GENETIC IDENTIFICATION OF DOMESTIC CAT BREEDS AND POPULATIONS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit under 35 U.S.C. § 119(e) of U.S. Provisional Application No. 61/487,987, filed on May 19, 2011, which is hereby incorporated herein in its entirety for all purposes.

STATEMENT OF GOVERNMENTAL SUPPORT

[0002] This invention was made with government support under Grant No. R24 RR0016094 awarded by the National Institutes of Health, National Center for Research Resources (NCRR). The government has certain rights in the invention.

FIELD OF THE INVENTION

[0003] The invention relates to determining the contribution of one or more feline populations to the genome of a feline using a predetermined set of genetic markers, including single nucleotide polymorphisms (SNPs), short tandem repeats (STRs) and DNA-based phenotypic markers.

BACKGROUND OF THE INVENTION

[0004] The domestication of the cat has been a slow and prolonged process, especially when compared to most species associated with human agricultural development. Indeed, the cat is often considered to be only semi-domesticated. Archaeological remains of cats in close proximity to and even buried alongside humans suggest that cats were first domesticated in Cyprus during the Neolithic age 5,000-10,000 BP (Vigne et al., (2004) Science 304, 259-259.) but popular culture suggests cats were domesticated in Egypt (Málek, (1993) *The cat in ancient Egypt* British Museum Pr. for the Trustees of the British Museum, London; Nowell, (1996) *Status Survey and Conservation Action Plan: Wild Cats* IUCN, Gland, Switzerland.). Genetic studies using STR and mtDNA analysis of feral and wildcats from throughout Africa and Eurasia identified the Near Eastern Arabian/Northern African wildcat subspecies (*Felis silvestris libyca*) as the species most closely related to the domestic cat (Driscoll et al., (2007) *Science* 317, 519-523). Other early human civilizations developed near the Yellow River region of China and the Indus Valley of present day Pakistan. However, sufficient sampling or documentation of wildcats in these regions is inadequate. Only the Fertile Crescent lies within the range of *F. s. lybica*, which has better documentation and sampling. In addition to the wildcat studies, an independent STR study of both feral and pedigreed cats found the highest genetic diversity of the sampled cats in the region of the eastern Mediterranean Sea, supporting a Fertile Crescent origin of cat domestication (Lipinski et al., (2008) *Genomics* 91, 12-21.). However, neither study sampled the cats of the Fertile Crescent and Egypt sufficiently to closely examine cat populations in this historically important region, which is necessary for pinpointing the site of cat domestication.

[0005] Genetic markers that arise through a variety of mutational mechanisms help to resolve population stratifications and trace historical migrations (Zeder et al., (2006) *Trends in Genetics* 22:139-155). STRs and have long been the preferred tool for genetic analyses of recently diverged populations, such as cat breeds, due to their high mutation rate and relative cost effectiveness in comparison to sequencing techniques (Brown et al., (1979) *Proc. Natl. Acad. Sci. USA*_76:1967-1971). Analysis of different areas of the mtDNA, particularly gene sequences provide evidence of the matrilineal history of the domesticated cat and of the closest common ancestor, the African wildcat from the Near East (Driscoll et al., 2007, *supra*). In addition, the mtDNA control region (CR), with its fast rate of mutation, provides evidence of recent admixture of most of the worldwide cat populations (Grahn et al., *Forensic Sci Int Genet.* (2011) 1:33-42). The advent of high-throughput SNP typing platforms allows the genotyping of many markers with slower mutation rates, rates which can help define a population's more ancient origins and provide finer-scale evidence for the first domesticated cat populations. Thus, genetic analysis of the same cat populations, using an assortment of DNA markers with a variety of mutation patterns, will better define cat population stratification but not obfuscate the more ancient lineages, further clarifying the domestication progression from ancient to modern cats.

[0006] Data presented herein shows that the domestic cat origins lie within the Northern region of the Fertile Crescent, where the earliest agriculture and civilizations began. Random bred domestic cat populations from around the world, specifically the region of the Fertile Crescent and Egypt, were genetically investigated to improve the resolution of cat population structures within this important site of cat domestication. Two types of genetic markers, STRs and SNPs, were genotyped in the same cat populations, including several larger populations from the Fertile Crescent region.

[0007] The genetic markers further find application in determining the breed pedigree or population origins of a subject feline. Over the past 125 years, mankind has imposed artificial selection to further the previously unchecked process of cat domestication resulting in pedigreed cats. Since the first USA cat show in 1895, which presented five breeds, the development of pedigreed cats has increased in popularity (Gebhardt (1991) *The Complete Cat Book*. Howell Book House, New York.). Forty-one breeds are currently recognized for competition by the Cat Fanciers' Association (CFA, on the internet at cfa.org/) and 57 are accepted by The International Cat Association (TICA, on the internet at tica.org/). A majority of the breeds recognized by these two large registries is also recognized around the world. A common, sometimes obsessive hobby of cat breeders is feline genealogy, or tracing the true genetic ancestry of the breed and even of one's own random bred pet cat. Many commercial service laboratories are marketing genetic tests for dogs, promising the elucidation of "the breed ancestry of your best friend". Random bred house cats, however, have a different story to their genetic origins. Whereas the average feline mutt found in the streets of most developed countries is more likely a cross-bred individual from multiple purebred breeds, the average random bred cat is not a descendant of their pedigreed counterparts. For cats, the opposite scenario is more likely - pedigreed feline stocks are the descendants of common street cats from distinct parts of the world that have been selected for a distinctive trait (Table 8) (CFA (1993) *The Cat Fanciers' Association Cat Encyclopedia*, Simon & Schuster, New York). Random bred cats are the original populations from which the breeds developed, not a population of pedigreed cats gone feral. In addition, also converse to most dog registries, to improve population health and reduce the effects of inbreeding depression, cat breeding associations often seek to diversify their breed populations with random bred cats from their ancestral origin. For this reason, most cat registries use the term "pedigreed" and not "purebred".

[0008] Two studies have evaluated the genetic distinction of cat breeds. Lipinski et al. ((2008) *Genomics*, 91:12-21) defined the connections between the random bred cat populations and their descendant pedigreed lines using a DNA marker panel containing two tetranucleotide and 36 dinucleotide STR markers. Five hundred fifty-five individuals were demarcated into 20 breeds. Four breeds could not be resolved at the breed level. Furthermore, the breeds sampled by Lipinski et al. were shown to be similar to the populations of street cats found in Europe, the Eastern Mediterranean and Southeast Asia. Menotti-Raymond et al. ((2008) *Genomics*, 91:1-11) used a panel of eleven tetranucleotide

STR markers and ten regions of SNPs in a subset of their sample set in order to characterize the delineation of cat breeds. Further attempts at population division caused lineages within breeds to resolve before that of the recognized sister breeds. Using only the STR markers, 1040 individuals were demarcated into 8 individual breeds and 9 additional breed groups. Twenty breeds could not be resolved at the breed level. These studies indicated that distinct populations and breeds of cats can be defined genetically, that breeds do have different worldwide regions of origin, tetranucleotide STRs do not perform as well with defining cat breeds as the dinucleotide markers, and that some breeds are so closely related that they cannot be distinguished with even the rapidly evolving dinucleotide STRs.

[0009] The 38 highly polymorphic markers of Lipinski et al. (2008), *supra*, and a recently developed panel of 148 intergenic autosomal SNPs were recently applied to an extensive sample of random bred street cats collected throughout the world (described herein). Nine hundred forty-four samples were collected from 37 locations spread throughout North and South America, Europe, Africa, and Asia. This study found that while both were efficient at distinguishing five long established lineages, a few geographically close populations were better delineated with either SNPs or STRs, most likely due to varying mutation rates between the markers.

[0010] Many methods of assignment testing have been developed in the past decade using common population genetic markers and a variety of statistical methods (Rannala & Mountain (1997) *Proc Natl Acad Sci U S A.* 94(17):9197-9201; Pritchard et al. (2000) *Genetics*, 155:945-959; Baudouin & Lebrun (2001) In: *Proc. Int. Symp. on Molecular Markers*, pp. 81-94; Paetkau et al. (2004) *Molecular Ecology*, 13:55-65). These methods have been applied to various breeding populations including pigs, cattle, and dogs (Schelling et al. (2005) *Journal of Animal Breeding and Genetics*, 122:71-77; Negrini et al. (2009) *Animal Genetics*, 40:18-26; Boitard et al. (2010) *Anim Genet.* 2010 41(6):608-18. In cattle, Negrini et al. (2009), *supra*, used 90 SNPs to both allocate and then assign 24 breeds under both the Baysean methods of Pritchard et al. (2000), *supra*, and Rannala & Mountain (1997), *supra*, and Baudouin & Lebrun (2001), *supra*, and the likelihood method of Paetkau et al. (2004), *supra*. Negrini et al. (2009) concluded that the methods implemented through Rannala & Mountain (Bayesian) (1997) and Petkau et al. (frequentist) (2004) worked best when attempting to assign unknown individuals to a known database of representative samples from each breed. Previous population studies used Bayesian clustering and neighbor-joining phylogenetic analyses to elucidate the cat breeds and the origins of random bred populations. The present invention demonstrates the utility of a panel of 148 evenly dispersed genome-wide SNPs for population assignment of cats. Different assignment techniques are examined and demonstrated in a species exhibiting many recent and extreme population bottlenecks, comparing the power and efficiency of this 148 SNP panel to 4-fold fewer microsatellites. The power of phenotypic DNA variants is demonstrated for sensitivity and specificity to support individual assignment, specifically for closely related cat breeds that are demarcated by single gene traits.

SUMMARY OF THE INVENTION

[0011] The present invention provides genetic markers useful for the determination of the the population of origin (*e.g.*, ancestral lineage and/or contributing breed(s)) of a test feline. Accordingly, in one aspect, the invention provides computer implemented methods for determining the contributions of feline populations to a feline genome. In some embodiments, the methods comprise:

(a) genotyping a sample comprising genomic DNA obtained from a test feline to determine the identity of one or both alleles of each marker of a set of markers, wherein the set of markers comprises a plurality of single nucleotide polymorphisms (SNPs) listed in Table 1;

(b) comparing the identity of one or both alleles for each of the markers in the set of markers determined to be present in the test feline genome to a database comprising one or more feline population profiles, wherein each feline population profile comprises genotype information for the set of markers in the feline population; and

(c) determining the contribution of the one or more feline populations to the test feline genome.

[0012] In a further aspect, the invention provides methods for defining one or more feline populations. In some embodiments, the methods comprise:

(a) determining the identity of one or both alleles for each marker of a set of markers in a test feline genome, wherein the set of markers comprises a plurality of single nucleotide polymorphisms (SNPs) listed in Table 1; and

(b) applying a computer-implemented statistical model to define one or more distinct feline populations, wherein one or more distinct feline populations are characterized by a set of allele frequencies for each marker of the set of markers comprising a plurality of SNPs listed in Table 1.

[0013] In a related aspect, the invention provides methods for determining the contributions of feline populations to a feline genome. In some embodiments, the methods comprise performing a genotyping assay on a sample comprising genomic DNA obtained from a test feline to determine the identity of one or both alleles present in the test feline genome for each marker of a set of markers, wherein the set of markers is indicative of the contribution of feline populations to the genome of the test feline, wherein the set of markers comprises a plurality of single nucleotide polymorphisms (SNPs) listed in Table 1.

[0014] In another aspect, the invention provides methods of assigning a feline individual to a population of origin (*e.g.*, an ancestral lineage and/or one or more contributing breeds), which comprises:

(a) genotyping the feline individual to identify one or both alleles of each marker of a set of markers to thereby identify the individual's genotype, wherein the set of markers comprises a plurality of single nucleotide polymorphisms (SNPs) listed in Table 1;

(b) applying a computer-implemented statistical model to assign the feline individual to one or more feline populations in a database, wherein the one or more feline populations are characterized by a set of allele frequencies for each marker of the set of markers; and

(c) assigning the feline individual to the one or more most likely populations identified in step (b). In some embodiments, the individual is assigned to the one or more most likely feline populations if the population genotype probability for the most likely feline populations exceeds the value of assignment to any other feline populations of the database.

[0015] With respect to the embodiments, in some embodiments, the plurality of SNPs comprises at least about 5 SNPs listed in Table 1, for example, at least about 10, 15, 20, 25, 30, 40, 50, 60, 70, 75, 80, 90, 100, 110, 120, 125, 130, 140 or 148 SNPs listed in Table 1. The SNPs listed in Table 1 are as depicted at position 61 of a polynucleotide selected from the group consisting of SEQ ID NO:1 to SEQ ID NO:148 listed in Table 1. In some embodiments, the plurality of SNPs comprises all 148 SNPs listed in Table 1, *e.g.*, as depicted at position 61 of polynucleotides SEQ ID NO:1 to SEQ ID NO:148 listed in Table 1.

[0016] For example, the plurality of SNPs listed in Table 1 are as depicted at position 61 of a polynucleotide selected from the group consisting of SEQ ID NO:1 to SEQ ID NO:148. In some embodiments, the set of markers comprises a plurality of SNPs, wherein the SNPs are selected from the group consisting of position 61 of SEQ ID NO:1, position 61 of SEQ ID NO:2, position 61 of SEQ ID NO:3, position 61 of SEQ ID NO:4, position 61 of SEQ ID NO:5, position 61 of SEQ ID NO:6, position 61 of SEQ ID NO:7, position 61 of SEQ ID NO:8, position 61 of SEQ ID NO:9, position 61 of SEQ ID NO:10, position 61 of SEQ ID NO:11, position 61 of SEQ ID NO:12, position 61 of SEQ ID NO:13, position 61 of SEQ ID NO:14, position 61 of SEQ ID NO:15, position 61 of SEQ ID NO:16, position 61 of SEQ ID NO:17, position 61 of SEQ ID NO:18, position 61 of SEQ ID NO:19, position 61 of SEQ ID NO:20, position 61 of SEQ ID NO:21, position 61 of SEQ ID NO:22, position 61 of SEQ ID NO:23, position 61 of SEQ ID NO:24, position 61 of SEQ ID NO:25, position 61 of SEQ ID NO:26, position 61 of SEQ ID NO:27, position 61 of SEQ ID NO:28, position 61 of SEQ ID NO:29, position 61 of SEQ ID NO:30, position 61 of SEQ ID NO:31, position 61 of SEQ ID NO:32, position 61 of SEQ ID NO:33, position 61 of SEQ ID NO:34, position 61 of SEQ ID NO:35, position 61 of SEQ ID NO:36, position 61 of SEQ ID NO:37, position 61 of SEQ ID NO:38, position 61 of SEQ ID NO:39, position 61 of SEQ ID NO:40, position 61 of SEQ ID NO:41, position 61 of SEQ ID NO:42, position 61 of SEQ ID NO:43, position 61 of SEQ ID NO:44, position 61 of SEQ ID NO:45, position 61 of SEQ ID NO:46, position 61 of SEQ ID NO:47, position 61 of SEQ ID NO:48, position 61 of SEQ ID NO:49, position 61 of SEQ ID NO:50, position 61 of SEQ ID NO:51, position 61 of SEQ ID NO:52, position 61 of SEQ ID NO:53, position 61 of SEQ ID NO:54, position 61 of SEQ ID NO:55, position 61 of SEQ ID NO:56, position 61 of SEQ ID NO:57, position 61 of SEQ ID NO:58, position 61 of SEQ ID NO:59, position 61 of SEQ ID NO:60, position 61 of SEQ ID NO:61, position 61 of SEQ ID NO:62, position 61 of SEQ ID NO:63, position 61 of SEQ ID NO:64, position 61 of SEQ ID NO:65, position 61 of SEQ ID NO:66, position 61 of SEQ ID NO:67, position 61 of SEQ ID NO:68, position 61 of SEQ ID NO:69, position 61 of SEQ ID NO:70, position 61 of SEQ ID NO:71, position 61 of SEQ ID NO:72, position 61 of SEQ ID NO:73, position 61 of SEQ ID NO:74, position 61 of SEQ ID NO:75, position 61 of SEQ ID NO:76, position 61 of SEQ ID NO:77, position 61 of SEQ ID NO:78, position 61 of SEQ ID NO:79, position 61 of SEQ ID NO:80, position 61 of SEQ ID NO:81, position 61 of SEQ ID NO:82, position 61 of SEQ ID NO:83, position 61 of SEQ ID NO:84, position 61 of SEQ ID NO:85, position 61 of SEQ ID NO:86, position 61 of SEQ ID NO:87, position 61 of SEQ ID NO:88, position 61 of SEQ ID NO:89, position 61 of SEQ ID NO:90, position 61 of SEQ ID NO:91, position 61 of SEQ ID NO:92, position 61 of SEQ ID NO:93, position 61 of SEQ ID NO:94, position 61 of SEQ ID NO:95, position 61 of SEQ ID NO:96, position 61 of SEQ ID NO:97, position 61 of SEQ ID NO:98, position 61 of SEQ ID NO:99, position 61 of SEQ ID NO:100, position 61 of SEQ ID NO:101, position 61 of SEQ ID NO:102, position 61 of SEQ ID NO:103, position 61 of SEQ ID NO:104, position 61 of SEQ ID NO:105, position 61 of SEQ ID NO:106, position 61 of SEQ ID NO:107, position 61 of SEQ ID NO:108, position 61 of SEQ ID NO:109, position 61 of SEQ ID NO:110, position 61 of SEQ ID NO:111, position 61 of SEQ ID NO:112, position 61 of SEQ ID NO:113, position 61 of SEQ ID NO:114, position 61 of SEQ ID NO:115, position 61 of SEQ ID NO:116, position 61 of SEQ ID NO:117, position 61 of SEQ ID NO:118, position 61 of SEQ ID NO:119, position 61 of SEQ ID NO:120, position 61 of SEQ ID NO:121, position 61 of SEQ ID NO:122, position 61 of SEQ ID NO:123, position 61 of SEQ ID NO:124, position 61 of SEQ ID NO:125, position 61 of SEQ ID NO:126, position 61 of SEQ ID NO:127, position 61 of SEQ ID NO:128, position 61 of SEQ ID NO:129, position 61 of SEQ ID NO:130, position 61 of SEQ ID NO:131, position 61 of SEQ ID NO:132, position 61 of SEQ ID NO:133, position 61 of SEQ ID NO:134, position 61 of SEQ ID NO:135, position 61 of SEQ ID NO:136, position 61 of SEQ ID NO:137, position 61 of SEQ ID NO:138, position 61 of SEQ ID NO:139, position 61 of SEQ ID NO:140, position 61 of SEQ ID NO:141, position 61 of SEQ ID NO:142, position 61 of SEQ ID NO:143, position 61 of SEQ ID NO:144, position 61 of SEQ ID NO:145, position 61 of SEQ ID NO:146, position 61 of SEQ ID NO:147, and position 61 of SEQ ID NO:148.

[0017] In some embodiments, the set of markers comprises a plurality of SNPs, wherein the SNPs are selected from the group consisting of chrA1_10141047, chrA1_133621071, chrA1_151648701, chrA1_175780586, chrA1_208054462, chrA1_223501140, chrA1_223506906, chrA1_225057933, chrA1_235579538, chrA1_27523501, chrA1_68485376, chrA1_69424718, chrA1_7429296, chrA1_8742286, chrA2_152258936, chrA2_201526186, chrA2_202225770, chrA2_44241149, chrA2_554046, chrA3_101420069, chrA3_11480952, chrA3_12082294, chrA3_130195244, chrA3_159537633, chrA3_162208567, chrA3_38781591, chrA3_75156179, chrA3_91058022, chrA3_99507784, chrB1_10420438, chrB1_12214271, chrB1_195678303, chrB1_199564532, chrB1_202966562, chrB1_54775572, chrB1_80161671, chrB1_88148379, chrB2_138312489, chrB2_146660650, chrB2_41509834, chrB2_45093345, chrB2_6949528, chrB3_104483970, chrB3_111000326, chrB3_13666494, chrB3_39203469, chrB3_51317931, chrB3_57141954, chrB3_77094074, chrB4_105706694, chrB4_142658074, chrB4_143006494, chrB4_144693308, chrB4_146486983, chrB4_147206961, chrB4_149532846, chrB4_1687419, chrB4_20001848, chrB4_21098349, chrB4_255106, chrB4_3093827, chrB4_40319102, chrB4_47638578, chrC1_116355295, chrC1_123164748, chrC1_181852965, chrC1_190502133, chrC1_215441574, chrC1_216852686, chrC1_24148281, chrC1_28702055, chrC1_34981315, chrC1_396397, chrC1_44520932, chrC1_52456776, chrC2_106991233, chrC2_147124460, chrC2_150774106, chrC2_156491175, chrC2_187325, chrC2_262401, chrC2_5215469, chrD1_101321498, chrD1_104941557, chrD1_105498119, chrD1_10789012, chrD1_11484008, chrD1_117527468, chrD1_125811329, chrD1_126256993, chrD1_126847301, chrD1_15984279, chrD1_16242433, chrD1_18390852, chrD1_18570323, chrD1_66177762, chrD2_1020904, chrD2_105772916, chrD2_1752007, chrD2_56777338, chrD2_717969, chrD2_74293444, chrD2_91989307, chrD3_103840114, chrD3_122502120, chrD3_1810839, chrD3_24565823, chrD3_24823793, chrD3_28838660, chrD4_41078218, chrD4_42000379, chrD4_63622083, chrE1_130875919, chrE1_131587399, chrE1_3912105, chrE1_4114158, chrE1_48228153, chrE1_48700963, chrE1_5453028, chrE2_22632289, chrE2_34027888, chrE2_35914023, chrE2_36986631, chrE2_38860686, chrE2_39211557, chrE2_65436639, chrE2_7950477, chrE2_8422942, chrE3_36044809, chrE3_55434272, chrE3_67006512, chrF1_20309325, chrF1_21799641, chrF1_26100599, chrF1_27124984, chrF1_38051725, chrF1_565223, chrF1_82068276, chrF1_82716202, chrF1_91517402, chrF2_26886470, chrF2_38395360, chrF2_46855978, chrF2_68572596, chrF2_74863327, chrF2_78303221, chrF2_79632602 and chrF2_8427817.

[0018] In some embodiments, the set of markers further comprises one or more microsatellite markers. For example, in some embodiments, the set of markers further comprises one or more STRs selected from the group consisting of FCA005, FCA008, FCA023, FCA026, FCA035, FCA043, FCA045, FCA058, FCA069, FCA075, FCA077, FCA080B, FCA088, FCA090, FCA094, FCA096, FCA097, FCA105, FCA123, FCA126, FCA132, FCA149, FCA211, FCA220, FCA223, FCA224, FCA229, FCA262, FCA293, FCA305, FCA310, FCA391, FCA441, FCA453, FCA628, FCA649, FCA678 and FCA698.

[0019] In various embodiments, prior to or in addition to genotyping, a most likely population of origin is based on one or more morphological features of the test feline. In some embodiments, prior to or in addition to genotyping, one or more morphological features of the test feline allow the exclusion of one or more of the candidate populations of origin. For example, the feline may be evaluated for coat color (*e.g.*, chocolate, cinnamon, dilute, orange, white), coat patterning (*e.g.*, agouti, tabby, spotted, ticked, calico, point coloring), coat texture (*e.g.*, straight or rex), coat length (*e.g.*, hairless, short or long), ear morphology (*e.g.*, normal, curled or folded), paw morphology (*e.g.*, normal or polydactyl), and tail morphology (*e.g.*, manx, bobtail, long).

[0020] In some embodiments, the set of markers further comprises one or more phenotypic markers. For example, in some embodiments, the set of markers further comprises one or more of the phenotypic markers selected from the group consisting of Phen_CMAH_G139A, Phen_ASIP_del, Phen_MLPH_T83del, Phen_MC1R_G250A, Phen_TYRP1_C298T, Phen_TYRP1_5IVS6, Phen_TYR_del975C, Phen_TYR_G715T, Phen_TYR_G940A, Phen_KIT_G1035C_BI, Phen_FGF5_475, Phen_FGF5_474, phen_FGF5_406, Phen_FGF5_356, Phen_GBL1_G1457C_SIA_KOR, Phen_HEXB_DelIntr_BUR, Phen_HEXB_del39C_KOR, Phen_GBE1_Ins_NFC, Phen_KRT71_G/Aintro4_SPX, Phen_MYBPC_G93C_MCC, Phen_MYBPC_C2460T_RAG, phen_MPO_ALC, Phen_PLAU_AG_ALC, Phen_FCAT_ALC, Phen_PKLR_13delE6_Aby, Phen_PKD1_C10063A_PER, Phen_SHH_A479G_Hw, Phen_CEP290_PRA_Aby, Phen_CRX_546_Aby, Phen_CMAH_del, Phen_HEXB_C667T_DSH, Phen_GM2A_Del_DSH, Phen_GRHPR_DSH, Phen_LPL_G1234A_DSH, Phen_LAMAN_del_PER, Phen_IDUA_del_DSH, Phen_ARSB_G1558A_SIA, Phen_ARSB_T1427C_Sia, Phen_GUSB_A1052G_DSH, Phen_MYBPC_A74T_Poly, Phen_NPC1_G2864C_PER, Phen_SHH_G257C_UK1, Phen_SHH_A481T_UK2, Phen_HMBS_del842_SIA, Phen-HMBS_189TT_SIA, Phen_CYP21B1, Phen_TAS1R2_CAT, Phen_TAS1R2_G8224A_CAT, Phen_CYP27B1_Rob, Phen_ZFX, KRT71-Del_Drex, P2RY5_CRex, WNK4_Burm_HKL, and CART1_del_Burm. In some embodiments, the set of markers further comprises one or more of the phenotypic markers selected from the group consisting of SEQ ID NO:149 to SEQ ID NO:202, shown in Table 3.

[0021] In some embodiments, the marker locus genotypes for each candidate population are in Hardy-Weinberg Equilibrium and/or Gametic Phase Equilibrium.

[0022] In various embodiments, the genotype information in each feline population profile comprises identities of one or both alleles of each marker of the set of markers. In some embodiments, the genotype information in each feline population profile comprises allele frequencies for one or both alleles of each marker of the set of markers. In various embodiments, the genotype information in each feline population profile comprises both the identities and the allele frequencies of one or both alleles of each marker of the set of markers.

[0023] In some embodiments, the database of feline population profiles comprises one or more feline population profiles. In various embodiments, the database of feline population profiles comprises a plurality of feline population profiles, for example, between about 5 and about 500 feline population profiles, for example, about 10-400, 15-300, or 20-200 feline population profiles, for example, about 5, 10, 15, 20, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, or more, feline population profiles.

[0024] In some embodiments, the database of feline populations profiles comprise one or more profiles of feline ancestral lineages, *i.e.*, randombred populations of origin. For example, the feline populations profiles may comprise the profiles of one or more ancestral lineages of random bred worldwide populations of cats, including, *e.g.*, Europe, Mediterranean, Egypt, Iraq/Iran, Arabian Sea, India, Southeast Asia, and East Asia. In some embodiments, the feline populations profiles may comprise the profiles of 1, 2, 3, 4, 5, 6, 7, 8, or more, ancestral lineages of random bred worldwide populations of cats.

[0025] In some embodiments, the database of feline populations profiles comprise profiles of one or more feline breeds. Breeds of interest are recognized by at least one cat breed registry. For example, the breed may be recognized by one or more cat registries selected from the group consisting of The International Cat Association (TICA); the Cat Fanciers’ Association (CFA); The Australian Cat Federation (ACF); Co-Ordinating Cat Council of Australia (CCC of A); Federation Internationale Feline (FIFe); Governing Council of the Cat Fancy (GCCF); The New Zealand Cat Fancy (NZCF); The Southern African Cat Council (SACC); The World Cat Federation (WCF); American Cat Fanciers Association (ACFA); The Traditional Cat Association, Inc. (TCA); International Progressive Cat Breeders' Alliance (IPCBA); Canadian Cat Association (CCA); Cat Fanciers' Federation (CFF); American Association of Cat Enthusiasts (AACE); Australian National Cats (WNCA); Capital Cats Incorporated (CCI); Catz Incorporated; Council of Federated Cat Clubs of Qld (CFCCQ); The Feline Association of NSW (TFA of NSW); Feline Control Council (FCC); Gold Coast Cat Club; The Governing Council of the Cat Fancy of South Australia (GCCFSA); NSW Cat Fanciers' Association (NSW CFA;); Queensland Feline Association (QFA); Queensland Independent Cat Council (QICC;);

Hong Kong Cat Lovers' Society; Korea Cat Club (KOCC); The Cat Federation of Southern Africa (CFSA); The Asian Cat Association (ACA); Bavarian Cat Fanciers' Association; and Feline Federation Europe.

[0026] In various embodiments, the database comprises profiles of a plurality of feline breeds, for example, profiles of at least about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, or more, feline breeds recognized by one or more cat registries. For example, in certain embodiments, the profiles of feline breeds are selected from the group consisting of Persian, Exotic Shorthair (SH), British SH, Scottish Fold, Chartreux, American SH, Sphynx, Japanese Bobtail, Cornish Rex, Ragdoll, Maine Coon, Abyssinian, Siberian, Norwegian FC, Manx, Egyptian Mau, Turkish Angora, Turkish Van, Bengal, Sokoke, Ocicat, Russian Blue, Australian Mist, Burmese, Birman, Havana Brown, Korat, Siamese and Singapura. In some embodiments, the profiles of feline breeds are selected from the group consisting of Abyssinian, American Bobtail, American Bobtail Shorthair (SH), American Curl, American Curl Longhair (LH), American Shorthair, American Wirehair, Balinese, Bengal, Birman, Bombay, British Shorthair, British Longhair, Burmese, Chartreux, Colorpoint Shorthair, Cornish Rex, Cymric, Devon Rex, Don-Skoy, Egyptian Mau, European Burmese, Exotic Shorthair, Havana Brown, Himalayan, Japanese Bobtail, Japanese Bobtail Longhair, Korat, LaPerm, Maine Coon, Manx, Munchkin, Munchkin Longhair, Nebelung, Norwegian Forest Cat, Ocicat, Oriental Longhair, Oriental Shorthair, Persian, Peterbald, Pixiebob, Pixiebob Longhair, RagaMuffin, Ragdoll, Russian Blue, Scottish Fold, Scottish Fold Longhair, Selkirk Rex, Selkirk Rex Longhair, Siamese, Siberian, Singapura, Snowshoe, Somali, Sphynx, Thai, Tonkinese, Toyger, Turkish Angora, and Turkish Van. The profiles of feline breeds may also include one or more of Chausie, Savannah, Bambino, Donskey, Highlander, Highlander Shorthair, Kurilian Bobtail, Kurilian Bobtail Longhair, Minskin, Ojos Azules, Ojos Azules Longhair, Serengeti and Sokoke.

[0027] In various embodiments, the test feline is suspected of having genetic contributions of 4 or fewer breeds. For example, a test feline may be suspected of being a purebred, having a genetic composition primarily contributed from a single breed, having a genetic composition primarily contributed by two distinct breeds, having a genetic composition primarily contributed by three distinct breeds, or having a genetic composition primarily contributed by four distinct breeds.

[0028] In some embodiments, the set of markers comprises a subset of the 148 SNP markers listed in Table 1 and the method determines the contributions of one or more feline populations to the test feline genome. In various embodiments, the set of markers comprises fewer than about 150 SNP markers and the method determines the contributions of 1, 2, 3 or 4 feline populations to the test feline genome.

[0029] The identity of one or both alleles of a marker can be determined using any method in the art. In some embodiments, the identity of one or both alleles of a marker is determined by amplifying genomic DNA of the test feline using primers specific for each of the set of markers and determining the size of the amplification product. In some embodiments, the identity of one or both alleles of a marker is determined by amplifying genomic DNA of the test feline using primers specific for each of the set of markers and sequencing the amplification product.

[0030] In some embodiments, the algorithm used to compare the identity of one or both alleles for each of the markers in the set of markers to a database comprising the one or more, or a plurality, of feline population profiles comprises a genotype clustering program. In some embodiments, the algorithm used to compare the identity of one or both alleles for each of the markers in the set of markers to a database comprising the one or more, or a plurality, of feline population profiles comprises an assignment program. In some embodiments, the algorithm used to compare the identity of one or both alleles for each of the markers in the set of markers to a database comprising the one or more, or a plurality, of feline population profiles comprises both a genotype clustering program and an assignment program. In some embodiments, the clustering program is a Bayesian clustering program. In some embodiments, the assignment program is a likelihood or frequentist program. In some embodiments, the test feline is assigned to the most likely population of origin if the population genotype probability for the most likely population of origin exceeds the value of assignment to any other population of the database.

[0031] In some embodiments, the contributions of two or more genetically related feline populations to the test feline genome are discriminated by comparing the alleles in the test feline genome to a database comprising profiles of the two or more genetically related feline populations. For example, in various embodiments, the two or more genetically related feline populations being discriminated are selected from the group consisting of (i) Persian and Exotic Shorthair (SH); (ii) British SH and Scottish Fold; (iii) Australian Mist and Burmese; (iv) Singapura and Burmese; (v) Birman and Korat, and (vi) Siamese and Havana Brown. As appropriate, one or more phenotypic markers can be determined, in addition to determining the identity of a plurality of the SNPs listed in Table 1, to help distinguish between the contributions of two or more genetically related feline populations to the test feline genome.

[0032] For example, the genotype of the FGF5 SNP, which causes long hair, can be determined to affirmatively assign a test feline to one or more breeds selected from the group consisting of Persian, Maine Coon, Turkish Angora, Turkish Van and Birman. Similarly, a FGF5 genotype indicative of the presence of long hair can be used to exclude assignment to one or more breeds selected from the group consisting of Abyssinian, Egyptian Mau, Sokoke, Ocicat, and short-haired varieties of other recognized feline breeds. In some embodiments, the genotypes of one or both alleles of one or more of the FGF5 SNPs depicted by SEQ ID NOs:159-162 are determined. In some embodiments, the genotypes of one or both alleles of all four of the FGF5 SNPs depicted by SEQ ID NOs:159-162 are determined.

[0033] In various embodiments, the methods further comprise reporting the results of the analysis. In some embodiments, the methods further comprise the step of providing a document displaying the contributions of one or more feline populations to the genome of the test feline genome. In various embodiments, the document provides additional information regarding the one or more feline populations that contributed to the genome of the test feline. In some embodiments, the document provides health-related information. In some embodiments, the document provides a certification of the contributions of one or more feline populations to the genome of the test feline. In some embodiments, the document provides a representation of the one or more feline populations that contributed to the genome of the test feline.

[0034] In another aspect, the invention provides one or more primer sets for determining the identity of one or both alleles a plurality of single nucleotide polymorphisms (SNPs) listed in Table 1. In various embodiments, primer sets for determining the identity of one or both alleles of at least about 5 SNPs, for example, at least about 10, 15, 20, 25, 30, 40, 50, 60, 70, 75, 80, 90, 100, 110, 120, 125, 130, 140, 148 SNPs listed in Table 1 are provided. The primer sets may be provided in a kit.

[0035] In a related aspect, the invention provides one or more computer-readable media. In some embodiments, the computer-readable media comprise:

(a) a data structure stored thereon for use in distinguishing feline populations, the data structure comprising:

(i) marker data, wherein the marker data identifies one or both alleles of each marker of a set of markers in one or more feline population profiles, wherein the set of markers comprises a plurality of single nucleotide polymorphisms (SNPs) listed in Table 1; and

(ii) genotype information data, wherein the genotype information data provides genotype information for each marker of a set of markers in a feline population, wherein a record comprises an instantiation of the marker data and an instantiation of the genotype information data and a set of records represents a feline population profile; and

(b) computer-executable instructions for controlling one or more computing devices to:

(i) identify one or both alleles in a test feline genome for each marker of the set of markers; and

(ii) determine the contributions of one or more feline populations to the test feline genome by comparing the identified alleles in the test feline genome to the database comprising one or more feline population profiles, wherein each feline population profile comprises genotype information for the set of markers in the feline population.

[0036] In a further aspect, the invention provides one or more computer-readable media comprising a data structure stored thereon for use in distinguishing feline populations. In some embodiments, the data structure comprises:

(a) marker data, wherein the marker data identifies one or both alleles of each marker of a set of markers in one or more feline population profiles, wherein the set of markers comprises a plurality of single nucleotide polymorphisms (SNPs) listed in Table 1; and

(b) genotype information data, wherein the genotype information data provides genotype information for each marker of a set of markers in a feline population, wherein a record comprises an instantiation of the marker data and an instantiation of the genotype information data and a set of records represents a feline population profile.

[0037] Further embodiments in the computer readable media are as described above and herein.

DEFINITIONS

[0038] Unless defined otherwise, all technical and scientific terms used herein generally have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Generally, the nomenclature used herein and the laboratory procedures in cell culture, molecular genetics, organic chemistry and nucleic acid chemistry and hybridization described below are those well known and commonly employed in the art. Standard techniques are used for nucleic acid and peptide synthesis. Generally, enzymatic reactions and purification steps are performed according to the manufacturer's specifications. The techniques and procedures are generally performed according to conventional methods in the art and various general references (see generally, Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL, 3rd ed. (2001) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. and Ausubel, *et al.*, Current Protocols in Molecular Biology, 1987-2011, John Wiley and Sons), which are provided throughout this document. The nomenclature used herein and the laboratory procedures in analytical chemistry, and organic synthetic described below are those well known and commonly employed in the art. Standard techniques, or modifications thereof, are used for chemical syntheses and chemical analyses.

[0039] The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. Genomic DNA or a polynucleotide that is the predominant species present in a preparation is substantially purified. The term "purified" denotes that a nucleic acid gives rise to essentially one band in an electrophoretic gel. Particularly, it means that the nucleic acid or genomic DNA is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure.

[0040] The terms "nucleic acid" and "polynucleotide" are used interchangeably herein to refer to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. The term encompasses nucleic acids containing known nucleotide analogs or modified backbone residues or linkages, which are synthetic, naturally occurring, and non-naturally occurring, which have similar binding properties as the reference nucleic acid, and which are metabolized in a manner similar to the reference nucleotides. Examples of such analogs include, without limitation, phosphorothioates, phosphoramidates, methyl phosphonates, chiral-methyl phosphonates, 2-O-methyl ribonucleotides, peptide-nucleic acids (PNAs).

[0041] Unless otherwise indicated, a particular nucleic acid sequence also encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer et al., Nucleic Acid Res. 19:5081 (1991); Ohtsuka et al., J. Biol. Chem. 260:2605 2608 (1985); Rossolini et al., Mol. Cell. Probes 8:91 98 (1994)). The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

[0042] The terms "identical" or percent "identity," in the context of two or more nucleic acid sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of nucleotides that are the same (*e.g.*, 80% identity, preferably 85%, 90%, 95%, 96%, 97%, 98%, 99% identity over a specified region such as the nucleic acid sequences of SEQ ID NOs:1-148 and SEQ ID NOs:149-202), when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using a known sequence comparison algorithm (*e.g.*, BLAST, ALIGN) set to default settings or by manual alignment and visual inspection. Such sequences are then said to be "substantially identical." This definition also refers to the complement of a test sequence. Preferably, the identity exists over a region that is at least about 25 nucleotides in length, or more preferably over a region that is 50-100 nucleotides in length, or over the full length of the contextual sequence flanking the genetic marker.

[0043] A "label" or "detectable label" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include radioisotopes (e.g., ^{3}H, ^{35}S, ^{32}P, ^{51}Cr, or ^{125}I) fluorescent dyes, electron-dense reagents, enzymes (e.g., alkaline phosphatase, horseradish peroxidase, or others commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins for which antisera or monoclonal antibodies are available (e.g., the polypeptide comprising a sequence encoded by SEQ ID NO:1 can be made detectable, e.g., by incorporating a radiolabel into the peptide, and used to detect antibodies specifically reactive with the peptide).

[0044] An "amplification reaction" refers to any chemical reaction, including an enzymatic reaction, which results in increased copies of a template nucleic acid sequence. Amplification reactions include polymerase chain reaction (PCR) and ligase chain reaction (LCR) (see U.S. Pat. Nos. 4,683,195 and 4,683,202; PCR Protocols: A Guide to Methods and Applications (Innis et al., eds, 1990)), strand displacement amplification (SDA) (Walker, et al. Nucleic Acids Res. 20(7):1691 (1992); Walker PCR Methods Appl 3(1):1 (1993)), transcription-mediated amplification (Phyffer, et al., J. Clin. Microbiol. 34:834 (1996); Vuorinen, et al., J. Clin. Microbiol. 33:1856 (1995)), nucleic acid sequence-based amplification (NASBA) (Compton, Nature 350(6313):91 (1991), rolling circle amplification (RCA) (Lisby, Mol. Biotechnol. 12(1):75 (1999)); Hatch et al., Genet. Anal. 15(2):35 (1999)) and branched DNA signal amplification (bDNA) (see, e.g., Iqbal et al., Mol. Cell Probes 13(4):315 (1999)).

[0045] "Amplifying" refers to submitting a solution to conditions sufficient to allow for amplification of a polynucleotide if all of the components of the reaction are intact. Components of an amplification reaction include, e.g., primers, a polynucleotide template, polymerase, nucleotides, and the like. Thus, an amplifying step can occur without producing a product if, for example, primers are degraded.

[0046] "Amplification reagents" refer to reagents used in an amplification reaction. These reagents can include, e.g., oligonucleotide primers; borate, phosphate, carbonate, barbital, Tris, etc. based buffers (see, U.S. Pat. No. 5,508,178); salts such as potassium or sodium chloride; magnesium; deoxynucleotide triphosphates (dNTPs); a nucleic acid polymerase such as Taq DNA polymerase; as well as DMSO; and stabilizing agents such as gelatin, bovine serum albumin, and non-ionic detergents (e.g. Tween-20).

[0047] A “plurality” refers to two or more, for example, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, 60, 70, 75, 80, 90, 100, 110, 120, 130, 140, 145, 148, 150, or more (*e.g.*, genetic markers, including SNPs, short tandem repeats (STRs), microsatellites, phenotypic markers; feline population profiles). In some embodiments, a plurality refers to concurrent or sequential determination of about 2-150, 5-148, 50-148, 100-148 markers, for example, about 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 145, 148, 150, or more, markers. In some embodiments, “plurality” refers to all markers listed in one or more tables, e.g., all markers listed in Table 1, and optionally also including all markers listed in Table 3.

[0048] A "single nucleotide polymorphism" or "SNP" refers to polynucleotide that differs from another polynucleotide by a single nucleotide exchange. For example, without limitation, exchanging one A for one C, G or T in the entire sequence of polynucleotide constitutes a SNP. Of course, it is possible to have more than one SNP in a particular polynucleotide. For example, at one locus in a polynucleotide, a C may be exchanged for a

T, at another locus a G may be exchanged for an A and so on. When referring to SNPs, the polynucleotide is most often DNA and the SNP is one that usually results in a change in the genotype that is associated with a corresponding change in phenotype of the organism in which the SNP occurs.

[0049] A "variant" is a difference in the nucleotide sequence among related polynucleotides. The difference may be the deletion of one or more nucleotides from the sequence of one polynucleotide compared to the sequence of a related polynucleotide, the addition of one or more nucleotides or the substitution of one nucleotide for another. The terms "mutation," "polymorphism" and "variant" are used interchangeably herein to describe such variants. As used herein, the term "variant" in the singular is to be construed to include multiple variances; i. e., two or more nucleotide additions, deletions and/or substitutions in the same polynucleotide. A "point mutation" refers to a single substitution of one nucleotide for another.

[0050] A nucleic acid "that distinguishes" as used herein refers to a polynucleotide(s) that distinguishes a first polymorphism (*e.g.*, a major allele of a SNP) from a second polymorphism (*e.g.*, a minor allele of the same SNP) at the same position in the genomic sequence. The nucleic acid that distinguishes can allow for polynucleotide extension and amplification after annealing to a polynucleotide comprising the first polymorphism, but will not allow for polynucleotide extension or amplification after annealing to a polynucleotide comprising the second polymorphism. In other embodiments, a nucleic acid that distinguishes a first polymorphism from a second polymorphism at the same position in the sequence will hybridize to a polynucleotide comprising the first polymorphism but will not hybridize to a polynucleotide comprising the second polymorphism. The invention provides polynucleotides that distinguish the SNPs and genetic markers listed in Table 1.

[0051] The term "primer" refers to a nucleic acid sequence that primes the synthesis of a polynucleotide in an amplification reaction. Typically a primer comprises fewer than about 100 nucleotides and preferably comprises fewer than about 30 nucleotides. Exemplary primers range from about 5 to about 25 nucleotides. The "integrity" of a primer refers to the ability of the primer to primer an amplification reaction. For example, the integrity of a primer is typically no longer intact after degradation of the primer sequences such as by endonuclease cleavage.

[0052] The term "subsequence" refers to a sequence of nucleotides that are contiguous within a second sequence but does not include all of the nucleotides of the second sequence.

[0053] A "target" or "target sequence" refers to a single or double stranded polynucleotide sequence sought to be amplified in an amplification reaction. Two target sequences are different if they comprise non-identical polynucleotide sequences.

[0054] As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

[0055] A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe.

[0056] "Biological sample" as used herein is a sample of biological tissue or fluid that contains genomic DNA. These samples can be tested by the methods described herein and include body fluids such as whole blood, serum, plasma, cerebrospinal fluid, urine, lymph fluids, and various external secretions of the respiratory, intestinal and genitourinary tracts, tears, saliva, milk, white blood cells, myelomas, and the like; and biological fluids such as cell extracts, cell culture supernatants; fixed tissue specimens; and fixed cell specimens. Biological samples may also include sections of tissues such as biopsy and autopsy samples or frozen sections taken for histologic purposes. A biological sample can also be skin cells, a cheek swab or a hair bulb sample. These samples are well known in the art. A biological sample is obtained from any mammal including, e.g., a cat. A biological sample may be suspended or dissolved in liquid materials such as buffers, extractants, solvents and the like.

[0057] The term “feline” refers to an animal that is a member of the family Felidae; including without limitation the subfamilies, Felinae, Pantherinae, and Acinonychinae; the genera Caracal, Catopuma, Felis, Herpailurus, Leopardus, Leptailurus, Lynx, Oncifelis, Oreailurus, Otocolobus, Prionailurus, Profelis, Puma, Neofelis, Panthera, Pardofelis, and Uncia; the species felis, lybica, jubatus, caracal, badia, bieti, chaus, margarita, nigripes, silvestris, gordonii, yaguarondi, pardalis, tigrinus, wiedi, serval, canadensis, lynx, pardinus, rufus, colocolo, geoffroyi, guigna, jacobita, manul, bengalensis, planiceps, rubiginosus, viverrinus, aurata, concolor, nebulosa, leo, onca, pardus, tigris, marmorata, and uncial.

[0058] The term "determining the contributions of feline populations" refers to estimating or inferring using statistical methods the contributions of feline populations to draw conclusions regarding whether one or more feline populations contributed to the genome of a test feline.

[0059] The term "feline population" refers to a group of felines related by descent, such as a domestic cat breed.

[0060] 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 International Cat Association (TICA) recognizes 57 Championship Breeds, 2 Advanced New Breeds and 10 Preliminary New Breeds (identified at tica.org). The Cat Fanciers’ Association (CFA) lists 40 breeds. The methods of the invention may be used to estimate the genetic contributions of any cat breed, including, but not limited to Abyssinian, American Bobtail, American Bobtail Shorthair (SH), American Curl, American Curl Longhair (LH), American Shorthair, American Wirehair, Balinese, Bengal, Birman, Bombay, British Shorthair, British Longhair, Burmese, Chartreux, Colorpoint Shorthair, Cornish Rex, Cymric, Devon Rex, Egyptian Mau, European Burmese, Exotic Shorthair, Havana Brown, Himalayan, Japanese Bobtail, Japanese Bobtail Longhair, Korat, LaPerm, Maine Coon, Manx, Munchkin, Munchkin Longhair, Nebelung, Norwegian Forest Cat, Ocicat, Oriental Longhair, Oriental Shorthair, Persian, Peterbald, Pixiebob, Pixiebob Longhair, RagaMuffin, Ragdoll, Russian Blue, Scottish Fold, Scottish Fold Longhair, Selkirk Rex, Selkirk Rex Longhair, Siamese, Siberian, Singapura, Snowshoe, Somali, Sphynx, Thai, Tonkinese, Toyger, Turkish Angora, Turkish Van, Chausie, Savannah, Bambino, Donskey, Highlander, Highlander Shorthair, Kurilian Bobtail, Kurilian Bobtail Longhair, Minskin, Ojos Azules, Ojos Azules Longhair, Serengeti and Sokoke, and mixtures thereof.

[0061] The term "marker" refers to any polymorphic genomic locus that is sufficiently informative across the feline populations used in the methods of the invention to be useful for estimating the genetic contribution of these feline populations to the genome of a test feline. A genomic locus is polymorphic if it has at least two alleles.

[0062] 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 feline 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.

[0063] Population-specific alleles are alleles that are present at some frequency in one feline population but have not been observed in the sampled feline from comparison feline 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.

[0064] A "set of markers" refers to a minimum number of markers that are sufficient for determining the genetic contribution of the feline populations used in the methods of the invention to the genome of a test feline. The minimum number of markers required depends on the informativeness of the markers for the particular feline populations that are being used, as further described below. The set of markers may comprise at least about 5, 10, 25, 50, 75, 100, 125, 150 markers, or more, as appropriate.

[0065] A "feline population profile" as used herein refers to the collection of genotype information for the set of markers in a feline population. Thus, a feline population profile may comprise genotype information for most or all alleles of most or all markers in the set of markers in the feline population.

[0066] 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 feline 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 feline population.

[0067] A "database of feline population profiles" refers to the collection of feline population profiles for all of the feline populations used in an exemplary method of the invention. In some embodiments, the database of feline population profiles comprises between about five and about 500 feline population profiles, such as about 20 feline population profiles, about 50 feline population profiles, or about 100 feline population profiles.

[0068] 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.

[0069] 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.

[0070] 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.

BRIEF DESCRIPTION OF THE DRAWINGS

[0071] Figure 1 illustrates a map of random bred cat sampling locations. The pie charts represent the percentage of the eight worldwide lineages found at each location. The shading indicates the strength of the predominating lineage for each region of the world.

[0072] Figures 2A-F illustrate Delta K plots of random bred cat population structuring. Graphs of both the mean Ln(K) and ΔK calculations based on the results of Bayesian clustering. Top) SNPs only, Middle) STRs only, Bottom) SNPs and STRs combined. Points where a peaks in a ΔK plot occur indicate population stratification with higher likelihood than those where valleys occur.

[0073] Figures 3A-F illustrate Bayesian clustering of random bred worldwide cat populations. Clustering of cat populations using STRUCTURE A) SNPs K=5, B) SNPs K=8, C) STRs K=5, D) STRs K=7, E) SNPS and STRs K=5, F) SNPs and STRs K=8.

[0074] Figures 4A-C illustrate alternate Bayesian clustering of worldwide cat populations. Alternate clustering of cat populations using STRUCTURE based on ΔK calculations. A) SNPs at K=11 and 23, B) STRs at K=9 and 13, and C) SNPs and STRs combined at K=10, 16, 18, and 22.

[0075] Figures 5A-B illustrate principal coordinate analysis of world cat populations. A) SNPs and B) STRs by sampling location calculated via Nei's Unbiased Distance. Colors indicate the eight random bred populations. Circles indicate the five lineages.

[0076] Figures 6A-B illustrate neighbor-joining trees of world cat populations. Bootstrap values over 50% indicated on nodes. Branch colors indicate the population as assigned by STRUCTURE. A) SNP-based phylogeny produced with Reynolds, Weir and Cockerham's genetic distance. B) STR-based tree produced with Nei's unbiased genetic distance.

[0077] Figures 7A-D illustrate log likelikhood and Delta K plots from the Bayesian clustering of cat breeds. Graphs of both the mean Ln(K) and ΔK calculations based on the results of Bayesian clustering. Points where a peaks in a ΔK plot occur indicate population stratification with higher likelihood than those where valleys occur.

[0078] Figure 8 illustrates Bayesian clustering of cat breeds. Clustering of breeds at K=17 and K=21 as calculated with SNPs and STRs respectively.

[0079] Figures 9A-B. Figure 9A illustrates alternate plots of Bayesian clustering analysis for SNPs. Figure 9B illustrates alternate plots of Bayesian clustering analysis for STRs.

[0080] Figures 10A-B illustrate principal coordinate analysis of cat breeds and worldwide random bred cat populations. Color shades indicate the population membership of the respective random bred populations.

[0081] Figures 11A-B. Figure 11A illustrates crossed assignment rate between breeds as a function of the Reynolds distance between populations using SNPs. Figure 11B illustrates crossed assignment rate between breeds as a function of the Reynolds distance between populations using STRs.

DETAILED DESCRIPTION

1. Introduction

[0082] The present invention is based, in part, on the discovery of a panel of biomarkers useful for the assignment of domestic cats to specific breeds or world populations based on the frequency of genetic markers in their genome. Assignment testing utilizes microsatellite and/or single nucleotide polymorphism (SNP) biomarkers, as well as genetic biomarkers that are known to confer a physical characteristic or disease state in the cat. The combined panel of over 200 different genetic tests can be used to determine if a cat is from a specific breed or random bred population of origin within a database of approximately 2000 cats. To conduct the test, the genotypes of the panel of biomarkers are determined in a biological sample of the cat (*e.g.*, blood, tissue, hair bulb, buccal swab) comprising genomic DNA. The genotypic "signature" over the panel of biomarkers of the test cat is compared against a database of the same panel of biomarkers with identified frequency associations with known cat breeds and random bred populations of origin. The frequency of the DNA variants of the test cat are compared to the database to match the test cat to the population with the most similar frequencies, allowing assignment to one or more breeds and/or ancestral lineages of origin. Using the biomarker panels described herein, it is possible to determine the geographical region of the genetic origins of the test cat, whether the test cat is highly related to a known breed, or whether the test cat has a parent or grandparent that is of a known breed. The present genetic assignment tests also find use breeding strategies, *e.g.*, to facilitate the selection of a mating partner that is genetically dissimilar, or as a new foundation for a breed stock.

2. Felines Subject to Testing

[0083] The methods find use in determining the contributing feline populations of origin of any feline, *e.g.*, any member of the family Felidae. Oftentimes, the feline will be a domesticated feline. In various embodiments, the feline is a member of the genus Felis. For example, the feline may be a member of *Felis silvestris* or *Felis catus*. The feline further can have one or more identifiable phenotypic or morphological features associated with one or more recognized cat breeds, by a cat registry. For example, the feline may have genetic contributions from a cat breed recognized by one or more cat registries selected from the group consisting of The International Cat Association (TICA; tica.org); the Cat Fanciers' Association (CFA; cfa.org); The Australian Cat Federation (ACF; acf.asn.au); Co-Ordinating Cat Council of Australia (CCC of A; cccofa.asn.au); Federation Internationale Feline (FIFe; fifeweb.org); Governing Council of the Cat Fancy (GCCF; gccfcats.org); The New Zealand Cat Fancy (NZCF; nzcatfancy.gen.nz); The Southern African Cat Council (SACC; tsacc.org.za); The World Cat Federation (WCF;wcf-online.de); American Cat Fanciers Association (ACFA; acfacat.com); The Traditional Cat

Association, Inc. (TCA; traditionalcats.com); International Progressive Cat Breeders' Alliance (IPCBA; ipcba.8k.com); Canadian Cat Association (CCA; cca-afc.com); Cat Fanciers' Federation (CFF; cffinc.org); American Association of Cat Enthusiasts (AACE; aaceinc.org); Australian National Cats (WNCA; ancats.com.au); Capital Cats Incorporated (CCI; cci.asn.au); Catz Incorporated (catzinc.org); Council of Federated Cat Clubs of Qld (CFCCQ; cfccq.org/index.html); The Feline Association of NSW (TFA of NSW; tfansw.webs.com); Feline Control Council (FCC; hotkey.net.au/%7Efccvic); Gold Coast Cat Club Inc. (goldcoastcatclub.com); The Governing Council of the Cat Fancy of South Australia (GCCFSA; users.chariot.net.au/~gccfsa/index.html); NSW Cat Fanciers' Association (NSW CFA; nswcfa.asn.au); Queensland Feline Association (QFA; qfeline.com); Queensland Independent Cat Council (QICC; qicc.org.au); Hong Kong Cat Lovers' Society (hkcls.com); Korea Cat Club (KOCC; kocc.or.kr/link/link.htm or ticakorea.org); The Cat Federation of Southern Africa (CFSA; .cfsa.co.za); The Asian Cat Association (ACA; asiancats.co.uk); Bavarian Cat Fanciers' Association (bavarian-cfa.de/bcfa.htm); and Feline Federation Europe (FFE; ffe-europe.de).

[0084] Illustrative breeds include without limitation Abyssinian, American Bobtail, American Bobtail Shorthair (SH), American Curl, American Curl Longhair (LH), American Shorthair, American Wirehair, Balinese, Bengal, Birman, Bombay, British Shorthair, British Longhair, Burmese, Chartreux, Colorpoint Shorthair, Cornish Rex, Cymric, Devon Rex, Egyptian Mau, European Burmese, Exotic Shorthair, Havana Brown, Himalayan, Japanese Bobtail, Japanese Bobtail Longhair, Korat, LaPerm, Maine Coon, Manx, Munchkin, Munchkin Longhair, Nebelung, Norwegian Forest Cat, Ocicat, Oriental Longhair, Oriental Shorthair, Persian, Peterbald, Pixiebob, Pixiebob Longhair, RagaMuffin, Ragdoll, Russian Blue, Scottish Fold, Scottish Fold Longhair, Selkirk Rex, Selkirk Rex Longhair, Siamese, Siberian, Singapura, Snowshoe, Somali, Sphynx, Thai, Tonkinese, Toyger, Turkish Angora, Turkish Van, Chausie, Savannah, Bambino, Donskey, Highlander, Highlander Shorthair, Kurilian Bobtail, Kurilian Bobtail Longhair, Minskin, Ojos Azules, Ojos Azules Longhair, Serengeti and Sokoke, and mixtures thereof.

[0085] The feline breed assignment tests were developed based on the understanding that 44 breeds are genetically definable of the world's 54 major breeds, not including longhaired and shorthaired varieties with the same breed name. The assignment test described herein attempted to include all breeds recognized in three or more of the following registries: CFA (USA), TICA (USA), GCCF (UK), and FIFe (Europe). However, the assignment of a cat to a breed was mainly based on USA populations. Cats representing breeds from other world regions will therefore be assigned to a cat breed in reference to the genetic structuring of USA cats.

[0086] Additional populations can also be added. For example, breeds that are considered preliminary or under development, as well as breeds specific to a particular geographic location (*e.g.*, breeds or populations specific to an island location), can be added to the databases described herein, first as a preliminary breed and then as an established breed. For example, the Selkirk Rex and American Curl breeds are under development. Also, additional analyses could be used to further refine population and breed definitions when compared on a less global and more regional scale.

[0087] It is recognized that the definitions of cat breeds vary between registries around the world, and that different breed registries accept and refuse different color varieties and variants, sometimes even defining a breed. For example, some registries define a Himalayan as a pointed Persian. For the sake of reference, the CFA definitions of breeds were used in the tests described herein to make assignments. Thus, a pointed Manx, which may be a defined breed in another cat registry, may seem to have an inappropriate assignment. Straight-eared Scottish Folds and tailed Manx may be difficult to define if not only by their breed heritage. These nuances of breed definitions need to be considered in the analysis and interpretation of results. It is further recognized that many breeds may have longhaired and shorthaired varieties, some using a different name, such as Manx and Cymric.

[0088] In various embodiments, the feline is a hybrid, *e.g.*, having genomic contributions from one or more wild felids. For example, the Bengal is a cross of various cat breeds and random bred cats with various sub-species of the Asian Leopard cat (*Felis bengalensis, a.k.a. Prionailurus bengalensis*). The Chaussie breed is a cross of various cat breeds and random bred cats with various sub-species of the Jungle cat (*Felis chaus*). The Savannah breed is a cross of various cat breeds and random bred cats with various sub-species of the Serval (*Felis Serval*). Some cat breeds are mixtures of these various hybrid breeds, *e.g.*, the Desert Lynx.

3. Biological Sample

[0089] The methods may comprise the step of obtaining a biological sample comprising genomic DNA from the feline to be tested. The biological sample may be obtained in the laboratory conducting the analysis or by another party (*e.g.*, a veterinarian, a guardian of the feline). The biological sample can be from solid tissue or a biological fluid that contains a nucleic acid comprising a single nucleotide polymorphism (SNP) described herein, e.g., a genomic DNA sample comprising a plurality of the genetic markers listed in Table 1, particularly the SNPs depicted in SEQ ID NOs:1-148. The biological sample can be tested by the methods described herein and include body fluids including whole blood, serum, plasma, cerebrospinal fluid, urine, lymph fluids, semen, and various external secretions of the respiratory, intestinal and genitourinary tracts, tears, saliva, milk, white blood cells, myelomas, and the like; and biological fluids such as cell extracts, cell culture supernatants; fixed tissue specimens; and fixed cell specimens. Biological samples can also be from solid tissue, including hair bulb, skin, cheek swab, biopsy or autopsy samples or frozen sections taken for histologic purposes. These samples are well known in the art. A biological sample is obtained from any feline to be tested for the genotype of the genetic markers as described herein. A biological sample can be suspended or dissolved in liquid materials such as buffers, extractants, solvents and the like.

4. Biomarkers Useful to Determine Breed and/or Population of Origin

[0090] Genetic markers useful for the determination of the contribution of one of more feline populations or breeds of origin are listed in Table 1. The methods of the invention analyze in a test feline the genotype of a plurality of genetic markers depicted as SEQ ID NOs:1-148 in Table 1, also identified by their chromosomal location.

Table 1 - SNP sequences useful for breed identification test

SEQ ID NO:	SNP ID	Sequence
1	A1_10141047	TCAATAGCAGGAGAAACAAGATCAAACCATGCCCGGGTTTCAATGCCTTGGGGAAATAAC[A/G]GAGAGAAGGAAACTTTATTAAGGCGATCCCGTCAACTCTACCCATTCCTCGGAGGCGTTT
2	A1_133621071	GTAAAACACGACAACATAGAATGACACTCACTGTGGCAGTCGAAAAGAGGTACTTGGCAA[A/G]TACCATGGGAATGTCATACGGGATGCATGCTACTGGAGGGATGTCTATAGCCTTTCCACT
3	A1_151648701	TAGCACCAGATCAAAAAATGAGTGGATTTCCCTGTCTAGCTCCTTCACCACCACAAGTTC[T/C]GCATGTTTGGTCTCATCAGGCCCCACGATGACATCCAGGGCAAAGTGCTCGCTGGGGGAC
4	A1_175780586	TTGTGGAATGACACCGTCAGAAAGGAGATTTCTTGGGCTACTGTGGTAGCTAGATTCCCG[T/C]GGAAGGGCGTGCCTTTCGGTTACAACGTATTGGTGCTAGGCTGCCTGGACCACTGGCTTT
5	A1_208054462	GAAACGGAGTCACAGGAAGTAAGGGTTGGTATTATATTTTTAGAAGTATTTATTGGGGGA[C/G]GGGGGATAAATAGGTGGGCTCAGAGAATAATATTTCCAAGGTCACAGGGCTAATGAGCCT

Table 1 - SNP sequences useful for breed identification test

SEQ ID NO:	SNP ID	Sequence
6	A1_223501140	AGTGATCCAAGGAGGTGACGAGGGACCATAAGCCTTGATTTATGACCTGAGGTTTCCATC[T/C]CAGAAGCCACATCATCAGTCCCTCTGGGAAAGAGTTTTAACTGGATGAACTGCCCTTCTA
7	A1_223506906	GTTCATTGAGTAAGATGTTCATCACCCTCTTCTTAGAAATAAATTCCCTTTGCTTCATCA[A/G]GGAATCATGAACCCTTAGAGCTAGAAACGACTTTGGAGGTTATGTGTTTAAGTGTTTTTG
8	A1_225057933	AATTACCCAATTCCTCCCTAGTTATCGTATTCAGTGACACAGATAACAAAAGTTAGAAGT[T/G]CTTCGATTCACATTCACAAAGATGCACCATGAAATCATAGTAACTTGGAGTAAGTGGCAG
9	A1_235579538	CTTTTGATTCTATTTTGGGTCACACGTGAAACCCACAGAACAATCGACAAAAGCCATTTC[A/G]TCTTCTCACTCTCTTCAGTTTACCCTTTTGCTTAGTTTATTTCATTTCGCCAACATTTTT
10	A1_27523501	ATGCAGTCCTGCCTAAATGTAGGAGAGTCCTGAAGATTTTCTGGATCTAATCTCTACCAT[T/G]TTGTGCCAAGTTTGAGGACTCATTATACTTTAGGCTTTATAAAATATTTCTCCTCTGGGT
11	A1_68485376	ATTATTTGCAGGATCTACGTTCATTACTTGAGACAGGACGATTCATTAAATGTTAGAAAT[T/C]AATTCGTGGAGCAAGTAAAAAGGTGGAAGAAGTGTTAGGAAAATCACTTGAGAAAACGTA
12	A1_69424718	AACTCAATCAATCCAGGCATCCTTGTCTGACCAGGAGGAAAAAATAAACACAGCAACGTG[A/G]AGGCGGAAGCTCGTGCTCTGGAAACAGTCAGACCTGACTCAATTCCAAGCTCCCGGATGT
13	A1_7429296	GAGTCAAGCTGTCGCTGTTTCTGGTGCAAAACCAGGCACAAGGTACACAGTGATATTAAA[A/G]GCTCGTGGGCAAAACACCTTCCTCAGCCCGGGAGCGACACCTGTGGCAATATAATTTGAT
14	A1_8742286	CCTTCCCTTACTGAGAGACAGTCAATAAACCTTCAGAGGAGGGCTAAGCATGACCCGCAG[T/G]GATCCAAGAACACACCAGAAGAAAGGGGATCATCACAGCCAATGCCAACGTAGGGAGTTG
15	A2_152258936	CTAAAACTTCATTTGGTTAAAACAGAAGAAGAGTCAAGCACTTCTCTTCCTTGTGAGCTA[T/C]CATGTAGCCAACACTCTGAACATAACATGCGCAACGGGAATATACTCAGCTTCCCAACTC
16	A2_201526186	TCGAGAAATAGGGGACACAGCAATTCAATCTCCTGGTTAAACCAAAGCTTAGATGAAGAC[A/G]TCTGGTTCTTTAAGCCTTTCTGCTGAAAATAATCATCCGAGGTACTAAGGTCCCTTTTGA
17	A2_202225770	GCAGAATTTGTCGTAAAGAGAATTCTCACACGTGAGGACTTTCCCTCTCTTGTGTTGCAT[T/C]GTCAAACTAGACCTGCATTTAGGCCCCTGGTTGTATAAACTCCAGCTTAGTTATCCAACG
18	A2_44241149	GTTTTTCCTGAACCTTCCCACCTTTAATGCATCCTGGAGCAGTCCTTCAGCCTGCTTCCC[T/G]CCAGTCTTCTTACTCTTTCATTTTAAATAATGTAATAACGTTGACATTTTCATTTAGAGT
19	A2_554046	GAACCCACTTTGCAGATGGGAGAACCATGGGGTTACACTTCGGCATCTCCCTGAAATCTG[A/G]TGAGACACGGAATGGAGGCCTTCTCAGCAGATACTGGGTGAGAGTCACATTGATGTGCTG
20	A3_101420069	CAGATTTCAGGGAGCAAAGGGATCAAATTAACTTTTCTCATGGTTCTATTTTTGTGACTC[A/C]ATTCTTTTGGAGGAGAGAGTCAGGATGACTGGTGGGATTTCCAGAAAAGCCAGAAACAGT
21	A3_12082294	CAGACACATTGGGATCATGAAAATCAGCCTCAGTTTCAAAAATAAATCTGTTACCTCCAT[T/C]AATCATGAAAAACAATTGGTCAATGGCCTGCAGGGGTGGCAGCTGTGTCAAAGCAGGGGC
22	A3_130195244	ATATGCTCAATAAATAACGATCACTCGTTTGCTTATTACTCGTTCGGGTGGGGATACAGA[T/C]GTATATACCTAAAATTACAAAACAGCGTAAGATCTGTCCTGGTTACATGTACCAGGTGAA

Table 1 - SNP sequences useful for breed identification test

SEQ ID NO:	SNP ID	Sequence
23	A3_159537633	CCGCAAGTTGGGCGGAGGTTAGGTGGGCAGACTCACCTTCTTGTCCATGAGGCAACCAAA[C/G]AGTAAGATGAAGACACCCTTAACGGGGGGATACGGGGATAAGTTAGTCACGGAGGAAGGA
24	A3_162208567	ACGAGTCGTGTTAAATAAATCGAGGATGGCATTGTTAGTCCTCTTTCCTAAGTAACCTTC[C/G]AGGCTGTCAGATAAGCTCTCCCTGTGGTTTCTGTTCTCTTTTAGAATGAGCCCTTCCTGA
25	A3_38781591	AGCATTTATCAAAGGAATGATAAGGAGTAAAGTAGAACATTAGTCCATAGGTGAAAGCCC[A/G]TGAGAAAAAAATTAAATGCCCAAGTCATTAAGTGCATGGCTTGACAAATTGTTTAAAAGg
26	A3_75156179	CTATACTAGTTTTATATCATCCTTGCCTGTTATGGATCGAACGAGTGTTTTTCCTGCTGT[A/G]CAAAAACGTTCCTTGACAATATATTTTCTACCAATAATCATTATTTTAATAAAACCAGTG
27	A3_91058022	GTTAAGCCCATCTAACTCCTGAATTTTTTCGTGTGATTGTTTCATAGAAAAGGTAAGCTT[T/G]CTGGGAAAGCAGGTATGGAGAATTTTTATTTTAAATCCTTGAAACTGTGACAGATGTTTA
28	A3_99507784	CAGCACAAACATCTCCTATTCCTTCCTTTCTCATTCCATAATCCTTTGAATATGCATCCA[A/T]TAAAACACTTAACACATTGTTCTGTGTCAGGAGTGTCTGTCTCTGATTAGACCAGCAGTT
29	B1_10420438	GGGTAGGGTTGGGAATGAGGGTGAAGGTAGAAGGAGGGATAGAAGGACAAGAAGAAGCAA[A/G]GAGCATCCTGGACAATCTGTGTCATTAGCTTCTGTTTGCACATGGCCAAGGCACTTGCTT
30	B1_12214271	CCTTCCTCTTCACCCTGCCTCTCGGGCATGAGTCACCATTTCCTCTTAAAATATGGAGAA[A/C]TACCAAACGTGGCTTTCATGTGGGTTGCACACGTGGTAATGACTGAGTTGGGAAGACCAC
31	B1_195678303	TGGAGGGCATCAGAGATGTTAGACACCATGGGCAGGCTTACCTTGAATTTTAGGTGCTCC[A/G]AGGCTCTGAGGTTCTCCATCATAAAGTCAAGGATTTGACAAGACTTGAAGTTGTTATTGA
32	B1_199564532	TACTTGGAAATGTTCATTTCTGAGCTTCCTGTCTGTCGTGGAATTGCTGGAGAATGGAAA[A/G]TGGGTTTCGTTTTCTCTGAGTAGTGAGGACTTTAAGCCTCTGCACACATTTGTTGCCTTT
33	B1_202966562	AGTCATCTATAACTCAGAAAAAATAAGCAACAGTATAATCCTTAACCTTGTTAACAGGGC[A/G]GGGGTGTAGGGGGCAAGCACAAACTAAAATGACACAGGGTATTTCACTAGTTTTTTTTTT
34	B1_54775572	TTTTAATGTATGCTCTTTTATAAAATCTGCATGGCCATTCCGTGTATATGCGTTTTTAGC[A/G]TGTGCATAAATGATATGTTCTGCGTCTCATTTGGTTTCTTATGGTTCAGTCAGCACTGTT
35	B1_80161671	tatGTAAACACTTATTGAGTATCTATTGCCCTAAAGGGATTCAACAACAGCTCGATCATA[A/G]TTATAAGGCACAAAAGAGAGATGAGTTTAAGTCTCTACTTTGATTTTAAAAACTTATATT
36	B1_88148379	CAAGGACCCAACTTGGGTCCCATCCCCATGCCCCACCTCACCCCACAGCAAGACGTCTTT[T/C]CCATATTCACTGCTCTTCCCTTGACTTCTGAGAGCTTTTGCAATCTACATTTTGACATTT
37	B2_138312489	TAGGAGGTTGATGAAAGGCATCCGGATCAGGGCCAAGGGTTTGATCAAAAGCCCAGTAAT[A/G]AGAGTGAGCAAAGTGTAATGTTAAAGAATCAGAGTGCATCCTACTCAGATGTGGCAAAGG
38	B2_146660650	ACAGATAAGTGTCCGTGTTCAGTGGGCTCAAGCCTCCTGGCTCAAGAGACTATGGTTTGA[T/C]CAGTCTTCTAGGTGAATCAAAGATAGCTGACTCTGAGGCTTTGACCCTGGATTTCAAGAG
39	B2_41509834	ACAGAGGGCAGTCACCATGGTCACTAGTGGGGACAACGAGGGAAGACTCTCAGGAGACAC[A/G]AAGGTCAGAGTTTACTCTAGTGCCAATAGTAATAACATTTACGAGGTCCCCACTGTGTGC

Table 1 - SNP sequences useful for breed identification test

SEQ ID NO:	SNP ID	Sequence
40	B2_45093345	AGCTCTACAGTTCTGGAAGCTTCCTTAGGCTCCTCCTCTACAGTCCTAGGCTCAGGCACA[T/C]TCTTCTGGGTGAGGAAGCATCTGTTCCAGAGGATGAGTGTTTCAAGGTTGACTTCCTGAA
41	B2_6949528	CAAATGGGCATAGGTGTTCAAAATTAAAATTAAGTCGTCTGGCATCCAGATGAGAGAAAT[A/G]GAAGTTAGAAGTCAGGGAGACGTTGTGCACTGGGCCCGTGATTTGCTGCAGGGCCTCCAT
42	B3_104483970	GGGTTACACTGTTTATGCGGTTGTACAGATCTACAGTTCTTAACAGTTGGGTTCTGCAGT[A/G]TATTACTCTGGTGTTAAATGGAGGATCATCTGTTTTAGATCACAGATTTATTATTCTATT
43	B3_111000326	AAGCAACCAAAAGGTGAACTGTTGATGAGCAGTGTCCTGCTTGATGATATTTATCATGTG[T/C]AGCCCCTCCTGAACGTTGACTCCGCGTCATGGCACACAATTTTCTGATGACAATATACTT
44	B3_13666494	AACAAAGCAGCCCAGCTTCTCAGGGAAGTCTTCTACCTGGGTGATTACTTAACCTTTCTA[C/G]AGTTCTGCGGTATTTTTCTCTAGGGCAAAGTCGTAAAACCGCCAGGTTTGGGTACAGCCC
45	B3_39203469	CCAGACAGCTGCCAGATCCGGGGGGTGGGGATGAGGGTAAAGGGGATGGGAGTTATCTCC[T/C]TGCCTTTATGGCTGGCACCTGGAGCCAGGCTGGGTGATTCAAAAGCACTTGGCCAGAGAC
46	B3_51317931	GGCAGTGTGGGAATAAATATTTATAGGCTGGGCTCTGAAACCAACATATTCTCATTTTTT[A/G]TAGAGCCTTGGGCCAGGCCTATGCCAAGTGAAAATTAATTTACCCAAGAATTTCTTTTCA
47	B3_57141954	TCCTGCCATCACAGTGGGCACCTGTCAGGTCACAACTACTGACCAAAGAGAAACCCAGCT[C/G]CTCACTTCTGCCCCTCCCACAGATAAGCAGAACCCCCAGGACCACCATCACTGTGAATGA
48	B3_77094074	GCCTGATGTTTTCTGGTTGGTGGGTGTATTTATCCTTGTTCCTTCTGTCCTGACCAAGTC[A/C]CTTGCTTCTACAGAGTGAATGGAGCCTAGACTAGCTAAAAATCAAGATTCTACCACTTAC
49	B4_105706694	ATTAGAAACATACCAATAAATGTTATTATTTGAAAAAAGATTTTAGACTCACTGAAGCCC[A/G]CAAATATTTAGGCTTTGCCCAAATTTATTTCTACACTACAGGAATTTGCTCAACTACTTT
50	B4_142658074	AGGCCAGAACAATAATATGCCCTTCCGGAAAGGTCTATCACATTCTCAGGAGGCAAAGGT[A/G]GCTTGAAAAAGCATACTGTAATGTACACATCTAGGAAGGTGGAAGGAGCCTTCACCTGAT
51	B4_143006494	TTTAATTATTAGTTGTACATGATGCATAACCACTGAACTTTCTCTGCATTAACAGGATGA[A/G]TATCAGGTAATTAGTGCTCTGACAGTGCTCTGATAATTAGTGCTCTGAGTCCTAGCATTT
52	B4_144693308	CTTCTCTTGGCCTGGAGAGAGCATTGAAGCCACTCCCTCTGTGGGTGCCTCGCTCCATAC[A/G]TAAACACATGTCTACCATATATACACAGGCACACACATTTGTCATTCCTTCCCAGAATGA
53	B4_146486983	AGTTTGTGCTCACTTGTGTTTTTTCCTAATTGTTTTATGTGGAAATGTTTTATCTTCATG[A/G]CAGCAGAACACATTCCTTGAGGAAAAAACAATATGTCTTCACTTTATTTTGTCCCCTAAT
54	B4_149532846	TGAGGCCTGGCCAGATCTCCCTGGCCATCTGGGTCCCCTGGCACAGCTTCCTTTGGTGAC[T/C]CGAGTAATCGTAACAGTTGCCATATAATTGAGGAGCGGCCATGGTGTGCCATACGTCAGC
55	B4_20001848	GGTGTAAGGAGAGAAAACGGAAAAGCTATTTTAACATGAGTTCTCTCAGAATGGCGTCAT[T/C]GTGAGACCCTTGTACTTTATTCTCTTTTTGCTTATCTGCATTGTTAAGTGATCTGTAGTA
56	B4_21098349	TTTGTTTGTTACAGGAGATTAAGGGCCTGGCTTCTCTTTGACTCTTTCAAGTTTACCCAA[A/G]TTCAGAAGTAGGATCACAACACAGCATTTTGTGTGGAGAACCATGTCTCAAATATACAAC

Table 1 - SNP sequences useful for breed identification test

SEQ ID NO:	SNP ID	Sequence
57	B4_255106	TCGCCCATATGGAGTGCAGCAGCCCCTCTGTTAAGGCAATTATCTCATTATCGTGGGACT[T/C]TTGAGGCTGTCTTTTATGCTCACCATGACTTTCTTAATGGGTTTCATCATGTTCGCCTTT
58	B4_3093827	GCCCCGTCATCCAAACTGTTCAACAGGGGAAGGGTGTGAGGCTGACCTATGTTGTCCACA[T/C]GACCCCAGAAGGTCTAAGAGAAGCAGGTGTCGTTGGTGCTCAGCAAGTGCCCAGAGCCCC
59	B4_40319102	TTCATAATGAAGCCTGGAATGCCTTCCTCCCAGTTCCATTTGTCCTGCTCCTCACCCCAT[T/C]ACTCTTTATTTCCTCTCCTGCTTAAGTTTTCTTCAGAGCTCCCACCCTGTGGGACATGCC
60	B4_47638578	ACCCCTGCCTCCTTTCCCTCATACCTAATAGGAGTCCTCTGTATGTTCACCAGTGCAGCT[A/G]AATCAAGCTGCTGAGAGTTAACCAAATAAAAGAAATAGGTCTAGCTCTCCTGTAACTGGC
61	C1_116355295	ATCTATCTGGCAGCCCTTCCACCAGCAGTGTATTTCCAAATATCCCACGGGGCTGTCCTC[T/C]GTCTCTACTGTGCCATCCTTTCTGTCTGGACCATCTAAACAGAGTTTTGGAAGCACCACA
62	C1_123164748	GTTAAGTGTAAGCTGCTGTATGGGGATTATCATTATTTCTTTTGTCAGTGAACCATCACT[A/G]CTCTTTGCTCCCTTGCCTCCCCACCTCTGTCTGCCCACCCCCTTCTTGCCAACCTTTCTT
63	C1_190502133	GCCCCTCTCATCTTGGGCAACACTTCACTGGGTGAGTGATTACAGCATTTTTCCTCTCAC[T/C]GCCAAGCTGGTCCTCCTGTCCCCTACTTTGCTCTCAGTCTATAAAAACTACTTTTTAAGG
64	C1_215441574	TGTTGACTAATGTGAATAATGATTCTTTTTTTCTATTAAGAAAAGAGAGGAACGCATCCA[A/C]GTATTGAGTACACTACCAGCCAGGAATGGTGTATTTTACAGGTGGGCATCTAATCTAAGA
65	C1_24148281	TGACTATCTTGCCCCCTTCCTTTTGTAGCAACCCTGTTCTCCAGGGTCTAGTAAGACAAG[A/G]CATGGGAAAACACTTTGCCGTTGCAAAAGCATTGTATAAAGTGATGCACAGAAAATGGGA
66	C1_28702055	TGTGAGGATATGGAGACATCACATAAACTAACAGACAACTAGACTTAATCAATGGTGGCT[A/C]ATTAGGAGAAGACTCAACAGTGGAAGCTTCTTAGTTGGGCACCGAAGGTTTCCTGGGAGC
67	C1_34981315	TGTTCAGATATTTGGGTGTTCTGGTTCAAAACTGGTTTCTCTCAAGATTCTGATAGACCT[T/C]GCCAGCTGCAGATCCCAGCCACCTTCAAACCCATCCTTAGGTGGCCTCCTCTCGAGACTC
68	C1_396397	AGACAGCGCCATGCCCGCATCCCGCCACCCTCCCCTCACGCGTCTTCCCTGGTAATTATG[A/G]TTTTCAAAACTCACCTGATATAAAATTTACCACTTAACCTTTTTTATTACTTACTTATTA
69	C1_44520932	TCAGGTACGAAGGCTCAGGTATGGAAGGCGGGTATTTTTTAGCCTTGAGAAAGGTTTAAG[A/G]TCAAGAAGGACAATGGGTTAAGCCATCTGAGCAAAGGATCATCTGGTCAGAGACAGGAAA
70	C1_52456776	GGGGAGAGCACATGGCGGGGAGTGGGGGGGCAGGTATACGAGATGTTGCTCCAGTGGAAC[A/G]GATAGAAAATGAGAGGAAGAGGTTAGACAGGAAGGGGTTCGGGTTGATGCTTAGTTCTAG
71	C2_106991233	AAAAGTTGTAGAAAGAAAAAGAAGCATACAAAAGTGCTCAGTGAAAAATGAGAGGATATC[A/G]CCCAAAGGCAAAGGAGCTACAAGCATGTATTGACATCATAGTACGGAGTACAGACTCAAA
72	C2_147124460	GTTCTCTTCACACACGCCAGGATATAAACACAAACTTTGCAAAGGCACTTGTGCCTCACC[T/C]GCTCATTTTCATGCATAAATCAACGGCTATTTCTTACACAAATGGAAACAAATTTAAATT
73	C2_150774106	TTCAGCAATGGTATAATATCTCTGCAGTCTGGATTACCCAACAGGCAGTTCAAATACACA[A/G]TTAGGTGTCCCAAACTTTTATTGCTATACTTTTTCATTTTTAATATACCTATGGAGAGTT

Table 1 - SNP sequences useful for breed identification test

SEQ ID NO:	SNP ID	Sequence
74	C2_156491175	TTGCTACTGCTACCAGGCACAGAGACTATTCTGCCAGGGCAGTTAATTTTCAATCAGGAT[A/G]CACATTTCAGGGTCTGGGGTGCAGGCATATGCAGTTAGGGCAAGTTCCCCAAGAGATTTT
75	C2_262401	TTGTTCCAAGCGGGAGGGTAGACCTGAGTTCTCTTGTCTGAATTATCCTATTTCCTCATT[T/C]TTTACCGTGGAGCCGTCTCCTCTGGCCCAGAAGCTTCCTGGAGCCGAGTCTATGGGTTGT
76	C2_5215469	TAAATAAAGGAGCAAATGAATATAATGGGCTTATTCAACTCTCAAGAATAAAGATGGGTC[A/G]CTGCTTTTAGGAAATGGGATGTGTAAACACCCACCCACACCGTCCTTCCCTTTCACCATG
77	D1_101321498	AGGAAGAAGGTTATGTTATCCAGTGTACCTGGTGTTCTAAGGGGAGGCTCTTGGAATTCA[A/G]ATACAGGCCTGTCTAATGCTGAAGGTCTTGACTTCTTGGCCAGGCCATCTTGTTTTCAGT
78	D1_104941557	GATATTCTGTACAGCTGTTGTGCAGCTTGTTGCCACAGCAATGGCTAAATTTCAAAGGTG[A/G]GCCCAGGATATGTGAAGTAGGGCATAGAAGATTTCCAACACACCCAGGAACCTTTCCGGG
79	D1_105498119	GCAGATGTCTTGTCAAAACAGAATAAGAAACTGTGAAGAAATAGTCTGTGAAACCCAGCC[A/G]TGTCCTGCTTCCTCTCATTTCTGGGGTAAAATAGCAGCGGGGGGAAAAATGGCTTTTAGT
80	D1_10789012	GTGAAGAAAGAGGAGTGATGGGGAAATCTGGGCTCACTAGGTGTAGCCACTCTCTCCTTT[A/G]GAATGTACTGGCTAAGCACTGACATGTTCTTACTATTCAGTTGCCTTCCTTATACAATTT
81	D1_11484008	TGGGTCCAACCTTTTAACCCATTTCTTCACCCATTTGTCTACAGTGGAGACACCAGAAGT[T/C]GTCTAGCATCTTAAGAACAATTGCTCTCACTCTGAATGGTGGGATAGTCTGGTTGCCTGG
82	D1_117527468	CACCGAAATCTCTTCCATCGATGTCCAGGTGGTGCCAATTGCAAAATATTGCTTCCCTTC[A/G]ATAGTATAAGGAAGTACACGGTCTTTTGCTCCGTACTCGTGAATAACGAATGGGAAGCTT
83	D1_125811329	CTGGCCTTTGGCTCAGGAATCTGTCGGCGAAACCAGTTCTGATTTCTTTTGCCCCAAATC[A/G]TTTGCTCAAAGGTAATGAATGCGGTGGCAATTCTCAGTTTGTGTCCTGCTGTAAATATCT
84	D1_126256993	CAGTGAAAGGGCACCTTACCAGCAAATAGGCTTAAGCGACGACCTTACATAAAGACAGGC[A/G]TTTGGAACCTTCTGCCCAGAGCAGCTCCACCCTGGAGATCCTGCCCAACTTCCTGATCGC
85	D1_126847301	ATGGGCATGGCTTCCCAAGACATATTTATGAATTGAGGATCTGATAGAGAAGGTAAGATG[A/G]GGTCAAAGTGGGGAAGTAGTCAGCTCTAAAACAAAAATGAGAAATCCCGGGGATTTTAAG
86	D1_15984279	GTGGCGTGAACCAAGATAGTAGAAAAAATGGTACCAGTTTCGGGGAGTCATCAAAGGGTG[A/G]TGTGTTATCTATCACTCATCTTCGGTACGGAATTCCTGCCTACCCTGAAGATAAGCCTGG
87	D1_18390852	TTCTTGTGAAAGCCTACCCTTCCCACACAGCTGCAGCTGCTTTGAATGAATGGGAGTTCA[T/C]CTGGGGGGAAATGGTCTATTGCTCTGGGGAATTGCTGTCCTCCCCAGAGGCTGGAGGGCA
88	D1_18570323	CCCCCCCCCAAGCTTGGGTGGGTTCTCTTACTAACAATTTGTAAGCACCTGGGAGATGCA[A/G]AGGTGCTTTTTATTAATTTCTTAACTTAAGGAAACATAGCTGAAAGGAAATTCTGGATTA
89	D1_66177762	AGACCAGAATGGGCACAAAAGGGGTGTTAAGAGAGTGCCACCTAATGGAAAATAGGAACG[T/C]CTCCCTGGGTTGCAGAGACAGGTTCCAGAGCCCCAGAGACCCAGAGCACCAGCCTTAAAA
90	D2_1020904	TGAGCTAAATTTGCTTTTTGTGAGAAATTGATGTCAGTGTTTTCACTGCATTTATGAACA[T/C]GTTATCATCTTTGGGAGAGAGACCAGAAGAGTAAAATTGAAGAAGAGTACAAAGGGATTG

Table 1 - SNP sequences useful for breed identification test

SEQ ID NO:	SNP ID	Sequence
91	D2_105772916	ATGGGAAGAACGGGGACCGCTCCCGAAAGTTCCGAGACTTTCTATCCTGGAAGAATGAAG[T/C]AATTCCCACTCTTGTCTCCAGCCGGGGAAGGGGGGGGTGGAGAGTCATGTGAGCCGCCCC
92	D2_1752007	AATGGAGGAATTTTGCCTTGTGAGCCTTCACTTACCAACAATGATGTGGGTACCTAACTT[T/C]TGGCGCATTGATCTCTTGACTTTGCTGTACAATTTTAACCTCTGCAGCTTTAATTATCTT
93	D2_56777338	TACCAGGTTGGAATCTTCCTTTCTGTGTTTTCTCTAGGGTTTCTAGGACACATCTGCTTC[A/G]TTTGCCCTAAATCTGAGTCCCACGGGGATGTGTAAACAGTTATTACATTTCCCGCAGGAC
94	D2_74293444	GGGGCCCAGACTGTGAGTGTGTGCAGAACCAGAAGAAATAGGAGTGGCCCATGTAGGCTG[T/C]TCCTTCTAGAAGTGCAAAGAAGAAGCTGGAGGACAGCTCAAGAAGGGTGTGGGGTCAGGG
95	D2_91989307	AGGAAGGATGACACTGACTGAATTCAGGCCCTGGGAACTTTAAATTTCAATCCTATCTCC[T/C]CTGCTTGACCACAGTGCTCACAGATAGGACCGTGTTTTTGTTGTGAACTTAATTACACAC
96	D3_103840114	GCAATGCTTCATTGTGGTTATTCCAGAGAAGACAGAGCAATCCAAGCCACCCCACTGATG[T/C]TCAGGAACAGGTCAACCAATTCATTTGGGGGCACAGCGTATCCTTATCCGTGCCACACCG
97	D3_122502120	AATAAGAGACTGCATTTCATTGAATCCTCTTTGAACCCGTTTTGCTATTCCAATAAAGAG[A/C]CCTGCAAGTCCTGATTTCTCTGGAAAATGAATAATAATCTTCTAATTTGTTGTTTCCTCA
98	D3_24565823	TTTATGGAATGGAAGATGAACCTTGATGGATGATAAAGCATGTCATGAAAGTGGATGCAC[A/G]GAAGGCCAGAATTCTTCAAGTTCACAAGAACCTGACCAGCGCAGTGACTTCTTTATGTAC
99	D3_24823793	TGGTCTCATGGCTGAGTCAGCACCTGTGCAGAGGCGCAGAGGCACTAGACTTCTCCCACT[C/G]GTTGCATTTAACTGAGGGGACACAGCCTGTGTGCTTCCTGTAGGGAACAGAACAAGTAAA
100	D3_28838660	CACACAGGCATAGCCAGAAGAAGGCAGCCAAGCCAGATGCTGGACCAGACTCCACAGTCT[T/C]CTGGAAAATCATGAGTTGAAAAGGAAACCCTTAGCCACCATATAATCTTGTGGCTTAGTA
101	D4_41078218	TAGCTGACTTTAATTCTCCCACAAAGAGAGGAAATTAGCCACATTATTTTAAAAAGAGAT[T/G]CTTCATTTTACAAAAAGATTGCTGAACATTTCCTAAATGACAATAGGACATTCAAAAAAT
102	D4_42000379	TTCCAGAGTGACGAGGACGCATAGTCGCTGCCCAGAGAAGATGAAGCACTCTGGAGAGAT[C/G]AAAGGCCATTGAGGCCTGAGTGGCTGTACAATTTAGCACTGGGGGTTCTATTCAGCAGTC
103	D4_63622083	CCTCAATGTATGGTGGTGGCTGAAAAGCTGTTGCAGCTTCATGCCCAGAAATGCACGTGT[A/G]TACATGAATACATGGGTTTGTGGATGGATTTTGCATGAGTGCATATGTGGGTCTGCATGT
104	E1_130875919	CTGCGTGACTGTAATTTTCCCCTTGAGCCCTGGATACAAATAAAGAGCCAGCTAATACTT[T/G]CTTTGCCCTTTTTCTACTCTCCCTTTGCTTAACCCACAGGTATTTACAAGGTTTTGGTTG
105	E1_3912105	GTGAGTAACATGGTCCACATACCCATGGAATGGGTGTCCTGAACAAGGTCTGGGCAGTAG[T/G]TGACAATGAACTGAAAATAAGTGGAGTCATTTCCATGACCGTAATGATAACTCTATGATG
106	E1_4114158	TTTTATTTTGTTGATTTAGCGAACATTTATCATGTGCCTTCCATGTGTGTGGTCCCAAAG[T/G]TGGAGTAGTATTGAATAAGGAGGGCAATTCTGACCCTCACCCAAGAGGCGGTATGAAGAA
107	E1_48228153	AACAGGAGAGTAGGGCTCATATTGATTAGATATCTGTCACGGGTTGGGAAGGTTTACCGT[A/C]ACTGTGCTATCCATTTTGCATATCAGTCTTCTGACATGTCCTCTTACATCCATTTTATAG

Table 1 - SNP sequences useful for breed identification test

SEQ ID NO:	SNP ID	Sequence
108	E1_48700963	GACGCTTAACCAACCGAGCCACCCGGGTGCCCCTCCTAGGAGGCGATCTTGAAAAGACAG[A/T]CATAACAGTGCTCCATTATGTGATTTTCAACTTTCTCAGTAAGCATTACAGACTGCCCAG
109	E1_5453028	TCATAAATTCCACCTCCTTTTGCAAAGGACTCCTATGCTTCAGCGTTTCATTTTAGATCG[A/G]TAGAATTTAAATTTTCTTGGAATTTTAAAATTCACAGAGAATCTGGTCTTTTCTTTTAAA
110	E2_22632289	GCAAGATTTGCTTTCCTCTGTATCACCGAGGCAGTTTGCTTCAAAGAACAACTATTTGAC[T/C]GGTCAGATGCTACTTGCAGGCAGAGGGGAGTCAAGCCTCAGCACCTTTGGGTGGCACATG
111	E2_34027888	TTTACTTGTAGTATAATAAATGCCATTAGCATGACTAATCACACACCTGATTAGACAAAC[T/C]GCCCCTCCTCCCCTAGTGTATTTCCTGGATCCTACACCCAATAAATCCAGCATTGATGCA
112	E2_35914023	GGAGGGCAGGGCCTGGTCTTACCCAGTATATCAGAAGCAGCCAGGGTCGGTCGCCTTCCC[T/C]CCATCAAGTGCTCCCTATGTCCTCCTTGGCTGCATTCTGTGAAAGCACTAGAAGGGAGCT
113	E2_36986631	TTAGGGGAGCAGGAGTTCAGAGACAGGCTTTTCTAAGGACAGGCTTTCAAAAAAAATGTG[T/G]TTTTTTTGGTTTATTTTACCCTTTTGAAGACCTCACAACGTATAGTAAGTCACGTCAGGG
114	E2_38860686	AAGCCATGTTGGACGATCTCCAGTCTCTGCGAAAACATGTGACACCATTGTACATTCCCC[T/C]GGTTAAAACACTTCATTCCCAGTTTTATTGTGTTGCCTGTGGCCCCTTACTTTTGAGGCT
115	E2_65436639	TCTGGGGGACGATGGACTCAGGAGGGGACCTGAGAAGTATGTAGGAGAAGGCAGGCTAAC[A/G]AAAGGAGGGAGAGTCAGCCGAGTACCAGAGGTGGGGGCAGAGAGGCTCAGTGAGGGAGCC
116	E2_7950477	TACATTCTAGTTCAGGATGGAATGAATGAGGGAAAGAAAAAGACGTTTTAATTCCTCAAG[T/G]CTTTCTGGTGTGCAAGTCCCTTTCTGGGAAAGCACAGGTGCTGGTCGAATTCGTTCCCTG
117	E2_8422942	GCTAATTTCTCTGAGAAATGGCTATGCCATGGGGACCTCCTGCTAAATGCATGCAACAGA[A/G]TATTCTAGAAGCATGCTAAAATAGATTCAGGGTCCCATGCCAGCCCACCTGGGCTTGCTA
118	E3_36044809	CAGTTAGTAAGCACTCCTTTGGTTAGTACAGAAAAAGTGAAATGTTGGAGGTGTGAGAAA[T/C]GCGGTTGGGGGCATGTTGAAGGACAGGGACACGCGCTTTGTGACTGCCAGGTTTTGAGAG
119	E3_55434272	TGCCGCTTCAGATTGGGGAGACAGGTTCAAGGTGACTGCCTCAACATACCCAAGTTCAGA[A/G]GGAGGAGCTCCGATCATACACTGTGTCTTCCCCGTGACACCACATGCCCTGCCCCTGAGG
120	F1_20309325	TCTGTGGAGGTGATGTGACAGCCAGGGCACTGTTGTCACCCAGAGAATACAGGCATTTGG[A/G]ACTGCTATTAAATCTACTGAAAGCCAGTCACTGCAGAAGAAGGCAAGCTATAGGCCTGCT
121	F1_21799641	TGACCCAGGGTCAAATTTGGTGGCCTCTTCCTTAGCGGTCAGCTTAGCAGTGAAGGTCTG[A/G]CACATGCTTCCACAGCACATGCTTCGATAAGTGGCTAACGAAGAAATGAATAAAAGAGCT
122	F1_26100599	CCAAAAGAAACAAAACTGCCAAGTAAAATTGCACTCCAAGAACTGGGCATATGCTTTATT[A/T]ACCCAAACCTCATGTTTATAAGACTCAGTACCGACTCTAATTCAGGCTAGTGGGTCACAA
123	F1_27124984	CACATTATTTGTCTGTTCCCACATGATCTCAATGAATGTAAATTCCTTTCATCCTGAAGT[A/G]GCCAGTAAGAACACACTCTTCCAGTGAGGCTCCCTTCCTTCAGACCTTTCTGATTTGCAC
124	F1_38051725	CTTTACAACGAAGAGGTACACATTGCTAATGGGAGTCACAGTACGGTGTGGGCAAAGGTT[A/G]ATTTTTTCTTAATTCTTGTAGAGGCGCCAAAAAGTACACACAACTCCTACTCAAGTTCAC

Table 1 - SNP sequences useful for breed identification test

SEQ ID NO:	SNP ID	Sequence
125	F1_565223	TGAGAGTTTGGACTTGAGGTATCCTCGTGTTAAAAACGTAGACATTGGTGTTTCGAAATG[A/G]TGGGAGAATCAGACATTGAATATAGTCAACGCGTTGTAAATTAACATTTCCTTCTAGTTG
126	F1_82716202	CTCCTTTTCCAATCTCATCTCTTATCAACTCTTTCTATGCACCTTATATTCAGGCTATAC[T/G]GAATTACTGGTGGTAGCCTGAAATGCTGACCTCTTTACTGGAATACCACCTTTTCCTTAT
127	F1_91517402	TGCTTATCCACCTAATAATATAATTCAGTAATAGCAATACAAAAGTATGATCTTTGTTTG[A/G]TCCCGATTCACACAACCCAACTGCAAAAAGACCGTTGAGGATATTTGGGTGCTTACTGGA
128	F2_26886470	TAACCTAAAAACGTACAGTGGGAATGCACGAGTACCCAGCAGTGCTTCAGGCAATGCGTG[A/G]CTTGTTAGTTTGCTATGTTTGGGGACAGATTCTTAATGTCCTCAAATAAAATTCCAGATA
129	F2_38395360	AAGACAGCTACATTCCAGAGGATCCAATTTTGCCTTGTAGAGTATAGACATCCATGGCAC[A/G]GGCCTTGAAATAGCCCAGCAGGGGGAATGGTTGAAACTCCAGGAGCTGTGCCTTTATAGA
130	F2_46855978	TTCCTTTTATGGCCTGGAGAAGGTTTTCTAACTTTCCGCTACATGCCATCCGGTCTGGTA[T/C]AACTGACGAAAACAATTGTTGAAAGTACTGTCCTCTGGTTAAATAAATTATGGTACGTCT
131	F2_74863327	TGACTGCACTTCCTTCTGAGCTGGAGGAGGGGCATACAATGCACCCACTAACTAGGTATG[T/C]GATTCCCGGTCCATCAGAACCTGCATTCCCACCAGCACCTTAGCCCCTCTCCACGTTCTC
132	F2_78303221	AAAGTGTCATCGATGCCCAAACCACGACTGATGAAGGATGGGAATCAAATCGTCTGTCTT[T/C]GTAGAGGCCACCAATGGTACTAACCACGCTGGAAACGAACGCCTGTTGGTTAAATGTACA
133	F2_79632602	CCAGTGTACCTTTTGGTAACCATTTGCATGGGTGTTTTGCTGCATTAGAACATGTGAGTC[C/G]CTCTAGCACTTGTGTGCGGGAATCCCACCACCAGGATAATCTGGAGGTCATGTTACGGAG
134	F2_8427817	ATTTTGTCACGTAAGCAACACTGGAATTCTGAATGTGTGTTCGCAGGCGCTCACATAATT[A/G]CCAACTGTGATTTTAGACGAGCCTGTGCCTCGGATCCCAATATTATTTATCATGCACGTT
135	C2_187325	AATCCTAACATTCATTAAAAGGAAACTGTAAGCCGCGACCGTGTGAGATCACGTGCTTCT[A/C]GATTTACAAAAGAATTCTAGTCCTTCAGCAGCTGTTTAAAAGTACTTTTAACTAACTAAA
136	D2_717969	aCAGATATTCTTTTTTATAGCCTTTTACTTATTAGAAGAACGATAGGTACTCGTGATACT[A/G]CGTTTTGAGCTCTGAGAAGATACGTAGAATCATTAAGTCACCGGGGGTAACTGTCGTCAG
137	B4_1687419	CTCTTGCTGCCCTAAAGGTGGACTGAAAATGGAGTTGGGTGATCATCCCCAGTGGATGCT[T/C]GTAGCACTTAGCTCATGATATGTGCTCTATAAATATCAGCCTTTATAAATTATTAGTGCT
138	D3_1810839	ACTTAACCCAGGGAATTCTTCCAGGAAGCACTTCAGAAAATGGAAAGCACCACATGGCAG[T/G]TTTCTTCTGGGTTTAAAAACTGCTATTTGCGGGTACCTTTGTTTGTATTTTCAAGCAGGA
139	A3_11480952	AGAACATTGACCTTGAATGCATGCAGTTTAGGAAGTGAAGGCCAGACCACCAAGGAGGCC[T/C]ATGTTGGCTGTGTTTTCACATCTTGCTTCCCCTGGGGAAACCAGGGCTGGGGCAGGAAGG
140	D1_16242433	GGTTTCTGGAAGTGCAATTCCTCAATATCCTGCCTCCCAACCAGGTAGGCAGGAGAGGAA[A/G]ACCTAAAATCTGCTGAATTACTTTCTTGAATTTGGCCTGTTTTCCAGGCTGTCTACTATG
141	E2_39211557	ACTAACGTCAAGACCCGTCTGCATCCCGAGGACAGGAAATAAGCAACTCTGTGCATTTGC[A/G]CAAGACCTTGCGGAAGACCTCATTACAGACGAGTGGATGTTTGCCCATCAAGCTCTTTGT

Table 1 - SNP sequences useful for breed identification test

SEQ ID NO:	SNP ID	Sequence
142	E3_67006512	CCCGGACGGCCCACTGTGAAGTTCTGCCCCGCATGTCCCTGAGCGTCATCCACCACCTGA[T/C]CAGCTCATAATAGAGCTGGACTCCCCAGCACTCCGGCATCCCTCCCCCTCCCACCTGGGA
143	F2_68572596	AGCTATTGTTCCAATAAAATTACTTCCTAAAACTGCACTCAAATTTCAATTTATCCCATG[T/C]GAATCTATTCAGCAATTTCCCCAACTTCTCTTAGCTGTCTGAAACCTCCTTTTCATATTT
144	F1_82068276	CTGTAGTAACATTCCATAATGAGAATATGAGATTATTCCGGATAGTCATAGACACAAGAT[A/C]CACTACCCTTCAGTCCCTGATAAATGCTCAGTGTCTGTGGTTTCCCTTCCATTATTATTT
145	E1_131587399	TCGCTGCTGGATGGCTGACGGTTTTTCAAAACCTGCAGAAAGAAACAAAGTTAGTTCTAA[T/C]CACACACTGGAAGCTCCTCGGTATCCCTGTTTAAGCCCTCACCCCCACCCCTCCTAACCC
146	B4_147206961	CCCCGATGTGGAAATGCTAGCTTGGGGCCCAAGTCTCTGTCTTAAGGGTAACAGGGAATG[A/G]TGTCTAGAAAGGACCTTGTGCCAAATGGCTGTGGCACATGCCATAAGGCATCCAGGTTGA
147	C1_181852965	CCTTCCTGAATTCTCTGCCCTCCCGTTCCTGCACCATTGAAATCCAGAGGGCATAAGTTC[A/G]TGAAACTAATAGCAAGTAGAGCGGCATAAACAGAAATAGTTCTTACTATAAATGGAGCCT
148	C1_216852686	GTTAGATTCAGGGAAATTTGCATGACCTGCCCGAGCTCAGTCTTCTGAGTGAAATGGAGA[T/C]CGTCACGAGGATGGAGTTGGCTCATGTGTGTGCATGTGCTTGTCAGCCTGTATACACCCA

Table 2a - Intergenic SNP minor allele frequencies by breed and population.

			Minor Allele Frequency																			
	Major Allele	Minor Allele	Total	Total Breeds	Total Random Bred	Abyssinian	American SH	Australian Mist	Bengal	Birman	British SH	Burmese	Chartreux	Cornish Rex	Egyptian Mau	Exotic SH	Havana Brown	Japanese Bob.	Korat	Maine Coon	Manx	Norwegian FC
chrA1_10141047	A	G	0.146	0.088	0.175	0.286	0.000	0.036	0.063	0.000	0.107	0.000	0.042	0.000	0.458	0.028	0.000	0.094	0.045	0.063	0.125	0.088
chrA1_133621071	C	T	0.270	0.315	0.245	0.167	0.769	0.367	0.528	0.526	0.667	0.079	0.500	0.467	0.643	0.316	0.045	0.250	0.065	0.316	0.406	0.412
chrA1_151648701	G	A	0.065	0.086	0.055	0.267	0.231	0.100	0.000	0.000	0.028	0.000	0.000	0.000	0.036	0.079	0.154	0.000	0.000	0.079	0.176	0.324
chrA1_175780586	G	A	0.394	0.572	0.306	0.500	0.400	0.933	0.563	0.421	0.750	0.750	0.500	0.667	0.773	0.583	0.545	0.528	0.618	0.656	0.533	0.500
chrA1_208054462	C	G	0.129	0.185	0.102	0.393	0.150	0.000	0.156	0.083	0.235	0.028	0.346	0.167	0.214	0.194	0.000	0.118	0.045	0.263	0.206	0.125
chrA1_223501140	A	G	0.133	0.193	0.099	0.533	0.083	0.100	0.344	0.475	0.083	0.083	0.063	0.000	0.321	0.176	0.818	0.000	0.000	0.237	0.235	0.059
chrA1_223506906	A	G	0.260	0.123	0.327	0.533	0.000	0.042	0.100	0.000	0.000	0.000	0.417	0.423	0.000	0.079	0.000	0.167	0.025	0.194	0.029	0.133
chrA1_225057933	C	A	0.233	0.128	0.283	0.400	0.038	0.067	0.139	0.375	0.028	0.132	0.250	0.233	0.115	0.026	0.038	0.417	0.060	0.053	0.265	0.028
chrA1_235579538	G	A	0.101	0.027	0.138	0.033	0.000	0.000	0.000	0.000	0.000	0.028	0.000	0.067	0.000	0.026	0.000	0.000	0.025	0.031	0.063	0.063
chrA1_27523501	C	A	0.564	0.473	0.605	0.233	0.308	0.714	0.500	0.850	0.406	0.342	0.231	0.000	0.536	0.333	0.458	0.235	0.682	0.412	0.441	0.472
chrA1_68485376	A	G	0.059	0.089	0.045	0.000	0.385	0.000	0.000	0.000	0.000	0.000	0.200	0.071	0.000	0.194	0.227	0.167	0.000	0.206	0.188	0.088
chrA1_69424718	C	T	0.378	0.311	0.410	0.100	0.154	0.393	0.265	0.289	0.194	0.395	0.409	0.467	0.400	0.500	0.192	0.235	0.550	0.105	0.412	0.357
chrA1_7429296	C	T	0.181	0.152	0.196	0.200	0.154	0.133	0.382	0.000	0.194	0.056	0.167	0.633	0.077	0.028	0.100	0.111	0.000	0.313	0.265	0.031
chrA1_8742286	G	T	0.373	0.278	0.416	0.067	0.346	0.167	0.000	0.650	0.278	0.447	0.292	0.667	0.000	0.026	0.583	0.368	0.208	0.278	0.313	0.417
chrA2_152258936	T	C	0.386	0.401	0.382	0.233	0.417	0.154	0.056	0.194	0.389	0.353	0.231	0.433	0.036	0.079	0.708	0.235	0.370	0.316	0.412	0.333
chrA2_201526186	C	T	0.191	0.211	0.182	0.393	0.154	0.286	0.056	0.025	0.083	0.105	0.042	0.067	0.654	0.316	0.042	0.553	0.160	0.361	0.294	0.278
chrA2_202225770	C	T	0.327	0.363	0.311	0.000	0.167	0.077	0.222	0.278	0.306	0.342	0.500	0.767	0.333	0.667	0.591	0.147	0.553	0.250	0.382	0.324
chrA2_44241149	G	T	0.016	0.008	0.019	0.000	0.000	0.000	0.000	0.200	0.000	0.000	0.000	0.000	0.038	0.000	0.000	0.000	0.000	0.000	0.000	0.000
chrA2_554046	T	C	0.149	0.122	0.165	0.700	0.000	0.033	0.531	0.000	0.056	0.026	0.115	0.000	0.538	0.000	0.125	0.158	0.040	0.316	0.000	0.000
chrA3_101420069	T	G	0.052	0.055	0.049	0.033	0.000	0.033	0.029	0.200	0.000	0.342	0.000	0.000	0.417	0.000	0.000	0.000	0.000	0.000	0.059	0.250
chrA3_11480952	C	T	0.025	0.024	0.026	0.000	0.083	0.292	0.000	0.000	0.028	0.000	0.000	0.000	0.000	0.000	0.000	0.026	0.000	0.053	0.100	0.000
chrA3_12082294	G	A	0.212	0.288	0.178	0.533	0.731	0.714	0.139	0.000	0.278	0.079	0.375	0.200	0.179	0.500	0.000	0.278	0.000	0.158	0.643	0.250
chrA3_130195244	T	C	0.188	0.184	0.188	0.643	0.136	0.536	0.393	0.306	0.000	0.237	0.083	0.000	0.389	0.079	0.150	0.417	0.000	0.219	0.125	0.167
chrA3_159537633	G	C	0.471	0.316	0.552	0.200	0.423	0.033	0.559	0.225	0.361	0.132	0.250	0.214	0.429	0.263	0.038	0.658	0.060	0.579	0.500	0.125
chrA3_162208567	C	G	0.265	0.374	0.206	0.333	0.500	0.107	0.500	0.889	0.594	0.031	0.318	0.577	0.393	0.658	0.083	0.176	0.000	0.412	0.469	0.533
chrA3_38781591	G	A	0.013	0.020	0.010	0.167	0.000	0.133	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.028

Table 2a - Intergenic SNP minor allele frequencies by breed and population.

			Minor Allele Frequency																			
	Major Allele	Minor Allele	Total	Total Breeds	Total Random Bred	Abyssinian	American SH	Australian Mist	Bengal	Birman	British SH	Burmese	Chartreux	Cornish Rex	Egyptian Mau	Exotic SH	Havana Brown	Japanese Bob.	Korat	Maine Coon	Manx	Norwegian FC
chrA3_75156179	G	A	0.240	0.228	0.249	0.533	0.462	0.433	0.029	0.000	0.029	0.000	0.000	0.000	0.115	0.026	0.192	0.222	0.042	0.583	0.250	0.441
chrA3_91058022	A	C	0.286	0.391	0.237	0.667	0.538	0.038	0.265	0.025	0.361	0.194	0.000	0.000	0.643	0.211	0.077	0.444	0.304	0.711	0.735	0.750
chrA3_99507784	A	T	0.324	0.251	0.356	0.071	0.192	0.367	0.088	0.625	0.147	0.342	0.042	0.033	0.625	0.158	0.077	0.500	0.435	0.206	0.188	0.206
chrB1_10420438	C	T	0.074	0.117	0.054	0.000	0.038	0.615	0.156	0.025	0.083	0.000	0.083	0.333	0.038	0.333	0.045	0.000	0.000	0.000	0.059	0.056
chrB1_12214271	T	G	0.432	0.413	0.438	0.500	0.250	0.100	0.265	0.842	0.389	0.289	0.222	0.600	0.231	0.471	0.115	0.526	0.182	0.421	0.441	0.222
chrB1_195678303	T	C	0.181	0.139	0.201	0.067	0.038	0.714	0.250	0.132	0.000	0.263	0.000	0.067	0.115	0.053	0.364	0.079	0.080	0.053	0.088	0.118
chrB1_199564532	G	A	0.091	0.119	0.078	0.633	0.115	0.000	0.324	0.000	0.028	0.000	0.000	0.000	0.538	0.139	0.038	0.139	0.042	0.000	0.088	0.147
chrB1_202966562	C	T	0.274	0.353	0.236	0.200	0.250	0.467	0.176	0.395	0.441	0.500	0.591	0.700	0.538	0.368	0.000	0.333	0.326	0.406	0.265	0.206
chrB1_54775572	G	A	0.119	0.125	0.118	0.933	0.000	0.167	0.028	0.000	0.278	0.000	0.292	0.000	0.036	0.211	0.000	0.222	0.000	0.184	0.029	0.088
chrB1_80161671	G	A	0.151	0.210	0.126	0.567	0.192	0.000	0.188	0.000	0.625	0.079	0.300	0.036	0.192	0.469	0.000	0.000	0.000	0.406	0.344	0.423
chrB1_88148379	T	C	0.395	0.353	0.420	0.467	0.385	0.036	0.556	0.075	0.588	0.000	0.292	0.033	0.786	0.222	0.292	0.118	0.409	0.441	0.353	0.324
chrB2_138312489	G	A	0.452	0.447	0.449	0.100	0.038	0.900	0.000	1.000	0.306	0.816	0.636	0.133	0.125	0.421	0.083	0.167	0.840	0.389	0.281	0.676
chrB2_146660650	C	T	0.019	0.035	0.012	0.100	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.026	0.000	0.000	0.271	0.000	0.000	0.000
chrB2_41509834	G	A	0.380	0.378	0.378	0.067	0.308	0.923	0.118	0.447	0.179	0.861	0.318	0.286	0.000	0.139	0.077	0.605	0.979	0.139	0.063	0.139
chrB2_45093345	A	G	0.364	0.406	0.344	0.786	0.583	0.154	0.200	0.263	0.559	0.028	0.409	0.654	0.077	0.658	0.125	0.088	0.261	0.667	0.618	0.536
chrB2_6949528	G	A	0.126	0.151	0.115	0.767	0.038	0.067	0.056	0.083	0.167	0.000	0.038	0.333	0.083	0.421	0.000	0.083	0.000	0.211	0.176	0.219
chrB3_104483970	G	A	0.324	0.324	0.318	0.233	0.000	0.533	0.222	0.900	0.083	0.842	0.250	0.200	0.269	0.026	0.923	0.441	0.783	0.167	0.147	0.056
chrB3_111000326	A	G	0.191	0.123	0.225	0.300	0.000	0.267	0.000	0.075	0.118	0.263	0.042	0.067	0.038	0.053	0.458	0.000	0.180	0.026	0.000	0.000
chrB3_13666494	C	G	0.491	0.560	0.454	0.567	0.583	0.833	0.472	0.625	0.500	0.868	0.269	0.900	0.077	0.722	0.846	0.676	0.813	0.611	0.382	0.353
chrB3_39203469	G	A	0.215	0.128	0.259	0.000	0.308	0.200	0.028	0.000	0.088	0.028	0.083	0.167	0.000	0.263	0.000	0.118	0.023	0.139	0.063	0.206
chrB3_51317931	C	T	0.304	0.322	0.293	0.571	0.038	0.433	0.000	0.471	0.000	0.737	0.385	0.167	0.000	0.053	0.846	0.083	0.978	0.088	0.147	0.083
chrB3_57141954	G	C	0.285	0.394	0.234	0.000	0.667	0.167	0.000	0.100	0.444	0.026	0.409	0.000	0.692	0.611	0.125	0.412	0.000	0.694	0.588	0.594
chrB3_77094074	A	C	0.082	0.135	0.060	0.033	0.231	0.364	0.206	0.031	0.250	0.088	0.150	0.192	0.091	0.200	0.050	0.067	0.000	0.361	0.094	0.100
chrB4_105706694	T	C	0.456	0.427	0.464	0.067	0.462	0.077	0.639	1.000	0.471	0.471	0.458	0.500	0.818	0.528	0.550	0.324	0.457	0.324	0.324	0.500
chrB4_142658074	A	G	0.137	0.175	0.115	0.600	0.045	0.143	0.233	0.553	0.265	0.026	0.273	0.071	0.167	0.088	0.000	0.412	0.000	0.053	0.206	0.333
chrB4_143006494	A	G	0.254	0.220	0.273	0.000	0.808	0.100	0.500	0.000	0.059	0.059	0.045	0.067	0.154	0.147	0.222	0.618	0.000	0.206	0.469	0.531
chrB4_144693308	G	A	0.390	0.401	0.380	0.385	0.773	0.667	0.367	0.947	0.194	0.889	0.292	0.321	0.107	0.158	0.636	0.206	1.000	0.324	0.529	0.219
chrB4_146486983	T	C	0.278	0.273	0.282	0.750	0.000	0.786	0.029	0.025	0.133	0.737	0.125	0.033	0.154	0.053	0.700	0.278	0.896	0.111	0.088	0.000

Table 2a - Intergenic SNP minor allele frequencies by breed and population.

			Minor Allele Frequency																		
	Major Allele	Minor Allele	Total	Total Breeds	Total Random Bred	Abyssinian	American SH	Australian Mist	Bengal	Birman	British SH	Burmese	Chartreux	Cornish Rex	Egyptian Mau	Exotic SH	Havana Brown	Japanese Bob.	Korat	Maine Coon	Manx	Norwegian FC
chrB4_147206961	T	C	0.382	0.446	0.354	0.679	0.050	0.750	0.194	0.235	0.115	0.778	0.450	0.600	0.273	0.143	0.808	0.321	0.896	0.208	0.235	0.200
chrB4_149532846	C	T	0.074	0.125	0.050	0.767	0.000	0.071	0.406	0.000	0.333	0.000	0.042	0.036	0.107	0.053	0.000	0.281	0.042	0.194	0.118	0.088
chrB4_1687419	C	T	0.057	0.024	0.077	0.000	0.000	0.000	0.031	0.000	0.028	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.056	0.031	0.294
chrB4_20001848	T	C	0.030	0.058	0.018	0.433	0.038	0.107	0.382	0.000	0.000	0.028	0.000	0.000	0.045	0.000	0.000	0.028	0.000	0.412	0.000	0.059
chrB4_21098349	C	T	0.406	0.479	0.376	0.750	0.708	0.300	0.375	0.125	0.844	0.389	1.000	0.607	0.182	0.567	0.077	0.447	0.000	0.618	0.781	0.676
chrB4_255106	G	A	0.063	0.095	0.047	0.400	0.250	0.000	0.321	0.000	0.029	0.000	0.364	0.250	0.038	0.206	0.000	0.000	0.000	0.088	0.059	0.028
chrB4_3093827	C	T	0.132	0.227	0.086	0.333	0.000	0.714	0.444	0.083	0.063	0.526	0.083	0.107	0.000	0.000	0.923	0.000	0.636	0.079	0.059	0.000
chrB4_40319102	C	T	0.546	0.478	0.578	0.393	0.167	0.786	0.647	0.421	0.438	0.778	0.000	0.633	0.625	0.559	0.955	0.781	0.222	0.353	0.206	0.294
chrB4_47638578	A	G	0.055	0.101	0.032	0.033	0.038	0.000	0.083	0.000	0.278	0.000	0.038	0.000	0.000	0.412	0.000	0.000	0.000	0.250	0.235	0.111
chrC1_116355295	C	T	0.272	0.295	0.258	0.167	0.154	0.267	0.118	0.525	0.294	0.158	0.346	0.000	0.042	0.158	0.000	0.184	0.413	0.618	0.647	0.500
chrC1_123164748	C	T	0.217	0.233	0.212	0.923	0.192	0.033	0.600	0.000	0.083	0.158	0.577	0.300	0.538	0.263	0.038	0.000	0.400	0.083	0.063	0.206
chrC1_181852965	G	A	0.216	0.301	0.156	0.278	0.417	0.400	0.438	0.115	0.556	0.167	0.214	0.500	0.200	0.542	0.444	0.400	0.029	0.423	0.063	0.167
chrC1_190502133	G	A	0.241	0.146	0.291	0.133	0.231	0.000	0.056	0.025	0.333	0.028	0.900	0.167	0.538	0.194	0.000	0.026	0.000	0.211	0.176	0.056
chrC1_215441574	C	A	0.374	0.430	0.348	0.267	0.154	0.615	0.647	0.118	0.176	0.763	0.417	0.857	0.808	0.605	0.091	0.344	0.455	0.118	0.559	0.250
chrC1_216852686	G	A	0.326	0.353	0.314	0.857	0.364	0.214	0.265	0.050	0.324	0.029	0.208	0.000	0.864	0.605	0.000	0.318	0.020	0.531	0.500	0.357
chrC1_24148281	T	C	0.202	0.198	0.206	0.033	0.231	0.143	0.147	0.075	0.406	0.053	0.308	0.321	0.036	0.132	0.792	0.000	0.000	0.735	0.382	0.222
chrC1_28702055	G	T	0.070	0.091	0.060	0.000	0.077	0.000	0.000	0.000	0.324	0.000	0.038	0.000	0.000	0.026	0.000	0.079	0.080	0.472	0.088	0.281
chrC1_34981315	A	G	0.043	0.044	0.043	0.000	0.038	0.067	0.028	0.000	0.000	0.026	0.000	0.000	0.000	0.000	0.000	0.000	0.042	0.000	0.118	0.036
chrC1_396397	G	A	0.254	0.269	0.244	0.000	0.292	0.367	0.471	0.579	0.500	0.079	0.273	0.615	0.179	0.447	0.000	0.222	0.000	0.267	0.344	0.324
chrC1_44520932	C	T	0.074	0.087	0.068	0.133	0.208	0.000	0.375	0.000	0.118	0.079	0.200	0.000	0.179	0.026	0.000	0.059	0.000	0.000	0.094	0.056
chrC1_52456776	G	A	0.477	0.510	0.459	0.000	0.808	0.385	0.438	0.938	0.556	0.467	0.167	0.767	0.393	0.711	0.458	0.692	0.696	0.500	0.469	0.393
chrC2_106991233	C	T	0.278	0.248	0.294	0.100	0.154	0.600	0.250	0.111	0.029	0.816	0.000	0.067	0.071	0.147	0.458	0.053	0.370	0.263	0.235	0.235
chrC2_147124460	T	C	0.377	0.327	0.404	0.733	0.115	0.429	0.500	0.079	0.333	0.105	0.417	0.467	0.769	0.105	0.545	0.579	0.021	0.316	0.559	0.361
chrC2_150774106	A	G	0.062	0.090	0.049	0.033	0.000	0.000	0.188	0.000	0.028	0.000	0.192	0.000	0.464	0.079	0.000	0.000	0.000	0.167	0.094	0.176
chrC2_156491175	T	C	0.479	0.463	0.488	0.250	0.346	0.800	0.500	0.158	0.444	0.722	0.500	0.067	0.071	0.219	0.909	0.618	0.760	0.294	0.294	0.267
chrC2_187325	C	A	0.193	0.195	0.192	0.433	0.136	0.464	0.353	0.265	0.029	0.579	0.000	0.357	0.042	0.028	0.727	0.033	0.150	0.059	0.000	0.063
chrC2_262401	G	A	0.264	0.299	0.245	0.467	0.083	0.714	0.441	0.350	0.111	0.947	0.000	0.429	0.036	0.026	0.808	0.176	0.913	0.265	0.029	0.031
chrC2_5215469	T	C	0.405	0.327	0.436	0.533	0.000	0.633	0.083	0.925	0.059	0.895	0.000	0.107	0.091	0.079	1.000	0.375	0.958	0.088	0.000	0.059

Table 2a - Intergenic SNP minor allele frequencies by breed and population.

	Major Allele	Minor Allele	Minor Allele Frequency																			
			Total	Total Breeds	Total Random Bred	Abyssinian	American SH	Australian Mist	Bengal	Birman	British SH	Burmese	Chartreux	Cornish Rex	Egyptian Mau	Exotic SH	Havana Brown	Japanese Bob.	Korat	Maine Coon	Manx	Norwegian FC
chrD1_101321498	A	G	0.315	0.399	0.276	0.700	0.708	0.321	0.036	0.206	0.611	0.053	0.708	0.300	0.385	0.579	0.000	0.222	0.048	0.658	0.500	0.765
chrD1_104941557	C	T	0.119	0.091	0.134	0.267	0.125	0.033	0.250	0.000	0.088	0.026	0.083	0.000	0.077	0.132	0.083	0.139	0.000	0.111	0.059	0.088
chrD1_105498119	T	C	0.121	0.144	0.109	0.179	0.042	0.033	0.382	0.083	0.281	0.000	0.462	0.200	0.000	0.342	0.038	0.000	0.020	0.105	0.176	0.200
chrD1_10789012	G	A	0.330	0.319	0.339	0.300	0.077	0.433	0.139	0.000	0.333	0.235	0.038	0.100	0.115	0.289	0.308	0.306	0.523	0.588	0.294	0.389
chrD1_11484008	C	T	0.138	0.076	0.170	0.133	0.000	0.000	0.038	0.000	0.000	0.026	0.000	0.071	0.107	0.026	0.250	0.235	0.159	0.000	0.000	0.059
chrD1_117527468	G	A	0.021	0.039	0.013	0.000	0.308	0.000	0.000	0.000	0.059	0.000	0.000	0.000	0.000	0.176	0.000	0.000	0.000	0.237	0.000	0.059
chrD1_125811329	G	A	0.243	0.313	0.205	0.133	0.500	0.233	0.441	0.500	0.222	0.395	0.143	0.333	0.250	0.219	0.500	0.206	0.955	0.214	0.313	0.265
chrD1_126256993	T	C	0.299	0.381	0.259	0.467	0.115	0.321	0.133	0.289	0.265	0.789	0.350	0.200	0.115	0.289	0.923	0.176	0.960	0.088	0.176	0.300
chrD1_126847301	T	C	0.086	0.086	0.086	0.033	0.269	0.167	0.029	0.265	0.056	0.026	0.000	0.542	0.000	0.000	0.000	0.375	0.000	0.029	0.038	0.118
chrD1_15984279	A	G	0.193	0.213	0.185	0.250	0.538	0.192	0.100	0.059	0.028	0.105	0.577	0.038	0.077	0.053	0.250	0.132	0.214	0.306	0.294	0.333
chrD1_16242433	G	A	0.284	0.337	0.263	0.227	0.150	0.650	0.294	0.105	0.083	0.731	0.200	0.455	0.083	0.393	0.417	0.333	0.375	0.344	0.250	0.118
chrD1_18390852	A	G	0.148	0.230	0.110	0.733	0.308	0.033	0.031	0.025	0.594	0.053	0.455	0.033	0.107	0.528	0.000	0.000	0.000	0.083	0.471	0.206
chrD1_18570323	A	G	0.401	0.370	0.412	0.167	0.385	0.067	0.441	0.842	0.278	0.211	0.455	0.500	0.538	0.316	0.917	0.382	0.600	0.441	0.367	0.333
chrD1_66177762	G	A	0.101	0.121	0.091	0.167	0.308	0.000	0.056	0.000	0.222	0.026	0.269	0.033	0.429	0.132	0.000	0.079	0.000	0.447	0.294	0.194
chrD2_1020904	A	G	0.466	0.336	0.531	0.100	0.346	0.500	0.471	0.150	0.194	0.711	0.038	0.214	0.321	0.605	0.231	0.313	0.140	0.389	0.382	0.294
chrD2_105772916	A	G	0.306	0.356	0.275	0.033	0.115	0.538	0.294	0.825	0.167	0.737	0.227	0.067	0.269	0.053	0.917	0.118	0.680	0.056	0.156	0.139
chrD2_1752007	G	A	0.131	0.182	0.108	0.333	0.038	0.375	0.111	0.000	0.000	0.342	0.000	0.133	0.000	0.079	0.875	0.235	0.200	0.250	0.029	0.059
chrD2_56777338	C	T	0.004	0.013	0.000	0.233	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.000	0.000	0.000
chrD2_717969	C	T	0.404	0.518	0.340	0.633	0.458	0.143	0.382	0.972	0.324	0.737	0.042	0.464	0.269	0.194	0.958	0.583	0.913	0.500	0.235	0.406
chrD2_74293444	C	T	0.195	0.191	0.197	0.000	0.167	0.071	0.029	0.158	0.056	0.158	0.000	0.615	0.731	0.194	0.227	0.056	0.208	0.139	0.313	0.324
chrD2_91989307	G	A	0.066	0.100	0.050	0.467	0.000	0.367	0.028	0.000	0.000	0.000	0.154	0.100	0.000	0.105	0.833	0.147	0.000	0.056	0.094	0.059
chrD3_103840114	C	T	0.042	0.054	0.036	0.100	0.038	0.033	0.000	0.000	0.056	0.000	0.038	0.000	0.269	0.000	0.000	0.000	0.000	0.000	0.000	0.000
chrD3_122502120	G	T	0.230	0.184	0.248	0.467	0.038	0.346	0.028	0.694	0.029	0.278	0.182	0.357	0.000	0.211	0.292	0.125	0.786	0.056	0.156	0.188
chrD3_1810839	T	G	0.349	0.405	0.319	0.923	0.545	0.250	0.179	0.167	0.471	0.278	0.350	0.714	0.458	0.500	0.000	0.300	0.000	0.767	0.600	0.692
chrD3_24565823	G	A	0.081	0.156	0.044	0.367	0.423	0.100	0.028	0.000	0.559	0.000	0.231	0.233	0.000	0.184	0.000	0.000	0.000	0.289	0.324	0.353
chrD3_24823793	C	G	0.193	0.132	0.224	0.000	0.038	0.133	0.000	0.225	0.028	0.342	0.269	0.500	0.000	0.079	0.818	0.079	0.326	0.026	0.059	0.056
chrD3_28838660	T	C	0.082	0.139	0.053	0.000	0.000	0.000	0.000	0.447	0.000	0.389	0.042	0.267	0.000	0.000	0.077	0.083	0.800	0.000	0.000	0.000
chrD4_41078218	A	C	0.448	0.430	0.456	0.071	0.500	0.083	0.406	0.579	0.125	0.206	0.364	0.821	0.417	0.605	0.364	0.567	0.412	0.658	0.536	0.324

Table 2a - Intergenic SNP minor allele frequencies by breed and population.

			Minor Allele Frequency																		
	Major Allele	Minor Allele	Total	Total Breeds	Total Random Bred	Abyssinian	American SH	Australian Mist	Bengal	Birman	British SH	Burmese	Chartreux	Cornish Rex	Egyptian Mau	Exotic SH	Havana Brown	Japanese Bob.	Korat	Maine Coon	Manx	Norwegian FC
chrD4_42000379	G	C	0.081	0.106	0.069	0.000	0.000	0.536	0.441	0.000	0.033	0.395	0.000	0.000	0.042	0.000	0.000	0.000	0.000	0.000	0.125	0.156
chrD4_63622083	G	A	0.138	0.198	0.111	0.308	0.750	0.100	0.000	0.083	0.176	0.056	0.500	0.633	0.179	0.353	0.000	0.028	0.022	0.028	0.375	0.367
chrE1_130875919	C	A	0.125	0.134	0.123	0.038	0.269	0.033	0.000	0.000	0.111	0.000	0.038	0.600	0.375	0.079	0.000	0.324	0.000	0.406	0.206	0.400
chrE1_131587399	G	A	0.089	0.143	0.056	0.071	0.385	0.536	0.100	0.500	0.528	0.000	0.450	0.100	0.036	0.211	0.154	0.028	0.000	0.184	0.000	0.194
chrE1_3912105	G	T	0.170	0.249	0.132	0.467	0.375	0.143	0.111	0.147	0.417	0.079	0.778	0.200	0.143	0.237	0.000	0.029	0.109	0.306	0.176	0.265
chrE1_4114158	g	t	0.477	0.499	0.467	0.400	0.417	0.433	0.083	0.000	0.056	0.316	0.000	0.300	0.500	0.000	0.731	0.105	0.521	0.063	0.094	0.028
chrE1_48228153	C	A	0.218	0.254	0.202	0.400	0.417	0.433	0.083	0.000	0.056	0.316	0.000	0.300	0.500	0.000	0.731	0.105	0.521	0.063	0.094	0.028
chrE1_48700963	A	T	0.062	0.093	0.048	0.733	0.000	0.143	0.088	0.000	0.111	0.000	0.000	0.100	0.077	0.056	0.000	0.000	0.000	0.278	0.294	0.206
chrE1_5453028	G	A	0.312	0.352	0.296	0.214	0.731	0.267	0.559	0.000	0.353	0.000	0.231	0.200	0.679	0.474	0.192	0.444	0.020	0.278	0.600	0.667
chrE2_22632289	G	A	0.439	0.411	0.449	0.750	0.731	0.385	0.688	0.861	0.382	0.079	0.308	0.115	0.346	0.441	0.708	0.389	0.545	0.184	0.206	0.250
chrE2_34027888	G	A	0.082	0.155	0.044	0.000	0.125	0.038	0.031	0.447	0.528	0.237	0.462	0.300	0.083	0.694	0.000	0.026	0.000	0.028	0.250	0.083
chrE2_35914023	C	T	0.215	0.195	0.226	0.700	0.417	0.033	0.028	0.000	0.118	0.026	0.038	0.200	0.143	0.000	0.038	0.563	0.043	0.056	0.688	0.444
chrE2_36986631	G	T	0.435	0.438	0.433	0.300	0.346	0.286	0.353	0.579	0.618	0.361	0.636	0.633	0.500	0.763	0.269	0.400	0.440	0.053	0.500	0.333
chrE2_38860686	C	T	0.132	0.188	0.106	0.667	0.423	0.214	0.118	0.000	0.088	0.026	0.227	0.500	0.125	0.222	0.000	0.139	0.022	0.211	0.429	0.250
chrE2_39211557	C	T	0.424	0.434	0.418	0.389	0.722	0.000	0.375	0.667	0.542	0.056	0.750	0.583	0.750	0.429	0.083	0.455	0.269	0.533	0.545	0.346
chrE2_65436639	C	T	0.277	0.296	0.267	0.567	0.308	0.533	0.222	0.194	0.056	0.556	0.167	0.393	0.321	0.211	0.885	0.105	0.313	0.250	0.235	0.250
chrE2_7950477	C	A	0.516	0.518	0.513	0.167	0.750	0.654	0.500	0.639	0.250	0.722	0.346	0.667	0.269	0.676	0.308	0.643	0.550	0.733	0.594	0.417
chrE2_8422942	A	G	0.082	0.050	0.098	0.133	0.000	0.000	0.000	0.000	0.000	0.000	0.273	0.214	0.000	0.000	0.000	0.000	0.020	0.028	0.029	0.200
chrE3_36044809	G	A	0.374	0.263	0.428	0.100	0.269	0.100	0.088	0.361	0.472	0.139	0.077	0.600	0.179	0.556	0.182	0.382	0.271	0.211	0.118	0.412
chrE3_55434272	C	T	0.347	0.361	0.341	0.800	0.417	0.107	0.094	0.200	0.306	0.026	0.462	0.000	0.077	0.441	0.625	0.667	0.217	0.500	0.441	0.300
chrE3_67006512	C	T	0.115	0.160	0.093	0.071	0.208	0.033	0.036	0.000	0.536	0.031	0.423	0.536	0.042	0.188	0.000	0.167	0.000	0.235	0.281	0.188
chrF1_20309325	G	A	0.085	0.127	0.065	0.367	0.000	0.000	0.235	0.200	0.000	0.278	0.000	0.067	0.375	0.026	0.615	0.000	0.083	0.026	0.029	0.000
chrF1_21799641	C	T	0.163	0.230	0.130	0.333	0.077	0.750	0.188	0.150	0.056	0.500	0.250	0.033	0.250	0.158	0.208	0.139	0.000	0.306	0.344	0.375
chrF1_26100599	A	T	0.220	0.308	0.180	0.133	0.292	0.167	0.139	0.079	0.433	0.143	0.154	0.308	0.038	0.289	0.292	0.571	0.152	0.237	0.406	0.531
chrF1_27124984	C	T	0.316	0.271	0.336	0.367	0.000	0.654	0.361	0.675	0.000	0.158	0.000	0.133	0.429	0.053	0.542	0.294	0.980	0.132	0.118	0.147
chrF1_38051725	A	G	0.470	0.448	0.480	0.167	0.308	0.733	0.188	0.417	0.639	0.395	0.538	0.567	0.536	0.417	0.615	0.206	0.500	0.139	0.607	0.471
chrF1_565223	G	A	0.496	0.529	0.483	0.107	0.154	0.500	0.676	0.368	0.694	0.684	0.417	0.538	0.821	0.184	0.400	0.471	0.500	0.342	0.471	0.656
chrF1_82068276	G	T	0.216	0.361	0.143	0.269	0.318	0.133	0.375	0.139	0.375	0.529	0.682	0.133	0.682	0.357	1.000	0.111	0.900	0.100	0.094	0.176

Table 2a - Intergenic SNP minor allele frequencies by breed and population.

			Minor Allele Frequency																			
	Major Allele	Minor Allele	Total	Total Breeds	Total Random Bred	Abyssinian	American SH	Australian Mist	Bengal	Birman	British SH	Burmese	Chartreux	Cornish Rex	Egyptian Mau	Exotic SH	Havana Brown	Japanese Bob.	Korat	Maine Coon	Manx	Norwegian FC
chrF1_82716202	C	A	0.196	0.181	0.204	0.067	0.038	0.067	0.389	0.026	0.222	0.000	0.333	0.067	0.269	0.139	0.000	0.029	0.000	0.395	0.471	0.361
chrF1_91517402	C	T	0.188	0.173	0.192	0.467	0.308	0.100	0.133	0.447	0.333	0.079	0.250	0.067	0.077	0.250	0.154	0.105	0.000	0.147	0.235	0.118
chrF2_26886470	G	A	0.298	0.322	0.282	0.100	0.115	0.607	0.059	0.650	0.361	0.889	0.417	0.000	0.000	0.361	0.875	0.194	0.739	0.000	0.088	0.059
chrF2_38395360	C	T	0.295	0.319	0.285	0.167	0.269	0.357	0.313	0.053	0.778	0.000	0.545	0.607	0.091	0.868	0.045	0.194	0.000	0.278	0.500	0.389
chrF2_46855978	T	C	0.329	0.359	0.314	0.333	0.385	0.367	0.156	0.342	0.313	0.441	0.182	0.233	0.357	0.474	0.500	0.316	0.457	0.263	0.375	0.324
chrF2_68572596	G	A	0.291	0.241	0.309	0.033	0.115	0.233	0.194	0.912	0.029	0.656	0.077	0.000	0.423	0.158	0.909	0.026	0.471	0.118	0.088	0.139
chrF2_74863327	G	A	0.253	0.264	0.249	0.267	0.083	0.567	0.294	0.132	0.206	0.316	0.167	0.200	0.321	0.105	0.682	0.118	0.340	0.053	0.147	0.139
chrF2_78303221	T	C	0.475	0.401	0.517	0.600	0.538	0.214	0.412	0.025	0.722	0.028	0.500	0.000	0.750	0.765	0.077	0.579	0.125	0.278	0.647	0.389
chrF2_79632602	G	C	0.026	0.039	0.019	0.100	0.000	0.000	0.000	0.000	0.111	0.000	0.000	0.200	0.000	0.211	0.000	0.000	0.000	0.028	0.029	0.000
chrF2_8427817	A	G	0.402	0.475	0.374	0.692	0.600	0.167	0.154	0.200	0.567	0.500	0.571	0.577	0.222	0.462	0.045	0.750	0.423	0.346	0.500	0.577

Table 2b - Intergenic SNP minor allele frequencies by breed and population.

			Minor Allele Frequency																				
	Major Allele	Minor Allele	Ocicat	Persian	Ragdoll	Russian Blue	Scottish Fold	Siamese	Siberian	Singapura	Sokoke	Sphynx	Turkish Angora	Turkish Van	Europe	East Med. Basin	Egypt	Iraq/Iran	Arabian Sea	India	South Asia	East Asia
chrA1_10141047	A	G	0.000	0.033	0.000	0.100	0.029	0.000	0.286	0.000	0.000	0.000	0.237	0.294	0.11	0.28	0.31	0.26	0.10	0.04	0.10	0.03
chrA1_133621071	C	T	0.250	0.333	0.600	0.000	0.529	0.000	0.133	0.029	0.000	0.559	0.143	0.184	0.304	0.222	0.309	0.283	0.189	0.316	0.129	0.108
chrA1_151648701	G	A	0.050	0.067	0.200	0.028	0.000	0.000	0.033	0.500	0.000	0.147	0.026	0.000	0.120	0.063	0.056	0.013	0.027	0.023	0.000	0.058
chrA1_175780586	G	A	0.833	0.400	0.357	0.382	0.794	0.767	0.462	0.563	0.250	0.433	0.333	0.618	0.423	0.410	0.299	0.085	0.088	0.162	0.581	0.363
chrA1_208054462	C	G	0.611	0.200	0.367	0.200	0.294	0.000	0.071	0.000	0.000	0.559	0.190	0.139	0.142	0.138	0.182	0.013	0.014	0.055	0.125	0.090

Table 2b - Intergenic SNP minor allele frequencies by breed and population.

	Major Allele	Minor Allele	Minor Allele Frequency																			
			Ocicat	Persian	Ragdoll	Russian Blue	Scottish Fold	Siamese	Siberian	Singapura	Sokoke	Sphynx	Turkish Angora	Turkish Van	Europe	East Med. Basin	Egypt	Iraq/Iran	Arabian Sea	India	South Asia	East Asia
chrA1_223501140	A	G	0.222	0.100	0.067	0.333	0.118	0.267	0.071	0.588	0.000	0.219	0.147	0.075	0.162	0.082	0.074	0.039	0.111	0.167	0.076	0.100
chrA1_223506906	A	G	0.000	0.000	0.033	0.000	0.000	0.000	0.091	0.625	0.000	0.179	0.194	0.147	0.154	0.195	0.329	0.367	0.708	0.425	0.183	0.529
chrA1_225057933	C	A	0.111	0.067	0.267	0.056	0.029	0.133	0.133	0.000	0.000	0.000	0.190	0.132	0.221	0.218	0.284	0.401	0.000	0.259	0.139	0.437
chrA1_235579538	G	A	0.000	0.036	0.036	0.000	0.000	0.033	0.036	0.000	0.071	0.059	0.000	0.132	0.054	0.144	0.090	0.299	0.324	0.125	0.056	0.071
chrA1_27523501	C	A	0.150	0.267	0.733	0.735	0.382	0.800	0.667	0.531	0.000	0.406	0.667	0.700	0.426	0.628	0.636	0.745	0.568	0.649	0.786	0.563
chrA1_68485376	A	G	0.000	0.107	0.067	0.000	0.118	0.000	0.067	0.000	0.000	0.235	0.053	0.184	0.141	0.076	0.009	0.000	0.000	0.006	0.015	0.014
chrA1_69424718	C	T	0.000	0.500	0.400	0.433	0.118	0.367	0.500	0.000	0.143	0.088	0.316	0.556	0.292	0.343	0.332	0.755	0.542	0.335	0.412	0.322
chrA1_7429296	C	T	0.050	0.167	0.100	0.000	0.382	0.000	0.000	0.000	0.375	0.533	0.105	0.028	0.183	0.150	0.161	0.244	0.581	0.296	0.028	0.125
chrA1_8742286	G	T	0.650	0.033	0.167	0.611	0.000	0.400	0.267	0.031	0.500	0.353	0.250	0.250	0.273	0.406	0.426	0.683	0.257	0.476	0.514	0.303
chrA2_152258936	T	C	0.833	0.333	0.600	0.853	0.324	0.333	0.357	1.000	0.714	0.567	0.711	0.361	0.409	0.399	0.319	0.565	0.446	0.314	0.471	0.182
chrA2_201526186	C	T	0.050	0.233	0.200	0.000	0.206	0.000	0.133	0.176	0.000	0.412	0.214	0.361	0.207	0.156	0.269	0.161	0.176	0.253	0.103	0.104
chrA2_202225770	C	T	0.650	0.633	0.333	0.094	0.324	0.733	0.308	0.107	0.000	0.563	0.300	0.375	0.317	0.319	0.232	0.203	0.108	0.440	0.672	0.338
chrA2_44241149	G	T	0.000	0.000	0.000	0.000	0.000	0.000	0.067	0.000	0.000	0.000	0.000	0.000	0.062	0.016	0.009	0.006	0.000	0.017	0.014	0.003
chrA2_554046	T	C	0.050	0.000	0.200	0.111	0.059	0.000	0.133	0.000	0.000	0.147	0.150	0.053	0.133	0.169	0.217	0.186	0.027	0.144	0.028	0.236
chrA3_101420069	T	G	0.000	0.000	0.000	0.000	0.000	0.000	0.200	0.000	0.000	0.118	0.000	0.000	0.056	0.057	0.065	0.000	0.054	0.087	0.000	0.061
chrA3_11480952	C	T	0.000	0.000	0.000	0.000	0.029	0.000	0.067	0.000	0.000	0.059	0.024	0.000	0.053	0.021	0.027	0.000	0.014	0.000	0.048	0.054
chrA3_12082294	G	A	0.313	0.467	0.300	0.400	0.406	0.000	0.286	0.833	0.000	0.118	0.071	0.225	0.336	0.171	0.252	0.126	0.095	0.063	0.103	0.119
chrA3_130195244	T	C	0.222	0.038	0.100	0.077	0.059	0.167	0.115	0.192	0.700	0.156	0.179	0.059	0.199	0.284	0.368	0.075	0.111	0.124	0.138	0.096
chrA3_159537633	G	C	0.050	0.333	0.433	0.222	0.176	0.233	0.367	0.088	0.000	0.344	0.475	0.825	0.472	0.595	0.650	0.699	0.405	0.506	0.243	0.481
chrA3_162208567	C	G	0.167	0.786	0.200	0.441	0.794	0.000	0.536	0.100	0.000	0.594	0.382	0.250	0.377	0.194	0.196	0.260	0.068	0.064	0.016	0.139
chrA3_38781591	G	A	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.158	0.053	0.022	0.016	0.004	0.006	0.000	0.011	0.000	0.000
chrA3_75156179	G	A	0.350	0.000	0.467	0.281	0.118	0.000	0.467	0.233	0.000	0.267	0.333	0.605	0.266	0.375	0.348	0.243	0.068	0.127	0.069	0.167
chrA3_91058022	A	C	0.313	0.433	0.633	0.233	0.147	0.133	0.633	0.706	0.786	0.294	0.625	0.342	0.484	0.256	0.241	0.104	0.230	0.106	0.121	0.165
chrA3_99507784	A	T	0.100	0.233	0.467	0.333	0.235	0.433	0.033	0.219	0.000	0.176	0.250	0.333	0.231	0.302	0.296	0.578	0.162	0.355	0.456	0.411
chrB1_10420438	C	T	0.444	0.267	0.333	0.000	0.125	0.000	0.167	0.000	0.500	0.118	0.071	0.025	0.104	0.082	0.034	0.023	0.027	0.034	0.014	0.033
chrB1_12214271	T	G	0.722	0.333	0.533	0.382	0.688	0.267	0.607	0.941	0.714	0.441	0.525	0.105	0.401	0.392	0.591	0.350	0.514	0.554	0.333	0.437
chrB1_195678303	T	C	0.056	0.067	0.133	0.500	0.029	0.033	0.143	0.000	0.667	0.088	0.175	0.132	0.102	0.258	0.230	0.358	0.351	0.116	0.071	0.107
chrB1_199564532	G	A	0.200	0.067	0.100	0.206	0.147	0.000	0.250	0.000	0.000	0.147	0.095	0.075	0.156	0.101	0.154	0.003	0.027	0.052	0.000	0.028
chrB1_202966562	C	T	0.100	0.400	0.267	0.833	0.382	0.167	0.462	0.125	0.000	0.500	0.250	0.316	0.381	0.263	0.198	0.183	0.149	0.184	0.235	0.175

Table 2b - Intergenic SNP minor allele frequencies by breed and population.

