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Doctoral Dissertation

Whole-genome population analysis of wild house mice (*Mus musculus*): population genetic structure in Eurasia and its surrounding areas and inference of expansion route associated with human activities

野生ハツカネズミ (*Mus musculus*) の全ゲノム集団解析：
ユーラシア大陸とその周辺地域における集団遺伝的構造
の解明と人間活動に伴った拡散経路の推定

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Abstract

House mouse (*Mus musculus*) is small commensal mammal that inhabit the worldwide and are thought to have been closely related to the history of human migration because of their preference for grains and nesting inside houses. Today, house mouse has been widely used in research, primarily in medical physiology and the life sciences. Humans established this house mouse as a laboratory mouse several hundred years ago and have used it as a model organism after finding similarities with humans. Although the experimental mouse strain has been studied by a great number of researchers, genetic background of the wild house mouse is not well studied. Until now, in the fields of ecology and phylogeography, studies of wild animals have mainly used specific genes in mitochondria and limited regions of the autosomal genome, such as microsatellites, to discuss relationships among species and subspecies. However, since mitochondria can only reveal maternal lineages and microsatellites have low resolution, more detailed analyses using autosomal genomes are required to reveal history of the species. In this study, we determined whole genomes of the wild house mouse to provide insight into the history of the species.

In PART I, we sequenced the whole genomes of wild house mouse samples collected from worldwide and analyzed their genetic diversity and phylogenetic relationships among subspecies. House mice are genetically diverse, yet their genetic background at the global level has not been fully understood. Previous studies have suggested that they originated in South Asia and diverged into three major subspecies, almost simultaneously, approximately 110,000–500,000 years ago; however, they have spread across the world with the migration of modern humans in prehistoric and historic times (~10,000 years ago to the present day) and have undergone secondary contact, which has complicated the genetic landscape of wild house mice. In this study, we sequenced the whole-genome sequences of 98 wild house mice collected from

Eurasia, particularly East Asia, Southeast Asia, and South Asia. Although wild house mice were found to consist of three major genetic groups corresponding to the three major subspecies, individuals representing admixtures between subspecies were more prevalent in East Asia than has been previously recognized. Furthermore, several samples exhibited an incongruent pattern of genealogies between mitochondrial and autosomal genomes. Using samples that likely retained the original genetic components of subspecies with the least admixture, we estimated the pattern and timing of divergence among the subspecies. The estimated divergence time of the three subspecies was 187,000–226,000 years ago.

In PART II, we focused our analysis on Madagascar house mouse sample as an example of the relationship between mice and humans. In Madagascar, the house mouse (*Mus musculus*) is widely believed to have colonized with human activities and is now one of the most abundant rodents on the island. However, its genetic background at the genomic level remains unclear, and clarifying this would help us to infer the timing of introduction and route of migration. In this study, we determined the whole-genome sequences of five Madagascar house mice captured from an inland location in Madagascar. We examined the genetic background of samples by analyzing the mitochondrial and autosomal genomes. We confirmed that the mitochondrial genome lineages of collected samples formed a single clade placed at one of the most basal positions in the *Mus musculus* species. Autosomal genomic sequences revealed that these samples are most closely related to the subspecies *M. m. castaneus* (CAS), but also contain a genetic component of the subspecies *M. m. domesticus* (DOM). The signature of a strong population bottleneck 1,000–3,000 years ago was observed in both mitochondrial and autosomal genomic data. In a comparison with global samples of *M. musculus*, the Madagascar samples showed strong genetic affinity to many CAS samples across a wide range of Indian Ocean coastal and insular regions, with divergence time estimated as around 4,000 years ago.

In PART III, we have analyzed East Asian wild house mouse, especially China and Japanese archipelago. Hybrids of MUS and CAS are widespread in East Asia. In Japan, mitochondrial analysis suggested that MUS and CAS types were divided between the northern and southern parts of the Japanese archipelago, but our autosomal analysis suggested that they showed different trends and were divided between the Sea of Japan side and the Pacific side. In China, mitochondria analysis suggested that the MUS and CAS types were separated by Yangtze River, but Y chromosome analysis suggested that the Y chromosome of MUS was completely dominant in China. This predominance of MUS-type chromosomes Y is seen in East Asia, including the Japanese archipelago.

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List of Abbreviations

DNA	deoxyribonucleic acid
mtDNA	mitochondrial DNA
<i>M. musculus</i>	<i>Mus musculus</i>
<i>M. spretus</i>	<i>Mus spretus</i>
<i>M. m. castaneus</i>	<i>Mus musculus castaneus</i>
<i>M. m. domesticus</i>	<i>Mus musculus domesticus</i>
<i>M. m. musculus</i>	<i>Mus musculus musculus</i>
<i>R. rattus</i>	<i>Rattus rattus</i>
CAS	<i>Mus musculus castaneus</i>
DOM	<i>Mus musculus domesticus</i>
MUS	<i>Mus musculus musculus</i>
MOL	<i>Mus musculus molossinus</i>
SPR	<i>Mus spretus</i> from Spain
NEP	Nepal wild house mouse
GEN	<i>Mus musculus gentilulus</i>
MDG	Madagascar wild house mouse
PCA	Principal Component Analysis
PC	principal component
PSMC	pairwise sequentially Markovian coalescent
MSMC	multiple sequentially Markovian coalescent
CI	confidence intervals
rCCR	relative cross-coalescent rate
DSFS	derived site frequency spectrum

LD	linkage disequilibrium
tMRCA	time to the most recent common ancestor
ML	maximum likelihood
HPD	highest posterior density

PART I: Insights into *Mus musculus* Population Structure across Eurasia Revealed by Whole-Genome Analysis

Introduction

The house mouse (*Mus musculus*) has been an important animal model in biomedical research for more than 100 years, and many inbred strains are currently available for research. Inbred laboratory strains are genetically diverse, originating from at least three wild subspecies (Yonekawa et al. 1980, 1982, 1981; Moriwaki et al. 1984; Bonhomme et al. 1987; Yang et al. 2007; Didion and de Villena 2013): *M. m. musculus* (MUS) from northern Eurasia, *M. m. castaneus* (CAS) from southern Asia, and *M. m. domesticus* (DOM) from western Europe. Hereafter we use these abbreviations to represent the subspecies. The first mouse reference genome sequence was created using the classical inbred strain C57BL/6J (Mouse Genome Sequencing Consortium 2002), and dozens of whole-genome sequences of laboratory mouse strains have been published ever since (Keane et al. 2011). The genome of the classical inbred strain is derived from approximately 94.3% DOM, 5.4% MUS, and 0.3% CAS (Keane et al. 2011), whereas the mitochondrial genome is that of DOM (Frazer et al. 2007). In addition, Frazer et al. 2007 estimated that 10% of the classical inbred strain genome is derived from *M. m. molossinus* (MOL), which is thought to have arisen from hybridization between MUS and CAS found in Japan (Yonekawa et al. 1988; Takada et al. 2013). Various strains of laboratory mice have been investigated, with some researchers analyzing the sequences of diverse mouse strains focusing on the origin of subspecies (e.g., Yang et al. 2011).

Despite intensive effort to sequence the genomes of laboratory mice, the genetic diversity of wild house mice has yet to be thoroughly investigated. Previous studies found that wild house mice are highly genetically diverse and have an estimated effective population size of around 10^5 (Baines and Harr 2007; Geraldine et al. 2008, 2011; Halligan et al. 2010, 2013). Classical inbred strains represent a small fraction of the genetic diversity of wild house mice (Salcedo et al. 2007). Previous studies have demonstrated a genome-wide pattern of polymorphisms in wild house mice, but such studies have mostly focused on CAS or DOM within limited geographic ranges (Halligan et al. 2013; Harr et al. 2016; Phifer-Rixey et al. 2018). Therefore, a large-scale genome sequencing study covering the Eurasian continent and surrounding islands will substantially improve our understanding of the worldwide genetic diversity of house mice.

Wild house mice are distributed almost worldwide, including on remote islands: CAS inhabits the Indian subcontinent and Southeast Asia; DOM inhabits North and South America, Africa, the Middle East, Australia, Southwestern Europe, and many surrounding and remote islands; and MUS inhabits Siberia, Central Asia, East Asia, and Northeastern Europe. In addition, more subspecies have been proposed by previous studies. For example, wild house mice found in Japan are considered to be a hybrid between CAS and MUS, forming the independent subspecies MOL (Yonekawa et al. 1988; Takada et al. 2013). Furthermore, mitochondrial phylogeny suggests that the subspecies *M. m. gentilulus* exists in the Arabian Peninsula (Prager et al. 1998) and that an unspecified potential subspecies exists in Nepal (Suzuki et al. 2013; Hardouin et al. 2015). Moreover, highly diversified nuclear genomes and mitochondrial lineages of *M. musculus* have been reported in Iran (Rajabi-Maham et al. 2012; Hardouin et al. 2015). The original homeland of *M. musculus* has been proposed as the northern part of the Indian subcontinent (Boursot et al. 1993; Din et al. 1996), and its common ancestors diverged into the three subspecies, almost simultaneously (Didion and de Villena 2013),

approximately 110,000–500,000 years ago (Boursot et al. 1996; Suzuki et al. 2004; Salcedo et al. 2007; Geraldès et al. 2008, 2011; Bonhomme and Searle 2012; Phifer-Rixey et al. 2020).

Wild house mice migrated and lived commensally with humans. With prehistoric and historic long-distance migration of humans, house mice, for which the staple food is grain, expanded their range with the development of agriculture and cultural exchange (Sage 1981; Moriwaki et al. 1986; Bonhomme et al. 2010; Gabriel et al. 2011; Jones et al. 2013). As the mice moved with humans, genetically diverse subspecies were brought into secondary contact (Boursot et al. 1993; Duvaux et al. 2011), which allowed admixture of their genomes (Bonhomme et al. 2007; Staubach et al. 2012; Liu et al. 2015), despite partial reproductive isolation between subspecies, for example, DOM and MUS (White et al. 2011). DOM and MUS make contact along a narrow hybrid zone in Europe, whereas CAS and MUS seem to have a broader hybrid zone (e.g., Vanlerberghe et al. 1986; Payseur et al. 2004; Dod et al. 2005; Raufaste et al. 2005; Macholn et al. 2007; Teeter et al. 2010, 2008; Jones et al. 2011; Wang et al. 2011; Ďureje et al. 2012) across Central and Eastern Asia (Boursot et al. 1993; Jing et al. 2014). Previous phylogenetic and phylogeographic studies have analyzed mitochondrial DNA sequences and limited nuclear gene sequence data from house mice (e.g., Liu et al. 2008). However, the prevalence of hybridization between subspecies in the global population has yet to be elucidated using genome-wide sequence data. In the pregenomic era, it was recognized that the genetic and phenotypic boundaries between subspecies, except for the boundary between DOM and MUS in western and central Europe, were obscure due to high variability within subspecies (Boursot et al. 1993). This obscurity may have been caused by the limited number of autosomal loci analyzed at that time.

The rapid advancement in sequencing technologies has enabled the use of whole-genome data to estimate population structures and phylogenetic histories. In this study, we sequenced the whole genomes of 98 wild house mice that had previously been collected from

across the Eurasian continent and Southeast Asian islands, particularly mouse samples from East, Southeast, and South Asia. Our analysis revealed that the hybridization between subspecies is prevalent beyond the hybrid zones at a higher level than was previously estimated, particularly that between CAS and MUS in East Asia. Moreover, we estimated the past population size of all individuals used in this study, which allows us to infer the population history of wild house mice that are commensal to humans with agricultural culture. These results improve our understanding of the genetic diversity of house mice at the global level and will facilitate future biomedical and evolutionary research.

Results

Genetic Diversity of Mus musculus

In this study, we analyzed 141 whole-genome-sequenced samples of *M. musculus* and *Mus spretus* (SPR). These included 98 newly sequenced *M. musculus* samples from Eurasia, including samples from Estonia (EST), Ukraine (UKR), Russia (RUS), Iran (IRN), Kazakhstan (KAZ), Pakistan (PAK), India (IND), Sri Lanka (LKA), Nepal (NPL), China (CHN), Vietnam (VNM), Indonesia (IDN), Taiwan (TWN), Korea (KOR), and Japan (JPN) (Figure 1-1). Data for the other 35 *M. musculus* and 8 SPR samples were previously published by Harr et al. (2016) including *M. musculus* samples from Germany (DEU), France (FRA), Iran (IRN), Czech Republic (CZE), Kazakhstan (KAZ), India (IND), and SPR samples from Spain. After filtering individuals with equal to or greater than third-degree kinship, which was inferred using the kinship coefficient, 128 samples were retained for further analysis, including 94 of our newly sequenced samples. The samples used in this study are listed in Table 1-1. Of the 94 newly sequenced samples, 61 were males and 33 were females. The sex of each of these samples is summarized in Table 1-2. After the variants were filtered, we obtained 134,030,288 SNVs and 31,618,947 indels for the dataset containing 128 samples of SPR and *M. musculus*, and 107,337,961 SNVs and 25,875,963 indels for the dataset containing 121 samples of *M. musculus*. The overall transition/transversion ratio of our samples was 2.23. The detailed filtering process is described in the Materials and Methods section.

As reported by Li et al. (2021), mitochondrial genome sequences were clustered into four distinct clades, three of which presumably corresponded to CAS, DOM, and MUS subspecies. The mitochondrial genomes of samples from Nepal (NPL01 and NPL02) diverged before the split between the CAS and DOM clades. When we classified our 94 newly sequenced samples according to mitochondrial haplogroups, the per-sample nucleotide diversity (heterozygosity) of the three subspecies was as follows: 0.00006–0.00757 for CAS (including

the NEP mitochondrial haplogroup), 0.00003–0.00450 for MUS, and 0.00040–0.00561 for DOM. The average ratio of nonsynonymous to synonymous polymorphic sites for each sample was 0.415. The basic statistics for each individual, including per-sample nucleotide diversity for all 94 newly sequenced samples, are presented in Table 1-3.

Genetic Structure of Wild House Mice

We conducted principal component analysis (PCA) of all 128 samples using 100,832,598 autosomal SNVs, including those from SPR (Figure 1-2). All *M. musculus* and *M. spretus* (SPR) were clearly differentiated along principal component 1 (PC1); principal component 2 (PC2) corresponded to variation within the *M. musculus* subspecies (Figure 1-2). In PC2, the *M. musculus* subspecies were differentiated into two clusters with some intermediate samples. Mitochondrial haplotypes and sampling locations indicated that these two clusters corresponded to the DOM and CAS–MUS groups.

We subsequently excluded SPR and replotted the PCA using 84,744,729 autosomal SNVs. Figure 1-3a presents the locations of samples colored according to the three genetic components identified in the PCA plot (Figure 1-3b). The PC score for each sample is presented in Table 1-4. Considering the sampling locations, these three clusters corresponded to the CAS, DOM, and MUS subspecies, whereas a wide range of admixture between the CAS and MUS clusters was observed (Figure 1-3b). In the PCA plot, Nepalese samples with distinct mitochondrial haplogroups were clustered with CAS samples. PC1 shows the genetic differences between MUS and CAS–DOM, whereas PC2 shows the genetic differences between DOM and CAS–MUS. As presented in Figure 1-3a and b, hybrid individuals were prevalent, particularly between CAS and MUS. The Chinese samples were scattered throughout a wide range of the CAS–MUS cline, and the Japanese samples were also scattered along this cline, although the range was narrower than that in the Chinese samples and skewed toward the MUS cluster. We also conducted PCA using only X-chromosomal SNVs (Figure

1-4). This pattern was the same as that obtained using autosomal SNVs; however, the plots were more tightly clustered at each vertex, indicating that admixture was less pronounced on the X chromosomes. For the X chromosomes, the PC scores for each sample are also presented in Table 1-4. PCA plots produced using autosomal and X-chromosomal data without linkage disequilibrium (LD) are presented in Figure 1-5 and 1-6.

In Figure 1-3b, samples from Germany, Bangladesh, and Korea are located at the vertices of a triangle (Table 1-4). However, this pattern does not necessarily imply that these samples are representatives of each of the three major subspecies; instead, the pattern may have been generated by the strong genetic drift in the three populations. To identify samples representing the lowest level of gene flow between subspecies, we computed the f_3 and f_4 statistics among different individuals (Table 1-5–1-7 and 1-8–1-13, respectively). Indian CAS samples from mountainous regions, western European DOM samples, and Korean MUS samples exhibited the lowest levels of gene flow compared with the other subspecies. Therefore, we selected an Indian sample (IND04), a Korean sample (KOR01), and a German sample (DEU01) as our reference samples of the CAS, MUS, and DOM subspecies, respectively.

Except for the aforementioned samples, most CAS–MUS samples exhibited some extent of admixture between subspecies. For example, compared with IND04, another Indian sample from Delhi (IND02) was slightly genetically closer to MUS (KOR01). The Z score of f_4 (SPR, KOR01; IND04, IND02) was 2.814 (Table 1-14). Compared with the IND03, IND04, and IND07 samples, other CAS samples from neighboring regions, such as Pakistan and Bangladesh, were more similar to MUS (KOR01) (Table 1-11 and 1-12). CAS samples from East and Southeast Asian regions also exhibited various levels of admixture with MUS genomes. Likewise, all MUS samples from Eastern Europe had a significantly closer relationship to DOM than the other Asian MUS samples. For example, the Z scores of f_4 (SPR, DEU01; KOR01, CZE01) and f_4 (SPR, DEU01; KOR01, KAZ01) were 14.724 and 11.104,

respectively (Table 1-11). The majority of MUS samples from East Asia, particularly those from Northern China and Japan, exhibited a high level of admixture with CAS. Compared with DOM samples from Western Europe, those from outside Western Europe, such as the Iranian and Russian samples, exhibited slightly but significantly closer affinity to MUS and CAS samples (Table 1-10 and 1-11). One sample collected from Kathmandu in Nepal (NPL02) was the most distantly related to the CAS, MUS, and DOM samples. Another sample from Nepal (NPL01) exhibited a similar pattern; however, compared with NPL02, NPL01 was more closely related to CAS.

The PCA plot produced using nuclear genome data was labeled with the four mitochondrial haplogroups (CAS, DOM, MUS, and NEP; Table 1-3) and is presented in Figure 1-3c. Most samples exhibited congruent patterns in their mitochondrial and nuclear genomes, although the patterns were incongruent in some samples. As presented in the PCA plot (Figure 1-3b and c), mitochondria–nuclear genome incongruence was more commonly observed in the MUS cluster than in the CAS or DOM cluster. For example, a sample from Khabarovsk in the Russian Far East (RUS13) had a DOM-type mitochondrial genome but a nuclear genome that was highly similar to that of MUS.

To infer the genomic ancestries of *M. musculus* genomes, we also conducted ADMIXTURE analysis (Figure 1-7). We analyzed 121 *M. musculus* samples by selecting K values from 1 to 5, where K is a predefined number of ancient components. We also performed cross-validation to infer the most suitable K value (Figure 1-8) and found that the cross-validation error rate was the lowest at $K=4$. At $K=3$, we confirmed the presence of three genetic components corresponding to CAS, DOM, and MUS, respectively. Most Japanese and Chinese samples exhibited a hybrid pattern with the CAS and MUS components. At $K=4$, another genetic component represented the specific genetic features of Japanese and Korean mice. The results of the ADMIXTURE analysis using X-chromosomal SNVs were largely the

same as those obtained using autosomal SNVs (Figure 1-9). The ADMIXTURE plots of autosomes and X chromosomes without LD are presented in Figure 1-10 and 1-11.

Inference of Past Demography Using PSMC and MSMC

To estimate the past demographic pattern of wild house mice, we conducted pairwise sequentially Markovian coalescent (PSMC) analysis for each individual. Figure 1-12 presents the PSMC plots of all individual samples. Although some of the samples exhibited unusual patterns, the trajectories of most samples could be largely classified into three categories representing CAS, DOM, and MUS (Figure 1-12).

We investigated past demography in more recent years by performing multiple sequentially Markovian coalescent (MSMC) analysis using the MSMC/MSMC2 software, which uses information on multiple haplotypes from each population. Figure 1-13 presents the results of four haplotypes from two Indian samples (IND03 and IND04) for CAS, eight haplotypes from four German samples (DEU01, DEU03, DEU04, and DEU06) for DOM, and eight haplotypes from four Korean samples (KOR01–03 and KOR05) for MUS. Because the number of analyzed haplotypes was smaller in CAS than in DOM and MUS, the demography of CAS in recent years (i.e., after ~10,000 years ago) may not be reliably estimated. To convert the generation number into years, we assumed a mutation rate of 5.7×10^{-9} per base pair per generation (Milholland et al. 2017) and a generation time of 1 year. Three subspecies followed different trajectories of population size change. The effective population size of CAS increased in an ancient time period around 100,000 years ago and later continued to decrease. After the decline, the effective population size of CAS reached its maximum level around 1,000–3,000 years ago. In contrast, both MUS and DOM genomes showed the signs of population shrinkage roughly 200,000 years ago. The trajectories of population sizes in DOM and MUS were similar prior to 100,000 years ago. DOM later experienced two rounds of population bottleneck and expansion, around 50,000 and 5,000 years ago. The trajectories of Korean MUS showed the

signature of recent population bottleneck and expansion, probably between 2,000 and 4,000 years ago.

Genetic Relationship among Three Subspecies

Previous phylogenetic studies, in which partial or complete mitochondrial genome sequences were used, demonstrated a sister relationship between CAS–DOM (Geraldes et al. 2008; Li et al. 2021) and CAS–MUS (Jing et al. 2014), and genome sequencing studies of wild-derived mouse strains suggested a CAS–MUS clade (White et al. 2009; Keane et al. 2011; Phifer-Rixey et al. 2020). In this study, we conducted f -statistics analysis using representative samples of each subspecies, that is, IND04 for CAS, DEU01 for DOM, and KOR01 for MUS. We calculated outgroup f_3 statistics for all pairs among the three target samples with SPR used as an outgroup (Figure 1-14). A larger f_3 statistic value indicates that two subspecies share a larger amount of genetic drift, that is, a closer relationship exists between the two subspecies. The f_3 value of the CAS–MUS pair was statistically larger than that of the other comparisons between subspecies ($P = 3.12 \times 10^{-8}$ between CAS–MUS and CAS–DOM, $P = 6.22 \times 10^{-7}$ between CAS–MUS and DOM–MUS; Tukey's test). To validate this result, we conducted four population tests using f_4 statistics. The Z scores for the f_4 (SPR, DEU01; IND04, KOR01), f_4 (SPR, IND04; DEU01, KOR01), and f_4 (SPR, KOR01; DEU01, IND04) values were 2.003, 28.518, and 16.001, respectively (Table 1-10, 1-8, and 1-13, respectively). These results support a close genetic relationship between CAS and MUS. Table 1-15–1-17 and 1-18–1-23 show the f_3 statistics and four f_4 statistics for chromosome X, respectively.

We also constructed a neighbor-joining tree using pairwise genetic distances between samples, initially with all samples including SPR as the outgroup (Figure 1-15 and 1-16). The initial tree showed a sister relationship between DOM and MUS with an exceptionally longer branch of the DOM clade, which contradicted the f_3 and f_4 statistics. However, two particular samples, CHN06 from Urumqi and RUS01 from Moscow, which exhibited a strong

hybridization signature between MUS and DOM, potentially distorted the pattern. To solve this problem, we reconstructed a tree excluding all potential hybrid individuals, that is, a phylogenetic tree constructed using only individuals with >80% signal for one subspecies ancestry from the ADMIXTURE results; consequently, we obtained the pattern of the CAS–MUS clade (Figure 1-17).

Estimation of Divergence Times between Subspecies

To estimate the divergence timing of the three subspecies, we conducted cross-subspecific MSMC analysis (Figure 1-18). Initially, we used Indian, German, and Korean samples as the representative samples for each subspecies, but we found that the strong population bottleneck that occurred in the ancestors of Korean samples made it difficult to accurately infer the population history before the bottleneck. Therefore, we used Kazakhstan samples as representatives of MUS. Although Kazakhstan samples exhibited some level of admixture with DOM, this would not affect the estimated subspecies divergence time if the admixture occurred relatively recently (i.e., after 10,000 years ago). The divergence times between CAS and DOM, CAS and MUS, and DOM and MUS were separately estimated using time points when the relative cross-coalescent rate (rCCR) was 0.5. The divergence between CAS and MUS was most recent (95% CI: 187,365–188,647), consistent with the earlier analyses. The divergence times between CAS and DOM and DOM and MUS were almost equal, that is, 223,614–225,306 and 245,411–247,175 years ago (95% CIs), respectively.

Discussion

Although house mice have been widely used in biomedical research, the global genetic landscape of wild house mice has not been clear. Previous studies have included analysis of the genome sequences of western European (DOM), Middle Eastern (CAS), and North American (DOM) samples (Staubach et al. 2012; Harr et al. 2016; Mack et al. 2018). This is the first genome-wide study of wild house mice that includes all three subspecies and focuses on the genetic diversity across the Eurasian continent and Southeast Asian islands. Furthermore, we elucidated the present and ancestral population structure of the species.

Wild house mice have a much larger effective population size than humans (Geraldes et al. 2008, 2011; Halligan et al. 2010, 2013). Based on a phylogenetic tree excluding hybrid individuals (Figure 1-17), we calculated the nucleotide diversity in each subspecies: 0.527% for CAS, 0.244% for DOM, and 0.225% for MUS. Given that the average human nucleotide diversity is 0.08–0.12%, our results confirm that the nucleotide diversity of wild house mice is much higher than that of humans (Perry et al. 2012; Prado-Martinez et al. 2013; Arbiza et al. 2014). These values are consistent with those in previous studies (Geraldes et al. 2008; Phifer-Rixey et al. 2014; Harr et al. 2016), which showed that CAS has the highest diversity in all subspecies.

The PCA results presented in Figure 1-3b revealed a wide spectrum of samples within the CAS and MUS genetic clines. In particular, the Japanese and Chinese samples were widely distributed along the PCA plot. Even samples from other locations, such as Southeast Asia, demonstrated an admixture signature to some extent. The ADMIXTURE results (Figure 1-7) were largely in agreement with the PCA results. Our analysis using the f_3 and f_4 statistics showed that samples from India, Germany, and Korea had the smallest genetic component derived from different subspecies. Although these samples do not necessarily represent genuine

subspecies with pure ancestry and without admixture between subspecies, this could be verified by additional sampling of wild mice in the Eurasian continent.

Our PSMC plots can be classified into three categories representing three subspecies, but relatively recent effective population size varied from sample to sample (Figure 1-12). For example, in MUS, comparing CHN03 (China: Aksu), EST01 (Estonia: Tallinn), and IRN06 (Iran: Mashhad), all showed similar population size changes until ~50,000 years ago, but the Chinese Aksu population more recently experienced a strong bottleneck 20,000–30,000 years ago and then an increase in population size about 10,000 years ago (Figure 1-12). A population size increase about 10,000 years ago was also observed in the Iranian Mashhad population, but the magnitude of population bottleneck and expansion was milder than that in the Chinese Aksu population. In contrast, the Estonian Tallinn population exhibited little increase in population size around 10,000 years ago; thus, the three populations experienced distinctly different region-dependent population size changes. As aforementioned, wild house mice in certain regions, such as Russia, the Japanese archipelago, and the Korean peninsula, were subject to an extreme population bottleneck, making it difficult to follow the past genetic demography of some individuals due to the substantial loss of polymorphic markers. For example, it was impossible to trace the population history of the RUS06 (Russia: Irkutsk), JPN13 (Japan: Ashiro), and KOR01 (Korea: Baengnyeong Island) samples before 100,000 years ago due to the strong bottleneck effect (Figure 1-12).

Our results could substantially alter the simple trinity view of *M. musculus* subspecies. The observed pattern implies that the admixture between CAS and MUS has continued to occur for 10,000 years in Asia and that many “MUS-like CAS” and “CAS-like MUS” samples exist. This complex pattern has not previously been captured using mitochondrial phylogeny. Indeed, we observed many cases with incongruence between mitochondrial and autosomal genotypes. In particular, many Japanese samples harbor CAS-type mitochondrial and MUS-like nuclear

genomes (Figure 1-3c). Based on a study of whole mitochondrial genome sequences, Li et al. (2021) suggested that the CAS-type mitochondrial genome was introduced to the Japanese archipelago in the late Neolithic period (~3,500 years ago) and that the MUS-type mitochondrial genome migrated later (~2,700 years ago) and quickly spread to the archipelago. The latter migration of house mice may coincide with the introduction of intense rice farming to the Japanese archipelago (Li et al. 2021). Such a pattern of nuclear–mitochondrial genotype mismatching has also been reported in house mice from New Zealand (Veale et al. 2018), Mainland China and Taiwan (Geraldès et al. 2008), and Madagascar (Fujiwara et al. 2021).

Interestingly, the incongruence between mitochondrial and autosomal genotypes was particularly prevalent among MUS. In samples with autosomal MUS genotypes, mitochondrial haplotypes corresponding to CAS, MUS, and DOM were identified. Previous studies reported a similar bias in the European hybrid zone of DOM–MUS, in which DOM-type haplotypes were observed in MUS, but MUS-type haplotypes were not observed in DOM (Božíková et al. 2005). Hybrid incompatibility associated with cytonuclear incompatibility is one possible explanation (Johnson 2010), but a reciprocal mtDNA transplant experiment revealed the opposite result, that is, that MUS-type (PWD) embryos with DOM-type (B6) mitochondria are more likely to be lethal than reciprocally transplanted embryos (Ma et al. 2016). Thus, additional ecological and experimental studies are required to reveal the cause of this bias.

Our analysis of past demography revealed different trajectories of population sizes in the three subspecies. Previous studies have suggested that the divergence of the three subspecies of *M. musculus* occurred 250,000 years ago for the substitution at the third codon position in mitochondrial Cyt *b* (Bonhomme and Searle 2012), 110,000–320,000 years ago for the isolation-with-migration model using whole-genome SNPs (Phifer-Rixey et al. 2020). Summarizing previous studies, the estimated divergence times fall within the range of 110,000–500,000 years ago (e.g., Boursot et al. 1996; Suzuki et al. 2004; Salcedo et al. 2007;

Duvaux et al. 2011; Geraldles et al. 2011, 2008; Bonhomme and Searle 2012; Suzuki et al. 2013). In our analysis based on the MSMC results, we estimated that the divergence of the three subspecies occurred 187,000–247,000 years ago and the most recent subspecies divergence, that of CAS and MUS, occurred ~188,000 years ago, which are within the range of previous estimates. It should be noted that these estimates of divergence timing are highly dependent on the germline mutation rate and generation time used in our study.

Interestingly, both DOM and MUS experienced a recent strong population bottleneck and expansion, which was likely associated with the spread of agriculture. Entries into the expansion phase were much earlier in German DOM (4,000–6,000 years ago) than in Korean MUS (2,000–4,000 years ago), and this difference may reflect the different histories of agriculture in the two regions. In contrast, the population size of CAS was smallest at ~10,000–20,000 years ago, but the reduction was much lower than that in the other subspecies. A less severe population bottleneck would explain the higher genetic diversity of CAS.

This study elucidates the genome-wide relationship among *M. musculus* subspecies. Our f_3 and f_4 statistics support the close relationship between CAS and MUS, which is consistent with the study of White et al. (2009), in which dense genome-wide SNP data from wild-derived inbred mouse strains was used. In the presence of rampant gene flow between populations, it is difficult to infer population splitting. In particular, we found that the removal of obvious hybrid samples drastically altered the topology of the evolutionary relationship of subspecies (Figure 1-16 and 1-17). Additional analyses using different data types (f_3 statistics and MSMC; Figure 1-14 and 1-18) indicated that the CAS–MUS clade is most likely. As a note of caution, bifurcating tree construction methods that do not assume any gene flow among taxon could potentially lead to biased results if hybrid samples were included in the analysis.

M. musculus has been widely used as an animal model in evolutionary genetics and biomedical research. Revealing the genetic background and evolutionary history of this species

will significantly contribute to the understanding of these models among research communities. In this study, we reported 98 novel whole-genome sequences of wild house mice, which were collected from a range of regions in the Eurasian continent and surrounding islands. Our analysis captured the genetic diversity of wild house mice on this continent, which has not previously been well studied, and revealed a complex pattern of admixture among three major subspecies. Indeed, the extent and geographic range of admixture was greater than previously thought, particularly between CAS and MUS; most of the samples from Southeast and East Asia showed some level of gene flow from different subspecies. The high-quality whole-genome sequencing data presented in this study will be important for future research on evolutionary ecology, population dynamics, and natural selection by introgression among subspecies of wild house mice.

Materials and Methods

Materials

Ninety-eight wild house mouse samples from across the Eurasian continent and surrounding remote islands were collected. These samples are identical to those used by Li et al. (2021), who reported and analyzed whole mitochondrial genome sequences. In addition, whole-genome sequencing data from 35 wild *M. musculus* and 8 SPRs, previously reported by Harr et al. (2016), were downloaded from the European Nucleotide Archive (PRJEB9450, PRJEB11742, PRJEB14167, PRJEB2176, and PRJEB11897). In this study, the mitochondrial haplogroup of each sample was determined using the data provided by Li et al. (2021). For the mitochondrial sequences of Harr et al. (2016) dataset, a maximum likelihood phylogenetic tree was created along with the mitochondrial sequences determined by Li et al. (2021) to assign mitochondrial haplogroups. Table 1-1–1-3 include detailed information on the samples, and the geographical sampling locations are presented in Figure 1-1.

Mapping Genomic Read Pairs and Single-Nucleotide Variant Calling

For the 98 wild house mouse samples, paired-end sequences of 100 bp in length were determined using the BGISEQ-500 platform. The quality of reads was checked and visualized using FastQC (Andrews 2010) and MultiQC (Ewels et al. 2016).

All raw reads were mapped to the GRCm38 (mm10) house mouse reference genome sequence using the bwa-mem algorithm with the “-M” option (Li and Durbin 2009). The samblaster program with “-M” option was used to mark PCR duplicate reads (Faust and Hall 2014). For the Harr et al. (2016) dataset, we used 43 samples with a median coverage of >20. All of the newly sequenced samples had a median coverage of at least >25 (Table 1-3). Raw SNV and insertion/deletion (indel) calls were performed using GATK4 HaplotypeCaller with the “-ERC GVCF” option (McKenna et al. 2010). All genomic variant call format (gVCF) files

were merged using the CombineGVCFs function, and the variants of all samples were jointly called using the GenotypeGVCFs function.

Raw SNVs and indels were processed using GATK4 Variant Quality Score Recalibration (VQSR), a machine learning process that uses known variants as a training dataset and predicts whether a new variant is a true positive or false positive. To run GATK4 VQSR, we used the files “mgp.v3.snps.rsIDdbSNPv137.vcf.gz” and “mgp.v3.indels.rsIDdbSNPv137.vcf.gz,” which were downloaded from the web server of the Sanger Institute (ftp://ftp-mouse.sanger.ac.uk/REL-1303-SNPs_Indels-GRCm38/), as training datasets for SNVs and indels, respectively. We also included hard-filtered SNV data as a training dataset. A hard-filtering process for SNVs was conducted using the following parameters: $QD < 2.0$; $FS > 60.0$; $MQ < 40.0$; $MQRankSum < -12.5$; and $ReadPosRankSum < -8.0$. In contrast, a HARD-filtering process for indels was performed using the following parameters: $QD < 2.0$; $FS > 200.0$; $InbreedingCoeff < -0.8$; $ReadPosRankSum < -20.0$; and $SOR > 10.0$. We assumed that SNVs and indels within the 90% tranche (i.e., 90% acceptance in all reliable training SNV datasets) were true-positive SNVs and indels, and these were used for downstream analyses. VQSR-passed SNVs were further filtered according to their mappability to the *M. musculus* reference genome, which was achieved using GenMap (Pockrandt et al. 2020). Mappability filtering retains highly unique regions in the reference genome. We computed mappability scores using the “-K 30” and “-E 2” options and analyzed sites with mappability values of 1.

Because we could not reliably distinguish the sex of some of our samples based on morphological records, we assigned sex based on the read depth coverages on the X and Y chromosomes (Table 1-2). We used samtools “depth” to calculate the coverage of each sample in the nonpseudoautosomal regions of the sex chromosomes that passed through the mappability filter. The ratios of average X-chromosomal to Y-chromosomal coverages

exhibited a clear bimodal distribution, 0.96–1.15 and 7.43–195.20, in which the samples within the ranges likely represented males and females, respectively.

Kinship inference among samples was performed using KING with the “–kinship” option (Manichaikul et al. 2010). According to KING, the expected ranges of kinship coefficients were >0.354 for duplicate/monozygotic twins, >0.177 and <0.354 for first-degree relationships, >0.0884 and <0.177 for second-degree relationships, >0.0442 and <0.0884 for third-degree relationships, and <0.0442 for unrelated individuals. We excluded 13 samples (12 *M. musculus* and 1 SPR) with relationships closer than third degree. In total, 128 samples (94 of our samples and 34 public samples) were retained after the filtering process.

Synonymous and nonsynonymous variants were assigned using SnpEff (Cingolani, Platts, et al. 2012) and SnpSift (Cingolani, Patel, et al. 2012) with house mouse gene annotation data version “GRCm38.101 (ftp://ftp.ensembl.org/pub/release-101/gtf/mus_musculus/).” This was calculated by counting the number of synonymous and nonsynonymous variants on a gene-by-gene basis.

Population Structure Analysis

Using VCFtools (Danecek et al. 2011), SNVs were further filtered and converted to the PLINK format (Purcell et al. 2007) containing only biallelic autosomal SNVs and retaining sites successfully genotyped in all samples. Typically, SNVs in LD are excluded from the population structure analysis; however, in our main analysis, we did not eliminate these SNVs as our mouse samples were highly structured at the subspecies level, and the elimination of these SNVs have removed too many SNVs and prevented analysis. We also created PCA and ADMIXTURE plots without LD (Figure 1-5, 1-6, 1-10, and 1-11) by specifying the following parameters: window size = 50 kb, window step size = 5, and variance inflation factor = 2. PCA was conducted using the smartpca program from Eigensoft (Patterson et al. 2006); default parameter settings were used with the exception of declining to remove outlier samples. The

color codes in Figure 1-3a and b were assigned according to Maxwell's color triangle. Outgroup f_3 statistics were computed using Admixtools, with the SPR population used as an outgroup via the "outgroupmode" option (Patterson et al. 2012). The f_4 statistics were also computed using Admixtools with the " f_4 mode" and "prints" options (Patterson et al. 2012). In addition, the ADMIXTURE (Alexander et al. 2009) software was used for population stratification. We computed cross-validation error values ($-cv$ option) from $K = 1$ to $K = 5$ for datasets that either included or excluded SPR. The identity-by-state (IBS) distance matrix between all pairs of individuals was calculated using the PLINK "--distance 1-ibs" option, and the matrix was used to construct a neighbor-joining tree (Saitou and Nei 1987) using the Ape package in R (Paradis et al. 2004).

Demographic Inference Using PSMC and MSMC/MSMC2

The sampled individuals were subjected to PSMC analysis (Li and Durbin 2011). To obtain the required input for PSMC, a consensus autosomal genome sequence for each individual, the "mpileup" samtools command was applied to the dataset using the "-C 50" options. For vcf2fq command of vcfutils.pl implemented in PSMC, we used option "-D 60, -d 10". PSMC analysis options (-t and -p) were selected according to the default settings suggested for the PSMC software. The time interval parameters were set to " $4 + 25 * 2 + 4 + 6$ " with 25 iterations. To show the standard errors of the population size (N_e) estimates, we conducted 100 replications using the bootstrap method for the representative samples of each subspecies.

MSMC (Schiffels and Durbin 2014) version 2 (MSMC2: <https://github.com/stschiff/msmc2>; Schiffels and Wang 2020; Malaspina et al. 2016) was used to estimate changes in N_e as well as the divergence time of subspecies. During the MSMC/MSMC2 analysis, we performed estimations using phased haplotype sequences as input. We estimated phased haplotypes using the ShapeIT4 software (Delaneau et al. 2019). The "Mapping Data for G2F1-Based Coordinates" from "Mouse Map Converter

(<http://cgd.jax.org/mousemapconverter/>)” were used to provide the recombination rate input file for MSMC2. Mappability was taken considered, and nonunique sequence positions were not used for calculations. The time interval parameters were set to “ $1 * 2 + 50 * 1 + 1 * 2 + 1 * 3$ ” with 20 iterations. To estimate the divergence time of subspecies, we used two haplotypes from each population (four haplotypes in total) as an input for MSMC2. According to Shiffels and Durbin (2014), the rCCR variable should be between 0 and 1 (however, the calculation is unavoidably >1 in some cases), with a value close to 1 indicating that two populations were one population at a specific point in time. Heuristically, $rCCR = 0.5$ is considered to indicate the estimated time at which the two populations separated. Bootstrap was conducted by cutting the original input data into 5-Mb blocks and randomly sampling such blocks to artificially create a 3-Gbp-length genome. Of these artificially created datasets, 20 were used for analysis. To estimate N_e over time, we used eight haplotypes from four samples of each MUS (KOR01–03 and 05) and DOM (DEU01, DEU03, DEU04, and DEU06) population and four haplotypes from two samples of CAS (IND03 and IND04). To estimate subspecies divergence, we used four haplotypes from two populations for each combination of CAS–MUS (IND04 and KAZ01), DOM–MUS (DEU07 and KAZ01), and CAS–DOM (IND04 and DEU07).

Figures and Legends

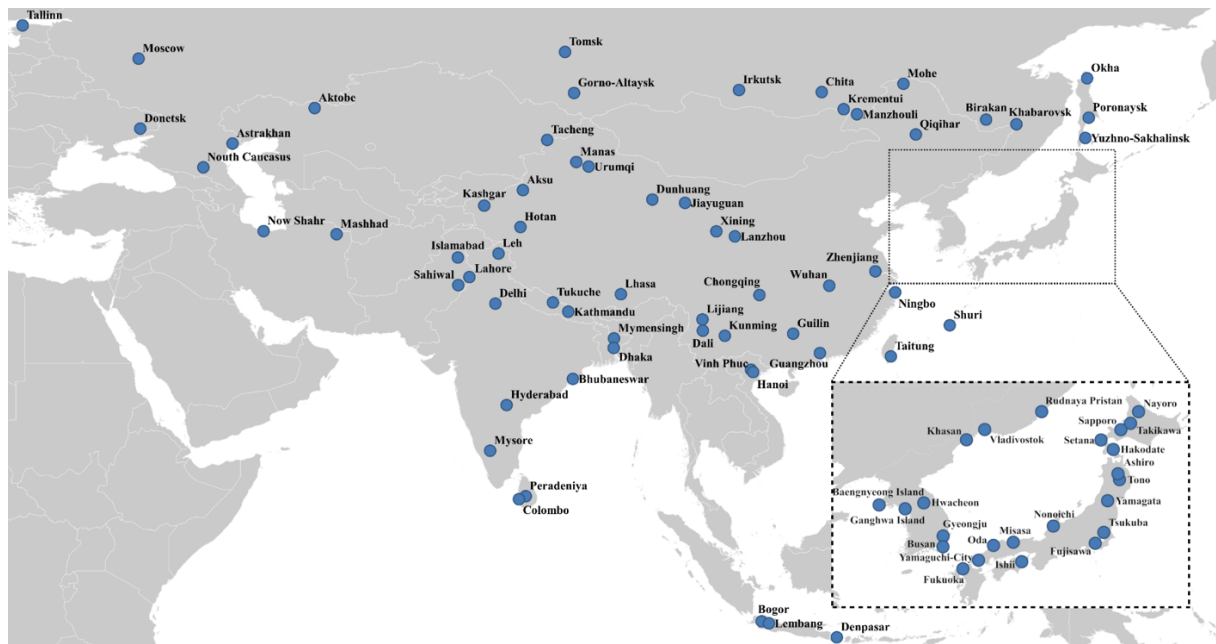


Figure 1-1 Geographic location map of collection sites.

Collection sites for wild house mouse samples used in this study. Blue dots indicate the approximate locations of new samples used in this study. At some sites, more than one individual was collected from the same location.

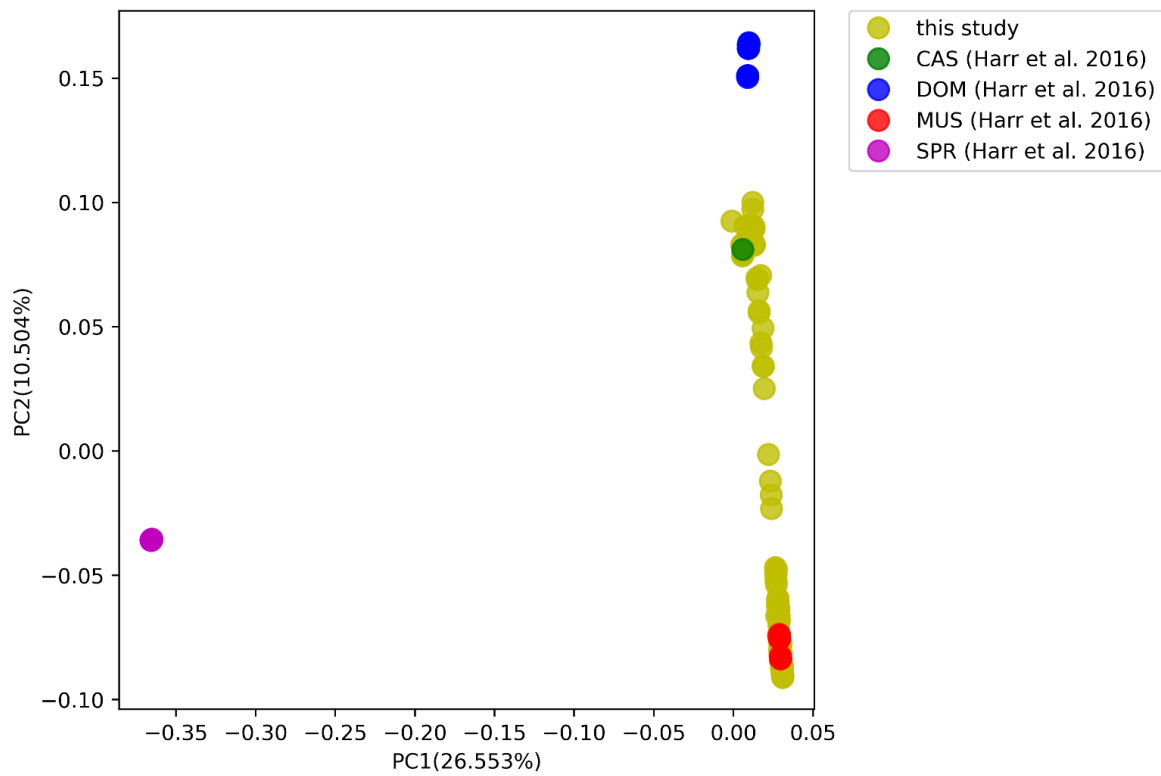


Figure 1-2 PCA results of *Mus musculus* and *Mus spretus* using autosome.

