
atcctggtat caaatctatc a		21

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SEQ ID NO: 143 moltype = DNA length = 25
FEATURE Location/Qualifiers
misc_feature 1..25
note = Oligonucleotide Primer
source 1..25
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 143
aatagactat gtaactgtct ctggc 25

SEQ ID NO: 144 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 144
gcaatggaaa gaggatggaa 20

SEQ ID NO: 145 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 145
gttgattggg agataatcca ca 22

SEQ ID NO: 146 moltype = DNA length = 23
FEATURE Location/Qualifiers
misc_feature 1..23
note = Oligonucleotide Primer
source 1..23
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 146
ttagagctta ctcatgatat ctg 23

SEQ ID NO: 147 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 147
cctggattat aagcatgaga gc 22

SEQ ID NO: 148 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 148
tttctgagcc acttttccat ag 22

SEQ ID NO: 149 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 149
gggggtgtcg gtggagttct 20

SEQ ID NO: 150 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20

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	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 150	
gccacctcat tccaaaaaga	20
SEQ ID NO: 151	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 151	
tatggagatg gagggcacac	20
SEQ ID NO: 152	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 152	
atgaggaggt gcaactatcc	20
SEQ ID NO: 153	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 153	
caggctttgt tgaggtgtca	20
SEQ ID NO: 154	moltype = DNA length = 19
FEATURE	Location/Qualifiers
misc_feature	1..19
	note = Oligonucleotide Primer
source	1..19
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 154	
aacactgaca tgcatccac	19
SEQ ID NO: 155	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 155	
tggtggataa atagataagg a	21
SEQ ID NO: 156	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 156	
attgcttgga taagaggggg	20
SEQ ID NO: 157	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 157	
tgtgagtagg gtagggcaag	20
SEQ ID NO: 158	moltype = DNA length = 21

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FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 158	
ggtgtcagga aaatgagacc a	21
SEQ ID NO: 159	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 159	
aggcctgctg tttctcttct	20
SEQ ID NO: 160	moltype = DNA length = 18
FEATURE	Location/Qualifiers
misc_feature	1..18
	note = Oligonucleotide Primer
source	1..18
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 160	
tccctttttg tggctgaa	18
SEQ ID NO: 161	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 161	
ggcataaatt gtctttgccc	20
SEQ ID NO: 162	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 162	
caagattcaa aacaagcaac c	21
SEQ ID NO: 163	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 163	
ccatggagag tggttattgc	20
SEQ ID NO: 164	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 164	
aatgacattg agcctgggaa	20
SEQ ID NO: 165	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct

-continued

SEQUENCE: 165
atagccttgg gaatttttgc 20

SEQ ID NO: 166 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 166
tatggacctt cgttcagagg 20

SEQ ID NO: 167 moltype = DNA length = 19
FEATURE Location/Qualifiers
misc_feature 1..19
note = Oligonucleotide Primer
source 1..19
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 167
tcataaggca aagaaaacc 19

SEQ ID NO: 168 moltype = DNA length = 21
FEATURE Location/Qualifiers
misc_feature 1..21
note = Oligonucleotide Primer
source 1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 168
ttgtcccttg tataactgat g 21

SEQ ID NO: 169 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 169
ttagacaaaa taggcttcaa 20

SEQ ID NO: 170 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 170
ttcagggaat tctttcttgg 20

SEQ ID NO: 171 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 171
ttgtatggag gtggggagag 20

SEQ ID NO: 172 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 172
agatggggcc taaccaaagt 20

SEQ ID NO: 173 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20

-continued

	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 173		
cccttctggc ctcctacaca		20
SEQ ID NO: 174	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 174		
caggttattc tgggctatgg		20
SEQ ID NO: 175	moltype = DNA length = 18	
FEATURE	Location/Qualifiers	
misc_feature	1..18	
	note = Oligonucleotide Primer	
source	1..18	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 175		
tattccacat cattcacc		18
SEQ ID NO: 176	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
misc_feature	1..21	
	note = Oligonucleotide Primer	
source	1..21	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 176		
atgcttcctg gtaagcaatc a		21
SEQ ID NO: 177	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
misc_feature	1..21	
	note = Oligonucleotide Primer	
source	1..21	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 177		
ccccttccag cttcggtgta g		21
SEQ ID NO: 178	moltype = DNA length = 22	
FEATURE	Location/Qualifiers	
misc_feature	1..22	
	note = Oligonucleotide Primer	
source	1..22	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 178		
gagaggagaa acaaccaaca cc		22
SEQ ID NO: 179	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
	note = Oligonucleotide Primer	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 179		
acacatacac gcccaattca		20
SEQ ID NO: 180	moltype = DNA length = 17	
FEATURE	Location/Qualifiers	
misc_feature	1..17	
	note = Oligonucleotide Primer	
source	1..17	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 180		
catcttgctc tctcaac		17

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SEQ ID NO: 181 moltype = DNA length = 21
FEATURE Location/Qualifiers
misc_feature 1..21
note = Oligonucleotide Primer
source 1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 181
acctggcctc ttctgttgtc t 21

SEQ ID NO: 182 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 182
caagctgaga gccatgtagg 20

SEQ ID NO: 183 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 183
gatagatcca agccaacacc 20

SEQ ID NO: 184 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 184
ccccaggacc atttgttaga 20

SEQ ID NO: 185 moltype = DNA length = 21
FEATURE Location/Qualifiers
misc_feature 1..21
note = Oligonucleotide Primer
source 1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 185
catttgtcat tgtggaaaac c 21

SEQ ID NO: 186 moltype = DNA length = 21
FEATURE Location/Qualifiers
misc_feature 1..21
note = Oligonucleotide Primer
source 1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 186
gtgctagtct ggctgtgctc a 21

SEQ ID NO: 187 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 187
tcatctccag cttttcatgg 20

SEQ ID NO: 188 moltype = DNA length = 19
FEATURE Location/Qualifiers
misc_feature 1..19
note = Oligonucleotide Primer
source 1..19

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	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 188	
atgtgaaccc cgcccaata	19
SEQ ID NO: 189	moltype = DNA length = 19
FEATURE	Location/Qualifiers
misc_feature	1..19
	note = Oligonucleotide Primer
source	1..19
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 189	
gagccctgtt ctcaggttg	19
SEQ ID NO: 190	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 190	
caataccctg ataccaaaac c	21
SEQ ID NO: 191	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 191	
aggccttctc tgtcctcttg	20
SEQ ID NO: 192	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 192	
tgtccaccca cagatgaatg	20
SEQ ID NO: 193	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 193	
ggatgcttgg gaatcttgaa	20
SEQ ID NO: 194	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 194	
tacaggcact ccttcctacg	20
SEQ ID NO: 195	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 195	
aggtttgggc tcctcattct	20
SEQ ID NO: 196	moltype = DNA length = 20

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FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 196	
gagacttaac acagtatttg	20
SEQ ID NO: 197	moltype = DNA length = 19
FEATURE	Location/Qualifiers
misc_feature	1..19
	note = Oligonucleotide Primer
source	1..19
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 197	
tcggggacat acttgaacc	19
SEQ ID NO: 198	moltype = DNA length = 19
FEATURE	Location/Qualifiers
misc_feature	1..19
	note = Oligonucleotide Primer
source	1..19
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 198	
aaccactatc caactttat	19
SEQ ID NO: 199	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Oligonucleotide Primer
source	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 199	
gaaagaggat gaagggtgtg	20
SEQ ID NO: 200	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 200	
caactaaggc agagaatacc a	21
SEQ ID NO: 201	moltype = DNA length = 19
FEATURE	Location/Qualifiers
misc_feature	1..19
	note = Oligonucleotide Primer
source	1..19
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 201	
cacgacgttg taaaacgac	19
SEQ ID NO: 202	moltype = DNA length = 337
FEATURE	Location/Qualifiers
misc_feature	1..337
	note = Wherein N = A or C or G or T
misc_feature	82
	allele = C to T
	note = allele - C to T
misc_feature	133
	allele = T to C
	note = allele - T to C
source	1..337
	mol_type = genomic DNA
	organism = Canis familiaris
SEQUENCE: 202	
gcttttggac aactttggat agactccttt ctctggaatg acttccagca tatggtgcag	60
cttcaaggcc agagaagaga ccagatgacc tttcaagtgt ccttccagtc caaagnnnnn	120
nnnttccaat actgagggtt ttcaaactgg tgttggtatt tgcttttcaa agagagacag	180

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actgagtttc tcatatcaaa tccctatagc ctcataaaag cacttttcag ttttattttc 240
catcagaaat tcctatgaaa agcatttgaa gtttcaaaag ctccctacac ccaagnngct 300
gattgagatt ttagcccaga gagtgacgta gatcaca 337

SEQ ID NO: 203 moltype = DNA length = 341
FEATURE Location/Qualifiers
misc_feature 1..341
note = Wherein N = A or C or G or T
misc_feature 285
allele = G to A
note = allele - G to A
source 1..341
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 203
gaattccaaa tgtcctgctt agggtccagc aggatagagg gatagnnnnn nnnnnnntga 60
ggtaggagga aacagtgact tttccagaaa cagtgcaaca tttctcctgc atttttaacc 120
tctatagatg atactcattt ctcattagcc agagttcctg cattccattg gcagtaagtt 180
gtccatcaga atccctgaaa nnacaacttt gggtgaactg gaagccattc acactttgcc 240
agttgggtaa tgccagttag tacatacctt tctcataagg ttttgaatac ctgnnnnnnn 300
nnnnnnncca atgaataccc acacccttgg tagatgaaag a 341