			Minor Allele Frequency																			
	Major Allele	Minor Allele	Ocicat	Persian	Ragdoll	Russian Blue	Scottish Fold	Siamese	Siberian	Singapura	Sokoke	Sphynx	Turkish Angora	Turkish Van	Europe	East Med. Basin	Egypt	Iraq/Iran	Arabian Sea	India	South Asia	East Asia
chrB1_54775572	G	A	0.000	0.100	0.033	0.059	0.176	0.000	0.000	0.324	0.000	0.059	0.190	0.075	0.188	0.204	0.135	0.059	0.216	0.000	0.097	0.028
chrB1_80161671	G	A	0.000	0.231	0.000	0.036	0.594	0.033	0.222	0.583	0.000	0.147	0.056	0.028	0.169	0.096	0.058	0.241	0.068	0.122	0.097	0.069
chrB1_88148379	T	C	0.150	0.267	0.567	0.265	0.382	0.500	0.643	0.235	0.333	0.156	0.525	0.605	0.360	0.477	0.483	0.443	0.622	0.369	0.182	0.371
chrB2_138312489	G	A	0.400	0.433	0.800	0.433	0.353	0.567	0.400	0.125	0.750	0.735	0.275	0.750	0.422	0.462	0.422	0.282	0.284	0.698	0.700	0.482
chrB2_146660650	C	T	0.050	0.000	0.000	0.000	0.000	0.000	0.000	0.467	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.014	0.034	0.139	0.010
chrB2_41509834	G	A	0.333	0.233	0.600	0.000	0.000	0.833	0.269	0.857	0.714	0.412	0.605	0.400	0.278	0.257	0.155	0.624	0.351	0.464	0.614	0.489
chrB2_45093345	A	G	0.333	0.700	0.500	0.063	0.625	0.067	0.808	0.393	0.100	0.469	0.389	0.474	0.542	0.433	0.404	0.093	0.257	0.227	0.258	0.347
chrB2_6949528	G	A	0.000	0.467	0.000	0.083	0.324	0.000	0.214	0.000	0.000	0.029	0.262	0.100	0.201	0.195	0.111	0.029	0.149	0.029	0.014	0.070
chrB3_104483970	G	A	0.333	0.133	0.367	0.719	0.000	0.821	0.233	0.471	0.143	0.029	0.050	0.132	0.202	0.328	0.321	0.172	0.122	0.506	0.855	0.420
chrB3_111000326	A	G	0.222	0.133	0.033	0.333	0.029	0.567	0.067	0.206	0.000	0.000	0.025	0.100	0.111	0.200	0.261	0.171	0.149	0.333	0.676	0.260
chrB3_13666494	C	G	0.667	0.667	0.767	0.563	0.706	0.667	0.286	0.563	0.083	0.353	0.361	0.225	0.475	0.439	0.504	0.255	0.243	0.560	0.765	0.528
chrB3_39203469	G	A	0.000	0.200	0.067	0.393	0.147	0.000	0.036	0.000	0.083	0.219	0.333	0.294	0.184	0.378	0.625	0.211	0.108	0.071	0.100	0.138
chrB3_51317931	C	T	0.786	0.250	0.233	0.056	0.029	0.893	0.167	1.000	0.125	0.219	0.353	0.325	0.138	0.294	0.276	0.407	0.095	0.390	0.750	0.254
chrB3_57141954	G	C	0.350	0.571	0.667	0.882	0.471	0.067	0.533	0.767	0.000	0.531	0.324	0.588	0.377	0.173	0.171	0.242	0.230	0.137	0.069	0.281
chrB3_77094074	A	C	0.417	0.036	0.033	0.115	0.467	0.000	0.000	0.000	0.300	0.143	0.105	0.000	0.168	0.006	0.022	0.007	0.139	0.056	0.067	0.059
chrB4_105706694	T	C	0.056	0.533	0.433	0.344	0.265	0.733	0.286	0.176	0.786	0.500	0.417	0.250	0.374	0.410	0.397	0.480	0.459	0.585	0.371	0.628
chrB4_142658074	A	G	0.000	0.200	0.300	0.059	0.353	0.000	0.227	0.000	0.000	0.125	0.167	0.194	0.108	0.190	0.187	0.066	0.014	0.030	0.065	0.121
chrB4_143006494	A	G	0.050	0.167	0.733	0.029	0.088	0.000	0.462	0.000	0.000	0.469	0.105	0.139	0.338	0.344	0.345	0.243	0.097	0.110	0.074	0.261
chrB4_144693308	G	A	0.625	0.167	0.133	0.156	0.029	0.833	0.367	0.333	0.750	0.406	0.190	0.289	0.311	0.426	0.460	0.450	0.473	0.335	0.469	0.215
chrB4_146486983	T	C	0.050	0.033	0.067	0.528	0.156	0.767	0.269	0.433	0.000	0.029	0.200	0.075	0.193	0.194	0.124	0.288	0.541	0.134	0.641	0.568
chrB4_147206961	T	C	0.556	0.179	0.292	0.719	0.000	0.900	0.500	0.938	0.917	0.222	0.294	0.100	0.350	0.276	0.434	0.293	0.176	0.544	0.750	0.291
chrB4_149532846	C	T	0.200	0.000	0.233	0.000	0.324	0.000	0.115	0.063	0.000	0.067	0.000	0.025	0.126	0.056	0.030	0.016	0.014	0.023	0.057	0.026
chrB4_1687419	C	T	0.000	0.000	0.000	0.000	0.000	0.000	0.115	0.000	0.000	0.063	0.000	0.029	0.108	0.141	0.145	0.013	0.000	0.009	0.000	0.006
chrB4_20001848	T	C	0.000	0.000	0.000	0.000	0.063	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.046	0.008	0.000	0.003	0.000	0.029	0.029	0.014
chrB4_21098349	C	T	0.350	0.500	0.808	0.250	0.923	0.000	0.462	0.281	0.000	0.647	0.737	0.475	0.581	0.408	0.375	0.359	0.357	0.318	0.118	0.239
chrB4_255106	G	A	0.050	0.200	0.067	0.000	0.147	0.036	0.000	0.133	0.071	0.000	0.071	0.105	0.120	0.025	0.065	0.036	0.000	0.006	0.015	0.031
chrB4_3093827	C	T	0.400	0.033	0.000	0.900	0.088	0.800	0.000	0.219	0.000	0.063	0.000	0.000	0.109	0.046	0.055	0.000	0.041	0.071	0.452	0.161
chrB4_40319102	C	T	0.688	0.643	0.767	0.000	0.412	0.867	0.467	0.813	0.500	0.118	0.316	0.368	0.468	0.470	0.600	0.500	0.730	0.560	0.818	0.812
chrB4_47638578	A	G	0.100	0.367	0.067	0.000	0.559	0.000	0.115	0.000	0.000	0.029	0.048	0.026	0.086	0.038	0.004	0.006	0.000	0.017	0.014	0.031

Table 2b - Intergenic SNP minor allele frequencies by breed and population.

			Minor Allele Frequency																			
	Major Allele	Minor Allele	Ocicat	Persian	Ragdoll	Russian Blue	Scottish Fold	Siamese	Siberian	Singapura	Sokoke	Sphynx	Turkish Angora	Turkish Van	Europe	East Med. Basin	Egypt	Iraq/Iran	Arabian Sea	India	South Asia	East Asia
chrC1_116355295	C	T	0.500	0.233	0.200	0.000	0.500	0.500	0.300	0.265	0.000	0.206	0.350	0.667	0.332	0.262	0.272	0.203	0.284	0.320	0.235	0.155
chrC1_123164748	C	T	0.150	0.167	0.067	0.000	0.088	0.000	0.467	0.588	0.000	0.059	0.389	0.275	0.261	0.237	0.196	0.267	0.000	0.229	0.242	0.120
chrC1_181852965	G	A	0.500	0.400	0.500	0.125	0.417	0.125	0.167	0.591	0.000	0.308	0.136	0.000	0.406	0.108	0.167	0.022	0.000	0.113	0.056	0.239
chrC1_190502133	G	A	0.300	0.133	0.000	0.139	0.235	0.133	0.067	0.000	0.000	0.000	0.200	0.275	0.176	0.381	0.293	0.576	0.306	0.215	0.028	0.127
chrC1_215441574	C	A	0.056	0.700	0.367	0.118	0.265	0.200	0.462	1.000	0.125	0.588	0.206	0.583	0.394	0.346	0.272	0.235	0.459	0.323	0.574	0.389
chrC1_216852686	G	A	0.250	0.607	0.500	0.375	0.265	0.000	0.375	0.607	0.750	0.133	0.605	0.529	0.356	0.339	0.507	0.312	0.200	0.231	0.340	0.211
chrC1_24148281	T	C	0.063	0.133	0.333	0.029	0.324	0.000	0.385	0.000	0.000	0.281	0.059	0.147	0.180	0.222	0.209	0.247	0.292	0.324	0.059	0.116
chrC1_28702055	G	T	0.000	0.000	0.000	0.000	0.294	0.000	0.133	0.000	0.000	0.382	0.050	0.100	0.122	0.041	0.000	0.129	0.027	0.029	0.043	0.024
chrC1_34981315	A	G	0.000	0.000	0.000	0.706	0.000	0.067	0.000	0.000	0.000	0.000	0.025	0.000	0.046	0.050	0.099	0.000	0.000	0.012	0.103	0.040
chrC1_396397	G	A	0.050	0.467	0.433	0.000	0.281	0.000	0.357	0.000	0.333	0.235	0.528	0.325	0.392	0.313	0.425	0.139	0.230	0.109	0.030	0.096
chrC1_44520932	C	T	0.250	0.033	0.000	0.000	0.063	0.033	0.033	0.000	0.000	0.000	0.194	0.441	0.134	0.087	0.137	0.003	0.014	0.040	0.015	0.024
chrC1_52456776	G	A	0.750	0.714	0.400	0.281	0.719	0.400	0.192	0.643	0.125	0.643	0.467	0.214	0.342	0.352	0.454	0.747	0.569	0.506	0.529	0.331
chrC2_106991233	C	T	0.438	0.067	0.000	0.147	0.000	0.786	0.100	0.700	0.000	0.206	0.525	0.125	0.261	0.250	0.274	0.279	0.068	0.335	0.578	0.402
chrC2_147124460	T	C	0.444	0.200	0.067	0.647	0.324	0.000	0.321	0.000	0.750	0.147	0.238	0.472	0.516	0.492	0.556	0.416	0.568	0.362	0.186	0.086
chrC2_150774106	A	G	0.000	0.033	0.000	0.607	0.000	0.000	0.367	0.000	0.000	0.029	0.132	0.050	0.072	0.057	0.059	0.032	0.014	0.012	0.014	0.060
chrC2_156491175	T	C	0.786	0.433	0.167	0.765	0.412	0.200	0.464	1.000	0.600	0.545	0.405	0.447	0.381	0.408	0.307	0.672	0.662	0.667	0.313	0.565
chrC2_187325	C	A	0.450	0.038	0.143	0.029	0.000	0.567	0.000	0.429	0.300	0.071	0.105	0.000	0.105	0.195	0.289	0.168	0.216	0.211	0.383	0.185
chrC2_262401	G	A	0.444	0.067	0.133	0.059	0.094	0.333	0.107	0.531	0.571	0.059	0.125	0.306	0.188	0.283	0.277	0.122	0.153	0.280	0.591	0.283
chrC2_5215469	T	C	0.050	0.000	0.400	0.344	0.088	0.800	0.179	0.286	0.417	0.235	0.286	0.395	0.241	0.342	0.250	0.728	0.500	0.313	0.838	0.628
chrD1_101321498	A	G	0.250	0.607	0.000	0.618	0.765	0.100	0.462	0.000	0.643	0.500	0.375	0.368	0.441	0.279	0.281	0.258	0.432	0.134	0.061	0.186
chrD1_104941557	C	T	0.200	0.100	0.000	0.028	0.088	0.000	0.107	0.000	0.000	0.438	0.024	0.105	0.144	0.197	0.147	0.136	0.243	0.052	0.014	0.084
chrD1_105498119	T	C	0.000	0.231	0.033	0.472	0.156	0.000	0.100	0.000	0.000	0.324	0.095	0.100	0.182	0.094	0.180	0.040	0.081	0.177	0.042	0.046
chrD1_10789012	G	A	0.389	0.133	0.333	0.111	0.176	0.267	0.467	1.000	0.750	0.412	0.306	0.400	0.322	0.362	0.230	0.401	0.149	0.149	0.368	0.524
chrD1_11484008	C	T	0.167	0.067	0.000	0.176	0.000	0.133	0.000	0.250	0.071	0.088	0.156	0.025	0.068	0.073	0.044	0.178	0.189	0.247	0.081	0.471
chrD1_117527468	G	A	0.100	0.067	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.125	0.000	0.040	0.011	0.004	0.003	0.000	0.000	0.000	0.010
chrD1_125811329	G	A	0.167	0.133	0.233	0.094	0.059	0.633	0.192	0.733	0.500	0.206	0.150	0.200	0.308	0.151	0.206	0.096	0.324	0.169	0.518	0.172
chrD1_126256993	T	C	0.833	0.267	0.333	0.559	0.059	0.667	0.500	0.676	0.250	0.375	0.325	0.056	0.233	0.228	0.188	0.144	0.378	0.221	0.819	0.361
chrD1_126847301	T	C	0.000	0.000	0.000	0.000	0.059	0.179	0.115	0.000	0.000	0.147	0.000	0.147	0.100	0.137	0.218	0.010	0.054	0.052	0.043	0.011
chrD1_15984279	A	G	0.222	0.100	0.000	0.794	0.059	0.033	0.417	0.000	0.167	0.235	0.289	0.316	0.245	0.278	0.265	0.050	0.014	0.100	0.368	0.124

Table 2b - Intergenic SNP minor allele frequencies by breed and population.

	Major Allele	Minor Allele	Minor Allele Frequency																			
			Ocicat	Persian	Ragdoll	Russian Blue	Scottish Fold	Siamese	Siberian	Singapura	Sokoke	Sphynx	Turkish Angora	Turkish Van	Europe	East Med. Basin	Egypt	Iraq/Iran	Arabian Sea	India	South Asia	East Asia
chrD1_16242433	G	A	0.167	0.333	0.583	0.125	0.118	0.792	0.409	1.000	0.300	0.300	0.235	0.346	0.336	0.256	0.273	0.139	0.143	0.198	0.517	0.340
chrD1_18390852	A	G	0.167	0.300	0.233	0.056	0.765	0.067	0.292	0.563	0.000	0.200	0.175	0.105	0.223	0.171	0.111	0.006	0.108	0.080	0.000	0.066
chrD1_18570323	A	G	0.300	0.286	0.167	0.361	0.147	0.533	0.500	0.029	0.500	0.324	0.214	0.475	0.401	0.409	0.561	0.243	0.527	0.430	0.379	0.450
chrD1_66177762	G	A	0.000	0.300	0.000	0.028	0.294	0.000	0.033	0.000	0.000	0.029	0.048	0.075	0.161	0.112	0.104	0.010	0.097	0.052	0.014	0.095
chrD2_1020904	A	G	0.000	0.400	0.167	0.188	0.000	0.033	0.321	0.813	0.571	0.382	0.619	0.605	0.420	0.437	0.689	0.631	0.703	0.667	0.329	0.475
chrD2_105772916	A	G	0.600	0.143	0.167	0.969	0.176	0.933	0.267	0.500	0.500	0.250	0.357	0.395	0.192	0.272	0.372	0.284	0.338	0.412	0.426	0.154
chrD2_1752007	G	A	0.200	0.133	0.300	0.625	0.088	0.533	0.000	0.000	0.000	0.088	0.167	0.053	0.135	0.056	0.043	0.133	0.041	0.147	0.250	0.135
chrD2_56777338	C	T	0.150	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
chrD2_717969	C	T	0.643	0.167	0.667	0.906	0.471	0.933	0.200	0.563	0.250	0.781	0.368	0.658	0.402	0.252	0.542	0.256	0.136	0.432	0.719	0.195
chrD2_74293444	C	T	0.200	0.200	0.100	0.059	0.059	0.633	0.286	0.000	0.071	0.235	0.250	0.150	0.208	0.151	0.155	0.122	0.189	0.134	0.118	0.430
chrD2_91989307	G	A	0.100	0.067	0.133	0.029	0.118	0.200	0.000	0.000	0.000	0.031	0.050	0.000	0.133	0.041	0.065	0.013	0.041	0.029	0.014	0.025
chrD3_103840114	C	T	0.150	0.000	0.000	0.000	0.000	0.000	0.000	0.750	0.000	0.000	0.100	0.100	0.022	0.040	0.043	0.039	0.135	0.046	0.000	0.011
chrD3_122502120	G	T	0.100	0.143	0.000	0.000	0.000	0.133	0.067	0.118	0.071	0.125	0.275	0.075	0.176	0.236	0.243	0.313	0.392	0.310	0.313	0.194
chrD3_1810839	T	G	0.071	0.423	0.500	0.000	0.800	0.000	0.643	0.292	0.167	0.667	0.292	0.750	0.603	0.528	0.427	0.065	0.129	0.211	0.143	0.104
chrD3_24565823	G	A	0.250	0.267	0.333	0.000	0.235	0.100	0.033	0.059	0.000	0.176	0.024	0.026	0.151	0.024	0.030	0.003	0.000	0.023	0.028	0.035
chrD3_24823793	C	G	0.050	0.000	0.000	0.056	0.000	0.367	0.033	0.133	0.583	0.125	0.025	0.025	0.073	0.184	0.186	0.197	0.541	0.339	0.250	0.368
chrD3_28838660	T	C	0.100	0.033	0.067	0.147	0.000	0.200	0.036	0.679	0.500	0.094	0.000	0.000	0.022	0.011	0.009	0.000	0.041	0.100	0.343	0.127
chrD4_41078218	A	C	0.700	0.536	0.733	0.231	0.438	0.400	0.654	0.000	0.900	0.038	0.429	0.550	0.458	0.491	0.482	0.493	0.919	0.402	0.212	0.313
chrD4_42000379	G	C	0.000	0.033	0.200	0.233	0.000	0.000	0.000	0.000	0.000	0.324	0.167	0.139	0.077	0.134	0.106	0.038	0.014	0.078	0.015	0.011
chrD4_63622083	G	A	0.000	0.429	0.500	0.292	0.294	0.000	0.179	0.029	0.333	0.000	0.075	0.139	0.241	0.082	0.065	0.069	0.083	0.135	0.061	0.088
chrE1_130875919	C	A	0.000	0.233	0.000	0.000	0.088	0.000	0.067	0.000	0.000	0.250	0.225	0.083	0.271	0.103	0.303	0.013	0.000	0.061	0.061	0.032
chrE1_131587399	G	A	0.056	0.269	0.100	0.000	0.382	0.000	0.000	0.000	0.000	0.176	0.083	0.000	0.141	0.047	0.022	0.013	0.000	0.023	0.056	0.083
chrE1_3912105	G	T	0.500	0.200	0.233	0.000	0.618	0.367	0.200	0.467	0.214	0.000	0.324	0.450	0.199	0.076	0.097	0.123	0.405	0.092	0.074	0.120
chrE1_4114158	g	t	0.200	0.067	0.033	0.382	0.147	0.500	0.367	0.676	0.333	0.147	0.071	0.474	0.438	0.461	0.415	0.507	0.365	0.458	0.439	0.550
chrE1_48228153	C	A	0.200	0.067	0.033	0.382	0.147	0.500	0.367	0.676	0.333	0.147	0.071	0.474	0.205	0.196	0.147	0.145	0.176	0.198	0.530	0.223
chrE1_48700963	A	T	0.222	0.100	0.067	0.111	0.029	0.000	0.036	0.000	0.000	0.000	0.025	0.050	0.096	0.060	0.048	0.000	0.027	0.034	0.000	0.053
chrE1_5453028	G	A	0.000	0.286	0.400	0.278	0.471	0.067	0.462	0.000	1.000	0.647	0.633	0.350	0.522	0.376	0.435	0.211	0.284	0.157	0.029	0.071
chrE2_22632289	G	A	0.850	0.500	0.300	0.094	0.353	0.833	0.500	0.031	0.917	0.529	0.200	0.389	0.373	0.389	0.421	0.374	0.608	0.371	0.724	0.656
chrE2_34027888	G	A	0.000	0.433	0.167	0.156	0.265	0.000	0.033	0.000	0.000	0.000	0.026	0.025	0.059	0.022	0.089	0.000	0.000	0.076	0.014	0.063

Table 2b - Intergenic SNP minor allele frequencies by breed and population.

			Minor Allele Frequency																			
	Major Allele	Minor Allele	Ocicat	Persian	Ragdoll	Russian Blue	Scottish Fold	Siamese	Siberian	Singapura	Sokoke	Sphynx	Turkish Angora	Turkish Van	Europe	East Med. Basin	Egypt	Iraq/Iran	Arabian Sea	India	South Asia	East Asia
chrE2_35914023	C	T	0.167	0.000	0.000	0.278	0.059	0.033	0.600	0.118	0.083	0.107	0.306	0.333	0.275	0.241	0.152	0.050	0.292	0.194	0.181	0.431
chrE2_36986631	G	T	0.200	0.786	0.533	0.333	0.625	0.200	0.467	0.313	0.143	0.324	0.750	0.526	0.410	0.603	0.618	0.392	0.257	0.471	0.281	0.191
chrE2_38860686	C	T	0.150	0.133	0.133	0.056	0.735	0.000	0.179	0.000	0.500	0.059	0.139	0.000	0.297	0.049	0.039	0.090	0.081	0.059	0.015	0.094
chrE2_39211557	C	T	0.389	0.464	0.542	0.300	0.708	0.464	0.500	0.000	0.833	0.462	0.227	0.333	0.440	0.422	0.495	0.411	0.324	0.402	0.407	0.357
chrE2_65436639	C	T	0.500	0.067	0.233	0.000	0.088	0.400	0.133	0.938	0.071	0.235	0.176	0.325	0.227	0.298	0.283	0.330	0.189	0.310	0.147	0.216
chrE2_7950477	C	A	0.722	0.500	0.467	0.806	0.471	0.667	0.433	0.063	0.400	0.781	0.528	0.368	0.457	0.497	0.417	0.566	0.597	0.579	0.677	0.504
chrE2_8422942	A	G	0.050	0.000	0.133	0.028	0.000	0.033	0.000	0.029	0.000	0.000	0.139	0.184	0.078	0.064	0.066	0.320	0.054	0.017	0.028	0.053
chrE3_36044809	G	A	0.000	0.400	0.536	0.028	0.382	0.067	0.133	0.344	0.286	0.500	0.175	0.200	0.237	0.411	0.548	0.530	0.243	0.282	0.191	0.686
chrE3_55434272	C	T	0.250	0.500	0.600	0.471	0.412	0.333	0.583	0.000	0.100	0.633	0.553	0.211	0.385	0.383	0.421	0.039	0.324	0.317	0.303	0.538
chrE3_67006512	C	T	0.056	0.067	0.357	0.000	0.235	0.000	0.091	0.000	0.000	0.100	0.265	0.333	0.129	0.123	0.109	0.083	0.045	0.032	0.030	0.077
chrF1_20309325	G	A	0.056	0.067	0.233	0.028	0.000	0.667	0.000	0.029	0.000	0.029	0.071	0.306	0.075	0.081	0.022	0.076	0.097	0.034	0.069	0.050
chrF1_21799641	C	T	0.400	0.300	0.400	0.469	0.147	0.067	0.433	0.281	0.000	0.156	0.071	0.050	0.331	0.079	0.113	0.048	0.108	0.098	0.042	0.108
chrF1_26100599	A	T	0.750	0.400	0.567	0.176	0.353	0.167	0.714	0.286	0.000	0.176	0.417	0.605	0.356	0.194	0.068	0.072	0.189	0.167	0.186	0.170
chrF1_27124984	C	T	0.150	0.033	0.200	0.059	0.029	0.767	0.071	0.577	0.929	0.125	0.094	0.026	0.206	0.253	0.297	0.373	0.292	0.429	0.667	0.461
chrF1_38051725	A	G	0.444	0.286	0.400	0.882	0.382	0.333	0.633	0.250	0.000	0.500	0.675	0.500	0.541	0.644	0.671	0.317	0.122	0.305	0.530	0.434
chrF1_565223	G	A	0.550	0.179	0.733	0.361	0.706	0.750	0.692	0.824	0.417	0.563	0.632	0.600	0.463	0.438	0.425	0.463	0.608	0.536	0.471	0.601
chrF1_82068276	G	T	0.938	0.444	0.143	0.000	0.417	0.700	0.115	0.882	0.333	0.269	0.056	0.079	0.187	0.065	0.059	0.007	0.015	0.250	0.379	0.289
chrF1_82716202	C	A	0.000	0.250	0.167	0.853	0.206	0.067	0.107	0.000	0.000	0.324	0.132	0.026	0.288	0.191	0.125	0.339	0.243	0.100	0.100	0.124
chrF1_91517402	C	T	0.350	0.133	0.233	0.029	0.382	0.033	0.107	0.000	0.000	0.235	0.200	0.225	0.214	0.223	0.184	0.176	0.351	0.327	0.044	0.064
chrF2_26886470	G	A	0.444	0.133	0.433	0.344	0.118	0.833	0.143	0.781	0.750	0.235	0.024	0.100	0.104	0.153	0.104	0.459	0.405	0.494	0.591	0.390
chrF2_38395360	C	T	0.643	0.833	0.367	0.235	0.765	0.033	0.269	0.000	0.214	0.156	0.333	0.025	0.349	0.270	0.279	0.334	0.338	0.360	0.029	0.184
chrF2_46855978	T	C	0.125	0.433	0.500	0.433	0.382	0.433	0.433	0.500	0.200	0.219	0.389	0.316	0.332	0.280	0.309	0.229	0.392	0.407	0.444	0.310
chrF2_68572596	G	A	0.688	0.107	0.133	0.156	0.118	0.964	0.107	0.667	0.125	0.176	0.105	0.000	0.211	0.270	0.318	0.302	0.500	0.323	0.717	0.313
chrF2_74863327	G	A	0.650	0.133	0.400	0.194	0.088	0.433	0.200	0.618	0.071	0.206	0.119	0.553	0.181	0.278	0.282	0.171	0.122	0.306	0.338	0.336
chrF2_78303221	T	C	0.000	0.633	0.500	0.194	0.500	0.000	0.769	0.265	0.857	0.469	0.595	0.275	0.478	0.531	0.470	0.743	0.716	0.429	0.273	0.405
chrF2_79632602	G	C	0.000	0.167	0.000	0.063	0.125	0.000	0.000	0.000	0.000	0.059	0.000	0.000	0.025	0.011	0.004	0.062	0.000	0.006	0.000	0.007
chrF2_8427817	A	G	0.222	0.464	0.267	0.679	0.412	0.433	0.417	1.000	0.100	0.781	0.556	0.533	0.390	0.408	0.387	0.227	0.257	0.378	0.350	0.489

[0091] As appropriate, the genotypes of at least about 3, 5, 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 145, 148 or more, SNPs from Table 1 are determined. In some embodiments, the expression levels of all listed SNPs of SEQ ID NOs:1-148 listed in Table 1 are determined.

[0092] In addition to determination of the plurality of SNPs listed in Table 1, one or more morphological features and/or the genotype of one or more phenotypic markers can be determined. The morphologic and phenotypic markers can relate to hair length, coat color, coat texture, ear, paw and tail morphology, or a known disease marker. For example, the feline may be evaluated for coat color (*e.g.*, chocolate, cinnamon, dilute, orange, white), coat patterning (*e.g.*, agouti, tabby, spotted, ticked, calico, point coloring), coat texture (*e.g.*, straight or rex), coat length (*e.g.*, hairless, short or long), ear morphology (*e.g.*, normal, curled or folded, paw morphology (*e.g.*, normal or polydactyl), and tail morphology (*e.g.*, manx, bobtail, long). Such phenotypic and morphologic features can be evaluated by visual inspection and/or genetic analysis of the feline.

[0093] Some phenotypic markers can be evaluated by genetic analysis, without visual inspection of the feline. In various embodiments, the methods may further comprise determining the genotype of one or more phenotypic markers identified in Table 3, *i.e.*, as SEQ ID NOs:149-202.

[0094] As appropriate, the genotypes of at least about 3, 5, 10, 15, 20, 25, 30, 40, 50, or more, phenotypic markers, *e.g.*, listed in Table 3, are determined. In some embodiments, the expression levels of all listed phenotypic marker of SEQ ID NOs:149-202 are determined.

[0095] Genetic markers for phenotypic traits, especially traits that are breed specific, find use to distinguish genetically related feline populations. For example, Birman or Siamese are homozygous for the G940A TYR mutation. This same mutation would exclude a Havanna Brown from very closely related breeds, *e.g.*, Siamese, Birman and Himalayan. Colorpoints in the chocolate variety, such as Havana Brown, cannot be homozygous for the mutation. A Korat, Russian Blue or Charteux are by definition solid blue; therefore no other colors or patterns are present. Thus, the presence of mutations that would exhibit other patterns and colors would exclude a cat as one of these breeds.

[0096] A genetic marker for long hair, *e.g.*, the A475C *FGF5* mutation, can be used as a means for identifying members of the Persian, Maine Coon, Turkish Angora, Turkish

Van and Birman breeds, and likewise a means for discrimination as an exclusion maker for breeds such as the Abyssinian, Egyptian Mau, Sokoke and Ocicat. The long hair mutations can also be used to distinguish different breeds that are long haired varietes within the breed family. For example, a Balinese is a longhaired Siamese and a Cymric is a longhaired Manx. Many cat breeds are designated as a breed, such as Oriental Longhair or Oriental Shorthair, just based on the *FGF5* mutations. The frequency of the long hair mutations could also be used to support a breed selection. For example, the Norwegian Forest Cat and the Ragdoll have *FGF5* mutations that are less common in other breeds.

[0097] Other single gene traits may be used to identify members of certain cat breeds as well. For example, the G715T TYR mutation, which defines Burmese points, is found in the genomes of felines of Burmese and Singapura breeds. The cinnamon mutation, C298T TYRP1, is common to the red Abyssinian. Certain dominant traits can be homozygous or heterozygous, such as the ear curl of American Curls or the bobtail of the Japanese Bobtail. Tonkinese felines are genetically compound heterozygous for the G940A and the G715T TYR mutations and can produce both pointed and sepia cats, and genetically resemble a Siamese or Burmese, respectively. However, breeding restrictions would not allow these Tonkinese variants to be registered as Siamese or Burmese. Additional phenotypic SNPs that find use include the Norwegian Forest Cat color variant amber (Peterschmitt et al. (2009) Animal Genetics, 40:547-552), three additional long-haired mutations (Kehler et al. (2007) Journal of Heredity, 98:555-566), and the mutations responsible for hairless of Sphynx and rexing of the Devon Rex (Gandolfi et al., Mamm Genome. (2010) (9-10):509-15). A mutation in *KIT* (c.1035_1036delinsCA) for Birman glove white spotting should be restricted to the Birman breed. Phenotypic genetic markers, as well as disease mutations, find use to further delineate cat breeds.

[0098] Accordingly, morphological and/or phenotypic markers find use to distinguish between genetically related feline breeds, *e.g.*, (i) Persian and Exotic Shorthair (SH); (ii) British SH and Scottish Fold; (iii) Australian Mist and Burmese; (iv) Singapura and Burmese; (v) Birman and Korat, and (vi) Siamese and Havana Brown. For example, determination of whether the feline has the phenotype for long hair can be used to distinguish between Persian and Exotic Shorthair; determination of whether the feline has curled ear morphology can be used to distinguish between British SH and Scottish Fold; determination of fur color and/or pattern can be used to distinguish between Australian Mist and Burmese; between Singapura and Burmese; between Birman and Korat; or between

Siamese and Havana Brown. Whereas a Burmese will lack barring and/or spotting, a Singapura possesses the dominant ticked tabby gene, Ta; and an Australian Mist will have spotting and barring. Whereas a Birman and a Siamese will have the mutation for Siamese points (*i.e*, homozygous for the G940A TYR mutation), a Korat and a Havana Brown will not.

[0099] The use of phenotypic markers to further refine the assignment of a test feline to a breed or ancestral population is demonstrated in Tables 4 and 5.

Table 3 – Phenotypic Markers useful for breed identification test

SEQ ID NO:	SNP ID	Sequence
149	Phen_CMAH_G139A	AATTTCTTGAGAAACAAGAAGACCRGCAAAGATTTCATTCTGTACAAGAGCAAGAATYGY[G/A]TGAGGGCGTGCAAGAACGTGTGCAAGCATCAAGGAGKCCTGTTCRTAAAAGACATCGAAG
150	Phen_ASIP_del	CCACCCTGCTGGTCTGCCTGTGCCTCCTCACTGCCTACAGTCACCTGGCACCTGAGGAAAAACCCAGAGATGACAGGAACCTGAGGAGCAACTCCT[CA/-]TGAACATGTTGGATCTCTCTTCTGTCTCTATTGTAGCGCTGAACAAGAAATCCAAAAAGATCAGCAGAAAAGAGGCGGAAAAGAAGAGATCTTCCAAGAAAAAGGCTTCG
151	Phen_MLPH_T83del	GGCAGAGATGGGGAAAAAACTGGATCTTTCCAAGCTCACGGACGACGAGGCCAAGCACATCTGGGAAGTGGTTCAGCGGGACTTTGATC[T/-]AGAAGGAAAGAAGAGGAAAGGCTGGGGTGAGTGTATGAGGCCGAGCCCGTCCCTCCGGTGTCCCCTGGAAGGGGGGGCCTCCCCGGGACGCTGGGGGTGAGCA
152	Phen_MC1R_G250A	CCTGGGGCTGGTGAGCGTGGTGGAGAACGTGCTGGTGGTGGCCGCCATTGCCAAGAACCGCAACCTGCACTCGCCCATGTATTACTTCATCTGTTGCCTGGCCGTGTCC[G/A]ACCTGCTGGTGAGCGTGAGCAGTGTGCTGGAGACGGCCGTCATGCTGCTGCTGGAGGCAGGCGCCCTGGCCGGCCGGGCCGCCGTGGTGCAGCGGCTGGA
153	Phen_TYRP1_C298T	CCGCATGATGGCAGAGATGATCGGGAGGCTTGGCCCACGAGGTTCTTCAACAGGACATGC[T/C]GATGCAATGGCAATTTCTCAGGACACAACTGTGGGACTTGCCGTCCTGGATGGAAAGGAG
154	Phen_TYRP1_5IVS6	CCTTCACAATTTGGCTCATCTATTCCTGAATGGAACAGGGGGACAAACCCATTTATCTCCAAACGATCCTATTTTTGTCCTCCTGCACACTTTCACTGACGCAGTCTTTGATGAATGGCTGAGGAGATATAATGCTGGTGA[G/A]ACATTCTCCTATGCTTTTTTGCAGGCTCAGCAAG
155	Phen_TYR_del975C	TTAGCCGATTGGAGGAGTACAATAGCCGTCAGGCTTTATGTGATGGAACTCCAGAGGGACCATTACTGCGCAATCCCGGAAACCATGACAAAGCCAGGACCCCAAGGCT[C/-]CCTCCTCTGCTGATGTGGAATTTTGCCTAAGTCTGACACAATATGAATCGGGTTCCATGGATAAAGCTGCA
156	Phen_TYR_G715T	TTCCTGCCTTGGCACAGACTCTTCTTGTTGCTGTGGGAACAAGAAATCCAGAAGCTGACC[T/G]GGGATGAGAACTTCACTATTCCATATTGGGATTGGCGAGATGCTAAAAGCTGTGA
157	Phen_TYR_G940A	TACAATAGCCGTCAGGCTTTATGTGATGGAACTCCAGAGGGACCATTACTGCGCAATCCC[A/G]GAAACCATGACAAAGCCAGGACCCCAAGGCTCCCCTCCTCTGCT

Table 3 – Phenotypic Markers useful for breed identification test

SEQ ID NO:	SNP ID	Sequence
158	Phen_KIT_G1035C_BI	TTTCATTAACATCTTCCCTATGATGAATACCACAATATTCGTGAATGATGGCGAGAATGTGGATCTGATTGTCGAATATGAGGCATATCCCAAGCCTGA[G/C]MACCAACGGTGGGTCTATATGAACAGAACCCTCACTGATAAATGGGAAGATTATCCCAAGTCTGACAACGAAAGTAATATCAGGTAAGAAAAAAGCCTTACGCTGAGGATCAGATGTTTTCC
159	Phen_FGF5_475	TGCTGAAAATATTATTACTATTTACAAGTTTTTCTTCTTTCCCCCCACCAGGCCAAATTT[A/C]CCGATGACTGCAAGTTCAGGGAGCGATTCCAAGAAAACAGCTATAATACCTATGCCTCAG
160	Phen_FGF5_474	TGCTGAAAATATTATTACTATTTACAAGTTTTTCTTCTTTCCCCCCACCAGGCCAAATT[T/-]ACCGATGACTGCAAGTTCAGGGAGCGATTCCAAGAAAACAGCTATAATACCTATGCCTCAG
161	phen_FGF5_406	ATTTCTGTCATCCTAGGTATTTTGGAAATATTTGCTGTGTCTCAGGGGATTGTAGGAATA[C/T]GAGGAGTTTTCAGCAACAAATTTTTAGCGATGTCAAAAAAAGGAAAACTCCATGCAAGTGTAAGTAGAACCACTTTATGTT
162	Phen_FGF5_356	GTGGAGCCCCTCGGGGCGCCGGACCGGCAGCCTCTACTGCAGAGTGGGCATCGGTTTCCATCTGCAGATCTACCCGGATTGGCAAAGTCAATGGCTCCCATGAAGCCAATA[T/-]GTTAAGTAAGTTGCTCGCCCTCCTGGCAAAGCGCGTCCTAAGCGGGCGATGGGGGGRTTCGGGAGGGACAGAGGCTATTCCCTGGCCCACAGGCGCACCTTCCGGAGCCCTGGCTCCTGGGACTCAGCTGTCCCTCGGAACC
163	Phen_GBL1_G1457C_SIA_KOR	CCCAGGGAGTCCTGGAGCGAAGTTACGTGATCACTCTGAACATAACAGGGCAAGCCGGAGCCACTCTGGACCTTCTGGTGGAGAACATGGGGC[G/C]TGTGAACTATGGCAGATACATCAATGATTTCAAGGTAGGACCAGCCTCGCTGTCGAGGTCGATAGGACTGTGTCTGTGCCACCCGAGGA
164	Phen_HEXB_DelIntr_BUR	ACCATGAACTGACCAAGGGACCAGTAATTGCCTCTGTCAGACTACTACTGCATTTTGCCTATTGCCTCTGCAACTACTTCATTTACAGCCATTCAATGATTT[TAATGTAGGTTCTCA/-]AGAACAGAAAAAACTTGTCATTGGTGGAGAAGCTTGTCTGTGGGGAGAATTTGTGGATGCAACTAACCTTACTCCAAGATTATGGTATGGAAT
165	Phen_HEXB_del39C_KOR	GGCTGGGGCTGGCGGCGCTGCTGGCGCTGCTGGCGGCCGTGGCCCCGCGCTCCTCCGCCGCCGCGGAGCCGCCCTGTGGCCTATGCCGCTCTCGGTGAAGACGTCTCCGCGCCTGCTGCA[C/-]CTCTCCCGCGACAACTTCTCCATCGGCTACGGCCCCTCGTCCACCGCCGGCCCCACCTGCTCCCTCCTGCAGGAAGCTTTTCGGCGATATCACGAATACATTTTTGGTTTCGACAAGAGG
166	Phen_GBE1_Ins_NFC	TTAAGAATATTCATTCTAGGGGCGCCTGGGTGGCGCAGTCGGTTAAGCGTCCGACTTCAGCCAGGTCACGATCTCGCGGTCTGTGAGTTCGAGCCCCGCGTCGGGCTCTGGGCTGATG[C/-]CCAGAGCCCGACGACATGGGTCAAACTCACCGACCGCGAGATCGTGTACCTGAGCTGAAGTCGGACGCTTCACCGTACTGAGCCACCCAGGC
167	Phen_KRT71_G/Aintro4_SPX	GCCAATAAGGAGGAGCTCCAGGCCAAGGTGGACTCCATGGATCAGGAGATCAAGTTTTTCAAGTGCCTCTATGAAGCC[G/A]TAAGTCTGTCTCTCCACCCACCCCTCTGAGGGCAGCCAGCGGGTAAAACTCTGTTCTGG
168	Phen_MYBPC_G93C_MCC	GCCTTCAGCAAGAAGCCAAGGTCAGTGGAAGTGGCAGCCAGCAGCTCTGCTGTGTTCGAG[C/G]CCGAGACAGAGCGGTCAGGAGTAAAGGTGCGCTGGCAGCGGGGGGGCAGTGACATCAGCG
169	Phen_MYBPC_C2460T_RAG	GTCCCCCCTTCATCAGGCTACATCCTGGAGCGCAAGAAGAAGAAGAGCTTCCGGTGGATG[T/C]GGCTGAACTTTGACCTGCTGCAGGAGCTGAGCCACGAGGCACGGCGCATGATTGAGGGCG

Table 3 – Phenotypic Markers useful for breed identification test

SEQ ID NO:	SNP ID	Sequence
170	phen_MPO_ALC	GTGCAGTTGGGGGATCGCAGAAGAGGGCTGGGCACATGCAGCTCCTGGTGCCAAGGTCAC[T/C]CCAGTGGGCAGGTCTTCACCAGGGAATCAAGGTCTCAAGGTATAATGCCATTCAGACTTG
171	Phen_PLAU_AG_ALC	TGTATCTAAGGAAGAATGTGAGGATGAGAGATATTAGAAAGAGGAGGAAATTCAGACAGG[T/C]GTTTTAGAGATCCTGTCAGGCCTTGCATGATTTCAGACCTGG
172	Phen_FCAT_ALC	AAAAGCTGATGTACTTGTGCCCAGGGAAGATGTCAATATTTACCATTAACTGTTGTGAAA[A/G]ATTCAACCAATGTACTCAGTTGAAGTTCTTTTCATTTTATTGGATTAAAAAAATCACTAT
173	Phen_PKLR_13delE6_Aby	CGCCCACCGGTGCCTGTTCCGTGCACGGCCCAGGCCCCAAGGTGGACAGGCAATAGGACACGGGTTCCTGATTTCCTGGGGGCCCACGCCCCGTGCCCCCGCTCCAC[G/A]ACTCTGCCCCCGGCTYGCCCCTGACCTGCGCTGGCTCTTCCCATGCCTGCAGGCCCGGAGGGGCTGGAGACCCACGTGGAGAACGGCGGCGTCCTGGGC
174	Phen_PKD1_C10063A_PER	CTCCCTCTGGGACCGGCCTCCTCGGAGCCGCTTCACCCGCGTCCAGCGGGCCACCTGTTG[A/C]GTCCTCCTCGTCTGCCTCTTCCTGGGCGCCAATGCTGTGTGGTACGGGGTCGTGGGAGAC
175	Phen_SHH_A479G_Hw	CCAGTGGCTAATTTGTCTCAGGCCTCCGTCTTAAAGAGACAC[A/G]GAAATGAGTAGGAAGTCCAGCGTGGTCTCAGAGAGCT
176	Phen_CEP290_PRA_Aby	AACAGAGAGGGAGCAAAAAGCTAAGAAATACACTGAAGACCTTGAGCAACAAGCAAGTAA[T/G]TTTTCTTTATGAGAAAATAATGCATTTCATCTCAAGCCACTCCTTGGCATTGTTTTAA
177	Phen_CRX_546_Aby	TCCCCCACCTCGGCCGTGGCCACGGTGTCCATCTGGAGTCCCGCCTCGGAGTCCCCTCTGCCCGAGGCCCAGCGGGCGGGGCTGGTGGCGGC[C/-]GGGCCCCCTCTGACCTCCGCGCCCTACGCCATGACCTACACCCCCGCCTCTGCTTTCTGCTCTTCCCCCTCGGCCTACGGGTCTCCGAGCTCCTATTTCAGTGGCC
178	Phen_CMAH_del	AGTAGTGAACCGCGTGCATATGCATCCTCCGTCTCATACTTTGTGGGAGCA[AACGAGCAACCGAAGCTG/-]AACGAGCAACCACCGTCCTTTCAGAATTCCCAGGGAGAGGCAGCTGCGGACCATGGGCAGGCAAGTGACAGGGGCATTGGGTCTGGAGGAACCCGAGACCAACACTGAGCA
179	Phen_HEXB_C667T_DSH	TCTCTGTCTCATGTTTATACACCAAACGATGTCCATACGGTGATTGAATATGCCAGATTA[T/C]GAGGGATTCGAGTCATACCAGAATTTGATAGCCCTGGACATACACAGTCTTGGGGAAAAG
180	Phen_GM2A_Del_DSH	TCACTGCCGGAGAGTGATTTCACCCTGCCCCAGCTGGAGGTGCCCGGCTGGCTTAGCTCTGGGCACTACCGCATCAAGAGGT[C/T]CCTCAGCAGCGGTGGGGAGCGTCTGGGCTGTGTCAAGATCTCTGCCTCTCTGAAGGGCAAATAATGTGGCACCAGCCACA
181	Phen_GRHPR_DSH	ACCTGGAGAGGATGATCTTCTCCCCCTGGGGGTTCTGGGTCTGTGAGTTTGCAGTGAGCCCTCATCTTTGCCCAAGGTGGGGTCCTCTTACCCACCCCTTCTCTCCTCACA[G/A]CGGTGGCTGGACCTCATGGAAGCCCCTGTGGATGTGTGGCTATGGACTCACGCAGAGCACTGTCGGCATCATCGGGCTGGGGCGC
182	Phen_LPL_G1234A_DSH	GAGCGATTCATACTTCAGCTGGTCAGACTGGTGGAGCAGCCCTGGGTTTACTATTGAGAAGATCAGAGTAAAAGCA[G/A]GAGAGACTCAAAAAAAGGTAATCTTCTGTTCCAGGGAGAAAGTATCTCATCTGCAGAAAGGAAAGGCATCTGTGGTATTTGTGAAATGCCATG

Table 3 – Phenotypic Markers useful for breed identification test

SEQ ID NO:	SNP ID	Sequence
183	Phen_LAMAN_del_PER	ACGGTCAGGAACTGCTTTTCCCAGCCTCGGTGCCTGCCCTGGGCTTCAGCATCTACTCAGTAAGCCAGGTGCCTG[GCCA/-]KCGCCCCCACGCCCACAAACCCCAGCCCAGATCCCAGCGGCCCTGGTCCCGTGTCTTGGCCATCCAAAATGAGCACATCCGGGC
184	Phen_IDUA_del_DSH	GGACATCCCGACCCCCTGGACCCCCGCAGGTCATTGCGCAGCACCAGAACCTGCTGGTGGCCAACACCAGCTCCCCCGTGCGCTACGCGCTCCTGAGCAAC[GAC/-]ACGCCTTCCTGAGCTACCACCCGCACCCCTTCACGCAGCGCACGCTCACGGCGCGCTTCCAGGTCAACAACACCCGCCCGCCGCACGTGCAGCTGCTGC
185	Phen_ARSB_G1558A_SIA	CTCCAGTTCTACCACAAACATTCAGTGCCTGTGCATTTCCCGGCACAG[A/G]ACCCCCGCTGTGACCCCAAGGGCACTGGGGCCTGGGGCCCTTGGGTATAGGAC
186	Phen_ARSB_T1427C_Sia	CGTCTCCATACAACGATTCTGCGATACCCTCATCAGACCCACCGACCAAGACCCTCTGGC[T/C]CTTTGATATTGATCAGGACCCAGAAGAAAGACATGACCTGTCAAGAGACTATCCCCATAT
187	Phen_GUSB_A1052G_DSH	GATTCGCACGGTGGCTGTCACAGAGCACCAGTTCCTCATCAATGGGACCTTTCTATTTCCACGGGGTCAACAAGCAC[G/A]AGGATGCAGATATCCGAGGGAAGGGCTTTGACTGGCCACTGCTGGTGAAGGACTTCAATTTGCTTCGCTGGCTCGGGGCCAACGCCTCCGCACCAGTCACTACCCCTA
188	Phen_MYBPC_A74T_Poly	CTTCAGCAAGAAGCCAAGGTCAGTGGAAGTGGCAGCCAGCAGCTCTGCTGTGTTCGAGSCCGAGACAGAGCGGTCAGGAGTAAAGGTGCGCTGGCAGCGGGGGGGCAGTGACATCAGCGCCAGTGACAAGTATGGCCTAGCARCCGAGGGCACGAGGCACACTCTGACAGTGCGGGACGTGGGCCCC[G/A]CCGACCAGGGACCCTACGCAGTCATCGCT
189	Phen_NPC1_G2864C_PER	GCTTTGCTCCCTCTTCCTGGATCGACGATTACTTTGATTGGGTCAAGCCTCAGTCTTCTT[C/G]CTGTAGAGTCTACAACAGCACCGATCGGTTCTGCAATGCTTCAGGTACTTTCATCTCCTT
190	Phen_SHH_G257C_UK1	TAATTAGACTGACCAGGTGGCAGCAAAGAGCCGGGTGCC[C/G]GTGCTGGGAAGGCCTATAAAGCTGAGCGCTGTGACAGCACA
191	Phen_SHH_A481T_UK2	CCAGTGGCTAATTTGTCTCAGGCCTCCGTCTTAAAGAGAC[A/T]CAGAAATGAGTAGGAAGTCCAGCGTGGTCTCAGAGAGCT
192	Phen_HMBS_del842_SIA	GTCCCCGTGCACGTCAAGTTGTCCACAAGAGCCCAGGTTTCTAACCAGTTCTCTCAGAATATGCTGAGATAACCATTTTCTTTCCCAGCTGTACCTGACAGGAG[GAG/-]TCTGGAGTCTAGACGGCTCAGATAGCATGCAAGAGACCATGCAGGCCACCATTTGTGTCACTGCCCAGGTGCCAAAGCTGGAGGGTGAGGGAGAGGGTGAG
193	Phen-HMBS_189TT_SIA	TTAGTACAGTGCTGGGCTCAGTAGGGGCTCGTTAAACGCCAATAGATGAGCACGTGACTGATTCTCTCCTCAGTTGCTATGTCCACCACAGGGGACAAGATT[-/T]CTTGATACTGCGCTCTCTAAGGTAACGTGTTCCCCCCAATCCCTTTCCCTCCTTTCTCTTTCCTTCCCCCAAAAGATTCACTCTGAGGCTTTTTCTTGACC
194	Phen_CYP21B1	GGAGGCACCCGCCTGGGTTTCTCAGTGCCCTGACAGCGCCCCCTCGCGCCCAGGGATAGCCGCCGTGCTCCTGGGTTCACGCCTGGGCTGCCTGGAGGCCGAAGTGCCTCCAGACACAGAGACCTTCATCCGCGCGGTGGGATCGGTATTTGTGTCCACGCTGCTGACCATGGCGATGCCTAGCTGGCTTCACC[G/-]CCTCGTGCCCGGACCCTGGGGCCGCCTCTGCCGAGACTGGG

Table 3 – Phenotypic Markers useful for breed identification test

SEQ ID NO:	SNP ID	Sequence
195	Phen_TAS1R2_CAT	CCCTCCTGGGCCACCAGATCTTTTTTGACCAGCGAGGGGACCTACTCATGCGCCTGGAGATCATCCAGGGACGGTGGGACCTGAGCCAGAAC[T/-]TTTCTGGAGCGTCGCCTCCTACTGCCCGGTGCTACGACGGCTGAGGGCCATCCGTGACGTCTCCTGGCACACGGCCAACAACAC
196	Phen_TAS1R2_G8224A_CAT	TTGCAGACGAGTTTGGCTGCCGGCCCTGCCCGAGTTGCGGGTGGTCCCGGAGGAACGACGCTTCGTGCTTCAAGCGGCGGCTGGCCTCCCTTGAATG[G/A]CGCGAGGCACCCGCCGTCGCTGTGGCCGTGCTGTCCATCCTGGGCTCCCTCTGCACCCTGGCCATCCTGGTGATCTTCTGGAGGCACCGCCACGCGCC
197	Phen_CYP27B1_Rob	GGAGGCACCCGCCTGGGTTTCTCAGTGCCCTGACAGCGCCCCCTCGCGCCCAGGGATAGCCGCCGTGCTCCTGGGTTCACGCCTGGGCTGCCTGGAGGCC[G/T]AAGTGCCTCCAGACACAGAGACCTTCATCCGCGCGGTGGGATCGGTATTTGTGTCCACGCTGCTGACCATGGCGATGCCTAGCTGGCTTCACC
198	Phen_ZFX	GGTTTTCGTCACCCGTCAGAGCTCAAGAAGCACATGCGAATCCATACTGGGGAGAAGCCGTACCAGTGCCAGTACTGCGA[G/A]TATAGGTCTGCAGACTCTTCTAACTTGAAAACGCATGTAAAAACTAAGCATAGTAAAGAGATGCCATTCAAGTGTGACATCTGTCTTCTGACT
199	KRT71-Del_Drex	GGTGGGCATCCCTGCCNGGGAATCAGCAAGCNCTAGTGNGATTTGGATTTGGATGACTCGAATTACCCCTTCCAGTTTTTGAACTTCTCCAACTCCCTGT[TTAGGCTTCCAACCTGGAGACGGCCATCGCCGATGCCGAGCAGCGGGGCGACAGTGCCCTGAAGGATGCCCGGGCCAAGCT/-][-/AGTTGGAG]GGACGAGCTGGA[-/T]GTCCGCCCTGCACCAGGCCAAGGAGGAGCTGGCCCGGATGCTGCGGGAGTACCAGGAGCTCATGAGCCTGAAGCTGGCCCTGGACATGGAGATCGCCACCTACC
200	P2RY5_CRex	ACACTTTGTATGGCCGCATGTTTAGTATGGTATTTGTGCTTGGGTTAATATCTAACTGTGTTGCCATATACATTTTCATCTGCACCCTCAAAGTGCGAAATGAAACTACAACATACATGATTAACTTGGCAATGTCAGACTTGCTTTTCGTTTTTACTTTACCCTTCAGGATTTTTTACTTTGCAACCCAGAATTGGCC[GTTT/-]GGAGATCAACTCTGTAAAATTTCAGTGATGCTATTCTATACCAACATGTATGGAAGCATTCTGTTCTTAACCTGTATTAGTGTCGATCGGTTTCTGGCAAT
201	WNK4_Burm_HKL	TGCCCCTCTGCTTCCCCCCTTCCGTCCACCACAGCAGCCCCTCTCCTCTCTCTGGCTAGTGCCTTCTCACTGGCTGTGATGACTGTGGCCCAGTCCCTGCTGTCTCCCTCACCTGGGCTCCTGTCCCAGTCTCCTCCAGCCCCTCCTGCTCCCCTCCCTAGCTTGCCCCTGCCCCCTCCCCCTGCTCCTTGTGGC[C/T]AGGATAGGCCTTCACCCCCAACAGCTGAGACCGAGAGTGAGGTGAGTAGGAAACCAAGAGGGATGGTTAGGGGAGCTCCACTCTGGATCATTTCCCTTCTCATGGACCCACACTTTGCAGGTCCCGCCAAATCCTGCTCGGCCACTC
202	CART1_del_Burm	CTCCCGTGAAGGGGATGCCAGAAAAGGGAGAACTAGATGAACTTGGGGATAAATGTGACAGCAACGTATCCAGCAGCAAGAAGCGGAGACACAGAACCACCTTCACCAGCCTGCAGCTCGAGGAGCTGGAGAAGGTCTTTCAGAAAACCCATTACCCGGATGTATACGTCAGAGAACAGCTTG[CTCTCAGGACTG/-]AGCTCACGGAGGCCAGAGTCCAGGTAGGAGCCAAATGAAGGACGTGGGTGTGCGTGTTGGGGGCCGGTGTGTGGAGATACTGTTAGAATAATTCAGTGGTTGCATTTTGCCAAAAGGAAGAAACTGATCCTCTCACTAAAGACTAGAACC

Table 4

No.				Defining Variant	Phenotypic SNPs / genotypes (Inclusive (I) / Exclusive (E))															
Registry	**Breed**	**Category**	**Family**	**for family**	**Agouti**	**Brown**	**Color**	**Dilute**	**Extension**	**Glove**	**Hairless**	**Inhibitor**	**Orange**	**Spotting**	**Tabby**	**Ticked**	**White**	**Long**	**Rex**	**Rex 2**
4	Abyssinian	1	Abyssinian		aa - E	bb = E	CC = I		E	E	E	E	E	E		I	E	L- = I	E	E
2	American Shorthair	1					cbcb = E		E	E	E							L- = I	E	E
4	Birman	1			aa = I		cscs = I		E	I	E			E			E	ll - I	E	E
4	British Shorthair	1	Persian				C- = I		E	E	E								E	E
4	Burmese	1	Burmese		aa = I		cbcb=I		E	E	E		E	E			E	L- = I	E	E
3	Chartreux	1			aa = I	BB, Bb = I	C- = I	dd = I	E	E	E		E	E			E		E	E
4	**Cornish Rex***	1		Rex			cbcb = E		E	E	E								I	E
4	Devon Rex	1					cbcb = E		E	E	E								E	rere = I
4	Egyptian Mau	1					C- = I		E	E	E		E	E			E		E	E
3	**Japanese Bobtail**	1					cbcb = E		E	E	E								E	E
4	Korat	1			aa = I	BB, Bb = I	C- = I	dd = I	E	E	E	E	E	E			E	L- = E	E	E
4	Maine Coon	1					C- = I		E	E	E							ll - I	E	E
4	**Manx**§	1					C- = I		E	E	E								E	E
4	Norwegian Forest	1					C- = I		I	E	E							ll - I	E	E
4	Persian	1	Persian				cbcb = E		E	E	E							ll - I	E	E
4	Russian Blue	1			aa = I	BB, Bb = I	cbcb = E	dd = I	E	E	E		E	E			E		E	E
4	Siamese	1	Siamese		aa = I	blbl = E	cscs = I		E	E	E			E			E		E	E
3	Turkish Angora	1					cbcb = E		E	E	E							ll - I	E	E
4	Turkish Van	1					cbcb = E		E	E	E							ll - I	E	E
X	Asian	2	Burmese						E	E	E								E	E
4	Balinese	2	Siamese	Long/Brown/Dilute	aa = I	blbl = E	cscs = I		E	E	E			E			E	ll = I	E	E
3	Bombay	2	Burmese	Color	aa = I	B- = I	C- = I	dd - E	E	E	E		E	E			E		E	E
2	Colorpoint	2	Siamese	Agouti			cscs = I		E	E	E								E	E
2	Cymric§	2	Manx	Long			cbcb = E		E	E	E							ll = I	E	E
4	Exotic Shorthair	2	Persian	Long			cbcb = E		E	E	E							L- = I	E	E
3	Havana Brown	2	Siamese	Color	aa = I	bb = I	C- = I	dd = E	E	E	E		E	E			E		E	E
X	Himalayan	2	Persian	Color			cscs = I		E	E	E							ll = I	E	E
4	Oriental	2	Siamese	Color			cscs = E		E	E	E								E	E

Table 4

No.				Defining Variant	Phenotypic SNPs / genotypes (Inclusive (I) / Exclusive (E))															
Registry	Breed	Category	Family	for family	Agouti	Brown	Color	Dilute	Extension	Glove	Hairless	Inhibitor	Orange	Spotting	Tabby	Ticked	White	Long	Rex	Rex 2
X	Ragamuffin	2	Ragdoll	Not pointed			C- = I		E	E	E							II - I	E	E
3	Singapura	2	Burmese	Agouti	aa - E		cbcb = I		E	E	E		E	E		I	E		E	E
4	Somali	2	Abysinnian	Long	aa - E	bb = E	cbcb = E		E	E	E		E	E			E	II - I	E	E
4	Sphynx	2	Devon Rex	Hairless/Rex					E	E	E								E	E
1	Tiffanie	2	Burmilla	Long/Silver					E	E	E	I = I						II = I	E	E
2	Scottish Fold	3	Persian	Fold			cbcb = E		E	E	E								E	E
X	European Shorthair	5					cbcb = E		E	E	E								E	E
4	Ragdoll	5	Ragdoll				cscs = I		E	E	E							II - I	E	E
4	Siberian	5					cbcb = E		E	E	E							II - I	E	E
2	Sokoke	5					cbcb = E		E	E	E								E	E
X	Australian Mist	6	Burmese						E	E	E								E	E
4	Burmese Non-USA	7			aa = I		cbcb = I		E	E	E			E			E		E	E
3	Tonkinese	2/6	Burmese/Siamese	Color	aa = I		cscb = I		E	E	E			E			E		E	E
3	Bengal	1/4/6	Aby/Mau	Ticked					E	E	E			E			E		E	E
3	Snowshoe	?	Birman?	bicolor, sh			cscs = I		E	E	E							L- = I	E	E
4	Ocicat	1 (6)	Aby/Siamese	Color/Ticked/Tabby	aa - E		cbcb = E		E	E	E			E			E		E	E

Disease info: F = disease SNP is frequent in the breed and may be breed specific

V = the SNP variant has different frequencies in different breeds.

Categories: 1 = founder breed (N = 19, genetically defined by SNPs)

2 = Breed variants (N = 16), distinguish with other phenotypic SNPs or DNA variants

3 = Breeds may be like random breds (N = 9), but if found mutation, could distinguish.

4 = Hybrid breed (N = 2), need wildcat diagnostics, Y STRs

5 = Random bred (N = 4), regional, 3 completed, Euro SH underway, but define as breeds in breed only comparison

6 = concoction breeds (N = 3), will show mixture, defining variants will be of assistance

7 = Foreign Burmese may have distinct gene pool from USA Burmese, separate breed

§Variant found, unpublished

*Could share fur type variant

Table 5

				Structural Trait						Disease Traits											
Breed	Cat.	Family	Defining Variant for family	Dwarf	Ear Curl	Fold	Bobtail	Tailless	Poly-dactyla	Blood Type B	Korat GM1	Korat GM2	Burmese GM2	NFC GSD	MCC HCM	Ragdoll HCM	Aby PRA CEP290	Aby PRA CRX	Persian PKD	Aby PKLR	MCC SMA
Abyssinian	1	Abyssinian		E	E	E	E	E	E	V							F	F		F	
American Shorthair	1			E	E	E	E	E	E	V									F		
Birman	1			E	E	E	E	E	E	V											
British Shorthair	1	Persian		E	E	E	E	E	E	V									F		
Burmese	1	Burmese		E	E	E	E	E	E	V			F								
Chartreux	1			E	E	E	E	E	E	V											
Cornish Rex*	1		Rex	E	E	E	E	E	E	V											
Devon Rex	1			E	E	E	E	E	E	V											
Egyptian Mau	1			E	E	E	E	E	E	V											
Japanese Bobtail	1			E	E	E	I	E	E	V											
Korat	1			E	E	E	E	E	E	V	F	F									
Maine Coon	1			E	E	E	E	E	F	V					F						F
Manx§	1			E	E	E	E	I	E	V											
Norwegian Forest	1			E	E	E	E	E	E	V				F							
Persian	1	Persian		E	E	E	E	E	E	V									F		
Russian Blue	1			E	E	E	E	E	E	V											
Siamese	1	Siamese		E	E	E	E	E	E	V							F				
Turkish Angora	1			E	E	E	E	E	E	V											
Turkish Van	1			E	E	E	E	E	E	V											
Asian	2	Burmese		E	E	E	E	E	E	V											
Balinese	2	Siamese	Long/Brown/Dilute	E	E	E	E	E	E	V											
Bombay	2	Burmese	Color	E	E	E	E	E	E	V											
Colorpoint	2	Siamese	Agouti	E	E	E	E	E	E	V											
Cymric§	2	Manx	Long	E	E	E	E	I	E	V											
Exotic Shorthair	2	Persian	Long	E	E	E	E	E	E	V									F		

Table 5

				Structural Trait						Disease Traits											
Breed	Cat.	Family	Defining Variant for family	Dwarf	Ear Curl	Fold	Bobtail	Tailless	Poly-dactyla	Blood Type B	Korat GM1	Korat GM2	Burmese GM2	NFC GSD	MCC HCM	Ragdoll HCM	Aby PRA CEP290	Aby PRA CRX	Persian PKD	Aby PKLR	MCC SMA
Havana Brown	2	Siamese	Color	E	E	E	E	E	E	V											
Himalayan	2	Persian	Color	E	E	E	E	E	E	V											
Oriental	2	Siamese	Color	E	E	E	E	E	E	V											
Ragamuffin	2	Ragdoll	Not pointed	E	E	E	E	E	E	V											
Singapura	2	Burmese	Agouti	E	E	E	E	E	E	V			F								
Somali	2	Abysinnian	Long	E	E	E	E	E	E	V							F	F		F	
Sphynx	2	Devon Rex	Hairless/Rex	E	E	E	E	E	E	V											
Tiffanie	2	Burmilla	Long/Silver	E	E	E	E	E	E	V			V						V		
Scottish Fold	3	Persian	Fold	E	E	I	E	E	E	V									F		
European Shorthair	5			E	E	E	E	E	E	V											
Ragdoll	5	Ragdoll		E	E	E	E	E	E	V						F					
Siberian	5			E	E	E	E	E	E	V											
Sokoke	5			E	E	E	E	E	E	V											
Australian Mist	6	Burmese		E	E	E	E	E	E	V											
Burmese Non-USA	7			E	E	E	E	E	E	V											
Tonkinese	2/6	Burmese/Siamese	Color	E	E	E	E	E	E	V											
Bengal	1/4/6	Aby/Mau	Ticked	E	E	E	E	E	E	V											
Snowshoe	?	Birman?	bicolor, sh	E	E	E	E	E	E	V											
Ocicat	1 (6)	Aby/Siamese	Color/Ticked/Tabby	E	E	E	E	E	E	V											

[0100] In addition to determination of the plurality of SNPs listed in Table 1, the genotype of one or more microsatellite markers and/or short tandem repeats (STRs) can be determined. For example, the genotype of one or more feline STRs selected from the group consisting of selected from the group consisting of FCA005, FCA008, FCA023, FCA026, FCA035, FCA043, FCA045, FCA058, FCA069, FCA075, FCA077, FCA080B, FCA088, FCA090, FCA094, FCA096, FCA097, FCA105, FCA123, FCA126, FCA132, FCA149, FCA211, FCA220, FCA223, FCA224, FCA229, FCA262, FCA293, FCA305, FCA310, FCA391, FCA441, FCA453, FCA628, FCA649, FCA678 and FCA698. The identity and location of feline microsatellites and STRs have been characterized and mapped, as described, *e.g.*, in Menotti-Raymond, *et al.*, *Genomics* (1999) 57(1):9-23; Menotti-Raymond, *et al.*, *Journal of Heredity* (2003) 94(1):95–106; and Menotti-Raymond, *et al.*, *Genomics* (2009) 93(4): 305–313.

[0101] As appropriate, the genotypes of at least about 3, 5, 10, 15, 20, 25, 30, 35, 38, or more, feline STRs are determined. In some embodiments, the expression levels of all STRs selected from FCA005, FCA008, FCA023, FCA026, FCA035, FCA043, FCA045, FCA058, FCA069, FCA075, FCA077, FCA080B, FCA088, FCA090, FCA094, FCA096, FCA097, FCA105, FCA123, FCA126, FCA132, FCA149, FCA211, FCA220, FCA223, FCA224, FCA229, FCA262, FCA293, FCA305, FCA310, FCA391, FCA441, FCA453, FCA628, FCA649, FCA678 and FCA698 are determined.

5. Methods of Detecting Biomarkers

[0102] In some embodiments, methods comprise obtaining the identity of one or both alleles in a test feline genome for each marker of a set of markers. The genetic markers described herein, including the SNPs, STRs and phenotypic markers, can be detected using any methods known in art, including without limitation amplification, sequencing and hybridization techniques. Detection techniques for evaluating nucleic acids for the presence of a single base change involve procedures well known in the field of molecular genetics. Methods for amplifying nucleic acids find use in carrying out the present methods. Ample guidance for performing the methods is provided in the art. Exemplary references include manuals such as PCR Technology: PRINCIPLES AND APPLICATIONS FOR DNA AMPLIFICATION (ed. H. A. Erlich, Freeman Press, NY, N.Y., 1992); PCR PROTOCOLS: A GUIDE TO METHODS AND APPLICATIONS (eds. Innis, et al., Academic Press, San Diego, Calif., 1990); CURRENT PROTOCOLS IN

MOLECULAR BIOLOGY, Ausubel, 1990-2008, including supplemental updates; Sambrook & Russell, Molecular Cloning, A Laboratory Manual (3rd Ed, 2001).

[0103] According to one aspect of the present invention, there is provided a method for assigning a feline to one or more breeds and/or populations of origin based on the genotypes of a set of gene polymorphisms. The method comprises the steps of first isolating a genomic DNA sample from a feline, and then detecting, *e.g.*, amplifying a region genomic DNA including the one or more of the genetic markers using an oligonucleotide pair to form nucleic acid amplification products of the one or more gene polymorphism sequences. Amplification can be by any of a number of methods known to those skilled in the art including PCR, and the invention is intended to encompass any suitable methods of DNA amplification. A number of DNA amplification techniques are suitable for use with the present invention. Conveniently, such amplification techniques include methods such as polymerase chain reaction (PCR), strand displacement amplification (SDA), nucleic acid sequence based amplification (NASBA), rolling circle amplification, T7 polymerase mediated amplification, T3 polymerase mediated amplification, SP6 polymerase mediated amplification, and GoldenGate amplification assays. The precise method of DNA amplification is not intended to be limiting, and other methods not listed here will be apparent to those skilled in the art and their use is within the scope of the invention.

[0104] In some embodiments, the polymerase chain reaction (PCR) process is used (see, e.g., U.S. Pat. Nos. 4,683,195 and 4,683,202. PCR involves the use of a thermostable DNA polymerase, known sequences as primers, and heating cycles, which separate the replicating deoxyribonucleic acid (DNA), strands and exponentially amplify a gene of interest. Any type of PCR, including quantitative PCR, RT-PCR, hot start PCR, LA-PCR, multiplex PCR, touchdown PCR, finds use. In some embodiments, real-time PCR is used.

[0105] The amplification products are then analyzed in order to detect the presence or absence of at least one polymorphism in the feline genome that is associated with the desired genotypes and/or phenotypes, as discussed herein. By practicing the methods of the present invention and analyzing the amplification products it is possible to determine the genotype of individual animals with respect to the polymorphism.

[0106] In some embodiments, the genetic markers may be detected by restriction fragment length polymorphism (RFLP) analysis of a PCR amplicon produced by amplification of genomic DNA with the oligonucleotide pair. In order to simplify detection of the amplification products and the restriction fragments, those of skill will appreciate that the amplified DNA will further comprise labeled moieties to permit detection of relatively small amounts of product. A variety of moieties are well known to those skilled in the art and include such labeling tags as fluorescent, bioluminescent, chemiluminescent, and radioactive or colorigenic moieties.

[0107] A variety of methods of detecting the presence and restriction digestion properties of amplification products are also suitable for use with the present invention. These can include methods such as gel electrophoresis, mass spectroscopy or the like. The present invention is also adapted to the use of single stranded DNA detection techniques such as fluorescence resonance energy transfer (FRET). For FRET analysis, hybridization anchor and detection probes may be used to hybridize to the amplification products. The probes sequences are selected such that in the presence of the SNP, for example, the resulting hybridization complex is more stable than if there is a G or C residue at a particular nucleotide position. By adjusting the hybridization conditions, it is therefore possible to distinguish between animals with the SNP and those without. A variety of parameters well known to those skilled in the art can be used to affect the ability of a hybridization complex to form. These include changes in temperature, ionic concentration, or the inclusion of chemical constituents like formamide that decrease complex stability. It is further possible to distinguish animals heterozygous for the SNP versus those that are homozygous for the same. The method of FRET analysis is well known to the art, and the conditions under which the presence or absence of the SNP would be detected by FRET are readily determinable.

[0108] Suitable sequence methods of detection also include e.g., dideoxy sequencing-based methods and Maxam and Gilbert sequence (see, e.g., Sambrook and Russell, supra). Suitable HPLC-based analyses include, e.g., denaturing HPLC (dHPLC) as described in e.g., Premstaller and Oefner, LC-GC Europe 1-9 (July 2002); Bennet et al., BMC Genetics 2:17 (2001); Schrimi et al., Biotechniques 28(4):740 (2000); and Nairz et al., PNAS USA 99(16):10575-10580 (2002); and ion-pair reversed phase HPLC-electrospray ionization mass spectrometry (ICEMS) as described in e.g., Oberacher et al.; Hum. Mutat. 21(1):86 (2003). Other methods for characterizing single base changes in alleles of genetic markers include, e.g., single base extensions (see, e.g., Kobayashi et al, Mol. Cell. Probes, 9:175-182, 1995); single-strand conformation polymorphism analysis, as described, e.g, in Orita et al., Proc. Nat. Acad. Sci. 86, 2766-2770 (1989), allele specific oligonucleotide hybridization (ASO) (e.g., Stoneking et al., Am. J. Hum. Genet. 48:70–382, 1991; Saiki et al., Nature 324, 163-166, 1986; EP 235,726; and WO 89/11548); and sequence-specific amplification or primer extension methods as described in, for example, WO 93/22456; U.S. Pat. Nos. 5,137,806; 5,595,890; 5,639,611; and U.S. Pat. No. 4,851,331; 5'-nuclease assays, as described in U.S. Pat. Nos. 5,210,015; 5,487,972; and 5,804,375; and Holland et al., 1988, Proc. Natl. Acad. Sci. USA 88:7276-7280.

[0109] Methods for detecting single base changes well known in the art often entail one of several general protocols: hybridization using sequence-specific oligonucleotides, primer extension, sequence-specific ligation, sequencing, or electrophoretic separation techniques, e.g., singled-stranded conformational polymorphism (SSCP) and heteroduplex analysis. Exemplary assays include 5' nuclease assays, template-directed dye-terminator incorporation, molecular beacon allele-specific oligonucleotide assays, single-base extension assays, and SNP scoring by real-time pyrophosphate sequences. Analysis of amplified sequences can be performed using various technologies such as microchips, fluorescence polarization assays, and matrix-assisted laser desorption ionization (MALDI) mass spectrometry. In addition to these frequently used methodologies for analysis of nucleic acid samples to detect single base changes, any method known in the art can be used to detect the presence of the genetic markers described herein.

[0110] For example FRET analysis can be used as a method of detection. Conveniently, hybridization probes comprising an anchor and detection probe, the design of which art is well known to those skilled in the art of FRET analysis, are labeled with a detectable moiety, and then under suitable conditions are hybridized an amplification product containing the genetic marker of interest in order to form a hybridization complex. A variety of parameters well known to those skilled in the art can be used to affect the ability of a hybridization complex to form. These include changes in temperature, ionic concentration, or the inclusion of chemical constituents like formamide that decrease complex stability. The presence or absence of the genetic marker is then determined by the stability of the hybridization complex. The parameters affecting hybridization and FRET analysis are well known to those skilled in the art. The amplification products and hybridization probes described herein are suitable for use with FRET analysis.

6. Methods of Analyzing Biomarkers

[0111] The methods comoprise determining the contributions of one or more feline populations (*e.g.*, ancestral lineage and/or breed contributions) to the test feline genome by comparing the alleles at the predetermined genetic markers in the test feline genome (*e.g.*, a plurality of the SNPs listed in Table 1; optionally one or more phenotypic markers and/or microsatellite markers) to a database comprising feline population profiles, wherein each feline population profile comprises genotype information for alleles of the markers in the set of markers in the feline population. For example, a feline population profile may comprise genotype information for each allele of each marker in the set of markers in the feline population. The genotype information in a feline 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 felines that are members of that feline 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 feline population. The collection of feline population profiles can be collected in a database for use in practicing the invention. In some embodiments, the database of feline population profiles comprises one or more feline population profiles. In various embodiments, the database of feline population profiles comprises a plurality of feline population profiles, *e.g.*, between about five and about 500 feline population profiles, such as about 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, or more, feline population profiles.

[0112] Determining the contributions of feline populations to the test feline genome can encompass both assigning a feline genome to one or more particular feline populations and/or determining the fraction of the feline genome that was derived from one or more feline populations. In one embodiment, the test feline is suspected of having at least about 25% of the feline genome, *e.g.*, at least about 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100%, derived from a single defined feline population (*e.g.*, ancestral lineage and/or breed).

[0113] Many methods of assignment testing have been developed in the past decade using common population genetic markers and a variety of statistical methods (Rannala & Mountain (1997) *Proc Natl Acad Sci U S A.* 94(17):9197-9201; Pritchard et al. (2000) *Genetics*, 155:945-959; Baudouin & Lebrun (2001) In: *Proc. Int. Symp. on Molecular Markers*, pp. 81-94; Paetkau et al. (2004) *Molecular Ecology*, 13:55-65). These methods have been applied to various breeding populations including pigs, cattle, and dogs (Schelling et al. (2005) *Journal of Animal Breeding and Genetics*, 122:71-77; Negrini et al. (2009) *Animal Genetics*, 40:18-26; Boitard et al. (2010) *Anim Genet.* 2010 41(6):608-18. *See also,* U.S. Patent Nos. 7,729,863 and 6,770,437. In some embodiments of the method, a

Bayesian model-based clustering approach is used, *e.g.*, as described by Rannala & Mountain, *supra*; Pritchard, *supra*; and/or Baudouin & Lebrun, *supra*.

[0114] There are two broad classes of clustering methods that are used to assign individuals to populations (Pritchard, *supra*). Distance-based methods calculate 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. In some embodiments of the method, a likelihood or frequentist model-based approach is used, *e.g.*, as described by Paetkau, *supra*; and/or Negrini, *supra*. 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.

[0115] 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), Geneclass2 (Piry et al., (2004) *Journal of Heredity* 95, 536-539) and STRUCTURE (Pritchard et al. (2000) Genetics 155:945-59).

[0116] 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.

[0117] 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 Rannala & Mountain (1997) Proc. Natl. Acad. Sci. U.S.A. 94:9197-9201, Paetkau et al. (2004) *Molecular Ecology*, 13:55-65 and Cornuet et al. (1999) Genetics 153:1989-2000 and variations thereof. Exemplary programs available for multi-locus genotype analysis include Doh (available on the internet at biology.ualberta.ca/jbrzusto/Doh.php) and GeneClass (available at montpellier.inra.fr/URLB/geneclass/genecass.htm). Cluster iterations can be combined, *e.g.*, through the program CLUMP (Jakobsson & Rosenberg, *Bioinformatics* 23(14):1801-6) and DISTRUCT (Rosenberg, (2004) *Molecular Ecology Notes* 4, 137-138) to create a consensus clustering. Migrants within populations can be detected, *e.g.*, using the program Geneclass2 (Piry et al., (2004) *Journal of Heredity* 95, 536-539.

[0118] In some embodiments, the methods of the invention comprise determining the probability that a specific feline population contributed to the genome of the test feline by determining the conditional probability that the alleles in the test feline genome would occur in the specific feline population divided by the sum of conditional probabilities that the alleles in the test feline genome would occur in each feline population in the database.

[0119] Some embodiments of the methods of the invention comprise discriminating between the contributions of two or more genetically related feline populations to the test feline genome by comparing the alleles in the test feline genome to a database comprising profiles of the two or more genetically related feline populations. In various embodiments, the two or more genetically related feline populations may comprise (i) Persian and Exotic Shorthair (SH); (ii) British SH and Scottish Fold; (iii) Australian Mist and Burmese; (iv) Singapura and Burmese; (v) Birman and Korat, and (vi) Siamese and Havana Brown.

[0120] Using an assignment algorithm on genotype information for all 148 SNPs listed in Table 1, 38 microsatellite markers and 5 phenotypic markers listed in Table 3 from 477 felines representing 29 feline breeds, the methods of the invention have been used to assign individual test felines to its breed with at least about 50% sensitivity and specificity, for example, at least about 60%, 70%, 75%, 80%, 85%, 90%, 95% sensitivity and specificity, or greater. As used herein, sensitivity specifically indicates the percentage of individuals sampled from a breed that could be assigned back to that breed. Specificity takes into account individuals sampled from other breeds that were misassigned to that breed. Sensitivity and specificity are properly used to describe the power of the testing in assignment testing. *See*, Example 2.

[0121] The methods of the invention are also useful for determining the contributions of feline populations to felines having genetic contributions from more than one breed or defined ancestral lineage. Preferably, the test feline has at least 25% of the markers, *e.g.*, at least about 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100% of the markers, associated with a defined ancestral lineage or breed. 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. 88:62-5), 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.

7. Reporting Results of Analysis

[0122] In various embodiments, the methods may further comprise the step of reporting the results of the assignment analysis, *e.g.*, to the purchaser, to the owner or guardian of the feline, to a breed registry, to a veterinarian or another interested individual. The methods may further comprise the step of providing a document displaying the contributions of one or more feline populations to the genome of the test feline genome. The document may be a chart, certificate, card, or any other kind of documentation. The document may be electronic or paper copy. The document may display the contributions of one or more feline populations to the test feline 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 feline 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 feline populations to the genome of the test feline genome.

[0123] In some embodiments, the document additionally provides information regarding the one or more feline populations that contributed to the genome of the test feline or the test feline. The information regarding feline populations that contributed to the genome of the test feline may include information related to the characteristics and origin of the feline population (*e.g.*, ancestral origin and/or contributing breed(s)) or any other kind of information that would be useful knowledge concerning the test feline. In some embodiment, the information includes health-related information. Many feline populations have predispositions to particular diseases or conditions. For example, heart disease in the Maine Coon and Ragdoll (Meurs et al. (2005) *Human Molecular Genetics*, 14:3587-3593; Meurs et al. (2007) *Genomics*, 90:261-264), polycystic kidney disease in the Persian (Lyons et al. 2004, *supra*), progressive retinal atrophy in the Abyssinian (Menotti-Raymond et al. (2007) *Journal of Heredity*, 98:211-220) and a craniofacial defect and hypokalemia in Burmese. Therefore, information regarding the contributions of one or more feline populations to the genome of the test feline genome is particularly valuable to mixed-breed feline 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 cat that is found to be a mixture of a breed with known association or predisposition for certain disease conditions could be proactively monitored for such disease conditions that occur with rare frequency in the general population of cats, but occur with significant frequency in these specific breeds.

[0124] Health-related information may also include potential treatments, special diets or products, diagnostic information, and insurance information.

8. Computer-Readable Media

[0125] In a further aspect, the invention provides one or more computer-readable media comprising a data structure stored thereon for use in distinguishing feline populations. In some embodiments, the data structure comprises: 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 feline genome or an estimate of the frequency of an allele of the marker in a feline 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 feline population profile.

[0126] 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. Computer readable media that are non-transitory find use. 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.

[0127] 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. In some embodiments, a data structure in the computer-readable medium can comprise 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 record provides a feline population profile. Thus, the data structure may be used to create a database of feline population profiles.

[0128] In some embodiments, the computer readable medium comprises a substrate having stored thereon: (a) a data structure for use in distinguishing feline 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 feline population profile; and (b) computer-executable instructions for implementing a method for determining the contributions of feline populations to a feline genome, comprising: (i) obtaining the identity of one or both alleles in a test feline genome for each marker of a set of markers; and (ii) determining the contributions of feline populations to the test feline genome by comparing the alleles in the test feline genome to a database comprising feline population profiles, wherein each feline population profile comprises genotype information for the set of markers in the feline population.

9. Kits

[0129] In another aspect, the invention provides nucleic acid sequences for determining the identity of one or both alleles in a feline genome for each marker of a set of markers, *e.g.*, as listed in Table 1. The nucleic acid sequences can be primer sets. In some embodiments, the primer sets are provided in a kit.

[0130] The invention further provides kits useful for determining the population of origin (*e.g.*, ancestral lineage and/or breed contributions) of a feline. In general, the kits comprise one or more oligonucleotide primer pairs as described herein suitable to amplify the portions of a feline genome comprising a plurality of the SNPs listed in Table 1. In some embodiments, the kit comprises oligonucleotide primer pairs for determining all 148 SNPs listed in Table 1. In various embodiments, the kits may further comprise one or more oligonucleotide primer pairs for determining one or more biomarkers listed in Table 3, *e.g.*, for determining the SNPs in one or more of SEQ ID NOs: 149-202. The kits comprise forward and reverse primers suitable for amplification of a genomic DNA sample taken from a feline. As described above, the biological sample can be from any tissue or fluid in which genomic DNA is present. Conveniently, the sample may be taken from blood, skin (*e.g.*, cheek swab) or a hair bulb.

EXAMPLES

[0131] The following examples are offered to illustrate, but not to limit the claimed invention.

Example 1

Genetic Structure of Worldwide Random Bred Cat Populations

[0132] This example describes the specific pinpointing of the geographic source of domestic cats. For this study, 944 cats from 37 random bred worldwide populations particularly from within the Middle East, Egypt and other Old World areas were genotyped at 148 SNPs and 38 cat-specific STRs. Thirty-eight wildcats were examined as outgroups. Principal Coordinate Analysis (PCA) and Bayesian clustering methods indicated eight modern worldwide cat populations belonging to at least five distinct ancestral groups; populations were geographically distributed, consistent with isolation by distance. Genetic indices were a gradient across the world, with the highest genetic diversity and lowest inbreeding in the region of historical Mesopotamia and the Levant, current day Iraq, Lebanon and Israel of the 37 sampled locations, more so than cats from Egypt, suggesting cats shared their cradle of domestication with the earliest human civilization and only later branching out towards Europe and Asia.

<u>Materials and Methods:</u>

[0133] *Cat Sample Collection*. This study included 944 domestic cats from 37 locations worldwide, including 20 locations and 481 cats novel to this study (Figure 1). Samples (n = 463) from a previous study included random bred cats from 17 locations (Lipinski et al., (2008) *Genomics* 91, 12-21). Samples were collected via buccal (cheek) swabs and extracted with a QIAamp DNA blood mini kit following the manufacturer's protocol (Qiagen, Valencia, CA, USA), or as whole blood spotted onto an FTA Card (Whatman International Ltd.) followed by a modified whole genome amplification (REPLI-g Mini Kit, Qiagen) as follows. A 0.12 cm punch was taken from the bloodstained card and washed with 5 minutes of gentle rocking a total of 5 times: 3 times with 0.5 ml of FTA purification mix made out of one part FTA-Reagents (Whatman International Ltd.), two parts PBS and 0.5% TWEEEN, and 2 washes with 0.5 mL of 1x TE Buffer (10 mL Tris HCl 1M, 2 mL EDTA 0.5M). This was dried at 60°C for 30 min. Two clean, dry punches were combined with 2.5 µl PBS and processed following the REPLI-g whole genome amplification kit protocol for amplification of genomic DNA from blood or cells (Qiagen, Valencia, CA, USA). Following whole genome amplification, consumed punches were discarded. Wildcat samples (N=38) were collected as part of other studies and provided as extracted DNA that had been whole genome amplified.

[0134] *SNP and STRs*. Thirty-eight autosomal STRs were genotyped following the PCR and analysis procedures of a previous study (Lipinski *et al*., 2008, *supra*). Unlinked non-coding autosomal SNPs (n=169), which were defined by one Abyssinian cat, were selected to represent all autosomes from the 1.9x coverage cat genomic sequence (Pontius, *et al*., 2007, (2007) *Genome Research* 17, 1675-1689). Primers were designed with the VeraCode Assay Designer software (Illumina Inc., San Diego, CA, USA). Only SNPs that received a design score of 0.75 or higher (with a mean design score of 0.95) (n = 162) were included in the analysis (Table 6).

[0135] Golden Gate Assay amplification and BeadXpress reads were performed per the manufacturer's protocol (Illumina Inc.) on 50-500ng of DNA or whole genome amplified product. BeadStudio software v. 3.1.3.0 with the Genotyping module v. 3.2.23 (Illumina Inc.) was used to analyze the data. Any samples with a call rate less than 0.80 (n = 21) were removed from further clustering analysis. Additionally, only SNPs with a Gentrain Score of > 0.55 (n = 148) were included in the study (Table 6).

Table 6
SNPs for the analysis of worldwide random bred cat populations.

Locus Name	Call Frequency	Minor Allele Frequency	Gentrain Score	Design Score
chrA1_10141047	0.753	0.099	0.8314	0.967
chrA1_133621071	0.822	0.316	0.6292	0.851
chrA1_151648701	0.82	0.161	0.9071	0.872
chrA1_175780586	0.745	0.257	0.797	0.908
chrA1_208054462	0.788	0.094	0.8803	1
chrA1_223501140	0.777	0.201	0.9354	0.979
chrA1_223506906	0.775	0.168	0.7732	0.911
chrA1_225057933	0.824	0.179	0.9035	0.934
chrA1_235579538	0.782	0.066	0.9023	0.953
chrA1_264488084	-	-	< 0.55	0.952
chrA1_27523501	0.816	0.408	0.7117	0.98
chrA1_68485376	0.806	0.116	0.6293	0.953
chrA1_69424718	0.796	0.369	0.8457	0.95
chrA1_7429296	0.755	0.121	0.933	0.976
chrA1_8742286	0.826	0.264	0.9066	0.9
chrA2_152258936	0.807	0.266	0.7745	0.941
chrA2_18603206	-	-	< 0.55	0.909
chrA2_201526186	0.822	0.253	0.9045	0.967
chrA2_202225770	0.794	0.222	0.9004	0.955
chrA2_44241149	0.834	0.014	0.8447	0.919
chrA2_554046	0.806	0.105	0.8098	0.754
chrA2_63928585	-	-	<0.55	0.977
chrA3_101420069	0.825	0.036	0.9005	0.949
chrA3_11480952	0.756	0.017	0.8013	0.847
chrA3_12082294	0.813	0.148	0.8723	0.941
chrA3_130195244	0.765	0.126	0.9275	0.915
chrA3_159537633	0.812	0.382	0.9266	0.986
chrA3_162208567	0.768	0.278	0.8971	0.959
chrA3_38781591	0.818	0.06	0.6781	0.913
chrA3_75156179	0.808	0.28	0.8108	0.991
chrA3_91058022	0.808	0.208	0.8533	0.969
chrA3_99507784	0.817	0.223	0.7373	0.94
chrB1_10420438	0.812	0.168	0.8177	0.973
chrB1_12214271	0.813	0.302	0.9113	0.977
chrB1_173872554	-	-	< 0.55	0.984
chrB1_195678303	0.82	0.122	0.8838	0.958
chrB1_199564532	0.816	0.068	0.8779	0.967
chrB1_202966562	0.807	0.304	0.9003	0.921
chrB1_54775572	0.826	0.086	0.7206	0.932

Table 6
SNPs for the analysis of worldwide random bred cat populations.

Locus Name	Call Frequency	Minor Allele Frequency	Gentrain Score	Design Score
chrB1_80161671	0.755	0.158	0.8431	0.971
chrB1_88148379	0.811	0.272	0.881	0.954
chrB2_138312489	0.816	0.315	0.9085	0.972
chrB2_146660650	0.834	0.013	0.9346	0.932
chrB2_165334691	-	-	< 0.55	0.978
chrB2_41509834	0.8	0.252	0.8068	0.988
chrB2_44611679	-	-	< 0.55	0.902
chrB2_45093345	0.779	0.252	0.8423	0.842
chrB2_6949528	0.824	0.096	0.9261	0.955
chrB3_104483970	0.818	0.223	0.8287	0.924
chrB3_111000326	0.827	0.129	0.8451	0.97
chrB3_13666494	0.813	0.337	0.8875	0.949
chrB3_144896949	-	-	< 0.55	0.93
chrB3_39203469	0.807	0.151	0.8987	0.91
chrB3_51317931	0.806	0.204	0.7156	0.96
chrB3_57141954	0.79	0.31	0.8199	0.814
chrB3_77094074	0.762	0.135	0.9005	0.945
chrB4_105706694	0.795	0.371	0.8855	0.936
chrB4_142658074	0.796	0.094	0.666	0.953
chrB4_143006494	0.79	0.18	0.8963	0.915
chrB4_144693308	0.806	0.267	0.925	0.906
chrB4_146486983	0.817	0.187	0.9402	0.978
chrB4_147206961	0.738	0.232	0.87	0.965
chrB4_149532846	0.756	0.108	0.856	0.992
chrB4_1687419	0.696	0.036	0.8797	0.992
chrB4_20001848	0.813	0.05	0.8896	0.983
chrB4_21098349	0.779	0.278	0.8934	0.929
chrB4_255106	0.8	0.154	0.8312	0.964
chrB4_3093827	0.812	0.094	0.9242	0.935
chrB4_40319102	0.79	0.363	0.8632	0.981
chrB4_47638578	0.813	0.084	0.9279	0.923
chrC1_104161375	-	-	< 0.55	0.909
chrC1_116355295	0.821	0.196	0.6692	0.924
chrC1_123164748	0.813	0.148	0.8197	0.94
chrC1_181852965	0.389	0.11	0.9008	0.954
chrC1_190502133	0.825	0.254	0.7788	0.968
chrC1_214768780	-	-	< 0.55	0.94
chrC1_215441574	0.794	0.255	0.863	0.956
chrC1_216852686	0.694	0.198	0.9473	0.958
chrC1_23778400	-	-	< 0.55	0.957
chrC1_24148281	0.811	0.143	0.8695	0.987
chrC1_28702055	0.819	0.168	0.9367	0.901
chrC1_34981315	0.814	0.031	0.8551	0.937
chrC1_396397	0.785	0.178	0.7129	0.976
chrC1_44520932	0.796	0.053	0.9208	0.982
chrC1_52456776	0.747	0.339	0.9	0.987
chrC2_106991233	0.802	0.302	0.8821	0.983
chrC2_147124460	0.824	0.394	0.8973	0.99
chrC2_150774106	0.821	0.046	0.7475	0.976
chrC2_156491175	0.799	0.376	0.8444	0.944

Table 6
SNPs for the analysis of worldwide random bred cat populations.

Locus Name	Call Frequency	Minor Allele Frequency	Gentrain Score	Design Score
chrC2_187325	0.689	0.116	0.7213	0.936
chrC2_262401	0.771	0.176	0.8529	0.981
chrC2_5215469	0.806	0.268	0.8223	0.958
chrC2_955732	-	-	< 0.55	0.947
chrD1_101321498	0.802	0.226	0.9247	0.904
chrD1_104941557	0.816	0.148	0.8874	0.956
chrD1_105498119	0.798	0.084	0.8834	0.942
chrD1_10789012	0.818	0.231	0.8845	0.904
chrD1_11484008	0.797	0.095	0.8929	0.922
chrD1_117527468	0.823	0.093	0.8557	0.931
chrD1_125811329	0.761	0.166	0.7921	0.906
chrD1_126256993	0.815	0.202	0.8932	0.977
chrD1_126847301	0.804	0.06	0.8391	0.96
chrD1_15984279	0.806	0.256	0.8615	0.964
chrD1_16242433	0.728	0.178	0.8532	0.988
chrD1_17005687	-	-	< 0.55	0.955
chrD1_18390852	0.816	0.213	0.933	0.902
chrD1_18570323	0.811	0.279	0.9196	0.943
chrD1_66177762	0.813	0.073	0.7002	0.974
chrD2_1020904	0.82	0.383	0.7066	0.922
chrD2_103984864	-	-	< 0.55	0.933
chrD2_105772916	0.808	0.211	0.8808	0.996
chrD2_1752007	0.81	0.09	0.8115	0.991
chrD2_56777338	0.832	0.004	0.7186	0.949
chrD2_717969	0.771	0.263	0.8805	0.932
chrD2_74293444	0.784	0.134	0.8692	0.985
chrD2_91989307	0.817	0.165	0.8417	0.945
chrD3_103840114	0.829	0.029	0.8386	0.867
chrD3_122502120	0.807	0.173	0.7726	0.982
chrD3_1810839	0.515	0.191	0.8856	0.951
chrD3_24565823	0.827	0.057	0.7063	0.93
chrD3_24823793	0.792	0.128	0.8819	0.901
chrD3_28838660	0.824	0.057	0.8921	0.968
chrD4_41078218	0.77	0.301	0.8384	0.84
chrD4_42000379	0.785	0.055	0.8177	0.941
chrD4_63622083	0.786	0.196	0.886	0.937
chrE1_130875919	0.803	0.09	0.6753	0.947
chrE1_131587399	0.762	0.146	0.8134	0.966
chrE1_3912105	0.81	0.119	0.9033	0.997
chrE1_4114158	0.81	0.366	0.8524	0.997
chrE1_48228153	0.814	0.155	0.8877	0.963
chrE1_48700963	0.828	0.043	0.8647	0.981
chrE1_5453028	0.822	0.347	0.9203	0.947
chrE2_22632289	0.804	0.298	0.8704	0.989
chrE2_34027888	0.807	0.168	0.6515	0.994
chrE2_35914023	0.805	0.152	0.906	0.834
chrE2_36986631	0.815	0.361	0.927	0.968
chrE2_38860686	0.811	0.212	0.7932	0.989
chrE2_39211557	0.651	0.24	0.6053	0.964
chrE2_65436639	0.818	0.253	0.9099	0.937

Table 6
SNPs for the analysis of worldwide random bred cat populations.

Locus Name	Call Frequency	Minor Allele Frequency	Gentrain Score	Design Score
chrE2_7950477	0.8	0.347	0.6547	0.989
chrE2_8422942	0.771	0.115	0.8173	0.96
chrE3_36044809	0.81	0.256	0.8796	0.833
chrE3_42164232	-	-	< 0.55	0.967
chrE3_55434272	0.782	0.241	0.7735	0.936
chrE3_67006512	0.681	0.071	0.8178	0.96
chrF1_20309325	0.824	0.059	0.7635	0.983
chrF1_21799641	0.824	0.122	0.8749	0.937
chrF1_26100599	0.804	0.271	0.8394	0.951
chrF1_27124984	0.814	0.213	0.9122	0.929
chrF1_38051725	0.819	0.331	0.9303	0.993
chrF1_565223	0.802	0.348	0.8739	0.958
chrF1_82068276	0.682	0.157	0.7686	0.91
chrF1_82716202	0.81	0.253	0.8563	0.943
chrF1_91517402	0.809	0.166	0.7746	0.933
chrF2_26886470	0.799	0.198	0.8643	0.957
chrF2_38395360	0.801	0.317	0.877	0.993
chrF2_46855978	0.808	0.277	0.7193	0.963
chrF2_68572596	0.796	0.191	0.8183	0.956
chrF2_74863327	0.82	0.18	0.9059	0.976
chrF2_78303221	0.812	0.4	0.911	0.911
chrF2_79632602	0.827	0.019	0.9445	0.959
chrF2_8427817	0.695	0.302	0.8707	0.955

Locus name includes the chromosome and location of each SNP.

[0136] *Data analysis*. Data sets were analyzed with the Bayesian clustering program STRUCTURE (Pritchard et al., (2000) *Genetics* 155, 945-959) under the admixture model with correlated allele frequencies and a burn-in of 100,000 with 100,000 additional iterations. Values of K were calculated from K = 1 to K = 25, each run was replicated 10 times. Posterior log likelihoods were used in the calculation of ΔK in order to best estimate the number of ancestral populations through the program Harvester (Evanno et al., (2005) *Molecular Ecology* 14, 2611-2620) (Figure 2). To assess the effects of varying marker types on the final results, STRUCTURE analysis was conducted on the data in three different permutations: only SNPs, only STRs, and SNPs and STRs together. Images were created with CLUMPP v. 1.1.2 (Jakobsson and Rosenberg, (2007) *Bioinformatics* 23(14):1801-6) to combine replicates and DISTRUCT v. 1.1 (Rosenberg, (2004) *Molecular Ecology Notes* 4, 137-138) to create final images. A map of cat domestication was created using an inverse distance function. Each point on the map has an interpolated likelihood for each cluster; the color is the most likely cluster. Color saturation is based on the value of the likelihood (e.g. low saturation means low likelihood) (Figure 1).

[0137] First generation migrants within populations identified by STRUCTURE were detected with the program Geneclass2 (Piry et al., (2004) *Journal of Heredity* 95, 536-539) under the Rannala and Mountain (*Proc Natl Acad Sci U S A*. (1997) 94(17):9197-201) Bayesian model, with 1000 Monte-Carlo re-sampling simulations (Paetkau et al., (2004) *Molecular Ecology* 13, 55-65), and the p-value threshold set at 0.01. From both STRs and SNPs, samples that were below the threshold of 0.01 for originating from the same lineage as that assigned for the majority of the cats from the same sampling location were considered recent immigrants and removed from subsequent analyses. These individuals were compared to the first generation migration test applied to the output from STRUCTURE as in previous studies (Randall et al., (2010) *Conservation Genetics* 11, 89-101), where individuals that clustered with a lineage other than that of the majority of their sampling location with a posterior probability of >0.5 were considered to be first generation immigrants to that sampling location (n = 56). All migrants were removed from further analyses (n = 63). FIS was calculated with Fstat v. 2.9.3.2 (Goudet, (1995) J Hered (1995) 86(6): 485-486) and observed and expected heterozygosites with GenAlEx v.6.3 (Peakall, Smouse, (2006) *Molecular Ecology Notes* 6, 288-295). F-statistics were calculated both by sampling location and based on the populations as assigned by STRUCTURE.

[0138] Principal coordinates analyses were conducted on a matrix of Nei's unbiased genetic distance and plotted via the standardized co-variance using the software GenAlEx (Peakall, Smouse, 2006, *supra*).

[0139] Phylogenetic trees were created with the software package PHYLIP version 3.67 (Felsenstein, (1989) *Cladistics* 5, 164-166). Allele frequencies for each data set were analyzed sequentially with SeqBoot, Genedist, Neighbor, and Consense to create a consensus tree. Trees were replicated with 1,000 bootstraps; genetic distance was calculated following Nei's unbiased method (Nei, Roychoudhury, (1974) *Genetics* 76:379-390) with the STRs to account for not only genetic drift, but also the fast mutation rate of the markers. The method of Reynolds et al. (Reynolds et al., (1983) *Genetics* 105, 767-779) was applied to the SNP data to account for genetic drift only. Final unrooted trees were produced with the neighbor-joining method and visualized with FigTree v1.3.1 (on the internet at tree.bio.ed.ac.uk/software/figtree).

Results:

[0140] The final analyses consisted of cat DNA samples (n = 944) from worldwide populations, including 463 domestic cats used previously (Lipinski et al., 2008, *supra*), and 481 domestic cat samples collected from 20 additional locations in the Middle East, Kenya, India, and Japan (Figure 1). Thirty-eight wildcats of known genetic origin (*F. silvestris silvestris* (Western Europe), *F. s. libyca* (assorted African locations), and *F.s. tristrami* (Israel)) (Lipinski et al., 2008, *supra*) were used as outgroups for the analyses. The 38 STRs had an average call rate of 92.3% and the 148 SNPs had an average call rate of 95.5%.

[0141] Bayesian clustering suggested a value of K = 5 (Figure 2) for both SNPs and STRs resulting in five groupings corresponding to Europe, Mediterranean (including Western portions of the Middle East), Iraq/Iran, South Asia, and East Asia (Figure 3A, C) (alternate plots are available as Figure 4). The sampling locations along the Indian Ocean, including India and Sri Lanka, appeared to be admixtures of all five ancestral lineages, which are more strongly depicted by the STR data (Figure 3C). A secondary peak in ΔK values was observed at K=7 in the STRs and K=8 in SNPs, however, the two marker types resolved with some discrepancies (Figure 3B, D). SNPs and STRs both separated the Egyptian cats from the other Mediterranean cats, STRs indicating a stronger distinction (Figure 3D) than the SNPs (Figure 3B). STRs additionally indicated the Arabian Sea (Dubai, Pate, and Lamu), to be distinct from the cats of India, Sri Lanka and Southern Asia (Thailand and Vietnam). SNPs were able to discern the Arabian Sea cats and the Southern Asian cats as distinct populations but maintained the cats of India as highly admixed.

[0142] When SNPs and STRs were combined for analysis, a consensus of both the individual SNP and STR analyses is observed, suggesting five distinct ancestral lineages (Figure 3E) and eight modern populations (Figure 3). The division between the Arabian Sea and the Indian populations is supported by the STR data, but not the SNP data set, while the division between Indian and South Asian populations is supported by the SNP but not the STR data. Besides the Indian cats, the cats from Taiwan and Sapporo, Japan have the most amount of admixture.

[0143] When analyzed for first generation migrants, 21 individuals had a p-value of less than 0.01 indicating that these cats were likely not native to the sampling location. Additionally, detection of first generation migrants using the posterior probabilities of assignment with STRUCTURE detected 56 individuals (42 additional migrants), for a combined total of 63 individuals when the cats from the two methods were combined (Table 7). Europe is the source for a majority of the migrant cats that are found in other parts of the world (33%). The remainder of migrant cats appears to have traveled a short distance to adjoining populations. Individuals that were categorized as first generation migrants were removed from further analyses.

Table 7

First generation migration test of eight worldwide cat populations*.

		Total First Generation Migrants from Each Source						
Lineage	**Sampling location**	**Europe**	**East Mediterranean**	**Egypt**	**Iraq/Iran**	**India**	**South Asia**	**East Asia**
Europe	Germany						1	
	Italy-Milan		4					
	Kenya-Nairobi			1		1		
East Mediterranean	Turkey	2		1			4	
	Cyprus			4				
	Lebanon	1		6			1	
	Israel	2						
Egypt	Cairo		6				2	1
	Luxor	1						
Arabian Sea	Dubai				1	1		
India	Sri Lanka	1	1					
South Asia	Vietnam					1		
East Asia	Taiwan	7				1		
	Japan-Oita						2	
	Japan-Kanazawa	2						
	Japan-Ohmiya						1	
	Japan-Sapporo	4					2	
	South Korea	1						
Total	N = 63	21	11	12	1	4	13	1

*Number of individuals that were determined migrants with a p-value < 0.01 calculated using Geneclass2 (Peakall, Smouse, 2006, *supra*). Populations with no detected migrants are not presented.

[0144] Population statistics are presented both for each sampling site (Table 8) and population (Table 9) including the average effective number of alleles, inbreeding coefficients (FIS) and observed heterozygosity (HO) based on SNPs and STRs. No population had a diagnostic / unique SNP. The range of the SNP minor allele frequencies (MAF) throughout the world suggests insignificant ascertainment bias (Table 10). The populations with the highest number of STR alleles were the Mediterranean lineage and the modern Egyptian population, the lowest were found in East Asia. Private alleles were most common in the lineages from the Arabian Sea/Asia, Mediterranean and Iraq/Iran, and the modern lineages of the Arabian Sea and Iraq/Iran.

Table 8

Cat population statistics based on sampling locations*.

Sampling Location		n (Migrants)	Private Alleles	F_{IS} (SNP)	F_{IS} (STR)	H_O (SNP)	H_O (STR)
Europe (sites=9)	USA-NY	9	2	0.032	0.128	0.312	0.639
	USA-MS	10	0	0.026	0.063	0.309	0.68
	USA-HI	10	0	0.084	0.142	0.304	0.615
	Brazil	29	1	0.014	0.072	0.3	0.652
	Finland	11	0	0.174	0.082	0.259	0.628
	Germany	28	3	0.209	0.101	0.255	0.626
	Italy-Milan	10	1	0.051	0.039	0.316	0.711
	Italy-Rome	15	2	0.018	0.098	0.315	0.651
	Kenya-Nairobi	34	6	-0.015	0.056	0.336	0.725
Eastern Mediterr. Basin (sites=4)	Turkey	44	4	0.118	0.064	0.267	0.689
	Cyprus	26	2	0.002	0.078	0.309	0.704
	Lebanon	50	4	0.025	0.058	0.298	0.717
	Israel-Tel Aviv	44	2	0.006	0.076	0.301	0.751
Egypt (sites=4)	Cairo	75	6	0.053	0.107	0.292	0.688
	Assuit	10	1	-0.064	0.031	0.298	0.704
	Luxor	27	5	-0.008	0.043	0.303	0.745
	Abu Simbel	5	1	0.027	0.099	0.286	0.673
Iraq/Iran (sites= 3)	Iraq-Western	12	1	-0.06	0.102	0.295	0.684
	Baghdad	33	7	-0.025	0.043	0.284	0.721
	Iran	110	4	0.045	0.121	0.239	0.646
Arabian Sea (sites=3)	Dubai	8	2	0.03	0.024	0.244	0.699
	Kenya-Pate	9	0	-0.015	0.056	0.241	0.597
	Kenya-Lamu	20	2	0.04	0.118	0.249	0.59
India (sites=5)	Udaipur/Agra	15	2	-0.08	0.073	0.268	0.68
	Hyderbad	20	2	-0.008	0.103	0.266	0.688
	Andhra	23	3	0.02	0.076	0.259	0.665
	Kolkata	7	1	0.07	0.144	0.261	0.639
	Sri Lanka	24	2	0.015	0.054	0.289	0.719
South Asia (sites=2)	Thailand	14	1	0.171	0.153	0.183	0.563
	Vietnam	19	0	0.038	0.065	0.261	0.639
East Asia (sites=7)	Taiwan	21	0	0.008	0.025	0.287	0.681
	Japan-Oita	15	1	0.11	0.101	0.248	0.613
	Japan-Kanazawa	13	0	0.1	0.111	0.237	0.604
	Japan-Ohmiya	15	0	0.071	0.163	0.259	0.594
	Japan-Sapporo	9	0	0.031	0.075	0.26	0.641
	China-Henan	20	3	0.012	0.043	0.219	0.627
	South Korea	37	0	0.044	0.04	0.246	0.619
Total	sites = 37	881 (63)	71			0.275	0.66

*First generation migrants were not included. N = sample size. F_{IS} = average inbreeding coefficient of an individual relative to its source population, H_O = observed heterozygosity.

Table 9

Population statistics of worldwide cat populations

Population	n	Total Alleles	Private Alleles	Aver. N_e	F_{IS}(SNP)	F_{IS}(STR)	H_O(SNP)	H_O(STR)
Ancient Basal Lineage								
Europe	156	452	5	4.908	0.087	0.107	0.302	0.678
Mediterranean	281	516	7	5.466	0.051	0.089	0.293	0.71
Iraq/Iran	155	408	7	4.866	0.038	0.118	0.252	0.682
Arabian Sea/Asia	159	455	9	5.197	0.102	0.153	0.254	0.657
East Asia	130	402	3	4.299	0.087	0.097	0.249	0.652
Modern Lineage								
Europe	156	452	5	4.941	0.087	0.107	0.302	0.678
East Mediterranean Basin	164	481	3	5.284	0.053	0.079	0.291	0.715
Egypt	117	447	3	5.353	0.04	0.096	0.295	0.704
Iraq/Iran	155	408	7	4.866	0.038	0.118	0.252	0.682
Arabian Sea	37	288	8	3.802	0.066	0.121	0.245	0.632
India	89	416	4	5.193	0.042	0.122	0.27	0.683
South Asia	33	285	4	3.554	0.112	0.11	0.225	0.617
East Asia	130	402	4	4.442	0.087	0.097	0.249	0.652

*First generation migrants were not included. n = sample size. Aver. N_e = average effective number of alleles F_{IS} = average inbreeding coefficient of an individual relative to its source population, H_O = observed heterozygosity.

Table 10
Minor Allele Frequency based on population

Locus	Europe	East Mediterranean	Egypt	Iraq/Iran	Arabian Sea	India	South Asia	East Asia
chrA1_10141047	0.108	0.277	0.308	0.260	0.100	.045	.097	.027
chrA1_133621071	0.304	0.222	0.309	0.283	0.189	.316	.129	.108
chrA1_151648701	0.120	0.063	0.056	0.013	0.027	.023	.000	.058
chrA1_175780586	0.423	0.410	0.299	0.085	0.088	.162	.581	.363
chrA1_208054462	0.142	0.138	0.182	0.013	0.014	.055	.125	.090
chrA1_223501140	0.162	0.082	0.074	0.039	0.111	.167	.076	.100
chrA1_223506906	0.154	0.195	0.329	0.367	0.708	.425	.183	.529
chrA1_225057933	0.221	0.218	0.284	0.401	0.000	.259	.139	.437
chrA1_235579538	0.054	0.144	0.090	0.299	0.324	.125	.056	.071
chrA1_27523501	0.574	0.372	0.364	0.255	0.432	.351	.214	.437
chrA1_68485376	0.141	0.076	0.009	0.000	0.000	.006	.015	.014
chrA1_69424718	0.292	0.343	0.332	0.755	0.542	.335	.412	.322
chrA1_7429296	0.183	0.150	0.161	0.244	0.581	.296	.028	.125
chrA1_8742286	0.273	0.406	0.426	0.683	0.257	.476	.514	.303
chrA2_152258936	0.409	0.399	0.319	0.565	0.446	.314	.471	.182
chrA2_201526186	0.207	0.156	0.269	0.161	0.176	.253	.103	.104
chrA2_202225770	0.317	0.319	0.232	0.203	0.108	.440	.672	.338
chrA2_44241149	0.062	0.016	0.009	0.006	0.000	.017	.014	.003
chrA2_554046	0.133	0.169	0.217	0.186	0.027	.144	.028	.236
chrA3_101420069	0.056	0.057	0.065	0.000	0.054	.087	.000	.061
chrA3_11480952	0.053	0.021	0.027	0.000	0.014	.000	.048	.054
chrA3_12082294	0.336	0.171	0.252	0.126	0.095	.063	.103	.119
chrA3_130195244	0.199	0.284	0.368	0.075	0.111	.124	.138	.096
chrA3_159537633	0.528	0.405	0.350	0.301	0.595	.494	.757	.519
chrA3_162208567	0.377	0.194	0.196	0.260	0.068	.064	.016	.139
chrA3_38781591	0.022	0.016	0.004	0.006	0.000			

Table 10
Minor Allele Frequency based on population

Locus	Europe	East Mediterranean	Egypt	Iraq/Iran	Arabian Sea	India	South Asia	East Asia
						.011	.000	.000
chrA3_75156179	0.266	0.375	0.348	0.243	0.068	.127	.069	.167
chrA3_91058022	0.484	0.256	0.241	0.104	0.230	.106	.121	.165
chrA3_99507784	0.231	0.302	0.296	0.578	0.162	.355	.456	.411
chrB1_10420438	0.104	0.082	0.034	0.023	0.027	.034	.014	.033
chrB1_12214271	0.401	0.392	0.591	0.350	0.514	.554	.333	.437
chrB1_195678303	0.102	0.258	0.230	0.358	0.351	.116	.071	.107
chrB1_199564532	0.156	0.101	0.154	0.003	0.027	.052	.000	.028
chrB1_202966562	0.381	0.263	0.198	0.183	0.149	.184	.235	.175
chrB1_54775572	0.188	0.204	0.135	0.059	0.216	.000	.097	.028
chrB1_80161671	0.169	0.096	0.058	0.241	0.068	.122	.097	.069
chrB1_88148379	0.360	0.477	0.483	0.443	0.622	.369	.182	.371
chrB2_138312489	0.422	0.462	0.422	0.282	0.284	.698	.700	.482
chrB2_146660650	0.000	0.000	0.004	0.000	0.014	.034	.139	.010
chrB2_41509834	0.278	0.257	0.155	0.624	0.351	.464	.614	.489
chrB2_45093345	0.542	0.433	0.404	0.093	0.257	.227	.258	.347
chrB2_6949528	0.201	0.195	0.111	0.029	0.149	.029	.014	.070
chrB3_104483970	0.202	0.328	0.321	0.172	0.122	.506	.855	.420
chrB3_111000326	0.111	0.200	0.261	0.171	0.149	.333	.676	.260
chrB3_13666494	0.475	0.439	0.504	0.255	0.243	.560	.765	.528
chrB3_39203469	0.184	0.378	0.625	0.211	0.108	.071	.100	.138
chrB3_51317931	0.138	0.294	0.276	0.407	0.095	.390	.750	.254
chrB3_57141954	0.377	0.173	0.171	0.242	0.230	.137	.069	.281
chrB3_77094074	0.168	0.006	0.022	0.007	0.139	.056	.067	.059
chrB4_105706694	0.374	0.410	0.397	0.480	0.459	.585	.371	.628
chrB4_142658074	0.108	0.190	0.187	0.066	0.014	.030	.065	.121
chrB4_143006494	0.338	0.344	0.345	0.243	0.097			

Table 10
Minor Allele Frequency based on population

Locus	Europe	East Mediterranean	Egypt	Iraq/Iran	Arabian Sea	India	South Asia	East Asia
						.110	.074	.261
chrB4_144693308	0.311	0.426	0.460	0.450	0.473	.335	.469	.215
chrB4_146486983	0.193	0.194	0.124	0.288	0.541	.134	.641	.568
chrB4_147206961	0.350	0.276	0.434	0.293	0.176	.544	.750	.291
chrB4_149532846	0.126	0.056	0.030	0.016	0.014	.023	.057	.026
chrB4_1687419	0.108	0.141	0.145	0.013	0.000	.009	.000	.006
chrB4_20001848	0.046	0.008	0.000	0.003	0.000	.029	.029	.014
chrB4_21098349	0.581	0.408	0.375	0.359	0.357	.318	.118	.239
chrB4_255106	0.120	0.025	0.065	0.036	0.000	.006	.015	.031
chrB4_3093827	0.109	0.046	0.055	0.000	0.041	.071	.452	.161
chrB4_40319102	0.532	0.530	0.400	0.500	0.270	.440	.182	.188
chrB4_47638578	0.086	0.038	0.004	0.006	0.000	.017	.014	.031
chrC1_116355295	0.332	0.262	0.272	0.203	0.284	.320	.235	.155
chrC1_123164748	0.261	0.237	0.196	0.267	0.000	.229	.242	.120
chrC1_181852965	0.406	0.108	0.167	0.022	0.000	.113	.056	.239
chrC1_190502133	0.176	0.381	0.293	0.576	0.306	.215	.028	.127
chrC1_215441574	0.394	0.346	0.272	0.235	0.459	.323	.574	.389
chrC1_216852686	0.356	0.339	0.507	0.312	0.200	.231	.340	.211
chrC1_24148281	0.180	0.222	0.209	0.247	0.292	.324	.059	.116
chrC1_28702055	0.122	0.041	0.000	0.129	0.027	.029	.043	.024
chrC1_34981315	0.046	0.050	0.099	0.000	0.000	.012	.103	.040
chrC1_396397	0.392	0.313	0.425	0.139	0.230	.109	.030	.096
chrC1_44520932	0.134	0.087	0.137	0.003	0.014	.040	.015	.024
chrC1_52456776	0.342	0.352	0.454	0.747	0.569	.506	.529	.331
chrC2_106991233	0.261	0.250	0.274	0.279	0.068	.335	.578	.402
chrC2_147124460	0.516	0.492	0.556	0.416	0.568	.362	.186	.086
chrC2_150774106	0.072	0.057	0.059	0.032	0.014			

Table 10
Minor Allele Frequency based on population

Locus	Europe	East Mediterranean	Egypt	Iraq/Iran	Arabian Sea	India	South Asia	East Asia
						.012	.014	.060
chrC2_156491175	0.381	0.408	0.307	0.672	0.662	.667	.313	.565
chrC2_187325	0.105	0.195	0.289	0.168	0.216	.211	.383	.185
chrC2_262401	0.188	0.283	0.277	0.122	0.153	.280	.591	.283
chrC2_5215469	0.241	0.342	0.250	0.728	0.500	.313	.838	.628
chrD1_101321498	0.441	0.279	0.281	0.258	0.432	.134	.061	.186
chrD1_104941557	0.144	0.197	0.147	0.136	0.243	.052	.014	.084
chrD1_105498119	0.182	0.094	0.180	0.040	0.081	.177	.042	.046
chrD1_10789012	0.322	0.362	0.230	0.401	0.149	.149	.368	.524
chrD1_11484008	0.068	0.073	0.044	0.178	0.189	.247	.081	.471
chrD1_117527468	0.040	0.011	0.004	0.003	0.000	.000	.000	.010
chrD1_125811329	0.308	0.151	0.206	0.096	0.324	.169	.518	.172
chrD1_126256993	0.233	0.228	0.188	0.144	0.378	.221	.819	.361
chrD1_126847301	0.100	0.137	0.218	0.010	0.054	.052	.043	.011
chrD1_15984279	0.245	0.278	0.265	0.050	0.014	.100	.368	.124
chrD1_16242433	0.336	0.256	0.273	0.139	0.143	.198	.517	.340
chrD1_18390852	0.223	0.171	0.111	0.006	0.108	.080	.000	.066
chrD1_18570323	0.401	0.409	0.561	0.243	0.527	.430	.379	.450
chrD1_66177762	0.161	0.112	0.104	0.010	0.097	.052	.014	.095
chrD2_1020904	0.580	0.563	0.311	0.369	0.297	.333	.671	.525
chrD2_105772916	0.192	0.272	0.372	0.284	0.338	.412	.426	.154
chrD2_1752007	0.135	0.056	0.043	0.133	0.041	.147	.250	.135
chrD2_56777338	0.000	0.000	0.000	0.000	0.000	.000	.000	.000
chrD2_717969	0.402	0.252	0.542	0.256	0.136	.432	.719	.195
chrD2_74293444	0.208	0.151	0.155	0.122	0.189	.134	.118	.430
chrD2_91989307	0.133	0.041	0.065	0.013	0.041	.029	.014	.025
chrD3_103840114	0.022	0.040	0.043	0.039	0.135			

Table 10
Minor Allele Frequency based on population

Locus	Europe	East Mediterranean	Egypt	Iraq/Iran	Arabian Sea	India	South Asia	East Asia
						.046	.000	.011
chrD3_122502120	0.176	0.236	0.243	0.313	0.392	.310	.313	.194
chrD3_1810839	0.603	0.528	0.427	0.065	0.129	.211	.143	.104
chrD3_24565823	0.151	0.024	0.030	0.003	0.000	.023	.028	.035
chrD3_24823793	0.073	0.184	0.186	0.197	0.541	.339	.250	.368
chrD3_28838660	0.022	0.011	0.009	0.000	0.041	.100	.343	.127
chrD4_41078218	0.458	0.491	0.482	0.493	0.919	.402	.212	.313
chrD4_42000379	0.077	0.134	0.106	0.038	0.014	.078	.015	.011
chrD4_63622083	0.241	0.082	0.065	0.069	0.083	.135	.061	.088
chrE1_130875919	0.271	0.103	0.303	0.013	0.000	.061	.061	.032
chrE1_131587399	0.141	0.047	0.022	0.013	0.000	.023	.056	.083
chrE1_3912105	0.199	0.076	0.097	0.123	0.405	.092	.074	.120
chrE1_4114158	0.438	0.461	0.415	0.507	0.365	.458	.439	.550
chrE1_48228153	0.205	0.196	0.147	0.145	0.176	.198	.530	.223
chrE1_48700963	0.096	0.060	0.048	0.000	0.027	.034	.000	.053
chrE1_5453028	0.522	0.376	0.435	0.211	0.284	.157	.029	.071
chrE2_22632289	0.373	0.389	0.421	0.374	0.608	.371	.724	.656
chrE2_34027888	0.059	0.022	0.089	0.000	0.000	.076	.014	.063
chrE2_35914023	0.275	0.241	0.152	0.050	0.292	.194	.181	.431
chrE2_36986631	0.410	0.603	0.618	0.392	0.257	.471	.281	.191
chrE2_38860686	0.297	0.049	0.039	0.090	0.081	.059	.015	.094
chrE2_39211557	0.440	0.422	0.495	0.411	0.324	.402	.407	.357
chrE2_65436639	0.227	0.298	0.283	0.330	0.189	.310	.147	.216
chrE2_7950477	0.543	0.503	0.583	0.434	0.403	.421	.323	.496
chrE2_8422942	0.078	0.064	0.066	0.320	0.054	.017	.028	.053
chrE3_36044809	0.237	0.411	0.548	0.530	0.243	.282	.191	.686
chrE3_55434272	0.385	0.383	0.421	0.039	0.324			

Table 10
Minor Allele Frequency based on population

Locus	Europe	East Mediterranean	Egypt	Iraq/Iran	Arabian Sea	India	South Asia	East Asia
						.317	.303	.538
chrE3_67006512	0.129	0.123	0.109	0.083	0.045	.032	.030	.077
chrF1_20309325	0.075	0.081	0.022	0.076	0.097	.034	.069	.050
chrF1_21799641	0.331	0.079	0.113	0.048	0.108	.098	.042	.108
chrF1_26100599	0.356	0.194	0.068	0.072	0.189	.167	.186	.170
chrF1_27124984	0.206	0.253	0.297	0.373	0.292	.429	.667	.461
chrF1_38051725	0.541	0.644	0.671	0.317	0.122	.305	.530	.434
chrF1_565223	0.537	0.562	0.575	0.537	0.392	.464	.529	.399
chrF1_82068276	0.187	0.065	0.059	0.007	0.015	.250	.379	.289
chrF1_82716202	0.288	0.191	0.125	0.339	0.243	.100	.100	.124
chrF1_91517402	0.214	0.223	0.184	0.176	0.351	.327	.044	.064
chrF2_26886470	0.104	0.153	0.104	0.459	0.405	.494	.591	.390
chrF2_38395360	0.349	0.270	0.279	0.334	0.338	.360	.029	.184
chrF2_46855978	0.332	0.280	0.309	0.229	0.392	.407	.444	.310
chrF2_68572596	0.211	0.270	0.318	0.302	0.500	.323	.717	.313
chrF2_74863327	0.181	0.278	0.282	0.171	0.122	.306	.338	.336
chrF2_78303221	0.522	0.469	0.530	0.257	0.284	.571	.727	.595
chrF2_79632602	0.025	0.011	0.004	0.062	0.000	.006	.000	.007
chrF2_8427817	0.390	0.408	0.387	0.227	0.257	.378	.350	.489

[0145] Principal coordinates analyses (PCA) (Figure 5) broadly correlated with the STRUCTURE analyses. PCA consistently grouped individuals from the same geographic cluster together as delineated by Bayesian clustering (Figure 3). Differences of SNP (Figure 5A) versus STR (Figure 5B) based analyses are most notably in the distance of the Arabian Sea populations from those of the Iraqi/Iranian populations (more distant with SNPs and less so with STRs). Also, SNPs position the South Asian populations close to that of the Indian populations as opposed to closer to the East Asian populations when STRs are used. Despite these slight changes in comparative distance, both PCA analyses show genetic distances to be correlated with that of geographical or physical distances of the populations and sampling sites.

[0146] The SNP (Figure 6A) and STR-based (Figure 6B) Neighbor-joining phylogenetic trees were also broadly concordant with the STRUCTURE and PCA defined lineages through forming groups along geographical lines. Very high bootstrap values are noted between cats that show strong associations in the other analyses, including, cats from Vietnam and Thailand, cats from the Kenyan Islands, Lamu and Pate, and Dubai, and those from various cities of Japan. However, at a fine-scale, minor discrepancies are observed. For example, mainland Kenyan cats, when analyzed with STRs, are in the middle of the European branch with a bootstrap value of 100%, but in the SNP-based tree, mainland Kenyan individuals are in between the European/Mediterranean and the Iraq/Iran/Asian clades with a lower bootstrap of 43%. Additionally, the northwestern populations in India weakly grouped with either the Iraq/Iran clade or the Indian depending upon the marker.

[0147] The wildcat outgroups also showed significant differences between markers. With SNPs, *Felis s. libyca* is more closely associated with the Mediterranean cats, while *F. s. silvestris* associated with the European cats. With STRs, the two wildcat groups form their own clade, in between the Mediterranean/European/ Iraqi/Irani populations and more eastern populations.

<u>Discussion</u>

[0148] Cultural histories, archeological evidence, and more recently, genetic investigations all support the theory of at least one cat domestication event in the 450,000 km2 region of the Fertile Crescent. The Fertile Crescent spreads from the land between the Tigris and Euphrates Rivers (currently Iraq), extending into modern Syria and Turkey, along the Mediterranean coast of Israel (the Levant region) and into the fertile regions of the Nile River Valley in Egypt. As agriculture and civilization spread, the provision of vermin population control to surrounding refuse piles and grain stores was an important benefit of the symbiotic relationship between the regional wildcats and humans. Bold wildcats may have repeatedly approached humans as the sedentary agricultural lifestyle proliferated throughout the Fertile Crescent. Over time, some cats may have moved with mobile tribes over short distances. Both natural and human-induced barriers have posed limits to feline migrations over the past 10,000 years, as well as varying human migrations due to stochastic political barriers. But as humans became increasingly mobile, so too have the cats, by hitching rides around the world on ships and colonizing new regions with limited founders. DNA sampling and genetic evaluations of modern cats provide only a present-day snapshot of cat population stratifications around the world. However, large DNA sample sets of cats from diverse geographical regions combined with an assortment of genetic markers with a variety of resolution powers can help define these cat populations, tracing recent migrations, and clarifying those more ancient relationships of the cats around the world.

[0149] This study focused on cat populations within the Fertile Crescent, Egypt, and eastern regions, examining the effect of different genetic markers on refining the site of cat domestication and clarifying the paths of migration. STRUCTURE analysis of SNPs and STRs genetically refined the cat population stratifications of the world, especially with the addition of cats from the Middle East and Asia. The previous STR study by Lipinski et al. (2008) suggests that worldwide cats divide into 4 basal lineages; Western European, Mediterranean basin, East African (Lamu and Pate), and Asian. By doubling the sample set and including 148 random SNP markers, the previous population demarcations were reinforced and an additional lineage in Iraq/Iran was detected. The previously defined African lineage, cats from the Kenyan islands of Lamu and Pate, appears to be rather a lineage that defines cats of Indian Ocean/Arabian Sea including cats from Dubai, India and Sri Lanka, Thailand, and Vietnam. The SNPs more clearly defined this lineage than the STRs.

[0150] Additional stratifications can be resolved, dividing cats into seven modern populations for each marker type, eight overall populations considering a combined analysis. These population divisions align mostly along geographic regions, specifically Europe (including the Americas), East Mediterranean Basin (Turkey, Cyprus, Lebanon, and Israel), Egypt, Iraq/Iran, Arabian Sea, India (including Sri Lanka), Southern Asia (Thailand and Vietnam), and Eastern Asia (Taiwan, Japan, China, and South Korea). Both marker types support Egyptian cats as distinctive, perhaps a result of ancient breeding practices causing drift or strong isolation due to cultural and geographical barriers in the region. SNPs and STRs were discordant with the distinction of the cats from India and Sri Lanka. With SNPs, the Indian cats group with cats around the Arabian Sea, but with STRs, these same cats cluster with a distinctive Southern Asian group. The slower mutation rate of SNPs should strengthen their resolving power in the older cat populations; STRs should illuminate the more recent migrations that may not be visible with SNPs. Perhaps the differences in the SNP versus STR demarcations suggest that historically the India cats arrived from the West, whereas more recent migrations have come from the East.

[0151] In support of recent cat movements, approximately 66% of migrants appear to have originated from geographically close neighbors. However, the cat migrants in Taiwan and Japan are most likely due to human-mediated movement subsequent to human colonization or migration by European people. For example, 9.5% of the Japanese cats and 24.1% of Taiwanese cats appear to have a significant portion of European ancestry. The Nairobi Kenyan cats appear to be highly correlated with that of Europe, consistent with the European colonization of Kenya, which is readily depicted by the STR neighbor-joining phylogenetic analysis. A similar result was indicated in the previous study with cats from Tunisia, which appeared to also have European origins (Lipinski et al., 2008). An individual example is a cat sample that was collected in Luxor, Egypt, a city deep within the Nile Valley. This longhaired cat belonged to a woman who had recently moved from the coastal Mediterranean city of Alexandria. Her cat clearly owes most of its ancestry to that of European cats. While signs of historical colonization by western countries can be detected, Iraq's short history of British rule resulted in very little influence of the European cats in the feral populations of Iraq and Iran. Overall, the stratification of cats from these analyses is sufficient to define regional origins of modern cats, and recent migrations can be tracked by the cat's genetic constitution.

[0152] PCA analyses depicted a great divide between the regions of Europe, East Mediterranean Basin, and Egypt versus cats from Southern Asian, and Eastern Asian populations, suggesting these larger regional groupings as the most genetically distinct. The phylogenetic relationships presented in the neighbor-joining trees also relay a significant difference between Eastern and Western domestic cats. Both approaches place the Irani/Iraqi and Arabian Sea groups somewhat in between the Eastern - Western divisions. The wildcat species group with the Western European clusters of cats, leaving speculation as to whether the significant divide between western and eastern cats is due to more than one domestication event, or the ancient diaspora of early cat domesticates, followed by a decrease of migration and isolationism.

[0153] Population statistics assist the identification of the older cat populations and lineages, indicating that Egypt and the Mediterranean lineage have the lowest inbreeding and highest heterozygosity based on STRs, as well as the highest averages for effective number of alleles of the populations included in this study. FIS calculations based on SNPs show the Asuit, Egypt and Iraqi/Irani lineage to have the least amount in inbreeding but likely not statistically significant from other Egyptian and Mediterranean areas. Additionally the Assuit collection was partially made up of cats that had been presented to the Veterinary School of Assuit University, and may likely represent cats from a variety of origins. Thus, the oldest cat lineages are represented in the Near East, primarily the Eastern Mediterranean countries and Egypt, supporting sites of cat domestication. The isolation of the cat populations in Iraq and Iran has undoubtedly prevented admixture, despite this, the population has not suffered from inbreeding. Cats from India, including Sri Lanka, show significant admixture with representation from all groups. Bootstrap values are low for the Indian cats, while STRUCTURE analysis indicated gene flow from surrounding areas, suggesting the Indian peninsula as a potential mixing pot for domestic cats. Overall, the regions of highest diversity focus around the location of the first human agricultural settlements, including Egypt, Israel, Lebanon, and Iraq.

[0154] Together, the various SNP and STR data of this study indicate that cats were first domesticated in the Fertile Crescent and Levant regions, potentially near Lebanon and Iraq. The Iraq/Iran clade is clearly delineated early in the Baysean clustering analysis as one of the first lineages, show little sign of admixture with the other lineages, and maintains a high diversity even when compared to the modern populations. Iraq has also had the benefit of relatively few influences from Europe; the modern populations found there are most likely to represent some of the first domesticated cats. The high diversity of other populations is a result of large numbers of migrations and introgressions from other regions of the world (such as northwestern India and northern Egypt). From the northern Fertile Crescent, domesticated cats have spread throughout the world, first out towards Iraq, the Eastern Mediterranean and then down through Egypt before extending to Asia and Europe. Since then, as Europeans traveled throughout the world, they brought with them their fellow felines, which have subsequently left their genetic pawprints in areas such as Kenya, Taiwan, Japan, and the Americas.

Example 2

Assessment of Genetic Assignment of Domestic Cats to Breeds and Worldwide Random Bred Populations

[0155] In this example, 477 cats representing 29 fancy breeds were analyzed with 38 microsatellites (STRs), 148 intergenic SNPs, and 5 causative and linked phenotypic SNPs. Results of this study suggest that contrary to previous studies, the frequentist methods of Paekau (accuracy SNPs = 0.78, STRs = 0.88) surpass the Bayesian methods of Rannala and Mountain (SNPs = 0.56, STRs = 0.83). Additionally, a post-assignment verification step with the phenotypic SNPs will accurately identify between 0.31 and 0.58 of the mis-assigned individuals.

Materials and Methods:

[0156] *Sample Collection.* Twenty-nine breeds were represented by 477 cats. This study included 354 cats from the work of Lipinski et al. ((2008) *Genomics* 91:12-21) that analyzed 22 breeds. The 123 additionally collected samples represented seven additional breeds (Scottish Fold, Cornish Rex, Ragdoll, Manx, Bengal, Ocicat, and Australian Mist). All cats were representatives of their breed as found within the USA, except for a few Turkish Angora and Turkish Vans from an international collaboration. All cats were pedigreed and verified to be unrelated to the grandparent level. Worldwide random bred data (N=944) was included from results discussed in Example 1 in order to assess the origins of each of the breed populations. New samples were collected via a buccal (cheek) swab and extracted following the manufacturer's protocol (Qiagen).

Table 11
Origins of cat Breeds*

	Indicative Phenotypic Traits		
Breed	**Inclusion**	**Exclusion**	**Origins Based on Historical Evidence[1]**
Persian	LH	SH	British RB, Siamese, Maine Coon
Exotic SH	SH	LH	Persian, American SH, Abyssinian, Burmese
British SH	SH	LH	British RB, Persian
Scottish Fold	Ear Fold		Scottish RB, British SH, American SH, Persian, Exotic SH
Chartreux	Blue		French RB, Persian, British SH
American SH	SH	LH	British RB, American RB, Persian, Burmese
Sphynx	Hairless		American RB
Japanese Bobtail	Bobtail		Japanese RB
Cornish Rex	Cornish curl		British RB, Siamese
Ragdoll	LH		American RB, Birman
Maine Coon	LH		American RB
Abyssinian	SH, Ticked, Agouti	LH	British RB, Egyptian RB, African RB
Siberian	LH		Russian RB[2]
Norwegian FC	LH		Norwegian RB
Manx	Tailless, SH	LH	British RB

Table 11
Origins of cat Breeds*

Breed	Indicative Phenotypic Traits Inclusion	Exclusion	Origins Based on Historical Evidence[1]
Egyptian Mau			Egyptian RB
Turkish Angora			Turkish RB
Turkish Van			Turkish RB
Bengal			Asian leopard cat, American RB
Sokoke			Kenyan randombred[3]
Ocicat	Spotted, SH	LH	Abyssinian, Siamese
Russian Blue	Blue, SH		British RB, Siamese
Australian Mist			Burmese, Abyssinian, Australian RB[4]
Burmese	Agouti, Sepia	Non-Agouti, Silver	Burmese RB, Siamese, European RB, British SH
Singapura	Agouti	Non-Agouti, Silver	Singaporean RB, Abyssinian
Birman	LH, Points		Burmese RB, various breed outcrosses
Korat	Blue, Non-agouti		Thai RB
Havana Brown	Chocolate, Non-Agouti	Points	Siamese, British SH, Russian Blue
Siamese	SH, Siamese Points, Non-Agouti		Thai RB

*RB = randombred, SH = shorthair, LH = Long hair. Unless noted origins are according to: [1]Gebhardt, 1991(Gebhardt (1991). The Complete Cat Book. Howell Book House, New York, [2]The Royal Canin Cat Encyclopedia, 2000, Groupe Royan Canin, Paris, France, [3]The International Cat Association (on the internet at tica.org), or [4]Australian Mist Breed Council (on the internet at australianmist.info/Home.html).

[0157] Thirty eight microsatellites were genotyped in the 123 newly acquired cats following the PCR and analysis procedures of Lipinski et al. (2008), *supra*. The 148 intergenic SNPs were assayed in all 477 breed cats for this study as described in Example 1. Five additional phenotypic SNPs were also evaluated in all cats. The phenotypic SNPs consisted of a causative mutation for the most common form of long hair in cats (FGF5 A475C) (Kehler et al. (2007) *J Hered* 98, 555-66.), Burmese and Siamese color points (TYR G715T and G940A, respectively) (Lyons et al. (2005) *Animal Genetics*, 36, 119-126), and the mutations for the color variants chocolate and cinnamon (Phen_TYRP1_5IVS6 and C298T) (Lyons et al. (2005) *Mammalian Genome*, 16, 356-366). Golden Gate Assay amplification and BeadXpress reads were performed per the manufacturer's protocol (Illumina Inc., San Diego) on 50-500ng of DNA, using the same oligo primer pool as used in Example 1. Each run of the SNP assay contained both an internal positive and negative control in order to validate repeatability and contamination.

[0158] *Population Statistics*. Hardy-Weinberg Equilibrium (HWE) with associated chi squared tests was performed by population, as well as observed and expected heterozygosites with GenAlEx v.6.3 (Peakall & Smouse 2006, *supra*). FIS and FST were calculated with Fstat v. 2.9.3.2 (Goudet 1995, *supra*). F-statistics were calculated both by sampling location, and based on the populations as assigned by STRUCTURE, regardless of sampling location. Reynold's genetic distance was calculated between all pairs of breeds due to the predicted recent separation of these populations (Reynolds et al. 1983, *supra*).

Population Structuring

[0159] *Bayesian Clustering*. Data sets were analyzed with the Bayesian clustering program STRUCTURE (Pritchard et al. 2000) under the admixture model with correlated allele frequencies and a burn-in of 100,000 with 100,000 additional iterations. Values of K were calculated from K = 1 to K = 33, each run was replicated 10 times. Posterior log likelihoods were used in the calculation of ΔK to best estimate the number of ancestral populations through the program Harvester (Evanno et al. 2005, *supra*). All ten iterations were then combined through the program CLUMP (Jakobsson & Rosenberg 2007, *supra*) to create a consensus clustering. To assess the effects of varying marker types on the final results, STRUCTURE analysis was conducted on the data with the two different permutations: SNPs and STRs.

[0160] *Principal Coordinate Analysis*. Principal components analyses were conducted through the calculation of Nei's genetic distance using the software GenAlEx v.6.3 (Peakall & Smouse 2006, *supra*). For the PCA plots, both the data in the present example and data from the worldwide random bred populations discussed in Example 1 were considered to show the relationship of the cat breeds and their random bred population origins.

[0161] *Breed Lineage Assignment*. Cat breed populations were assigned to the eight ancestral lineages of random bred worldwide populations of cats (Europe, Mediterranean, Egypt, Iraq/Iran, Arabian Sea, India, Southeast Asia, and East Asia) identified in Example 1 by calculating –log(Likelihood) values using the Bayesian population assignment methods available in the software Geneclass2 (Piry et al. 2004, *supra*).

[0162] *Assignment Testing*. Ten sets of 50 individuals were randomly selected from the sample set and assigned to a population of origin using the remaining samples as the reference populations. The Bayesian method of Rannala and Mountain (1997), *supra*, and the Frequentist method suggested by Paetkau et al. (2004), *supra*, were compared as they performed best in the previous assignment study of Negrini et al. (2009) *Animal Genetics*, 40:18-26) when compared to the Pritchard et al. (2000) *Genetics*, 155:945-959) and the Baudoulin & Lebrun methods (2001) *Proc. Int. Symp. on Molecular Markers*, pp. 81-94. Additionally, the assignment tests were performed in three iterations: intergenic SNPs, intergenic and phenotypic SNPs combined, and STRs. Tallies of type I error (an individual not reassigning to its population of origin) and type II error (an individual not from that population assigning to it) were used to calculate the sensitivity and specificity of the assignment method (Negrini et al. 2009, *supra*).

[0163] Phenotypic SNPs were also used post-assignment test to compare both STRs with and without phenotypic SNP input, as well as comparing the use of phenotypic SNPs combined with intergenic SNPs for the assignment test as opposed to only post assignment testing. Cats were considered mis-assigned if they had genotypes exclusionary for the breed. For example, an individual assigned to the Exotic short haired group was identified as mis-assigned if it was homozygous for long-hair.

<u>Results:</u>

[0164] *Summary Statistics*. Pedigreed cats (N = 477), representing 29 recognized breeds were included in this study (Table 12). The number of cats per breed ranged from 7 to 25 with an average of 16.4 individuals per breed. STRs had a call rate of 88.2% and SNPs had a 94.0% average call rate. While the chi-squared goodness-of-fit test indicated that 126 of the 148 SNPs and 36 of the 38 STRs were not in HW equilibrium in at least one breed group, only one SNP marker (chrF2_46855978) was found to be not in HW equilibrium in more than 50% of the breeds (Table 13). Twenty-seven breeds have 10-25 SNPs not in HWE; however the Russian Blue and Turkish Van breeds have 31 and 33 of the total 186 genetic markers out of HWE. This is suggestive of potential population substructuring or recent inbreeding. The frequency of the genotypes and alleles for the phenotypic SNPs were calculated by counting (Table 14). The FGF5 A475C mutation causing long coated cats in the homozygous state was by far the most prevalent of the phenotypic SNPs as it was found in all but eight of the breeds. In contrast, cinnamon, caused by TYRP1 C298T, was only seen in five breeds two of which had a frequency lower than 0.1.

Table 12

Population statistics of cat breeds.