The principal component analysis (PCA) plot using *Mus musculus* and *Mus spretus* whole genome sequences. For comparison, the public data for MUS, CAS, and DOM samples are marked separately from our analyzed samples.

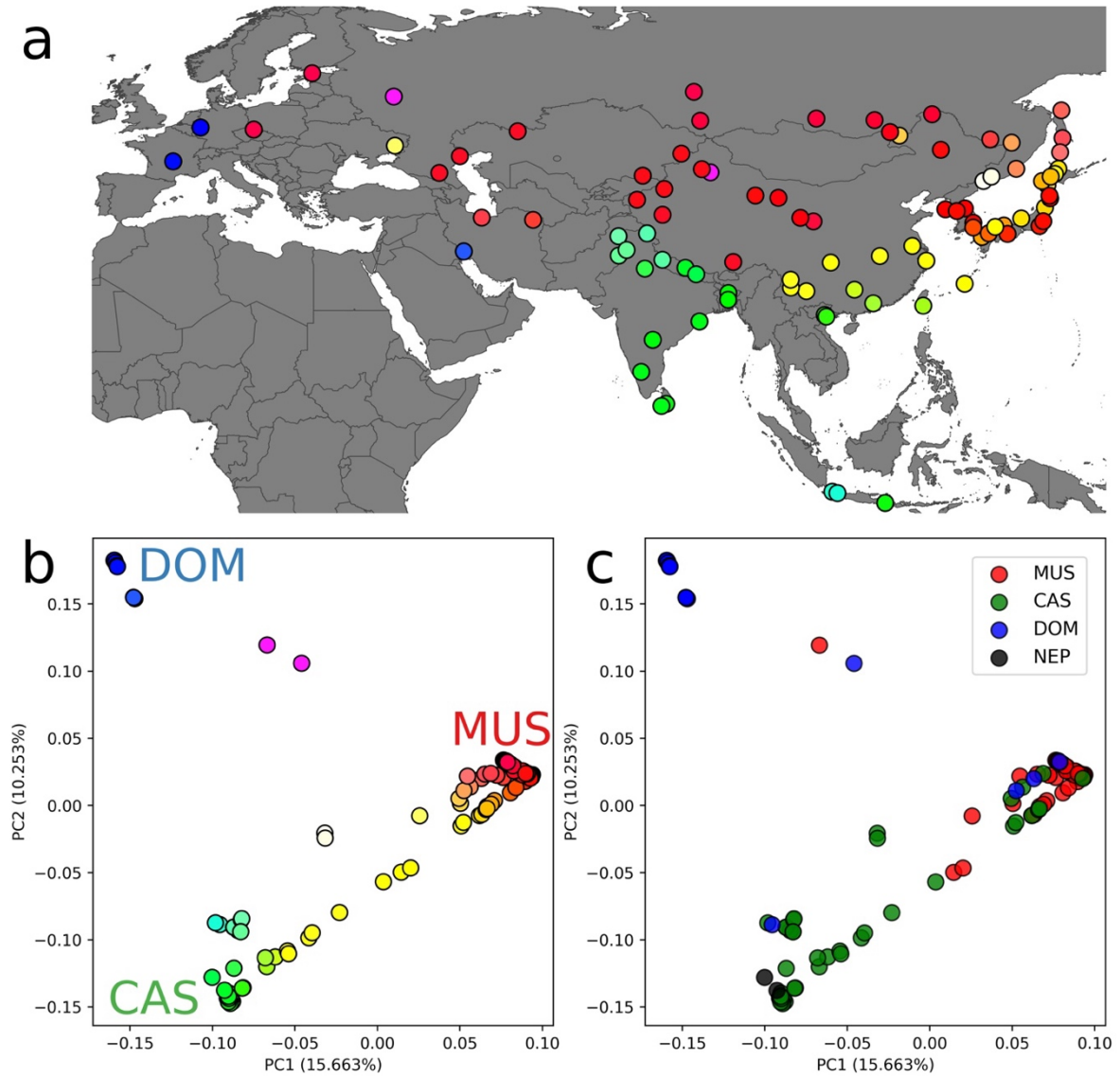


Figure 1-3 PCA results in wild house mice.

(a) Geographical map of sampling locations. Circles represent each individual, and the assigned color is the same as that in panel (b). Figure 1-1 presents the detailed names of sample collection sites. (b) PCA plot of wild house mice produced using autosomal SNVs. The x and y axes represent PC1 and PC2, respectively. Circles are colored according to “Maxwell’s color triangle,” assigning three vertices to the RGB colors. Red, green, and blue color intensities correspond to the MUS, CAS, and DOM genetic components, respectively. The proportion of variance for each PC is shown in parentheses on the axis label. (c) PCA plot of wild house mice produced using autosomal SNVs labeled with the mitochondrial genome haplogroup of each

sample. NEP represents the mitochondrial haplogroup of Nepalese origin. The proportion of variance for each PC is shown in parentheses on the axis label.

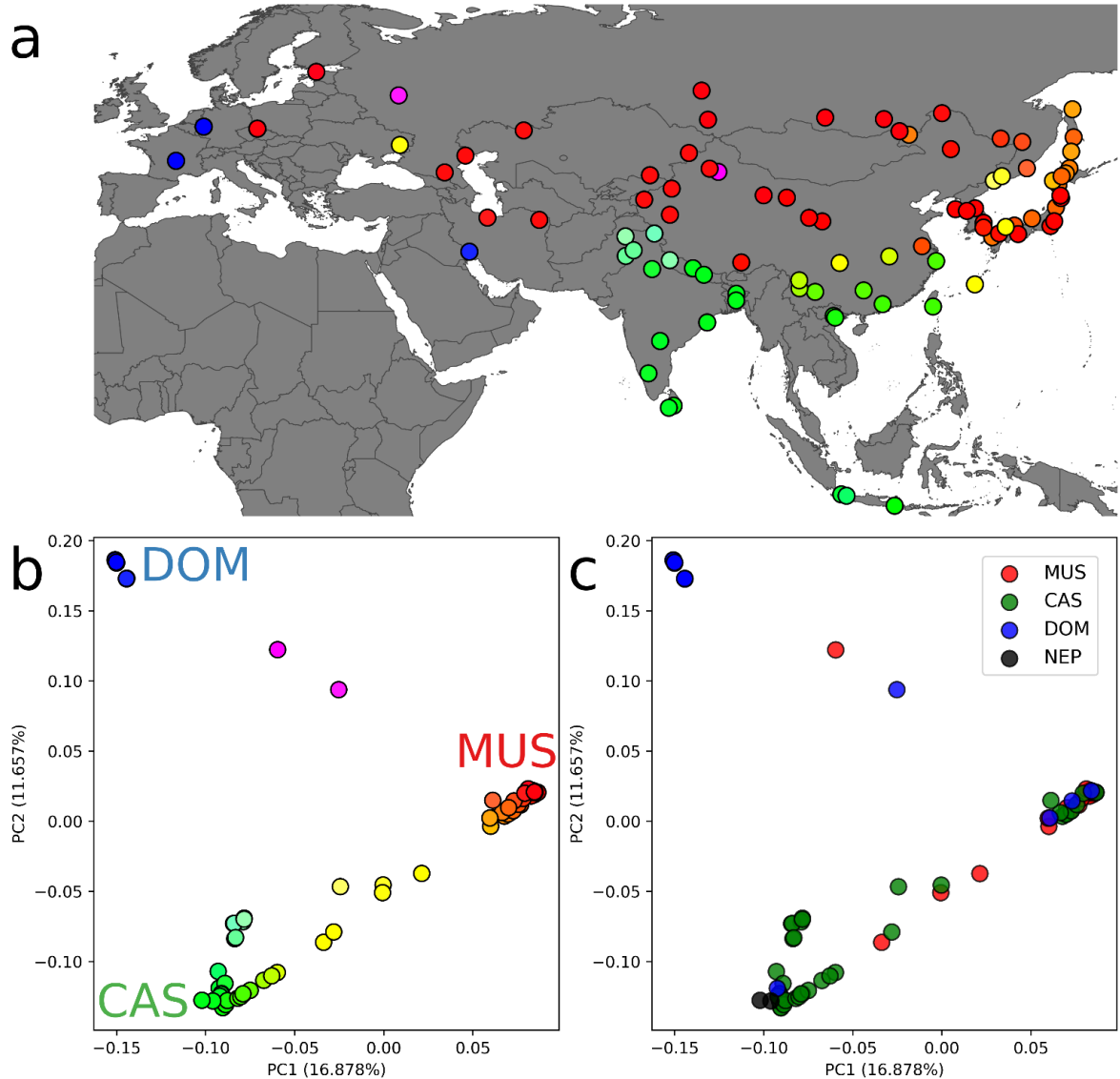


Figure 1-4 PCA results of X chromosome in wild house mouse.

(a) A geographical map of sampling locations. The circle represents each individual and the assigned color is the same as the color in panel b. Figure 1-1 shows the detailed names of sample collection sites. (b) PCA plot of wild house mice using X chromosomal SNVs. The x and y axes represent the eigenvalues of PC1 and PC2, respectively. The circles are colored according to “Maxwell’s color triangle,” assigning three vertices to the RGB colors. The red, green, and blue color intensities correspond to MUS, CAS, and DOM genetic components, respectively. The proportion of variance for each eigenvalue is shown in parentheses on the

axis label. (c) PCA plot of wild house mice using X chromosomal SNVs labeled with the mitochondrial genome haplogroup of each sample. The proportion of variance for each eigenvalue is shown in parentheses on the axis label.

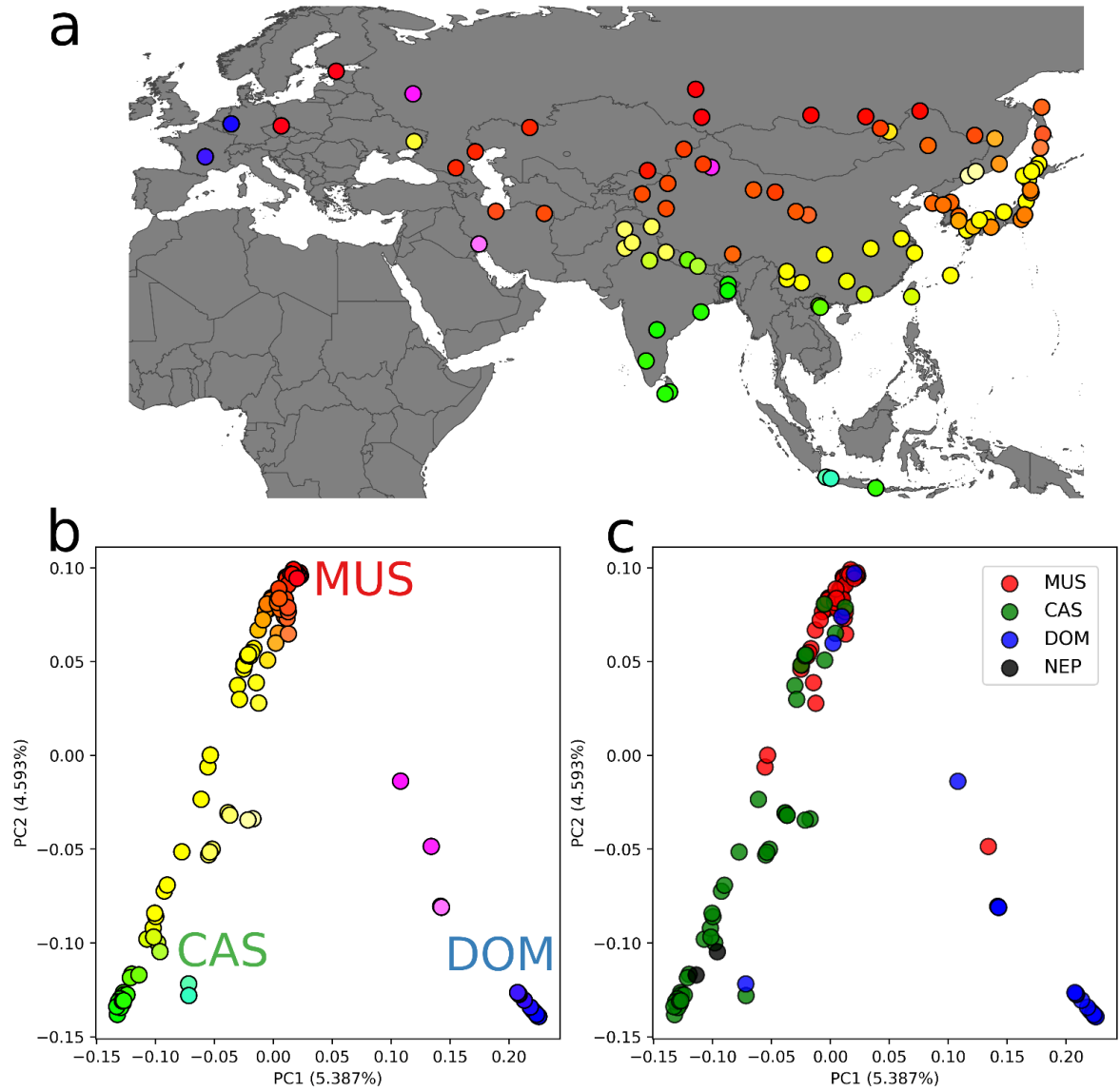


Figure 1-5 LD pruned PCA results in wild house mice.

(a) A geographical map of sampling locations. The circle represents each individual and the assigned color is the same as the color in panel b. Figure 1-1 shows the detailed names of sample collection sites. (b) PCA plot of wild house mice using autosomal SNVs. The x and y axes represent the PC1 and PC2, respectively. The circles are colored according to “Maxwell’s color triangle,” assigning three vertices to the RGB colors. The red, green, and blue color intensities correspond to MUS, CAS, and DOM genetic components, respectively. The proportion of variance for each PC is shown in parentheses on the axis label. (c) PCA plot of

wild house mice using autosomal SNVs labeled with the mitochondrial genome haplogroup of each sample. NEP represents an independent mitochondrial haplogroup of Nepalese origin. The proportion of variance for each PC is shown in parentheses on the axis label.

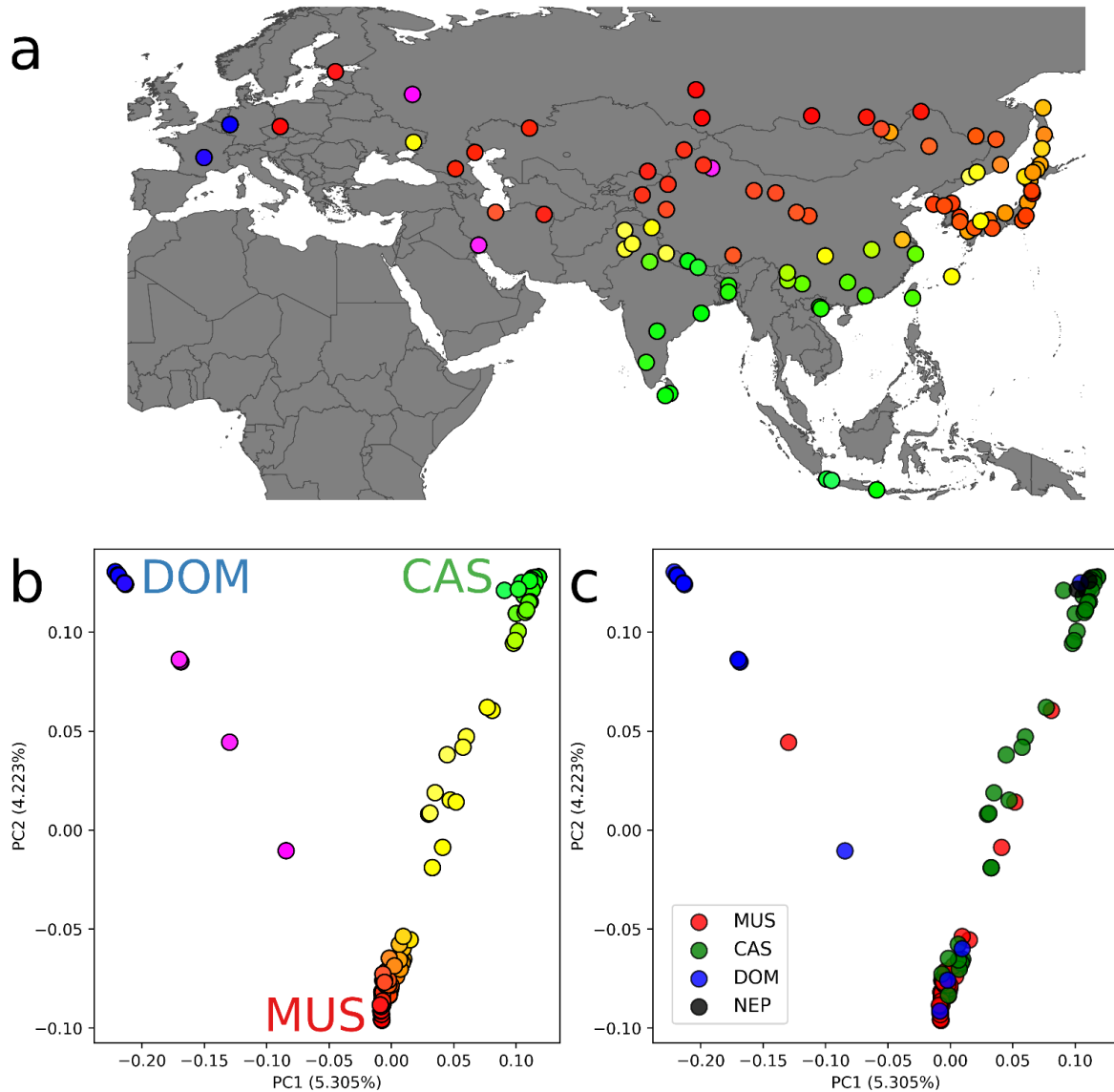


Figure 1-6 LD pruned PCA results of X chromosome in wild house mouse.

(a) A geographical map of sampling locations. The circle represents each individual and the assigned color is the same as the color in panel b. Figure 1-1 shows the detailed names of sample collection sites. (b) PCA plot of wild house mice using X chromosomal SNVs. The x and y axes represent the PC1 and PC2, respectively. The circles are colored according to “Maxwell’s color triangle,” assigning three vertices to the RGB colors. The red, green, and blue color intensities correspond to MUS, CAS, and DOM genetic components, respectively. The proportion of variance for each PC is shown in parentheses on the axis label. (c) PCA plot of wild house mice using X chromosomal SNVs labeled with the mitochondrial genome

haplogroup of each sample. NEP represents an independent mitochondrial haplogroup of Nepalese origin. The proportion of variance for each PC is shown in parentheses on the axis label.

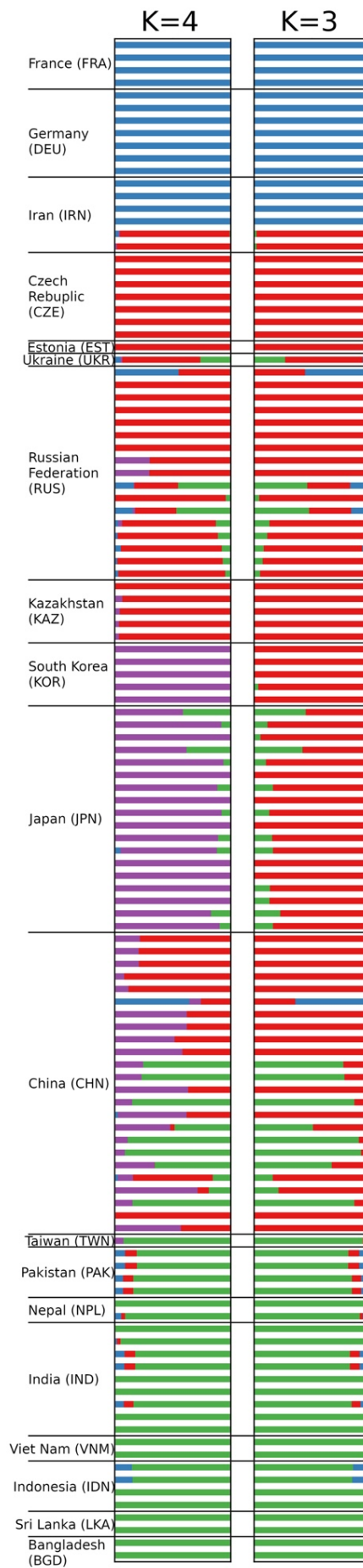


Figure 1-7 ADMIXTURE plot using autosomal data.

Plot showing the proportion of estimated subspecies genetic components. Results for cluster $K = 3$ and $K = 4$ are presented. Samples with the same country code are ordered according to the sampling site from west to east and north to south.

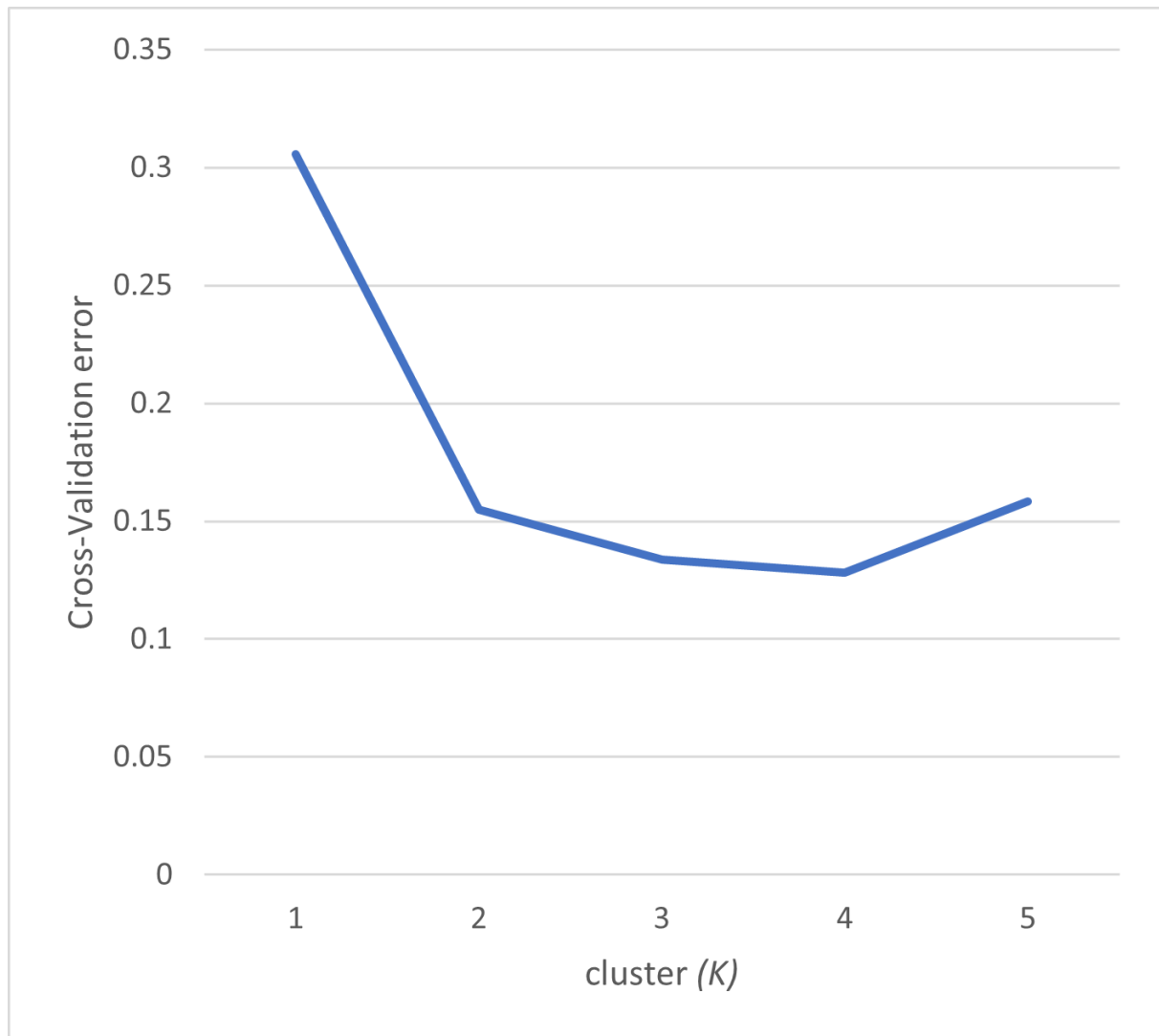


Figure 1-8 The cross-validation error values of ADMIXTURE analysis.

The better value of cluster K exhibits the lower cross-validation error value. The $K=4$ shows the best lowest value.

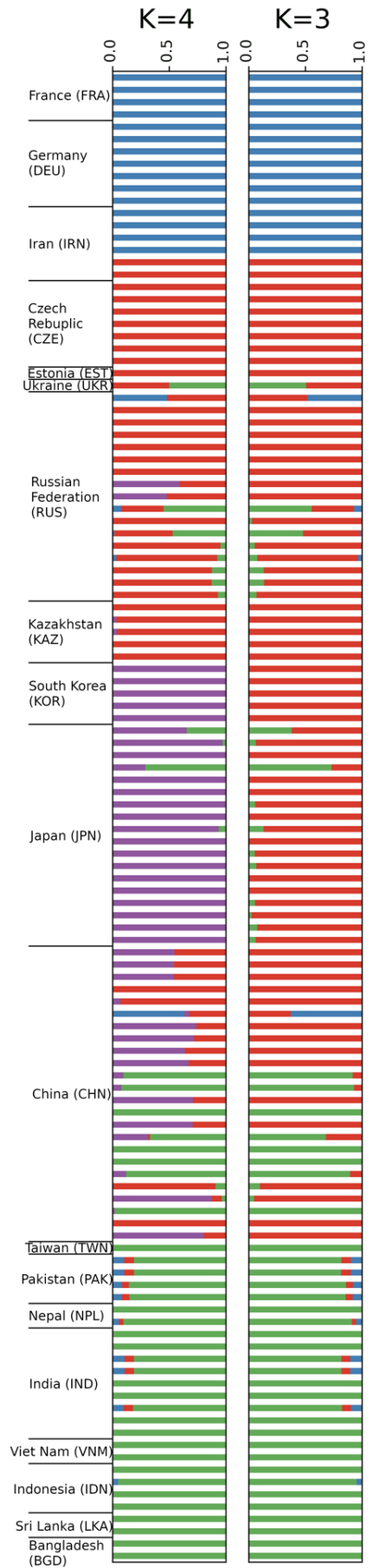


Figure 1-9 ADMIXTURE plot using X chromosome.

The proportion of estimated subspecies genetic components are shown. The results of cluster $K = 3$ and $K = 4$ are presented. In each country code, the samples are lined up according to longitude and latitude. From top to bottom, it represents samples from west to east and north to south.

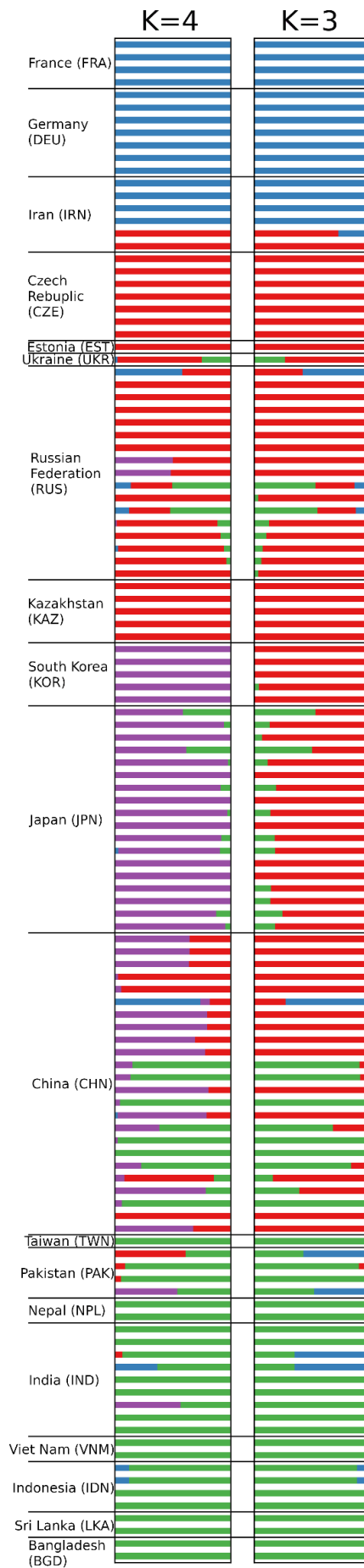


Figure 1-10 LD pruned ADMIXTURE plot of autosomes.

The plot shows the proportion of estimated subspecies genetic components. Results for cluster $K = 3$ and $K = 4$ are presented. Samples with the same country code are ordered according to sampling site from west to east and north to south.

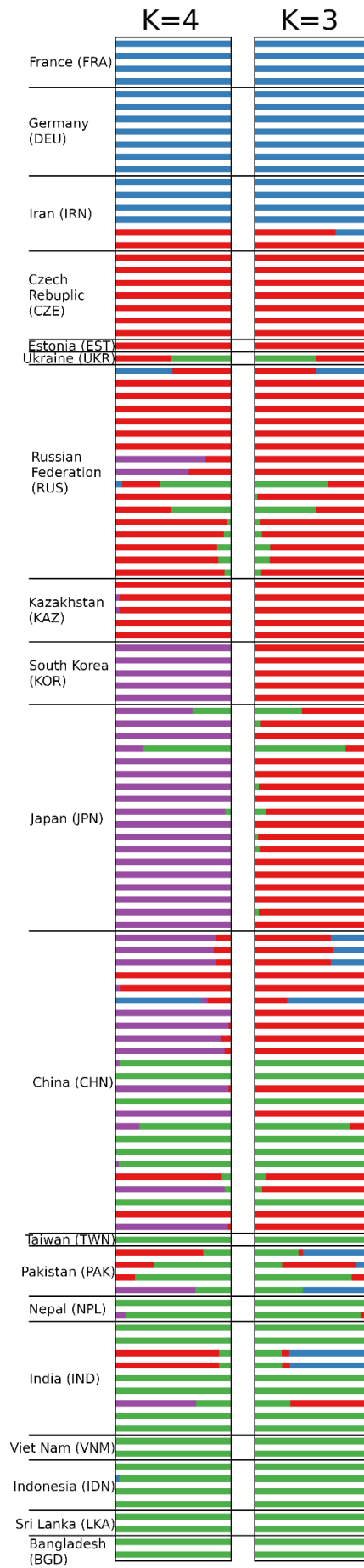
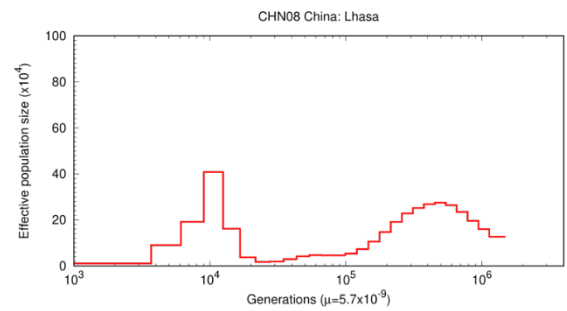
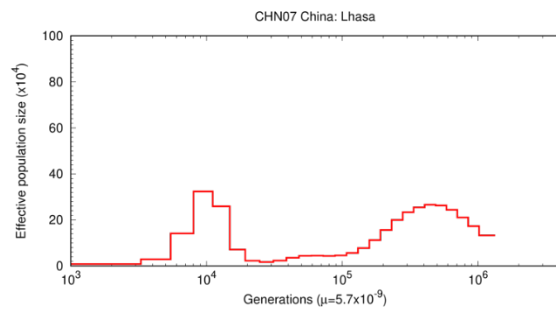
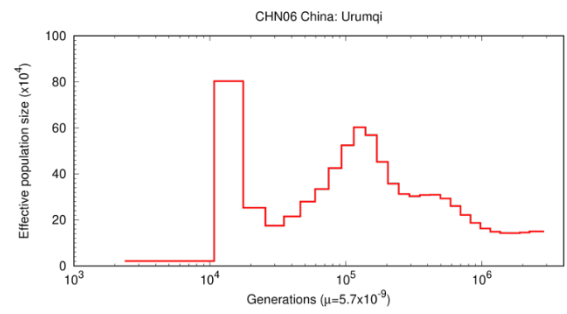
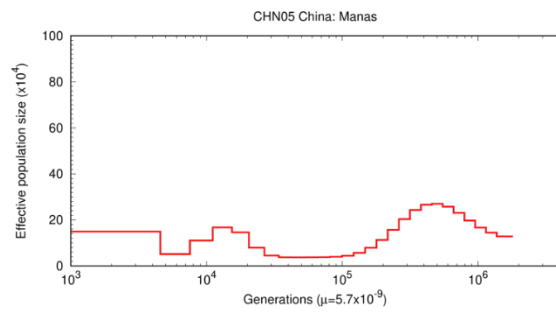
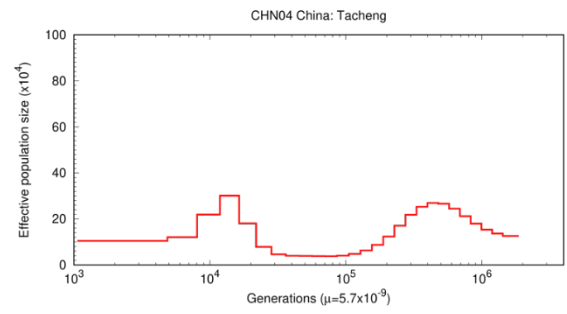
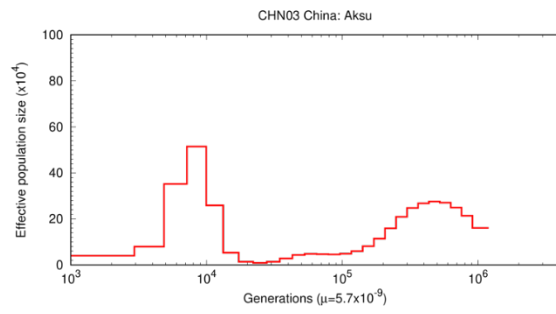
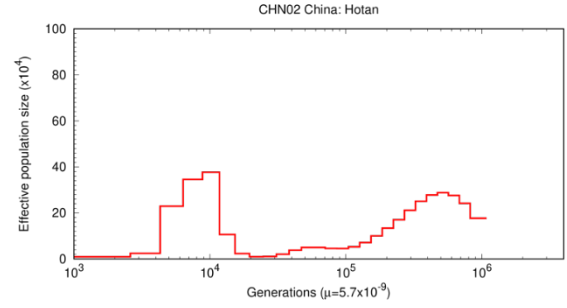
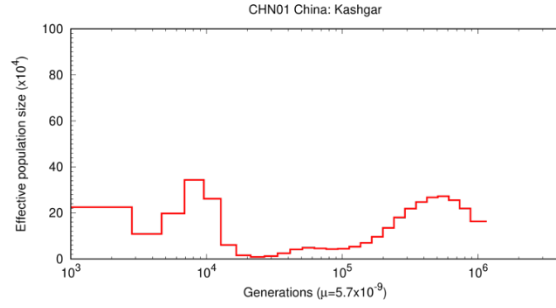
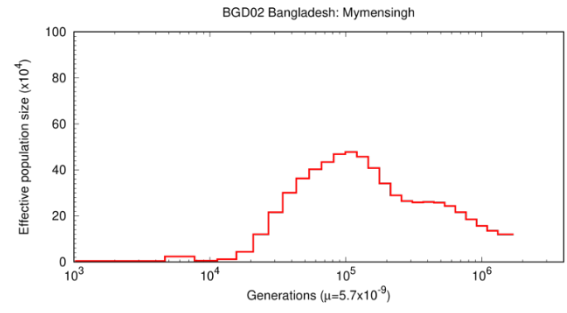
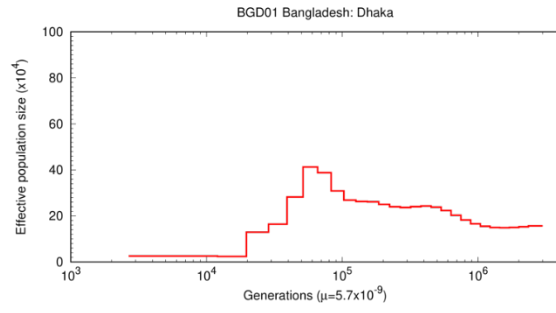
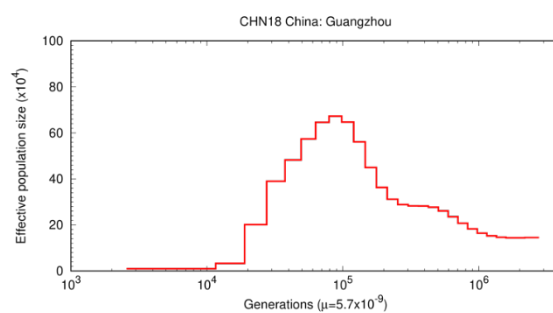
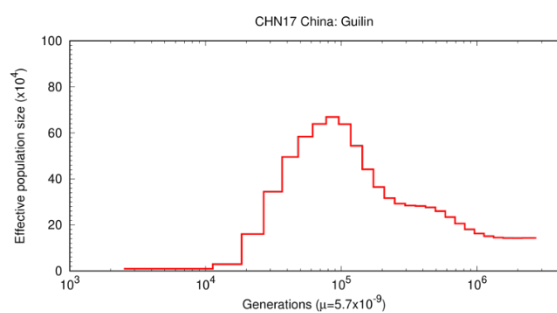
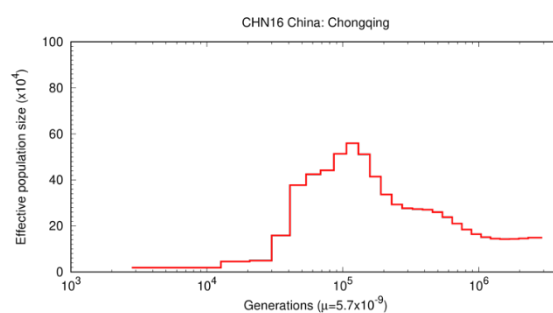
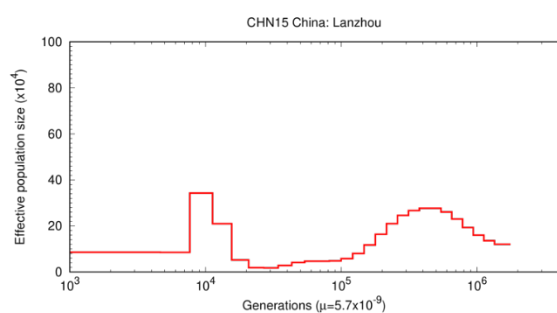
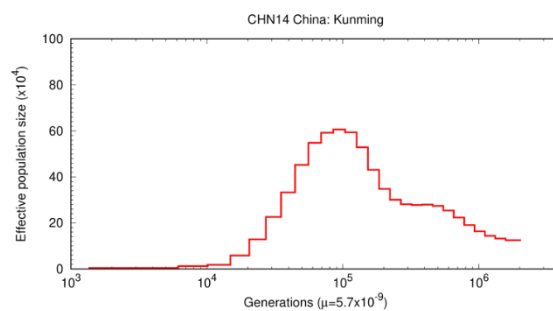
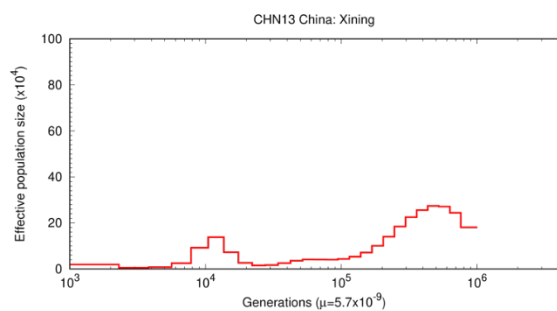
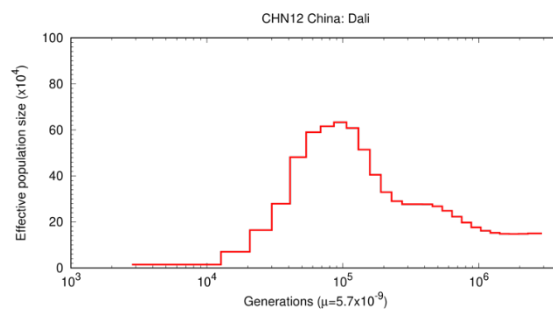
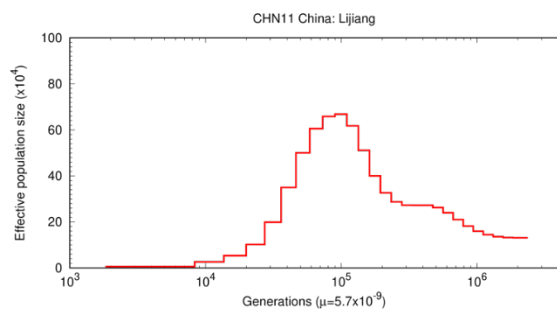
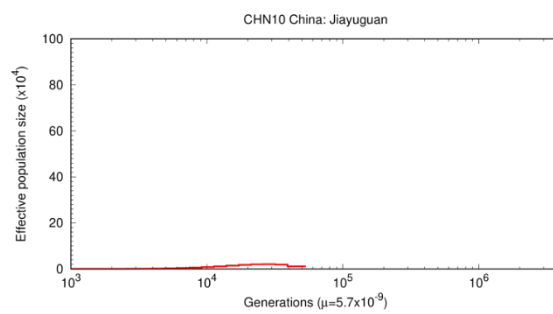
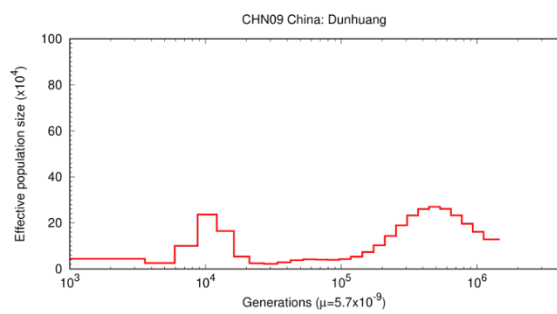
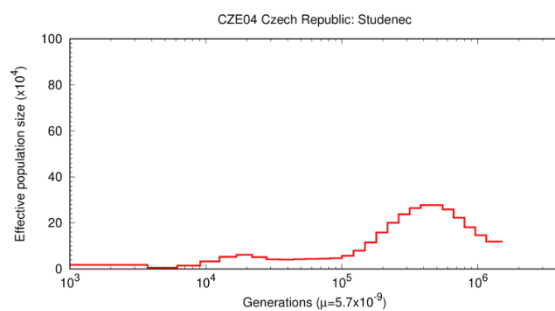
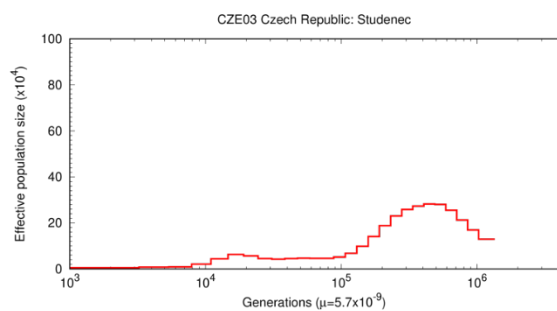
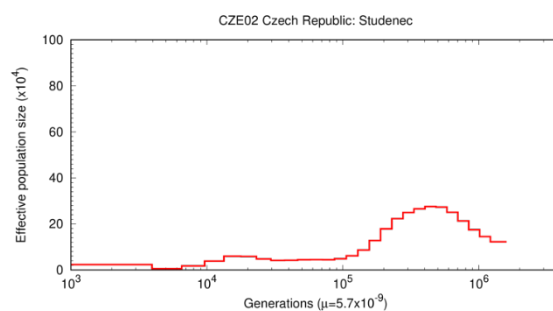
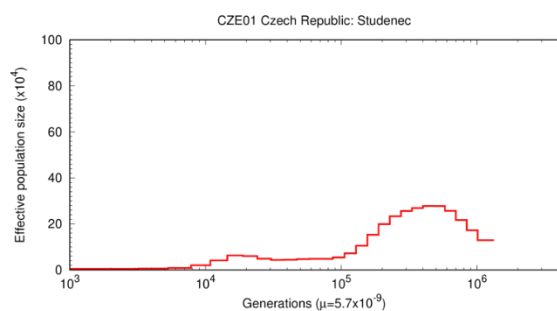
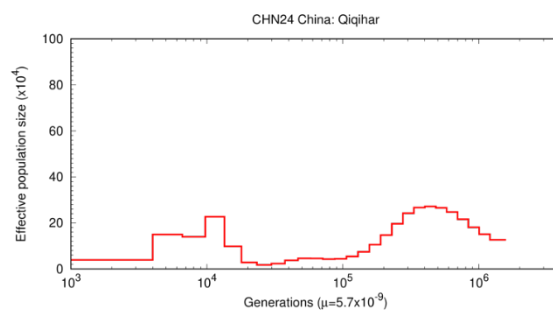
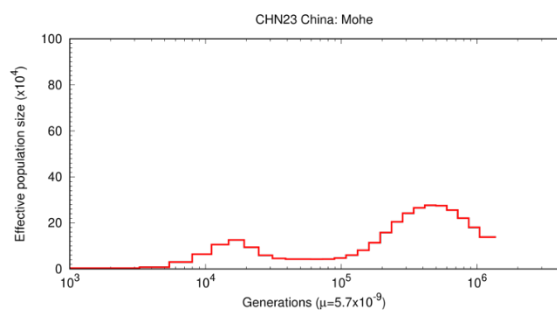
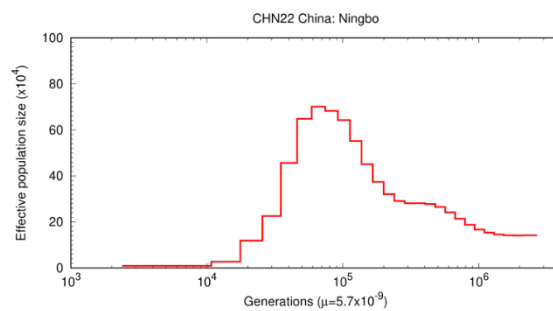
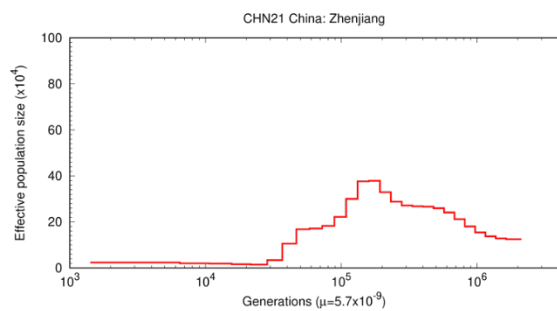
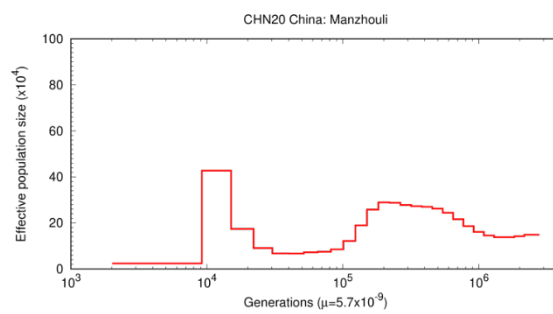
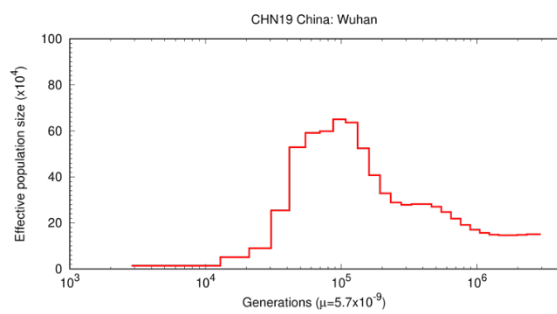


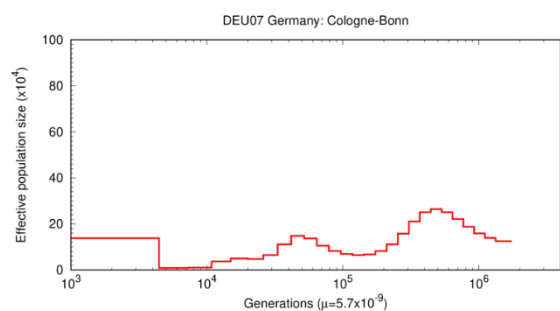
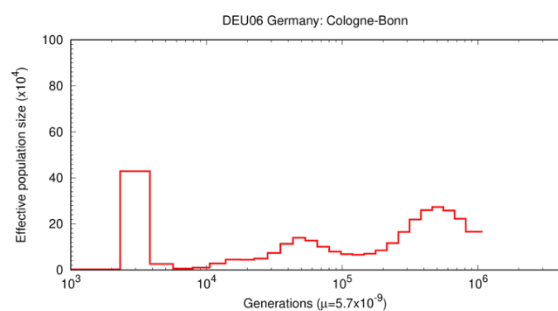
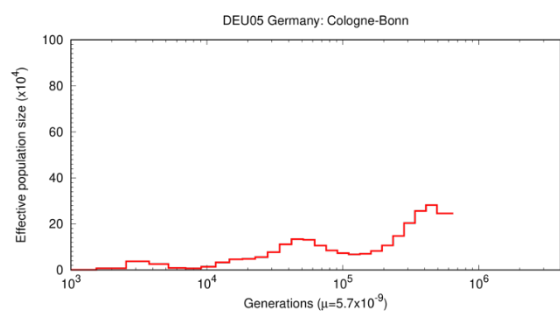
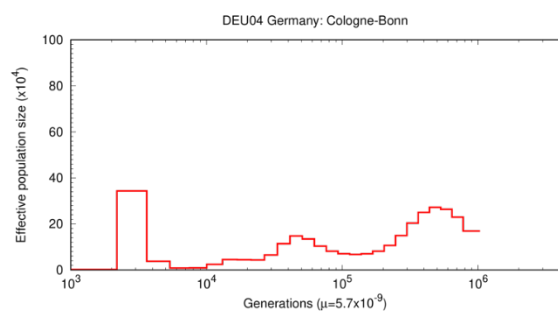
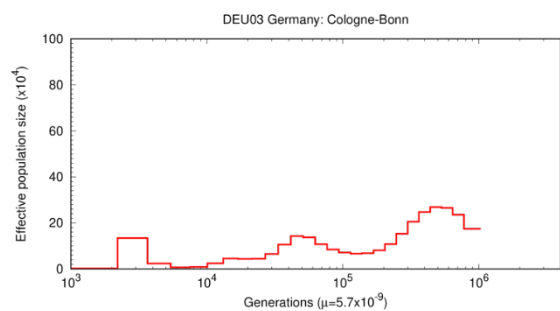
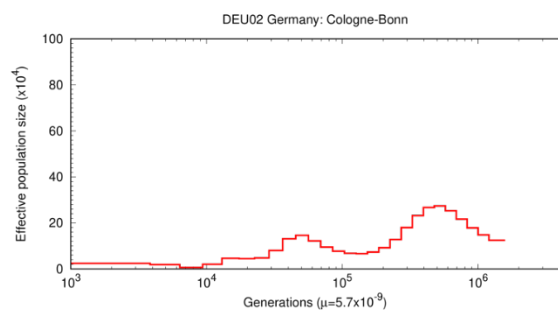
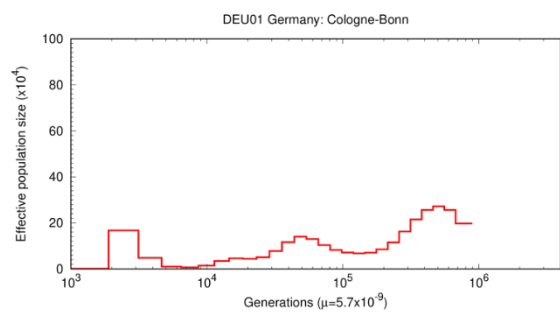
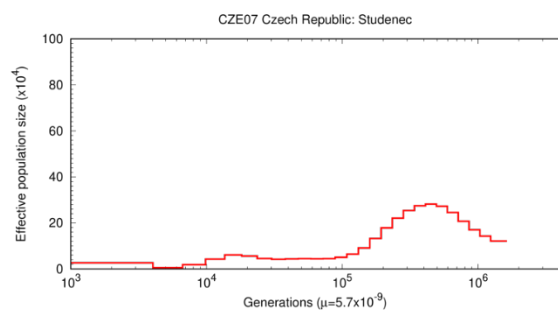
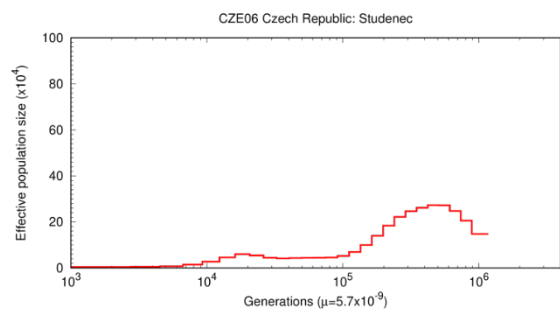
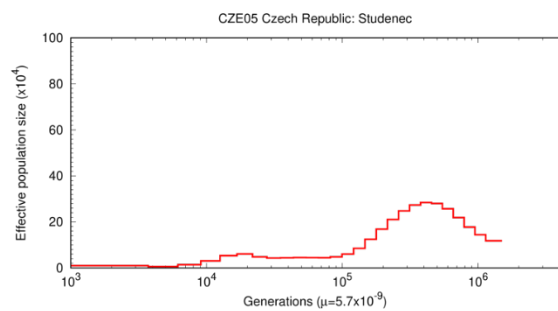
Figure 1-11 LD pruned ADMIXTURE plot of X chromosome.