SEQ ID NO: 204 moltype = DNA length = 302
FEATURE Location/Qualifiers
misc_feature 1..302
note = Wherein N = A or C or G or T
misc_feature 50
allele = Deletion A
note = allele - Deletion A
misc_feature 93
allele = C to G
note = allele - C to G
misc_feature 128
allele = C to G
note = allele - C to G
misc_feature 257
allele = C to T
note = allele - C to T
misc_feature 271
allele = G to T
note = allele - G to T
source 1..302
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 204
aagcatactt ccctgaaatg aggcttcact atctgatttg ctttggctaa taaatataaa 60
tagaagtgag atgggtcact tctaggctgt agctttaagg gcaggatgtg tgtcgctaaa 120
ttctcctctt ctcctgccat aatgactgac atcagnnntt ctccatcagc ttggggcctg 180
aagtgtaatg atgtagagaa gaaccaggct tatgtaagtg aggaataaac aaccttgtta 240
gaaactacag atatggcggt gtttattact gcagcataat ccaacacttt atggctgata 300
ca 302

SEQ ID NO: 205 moltype = DNA length = 408
FEATURE Location/Qualifiers
misc_feature 1..408
note = Wherein N = A or C or G or T
misc_feature 57
allele = T to C
note = allele - T to C
source 1..408
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 205
agtcaaatcg ttcattggat tcccttgcac tcagagctta tgagaagagc tgacaatgta 60
ctcagcagcc gtgtccttct tcctaaatta ttggctttta tttcatcaga gtgaaagccc 120
ttnnnnnnnc agggtttgaa attgccatca cttcaaattt cctataagca cttcttgcat 180
gtgaatgttt actgaatgca gttaactgtt ttctaaattt aactagcttt aacgaatttg 240
attttcaaac tgaaaaagaa ataattgatg tcaatttcat ttcaattcca caaagagaat 300
gggggggtggg caatgcagaa atcatgtcct gaagcattta cttttatttt ttaatttttt 360
aaagatttgt ttatttgaga gacagagaga gggagtacat tcaagcag 408

SEQ ID NO: 206 moltype = DNA length = 381
FEATURE Location/Qualifiers
misc_feature 1..381
note = Wherein N = A or C or G or T
misc_feature 156

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                     allele = Insert T
                     note = allele - Insert T
misc_feature         258
                     allele = C to T
                     note = allele - C to T
misc_feature         303
                     allele = C to T
                     note = allele - C to T
misc_feature         312
                     allele = Insert A
                     note = allele - Insert A
source               1..381
                     mol_type = genomic DNA
                     organism = Canis familiaris
SEQUENCE: 206
aaaaggtggc acatatgaaa agttgttgtt ttttttttc ctaatgtcat ggcctgtcac  60
ttagacaaaa agcataatga gggaagtttc taagaattat annnnnnnnn nngctaatca  120
aattttaagg aatgtatatg gtggtgaggt gaaggatcaa gatggcagtt gtttgcaaag  180
gaaaggaagg tggaaataaa ggagtatcca agagggataa tataacaaaa aattattgag  240
tttcagagaa atcaggtgaa tggaagatgt aacagggctc taacatgaan ntggtccaag  300
nngattcaac ataaaaatta ccagtcatgg gtgcctgagt tgttcaaagt cagttaagcc  360
tcccttaagc ctctgactct t                                            381

SEQ ID NO: 207       moltype = DNA  length = 344
FEATURE              Location/Qualifiers
misc_feature         1..344
                     note = Wherein N = A or C or G or T
misc_feature         254
                     allele = G to A
                     note = allele - G to A
source               1..344
                     mol_type = genomic DNA
                     organism = Canis familiaris
SEQUENCE: 207
ggggtttcta ttccattttc accacgtttg aaggacaaat tgaggctgcc ctcatacaaa  60
tgcccctggg cnnnnnnatt agggttgggg ttgggggnnn nnnnnnnngg ccagaattcc  120
tctctcaccc aacaggggag gcagtaatgc cttattttgc cgtcttgggt ggtgacagta  180
gtgagagctt ggttctgggg ctaaacagag acagccttgc caacagatgt cagctcacca  240
gaagtggtca agcgtttctc aaagtagcca cagtgctggg agcagccaag gctttcnnnn  300
nnnnannatn gaaactcaaa ctgtgtcaac agtatgcatt ccaa                   344

SEQ ID NO: 208       moltype = DNA  length = 370
FEATURE              Location/Qualifiers
misc_feature         1..370
                     note = Wherein N = A or C or G or T
misc_feature         165
                     allele = G to C
                     note = allele - G to C
source               1..370
                     mol_type = genomic DNA
                     organism = Canis familiaris
SEQUENCE: 208
acctcatgta tgtcttgttc cccaagaacc cttcgtccag ggatttttt tttaaatgta  60
tttattcatg agagacagag agagagagag agaatggggc agagacacag gcagagggag  120
aagcaggctc cacacnnnnn nnnnnnngtg gggactcgat cccgggtctc caggatcagg  180
ccctggactg aaggtagtgc taaaccgctg agccacctgg gctgcccagc ctaatctttt  240
ttgttgttgt tgttttgttt tgtttttta agattctatt tattttagag agagagggtt  300
aaaaaaactt tagcagactc catgctcagc acnngcccca tgagggctcg atctcaggac  360
cccaagatca                                                         370

SEQ ID NO: 209       moltype = DNA  length = 337
FEATURE              Location/Qualifiers
misc_feature         1..337
                     note = Wherein N = A or C or G or T
misc_feature         66
                     allele = T to A
                     note = allele - T to A
source               1..337
                     mol_type = genomic DNA
                     organism = Canis familiaris
SEQUENCE: 209
ctctgctagg agaaaaggag agaaactact gcttttccta tggattttaa cctccacctt  60
tcaatttttt cccctgggta agggacaggg taggattgga acagngggca ggcagattgt  120
nnnnnnnnnn tatctgggat tgaatatggg ttgtaatagc tttagaaatt gtcatttctc  180
ttgccttgac cagccagttt tctgggaagt agaggatatg aaagcatttg tgctcttcca  240
gaataagatg tgtattcatg aaattagttg ttgctcttaa ataaaatgct tccttatgta  300
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caaaattctc nagcaggctg aatggactga attgtgt 337

SEQ ID NO: 210 moltype = DNA length = 480
FEATURE Location/Qualifiers
misc_feature 1..480
note = Wherein N = A or C or G or T
misc_feature 384
allele = A to G
note = allele - A to G
source 1..480
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 210
caaatggttc aagaggagat tcttgtaata gttctgctat tggcaaggtg gtaggaggag 60
gctttcagga cacagcagca aggtgtttta nnnnnnnnnn nctcactgtg ttatggctct 120
cctgaggttc cagtccattg ggagtatatg ggtgaaacct taaatctcaa agggatcttc 180
cttaagactg acatgtacta tagtcagtca cttgatacat gaggcagatg acccagacaa 240
aagtggctac tactagggtg tccacatatg gctacacagt agaatcacct ggagagcttt 300
tacgatccca gtgcccaagt cataacctat tcaaattaaa ttacagtgtt ggggcnnnga 360
gtcagatagc aatatttttt aaagacccca gctgattcca gtgcattgca ccttttgcaa 420
ctaatgggct tatgatttat ctaacatcac acaagtgggg acaggaacct acaatggtta 480

SEQ ID NO: 211 moltype = DNA length = 313
FEATURE Location/Qualifiers
misc_feature 1..313
note = Wherein N = A or C or G or T
misc_feature 88
allele = T to C
note = allele - T to C
misc_feature 138
allele = C to A
note = allele - C to A
misc_feature 266
allele = T to G
note = allele - T to G
source 1..313
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 211
aaagtaaaat caggtattct cctcctaact atgaaganan nntaattttt agagtgaaat 60
ctgagttaac aactcctaca atcacaatct tgtttgccaa tccagcgtta tgagctgccc 120
atcccagaag aaaaaaactn nnnnnnnttg tggtgttatg aaatgagcct gcctatggac 180
tccaaaaaaa gctagatcca gggtgcaatg tccatctttg gtcatgccta tcccctcatt 240
ccagtaattg accaacattt aggagttagt gtttttcccc tatgcttact acttcagata 300
gatatgcatg cca 313

SEQ ID NO: 212 moltype = DNA length = 353
FEATURE Location/Qualifiers
misc_feature 1..353
note = Wherein N = A or C or G or T
misc_feature 317
allele = T to A
note = allele - T to A
source 1..353
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 212
caccctcaag aagttaaagc acaactcttc acccctaag tatgggctac acagtgactt 60
ccttcgaaag aggacagttt gggaaggggg aaaaacagga nnnnnnnnnn ngagaagcct 120
aataaatact atcttagcca ggtgactaag gctggcaaca tcaagagcta tgtcaaataa 180
catatgccct tgatataata tgataagaat ggcactgtag acttcctccc tcaaatcctt 240
aaccactatc taatcatgag aaaaatatta gacaaccaaa attgaaggac atactacaaa 300
atatctaact actacttctc aaaaccgtca annccagtct tctcaaaacc agg 353

SEQ ID NO: 213 moltype = DNA length = 336
FEATURE Location/Qualifiers
misc_feature 1..336
note = Wherein N = A or C or G or T
misc_feature 58
allele = G to C
note = allele - G to C
misc_feature 108
allele = A to T
note = allele - A to T
source 1..336
mol_type = genomic DNA