Breed	N	Total Alleles (SNP)	Total Alleles (STR)	PA B(STR)	PA W(STR)	Na (SNP)	Na (STR)	Ho (SNP)	Ho (STR)	F_{IS} (SNP)	F_{IS}(STR)
Persian	15	276	181	1	0	1.865	4.763	0.285	0.502	-0.023	0.145
Exotic SH	19	279	178	1	1	1.885	4.684	0.253	0.526	0.073	0.068
British SH	18	276	192	2	0	1.865	5.053	0.242	0.546	0.101	0.064
Scottish Fold	17	269	180	2	1	1.818	4.737	0.261	0.574	0.001	0.047
Chartreux	13	264	151	0	0	1.784	3.974	0.237	0.557	0.1	0.042
American SH	13	269	168	0	0	1.818	4.421	0.281	0.552	-0.023	0.035
Sphynx	17	277	178	2	0	1.872	4.684	0.271	0.549	0.047	0.05
Japanese Bob.	19	267	191	4	0	1.804	5.026	0.223	0.578	0.146	0.076
Cornish Rex	15	262	163	2	0	1.77	4.289	0.238	0.555	0.049	0.026
Ragdoll	15	265	178	4	0	1.791	4.684	0.29	0.624	-0.057	0.001
Maine Coon	19	282	210	2	1	1.905	5.526	0.256	0.602	0.114	0.043
Abyssinian	15	277	130	1	1	1.872	3.421	0.287	0.415	0.022	0.11
Siberian	17	275	227	4	2	1.858	5.974	0.26	0.705	0.093	-0.06
Norwegian FC	16	284	248	8	0	1.919	6.447	0.28	0.667	0.063	0.023
Manx	17	282	233	6	2	1.905	6.132	0.304	0.696	-0.002	-0.018
Egyptian Mau	14	268	160	1	0	1.811	4.211	0.246	0.495	0.029	0.114
Turkish Angora	21	284	275	10	1	1.919	7.237	0.251	0.674	0.109	0.055
Turkish Van	20	277	259	6	0	1.872	6.816	0.236	0.595	0.12	0.123
Bengal	18	274	192	10	2	1.851	5.053	0.244	0.579	0.065	0.038
Sokoke	7	222	92	0	0	1.5	2.421	0.166	0.368	0.003	0.004
Ocicat	10	264	142	3	2	1.784	3.737	0.236	0.495	0.035	0.048
Russian Blue	17	259	146	2	1	1.75	3.842	0.185	0.453	0.16	0.063
Australian Mist	15	273	156	4	0	1.845	4.105	0.268	0.569	-0.01	-0.045
Burmese	19	262	158	2	1	1.77	4.158	0.196	0.423	0.08	0.158
Birman	20	247	133	3	0	1.669	3.5	0.169	0.437	0.134	0.027
Havana Brown	14	245	113	1	0	1.655	2.974	0.168	0.423	0.115	-0.015
Korat	25	246	150	2	0	1.662	3.947	0.168	0.516	0.077	0.032
Siamese	15	242	133	2	1	1.635	3.5	0.2	0.466	0.002	0.024
Singapura	17	232	94	1	0	1.568	2.474	0.182	0.342	0.055	0.019
Total	477	296	490			1.794	4.544	0.237	0.534	0.058	0.044

N implies number of samples, PA_B implies private alleles between breeds, PA_W implies private alleles between breeds and worldwide randombred populations, Na implies average effective number of alleles, Ho implies observed heterozygosity, F_{IS} implies inbreeding coefficient

Table 13 - Chi-squared test for Hardy-Weinberg Equilibrium by cat breed

	Persian	Exotic SH	British SH	Scottish Fold	Chartreux	American SH	Sphynx	Japanese Bobtail	Cornish Rex	Ragdoll	Maine Coon	Abyssinian	Siberian	Norwegian FC	Manx	Egyptian Mau	Turkish Angora	Turkish Van	Bengal	Sokoke	Ocicat	Russian Blue	Australian Mist	Burmese	Birman	Havana Brown	Korat	Siamese	Singapura	Total
chrA1 10141047	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns				•	•	•	6
chrA1 133621071	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	2
chrA1 151648701	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns			ns	ns	ns	ns	1
chrA1 175780586	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	•	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	4
chrA1 208054462	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	1
chrA1 223501140	ns	ns	•	ns	ns	•	ns	ns	•	ns	ns	ns	•	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	5
chrA1 223506906	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns				ns	ns	ns	3
chrA1 225057933	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	•	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	3
chrA1 235579538	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	0
chrA1 27523501	ns	ns	ns	ns	•	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	•	•	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	5
chrA1 68485376	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns			ns	ns	ns	ns	1
chrA1 69424718	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	•	ns	ns	ns	3
chrA1 7429296	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	0
chrA1 8742286	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	1
chrA2 152258936	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
chrA2 201526186	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	0
chrA2 202225770	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	•	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	4
chrA2 44241149	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	0
chrA2 554046	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns		•	ns	ns	ns	2
chrA3 101420069	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
chrA3 11480952	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	ns	ns	ns	ns	ns		ns							0
chrA3 12082294	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	1
chrA3 130195244	ns	•	•	•	•	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	7
chrA3 159537633	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	3

Table 13 - Chi-squared test for Hardy-Weinberg Equilibrium by cat breed

	Persian	Exotic SH	British SH	Scottish Fold	Chartreux	American SH	Sphynx	Japanese Bobtail	Cornish Rex	Ragdoll	Maine Coon	Abyssinian	Siberian	Norwegian FC	Manx	Egyptian Mau	Turkish Angora	Turkish Van	Bengal	Sokoke	Ocicat	Russian Blue	Australian Mist	Burmese	Birman	Havana Brown	Korat	Siamese	Singapura	Total
chrA3 162208567	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	1
chrA3 38781591	ns	ns	•	ns	•	•	ns	•	ns	ns	•	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns							7
chrA3 75156179	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns			•	ns	ns	ns	2
chrA3 91058022	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	2
chrA3 99507784	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	•	ns	ns	ns	ns	2
chrB1 10420438	ns	ns	ns	ns	•	ns	ns	•	ns	ns	•	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	4
chrB1 12214271	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	0
chrB1 195678303	ns	ns	ns	ns	ns	ns	ns	•	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	2
chrB1 199564532	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns			ns	ns	ns	ns	1
chrB1 202966562	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	2
chrB1 54775572	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns						ns	0
chrB1 80161671	•	ns	ns	ns	•	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	•		•	•	ns	ns	7
chrB1 88148379	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
chrB2 138312489	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	1
chrB2 146660650	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns				ns	ns	ns	0
chrB2 41509834	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	2
chrB2 45093345	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	0
chrB2 6949528	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	•	•	•	•	•	•	7
chrB3 104483970	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	2
chrB3 111000326	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	•	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	4
chrB3 13666494	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	0
chrB3 39203469	•	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	2
chrB3 51317931	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	2
chrB3 57141954	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	•	ns	3

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	Persian	Exotic SH	British SH	Scottish Fold	Chartreux	American SH	Sphynx	Japanese Bobtail	Cornish Rex	Ragdoll	Maine Coon	Abyssinian	Siberian	Norwegian FC	Manx	Egyptian Mau	Turkish Angora	Turkish Van	Bengal	Sokoke	Ocicat	Russian Blue	Australian Mist	Burmese	Birman	Havana Brown	Korat	Siamese	Singapura	Total
chrB3 77094074	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	•	•	ns	ns	ns	ns	ns	ns	4
chrB4 105706694	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	•	ns	ns	ns	ns	ns	ns		ns	ns	ns	•	3
chrB4 142658074	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	2
chrB4 143006494	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	•		ns	ns	ns	ns	3
chrB4 144693308	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
chrB4 146486983	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	•	ns	ns	ns	ns	•	4
chrB4 147206961	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
chrB4 149532846	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	•	ns	ns	•	ns	ns	•				ns	ns	ns	4
chrB4 1687419	•	•	ns	ns	ns		•	ns	ns	ns	ns		ns	•	ns	ns	ns	ns	ns	ns	ns		ns							4
chrB4 20001848	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	0
chrB4 21098349	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
chrB4 255106	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns					ns	ns	1
chrB4 3093827	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	•	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	4
chrB4 40319102	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	•	ns	•	ns	ns	ns	•	ns	ns	ns	ns	5
chrB4 47638578	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	•	ns	•	ns	ns							3
chrC1 116355295	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	3
chrC1 123164748	ns	ns	•	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	2
chrC1 181852965	ns	ns	ns	ns	ns	ns	ns	ns	•	•	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	4
chrC1 190502133	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
chrC1 215441574	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
chrC1 216852686	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	•	ns	ns	•	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	4
chrC1 24148281	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	•	•	ns	ns	ns	ns	3
chrC1 28702055	ns	ns	ns	ns	ns	•	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns				ns	ns	ns	3
chrC1 34981315	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns		ns	ns	ns	ns	1

Table 13 - Chi-squared test for Hardy-Weinberg Equilibrium by cat breed

	Persian	Exotic SH	British SH	Scottish Fold	Chartreux	American SH	Sphynx	Japanese Bobtail	Cornish Rex	Ragdoll	Maine Coon	Abyssinian	Siberian	Norwegian FC	Manx	Egyptian Mau	Turkish Angora	Turkish Van	Bengal	Sokoke	Ocicat	Russian Blue	Australian Mist	Burmese	Birman	Havana Brown	Korat	Siamese	Singapura	Total
chrC1 396397	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
chrC1 44520932	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	1
chrC1 52456776	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	•	ns	ns	•	ns	ns	ns	ns	ns	ns	•	4
chrC2 106991233	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	2
chrC2 147124460	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
chrC2 150774106	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns							0
chrC2 156491175	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	2
chrC2 187325	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	3
chrC2 262401	ns	ns	ns	ns	ns	ns	•	•	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	4
chrC2 5215469	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	2
chrD1 101321498	•	ns	ns	ns	•	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	•	•	•	7
chrD1 104941557	ns	ns	•	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	2
chrD1 105498119	ns	ns	ns	ns	•	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	3
chrD1 10789012	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	1
chrD1 11484008	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	0
chrD1 117527468	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	ns	ns	ns	ns	ns		ns							0
chrD1 125811329	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	2
chrD1 126256993	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	•	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	3
chrD1 126847301	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	•	•	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	4
chrD1 15984279	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	1
chrD1 16242433	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	2
chrD1 18390852	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	•	•	ns	ns	•	ns	•	ns	ns	ns	ns	ns	ns	ns	5
chrD1 18570323	ns	•	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	•	ns	ns	ns	4
chrD1 66177762	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	2

Table 13 - Chi-squared test for Hardy-Weinberg Equilibrium by cat breed

	Persian	Exotic SH	British SH	Scottish Fold	Chartreux	American SH	Sphynx	Japanese Bobtail	Cornish Rex	Ragdoll	Maine Coon	Abyssinian	Siberian	Norwegian FC	Manx	Egyptian Mau	Turkish Angora	Turkish Van	Bengal	Sokoke	Ocicat	Russian Blue	Australian Mist	Burmese	Birman	Havana Brown	Korat	Siamese	Singapura	Total
chrD2 1020904	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	2
chrD2 105772916	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
chrD2 1752007	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	•	ns	ns	•	ns	ns	ns	•	•	ns	ns	ns		ns	ns	ns	ns	5
chrD2 56777338	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns				ns	ns	ns	0
chrD2 717969	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	•	ns	ns	ns	ns	ns	ns	•	•	ns	4
chrD2 74293444	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	•	•	5
chrD2 91989307	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•			ns	ns	ns	ns	3
chrD3 103840114	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns						ns	1
chrD3 122502120	ns	ns	ns	•	ns	ns	ns	ns	•	•	ns	ns	ns	•	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	5
chrD3 1810839	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	•	ns	•	ns	ns	ns	ns	•	ns	ns	ns	ns	5
chrD3 24565823	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns					ns	ns	0
chrD3 24823793	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	2
chrD3 28838660	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	•	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	4
chrD4 41078218	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	1
chrD4 42000379	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns		ns	ns	ns	ns	2
chrD4 63622083	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	2
chrE1 130875919	ns	ns	ns	ns	ns	ns	•	•	ns	ns	ns	ns	ns	ns	ns	ns	•	•	ns	ns	ns	ns	ns							4
chrE1 131587399	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	•	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	3
chrE1 3912105	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	0
chrE1 4114158	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	•	ns	3
chrE1 48228153	•	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	3
chrE1 48700963	ns	•	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns							2
chrE1 5453028	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns			•	ns	ns	ns	2
chrE2 22632289	ns	•	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	3

Table 13 - Chi-squared test for Hardy-Weinberg Equilibrium by cat breed

	Persian	Exotic SH	British SH	Scottish Fold	Chartreux	American SH	Sphynx	Japanese Bobtail	Cornish Rex	Ragdoll	Maine Coon	Abyssinian	Siberian	Norwegian FC	Manx	Egyptian Mau	Turkish Angora	Turkish Van	Bengal	Sokoke	Ocicat	Russian Blue	Australian Mist	Burmese	Birman	Havana Brown	Korat	Siamese	Singapura	Total
chrE2 34027888	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	•	•	•	•	7
chrE2 35914023	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	0
chrE2 36986631	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
chrE2 38860686	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns		ns	ns	ns	ns	1
chrE2 39211557	ns	•	ns	ns	•	•	•	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	•	•	ns	ns	ns	ns	ns	•	ns	ns	9
chrE2 65436639	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	2
chrE2 7950477	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	2
chrE2 8422942	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns				ns	ns	ns	0
chrE3 36044809	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	•	ns	ns	ns	ns	ns	ns	•	ns	•	ns	ns	ns	ns	ns	•	ns	ns	5
chrE3 55434272	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	0
chrE3 67006512	ns	ns	•	ns	•	ns	ns	•	ns	ns	•	•	•	ns	ns	ns	•	ns	ns	ns	ns	•	ns	ns		ns	ns	ns	ns	8
chrF1 20309325	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	2
chrF1 21799641	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
chrF1 26100599	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	1
chrF1 27124984	ns	ns	•	ns	•	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	4
chrF1 38051725	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
chrF1 565223	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	2
chrF1 82068276	ns	ns	•	ns	ns	ns	•	ns	ns	ns	•	ns	•	ns	•	•	ns	•	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	8
chrF1 82716202	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
chrF1 91517402	ns	ns	•	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	3
chrF2 26886470	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	2
chrF2 38395360	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	2
chrF2 46855978	•	•	ns	•	ns	•	ns	•	ns	•	ns	ns	•	•	•	•	•	•	ns	ns	ns	•	•	•	•	•	•	•	•	20
chrF2 68572596	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	•	•	ns	ns	ns	•	6

Table 13 - Chi-squared test for Hardy-Weinberg Equilibrium by cat breed

	Persian	Exotic SH	British SH	Scottish Fold	Chartreux	American SH	Sphynx	Japanese Bobtail	Cornish Rex	Ragdoll	Maine Coon	Abyssinian	Siberian	Norwegian FC	Manx	Egyptian Mau	Turkish Angora	Turkish Van	Bengal	Sokoke	Ocicat	Russian Blue	Australian Mist	Burmese	Birman	Havana Brown	Korat	Siamese	Singapura	Total
chrF2 74863327	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	2
chrF2 78303221	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	3
chrF2 79632602	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns							0
chrF2 8427817	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
FCA005	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	3
FCA008	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	•	ns	ns	ns	ns	2
FCA023	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	2
FCA026	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
FCA035	•	ns	ns	•	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	•	ns	ns	•	•	•	ns	ns	ns	ns	ns	8
FCA043	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	2
FCA045	ns	•	ns	ns	ns	ns	•	ns	ns	ns	ns	•	•	ns	ns	ns	ns	ns	•	ns	•	ns	ns	•	•	ns	ns	ns	ns	8
FCA058	ns	•	ns	ns	ns	ns	•	ns	ns	ns	•	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	5
FCA069	ns	ns		ns			ns		ns	ns			ns	ns	ns	ns	ns	ns	ns	ns	ns		ns							0
FCA075	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	•	ns	•	•	ns	ns	•	ns	•	ns	ns	ns	ns	ns	ns	ns	6
FCA077	ns	•	ns	ns	•	ns	•	ns	ns	ns	ns	•	ns	ns	ns	•	•	•	ns	•	ns	•	ns	ns	ns	ns	ns	ns	ns	9
FCA080B	ns	ns	ns	ns	ns	ns	ns	•	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	3
FCA088	•	•	•	•	ns	•	•	ns	•	•	•	ns	ns	ns	•	•	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	12
FCA090	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	2
FCA094	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns						ns	1
FCA096	ns	ns	ns	•	ns	ns	ns	ns	ns	•	ns	ns	•	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	•	•	ns	ns	ns	6
FCA097	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns		ns	ns	•	ns	1
FCA105	ns	ns	ns	•	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	3
FCA123	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	2
FCA126	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	4

Table 13 - Chi-squared test for Hardy-Weinberg Equilibrium by cat breed

	Persian	Exotic SH	British SH	Scottish Fold	Chartreux	American SH	Sphynx	Japanese Bobtail	Cornish Rex	Ragdoll	Maine Coon	Abyssinian	Siberian	Norwegian FC	Manx	Egyptian Mau	Turkish Angora	Turkish Van	Bengal	Sokoke	Ocicat	Russian Blue	Australian Mist	Burmese	Birman	Havana Brown	Korat	Siamese	Singapura	Total
FCA132	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	•	ns	ns	•	ns	ns	4
FCA149	ns	ns	ns	•	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	4
FCA211	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	2
FCA220	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	3
FCA223	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	•	•	ns	ns	•	ns	•	ns	•	ns	ns	ns	ns	ns	ns	ns	•	ns	7
FCA224	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	•	ns	•	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	4
FCA229	ns	•	ns	ns	•	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	5
FCA262	•	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	•	ns	•	ns	ns	ns	ns	ns	ns	•	ns	•	ns	ns	6
FCA293	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	1
FCA305	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	•	ns	•	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	4
FCA310	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	0
FCA391	ns	•	•	ns	ns	•	•	ns	•	ns	•	•	•	ns	•	ns	•	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	11
FCA441	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
FCA453	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	1
FCA628	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	•	•	ns	4
FCA649	ns	ns	ns	•	ns	•	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	•	ns	ns	5
FCA678	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	3
FCA698	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	•	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	2
Total	14	21	17	11	18	21	20	25	13	11	23	17	20	16	15	25	25	31	14	14	10	33	12	17	23	16	18	13	16	

ns = not significantly out of Hardy-Weinberg Equilibrium, • = significantly out of HWE with p-value < 0.05

Table 14 - Phenotypic SNP Frequencies

	Long Hair FGF5 A475C					Burmese Points TYR G715T					Siamese Points TYR G940A					Chocolate Phen_TYRP1_5IVS6					Cinnamon TYRP1 C298T				
Breed	N	AA	AC	CC	Freq. C	N	GG	GT	TT	Freq. T	N	GG	GA	AA	Freq. A	N	CC	CG	GG	Freq.	N	CC	CT	TT	Freq . T
Persian	15	0	1	14	**0.97**	15	15	0	0	**0**	15	5	4	6	**0.53**	15	12	2	1	**0.13**	15	15	0	0	**0**
Exotic SH	17	5	10	2	**0.41**	19	19	0	0	**0**	17	14	2	1	**0.12**	19	15	3	1	**0.13**	19	19	0	0	**0**
British SH	18	16	2	0	**0.06**	18	18	0	0	**0**	17	13	0	4	**0.24**	18	11	2	5	**0.33**	18	15	3	0	**0.08**
Scottish Fold	16	13	3	0	**0.09**	17	17	0	0	**0**	15	14	1	0	**0.03**	17	13	4	0	**0.12**	17	17	0	0	**0**
Chartreux	10	5	5	0	**0.25**	13	13	0	0	**0**	11	11	0	0	**0**	13	13	0	0	**0**	13	13	0	0	**0**
American SH	13	10	2	1	**0.15**	13	11	2	0	**0.08**	13	13	0	0	**0**	13	12	0	1	**0.08**	13	13	0	0	**0**
Sphynx	16	9	1	6	**0.41**	16	6	6	4	**0.44**	12	9	1	2	**0.21**	17	8	5	4	**0.38**	17	17	0	0	**0**
Japanese Bobt	14	8	2	4	**0.36**	18	18	0	0	**0**	15	13	2	0	**0.07**	19	19	0	0	**0**	19	19	0	0	**0**
Cornish Rex	15	14	1	0	**0.03**	15	15	0	0	**0**	14	3	4	1	**0.21**	14	13	1	0	**0.04**	15	15	0	0	**0**
Ragdoll	15	4	3	8	**0.63**	15	15	0	0	**0**	15	0	0	15	**1**	15	13	2	0	**0.07**	15	15	0	0	**0**
Maine Coon	14	0	0	14	**1**	18	18	0	0	**0**	17	17	0	0	**0**	19	16	2	1	**0.11**	19	19	0	0	**0**
Abyssinian	15	15	0	0	**0**	15	15	0	0	**0**	15	15	0	0	**0**	15	12	3	0	**0.1**	15	4	6	5	**0.53**
Siberian	14	1	3	10	**0.82**	16	16	0	0	**0**	15	8	6	1	**0.27**	17	16	1	0	**0.03**	17	17	0	0	**0**
Norwegian FC	13	8	3	2	**0.27**	16	16	0	0	**0**	15	15	0	0	**0**	16	15	0	1	**0.06**	16	16	0	0	**0**
Manx	15	8	6	1	**0.27**	17	17	0	0	**0**	16	16	0	0	**0**	17	16	1	0	**0.03**	17	17	0	0	**0**
Egyptian Mau	12	12	0	0	**0**	14	14	0	0	**0**	12	12	0	0	**0**	14	14	0	0	**0**	14	14	0	0	**0**
Turkish Angora	20	0	0	20	**1**	21	21	0	0	**0**	20	17	1	2	**0.13**	20	15	5	0	**0.13**	21	21	0	0	**0**
Turkish Van	18	0	0	18	**1**	19	19	0	0	**0**	20	19	1	0	**0.03**	19	14	2	3	**0.21**	20	20	0	0	**0**
Bengal	16	15	1	0	**0.03**	18	16	2	0	**0.06**	14	9	4	1	**0.21**	18	16	2	0	**0.06**	17	17	0	0	**0**
Sokoke	6	6	0	0	**0**	7	7	0	0	**0**	4	3	0	1	**0.25**	6	5	1	0	**0.08**	7	7	0	0	**0**
Ocicat	8	8	0	0	**0**	10	10	0	0	**0**	9	9	0	0	**0**	10	4	1	5	**0.55**	10	6	3	1	**0.25**
Russian Blue	15	14	0	1	**0.07**	17	16	1	0	**0.03**	15	11	3	1	**0.17**	17	17	0	0	**0**	17	17	0	0	**0**
Australian Mist	13	11	2	0	**0.08**	15	2	0	13	**0.87**	12	10	1	1	**0.13**	15	6	6	3	**0.4**	15	7	7	1	**0.3**
Burmese	19	19	0	0	**0**	19	0	1	18	**0.97**	16	16	0	0	**0**	19	9	4	6	**0.42**	19	18	0	1	**0.05**
Birman	19	0	0	19	**1**	20	20	0	0	**0**	16	0	0	16	**1**	20	12	5	3	**0.28**	20	20	0	0	**0**
Havana Brown	11	11	0	0	**0**	14	14	0	0	**0**	12	10	1	1	**0.13**	14	0	1	13	**0.96**	14	14	0	0	**0**
Korat	23	22	1	0	**0.02**	25	25	0	0	**0**	21	20	1	0	**0.02**	25	1	2	22	**0.92**	25	25	0	0	**0**
Siamese	15	15	0	0	**0**	15	15	0	0	**0**	13	0	0	13	**1**	15	2	6	7	**0.67**	15	15	0	0	**0**
Singapura	16	16	0	0	**0**	15	0	0	15	**1**	14	14	0	0	**0**	17	17	0	0	**0**	17	17	0	0	**0**

[0165] *Genetic Diversity*. The population genetic data is presented in Table 12. The average effective number of SNP alleles observed averaged 1.794 across breeds, ranging from 1.500 in Sokoke to 1.919 in Norwegian Forest and Turkish Angora. The average effective number of STR alleles observed averaged 4.54 across breeds, ranging from 2.42 in Sokoke to 7.23 in Turkish Angora. Private STR alleles within breeds ranged from 0 - 10, however, when the breeds were compared to worldwide random bred populations, private alleles within breeds dropped to between 0 – 2 per breed. No SNPs had private alleles in a breed.

[0166] The average SNP-based observed heterozygosity was 0.287, ranging from 0.166 in Sokoke to 0.304 in Manx. The average STR-based observed heterozygosity was 0.534, ranging from 0.342 in Singapura to 0.705 in Siberian. Inbreeding coefficients (FIS) were lowest in the Ragdoll (-0.057) and Siberian (-0.060) with SNPs and STRs, respectively, and highest within the Australian Mist Cats (0.160) and Burmese (0.158). Between population variation FST values were 0.237 ± 0.007 with SNPs and 0.269 ± 0.019 with STRs.

[0167] *Breed Clustering*. The most likely value of K, the number of structured groupings, could not be decisively determined. A significant difference between the log likelihoods was not evident for either marker type between $K = 17 – 33$ (Figure 7), however, a plateau was suggested near $K = 21$ for STRs and $K = 17$ for SNPs (Figure 8). As a result, a combination of the ΔK plots and common sense directed selection of the most likely number of populations. For STRs, at $K > 24$ (Figure 9B), different lineages within specific breeds, such as Norwegian Forest Cat and Turkish Angora, became apparent before five other breed groups would split: Persian / Exotic SH, British SH / Scottish Fold, Australian Mist / Burmese, Birman / Korat, and Siamese / Havana Brown. Similar results were found for the SNPs-based analyses; however the associations of the Asian based breeds varied. SNPs appear to resolve the Birman and Singapura breeds from the other Asian breeds more readily. Considering both SNPs and STRs, Persians appear to have influenced several younger and older breeds: Exotic shorthair, Scottish Fold, British Shorthair and Chartreux. For breeds with Asian heritage, Siamese have a strong influence on the Havana Brown, Korats, Birmans, and Singapura (Figure 8).

[0168] The principal coordinate analyses indicate the relationship of the sub-groups of breeds and their likely closest random bred origins (Figure 10). The breeds that originated solely from European and American random bred cats cluster with the random bred populations of Europe and America. Likewise, breeds with Asian decent grouped with the South Asian populations of random bred cats, and the Sokoke shows a strong influence from its roots in Kenya. The breeds that do not share similar coordinates with a random bred population such as, Russian Blue, Ocicat, Singapura, Australian Mist and Birman, show a strong influence from both Europe and Asia.

[0169] Using Bayesian clustering, the breeds were then assigned back to the eight random bred lineages discussed in Example 1 (Table 15). Four regional areas have contributed to the development of cat breeds. Asian breeds, such as Birman, Burmese, Siamese and others grouped with Southern Asian cats, Western breeds, such as Persian, Norwegian Forest Cat, Maine Coon and others grouped with the Western European random bred cats. Turkish Angora and Turkish Van assigned to the Eastern Mediterranean cats and the Sokoke to the Arabian Sea region. Three breeds showed regional variation depending on the marker type used for assignment. When analyzed with data from SNPs and STRs, the Turkish Angora assigned to the Eastern Mediterranean or Europe, Bengal assigned to the Arabian Sea or Europe, and the Ocicat assigned to Europe or South Asia, respectively.

Table 15a Assignment of cat breeds to random bred cat populations using SNPs.

Breed	SNPs (N=148)								
	Lineage	"-log(L)"							
		Europe	East Med	South Med	IraqIran	Arabian	India	South Asia	East Asia
Birman	South Asia	562.439	514.619	489.325	571.811	466.884	398.272	357.638	494.121
Burmese	South Asia	537.957	494.594	510.756	554.652	452.18	353.1	232.359	408.667
H. Brown	South Asia	498.346	470.353	477.771	538.807	421.824	376.835	266.337	404.7
Korat	South Asia	783.086	710.194	728.915	728.005	569.748	497.518	241.988	544.729
Siamese	South Asia	521.766	481.206	493.075	520.538	417.91	356.165	196.049	363.29
Singapura	South Asia	610.855	635.495	634.003	697.695	541.126	518.324	402.416	539.635
Abyssinian	Europe	425.881	506.972	520.173	739.043	523.387	571.166	539.713	582.183
Russian Blue	South Asia	426.363	443.64	443.657	549.342	451.198	439.924	406.281	478.247
American SH	Europe	214.445	294.034	300.891	436.278	342.32	356.071	430.155	363.917
British SH	Europe	266.189	351.574	383.015	509.425	386.181	402.229	499.062	426.489
Chartreux	Europe	243.214	287.905	310.595	392.542	328.31	306.122	390.676	340.836
Japanese Bob.	Europe	241.661	256.018	267.56	369.44	306.997	289.681	354.146	274.931
Maine Coon	Europe	233.644	336.954	359.517	507.38	383.73	400.377	481.154	409.93
Norwegian FC	Europe	186.918	268.319	297.021	459.99	364.374	361.486	460.332	367.953
Persian	Europe	210.224	280.822	298.776	425.561	327.435	320.381	410.002	328.219
Exotic SH	Europe	275.475	367.195	380.41	532.774	391.854	408.132	500.594	423.104
Sphynx	Europe	229.867	268.333	294.366	421.316	343.479	304.696	385.86	333.086
Siberian	Europe	177.505	205.628	244.135	368.507	282.501	286.135	350.747	277.186
Egyptian Mau	Europe	278.503	303.627	303.291	421.446	345.331	349.259	422.453	366.832
Sokoke	W Indian	215.491	213.151	215.151	222.711	175.088	194.761	214.181	212.471

Table 15a Assignment of cat breeds to random bred cat populations using SNPs.

Breed	SNPs (N=148)								
	Lineage	"-log(L)"							
		Europe	East Med	South Me	IraqIran	Arabian	India	South Asia	East Asia
Turkish Angora *	Europe	206.309	215.369	239.522	346.148	308.088	297.611	395.989	324.211
Turksih Van	East Med	251.489	233.29	268.56	383.923	339.409	320.684	396.447	367.681
Cornish Rex	Europe	317.191	368.372	358.46	488.121	383.104	360.937	413.799	403.094
Manx	Europe	183.172	266.261	293.483	465.86	343.149	354.55	469.19	382.31
Ragdoll	Europe	238.285	277.549	295.736	393.95	342.598	302.199	364.068	309.321
Scottish Fold	Europe	285.089	410.698	439.66	579.88	419.796	453.876	548.531	480.68
Australian Mist	South Asia	366.442	372.814	392.118	473.959	391.023	357.53	299.831	371.146
Bengal*	Europe	277.481	312.259	314.506	444.415	343.165	327.977	410.917	369.303
Ocicat*	South Asia	250.81	272.05	285.371	362.082	289.028	245.677	244.482	272.293

*Indicates breeds that assigned to varying origins based on the genetic marker type.

Table 15b Assignment of cat breeds to random bred cat populations using STRs.

Breed	STRs (N=38)								
	Lineage	"-log(L)"							
		Europe	East Me	South Me	IraqIran	Arabian	India	South Asia	East Asia
Birman	South Asia	619.802	624.199	691.233	784.48	627.696	611.122	404.846	619.715
Burmese	South Asia	538.86	574.707	602.871	650.149	543.725	469.352	328.296	480.689
H. Brown	South Asia	405.814	452.844	463.474	490.494	410.516	391.736	290.886	348.305
Korat	South Asia	724.631	720.932	769.557	773.995	605.694	574.06	298.912	623.147
Siamese	South Asia	440.302	476.476	511.011	515.028	452.232	377.384	268.941	373.961
Singapura	South Asia	529.943	593.678	581.331	723.339	530.853	516.217	377.292	562.624
Abyssinian	Europe	391.775	431.049	448.175	569.783	452.082	452.751	420.303	462.802
Russian Blue	South Asia	459.628	550.271	565.88	694.372	553.199	522.684	440.046	531.117
American SH	Europe	284.004	352.415	373.617	519.61	407.953	404.881	411.122	413.971
British SH	Europe	365.836	462.364	494.534	697.257	542.932	520.762	538.64	553.998
Chartreux	Europe	288.091	333.218	364.422	471.369	420.547	380.17	383.442	377.357
Japanese Bob.	Europe	442.684	492.594	504.049	586.241	498.245	472.916	486.841	466.728
Maine Coon	Europe	325.993	413.915	454.08	635.061	519.562	481.193	513.901	510.841
Norwegian FC	Europe	265.706	325.855	373.736	530.702	476.455	437.795	466.9	454.453
Persian	Europe	304.615	380.994	409.462	529.928	455.066	438.168	449.052	414.575
Exotic SH	Europe	431.298	514.268	536.769	706.318	563.227	579.773	541.912	574.013
Sphynx	Europe	381.955	446.644	456.938	607.529	461.321	471.637	426.769	491.009
Siberian	Europe	272.587	305.993	346.585	514.722	453.233	405.521	428.93	411.038
Egyptian Mau	Europe	322.916	350.668	362.843	446.658	386.768	374.387	399.565	412.49
Sokoke	W Indian	275.548	271.011	274.846	286.448	218.947	248.466	244.002	300.134
Turkish Angora *	East Med	398.178	381.553	406.446	556.699	524.253	483.876	549.764	539.647
Turksih Van	East Med	452.401	387.724	427.429	577.663	525.23	477.131	505.265	549.053
Cornish Rex	Europe	369.25	437.788	446.038	555.609	468.858	428.47	394.753	477.392
Manx	Europe	280.006	354.58	393.541	589.955	496.761	463.125	499.578	482.289
Ragdoll	Europe	341.134	393.51	404.545	592.622	471.899	425.202	397.716	405.643
Scottish Fold	Europe	353.106	438.254	455.217	674.159	506.12	514.422	530.18	525.99
Australian Mist	South Asia	372.752	415.4	428.335	503.159	433.821	388.385	318.639	384.275

Table 15b Assignment of cat breeds to random bred cat populations using STRs.

Breed	STRs (N=38)								
	Lineage	"-log(L)"							
		Europe	East Me	South Me	IraqIran	Arabian	India	South Asia	East Asia
Bengal*	W Indian	496.347	512.793	499.54	583.542	490.251	513.431	503.627	594.543
Ocicat*	Europe	283.111	305.428	301.617	383.669	328.11	300.313	287.939	319.107

*Indicates breeds that assigned to varying origins based on the genetic marker type.

[0170] *Assignment Testing.* The accuracy of assignment testing varied depending upon not only the assignment method, but also the marker type used to differentiate the cat breeds. For example, when comparing the Bayesian method of Rannala & Mountain (1997) versus the Frequentist method of Paetkau et al. (2004), *supra*, the average sensitivity of assignment for the 148 non-phenotypic SNPs was 0.56 and 0.78, respectively (Table 16). When the five phenotypic SNPs were included with the random SNPs, the average assignment sensitivity was 0.54 and 0.83, respectively. Overall, the STRs had higher average sensitivities of 0.83 and 0.88, respectively. In six breeds, adding phenotypic SNPs into the Frequentist assignment of individuals reduced the sensitivity of the test, and in five breeds it reduced specificity. As this may be due to the strength of selection imposed on these markers we looked to use the phenotypic SNPs as a method of post assignment verification of breed origin for these cats. For many breeds these single-gene traits are the sole selection criteria for breed allocation, and can be seen in the frequency of the causative mutation in the breed (Table 14). Using just the five phenotypic SNPs included in this study, it was possible to correct for miss-assignment of individuals post-assignment testing in 57.5% of the individuals miss-assigned by the Bayesian method and in 50% of the individuals incorrectly assigned by the Frequentist method (Table 17). This would increase the sensitivity and specificity of the Bayesian method to 0.746 and 0.772 respectively, and the Frequentist to 0.89 and 0.888, resulting in better resolution than the use of STRs alone. The influence of recent breed development on the mis-allocation of individuals may be further visualized by plotting the crossed assignment rate as a function of the Reynold's distance between breeds (Figure 14). In all cases, the crossed assignment rate increased as the distance between breeds decreased.

Table 16a - Assignment accuracy with the Bayesian method of Rannala & Mountain (Rannala & Mountain 1997).

		Intergenic SNPs					Intergenic and phenotypic SNPs					STRs				
Breed	n	E_I	E_{II}	Sens.	Spec.	Ave. Prob	E_I	E_{II}	Sens.	Spec.	Ave. Prob.	E_I	E_{II}	Sens.	Spec.	Ave. Prob.
Persian	12	12	0	0	*	*	10	0	0.17	1	*	2	13	0.83	0.43	0.57
Exotic SH	22	16	8	0.27	0.43	1	17	6	0.23	0.45	1	6	1	0.73	0.94	0.69
British SH	17	17	10	0	0	1	13	5	0.24	0.44	0.99	7	1	0.59	0.91	0.24
Scottish Fold	19	18	0	0.05	1	1	16	0	0.16	1	1	6	0	0.68	1	0.67
Chartreux	11	1	13	0.91	0.43	1	1	7	0.91	0.59	1	1	1	0.91	0.91	0.61
American SH	17	8	0	0.53	1	0.99	11	0	0.35	1	1	4	0	0.76	1	0.54
Sphynx	25	16	0	0.36	1	0.99	14	0	0.44	1	0.99	3	0	0.88	1	0.34
Japanese Bob.	18	2	33	0.89	0.33	1	7	34	0.61	0.24	1	1	0	0.94	1	0.55
Cornish Rex	23	12	0	0.48	1	0.97	14	0	0.39	1	0.98	5	0	0.78	1	0.58
Ragdoll	16	16	0	0	*	*	16	0	0	*	*	5	0	0.69	1	0.6
Maine Coon	27	3	21	0.89	0.53	1	10	32	0.63	0.35	1	6	1	0.78	0.95	0.61
Abyssinian	11	4	0	0.64	1	0.98	4	0	0.64	1	0.98	2	0	0.82	1	0.54
Siberian	9	9	0	0	*	*	6	23	0.33	0.12	1	1	9	0.89	0.47	0.27
Manx	22	20	1	0.09	0.67	1	21	1	0.05	0.5	1	4	16	0.82	0.53	0.48
Egyptian Mau	14	3	0	0.79	1	1	4	0	0.71	1	1	1	0	0.93	1	0.59
Turkish Angora	18	5	125	0.72	0.09	1	11	134	0.39	0.05	1	11	2	0.39	0.78	0.46
Turkish Van	14	10	3	0.29	0.57	0.98	13	3	0.07	0.25	0.99	3	3	0.79	0.79	0.69
Bengal	23	7	0	0.7	1	1	2	0	0.91	1	0.99	0	0	1	1	0.79
Sokoke	5	0	0	1	1	1	0	0	1	1	1	0	0	1	1	0.81
Ocicat	7	4	0	0.43	1	0.99	3	1	0.57	0.8	0.99	1	0	0.86	1	0.63
Russian Blue	19	0	0	1	1	1	4	0	0.79	1	1	3	0	0.84	1	0.93
Australian Mist	20	0	1	1	0.95	1	0	2	1	0.91	1	2	15	0.9	0.55	0.92
Burmese	16	4	1	0.75	0.92	1	2	0	0.88	1	1	4	1	0.75	0.92	0.86
Birman	22	4	0	0.82	1	0.96	6	0	0.73	1	0.99	1	0	0.95	1	0.72
Havana Brown	15	2	2	0.87	0.87	1	2	1	0.87	0.93	1	0	0	1	1	0.93
Korat	24	0	15	1	0.62	1	0	17	1	0.59	1	2	0	0.92	1	0.55
Norwegian FC	16	8	4	0.5	0.67	1	5	25	0.69	0.31	1	2	25	0.88	0.36	0.41
Siamese	19	19	0	0	*	*	19	0	0	*	*	1	0	0.95	1	0.63
Singapura	19	1	0	0.95	1	1	0	0	1	1	1	2	0	0.89	1	0.86
All Breeds	500	221	237	0.56	0.54	0.99	231	291	0.54	0.48	1	86	88	0.83	0.82	0.63

* Essentially zero due to lack of sensitivity, n = Number of samples from this breed tested over ten iterations, E_I = Members of a breed that were incorrectly assigned to another breed, E_{II} = Members of a different breed that were incorrectly assigned to the breed in question, Sens. = Sensitivity, Spec. = Specificity, Ave. Prob. = Average Probability of assignment.

Table 16b - Assignment accuracy with the Frequentist method of Paetkau *et al.* (Paetkau *et al.* 2004).

		Intergenic SNPs					Intergenic and phenotypic SNPs					STRs				
Breed	n	E_I	E_{II}	Sens.	Spec.	Ave. Prob	E_I	E_{II}	Sens.	Spec.	Ave. Prob.	E_I	E_{II}	Sens.	Spec.	Ave. Prob.
Persian	12	9	19	0.25	0.14	0.39	6	10	0.5	0.38	0.45	1	6	0.92	0.65	0.26
Exotic SH	22	19	7	0.14	0.3	0.43	10	5	0.55	0.71	0.37	4	1	0.82	0.95	0.39
British SH	17	10	6	0.41	0.54	0.45	5	4	0.71	0.75	0.33	5	3	0.71	0.8	0.16
Scottish Fold	19	10	0	0.47	1	0.84	10	0	0.47	1	0.85	2	0	0.89	1	0.45
Chartreux	11	2	0	0.82	1	0.31	2	0	0.82	1	0.31	0	0	1	1	0.15
American SH	17	1	0	0.94	1	0.53	4	0	0.76	1	0.6	2	0	0.88	1	0.27
Sphynx	25	3	2	0.88	0.92	0.32	3	2	0.88	0.92	0.31	1	0	0.96	1	0.25
Japanese Bobtail	18	4	0	0.78	1	0.29	3	0	0.83	1	0.26	1	0	0.94	1	0.29
Cornish Rex	23	5	0	0.78	1	0.29	4	1	0.83	0.95	0.3	2	0	0.91	1	0.25
Ragdoll	16	3	0	0.81	1	0.26	2	0	0.88	1	0.26	4	0	0.75	1	0.32
Maine Coon	27	5	8	0.81	0.73	0.44	1	13	0.96	0.67	0.44	6	5	0.78	0.81	0.35
Abyssinian	11	0	0	1	1	0.32	0	0	1	1	0.32	2	0	0.82	1	0.33
Siberian	9	5	3	0.44	0.57	0.19	4	3	0.56	0.63	0.22	0	18	1	0.33	0.11
Manx	22	8	11	0.64	0.56	0.33	5	9	0.77	0.65	0.4	4	12	0.82	0.6	0.14
Egyptian Mau	14	1	0	0.93	1	0.29	2	0	0.86	1	0.32	3	0	0.79	1	0.18
Turkish Angora	18	10	1	0.44	0.89	0.23	6	8	0.67	0.6	0.37	9	7	0.5	0.56	0.21
Turkish Van	14	5	3	0.64	0.75	0.27	4	2	0.71	0.83	0.37	2	3	0.86	0.8	0.18
Bengal	23	2	0	0.91	1	0.43	2	0	0.91	1	0.43	0	0	1	1	0.21
Sokoke	5	0	0	1	1	0.41	0	0	1	1	0.42	0	0	1	1	0.46
Ocicat	7	0	1	1	0.88	0.27	0	2	1	0.78	0.3	1	1	0.86	0.86	0.1
Russian Blue	19	0	0	1	1	0.31	1	0	0.95	1	0.32	3	0	0.84	1	0.39
Australian Mist	20	0	2	1	0.91	0.57	0	3	1	0.87	0.58	2	1	0.9	0.95	0.27
Burmese	16	2	2	0.88	0.88	0.51	3	0	0.81	1	0.51	0	2	1	0.89	0.26
Birman	22	1	0	0.95	1	0.39	1	0	0.95	1	0.38	1	0	0.95	1	0.34
Havana Brown	15	1	0	0.93	1	0.48	2	1	0.87	0.93	0.49	0	0	1	1	0.37
Korat	24	1	0	0.96	1	0.41	0	0	1	1	0.42	0	0	1	1	0.45
Norwegian FC	16	1	46	0.94	0.25	0.33	3	20	0.81	0.39	0.37	1	3	0.94	0.83	0.06
Siamese	19	1	0	0.95	1	0.33	0	0	1	1	0.32	0	0	1	1	0.17
Singapura	19	1	0	0.95	1	0.45	0	0	1	1	0.44	3	0	0.84	1	0.32
All Breeds	500	110	111	0.78	0.78	0.39	83	83	0.83	0.83	0.39	59	62	0.88	0.88	0.27

* Essentially zero due to lack of sensitivity, n = Number of samples from this breed tested over ten iterations, E_I = Members of a breed that were incorrectly assigned to another breed, E_{II} = Members of a different breed that were incorrectly assigned to the breed in question, Sens. = Sensitivity, Spec. = Specificity, Ave. Prob. = Average Probability of assignment.

Table 17

Total mis-assigned individuals identified post-assignment by phenotypic SNPs.

	Assigned by SNPs				Assigned by STRs			
	Bayesian		Frequentist		Bayesian		Frequentist	
	Total	Freq.	Total	Freq.	Total	Freq.	Total	Freq.
Long Hair	105	0.49	37	0.34	11	0.128	11	0.18
Burmese Points	15	0.07	3	0.03	1	0.016	2	0.03
Siamese Points	15	0.07	16	0.15	6	0.07	3	0.05
Chocolate	8	0.04	0	0	2	0.023	0	0
Cinnamon	14	0.07	5	0.05	4	0.047	4	0.07
Total*	127	0.58	55	0.5	22	0.256	19	0.31

Frequency (SNPs: Bayesian = 221, Frequentist = 110 STRs: Bayesian = 86, Frequentist = 62) *A few individuals were identified as mis-assigned with multiple phenotypic SNPs.

Discussion:

[0171] The artificial selection and population dynamics of domestic cats and its associated fancy breeds are unique amongst domesticated species. Cats are one of the more recent mammalian domesticates, arguably they exist in a unique quasi-domesticated state. Unlike other agricultural species and the domestic dog, for thousands of years, cats have had minimal artificial selection pressures on their form and function as they have naturally performed their required task of vermin control. Cats are transported between countries via accidental human-mediated travel or by direct importations, reducing barriers to gene flow; however, rabies control legislation has reduced the migration of cats between some countries. Overlapping niches between the wildcat progenitors, random bred feral cats, random bred house cats, and fancy breeds likely produces continual, however limited, gene flow throughout domestic cat world.

[0172] The overall selection on the cat genome may be predicted as less intense than in other domesticated species and their breeds. The cat fancy is less than 200 years old, and a majority of cat breeds were developed in the past 50 – 75 years. Human selection has focused on aesthetic qualities, such as coat colors and fur types, as opposed to complex behaviors, such as hunting skills, meat or milk production. Many of the cat's phenotypic traits, even ones that affect body and appendage morphologies, are simple traits with basic Mendelian inheritance patterns. One simple genetic change, such as long hair of the Persian versus short hair of the Exotic Shorthair, can be the defining characteristic between two breeds. Cat registries have recognized that some breeds are "natural", such as the Korat and Turkish Van, being specific population isolates, therefore random bred cats of similar origins can be used to augment the gene pools of these selected breeds. Other breeds are recognized as "hybrids", developed from purposeful cross-breeding. Breeds that are interspecies hybrids also exist in the cat fancy, such as the Bengal, which is a hybrid between an Asian leopard cat and various domestic breeds, such as Abyssinian and Egyptian Mau. Thus, some cat breeds may be a concoction of various genetic backgrounds.

[0173] Breed assignment studies of cats can be of great value to humans and the cat itself in a variety of applications. As models for human disease, cat population structuring is important to the proper selection of cases and controls in the study design of genome-wide association studies. Cross-bred cats may unknowing transport undesired mutations into naïve breed populations, and affect the breed's health and veterinary care. Polycystic kidney disease (PKD) is found in roughly 40% of Persians worldwide and has been documented in breeds with Persian influence, such as Scottish Folds and British Shorthairs (Lyons et al. (2004) *Journal of the American Society of Nephrology*, 15:2548-2555). The identification of migrants or hybridized individuals may affect the registration policies of a breed association. Out of curiosity, many of the lay public may like to know the origins of their cat and if their cat has pedigreed roots. Thus, this study has focused on the feasibility and power of genetic markers to delineate 29 of the world's cat breeds. SNPs and STRs were evaluated to assess the effects of genetic markers with different mutation rates on domestic cat regional clustering, breed clustering, and individual breed assignment. The selected 29 breeds were expected to represent the major breeds of the cat fancy. Several breeds were purposely selected that had been clearly derived from another breed, such as Persians and Exotics, while others were selected because they were recently developed hybrid breeds, such as the Ocicat and the Australian Mist. More slowly evolving SNPs and relatively quickly evolving STRs were examined as to their power to resolve these cat breeds that have different patterns and ages of ancestry.

[0174] *Genetic Diversity*. Significant genetic variation is present in many cat breeds. The Turkish Angora, a breed from Turkey, an area near the seat of cat domestication, had the highest effective number of alleles for both SNPs and STRs. A continuum of increasing heterozygosity and decreasing inbreeding, whether SNP- or STR-based, is found between the least variable and most variable domesticated cat breeds. Two of the more popular breeds of the USA and the world are Persians and Bengals (on the internet at tica.org/). Persians were one of the first breeds to be recognized and Bengals, although only introduced in the past 40 years have risen to worldwide fame. Both breeds had moderate levels of heterozygosity and inbreeding. Several less popular breeds, such as the Cornish Rex, had fairly high levels of variation and low inbreeding. Two relatively new breeds, the Siberian and Ragdoll, have high variation, perhaps a reflection of their recent development from random bred populations. Thus, levels of variation and inbreeding cannot entirely be predicted based on breed popularity and breed age, implying management by the cat breeders may be the most significant dynamic for breed genetic population health. Interestingly, the Burmese had one of the highest levels of inbreeding and lowest levels of genetic variation. Burmese were established in the post-World War II breed boom, and has been a moderately popular breed. However, concerns for two diseases, a craniofacial defect and hypokalemia, has limited migration of cats between countries and within the USA. Fractionation of the breeding pool by color preferences within the USA has also caused poor breeding dynamics. Thus, a reduction in observed heterozygosity due to the Wahlund-effect may be likely, resulting in an under-estimation of the already severely high inbreeding coefficients, possibly sending the Burmese into extinction. A breed management plan that balances diversity, health and breed type may need to be implemented to help the Burmese breed survive.

[0175] *Breed Clustering*. The most likely value of K, the number of structured groupings, could not be decisively determined. Several factors that violate many of the assumptions in the models implemented by Structure may have caused this difficulty. Cat breeds have variation in age of development, significantly different genetic population origins, and the variation in breeding practices can create distinct lines within one breed that may be as unique as one of the more recently established breeds. Many breeds were created through the crossing of two often highly divergent populations of cats resulting in a hybrid of sorts while other breeds still allow the introduction of cats from random bred populations. However, the Bayesian cluster analysis supported the breed demarcations from previous studies, especially the STR analyses of Lipinski et al. (2007) *Animal Genetics*, 38, 371-377. Previously, 22 breeds, which included 15 of 16 "foundation" cat breeds designated by the Cat Fanciers Association, delineated as 17-18 separate populations. This study added seven additional breeds, including the missing 16th "foundation" breed, the Manx. As in previous studies, the novel breeds that were not deemed significantly distinct from another breed can be very clearly explained by the breed history. The two large breed families of Siamese and Persians were re-identified and the Persian family expanded with Scottish Folds. In addition to the previously recognized grouping of the Siamese / Havana Brown, the

Australian Mist, which was created by cross-breeding with Burmese, grouped with the Burmese. However, more recent breeds, such as Ragdoll and Bengal, are resolved as separate breed populations, suggesting STRs alone can differentiate about 24 of 29 breeds, as well as Turkish-origin versus USA-origin Turkish Angoras. At K = 17, SNPs could not differentiate the Singapura, however, the Birman separation from other Asiatic breeds could be defined. Thus, both sets of markers provide valuable insight to the relationship of the breeds.

[0176] *Regional Clustering*. Regardless of the marker assayed and using both Bayesian assignment testing and principal coordinate analyses, the majority of the breeds assigned back to the random bred population most influential to the creation of that breed, as suggested by popular breed histories. Sixteen breeds originate from European populations, six breeds form South Asian populations, two breeds from the Eastern Mediterranean, the Turkish Van and the Turkish Angora, and the Sokoke from the Arabian Sea region. However, some exceptions were noted depending on the marker of analysis. For SNPs versus STRs, the Turkish Angora assigned to the Eastern Mediterranean or Europe, respectively, Bengal assigned to the Arabian Sea or Europe, respectively, and the Ocicat assigned to Europe or South Asia, respectively. The Turkish Angora breed was reconstituted from the Persian (European) pedigree post World Wars and recently, has been increasing genetic diversity via the outcrossing of pedigreed Turkish Angora cats to the random bred cats of Turkey. The identified lineages within the breed may be identifying the recent influx of random bred cats. The confusion in the Bengal and the Ocicat assignments could be a result of the contribution of the Abyssinian and Egyptian Mau and the Abyssinian and the Siamese, respectively, which are breeds with different regional assignments.

[0177] *Assignment Testing*. Overall, the Frequentist method of Paetkau et al. (2004), *supra*, outperformed the Bayesian method of Rannala and Mountain (1997), *supra*. In addition, while the 38 highly polymorphic STRs consistently outperformed the SNPs, the addition of phenotypic SNPs as a post-assignment verification significantly improved the assignment rates using the frequentist method. For the 29 breeds, when intergenic SNPs were used with the frequentist method for assignment, the sensitivity of assignment was equal to or better than that of the STRs in 12 breeds and the specificity in 19 breeds. With the addition of only five phenotypic determining SNPs, specificity improved to 15 breeds, equaling or surpassing in the sensitivity of assignment of the STRs and 19 breeds equaling or outperforming in specificity of assignment.

[0178] In six breeds, adding phenotypic SNPs into the frequentist assignment of individuals reduced the sensitivity of the test, and in five breeds it reduced specificity. As this may be due to the strength of selection imposed on these markers we looked to use the phenotypic SNPs as a method of post assignment verification of breed origin for these cats. For many breeds these single-gene traits are the sole selection criteria for breed allocation, and can be seen in the frequency of the causative mutation in the breed (Table 14). In general, breeds that were more inbred and both not used in outcrosses, nor developed through the crossing of pre-existing breeds had a higher accuracy in reassignment. Breeds such as the Russian Blue, Sokoke and Abyssinian are examples of such. In contrast, breeds where outcrossing is common either with other breeds or random bred populations tended to confuse the assignment algorithm and had a high probability of both Type I and II error. These would be breeds such as the Persians, Turkish Angoras, Siamese and Ragdoll. The most common error in assignment by far was cross assignment between Exotic shorthairs and Persians –a problem easily remedied through exploiting the FGF5 SNP shown to cause long hair in Persians.

[0179] The influence of recent breed development on the mis-allocation of individuals may be further visualized by plotting the crossed assignment rate as a function of the Reynold’s distance between breeds (Figure 11). In all cases, the crossed assignment rate increased as the distance between breeds decreased. This correlates exactly with what would be expected. Breeds that are considered separate solely on a color variant or hair length would be very close genetically and as a result, more prone to cross assignment.

[0180] The advantage was tipped in favor of SNPs when the five phenotypic SNPs were included as a post-assignment check. Initially, cats could be localized to a regional population and a breed family by STRs and / or SNPs. Secondary differentiation within the breed family could be determined by genotyping mutations for phenotypic traits, especially traits that are breed specific to or fixed within a breed. Some traits are required for breed membership; a Birman or Siamese must be pointed, implying homozygous for the G940A TYR mutation. Some traits are grounds for exclusion, all Korats are solid blue, no other colors or patterns are acceptable. Therefore, a trait such as the long haired A475C FGF5 mutation could be used as a means for identifying members of the Persian, Maine Coon, Turkish Angora, Turkish Van and Birman breeds, and likewise a means for discrimination as an exclusion maker for breeds such as the Abyssinian, Egyptian Mau, Sokoke and Ocicat. Other single gene traits may be used to identify members of a small family of cat breeds as well, such as the Burmese points, G715T TYR, are a prerequisite for membership to the Burmese and Singapura breeds, and Siamese points, G940A TYR, as their name suggests, are a requirement for Birmans, Himalayans and, of course, Siamese cats. The cinnamon mutation, C298T TYRP1, is very rare and is common to the red Abyssinian. Certain dominant traits can be homozygous or heterozygous, such as the ear curl of American Curls or the bobtail of the Japanese Bobtail. Some dominant traits are homozygous lethal in utero, such as tailless of the Manx (Todd (1961) *Journal of Heredity*, 52:228-232), or cause health problems, such as osteochondroplasia caused by the ear fold mutation in Scottish Folds (Malik et al. (1999) *Australian Veterinary Journal*, 77:85-92). As a result, the breed may have cats that conform to the breed except do not express the breed-specific trait, such as straight-eared Scottish Folds, or tailed Manx. These varieties would currently be difficult to distinguish within the breed family or region.

[0181] Cat fancy registries may not agree with assignments due to breeding restrictions. The Tonkinese, which is genetically compound heterozygous for the G940A and the G715T TYR mutations, can produce both pointed and sepia cats, thus they would genetically resemble a Siamese or Burmese, respectively. However, breeding restrictions would not allow these Tonkinese variants to be registered as Siamese or Burmese. Since the development of this SNP panel, additional phenotypic SNPs have been discovered in cats including the Norwegian Forest Cat color variant amber (Peterschmitt et al. (2009) *Animal Genetics*, 40:547-552), three additional long-haired mutations (Kehler et al. (2007) *Journal of Heredity*, 98:555-566), and the mutations responsible for hairless of Sphynx and rexing of the Devon Rex (Gandolfi et al., Mamm Genome. (2010) (9-10):509-15). These additional mutations, as well as disease mutations, could further delineate cat breeds.

[0182] *Conclusions*. Aside from the public interest in knowing their prized family pet is descendent from a celebrated pedigree, breed assignment is a vital tool in tracing the spread of genetically inherited diseases throughout the cat world. Much like humans and dogs, certain populations of cats are known to be at higher risk for particular diseases, such as heart disease in the Maine Coon and Ragdoll (Meurs et al. (2005) *Human Molecular Genetics*, 14:3587-3593; Meurs et al. (2007) *Genomics*, 90:261-264), polycystic kidney disease in the Persian (Lyons et al. 2004, *supra*), and progressive retinal atrophy in the Abyssinian (Menotti-Raymond et al. (2007) *Journal of Heredity*, 98:211-220). Knowing if a particular feline descended from one of these at risk populations may influence treatments in a clinical setting and help us to better care for our animal companions. With additional phenotypic and perhaps disease-causing SNPs, the power of this STR / SNP panel to accurately assign individuals to specific cat breeds would be greatly increased, in particular those breeds that are defined expressively by single-gene traits.

Example 3

Tables of Population Clustering at Different K Values

Table 18 - Population clustering of each pedigreed individual in the database by STRs at K = 21

Feline Population	ID No.	Missing Data	Groups																				
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Persian	1250	7	0.7866	0.0682	0.0114	0.0031	0.0048	0.0039	0.0064	0.0035	0.0031	0.039	0.0066	0.0059	0.0096	0.0033	0.0022	0.0014	0.0065	0.0085	0.0035	0.0099	0.0126
Persian	1939	13	0.5479	0.0033	0.134	0.0038	0.022	0.002	0.004	0.0053	0.001	0.003	0.2157	0.002	0.0043	0.0023	0.0033	0.0033	0.0021	0.0033	0.001	0.0354	0.001
Persian	2071	18	0.7477	0.0207	0.0379	0.0036	0.0045	0.0095	0.0277	0.0095	0.0033	0.0028	0.006	0.0073	0.0095	0.0048	0.0032	0.0043	0.003	0.0199	0.0082	0.0066	0.0599
Persian	2088	21	0.9342	0.0063	0.0037	0.0028	0.0063	0.0038	0.0028	0.006	0.0021	0.002	0.0034	0.0092	0.0019	0.0026	0.0023	0.0017	0.0018	0.0019	0.002	0.0021	0.001
Persian	2140	10	0.8648	0.0117	0.0038	0.0056	0.0028	0.0059	0.0063	0.0127	0.003	0.0079	0.0117	0.0031	0.0047	0.0023	0.0019	0.0024	0.0199	0.0065	0.0036	0.0135	0.0059
Persian	2174	10	0.9585	0.002	0.0016	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.0019	0.002	0.0018	0.0021	0.0116	0.0022	0.0013	0.001	0.001	0.003	0.001
Persian	2209	10	0.6727	0.0023	0.0058	0.0048	0.0176	0.002	0.0021	0.0022	0.002	0.1571	0.0055	0.0065	0.002	0.0022	0.0017	0.0019	0.0032	0.0043	0.0818	0.0081	0.0142
Persian	2215	18	0.6827	0.0013	0.0057	0.0227	0.001	0.0086	0.0058	0.0137	0.0108	0.0209	0.066	0.0157	0.0094	0.0021	0.0012	0.0026	0.0023	0.0027	0.0026	0.1183	0.0038
Persian	2890	10	0.9745	0.0012	0.002	0.001	0.0011	0.001	0.0019	0.0018	0.0012	0.001	0.0011	0.001	0.001	0.001	0.001	0.001	0.0018	0.001	0.001	0.0017	0.0017
Persian	2977	15	0.3524	0.0062	0.1847	0.003	0.0022	0.001	0.0047	0.0155	0.0019	0.0392	0.2965	0.002	0.0065	0.0022	0.0115	0.0027	0.001	0.001	0.002	0.0628	0.001
Persian	4143	7	0.5399	0.0015	0.1206	0.0053	0.0036	0.0022	0.0029	0.025	0.0077	0.0071	0.2098	0.002	0.0026	0.0058	0.0025	0.0027	0.0072	0.0019	0.0046	0.0437	0.0013
Persian	4168	7	0.88	0.0049	0.0032	0.0038	0.0527	0.002	0.02	0.002	0.001	0.003	0.0036	0.0022	0.0025	0.0023	0.0023	0.0019	0.0031	0.0014	0.0017	0.0052	0.0013
Persian	4169	7	0.9097	0.0074	0.0108	0.0041	0.002	0.0202	0.0075	0.0028	0.0021	0.0051	0.0068	0.0036	0.0023	0.0018	0.0027	0.0017	0.0016	0.002	0.0018	0.0028	0.0013
Persian	4950	7	0.8748	0.0039	0.0049	0.0049	0.0019	0.0125	0.0026	0.0055	0.001	0.0039	0.0077	0.0049	0.0132	0.0051	0.003	0.007	0.0036	0.0037	0.0302	0.003	0.0027
Persian	4953	15	0.9194	0.0027	0.0058	0.0024	0.0021	0.0012	0.0022	0.0098	0.002	0.0025	0.0045	0.0217	0.0057	0.0044	0.0035	0.0014	0.002	0.001	0.001	0.0031	0.0016
Exotic SH	258	15	0.8256	0.0051	0.003	0.0113	0.0015	0.005	0.0082	0.002	0.002	0.0024	0.006	0.0037	0.0833	0.0028	0.0021	0.0014	0.002	0.0238	0.0044	0.0031	0.0013
Exotic SH	259	7	0.9005	0.0029	0.0057	0.0075	0.004	0.0066	0.0102	0.0187	0.001	0.0034	0.0026	0.0025	0.0044	0.0011	0.0014	0.0013	0.001	0.001	0.001	0.0215	0.0017
Exotic SH	260	5	0.9608	0.0037	0.0023	0.0028	0.0035	0.0024	0.0021	0.0034	0.001	0.002	0.002	0.001	0.002	0.0018	0.0015	0.0019	0.001	0.001	0.0012	0.0016	0.001
Exotic SH	261	7	0.8958	0.0065	0.0091	0.0085	0.0025	0.0053	0.001	0.0033	0.002	0.0073	0.0114	0.0092	0.0071	0.0072	0.0112	0.0024	0.0012	0.001	0.003	0.0036	0.0013
Exotic SH	262	7	0.9025	0.018	0.0032	0.0158	0.0016	0.0069	0.0028	0.0068	0.0041	0.003	0.0037	0.002	0.0034	0.0046	0.0036	0.0025	0.0019	0.0043	0.0033	0.0048	0.0013
Exotic SH	263	10	0.9234	0.0056	0.0041	0.0091	0.0024	0.0019	0.0022	0.01	0.0013	0.0072	0.0044	0.005	0.0021	0.0034	0.0019	0.0024	0.0026	0.0022	0.001	0.0066	0.0012
Exotic SH	264	7	0.6501	0.0031	0.0266	0.1467	0.0838	0.0011	0.0107	0.0014	0.002	0.0138	0.0077	0.0023	0.0104	0.0012	0.0024	0.0062	0.0082	0.0057	0.0027	0.0115	0.0023
Exotic SH	265	18	0.8689	0.0033	0.005	0.0032	0.0029	0.006	0.008	0.003	0.0034	0.01	0.0069	0.002	0.0026	0.0033	0.0025	0.0021	0.0058	0.006	0.0061	0.004	0.045
Exotic SH	266	7	0.9553	0.002	0.0021	0.0041	0.004	0.001	0.0019	0.002	0.001	0.0017	0.0022	0.001	0.001	0.0016	0.001	0.001	0.0116	0.001	0.002	0.0015	0.001
Exotic SH	267	7	0.9372	0.0019	0.0015	0.016	0.002	0.002	0.0029	0.002	0.0017	0.0019	0.0019	0.001	0.0015	0.0041	0.0045	0.0089	0.0015	0.0019	0.0018	0.0025	0.0013
Exotic SH	268	18	0.8783	0.009	0.0056	0.0105	0.0021	0.0018	0.0052	0.0024	0.0023	0.0039	0.0053	0.0054	0.0024	0.0023	0.007	0.0016	0.0233	0.0034	0.0219	0.0028	0.0034
Exotic SH	269	5	0.9549	0.0019	0.0031	0.0046	0.0028	0.0019	0.0018	0.0033	0.0011	0.0018	0.0023	0.0026	0.0019	0.0015	0.0023	0.0017	0.0018	0.0018	0.0035	0.0016	0.0019
Exotic SH	270	5	0.9377	0.0061	0.0022	0.0131	0.002	0.0042	0.0025	0.0027	0.001	0.0022	0.0024	0.0012	0.0028	0.0011	0.001	0.0011	0.0022	0.0011	0.001	0.0112	0.0012
Exotic SH	271	7	0.9563	0.0043	0.0029	0.0018	0.0021	0.0023	0.001	0.0032	0.002	0.002	0.0024	0.0019	0.0019	0.0019	0.0016	0.0019	0.0018	0.0025	0.0022	0.003	0.001
Exotic SH	272	7	0.7489	0.0021	0.003	0.1869	0.0021	0.0023	0.0023	0.005	0.0033	0.0044	0.0033	0.002	0.0037	0.0021	0.0085	0.0024	0.0018	0.0032	0.0036	0.0074	0.0016
Exotic SH	273	5	0.9224	0.0056	0.0036	0.0036	0.0019	0.0028	0.002	0.0032	0.0045	0.0057	0.006	0.0073	0.0028	0.0035	0.0025	0.0016	0.0114	0.0019	0.0018	0.0033	0.0026
Exotic SH	274	15	0.9178	0.0023	0.0066	0.0013	0.0054	0.004	0.0073	0.0041	0.0026	0.0034	0.0056	0.0018	0.0062	0.002	0.0035	0.003	0.0137	0.0022	0.001	0.004	0.0022
Exotic SH	275	10	0.8779	0.002	0.0029	0.0111	0.0021	0.0028	0.0241	0.0014	0.0104	0.002	0.0022	0.0018	0.0018	0.0016	0.0011	0.0017	0.0054	0.0022	0.0377	0.0031	0.0047
Exotic SH	276	7	0.9058	0.0039	0.0076	0.008	0.0011	0.0021	0.0044	0.0058	0.0032	0.0043	0.0064	0.0028	0.0022	0.0029	0.0017	0.0012	0.002	0.0036	0.0014	0.004	0.0255
British SH	156	5	0.6905	0.0221	0.0172	0.0044	0.002	0.0108	0.0018	0.0048	0.0112	0.005	0.0087	0.0042	0.006	0.004	0.0027	0.0013	0.002	0.0028	0.001	0.1936	0.004
British SH	157	5	0.7973	0.0148	0.0172	0.0053	0.009	0.0068	0.0057	0.0077	0.0082	0.004	0.006	0.0034	0.0078	0.0032	0.002	0.0017	0.001	0.0028	0.0041	0.0852	0.0068
British SH	158	5	0.5086	0.0079	0.1649	0.002	0.0095	0.003	0.004	0.0117	0.003	0.0101	0.1597	0.0021	0.0036	0.0024	0.0023	0.0024	0.0011	0.0017	0.001	0.0928	0.0062

Table 18 - Population clustering of each pedigreed individual in the database by STRs at K = 21

Feline	ID	Missing	Groups																				
Population	No.	Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
British SH	159	5	0.6213	0.063	0.0035	0.0065	0.0274	0.0029	0.0031	0.0062	0.0025	0.0458	0.0077	0.003	0.002	0.0061	0.0027	0.0023	0.0042	0.0081	0.0037	0.1741	0.0039
British SH	160	7	0.7633	0.0026	0.01	0.002	0.0018	0.0025	0.001	0.0037	0.0021	0.0018	0.0016	0.001	0.0019	0.0021	0.001	0.001	0.001	0.001	0.001	0.1958	0.0018
British SH	161	5	0.6705	0.017	0.0622	0.002	0.0021	0.0085	0.0056	0.0081	0.002	0.003	0.0025	0.0025	0.0032	0.0025	0.0017	0.0022	0.0141	0.0013	0.001	0.1828	0.0052
British SH	162	5	0.5013	0.0683	0.188	0.002	0.002	0.0024	0.0019	0.0047	0.0036	0.0104	0.0055	0.0038	0.0044	0.0061	0.0026	0.0018	0.0359	0.0021	0.0011	0.151	0.0012
British SH	163	5	0.4522	0.1998	0.0046	0.0033	0.0609	0.004	0.0053	0.0056	0.0021	0.0215	0.0036	0.0137	0.0077	0.003	0.006	0.0013	0.0352	0.0025	0.0421	0.1228	0.0028
British SH	164	5	0.5118	0.0989	0.1951	0.003	0.0029	0.0044	0.0013	0.0049	0.002	0.0234	0.0037	0.002	0.0028	0.0019	0.0077	0.0013	0.0034	0.001	0.0027	0.124	0.0018
British SH	165	10	0.6535	0.0691	0.0123	0.003	0.0018	0.0059	0.0061	0.0059	0.0039	0.0145	0.0055	0.0208	0.0065	0.002	0.0023	0.0059	0.0028	0.0021	0.0014	0.1721	0.0025
British SH	166	7	0.8077	0.0026	0.007	0.019	0.0107	0.0063	0.0122	0.0104	0.0106	0.0029	0.0032	0.0041	0.0026	0.0034	0.0011	0.0026	0.0067	0.0023	0.011	0.0688	0.0046
British SH	167	7	0.4173	0.038	0.314	0.0094	0.0059	0.002	0.0196	0.0156	0.002	0.023	0.0386	0.002	0.0138	0.005	0.0015	0.0022	0.0145	0.0044	0.0044	0.0638	0.003
British SH	168	5	0.721	0.0019	0.0027	0.003	0.0019	0.0017	0.0259	0.003	0.0056	0.003	0.0101	0.0145	0.002	0.0019	0.0034	0.0038	0.0012	0.0404	0.0052	0.1342	0.0136
British SH	169	5	0.8963	0.004	0.0084	0.004	0.0042	0.002	0.0066	0.0042	0.0082	0.0037	0.0057	0.0047	0.014	0.0036	0.0024	0.003	0.0011	0.001	0.0084	0.0125	0.002
British SH	170	7	0.7456	0.0052	0.0136	0.002	0.001	0.001	0.001	0.0281	0.0018	0.0027	0.0034	0.002	0.0055	0.0011	0.009	0.0024	0.001	0.001	0.0011	0.1704	0.001
British SH	171	5	0.7699	0.0017	0.0014	0.0027	0.001	0.0032	0.0038	0.0025	0.0042	0.0021	0.0027	0.0032	0.0021	0.0032	0.001	0.0017	0.0012	0.0013	0.001	0.1891	0.001
British SH	172	5	0.7388	0.0026	0.0021	0.0022	0.002	0.0033	0.0011	0.0034	0.0019	0.0012	0.0012	0.001	0.001	0.0011	0.001	0.0016	0.0025	0.0085	0.0028	0.2084	0.0123
British SH	173	7	0.6843	0.0123	0.0075	0.002	0.0019	0.0631	0.0031	0.0052	0.0035	0.003	0.0032	0.0018	0.003	0.0061	0.007	0.0016	0.0053	0.0014	0.001	0.1806	0.0031
Scottish Fold	5655	7	0.6005	0.0301	0.0652	0.0178	0.0021	0.0022	0.0048	0.0196	0.0109	0.0086	0.019	0.0021	0.0105	0.0077	0.001	0.0013	0.0578	0.0038	0.0021	0.1304	0.0025
Scottish Fold	5669	2	0.7467	0.0172	0.0347	0.0032	0.0048	0.0032	0.024	0.0113	0.0178	0.0021	0.0278	0.002	0.0057	0.0016	0.0016	0.0025	0.0097	0.0017	0.001	0.0803	0.001
Scottish Fold	7205	5	0.5549	0.1066	0.1134	0.0039	0.0027	0.0024	0.0331	0.0033	0.0029	0.0128	0.009	0.0014	0.0031	0.002	0.003	0.0176	0.0037	0.0023	0.0032	0.1174	0.0013
Scottish Fold	7260	7	0.4461	0.0055	0.0897	0.0059	0.0046	0.0054	0.0028	0.0026	0.0785	0.0443	0.2661	0.0025	0.002	0.0011	0.0013	0.0032	0.0035	0.001	0.001	0.0319	0.001
Scottish Fold	8552	7	0.7094	0.0031	0.0065	0.0077	0.004	0.0023	0.0042	0.0148	0.0029	0.0067	0.0063	0.0019	0.0078	0.0023	0.002	0.0109	0.0085	0.0013	0.0013	0.1806	0.0156
Scottish Fold	9823	5	0.7631	0.0033	0.0035	0.0022	0.0017	0.0018	0.0012	0.0028	0.0027	0.0029	0.0042	0.0029	0.0018	0.0011	0.0011	0.0022	0.0018	0.0017	0.001	0.1957	0.0013
Scottish Fold	9824	5	0.7671	0.0015	0.0045	0.0018	0.002	0.0017	0.002	0.0115	0.0018	0.002	0.0041	0.001	0.0013	0.0012	0.0013	0.0014	0.001	0.0015	0.001	0.1885	0.0018
Scottish Fold	9825	7	0.7611	0.0037	0.0031	0.0024	0.003	0.0021	0.0018	0.0028	0.0028	0.0035	0.0032	0.0018	0.002	0.0014	0.0015	0.0019	0.001	0.0019	0.0014	0.1948	0.0028
Scottish Fold	9826	5	0.7696	0.0032	0.0035	0.0018	0.0018	0.0028	0.001	0.0025	0.0017	0.0018	0.0023	0.0017	0.001	0.001	0.0011	0.0017	0.0018	0.001	0.001	0.1967	0.001
Scottish Fold	9827	7	0.7742	0.0012	0.0029	0.0019	0.003	0.001	0.001	0.0028	0.0011	0.002	0.0018	0.0015	0.0014	0.001	0.001	0.0022	0.002	0.001	0.001	0.195	0.001
Scottish Fold	9831	5	0.7659	0.0028	0.0026	0.002	0.0021	0.002	0.001	0.0033	0.0041	0.002	0.0019	0.002	0.0019	0.0017	0.0011	0.0029	0.0018	0.0018	0.001	0.1943	0.0018
Scottish Fold	9832	7	0.7597	0.0036	0.0037	0.002	0.004	0.0019	0.0018	0.0037	0.0024	0.0029	0.0058	0.0018	0.0018	0.0011	0.0015	0.0031	0.001	0.001	0.0016	0.1946	0.001
Scottish Fold	9929	7	0.7189	0.0385	0.0118	0.0024	0.003	0.001	0.0121	0.004	0.0019	0.0503	0.0078	0.0015	0.0296	0.0065	0.0028	0.0028	0.002	0.0017	0.001	0.0995	0.001
Scottish Fold	9930	7	0.5752	0.2529	0.0055	0.002	0.0033	0.0032	0.0094	0.002	0.0029	0.0158	0.0039	0.001	0.002	0.0033	0.0016	0.0021	0.0011	0.001	0.001	0.1097	0.001
Scottish Fold	9931	7	0.5005	0.3098	0.0049	0.0023	0.0079	0.0015	0.0074	0.0027	0.0023	0.0052	0.0049	0.0031	0.0043	0.0026	0.004	0.0038	0.001	0.0027	0.001	0.1271	0.001
Scottish Fold	9937	5	0.3795	0.3982	0.0214	0.0035	0.001	0.0049	0.0064	0.0155	0.0029	0.0072	0.0167	0.001	0.0056	0.0021	0.0019	0.0027	0.0017	0.0034	0.0027	0.1204	0.0013
Scottish Fold	9965	5	0.4471	0.1745	0.2081	0.0056	0.002	0.002	0.0017	0.002	0.0023	0.0057	0.0063	0.001	0.0037	0.0012	0.0095	0.0029	0.0019	0.001	0.0018	0.1188	0.001
Chartreux	1772	7	0.0063	0.8977	0.0381	0.0023	0.0046	0.0047	0.0033	0.0023	0.0016	0.0021	0.0022	0.0018	0.0052	0.0018	0.0014	0.0017	0.0086	0.002	0.0043	0.0051	0.0029
Chartreux	2226	15	0.0037	0.8556	0.0077	0.0397	0.0043	0.0042	0.0065	0.0067	0.004	0.0123	0.0052	0.0033	0.0197	0.0022	0.0032	0.0026	0.0095	0.0014	0.0019	0.005	0.0013
Chartreux	2229	26	0.028	0.7448	0.0033	0.0025	0.0026	0.0044	0.0019	0.1111	0.009	0.0064	0.004	0.0019	0.0032	0.0041	0.0041	0.0025	0.0011	0.0011	0.0028	0.06	0.0013
Chartreux	2524	5	0.0025	0.7292	0.1568	0.0113	0.0046	0.0062	0.0095	0.0022	0.008	0.0094	0.0156	0.004	0.0038	0.0036	0.0042	0.0051	0.0025	0.0057	0.0024	0.0074	0.006
Chartreux	2787	13	0.0032	0.86	0.0504	0.0167	0.0028	0.002	0.0032	0.0039	0.0028	0.0032	0.0076	0.003	0.0026	0.0057	0.005	0.0044	0.0047	0.0044	0.0047	0.006	0.0038
Chartreux	2805	15	0.0671	0.7312	0.0491	0.0042	0.0054	0.001	0.001	0.0027	0.0026	0.0039	0.0091	0.0192	0.0018	0.0017	0.0025	0.0012	0.0026	0.0025	0.0012	0.0866	0.0033
Chartreux	2813	26	0.1312	0.5713	0.1405	0.0048	0.0038	0.006	0.0033	0.0076	0.0021	0.0173	0.0049	0.0074	0.002	0.0021	0.0094	0.0039	0.0041	0.0043	0.0023	0.0684	0.0034

Table 18 - Population clustering of each pedigreed individual in the database by STRs at K = 21

Feline Population	ID No.	Missing Data	Groups																				
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Chartreux	2979	21	0.2175	0.663	0.0037	0.0045	0.0032	0.0046	0.0067	0.0022	0.0021	0.0025	0.0054	0.002	0.0048	0.0088	0.0059	0.008	0.003	0.002	0.0056	0.0433	0.0012
Chartreux	4059	13	0.006	0.956	0.002	0.0026	0.0026	0.0013	0.001	0.0013	0.001	0.0022	0.0027	0.0048	0.0013	0.0014	0.0017	0.0012	0.0019	0.0023	0.0021	0.0026	0.002
Chartreux	4063	28	0.0128	0.9451	0.0033	0.0035	0.0014	0.0014	0.0022	0.0012	0.002	0.0023	0.0028	0.0016	0.0021	0.002	0.0021	0.0023	0.004	0.0018	0.0021	0.0027	0.0012
Chartreux	5606	13	0.0031	0.9692	0.0023	0.0013	0.0016	0.0017	0.0013	0.0017	0.0011	0.0013	0.0023	0.001	0.001	0.0011	0.0015	0.0011	0.0023	0.001	0.0013	0.0018	0.001
Chartreux	5609	10	0.0013	0.9309	0.0016	0.0028	0.0087	0.0021	0.0033	0.0025	0.0074	0.0024	0.0029	0.002	0.0036	0.0055	0.0013	0.0016	0.0041	0.0041	0.0024	0.0054	0.0041
Chartreux	5611	18	0.0236	0.9192	0.0023	0.0114	0.0021	0.0024	0.0017	0.0091	0.0014	0.0023	0.0032	0.0031	0.002	0.0022	0.0018	0.0011	0.0034	0.0015	0.0013	0.0037	0.0012
American SH	143	5	0.0105	0.2447	0.5894	0.008	0.0023	0.01	0.002	0.0088	0.0017	0.003	0.0082	0.079	0.005	0.0024	0.0027	0.0047	0.009	0.0013	0.001	0.0043	0.002
American SH	144	5	0.0025	0.2937	0.6791	0.0031	0.001	0.001	0.001	0.001	0.0023	0.0023	0.0017	0.001	0.001	0.001	0.0012	0.0011	0.001	0.001	0.001	0.0011	0.0019
American SH	145	5	0.0092	0.2629	0.6655	0.0041	0.006	0.002	0.0013	0.0055	0.0023	0.0055	0.0044	0.0023	0.004	0.0024	0.0046	0.0014	0.0023	0.0023	0.001	0.0087	0.0023
American SH	146	5	0.0259	0.1959	0.5457	0.0053	0.0016	0.0105	0.0231	0.0304	0.0032	0.0455	0.0179	0.001	0.0021	0.0027	0.0011	0.0021	0.0401	0.002	0.0018	0.0383	0.0039
American SH	3652	15	0.0039	0.2904	0.6406	0.0052	0.0019	0.0097	0.0024	0.0057	0.0028	0.004	0.0094	0.001	0.0039	0.003	0.001	0.0012	0.0048	0.0018	0.0012	0.0036	0.0025
American SH	3653	5	0.0095	0.2145	0.5634	0.0112	0.0516	0.003	0.0049	0.0235	0.0107	0.0135	0.0269	0.0051	0.022	0.0036	0.0033	0.0037	0.0035	0.0143	0.001	0.0056	0.0052
American SH	4363	10	0.0132	0.277	0.673	0.0011	0.0013	0.0026	0.0025	0.0018	0.0045	0.0031	0.0023	0.002	0.0013	0.0017	0.001	0.0017	0.002	0.001	0.001	0.0034	0.0025
American SH	4370	7	0.0111	0.2027	0.5732	0.0052	0.0131	0.0154	0.0298	0.0066	0.0025	0.0449	0.0106	0.001	0.0163	0.016	0.0043	0.0141	0.0023	0.0035	0.0124	0.0071	0.0078
American SH	4373	18	0.006	0.2785	0.6691	0.002	0.0021	0.001	0.0015	0.0014	0.0013	0.0036	0.002	0.0141	0.0024	0.0021	0.0022	0.0019	0.0023	0.001	0.001	0.0019	0.0026
American SH	6404	13	0.0045	0.1919	0.6085	0.0108	0.048	0.0023	0.002	0.0033	0.0025	0.0046	0.0041	0.003	0.0554	0.0014	0.0041	0.007	0.0376	0.0016	0.0022	0.0036	0.0015
American SH	6406	7	0.1731	0.1501	0.5087	0.0093	0.0039	0.0624	0.0041	0.0121	0.002	0.0062	0.0153	0.0031	0.0074	0.0021	0.0061	0.0043	0.002	0.0017	0.0064	0.0184	0.0013
American SH	6410	7	0.2401	0.2059	0.4241	0.0035	0.0037	0.0022	0.0019	0.0039	0.0014	0.0057	0.0038	0.0027	0.0033	0.0014	0.0026	0.0023	0.0036	0.002	0.0041	0.0803	0.0015
American SH	6421	13	0.0173	0.2621	0.4855	0.0056	0.008	0.0156	0.004	0.045	0.0057	0.0076	0.0104	0.0434	0.0146	0.0079	0.0043	0.0161	0.002	0.0054	0.0042	0.0258	0.0095
American SH	2259	5	0.0059	0.2719	0.6448	0.0012	0.0072	0.002	0.0037	0.0037	0.0178	0.0034	0.004	0.002	0.0032	0.0021	0.0066	0.0021	0.0035	0.0021	0.0054	0.0028	0.0045
Sphynx	277	10	0.0077	0.003	0.0031	0.8871	0.0068	0.0256	0.0058	0.0026	0.0044	0.002	0.003	0.002	0.0021	0.0035	0.0018	0.0034	0.0021	0.0064	0.0081	0.0045	0.0151
Sphynx	278	7	0.0054	0.0143	0.0078	0.9134	0.002	0.001	0.003	0.0027	0.002	0.0054	0.0103	0.0028	0.002	0.0029	0.0063	0.004	0.0064	0.002	0.0027	0.0023	0.0013
Sphynx	279	7	0.0035	0.0038	0.0026	0.8939	0.003	0.012	0.0057	0.0314	0.003	0.0022	0.0045	0.0018	0.002	0.0023	0.001	0.0026	0.002	0.0061	0.0018	0.0126	0.0023
Sphynx	280	7	0.0046	0.0045	0.0092	0.9188	0.0024	0.002	0.0074	0.003	0.0021	0.0029	0.0078	0.0035	0.0037	0.0017	0.002	0.003	0.01	0.0013	0.002	0.0026	0.0055
Sphynx	281	7	0.0053	0.003	0.0075	0.8739	0.0047	0.0327	0.0077	0.0021	0.0032	0.0066	0.0031	0.002	0.0091	0.0034	0.0016	0.0041	0.002	0.0112	0.0023	0.0058	0.0087
Sphynx	282	7	0.0035	0.002	0.0022	0.9577	0.001	0.002	0.002	0.002	0.0022	0.002	0.0021	0.0066	0.002	0.001	0.001	0.001	0.001	0.0021	0.002	0.0023	0.0022
Sphynx	283	10	0.0587	0.0023	0.0041	0.8182	0.002	0.0043	0.003	0.0705	0.0021	0.0047	0.0028	0.0038	0.0029	0.0012	0.0013	0.001	0.003	0.001	0.0054	0.0065	0.0011
Sphynx	284	7	0.0037	0.0155	0.0104	0.8288	0.0012	0.0083	0.002	0.0068	0.0446	0.0094	0.0372	0.0028	0.0026	0.0025	0.0021	0.0052	0.005	0.0027	0.002	0.0046	0.0027
Sphynx	285	7	0.0025	0.0021	0.0032	0.9417	0.0033	0.002	0.0033	0.002	0.003	0.0026	0.0026	0.0029	0.003	0.0024	0.0022	0.0052	0.0031	0.0026	0.0037	0.0039	0.0027
Sphynx	286	7	0.003	0.0029	0.002	0.9484	0.0012	0.002	0.0019	0.0041	0.003	0.002	0.0029	0.0056	0.0015	0.0016	0.001	0.001	0.0034	0.0039	0.0014	0.005	0.0022
Sphynx	287	10	0.0259	0.0163	0.105	0.7	0.0097	0.0042	0.0056	0.0048	0.0032	0.008	0.0115	0.0318	0.0102	0.0038	0.0026	0.0029	0.0042	0.0082	0.017	0.0108	0.0142
Sphynx	288	7	0.0022	0.0091	0.0029	0.9489	0.001	0.0134	0.002	0.0012	0.0029	0.002	0.002	0.001	0.003	0.0011	0.001	0.0011	0.0011	0.001	0.001	0.0011	0.001
Sphynx	289	7	0.0037	0.016	0.0053	0.8831	0.001	0.0029	0.0018	0.0058	0.0316	0.0034	0.0063	0.0099	0.0059	0.0044	0.0034	0.0027	0.0027	0.0013	0.001	0.0062	0.0017
Sphynx	290	10	0.0031	0.0028	0.0035	0.9513	0.0028	0.0029	0.001	0.003	0.0014	0.002	0.0034	0.0013	0.004	0.0019	0.0027	0.0054	0.001	0.0025	0.0013	0.0017	0.001
Sphynx	291	5	0.0053	0.0147	0.0173	0.874	0.0046	0.0072	0.0021	0.0106	0.0023	0.008	0.0075	0.0039	0.0118	0.0045	0.0041	0.0027	0.005	0.0033	0.0015	0.0077	0.0019
Sphynx	292	5	0.0054	0.0035	0.0023	0.9266	0.0011	0.0055	0.0039	0.0044	0.0038	0.002	0.0028	0.002	0.004	0.0027	0.0013	0.0021	0.001	0.0091	0.002	0.0043	0.0102
Sphynx	293	7	0.0018	0.0061	0.0076	0.7433	0.0061	0.0041	0.031	0.004	0.022	0.0235	0.032	0.0083	0.0036	0.0166	0.0232	0.0185	0.0062	0.0089	0.0057	0.0084	0.019
Japanese BT	1949	7	0.0029	0.0019	0.0026	0.003	0.9335	0.0031	0.0013	0.0058	0.0013	0.0087	0.0043	0.0017	0.0105	0.0044	0.003	0.0025	0.001	0.001	0.0022	0.0038	0.0015
Japanese BT	1966	10	0.0131	0.0107	0.0875	0.0202	0.7777	0.0023	0.002	0.0071	0.0059	0.0106	0.0152	0.0183	0.0034	0.0023	0.0021	0.002	0.0037	0.0015	0.0013	0.0055	0.0076

Table 18 - Population clustering of each pedigreed individual in the database by STRs at K = 21

Feline	ID	Missing	Groups																			
Population	No.	Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Japanese BT	2661	10	0.001	0.001	0.001	0.001	0.9798	0.001	0.0011	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	0.001
Japanese BT	2663	5	0.001	0.0012	0.001	0.001	0.9745	0.001	0.002	0.001	0.0019	0.001	0.001	0.002	0.0017	0.0013	0.001	0.0011	0.002	0.001	0.001	0.001	0.0013
Japanese BT	2666	7	0.0029	0.0063	0.0089	0.0055	0.8864	0.011	0.0132	0.002	0.0021	0.0092	0.003	0.0023	0.0029	0.0016	0.0029	0.0028	0.0075	0.0047	0.0147	0.0056	0.0044
Japanese BT	2668	10	0.0016	0.0042	0.0156	0.0024	0.8897	0.003	0.0035	0.0029	0.0046	0.0047	0.0211	0.003	0.0027	0.0031	0.002	0.0076	0.002	0.0066	0.0032	0.0034	0.0131
Japanese BT	2973	13	0.0019	0.0023	0.0044	0.002	0.9499	0.0024	0.0018	0.0013	0.0033	0.002	0.004	0.002	0.005	0.003	0.0018	0.0025	0.002	0.001	0.0017	0.0024	0.0033
Japanese BT	3324	10	0.0031	0.002	0.0017	0.001	0.9731	0.001	0.0019	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.0019	0.001	0.001	0.001	0.001	0.0016	0.0017
Japanese BT	3355	5	0.002	0.0031	0.0017	0.001	0.9594	0.0011	0.003	0.0021	0.0037	0.002	0.002	0.001	0.0011	0.0021	0.001	0.0024	0.001	0.0023	0.0018	0.0042	0.0019
Japanese BT	3356	15	0.0047	0.0174	0.003	0.006	0.8809	0.0049	0.009	0.011	0.003	0.0057	0.0062	0.002	0.0283	0.0019	0.002	0.0055	0.002	0.0012	0.0013	0.003	0.001
Japanese BT	3523	7	0.0016	0.0048	0.0049	0.002	0.9443	0.002	0.003	0.002	0.0055	0.002	0.0038	0.004	0.0029	0.0027	0.0026	0.0028	0.002	0.002	0.001	0.0021	0.002
Japanese BT	3621	7	0.0044	0.002	0.0023	0.001	0.9505	0.002	0.0039	0.0012	0.003	0.001	0.002	0.001	0.002	0.0025	0.0038	0.0094	0.003	0.001	0.0011	0.0019	0.001
Japanese BT	3622	10	0.0076	0.0035	0.0043	0.004	0.802	0.002	0.005	0.0432	0.0125	0.0094	0.008	0.002	0.0045	0.0052	0.002	0.0022	0.0258	0.0186	0.0026	0.0319	0.0038
Japanese BT	3673	5	0.0019	0.003	0.0037	0.0017	0.6722	0.0041	0.0031	0.0102	0.2051	0.0117	0.0084	0.002	0.0148	0.0058	0.0023	0.029	0.0054	0.0068	0.0021	0.0025	0.0042
Japanese BT	3691	5	0.0039	0.0031	0.003	0.002	0.9432	0.001	0.0049	0.001	0.0048	0.002	0.0015	0.001	0.001	0.0011	0.0018	0.0022	0.0039	0.0026	0.007	0.0031	0.0059
Japanese BT	3693	5	0.0018	0.0013	0.0024	0.001	0.9627	0.0015	0.0027	0.001	0.003	0.003	0.002	0.002	0.001	0.0019	0.0028	0.0012	0.0015	0.0013	0.002	0.0026	0.0013
Japanese BT	4027	13	0.0051	0.0289	0.0052	0.0014	0.8401	0.0024	0.0142	0.004	0.0043	0.0082	0.0089	0.001	0.0113	0.0017	0.0015	0.0018	0.0481	0.0013	0.004	0.0035	0.003
Japanese BT	4030	13	0.0031	0.0038	0.0025	0.0157	0.876	0.0089	0.0058	0.002	0.0036	0.003	0.005	0.0063	0.0088	0.0039	0.0038	0.0265	0.003	0.006	0.006	0.0036	0.0028
Japanese BT	4043	10	0.0066	0.004	0.0074	0.0104	0.7678	0.0309	0.086	0.0065	0.0074	0.0043	0.0052	0.0025	0.004	0.002	0.0021	0.0037	0.01	0.0051	0.0026	0.0042	0.0273
Cornish Rex	2497	7	0.0019	0.0042	0.0039	0.002	0.001	0.933	0.002	0.002	0.0011	0.002	0.0064	0.0023	0.002	0.0019	0.0019	0.002	0.001	0.0051	0.0122	0.002	0.0101
Cornish Rex	2863	0	0.002	0.001	0.0017	0.003	0.0036	0.954	0.0021	0.002	0.0072	0.001	0.001	0.001	0.001	0.0019	0.001	0.0012	0.001	0.0045	0.001	0.0042	0.0045
Cornish Rex	2872	13	0.001	0.0018	0.002	0.0013	0.001	0.9531	0.002	0.001	0.0025	0.002	0.002	0.001	0.002	0.0014	0.0019	0.002	0.001	0.0057	0.0056	0.0019	0.0077
Cornish Rex	3283	2	0.0026	0.0026	0.005	0.004	0.0123	0.8988	0.002	0.003	0.0043	0.002	0.0022	0.002	0.0021	0.0029	0.0024	0.0034	0.0035	0.0307	0.0047	0.0058	0.0036
Cornish Rex	3306	15	0.0018	0.0034	0.0023	0.0024	0.002	0.8649	0.0177	0.002	0.0042	0.011	0.0053	0.002	0.0057	0.0037	0.0084	0.0069	0.0047	0.0077	0.0116	0.0093	0.023
Cornish Rex	3931	10	0.001	0.0014	0.0016	0.002	0.0032	0.9654	0.0013	0.002	0.0011	0.0031	0.0026	0.001	0.002	0.0012	0.002	0.0012	0.002	0.0018	0.001	0.0014	0.0017
Cornish Rex	3955	7	0.0151	0.0186	0.0076	0.0022	0.001	0.889	0.0191	0.0021	0.0019	0.0052	0.0099	0.0023	0.0059	0.0033	0.0021	0.0022	0.0016	0.0026	0.0025	0.0041	0.0016
Cornish Rex	3992	23	0.0181	0.0022	0.0042	0.0013	0.002	0.9222	0.002	0.0035	0.0067	0.0034	0.0027	0.001	0.0023	0.002	0.001	0.0032	0.002	0.004	0.0033	0.0107	0.0021
Cornish Rex	5790	2	0.018	0.0106	0.0146	0.0067	0.1444	0.7143	0.0035	0.0063	0.0108	0.0043	0.0234	0.0069	0.0054	0.0041	0.0033	0.002	0.0019	0.0024	0.0047	0.0084	0.0042
Cornish Rex	7031	0	0.0023	0.0142	0.0032	0.0111	0.0061	0.8151	0.003	0.0027	0.0023	0.0052	0.004	0.0167	0.0046	0.0131	0.0199	0.0166	0.0019	0.0341	0.0036	0.0173	0.0032
Cornish Rex	7036	0	0.0036	0.0023	0.0029	0.002	0.002	0.8666	0.0164	0.001	0.0031	0.0033	0.003	0.0011	0.002	0.002	0.0027	0.0034	0.0241	0.0043	0.0048	0.0034	0.046
Cornish Rex	8528	18	0.001	0.001	0.002	0.002	0.0022	0.9638	0.002	0.0026	0.0013	0.002	0.0022	0.002	0.001	0.001	0.001	0.0016	0.0023	0.0026	0.0021	0.0028	0.0015
Cornish Rex	8529	2	0.0018	0.002	0.0018	0.0019	0.001	0.9633	0.002	0.002	0.001	0.002	0.0026	0.0019	0.002	0.001	0.001	0.0011	0.001	0.0017	0.0013	0.0014	0.0062
Cornish Rex	8530	0	0.0012	0.0026	0.0013	0.0011	0.0017	0.9591	0.0021	0.002	0.0064	0.001	0.003	0.001	0.0028	0.0016	0.001	0.0012	0.001	0.0031	0.002	0.0021	0.0027
Cornish Rex	8543	5	0.001	0.0018	0.0071	0.002	0.001	0.9612	0.001	0.002	0.0022	0.002	0.0026	0.002	0.0022	0.0021	0.0015	0.001	0.002	0.001	0.001	0.0016	0.0017
Ragdoll	7429	5	0.002	0.0036	0.0045	0.002	0.0022	0.0042	0.9378	0.001	0.001	0.0063	0.0026	0.002	0.0021	0.0042	0.002	0.0052	0.0082	0.0023	0.002	0.0033	0.0015
Ragdoll	8362	2	0.0118	0.0024	0.0051	0.0012	0.003	0.003	0.9272	0.002	0.0081	0.003	0.0028	0.002	0.0025	0.0017	0.0019	0.0028	0.0106	0.001	0.003	0.0029	0.002
Ragdoll	8366	0	0.0018	0.002	0.0026	0.0015	0.004	0.002	0.9558	0.002	0.0022	0.0047	0.0025	0.001	0.0022	0.0014	0.002	0.0015	0.001	0.0023	0.002	0.0021	0.0034
Ragdoll	8367	5	0.0208	0.0035	0.004	0.0029	0.0018	0.0017	0.921	0.0069	0.0048	0.0031	0.0027	0.0049	0.0045	0.0011	0.0021	0.0025	0.002	0.002	0.0025	0.0028	0.0024
Ragdoll	8368	7	0.0044	0.001	0.0027	0.002	0.0027	0.0013	0.9534	0.002	0.002	0.002	0.0021	0.002	0.0019	0.0012	0.0014	0.002	0.003	0.004	0.0024	0.0025	0.004
Ragdoll	8372	13	0.425	0.0027	0.0023	0.0037	0.0052	0.0051	0.5111	0.0031	0.0031	0.002	0.0024	0.003	0.003	0.0021	0.0016	0.0013	0.003	0.003	0.0087	0.0049	0.0037
Ragdoll	8377	0	0.001	0.001	0.001	0.0012	0.002	0.002	0.9636	0.001	0.0011	0.0011	0.0013	0.002	0.001	0.002	0.002	0.0029	0.002	0.004	0.0042	0.0018	0.0018

Table 18 - Population clustering of each pedigreed individual in the database by STRs at K = 21

Feline	ID	Missing	Groups																			
Population	No.	Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Ragdoll	9292	0	0.0151	0.0038	0.0055	0.0021	0.001	0.0125	0.8937	0.0086	0.0041	0.0035	0.0029	0.002	0.0086	0.0023	0.001	0.0024	0.0052	0.0033	0.0027	0.0057	0.0139
Ragdoll	9295	5	0.004	0.002	0.0024	0.0066	0.007	0.004	0.8912	0.001	0.0121	0.002	0.0106	0.002	0.0029	0.0032	0.0032	0.0077	0.0052	0.0191	0.0044	0.0052	0.0042
Ragdoll	9299	0	0.0091	0.0038	0.0301	0.0093	0.0069	0.0026	0.666	0.0273	0.0051	0.0123	0.0978	0.0147	0.0223	0.0045	0.0028	0.0134	0.0117	0.0056	0.0232	0.0151	0.0164
Ragdoll	9300	10	0.0019	0.0022	0.0059	0.003	0.002	0.0047	0.9335	0.002	0.0054	0.0035	0.0051	0.001	0.0027	0.0097	0.0014	0.0011	0.002	0.0027	0.003	0.0049	0.0023
Ragdoll	9301	2	0.0056	0.0033	0.0153	0.0024	0.0039	0.0034	0.9086	0.003	0.0059	0.0061	0.0064	0.001	0.0031	0.0034	0.0015	0.0033	0.0055	0.004	0.0073	0.0031	0.0039
Ragdoll	9302	2	0.0049	0.0027	0.0041	0.003	0.0021	0.0052	0.9162	0.0081	0.0072	0.0053	0.0083	0.0082	0.0051	0.0021	0.0034	0.0022	0.002	0.002	0.0032	0.0029	0.0018
Ragdoll	9304	10	0.0037	0.0046	0.0049	0.0078	0.003	0.0161	0.9128	0.0031	0.0011	0.0021	0.0018	0.0042	0.003	0.0019	0.0019	0.0034	0.0097	0.0051	0.002	0.0058	0.0019
Ragdoll	9305	0	0.003	0.003	0.0023	0.0065	0.001	0.001	0.9288	0.003	0.002	0.002	0.0028	0.001	0.001	0.0015	0.0056	0.0016	0.001	0.0029	0.0249	0.0025	0.0025
Maine Coon	2950	5	0.002	0.0026	0.0073	0.0039	0.002	0.0028	0.002	0.942	0.0049	0.0047	0.0045	0.003	0.005	0.0021	0.0026	0.0013	0.0013	0.001	0.0015	0.0019	0.0016
Maine Coon	2959	13	0.0039	0.0083	0.0084	0.0024	0.0019	0.0079	0.0134	0.8793	0.0085	0.0044	0.0056	0.0087	0.0075	0.0062	0.0033	0.0028	0.0059	0.0045	0.0044	0.0052	0.0075
Maine Coon	3304	18	0.0123	0.0104	0.0435	0.0023	0.0012	0.0072	0.0818	0.7136	0.002	0.003	0.0795	0.003	0.0031	0.0028	0.0028	0.003	0.0077	0.0013	0.001	0.0175	0.001
Maine Coon	3311	5	0.0016	0.002	0.0033	0.002	0.001	0.0029	0.002	0.9501	0.002	0.002	0.0055	0.0022	0.0022	0.0034	0.001	0.0014	0.001	0.0034	0.0013	0.0065	0.0032
Maine Coon	3495	13	0.0047	0.0044	0.0098	0.003	0.0113	0.0025	0.0021	0.8838	0.0011	0.0174	0.0195	0.0028	0.0133	0.0019	0.0067	0.002	0.0043	0.0027	0.001	0.0029	0.0027
Maine Coon	3925	13	0.0072	0.0089	0.0029	0.002	0.0042	0.0031	0.001	0.9303	0.0035	0.002	0.0043	0.0031	0.0026	0.0099	0.0019	0.0028	0.001	0.0017	0.0019	0.004	0.0017
Maine Coon	3941	5	0.0045	0.0025	0.0062	0.0028	0.0056	0.0081	0.0054	0.9368	0.0018	0.0039	0.0037	0.002	0.003	0.0018	0.0022	0.0029	0.0012	0.001	0.0013	0.0024	0.001
Maine Coon	9198	10	0.0043	0.0159	0.0367	0.0081	0.0045	0.01	0.0249	0.3824	0.0031	0.0077	0.0072	0.0114	0.1519	0.0039	0.0108	0.0067	0.0185	0.092	0.003	0.1198	0.0773
Maine Coon	9775	7	0.0048	0.0014	0.0023	0.002	0.002	0.0036	0.0011	0.9566	0.0015	0.002	0.0026	0.0045	0.0029	0.0014	0.0012	0.0021	0.002	0.0017	0.0014	0.0019	0.001
Maine Coon	10662	13	0.002	0.0027	0.0026	0.001	0.0019	0.0031	0.0019	0.9558	0.0031	0.002	0.0025	0.002	0.002	0.0026	0.001	0.001	0.0045	0.0022	0.0023	0.0025	0.0013
Maine Coon	11544	13	0.0058	0.0036	0.0023	0.0066	0.0053	0.0094	0.002	0.916	0.0058	0.0106	0.0081	0.0052	0.003	0.0028	0.0015	0.0021	0.003	0.0012	0.002	0.0027	0.0011
Maine Coon	217	7	0.0066	0.0018	0.0021	0.002	0.002	0.002	0.002	0.9577	0.0056	0.002	0.0023	0.001	0.0019	0.001	0.0011	0.0012	0.002	0.001	0.001	0.002	0.0017
Maine Coon	218	5	0.1421	0.0922	0.0719	0.0067	0.0047	0.0057	0.217	0.0225	0.0217	0.0049	0.098	0.0076	0.0157	0.0047	0.0046	0.0046	0.1483	0.0197	0.0119	0.0844	0.011
Maine Coon	219	7	0.006	0.001	0.0012	0.002	0.001	0.001	0.002	0.9616	0.0024	0.002	0.0021	0.002	0.002	0.0017	0.0029	0.0011	0.002	0.001	0.0013	0.0027	0.001
Maine Coon	220	7	0.0054	0.0141	0.0185	0.0091	0.5015	0.2302	0.002	0.1042	0.0058	0.0231	0.0309	0.004	0.004	0.0032	0.002	0.0036	0.0138	0.0065	0.0032	0.0089	0.0061
Maine Coon	221	5	0.0073	0.0104	0.0101	0.0065	0.002	0.0168	0.0038	0.879	0.0018	0.0092	0.012	0.0069	0.0088	0.002	0.0058	0.0033	0.0048	0.0014	0.0013	0.0058	0.001
Maine Coon	222	5	0.0057	0.3721	0.0464	0.0217	0.0032	0.0192	0.0066	0.3519	0.0043	0.0456	0.0454	0.0093	0.0131	0.0077	0.0046	0.0091	0.001	0.0043	0.002	0.0242	0.0027
Maine Coon	223	5	0.0066	0.0196	0.0285	0.0141	0.003	0.0256	0.0156	0.7372	0.0548	0.0153	0.0317	0.007	0.0055	0.005	0.0023	0.0084	0.0053	0.0011	0.0012	0.0097	0.0026
Maine Coon	224	5	0.0058	0.0033	0.0146	0.0027	0.0109	0.0052	0.146	0.6608	0.0117	0.0106	0.018	0.0119	0.0199	0.0029	0.0012	0.0043	0.0028	0.019	0.0091	0.0206	0.0188
Abyssinian	110	5	0.0022	0.0066	0.0073	0.0065	0.0053	0.0065	0.0021	0.0057	0.7717	0.0041	0.0038	0.002	0.0031	0.0022	0.0021	0.0848	0.0683	0.0017	0.0011	0.0027	0.0102
Abyssinian	111	7	0.0035	0.0067	0.0073	0.0099	0.007	0.0362	0.002	0.0115	0.749	0.008	0.0267	0.0108	0.0087	0.0037	0.0012	0.0881	0.001	0.0052	0.0034	0.0059	0.0041
Abyssinian	112	7	0.0015	0.0011	0.0015	0.0011	0.0011	0.0015	0.0011	0.0013	0.8729	0.0021	0.0046	0.002	0.0011	0.0015	0.0011	0.0952	0.004	0.0012	0.0011	0.0015	0.0014
Abyssinian	113	7	0.003	0.0095	0.0062	0.007	0.002	0.0034	0.0014	0.0037	0.7841	0.0086	0.0208	0.0026	0.0655	0.0037	0.0015	0.0681	0.001	0.0014	0.0011	0.0042	0.0012
Abyssinian	114	5	0.0015	0.0021	0.0015	0.0024	0.001	0.0023	0.0021	0.0017	0.8763	0.002	0.0019	0.0011	0.0011	0.002	0.0015	0.092	0.0011	0.0014	0.0011	0.0026	0.0013
Abyssinian	115	5	0.0018	0.0018	0.0039	0.001	0.0018	0.0041	0.0013	0.0023	0.8641	0.0021	0.0021	0.001	0.0034	0.0016	0.0023	0.0957	0.0013	0.001	0.001	0.0025	0.0039
Abyssinian	116	5	0.0011	0.0011	0.0012	0.0012	0.001	0.001	0.0036	0.001	0.8786	0.001	0.0013	0.0011	0.0018	0.0014	0.001	0.0953	0.001	0.0011	0.0014	0.001	0.0028
Abyssinian	117	5	0.001	0.001	0.0013	0.0154	0.001	0.0011	0.0019	0.0011	0.8719	0.001	0.0019	0.0032	0.001	0.001	0.001	0.0878	0.0011	0.0018	0.0017	0.0013	0.0015
Abyssinian	118	7	0.0011	0.0011	0.0011	0.0022	0.0011	0.001	0.0021	0.0016	0.8817	0.0014	0.0013	0.001	0.0012	0.0014	0.001	0.0893	0.001	0.0025	0.0023	0.0018	0.0028
Abyssinian	119	7	0.0021	0.0051	0.0017	0.0069	0.0016	0.0019	0.013	0.0033	0.8471	0.0021	0.0033	0.0011	0.0053	0.0018	0.001	0.0912	0.001	0.0047	0.0016	0.0024	0.0018
Abyssinian	120	5	0.0017	0.0025	0.0024	0.001	0.0013	0.002	0.0017	0.0011	0.8723	0.001	0.0012	0.002	0.002	0.002	0.001	0.0978	0.0011	0.0011	0.0015	0.0015	0.0018
Abyssinian	121	5	0.002	0.0022	0.0032	0.0022	0.0021	0.0011	0.0011	0.0022	0.8466	0.002	0.004	0.0021	0.0031	0.0021	0.0032	0.0961	0.0022	0.0021	0.0066	0.0033	0.0105

Table 18 - Population clustering of each pedigreed individual in the database by STRs at K = 21

Feline	ID	Missing	Groups																				
Population	No.	Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Abyssinian	122	7	0.0021	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.8636	0.001	0.002	0.0027	0.001	0.001	0.0014	0.0944	0.0017	0.0039	0.001	0.0014	0.0148
Abyssinian	123	5	0.0011	0.001	0.0013	0.0013	0.0016	0.001	0.0024	0.0022	0.8692	0.0032	0.0017	0.0021	0.003	0.0013	0.0067	0.0929	0.0012	0.0023	0.0017	0.0016	0.0012
Abyssinian	6934	28	0.0051	0.0051	0.0039	0.0011	0.0013	0.0024	0.0048	0.0019	0.749	0.0023	0.002	0.003	0.0021	0.0023	0.0034	0.0831	0.0949	0.0046	0.0011	0.0033	0.0233
Siberian	3273	21	0.0042	0.0092	0.012	0.0037	0.0059	0.002	0.002	0.0059	0.0094	0.8101	0.0113	0.0041	0.0246	0.0635	0.0044	0.0047	0.002	0.002	0.0045	0.0132	0.0014
Siberian	4593	21	0.003	0.0049	0.0049	0.0028	0.0062	0.0025	0.0022	0.004	0.0026	0.9239	0.0109	0.0025	0.002	0.002	0.0109	0.0025	0.004	0.002	0.0025	0.002	0.0017
Siberian	4829	7	0.002	0.003	0.0037	0.0053	0.003	0.002	0.003	0.0154	0.0033	0.9021	0.0146	0.002	0.0049	0.0023	0.0055	0.0047	0.0111	0.0025	0.0028	0.0044	0.0025
Siberian	4928	5	0.3394	0.007	0.0064	0.0022	0.001	0.001	0.0018	0.0062	0.001	0.5831	0.0044	0.0016	0.0032	0.0015	0.0019	0.0018	0.0022	0.0022	0.002	0.028	0.0021
Siberian	4930	7	0.0032	0.0153	0.0025	0.0018	0.0017	0.001	0.0031	0.002	0.0011	0.8832	0.0028	0.0029	0.0022	0.0145	0.0107	0.002	0.0414	0.002	0.0022	0.0034	0.001
Siberian	5101	13	0.0051	0.0033	0.0024	0.0011	0.001	0.001	0.0029	0.0034	0.002	0.9575	0.0021	0.0018	0.0019	0.0019	0.0018	0.0025	0.0026	0.001	0.001	0.0027	0.001
Siberian	5105	15	0.0036	0.0023	0.0054	0.002	0.0055	0.0065	0.0133	0.0023	0.0024	0.8245	0.003	0.0289	0.0061	0.0679	0.0054	0.0029	0.0015	0.0017	0.0022	0.011	0.0015
Siberian	5107	5	0.0091	0.0067	0.0403	0.0062	0.0122	0.0739	0.003	0.0039	0.0037	0.7549	0.0113	0.0081	0.0072	0.0144	0.0019	0.0028	0.002	0.003	0.0176	0.0102	0.0076
Siberian	5110	10	0.0022	0.0027	0.0054	0.0117	0.0359	0.002	0.002	0.3551	0.002	0.5514	0.0041	0.002	0.0064	0.0021	0.002	0.0029	0.0012	0.003	0.0017	0.0027	0.0016
Siberian	5118	7	0.0025	0.003	0.0082	0.0064	0.002	0.002	0.0073	0.0021	0.0051	0.8052	0.0533	0.0069	0.0053	0.0108	0.0089	0.0018	0.0283	0.0289	0.001	0.0061	0.0047
Siberian	5120	5	0.002	0.0029	0.0047	0.003	0.0039	0.0098	0.0037	0.0054	0.0021	0.8584	0.0526	0.0091	0.0038	0.0031	0.0034	0.0046	0.0093	0.0086	0.002	0.0038	0.0038
Siberian	5632	5	0.0368	0.0162	0.0087	0.004	0.0059	0.0046	0.0058	0.0779	0.0063	0.6382	0.0097	0.0329	0.0047	0.0024	0.002	0.0014	0.0044	0.013	0.0262	0.0077	0.0911
Siberian	6474	5	0.0032	0.0037	0.0026	0.0028	0.0894	0.0059	0.0162	0.0028	0.002	0.8405	0.0036	0.001	0.0049	0.0036	0.0052	0.0014	0.0018	0.0013	0.0026	0.0032	0.0023
Siberian	11562	15	0.0049	0.0091	0.0381	0.0061	0.002	0.0022	0.0133	0.0083	0.0175	0.7766	0.0398	0.003	0.0139	0.0059	0.0045	0.0045	0.0042	0.0053	0.0241	0.0111	0.0055
Siberian	11582	10	0.046	0.0051	0.0074	0.0069	0.0093	0.0043	0.0118	0.0204	0.0271	0.6859	0.0968	0.0251	0.0024	0.007	0.0081	0.0135	0.002	0.0037	0.001	0.0143	0.002
Siberian	11559	13	0.0042	0.0046	0.0048	0.002	0.0037	0.0099	0.0052	0.004	0.0103	0.9102	0.0105	0.002	0.003	0.0024	0.0011	0.0022	0.0072	0.0053	0.0017	0.0034	0.0023
Siberian	11560	13	0.0116	0.0096	0.0087	0.0067	0.0032	0.0029	0.0214	0.02	0.0017	0.7299	0.0303	0.0089	0.0802	0.0048	0.0318	0.0051	0.002	0.0012	0.0044	0.0119	0.0036
Norwegian FC	2942	15	0.0076	0.0048	0.0046	0.0052	0.0067	0.002	0.002	0.0062	0.0018	0.0224	0.8878	0.0251	0.0036	0.0019	0.0011	0.0029	0.002	0.0044	0.0027	0.003	0.0022
Norwegian FC	3610	47	0.0083	0.1843	0.0307	0.0031	0.0046	0.0042	0.0038	0.0375	0.0041	0.0255	0.4997	0.0725	0.039	0.0189	0.0113	0.0038	0.0215	0.002	0.0047	0.0153	0.005
Norwegian FC	3611	13	0.2644	0.01	0.0142	0.0029	0.0031	0.0204	0.0076	0.3742	0.0146	0.0658	0.1256	0.0018	0.0073	0.0107	0.002	0.0014	0.0062	0.0022	0.002	0.0615	0.002
Norwegian FC	3612	7	0.003	0.004	0.0019	0.0025	0.0033	0.0052	0.0025	0.004	0.0019	0.021	0.9191	0.0078	0.0027	0.0029	0.0032	0.0025	0.0032	0.002	0.0017	0.0027	0.003
Norwegian FC	3617	26	0.0042	0.0107	0.0124	0.0084	0.0027	0.003	0.0032	0.019	0.0021	0.8151	0.0663	0.0106	0.009	0.0035	0.006	0.0063	0.0031	0.004	0.002	0.0059	0.0024
Norwegian FC	3661	31	0.0053	0.0473	0.015	0.002	0.0033	0.0035	0.0052	0.0054	0.0132	0.0095	0.8189	0.0045	0.0037	0.0078	0.0095	0.0036	0.0061	0.0157	0.002	0.0146	0.004
Norwegian FC	4815	7	0.0033	0.013	0.0766	0.0174	0.0043	0.0119	0.0151	0.026	0.0092	0.027	0.6794	0.0062	0.007	0.0066	0.0021	0.004	0.004	0.0047	0.0034	0.0552	0.0236
Norwegian FC	4816	2	0.0021	0.0027	0.0257	0.0011	0.002	0.0021	0.0059	0.0182	0.0083	0.0068	0.8951	0.0039	0.0023	0.0016	0.0031	0.0023	0.001	0.0016	0.001	0.0119	0.0012
Norwegian FC	6004	18	0.0049	0.0053	0.0183	0.0089	0.0046	0.0152	0.0065	0.0154	0.0021	0.0161	0.7258	0.0282	0.0522	0.0683	0.0038	0.0023	0.001	0.0027	0.0017	0.0148	0.002
Norwegian FC	6932	44	0.007	0.0029	0.0041	0.0092	0.0036	0.0061	0.0079	0.0048	0.0027	0.0141	0.6163	0.0163	0.0076	0.0032	0.0154	0.0039	0.2592	0.0062	0.003	0.0039	0.0027
Norwegian FC	9321	2	0.0029	0.0426	0.0147	0.0145	0.0087	0.0042	0.0191	0.622	0.0033	0.0099	0.1254	0.0072	0.0961	0.0046	0.0021	0.0033	0.0105	0.0013	0.001	0.0052	0.0013
Norwegian FC	10367	34	0.0079	0.0132	0.0173	0.0076	0.0031	0.0138	0.0068	0.0053	0.0111	0.1797	0.6539	0.0315	0.0076	0.0032	0.0026	0.0047	0.0128	0.006	0.0022	0.0073	0.0024
Norwegian FC	10682	13	0.0094	0.0036	0.0049	0.005	0.0609	0.0034	0.0029	0.0096	0.0035	0.0196	0.8214	0.0143	0.0082	0.0058	0.0051	0.0049	0.0069	0.0024	0.0023	0.0048	0.0012
Norwegian FC	11548	18	0.0086	0.0763	0.1058	0.0041	0.002	0.0076	0.0044	0.0129	0.0039	0.0455	0.5909	0.0508	0.0351	0.002	0.0139	0.0136	0.0038	0.0051	0.0057	0.0053	0.0025
Norwegian FC	242	7	0.0031	0.2604	0.0126	0.0044	0.001	0.0032	0.0084	0.0433	0.0505	0.0706	0.476	0.0048	0.0065	0.0211	0.0038	0.0046	0.002	0.0064	0.0022	0.0095	0.0057
Manx	2928	15	0.0049	0.0053	0.1084	0.0037	0.002	0.0123	0.002	0.1142	0.0065	0.0166	0.6578	0.0049	0.0038	0.0021	0.0019	0.0021	0.0034	0.0017	0.001	0.0436	0.0017
Manx	2980	31	0.0048	0.0083	0.2651	0.0023	0.0078	0.002	0.0176	0.0103	0.0189	0.0232	0.5133	0.0093	0.0045	0.0063	0.0033	0.003	0.002	0.0013	0.0015	0.0934	0.0017
Manx	3926	10	0.0027	0.0036	0.2563	0.0021	0.003	0.0061	0.0035	0.0053	0.0058	0.0035	0.56	0.0398	0.005	0.0036	0.0022	0.0019	0.001	0.002	0.0023	0.089	0.0012
Manx	4378	0	0.0121	0.1224	0.1639	0.0065	0.0039	0.0208	0.0076	0.0326	0.0059	0.004	0.5237	0.0074	0.0033	0.0033	0.0021	0.0032	0.0037	0.0013	0.0013	0.0694	0.0017

Table 18 - Population clustering of each pedigreed individual in the database by STRs at K = 21

Feline	ID	Missing	Groups																				
Population	No.	Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Manx	5757	2	0.0059	0.005	0.1857	0.0032	0.0043	0.0118	0.002	0.2705	0.0023	0.0032	0.4171	0.0031	0.0031	0.0026	0.0031	0.0029	0.002	0.001	0.0045	0.0657	0.001
Manx	6294	5	0.3341	0.0022	0.167	0.0036	0.002	0.0015	0.0122	0.0063	0.0035	0.008	0.326	0.0024	0.0111	0.0166	0.0022	0.0013	0.0014	0.0037	0.0013	0.0915	0.0021
Manx	6296	10	0.0018	0.0074	0.3603	0.0042	0.001	0.0205	0.0024	0.0061	0.0013	0.0101	0.4823	0.0022	0.0048	0.0033	0.001	0.0019	0.0035	0.0014	0.0017	0.0805	0.0023
Manx	6299	5	0.0035	0.0163	0.2518	0.0025	0.0054	0.022	0.003	0.0221	0.0287	0.0155	0.4937	0.0022	0.0133	0.0119	0.002	0.0021	0.001	0.002	0.001	0.0976	0.0025
Manx	7079	5	0.0189	0.024	0.2636	0.012	0.0049	0.0045	0.0104	0.0067	0.0044	0.0152	0.4918	0.0046	0.016	0.0023	0.0121	0.0055	0.0138	0.0019	0.0021	0.083	0.0023
Manx	7082	5	0.0314	0.0239	0.0066	0.0078	0.0035	0.0129	0.0131	0.0171	0.0063	0.0412	0.7496	0.0087	0.0085	0.0127	0.0099	0.0044	0.002	0.0041	0.0167	0.0117	0.0078
Manx	7083	0	0.0021	0.017	0.0032	0.0023	0.0163	0.003	0.009	0.0033	0.0055	0.0042	0.8929	0.0069	0.0026	0.0033	0.0026	0.0019	0.001	0.0021	0.0141	0.0032	0.0034
Manx	7105	2	0.0048	0.0022	0.2381	0.0086	0.0058	0.0161	0.0789	0.0026	0.0046	0.005	0.4752	0.0509	0.0089	0.0057	0.0019	0.0036	0.0019	0.0023	0.002	0.0786	0.0023
Manx	7108	0	0.0227	0.0037	0.2805	0.0108	0.002	0.0059	0.0071	0.0028	0.0019	0.0046	0.5445	0.0014	0.003	0.0011	0.0017	0.001	0.002	0.002	0.0031	0.0959	0.0023
Manx	7112	2	0.0288	0.0056	0.2782	0.0175	0.003	0.0084	0.0095	0.0027	0.0017	0.0041	0.5021	0.005	0.0176	0.0045	0.0045	0.0021	0.0019	0.0029	0.0034	0.0944	0.0022
Manx	7708	5	0.2924	0.0192	0.0126	0.0042	0.004	0.0047	0.0132	0.0132	0.0019	0.3028	0.0799	0.1553	0.0212	0.0114	0.0012	0.0095	0.0047	0.0013	0.002	0.044	0.0013
Manx	9084	18	0.0062	0.0058	0.281	0.0054	0.0037	0.0036	0.0042	0.0047	0.003	0.0035	0.5503	0.006	0.0057	0.0047	0.0031	0.0058	0.003	0.0023	0.002	0.0948	0.0012
Manx	9091	7	0.0329	0.0101	0.1494	0.005	0.008	0.0087	0.0031	0.0236	0.0235	0.0579	0.4568	0.0469	0.0832	0.0035	0.0028	0.0074	0.0112	0.0075	0.002	0.054	0.0026
Egyptian Mau	1812	5	0.0044	0.0029	0.0036	0.0046	0.001	0.001	0.0033	0.0051	0.0052	0.002	0.0061	0.9301	0.0101	0.0034	0.0019	0.0029	0.001	0.0036	0.001	0.0051	0.0016
Egyptian Mau	2431	18	0.0021	0.0029	0.0025	0.0029	0.0062	0.0099	0.0016	0.0126	0.001	0.002	0.002	0.9326	0.003	0.002	0.0042	0.0034	0.001	0.0025	0.0017	0.0019	0.002
Egyptian Mau	2433	7	0.0011	0.0036	0.0019	0.002	0.001	0.001	0.0073	0.001	0.001	0.0042	0.0024	0.8827	0.0033	0.003	0.0059	0.0628	0.0034	0.0035	0.002	0.0053	0.0016
Egyptian Mau	3331	26	0.0029	0.0027	0.0023	0.0067	0.0019	0.0162	0.012	0.0079	0.0114	0.003	0.003	0.8547	0.0038	0.0028	0.0026	0.0108	0.002	0.0347	0.0094	0.0044	0.0048
Egyptian Mau	3332	15	0.001	0.0012	0.0023	0.0016	0.002	0.002	0.0043	0.0041	0.001	0.0018	0.002	0.9613	0.0027	0.0024	0.002	0.0019	0.001	0.001	0.0015	0.0016	0.0013
Egyptian Mau	5545	15	0.0049	0.0032	0.0098	0.0026	0.0062	0.003	0.0011	0.004	0.002	0.0075	0.0047	0.9225	0.0034	0.0029	0.002	0.0055	0.004	0.003	0.0018	0.0033	0.0027
Egyptian Mau	5553	15	0.0035	0.0052	0.0065	0.0041	0.0244	0.0154	0.0023	0.0047	0.0029	0.002	0.0102	0.7988	0.011	0.0078	0.006	0.0782	0.001	0.0017	0.0104	0.0026	0.0013
Egyptian Mau	5567	28	0.0077	0.0254	0.0033	0.0044	0.0075	0.0033	0.0051	0.004	0.0033	0.005	0.0158	0.8821	0.0031	0.0032	0.0011	0.0052	0.0094	0.0027	0.0024	0.0043	0.0016
Egyptian Mau	5568	28	0.002	0.0015	0.0032	0.0041	0.0013	0.001	0.001	0.0019	0.0022	0.0019	0.0027	0.9561	0.0021	0.0032	0.0017	0.0023	0.003	0.0023	0.0019	0.003	0.0016
Egyptian Mau	7475	13	0.0068	0.0013	0.002	0.0021	0.001	0.002	0.001	0.0038	0.001	0.0011	0.002	0.9649	0.001	0.0011	0.0015	0.001	0.0012	0.001	0.001	0.0021	0.001
Egyptian Mau	7476	28	0.0094	0.0157	0.0774	0.002	0.0636	0.002	0.002	0.0042	0.0035	0.0061	0.0122	0.6551	0.0265	0.0139	0.0072	0.0038	0.0019	0.0084	0.0683	0.0038	0.013
Egyptian Mau	7479	34	0.002	0.0011	0.0013	0.0023	0.0034	0.0023	0.0056	0.0021	0.0017	0.002	0.002	0.7461	0.0014	0.0069	0.0015	0.0038	0.0114	0.0336	0.0062	0.0791	0.0842
Egyptian Mau	7480	28	0.001	0.001	0.0013	0.001	0.0025	0.002	0.001	0.001	0.001	0.001	0.0024	0.9743	0.002	0.0011	0.0011	0.001	0.001	0.001	0.001	0.0012	0.001
Egyptian Mau	11410	13	0.017	0.0195	0.0022	0.0197	0.0017	0.0352	0.0019	0.0184	0.0022	0.002	0.012	0.6149	0.0165	0.0033	0.0074	0.2079	0.0035	0.0033	0.0016	0.0088	0.001
Turk. Angora	607	15	0.0696	0.0333	0.0401	0.0083	0.0253	0.0088	0.002	0.0285	0.0306	0.0681	0.0823	0.0252	0.4761	0.0349	0.0358	0.0037	0.0066	0.0036	0.0012	0.014	0.002
Turk. Angora	1832	13	0.0028	0.0025	0.0024	0.0042	0.002	0.002	0.0026	0.0084	0.0042	0.0038	0.0072	0.0031	0.9312	0.003	0.0017	0.0059	0.002	0.0034	0.001	0.0036	0.003
Turk. Angora	1845	13	0.001	0.0013	0.0017	0.001	0.0021	0.001	0.0021	0.0011	0.0019	0.0017	0.0024	0.0022	0.9687	0.0018	0.0011	0.0012	0.001	0.0018	0.002	0.0012	0.0017
Turk. Angora	2848	18	0.0114	0.0719	0.079	0.0184	0.0083	0.0574	0.0086	0.0169	0.0051	0.0042	0.0893	0.0319	0.497	0.0227	0.0027	0.0081	0.0031	0.0042	0.0055	0.0316	0.0226
Turk. Angora	2862	21	0.0043	0.0023	0.0039	0.002	0.0047	0.0023	0.0125	0.004	0.003	0.002	0.0026	0.0021	0.9333	0.0041	0.0035	0.0034	0.002	0.0017	0.0011	0.0024	0.0027
Turk. Angora	5552	7	0.0031	0.003	0.0073	0.0058	0.0059	0.0038	0.0057	0.0037	0.0047	0.0043	0.0025	0.0021	0.9191	0.0016	0.0033	0.0021	0.001	0.0064	0.0062	0.005	0.0034
Turk. Angora	5563	5	0.0093	0.0014	0.0046	0.005	0.0032	0.0073	0.0021	0.0071	0.0014	0.0021	0.0078	0.0054	0.9209	0.002	0.0048	0.005	0.0019	0.0013	0.0021	0.004	0.0013
Turk. Angora	5564	5	0.0017	0.0089	0.0119	0.0021	0.002	0.0271	0.0037	0.0037	0.0268	0.0534	0.0636	0.0066	0.7368	0.0048	0.0312	0.0047	0.001	0.001	0.001	0.0062	0.0017
Turk. Angora	6350	10	0.0024	0.0046	0.0036	0.0021	0.0121	0.0057	0.0022	0.0027	0.0027	0.0081	0.0045	0.0065	0.9169	0.0044	0.0059	0.0031	0.0015	0.0026	0.0033	0.003	0.0021
Turk. Angora	9541	0	0.002	0.0055	0.0082	0.0072	0.0041	0.0047	0.002	0.002	0.0021	0.421	0.0049	0.0106	0.3367	0.0118	0.1236	0.0329	0.0026	0.0049	0.0054	0.0048	0.003
Turk. Angora	9542	23	0.0017	0.0013	0.0013	0.001	0.001	0.0017	0.0011	0.001	0.001	0.0011	0.0011	0.0016	0.0012	0.0023	0.879	0.0963	0.0011	0.0014	0.0012	0.0015	0.0011
Turk. Angora	9584	10	0.0028	0.0478	0.0107	0.0092	0.0732	0.002	0.0044	0.0064	0.0287	0.3881	0.0246	0.0044	0.2958	0.0504	0.0187	0.0063	0.0037	0.0028	0.0037	0.0135	0.0027

Table 18 - Population clustering of each pedigreed individual in the database by STRs at K = 21

Feline	ID	Missing	Groups																				
Population	No.	Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Turk. Angora	9586	2	0.0455	0.0084	0.0233	0.0068	0.0122	0.014	0.051	0.0122	0.0054	0.0351	0.3795	0.0211	0.3065	0.0257	0.0029	0.0021	0.002	0.0027	0.0013	0.0336	0.0087
Turk. Angora	9608	10	0.0033	0.005	0.0146	0.003	0.0031	0.0021	0.0053	0.046	0.0101	0.0193	0.1131	0.003	0.1273	0.538	0.0019	0.0025	0.002	0.0068	0.0022	0.0839	0.0073
Turk. Angora	9609	7	0.0045	0.0029	0.0043	0.006	0.0045	0.0029	0.0091	0.0021	0.0029	0.0107	0.0044	0.0044	0.1047	0.6694	0.0581	0.0145	0.0011	0.0017	0.0028	0.0865	0.0025
Turk. Angora	9610	13	0.0076	0.0104	0.0027	0.0025	0.0057	0.004	0.0125	0.0035	0.0134	0.003	0.0037	0.0033	0.0947	0.7216	0.0017	0.0013	0.0046	0.003	0.0038	0.094	0.003
Turk. Angora	9611	5	0.0011	0.001	0.0011	0.001	0.001	0.0011	0.0011	0.0011	0.0011	0.0011	0.001	0.0011	0.0964	0.7792	0.0073	0.0012	0.0011	0.0011	0.0011	0.0986	0.0012
Turk. Angora	9612	5	0.002	0.0027	0.0124	0.004	0.0035	0.003	0.002	0.2123	0.0041	0.0187	0.0084	0.0215	0.0823	0.5342	0.0026	0.0013	0.0049	0.0022	0.0019	0.0719	0.0042
Turk. Angora	9613	2	0.005	0.0032	0.0057	0.0076	0.0136	0.0065	0.0033	0.0332	0.0198	0.0056	0.0069	0.0551	0.7127	0.0029	0.006	0.0899	0.0015	0.0141	0.0017	0.0034	0.0023
Turk. Angora	9614	2	0.0011	0.0011	0.0011	0.001	0.0021	0.0032	0.0013	0.0017	0.001	0.0032	0.0023	0.0021	0.0961	0.7776	0.0017	0.0011	0.001	0.001	0.001	0.0983	0.001
Turk. Angora	9615	7	0.0021	0.0019	0.0014	0.001	0.001	0.002	0.0023	0.0017	0.0019	0.0023	0.0022	0.0011	0.0948	0.7738	0.0027	0.0018	0.0019	0.0022	0.0014	0.0986	0.0019
Turkish Van	1789	13	0.001	0.0012	0.0015	0.001	0.0014	0.001	0.001	0.001	0.001	0.0011	0.0011	0.0015	0.0011	0.001	0.8809	0.0981	0.0011	0.001	0.001	0.001	0.001
Turkish Van	3013	18	0.0016	0.0045	0.0087	0.0016	0.0024	0.0015	0.0014	0.0015	0.0013	0.0018	0.0052	0.0055	0.0045	0.004	0.8524	0.0948	0.0011	0.001	0.0011	0.0018	0.0023
Turkish Van	3056	5	0.0025	0.0372	0.0025	0.0105	0.0025	0.0042	0.001	0.0087	0.0063	0.0111	0.0133	0.002	0.0069	0.0031	0.771	0.0915	0.0038	0.0023	0.0135	0.0039	0.0021
Turkish Van	4090	15	0.0022	0.0026	0.003	0.0015	0.0023	0.0014	0.0024	0.0015	0.0026	0.0025	0.0025	0.0023	0.0016	0.0016	0.8667	0.0966	0.0015	0.0012	0.001	0.0014	0.0016
Turkish Van	7662	21	0.0022	0.0035	0.0033	0.0037	0.0021	0.0048	0.0029	0.002	0.0019	0.0045	0.0047	0.0036	0.0168	0.0301	0.8133	0.0742	0.0024	0.0129	0.0042	0.0049	0.002
Turkish Van	7663	34	0.0092	0.0231	0.0065	0.0049	0.0072	0.0041	0.0054	0.0055	0.002	0.0076	0.0059	0.0047	0.0057	0.0249	0.6873	0.1447	0.0048	0.014	0.0094	0.0181	0.005
Turkish Van	7666	39	0.0076	0.0032	0.0051	0.0033	0.0223	0.0011	0.0125	0.0028	0.0044	0.0045	0.0056	0.006	0.0047	0.003	0.7513	0.1171	0.002	0.0046	0.0287	0.0029	0.0073
Turkish Van	7667	36	0.0034	0.0043	0.0041	0.002	0.042	0.0078	0.0024	0.0091	0.0097	0.0734	0.006	0.0033	0.0059	0.0093	0.711	0.0879	0.0024	0.0052	0.0019	0.0065	0.0025
Turkish Van	9322	5	0.0109	0.1919	0.0066	0.0023	0.0019	0.0063	0.0054	0.0033	0.0017	0.0302	0.0053	0.0026	0.0106	0.0023	0.637	0.0605	0.0018	0.002	0.0112	0.0034	0.0027
Turkish Van	9535	2	0.0042	0.0034	0.0045	0.002	0.002	0.0015	0.001	0.0027	0.0018	0.0184	0.009	0.001	0.0036	0.0353	0.82	0.0761	0.0043	0.001	0.0013	0.0055	0.0013
Turkish Van	9538	0	0.0036	0.0031	0.0044	0.0038	0.0019	0.0025	0.0023	0.0024	0.0024	0.0034	0.0028	0.0072	0.0053	0.0039	0.8435	0.0946	0.0015	0.0036	0.0016	0.0023	0.0039
Turkish Van	9539	0	0.0104	0.1031	0.0312	0.0032	0.0022	0.0021	0.0024	0.0041	0.084	0.048	0.0133	0.0117	0.0116	0.0107	0.5446	0.0595	0.001	0.0027	0.0386	0.0129	0.0025
Turkish Van	9543	0	0.0022	0.0077	0.0183	0.0033	0.0059	0.0049	0.0387	0.0042	0.01	0.0855	0.0432	0.0042	0.6395	0.0083	0.0156	0.0709	0.0026	0.003	0.0132	0.0124	0.0062
Turkish Van	9563	2	0.0225	0.0161	0.0443	0.0118	0.0041	0.0062	0.0038	0.0162	0.0069	0.0116	0.0293	0.0145	0.0123	0.0084	0.5507	0.2153	0.0086	0.0033	0.0029	0.0096	0.0014
Turkish Van	9564	2	0.0014	0.0052	0.0095	0.0019	0.0042	0.0039	0.0068	0.0016	0.0017	0.0071	0.0026	0.0019	0.0057	0.0077	0.8296	0.1002	0.0017	0.001	0.001	0.003	0.0022
Turkish Van	9573	0	0.002	0.0013	0.0021	0.0014	0.0024	0.001	0.0017	0.0031	0.0034	0.0023	0.002	0.0024	0.0063	0.0022	0.8454	0.1118	0.001	0.0019	0.0028	0.0022	0.0013
Turkish Van	9574	0	0.0021	0.003	0.0047	0.009	0.002	0.0014	0.0039	0.002	0.0033	0.015	0.0052	0.0096	0.0072	0.1311	0.6738	0.0764	0.016	0.0076	0.003	0.0215	0.0023
Turkish Van	9575	0	0.003	0.0013	0.0211	0.005	0.0038	0.0081	0.0072	0.003	0.031	0.6143	0.0709	0.0073	0.0119	0.0115	0.1241	0.0357	0.0029	0.0085	0.0031	0.0143	0.0121
Turkish Van	9576	2	0.002	0.0042	0.0059	0.0148	0.1006	0.003	0.0149	0.002	0.0502	0.4899	0.0374	0.002	0.0777	0.0106	0.0205	0.0064	0.003	0.0757	0.0331	0.0073	0.0388
Turkish Van	9581	5	0.0039	0.0038	0.0051	0.0053	0.0049	0.0039	0.0112	0.0039	0.0064	0.691	0.0077	0.0048	0.0368	0.1393	0.0099	0.0068	0.0022	0.0165	0.0098	0.0252	0.0016
Bengal	2518	52	0.0177	0.0044	0.0067	0.004	0.0024	0.0037	0.012	0.0031	0.0825	0.0075	0.0068	0.0123	0.0438	0.0073	0.0124	0.7459	0.0019	0.0051	0.0044	0.008	0.0082
Bengal	3455	44	0.002	0.0022	0.0028	0.0023	0.0015	0.002	0.002	0.0021	0.0017	0.0026	0.002	0.002	0.0021	0.002	0.0288	0.9157	0.0049	0.0057	0.0086	0.0026	0.0045
Bengal	3478	39	0.0017	0.0023	0.0065	0.0046	0.001	0.0025	0.0023	0.0044	0.0035	0.003	0.0145	0.0785	0.011	0.0033	0.0126	0.8365	0.001	0.0027	0.0019	0.0042	0.002
Bengal	3522	18	0.0039	0.0072	0.0059	0.0032	0.0034	0.0065	0.0112	0.006	0.033	0.0044	0.0201	0.0022	0.0069	0.0568	0.0019	0.8101	0.002	0.0016	0.0022	0.0078	0.0037
Bengal	3541	18	0.0084	0.0028	0.0054	0.0025	0.0038	0.0018	0.0171	0.0044	0.0019	0.0202	0.0034	0.0085	0.0025	0.0025	0.0015	0.9003	0.0048	0.0012	0.0011	0.0043	0.0016
Bengal	3550	31	0.0011	0.0021	0.003	0.0029	0.0022	0.0059	0.0048	0.0019	0.0051	0.0028	0.0029	0.0031	0.0102	0.0036	0.0023	0.9346	0.0011	0.0023	0.0025	0.0022	0.0034
Bengal	6678	0	0.0011	0.0025	0.0031	0.0042	0.0025	0.0019	0.0025	0.001	0.0069	0.0021	0.002	0.0069	0.0035	0.0033	0.0028	0.9321	0.0011	0.0099	0.0032	0.0057	0.0017
Bengal	6899	0	0.0148	0.0024	0.008	0.0091	0.0229	0.0988	0.009	0.012	0.01	0.004	0.0236	0.0024	0.0061	0.0049	0.0047	0.7319	0.0028	0.0046	0.0125	0.0062	0.0094
Bengal	6902	0	0.0015	0.0018	0.0023	0.0013	0.0017	0.0021	0.001	0.0016	0.0014	0.0011	0.0015	0.006	0.0022	0.0017	0.0013	0.9347	0.0305	0.001	0.0015	0.0016	0.0022
Bengal	6907	2	0.0024	0.0012	0.0049	0.0052	0.0053	0.0022	0.0042	0.0049	0.0594	0.0151	0.0043	0.0025	0.007	0.0138	0.0017	0.8549	0.0029	0.001	0.0017	0.0037	0.0016

Table 18 - Population clustering of each pedigreed individual in the database by STRs at K = 21

Feline	ID	Missing	Groups																				
Population	No.	Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Bengal	8399	2	0.0059	0.0156	0.0011	0.0052	0.0144	0.0093	0.0025	0.0027	0.0078	0.0021	0.0023	0.1794	0.0029	0.0057	0.0018	0.6801	0.0023	0.0115	0.0093	0.007	0.0311
Bengal	8400	13	0.0015	0.002	0.0024	0.0025	0.0028	0.0085	0.0043	0.0041	0.003	0.0023	0.0034	0.0035	0.0028	0.0012	0.0022	0.9358	0.0016	0.0049	0.0022	0.002	0.007
Bengal	8766	13	0.001	0.002	0.0023	0.0016	0.0011	0.0026	0.0015	0.0015	0.0029	0.0023	0.0022	0.0101	0.0112	0.0118	0.0113	0.9187	0.0011	0.0041	0.0012	0.0056	0.0039
Bengal	9053	10	0.0071	0.0029	0.0037	0.0022	0.009	0.015	0.0244	0.0036	0.0025	0.005	0.009	0.0225	0.0132	0.0024	0.0028	0.8564	0.0042	0.0053	0.0021	0.0039	0.0027
Bengal	9800	2	0.0015	0.0021	0.0022	0.0023	0.0019	0.0023	0.0027	0.0011	0.003	0.0013	0.0022	0.0012	0.0012	0.0016	0.0014	0.9639	0.0019	0.0021	0.0012	0.0018	0.0011
Bengal	10344	23	0.0013	0.0013	0.0027	0.0025	0.0022	0.0023	0.0034	0.0015	0.0021	0.0022	0.0011	0.0032	0.0027	0.006	0.0016	0.9561	0.0021	0.001	0.0015	0.0021	0.001
Bengal	10946	0	0.004	0.0092	0.0351	0.005	0.0045	0.002	0.002	0.0053	0.054	0.0041	0.0056	0.0163	0.0019	0.0054	0.0039	0.7789	0.0073	0.0027	0.003	0.0087	0.0411
Bengal	11194	18	0.003	0.007	0.1181	0.0076	0.0136	0.0113	0.0063	0.0023	0.015	0.003	0.0062	0.0025	0.0051	0.0044	0.0078	0.7445	0.0128	0.0022	0.021	0.0047	0.0017
Sokoke	1890	7	0.001	0.001	0.001	0.0012	0.001	0.0014	0.001	0.001	0.0012	0.001	0.0013	0.001	0.001	0.099	0.4893	0.2931	0.001	0.0019	0.0018	0.0988	0.001
Sokoke	1898	31	0.001	0.001	0.001	0.0013	0.0033	0.001	0.0027	0.001	0.0017	0.0017	0.001	0.001	0.0012	0.0985	0.4716	0.2823	0.001	0.0086	0.0062	0.1059	0.007
Sokoke	2054	7	0.001	0.001	0.001	0.0012	0.0013	0.001	0.0013	0.001	0.001	0.0013	0.0013	0.0013	0.001	0.0992	0.4901	0.2909	0.001	0.0013	0.0027	0.0989	0.0012
Sokoke	2061	34	0.0031	0.0044	0.0046	0.0023	0.0017	0.0018	0.0023	0.003	0.0016	0.0026	0.0026	0.0016	0.0017	0.0974	0.4793	0.2818	0.0012	0.003	0.0024	0.0979	0.0037
Sokoke	2063	15	0.001	0.002	0.0015	0.0014	0.0021	0.0037	0.0052	0.0027	0.003	0.0038	0.0027	0.0017	0.0011	0.0974	0.4689	0.2882	0.001	0.0037	0.0077	0.0975	0.0036
Sokoke	2067	42	0.0049	0.0057	0.0027	0.0706	0.0016	0.0271	0.0021	0.0022	0.0025	0.0059	0.0024	0.0046	0.0021	0.0796	0.3918	0.2925	0.0023	0.009	0.0052	0.082	0.0033
Sokoke	6615	23	0.001	0.0078	0.0045	0.0029	0.0016	0.0109	0.0023	0.0013	0.0105	0.0039	0.0051	0.0017	0.0075	0.0905	0.4162	0.2424	0.0014	0.0078	0.0017	0.0923	0.0866
Ocicat	2933	44	0.0033	0.0026	0.0085	0.0063	0.0094	0.0072	0.0828	0.4183	0.019	0.0068	0.007	0.002	0.0035	0.0118	0.0021	0.0022	0.003	0.0688	0.0055	0.06	0.2699
Ocicat	2951	21	0.001	0.007	0.0028	0.0011	0.0022	0.0029	0.0038	0.0029	0.678	0.0048	0.0067	0.0023	0.0086	0.0907	0.0027	0.0074	0.0028	0.0393	0.0205	0.0972	0.0153
Ocicat	2954	26	0.0019	0.0021	0.019	0.089	0.0018	0.0028	0.002	0.0055	0.6232	0.0217	0.0041	0.002	0.0044	0.0907	0.0039	0.0233	0.001	0.0054	0.0018	0.0889	0.0055
Ocicat	3514	47	0.0056	0.0086	0.0032	0.0061	0.0023	0.0022	0.0054	0.0072	0.6771	0.0061	0.0257	0.0021	0.0094	0.0951	0.0033	0.0036	0.001	0.029	0.0041	0.0979	0.005
Ocicat	5744	5	0.0075	0.0048	0.0075	0.0106	0.0075	0.0101	0.0037	0.011	0.5248	0.0095	0.0071	0.0072	0.0098	0.0995	0.0032	0.003	0.0153	0.1045	0.0032	0.1311	0.0191
Ocicat	9966	13	0.0055	0.0017	0.0022	0.0025	0.003	0.0451	0.0659	0.0076	0.3938	0.0044	0.0126	0.0013	0.0245	0.0975	0.0064	0.0052	0.003	0.1382	0.0086	0.1019	0.0692
Ocicat	9967	2	0.0603	0.0031	0.0054	0.0037	0.0026	0.0023	0.0077	0.0051	0.4946	0.0045	0.0026	0.002	0.0064	0.084	0.005	0.003	0.006	0.0861	0.0095	0.1648	0.0414
Ocicat	10400	2	0.0025	0.0042	0.0108	0.0035	0.0017	0.0168	0.0046	0.0032	0.5573	0.0124	0.0071	0.0311	0.006	0.0823	0.0022	0.02	0.0051	0.0894	0.0051	0.0898	0.0449
Ocicat	10652	2	0.0102	0.0067	0.0076	0.0042	0.0143	0.0019	0.0017	0.0073	0.6008	0.0077	0.0075	0.0027	0.0188	0.1089	0.0011	0.0036	0.0057	0.0537	0.0015	0.1257	0.0085
Ocicat	10654	0	0.0292	0.0017	0.0065	0.0087	0.001	0.0152	0.0254	0.0129	0.5538	0.0017	0.0029	0.0014	0.0035	0.0967	0.0026	0.0018	0.0017	0.0669	0.0083	0.1257	0.0323
Russian Blue	1834	7	0.001	0.0015	0.0017	0.0021	0.001	0.002	0.001	0.001	0.001	0.002	0.0021	0.0015	0.0019	0.0016	0.002	0.0026	0.9642	0.0026	0.002	0.0036	0.0016
Russian Blue	1835	5	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	0.001	0.001	0.001	0.98	0.001	0.001	0.001	0.001
Russian Blue	2505	13	0.001	0.0022	0.0011	0.001	0.001	0.001	0.001	0.001	0.001	0.0027	0.001	0.0011	0.001	0.001	0.0019	0.0088	0.9667	0.001	0.0022	0.0011	0.0011
Russian Blue	4068	13	0.001	0.001	0.0013	0.0011	0.001	0.003	0.002	0.002	0.001	0.0019	0.001	0.001	0.001	0.0014	0.0014	0.0011	0.9697	0.0016	0.0033	0.0019	0.0013
Russian Blue	4072	23	0.0032	0.0024	0.002	0.002	0.002	0.0011	0.001	0.002	0.0019	0.002	0.0028	0.0022	0.002	0.0019	0.0092	0.0014	0.9493	0.0074	0.0011	0.0015	0.0015
Russian Blue	4074	10	0.0035	0.0048	0.0034	0.002	0.0012	0.0108	0.001	0.2168	0.002	0.0038	0.0028	0.0032	0.0019	0.001	0.001	0.0011	0.7309	0.0029	0.002	0.0026	0.0013
Russian Blue	4076	10	0.002	0.0029	0.002	0.002	0.001	0.001	0.001	0.002	0.0019	0.002	0.0013	0.0024	0.001	0.001	0.0012	0.0012	0.9687	0.0014	0.001	0.0019	0.0011
Russian Blue	4077	7	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	0.001	0.001	0.001	0.9792	0.001	0.001	0.001	0.0018
Russian Blue	4078	10	0.0029	0.0047	0.0066	0.0067	0.003	0.0069	0.003	0.0034	0.0031	0.004	0.0037	0.003	0.0058	0.0046	0.0033	0.0112	0.915	0.002	0.0019	0.0032	0.002
Russian Blue	4302	10	0.0011	0.001	0.0017	0.001	0.0027	0.001	0.0012	0.0018	0.0012	0.0013	0.001	0.003	0.0019	0.0012	0.001	0.001	0.9453	0.0022	0.0012	0.0025	0.0257
Russian Blue	4867	23	0.0018	0.0034	0.0037	0.0022	0.002	0.001	0.0053	0.0047	0.0213	0.0082	0.003	0.001	0.0025	0.0015	0.0015	0.0051	0.9252	0.001	0.0018	0.002	0.0017
Russian Blue	4869	21	0.002	0.0038	0.002	0.002	0.0024	0.0019	0.0028	0.0012	0.001	0.002	0.002	0.002	0.001	0.0019	0.0018	0.0013	0.9566	0.0025	0.0049	0.0035	0.0014
Russian Blue	5216	7	0.028	0.0027	0.0043	0.002	0.0022	0.0244	0.1649	0.0581	0.0577	0.0026	0.0138	0.0025	0.0037	0.0059	0.002	0.0036	0.5907	0.0047	0.0111	0.009	0.0062
Russian Blue	5630	34	0.0051	0.0036	0.005	0.0059	0.001	0.004	0.002	0.003	0.0019	0.0037	0.0032	0.0037	0.0028	0.0019	0.0029	0.0036	0.9353	0.002	0.0052	0.0026	0.0016