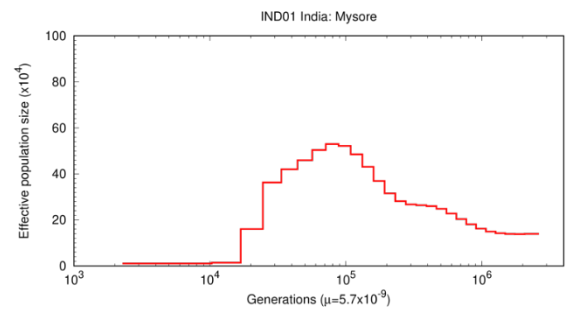
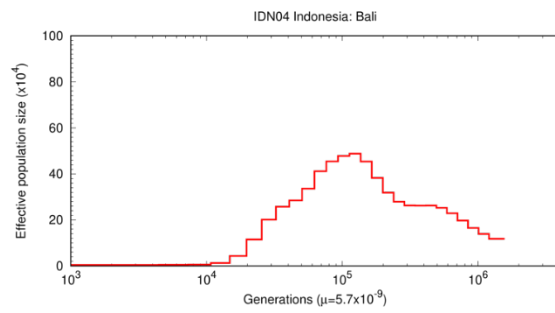
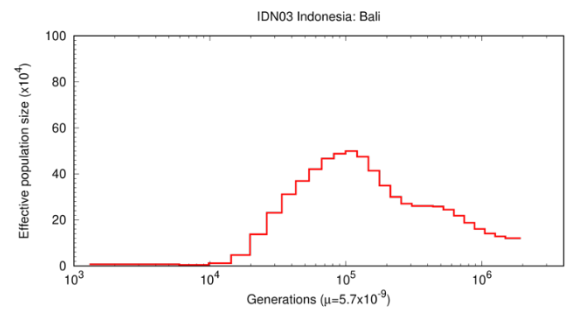
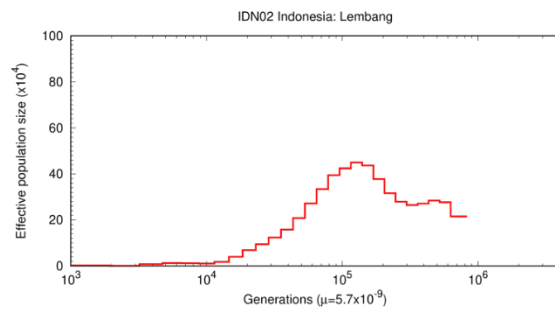
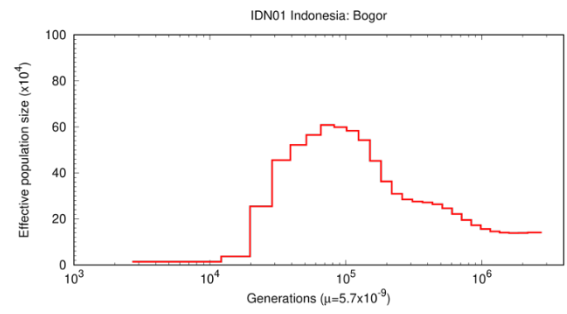
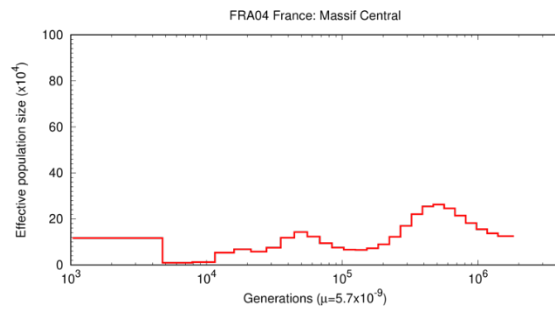
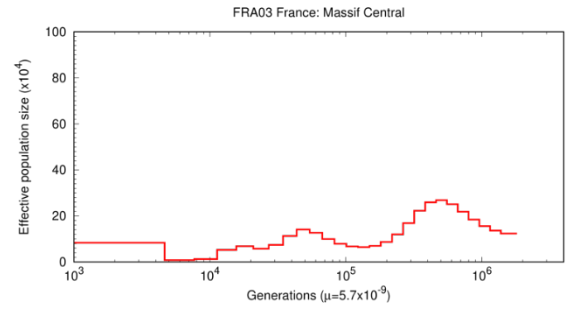
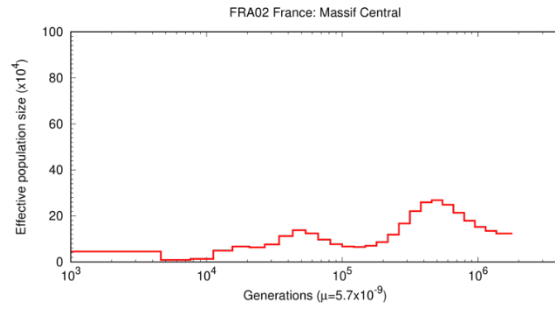
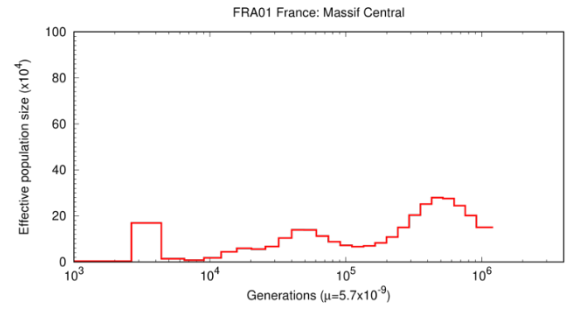
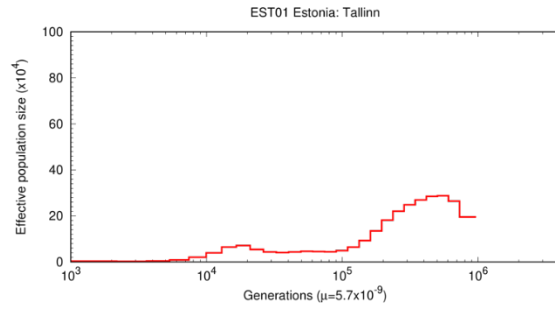
The proportion of estimated subspecies genetic components are shown. The results of cluster $K = 3$ and $K = 4$ are presented. In each country code, the samples are lined up according to longitude and latitude. From top to bottom, it represents samples from west to east and north to south.

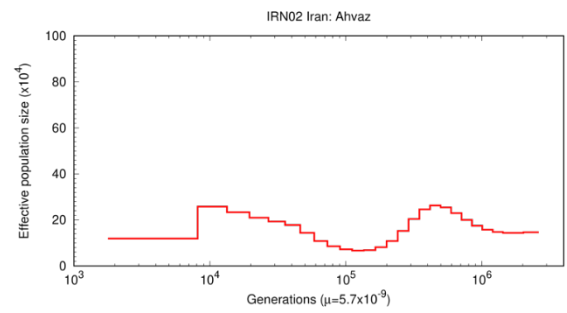
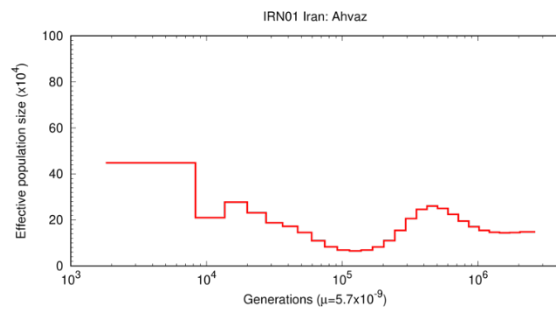
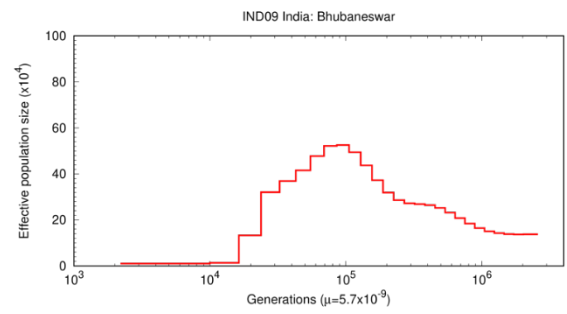
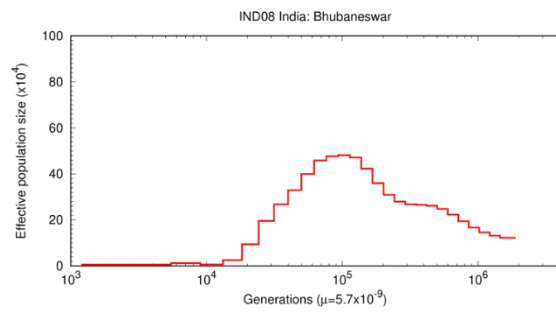
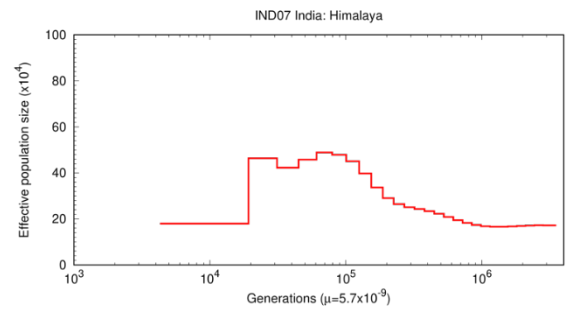
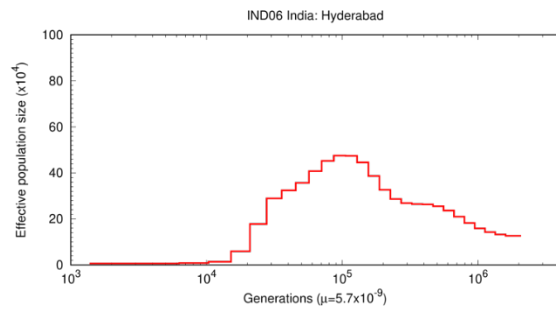
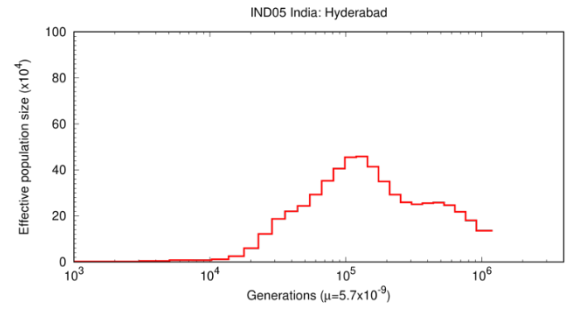
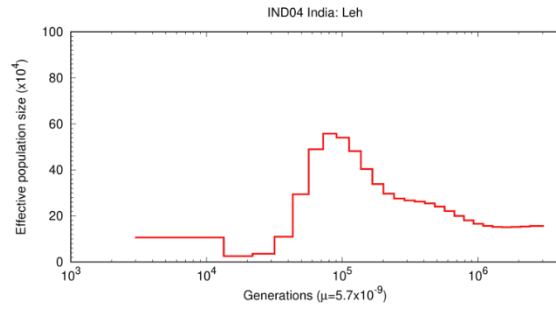
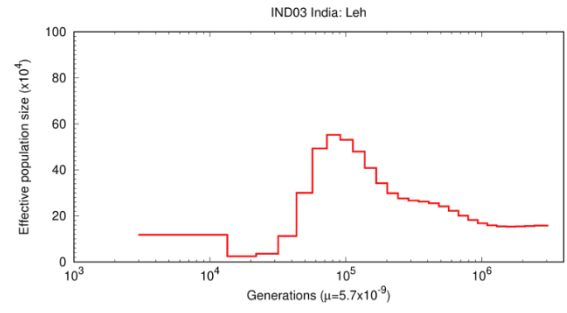
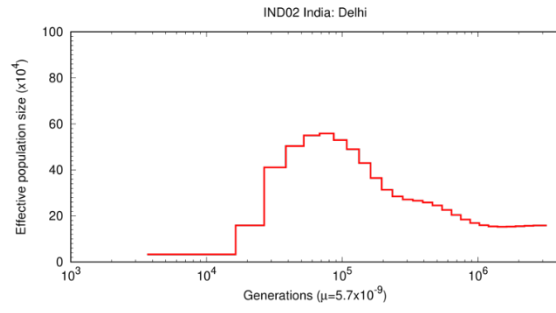


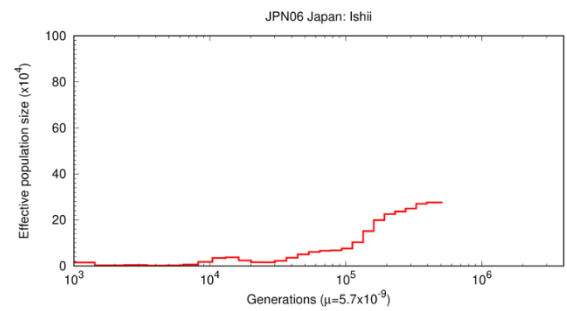
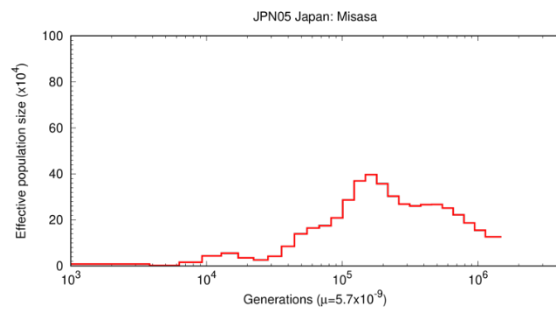
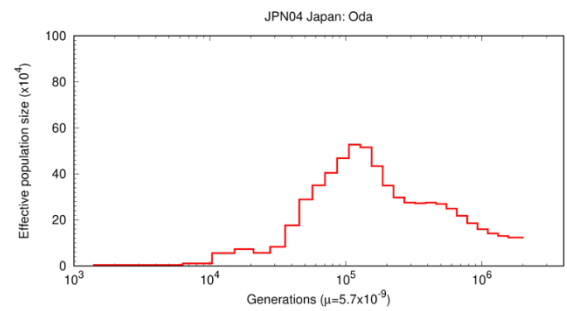
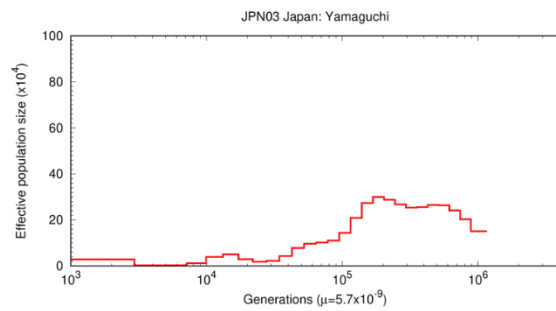
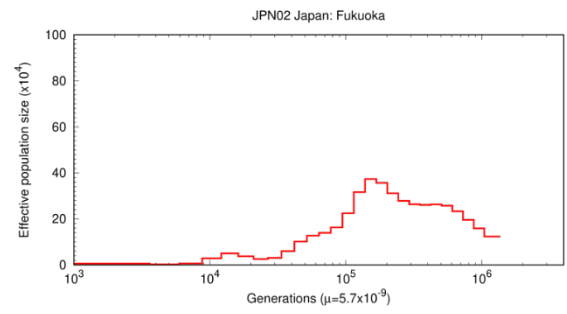
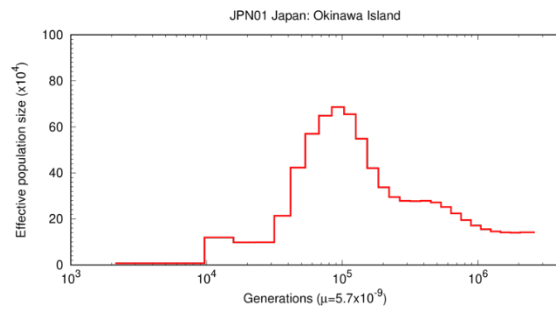
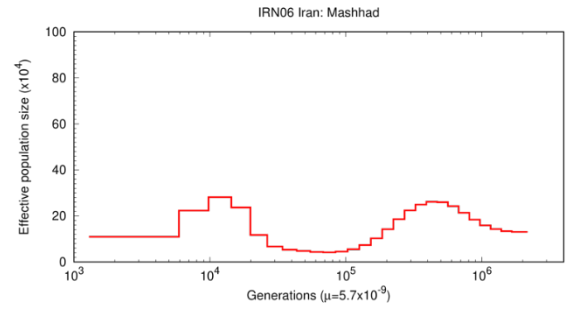
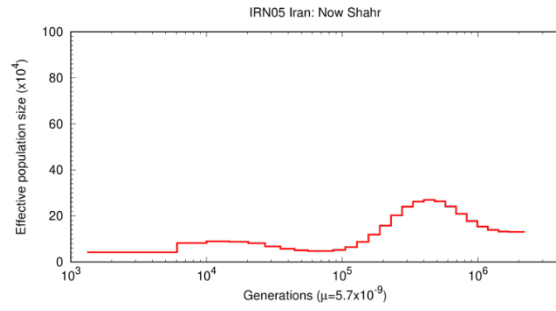
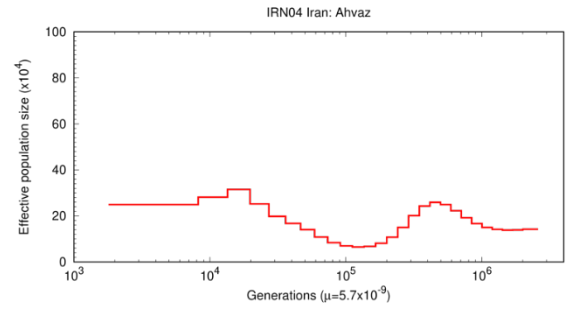
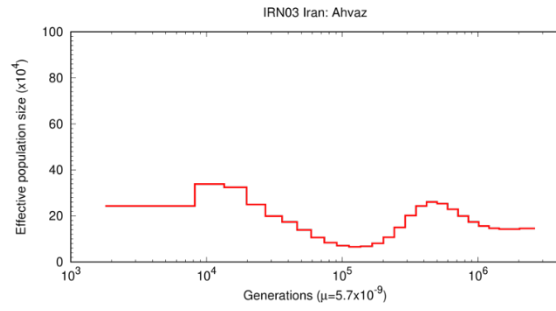


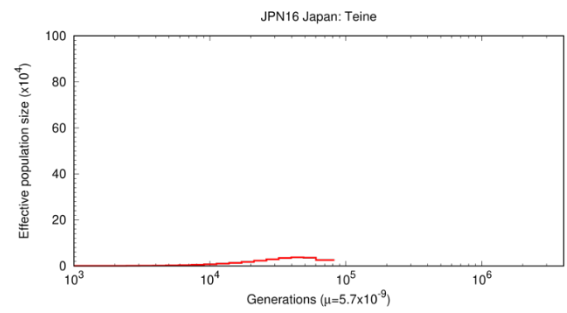
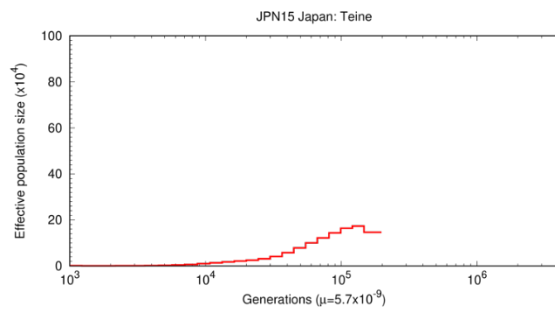
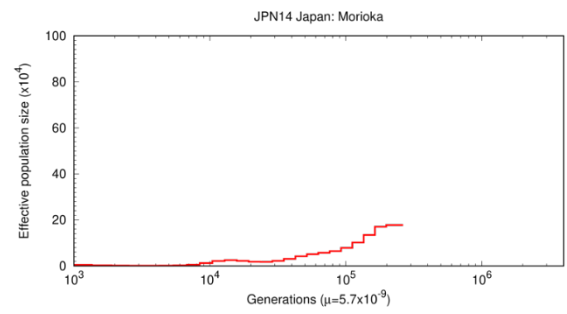
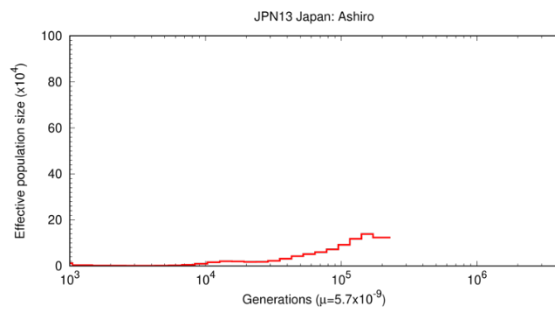
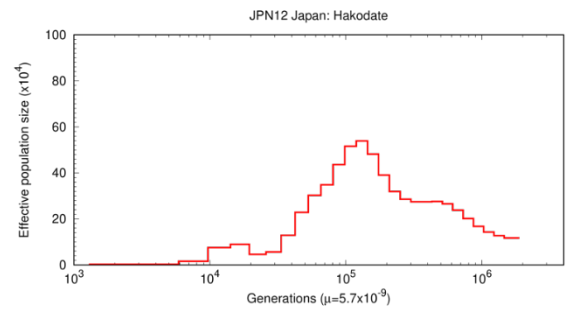
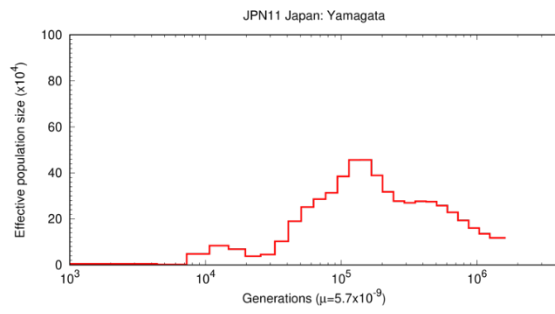
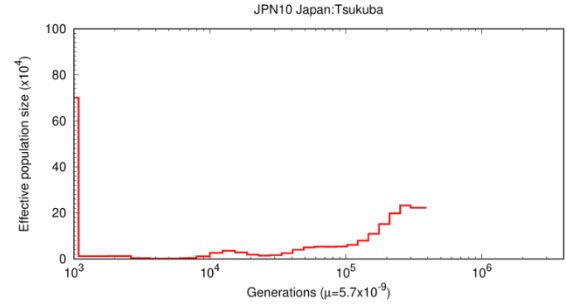
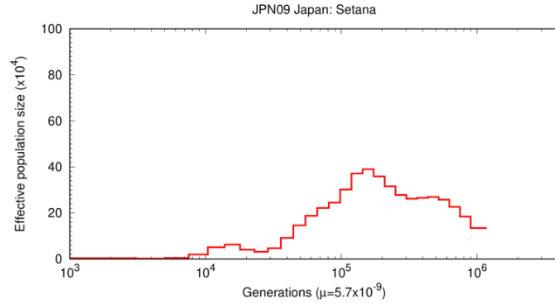
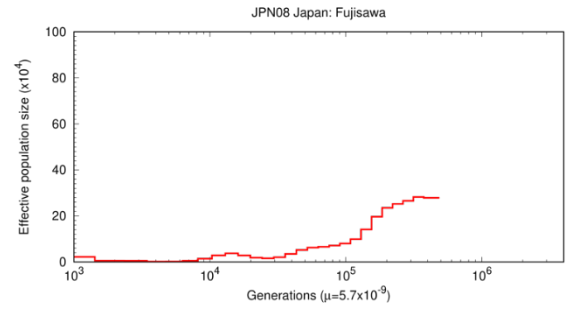
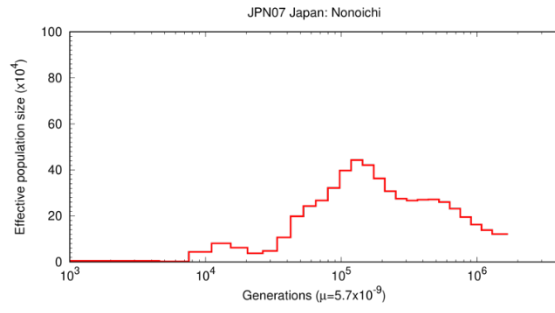


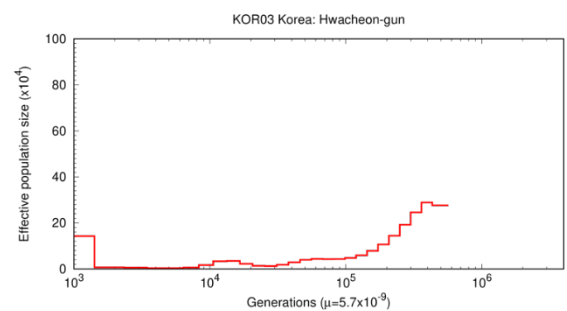
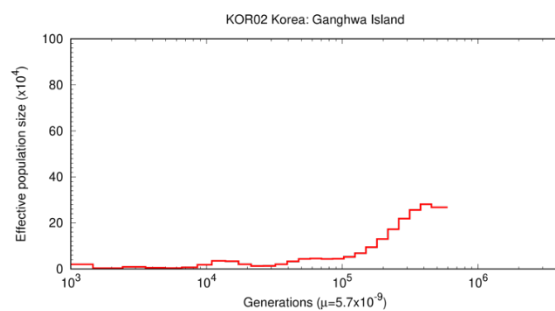
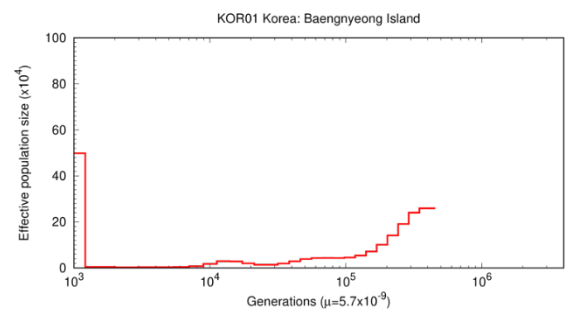
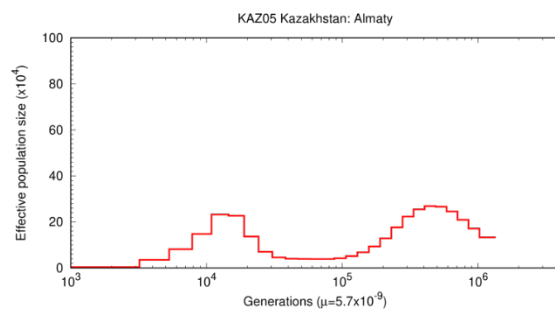
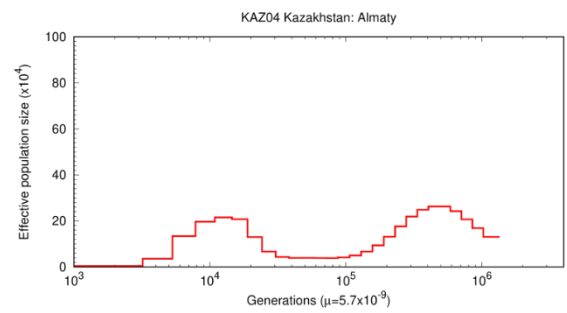
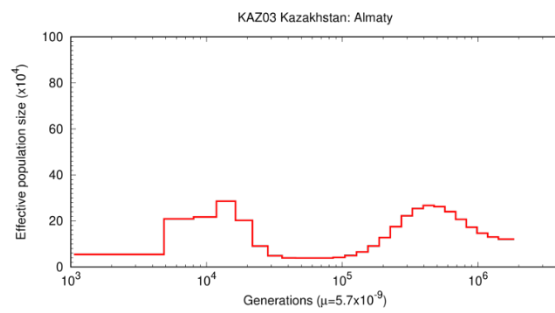
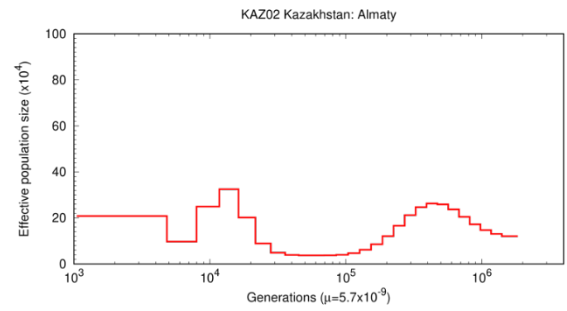
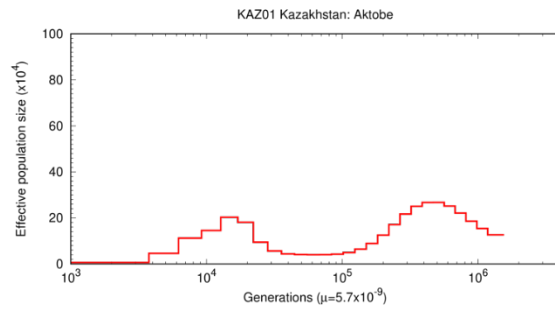
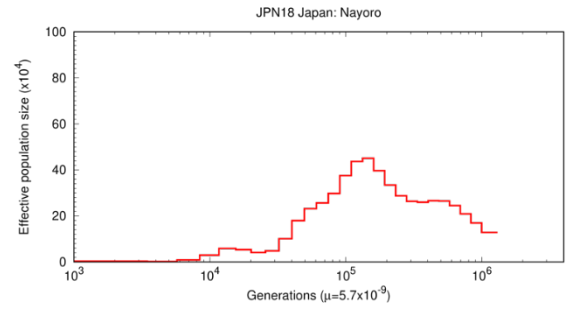
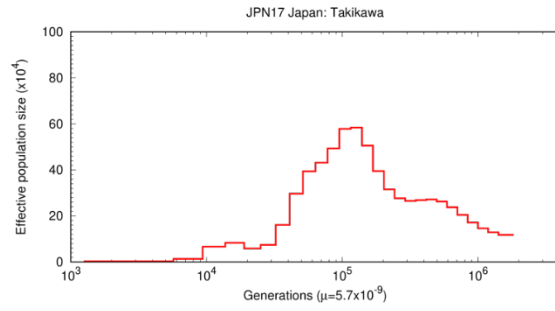


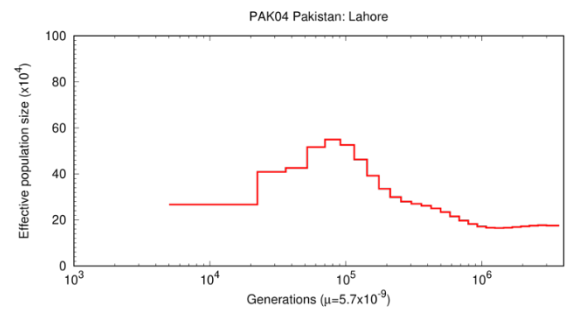
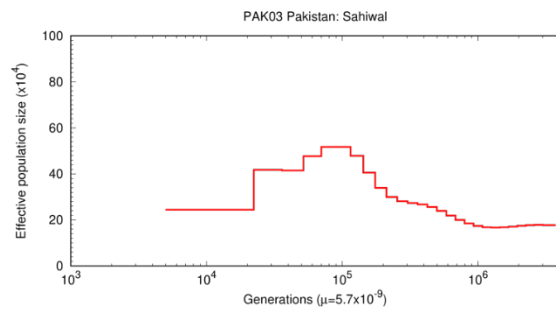
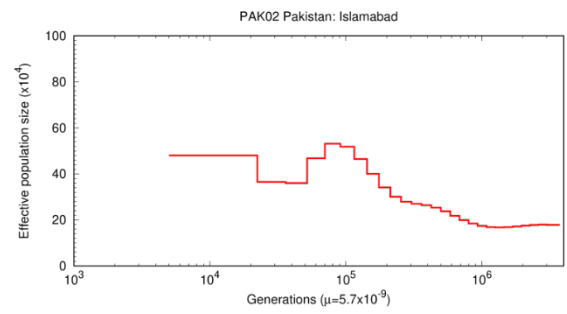
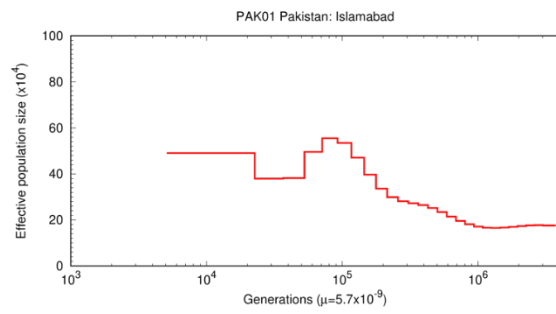
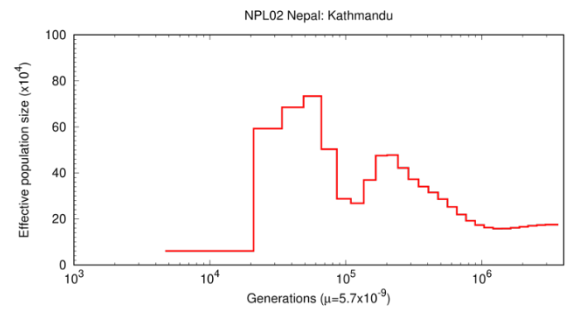
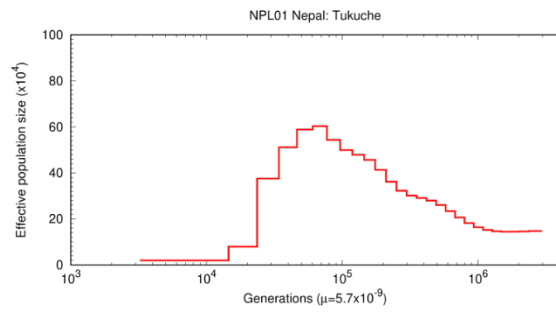
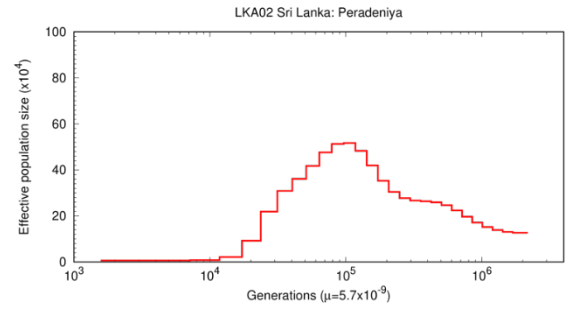
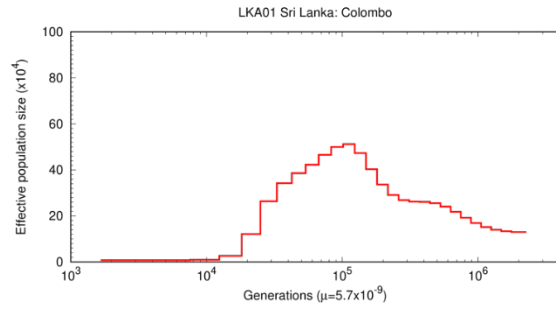
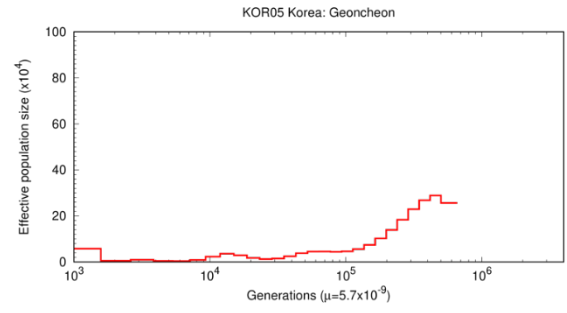
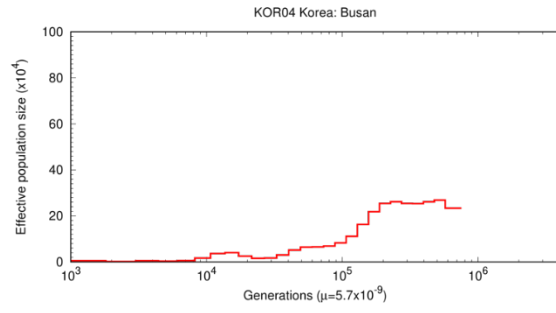


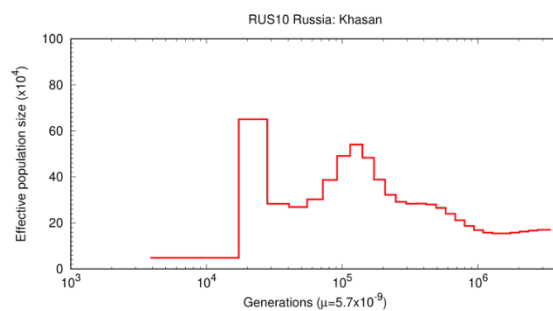
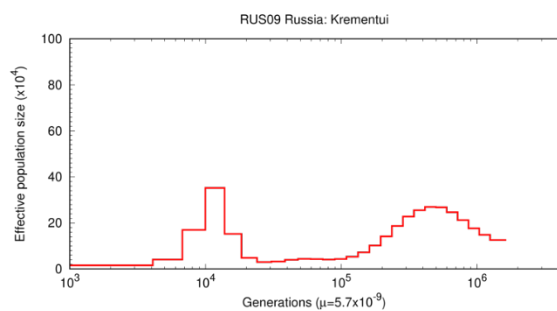
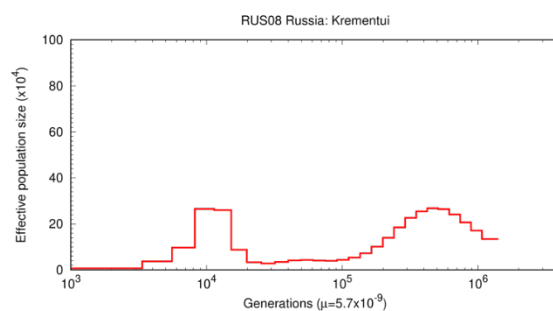
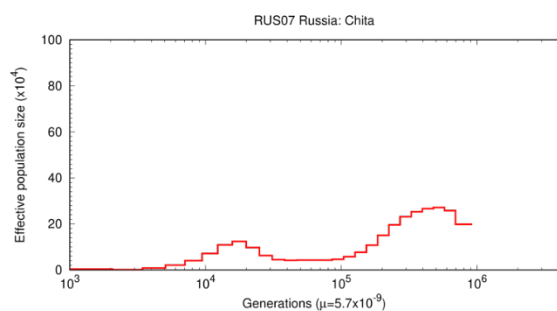
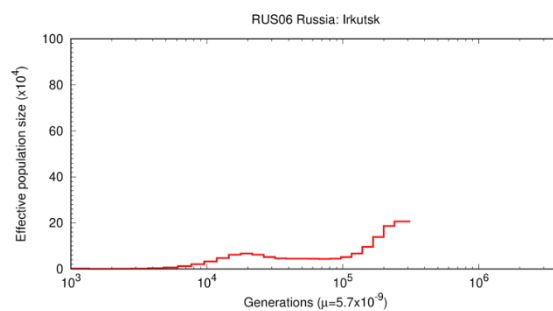
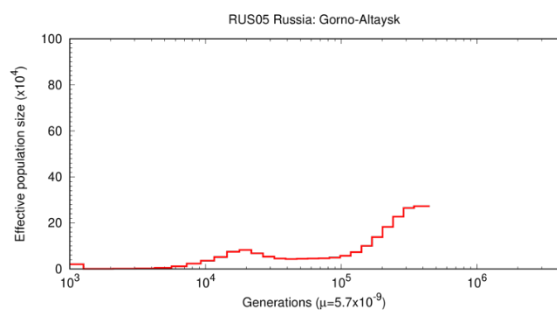
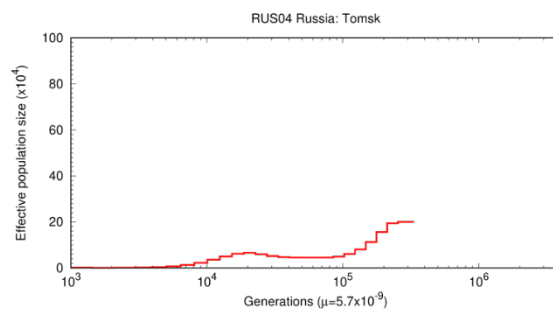
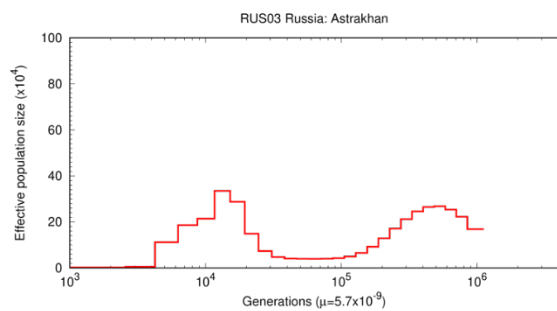
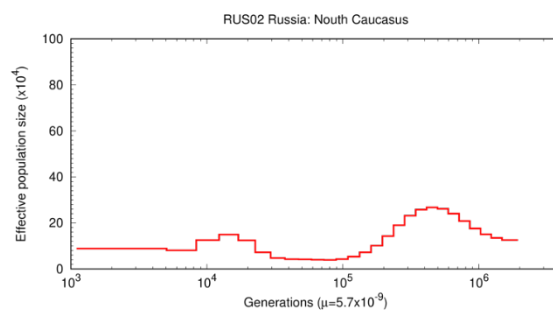
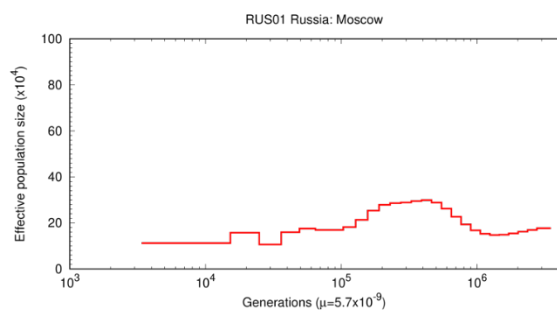