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organism = Canis familiaris

SEQUENCE: 213

tagggacac agtttctaaa ggctgttcac agtttctaga ggcctcccac agtttctgaa 60
ggacttttgc agctccctga tacatgaggt cctccaatgt ggccaataat ttaatccagn 120
nnnnnnnnnn ngcctctaga gttagtgtgc tagcaagatg gagtcttctg taacataacc 180
taagcacgag aatgacatcc tgtcaccttt tccgtatttt attgctttgc aacaaatcac 240
tggtcctgct caccctcaga gggaggcaga agatacaggg agataactcc taaacactaa 300
gagacaaaga aaatgagggc ttcttacatg tctgtc 336

SEQ ID NO: 214 moltype = DNA length = 377
FEATURE Location/Qualifiers
misc_feature 1..377
note = Wherein N = A or C or G or T
misc_feature 129
allele = G to A
note = allele - G to A
misc_feature 170
allele = Insert T
note = allele - Insert T
source 1..377
mol_type = genomic DNA
organism = Canis familiaris

SEQUENCE: 214

tctcaaactg ttgaagacca acagaatgat aaaatcttga aagcaacann nnnnnaaaac 60
attcatcata tacaaaggaa caatgagatt aacaattaac ttctcaaaag agataataga 120
ggccagaagt cagtggatga catattcaaa gtnnnnnnnn nnnnnnnnnn nnctcaacca 180
actgaacaaa acaaaaaatg aagatgaaan ngacacttag gtgactctgt cagnnnaaca 240
tgcttctctt gatcttgggg tcatgagttt gagtgcagag attatttaag gaaataaata 300
aaacctgtat atctttttaa atgaaaatga acatattccc agaaaaagat tgaaagaatt 360
tgttcctagc agagacc 377

SEQ ID NO: 215 moltype = DNA length = 312
FEATURE Location/Qualifiers
misc_feature 1..312
note = Wherein N = A or C or G or T
misc_feature 76
allele = C to T
note = allele - C to T
misc_feature 108
allele = G to A
note = allele - G to A
misc_feature 229
allele = G to A
note = allele - G to A
misc_feature 238
allele = T to C
note = allele - T to C
misc_feature 263
allele = A to G
note = allele - A to G
source 1..312
mol_type = genomic DNA
organism = Canis familiaris

SEQUENCE: 215

catgtgaccc ttcctatgag actgtcacag aaccagccca cactcgggtt ggccggacct 60
gggtcaatcc tcagccgcca nnnnnnnnnn naggtgcagt gtgcccggag ggagcgatgg 120
cgtgagctaa gcctggggca ctggtatcct ccagcagtga ggagggaggc accccaaaan 180
ntgctttaaa tgatcctaac agaaccccac agcgacagac attagccagg agggaagtga 240
ccaagtaaac ctgaaccgag acaggaggct ttattcaaga tcattctcat caaccaaatt 300
gcctctactt tc 312

SEQ ID NO: 216 moltype = DNA length = 316
FEATURE Location/Qualifiers
misc_feature 1..316
note = Wherein N = A or C or G or T
misc_feature 212
allele = T to C
note = allele - T to C
source 1..316
mol_type = genomic DNA
organism = Canis familiaris

SEQUENCE: 216

ggaagacccc aactctatta ttgcaggcat gccagtcctc gaggtctgga aatcaaagca 60
ggtaaagttt cagacttgtg tttcattcta acaatcaagt atctcttaaa acatgnnnnn 120
nnnattgtcc tggttcactt ggtgagaaat gctgatgcct cttaggagta ctaggagcta 180
gagcaggggt agtgctctcg ctatccagct tttgtctatt tggtgatcat cagagaaccc 240

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aagagaatgc cctgctcacc attagaacta gatgatatta tctgggtgga ttaacaaaat 300
ctgtaaccac agctga 316

SEQ ID NO: 217 moltype = DNA length = 423
FEATURE Location/Qualifiers
misc_feature 1..423
note = Wherein N = A or C or G or T
misc_feature 274
allele = T to C
note = allele - T to C
source 1..423
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 217
agtcttttgg tcctaaacat ggtagaaaac atctttgttg cattttttag aattaatcta 60
ttttaaattg acatattttg catgtaatat atttttcagg tatataaann nnnnnnnnna 120
tatttttata cactgcaaaa gatccccata tctggttaac atttgtcacc ttatatggta 180
aaaaaaattt tacaaaattt attcttgtga tgaaaactta agatttactc ttagcaactt 240
gcacatatac aatacagtag tagccaactt gctatctgtt atatcttcac tttgttgctg 300
tgtctaagaa gtgacagatg ccagtagagg tgtgggatcc tatatganna aatcccagta 360
tctgacattg cagagccttc tacctgccac ctctgagnca ccagtcagtg aggagtcaca 420
gtg 423

SEQ ID NO: 218 moltype = DNA length = 304
FEATURE Location/Qualifiers
misc_feature 1..304
note = Wherein N = A or C or G or T
misc_feature 112
allele = G to A
note = allele - G to A
source 1..304
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 218
agacacatgc attttcccag ctgacttttt gcacccagtg gctcataatc acaatcacat 60
gttatcaact tgcctcatag acccatttttt tcagccnnnn nnnnnnngnc agtgtcacat 120
ctcaatacag tggccagaaa agtggttctt gcccctggtt tgcttaacct gagtatcatg 180
gggaacactg tcttctgaat tctagctgtg tgatctgtgt tcctatttat aaccatgttt 240
tatctttcag acctgacaca actagtctga tttggacatt ttgctcctgt tcacaatgaa 300
gatt 304

SEQ ID NO: 219 moltype = DNA length = 316
FEATURE Location/Qualifiers
misc_feature 1..316
note = Wherein N = A or C or G or T
misc_feature 73
allele = G to A
note = allele - G to A
misc_feature 136
allele = A to G
note = allele - A to G
source 1..316
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 219
gtccaaagtt ggagatgata ggttctctca caataataat gtattgtttt cctcttacac 60
cctcactagg cagtccactg ctgacccaac tgnnnnnnnn tgcactatat caatttctga 120
ctttatggag ataaaatagc tgtgatgtac ccagcttata ataaccctcc ttctacttag 180
agccacttgt tctctcctca gttttatttt actcctgaaa aaaaccctct tctcttttaa 240
actctattca taggtccttc acatcatttt aatcaaaaga tttcagggtc ttctataaca 300
acatttccca gtttca 316

SEQ ID NO: 220 moltype = DNA length = 330
FEATURE Location/Qualifiers
misc_feature 1..330
note = Wherein N = A or C or G or T
misc_feature 89
allele = C to T
note = allele - C to T
source 1..330
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 220
aaagcccagc tgttgtctgg agccctgnnn nnnngaaaca ctggactttc caggccctcc 60
cttgaccttg actttcaagg gctctgtccg gatgcccttg ccttctcctg cctgnnnnnn 120
nnngggagca aaggaagctg gagctctggt tgttgcacaa cagaaagtcc tggctcctga 180

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cactgagtga ttaaatgtga ttttttcttt aagaaaaaag aagcctttta tcatactcct 240
agggctgtca gaaaccattc cggtagattt tcctaagtct tgtttttca gatgcgaaag 300
tgggannccg tagctgtcct caccctatct 330

SEQ ID NO: 221 moltype = DNA length = 325
FEATURE Location/Qualifiers
misc_feature 1..325
note = Wherein N = A or C or G or T
misc_feature 93
allele = C to T
note = allele - C to T
source 1..325
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 221
cctgtccttt agaatcctca tcttgtacat gagagaggga tgaagacagg gaaggcagga 60
gggacggagg gagaaggaag tagctggcta ttcttctgaa ttagaatatg atannnnnnn 120
nnttttaaat cgaaaaatag gaaaaattca aaatctgaca attagcagag ggctttttgc 180
cctcagaata ttgcaaagaa tgaacaatca ttttataatt atgtcctttt tgtattttgt 240
atttttgtat ggaagttaac acttccatag taacatacat cttctagant tatgacctcc 300
tttccctctg gtgcttgaat gtgta 325

SEQ ID NO: 222 moltype = DNA length = 325
FEATURE Location/Qualifiers
misc_feature 1..325
note = Wherein N = A or C or G or T
misc_feature 131
allele = Insert 2 "A"s
note = allele - Insert 2 "A"s
misc_feature 202
allele = C to T
note = allele - C to T
misc_feature 242
allele = C to T
note = allele - C to T
source 1..325
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 222
agtcatttat tgaagcaaag ggtgcaggga agggaaggag tagaaaataa aaatgaaaag 60
gaagattaag atcatattca aaaggccctt ataaaattca tttttggata aatctacaac 120
ggnnnnnnnn naccccaaat ttggatattt ggtctatttt cagtctctca tccatgtcaa 180
ttaacattag aagcaggaag ccctgtcctg ggactaatgg ctggctcaga gtcatgctac 240
ttgacccgat gccctgtaac tctacaatca tgggcagggt gccaagcaag aacaagcact 300
ccacactcaa tccaggtgta cagag 325

SEQ ID NO: 223 moltype = DNA length = 315
FEATURE Location/Qualifiers
misc_feature 1..315
note = Wherein N = A or C or G or T
misc_feature 50
allele = T to C
note = allele - T to C
misc_feature 102
allele = Delete 8 Bases
note = allele - Delete 8 Bases
misc_feature 130
allele = G to A
note = allele - G to A
source 1..315
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 223
cgatatttag gaatgaagcc acattctttt catgacaaag catatgacct actctacaat 60
ctcctgaagc cagaatgctc ntacnctagt agtgaacaga gatctgaaga tctgaagaaa 120
ccaaacatag taaaagaaaa gacactgaga ggagagaagg ggcaagatgc agtgactctc 180
gcaatgcagt gacttaaggc accaaaccca tcagctagct atttaaatag ttggaaaata 240
agagtaaaag ccaagaaaca aaagataaga ttgttattaa agggcagana cnncgaagtg 300
cctatttgca tacca 315