Table 18 - Population clustering of each pedigreed individual in the database by STRs at K = 21

Feline Population	ID No.	Missing Data	Groups																				
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Russian Blue	5631	15	0.0044	0.0172	0.0088	0.0043	0.002	0.002	0.0025	0.001	0.0035	0.0039	0.0023	0.0048	0.0012	0.0022	0.002	0.0021	0.9265	0.002	0.002	0.0026	0.0027
Russian Blue	5704	7	0.0014	0.001	0.0017	0.001	0.001	0.001	0.002	0.0018	0.001	0.0018	0.0014	0.001	0.001	0.001	0.001	0.001	0.9758	0.001	0.001	0.0011	0.001
Russian Blue	5709	15	0.0022	0.0029	0.0017	0.0036	0.002	0.003	0.001	0.002	0.001	0.0013	0.001	0.002	0.001	0.0011	0.0012	0.001	0.9667	0.0019	0.001	0.0014	0.001
Aust. Mist	4716	86	0.0221	0.0471	0.1068	0.0059	0.034	0.0167	0.0471	0.0124	0.0071	0.0291	0.024	0.0186	0.0092	0.0107	0.1018	0.023	0.1247	0.3026	0.0111	0.0283	0.0175
Aust. Mist	4718	2	0.0317	0.0024	0.0108	0.0037	0.0023	0.0081	0.001	0.0317	0.008	0.0528	0.0629	0.0488	0.0129	0.0059	0.0019	0.0048	0.001	0.6997	0.0018	0.0059	0.002
Aust. Mist	4720	15	0.0024	0.002	0.0044	0.0047	0.0048	0.002	0.0072	0.0042	0.014	0.0083	0.0069	0.002	0.0091	0.0055	0.0016	0.0027	0.0019	0.8976	0.0024	0.0133	0.003
Aust. Mist	4722	13	0.0117	0.0035	0.0079	0.0103	0.0051	0.0037	0.0264	0.0275	0.0057	0.0127	0.0258	0.0036	0.0069	0.0051	0.0011	0.0024	0.0021	0.8215	0.0013	0.0138	0.002
Aust. Mist	4723	10	0.0038	0.0023	0.0051	0.0081	0.0065	0.0093	0.0296	0.0107	0.004	0.0124	0.0374	0.0025	0.023	0.0059	0.0075	0.0037	0.0016	0.7855	0.0068	0.0075	0.0267
Aust. Mist	4724	84	0.013	0.0498	0.0201	0.0089	0.0067	0.0114	0.011	0.0134	0.0217	0.0258	0.0154	0.0092	0.6192	0.0728	0.0299	0.0174	0.003	0.0061	0.0054	0.0357	0.0043
Aust. Mist	4725	21	0.004	0.0142	0.0084	0.0155	0.0224	0.0023	0.0029	0.0171	0.0147	0.0142	0.0278	0.0103	0.0061	0.0058	0.0041	0.0475	0.0111	0.749	0.0077	0.0075	0.0074
Aust. Mist	4727	0	0.002	0.0024	0.0061	0.007	0.0033	0.0588	0.002	0.0028	0.0064	0.0219	0.1028	0.0066	0.0022	0.003	0.0016	0.0037	0.0024	0.7511	0.0047	0.0034	0.0058
Aust. Mist	4731	26	0.0034	0.001	0.002	0.2342	0.002	0.0079	0.0137	0.003	0.0108	0.0026	0.0028	0.002	0.0041	0.0018	0.0015	0.0015	0.0012	0.6965	0.002	0.0037	0.0023
Aust. Mist	4736	44	0.0019	0.0014	0.0026	0.0022	0.0017	0.0021	0.0021	0.0033	0.006	0.0053	0.0063	0.001	0.0074	0.0128	0.0047	0.0021	0.001	0.9273	0.002	0.0048	0.002
Aust. Mist	4739	28	0.0026	0.0076	0.0048	0.0174	0.0022	0.0115	0.0029	0.0094	0.0084	0.0034	0.0362	0.015	0.0036	0.0022	0.0018	0.0026	0.002	0.8503	0.0067	0.0066	0.0027
Aust. Mist	6184	2	0.0067	0.0079	0.0101	0.0051	0.002	0.0376	0.0044	0.0024	0.0033	0.0035	0.0225	0.0023	0.0022	0.0024	0.0027	0.0022	0.002	0.8309	0.0039	0.0072	0.0387
Aust. Mist	6187	2	0.0184	0.0078	0.0261	0.0051	0.0036	0.0121	0.0088	0.0101	0.0117	0.0103	0.0233	0.0034	0.0053	0.0066	0.0029	0.0042	0.0084	0.7978	0.0113	0.0163	0.0066
Aust. Mist	6188	7	0.0053	0.0143	0.032	0.0228	0.0071	0.0145	0.0049	0.0338	0.0811	0.0126	0.0737	0.002	0.0106	0.0063	0.002	0.0173	0.0036	0.5904	0.0042	0.0133	0.0482
Aust. Mist	6189	7	0.0164	0.0073	0.0061	0.0167	0.0065	0.0042	0.002	0.0052	0.0022	0.0085	0.0064	0.002	0.0014	0.002	0.0011	0.0017	0.0049	0.8746	0.0174	0.0106	0.0028
Burmese	21	5	0.0049	0.0027	0.002	0.0026	0.0049	0.001	0.0022	0.001	0.0043	0.0068	0.0025	0.001	0.001	0.0012	0.0012	0.0011	0.003	0.9204	0.0034	0.0172	0.0156
Burmese	22	5	0.0013	0.0013	0.0013	0.0036	0.001	0.0027	0.0016	0.0014	0.0013	0.0017	0.0018	0.0025	0.0015	0.0014	0.0027	0.0079	0.0026	0.9442	0.009	0.0033	0.0059
Burmese	23	5	0.0018	0.0023	0.0017	0.001	0.0011	0.0021	0.0029	0.0018	0.0016	0.0021	0.0024	0.0025	0.0021	0.0012	0.0024	0.0017	0.0012	0.888	0.002	0.0026	0.0755
Burmese	24	7	0.0019	0.002	0.0019	0.002	0.0021	0.0021	0.0189	0.0224	0.002	0.0039	0.0051	0.0333	0.0605	0.0033	0.0018	0.0011	0.0027	0.8254	0.0024	0.0026	0.0027
Burmese	25	5	0.001	0.0011	0.001	0.002	0.0021	0.001	0.0026	0.0015	0.0034	0.0011	0.0017	0.002	0.002	0.0017	0.0023	0.0019	0.001	0.9163	0.0404	0.004	0.0099
Burmese	26	7	0.0025	0.009	0.0026	0.01	0.0029	0.0033	0.002	0.001	0.0022	0.0085	0.0034	0.001	0.0037	0.0025	0.0011	0.0017	0.0016	0.9098	0.0091	0.0067	0.0154
Burmese	27	7	0.0024	0.0018	0.0021	0.002	0.001	0.0055	0.0312	0.0019	0.0043	0.0054	0.0033	0.0099	0.0015	0.0027	0.0017	0.005	0.0047	0.8194	0.0064	0.0725	0.0153
Burmese	28	10	0.0127	0.0012	0.0025	0.001	0.002	0.001	0.002	0.0026	0.0049	0.0013	0.0018	0.0016	0.001	0.0012	0.0012	0.0011	0.0019	0.9462	0.001	0.0063	0.0055
Burmese	29	7	0.001	0.0013	0.0013	0.0013	0.001	0.001	0.0011	0.001	0.0021	0.002	0.0023	0.0132	0.0014	0.0041	0.0077	0.0013	0.001	0.9405	0.0062	0.0024	0.0068
Burmese	4401	13	0.0018	0.0011	0.001	0.0014	0.0031	0.0014	0.0023	0.0044	0.0027	0.0022	0.0022	0.0015	0.0013	0.0029	0.0071	0.0076	0.002	0.8144	0.13	0.0033	0.0063
Burmese	4691	18	0.0054	0.007	0.0085	0.0042	0.0211	0.0636	0.0022	0.0086	0.0017	0.019	0.0074	0.0021	0.0034	0.0173	0.0365	0.009	0.0075	0.7569	0.0019	0.0098	0.007
Burmese	4781	18	0.001	0.0026	0.001	0.0013	0.001	0.0025	0.0013	0.0013	0.0013	0.001	0.0012	0.001	0.001	0.0017	0.0025	0.0017	0.0013	0.9301	0.0079	0.0021	0.0351
Burmese	4782	18	0.0031	0.0011	0.0021	0.002	0.001	0.002	0.003	0.001	0.0041	0.0012	0.0031	0.0013	0.002	0.0018	0.0015	0.0022	0.001	0.8325	0.0021	0.0032	0.1287
Burmese	5425	7	0.0015	0.002	0.0027	0.004	0.001	0.002	0.0013	0.0021	0.0045	0.0042	0.0053	0.0047	0.0086	0.0023	0.0139	0.0025	0.0017	0.8858	0.0029	0.0035	0.0434
Burmese	5800	15	0.0035	0.0045	0.0018	0.0022	0.001	0.0026	0.0065	0.0042	0.0018	0.002	0.0028	0.002	0.0013	0.0027	0.0028	0.0027	0.002	0.8922	0.0055	0.007	0.0489
Burmese	6182	13	0.0038	0.0015	0.0037	0.0013	0.001	0.001	0.0028	0.0044	0.0013	0.0088	0.0038	0.0027	0.0013	0.0012	0.0032	0.001	0.0303	0.9028	0.0028	0.0046	0.0166
Burmese	6471	18	0.0011	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.0066	0.001	0.001	0.0029	0.001	0.0018	0.0022	0.0022	0.001	0.8969	0.0229	0.0066	0.0458
Burmese	6962	15	0.0013	0.0013	0.0022	0.001	0.0011	0.0013	0.0026	0.001	0.001	0.0014	0.0013	0.001	0.001	0.0019	0.0022	0.001	0.0024	0.7499	0.2	0.0028	0.0223
Burmese	6964	23	0.0017	0.0028	0.0018	0.0018	0.001	0.0048	0.0023	0.0014	0.0098	0.0024	0.0034	0.0013	0.0027	0.0026	0.002	0.0026	0.0013	0.9276	0.0186	0.0026	0.0055
Birman	1760	7	0.0036	0.0092	0.0078	0.01	0.001	0.001	0.0036	0.0051	0.0011	0.0039	0.0054	0.001	0.0104	0.0031	0.001	0.001	0.0122	0.001	0.914	0.0025	0.002
Birman	2917	28	0.001	0.0011	0.0011	0.001	0.002	0.0018	0.0037	0.002	0.0012	0.001	0.0017	0.001	0.001	0.0015	0.001	0.001	0.0018	0.001	0.9712	0.0016	0.0013

Table 18 - Population clustering of each pedigreed individual in the database by STRs at K = 21

Feline	ID	Missing	Groups																				
Population	No.	Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Birman	3910	10	0.0034	0.0142	0.002	0.0018	0.0102	0.0017	0.0026	0.0011	0.0011	0.002	0.0032	0.0015	0.0035	0.0018	0.0026	0.0019	0.003	0.0013	0.9382	0.0018	0.0011
Birman	5029	7	0.0024	0.0098	0.0042	0.0064	0.001	0.0051	0.0034	0.0019	0.0158	0.0042	0.0088	0.0065	0.0024	0.0018	0.0013	0.0018	0.0029	0.0017	0.9133	0.0036	0.0017
Birman	5033	7	0.001	0.001	0.0011	0.0011	0.001	0.0033	0.0017	0.001	0.0017	0.001	0.001	0.001	0.001	0.0012	0.0012	0.0016	0.001	0.0023	0.9717	0.0011	0.003
Birman	5034	5	0.0145	0.0221	0.003	0.0038	0.0178	0.002	0.0032	0.003	0.0029	0.0061	0.0065	0.002	0.0039	0.0033	0.0018	0.0011	0.0115	0.005	0.8733	0.0089	0.0042
Birman	5038	10	0.0168	0.0049	0.0044	0.0032	0.0034	0.0024	0.0025	0.0035	0.0016	0.0026	0.0033	0.0049	0.0026	0.0023	0.0021	0.0017	0.0237	0.0032	0.9049	0.0038	0.0023
Birman	5151	7	0.0034	0.0038	0.0031	0.0015	0.0017	0.0027	0.003	0.0021	0.0024	0.0019	0.0061	0.001	0.0048	0.0017	0.0086	0.0015	0.0018	0.0027	0.9408	0.0024	0.003
Birman	5576	23	0.0038	0.0011	0.0018	0.0013	0.0036	0.001	0.002	0.0019	0.0038	0.001	0.001	0.001	0.001	0.001	0.0011	0.0011	0.0017	0.0016	0.9656	0.0016	0.002
Birman	5578	15	0.0169	0.0116	0.0041	0.056	0.0221	0.0129	0.012	0.0078	0.0093	0.002	0.005	0.0044	0.0038	0.0082	0.0021	0.0039	0.0072	0.021	0.6749	0.0617	0.0529
Birman	6448	10	0.0046	0.0016	0.0018	0.0029	0.0016	0.0017	0.0024	0.0017	0.001	0.0027	0.0017	0.016	0.0017	0.0011	0.001	0.002	0.0031	0.002	0.9452	0.0019	0.0023
Birman	6450	15	0.0019	0.001	0.001	0.002	0.0016	0.001	0.0027	0.0036	0.0018	0.001	0.001	0.001	0.001	0.0016	0.001	0.001	0.0011	0.0026	0.9655	0.0025	0.0041
Birman	6526	21	0.001	0.001	0.001	0.001	0.001	0.001	0.0011	0.001	0.001	0.001	0.001	0.001	0.001	0.0011	0.0011	0.001	0.001	0.001	0.9793	0.001	0.0014
Birman	6527	13	0.001	0.001	0.0017	0.001	0.0038	0.0017	0.001	0.0025	0.0019	0.0017	0.0017	0.0028	0.0016	0.0013	0.001	0.001	0.0017	0.0013	0.9661	0.0022	0.002
Birman	6528	15	0.0013	0.001	0.0017	0.001	0.0018	0.0011	0.001	0.0014	0.0018	0.0017	0.0018	0.001	0.001	0.0012	0.0017	0.0011	0.001	0.002	0.9711	0.0016	0.0027
Birman	6529	15	0.0122	0.0034	0.0018	0.0019	0.0036	0.0023	0.0152	0.0017	0.0017	0.0017	0.0018	0.0017	0.0027	0.002	0.0075	0.0021	0.0016	0.001	0.9315	0.0016	0.001
Birman	6604	5	0.0019	0.0025	0.0035	0.003	0.0029	0.0046	0.0153	0.0042	0.0028	0.0043	0.003	0.001	0.002	0.002	0.0013	0.0022	0.001	0.0016	0.9354	0.0033	0.0021
Birman	6607	10	0.0022	0.0017	0.0017	0.001	0.0011	0.0017	0.0017	0.001	0.0017	0.0011	0.0014	0.001	0.0021	0.001	0.0064	0.0013	0.002	0.001	0.9668	0.0011	0.001
Birman	6608	5	0.0014	0.0017	0.0029	0.002	0.0025	0.0091	0.0222	0.0027	0.0016	0.0019	0.0045	0.0022	0.0027	0.0019	0.0011	0.002	0.001	0.0016	0.9313	0.0017	0.002
Birman	6609	10	0.0451	0.0027	0.0033	0.0017	0.0034	0.0014	0.0176	0.0017	0.0018	0.0039	0.0062	0.002	0.0011	0.0072	0.001	0.0011	0.0043	0.0044	0.8781	0.0085	0.0035
Havana Brn.	787	7	0.0035	0.0021	0.0028	0.0035	0.0022	0.001	0.0039	0.0019	0.0015	0.0014	0.0035	0.001	0.0013	0.0014	0.0012	0.0019	0.004	0.3056	0.0015	0.384	0.2708
Havana Brn.	2415	47	0.0036	0.0019	0.0017	0.0026	0.0146	0.002	0.0023	0.0026	0.0058	0.0016	0.0025	0.0013	0.0026	0.0019	0.0013	0.0029	0.0054	0.2886	0.003	0.3842	0.2676
Havana Brn.	2500	10	0.0057	0.0042	0.0021	0.003	0.0017	0.001	0.002	0.0028	0.0035	0.002	0.0028	0.0032	0.002	0.002	0.0017	0.0012	0.0033	0.2846	0.002	0.3804	0.2888
Havana Brn.	2501	36	0.0014	0.0012	0.0014	0.0013	0.002	0.001	0.0036	0.0022	0.0021	0.0011	0.0018	0.002	0.0017	0.0014	0.001	0.001	0.0016	0.292	0.003	0.3808	0.2964
Havana Brn.	2502	28	0.002	0.0024	0.0016	0.0016	0.001	0.0014	0.0023	0.0013	0.0021	0.0013	0.0018	0.0013	0.0013	0.0012	0.001	0.001	0.0013	0.2923	0.0018	0.3911	0.2889
Havana Brn.	3312	34	0.0016	0.0019	0.0014	0.0016	0.0016	0.001	0.0026	0.002	0.0026	0.002	0.0019	0.0016	0.0013	0.0012	0.0013	0.0011	0.0022	0.2879	0.0052	0.3881	0.2899
Havana Brn.	3404	10	0.001	0.003	0.0033	0.0017	0.0043	0.0017	0.0017	0.0101	0.0032	0.0031	0.0022	0.0017	0.002	0.0029	0.0017	0.0021	0.0033	0.2916	0.0017	0.3814	0.2763
Havana Brn.	3513	13	0.0019	0.0037	0.003	0.0017	0.0032	0.0027	0.0919	0.0035	0.0011	0.0056	0.0154	0.0011	0.0023	0.0015	0.0015	0.0016	0.0023	0.2551	0.0032	0.3547	0.243
Havana Brn.	5707	7	0.0019	0.0025	0.002	0.0019	0.0032	0.0019	0.0017	0.0117	0.0016	0.0014	0.0017	0.0031	0.0014	0.0018	0.001	0.0013	0.0048	0.2854	0.001	0.3918	0.2769
Havana Brn.	5708	13	0.0029	0.0035	0.0031	0.0199	0.0014	0.0017	0.0018	0.0177	0.0041	0.0141	0.0031	0.0134	0.0047	0.0017	0.007	0.003	0.0022	0.2806	0.0012	0.3648	0.248
Havana Brn.	6972	13	0.0034	0.0161	0.0026	0.0097	0.0107	0.0021	0.0023	0.0082	0.0013	0.0033	0.0023	0.0017	0.0046	0.002	0.0011	0.001	0.0101	0.2627	0.0014	0.3858	0.2675
Havana Brn.	6973	21	0.0015	0.0046	0.004	0.0079	0.0086	0.002	0.0026	0.002	0.0017	0.003	0.0021	0.0017	0.0035	0.0022	0.0013	0.002	0.0057	0.267	0.0021	0.387	0.2875
Havana Brn.	10350	13	0.0031	0.0014	0.0019	0.0016	0.0016	0.0034	0.0017	0.0062	0.0032	0.0019	0.0029	0.0069	0.0019	0.002	0.001	0.0015	0.0016	0.2849	0.0023	0.3909	0.2781
Havana Brn.	5554	28	0.0014	0.0021	0.0024	0.0019	0.0059	0.001	0.0026	0.0023	0.0014	0.0017	0.0019	0.0033	0.0024	0.0012	0.001	0.0021	0.0078	0.2725	0.0013	0.3811	0.3027
Korat	4708	5	0.0017	0.0034	0.0021	0.0031	0.002	0.0048	0.006	0.0013	0.0064	0.0022	0.0025	0.0033	0.0029	0.0038	0.002	0.0021	0.0018	0.0018	0.6506	0.0031	0.2931
Korat	4711	5	0.001	0.0018	0.001	0.002	0.001	0.002	0.0018	0.001	0.0011	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.0017	0.6819	0.0014	0.2943
Korat	5059	7	0.001	0.0018	0.001	0.0016	0.0019	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.0011	0.0014	0.0014	0.001	0.0112	0.6496	0.0283	0.2907
Korat	5069	5	0.0043	0.0195	0.0047	0.0173	0.002	0.006	0.0011	0.0022	0.0038	0.0034	0.0032	0.0067	0.0023	0.0111	0.005	0.0049	0.0012	0.0154	0.6021	0.0085	0.2753
Korat	5098	7	0.001	0.0022	0.0012	0.0024	0.0049	0.0026	0.002	0.001	0.0011	0.0013	0.0013	0.0011	0.0013	0.0015	0.0014	0.002	0.0013	0.003	0.6807	0.0018	0.2848
Korat	5175	5	0.001	0.0013	0.001	0.001	0.001	0.002	0.0029	0.001	0.0017	0.0011	0.0016	0.0011	0.0019	0.0012	0.0011	0.0012	0.0013	0.0103	0.649	0.0241	0.2932
Korat	5176	5	0.001	0.0014	0.0022	0.0027	0.002	0.001	0.0014	0.0019	0.0029	0.0031	0.0017	0.001	0.0011	0.0016	0.0019	0.002	0.001	0.0296	0.5911	0.058	0.2913

Table 18 - Population clustering of each pedigreed individual in the database by STRs at K = 21

Feline Population	ID No.	Missing Data	Groups																				
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Korat	5177	5	0.001	0.001	0.001	0.002	0.001	0.0014	0.0012	0.001	0.0015	0.001	0.0014	0.001	0.001	0.0012	0.0146	0.0016	0.0014	0.171	0.5363	0.006	0.2524
Korat	5178	7	0.001	0.0023	0.0011	0.002	0.0013	0.0013	0.002	0.001	0.002	0.0013	0.0015	0.0022	0.0017	0.0021	0.0022	0.0012	0.002	0.002	0.679	0.0016	0.2892
Korat	5224	5	0.0016	0.0017	0.002	0.0011	0.0017	0.0034	0.002	0.0017	0.0011	0.0018	0.0026	0.0033	0.002	0.0014	0.0018	0.0029	0.0035	0.0034	0.6672	0.0055	0.2883
Korat	5237	7	0.0126	0.0096	0.007	0.0088	0.0038	0.002	0.002	0.0026	0.0043	0.0018	0.0029	0.0234	0.0029	0.0066	0.0118	0.0138	0.001	0.0083	0.6129	0.0075	0.2544
Korat	5240	5	0.001	0.001	0.0014	0.002	0.0011	0.0017	0.001	0.001	0.0014	0.001	0.001	0.001	0.0012	0.0015	0.002	0.0014	0.0012	0.0052	0.6789	0.0026	0.2914
Korat	5242	5	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.0011	0.001	0.001	0.001	0.001	0.0011	0.0011	0.001	0.0018	0.0024	0.6841	0.0026	0.2928
Korat	5244	5	0.001	0.0011	0.001	0.002	0.0015	0.0015	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.0011	0.0011	0.0013	0.0013	0.0022	0.6983	0.002	0.2766
Korat	5284	7	0.001	0.001	0.001	0.001	0.0021	0.002	0.002	0.001	0.0033	0.001	0.0014	0.0013	0.001	0.0017	0.0017	0.0013	0.001	0.1027	0.5843	0.0074	0.2808
Korat	5344	5	0.001	0.001	0.0011	0.001	0.001	0.0013	0.0065	0.002	0.005	0.0017	0.0014	0.001	0.0014	0.0021	0.002	0.0024	0.0034	0.0041	0.6631	0.0053	0.2922
Korat	5481	5	0.001	0.0017	0.0016	0.0045	0.001	0.0064	0.0014	0.0017	0.0028	0.0014	0.0019	0.0013	0.0017	0.0019	0.0024	0.0033	0.0019	0.0115	0.6558	0.0034	0.2915
Korat	5512	5	0.001	0.0013	0.0011	0.0037	0.0013	0.0028	0.001	0.001	0.002	0.0019	0.0013	0.0017	0.002	0.0011	0.0012	0.0021	0.0013	0.0057	0.6975	0.0028	0.2662
Korat	5514	5	0.0017	0.0021	0.0022	0.0017	0.001	0.002	0.001	0.0017	0.0011	0.001	0.0015	0.001	0.001	0.0011	0.0011	0.001	0.001	0.0025	0.6633	0.0023	0.3086
Korat	5595	5	0.001	0.001	0.0016	0.0023	0.002	0.0026	0.001	0.001	0.0011	0.002	0.0017	0.0026	0.0015	0.0035	0.0052	0.0029	0.002	0.0954	0.576	0.0105	0.2831
Korat	5597	7	0.001	0.002	0.0032	0.0032	0.0016	0.0033	0.0017	0.002	0.0073	0.002	0.0037	0.0034	0.0027	0.0043	0.003	0.0054	0.001	0.0474	0.6235	0.0046	0.2736
Korat	6375	5	0.001	0.0012	0.0013	0.001	0.0034	0.0021	0.003	0.002	0.0042	0.002	0.0022	0.001	0.0158	0.0975	0.0045	0.0051	0.0017	0.0791	0.4248	0.088	0.2591
Korat	6376	7	0.001	0.0017	0.0022	0.0019	0.0017	0.0051	0.001	0.001	0.0028	0.0022	0.0116	0.0017	0.0018	0.0028	0.001	0.0022	0.0017	0.0668	0.4568	0.0718	0.3611
Korat	6377	5	0.001	0.0011	0.0014	0.0018	0.0012	0.0514	0.0023	0.0023	0.0045	0.0025	0.0021	0.003	0.0012	0.0073	0.0016	0.0018	0.0021	0.1067	0.429	0.0903	0.2853
Korat	6378	5	0.0023	0.0021	0.0019	0.002	0.0021	0.0191	0.0044	0.0022	0.0087	0.0036	0.0023	0.0014	0.0032	0.0067	0.0104	0.0018	0.0026	0.1016	0.4425	0.1102	0.2689
Siamese	2868	7	0.001	0.0021	0.0014	0.0021	0.0032	0.0053	0.001	0.002	0.006	0.0014	0.0017	0.001	0.001	0.0026	0.005	0.0027	0.0011	0.3468	0.0293	0.3171	0.2662
Siamese	6686	28	0.0068	0.0021	0.0022	0.0028	0.0014	0.0012	0.0037	0.0025	0.002	0.1366	0.0042	0.0063	0.0135	0.0029	0.0059	0.0024	0.0023	0.2729	0.002	0.3335	0.1927
Siamese	6688	10	0.0019	0.0022	0.0018	0.0059	0.005	0.0036	0.0113	0.002	0.0074	0.0037	0.0033	0.0027	0.0038	0.0026	0.0027	0.0027	0.0035	0.3084	0.006	0.3178	0.3017
Siamese	6690	18	0.0014	0.0049	0.0029	0.0092	0.0019	0.0023	0.0013	0.0013	0.0025	0.0031	0.0021	0.0015	0.0015	0.0034	0.0025	0.0053	0.0038	0.2853	0.002	0.3935	0.2683
Siamese	6696	15	0.001	0.0012	0.0023	0.0024	0.0013	0.0028	0.0055	0.0018	0.0032	0.0018	0.0013	0.001	0.0021	0.002	0.0035	0.0018	0.0068	0.2498	0.1412	0.3094	0.2578
Siamese	7839	10	0.001	0.001	0.0011	0.001	0.0016	0.0014	0.003	0.001	0.0021	0.001	0.001	0.001	0.0011	0.003	0.0012	0.001	0.001	0.2979	0.0073	0.3802	0.2911
Siamese	8181	10	0.001	0.0017	0.0019	0.0016	0.0017	0.0014	0.0026	0.0016	0.0014	0.0016	0.0025	0.0014	0.001	0.0011	0.001	0.0013	0.0016	0.2929	0.0022	0.3904	0.2881
Siamese	8182	7	0.001	0.001	0.001	0.0013	0.001	0.0013	0.0013	0.0016	0.0013	0.0012	0.001	0.0017	0.001	0.0011	0.001	0.0033	0.001	0.3154	0.0023	0.3818	0.2784
Siamese	8184	13	0.0016	0.0023	0.0018	0.003	0.0017	0.0169	0.0509	0.003	0.0035	0.0109	0.003	0.003	0.002	0.0028	0.0026	0.0093	0.0023	0.3273	0.0057	0.3575	0.1889
Siamese	8185	10	0.0037	0.0033	0.0025	0.0028	0.0019	0.0076	0.0197	0.0033	0.0045	0.0138	0.0031	0.002	0.0022	0.004	0.019	0.0051	0.0212	0.259	0.008	0.3659	0.2473
Siamese	8187	5	0.0016	0.0014	0.0013	0.0027	0.0022	0.002	0.0051	0.0013	0.0016	0.0015	0.0013	0.001	0.0013	0.0016	0.0014	0.0019	0.0014	0.2767	0.128	0.3118	0.2529
Siamese	8251	13	0.0024	0.0075	0.0029	0.0014	0.001	0.0266	0.0111	0.001	0.0025	0.0019	0.0024	0.0025	0.0022	0.0055	0.001	0.0011	0.0026	0.2803	0.0854	0.2768	0.2819
Siamese	8253	5	0.001	0.002	0.0037	0.0023	0.0029	0.0026	0.0121	0.001	0.0038	0.0015	0.0012	0.0013	0.0016	0.0025	0.001	0.0029	0.0042	0.3692	0.0088	0.2998	0.2745
Siamese	8258	10	0.0011	0.0034	0.0011	0.002	0.0011	0.0015	0.0015	0.0013	0.0015	0.002	0.001	0.0013	0.001	0.0016	0.0019	0.0013	0.0027	0.2845	0.0262	0.3747	0.2873
Siamese	8259	5	0.0013	0.0014	0.0027	0.0042	0.0043	0.0159	0.0036	0.002	0.0022	0.0026	0.0034	0.0017	0.002	0.0024	0.0027	0.0027	0.0025	0.2744	0.0365	0.3478	0.2838
Singapura	3428	39	0.001	0.0024	0.0019	0.007	0.0035	0.002	0.0042	0.0026	0.0039	0.0027	0.0028	0.0053	0.002	0.003	0.0026	0.0019	0.0046	0.0455	0.0172	0.0123	0.8716
Singapura	3919	26	0.001	0.0012	0.0012	0.001	0.001	0.0013	0.0013	0.0013	0.0025	0.001	0.0012	0.001	0.0013	0.0014	0.0013	0.001	0.001	0.0016	0.001	0.0021	0.9743
Singapura	4464	7	0.001	0.0012	0.0013	0.001	0.001	0.0027	0.0021	0.0012	0.0017	0.001	0.0011	0.0011	0.0013	0.0016	0.001	0.001	0.0017	0.0028	0.0011	0.0011	0.972
Singapura	4467	7	0.001	0.001	0.0011	0.001	0.001	0.0012	0.0013	0.001	0.0018	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.0021	0.0025	0.0013	0.0014	0.9753
Singapura	4468	31	0.001	0.0013	0.0013	0.0013	0.001	0.0013	0.0013	0.0013	0.0018	0.0013	0.0013	0.0016	0.0016	0.0013	0.001	0.0011	0.0013	0.0063	0.001	0.0012	0.9694
Singapura	4469	7	0.001	0.0012	0.0016	0.001	0.001	0.0013	0.0013	0.0013	0.0039	0.0013	0.0013	0.0013	0.0013	0.0016	0.001	0.001	0.001	0.0027	0.0013	0.0014	0.9713

Table 18 - Population clustering of each pedigreed individual in the database by STRs at K = 21

Feline	ID	Missing	Groups																				
Population	No.	Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Singapura	4470	5	0.001	0.0012	0.0016	0.001	0.001	0.0013	0.0013	0.001	0.0013	0.0013	0.0012	0.0013	0.0013	0.0016	0.001	0.0039	0.0011	0.0026	0.001	0.0012	0.9718
Singapura	4471	5	0.001	0.0012	0.0016	0.001	0.001	0.001	0.0013	0.001	0.0086	0.0013	0.0014	0.0013	0.0013	0.0012	0.001	0.001	0.0044	0.0016	0.0037	0.0013	0.9628
Singapura	4472	5	0.001	0.0012	0.0029	0.0021	0.0013	0.0011	0.0013	0.001	0.0768	0.0013	0.0029	0.0028	0.0016	0.0013	0.0013	0.0011	0.001	0.0022	0.0013	0.0014	0.8931
Singapura	4473	18	0.002	0.0012	0.0015	0.0013	0.005	0.0013	0.0046	0.002	0.0019	0.0023	0.0016	0.004	0.0039	0.001	0.001	0.001	0.001	0.0027	0.0022	0.0022	0.9563
Singapura	4474	28	0.0037	0.002	0.0044	0.0044	0.0027	0.0023	0.0051	0.0039	0.0373	0.0026	0.0049	0.0037	0.002	0.0043	0.0026	0.0016	0.0026	0.0383	0.0019	0.005	0.8648
Singapura	4485	31	0.0016	0.0019	0.002	0.002	0.001	0.002	0.0023	0.001	0.0056	0.002	0.002	0.0022	0.0023	0.0044	0.0016	0.0017	0.0017	0.0028	0.0045	0.0034	0.952
Singapura	4486	18	0.0012	0.0019	0.0027	0.001	0.001	0.0023	0.0019	0.0019	0.0067	0.0016	0.0014	0.0016	0.0015	0.0043	0.0013	0.0013	0.0013	0.0044	0.0013	0.0016	0.9578
Singapura	4487	18	0.001	0.0058	0.0045	0.0016	0.0015	0.001	0.0031	0.0012	0.0055	0.0028	0.0028	0.002	0.0014	0.0016	0.002	0.001	0.0029	0.0068	0.0381	0.0037	0.9096
Singapura	4488	21	0.0012	0.0027	0.0041	0.002	0.001	0.0064	0.0027	0.0016	0.0196	0.0036	0.0024	0.0011	0.0013	0.0017	0.0013	0.0014	0.0015	0.0038	0.0022	0.003	0.9353
Singapura	6597	5	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.0018	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.0061	0.0013	0.0018	0.9731
Singapura	6975	21	0.0016	0.0015	0.002	0.0019	0.001	0.0023	0.003	0.0017	0.0152	0.0019	0.002	0.001	0.002	0.0018	0.0014	0.0011	0.0017	0.0072	0.001	0.0026	0.9461

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline	ID	Missing	Groups																
Population	No.	Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Persian	1250	9	0.0065	0.0352	0.0036	0.001	0.0034	0.0042	0.0203	0.0035	0.0022	0.0068	0.885	0.0044	0.0073	0.0052	0.0029	0.0046	0.0039
Persian	1939	4	0.0011	0.0013	0.001	0.001	0.0019	0.0027	0.001	0.001	0.001	0.001	0.9786	0.001	0.002	0.0011	0.002	0.001	0.0013
Persian	2071	8	0.0024	0.0046	0.0022	0.0029	0.0605	0.002	0.002	0.0023	0.0025	0.003	0.8831	0.0022	0.0027	0.002	0.011	0.0057	0.0089
Persian	2088	0	0.0125	0.0039	0.0021	0.0192	0.0684	0.0023	0.0026	0.0022	0.0011	0.0079	0.8201	0.0024	0.003	0.003	0.0198	0.002	0.0275
Persian	2140	7	0.001	0.0019	0.0014	0.0041	0.002	0.0044	0.0023	0.0016	0.001	0.002	0.966	0.0024	0.0018	0.0019	0.0025	0.002	0.0017
Persian	2174	2	0.0018	0.0012	0.0015	0.0035	0.0071	0.002	0.002	0.0018	0.002	0.0018	0.9602	0.0011	0.0011	0.0016	0.0055	0.003	0.0028
Persian	2209	4	0.0031	0.0063	0.003	0.002	0.0068	0.0051	0.0107	0.0099	0.0018	0.003	0.8757	0.0045	0.0073	0.0173	0.0339	0.0048	0.0048
Persian	2215	21	0.0024	0.0048	0.0052	0.0118	0.0062	0.0033	0.0039	0.0033	0.0018	0.0078	0.9129	0.0035	0.0033	0.0083	0.0125	0.0054	0.0036
Persian	2890	8	0.0029	0.003	0.0255	0.0033	0.0126	0.0033	0.0102	0.0077	0.002	0.0061	0.8256	0.0146	0.0057	0.0188	0.0133	0.003	0.0423
Persian	2977	3	0.0406	0.0043	0.0029	0.0037	0.0896	0.006	0.0202	0.0123	0.0022	0.0099	0.7185	0.0189	0.0121	0.0089	0.0172	0.0105	0.0223
Persian	4143	8	0.0031	0.0033	0.0032	0.0163	0.004	0.0074	0.003	0.0081	0.0032	0.0065	0.9183	0.0026	0.0066	0.0038	0.0039	0.0028	0.004
Persian	4168	4	0.0048	0.0061	0.0031	0.0112	0.0092	0.001	0.0067	0.0041	0.0028	0.0055	0.9075	0.0039	0.0037	0.0093	0.0074	0.0083	0.0054
Persian	4169	2	0.002	0.0056	0.001	0.001	0.002	0.0026	0.002	0.002	0.001	0.0028	0.9684	0.0011	0.002	0.0017	0.001	0.002	0.0018
Persian	4950	0	0.0019	0.002	0.0013	0.0045	0.001	0.0032	0.0025	0.0031	0.001	0.003	0.9638	0.0011	0.003	0.0026	0.0018	0.0022	0.002
Persian	4953	1	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.0009	0.001	0.9831	0.001	0.001	0.001	0.0011	0.001	0.001
Exotic SH	258	0	0.001	0.001	0.001	0.0029	0.0044	0.003	0.001	0.0011	0.001	0.001	0.9748	0.001	0.001	0.001	0.002	0.0012	0.0016
Exotic SH	259	3	0.0038	0.0114	0.002	0.005	0.0171	0.0027	0.0022	0.0044	0.0032	0.0029	0.9282	0.0021	0.003	0.0022	0.0024	0.002	0.0054
Exotic SH	260	4	0.0061	0.0047	0.0048	0.0044	0.0107	0.002	0.0304	0.0067	0.001	0.0068	0.8873	0.0063	0.0063	0.0102	0.0028	0.004	0.0054
Exotic SH	261	4	0.001	0.002	0.001	0.001	0.0021	0.0034	0.001	0.001	0.0007	0.001	0.9791	0.0011	0.001	0.001	0.0016	0.001	0.001
Exotic SH	262	4	0.0236	0.0035	0.0076	0.0029	0.0228	0.0118	0.022	0.0024	0.0022	0.0079	0.818	0.0113	0.0316	0.0032	0.0045	0.002	0.0226
Exotic SH	263	7	0.001	0.002	0.001	0.0031	0.5009	0.001	0.002	0.0012	0.001	0.0012	0.0102	0.001	0.0013	0.0038	0.4582	0.0032	0.0078
Exotic SH	264	2	0.0011	0.002	0.001	0.0012	0.6721	0.0019	0.001	0.0013	0.001	0.0014	0.0029	0.001	0.001	0.001	0.3058	0.002	0.0023
Exotic SH	265	3	0.0022	0.0096	0.0024	0.0015	0.3718	0.002	0.0031	0.0022	0.001	0.0031	0.0071	0.0019	0.0024	0.0067	0.5751	0.0027	0.0053
Exotic SH	266	5	0.0011	0.0031	0.001	0.001	0.4978	0.0045	0.0021	0.002	0.0016	0.0015	0.003	0.001	0.001	0.0014	0.4721	0.0021	0.0037
Exotic SH	267	4	0.0206	0.0043	0.053	0.0031	0.475	0.0068	0.0024	0.0213	0.0133	0.0076	0.0038	0.0145	0.0051	0.0194	0.2797	0.0391	0.0308
Exotic SH	268	5	0.0016	0.001	0.001	0.0036	0.5358	0.003	0.002	0.0028	0.0018	0.0022	0.0028	0.0018	0.002	0.0021	0.4301	0.001	0.0054
Exotic SH	269	4	0.0026	0.0031	0.0018	0.0034	0.6168	0.0054	0.0024	0.0031	0.001	0.0026	0.0057	0.002	0.002	0.0027	0.3267	0.0032	0.0156
Exotic SH	270	9	0.0473	0.0046	0.007	0.002	0.2903	0.0024	0.0103	0.0031	0.0103	0.0388	0.1262	0.0065	0.0387	0.0092	0.3427	0.003	0.0577
Exotic SH	271	0	0.002	0.005	0.0013	0.0102	0.3558	0.0029	0.0029	0.003	0.001	0.0022	0.0061	0.0033	0.0026	0.0025	0.5466	0.0013	0.0514
Exotic SH	272	1	0.0019	0.0019	0.0011	0.0015	0.5542	0.0013	0.0025	0.002	0.0011	0.0018	0.0021	0.0012	0.001	0.0019	0.4172	0.0028	0.0045
Exotic SH	273	1	0.018	0.0317	0.1202	0.0049	0.1133	0.0028	0.0104	0.0078	0.0064	0.0669	0.0078	0.0127	0.0047	0.0297	0.5325	0.0127	0.0176
Exotic SH	274	1	0.0045	0.0104	0.002	0.0015	0.3267	0.0064	0.0043	0.0055	0.0018	0.0031	0.0243	0.002	0.0023	0.0094	0.5775	0.0069	0.0114
Exotic SH	275	0	0.0023	0.0028	0.0011	0.0064	0.544	0.0033	0.0019	0.0028	0.001	0.002	0.006	0.0013	0.0018	0.0025	0.4129	0.0043	0.0036
Exotic SH	276	2	0.004	0.0079	0.0026	0.0026	0.5834	0.0038	0.0087	0.0073	0.003	0.0111	0.0132	0.0054	0.0101	0.0037	0.321	0.0029	0.0093
British SH	156	9	0.0043	0.0055	0.0051	0.0025	0.4419	0.0029	0.0048	0.004	0.001	0.0027	0.003	0.0024	0.0022	0.0031	0.4866	0.003	0.0249

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline Population	ID No.	Missing Data	Groups 1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
British SH	157	1	0.2103	0.0049	0.0068	0.0238	0.1071	0.0029	0.0176	0.0041	0.002	0.013	0.1852	0.0434	0.0066	0.0059	0.3426	0.0077	0.0161
British SH	158	5	0.0011	0.0011	0.001	0.0022	0.6183	0.002	0.001	0.001	0.001	0.001	0.0028	0.001	0.001	0.001	0.3604	0.0012	0.0029
British SH	159	3	0.0011	0.0011	0.001	0.0027	0.6988	0.0013	0.0011	0.001	0.001	0.001	0.0038	0.001	0.001	0.001	0.2635	0.001	0.0186
British SH	160	5	0.0023	0.0066	0.001	0.0021	0.4154	0.0026	0.002	0.005	0.0012	0.0019	0.0151	0.002	0.002	0.0049	0.5274	0.0036	0.0049
British SH	161	2	0.0038	0.0025	0.0055	0.0062	0.6298	0.0044	0.0081	0.0034	0.0017	0.012	0.0099	0.0127	0.0044	0.0036	0.0022	0.0054	0.2845
British SH	162	17	0.0022	0.0029	0.0209	0.0052	0.5835	0.001	0.0139	0.0027	0.0029	0.0191	0.0049	0.036	0.002	0.0068	0.0019	0.0024	0.2917
British SH	163	15	0.0135	0.0028	0.0078	0.0055	0.5922	0.0034	0.0139	0.0037	0.0111	0.005	0.0015	0.0074	0.0029	0.0028	0.0057	0.0292	0.2916
British SH	164	8	0.0046	0.0016	0.006	0.0284	0.5898	0.0022	0.0133	0.0024	0.0054	0.0066	0.0156	0.0062	0.0038	0.0031	0.0087	0.0035	0.2988
British SH	165	15	0.1608	0.002	0.0035	0.0038	0.4208	0.0108	0.0313	0.0287	0.0118	0.1931	0.002	0.0171	0.0098	0.0042	0.0057	0.0362	0.0584
British SH	166	5	0.0057	0.008	0.0032	0.0058	0.6486	0.0062	0.0017	0.002	0.0031	0.0051	0.0058	0.0034	0.0035	0.0021	0.0043	0.0036	0.2879
British SH	167	18	0.0014	0.0012	0.0011	0.0032	0.6795	0.001	0.0018	0.0011	0.001	0.0015	0.005	0.0013	0.0017	0.0015	0.0058	0.0016	0.2903
British SH	168	15	0.0023	0.0018	0.002	0.0081	0.663	0.0049	0.0025	0.0022	0.0017	0.0029	0.0011	0.0023	0.0015	0.0014	0.0044	0.0022	0.2957
British SH	169	12	0.0059	0.0017	0.0017	0.0022	0.6667	0.005	0.0022	0.001	0.0035	0.0016	0.0047	0.0016	0.0014	0.0017	0.0025	0.0023	0.2943
British SH	170	1	0.0577	0.0023	0.0047	0.0055	0.6134	0.0012	0.0064	0.0022	0.0091	0.0197	0.0064	0.0031	0.0031	0.002	0.002	0.0051	0.2561
British SH	171	0	0.005	0.0027	0.0034	0.0023	0.6278	0.0111	0.0096	0.0014	0.0015	0.0075	0.0018	0.007	0.0027	0.0015	0.0183	0.0057	0.2907
British SH	172	2	0.0017	0.0011	0.0031	0.0128	0.6267	0.004	0.0012	0.0015	0.0017	0.0013	0.0015	0.0016	0.001	0.0017	0.0487	0.0016	0.2888
British SH	173	2	0.0036	0.004	0.0074	0.0219	0.5993	0.0111	0.0018	0.0025	0.0018	0.0079	0.001	0.0045	0.0017	0.0097	0.0261	0.005	0.2907
Scottish Fold	5655	12	0.001	0.001	0.002	0.0021	0.8314	0.144	0.001	0.0019	0.002	0.0015	0.002	0.0023	0.0015	0.0012	0.0015	0.001	0.0026
Scottish Fold	5669	3	0.0015	0.001	0.0011	0.001	0.9817	0.001	0.001	0.001	0.001	0.001	0.0016	0.0011	0.001	0.001	0.001	0.001	0.002
Scottish Fold	7205	21	0.0061	0.0018	0.002	0.0031	0.8988	0.002	0.0039	0.0082	0.0032	0.005	0.0122	0.0033	0.0018	0.0377	0.002	0.0037	0.0052
Scottish Fold	7260	6	0.005	0.0027	0.004	0.0052	0.9178	0.008	0.0069	0.0035	0.0066	0.0026	0.0082	0.0019	0.0027	0.0026	0.0081	0.0111	0.0031
Scottish Fold	8552	16	0.0026	0.0036	0.002	0.0029	0.9355	0.0029	0.0024	0.002	0.001	0.0021	0.0288	0.0018	0.0019	0.0021	0.002	0.0028	0.0037
Scottish Fold	9823	12	0.0018	0.001	0.001	0.0049	0.9614	0.0023	0.0034	0.0016	0.001	0.0028	0.002	0.0011	0.0015	0.0013	0.0038	0.002	0.0071
Scottish Fold	9824	4	0.0018	0.001	0.002	0.0012	0.9613	0.0024	0.0026	0.0019	0.001	0.003	0.0047	0.0019	0.0023	0.0026	0.0019	0.0039	0.0045
Scottish Fold	9825	4	0.0028	0.0031	0.0076	0.0011	0.8719	0.0121	0.0151	0.0111	0.0023	0.0173	0.0054	0.0065	0.005	0.0183	0.0029	0.0083	0.0092
Scottish Fold	9826	11	0.001	0.0015	0.001	0.0076	0.9714	0.0017	0.001	0.001	0.001	0.0011	0.002	0.001	0.001	0.001	0.0035	0.0013	0.0019

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline Population	ID No.	Missing Data	Groups																
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Scottish Fold	9827	10	0.0016	0.0015	0.0018	0.0044	0.919	0.0123	0.0025	0.0126	0.0041	0.0035	0.0021	0.0036	0.0016	0.0075	0.0054	0.0114	0.0052
Scottish Fold	9831	6	0.0038	0.006	0.0034	0.0025	0.9008	0.0036	0.0097	0.0178	0.002	0.0052	0.0057	0.0035	0.0025	0.016	0.0025	0.0091	0.0059
Scottish Fold	9832	2	0.0061	0.0022	0.0024	0.0012	0.9544	0.002	0.003	0.002	0.002	0.003	0.0053	0.0031	0.0017	0.0026	0.0027	0.0027	0.0036
Scottish Fold	9929	16	0.0028	0.0036	0.0064	0.0037	0.9049	0.0045	0.0033	0.0067	0.0027	0.0115	0.0072	0.0137	0.0037	0.0101	0.0041	0.0029	0.0082
Scottish Fold	9930	4	0.0036	0.0018	0.0012	0.0023	0.9601	0.0017	0.0029	0.0031	0.0048	0.002	0.0036	0.002	0.0014	0.0024	0.0016	0.0025	0.003
Scottish Fold	9931	8	0.0045	0.0027	0.0023	0.0032	0.9064	0.0127	0.0113	0.0045	0.0139	0.0087	0.0033	0.0033	0.0043	0.0023	0.003	0.008	0.0056
Scottish Fold	9937	10	0.0017	0.0013	0.0017	0.0019	0.961	0.0043	0.002	0.0025	0.001	0.0023	0.0047	0.0019	0.0017	0.0033	0.0032	0.0029	0.0026
Scottish Fold	9965	6	0.0057	0.0017	0.0086	0.0066	0.9227	0.0042	0.0075	0.003	0.0042	0.0075	0.0069	0.0026	0.0043	0.0028	0.001	0.0063	0.0044
Chartreux	1772	8	0.0011	0.001	0.0019	0.0016	0.969	0.0014	0.0025	0.0021	0.0017	0.0017	0.0026	0.0015	0.001	0.0028	0.0034	0.002	0.0027
Chartreux	2226	2	0.001	0.001	0.001	0.001	0.9828	0.001	0.001	0.001	0.001	0.001	0.0013	0.001	0.001	0.001	0.001	0.001	0.0019
Chartreux	2229	4	0.0034	0.0021	0.0021	0.001	0.949	0.0036	0.0027	0.0018	0.0012	0.0024	0.0036	0.003	0.0019	0.003	0.0071	0.0031	0.009
Chartreux	2524	6	0.0023	0.0033	0.0012	0.0023	0.9603	0.0026	0.0014	0.002	0.0013	0.0019	0.0086	0.0015	0.0015	0.0021	0.0019	0.002	0.0038
Chartreux	2787	0	0.0046	0.0038	0.0031	0.0046	0.8816	0.0076	0.0072	0.0091	0.0011	0.0045	0.0033	0.0035	0.0032	0.0216	0.021	0.0082	0.0119
Chartreux	2805	10	0.0021	0.0066	0.003	0.0042	0.8308	0.045	0.0029	0.0158	0.002	0.0029	0.0089	0.0047	0.002	0.0045	0.0481	0.0086	0.0078
Chartreux	2813	19	0.0256	0.0031	0.0042	0.0083	0.8391	0.0049	0.0044	0.0235	0.0171	0.0053	0.0123	0.0048	0.0186	0.0099	0.0028	0.0046	0.0114
Chartreux	2979	2	0.0048	0.0132	0.0033	0.011	0.9009	0.0078	0.0036	0.0093	0.0058	0.0075	0.003	0.0045	0.0037	0.0058	0.003	0.0056	0.0072
Chartreux	4059	7	0.0048	0.002	0.0031	0.0119	0.767	0.0164	0.0069	0.0047	0.001	0.0041	0.0941	0.0025	0.0021	0.0054	0.0033	0.0076	0.063
Chartreux	4063	1	0.0081	0.0036	0.0024	0.0024	0.7695	0.0029	0.0024	0.0124	0.002	0.0026	0.009	0.0033	0.0016	0.0553	0.0047	0.0021	0.1157
Chartreux	5606	0	0.0028	0.0027	0.0107	0.0281	0.8417	0.0139	0.003	0.0046	0.0018	0.0044	0.0282	0.0049	0.0044	0.006	0.0058	0.0054	0.0317
Chartreux	5609	1	0.005	0.0154	0.003	0.0027	0.7679	0.003	0.0048	0.0075	0.0036	0.0083	0.0259	0.0073	0.0044	0.0048	0.0036	0.017	0.1158
Chartreux	5611	0	0.002	0.0053	0.003	0.0018	0.8149	0.0021	0.0035	0.002	0.0019	0.0027	0.0043	0.0027	0.002	0.0029	0.0034	0.0054	0.1401
American SH	143	2	0.002	0.0019	0.0025	0.0865	0.7379	0.0022	0.0073	0.0019	0.001	0.0038	0.0056	0.0019	0.0012	0.0095	0.0024	0.002	0.1304
American SH	144	0	0.0264	0.0038	0.0049	0.0021	0.682	0.0037	0.0033	0.005	0.001	0.0035	0.0418	0.0094	0.0028	0.0124	0.002	0.0111	0.1848
American SH	145	0	0.0095	0.0018	0.0019	0.0047	0.6966	0.0041	0.0025	0.0054	0.0017	0.0028	0.0106	0.0051	0.001	0.0033	0.0013	0.01	0.2377

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline	ID	Missing	Groups																
Population	No.	Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
American SH	146	0	0.002	0.0063	0.0043	0.0029	0.8084	0.002	0.0149	0.0036	0.002	0.003	0.0077	0.0033	0.0043	0.0055	0.008	0.0035	0.1183
American SH	3652	0	0.0011	0.004	0.0019	0.0015	0.7862	0.0017	0.0052	0.0021	0.0011	0.0015	0.0231	0.0021	0.0019	0.0023	0.002	0.002	0.1603
American SH	3653	0	0.0116	0.0014	0.0101	0.0028	0.7964	0.006	0.0052	0.0071	0.007	0.0051	0.0078	0.0041	0.0051	0.003	0.0081	0.0035	0.1157
American SH	4363	0	0.0045	0.001	0.0035	0.0492	0.764	0.0014	0.0062	0.0053	0.0022	0.005	0.0123	0.0041	0.0084	0.0056	0.002	0.0014	0.1239
American SH	4370	0	0.0059	0.0082	0.0032	0.0024	0.8816	0.004	0.0032	0.0039	0.001	0.0021	0.0205	0.0037	0.0061	0.0052	0.0028	0.002	0.0442
American SH	4373	1	0.0073	0.0045	0.0036	0.0012	0.7815	0.0014	0.0028	0.0046	0.001	0.0021	0.0082	0.0043	0.0029	0.0582	0.0032	0.0055	0.1077
American SH	6404	0	0.0171	0.025	0.0048	0.0077	0.7794	0.0292	0.0055	0.0063	0.0027	0.0027	0.0329	0.0057	0.0066	0.0063	0.0342	0.007	0.0269
American SH	6406	6	0.002	0.0078	0.0022	0.0032	0.4852	0.0031	0.014	0.0038	0.2669	0.0034	0.0053	0.0055	0.0033	0.0047	0.0047	0.0056	0.1793
American SH	6410	11	0.0019	0.001	0.002	0.002	0.3294	0.0021	0.0019	0.0021	0.4475	0.0019	0.0013	0.0019	0.0012	0.0031	0.0024	0.0016	0.1967
American SH	6421	0	0.0018	0.0018	0.0015	0.0018	0.5073	0.003	0.0036	0.002	0.2659	0.0019	0.001	0.0018	0.0018	0.0024	0.0025	0.0025	0.1975
American SH	2259	10	0.0019	0.002	0.0019	0.0017	0.4169	0.0048	0.0023	0.0039	0.3483	0.0026	0.0036	0.0015	0.0014	0.002	0.0089	0.0035	0.1928
Sphynx	277	4	0.001	0.0011	0.001	0.001	0.3356	0.0016	0.0016	0.0018	0.4479	0.0013	0.001	0.001	0.001	0.0017	0.0025	0.0011	0.1978
Sphynx	278	5	0.001	0.001	0.0014	0.001	0.4198	0.0026	0.0018	0.0017	0.3616	0.0013	0.001	0.0012	0.0011	0.0017	0.0025	0.0019	0.1973
Sphynx	279	0	0.0017	0.0012	0.0016	0.001	0.3979	0.0051	0.0037	0.003	0.3736	0.0018	0.001	0.0021	0.0026	0.0028	0.0024	0.0025	0.196
Sphynx	280	6	0.001	0.001	0.001	0.001	0.4469	0.0015	0.001	0.0015	0.3394	0.001	0.0012	0.001	0.001	0.0012	0.0034	0.0012	0.1956
Sphynx	281	14	0.0018	0.0013	0.0013	0.001	0.3006	0.0037	0.0018	0.0021	0.4772	0.0017	0.001	0.0012	0.0017	0.001	0.003	0.0014	0.1982
Sphynx	282	8	0.0016	0.0018	0.0021	0.0022	0.3815	0.001	0.0022	0.0028	0.399	0.0022	0.0021	0.0012	0.0021	0.003	0.0028	0.0033	0.1892
Sphynx	283	1	0.0016	0.0014	0.001	0.0015	0.4405	0.0022	0.0025	0.0023	0.3356	0.0017	0.001	0.0018	0.0012	0.0027	0.0037	0.0018	0.1975
Sphynx	284	14	0.0024	0.001	0.0018	0.0018	0.3368	0.0043	0.002	0.0044	0.4309	0.0021	0.0017	0.0019	0.0024	0.0025	0.0031	0.0018	0.1991
Sphynx	285	4	0.0018	0.0018	0.0028	0.0021	0.5105	0.0021	0.0051	0.0059	0.2202	0.0033	0.0024	0.0024	0.0023	0.0279	0.0108	0.0052	0.1934
Sphynx	286	22	0.0033	0.0035	0.0062	0.0018	0.5472	0.0085	0.0109	0.0038	0.1648	0.0035	0.0018	0.0034	0.0052	0.0033	0.0282	0.0106	0.194
Sphynx	287	9	0.008	0.0073	0.0055	0.0028	0.4222	0.0031	0.0277	0.0152	0.2448	0.0076	0.002	0.0088	0.0084	0.0592	0.0109	0.009	0.1575
Sphynx	288	2	0.001	0.001	0.001	0.0018	0.4424	0.0012	0.002	0.0021	0.3381	0.0014	0.001	0.0015	0.0011	0.0016	0.0028	0.0018	0.1982
Sphynx	289	1	0.0023	0.001	0.002	0.0033	0.4343	0.0022	0.0025	0.0031	0.3368	0.0021	0.0046	0.0019	0.0018	0.0024	0.0036	0.0028	0.1933

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline Population	ID No.	Missing Data	Groups																
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Sphynx	290	2	0.019	0.0033	0.0051	0.0041	0.0021	0.003	0.0032	0.0052	0.9015	0.0065	0.0099	0.0064	0.0065	0.0065	0.0019	0.0064	0.0094
Sphynx	291	2	0.0034	0.008	0.011	0.1264	0.0022	0.0035	0.0056	0.1043	0.6641	0.0092	0.0028	0.0064	0.0046	0.0144	0.0095	0.0072	0.0174
Sphynx	292	1	0.0114	0.0097	0.0121	0.0037	0.0093	0.0075	0.0074	0.0032	0.8437	0.0103	0.0103	0.0093	0.0068	0.0056	0.004	0.0273	0.0183
Sphynx	293	1	0.0074	0.0929	0.0113	0.0109	0.0029	0.0046	0.0032	0.0129	0.75	0.0113	0.0047	0.0049	0.0167	0.0166	0.0061	0.0101	0.0336
Japanese BT	1949	6	0.0045	0.0053	0.0168	0.0019	0.0016	0.0019	0.0046	0.0039	0.8907	0.005	0.0051	0.0212	0.0157	0.0053	0.0042	0.007	0.0053
Japanese BT	1966	4	0.0064	0.0179	0.0132	0.0025	0.0053	0.0055	0.0068	0.0134	0.7273	0.0113	0.0109	0.1083	0.0215	0.0158	0.0022	0.0035	0.0282
Japanese BT	2661	0	0.0199	0.0014	0.0037	0.0137	0.0015	0.0025	0.0029	0.0088	0.9117	0.0036	0.0016	0.0075	0.0022	0.0023	0.001	0.0023	0.0134
Japanese BT	2663	4	0.0038	0.0013	0.0014	0.0017	0.0017	0.001	0.0024	0.0017	0.9681	0.001	0.004	0.0017	0.002	0.002	0.002	0.0021	0.0021
Japanese BT	2666	4	0.0222	0.0022	0.0155	0.0039	0.0019	0.002	0.0043	0.0111	0.8141	0.0165	0.0028	0.0173	0.0376	0.0033	0.0075	0.0109	0.0269
Japanese BT	2668	0	0.044	0.0029	0.0065	0.0095	0.005	0.0037	0.0064	0.0082	0.8562	0.0077	0.0027	0.0071	0.0053	0.0093	0.0055	0.006	0.0141
Japanese BT	2973	3	0.0102	0.006	0.0298	0.0063	0.0133	0.0044	0.0068	0.0068	0.8237	0.0071	0.0017	0.0039	0.0049	0.0256	0.0061	0.0055	0.0379
Japanese BT	3324	1	0.0518	0.0049	0.0084	0.0028	0.0024	0.0124	0.0151	0.0103	0.7868	0.0047	0.0053	0.0107	0.0076	0.0125	0.0026	0.052	0.0095
Japanese BT	3355	2	0.0061	0.0017	0.0048	0.0013	0.001	0.0018	0.0017	0.0025	0.9616	0.0026	0.0017	0.0027	0.0028	0.0019	0.001	0.0019	0.0029
Japanese BT	3356	3	0.0293	0.0032	0.0062	0.0035	0.0023	0.0037	0.0037	0.006	0.8994	0.0032	0.0036	0.0069	0.0082	0.0042	0.0028	0.0056	0.0083
Japanese BT	3523	1	0.0032	0.0036	0.008	0.1776	0.0243	0.0097	0.0023	0.0055	0.694	0.009	0.0107	0.0058	0.0046	0.0114	0.0063	0.0058	0.0181
Japanese BT	3621	12	0.001	0.001	0.002	0.9746	0.001	0.001	0.0017	0.0028	0.001	0.0017	0.001	0.0012	0.0017	0.0028	0.001	0.003	0.0015
Japanese BT	3622	6	0.0011	0.001	0.001	0.9805	0.0011	0.001	0.001	0.0011	0.001	0.001	0.0028	0.0011	0.0017	0.0012	0.001	0.001	0.0014
Japanese BT	3673	0	0.0088	0.0025	0.0029	0.9363	0.0047	0.0081	0.003	0.0051	0.002	0.0028	0.0039	0.0029	0.002	0.002	0.0048	0.0041	0.0041
Japanese BT	3691	11	0.001	0.001	0.001	0.978	0.0023	0.002	0.001	0.0018	0.001	0.001	0.0011	0.0012	0.001	0.0013	0.0023	0.0015	0.0015
Japanese	3693	8	0.0043	0.001	0.0049	0.8894	0.0014	0.0027	0.0067	0.0491	0.0067	0.005	0.001	0.0062	0.0081	0.0033	0.002	0.002	0.0062

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline Population	ID No.	Missing Data	Groups																
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
BT																			
Japanese BT	4027	23	0.003	0.0056	0.0127	0.9234	0.0047	0.0103	0.0022	0.003	0.0046	0.0031	0.0056	0.004	0.005	0.0012	0.004	0.0041	0.0035
Japanese BT	4030	14	0.0019	0.0014	0.0019	0.9649	0.0032	0.004	0.0027	0.003	0.001	0.0021	0.002	0.0013	0.0015	0.002	0.003	0.002	0.0021
Japanese BT	4043	14	0.0024	0.0014	0.0028	0.9753	0.001	0.0011	0.001	0.0016	0.001	0.0016	0.001	0.0027	0.002	0.0011	0.0012	0.001	0.0018
Cornish Rex	2497	14	0.0042	0.002	0.0029	0.9274	0.0021	0.0053	0.0049	0.0094	0.0011	0.0028	0.0079	0.0073	0.0033	0.0037	0.0041	0.0084	0.0032
Cornish Rex	2863	8	0.0068	0.002	0.0077	0.925	0.0018	0.006	0.006	0.0074	0.0027	0.0038	0.0027	0.004	0.0057	0.0046	0.0032	0.0062	0.0044
Cornish Rex	2872	5	0.0026	0.0046	0.0042	0.9097	0.0056	0.003	0.0045	0.0052	0.0181	0.0089	0.0021	0.0045	0.0096	0.0023	0.0057	0.0047	0.0047
Cornish Rex	3283	16	0.0126	0.03	0.0028	0.7524	0.0036	0.002	0.0223	0.0107	0.0055	0.0402	0.0064	0.0072	0.0125	0.0416	0.0056	0.0255	0.0191
Cornish Rex	3306	0	0.0124	0.0132	0.0132	0.7913	0.0172	0.0064	0.0151	0.0077	0.0012	0.0246	0.0109	0.0351	0.0106	0.0036	0.0023	0.0094	0.0258
Cornish Rex	3931	12	0.0301	0.0025	0.0055	0.008	0.5654	0.0078	0.0166	0.0059	0.0065	0.0108	0.0034	0.0185	0.0032	0.0036	0.0066	0.0223	0.2832
Cornish Rex	3955	4	0.0039	0.0181	0.0056	0.8535	0.0047	0.0041	0.0063	0.0122	0.0055	0.0098	0.0016	0.0038	0.0084	0.0112	0.0358	0.0074	0.0081
Cornish Rex	3992	2	0.0021	0.001	0.001	0.9741	0.0018	0.0021	0.0015	0.0017	0.001	0.002	0.002	0.0015	0.0015	0.002	0.001	0.002	0.0017
Cornish Rex	5790	1	0.002	0.0023	0.0022	0.9484	0.0025	0.002	0.0046	0.0048	0.0032	0.0038	0.0017	0.0022	0.003	0.0044	0.0021	0.0075	0.0033
Cornish Rex	7031	3	0.0021	0.001	0.0028	0.9665	0.0018	0.002	0.0018	0.002	0.0012	0.0028	0.0035	0.002	0.003	0.0017	0.0015	0.0022	0.0021
Cornish Rex	7036	15	0.0053	0.0082	0.1478	0.0082	0.0026	0.0031	0.0135	0.008	0.0051	0.0287	0.0032	0.6506	0.0242	0.0132	0.0062	0.0663	0.0059
Cornish Rex	8528	2	0.0024	0.003	0.2225	0.001	0.0011	0.002	0.0092	0.005	0.001	0.0203	0.0025	0.6794	0.0339	0.005	0.0017	0.0035	0.0065
Cornish Rex	8529	6	0.0034	0.0197	0.1784	0.0015	0.0065	0.0213	0.0166	0.0034	0.0055	0.0052	0.0136	0.6886	0.006	0.0051	0.009	0.012	0.0042
Cornish Rex	8530	2	0.003	0.0029	0.1972	0.0014	0.001	0.0021	0.0042	0.002	0.001	0.0047	0.001	0.7671	0.0038	0.0022	0.001	0.0022	0.0032

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline Population	ID No.	Missing Data	Groups																
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Cornish Rex	8543	10	0.0069	0.0021	0.0046	0.0138	0.001	0.005	0.002	0.8884	0.0044	0.037	0.0017	0.0057	0.0055	0.0034	0.0014	0.0145	0.0026
Ragdoll	7429	4	0.0035	0.0033	0.1846	0.0064	0.001	0.0034	0.0098	0.0119	0.0026	0.0084	0.002	0.7138	0.0101	0.0083	0.0034	0.0075	0.02
Ragdoll	8362	2	0.0059	0.0021	0.1897	0.0033	0.0018	0.0031	0.0024	0.0092	0.0012	0.0054	0.0043	0.7526	0.0041	0.0033	0.0013	0.0057	0.0046
Ragdoll	8366	0	0.0072	0.1174	0.0959	0.0013	0.0014	0.0023	0.003	0.0026	0.0025	0.0052	0.003	0.5522	0.1919	0.003	0.001	0.0031	0.007
Ragdoll	8367	2	0.0059	0.0028	0.1976	0.0022	0.0043	0.0029	0.0078	0.0042	0.0011	0.0267	0.0028	0.7227	0.0049	0.0049	0.001	0.0041	0.004
Ragdoll	8368	4	0.0035	0.0147	0.1672	0.0012	0.0051	0.0111	0.004	0.0029	0.0027	0.0047	0.0045	0.7554	0.0079	0.0037	0.0022	0.0037	0.0055
Ragdoll	8372	2	0.0402	0.021	0.1437	0.002	0.0033	0.0063	0.0138	0.0148	0.0028	0.0163	0.0167	0.571	0.1194	0.0059	0.0054	0.0062	0.0112
Ragdoll	8377	3	0.0132	0.0058	0.0606	0.0084	0.0039	0.018	0.008	0.0067	0.0018	0.0082	0.0054	0.5088	0.2876	0.0196	0.0061	0.0047	0.0332
Ragdoll	9292	0	0.0051	0.0028	0.1696	0.0022	0.0013	0.0053	0.0024	0.0046	0.0038	0.006	0.0025	0.7707	0.0028	0.0089	0.0024	0.0023	0.0073
Ragdoll	9295	0	0.0045	0.002	0.0046	0.0015	0.0013	0.002	0.0055	0.0069	0.001	0.0066	0.0024	0.0034	0.9344	0.0142	0.002	0.0039	0.0038
Ragdoll	9299	1	0.0027	0.0062	0.0081	0.001	0.0028	0.0017	0.004	0.002	0.0021	0.0056	0.0079	0.0064	0.9385	0.0029	0.001	0.002	0.0051
Ragdoll	9300	0	0.0039	0.0298	0.0234	0.1373	0.0021	0.0043	0.0089	0.0129	0.001	0.3176	0.0094	0.0849	0.3055	0.0124	0.0106	0.0184	0.0175
Ragdoll	9301	2	0.0226	0.1856	0.0085	0.1741	0.0082	0.003	0.0082	0.0167	0.002	0.0135	0.0061	0.0203	0.4666	0.0228	0.0091	0.0157	0.0171
Ragdoll	9302	2	0.003	0.0023	0.0148	0.001	0.001	0.0027	0.0111	0.0089	0.0021	0.1519	0.002	0.038	0.6837	0.0467	0.0013	0.0044	0.025
Ragdoll	9304	2	0.0125	0.003	0.0083	0.0011	0.003	0.0142	0.0049	0.0067	0.002	0.0268	0.002	0.0047	0.8808	0.0135	0.0038	0.0036	0.0091
Ragdoll	9305	2	0.0136	0.0032	0.0076	0.0027	0.002	0.0046	0.0143	0.0243	0.0037	0.0036	0.0025	0.0051	0.8859	0.0101	0.0021	0.0083	0.0065
Maine Coon	2950	1	0.0041	0.0033	0.0417	0.0174	0.0048	0.0079	0.0234	0.0356	0.0061	0.0324	0.0051	0.0254	0.6881	0.0283	0.0035	0.0457	0.0271
Maine Coon	2959	2	0.0642	0.005	0.0807	0.0107	0.0049	0.0049	0.0179	0.0069	0.0341	0.0156	0.0028	0.0715	0.6367	0.0136	0.0046	0.0105	0.0155
Maine Coon	3304	9	0.0088	0.002	0.0151	0.0125	0.0046	0.0102	0.0305	0.0696	0.0035	0.0272	0.002	0.0108	0.7572	0.0116	0.0037	0.0158	0.0148
Maine Coon	3311	6	0.0035	0.0027	0.0069	0.0058	0.0021	0.005	0.0027	0.0067	0.0083	0.0052	0.002	0.0046	0.9005	0.0148	0.0022	0.0039	0.0231
Maine Coon	3495	3	0.0221	0.006	0.1272	0.0179	0.0087	0.0033	0.0572	0.0087	0.002	0.0563	0.0139	0.1512	0.4019	0.0177	0.0072	0.0685	0.0303
Maine Coon	3925	2	0.002	0.002	0.0049	0.0401	0.0084	0.0036	0.0107	0.0037	0.0052	0.003	0.0268	0.0037	0.8522	0.0074	0.0056	0.0103	0.0105
Maine Coon	3941	2	0.008	0.0075	0.0086	0.0021	0.0043	0.006	0.0066	0.0036	0.0027	0.0055	0.0027	0.0108	0.8893	0.0213	0.0032	0.0039	0.0139
Maine Coon	9198	14	0.0021	0.0016	0.0082	0.002	0.001	0.002	0.0066	0.0052	0.0022	0.0591	0.001	0.0047	0.8941	0.0011	0.001	0.002	0.0061
Maine Coon	9775	2	0.0042	0.0091	0.0186	0.028	0.0035	0.0075	0.0223	0.0052	0.001	0.0329	0.0032	0.0086	0.8173	0.0145	0.0025	0.008	0.0135

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline Population	ID No.	Missing Data	Groups																
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Maine Coon	10662	16	0.0047	0.0044	0.002	0.001	0.0018	0.0017	0.0034	0.0069	0.2196	0.0031	0.0023	0.0028	0.6859	0.0049	0.002	0.0029	0.0506
Maine Coon	11544	8	0.0036	0.0041	0.0079	0.0025	0.0026	0.0028	0.0173	0.0113	0.002	0.0074	0.0034	0.0044	0.9072	0.011	0.0034	0.0034	0.0057
Maine Coon	217	14	0.0534	0.005	0.0128	0.1373	0.0072	0.002	0.0071	0.0107	0.0036	0.0103	0.0021	0.0139	0.3961	0.161	0.0107	0.0066	0.1601
Maine Coon	218	3	0.0027	0.0258	0.0107	0.0061	0.0018	0.0011	0.0054	0.0536	0.0237	0.0096	0.003	0.0071	0.5809	0.0884	0.0025	0.0064	0.1711
Maine Coon	219	9	0.0044	0.0243	0.0025	0.0111	0.0033	0.0057	0.0071	0.0067	0.0027	0.0096	0.0102	0.004	0.648	0.0881	0.0023	0.0044	0.1657
Maine Coon	220	1	0.062	0.1609	0.012	0.0244	0.0057	0.0119	0.0034	0.0882	0.0038	0.0109	0.0313	0.0126	0.1559	0.2167	0.0036	0.0021	0.1946
Maine Coon	221	8	0.004	0.0133	0.011	0.1828	0.0124	0.0075	0.0034	0.0125	0.1474	0.0048	0.0109	0.0093	0.3585	0.0705	0.002	0.0109	0.1387
Maine Coon	222	5	0.0061	0.0081	0.0054	0.0496	0.0206	0.0036	0.0094	0.0155	0.002	0.019	0.0236	0.0065	0.5996	0.0772	0.0039	0.0039	0.146
Maine Coon	223	20	0.0045	0.0031	0.0045	0.0054	0.0056	0.0059	0.0212	0.1216	0.0018	0.5962	0.0023	0.0044	0.0321	0.0775	0.0037	0.0119	0.0983
Maine Coon	224	6	0.0032	0.0275	0.0028	0.0152	0.0035	0.0018	0.0043	0.0078	0.002	0.0096	0.0071	0.0069	0.6352	0.1041	0.0038	0.0034	0.1618
Abyssinian	110	13	0.0709	0.01	0.041	0.0175	0.0272	0.0456	0.0126	0.0118	0.0042	0.0088	0.0875	0.0571	0.1872	0.2001	0.0201	0.0051	0.1932
Abyssinian	111	26	0.0031	0.0401	0.0095	0.0534	0.0012	0.0055	0.0028	0.02	0.0071	0.0184	0.0018	0.0209	0.4782	0.116	0.0016	0.0026	0.2179
Abyssinian	112	10	0.0036	0.0064	0.0054	0.0068	0.0077	0.0258	0.0035	0.0057	0.0027	0.007	0.004	0.0936	0.4985	0.1167	0.0097	0.0027	0.2003
Abyssinian	113	10	0.0051	0.0088	0.0081	0.0027	0.0034	0.0023	0.0037	0.0137	0.0222	0.0075	0.0017	0.0176	0.4555	0.2409	0.0036	0.0034	0.1997
Abyssinian	114	1	0.0069	0.0056	0.0041	0.0065	0.0058	0.0085	0.0046	0.0051	0.0963	0.0047	0.0042	0.0076	0.5434	0.0907	0.0113	0.0039	0.1909
Abyssinian	115	18	0.015	0.0279	0.0223	0.004	0.0109	0.0054	0.0042	0.0324	0.003	0.0899	0.01	0.0574	0.0087	0.0077	0.0147	0.6734	0.013
Abyssinian	116	15	0.0029	0.0072	0.0237	0.0019	0.0027	0.0088	0.005	0.0044	0.0179	0.0079	0.002	0.01	0.0065	0.005	0.0063	0.8827	0.0051
Abyssinian	117	5	0.0025	0.0018	0.002	0.0018	0.001	0.001	0.002	0.0026	0.0018	0.0019	0.0012	0.002	0.0018	0.0039	0.001	0.9701	0.0016
Abyssinian	118	4	0.0023	0.001	0.0011	0.0042	0.0022	0.0068	0.0046	0.0049	0.0011	0.0024	0.0021	0.0012	0.001	0.0049	0.0531	0.9052	0.0019
Abyssinian	119	5	0.0609	0.0099	0.0263	0.0043	0.0555	0.0154	0.0129	0.007	0.0033	0.0498	0.0337	0.0114	0.0106	0.0103	0.0093	0.6646	0.0149
Abyssinian	120	10	0.0098	0.0054	0.0051	0.0052	0.0104	0.1715	0.0071	0.0035	0.0091	0.0044	0.0174	0.0068	0.0031	0.0036	0.0015	0.73	0.0062
Abyssinian	121	2	0.0044	0.002	0.0083	0.0078	0.002	0.002	0.0059	0.0111	0.002	0.0105	0.002	0.0227	0.0036	0.0038	0.0023	0.9031	0.0064
Abyssinian	122	4	0.0048	0.0033	0.0021	0.0057	0.0157	0.0728	0.0187	0.0112	0.001	0.0077	0.0218	0.0025	0.002	0.0097	0.003	0.8142	0.0038
Abyssinian	123	18	0.016	0.01	0.0047	0.002	0.0686	0.0075	0.0511	0.0213	0.0053	0.026	0.0051	0.0213	0.0277	0.0106	0.0097	0.6973	0.0157
Abyssinian	6934	9	0.0028	0.0032	0.0069	0.0048	0.0035	0.008	0.005	0.0069	0.0016	0.0166	0.0968	0.0036	0.0062	0.0057	0.0044	0.821	0.003

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline Population	ID No.	Missing Data	Groups																
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Siberian	3273	10	0.0026	0.0125	0.0022	0.0033	0.0058	0.1109	0.0121	0.0111	0.0076	0.0022	0.002	0.0054	0.0028	0.0035	0.0047	0.8075	0.0038
Siberian	4593	6	0.002	0.0102	0.0053	0.0037	0.0031	0.002	0.0094	0.0068	0.0021	0.0052	0.0035	0.0042	0.0032	0.004	0.003	0.9295	0.0028
Siberian	4829	6	0.0053	0.002	0.0046	0.0029	0.0017	0.0032	0.0104	0.0073	0.002	0.02	0.0127	0.011	0.0077	0.0039	0.002	0.9003	0.003
Siberian	4928	6	0.0188	0.008	0.1093	0.0067	0.0264	0.0181	0.0125	0.0057	0.0034	0.0221	0.0127	0.1924	0.0034	0.0104	0.002	0.5319	0.0161
Siberian	4930	14	0.0446	0.006	0.0065	0.002	0.0033	0.0031	0.0036	0.0058	0.0041	0.0031	0.0016	0.0034	0.0071	0.0048	0.0093	0.8871	0.0047
Siberian	5101	9	0.0019	0.0058	0.0039	0.002	0.001	0.0019	0.0054	0.0027	0.002	0.0034	0.0081	0.004	0.009	0.0032	0.0027	0.9403	0.0027
Siberian	5105	2	0.0043	0.0077	0.0192	0.0121	0.0069	0.0091	0.0123	0.0085	0.0038	0.0077	0.0114	0.0095	0.0064	0.0104	0.0272	0.8356	0.0079
Siberian	5107	6	0.0046	0.0035	0.0037	0.0074	0.1061	0.0989	0.0121	0.0067	0.0016	0.0057	0.0687	0.0022	0.002	0.0032	0.0051	0.6631	0.0055
Siberian	5110	9	0.0601	0.0042	0.2709	0.0029	0.0016	0.0923	0.0033	0.0052	0.0021	0.0294	0.002	0.2111	0.0045	0.0047	0.0056	0.2615	0.0386
Siberian	5118	6	0.0041	0.0012	0.8928	0.0045	0.003	0.0022	0.0049	0.0063	0.0043	0.0033	0.0073	0.0037	0.0023	0.0525	0.0012	0.003	0.0034
Siberian	5120	18	0.0175	0.0125	0.8265	0.0026	0.0019	0.0044	0.0124	0.0084	0.0037	0.012	0.0029	0.0488	0.0159	0.0029	0.002	0.0198	0.0059
Siberian	5632	12	0.0041	0.0084	0.6525	0.0155	0.0038	0.0165	0.0047	0.0039	0.0164	0.0346	0.0076	0.1406	0.0655	0.0034	0.0041	0.0106	0.0077
Siberian	6474	18	0.0033	0.0037	0.8813	0.0037	0.0011	0.0021	0.0028	0.0059	0.0015	0.0065	0.002	0.0108	0.0093	0.0138	0.002	0.0455	0.0046
Siberian	11562	2	0.0066	0.0021	0.7764	0.002	0.0146	0.0046	0.0147	0.0324	0.0307	0.043	0.0075	0.0171	0.0078	0.0077	0.0071	0.0073	0.0184
Siberian	11582	10	0.0083	0.0034	0.8619	0.0091	0.0021	0.0048	0.0033	0.039	0.0051	0.0078	0.0032	0.0109	0.0151	0.0062	0.0037	0.0064	0.0097
Siberian	11559	24	0.0029	0.0021	0.9554	0.0011	0.001	0.0022	0.0034	0.004	0.0026	0.0039	0.0016	0.0034	0.0031	0.0073	0.001	0.0024	0.0026
Siberian	11560	1	0.0574	0.0134	0.5024	0.0201	0.021	0.008	0.0077	0.0268	0.0747	0.1203	0.0138	0.0523	0.0145	0.009	0.0127	0.0066	0.0391
Norwegian FC	2942	2	0.0037	0.0055	0.8857	0.0045	0.0023	0.0015	0.0051	0.011	0.004	0.0109	0.0019	0.029	0.0113	0.0034	0.0046	0.0059	0.0097
Norwegian FC	3610	1	0.0047	0.0128	0.9192	0.0018	0.0019	0.0024	0.0137	0.0054	0.0012	0.0058	0.0025	0.0068	0.0096	0.0031	0.0012	0.0045	0.0034
Norwegian FC	3611	1	0.0189	0.0207	0.8418	0.0025	0.0023	0.0046	0.0075	0.0036	0.0017	0.0094	0.0036	0.0248	0.0053	0.012	0.002	0.0356	0.0037
Norwegian FC	3612	10	0.004	0.0076	0.9207	0.0052	0.0018	0.002	0.002	0.0024	0.0047	0.0065	0.001	0.0128	0.0144	0.0021	0.0048	0.0027	0.0053
Norwegian FC	3617	1	0.0072	0.0024	0.3296	0.0089	0.0128	0.0027	0.0114	0.009	0.0075	0.3362	0.0073	0.0719	0.0134	0.0385	0.0118	0.0059	0.1235
Norwegian FC	3661	2	0.0027	0.0022	0.9535	0.003	0.0019	0.002	0.0044	0.0028	0.0031	0.0029	0.0019	0.0029	0.0028	0.0051	0.0033	0.0025	0.003
Norwegian FC	4815	0	0.0277	0.0148	0.0825	0.0287	0.0057	0.0475	0.0536	0.1629	0.0088	0.1034	0.0073	0.0381	0.085	0.1571	0.0171	0.0787	0.0809
Norwegian FC	4816	0	0.0029	0.0025	0.5885	0.0041	0.002	0.013	0.0123	0.0038	0.0026	0.0809	0.0034	0.1778	0.005	0.0033	0.0048	0.0617	0.0314
Norwegian FC	6004	2	0.1582	0.0155	0.4053	0.0133	0.0316	0.002	0.0185	0.0284	0.0547	0.0687	0.0162	0.037	0.0233	0.0176	0.0131	0.0324	0.0644

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline	ID	Missing	Groups																
Population	No.	Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Norwegian FC	6932	8	0.0414	0.0475	0.6597	0.0015	0.0023	0.0054	0.0117	0.0096	0.1112	0.0152	0.002	0.0065	0.0059	0.0342	0.0085	0.0309	0.0066
Norwegian FC	9321	7	0.007	0.0068	0.7523	0.005	0.0028	0.0036	0.0058	0.0099	0.013	0.1302	0.0032	0.0248	0.0086	0.0031	0.002	0.009	0.0128
Norwegian FC	10367	0	0.0021	0.0042	0.1867	0.0035	0.002	0.0011	0.0071	0.003	0.0026	0.0129	0.0036	0.7461	0.0053	0.0107	0.0025	0.0024	0.0042
Norwegian FC	10682	18	0.0075	0.002	0.3517	0.0028	0.0046	0.0031	0.0078	0.0359	0.0046	0.2105	0.0095	0.1456	0.0164	0.0196	0.0081	0.0033	0.1671
Norwegian FC	11548	11	0.0031	0.0014	0.003	0.0019	0.001	0.0027	0.002	0.9126	0.0042	0.0426	0.0015	0.0031	0.0041	0.0039	0.001	0.0095	0.0024
Norwegian FC	242	8	0.0056	0.0137	0.0239	0.0149	0.0031	0.0072	0.0096	0.396	0.0014	0.1297	0.0153	0.0735	0.147	0.0118	0.0067	0.0047	0.1359
Manx	2928	18	0.0041	0.0073	0.0409	0.002	0.002	0.0254	0.0123	0.23	0.0055	0.3063	0.0021	0.0588	0.1812	0.0041	0.0028	0.0121	0.1031
Manx	2980	9	0.0179	0.0211	0.1271	0.0136	0.0062	0.0156	0.016	0.042	0.0067	0.2808	0.0096	0.202	0.0118	0.0233	0.007	0.0075	0.1918
Manx	3926	19	0.0185	0.0029	0.3123	0.0089	0.001	0.0028	0.0046	0.1822	0.003	0.1788	0.001	0.0926	0.0051	0.0099	0.001	0.0029	0.1725
Manx	4378	1	0.0097	0.0176	0.1723	0.0035	0.0035	0.0039	0.0051	0.0076	0.0034	0.45	0.0042	0.089	0.0512	0.0037	0.0044	0.0028	0.1681
Manx	5757	1	0.0052	0.0105	0.232	0.0023	0.0019	0.0066	0.0085	0.0088	0.0106	0.4071	0.0034	0.1137	0.0038	0.0103	0.0018	0.0053	0.1682
Manx	6294	0	0.0072	0.0036	0.0713	0.0036	0.0013	0.002	0.0131	0.0049	0.003	0.5938	0.0021	0.1068	0.0116	0.0024	0.0033	0.0041	0.1659
Manx	6296	1	0.0071	0.0151	0.0902	0.0028	0.0023	0.0035	0.033	0.0187	0.0037	0.4694	0.0052	0.1305	0.0307	0.0072	0.002	0.0038	0.1748
Manx	6299	3	0.0039	0.0081	0.2136	0.0118	0.0014	0.0084	0.0056	0.2642	0.0094	0.1142	0.0024	0.1602	0.009	0.0031	0.0025	0.0032	0.1791
Manx	7079	3	0.0021	0.0051	0.0863	0.0041	0.0019	0.001	0.0069	0.0087	0.003	0.6472	0.0061	0.0799	0.0094	0.0039	0.0018	0.0065	0.1261
Manx	7082	0	0.0039	0.0041	0.2686	0.0016	0.0015	0.0016	0.0041	0.0052	0.0039	0.36	0.002	0.159	0.0097	0.0054	0.001	0.0056	0.1629
Manx	7083	0	0.0027	0.0074	0.0887	0.0019	0.0022	0.0032	0.0256	0.0067	0.0022	0.5248	0.0069	0.1002	0.0267	0.0037	0.0041	0.0202	0.1728
Manx	7105	8	0.0142	0.0023	0.0435	0.0106	0.0591	0.0126	0.6295	0.0726	0.0024	0.0362	0.0127	0.0242	0.0097	0.0108	0.0072	0.0229	0.0295
Manx	7108	5	0.0045	0.006	0.0212	0.0033	0.0031	0.012	0.2192	0.5462	0.0015	0.0203	0.0069	0.0344	0.003	0.0561	0.0047	0.0101	0.0473
Manx	7112	17	0.0146	0.0067	0.0712	0.0059	0.001	0.003	0.0072	0.0888	0.0091	0.4508	0.001	0.1166	0.0185	0.0154	0.0039	0.0449	0.1414
Manx	7708	0	0.0169	0.003	0.0062	0.0106	0.002	0.002	0.0078	0.0485	0.0028	0.0244	0.0022	0.0055	0.821	0.0264	0.0039	0.0047	0.012
Manx	9084	2	0.0229	0.007	0.0111	0.0202	0.0074	0.0144	0.0327	0.0062	0.0106	0.2454	0.0048	0.0199	0.4794	0.0184	0.0632	0.0158	0.0207
Manx	9091	1	0.0048	0.331	0.0181	0.0023	0.0037	0.014	0.1974	0.045	0.0041	0.0283	0.0029	0.0613	0.2251	0.0251	0.0031	0.003	0.0309
Egyptian Mau	1812	0	0.1072	0.017	0.009	0.0031	0.0189	0.003	0.0834	0.0363	0.0033	0.0102	0.0073	0.0141	0.625	0.0273	0.0061	0.0061	0.0226
Egyptian Mau	2431	0	0.0165	0.0103	0.0169	0.0099	0.0021	0.0191	0.0094	0.0223	0.0038	0.0368	0.003	0.0568	0.7314	0.005	0.0037	0.0179	0.0351
Egyptian Mau	2433	1	0.0038	0.0048	0.0051	0.0011	0.001	0.002	0.0088	0.0115	0.0017	0.01	0.0027	0.0144	0.8833	0.0126	0.0011	0.0127	0.0233

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline Population	ID No.	Missing Data	Groups																
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Egyptian Mau	3331	0	0.0073	0.0708	0.0036	0.007	0.0184	0.0054	0.0382	0.0123	0.0019	0.0068	0.0084	0.0048	0.746	0.0016	0.0451	0.0071	0.0154
Egyptian Mau	3332	0	0.0057	0.0179	0.0071	0.005	0.0256	0.0055	0.0198	0.0138	0.0032	0.0285	0.0107	0.0159	0.7932	0.0084	0.0133	0.0113	0.015
Egyptian Mau	5545	6	0.0065	0.0175	0.0144	0.0032	0.0027	0.0026	0.0054	0.0167	0.002	0.0058	0.0019	0.0172	0.8843	0.0048	0.0029	0.0073	0.0048
Egyptian Mau	5553	11	0.0502	0.0171	0.0193	0.0057	0.0024	0.0046	0.006	0.0092	0.0019	0.0134	0.004	0.0208	0.7785	0.0162	0.002	0.0185	0.0302
Egyptian Mau	5567	0	0.0032	0.0046	0.0261	0.0288	0.0336	0.0037	0.0841	0.0309	0.006	0.0142	0.0035	0.0215	0.6683	0.004	0.0136	0.0196	0.0344
Egyptian Mau	5568	8	0.0236	0.0063	0.016	0.0054	0.002	0.0183	0.1136	0.0176	0.0032	0.063	0.0054	0.0422	0.6282	0.0059	0.0023	0.0133	0.0337
Egyptian Mau	7475	0	0.0115	0.0672	0.0046	0.0062	0.0317	0.0238	0.0303	0.0217	0.0024	0.0079	0.0203	0.0287	0.7119	0.0052	0.0051	0.0116	0.0099
Egyptian Mau	7476	0	0.0036	0.0064	0.0037	0.0039	0.0029	0.002	0.0066	0.004	0.0023	0.0053	0.0036	0.0034	0.8813	0.0029	0.0036	0.0615	0.0031
Egyptian Mau	7479	0	0.003	0.0076	0.0043	0.0077	0.0056	0.0029	0.2979	0.0047	0.002	0.0047	0.006	0.0035	0.6308	0.0031	0.0033	0.0098	0.0031
Egyptian Mau	7480	2	0.005	0.0095	0.002	0.002	0.021	0.0071	0.0036	0.0029	0.0018	0.0032	0.0319	0.0024	0.8849	0.0016	0.0028	0.0041	0.0142
Egyptian Mau	11410	5	0.002	0.0123	0.0833	0.004	0.0073	0.001	0.0036	0.003	0.0217	0.0112	0.0019	0.0195	0.8121	0.004	0.0015	0.0041	0.0076
Turk. Angora	607	1	0.0123	0.0055	0.0131	0.0043	0.0049	0.01	0.0625	0.0808	0.002	0.033	0.0049	0.0172	0.6397	0.0066	0.0076	0.0825	0.0132
Turk. Angora	1832	5	0.0021	0.0333	0.0048	0.0023	0.001	0.002	0.0074	0.0044	0.001	0.0079	0.002	0.0025	0.9204	0.0031	0.001	0.0027	0.0021
Turk. Angora	1845	6	0.0101	0.015	0.0083	0.001	0.0023	0.0024	0.0059	0.0128	0.0097	0.0224	0.0024	0.0194	0.7297	0.0208	0.0021	0.1201	0.0156
Turk. Angora	2848	0	0.0269	0.0038	0.0064	0.0018	0.0047	0.008	0.0878	0.0112	0.0239	0.0072	0.0054	0.0089	0.7786	0.0076	0.0031	0.004	0.0106
Turk. Angora	2862	4	0.0041	0.0061	0.0045	0.001	0.0027	0.0021	0.0031	0.0023	0.0019	0.0027	0.0016	0.0082	0.9461	0.0037	0.0047	0.001	0.0041
Turk. Angora	5552	1	0.0074	0.0031	0.0087	0.003	0.0055	0.0043	0.0085	0.0383	0.0035	0.0172	0.0021	0.0073	0.7871	0.0077	0.03	0.0581	0.0082
Turk.	5563	0	0.0063	0.0055	0.0027	0.0029	0.0031	0.0023	0.0046	0.0064	0.0031	0.0041	0.0072	0.005	0.929	0.0051	0.002	0.0044	0.0063

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline Population	ID No.	Missing Data	Groups																
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Angora																			
Turk. Angora	5564	10	0.0049	0.0019	0.0028	0.0057	0.0014	0.002	0.0033	0.0057	0.002	0.0042	0.0029	0.0035	0.9505	0.0024	0.001	0.0022	0.0036
Turk. Angora	6350	5	0.0318	0.0117	0.0086	0.004	0.0103	0.0799	0.087	0.0112	0.0051	0.0229	0.0123	0.007	0.6462	0.0047	0.0121	0.0087	0.0364
Turk. Angora	9541	8	0.0064	0.0278	0.0066	0.0024	0.0194	0.0021	0.0854	0.0181	0.0046	0.0028	0.0049	0.0071	0.7741	0.0039	0.019	0.0042	0.0111
Turk. Angora	9542	1	0.003	0.0074	0.0029	0.002	0.0063	0.023	0.0289	0.0351	0.0028	0.0224	0.0055	0.0156	0.7847	0.0042	0.0066	0.0415	0.0081
Turk. Angora	9584	1	0.0173	0.0346	0.0453	0.0024	0.0032	0.0038	0.0736	0.0299	0.0044	0.0689	0.0024	0.0811	0.4471	0.0129	0.0032	0.1383	0.0316
Turk. Angora	9586	2	0.0035	0.0074	0.0163	0.0052	0.0021	0.0014	0.0244	0.0043	0.0024	0.0055	0.0038	0.0671	0.837	0.0047	0.003	0.0062	0.0057
Turk. Angora	9608	2	0.0032	0.0648	0.0072	0.0046	0.0039	0.005	0.006	0.0127	0.0016	0.0089	0.0036	0.0065	0.8319	0.0072	0.0197	0.0057	0.0075
Turk. Angora	9609	10	0.0139	0.0308	0.0048	0.0022	0.0031	0.021	0.0041	0.0252	0.005	0.0154	0.0056	0.0068	0.8347	0.0043	0.0052	0.0115	0.0063
Turk. Angora	9610	7	0.0034	0.0128	0.0034	0.001	0.0187	0.0078	0.0065	0.0096	0.0123	0.006	0.0085	0.0052	0.8537	0.0102	0.011	0.0033	0.0266
Turk. Angora	9611	2	0.02	0.0027	0.0063	0.0136	0.0012	0.008	0.0077	0.0234	0.0019	0.1127	0.0028	0.0121	0.7586	0.0039	0.0089	0.011	0.0053
Turk. Angora	9612	9	0.0049	0.002	0.0055	0.0422	0.0029	0.0046	0.0404	0.0304	0.0025	0.7876	0.0061	0.0044	0.0042	0.0079	0.0031	0.0475	0.0037
Turk. Angora	9613	1	0.0022	0.0145	0.0199	0.0112	0.0122	0.0057	0.0052	0.0037	0.0036	0.8433	0.0266	0.0092	0.0114	0.0062	0.0099	0.0051	0.0101
Turk. Angora	9614	0	0.0294	0.0139	0.0048	0.0046	0.0287	0.0208	0.0258	0.0084	0.0019	0.766	0.0355	0.0125	0.0057	0.0178	0.0026	0.0111	0.0105
Turk. Angora	9615	2	0.0076	0.0043	0.0036	0.0051	0.0111	0.0038	0.0035	0.0033	0.0018	0.8982	0.018	0.0048	0.0037	0.0033	0.0159	0.0032	0.0088
Turkish Van	1789	6	0.0059	0.0062	0.0181	0.0032	0.0022	0.0025	0.0337	0.0081	0.009	0.8286	0.0034	0.0064	0.018	0.0032	0.0025	0.0406	0.0084
Turkish Van	3013	1	0.006	0.0121	0.0043	0.0308	0.0044	0.0035	0.0111	0.005	0.0012	0.852	0.0031	0.006	0.0058	0.0112	0.0059	0.0314	0.0061
Turkish Van	3056	2	0.0049	0.017	0.0059	0.0028	0.0037	0.0061	0.0042	0.0042	0.0028	0.8905	0.0165	0.0096	0.0066	0.0077	0.0038	0.0052	0.0085

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline	ID	Missing	Groups																
Population	No.	Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Turkish Van	4090	7	0.0259	0.0036	0.0068	0.0089	0.0169	0.0053	0.0051	0.0084	0.0019	0.787	0.0808	0.0094	0.0064	0.0034	0.0114	0.0044	0.0144
Turkish Van	7662	2	0.0044	0.0022	0.0397	0.0344	0.0037	0.0079	0.0075	0.0077	0.001	0.8116	0.0339	0.0197	0.0045	0.0039	0.0076	0.0066	0.0037
Turkish Van	7663	3	0.0046	0.0051	0.0026	0.0021	0.0044	0.0074	0.0054	0.0055	0.0015	0.9341	0.003	0.0058	0.0036	0.0033	0.0024	0.0041	0.0051
Turkish Van	7666	1	0.0023	0.005	0.0307	0.0021	0.0172	0.0031	0.014	0.01	0.0029	0.6741	0.17	0.0051	0.0039	0.0209	0.005	0.0285	0.0051
Turkish Van	7667	17	0.0174	0.0049	0.0862	0.1776	0.0035	0.005	0.0044	0.0469	0.0017	0.6215	0.0019	0.0079	0.004	0.0037	0.0025	0.007	0.0038
Turkish Van	9322	4	0.0055	0.0101	0.0184	0.002	0.201	0.0143	0.0041	0.004	0.0072	0.6373	0.0036	0.009	0.0439	0.0055	0.0088	0.005	0.0202
Turkish Van	9535	6	0.002	0.0217	0.0059	0.0026	0.002	0.0017	0.0037	0.0047	0.0027	0.9194	0.0029	0.0095	0.0037	0.0038	0.002	0.0082	0.0036
Turkish Van	9538	4	0.0105	0.0042	0.0586	0.002	0.0148	0.0033	0.0152	0.0041	0.0175	0.7686	0.0022	0.0064	0.0047	0.0035	0.0493	0.0161	0.019
Turkish Van	9539	2	0.0061	0.002	0.0134	0.0032	0.0018	0.004	0.0092	0.0052	0.0018	0.8995	0.0021	0.0096	0.0112	0.0037	0.0029	0.0167	0.0076
Turkish Van	9543	6	0.0047	0.0047	0.0114	0.0095	0.0154	0.0137	0.0179	0.0112	0.0022	0.8275	0.0191	0.0193	0.0097	0.004	0.0035	0.0191	0.0072
Turkish Van	9563	12	0.0055	0.0043	0.0043	0.0745	0.1379	0.0035	0.0125	0.4148	0.0053	0.0096	0.0038	0.0043	0.0039	0.2531	0.049	0.0062	0.0075
Turkish Van	9564	0	0.0069	0.0049	0.0764	0.01	0.0354	0.0123	0.0251	0.199	0.0048	0.3185	0.0108	0.0908	0.0052	0.0221	0.0028	0.0037	0.1713
Turkish Van	9573	2	0.046	0.0028	0.087	0.0052	0.0023	0.0031	0.0139	0.099	0.0039	0.2677	0.0021	0.1381	0.0025	0.0822	0.0019	0.0627	0.1797
Turkish Van	9574	6	0.0057	0.0228	0.0766	0.0064	0.0025	0.028	0.0801	0.2059	0.0027	0.0873	0.0039	0.2216	0.0119	0.0282	0.0042	0.0332	0.179
Turkish Van	9575	10	0.0254	0.0032	0.007	0.0125	0.0047	0.0118	0.7715	0.02	0.0047	0.0294	0.0139	0.0285	0.0038	0.0253	0.0047	0.004	0.0295
Turkish Van	9576	9	0.0093	0.0097	0.0116	0.0106	0.0037	0.0389	0.1459	0.4242	0.0014	0.0252	0.0067	0.0886	0.0074	0.0969	0.0032	0.0154	0.1013
Turkish Van	9581	12	0.0399	0.0051	0.0998	0.0062	0.0073	0.0495	0.0086	0.2752	0.0063	0.0491	0.0023	0.0861	0.0738	0.0262	0.0172	0.1126	0.1347
Bengal	2518	10	0.0252	0.0014	0.0094	0.0101	0.0029	0.0186	0.033	0.4085	0.0023	0.2062	0.002	0.0851	0.0119	0.0084	0.0054	0.0157	0.1539

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline Population	ID No.	Missing Data	Groups																
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Bengal	3455	3	0.0111	0.0068	0.0243	0.002	0.0082	0.0024	0.3067	0.1636	0.1962	0.0546	0.004	0.0082	0.0207	0.1638	0.0072	0.0052	0.015
Bengal	3478	18	0.0132	0.0051	0.0248	0.0701	0.0048	0.026	0.0113	0.6078	0.0202	0.0643	0.0057	0.0446	0.0064	0.0052	0.0059	0.0153	0.0694
Bengal	3522	12	0.0073	0.0028	0.1736	0.0035	0.0017	0.0092	0.0042	0.012	0.0025	0.4492	0.002	0.1066	0.0034	0.0287	0.002	0.0046	0.1867
Bengal	3541	1	0.0224	0.0054	0.0121	0.0429	0.0397	0.0037	0.2309	0.263	0.0212	0.0592	0.0197	0.0701	0.0095	0.0098	0.0459	0.0221	0.1224
Bengal	3550	0	0.0182	0.0194	0.0483	0.0036	0.0095	0.0048	0.0395	0.1681	0.0178	0.0715	0.0513	0.2959	0.01	0.0168	0.0046	0.0594	0.1613
Bengal	6678	2	0.0182	0.0042	0.1058	0.0067	0.001	0.0029	0.022	0.2968	0.0027	0.1273	0.0011	0.1697	0.0131	0.0093	0.0024	0.0113	0.2055
Bengal	6899	2	0.0139	0.0085	0.0159	0.0037	0.0039	0.0031	0.5038	0.1083	0.1169	0.0155	0.0033	0.0669	0.0119	0.0273	0.0017	0.0222	0.0733
Bengal	6902	12	0.6799	0.0038	0.0087	0.0053	0.0054	0.0143	0.0251	0.0144	0.0033	0.0067	0.0416	0.0672	0.0059	0.0104	0.0026	0.0389	0.0665
Bengal	6907	6	0.6325	0.0039	0.0069	0.0069	0.0055	0.0014	0.0071	0.0155	0.0481	0.0168	0.0042	0.1132	0.0162	0.0068	0.011	0.0088	0.0953
Bengal	8399	6	0.6618	0.0053	0.0467	0.002	0.0022	0.0061	0.0064	0.023	0.0029	0.0086	0.0031	0.0979	0.0116	0.0296	0.0012	0.0074	0.0842
Bengal	8400	6	0.7636	0.002	0.0027	0.0015	0.001	0.0019	0.0046	0.0028	0.0031	0.0034	0.003	0.0959	0.0073	0.0055	0.0012	0.0035	0.097
Bengal	8766	14	0.7295	0.0012	0.004	0.0135	0.0061	0.0028	0.0079	0.0058	0.001	0.0056	0.0125	0.0926	0.0032	0.0126	0.0067	0.0025	0.0925
Bengal	9053	15	0.7742	0.002	0.0032	0.0019	0.0015	0.0012	0.0022	0.0036	0.001	0.0026	0.001	0.0982	0.0029	0.0034	0.001	0.002	0.0981
Bengal	9800	6	0.6652	0.0093	0.0164	0.064	0.0024	0.0052	0.0044	0.0064	0.0118	0.0054	0.0058	0.099	0.006	0.0042	0.003	0.0093	0.0822
Bengal	10344	12	0.7778	0.0024	0.0033	0.001	0.001	0.0034	0.006	0.0035	0.004	0.0051	0.0022	0.087	0.0079	0.0013	0.0012	0.0078	0.0851
Bengal	10946	12	0.6542	0.0026	0.0033	0.0117	0.0036	0.0076	0.0052	0.0471	0.0562	0.008	0.002	0.0893	0.0019	0.0063	0.002	0.0053	0.0937
Bengal	11194	1	0.776	0.002	0.002	0.002	0.0018	0.0022	0.002	0.0025	0.0015	0.0018	0.0022	0.0976	0.0022	0.003	0.0012	0.002	0.098
Sokoke	1890	2	0.6563	0.004	0.0092	0.006	0.001	0.0013	0.0073	0.0195	0.0059	0.0141	0.0022	0.0971	0.0255	0.0373	0.0019	0.0087	0.1028
Sokoke	1898	4	0.8122	0.0028	0.0028	0.0024	0.0022	0.0032	0.0042	0.0022	0.0037	0.004	0.0012	0.074	0.0019	0.0032	0.004	0.0043	0.0717
Sokoke	2054	2	0.7688	0.002	0.0021	0.0025	0.0025	0.002	0.002	0.0033	0.0041	0.0023	0.0017	0.0979	0.0029	0.0023	0.0021	0.003	0.0985
Sokoke	2061	2	0.7072	0.0022	0.0148	0.0454	0.0013	0.005	0.0025	0.0071	0.0037	0.0039	0.002	0.0923	0.005	0.0116	0.0025	0.0026	0.0909
Sokoke	2063	18	0.0038	0.1292	0.0061	0.0023	0.0025	0.7543	0.0054	0.0099	0.0048	0.0169	0.0036	0.0122	0.0049	0.0225	0.003	0.0115	0.0071
Sokoke	2067	16	0.0024	0.003	0.0011	0.001	0.0026	0.9686	0.002	0.002	0.0018	0.0014	0.0021	0.0019	0.0023	0.0026	0.002	0.001	0.0022
Sokoke	6615	6	0.001	0.001	0.001	0.0011	0.002	0.9815	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.0012	0.001	0.0012	0.001
Ocicat	2933	13	0.0103	0.0046	0.0028	0.0058	0.0073	0.9242	0.003	0.003	0.0011	0.0025	0.0101	0.0036	0.0042	0.0048	0.0042	0.0036	0.0049
Ocicat	2951	3	0.0018	0.0067	0.002	0.0023	0.0244	0.9116	0.002	0.0053	0.0021	0.0025	0.0043	0.0019	0.002	0.002	0.0211	0.0037	0.0043
Ocicat	2954	6	0.0022	0.0022	0.0014	0.0012	0.005	0.968	0.002	0.0021	0.001	0.0021	0.002	0.0012	0.001	0.0018	0.0025	0.0019	0.0024
Ocicat	3514	10	0.0078	0.008	0.0027	0.0059	0.0936	0.6685	0.0088	0.0083	0.002	0.0063	0.1174	0.0051	0.0053	0.003	0.0044	0.0161	0.0368
Ocicat	5744	0	0.0041	0.0061	0.0121	0.0033	0.0161	0.0044	0.0141	0.5178	0.0057	0.0152	0.0075	0.0101	0.0153	0.002	0.2625	0.0963	0.0074
Ocicat	9966	12	0.0174	0.0085	0.003	0.0021	0.0021	0.0084	0.011	0.8611	0.0072	0.0044	0.0027	0.0052	0.017	0.0201	0.001	0.024	0.0048
Ocicat	9967	14	0.002	0.0027	0.0023	0.0067	0.0169	0.0037	0.0099	0.8953	0.0022	0.0071	0.0153	0.0044	0.0022	0.0096	0.004	0.011	0.0047
Ocicat	10400	17	0.1411	0.0104	0.0184	0.0047	0.031	0.0028	0.0073	0.3582	0.0197	0.0468	0.0862	0.1401	0.0405	0.0201	0.0032	0.0154	0.0542
Ocicat	10652	20	0.011	0.003	0.0038	0.0113	0.0035	0.0062	0.006	0.8187	0.0022	0.0073	0.0036	0.0051	0.0056	0.0716	0.0272	0.0065	0.0074
Ocicat	10654	11	0.0038	0.0012	0.0039	0.0018	0.001	0.0043	0.003	0.9572	0.0062	0.0031	0.001	0.0019	0.0013	0.0041	0.001	0.0032	0.002
Russian	1834	14	0.005	0.0036	0.0099	0.0051	0.002	0.0077	0.1095	0.735	0.0043	0.0376	0.0025	0.0115	0.0104	0.0185	0.0133	0.0052	0.019

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline Population	ID No.	Missing Data	Groups																
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Blue																			
Russian Blue	1835	13	0.0052	0.0272	0.1582	0.0055	0.0064	0.001	0.0117	0.6653	0.0218	0.0157	0.0026	0.0107	0.0128	0.0183	0.02	0.0067	0.0109
Russian Blue	2505	6	0.0047	0.0123	0.0034	0.0309	0.0564	0.0114	0.0051	0.7558	0.0163	0.0085	0.0024	0.0058	0.003	0.0351	0.0056	0.0115	0.0318
Russian Blue	4068	8	0.0097	0.012	0.028	0.0026	0.0051	0.0072	0.0724	0.1258	0.0045	0.0752	0.0203	0.0113	0.0098	0.1044	0.0172	0.4776	0.017
Russian Blue	4072	2	0.0012	0.002	0.0023	0.0028	0.002	0.0043	0.0051	0.0977	0.002	0.0064	0.0032	0.0057	0.002	0.8561	0.0012	0.0029	0.0031
Russian Blue	4074	14	0.0703	0.0027	0.4326	0.0085	0.0043	0.04	0.1037	0.0966	0.0033	0.0339	0.0881	0.0213	0.0079	0.0074	0.0113	0.0599	0.0081
Russian Blue	4076	9	0.03	0.01	0.039	0.0039	0.002	0.0059	0.0035	0.4242	0.0048	0.0651	0.0013	0.2547	0.0022	0.014	0.0029	0.0839	0.0526
Russian Blue	4077	2	0.0558	0.0157	0.0121	0.0078	0.0048	0.0026	0.045	0.7749	0.0073	0.0074	0.0071	0.0075	0.0136	0.0156	0.0021	0.0104	0.0103
Russian Blue	4078	21	0.0112	0.0114	0.0105	0.0169	0.0311	0.0213	0.0115	0.6287	0.0112	0.0548	0.0114	0.0171	0.0288	0.0841	0.0187	0.0102	0.0211
Russian Blue	4302	14	0.0029	0.0029	0.0025	0.0022	0.0042	0.0047	0.003	0.9139	0.0015	0.0038	0.0157	0.0032	0.0042	0.0205	0.0063	0.0055	0.003
Russian Blue	4867	6	0.0039	0.0048	0.0045	0.0151	0.0014	0.0027	0.0088	0.9054	0.0025	0.0071	0.0026	0.0063	0.0167	0.0059	0.0025	0.0044	0.0054
Russian Blue	4869	9	0.0314	0.0097	0.0185	0.0058	0.0122	0.0034	0.0122	0.7102	0.0122	0.0151	0.0104	0.005	0.0068	0.1176	0.0032	0.0169	0.0095
Russian Blue	5216	0	0.0045	0.0818	0.0424	0.0021	0.0026	0.0017	0.005	0.5951	0.0028	0.0128	0.0011	0.0194	0.1819	0.0145	0.0047	0.0187	0.0089
Russian Blue	5630	2	0.0036	0.0054	0.0039	0.0275	0.004	0.0053	0.0136	0.8921	0.0023	0.0052	0.0045	0.0029	0.0066	0.0034	0.0092	0.0064	0.0041
Russian Blue	5631	6	0.0075	0.0156	0.0049	0.003	0.003	0.0196	0.0095	0.7978	0.0109	0.0076	0.0034	0.012	0.0724	0.0114	0.004	0.004	0.0134
Russian Blue	5704	12	0.0048	0.005	0.005	0.0354	0.004	0.0435	0.031	0.0949	0.0018	0.0071	0.0023	0.0043	0.003	0.7369	0.0139	0.0022	0.0049
Russian Blue	5709	5	0.0048	0.0023	0.0025	0.009	0.0211	0.001	0.0056	0.0858	0.0058	0.002	0.0066	0.0025	0.0016	0.7793	0.0461	0.0148	0.0092
Aust. Mist	4716	10	0.0013	0.004	0.0035	0.002	0.001	0.002	0.0069	0.0865	0.002	0.0043	0.0018	0.0057	0.0865	0.7681	0.003	0.0021	0.0194
Aust. Mist	4718	20	0.0085	0.0031	0.0161	0.0039	0.0021	0.0031	0.0043	0.0923	0.0018	0.0182	0.0012	0.0104	0.0043	0.8184	0.002	0.0037	0.0066

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline Population	ID No.	Missing Data	Groups																
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Aust. Mist	4720	1	0.0189	0.0035	0.0129	0.0155	0.0078	0.0051	0.029	0.1144	0.0077	0.0256	0.0113	0.0064	0.006	0.7032	0.0058	0.0141	0.0129
Aust. Mist	4722	2	0.0153	0.0041	0.0118	0.0031	0.003	0.0035	0.0047	0.3428	0.0097	0.0089	0.0021	0.0078	0.005	0.4904	0.0061	0.0756	0.0062
Aust. Mist	4723	1	0.0047	0.0044	0.0082	0.0028	0.0158	0.0073	0.0142	0.0881	0.0016	0.0291	0.0054	0.007	0.0043	0.753	0.0404	0.0031	0.0106
Aust. Mist	4724	6	0.0023	0.0117	0.0025	0.0028	0.003	0.0053	0.0058	0.0995	0.0013	0.0043	0.0031	0.0076	0.0036	0.827	0.003	0.0142	0.003
Aust. Mist	4725	8	0.0079	0.0026	0.1771	0.0096	0.0046	0.002	0.002	0.0801	0.0035	0.0058	0.0162	0.0072	0.0021	0.6691	0.0012	0.0031	0.0059
Aust. Mist	4727	2	0.012	0.0021	0.0015	0.0041	0.0024	0.0019	0.0044	0.0973	0.002	0.0028	0.0072	0.0023	0.0019	0.8403	0.0116	0.0038	0.0025
Aust. Mist	4731	3	0.0019	0.0038	0.0039	0.0023	0.0046	0.0015	0.0054	0.1014	0.0027	0.0037	0.0019	0.0034	0.0021	0.8452	0.0059	0.0049	0.0054
Aust. Mist	4736	16	0.0058	0.1341	0.0457	0.001	0.001	0.002	0.005	0.1049	0.0036	0.0319	0.0015	0.0547	0.0105	0.5603	0.001	0.0164	0.0205
Aust. Mist	4739	2	0.0326	0.0087	0.0589	0.03	0.0061	0.0041	0.0336	0.4825	0.0077	0.0347	0.008	0.013	0.0267	0.1074	0.0047	0.1187	0.0226
Aust. Mist	6184	0	0.0074	0.0031	0.0042	0.0031	0.0032	0.0019	0.0127	0.1207	0.0025	0.0176	0.0064	0.0162	0.0066	0.7254	0.0017	0.0606	0.0067
Aust. Mist	6187	1	0.0079	0.002	0.0185	0.002	0.001	0.002	0.0043	0.103	0.0077	0.0059	0.0028	0.0094	0.0045	0.813	0.001	0.008	0.007
Aust. Mist	6188	5	0.0024	0.0022	0.0016	0.0018	0.0019	0.0025	0.0021	0.1	0.001	0.002	0.002	0.0021	0.002	0.8705	0.002	0.0021	0.0018
Aust. Mist	6189	3	0.0052	0.002	0.0222	0.0031	0.0022	0.0038	0.0215	0.1087	0.0056	0.0094	0.002	0.0048	0.0036	0.7811	0.003	0.0173	0.0045
Burmese	21	5	0.1445	0.02	0.005	0.0155	0.018	0.0308	0.121	0.1126	0.0265	0.3899	0.0135	0.0204	0.0182	0.0136	0.0149	0.0162	0.0194
Burmese	22	6	0.0123	0.0035	0.0092	0.0028	0.0039	0.0031	0.0539	0.2275	0.0053	0.4045	0.018	0.0349	0.0026	0.0225	0.007	0.1359	0.053
Burmese	23	7	0.0179	0.1323	0.0207	0.036	0.011	0.0099	0.0057	0.1692	0.0074	0.2078	0.0129	0.1253	0.0081	0.0841	0.0125	0.0334	0.1056
Burmese	24	2	0.0012	0.9257	0.001	0.0035	0.0322	0.0079	0.002	0.001	0.001	0.001	0.0048	0.0011	0.0017	0.001	0.0073	0.0019	0.0056
Burmese	25	0	0.003	0.948	0.0022	0.002	0.005	0.0024	0.0032	0.002	0.001	0.0041	0.002	0.0041	0.003	0.002	0.0069	0.006	0.0031
Burmese	26	3	0.0039	0.9451	0.002	0.0012	0.0019	0.0011	0.0075	0.0014	0.0024	0.0021	0.002	0.0023	0.002	0.0016	0.0028	0.019	0.0017
Burmese	27	2	0.0024	0.9565	0.002	0.0013	0.0029	0.0042	0.0029	0.0015	0.001	0.0026	0.0059	0.0027	0.003	0.0032	0.0029	0.0028	0.0022
Burmese	28	1	0.0041	0.8728	0.0133	0.002	0.0039	0.003	0.0032	0.0021	0.0017	0.0053	0.004	0.0388	0.0239	0.0028	0.0074	0.0059	0.0058
Burmese	29	3	0.0021	0.9592	0.0028	0.002	0.0024	0.0012	0.002	0.0029	0.0025	0.0028	0.0011	0.0025	0.0038	0.0035	0.003	0.0036	0.0026
Burmese	4401	12	0.0018	0.9677	0.0019	0.001	0.0025	0.0039	0.0029	0.0013	0.001	0.0015	0.0044	0.0016	0.0023	0.0011	0.0016	0.002	0.0015
Burmese	4691	12	0.0083	0.8251	0.0059	0.0067	0.0059	0.0182	0.004	0.0139	0.002	0.0186	0.0062	0.0282	0.0163	0.0106	0.002	0.0063	0.0219
Burmese	4781	1	0.0035	0.8873	0.0034	0.0025	0.0149	0.0018	0.0082	0.0071	0.0071	0.0093	0.0034	0.0145	0.0061	0.0122	0.0028	0.0023	0.0135
Burmese	4782	1	0.0509	0.7588	0.0131	0.0314	0.0036	0.0072	0.0059	0.0083	0.0033	0.0314	0.0015	0.0124	0.0223	0.0081	0.0074	0.0141	0.0203
Burmese	5425	1	0.0193	0.7378	0.0057	0.0555	0.0079	0.0133	0.0036	0.0186	0.0021	0.0288	0.0276	0.007	0.0109	0.0242	0.0017	0.0046	0.0315
Burmese	5800	11	0.0028	0.9277	0.0024	0.0025	0.0031	0.0017	0.0055	0.0055	0.0021	0.0024	0.0093	0.0018	0.004	0.0042	0.0174	0.003	0.0046
Burmese	6182	2	0.0018	0.9522	0.0026	0.002	0.0028	0.002	0.0035	0.0022	0.002	0.0038	0.005	0.003	0.0044	0.0043	0.0026	0.0031	0.0027
Burmese	6471	2	0.0019	0.9607	0.002	0.0016	0.002	0.003	0.0022	0.0036	0.0028	0.0026	0.001	0.0024	0.0036	0.0022	0.0013	0.0048	0.0023
Burmese	6962	2	0.0045	0.9231	0.002	0.002	0.0057	0.0071	0.0022	0.0033	0.003	0.0041	0.0182	0.0039	0.0025	0.0084	0.0027	0.0031	0.0042
Burmese	6964	13	0.0119	0.0088	0.1073	0.0061	0.0071	0.0168	0.0166	0.1634	0.004	0.1736	0.0031	0.241	0.0035	0.0411	0.0095	0.0263	0.16
Birman	1760	14	0.0349	0.0083	0.0799	0.0857	0.002	0.007	0.0052	0.0726	0.012	0.0503	0.002	0.438	0.0198	0.0105	0.002	0.0172	0.1526
Birman	2917	8	0.0197	0.0069	0.3869	0.0079	0.0034	0.0037	0.0162	0.0165	0.0039	0.0934	0.0056	0.2611	0.0075	0.0111	0.0107	0.0135	0.1321
Birman	3910	2	0.0404	0.0101	0.147	0.0234	0.001	0.002	0.013	0.0452	0.0134	0.0424	0.0018	0.0313	0.5564	0.0088	0.0036	0.0025	0.0578

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline Population	ID No.	Missing Data	Groups																
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Birman	5029	1	0.0236	0.0052	0.159	0.0025	0.0054	0.0032	0.03	0.0177	0.0279	0.1649	0.0023	0.1807	0.1692	0.0112	0.0053	0.0196	0.1724
Birman	5033	1	0.0039	0.0091	0.0568	0.0144	0.0015	0.0257	0.1181	0.0605	0.0024	0.0854	0.0023	0.1599	0.0906	0.0072	0.033	0.1732	0.1559
Birman	5034	0	0.0032	0.0051	0.1896	0.0028	0.0245	0.0045	0.006	0.1924	0.0124	0.0835	0.0155	0.2938	0.0187	0.0057	0.0058	0.0037	0.1328
Birman	5038	1	0.0039	0.0045	0.161	0.0744	0.0017	0.0028	0.0235	0.0091	0.0041	0.1452	0.0032	0.3542	0.0358	0.0071	0.008	0.0066	0.1549
Birman	5151	1	0.0156	0.0036	0.0887	0.0097	0.0019	0.0034	0.0045	0.215	0.0108	0.0848	0.002	0.3419	0.0219	0.0066	0.0034	0.0096	0.1766
Birman	5576	0	0.004	0.0123	0.1089	0.0063	0.001	0.0014	0.0049	0.0209	0.0027	0.4963	0.0026	0.0974	0.0227	0.0468	0.0017	0.0039	0.1662
Birman	5578	0	0.0087	0.0058	0.1156	0.0134	0.0036	0.0034	0.0106	0.0085	0.0025	0.4583	0.0049	0.0961	0.0632	0.0129	0.0107	0.0045	0.1772
Birman	6448	2	0.0033	0.0086	0.0945	0.0034	0.0014	0.0031	0.0149	0.2019	0.0057	0.0963	0.003	0.3349	0.0413	0.0036	0.0013	0.0033	0.1795
Birman	6450	6	0.0115	0.003	0.1261	0.0034	0.002	0.0014	0.0092	0.0937	0.0045	0.1289	0.002	0.3749	0.0069	0.0205	0.0023	0.0194	0.1902
Birman	6526	5	0.0045	0.0078	0.0858	0.0017	0.0014	0.0021	0.0056	0.0891	0.0034	0.1287	0.0027	0.4452	0.0161	0.0036	0.001	0.0169	0.1843
Birman	6527	5	0.0395	0.0055	0.019	0.0078	0.0045	0.0168	0.052	0.0581	0.0155	0.0424	0.0042	0.1022	0.4828	0.0618	0.0038	0.0152	0.069
Birman	6528	0	0.0127	0.053	0.0894	0.0117	0.001	0.001	0.0062	0.1642	0.0012	0.1261	0.0036	0.2747	0.0704	0.0051	0.0018	0.0081	0.1698
Birman	6529	2	0.0093	0.0208	0.0605	0.0035	0.0032	0.0139	0.2812	0.0861	0.0068	0.0755	0.0061	0.2131	0.0426	0.0195	0.0052	0.0154	0.1372
Birman	6604	2	0.0078	0.0031	0.0086	0.0082	0.0033	0.0161	0.8459	0.0342	0.0075	0.0195	0.0036	0.0098	0.0052	0.0062	0.0071	0.008	0.0059
Birman	6607	0	0.002	0.0043	0.0027	0.0029	0.0081	0.0038	0.9448	0.0029	0.003	0.0036	0.0021	0.0016	0.002	0.0032	0.0054	0.0038	0.0038
Birman	6608	0	0.0066	0.002	0.0107	0.004	0.0035	0.0041	0.8995	0.0021	0.0021	0.0052	0.0157	0.007	0.0196	0.0029	0.0029	0.0059	0.0062
Birman	6609	1	0.0044	0.0062	0.0031	0.002	0.002	0.0021	0.8791	0.0237	0.002	0.0088	0.0015	0.003	0.008	0.0438	0.002	0.0056	0.0027
Havana Brn.	787	2	0.0022	0.0056	0.0019	0.0025	0.0038	0.0049	0.9431	0.0021	0.001	0.0028	0.0132	0.0022	0.0029	0.0039	0.0027	0.0027	0.0025
Havana Brn.	2415	0	0.0061	0.0968	0.007	0.0097	0.006	0.0081	0.7292	0.0063	0.0145	0.0058	0.0198	0.0092	0.022	0.0061	0.0065	0.0316	0.0153
Havana Brn.	2500	0	0.0049	0.0062	0.0061	0.0026	0.0265	0.0026	0.8498	0.0043	0.0059	0.0039	0.0062	0.0076	0.0048	0.0141	0.0314	0.0122	0.011
Havana Brn.	2501	0	0.0032	0.0031	0.006	0.002	0.002	0.002	0.9278	0.0025	0.001	0.005	0.0027	0.0066	0.0033	0.0164	0.005	0.0091	0.0023
Havana Brn.	2502	3	0.006	0.0075	0.0081	0.002	0.147	0.0077	0.7075	0.0047	0.0014	0.0136	0.023	0.0151	0.0116	0.0067	0.0163	0.0037	0.0181
Havana Brn.	3312	1	0.0034	0.0051	0.0036	0.0023	0.0014	0.002	0.9295	0.0046	0.001	0.0143	0.0063	0.0031	0.0082	0.0045	0.002	0.0052	0.0034
Havana Brn.	3404	1	0.0199	0.0134	0.0033	0.0036	0.0024	0.0108	0.8823	0.0065	0.0031	0.0038	0.002	0.0116	0.0103	0.0034	0.0037	0.0122	0.0077
Havana Brn.	3513	0	0.0027	0.0019	0.0037	0.0028	0.0168	0.0049	0.8938	0.0032	0.0064	0.0062	0.0192	0.0044	0.0051	0.003	0.0102	0.0035	0.0123
Havana Brn.	5707	0	0.0034	0.002	0.004	0.0013	0.0025	0.0026	0.9396	0.0053	0.002	0.0052	0.003	0.0043	0.0069	0.005	0.0027	0.0078	0.0024

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline	ID	Missing	Groups																
Population	No.	Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Havana Brn.	5708	2	0.0044	0.0042	0.0032	0.003	0.003	0.002	0.9191	0.0051	0.0021	0.0032	0.0066	0.0039	0.0051	0.0054	0.0028	0.0231	0.0038
Havana Brn.	6972	0	0.0136	0.0053	0.0025	0.002	0.0041	0.0082	0.8921	0.0073	0.0223	0.0039	0.0028	0.0034	0.0021	0.0078	0.0025	0.0127	0.0074
Havana Brn.	6973	0	0.0267	0.0151	0.1473	0.0027	0.001	0.002	0.034	0.0032	0.0082	0.4883	0.002	0.0601	0.1698	0.0119	0.0053	0.0097	0.0126
Havana Brn.	10350	4	0.0066	0.0033	0.1676	0.0017	0.001	0.0047	0.0068	0.0096	0.0527	0.0097	0.0013	0.0571	0.6417	0.0088	0.002	0.0095	0.016
Havana Brn.	5554	0	0.0042	0.0078	0.1527	0.0044	0.001	0.0018	0.0071	0.0053	0.0063	0.044	0.002	0.0116	0.7164	0.0213	0.0016	0.0087	0.0038
Korat	4708	2	0.0046	0.0024	0.0972	0.0019	0.001	0.002	0.0165	0.0152	0.0023	0.0781	0.0011	0.2501	0.3313	0.0255	0.0012	0.0103	0.1593
Korat	4711	1	0.0044	0.0075	0.0304	0.001	0.002	0.0022	0.0037	0.0028	0.0021	0.0053	0.0024	0.0299	0.8859	0.0036	0.0092	0.0035	0.004
Korat	5059	4	0.0019	0.002	0.0053	0.0019	0.001	0.0018	0.002	0.002	0.0012	0.0031	0.0025	0.0019	0.9649	0.0015	0.001	0.0043	0.0017
Korat	5069	2	0.0014	0.0022	0.0037	0.002	0.001	0.001	0.0021	0.0021	0.0025	0.0032	0.0018	0.0026	0.9658	0.0027	0.001	0.002	0.0029
Korat	5098	3	0.0019	0.0033	0.0025	0.001	0.001	0.001	0.0013	0.0013	0.0011	0.0021	0.0012	0.0019	0.9746	0.0012	0.001	0.0019	0.0017
Korat	5175	2	0.0018	0.0019	0.0053	0.001	0.001	0.0013	0.0021	0.0017	0.0022	0.002	0.0015	0.0021	0.9696	0.002	0.001	0.002	0.0015
Korat	5176	1	0.0031	0.002	0.0044	0.0018	0.001	0.0032	0.0024	0.0025	0.0018	0.0064	0.0031	0.0038	0.9548	0.0027	0.0018	0.0029	0.0023
Korat	5177	2	0.002	0.0029	0.0027	0.0019	0.0012	0.0014	0.004	0.0022	0.0012	0.0032	0.0048	0.002	0.9616	0.0031	0.0011	0.0029	0.0018
Korat	5178	4	0.0025	0.0032	0.0039	0.001	0.001	0.0018	0.0029	0.0019	0.0014	0.002	0.002	0.0023	0.9675	0.0021	0.001	0.0017	0.0018
Korat	5224	1	0.0096	0.0038	0.0353	0.1421	0.0034	0.004	0.021	0.0186	0.0076	0.038	0.0049	0.0131	0.6445	0.0266	0.0094	0.0076	0.0105
Korat	5237	0	0.0047	0.0022	0.0044	0.0377	0.0045	0.0098	0.0036	0.017	0.0028	0.0045	0.0035	0.0049	0.8773	0.0084	0.0033	0.0055	0.0059
Korat	5240	2	0.0075	0.0035	0.011	0.0576	0.0122	0.0039	0.1226	0.0067	0.0449	0.0147	0.002	0.0291	0.633	0.0061	0.0093	0.0218	0.0141
Korat	5242	4	0.014	0.0026	0.0042	0.0101	0.0791	0.002	0.0092	0.0028	0.0605	0.0034	0.006	0.0034	0.7478	0.0023	0.0074	0.0052	0.04
Korat	5244	3	0.0057	0.012	0.0171	0.0095	0.0021	0.002	0.0041	0.0054	0.0021	0.0232	0.0042	0.0087	0.8595	0.0055	0.003	0.028	0.0079
Korat	5284	2	0.0043	0.0044	0.0063	0.0038	0.0124	0.0132	0.0103	0.0081	0.0055	0.011	0.01	0.0145	0.0033	0.0027	0.8711	0.0075	0.0116
Korat	5344	3	0.0051	0.0018	0.0137	0.0036	0.0035	0.0091	0.0147	0.0064	0.0061	0.0094	0.002	0.0108	0.0029	0.0097	0.8823	0.0144	0.0045
Korat	5481	2	0.0049	0.0012	0.0053	0.0152	0.0048	0.0035	0.0043	0.0267	0.0557	0.0037	0.0057	0.0034	0.002	0.0064	0.8313	0.0206	0.0052
Korat	5512	3	0.0192	0.001	0.0035	0.0015	0.026	0.0035	0.0069	0.002	0.0407	0.0029	0.0027	0.0018	0.0042	0.0028	0.8697	0.0063	0.0053
Korat	5514	0	0.0027	0.0026	0.0078	0.1579	0.003	0.004	0.0048	0.007	0.0024	0.012	0.002	0.0157	0.0092	0.0023	0.7572	0.0049	0.0045
Korat	5595	22	0.004	0.1207	0.2523	0.0749	0.004	0.0033	0.0338	0.0049	0.0145	0.1431	0.0036	0.0701	0.0237	0.003	0.1927	0.0245	0.0271
Korat	5597	5	0.0042	0.0251	0.0273	0.0033	0.0063	0.0069	0.0213	0.0036	0.0075	0.0118	0.0034	0.0529	0.0051	0.0049	0.7622	0.0379	0.0162
Korat	6375	2	0.0038	0.007	0.0217	0.0071	0.0032	0.0196	0.0103	0.0063	0.0021	0.0058	0.0043	0.0485	0.0101	0.0108	0.8213	0.0107	0.0074
Korat	6376	20	0.0068	0.003	0.0032	0.0056	0.0129	0.0288	0.0054	0.006	0.0087	0.0056	0.0247	0.003	0.0044	0.0026	0.8672	0.0077	0.0044
Korat	6377	15	0.0029	0.0039	0.0025	0.0044	0.0071	0.0051	0.0027	0.0036	0.0017	0.0029	0.0031	0.0026	0.003	0.003	0.9445	0.0027	0.0043
Korat	6378	7	0.0031	0.0251	0.0222	0.002	0.0022	0.0024	0.0206	0.0113	0.0433	0.012	0.0089	0.0165	0.0235	0.0075	0.7825	0.0094	0.0075

Table 19 - Population clustering of each pedigreed individual in the database by SNPs at K = 17

Feline	ID	Missing	Groups																
Population	No.	Data	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Siamese	2868	0	0.0406	0.0044	0.0239	0.0091	0.044	0.0031	0.0097	0.0034	0.0048	0.0125	0.0148	0.0166	0.0155	0.005	0.7727	0.0028	0.0171
Siamese	6686	2	0.002	0.0056	0.0049	0.0029	0.004	0.0712	0.0112	0.0035	0.0027	0.0044	0.002	0.0039	0.0083	0.005	0.8617	0.0028	0.0039
Siamese	6688	4	0.013	0.0143	0.0047	0.0061	0.0027	0.0063	0.0042	0.1075	0.0282	0.0915	0.0068	0.0103	0.0535	0.0236	0.6112	0.0045	0.0117
Siamese	6690	2	0.018	0.0032	0.0023	0.002	0.0029	0.0051	0.0067	0.0153	0.0164	0.0045	0.0041	0.0043	0.0055	0.0157	0.8787	0.0075	0.0078
Siamese	6696	18	0.5406	0.0018	0.0035	0.0026	0.002	0.0397	0.0032	0.0037	0.0011	0.0043	0.0017	0.0029	0.0026	0.002	0.3829	0.0023	0.0031
Siamese	7839	14	0.8253	0.0174	0.0091	0.001	0.0061	0.0205	0.004	0.0035	0.0028	0.0038	0.0643	0.0094	0.0117	0.0044	0.0064	0.0064	0.0039
Siamese	8181	18	0.5983	0.0058	0.0172	0.001	0.0028	0.006	0.005	0.0021	0.0078	0.0035	0.0022	0.015	0.3146	0.0028	0.0029	0.0087	0.0043
Siamese	8182	8	0.915	0.0055	0.0102	0.0032	0.0023	0.0147	0.0064	0.0046	0.002	0.0069	0.0017	0.0061	0.0036	0.0032	0.0055	0.0049	0.0042
Siamese	8184	6	0.821	0.0218	0.0064	0.0124	0.0037	0.0023	0.0033	0.0085	0.0043	0.0171	0.0033	0.007	0.0049	0.002	0.0625	0.0123	0.0073
Siamese	8185	8	0.3645	0.007	0.0472	0.0054	0.0118	0.0068	0.0061	0.0083	0.0025	0.0264	0.003	0.128	0.0069	0.0113	0.0832	0.2143	0.0674
Siamese	8187	2	0.8651	0.0037	0.0104	0.0035	0.0033	0.0037	0.0165	0.015	0.0075	0.0067	0.0023	0.0049	0.0325	0.0066	0.0055	0.0051	0.0077
Siamese	8251	1	0.7731	0.0072	0.0046	0.004	0.0167	0.002	0.0071	0.0175	0.0816	0.009	0.0053	0.0051	0.004	0.0129	0.0107	0.0168	0.0224
Siamese	8253	3	0.8016	0.002	0.012	0.0994	0.0063	0.0012	0.0057	0.0176	0.0052	0.0052	0.0069	0.0037	0.0051	0.0114	0.0042	0.0061	0.0063
Siamese	8258	4	0.8358	0.008	0.052	0.0013	0.0024	0.002	0.0183	0.0028	0.0077	0.0097	0.0123	0.0089	0.0165	0.0055	0.002	0.0081	0.0067
Siamese	8259	0	0.6547	0.0047	0.0057	0.0282	0.0404	0.0071	0.008	0.0118	0.0075	0.0068	0.0051	0.01	0.0036	0.0049	0.1246	0.0137	0.0632
Singapura	3428	2	0.9	0.0079	0.006	0.0019	0.0027	0.004	0.0034	0.0057	0.0022	0.0064	0.0162	0.0083	0.0077	0.0152	0.0018	0.0056	0.005
Singapura	3919	8	0.7495	0.002	0.0025	0.0048	0.0088	0.0153	0.0231	0.004	0.0026	0.0032	0.0055	0.0019	0.0031	0.0025	0.1614	0.0066	0.0031
Singapura	4464	3	0.864	0.0053	0.0027	0.0103	0.0087	0.0101	0.0076	0.0067	0.002	0.0085	0.0166	0.0057	0.0067	0.0036	0.0277	0.0078	0.0059
Singapura	4467	0	0.8436	0.0086	0.0114	0.0032	0.0023	0.0043	0.0059	0.0041	0.0037	0.0791	0.0039	0.0066	0.0045	0.0024	0.0031	0.0073	0.006
Singapura	4468	0	0.8299	0.0052	0.0074	0.0012	0.0126	0.0518	0.0036	0.0051	0.0031	0.0063	0.0077	0.0147	0.017	0.0048	0.0147	0.0039	0.0109
Singapura	4469	1	0.8894	0.0037	0.0024	0.0133	0.0057	0.002	0.0065	0.0101	0.005	0.004	0.0154	0.0028	0.0029	0.0042	0.0149	0.0123	0.0054
Singapura	4470	17	0.8528	0.0193	0.0055	0.0221	0.0041	0.0104	0.0061	0.0083	0.0034	0.0127	0.0018	0.0045	0.0115	0.0053	0.0127	0.0097	0.0098
Singapura	4471	16	0.0649	0.0063	0.0545	0.033	0.2708	0.0044	0.0181	0.0261	0.1831	0.0267	0.0136	0.0098	0.0073	0.023	0.0071	0.0798	0.1715
Singapura	4472	6	0.0051	0.1693	0.047	0.0032	0.4249	0.0062	0.0704	0.041	0.0874	0.0046	0.0051	0.012	0.0094	0.0187	0.0051	0.0045	0.086
Singapura	4473	10	0.0193	0.0049	0.0063	0.0138	0.2706	0.0159	0.347	0.0294	0.0044	0.0444	0.0077	0.0088	0.033	0.0392	0.0043	0.0204	0.1305
Singapura	4474	18	0.0402	0.0065	0.02	0.0023	0.2262	0.0572	0.0754	0.0045	0.0029	0.0156	0.0042	0.0505	0.3651	0.0042	0.0075	0.0097	0.1081
Singapura	4485	1	0.0143	0.0627	0.0307	0.0033	0.3816	0.0049	0.0231	0.0138	0.0794	0.0061	0.0031	0.018	0.2459	0.0281	0.0122	0.0058	0.067
Singapura	4486	13	0.0046	0.0032	0.005	0.0079	0.1946	0.0229	0.208	0.006	0.0055	0.016	0.0417	0.0164	0.1886	0.0155	0.1575	0.0033	0.1032
Singapura	4487	2	0.0064	0.012	0.0231	0.0121	0.3331	0.0038	0.0161	0.0542	0.0221	0.0358	0.0042	0.0331	0.0119	0.2805	0.0028	0.0041	0.1445
Singapura	4488	0	0.0044	0.018	0.1542	0.0027	0.3062	0.1154	0.0068	0.0076	0.1604	0.0059	0.0023	0.0518	0.0184	0.005	0.009	0.0046	0.1272
Singapura	6597	0	0.0069	0.003	0.2742	0.0039	0.271	0.0051	0.0774	0.0194	0.0071	0.0199	0.0051	0.0762	0.0514	0.034	0.0111	0.0151	0.1191
Singapura	6975	2	0.0134	0.073	0.0316	0.0221	0.1489	0.0314	0.0889	0.0072	0.1075	0.0161	0.023	0.0426	0.214	0.0108	0.0101	0.0117	0.1476

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
USA-NY	2547	1	0.821	0.021	0.037	0.08	0.041
USA-NY	2559	0	0.556	0.088	0.156	0.187	0.012
USA-NY	2568	0	0.964	0.01	0.011	0.006	0.009
USA-NY	2569	1	0.921	0.01	0.017	0.027	0.025
USA-NY	2572	0	0.903	0.01	0.046	0.02	0.022
USA-NY	2578	20	0.768	0.017	0.084	0.05	0.082
USA-NY	2590	0	0.901	0.023	0.043	0.022	0.012
USA-NY	2591	1	0.929	0.01	0.022	0.01	0.029
USA-NY	2597	1	0.864	0.018	0.032	0.024	0.062
USA-MS	9971	2	0.896	0.039	0.023	0.026	0.016
USA-MS	9972	2	0.778	0.027	0.104	0.019	0.072
USA-MS	9974	2	0.687	0.259	0.03	0.011	0.014
USA-MS	9977	4	0.941	0.007	0.024	0.018	0.011
USA-MS	9980	1	0.878	0.034	0.034	0.023	0.032
USA-MS	9983	1	0.924	0.007	0.024	0.017	0.029
USA-MS	9985	2	0.706	0.226	0.021	0.013	0.034
USA-MS	9987	2	0.641	0.084	0.187	0.071	0.018
USA-MS	9989	2	0.933	0.025	0.017	0.013	0.012
USA-MS	9992	2	0.883	0.013	0.051	0.017	0.036
USA-HI	5366	1	0.751	0.026	0.042	0.156	0.025
USA-HI	5367	0	0.775	0.054	0.024	0.08	0.068
USA-HI	5371	0	0.898	0.023	0.047	0.012	0.019
USA-HI	5372	0	0.564	0.043	0.263	0.031	0.099
USA-HI	5379	0	0.858	0.014	0.064	0.032	0.032
USA-HI	5380	1	0.941	0.005	0.032	0.014	0.007
USA-HI	5383	1	0.39	0.054	0.039	0.101	0.416
USA-HI	5384	2	0.879	0.012	0.044	0.032	0.034
USA-HI	5401	1	0.938	0.016	0.021	0.013	0.013
USA-HI	5402	0	0.838	0.073	0.025	0.047	0.017
Brazil	7961	0	0.861	0.022	0.067	0.029	0.021
Brazil	7962	2	0.763	0.06	0.095	0.057	0.026
Brazil	7963	15	0.544	0.3	0.095	0.047	0.014
Brazil	7964	1	0.871	0.009	0.077	0.027	0.016
Brazil	7965	18	0.934	0.015	0.013	0.024	0.014