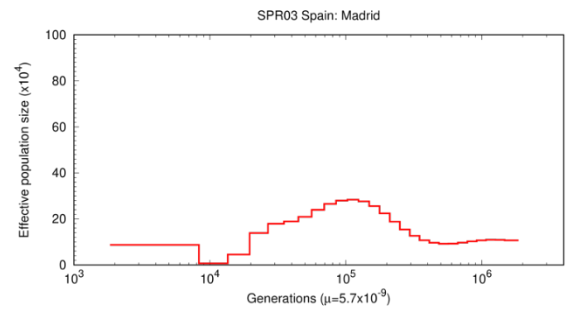
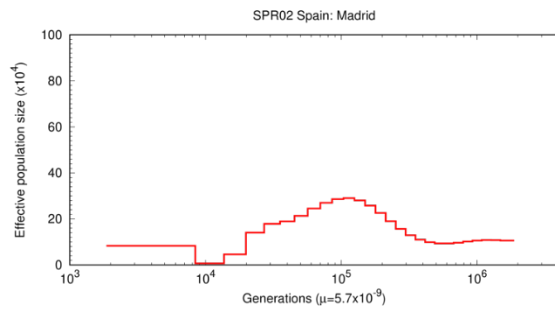
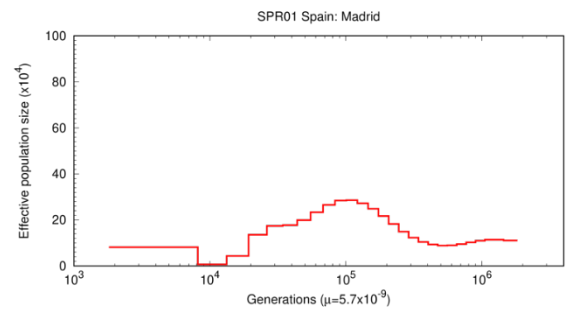
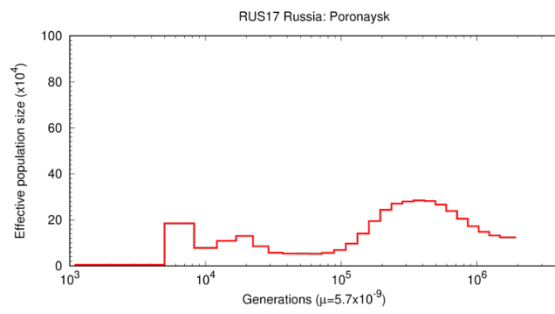
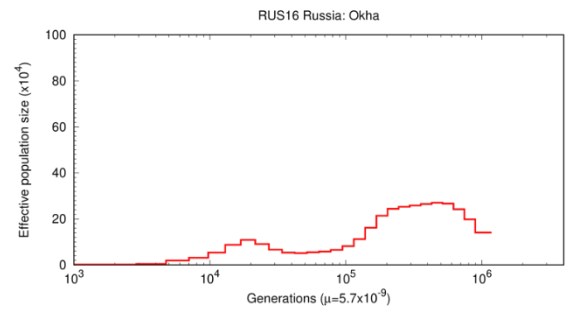
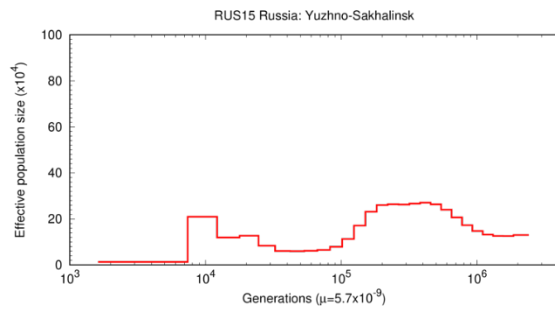
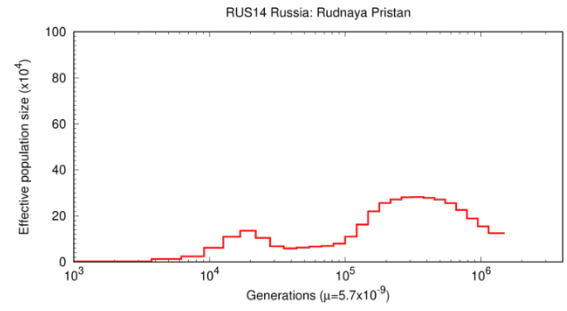
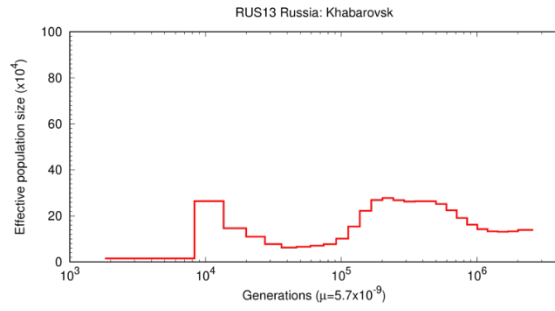
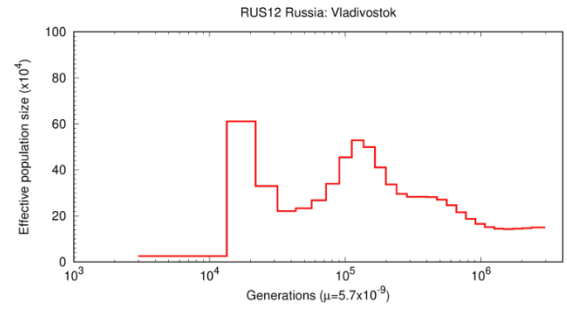
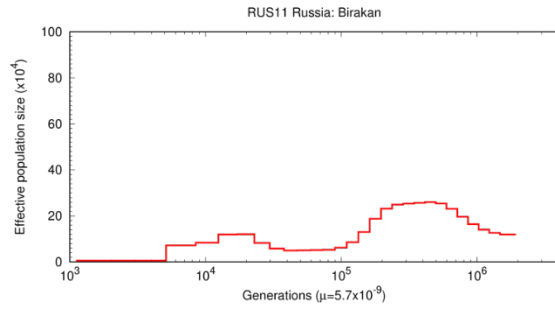












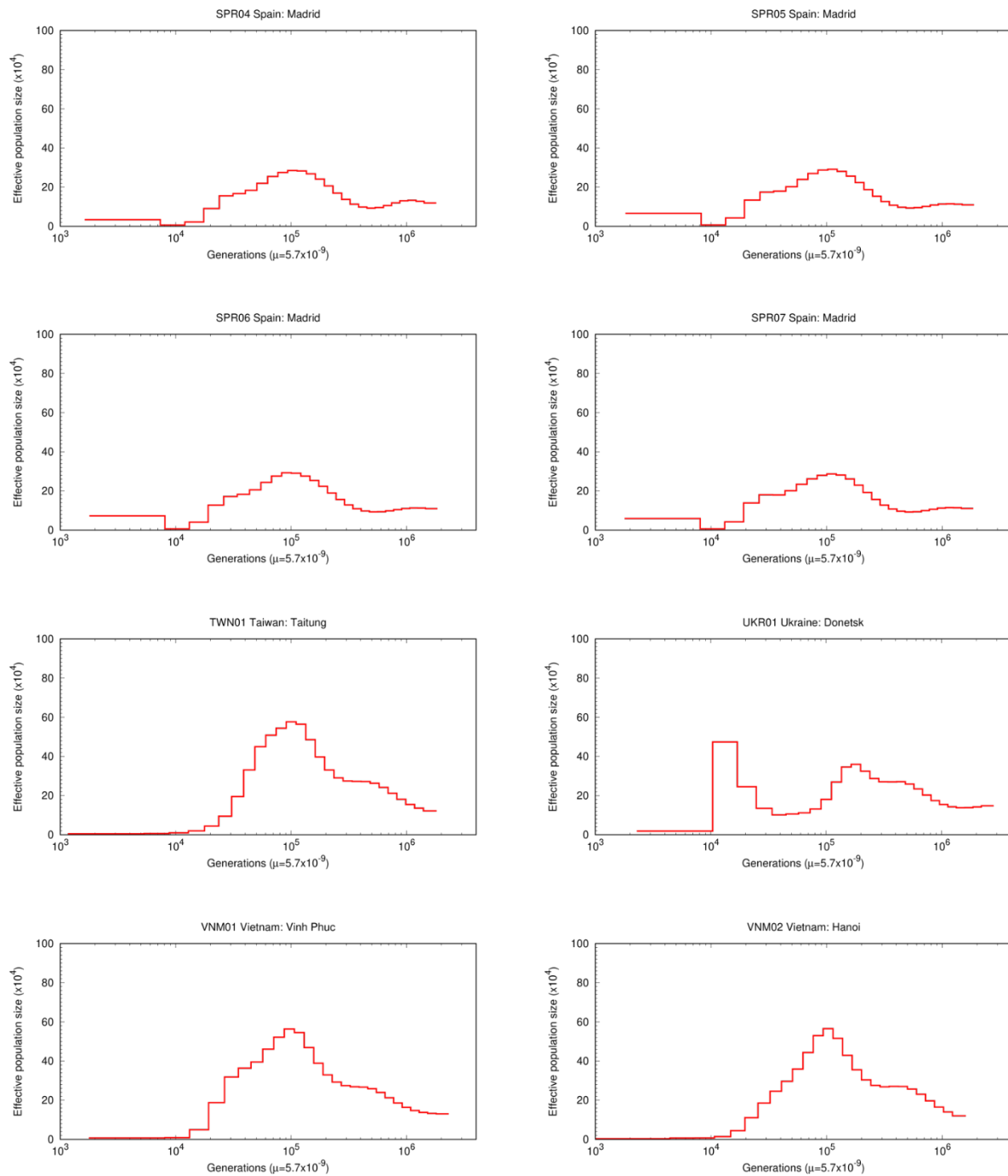


Figure 1-12 The PSMC results of all individual samples used in this study.

The figures are sorted according to the alphabetical order of the sample codes. The title of each plot shows the sample code and the collection site.

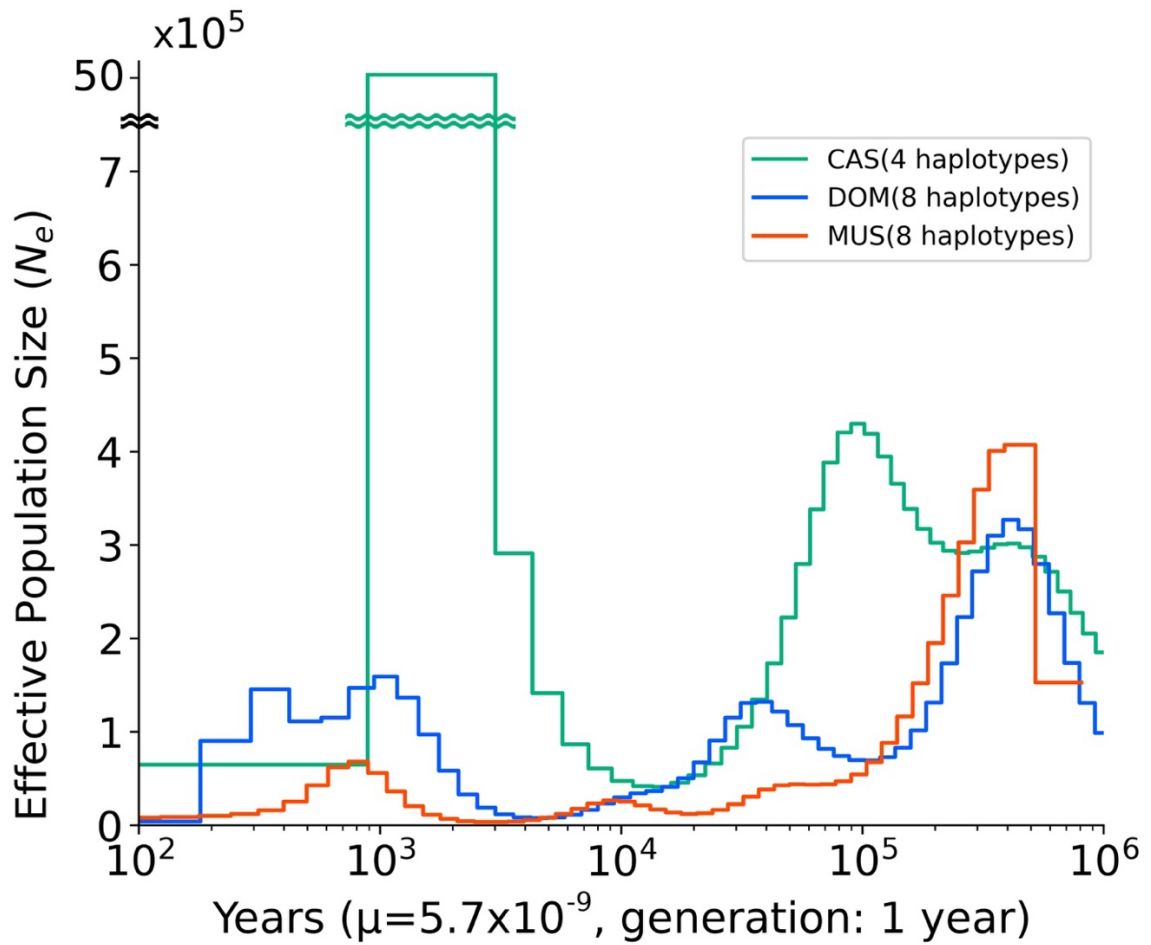


Figure 1-13 Inferred population sizes determined using MSMC analysis.

The x axis represents time before the present assuming a mutation rate of 0.57×10^{-8} per site per generation and a generation time of 1 year. y axis represents the effective population size. The red, green, and blue lines represent past population sizes of Korean (MUS), Indian (CAS), and German (DOM) samples, respectively.

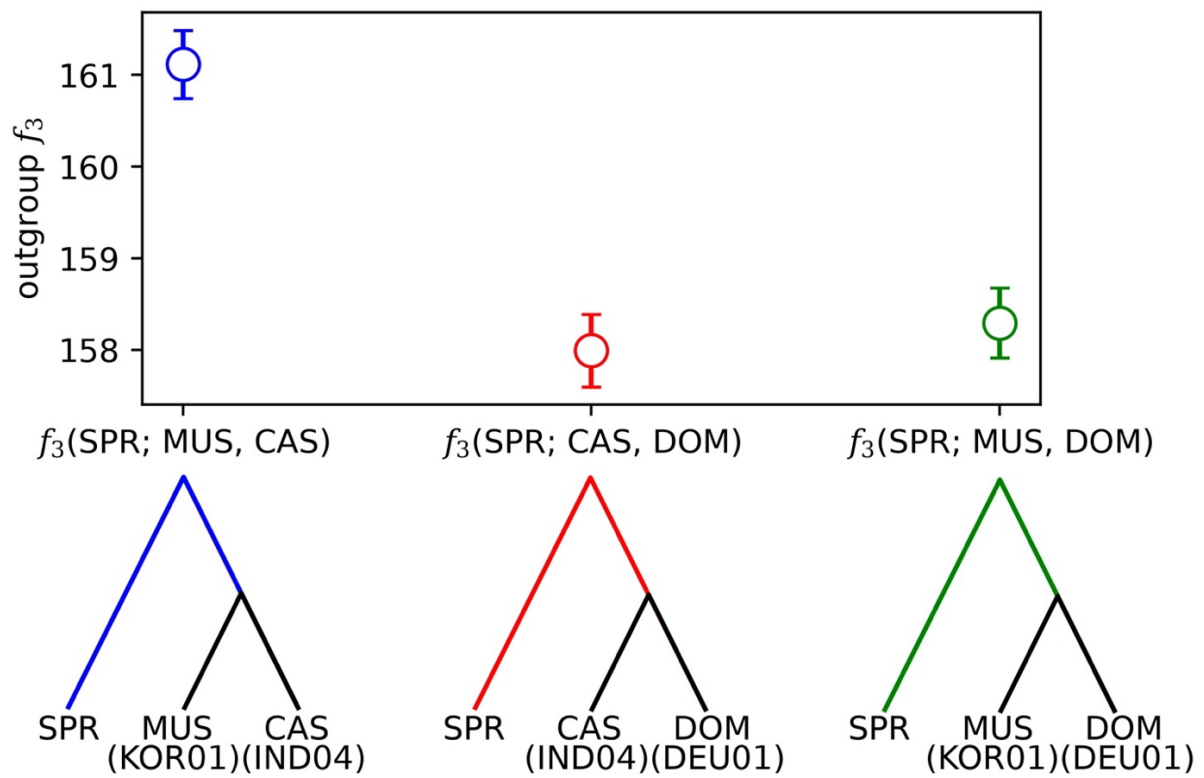


Figure 1-14 Genetic distances between subspecies using outgroup f_3 statistics.

The y axis indicates the outgroup f_3 statistics with SPR used as the outgroup. Higher f_3 values indicate that the two target populations shared more genetic drift, implying that the two populations diverged more recently or that a larger amount of gene flow had occurred between the populations.

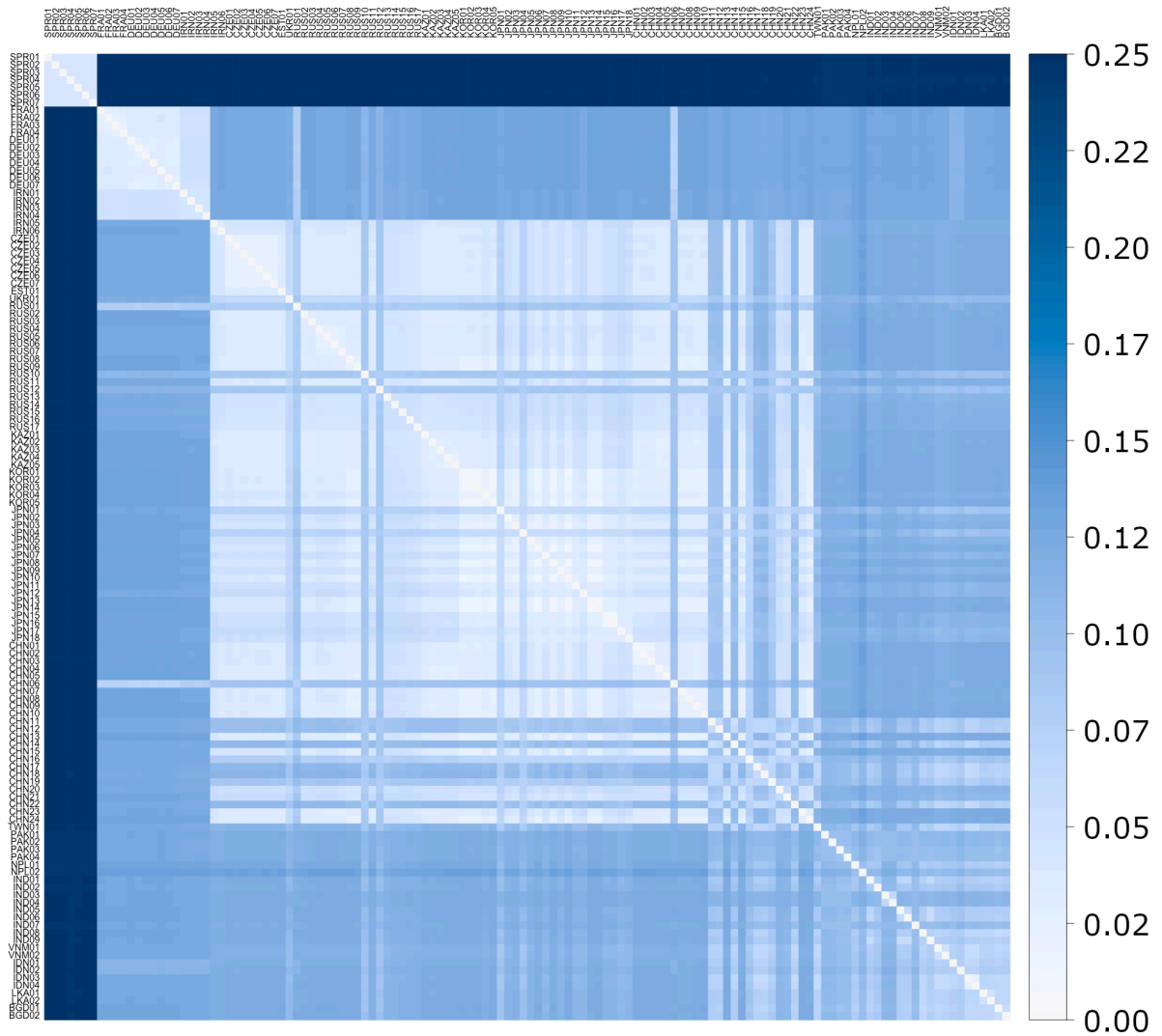


Figure 1-15 Identity-By-State distance plot.

The plot of all pairwise genetic distances between samples (identity-by-state distance). The light-colored cells indicate that the genetic distances between the two samples are close.

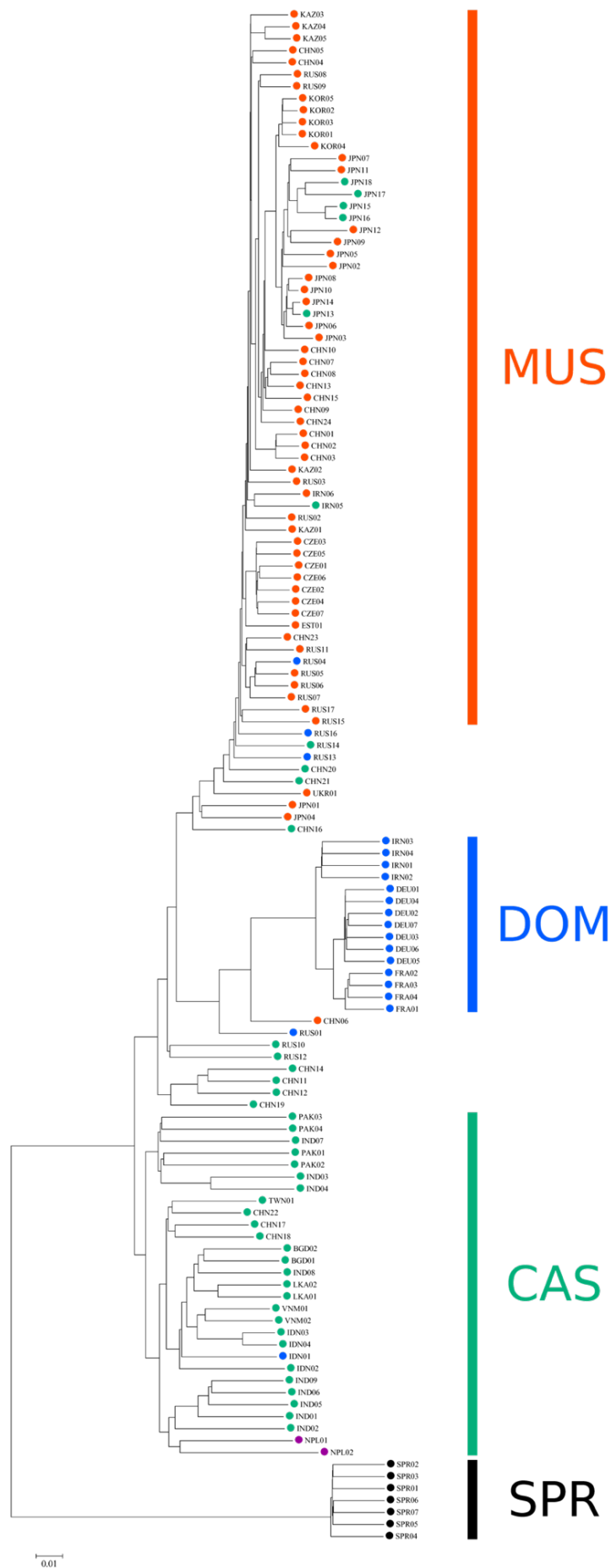


Figure 1-16 Neighbor-joining tree with all samples used in this study.

The neighbor-joining tree inferred using all pairwise genetic distance presented in Figure 1-15.

The circles next to sample names represent the mtDNA haplogroups of samples.

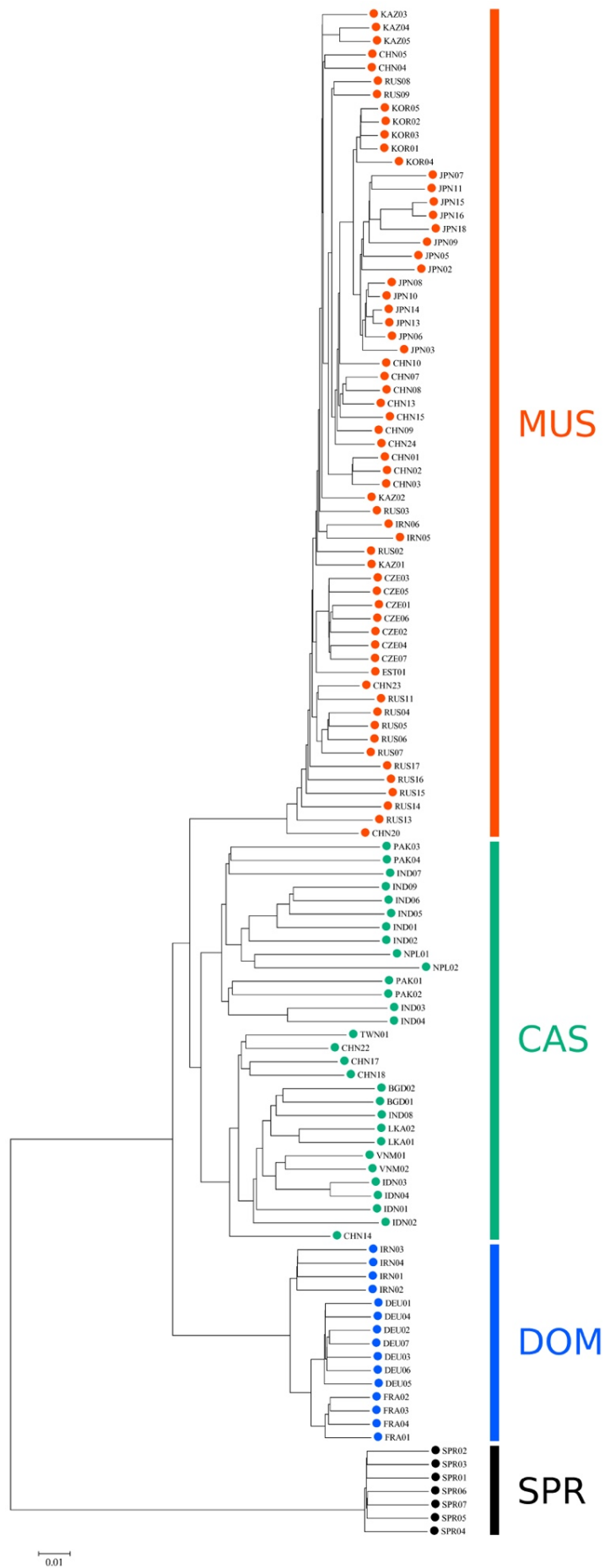


Figure 1-17 Neighbor-joining tree of the *M. musculus* subspecies.

Hybrid individuals were excluded from the reconstruction. Red, green, and blue correspond to MUS, CAS, and DOM, respectively. SPR was used as the outgroup of *M. musculus*.

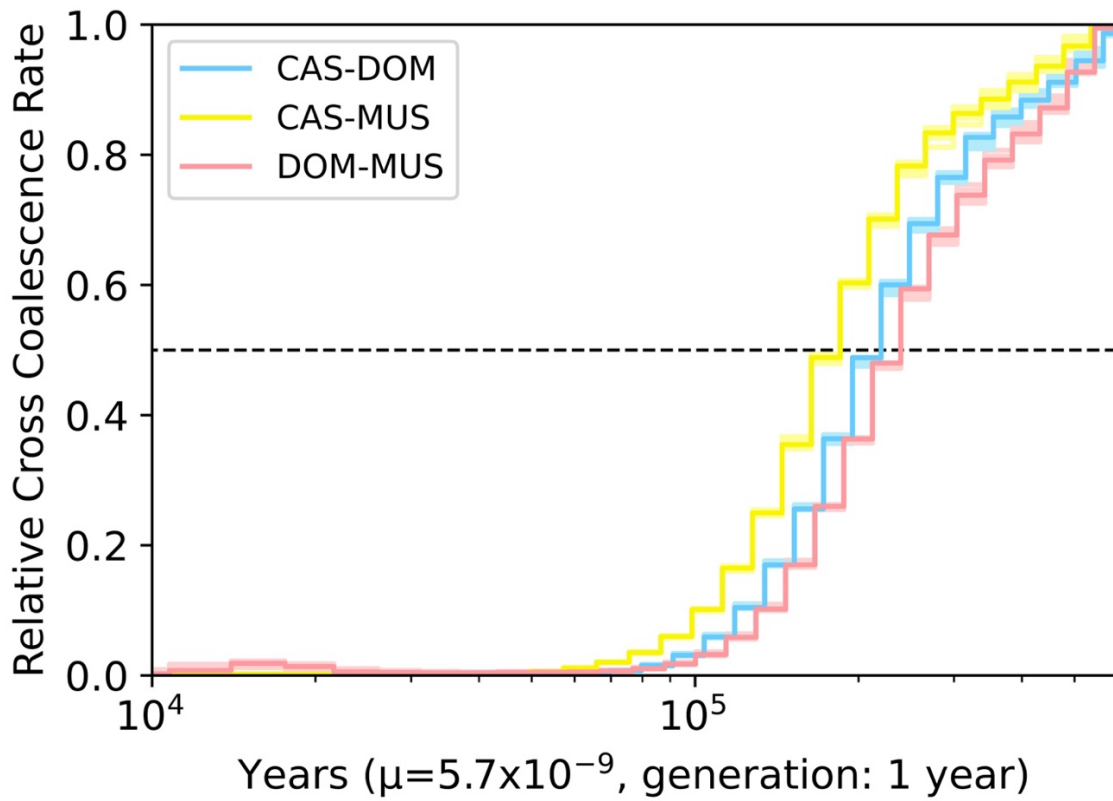


Figure 1-18 Multiple sequentially Markovian coalescent (MSMC) plot of each subspecies.

Diagram showing the divergence process of the *M. musculus* subspecies by the cross-coalescence rate using to the MSMC method. x axis represents the time before the present assuming a mutation rate of 0.57×10^{-8} per site per generation and a generation time of 1 year. The y axis represents relative cross-coalescence rates (rCCRs). The magenta, cyan, and yellow lines correspond to the DOM–MUS, CAS–DOM, and CAS–MUS rCCR changes, respectively. The dotted line shows the $rCCR = 0.5$ point, which is heuristically identified as the estimated time at which the two populations split.

Tables

Table 1-1 The list of samples used in this study.

The list of samples used in this study.

Sample Code	Sample ID	Species	Location	Reference
BGD01	HI0373	<i>Mus musculus</i>	Bangladesh: Dhaka	this study
BGD02	HI0347	<i>Mus musculus</i>	Bangladesh: Mymensingh	this study
CHN01	MG0686	<i>Mus musculus</i>	China: Kashgar	this study
CHN02	MG0747	<i>Mus musculus</i>	China: Hotan	this study
CHN03	MG0608	<i>Mus musculus</i>	China: Aksu	this study
CHN04	MG0611	<i>Mus musculus</i>	China: Tacheng	this study
CHN05	MG0597	<i>Mus musculus</i>	China: Manas	this study
CHN06	MG0577	<i>Mus musculus</i>	China: Urumqi	this study
CHN07	MG0716	<i>Mus musculus</i>	China: Lhasa	this study
CHN08	MG0721	<i>Mus musculus</i>	China: Lhasa	this study
CHN09	MG0871	<i>Mus musculus</i>	China: Dunhuang	this study
CHN10	MG5086	<i>Mus musculus</i>	China: Jiayuguan	this study
CHN11	MG0917	<i>Mus musculus</i>	China: Lijiang	this study
CHN12	MG0797	<i>Mus musculus</i>	China: Dali	this study
CHN13	MG0565	<i>Mus musculus</i>	China: Xining	this study
CHN14	MG0529	<i>Mus musculus</i>	China: Kunming	this study
CHN15	MG0507	<i>Mus musculus</i>	China: Lanzhou	this study
CHN16	MG0709	<i>Mus musculus</i>	China: Chongqing	this study
CHN17	MG0501	<i>Mus musculus</i>	China: Guilin	this study
CHN18	MG0504	<i>Mus musculus</i>	China: Guangzhou	this study
CHN19	MG0908	<i>Mus musculus</i>	China: Wuhan	this study
CHN20	MG0863	<i>Mus musculus</i>	China: Manzhouli	this study
CHN21	MG0713	<i>Mus musculus</i>	China: Zhenjiang	this study
CHN22	MG0795	<i>Mus musculus</i>	China: Ningbo	this study
CHN23	MG0631	<i>Mus musculus</i>	China: Mohe	this study
CHN24	MG0992	<i>Mus musculus</i>	China: Qiqihar	this study
CZE01	ERS957497	<i>Mus musculus</i>	Czech Republic: Studenec	*Harr et al. 2016
CZE02	ERS957498	<i>Mus musculus</i>	Czech Republic: Studenec	*Harr et al. 2016
CZE03	ERS957499	<i>Mus musculus</i>	Czech Republic: Studenec	*Harr et al. 2016
CZE04	ERS957500	<i>Mus musculus</i>	Czech Republic: Studenec	*Harr et al. 2016
CZE05	ERS957501	<i>Mus musculus</i>	Czech Republic: Studenec	*Harr et al. 2016
CZE06	ERS957502	<i>Mus musculus</i>	Czech Republic: Studenec	*Harr et al. 2016
CZE07	ERS957503	<i>Mus musculus</i>	Czech Republic: Studenec	*Harr et al. 2016
DEU01	ERS739373	<i>Mus musculus</i>	Germany: Cologne-Bonn	*Harr et al. 2016
DEU02	ERS739374	<i>Mus musculus</i>	Germany: Cologne-Bonn	*Harr et al. 2016
DEU03	ERS739375	<i>Mus musculus</i>	Germany: Cologne-Bonn	*Harr et al. 2016
DEU04	ERS739376	<i>Mus musculus</i>	Germany: Cologne-Bonn	*Harr et al. 2016
DEU05	ERS739377	<i>Mus musculus</i>	Germany: Cologne-Bonn	*Harr et al. 2016
DEU06	ERS739378	<i>Mus musculus</i>	Germany: Cologne-Bonn	*Harr et al. 2016
DEU07	ERS739379	<i>Mus musculus</i>	Germany: Cologne-Bonn	*Harr et al. 2016
EST01	MG3044	<i>Mus musculus</i>	Estonia: Tallinn	this study
FRA01	ERS739382	<i>Mus musculus</i>	France: Massif Central	*Harr et al. 2016
FRA02	ERS739385	<i>Mus musculus</i>	France: Massif Central	*Harr et al. 2016

FRA03	ERS739386	<i>Mus musculus</i>	France: Massif Central	*Harr et al. 2016
FRA04	ERS739388	<i>Mus musculus</i>	France: Massif Central	*Harr et al. 2016
IDN01	HI0112	<i>Mus musculus</i>	Indonesia: Bogor	this study
IDN02	HI0134	<i>Mus musculus</i>	Indonesia: Lembang	this study
IDN03	HI0115	<i>Mus musculus</i>	Indonesia: Bali	this study
IDN04	HI0116	<i>Mus musculus</i>	Indonesia: Bali	this study
IND01	HI0274	<i>Mus musculus</i>	India: Mysore	this study
IND02	HI0185	<i>Mus musculus</i>	India: Delhi	this study
IND03	HI0159	<i>Mus musculus</i>	India: Leh	this study
IND04	HI0161	<i>Mus musculus</i>	India: Leh	this study
IND05	HI0328	<i>Mus musculus</i>	India: Hyderabad	this study
IND06	HI0329	<i>Mus musculus</i>	India: Hyderabad	this study
IND07	ERS003044	<i>Mus musculus</i>	India: Himalaya	*Harr et al. 2016
IND08	HI0313	<i>Mus musculus</i>	India: Bhubaneswar	this study
IND09	HI0321	<i>Mus musculus</i>	India: Bhubaneswar	this study
IRN01	ERS739389	<i>Mus musculus</i>	Iran: Ahvaz	*Harr et al. 2016
IRN02	ERS739393	<i>Mus musculus</i>	Iran: Ahvaz	*Harr et al. 2016
IRN03	ERS739395	<i>Mus musculus</i>	Iran: Ahvaz	*Harr et al. 2016
IRN04	ERS739396	<i>Mus musculus</i>	Iran: Ahvaz	*Harr et al. 2016
IRN05	MG5135	<i>Mus musculus</i>	Iran: Now Shahr	this study
IRN06	MG0417	<i>Mus musculus</i>	Iran: Mashhad	this study
JPN01	HS2788	<i>Mus musculus</i>	Japan: Okinawa Island	this study
JPN02	HS4272	<i>Mus musculus</i>	Japan: Fukuoka	this study
JPN03	HS4273	<i>Mus musculus</i>	Japan: Yamaguchi	this study
JPN04	HS4411	<i>Mus musculus</i>	Japan: Oda	this study
JPN05	HS4097	<i>Mus musculus</i>	Japan: Misasa	this study
JPN06	HS4120	<i>Mus musculus</i>	Japan: Ishii	this study
JPN07	HS2815	<i>Mus musculus</i>	Japan: Nonoichi	this study
JPN08	HS4056	<i>Mus musculus</i>	Japan: Fujisawa	this study
JPN09	HS4271	<i>Mus musculus</i>	Japan: Setana	this study
JPN10	HS4169	<i>Mus musculus</i>	Japan: Tsukuba	this study
JPN11	HS3534	<i>Mus musculus</i>	Japan: Yamagata	this study
JPN12	HS2323	<i>Mus musculus</i>	Japan: Hakodate	this study
JPN13	MG0230	<i>Mus musculus</i>	Japan: Ashiro	this study
JPN14	HS3538	<i>Mus musculus</i>	Japan: Tono	this study
JPN15	MG0296	<i>Mus musculus</i>	Japan: Teine	this study
JPN16	MG0297	<i>Mus musculus</i>	Japan: Teine	this study
JPN17	HS2445	<i>Mus musculus</i>	Japan: Takikawa	this study
JPN18	HS2326	<i>Mus musculus</i>	Japan: Nayoro	this study
KAZ01	HS1464	<i>Mus musculus</i>	Kazakhstan: Aktobe	this study
KAZ02	ERS957504	<i>Mus musculus</i>	Kazakhstan: Almaty	*Harr et al. 2016
KAZ03	ERS957506	<i>Mus musculus</i>	Kazakhstan: Almaty	*Harr et al. 2016
KAZ04	ERS957508	<i>Mus musculus</i>	Kazakhstan: Almaty	*Harr et al. 2016
KAZ05	ERS957510	<i>Mus musculus</i>	Kazakhstan: Almaty	*Harr et al. 2016
KOR01	HS0682	<i>Mus musculus</i>	South Korea: Baengnyeong Island	this study
KOR02	HS4238	<i>Mus musculus</i>	South Korea: Ganghwa Island	this study
KOR03	HS4233	<i>Mus musculus</i>	South Korea: Hwacheon-gun	this study
KOR04	MG0444	<i>Mus musculus</i>	South Korea: Busan	this study
KOR05	HS1368	<i>Mus musculus</i>	South Korea: Geoncheon	this study

LKA01	HI0488	<i>Mus musculus</i>	Sri Lanka: Colombo	this study
LKA02	HI0484	<i>Mus musculus</i>	Sri Lanka: Peradeniya	this study
NPL01	HS1467	<i>Mus musculus</i>	Nepal: Tukuhe	this study
NPL02	HS1523	<i>Mus musculus</i>	Nepal: Kathmandu	this study
PAK01	HI0173	<i>Mus musculus</i>	Pakistan: Islamabad	this study
PAK02	HI0175	<i>Mus musculus</i>	Pakistan: Islamabad	this study
PAK03	HI0261	<i>Mus musculus</i>	Pakistan: Sahiwal	this study
PAK04	HI0264	<i>Mus musculus</i>	Pakistan: Lahore	this study
RUS01	MG3056	<i>Mus musculus</i>	Russia: Moscow	this study
RUS02	MG3010	<i>Mus musculus</i>	Russia: Nouth Caucasus	this study
RUS03	HS3612	<i>Mus musculus</i>	Russia: Astrakhan	this study
RUS04	HS3604	<i>Mus musculus</i>	Russia: Tomsk	this study
RUS05	HS3605	<i>Mus musculus</i>	Russia: Gorno-Altaysk	this study
RUS06	HS3608	<i>Mus musculus</i>	Russia: Irkutsk	this study
RUS07	MG3012	<i>Mus musculus</i>	Russia: Chita	this study
RUS08	MG3007	<i>Mus musculus</i>	Russia: Krementui	this study
RUS09	MG3008	<i>Mus musculus</i>	Russia: Krementui	this study
RUS10	HS1411	<i>Mus musculus</i>	Russia: Khasan	this study
RUS11	MG3026	<i>Mus musculus</i>	Russia: Birakan	this study
RUS12	MG3025	<i>Mus musculus</i>	Russia: Vladivostok	this study
RUS13	MG3037	<i>Mus musculus</i>	Russia: Khabarovsk	this study
RUS14	MG3018	<i>Mus musculus</i>	Russia: Rudnaya Pristan	this study
RUS15	MG3048	<i>Mus musculus</i>	Russia: Yuzhno-Sakhalinsk	this study
RUS16	HS3607	<i>Mus musculus</i>	Russia: Okha	this study
RUS17	MG3045	<i>Mus musculus</i>	Russia: Poronaysk	this study
SPR01	ERS957512	<i>Mus spretus</i>	Spain: Madrid	*Harr et al. 2016
SPR02	ERS957513	<i>Mus spretus</i>	Spain: Madrid	*Harr et al. 2016
SPR03	ERS957514	<i>Mus spretus</i>	Spain: Madrid	*Harr et al. 2016
SPR04	ERS957515	<i>Mus spretus</i>	Spain: Madrid	*Harr et al. 2016
SPR05	ERS957516	<i>Mus spretus</i>	Spain: Madrid	*Harr et al. 2016
SPR06	ERS957517	<i>Mus spretus</i>	Spain: Madrid	*Harr et al. 2016
SPR07	ERS957519	<i>Mus spretus</i>	Spain: Madrid	*Harr et al. 2016
TWN01	HS2400	<i>Mus musculus</i>	Taiwan: Taitung	this study
UKR01	MG3066	<i>Mus musculus</i>	Ukraine: Donetsk	this study
VNM01	HI0505	<i>Mus musculus</i>	Viet Nam: Vinh Phuc	this study
VNM02	HI0520	<i>Mus musculus</i>	Viet Nam: Hanoi	this study

*Harr, B. et al. Genomic resources for wild populations of the house mouse, *Mus musculus* and its close relative *Mus spretus*. Sci Data 3, 160075 (2016).