SEQ ID NO: 224 moltype = DNA length = 315
FEATURE Location/Qualifiers
misc_feature 1..315
note = Wherein N = A or C or G or T
misc_feature 116
allele = C to T

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                     note = allele - C to T
misc_feature         282
                     allele = A to G
                     note = allele - A to G
source               1..315
                     mol_type = genomic DNA
                     organism = Canis familiaris
SEQUENCE: 224
aaatatctgt ttctgaaata tctccctaaa aaactgtata tgtctgtatg catacaattc  60
acgtagtata cagctaccgt gaacgtttct tgcatgatgt cagccagtag ggannnnnnn  120
nnnngaccaa actatagctt ttgacccatg agcatcaggc tgctaaatcc ccgcaagggc  180
cttttacaac tttatcctgg gcagaagaat tttccttggt gtgtttctct cactggtgtg  240
tctctttcag ctacttgttt tgtgttctga taagcagtta gagctcgtaa tgacactatt  300
acgggctaga tctgc                                                   315

SEQ ID NO: 225       moltype = DNA  length = 324
FEATURE              Location/Qualifiers
misc_feature         1..324
                     note = Wherein N = A or C or G or T
misc_feature         84
                     allele = Delete T
                     note = allele - Delete T
misc_feature         242
                     allele = G to A
                     note = allele - G to A
misc_feature         243
                     allele = C to T
                     note = allele - C to T
source               1..324
                     mol_type = genomic DNA
                     organism = Canis familiaris
SEQUENCE: 225
tttcctttgc ttctggtgct ggannnnnnc tttnnntggg aatttcatct cctgttttta  60
agaaaaagaa agatcagggt gtttttcttg tatttgctat ttttcaagtg cctctaactc  120
aaaataacac tcgtaccaca gtgatgtatt ttggggnnnn nnnnnctgcc accctcagtg  180
tgtatatgta tttgtcaaaa gccagtgaat tatgcattta aaataggtac atttttattc  240
gatgtaagct aataccacaa tacaatttga tagaattttt aaaatagttt aaaaatagcc  300
cccaaaagcc agaagagtta gcaa                                         324

SEQ ID NO: 226       moltype = DNA  length = 421
FEATURE              Location/Qualifiers
misc_feature         1..421
                     note = Wherein N = A or C or G or T
misc_feature         224
                     allele = T to C
                     note = allele - T to C
misc_feature         246
                     allele = G to A
                     note = allele - G to A
misc_feature         249
                     allele = Insert A
                     note = allele - Insert A
misc_feature         251
                     allele = Delete A
                     note = allele - Delete A
misc_feature         378
                     allele = A to C
                     note = allele - A to C
source               1..421
                     mol_type = genomic DNA
                     organism = Canis familiaris
SEQUENCE: 226
ttggtttgat cacctatgga aggctgaaca aatccgggta ggattagatc gnnnnnnggg  60
agagaacaat tctccttgcc ctctttgggt ctctggctga ttctgaggat taaactgact  120
taagacaggg taacaggaga aaagtgtaga cacattattg aattntnnnn nnacatggga  180
ggccttcact tcacaaggga gtgaagaccc agggacatga ccaaagcagg aagattttaa  240
accttctgac aaagaaacaa tgagtttgtg aagaattgac aaggcacagg gatttgggtt  300
aggggtagta aatgctgaaa aattaaggtt tgtttataca gccttctcag ccctaaagcc  360
cctcttggtg ataaggctgt gtcccctcct tcagtacaag gggaagttgt atctcacatg  420
t                                                                  421

SEQ ID NO: 227       moltype = DNA  length = 395
FEATURE              Location/Qualifiers
misc_feature         1..395
                     note = Wherein N = A or C or G or T
misc_feature         199
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```
                     allele = A to C
                     note = allele - A to C
misc_feature         224
                     allele = G to A
                     note = allele - G to A
source               1..395
                     mol_type = genomic DNA
                     organism = Canis familiaris
SEQUENCE: 227
acacataact gaagcacacc agcaatatga cagtannnnn nnnnnnnnag ggaaaaaatg  60
tatgaacagg atgttgaggt tttactttta cttgttgcat tcccttaaaa aataataacc  120
attatggcaa aaatatggac ttcattttag tggtatctgt gtattcatat tattttgcac  180
ttttctaagg tttgcattat ctcacaattg aaaagaaaaa cacgagctaa gtaaaatgtt  240
aacatatatt attgctacat ttaaaagnnn acaggaagtt taaaaacaaa tgcacccatt  300
attcattaat ttttcactgc tattaagttt aatcaactct tagttttctc tctcagncct  360
aagtagatta tttcaaggaa gtcatgctca atctt                             395

SEQ ID NO: 228       moltype = DNA  length = 439
FEATURE              Location/Qualifiers
misc_feature         1..439
                     note = Wherein N = A or C or G or T
misc_feature         249
                     allele = C to T
                     note = allele - C to T
misc_feature         250
                     allele = C to T
                     note = allele - C to T
misc_feature         254
                     allele = G to A
                     note = allele - G to A
misc_feature         312
                     allele = A to G
                     note = allele - A to G
source               1..439
                     mol_type = genomic DNA
                     organism = Canis familiaris
SEQUENCE: 228
taggtgcatc ccattctcag ggggccattg gggccacagc agccttcccn nnnngcctnn  60
nnnnnnnnnn gccgtggtgt ttcctctgcn nnnnnccagg ctggggcggc aggcaggggt  120
ggggcctccc ttggagaaan nnnagctgcc tctgtcctgg gctgggctga gctgggagag  180
gccacgccag gtccttctgc ccagatgcca cctcctcccc gctcctcttg gcctctccag  240
ccgcaggccc ggcgcctccc anngagtggg acctgctcct gtgagtcagn nnnnngacnn  300
nnnnngtgca cagatnnact atannnngta tnnnactggt catgtgttta tttnnnngag  360
tatcnnnnnn nnncnnacaa gcaattaatg cgcgnaaccc tngatnncat nnattnnann  420
gctcaaggcg aggcaaatt                                               439

SEQ ID NO: 229       moltype = DNA  length = 342
FEATURE              Location/Qualifiers
misc_feature         1..342
                     note = Wherein N = A or C or G or T
misc_feature         181
                     allele = C to T
                     note = allele - C to T
misc_feature         224
                     allele = Delete 2 Bases
                     note = allele - Delete 2 Bases
source               1..342
                     mol_type = genomic DNA
                     organism = Canis familiaris
SEQUENCE: 229
ccaatgatct tgcacagtta tgttacnnnn nnnnnctttа aaaaacatat aactgagtac  60
ggtggttccn nnnnnacatc ctttaattgc tccccagcat ctaaaggaca atgcccnnnc  120
tcctgaacac ggatacggat ccccacctca nngtcctgtc catttctctc gtatcacttg  180
ccatccacca actccagctc atttactgcc atggaaacaa agagagccat caaatttgag  240
atgttttatg ttacnnnnnn ntttagctga aacatctttt ttttgtctag ttatagtcct  300
aatcttcttt cannnnnntc cactccaata ccacctctac ca                     342

SEQ ID NO: 230       moltype = DNA  length = 357
FEATURE              Location/Qualifiers
misc_feature         1..357
                     note = Wherein N = A or C or G or T
misc_feature         261
                     allele = A to C
                     note = allele - A to C
misc_feature         264
                     allele = T to C
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```
                     note = allele - T to C
source               1..357
                     mol_type = genomic DNA
                     organism = Canis familiaris
SEQUENCE: 230
caaatgttaa atggacatct gcnnnnnnnn nnnctgcacn nggctannnn nngnnggnnn  60
gaaannnnct ttgtcttcat gnnnttggnn nnnnntcann nnnngagcnn nnncgtgcca  120
nnnnnnnnnn nnngtgaata atttaatgtc tgaatcagac atgattctga acttctttgt  180
tttacagatg aggaaattga acttatctgt gtctgcttca accccaggat ttccttattc  240
tttgattcaa aacttgacct aaataatcct gtagaannat agagaaaagg gtcgtcgaaa  300
tgctcgtgat acggaaatga gagtctgatt gtcatgttct ttctcaggcc tctatca     357

SEQ ID NO: 231        moltype = DNA  length = 317
FEATURE               Location/Qualifiers
misc_feature          1..317
                      note = Wherein N = A or C or G or T
misc_feature          112
                      allele = A to G
                      note = allele - A to G
misc_feature          168
                      allele = A to G
                      note = allele - A to G
source                1..317
                      mol_type = genomic DNA
                      organism = Canis familiaris
SEQUENCE: 231
ggtaaaccag aagttcccca ggtgaaatgg cttttcctcc attaccctcc ccagtcacac  60
aaccagagga aagtgggctg aaactgagca ttcagngata gaggatgggg tgctgagtgn  120
nctnnnnnna cggaggtccc ataggtccaa gggctgaacc caggtacagg gggcgtgaga  180
aaggggcctg agaggtctac gggagactgg aaactctggg ggcgcagaag cgggggaaga  240
accctggcga tcacgcctgc gggctggcaa agggacggaa aacccaanng gggagaganc  300
ttgagccttc gcaacag                                                 317