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Brazil	7966	1	0.858	0.024	0.085	0.012	0.021
Brazil	7968	22	0.775	0.026	0.044	0.12	0.035
Brazil	7969	0	0.953	0.008	0.016	0.011	0.012
Brazil	7970	0	0.934	0.013	0.015	0.023	0.015
Brazil	7971	0	0.924	0.012	0.025	0.015	0.023
Brazil	7972	0	0.865	0.012	0.096	0.014	0.013
Brazil	7973	0	0.915	0.015	0.026	0.028	0.016
Brazil	7974	3	0.869	0.022	0.073	0.022	0.014
Brazil	7975	3	0.888	0.013	0.036	0.04	0.022
Brazil	7976	0	0.902	0.019	0.034	0.025	0.02
Brazil	7977	1	0.895	0.006	0.059	0.029	0.011
Brazil	7978	1	0.804	0.02	0.052	0.101	0.023
Brazil	7979	1	0.861	0.043	0.041	0.034	0.021
Brazil	7980	2	0.64	0.014	0.252	0.058	0.036
Brazil	7981	2	0.768	0.009	0.025	0.188	0.009
Brazil	7982	15	0.707	0.141	0.037	0.093	0.022
Brazil	7983	1	0.659	0.074	0.15	0.062	0.054
Brazil	7984	6	0.614	0.25	0.054	0.07	0.013
Brazil	7985	2	0.705	0.054	0.145	0.084	0.012
Brazil	7986	2	0.755	0.136	0.073	0.026	0.01
Brazil	7987	1	0.854	0.025	0.091	0.02	0.01
Brazil	7988	0	0.747	0.073	0.041	0.126	0.013
Brazil	7989	0	0.568	0.376	0.023	0.018	0.015
Brazil	7990	0	0.717	0.222	0.028	0.019	0.014
Finland	8077	8	0.86	0.011	0.075	0.024	0.03
Finland	8084	6	0.824	0.008	0.049	0.047	0.073
Finland	8086	4	0.829	0.035	0.072	0.039	0.024
Finland	8089	4	0.688	0.029	0.097	0.075	0.111
Finland	8093	16	0.863	0.013	0.032	0.055	0.037
Finland	8094	3	0.904	0.01	0.028	0.018	0.04
Finland	8096	3	0.941	0.005	0.017	0.008	0.028
Finland	8107	22	0.953	0.006	0.014	0.011	0.016
Finland	8110	5	0.96	0.009	0.015	0.007	0.01
Finland	8116	8	0.857	0.04	0.031	0.045	0.028

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Finland	8120	19	0.933	0.015	0.02	0.023	0.008
Germany	8711	2	0.884	0.009	0.052	0.038	0.016
Germany	8712	3	0.931	0.008	0.023	0.013	0.026
Germany	8713	2	0.681	0.012	0.264	0.027	0.016
Germany	8714	2	0.744	0.021	0.128	0.03	0.077
Germany	8715	4	0.914	0.006	0.033	0.012	0.034
Germany	8716	4	0.898	0.021	0.027	0.033	0.021
Germany	8717	12	0.899	0.015	0.037	0.019	0.03
Germany	8720	2	0.271	0.657	0.046	0.01	0.017
Germany	8721	10	0.909	0.014	0.052	0.013	0.013
Germany	8727	0	0.937	0.01	0.02	0.022	0.01
Germany	8728	10	0.857	0.018	0.045	0.025	0.054
Germany	8729	1	0.948	0.011	0.013	0.013	0.015
Germany	8730	22	0.767	0.022	0.015	0.173	0.023
Germany	8731	12	0.953	0.005	0.014	0.015	0.013
Germany	8732	3	0.892	0.006	0.073	0.01	0.019
Germany	8733	14	0.833	0.034	0.047	0.027	0.059
Germany	8734	0	0.938	0.007	0.033	0.008	0.016
Germany	8735	0	0.851	0.021	0.082	0.027	0.017
Germany	8736	0	0.933	0.008	0.041	0.011	0.007
Germany	8737	2	0.944	0.01	0.016	0.012	0.019
Germany	8738	10	0.866	0.008	0.097	0.012	0.018
Germany	8739	0	0.913	0.005	0.065	0.008	0.009
Germany	8741	12	0.147	0.008	0.813	0.012	0.02
Germany	8742	10	0.902	0.025	0.047	0.011	0.014
Germany	8744	6	0.555	0.088	0.324	0.024	0.008
Germany	8745	22	0.918	0.008	0.045	0.013	0.016
Germany	8746	0	0.896	0.025	0.035	0.016	0.028
Germany	8747	12	0.959	0.01	0.014	0.008	0.009
Germany	8749	0	0.939	0.012	0.016	0.016	0.017
Italy-Milan	8050	0	0.712	0.04	0.139	0.017	0.092
Italy-Milan	8057	1	0.619	0.116	0.092	0.047	0.127
Italy-Milan	8060	0	0.657	0.074	0.037	0.018	0.213
Italy-Milan	8061	2	0.653	0.231	0.083	0.016	0.017

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Italy-Milan	8062	1	0.39	0.034	0.525	0.011	0.04
Italy-Milan	8065	4	0.625	0.013	0.309	0.015	0.039
Italy-Milan	8066	0	0.329	0.072	0.489	0.018	0.092
Italy-Milan	8067	2	0.553	0.06	0.304	0.027	0.055
Italy-Milan	8068	0	0.599	0.017	0.311	0.03	0.042
Italy-Milan	8069	0	0.692	0.09	0.132	0.046	0.04
Italy-Milan	8071	2	0.732	0.026	0.161	0.05	0.03
Italy-Milan	8072	2	0.315	0.275	0.273	0.117	0.02
Italy-Milan	8073	0	0.753	0.011	0.183	0.023	0.031
Italy-Milan	8074	1	0.71	0.167	0.091	0.018	0.013
Italy-Rome	8586	1	0.475	0.012	0.439	0.031	0.042
Italy-Rome	8589	2	0.903	0.016	0.046	0.017	0.019
Italy-Rome	8592	1	0.54	0.026	0.123	0.127	0.185
Italy-Rome	8594	1	0.783	0.033	0.116	0.051	0.017
Italy-Rome	8595	0	0.705	0.064	0.147	0.033	0.051
Italy-Rome	8596	1	0.353	0.02	0.585	0.017	0.025
Italy-Rome	8597	0	0.779	0.077	0.07	0.041	0.033
Italy-Rome	8599	0	0.925	0.023	0.02	0.017	0.015
Italy-Rome	8601	2	0.667	0.034	0.198	0.074	0.026
Italy-Rome	8602	2	0.807	0.045	0.087	0.024	0.037
Italy-Rome	8603	0	0.864	0.03	0.049	0.042	0.016
Italy-Rome	8604	2	0.241	0.01	0.591	0.139	0.018
Italy-Rome	8609	1	0.898	0.011	0.059	0.017	0.014
Italy-Rome	8610	1	0.529	0.051	0.245	0.1	0.075
Italy-Rome	8611	2	0.711	0.049	0.173	0.021	0.045
Turkey	6477	7	0.206	0.007	0.754	0.008	0.024
Turkey	6478	12	0.065	0.055	0.673	0.087	0.12
Turkey	6480	11	0.039	0.012	0.917	0.011	0.022
Turkey	6481	12	0.067	0.647	0.064	0.08	0.142
Turkey	6482	14	0.047	0.008	0.893	0.04	0.012
Turkey	6484	7	0.087	0.019	0.855	0.021	0.019
Turkey	6486	8	0.729	0.025	0.193	0.019	0.035
Turkey	6487	15	0.279	0.012	0.648	0.035	0.025
Turkey	6488	12	0.078	0.011	0.778	0.059	0.075

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Turkey	6491	15	0.018	0.482	0.022	0.04	0.439
Turkey	6494	11	0.227	0.098	0.551	0.044	0.08
Turkey	6496	12	0.062	0.038	0.793	0.058	0.049
Turkey	6499	12	0.625	0.026	0.282	0.037	0.031
Turkey	6500	15	0.261	0.01	0.576	0.066	0.088
Turkey	6502	6	0.142	0.024	0.647	0.083	0.104
Turkey	6503	1	0.161	0.012	0.78	0.018	0.03
Turkey	6507	14	0.03	0.016	0.891	0.04	0.023
Turkey	6510	10	0.035	0.187	0.676	0.068	0.033
Turkey	6512	15	0.2	0.01	0.381	0.034	0.374
Turkey	6513	14	0.731	0.038	0.13	0.044	0.057
Turkey	6514	9	0.012	0.95	0.014	0.008	0.016
Turkey	6516	12	0.94	0.012	0.023	0.013	0.012
Turkey	6519	7	0.574	0.02	0.183	0.11	0.112
Turkey	6520	15	0.229	0.012	0.658	0.025	0.076
Turkey	6521	12	0.707	0.018	0.198	0.049	0.029
Turkey	6729	1	0.101	0.029	0.05	0.115	0.704
Turkey	6730	1	0.039	0.009	0.928	0.009	0.015
Turkey	6731	2	0.363	0.023	0.475	0.035	0.104
Turkey	6732	0	0.024	0.077	0.803	0.055	0.041
Turkey	6733	3	0.051	0.022	0.845	0.038	0.044
Turkey	6734	0	0.023	0.026	0.808	0.015	0.128
Turkey	6735	2	0.024	0.006	0.948	0.009	0.013
Turkey	6736	1	0.288	0.011	0.634	0.018	0.048
Turkey	6738	2	0.183	0.004	0.798	0.006	0.008
Turkey	6739	2	0.327	0.02	0.563	0.018	0.073
Turkey	6740	0	0.961	0.006	0.013	0.01	0.01
Turkey	6741	0	0.094	0.839	0.019	0.024	0.023
Turkey	6742	2	0.273	0.025	0.479	0.032	0.191
Turkey	6743	1	0.193	0.014	0.771	0.009	0.012
Turkey	6745	0	0.068	0.009	0.824	0.037	0.063
Turkey	6746	1	0.233	0.259	0.127	0.22	0.161
Turkey	6748	1	0.186	0.054	0.455	0.046	0.258
Turkey	6749	0	0.042	0.026	0.887	0.02	0.027

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Turkey	6750	3	0.398	0.025	0.522	0.025	0.03
Turkey	6753	0	0.333	0.014	0.565	0.029	0.059
Turkey	6754	2	0.335	0.018	0.466	0.059	0.122
Turkey	6755	1	0.271	0.007	0.656	0.019	0.046
Turkey	6756	0	0.16	0.012	0.786	0.023	0.019
Turkey	6758	1	0.082	0.03	0.826	0.046	0.016
Turkey	6759	2	0.424	0.015	0.46	0.034	0.067
Turkey	6760	1	0.654	0.009	0.201	0.023	0.113
Cyprus	10128	3	0.061	0.036	0.805	0.07	0.027
Cyprus	10129	0	0.638	0.065	0.112	0.074	0.112
Cyprus	10130	2	0.06	0.009	0.909	0.011	0.011
Cyprus	10131	1	0.326	0.039	0.29	0.312	0.033
Cyprus	10132	0	0.009	0.096	0.773	0.042	0.08
Cyprus	10133	0	0.162	0.125	0.653	0.044	0.017
Cyprus	10134	0	0.279	0.02	0.638	0.029	0.034
Cyprus	10135	2	0.2	0.019	0.562	0.032	0.186
Cyprus	10136	2	0.437	0.01	0.283	0.031	0.24
Cyprus	10137	1	0.049	0.01	0.908	0.013	0.02
Cyprus	10138	2	0.017	0.053	0.883	0.022	0.025
Cyprus	10139	3	0.08	0.045	0.749	0.098	0.028
Cyprus	10140	0	0.067	0.025	0.844	0.05	0.015
Cyprus	10141	0	0.035	0.01	0.929	0.014	0.012
Cyprus	10142	1	0.042	0.06	0.789	0.02	0.089
Cyprus	10143	0	0.016	0.019	0.871	0.076	0.017
Cyprus	10144	2	0.04	0.039	0.566	0.041	0.313
Cyprus	10145	1	0.107	0.022	0.794	0.047	0.029
Cyprus	10146	0	0.032	0.008	0.69	0.024	0.246
Cyprus	10147	1	0.129	0.014	0.766	0.052	0.039
Cyprus	10148	0	0.054	0.033	0.843	0.025	0.045
Cyprus	10149	2	0.039	0.046	0.833	0.02	0.063
Cyprus	10150	0	0.196	0.029	0.667	0.071	0.037
Cyprus	10151	2	0.022	0.024	0.9	0.031	0.022
Cyprus	10152	2	0.375	0.008	0.525	0.02	0.073
Cyprus	10153	1	0.031	0.008	0.732	0.186	0.043

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Cyprus	10154	2	0.035	0.048	0.869	0.027	0.02
Cyprus	10155	2	0.026	0.038	0.888	0.027	0.021
Cyprus	10156	5	0.018	0.025	0.84	0.017	0.099
Cyprus	10157	2	0.106	0.023	0.529	0.019	0.323
Lebanon	10235	21	0.039	0.084	0.688	0.098	0.091
Lebanon	10236	25	0.018	0.021	0.786	0.132	0.043
Lebanon	10237	19	0.031	0.06	0.583	0.266	0.06
Lebanon	10238	2	0.353	0.055	0.459	0.055	0.077
Lebanon	10239	16	0.056	0.014	0.821	0.025	0.084
Lebanon	10240	20	0.049	0.025	0.825	0.031	0.069
Lebanon	10241	5	0.038	0.033	0.621	0.148	0.16
Lebanon	10242	0	0.192	0.159	0.567	0.042	0.04
Lebanon	10243	1	0.057	0.028	0.742	0.043	0.131
Lebanon	10244	18	0.04	0.032	0.819	0.058	0.051
Lebanon	10245	6	0.058	0.03	0.715	0.02	0.178
Lebanon	10246	18	0.201	0.078	0.564	0.035	0.122
Lebanon	10247	26	0.017	0.04	0.764	0.048	0.131
Lebanon	10248	22	0.031	0.053	0.709	0.11	0.097
Lebanon	10249	18	0.378	0.044	0.506	0.031	0.04
Lebanon	10250	27	0.051	0.014	0.881	0.022	0.032
Lebanon	10251	4	0.029	0.025	0.814	0.038	0.094
Lebanon	10252	14	0.261	0.061	0.193	0.031	0.455
Lebanon	10253	4	0.047	0.163	0.108	0.027	0.655
Lebanon	10254	13	0.043	0.015	0.821	0.096	0.025
Lebanon	10255	7	0.124	0.125	0.564	0.043	0.144
Lebanon	10256	10	0.191	0.032	0.336	0.036	0.405
Lebanon	10257	3	0.434	0.169	0.352	0.028	0.018
Lebanon	10258	19	0.017	0.037	0.616	0.227	0.103
Lebanon	10259	0	0.043	0.5	0.339	0.104	0.014
Lebanon	10260	17	0.166	0.023	0.756	0.023	0.033
Lebanon	10261	14	0.02	0.118	0.776	0.058	0.027
Lebanon	10262	22	0.015	0.013	0.87	0.024	0.077
Lebanon	10263	2	0.078	0.025	0.707	0.035	0.154
Lebanon	10264	3	0.188	0.035	0.583	0.09	0.105

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Lebanon	10265	10	0.035	0.022	0.884	0.028	0.031
Lebanon	10266	5	0.013	0.06	0.852	0.054	0.022
Lebanon	10267	12	0.865	0.016	0.038	0.017	0.065
Lebanon	10268	17	0.049	0.082	0.716	0.116	0.037
Lebanon	10270	10	0.236	0.424	0.276	0.034	0.03
Lebanon	10271	1	0.021	0.154	0.637	0.045	0.143
Lebanon	10273	4	0.076	0.064	0.59	0.23	0.041
Lebanon	10274	3	0.145	0.019	0.782	0.041	0.014
Lebanon	10276	4	0.029	0.011	0.829	0.023	0.107
Lebanon	10277	4	0.256	0.08	0.518	0.107	0.039
Lebanon	10278	3	0.029	0.012	0.713	0.044	0.202
Lebanon	10279	2	0.077	0.02	0.653	0.037	0.213
Lebanon	10280	2	0.051	0.054	0.767	0.089	0.04
Lebanon	10281	7	0.09	0.015	0.825	0.038	0.032
Lebanon	10282	2	0.062	0.104	0.694	0.108	0.031
Lebanon	10283	16	0.019	0.019	0.869	0.031	0.063
Lebanon	10284	14	0.091	0.041	0.581	0.062	0.225
Lebanon	10285	1	0.027	0.028	0.901	0.007	0.036
Lebanon	10286	3	0.253	0.212	0.232	0.2	0.104
Lebanon	10287	1	0.334	0.026	0.499	0.064	0.078
Lebanon	10288	25	0.34	0.037	0.277	0.283	0.063
Lebanon	10289	2	0.021	0.024	0.812	0.048	0.094
Lebanon	10290	3	0.044	0.037	0.772	0.05	0.097
Lebanon	10291	8	0.097	0.053	0.611	0.09	0.149
Lebanon	10292	6	0.096	0.097	0.664	0.024	0.119
Lebanon	10294	9	0.045	0.111	0.751	0.07	0.024
Lebanon	10295	6	0.117	0.175	0.512	0.112	0.083
Lebanon	10297	5	0.093	0.04	0.57	0.043	0.254
Lebanon	10298	7	0.036	0.026	0.786	0.045	0.107
Lebanon	10299	20	0.144	0.047	0.66	0.035	0.113
Lebanon	10300	25	0.06	0.041	0.764	0.045	0.091
Israel	4962	0	0.259	0.016	0.414	0.097	0.213
Israel	4963	0	0.122	0.019	0.758	0.059	0.041
Israel	4964	0	0.018	0.042	0.68	0.028	0.232

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Israel	4966	2	0.046	0.025	0.878	0.026	0.025
Israel	4967	1	0.302	0.029	0.316	0.018	0.335
Israel	4968	2	0.016	0.029	0.876	0.046	0.034
Israel	4969	1	0.661	0.162	0.045	0.098	0.033
Israel	4970	0	0.074	0.032	0.816	0.047	0.031
Israel	4971	0	0.026	0.011	0.919	0.012	0.032
Israel	4972	0	0.11	0.027	0.61	0.14	0.113
Israel	4973	2	0.063	0.034	0.787	0.064	0.053
Israel	4974	1	0.05	0.027	0.822	0.053	0.048
Israel	4975	0	0.103	0.026	0.793	0.031	0.047
Israel	4976	0	0.136	0.054	0.511	0.061	0.239
Israel	4977	0	0.378	0.029	0.29	0.022	0.281
Israel	4978	1	0.037	0.031	0.695	0.096	0.141
Israel	4979	1	0.058	0.033	0.583	0.078	0.248
Israel	4980	1	0.31	0.019	0.578	0.021	0.071
Israel	4981	2	0.109	0.07	0.192	0.565	0.063
Israel	4982	3	0.039	0.057	0.819	0.023	0.061
Israel	4983	0	0.109	0.138	0.549	0.076	0.129
Israel	4984	2	0.238	0.072	0.37	0.027	0.292
Israel	4985	16	0.099	0.021	0.783	0.075	0.022
Israel	4986	1	0.057	0.162	0.689	0.027	0.065
Israel	4988	0	0.092	0.107	0.705	0.065	0.03
Israel	4989	4	0.091	0.104	0.604	0.18	0.02
Israel	4990	2	0.051	0.249	0.341	0.331	0.029
Israel	4992	6	0.063	0.011	0.519	0.045	0.362
Israel	4993	10	0.051	0.03	0.827	0.036	0.055
Israel	4994	2	0.016	0.013	0.94	0.013	0.018
Israel	4995	1	0.129	0.147	0.468	0.242	0.015
Israel	4996	0	0.029	0.014	0.742	0.193	0.022
Israel	4997	0	0.045	0.17	0.563	0.191	0.031
Israel	4998	0	0.21	0.021	0.404	0.032	0.333
Israel	5000	1	0.025	0.013	0.907	0.025	0.03
Israel	5001	1	0.376	0.051	0.478	0.076	0.02
Israel	5002	0	0.072	0.117	0.748	0.047	0.015

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Israel	5003	1	0.307	0.259	0.151	0.101	0.182
Israel	5004	0	0.023	0.156	0.611	0.052	0.158
Israel	5005	0	0.218	0.012	0.707	0.035	0.028
Israel	5006	1	0.089	0.053	0.72	0.024	0.113
Israel	5007	1	0.033	0.103	0.711	0.117	0.036
Israel	5008	0	0.356	0.115	0.374	0.097	0.058
Israel	5009	0	0.03	0.292	0.534	0.028	0.116
Israel	5010	1	0.042	0.01	0.886	0.011	0.051
Israel	5011	0	0.016	0.024	0.881	0.05	0.03
Egypt-Cairo	8190	0	0.058	0.054	0.795	0.048	0.045
Egypt-Cairo	8192	2	0.142	0.014	0.796	0.017	0.031
Egypt-Cairo	8193	0	0.384	0.049	0.429	0.044	0.094
Egypt-Cairo	8196	1	0.029	0.039	0.774	0.065	0.094
Egypt-Cairo	8203	1	0.029	0.012	0.922	0.012	0.025
Egypt-Cairo	8215	1	0.085	0.044	0.698	0.064	0.109
Egypt-Cairo	8198	2	0.028	0.047	0.867	0.021	0.038
Egypt-Cairo	8194	0	0.106	0.059	0.738	0.035	0.062
Egypt-Cairo	8211	10	0.025	0.008	0.938	0.012	0.017
Egypt-Cairo	8216	1	0.039	0.136	0.793	0.01	0.022
Egypt-Cairo	8195	1	0.165	0.013	0.772	0.022	0.029
Egypt-Cairo	8199	9	0.051	0.015	0.863	0.045	0.026
Egypt-Cairo	8200	16	0.038	0.029	0.885	0.022	0.026
Egypt-Cairo	8201	0	0.205	0.123	0.6	0.018	0.053
Egypt-Cairo	8202	2	0.033	0.679	0.111	0.055	0.122
Egypt-Cairo	8204	2	0.023	0.012	0.93	0.023	0.012
Egypt-Cairo	8208	0	0.011	0.027	0.839	0.012	0.11
Egypt-Cairo	8210	3	0.032	0.014	0.731	0.148	0.074
Egypt-Cairo	8214	2	0.061	0.225	0.599	0.032	0.083
Egypt-Cairo	8191	1	0.024	0.014	0.928	0.017	0.018
Egypt-Cairo	8197	0	0.032	0.043	0.897	0.012	0.015
Egypt-Cairo	8205	0	0.011	0.011	0.766	0.06	0.151
Egypt-Cairo	8206	1	0.01	0.044	0.856	0.05	0.04
Egypt-Cairo	8207	2	0.023	0.1	0.813	0.033	0.031
Egypt-Cairo	8209	1	0.013	0.018	0.883	0.027	0.059

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Egypt-Cairo	8212	0	0.04	0.095	0.787	0.016	0.062
Egypt-Cairo	8213	0	0.043	0.053	0.832	0.023	0.049
Egypt-Cairo	9942	3	0.033	0.02	0.866	0.051	0.031
Egypt-Cairo	9943	0	0.182	0.418	0.375	0.011	0.014
Egypt-Cairo	9944	4	0.583	0.053	0.049	0.053	0.263
Egypt-Cairo	9945	0	0.009	0.044	0.864	0.024	0.059
Egypt-Cairo	9946	0	0.029	0.024	0.898	0.033	0.016
Egypt-Cairo	9947	2	0.017	0.038	0.786	0.023	0.137
Egypt-Cairo	9948	0	0.157	0.017	0.795	0.011	0.02
Egypt-Cairo	9949	0	0.029	0.2	0.708	0.045	0.018
Egypt-Cairo	9950	1	0.046	0.009	0.921	0.012	0.012
Egypt-Cairo	9951	2	0.024	0.095	0.756	0.026	0.099
Egypt-Cairo	9952	1	0.01	0.013	0.667	0.021	0.289
Egypt-Cairo	9953	4	0.659	0.087	0.143	0.063	0.048
Egypt-Cairo	9954	0	0.028	0.52	0.405	0.032	0.015
Egypt-Cairo	9955	3	0.187	0.047	0.665	0.029	0.072
Egypt-Cairo	9956	5	0.021	0.252	0.605	0.106	0.016
Egypt-Cairo	9957	1	0.241	0.025	0.39	0.061	0.282
Egypt-Cairo	9958	1	0.02	0.141	0.784	0.023	0.032
Egypt-Cairo	9959	2	0.075	0.224	0.376	0.073	0.252
Egypt-Cairo	9960	1	0.015	0.044	0.881	0.026	0.035
Egypt-Cairo	9961	5	0.024	0.457	0.362	0.12	0.037
Egypt-Cairo	9962	2	0.154	0.065	0.744	0.023	0.014
Egypt-Cairo	9963	4	0.032	0.021	0.886	0.036	0.024
Egypt-Cairo	9964	2	0.048	0.118	0.726	0.033	0.075
Egypt-Cairo	10021	8	0.024	0.021	0.926	0.01	0.018
Egypt-Cairo	10022	1	0.015	0.016	0.914	0.021	0.035
Egypt-Cairo	10023	0	0.013	0.014	0.891	0.011	0.071
Egypt-Cairo	10024	2	0.014	0.006	0.966	0.007	0.007
Egypt-Cairo	10025	2	0.024	0.026	0.784	0.055	0.111
Egypt-Cairo	10026	21	0.099	0.023	0.803	0.06	0.015
Egypt-Cairo	10027	1	0.021	0.016	0.928	0.017	0.018
Egypt-Cairo	10028	1	0.069	0.01	0.877	0.018	0.026
Egypt-Cairo	10029	4	0.037	0.014	0.91	0.014	0.025

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Egypt-Cairo	10030	1	0.013	0.012	0.946	0.014	0.015
Egypt-Cairo	10031	3	0.016	0.015	0.93	0.027	0.014
Egypt-Cairo	10032	0	0.03	0.015	0.903	0.016	0.036
Egypt-Cairo	10033	1	0.014	0.016	0.881	0.011	0.078
Egypt-Cairo	10034	1	0.059	0.016	0.879	0.022	0.024
Egypt-Cairo	10035	4	0.033	0.024	0.762	0.053	0.128
Egypt-Cairo	10037	5	0.372	0.016	0.532	0.043	0.037
Egypt-Cairo	10042	1	0.116	0.026	0.784	0.058	0.017
Egypt-Cairo	10043	1	0.059	0.02	0.822	0.015	0.084
Egypt-Cairo	10044	4	0.036	0.019	0.819	0.091	0.034
Egypt-Cairo	10045	1	0.099	0.008	0.865	0.013	0.015
Egypt-Cairo	10046	0	0.021	0.023	0.891	0.024	0.04
Egypt-Cairo	10047	0	0.016	0.019	0.921	0.016	0.029
Egypt-Cairo	10048	1	0.018	0.059	0.775	0.099	0.049
Egypt-Cairo	10083	25	0.054	0.012	0.792	0.095	0.047
Egypt-Cairo	10040	3	0.024	0.02	0.89	0.032	0.034
Egypt-Cairo	10041	1	0.012	0.016	0.733	0.047	0.192
Egypt-Cairo	10049	10	0.028	0.059	0.838	0.045	0.029
Egypt-Cairo	10084	8	0.109	0.034	0.799	0.039	0.019
Egypt-Cairo	10085	18	0.056	0.038	0.884	0.01	0.012
Egypt-Cairo	10087	4	0.133	0.009	0.799	0.023	0.035
Egypt-Cairo	10090	3	0.105	0.042	0.77	0.022	0.062
Egypt-Cairo	9968	0	0.031	0.017	0.822	0.095	0.034
Egypt-Asuit	10091	1	0.025	0.015	0.918	0.025	0.017
Egypt-Asuit	10093	4	0.061	0.01	0.904	0.015	0.011
Egypt-Asuit	10094	4	0.059	0.017	0.878	0.03	0.016
Egypt-Asuit	10095	16	0.159	0.022	0.78	0.025	0.015
Egypt-Asuit	10096	2	0.037	0.026	0.821	0.103	0.013
Egypt-Asuit	10098	2	0.091	0.01	0.878	0.012	0.009
Egypt-Asuit	10099	0	0.03	0.008	0.922	0.022	0.018
Egypt-Asuit	10100	2	0.164	0.064	0.635	0.103	0.033
Egypt-Asuit	10101	2	0.018	0.026	0.914	0.02	0.021
Egypt-Asuit	10102	2	0.017	0.015	0.936	0.017	0.015
Egypt-Luxor	10038	1	0.02	0.075	0.858	0.027	0.021

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Egypt-Luxor	10039	6	0.012	0.035	0.904	0.035	0.013
Egypt-Luxor	10050	2	0.012	0.042	0.895	0.032	0.02
Egypt-Luxor	10051	1	0.013	0.018	0.856	0.093	0.019
Egypt-Luxor	10052	14	0.026	0.027	0.885	0.05	0.011
Egypt-Luxor	10053	3	0.015	0.071	0.612	0.157	0.144
Egypt-Luxor	10054	2	0.014	0.01	0.903	0.024	0.049
Egypt-Luxor	10055	2	0.011	0.062	0.863	0.044	0.021
Egypt-Luxor	10056	2	0.072	0.069	0.794	0.033	0.032
Egypt-Luxor	10057	13	0.029	0.011	0.91	0.035	0.015
Egypt-Luxor	10058	8	0.031	0.016	0.873	0.036	0.044
Egypt-Luxor	10060	5	0.033	0.022	0.912	0.02	0.012
Egypt-Luxor	10061	0	0.055	0.046	0.857	0.029	0.014
Egypt-Luxor	10062	3	0.028	0.013	0.885	0.015	0.058
Egypt-Luxor	10063	0	0.293	0.049	0.435	0.12	0.103
Egypt-Luxor	10064	1	0.138	0.016	0.814	0.015	0.017
Egypt-Luxor	10065	0	0.031	0.035	0.8	0.052	0.082
Egypt-Luxor	10066	4	0.048	0.066	0.827	0.039	0.02
Egypt-Luxor	10067	4	0.027	0.013	0.875	0.033	0.052
Egypt-Luxor	10068	9	0.104	0.019	0.832	0.026	0.019
Egypt-Luxor	10069	3	0.025	0.009	0.774	0.036	0.157
Egypt-Luxor	10070	2	0.058	0.044	0.856	0.028	0.014
Egypt-Luxor	10071	4	0.019	0.014	0.919	0.012	0.036
Egypt-Luxor	10072	2	0.032	0.021	0.872	0.034	0.04
Egypt-Luxor	10073	0	0.928	0.006	0.019	0.024	0.023
Egypt-Luxor	10074	0	0.021	0.008	0.945	0.008	0.019
Egypt-Luxor	10079	6	0.073	0.018	0.873	0.019	0.017
Egypt-Luxor	10080	6	0.012	0.023	0.931	0.022	0.013
Egypt-Abu Simbel	10076	11	0.057	0.03	0.813	0.06	0.04
Egypt-Abu Simbel	10077	18	0.02	0.009	0.925	0.024	0.021
Egypt-Abu Simbel	10081	19	0.047	0.023	0.841	0.017	0.072
Egypt-Abu Simbel	10089	2	0.039	0.019	0.899	0.024	0.019
Egypt-Abu Simbel	10092	2	0.048	0.008	0.908	0.02	0.016
Iraq-West	9587	12	0.148	0.012	0.159	0.031	0.65
Iraq-West	10202	2	0.063	0.013	0.391	0.018	0.515
Iraq-West	10204	13	0.086	0.013	0.271	0.022	0.608
Iraq-West	11854	23	0.058	0.064	0.141	0.044	0.692
Iraq-West	11860	8	0.048	0.014	0.196	0.071	0.671
Iraq-West	11861	2	0.031	0.056	0.061	0.033	0.819
Iraq-West	11863	2	0.066	0.011	0.174	0.012	0.737
Iraq-West	11864	1	0.098	0.021	0.144	0.015	0.722
Iraq-West	11888	2	0.043	0.301	0.062	0.038	0.556
Iraq-West	11889	3	0.029	0.009	0.102	0.013	0.848
Iraq-West	11890	20	0.05	0.038	0.126	0.048	0.738
Iraq-West	11891	18	0.028	0.041	0.078	0.029	0.824
Iraq-Baghdad	11847	0	0.026	0.009	0.126	0.017	0.823
Iraq-Baghdad	11848	1	0.04	0.03	0.071	0.017	0.842
Iraq-Baghdad	11849	0	0.078	0.006	0.282	0.013	0.621
Iraq-Baghdad	11850	1	0.072	0.061	0.077	0.033	0.757
Iraq-Baghdad	11852	18	0.015	0.022	0.021	0.018	0.924
Iraq-Baghdad	11853	9	0.02	0.096	0.338	0.031	0.515
Iraq-Baghdad	11855	22	0.024	0.027	0.078	0.023	0.849
Iraq-Baghdad	11856	1	0.063	0.015	0.132	0.01	0.78
Iraq-Baghdad	11857	2	0.114	0.01	0.127	0.021	0.728
Iraq-Baghdad	11858	0	0.016	0.085	0.243	0.059	0.598
Iraq-Baghdad	11859	3	0.055	0.013	0.091	0.023	0.818
Iraq-Baghdad	11862	1	0.048	0.009	0.333	0.012	0.599
Iraq-Baghdad	11865	2	0.036	0.048	0.313	0.082	0.521
Iraq-Baghdad	11868	10	0.018	0.123	0.058	0.048	0.752
Iraq-Baghdad	11869	8	0.054	0.014	0.117	0.023	0.793
Iraq-Baghdad	11870	1	0.26	0.03	0.36	0.018	0.333
Iraq-Baghdad	11871	2	0.138	0.012	0.184	0.089	0.577
Iraq-Baghdad	11872	4	0.021	0.011	0.023	0.011	0.934
Iraq-Baghdad	11873	2	0.05	0.03	0.367	0.027	0.526

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population				
			1	2	3	4	5
Iraq-Baghdad	11874	0	0.042	0.018	0.215	0.102	0.624
Iraq-Baghdad	11875	1	0.025	0.018	0.205	0.011	0.742
Iraq-Baghdad	11876	1	0.017	0.064	0.078	0.012	0.83
Iraq-Baghdad	11877	2	0.021	0.057	0.429	0.027	0.466
Iraq-Baghdad	11878	2	0.181	0.017	0.11	0.01	0.682
Iraq-Baghdad	11879	0	0.024	0.213	0.027	0.022	0.715
Iraq-Baghdad	11880	3	0.082	0.028	0.224	0.079	0.586
Iraq-Baghdad	11881	2	0.19	0.009	0.179	0.037	0.584
Iraq-Baghdad	11882	0	0.027	0.07	0.137	0.033	0.733
Iraq-Baghdad	11883	2	0.123	0.018	0.28	0.049	0.53
Iraq-Baghdad	11884	17	0.058	0.027	0.164	0.048	0.704
Iraq-Baghdad	11885	0	0.009	0.282	0.294	0.012	0.404
Iraq-Baghdad	11886	2	0.032	0.049	0.191	0.066	0.661
Iraq-Baghdad	11887	16	0.051	0.069	0.14	0.016	0.724
Iran	9419	22	0.018	0.031	0.036	0.019	0.896
Iran	9420	17	0.053	0.049	0.175	0.088	0.636
Iran	9421	20	0.018	0.011	0.1	0.07	0.801
Iran	9422	18	0.017	0.012	0.079	0.07	0.822
Iran	9424	25	0.011	0.022	0.019	0.021	0.928
Iran	9425	4	0.014	0.038	0.134	0.039	0.774
Iran	9426	6	0.023	0.024	0.032	0.205	0.717
Iran	9427	3	0.014	0.157	0.029	0.031	0.769
Iran	9428	2	0.025	0.073	0.303	0.11	0.489
Iran	9429	0	0.024	0.147	0.067	0.082	0.68
Iran	9430	10	0.043	0.015	0.398	0.025	0.52
Iran	9431	0	0.014	0.035	0.052	0.027	0.872
Iran	9432	1	0.01	0.182	0.024	0.029	0.754
Iran	9433	1	0.073	0.023	0.085	0.12	0.698
Iran	9434	0	0.022	0.013	0.044	0.011	0.91
Iran	9435	2	0.012	0.027	0.02	0.028	0.913
Iran	9436	18	0.014	0.017	0.019	0.025	0.925
Iran	9437	1	0.011	0.015	0.018	0.024	0.932
Iran	9438	1	0.009	0.026	0.019	0.06	0.886
Iran	9439	0	0.008	0.007	0.009	0.015	0.96

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population				
			1	2	3	4	5
Iran	9440	1	0.013	0.007	0.016	0.011	0.953
Iran	9441	1	0.008	0.007	0.009	0.015	0.961
Iran	9442	2	0.008	0.018	0.024	0.029	0.922
Iran	9443	0	0.015	0.027	0.019	0.018	0.921
Iran	9444	0	0.01	0.056	0.018	0.026	0.891
Iran	9445	1	0.01	0.015	0.016	0.04	0.92
Iran	9446	2	0.012	0.028	0.012	0.02	0.928
Iran	9447	22	0.014	0.013	0.017	0.02	0.937
Iran	9448	0	0.01	0.009	0.019	0.037	0.925
Iran	9449	0	0.008	0.023	0.013	0.122	0.834
Iran	9450	0	0.01	0.011	0.014	0.016	0.949
Iran	9451	2	0.007	0.019	0.008	0.019	0.947
Iran	9452	0	0.014	0.011	0.01	0.013	0.952
Iran	9453	2	0.007	0.014	0.017	0.01	0.953
Iran	9454	0	0.006	0.012	0.007	0.013	0.962
Iran	9455	1	0.025	0.037	0.049	0.013	0.875
Iran	9456	4	0.006	0.015	0.009	0.01	0.96
Iran	9457	2	0.01	0.022	0.012	0.012	0.945
Iran	9458	0	0.005	0.006	0.007	0.017	0.965
Iran	9459	2	0.01	0.018	0.018	0.012	0.942
Iran	9460	0	0.012	0.031	0.026	0.065	0.866
Iran	9461	1	0.036	0.011	0.037	0.018	0.898
Iran	9462	0	0.013	0.009	0.011	0.024	0.942
Iran	9463	0	0.007	0.015	0.009	0.025	0.944
Iran	9464	0	0.012	0.037	0.013	0.051	0.886
Iran	9465	1	0.012	0.01	0.02	0.013	0.945
Iran	9466	0	0.007	0.013	0.008	0.031	0.941
Iran	9468	1	0.007	0.026	0.01	0.039	0.918
Iran	9469	0	0.017	0.011	0.017	0.079	0.875
Iran	9470	1	0.008	0.017	0.014	0.059	0.901
Iran	9471	0	0.04	0.015	0.048	0.05	0.847
Iran	9472	0	0.008	0.102	0.014	0.076	0.8
Iran	9473	0	0.02	0.011	0.012	0.018	0.94
Iran	9474	0	0.045	0.028	0.036	0.053	0.839

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Iran	9475	0	0.014	0.015	0.018	0.059	0.894
Iran	9476	2	0.038	0.017	0.03	0.016	0.9
Iran	9477	1	0.019	0.054	0.023	0.01	0.894
Iran	9478	0	0.018	0.015	0.024	0.049	0.893
Iran	9479	1	0.016	0.009	0.018	0.007	0.95
Iran	9480	1	0.007	0.021	0.016	0.012	0.945
Iran	9481	1	0.017	0.049	0.007	0.091	0.836
Iran	9482	1	0.01	0.013	0.007	0.022	0.948
Iran	9483	2	0.029	0.014	0.1	0.172	0.685
Iran	9484	2	0.029	0.012	0.125	0.013	0.822
Iran	9485	0	0.012	0.01	0.018	0.069	0.891
Iran	9486	1	0.008	0.008	0.009	0.015	0.959
Iran	9487	1	0.018	0.013	0.026	0.025	0.918
Iran	9488	1	0.022	0.172	0.048	0.011	0.748
Iran	9489	0	0.04	0.017	0.046	0.03	0.867
Iran	9490	0	0.026	0.007	0.014	0.039	0.915
Iran	9491	0	0.008	0.035	0.013	0.02	0.924
Iran	9492	2	0.017	0.026	0.028	0.011	0.918
Iran	9493	1	0.016	0.014	0.014	0.032	0.924
Iran	9494	1	0.008	0.011	0.011	0.018	0.952
Iran	9495	0	0.012	0.014	0.013	0.013	0.948
Iran	9497	1	0.008	0.013	0.011	0.043	0.926
Iran	9498	0	0.009	0.011	0.01	0.023	0.947
Iran	9499	2	0.013	0.007	0.016	0.042	0.922
Iran	9500	0	0.01	0.012	0.01	0.014	0.954
Iran	9501	1	0.023	0.014	0.016	0.01	0.938
Iran	9502	4	0.011	0.016	0.016	0.007	0.95
Iran	9503	2	0.107	0.016	0.046	0.022	0.809
Iran	9504	1	0.009	0.008	0.01	0.01	0.964
Iran	9505	2	0.033	0.013	0.026	0.01	0.918
Iran	9506	6	0.052	0.05	0.024	0.035	0.839
Iran	9507	0	0.083	0.015	0.042	0.036	0.824
Iran	9508	2	0.01	0.008	0.009	0.012	0.961
Iran	9509	2	0.016	0.012	0.013	0.056	0.903

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Iran	9510	2	0.009	0.014	0.011	0.025	0.94
Iran	9511	0	0.011	0.032	0.024	0.049	0.884
Iran	9512	1	0.007	0.008	0.011	0.021	0.953
Iran	9513	2	0.013	0.016	0.02	0.024	0.927
Iran	9514	2	0.027	0.023	0.062	0.025	0.864
Iran	9515	2	0.005	0.015	0.007	0.014	0.959
Iran	9516	5	0.009	0.012	0.015	0.026	0.938
Iran	9517	0	0.01	0.01	0.01	0.02	0.95
Iran	9518	1	0.007	0.026	0.009	0.011	0.947
Iran	9519	0	0.01	0.012	0.017	0.03	0.932
Iran	9520	1	0.006	0.009	0.008	0.01	0.966
Iran	9521	4	0.011	0.012	0.009	0.058	0.911
Iran	9522	7	0.006	0.009	0.011	0.01	0.965
Iran	9523	0	0.027	0.016	0.017	0.014	0.925
Iran	9524	0	0.006	0.009	0.009	0.023	0.953
Iran	9526	2	0.005	0.007	0.006	0.016	0.966
Iran	9527	1	0.009	0.046	0.015	0.026	0.904
Iran	9528	3	0.01	0.016	0.013	0.069	0.893
Iran	9529	1	0.012	0.017	0.016	0.009	0.945
Iran	9530	4	0.008	0.007	0.017	0.016	0.952
Iran	9531	2	0.01	0.048	0.017	0.028	0.897
Iran	9532	16	0.192	0.211	0.184	0.011	0.402
Dubai	10104	0	0.228	0.013	0.22	0.025	0.514
Dubai	10105	2	0.069	0.113	0.169	0.022	0.627
Dubai	10106	0	0.051	0.169	0.08	0.05	0.65
Dubai	10107	0	0.055	0.037	0.059	0.154	0.695
Dubai	10108	2	0.076	0.145	0.295	0.074	0.41
Dubai	10109	1	0.034	0.083	0.048	0.332	0.503
Dubai	10110	2	0.084	0.095	0.299	0.027	0.495
Dubai	10111	2	0.082	0.014	0.089	0.015	0.8
Dubai	10112	0	0.035	0.11	0.098	0.043	0.715
Dubai	10120	0	0.032	0.028	0.063	0.193	0.685
Kenya-Nairobi	9833	2	0.771	0.027	0.052	0.022	0.127
Kenya-Nairobi	9834	0	0.186	0.038	0.415	0.29	0.071

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Kenya-Nairobi	9835	0	0.016	0.069	0.818	0.022	0.076
Kenya-Nairobi	9836	2	0.61	0.182	0.133	0.051	0.023
Kenya-Nairobi	9837	3	0.738	0.178	0.043	0.022	0.019
Kenya-Nairobi	9838	4	0.532	0.079	0.325	0.019	0.045
Kenya-Nairobi	9839	1	0.76	0.035	0.068	0.039	0.097
Kenya-Nairobi	9840	4	0.757	0.072	0.043	0.022	0.105
Kenya-Nairobi	9841	4	0.757	0.058	0.033	0.048	0.104
Kenya-Nairobi	9842	2	0.532	0.039	0.309	0.057	0.064
Kenya-Nairobi	9843	6	0.568	0.197	0.112	0.037	0.085
Kenya-Nairobi	9844	4	0.639	0.201	0.058	0.045	0.058
Kenya-Nairobi	9845	2	0.737	0.147	0.062	0.022	0.033
Kenya-Nairobi	9846	1	0.612	0.054	0.076	0.014	0.243
Kenya-Nairobi	9847	4	0.665	0.103	0.047	0.092	0.093
Kenya-Nairobi	9848	4	0.679	0.049	0.167	0.042	0.062
Kenya-Nairobi	9849	2	0.478	0.148	0.089	0.255	0.03
Kenya-Nairobi	9850	2	0.771	0.052	0.054	0.02	0.103
Kenya-Nairobi	9851	2	0.321	0.26	0.156	0.072	0.19
Kenya-Nairobi	9852	4	0.394	0.21	0.136	0.174	0.087
Kenya-Nairobi	9853	4	0.583	0.17	0.088	0.077	0.082
Kenya-Nairobi	9854	2	0.515	0.281	0.121	0.047	0.036
Kenya-Nairobi	9855	2	0.523	0.103	0.071	0.153	0.151
Kenya-Nairobi	9856	3	0.564	0.118	0.086	0.037	0.195
Kenya-Nairobi	9857	2	0.789	0.047	0.099	0.018	0.047
Kenya-Nairobi	9858	0	0.579	0.037	0.051	0.105	0.227
Kenya-Nairobi	9859	1	0.761	0.045	0.061	0.109	0.024
Kenya-Nairobi	9860	2	0.726	0.108	0.032	0.103	0.03
Kenya-Nairobi	9861	1	0.666	0.054	0.096	0.098	0.086
Kenya-Nairobi	9862	1	0.717	0.158	0.06	0.024	0.041
Kenya-Nairobi	9863	1	0.379	0.18	0.132	0.271	0.039
Kenya-Nairobi	9864	1	0.368	0.226	0.22	0.076	0.11
Kenya-Nairobi	9865	2	0.859	0.021	0.042	0.055	0.023
Kenya-Nairobi	9866	2	0.623	0.216	0.031	0.054	0.075
Kenya-Nairobi	9867	0	0.752	0.028	0.058	0.11	0.052
Kenya-Nairobi	9868	5	0.585	0.312	0.03	0.025	0.048

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Kenya-Pate	2000	0	0.04	0.039	0.047	0.306	0.568
Kenya-Pate	2001	0	0.076	0.067	0.015	0.098	0.744
Kenya-Pate	2002	0	0.084	0.059	0.016	0.087	0.754
Kenya-Pate	2003	0	0.219	0.013	0.036	0.061	0.672
Kenya-Pate	2004	1	0.029	0.201	0.26	0.115	0.395
Kenya-Pate	2006	2	0.227	0.015	0.051	0.408	0.3
Kenya-Pate	2007	3	0.14	0.011	0.201	0.319	0.329
Kenya-Pate	2009	0	0.087	0.05	0.147	0.122	0.594
Kenya-Pate	2011	0	0.049	0.043	0.132	0.324	0.453
Kenya-Lamu	1848	14	0.07	0.028	0.292	0.389	0.222
Kenya-Lamu	2014	4	0.112	0.016	0.048	0.186	0.639
Kenya-Lamu	2015	0	0.264	0.224	0.023	0.118	0.371
Kenya-Lamu	2016	0	0.019	0.22	0.034	0.151	0.576
Kenya-Lamu	2018	0	0.484	0.056	0.013	0.073	0.373
Kenya-Lamu	2019	0	0.156	0.047	0.454	0.082	0.261
Kenya-Lamu	2021	1	0.198	0.061	0.095	0.282	0.364
Kenya-Lamu	2023	1	0.049	0.042	0.083	0.232	0.593
Kenya-Lamu	2024	2	0.087	0.024	0.105	0.189	0.595
Kenya-Lamu	2025	3	0.155	0.012	0.056	0.3	0.477
Kenya-Lamu	2026	1	0.138	0.022	0.208	0.091	0.542
Kenya-Lamu	2027	2	0.06	0.01	0.033	0.558	0.339
Kenya-Lamu	2029	1	0.09	0.03	0.11	0.211	0.56
Kenya-Lamu	2030	0	0.118	0.01	0.072	0.038	0.761
Kenya-Lamu	2031	0	0.067	0.025	0.041	0.23	0.636
Kenya-Lamu	2032	0	0.039	0.023	0.1	0.22	0.619
Kenya-Lamu	2033	0	0.112	0.022	0.071	0.048	0.746
Kenya-Lamu	3241	0	0.115	0.017	0.235	0.032	0.601
Kenya-Lamu	3246	0	0.3	0.192	0.049	0.081	0.378
Kenya-Lamu	3247	0	0.141	0.031	0.119	0.488	0.221
India-Udaipur	11835	7	0.023	0.368	0.021	0.12	0.469
India-Udaipur	11836	3	0.163	0.076	0.088	0.187	0.487
India-Udaipur	11837	1	0.014	0.099	0.051	0.408	0.429
India-Agra	11823	2	0.029	0.258	0.189	0.243	0.281
India-Agra	11824	2	0.036	0.023	0.371	0.038	0.533

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population				
			1	2	3	4	5
India-Agra	11825	2	0.012	0.031	0.022	0.356	0.58
India-Agra	11826	6	0.015	0.023	0.058	0.569	0.335
India-Agra	11827	25	0.046	0.105	0.111	0.104	0.634
India-Agra	11828	2	0.036	0.042	0.72	0.07	0.132
India-Agra	11829	4	0.02	0.06	0.041	0.281	0.598
India-Agra	11830	8	0.042	0.024	0.093	0.193	0.648
India-Agra	11831	2	0.015	0.029	0.027	0.205	0.724
India-Agra	11832	2	0.017	0.096	0.024	0.175	0.687
India-Agra	11833	20	0.037	0.364	0.196	0.126	0.276
India-Agra	11834	2	0.019	0.023	0.051	0.563	0.344
India-Hyderbad	11802	14	0.018	0.609	0.244	0.048	0.081
India-Hyderbad	11803	7	0.018	0.207	0.074	0.045	0.657
India-Hyderbad	11804	4	0.01	0.385	0.033	0.242	0.33
India-Hyderbad	11805	11	0.023	0.284	0.308	0.035	0.351
India-Hyderbad	11807	13	0.141	0.369	0.175	0.201	0.113
India-Hyderbad	11808	10	0.158	0.156	0.284	0.261	0.141
India-Hyderbad	11809	4	0.201	0.224	0.085	0.1	0.39
India-Hyderbad	11810	0	0.033	0.041	0.054	0.434	0.438
India-Hyderbad	11811	0	0.173	0.064	0.458	0.179	0.126
India-Hyderbad	11812	0	0.021	0.253	0.143	0.137	0.447
India-Hyderbad	11813	2	0.068	0.5	0.333	0.034	0.064
India-Hyderbad	11814	2	0.021	0.272	0.164	0.016	0.527

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population				
			1	2	3	4	5
India-Hyderbad	11815	2	0.023	0.273	0.629	0.027	0.048
India-Hyderbad	11816	4	0.027	0.032	0.054	0.226	0.661
India-Hyderbad	11817	2	0.017	0.493	0.264	0.044	0.182
India-Hyderbad	11818	1	0.534	0.372	0.04	0.012	0.042
India-Hyderbad	11819	6	0.031	0.033	0.086	0.233	0.617
India-Hyderbad	11820	6	0.01	0.379	0.044	0.074	0.494
India-Hyderbad	11821	17	0.028	0.572	0.228	0.033	0.139
India-Hyderbad	11822	2	0.042	0.235	0.167	0.076	0.48
India-Andhra	10159	1	0.069	0.286	0.097	0.065	0.484
India-Andhra	10160	1	0.017	0.605	0.023	0.307	0.048
India-Andhra	10161	2	0.105	0.382	0.086	0.054	0.373
India-Andhra	10162	5	0.062	0.599	0.041	0.04	0.258
India-Andhra	10163	0	0.039	0.452	0.043	0.041	0.424
India-Andhra	10164	2	0.396	0.382	0.066	0.043	0.114
India-Andhra	10165	1	0.079	0.752	0.095	0.02	0.054
India-Andhra	10166	2	0.038	0.477	0.112	0.031	0.342
India-Andhra	10167	0	0.025	0.717	0.033	0.087	0.138
India-Andhra	10168	1	0.141	0.632	0.133	0.048	0.045
India-Andhra	10169	7	0.061	0.512	0.111	0.065	0.251
India-Andhra	10170	6	0.02	0.49	0.349	0.071	0.069
India-Andhra	10171	1	0.393	0.389	0.069	0.041	0.107
India-Andhra	10172	2	0.046	0.572	0.098	0.038	0.247
India-Andhra	10173	2	0.075	0.647	0.085	0.018	0.175
India-Andhra	10174	3	0.043	0.4	0.104	0.367	0.086
India-Andhra	10175	2	0.061	0.296	0.234	0.358	0.051
India-Andhra	10176	2	0.065	0.303	0.29	0.214	0.127

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
India-Andhra	10177	0	0.327	0.448	0.017	0.122	0.086
India-Andhra	10178	2	0.061	0.66	0.075	0.05	0.155
India-Andhra	10179	5	0.036	0.547	0.024	0.042	0.351
India-Andhra	10180	12	0.081	0.287	0.081	0.216	0.335
India-Andhra	10181	4	0.058	0.537	0.056	0.103	0.246
India-Kolkata	10113	0	0.019	0.019	0.062	0.573	0.326
India-Kolkata	10114	1	0.038	0.588	0.115	0.088	0.171
India-Kolkata	10115	1	0.021	0.222	0.504	0.191	0.062
India-Kolkata	10116	1	0.008	0.538	0.022	0.054	0.377
India-Kolkata	10117	2	0.029	0.415	0.407	0.06	0.089
India-Kolkata	10118	0	0.137	0.423	0.253	0.11	0.076
India-Kolkata	10119	2	0.175	0.202	0.231	0.076	0.316
Sri Lanka	8780	2	0.173	0.057	0.098	0.563	0.11
Sri Lanka	8781	0	0.256	0.312	0.08	0.296	0.056
Sri Lanka	8782	0	0.093	0.207	0.431	0.202	0.067
Sri Lanka	8783	0	0.082	0.224	0.64	0.022	0.033
Sri Lanka	8784	0	0.482	0.348	0.074	0.074	0.023
Sri Lanka	8785	11	0.332	0.321	0.03	0.133	0.183
Sri Lanka	8786	0	0.121	0.134	0.094	0.449	0.202
Sri Lanka	8787	0	0.529	0.18	0.082	0.099	0.11
Sri Lanka	8788	4	0.078	0.234	0.534	0.065	0.088
Sri Lanka	8789	2	0.164	0.333	0.384	0.085	0.034
Sri Lanka	8790	1	0.279	0.568	0.095	0.012	0.047
Sri Lanka	8791	0	0.159	0.316	0.429	0.058	0.038
Sri Lanka	8792	0	0.029	0.054	0.461	0.193	0.264
Sri Lanka	8793	1	0.146	0.083	0.333	0.101	0.337
Sri Lanka	8794	1	0.117	0.075	0.257	0.211	0.339
Sri Lanka	8795	1	0.399	0.138	0.162	0.207	0.094
Sri Lanka	8796	3	0.049	0.189	0.198	0.384	0.18
Sri Lanka	8797	0	0.293	0.437	0.069	0.035	0.165
Sri Lanka	8798	0	0.055	0.077	0.51	0.303	0.054
Sri Lanka	8799	1	0.364	0.205	0.132	0.089	0.21
Sri Lanka	8800	0	0.55	0.254	0.08	0.048	0.068
Sri Lanka	8801	4	0.306	0.149	0.254	0.165	0.125

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Sri Lanka	8802	2	0.359	0.129	0.126	0.316	0.07
Sri Lanka	8803	4	0.151	0.403	0.128	0.277	0.041
Thailand	11688	6	0.03	0.94	0.011	0.012	0.007
Thailand	11689	13	0.009	0.942	0.008	0.032	0.009
Thailand	11691	20	0.026	0.921	0.016	0.023	0.013
Thailand	11698	17	0.006	0.972	0.009	0.007	0.006
Thailand	11702	10	0.006	0.95	0.006	0.03	0.008
Thailand	11703	12	0.007	0.958	0.009	0.018	0.007
Thailand	11705	21	0.014	0.873	0.034	0.026	0.053
Thailand	11707	3	0.005	0.96	0.007	0.018	0.01
Thailand	11708	22	0.009	0.95	0.009	0.022	0.01
Thailand	11709	12	0.006	0.958	0.008	0.013	0.014
Thailand	11710	8	0.016	0.921	0.019	0.029	0.015
Thailand	11711	7	0.011	0.951	0.01	0.016	0.012
Thailand	11714	5	0.015	0.944	0.012	0.012	0.017
Thailand	11715	16	0.016	0.8	0.015	0.02	0.148
Thailand	11717	15	0.005	0.951	0.008	0.014	0.022
Thailand	11718	0	0.004	0.973	0.004	0.01	0.008
Thailand	11720	3	0.004	0.98	0.004	0.006	0.006
Vietnam	8844	4	0.023	0.93	0.009	0.02	0.018
Vietnam	8845	1	0.025	0.788	0.053	0.029	0.104
Vietnam	8846	0	0.021	0.92	0.033	0.013	0.014
Vietnam	8847	9	0.01	0.957	0.009	0.018	0.006
Vietnam	8848	6	0.009	0.945	0.014	0.02	0.011
Vietnam	8849	2	0.026	0.87	0.048	0.036	0.02
Vietnam	8850	0	0.085	0.795	0.042	0.038	0.041
Vietnam	8851	0	0.032	0.774	0.094	0.013	0.087
Vietnam	8852	13	0.046	0.813	0.06	0.063	0.019
Vietnam	8853	1	0.13	0.713	0.102	0.036	0.019
Vietnam	8854	5	0.02	0.832	0.04	0.056	0.051
Vietnam	8855	0	0.277	0.639	0.06	0.015	0.009
Vietnam	8856	0	0.03	0.857	0.038	0.034	0.041
Vietnam	8857	2	0.058	0.664	0.228	0.036	0.014
Vietnam	8858	0	0.098	0.625	0.25	0.01	0.018

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Vietnam	8859	6	0.049	0.774	0.093	0.059	0.025
Vietnam	8860	0	0.017	0.701	0.049	0.146	0.087
Vietnam	8861	0	0.026	0.66	0.133	0.136	0.045
Vietnam	8862	0	0.087	0.507	0.112	0.038	0.257
Vietnam	8863	0	0.2	0.61	0.146	0.017	0.027
Taiwan	8681	3	0.593	0.043	0.015	0.333	0.015
Taiwan	8682	0	0.204	0.461	0.057	0.171	0.107
Taiwan	8683	2	0.06	0.125	0.409	0.276	0.13
Taiwan	8684	2	0.6	0.06	0.019	0.281	0.039
Taiwan	8685	2	0.026	0.355	0.022	0.562	0.036
Taiwan	8686	6	0.158	0.096	0.068	0.572	0.106
Taiwan	8687	6	0.019	0.585	0.098	0.262	0.035
Taiwan	8688	21	0.098	0.335	0.047	0.382	0.138
Taiwan	8689	5	0.027	0.056	0.034	0.537	0.346
Taiwan	8690	0	0.016	0.215	0.017	0.693	0.059
Taiwan	8691	14	0.068	0.254	0.036	0.56	0.081
Taiwan	8692	3	0.127	0.5	0.063	0.215	0.094
Taiwan	8693	0	0.174	0.196	0.033	0.489	0.108
Taiwan	8694	0	0.28	0.228	0.086	0.299	0.107
Taiwan	8695	0	0.089	0.297	0.091	0.509	0.014
Taiwan	8696	8	0.968	0.005	0.013	0.008	0.006
Taiwan	8697	0	0.723	0.034	0.019	0.193	0.031
Taiwan	8698	4	0.948	0.008	0.014	0.019	0.011
Taiwan	8699	6	0.057	0.239	0.077	0.428	0.199
Taiwan	8700	1	0.337	0.2	0.048	0.38	0.036
Taiwan	8701	2	0.099	0.191	0.015	0.67	0.026
Taiwan	8702	1	0.33	0.101	0.036	0.509	0.023
Taiwan	8703	1	0.8	0.083	0.042	0.041	0.034
Taiwan	8704	0	0.016	0.162	0.154	0.654	0.013
Taiwan	8705	1	0.025	0.26	0.043	0.631	0.041
Taiwan	8706	0	0.111	0.13	0.199	0.288	0.273
Taiwan	8707	4	0.031	0.177	0.088	0.522	0.182
Taiwan	8708	0	0.93	0.027	0.014	0.013	0.017
Taiwan	8709	2	0.021	0.212	0.022	0.72	0.025

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Japan-Oita	11967	4	0.04	0.679	0.054	0.195	0.032
Japan-Oita	11968	5	0.319	0.298	0.031	0.329	0.022
Japan-Oita	11969	5	0.135	0.292	0.108	0.447	0.018
Japan-Oita	11970	16	0.031	0.847	0.077	0.029	0.016
Japan-Oita	11971	8	0.032	0.538	0.156	0.122	0.152
Japan-Oita	11972	3	0.067	0.468	0.252	0.182	0.032
Japan-Oita	11973	2	0.398	0.043	0.014	0.53	0.014
Japan-Oita	11974	20	0.015	0.45	0.023	0.485	0.027
Japan-Oita	11975	22	0.275	0.545	0.052	0.116	0.013
Japan-Oita	11976	16	0.033	0.602	0.015	0.316	0.034
Japan-Oita	11977	4	0.014	0.629	0.01	0.295	0.052
Japan-Oita	11979	12	0.147	0.667	0.024	0.113	0.049
Japan-Oita	11980	21	0.013	0.694	0.03	0.148	0.115
Japan-Oita	11981	18	0.012	0.164	0.012	0.798	0.014
Japan-Oita	11982	4	0.025	0.427	0.018	0.472	0.058
Japan-Oita	11985	11	0.033	0.255	0.043	0.639	0.03
Japan-Oita	11986	6	0.364	0.431	0.036	0.146	0.023
Japan-Kanazawa	11929	6	0.933	0.008	0.015	0.02	0.024
Japan-Kanazawa	11931	20	0.033	0.12	0.014	0.794	0.038
Japan-Kanazawa	11932	6	0.123	0.124	0.028	0.701	0.024
Japan-Kanazawa	11933	14	0.132	0.042	0.048	0.767	0.011
Japan-Kanazawa	11934	3	0.145	0.042	0.023	0.783	0.007
Japan-Kanazawa	11936	8	0.065	0.419	0.029	0.459	0.027
Japan-Kanazawa	11937	27	0.035	0.033	0.019	0.889	0.025
Japan-Kanazawa	11939	20	0.022	0.321	0.011	0.637	0.009
Japan-	11940	12	0.018	0.116	0.014	0.838	0.014

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Kanazawa							
Japan-Kanazawa	11941	6	0.029	0.334	0.016	0.607	0.014
Japan-Kanazawa	11942	9	0.011	0.04	0.009	0.93	0.01
Japan-Kanazawa	11943	17	0.018	0.467	0.02	0.45	0.045
Japan-Kanazawa	11944	7	0.508	0.119	0.256	0.049	0.069
Japan-Kanazawa	11945	18	0.048	0.132	0.025	0.781	0.014
Japan-Kanazawa	11946	16	0.006	0.029	0.009	0.949	0.006
Japan-Ohmiya	11947	4	0.085	0.12	0.106	0.672	0.017
Japan-Ohmiya	11948	17	0.009	0.031	0.013	0.924	0.024
Japan-Ohmiya	11951	22	0.06	0.049	0.064	0.731	0.096
Japan-Ohmiya	11953	2	0.011	0.267	0.015	0.693	0.014
Japan-Ohmiya	11954	2	0.064	0.066	0.029	0.814	0.026
Japan-Ohmiya	11955	5	0.237	0.019	0.014	0.707	0.022
Japan-Ohmiya	11956	2	0.009	0.722	0.025	0.233	0.011
Japan-Ohmiya	11957	3	0.063	0.077	0.086	0.755	0.019
Japan-Ohmiya	11959	4	0.02	0.196	0.016	0.757	0.011
Japan-Ohmiya	11960	3	0.014	0.551	0.011	0.413	0.011
Japan-Ohmiya	11961	3	0.033	0.17	0.02	0.76	0.017
Japan-Ohmiya	11962	4	0.328	0.13	0.047	0.469	0.027
Japan-Ohmiya	11963	3	0.026	0.155	0.03	0.699	0.091
Japan-Ohmiya	11964	4	0.053	0.025	0.02	0.879	0.024
Japan-Ohmiya	11965	4	0.046	0.141	0.16	0.557	0.096
Japan-Ohmiya	11966	5	0.089	0.179	0.077	0.565	0.09
Japan-Sapporo	11907	7	0.059	0.118	0.026	0.675	0.122
Japan-Sapporo	11909	9	0.955	0.011	0.01	0.011	0.012
Japan-	11911	17	0.304	0.053	0.029	0.593	0.02

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Sapporo							
Japan-Sapporo	11913	16	0.046	0.345	0.129	0.455	0.025
Japan-Sapporo	11914	4	0.033	0.315	0.194	0.412	0.046
Japan-Sapporo	11915	7	0.012	0.819	0.01	0.148	0.011
Japan-Sapporo	11916	7	0.926	0.021	0.034	0.007	0.012
Japan-Sapporo	11917	4	0.905	0.011	0.017	0.018	0.049
Japan-Sapporo	11918	13	0.087	0.207	0.045	0.613	0.048
Japan-Sapporo	11921	5	0.012	0.378	0.038	0.526	0.046
Japan-Sapporo	11922	6	0.016	0.058	0.015	0.507	0.404
Japan-Sapporo	11923	7	0.005	0.408	0.007	0.57	0.009
Japan-Sapporo	11924	6	0.58	0.192	0.056	0.158	0.014
Japan-Sapporo	11925	9	0.011	0.9	0.017	0.04	0.032
Japan-Sapporo	11926	11	0.083	0.032	0.318	0.513	0.054
China-Henan	8869	2	0.007	0.014	0.022	0.851	0.106
China-Henan	8870	0	0.01	0.016	0.017	0.932	0.025
China-Henan	8871	0	0.013	0.012	0.021	0.926	0.028
China-Henan	8872	1	0.021	0.027	0.046	0.885	0.021
China-Henan	8873	1	0.006	0.011	0.013	0.925	0.045
China-Henan	8874	8	0.008	0.069	0.016	0.793	0.114
China-Henan	8875	1	0.008	0.008	0.012	0.953	0.02
China-Henan	8876	0	0.007	0.012	0.011	0.953	0.018
China-Henan	8877	0	0.062	0.01	0.019	0.882	0.027

Table 20 - Population clustering of each random bred individual in the database by SNPs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
China-Henan	8878	2	0.012	0.01	0.026	0.904	0.049
China-Henan	8879	2	0.015	0.009	0.016	0.944	0.016
China-Henan	8880	0	0.078	0.009	0.03	0.857	0.026
China-Henan	8881	2	0.01	0.013	0.018	0.912	0.047
China-Henan	8882	2	0.015	0.012	0.02	0.913	0.04
China-Henan	8883	0	0.013	0.014	0.01	0.853	0.11
China-Henan	8884	0	0.008	0.007	0.009	0.949	0.027
China-Henan	8885	0	0.024	0.012	0.048	0.773	0.144
China-Henan	8886	0	0.007	0.009	0.013	0.913	0.059
China-Henan	8887	1	0.009	0.042	0.021	0.886	0.043
China-Henan	8888	1	0.01	0.007	0.009	0.963	0.011
South Korea	2769	4	0.018	0.018	0.061	0.812	0.091
South Korea	2772	12	0.01	0.01	0.008	0.961	0.011
South Korea	2775	8	0.015	0.075	0.025	0.828	0.057
South Korea	2776	25	0.008	0.038	0.011	0.908	0.035
South Korea	2779	0	0.03	0.046	0.023	0.849	0.052
South Korea	2784	2	0.018	0.016	0.056	0.817	0.094
South Korea	2785	1	0.011	0.033	0.018	0.909	0.029
South Korea	2786	2	0.011	0.042	0.021	0.918	0.009
South Korea	7671	1	0.121	0.014	0.064	0.775	0.025
South Korea	7672	0	0.009	0.102	0.019	0.843	0.026
South Korea	7673	0	0.014	0.015	0.047	0.892	0.033
South Korea	7674	1	0.12	0.015	0.114	0.581	0.171
South Korea	7675	2	0.009	0.021	0.011	0.943	0.016
South Korea	7676	2	0.154	0.028	0.05	0.753	0.014
South Korea	7677	14	0.835	0.041	0.054	0.054	0.016
South Korea	7678	0	0.024	0.018	0.014	0.928	0.016
South Korea	7679	2	0.015	0.023	0.036	0.905	0.021
South Korea	7680	8	0.168	0.012	0.045	0.744	0.031
South Korea	7681	2	0.017	0.063	0.018	0.888	0.014
South Korea	7682	0	0.008	0.051	0.01	0.921	0.01
South Korea	7683	0	0.008	0.012	0.008	0.952	0.021
South Korea	7684	1	0.561	0.014	0.025	0.291	0.11
South Korea	7685	6	0.03	0.134	0.098	0.628	0.109
South Korea	7686	2	0.03	0.008	0.037	0.888	0.036
South Korea	7687	4	0.121	0.133	0.049	0.676	0.021
South Korea	7688	13	0.326	0.024	0.014	0.622	0.015
South Korea	7689	0	0.01	0.008	0.01	0.877	0.095
South Korea	7690	0	0.061	0.027	0.115	0.757	0.04
South Korea	7691	2	0.01	0.179	0.013	0.786	0.013
South Korea	7692	0	0.057	0.026	0.073	0.767	0.077
South Korea	7693	0	0.021	0.049	0.03	0.86	0.04
South Korea	7694	1	0.007	0.056	0.016	0.905	0.016
South Korea	7695	9	0.081	0.009	0.121	0.741	0.049
South Korea	7696	2	0.015	0.01	0.018	0.939	0.018
South Korea	7697	2	0.061	0.014	0.045	0.832	0.048
South Korea	7698	2	0.023	0.363	0.111	0.489	0.013
South Korea	7699	0	0.043	0.031	0.065	0.846	0.014
South Korea	7700	6	0.012	0.035	0.018	0.916	0.019

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
USA-NY	2547	2	0.006	0.013	0.111	0.821	0.049
USA-NY	2559	13	0.004	0.006	0.176	0.803	0.011
USA-NY	2568	2	0.017	0.004	0.01	0.963	0.006
USA-NY	2569	21	0.022	0.015	0.028	0.923	0.013
USA-NY	2572	5	0.012	0.007	0.016	0.863	0.102
USA-NY	2578	5	0.005	0.008	0.01	0.962	0.016
USA-NY	2590	5	0.005	0.003	0.037	0.935	0.019
USA-NY	2591	7	0.031	0.01	0.017	0.929	0.012
USA-NY	2597	15	0.011	0.014	0.018	0.865	0.092
USA-MS	9971	5	0.011	0.011	0.018	0.888	0.072
USA-MS	9972	0	0.013	0.019	0.021	0.857	0.089
USA-MS	9974	2	0.011	0.01	0.023	0.908	0.048
USA-MS	9977	10	0.015	0.012	0.017	0.936	0.02
USA-MS	9980	7	0.007	0.017	0.043	0.922	0.012
USA-MS	9983	7	0.006	0.008	0.011	0.951	0.024
USA-MS	9985	5	0.133	0.004	0.051	0.795	0.017
USA-MS	9987	10	0.01	0.015	0.025	0.92	0.031
USA-MS	9989	2	0.05	0.009	0.042	0.875	0.024
USA-MS	9992	7	0.016	0.009	0.136	0.754	0.085
USA-HI	5366	10	0.161	0.005	0.057	0.681	0.097
USA-HI	5367	7	0.017	0.016	0.092	0.8	0.074
USA-HI	5371	5	0.064	0.024	0.319	0.448	0.144
USA-HI	5372	7	0.02	0.011	0.047	0.762	0.161
USA-HI	5379	2	0.051	0.021	0.03	0.878	0.019
USA-HI	5380	2	0.016	0.007	0.019	0.948	0.01
USA-HI	5383	10	0.025	0.122	0.386	0.43	0.037
USA-HI	5384	18	0.005	0.007	0.175	0.805	0.008
USA-HI	5401	5	0.063	0.005	0.442	0.466	0.024
USA-HI	5402	7	0.117	0.057	0.066	0.741	0.018
Brazil	7961	2	0.011	0.005	0.02	0.959	0.005
Brazil	7962	2	0.004	0.003	0.077	0.907	0.008
Brazil	7963	23	0.008	0.006	0.014	0.791	0.181
Brazil	7964	5	0.013	0.005	0.009	0.958	0.014
Brazil	7965	65	0.007	0.008	0.014	0.958	0.014

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Brazil	7966	5	0.005	0.015	0.011	0.96	0.009
Brazil	7968	23	0.009	0.008	0.018	0.953	0.011
Brazil	7969	2	0.006	0.005	0.01	0.971	0.009
Brazil	7970	2	0.005	0.005	0.016	0.96	0.014
Brazil	7971	2	0.013	0.006	0.007	0.968	0.007
Brazil	7972	2	0.007	0.009	0.011	0.968	0.006
Brazil	7973	2	0.015	0.006	0.015	0.958	0.007
Brazil	7974	2	0.009	0.008	0.014	0.955	0.014
Brazil	7975	13	0.019	0.005	0.017	0.943	0.017
Brazil	7976	2	0.008	0.004	0.007	0.976	0.005
Brazil	7977	7	0.009	0.004	0.016	0.967	0.005
Brazil	7978	2	0.007	0.006	0.011	0.962	0.015
Brazil	7979	5	0.022	0.007	0.014	0.943	0.014
Brazil	7980	2	0.026	0.025	0.262	0.675	0.013
Brazil	7981	5	0.145	0.009	0.02	0.791	0.036
Brazil	7982	42	0.038	0.014	0.055	0.832	0.062
Brazil	7983	15	0.007	0.009	0.03	0.768	0.186
Brazil	7984	50	0.136	0.024	0.137	0.6	0.103
Brazil	7985	21	0.006	0.006	0.012	0.964	0.011
Brazil	7986	10	0.033	0.01	0.032	0.905	0.021
Brazil	7987	5	0.009	0.006	0.017	0.886	0.081
Brazil	7988	2	0.015	0.027	0.049	0.843	0.066
Brazil	7989	5	0.02	0.011	0.018	0.893	0.057
Brazil	7990	5	0.005	0.004	0.007	0.973	0.012
Finland	8077	23	0.004	0.007	0.008	0.976	0.005
Finland	8084	31	0.037	0.008	0.024	0.88	0.051
Finland	8086	13	0.005	0.007	0.028	0.954	0.006
Finland	8089	26	0.016	0.017	0.02	0.914	0.033
Finland	8093	18	0.004	0.005	0.373	0.612	0.005
Finland	8094	34	0.013	0.072	0.104	0.78	0.03
Finland	8096	23	0.006	0.013	0.138	0.834	0.009
Finland	8107	31	0.004	0.004	0.008	0.979	0.005
Finland	8110	28	0.013	0.021	0.238	0.606	0.123
Finland	8116	44	0.015	0.02	0.034	0.914	0.017

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population				
			1	2	3	4	5
Finland	8120	28	0.015	0.014	0.087	0.878	0.006
Germany	8711	13	0.004	0.004	0.007	0.981	0.004
Germany	8712	2	0.012	0.019	0.007	0.946	0.016
Germany	8713	7	0.039	0.034	0.022	0.885	0.02
Germany	8714	5	0.007	0.014	0.017	0.952	0.011
Germany	8715	5	0.005	0.006	0.011	0.972	0.007
Germany	8716	2	0.005	0.006	0.012	0.972	0.006
Germany	8717	7	0.006	0.006	0.013	0.968	0.007
Germany	8720	5	0.038	0.007	0.012	0.493	0.45
Germany	8721	10	0.005	0.014	0.063	0.911	0.006
Germany	8727	7	0.006	0.006	0.133	0.84	0.015
Germany	8728	10	0.005	0.004	0.006	0.977	0.007
Germany	8729	7	0.003	0.003	0.011	0.98	0.004
Germany	8730	21	0.011	0.004	0.132	0.843	0.01
Germany	8731	13	0.008	0.006	0.022	0.957	0.008
Germany	8732	7	0.006	0.004	0.012	0.961	0.016
Germany	8733	23	0.015	0.011	0.013	0.944	0.016
Germany	8734	7	0.004	0.002	0.011	0.978	0.004
Germany	8735	7	0.005	0.004	0.01	0.973	0.007
Germany	8736	5	0.015	0.116	0.022	0.836	0.011
Germany	8737	10	0.021	0.024	0.068	0.848	0.039
Germany	8738	10	0.009	0.145	0.023	0.814	0.01
Germany	8739	7	0.005	0.005	0.01	0.966	0.013
Germany	8741	7	0.005	0.003	0.007	0.978	0.006
Germany	8742	7	0.009	0.005	0.007	0.975	0.004
Germany	8744	7	0.163	0.026	0.1	0.672	0.039
Germany	8745	26	0.008	0.01	0.049	0.917	0.015
Germany	8746	5	0.004	0.004	0.008	0.977	0.007
Germany	8747	18	0.012	0.004	0.014	0.959	0.01
Germany	8749	7	0.004	0.005	0.006	0.98	0.004
Italy-Milan	8050	5	0.303	0.027	0.04	0.597	0.032
Italy-Milan	8057	5	0.009	0.039	0.23	0.578	0.145
Italy-Milan	8060	2	0.008	0.007	0.224	0.717	0.044
Italy-Milan	8061	5	0.04	0.055	0.521	0.298	0.085

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population				
			1	2	3	4	5
Italy-Milan	8062	10	0.017	0.01	0.441	0.511	0.021
Italy-Milan	8065	10	0.02	0.007	0.576	0.384	0.013
Italy-Milan	8066	2	0.006	0.006	0.011	0.927	0.05
Italy-Milan	8067	2	0.006	0.016	0.37	0.555	0.053
Italy-Milan	8068	7	0.01	0.008	0.627	0.337	0.019
Italy-Milan	8069	2	0.021	0.024	0.251	0.529	0.175
Italy-Milan	8071	5	0.01	0.008	0.017	0.95	0.015
Italy-Milan	8072	7	0.084	0.054	0.135	0.698	0.03
Italy-Milan	8073	5	0.027	0.033	0.164	0.739	0.037
Italy-Milan	8074	5	0.026	0.004	0.015	0.603	0.352
Italy-Rome	8586	2	0.08	0.021	0.294	0.583	0.022
Italy-Rome	8589	7	0.079	0.007	0.154	0.742	0.018
Italy-Rome	8592	7	0.013	0.119	0.219	0.628	0.021
Italy-Rome	8594	2	0.01	0.095	0.037	0.836	0.021
Italy-Rome	8595	5	0.031	0.173	0.149	0.548	0.098
Italy-Rome	8596	2	0.05	0.012	0.415	0.507	0.017
Italy-Rome	8597	2	0.021	0.039	0.199	0.721	0.019
Italy-Rome	8599	5	0.074	0.007	0.258	0.647	0.014
Italy-Rome	8601	2	0.034	0.242	0.03	0.676	0.017
Italy-Rome	8602	5	0.011	0.015	0.24	0.716	0.018
Italy-Rome	8603	5	0.007	0.026	0.078	0.863	0.026
Italy-Rome	8604	7	0.232	0.027	0.029	0.684	0.028
Italy-Rome	8609	5	0.018	0.014	0.515	0.438	0.015
Italy-Rome	8610	7	0.008	0.005	0.247	0.731	0.008
Italy-Rome	8611	2	0.01	0.094	0.155	0.732	0.009
Turkey	6477	5	0.009	0.052	0.866	0.067	0.006
Turkey	6478	10	0.006	0.018	0.944	0.023	0.009
Turkey	6480	7	0.014	0.01	0.779	0.129	0.069
Turkey	6481	5	0.034	0.005	0.026	0.069	0.866
Turkey	6482	7	0.02	0.118	0.378	0.44	0.045
Turkey	6484	5	0.008	0.01	0.894	0.067	0.022
Turkey	6486	5	0.007	0.031	0.766	0.156	0.04
Turkey	6487	7	0.011	0.011	0.938	0.033	0.006
Turkey	6488	7	0.026	0.031	0.774	0.154	0.015

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Turkey	6491	13	0.556	0.005	0.036	0.304	0.1
Turkey	6494	7	0.031	0.063	0.445	0.437	0.024
Turkey	6496	5	0.019	0.01	0.622	0.199	0.15
Turkey	6499	7	0.019	0.015	0.406	0.548	0.012
Turkey	6500	15	0.005	0.006	0.941	0.043	0.005
Turkey	6502	7	0.02	0.006	0.89	0.071	0.013
Turkey	6503	10	0.035	0.013	0.605	0.296	0.051
Turkey	6507	5	0.015	0.008	0.853	0.118	0.006
Turkey	6510	5	0.012	0.004	0.159	0.819	0.006
Turkey	6512	7	0.025	0.012	0.894	0.049	0.019
Turkey	6513	5	0.008	0.053	0.775	0.086	0.078
Turkey	6514	5	0.378	0.009	0.009	0.02	0.584
Turkey	6516	5	0.003	0.011	0.019	0.953	0.013
Turkey	6519	5	0.007	0.015	0.625	0.338	0.015
Turkey	6520	5	0.008	0.006	0.335	0.632	0.02
Turkey	6521	7	0.049	0.029	0.747	0.161	0.013
Turkey	6729	5	0.055	0.336	0.555	0.029	0.025
Turkey	6730	5	0.026	0.011	0.504	0.451	0.008
Turkey	6731	7	0.005	0.049	0.422	0.507	0.017
Turkey	6732	7	0.062	0.166	0.354	0.256	0.162
Turkey	6733	7	0.055	0.021	0.499	0.374	0.05
Turkey	6734	5	0.044	0.01	0.568	0.346	0.032
Turkey	6735	7	0.006	0.021	0.951	0.012	0.01
Turkey	6736	2	0.006	0.017	0.881	0.087	0.009
Turkey	6738	7	0.016	0.032	0.847	0.076	0.029
Turkey	6739	13	0.011	0.06	0.42	0.491	0.018
Turkey	6740	5	0.004	0.004	0.004	0.982	0.006
Turkey	6741	7	0.041	0.006	0.011	0.021	0.921
Turkey	6742	13	0.036	0.031	0.444	0.34	0.15
Turkey	6743	5	0.013	0.063	0.51	0.368	0.046
Turkey	6745	7	0.04	0.018	0.093	0.841	0.008
Turkey	6746	5	0.073	0.028	0.067	0.468	0.363
Turkey	6748	10	0.008	0.012	0.859	0.103	0.018
Turkey	6749	10	0.012	0.067	0.036	0.878	0.006

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Turkey	6750	5	0.005	0.005	0.314	0.669	0.007
Turkey	6753	10	0.115	0.083	0.612	0.129	0.062
Turkey	6754	10	0.005	0.22	0.525	0.242	0.008
Turkey	6755	10	0.042	0.018	0.566	0.361	0.012
Turkey	6756	10	0.005	0.015	0.421	0.551	0.008
Turkey	6758	13	0.073	0.059	0.718	0.136	0.015
Turkey	6759	13	0.013	0.006	0.892	0.071	0.018
Turkey	6760	7	0.008	0.019	0.261	0.665	0.048
Cyprus	10128	2	0.041	0.009	0.875	0.061	0.014
Cyprus	10129	5	0.005	0.008	0.705	0.274	0.008
Cyprus	10130	7	0.013	0.01	0.519	0.408	0.05
Cyprus	10131	2	0.024	0.017	0.788	0.021	0.15
Cyprus	10132	2	0.01	0.019	0.888	0.059	0.024
Cyprus	10133	15	0.009	0.027	0.856	0.089	0.019
Cyprus	10134	5	0.006	0.027	0.934	0.013	0.019
Cyprus	10135	5	0.017	0.005	0.802	0.03	0.146
Cyprus	10136	5	0.027	0.091	0.486	0.372	0.024
Cyprus	10137	2	0.04	0.269	0.603	0.079	0.009
Cyprus	10138	2	0.012	0.036	0.92	0.015	0.016
Cyprus	10139	2	0.02	0.047	0.584	0.017	0.331
Cyprus	10140	0	0.006	0.027	0.882	0.07	0.014
Cyprus	10141	5	0.019	0.034	0.394	0.54	0.013
Cyprus	10142	2	0.043	0.022	0.871	0.014	0.049
Cyprus	10143	5	0.012	0.015	0.953	0.014	0.006
Cyprus	10144	7	0.008	0.006	0.931	0.039	0.016
Cyprus	10145	5	0.005	0.008	0.906	0.076	0.005
Cyprus	10146	0	0.012	0.008	0.922	0.01	0.048
Cyprus	10147	5	0.004	0.006	0.899	0.085	0.007
Cyprus	10148	7	0.036	0.029	0.791	0.06	0.084
Cyprus	10149	7	0.021	0.2	0.436	0.321	0.023
Cyprus	10150	2	0.011	0.019	0.925	0.019	0.026
Cyprus	10151	2	0.019	0.042	0.88	0.04	0.018
Cyprus	10152	5	0.048	0.015	0.887	0.016	0.035
Cyprus	10153	0	0.015	0.02	0.924	0.026	0.014

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Cyprus	10154	0	0.011	0.129	0.709	0.038	0.112
Cyprus	10155	5	0.016	0.008	0.851	0.018	0.107
Cyprus	10156	7	0.125	0.017	0.752	0.09	0.016
Cyprus	10157	2	0.009	0.042	0.931	0.01	0.009
Lebanon	10235	10	0.045	0.046	0.769	0.069	0.07
Lebanon	10236	13	0.045	0.024	0.843	0.047	0.04
Lebanon	10237	5	0.044	0.01	0.56	0.024	0.363
Lebanon	10238	5	0.011	0.042	0.905	0.013	0.029
Lebanon	10239	5	0.01	0.011	0.953	0.015	0.011
Lebanon	10240	15	0.029	0.033	0.778	0.037	0.122
Lebanon	10241	13	0.105	0.053	0.53	0.265	0.047
Lebanon	10242	7	0.007	0.031	0.883	0.066	0.014
Lebanon	10243	10	0.058	0.05	0.76	0.039	0.093
Lebanon	10244	5	0.049	0.104	0.786	0.02	0.042
Lebanon	10245	13	0.01	0.268	0.592	0.072	0.058
Lebanon	10246	2	0.004	0.024	0.94	0.013	0.018
Lebanon	10247	18	0.012	0.289	0.671	0.015	0.014
Lebanon	10248	7	0.007	0.01	0.884	0.089	0.01
Lebanon	10249	13	0.013	0.016	0.181	0.75	0.04
Lebanon	10250	2	0.023	0.138	0.748	0.081	0.01
Lebanon	10251	2	0.006	0.013	0.872	0.097	0.012
Lebanon	10252	5	0.019	0.09	0.579	0.3	0.011
Lebanon	10253	15	0.006	0.008	0.938	0.042	0.005
Lebanon	10254	13	0.023	0.04	0.867	0.016	0.053
Lebanon	10255	7	0.026	0.174	0.702	0.078	0.02
Lebanon	10256	18	0.007	0.008	0.969	0.01	0.006
Lebanon	10257	5	0.026	0.071	0.84	0.007	0.056
Lebanon	10258	7	0.008	0.015	0.933	0.024	0.02
Lebanon	10259	10	0.014	0.01	0.058	0.085	0.833
Lebanon	10260	2	0.011	0.021	0.939	0.011	0.018
Lebanon	10261	10	0.015	0.077	0.824	0.069	0.015
Lebanon	10262	5	0.068	0.062	0.678	0.139	0.052
Lebanon	10263	7	0.008	0.011	0.949	0.011	0.021
Lebanon	10264	5	0.017	0.015	0.808	0.092	0.067

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Lebanon	10265	7	0.009	0.12	0.841	0.02	0.01
Lebanon	10266	0	0.013	0.014	0.822	0.037	0.114
Lebanon	10267	18	0.008	0.007	0.893	0.085	0.007
Lebanon	10268	5	0.018	0.005	0.914	0.028	0.035
Lebanon	10270	13	0.107	0.117	0.637	0.027	0.113
Lebanon	10271	18	0.032	0.22	0.088	0.524	0.136
Lebanon	10273	10	0.053	0.068	0.517	0.309	0.052
Lebanon	10274	13	0.065	0.009	0.307	0.029	0.591
Lebanon	10276	10	0.005	0.014	0.931	0.015	0.035
Lebanon	10277	2	0.18	0.045	0.669	0.087	0.019
Lebanon	10278	15	0.039	0.02	0.89	0.026	0.025
Lebanon	10279	0	0.01	0.051	0.835	0.015	0.089
Lebanon	10280	0	0.021	0.046	0.497	0.056	0.381
Lebanon	10281	10	0.009	0.046	0.925	0.01	0.01
Lebanon	10282	10	0.011	0.022	0.906	0.012	0.049
Lebanon	10283	23	0.008	0.01	0.945	0.021	0.016
Lebanon	10284	23	0.04	0.105	0.607	0.051	0.197
Lebanon	10285	2	0.168	0.017	0.727	0.063	0.025
Lebanon	10286	15	0.02	0.305	0.551	0.015	0.108
Lebanon	10287	5	0.074	0.055	0.321	0.38	0.171
Lebanon	10288	13	0.01	0.004	0.023	0.958	0.005
Lebanon	10289	13	0.009	0.029	0.931	0.01	0.021
Lebanon	10290	5	0.095	0.033	0.59	0.011	0.271
Lebanon	10291	15	0.066	0.147	0.732	0.023	0.033
Lebanon	10292	13	0.054	0.077	0.386	0.032	0.45
Lebanon	10294	2	0.033	0.056	0.74	0.062	0.109
Lebanon	10295	7	0.023	0.08	0.781	0.05	0.066
Lebanon	10297	5	0.03	0.128	0.798	0.025	0.02
Lebanon	10298	10	0.029	0.495	0.38	0.018	0.079
Lebanon	10299	2	0.114	0.085	0.247	0.388	0.166
Lebanon	10300	2	0.021	0.083	0.835	0.018	0.042
Israel	4962	7	0.007	0.152	0.79	0.033	0.019
Israel	4963	5	0.017	0.031	0.893	0.028	0.031
Israel	4964	7	0.013	0.102	0.333	0.531	0.02

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Israel	4966	5	0.008	0.009	0.898	0.03	0.054
Israel	4967	5	0.108	0.021	0.519	0.317	0.036
Israel	4968	7	0.028	0.041	0.877	0.024	0.03
Israel	4969	2	0.065	0.018	0.557	0.307	0.053
Israel	4970	7	0.022	0.054	0.691	0.138	0.096
Israel	4971	2	0.065	0.077	0.75	0.038	0.069
Israel	4972	10	0.03	0.016	0.828	0.089	0.037
Israel	4973	5	0.01	0.011	0.951	0.017	0.012
Israel	4974	5	0.009	0.029	0.888	0.052	0.023
Israel	4975	2	0.007	0.015	0.832	0.132	0.014
Israel	4976	5	0.007	0.016	0.629	0.302	0.046
Israel	4977	15	0.01	0.035	0.625	0.316	0.014
Israel	4978	10	0.019	0.107	0.634	0.179	0.061
Israel	4979	7	0.01	0.024	0.91	0.048	0.007
Israel	4980	2	0.157	0.161	0.421	0.113	0.148
Israel	4981	15	0.158	0.039	0.778	0.013	0.012
Israel	4982	10	0.012	0.008	0.676	0.269	0.035
Israel	4983	7	0.109	0.03	0.027	0.797	0.036
Israel	4984	2	0.033	0.006	0.009	0.926	0.025
Israel	4985	21	0.034	0.012	0.865	0.022	0.067
Israel	4986	5	0.015	0.013	0.947	0.016	0.01
Israel	4988	13	0.027	0.03	0.896	0.02	0.028
Israel	4989	5	0.016	0.059	0.825	0.01	0.091
Israel	4990	5	0.034	0.011	0.88	0.039	0.036
Israel	4992	7	0.007	0.007	0.763	0.213	0.01
Israel	4993	7	0.008	0.011	0.95	0.02	0.011
Israel	4994	5	0.007	0.006	0.97	0.012	0.005
Israel	4995	5	0.026	0.063	0.85	0.02	0.041
Israel	4996	2	0.02	0.026	0.933	0.012	0.009
Israel	4997	15	0.012	0.086	0.853	0.017	0.032
Israel	4998	10	0.019	0.037	0.583	0.322	0.039
Israel	5000	7	0.025	0.021	0.752	0.017	0.185
Israel	5001	5	0.013	0.051	0.791	0.128	0.018
Israel	5002	7	0.012	0.012	0.855	0.098	0.024

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Israel	5003	7	0.028	0.01	0.883	0.071	0.008
Israel	5004	15	0.015	0.028	0.313	0.513	0.131
Israel	5005	7	0.008	0.018	0.837	0.116	0.021
Israel	5006	10	0.006	0.012	0.95	0.027	0.005
Israel	5007	5	0.269	0.01	0.145	0.464	0.112
Israel	5008	5	0.011	0.035	0.912	0.025	0.017
Israel	5009	13	0.055	0.101	0.376	0.381	0.087
Israel	5010	15	0.008	0.009	0.927	0.048	0.008
Israel	5011	13	0.016	0.043	0.792	0.119	0.029
Egypt-Cairo	8190	15	0.01	0.01	0.895	0.065	0.022
Egypt-Cairo	8192	18	0.015	0.033	0.668	0.099	0.186
Egypt-Cairo	8193	18	0.005	0.019	0.957	0.009	0.01
Egypt-Cairo	8196	15	0.038	0.015	0.85	0.021	0.076
Egypt-Cairo	8203	15	0.024	0.008	0.927	0.022	0.02
Egypt-Cairo	8215	10	0.008	0.007	0.97	0.008	0.008
Egypt-Cairo	8198	10	0.021	0.015	0.889	0.057	0.017
Egypt-Cairo	8194	7	0.019	0.014	0.849	0.099	0.019
Egypt-Cairo	8211	5	0.011	0.03	0.928	0.022	0.009
Egypt-Cairo	8216	7	0.013	0.011	0.72	0.246	0.011
Egypt-Cairo	8195	5	0.035	0.02	0.853	0.013	0.079
Egypt-Cairo	8199	2	0.006	0.01	0.943	0.008	0.033
Egypt-Cairo	8200	5	0.01	0.018	0.915	0.051	0.006
Egypt-Cairo	8201	5	0.102	0.101	0.748	0.024	0.025
Egypt-Cairo	8202	5	0.038	0.02	0.042	0.034	0.866
Egypt-Cairo	8204	5	0.022	0.009	0.917	0.02	0.032
Egypt-Cairo	8208	2	0.08	0.016	0.78	0.099	0.025
Egypt-Cairo	8210	5	0.007	0.05	0.891	0.013	0.04
Egypt-Cairo	8214	2	0.006	0.006	0.977	0.007	0.004
Egypt-Cairo	8191	5	0.074	0.045	0.784	0.051	0.046
Egypt-Cairo	8197	2	0.01	0.02	0.915	0.008	0.047
Egypt-Cairo	8205	2	0.023	0.011	0.83	0.076	0.059
Egypt-Cairo	8206	2	0.017	0.008	0.841	0.091	0.043
Egypt-Cairo	8207	2	0.027	0.013	0.894	0.023	0.044
Egypt-Cairo	8209	2	0.008	0.006	0.939	0.041	0.005

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Egypt-Cairo	8212	2	0.009	0.009	0.969	0.008	0.005
Egypt-Cairo	8213	2	0.008	0.011	0.964	0.011	0.006
Egypt-Cairo	9942	0	0.035	0.223	0.7	0.011	0.031
Egypt-Cairo	9943	15	0.336	0.014	0.01	0.252	0.388
Egypt-Cairo	9944	7	0.004	0.028	0.907	0.052	0.01
Egypt-Cairo	9945	2	0.012	0.015	0.797	0.161	0.015
Egypt-Cairo	9946	13	0.048	0.03	0.803	0.018	0.1
Egypt-Cairo	9947	7	0.01	0.038	0.917	0.021	0.014
Egypt-Cairo	9948	0	0.02	0.007	0.901	0.051	0.019
Egypt-Cairo	9949	0	0.022	0.019	0.894	0.05	0.016
Egypt-Cairo	9950	0	0.019	0.015	0.807	0.096	0.062
Egypt-Cairo	9951	5	0.012	0.004	0.952	0.02	0.012
Egypt-Cairo	9952	15	0.01	0.01	0.689	0.277	0.013
Egypt-Cairo	9953	21	0.009	0.085	0.731	0.158	0.017
Egypt-Cairo	9954	2	0.14	0.007	0.816	0.019	0.019
Egypt-Cairo	9955	0	0.061	0.007	0.214	0.566	0.152
Egypt-Cairo	9956	18	0.043	0.019	0.899	0.027	0.012
Egypt-Cairo	9957	5	0.09	0.009	0.868	0.02	0.013
Egypt-Cairo	9958	15	0.038	0.007	0.876	0.044	0.035
Egypt-Cairo	9959	5	0.03	0.027	0.687	0.214	0.043
Egypt-Cairo	9960	2	0.03	0.053	0.882	0.024	0.011
Egypt-Cairo	9961	5	0.074	0.014	0.205	0.15	0.557
Egypt-Cairo	9962	7	0.01	0.069	0.882	0.019	0.02
Egypt-Cairo	9963	2	0.021	0.013	0.925	0.025	0.016
Egypt-Cairo	9964	0	0.009	0.006	0.942	0.023	0.02
Egypt-Cairo	10021	0	0.006	0.009	0.971	0.008	0.007
Egypt-Cairo	10022	0	0.03	0.006	0.924	0.023	0.016
Egypt-Cairo	10023	0	0.01	0.004	0.958	0.006	0.021
Egypt-Cairo	10024	0	0.015	0.009	0.911	0.057	0.009
Egypt-Cairo	10025	0	0.005	0.014	0.819	0.149	0.013
Egypt-Cairo	10026	2	0.045	0.009	0.914	0.022	0.011
Egypt-Cairo	10027	0	0.019	0.023	0.639	0.089	0.229
Egypt-Cairo	10028	0	0.013	0.026	0.941	0.006	0.015
Egypt-Cairo	10029	0	0.008	0.021	0.959	0.006	0.006

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Egypt-Cairo	10030	0	0.03	0.009	0.902	0.048	0.011
Egypt-Cairo	10031	2	0.005	0.018	0.964	0.005	0.008
Egypt-Cairo	10032	0	0.006	0.027	0.956	0.005	0.006
Egypt-Cairo	10033	2	0.014	0.005	0.956	0.006	0.019
Egypt-Cairo	10034	0	0.008	0.008	0.965	0.01	0.009
Egypt-Cairo	10035	0	0.175	0.012	0.765	0.01	0.038
Egypt-Cairo	10037	5	0.011	0.014	0.843	0.081	0.052
Egypt-Cairo	10042	0	0.026	0.031	0.834	0.029	0.08
Egypt-Cairo	10043	7	0.005	0.009	0.924	0.047	0.016
Egypt-Cairo	10044	2	0.009	0.007	0.954	0.016	0.014
Egypt-Cairo	10045	2	0.017	0.012	0.933	0.017	0.021
Egypt-Cairo	10046	0	0.039	0.007	0.891	0.025	0.038
Egypt-Cairo	10047	0	0.022	0.025	0.922	0.012	0.019
Egypt-Cairo	10048	2	0.02	0.004	0.909	0.05	0.018
Egypt-Cairo	10083	21	0.01	0.006	0.907	0.062	0.014
Egypt-Cairo	10040	0	0.045	0.019	0.463	0.437	0.036
Egypt-Cairo	10041	0	0.031	0.01	0.487	0.439	0.033
Egypt-Cairo	10049	5	0.028	0.028	0.89	0.024	0.03
Egypt-Cairo	10084	2	0.015	0.012	0.93	0.017	0.027
Egypt-Cairo	10085	23	0.012	0.011	0.861	0.066	0.049
Egypt-Cairo	10087	5	0.007	0.004	0.973	0.008	0.008
Egypt-Cairo	10090	7	0.067	0.009	0.871	0.02	0.033
Egypt-Cairo	9968	0	0.006	0.027	0.911	0.039	0.017
Egypt-Asuit	10091	2	0.007	0.007	0.956	0.021	0.009
Egypt-Asuit	10093	0	0.006	0.005	0.962	0.016	0.011
Egypt-Asuit	10094	5	0.008	0.007	0.959	0.012	0.015
Egypt-Asuit	10095	2	0.005	0.009	0.959	0.012	0.016
Egypt-Asuit	10096	0	0.015	0.005	0.96	0.011	0.009
Egypt-Asuit	10098	0	0.006	0.004	0.975	0.007	0.007
Egypt-Asuit	10099	5	0.007	0.005	0.974	0.006	0.008
Egypt-Asuit	10100	2	0.093	0.042	0.721	0.081	0.063
Egypt-Asuit	10101	2	0.021	0.017	0.919	0.015	0.028
Egypt-Asuit	10102	0	0.023	0.014	0.772	0.009	0.182
Egypt-Luxor	10038	0	0.044	0.008	0.915	0.01	0.023

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population				
			1	2	3	4	5
Egypt-Luxor	10039	2	0.005	0.051	0.932	0.008	0.005
Egypt-Luxor	10050	2	0.048	0.015	0.897	0.009	0.031
Egypt-Luxor	10051	0	0.005	0.005	0.969	0.012	0.009
Egypt-Luxor	10052	0	0.018	0.015	0.81	0.023	0.134
Egypt-Luxor	10053	0	0.006	0.074	0.863	0.027	0.03
Egypt-Luxor	10054	0	0.065	0.02	0.877	0.021	0.018
Egypt-Luxor	10055	0	0.008	0.01	0.956	0.014	0.012
Egypt-Luxor	10056	0	0.049	0.024	0.91	0.009	0.008
Egypt-Luxor	10057	7	0.026	0.079	0.858	0.016	0.02
Egypt-Luxor	10058	0	0.01	0.008	0.962	0.014	0.006
Egypt-Luxor	10060	0	0.011	0.011	0.922	0.047	0.009
Egypt-Luxor	10061	0	0.443	0.008	0.449	0.017	0.084
Egypt-Luxor	10062	5	0.023	0.01	0.893	0.063	0.011
Egypt-Luxor	10063	2	0.024	0.071	0.841	0.026	0.039
Egypt-Luxor	10064	0	0.029	0.013	0.88	0.021	0.057
Egypt-Luxor	10065	0	0.008	0.015	0.893	0.03	0.054
Egypt-Luxor	10066	2	0.05	0.015	0.841	0.067	0.026
Egypt-Luxor	10067	2	0.005	0.018	0.961	0.008	0.008
Egypt-Luxor	10068	0	0.119	0.004	0.812	0.014	0.05
Egypt-Luxor	10069	2	0.007	0.009	0.958	0.012	0.014
Egypt-Luxor	10070	0	0.422	0.007	0.465	0.021	0.085
Egypt-Luxor	10071	2	0.143	0.023	0.772	0.017	0.045
Egypt-Luxor	10072	2	0.03	0.008	0.946	0.008	0.008
Egypt-Luxor	10073	5	0.008	0.006	0.04	0.935	0.011
Egypt-Luxor	10074	0	0.008	0.005	0.972	0.008	0.007
Egypt-Luxor	10079	0	0.007	0.014	0.778	0.085	0.116
Egypt-Luxor	10080	0	0.021	0.017	0.591	0.059	0.311
Egypt-Abu Simbel	10076	5	0.088	0.007	0.857	0.019	0.03
Egypt-Abu Simbel	10077	13	0.019	0.007	0.888	0.009	0.077
Egypt-Abu Simbel	10081	7	0.02	0.01	0.927	0.015	0.028
Egypt-Abu Simbel	10089	0	0.004	0.004	0.881	0.102	0.008
Egypt-Abu Simbel	10092	0	0.013	0.01	0.962	0.006	0.009
Iraq-West	9587	0	0.02	0.725	0.091	0.026	0.138
Iraq-West	10202	23	0.015	0.746	0.191	0.031	0.017
Iraq-West	10204	23	0.006	0.763	0.166	0.051	0.013
Iraq-West	11854	0	0.037	0.879	0.06	0.013	0.009
Iraq-West	11860	21	0.008	0.881	0.017	0.006	0.088
Iraq-West	11861	7	0.257	0.549	0.157	0.02	0.017
Iraq-West	11863	21	0.016	0.94	0.009	0.022	0.012
Iraq-West	11864	2	0.033	0.901	0.026	0.007	0.032
Iraq-West	11888	5	0.015	0.946	0.007	0.004	0.028
Iraq-West	11889	7	0.016	0.7	0.03	0.224	0.029
Iraq-West	11890	2	0.103	0.695	0.157	0.015	0.031
Iraq-West	11891	0	0.009	0.632	0.308	0.037	0.014
Iraq-Baghdad	11847	5	0.017	0.858	0.081	0.015	0.029
Iraq-Baghdad	11848	0	0.081	0.773	0.017	0.013	0.116
Iraq-Baghdad	11849	5	0.055	0.782	0.108	0.014	0.042
Iraq-Baghdad	11850	0	0.021	0.902	0.017	0.045	0.015
Iraq-Baghdad	11852	0	0.02	0.868	0.039	0.016	0.057
Iraq-Baghdad	11853	5	0.029	0.908	0.02	0.009	0.035
Iraq-Baghdad	11855	5	0.021	0.874	0.049	0.01	0.047
Iraq-Baghdad	11856	2	0.008	0.842	0.064	0.052	0.034
Iraq-Baghdad	11857	0	0.016	0.578	0.158	0.233	0.014
Iraq-Baghdad	11858	2	0.008	0.956	0.013	0.012	0.011
Iraq-Baghdad	11859	5	0.017	0.85	0.056	0.026	0.051
Iraq-Baghdad	11862	2	0.274	0.562	0.06	0.083	0.02
Iraq-Baghdad	11865	5	0.197	0.624	0.107	0.011	0.061
Iraq-Baghdad	11868	2	0.009	0.965	0.011	0.007	0.009
Iraq-Baghdad	11869	2	0.027	0.652	0.083	0.224	0.014
Iraq-Baghdad	11870	0	0.102	0.707	0.111	0.057	0.022
Iraq-Baghdad	11871	5	0.011	0.507	0.416	0.009	0.056
Iraq-Baghdad	11872	2	0.005	0.711	0.25	0.021	0.012
Iraq-Baghdad	11873	7	0.042	0.551	0.379	0.008	0.02

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Iraq-Baghdad	11874	2	0.062	0.859	0.054	0.016	0.01
Iraq-Baghdad	11875	15	0.186	0.587	0.013	0.011	0.204
Iraq-Baghdad	11876	21	0.029	0.806	0.082	0.013	0.07
Iraq-Baghdad	11877	7	0.068	0.848	0.055	0.012	0.017
Iraq-Baghdad	11878	7	0.015	0.535	0.374	0.055	0.02
Iraq-Baghdad	11879	2	0.021	0.771	0.029	0.01	0.168
Iraq-Baghdad	11880	10	0.01	0.906	0.053	0.012	0.018
Iraq-Baghdad	11881	0	0.115	0.634	0.155	0.069	0.027
Iraq-Baghdad	11882	15	0.017	0.826	0.122	0.018	0.017
Iraq-Baghdad	11883	0	0.013	0.67	0.108	0.182	0.026
Iraq-Baghdad	11884	0	0.015	0.961	0.006	0.005	0.012
Iraq-Baghdad	11885	0	0.011	0.949	0.021	0.005	0.013
Iraq-Baghdad	11886	0	0.088	0.605	0.236	0.014	0.058
Iraq-Baghdad	11887	13	0.05	0.814	0.066	0.016	0.054
Iran	9419	2	0.043	0.769	0.047	0.128	0.012
Iran	9420	2	0.131	0.822	0.015	0.008	0.023
Iran	9421	5	0.013	0.95	0.018	0.012	0.006
Iran	9422	5	0.13	0.751	0.088	0.02	0.011
Iran	9424	7	0.125	0.853	0.006	0.005	0.011
Iran	9425	7	0.017	0.965	0.005	0.004	0.008
Iran	9426	2	0.012	0.957	0.008	0.013	0.01
Iran	9427	2	0.006	0.963	0.01	0.012	0.009
Iran	9428	5	0.01	0.968	0.007	0.007	0.008
Iran	9429	15	0.095	0.821	0.029	0.017	0.039
Iran	9430	7	0.05	0.865	0.031	0.021	0.033
Iran	9431	7	0.064	0.747	0.038	0.021	0.129
Iran	9432	13	0.008	0.957	0.006	0.006	0.023
Iran	9433	5	0.034	0.931	0.013	0.01	0.013
Iran	9434	7	0.127	0.754	0.013	0.041	0.065
Iran	9435	5	0.017	0.923	0.007	0.009	0.043
Iran	9436	2	0.008	0.962	0.012	0.01	0.008
Iran	9437	2	0.009	0.952	0.013	0.01	0.017
Iran	9438	2	0.015	0.956	0.005	0.007	0.017
Iran	9439	5	0.155	0.729	0.043	0.028	0.044

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Iran	9440	2	0.005	0.963	0.014	0.004	0.014
Iran	9441	7	0.006	0.974	0.005	0.005	0.009
Iran	9442	5	0.014	0.873	0.019	0.023	0.071
Iran	9443	10	0.013	0.953	0.009	0.013	0.013
Iran	9444	5	0.006	0.981	0.005	0.004	0.004
Iran	9445	5	0.004	0.983	0.003	0.003	0.006
Iran	9446	10	0.014	0.962	0.006	0.005	0.013
Iran	9447	7	0.007	0.967	0.005	0.009	0.012
Iran	9448	13	0.005	0.977	0.005	0.005	0.008
Iran	9449	5	0.003	0.985	0.004	0.004	0.004
Iran	9450	7	0.025	0.947	0.016	0.005	0.006
Iran	9451	10	0.098	0.867	0.011	0.007	0.016
Iran	9452	2	0.01	0.952	0.008	0.009	0.022
Iran	9453	7	0.004	0.978	0.006	0.007	0.005
Iran	9454	7	0.005	0.98	0.006	0.005	0.005
Iran	9455	13	0.008	0.958	0.011	0.008	0.014
Iran	9456	2	0.021	0.926	0.015	0.017	0.02
Iran	9457	5	0.004	0.975	0.01	0.006	0.005
Iran	9458	2	0.014	0.958	0.01	0.005	0.012
Iran	9459	5	0.006	0.978	0.004	0.004	0.007
Iran	9460	10	0.014	0.925	0.018	0.023	0.02
Iran	9461	10	0.005	0.973	0.006	0.006	0.01
Iran	9462	10	0.008	0.941	0.008	0.019	0.024
Iran	9463	15	0.008	0.965	0.012	0.006	0.009
Iran	9464	7	0.011	0.972	0.006	0.004	0.007
Iran	9465	5	0.005	0.968	0.009	0.008	0.01
Iran	9466	13	0.006	0.931	0.027	0.014	0.022
Iran	9468	10	0.029	0.916	0.016	0.029	0.01
Iran	9469	10	0.038	0.861	0.029	0.028	0.043
Iran	9470	13	0.022	0.921	0.017	0.021	0.018
Iran	9471	7	0.005	0.969	0.008	0.01	0.008
Iran	9472	10	0.01	0.958	0.015	0.006	0.01
Iran	9473	5	0.01	0.969	0.006	0.006	0.01
Iran	9474	7	0.006	0.959	0.014	0.011	0.01

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population				
			1	2	3	4	5
Iran	9475	7	0.004	0.962	0.015	0.009	0.009
Iran	9476	7	0.012	0.975	0.006	0.004	0.004
Iran	9477	7	0.068	0.902	0.009	0.012	0.008
Iran	9478	5	0.031	0.796	0.017	0.012	0.144
Iran	9479	7	0.012	0.975	0.004	0.004	0.005
Iran	9480	13	0.017	0.939	0.008	0.013	0.022
Iran	9481	10	0.008	0.958	0.018	0.009	0.007
Iran	9482	5	0.039	0.878	0.033	0.021	0.03
Iran	9483	13	0.195	0.73	0.013	0.014	0.047
Iran	9484	2	0.007	0.713	0.187	0.079	0.015
Iran	9485	10	0.101	0.862	0.013	0.006	0.019
Iran	9486	10	0.007	0.944	0.012	0.027	0.009
Iran	9487	5	0.011	0.951	0.008	0.006	0.024
Iran	9488	10	0.007	0.967	0.01	0.009	0.007
Iran	9489	15	0.009	0.922	0.01	0.007	0.052
Iran	9490	13	0.014	0.961	0.005	0.007	0.014
Iran	9491	7	0.006	0.981	0.005	0.004	0.005
Iran	9492	10	0.005	0.969	0.006	0.007	0.014
Iran	9493	2	0.023	0.952	0.008	0.008	0.01
Iran	9494	7	0.004	0.972	0.012	0.006	0.006
Iran	9495	5	0.007	0.971	0.005	0.006	0.011
Iran	9497	10	0.005	0.971	0.005	0.006	0.012
Iran	9498	10	0.013	0.965	0.008	0.006	0.008
Iran	9499	5	0.102	0.868	0.009	0.006	0.015
Iran	9500	7	0.006	0.97	0.004	0.005	0.015
Iran	9501	2	0.009	0.854	0.035	0.047	0.056
Iran	9502	5	0.279	0.693	0.012	0.009	0.007
Iran	9503	7	0.008	0.973	0.004	0.004	0.011
Iran	9504	5	0.004	0.984	0.005	0.004	0.003
Iran	9505	5	0.007	0.985	0.003	0.002	0.003
Iran	9506	7	0.01	0.919	0.009	0.019	0.043
Iran	9507	31	0.044	0.885	0.028	0.015	0.028
Iran	9508	10	0.121	0.844	0.009	0.006	0.02
Iran	9509	18	0.043	0.929	0.01	0.009	0.01
Iran	9510	15	0.069	0.908	0.007	0.007	0.009
Iran	9511	13	0.007	0.959	0.008	0.02	0.006
Iran	9512	28	0.015	0.812	0.03	0.117	0.026
Iran	9513	21	0.007	0.952	0.013	0.013	0.015
Iran	9514	15	0.015	0.773	0.123	0.053	0.036
Iran	9515	13	0.008	0.791	0.01	0.165	0.025
Iran	9516	15	0.01	0.922	0.015	0.016	0.037
Iran	9517	13	0.059	0.823	0.019	0.04	0.058
Iran	9518	13	0.026	0.712	0.04	0.199	0.024
Iran	9519	18	0.008	0.887	0.016	0.074	0.015
Iran	9520	15	0.006	0.86	0.023	0.086	0.025
Iran	9521	21	0.01	0.874	0.017	0.02	0.078
Iran	9522	15	0.075	0.642	0.191	0.05	0.042
Iran	9523	13	0.011	0.835	0.104	0.037	0.014
Iran	9524	15	0.054	0.923	0.007	0.005	0.01
Iran	9526	15	0.12	0.853	0.009	0.005	0.012
Iran	9527	13	0.028	0.852	0.023	0.024	0.073
Iran	9528	15	0.007	0.977	0.004	0.005	0.006
Iran	9529	15	0.03	0.935	0.005	0.003	0.027
Iran	9530	10	0.047	0.926	0.009	0.009	0.01
Iran	9531	15	0.033	0.784	0.05	0.045	0.088
Iran	9532	5	0.006	0.974	0.006	0.006	0.008
Dubai	10104	2	0.004	0.298	0.178	0.038	0.482
Dubai	10105	2	0.024	0.189	0.018	0.018	0.751
Dubai	10106	18	0.007	0.023	0.015	0.007	0.947
Dubai	10107	5	0.165	0.384	0.039	0.045	0.367
Dubai	10108	2	0.034	0.029	0.026	0.011	0.9
Dubai	10109	18	0.194	0.53	0.023	0.029	0.224
Dubai	10110	7	0.016	0.364	0.025	0.045	0.55
Dubai	10111	13	0.009	0.019	0.017	0.006	0.949
Dubai	10112	7	0.037	0.024	0.098	0.046	0.794
Dubai	10120	15	0.008	0.059	0.016	0.017	0.9
Kenya-Nairobi	9833	13	0.047	0.202	0.023	0.593	0.135
Kenya-Nairobi	9834	0	0.02	0.009	0.017	0.709	0.245

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Kenya-Nairobi	9835	0	0.208	0.009	0.075	0.534	0.173
Kenya-Nairobi	9836	2	0.033	0.013	0.01	0.673	0.27
Kenya-Nairobi	9837	0	0.116	0.056	0.028	0.759	0.041
Kenya-Nairobi	9838	2	0.024	0.239	0.087	0.614	0.036
Kenya-Nairobi	9839	0	0.03	0.02	0.036	0.221	0.694
Kenya-Nairobi	9840	0	0.012	0.017	0.325	0.466	0.18
Kenya-Nairobi	9841	2	0.013	0.01	0.016	0.805	0.157
Kenya-Nairobi	9842	2	0.127	0.053	0.041	0.71	0.069
Kenya-Nairobi	9843	0	0.014	0.011	0.017	0.752	0.206
Kenya-Nairobi	9844	2	0.062	0.01	0.018	0.821	0.089
Kenya-Nairobi	9845	0	0.056	0.024	0.188	0.69	0.042
Kenya-Nairobi	9846	2	0.157	0.016	0.033	0.579	0.216
Kenya-Nairobi	9847	0	0.022	0.02	0.016	0.839	0.103
Kenya-Nairobi	9848	0	0.112	0.033	0.214	0.583	0.058
Kenya-Nairobi	9849	5	0.024	0.009	0.062	0.19	0.715
Kenya-Nairobi	9850	7	0.018	0.022	0.067	0.784	0.109
Kenya-Nairobi	9851	2	0.008	0.008	0.008	0.518	0.457
Kenya-Nairobi	9852	7	0.005	0.008	0.092	0.52	0.375
Kenya-Nairobi	9853	2	0.029	0.083	0.016	0.766	0.107
Kenya-Nairobi	9854	0	0.007	0.088	0.035	0.824	0.046
Kenya-Nairobi	9855	2	0.009	0.023	0.166	0.517	0.285
Kenya-Nairobi	9856	2	0.013	0.008	0.024	0.665	0.29
Kenya-Nairobi	9857	23	0.13	0.014	0.043	0.505	0.309
Kenya-Nairobi	9858	15	0.057	0.009	0.015	0.837	0.081
Kenya-Nairobi	9859	15	0.105	0.021	0.007	0.817	0.05
Kenya-Nairobi	9860	5	0.071	0.016	0.012	0.839	0.062
Kenya-Nairobi	9861	2	0.007	0.013	0.048	0.897	0.035
Kenya-Nairobi	9862	7	0.028	0.006	0.094	0.505	0.367
Kenya-Nairobi	9863	2	0.02	0.011	0.008	0.612	0.35
Kenya-Nairobi	9864	7	0.005	0.087	0.022	0.683	0.204
Kenya-Nairobi	9865	10	0.06	0.065	0.079	0.36	0.436
Kenya-Nairobi	9866	7	0.032	0.007	0.177	0.641	0.143
Kenya-Nairobi	9867	0	0.044	0.052	0.085	0.361	0.458
Kenya-Nairobi	9868	5	0.008	0.014	0.286	0.523	0.169

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Kenya-Pate	2000	7	0.005	0.007	0.042	0.175	0.77
Kenya-Pate	2001	13	0.005	0.166	0.016	0.006	0.807
Kenya-Pate	2002	2	0.01	0.174	0.013	0.005	0.798
Kenya-Pate	2003	2	0.024	0.017	0.014	0.016	0.928
Kenya-Pate	2004	10	0.007	0.031	0.058	0.024	0.88
Kenya-Pate	2006	7	0.075	0.064	0.044	0.014	0.802
Kenya-Pate	2007	7	0.01	0.036	0.032	0.033	0.888
Kenya-Pate	2009	28	0.007	0.017	0.313	0.053	0.61
Kenya-Pate	2011	13	0.006	0.004	0.026	0.012	0.953
Kenya-Lamu	1848	10	0.015	0.014	0.023	0.013	0.935
Kenya-Lamu	2014	5	0.005	0.01	0.042	0.011	0.932
Kenya-Lamu	2015	7	0.023	0.019	0.775	0.023	0.16
Kenya-Lamu	2016	7	0.007	0.009	0.066	0.07	0.848
Kenya-Lamu	2018	2	0.01	0.036	0.373	0.055	0.526
Kenya-Lamu	2019	7	0.007	0.009	0.055	0.04	0.889
Kenya-Lamu	2021	7	0.005	0.187	0.033	0.022	0.753
Kenya-Lamu	2023	13	0.008	0.008	0.074	0.042	0.867
Kenya-Lamu	2024	2	0.006	0.042	0.017	0.009	0.927
Kenya-Lamu	2025	5	0.02	0.039	0.106	0.012	0.823
Kenya-Lamu	2026	18	0.006	0.008	0.032	0.006	0.949
Kenya-Lamu	2027	26	0.014	0.092	0.047	0.053	0.794
Kenya-Lamu	2029	5	0.006	0.033	0.016	0.008	0.938
Kenya-Lamu	2030	5	0.006	0.011	0.024	0.132	0.827
Kenya-Lamu	2031	18	0.038	0.079	0.163	0.301	0.419
Kenya-Lamu	2032	10	0.01	0.251	0.023	0.02	0.696
Kenya-Lamu	2033	13	0.008	0.02	0.13	0.023	0.818
Kenya-Lamu	3241	18	0.045	0.011	0.073	0.061	0.81
Kenya-Lamu	3246	7	0.015	0.021	0.832	0.017	0.114
Kenya-Lamu	3247	13	0.01	0.024	0.073	0.127	0.765
India-Udaipur	11835	10	0.237	0.215	0.16	0.034	0.354
India-Udaipur	11836	5	0.027	0.34	0.026	0.01	0.596
India-Udaipur	11837	5	0.038	0.32	0.017	0.007	0.618
India-Agra	11823	0	0.008	0.447	0.015	0.008	0.522
India-Agra	11824	0	0.007	0.223	0.016	0.006	0.747

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
India-Agra	11825	2	0.013	0.494	0.012	0.013	0.468
India-Agra	11826	7	0.007	0.473	0.007	0.007	0.506
India-Agra	11827	0	0.008	0.407	0.015	0.005	0.566
India-Agra	11828	5	0.019	0.35	0.033	0.007	0.591
India-Agra	11829	5	0.012	0.166	0.035	0.023	0.764
India-Agra	11830	5	0.009	0.37	0.014	0.005	0.602
India-Agra	11831	5	0.01	0.442	0.041	0.013	0.495
India-Agra	11832	0	0.009	0.509	0.012	0.006	0.464
India-Agra	11833	2	0.022	0.47	0.015	0.006	0.487
India-Agra	11834	5	0.007	0.48	0.007	0.007	0.499
India-Hyderbad	11802	7	0.047	0.013	0.443	0.044	0.452
India-Hyderbad	11803	7	0.014	0.04	0.134	0.011	0.8
India-Hyderbad	11804	10	0.408	0.092	0.012	0.011	0.476
India-Hyderbad	11805	5	0.038	0.016	0.02	0.025	0.901
India-Hyderbad	11807	2	0.019	0.03	0.011	0.006	0.934
India-Hyderbad	11808	2	0.125	0.006	0.009	0.012	0.847
India-Hyderbad	11809	2	0.005	0.076	0.105	0.125	0.689
India-Hyderbad	11810	0	0.047	0.02	0.077	0.016	0.84
India-Hyderbad	11811	0	0.019	0.018	0.015	0.007	0.941
India-Hyderbad	11812	13	0.072	0.244	0.013	0.005	0.666
India-Hyderbad	11813	10	0.319	0.127	0.032	0.01	0.512
India-Hyderbad	11814	0	0.013	0.014	0.01	0.007	0.956

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
India-Hyderbad	11815	0	0.024	0.048	0.008	0.007	0.913
India-Hyderbad	11816	0	0.007	0.023	0.019	0.007	0.944
India-Hyderbad	11817	5	0.016	0.012	0.009	0.008	0.956
India-Hyderbad	11818	2	0.048	0.01	0.007	0.005	0.929
India-Hyderbad	11819	0	0.007	0.022	0.02	0.007	0.943
India-Hyderbad	11820	5	0.075	0.022	0.008	0.006	0.888
India-Hyderbad	11821	0	0.046	0.035	0.04	0.012	0.867
India-Hyderbad	11822	0	0.065	0.012	0.044	0.017	0.862
India-Andhra	10159	5	0.087	0.005	0.019	0.014	0.875
India-Andhra	10160	2	0.232	0.01	0.01	0.011	0.736
India-Andhra	10161	0	0.012	0.014	0.007	0.011	0.956
India-Andhra	10162	5	0.016	0.011	0.011	0.011	0.952
India-Andhra	10163	0	0.076	0.013	0.008	0.006	0.898
India-Andhra	10164	2	0.186	0.072	0.008	0.006	0.728
India-Andhra	10165	0	0.015	0.018	0.01	0.009	0.947
India-Andhra	10166	5	0.021	0.009	0.035	0.039	0.897
India-Andhra	10167	2	0.026	0.009	0.24	0.045	0.68
India-Andhra	10168	2	0.026	0.037	0.024	0.009	0.904
India-Andhra	10169	5	0.077	0.007	0.025	0.034	0.857
India-Andhra	10170	0	0.097	0.008	0.032	0.034	0.829
India-Andhra	10171	2	0.188	0.073	0.009	0.006	0.725
India-Andhra	10172	5	0.079	0.045	0.027	0.085	0.764
India-Andhra	10173	5	0.021	0.005	0.013	0.006	0.955
India-Andhra	10174	5	0.013	0.004	0.021	0.018	0.944
India-Andhra	10175	5	0.018	0.017	0.018	0.091	0.856
India-Andhra	10176	0	0.237	0.029	0.019	0.015	0.699

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
India-Andhra	10177	0	0.102	0.014	0.021	0.013	0.85
India-Andhra	10178	5	0.02	0.025	0.011	0.014	0.93
India-Andhra	10179	2	0.017	0.006	0.016	0.042	0.919
India-Andhra	10180	2	0.009	0.016	0.167	0.075	0.732
India-Andhra	10181	7	0.228	0.007	0.019	0.015	0.731
India-Kolkata	10113	7	0.019	0.013	0.018	0.019	0.931
India-Kolkata	10114	2	0.018	0.017	0.014	0.008	0.943
India-Kolkata	10115	0	0.02	0.012	0.071	0.028	0.869
India-Kolkata	10116	7	0.023	0.009	0.011	0.009	0.949
India-Kolkata	10117	5	0.359	0.043	0.087	0.018	0.494
India-Kolkata	10118	13	0.042	0.07	0.078	0.015	0.794
India-Kolkata	10119	7	0.008	0.016	0.091	0.059	0.825
Sri Lanka	8780	0	0.065	0.022	0.048	0.054	0.812
Sri Lanka	8781	5	0.022	0.023	0.106	0.1	0.75
Sri Lanka	8782	15	0.023	0.035	0.097	0.12	0.726
Sri Lanka	8783	0	0.02	0.026	0.053	0.03	0.871
Sri Lanka	8784	5	0.099	0.026	0.02	0.03	0.825
Sri Lanka	8785	7	0.025	0.162	0.09	0.107	0.616
Sri Lanka	8786	0	0.018	0.065	0.268	0.131	0.517
Sri Lanka	8787	0	0.008	0.023	0.027	0.251	0.691
Sri Lanka	8788	5	0.015	0.164	0.025	0.054	0.742
Sri Lanka	8789	2	0.012	0.041	0.049	0.515	0.383
Sri Lanka	8790	0	0.011	0.009	0.037	0.172	0.772
Sri Lanka	8791	5	0.01	0.047	0.01	0.006	0.926
Sri Lanka	8792	2	0.007	0.012	0.032	0.2	0.749
Sri Lanka	8793	5	0.006	0.022	0.027	0.351	0.595
Sri Lanka	8794	5	0.015	0.02	0.069	0.295	0.602
Sri Lanka	8795	0	0.03	0.01	0.1	0.041	0.82
Sri Lanka	8796	7	0.063	0.007	0.126	0.084	0.72
Sri Lanka	8797	2	0.059	0.089	0.013	0.45	0.389
Sri Lanka	8798	2	0.028	0.042	0.065	0.068	0.797
Sri Lanka	8799	7	0.004	0.017	0.007	0.235	0.737
Sri Lanka	8800	10	0.292	0.031	0.044	0.329	0.304
Sri Lanka	8801	10	0.008	0.159	0.022	0.098	0.713

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Sri Lanka	8802	2	0.005	0.035	0.007	0.522	0.43
Sri Lanka	8803	15	0.015	0.011	0.033	0.051	0.89
Thailand	11688	7	0.036	0.005	0.004	0.006	0.949
Thailand	11689	15	0.033	0.022	0.007	0.008	0.93
Thailand	11691	55	0.639	0.022	0.017	0.021	0.301
Thailand	11698	23	0.459	0.009	0.014	0.017	0.502
Thailand	11702	10	0.026	0.005	0.006	0.016	0.947
Thailand	11703	13	0.084	0.008	0.005	0.007	0.896
Thailand	11705	21	0.022	0.006	0.013	0.007	0.952
Thailand	11707	10	0.086	0.007	0.007	0.006	0.893
Thailand	11708	2	0.091	0.008	0.022	0.01	0.87
Thailand	11709	15	0.049	0.006	0.012	0.01	0.923
Thailand	11710	15	0.105	0.005	0.009	0.012	0.868
Thailand	11711	2	0.294	0.006	0.004	0.006	0.689
Thailand	11714	13	0.029	0.007	0.01	0.014	0.94
Thailand	11715	21	0.108	0.013	0.006	0.015	0.858
Thailand	11717	13	0.036	0.009	0.011	0.012	0.932
Thailand	11718	7	0.097	0.009	0.019	0.03	0.845
Thailand	11720	7	0.103	0.006	0.009	0.007	0.875
Vietnam	8844	5	0.03	0.006	0.007	0.007	0.95
Vietnam	8845	13	0.011	0.01	0.007	0.008	0.964
Vietnam	8846	13	0.053	0.007	0.024	0.06	0.856
Vietnam	8847	15	0.05	0.021	0.011	0.252	0.666
Vietnam	8848	10	0.012	0.009	0.014	0.105	0.859
Vietnam	8849	2	0.041	0.005	0.026	0.012	0.916
Vietnam	8850	5	0.247	0.007	0.02	0.463	0.262
Vietnam	8851	10	0.029	0.029	0.015	0.017	0.91
Vietnam	8852	13	0.119	0.017	0.095	0.195	0.574
Vietnam	8853	10	0.018	0.011	0.262	0.062	0.647
Vietnam	8854	7	0.19	0.131	0.021	0.4	0.259
Vietnam	8855	10	0.278	0.008	0.008	0.008	0.699
Vietnam	8856	10	0.015	0.007	0.141	0.018	0.82
Vietnam	8857	7	0.012	0.04	0.014	0.028	0.905
Vietnam	8858	13	0.227	0.005	0.008	0.011	0.748

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Vietnam	8859	13	0.249	0.015	0.011	0.019	0.707
Vietnam	8860	10	0.116	0.015	0.175	0.318	0.376
Vietnam	8861	10	0.048	0.04	0.04	0.096	0.776
Vietnam	8862	7	0.087	0.005	0.013	0.01	0.885
Vietnam	8863	15	0.232	0.01	0.024	0.038	0.695
Taiwan	8681	7	0.248	0.018	0.013	0.71	0.012
Taiwan	8682	2	0.862	0.027	0.007	0.006	0.098
Taiwan	8683	7	0.803	0.015	0.015	0.104	0.063
Taiwan	8684	7	0.214	0.013	0.028	0.709	0.036
Taiwan	8685	2	0.694	0.005	0.012	0.154	0.135
Taiwan	8686	7	0.589	0.011	0.021	0.353	0.027
Taiwan	8687	2	0.437	0.049	0.066	0.086	0.362
Taiwan	8688	47	0.702	0.011	0.025	0.025	0.238
Taiwan	8689	5	0.584	0.035	0.046	0.138	0.197
Taiwan	8690	7	0.684	0.075	0.015	0.027	0.2
Taiwan	8691	26	0.39	0.008	0.035	0.023	0.544
Taiwan	8692	5	0.907	0.008	0.01	0.017	0.058
Taiwan	8693	7	0.912	0.009	0.021	0.032	0.026
Taiwan	8694	5	0.189	0.004	0.007	0.473	0.327
Taiwan	8695	2	0.854	0.009	0.073	0.036	0.029
Taiwan	8696	23	0.037	0.005	0.013	0.929	0.015
Taiwan	8697	5	0.009	0.01	0.025	0.95	0.006
Taiwan	8698	7	0.007	0.004	0.009	0.974	0.006
Taiwan	8699	10	0.432	0.08	0.075	0.25	0.164
Taiwan	8700	7	0.562	0.018	0.119	0.098	0.203
Taiwan	8701	2	0.691	0.014	0.027	0.214	0.055
Taiwan	8702	5	0.599	0.019	0.249	0.083	0.05
Taiwan	8703	7	0.009	0.005	0.02	0.959	0.006
Taiwan	8704	2	0.733	0.017	0.036	0.076	0.139
Taiwan	8705	5	0.624	0.025	0.023	0.02	0.308
Taiwan	8706	7	0.855	0.01	0.019	0.017	0.099
Taiwan	8707	7	0.865	0.044	0.01	0.032	0.05
Taiwan	8708	15	0.022	0.006	0.009	0.952	0.012
Taiwan	8709	13	0.703	0.036	0.076	0.063	0.122

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Japan-Oita	11967	5	0.909	0.013	0.027	0.021	0.029
Japan-Oita	11968	7	0.41	0.008	0.02	0.023	0.538
Japan-Oita	11969	7	0.899	0.011	0.025	0.04	0.025
Japan-Oita	11970	7	0.738	0.044	0.047	0.037	0.134
Japan-Oita	11971	7	0.879	0.011	0.008	0.057	0.046
Japan-Oita	11972	5	0.962	0.005	0.006	0.009	0.017
Japan-Oita	11973	7	0.823	0.039	0.024	0.059	0.056
Japan-Oita	11974	21	0.768	0.01	0.025	0.026	0.171
Japan-Oita	11975	10	0.668	0.004	0.028	0.035	0.264
Japan-Oita	11976	13	0.616	0.009	0.021	0.338	0.017
Japan-Oita	11977	7	0.564	0.006	0.012	0.398	0.02
Japan-Oita	11979	10	0.888	0.011	0.025	0.013	0.063
Japan-Oita	11980	7	0.92	0.009	0.012	0.029	0.03
Japan-Oita	11981	7	0.957	0.006	0.005	0.004	0.028
Japan-Oita	11982	13	0.764	0.006	0.016	0.111	0.103
Japan-Oita	11985	10	0.741	0.007	0.036	0.007	0.209
Japan-Oita	11986	10	0.608	0.021	0.206	0.126	0.039
Japan-Kanazawa	11929	10	0.005	0.004	0.007	0.979	0.005
Japan-Kanazawa	11931	10	0.828	0.01	0.01	0.069	0.083
Japan-Kanazawa	11932	7	0.714	0.013	0.013	0.227	0.032
Japan-Kanazawa	11933	15	0.748	0.006	0.011	0.014	0.221
Japan-Kanazawa	11934	7	0.922	0.004	0.012	0.045	0.018
Japan-Kanazawa	11936	7	0.903	0.006	0.015	0.021	0.056
Japan-Kanazawa	11937	10	0.958	0.005	0.009	0.02	0.008
Japan-Kanazawa	11939	10	0.881	0.023	0.011	0.029	0.056
Japan-	11940	10	0.949	0.022	0.011	0.008	0.011

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Kanazawa							
Japan-Kanazawa	11941	10	0.925	0.031	0.02	0.011	0.013
Japan-Kanazawa	11942	7	0.875	0.008	0.018	0.009	0.091
Japan-Kanazawa	11943	28	0.634	0.065	0.056	0.06	0.186
Japan-Kanazawa	11944	39	0.019	0.014	0.027	0.92	0.02
Japan-Kanazawa	11945	10	0.855	0.011	0.01	0.048	0.077
Japan-Kanazawa	11946	10	0.954	0.006	0.015	0.013	0.013
Japan-Ohmiya	11947	5	0.842	0.008	0.043	0.067	0.04
Japan-Ohmiya	11948	10	0.691	0.039	0.149	0.105	0.016
Japan-Ohmiya	11951	5	0.76	0.041	0.036	0.065	0.098
Japan-Ohmiya	11953	7	0.94	0.006	0.015	0.015	0.024
Japan-Ohmiya	11954	5	0.628	0.014	0.033	0.2	0.125
Japan-Ohmiya	11955	7	0.523	0.006	0.032	0.194	0.246
Japan-Ohmiya	11956	7	0.813	0.012	0.015	0.053	0.107
Japan-Ohmiya	11957	2	0.7	0.027	0.056	0.204	0.013
Japan-Ohmiya	11959	18	0.687	0.01	0.211	0.079	0.013
Japan-Ohmiya	11960	2	0.924	0.023	0.007	0.015	0.031
Japan-Ohmiya	11961	5	0.964	0.008	0.015	0.006	0.007
Japan-Ohmiya	11962	13	0.839	0.013	0.011	0.013	0.124
Japan-Ohmiya	11963	2	0.712	0.007	0.009	0.252	0.021
Japan-Ohmiya	11964	5	0.646	0.034	0.031	0.167	0.121
Japan-Ohmiya	11965	7	0.925	0.005	0.012	0.008	0.05
Japan-Ohmiya	11966	2	0.8	0.014	0.025	0.111	0.05
Japan-Sapporo	11907	2	0.915	0.01	0.021	0.032	0.023
Japan-Sapporo	11909	7	0.015	0.007	0.014	0.951	0.013
Japan-	11911	5	0.533	0.015	0.018	0.422	0.013

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Sapporo							
Japan-Sapporo	11913	7	0.543	0.004	0.009	0.433	0.01
Japan-Sapporo	11914	13	0.736	0.006	0.008	0.236	0.013
Japan-Sapporo	11915	10	0.562	0.022	0.032	0.029	0.355
Japan-Sapporo	11916	5	0.036	0.004	0.13	0.782	0.048
Japan-Sapporo	11917	5	0.04	0.013	0.053	0.873	0.021
Japan-Sapporo	11918	7	0.528	0.016	0.024	0.342	0.09
Japan-Sapporo	11921	7	0.9	0.01	0.009	0.009	0.072
Japan-Sapporo	11922	5	0.909	0.004	0.01	0.06	0.017
Japan-Sapporo	11923	7	0.665	0.009	0.023	0.221	0.082
Japan-Sapporo	11924	5	0.121	0.01	0.012	0.602	0.254
Japan-Sapporo	11925	7	0.887	0.005	0.009	0.007	0.093
Japan-Sapporo	11926	5	0.528	0.007	0.039	0.408	0.017
China-Henan	8869	2	0.847	0.012	0.071	0.062	0.009
China-Henan	8870	5	0.977	0.009	0.004	0.004	0.007
China-Henan	8871	5	0.81	0.158	0.014	0.008	0.01
China-Henan	8872	2	0.954	0.019	0.006	0.008	0.013
China-Henan	8873	5	0.95	0.01	0.018	0.013	0.008
China-Henan	8874	5	0.91	0.043	0.014	0.005	0.029
China-Henan	8875	5	0.986	0.003	0.004	0.004	0.004
China-Henan	8876	5	0.985	0.003	0.003	0.004	0.005
China-Henan	8877	7	0.874	0.026	0.018	0.006	0.076

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population				
			1	2	3	4	5
China-Henan	8878	5	0.977	0.004	0.011	0.004	0.004
China-Henan	8879	2	0.96	0.016	0.005	0.004	0.016
China-Henan	8880	7	0.954	0.022	0.007	0.009	0.008
China-Henan	8881	5	0.88	0.049	0.058	0.005	0.009
China-Henan	8882	5	0.872	0.012	0.027	0.031	0.057
China-Henan	8883	2	0.973	0.006	0.008	0.005	0.007
China-Henan	8884	2	0.892	0.029	0.011	0.003	0.065
China-Henan	8885	2	0.971	0.005	0.008	0.008	0.008
China-Henan	8886	2	0.969	0.008	0.012	0.005	0.006
China-Henan	8887	2	0.872	0.071	0.029	0.021	0.007
China-Henan	8888	2	0.936	0.027	0.012	0.014	0.011
South Korea	2769	5	0.981	0.004	0.005	0.005	0.005
South Korea	2772	47	0.958	0.01	0.008	0.006	0.018
South Korea	2775	13	0.964	0.007	0.01	0.011	0.008
South Korea	2776	13	0.825	0.006	0.056	0.042	0.072
South Korea	2779	2	0.96	0.01	0.006	0.006	0.018
South Korea	2784	2	0.98	0.006	0.004	0.004	0.006
South Korea	2785	2	0.863	0.096	0.018	0.015	0.009
South Korea	2786	2	0.976	0.003	0.006	0.011	0.005
South Korea	7671	2	0.965	0.006	0.012	0.009	0.008
South Korea	7672	2	0.957	0.005	0.008	0.01	0.02
South Korea	7673	2	0.93	0.028	0.026	0.011	0.005
South Korea	7674	2	0.901	0.01	0.032	0.046	0.011
South Korea	7675	10	0.965	0.005	0.012	0.011	0.007
South Korea	7676	7	0.947	0.018	0.011	0.013	0.011
South Korea	7677	15	0.385	0.29	0.056	0.259	0.01
South Korea	7678	2	0.952	0.011	0.013	0.018	0.006
South Korea	7679	5	0.974	0.007	0.007	0.006	0.005
South Korea	7680	7	0.924	0.007	0.03	0.03	0.009
South Korea	7681	13	0.736	0.016	0.224	0.016	0.007
South Korea	7682	5	0.955	0.005	0.021	0.009	0.01
South Korea	7683	7	0.976	0.006	0.005	0.005	0.009
South Korea	7684	7	0.588	0.012	0.316	0.041	0.043
South Korea	7685	18	0.941	0.006	0.011	0.019	0.022

Table 21 - Population clustering of each random bred individual in the database by STRs at K = 5

Sampling Location	ID No.	Missing Data	Population				
			1	2	3	4	5
South Korea	7686	10	0.934	0.007	0.014	0.037	0.008
South Korea	7687	10	0.699	0.005	0.03	0.068	0.197
South Korea	7688	2	0.362	0.005	0.032	0.538	0.063
South Korea	7689	10	0.966	0.007	0.008	0.011	0.009
South Korea	7690	10	0.928	0.004	0.014	0.01	0.044
South Korea	7691	7	0.945	0.01	0.015	0.014	0.016
South Korea	7692	5	0.88	0.016	0.029	0.014	0.061
South Korea	7693	2	0.739	0.017	0.118	0.086	0.04
South Korea	7694	5	0.981	0.003	0.005	0.004	0.006
South Korea	7695	7	0.784	0.011	0.125	0.066	0.014
South Korea	7696	5	0.974	0.009	0.006	0.006	0.005
South Korea	7697	10	0.95	0.019	0.008	0.01	0.013
South Korea	7698	23	0.64	0.04	0.085	0.033	0.202
South Korea	7699	7	0.945	0.015	0.018	0.008	0.014
South Korea	7700	7	0.886	0.026	0.027	0.012	0.049

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
USA-NY	2547	1	0.008	0.079	0.08	0.823	0.011
USA-NY	2559	3	0.008	0.011	0.315	0.663	0.003
USA-NY	2568	0	0.004	0.004	0.004	0.986	0.002
USA-NY	2569	5	0.01	0.007	0.011	0.96	0.013
USA-NY	2572	1	0.008	0.024	0.017	0.945	0.006
USA-NY	2578	17	0.005	0.034	0.018	0.928	0.015
USA-NY	2590	1	0.006	0.008	0.028	0.956	0.002
USA-NY	2591	2	0.008	0.007	0.011	0.964	0.01
USA-NY	2597	4	0.015	0.036	0.018	0.897	0.035
USA-MS	9971	3	0.017	0.041	0.012	0.921	0.01
USA-MS	9972	2	0.011	0.119	0.026	0.822	0.023
USA-MS	9974	2	0.028	0.047	0.019	0.897	0.009
USA-MS	9977	5	0.015	0.005	0.011	0.962	0.007
USA-MS	9980	2	0.01	0.027	0.027	0.923	0.013
USA-MS	9983	2	0.007	0.012	0.009	0.961	0.011
USA-MS	9985	3	0.171	0.012	0.031	0.783	0.004
USA-MS	9987	3	0.054	0.028	0.065	0.841	0.012
USA-MS	9989	2	0.023	0.012	0.013	0.947	0.004
USA-MS	9992	3	0.016	0.012	0.133	0.826	0.012
USA-HI	5366	3	0.201	0.044	0.026	0.726	0.004
USA-HI	5367	1	0.061	0.122	0.028	0.765	0.024
USA-HI	5371	1	0.032	0.028	0.207	0.711	0.022
USA-HI	5372	2	0.019	0.193	0.099	0.674	0.016
USA-HI	5379	1	0.035	0.009	0.047	0.889	0.021
USA-HI	5380	1	0.007	0.004	0.017	0.969	0.003
USA-HI	5383	3	0.032	0.111	0.111	0.465	0.28
USA-HI	5384	5	0.003	0.011	0.097	0.88	0.008
USA-HI	5401	2	0.037	0.025	0.05	0.883	0.005
USA-HI	5402	2	0.128	0.01	0.028	0.81	0.023
Brazil	7961	1	0.009	0.005	0.021	0.961	0.004
Brazil	7962	2	0.008	0.012	0.092	0.885	0.003
Brazil	7963	17	0.091	0.164	0.022	0.72	0.004