Table 1-2 Check sample sex by counting X and Y chromosomes.**Check sample sex by counting X and Y chromosomes**

Sample Code	Sample	Chromosome X Total Depth	Chromosome Y Total Depth	Chromosome X (Normalized)	Chromosome Y (Normalized)	X/Y ratio	Sex
BGD01	HI0373	2,556,841,016	3,368,901	28.23	3.80	7.43	F
BGD02	HI0347	3,084,117,474	307,301	34.06	0.35	98.28	F
CHN01	MG0686	1,482,780,655	14,259,050	16.37	16.08	1.02	M
CHN02	MG0747	3,086,253,259	625,491	34.08	0.71	48.32	F
CHN03	MG0608	1,633,354,526	15,581,390	18.04	17.57	1.03	M
CHN04	MG0611	1,367,378,538	12,753,383	15.10	14.38	1.05	M
CHN05	MG0597	1,609,732,481	15,391,577	17.78	17.36	1.02	M
CHN06	MG0577	2,975,154,512	451,461	32.85	0.51	64.53	F
CHN07	MG0716	1,504,939,236	14,540,348	16.62	16.40	1.01	M
CHN08	MG0721	3,104,237,452	499,274	34.28	0.56	60.89	F
CHN09	MG0871	1,489,069,686	14,328,983	16.44	16.16	1.02	M
CHN10	MG5086	1,496,824,347	14,191,783	16.53	16.00	1.03	M
CHN11	MG0917	1,535,423,557	13,594,927	16.95	15.33	1.11	M
CHN12	MG0797	1,572,431,456	14,052,379	17.36	15.85	1.10	M
CHN13	MG0565	2,937,834,046	645,882	32.44	0.73	44.54	F
CHN14	MG0529	1,609,058,491	14,173,593	17.77	15.98	1.11	M
CHN15	MG0507	1,410,821,670	13,195,635	15.58	14.88	1.05	M
CHN16	MG0709	2,739,498,888	494,890	30.25	0.56	54.21	F
CHN17	MG0501	2,712,914,539	732,892	29.96	0.83	36.25	F
CHN18	MG0504	1,463,710,826	12,764,489	16.16	14.39	1.12	M
CHN19	MG0908	1,402,263,782	12,999,602	15.48	14.66	1.06	M
CHN20	MG0863	1,537,871,250	14,982,743	16.98	16.89	1.01	M
CHN21	MG0713	1,566,712,641	14,341,395	17.30	16.17	1.07	M
CHN22	MG0795	3,208,938,768	254,355	35.43	0.29	123.55	F
CHN23	MG0631	2,995,929,905	293,551	33.08	0.33	99.94	F
CHN24	MG0992	3,025,774,556	537,599	33.41	0.61	55.12	F
EST01	MG3044	1,369,499,302	12,720,373	15.12	14.34	1.05	M
IDN01	HI0112	1,417,816,563	13,711,793	15.66	15.46	1.01	M
IDN02	HI0134	1,416,464,945	13,040,386	15.64	14.70	1.06	M
IDN03	HI0115	1,553,691,234	886,055	17.16	1.00	17.17	F
IDN04	HI0116	2,967,792,895	246,139	32.77	0.28	118.07	F
IND01	HI0274	3,014,590,988	151,233	33.29	0.17	195.20	F
IND02	HI0185	1,541,705,192	13,813,583	17.02	15.58	1.09	M
IND03	HI0159	1,678,928,350	14,991,851	18.54	16.91	1.10	M
IND04	HI0161	1,578,911,943	15,261,250	17.44	17.21	1.01	M
IND05	HI0328	1,514,940,676	13,767,715	16.73	15.52	1.08	M
IND06	HI0329	3,089,678,700	202,705	34.12	0.23	149.26	F
IND08	HI0313	3,104,773,116	179,520	34.28	0.20	169.36	F
IND09	HI0321	1,536,385,692	14,041,796	16.97	15.83	1.07	M
IRN05	MG5135	2,882,173,864	459,052	31.83	0.52	61.48	F
IRN06	MG0417	1,522,361,434	13,335,607	16.81	15.04	1.12	M
JPN01	HS2788	1,641,722,149	15,768,836	18.13	17.78	1.02	M
JPN02	HS4272	1,526,083,240	14,684,112	16.85	16.56	1.02	M
JPN03	HS4273	3,122,715,953	382,460	34.48	0.43	79.96	F
JPN04	HS4411	1,597,191,365	15,212,526	17.64	17.15	1.03	M
JPN05	HS4097	1,485,164,545	15,154,583	16.40	17.09	0.96	M
JPN06	HS4120	3,178,019,242	516,666	35.09	0.58	60.24	F
JPN07	HS2815	1,601,956,565	15,886,297	17.69	17.91	0.99	M
JPN08	HS4056	2,920,255,444	559,921	32.25	0.63	51.07	F
JPN09	HS4271	1,414,765,218	13,733,703	15.62	15.49	1.01	M
JPN10	HS4169	1,481,569,657	14,495,597	16.36	16.35	1.00	M
JPN11	HS3534	1,491,349,339	15,171,912	16.47	17.11	0.96	M
JPN12	HS2323	1,549,147,798	14,563,988	17.11	16.42	1.04	M
JPN13	MG0230	1,423,329,719	14,430,719	15.72	16.27	0.97	M
JPN14	HS3538	2,931,017,230	725,905	32.37	0.82	39.54	F

JPN15	MG0296	1,430,678,798	13,957,335	15.80	15.74	1.00	M
JPN16	MG0297	2,751,319,104	340,044	30.38	0.38	79.23	F
JPN17	HS2445	1,539,233,686	15,070,034	17.00	16.99	1.00	M
JPN18	HS2326	1,526,911,931	14,865,826	16.86	16.76	1.01	M
KAZ01	HS1464	1,607,805,041	14,491,589	17.75	16.34	1.09	M
KOR01	HS0682	1,483,027,922	14,586,083	16.38	16.45	1.00	M
KOR02	HS4238	3,106,143,974	583,624	34.30	0.66	52.12	F
KOR03	HS4233	1,550,889,255	15,443,608	17.13	17.41	0.98	M
KOR04	MG0444	1,419,166,134	13,925,957	15.67	15.70	1.00	M
KOR05	HS1368	1,511,602,816	15,125,500	16.69	17.06	0.98	M
LKA01	HI0488	1,645,521,259	14,772,680	18.17	16.66	1.09	M
LKA02	HI0484	1,730,217,698	15,457,554	19.11	17.43	1.10	M
NPL01	HS1467	1,611,997,181	14,317,536	17.80	16.14	1.10	M
NPL02	HS1523	1,645,770,789	15,331,655	18.17	17.29	1.05	M
PAK01	HI0173	3,218,041,328	339,783	35.54	0.38	92.75	F
PAK02	HI0175	3,422,569,562	275,393	37.79	0.31	121.70	F
PAK03	HI0261	1,714,240,346	15,104,261	18.93	17.03	1.11	M
PAK04	HI0264	1,666,014,193	14,294,775	18.40	16.12	1.14	M
RUS01	MG3056	2,954,074,054	386,577	32.62	0.44	74.83	F
RUS02	MG3010	1,307,062,188	12,533,737	14.43	14.13	1.02	M
RUS03	HS3612	1,628,161,002	15,781,252	17.98	17.80	1.01	M
RUS04	HS3604	3,200,900,718	470,350	35.35	0.53	66.64	F
RUS05	HS3605	1,644,273,463	14,594,513	18.16	16.46	1.10	M
RUS06	HS3608	1,647,212,231	14,860,569	18.19	16.76	1.09	M
RUS07	MG3012	2,879,671,508	240,350	31.80	0.27	117.33	F
RUS08	MG3007	1,645,839,078	15,189,995	18.17	17.13	1.06	M
RUS09	MG3008	2,748,049,287	603,505	30.35	0.68	44.59	F
RUS10	HS1411	1,602,800,977	15,065,712	17.70	16.99	1.04	M
RUS11	MG3026	1,449,373,053	12,300,109	16.00	13.87	1.15	M
RUS12	MG3025	2,986,291,346	490,757	32.98	0.55	59.59	F
RUS13	MG3037	2,776,988,436	617,210	30.66	0.70	44.06	F
RUS14	MG3018	1,550,065,017	13,458,573	17.12	15.18	1.13	M
RUS15	MG3048	2,618,810,319	371,710	28.92	0.42	68.99	F
RUS16	HS3607	1,673,229,397	14,321,425	18.48	16.15	1.14	M
RUS17	MG3045	3,008,203,389	171,604	33.22	0.19	171.67	F
TWN01	HS2400	1,611,175,870	14,672,477	17.79	16.54	1.08	M
UKR01	MG3066	1,548,970,932	13,381,953	17.10	15.09	1.13	M
VNM01	HI0505	1,447,706,945	13,516,401	15.99	15.24	1.05	M
VNM02	HI0520	1,521,400,410	13,330,960	16.80	15.03	1.12	M

Table 1-3 Summary of the whole genome sequencing of the house mouse.

Summary of the whole genome sequencing of the house mouse											
Sample Code	Sample ID	Location	*mtDNA Haplogroup	Median Coverage	Ts/Tv	Per-Sample Nucleotide Diversity	Nonsynonymous	Synonymous	Nonsynonymous /Synonymous	**Latitude	**Longitude
BGD01	HI0373	Bangladesh: Dhaka	CAS	29	2.223	0.00575	105,814	259,916	0.407	23.702000	90.366944
BGD02	HI0347	Bangladesh: Mymensingh	CAS	31	2.223	0.00240	90,608	219,566	0.413	24.753889	90.403056
CHN01	MG0686	China: Kashgar	MUS	30	2.239	0.00124	87,348	200,878	0.435	39.468100	75.993800
CHN02	MG0747	China: Hotan	MUS	33	2.234	0.00118	86,087	199,539	0.431	37.100000	80.016667
CHN03	MG0608	China: Aksu	MUS	32	2.239	0.00132	89,201	204,317	0.437	41.185000	80.290400
CHN04	MG0611	China: Tacheng	MUS	28	2.236	0.00219	93,668	214,670	0.436	46.751700	82.986900
CHN05	MG0597	China: Manas	MUS	32	2.236	0.00207	92,712	212,896	0.435	44.300000	86.216667
CHN06	MG0577	China: Urumqi	MUS	29	2.257	0.00450	62,427	145,088	0.430	43.800000	87.583333
CHN07	MG0716	China: Lhasa	MUS	29	2.236	0.00154	87,797	203,111	0.432	29.653400	91.171900
CHN08	MG0721	China: Lhasa	MUS	31	2.229	0.00172	87,560	202,997	0.431	29.653400	91.171900
CHN09	MG0871	China: Dunhuang	MUS	29	2.237	0.00165	89,469	206,049	0.434	40.142100	94.661900
CHN10	MG5086	China: Jiayuguan	MUS	29	2.238	0.00003	79,912	187,758	0.426	39.773200	98.288200
CHN11	MG0917	China: Lijiang	CAS	29	2.234	0.00364	97,041	231,501	0.419	26.855200	100.225900
CHN12	MG0797	China: Dali	CAS	32	2.230	0.00488	101,695	244,586	0.416	25.606500	100.267600
CHN13	MG0565	China: Xining	MUS	29	2.229	0.00110	85,700	198,964	0.431	36.616667	101.766667
CHN14	MG0529	China: Kunming	CAS	32	2.233	0.00299	93,665	224,367	0.417	25.046400	102.709400
CHN15	MG0507	China: Lanzhou	MUS	29	2.237	0.00210	89,530	209,616	0.427	36.060600	103.826800
CHN16	MG0709	China: Chongqing	CAS	27	2.227	0.00483	102,828	244,294	0.421	29.563700	106.550400
CHN17	MG0501	China: Guilin	CAS	29	2.225	0.00456	99,498	241,565	0.412	25.275000	110.296000
CHN18	MG0504	China: Guangzhou	CAS	30	2.232	0.00463	99,674	239,400	0.416	23.132000	113.266000
CHN19	MG0908	China: Wuhan	CAS	29	2.231	0.00497	100,278	242,033	0.414	30.593400	114.304600
CHN20	MG0863	China: Manzhouli	CAS	32	2.233	0.00384	95,938	226,639	0.423	49.598000	117.379000
CHN21	MG0713	China: Zhenjiang	CAS	32	2.237	0.00286	94,521	221,920	0.426	32.188000	119.424000
CHN22	MG0795	China: Ningbo	CAS	33	2.225	0.00439	98,385	236,591	0.416	29.860300	121.624500
CHN23	MG0631	China: Mohe	MUS	31	2.229	0.00159	89,487	206,801	0.433	52.972000	122.539000
CHN24	MG0992	China: Qiqihar	MUS	32	2.228	0.00180	91,229	208,853	0.437	47.354900	123.918200
EST01	MG3044	Estonia: Tallinn	MUS	29	2.240	0.00112	83,282	195,115	0.427	59.437222	24.745278
IDN01	HI0112	Indonesia: Bogor	DOM	25	2.228	0.00464	93,169	226,203	0.412	-6.600000	106.800000
IDN02	HI0134	Indonesia: Lembang	CAS	29	2.226	0.00115	77,394	184,667	0.419	-6.817000	107.617000
IDN03	HI0115	Indonesia: Bali	CAS	31	2.222	0.00283	92,293	225,657	0.409	-8.369167	115.138333
IDN04	HI0116	Indonesia: Bali	CAS	30	2.223	0.00221	89,434	216,788	0.413	-8.369167	115.138333
IND01	HI0274	India: Mysore	CAS	30	2.223	0.00431	98,835	241,363	0.409	12.308611	76.653056
IND02	HI0185	India: Delhi	CAS	30	2.227	0.00597	105,968	262,733	0.403	28.610000	77.230000
IND03	HI0159	India: Leh	CAS	31	2.229	0.00535	102,315	251,754	0.406	34.160000	77.580000
IND04	HI0161	India: Leh	CAS	29	2.230	0.00535	102,608	252,742	0.406	34.160000	77.580000
IND05	HI0328	India: Hyderabad	CAS	29	2.230	0.00169	86,449	210,375	0.411	17.370000	78.480000
IND06	HI0329	India: Hyderabad	CAS	31	2.223	0.00307	94,057	228,423	0.412	17.370000	78.480000
IND08	HI0313	India: Bhubaneswar	CAS	31	2.222	0.00275	94,042	227,152	0.414	20.270000	85.840000
IND09	HI0321	India: Bhubaneswar	CAS	30	2.229	0.00422	97,981	240,748	0.407	20.270000	85.840000
IRN05	MG5135	Iran: Now Shahr	CAS	30	2.232	0.00276	93,123	216,076	0.431	36.648889	51.496111
IRN06	MG0417	Iran: Mashhad	MUS	30	2.237	0.00263	94,011	217,271	0.433	36.300000	59.600000
JPN01	HS2788	Japan: Okinawa Island	MUS	32	2.233	0.00407	98,270	234,804	0.419	26.212444	127.680917
JPN02	HS4272	Japan: Fukuoka	MUS	30	2.236	0.00182	88,270	207,779	0.425	33.590139	130.401722
JPN03	HS4273	Japan: Yamaguchi	MUS	32	2.228	0.00145	87,004	202,486	0.430	34.178028	131.473778
JPN04	HS4411	Japan: Oda	MUS	31	2.234	0.00292	92,692	219,473	0.422	35.192083	132.499361
JPN05	HS4097	Japan: Misasa	MUS	29	2.235	0.00194	89,771	209,221	0.429	35.408444	133.861778
JPN06	HS4120	Japan: Ishii	MUS	29	2.228	0.00065	82,533	192,646	0.428	34.074167	134.440556
JPN07	HS2815	Japan: Nonoichi	MUS	32	2.235	0.00230	88,618	210,353	0.421	36.519417	136.609778
JPN08	HS4056	Japan: Fujisawa	MUS	29	2.229	0.00063	81,918	190,971	0.429	35.338833	139.491111
JPN09	HS4271	Japan: Setana	MUS	26	2.234	0.00157	85,858	202,211	0.425	42.417111	139.883028
JPN10	HS4169	Japan: Tsukuba	MUS	30	2.235	0.00044	82,100	191,043	0.430	36.083472	140.076444
JPN11	HS3534	Japan: Yamagata	MUS	29	2.234	0.00220	91,093	212,232	0.429	38.255417	140.339611
JPN12	HS2323	Japan: Hakodate	MUS	31	2.236	0.00267	89,954	211,610	0.425	41.768667	140.728917
JPN13	MG0230	Japan: Ashiro	CAS	31	2.235	0.00019	79,837	188,062	0.425	40.101389	141.052028
JPN14	HS3538	Japan: Tono	MUS	29	2.227	0.00025	80,578	188,213	0.428	39.702083	141.154500
JPN15	MG0296	Japan: Teine	CAS	29	2.236	0.00018	79,317	188,238	0.421	43.121917	141.245833
JPN16	MG0297	Japan: Teine	CAS	28	2.228	0.00006	78,973	188,246	0.420	43.121917	141.245833
JPN17	HS2445	Japan: Takikawa	CAS	30	2.233	0.00259	90,463	215,400	0.420	43.557833	141.910417
JPN18	HS2326	Japan: Nayoro	CAS	30	2.234	0.00177	87,401	207,303	0.422	44.355833	142.463333
KAZ01	HS1464	Kazakhstan: Aktobe	MUS	31	2.237	0.00178	89,227	207,464	0.430	50.283333	57.166667
KOR01	HS0682	South Korea: Baengnyeong Island	MUS	28	2.235	0.00052	82,910	192,288	0.431	37.966667	124.650000
KOR02	HS4238	South Korea: Ganghwa Island	MUS	31	2.229	0.00068	83,386	193,629	0.431	37.700000	126.433333
KOR03	HS4233	South Korea: Hwacheon-gun	MUS	31	2.236	0.00064	83,090	193,505	0.429	38.107500	127.714444
KOR04	MG0444	South Korea: Busan	MUS	30	2.234	0.00093	83,954	195,828	0.429	35.100000	129.033333
KOR05	HS1368	South Korea: Geoncheon	MUS	28	2.236	0.00074	83,724	194,017	0.432	35.837686	129.045187
LKA01	HI0488	Sri Lanka: Colombo	CAS	32	2.229	0.00341	94,919	231,263	0.410	6.934444	79.842778
LKA02	HI0484	Sri Lanka: Peradeniya	CAS	33	2.228	0.00329	95,234	230,020	0.414	7.266667	80.600000
NPL01	HS1467	Nepal: Tukuhe	NEP	32	2.223	0.00528	106,253	259,487	0.409	28.740000	83.620000
NPL02	HS1523	Nepal: Kathmandu	NEP	32	2.220	0.00700	118,218	290,401	0.407	27.717200	85.324000
PAK01	HI0173	Pakistan: Islamabad	CAS	32	2.222	0.00757	110,301	277,816	0.397	33.716667	73.066667
PAK02	HI0175	Pakistan: Islamabad	CAS	34	2.221	0.00750	110,154	276,926	0.398	33.716667	73.066667
PAK03	HI0261	Pakistan: Sahiwal	CAS	33	2.229	0.00751	110,831	278,758	0.398	30.661111	73.108333
PAK04	HI0264	Pakistan: Lahore	CAS	34	2.228	0.00753	110,118	276,433	0.398	31.549722	74.343611
RUS01	MG3056	Russia: Moscow	DOM	28	2.235	0.00561	79,502	184,256	0.431	55.755833	37.617222
RUS02	MG3010	Russia: Nouth Caucasus	MUS	28	2.237	0.00230	92,111	214,251	0.430	43.711400	44.806100
RUS03	HS3612	Russia: Astrakhan	MUS	31	2.237	0.00127	87,079	204,096	0.427	46.350000	48.050000
RUS04	HS3604	Russia: Tomsrk	DOM	33	2.230	0.00040	78,805	187,296	0.421	56.500000	84.966667
RUS05	HS3605	Russia: Gorno-Altaysk	MUS	33	2.238	0.00058	80,774	191,052	0.423	51.950000	85.966667
RUS06	HS3608	Russia: Irkutsk	MUS	32	2.240	0.00037	79,987	190,541	0.420	52.283333	104.283333
RUS07	MG3012	Russia: Chita	MUS	30	2.231	0.00105	84,584	197,942	0.427	52.466000	113.466667
RUS08	MG3007	Russia: Krementui	MUS	34	2.237	0.00160	88,512	205,076	0.432	50.155148	115.906841
RUS09	MG3008	Russia: Krementui	MUS	30	2.231	0.00187	90,658	209,195	0.433	50.155148	115.906841
RUS10	HS1411	Russia: Khasan	CAS	30	2.239	0.00608	98,812	237,456	0.416	42.428333	130.645556
RUS11	MG3026	Russia: Birakan	MUS	31	2.238	0.00240	91,232	214,488	0.425	49.000833	131.720000
RUS12	MG3025	Russia: Vladivostok	CAS	30	2.230	0.00498	95,067	226,373	0.420	43.133333	131.900000

RUS13	MG3037	Russia: Khabarovsk	DOM	31	2.232	0.00359	94,667	222,625	0.425	48.483333	135.083333
RUS14	MG3018	Russia: Rudnaya Pristan	CAS	31	2.238	0.00191	85,980	203,350	0.423	44.358611	135.810278
RUS15	MG3048	Russia: Yuzhno-Sakhalinsk	MUS	25	2.229	0.00325	95,056	219,938	0.432	46.966667	142.733333
RUS16	HS3607	Russia: Okha	DOM	33	2.236	0.00147	83,554	198,567	0.421	53.583333	142.933333
RUS17	MG3045	Russia: Poronaysk	MUS	31	2.231	0.00239	91,198	212,474	0.429	49.216667	143.116667
TWN01	HS2400	Taiwan: Taitung	CAS	31	2.232	0.00276	90,082	217,314	0.415	22.758333	121.144444
UKR01	MG3066	Ukraine: Donetsk	MUS	30	2.234	0.00417	96,190	227,733	0.422	48.002778	37.805278
VNM01	HI0505	Viet Nam: Vinh Phuc	CAS	29	2.229	0.00356	94,824	229,754	0.413	21.300000	105.600000
VNM02	HI0520	Viet Nam: Hanoi	CAS	32	2.232	0.00227	89,245	217,339	0.411	21.028472	105.854167

*Li, Y. et al. House mouse *Mus musculus* dispersal in East Eurasia inferred from 98 newly determined complete mitochondrial genome sequences. Heredity 126, 132–147 (2021).

**Latitude and longitude are not absolute points of sample collection, but rather approximate locations.

Table 1-4 The eigenvalues of autosomes and X chromosomes of each samples by principal component analysis (PCA)

The eigenvalues of autosomes and X chromosomes of each samples by principal component analysis (PCA)				
Sample Code	PC1 (Autosome)	PC2 (Autosome)	PC1 (X chromosome)	PC2 (X chromosome)
BGD01	-0.0903	-0.1462	-0.0909	-0.1268
BGD02	-0.0893	-0.1474	-0.0907	-0.1272
CHN01	0.0872	0.0236	0.0823	0.0206
CHN02	0.0855	0.0250	0.0816	0.0203
CHN03	0.0864	0.0236	0.0821	0.0205
CHN04	0.0864	0.0244	0.0834	0.021
CHN05	0.0868	0.0242	0.0836	0.0212
CHN06	-0.0669	0.1195	-0.0596	0.1223
CHN07	0.0871	0.0236	0.085	0.0208
CHN08	0.0851	0.0248	0.0844	0.0206
CHN09	0.0899	0.0238	0.0846	0.0209
CHN10	0.0910	0.0239	0.0845	0.0207
CHN11	-0.0396	-0.0948	-0.0629	-0.1102
CHN12	-0.0416	-0.0985	-0.0674	-0.1134
CHN13	0.0909	0.0236	0.0845	0.0207
CHN14	-0.0545	-0.1083	-0.075	-0.1205
CHN15	0.0808	0.0294	0.0847	0.0208
CHN16	0.0036	-0.0568	-0.0281	-0.0789
CHN17	-0.0620	-0.1128	-0.0785	-0.1228
CHN18	-0.0680	-0.1134	-0.0803	-0.125
CHN19	-0.0230	-0.0797	-0.0598	-0.1078
CHN20	0.0494	0.0052	0.0665	0.0062
CHN21	0.0521	-0.0126	0.0756	0.012
CHN22	-0.0539	-0.1104	-0.0791	-0.123
CHN23	0.0831	0.0286	0.0836	0.0212
CHN24	0.0880	0.0228	0.0846	0.0205
CZE01	0.0764	0.0338	0.0843	0.0214
CZE02	0.0778	0.0331	0.0838	0.0217
CZE03	0.0773	0.0329	0.083	0.0221
CZE04	0.0782	0.0329	0.0834	0.0218
CZE05	0.0770	0.0334	0.0838	0.0216
CZE06	0.0779	0.0332	0.084	0.0215
CZE07	0.0780	0.0330	0.0834	0.0219
DEU01	-0.1597	0.1825	-0.1508	0.1861
DEU02	-0.1593	0.1818	-0.1508	0.1862
DEU03	-0.1595	0.1825	-0.1507	0.186
DEU04	-0.1591	0.1817	-0.1507	0.1862
DEU05	-0.1593	0.1825	-0.1509	0.1864
DEU06	-0.1595	0.1825	-0.1508	0.1864
DEU07	-0.1588	0.1808	-0.1509	0.186
EST01	0.0788	0.0322	0.0811	0.0231
FRA01	-0.1580	0.1785	-0.1501	0.1841
FRA02	-0.1578	0.1782	-0.15	0.1843
FRA03	-0.1577	0.1780	-0.1501	0.1843
FRA04	-0.1577	0.1778	-0.1502	0.1847
IDN01	-0.0956	-0.0887	-0.0925	-0.119
IDN02	-0.0982	-0.0874	-0.093	-0.107
IDN03	-0.0878	-0.1459	-0.0905	-0.1326
IDN04	-0.0887	-0.1446	-0.0904	-0.1329
IND01	-0.0902	-0.1397	-0.0911	-0.1228
IND02	-0.0870	-0.1212	-0.0892	-0.1156
IND03	-0.0872	-0.0906	-0.0844	-0.0729
IND04	-0.0870	-0.0906	-0.084	-0.0728

IND05	-0.0911	-0.1434	-0.0919	-0.1251
IND06	-0.0909	-0.1427	-0.0914	-0.1232
IND07	-0.0845	-0.0931	-0.079	-0.0716
IND08	-0.0892	-0.1466	-0.0911	-0.1247
IND09	-0.0907	-0.1417	-0.0916	-0.1261
IRN01	-0.1474	0.1544	-0.1443	0.1732
IRN02	-0.1471	0.1540	-0.1445	0.1729
IRN03	-0.1479	0.1550	-0.1444	0.1728
IRN04	-0.1478	0.1548	-0.1445	0.173
IRN05	0.0687	0.0239	0.0792	0.02
IRN06	0.0762	0.0208	0.0809	0.0204
JPN01	0.0144	-0.0497	0.0213	-0.0372
JPN02	0.0689	0.0009	0.0715	0.0068
JPN03	0.0806	0.0095	0.0844	0.0189
JPN04	0.0201	-0.0465	-0.0338	-0.0863
JPN05	0.0709	0.0036	0.0768	0.0116
JPN06	0.0895	0.0179	0.0861	0.0203
JPN07	0.0618	-0.0075	0.0725	0.0078
JPN08	0.0897	0.0205	0.0855	0.0198
JPN09	0.0666	-0.0007	0.06	-0.0036
JPN10	0.0934	0.0211	0.0864	0.0206
JPN11	0.0632	-0.0067	0.0721	0.0072
JPN12	0.0503	0.0016	0.0708	0.006
JPN13	0.0926	0.0202	0.0865	0.0206
JPN14	0.0926	0.0212	0.0865	0.0206
JPN15	0.0659	-0.0030	0.0697	0.0051
JPN16	0.0664	-0.0023	0.0727	0.0075
JPN17	0.0507	-0.0152	0.0677	0.0036
JPN18	0.0619	-0.0075	0.0694	0.0051
KAZ01	0.0829	0.0262	0.0835	0.0213
KAZ02	0.0861	0.0244	0.0828	0.021
KAZ03	0.0851	0.0250	0.0828	0.0209
KAZ04	0.0862	0.0252	0.0835	0.0211
KAZ05	0.0860	0.0251	0.0835	0.0212
KOR01	0.0939	0.0229	0.0862	0.0207
KOR02	0.0928	0.0219	0.086	0.0207
KOR03	0.0936	0.0225	0.0861	0.0207
KOR04	0.0839	0.0133	0.0827	0.018
KOR05	0.0930	0.0222	0.0861	0.0207
LKA01	-0.0903	-0.1422	-0.092	-0.1247
LKA02	-0.0901	-0.1437	-0.0912	-0.1281
NPL01	-0.0927	-0.1376	-0.096	-0.1281
NPL02	-0.1002	-0.1280	-0.1021	-0.1276
PAK01	-0.0826	-0.0850	-0.0784	-0.0691
PAK02	-0.0823	-0.0843	-0.0784	-0.0698
PAK03	-0.0829	-0.0939	-0.0837	-0.0837
PAK04	-0.0829	-0.0940	-0.0832	-0.0829
RUS01	-0.0460	0.1059	-0.0253	0.0938
RUS02	0.0827	0.0257	0.0832	0.021
RUS03	0.0849	0.0253	0.0832	0.021
RUS04	0.0786	0.0325	0.0839	0.0218
RUS05	0.0804	0.0310	0.0839	0.0217
RUS06	0.0814	0.0298	0.084	0.0215
RUS07	0.0820	0.0295	0.0831	0.0218
RUS08	0.0885	0.0255	0.0848	0.0209
RUS09	0.0880	0.0258	0.0843	0.0209
RUS10	-0.0319	-0.0206	-0.0244	-0.0466

RUS11	0.0723	0.0225	0.0782	0.0162
RUS12	-0.0317	-0.0243	-0.0004	-0.0454
RUS13	0.0524	0.0111	0.0731	0.0145
RUS14	0.0562	0.0138	0.0612	0.0149
RUS15	0.0546	0.0218	0.0596	0.0023
RUS16	0.0630	0.0201	0.0606	0.0024
RUS17	0.0652	0.0234	0.0701	0.0097
TWN01	-0.0671	-0.1200	-0.082	-0.1262
UKR01	0.0256	-0.0077	-0.0007	-0.0509
VNM01	-0.0815	-0.1357	-0.0888	-0.1307
VNM02	-0.0819	-0.1360	-0.0878	-0.1278

Table 1-5 The outgroup f_3 statistics result of autosome with SPR as outgroup. f_3 (CAS, X: SPR)

The outgroup f_3 statistics result of autosome with SPR as outgroup. f_3(CAS, X; SPR)								
Source1	Source2	Target	Source2 mtDNA Haplogroup	f_3 statistics	Std.Err	Z	SNPs	
IND04	IND03	SPR	CAS	182.612237	0.446592	408.902	41,316,659	
IND04	PAK01	SPR	CAS	166.346980	0.385277	431.760	44,821,432	
IND04	PAK02	SPR	CAS	166.114768	0.398941	416.389	44,819,245	
IND04	PAK04	SPR	CAS	165.256554	0.397463	415.778	44,983,613	
IND04	PAK03	SPR	CAS	165.005197	0.396924	415.710	45,024,181	
IND04	IND02	SPR	CAS	164.853710	0.397010	415.238	44,369,741	
IND04	BGD02	SPR	CAS	164.796617	0.398664	413.372	42,826,671	
IND04	IND05	SPR	CAS	164.749192	0.400784	411.068	42,511,816	
IND04	IND01	SPR	CAS	164.723086	0.399450	412.375	43,674,415	
IND04	LKA02	SPR	CAS	164.715305	0.400132	411.653	43,232,300	
IND04	IND06	SPR	CAS	164.706158	0.397115	414.757	43,130,254	
IND04	BGD01	SPR	CAS	164.699793	0.396604	415.276	44,438,207	
IND04	IND09	SPR	CAS	164.687444	0.399003	412.747	43,640,450	
IND04	LKA01	SPR	CAS	164.670444	0.398839	412.874	43,284,124	
IND04	IND07	SPR	CAS	164.651394	0.395467	416.347	44,899,513	
IND04	IDN03	SPR	CAS	164.579575	0.400385	411.053	43,043,092	
IND04	IDN04	SPR	CAS	164.575480	0.400304	411.127	42,775,321	
IND04	IND08	SPR	CAS	164.573734	0.398880	412.590	43,011,755	
IND04	VNM01	SPR	CAS	164.459897	0.400260	410.883	43,386,303	
IND04	VNM02	SPR	CAS	164.445382	0.396137	415.123	42,821,334	
IND04	TWN01	SPR	CAS	164.102364	0.397194	413.155	43,087,041	
IND04	CHN18	SPR	CAS	163.974090	0.398340	411.643	43,940,653	
IND04	CHN17	SPR	CAS	163.902282	0.398055	411.758	43,926,574	
IND04	CHN22	SPR	CAS	163.887333	0.397448	412.349	43,854,376	
IND04	CHN14	SPR	CAS	163.737400	0.395216	414.298	43,253,155	
IND04	CHN12	SPR	CAS	163.590348	0.396487	412.599	44,128,745	
IND04	CHN11	SPR	CAS	163.490392	0.395779	413.085	43,596,955	
IND04	IDN01	SPR	DOM	163.470850	0.402595	406.043	43,995,590	
IND04	IDN02	SPR	CAS	163.353219	0.410333	398.099	42,445,946	
IND04	CHN19	SPR	CAS	163.249393	0.396904	411.307	44,231,709	
IND04	CHN16	SPR	CAS	162.808216	0.389812	417.658	44,257,647	
IND04	JPN01	SPR	MUS	162.740230	0.390833	416.393	43,926,564	
IND04	JPN04	SPR	MUS	162.628183	0.388754	418.332	43,430,374	
IND04	NPL01	SPR	NEP	162.398494	0.436670	371.902	44,383,678	
IND04	RUS12	SPR	CAS	162.219840	0.398148	407.436	44,391,978	
IND04	RUS10	SPR	CAS	162.161916	0.394333	411.231	44,912,866	
IND04	JPN17	SPR	CAS	162.028410	0.380347	426.001	43,371,013	
IND04	CHN21	SPR	CAS	161.902072	0.383914	421.715	43,541,208	
IND04	UKR01	SPR	MUS	161.862031	0.382776	422.864	44,148,753	
IND04	JPN18	SPR	CAS	161.851155	0.380071	425.845	43,036,750	
IND04	JPN07	SPR	MUS	161.838379	0.380061	425.823	43,283,637	
IND04	JPN15	SPR	CAS	161.734939	0.379063	426.670	42,326,504	
IND04	JPN11	SPR	MUS	161.714620	0.380447	425.065	43,255,514	

IND04	JPN16	SPR	CAS	161.698887	0.377128	428.764	42,279,391
IND04	JPN12	SPR	MUS	161.694222	0.379557	426.007	43,468,397
IND04	JPN02	SPR	MUS	161.680754	0.381065	424.287	43,099,526
IND04	JPN09	SPR	MUS	161.656828	0.379142	426.376	42,978,733
IND04	CHN20	SPR	CAS	161.565200	0.381392	423.619	44,084,031
IND04	JPN05	SPR	MUS	161.492129	0.378515	426.647	43,182,337
IND04	RUS13	SPR	DOM	161.466624	0.383996	420.490	43,981,205
IND04	JPN03	SPR	MUS	161.421360	0.375565	429.810	42,979,639
IND04	KOR04	SPR	MUS	161.342522	0.375375	429.817	42,754,845
IND04	RUS14	SPR	CAS	161.338137	0.380514	424.001	43,191,345
IND04	IRN06	SPR	MUS	161.332035	0.378138	426.649	43,660,660
IND04	RUS16	SPR	DOM	161.262349	0.379359	425.092	43,022,910
IND04	JPN06	SPR	MUS	161.255325	0.375030	429.980	42,641,019
IND04	RUS11	SPR	MUS	161.247267	0.378377	426.155	43,498,349
IND04	IRN05	SPR	CAS	161.211786	0.374531	430.436	43,712,028
IND04	JPN08	SPR	MUS	161.183588	0.376648	427.942	42,644,405
IND04	KAZ02	SPR	MUS	161.155247	0.372748	432.344	43,503,814
IND04	KAZ01	SPR	MUS	161.153775	0.373163	431.859	43,271,577
IND04	RUS02	SPR	MUS	161.151099	0.375992	428.603	43,540,507
IND04	RUS15	SPR	CAS	161.149118	0.380736	423.257	43,883,635
IND04	JPN13	SPR	MUS	161.147668	0.372958	432.080	42,432,308
IND04	KAZ04	SPR	MUS	161.135903	0.374704	430.036	43,174,512
IND04	JPN10	SPR	MUS	161.132760	0.373912	430.938	42,567,191
IND04	JPN14	SPR	MUS	161.123936	0.374845	429.842	42,466,795
IND04	KOR03	SPR	MUS	161.123161	0.373912	430.912	42,685,415
IND04	RUS03	SPR	MUS	161.122472	0.374322	430.438	43,014,234
IND04	KOR05	SPR	MUS	161.122438	0.374031	430.773	42,737,733
IND04	KOR02	SPR	MUS	161.118386	0.373234	431.682	42,701,807
IND04	KOR01	SPR	MUS	161.116092	0.373595	431.259	42,624,527
IND04	CHN07	SPR	MUS	161.113821	0.375240	429.363	43,137,078
IND04	CHN09	SPR	MUS	161.102751	0.374612	430.052	43,225,391
IND04	CHN01	SPR	MUS	161.094227	0.373660	431.125	42,998,101
IND04	CHN13	SPR	MUS	161.093526	0.374744	429.876	42,931,602
IND04	CHN02	SPR	MUS	161.084335	0.374801	429.786	42,949,942
IND04	RUS08	SPR	MUS	161.076495	0.373544	431.212	43,192,743
IND04	RUS17	SPR	MUS	161.074953	0.375891	428.515	43,502,262
IND04	RUS09	SPR	MUS	161.072759	0.376590	427.714	43,325,250
IND04	CHN10	SPR	MUS	161.069671	0.374849	429.692	42,350,767
IND04	RUS06	SPR	MUS	161.067765	0.376336	427.989	42,537,657
IND04	KAZ05	SPR	MUS	161.065952	0.373193	431.589	43,182,917
IND04	CHN04	SPR	MUS	161.065121	0.373102	431.692	43,521,472
IND04	CHN08	SPR	MUS	161.064276	0.375502	428.931	43,229,281
IND04	RUS05	SPR	MUS	161.062253	0.376115	428.226	42,635,214
IND04	KAZ03	SPR	MUS	161.055030	0.373483	431.225	43,520,110
IND04	RUS07	SPR	MUS	161.050702	0.375255	429.177	42,890,492
IND04	CHN05	SPR	MUS	161.041647	0.373399	431.285	43,460,944
IND04	CHN24	SPR	MUS	161.034386	0.374590	429.895	43,298,501
IND04	RUS04	SPR	DOM	161.018430	0.377803	426.197	42,551,616

IND04	CHN03	SPR	MUS	161.016337	0.372996	431.684	43,038,329
IND04	CZE02	SPR	MUS	161.002095	0.375657	428.588	43,333,573
IND04	CZE06	SPR	MUS	160.990187	0.375475	428.765	43,061,262
IND04	CHN23	SPR	MUS	160.981637	0.374603	429.740	43,178,551
IND04	CZE04	SPR	MUS	160.969109	0.378823	424.919	43,281,542
IND04	CHN15	SPR	MUS	160.965475	0.378181	425.631	43,430,606
IND04	CZE07	SPR	MUS	160.931959	0.378861	424.778	43,347,409
IND04	CZE05	SPR	MUS	160.916132	0.373174	431.209	43,282,609
IND04	CZE03	SPR	MUS	160.899000	0.374867	429.216	43,190,284
IND04	EST01	SPR	MUS	160.895208	0.384402	418.560	42,928,694
IND04	CZE01	SPR	MUS	160.873979	0.376967	426.758	43,192,912
IND04	RUS01	SPR	DOM	159.538852	0.385310	414.053	45,132,878
IND04	CHN06	SPR	MUS	159.285734	0.387420	411.145	44,570,949
IND04	IRN02	SPR	DOM	158.296554	0.384655	411.528	44,331,362
IND04	IRN04	SPR	DOM	158.269609	0.383557	412.636	44,349,230
IND04	IRN01	SPR	DOM	158.262651	0.384098	412.037	44,359,816
IND04	IRN03	SPR	DOM	158.235016	0.384011	412.058	44,343,823
IND04	DEU04	SPR	DOM	158.065784	0.392196	403.027	43,188,614
IND04	DEU03	SPR	DOM	158.044179	0.394258	400.865	43,187,697
IND04	DEU06	SPR	DOM	158.029085	0.395484	399.584	43,214,421
IND04	DEU07	SPR	DOM	158.026652	0.393499	401.594	43,671,821
IND04	FRA04	SPR	DOM	158.003910	0.396145	398.854	43,726,421
IND04	FRA03	SPR	DOM	158.000919	0.397098	397.889	43,708,212
IND04	DEU01	SPR	DOM	157.993716	0.395962	399.012	43,102,382
IND04	FRA01	SPR	DOM	157.962848	0.392530	402.423	43,298,629
IND04	FRA02	SPR	DOM	157.940386	0.402497	392.401	43,698,221
IND04	DEU05	SPR	DOM	157.938529	0.397480	397.350	42,988,752
IND04	DEU02	SPR	DOM	157.880747	0.407673	387.273	43,536,716
IND04	NPL02	SPR	NEP	157.436513	0.457804	343.895	45,747,076

Table 1-6 The outgroup f_3 statistics result of autosome with SPR as outgroup. f_3 (DOM, X: SPR)

The outgroup f_3 statistics result of autosome with SPR as outgroup. f_3 (DOM, X; SPR)								
Source1	Source2	Target	Source2 mtDNA Haplogroup	f_3 statistics	Std.Err	Z	SNPs	
DEU01	DEU04	SPR	DOM	206.659053	0.432096	478.271	35,832,948	
DEU01	DEU03	SPR	DOM	206.503162	0.430884	479.255	35,841,723	
DEU01	DEU06	SPR	DOM	206.448170	0.426418	484.146	35,864,428	
DEU01	DEU07	SPR	DOM	206.371651	0.430922	478.907	36,167,594	
DEU01	DEU05	SPR	DOM	206.299431	0.455983	452.428	35,727,538	
DEU01	DEU02	SPR	DOM	206.295498	0.460603	447.881	36,069,263	
DEU01	FRA04	SPR	DOM	202.181080	0.434840	464.956	36,731,747	
DEU01	FRA03	SPR	DOM	202.141808	0.446287	452.941	36,727,640	
DEU01	FRA01	SPR	DOM	202.004700	0.436197	463.104	36,439,520	
DEU01	FRA02	SPR	DOM	201.959624	0.448131	450.671	36,723,292	
DEU01	IRN03	SPR	DOM	195.811149	0.429355	456.059	38,031,960	
DEU01	IRN04	SPR	DOM	195.708594	0.429941	455.199	38,047,320	
DEU01	IRN01	SPR	DOM	195.652792	0.428044	457.086	38,063,274	
DEU01	IRN02	SPR	DOM	195.515984	0.428813	455.947	38,058,512	
DEU01	CHN06	SPR	MUS	187.354329	0.785226	238.599	39,210,126	
DEU01	RUS01	SPR	DOM	182.787664	0.776460	235.411	40,200,464	
DEU01	RUS10	SPR	CAS	166.758340	0.532465	313.182	42,366,906	
DEU01	IDN02	SPR	CAS	166.641239	0.530049	314.389	39,954,691	
DEU01	RUS12	SPR	CAS	166.368286	0.507121	328.064	41,875,972	
DEU01	IDN01	SPR	DOM	166.181182	0.470143	353.470	41,639,382	
DEU01	UKR01	SPR	MUS	161.695593	0.418692	386.192	42,124,040	
DEU01	RUS15	SPR	MUS	161.640952	0.436173	370.589	41,678,462	
DEU01	JPN12	SPR	MUS	160.963066	0.462389	348.112	41,410,614	
DEU01	RUS13	SPR	DOM	160.902693	0.423278	380.135	41,954,625	
DEU01	CZE01	SPR	MUS	160.742904	0.391455	410.629	40,990,914	
DEU01	RUS14	SPR	CAS	160.704742	0.418722	383.798	41,106,687	
DEU01	RUS16	SPR	DOM	160.671185	0.421959	380.774	40,917,464	
DEU01	RUS17	SPR	MUS	160.667395	0.411806	390.153	41,383,966	
DEU01	CHN20	SPR	CAS	160.632571	0.394309	407.378	42,118,814	
DEU01	CZE05	SPR	MUS	160.611502	0.387331	414.662	41,105,126	
DEU01	CZE02	SPR	MUS	160.570869	0.380154	422.384	41,173,629	
DEU01	CZE06	SPR	MUS	160.557744	0.381064	421.341	40,898,252	
DEU01	CZE03	SPR	MUS	160.459684	0.380570	421.629	41,028,048	
DEU01	CZE07	SPR	MUS	160.434358	0.383339	418.519	41,196,430	
DEU01	CZE04	SPR	MUS	160.426439	0.376627	425.956	41,136,385	
DEU01	RUS04	SPR	DOM	160.377292	0.454565	352.815	40,403,696	
DEU01	CHN18	SPR	CAS	160.318048	0.402591	398.216	42,418,510	
DEU01	CHN15	SPR	MUS	160.239017	0.444951	360.127	41,292,186	
DEU01	EST01	SPR	MUS	160.146242	0.398360	402.014	40,800,222	
DEU01	RUS05	SPR	MUS	159.993917	0.417407	383.304	40,531,368	
DEU01	RUS11	SPR	MUS	159.909533	0.391013	408.962	41,493,657	
DEU01	TWN01	SPR	CAS	159.731385	0.413599	386.198	41,538,238	
DEU01	RUS06	SPR	MUS	159.730250	0.400556	398.771	40,468,781	

DEU01	CHN17	SPR	CAS	159.717054	0.395421	403.916	42,470,264
DEU01	IRN05	SPR	CAS	159.713846	0.377167	423.457	41,736,259
DEU01	CHN14	SPR	CAS	159.638501	0.400978	398.123	41,683,111
DEU01	RUS07	SPR	MUS	159.637271	0.388071	411.361	40,836,561
DEU01	CHN11	SPR	CAS	159.610175	0.405924	393.202	42,051,517
DEU01	CHN19	SPR	CAS	159.425762	0.394686	403.931	42,758,597
DEU01	CHN23	SPR	MUS	159.311268	0.385161	413.623	41,169,077
DEU01	IDN04	SPR	CAS	159.294726	0.399530	398.705	41,290,962
DEU01	CHN22	SPR	CAS	159.273400	0.391527	406.801	42,447,493
DEU01	VNM02	SPR	CAS	159.249227	0.407234	391.051	41,348,066
DEU01	CHN12	SPR	CAS	159.177240	0.401666	396.293	42,734,480
DEU01	CHN08	SPR	MUS	159.114139	0.419687	379.125	41,246,040
DEU01	VNM01	SPR	CAS	159.104252	0.395021	402.774	42,024,341
DEU01	CHN16	SPR	CAS	159.099801	0.388245	409.793	42,761,593
DEU01	IDN03	SPR	CAS	158.972369	0.394437	403.036	41,643,310
DEU01	KAZ01	SPR	MUS	158.949263	0.383276	414.713	41,337,198
DEU01	JPN01	SPR	MUS	158.873064	0.396782	400.404	42,400,001
DEU01	RUS02	SPR	MUS	158.857641	0.384307	413.362	41,633,056
DEU01	JPN09	SPR	MUS	158.826691	0.390885	406.325	41,140,863
DEU01	JPN16	SPR	CAS	158.813616	0.422345	376.028	40,364,830
DEU01	JPN17	SPR	CAS	158.787386	0.389218	407.966	41,666,264
DEU01	JPN15	SPR	CAS	158.780375	0.412140	385.258	40,427,670
DEU01	JPN05	SPR	MUS	158.770555	0.405893	391.163	41,346,398
DEU01	RUS09	SPR	MUS	158.767853	0.384923	412.466	41,398,929
DEU01	JPN02	SPR	MUS	158.753623	0.398881	397.998	41,291,341
DEU01	CHN07	SPR	MUS	158.746438	0.394209	402.696	41,203,847
DEU01	CHN21	SPR	CAS	158.744021	0.390589	406.422	41,832,181
DEU01	LKA01	SPR	CAS	158.717519	0.393159	403.698	41,985,204
DEU01	CHN02	SPR	MUS	158.697955	0.398383	398.355	41,004,348
DEU01	JPN04	SPR	MUS	158.693103	0.383531	413.769	41,842,345
DEU01	RUS08	SPR	MUS	158.690452	0.385424	411.730	41,265,849
DEU01	JPN08	SPR	MUS	158.660533	0.395527	401.137	40,701,833
DEU01	IRN06	SPR	MUS	158.635844	0.382839	414.366	41,834,403
DEU01	JPN07	SPR	MUS	158.600486	0.392626	403.948	41,556,636
DEU01	RUS03	SPR	MUS	158.599638	0.382042	415.136	41,100,484
DEU01	LKA02	SPR	CAS	158.579756	0.391764	404.784	41,945,111
DEU01	JPN18	SPR	CAS	158.562430	0.385619	411.189	41,282,260
DEU01	KAZ04	SPR	MUS	158.543763	0.384236	412.621	41,271,408
DEU01	KAZ03	SPR	MUS	158.532424	0.380162	417.013	41,633,898
DEU01	KAZ05	SPR	MUS	158.509148	0.384703	412.030	41,278,031
DEU01	CHN24	SPR	MUS	158.503242	0.382891	413.964	41,400,010
DEU01	JPN11	SPR	MUS	158.449025	0.388557	407.788	41,518,137
DEU01	JPN03	SPR	MUS	158.424945	0.386211	410.203	41,157,265
DEU01	JPN14	SPR	MUS	158.419439	0.384986	411.494	40,528,340
DEU01	KAZ02	SPR	MUS	158.418140	0.379361	417.592	41,645,063
DEU01	JPN06	SPR	MUS	158.403694	0.384531	411.939	40,744,928
DEU01	BGD01	SPR	CAS	158.369736	0.386042	410.239	43,398,639
DEU01	PAK03	SPR	CAS	158.344765	0.383851	412.517	44,183,136