SEQ ID NO: 232        moltype = DNA  length = 325
FEATURE               Location/Qualifiers
misc_feature          1..325
                      note = Wherein N = A or C or G or T
misc_feature          121
                      allele = T to C
                      note = allele - T to C
misc_feature          196
                      allele = G to A
                      note = allele - G to A
source                1..325
                      mol_type = genomic DNA
                      organism = Canis familiaris
SEQUENCE: 232
atttacatgg cagtgtgttc tggttatcta cttctgtata acaaatgacc ttaaaattta  60
gtggcttaaa acagtaattc atcattataa ttcacagttc ttngngttga ctgggccctc  120
ttgggtagtt cttgcttgca atctctcatg gagttgtagt caggtacagg ctgggagggg  180
ctgcaattct ctggaggttt tagtgagccc agcatccaaa atggtgccct catatggctg  240
gtgattgata gtggctgctg tctgggagct cagctggaac tatcaaatgg actgtcctca  300
tgtggctcat gttatgtggg ctttt                                       325

SEQ ID NO: 233        moltype = DNA  length = 250
FEATURE               Location/Qualifiers
misc_feature          1..250
                      note = Wherein N = A or C or G or T
misc_feature          67
                      allele = A to G
                      note = allele - A to G
misc_feature          71
                      allele = A to C
                      note = allele - A to C
misc_feature          165
                      allele = G to A
                      note = allele - G to A
misc_feature          221
                      allele = C to A
                      note = allele - C to A
source                1..250
                      mol_type = genomic DNA
                      organism = Canis familiaris
SEQUENCE: 233
attccatttt aggtctgcat aaaggcaaca atgttgtcaa aagtttagnn nnnnnnnnnn  60
nntaaaacca atgaatcacg gaagtactaa ttagtaaaag ttgatcatgc acacagagtt  120
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ctaaataagt aaattaatgg agagacataa tacacttatg gattgtagaa tttaagatgt 180
tagtcatctc caaatttttc aaaagatata ataaaatttc catcaacttc ttggcaggca 240
ctctctaaaa 250

SEQ ID NO: 234 moltype = DNA length = 245
FEATURE Location/Qualifiers
misc_feature 1..245
note = Wherein N = A or C or G or T
misc_feature 97
allele = A to G
note = allele - A to G
misc_feature 224
allele = Insert T
note = allele - Insert T
source 1..245
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 234
aaactctcct atttcacatt gaccattttt ctatgaatga aggaataata tttttataac 60
cctgttcccc tccctctgaa tgttttatga aaagaannnn nnnnnnnnnn nnaaaattca 120
agaagtgaaa ggaaaattga attttccttc ctcagagaag aagtttaaat caatcatcct 180
tgagaaaaat ctaaatggtc caaattatct ggagccattt tttgtaagat tggatttgcc 240
agttc 245

SEQ ID NO: 235 moltype = DNA length = 297
FEATURE Location/Qualifiers
misc_feature 1..297
note = Wherein N = A or C or G or T
misc_feature 67
allele = A to G
note = allele - A to G
misc_feature 73
allele = A to C
note = allele - A to C
misc_feature 100
allele = T to C
note = allele - T to C
misc_feature 108
allele = C to T
note = allele - C to T
misc_feature 127
allele = T to A
note = allele - T to A
misc_feature 147
allele = T to G
note = allele - T to G
misc_feature 186
allele = A to G
note = allele - A to G
source 1..297
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 235
acaaaagaac cctcctgtct ctgtaaccan nnncaagaag gacagtaagg ctgggtcctt 60
atgtaaacga gcctgagtac atatctaagt gctctcatgc ttaagggcag aagttccctn 120
nnnnnnnnnn aaagtaaagg cagagataat ttcatctctg aggggaaagg gtaaaataat 180
gcttcagcaa tcactcaaat aggggcaggg agcatctgaa aaggattaat tcacccgtgc 240
aatagatatc tagctaaatc tctactatga gtattttctc tttctttcct ttaagat 297

SEQ ID NO: 236 moltype = DNA length = 338
FEATURE Location/Qualifiers
misc_feature 1..338
note = Wherein N = A or C or G or T
misc_feature 100
allele = C to A
note = allele - C to A
misc_feature 273
allele = A to G
note = allele - A to G
source 1..338
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 236
cttttggctt tctctgaatt tgcataaact ccagtaatct ttttttttccc cctgggttga 60
taatagtgtt tgtgttaaaa tcacaccttc ttttcatttc ttgcatgcat ataggctttt 120
ctcctgtttg tggacacaag tgcttttatc tcactctgca atcagtcaca accccgggtg 180

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gaggcaggga acatttgcta caatatttcc tatataaaca gtttcactgt aaaaggaaca 240
atatggctct aattttgatg tatgatcagt ttagaaatat gcaaacacat ttgaatatac 300
atcctgtaca tgacaacagc aatgtgaaat tggataca 338

SEQ ID NO: 237 moltype = DNA length = 304
FEATURE Location/Qualifiers
misc_feature 1..304
note = Wherein N = A or C or G or T
misc_feature 131
allele = T to C
note = allele - T to C
source 1..304
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 237
taagttccac ctgtattgca tcagattgtt gttgaaaaac actgccaata attgcttttn 60
nnnttgccag gctagttggg agtggaaagg gggctggaac tatggaatca gacctaacta 120
tgatctactt cggtccctaa atccctgagt aacaacagca ggcagagcag tgaacctctc 180
tgatctacag tttctgcctc tgcaaaatgg gggtcattct tcccacctca tggaacaccc 240
tgtggtcttc agcctatttc tagcccgggg taggtgctca gagaagacaa gtgatgatgg 300
gttt 304

SEQ ID NO: 238 moltype = DNA length = 412
FEATURE Location/Qualifiers
misc_feature 1..412
note = Wherein N = A or C or G or T
misc_feature 55
allele = Delete T
note = allele - Delete T
misc_feature 160
allele = A to T
note = allele - A to T
misc_feature 197
allele = C to T
note = allele - C to T
misc_feature 290
allele = T to C
note = allele - T to C
source 1..412
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 238
gatcttttgt gctcagtgag agaantnnnn nttcaannnn nnnnnnnngn atccaacaaa 60
tacaaaaagc nnnnnaacat aaaatagaca tttataagtc acttgtatgt atattggctt 120
tttgtaaatt aaatcatgtt ttatataaca ttagaaccct gttgggtaag gccccctgaa 180
gtaaatggtt tgtaatagaa ataaattgcc ctaccacttg tgatgagcat agcataacaa 240
ccaaagttgt tgaatcactt tgttgtacac ctgaaactaa tgtaacattg tgtgtcaact 300
atactaaaaa ataataataa ataagttttt atttttaata actgctaaaa taaattaaaa 360
atgagtagtg atcctcgttt cagnaatacc tgaaacattt atctgcttat ga 412

SEQ ID NO: 239 moltype = DNA length = 300
FEATURE Location/Qualifiers
misc_feature 1..300
note = Wherein N = A or C or G or T
misc_feature 93
allele = A to G
note = allele - A to G
source 1..300
mol_type = genomic DNA
organism = Canis familiaris
SEQUENCE: 239
ccttatccta ccacagcttc agccatgtct ccagggcctg tgggatccta gagcactcca 60
tcaaggaagc agngtgaggt gagggggggag ctacannnnn ggcggattga cttgtatctc 120
cacnnnnnnn ttcctgtcac attttgatga tctgtcctca ggtttatgac aaatgcttat 180
tacatggtgt atggagacca gtatacagaa acactcttgt ttcctgtaac tcattctttt 240
tatttttgaa ttcctacttg atactcctgt ctaaaatgag ccctaaatat cacaaactca 300

SEQ ID NO: 240 moltype = DNA length = 300
FEATURE Location/Qualifiers
misc_feature 1..300
note = Wherein N = A or C or G or T
misc_feature 136
allele = C to T
note = allele - C to T
misc_feature 175
allele = C to T