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Brazil	7964	2	0.009	0.009	0.012	0.965	0.006
Brazil	7965	27	0.007	0.006	0.005	0.978	0.005
Brazil	7966	2	0.004	0.011	0.018	0.955	0.012
Brazil	7968	23	0.016	0.009	0.017	0.949	0.009
Brazil	7969	1	0.003	0.004	0.005	0.985	0.003
Brazil	7970	1	0.006	0.007	0.007	0.977	0.004
Brazil	7971	1	0.007	0.004	0.006	0.979	0.005
Brazil	7972	1	0.004	0.005	0.012	0.973	0.006
Brazil	7973	0	0.012	0.004	0.009	0.97	0.005
Brazil	7974	3	0.008	0.008	0.018	0.961	0.006
Brazil	7975	5	0.013	0.01	0.013	0.96	0.005
Brazil	7976	1	0.007	0.004	0.006	0.979	0.004
Brazil	7977	2	0.006	0.004	0.02	0.968	0.003
Brazil	7978	1	0.014	0.03	0.012	0.938	0.006
Brazil	7979	2	0.023	0.011	0.014	0.946	0.006
Brazil	7980	2	0.013	0.025	0.291	0.656	0.015
Brazil	7981	2	0.157	0.008	0.013	0.818	0.004
Brazil	7982	20	0.077	0.116	0.024	0.775	0.008
Brazil	7983	4	0.02	0.148	0.052	0.768	0.012
Brazil	7984	15	0.344	0.009	0.027	0.614	0.006
Brazil	7985	5	0.014	0.019	0.021	0.942	0.005
Brazil	7986	3	0.088	0.012	0.038	0.857	0.005
Brazil	7987	2	0.013	0.034	0.038	0.911	0.004
Brazil	7988	0	0.118	0.035	0.029	0.809	0.009
Brazil	7989	1	0.151	0.1	0.013	0.73	0.006
Brazil	7990	1	0.019	0.022	0.008	0.947	0.004
Finland	8077	11	0.003	0.005	0.012	0.973	0.007
Finland	8084	11	0.023	0.024	0.034	0.905	0.013
Finland	8086	5	0.007	0.009	0.058	0.918	0.008
Finland	8089	8	0.019	0.104	0.018	0.827	0.032
Finland	8093	16	0.005	0.005	0.204	0.78	0.006
Finland	8094	9	0.011	0.017	0.058	0.835	0.079

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Finland	8096	7	0.003	0.004	0.021	0.959	0.014
Finland	8107	24	0.002	0.004	0.005	0.986	0.003
Finland	8110	10	0.005	0.029	0.042	0.915	0.008
Finland	8116	16	0.016	0.03	0.013	0.93	0.01
Finland	8120	21	0.012	0.004	0.025	0.954	0.005
Germany	8711	4	0.004	0.003	0.008	0.981	0.004
Germany	8712	3	0.006	0.013	0.006	0.955	0.02
Germany	8713	3	0.025	0.02	0.062	0.869	0.023
Germany	8714	2	0.008	0.01	0.026	0.928	0.028
Germany	8715	4	0.003	0.004	0.012	0.974	0.007
Germany	8716	3	0.005	0.005	0.009	0.975	0.005
Germany	8717	11	0.005	0.005	0.009	0.975	0.006
Germany	8720	3	0.49	0.093	0.015	0.396	0.005
Germany	8721	10	0.004	0.005	0.039	0.944	0.007
Germany	8727	1	0.005	0.01	0.027	0.954	0.004
Germany	8728	10	0.004	0.009	0.006	0.977	0.004
Germany	8729	2	0.002	0.003	0.005	0.987	0.002
Germany	8730	22	0.028	0.016	0.052	0.9	0.004
Germany	8731	12	0.003	0.005	0.007	0.981	0.003
Germany	8732	4	0.003	0.01	0.013	0.971	0.003
Germany	8733	16	0.021	0.014	0.013	0.938	0.015
Germany	8734	1	0.002	0.003	0.009	0.984	0.002
Germany	8735	2	0.007	0.004	0.009	0.977	0.004
Germany	8736	1	0.006	0.006	0.031	0.939	0.018
Germany	8737	3	0.007	0.013	0.016	0.95	0.013
Germany	8738	10	0.004	0.007	0.049	0.864	0.076
Germany	8739	2	0.003	0.005	0.011	0.978	0.003
Germany	8741	11	0.004	0.006	0.019	0.967	0.004
Germany	8742	9	0.006	0.004	0.008	0.979	0.003
Germany	8744	6	0.094	0.013	0.316	0.572	0.006
Germany	8745	23	0.004	0.009	0.027	0.953	0.007
Germany	8746	1	0.004	0.01	0.007	0.975	0.004

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Germany	8747	13	0.004	0.006	0.006	0.982	0.003
Germany	8749	2	0.003	0.003	0.005	0.984	0.005
Italy-Milan	8050	1	0.105	0.012	0.095	0.673	0.115
Italy-Milan	8057	2	0.051	0.1	0.207	0.578	0.064
Italy-Milan	8060	1	0.016	0.045	0.21	0.707	0.022
Italy-Milan	8061	2	0.104	0.028	0.295	0.552	0.022
Italy-Milan	8062	3	0.007	0.012	0.583	0.392	0.006
Italy-Milan	8065	5	0.005	0.008	0.488	0.493	0.005
Italy-Milan	8066	1	0.029	0.058	0.107	0.786	0.021
Italy-Milan	8067	2	0.008	0.016	0.467	0.492	0.017
Italy-Milan	8068	2	0.008	0.013	0.509	0.465	0.006
Italy-Milan	8069	1	0.033	0.129	0.201	0.614	0.023
Italy-Milan	8071	3	0.015	0.013	0.04	0.923	0.01
Italy-Milan	8072	3	0.272	0.015	0.201	0.501	0.011
Italy-Milan	8073	1	0.013	0.009	0.263	0.694	0.02
Italy-Milan	8074	2	0.184	0.061	0.025	0.726	0.003
Italy-Rome	8586	1	0.014	0.021	0.475	0.478	0.011
Italy-Rome	8589	3	0.039	0.015	0.092	0.848	0.005
Italy-Rome	8592	2	0.013	0.018	0.14	0.626	0.202
Italy-Rome	8594	1	0.02	0.02	0.112	0.808	0.039
Italy-Rome	8595	1	0.042	0.044	0.188	0.606	0.12
Italy-Rome	8596	1	0.011	0.01	0.542	0.43	0.007
Italy-Rome	8597	1	0.034	0.012	0.188	0.73	0.036
Italy-Rome	8599	1	0.053	0.007	0.077	0.858	0.005
Italy-Rome	8601	2	0.037	0.014	0.081	0.701	0.167
Italy-Rome	8602	3	0.01	0.023	0.26	0.694	0.013
Italy-Rome	8603	1	0.012	0.01	0.044	0.915	0.019
Italy-Rome	8604	3	0.207	0.011	0.118	0.645	0.019
Italy-Rome	8609	2	0.007	0.006	0.364	0.616	0.007
Italy-Rome	8610	2	0.01	0.011	0.4	0.572	0.007
Italy-Rome	8611	2	0.007	0.01	0.295	0.648	0.04
Turkey	6477	6	0.004	0.003	0.856	0.109	0.028

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Turkey	6478	12	0.01	0.011	0.922	0.017	0.041
Turkey	6480	10	0.006	0.018	0.922	0.048	0.006
Turkey	6481	11	0.587	0.356	0.032	0.019	0.005
Turkey	6482	12	0.014	0.02	0.698	0.259	0.01
Turkey	6484	6	0.007	0.015	0.88	0.093	0.005
Turkey	6486	8	0.006	0.026	0.648	0.305	0.016
Turkey	6487	13	0.006	0.005	0.886	0.095	0.007
Turkey	6488	11	0.013	0.009	0.838	0.097	0.044
Turkey	6491	15	0.691	0.088	0.044	0.167	0.01
Turkey	6494	10	0.032	0.018	0.494	0.382	0.074
Turkey	6496	11	0.027	0.063	0.787	0.114	0.009
Turkey	6499	11	0.01	0.011	0.444	0.527	0.009
Turkey	6500	15	0.004	0.005	0.889	0.096	0.005
Turkey	6502	6	0.021	0.014	0.861	0.095	0.009
Turkey	6503	3	0.013	0.007	0.691	0.278	0.01
Turkey	6507	12	0.01	0.004	0.939	0.041	0.006
Turkey	6510	9	0.04	0.011	0.515	0.429	0.005
Turkey	6512	13	0.015	0.019	0.887	0.044	0.035
Turkey	6513	12	0.007	0.058	0.628	0.277	0.03
Turkey	6514	8	0.951	0.018	0.011	0.008	0.013
Turkey	6516	10	0.003	0.008	0.008	0.976	0.006
Turkey	6519	6	0.01	0.016	0.519	0.439	0.017
Turkey	6520	13	0.006	0.007	0.536	0.444	0.006
Turkey	6521	11	0.017	0.012	0.579	0.381	0.012
Turkey	6729	2	0.036	0.079	0.306	0.067	0.512
Turkey	6730	2	0.006	0.005	0.788	0.197	0.004
Turkey	6731	3	0.005	0.014	0.549	0.397	0.035
Turkey	6732	2	0.086	0.116	0.656	0.055	0.087
Turkey	6733	4	0.028	0.023	0.879	0.059	0.012
Turkey	6734	1	0.023	0.012	0.906	0.047	0.013
Turkey	6735	3	0.003	0.003	0.977	0.009	0.007
Turkey	6736	1	0.004	0.011	0.765	0.21	0.01

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Turkey	6738	3	0.003	0.005	0.848	0.138	0.006
Turkey	6739	4	0.006	0.038	0.506	0.403	0.047
Turkey	6740	1	0.002	0.004	0.003	0.988	0.003
Turkey	6741	2	0.858	0.064	0.015	0.059	0.004
Turkey	6742	4	0.026	0.054	0.677	0.189	0.055
Turkey	6743	2	0.006	0.012	0.664	0.308	0.009
Turkey	6745	1	0.013	0.007	0.56	0.403	0.018
Turkey	6746	2	0.324	0.218	0.056	0.346	0.055
Turkey	6748	3	0.011	0.077	0.815	0.08	0.017
Turkey	6749	2	0.018	0.006	0.434	0.51	0.031
Turkey	6750	3	0.004	0.006	0.503	0.484	0.003
Turkey	6753	2	0.021	0.014	0.626	0.277	0.062
Turkey	6754	3	0.004	0.006	0.508	0.283	0.198
Turkey	6755	3	0.009	0.005	0.727	0.248	0.012
Turkey	6756	2	0.003	0.006	0.629	0.356	0.006
Turkey	6758	3	0.041	0.018	0.796	0.124	0.02
Turkey	6759	4	0.007	0.023	0.73	0.235	0.005
Turkey	6760	2	0.005	0.017	0.385	0.577	0.017
Cyprus	10128	3	0.031	0.013	0.907	0.041	0.008
Cyprus	10129	1	0.007	0.009	0.514	0.455	0.014
Cyprus	10130	3	0.004	0.012	0.866	0.114	0.004
Cyprus	10131	1	0.084	0.078	0.776	0.051	0.012
Cyprus	10132	0	0.017	0.031	0.924	0.007	0.02
Cyprus	10133	3	0.013	0.018	0.853	0.101	0.015
Cyprus	10134	1	0.005	0.041	0.915	0.027	0.013
Cyprus	10135	2	0.011	0.17	0.755	0.059	0.006
Cyprus	10136	3	0.009	0.015	0.542	0.332	0.102
Cyprus	10137	1	0.01	0.005	0.86	0.026	0.099
Cyprus	10138	2	0.01	0.015	0.953	0.007	0.015
Cyprus	10139	3	0.088	0.095	0.773	0.015	0.03
Cyprus	10140	0	0.008	0.011	0.914	0.057	0.011
Cyprus	10141	1	0.007	0.008	0.908	0.07	0.007

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Cyprus	10142	1	0.017	0.031	0.917	0.01	0.025
Cyprus	10143	1	0.007	0.005	0.973	0.007	0.008
Cyprus	10144	3	0.01	0.099	0.867	0.014	0.01
Cyprus	10145	2	0.005	0.005	0.922	0.061	0.007
Cyprus	10146	0	0.007	0.045	0.923	0.008	0.017
Cyprus	10147	2	0.004	0.006	0.875	0.111	0.004
Cyprus	10148	1	0.02	0.046	0.894	0.02	0.02
Cyprus	10149	3	0.012	0.028	0.789	0.061	0.111
Cyprus	10150	1	0.014	0.008	0.913	0.051	0.014
Cyprus	10151	2	0.013	0.02	0.935	0.012	0.019
Cyprus	10152	2	0.011	0.008	0.865	0.094	0.021
Cyprus	10153	1	0.023	0.007	0.931	0.016	0.022
Cyprus	10154	1	0.01	0.109	0.823	0.018	0.04
Cyprus	10155	3	0.011	0.126	0.85	0.009	0.004
Cyprus	10156	5	0.038	0.012	0.907	0.016	0.027
Cyprus	10157	2	0.006	0.008	0.859	0.012	0.117
Lebanon	10235	19	0.08	0.068	0.789	0.023	0.039
Lebanon	10236	22	0.033	0.101	0.842	0.01	0.015
Lebanon	10237	16	0.177	0.192	0.604	0.018	0.009
Lebanon	10238	3	0.015	0.038	0.842	0.054	0.05
Lebanon	10239	14	0.007	0.009	0.962	0.012	0.01
Lebanon	10240	19	0.029	0.062	0.835	0.04	0.035
Lebanon	10241	6	0.128	0.044	0.688	0.068	0.072
Lebanon	10242	2	0.014	0.015	0.852	0.1	0.02
Lebanon	10243	3	0.04	0.039	0.819	0.027	0.075
Lebanon	10244	15	0.026	0.05	0.861	0.011	0.051
Lebanon	10245	7	0.007	0.039	0.713	0.024	0.217
Lebanon	10246	15	0.008	0.014	0.911	0.022	0.045
Lebanon	10247	24	0.011	0.012	0.727	0.005	0.245
Lebanon	10248	19	0.012	0.02	0.916	0.042	0.01
Lebanon	10249	17	0.014	0.051	0.339	0.587	0.009
Lebanon	10250	22	0.011	0.009	0.841	0.041	0.097

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Lebanon	10251	3	0.005	0.03	0.929	0.023	0.012
Lebanon	10252	12	0.014	0.016	0.385	0.332	0.254
Lebanon	10253	6	0.015	0.013	0.89	0.02	0.063
Lebanon	10254	13	0.032	0.021	0.919	0.012	0.016
Lebanon	10255	7	0.027	0.009	0.699	0.062	0.203
Lebanon	10256	12	0.008	0.007	0.958	0.011	0.016
Lebanon	10257	3	0.078	0.046	0.83	0.027	0.02
Lebanon	10258	17	0.018	0.029	0.917	0.008	0.028
Lebanon	10259	2	0.547	0.087	0.328	0.032	0.007
Lebanon	10260	14	0.008	0.008	0.957	0.015	0.012
Lebanon	10261	13	0.029	0.012	0.909	0.017	0.032
Lebanon	10262	18	0.025	0.014	0.875	0.017	0.069
Lebanon	10263	3	0.009	0.015	0.946	0.014	0.017
Lebanon	10264	3	0.032	0.052	0.773	0.119	0.024
Lebanon	10265	9	0.006	0.007	0.927	0.01	0.049
Lebanon	10266	4	0.018	0.077	0.886	0.01	0.008
Lebanon	10267	13	0.004	0.006	0.54	0.439	0.01
Lebanon	10268	15	0.07	0.011	0.897	0.017	0.005
Lebanon	10270	10	0.315	0.025	0.591	0.038	0.031
Lebanon	10271	4	0.041	0.271	0.514	0.057	0.117
Lebanon	10273	5	0.173	0.018	0.67	0.1	0.039
Lebanon	10274	5	0.057	0.082	0.801	0.054	0.005
Lebanon	10276	5	0.004	0.012	0.957	0.01	0.016
Lebanon	10277	4	0.174	0.011	0.677	0.113	0.025
Lebanon	10278	5	0.016	0.017	0.914	0.01	0.043
Lebanon	10279	1	0.008	0.104	0.787	0.013	0.088
Lebanon	10280	2	0.033	0.244	0.681	0.019	0.023
Lebanon	10281	8	0.007	0.008	0.954	0.013	0.019
Lebanon	10282	3	0.039	0.015	0.921	0.01	0.015
Lebanon	10283	18	0.005	0.037	0.943	0.007	0.009
Lebanon	10284	16	0.046	0.061	0.693	0.03	0.169
Lebanon	10285	1	0.021	0.028	0.92	0.016	0.015

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Lebanon	10286	5	0.166	0.053	0.583	0.02	0.178
Lebanon	10287	2	0.043	0.039	0.519	0.334	0.065
Lebanon	10288	22	0.042	0.01	0.087	0.856	0.006
Lebanon	10289	4	0.009	0.024	0.922	0.007	0.038
Lebanon	10290	3	0.071	0.167	0.722	0.008	0.032
Lebanon	10291	9	0.038	0.13	0.71	0.016	0.107
Lebanon	10292	7	0.017	0.401	0.528	0.027	0.028
Lebanon	10294	8	0.105	0.018	0.835	0.022	0.02
Lebanon	10295	6	0.057	0.053	0.771	0.033	0.087
Lebanon	10297	5	0.018	0.014	0.729	0.021	0.217
Lebanon	10298	8	0.014	0.071	0.687	0.008	0.22
Lebanon	10299	17	0.054	0.07	0.488	0.276	0.111
Lebanon	10300	20	0.021	0.024	0.866	0.012	0.078
Israel	4962	1	0.006	0.042	0.7	0.067	0.184
Israel	4963	1	0.017	0.039	0.898	0.029	0.017
Israel	4964	2	0.013	0.014	0.841	0.059	0.073
Israel	4966	2	0.008	0.036	0.929	0.021	0.006
Israel	4967	2	0.029	0.064	0.57	0.285	0.053
Israel	4968	3	0.027	0.017	0.91	0.012	0.035
Israel	4969	1	0.222	0.024	0.142	0.594	0.018
Israel	4970	1	0.023	0.017	0.814	0.115	0.03
Israel	4971	1	0.018	0.007	0.918	0.014	0.043
Israel	4972	2	0.036	0.018	0.853	0.069	0.024
Israel	4973	2	0.01	0.02	0.947	0.014	0.009
Israel	4974	2	0.009	0.016	0.919	0.03	0.026
Israel	4975	1	0.007	0.009	0.884	0.087	0.013
Israel	4976	1	0.015	0.049	0.735	0.152	0.049
Israel	4977	3	0.007	0.018	0.559	0.327	0.09
Israel	4978	3	0.028	0.041	0.75	0.046	0.135
Israel	4979	2	0.014	0.008	0.868	0.023	0.088
Israel	4980	1	0.035	0.088	0.66	0.131	0.085
Israel	4981	5	0.311	0.008	0.624	0.011	0.045

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Israel	4982	4	0.012	0.079	0.817	0.083	0.009
Israel	4983	1	0.333	0.021	0.081	0.518	0.046
Israel	4984	2	0.24	0.028	0.024	0.679	0.028
Israel	4985	17	0.034	0.016	0.904	0.038	0.008
Israel	4986	2	0.019	0.016	0.933	0.015	0.017
Israel	4988	3	0.042	0.026	0.89	0.026	0.016
Israel	4989	4	0.102	0.019	0.834	0.013	0.032
Israel	4990	2	0.291	0.014	0.671	0.018	0.007
Israel	4992	6	0.007	0.009	0.9	0.068	0.016
Israel	4993	9	0.007	0.011	0.958	0.013	0.011
Israel	4994	2	0.003	0.005	0.981	0.006	0.005
Israel	4995	2	0.191	0.01	0.763	0.018	0.018
Israel	4996	1	0.026	0.004	0.938	0.009	0.022
Israel	4997	3	0.106	0.011	0.812	0.011	0.06
Israel	4998	2	0.014	0.034	0.603	0.222	0.127
Israel	5000	2	0.04	0.016	0.917	0.008	0.018
Israel	5001	2	0.012	0.022	0.679	0.272	0.015
Israel	5002	2	0.022	0.036	0.891	0.047	0.005
Israel	5003	2	0.11	0.025	0.643	0.185	0.038
Israel	5004	3	0.114	0.059	0.711	0.057	0.059
Israel	5005	2	0.006	0.016	0.806	0.161	0.011
Israel	5006	3	0.005	0.008	0.925	0.036	0.026
Israel	5007	2	0.257	0.026	0.632	0.079	0.005
Israel	5008	1	0.022	0.024	0.88	0.047	0.026
Israel	5009	3	0.217	0.02	0.649	0.038	0.076
Israel	5010	4	0.004	0.007	0.955	0.026	0.009
Israel	5011	2	0.017	0.009	0.933	0.017	0.023
Egypt-Cairo	8190	3	0.015	0.017	0.916	0.043	0.01
Egypt-Cairo	8192	5	0.007	0.072	0.746	0.148	0.026
Egypt-Cairo	8193	4	0.007	0.018	0.936	0.023	0.017
Egypt-Cairo	8196	4	0.04	0.071	0.863	0.009	0.017
Egypt-Cairo	8203	4	0.009	0.006	0.965	0.013	0.006

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Egypt-Cairo	8215	3	0.008	0.012	0.961	0.009	0.01
Egypt-Cairo	8198	3	0.015	0.015	0.938	0.022	0.01
Egypt-Cairo	8194	1	0.019	0.019	0.869	0.076	0.017
Egypt-Cairo	8211	9	0.005	0.004	0.971	0.009	0.01
Egypt-Cairo	8216	2	0.01	0.012	0.9	0.071	0.007
Egypt-Cairo	8195	2	0.009	0.052	0.909	0.02	0.01
Egypt-Cairo	8199	8	0.005	0.045	0.937	0.007	0.007
Egypt-Cairo	8200	13	0.006	0.005	0.942	0.032	0.015
Egypt-Cairo	8201	1	0.026	0.063	0.786	0.037	0.087
Egypt-Cairo	8202	2	0.614	0.27	0.066	0.019	0.032
Egypt-Cairo	8204	2	0.012	0.011	0.965	0.009	0.004
Egypt-Cairo	8208	1	0.015	0.024	0.929	0.009	0.023
Egypt-Cairo	8210	3	0.009	0.053	0.885	0.008	0.045
Egypt-Cairo	8214	2	0.007	0.007	0.971	0.006	0.01
Egypt-Cairo	8191	2	0.028	0.014	0.91	0.02	0.028
Egypt-Cairo	8197	1	0.005	0.041	0.938	0.007	0.008
Egypt-Cairo	8205	1	0.019	0.027	0.922	0.01	0.021
Egypt-Cairo	8206	1	0.022	0.018	0.945	0.007	0.008
Egypt-Cairo	8207	2	0.035	0.026	0.92	0.009	0.01
Egypt-Cairo	8209	1	0.005	0.004	0.971	0.011	0.008
Egypt-Cairo	8212	1	0.006	0.007	0.97	0.007	0.009
Egypt-Cairo	8213	1	0.005	0.009	0.967	0.009	0.009
Egypt-Cairo	9942	2	0.033	0.011	0.817	0.008	0.132
Egypt-Cairo	9943	3	0.47	0.055	0.058	0.404	0.013
Egypt-Cairo	9944	4	0.006	0.017	0.521	0.341	0.116
Egypt-Cairo	9945	0	0.007	0.031	0.928	0.014	0.019
Egypt-Cairo	9946	3	0.06	0.034	0.883	0.011	0.012
Egypt-Cairo	9947	3	0.008	0.028	0.909	0.008	0.048
Egypt-Cairo	9948	0	0.012	0.006	0.882	0.095	0.005
Egypt-Cairo	9949	0	0.032	0.016	0.925	0.019	0.008
Egypt-Cairo	9950	1	0.006	0.013	0.932	0.043	0.006
Egypt-Cairo	9951	2	0.012	0.013	0.961	0.01	0.005

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Egypt-Cairo	9952	4	0.006	0.018	0.942	0.009	0.024
Egypt-Cairo	9953	8	0.013	0.013	0.319	0.535	0.12
Egypt-Cairo	9954	1	0.324	0.014	0.651	0.007	0.004
Egypt-Cairo	9955	2	0.032	0.18	0.376	0.404	0.008
Egypt-Cairo	9956	8	0.171	0.018	0.789	0.011	0.01
Egypt-Cairo	9957	2	0.066	0.012	0.875	0.027	0.019
Egypt-Cairo	9958	4	0.053	0.015	0.914	0.012	0.006
Egypt-Cairo	9959	2	0.036	0.339	0.553	0.05	0.021
Egypt-Cairo	9960	1	0.023	0.007	0.924	0.013	0.033
Egypt-Cairo	9961	5	0.529	0.059	0.384	0.022	0.006
Egypt-Cairo	9962	3	0.009	0.033	0.914	0.031	0.013
Egypt-Cairo	9963	3	0.015	0.007	0.954	0.014	0.009
Egypt-Cairo	9964	1	0.034	0.047	0.892	0.019	0.008
Egypt-Cairo	10021	6	0.003	0.007	0.979	0.006	0.006
Egypt-Cairo	10022	1	0.011	0.013	0.962	0.008	0.006
Egypt-Cairo	10023	0	0.005	0.011	0.975	0.004	0.005
Egypt-Cairo	10024	1	0.004	0.003	0.978	0.012	0.003
Egypt-Cairo	10025	2	0.007	0.012	0.924	0.037	0.019
Egypt-Cairo	10026	17	0.022	0.006	0.941	0.026	0.005
Egypt-Cairo	10027	1	0.009	0.086	0.879	0.018	0.009
Egypt-Cairo	10028	1	0.007	0.008	0.964	0.007	0.013
Egypt-Cairo	10029	3	0.004	0.005	0.973	0.005	0.013
Egypt-Cairo	10030	1	0.009	0.005	0.971	0.01	0.005
Egypt-Cairo	10031	3	0.004	0.006	0.98	0.003	0.007
Egypt-Cairo	10032	0	0.004	0.006	0.964	0.005	0.021
Egypt-Cairo	10033	1	0.006	0.01	0.975	0.004	0.006
Egypt-Cairo	10034	1	0.005	0.01	0.97	0.009	0.005
Egypt-Cairo	10035	3	0.067	0.059	0.848	0.008	0.019
Egypt-Cairo	10037	5	0.006	0.035	0.731	0.219	0.008
Egypt-Cairo	10042	1	0.03	0.055	0.85	0.051	0.013
Egypt-Cairo	10043	2	0.004	0.014	0.935	0.037	0.01
Egypt-Cairo	10044	4	0.012	0.008	0.964	0.01	0.005

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Egypt-Cairo	10045	1	0.008	0.01	0.951	0.026	0.005
Egypt-Cairo	10046	0	0.022	0.015	0.946	0.01	0.007
Egypt-Cairo	10047	0	0.009	0.014	0.954	0.007	0.016
Egypt-Cairo	10048	1	0.049	0.017	0.918	0.012	0.003
Egypt-Cairo	10083	24	0.013	0.008	0.936	0.037	0.007
Egypt-Cairo	10040	2	0.017	0.025	0.912	0.035	0.011
Egypt-Cairo	10041	1	0.015	0.054	0.904	0.018	0.01
Egypt-Cairo	10049	9	0.019	0.055	0.901	0.012	0.013
Egypt-Cairo	10084	7	0.019	0.021	0.923	0.03	0.007
Egypt-Cairo	10085	19	0.007	0.03	0.89	0.068	0.004
Egypt-Cairo	10087	4	0.004	0.008	0.976	0.009	0.003
Egypt-Cairo	10090	4	0.021	0.107	0.84	0.023	0.009
Egypt-Cairo	9968	0	0.007	0.02	0.936	0.019	0.018
Egypt-Asuit	10091	1	0.004	0.007	0.974	0.01	0.005
Egypt-Asuit	10093	3	0.003	0.012	0.964	0.018	0.003
Egypt-Asuit	10094	4	0.005	0.015	0.961	0.014	0.004
Egypt-Asuit	10095	13	0.005	0.02	0.939	0.032	0.004
Egypt-Asuit	10096	1	0.012	0.01	0.967	0.008	0.003
Egypt-Asuit	10098	1	0.003	0.006	0.98	0.009	0.003
Egypt-Asuit	10099	1	0.004	0.008	0.979	0.006	0.004
Egypt-Asuit	10100	2	0.082	0.107	0.694	0.097	0.02
Egypt-Asuit	10101	2	0.009	0.026	0.949	0.006	0.01
Egypt-Asuit	10102	1	0.023	0.022	0.94	0.005	0.01
Egypt-Luxor	10038	1	0.076	0.029	0.884	0.006	0.004
Egypt-Luxor	10039	5	0.004	0.005	0.967	0.004	0.021
Egypt-Luxor	10050	2	0.032	0.017	0.936	0.005	0.01
Egypt-Luxor	10051	1	0.005	0.008	0.979	0.005	0.004
Egypt-Luxor	10052	11	0.022	0.053	0.908	0.011	0.005
Egypt-Luxor	10053	2	0.013	0.042	0.827	0.007	0.111
Egypt-Luxor	10054	2	0.016	0.008	0.955	0.007	0.015
Egypt-Luxor	10055	1	0.012	0.012	0.963	0.005	0.007
Egypt-Luxor	10056	2	0.026	0.014	0.93	0.012	0.018
Egypt-Luxor	10057	12	0.009	0.01	0.949	0.01	0.021
Egypt-Luxor	10058	6	0.006	0.006	0.973	0.008	0.007
Egypt-Luxor	10060	4	0.005	0.008	0.959	0.022	0.005
Egypt-Luxor	10061	0	0.254	0.012	0.714	0.016	0.005
Egypt-Luxor	10062	3	0.007	0.01	0.947	0.026	0.01
Egypt-Luxor	10063	1	0.051	0.098	0.735	0.056	0.061
Egypt-Luxor	10064	1	0.007	0.068	0.893	0.027	0.005
Egypt-Luxor	10065	0	0.01	0.122	0.835	0.014	0.018
Egypt-Luxor	10066	3	0.028	0.066	0.859	0.039	0.008
Egypt-Luxor	10067	4	0.004	0.01	0.967	0.005	0.014
Egypt-Luxor	10068	7	0.044	0.031	0.905	0.017	0.003
Egypt-Luxor	10069	3	0.005	0.011	0.964	0.006	0.014
Egypt-Luxor	10070	1	0.244	0.013	0.718	0.021	0.004
Egypt-Luxor	10071	3	0.015	0.027	0.935	0.006	0.016
Egypt-Luxor	10072	2	0.013	0.009	0.963	0.007	0.008
Egypt-Luxor	10073	1	0.005	0.009	0.016	0.964	0.006
Egypt-Luxor	10074	0	0.003	0.004	0.983	0.006	0.004
Egypt-Luxor	10079	4	0.006	0.056	0.864	0.068	0.007
Egypt-Luxor	10080	5	0.014	0.212	0.752	0.016	0.006
Egypt-Abu Simbel	10076	10	0.039	0.028	0.904	0.023	0.007
Egypt-Abu Simbel	10077	17	0.01	0.024	0.954	0.006	0.006
Egypt-Abu Simbel	10081	17	0.011	0.022	0.944	0.013	0.009
Egypt-Abu Simbel	10089	1	0.004	0.009	0.919	0.065	0.003
Egypt-Abu Simbel	10092	2	0.005	0.006	0.979	0.005	0.005
Iraq-West	9587	9	0.012	0.039	0.25	0.046	0.653
Iraq-West	10202	6	0.007	0.006	0.331	0.023	0.634
Iraq-West	10204	15	0.004	0.011	0.277	0.048	0.661

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Iraq-West	11854	18	0.03	0.014	0.14	0.012	0.804
Iraq-West	11860	10	0.012	0.034	0.052	0.009	0.893
Iraq-West	11861	3	0.088	0.068	0.151	0.018	0.674
Iraq-West	11863	5	0.007	0.011	0.041	0.057	0.884
Iraq-West	11864	1	0.011	0.033	0.112	0.027	0.818
Iraq-West	11888	2	0.093	0.061	0.015	0.006	0.824
Iraq-West	11889	4	0.006	0.024	0.06	0.119	0.791
Iraq-West	11890	16	0.062	0.047	0.214	0.012	0.664
Iraq-West	11891	15	0.007	0.025	0.333	0.014	0.621
Iraq-Baghdad	11847	1	0.007	0.007	0.161	0.009	0.816
Iraq-Baghdad	11848	1	0.036	0.157	0.024	0.013	0.77
Iraq-Baghdad	11849	1	0.006	0.012	0.303	0.022	0.657
Iraq-Baghdad	11850	1	0.028	0.011	0.025	0.076	0.859
Iraq-Baghdad	11852	14	0.013	0.068	0.022	0.008	0.89
Iraq-Baghdad	11853	8	0.039	0.047	0.099	0.01	0.805
Iraq-Baghdad	11855	19	0.014	0.04	0.059	0.01	0.877
Iraq-Baghdad	11856	1	0.004	0.032	0.149	0.042	0.773
Iraq-Baghdad	11857	2	0.008	0.01	0.203	0.153	0.626
Iraq-Baghdad	11858	1	0.021	0.016	0.113	0.013	0.837
Iraq-Baghdad	11859	3	0.008	0.012	0.091	0.044	0.845
Iraq-Baghdad	11862	1	0.025	0.01	0.272	0.066	0.627
Iraq-Baghdad	11865	3	0.154	0.022	0.213	0.01	0.601
Iraq-Baghdad	11868	8	0.02	0.022	0.036	0.007	0.916
Iraq-Baghdad	11869	7	0.011	0.012	0.124	0.151	0.701
Iraq-Baghdad	11870	1	0.019	0.018	0.29	0.139	0.532
Iraq-Baghdad	11871	2	0.01	0.073	0.388	0.017	0.512
Iraq-Baghdad	11872	3	0.003	0.017	0.159	0.02	0.8
Iraq-Baghdad	11873	3	0.016	0.017	0.464	0.005	0.499
Iraq-Baghdad	11874	1	0.035	0.007	0.191	0.016	0.751
Iraq-Baghdad	11875	4	0.04	0.185	0.029	0.008	0.738
Iraq-Baghdad	11876	5	0.011	0.133	0.104	0.005	0.747
Iraq-Baghdad	11877	3	0.033	0.015	0.256	0.006	0.69

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Iraq-Baghdad	11878	3	0.006	0.01	0.307	0.071	0.605
Iraq-Baghdad	11879	1	0.049	0.127	0.025	0.012	0.787
Iraq-Baghdad	11880	4	0.015	0.014	0.176	0.017	0.779
Iraq-Baghdad	11881	2	0.014	0.009	0.296	0.076	0.605
Iraq-Baghdad	11882	3	0.013	0.006	0.219	0.008	0.755
Iraq-Baghdad	11883	2	0.011	0.023	0.179	0.154	0.634
Iraq-Baghdad	11884	13	0.026	0.016	0.034	0.015	0.909
Iraq-Baghdad	11885	0	0.013	0.034	0.228	0.003	0.721
Iraq-Baghdad	11886	2	0.057	0.088	0.232	0.008	0.615
Iraq-Baghdad	11887	15	0.01	0.245	0.088	0.01	0.647
Iran	9419	18	0.012	0.027	0.049	0.068	0.844
Iran	9420	14	0.122	0.044	0.038	0.013	0.784
Iran	9421	17	0.01	0.01	0.059	0.01	0.911
Iran	9422	15	0.05	0.019	0.135	0.008	0.788
Iran	9424	21	0.03	0.012	0.006	0.004	0.949
Iran	9425	4	0.018	0.009	0.01	0.003	0.959
Iran	9426	5	0.034	0.017	0.011	0.019	0.919
Iran	9427	3	0.009	0.013	0.01	0.007	0.962
Iran	9428	2	0.029	0.087	0.031	0.013	0.841
Iran	9429	3	0.116	0.103	0.023	0.011	0.746
Iran	9430	9	0.02	0.081	0.138	0.035	0.726
Iran	9431	1	0.025	0.236	0.02	0.006	0.713
Iran	9432	3	0.021	0.023	0.007	0.004	0.946
Iran	9433	2	0.052	0.016	0.027	0.032	0.872
Iran	9434	2	0.033	0.029	0.018	0.043	0.877
Iran	9435	2	0.017	0.017	0.005	0.005	0.956
Iran	9436	15	0.005	0.011	0.009	0.005	0.969
Iran	9437	1	0.006	0.018	0.008	0.005	0.962
Iran	9438	1	0.014	0.005	0.004	0.003	0.974
Iran	9439	1	0.018	0.019	0.008	0.008	0.946
Iran	9440	1	0.002	0.007	0.006	0.002	0.982
Iran	9441	2	0.003	0.005	0.003	0.003	0.987

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Iran	9442	2	0.012	0.019	0.01	0.005	0.954
Iran	9443	2	0.007	0.008	0.005	0.005	0.975
Iran	9444	1	0.005	0.003	0.003	0.002	0.985
Iran	9445	2	0.004	0.003	0.003	0.002	0.988
Iran	9446	3	0.01	0.008	0.004	0.004	0.975
Iran	9447	19	0.004	0.015	0.004	0.005	0.972
Iran	9448	3	0.004	0.006	0.004	0.003	0.983
Iran	9449	1	0.005	0.003	0.003	0.002	0.987
Iran	9450	2	0.007	0.004	0.006	0.003	0.979
Iran	9451	3	0.018	0.009	0.004	0.003	0.967
Iran	9452	1	0.006	0.006	0.004	0.006	0.979
Iran	9453	3	0.002	0.003	0.004	0.002	0.989
Iran	9454	1	0.003	0.003	0.003	0.002	0.99
Iran	9455	3	0.006	0.016	0.013	0.007	0.957
Iran	9456	3	0.007	0.009	0.004	0.003	0.977
Iran	9457	3	0.003	0.004	0.005	0.004	0.985
Iran	9458	1	0.005	0.005	0.003	0.002	0.985
Iran	9459	2	0.004	0.008	0.003	0.003	0.983
Iran	9460	2	0.013	0.012	0.012	0.009	0.955
Iran	9461	3	0.004	0.009	0.005	0.007	0.975
Iran	9462	2	0.006	0.017	0.004	0.009	0.965
Iran	9463	3	0.006	0.006	0.004	0.003	0.981
Iran	9464	2	0.009	0.005	0.003	0.003	0.98
Iran	9465	2	0.003	0.007	0.008	0.004	0.978
Iran	9466	3	0.005	0.031	0.009	0.004	0.95
Iran	9468	3	0.023	0.007	0.007	0.007	0.956
Iran	9469	2	0.031	0.007	0.009	0.015	0.937
Iran	9470	3	0.025	0.009	0.009	0.007	0.95
Iran	9471	2	0.006	0.008	0.011	0.015	0.96
Iran	9472	2	0.021	0.012	0.008	0.003	0.956
Iran	9473	1	0.005	0.008	0.003	0.004	0.98
Iran	9474	1	0.006	0.009	0.013	0.013	0.959

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Iran	9475	2	0.004	0.01	0.008	0.006	0.973
Iran	9476	3	0.005	0.004	0.005	0.004	0.981
Iran	9477	2	0.017	0.006	0.007	0.008	0.962
Iran	9478	1	0.023	0.065	0.011	0.007	0.894
Iran	9479	2	0.004	0.003	0.003	0.003	0.987
Iran	9480	3	0.009	0.027	0.006	0.004	0.954
Iran	9481	3	0.039	0.012	0.007	0.014	0.928
Iran	9482	2	0.014	0.037	0.007	0.008	0.934
Iran	9483	4	0.206	0.017	0.018	0.01	0.75
Iran	9484	2	0.004	0.017	0.192	0.04	0.747
Iran	9485	2	0.046	0.01	0.008	0.004	0.932
Iran	9486	3	0.004	0.009	0.006	0.008	0.973
Iran	9487	2	0.007	0.022	0.007	0.004	0.96
Iran	9488	3	0.007	0.008	0.017	0.009	0.959
Iran	9489	3	0.007	0.032	0.015	0.009	0.936
Iran	9490	3	0.006	0.008	0.003	0.005	0.977
Iran	9491	2	0.004	0.004	0.003	0.002	0.987
Iran	9492	3	0.004	0.011	0.006	0.006	0.973
Iran	9493	1	0.014	0.005	0.004	0.005	0.971
Iran	9494	2	0.003	0.004	0.005	0.003	0.985
Iran	9495	1	0.004	0.007	0.004	0.004	0.981
Iran	9497	3	0.006	0.012	0.004	0.003	0.975
Iran	9498	2	0.006	0.004	0.004	0.003	0.984
Iran	9499	3	0.023	0.006	0.006	0.004	0.962
Iran	9500	2	0.004	0.009	0.003	0.003	0.982
Iran	9501	1	0.005	0.04	0.014	0.03	0.91
Iran	9502	4	0.017	0.005	0.011	0.005	0.963
Iran	9503	3	0.007	0.02	0.006	0.011	0.956
Iran	9504	2	0.002	0.003	0.003	0.002	0.99
Iran	9505	2	0.003	0.003	0.003	0.003	0.989
Iran	9506	6	0.012	0.077	0.006	0.033	0.872
Iran	9507	6	0.013	0.051	0.023	0.048	0.865

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Iran	9508	3	0.011	0.011	0.004	0.003	0.971
Iran	9509	5	0.019	0.006	0.005	0.005	0.965
Iran	9510	4	0.015	0.006	0.003	0.003	0.972
Iran	9511	3	0.006	0.006	0.007	0.007	0.974
Iran	9512	6	0.009	0.01	0.008	0.008	0.966
Iran	9513	5	0.006	0.021	0.008	0.007	0.958
Iran	9514	4	0.013	0.016	0.105	0.019	0.848
Iran	9515	4	0.006	0.016	0.004	0.007	0.967
Iran	9516	7	0.008	0.021	0.007	0.006	0.958
Iran	9517	3	0.029	0.009	0.006	0.009	0.947
Iran	9518	3	0.012	0.036	0.01	0.012	0.931
Iran	9519	4	0.007	0.013	0.009	0.017	0.954
Iran	9520	4	0.003	0.021	0.006	0.006	0.963
Iran	9521	8	0.008	0.114	0.006	0.008	0.864
Iran	9522	9	0.024	0.019	0.04	0.006	0.912
Iran	9523	3	0.005	0.021	0.038	0.024	0.913
Iran	9524	3	0.01	0.005	0.003	0.002	0.98
Iran	9526	4	0.009	0.005	0.003	0.002	0.98
Iran	9527	3	0.016	0.058	0.011	0.006	0.909
Iran	9528	5	0.007	0.005	0.003	0.003	0.981
Iran	9529	4	0.009	0.014	0.003	0.002	0.972
Iran	9530	5	0.007	0.006	0.005	0.003	0.979
Iran	9531	4	0.018	0.102	0.024	0.01	0.846
Iran	9532	14	0.011	0.014	0.033	0.028	0.914
Dubai	10104	1	0.002	0.796	0.055	0.02	0.127
Dubai	10105	2	0.011	0.746	0.011	0.01	0.222
Dubai	10106	4	0.006	0.941	0.006	0.004	0.042
Dubai	10107	1	0.047	0.476	0.024	0.03	0.424
Dubai	10108	2	0.048	0.843	0.047	0.009	0.054
Dubai	10109	4	0.125	0.501	0.009	0.009	0.356
Dubai	10110	3	0.006	0.791	0.013	0.014	0.176
Dubai	10111	4	0.004	0.937	0.008	0.004	0.048

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
Dubai	10112	2	0.036	0.808	0.081	0.011	0.064
Dubai	10120	3	0.006	0.871	0.008	0.006	0.109
Kenya-Nairobi	9833	4	0.019	0.044	0.01	0.694	0.234
Kenya-Nairobi	9834	0	0.083	0.332	0.029	0.54	0.017
Kenya-Nairobi	9835	0	0.039	0.353	0.533	0.068	0.007
Kenya-Nairobi	9836	2	0.044	0.322	0.009	0.619	0.005
Kenya-Nairobi	9837	2	0.163	0.035	0.023	0.758	0.021
Kenya-Nairobi	9838	4	0.012	0.135	0.218	0.545	0.091
Kenya-Nairobi	9839	1	0.032	0.439	0.013	0.498	0.017
Kenya-Nairobi	9840	3	0.013	0.306	0.082	0.579	0.02
Kenya-Nairobi	9841	3	0.02	0.219	0.01	0.739	0.012
Kenya-Nairobi	9842	2	0.038	0.286	0.045	0.603	0.028
Kenya-Nairobi	9843	4	0.034	0.327	0.017	0.612	0.01
Kenya-Nairobi	9844	3	0.096	0.155	0.017	0.722	0.01
Kenya-Nairobi	9845	1	0.038	0.17	0.113	0.668	0.011
Kenya-Nairobi	9846	1	0.061	0.332	0.019	0.565	0.022
Kenya-Nairobi	9847	3	0.023	0.216	0.012	0.737	0.012
Kenya-Nairobi	9848	3	0.069	0.173	0.141	0.604	0.013
Kenya-Nairobi	9849	2	0.029	0.653	0.016	0.297	0.004
Kenya-Nairobi	9850	3	0.016	0.118	0.052	0.779	0.035
Kenya-Nairobi	9851	2	0.016	0.527	0.01	0.436	0.012
Kenya-Nairobi	9852	4	0.012	0.534	0.033	0.415	0.006
Kenya-Nairobi	9853	4	0.039	0.315	0.01	0.601	0.035
Kenya-Nairobi	9854	2	0.012	0.286	0.047	0.617	0.039
Kenya-Nairobi	9855	2	0.015	0.383	0.048	0.534	0.02
Kenya-Nairobi	9856	3	0.013	0.39	0.026	0.563	0.009
Kenya-Nairobi	9857	6	0.108	0.163	0.031	0.683	0.015
Kenya-Nairobi	9858	3	0.028	0.318	0.01	0.635	0.01
Kenya-Nairobi	9859	4	0.199	0.018	0.006	0.766	0.011
Kenya-Nairobi	9860	2	0.167	0.11	0.01	0.705	0.008
Kenya-Nairobi	9861	1	0.011	0.178	0.048	0.744	0.02
Kenya-Nairobi	9862	2	0.037	0.337	0.049	0.571	0.004

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Kenya-Nairobi	9863	1	0.035	0.536	0.006	0.417	0.006
Kenya-Nairobi	9864	2	0.01	0.393	0.021	0.53	0.045
Kenya-Nairobi	9865	4	0.062	0.277	0.022	0.614	0.025
Kenya-Nairobi	9866	3	0.075	0.222	0.06	0.635	0.008
Kenya-Nairobi	9867	0	0.059	0.319	0.019	0.578	0.025
Kenya-Nairobi	9868	5	0.021	0.219	0.132	0.606	0.021
Kenya-Pate	2000	2	0.006	0.916	0.024	0.045	0.009
Kenya-Pate	2001	3	0.004	0.97	0.003	0.003	0.02
Kenya-Pate	2002	1	0.006	0.948	0.004	0.003	0.038
Kenya-Pate	2003	0	0.006	0.974	0.005	0.009	0.007
Kenya-Pate	2004	3	0.007	0.963	0.015	0.005	0.01
Kenya-Pate	2006	3	0.021	0.92	0.01	0.015	0.034
Kenya-Pate	2007	4	0.005	0.963	0.012	0.011	0.008
Kenya-Pate	2009	6	0.005	0.86	0.083	0.034	0.018
Kenya-Pate	2011	3	0.004	0.982	0.008	0.003	0.003
Kenya-Lamu	1848	13	0.009	0.969	0.008	0.009	0.005
Kenya-Lamu	2014	4	0.005	0.922	0.02	0.019	0.033
Kenya-Lamu	2015	2	0.009	0.89	0.063	0.032	0.006
Kenya-Lamu	2016	2	0.007	0.963	0.015	0.009	0.007
Kenya-Lamu	2018	1	0.004	0.841	0.02	0.127	0.008
Kenya-Lamu	2019	2	0.005	0.923	0.04	0.027	0.005
Kenya-Lamu	2021	2	0.006	0.866	0.018	0.027	0.083
Kenya-Lamu	2023	3	0.005	0.976	0.006	0.008	0.005
Kenya-Lamu	2024	2	0.003	0.977	0.005	0.004	0.01
Kenya-Lamu	2025	3	0.009	0.946	0.016	0.009	0.02
Kenya-Lamu	2026	4	0.005	0.938	0.046	0.006	0.006
Kenya-Lamu	2027	6	0.017	0.916	0.008	0.02	0.039
Kenya-Lamu	2029	2	0.003	0.981	0.005	0.003	0.008
Kenya-Lamu	2030	1	0.003	0.962	0.007	0.02	0.008
Kenya-Lamu	2031	4	0.009	0.929	0.017	0.017	0.029
Kenya-Lamu	2032	2	0.007	0.833	0.011	0.008	0.142
Kenya-Lamu	2033	2	0.003	0.971	0.012	0.004	0.009

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Kenya-Lamu	3241	4	0.013	0.917	0.036	0.026	0.008
Kenya-Lamu	3246	2	0.006	0.908	0.052	0.028	0.007
Kenya-Lamu	3247	3	0.013	0.865	0.017	0.091	0.013
India-Udaipur	11835	8	0.357	0.374	0.024	0.01	0.235
India-Udaipur	11836	3	0.031	0.581	0.013	0.012	0.363
India-Udaipur	11837	2	0.063	0.682	0.01	0.003	0.242
India-Agra	11823	1	0.04	0.553	0.014	0.005	0.389
India-Agra	11824	2	0.006	0.739	0.024	0.005	0.226
India-Agra	11825	2	0.099	0.353	0.009	0.007	0.532
India-Agra	11826	6	0.044	0.52	0.008	0.004	0.425
India-Agra	11827	19	0.012	0.555	0.012	0.004	0.417
India-Agra	11828	2	0.023	0.618	0.118	0.007	0.233
India-Agra	11829	4	0.018	0.633	0.012	0.008	0.329
India-Agra	11830	8	0.013	0.546	0.008	0.004	0.429
India-Agra	11831	3	0.061	0.39	0.034	0.007	0.507
India-Agra	11832	2	0.016	0.466	0.007	0.003	0.508
India-Agra	11833	16	0.049	0.634	0.018	0.004	0.294
India-Agra	11834	3	0.051	0.484	0.008	0.005	0.452
India-Hyderbad	11802	13	0.104	0.604	0.271	0.011	0.009
India-Hyderbad	11803	7	0.021	0.883	0.05	0.004	0.043
India-Hyderbad	11804	5	0.445	0.516	0.005	0.003	0.031
India-Hyderbad	11805	10	0.042	0.901	0.023	0.01	0.023
India-Hyderbad	11807	11	0.099	0.858	0.014	0.008	0.02
India-Hyderbad	11808	9	0.251	0.72	0.01	0.014	0.005
India-Hyderbad	11809	3	0.008	0.73	0.053	0.141	0.068

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
India-Hyderbad	11810	0	0.234	0.66	0.049	0.007	0.05
India-Hyderbad	11811	0	0.015	0.949	0.017	0.012	0.007
India-Hyderbad	11812	3	0.097	0.715	0.009	0.003	0.176
India-Hyderbad	11813	4	0.392	0.543	0.037	0.006	0.023
India-Hyderbad	11814	2	0.024	0.908	0.021	0.005	0.042
India-Hyderbad	11815	2	0.134	0.802	0.025	0.008	0.031
India-Hyderbad	11816	3	0.007	0.954	0.007	0.004	0.029
India-Hyderbad	11817	2	0.134	0.837	0.011	0.004	0.014
India-Hyderbad	11818	1	0.057	0.86	0.019	0.057	0.006
India-Hyderbad	11819	4	0.007	0.954	0.009	0.005	0.024
India-Hyderbad	11820	5	0.152	0.817	0.007	0.003	0.021
India-Hyderbad	11821	13	0.309	0.647	0.024	0.005	0.015
India-Hyderbad	11822	2	0.17	0.764	0.037	0.008	0.021
India-Andhra	10159	2	0.313	0.638	0.025	0.012	0.012
India-Andhra	10160	1	0.455	0.529	0.005	0.004	0.006
India-Andhra	10161	2	0.051	0.922	0.005	0.008	0.014
India-Andhra	10162	5	0.188	0.782	0.008	0.009	0.014
India-Andhra	10163	0	0.122	0.86	0.005	0.005	0.009
India-Andhra	10164	2	0.314	0.611	0.01	0.013	0.053

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
India-Andhra	10165	1	0.08	0.895	0.008	0.007	0.011
India-Andhra	10166	3	0.064	0.887	0.023	0.019	0.007
India-Andhra	10167	1	0.199	0.732	0.04	0.024	0.005
India-Andhra	10168	1	0.127	0.822	0.025	0.012	0.015
India-Andhra	10169	6	0.217	0.749	0.011	0.018	0.005
India-Andhra	10170	4	0.293	0.664	0.025	0.013	0.004
India-Andhra	10171	1	0.323	0.598	0.011	0.012	0.056
India-Andhra	10172	2	0.106	0.837	0.011	0.02	0.026
India-Andhra	10173	2	0.223	0.752	0.011	0.009	0.005
India-Andhra	10174	3	0.194	0.784	0.01	0.009	0.003
India-Andhra	10175	2	0.105	0.793	0.024	0.067	0.011
India-Andhra	10176	2	0.358	0.585	0.025	0.011	0.021
India-Andhra	10177	0	0.271	0.632	0.009	0.077	0.01
India-Andhra	10178	3	0.152	0.822	0.007	0.007	0.012
India-Andhra	10179	4	0.048	0.924	0.005	0.018	0.004
India-Andhra	10180	10	0.113	0.676	0.113	0.066	0.032
India-Andhra	10181	5	0.368	0.608	0.01	0.007	0.006
India-Kolkata	10113	2	0.056	0.91	0.014	0.007	0.013
India-Kolkata	10114	1	0.09	0.889	0.007	0.004	0.01
India-Kolkata	10115	1	0.086	0.806	0.088	0.012	0.008
India-Kolkata	10116	2	0.072	0.911	0.006	0.003	0.01
India-Kolkata	10117	2	0.283	0.621	0.076	0.007	0.014
India-Kolkata	10118	3	0.197	0.543	0.204	0.022	0.034
India-Kolkata	10119	3	0.035	0.73	0.093	0.096	0.046
Sri Lanka	8780	1	0.194	0.677	0.023	0.095	0.01
Sri Lanka	8781	1	0.18	0.657	0.037	0.117	0.009
Sri Lanka	8782	3	0.055	0.759	0.101	0.07	0.015
Sri Lanka	8783	0	0.014	0.827	0.108	0.041	0.01
Sri Lanka	8784	1	0.283	0.439	0.016	0.25	0.012
Sri Lanka	8785	10	0.033	0.768	0.015	0.151	0.033
Sri Lanka	8786	0	0.061	0.675	0.124	0.097	0.043
Sri Lanka	8787	0	0.006	0.747	0.011	0.229	0.007

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Sri Lanka	8788	4	0.061	0.697	0.077	0.076	0.088
Sri Lanka	8789	2	0.065	0.448	0.107	0.363	0.017
Sri Lanka	8790	1	0.054	0.64	0.021	0.279	0.007
Sri Lanka	8791	1	0.032	0.892	0.046	0.017	0.013
Sri Lanka	8792	0	0.016	0.772	0.085	0.104	0.023
Sri Lanka	8793	2	0.011	0.653	0.027	0.282	0.027
Sri Lanka	8794	2	0.024	0.62	0.079	0.236	0.041
Sri Lanka	8795	1	0.076	0.651	0.059	0.208	0.007
Sri Lanka	8796	4	0.272	0.621	0.071	0.03	0.006
Sri Lanka	8797	1	0.087	0.487	0.008	0.355	0.063
Sri Lanka	8798	1	0.134	0.528	0.259	0.059	0.02
Sri Lanka	8799	2	0.007	0.69	0.005	0.285	0.013
Sri Lanka	8800	2	0.227	0.375	0.02	0.365	0.013
Sri Lanka	8801	5	0.006	0.755	0.013	0.197	0.029
Sri Lanka	8802	2	0.019	0.591	0.006	0.371	0.013
Sri Lanka	8803	6	0.131	0.771	0.03	0.061	0.006
Thailand	11688	6	0.965	0.018	0.004	0.01	0.003
Thailand	11689	13	0.94	0.024	0.004	0.004	0.028
Thailand	11691	27	0.959	0.019	0.008	0.008	0.005
Thailand	11698	18	0.978	0.008	0.007	0.003	0.004
Thailand	11702	10	0.977	0.012	0.004	0.004	0.003
Thailand	11703	12	0.983	0.007	0.003	0.003	0.004
Thailand	11705	21	0.853	0.107	0.027	0.005	0.009
Thailand	11707	4	0.972	0.017	0.005	0.003	0.004
Thailand	11708	18	0.897	0.055	0.028	0.012	0.009
Thailand	11709	12	0.974	0.011	0.007	0.004	0.005
Thailand	11710	9	0.974	0.01	0.008	0.004	0.004
Thailand	11711	6	0.975	0.012	0.003	0.006	0.005
Thailand	11714	6	0.883	0.09	0.01	0.006	0.012
Thailand	11715	17	0.814	0.061	0.006	0.008	0.111
Thailand	11717	15	0.877	0.1	0.005	0.003	0.015
Thailand	11718	2	0.965	0.018	0.004	0.007	0.005

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Thailand	11720	4	0.982	0.008	0.004	0.002	0.004
Vietnam	8844	4	0.845	0.137	0.004	0.007	0.007
Vietnam	8845	3	0.694	0.269	0.014	0.007	0.016
Vietnam	8846	3	0.545	0.408	0.031	0.012	0.004
Vietnam	8847	10	0.933	0.021	0.009	0.029	0.008
Vietnam	8848	6	0.778	0.187	0.017	0.013	0.005
Vietnam	8849	2	0.87	0.054	0.057	0.015	0.005
Vietnam	8850	1	0.735	0.022	0.014	0.222	0.007
Vietnam	8851	2	0.713	0.088	0.067	0.031	0.1
Vietnam	8852	13	0.721	0.067	0.157	0.043	0.011
Vietnam	8853	3	0.605	0.134	0.201	0.055	0.006
Vietnam	8854	5	0.739	0.048	0.039	0.05	0.125
Vietnam	8855	2	0.738	0.021	0.046	0.19	0.005
Vietnam	8856	2	0.634	0.164	0.185	0.01	0.008
Vietnam	8857	3	0.35	0.608	0.018	0.015	0.009
Vietnam	8858	2	0.673	0.084	0.175	0.062	0.006
Vietnam	8859	7	0.647	0.319	0.015	0.01	0.009
Vietnam	8860	2	0.784	0.051	0.114	0.04	0.01
Vietnam	8861	2	0.608	0.212	0.118	0.022	0.041
Vietnam	8862	2	0.414	0.55	0.016	0.012	0.009
Vietnam	8863	3	0.624	0.071	0.104	0.178	0.022
Taiwan	8681	4	0.326	0.005	0.005	0.658	0.005
Taiwan	8682	0	0.876	0.052	0.014	0.019	0.04
Taiwan	8683	3	0.7	0.03	0.071	0.152	0.047
Taiwan	8684	3	0.36	0.005	0.008	0.619	0.008
Taiwan	8685	2	0.898	0.033	0.011	0.054	0.004
Taiwan	8686	6	0.672	0.016	0.017	0.283	0.012
Taiwan	8687	5	0.801	0.035	0.1	0.026	0.038
Taiwan	8688	26	0.821	0.111	0.019	0.033	0.016
Taiwan	8689	5	0.715	0.023	0.035	0.064	0.163
Taiwan	8690	2	0.892	0.017	0.008	0.011	0.073
Taiwan	8691	16	0.776	0.137	0.023	0.053	0.011

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Taiwan	8692	3	0.922	0.018	0.012	0.034	0.013
Taiwan	8693	2	0.807	0.033	0.015	0.134	0.011
Taiwan	8694	1	0.541	0.02	0.005	0.428	0.007
Taiwan	8695	1	0.837	0.01	0.063	0.086	0.005
Taiwan	8696	11	0.01	0.005	0.005	0.976	0.003
Taiwan	8697	1	0.021	0.014	0.017	0.932	0.016
Taiwan	8698	4	0.004	0.004	0.005	0.985	0.003
Taiwan	8699	6	0.493	0.244	0.056	0.08	0.128
Taiwan	8700	2	0.659	0.031	0.054	0.241	0.015
Taiwan	8701	2	0.777	0.016	0.007	0.194	0.006
Taiwan	8702	2	0.627	0.036	0.058	0.261	0.017
Taiwan	8703	2	0.012	0.012	0.014	0.958	0.005
Taiwan	8704	1	0.843	0.032	0.104	0.016	0.005
Taiwan	8705	2	0.827	0.113	0.023	0.013	0.023
Taiwan	8706	2	0.755	0.053	0.085	0.074	0.033
Taiwan	8707	5	0.844	0.015	0.014	0.022	0.105
Taiwan	8708	3	0.01	0.007	0.005	0.974	0.004
Taiwan	8709	4	0.911	0.024	0.023	0.025	0.018
Japan-Oita	11967	4	0.936	0.018	0.024	0.014	0.008
Japan-Oita	11968	5	0.741	0.045	0.022	0.188	0.005
Japan-Oita	11969	5	0.849	0.009	0.05	0.085	0.007
Japan-Oita	11970	15	0.848	0.02	0.104	0.013	0.015
Japan-Oita	11971	8	0.893	0.047	0.018	0.025	0.017
Japan-Oita	11972	3	0.945	0.014	0.02	0.015	0.006
Japan-Oita	11973	3	0.716	0.009	0.008	0.26	0.008
Japan-Oita	11974	20	0.914	0.054	0.016	0.008	0.008
Japan-Oita	11975	19	0.759	0.066	0.03	0.143	0.003
Japan-Oita	11976	16	0.843	0.007	0.01	0.133	0.006
Japan-Oita	11977	5	0.924	0.013	0.011	0.045	0.007
Japan-Oita	11979	11	0.946	0.018	0.012	0.014	0.009
Japan-Oita	11980	18	0.949	0.022	0.011	0.009	0.009
Japan-Oita	11981	16	0.985	0.006	0.003	0.002	0.004

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Japan-Oita	11982	6	0.923	0.018	0.011	0.04	0.008
Japan-Oita	11985	11	0.952	0.012	0.023	0.007	0.005
Japan-Oita	11986	7	0.668	0.008	0.037	0.28	0.007
Japan-Kanazawa	11929	7	0.003	0.004	0.004	0.984	0.004
Japan-Kanazawa	11931	18	0.926	0.025	0.005	0.034	0.01
Japan-Kanazawa	11932	6	0.772	0.009	0.006	0.207	0.007
Japan-Kanazawa	11933	14	0.844	0.078	0.018	0.055	0.004
Japan-Kanazawa	11934	4	0.88	0.004	0.006	0.108	0.002
Japan-Kanazawa	11936	8	0.952	0.011	0.01	0.023	0.004
Japan-Kanazawa	11937	23	0.957	0.008	0.008	0.023	0.005
Japan-Kanazawa	11939	18	0.965	0.014	0.005	0.01	0.005
Japan-Kanazawa	11940	12	0.97	0.007	0.007	0.006	0.011
Japan-Kanazawa	11941	7	0.954	0.006	0.014	0.009	0.017
Japan-Kanazawa	11942	9	0.956	0.031	0.005	0.004	0.004
Japan-Kanazawa	11943	19	0.858	0.064	0.02	0.014	0.045
Japan-Kanazawa	11944	13	0.035	0.104	0.072	0.762	0.026
Japan-Kanazawa	11945	16	0.919	0.015	0.008	0.051	0.007
Japan-	11946	15	0.98	0.007	0.006	0.005	0.003

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Kanazawa							
Japan-Ohmiya	11947	4	0.841	0.008	0.074	0.073	0.005
Japan-Ohmiya	11948	16	0.834	0.023	0.052	0.024	0.067
Japan-Ohmiya	11951	18	0.778	0.057	0.031	0.081	0.053
Japan-Ohmiya	11953	3	0.982	0.004	0.006	0.005	0.004
Japan-Ohmiya	11954	3	0.763	0.009	0.01	0.208	0.01
Japan-Ohmiya	11955	5	0.678	0.013	0.007	0.296	0.005
Japan-Ohmiya	11956	3	0.964	0.017	0.008	0.007	0.005
Japan-Ohmiya	11957	3	0.762	0.025	0.071	0.129	0.013
Japan-Ohmiya	11959	6	0.862	0.014	0.07	0.047	0.006
Japan-Ohmiya	11960	3	0.982	0.005	0.003	0.005	0.005
Japan-Ohmiya	11961	3	0.962	0.008	0.015	0.01	0.005
Japan-Ohmiya	11962	5	0.77	0.039	0.019	0.165	0.007
Japan-Ohmiya	11963	3	0.85	0.031	0.01	0.102	0.007
Japan-Ohmiya	11964	4	0.747	0.05	0.012	0.171	0.02
Japan-Ohmiya	11965	4	0.718	0.246	0.022	0.008	0.005
Japan-Ohmiya	11966	4	0.847	0.022	0.026	0.089	0.017
Japan-Sapporo	11907	6	0.929	0.011	0.016	0.028	0.015
Japan-Sapporo	11909	9	0.007	0.005	0.005	0.979	0.004
Japan-Sapporo	11911	15	0.582	0.008	0.008	0.392	0.009
Japan-Sapporo	11913	14	0.681	0.012	0.011	0.292	0.004
Japan-Sapporo	11914	6	0.761	0.027	0.017	0.189	0.006
Japan-Sapporo	11915	8	0.955	0.013	0.01	0.013	0.01
Japan-Sapporo	11916	6	0.011	0.013	0.046	0.926	0.003
Japan-	11917	4	0.018	0.033	0.02	0.911	0.018

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling Location	ID No.	Missing Data	Population 1	2	3	4	5
Sapporo							
Japan-Sapporo	11918	12	0.65	0.083	0.016	0.238	0.012
Japan-Sapporo	11921	5	0.923	0.047	0.01	0.005	0.015
Japan-Sapporo	11922	5	0.795	0.165	0.008	0.024	0.008
Japan-Sapporo	11923	7	0.938	0.028	0.008	0.021	0.005
Japan-Sapporo	11924	5	0.401	0.011	0.009	0.574	0.005
Japan-Sapporo	11925	9	0.972	0.016	0.005	0.003	0.004
Japan-Sapporo	11926	10	0.579	0.009	0.152	0.25	0.011
China-Henan	8869	2	0.882	0.009	0.051	0.011	0.047
China-Henan	8870	1	0.981	0.005	0.004	0.003	0.008
China-Henan	8871	1	0.788	0.014	0.014	0.005	0.179
China-Henan	8872	1	0.961	0.008	0.009	0.006	0.016
China-Henan	8873	2	0.953	0.005	0.011	0.004	0.027
China-Henan	8874	8	0.845	0.028	0.005	0.003	0.12
China-Henan	8875	2	0.985	0.004	0.004	0.003	0.003
China-Henan	8876	1	0.985	0.005	0.004	0.003	0.003
China-Henan	8877	2	0.817	0.061	0.025	0.023	0.074
China-Henan	8878	3	0.952	0.007	0.03	0.004	0.007
China-Henan	8879	2	0.971	0.009	0.005	0.003	0.012
China-Henan	8880	2	0.877	0.015	0.009	0.036	0.063
China-Henan	8881	2	0.836	0.013	0.053	0.003	0.095
China-Henan	8882	2	0.906	0.034	0.023	0.014	0.022
China-Henan	8883	0	0.969	0.005	0.005	0.004	0.016
China-Henan	8884	0	0.89	0.031	0.006	0.002	0.071
China-Henan	8885	1	0.92	0.019	0.021	0.012	0.028

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
China-Henan	8886	1	0.97	0.004	0.009	0.004	0.013
China-Henan	8887	1	0.844	0.009	0.02	0.008	0.118
China-Henan	8888	1	0.948	0.01	0.008	0.01	0.024
South Korea	2769	4	0.972	0.003	0.008	0.004	0.013
South Korea	2772	19	0.97	0.014	0.005	0.004	0.007
South Korea	2775	9	0.97	0.007	0.007	0.006	0.011
South Korea	2776	23	0.922	0.042	0.024	0.007	0.006
South Korea	2779	1	0.967	0.01	0.005	0.006	0.012
South Korea	2784	2	0.959	0.011	0.009	0.004	0.017
South Korea	2785	1	0.892	0.007	0.009	0.007	0.085
South Korea	2786	2	0.986	0.003	0.005	0.004	0.002
South Korea	7671	1	0.897	0.004	0.038	0.053	0.007
South Korea	7672	0	0.954	0.027	0.009	0.004	0.006
South Korea	7673	1	0.862	0.004	0.066	0.009	0.059
South Korea	7674	1	0.727	0.028	0.086	0.114	0.045
South Korea	7675	3	0.981	0.004	0.006	0.005	0.004
South Korea	7676	3	0.907	0.009	0.019	0.053	0.012
South Korea	7677	14	0.162	0.011	0.034	0.613	0.18
South Korea	7678	1	0.938	0.006	0.01	0.036	0.01
South Korea	7679	2	0.969	0.005	0.011	0.005	0.011
South Korea	7680	8	0.799	0.008	0.061	0.118	0.013
South Korea	7681	4	0.909	0.004	0.067	0.009	0.012
South Korea	7682	1	0.977	0.006	0.009	0.004	0.004
South Korea	7683	2	0.975	0.009	0.004	0.003	0.009
South Korea	7684	2	0.436	0.019	0.083	0.436	0.026
South Korea	7685	8	0.901	0.039	0.029	0.017	0.013
South Korea	7686	3	0.903	0.007	0.023	0.056	0.011
South Korea	7687	5	0.846	0.017	0.02	0.113	0.004
South Korea	7688	11	0.535	0.005	0.006	0.45	0.003
South Korea	7689	2	0.957	0.006	0.007	0.008	0.022
South Korea	7690	2	0.902	0.027	0.041	0.023	0.007
South Korea	7691	3	0.973	0.009	0.007	0.005	0.005

Table 22 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 5

Sampling	ID	Missing	Population				
Location	No.	Data	1	2	3	4	5
South Korea	7692	1	0.851	0.033	0.064	0.023	0.028
South Korea	7693	0	0.805	0.077	0.069	0.028	0.022
South Korea	7694	2	0.981	0.008	0.005	0.002	0.004
South Korea	7695	9	0.695	0.009	0.229	0.051	0.015
South Korea	7696	2	0.974	0.004	0.008	0.006	0.008
South Korea	7697	3	0.899	0.009	0.016	0.039	0.037
South Korea	7698	6	0.82	0.013	0.143	0.01	0.014
South Korea	7699	2	0.952	0.004	0.025	0.01	0.009
South Korea	7700	6	0.957	0.01	0.01	0.006	0.017

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
USA-NY	2547	1	0.8149	0.02	0.0204	0.0175	0.0471	0.0288	0.0087	0.0426
USA-NY	2559	0	0.5437	0.0368	0.1514	0.0059	0.0184	0.0713	0.05	0.1224
USA-NY	2568	0	0.965	0.0055	0.0054	0.0042	0.0058	0.007	0.0041	0.003
USA-NY	2569	1	0.9214	0.0148	0.0084	0.0146	0.0116	0.0116	0.0043	0.0133
USA-NY	2572	0	0.9093	0.0225	0.0219	0.0134	0.0058	0.0128	0.0043	0.01
USA-NY	2578	20	0.7478	0.076	0.0405	0.0482	0.0264	0.0316	0.0068	0.0227
USA-NY	2590	0	0.9116	0.0158	0.0259	0.0058	0.0066	0.0107	0.0132	0.0104
USA-NY	2591	1	0.9247	0.0181	0.0102	0.017	0.0111	0.009	0.0048	0.0051
USA-NY	2597	1	0.8567	0.0364	0.0148	0.0483	0.013	0.0119	0.008	0.0109
USA-MS	9971	2	0.899	0.0149	0.0137	0.0077	0.0168	0.0113	0.0212	0.0154
USA-MS	9972	2	0.7381	0.0906	0.039	0.0276	0.044	0.0422	0.01	0.0085
USA-MS	9974	2	0.6857	0.0156	0.0155	0.0066	0.0062	0.009	0.2562	0.0052
USA-MS	9977	4	0.9489	0.0096	0.0125	0.0053	0.0063	0.0054	0.0031	0.0089
USA-MS	9980	1	0.8555	0.0296	0.0143	0.0142	0.0263	0.0319	0.0177	0.0105
USA-MS	9983	1	0.9283	0.0123	0.0146	0.0164	0.01	0.0067	0.0031	0.0086
USA-MS	9985	2	0.683	0.0179	0.0106	0.0162	0.024	0.0111	0.2318	0.0054
USA-MS	9987	2	0.5845	0.1533	0.104	0.0077	0.0244	0.0302	0.0569	0.039
USA-MS	9989	2	0.9404	0.008	0.0105	0.0061	0.0053	0.0112	0.0113	0.0072
USA-MS	9992	2	0.8732	0.0381	0.0277	0.0305	0.0064	0.0104	0.0052	0.0085
USA-HI	5366	1	0.7618	0.0147	0.0289	0.0152	0.0118	0.0569	0.013	0.0977
USA-HI	5367	0	0.7171	0.0163	0.0098	0.0367	0.0951	0.0654	0.0198	0.0398
USA-HI	5371	0	0.8947	0.0277	0.0266	0.0112	0.0058	0.0148	0.0128	0.0064
USA-HI	5372	0	0.4323	0.3105	0.0857	0.0461	0.0248	0.0755	0.0139	0.0111
USA-HI	5379	0	0.8471	0.0419	0.032	0.0197	0.0097	0.0275	0.0062	0.0159
USA-HI	5380	1	0.952	0.0093	0.018	0.0031	0.0032	0.0054	0.0024	0.0066
USA-HI	5383	1	0.3502	0.054	0.0307	0.2709	0.1737	0.0285	0.0282	0.0639
USA-HI	5384	2	0.87	0.0266	0.0253	0.0211	0.0215	0.016	0.0051	0.0144
USA-HI	5401	1	0.9419	0.0095	0.0105	0.0071	0.0087	0.0091	0.0071	0.0061
USA-HI	5402	0	0.8481	0.0151	0.0136	0.008	0.0124	0.0436	0.0356	0.0236
Brazil	7961	0	0.8658	0.0254	0.0433	0.0113	0.0071	0.0212	0.0099	0.016
Brazil	7962	2	0.7395	0.0339	0.0842	0.0109	0.0262	0.0436	0.0336	0.028
Brazil	7963	15	0.5211	0.0423	0.1078	0.0069	0.0148	0.0649	0.213	0.0291
Brazil	7964	1	0.874	0.0134	0.0684	0.0095	0.0065	0.0122	0.0041	0.0119
Brazil	7965	18	0.9426	0.0072	0.0058	0.0064	0.0115	0.0075	0.0079	0.0111
Brazil	7966	1	0.8629	0.0244	0.0471	0.0104	0.0092	0.0298	0.0105	0.0057
Brazil	7968	22	0.7997	0.0217	0.0308	0.0207	0.0208	0.0175	0.0144	0.0744
Brazil	7969	0	0.9541	0.0086	0.0081	0.0058	0.0079	0.0069	0.0041	0.0045
Brazil	7970	0	0.9429	0.0073	0.0083	0.0071	0.0103	0.0077	0.0057	0.0107
Brazil	7971	0	0.9351	0.0138	0.0123	0.0134	0.0059	0.0056	0.006	0.0079
Brazil	7972	0	0.8774	0.037	0.0451	0.0063	0.0071	0.0157	0.0049	0.0065
Brazil	7973	0	0.921	0.0144	0.0116	0.0092	0.0076	0.0119	0.0076	0.0167
Brazil	7974	3	0.858	0.0185	0.0765	0.0068	0.0058	0.0124	0.0107	0.0113
Brazil	7975	3	0.907	0.012	0.0212	0.0134	0.0058	0.0132	0.0061	0.0213
Brazil	7976	0	0.9157	0.0133	0.0197	0.0105	0.0056	0.014	0.0076	0.0136
Brazil	7977	1	0.8937	0.0299	0.0357	0.0067	0.0053	0.0082	0.0027	0.0178
Brazil	7978	1	0.8036	0.0277	0.0283	0.0107	0.0443	0.019	0.0094	0.0569
Brazil	7979	1	0.8596	0.0299	0.0212	0.0118	0.012	0.0164	0.0305	0.0186
Brazil	7980	2	0.6096	0.0259	0.1856	0.0116	0.0943	0.0485	0.0048	0.0198
Brazil	7981	2	0.7936	0.0137	0.0128	0.0045	0.011	0.0078	0.0051	0.1515
Brazil	7982	15	0.6989	0.0203	0.0196	0.0111	0.0546	0.0793	0.0716	0.0446
Brazil	7983	1	0.6454	0.0622	0.1221	0.0347	0.0236	0.0401	0.0362	0.0356
Brazil	7984	6	0.6041	0.0144	0.0595	0.0065	0.0114	0.0157	0.2475	0.0409
Brazil	7985	2	0.7088	0.0774	0.0858	0.005	0.0175	0.0212	0.0299	0.0545
Brazil	7986	2	0.7468	0.0334	0.0551	0.0052	0.0135	0.0204	0.1129	0.0127
Brazil	7987	1	0.8607	0.0225	0.07	0.005	0.0063	0.0125	0.0127	0.0103
Brazil	7988	0	0.7416	0.0334	0.0174	0.0057	0.0215	0.0439	0.0439	0.0927

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling	ID	Missing	Population							
Location	No.	Data	1	2	3	4	5	6	7	8
Brazil	7989	0	0.5809	0.0098	0.0116	0.0082	0.0067	0.0126	0.3619	0.0083
Brazil	7990	0	0.7188	0.0135	0.013	0.0067	0.0065	0.012	0.22	0.0096
Finland	8077	8	0.8471	0.06	0.0289	0.017	0.0118	0.0194	0.0046	0.0111
Finland	8084	6	0.8304	0.0319	0.0287	0.0471	0.0208	0.0151	0.0035	0.0225
Finland	8086	4	0.8111	0.0661	0.0384	0.0153	0.0093	0.0213	0.019	0.0195
Finland	8089	4	0.5705	0.1316	0.0331	0.0403	0.0242	0.166	0.0085	0.0259
Finland	8093	16	0.8786	0.0208	0.0151	0.0226	0.0116	0.0188	0.0055	0.027
Finland	8094	3	0.8916	0.0249	0.0131	0.0211	0.0106	0.026	0.0041	0.0086
Finland	8096	3	0.9442	0.0119	0.0073	0.0187	0.0069	0.0045	0.0021	0.0044
Finland	8107	22	0.9514	0.0083	0.0062	0.0071	0.0119	0.0084	0.0021	0.0046
Finland	8110	5	0.9633	0.0077	0.007	0.0043	0.0047	0.0068	0.0031	0.0031
Finland	8116	8	0.7999	0.012	0.0255	0.0115	0.0848	0.0334	0.0146	0.0183
Finland	8120	19	0.9402	0.0122	0.0102	0.004	0.0083	0.0069	0.0071	0.0111
Germany	8711	2	0.891	0.0204	0.0373	0.0088	0.009	0.008	0.0044	0.0211
Germany	8712	3	0.9323	0.0166	0.0095	0.0157	0.0076	0.0089	0.0038	0.0056
Germany	8713	2	0.6576	0.0447	0.2334	0.0079	0.018	0.0198	0.0046	0.014
Germany	8714	2	0.6758	0.1335	0.0649	0.0423	0.0232	0.0372	0.0092	0.0138
Germany	8715	4	0.9043	0.0384	0.0117	0.0192	0.011	0.006	0.0031	0.0063
Germany	8716	4	0.9015	0.0213	0.0147	0.0122	0.0088	0.0135	0.0085	0.0195
Germany	8717	12	0.9087	0.0177	0.0199	0.0174	0.0061	0.0137	0.0061	0.0104
Germany	8720	2	0.2269	0.0804	0.04	0.0094	0.0096	0.0335	0.5953	0.0049
Germany	8721	10	0.9045	0.0397	0.023	0.0062	0.0066	0.0082	0.0059	0.0059
Germany	8727	0	0.9441	0.0077	0.0097	0.0057	0.008	0.0092	0.0043	0.0113
Germany	8728	10	0.8226	0.0286	0.026	0.0247	0.0617	0.0168	0.009	0.0107
Germany	8729	1	0.953	0.0086	0.0064	0.0076	0.007	0.0064	0.0045	0.0065
Germany	8730	22	0.7621	0.0083	0.0079	0.0101	0.0613	0.0139	0.0096	0.1268
Germany	8731	12	0.9541	0.007	0.007	0.0054	0.0124	0.0058	0.0021	0.0062
Germany	8732	3	0.8954	0.0342	0.0309	0.0086	0.0158	0.0076	0.0029	0.0046
Germany	8733	14	0.8288	0.033	0.0282	0.0301	0.0323	0.0167	0.0173	0.0136
Germany	8734	0	0.9398	0.0174	0.0135	0.0084	0.0072	0.0073	0.0027	0.0037
Germany	8735	0	0.853	0.0417	0.0469	0.0111	0.0048	0.0155	0.0112	0.0158
Germany	8736	0	0.9326	0.019	0.0249	0.004	0.0043	0.006	0.004	0.0052
Germany	8737	2	0.9447	0.01	0.0089	0.0093	0.0085	0.0086	0.0042	0.0058
Germany	8738	10	0.8424	0.0646	0.0574	0.0086	0.0088	0.0097	0.0031	0.0054
Germany	8739	0	0.9201	0.0206	0.0394	0.0049	0.0039	0.0055	0.0021	0.0035
Germany	8741	12	0.0993	0.1491	0.7016	0.0089	0.0123	0.0205	0.0031	0.0052
Germany	8742	10	0.8989	0.0282	0.0222	0.0063	0.0079	0.0193	0.0117	0.0055
Germany	8744	6	0.5045	0.1384	0.2209	0.0039	0.01	0.0523	0.0603	0.0098
Germany	8745	22	0.9016	0.0364	0.0197	0.0071	0.0116	0.0142	0.0032	0.0062
Germany	8746	0	0.8691	0.0171	0.0171	0.0118	0.0437	0.025	0.0095	0.0067
Germany	8747	12	0.9586	0.0065	0.0069	0.004	0.0084	0.0081	0.0041	0.0034
Germany	8749	0	0.9421	0.0094	0.0083	0.0098	0.0077	0.0103	0.005	0.0074
Italy-Milan	8050	0	0.602	0.203	0.0706	0.0627	0.0118	0.0239	0.0174	0.0087
Italy-Milan	8057	1	0.5543	0.14	0.0371	0.0592	0.0589	0.0641	0.0616	0.0247
Italy-Milan	8060	0	0.6467	0.053	0.0189	0.1859	0.0132	0.0147	0.0584	0.0092
Italy-Milan	8061	2	0.6295	0.0815	0.0415	0.0086	0.0065	0.0403	0.1821	0.01
Italy-Milan	8062	1	0.2173	0.6024	0.1243	0.0111	0.0142	0.0139	0.0121	0.0047
Italy-Milan	8065	4	0.2969	0.6124	0.0434	0.0103	0.0101	0.0181	0.0037	0.0051
Italy-Milan	8066	0	0.1381	0.6217	0.1306	0.0407	0.0104	0.019	0.0315	0.008
Italy-Milan	8067	2	0.4805	0.2641	0.133	0.0413	0.007	0.0244	0.0376	0.0122
Italy-Milan	8068	0	0.3707	0.4037	0.1242	0.0138	0.0367	0.0319	0.0078	0.0111
Italy-Milan	8069	0	0.5977	0.1327	0.0543	0.0159	0.0155	0.1351	0.0308	0.0179
Italy-Milan	8071	2	0.6873	0.1343	0.0781	0.0153	0.0114	0.0309	0.0108	0.0318
Italy-Milan	8072	2	0.2072	0.2507	0.1594	0.0083	0.0245	0.0491	0.199	0.1017
Italy-Milan	8073	0	0.6913	0.0349	0.1821	0.0146	0.0145	0.048	0.0041	0.0106
Italy-Milan	8074	1	0.7195	0.0239	0.0693	0.0058	0.0104	0.0327	0.1294	0.009

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Italy-Rome	8586	1	0.4396	0.1849	0.2332	0.0171	0.0406	0.0685	0.0044	0.0118
Italy-Rome	8589	2	0.9124	0.0137	0.0244	0.0094	0.0088	0.0145	0.0083	0.0085
Italy-Rome	8592	1	0.3862	0.2207	0.0434	0.0751	0.0496	0.1617	0.0073	0.056
Italy-Rome	8594	1	0.7447	0.1067	0.0561	0.0071	0.0201	0.021	0.0161	0.0281
Italy-Rome	8595	0	0.6873	0.051	0.1204	0.0247	0.0268	0.0388	0.0332	0.0177
Italy-Rome	8596	1	0.2942	0.1279	0.481	0.0122	0.0055	0.063	0.0075	0.0088
Italy-Rome	8597	0	0.7674	0.0273	0.0603	0.0181	0.0133	0.0584	0.0332	0.0219
Italy-Rome	8599	0	0.9274	0.0083	0.0134	0.0072	0.0111	0.0111	0.013	0.0085
Italy-Rome	8601	2	0.5432	0.2255	0.1248	0.0126	0.0187	0.0143	0.0186	0.0423
Italy-Rome	8602	2	0.7002	0.0579	0.0404	0.0131	0.012	0.1561	0.0116	0.0087
Italy-Rome	8603	0	0.8695	0.0332	0.0264	0.0085	0.0066	0.0116	0.0165	0.0277
Italy-Rome	8604	2	0.1576	0.2738	0.4345	0.0077	0.0203	0.0174	0.0043	0.0843
Italy-Rome	8609	1	0.8883	0.0327	0.0297	0.0066	0.0104	0.0189	0.0048	0.0085
Italy-Rome	8610	1	0.385	0.2904	0.1399	0.0329	0.0272	0.0516	0.0195	0.0536
Italy-Rome	8611	2	0.6267	0.1049	0.1002	0.0186	0.0145	0.1139	0.0129	0.0083
Turkey	6477	2	0.7494	0.0419	0.0268	0.1058	0.035	0.0163	0.0152	0.0095
Turkey	6478	0	0.0803	0.4344	0.1166	0.0208	0.0151	0.1532	0.0122	0.1676
Turkey	6480	0	0.0088	0.1331	0.6852	0.0481	0.0197	0.0672	0.0294	0.0086
Turkey	6481	2	0.5551	0.0603	0.0425	0.006	0.1769	0.0823	0.0593	0.0175
Turkey	6482	3	0.7276	0.018	0.0275	0.0091	0.0089	0.0662	0.1312	0.0116
Turkey	6484	4	0.3921	0.3362	0.1122	0.0164	0.039	0.0732	0.0233	0.0076
Turkey	6486	1	0.7103	0.0467	0.0446	0.0456	0.0815	0.0353	0.0171	0.0189
Turkey	6487	4	0.6456	0.0329	0.0191	0.034	0.1001	0.1411	0.0187	0.0085
Turkey	6488	4	0.7409	0.0323	0.0184	0.0645	0.0394	0.0483	0.0281	0.0281
Turkey	6491	2	0.35	0.1655	0.105	0.0115	0.3306	0.0154	0.0094	0.0126
Turkey	6494	6	0.4972	0.1157	0.0744	0.0423	0.0358	0.0921	0.1229	0.0194
Turkey	6496	4	0.6051	0.0426	0.0421	0.0345	0.0257	0.0234	0.2017	0.0249
Turkey	6499	2	0.6808	0.0265	0.0377	0.0148	0.0379	0.124	0.0683	0.0099
Turkey	6500	1	0.4518	0.0472	0.0307	0.0451	0.3319	0.0737	0.0139	0.0057
Turkey	6502	4	0.5497	0.0364	0.0171	0.0339	0.0523	0.2541	0.0238	0.0327
Turkey	6503	4	0.5737	0.0299	0.031	0.0083	0.3192	0.0205	0.0097	0.0077
Turkey	6507	2	0.2732	0.0622	0.0209	0.007	0.0667	0.4754	0.0265	0.068
Turkey	6510	2	0.7601	0.0349	0.039	0.063	0.0315	0.0368	0.0253	0.0093
Turkey	6512	2	0.202	0.1712	0.0851	0.0909	0.0248	0.2593	0.1215	0.0451
Turkey	6513	4	0.2724	0.0715	0.0486	0.0246	0.0906	0.3703	0.0736	0.0485
Turkey	6514	4	0.4091	0.0938	0.0246	0.0141	0.316	0.0498	0.0698	0.0229
Turkey	6516	2	0.3466	0.1908	0.0483	0.0129	0.0244	0.2886	0.0674	0.0211
Turkey	6519	2	0.3946	0.0957	0.0172	0.0326	0.0557	0.3361	0.0216	0.0464
Turkey	6520	3	0.4668	0.1244	0.0515	0.0792	0.1229	0.0814	0.0576	0.0161
Turkey	6521	2	0.7308	0.105	0.0422	0.02	0.019	0.0549	0.019	0.0091
Turkey	6729	0	0.4579	0.0228	0.0212	0.0354	0.3831	0.0485	0.0119	0.0192
Turkey	6730	1	0.7362	0.0366	0.0376	0.0105	0.0759	0.0175	0.0251	0.0606
Turkey	6731	2	0.6791	0.0206	0.0183	0.0125	0.0566	0.1118	0.0396	0.0614
Turkey	6732	1	0.6	0.0921	0.0549	0.0515	0.0191	0.1021	0.0248	0.0556
Turkey	6733	1	0.5933	0.0173	0.0308	0.0119	0.0382	0.262	0.0391	0.0074
Turkey	6734	1	0.1613	0.0897	0.0354	0.0074	0.1713	0.4542	0.0357	0.045
Turkey	6735	1	0.2061	0.058	0.0414	0.0124	0.0153	0.6383	0.0141	0.0144
Turkey	6736	2	0.7785	0.0174	0.022	0.0098	0.1306	0.0143	0.0091	0.0183
Turkey	6738	2	0.6074	0.0168	0.021	0.0468	0.0848	0.0218	0.1739	0.0275
Turkey	6739	0	0.6749	0.0327	0.0206	0.0164	0.1628	0.0481	0.0092	0.0353
Turkey	6740	5	0.5768	0.025	0.0172	0.0248	0.0369	0.0204	0.2859	0.013
Turkey	6741	7	0.1037	0.4046	0.4554	0.0117	0.0072	0.0101	0.003	0.0043
Turkey	6742	12	0.0268	0.1655	0.5709	0.0336	0.1129	0.04	0.0145	0.0359
Turkey	6743	11	0.0125	0.7056	0.2448	0.009	0.0066	0.0131	0.0041	0.0043
Turkey	6745	12	0.0191	0.036	0.023	0.0271	0.1568	0.2601	0.4483	0.0297
Turkey	6746	14	0.0255	0.3924	0.5028	0.0046	0.0463	0.0074	0.0033	0.0176

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Turkey	6748	7	0.0347	0.637	0.2716	0.0067	0.0156	0.0175	0.0082	0.0086
Turkey	6749	8	0.5575	0.2392	0.0994	0.0114	0.0476	0.027	0.0099	0.008
Turkey	6750	15	0.1611	0.4095	0.3553	0.0091	0.0127	0.0304	0.0048	0.0171
Turkey	6753	12	0.0288	0.405	0.4555	0.0392	0.0101	0.0286	0.0041	0.0287
Turkey	6754	15	0.0058	0.0079	0.0078	0.0338	0.5464	0.0173	0.3679	0.0131
Turkey	6755	11	0.1046	0.4561	0.2677	0.0321	0.0123	0.0745	0.0308	0.0219
Turkey	6756	12	0.0218	0.6947	0.193	0.0139	0.0191	0.0177	0.0153	0.0245
Turkey	6758	12	0.4593	0.3022	0.1461	0.0142	0.009	0.043	0.0089	0.0172
Turkey	6759	15	0.0881	0.6066	0.154	0.0211	0.0945	0.0106	0.004	0.0211
Turkey	6760	6	0.0683	0.3367	0.3902	0.0476	0.0468	0.0593	0.0115	0.0396
Cyprus	10128	1	0.0529	0.6925	0.2097	0.011	0.0054	0.017	0.0047	0.0068
Cyprus	10129	14	0.0154	0.7548	0.1735	0.0081	0.0113	0.0143	0.0067	0.016
Cyprus	10130	10	0.0153	0.1691	0.5096	0.012	0.1362	0.0238	0.1032	0.0309
Cyprus	10131	15	0.0505	0.7148	0.0468	0.1358	0.0149	0.0193	0.004	0.0139
Cyprus	10132	14	0.6346	0.1209	0.1012	0.0248	0.0249	0.061	0.0129	0.0195
Cyprus	10133	9	0.008	0.0136	0.0101	0.0093	0.0109	0.0109	0.9332	0.004
Cyprus	10134	12	0.9429	0.0101	0.0127	0.0065	0.0077	0.0083	0.0057	0.0061
Cyprus	10135	7	0.2713	0.4963	0.069	0.0471	0.0326	0.0256	0.0073	0.0508
Cyprus	10136	15	0.1118	0.3276	0.4577	0.0424	0.015	0.0291	0.0044	0.0119
Cyprus	10137	12	0.4979	0.375	0.0541	0.0105	0.0115	0.0244	0.0055	0.0211
Cyprus	10138	1	0.0484	0.0878	0.0213	0.5443	0.0482	0.1812	0.011	0.0578
Cyprus	10139	1	0.0171	0.5866	0.3635	0.0056	0.0112	0.0087	0.0032	0.0041
Cyprus	10140	2	0.1454	0.6382	0.1156	0.0224	0.0343	0.0245	0.0077	0.0119
Cyprus	10141	0	0.011	0.3811	0.4365	0.0197	0.0261	0.0685	0.0329	0.0243
Cyprus	10142	3	0.0155	0.69	0.21	0.014	0.0278	0.0197	0.0083	0.0147
Cyprus	10143	0	0.0095	0.6003	0.2972	0.0532	0.0097	0.0131	0.0102	0.0069
Cyprus	10144	2	0.011	0.5562	0.4086	0.0064	0.0047	0.0066	0.0027	0.0038
Cyprus	10145	1	0.1119	0.6666	0.1659	0.012	0.019	0.0147	0.0039	0.006
Cyprus	10146	2	0.0626	0.714	0.2033	0.0031	0.0062	0.0061	0.0018	0.0029
Cyprus	10147	2	0.2089	0.411	0.1097	0.0156	0.0224	0.2223	0.0046	0.0055
Cyprus	10148	0	0.9578	0.0103	0.0061	0.0056	0.0073	0.0055	0.003	0.0044
Cyprus	10149	0	0.0991	0.0105	0.0218	0.0139	0.0333	0.0126	0.7939	0.0149
Cyprus	10150	2	0.0999	0.7136	0.0788	0.0547	0.0123	0.0206	0.0083	0.0119
Cyprus	10151	1	0.1075	0.3023	0.5569	0.0056	0.0078	0.0101	0.0058	0.0041
Cyprus	10152	0	0.0256	0.4862	0.407	0.0229	0.0314	0.0089	0.0034	0.0147
Cyprus	10153	1	0.0887	0.1397	0.0314	0.0372	0.0548	0.4654	0.0749	0.1077
Cyprus	10154	1	0.0771	0.1913	0.1746	0.0214	0.3335	0.1737	0.0149	0.0134
Cyprus	10155	0	0.0231	0.1207	0.7555	0.0115	0.0318	0.0397	0.0085	0.0092
Cyprus	10156	3	0.2038	0.6156	0.1279	0.0083	0.0096	0.0162	0.009	0.0097
Cyprus	10157	0	0.2116	0.3524	0.3623	0.0318	0.0071	0.0152	0.0056	0.014
Lebanon	10235	2	0.1141	0.7295	0.0705	0.0221	0.0221	0.0106	0.0072	0.0239
Lebanon	10236	1	0.131	0.3684	0.4463	0.018	0.0122	0.0119	0.003	0.0092
Lebanon	10237	0	0.0692	0.6794	0.2001	0.0059	0.0161	0.0161	0.0044	0.0088
Lebanon	10238	1	0.0431	0.5284	0.3114	0.0057	0.0118	0.0724	0.0113	0.0159
Lebanon	10239	2	0.3051	0.3118	0.2237	0.0234	0.0639	0.0542	0.0051	0.0129
Lebanon	10240	1	0.3692	0.5016	0.0435	0.0372	0.0281	0.0076	0.0033	0.0095
Lebanon	10241	3	0.029	0.1906	0.5794	0.0148	0.0082	0.1375	0.0108	0.0297
Lebanon	10242	0	0.5443	0.1975	0.0467	0.0775	0.0139	0.0505	0.0271	0.0425
Lebanon	10243	2	0.0346	0.2644	0.6365	0.0048	0.0071	0.0436	0.0039	0.0052
Lebanon	10244	1	0.2191	0.2947	0.1575	0.018	0.0127	0.0572	0.0227	0.218
Lebanon	10245	0	0.0041	0.3287	0.4552	0.0401	0.0217	0.0702	0.0564	0.0237
Lebanon	10246	0	0.0761	0.1966	0.5194	0.0081	0.0108	0.0996	0.0665	0.0229
Lebanon	10247	0	0.1617	0.422	0.3287	0.0142	0.0243	0.0291	0.0079	0.0121
Lebanon	10248	2	0.0695	0.3312	0.3294	0.0517	0.129	0.0701	0.0078	0.0113
Lebanon	10249	2	0.2897	0.351	0.136	0.1631	0.0205	0.0223	0.0041	0.0133
Lebanon	10250	1	0.0175	0.6093	0.3216	0.0079	0.0056	0.0276	0.0046	0.0059

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling	ID	Missing	Population							
Location	No.	Data	1	2	3	4	5	6	7	8
Lebanon	10251	2	0.0074	0.4529	0.4552	0.0124	0.0128	0.022	0.0275	0.0098
Lebanon	10252	3	0.0315	0.531	0.3055	0.0125	0.0184	0.0215	0.022	0.0576
Lebanon	10253	0	0.0272	0.4327	0.4627	0.0071	0.0093	0.022	0.0125	0.0265
Lebanon	10254	0	0.013	0.4075	0.5161	0.0055	0.0076	0.0395	0.0041	0.0067
Lebanon	10255	1	0.0163	0.7811	0.1209	0.0242	0.0105	0.0153	0.0235	0.0082
Lebanon	10256	0	0.0067	0.6663	0.2554	0.007	0.008	0.0226	0.0066	0.0274
Lebanon	10257	2	0.0156	0.3061	0.2404	0.0953	0.1756	0.1349	0.0158	0.0162
Lebanon	10258	1	0.0441	0.2025	0.5791	0.0117	0.0319	0.1051	0.0089	0.0167
Lebanon	10259	0	0.0136	0.1684	0.5525	0.1331	0.0783	0.0418	0.0031	0.0092
Lebanon	10260	1	0.0325	0.7087	0.1834	0.0113	0.0249	0.0138	0.005	0.0204
Lebanon	10261	0	0.0256	0.4343	0.4421	0.0176	0.0225	0.0318	0.0139	0.0121
Lebanon	10262	2	0.0174	0.1123	0.6791	0.0286	0.0205	0.1162	0.0173	0.0086
Lebanon	10263	0	0.0822	0.5951	0.2266	0.0146	0.0099	0.0179	0.0154	0.0383
Lebanon	10264	2	0.0098	0.1393	0.6933	0.0094	0.0194	0.1066	0.0096	0.0126
Lebanon	10265	2	0.2518	0.5535	0.1258	0.0343	0.0118	0.0121	0.0031	0.0075
Lebanon	10266	1	0.0121	0.6189	0.2274	0.0184	0.0179	0.0114	0.0036	0.0903
Lebanon	10267	2	0.0145	0.0925	0.7665	0.01	0.008	0.0768	0.02	0.0117
Lebanon	10268	2	0.0086	0.7006	0.2164	0.007	0.0246	0.0201	0.0127	0.01
Lebanon	10270	5	0.0078	0.2784	0.5489	0.0671	0.0104	0.0696	0.0105	0.0073
Lebanon	10271	2	0.0592	0.1565	0.4237	0.2265	0.0317	0.0822	0.0117	0.0085
Lebanon	10273	21	0.0179	0.2355	0.3902	0.0298	0.0393	0.2248	0.0227	0.0397
Lebanon	10274	25	0.0083	0.1596	0.3479	0.011	0.1331	0.2895	0.0055	0.0451
Lebanon	10276	19	0.0122	0.4411	0.2162	0.0271	0.0447	0.0813	0.0266	0.1508
Lebanon	10277	2	0.2434	0.1635	0.3474	0.0265	0.0294	0.1519	0.016	0.0219
Lebanon	10278	16	0.0202	0.5363	0.2975	0.0299	0.0435	0.057	0.0053	0.0102
Lebanon	10279	20	0.0225	0.4778	0.3676	0.0301	0.0219	0.0557	0.0103	0.0141
Lebanon	10280	5	0.0196	0.3098	0.3519	0.1155	0.0146	0.0971	0.0159	0.0755
Lebanon	10281	0	0.0866	0.43	0.3027	0.0157	0.0121	0.0371	0.0903	0.0254
Lebanon	10282	1	0.0189	0.6503	0.1991	0.0636	0.0129	0.0302	0.01	0.0149
Lebanon	10283	18	0.0201	0.2162	0.4903	0.0206	0.0243	0.1927	0.0096	0.0263
Lebanon	10284	6	0.0176	0.6474	0.1881	0.0504	0.0498	0.0254	0.0124	0.0089
Lebanon	10285	18	0.1226	0.3423	0.3331	0.0904	0.009	0.0365	0.0479	0.0183
Lebanon	10286	26	0.0077	0.2736	0.5223	0.0707	0.0479	0.0337	0.019	0.0251
Lebanon	10287	22	0.0129	0.2714	0.2604	0.02	0.334	0.0452	0.0188	0.0372
Lebanon	10288	18	0.2136	0.5667	0.1054	0.0121	0.0206	0.0586	0.0122	0.0108
Lebanon	10289	27	0.0223	0.6432	0.267	0.0126	0.0128	0.0268	0.0061	0.0093
Lebanon	10290	4	0.0102	0.6603	0.1905	0.0261	0.0335	0.0558	0.0079	0.0156
Lebanon	10291	14	0.1626	0.2685	0.1163	0.2976	0.0265	0.0856	0.027	0.0158
Lebanon	10292	4	0.0066	0.0454	0.0192	0.1971	0.65	0.0187	0.0473	0.0157
Lebanon	10294	13	0.0168	0.5621	0.2948	0.0095	0.0255	0.0324	0.0068	0.0521
Lebanon	10295	7	0.0554	0.2153	0.4258	0.1033	0.0102	0.096	0.0685	0.0255
Lebanon	10297	10	0.0786	0.3293	0.1791	0.156	0.1776	0.0507	0.0119	0.0168
Lebanon	10298	3	0.3815	0.0979	0.3208	0.0101	0.0094	0.0492	0.1168	0.0143
Lebanon	10299	19	0.0086	0.2198	0.4538	0.0589	0.0289	0.0341	0.0202	0.1758
Lebanon	10300	0	0.0235	0.0561	0.3501	0.0066	0.012	0.021	0.4725	0.0582
Israel	4962	17	0.1057	0.4387	0.3541	0.0149	0.0081	0.0578	0.0113	0.0094
Israel	4963	14	0.0091	0.4248	0.4223	0.014	0.0071	0.0206	0.0623	0.0398
Israel	4964	22	0.0062	0.6755	0.2503	0.0322	0.009	0.0094	0.0061	0.0113
Israel	4966	2	0.0324	0.2986	0.4524	0.0784	0.0601	0.051	0.0117	0.0153
Israel	4967	3	0.0829	0.5028	0.2313	0.0468	0.0219	0.0598	0.0133	0.0413
Israel	4968	10	0.0151	0.0844	0.7741	0.0154	0.0114	0.0789	0.0096	0.0111
Israel	4969	5	0.0059	0.2667	0.5593	0.0108	0.0091	0.0928	0.0261	0.0293
Israel	4970	12	0.8446	0.0281	0.0221	0.0303	0.0512	0.009	0.0076	0.0071
Israel	4971	17	0.0191	0.1511	0.6555	0.0163	0.0361	0.0249	0.0421	0.0549
Israel	4972	10	0.1452	0.183	0.2077	0.015	0.0226	0.0246	0.3872	0.0148
Israel	4973	1	0.0109	0.1992	0.4756	0.0889	0.0718	0.0411	0.0899	0.0226

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Israel	4974	4	0.0353	0.3558	0.3084	0.0231	0.0086	0.0229	0.045	0.2008
Israel	4975	3	0.0846	0.1692	0.6612	0.0056	0.0122	0.0406	0.0077	0.019
Israel	4976	4	0.0101	0.6943	0.2099	0.0369	0.0266	0.0095	0.0043	0.0085
Israel	4977	4	0.1199	0.4947	0.1893	0.0186	0.0077	0.0857	0.0299	0.0542
Israel	4978	3	0.0138	0.1679	0.6089	0.1524	0.0127	0.0187	0.0057	0.0198
Israel	4979	2	0.0249	0.6712	0.1467	0.0868	0.0192	0.0267	0.0078	0.0167
Israel	4980	2	0.0254	0.1236	0.6685	0.0217	0.0292	0.0681	0.0209	0.0426
Israel	4981	7	0.0324	0.6631	0.2448	0.0095	0.0177	0.0128	0.0064	0.0133
Israel	4982	2	0.0311	0.1899	0.5462	0.0155	0.0111	0.0664	0.066	0.0738
Israel	4983	16	0.0086	0.0816	0.7355	0.02	0.063	0.0747	0.0054	0.0113
Israel	4984	14	0.0372	0.0939	0.6094	0.1373	0.0102	0.0654	0.0164	0.0303
Israel	4985	1	0.0111	0.0972	0.7576	0.0152	0.0359	0.0681	0.0118	0.0031
Israel	4986	3	0.1134	0.2036	0.1339	0.0376	0.0307	0.2596	0.086	0.1351
Israel	4988	1	0.2149	0.0893	0.5612	0.0422	0.0088	0.0399	0.0102	0.0336
Israel	4989	25	0.2301	0.2447	0.1459	0.0268	0.0329	0.1	0.0166	0.2031
Israel	4990	2	0.0083	0.6561	0.2341	0.0357	0.0149	0.021	0.0095	0.0204
Israel	4992	3	0.0203	0.422	0.3707	0.039	0.0174	0.0941	0.0133	0.0232
Israel	4993	8	0.0377	0.3123	0.3383	0.038	0.1205	0.1062	0.0146	0.0323
Israel	4994	6	0.0371	0.4967	0.1587	0.0202	0.14	0.1128	0.0268	0.0076
Israel	4995	9	0.0151	0.4571	0.364	0.0107	0.0117	0.0213	0.0821	0.038
Israel	4996	6	0.0611	0.1476	0.4386	0.0629	0.013	0.1088	0.092	0.076
Israel	4997	5	0.0482	0.1031	0.4904	0.1692	0.0275	0.1271	0.0174	0.0171
Israel	4998	7	0.0124	0.0487	0.7184	0.0374	0.0448	0.1138	0.0077	0.0169
Israel	5000	20	0.0857	0.1338	0.5661	0.0637	0.0303	0.0858	0.0204	0.0142
Israel	5001	25	0.0256	0.4044	0.3805	0.0392	0.0425	0.0704	0.0173	0.0202
Israel	5002	0	0.1693	0.1751	0.2846	0.0633	0.2199	0.0534	0.0054	0.029
Israel	5003	0	0.0578	0.2144	0.3998	0.011	0.0883	0.2096	0.005	0.0141
Israel	5004	0	0.0088	0.2362	0.4943	0.1704	0.0097	0.0501	0.0172	0.0132
Israel	5005	2	0.0187	0.1387	0.7404	0.0098	0.0382	0.0349	0.0084	0.0109
Israel	5006	1	0.1279	0.4641	0.1387	0.0929	0.1334	0.0243	0.0116	0.0072
Israel	5007	2	0.0073	0.0527	0.7963	0.0172	0.0085	0.086	0.012	0.02
Israel	5008	1	0.6522	0.0283	0.0259	0.019	0.0133	0.0824	0.102	0.0769
Israel	5009	0	0.0301	0.3734	0.505	0.0155	0.0111	0.0265	0.0166	0.0218
Israel	5010	0	0.0104	0.3837	0.5676	0.0137	0.0068	0.0068	0.005	0.006
Israel	5011	0	0.0442	0.2644	0.4944	0.0695	0.0179	0.0141	0.0126	0.083
Egypt-Cairo	8190	2	0.0229	0.3802	0.3973	0.018	0.1106	0.0319	0.0131	0.026
Egypt-Cairo	8192	1	0.0234	0.2141	0.5805	0.0239	0.0155	0.1101	0.0097	0.0228
Egypt-Cairo	8193	0	0.0402	0.5017	0.3644	0.0209	0.0121	0.035	0.012	0.0137
Egypt-Cairo	8196	0	0.0628	0.1656	0.4636	0.1446	0.0721	0.0291	0.0314	0.0307
Egypt-Cairo	8203	0	0.2673	0.175	0.2104	0.169	0.0268	0.132	0.0099	0.0095
Egypt-Cairo	8215	1	0.0156	0.3212	0.3801	0.0625	0.1323	0.0383	0.0126	0.0373
Egypt-Cairo	8198	1	0.0215	0.3737	0.2784	0.1419	0.1073	0.026	0.017	0.0341
Egypt-Cairo	8194	1	0.1308	0.3771	0.3105	0.015	0.1322	0.0195	0.0063	0.0086
Egypt-Cairo	8211	2	0.0612	0.0647	0.1698	0.0381	0.0099	0.0956	0.0255	0.5353
Egypt-Cairo	8216	3	0.0196	0.058	0.5911	0.0189	0.0144	0.2778	0.0117	0.0085
Egypt-Cairo	8195	0	0.0451	0.3903	0.2232	0.0341	0.116	0.0949	0.06	0.0363
Egypt-Cairo	8199	2	0.083	0.5569	0.1061	0.0628	0.1049	0.0495	0.0243	0.0126
Egypt-Cairo	8200	16	0.0533	0.1033	0.7252	0.0127	0.0073	0.0533	0.0084	0.0364
Egypt-Cairo	8201	1	0.0246	0.3423	0.352	0.0326	0.0172	0.1288	0.0899	0.0126
Egypt-Cairo	8202	0	0.0434	0.1732	0.5444	0.0133	0.0163	0.1345	0.0449	0.03
Egypt-Cairo	8204	4	0.0525	0.2221	0.4149	0.0127	0.0049	0.0999	0.0801	0.1129
Egypt-Cairo	8208	2	0.0207	0.0595	0.321	0.0153	0.015	0.139	0.1903	0.2391
Egypt-Cairo	8210	6	0.0249	0.4847	0.185	0.1692	0.0968	0.0153	0.0043	0.0199
Egypt-Cairo	8214	10	0.0194	0.3837	0.4908	0.0224	0.0316	0.0164	0.0181	0.0176
Egypt-Cairo	8191	2	0.0068	0.6047	0.3252	0.0076	0.0098	0.0347	0.0052	0.006
Egypt-Cairo	8197	1	0.0602	0.1212	0.4084	0.0076	0.0053	0.0931	0.113	0.1912

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling	ID	Missing	Population							
Location	No.	Data	1	2	3	4	5	6	7	8
Egypt-Cairo	8205	0	0.0127	0.2425	0.5066	0.0131	0.0063	0.0902	0.007	0.1216
Egypt-Cairo	8206	0	0.0198	0.1813	0.4052	0.0195	0.0065	0.1075	0.1409	0.1194
Egypt-Cairo	8207	0	0.1309	0.2393	0.2543	0.2481	0.0459	0.0593	0.0089	0.0132
Egypt-Cairo	8209	1	0.0111	0.5614	0.3539	0.0156	0.0103	0.03	0.0065	0.0112
Egypt-Cairo	8212	1	0.2888	0.1058	0.4111	0.0079	0.0376	0.0954	0.02	0.0334
Egypt-Cairo	8213	0	0.0286	0.4116	0.3308	0.0053	0.0328	0.1381	0.0377	0.0151
Egypt-Cairo	9942	1	0.2027	0.1753	0.0885	0.1089	0.0375	0.1801	0.1496	0.0574
Egypt-Cairo	9943	0	0.0094	0.078	0.567	0.1313	0.0198	0.0831	0.0815	0.03
Egypt-Cairo	9944	0	0.0965	0.5944	0.225	0.0099	0.0247	0.0307	0.0045	0.0143
Egypt-Cairo	9945	1	0.0506	0.0897	0.655	0.0677	0.0131	0.0945	0.0199	0.0094
Egypt-Cairo	9946	1	0.0132	0.3816	0.3723	0.0148	0.0542	0.0428	0.0532	0.0678
Egypt-Cairo	9947	0	0.1948	0.2128	0.3182	0.0204	0.1216	0.0341	0.063	0.0351
Egypt-Cairo	9948	0	0.0145	0.3067	0.2668	0.0735	0.0161	0.0392	0.2709	0.0124
Egypt-Cairo	9949	1	0.0135	0.7171	0.2183	0.0157	0.0112	0.016	0.0035	0.0047
Egypt-Cairo	9950	0	0.0068	0.2971	0.5737	0.013	0.008	0.064	0.0095	0.0279
Egypt-Cairo	9951	0	0.0175	0.0427	0.7607	0.0215	0.006	0.1108	0.0208	0.02
Egypt-Cairo	9952	2	0.066	0.611	0.2515	0.0089	0.0253	0.0236	0.0067	0.007
Egypt-Cairo	9953	0	0.2966	0.0623	0.485	0.0529	0.0145	0.0446	0.0209	0.0233
Egypt-Cairo	9954	1	0.0129	0.3399	0.4646	0.0399	0.0519	0.0433	0.0196	0.028
Egypt-Cairo	9955	1	0.0111	0.6656	0.28	0.0086	0.0068	0.0179	0.0048	0.0052
Egypt-Cairo	9956	1	0.0357	0.4529	0.1909	0.03	0.0188	0.2412	0.0107	0.0198
Egypt-Cairo	9957	2	0.0117	0.1107	0.7133	0.0175	0.0103	0.1064	0.0205	0.0096
Egypt-Cairo	9958	0	0.0325	0.0562	0.7217	0.0261	0.0109	0.1188	0.0214	0.0124
Egypt-Cairo	9959	10	0.0144	0.157	0.7767	0.0081	0.0081	0.0258	0.0034	0.0065
Egypt-Cairo	9960	1	0.0165	0.0877	0.7731	0.0106	0.0113	0.0271	0.0687	0.0049
Egypt-Cairo	9961	1	0.0943	0.0716	0.7391	0.0127	0.0355	0.0323	0.0051	0.0095
Egypt-Cairo	9962	9	0.0259	0.465	0.3561	0.0105	0.0193	0.0979	0.0056	0.0197
Egypt-Cairo	9963	16	0.0193	0.0765	0.8057	0.0117	0.0081	0.0601	0.0094	0.0091
Egypt-Cairo	9964	0	0.1236	0.1321	0.5508	0.0213	0.0188	0.0839	0.0618	0.0077
Egypt-Cairo	10021	2	0.0135	0.1514	0.0451	0.0527	0.0406	0.1013	0.57	0.0253
Egypt-Cairo	10022	2	0.0122	0.1959	0.6576	0.005	0.0091	0.1049	0.0041	0.0112
Egypt-Cairo	10023	0	0.005	0.0735	0.778	0.0616	0.0101	0.0563	0.01	0.0054
Egypt-Cairo	10024	3	0.0169	0.4188	0.3592	0.0376	0.0317	0.0431	0.0067	0.0859
Egypt-Cairo	10025	2	0.0198	0.5359	0.1328	0.035	0.0093	0.1445	0.1099	0.0128
Egypt-Cairo	10026	1	0.009	0.6837	0.2687	0.0071	0.0049	0.0138	0.0061	0.0067
Egypt-Cairo	10027	0	0.0147	0.2904	0.6285	0.0065	0.0196	0.0159	0.0194	0.0051
Egypt-Cairo	10028	0	0.0051	0.232	0.5443	0.1234	0.0096	0.0457	0.0042	0.0357
Egypt-Cairo	10029	1	0.0041	0.3348	0.5404	0.0218	0.0103	0.0487	0.0144	0.0256
Egypt-Cairo	10030	2	0.0092	0.0484	0.7438	0.0126	0.0088	0.1259	0.0372	0.0141
Egypt-Cairo	10031	1	0.0057	0.3257	0.5443	0.037	0.0064	0.0623	0.0064	0.0122
Egypt-Cairo	10032	0	0.0187	0.4441	0.3494	0.0245	0.0217	0.0899	0.045	0.0068
Egypt-Cairo	10033	0	0.0185	0.4404	0.3175	0.0151	0.0204	0.16	0.0194	0.0088
Egypt-Cairo	10034	3	0.0137	0.0783	0.8012	0.013	0.0476	0.0211	0.0067	0.0184
Egypt-Cairo	10035	0	0.1083	0.0724	0.4031	0.0059	0.008	0.0392	0.3585	0.0047
Egypt-Cairo	10037	4	0.5388	0.026	0.0306	0.1271	0.0983	0.1358	0.0206	0.0228
Egypt-Cairo	10042	0	0.0041	0.0523	0.7491	0.0206	0.0284	0.1233	0.0133	0.0089
Egypt-Cairo	10043	0	0.0141	0.268	0.65	0.008	0.0083	0.0268	0.0099	0.0148
Egypt-Cairo	10044	2	0.0069	0.2254	0.5655	0.0438	0.1039	0.0325	0.0138	0.0082
Egypt-Cairo	10045	0	0.0585	0.5482	0.3471	0.0091	0.005	0.0189	0.0084	0.0049
Egypt-Cairo	10046	0	0.0134	0.1061	0.591	0.009	0.0083	0.1383	0.1093	0.0246
Egypt-Cairo	10047	1	0.0273	0.0925	0.8261	0.0058	0.0048	0.0342	0.0033	0.0061
Egypt-Cairo	10048	2	0.01	0.1433	0.6051	0.0463	0.0112	0.1426	0.0303	0.0112
Egypt-Cairo	10083	1	0.0043	0.2661	0.478	0.1238	0.0798	0.0342	0.0049	0.0089
Egypt-Cairo	10040	4	0.6381	0.0808	0.0771	0.0312	0.0114	0.0909	0.0394	0.031
Egypt-Cairo	10041	0	0.0085	0.0254	0.4525	0.0067	0.0123	0.045	0.4357	0.014
Egypt-Cairo	10049	3	0.1062	0.4291	0.2275	0.0175	0.0533	0.1448	0.0119	0.0097

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling	ID	Missing	Population							
Location	No.	Data	1	2	3	4	5	6	7	8
Egypt-Cairo	10084	5	0.0095	0.0359	0.6399	0.0065	0.0182	0.0409	0.1638	0.0853
Egypt-Cairo	10085	1	0.1073	0.3931	0.2318	0.1681	0.024	0.0328	0.0105	0.0324
Egypt-Cairo	10087	1	0.0108	0.1416	0.6616	0.0217	0.0101	0.0382	0.1055	0.0105
Egypt-Cairo	10090	2	0.0123	0.0163	0.0292	0.0152	0.0378	0.8679	0.0111	0.0102
Egypt-Cairo	9968	1	0.0063	0.0512	0.8014	0.018	0.0099	0.0823	0.0203	0.0106
Egypt-Asuit	10091	5	0.0129	0.1401	0.2491	0.0189	0.0152	0.0851	0.388	0.0908
Egypt-Asuit	10093	2	0.0676	0.021	0.8179	0.0051	0.0199	0.0263	0.0338	0.0085
Egypt-Asuit	10094	4	0.015	0.0678	0.8376	0.0111	0.0079	0.0307	0.0109	0.0191
Egypt-Asuit	10095	2	0.0176	0.491	0.2695	0.0278	0.0364	0.0882	0.0542	0.0152
Egypt-Asuit	10096	8	0.0125	0.0991	0.8423	0.0092	0.012	0.0125	0.0078	0.0045
Egypt-Asuit	10098	1	0.0062	0.0283	0.9124	0.0137	0.0096	0.0158	0.0062	0.0078
Egypt-Asuit	10099	0	0.0057	0.5676	0.3607	0.0357	0.0065	0.0125	0.0063	0.005
Egypt-Asuit	10100	2	0.0065	0.0379	0.9349	0.0037	0.0032	0.0082	0.0024	0.0032
Egypt-Asuit	10101	2	0.011	0.4772	0.3538	0.0563	0.0174	0.0473	0.0131	0.024
Egypt-Asuit	10102	21	0.0412	0.0342	0.8202	0.0075	0.0062	0.0494	0.0104	0.0309
Egypt-Luxor	10038	1	0.0095	0.1167	0.8346	0.0083	0.0055	0.0114	0.0069	0.0071
Egypt-Luxor	10039	1	0.0339	0.5228	0.4006	0.01	0.0098	0.0112	0.0041	0.0076
Egypt-Luxor	10050	4	0.0158	0.3732	0.5702	0.011	0.0076	0.0102	0.0057	0.0063
Egypt-Luxor	10051	1	0.0052	0.0362	0.9234	0.0064	0.0043	0.0137	0.0048	0.006
Egypt-Luxor	10052	3	0.0067	0.0409	0.9124	0.0063	0.0075	0.0106	0.0054	0.0102
Egypt-Luxor	10053	0	0.0124	0.3867	0.5491	0.0155	0.0093	0.0133	0.0065	0.0072
Egypt-Luxor	10054	1	0.0059	0.568	0.358	0.0358	0.0066	0.0136	0.007	0.0051
Egypt-Luxor	10055	1	0.0269	0.451	0.4258	0.01	0.0132	0.0582	0.0057	0.0092
Egypt-Luxor	10056	4	0.0147	0.3087	0.4245	0.0779	0.012	0.1329	0.0075	0.0218
Egypt-Luxor	10057	5	0.2909	0.0629	0.5261	0.0169	0.0193	0.061	0.0059	0.017
Egypt-Luxor	10058	1	0.0606	0.0554	0.7784	0.0078	0.0368	0.0273	0.0109	0.0228
Egypt-Luxor	10060	1	0.0241	0.13	0.7326	0.0325	0.0454	0.021	0.0072	0.0072
Egypt-Luxor	10061	4	0.016	0.2821	0.5926	0.0196	0.0094	0.0149	0.0101	0.0553
Egypt-Luxor	10062	1	0.0528	0.5586	0.3523	0.0058	0.0063	0.0149	0.0037	0.0055
Egypt-Luxor	10063	0	0.0102	0.3006	0.6085	0.0177	0.0096	0.0312	0.0099	0.0123
Egypt-Luxor	10064	0	0.0064	0.0237	0.9192	0.013	0.0083	0.0162	0.0068	0.0064
Egypt-Luxor	10065	1	0.0072	0.4304	0.3769	0.0263	0.0203	0.0625	0.0287	0.0477
Egypt-Luxor	10066	25	0.0228	0.1488	0.7166	0.0218	0.0294	0.0103	0.0055	0.0449
Egypt-Luxor	10067	3	0.0104	0.0919	0.7963	0.02	0.0112	0.0471	0.0078	0.0154
Egypt-Luxor	10068	1	0.0053	0.3155	0.4241	0.0822	0.0534	0.0914	0.0058	0.0223
Egypt-Luxor	10069	10	0.0136	0.394	0.2434	0.0086	0.0143	0.3002	0.0133	0.0126
Egypt-Luxor	10070	8	0.0386	0.0718	0.8112	0.0063	0.0337	0.0091	0.0164	0.0129
Egypt-Luxor	10071	18	0.0218	0.2886	0.6104	0.0046	0.0379	0.0169	0.0153	0.0046
Egypt-Luxor	10072	4	0.057	0.115	0.7388	0.0104	0.0559	0.0116	0.0031	0.0082
Egypt-Luxor	10073	3	0.046	0.0773	0.6397	0.0144	0.1639	0.0411	0.0107	0.007
Egypt-Luxor	10074	0	0.0141	0.0676	0.6902	0.0105	0.0886	0.0962	0.0052	0.0276
Egypt-Luxor	10079	1	0.01	0.0313	0.8109	0.0064	0.0078	0.1212	0.0041	0.0083
Egypt-Luxor	10080	4	0.0202	0.0154	0.9187	0.0041	0.0043	0.0279	0.0035	0.0059
Egypt-Abu Simbel	10076	4	0.0226	0.0287	0.8049	0.0065	0.0137	0.1095	0.0052	0.0089
Egypt-Abu Simbel	10077	16	0.0834	0.0704	0.7314	0.0072	0.0141	0.0732	0.0097	0.0107
Egypt-Abu Simbel	10081	2	0.0147	0.0333	0.7654	0.0052	0.0132	0.1181	0.0074	0.0427
Egypt-Abu Simbel	10089	2	0.0313	0.0115	0.9013	0.0041	0.0061	0.0382	0.0033	0.0041
Egypt-Abu Simbel	10092	0	0.0109	0.0178	0.9023	0.0066	0.0115	0.0394	0.003	0.0085
Iraq-West	9587	2	0.0806	0.076	0.6246	0.0115	0.091	0.0491	0.0236	0.0435
Iraq-West	10202	2	0.0064	0.0166	0.8825	0.0103	0.0111	0.0563	0.0083	0.0084
Iraq-West	10204	2	0.0082	0.0809	0.8137	0.0069	0.0067	0.0688	0.0054	0.0094
Iraq-West	11854	1	0.0081	0.0965	0.6933	0.0072	0.0674	0.0967	0.0215	0.0094
Iraq-West	11860	6	0.0051	0.0147	0.9229	0.0051	0.0043	0.0223	0.0129	0.0127
Iraq-West	11861	2	0.0059	0.0491	0.8123	0.0101	0.0055	0.0885	0.0143	0.0143
Iraq-West	11863	1	0.0063	0.0338	0.8286	0.0084	0.0142	0.0583	0.0079	0.0425
Iraq-West	11864	14	0.0117	0.045	0.8229	0.0047	0.0194	0.0662	0.011	0.0191

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling	ID	Missing	Population							
Location	No.	Data	1	2	3	4	5	6	7	8
Iraq-West	11888	3	0.0058	0.0677	0.5868	0.0691	0.0575	0.0915	0.0301	0.0914
Iraq-West	11889	2	0.0063	0.2702	0.653	0.0228	0.0179	0.0152	0.004	0.0106
Iraq-West	11890	2	0.0044	0.0586	0.8357	0.0095	0.0112	0.028	0.0301	0.0225
Iraq-West	11891	2	0.0343	0.1488	0.6589	0.0119	0.0251	0.0838	0.0228	0.0143
Iraq-Baghdad	11847	13	0.0152	0.216	0.6415	0.0071	0.0071	0.0929	0.0037	0.0165
Iraq-Baghdad	11848	8	0.0152	0.1072	0.7644	0.024	0.0099	0.0587	0.0072	0.0134
Iraq-Baghdad	11849	5	0.0203	0.1896	0.7205	0.0054	0.0185	0.0287	0.0085	0.0085
Iraq-Baghdad	11850	0	0.0202	0.0986	0.8189	0.0056	0.0128	0.0116	0.0198	0.0125
Iraq-Baghdad	11852	3	0.0117	0.0731	0.803	0.0288	0.0166	0.0554	0.0051	0.0063
Iraq-Baghdad	11853	0	0.199	0.2937	0.1206	0.026	0.0482	0.2737	0.0104	0.0283
Iraq-Baghdad	11855	1	0.082	0.2489	0.5995	0.0068	0.0125	0.038	0.0061	0.0062
Iraq-Baghdad	11856	0	0.0126	0.0754	0.6803	0.0336	0.0318	0.134	0.0121	0.0202
Iraq-Baghdad	11857	4	0.0202	0.2615	0.5334	0.0073	0.0176	0.1268	0.0181	0.0151
Iraq-Baghdad	11858	4	0.0096	0.0304	0.8845	0.0187	0.0192	0.0205	0.0045	0.0126
Iraq-Baghdad	11859	9	0.0446	0.0971	0.7963	0.0086	0.0129	0.0235	0.0071	0.0099
Iraq-Baghdad	11862	3	0.0129	0.1648	0.5964	0.0929	0.053	0.0618	0.0031	0.0151
Iraq-Baghdad	11865	2	0.0211	0.0974	0.8228	0.0055	0.0122	0.0105	0.0189	0.0116
Iraq-Baghdad	11868	4	0.009	0.081	0.8525	0.0166	0.0127	0.0184	0.0048	0.0051
Iraq-Baghdad	11869	2	0.0199	0.2129	0.6427	0.0188	0.0295	0.0543	0.0075	0.0144
Iraq-Baghdad	11870	0	0.9272	0.0089	0.0112	0.0127	0.0128	0.0128	0.0025	0.0119
Iraq-Baghdad	11871	0	0.01	0.0489	0.8995	0.0107	0.005	0.0187	0.0039	0.0033
Iraq-Baghdad	11872	6	0.0302	0.3878	0.5101	0.0081	0.0112	0.0372	0.0066	0.0088
Iraq-Baghdad	11873	6	0.0059	0.124	0.7839	0.0056	0.0387	0.0225	0.0103	0.0091
Iraq-Baghdad	11874	11	0.0248	0.0922	0.7799	0.0168	0.0186	0.0324	0.0102	0.0251
Iraq-Baghdad	11875	18	0.0083	0.0441	0.8968	0.01	0.0079	0.0188	0.0037	0.0104
Iraq-Baghdad	11876	19	0.0152	0.4873	0.3901	0.0252	0.045	0.0205	0.01	0.0067
Iraq-Baghdad	11877	2	0.0156	0.3172	0.6022	0.0081	0.0261	0.0108	0.0093	0.0107
Iraq-Baghdad	11878	2	0.0182	0.0563	0.8797	0.0061	0.0202	0.0089	0.0032	0.0074
Iraq-Baghdad	11879	12	0.0828	0.2126	0.122	0.4716	0.0587	0.0331	0.0049	0.0143
Iraq-Baghdad	11880	2	0.0275	0.4851	0.0963	0.3449	0.0129	0.0176	0.0063	0.0094
Iraq-Baghdad	11881	13	0.0309	0.4225	0.073	0.435	0.0096	0.0137	0.0046	0.0107
Iraq-Baghdad	11882	23	0.0226	0.1957	0.0664	0.3916	0.1907	0.0843	0.0275	0.0212
Iraq-Baghdad	11883	8	0.0227	0.2335	0.0854	0.5987	0.0055	0.0132	0.0072	0.0339
Iraq-Baghdad	11884	2	0.0106	0.0849	0.0228	0.5902	0.119	0.1462	0.0144	0.0119
Iraq-Baghdad	11885	2	0.0346	0.2034	0.0962	0.6267	0.0175	0.0112	0.0049	0.0056
Iraq-Baghdad	11886	1	0.0367	0.3376	0.0432	0.5355	0.0084	0.0246	0.0076	0.0064
Iraq-Baghdad	11887	2	0.0189	0.1157	0.0338	0.5075	0.0081	0.0447	0.2487	0.0226
Iran	9419	3	0.0118	0.2221	0.0463	0.6745	0.0189	0.0167	0.0034	0.0063
Iran	9420	20	0.0173	0.3386	0.0368	0.5055	0.0381	0.0247	0.0152	0.0238
Iran	9421	18	0.0121	0.2742	0.0283	0.5848	0.0359	0.035	0.0163	0.0134
Iran	9422	0	0.0098	0.2846	0.0268	0.6544	0.0071	0.0061	0.0034	0.0078
Iran	9424	1	0.0183	0.0989	0.0361	0.6938	0.0204	0.1165	0.0089	0.0071
Iran	9425	0	0.0289	0.4359	0.0573	0.4261	0.027	0.0169	0.0021	0.0057
Iran	9426	1	0.0299	0.2645	0.0334	0.572	0.0308	0.0186	0.0344	0.0164
Iran	9427	18	0.0069	0.1064	0.0097	0.8224	0.0231	0.0126	0.0102	0.0086
Iran	9428	9	0.0065	0.4848	0.0573	0.3387	0.021	0.0312	0.0457	0.0147
Iran	9429	22	0.01	0.2284	0.0242	0.673	0.0131	0.0325	0.0093	0.0094
Iran	9430	1	0.0315	0.2226	0.0834	0.6039	0.0343	0.0135	0.0066	0.0042
Iran	9431	2	0.0462	0.3501	0.0301	0.5301	0.0149	0.0159	0.0038	0.0089
Iran	9432	0	0.0056	0.3826	0.049	0.4477	0.0148	0.0268	0.0476	0.0259
Iran	9433	3	0.0282	0.2226	0.0533	0.6615	0.0105	0.0076	0.0056	0.0106
Iran	9434	1	0.0122	0.5052	0.0315	0.4262	0.0089	0.0068	0.004	0.0052
Iran	9435	2	0.015	0.3905	0.0836	0.4113	0.0086	0.0234	0.0253	0.0424
Iran	9436	10	0.0093	0.1247	0.0347	0.6786	0.0129	0.0502	0.061	0.0286
Iran	9437	8	0.0226	0.2728	0.0449	0.6013	0.0141	0.029	0.0059	0.0095
Iran	9438	1	0.082	0.5305	0.1228	0.0737	0.1182	0.0565	0.0093	0.0069

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Iran	9439	2	0.066	0.3368	0.0813	0.3698	0.05	0.0421	0.0042	0.0497
Iran	9440	4	0.0101	0.202	0.0088	0.7326	0.0247	0.011	0.0053	0.0055
Iran	9441	2	0.0153	0.4654	0.0932	0.3348	0.043	0.0231	0.0139	0.0114
Iran	9442	0	0.0157	0.3089	0.0769	0.5043	0.0103	0.014	0.0079	0.062
Iran	9443	1	0.0095	0.3381	0.0434	0.5637	0.0087	0.0238	0.0073	0.0055
Iran	9444	1	0.007	0.1664	0.0319	0.6336	0.0796	0.0469	0.0296	0.005
Iran	9445	2	0.0077	0.474	0.1321	0.3021	0.0109	0.0286	0.0294	0.0152
Iran	9446	2	0.0959	0.3054	0.0517	0.5078	0.0122	0.0154	0.0065	0.005
Iran	9447	0	0.0145	0.1241	0.0154	0.6357	0.0138	0.0262	0.1564	0.0139
Iran	9448	3	0.0419	0.3079	0.0755	0.4535	0.0086	0.0624	0.0104	0.0398
Iran	9449	2	0.0425	0.537	0.0263	0.3502	0.0149	0.0102	0.0034	0.0155
Iran	9450	0	0.0094	0.2644	0.0351	0.6021	0.008	0.0116	0.0544	0.015
Iran	9451	2	0.0455	0.3321	0.1815	0.3716	0.0184	0.0191	0.0075	0.0244
Iran	9452	17	0.0271	0.3026	0.0492	0.5503	0.0107	0.0259	0.0108	0.0234
Iran	9453	0	0.0038	0.3402	0.1015	0.2946	0.0099	0.0701	0.1736	0.0064
Iran	9454	2	0.0112	0.2873	0.038	0.4008	0.0475	0.1819	0.014	0.0193
Iran	9455	16	0.0133	0.1809	0.0621	0.4158	0.0566	0.2518	0.0135	0.006
Iran	9456	22	0.0085	0.1605	0.0176	0.6798	0.0626	0.0489	0.0133	0.0089
Iran	9457	17	0.0212	0.2918	0.0719	0.3444	0.0938	0.116	0.0175	0.0434
Iran	9458	20	0.0081	0.1583	0.048	0.5994	0.1141	0.029	0.0042	0.0389
Iran	9459	18	0.0073	0.1305	0.0341	0.6046	0.1608	0.0264	0.0041	0.0322
Iran	9460	25	0.0046	0.0706	0.0094	0.4993	0.2799	0.1181	0.0077	0.0104
Iran	9461	4	0.0059	0.1872	0.0737	0.6339	0.024	0.0375	0.0151	0.0227
Iran	9462	6	0.0132	0.0195	0.0181	0.7147	0.0383	0.0161	0.0127	0.1674
Iran	9463	3	0.0069	0.0243	0.0162	0.7772	0.0141	0.0512	0.0941	0.0159
Iran	9464	2	0.0079	0.2171	0.0972	0.1407	0.4055	0.0609	0.031	0.0396
Iran	9465	0	0.0121	0.1648	0.0351	0.485	0.0664	0.1019	0.0756	0.0591
Iran	9466	10	0.0164	0.2698	0.157	0.273	0.1512	0.1163	0.0046	0.0117
Iran	9468	0	0.0059	0.1664	0.0221	0.6426	0.1134	0.0238	0.014	0.0118
Iran	9469	1	0.0058	0.0784	0.0186	0.7109	0.007	0.0373	0.1248	0.0172
Iran	9470	1	0.0397	0.1706	0.0461	0.5045	0.023	0.1513	0.0076	0.0572
Iran	9471	0	0.0102	0.2077	0.0195	0.7203	0.0103	0.0221	0.0048	0.0051
Iran	9472	2	0.0058	0.0849	0.0109	0.8451	0.0097	0.0164	0.0122	0.015
Iran	9473	18	0.0068	0.14	0.0127	0.7593	0.0315	0.0286	0.007	0.0141
Iran	9474	1	0.0056	0.0115	0.0107	0.8495	0.0875	0.0189	0.0059	0.0104
Iran	9475	1	0.0038	0.0082	0.0086	0.9267	0.006	0.0065	0.0138	0.0264
Iran	9476	0	0.0037	0.0054	0.0047	0.948	0.0216	0.0058	0.0032	0.0076
Iran	9477	1	0.006	0.0109	0.0061	0.9563	0.0061	0.0073	0.0028	0.0045
Iran	9478	1	0.004	0.0072	0.0043	0.9626	0.0063	0.006	0.0024	0.0072
Iran	9479	2	0.0033	0.019	0.0111	0.9292	0.0109	0.0066	0.0074	0.0125
Iran	9480	0	0.0069	0.0158	0.0086	0.9184	0.0103	0.0195	0.0129	0.0076
Iran	9481	0	0.0044	0.0135	0.0077	0.9079	0.0079	0.012	0.0341	0.0125
Iran	9482	1	0.0043	0.0101	0.0074	0.9378	0.0085	0.0056	0.0067	0.0196
Iran	9483	2	0.0055	0.007	0.0069	0.9349	0.0168	0.0066	0.0136	0.0087
Iran	9484	22	0.007	0.0352	0.0097	0.8954	0.0236	0.0134	0.0052	0.0105
Iran	9485	0	0.0051	0.0096	0.0118	0.9042	0.0398	0.0092	0.004	0.0163
Iran	9486	0	0.0038	0.0059	0.0082	0.8812	0.0084	0.0106	0.0097	0.0722
Iran	9487	0	0.0056	0.0093	0.0075	0.9456	0.0078	0.0127	0.0041	0.0074
Iran	9488	2	0.0031	0.0053	0.004	0.9468	0.0098	0.0135	0.0087	0.0088
Iran	9489	0	0.0063	0.0065	0.0049	0.9617	0.005	0.0051	0.0049	0.0056
Iran	9490	2	0.003	0.0087	0.0062	0.9607	0.0051	0.0056	0.0066	0.0041
Iran	9491	0	0.0028	0.0048	0.0031	0.9666	0.0062	0.0049	0.0057	0.0059
Iran	9492	1	0.0137	0.0342	0.0268	0.8536	0.0123	0.0378	0.0146	0.007
Iran	9493	4	0.0027	0.0048	0.0041	0.9608	0.0092	0.0073	0.0061	0.005
Iran	9494	2	0.0048	0.007	0.0061	0.944	0.013	0.0082	0.0118	0.0051
Iran	9495	0	0.0021	0.0036	0.0031	0.9698	0.007	0.0045	0.003	0.0069

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Iran	9497	2	0.0058	0.0265	0.0102	0.9101	0.0211	0.0127	0.0073	0.0063
Iran	9498	0	0.0058	0.0115	0.0152	0.8991	0.0074	0.0151	0.0125	0.0334
Iran	9499	1	0.0197	0.0259	0.0198	0.8715	0.0261	0.024	0.0048	0.0082
Iran	9500	0	0.0061	0.0063	0.0055	0.9417	0.0149	0.0108	0.0039	0.0108
Iran	9501	0	0.0035	0.0077	0.0051	0.94	0.0138	0.0095	0.007	0.0134
Iran	9502	0	0.0061	0.007	0.0071	0.9027	0.0069	0.0279	0.0154	0.0269
Iran	9503	1	0.0055	0.011	0.0103	0.9454	0.0105	0.0072	0.0048	0.0053
Iran	9504	0	0.0033	0.005	0.0043	0.905	0.0524	0.0089	0.0062	0.0149
Iran	9505	1	0.0041	0.0066	0.0042	0.926	0.0092	0.02	0.0111	0.0187
Iran	9506	0	0.0093	0.0318	0.0091	0.8752	0.0058	0.0117	0.0045	0.0527
Iran	9507	1	0.0041	0.0173	0.0071	0.9004	0.0108	0.0147	0.0069	0.0387
Iran	9508	0	0.0182	0.1299	0.0174	0.7366	0.0197	0.0467	0.0059	0.0256
Iran	9509	0	0.0041	0.0124	0.0084	0.8008	0.0204	0.0493	0.0524	0.0522
Iran	9510	0	0.0095	0.0162	0.0065	0.8724	0.0642	0.0183	0.0045	0.0084
Iran	9511	0	0.0251	0.0262	0.0174	0.8654	0.0076	0.015	0.0139	0.0294
Iran	9512	0	0.0074	0.0227	0.0094	0.862	0.0339	0.0316	0.0062	0.0267
Iran	9513	2	0.0196	0.0121	0.0201	0.8927	0.0239	0.018	0.0073	0.0063
Iran	9514	1	0.0101	0.0183	0.014	0.8726	0.024	0.0258	0.0306	0.0046
Iran	9515	0	0.01	0.016	0.021	0.8647	0.0391	0.0183	0.0069	0.024
Iran	9516	1	0.0082	0.0147	0.0107	0.946	0.0077	0.0047	0.0049	0.0031
Iran	9517	1	0.0039	0.0446	0.0078	0.8479	0.0578	0.0214	0.011	0.0056
Iran	9518	1	0.0101	0.0059	0.0039	0.8436	0.0062	0.0149	0.0374	0.078
Iran	9519	1	0.0057	0.0058	0.0041	0.8319	0.1185	0.0174	0.0057	0.0109
Iran	9520	2	0.0143	0.2207	0.0603	0.5458	0.0131	0.0214	0.0057	0.1186
Iran	9521	2	0.0159	0.0991	0.0646	0.7526	0.0178	0.0398	0.0041	0.0061
Iran	9522	0	0.0066	0.0185	0.0081	0.8807	0.0171	0.0163	0.0047	0.048
Iran	9523	1	0.0046	0.0062	0.0051	0.8773	0.085	0.0116	0.0036	0.0066
Iran	9524	1	0.0102	0.0173	0.0179	0.899	0.0108	0.0253	0.0057	0.0138
Iran	9526	1	0.0105	0.0321	0.0265	0.784	0.007	0.0246	0.1105	0.0048
Iran	9527	0	0.0208	0.0141	0.0281	0.894	0.0083	0.014	0.0069	0.0138
Iran	9528	0	0.0121	0.0072	0.0069	0.9274	0.0182	0.0071	0.0028	0.0183
Iran	9529	0	0.0039	0.0099	0.0064	0.9197	0.0118	0.0199	0.0188	0.0096
Iran	9530	2	0.0089	0.0229	0.0142	0.9044	0.0167	0.0134	0.0144	0.0051
Iran	9531	1	0.0072	0.0079	0.0072	0.938	0.009	0.008	0.0074	0.0153
Iran	9532	1	0.0032	0.0052	0.0046	0.9605	0.0068	0.006	0.005	0.0087
Dubai	10104	0	0.006	0.0063	0.0064	0.9482	0.0142	0.0072	0.0057	0.006
Dubai	10105	1	0.0043	0.0069	0.006	0.9264	0.0161	0.008	0.0063	0.026
Dubai	10106	0	0.004	0.0054	0.0049	0.9584	0.0066	0.0057	0.0053	0.0097
Dubai	10107	2	0.0062	0.0075	0.0083	0.9342	0.016	0.0061	0.0032	0.0185
Dubai	10108	0	0.0046	0.011	0.0054	0.9408	0.0177	0.0077	0.0057	0.0071
Dubai	10109	1	0.0113	0.0345	0.0079	0.9148	0.0113	0.0097	0.0062	0.0043
Dubai	10110	4	0.0052	0.0131	0.0087	0.9452	0.0066	0.0115	0.0066	0.0031
Dubai	10111	2	0.0726	0.0257	0.0311	0.7494	0.0628	0.0435	0.0059	0.0089
Dubai	10112	1	0.0043	0.0079	0.0053	0.959	0.0094	0.0068	0.0032	0.0041
Dubai	10120	2	0.016	0.0147	0.0155	0.9253	0.0098	0.0096	0.0052	0.0039
Kenya-Nairobi	9833	6	0.0363	0.0507	0.0138	0.7907	0.0288	0.0335	0.0288	0.0174
Kenya-Nairobi	9834	0	0.0397	0.0263	0.0246	0.7146	0.0821	0.0918	0.0053	0.0155
Kenya-Nairobi	9835	2	0.0043	0.0137	0.0046	0.9266	0.0341	0.0078	0.0039	0.005
Kenya-Nairobi	9836	2	0.0079	0.0173	0.0068	0.8738	0.0434	0.0155	0.0053	0.03
Kenya-Nairobi	9837	2	0.004	0.006	0.0052	0.9521	0.008	0.0074	0.0066	0.0107
Kenya-Nairobi	9838	0	0.0052	0.011	0.011	0.8914	0.0118	0.0332	0.0137	0.0227
Kenya-Nairobi	9839	1	0.003	0.0058	0.005	0.9573	0.0102	0.0049	0.0037	0.0101
Kenya-Nairobi	9840	2	0.0064	0.0133	0.0119	0.8319	0.0985	0.0209	0.0061	0.011
Kenya-Nairobi	9841	2	0.0116	0.0353	0.0295	0.8798	0.0083	0.0124	0.0111	0.012
Kenya-Nairobi	9842	2	0.0024	0.0066	0.0033	0.9578	0.0084	0.008	0.0067	0.0068
Kenya-Nairobi	9843	5	0.0042	0.0105	0.0078	0.9335	0.0169	0.008	0.006	0.0131