DEU01	CHN13	SPR	MUS	158.344614	0.380014	416.680	41,032,175
DEU01	KOR04	SPR	MUS	158.340208	0.382071	414.426	40,898,876
DEU01	CHN04	SPR	MUS	158.335191	0.379996	416.676	41,660,382
DEU01	KOR05	SPR	MUS	158.328826	0.381874	414.611	40,830,825
DEU01	CHN03	SPR	MUS	158.328184	0.381854	414.630	41,135,745
DEU01	KOR02	SPR	MUS	158.327960	0.381181	415.361	40,793,148
DEU01	CHN09	SPR	MUS	158.326368	0.382720	413.688	41,349,946
DEU01	CHN01	SPR	MUS	158.321906	0.382780	413.611	41,103,829
DEU01	PAK02	SPR	CAS	158.319792	0.385234	410.971	44,173,827
DEU01	JPN10	SPR	MUS	158.315953	0.382701	413.681	40,653,079
DEU01	CHN10	SPR	MUS	158.308170	0.381756	414.684	40,413,678
DEU01	JPN13	SPR	CAS	158.302250	0.381713	414.715	40,513,544
DEU01	KOR01	SPR	MUS	158.293916	0.381910	414.480	40,710,525
DEU01	CHN05	SPR	MUS	158.286309	0.379755	416.812	41,596,914
DEU01	KOR03	SPR	MUS	158.277527	0.383790	412.407	40,778,748
DEU01	BGD02	SPR	CAS	158.265689	0.385555	410.488	41,523,029
DEU01	IND02	SPR	CAS	158.250108	0.384380	411.702	43,373,729
DEU01	IND09	SPR	CAS	158.249267	0.388962	406.850	42,478,447
DEU01	PAK04	SPR	CAS	158.239127	0.384541	411.502	44,199,582
DEU01	IND01	SPR	CAS	158.231489	0.390473	405.230	42,527,736
DEU01	IND05	SPR	CAS	158.227014	0.390317	405.380	41,150,368
DEU01	PAK01	SPR	CAS	158.198840	0.386787	409.007	44,230,689
DEU01	IND06	SPR	CAS	158.179569	0.389974	405.616	41,879,765
DEU01	IND07	SPR	CAS	158.120801	0.385720	409.937	43,994,392
DEU01	IND08	SPR	CAS	158.119912	0.386906	408.678	41,721,879
DEU01	IND03	SPR	CAS	158.012481	0.396034	398.987	43,101,451
DEU01	IND04	SPR	CAS	157.993716	0.395962	399.012	43,102,382
DEU01	NPL01	SPR	NEP	156.657170	0.409525	382.534	43,164,210
DEU01	NPL02	SPR	NEP	153.318253	0.426110	359.809	44,356,506

Table 1-7 The outgroup f_3 statistics result of autosome with SPR as outgroup. f_3 (MUS, X: SPR)

The outgroup f_3 statistics result of autosome with SPR as outgroup. f_3 (MUS, X: SPR)							
Source1	Source2	Target	Source2 mtDNA Haplogroup	f_3 statistics	Std.Err	Z	SNPs
KOR01	KOR03	SPR	MUS	216.804662	0.399407	542.816	34,661,172
KOR01	KOR05	SPR	MUS	216.580433	0.402285	538.376	34,715,893
KOR01	KOR02	SPR	MUS	216.474593	0.405523	533.815	34,709,913
KOR01	JPN10	SPR	MUS	215.616189	0.407820	528.704	34,734,511
KOR01	JPN14	SPR	MUS	215.364068	0.433413	496.903	34,695,846
KOR01	JPN13	SPR	CAS	215.228779	0.441086	487.951	34,688,755
KOR01	JPN08	SPR	MUS	214.552179	0.472519	454.060	34,913,792
KOR01	JPN06	SPR	MUS	214.449595	0.456808	469.452	34,925,710
KOR01	KOR04	SPR	MUS	213.320735	0.464264	459.482	35,123,629
KOR01	CHN13	SPR	MUS	211.574861	0.416056	508.525	35,434,064
KOR01	JPN03	SPR	MUS	211.529471	0.452317	467.657	35,500,658
KOR01	CHN10	SPR	MUS	211.014397	0.410983	513.439	35,056,202
KOR01	CHN24	SPR	MUS	210.744421	0.453567	464.638	35,793,776
KOR01	CHN09	SPR	MUS	210.449456	0.409835	513.498	35,774,768
KOR01	CHN07	SPR	MUS	210.430781	0.437960	480.479	35,715,673
KOR01	CHN08	SPR	MUS	210.074767	0.449029	467.842	35,821,184
KOR01	RUS08	SPR	MUS	209.431784	0.413909	505.985	35,858,269
KOR01	CHN15	SPR	MUS	209.345074	0.533697	392.254	36,042,481
KOR01	RUS09	SPR	MUS	209.282106	0.431416	485.105	35,974,652
KOR01	JPN05	SPR	MUS	208.383043	0.556026	374.772	36,010,764
KOR01	CHN01	SPR	MUS	207.964927	0.406535	511.555	35,882,052
KOR01	JPN02	SPR	MUS	207.937465	0.515163	403.634	36,005,597
KOR01	CHN02	SPR	MUS	207.639435	0.427918	485.232	35,876,258
KOR01	CHN03	SPR	MUS	207.632863	0.428941	484.059	35,944,252
KOR01	CHN05	SPR	MUS	207.253785	0.421932	491.202	36,316,568
KOR01	JPN09	SPR	MUS	206.941677	0.559767	369.693	36,007,927
KOR01	CHN04	SPR	MUS	206.753272	0.421524	490.489	36,423,273
KOR01	KAZ02	SPR	MUS	206.610926	0.403930	511.502	36,434,177
KOR01	KAZ04	SPR	MUS	206.501918	0.416814	495.430	36,177,821
KOR01	JPN16	SPR	CAS	206.347051	0.586132	352.049	35,503,164
KOR01	KAZ05	SPR	MUS	206.297635	0.429920	479.851	36,204,059
KOR01	JPN15	SPR	CAS	206.142125	0.582176	354.089	35,564,800
KOR01	KAZ03	SPR	MUS	206.140506	0.429548	479.901	36,493,257
KOR01	RUS03	SPR	MUS	205.843964	0.407223	505.482	36,117,943
KOR01	JPN11	SPR	MUS	205.681966	0.534841	384.567	36,377,236
KOR01	JPN07	SPR	MUS	205.479870	0.548312	374.750	36,434,327
KOR01	JPN18	SPR	CAS	205.087849	0.559539	366.530	36,267,627
KOR01	RUS02	SPR	MUS	205.041379	0.413644	495.695	36,640,215
KOR01	KAZ01	SPR	MUS	205.002188	0.417064	491.537	36,421,996
KOR01	CHN23	SPR	MUS	204.913054	0.435276	470.766	36,338,095
KOR01	RUS07	SPR	MUS	204.853351	0.434734	471.215	36,115,092
KOR01	RUS06	SPR	MUS	204.093397	0.450165	453.375	35,905,198
KOR01	RUS05	SPR	MUS	203.867951	0.457525	445.589	36,006,963

KOR01	EST01	SPR	MUS	203.761505	0.442060	460.936	36,246,337
KOR01	RUS04	SPR	DOM	203.519960	0.502741	404.821	35,968,826
KOR01	CZE07	SPR	MUS	203.502336	0.432024	471.044	36,627,159
KOR01	CZE04	SPR	MUS	203.466432	0.447885	454.282	36,580,135
KOR01	CZE02	SPR	MUS	203.425764	0.435386	467.231	36,628,449
KOR01	CZE06	SPR	MUS	203.387128	0.446551	455.462	36,406,037
KOR01	CZE05	SPR	MUS	203.161289	0.438510	463.299	36,605,406
KOR01	CZE03	SPR	MUS	203.116844	0.449835	451.537	36,534,412
KOR01	IRN06	SPR	MUS	202.998907	0.414551	489.683	36,988,430
KOR01	CZE01	SPR	MUS	202.932518	0.467088	434.463	36,554,490
KOR01	JPN12	SPR	MUS	202.822746	0.601602	337.138	36,838,087
KOR01	RUS11	SPR	MUS	202.595343	0.489693	413.719	36,882,293
KOR01	CHN21	SPR	CAS	201.822879	0.599252	336.792	37,047,331
KOR01	JPN17	SPR	CAS	201.706629	0.592979	340.158	36,918,918
KOR01	IRN05	SPR	CAS	201.158185	0.428841	469.074	37,216,166
KOR01	RUS17	SPR	MUS	200.612116	0.563715	355.875	37,084,340
KOR01	RUS16	SPR	DOM	200.183792	0.530816	377.125	36,727,333
KOR01	RUS14	SPR	CAS	198.400873	0.587497	337.706	37,073,739
KOR01	RUS15	SPR	MUS	198.172935	0.548180	361.511	37,677,762
KOR01	CHN20	SPR	CAS	198.094544	0.585314	338.441	37,868,204
KOR01	RUS13	SPR	DOM	197.720502	0.549025	360.130	37,835,353
KOR01	JPN04	SPR	MUS	192.885634	0.549953	350.731	37,901,139
KOR01	JPN01	SPR	MUS	191.479402	0.527727	362.838	38,520,819
KOR01	UKR01	SPR	MUS	191.133931	0.649186	294.421	38,724,563
KOR01	CHN16	SPR	CAS	187.712882	0.475206	395.014	39,254,198
KOR01	CHN19	SPR	CAS	180.141102	0.452585	398.027	40,101,030
KOR01	RUS01	SPR	DOM	179.416863	0.788365	227.581	40,532,865
KOR01	RUS12	SPR	CAS	177.968712	0.599913	296.658	40,429,511
KOR01	RUS10	SPR	CAS	177.951343	0.546713	325.493	40,921,213
KOR01	CHN06	SPR	MUS	176.625570	0.787466	224.296	40,191,163
KOR01	CHN11	SPR	CAS	175.551709	0.501894	349.779	40,020,627
KOR01	CHN12	SPR	CAS	174.756803	0.552213	316.467	40,675,665
KOR01	CHN14	SPR	CAS	171.090001	0.451319	379.089	40,244,591
KOR01	CHN22	SPR	CAS	171.063469	0.420737	406.581	40,867,961
KOR01	CHN17	SPR	CAS	168.946776	0.402685	419.551	41,217,922
KOR01	TWN01	SPR	CAS	167.413986	0.409165	409.160	40,531,967
KOR01	CHN18	SPR	CAS	167.401123	0.394298	424.555	41,431,140
KOR01	VNM02	SPR	CAS	163.589790	0.384053	425.956	40,745,073
KOR01	VNM01	SPR	CAS	163.564365	0.377641	433.121	41,384,704
KOR01	IDN01	SPR	DOM	162.161598	0.377082	430.043	42,106,736
KOR01	IDN02	SPR	CAS	161.792976	0.372366	434.500	40,369,114
KOR01	IDN03	SPR	CAS	161.732496	0.370757	436.222	41,241,030
KOR01	PAK03	SPR	CAS	161.719629	0.362326	446.338	43,650,799
KOR01	PAK04	SPR	CAS	161.666930	0.363321	444.970	43,664,420
KOR01	IDN04	SPR	CAS	161.633380	0.369212	437.779	40,938,224
KOR01	BGD02	SPR	CAS	161.595935	0.365075	442.638	41,047,018
KOR01	PAK02	SPR	CAS	161.574400	0.361777	446.613	43,658,551
KOR01	LKA01	SPR	CAS	161.556053	0.365267	442.296	41,564,042

KOR01	LKA02	SPR	CAS	161.554276	0.367122	440.057	41,506,233
KOR01	IND05	SPR	CAS	161.523585	0.370019	436.528	40,682,172
KOR01	IND02	SPR	CAS	161.522431	0.364885	442.667	42,871,632
KOR01	BGD01	SPR	CAS	161.511575	0.363142	444.761	42,912,837
KOR01	IND09	SPR	CAS	161.505283	0.367673	439.264	41,992,374
KOR01	PAK01	SPR	CAS	161.491488	0.359719	448.937	43,711,614
KOR01	IND06	SPR	CAS	161.466309	0.366319	440.781	41,405,331
KOR01	IND08	SPR	CAS	161.447792	0.365683	441.497	41,243,759
KOR01	IND01	SPR	CAS	161.441610	0.364969	442.343	42,048,413
KOR01	IND04	SPR	CAS	161.116092	0.373595	431.259	42,624,527
KOR01	IND07	SPR	CAS	161.090050	0.366364	439.700	43,517,885
KOR01	IND03	SPR	CAS	161.059219	0.371219	433.866	42,632,088
KOR01	NPL01	SPR	NEP	159.512390	0.402897	395.914	42,718,577
KOR01	IRN02	SPR	DOM	158.871025	0.371416	427.744	41,991,854
KOR01	IRN01	SPR	DOM	158.830326	0.371186	427.900	42,022,316
KOR01	IRN04	SPR	DOM	158.752798	0.370077	428.973	42,019,319
KOR01	IRN03	SPR	DOM	158.738335	0.371496	427.295	42,012,048
KOR01	DEU04	SPR	DOM	158.422654	0.382486	414.192	40,794,325
KOR01	DEU03	SPR	DOM	158.380240	0.382335	414.244	40,797,113
KOR01	DEU07	SPR	DOM	158.359855	0.381178	415.449	41,312,238
KOR01	DEU06	SPR	DOM	158.334888	0.382700	413.731	40,829,225
KOR01	FRA03	SPR	DOM	158.323509	0.384646	411.609	41,352,198
KOR01	FRA04	SPR	DOM	158.309363	0.382882	413.467	41,372,623
KOR01	DEU01	SPR	DOM	158.293916	0.381910	414.480	40,710,525
KOR01	DEU05	SPR	DOM	158.273643	0.385655	410.402	40,584,734
KOR01	FRA02	SPR	DOM	158.264514	0.390563	405.221	41,341,414
KOR01	FRA01	SPR	DOM	158.257380	0.379712	416.783	40,919,004
KOR01	DEU02	SPR	DOM	158.168431	0.396190	399.223	41,173,592
KOR01	NPL02	SPR	NEP	155.106123	0.427025	363.225	44,017,384

Table 1-8 The f_4 statistics result of autosome. f_4 (SPR, CAS; DOM, X)The f_4 statistics result of autosome. f_4 (SPR, CAS; DOM, X)

Pop1(W)	Pop2(X)	Pop3(Y)	Pop4(Z)	Pop4(Z) mtDNA Haplogroup	f_4 statistics	Standard Error	Z	BABA	ABBA	Number of SNPs that all population have data
SPR	IND04	DEU01	NPL02	NEP	-0.000557	0.000226	-2.469	1,880,597	1,936,781	100,832,598
SPR	IND04	DEU01	DEU02	DOM	-0.000113	0.000108	-1.050	327,853	339,244	100,832,598
SPR	IND04	DEU01	DEU05	DOM	-0.000055	0.000079	-0.695	328,795	334,360	100,832,598
SPR	IND04	DEU01	FRA01	DOM	-0.000031	0.000055	-0.562	420,122	423,234	100,832,598
SPR	IND04	DEU01	FRA02	DOM	-0.000053	0.000101	-0.527	421,727	427,105	100,832,598
SPR	IND04	DEU01	FRA03	DOM	0.000007	0.000069	0.104	418,566	417,840	100,832,598
SPR	IND04	DEU01	FRA04	DOM	0.000010	0.000062	0.164	417,194	416,166	100,832,598
SPR	IND04	DEU01	DEU07	DOM	0.000033	0.000057	0.574	329,958	326,637	100,832,598
SPR	IND04	DEU01	DEU06	DOM	0.000035	0.000041	0.858	328,137	324,571	100,832,598
SPR	IND04	DEU01	DEU03	DOM	0.000050	0.000039	1.299	328,252	323,163	100,832,598
SPR	IND04	DEU01	DEU04	DOM	0.000072	0.000036	1.995	325,626	318,359	100,832,598
SPR	IND04	DEU01	IRN01	DOM	0.000269	0.000081	3.315	580,395	553,278	100,832,598
SPR	IND04	DEU01	IRN04	DOM	0.000276	0.000079	3.473	579,542	551,723	100,832,598
SPR	IND04	DEU01	IRN03	DOM	0.000241	0.000068	3.545	574,486	550,155	100,832,598
SPR	IND04	DEU01	IRN02	DOM	0.000303	0.000078	3.875	586,477	555,942	100,832,598
SPR	IND04	DEU01	CHN06	MUS	0.001292	0.000091	14.265	952,288	822,010	100,832,598
SPR	IND04	DEU01	RUS01	DOM	0.001545	0.000101	15.284	1,091,349	935,549	100,832,598
SPR	IND04	DEU01	NPL01	NEP	0.004405	0.000200	21.994	2,078,359	1,634,213	100,832,598
SPR	IND04	DEU01	CHN05	MUS	0.003048	0.000117	26.084	1,914,155	1,606,824	100,832,598
SPR	IND04	DEU01	CHN04	MUS	0.003071	0.000118	26.089	1,914,002	1,604,304	100,832,598
SPR	IND04	DEU01	CHN23	MUS	0.002988	0.000114	26.140	1,879,200	1,577,921	100,832,598
SPR	IND04	DEU01	KAZ05	MUS	0.003072	0.000116	26.474	1,908,783	1,599,002	100,832,598
SPR	IND04	DEU01	CZE03	MUS	0.002905	0.000110	26.523	1,840,488	1,547,541	100,832,598
SPR	IND04	DEU01	RUS15	MUS	0.003155	0.000117	26.981	1,823,200	1,505,033	100,832,598
SPR	IND04	DEU01	RUS17	MUS	0.003081	0.000111	27.660	1,844,853	1,534,164	100,832,598
SPR	IND04	DEU01	CHN24	MUS	0.003041	0.000110	27.671	1,906,630	1,600,032	100,832,598
SPR	IND04	DEU01	KAZ03	MUS	0.003061	0.000110	27.951	1,906,829	1,598,148	100,832,598
SPR	IND04	DEU01	CHN01	MUS	0.003101	0.000110	28.141	1,914,744	1,602,111	100,832,598
SPR	IND04	DEU01	RUS04	DOM	0.003025	0.000107	28.158	1,849,278	1,544,288	100,832,598
SPR	IND04	DEU01	CZE01	MUS	0.002922	0.000103	28.300	1,836,192	1,541,518	100,832,598
SPR	IND04	DEU01	JPN10	MUS	0.003139	0.000111	28.396	1,918,024	1,601,506	100,832,598
SPR	IND04	DEU01	JPN13	CAS	0.003154	0.000111	28.445	1,919,796	1,601,775	100,832,598
SPR	IND04	DEU01	CHN03	MUS	0.003023	0.000106	28.479	1,910,474	1,605,695	100,832,598
SPR	IND04	DEU01	CZE01	MUS	0.002880	0.000101	28.502	1,830,520	1,540,095	100,832,598
SPR	IND04	DEU01	KOR01	MUS	0.003122	0.000109	28.518	1,917,648	1,602,811	100,832,598
SPR	IND04	DEU01	JPN14	MUS	0.003130	0.000110	28.537	1,914,344	1,598,716	100,832,598
SPR	IND04	DEU01	CHN02	MUS	0.003091	0.000108	28.545	1,902,698	1,591,063	100,832,598
SPR	IND04	DEU01	RUS03	MUS	0.003129	0.000109	28.660	1,908,636	1,593,156	100,832,598
SPR	IND04	DEU01	CZE06	MUS	0.002996	0.000104	28.846	1,841,961	1,539,820	100,832,598
SPR	IND04	DEU01	EST01	MUS	0.002901	0.000100	28.884	1,847,369	1,554,804	100,832,598
SPR	IND04	DEU01	JPN08	MUS	0.003190	0.000110	28.938	1,910,972	1,589,329	100,832,598
SPR	IND04	DEU01	RUS06	MUS	0.003074	0.000106	28.974	1,870,806	1,560,842	100,832,598
SPR	IND04	DEU01	KOR05	MUS	0.003129	0.000108	28.999	1,916,702	1,601,225	100,832,598
SPR	IND04	DEU01	JPN06	MUS	0.003262	0.000112	28.999	1,924,120	1,595,243	100,832,598
SPR	IND04	DEU01	RUS05	MUS	0.003069	0.000106	29.025	1,862,961	1,553,553	100,832,598
SPR	IND04	DEU01	KOR02	MUS	0.003125	0.000107	29.075	1,916,280	1,601,212	100,832,598
SPR	IND04	DEU01	KOR03	MUS	0.003129	0.000108	29.103	1,918,699	1,603,148	100,832,598
SPR	IND04	DEU01	RUS08	MUS	0.003083	0.000106	29.155	1,902,548	1,591,703	100,832,598
SPR	IND04	DEU01	KAZ02	MUS	0.003162	0.000108	29.157	1,916,271	1,597,486	100,832,598
SPR	IND04	DEU01	KAZ04	MUS	0.003142	0.000107	29.355	1,910,578	1,593,744	100,832,598
SPR	IND04	DEU01	CHN09	MUS	0.003109	0.000106	29.375	1,915,107	1,601,615	100,832,598
SPR	IND04	DEU01	JPN05	MUS	0.003498	0.000118	29.547	1,931,543	1,578,789	100,832,598
SPR	IND04	DEU01	RUS02	MUS	0.003157	0.000106	29.671	1,901,644	1,583,277	100,832,598
SPR	IND04	DEU01	CHN08	MUS	0.003071	0.000103	29.772	1,890,012	1,580,400	100,832,598
SPR	IND04	DEU01	CHN07	MUS	0.003120	0.000105	29.835	1,903,987	1,589,378	100,832,598
SPR	IND04	DEU01	RUS07	MUS	0.003057	0.000102	29.858	1,872,851	1,564,608	100,832,598
SPR	IND04	DEU01	IRN05	CAS	0.003218	0.000108	29.867	1,877,903	1,553,417	100,832,598
SPR	IND04	DEU01	CZE07	MUS	0.002938	0.000097	30.201	1,841,845	1,545,575	100,832,598
SPR	IND04	DEU01	KAZ01	MUS	0.003160	0.000104	30.256	1,899,239	1,580,602	100,832,598
SPR	IND04	DEU01	JPN09	MUS	0.003663	0.000120	30.440	1,939,525	1,570,164	100,832,598
SPR	IND04	DEU01	CZE02	MUS	0.003008	0.000099	30.509	1,842,788	1,539,445	100,832,598
SPR	IND04	DEU01	IRN06	MUS	0.003338	0.000109	30.527	1,920,173	1,583,561	100,832,598
SPR	IND04	DEU01	KOR04	MUS	0.003349	0.000109	30.632	1,931,491	1,593,822	100,832,598
SPR	IND04	DEU01	RUS16	DOM	0.003269	0.000106	30.720	1,857,096	1,527,511	100,832,598
SPR	IND04	DEU01	JPN11	MUS	0.003721	0.000121	30.741	1,955,644	1,580,456	100,832,598
SPR	IND04	DEU01	CHN15	MUS	0.002972	0.000096	30.987	1,850,363	1,550,713	100,832,598
SPR	IND04	DEU01	JPN03	MUS	0.003428	0.000110	31.278	1,934,135	1,588,517	100,832,598
SPR	IND04	DEU01	JPN16	CAS	0.003705	0.000118	31.372	1,942,294	1,568,692	100,832,598
SPR	IND04	DEU01	RUS14	CAS	0.003344	0.000106	31.432	1,860,562	1,523,336	100,832,598
SPR	IND04	DEU01	CHN10	MUS	0.003076	0.000098	31.527	1,913,713	1,603,557	100,832,598

SPR	IND04	DEU01	RUS09	MUS	0.003079	0.000098	31.545	1,899,891	1,589,424	100,832,598
SPR	IND04	DEU01	CHN20	CAS	0.003571	0.000113	31.572	1,879,451	1,519,329	100,832,598
SPR	IND04	DEU01	JPN15	CAS	0.003741	0.000117	32.024	1,945,643	1,568,406	100,832,598
SPR	IND04	DEU01	JPN07	MUS	0.003845	0.000119	32.374	1,958,725	1,571,058	100,832,598
SPR	IND04	DEU01	CHN13	MUS	0.003100	0.000096	32.400	1,913,837	1,601,275	100,832,598
SPR	IND04	DEU01	RUS11	MUS	0.003254	0.000100	32.449	1,877,757	1,549,693	100,832,598
SPR	IND04	DEU01	RUS13	DOM	0.003473	0.000106	32.796	1,864,263	1,514,081	100,832,598
SPR	IND04	DEU01	JPN02	MUS	0.003687	0.000112	33.040	1,941,563	1,569,789	100,832,598
SPR	IND04	DEU01	JPN12	MUS	0.003701	0.000111	33.237	1,879,860	1,506,728	100,832,598
SPR	IND04	DEU01	CHN21	CAS	0.003908	0.000115	34.106	1,957,999	1,563,909	100,832,598
SPR	IND04	DEU01	JPN18	CAS	0.003857	0.000113	34.127	1,959,451	1,570,496	100,832,598
SPR	IND04	DEU01	CZE04	MUS	0.002975	0.000086	34.421	1,844,833	1,544,816	100,832,598
SPR	IND04	DEU01	JPN17	CAS	0.004035	0.000115	35.149	1,964,887	1,558,058	100,832,598
SPR	IND04	DEU01	UKR01	MUS	0.003868	0.000106	36.517	1,868,729	1,478,676	100,832,598
SPR	IND04	DEU01	RUS12	CAS	0.004226	0.000116	36.542	1,755,169	1,329,038	100,832,598
SPR	IND04	DEU01	RUS10	CAS	0.004168	0.000112	37.221	1,741,238	1,320,948	100,832,598
SPR	IND04	DEU01	JPN04	MUS	0.004634	0.000117	39.694	2,010,719	1,543,414	100,832,598
SPR	IND04	DEU01	JPN01	MUS	0.004747	0.000114	41.793	2,012,346	1,533,743	100,832,598
SPR	IND04	DEU01	IDN02	CAS	0.005360	0.000117	45.657	1,831,562	1,291,150	100,832,598
SPR	IND04	DEU01	CHN14	CAS	0.005744	0.000126	45.764	2,059,443	1,480,292	100,832,598
SPR	IND04	DEU01	CHN11	CAS	0.005497	0.000119	46.147	2,044,115	1,489,871	100,832,598
SPR	IND04	DEU01	CHN16	CAS	0.004815	0.000102	47.011	2,010,572	1,525,114	100,832,598
SPR	IND04	DEU01	IDN01	DOM	0.005477	0.000116	47.235	1,849,864	1,297,590	100,832,598
SPR	IND04	DEU01	CHN12	CAS	0.005597	0.000118	47.332	2,062,919	1,498,596	100,832,598
SPR	IND04	DEU01	CHN18	CAS	0.005980	0.000121	49.473	2,054,090	1,451,073	100,832,598
SPR	IND04	DEU01	CHN17	CAS	0.005909	0.000116	51.114	2,068,612	1,472,836	100,832,598
SPR	IND04	DEU01	CHN22	CAS	0.005894	0.000111	53.062	2,080,360	1,486,091	100,832,598
SPR	IND04	DEU01	TWN01	CAS	0.006109	0.000114	53.472	2,080,578	1,464,627	100,832,598
SPR	IND04	DEU01	IND08	CAS	0.006580	0.000122	54.111	2,163,780	1,500,299	100,832,598
SPR	IND04	DEU01	CHN19	CAS	0.005256	0.000097	54.200	2,030,495	1,500,551	100,832,598
SPR	IND04	DEU01	VNM01	CAS	0.006466	0.000114	56.807	2,124,272	1,472,270	100,832,598
SPR	IND04	DEU01	VNM02	CAS	0.006452	0.000113	56.956	2,118,324	1,467,786	100,832,598
SPR	IND04	DEU01	PAK01	CAS	0.008353	0.000144	58.115	2,290,644	1,448,363	100,832,598
SPR	IND04	DEU01	LKA01	CAS	0.006677	0.000115	58.127	2,150,480	1,477,248	100,832,598
SPR	IND04	DEU01	BGD02	CAS	0.006803	0.000117	58.284	2,170,827	1,484,873	100,832,598
SPR	IND04	DEU01	IDN04	CAS	0.006582	0.000113	58.436	2,127,552	1,463,896	100,832,598
SPR	IND04	DEU01	IND06	CAS	0.006712	0.000114	58.852	2,169,042	1,492,209	100,832,598
SPR	IND04	DEU01	IND07	CAS	0.006658	0.000113	59.130	2,167,441	1,496,130	100,832,598
SPR	IND04	DEU01	LKA02	CAS	0.006722	0.000113	59.511	2,158,601	1,480,846	100,832,598
SPR	IND04	DEU01	IND09	CAS	0.006694	0.000112	59.647	2,164,424	1,489,478	100,832,598
SPR	IND04	DEU01	IND02	CAS	0.006860	0.000114	59.990	2,177,399	1,485,688	100,832,598
SPR	IND04	DEU01	IND01	CAS	0.006729	0.000111	60.657	2,168,935	1,490,395	100,832,598
SPR	IND04	DEU01	IND05	CAS	0.006755	0.000111	60.998	2,169,343	1,488,170	100,832,598
SPR	IND04	DEU01	IDN03	CAS	0.006586	0.000107	61.270	2,137,682	1,473,613	100,832,598
SPR	IND04	DEU01	PAK03	CAS	0.007011	0.000114	61.529	2,185,219	1,478,233	100,832,598
SPR	IND04	DEU01	BGD01	CAS	0.006706	0.000109	61.552	2,171,680	1,495,489	100,832,598
SPR	IND04	DEU01	PAK04	CAS	0.007263	0.000112	64.622	2,207,709	1,475,378	100,832,598
SPR	IND04	DEU01	PAK02	CAS	0.008121	0.000118	69.056	2,267,109	1,448,242	100,832,598
SPR	IND04	DEU01	IND03	CAS	0.024619	0.000269	91.683	3,498,971	1,016,621	100,832,598

Table 1-9 The f_4 statistics result of autosome. f_4 (SPR, CAS; MUS, X)The f_4 statistics result of autosome. f_4 (SPR, CAS; MUS, X)

Pop1(W)	Pop2(X)	Pop3(Y)	Pop4(Z)	Pop4(Z) mtDNA Haplogroup	f_4 statistics	Standard Error	Z	BABA	ABBA	Number of SNPs that all population have data
SPR	IND04	KOR01	IRN01	DOM	-0.002853	0.000072	-39.723	1,596,176	1,883,896	100,832,598
SPR	IND04	KOR01	IRN04	DOM	-0.002846	0.000072	-39.361	1,599,056	1,886,074	100,832,598
SPR	IND04	KOR01	IRN02	DOM	-0.002820	0.000074	-38.076	1,596,485	1,880,787	100,832,598
SPR	IND04	KOR01	IRN03	DOM	-0.002881	0.000076	-38.039	1,598,824	1,889,330	100,832,598
SPR	IND04	KOR01	DEU07	DOM	-0.003089	0.000091	-33.812	1,601,826	1,913,342	100,832,598
SPR	IND04	KOR01	DEU06	DOM	-0.003087	0.000098	-31.563	1,603,190	1,914,461	100,832,598
SPR	IND04	KOR01	DEU03	DOM	-0.003072	0.000101	-30.543	1,601,626	1,911,375	100,832,598
SPR	IND04	KOR01	FRA01	DOM	-0.003153	0.000104	-30.432	1,602,527	1,920,477	100,832,598
SPR	IND04	KOR01	DEU04	DOM	-0.003050	0.000101	-30.349	1,602,004	1,909,574	100,832,598
SPR	IND04	KOR01	FRA03	DOM	-0.003115	0.000105	-29.803	1,601,680	1,915,791	100,832,598
SPR	IND04	KOR01	DEU01	DOM	-0.003122	0.000109	-28.518	1,602,811	1,917,648	100,832,598
SPR	IND04	KOR01	DEU05	DOM	-0.003178	0.000116	-27.299	1,601,344	1,921,746	100,832,598
SPR	IND04	KOR01	FRA04	DOM	-0.003112	0.000116	-26.776	1,603,085	1,916,894	100,832,598
SPR	IND04	KOR01	FRA02	DOM	-0.003176	0.000123	-25.835	1,601,122	1,921,337	100,832,598
SPR	IND04	KOR01	DEU02	DOM	-0.003235	0.000130	-24.876	1,602,055	1,928,283	100,832,598
SPR	IND04	KOR01	RUS01	DOM	-0.001577	0.000068	-23.134	1,046,738	1,205,775	100,832,598
SPR	IND04	KOR01	CHN06	MUS	-0.001830	0.000083	-22.089	1,126,345	1,310,905	100,832,598
SPR	IND04	KOR01	NPL02	NEP	-0.003680	0.000213	-17.257	1,708,693	2,079,714	100,832,598
SPR	IND04	KOR01	CZE05	MUS	-0.000200	0.000047	-4.266	404,583	424,746	100,832,598
SPR	IND04	KOR01	CZE06	MUS	-0.000126	0.000030	-4.160	400,578	413,274	100,832,598
SPR	IND04	KOR01	CZE03	MUS	-0.000217	0.000053	-4.087	404,225	426,115	100,832,598
SPR	IND04	KOR01	CZE07	MUS	-0.000184	0.000052	-3.545	395,145	413,711	100,832,598
SPR	IND04	KOR01	CZE01	MUS	-0.000242	0.000073	-3.312	409,321	433,734	100,832,598
SPR	IND04	KOR01	CZE02	MUS	-0.000114	0.000036	-3.169	400,798	412,293	100,832,598
SPR	IND04	KOR01	CHN23	MUS	-0.000134	0.000048	-2.781	359,666	373,223	100,832,598
SPR	IND04	KOR01	EST01	MUS	-0.000221	0.000084	-2.637	385,568	407,841	100,832,598
SPR	IND04	KOR01	CHN15	MUS	-0.000151	0.000058	-2.601	264,584	279,771	100,832,598
SPR	IND04	KOR01	RUS04	DOM	-0.000098	0.000043	-2.294	397,950	407,797	100,832,598
SPR	IND04	KOR01	CZE04	MUS	-0.000147	0.000070	-2.110	397,836	412,656	100,832,598
SPR	IND04	KOR01	CHN03	MUS	-0.000100	0.000051	-1.967	289,448	299,506	100,832,598
SPR	IND04	KOR01	CHN08	MUS	-0.000052	0.000028	-1.823	248,055	253,280	100,832,598
SPR	IND04	KOR01	RUS07	MUS	-0.000065	0.000037	-1.773	364,511	371,105	100,832,598
SPR	IND04	KOR01	CHN05	MUS	-0.000074	0.000043	-1.733	298,899	306,405	100,832,598
SPR	IND04	KOR01	RUS08	MUS	-0.000040	0.000024	-1.671	256,212	260,205	100,832,598
SPR	IND04	KOR01	CHN24	MUS	-0.000082	0.000050	-1.649	230,721	238,960	100,832,598
SPR	IND04	KOR01	RUS05	MUS	-0.000054	0.000037	-1.464	390,229	395,657	100,832,598
SPR	IND04	KOR01	CHN02	MUS	-0.000032	0.000022	-1.413	291,745	294,948	100,832,598
SPR	IND04	KOR01	KAZ03	MUS	-0.000061	0.000045	-1.355	327,444	333,601	100,832,598
SPR	IND04	KOR01	RUS09	MUS	-0.000043	0.000033	-1.314	259,970	264,340	100,832,598
SPR	IND04	KOR01	RUS06	MUS	-0.000048	0.000039	-1.230	384,569	389,442	100,832,598
SPR	IND04	KOR01	CHN04	MUS	-0.000051	0.000045	-1.142	312,891	318,030	100,832,598
SPR	IND04	KOR01	KAZ05	MUS	-0.000050	0.000044	-1.142	323,776	328,831	100,832,598
SPR	IND04	KOR01	CHN10	MUS	-0.000046	0.000044	-1.051	216,959	221,640	100,832,598
SPR	IND04	KOR01	CHN01	MUS	-0.000022	0.000021	-1.041	283,202	285,407	100,832,598
SPR	IND04	KOR01	RUS17	MUS	-0.000041	0.000053	-0.777	493,606	497,755	100,832,598
SPR	IND04	KOR01	CHN09	MUS	-0.000013	0.000021	-0.648	230,573	231,919	100,832,598
SPR	IND04	KOR01	CHN13	MUS	-0.000023	0.000055	-0.411	205,630	207,906	100,832,598
SPR	IND04	KOR01	CHN07	MUS	-0.000002	0.000023	-0.098	239,910	240,139	100,832,598
SPR	IND04	KOR01	KOR02	MUS	0.000002	0.000016	0.145	116,749	116,518	100,832,598
SPR	IND04	KOR01	RUS03	MUS	0.000006	0.000032	0.200	337,241	336,597	100,832,598
SPR	IND04	KOR01	JPN14	MUS	0.000008	0.000020	0.402	141,895	141,104	100,832,598
SPR	IND04	KOR01	KOR05	MUS	0.000006	0.000013	0.476	113,898	113,258	100,832,598
SPR	IND04	KOR01	KOR03	MUS	0.000007	0.000015	0.486	108,310	107,598	100,832,598
SPR	IND04	KOR01	RUS15	MUS	0.000033	0.000060	0.550	573,776	570,446	100,832,598
SPR	IND04	KOR01	KAZ04	MUS	0.000020	0.000022	0.899	320,601	318,604	100,832,598
SPR	IND04	KOR01	JPN10	MUS	0.000017	0.000018	0.945	134,898	133,218	100,832,598
SPR	IND04	KOR01	RUS02	MUS	0.000035	0.000028	1.265	359,059	355,529	100,832,598
SPR	IND04	KOR01	KAZ01	MUS	0.000038	0.000029	1.313	361,195	357,395	100,832,598
SPR	IND04	KOR01	KAZ02	MUS	0.000039	0.000026	1.519	319,792	315,844	100,832,598
SPR	IND04	KOR01	JPN13	CAS	0.000032	0.000019	1.694	147,124	143,940	100,832,598
SPR	IND04	KOR01	JPN08	MUS	0.000067	0.000038	1.769	169,005	162,199	100,832,598
SPR	IND04	KOR01	RUS11	MUS	0.000131	0.000051	2.576	448,089	434,863	100,832,598
SPR	IND04	KOR01	RUS16	DOM	0.000146	0.000045	3.233	520,699	505,952	100,832,598
SPR	IND04	KOR01	IRN05	CAS	0.000096	0.000027	3.533	468,502	458,853	100,832,598
SPR	IND04	KOR01	RUS14	CAS	0.000222	0.000050	4.401	582,007	559,618	100,832,598
SPR	IND04	KOR01	JPN06	MUS	0.000139	0.000025	5.566	175,907	161,867	100,832,598
SPR	IND04	KOR01	IRN06	MUS	0.000216	0.000036	5.965	424,571	402,797	100,832,598
SPR	IND04	KOR01	JPN05	MUS	0.000376	0.000055	6.825	367,951	330,034	100,832,598
SPR	IND04	KOR01	NPL01	NEP	0.001282	0.000181	7.089	1,859,531	1,730,223	100,832,598
SPR	IND04	KOR01	RUS13	DOM	0.000351	0.000049	7.162	612,098	576,753	100,832,598

SPR	IND04	KOR01	KOR04	MUS	0.000226	0.000026	8.738	219,524	196,692	100,832,598
SPR	IND04	KOR01	CHN20	CAS	0.000449	0.000050	8.908	619,537	574,252	100,832,598
SPR	IND04	KOR01	JPN11	MUS	0.000599	0.000057	10.440	460,240	399,889	100,832,598
SPR	IND04	KOR01	JPN03	MUS	0.000305	0.000028	10.831	270,555	239,774	100,832,598
SPR	IND04	KOR01	JPN02	MUS	0.000565	0.000050	11.397	391,778	334,842	100,832,598
SPR	IND04	KOR01	UKR01	MUS	0.000746	0.000062	12.006	840,120	764,905	100,832,598
SPR	IND04	KOR01	JPN09	MUS	0.000541	0.000045	12.093	420,029	365,505	100,832,598
SPR	IND04	KOR01	JPN16	CAS	0.000583	0.000047	12.479	439,126	380,361	100,832,598
SPR	IND04	KOR01	JPN12	MUS	0.000578	0.000046	12.580	539,499	481,205	100,832,598
SPR	IND04	KOR01	JPN15	CAS	0.000619	0.000047	13.225	446,679	384,279	100,832,598
SPR	IND04	KOR01	RUS12	CAS	0.001104	0.000083	13.337	1,267,967	1,156,673	100,832,598
SPR	IND04	KOR01	RUS10	CAS	0.001046	0.000074	14.083	1,261,808	1,156,355	100,832,598
SPR	IND04	KOR01	JPN18	CAS	0.000735	0.000051	14.344	485,280	411,161	100,832,598
SPR	IND04	KOR01	CHN21	CAS	0.000786	0.000051	15.482	560,139	480,886	100,832,598
SPR	IND04	KOR01	JPN07	MUS	0.000722	0.000046	15.602	472,514	399,684	100,832,598
SPR	IND04	KOR01	JPN17	CAS	0.000912	0.000051	17.774	592,871	500,880	100,832,598
SPR	IND04	KOR01	IDN02	CAS	0.002237	0.000102	22.036	1,839,256	1,613,681	100,832,598
SPR	IND04	KOR01	JPN01	MUS	0.001624	0.000064	25.425	934,751	770,985	100,832,598
SPR	IND04	KOR01	JPN04	MUS	0.001512	0.000059	25.647	887,851	735,383	100,832,598
SPR	IND04	KOR01	IDN01	DOM	0.002355	0.000091	25.833	1,832,839	1,595,402	100,832,598
SPR	IND04	KOR01	CHN11	CAS	0.002374	0.000090	26.291	1,440,693	1,201,286	100,832,598
SPR	IND04	KOR01	CHN16	CAS	0.001692	0.000061	27.832	1,032,862	862,241	100,832,598
SPR	IND04	KOR01	CHN19	CAS	0.002133	0.000076	28.150	1,287,559	1,072,453	100,832,598
SPR	IND04	KOR01	CHN14	CAS	0.002621	0.000088	29.627	1,586,847	1,322,534	100,832,598
SPR	IND04	KOR01	CHN12	CAS	0.002474	0.000082	29.997	1,468,688	1,219,203	100,832,598
SPR	IND04	KOR01	CHN17	CAS	0.002786	0.000092	30.205	1,661,613	1,380,675	100,832,598
SPR	IND04	KOR01	CHN18	CAS	0.002858	0.000089	32.266	1,710,734	1,422,554	100,832,598
SPR	IND04	KOR01	CHN22	CAS	0.002771	0.000075	36.966	1,595,978	1,316,547	100,832,598
SPR	IND04	KOR01	TWN01	CAS	0.002986	0.000078	38.231	1,716,531	1,415,417	100,832,598
SPR	IND04	KOR01	IND08	CAS	0.003458	0.000090	38.611	1,926,326	1,577,683	100,832,598
SPR	IND04	KOR01	IDN04	CAS	0.003459	0.000084	41.187	1,919,904	1,571,085	100,832,598
SPR	IND04	KOR01	VNM01	CAS	0.003344	0.000081	41.266	1,854,998	1,517,833	100,832,598
SPR	IND04	KOR01	VNM02	CAS	0.003329	0.000079	42.140	1,852,257	1,516,556	100,832,598
SPR	IND04	KOR01	IDN03	CAS	0.003463	0.000082	42.468	1,917,367	1,568,136	100,832,598
SPR	IND04	KOR01	PAK01	CAS	0.005231	0.000120	43.531	2,051,339	1,523,895	100,832,598
SPR	IND04	KOR01	LKA02	CAS	0.003599	0.000082	43.680	1,930,670	1,567,752	100,832,598
SPR	IND04	KOR01	LKA01	CAS	0.003554	0.000078	45.483	1,927,044	1,568,650	100,832,598
SPR	IND04	KOR01	IND09	CAS	0.003571	0.000078	45.977	1,930,530	1,570,422	100,832,598
SPR	IND04	KOR01	IND05	CAS	0.003633	0.000079	46.200	1,932,412	1,566,077	100,832,598
SPR	IND04	KOR01	IND06	CAS	0.003590	0.000077	46.517	1,932,792	1,570,797	100,832,598
SPR	IND04	KOR01	BGD02	CAS	0.003681	0.000078	47.176	1,932,457	1,561,340	100,832,598
SPR	IND04	KOR01	IND07	CAS	0.003535	0.000075	47.344	1,943,508	1,587,034	100,832,598
SPR	IND04	KOR01	IND01	CAS	0.003607	0.000076	47.497	1,935,849	1,572,146	100,832,598
SPR	IND04	KOR01	BGD01	CAS	0.003584	0.000075	47.926	1,941,514	1,580,160	100,832,598
SPR	IND04	KOR01	IND02	CAS	0.003738	0.000077	48.628	1,941,110	1,564,236	100,832,598
SPR	IND04	KOR01	PAK03	CAS	0.003889	0.000076	51.085	1,945,790	1,553,641	100,832,598
SPR	IND04	KOR01	PAK04	CAS	0.004140	0.000076	54.766	1,966,026	1,548,533	100,832,598
SPR	IND04	KOR01	PAK02	CAS	0.004999	0.000083	60.170	2,030,210	1,526,181	100,832,598
SPR	IND04	KOR01	IND03	CAS	0.021496	0.000258	83.461	3,244,535	1,077,023	100,832,598

Table 1-10 The f_4 statistics result of autosome. f_4 (SPR, DOM; CAS, X)The f_4 statistics result of autosome. f_4 (SPR, DOM; CAS, X)