-continued

```
                     note = allele - C to T
misc_feature         191
                     allele = G to C
                     note = allele - G to C
source               1..300
                     mol_type = genomic DNA
                     organism = Canis familiaris
SEQUENCE: 240
acccacagaa tccacaagca taattattgt ttaaagcctt tgtatttgga gccgattgtt  60
acaacagcaa ttatttttt aaaaattgta tttatttatt catgagagac acagaannnn  120
nnnnnnnnnn nnngacacag tgnnnnnnnn gaagcaggct ctctgtgggg agcccgatgt  180
gggactcgat gcctgggccc caatcacact ctgagccaaa ggcaaatact cacccactga  240
cccactcagg tgcccctata ccagcaatta gaacactagg cttgtcctta cacctatttt  300

SEQ ID NO: 241        moltype = DNA  length = 304
FEATURE               Location/Qualifiers
misc_feature          1..304
                     note = Wherein N = A or C or G or T
misc_feature         263
                     allele = C to T
                     note = allele - C to T
misc_feature         266
                     allele = T to C
                     note = allele - T to C
source               1..304
                     mol_type = genomic DNA
                     organism = Canis familiaris
SEQUENCE: 241
catctgctgg cacaacttcc tcttgctctg gggaggtcag ttttttctgt tttagtcaaa  60
ctcttcaact gattagatga ggtccacctg cattatgaag ggatatctgc tttannnnnn  120
nnnnnactga tttgaattcc aaaacacctt cacaaaaaac attccaaatg ttgtttgagc  180
aaatatctgg gcaccatggt ccagtcaggt tgacacaaaa ttaacagtca caccactatg  240
agtcctgtgt atccatatta tttctttaag ctacgtttat gaaagtgaaa tctaatagga  300
tgca                                                              304

SEQ ID NO: 242        moltype = DNA  length = 342
FEATURE               Location/Qualifiers
misc_feature          1..342
                     note = Wherein N = A or C or G or T
misc_feature         47
                     allele = G to A
                     note = allele - G to A
misc_feature         133
                     allele = C to T
                     note = allele - C to T
misc_feature         173
                     allele = G to A
                     note = allele - G to A
misc_feature         210
                     allele = G to A
                     note = allele - G to A
misc_feature         302
                     allele = C to T
                     note = allele - C to T
misc_feature         319
                     allele = C to A
                     note = allele - C to A
source               1..342
                     mol_type = genomic DNA
                     organism = Canis familiaris
SEQUENCE: 242
tattgagccc aactgtatac ccgagcctgc gcttggtgct gaggggggtag tggtggcaac  60
actgagcctt taccatccac tccaccgcac tcacagtgag atgaggatca gcacataaac  120
ccgggattcc agcgtgggac acgctgagac agaaggcaac ctgaggcaga cgggggggtta  180
gggtgggtgg gacaggcagc catgannnnn nggacnnnnn tcannnnnna tgannannag  240
acacagatcn nnngttngan nagagagggt cattcnnnnn ggcaggagca gcgcgtgcaa  300
annngccatg atgcccagnn tgctgtgtca tgggaaccag at                     342

SEQ ID NO: 243        moltype = DNA  length = 331
FEATURE               Location/Qualifiers
misc_feature          1..331
                     note = Wherein N = A or C or G or T
misc_feature         54
                     allele = Insert A
                     note = allele - Insert A
source               1..331
```

-continued

```
                     mol_type = genomic DNA
                     organism = Canis familiaris
SEQUENCE: 243
tgacagtaag ttgtgcaggt tccttttctt tccccccaaa tgagtctttt actatttttt  60
ttctaannnn agctaccttc agnnnnnnnn nnnnnncnaa gtcaannnnn acacatccct  120
tgacacagac acctaaatct ctgtaatttt tgagcaagaa cttgatttgc tatatgccat  180
aagctaaatg gatagtttgg ggcacacatt tgtctggaga caaagccttg ctctaaacaa  240
cagtttaaaa tgtttcagtg agcacctatt gaaagtgata tattatgcaa gcaatttctt  300
tgtagttatg cgtagaaaca gctcagctac t                                 331

SEQ ID NO: 244       moltype = DNA  length = 22
FEATURE              Location/Qualifiers
misc_feature         1..22
                     note = Oligonucleotide Primer
source               1..22
                     mol_type = other DNA
                     organism = synthetic construct
SEQUENCE: 244
gcttttggac aactttggat ag                                           22

SEQ ID NO: 245       moltype = DNA  length = 22
FEATURE              Location/Qualifiers
misc_feature         1..22
                     note = Oligonucleotide Primer
source               1..22
                     mol_type = other DNA
                     organism = synthetic construct
SEQUENCE: 245
gaattccaaa tgtcctgctt ag                                           22

SEQ ID NO: 246       moltype = DNA  length = 22
FEATURE              Location/Qualifiers
misc_feature         1..22
                     note = Oligonucleotide Primer
source               1..22
                     mol_type = other DNA
                     organism = synthetic construct
SEQUENCE: 246
aagcatactt ccctgaaatg ag                                           22

SEQ ID NO: 247       moltype = DNA  length = 22
FEATURE              Location/Qualifiers
misc_feature         1..22
                     note = Oligonucleotide Primer
source               1..22
                     mol_type = other DNA
                     organism = synthetic construct
SEQUENCE: 247
agtcaaatcg ttcattggat tc                                           22

SEQ ID NO: 248       moltype = DNA  length = 22
FEATURE              Location/Qualifiers
misc_feature         1..22
                     note = Oligonucleotide Primer
source               1..22
                     mol_type = other DNA
                     organism = synthetic construct
SEQUENCE: 248
aaaaggtggc acatatgaaa ag                                           22

SEQ ID NO: 249       moltype = DNA  length = 22
FEATURE              Location/Qualifiers
misc_feature         1..22
                     note = Oligonucleotide Primer
source               1..22
                     mol_type = other DNA
                     organism = synthetic construct
SEQUENCE: 249
ggggtttcta ttccattttc ac                                           22

SEQ ID NO: 250       moltype = DNA  length = 22
FEATURE              Location/Qualifiers
misc_feature         1..22
                     note = Oligonucleotide Primer
source               1..22
                     mol_type = other DNA
```

-continued

	organism = synthetic construct
SEQUENCE: 250	
acctcatgta tgtcttgttc cc	22
SEQ ID NO: 251	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 251	
ctctgctagg agaaaaggag ag	22
SEQ ID NO: 252	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 252	
caaatggttc aagaggagat tc	22
SEQ ID NO: 253	moltype = DNA length = 25
FEATURE	Location/Qualifiers
misc_feature	1..25
	note = Oligonucleotide Primer
source	1..25
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 253	
aaagtaaaat caggtattct cctcc	25
SEQ ID NO: 254	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 254	
caccctcaag aagttaaagc ac	22
SEQ ID NO: 255	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 255	
taggggacac agtttctaaa gg	22
SEQ ID NO: 256	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 256	
tctcaaactg ttgaagacca ac	22
SEQ ID NO: 257	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 257	
catgtgaccc ttcctatgag ac	22
SEQ ID NO: 258	moltype = DNA length = 23
FEATURE	Location/Qualifiers

-continued

misc_feature 1..23
note = Oligonucleotide Primer
source 1..23
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 258
ggaagacccc aactctatta ttg 23

SEQ ID NO: 259 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 259
agtcttttgg tcctaaacat gg 22

SEQ ID NO: 260 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 260
agacacatgc attttcccag 20

SEQ ID NO: 261 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 261
gtccaaagtt ggagatgata gg 22

SEQ ID NO: 262 moltype = DNA length = 19
FEATURE Location/Qualifiers
misc_feature 1..19
note = Oligonucleotide Primer
source 1..19
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 262
aaagcccagc tgttgtctg 19

SEQ ID NO: 263 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 263
cctgtccttt agaatcctca tc 22

SEQ ID NO: 264 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 264
agtcatttat tgaagcaaag gg 22

SEQ ID NO: 265 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 265

-continued

cgatatttag gaatgaagcc ac 22

SEQ ID NO: 266 moltype = DNA length = 26
FEATURE Location/Qualifiers
misc_feature 1..26
note = Oligonucleotide Primer
source 1..26
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 266
aaatatctgt ttctgaaata tctccc 26

SEQ ID NO: 267 moltype = DNA length = 19
FEATURE Location/Qualifiers
misc_feature 1..19
note = Oligonucleotide Primer
source 1..19
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 267
tttcctttgc ttctggtgc 19

SEQ ID NO: 268 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 268
ttggtttgat cacctatgga ag 22

SEQ ID NO: 269 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 269
acacataact gaagcacacc ag 22

SEQ ID NO: 270 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 270
taggtgcatc ccattctcag 20

SEQ ID NO: 271 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 271
ccaatgatct tgcacagtta tg 22

SEQ ID NO: 272 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 272
caaatgttaa atggacatct gc 22

SEQ ID NO: 273 moltype = DNA length = 21
FEATURE Location/Qualifiers
misc_feature 1..21
note = Oligonucleotide Primer

-continued

source 1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 273
ggtaaaccag aagttcccca g 21

SEQ ID NO: 274 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 274
atttacatgg cagtgtgttc tg 22

SEQ ID NO: 275 moltype = DNA length = 24
FEATURE Location/Qualifiers
misc_feature 1..24
note = Oligonucleotide Primer
source 1..24
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 275
attccatttt aggtctgcat aaag 24

SEQ ID NO: 276 moltype = DNA length = 24
FEATURE Location/Qualifiers
misc_feature 1..24
note = Oligonucleotide Primer
source 1..24
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 276
aaactctcct atttcacatt gacc 24

SEQ ID NO: 277 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 277
gaaccctcct gtctctgtaa cc 22

SEQ ID NO: 278 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 278
cttttggctt tctctgaatt tg 22

SEQ ID NO: 279 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 279
taagttccac ctgtattgca tc 22

SEQ ID NO: 280 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 280
gatcttttgt gctcagtgag ag 22

-continued

SEQ ID NO: 281	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 281	
ccttatccta ccacagcttc ag	22
SEQ ID NO: 282	moltype = DNA length = 19
FEATURE	Location/Qualifiers
misc_feature	1..19
	note = Oligonucleotide Primer
source	1..19
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 282	
acccacagaa tccacaagc	19
SEQ ID NO: 283	moltype = DNA length = 19
FEATURE	Location/Qualifiers
misc_feature	1..19
	note = Oligonucleotide Primer
source	1..19
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 283	
catctgctgg cacaacttc	19
SEQ ID NO: 284	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 284	
tattgagccc aactgtatac cc	22
SEQ ID NO: 285	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 285	
tgacagtaag ttgtgcaggt tc	22
SEQ ID NO: 286	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 286	
tgtgatctac gtcactctct gg	22
SEQ ID NO: 287	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 287	
tctttcatct accaagggtg tg	22
SEQ ID NO: 288	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA