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Kenya-Nairobi	9844	0	0.0055	0.0074	0.0049	0.9529	0.0074	0.0071	0.0047	0.0101
Kenya-Nairobi	9845	1	0.0031	0.0194	0.0044	0.9285	0.0109	0.0163	0.0122	0.0052
Kenya-Nairobi	9846	0	0.0047	0.0131	0.0085	0.9261	0.0112	0.015	0.0054	0.016
Kenya-Nairobi	9847	1	0.003	0.0073	0.0045	0.9465	0.0233	0.0072	0.0039	0.0043
Kenya-Nairobi	9848	4	0.0053	0.0071	0.0049	0.8729	0.0509	0.0216	0.0053	0.032
Kenya-Nairobi	9849	7	0.003	0.0134	0.0056	0.9533	0.0066	0.0102	0.0033	0.0046
Kenya-Nairobi	9850	0	0.0162	0.0123	0.01	0.9057	0.0265	0.0168	0.0055	0.0069
Kenya-Nairobi	9851	0	0.0029	0.0044	0.0049	0.9612	0.0069	0.0053	0.004	0.0104
Kenya-Nairobi	9852	2	0.002	0.0035	0.0031	0.9699	0.0072	0.0044	0.003	0.0069
Kenya-Nairobi	9853	1	0.0046	0.0126	0.009	0.9132	0.0077	0.0213	0.0196	0.012
Kenya-Nairobi	9854	3	0.0054	0.0093	0.0073	0.8978	0.0259	0.0081	0.008	0.0382
Kenya-Nairobi	9855	1	0.0053	0.0114	0.0074	0.9514	0.0044	0.0091	0.0066	0.0044
Kenya-Nairobi	9856	4	0.0038	0.0079	0.0083	0.9519	0.0094	0.0094	0.003	0.0063
Kenya-Nairobi	9857	2	0.005	0.0137	0.0107	0.9051	0.0079	0.0235	0.0202	0.0139
Kenya-Nairobi	9858	16	0.0856	0.2827	0.1344	0.2372	0.045	0.0749	0.1346	0.0057
Kenya-Nairobi	9859	0	0.0443	0.0577	0.0392	0.0221	0.7812	0.0465	0.0033	0.0056
Kenya-Nairobi	9860	2	0.0223	0.065	0.0999	0.2842	0.4256	0.0516	0.0438	0.0076
Kenya-Nairobi	9861	0	0.0059	0.0143	0.0108	0.0936	0.414	0.4349	0.0157	0.0109
Kenya-Nairobi	9862	0	0.0221	0.0878	0.0293	0.4245	0.2995	0.0601	0.015	0.0617
Kenya-Nairobi	9863	2	0.018	0.1869	0.0748	0.0481	0.572	0.05	0.0301	0.0201
Kenya-Nairobi	9864	1	0.0098	0.0196	0.015	0.0986	0.3897	0.2668	0.0234	0.1771
Kenya-Nairobi	9865	2	0.0151	0.0434	0.0495	0.0477	0.7614	0.0467	0.0295	0.0068
Kenya-Nairobi	9866	2	0.0123	0.032	0.0193	0.3694	0.4188	0.1399	0.0035	0.0048
Kenya-Nairobi	9867	0	0.0072	0.1017	0.0197	0.2399	0.5035	0.0807	0.0314	0.0159
Kenya-Nairobi	9868	0	0.0093	0.0227	0.0255	0.1019	0.7605	0.0376	0.0059	0.0366
Kenya-Pate	2000	0	0.0052	0.0117	0.009	0.0424	0.8919	0.0098	0.0058	0.0242
Kenya-Pate	2001	0	0.0043	0.004	0.0031	0.0101	0.9608	0.0053	0.0061	0.0063
Kenya-Pate	2002	0	0.0049	0.0045	0.0034	0.012	0.9574	0.0052	0.0058	0.0068
Kenya-Pate	2003	0	0.0048	0.0055	0.0046	0.0064	0.9661	0.0057	0.0022	0.0047
Kenya-Pate	2004	1	0.0048	0.0155	0.0154	0.0097	0.9015	0.0212	0.0234	0.0085
Kenya-Pate	2006	2	0.0161	0.0081	0.0064	0.0094	0.933	0.0054	0.0034	0.0182
Kenya-Pate	2007	3	0.009	0.0132	0.0127	0.008	0.9199	0.0113	0.0031	0.0228
Kenya-Pate	2009	0	0.0115	0.0371	0.0233	0.0391	0.8493	0.0197	0.0096	0.0103
Kenya-Pate	2011	0	0.0068	0.013	0.0124	0.0193	0.8722	0.0444	0.0103	0.0216
Kenya-Lamu	1848	14	0.0132	0.0251	0.0246	0.0071	0.8378	0.0481	0.007	0.0371
Kenya-Lamu	2014	4	0.0284	0.0363	0.0118	0.2268	0.6639	0.0102	0.0049	0.0177
Kenya-Lamu	2015	0	0.0078	0.0051	0.004	0.0044	0.92	0.0186	0.0303	0.0098
Kenya-Lamu	2016	0	0.0038	0.0098	0.0077	0.0241	0.8601	0.024	0.0562	0.0143
Kenya-Lamu	2018	0	0.0457	0.0063	0.0046	0.0064	0.9204	0.0063	0.0052	0.0051
Kenya-Lamu	2019	0	0.0312	0.058	0.0697	0.0084	0.7664	0.05	0.0081	0.0083
Kenya-Lamu	2021	1	0.0608	0.0443	0.0317	0.0414	0.7045	0.0266	0.0148	0.0759
Kenya-Lamu	2023	1	0.0036	0.0043	0.0048	0.0074	0.9602	0.0059	0.0063	0.0075
Kenya-Lamu	2024	2	0.0042	0.0076	0.0055	0.0098	0.9542	0.0078	0.005	0.0059
Kenya-Lamu	2025	3	0.0085	0.0059	0.0051	0.0072	0.9553	0.0055	0.003	0.0095
Kenya-Lamu	2026	1	0.0107	0.0203	0.0361	0.0128	0.8933	0.0115	0.005	0.0103
Kenya-Lamu	2027	2	0.0073	0.0069	0.0056	0.0089	0.8997	0.0111	0.0056	0.0549
Kenya-Lamu	2029	1	0.0041	0.0066	0.0055	0.0081	0.9574	0.0078	0.0051	0.0054
Kenya-Lamu	2030	0	0.0075	0.0091	0.0084	0.0295	0.924	0.0103	0.0031	0.0081
Kenya-Lamu	2031	0	0.0079	0.0112	0.0109	0.068	0.845	0.0258	0.0064	0.0248
Kenya-Lamu	2032	0	0.0067	0.0152	0.0182	0.0572	0.8627	0.0123	0.0067	0.0211
Kenya-Lamu	2033	0	0.0031	0.0057	0.0052	0.0077	0.9657	0.0063	0.0031	0.0032
Kenya-Lamu	3241	0	0.0157	0.0341	0.0258	0.0169	0.8764	0.0174	0.0059	0.0078
Kenya-Lamu	3246	0	0.0153	0.0057	0.0054	0.0051	0.8894	0.0239	0.0425	0.0127
Kenya-Lamu	3247	0	0.0115	0.0075	0.0128	0.0071	0.9151	0.0131	0.0103	0.0226
India-Udaipur	11835	7	0.0061	0.0114	0.0059	0.1045	0.0078	0.7642	0.0528	0.0473
India-Udaipur	11836	3	0.042	0.0331	0.0254	0.145	0.0099	0.6785	0.01	0.056

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
India-Udaipur	11837	1	0.004	0.0141	0.0095	0.051	0.261	0.541	0.0213	0.0981
India-Agra	11823	2	0.0092	0.0847	0.0329	0.0969	0.0133	0.5361	0.066	0.1609
India-Agra	11824	2	0.0125	0.0799	0.165	0.2201	0.2554	0.2475	0.0063	0.0133
India-Agra	11825	2	0.005	0.0962	0.0116	0.3637	0.0219	0.2722	0.0092	0.2202
India-Agra	11826	6	0.0057	0.0421	0.0194	0.1086	0.0279	0.3254	0.0062	0.4647
India-Agra	11827	25	0.0189	0.1981	0.0543	0.3265	0.0422	0.2944	0.0284	0.0371
India-Agra	11828	2	0.0145	0.458	0.1678	0.0208	0.1538	0.1515	0.0116	0.022
India-Agra	11829	4	0.0081	0.0272	0.0146	0.4481	0.0288	0.3092	0.0176	0.1465
India-Agra	11830	8	0.0147	0.1537	0.034	0.3953	0.025	0.3117	0.0069	0.0586
India-Agra	11831	2	0.0064	0.1822	0.0122	0.5332	0.024	0.1034	0.0118	0.1268
India-Agra	11832	2	0.0063	0.0759	0.0089	0.3934	0.0181	0.416	0.0196	0.0617
India-Agra	11833	20	0.0075	0.0314	0.0226	0.019	0.2423	0.5895	0.0604	0.0273
India-Agra	11834	2	0.0069	0.0522	0.0185	0.1321	0.0223	0.2839	0.0065	0.4776
India-Hyderbad	11802	14	0.0042	0.0218	0.0173	0.012	0.0117	0.8432	0.0773	0.0125
India-Hyderbad	11803	7	0.0034	0.0178	0.0084	0.0692	0.0576	0.8204	0.0126	0.0106
India-Hyderbad	11804	4	0.0032	0.0077	0.006	0.0273	0.037	0.8421	0.0376	0.0391
India-Hyderbad	11805	11	0.0047	0.014	0.0223	0.0195	0.0653	0.8498	0.0174	0.007
India-Hyderbad	11807	13	0.033	0.0199	0.0322	0.0125	0.0627	0.7689	0.0353	0.0356
India-Hyderbad	11808	10	0.0344	0.0211	0.0303	0.0106	0.1872	0.6834	0.0105	0.0224
India-Hyderbad	11809	4	0.0459	0.0738	0.0135	0.0425	0.0543	0.7282	0.0195	0.0224
India-Hyderbad	11810	0	0.0079	0.0155	0.0185	0.0845	0.2349	0.4859	0.0097	0.1431
India-Hyderbad	11811	0	0.0567	0.0178	0.0748	0.0102	0.0569	0.7598	0.0056	0.0182
India-Hyderbad	11812	0	0.0038	0.0081	0.0104	0.0168	0.0676	0.8639	0.0144	0.015
India-Hyderbad	11813	2	0.0076	0.014	0.0161	0.0071	0.029	0.8419	0.0732	0.0112
India-Hyderbad	11814	2	0.0047	0.0216	0.0166	0.0558	0.0214	0.8582	0.0173	0.0044
India-Hyderbad	11815	2	0.007	0.0477	0.0329	0.0081	0.0133	0.8657	0.0187	0.0066
India-Hyderbad	11816	4	0.0065	0.0184	0.0085	0.1971	0.0851	0.6486	0.0055	0.0303
India-Hyderbad	11817	2	0.0034	0.0134	0.0134	0.014	0.0219	0.8772	0.0483	0.0084
India-Hyderbad	11818	1	0.4405	0.0183	0.0304	0.0141	0.1267	0.1626	0.2022	0.0052
India-Hyderbad	11819	6	0.0084	0.0344	0.013	0.1712	0.113	0.6199	0.0056	0.0345
India-Hyderbad	11820	6	0.0031	0.0106	0.0103	0.0557	0.0429	0.8148	0.044	0.0185
India-Hyderbad	11821	17	0.0083	0.0393	0.0389	0.0207	0.0645	0.6513	0.164	0.0131
India-Hyderbad	11822	2	0.0053	0.0107	0.0154	0.0874	0.0654	0.781	0.0207	0.0141
India-Andhra	10159	1	0.0178	0.0229	0.0272	0.1705	0.0107	0.678	0.0476	0.0253
India-Andhra	10160	1	0.0053	0.0081	0.0078	0.0122	0.0113	0.6141	0.2167	0.1245
India-Andhra	10161	2	0.017	0.0228	0.0131	0.0369	0.081	0.7808	0.0375	0.0109
India-Andhra	10162	5	0.011	0.0102	0.0109	0.0441	0.0105	0.7626	0.14	0.0107
India-Andhra	10163	0	0.0082	0.0122	0.0107	0.0217	0.0695	0.8088	0.0566	0.0123
India-Andhra	10164	2	0.0944	0.0255	0.0181	0.0228	0.01	0.7638	0.0512	0.0143
India-Andhra	10165	1	0.0257	0.0258	0.0469	0.0194	0.0456	0.3363	0.491	0.0092
India-Andhra	10166	2	0.0093	0.0764	0.0299	0.089	0.0732	0.4868	0.2196	0.0158
India-Andhra	10167	0	0.0064	0.0069	0.0082	0.0168	0.0345	0.5586	0.3478	0.0208
India-Andhra	10168	1	0.0344	0.0209	0.0539	0.0102	0.0223	0.6305	0.2121	0.0157
India-Andhra	10169	7	0.0054	0.0086	0.0069	0.0091	0.0682	0.8535	0.0407	0.0076
India-Andhra	10170	6	0.007	0.0348	0.0499	0.0104	0.0949	0.6735	0.1065	0.0231
India-Andhra	10171	1	0.0923	0.0251	0.017	0.0237	0.01	0.7657	0.0524	0.0139
India-Andhra	10172	2	0.0062	0.0085	0.0097	0.0117	0.0988	0.7613	0.0956	0.0082
India-Andhra	10173	2	0.0118	0.0172	0.0179	0.0146	0.0337	0.7665	0.1328	0.0054
India-Andhra	10174	3	0.0069	0.008	0.0119	0.0069	0.048	0.7983	0.0757	0.0443
India-Andhra	10175	2	0.0237	0.0391	0.0716	0.0133	0.0384	0.6239	0.0584	0.1315
India-Andhra	10176	2	0.009	0.0312	0.0162	0.0138	0.0198	0.8628	0.0219	0.0253
India-Andhra	10177	0	0.197	0.0094	0.0075	0.0358	0.0224	0.5453	0.1257	0.0569
India-Andhra	10178	2	0.0072	0.0068	0.0073	0.0083	0.0467	0.7306	0.1842	0.0089
India-Andhra	10179	5	0.0069	0.0074	0.0051	0.0096	0.4515	0.3078	0.2017	0.01
India-Andhra	10180	12	0.0208	0.0108	0.0204	0.0853	0.017	0.7135	0.0499	0.0823
India-Andhra	10181	4	0.0082	0.0122	0.0088	0.0236	0.0517	0.7971	0.0831	0.0153

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
India-Kolkata	10113	0	0.0052	0.0125	0.0102	0.029	0.1619	0.6324	0.0043	0.1446
India-Kolkata	10114	1	0.0061	0.0247	0.0096	0.0138	0.0528	0.6832	0.1886	0.0212
India-Kolkata	10115	1	0.0086	0.0669	0.0544	0.0112	0.0392	0.7438	0.036	0.0399
India-Kolkata	10116	1	0.0029	0.0415	0.0078	0.0999	0.0282	0.5887	0.2034	0.0275
India-Kolkata	10117	2	0.0071	0.065	0.0279	0.0109	0.0467	0.752	0.0788	0.0117
India-Kolkata	10118	0	0.0614	0.1603	0.0992	0.0215	0.0198	0.4194	0.1579	0.0606
India-Kolkata	10119	2	0.0806	0.1532	0.093	0.0886	0.0581	0.4495	0.0433	0.0338
Sri Lanka	8780	2	0.0483	0.0296	0.0217	0.0139	0.2366	0.4524	0.0142	0.1833
Sri Lanka	8781	0	0.0532	0.041	0.0196	0.0108	0.1335	0.5079	0.0895	0.1444
Sri Lanka	8782	0	0.0157	0.0255	0.0527	0.0088	0.1014	0.7458	0.0217	0.0284
Sri Lanka	8783	0	0.0374	0.1252	0.3072	0.01	0.0178	0.4467	0.0479	0.0078
Sri Lanka	8784	0	0.325	0.0999	0.0303	0.0077	0.0251	0.3352	0.145	0.0318
Sri Lanka	8785	11	0.1125	0.0236	0.0124	0.0241	0.0657	0.6425	0.07	0.0493
Sri Lanka	8786	0	0.023	0.0245	0.0169	0.0199	0.1936	0.534	0.0352	0.1528
Sri Lanka	8787	0	0.0798	0.0175	0.0111	0.0058	0.0817	0.7888	0.0069	0.0084
Sri Lanka	8788	4	0.028	0.0329	0.1215	0.0099	0.1415	0.6453	0.0127	0.0082
Sri Lanka	8789	2	0.0987	0.0681	0.3622	0.0137	0.0776	0.0823	0.2557	0.0415
Sri Lanka	8790	1	0.1667	0.0812	0.0367	0.0161	0.0178	0.293	0.3834	0.0051
Sri Lanka	8791	0	0.0654	0.2282	0.1887	0.0127	0.0226	0.3205	0.1378	0.0241
Sri Lanka	8792	0	0.0088	0.0218	0.0532	0.0387	0.0712	0.7818	0.0059	0.0185
Sri Lanka	8793	1	0.0555	0.0196	0.0741	0.0453	0.1449	0.6362	0.0115	0.0128
Sri Lanka	8794	1	0.0398	0.0214	0.0567	0.108	0.0686	0.6686	0.0094	0.0276
Sri Lanka	8795	1	0.2526	0.037	0.0715	0.015	0.2086	0.3528	0.0308	0.0317
Sri Lanka	8796	3	0.0161	0.0396	0.0499	0.0333	0.0951	0.5129	0.0376	0.2155
Sri Lanka	8797	0	0.1746	0.0544	0.033	0.0399	0.0406	0.4824	0.1572	0.0179
Sri Lanka	8798	0	0.0309	0.143	0.1005	0.0175	0.0219	0.5893	0.0142	0.0827
Sri Lanka	8799	1	0.1612	0.0172	0.0354	0.0121	0.0628	0.6906	0.0111	0.0096
Sri Lanka	8800	0	0.3314	0.044	0.0257	0.0131	0.0691	0.4522	0.0502	0.0143
Sri Lanka	8801	4	0.0764	0.0262	0.0279	0.0087	0.0666	0.7749	0.008	0.0113
Sri Lanka	8802	2	0.1278	0.0192	0.0323	0.0063	0.1581	0.618	0.0112	0.0271
Sri Lanka	8803	4	0.0681	0.0233	0.0951	0.0138	0.0774	0.2957	0.2675	0.1592
Thailand	11688	6	0.0257	0.0075	0.0062	0.0031	0.0135	0.0056	0.9335	0.0049
Thailand	11689	13	0.0048	0.0061	0.0044	0.0048	0.0034	0.0059	0.9535	0.0171
Thailand	11691	20	0.0251	0.0114	0.015	0.0095	0.0087	0.0359	0.8786	0.0158
Thailand	11698	17	0.0053	0.0053	0.0049	0.003	0.0021	0.0074	0.9678	0.0042
Thailand	11702	10	0.0028	0.0021	0.0028	0.0039	0.0036	0.004	0.9671	0.0137
Thailand	11703	12	0.0043	0.0051	0.0068	0.0038	0.0051	0.0089	0.9549	0.0111
Thailand	11705	21	0.0079	0.0217	0.0207	0.0319	0.0452	0.0343	0.825	0.0133
Thailand	11707	3	0.0027	0.0041	0.0038	0.0058	0.0045	0.0084	0.9625	0.0082
Thailand	11708	22	0.0041	0.0043	0.0043	0.0048	0.0069	0.0076	0.958	0.01
Thailand	11709	12	0.0042	0.0067	0.0054	0.0113	0.007	0.0126	0.9452	0.0076
Thailand	11710	8	0.0103	0.0109	0.0105	0.0108	0.0054	0.0085	0.9252	0.0184
Thailand	11711	7	0.007	0.005	0.0062	0.0071	0.007	0.0056	0.9535	0.0086
Thailand	11714	5	0.008	0.0072	0.0071	0.0102	0.0046	0.0073	0.9496	0.006
Thailand	11715	16	0.0084	0.0247	0.0085	0.1675	0.0371	0.0166	0.7256	0.0116
Thailand	11717	15	0.0029	0.0047	0.0046	0.0135	0.0117	0.0113	0.944	0.0073
Thailand	11718	0	0.002	0.0027	0.0026	0.0045	0.0031	0.0047	0.9753	0.0051
Thailand	11720	3	0.0021	0.0022	0.002	0.0027	0.0033	0.0035	0.9812	0.003
Vietnam	8844	4	0.0242	0.0111	0.0055	0.0109	0.0094	0.0157	0.9109	0.0123
Vietnam	8845	1	0.0198	0.0318	0.0363	0.1173	0.0139	0.0218	0.7387	0.0205
Vietnam	8846	0	0.011	0.0185	0.0225	0.0079	0.007	0.1624	0.7642	0.0065
Vietnam	8847	9	0.0054	0.0045	0.0043	0.0031	0.0042	0.0056	0.9658	0.0071
Vietnam	8848	6	0.0056	0.0154	0.011	0.0091	0.0184	0.0285	0.8964	0.0156
Vietnam	8849	2	0.02	0.0343	0.0484	0.0152	0.0065	0.0387	0.8094	0.0275
Vietnam	8850	0	0.049	0.0845	0.0215	0.0315	0.0215	0.0365	0.7385	0.0171
Vietnam	8851	0	0.0213	0.0755	0.0617	0.0779	0.0063	0.0309	0.7192	0.0073

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Vietnam	8852	13	0.0309	0.0609	0.0264	0.0089	0.0479	0.0573	0.7288	0.0388
Vietnam	8853	1	0.0866	0.0949	0.0549	0.0089	0.0181	0.1195	0.5948	0.0222
Vietnam	8854	5	0.0106	0.032	0.0214	0.0422	0.0305	0.0814	0.7395	0.0424
Vietnam	8855	0	0.2697	0.0221	0.0583	0.0046	0.006	0.011	0.6205	0.0078
Vietnam	8856	0	0.019	0.02	0.0443	0.0305	0.0078	0.0911	0.7695	0.0178
Vietnam	8857	2	0.0242	0.0345	0.1661	0.0048	0.0235	0.2018	0.5294	0.0157
Vietnam	8858	0	0.0484	0.0271	0.2905	0.0087	0.0084	0.0247	0.5874	0.0048
Vietnam	8859	6	0.0192	0.0786	0.0386	0.0108	0.1204	0.0308	0.6787	0.023
Vietnam	8860	0	0.0082	0.0541	0.0207	0.0565	0.052	0.0793	0.633	0.0961
Vietnam	8861	0	0.0109	0.0996	0.0894	0.0327	0.0294	0.04	0.6182	0.08
Vietnam	8862	0	0.0316	0.2645	0.0297	0.1359	0.0257	0.0767	0.4134	0.0226
Vietnam	8863	0	0.1561	0.0374	0.1777	0.0192	0.0061	0.0226	0.5736	0.0073
Taiwan	8681	3	0.5988	0.01	0.0074	0.0077	0.0137	0.0123	0.0294	0.3207
Taiwan	8682	0	0.1407	0.0589	0.0403	0.0813	0.0511	0.1265	0.3831	0.1182
Taiwan	8683	2	0.0227	0.2842	0.1142	0.0669	0.0188	0.2839	0.031	0.1783
Taiwan	8684	2	0.5912	0.0131	0.0096	0.0279	0.0045	0.0134	0.028	0.3123
Taiwan	8685	2	0.0113	0.0172	0.01	0.0116	0.099	0.049	0.2604	0.5414
Taiwan	8686	6	0.069	0.0477	0.0286	0.0421	0.1558	0.122	0.0335	0.5014
Taiwan	8687	6	0.0088	0.0926	0.0465	0.0204	0.0105	0.0898	0.4907	0.2408
Taiwan	8688	21	0.0626	0.0533	0.0285	0.0877	0.0447	0.1327	0.2007	0.3898
Taiwan	8689	5	0.0135	0.0156	0.0206	0.3609	0.0099	0.0198	0.0249	0.5348
Taiwan	8690	0	0.0077	0.0124	0.0098	0.0463	0.011	0.0484	0.1458	0.7187
Taiwan	8691	14	0.0466	0.0359	0.0193	0.0622	0.0321	0.0544	0.1959	0.5536
Taiwan	8692	3	0.0917	0.0914	0.0458	0.0772	0.0417	0.0507	0.4872	0.1143
Taiwan	8693	0	0.0435	0.0138	0.0129	0.0251	0.0746	0.5199	0.0429	0.2673
Taiwan	8694	0	0.1651	0.2053	0.0361	0.0669	0.061	0.0144	0.1864	0.2647
Taiwan	8695	0	0.0535	0.0809	0.0499	0.0088	0.0067	0.0792	0.2074	0.5136
Taiwan	8696	8	0.9708	0.0054	0.0067	0.003	0.0048	0.0035	0.0021	0.0037
Taiwan	8697	0	0.7175	0.0103	0.0097	0.016	0.0197	0.0769	0.0123	0.1375
Taiwan	8698	4	0.9531	0.007	0.0075	0.0066	0.0069	0.0061	0.0038	0.009
Taiwan	8699	6	0.0158	0.0156	0.0465	0.052	0.1473	0.4495	0.0796	0.1938
Taiwan	8700	1	0.3523	0.0295	0.0328	0.0258	0.0187	0.0195	0.2145	0.3069
Taiwan	8701	2	0.0741	0.0103	0.0087	0.0117	0.0542	0.0285	0.1495	0.663
Taiwan	8702	1	0.296	0.0349	0.0211	0.01	0.0348	0.0598	0.0466	0.4967
Taiwan	8703	1	0.7562	0.0119	0.0362	0.0128	0.0408	0.0954	0.0288	0.0179
Taiwan	8704	0	0.0066	0.0228	0.1598	0.0054	0.0339	0.0218	0.1195	0.6302
Taiwan	8705	1	0.0115	0.0213	0.0286	0.0238	0.0267	0.0476	0.1907	0.6498
Taiwan	8706	0	0.07	0.0952	0.1384	0.2491	0.0243	0.1176	0.0711	0.2342
Taiwan	8707	4	0.0125	0.0975	0.0375	0.1074	0.0341	0.1234	0.0811	0.5065
Taiwan	8708	0	0.9342	0.0096	0.0068	0.008	0.0091	0.0137	0.0125	0.0061
Taiwan	8709	2	0.0098	0.0188	0.0101	0.0127	0.0232	0.0157	0.1617	0.748
Japan-Oita	11967	4	0.021	0.0383	0.0357	0.0133	0.1053	0.0625	0.5731	0.1507
Japan-Oita	11968	5	0.274	0.0194	0.0228	0.009	0.1373	0.0239	0.2583	0.2554
Japan-Oita	11969	5	0.0936	0.0207	0.1672	0.0084	0.0136	0.037	0.2395	0.4199
Japan-Oita	11970	16	0.019	0.0622	0.0634	0.0084	0.0164	0.0263	0.789	0.0153
Japan-Oita	11971	8	0.0111	0.0531	0.0573	0.0524	0.0256	0.4899	0.2553	0.0552
Japan-Oita	11972	3	0.0272	0.1819	0.1543	0.0177	0.0168	0.0868	0.3903	0.1249
Japan-Oita	11973	2	0.4089	0.007	0.0087	0.0072	0.0083	0.0138	0.0185	0.5276
Japan-Oita	11974	20	0.0084	0.012	0.0207	0.0139	0.0286	0.0498	0.3617	0.5049
Japan-Oita	11975	22	0.2289	0.0883	0.0279	0.006	0.021	0.078	0.4869	0.0631
Japan-Oita	11976	16	0.02	0.0092	0.0093	0.0171	0.0179	0.0433	0.5176	0.3656
Japan-Oita	11977	4	0.0072	0.0064	0.0048	0.0393	0.0498	0.0245	0.5591	0.3089
Japan-Oita	11979	12	0.1335	0.0164	0.0181	0.0454	0.0164	0.0077	0.6835	0.079
Japan-Oita	11980	21	0.0073	0.0185	0.0206	0.1152	0.0311	0.0344	0.6555	0.1173
Japan-Oita	11981	18	0.0059	0.0057	0.0063	0.0067	0.0131	0.0065	0.2067	0.749
Japan-Oita	11982	4	0.0151	0.02	0.0122	0.0359	0.0315	0.0153	0.3762	0.4938

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Japan-Oita	11985	11	0.0182	0.0207	0.0232	0.0194	0.0077	0.016	0.2148	0.6799
Japan-Oita	11986	6	0.373	0.0219	0.0269	0.0133	0.0142	0.0311	0.4005	0.1191
Japan-Kanazawa	11929	6	0.9291	0.0104	0.0082	0.0119	0.0167	0.0109	0.0034	0.0094
Japan-Kanazawa	11931	20	0.0207	0.0098	0.0082	0.0283	0.0133	0.0323	0.0707	0.8167
Japan-Kanazawa	11932	6	0.0855	0.028	0.0167	0.0122	0.0159	0.0493	0.0933	0.6991
Japan-Kanazawa	11933	14	0.1065	0.0226	0.0316	0.005	0.0118	0.023	0.0168	0.7827
Japan-Kanazawa	11934	3	0.1539	0.0144	0.014	0.0031	0.01	0.0092	0.0249	0.7705
Japan-Kanazawa	11936	8	0.0408	0.0238	0.0173	0.0188	0.0136	0.09	0.3327	0.463
Japan-Kanazawa	11937	27	0.0204	0.0126	0.0089	0.0128	0.0235	0.0146	0.0137	0.8935
Japan-Kanazawa	11939	20	0.016	0.0055	0.0072	0.004	0.0344	0.0396	0.2948	0.5985
Japan-Kanazawa	11940	12	0.0119	0.0091	0.0074	0.0067	0.0188	0.0229	0.0872	0.836
Japan-Kanazawa	11941	6	0.0181	0.0114	0.0093	0.0071	0.0103	0.0489	0.2794	0.6155
Japan-Kanazawa	11942	9	0.0061	0.0037	0.0048	0.0045	0.0074	0.0064	0.0203	0.9468
Japan-Kanazawa	11943	17	0.0137	0.0175	0.0185	0.0315	0.0386	0.0523	0.4918	0.3361
Japan-Kanazawa	11944	7	0.3983	0.1001	0.1915	0.0224	0.0393	0.2042	0.0291	0.0151
Japan-Kanazawa	11945	18	0.0354	0.0111	0.0169	0.0069	0.0137	0.0272	0.0745	0.8143
Japan-Kanazawa	11946	16	0.0031	0.0031	0.0055	0.0031	0.0048	0.0068	0.0146	0.959
Japan-Ohmiya	11947	4	0.0618	0.0347	0.094	0.0089	0.006	0.0278	0.0664	0.7005
Japan-Ohmiya	11948	17	0.0042	0.0069	0.0065	0.0134	0.0081	0.0145	0.0152	0.9312
Japan-Ohmiya	11951	22	0.0305	0.0252	0.0508	0.0404	0.0717	0.0682	0.0182	0.6948
Japan-Ohmiya	11953	2	0.0057	0.0087	0.007	0.0075	0.0057	0.0103	0.2061	0.749
Japan-Ohmiya	11954	2	0.0462	0.0192	0.0192	0.0149	0.0076	0.0294	0.0259	0.8376
Japan-Ohmiya	11955	5	0.2035	0.015	0.0058	0.0133	0.0102	0.0115	0.0075	0.7332
Japan-Ohmiya	11956	2	0.0055	0.009	0.0343	0.0063	0.0117	0.0239	0.6507	0.2586
Japan-Ohmiya	11957	3	0.0187	0.0116	0.04	0.0058	0.2075	0.0208	0.0324	0.6631
Japan-Ohmiya	11959	4	0.011	0.0112	0.0096	0.0054	0.0107	0.0139	0.1684	0.7698
Japan-Ohmiya	11960	3	0.0066	0.0058	0.0055	0.0061	0.0093	0.0075	0.5186	0.4406
Japan-Ohmiya	11961	3	0.022	0.0123	0.0126	0.0081	0.0424	0.0181	0.1068	0.7777
Japan-Ohmiya	11962	4	0.2858	0.0341	0.0282	0.0099	0.1244	0.0417	0.067	0.4088
Japan-Ohmiya	11963	3	0.0125	0.0174	0.0152	0.0425	0.0909	0.056	0.0778	0.6876
Japan-Ohmiya	11964	4	0.0329	0.0136	0.0096	0.0109	0.0526	0.0321	0.0095	0.8388
Japan-Ohmiya	11965	4	0.0088	0.0207	0.0208	0.0111	0.381	0.2777	0.0351	0.2449
Japan-Ohmiya	11966	5	0.0452	0.053	0.0528	0.0525	0.0226	0.0939	0.0674	0.6125
Japan-Sapporo	11907	7	0.0364	0.0416	0.0118	0.0787	0.0528	0.0316	0.0609	0.6862
Japan-Sapporo	11909	9	0.9613	0.0058	0.0044	0.0057	0.0069	0.0056	0.005	0.0053
Japan-Sapporo	11911	17	0.2459	0.029	0.0119	0.0083	0.0166	0.1486	0.0251	0.5147
Japan-Sapporo	11913	16	0.0174	0.058	0.0467	0.0098	0.019	0.4068	0.157	0.2853
Japan-Sapporo	11914	4	0.012	0.0358	0.0505	0.0105	0.1369	0.3908	0.1625	0.201
Japan-Sapporo	11915	7	0.01	0.0066	0.006	0.0059	0.0088	0.0141	0.757	0.1915
Japan-Sapporo	11916	7	0.9309	0.0148	0.0163	0.0063	0.0064	0.0111	0.0109	0.0033
Japan-Sapporo	11917	4	0.9094	0.0145	0.0079	0.0298	0.0155	0.0086	0.005	0.0093
Japan-Sapporo	11918	13	0.0492	0.0158	0.0276	0.0232	0.0258	0.2314	0.0766	0.5504
Japan-Sapporo	11921	5	0.0053	0.0176	0.0244	0.0277	0.0676	0.0419	0.3003	0.5152
Japan-Sapporo	11922	6	0.0045	0.0057	0.0085	0.1235	0.4193	0.1359	0.0249	0.2776
Japan-Sapporo	11923	7	0.002	0.0037	0.0038	0.0046	0.0079	0.0055	0.3865	0.586
Japan-Sapporo	11924	6	0.5659	0.0661	0.0311	0.0065	0.013	0.0333	0.1571	0.127
Japan-Sapporo	11925	9	0.0071	0.0156	0.0112	0.0244	0.0368	0.0272	0.8529	0.0249
Japan-Sapporo	11926	11	0.041	0.3068	0.1245	0.0288	0.0075	0.017	0.0207	0.4536
China-Henan	8869	2	0.0031	0.0173	0.0141	0.0728	0.0267	0.0176	0.0062	0.8422
China-Henan	8870	0	0.0051	0.0107	0.0083	0.0139	0.0095	0.0124	0.007	0.9331
China-Henan	8871	0	0.0072	0.0145	0.0107	0.0127	0.0149	0.0183	0.0049	0.9168
China-Henan	8872	1	0.0096	0.0233	0.0223	0.0089	0.0087	0.0596	0.0081	0.8595
China-Henan	8873	1	0.0027	0.0065	0.006	0.0255	0.0043	0.0095	0.0043	0.9412
China-Henan	8874	8	0.004	0.0203	0.0096	0.0693	0.0166	0.0775	0.026	0.7768
China-Henan	8875	1	0.0031	0.0061	0.005	0.0099	0.0079	0.0068	0.0036	0.9576
China-Henan	8876	0	0.0032	0.0059	0.0058	0.0096	0.0074	0.0075	0.0046	0.956

Table 23 - Population clustering of each random bred individual in the database by SNPs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
China-Henan	8877	0	0.0398	0.0179	0.0083	0.0151	0.0095	0.0141	0.0043	0.8911
China-Henan	8878	2	0.0057	0.0168	0.0133	0.024	0.0532	0.0121	0.004	0.8709
China-Henan	8879	2	0.0076	0.0089	0.0085	0.0067	0.0202	0.0226	0.0033	0.9222
China-Henan	8880	0	0.0492	0.0263	0.0167	0.0134	0.0133	0.0187	0.0034	0.859
China-Henan	8881	2	0.0046	0.0139	0.0091	0.0203	0.0713	0.0113	0.0052	0.8643
China-Henan	8882	2	0.0067	0.0125	0.009	0.0276	0.0057	0.0142	0.0052	0.9191
China-Henan	8883	0	0.0079	0.0073	0.0051	0.099	0.0061	0.0108	0.0071	0.8567
China-Henan	8884	0	0.0042	0.0055	0.0044	0.0183	0.0065	0.0054	0.0032	0.9525
China-Henan	8885	0	0.011	0.0548	0.0223	0.1045	0.0156	0.0245	0.0042	0.7631
China-Henan	8886	0	0.0036	0.0093	0.0065	0.0363	0.0093	0.0095	0.004	0.9215
China-Henan	8887	1	0.0041	0.0114	0.0114	0.0233	0.0122	0.0477	0.0186	0.8714
China-Henan	8888	1	0.0056	0.0048	0.0048	0.0061	0.009	0.0107	0.0029	0.9561
South Korea	2769	4	0.0072	0.0421	0.0367	0.0598	0.0161	0.0142	0.0083	0.8156
South Korea	2772	12	0.0053	0.0043	0.0043	0.0058	0.0074	0.0105	0.0049	0.9575
South Korea	2775	8	0.0077	0.0171	0.015	0.0299	0.0179	0.0225	0.0434	0.8465
South Korea	2776	25	0.0037	0.0062	0.0066	0.0162	0.0219	0.0106	0.0263	0.9085
South Korea	2779	0	0.017	0.0281	0.0133	0.0242	0.0734	0.0106	0.0255	0.8078
South Korea	2784	2	0.0074	0.029	0.0334	0.0394	0.0898	0.0494	0.0057	0.746
South Korea	2785	1	0.005	0.0068	0.0125	0.0145	0.0842	0.014	0.014	0.849
South Korea	2786	2	0.0055	0.0089	0.0108	0.0042	0.0064	0.0083	0.0226	0.9333
South Korea	7671	1	0.0629	0.0954	0.0266	0.0128	0.0074	0.0095	0.0066	0.7788
South Korea	7672	0	0.0043	0.0185	0.0101	0.0149	0.0122	0.0343	0.0522	0.8535
South Korea	7673	0	0.0078	0.0278	0.0259	0.0187	0.0102	0.0132	0.0056	0.8907
South Korea	7674	1	0.0524	0.0798	0.049	0.056	0.2326	0.0283	0.0061	0.4958
South Korea	7675	2	0.0045	0.0081	0.0056	0.008	0.0075	0.0069	0.0098	0.9496
South Korea	7676	2	0.1262	0.0274	0.0318	0.0066	0.0068	0.0227	0.0105	0.7681
South Korea	7677	14	0.8348	0.0273	0.0359	0.008	0.0105	0.0363	0.018	0.0291
South Korea	7678	0	0.0134	0.0081	0.0064	0.0084	0.0091	0.0166	0.0062	0.9318
South Korea	7679	2	0.0076	0.026	0.0171	0.0121	0.0113	0.0112	0.0104	0.9043
South Korea	7680	8	0.1295	0.0645	0.0252	0.0164	0.0099	0.0178	0.0049	0.7318
South Korea	7681	2	0.0096	0.0111	0.0106	0.0068	0.0053	0.0199	0.0238	0.9129
South Korea	7682	0	0.0037	0.005	0.0046	0.0051	0.0069	0.0084	0.0318	0.9345
South Korea	7683	0	0.0041	0.0054	0.0045	0.012	0.0167	0.0196	0.0045	0.9332
South Korea	7684	1	0.5642	0.0237	0.0143	0.0745	0.0554	0.0179	0.0073	0.2427
South Korea	7685	6	0.0109	0.0423	0.0363	0.0278	0.242	0.0438	0.0953	0.5016
South Korea	7686	2	0.0171	0.0165	0.0213	0.0202	0.0356	0.0095	0.0032	0.8766
South Korea	7687	4	0.0938	0.0308	0.0355	0.0087	0.0375	0.0152	0.0728	0.7057
South Korea	7688	13	0.3179	0.0088	0.0074	0.007	0.0088	0.0065	0.0112	0.6324
South Korea	7689	0	0.0041	0.0105	0.0046	0.0754	0.0105	0.0058	0.0035	0.8856
South Korea	7690	0	0.0275	0.092	0.0544	0.0206	0.0092	0.028	0.0088	0.7595
South Korea	7691	2	0.0045	0.0057	0.0069	0.0072	0.0065	0.0199	0.1218	0.8275
South Korea	7692	0	0.0355	0.0478	0.0443	0.0599	0.0246	0.0423	0.0105	0.7351
South Korea	7693	0	0.0089	0.0127	0.0161	0.0138	0.0918	0.0349	0.0177	0.8041
South Korea	7694	1	0.0032	0.0161	0.0076	0.0076	0.0396	0.0335	0.0269	0.8655
South Korea	7695	9	0.0515	0.0557	0.0928	0.0239	0.0143	0.0252	0.0032	0.7335
South Korea	7696	2	0.0073	0.0103	0.0095	0.0084	0.0103	0.0142	0.0041	0.9359
South Korea	7697	2	0.0357	0.0343	0.0234	0.0288	0.0502	0.0116	0.006	0.81
South Korea	7698	2	0.0112	0.0263	0.1216	0.007	0.0041	0.0243	0.3231	0.4825
South Korea	7699	0	0.0235	0.0274	0.0444	0.008	0.0058	0.0109	0.0186	0.8614
South Korea	7700	6	0.0052	0.0078	0.0104	0.0093	0.0059	0.0098	0.0161	0.9355

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling	ID	Missing	Population						
Location	No.	Data	1	2	3	4	5	6	7
USA-NY	2547	2	0.72	0.045	0.006	0.044	0.173	0.004	0.008
USA-NY	2559	13	0.738	0.229	0.005	0.006	0.016	0.003	0.004
USA-NY	2568	2	0.96	0.007	0.005	0.005	0.01	0.012	0.003
USA-NY	2569	21	0.902	0.014	0.005	0.011	0.042	0.015	0.011
USA-NY	2572	5	0.876	0.014	0.047	0.042	0.009	0.008	0.005
USA-NY	2578	5	0.937	0.008	0.004	0.019	0.025	0.003	0.005
USA-NY	2590	5	0.929	0.025	0.006	0.014	0.02	0.004	0.002
USA-NY	2591	7	0.916	0.011	0.014	0.007	0.021	0.023	0.007
USA-NY	2597	15	0.845	0.011	0.006	0.11	0.011	0.006	0.01
USA-MS	9971	5	0.875	0.017	0.005	0.077	0.011	0.007	0.007
USA-MS	9972	0	0.785	0.01	0.01	0.096	0.078	0.008	0.013
USA-MS	9974	2	0.907	0.021	0.024	0.024	0.01	0.008	0.007
USA-MS	9977	10	0.916	0.01	0.004	0.029	0.018	0.013	0.01
USA-MS	9980	7	0.904	0.04	0.017	0.005	0.017	0.004	0.011
USA-MS	9983	7	0.946	0.008	0.011	0.018	0.008	0.004	0.005
USA-MS	9985	5	0.786	0.062	0.004	0.03	0.02	0.095	0.002
USA-MS	9987	10	0.897	0.026	0.006	0.031	0.023	0.006	0.011
USA-MS	9989	2	0.865	0.019	0.007	0.021	0.053	0.03	0.005
USA-MS	9992	7	0.687	0.097	0.012	0.075	0.114	0.009	0.006
USA-HI	5366	10	0.628	0.057	0.071	0.04	0.063	0.137	0.003
USA-HI	5367	7	0.574	0.011	0.011	0.055	0.333	0.008	0.008
USA-HI	5371	5	0.46	0.329	0.01	0.119	0.024	0.037	0.021
USA-HI	5372	7	0.74	0.041	0.012	0.165	0.023	0.012	0.007
USA-HI	5379	2	0.875	0.024	0.005	0.019	0.026	0.036	0.014
USA-HI	5380	2	0.915	0.009	0.016	0.005	0.038	0.012	0.005
USA-HI	5383	10	0.366	0.266	0.113	0.012	0.154	0.014	0.075
USA-HI	5384	18	0.753	0.13	0.016	0.004	0.088	0.003	0.005
USA-HI	5401	5	0.274	0.09	0.041	0.009	0.548	0.035	0.003
USA-HI	5402	7	0.714	0.064	0.008	0.018	0.063	0.086	0.046
Brazil	7961	2	0.944	0.009	0.004	0.003	0.028	0.008	0.003
Brazil	7962	2	0.885	0.089	0.006	0.005	0.01	0.003	0.002
Brazil	7963	23	0.805	0.012	0.026	0.137	0.01	0.005	0.004
Brazil	7964	5	0.945	0.007	0.021	0.006	0.007	0.009	0.004
Brazil	7965	65	0.954	0.008	0.008	0.009	0.011	0.005	0.006
Brazil	7966	5	0.955	0.006	0.004	0.007	0.013	0.004	0.011
Brazil	7968	23	0.952	0.013	0.005	0.007	0.011	0.006	0.006
Brazil	7969	2	0.968	0.007	0.004	0.008	0.006	0.004	0.003
Brazil	7970	2	0.956	0.01	0.01	0.009	0.008	0.003	0.003
Brazil	7971	2	0.967	0.004	0.005	0.004	0.007	0.008	0.004
Brazil	7972	2	0.962	0.005	0.008	0.003	0.011	0.004	0.006
Brazil	7973	2	0.921	0.007	0.009	0.004	0.045	0.01	0.004
Brazil	7974	2	0.952	0.009	0.009	0.007	0.011	0.006	0.005
Brazil	7975	13	0.94	0.007	0.009	0.01	0.017	0.013	0.003
Brazil	7976	2	0.975	0.004	0.004	0.003	0.005	0.005	0.003
Brazil	7977	7	0.956	0.009	0.005	0.003	0.017	0.007	0.003
Brazil	7978	2	0.942	0.007	0.032	0.005	0.006	0.004	0.003
Brazil	7979	5	0.933	0.009	0.017	0.007	0.013	0.017	0.005
Brazil	7980	2	0.63	0.065	0.005	0.009	0.252	0.02	0.019
Brazil	7981	5	0.798	0.023	0.01	0.023	0.015	0.124	0.007
Brazil	7982	42	0.843	0.039	0.02	0.037	0.026	0.026	0.009
Brazil	7983	15	0.74	0.022	0.007	0.195	0.026	0.005	0.006
Brazil	7984	50	0.588	0.061	0.011	0.106	0.118	0.097	0.019
Brazil	7985	21	0.956	0.009	0.012	0.006	0.008	0.004	0.004
Brazil	7986	10	0.911	0.033	0.006	0.017	0.009	0.018	0.007
Brazil	7987	5	0.84	0.01	0.012	0.096	0.032	0.006	0.004
Brazil	7988	2	0.821	0.045	0.013	0.071	0.02	0.01	0.021

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling	ID	Missing	Population						
Location	No.	Data	1	2	3	4	5	6	7
Brazil	7989	5	0.889	0.011	0.03	0.033	0.014	0.014	0.008
Brazil	7990	5	0.967	0.005	0.008	0.008	0.006	0.003	0.003
Finland	8077	23	0.961	0.006	0.004	0.003	0.017	0.003	0.006
Finland	8084	31	0.612	0.007	0.006	0.052	0.301	0.018	0.005
Finland	8086	13	0.914	0.027	0.006	0.004	0.04	0.004	0.005
Finland	8089	26	0.915	0.013	0.024	0.013	0.015	0.011	0.009
Finland	8093	18	0.441	0.046	0.006	0.003	0.499	0.003	0.003
Finland	8094	34	0.732	0.067	0.019	0.026	0.091	0.01	0.056
Finland	8096	23	0.555	0.019	0.007	0.005	0.402	0.004	0.008
Finland	8107	31	0.975	0.006	0.003	0.004	0.007	0.003	0.003
Finland	8110	28	0.213	0.029	0.006	0.109	0.622	0.009	0.011
Finland	8116	44	0.906	0.015	0.015	0.01	0.03	0.011	0.013
Finland	8120	28	0.685	0.033	0.004	0.005	0.254	0.01	0.01
Germany	8711	13	0.977	0.004	0.003	0.003	0.008	0.003	0.003
Germany	8712	2	0.946	0.004	0.008	0.011	0.007	0.01	0.014
Germany	8713	7	0.867	0.013	0.015	0.013	0.034	0.029	0.029
Germany	8714	5	0.933	0.009	0.004	0.01	0.028	0.005	0.012
Germany	8715	5	0.963	0.008	0.004	0.005	0.012	0.004	0.005
Germany	8716	2	0.966	0.008	0.005	0.004	0.011	0.003	0.004
Germany	8717	7	0.962	0.008	0.005	0.005	0.012	0.004	0.004
Germany	8720	5	0.398	0.007	0.004	0.569	0.007	0.01	0.004
Germany	8721	10	0.85	0.023	0.014	0.003	0.096	0.004	0.009
Germany	8727	7	0.719	0.162	0.011	0.008	0.091	0.004	0.005
Germany	8728	10	0.974	0.004	0.005	0.005	0.006	0.004	0.003
Germany	8729	7	0.975	0.007	0.003	0.003	0.008	0.002	0.002
Germany	8730	21	0.811	0.036	0.005	0.008	0.13	0.008	0.003
Germany	8731	13	0.933	0.016	0.004	0.005	0.032	0.006	0.004
Germany	8732	7	0.954	0.009	0.007	0.011	0.011	0.004	0.003
Germany	8733	23	0.907	0.007	0.048	0.007	0.015	0.008	0.007
Germany	8734	7	0.972	0.007	0.003	0.003	0.01	0.003	0.002
Germany	8735	7	0.936	0.006	0.002	0.01	0.038	0.004	0.003
Germany	8736	5	0.835	0.011	0.006	0.006	0.031	0.011	0.099
Germany	8737	10	0.709	0.016	0.025	0.019	0.201	0.013	0.016
Germany	8738	10	0.716	0.007	0.005	0.008	0.177	0.006	0.081
Germany	8739	7	0.952	0.005	0.015	0.006	0.015	0.004	0.004
Germany	8741	7	0.969	0.005	0.003	0.005	0.011	0.004	0.003
Germany	8742	7	0.968	0.004	0.002	0.004	0.012	0.007	0.003
Germany	8744	7	0.635	0.042	0.01	0.031	0.119	0.144	0.019
Germany	8745	26	0.779	0.025	0.01	0.01	0.163	0.005	0.007
Germany	8746	5	0.968	0.005	0.009	0.004	0.007	0.003	0.003
Germany	8747	18	0.957	0.009	0.004	0.008	0.012	0.008	0.003
Germany	8749	7	0.975	0.005	0.004	0.003	0.007	0.003	0.004
Italy-Milan	8050	5	0.469	0.016	0.005	0.053	0.166	0.271	0.019
Italy-Milan	8057	5	0.098	0.011	0.006	0.035	0.837	0.005	0.008
Italy-Milan	8060	2	0.65	0.074	0.03	0.021	0.215	0.006	0.005
Italy-Milan	8061	5	0.179	0.077	0.088	0.047	0.556	0.027	0.026
Italy-Milan	8062	10	0.412	0.195	0.013	0.012	0.349	0.013	0.006
Italy-Milan	8065	10	0.397	0.489	0.016	0.007	0.073	0.013	0.005
Italy-Milan	8066	2	0.873	0.005	0.008	0.068	0.037	0.005	0.004
Italy-Milan	8067	2	0.471	0.24	0.121	0.017	0.137	0.005	0.01
Italy-Milan	8068	7	0.126	0.061	0.012	0.015	0.773	0.008	0.006
Italy-Milan	8069	2	0.109	0.008	0.011	0.111	0.74	0.013	0.008
Italy-Milan	8071	5	0.933	0.011	0.02	0.007	0.017	0.007	0.005
Italy-Milan	8072	7	0.21	0.024	0.004	0.021	0.694	0.03	0.017
Italy-Milan	8073	5	0.612	0.081	0.003	0.064	0.205	0.014	0.021
Italy-Milan	8074	5	0.603	0.012	0.011	0.347	0.008	0.016	0.003

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling	ID	Missing	Population						
Location	No.	Data	1	2	3	4	5	6	7
Italy-Rome	8586	2	0.431	0.148	0.043	0.009	0.311	0.045	0.013
Italy-Rome	8589	7	0.633	0.103	0.007	0.012	0.187	0.053	0.005
Italy-Rome	8592	7	0.349	0.064	0.005	0.022	0.493	0.008	0.059
Italy-Rome	8594	2	0.728	0.017	0.007	0.014	0.165	0.006	0.064
Italy-Rome	8595	5	0.361	0.092	0.011	0.08	0.31	0.021	0.125
Italy-Rome	8596	2	0.481	0.135	0.016	0.011	0.31	0.039	0.009
Italy-Rome	8597	2	0.635	0.188	0.006	0.014	0.124	0.012	0.022
Italy-Rome	8599	5	0.609	0.27	0.003	0.016	0.045	0.052	0.004
Italy-Rome	8601	2	0.645	0.02	0.009	0.01	0.043	0.026	0.247
Italy-Rome	8602	5	0.616	0.104	0.007	0.011	0.243	0.008	0.01
Italy-Rome	8603	5	0.82	0.096	0.005	0.021	0.035	0.004	0.019
Italy-Rome	8604	7	0.602	0.012	0.01	0.019	0.107	0.23	0.02
Italy-Rome	8609	5	0.365	0.473	0.006	0.015	0.121	0.011	0.009
Italy-Rome	8610	7	0.672	0.037	0.008	0.005	0.27	0.005	0.004
Italy-Rome	8611	2	0.604	0.097	0.011	0.005	0.215	0.008	0.06
Turkey	6477	5	0.013	0.109	0.003	0.004	0.843	0.007	0.021
Turkey	6478	10	0.016	0.532	0.005	0.007	0.424	0.004	0.012
Turkey	6480	7	0.101	0.461	0.028	0.024	0.369	0.009	0.008
Turkey	6481	5	0.027	0.009	0.007	0.891	0.054	0.009	0.004
Turkey	6482	7	0.165	0.017	0.015	0.033	0.731	0.014	0.025
Turkey	6484	5	0.021	0.024	0.024	0.006	0.913	0.006	0.005
Turkey	6486	5	0.014	0.01	0.011	0.014	0.931	0.005	0.016
Turkey	6487	7	0.01	0.025	0.002	0.004	0.95	0.005	0.004
Turkey	6488	7	0.048	0.361	0.004	0.02	0.532	0.016	0.018
Turkey	6491	13	0.3	0.043	0.011	0.289	0.012	0.342	0.003
Turkey	6494	7	0.17	0.069	0.005	0.009	0.694	0.017	0.037
Turkey	6496	5	0.08	0.037	0.019	0.09	0.756	0.013	0.006
Turkey	6499	7	0.277	0.032	0.081	0.005	0.582	0.015	0.008
Turkey	6500	15	0.029	0.037	0.004	0.003	0.92	0.004	0.004
Turkey	6502	7	0.058	0.209	0.032	0.007	0.674	0.016	0.006
Turkey	6503	10	0.054	0.013	0.005	0.034	0.879	0.011	0.004
Turkey	6507	5	0.038	0.05	0.003	0.005	0.887	0.011	0.006
Turkey	6510	5	0.616	0.017	0.003	0.004	0.35	0.008	0.002
Turkey	6512	7	0.012	0.031	0.015	0.009	0.898	0.026	0.008
Turkey	6513	5	0.059	0.338	0.064	0.029	0.457	0.007	0.046
Turkey	6514	5	0.015	0.006	0.005	0.87	0.014	0.084	0.006
Turkey	6516	5	0.935	0.009	0.017	0.007	0.021	0.002	0.008
Turkey	6519	5	0.081	0.071	0.006	0.007	0.824	0.005	0.007
Turkey	6520	5	0.105	0.041	0.003	0.009	0.834	0.004	0.003
Turkey	6521	7	0.027	0.015	0.01	0.006	0.916	0.019	0.008
Turkey	6729	5	0.01	0.026	0.038	0.01	0.513	0.04	0.364
Turkey	6730	5	0.14	0.039	0.012	0.005	0.772	0.027	0.005
Turkey	6731	7	0.278	0.022	0.005	0.007	0.664	0.003	0.02
Turkey	6732	7	0.076	0.034	0.02	0.087	0.632	0.055	0.096
Turkey	6733	7	0.022	0.016	0.005	0.015	0.92	0.016	0.006
Turkey	6734	5	0.067	0.022	0.009	0.025	0.837	0.036	0.004
Turkey	6735	7	0.004	0.011	0.005	0.004	0.965	0.004	0.006
Turkey	6736	2	0.057	0.494	0.004	0.007	0.419	0.005	0.013
Turkey	6738	7	0.015	0.062	0.013	0.011	0.871	0.013	0.015
Turkey	6739	13	0.129	0.031	0.012	0.011	0.794	0.006	0.017
Turkey	6740	5	0.979	0.003	0.005	0.004	0.004	0.003	0.003
Turkey	6741	7	0.012	0.006	0.007	0.948	0.013	0.011	0.003
Turkey	6742	13	0.017	0.012	0.004	0.049	0.895	0.014	0.008
Turkey	6743	5	0.122	0.037	0.014	0.022	0.778	0.008	0.02
Turkey	6745	7	0.647	0.028	0.006	0.005	0.275	0.028	0.012
Turkey	6746	5	0.21	0.019	0.009	0.361	0.348	0.035	0.017

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling	ID	Missing	Population						
Location	No.	Data	1	2	3	4	5	6	7
Turkey	6748	10	0.081	0.213	0.011	0.012	0.668	0.005	0.009
Turkey	6749	10	0.737	0.016	0.002	0.006	0.183	0.008	0.048
Turkey	6750	5	0.156	0.018	0.007	0.003	0.811	0.003	0.002
Turkey	6753	10	0.041	0.031	0.007	0.043	0.768	0.076	0.033
Turkey	6754	10	0.016	0.007	0.004	0.005	0.93	0.003	0.034
Turkey	6755	10	0.265	0.167	0.004	0.012	0.515	0.027	0.011
Turkey	6756	10	0.214	0.021	0.005	0.004	0.748	0.003	0.005
Turkey	6758	13	0.045	0.054	0.007	0.009	0.83	0.03	0.025
Turkey	6759	13	0.021	0.108	0.012	0.012	0.833	0.01	0.004
Turkey	6760	7	0.121	0.014	0.023	0.006	0.826	0.005	0.007
Cyprus	10128	2	0.024	0.018	0.011	0.008	0.905	0.028	0.006
Cyprus	10129	5	0.176	0.174	0.012	0.005	0.624	0.003	0.005
Cyprus	10130	7	0.097	0.017	0.013	0.013	0.85	0.006	0.004
Cyprus	10131	2	0.016	0.258	0.006	0.175	0.516	0.013	0.015
Cyprus	10132	2	0.034	0.176	0.031	0.019	0.717	0.008	0.014
Cyprus	10133	15	0.046	0.032	0.015	0.009	0.88	0.005	0.014
Cyprus	10134	5	0.01	0.301	0.046	0.008	0.61	0.005	0.021
Cyprus	10135	5	0.028	0.565	0.062	0.075	0.251	0.015	0.004
Cyprus	10136	5	0.171	0.069	0.043	0.01	0.651	0.023	0.034
Cyprus	10137	2	0.034	0.061	0.007	0.005	0.592	0.023	0.278
Cyprus	10138	2	0.015	0.521	0.013	0.012	0.394	0.01	0.035
Cyprus	10139	2	0.011	0.524	0.031	0.295	0.08	0.018	0.041
Cyprus	10140	0	0.02	0.04	0.011	0.007	0.904	0.004	0.014
Cyprus	10141	5	0.469	0.128	0.013	0.008	0.343	0.013	0.025
Cyprus	10142	2	0.006	0.056	0.055	0.011	0.831	0.027	0.013
Cyprus	10143	5	0.015	0.596	0.005	0.004	0.352	0.011	0.016
Cyprus	10144	7	0.023	0.111	0.012	0.014	0.831	0.005	0.004
Cyprus	10145	5	0.021	0.018	0.003	0.003	0.946	0.004	0.005
Cyprus	10146	0	0.007	0.786	0.025	0.028	0.138	0.01	0.006
Cyprus	10147	5	0.013	0.016	0.004	0.004	0.957	0.002	0.003
Cyprus	10148	7	0.03	0.775	0.015	0.05	0.075	0.032	0.023
Cyprus	10149	7	0.191	0.066	0.044	0.009	0.502	0.011	0.178
Cyprus	10150	2	0.015	0.693	0.006	0.028	0.237	0.007	0.014
Cyprus	10151	2	0.012	0.029	0.004	0.012	0.909	0.011	0.022
Cyprus	10152	5	0.014	0.709	0.006	0.044	0.175	0.039	0.013
Cyprus	10153	0	0.007	0.013	0.004	0.007	0.951	0.008	0.009
Cyprus	10154	0	0.033	0.467	0.011	0.087	0.272	0.009	0.121
Cyprus	10155	5	0.009	0.034	0.086	0.029	0.826	0.011	0.005
Cyprus	10156	7	0.107	0.373	0.005	0.018	0.39	0.089	0.018
Cyprus	10157	2	0.008	0.908	0.006	0.006	0.045	0.006	0.021
Lebanon	10235	10	0.073	0.732	0.016	0.049	0.064	0.03	0.036
Lebanon	10236	13	0.019	0.036	0.014	0.035	0.84	0.041	0.014
Lebanon	10237	5	0.021	0.4	0.072	0.226	0.22	0.053	0.009
Lebanon	10238	5	0.01	0.82	0.012	0.029	0.073	0.009	0.047
Lebanon	10239	5	0.012	0.348	0.006	0.009	0.611	0.008	0.007
Lebanon	10240	15	0.02	0.216	0.009	0.089	0.615	0.024	0.027
Lebanon	10241	13	0.04	0.018	0.015	0.028	0.81	0.064	0.025
Lebanon	10242	7	0.049	0.281	0.024	0.009	0.607	0.005	0.026
Lebanon	10243	10	0.021	0.082	0.022	0.043	0.732	0.032	0.067
Lebanon	10244	5	0.013	0.065	0.012	0.035	0.76	0.035	0.08
Lebanon	10245	13	0.047	0.167	0.034	0.027	0.459	0.008	0.258
Lebanon	10246	2	0.01	0.905	0.009	0.011	0.045	0.003	0.016
Lebanon	10247	18	0.012	0.598	0.013	0.009	0.067	0.008	0.293
Lebanon	10248	7	0.1	0.804	0.024	0.005	0.055	0.005	0.007
Lebanon	10249	13	0.538	0.035	0.01	0.018	0.384	0.008	0.007
Lebanon	10250	2	0.026	0.046	0.007	0.005	0.786	0.017	0.113

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling	ID	Missing	Population						
Location	No.	Data	1	2	3	4	5	6	7
Lebanon	10251	2	0.094	0.793	0.012	0.007	0.08	0.004	0.01
Lebanon	10252	5	0.086	0.027	0.011	0.006	0.83	0.009	0.031
Lebanon	10253	15	0.041	0.854	0.005	0.003	0.088	0.004	0.006
Lebanon	10254	13	0.008	0.053	0.011	0.031	0.865	0.015	0.017
Lebanon	10255	7	0.05	0.648	0.01	0.015	0.1	0.018	0.16
Lebanon	10256	18	0.008	0.827	0.006	0.005	0.14	0.007	0.008
Lebanon	10257	5	0.004	0.114	0.048	0.02	0.74	0.013	0.062
Lebanon	10258	7	0.024	0.408	0.022	0.01	0.518	0.007	0.012
Lebanon	10259	10	0.078	0.066	0.017	0.791	0.032	0.008	0.008
Lebanon	10260	2	0.005	0.053	0.02	0.006	0.891	0.007	0.018
Lebanon	10261	10	0.047	0.225	0.008	0.011	0.634	0.011	0.064
Lebanon	10262	5	0.087	0.169	0.015	0.034	0.612	0.041	0.041
Lebanon	10263	7	0.008	0.424	0.005	0.022	0.528	0.005	0.008
Lebanon	10264	5	0.018	0.015	0.009	0.03	0.908	0.01	0.01
Lebanon	10265	7	0.014	0.428	0.007	0.007	0.428	0.007	0.109
Lebanon	10266	0	0.032	0.736	0.03	0.105	0.073	0.012	0.012
Lebanon	10267	18	0.099	0.575	0.004	0.007	0.303	0.006	0.006
Lebanon	10268	5	0.025	0.781	0.01	0.042	0.128	0.011	0.003
Lebanon	10270	13	0.023	0.58	0.012	0.184	0.049	0.065	0.088
Lebanon	10271	18	0.18	0.011	0.049	0.082	0.545	0.026	0.107
Lebanon	10273	10	0.186	0.116	0.019	0.029	0.567	0.039	0.044
Lebanon	10274	13	0.027	0.164	0.037	0.53	0.204	0.032	0.007
Lebanon	10276	10	0.011	0.887	0.007	0.022	0.062	0.003	0.008
Lebanon	10277	2	0.072	0.27	0.005	0.02	0.43	0.162	0.04
Lebanon	10278	15	0.023	0.208	0.067	0.011	0.645	0.035	0.011
Lebanon	10279	0	0.008	0.066	0.026	0.031	0.837	0.007	0.025
Lebanon	10280	0	0.021	0.061	0.044	0.232	0.589	0.015	0.038
Lebanon	10281	10	0.007	0.424	0.007	0.007	0.509	0.008	0.038
Lebanon	10282	10	0.01	0.753	0.011	0.062	0.142	0.007	0.016
Lebanon	10283	23	0.007	0.012	0.077	0.005	0.888	0.005	0.006
Lebanon	10284	23	0.032	0.125	0.213	0.036	0.514	0.022	0.057
Lebanon	10285	2	0.035	0.131	0.017	0.019	0.676	0.111	0.011
Lebanon	10286	15	0.009	0.088	0.007	0.169	0.446	0.013	0.268
Lebanon	10287	5	0.142	0.04	0.036	0.08	0.629	0.043	0.03
Lebanon	10288	13	0.949	0.017	0.003	0.005	0.018	0.007	0.002
Lebanon	10289	13	0.008	0.547	0.008	0.019	0.389	0.007	0.022
Lebanon	10290	5	0.008	0.077	0.236	0.082	0.484	0.089	0.023
Lebanon	10291	15	0.011	0.089	0.03	0.013	0.69	0.045	0.122
Lebanon	10292	13	0.013	0.028	0.032	0.161	0.681	0.028	0.057
Lebanon	10294	2	0.066	0.289	0.023	0.095	0.455	0.025	0.047
Lebanon	10295	7	0.055	0.594	0.066	0.033	0.167	0.018	0.067
Lebanon	10297	5	0.01	0.027	0.007	0.015	0.813	0.021	0.108
Lebanon	10298	10	0.013	0.108	0.061	0.036	0.249	0.021	0.51
Lebanon	10299	2	0.246	0.057	0.208	0.034	0.342	0.083	0.03
Lebanon	10300	2	0.008	0.03	0.005	0.028	0.893	0.009	0.027
Israel	4962	7	0.009	0.029	0.013	0.008	0.904	0.004	0.034
Israel	4963	5	0.007	0.021	0.006	0.02	0.92	0.014	0.012
Israel	4964	7	0.201	0.042	0.006	0.016	0.693	0.009	0.033
Israel	4966	5	0.017	0.139	0.025	0.022	0.785	0.005	0.006
Israel	4967	5	0.052	0.021	0.019	0.015	0.784	0.097	0.012
Israel	4968	7	0.009	0.011	0.008	0.025	0.912	0.022	0.013
Israel	4969	2	0.076	0.014	0.015	0.022	0.831	0.032	0.01
Israel	4970	7	0.026	0.018	0.013	0.045	0.867	0.012	0.02
Israel	4971	2	0.006	0.005	0.006	0.014	0.929	0.022	0.019
Israel	4972	10	0.013	0.009	0.046	0.007	0.903	0.015	0.006
Israel	4973	5	0.006	0.009	0.026	0.005	0.942	0.006	0.005

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling Location	ID No.	Missing Data	Population						
			1	2	3	4	5	6	7
Israel	4974	5	0.015	0.009	0.006	0.012	0.945	0.005	0.009
Israel	4975	2	0.015	0.01	0.004	0.011	0.949	0.004	0.006
Israel	4976	5	0.072	0.037	0.04	0.021	0.817	0.004	0.009
Israel	4977	15	0.067	0.016	0.006	0.006	0.89	0.004	0.012
Israel	4978	10	0.017	0.005	0.009	0.013	0.928	0.007	0.021
Israel	4979	7	0.012	0.023	0.005	0.005	0.941	0.007	0.007
Israel	4980	2	0.084	0.093	0.011	0.118	0.458	0.106	0.129
Israel	4981	15	0.009	0.22	0.006	0.009	0.588	0.136	0.032
Israel	4982	10	0.066	0.008	0.014	0.019	0.882	0.006	0.005
Israel	4983	7	0.784	0.019	0.005	0.072	0.035	0.06	0.025
Israel	4984	2	0.924	0.006	0.005	0.029	0.009	0.022	0.005
Israel	4985	21	0.009	0.028	0.005	0.084	0.851	0.014	0.009
Israel	4986	5	0.004	0.008	0.007	0.005	0.959	0.009	0.008
Israel	4988	13	0.009	0.013	0.015	0.013	0.919	0.012	0.019
Israel	4989	5	0.006	0.141	0.005	0.137	0.647	0.009	0.055
Israel	4990	5	0.015	0.06	0.003	0.058	0.839	0.016	0.008
Israel	4992	7	0.018	0.009	0.005	0.005	0.956	0.004	0.004
Israel	4993	7	0.006	0.009	0.028	0.004	0.941	0.005	0.006
Israel	4994	5	0.004	0.008	0.003	0.003	0.974	0.004	0.003
Israel	4995	5	0.009	0.031	0.003	0.063	0.849	0.01	0.034
Israel	4996	2	0.009	0.149	0.003	0.01	0.803	0.014	0.013
Israel	4997	15	0.006	0.036	0.005	0.023	0.873	0.007	0.049
Israel	4998	10	0.034	0.011	0.005	0.018	0.916	0.007	0.01
Israel	5000	7	0.011	0.039	0.01	0.16	0.758	0.011	0.011
Israel	5001	5	0.041	0.049	0.006	0.014	0.856	0.007	0.028
Israel	5002	7	0.028	0.068	0.025	0.01	0.855	0.007	0.007
Israel	5003	7	0.023	0.019	0.012	0.005	0.914	0.019	0.007
Israel	5004	15	0.172	0.035	0.014	0.11	0.651	0.008	0.011
Israel	5005	7	0.022	0.017	0.011	0.01	0.927	0.004	0.008
Israel	5006	10	0.014	0.057	0.005	0.004	0.908	0.005	0.007
Israel	5007	5	0.208	0.034	0.027	0.071	0.463	0.192	0.005
Israel	5008	5	0.018	0.223	0.037	0.008	0.682	0.008	0.024
Israel	5009	13	0.277	0.138	0.006	0.106	0.371	0.034	0.067
Israel	5010	15	0.01	0.023	0.004	0.004	0.951	0.004	0.004
Israel	5011	13	0.019	0.011	0.009	0.012	0.926	0.006	0.016
Egypt-Cairo	8190	15	0.045	0.903	0.022	0.009	0.011	0.005	0.006
Egypt-Cairo	8192	18	0.1	0.682	0.066	0.077	0.027	0.012	0.037
Egypt-Cairo	8193	18	0.007	0.895	0.013	0.005	0.054	0.004	0.023
Egypt-Cairo	8196	15	0.009	0.875	0.008	0.038	0.041	0.021	0.009
Egypt-Cairo	8203	15	0.014	0.886	0.004	0.031	0.037	0.022	0.006
Egypt-Cairo	8215	10	0.005	0.955	0.003	0.007	0.021	0.004	0.005
Egypt-Cairo	8198	10	0.055	0.872	0.026	0.009	0.017	0.011	0.01
Egypt-Cairo	8194	7	0.101	0.82	0.025	0.008	0.023	0.013	0.01
Egypt-Cairo	8211	5	0.014	0.384	0.005	0.008	0.555	0.008	0.026
Egypt-Cairo	8216	7	0.312	0.633	0.01	0.006	0.023	0.008	0.009
Egypt-Cairo	8195	5	0.011	0.708	0.028	0.039	0.15	0.04	0.024
Egypt-Cairo	8199	2	0.005	0.917	0.041	0.007	0.022	0.004	0.005
Egypt-Cairo	8200	5	0.04	0.351	0.003	0.004	0.581	0.007	0.013
Egypt-Cairo	8201	5	0.014	0.036	0.042	0.009	0.729	0.095	0.076
Egypt-Cairo	8202	5	0.018	0.045	0.008	0.886	0.018	0.011	0.015
Egypt-Cairo	8204	5	0.019	0.781	0.009	0.031	0.139	0.016	0.006
Egypt-Cairo	8208	2	0.111	0.69	0.011	0.017	0.09	0.069	0.012
Egypt-Cairo	8210	5	0.007	0.86	0.019	0.02	0.053	0.004	0.037
Egypt-Cairo	8214	2	0.004	0.976	0.003	0.003	0.006	0.004	0.004
Egypt-Cairo	8191	5	0.034	0.534	0.018	0.032	0.254	0.083	0.046
Egypt-Cairo	8197	2	0.006	0.698	0.108	0.017	0.14	0.007	0.024

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling Location	ID No.	Missing Data	Population						
			1	2	3	4	5	6	7
Egypt-Cairo	8205	2	0.088	0.597	0.009	0.055	0.224	0.018	0.008
Egypt-Cairo	8206	2	0.068	0.744	0.008	0.031	0.134	0.01	0.006
Egypt-Cairo	8207	2	0.014	0.913	0.034	0.012	0.008	0.014	0.006
Egypt-Cairo	8209	2	0.075	0.824	0.003	0.004	0.082	0.007	0.005
Egypt-Cairo	8212	2	0.004	0.976	0.002	0.004	0.005	0.005	0.005
Egypt-Cairo	8213	2	0.007	0.968	0.003	0.004	0.007	0.005	0.006
Egypt-Cairo	9942	0	0.009	0.678	0.006	0.017	0.03	0.022	0.239
Egypt-Cairo	9943	15	0.2	0.006	0.003	0.669	0.006	0.109	0.007
Egypt-Cairo	9944	7	0.051	0.753	0.006	0.007	0.151	0.003	0.03
Egypt-Cairo	9945	2	0.107	0.845	0.007	0.009	0.015	0.006	0.01
Egypt-Cairo	9946	13	0.017	0.514	0.061	0.06	0.283	0.039	0.027
Egypt-Cairo	9947	7	0.018	0.868	0.019	0.007	0.05	0.007	0.03
Egypt-Cairo	9948	0	0.035	0.908	0.005	0.012	0.026	0.008	0.006
Egypt-Cairo	9949	0	0.029	0.917	0.007	0.01	0.018	0.011	0.008
Egypt-Cairo	9950	0	0.085	0.578	0.046	0.026	0.24	0.015	0.01
Egypt-Cairo	9951	5	0.009	0.055	0.012	0.005	0.907	0.008	0.003
Egypt-Cairo	9952	15	0.159	0.104	0.01	0.008	0.705	0.007	0.008
Egypt-Cairo	9953	21	0.06	0.048	0.008	0.01	0.828	0.005	0.041
Egypt-Cairo	9954	2	0.013	0.132	0.028	0.008	0.715	0.099	0.005
Egypt-Cairo	9955	0	0.506	0.166	0.006	0.212	0.077	0.027	0.005
Egypt-Cairo	9956	18	0.018	0.141	0.007	0.007	0.783	0.034	0.01
Egypt-Cairo	9957	5	0.014	0.886	0.005	0.011	0.011	0.066	0.006
Egypt-Cairo	9958	15	0.04	0.808	0.045	0.015	0.056	0.032	0.005
Egypt-Cairo	9959	5	0.137	0.093	0.006	0.065	0.663	0.017	0.017
Egypt-Cairo	9960	2	0.025	0.807	0.004	0.009	0.064	0.03	0.061
Egypt-Cairo	9961	5	0.066	0.319	0.006	0.556	0.027	0.018	0.008
Egypt-Cairo	9962	7	0.017	0.724	0.106	0.008	0.071	0.009	0.065
Egypt-Cairo	9963	2	0.031	0.808	0.032	0.01	0.096	0.014	0.008
Egypt-Cairo	9964	0	0.021	0.913	0.004	0.022	0.027	0.007	0.005
Egypt-Cairo	10021	0	0.005	0.96	0.01	0.004	0.009	0.004	0.007
Egypt-Cairo	10022	0	0.016	0.939	0.005	0.008	0.014	0.015	0.004
Egypt-Cairo	10023	0	0.005	0.947	0.007	0.012	0.019	0.006	0.003
Egypt-Cairo	10024	0	0.064	0.875	0.006	0.005	0.035	0.009	0.007
Egypt-Cairo	10025	0	0.04	0.035	0.006	0.009	0.891	0.003	0.015
Egypt-Cairo	10026	2	0.02	0.603	0.019	0.005	0.309	0.038	0.007
Egypt-Cairo	10027	0	0.063	0.649	0.223	0.022	0.02	0.01	0.012
Egypt-Cairo	10028	0	0.004	0.952	0.006	0.006	0.01	0.007	0.016
Egypt-Cairo	10029	0	0.004	0.968	0.006	0.003	0.006	0.004	0.01
Egypt-Cairo	10030	0	0.046	0.879	0.004	0.01	0.04	0.014	0.006
Egypt-Cairo	10031	2	0.003	0.961	0.01	0.004	0.007	0.003	0.012
Egypt-Cairo	10032	0	0.004	0.964	0.005	0.004	0.005	0.003	0.014
Egypt-Cairo	10033	2	0.004	0.95	0.008	0.01	0.016	0.009	0.004
Egypt-Cairo	10034	0	0.006	0.967	0.008	0.004	0.007	0.004	0.004
Egypt-Cairo	10035	0	0.007	0.763	0.086	0.009	0.021	0.107	0.007
Egypt-Cairo	10037	5	0.054	0.842	0.068	0.009	0.012	0.006	0.008
Egypt-Cairo	10042	0	0.031	0.747	0.035	0.034	0.108	0.018	0.027
Egypt-Cairo	10043	7	0.032	0.892	0.005	0.012	0.047	0.003	0.008
Egypt-Cairo	10044	2	0.014	0.934	0.005	0.008	0.027	0.006	0.005
Egypt-Cairo	10045	2	0.011	0.929	0.02	0.012	0.013	0.008	0.008
Egypt-Cairo	10046	0	0.017	0.912	0.006	0.022	0.018	0.021	0.004
Egypt-Cairo	10047	0	0.009	0.938	0.004	0.015	0.01	0.012	0.013
Egypt-Cairo	10048	2	0.031	0.927	0.005	0.013	0.012	0.011	0.002
Egypt-Cairo	10083	21	0.057	0.684	0.006	0.013	0.228	0.007	0.005
Egypt-Cairo	10040	0	0.301	0.252	0.024	0.019	0.365	0.027	0.011
Egypt-Cairo	10041	0	0.4	0.331	0.02	0.018	0.203	0.022	0.007
Egypt-Cairo	10049	5	0.015	0.901	0.011	0.016	0.02	0.015	0.022

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling Location	ID No.	Missing Data	Population						
			1	2	3	4	5	6	7
Egypt-Cairo	10084	2	0.012	0.456	0.037	0.015	0.461	0.01	0.009
Egypt-Cairo	10085	23	0.047	0.321	0.052	0.02	0.544	0.009	0.008
Egypt-Cairo	10087	5	0.007	0.936	0.005	0.005	0.04	0.005	0.002
Egypt-Cairo	10090	7	0.017	0.667	0.029	0.02	0.214	0.046	0.008
Egypt-Cairo	9968	0	0.022	0.929	0.01	0.007	0.014	0.004	0.014
Egypt-Asuit	10091	2	0.015	0.955	0.003	0.006	0.012	0.005	0.004
Egypt-Asuit	10093	0	0.008	0.966	0.012	0.003	0.005	0.004	0.003
Egypt-Asuit	10094	5	0.007	0.963	0.008	0.007	0.007	0.005	0.004
Egypt-Asuit	10095	2	0.009	0.927	0.009	0.008	0.033	0.003	0.01
Egypt-Asuit	10096	0	0.007	0.967	0.004	0.005	0.006	0.008	0.003
Egypt-Asuit	10098	0	0.005	0.974	0.006	0.003	0.005	0.004	0.003
Egypt-Asuit	10099	5	0.004	0.968	0.011	0.003	0.006	0.005	0.003
Egypt-Asuit	10100	2	0.069	0.321	0.182	0.015	0.315	0.069	0.03
Egypt-Asuit	10101	2	0.011	0.901	0.01	0.012	0.025	0.02	0.021
Egypt-Asuit	10102	0	0.005	0.742	0.007	0.215	0.013	0.011	0.007
Egypt-Luxor	10038	0	0.008	0.928	0.006	0.017	0.011	0.026	0.005
Egypt-Luxor	10039	2	0.005	0.96	0.004	0.003	0.007	0.003	0.019
Egypt-Luxor	10050	2	0.009	0.887	0.019	0.014	0.017	0.043	0.01
Egypt-Luxor	10051	0	0.008	0.934	0.011	0.005	0.036	0.003	0.004
Egypt-Luxor	10052	0	0.012	0.882	0.016	0.049	0.023	0.009	0.009
Egypt-Luxor	10053	0	0.023	0.419	0.016	0.023	0.449	0.004	0.066
Egypt-Luxor	10054	0	0.015	0.858	0.003	0.013	0.022	0.081	0.008
Egypt-Luxor	10055	0	0.01	0.917	0.025	0.006	0.029	0.005	0.008
Egypt-Luxor	10056	0	0.006	0.919	0.01	0.006	0.014	0.03	0.015
Egypt-Luxor	10057	7	0.016	0.632	0.007	0.019	0.223	0.033	0.07
Egypt-Luxor	10058	0	0.01	0.949	0.01	0.003	0.016	0.006	0.006
Egypt-Luxor	10060	0	0.033	0.195	0.01	0.005	0.741	0.009	0.007
Egypt-Luxor	10061	0	0.012	0.479	0.03	0.044	0.013	0.417	0.005
Egypt-Luxor	10062	5	0.036	0.901	0.007	0.007	0.028	0.016	0.007
Egypt-Luxor	10063	2	0.022	0.642	0.028	0.023	0.188	0.016	0.082
Egypt-Luxor	10064	0	0.013	0.72	0.206	0.01	0.031	0.013	0.007
Egypt-Luxor	10065	0	0.024	0.729	0.204	0.013	0.015	0.005	0.009
Egypt-Luxor	10066	2	0.032	0.856	0.038	0.014	0.015	0.037	0.008
Egypt-Luxor	10067	2	0.006	0.931	0.006	0.005	0.032	0.003	0.016
Egypt-Luxor	10068	0	0.011	0.806	0.006	0.038	0.041	0.095	0.003
Egypt-Luxor	10069	2	0.007	0.936	0.018	0.008	0.018	0.005	0.008
Egypt-Luxor	10070	0	0.015	0.5	0.027	0.041	0.012	0.4	0.005
Egypt-Luxor	10071	2	0.012	0.575	0.015	0.034	0.223	0.123	0.018
Egypt-Luxor	10072	2	0.008	0.867	0.009	0.005	0.073	0.032	0.006
Egypt-Luxor	10073	5	0.926	0.038	0.008	0.008	0.01	0.006	0.005
Egypt-Luxor	10074	0	0.007	0.785	0.008	0.004	0.185	0.007	0.004
Egypt-Luxor	10079	0	0.088	0.607	0.011	0.191	0.09	0.004	0.009
Egypt-Luxor	10080	0	0.044	0.55	0.314	0.033	0.038	0.012	0.009
Egypt-Abu Simbel	10076	5	0.015	0.81	0.027	0.015	0.074	0.054	0.006
Egypt-Abu Simbel	10077	13	0.005	0.906	0.017	0.036	0.017	0.013	0.005
Egypt-Abu Simbel	10081	7	0.013	0.655	0.023	0.016	0.268	0.018	0.007
Egypt-Abu Simbel	10089	0	0.116	0.761	0.027	0.004	0.086	0.003	0.003
Egypt-Abu Simbel	10092	0	0.005	0.957	0.01	0.004	0.011	0.008	0.004
Iraq-West	9587	0	0.02	0.056	0.017	0.096	0.062	0.012	0.736
Iraq-West	10202	23	0.01	0.012	0.006	0.012	0.316	0.009	0.636
Iraq-West	10204	23	0.037	0.102	0.009	0.008	0.086	0.004	0.754
Iraq-West	11854	0	0.007	0.027	0.003	0.009	0.041	0.025	0.888
Iraq-West	11860	21	0.004	0.012	0.012	0.06	0.013	0.005	0.892
Iraq-West	11861	7	0.011	0.082	0.012	0.009	0.107	0.246	0.534
Iraq-West	11863	21	0.016	0.006	0.006	0.01	0.009	0.011	0.943
Iraq-West	11864	2	0.005	0.018	0.006	0.026	0.022	0.023	0.9

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling Location	ID No.	Missing Data	Population						
			1	2	3	4	5	6	7
Iraq-West	11888	5	0.003	0.004	0.122	0.007	0.005	0.01	0.85
Iraq-West	11889	7	0.187	0.014	0.012	0.017	0.058	0.012	0.7
Iraq-West	11890	2	0.008	0.231	0.041	0.008	0.016	0.068	0.629
Iraq-West	11891	0	0.019	0.06	0.01	0.007	0.282	0.007	0.616
Iraq-Baghdad	11847	5	0.01	0.038	0.006	0.022	0.082	0.01	0.832
Iraq-Baghdad	11848	0	0.01	0.013	0.011	0.111	0.015	0.059	0.78
Iraq-Baghdad	11849	5	0.01	0.127	0.004	0.047	0.017	0.033	0.761
Iraq-Baghdad	11850	0	0.039	0.016	0.004	0.015	0.011	0.016	0.899
Iraq-Baghdad	11852	0	0.01	0.02	0.057	0.021	0.025	0.013	0.854
Iraq-Baghdad	11853	5	0.006	0.015	0.008	0.026	0.014	0.017	0.913
Iraq-Baghdad	11855	5	0.006	0.013	0.067	0.015	0.062	0.013	0.824
Iraq-Baghdad	11856	2	0.027	0.026	0.016	0.012	0.072	0.005	0.844
Iraq-Baghdad	11857	0	0.173	0.156	0.007	0.011	0.084	0.011	0.558
Iraq-Baghdad	11858	2	0.008	0.008	0.004	0.01	0.011	0.005	0.954
Iraq-Baghdad	11859	5	0.02	0.035	0.014	0.036	0.038	0.011	0.846
Iraq-Baghdad	11862	2	0.059	0.033	0.013	0.011	0.062	0.262	0.561
Iraq-Baghdad	11865	5	0.007	0.07	0.008	0.08	0.067	0.147	0.62
Iraq-Baghdad	11868	2	0.005	0.008	0.008	0.006	0.009	0.006	0.958
Iraq-Baghdad	11869	2	0.116	0.024	0.007	0.009	0.228	0.018	0.598
Iraq-Baghdad	11870	0	0.031	0.146	0.004	0.025	0.039	0.077	0.679
Iraq-Baghdad	11871	5	0.006	0.361	0.015	0.031	0.067	0.008	0.513
Iraq-Baghdad	11872	2	0.016	0.169	0.014	0.007	0.082	0.004	0.707
Iraq-Baghdad	11873	7	0.005	0.369	0.016	0.01	0.045	0.028	0.526
Iraq-Baghdad	11874	2	0.01	0.029	0.008	0.007	0.053	0.048	0.847
Iraq-Baghdad	11875	15	0.008	0.007	0.062	0.124	0.016	0.175	0.608
Iraq-Baghdad	11876	21	0.009	0.06	0.038	0.033	0.035	0.018	0.808
Iraq-Baghdad	11877	7	0.008	0.048	0.054	0.006	0.017	0.047	0.82
Iraq-Baghdad	11878	7	0.027	0.064	0.005	0.015	0.373	0.009	0.508
Iraq-Baghdad	11879	2	0.007	0.022	0.012	0.187	0.018	0.015	0.74
Iraq-Baghdad	11880	10	0.008	0.043	0.015	0.01	0.03	0.007	0.886
Iraq-Baghdad	11881	0	0.046	0.071	0.011	0.016	0.158	0.079	0.62
Iraq-Baghdad	11882	15	0.012	0.075	0.007	0.012	0.067	0.013	0.815
Iraq-Baghdad	11883	0	0.041	0.006	0.011	0.008	0.327	0.008	0.598
Iraq-Baghdad	11884	0	0.004	0.004	0.006	0.009	0.005	0.01	0.962
Iraq-Baghdad	11885	0	0.003	0.017	0.004	0.012	0.012	0.008	0.943
Iraq-Baghdad	11886	0	0.008	0.131	0.01	0.041	0.126	0.075	0.609
Iraq-Baghdad	11887	13	0.012	0.092	0.027	0.021	0.014	0.035	0.799
Iran	9419	2	0.091	0.034	0.009	0.008	0.046	0.032	0.779
Iran	9420	2	0.005	0.013	0.01	0.013	0.008	0.094	0.855
Iran	9421	5	0.01	0.013	0.005	0.005	0.012	0.01	0.945
Iran	9422	5	0.013	0.065	0.005	0.01	0.054	0.11	0.742
Iran	9424	7	0.004	0.005	0.002	0.013	0.004	0.092	0.88
Iran	9425	7	0.002	0.004	0.005	0.006	0.004	0.011	0.968
Iran	9426	2	0.009	0.006	0.041	0.004	0.005	0.008	0.927
Iran	9427	2	0.008	0.006	0.012	0.005	0.008	0.004	0.958
Iran	9428	5	0.006	0.006	0.003	0.007	0.005	0.007	0.967
Iran	9429	15	0.012	0.025	0.05	0.022	0.015	0.065	0.811
Iran	9430	7	0.012	0.009	0.01	0.027	0.064	0.034	0.843
Iran	9431	7	0.012	0.062	0.013	0.106	0.017	0.053	0.738
Iran	9432	13	0.004	0.004	0.048	0.01	0.005	0.005	0.924
Iran	9433	5	0.007	0.007	0.006	0.01	0.011	0.025	0.933
Iran	9434	7	0.033	0.01	0.006	0.096	0.014	0.084	0.757
Iran	9435	5	0.007	0.006	0.017	0.028	0.005	0.011	0.925
Iran	9436	2	0.006	0.007	0.005	0.006	0.013	0.006	0.958
Iran	9437	2	0.007	0.009	0.008	0.011	0.012	0.006	0.948
Iran	9438	2	0.005	0.004	0.011	0.013	0.004	0.01	0.953

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling Location	ID No.	Missing Data	Population						
			1	2	3	4	5	6	7
Iran	9439	5	0.02	0.023	0.016	0.034	0.049	0.115	0.744
Iran	9440	2	0.003	0.009	0.014	0.006	0.008	0.003	0.958
Iran	9441	7	0.003	0.004	0.009	0.005	0.004	0.004	0.971
Iran	9442	5	0.019	0.013	0.067	0.033	0.012	0.009	0.846
Iran	9443	10	0.009	0.006	0.008	0.01	0.008	0.009	0.951
Iran	9444	5	0.002	0.003	0.002	0.003	0.004	0.004	0.981
Iran	9445	5	0.002	0.002	0.003	0.004	0.002	0.003	0.983
Iran	9446	10	0.004	0.004	0.007	0.007	0.003	0.009	0.965
Iran	9447	7	0.007	0.005	0.011	0.006	0.003	0.005	0.963
Iran	9448	13	0.003	0.003	0.005	0.005	0.004	0.003	0.977
Iran	9449	5	0.003	0.003	0.002	0.003	0.003	0.002	0.985
Iran	9450	7	0.004	0.012	0.005	0.005	0.007	0.017	0.95
Iran	9451	10	0.005	0.008	0.004	0.02	0.009	0.061	0.893
Iran	9452	2	0.006	0.005	0.005	0.023	0.006	0.006	0.949
Iran	9453	7	0.005	0.005	0.004	0.003	0.004	0.003	0.977
Iran	9454	7	0.003	0.005	0.003	0.004	0.004	0.003	0.979
Iran	9455	13	0.006	0.008	0.011	0.01	0.006	0.006	0.952
Iran	9456	2	0.011	0.009	0.006	0.018	0.012	0.013	0.932
Iran	9457	5	0.004	0.007	0.004	0.004	0.005	0.003	0.973
Iran	9458	2	0.004	0.007	0.006	0.009	0.006	0.01	0.958
Iran	9459	5	0.003	0.003	0.009	0.004	0.003	0.004	0.974
Iran	9460	10	0.016	0.01	0.047	0.008	0.012	0.009	0.899
Iran	9461	10	0.004	0.003	0.004	0.008	0.004	0.004	0.973
Iran	9462	10	0.012	0.006	0.014	0.017	0.007	0.006	0.938
Iran	9463	15	0.004	0.007	0.007	0.006	0.01	0.006	0.959
Iran	9464	7	0.003	0.005	0.004	0.005	0.004	0.008	0.972
Iran	9465	5	0.006	0.007	0.004	0.009	0.005	0.003	0.966
Iran	9466	13	0.01	0.017	0.048	0.008	0.013	0.004	0.901
Iran	9468	10	0.02	0.009	0.006	0.009	0.02	0.021	0.914
Iran	9469	10	0.02	0.021	0.02	0.035	0.017	0.024	0.863
Iran	9470	13	0.015	0.013	0.006	0.018	0.011	0.014	0.923
Iran	9471	7	0.007	0.005	0.004	0.007	0.009	0.004	0.964
Iran	9472	10	0.004	0.01	0.006	0.007	0.008	0.007	0.957
Iran	9473	5	0.004	0.004	0.008	0.006	0.005	0.007	0.967
Iran	9474	7	0.007	0.01	0.035	0.005	0.008	0.004	0.931
Iran	9475	7	0.006	0.008	0.008	0.005	0.01	0.003	0.96
Iran	9476	7	0.003	0.003	0.003	0.002	0.004	0.008	0.976
Iran	9477	7	0.009	0.006	0.003	0.009	0.008	0.043	0.922
Iran	9478	5	0.008	0.008	0.065	0.058	0.026	0.021	0.815
Iran	9479	7	0.002	0.003	0.003	0.004	0.003	0.009	0.977
Iran	9480	13	0.008	0.005	0.005	0.019	0.008	0.012	0.942
Iran	9481	10	0.005	0.015	0.01	0.004	0.006	0.006	0.954
Iran	9482	5	0.013	0.023	0.007	0.024	0.023	0.03	0.88
Iran	9483	13	0.009	0.008	0.006	0.056	0.015	0.175	0.732
Iran	9484	2	0.033	0.128	0.005	0.01	0.132	0.005	0.688
Iran	9485	10	0.004	0.007	0.008	0.011	0.01	0.081	0.877
Iran	9486	10	0.02	0.008	0.006	0.007	0.01	0.005	0.944
Iran	9487	5	0.004	0.006	0.013	0.015	0.006	0.008	0.948
Iran	9488	10	0.006	0.008	0.003	0.006	0.007	0.005	0.964
Iran	9489	15	0.005	0.007	0.035	0.022	0.008	0.006	0.916
Iran	9490	13	0.005	0.003	0.006	0.01	0.005	0.009	0.962
Iran	9491	7	0.003	0.003	0.004	0.003	0.004	0.005	0.979
Iran	9492	10	0.005	0.005	0.005	0.01	0.004	0.003	0.968
Iran	9493	2	0.005	0.006	0.005	0.008	0.004	0.015	0.956
Iran	9494	7	0.004	0.007	0.003	0.004	0.011	0.003	0.968
Iran	9495	5	0.004	0.003	0.013	0.006	0.004	0.005	0.964

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling Location	ID No.	Missing Data	Population						
			1	2	3	4	5	6	7
Iran	9497	10	0.004	0.004	0.056	0.004	0.004	0.004	0.924
Iran	9498	10	0.004	0.005	0.005	0.005	0.006	0.008	0.967
Iran	9499	5	0.005	0.007	0.011	0.012	0.007	0.071	0.888
Iran	9500	7	0.003	0.003	0.012	0.008	0.003	0.004	0.968
Iran	9501	2	0.036	0.027	0.034	0.031	0.023	0.006	0.842
Iran	9502	5	0.006	0.009	0.003	0.007	0.011	0.228	0.736
Iran	9503	7	0.003	0.003	0.007	0.009	0.003	0.005	0.971
Iran	9504	5	0.003	0.003	0.002	0.002	0.004	0.003	0.983
Iran	9505	5	0.002	0.002	0.002	0.002	0.002	0.005	0.985
Iran	9506	7	0.015	0.006	0.027	0.027	0.008	0.008	0.91
Iran	9507	31	0.01	0.038	0.039	0.015	0.011	0.036	0.852
Iran	9508	10	0.004	0.006	0.02	0.012	0.008	0.092	0.858
Iran	9509	18	0.006	0.005	0.005	0.008	0.01	0.031	0.934
Iran	9510	15	0.005	0.004	0.01	0.005	0.006	0.049	0.921
Iran	9511	13	0.014	0.005	0.005	0.004	0.007	0.005	0.96
Iran	9512	28	0.069	0.014	0.099	0.009	0.031	0.011	0.768
Iran	9513	21	0.008	0.006	0.012	0.007	0.019	0.005	0.943
Iran	9514	15	0.024	0.057	0.033	0.021	0.106	0.012	0.748
Iran	9515	13	0.167	0.007	0.018	0.016	0.007	0.006	0.78
Iran	9516	15	0.009	0.008	0.081	0.011	0.01	0.006	0.876
Iran	9517	13	0.027	0.012	0.009	0.053	0.028	0.056	0.814
Iran	9518	13	0.172	0.022	0.02	0.02	0.041	0.018	0.708
Iran	9519	18	0.05	0.01	0.009	0.011	0.016	0.005	0.9
Iran	9520	15	0.063	0.014	0.085	0.009	0.013	0.004	0.812
Iran	9521	21	0.009	0.009	0.132	0.02	0.008	0.006	0.816
Iran	9522	15	0.024	0.069	0.006	0.036	0.191	0.048	0.626
Iran	9523	13	0.021	0.081	0.025	0.008	0.043	0.008	0.814
Iran	9524	15	0.004	0.006	0.004	0.008	0.005	0.046	0.928
Iran	9526	15	0.004	0.006	0.006	0.01	0.006	0.091	0.877
Iran	9527	13	0.015	0.014	0.024	0.042	0.025	0.022	0.859
Iran	9528	15	0.004	0.003	0.004	0.005	0.003	0.005	0.977
Iran	9529	15	0.002	0.003	0.005	0.022	0.003	0.025	0.938
Iran	9530	10	0.006	0.006	0.006	0.007	0.006	0.032	0.936
Iran	9531	15	0.025	0.038	0.05	0.031	0.032	0.02	0.804
Iran	9532	5	0.004	0.004	0.004	0.005	0.006	0.004	0.973
Dubai	10104	2	0.009	0.053	0.676	0.017	0.021	0.003	0.222
Dubai	10105	2	0.011	0.007	0.762	0.021	0.01	0.074	0.115
Dubai	10106	18	0.009	0.011	0.661	0.19	0.064	0.01	0.057
Dubai	10107	5	0.044	0.026	0.293	0.075	0.033	0.155	0.375
Dubai	10108	2	0.008	0.02	0.309	0.574	0.02	0.044	0.026
Dubai	10109	18	0.013	0.008	0.424	0.022	0.015	0.102	0.415
Dubai	10110	7	0.015	0.006	0.821	0.006	0.009	0.011	0.132
Dubai	10111	13	0.004	0.015	0.791	0.141	0.02	0.009	0.02
Dubai	10112	7	0.021	0.019	0.521	0.077	0.283	0.053	0.027
Dubai	10120	15	0.01	0.009	0.759	0.073	0.017	0.011	0.12
Kenya-Nairobi	9833	13	0.551	0.011	0.027	0.123	0.059	0.029	0.2
Kenya-Nairobi	9834	0	0.732	0.015	0.019	0.202	0.011	0.014	0.007
Kenya-Nairobi	9835	0	0.449	0.088	0.241	0.025	0.012	0.18	0.006
Kenya-Nairobi	9836	2	0.724	0.008	0.027	0.19	0.009	0.029	0.013
Kenya-Nairobi	9837	0	0.762	0.048	0.014	0.032	0.011	0.078	0.055
Kenya-Nairobi	9838	2	0.559	0.048	0.087	0.01	0.078	0.016	0.202
Kenya-Nairobi	9839	0	0.173	0.028	0.388	0.341	0.02	0.038	0.012
Kenya-Nairobi	9840	0	0.475	0.207	0.013	0.175	0.108	0.008	0.014
Kenya-Nairobi	9841	2	0.821	0.021	0.078	0.05	0.011	0.011	0.008
Kenya-Nairobi	9842	2	0.686	0.03	0.113	0.019	0.022	0.091	0.04
Kenya-Nairobi	9843	0	0.833	0.013	0.051	0.07	0.012	0.013	0.009

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling Location	ID No.	Missing Data	Population						
			1	2	3	4	5	6	7
Kenya-Nairobi	9844	2	0.753	0.01	0.182	0.012	0.009	0.029	0.005
Kenya-Nairobi	9845	0	0.67	0.08	0.056	0.013	0.118	0.046	0.018
Kenya-Nairobi	9846	2	0.567	0.013	0.006	0.295	0.027	0.08	0.011
Kenya-Nairobi	9847	0	0.81	0.008	0.117	0.017	0.022	0.016	0.01
Kenya-Nairobi	9848	0	0.553	0.102	0.02	0.027	0.182	0.092	0.024
Kenya-Nairobi	9849	5	0.151	0.054	0.024	0.664	0.084	0.016	0.008
Kenya-Nairobi	9850	7	0.637	0.017	0.035	0.045	0.244	0.01	0.013
Kenya-Nairobi	9851	2	0.535	0.006	0.043	0.389	0.014	0.006	0.007
Kenya-Nairobi	9852	7	0.473	0.063	0.407	0.009	0.039	0.003	0.005
Kenya-Nairobi	9853	2	0.752	0.014	0.107	0.039	0.011	0.02	0.058
Kenya-Nairobi	9854	0	0.785	0.024	0.045	0.023	0.044	0.005	0.075
Kenya-Nairobi	9855	2	0.461	0.281	0.125	0.074	0.038	0.007	0.015
Kenya-Nairobi	9856	2	0.685	0.018	0.192	0.075	0.015	0.01	0.005
Kenya-Nairobi	9857	23	0.434	0.033	0.007	0.449	0.03	0.039	0.009
Kenya-Nairobi	9858	15	0.854	0.013	0.032	0.042	0.011	0.042	0.006
Kenya-Nairobi	9859	15	0.87	0.005	0.029	0.029	0.005	0.047	0.015
Kenya-Nairobi	9860	5	0.864	0.014	0.036	0.025	0.006	0.043	0.012
Kenya-Nairobi	9861	2	0.764	0.028	0.183	0.005	0.009	0.004	0.007
Kenya-Nairobi	9862	7	0.456	0.037	0.03	0.336	0.119	0.016	0.004
Kenya-Nairobi	9863	2	0.666	0.007	0.09	0.202	0.005	0.019	0.011
Kenya-Nairobi	9864	7	0.7	0.02	0.044	0.123	0.018	0.004	0.091
Kenya-Nairobi	9865	10	0.37	0.103	0.033	0.334	0.029	0.054	0.076
Kenya-Nairobi	9866	7	0.532	0.191	0.058	0.061	0.134	0.019	0.005
Kenya-Nairobi	9867	0	0.313	0.031	0.02	0.454	0.123	0.023	0.037
Kenya-Nairobi	9868	5	0.454	0.373	0.059	0.047	0.05	0.005	0.011
Kenya-Pate	2000	7	0.076	0.02	0.844	0.008	0.045	0.004	0.003
Kenya-Pate	2001	13	0.002	0.003	0.983	0.002	0.003	0.002	0.004
Kenya-Pate	2002	2	0.002	0.003	0.97	0.003	0.003	0.008	0.011
Kenya-Pate	2003	2	0.005	0.005	0.919	0.009	0.003	0.054	0.005
Kenya-Pate	2004	10	0.007	0.016	0.901	0.023	0.025	0.016	0.011
Kenya-Pate	2006	7	0.004	0.007	0.774	0.01	0.006	0.08	0.12
Kenya-Pate	2007	7	0.004	0.004	0.977	0.004	0.004	0.004	0.004
Kenya-Pate	2009	28	0.014	0.022	0.941	0.003	0.013	0.003	0.004
Kenya-Pate	2011	13	0.01	0.015	0.895	0.043	0.026	0.008	0.004
Kenya-Lamu	1848	10	0.01	0.004	0.865	0.034	0.01	0.068	0.009
Kenya-Lamu	2014	5	0.006	0.02	0.934	0.019	0.012	0.003	0.006
Kenya-Lamu	2015	7	0.01	0.051	0.655	0.006	0.261	0.01	0.007
Kenya-Lamu	2016	7	0.032	0.014	0.907	0.009	0.026	0.006	0.004
Kenya-Lamu	2018	2	0.029	0.067	0.863	0.005	0.027	0.004	0.004
Kenya-Lamu	2019	7	0.034	0.048	0.823	0.057	0.021	0.011	0.007
Kenya-Lamu	2021	7	0.008	0.006	0.936	0.011	0.006	0.005	0.028
Kenya-Lamu	2023	13	0.006	0.004	0.975	0.004	0.004	0.005	0.002
Kenya-Lamu	2024	2	0.003	0.003	0.984	0.003	0.003	0.002	0.003
Kenya-Lamu	2025	5	0.005	0.008	0.95	0.004	0.01	0.009	0.015
Kenya-Lamu	2026	18	0.003	0.007	0.963	0.006	0.012	0.005	0.004
Kenya-Lamu	2027	26	0.088	0.016	0.773	0.047	0.021	0.021	0.033
Kenya-Lamu	2029	5	0.003	0.003	0.984	0.003	0.003	0.003	0.003
Kenya-Lamu	2030	5	0.022	0.005	0.939	0.013	0.013	0.004	0.004
Kenya-Lamu	2031	18	0.045	0.02	0.896	0.007	0.015	0.008	0.009
Kenya-Lamu	2032	10	0.006	0.007	0.952	0.006	0.006	0.006	0.017
Kenya-Lamu	2033	13	0.011	0.028	0.908	0.017	0.018	0.007	0.011
Kenya-Lamu	3241	18	0.018	0.029	0.808	0.039	0.013	0.084	0.008
Kenya-Lamu	3246	7	0.034	0.131	0.682	0.011	0.119	0.014	0.008
Kenya-Lamu	3247	13	0.188	0.011	0.714	0.029	0.037	0.009	0.012
India-Udaipur	11835	10	0.024	0.075	0.112	0.159	0.137	0.268	0.225
India-Udaipur	11836	5	0.009	0.02	0.075	0.422	0.044	0.023	0.407

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling	ID	Missing	Population						
Location	No.	Data	1	2	3	4	5	6	7
India-Udaipur	11837	5	0.005	0.02	0.053	0.551	0.009	0.021	0.341
India-Agra	11823	0	0.006	0.018	0.014	0.452	0.007	0.006	0.497
India-Agra	11824	0	0.005	0.016	0.108	0.585	0.016	0.007	0.263
India-Agra	11825	2	0.009	0.01	0.006	0.475	0.007	0.007	0.487
India-Agra	11826	7	0.004	0.005	0.003	0.536	0.004	0.004	0.444
India-Agra	11827	0	0.003	0.006	0.005	0.565	0.012	0.004	0.404
India-Agra	11828	5	0.006	0.024	0.034	0.517	0.044	0.01	0.365
India-Agra	11829	5	0.016	0.032	0.012	0.746	0.045	0.007	0.141
India-Agra	11830	5	0.003	0.007	0.005	0.593	0.012	0.005	0.376
India-Agra	11831	5	0.01	0.031	0.013	0.442	0.027	0.007	0.469
India-Agra	11832	0	0.004	0.009	0.015	0.416	0.007	0.006	0.544
India-Agra	11833	2	0.005	0.029	0.058	0.379	0.01	0.017	0.502
India-Agra	11834	5	0.004	0.005	0.004	0.518	0.004	0.004	0.462
India-Hyderbad	11802	7	0.032	0.463	0.016	0.353	0.086	0.038	0.012
India-Hyderbad	11803	7	0.007	0.066	0.031	0.708	0.133	0.008	0.047
India-Hyderbad	11804	10	0.007	0.008	0.213	0.23	0.011	0.464	0.067
India-Hyderbad	11805	5	0.021	0.017	0.037	0.858	0.019	0.033	0.015
India-Hyderbad	11807	2	0.004	0.013	0.014	0.91	0.007	0.009	0.042
India-Hyderbad	11808	2	0.011	0.008	0.012	0.88	0.009	0.075	0.004
India-Hyderbad	11809	2	0.111	0.065	0.007	0.655	0.085	0.003	0.073
India-Hyderbad	11810	0	0.015	0.134	0.024	0.766	0.026	0.021	0.014
India-Hyderbad	11811	0	0.005	0.008	0.435	0.516	0.013	0.012	0.011
India-Hyderbad	11812	13	0.004	0.009	0.012	0.663	0.013	0.041	0.259
India-Hyderbad	11813	10	0.006	0.01	0.007	0.712	0.063	0.122	0.08
India-Hyderbad	11814	0	0.007	0.013	0.041	0.904	0.008	0.012	0.014
India-Hyderbad	11815	0	0.007	0.011	0.153	0.756	0.006	0.019	0.049
India-Hyderbad	11816	0	0.005	0.031	0.011	0.917	0.015	0.004	0.017
India-Hyderbad	11817	5	0.006	0.009	0.013	0.947	0.006	0.009	0.01
India-Hyderbad	11818	2	0.004	0.005	0.023	0.916	0.007	0.022	0.025
India-Hyderbad	11819	0	0.006	0.035	0.01	0.913	0.016	0.004	0.017
India-Hyderbad	11820	5	0.006	0.011	0.137	0.724	0.006	0.087	0.03
India-Hyderbad	11821	0	0.017	0.125	0.046	0.748	0.019	0.028	0.018
India-Hyderbad	11822	0	0.008	0.015	0.071	0.75	0.077	0.068	0.01
India-Andhra	10159	5	0.01	0.015	0.006	0.92	0.008	0.038	0.004
India-Andhra	10160	2	0.009	0.012	0.068	0.635	0.005	0.259	0.013
India-Andhra	10161	0	0.008	0.005	0.006	0.959	0.006	0.006	0.009
India-Andhra	10162	5	0.006	0.006	0.01	0.953	0.008	0.007	0.009
India-Andhra	10163	0	0.005	0.007	0.104	0.784	0.01	0.075	0.015
India-Andhra	10164	2	0.004	0.006	0.01	0.712	0.009	0.174	0.086
India-Andhra	10165	0	0.008	0.015	0.114	0.821	0.008	0.009	0.025
India-Andhra	10166	5	0.023	0.017	0.33	0.577	0.032	0.015	0.006
India-Andhra	10167	2	0.029	0.197	0.064	0.597	0.085	0.022	0.006
India-Andhra	10168	2	0.005	0.021	0.006	0.907	0.015	0.016	0.03
India-Andhra	10169	5	0.017	0.024	0.007	0.91	0.01	0.027	0.004
India-Andhra	10170	0	0.02	0.031	0.017	0.824	0.031	0.068	0.008
India-Andhra	10171	2	0.004	0.006	0.01	0.713	0.009	0.173	0.085
India-Andhra	10172	5	0.072	0.02	0.007	0.808	0.015	0.034	0.045
India-Andhra	10173	5	0.004	0.013	0.015	0.946	0.007	0.012	0.003
India-Andhra	10174	5	0.01	0.013	0.003	0.957	0.009	0.006	0.002
India-Andhra	10175	5	0.087	0.015	0.012	0.851	0.012	0.009	0.014
India-Andhra	10176	0	0.009	0.013	0.013	0.713	0.021	0.191	0.04
India-Andhra	10177	0	0.01	0.015	0.01	0.863	0.019	0.072	0.011
India-Andhra	10178	5	0.008	0.006	0.007	0.942	0.009	0.01	0.018
India-Andhra	10179	2	0.045	0.031	0.021	0.882	0.008	0.007	0.005
India-Andhra	10180	2	0.024	0.074	0.005	0.758	0.124	0.005	0.01
India-Andhra	10181	7	0.009	0.015	0.013	0.767	0.011	0.18	0.005

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling	ID	Missing	Population						
Location	No.	Data	1	2	3	4	5	6	7
India-Kolkata	10113	7	0.014	0.019	0.075	0.833	0.025	0.019	0.014
India-Kolkata	10114	2	0.006	0.015	0.014	0.933	0.01	0.01	0.013
India-Kolkata	10115	0	0.029	0.115	0.024	0.769	0.037	0.018	0.008
India-Kolkata	10116	7	0.007	0.012	0.023	0.926	0.01	0.014	0.008
India-Kolkata	10117	5	0.011	0.045	0.262	0.138	0.045	0.48	0.019
India-Kolkata	10118	13	0.011	0.162	0.043	0.652	0.012	0.018	0.101
India-Kolkata	10119	7	0.021	0.028	0.013	0.834	0.088	0.005	0.012
Sri Lanka	8780	0	0.048	0.027	0.016	0.796	0.072	0.026	0.014
Sri Lanka	8781	5	0.046	0.043	0.011	0.796	0.083	0.009	0.012
Sri Lanka	8782	15	0.094	0.096	0.026	0.702	0.044	0.016	0.022
Sri Lanka	8783	0	0.031	0.051	0.06	0.718	0.078	0.016	0.046
Sri Lanka	8784	5	0.02	0.01	0.036	0.852	0.02	0.043	0.02
Sri Lanka	8785	7	0.077	0.09	0.024	0.545	0.064	0.015	0.185
Sri Lanka	8786	0	0.066	0.096	0.017	0.52	0.236	0.013	0.052
Sri Lanka	8787	0	0.242	0.025	0.009	0.68	0.017	0.005	0.022
Sri Lanka	8788	5	0.03	0.012	0.005	0.776	0.024	0.006	0.146
Sri Lanka	8789	2	0.419	0.025	0.007	0.429	0.089	0.006	0.024
Sri Lanka	8790	0	0.123	0.03	0.004	0.806	0.026	0.006	0.005
Sri Lanka	8791	5	0.007	0.01	0.07	0.811	0.011	0.009	0.082
Sri Lanka	8792	2	0.105	0.016	0.01	0.824	0.034	0.004	0.007
Sri Lanka	8793	5	0.211	0.01	0.015	0.693	0.054	0.003	0.013
Sri Lanka	8794	5	0.124	0.043	0.005	0.744	0.064	0.008	0.012
Sri Lanka	8795	0	0.021	0.092	0.032	0.807	0.025	0.016	0.007
Sri Lanka	8796	7	0.06	0.092	0.013	0.76	0.05	0.02	0.005
Sri Lanka	8797	2	0.416	0.009	0.018	0.381	0.042	0.037	0.097
Sri Lanka	8798	2	0.033	0.029	0.006	0.787	0.098	0.014	0.034
Sri Lanka	8799	7	0.183	0.006	0.117	0.666	0.007	0.003	0.018
Sri Lanka	8800	10	0.314	0.034	0.05	0.318	0.035	0.226	0.023
Sri Lanka	8801	10	0.125	0.03	0.334	0.278	0.019	0.008	0.205
Sri Lanka	8802	2	0.527	0.004	0.009	0.425	0.007	0.004	0.024
Sri Lanka	8803	15	0.044	0.023	0.174	0.671	0.066	0.011	0.012
Thailand	11688	7	0.003	0.003	0.003	0.976	0.003	0.009	0.003
Thailand	11689	15	0.004	0.005	0.003	0.964	0.004	0.009	0.011
Thailand	11691	55	0.012	0.01	0.01	0.71	0.013	0.232	0.013
Thailand	11698	23	0.015	0.008	0.006	0.641	0.01	0.315	0.005
Thailand	11702	10	0.009	0.004	0.006	0.965	0.005	0.009	0.003
Thailand	11703	13	0.004	0.003	0.003	0.971	0.003	0.013	0.004
Thailand	11705	21	0.003	0.005	0.004	0.969	0.009	0.006	0.003
Thailand	11707	10	0.004	0.004	0.005	0.966	0.005	0.013	0.003
Thailand	11708	2	0.008	0.025	0.025	0.893	0.013	0.029	0.006
Thailand	11709	15	0.005	0.005	0.004	0.968	0.005	0.009	0.003
Thailand	11710	15	0.006	0.006	0.004	0.957	0.005	0.018	0.004
Thailand	11711	2	0.004	0.003	0.007	0.925	0.003	0.054	0.004
Thailand	11714	13	0.01	0.005	0.021	0.931	0.012	0.016	0.005
Thailand	11715	21	0.007	0.004	0.004	0.95	0.005	0.023	0.007
Thailand	11717	13	0.006	0.006	0.003	0.966	0.005	0.008	0.005
Thailand	11718	7	0.022	0.018	0.012	0.895	0.011	0.036	0.006
Thailand	11720	7	0.003	0.003	0.002	0.967	0.006	0.016	0.003
Vietnam	8844	5	0.004	0.005	0.007	0.959	0.005	0.015	0.005
Vietnam	8845	13	0.005	0.006	0.01	0.961	0.005	0.006	0.007
Vietnam	8846	13	0.083	0.024	0.027	0.791	0.033	0.038	0.005
Vietnam	8847	15	0.182	0.006	0.005	0.765	0.013	0.016	0.013
Vietnam	8848	10	0.096	0.013	0.01	0.858	0.013	0.005	0.005
Vietnam	8849	2	0.009	0.013	0.006	0.937	0.018	0.013	0.004
Vietnam	8850	5	0.423	0.013	0.011	0.378	0.026	0.144	0.005
Vietnam	8851	10	0.009	0.009	0.004	0.95	0.008	0.009	0.011

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling Location	ID No.	Missing Data	Population						
			1	2	3	4	5	6	7
Vietnam	8852	13	0.074	0.011	0.015	0.561	0.269	0.064	0.007
Vietnam	8853	10	0.021	0.028	0.005	0.591	0.341	0.008	0.006
Vietnam	8854	7	0.209	0.007	0.004	0.6	0.069	0.055	0.055
Vietnam	8855	10	0.004	0.005	0.004	0.905	0.005	0.072	0.005
Vietnam	8856	10	0.006	0.03	0.003	0.869	0.083	0.005	0.003
Vietnam	8857	7	0.023	0.011	0.011	0.908	0.014	0.006	0.028
Vietnam	8858	13	0.006	0.006	0.004	0.915	0.005	0.061	0.003
Vietnam	8859	13	0.015	0.006	0.008	0.728	0.013	0.22	0.01
Vietnam	8860	10	0.195	0.132	0.031	0.409	0.164	0.059	0.009
Vietnam	8861	10	0.08	0.016	0.016	0.711	0.137	0.021	0.02
Vietnam	8862	7	0.011	0.015	0.046	0.844	0.009	0.072	0.004
Vietnam	8863	15	0.022	0.02	0.011	0.831	0.017	0.092	0.007
Taiwan	8681	7	0.737	0.01	0.008	0.009	0.011	0.21	0.015
Taiwan	8682	2	0.004	0.004	0.006	0.243	0.006	0.72	0.017
Taiwan	8683	7	0.077	0.012	0.012	0.069	0.019	0.8	0.011
Taiwan	8684	7	0.735	0.03	0.008	0.035	0.011	0.17	0.011
Taiwan	8685	2	0.094	0.006	0.006	0.283	0.013	0.595	0.003
Taiwan	8686	7	0.332	0.008	0.012	0.029	0.044	0.567	0.008
Taiwan	8687	2	0.056	0.024	0.034	0.349	0.094	0.406	0.038
Taiwan	8688	47	0.021	0.023	0.035	0.199	0.012	0.702	0.008
Taiwan	8689	5	0.098	0.014	0.165	0.047	0.051	0.596	0.029
Taiwan	8690	7	0.015	0.006	0.007	0.421	0.017	0.495	0.039
Taiwan	8691	26	0.018	0.032	0.02	0.579	0.025	0.319	0.007
Taiwan	8692	5	0.011	0.007	0.011	0.118	0.007	0.841	0.005
Taiwan	8693	7	0.027	0.012	0.006	0.046	0.022	0.881	0.006
Taiwan	8694	5	0.379	0.006	0.003	0.564	0.005	0.041	0.003
Taiwan	8695	2	0.025	0.089	0.043	0.014	0.012	0.812	0.005
Taiwan	8696	23	0.929	0.012	0.006	0.014	0.009	0.027	0.004
Taiwan	8697	5	0.914	0.011	0.005	0.004	0.052	0.006	0.008
Taiwan	8698	7	0.972	0.006	0.004	0.004	0.006	0.004	0.003
Taiwan	8699	10	0.18	0.029	0.007	0.213	0.114	0.384	0.073
Taiwan	8700	7	0.051	0.055	0.006	0.425	0.049	0.399	0.015
Taiwan	8701	2	0.166	0.018	0.004	0.173	0.019	0.611	0.01
Taiwan	8702	5	0.058	0.273	0.02	0.029	0.039	0.568	0.013
Taiwan	8703	7	0.95	0.018	0.003	0.006	0.013	0.007	0.003
Taiwan	8704	2	0.02	0.008	0.027	0.058	0.145	0.731	0.011
Taiwan	8705	5	0.013	0.022	0.019	0.332	0.013	0.585	0.016
Taiwan	8706	7	0.011	0.013	0.023	0.088	0.014	0.844	0.008
Taiwan	8707	7	0.029	0.016	0.004	0.125	0.004	0.784	0.037
Taiwan	8708	15	0.952	0.006	0.007	0.009	0.008	0.015	0.004
Taiwan	8709	13	0.034	0.024	0.013	0.118	0.119	0.669	0.024
Japan-Oita	11967	5	0.015	0.015	0.011	0.038	0.017	0.894	0.009
Japan-Oita	11968	7	0.017	0.024	0.011	0.644	0.023	0.274	0.007
Japan-Oita	11969	7	0.034	0.02	0.01	0.027	0.014	0.888	0.007
Japan-Oita	11970	7	0.024	0.03	0.013	0.209	0.035	0.663	0.027
Japan-Oita	11971	7	0.043	0.004	0.024	0.041	0.009	0.871	0.007
Japan-Oita	11972	5	0.007	0.004	0.008	0.015	0.005	0.957	0.004
Japan-Oita	11973	7	0.037	0.016	0.092	0.025	0.012	0.797	0.021
Japan-Oita	11974	21	0.02	0.017	0.021	0.156	0.021	0.757	0.008
Japan-Oita	11975	10	0.027	0.01	0.007	0.376	0.017	0.559	0.003
Japan-Oita	11976	13	0.324	0.014	0.004	0.031	0.022	0.597	0.007
Japan-Oita	11977	7	0.342	0.008	0.005	0.028	0.045	0.568	0.004
Japan-Oita	11979	10	0.009	0.015	0.036	0.023	0.017	0.894	0.007
Japan-Oita	11980	7	0.021	0.007	0.017	0.022	0.011	0.916	0.007
Japan-Oita	11981	7	0.003	0.003	0.01	0.021	0.003	0.955	0.004
Japan-Oita	11982	13	0.061	0.006	0.007	0.173	0.028	0.721	0.004

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling Location	ID No.	Missing Data	Population						
			1	2	3	4	5	6	7
Japan-Oita	11985	10	0.005	0.018	0.007	0.295	0.015	0.656	0.004
Japan-Oita	11986	10	0.121	0.123	0.007	0.06	0.074	0.599	0.016
Japan-Kanazawa	11929	10	0.976	0.004	0.003	0.003	0.007	0.003	0.003
Japan-Kanazawa	11931	10	0.059	0.011	0.009	0.107	0.006	0.8	0.008
Japan-Kanazawa	11932	7	0.227	0.012	0.005	0.046	0.009	0.691	0.01
Japan-Kanazawa	11933	15	0.005	0.004	0.247	0.017	0.004	0.72	0.003
Japan-Kanazawa	11934	7	0.027	0.008	0.009	0.015	0.012	0.927	0.003
Japan-Kanazawa	11936	7	0.012	0.008	0.006	0.107	0.012	0.852	0.004
Japan-Kanazawa	11937	10	0.014	0.005	0.003	0.011	0.008	0.956	0.003
Japan-Kanazawa	11939	10	0.022	0.006	0.007	0.093	0.012	0.846	0.014
Japan-Kanazawa	11940	10	0.006	0.007	0.007	0.008	0.007	0.95	0.015
Japan-Kanazawa	11941	10	0.008	0.014	0.004	0.019	0.014	0.921	0.021
Japan-Kanazawa	11942	7	0.006	0.011	0.053	0.048	0.011	0.865	0.006
Japan-Kanazawa	11943	28	0.039	0.024	0.009	0.309	0.034	0.546	0.039
Japan-Kanazawa	11944	39	0.888	0.032	0.04	0.011	0.009	0.011	0.008
Japan-Kanazawa	11945	10	0.038	0.006	0.025	0.045	0.008	0.869	0.009
Japan-Kanazawa	11946	10	0.01	0.029	0.012	0.009	0.004	0.932	0.004
Japan-Ohmiya	11947	5	0.065	0.046	0.014	0.038	0.014	0.817	0.007
Japan-Ohmiya	11948	10	0.071	0.121	0.015	0.01	0.059	0.693	0.03
Japan-Ohmiya	11951	5	0.052	0.031	0.017	0.113	0.019	0.739	0.028
Japan-Ohmiya	11953	7	0.009	0.009	0.005	0.04	0.014	0.918	0.004
Japan-Ohmiya	11954	5	0.177	0.044	0.008	0.194	0.015	0.552	0.01
Japan-Ohmiya	11955	7	0.108	0.023	0.193	0.09	0.017	0.564	0.004
Japan-Ohmiya	11956	7	0.042	0.011	0.015	0.137	0.016	0.77	0.009
Japan-Ohmiya	11957	2	0.189	0.028	0.012	0.008	0.048	0.696	0.019
Japan-Ohmiya	11959	18	0.049	0.253	0.008	0.01	0.012	0.662	0.005
Japan-Ohmiya	11960	2	0.013	0.006	0.004	0.065	0.004	0.887	0.021
Japan-Ohmiya	11961	5	0.004	0.014	0.003	0.007	0.008	0.959	0.005
Japan-Ohmiya	11962	13	0.01	0.007	0.014	0.192	0.006	0.761	0.01
Japan-Ohmiya	11963	2	0.248	0.005	0.007	0.021	0.01	0.703	0.005
Japan-Ohmiya	11964	5	0.161	0.022	0.019	0.142	0.021	0.606	0.029
Japan-Ohmiya	11965	7	0.006	0.009	0.021	0.023	0.006	0.932	0.003
Japan-Ohmiya	11966	2	0.103	0.026	0.017	0.035	0.014	0.795	0.01
Japan-Sapporo	11907	2	0.016	0.015	0.011	0.026	0.015	0.908	0.008
Japan-Sapporo	11909	7	0.941	0.008	0.004	0.014	0.017	0.012	0.005
Japan-Sapporo	11911	5	0.329	0.005	0.006	0.011	0.107	0.531	0.011
Japan-Sapporo	11913	7	0.437	0.005	0.009	0.006	0.008	0.532	0.003
Japan-Sapporo	11914	13	0.254	0.004	0.004	0.014	0.008	0.711	0.004
Japan-Sapporo	11915	10	0.017	0.028	0.011	0.625	0.011	0.294	0.013
Japan-Sapporo	11916	5	0.738	0.051	0.005	0.06	0.122	0.02	0.003
Japan-Sapporo	11917	5	0.838	0.04	0.036	0.007	0.034	0.035	0.009
Japan-Sapporo	11918	7	0.343	0.025	0.019	0.056	0.02	0.522	0.014
Japan-Sapporo	11921	7	0.006	0.006	0.016	0.05	0.007	0.907	0.008
Japan-Sapporo	11922	5	0.042	0.006	0.004	0.029	0.013	0.904	0.003
Japan-Sapporo	11923	7	0.192	0.009	0.015	0.086	0.037	0.655	0.006
Japan-Sapporo	11924	5	0.505	0.006	0.014	0.371	0.041	0.056	0.008
Japan-Sapporo	11925	7	0.005	0.006	0.01	0.086	0.005	0.883	0.004
Japan-Sapporo	11926	5	0.391	0.059	0.005	0.014	0.011	0.515	0.005
China-Henan	8869	2	0.047	0.076	0.003	0.009	0.028	0.828	0.009
China-Henan	8870	5	0.003	0.002	0.002	0.006	0.003	0.978	0.006
China-Henan	8871	5	0.006	0.017	0.019	0.005	0.008	0.843	0.103
China-Henan	8872	2	0.006	0.005	0.008	0.011	0.004	0.953	0.014
China-Henan	8873	5	0.009	0.008	0.005	0.006	0.018	0.948	0.007
China-Henan	8874	5	0.004	0.013	0.012	0.018	0.007	0.913	0.033
China-Henan	8875	5	0.003	0.003	0.003	0.002	0.002	0.985	0.002
China-Henan	8876	5	0.003	0.002	0.004	0.003	0.002	0.983	0.002

Table 24 - Population clustering of each random bred individual in the database by STRs at K = 7

Sampling Location	ID No.	Missing Data	Population						
			1	2	3	4	5	6	7
China-Henan	8877	7	0.005	0.017	0.021	0.03	0.007	0.903	0.018
China-Henan	8878	5	0.003	0.007	0.003	0.003	0.006	0.976	0.002
China-Henan	8879	2	0.003	0.004	0.005	0.018	0.004	0.955	0.012
China-Henan	8880	7	0.006	0.005	0.014	0.004	0.004	0.954	0.013
China-Henan	8881	5	0.003	0.039	0.005	0.006	0.026	0.885	0.036
China-Henan	8882	5	0.022	0.016	0.019	0.04	0.02	0.874	0.009
China-Henan	8883	2	0.003	0.005	0.004	0.005	0.006	0.971	0.005
China-Henan	8884	2	0.002	0.011	0.036	0.021	0.004	0.907	0.02
China-Henan	8885	2	0.005	0.005	0.009	0.004	0.005	0.968	0.003
China-Henan	8886	2	0.003	0.009	0.005	0.004	0.006	0.967	0.006
China-Henan	8887	2	0.016	0.016	0.014	0.004	0.017	0.876	0.057
China-Henan	8888	2	0.01	0.012	0.003	0.014	0.008	0.933	0.02
South Korea	2769	5	0.004	0.003	0.002	0.005	0.004	0.979	0.003
South Korea	2772	47	0.004	0.005	0.011	0.012	0.005	0.955	0.007
South Korea	2775	13	0.007	0.006	0.006	0.005	0.013	0.959	0.005
South Korea	2776	13	0.026	0.015	0.014	0.047	0.071	0.824	0.004
South Korea	2779	2	0.004	0.004	0.007	0.016	0.005	0.957	0.007
South Korea	2784	2	0.003	0.003	0.002	0.007	0.003	0.978	0.004
South Korea	2785	2	0.011	0.011	0.005	0.009	0.015	0.865	0.084
South Korea	2786	2	0.007	0.004	0.002	0.005	0.005	0.975	0.002
South Korea	7671	2	0.007	0.007	0.004	0.008	0.011	0.96	0.004
South Korea	7672	2	0.007	0.006	0.019	0.008	0.006	0.952	0.004
South Korea	7673	2	0.006	0.01	0.003	0.003	0.027	0.93	0.019
South Korea	7674	2	0.021	0.007	0.006	0.008	0.079	0.874	0.006
South Korea	7675	10	0.008	0.007	0.003	0.006	0.012	0.961	0.003
South Korea	7676	7	0.009	0.007	0.013	0.008	0.009	0.941	0.013
South Korea	7677	15	0.232	0.023	0.006	0.006	0.084	0.365	0.284
South Korea	7678	2	0.014	0.008	0.005	0.005	0.009	0.952	0.008
South Korea	7679	5	0.004	0.006	0.004	0.004	0.005	0.973	0.005
South Korea	7680	7	0.019	0.014	0.011	0.005	0.021	0.925	0.005
South Korea	7681	13	0.013	0.154	0.003	0.007	0.053	0.758	0.013
South Korea	7682	5	0.006	0.016	0.005	0.008	0.011	0.951	0.003
South Korea	7683	7	0.003	0.003	0.004	0.008	0.004	0.974	0.004
South Korea	7684	7	0.029	0.177	0.009	0.048	0.157	0.57	0.009
South Korea	7685	18	0.014	0.008	0.006	0.022	0.008	0.937	0.005
South Korea	7686	10	0.027	0.01	0.004	0.007	0.013	0.934	0.005
South Korea	7687	10	0.062	0.049	0.056	0.125	0.01	0.695	0.004
South Korea	7688	2	0.501	0.03	0.025	0.055	0.03	0.356	0.004
South Korea	7689	10	0.007	0.006	0.006	0.006	0.007	0.963	0.005
South Korea	7690	10	0.006	0.01	0.011	0.025	0.008	0.938	0.003
South Korea	7691	7	0.008	0.008	0.016	0.008	0.015	0.938	0.007
South Korea	7692	5	0.008	0.015	0.01	0.058	0.026	0.87	0.012
South Korea	7693	2	0.052	0.047	0.03	0.021	0.106	0.734	0.011
South Korea	7694	5	0.003	0.003	0.003	0.005	0.003	0.98	0.002
South Korea	7695	7	0.039	0.04	0.063	0.004	0.075	0.774	0.006
South Korea	7696	5	0.004	0.003	0.003	0.004	0.006	0.972	0.007
South Korea	7697	10	0.007	0.005	0.005	0.012	0.008	0.949	0.014
South Korea	7698	23	0.027	0.042	0.017	0.213	0.055	0.612	0.034
South Korea	7699	7	0.005	0.01	0.004	0.014	0.014	0.941	0.011
South Korea	7700	7	0.007	0.013	0.005	0.061	0.028	0.865	0.02

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling	ID	Missing	Population							
Location	No.	Data	1	2	3	4	5	6	7	8
USA-NY	2547	1	0.086	0.006	0.006	0.775	0.077	0.037	0.004	0.009
USA-NY	2559	3	0.009	0.002	0.008	0.618	0.006	0.348	0.004	0.004
USA-NY	2568	0	0.003	0.002	0.003	0.98	0.003	0.003	0.003	0.003
USA-NY	2569	5	0.015	0.008	0.004	0.942	0.009	0.005	0.011	0.005
USA-NY	2572	1	0.009	0.005	0.007	0.931	0.02	0.016	0.005	0.009
USA-NY	2578	17	0.041	0.008	0.003	0.883	0.048	0.009	0.003	0.005
USA-NY	2590	1	0.013	0.002	0.008	0.942	0.007	0.022	0.003	0.004
USA-NY	2591	2	0.015	0.009	0.004	0.944	0.004	0.007	0.007	0.011
USA-NY	2597	4	0.023	0.028	0.03	0.863	0.035	0.01	0.005	0.006
USA-MS	9971	3	0.009	0.007	0.058	0.885	0.024	0.007	0.005	0.006
USA-MS	9972	2	0.058	0.017	0.019	0.787	0.087	0.014	0.003	0.014
USA-MS	9974	2	0.01	0.005	0.119	0.823	0.022	0.011	0.003	0.007
USA-MS	9977	5	0.013	0.005	0.013	0.946	0.006	0.006	0.008	0.002
USA-MS	9980	2	0.01	0.01	0.011	0.904	0.013	0.028	0.004	0.019
USA-MS	9983	2	0.006	0.008	0.011	0.942	0.007	0.009	0.003	0.013
USA-MS	9985	3	0.009	0.002	0.228	0.719	0.005	0.028	0.005	0.004
USA-MS	9987	3	0.055	0.006	0.081	0.778	0.02	0.043	0.008	0.008
USA-MS	9989	2	0.015	0.003	0.03	0.914	0.019	0.007	0.008	0.003
USA-MS	9992	3	0.068	0.009	0.062	0.785	0.008	0.06	0.003	0.006
USA-HI	5366	3	0.023	0.003	0.018	0.712	0.021	0.019	0.176	0.028
USA-HI	5367	1	0.089	0.016	0.057	0.735	0.057	0.007	0.01	0.029
USA-HI	5371	1	0.026	0.015	0.018	0.696	0.047	0.185	0.01	0.004
USA-HI	5372	2	0.065	0.008	0.013	0.625	0.253	0.025	0.005	0.006
USA-HI	5379	1	0.067	0.016	0.016	0.84	0.01	0.023	0.026	0.004
USA-HI	5380	1	0.018	0.002	0.002	0.954	0.002	0.009	0.009	0.004
USA-HI	5383	3	0.028	0.199	0.011	0.401	0.015	0.147	0.017	0.182
USA-HI	5384	5	0.025	0.005	0.002	0.847	0.004	0.098	0.003	0.015
USA-HI	5401	2	0.039	0.004	0.02	0.848	0.007	0.026	0.024	0.033
USA-HI	5402	2	0.017	0.021	0.045	0.809	0.016	0.024	0.063	0.005
Brazil	7961	1	0.017	0.003	0.002	0.949	0.003	0.013	0.009	0.003
Brazil	7962	2	0.009	0.002	0.007	0.816	0.008	0.149	0.003	0.005
Brazil	7963	17	0.008	0.002	0.336	0.625	0.008	0.01	0.003	0.009
Brazil	7964	2	0.006	0.004	0.004	0.95	0.004	0.015	0.009	0.009
Brazil	7965	27	0.005	0.003	0.008	0.968	0.003	0.004	0.003	0.006
Brazil	7966	2	0.02	0.011	0.007	0.93	0.014	0.013	0.002	0.003
Brazil	7968	23	0.012	0.006	0.007	0.935	0.007	0.013	0.014	0.005
Brazil	7969	1	0.004	0.002	0.004	0.978	0.003	0.004	0.002	0.002
Brazil	7970	1	0.004	0.002	0.008	0.969	0.003	0.005	0.003	0.006
Brazil	7971	1	0.006	0.004	0.004	0.972	0.003	0.004	0.005	0.003
Brazil	7972	1	0.012	0.004	0.001	0.965	0.003	0.007	0.004	0.005
Brazil	7973	0	0.014	0.003	0.004	0.956	0.004	0.006	0.01	0.004
Brazil	7974	3	0.012	0.004	0.007	0.946	0.006	0.016	0.004	0.004
Brazil	7975	5	0.01	0.003	0.004	0.946	0.011	0.007	0.015	0.004
Brazil	7976	1	0.004	0.003	0.004	0.973	0.003	0.005	0.006	0.003
Brazil	7977	2	0.008	0.002	0.001	0.956	0.002	0.018	0.009	0.003
Brazil	7978	1	0.009	0.003	0.005	0.876	0.006	0.007	0.009	0.084
Brazil	7979	2	0.014	0.004	0.011	0.929	0.007	0.008	0.016	0.011
Brazil	7980	2	0.029	0.009	0.002	0.643	0.015	0.268	0.022	0.01
Brazil	7981	2	0.004	0.002	0.005	0.766	0.003	0.006	0.209	0.005
Brazil	7982	20	0.017	0.006	0.011	0.755	0.14	0.01	0.042	0.019
Brazil	7983	4	0.04	0.007	0.108	0.713	0.094	0.025	0.004	0.007
Brazil	7984	15	0.017	0.005	0.277	0.606	0.011	0.035	0.042	0.006
Brazil	7985	5	0.015	0.003	0.007	0.922	0.012	0.015	0.01	0.015
Brazil	7986	3	0.007	0.004	0.104	0.813	0.008	0.048	0.012	0.005
Brazil	7987	2	0.028	0.003	0.08	0.835	0.025	0.021	0.003	0.005
Brazil	7988	0	0.014	0.006	0.092	0.807	0.035	0.023	0.01	0.012

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Brazil	7989	1	0.008	0.004	0.263	0.69	0.015	0.008	0.005	0.008
Brazil	7990	1	0.005	0.002	0.105	0.867	0.008	0.004	0.003	0.005
Finland	8077	11	0.047	0.008	0.002	0.928	0.003	0.006	0.003	0.004
Finland	8084	11	0.263	0.006	0.005	0.69	0.014	0.004	0.013	0.004
Finland	8086	5	0.061	0.006	0.003	0.881	0.008	0.033	0.004	0.004
Finland	8089	8	0.014	0.015	0.005	0.798	0.116	0.012	0.018	0.022
Finland	8093	16	0.175	0.004	0.002	0.749	0.004	0.058	0.004	0.005
Finland	8094	9	0.04	0.076	0.015	0.808	0.019	0.032	0.003	0.008
Finland	8096	7	0.046	0.01	0.002	0.927	0.002	0.007	0.002	0.004
Finland	8107	24	0.004	0.002	0.001	0.982	0.003	0.003	0.002	0.003
Finland	8110	10	0.064	0.006	0.004	0.859	0.047	0.013	0.003	0.004
Finland	8116	16	0.01	0.006	0.009	0.899	0.012	0.011	0.009	0.044
Finland	8120	21	0.03	0.004	0.003	0.929	0.003	0.015	0.012	0.004
Germany	8711	4	0.006	0.002	0.002	0.976	0.002	0.005	0.003	0.003
Germany	8712	3	0.008	0.015	0.003	0.951	0.011	0.003	0.004	0.005
Germany	8713	3	0.073	0.015	0.004	0.822	0.008	0.03	0.031	0.016
Germany	8714	2	0.061	0.024	0.007	0.878	0.009	0.013	0.004	0.004
Germany	8715	4	0.014	0.005	0.002	0.964	0.003	0.006	0.002	0.003
Germany	8716	3	0.008	0.004	0.003	0.968	0.005	0.006	0.004	0.003
Germany	8717	11	0.008	0.005	0.003	0.968	0.006	0.005	0.003	0.002
Germany	8720	3	0.009	0.004	0.61	0.348	0.017	0.007	0.003	0.003
Germany	8721	10	0.101	0.004	0.002	0.87	0.002	0.012	0.002	0.006
Germany	8727	1	0.021	0.004	0.002	0.931	0.007	0.024	0.004	0.007
Germany	8728	10	0.006	0.003	0.003	0.964	0.005	0.005	0.003	0.01
Germany	8729	2	0.005	0.002	0.002	0.983	0.002	0.003	0.002	0.002
Germany	8730	22	0.048	0.002	0.007	0.869	0.007	0.015	0.038	0.014
Germany	8731	12	0.007	0.002	0.002	0.974	0.003	0.005	0.004	0.004
Germany	8732	4	0.015	0.003	0.002	0.956	0.006	0.009	0.003	0.007
Germany	8733	16	0.018	0.01	0.041	0.855	0.004	0.007	0.005	0.06
Germany	8734	1	0.008	0.002	0.001	0.976	0.002	0.007	0.002	0.002
Germany	8735	2	0.022	0.003	0.007	0.952	0.005	0.005	0.004	0.002
Germany	8736	1	0.026	0.015	0.002	0.919	0.005	0.023	0.007	0.003
Germany	8737	3	0.037	0.011	0.005	0.916	0.006	0.007	0.005	0.014
Germany	8738	10	0.191	0.038	0.002	0.751	0.004	0.008	0.002	0.003
Germany	8739	2	0.012	0.002	0.002	0.967	0.002	0.008	0.002	0.005
Germany	8741	11	0.04	0.003	0.002	0.935	0.006	0.008	0.003	0.003
Germany	8742	9	0.022	0.003	0.006	0.956	0.004	0.004	0.004	0.002
Germany	8744	6	0.23	0.004	0.085	0.539	0.008	0.108	0.02	0.006
Germany	8745	23	0.084	0.005	0.002	0.888	0.004	0.01	0.003	0.006
Germany	8746	1	0.007	0.003	0.004	0.958	0.004	0.005	0.002	0.016
Germany	8747	13	0.004	0.002	0.003	0.978	0.004	0.004	0.003	0.003
Germany	8749	2	0.007	0.004	0.002	0.976	0.003	0.003	0.002	0.003
Italy-Milan	8050	1	0.353	0.055	0.02	0.483	0.016	0.01	0.058	0.005
Italy-Milan	8057	2	0.633	0.011	0.058	0.265	0.018	0.005	0.004	0.006
Italy-Milan	8060	1	0.353	0.011	0.046	0.551	0.009	0.015	0.003	0.012
Italy-Milan	8061	2	0.327	0.012	0.154	0.464	0.009	0.019	0.006	0.009
Italy-Milan	8062	3	0.644	0.004	0.005	0.273	0.007	0.056	0.004	0.006
Italy-Milan	8065	5	0.032	0.004	0.004	0.508	0.004	0.434	0.004	0.009
Italy-Milan	8066	1	0.349	0.007	0.082	0.529	0.018	0.006	0.003	0.005
Italy-Milan	8067	2	0.065	0.016	0.041	0.513	0.006	0.338	0.003	0.019
Italy-Milan	8068	2	0.543	0.004	0.007	0.353	0.007	0.075	0.004	0.009
Italy-Milan	8069	1	0.412	0.008	0.039	0.429	0.083	0.018	0.005	0.006
Italy-Milan	8071	3	0.045	0.006	0.006	0.894	0.007	0.016	0.01	0.016
Italy-Milan	8072	3	0.507	0.006	0.083	0.259	0.029	0.042	0.07	0.004
Italy-Milan	8073	1	0.124	0.015	0.01	0.66	0.013	0.169	0.006	0.003
Italy-Milan	8074	2	0.008	0.002	0.292	0.66	0.013	0.017	0.003	0.005

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Italy-Rome	8586	1	0.061	0.009	0.003	0.517	0.009	0.359	0.014	0.027
Italy-Rome	8589	3	0.088	0.003	0.005	0.788	0.015	0.072	0.025	0.005
Italy-Rome	8592	2	0.458	0.075	0.005	0.394	0.034	0.018	0.011	0.005
Italy-Rome	8594	1	0.241	0.017	0.016	0.679	0.011	0.024	0.006	0.007
Italy-Rome	8595	1	0.122	0.091	0.016	0.565	0.093	0.09	0.015	0.008
Italy-Rome	8596	1	0.161	0.006	0.007	0.459	0.009	0.345	0.008	0.005
Italy-Rome	8597	1	0.053	0.026	0.016	0.704	0.012	0.174	0.011	0.004
Italy-Rome	8599	1	0.024	0.004	0.015	0.854	0.009	0.061	0.029	0.003
Italy-Rome	8601	2	0.112	0.144	0.006	0.645	0.01	0.036	0.038	0.009
Italy-Rome	8602	3	0.237	0.006	0.006	0.635	0.036	0.071	0.005	0.004
Italy-Rome	8603	1	0.021	0.012	0.015	0.882	0.012	0.05	0.005	0.003
Italy-Rome	8604	3	0.142	0.007	0.003	0.547	0.004	0.025	0.263	0.008
Italy-Rome	8609	2	0.149	0.006	0.005	0.612	0.007	0.211	0.006	0.004
Italy-Rome	8610	2	0.235	0.005	0.005	0.59	0.007	0.139	0.01	0.01
Italy-Rome	8611	2	0.421	0.021	0.004	0.504	0.007	0.032	0.004	0.007
Turkey	6477	3	0.924	0.003	0.006	0.044	0.007	0.008	0.005	0.003
Turkey	6478	12	0.927	0.004	0.003	0.013	0.005	0.032	0.014	0.003
Turkey	6480	9	0.703	0.003	0.017	0.227	0.005	0.018	0.02	0.008
Turkey	6481	13	0.93	0.015	0.003	0.008	0.007	0.01	0.018	0.009
Turkey	6482	8	0.012	0.005	0.959	0.006	0.004	0.005	0.005	0.004
Turkey	6484	10	0.01	0.005	0.003	0.965	0.005	0.004	0.002	0.006
Turkey	6486	6	0.896	0.005	0.004	0.067	0.006	0.01	0.006	0.007
Turkey	6487	13	0.906	0.002	0.003	0.052	0.005	0.026	0.003	0.003
Turkey	6488	11	0.748	0.005	0.003	0.203	0.006	0.015	0.014	0.007
Turkey	6491	6	0.781	0.014	0.002	0.039	0.003	0.157	0.003	0.002
Turkey	6494	12	0.241	0.026	0.01	0.014	0.008	0.688	0.006	0.007
Turkey	6496	10	0.875	0.004	0.004	0.011	0.008	0.086	0.003	0.009
Turkey	6499	11	0.096	0.008	0.679	0.034	0.088	0.028	0.008	0.059
Turkey	6500	12	0.839	0.004	0.007	0.098	0.006	0.015	0.007	0.023
Turkey	6502	6	0.904	0.004	0.004	0.029	0.01	0.035	0.004	0.01
Turkey	6503	8	0.932	0.005	0.006	0.029	0.008	0.007	0.003	0.012
Turkey	6507	13	0.928	0.003	0.002	0.031	0.004	0.025	0.005	0.002
Turkey	6510	11	0.763	0.016	0.003	0.024	0.018	0.162	0.012	0.003
Turkey	6512	12	0.569	0.021	0.004	0.221	0.039	0.11	0.005	0.03
Turkey	6513	15	0.026	0.009	0.534	0.13	0.008	0.025	0.026	0.242
Turkey	6514	10	0.516	0.05	0.006	0.293	0.021	0.088	0.022	0.004
Turkey	6516	11	0.893	0.004	0.021	0.028	0.025	0.01	0.009	0.011
Turkey	6519	11	0.59	0.005	0.003	0.358	0.004	0.016	0.009	0.014
Turkey	6520	15	0.859	0.004	0.002	0.076	0.003	0.045	0.005	0.008
Turkey	6521	6	0.724	0.007	0.006	0.068	0.006	0.136	0.021	0.034
Turkey	6729	2	0.374	0.456	0.004	0.023	0.024	0.012	0.072	0.035
Turkey	6730	2	0.767	0.003	0.002	0.099	0.003	0.11	0.007	0.01
Turkey	6731	3	0.794	0.012	0.004	0.161	0.006	0.016	0.002	0.004
Turkey	6732	2	0.7	0.038	0.018	0.024	0.124	0.04	0.038	0.018
Turkey	6733	4	0.93	0.005	0.008	0.013	0.009	0.018	0.01	0.007
Turkey	6734	1	0.891	0.006	0.013	0.019	0.011	0.038	0.013	0.009
Turkey	6735	3	0.974	0.003	0.002	0.003	0.002	0.011	0.002	0.003
Turkey	6736	1	0.338	0.008	0.002	0.198	0.01	0.436	0.003	0.005
Turkey	6738	3	0.936	0.003	0.001	0.021	0.003	0.029	0.002	0.004
Turkey	6739	4	0.62	0.017	0.004	0.3	0.025	0.021	0.003	0.01
Turkey	6740	1	0.003	0.002	0.001	0.984	0.002	0.002	0.002	0.003
Turkey	6741	2	0.021	0.007	0.824	0.066	0.016	0.008	0.021	0.036
Turkey	6742	4	0.906	0.01	0.007	0.03	0.027	0.007	0.008	0.004
Turkey	6743	2	0.813	0.004	0.007	0.139	0.007	0.019	0.003	0.008
Turkey	6745	1	0.791	0.007	0.002	0.159	0.004	0.014	0.017	0.006
Turkey	6746	2	0.435	0.018	0.208	0.119	0.173	0.01	0.026	0.011