Pop1(W)	Pop2(X)	Pop3(Y)	Pop4(Z)	Pop4(Z) mtDNA Haplogroup	f_4 statistics	Standard Error	Z	BABA	ABBA	Number of SNPs that all population have data
SPR	DEU01	IND04	NPL02	NEP	-0.004675	0.00016	-29.263	1,465,342	1,936,781	100,832,598
SPR	DEU01	IND04	NPL01	NEP	-0.001337	0.00019	-7.236	1,499,446	1,634,213	100,832,598
SPR	DEU01	IND04	IND03	CAS	0.000019	0.00003	0.583	1,018,514	1,016,621	100,832,598
SPR	DEU01	IND04	IND08	CAS	0.000126	0.00015	0.872	1,513,024	1,500,299	100,832,598
SPR	DEU01	IND04	IND07	CAS	0.000127	0.00013	0.949	1,508,945	1,496,130	100,832,598
SPR	DEU01	IND04	IND06	CAS	0.000186	0.00014	1.309	1,510,949	1,492,209	100,832,598
SPR	DEU01	IND04	IND05	CAS	0.000233	0.00015	1.592	1,511,694	1,488,170	100,832,598
SPR	DEU01	IND04	IND01	CAS	0.000238	0.00015	1.613	1,514,370	1,490,395	100,832,598
SPR	DEU01	IND04	PAK04	CAS	0.000245	0.00014	1.738	1,500,123	1,475,378	100,832,598
SPR	DEU01	IND04	IND09	CAS	0.000256	0.00014	1.807	1,515,246	1,489,478	100,832,598
SPR	DEU01	IND04	IND02	CAS	0.000256	0.00014	1.827	1,511,541	1,485,688	100,832,598
SPR	DEU01	IND04	KOR03	MUS	0.000284	0.00015	1.895	1,631,766	1,603,148	100,832,598
SPR	DEU01	IND04	BGD02	CAS	0.000272	0.00014	1.902	1,512,296	1,484,873	100,832,598
SPR	DEU01	IND04	CHN05	MUS	0.000293	0.00015	1.931	1,636,327	1,606,824	100,832,598
SPR	DEU01	IND04	KOR01	MUS	0.000300	0.00015	2.003	1,633,081	1,602,811	100,832,598
SPR	DEU01	IND04	JPN13	CAS	0.000309	0.00015	2.043	1,632,885	1,601,775	100,832,598
SPR	DEU01	IND04	CHN10	MUS	0.000314	0.00015	2.058	1,635,264	1,603,557	100,832,598
SPR	DEU01	IND04	CHN03	MUS	0.000334	0.00016	2.086	1,639,421	1,605,695	100,832,598
SPR	DEU01	IND04	JPN10	MUS	0.000322	0.00015	2.136	1,633,998	1,601,506	100,832,598
SPR	DEU01	IND04	CHN01	MUS	0.000328	0.00015	2.166	1,635,203	1,602,111	100,832,598
SPR	DEU01	IND04	KOR05	MUS	0.000335	0.00015	2.197	1,635,015	1,601,225	100,832,598
SPR	DEU01	IND04	KOR02	MUS	0.000334	0.00015	2.204	1,634,914	1,601,212	100,832,598
SPR	DEU01	IND04	CHN09	MUS	0.000333	0.00015	2.220	1,635,157	1,601,615	100,832,598
SPR	DEU01	IND04	CHN04	MUS	0.000341	0.00015	2.238	1,638,736	1,604,304	100,832,598
SPR	DEU01	IND04	CHN13	MUS	0.000351	0.00016	2.265	1,636,657	1,601,275	100,832,598
SPR	DEU01	IND04	KOR04	MUS	0.000346	0.00015	2.299	1,628,760	1,593,822	100,832,598
SPR	DEU01	IND04	PAK02	CAS	0.000326	0.00014	2.328	1,481,122	1,448,242	100,832,598
SPR	DEU01	IND04	PAK03	CAS	0.000351	0.00014	2.496	1,513,630	1,478,233	100,832,598
SPR	DEU01	IND04	JPN14	MUS	0.000426	0.00017	2.563	1,641,642	1,598,716	100,832,598
SPR	DEU01	IND04	JPN06	MUS	0.000410	0.00016	2.592	1,636,582	1,595,243	100,832,598
SPR	DEU01	IND04	PAK01	CAS	0.000205	0.00008	2.616	1,469,046	1,448,363	100,832,598
SPR	DEU01	IND04	BGD01	CAS	0.000376	0.00014	2.647	1,533,404	1,495,489	100,832,598
SPR	DEU01	IND04	JPN03	MUS	0.000431	0.00015	2.796	1,631,998	1,588,517	100,832,598
SPR	DEU01	IND04	KAZ02	MUS	0.000424	0.00015	2.812	1,640,281	1,597,486	100,832,598
SPR	DEU01	IND04	JPN11	MUS	0.000455	0.00016	2.855	1,626,366	1,580,456	100,832,598
SPR	DEU01	IND04	KAZ05	MUS	0.000515	0.00016	3.183	1,650,974	1,599,002	100,832,598
SPR	DEU01	IND04	CHN24	MUS	0.000510	0.00016	3.233	1,651,408	1,600,032	100,832,598
SPR	DEU01	IND04	KAZ03	MUS	0.000539	0.00016	3.331	1,652,468	1,598,148	100,832,598
SPR	DEU01	IND04	JPN08	MUS	0.000667	0.00020	3.418	1,656,566	1,589,329	100,832,598
SPR	DEU01	IND04	KAZ04	MUS	0.000550	0.00016	3.457	1,649,206	1,593,744	100,832,598
SPR	DEU01	IND04	JPN18	CAS	0.000569	0.00016	3.640	1,627,841	1,570,496	100,832,598
SPR	DEU01	IND04	JPN16	CAS	0.000820	0.00022	3.702	1,651,365	1,568,692	100,832,598
SPR	DEU01	IND04	JPN07	MUS	0.000607	0.00016	3.732	1,632,240	1,571,058	100,832,598
SPR	DEU01	IND04	CHN02	MUS	0.000704	0.00019	3.740	1,662,073	1,591,063	100,832,598
SPR	DEU01	IND04	JPN15	CAS	0.000787	0.00021	3.832	1,647,727	1,568,406	100,832,598
SPR	DEU01	IND04	LKA02	CAS	0.000586	0.00015	3.854	1,539,937	1,480,846	100,832,598
SPR	DEU01	IND04	RUS03	MUS	0.000606	0.00015	3.975	1,654,252	1,593,156	100,832,598
SPR	DEU01	IND04	JPN05	MUS	0.000777	0.00020	3.977	1,657,119	1,578,789	100,832,598
SPR	DEU01	IND04	CHN07	MUS	0.000753	0.00018	4.112	1,665,277	1,589,378	100,832,598
SPR	DEU01	IND04	CHN21	CAS	0.000750	0.00018	4.297	1,639,565	1,563,909	100,832,598
SPR	DEU01	IND04	IRN06	MUS	0.000642	0.00015	4.311	1,648,309	1,583,561	100,832,598
SPR	DEU01	IND04	JPN02	MUS	0.000760	0.00018	4.327	1,646,413	1,569,789	100,832,598
SPR	DEU01	IND04	JPN04	MUS	0.000699	0.00016	4.472	1,613,935	1,543,414	100,832,598
SPR	DEU01	IND04	RUS08	MUS	0.000697	0.00016	4.484	1,661,957	1,591,703	100,832,598
SPR	DEU01	IND04	LKA01	CAS	0.000724	0.00016	4.567	1,550,231	1,477,248	100,832,598
SPR	DEU01	IND04	JPN09	MUS	0.000833	0.00017	4.817	1,654,155	1,570,164	100,832,598
SPR	DEU01	IND04	RUS09	MUS	0.000774	0.00016	4.819	1,667,482	1,589,424	100,832,598
SPR	DEU01	IND04	JPN17	CAS	0.000794	0.00016	4.838	1,638,086	1,558,058	100,832,598
SPR	DEU01	IND04	CHN08	MUS	0.001120	0.00022	5.104	1,693,375	1,580,400	100,832,598
SPR	DEU01	IND04	JPN01	MUS	0.000879	0.00016	5.404	1,622,409	1,533,743	100,832,598
SPR	DEU01	IND04	RUS02	MUS	0.000864	0.00016	5.590	1,670,388	1,583,277	100,832,598
SPR	DEU01	IND04	IDN03	CAS	0.000979	0.00017	5.623	1,572,293	1,473,613	100,832,598
SPR	DEU01	IND04	KAZ01	MUS	0.000956	0.00016	5.968	1,676,953	1,580,602	100,832,598
SPR	DEU01	IND04	CHN16	CAS	0.001106	0.00018	6.286	1,636,643	1,525,114	100,832,598
SPR	DEU01	IND04	IDN04	CAS	0.001301	0.00020	6.401	1,595,080	1,463,896	100,832,598
SPR	DEU01	IND04	VNM01	CAS	0.001111	0.00016	6.827	1,584,248	1,472,270	100,832,598
SPR	DEU01	IND04	CHN12	CAS	0.001184	0.00017	6.886	1,617,934	1,498,596	100,832,598
SPR	DEU01	IND04	VNM02	CAS	0.001256	0.00017	7.205	1,594,382	1,467,786	100,832,598
SPR	DEU01	IND04	CHN22	CAS	0.001280	0.00017	7.401	1,615,125	1,486,091	100,832,598
SPR	DEU01	IND04	CHN19	CAS	0.001432	0.00019	7.408	1,644,948	1,500,551	100,832,598
SPR	DEU01	IND04	CHN15	MUS	0.002245	0.00030	7.477	1,777,113	1,550,713	100,832,598

SPR	DEU01	IND04	CHN23	MUS	0.001318	0.00017	7.872	1,710,773	1,577,921	100,832,598
SPR	DEU01	IND04	RUS05	MUS	0.002000	0.00025	7.923	1,755,238	1,553,553	100,832,598
SPR	DEU01	IND04	RUS04	DOM	0.002384	0.00030	7.974	1,784,631	1,544,288	100,832,598
SPR	DEU01	IND04	TWN01	CAS	0.001738	0.00021	8.304	1,639,841	1,464,627	100,832,598
SPR	DEU01	IND04	RUS06	MUS	0.001737	0.00021	8.469	1,735,941	1,560,842	100,832,598
SPR	DEU01	IND04	CHN11	CAS	0.001616	0.00018	8.773	1,652,863	1,489,871	100,832,598
SPR	DEU01	IND04	CHN14	CAS	0.001645	0.00018	9.010	1,646,140	1,480,292	100,832,598
SPR	DEU01	IND04	RUS07	MUS	0.001644	0.00018	9.185	1,730,332	1,564,608	100,832,598
SPR	DEU01	IND04	CHN17	CAS	0.001723	0.00018	9.824	1,646,605	1,472,836	100,832,598
SPR	DEU01	IND04	RUS11	MUS	0.001916	0.00019	10.041	1,742,870	1,549,693	100,832,598
SPR	DEU01	IND04	RUS16	DOM	0.002677	0.00026	10.299	1,797,487	1,527,511	100,832,598
SPR	DEU01	IND04	RUS14	CAS	0.002711	0.00025	10.674	1,796,695	1,523,336	100,832,598
SPR	DEU01	IND04	JPN12	MUS	0.002969	0.00027	10.938	1,806,135	1,506,728	100,832,598
SPR	DEU01	IND04	RUS17	MUS	0.002674	0.00024	10.983	1,803,758	1,534,164	100,832,598
SPR	DEU01	IND04	IRN05	CAS	0.001720	0.00016	11.012	1,726,862	1,553,417	100,832,598
SPR	DEU01	IND04	EST01	MUS	0.002153	0.00019	11.228	1,771,849	1,554,804	100,832,598
SPR	DEU01	IND04	CHN18	CAS	0.002324	0.00020	11.486	1,685,442	1,451,073	100,832,598
SPR	DEU01	IND04	CHN20	CAS	0.002639	0.00022	12.039	1,785,412	1,519,329	100,832,598
SPR	DEU01	IND04	CZE01	MUS	0.002749	0.00022	12.260	1,817,303	1,540,095	100,832,598
SPR	DEU01	IND04	RUS13	DOM	0.002909	0.00024	12.299	1,807,400	1,514,081	100,832,598
SPR	DEU01	IND04	CZE04	MUS	0.002433	0.00019	13.118	1,790,114	1,544,816	100,832,598
SPR	DEU01	IND04	RUS15	MUS	0.003647	0.00028	13.240	1,872,793	1,505,033	100,832,598
SPR	DEU01	IND04	CZE03	MUS	0.002466	0.00019	13.331	1,796,191	1,547,541	100,832,598
SPR	DEU01	IND04	UKR01	MUS	0.003702	0.00027	13.592	1,851,946	1,478,676	100,832,598
SPR	DEU01	IND04	CZE06	MUS	0.002564	0.00019	13.637	1,798,357	1,539,820	100,832,598
SPR	DEU01	IND04	CZE07	MUS	0.002441	0.00018	13.767	1,791,671	1,545,575	100,832,598
SPR	DEU01	IND04	CZE02	MUS	0.002577	0.00018	14.001	1,799,307	1,539,445	100,832,598
SPR	DEU01	IND04	CZE05	MUS	0.002618	0.00019	14.035	1,805,476	1,541,518	100,832,598
SPR	DEU01	IND04	IDN02	CAS	0.008648	0.00041	20.917	2,163,102	1,291,150	100,832,598
SPR	DEU01	IND04	RUS12	CAS	0.008375	0.00039	21.351	2,173,468	1,329,038	100,832,598
SPR	DEU01	IND04	RUS10	CAS	0.008765	0.00040	22.008	2,204,708	1,320,948	100,832,598
SPR	DEU01	IND04	IDN01	DOM	0.008187	0.00033	24.594	2,123,153	1,297,590	100,832,598
SPR	DEU01	IND04	RUS01	DOM	0.024794	0.00068	36.535	3,435,587	935,549	100,832,598
SPR	DEU01	IND04	CHN06	MUS	0.029361	0.00069	42.657	3,782,517	822,010	100,832,598
SPR	DEU01	IND04	IRN02	DOM	0.037522	0.00018	100.000	4,339,409	555,942	100,832,598
SPR	DEU01	IND04	IRN01	DOM	0.037659	0.00018	100.000	4,350,540	553,278	100,832,598
SPR	DEU01	IND04	IRN04	DOM	0.037715	0.00019	100.000	4,354,612	551,723	100,832,598
SPR	DEU01	IND04	IRN03	DOM	0.037817	0.00019	100.000	4,363,385	550,155	100,832,598
SPR	DEU01	IND04	FRA02	DOM	0.043966	0.00023	100.000	4,860,301	427,105	100,832,598
SPR	DEU01	IND04	FRA01	DOM	0.044011	0.00024	100.000	4,860,976	423,234	100,832,598
SPR	DEU01	IND04	FRA03	DOM	0.044148	0.00022	100.000	4,869,407	417,840	100,832,598
SPR	DEU01	IND04	FRA04	DOM	0.044187	0.00022	100.000	4,871,693	416,166	100,832,598
SPR	DEU01	IND04	DEU02	DOM	0.048302	0.00025	100.000	5,209,638	339,244	100,832,598
SPR	DEU01	IND04	DEU05	DOM	0.048306	0.00026	100.000	5,205,150	334,360	100,832,598
SPR	DEU01	IND04	DEU07	DOM	0.048378	0.00022	100.000	5,204,710	326,637	100,832,598
SPR	DEU01	IND04	DEU06	DOM	0.048454	0.00022	100.000	5,210,359	324,571	100,832,598
SPR	DEU01	IND04	DEU03	DOM	0.048509	0.00022	100.000	5,214,497	323,163	100,832,598
SPR	DEU01	IND04	DEU04	DOM	0.048665	0.00022	100.000	5,225,412	318,359	100,832,598

Table 1-11 The f_4 statistics result of autosome. f_4 (SPR, DOM; MUS, X)The f_4 statistics result of autosome. f_4 (SPR, DOM; MUS, X)

Pop1(W)	Pop2(X)	Pop3(Y)	Pop4(Z)	Pop4(Z) mtDNA Haplogroup	f_4 statistics	Standard Error	Z	BABA	ABBA	Number of SNPs that all population have data
SPR	DEU01	KOR01	NPL02	NEP	-0.004976	0.00016	-31.146	1,533,683	2,035,392	100,832,598
SPR	DEU01	KOR01	NPL01	NEP	-0.001637	0.000131	-12.521	1,579,748	1,744,785	100,832,598
SPR	DEU01	KOR01	IND07	CAS	-0.000173	0.000063	-2.73	1,608,640	1,626,095	100,832,598
SPR	DEU01	KOR01	IND08	CAS	-0.000174	0.000074	-2.363	1,598,507	1,616,052	100,832,598
SPR	DEU01	KOR01	IND04	CAS	-0.0003	0.00015	-2.003	1,602,811	1,633,081	100,832,598
SPR	DEU01	KOR01	IND03	CAS	-0.000281	0.00015	-1.877	1,605,662	1,634,040	100,832,598
SPR	DEU01	KOR01	IND06	CAS	-0.000114	0.000069	-1.652	1,600,651	1,612,181	100,832,598
SPR	DEU01	KOR01	PAK01	CAS	-0.000095	0.000095	-1.005	1,602,379	1,611,966	100,832,598
SPR	DEU01	KOR01	IND01	CAS	-0.000062	0.000069	-0.898	1,604,627	1,610,922	100,832,598
SPR	DEU01	KOR01	PAK04	CAS	-0.000055	0.000063	-0.874	1,597,623	1,603,148	100,832,598
SPR	DEU01	KOR01	IND05	CAS	-0.000067	0.000079	-0.849	1,601,502	1,608,248	100,832,598
SPR	DEU01	KOR01	KOR03	MUS	-0.000016	0.00002	-0.823	104,318	105,970	100,832,598
SPR	DEU01	KOR01	IND02	CAS	-0.000044	0.000064	-0.69	1,603,245	1,607,662	100,832,598
SPR	DEU01	KOR01	IND09	CAS	-0.000045	0.000068	-0.661	1,603,396	1,607,898	100,832,598
SPR	DEU01	KOR01	BGD02	CAS	-0.000028	0.000068	-0.417	1,600,643	1,603,490	100,832,598
SPR	DEU01	KOR01	CHN05	MUS	-0.000008	0.00004	-0.19	297,265	298,032	100,832,598
SPR	DEU01	KOR01	CHN10	MUS	0.000014	0.000039	0.37	215,582	214,145	100,832,598
SPR	DEU01	KOR01	JPN13	CAS	0.000008	0.000022	0.374	141,987	141,147	100,832,598
SPR	DEU01	KOR01	PAK02	CAS	0.000026	0.000064	0.404	1,605,518	1,602,909	100,832,598
SPR	DEU01	KOR01	CHN03	MUS	0.000034	0.000062	0.557	292,234	288,779	100,832,598
SPR	DEU01	KOR01	PAK03	CAS	0.000051	0.000062	0.818	1,602,841	1,597,714	100,832,598
SPR	DEU01	KOR01	CHN04	MUS	0.000041	0.00004	1.024	313,463	309,301	100,832,598
SPR	DEU01	KOR01	JPN10	MUS	0.000022	0.00002	1.093	131,709	129,486	100,832,598
SPR	DEU01	KOR01	BGD01	CAS	0.000076	0.000069	1.1	1,620,202	1,612,557	100,832,598
SPR	DEU01	KOR01	CHN13	MUS	0.000051	0.000046	1.112	205,614	200,502	100,832,598
SPR	DEU01	KOR01	CHN01	MUS	0.000028	0.000025	1.129	280,447	277,625	100,832,598
SPR	DEU01	KOR01	CHN09	MUS	0.000032	0.000024	1.327	228,506	225,233	100,832,598
SPR	DEU01	KOR01	KOR05	MUS	0.000035	0.000023	1.521	113,298	109,778	100,832,598
SPR	DEU01	KOR01	KOR02	MUS	0.000034	0.000022	1.565	115,436	112,003	100,832,598
SPR	DEU01	KOR01	JPN14	MUS	0.000126	0.000072	1.733	146,503	133,846	100,832,598
SPR	DEU01	KOR01	KOR04	MUS	0.000046	0.000026	1.805	199,875	195,207	100,832,598
SPR	DEU01	KOR01	JPN06	MUS	0.00011	0.00005	2.185	170,205	159,136	100,832,598
SPR	DEU01	KOR01	JPN11	MUS	0.000155	0.000068	2.277	414,184	398,544	100,832,598
SPR	DEU01	KOR01	JPN08	MUS	0.000367	0.000126	2.92	186,678	149,711	100,832,598
SPR	DEU01	KOR01	JPN16	CAS	0.000052	0.000171	3.048	419,761	367,359	100,832,598
SPR	DEU01	KOR01	KAZ05	MUS	0.000215	0.000069	3.139	335,879	314,177	100,832,598
SPR	DEU01	KOR01	JPN15	CAS	0.000486	0.000147	3.299	422,284	373,233	100,832,598
SPR	DEU01	KOR01	CHN02	MUS	0.000404	0.000121	3.342	315,839	275,099	100,832,598
SPR	DEU01	KOR01	LKA02	CAS	0.000286	0.000084	3.387	1,625,434	1,596,612	100,832,598
SPR	DEU01	KOR01	JPN03	MUS	0.000131	0.000036	3.602	249,998	236,786	100,832,598
SPR	DEU01	KOR01	JPN05	MUS	0.000477	0.00013	3.655	363,454	315,393	100,832,598
SPR	DEU01	KOR01	CHN24	MUS	0.000209	0.000054	3.844	245,047	223,940	100,832,598
SPR	DEU01	KOR01	CHN07	MUS	0.000453	0.000107	4.211	266,681	221,052	100,832,598
SPR	DEU01	KOR01	KAZ04	MUS	0.00025	0.000059	4.248	329,829	304,636	100,832,598
SPR	DEU01	KOR01	JPN07	MUS	0.000307	0.000072	4.271	428,101	397,189	100,832,598
SPR	DEU01	KOR01	JPN18	CAS	0.000269	0.000062	4.342	437,092	410,017	100,832,598
SPR	DEU01	KOR01	KAZ02	MUS	0.000124	0.000028	4.388	318,986	306,460	100,832,598
SPR	DEU01	KOR01	LKA01	CAS	0.000424	0.000095	4.451	1,634,997	1,592,284	100,832,598
SPR	DEU01	KOR01	CHN21	CAS	0.00045	0.000101	4.468	518,004	472,618	100,832,598
SPR	DEU01	KOR01	JPN02	MUS	0.00046	0.000101	4.533	372,042	325,689	100,832,598
SPR	DEU01	KOR01	KAZ03	MUS	0.000239	0.000048	4.939	340,693	316,643	100,832,598
SPR	DEU01	KOR01	CHN08	MUS	0.00082	0.000159	5.174	302,963	220,257	100,832,598
SPR	DEU01	KOR01	JPN09	MUS	0.000533	0.000094	5.672	406,033	352,312	100,832,598
SPR	DEU01	KOR01	IDN03	CAS	0.000678	0.000119	5.698	1,649,160	1,580,750	100,832,598
SPR	DEU01	KOR01	JPN04	MUS	0.000399	0.000068	5.845	776,884	736,633	100,832,598
SPR	DEU01	KOR01	JPN17	CAS	0.000493	0.000079	6.263	543,007	493,249	100,832,598
SPR	DEU01	KOR01	IDN04	CAS	0.001001	0.000157	6.377	1,675,411	1,574,496	100,832,598
SPR	DEU01	KOR01	JPN01	MUS	0.000579	0.000087	6.683	827,799	769,402	100,832,598
SPR	DEU01	KOR01	CHN15	MUS	0.001945	0.000273	7.133	405,814	209,684	100,832,598
SPR	DEU01	KOR01	CHN16	CAS	0.000806	0.000109	7.391	933,197	851,937	100,832,598
SPR	DEU01	KOR01	RUS03	MUS	0.000306	0.00004	7.554	350,049	319,222	100,832,598
SPR	DEU01	KOR01	RUS04	DOM	0.002083	0.000265	7.864	542,709	332,637	100,832,598
SPR	DEU01	KOR01	CHN12	CAS	0.000883	0.000112	7.868	1,302,929	1,213,861	100,832,598
SPR	DEU01	KOR01	VNM01	CAS	0.00081	0.000103	7.904	1,607,030	1,525,322	100,832,598
SPR	DEU01	KOR01	RUS09	MUS	0.000474	0.00006	7.934	289,639	241,851	100,832,598
SPR	DEU01	KOR01	VNM02	CAS	0.000955	0.000115	8.294	1,615,619	1,519,292	100,832,598
SPR	DEU01	KOR01	RUS08	MUS	0.000397	0.000047	8.393	280,523	240,539	100,832,598
SPR	DEU01	KOR01	RUS05	MUS	0.0017	0.000199	8.528	504,299	332,884	100,832,598
SPR	DEU01	KOR01	CHN19	CAS	0.001132	0.000132	8.543	1,169,077	1,054,950	100,832,598
SPR	DEU01	KOR01	IRN06	MUS	0.000342	0.000039	8.745	422,797	388,319	100,832,598
SPR	DEU01	KOR01	TWN01	CAS	0.001437	0.000162	8.895	1,542,118	1,397,174	100,832,598

SPR	DEU01	KOR01	CHN22	CAS	0.000979	0.000101	9.671	1,410,227	1,311,463	100,832,598
SPR	DEU01	KOR01	RUS06	MUS	0.001436	0.000144	9.956	479,373	334,544	100,832,598
SPR	DEU01	KOR01	CHN11	CAS	0.001316	0.000127	10.342	1,311,583	1,178,861	100,832,598
SPR	DEU01	KOR01	CHN14	CAS	0.001345	0.000122	11.012	1,437,511	1,301,933	100,832,598
SPR	DEU01	KOR01	KAZ01	MUS	0.000655	0.000059	11.104	396,609	330,529	100,832,598
SPR	DEU01	KOR01	JPN12	MUS	0.002669	0.000236	11.329	672,267	403,130	100,832,598
SPR	DEU01	KOR01	RUS16	DOM	0.002377	0.000204	11.661	663,079	423,373	100,832,598
SPR	DEU01	KOR01	RUS14	CAS	0.002411	0.000206	11.694	717,843	474,753	100,832,598
SPR	DEU01	KOR01	RUS17	MUS	0.002373	0.000202	11.761	648,278	408,954	100,832,598
SPR	DEU01	KOR01	RUS02	MUS	0.000564	0.000045	12.54	387,624	330,782	100,832,598
SPR	DEU01	KOR01	CHN17	CAS	0.001423	0.000112	12.738	1,501,950	1,358,452	100,832,598
SPR	DEU01	KOR01	CHN23	MUS	0.001017	0.00008	12.747	431,808	329,226	100,832,598
SPR	DEU01	KOR01	CHN18	CAS	0.002024	0.000154	13.109	1,586,588	1,382,489	100,832,598
SPR	DEU01	KOR01	RUS11	MUS	0.001616	0.000121	13.356	539,334	376,427	100,832,598
SPR	DEU01	KOR01	RUS07	MUS	0.001343	0.000099	13.553	454,486	319,032	100,832,598
SPR	DEU01	KOR01	RUS13	DOM	0.002609	0.000192	13.582	753,746	490,697	100,832,598
SPR	DEU01	KOR01	RUS15	MUS	0.003347	0.000238	14.073	790,981	453,491	100,832,598
SPR	DEU01	KOR01	CHN20	CAS	0.002339	0.000161	14.502	732,124	496,311	100,832,598
SPR	DEU01	KOR01	CZE01	MUS	0.002449	0.000166	14.724	589,004	342,066	100,832,598
SPR	DEU01	KOR01	EST01	MUS	0.001852	0.000123	15.089	518,621	331,847	100,832,598
SPR	DEU01	KOR01	UKR01	MUS	0.003402	0.000222	15.353	999,683	656,683	100,832,598
SPR	DEU01	KOR01	CZE03	MUS	0.002166	0.000121	17.916	562,298	343,918	100,832,598
SPR	DEU01	KOR01	CZE05	MUS	0.002318	0.000126	18.392	570,604	336,916	100,832,598
SPR	DEU01	KOR01	CZE04	MUS	0.002133	0.000115	18.548	548,705	333,677	100,832,598
SPR	DEU01	KOR01	CZE06	MUS	0.002264	0.00012	18.853	559,564	331,297	100,832,598
SPR	DEU01	KOR01	CZE02	MUS	0.002277	0.000115	19.846	559,401	329,810	100,832,598
SPR	DEU01	KOR01	CZE07	MUS	0.00214	0.000106	20.227	548,318	332,491	100,832,598
SPR	DEU01	KOR01	IDN02	CAS	0.008347	0.000389	21.452	2,203,206	1,361,523	100,832,598
SPR	DEU01	KOR01	RUS12	CAS	0.008074	0.000368	21.94	1,713,113	898,953	100,832,598
SPR	DEU01	KOR01	RUS10	CAS	0.008464	0.000375	22.553	1,741,598	888,108	100,832,598
SPR	DEU01	KOR01	IDN01	DOM	0.007887	0.000313	25.22	2,155,865	1,360,572	100,832,598
SPR	DEU01	KOR01	IRN05	CAS	0.00142	0.000052	27.56	548,697	405,522	100,832,598
SPR	DEU01	KOR01	RUS01	DOM	0.024494	0.000664	36.889	2,852,867	383,099	100,832,598
SPR	DEU01	KOR01	CHN06	MUS	0.02906	0.000677	42.92	3,278,476	348,239	100,832,598
SPR	DEU01	KOR01	IRN02	DOM	0.037222	0.000154	100	4,321,272	568,074	100,832,598
SPR	DEU01	KOR01	IRN01	DOM	0.037359	0.000156	100	4,332,448	565,455	100,832,598
SPR	DEU01	KOR01	IRN04	DOM	0.037415	0.000156	100	4,339,500	566,881	100,832,598
SPR	DEU01	KOR01	IRN03	DOM	0.037517	0.000156	100	4,346,891	563,930	100,832,598
SPR	DEU01	KOR01	FRA02	DOM	0.043666	0.00021	100	4,844,844	441,918	100,832,598
SPR	DEU01	KOR01	FRA01	DOM	0.043711	0.000217	100	4,847,191	439,719	100,832,598
SPR	DEU01	KOR01	FRA03	DOM	0.043848	0.000197	100	4,854,590	433,294	100,832,598
SPR	DEU01	KOR01	FRA04	DOM	0.043887	0.000192	100	4,857,662	432,405	100,832,598
SPR	DEU01	KOR01	DEU02	DOM	0.048002	0.000229	100	5,193,049	352,924	100,832,598
SPR	DEU01	KOR01	DEU05	DOM	0.048006	0.000241	100	5,186,877	346,356	100,832,598
SPR	DEU01	KOR01	DEU07	DOM	0.048078	0.000191	100	5,185,853	338,050	100,832,598
SPR	DEU01	KOR01	DEU06	DOM	0.048154	0.00019	100	5,192,481	336,963	100,832,598
SPR	DEU01	KOR01	DEU03	DOM	0.048209	0.000189	100	5,194,798	333,734	100,832,598
SPR	DEU01	KOR01	DEU04	DOM	0.048365	0.000196	100	5,206,366	329,584	100,832,598

Table 1-12 The f_4 statistics result of autosome. f_4 (SPR, MUS; CAS, X)The f_4 statistics result of autosome. f_4 (SPR, MUS; CAS, X)

Pop1(W)	Pop2(X)	Pop3(Y)	Pop4(Z)	Pop4(Z) mtDNA Haplogroup	f_4 statistics	Standard Error	Z	BABA	ABBA	Number of SNPs that all population have data
SPR	KOR01	IND04	NPL02	NEP	-0.00601	0.000189	-31.788	1,473,713	2,079,714	100,832,598
SPR	KOR01	IND04	DEU07	DOM	-0.00276	0.000168	-16.425	1,635,424	1,913,342	100,832,598
SPR	KOR01	IND04	FRA01	DOM	-0.00286	0.000175	-16.347	1,632,225	1,920,477	100,832,598
SPR	KOR01	IND04	DEU06	DOM	-0.00278	0.000171	-16.243	1,634,025	1,914,461	100,832,598
SPR	KOR01	IND04	DEU01	DOM	-0.00282	0.000176	-16.001	1,633,081	1,917,648	100,832,598
SPR	KOR01	IND04	FRA03	DOM	-0.00279	0.000175	-15.945	1,634,208	1,915,791	100,832,598
SPR	KOR01	IND04	DEU03	DOM	-0.00274	0.000174	-15.688	1,635,512	1,911,375	100,832,598
SPR	KOR01	IND04	FRA04	DOM	-0.00281	0.000182	-15.455	1,633,884	1,916,894	100,832,598
SPR	KOR01	IND04	DEU05	DOM	-0.00284	0.000184	-15.453	1,635,135	1,921,746	100,832,598
SPR	KOR01	IND04	DEU02	DOM	-0.00295	0.000192	-15.386	1,631,063	1,928,283	100,832,598
SPR	KOR01	IND04	FRA02	DOM	-0.00285	0.000186	-15.346	1,633,805	1,921,337	100,832,598
SPR	KOR01	IND04	DEU04	DOM	-0.00269	0.000177	-15.249	1,637,988	1,909,574	100,832,598
SPR	KOR01	IND04	IRN03	DOM	-0.00238	0.000160	-14.838	1,649,575	1,889,330	100,832,598
SPR	KOR01	IND04	IRN04	DOM	-0.00236	0.000160	-14.811	1,647,777	1,886,074	100,832,598
SPR	KOR01	IND04	IRN01	DOM	-0.00229	0.000160	-14.281	1,653,417	1,883,896	100,832,598
SPR	KOR01	IND04	IRN02	DOM	-0.00225	0.000160	-14.042	1,654,411	1,880,787	100,832,598
SPR	KOR01	IND04	NPL01	NEP	-0.00160	0.000210	-7.637	1,568,518	1,730,223	100,832,598
SPR	KOR01	IND04	IND03	CAS	-0.00006	0.000039	-1.471	1,071,289	1,077,023	100,832,598
SPR	KOR01	IND04	IND07	CAS	-0.00003	0.000140	-0.187	1,584,408	1,587,034	100,832,598
SPR	KOR01	IND04	IND08	CAS	0.00033	0.000154	2.160	1,611,129	1,577,683	100,832,598
SPR	KOR01	IND04	IND01	CAS	0.00033	0.000148	2.204	1,604,969	1,572,146	100,832,598
SPR	KOR01	IND04	IND06	CAS	0.00035	0.000146	2.398	1,606,110	1,570,797	100,832,598
SPR	KOR01	IND04	BGD01	CAS	0.00040	0.000148	2.674	1,620,038	1,580,160	100,832,598
SPR	KOR01	IND04	IND09	CAS	0.00039	0.000145	2.680	1,609,665	1,570,422	100,832,598
SPR	KOR01	IND04	IND05	CAS	0.00041	0.000146	2.798	1,607,166	1,566,077	100,832,598
SPR	KOR01	IND04	IND02	CAS	0.00041	0.000144	2.814	1,605,208	1,564,236	100,832,598
SPR	KOR01	IND04	LKA02	CAS	0.00044	0.000148	2.967	1,611,935	1,567,752	100,832,598
SPR	KOR01	IND04	LKA01	CAS	0.00044	0.000148	2.973	1,613,012	1,568,650	100,832,598
SPR	KOR01	IND04	PAK02	CAS	0.00046	0.000147	3.125	1,572,393	1,526,181	100,832,598
SPR	KOR01	IND04	BGD02	CAS	0.00048	0.000149	3.218	1,609,724	1,561,340	100,832,598
SPR	KOR01	IND04	IDN04	CAS	0.00052	0.000155	3.347	1,623,244	1,571,085	100,832,598
SPR	KOR01	IND04	PAK04	CAS	0.00055	0.000147	3.752	1,604,075	1,548,533	100,832,598
SPR	KOR01	IND04	IDN02	CAS	0.00068	0.000176	3.840	1,681,933	1,613,681	100,832,598
SPR	KOR01	IND04	IDN03	CAS	0.00062	0.000156	3.953	1,630,289	1,568,136	100,832,598
SPR	KOR01	IND04	PAK03	CAS	0.00060	0.000147	4.102	1,614,498	1,553,641	100,832,598
SPR	KOR01	IND04	PAK01	CAS	0.00038	0.000082	4.551	1,561,747	1,523,895	100,832,598
SPR	KOR01	IND04	IDN01	DOM	0.00105	0.000179	5.833	1,700,823	1,595,402	100,832,598
SPR	KOR01	IND04	VNM02	CAS	0.00247	0.000201	12.317	1,765,985	1,516,556	100,832,598
SPR	KOR01	IND04	VNM01	CAS	0.00245	0.000197	12.440	1,764,699	1,517,833	100,832,598
SPR	KOR01	IND04	CHN06	MUS	0.01551	0.000718	21.601	2,874,766	1,310,905	100,832,598
SPR	KOR01	IND04	TWN01	CAS	0.00630	0.000275	22.899	2,050,450	1,415,417	100,832,598
SPR	KOR01	IND04	CHN18	CAS	0.00629	0.000254	24.696	2,056,290	1,422,554	100,832,598
SPR	KOR01	IND04	RUS01	DOM	0.01830	0.000705	25.972	3,051,090	1,205,775	100,832,598
SPR	KOR01	IND04	CHN17	CAS	0.00783	0.000280	28.000	2,170,263	1,380,675	100,832,598
SPR	KOR01	IND04	CHN12	CAS	0.01364	0.000480	28.425	2,594,631	1,219,203	100,832,598
SPR	KOR01	IND04	CHN14	CAS	0.00997	0.000326	30.611	2,328,229	1,322,534	100,832,598
SPR	KOR01	IND04	RUS12	CAS	0.01685	0.000523	32.239	2,855,966	1,156,673	100,832,598
SPR	KOR01	IND04	CHN22	CAS	0.00995	0.000304	32.737	2,319,566	1,316,547	100,832,598
SPR	KOR01	IND04	CHN11	CAS	0.01444	0.000407	35.447	2,656,866	1,201,286	100,832,598
SPR	KOR01	IND04	RUS10	CAS	0.01684	0.000457	36.862	2,853,897	1,156,355	100,832,598
SPR	KOR01	IND04	CHN19	CAS	0.01903	0.000364	52.257	2,990,794	1,072,453	100,832,598
SPR	KOR01	IND04	UKR01	MUS	0.03002	0.000518	58.003	3,791,682	764,905	100,832,598
SPR	KOR01	IND04	JPN01	MUS	0.03036	0.000464	65.492	3,832,596	770,985	100,832,598
SPR	KOR01	IND04	JPN04	MUS	0.03177	0.000464	68.411	3,938,788	735,383	100,832,598
SPR	KOR01	IND04	CHN16	CAS	0.02660	0.000377	70.482	3,544,064	862,241	100,832,598
SPR	KOR01	IND04	CHN21	CAS	0.04071	0.000533	76.315	4,585,457	480,886	100,832,598
SPR	KOR01	IND04	RUS14	CAS	0.03729	0.000474	78.635	4,319,139	559,618	100,832,598
SPR	KOR01	IND04	CHN20	CAS	0.03698	0.000467	79.226	4,302,886	574,252	100,832,598
SPR	KOR01	IND04	JPN12	MUS	0.04171	0.000520	80.250	4,686,595	481,205	100,832,598
SPR	KOR01	IND04	JPN17	CAS	0.04059	0.000499	81.323	4,593,729	500,880	100,832,598
SPR	KOR01	IND04	RUS13	DOM	0.03660	0.000436	83.954	4,267,670	576,753	100,832,598
SPR	KOR01	IND04	RUS15	MUS	0.03706	0.000433	85.632	4,306,983	570,446	100,832,598
SPR	KOR01	IND04	JPN16	CAS	0.04523	0.000501	90.303	4,941,117	380,361	100,832,598
SPR	KOR01	IND04	JPN15	CAS	0.04503	0.000498	90.470	4,924,371	384,279	100,832,598
SPR	KOR01	IND04	RUS17	MUS	0.03950	0.000422	93.571	4,480,241	497,755	100,832,598
SPR	KOR01	IND04	JPN09	MUS	0.04583	0.000472	97.038	4,986,218	365,505	100,832,598
SPR	KOR01	IND04	JPN18	CAS	0.04397	0.000453	97.154	4,844,948	411,161	100,832,598
SPR	KOR01	IND04	JPN07	MUS	0.04436	0.000454	97.684	4,872,999	399,684	100,832,598
SPR	KOR01	IND04	JPN11	MUS	0.04457	0.000453	98.280	4,893,582	399,889	100,832,598
SPR	KOR01	IND04	RUS16	DOM	0.03907	0.000391	99.877	4,445,250	505,952	100,832,598
SPR	KOR01	IND04	IRN05	CAS	0.04004	0.000226	100.000	4,496,401	458,853	100,832,598

SPR	KOR01	IND04	RUS11	MUS	0.04148	0.000348	100.000	4,617,323	434,863	100,832,598
SPR	KOR01	IND04	CZE01	MUS	0.04182	0.000305	100.000	4,650,193	433,734	100,832,598
SPR	KOR01	IND04	IRN06	MUS	0.04188	0.000227	100.000	4,625,950	402,797	100,832,598
SPR	KOR01	IND04	CZE03	MUS	0.04200	0.000279	100.000	4,661,160	426,115	100,832,598
SPR	KOR01	IND04	CZE05	MUS	0.04205	0.000270	100.000	4,664,272	424,746	100,832,598
SPR	KOR01	IND04	CZE06	MUS	0.04227	0.000250	100.000	4,675,572	413,274	100,832,598
SPR	KOR01	IND04	CZE02	MUS	0.04231	0.000241	100.000	4,678,487	412,293	100,832,598
SPR	KOR01	IND04	CZE04	MUS	0.04235	0.000260	100.000	4,682,951	412,656	100,832,598
SPR	KOR01	IND04	CZE07	MUS	0.04239	0.000241	100.000	4,687,626	413,711	100,832,598
SPR	KOR01	IND04	RUS04	DOM	0.04240	0.000350	100.000	4,683,490	407,797	100,832,598
SPR	KOR01	IND04	EST01	MUS	0.04265	0.000266	100.000	4,707,888	407,841	100,832,598
SPR	KOR01	IND04	RUS05	MUS	0.04275	0.000281	100.000	4,706,438	395,657	100,832,598
SPR	KOR01	IND04	RUS06	MUS	0.04298	0.000276	100.000	4,722,955	389,442	100,832,598
SPR	KOR01	IND04	RUS07	MUS	0.04374	0.000245	100.000	4,781,246	371,105	100,832,598
SPR	KOR01	IND04	CHN23	MUS	0.04380	0.000274	100.000	4,789,385	373,223	100,832,598
SPR	KOR01	IND04	KAZ01	MUS	0.04389	0.000226	100.000	4,782,544	357,395	100,832,598
SPR	KOR01	IND04	RUS02	MUS	0.04393	0.000220	100.000	4,784,630	355,529	100,832,598
SPR	KOR01	IND04	RUS03	MUS	0.04473	0.000216	100.000	4,846,625	336,597	100,832,598
SPR	KOR01	IND04	KAZ03	MUS	0.04502	0.000258	100.000	4,873,530	333,601	100,832,598
SPR	KOR01	IND04	KAZ05	MUS	0.04518	0.000268	100.000	4,884,604	328,831	100,832,598
SPR	KOR01	IND04	KAZ04	MUS	0.04539	0.000224	100.000	4,894,974	318,604	100,832,598
SPR	KOR01	IND04	KAZ02	MUS	0.04550	0.000212	100.000	4,903,206	315,844	100,832,598
SPR	KOR01	IND04	CHN04	MUS	0.04564	0.000257	100.000	4,919,746	318,030	100,832,598
SPR	KOR01	IND04	CHN05	MUS	0.04614	0.000258	100.000	4,958,589	306,405	100,832,598
SPR	KOR01	IND04	CHN03	MUS	0.04652	0.000269	100.000	4,989,913	299,506	100,832,598
SPR	KOR01	IND04	CHN02	MUS	0.04652	0.000247	100.000	4,986,017	294,948	100,832,598
SPR	KOR01	IND04	JPN02	MUS	0.04682	0.000420	100.000	5,055,962	334,842	100,832,598
SPR	KOR01	IND04	CHN01	MUS	0.04685	0.000214	100.000	5,009,297	285,407	100,832,598
SPR	KOR01	IND04	JPN05	MUS	0.04727	0.000470	100.000	5,096,084	330,034	100,832,598
SPR	KOR01	IND04	RUS09	MUS	0.04817	0.000257	100.000	5,121,044	264,340	100,832,598
SPR	KOR01	IND04	CHN15	MUS	0.04823	0.000394	100.000	5,142,825	279,771	100,832,598
SPR	KOR01	IND04	RUS08	MUS	0.04832	0.000244	100.000	5,132,001	260,205	100,832,598
SPR	KOR01	IND04	CHN08	MUS	0.04896	0.000300	100.000	5,189,910	253,280	100,832,598
SPR	KOR01	IND04	CHN07	MUS	0.04932	0.000272	100.000	5,212,667	240,139	100,832,598
SPR	KOR01	IND04	CHN09	MUS	0.04933	0.000225	100.000	5,206,330	231,919	100,832,598
SPR	KOR01	IND04	CHN24	MUS	0.04963	0.000313	100.000	5,243,113	238,960	100,832,598
SPR	KOR01	IND04	CHN10	MUS	0.04990	0.000242	100.000	5,253,015	221,640	100,832,598
SPR	KOR01	IND04	JPN03	MUS	0.05041	0.000335	100.000	5,323,086	239,774	100,832,598
SPR	KOR01	IND04	CHN13	MUS	0.05046	0.000244	100.000	5,295,794	207,906	100,832,598
SPR	KOR01	IND04	KOR04	MUS	0.05221	0.000321	100.000	5,460,622	196,692	100,832,598
SPR	KOR01	IND04	JPN06	MUS	0.05333	0.000323	100.000	5,539,623	161,867	100,832,598
SPR	KOR01	IND04	JPN08	MUS	0.05344	0.000339	100.000	5,550,298	162,199	100,832,598
SPR	KOR01	IND04	JPN13	CAS	0.05411	0.000291	100.000	5,600,263	143,940	100,832,598
SPR	KOR01	IND04	JPN14	MUS	0.05425	0.000284	100.000	5,611,068	141,104	100,832,598
SPR	KOR01	IND04	JPN10	MUS	0.05450	0.000263	100.000	5,628,604	133,218	100,832,598
SPR	KOR01	IND04	KOR02	MUS	0.05536	0.000238	100.000	5,698,459	116,518	100,832,598
SPR	KOR01	IND04	KOR05	MUS	0.05546	0.000234	100.000	5,705,872	113,258	100,832,598
SPR	KOR01	IND04	KOR03	MUS	0.05569	0.000232	100.000	5,722,821	107,598	100,832,598

Table 1-13 The f_4 statistics result of autosome. f_4 (SPR, MUS; DOM, X)The f_4 statistics result of autosome. f_4 (SPR, MUS; DOM, X)