-continued

	organism = synthetic construct
SEQUENCE: 288	
tgtatcagcc ataaagtgtt gg	22
SEQ ID NO: 289	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 289	
ctgcttgaat gtactccctc tc	22
SEQ ID NO: 290	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 290	
aagagtcaga ggcttaaggg ag	22
SEQ ID NO: 291	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 291	
ttggaatgca tactgttgac ac	22
SEQ ID NO: 292	moltype = DNA length = 18
FEATURE	Location/Qualifiers
misc_feature	1..18
	note = Oligonucleotide Primer
source	1..18
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 292	
tgatcttggg gtcctgag	18
SEQ ID NO: 293	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 293	
acacaattca gtccattcag c	21
SEQ ID NO: 294	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 294	
taaccattgt aggttcctgt cc	22
SEQ ID NO: 295	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 295	
tggcatgcat atctatctga ag	22
SEQ ID NO: 296	moltype = DNA length = 20
FEATURE	Location/Qualifiers

-continued

misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 296
cctggttttg agaagactgg 20

SEQ ID NO: 297 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 297
gacagacatg taagaagccc tc 22

SEQ ID NO: 298 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 298
ggtctctgct aggaacaaat tc 22

SEQ ID NO: 299 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 299
gaaagtagag gcaatttggt tg 22

SEQ ID NO: 300 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 300
tcagctgtgg ttacagattt tg 22

SEQ ID NO: 301 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 301
cactgtgact cctcactgac tg 22

SEQ ID NO: 302 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 302
aatcttcatt gtgaacagga gc 22

SEQ ID NO: 303 moltype = DNA length = 24
FEATURE Location/Qualifiers
misc_feature 1..24
note = Oligonucleotide Primer
source 1..24
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 303

-continued

tgaaactggg aaatgttgtt atag 24

SEQ ID NO: 304 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 304
agatagggtg aggacagcta cg 22

SEQ ID NO: 305 moltype = DNA length = 21
FEATURE Location/Qualifiers
misc_feature 1..21
note = Oligonucleotide Primer
source 1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 305
tacacattca agcaccagag g 21

SEQ ID NO: 306 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 306
ctctgtacac ctggattgag tg 22

SEQ ID NO: 307 moltype = DNA length = 21
FEATURE Location/Qualifiers
misc_feature 1..21
note = Oligonucleotide Primer
source 1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 307
tggtatgcaa ataggcactt c 21

SEQ ID NO: 308 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 308
gcagatctag cccgtaatag tg 22

SEQ ID NO: 309 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 309
ttgctaactc ttctggcttt tg 22

SEQ ID NO: 310 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 310
acatgtgaga tacaacttcc cc 22

SEQ ID NO: 311 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer

-continued

source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 311	
aagattgagc atgacttcct tg	22
SEQ ID NO: 312	moltype = DNA length = 18
FEATURE	Location/Qualifiers
misc_feature	1..18
	note = Oligonucleotide Primer
source	1..18
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 312	
aatttgcctc gccttgag	18
SEQ ID NO: 313	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 313	
tggtagaggt ggtattggag tg	22
SEQ ID NO: 314	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 314	
tgatagaggc ctgagaaaga ac	22
SEQ ID NO: 315	moltype = DNA length = 18
FEATURE	Location/Qualifiers
misc_feature	1..18
	note = Oligonucleotide Primer
source	1..18
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 315	
ctgttgcgaa ggctcaag	18
SEQ ID NO: 316	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 316	
aaaagcccac ataacatgag c	21
SEQ ID NO: 317	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
	note = Oligonucleotide Primer
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 317	
ttttagagag tgcctgccaa g	21
SEQ ID NO: 318	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 318	
gaactggcaa atccaatctt ac	22

-continued

SEQ ID NO: 319 moltype = DNA length = 24
FEATURE Location/Qualifiers
misc_feature 1..24
note = Oligonucleotide Primer
source 1..24
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 319
agcaacttga atcttaaagg aaag 24

SEQ ID NO: 320 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 320
tgtatccaat ttcacattgc tg 22

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note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 321
aaacccatca tcacttgtct tc 22

SEQ ID NO: 322 moltype = DNA length = 24
FEATURE Location/Qualifiers
misc_feature 1..24
note = Oligonucleotide Primer
source 1..24
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 322
tcataagcag ataaatgttt cagg 24

SEQ ID NO: 323 moltype = DNA length = 23
FEATURE Location/Qualifiers
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note = Oligonucleotide Primer
source 1..23
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 323
tgagtttgtg atatttaggg ctc 23

SEQ ID NO: 324 moltype = DNA length = 22
FEATURE Location/Qualifiers
misc_feature 1..22
note = Oligonucleotide Primer
source 1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 324
aaaataggtg taaggacaag cc 22

SEQ ID NO: 325 moltype = DNA length = 24
FEATURE Location/Qualifiers
misc_feature 1..24
note = Oligonucleotide Primer
source 1..24
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 325
tgcatcctat tagatttcac tttc 24

SEQ ID NO: 326 moltype = DNA length = 20
FEATURE Location/Qualifiers
misc_feature 1..20
note = Oligonucleotide Primer
source 1..20
mol_type = other DNA

-continued

	organism = synthetic construct
SEQUENCE: 326	
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SEQ ID NO: 327	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Oligonucleotide Primer
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 327	
agtagctgag ctgtttctac gc	22

1-23. (canceled)

24. A method for identifying a breed in a mixed-breed canid and managing healthcare of the mixed-breed canid based on a medical predisposition of the breed, wherein a genome of the mixed-breed canid is from two or more domestic breeds, the method comprising:

(i) contacting the genome of the mixed-breed canid with at least two primers selected from the group consisting of SEQ ID NOs: 1-200 and 244-327;

(ii) amplifying sequences of the genome of the mixed-breed canid to obtain amplicons of at least 50 microsatellite markers and at least 50 single nucleotide polymorphism markers,

wherein the at least 50 microsatellite markers are selected from REN285G14, C01.673, REN112I02, REN172C02, FH2793, REN143K19, FH2890, C02.466, C02.894, C02.342, FH2895, REN157C08, C03.445, FH2732, FH2776, REN160J02, REN262N08, REN92G21, REN285I23, C05.414, FH2752, REN210I14, REN37H09, REN97M11, REN286L19, FH2860, REN204K13, C08.373, C08.618, C09.173, C09.474, FH2885, C10.781, REN73F08, REN154G10, REN164B05, FH2874, C11.873, REN258L11, REN213F01, REN208M20, REN94K11, REN120P21, REN286P03, C13.758, C14.866, FH3072, FH3802, REN06C11, REN144M10, REN85N14, FH3096, C17.402, REN50B03, REN112G10, REN186N13, FH2795, C18.460, FH2783, REN91I14, REN274F18, FH2887, FH3109, REN293N22, FH2914, FH3069, REN49F22, REN107H05, REN78I16, FH3078, C23.277, REN181K04, REN106I06, FH3083, REN54E19, C25.213, REN87021, C26.733, C27.442, C27.436, REN72K15, FH2759, FH2785, REN239K24, FH3082, REN51C16, FH3053, REN43H24, FH2712, FH2875, FH2790, REN291M20, REN160M18, FH3060, REN314H10, REN01G01, REN112C08, REN106I07, FH2708, and REN86G15; and

wherein the at least 50 single nucleotide polymorphism markers are selected from 372-c5t-82, 372-c5t-133, 372-c15t-285, 372-e2s-271, 372-e2s-257, 372-e2s-128, 372-e2s-93, 372-e2s-50, 372-e13t-57, 372-e15t-312, 372-e15t-301, 372-e15t-258, 372-e15t-156, 372-e16s-254, 372-e18t-165, 372-g17t-66, 372-i23s-384, 372-m6t-138, 372-m6t-88, 372-m6t-266, 372-m7s-317, 372-m9t-108, 372-m9t-58, 372-m18t-170, 372-m18t-129, 372-m23t-76, 372-m23t-108, 372-m23t-229, 372-m23t-238, 372-m23t-263, 372-o13s-212, 373-a10s-274, 373-a15t-112, 373-a17t-73, 373-a17t-136, 373-a21s-89, 373-c13s-93, 373-c15t-242, 373-c15t-202, 373-c15t-131, 373-e1t-50, 373-e1t-102, 373-e1t-130, 373-e21t-282, 373-e21t-116, 373-g7t-243, 373-g7t-242, 373-g7t-84, 373-g19t-249, 373-g19t-251, 373-g19t-246, 373-g19t-224, 373-g19t-378, 373-i8s-199, 373-i8s-224, 373416s-312, 373416s-254, 373416s-250, 373416s-249, 373-k8s-181, 373-k8s-224, 373-k10t-261, 373-k10t-264, 372-c5s-112, 372-c5s-168, 372-c15s-121, 372-c15s-196, 372-e15s-67, 372-e15s-71, 372-e15s-165, 372-e15s-221, 372-i23t-97, 372-i23t-224, 372-m6s-67, 372-m6s-73, 372-m6s-100, 372-m6s-108, 372-m6s-127, 372-m6s-147, 372-m6s-186, 372-m7t-100, 372-m7t-273, 372-m18s-131, 373-a14t-290, 373-a14t-197, 373-a14t-160, 373-a14t-55, 373-a21t-93, 373-e21s-136, 373-e21s-175, 373-e21s-191, 373-g7s-263, 373-g7s-266, 373416t-47, 373416t-133, 373416t-173, 373416t-210, 373416t-302, 373416t-319, and 373-k16t-54;

(iii) sequencing the amplicons of the at least 50 microsatellite markers and the at least 50 single nucleotide polymorphism markers to produce a plurality of sequences; and