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Turkey	6748	3	0.829	0.01	0.017	0.033	0.026	0.047	0.004	0.035
Turkey	6749	2	0.824	0.007	0.013	0.135	0.004	0.01	0.004	0.002
Turkey	6750	3	0.571	0.002	0.002	0.371	0.004	0.043	0.003	0.005
Turkey	6753	2	0.706	0.028	0.005	0.167	0.02	0.042	0.028	0.004
Turkey	6754	3	0.914	0.033	0.004	0.032	0.004	0.007	0.003	0.003
Turkey	6755	3	0.918	0.005	0.003	0.05	0.003	0.011	0.007	0.003
Turkey	6756	2	0.782	0.003	0.002	0.187	0.003	0.018	0.002	0.004
Turkey	6758	3	0.755	0.009	0.005	0.066	0.017	0.118	0.025	0.005
Turkey	6759	4	0.832	0.004	0.003	0.085	0.011	0.045	0.008	0.013
Turkey	6760	2	0.77	0.005	0.002	0.189	0.003	0.006	0.003	0.021
Cyprus	10128	3	0.908	0.004	0.003	0.018	0.017	0.015	0.031	0.004
Cyprus	10129	1	0.478	0.008	0.004	0.354	0.006	0.136	0.005	0.008
Cyprus	10130	3	0.797	0.002	0.003	0.096	0.012	0.083	0.003	0.005
Cyprus	10131	1	0.735	0.008	0.022	0.027	0.116	0.061	0.026	0.005
Cyprus	10132	0	0.667	0.014	0.017	0.005	0.02	0.245	0.008	0.024
Cyprus	10133	3	0.892	0.008	0.01	0.035	0.009	0.032	0.006	0.008
Cyprus	10134	1	0.793	0.01	0.003	0.017	0.012	0.131	0.005	0.03
Cyprus	10135	2	0.576	0.004	0.004	0.042	0.033	0.245	0.01	0.085
Cyprus	10136	3	0.697	0.039	0.002	0.206	0.009	0.017	0.015	0.015
Cyprus	10137	1	0.886	0.061	0.002	0.007	0.006	0.026	0.01	0.003
Cyprus	10138	2	0.551	0.013	0.007	0.006	0.012	0.397	0.006	0.007
Cyprus	10139	3	0.386	0.026	0.027	0.014	0.082	0.389	0.044	0.032
Cyprus	10140	0	0.939	0.006	0.004	0.011	0.006	0.023	0.005	0.006
Cyprus	10141	1	0.828	0.004	0.003	0.04	0.007	0.106	0.006	0.007
Cyprus	10142	1	0.879	0.011	0.007	0.005	0.017	0.05	0.009	0.021
Cyprus	10143	1	0.858	0.006	0.002	0.005	0.005	0.115	0.007	0.003
Cyprus	10144	3	0.83	0.007	0.005	0.008	0.048	0.057	0.005	0.039
Cyprus	10145	2	0.942	0.004	0.002	0.027	0.003	0.015	0.004	0.003
Cyprus	10146	0	0.12	0.014	0.003	0.007	0.019	0.793	0.006	0.038
Cyprus	10147	2	0.968	0.002	0.002	0.012	0.003	0.007	0.002	0.004
Cyprus	10148	1	0.158	0.016	0.018	0.016	0.04	0.729	0.01	0.013
Cyprus	10149	3	0.772	0.093	0.006	0.024	0.025	0.039	0.007	0.033
Cyprus	10150	1	0.819	0.006	0.013	0.017	0.008	0.126	0.008	0.003
Cyprus	10151	2	0.913	0.009	0.005	0.005	0.014	0.041	0.009	0.004
Cyprus	10152	2	0.762	0.013	0.006	0.06	0.007	0.138	0.01	0.004
Cyprus	10153	1	0.945	0.008	0.002	0.005	0.004	0.011	0.021	0.004
Cyprus	10154	1	0.144	0.018	0.005	0.025	0.163	0.635	0.006	0.004
Cyprus	10155	3	0.885	0.003	0.009	0.004	0.016	0.022	0.005	0.056
Cyprus	10156	5	0.856	0.02	0.007	0.006	0.01	0.074	0.023	0.005
Cyprus	10157	2	0.239	0.127	0.005	0.011	0.005	0.6	0.005	0.007
Lebanon	10235	9	0.226	0.643	0.008	0.031	0.016	0.056	0.007	0.012
Lebanon	10236	6	0.411	0.555	0.006	0.005	0.006	0.009	0.004	0.003
Lebanon	10237	15	0.071	0.642	0.002	0.026	0.008	0.242	0.004	0.004
Lebanon	10238	18	0.083	0.787	0.007	0.01	0.018	0.065	0.026	0.005
Lebanon	10239	10	0.03	0.88	0.005	0.006	0.031	0.036	0.007	0.005
Lebanon	10240	3	0.108	0.645	0.005	0.008	0.046	0.074	0.098	0.017
Lebanon	10241	5	0.038	0.878	0.005	0.037	0.006	0.022	0.005	0.008
Lebanon	10242	1	0.12	0.778	0.005	0.012	0.037	0.037	0.007	0.004
Lebanon	10243	2	0.009	0.806	0.097	0.004	0.012	0.009	0.019	0.043
Lebanon	10244	4	0.084	0.777	0.003	0.08	0.015	0.027	0.006	0.009
Lebanon	10245	16	0.036	0.65	0.006	0.008	0.012	0.188	0.062	0.038
Lebanon	10246	15	0.314	0.593	0.003	0.007	0.016	0.054	0.005	0.009
Lebanon	10247	1	0.133	0.795	0.004	0.004	0.004	0.051	0.004	0.004
Lebanon	10248	1	0.016	0.738	0.024	0.008	0.183	0.015	0.01	0.006
Lebanon	10249	1	0.04	0.646	0.002	0.018	0.01	0.274	0.007	0.004
Lebanon	10250	1	0.021	0.837	0.057	0.046	0.007	0.02	0.008	0.004

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling	ID	Missing	Population							
Location	No.	Data	1	2	3	4	5	6	7	8
Lebanon	10251	14	0.012	0.878	0.007	0.006	0.025	0.014	0.008	0.052
Lebanon	10252	8	0.037	0.774	0.014	0.006	0.045	0.098	0.019	0.007
Lebanon	10253	19	0.08	0.836	0.004	0.005	0.015	0.021	0.011	0.027
Lebanon	10254	1	0.124	0.767	0.003	0.029	0.008	0.049	0.002	0.016
Lebanon	10255	2	0.168	0.618	0.004	0.118	0.005	0.076	0.005	0.006
Lebanon	10256	1	0.054	0.822	0.041	0.009	0.01	0.053	0.008	0.005
Lebanon	10257	3	0.027	0.833	0.006	0.025	0.009	0.085	0.007	0.009
Lebanon	10258	1	0.291	0.591	0.004	0.032	0.007	0.037	0.033	0.005
Lebanon	10259	3	0.19	0.585	0.036	0.006	0.035	0.075	0.069	0.004
Lebanon	10260	8	0.02	0.897	0.014	0.005	0.019	0.026	0.011	0.007
Lebanon	10261	7	0.202	0.66	0.007	0.078	0.006	0.033	0.007	0.006
Lebanon	10262	1	0.187	0.504	0.007	0.086	0.018	0.181	0.011	0.005
Lebanon	10263	2	0.021	0.503	0.003	0.008	0.025	0.41	0.01	0.02
Lebanon	10264	3	0.079	0.788	0.003	0.016	0.009	0.086	0.002	0.018
Lebanon	10265	3	0.017	0.485	0.007	0.003	0.005	0.46	0.01	0.012
Lebanon	10266	1	0.121	0.715	0.003	0.007	0.004	0.061	0.085	0.005
Lebanon	10267	4	0.052	0.742	0.046	0.005	0.088	0.02	0.015	0.031
Lebanon	10268	5	0.033	0.749	0.023	0.004	0.036	0.109	0.004	0.042
Lebanon	10270	3	0.031	0.67	0.007	0.004	0.006	0.252	0.02	0.01
Lebanon	10271	3	0.225	0.578	0.004	0.042	0.01	0.133	0.005	0.003
Lebanon	10273	1	0.021	0.71	0.053	0.006	0.188	0.009	0.007	0.006
Lebanon	10274	4	0.121	0.754	0.005	0.009	0.009	0.085	0.01	0.007
Lebanon	10276	2	0.193	0.585	0.003	0.044	0.007	0.13	0.032	0.006
Lebanon	10277	3	0.084	0.757	0.013	0.005	0.005	0.125	0.007	0.004
Lebanon	10278	2	0.298	0.593	0.004	0.057	0.009	0.021	0.011	0.007
Lebanon	10279	13	0.034	0.894	0.015	0.01	0.01	0.014	0.017	0.007
Lebanon	10280	0	0.048	0.682	0.029	0.002	0.114	0.119	0.004	0.003
Lebanon	10281	2	0.172	0.609	0.011	0.005	0.069	0.08	0.045	0.009
Lebanon	10282	15	0.021	0.668	0.007	0.008	0.13	0.136	0.008	0.022
Lebanon	10283	18	0.06	0.826	0.005	0.042	0.017	0.028	0.011	0.011
Lebanon	10284	14	0.02	0.742	0.007	0.008	0.026	0.03	0.153	0.013
Lebanon	10285	17	0.03	0.892	0.003	0.007	0.005	0.034	0.018	0.011
Lebanon	10286	15	0.036	0.752	0.002	0.006	0.008	0.062	0.125	0.008
Lebanon	10287	21	0.003	0.927	0.007	0.003	0.024	0.004	0.028	0.003
Lebanon	10288	4	0.006	0.949	0.006	0.002	0.007	0.008	0.016	0.006
Lebanon	10289	5	0.006	0.848	0.004	0.008	0.004	0.006	0.037	0.087
Lebanon	10290	3	0.006	0.949	0.013	0.004	0.007	0.007	0.004	0.01
Lebanon	10291	2	0.018	0.827	0.008	0.01	0.072	0.023	0.027	0.015
Lebanon	10292	3	0.022	0.73	0.019	0.008	0.066	0.021	0.093	0.041
Lebanon	10294	9	0.215	0.684	0.005	0.011	0.036	0.018	0.014	0.016
Lebanon	10295	1	0.012	0.7	0.006	0.004	0.23	0.017	0.016	0.014
Lebanon	10297	3	0.004	0.905	0.055	0.003	0.013	0.005	0.006	0.009
Lebanon	10298	2	0.022	0.841	0.007	0.023	0.02	0.014	0.067	0.006
Lebanon	10299	2	0.021	0.846	0.023	0.027	0.052	0.011	0.015	0.005
Lebanon	10300	2	0.003	0.943	0.015	0.003	0.012	0.005	0.009	0.01
Israel	4962	15	0.008	0.96	0.003	0.004	0.009	0.006	0.005	0.006
Israel	4963	1	0.006	0.953	0.004	0.003	0.008	0.004	0.004	0.017
Israel	4964	1	0.003	0.966	0.011	0.002	0.004	0.002	0.008	0.004
Israel	4966	1	0.007	0.924	0.004	0.006	0.008	0.005	0.025	0.022
Israel	4967	1	0.005	0.974	0.001	0.002	0.006	0.004	0.002	0.007
Israel	4968	2	0.002	0.982	0.001	0.002	0.004	0.002	0.003	0.004
Israel	4969	2	0.007	0.928	0.01	0.004	0.008	0.01	0.006	0.027
Israel	4970	2	0.004	0.965	0.008	0.004	0.007	0.003	0.004	0.005
Israel	4971	1	0.003	0.981	0.004	0.001	0.003	0.002	0.003	0.002
Israel	4972	2	0.002	0.985	0.002	0.001	0.002	0.002	0.003	0.002
Israel	4973	3	0.002	0.969	0.004	0.002	0.005	0.003	0.007	0.007

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling	ID	Missing	Population							
Location	No.	Data	1	2	3	4	5	6	7	8
Israel	4974	19	0.002	0.961	0.002	0.004	0.01	0.004	0.004	0.012
Israel	4975	3	0.003	0.978	0.002	0.002	0.003	0.003	0.003	0.005
Israel	4976	1	0.002	0.984	0.002	0.001	0.002	0.002	0.004	0.002
Israel	4977	2	0.004	0.971	0.002	0.003	0.003	0.005	0.008	0.003
Israel	4978	3	0.003	0.957	0.005	0.002	0.014	0.003	0.013	0.003
Israel	4979	1	0.003	0.973	0.008	0.004	0.005	0.002	0.003	0.003
Israel	4980	3	0.002	0.986	0.002	0.002	0.002	0.002	0.002	0.002
Israel	4981	1	0.002	0.986	0.002	0.001	0.002	0.002	0.002	0.002
Israel	4982	3	0.011	0.946	0.008	0.005	0.013	0.008	0.004	0.006
Israel	4983	3	0.003	0.972	0.004	0.003	0.007	0.003	0.004	0.004
Israel	4984	3	0.004	0.98	0.002	0.003	0.003	0.003	0.002	0.003
Israel	4985	1	0.002	0.981	0.002	0.001	0.003	0.002	0.005	0.004
Israel	4986	2	0.002	0.974	0.003	0.002	0.004	0.002	0.003	0.011
Israel	4988	2	0.007	0.941	0.007	0.006	0.007	0.007	0.013	0.013
Israel	4989	3	0.005	0.97	0.004	0.004	0.007	0.003	0.002	0.005
Israel	4990	2	0.004	0.956	0.004	0.006	0.011	0.002	0.004	0.012
Israel	4992	3	0.004	0.973	0.004	0.002	0.004	0.003	0.004	0.006
Israel	4993	2	0.002	0.972	0.005	0.002	0.005	0.003	0.008	0.003
Israel	4994	2	0.005	0.972	0.002	0.003	0.006	0.007	0.002	0.003
Israel	4995	3	0.004	0.904	0.003	0.003	0.006	0.008	0.003	0.069
Israel	4996	3	0.006	0.944	0.008	0.006	0.007	0.005	0.02	0.003
Israel	4997	2	0.007	0.923	0.008	0.01	0.007	0.009	0.031	0.005
Israel	4998	3	0.008	0.932	0.008	0.004	0.013	0.005	0.025	0.004
Israel	5000	2	0.014	0.95	0.003	0.012	0.007	0.005	0.005	0.005
Israel	5001	2	0.004	0.944	0.011	0.002	0.014	0.005	0.015	0.005
Israel	5002	1	0.002	0.971	0.002	0.003	0.004	0.002	0.004	0.011
Israel	5003	1	0.014	0.943	0.005	0.01	0.004	0.007	0.005	0.012
Israel	5004	2	0.007	0.964	0.002	0.004	0.006	0.005	0.004	0.009
Israel	5005	3	0.003	0.976	0.002	0.003	0.002	0.004	0.006	0.004
Israel	5006	2	0.006	0.957	0.012	0.005	0.006	0.005	0.007	0.002
Israel	5007	1	0.009	0.862	0.008	0.005	0.018	0.007	0.02	0.073
Israel	5008	2	0.002	0.984	0.002	0.002	0.002	0.003	0.003	0.002
Israel	5009	3	0.005	0.938	0.011	0.003	0.028	0.004	0.004	0.006
Israel	5010	3	0.004	0.925	0.014	0.01	0.012	0.005	0.027	0.005
Israel	5011	2	0.005	0.921	0.005	0.006	0.029	0.005	0.017	0.013
Egypt-Cairo	8190	4	0.016	0.714	0.008	0.007	0.013	0.009	0.23	0.004
Egypt-Cairo	8192	2	0.128	0.712	0.003	0.017	0.031	0.103	0.003	0.004
Egypt-Cairo	8193	2	0.006	0.886	0.004	0.002	0.007	0.004	0.086	0.005
Egypt-Cairo	8196	3	0.004	0.965	0.002	0.007	0.005	0.003	0.003	0.01
Egypt-Cairo	8203	2	0.005	0.947	0.003	0.003	0.021	0.006	0.005	0.009
Egypt-Cairo	8215	3	0.022	0.934	0.015	0.007	0.011	0.007	0.003	0.002
Egypt-Cairo	8198	3	0.012	0.913	0.004	0.006	0.032	0.011	0.004	0.016
Egypt-Cairo	8194	3	0.003	0.968	0.002	0.004	0.006	0.002	0.009	0.005
Egypt-Cairo	8211	2	0.002	0.981	0.003	0.002	0.003	0.002	0.004	0.003
Egypt-Cairo	8216	3	0.005	0.965	0.005	0.004	0.008	0.005	0.002	0.005
Egypt-Cairo	8195	1	0.004	0.963	0.005	0.004	0.005	0.003	0.012	0.004
Egypt-Cairo	8199	2	0.003	0.981	0.002	0.002	0.003	0.003	0.002	0.003
Egypt-Cairo	8200	1	0.002	0.967	0.004	0.003	0.003	0.002	0.003	0.016
Egypt-Cairo	8201	3	0.003	0.938	0.002	0.002	0.003	0.003	0.005	0.045
Egypt-Cairo	8202	2	0.003	0.978	0.002	0.002	0.003	0.002	0.006	0.003
Egypt-Cairo	8204	3	0.004	0.926	0.004	0.003	0.004	0.004	0.046	0.01
Egypt-Cairo	8208	2	0.002	0.973	0.004	0.002	0.004	0.002	0.003	0.011
Egypt-Cairo	8210	1	0.007	0.907	0.005	0.024	0.025	0.012	0.003	0.017
Egypt-Cairo	8214	4	0.007	0.951	0.006	0.003	0.006	0.008	0.016	0.002
Egypt-Cairo	8191	3	0.004	0.945	0.006	0.008	0.014	0.004	0.004	0.014
Egypt-Cairo	8197	2	0.002	0.988	0.001	0.002	0.002	0.002	0.002	0.002

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling	ID	Missing	Population							
Location	No.	Data	1	2	3	4	5	6	7	8
Egypt-Cairo	8205	2	0.002	0.986	0.002	0.002	0.002	0.002	0.003	0.002
Egypt-Cairo	8206	6	0.006	0.872	0.013	0.027	0.037	0.005	0.005	0.034
Egypt-Cairo	8207	6	0.017	0.828	0.003	0.037	0.042	0.018	0.021	0.035
Egypt-Cairo	8209	3	0.003	0.947	0.004	0.002	0.004	0.003	0.013	0.023
Egypt-Cairo	8212	5	0.005	0.946	0.004	0.004	0.004	0.003	0.031	0.005
Egypt-Cairo	8213	4	0.003	0.947	0.003	0.002	0.004	0.002	0.034	0.005
Egypt-Cairo	9942	3	0.006	0.967	0.003	0.005	0.006	0.004	0.005	0.003
Egypt-Cairo	9943	6	0.009	0.92	0.003	0.005	0.003	0.004	0.007	0.049
Egypt-Cairo	9944	5	0.01	0.944	0.003	0.004	0.009	0.004	0.004	0.023
Egypt-Cairo	9945	4	0.12	0.814	0.01	0.008	0.01	0.019	0.007	0.012
Egypt-Cairo	9946	4	0.004	0.951	0.011	0.005	0.01	0.003	0.003	0.013
Egypt-Cairo	9947	7	0.005	0.925	0.005	0.004	0.005	0.004	0.004	0.048
Egypt-Cairo	9948	3	0.007	0.934	0.006	0.006	0.006	0.004	0.031	0.006
Egypt-Cairo	9949	3	0.012	0.914	0.012	0.009	0.026	0.006	0.005	0.017
Egypt-Cairo	9950	4	0.01	0.945	0.005	0.013	0.009	0.005	0.004	0.009
Egypt-Cairo	9951	4	0.005	0.909	0.002	0.005	0.007	0.004	0.002	0.067
Egypt-Cairo	9952	8	0.004	0.827	0.003	0.004	0.027	0.003	0.007	0.124
Egypt-Cairo	9953	9	0.043	0.889	0.009	0.003	0.018	0.018	0.015	0.005
Egypt-Cairo	9954	3	0.019	0.891	0.002	0.018	0.009	0.024	0.005	0.033
Egypt-Cairo	9955	3	0.002	0.963	0.002	0.001	0.004	0.002	0.022	0.003
Egypt-Cairo	9956	4	0.002	0.963	0.002	0.001	0.004	0.002	0.022	0.004
Egypt-Cairo	9957	3	0.008	0.877	0.006	0.005	0.076	0.008	0.014	0.006
Egypt-Cairo	9958	5	0.002	0.976	0.004	0.002	0.003	0.002	0.005	0.005
Egypt-Cairo	9959	4	0.002	0.966	0.005	0.002	0.013	0.002	0.007	0.002
Egypt-Cairo	9960	5	0.003	0.972	0.002	0.003	0.004	0.004	0.009	0.003
Egypt-Cairo	9961	4	0.017	0.84	0.007	0.007	0.061	0.027	0.018	0.023
Egypt-Cairo	9962	14	0.044	0.872	0.041	0.016	0.009	0.011	0.003	0.005
Egypt-Cairo	9963	1	0.084	0.107	0.002	0.012	0.144	0.025	0.002	0.625
Egypt-Cairo	9964	2	0.011	0.259	0.021	0.013	0.039	0.025	0.014	0.617
Egypt-Cairo	10021	4	0.007	0.044	0.005	0.003	0.488	0.004	0.004	0.444
Egypt-Cairo	10022	1	0.014	0.431	0.01	0.032	0.062	0.034	0.099	0.318
Egypt-Cairo	10023	2	0.022	0.033	0.016	0.007	0.487	0.042	0.028	0.364
Egypt-Cairo	10024	4	0.009	0.33	0.012	0.006	0.041	0.005	0.178	0.42
Egypt-Cairo	10025	3	0.015	0.18	0.005	0.015	0.012	0.01	0.008	0.755
Egypt-Cairo	10026	4	0.006	0.042	0.003	0.003	0.395	0.007	0.003	0.542
Egypt-Cairo	10027	2	0.169	0.077	0.025	0.006	0.221	0.013	0.026	0.463
Egypt-Cairo	10028	3	0.01	0.18	0.004	0.005	0.083	0.008	0.011	0.699
Egypt-Cairo	10029	19	0.078	0.04	0.04	0.022	0.068	0.716	0.023	0.014
Egypt-Cairo	10030	22	0.797	0.008	0.007	0.005	0.067	0.053	0.029	0.035
Egypt-Cairo	10031	16	0.668	0.005	0.046	0.01	0.116	0.032	0.077	0.045
Egypt-Cairo	10032	3	0.324	0.053	0.016	0.051	0.03	0.51	0.006	0.01
Egypt-Cairo	10033	14	0.908	0.007	0.004	0.009	0.007	0.057	0.004	0.006
Egypt-Cairo	10034	19	0.87	0.014	0.016	0.012	0.045	0.029	0.008	0.006
Egypt-Cairo	10035	6	0.772	0.02	0.01	0.015	0.038	0.015	0.123	0.008
Egypt-Cairo	10037	2	0.806	0.014	0.016	0.05	0.011	0.084	0.006	0.013
Egypt-Cairo	10042	3	0.867	0.053	0.011	0.008	0.021	0.02	0.012	0.009
Egypt-Cairo	10043	15	0.809	0.026	0.004	0.007	0.063	0.054	0.027	0.01
Egypt-Cairo	10044	7	0.717	0.164	0.01	0.014	0.018	0.05	0.005	0.021
Egypt-Cairo	10045	15	0.658	0.036	0.014	0.019	0.014	0.251	0.003	0.005
Egypt-Cairo	10046	24	0.199	0.252	0.005	0.004	0.011	0.505	0.009	0.015
Egypt-Cairo	10047	19	0.6	0.008	0.006	0.02	0.005	0.251	0.008	0.104
Egypt-Cairo	10048	17	0.595	0.005	0.007	0.359	0.01	0.013	0.004	0.006
Egypt-Cairo	10083	22	0.887	0.051	0.003	0.014	0.005	0.024	0.011	0.006
Egypt-Cairo	10040	3	0.92	0.007	0.004	0.007	0.012	0.022	0.004	0.025
Egypt-Cairo	10041	12	0.802	0.065	0.007	0.079	0.012	0.016	0.008	0.011
Egypt-Cairo	10049	6	0.741	0.051	0.012	0.009	0.004	0.089	0.011	0.083

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Egypt-Cairo	10084	13	0.925	0.006	0.008	0.005	0.01	0.019	0.017	0.01
Egypt-Cairo	10085	7	0.4	0.177	0.022	0.047	0.011	0.328	0.011	0.005
Egypt-Cairo	10087	12	0.661	0.012	0.004	0.009	0.006	0.295	0.006	0.008
Egypt-Cairo	10090	3	0.88	0.009	0.032	0.008	0.026	0.027	0.011	0.006
Egypt-Cairo	9968	17	0.196	0.023	0.008	0.007	0.016	0.702	0.021	0.028
Egypt-Asuit	10091	2	0.037	0.005	0.553	0.021	0.014	0.36	0.006	0.005
Egypt-Asuit	10093	14	0.953	0.008	0.004	0.005	0.004	0.017	0.004	0.006
Egypt-Asuit	10094	13	0.865	0.018	0.016	0.008	0.015	0.061	0.012	0.003
Egypt-Asuit	10095	18	0.898	0.019	0.009	0.009	0.013	0.032	0.013	0.006
Egypt-Asuit	10096	3	0.893	0.009	0.006	0.007	0.008	0.064	0.004	0.008
Egypt-Asuit	10098	3	0.894	0.009	0.009	0.03	0.025	0.014	0.011	0.008
Egypt-Asuit	10099	9	0.889	0.022	0.004	0.005	0.007	0.065	0.004	0.004
Egypt-Asuit	10100	4	0.082	0.006	0.026	0.006	0.135	0.728	0.008	0.009
Egypt-Asuit	10101	13	0.519	0.007	0.003	0.364	0.003	0.094	0.004	0.005
Egypt-Asuit	10102	15	0.046	0.003	0.133	0.015	0.004	0.782	0.007	0.009
Egypt-Luxor	10038	10	0.168	0.023	0.341	0.038	0.009	0.399	0.009	0.012
Egypt-Luxor	10039	4	0.685	0.068	0.035	0.014	0.114	0.01	0.013	0.062
Egypt-Luxor	10050	5	0.685	0.022	0.032	0.071	0.02	0.065	0.096	0.009
Egypt-Luxor	10051	5	0.365	0.004	0.065	0.062	0.051	0.416	0.015	0.021
Egypt-Luxor	10052	5	0.369	0.017	0.003	0.008	0.007	0.582	0.003	0.011
Egypt-Luxor	10053	4	0.605	0.018	0.011	0.091	0.032	0.1	0.14	0.003
Egypt-Luxor	10054	5	0.382	0.043	0.003	0.012	0.012	0.489	0.032	0.027
Egypt-Luxor	10055	1	0.897	0.03	0.004	0.005	0.032	0.01	0.004	0.018
Egypt-Luxor	10056	2	0.725	0.011	0.018	0.011	0.173	0.027	0.012	0.021
Egypt-Luxor	10057	8	0.911	0.012	0.003	0.007	0.005	0.048	0.007	0.006
Egypt-Luxor	10058	3	0.395	0.014	0.04	0.008	0.018	0.505	0.015	0.006
Egypt-Luxor	10060	18	0.847	0.005	0.002	0.004	0.009	0.033	0.004	0.095
Egypt-Luxor	10061	16	0.254	0.159	0.038	0.026	0.042	0.428	0.017	0.037
Egypt-Luxor	10062	1	0.246	0.012	0.024	0.014	0.009	0.642	0.008	0.045
Egypt-Luxor	10063	5	0.614	0.097	0.14	0.008	0.1	0.018	0.015	0.007
Egypt-Luxor	10064	2	0.413	0.041	0.012	0.287	0.073	0.132	0.033	0.008
Egypt-Luxor	10065	22	0.081	0.004	0.006	0.81	0.009	0.031	0.055	0.005
Egypt-Luxor	10066	4	0.875	0.025	0.004	0.004	0.022	0.057	0.008	0.006
Egypt-Luxor	10067	3	0.687	0.02	0.018	0.006	0.108	0.065	0.051	0.045
Egypt-Luxor	10068	9	0.589	0.088	0.004	0.011	0.058	0.147	0.056	0.047
Egypt-Luxor	10069	7	0.62	0.032	0.033	0.016	0.187	0.043	0.006	0.064
Egypt-Luxor	10070	8	0.781	0.009	0.159	0.007	0.007	0.022	0.006	0.008
Egypt-Luxor	10071	6	0.37	0.08	0.025	0.045	0.034	0.398	0.03	0.019
Egypt-Luxor	10072	5	0.697	0.203	0.008	0.014	0.019	0.04	0.014	0.005
Egypt-Luxor	10073	8	0.516	0.219	0.005	0.005	0.053	0.164	0.015	0.022
Egypt-Luxor	10074	17	0.371	0.074	0.024	0.241	0.03	0.146	0.024	0.089
Egypt-Luxor	10079	20	0.927	0.015	0.017	0.005	0.016	0.01	0.006	0.005
Egypt-Luxor	10080	1	0.831	0.062	0.002	0.021	0.017	0.035	0.006	0.027
Egypt-Abu Simbel	10076	1	0.923	0.005	0.006	0.007	0.024	0.012	0.012	0.01
Egypt-Abu Simbel	10077	2	0.824	0.048	0.01	0.025	0.016	0.068	0.006	0.003
Egypt-Abu Simbel	10081	2	0.91	0.004	0.008	0.007	0.011	0.042	0.003	0.015
Egypt-Abu Simbel	10089	2	0.771	0.024	0.006	0.064	0.023	0.03	0.024	0.057
Egypt-Abu Simbel	10092	3	0.87	0.012	0.011	0.005	0.033	0.031	0.033	0.005
Iraq-West	9587	1	0.218	0.013	0.107	0.541	0.027	0.024	0.056	0.013
Iraq-West	10202	1	0.931	0.009	0.013	0.015	0.007	0.012	0.007	0.006
Iraq-West	10204	1	0.961	0.01	0.003	0.004	0.004	0.007	0.006	0.003
Iraq-West	11854	2	0.914	0.006	0.005	0.01	0.004	0.011	0.024	0.026
Iraq-West	11860	2	0.913	0.004	0.004	0.004	0.005	0.007	0.008	0.053
Iraq-West	11861	2	0.95	0.009	0.005	0.01	0.008	0.008	0.005	0.005
Iraq-West	11863	1	0.95	0.004	0.006	0.017	0.007	0.011	0.003	0.003
Iraq-West	11864	1	0.814	0.013	0.034	0.042	0.014	0.035	0.004	0.043

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Iraq-West	11888	3	0.854	0.022	0.004	0.095	0.008	0.008	0.003	0.006
Iraq-West	11889	3	0.915	0.031	0.011	0.007	0.009	0.005	0.009	0.014
Iraq-West	11890	2	0.925	0.025	0.005	0.007	0.004	0.016	0.009	0.01
Iraq-West	11891	1	0.794	0.03	0.005	0.069	0.039	0.019	0.024	0.021
Iraq-Baghdad	11847	5	0.402	0.024	0.005	0.008	0.01	0.196	0.352	0.003
Iraq-Baghdad	11848	4	0.861	0.005	0.011	0.023	0.069	0.018	0.004	0.009
Iraq-Baghdad	11849	1	0.183	0.055	0.242	0.425	0.017	0.037	0.032	0.009
Iraq-Baghdad	11850	2	0.052	0.015	0.25	0.636	0.011	0.013	0.01	0.012
Iraq-Baghdad	11852	17	0.861	0.005	0.007	0.013	0.029	0.065	0.016	0.003
Iraq-Baghdad	11853	2	0.952	0.008	0.007	0.003	0.01	0.007	0.007	0.005
Iraq-Baghdad	11855	3	0.901	0.01	0.015	0.009	0.021	0.016	0.017	0.01
Iraq-Baghdad	11856	4	0.749	0.023	0.062	0.007	0.061	0.079	0.016	0.002
Iraq-Baghdad	11857	2	0.695	0.005	0.126	0.008	0.031	0.054	0.078	0.003
Iraq-Baghdad	11858	6	0.955	0.007	0.003	0.009	0.004	0.008	0.005	0.009
Iraq-Baghdad	11859	9	0.927	0.005	0.004	0.005	0.004	0.012	0.005	0.04
Iraq-Baghdad	11862	2	0.976	0.002	0.001	0.003	0.004	0.009	0.003	0.003
Iraq-Baghdad	11865	2	0.837	0.01	0.084	0.008	0.021	0.016	0.021	0.002
Iraq-Baghdad	11868	1	0.76	0.009	0.005	0.005	0.004	0.178	0.037	0.002
Iraq-Baghdad	11869	3	0.808	0.038	0.089	0.006	0.013	0.033	0.01	0.003
Iraq-Baghdad	11870	2	0.879	0.028	0.006	0.037	0.025	0.011	0.006	0.007
Iraq-Baghdad	11871	2	0.923	0.007	0.033	0.005	0.009	0.013	0.005	0.005
Iraq-Baghdad	11872	2	0.755	0.006	0.006	0.169	0.02	0.032	0.008	0.005
Iraq-Baghdad	11873	2	0.915	0.003	0.016	0.009	0.01	0.022	0.005	0.02
Iraq-Baghdad	11874	2	0.782	0.014	0.009	0.044	0.018	0.024	0.092	0.016
Iraq-Baghdad	11875	3	0.674	0.013	0.25	0.011	0.011	0.03	0.004	0.007
Iraq-Baghdad	11876	2	0.896	0.005	0.004	0.05	0.005	0.026	0.003	0.011
Iraq-Baghdad	11877	3	0.654	0.013	0.003	0.018	0.007	0.297	0.004	0.004
Iraq-Baghdad	11878	2	0.706	0.004	0.059	0.022	0.023	0.037	0.124	0.024
Iraq-Baghdad	11879	1	0.701	0.012	0.028	0.022	0.006	0.167	0.007	0.058
Iraq-Baghdad	11880	3	0.53	0.041	0.275	0.015	0.007	0.12	0.007	0.004
Iraq-Baghdad	11881	4	0.964	0.003	0.002	0.006	0.004	0.015	0.002	0.003
Iraq-Baghdad	11882	2	0.955	0.007	0.009	0.005	0.006	0.009	0.005	0.004
Iraq-Baghdad	11883	3	0.012	0.007	0.013	0.032	0.01	0.914	0.006	0.007
Iraq-Baghdad	11884	5	0.057	0.023	0.01	0.143	0.017	0.667	0.005	0.078
Iraq-Baghdad	11885	4	0.03	0.027	0.003	0.018	0.019	0.891	0.005	0.007
Iraq-Baghdad	11886	4	0.034	0.012	0.015	0.004	0.04	0.864	0.017	0.014
Iraq-Baghdad	11887	4	0.039	0.005	0.017	0.012	0.008	0.908	0.007	0.003
Iran	9419	3	0.03	0.008	0.004	0.007	0.025	0.917	0.006	0.004
Iran	9420	3	0.016	0.01	0.01	0.026	0.009	0.91	0.006	0.012
Iran	9421	1	0.022	0.015	0.015	0.105	0.008	0.814	0.009	0.012
Iran	9422	9	0.673	0.007	0.003	0.006	0.003	0.301	0.004	0.003
Iran	9424	2	0.039	0.008	0.025	0.12	0.006	0.79	0.004	0.008
Iran	9425	2	0.325	0.01	0.004	0.022	0.014	0.58	0.012	0.032
Iran	9426	8	0.025	0.005	0.002	0.005	0.016	0.923	0.005	0.018
Iran	9427	13	0.273	0.015	0.003	0.042	0.005	0.654	0.006	0.002
Iran	9428	1	0.491	0.077	0.007	0.037	0.069	0.27	0.029	0.019
Iran	9429	2	0.035	0.047	0.616	0.011	0.112	0.157	0.01	0.013
Iran	9430	2	0.133	0.003	0.006	0.01	0.013	0.822	0.008	0.005
Iran	9431	1	0.081	0.022	0.005	0.012	0.027	0.829	0.019	0.006
Iran	9432	3	0.174	0.065	0.004	0.007	0.042	0.681	0.008	0.021
Iran	9433	2	0.01	0.009	0.004	0.005	0.006	0.957	0.006	0.003
Iran	9434	2	0.373	0.025	0.011	0.016	0.011	0.537	0.02	0.007
Iran	9435	1	0.064	0.008	0.009	0.006	0.01	0.851	0.003	0.05
Iran	9436	1	0.08	0.023	0.004	0.012	0.057	0.788	0.032	0.005
Iran	9437	1	0.034	0.006	0.012	0.005	0.026	0.904	0.007	0.004
Iran	9438	2	0.008	0.006	0.028	0.009	0.009	0.92	0.01	0.011

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling	ID	Missing	Population							
Location	No.	Data	1	2	3	4	5	6	7	8
Iran	9439	1	0.175	0.007	0.002	0.016	0.007	0.784	0.006	0.002
Iran	9440	1	0.004	0.007	0.003	0.005	0.007	0.968	0.004	0.002
Iran	9441	1	0.007	0.007	0.003	0.008	0.007	0.961	0.005	0.003
Iran	9442	2	0.071	0.169	0.015	0.006	0.006	0.709	0.015	0.008
Iran	9443	3	0.013	0.007	0.513	0.355	0.07	0.034	0.005	0.002
Iran	9444	4	0.023	0.139	0.005	0.344	0.007	0.47	0.003	0.009
Iran	9445	0	0.022	0.016	0.007	0.014	0.027	0.897	0.005	0.012
Iran	9446	3	0.409	0.008	0.034	0.009	0.023	0.486	0.015	0.016
Iran	9447	3	0.041	0.053	0.004	0.007	0.014	0.821	0.006	0.054
Iran	9448	0	0.127	0.005	0.014	0.076	0.006	0.767	0.003	0.003
Iran	9449	0	0.027	0.006	0.027	0.016	0.024	0.886	0.009	0.004
Iran	9450	1	0.117	0.004	0.002	0.056	0.008	0.802	0.005	0.006
Iran	9451	2	0.036	0.004	0.009	0.009	0.014	0.91	0.007	0.012
Iran	9452	4	0.468	0.015	0.003	0.007	0.008	0.476	0.004	0.02
Iran	9453	8	0.449	0.071	0.01	0.426	0.013	0.022	0.005	0.004
Iran	9454	1	0.005	0.002	0.186	0.004	0.007	0.725	0.052	0.017
Iran	9455	2	0.015	0.005	0.039	0.381	0.185	0.361	0.006	0.007
Iran	9456	8	0.016	0.007	0.035	0.01	0.011	0.825	0.089	0.008
Iran	9457	2	0.047	0.016	0.006	0.032	0.014	0.751	0.129	0.005
Iran	9458	4	0.031	0.006	0.108	0.011	0.005	0.82	0.008	0.01
Iran	9459	2	0.271	0.009	0.008	0.071	0.49	0.136	0.008	0.007
Iran	9460	1	0.054	0.046	0.013	0.011	0.007	0.854	0.011	0.003
Iran	9461	5	0.029	0.006	0.393	0.012	0.054	0.491	0.012	0.004
Iran	9462	3	0.032	0.013	0.009	0.027	0.007	0.849	0.005	0.058
Iran	9463	3	0.066	0.007	0.009	0.016	0.004	0.871	0.012	0.015
Iran	9464	1	0.093	0.007	0.066	0.021	0.032	0.772	0.004	0.006
Iran	9465	6	0.01	0.005	0.002	0.004	0.003	0.964	0.003	0.009
Iran	9466	1	0.005	0.003	0.003	0.005	0.006	0.97	0.005	0.003
Iran	9468	0	0.119	0.005	0.003	0.003	0.01	0.851	0.004	0.005
Iran	9469	1	0.009	0.002	0.002	0.009	0.003	0.971	0.002	0.002
Iran	9470	2	0.933	0.015	0.004	0.01	0.01	0.019	0.004	0.006
Iran	9471	17	0.095	0.004	0.003	0.031	0.006	0.821	0.036	0.005
Iran	9472	1	0.009	0.007	0.004	0.011	0.023	0.91	0.005	0.031
Iran	9473	1	0.012	0.011	0.003	0.004	0.005	0.957	0.004	0.004
Iran	9474	3	0.006	0.008	0.001	0.004	0.003	0.971	0.003	0.004
Iran	9475	1	0.008	0.003	0.004	0.007	0.004	0.969	0.004	0.002
Iran	9476	3	0.009	0.006	0.002	0.002	0.003	0.97	0.003	0.005
Iran	9477	0	0.008	0.012	0.002	0.003	0.004	0.966	0.002	0.003
Iran	9478	1	0.077	0.006	0.003	0.003	0.007	0.895	0.005	0.005
Iran	9479	1	0.012	0.003	0.003	0.008	0.004	0.962	0.003	0.006
Iran	9480	3	0.031	0.011	0.003	0.006	0.017	0.789	0.106	0.037
Iran	9481	5	0.011	0.007	0.003	0.243	0.007	0.694	0.005	0.031
Iran	9482	1	0.06	0.015	0.014	0.05	0.014	0.804	0.01	0.033
Iran	9483	2	0.286	0.008	0.005	0.043	0.013	0.636	0.002	0.008
Iran	9484	4	0.011	0.005	0.004	0.008	0.006	0.953	0.008	0.004
Iran	9485	1	0.058	0.004	0.006	0.05	0.006	0.865	0.003	0.007
Iran	9486	0	0.014	0.004	0.007	0.008	0.011	0.941	0.01	0.004
Iran	9487	0	0.005	0.007	0.004	0.004	0.012	0.961	0.004	0.003
Iran	9488	1	0.021	0.003	0.014	0.009	0.018	0.904	0.025	0.006
Iran	9489	24	0.069	0.005	0.007	0.052	0.006	0.843	0.009	0.009
Iran	9490	2	0.149	0.007	0.005	0.047	0.025	0.741	0.014	0.011
Iran	9491	1	0.372	0.008	0.004	0.022	0.03	0.515	0.018	0.031
Iran	9492	9	0.061	0.016	0.007	0.009	0.052	0.827	0.014	0.014
Iran	9493	7	0.019	0.004	0.024	0.019	0.006	0.89	0.006	0.032
Iran	9494	19	0.362	0.003	0.024	0.062	0.009	0.486	0.003	0.051
Iran	9495	4	0.059	0.002	0.003	0.015	0.003	0.903	0.003	0.012

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Iran	9497	4	0.049	0.007	0.01	0.023	0.02	0.784	0.008	0.098
Iran	9498	0	0.027	0.015	0.004	0.015	0.007	0.905	0.005	0.022
Iran	9499	1	0.005	0.003	0.002	0.007	0.006	0.973	0.003	0.002
Iran	9500	3	0.005	0.002	0.001	0.008	0.004	0.974	0.003	0.004
Iran	9501	4	0.006	0.002	0.002	0.008	0.006	0.967	0.003	0.005
Iran	9502	13	0.024	0.005	0.005	0.019	0.006	0.933	0.003	0.006
Iran	9503	1	0.006	0.002	0.002	0.006	0.005	0.962	0.013	0.003
Iran	9504	1	0.004	0.002	0.001	0.006	0.003	0.978	0.003	0.004
Iran	9505	1	0.005	0.003	0.001	0.003	0.003	0.975	0.003	0.007
Iran	9506	2	0.107	0.013	0.014	0.079	0.015	0.536	0.059	0.177
Iran	9507	2	0.016	0.013	0.004	0.004	0.016	0.93	0.01	0.006
Iran	9508	1	0.031	0.006	0.028	0.004	0.023	0.893	0.008	0.006
Iran	9509	1	0.008	0.003	0.074	0.004	0.009	0.885	0.009	0.007
Iran	9510	5	0.004	0.006	0.002	0.003	0.003	0.978	0.002	0.002
Iran	9511	2	0.014	0.006	0.006	0.004	0.016	0.928	0.021	0.005
Iran	9512	1	0.022	0.002	0.003	0.004	0.004	0.95	0.004	0.011
Iran	9513	11	0.014	0.004	0.011	0.008	0.024	0.921	0.007	0.011
Iran	9514	2	0.038	0.091	0.019	0.006	0.018	0.798	0.007	0.024
Iran	9515	2	0.015	0.007	0.003	0.005	0.006	0.945	0.018	0.002
Iran	9516	1	0.024	0.007	0.01	0.004	0.006	0.932	0.005	0.013
Iran	9517	2	0.017	0.011	0.009	0.009	0.01	0.917	0.018	0.01
Iran	9518	12	0.167	0.021	0.003	0.009	0.018	0.762	0.016	0.004
Iran	9519	6	0.008	0.004	0.002	0.006	0.003	0.966	0.005	0.006
Iran	9520	4	0.108	0.004	0.003	0.027	0.005	0.836	0.005	0.013
Iran	9521	0	0.007	0.003	0.1	0.01	0.007	0.823	0.039	0.012
Iran	9522	3	0.058	0.008	0.003	0.019	0.006	0.893	0.005	0.008
Iran	9523	1	0.153	0.089	0.018	0.07	0.079	0.552	0.015	0.024
Iran	9524	1	0.034	0.004	0.002	0.044	0.017	0.851	0.005	0.043
Iran	9526	0	0.015	0.011	0.01	0.012	0.018	0.772	0.005	0.158
Iran	9527	3	0.008	0.005	0.011	0.015	0.019	0.906	0.015	0.022
Iran	9528	4	0.028	0.014	0.002	0.004	0.008	0.935	0.003	0.006
Iran	9529	7	0.013	0.002	0.006	0.013	0.039	0.899	0.023	0.004
Iran	9530	3	0.034	0.017	0.003	0.004	0.007	0.907	0.004	0.023
Iran	9531	1	0.007	0.003	0.105	0.013	0.006	0.823	0.033	0.01
Iran	9532	3	0.025	0.009	0.003	0.004	0.048	0.898	0.007	0.005
Dubai	10104	2	0.102	0.007	0.004	0.009	0.005	0.842	0.018	0.013
Dubai	10105	1	0.004	0.004	0.002	0.948	0.007	0.024	0.006	0.006
Dubai	10106	0	0.018	0.004	0.002	0.004	0.002	0.964	0.002	0.003
Dubai	10107	4	0.072	0.004	0.007	0.098	0.172	0.64	0.003	0.005
Dubai	10108	5	0.017	0.004	0.022	0.011	0.015	0.697	0.005	0.23
Dubai	10109	10	0.051	0.006	0.009	0.013	0.023	0.859	0.026	0.014
Dubai	10110	17	0.014	0.004	0.005	0.004	0.011	0.948	0.008	0.006
Dubai	10111	17	0.163	0.007	0.011	0.011	0.008	0.752	0.007	0.041
Dubai	10112	1	0.021	0.002	0.003	0.062	0.004	0.885	0.002	0.022
Dubai	10120	2	0.008	0.002	0.002	0.004	0.003	0.968	0.004	0.009
Kenya-Nairobi	9833	4	0.012	0.229	0.031	0.678	0.022	0.005	0.008	0.016
Kenya-Nairobi	9834	0	0.013	0.008	0.008	0.516	0.376	0.029	0.039	0.012
Kenya-Nairobi	9835	0	0.015	0.007	0.02	0.043	0.093	0.708	0.022	0.093
Kenya-Nairobi	9836	2	0.009	0.004	0.138	0.637	0.09	0.008	0.01	0.104
Kenya-Nairobi	9837	2	0.008	0.024	0.062	0.74	0.092	0.036	0.032	0.006
Kenya-Nairobi	9838	4	0.208	0.082	0.005	0.521	0.035	0.07	0.008	0.071
Kenya-Nairobi	9839	1	0.011	0.015	0.061	0.509	0.062	0.015	0.033	0.295
Kenya-Nairobi	9840	3	0.058	0.018	0.045	0.592	0.193	0.065	0.004	0.026
Kenya-Nairobi	9841	3	0.012	0.011	0.026	0.777	0.057	0.012	0.012	0.093
Kenya-Nairobi	9842	2	0.015	0.016	0.009	0.567	0.02	0.061	0.035	0.277
Kenya-Nairobi	9843	4	0.009	0.014	0.149	0.62	0.093	0.028	0.008	0.078

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Kenya-Nairobi	9844	3	0.006	0.006	0.064	0.681	0.009	0.012	0.026	0.195
Kenya-Nairobi	9845	1	0.042	0.011	0.018	0.657	0.068	0.121	0.018	0.065
Kenya-Nairobi	9846	1	0.086	0.035	0.184	0.558	0.08	0.012	0.01	0.037
Kenya-Nairobi	9847	3	0.018	0.01	0.005	0.739	0.106	0.006	0.018	0.098
Kenya-Nairobi	9848	3	0.051	0.011	0.008	0.594	0.032	0.115	0.048	0.143
Kenya-Nairobi	9849	2	0.018	0.003	0.013	0.311	0.607	0.014	0.014	0.021
Kenya-Nairobi	9850	3	0.136	0.03	0.016	0.722	0.056	0.011	0.006	0.024
Kenya-Nairobi	9851	2	0.016	0.01	0.033	0.428	0.474	0.007	0.006	0.026
Kenya-Nairobi	9852	4	0.034	0.006	0.074	0.44	0.039	0.049	0.004	0.355
Kenya-Nairobi	9853	4	0.008	0.037	0.044	0.614	0.123	0.011	0.012	0.151
Kenya-Nairobi	9854	2	0.117	0.055	0.028	0.606	0.098	0.044	0.005	0.048
Kenya-Nairobi	9855	2	0.047	0.025	0.033	0.552	0.121	0.042	0.009	0.17
Kenya-Nairobi	9856	3	0.018	0.006	0.087	0.573	0.066	0.028	0.004	0.217
Kenya-Nairobi	9857	6	0.018	0.01	0.123	0.668	0.14	0.021	0.012	0.008
Kenya-Nairobi	9858	3	0.006	0.009	0.009	0.651	0.096	0.008	0.035	0.185
Kenya-Nairobi	9859	4	0.005	0.008	0.182	0.699	0.004	0.005	0.013	0.085
Kenya-Nairobi	9860	2	0.004	0.008	0.132	0.694	0.024	0.012	0.031	0.094
Kenya-Nairobi	9861	1	0.015	0.013	0.008	0.722	0.014	0.055	0.006	0.168
Kenya-Nairobi	9862	2	0.018	0.004	0.126	0.571	0.174	0.068	0.005	0.035
Kenya-Nairobi	9863	1	0.005	0.005	0.105	0.459	0.262	0.005	0.011	0.148
Kenya-Nairobi	9864	2	0.028	0.042	0.016	0.512	0.35	0.022	0.003	0.026
Kenya-Nairobi	9865	4	0.012	0.027	0.008	0.643	0.166	0.029	0.069	0.046
Kenya-Nairobi	9866	3	0.028	0.008	0.108	0.629	0.041	0.076	0.016	0.093
Kenya-Nairobi	9867	0	0.023	0.021	0.009	0.58	0.302	0.009	0.029	0.027
Kenya-Nairobi	9868	5	0.048	0.018	0.126	0.571	0.047	0.13	0.005	0.055
Kenya-Pate	2000	2	0.043	0.005	0.003	0.018	0.009	0.014	0.006	0.902
Kenya-Pate	2001	3	0.002	0.003	0.002	0.001	0.002	0.001	0.002	0.987
Kenya-Pate	2002	1	0.002	0.009	0.002	0.001	0.002	0.002	0.007	0.975
Kenya-Pate	2003	0	0.002	0.004	0.003	0.003	0.006	0.004	0.024	0.953
Kenya-Pate	2004	3	0.013	0.008	0.016	0.004	0.034	0.033	0.011	0.881
Kenya-Pate	2006	3	0.006	0.049	0.002	0.004	0.007	0.003	0.11	0.82
Kenya-Pate	2007	4	0.005	0.005	0.002	0.005	0.005	0.006	0.007	0.965
Kenya-Pate	2009	6	0.03	0.005	0.003	0.012	0.005	0.023	0.003	0.918
Kenya-Pate	2011	3	0.012	0.003	0.008	0.005	0.092	0.01	0.006	0.864
Kenya-Lamu	1848	13	0.01	0.005	0.007	0.009	0.048	0.005	0.083	0.834
Kenya-Lamu	2014	4	0.038	0.055	0.006	0.019	0.01	0.01	0.004	0.859
Kenya-Lamu	2015	2	0.055	0.004	0.03	0.01	0.009	0.012	0.011	0.87
Kenya-Lamu	2016	2	0.014	0.005	0.043	0.006	0.008	0.008	0.005	0.91
Kenya-Lamu	2018	1	0.009	0.003	0.002	0.055	0.005	0.013	0.002	0.912
Kenya-Lamu	2019	2	0.054	0.005	0.018	0.023	0.04	0.069	0.005	0.785
Kenya-Lamu	2021	2	0.012	0.061	0.014	0.019	0.024	0.013	0.012	0.845
Kenya-Lamu	2023	3	0.002	0.002	0.002	0.002	0.002	0.002	0.003	0.983
Kenya-Lamu	2024	2	0.002	0.003	0.002	0.001	0.002	0.002	0.002	0.986
Kenya-Lamu	2025	3	0.004	0.008	0.002	0.003	0.003	0.003	0.007	0.971
Kenya-Lamu	2026	4	0.015	0.003	0.004	0.003	0.003	0.017	0.004	0.95
Kenya-Lamu	2027	6	0.007	0.018	0.012	0.029	0.034	0.006	0.053	0.841
Kenya-Lamu	2029	2	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.985
Kenya-Lamu	2030	1	0.01	0.006	0.002	0.01	0.047	0.005	0.003	0.918
Kenya-Lamu	2031	4	0.009	0.016	0.004	0.013	0.013	0.014	0.011	0.92
Kenya-Lamu	2032	2	0.01	0.035	0.004	0.004	0.006	0.008	0.007	0.926
Kenya-Lamu	2033	2	0.005	0.007	0.004	0.003	0.011	0.007	0.002	0.961
Kenya-Lamu	3241	4	0.016	0.007	0.004	0.016	0.059	0.033	0.029	0.836
Kenya-Lamu	3246	2	0.025	0.005	0.043	0.032	0.028	0.014	0.014	0.838
Kenya-Lamu	3247	3	0.035	0.005	0.023	0.089	0.02	0.007	0.01	0.812
India-Udaipur	11835	8	0.009	0.11	0.035	0.006	0.758	0.008	0.059	0.013
India-Udaipur	11836	3	0.008	0.125	0.002	0.007	0.831	0.006	0.014	0.006

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
India-Udaipur	11837	2	0.006	0.226	0.01	0.002	0.651	0.007	0.024	0.075
India-Agra	11823	1	0.007	0.29	0.007	0.003	0.667	0.01	0.009	0.007
India-Agra	11824	2	0.03	0.157	0.002	0.004	0.72	0.012	0.004	0.071
India-Agra	11825	2	0.004	0.422	0.01	0.004	0.539	0.006	0.011	0.004
India-Agra	11826	6	0.004	0.297	0.005	0.002	0.671	0.003	0.014	0.003
India-Agra	11827	19	0.008	0.304	0.004	0.002	0.67	0.004	0.004	0.003
India-Agra	11828	2	0.346	0.091	0.004	0.003	0.52	0.009	0.007	0.018
India-Agra	11829	4	0.012	0.199	0.004	0.004	0.754	0.007	0.011	0.009
India-Agra	11830	8	0.006	0.312	0.003	0.002	0.665	0.003	0.005	0.003
India-Agra	11831	3	0.013	0.462	0.027	0.005	0.463	0.016	0.008	0.005
India-Agra	11832	2	0.003	0.417	0.004	0.002	0.56	0.004	0.006	0.004
India-Agra	11833	16	0.015	0.28	0.022	0.003	0.57	0.02	0.016	0.074
India-Agra	11834	3	0.004	0.342	0.006	0.002	0.627	0.004	0.012	0.003
India-Hyderbad	11802	13	0.016	0.005	0.01	0.008	0.826	0.119	0.01	0.005
India-Hyderbad	11803	7	0.018	0.023	0.004	0.003	0.928	0.008	0.005	0.012
India-Hyderbad	11804	5	0.004	0.029	0.005	0.002	0.678	0.003	0.264	0.014
India-Hyderbad	11805	10	0.011	0.009	0.01	0.005	0.926	0.015	0.009	0.014
India-Hyderbad	11807	11	0.006	0.008	0.022	0.005	0.936	0.008	0.007	0.008
India-Hyderbad	11808	9	0.016	0.003	0.036	0.016	0.834	0.008	0.061	0.026
India-Hyderbad	11809	3	0.067	0.032	0.007	0.101	0.773	0.011	0.003	0.006
India-Hyderbad	11810	0	0.01	0.045	0.017	0.005	0.697	0.082	0.062	0.081
India-Hyderbad	11811	0	0.009	0.004	0.003	0.009	0.757	0.011	0.009	0.198
India-Hyderbad	11812	3	0.007	0.086	0.013	0.002	0.859	0.005	0.015	0.014
India-Hyderbad	11813	4	0.023	0.016	0.126	0.003	0.793	0.007	0.029	0.004
India-Hyderbad	11814	2	0.006	0.019	0.009	0.003	0.938	0.01	0.004	0.01
India-Hyderbad	11815	2	0.011	0.024	0.053	0.005	0.844	0.027	0.007	0.029
India-Hyderbad	11816	3	0.007	0.016	0.002	0.003	0.952	0.006	0.005	0.009
India-Hyderbad	11817	2	0.003	0.005	0.035	0.002	0.941	0.005	0.004	0.005
India-Hyderbad	11818	1	0.008	0.007	0.107	0.069	0.76	0.014	0.005	0.03
India-Hyderbad	11819	4	0.009	0.016	0.002	0.003	0.948	0.008	0.005	0.009
India-Hyderbad	11820	5	0.003	0.022	0.009	0.002	0.865	0.007	0.048	0.044
India-Hyderbad	11821	13	0.021	0.01	0.192	0.006	0.662	0.057	0.014	0.037
India-Hyderbad	11822	2	0.015	0.012	0.009	0.004	0.902	0.008	0.037	0.014
India-Andhra	10159	2	0.007	0.006	0.01	0.008	0.919	0.014	0.032	0.003
India-Andhra	10160	1	0.002	0.003	0.008	0.002	0.752	0.004	0.225	0.004
India-Andhra	10161	2	0.004	0.006	0.021	0.006	0.948	0.004	0.005	0.007
India-Andhra	10162	5	0.004	0.004	0.016	0.003	0.964	0.003	0.004	0.003
India-Andhra	10163	0	0.004	0.007	0.009	0.004	0.937	0.003	0.018	0.017
India-Andhra	10164	2	0.006	0.02	0.012	0.007	0.917	0.005	0.03	0.003
India-Andhra	10165	1	0.006	0.01	0.073	0.004	0.87	0.007	0.004	0.026
India-Andhra	10166	3	0.025	0.006	0.08	0.013	0.71	0.009	0.008	0.15
India-Andhra	10167	1	0.013	0.003	0.064	0.013	0.85	0.036	0.012	0.009
India-Andhra	10168	1	0.008	0.007	0.027	0.006	0.922	0.02	0.006	0.003
India-Andhra	10169	6	0.004	0.003	0.112	0.008	0.848	0.012	0.007	0.006
India-Andhra	10170	4	0.037	0.004	0.146	0.007	0.702	0.036	0.045	0.022
India-Andhra	10171	1	0.006	0.021	0.013	0.006	0.91	0.004	0.036	0.003
India-Andhra	10172	2	0.007	0.02	0.017	0.012	0.916	0.006	0.01	0.013
India-Andhra	10173	2	0.005	0.003	0.321	0.004	0.648	0.008	0.003	0.009
India-Andhra	10174	3	0.003	0.002	0.021	0.004	0.958	0.004	0.006	0.002
India-Andhra	10175	2	0.009	0.005	0.007	0.044	0.891	0.019	0.018	0.006
India-Andhra	10176	2	0.013	0.011	0.005	0.005	0.885	0.008	0.071	0.003
India-Andhra	10177	0	0.008	0.006	0.016	0.09	0.833	0.005	0.034	0.008
India-Andhra	10178	3	0.003	0.005	0.024	0.004	0.953	0.003	0.005	0.004
India-Andhra	10179	4	0.005	0.004	0.018	0.016	0.901	0.006	0.007	0.044
India-Andhra	10180	10	0.029	0.015	0.017	0.026	0.849	0.051	0.009	0.004
India-Andhra	10181	5	0.004	0.003	0.023	0.004	0.898	0.005	0.057	0.006

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
India-Kolkata	10113	2	0.008	0.009	0.003	0.004	0.899	0.005	0.035	0.037
India-Kolkata	10114	1	0.005	0.006	0.026	0.003	0.942	0.004	0.009	0.006
India-Kolkata	10115	1	0.029	0.005	0.016	0.01	0.88	0.036	0.015	0.01
India-Kolkata	10116	2	0.004	0.006	0.022	0.002	0.941	0.003	0.015	0.008
India-Kolkata	10117	2	0.059	0.018	0.049	0.005	0.683	0.036	0.071	0.079
India-Kolkata	10118	3	0.009	0.025	0.09	0.012	0.558	0.267	0.018	0.021
India-Kolkata	10119	3	0.055	0.022	0.052	0.061	0.723	0.062	0.004	0.021
Sri Lanka	8780	1	0.025	0.007	0.006	0.088	0.767	0.011	0.079	0.018
Sri Lanka	8781	1	0.031	0.006	0.025	0.098	0.788	0.011	0.032	0.01
Sri Lanka	8782	3	0.024	0.005	0.006	0.056	0.852	0.035	0.011	0.011
Sri Lanka	8783	0	0.109	0.006	0.007	0.028	0.816	0.023	0.004	0.008
Sri Lanka	8784	1	0.017	0.007	0.072	0.25	0.607	0.007	0.033	0.008
Sri Lanka	8785	10	0.013	0.021	0.007	0.089	0.825	0.014	0.014	0.017
Sri Lanka	8786	0	0.188	0.025	0.013	0.046	0.625	0.024	0.031	0.048
Sri Lanka	8787	0	0.007	0.005	0.005	0.169	0.799	0.007	0.003	0.005
Sri Lanka	8788	4	0.058	0.082	0.026	0.069	0.724	0.028	0.004	0.009
Sri Lanka	8789	2	0.139	0.01	0.127	0.298	0.374	0.039	0.004	0.008
Sri Lanka	8790	1	0.015	0.003	0.07	0.184	0.718	0.005	0.003	0.002
Sri Lanka	8791	1	0.03	0.01	0.021	0.017	0.892	0.01	0.007	0.013
Sri Lanka	8792	0	0.05	0.011	0.005	0.042	0.855	0.026	0.004	0.007
Sri Lanka	8793	2	0.042	0.016	0.008	0.215	0.685	0.009	0.004	0.02
Sri Lanka	8794	2	0.033	0.019	0.005	0.173	0.742	0.018	0.007	0.004
Sri Lanka	8795	1	0.042	0.005	0.016	0.161	0.709	0.033	0.014	0.02
Sri Lanka	8796	4	0.068	0.004	0.007	0.021	0.746	0.034	0.111	0.009
Sri Lanka	8797	1	0.011	0.061	0.031	0.325	0.545	0.005	0.013	0.009
Sri Lanka	8798	1	0.107	0.011	0.005	0.061	0.763	0.028	0.022	0.003
Sri Lanka	8799	2	0.003	0.008	0.009	0.263	0.664	0.004	0.002	0.047
Sri Lanka	8800	2	0.014	0.01	0.068	0.37	0.465	0.011	0.041	0.02
Sri Lanka	8801	5	0.011	0.019	0.004	0.201	0.709	0.007	0.004	0.044
Sri Lanka	8802	2	0.006	0.007	0.024	0.4	0.54	0.004	0.004	0.015
Sri Lanka	8803	6	0.036	0.005	0.103	0.055	0.7	0.019	0.015	0.067
Thailand	11688	6	0.002	0.001	0.984	0.003	0.003	0.002	0.002	0.003
Thailand	11689	13	0.003	0.022	0.937	0.004	0.009	0.008	0.014	0.003
Thailand	11691	27	0.012	0.007	0.909	0.018	0.026	0.009	0.014	0.005
Thailand	11698	18	0.005	0.003	0.937	0.007	0.014	0.007	0.026	0.002
Thailand	11702	10	0.002	0.002	0.973	0.003	0.008	0.003	0.005	0.003
Thailand	11703	12	0.002	0.002	0.983	0.002	0.004	0.002	0.004	0.002
Thailand	11705	21	0.035	0.009	0.824	0.003	0.104	0.008	0.01	0.007
Thailand	11707	4	0.004	0.002	0.976	0.003	0.006	0.003	0.004	0.003
Thailand	11708	18	0.006	0.003	0.954	0.003	0.005	0.007	0.009	0.013
Thailand	11709	12	0.003	0.003	0.979	0.002	0.005	0.003	0.003	0.004
Thailand	11710	9	0.006	0.004	0.959	0.006	0.007	0.007	0.006	0.003
Thailand	11711	6	0.002	0.006	0.948	0.004	0.008	0.003	0.024	0.006
Thailand	11714	6	0.008	0.01	0.95	0.004	0.011	0.003	0.008	0.006
Thailand	11715	17	0.009	0.089	0.753	0.006	0.094	0.004	0.035	0.009
Thailand	11717	15	0.003	0.005	0.969	0.003	0.008	0.003	0.006	0.003
Thailand	11718	2	0.004	0.005	0.969	0.004	0.003	0.006	0.007	0.003
Thailand	11720	4	0.001	0.001	0.99	0.001	0.002	0.001	0.001	0.001
Vietnam	8844	4	0.008	0.01	0.806	0.007	0.123	0.004	0.035	0.008
Vietnam	8845	3	0.02	0.079	0.748	0.007	0.099	0.026	0.01	0.01
Vietnam	8846	3	0.022	0.003	0.65	0.014	0.265	0.038	0.004	0.005
Vietnam	8847	10	0.005	0.004	0.966	0.01	0.005	0.003	0.005	0.003
Vietnam	8848	6	0.03	0.006	0.883	0.01	0.031	0.015	0.004	0.02
Vietnam	8849	2	0.032	0.007	0.829	0.01	0.024	0.067	0.028	0.003
Vietnam	8850	1	0.114	0.007	0.659	0.149	0.01	0.009	0.042	0.009
Vietnam	8851	2	0.03	0.126	0.767	0.012	0.015	0.043	0.004	0.002

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Vietnam	8852	13	0.201	0.004	0.701	0.025	0.018	0.024	0.009	0.017
Vietnam	8853	3	0.32	0.004	0.601	0.012	0.027	0.027	0.005	0.005
Vietnam	8854	5	0.056	0.163	0.636	0.037	0.069	0.008	0.028	0.004
Vietnam	8855	2	0.029	0.003	0.743	0.134	0.009	0.045	0.033	0.003
Vietnam	8856	2	0.077	0.005	0.693	0.005	0.13	0.085	0.004	0.002
Vietnam	8857	3	0.016	0.006	0.472	0.015	0.442	0.035	0.005	0.008
Vietnam	8858	2	0.077	0.005	0.709	0.06	0.017	0.112	0.015	0.004
Vietnam	8859	7	0.048	0.014	0.658	0.015	0.069	0.015	0.147	0.035
Vietnam	8860	2	0.19	0.01	0.619	0.011	0.009	0.083	0.055	0.023
Vietnam	8861	2	0.245	0.026	0.576	0.01	0.07	0.021	0.044	0.009
Vietnam	8862	2	0.04	0.009	0.44	0.02	0.39	0.023	0.04	0.039
Vietnam	8863	3	0.093	0.012	0.613	0.048	0.015	0.197	0.015	0.006
Taiwan	8681	4	0.005	0.005	0.014	0.654	0.004	0.004	0.309	0.005
Taiwan	8682	0	0.011	0.034	0.381	0.01	0.105	0.008	0.443	0.007
Taiwan	8683	3	0.058	0.023	0.103	0.119	0.086	0.04	0.562	0.009
Taiwan	8684	3	0.007	0.008	0.06	0.65	0.005	0.006	0.261	0.003
Taiwan	8685	2	0.012	0.003	0.352	0.037	0.035	0.007	0.544	0.01
Taiwan	8686	6	0.035	0.008	0.19	0.258	0.014	0.007	0.464	0.024
Taiwan	8687	5	0.087	0.028	0.44	0.011	0.044	0.054	0.329	0.007
Taiwan	8688	26	0.016	0.014	0.288	0.03	0.111	0.013	0.499	0.028
Taiwan	8689	5	0.039	0.15	0.143	0.035	0.009	0.014	0.525	0.086
Taiwan	8690	2	0.012	0.067	0.312	0.009	0.036	0.005	0.553	0.006
Taiwan	8691	16	0.023	0.008	0.324	0.046	0.111	0.019	0.436	0.033
Taiwan	8692	3	0.014	0.009	0.478	0.025	0.01	0.006	0.45	0.009
Taiwan	8693	2	0.018	0.007	0.212	0.105	0.092	0.008	0.547	0.01
Taiwan	8694	1	0.005	0.004	0.443	0.437	0.017	0.004	0.087	0.003
Taiwan	8695	1	0.019	0.003	0.21	0.056	0.009	0.064	0.629	0.011
Taiwan	8696	11	0.004	0.002	0.003	0.972	0.004	0.004	0.009	0.003
Taiwan	8697	1	0.025	0.011	0.005	0.898	0.02	0.008	0.029	0.005
Taiwan	8698	4	0.003	0.002	0.002	0.981	0.002	0.003	0.004	0.002
Taiwan	8699	6	0.036	0.081	0.04	0.045	0.507	0.05	0.231	0.011
Taiwan	8700	2	0.087	0.014	0.278	0.213	0.025	0.022	0.355	0.006
Taiwan	8701	2	0.004	0.005	0.159	0.205	0.045	0.005	0.574	0.004
Taiwan	8702	2	0.059	0.011	0.182	0.238	0.018	0.024	0.448	0.021
Taiwan	8703	2	0.005	0.004	0.008	0.94	0.012	0.017	0.009	0.005
Taiwan	8704	1	0.086	0.003	0.263	0.007	0.007	0.018	0.574	0.042
Taiwan	8705	2	0.01	0.015	0.268	0.008	0.082	0.026	0.572	0.019
Taiwan	8706	2	0.061	0.026	0.208	0.045	0.049	0.062	0.523	0.026
Taiwan	8707	5	0.004	0.088	0.29	0.017	0.035	0.026	0.536	0.004
Taiwan	8708	3	0.004	0.003	0.007	0.967	0.005	0.003	0.006	0.005
Taiwan	8709	4	0.024	0.011	0.285	0.014	0.015	0.009	0.63	0.013
Japan-Oita	11967	2	0.039	0.025	0.004	0.01	0.019	0.04	0.857	0.005
Japan-Oita	11968	1	0.004	0.006	0.004	0.002	0.007	0.002	0.972	0.003
Japan-Oita	11969	1	0.006	0.053	0.003	0.004	0.009	0.008	0.892	0.025
Japan-Oita	11970	1	0.004	0.01	0.031	0.008	0.036	0.01	0.894	0.006
Japan-Oita	11971	2	0.009	0.008	0.004	0.003	0.006	0.006	0.961	0.003
Japan-Oita	11972	8	0.004	0.073	0.012	0.002	0.075	0.007	0.819	0.008
Japan-Oita	11973	2	0.002	0.001	0.002	0.001	0.002	0.002	0.987	0.003
Japan-Oita	11974	1	0.002	0.002	0.004	0.002	0.002	0.002	0.983	0.003
Japan-Oita	11975	2	0.007	0.009	0.002	0.008	0.04	0.008	0.914	0.012
Japan-Oita	11976	3	0.006	0.003	0.002	0.002	0.003	0.006	0.975	0.005
Japan-Oita	11977	2	0.003	0.007	0.016	0.002	0.024	0.003	0.939	0.006
Japan-Oita	11979	2	0.005	0.009	0.002	0.015	0.005	0.006	0.948	0.012
Japan-Oita	11980	2	0.017	0.03	0.003	0.002	0.007	0.023	0.908	0.007
Japan-Oita	11981	2	0.016	0.01	0.004	0.012	0.042	0.014	0.889	0.012
Japan-Oita	11982	0	0.005	0.021	0.013	0.004	0.006	0.003	0.944	0.004

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
Japan-Oita	11985	0	0.003	0.023	0.003	0.002	0.014	0.005	0.928	0.022
Japan-Oita	11986	1	0.008	0.008	0.003	0.006	0.005	0.009	0.952	0.009
Japan-Kanazawa	11929	1	0.005	0.011	0.003	0.002	0.003	0.005	0.967	0.005
Japan-Kanazawa	11931	1	0.01	0.054	0.007	0.005	0.013	0.012	0.889	0.01
Japan-Kanazawa	11932	1	0.005	0.007	0.003	0.006	0.018	0.006	0.952	0.002
Japan-Kanazawa	11933	4	0.005	0.006	0.006	0.003	0.004	0.006	0.968	0.002
Japan-Kanazawa	11934	19	0.003	0.003	0.009	0.003	0.012	0.003	0.961	0.007
Japan-Kanazawa	11936	9	0.012	0.009	0.017	0.007	0.01	0.005	0.933	0.007
Japan-Kanazawa	11937	23	0.016	0.004	0.016	0.005	0.087	0.007	0.856	0.008
Japan-Kanazawa	11939	1	0.005	0.009	0.038	0.004	0.007	0.004	0.919	0.016
Japan-Kanazawa	11940	2	0.005	0.006	0.007	0.002	0.013	0.003	0.959	0.004
Japan-Kanazawa	11941	1	0.011	0.084	0.01	0.004	0.007	0.006	0.863	0.015
Japan-Kanazawa	11942	2	0.004	0.001	0.014	0.005	0.003	0.004	0.967	0.001
Japan-Kanazawa	11943	1	0.032	0.004	0.004	0.023	0.005	0.01	0.921	0.003
Japan-Kanazawa	11944	0	0.005	0.003	0.009	0.003	0.017	0.005	0.943	0.015
Japan-Kanazawa	11945	1	0.066	0.014	0.006	0.005	0.004	0.013	0.891	0.003
Japan-Kanazawa	11946	1	0.203	0.014	0.004	0.03	0.008	0.006	0.721	0.015
Japan-Ohmiya	11947	3	0.005	0.003	0.007	0.003	0.004	0.003	0.972	0.002
Japan-Ohmiya	11948	3	0.011	0.005	0.006	0.052	0.01	0.015	0.896	0.006
Japan-Ohmiya	11951	14	0.02	0.087	0.003	0.572	0.015	0.022	0.278	0.003
Japan-Ohmiya	11953	1	0.007	0.005	0.004	0.016	0.005	0.004	0.953	0.005
Japan-Ohmiya	11954	2	0.005	0.004	0.003	0.004	0.003	0.006	0.971	0.003
Japan-Ohmiya	11955	8	0.013	0.004	0.002	0.123	0.005	0.01	0.837	0.006
Japan-Ohmiya	11956	4	0.03	0.007	0.007	0.007	0.007	0.059	0.882	0.002
Japan-Ohmiya	11957	1	0.004	0.002	0.012	0.002	0.01	0.005	0.963	0.003
Japan-Ohmiya	11959	2	0.002	0.004	0.003	0.002	0.008	0.002	0.973	0.006
Japan-Ohmiya	11960	2	0.065	0.028	0.007	0.392	0.024	0.04	0.433	0.011
Japan-Ohmiya	11961	8	0.018	0.006	0.047	0.015	0.059	0.016	0.806	0.033
Japan-Ohmiya	11962	3	0.01	0.004	0.003	0.02	0.004	0.009	0.944	0.005
Japan-Ohmiya	11963	5	0.01	0.003	0.309	0.085	0.005	0.026	0.523	0.039
Japan-Ohmiya	11964	11	0.006	0.002	0.139	0.447	0.003	0.005	0.385	0.013
Japan-Ohmiya	11965	2	0.003	0.008	0.002	0.003	0.003	0.002	0.973	0.005
Japan-Ohmiya	11966	2	0.019	0.004	0.006	0.01	0.046	0.022	0.885	0.008
Japan-Sapporo	11907	3	0.009	0.005	0.04	0.004	0.015	0.005	0.912	0.009
Japan-Sapporo	11909	1	0.024	0.014	0.007	0.011	0.131	0.013	0.792	0.009
Japan-Sapporo	11911	0	0.07	0.007	0.024	0.019	0.021	0.013	0.75	0.096
Japan-Sapporo	11913	2	0.004	0.003	0.024	0.002	0.007	0.003	0.952	0.006
Japan-Sapporo	11914	9	0.11	0.007	0.003	0.051	0.003	0.055	0.739	0.031
Japan-Sapporo	11915	2	0.005	0.006	0.002	0.003	0.003	0.003	0.977	0.002
Japan-Sapporo	11916	3	0.011	0.023	0.007	0.016	0.009	0.007	0.915	0.012
Japan-Sapporo	11917	6	0.046	0.007	0.349	0.006	0.011	0.122	0.455	0.004
Japan-Sapporo	11918	2	0.041	0.006	0.024	0.009	0.006	0.013	0.897	0.003
Japan-Sapporo	11921	6	0.016	0.012	0.017	0.005	0.025	0.008	0.915	0.003
Japan-Sapporo	11922	4	0.02	0.006	0.369	0.008	0.009	0.011	0.567	0.011
Japan-Sapporo	11923	5	0.021	0.004	0.425	0.164	0.021	0.04	0.307	0.018
Japan-Sapporo	11924	5	0.008	0.005	0.347	0.051	0.005	0.077	0.501	0.006
Japan-Sapporo	11925	15	0.039	0.01	0.591	0.01	0.011	0.101	0.233	0.005
Japan-Sapporo	11926	8	0.027	0.015	0.406	0.017	0.045	0.01	0.47	0.01
China-Henan	8869	3	0.018	0.004	0.257	0.009	0.037	0.007	0.661	0.007
China-Henan	8870	3	0.005	0.007	0.105	0.263	0.01	0.005	0.595	0.011
China-Henan	8871	20	0.011	0.006	0.314	0.007	0.073	0.013	0.56	0.017
China-Henan	8872	19	0.022	0.002	0.432	0.131	0.119	0.013	0.276	0.005
China-Henan	8873	16	0.016	0.005	0.418	0.138	0.014	0.008	0.399	0.003
China-Henan	8874	5	0.014	0.007	0.535	0.03	0.005	0.006	0.394	0.008
China-Henan	8875	11	0.007	0.007	0.435	0.012	0.006	0.011	0.512	0.01
China-Henan	8876	18	0.006	0.007	0.4	0.007	0.011	0.008	0.545	0.017

Table 25 - Population clustering of each random bred individual in the database by SNPs and STRs at K = 8

Sampling Location	ID No.	Missing Data	Population							
			1	2	3	4	5	6	7	8
China-Henan	8877	16	0.002	0.003	0.317	0.002	0.004	0.002	0.665	0.005
China-Henan	8878	6	0.023	0.005	0.399	0.025	0.014	0.004	0.525	0.006
China-Henan	8879	11	0.01	0.004	0.338	0.006	0.028	0.018	0.594	0.003
China-Henan	8880	7	0.017	0.005	0.249	0.273	0.01	0.03	0.412	0.004
China-Henan	8881	7	0.003	0.003	0.001	0.981	0.003	0.003	0.003	0.003
China-Henan	8882	18	0.003	0.007	0.163	0.04	0.045	0.005	0.729	0.007
China-Henan	8883	6	0.006	0.006	0.111	0.205	0.028	0.005	0.634	0.004
China-Henan	8884	14	0.004	0.002	0.118	0.021	0.013	0.009	0.667	0.166
China-Henan	8885	4	0.004	0.001	0.09	0.156	0.004	0.003	0.737	0.005
China-Henan	8886	8	0.007	0.003	0.429	0.014	0.01	0.007	0.527	0.003
China-Henan	8887	23	0.007	0.005	0.013	0.025	0.01	0.004	0.933	0.004
China-Henan	8888	18	0.004	0.004	0.324	0.007	0.013	0.003	0.639	0.006
South Korea	2769	12	0.005	0.007	0.136	0.006	0.009	0.006	0.823	0.008
South Korea	2772	7	0.009	0.012	0.218	0.007	0.01	0.008	0.734	0.003
South Korea	2775	9	0.003	0.003	0.077	0.005	0.048	0.005	0.836	0.022
South Korea	2776	19	0.015	0.026	0.379	0.011	0.095	0.014	0.45	0.009
South Korea	2779	13	0.029	0.013	0.079	0.708	0.026	0.086	0.006	0.052
South Korea	2784	16	0.005	0.005	0.264	0.038	0.011	0.005	0.656	0.015
South Korea	2785	15	0.002	0.002	0.043	0.004	0.006	0.014	0.923	0.006
South Korea	2786	4	0.023	0.004	0.144	0.083	0.011	0.06	0.672	0.004
South Korea	7671	16	0.032	0.029	0.009	0.017	0.011	0.019	0.861	0.021
South Korea	7672	18	0.008	0.025	0.05	0.064	0.119	0.06	0.653	0.022
South Korea	7673	3	0.005	0.003	0.294	0.003	0.004	0.004	0.684	0.002
South Korea	7674	3	0.008	0.009	0.217	0.198	0.019	0.008	0.538	0.003
South Korea	7675	5	0.004	0.003	0.096	0.273	0.008	0.006	0.581	0.029
South Korea	7676	3	0.007	0.004	0.519	0.005	0.01	0.009	0.439	0.007
South Korea	7677	3	0.05	0.007	0.016	0.102	0.009	0.03	0.724	0.063
South Korea	7678	6	0.018	0.003	0.034	0.039	0.009	0.091	0.797	0.009
South Korea	7679	3	0.002	0.004	0.465	0.004	0.004	0.002	0.517	0.002
South Korea	7680	3	0.013	0.004	0.072	0.005	0.011	0.009	0.88	0.006
South Korea	7681	5	0.009	0.005	0.221	0.157	0.06	0.012	0.521	0.014
South Korea	7682	3	0.012	0.007	0.147	0.11	0.042	0.005	0.656	0.021
South Korea	7683	4	0.01	0.018	0.059	0.157	0.115	0.006	0.614	0.021
South Korea	7684	4	0.008	0.003	0.12	0.006	0.084	0.013	0.602	0.163
South Korea	7685	4	0.012	0.011	0.149	0.104	0.048	0.028	0.637	0.012
South Korea	7686	6	0.014	0.014	0.204	0.02	0.016	0.008	0.716	0.01
South Korea	7687	9	0.005	0.003	0.005	0.971	0.005	0.003	0.005	0.003
South Korea	7688	15	0.014	0.008	0.033	0.403	0.013	0.003	0.522	0.004
South Korea	7689	14	0.013	0.003	0.166	0.291	0.014	0.008	0.496	0.009
South Korea	7690	6	0.014	0.005	0.198	0.174	0.075	0.007	0.521	0.005
South Korea	7691	8	0.004	0.009	0.664	0.009	0.009	0.016	0.286	0.003
South Korea	7692	6	0.034	0.002	0.013	0.896	0.018	0.028	0.006	0.003
South Korea	7693	4	0.012	0.01	0.003	0.892	0.006	0.009	0.023	0.045
South Korea	7694	12	0.013	0.01	0.179	0.223	0.087	0.02	0.448	0.02
South Korea	7695	5	0.006	0.009	0.316	0.003	0.035	0.006	0.602	0.022
South Korea	7696	5	0.006	0.004	0.073	0.016	0.226	0.004	0.642	0.028
South Korea	7697	7	0.012	0.003	0.352	0.016	0.025	0.005	0.568	0.019
South Korea	7698	5	0.038	0.005	0.341	0.557	0.009	0.006	0.037	0.007
South Korea	7699	9	0.004	0.003	0.583	0.002	0.014	0.004	0.379	0.011
South Korea	7700	10	0.031	0.008	0.025	0.288	0.016	0.108	0.52	0.003

[0183] It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference in their entirety for all purposes.

CLAIMS

What is claimed is:

1. A computer implemented method for determining the contributions of feline populations to a feline genome, comprising:

(a) genotyping a sample comprising genomic DNA obtained from a test feline to determine the identity of one or both alleles of each marker of a set of markers, wherein the set of markers comprises a plurality of single nucleotide polymorphisms (SNPs) listed in Table 1;

(b) comparing the identity of one or both alleles for each of the markers in the set of markers determined to be present in the test feline genome to a database comprising one or more feline population profiles, wherein each feline population profile comprises genotype information for the set of markers in the feline population; and

(c) determining the contribution of the one or more feline populations to the test feline genome.

2. The method of claim 1, wherein the plurality of SNPs comprises at least about 100 SNPs listed in Table 1.

3. The method of claim 1, wherein the plurality of SNPs comprises all 148 SNPs listed in Table 1.

4. The method of any one of claims 1 to 3, wherein the set of markers further comprises one or more microsatellite markers.

5. The method of claim 4, wherein the set of markers further comprises one or more short tandem repeats (STRs) selected from the group consisting of FCA005, FCA008, FCA023, FCA026, FCA035, FCA043, FCA045, FCA058, FCA069, FCA075, FCA077, FCA080B, FCA088, FCA090, FCA094, FCA096, FCA097, FCA105, FCA123, FCA126, FCA132, FCA149, FCA211, FCA220, FCA223, FCA224, FCA229, FCA262, FCA293, FCA305, FCA310, FCA391, FCA441, FCA453, FCA628, FCA649, FCA678 and FCA698.

6. The method of any one of claims 1 to 5, wherein the set of markers further comprises one or more phenotypic markers.

7. The method of claim 6, wherein the one or more phenotypic markers are selected from the group consisting of Phen_CMAH_G139A, Phen_ASIP_del, Phen_MLPH_T83del, Phen_MC1R_G250A, Phen_TYRP1_C298T, Phen_TYRP1_5IVS6, Phen_TYR_del975C, Phen_TYR_G715T, Phen_TYR_G940A, Phen_KIT_G1035C_BI, Phen_FGF5_475, Phen_FGF5_474, phen_FGF5_406, Phen_FGF5_356, Phen_GBL1_G1457C_SIA_KOR, Phen_HEXB_DelIntr_BUR, Phen_HEXB_del39C_KOR, Phen_GBE1_Ins_NFC, Phen_KRT71_G/Aintro4_SPX, Phen_MYBPC_G93C_MCC, Phen_MYBPC_C2460T_RAG, phen_MPO_ALC, Phen_PLAU_AG_ALC, Phen_FCAT_ALC, Phen_PKLR_13delE6_Aby, Phen_PKD1_C10063A_PER, Phen_SHH_A479G_Hw, Phen_CEP290_PRA_Aby, Phen_CRX_546_Aby, Phen_CMAH_del, Phen_HEXB_C667T_DSH, Phen_GM2A_Del_DSH, Phen_GRHPR_DSH, Phen_LPL_G1234A_DSH, Phen_LAMAN_del_PER, Phen_IDUA_del_DSH, Phen_ARSB_G1558A_SIA, Phen_ARSB_T1427C_Sia, Phen_GUSB_A1052G_DSH, Phen_MYBPC_A74T_Poly, Phen_NPC1_G2864C_PER, Phen_SHH_G257C_UK1, Phen_SHH_A481T_UK2, Phen_HMBS_del842_SIA, Phen-HMBS_189TT_SIA, Phen_CYP21B1, Phen_TAS1R2_CAT, Phen_TAS1R2_G8224A_CAT, Phen_CYP27B1_Rob, Phen_ZFX, KRT71-Del_Drex, P2RY5_CRex, WNK4_Burm_HKL and CART1_del_Burm.

8. The method of any one of claims 1 to 7, wherein the genotype information in each feline population profile comprises identities of one or both alleles of each marker of the set of markers.

9. The method of any one of claims 1 to 8, wherein the genotype information in each feline population profile comprises allele frequencies for one or both alleles of each marker of the set of markers.

10. The method of any one of claims 1 to 9, wherein the database of feline population profiles comprises a plurality of feline population profiles.

11. The method of any one of claims 1 to 10, wherein the database of feline populations profiles comprises profiles for at least one feline breed.

12. The method of any one of claims 1 to 11, wherein the set of markers comprises a subset of the 148 SNP markers listed in Table 1 and wherein the method determines the contributions of one or more feline populations to the test feline genome.

13. The method of any one of claims 1 to 12, wherein step (a) comprises amplifying genomic DNA of the test feline using primers specific for each of the set of markers and determining the size of the amplification product.

14. The method of any one of claims 1 to 12, wherein step (a) comprises amplifying genomic DNA of the test feline using primers specific for each of the set of markers and sequencing the amplification product.

15. The method of any one of claims 1 to 14, wherein the algorithm according to step (b) comprises a genotype clustering program.

16. The method of any one of claims 1 to 15, wherein the algorithm according to step (b) comprises an assignment algorithm.

17. The method of any one of claims 1 to 16, wherein step (b) comprises discriminating between the contributions of two or more genetically related feline populations to the test feline genome by comparing the alleles in the test feline genome to a database comprising profiles of the two or more genetically related feline populations.

18. The method of claim 17, wherein the two or more genetically related feline populations are selected from the group consisting of:

(i) Persian and Exotic Shorthair (SH);
(ii) British SH and Scottish Fold;
(iii) Australian Mist and Burmese;
(iv) Singapura and Burmese;
(v) Birman and Korat; and
(vi) Siamese and Havana Brown.

19. The method of any one of claims 1 to 18, further comprising the step of providing a document displaying the contributions of one or more feline populations to the genome of the test feline genome.

20. The method of claim 19, wherein the document provides additional information regarding the one or more feline populations that contributed to the genome of the test feline.

21. The method of claim 20, wherein the additional information is health-related information.

22. The method of claim 20, wherein the document provides a certification of the contributions of one or more feline populations to the genome of the test feline.

23. The method of claim 20, wherein the document provides a representation of the one or more feline populations that contributed to the genome of the test feline.

24. A method for defining one or more feline populations, comprising:

(a) determining the identity of one or both alleles for each marker of a set of markers in a test feline genome, wherein the set of markers comprises a plurality of single nucleotide polymorphisms (SNPs) listed in Table 1; and

(b) applying a computer-implemented statistical model to define one or more distinct feline populations, wherein one or more distinct feline populations are characterized by a set of allele frequencies for each marker in the set of markers comprising a plurality of SNPs listed in Table 1.

25. One or more computer-readable media comprising:

(a) a data structure stored thereon for use in distinguishing feline populations, the data structure comprising:

(i) marker data, wherein the marker data identifies one or both alleles of each marker of a set of markers in one or more feline population profiles, wherein the set of markers comprises a plurality of single nucleotide polymorphisms (SNPs) listed in Table 1; and

(ii) genotype information data, wherein the genotype information data provides genotype information for each marker of a set of markers in a feline population, wherein a record comprises an instantiation of the marker data and an instantiation of the genotype information data and a set of records represents a feline population profile; and

(b) computer-executable instructions for controlling one or more computing devices to:

(i) identify one or both alleles in a test feline genome for each marker of the set of markers; and

(ii) determine the contributions of one or more feline populations to the test feline genome by comparing the identified alleles in the test feline genome to the database comprising one or more feline population profiles, wherein each feline population profile comprises genotype information for the set of markers in the feline population.

26. One or more computer-readable media comprising a data structure stored thereon for use in distinguishing feline populations, the data structure comprising:

(a) marker data, wherein the marker data identifies one or both alleles of each marker of a set of markers in one or more feline population profiles, wherein the set of markers comprises a plurality of single nucleotide polymorphisms (SNPs) listed in Table 1; and

(b) genotype information data, wherein the genotype information data provides genotype information for each marker of a set of markers in a feline population, wherein a record comprises an instantiation of the marker data and an instantiation of the genotype information data and a set of records represents a feline population profile.

27. The computer readable media of any one of claims 25 to 26, wherein the plurality of SNPs comprises at least about 100 SNPs listed in Table 1.

28. The computer readable media of any one of claims 25 to 26, wherein the plurality of SNPs comprises all 148 SNPs listed in Table 1.

29. The computer readable media of any one of claims 25 to 28, wherein the set of markers further comprises one or more microsatellite markers.

30. The computer readable media of claim 29, wherein the set of markers further comprises one or more short tandem repeats (STRs) selected from the group consisting of FCA005, FCA008, FCA023, FCA026, FCA035, FCA043, FCA045, FCA058, FCA069, FCA075, FCA077, FCA080B, FCA088, FCA090, FCA094, FCA096, FCA097, FCA105, FCA123, FCA126, FCA132, FCA149, FCA211, FCA220, FCA223, FCA224, FCA229, FCA262, FCA293, FCA305, FCA310, FCA391, FCA441, FCA453, FCA628, FCA649, FCA678 and FCA698.

31. The computer readable media of any one of claims 25 to 30, wherein the set of markers further comprises one or more phenotypic markers.

32. The computer readable media of claim 31, wherein the one or more phenotypic markers are selected from the group consisting of Phen_CMAH_G139A, Phen_ASIP_del, Phen_MLPH_T83del, Phen_MC1R_G250A, Phen_TYRP1_C298T, Phen_TYRP1_5IVS6, Phen_TYR_del975C, Phen_TYR_G715T, Phen_TYR_G940A, Phen_KIT_G1035C_BI, Phen_FGF5_475, Phen_FGF5_474, phen_FGF5_406, Phen_FGF5_356, Phen_GBL1_G1457C_SIA_KOR, Phen_HEXB_DelIntr_BUR, Phen_HEXB_del39C_KOR, Phen_GBE1_Ins_NFC, Phen_KRT71_G/Aintro4_SPX, Phen_MYBPC_G93C_MCC, Phen_MYBPC_C2460T_RAG, phen_MPO_ALC, Phen_PLAU_AG_ALC, Phen_FCAT_ALC, Phen_PKLR_13delE6_Aby, Phen_PKD1_C10063A_PER, Phen_SHH_A479G_Hw, Phen_CEP290_PRA_Aby, Phen_CRX_546_Aby, Phen_CMAH_del, Phen_HEXB_C667T_DSH, Phen_GM2A_Del_DSH, Phen_GRHPR_DSH, Phen_LPL_G1234A_DSH, Phen_LAMAN_del_PER, Phen_IDUA_del_DSH, Phen_ARSB_G1558A_SIA, Phen_ARSB_T1427C_Sia, Phen_GUSB_A1052G_DSH, Phen_MYBPC_A74T_Poly, Phen_NPC1_G2864C_PER, Phen_SHH_G257C_UK1, Phen_SHH_A481T_UK2, Phen_HMBS_del842_SIA, Phen-HMBS_189TT_SIA, Phen_CYP21B1, Phen_TAS1R2_CAT, Phen_TAS1R2_G8224A_CAT, Phen_CYP27B1_Rob, Phen_ZFX, KRT71-Del_Drex, P2RY5_CRex, WNK4_Burm_HKL and CART1_del_Burm.

33. A method for determining the contributions of feline populations to a feline genome, comprising performing a genotyping assay on a sample comprising genomic DNA obtained from a test feline to determine the identity of one or both alleles present in the test feline genome for each marker of a set of markers, wherein the set of markers is indicative of the contribution of feline populations to the genome of the test feline, wherein the set of markers comprises a plurality of single nucleotide polymorphisms (SNPs) listed in Table 1.

34. A method of assigning a feline individual to a population of origin, which comprises:

(a) genotyping the feline individual to identify one or both alleles of each marker of a set of markers to thereby identify the individual's genotype, wherein the set of markers comprises a plurality of single nucleotide polymorphisms (SNPs) listed in Table 1;

(b) applying a computer-implemented statistical model to assign the feline individual to one or more feline populations in a database, wherein the one or more feline populations are characterized by a set of allele frequencies for each marker in the set of markers; and

(c) assigning the feline individual to the one or more most likely populations identified in step (b).

35. The method of claim 34, wherein the individual is assigned to the one or more most likely feline populations if the population genotype probability for the most likely feline populations exceed the value of assignment to any other feline populations of the database.

36. The method of any one of claims 34 to 35, wherein the set of markers further comprises one or more STRs selected from the group consisting of FCA005, FCA008, FCA023, FCA026, FCA035, FCA043, FCA045, FCA058, FCA069, FCA075, FCA077, FCA080B, FCA088, FCA090, FCA094, FCA096, FCA097, FCA105, FCA123, FCA126, FCA132, FCA149, FCA211, FCA220, FCA223, FCA224, FCA229, FCA262, FCA293, FCA305, FCA310, FCA391, FCA441, FCA453, FCA628, FCA649, FCA678 and FCA698.

37. The method of any one of claims 34 to 36, wherein the set of markers further comprises one or more of the phenotypic markers selected from the group consisting of Phen_CMAH_G139A, Phen_ASIP_del, Phen_MLPH_T83del, Phen_MC1R_G250A, Phen_TYRP1_C298T, Phen_TYRP1_5IVS6, Phen_TYR_del975C, Phen_TYR_G715T, Phen_TYR_G940A, Phen_KIT_G1035C_BI, Phen_FGF5_475, Phen_FGF5_474, phen_FGF5_406, Phen_FGF5_356, Phen_GBL1_G1457C_SIA_KOR, Phen_HEXB_DelIntr_BUR, Phen_HEXB_del39C_KOR, Phen_GBE1_Ins_NFC, Phen_KRT71_G/Aintro4_SPX, Phen_MYBPC_G93C_MCC, Phen_MYBPC_C2460T_RAG, phen_MPO_ALC, Phen_PLAU_AG_ALC, Phen_FCAT_ALC, Phen_PKLR_13delE6_Aby, Phen_PKD1_C10063A_PER, Phen_SHH_A479G_Hw, Phen_CEP290_PRA_Aby, Phen_CRX_546_Aby, Phen_CMAH_del, Phen_HEXB_C667T_DSH, Phen_GM2A_Del_DSH, Phen_GRHPR_DSH, Phen_LPL_G1234A_DSH, Phen_LAMAN_del_PER, Phen_IDUA_del_DSH, Phen_ARSB_G1558A_SIA, Phen_ARSB_T1427C_Sia, Phen_GUSB_A1052G_DSH, Phen_MYBPC_A74T_Poly, Phen_NPC1_G2864C_PER, Phen_SHH_G257C_UK1, Phen_SHH_A481T_UK2, Phen_HMBS_del842_SIA, Phen-HMBS_189TT_SIA, Phen_CYP21B1, Phen_TAS1R2_CAT,

Phen_TAS1R2_G8224A_CAT, Phen_CYP27B1_Rob, Phen_ZFX, KRT71-Del_Drex, P2RY5_CRex, WNK4_Burm_HKL and CART1_del_Burm.

38. The method of any one of claims 34 to 37, wherein prior to genotyping, a most likely population of origin is based on one or more morphological features of the individual.

39. The method of any one of claims 34 to 37, wherein prior to genotyping, one or more morphological features of the individual allow the exclusion of one or more of the candidate populations of origin.

40. The method of any one of claims 34 to 39, wherein marker locus genotypes for said each candidate population are in Hardy-Weinberg Equilibrium and Gametic Phase Equilibrium.

GENETIC IDENTIFICATION OF DOMESTIC CAT BREEDS AND POPULATIONS

ABSTRACT OF THE DISCLOSURE

[0184] This invention provides genetic markers for use in identifying and assigning the population of origin of a feline.

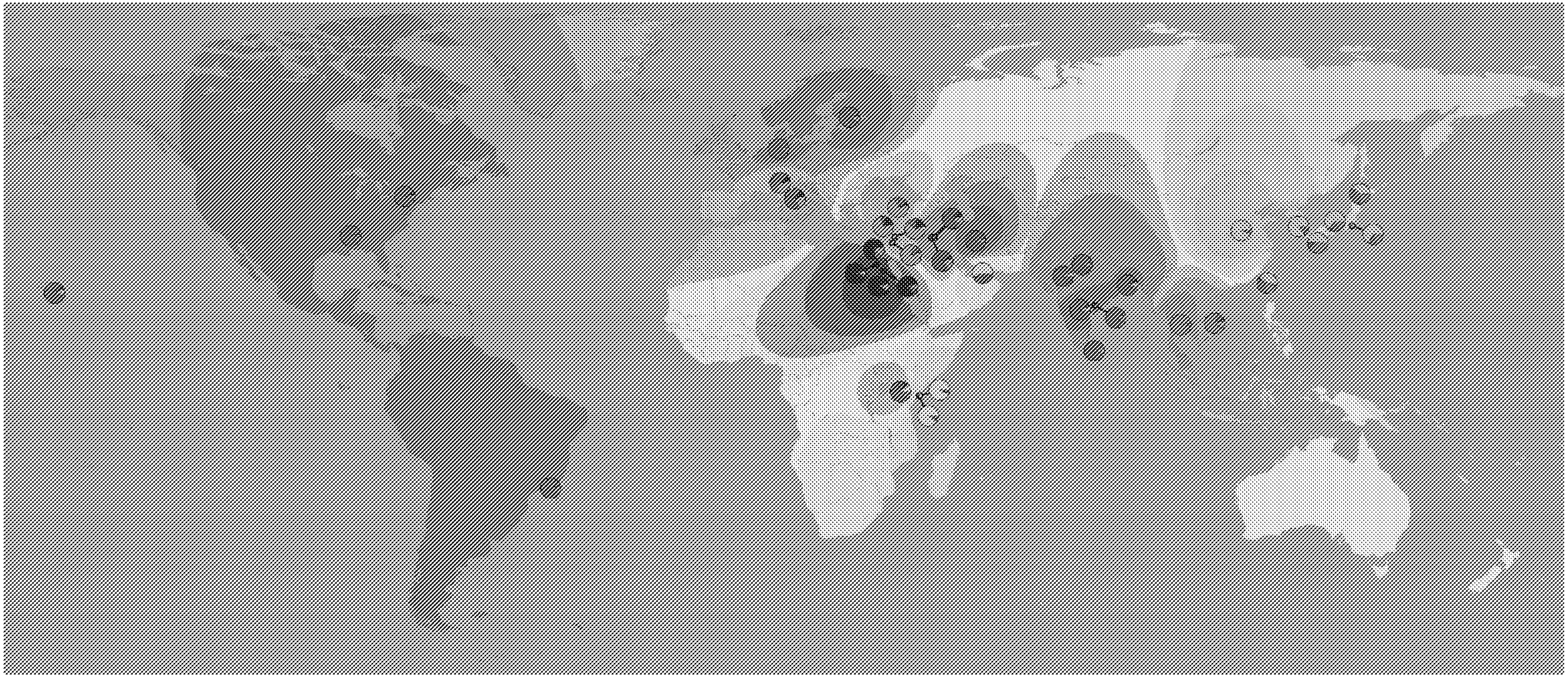
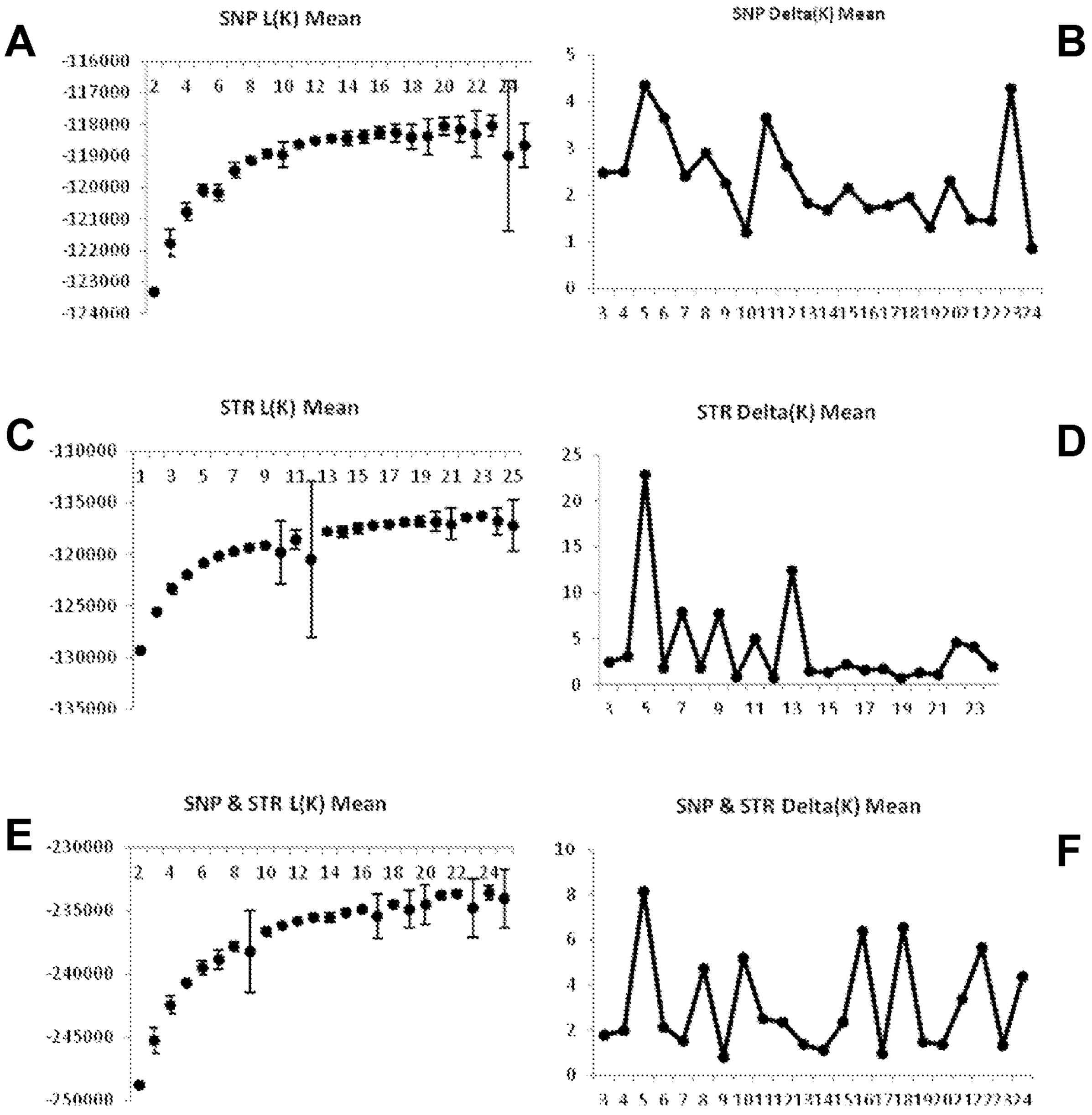


Fig. 1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B
SNP Delta(K) Mean
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4
3
2
1
0
3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24
C
STR L(K) Mean
-110000
-115000
-120000
-125000
-130000
-135000
1 3 5 7 9 11 13 15 17 19 21 23 25
D
STR Delta(K) Mean
25
20
15
10
5
0
3 5 7 9 11 13 15 17 19 21 23
E
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-240000
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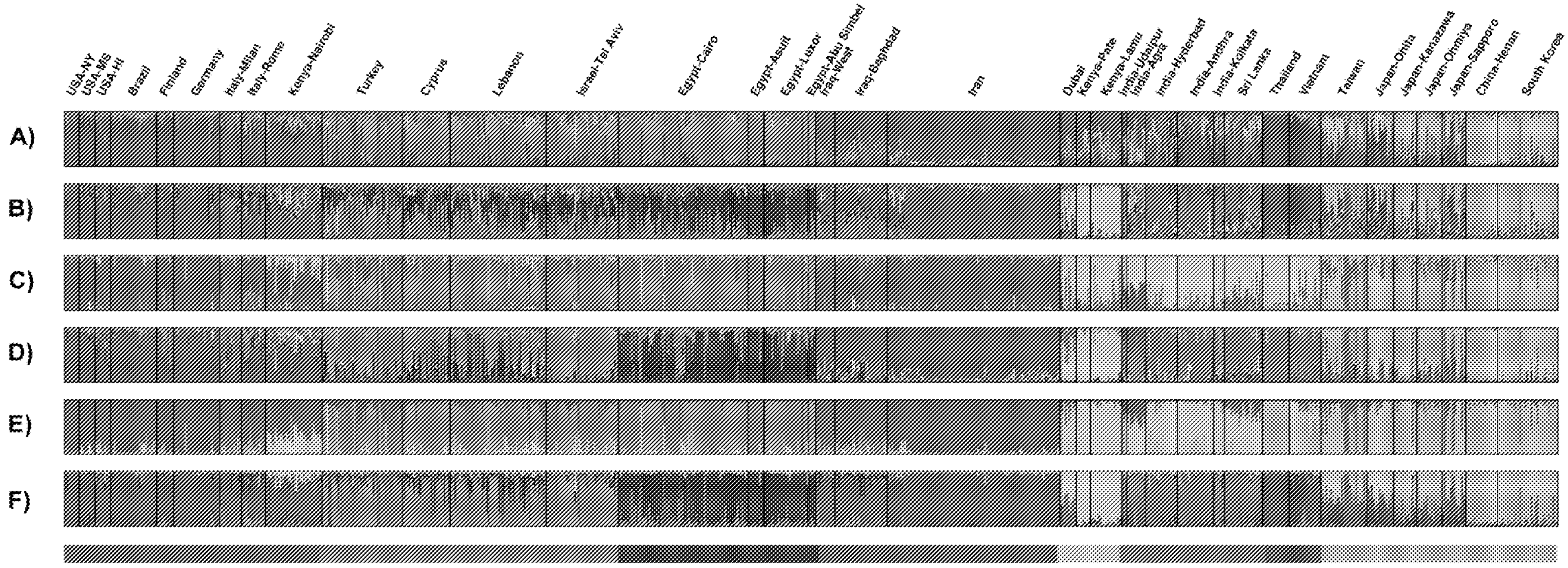
3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

Fig. 2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Israel-Tel Aviv
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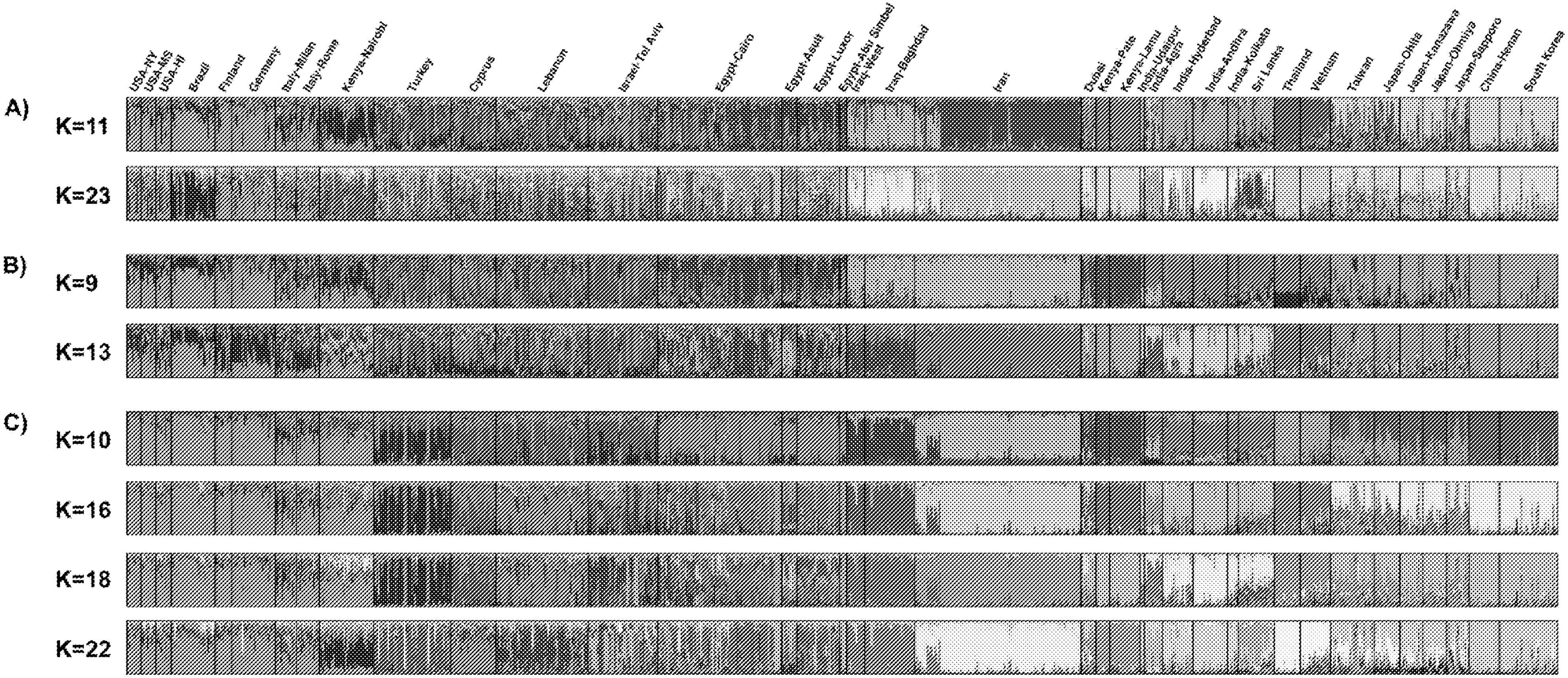
Egypt-Asuit
Egypt-Luxor
Egypt-Abu Simbel
Iraq-West
Iraq-Baghdad
Iran
Dubai
Kenya-Pate
Kenya-Lamu
India-Udaipur
India-Agra
India-Hyderbad
India-Andhra
India-Kolkata
Sri Lanka
Thailand
Vietnam
Taiwan
Japan-Ohita
Japan-Kanazawa
Japan-Ohmiya
Japan-Sapporo
China-Henan
South Korea
A)
B)
C)
D)
E)
F)

Fig. 3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Kenya-Nairobi
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Israel-Tel Aviv
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Egypt-Abu Simbel
Iraq-West
Iraq-Baghdad
Iran
Dubai
Kenya-Pate
Kenya-Lamu
India-Udaipur
India-Agra
India-Hyderbad
India-Andhra
India-Kolkata
Sri Lanka
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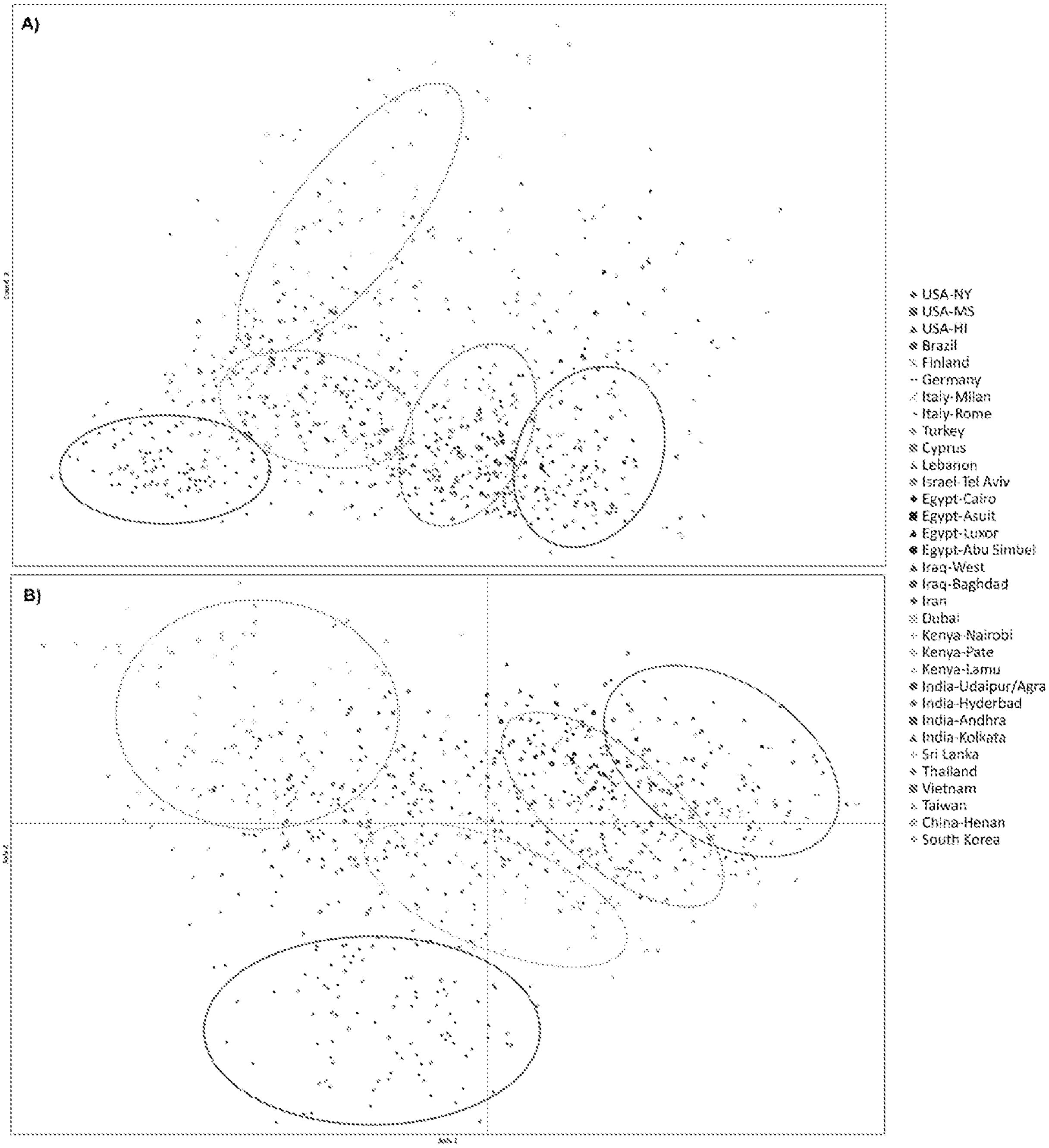
Japan-Sapporo
China-Henan
South Korea

Fig. 4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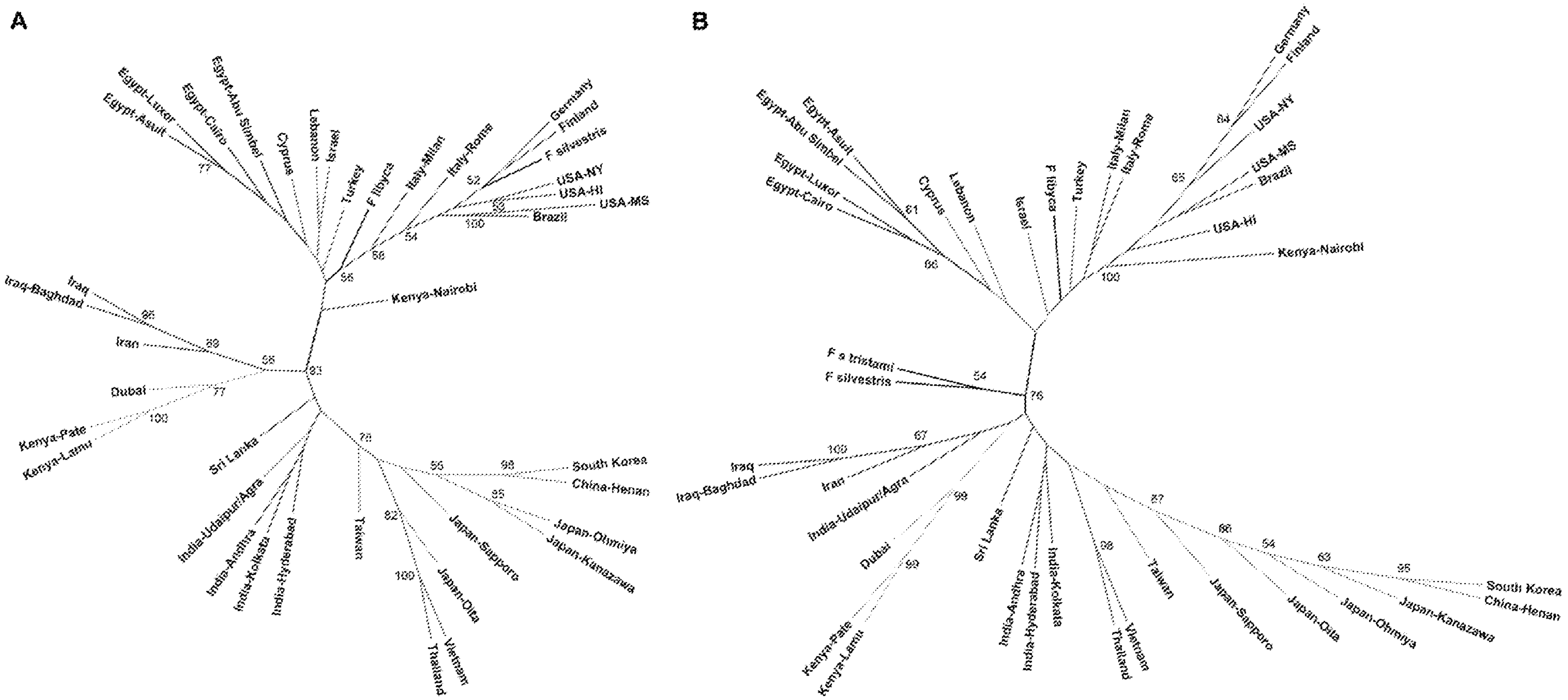
Egypt-Asuit
Egypt-Luxor
Egypt-Abu Simbel
Iraq-West
Iraq-Baghdad
Iran
Dubai
Kenya-Nairobi
Kenya-Pate
Kenya-Lamu
India-Udaipur/Agra
India-Hyderbad
India-Andhra
India-Kolkata
Sri Lanka
Thailand
Vietnam
Taiwan
China-Henan
South Korea

Fig. 5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Italy-Roma
Germany
Finland
F silvestris
USA-NY
USA-HI
USA-MS
Brazil
77
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100
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56
Kenya-Nairobi
Iraq
Iraq-Baghdad
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83
Dubai
77
100
Kenya-Pate
Kenya-Lamu
Sri Lanka
India-Udaipur/Agra
India-Andhra
India-Kolkata
India-Hyderabad
Taiwan
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98
South Korea
China-Henan
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Japan-Ohmiya
Japan-Kanazawa
82
Japan-Sapporo
100
Japan-Oita
Vietnam
Thailand
B
Egypt-Abu Simbel
Egypt-Asuit
Egypt-Luxor
Egypt-Cairo
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F libyca
Turkey
Italy-Milan
Italy-Roma
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Finland
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USA-NY
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Brazil
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Kenya-Nairobi
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F silvestris
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Iraq-Baghdad
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Kenya-Lamu
Sri Lanka
India-Andhra
India-Hyderabad
India-Kolkata
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Thailand
Vietnam
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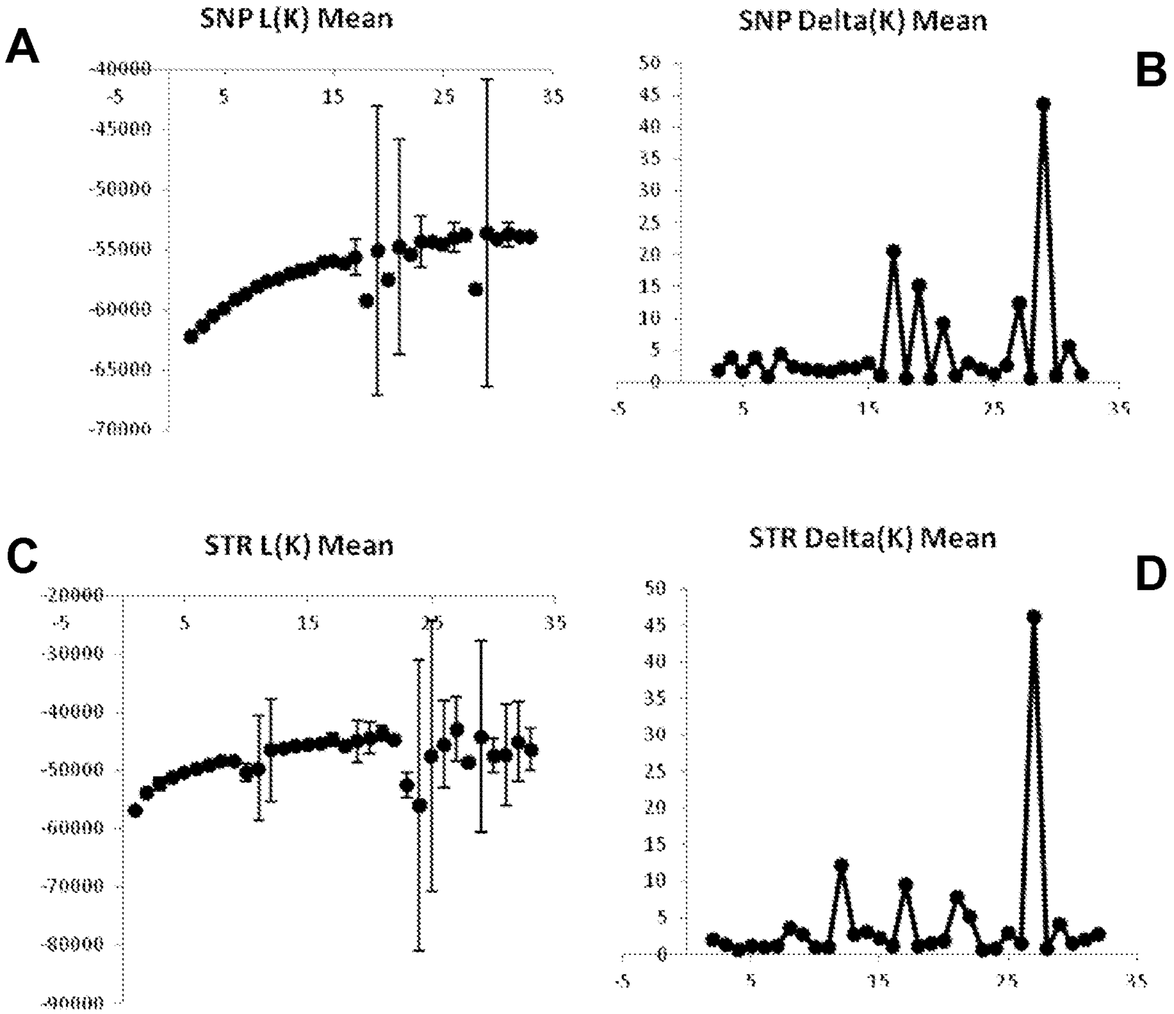
Japan-Kanazawa
South Korea
China-Henan

Fig. 6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-55000
-60000
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-70000
-5
5
15
25
35
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SNP Delta(K) Mean
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45
40
35
30
25
20
15
10
5
0
-5
5
15
25
35
C
STR L(K) Mean
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-30000
-40000
-50000
-60000
-70000
-80000
-90000
-5
5
15
25
35
D
STR Delta(K) Mean
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35
30
25
20
15
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5
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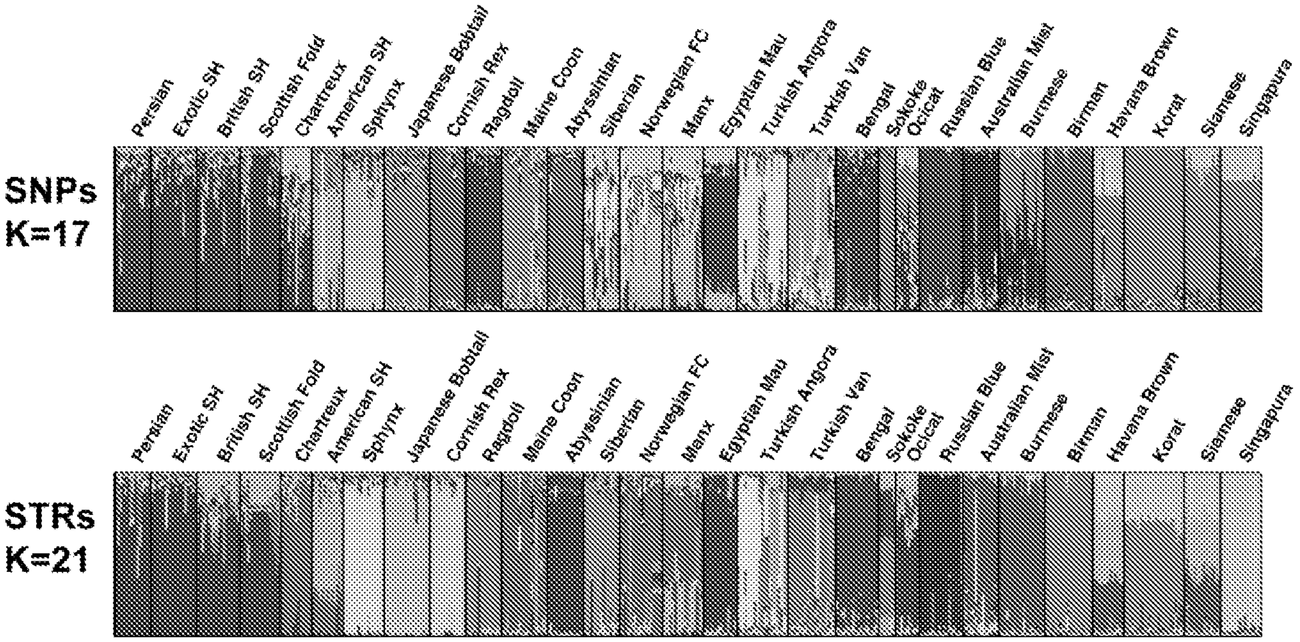
5
15
25
35

Fig. 7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Exotic SH
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Chartreux
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Sphynx
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Abyssinian
Siberian
Norwegian FC
Manx
Egyptian Mau
Turkish Angora
Turkish Van
Bengal
Sokoke
Ocicat
Russian Blue
Australian Mist
Burmese
Birman
Havana Brown
Korat
Siamese
Singapura
STRs
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Exotic SH
British SH
Scottish Fold
Chartreux
American SH
Sphynx
Japanese Bobtail
Cornish Rex
Ragdoll
Maine Coon
Abyssinian
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Manx
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Turkish Angora
Turkish Van
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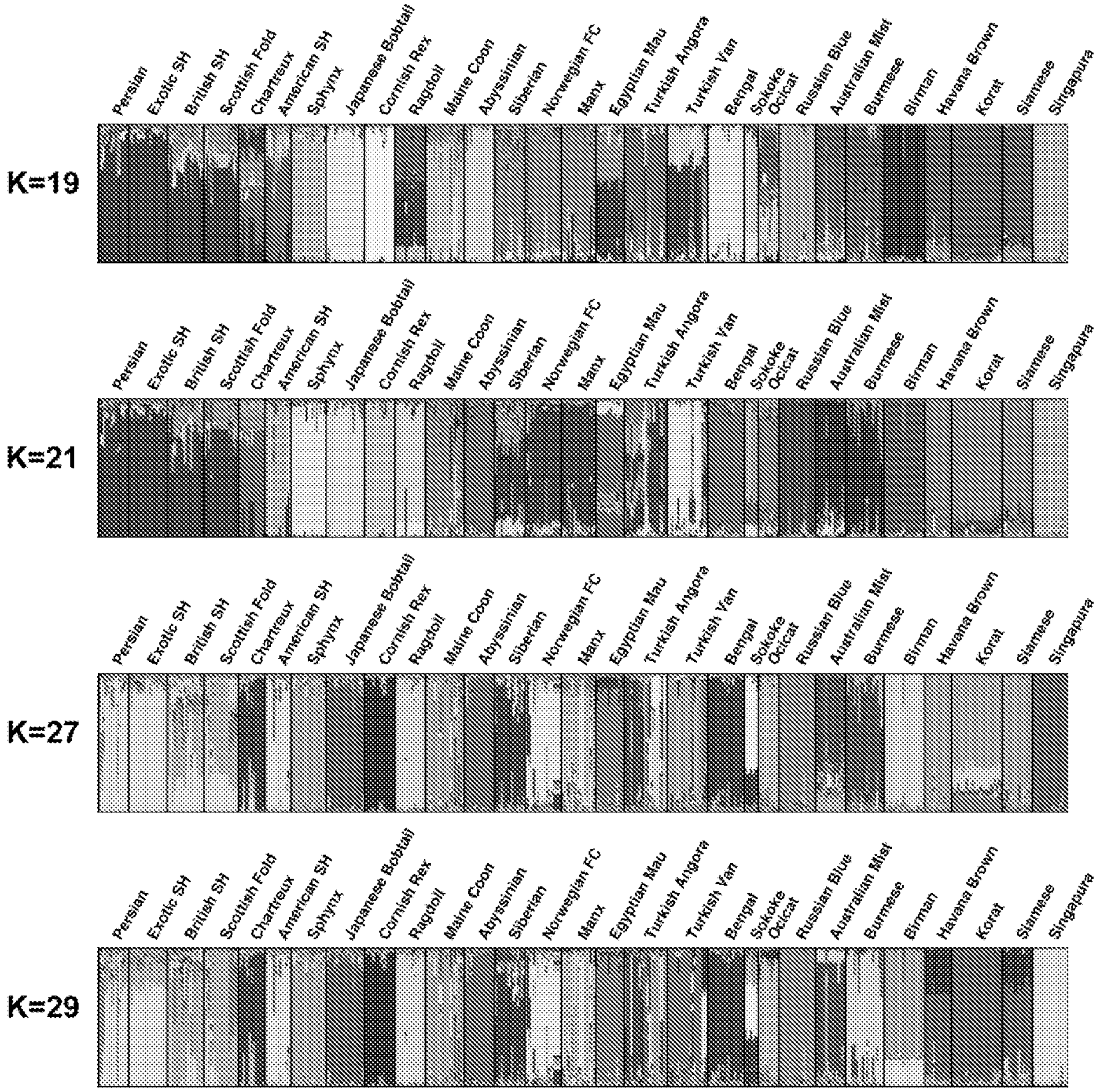
Siamese
Singapura

Fig. 8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Sphynx
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Ragdoll
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Norwegian FC
Manx
Egyptian Mau
Turkish Angora
Turkish Van
Bengal
Sokoke
Ocicat
Russian Blue
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Siamese
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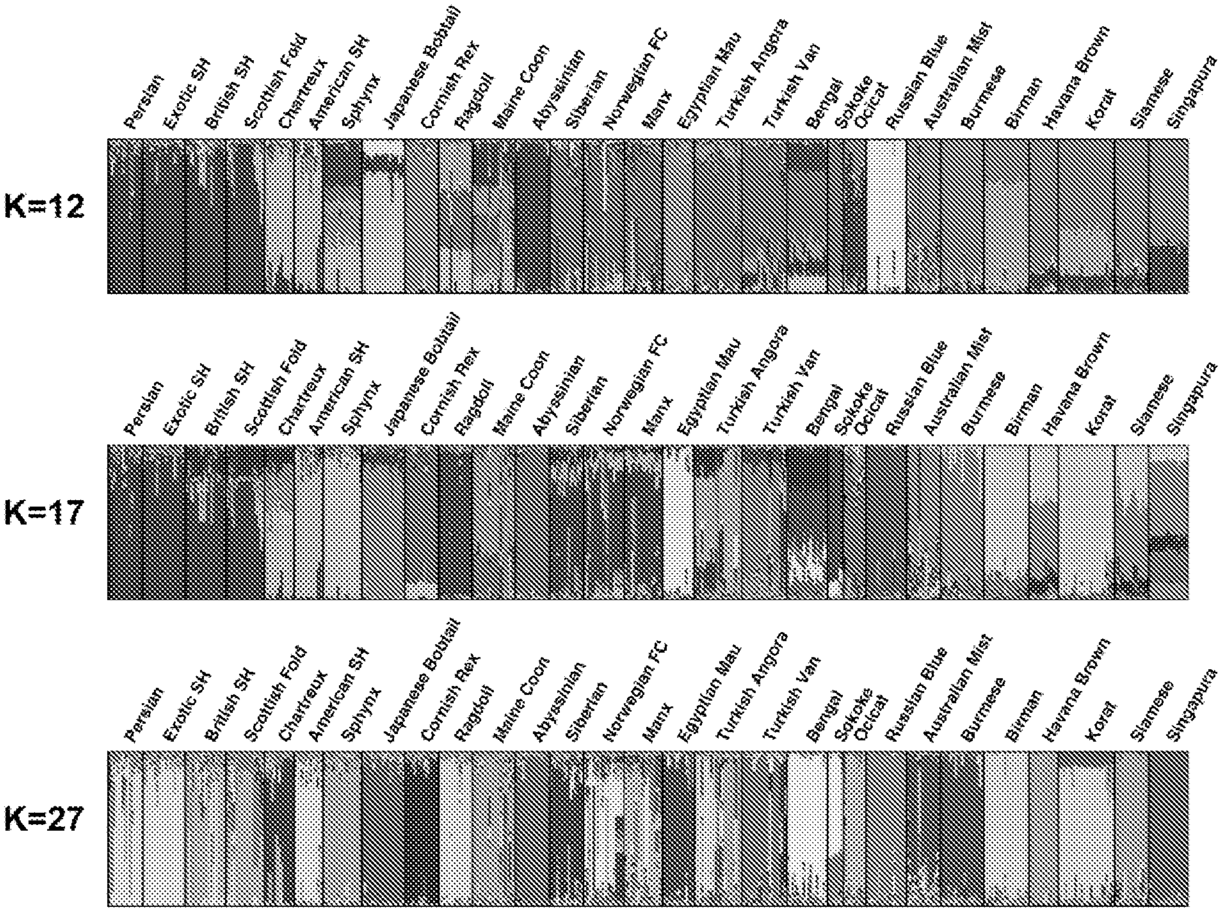
K=21
K=27
K=29

Fig. 9A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Ocicat
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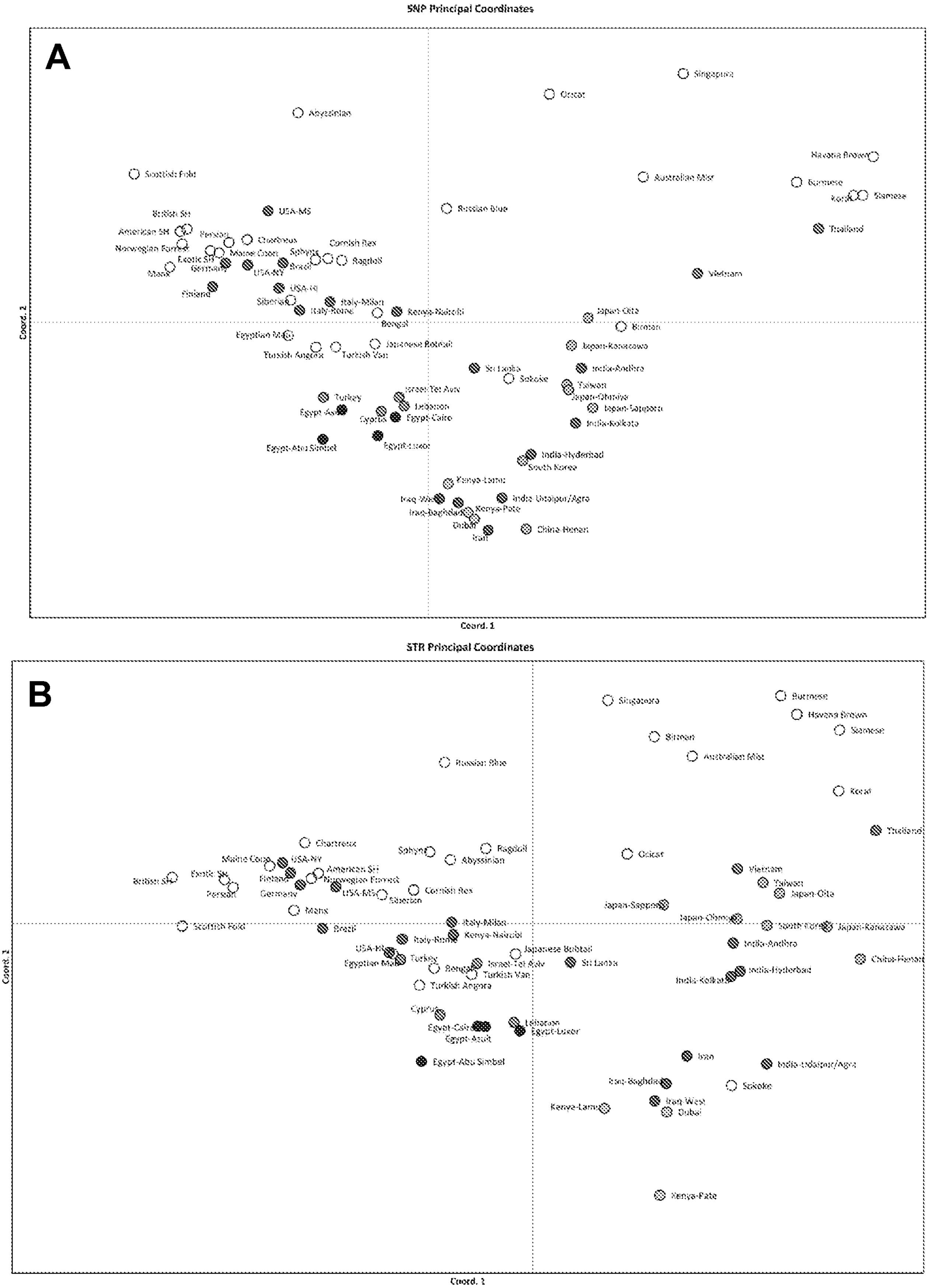
Fig. 9B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Exotic SH
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Germany
Brazil
Manx
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Egypt-Cairo
India-Kolkata
Egypt-Abu Simbel
Egypt-Luxor
India-Hyderbad
South Korea
Kenya-Lamu
Iraq-West
India-Udaipur/Agra
Iraq-Baghdad
Kenya-Pate
Dubai
China-Henan
Iran
Coord. 2
Coord. 1
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B
Singapura
Burmese
Havana Brown
Siamese
Birman
Australian Mist
Russian Blue
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Thailand
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Sphynx
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India-Andhra
Japanese Bobtail
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Bengal
India-Hyderbad
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India-Kolkata
Turkish Angora
Cyprus
Lebanon
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Iran
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India-Udaipur/Agra
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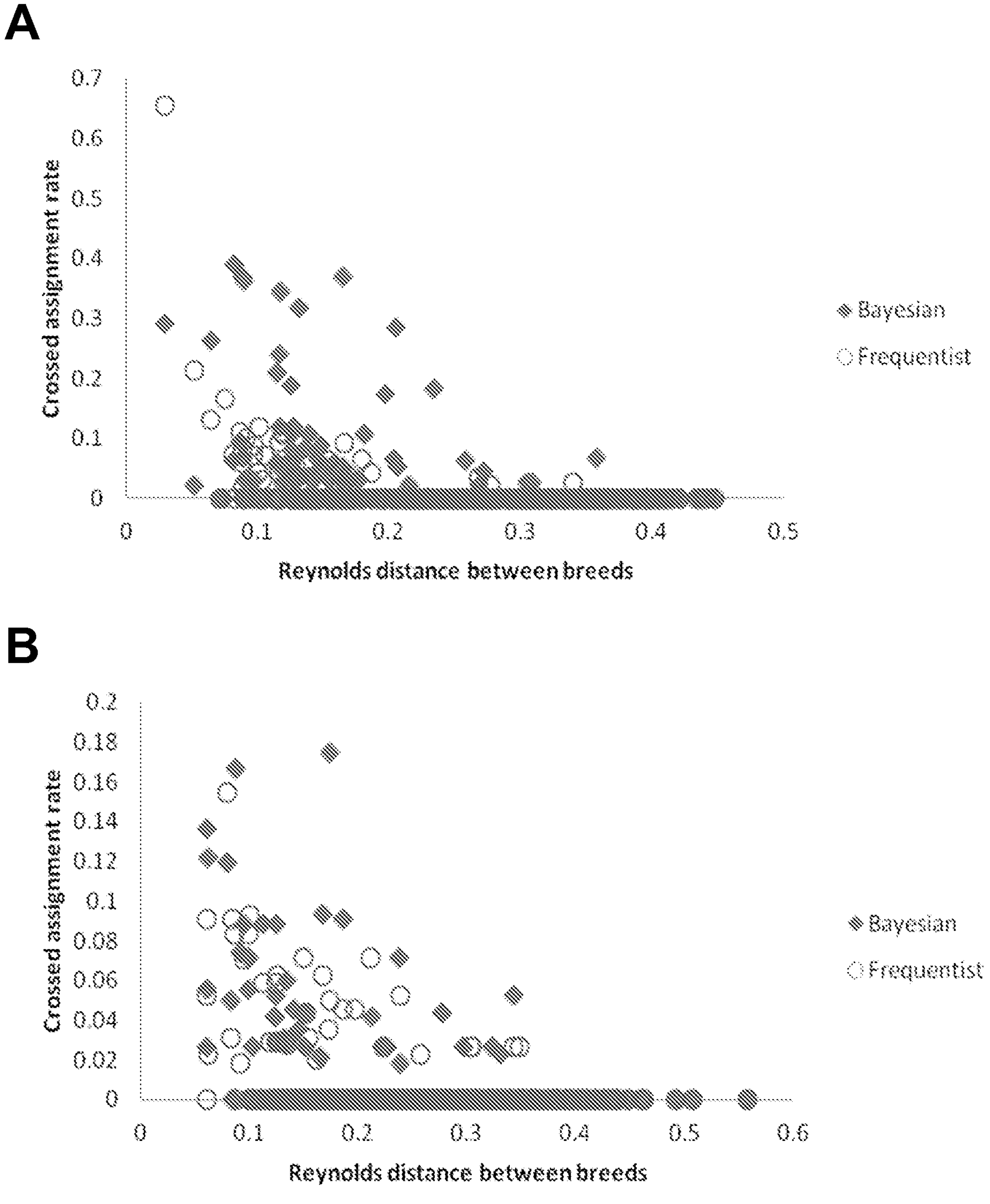
Coord. 2
Coord. 1

Fig. 10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0.5
0.4
0.3
0.2
0.1
0
0
0.1
0.2
0.3
0.4
0.5
Reynolds distance between breeds
Bayesian
Frequentist
B
Crossed assignment rate
0.2
0.18
0.16
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0
0.1
0.2
0.3
0.4
0.5
0.6
Reynolds distance between breeds
Bayesian
Frequentist

Fig. 11