(iv) executing, with a processor, computer-readable instructions stored on a computer-readable medium to cause the processor to determine, with a plurality of computational steps, the breed of the mixed-breed canid based on the plurality of sequences, wherein the plurality of computational steps comprises:

(a) inputting the sequences of the amplicons of the at least 50 microsatellite markers and the at least 50 single nucleotide polymorphism markers into a data structure stored in the computer readable medium, wherein the data structure comprises a marker field corresponding to the at least 50 microsatellite markers and the at least 50 single nucleotide polymorphism markers and a genotyping information field comprising the allele identities of the at least 50 microsatellite markers and the at least 50 single nucleotide polymorphism markers;

(b) comparing the marker field and the genotyping information field of the data structure to a database, wherein the database comprises allele identity and allele frequency information of the at least 50 microsatellite markers and the at least 50 single nucleotide polymorphism markers of a plurality of domestic dog breeds, wherein the plurality of domestic dog breeds comprises at least five domestic dog breeds;

(c) identifying the two or more domestic dog breeds of the mixed-breed canid from the allele-identities provided in the data structure; and

(d) calculating a fraction of the genome of the mixed-breed canid that is from each of the plurality of domestic dog breeds, at parent, grandparent, and great-grandparent levels, and wherein the fraction of the genome of the mixed-breed canid from each of the two or more domestic dog breeds is at least 5%;

(v) identifying the medical predisposition based on the breed; and

(vi) testing the mixed-breed canid for a disease or a condition based on the medical predisposition.

25. The method of claim **24**, wherein the plurality of domestic dog breeds comprises Mastiff, Dachshund, Bull Mastiff, Beagle, and Golden Retriever.

26. The method of claim **24**, wherein the plurality of domestic dog breeds comprises:

(i) Belgian Sheep Dog and Belgian Tervuren,

(ii) Collie and Shetland Sheep Dog,

(iii) Whippet and Greyhound,

(iv) Siberian Husky and Alaskan Malamute,

(v) Greater Swiss Mountain Dog and Bernese Mountain Dog,

(vi) West Highland White Terrier and Cairn Terrier, and/or

(vii) Lhasa Apso, Shih Tzu, and Pekinese.

27. The method of claim **24**, wherein the plurality of domestic dog breeds comprises between 5 and 500 domestic dog breeds.

28. The method of claim **24**, wherein (iv)(c) identifying further comprises:

(1) obtaining a health recommendation based on the identified breed, wherein the health recommendation comprises treatments, special diets, or special products; and

(2) generating a document comprising the health recommendation, wherein the document comprises information of diseases and predispositions of the mixed breed canid.

29. The method of claim **24**, wherein (d)(iii) identifying further comprises:

(i) discriminating between the fraction of the genome of the mixed-breed canid that is selected from the group consisting of:

(a) Belgian Sheep Dog and Belgian Tervuren,

(b) Collie and Shetland Sheep Dog,

(c) Whippet and Greyhound,

(d) Siberian Husky and Alaskan Malamute,

(e) Greater Swiss Mountain Dog and Bernese Mountain Dog,

(f) West Highland White Terrier and Cairn Terrier, and/or

(g) Lhasa Apso, Shih Tzu, and Pekinese.

30. A kit for performing the method of claim **24**.

31. A kit for identifying a breed in a mixed-breed canid and managing healthcare of the mixed-breed canid based on a medical predisposition of the breed, wherein a genome of the mixed-breed canid is from two or more domestic breeds, the kit comprising:

at least two primers selected from the group consisting of SEQ ID NOs: 1-200 and 244-327, wherein the at least two primers are to contact a genome of a mixed-breed canid and amplify sequences of the genome of the mixed-breed canid to obtain amplicons of at least 50 microsatellite markers and at least 50 single nucleotide polymorphism markers;

wherein the at least 50 microsatellite markers are selected from REN285G14, C01.673, REN112102, REN172C02, FH2793, REN143K19, FH2890, C02.466, C02.894, C02.342, FH2895, REN157C08, C03.445, FH2732, FH2776, REN160J02, REN262N08, REN92G21, REN285I23, C05.414, FH2752, REN210I14, REN37H09, REN97M11, REN286L19, FH2860, REN204K13, C08.373, C08.618, C09.173, C09.474, FH2885, C10.781, REN73F08, REN154G10, REN164B05, FH2874, C11.873, REN258L11, REN213F01, REN208M20, REN94K11, REN120P21, REN286P03, C13.758, C14.866, FH3072, FH3802, REN06C11, REN144M10, REN85N14, FH3096, C17.402, REN50B03, REN112G10, REN186N13, FH2795, C18.460, FH2783, REN91114, REN274F18, FH2887, FH3109, REN293N22, FH2914, FH3069, REN49F22, REN107H05, REN78116, FH3078, C23.277, REN181K04, REN106106, FH3083, REN54E19, C25.213, REN87021, C26.733, C27.442, C27.436, REN72K15, FH2759, FH2785, REN239K24, FH3082, REN51C16, FH3053, REN43H24, FH2712, FH2875, FH2790, REN291M20, REN160M18, FH3060, REN314H10, REN01G01, REN112C08, REN106107, FH2708, and REN86G15; and

wherein the at least 50 single nucleotide polymorphism markers are selected from 372-c5t-82, 372-c5t-133, 372-c15t-285, 372-e2s-271, 372-e2s-257, 372-e2s-128, 372-e2s-93, 372-e2s-50, 372-e13t-57, 372-e15t-312, 372-e15t-301, 372-e15t-258, 372-e15t-156, 372-e16s-254, 372-e18t-165, 372-g17t-66, 372-i23s-384, 372-m6t-138, 372-m6t-88, 372-m6t-266, 372-m7s-317, 372-m9t-108, 372-m9t-58, 372-m18t-170, 372-m18t-129, 372-m23t-76, 372-m23t-108, 372-m23t-229, 372-m23t-238, 372-m23t-263, 372-o13s-212, 373-a10s-274, 373-a15t-112, 373-a17t-73, 373-a17t-136, 373-a21s-89, 373-c13s-93, 373-c15t-242, 373-c15t-202, 373-c15t-131, 373-e1t-50, 373-e1t-102, 373-e1t-130, 373-e21t-282, 373-e21t-116, 373-g7t-243, 373-g7t-242, 373-g7t-84, 373-g19t-249, 373-g19t-251, 373-g19t-246, 373-g19t-224, 373-g19t-378, 373-i8s-199, 373-i8s-224, 373-i16s-312, 373416s-254, 373416s-250, 373416s-249, 373-k8s-181, 373-k8s-224, 373-k10t-261, 373-k10t-264, 372-c5s-112, 372-c5s-168, 372-c15s-121, 372-c15s-196, 372-e15s-67, 372-e15s-71, 372-e15s-165, 372-e15s-221, 372-i23t-97, 372-i23t-224, 372-m6s-67, 372-m6s-73, 372-m6s-100, 372-m6s-108, 372-m6s-127, 372-m6s-147, 372-m6s-186, 372-m7t-100, 372-m7t-273, 372-m18s-131, 373-a14t-290, 373-a14t-197, 373-a14t-160, 373-a14t-55, 373-a21t-93, 373-e21s-136, 373-e21s-175, 373-e21s-191, 373-g7s-263, 373-g7s-266, 373416t-47, 373416t-133, 373416t-173, 373416t-210, 373416t-302, 373416t-319, and 373-k16t-54.

32. The kit of claim **31**, wherein the amplicons of the at least 50 microsatellite markers and the at least 50 single nucleotide polymorphism markers are to produce a plurality of sequences for:

(i) determination of the breed of the mixed-breed canid;

(ii) identification of the medical predisposition based on the breed; and

(iii) evaluation of the mixed-breed canid for a disease or a condition based on the medical predisposition.

33. The kit of claim **31**, wherein the two or more domestic dog breeds comprises two or more of Mastiff, Dachshund, Bull Mastiff, Beagle, and Golden Retriever.

34. The kit of claim **31**, wherein the two or more domestic dog breeds comprises:

(i) Belgian Sheep Dog and Belgian Tervuren,

(ii) Collie and Shetland Sheep Dog,

(iii) Whippet and Greyhound,

(iv) Siberian Husky and Alaskan Malamute,

(v) Greater Swiss Mountain Dog and Bernese Mountain Dog,

(vi) West Highland White Terrier and Cairn Terrier, and/or

(vii) Lhasa Apso, Shih Tzu, and Pekinese.

35. The kit of claim **31**, wherein the two or more domestic dog breeds comprises between 5 and 500 domestic dog breeds.

36. The kit of claim **31**, wherein the determination of the breed of the mixed-breed canid is for:

(i) obtaining a health recommendation based on the breed, wherein the health recommendation comprises treatments, special diets, or special products; and

(ii) generating a document comprising the health recommendation, wherein the document comprises information of diseases and predispositions of the mixed breed canid.

37. The kit of claim **31**, wherein the determination of the breed of the mixed-breed canid comprises:

(i) discriminating between the fraction of the genome of the mixed-breed canid that is selected from the group consisting of:

(a) Belgian Sheep Dog and Belgian Tervuren,

(b) Collie and Shetland Sheep Dog,

(c) Whippet and Greyhound,

(d) Siberian Husky and Alaskan Malamute,

(e) Greater Swiss Mountain Dog and Bernese Mountain Dog,

(f) West Highland White Terrier and Cairn Terrier, and/or

(g) Lhasa Apso, Shih Tzu, and Pekinese.

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