Pop1(W)	Pop2(X)	Pop3(Y)	Pop4(Z)	Pop4(Z) mtDNA Haplogroup	f_4 statistics	Standard Error	Z	BABA	ABBA	Number of SNPs that all population have data
SPR	KOR01	DEU01	NPL02	NEP	-0.003188	0.0002	-15.914	1,713,958	2,035,392	100,832,598
SPR	KOR01	DEU01	DEU02	DOM	-0.000125	0.0001	-1.099	340,271	352,924	100,832,598
SPR	KOR01	DEU01	FRA01	DOM	-0.000037	0.0001	-0.655	436,035	439,719	100,832,598
SPR	KOR01	DEU01	FRA02	DOM	-0.000029	0.0001	-0.271	438,953	441,918	100,832,598
SPR	KOR01	DEU01	DEU05	DOM	-0.000020	0.0001	-0.216	344,312	346,356	100,832,598
SPR	KOR01	DEU01	FRA04	DOM	0.000015	0.0001	0.223	433,963	432,405	100,832,598
SPR	KOR01	DEU01	FRA03	DOM	0.000030	0.0001	0.373	436,278	433,294	100,832,598
SPR	KOR01	DEU01	DEU06	DOM	0.000041	0.0000	0.887	341,094	336,963	100,832,598
SPR	KOR01	DEU01	DEU07	DOM	0.000066	0.0001	0.964	344,699	338,050	100,832,598
SPR	KOR01	DEU01	DEU03	DOM	0.000086	0.0000	2.004	342,439	333,734	100,832,598
SPR	KOR01	DEU01	DEU04	DOM	0.000129	0.0001	2.463	342,565	329,584	100,832,598
SPR	KOR01	DEU01	IRN04	DOM	0.000459	0.0001	5.298	613,151	566,881	100,832,598
SPR	KOR01	DEU01	IRN01	DOM	0.000536	0.0001	5.929	619,543	565,455	100,832,598
SPR	KOR01	DEU01	IRN03	DOM	0.000444	0.0001	5.975	608,742	563,930	100,832,598
SPR	KOR01	DEU01	NPL01	NEP	0.001218	0.0002	6.651	1,867,647	1,744,785	100,832,598
SPR	KOR01	DEU01	IRN02	DOM	0.000577	0.0001	6.906	626,265	568,074	100,832,598
SPR	KOR01	DEU01	IND03	CAS	0.002765	0.0002	15.768	1,912,873	1,634,040	100,832,598
SPR	KOR01	DEU01	IND04	CAS	0.002822	0.0002	16.001	1,917,648	1,633,081	100,832,598
SPR	KOR01	DEU01	PAK01	CAS	0.003198	0.0001	25.173	1,934,385	1,611,966	100,832,598
SPR	KOR01	DEU01	IDN02	CAS	0.003499	0.0001	25.534	1,714,343	1,361,523	100,832,598
SPR	KOR01	DEU01	IND07	CAS	0.002796	0.0001	25.784	1,908,037	1,626,095	100,832,598
SPR	KOR01	DEU01	CHN06	MUS	0.018332	0.0007	25.818	2,196,668	348,239	100,832,598
SPR	KOR01	DEU01	IDN01	DOM	0.003868	0.0001	26.895	1,750,560	1,360,572	100,832,598
SPR	KOR01	DEU01	IND08	CAS	0.003154	0.0001	27.149	1,934,065	1,616,052	100,832,598
SPR	KOR01	DEU01	IND06	CAS	0.003172	0.0001	28.778	1,932,062	1,612,181	100,832,598
SPR	KOR01	DEU01	IDN01	CAS	0.003148	0.0001	29.002	1,928,312	1,610,922	100,832,598
SPR	KOR01	DEU01	IND09	CAS	0.003211	0.0001	29.179	1,931,709	1,607,898	100,832,598
SPR	KOR01	DEU01	IND05	CAS	0.003230	0.0001	29.308	1,933,904	1,608,248	100,832,598
SPR	KOR01	DEU01	LKA01	CAS	0.003262	0.0001	29.401	1,921,214	1,592,284	100,832,598
SPR	KOR01	DEU01	IDN04	CAS	0.003339	0.0001	29.757	1,911,223	1,574,496	100,832,598
SPR	KOR01	DEU01	BGD02	CAS	0.003302	0.0001	29.845	1,936,441	1,603,490	100,832,598
SPR	KOR01	DEU01	LKA02	CAS	0.003260	0.0001	29.904	1,925,363	1,596,612	100,832,598
SPR	KOR01	DEU01	RUS01	DOM	0.021123	0.0007	29.972	2,512,980	383,099	100,832,598
SPR	KOR01	DEU01	BGD01	CAS	0.003218	0.0001	30.117	1,937,002	1,612,557	100,832,598
SPR	KOR01	DEU01	IND02	CAS	0.003229	0.0001	30.230	1,933,202	1,607,662	100,832,598
SPR	KOR01	DEU01	IDN03	CAS	0.003439	0.0001	30.362	1,927,471	1,580,750	100,832,598
SPR	KOR01	DEU01	VNM02	CAS	0.005296	0.0002	30.500	2,053,289	1,519,292	100,832,598
SPR	KOR01	DEU01	PAK02	CAS	0.003280	0.0001	31.493	1,933,689	1,602,909	100,832,598
SPR	KOR01	DEU01	PAK03	CAS	0.003426	0.0001	32.050	1,943,138	1,597,714	100,832,598
SPR	KOR01	DEU01	PAK04	CAS	0.003373	0.0001	32.289	1,943,257	1,603,148	100,832,598
SPR	KOR01	DEU01	VNM01	CAS	0.005270	0.0002	32.462	2,056,755	1,525,322	100,832,598
SPR	KOR01	DEU01	CHN12	CAS	0.016463	0.0005	34.442	2,873,857	1,213,861	100,832,598
SPR	KOR01	DEU01	TWN01	CAS	0.009120	0.0003	34.486	2,316,774	1,397,174	100,832,598
SPR	KOR01	DEU01	CHN18	CAS	0.009107	0.0002	37.650	2,300,793	1,382,489	100,832,598
SPR	KOR01	DEU01	RUS12	CAS	0.019675	0.0005	38.758	2,882,814	898,953	100,832,598
SPR	KOR01	DEU01	CHN14	CAS	0.012796	0.0003	40.120	2,592,196	1,301,933	100,832,598
SPR	KOR01	DEU01	CHN17	CAS	0.010653	0.0003	40.203	2,432,607	1,358,452	100,832,598
SPR	KOR01	DEU01	CHN11	CAS	0.017258	0.0004	43.339	2,919,009	1,178,861	100,832,598
SPR	KOR01	DEU01	RUS10	CAS	0.019657	0.0005	43.641	2,870,217	888,108	100,832,598
SPR	KOR01	DEU01	CHN22	CAS	0.012770	0.0003	43.776	2,599,050	1,311,463	100,832,598
SPR	KOR01	DEU01	CHN19	CAS	0.021847	0.0003	62.547	3,257,859	1,054,950	100,832,598
SPR	KOR01	DEU01	UKR01	MUS	0.032840	0.0005	63.991	3,968,027	656,683	100,832,598
SPR	KOR01	DEU01	JPN01	MUS	0.033185	0.0004	73.829	4,115,581	769,402	100,832,598
SPR	KOR01	DEU01	JPN04	MUS	0.034592	0.0005	76.713	4,224,606	736,633	100,832,598
SPR	KOR01	DEU01	CHN16	CAS	0.029419	0.0004	80.237	3,818,328	851,937	100,832,598
SPR	KOR01	DEU01	CHN21	CAS	0.043529	0.0005	82.849	4,861,757	472,618	100,832,598
SPR	KOR01	DEU01	RUS14	CAS	0.040107	0.0005	86.262	4,518,842	474,753	100,832,598
SPR	KOR01	DEU01	JPN12	MUS	0.044529	0.0005	86.726	4,893,087	403,130	100,832,598
SPR	KOR01	DEU01	JPN17	CAS	0.043413	0.0005	86.959	4,870,666	493,249	100,832,598
SPR	KOR01	DEU01	CHN20	CAS	0.039801	0.0005	87.931	4,509,512	496,311	100,832,598
SPR	KOR01	DEU01	RUS13	DOM	0.039427	0.0004	92.172	4,466,182	490,697	100,832,598
SPR	KOR01	DEU01	RUS15	MUS	0.039879	0.0004	92.879	4,474,596	453,491	100,832,598
SPR	KOR01	DEU01	JPN16	CAS	0.048053	0.0005	98.447	5,212,681	367,359	100,832,598
SPR	KOR01	DEU01	JPN15	CAS	0.047848	0.0005	98.488	5,197,893	373,233	100,832,598
SPR	KOR01	DEU01	RUS16	DOM	0.041890	0.0004	100.000	4,647,238	423,373	100,832,598
SPR	KOR01	DEU01	RUS17	MUS	0.042318	0.0004	100.000	4,676,008	408,954	100,832,598
SPR	KOR01	DEU01	IRN05	CAS	0.042864	0.0002	100.000	4,727,637	405,522	100,832,598
SPR	KOR01	DEU01	RUS11	MUS	0.044301	0.0003	100.000	4,843,455	376,427	100,832,598
SPR	KOR01	DEU01	CZE01	MUS	0.044639	0.0003	100.000	4,843,092	342,066	100,832,598
SPR	KOR01	DEU01	IRN06	MUS	0.044705	0.0002	100.000	4,896,040	388,319	100,832,598
SPR	KOR01	DEU01	CZE03	MUS	0.044823	0.0003	100.000	4,863,531	343,918	100,832,598

SPR	KOR01	DEU01	CZE05	MUS	0.044867	0.0003	100.000	4,861,010	336,916	100,832,598
SPR	KOR01	DEU01	CZE06	MUS	0.045093	0.0002	100.000	4,878,162	331,297	100,832,598
SPR	KOR01	DEU01	CZE02	MUS	0.045132	0.0002	100.000	4,880,572	329,810	100,832,598
SPR	KOR01	DEU01	CZE04	MUS	0.045173	0.0002	100.000	4,888,539	333,677	100,832,598
SPR	KOR01	DEU01	CZE07	MUS	0.045208	0.0002	100.000	4,890,974	332,491	100,832,598
SPR	KOR01	DEU01	RUS04	DOM	0.045226	0.0003	100.000	4,892,896	332,637	100,832,598
SPR	KOR01	DEU01	EST01	MUS	0.045468	0.0002	100.000	4,916,462	331,847	100,832,598
SPR	KOR01	DEU01	RUS05	MUS	0.045574	0.0003	100.000	4,928,232	332,884	100,832,598
SPR	KOR01	DEU01	RUS06	MUS	0.045799	0.0003	100.000	4,952,624	334,544	100,832,598
SPR	KOR01	DEU01	RUS07	MUS	0.046559	0.0002	100.000	5,013,741	319,032	100,832,598
SPR	KOR01	DEU01	CHN23	MUS	0.046619	0.0003	100.000	5,029,955	329,226	100,832,598
SPR	KOR01	DEU01	KAZ01	MUS	0.046708	0.0002	100.000	5,040,245	330,529	100,832,598
SPR	KOR01	DEU01	RUS02	MUS	0.046747	0.0002	100.000	5,044,450	330,782	100,832,598
SPR	KOR01	DEU01	JPN18	CAS	0.046794	0.0004	100.000	5,128,370	410,017	100,832,598
SPR	KOR01	DEU01	JPN07	MUS	0.047186	0.0004	100.000	5,155,071	397,189	100,832,598
SPR	KOR01	DEU01	JPN11	MUS	0.047388	0.0004	100.000	5,176,804	398,544	100,832,598
SPR	KOR01	DEU01	RUS03	MUS	0.047550	0.0002	100.000	5,113,817	319,222	100,832,598
SPR	KOR01	DEU01	KAZ03	MUS	0.047847	0.0003	100.000	5,141,139	316,643	100,832,598
SPR	KOR01	DEU01	KAZ05	MUS	0.048004	0.0003	100.000	5,154,516	314,177	100,832,598
SPR	KOR01	DEU01	KAZ04	MUS	0.048208	0.0002	100.000	5,165,574	304,636	100,832,598
SPR	KOR01	DEU01	KAZ02	MUS	0.048317	0.0002	100.000	5,178,390	306,460	100,832,598
SPR	KOR01	DEU01	CHN04	MUS	0.048459	0.0003	100.000	5,195,583	309,301	100,832,598
SPR	KOR01	DEU01	JPN09	MUS	0.048648	0.0005	100.000	5,257,592	352,312	100,832,598
SPR	KOR01	DEU01	CHN05	MUS	0.048960	0.0003	100.000	5,234,783	298,032	100,832,598
SPR	KOR01	DEU01	CHN03	MUS	0.049339	0.0003	100.000	5,263,753	288,779	100,832,598
SPR	KOR01	DEU01	CHN02	MUS	0.049346	0.0002	100.000	5,250,736	275,099	100,832,598
SPR	KOR01	DEU01	JPN02	MUS	0.049644	0.0004	100.000	5,331,377	325,689	100,832,598
SPR	KOR01	DEU01	CHN01	MUS	0.049671	0.0002	100.000	5,286,082	277,625	100,832,598
SPR	KOR01	DEU01	JPN05	MUS	0.050089	0.0005	100.000	5,366,010	315,393	100,832,598
SPR	KOR01	DEU01	RUS09	MUS	0.050988	0.0002	100.000	5,383,123	241,851	100,832,598
SPR	KOR01	DEU01	CHN15	MUS	0.051051	0.0004	100.000	5,357,305	209,684	100,832,598
SPR	KOR01	DEU01	RUS08	MUS	0.051138	0.0002	100.000	5,396,903	240,539	100,832,598
SPR	KOR01	DEU01	CHN08	MUS	0.051781	0.0003	100.000	5,441,455	220,257	100,832,598
SPR	KOR01	DEU01	CHN07	MUS	0.052137	0.0003	100.000	5,478,148	221,052	100,832,598
SPR	KOR01	DEU01	CHN09	MUS	0.052156	0.0002	100.000	5,484,212	225,233	100,832,598
SPR	KOR01	DEU01	CHN24	MUS	0.052451	0.0003	100.000	5,512,660	223,940	100,832,598
SPR	KOR01	DEU01	CHN10	MUS	0.052720	0.0002	100.000	5,530,088	214,145	100,832,598
SPR	KOR01	DEU01	JPN03	MUS	0.053236	0.0003	100.000	5,604,665	236,786	100,832,598
SPR	KOR01	DEU01	CHN13	MUS	0.053281	0.0002	100.000	5,572,958	200,502	100,832,598
SPR	KOR01	DEU01	KOR04	MUS	0.055027	0.0003	100.000	5,743,704	195,207	100,832,598
SPR	KOR01	DEU01	JPN06	MUS	0.056156	0.0003	100.000	5,821,459	159,136	100,832,598
SPR	KOR01	DEU01	JPN08	MUS	0.056258	0.0003	100.000	5,822,378	149,711	100,832,598
SPR	KOR01	DEU01	JPN13	CAS	0.056935	0.0003	100.000	5,882,037	141,147	100,832,598
SPR	KOR01	DEU01	JPN14	MUS	0.057070	0.0003	100.000	5,888,378	133,846	100,832,598
SPR	KOR01	DEU01	JPN10	MUS	0.057322	0.0003	100.000	5,909,440	129,486	100,832,598
SPR	KOR01	DEU01	KOR02	MUS	0.058181	0.0002	100.000	5,978,512	112,003	100,832,598
SPR	KOR01	DEU01	KOR05	MUS	0.058287	0.0002	100.000	5,986,959	109,778	100,832,598
SPR	KOR01	DEU01	KOR03	MUS	0.058511	0.0002	100.000	6,005,761	105,970	100,832,598

Table 1-14 The f_4 statistics result of autosome. Verification of gene flow between IND samples. f_4 (SPR, MUS; CAS(IND), X(IND))

The f_4 statistics result of autosome. Verification of gene flow between IND samples. f_4 (SPR, MUS; CAS(IND), X(IND))

Pop1(W)	Pop2(X)	Pop3(Y)	Pop4(Z)	f_4 statistics	Standard Error	Z	BABA	ABBA	Number of SNPs that all population have data
SPR	KOR01	IND03	IND01	0.000382	0.000147	2.599	1,607,589	1,569,032	100,832,598
SPR	KOR01	IND03	IND02	0.000463	0.000144	3.210	1,607,451	1,560,744	100,832,598
SPR	KOR01	IND03	IND04	0.000057	0.000039	1.471	1,077,023	1,071,289	100,832,598
SPR	KOR01	IND03	IND05	0.000464	0.000146	3.190	1,610,448	1,563,625	100,832,598
SPR	KOR01	IND03	IND06	0.000407	0.000146	2.797	1,609,296	1,568,248	100,832,598
SPR	KOR01	IND03	IND07	0.000031	0.000139	0.221	1,586,213	1,583,104	100,832,598
SPR	KOR01	IND03	IND08	0.000389	0.000152	2.556	1,613,654	1,574,473	100,832,598
SPR	KOR01	IND03	IND09	0.000446	0.000144	3.087	1,611,185	1,566,207	100,832,598
SPR	KOR01	IND04	IND01	0.000326	0.000148	2.204	1,604,969	1,572,146	100,832,598
SPR	KOR01	IND04	IND02	0.000406	0.000144	2.814	1,605,208	1,564,236	100,832,598
SPR	KOR01	IND04	IND03	-0.000057	0.000039	-1.471	1,071,289	1,077,023	100,832,598
SPR	KOR01	IND04	IND05	0.000407	0.000146	2.798	1,607,166	1,566,077	100,832,598
SPR	KOR01	IND04	IND06	0.000350	0.000146	2.398	1,606,110	1,570,797	100,832,598
SPR	KOR01	IND04	IND07	-0.000026	0.000140	-0.187	1,584,408	1,587,034	100,832,598
SPR	KOR01	IND04	IND08	0.000332	0.000154	2.160	1,611,129	1,577,683	100,832,598
SPR	KOR01	IND04	IND09	0.000389	0.000145	2.680	1,609,665	1,570,422	100,832,598
SPR	KOR01	IND07	IND01	0.000352	0.000054	6.486	1,526,539	1,491,090	100,832,598
SPR	KOR01	IND07	IND02	0.000432	0.000049	8.842	1,546,317	1,502,719	100,832,598
SPR	KOR01	IND07	IND03	-0.000031	0.000139	-0.221	1,583,104	1,586,213	100,832,598
SPR	KOR01	IND07	IND04	0.000026	0.000140	0.187	1,587,034	1,584,408	100,832,598
SPR	KOR01	IND07	IND05	0.000434	0.000055	7.822	1,529,699	1,485,985	100,832,598
SPR	KOR01	IND07	IND06	0.000376	0.000051	7.310	1,527,937	1,489,998	100,832,598
SPR	KOR01	IND07	IND08	0.000358	0.000065	5.484	1,528,506	1,492,434	100,832,598
SPR	KOR01	IND07	IND09	0.000415	0.000051	8.187	1,530,247	1,488,378	100,832,598

Table 1-15 The outgroup f_3 statistics result of X chromosome with SPR as outgroup. $f_3(\text{CAS}, \text{X}; \text{SPR})$

The outgroup f_3 statistics result of X chromosome with SPR as outgroup. $f_3(\text{CAS}, \text{X}; \text{SPR})$

Source1	Source2	Target	Source2 mtDNA Haplogroup	f_3 statistics	Std.Err	Z	SNPs
IND04	IND03	SPR	CAS	294.778733	3.001623	98.206	1,213,419
IND04	PAK02	SPR	CAS	270.516892	3.194919	84.671	1,383,593
IND04	PAK01	SPR	CAS	269.572997	3.085307	87.373	1,388,434
IND04	PAK04	SPR	CAS	268.309040	3.168168	84.689	1,291,189
IND04	PAK03	SPR	CAS	267.342863	3.099119	86.264	1,293,654
IND04	IND02	SPR	CAS	267.174917	3.112029	85.852	1,295,058
IND04	LKA02	SPR	CAS	266.844230	3.130214	85.248	1,296,457
IND04	IND06	SPR	CAS	266.823682	3.193196	83.560	1,315,324
IND04	IND08	SPR	CAS	266.746828	3.140388	84.941	1,310,961
IND04	IND09	SPR	CAS	266.724106	3.156432	84.502	1,296,211
IND04	IND01	SPR	CAS	266.703701	3.164744	84.273	1,330,491
IND04	IND05	SPR	CAS	266.654797	3.163272	84.297	1,296,785
IND04	LKA01	SPR	CAS	266.651280	3.184258	83.740	1,296,880
IND04	IND07	SPR	CAS	266.643080	3.186216	83.686	1,396,948
IND04	BGD01	SPR	CAS	266.636472	3.115107	85.595	1,332,659
IND04	BGD02	SPR	CAS	266.634511	3.155362	84.502	1,333,133
IND04	IDN03	SPR	CAS	266.518047	3.152915	84.531	1,297,502
IND04	IDN04	SPR	CAS	266.470939	3.146506	84.688	1,299,953
IND04	TWN01	SPR	CAS	266.254375	3.110509	85.598	1,297,749
IND04	VNM01	SPR	CAS	266.179315	3.132419	84.976	1,298,059
IND04	CHN17	SPR	CAS	266.166361	3.167234	84.037	1,327,851
IND04	CHN22	SPR	CAS	266.128237	3.086775	86.216	1,325,851
IND04	VNM02	SPR	CAS	266.121914	3.129086	85.048	1,297,806
IND04	CHN18	SPR	CAS	266.119633	3.129255	85.042	1,298,416
IND04	IDN02	SPR	CAS	266.056290	3.134522	84.879	1,298,485
IND04	IDN01	SPR	DOM	265.839097	3.155707	84.241	1,299,482
IND04	CHN14	SPR	CAS	265.794436	3.102669	85.666	1,299,440
IND04	CHN11	SPR	CAS	265.456524	3.147413	84.341	1,301,440
IND04	CHN12	SPR	CAS	265.221028	3.121759	84.959	1,301,435
IND04	CHN19	SPR	CAS	264.947456	3.058539	86.626	1,302,787
IND04	JPN04	SPR	MUS	264.063612	3.268240	80.797	1,307,398
IND04	CHN16	SPR	CAS	263.257133	2.939162	89.569	1,367,699
IND04	NPL01	SPR	NEP	262.710370	3.994415	65.769	1,307,058
IND04	UKR01	SPR	MUS	261.958677	3.090406	84.765	1,315,240
IND04	RUS10	SPR	CAS	261.634645	2.963340	88.290	1,316,061
IND04	RUS12	SPR	CAS	261.123165	3.037257	85.973	1,366,111
IND04	JPN01	SPR	MUS	260.352992	3.068399	84.850	1,321,251
IND04	JPN09	SPR	MUS	258.489399	3.081111	83.895	1,329,409
IND04	JPN18	SPR	CAS	257.762259	2.999806	85.926	1,332,196
IND04	JPN17	SPR	CAS	257.686272	2.930681	87.927	1,332,156
IND04	JPN15	SPR	CAS	257.631510	2.937922	87.692	1,332,567
IND04	JPN12	SPR	MUS	257.584354	2.892880	89.041	1,332,509
IND04	JPN07	SPR	MUS	257.447306	2.871021	89.671	1,333,189
IND04	JPN11	SPR	MUS	257.389145	2.826434	91.065	1,333,982

IND04	RUS15	SPR	MUS	257.378473	2.652659	97.027	1,384,743
IND04	JPN02	SPR	MUS	257.343201	2.814070	91.449	1,333,894
IND04	JPN16	SPR	CAS	257.314894	2.842731	90.517	1,333,788
IND04	RUS17	SPR	MUS	257.127743	2.761649	93.107	1,363,640
IND04	RUS14	SPR	CAS	257.115835	2.900677	88.640	1,334,703
IND04	JPN05	SPR	MUS	257.094871	2.822922	91.074	1,334,716
IND04	RUS16	SPR	DOM	257.068703	2.635651	97.535	1,334,518
IND04	CHN20	SPR	CAS	257.030721	2.668027	96.337	1,334,869
IND04	RUS11	SPR	MUS	256.715198	2.731061	93.998	1,336,578
IND04	RUS13	SPR	DOM	256.714556	2.651501	96.819	1,363,465
IND04	CHN21	SPR	CAS	256.650858	2.729501	94.028	1,336,432
IND04	KOR04	SPR	MUS	256.415386	2.714624	94.457	1,337,252
IND04	JPN03	SPR	MUS	256.341895	2.701112	94.902	1,343,655
IND04	RUS07	SPR	MUS	256.324473	2.679579	95.658	1,338,026
IND04	RUS03	SPR	MUS	256.322833	2.690819	95.258	1,337,910
IND04	JPN08	SPR	MUS	256.317889	2.716201	94.366	1,342,006
IND04	CHN05	SPR	MUS	256.315417	2.686697	95.402	1,337,943
IND04	IRN05	SPR	CAS	256.309903	2.688483	95.336	1,363,664
IND04	RUS06	SPR	MUS	256.291364	2.684318	95.477	1,338,058
IND04	RUS04	SPR	DOM	256.288000	2.686323	95.405	1,338,280
IND04	KAZ03	SPR	MUS	256.285647	2.686141	95.410	1,363,399
IND04	CHN04	SPR	MUS	256.285160	2.692917	95.170	1,337,995
IND04	CHN03	SPR	MUS	256.276627	2.685586	95.427	1,336,728
IND04	CZE01	SPR	MUS	256.276188	2.686643	95.389	1,339,205
IND04	CHN23	SPR	MUS	256.275760	2.686287	95.401	1,350,858
IND04	CHN10	SPR	MUS	256.275059	2.687883	95.345	1,337,317
IND04	KAZ05	SPR	MUS	256.274274	2.685649	95.424	1,338,158
IND04	RUS02	SPR	MUS	256.263935	2.681364	95.572	1,337,949
IND04	CZE02	SPR	MUS	256.263697	2.690969	95.231	1,338,123
IND04	RUS05	SPR	MUS	256.262176	2.690652	95.242	1,338,304
IND04	KAZ02	SPR	MUS	256.260287	2.690306	95.253	1,363,665
IND04	CHN01	SPR	MUS	256.260085	2.684413	95.462	1,336,910
IND04	KAZ01	SPR	MUS	256.259324	2.690287	95.254	1,338,271
IND04	CZE04	SPR	MUS	256.258884	2.688568	95.314	1,353,247
IND04	CHN13	SPR	MUS	256.258112	2.692850	95.162	1,348,577
IND04	IRN06	SPR	MUS	256.257779	2.683062	95.509	1,337,715
IND04	RUS08	SPR	MUS	256.257209	2.692859	95.162	1,337,634
IND04	KOR03	SPR	MUS	256.252027	2.691892	95.194	1,337,987
IND04	CZE03	SPR	MUS	256.247024	2.691379	95.210	1,354,927
IND04	CHN15	SPR	MUS	256.246774	2.695143	95.077	1,337,504
IND04	JPN06	SPR	MUS	256.246085	2.687678	95.341	1,341,541
IND04	CHN02	SPR	MUS	256.244398	2.683785	95.479	1,349,832
IND04	KOR05	SPR	MUS	256.244136	2.695269	95.072	1,337,814
IND04	JPN14	SPR	MUS	256.240892	2.684200	95.463	1,339,452
IND04	EST01	SPR	MUS	256.239834	2.689592	95.271	1,338,176
IND04	KOR02	SPR	MUS	256.236637	2.697291	94.998	1,343,562
IND04	CZE07	SPR	MUS	256.236495	2.688131	95.321	1,352,694
IND04	RUS09	SPR	MUS	256.236316	2.692510	95.166	1,356,216

IND04	CZE06	SPR	MUS	256.236293	2.685066	95.430	1,338,175
IND04	JPN13	SPR	CAS	256.236150	2.688120	95.322	1,338,101
IND04	KAZ04	SPR	MUS	256.235390	2.689872	95.259	1,338,226
IND04	CHN08	SPR	MUS	256.234641	2.693155	95.143	1,352,350
IND04	CHN07	SPR	MUS	256.233060	2.693070	95.145	1,337,433
IND04	CZE05	SPR	MUS	256.231587	2.690078	95.251	1,343,797
IND04	CHN24	SPR	MUS	256.230327	2.699347	94.923	1,354,304
IND04	JPN10	SPR	MUS	256.227665	2.689845	95.257	1,338,101
IND04	KOR01	SPR	MUS	256.225003	2.694874	95.079	1,337,921
IND04	CHN09	SPR	MUS	256.219631	2.690001	95.249	1,337,617
IND04	RUS01	SPR	DOM	255.970172	2.738144	93.483	1,489,582
IND04	CHN06	SPR	MUS	255.581122	2.790142	91.601	1,459,613
IND04	IRN01	SPR	DOM	255.520038	2.851835	89.598	1,337,545
IND04	IRN04	SPR	DOM	255.483245	2.850787	89.619	1,337,773
IND04	IRN02	SPR	DOM	255.462210	2.845622	89.774	1,337,685
IND04	IRN03	SPR	DOM	255.432833	2.859955	89.314	1,337,933
IND04	FRA01	SPR	DOM	255.387625	2.868380	89.035	1,338,728
IND04	DEU02	SPR	DOM	255.369157	2.845738	89.737	1,339,281
IND04	FRA02	SPR	DOM	255.366614	2.859212	89.314	1,338,580
IND04	FRA03	SPR	DOM	255.365093	2.858391	89.339	1,338,545
IND04	DEU03	SPR	DOM	255.362312	2.865033	89.131	1,339,166
IND04	DEU04	SPR	DOM	255.358985	2.854639	89.454	1,339,311
IND04	DEU05	SPR	DOM	255.357749	2.851517	89.552	1,339,005
IND04	DEU07	SPR	DOM	255.354611	2.851652	89.546	1,339,398
IND04	FRA04	SPR	DOM	255.340921	2.849481	89.610	1,338,586
IND04	DEU01	SPR	DOM	255.327183	2.852104	89.522	1,339,185
IND04	DEU06	SPR	DOM	255.284614	2.860292	89.251	1,339,281
IND04	NPL02	SPR	NEP	254.512195	4.752896	53.549	1,328,937

Table 1-16 The outgroup f_3 statistics result of X chromosome with SPR as outgroup. $f_3(\text{DOM}, \text{X}; \text{SPR})$

The outgroup f_3 statistics result of X chromosome with SPR as outgroup. $f_3(\text{DOM}, \text{X}; \text{SPR})$							
Source1	Source2	Target	Source2 mtDNA Haplogroup	f_3 statistics	Std.Err	Z	SNPs
DEU01	DEU04	SPR	DOM	310.9467	2.820462	110.247	1,181,846
DEU01	DEU06	SPR	DOM	310.8887	2.870605	108.301	1,181,751
DEU01	DEU05	SPR	DOM	310.5003	2.904943	106.887	1,182,887
DEU01	DEU02	SPR	DOM	310.0558	2.792531	111.030	1,184,516
DEU01	DEU03	SPR	DOM	309.9135	2.836881	109.244	1,184,769
DEU01	DEU07	SPR	DOM	309.7052	2.795281	110.796	1,185,619
DEU01	FRA04	SPR	DOM	306.9493	2.831248	108.415	1,193,000
DEU01	FRA03	SPR	DOM	306.6254	2.779005	110.336	1,193,992
DEU01	FRA02	SPR	DOM	306.4602	2.772546	110.534	1,194,533
DEU01	FRA01	SPR	DOM	306.2902	2.746987	111.500	1,195,226
DEU01	IRN01	SPR	DOM	301.2526	2.762614	109.046	1,209,379
DEU01	IRN02	SPR	DOM	300.9885	2.760408	109.038	1,210,173
DEU01	IRN03	SPR	DOM	300.9311	2.732610	110.126	1,210,503
DEU01	IRN04	SPR	DOM	300.9280	2.755152	109.224	1,210,518
DEU01	CHN06	SPR	MUS	287.2546	3.809536	75.404	1,338,635
DEU01	RUS01	SPR	DOM	277.7732	2.870543	96.767	1,395,195
DEU01	IDN02	SPR	CAS	258.7534	3.421305	75.630	1,328,452
DEU01	RUS10	SPR	CAS	258.5873	3.808880	67.891	1,333,274
DEU01	IDN01	SPR	DOM	256.9549	2.854818	90.007	1,334,049
DEU01	LKA01	SPR	CAS	255.3317	2.773531	92.060	1,338,754
DEU01	IND04	SPR	CAS	255.3272	2.852104	89.522	1,339,185
DEU01	IND03	SPR	CAS	255.3074	2.901485	87.992	1,339,253
DEU01	PAK03	SPR	CAS	255.2087	2.842276	89.790	1,338,003
DEU01	PAK04	SPR	CAS	255.1939	2.853091	89.445	1,338,433
DEU01	PAK01	SPR	CAS	255.1568	2.802206	91.056	1,451,085
DEU01	PAK02	SPR	CAS	255.0915	2.828871	90.174	1,449,460
DEU01	LKA02	SPR	CAS	255.0259	2.820021	90.434	1,339,809
DEU01	VNM02	SPR	CAS	255.0236	2.814484	90.611	1,339,027
DEU01	CHN22	SPR	CAS	254.9166	2.838149	89.818	1,368,941
DEU01	IDN03	SPR	CAS	254.8947	2.839926	89.754	1,340,276
DEU01	IND08	SPR	CAS	254.8845	2.801105	90.994	1,355,553
DEU01	RUS12	SPR	CAS	254.8809	2.787654	91.432	1,394,456
DEU01	IND06	SPR	CAS	254.8514	2.804984	90.857	1,360,698
DEU01	IND05	SPR	CAS	254.8374	2.815832	90.502	1,340,161
DEU01	TWN01	SPR	CAS	254.8293	2.826940	90.143	1,339,955
DEU01	CHN17	SPR	CAS	254.8285	2.863036	89.006	1,371,637
DEU01	IDN04	SPR	CAS	254.8211	2.840233	89.718	1,342,994
DEU01	IND07	SPR	CAS	254.7826	2.811084	90.635	1,448,645
DEU01	BGD01	SPR	CAS	254.7825	2.823382	90.240	1,378,707
DEU01	IND02	SPR	CAS	254.7799	2.818064	90.410	1,340,141
DEU01	CHN14	SPR	CAS	254.7484	2.902239	87.777	1,340,502
DEU01	CHN18	SPR	CAS	254.7185	2.846947	89.471	1,340,532
DEU01	BGD02	SPR	CAS	254.7173	2.822923	90.232	1,379,459
DEU01	VNM01	SPR	CAS	254.6860	2.842438	89.601	1,340,482

DEU01	IND01	SPR	CAS	254.6532	2.809156	90.651	1,377,163
DEU01	RUS14	SPR	CAS	254.6319	3.069110	82.966	1,350,231
DEU01	CHN11	SPR	CAS	254.6221	2.880176	88.405	1,341,883
DEU01	IND09	SPR	CAS	254.6126	2.817251	90.376	1,340,486
DEU01	CHN12	SPR	CAS	254.5986	2.869271	88.733	1,341,233
DEU01	CHN19	SPR	CAS	254.4980	2.867886	88.741	1,342,067
DEU01	UKR01	SPR	MUS	254.3922	2.787007	91.278	1,345,943
DEU01	CHN16	SPR	CAS	254.3364	2.824860	90.035	1,405,539
DEU01	JPN04	SPR	MUS	254.2850	2.906444	87.490	1,344,701
DEU01	JPN01	SPR	MUS	253.3190	2.917131	86.838	1,350,374
DEU01	EST01	SPR	MUS	253.0634	2.796878	90.481	1,355,758
DEU01	RUS15	SPR	MUS	253.0346	2.784931	90.858	1,407,333
DEU01	JPN09	SPR	MUS	252.9588	2.876974	87.925	1,354,024
DEU01	JPN18	SPR	CAS	252.9214	2.903192	87.118	1,354,762
DEU01	RUS13	SPR	DOM	252.8869	2.817214	89.765	1,382,910
DEU01	JPN15	SPR	CAS	252.8472	2.872231	88.032	1,354,960
DEU01	JPN07	SPR	MUS	252.7868	2.863201	88.288	1,355,204
DEU01	RUS16	SPR	DOM	252.7476	2.755652	91.720	1,355,496
DEU01	JPN17	SPR	CAS	252.7047	2.868337	88.101	1,355,128
DEU01	CHN20	SPR	CAS	252.6957	2.801484	90.201	1,355,908
DEU01	CZE03	SPR	MUS	252.6823	2.818893	89.639	1,373,156
DEU01	JPN16	SPR	CAS	252.6644	2.849661	88.665	1,355,770
DEU01	RUS17	SPR	MUS	252.6566	2.839374	88.983	1,385,845
DEU01	JPN11	SPR	MUS	252.6398	2.858045	88.396	1,356,266
DEU01	RUS07	SPR	MUS	252.6075	2.783048	90.766	1,357,233
DEU01	CZE07	SPR	MUS	252.5942	2.820138	89.568	1,371,454
DEU01	JPN12	SPR	MUS	252.5924	2.847906	88.694	1,355,513
DEU01	JPN02	SPR	MUS	252.5895	2.824342	89.433	1,356,185
DEU01	CZE04	SPR	MUS	252.5594	2.825028	89.401	1,372,134
DEU01	CHN21	SPR	CAS	252.5441	2.830907	89.210	1,356,799
DEU01	RUS11	SPR	MUS	252.5309	2.819421	89.568	1,357,179
DEU01	JPN05	SPR	MUS	252.5039	2.861564	88.240	1,356,522
DEU01	CZE02	SPR	MUS	252.4937	2.807123	89.948	1,357,493
DEU01	KOR04	SPR	MUS	252.4820	2.832544	89.136	1,357,104
DEU01	RUS04	SPR	DOM	252.4762	2.822204	89.461	1,357,764
DEU01	RUS05	SPR	MUS	252.4692	2.825246	89.362	1,357,740
DEU01	IRN05	SPR	CAS	252.4643	2.812649	89.760	1,383,266
DEU01	CZE05	SPR	MUS	252.4551	2.812931	89.748	1,363,042
DEU01	CHN23	SPR	MUS	252.4470	2.819707	89.530	1,370,315
DEU01	CZE06	SPR	MUS	252.4450	2.821066	89.486	1,357,605
DEU01	JPN03	SPR	MUS	252.4442	2.838942	88.922	1,363,532
DEU01	IRN06	SPR	MUS	252.4242	2.812140	89.762	1,357,277
DEU01	JPN08	SPR	MUS	252.4132	2.831756	89.137	1,361,828
DEU01	KAZ02	SPR	MUS	252.4064	2.816352	89.622	1,383,382
DEU01	RUS03	SPR	MUS	252.4047	2.825198	89.341	1,357,715
DEU01	CZE01	SPR	MUS	252.4043	2.818960	89.538	1,358,872
DEU01	KAZ04	SPR	MUS	252.4018	2.821885	89.444	1,357,776
DEU01	KAZ01	SPR	MUS	252.4011	2.829839	89.193	1,357,895
DEU01	KAZ05	SPR	MUS	252.3974	2.817071	89.596	1,357,837

DEU01	KAZ03	SPR	MUS	252.3910	2.822994	89.405	1,383,200
DEU01	CHN05	SPR	MUS	252.3850	2.822078	89.432	1,357,786
DEU01	RUS06	SPR	MUS	252.3789	2.820463	89.481	1,357,845
DEU01	JPN13	SPR	CAS	252.3753	2.821837	89.437	1,357,734
DEU01	JPN10	SPR	MUS	252.3688	2.819140	89.520	1,357,726
DEU01	RUS02	SPR	MUS	252.3681	2.814422	89.670	1,357,695
DEU01	CHN04	SPR	MUS	252.3660	2.823393	89.384	1,357,804
DEU01	JPN06	SPR	MUS	252.3659	2.820625	89.472	1,361,263
DEU01	JPN14	SPR	MUS	252.3655	2.820766	89.467	1,359,124
DEU01	KOR02	SPR	MUS	252.3646	2.824384	89.352	1,363,232
DEU01	CHN01	SPR	MUS	252.3646	2.815643	89.629	1,356,642
DEU01	CHN07	SPR	MUS	252.3629	2.825407	89.319	1,357,089
DEU01	CHN08	SPR	MUS	252.3618	2.824278	89.354	1,372,022
DEU01	KOR05	SPR	MUS	252.3606	2.822177	89.421	1,357,512
DEU01	KOR03	SPR	MUS	252.3565	2.824618	89.342	1,357,717
DEU01	RUS09	SPR	MUS	252.3546	2.825018	89.328	1,375,919
DEU01	CHN03	SPR	MUS	252.3519	2.816216	89.607	1,356,550
DEU01	RUS08	SPR	MUS	252.3464	2.822633	89.401	1,357,423
DEU01	CHN10	SPR	MUS	252.3456	2.823298	89.380	1,357,151
DEU01	KOR01	SPR	MUS	252.3445	2.823176	89.383	1,357,611
DEU01	CHN24	SPR	MUS	252.3408	2.825942	89.294	1,374,005
DEU01	CHN13	SPR	MUS	252.3395	2.822760	89.395	1,368,403
DEU01	CHN09	SPR	MUS	252.3361	2.825876	89.295	1,357,312
DEU01	CHN02	SPR	MUS	252.3338	2.817520	89.559	1,369,631
DEU01	CHN15	SPR	MUS	252.3317	2.831536	89.115	1,357,296
DEU01	NPL01	SPR	NEP	252.1228	3.343516	75.407	1,346,744
DEU01	NPL02	SPR	NEP	246.4593	3.828414	64.376	1,361,079

Table 1-17 The outgroup f_3 statistics result of X chromosome with SPR as outgroup. $f_3(\text{CAS}, \text{X}; \text{SPR})$

The outgroup f_3 statistics result of X chromosome with SPR as outgroup. $f_3(\text{MUS}, \text{X}; \text{SPR})$

Source1	Source2	Target	Source2 mtDNA Haplogroup	f_3 statistics	Std.Err	Z	SNPs
KOR01	KOR05	SPR	MUS	316.565044	2.766342	114.435	1,167,443
KOR01	KOR03	SPR	MUS	316.477767	2.779350	113.868	1,167,898
KOR01	KOR02	SPR	MUS	316.382183	2.794387	113.221	1,171,833
KOR01	JPN10	SPR	MUS	316.214487	2.766237	114.312	1,168,722
KOR01	JPN13	SPR	CAS	316.174723	2.765015	114.348	1,168,864
KOR01	JPN14	SPR	MUS	316.169648	2.768820	114.189	1,170,007
KOR01	JPN06	SPR	MUS	316.124928	2.771811	114.050	1,171,606
KOR01	JPN08	SPR	MUS	315.867637	2.679012	117.905	1,172,767
KOR01	JPN03	SPR	MUS	315.378036	2.758738	114.320	1,175,180
KOR01	KOR04	SPR	MUS	314.933096	2.683415	117.363	1,172,254
KOR01	CHN24	SPR	MUS	313.542133	2.704864	115.918	1,189,103
KOR01	CHN15	SPR	MUS	312.624538	2.701311	115.731	1,178,889
KOR01	CHN13	SPR	MUS	312.525068	2.652521	117.822	1,187,934
KOR01	CHN07	SPR	MUS	312.511996	2.655245	117.696	1,179,116
KOR01	CHN08	SPR	MUS	312.491115	2.680231	116.591	1,190,942
KOR01	RUS08	SPR	MUS	312.374758	2.665898	117.174	1,179,795
KOR01	CHN10	SPR	MUS	312.233884	2.711720	115.142	1,179,945
KOR01	JPN05	SPR	MUS	312.121318	2.837294	110.007	1,180,147
KOR01	CHN09	SPR	MUS	312.018401	2.702336	115.462	1,180,726
KOR01	RUS09	SPR	MUS	311.703330	2.636667	118.219	1,196,154
KOR01	JPN07	SPR	MUS	310.855899	2.901349	107.142	1,183,416
KOR01	CHN21	SPR	CAS	310.642104	2.739532	113.392	1,184,951
KOR01	JPN16	SPR	CAS	310.573081	3.126026	99.351	1,184,445
KOR01	JPN11	SPR	MUS	310.568803	3.136319	99.023	1,184,920
KOR01	JPN02	SPR	MUS	310.525188	2.743851	113.171	1,184,834
KOR01	JPN12	SPR	MUS	310.155402	3.251327	95.393	1,185,235
KOR01	CHN05	SPR	MUS	309.818179	2.686643	115.318	1,187,908
KOR01	JPN15	SPR	CAS	309.464176	3.163964	97.809	1,187,513
KOR01	JPN18	SPR	CAS	309.436533	2.845446	108.748	1,187,630
KOR01	KAZ02	SPR	MUS	309.358253	2.696935	114.707	1,210,113
KOR01	KAZ03	SPR	MUS	309.344348	2.711715	114.077	1,209,910
KOR01	KAZ05	SPR	MUS	309.169759	2.655432	116.429	1,189,926
KOR01	CHN04	SPR	MUS	309.160347	2.680368	115.342	1,189,828
KOR01	KAZ04	SPR	MUS	309.134867	2.731068	113.192	1,189,988
KOR01	CHN03	SPR	MUS	309.061638	2.810028	109.985	1,188,825
KOR01	CHN01	SPR	MUS	309.046426	2.788645	110.823	1,188,996
KOR01	CHN02	SPR	MUS	309.022420	2.801500	110.306	1,200,218
KOR01	RUS03	SPR	MUS	308.746138	2.778329	111.127	1,191,090
KOR01	RUS05	SPR	MUS	308.668844	2.707158	114.020	1,191,551
KOR01	JPN17	SPR	CAS	308.657768	2.919075	105.738	1,189,661
KOR01	KAZ01	SPR	MUS	308.584800	2.698074	114.372	1,191,735
KOR01	CHN23	SPR	MUS	308.554816	2.736809	112.743	1,202,355
KOR01	RUS04	SPR	DOM	308.523799	2.741634	112.533	1,192,010
KOR01	RUS02	SPR	MUS	308.483262	2.707574	113.933	1,191,742

KOR01	RUS06	SPR	MUS	308.478746	2.752318	112.080	1,191,958
KOR01	RUS07	SPR	MUS	308.471093	2.804755	109.981	1,192,026
KOR01	CZE06	SPR	MUS	308.385076	2.781298	110.878	1,192,184
KOR01	CZE01	SPR	MUS	308.363577	2.738342	112.610	1,193,277
KOR01	CZE07	SPR	MUS	308.281625	2.748985	112.144	1,204,644
KOR01	CZE05	SPR	MUS	308.233791	2.792652	110.373	1,197,299
KOR01	CZE04	SPR	MUS	308.211508	2.753180	111.947	1,205,345
KOR01	CZE02	SPR	MUS	308.164911	2.736964	112.594	1,192,871
KOR01	CZE03	SPR	MUS	308.106144	2.773208	111.101	1,206,916
KOR01	EST01	SPR	MUS	307.913443	2.831062	108.763	1,193,597
KOR01	RUS11	SPR	MUS	307.635783	2.972024	103.511	1,194,225
KOR01	IRN06	SPR	MUS	307.621261	2.777999	110.735	1,194,063
KOR01	IRN05	SPR	CAS	307.130661	2.726857	112.632	1,217,228
KOR01	JPN09	SPR	MUS	306.355628	3.631733	84.355	1,196,188
KOR01	RUS13	SPR	DOM	305.561913	3.273550	93.343	1,221,809
KOR01	RUS17	SPR	MUS	304.655061	3.236759	94.123	1,225,720
KOR01	CHN20	SPR	CAS	303.526000	3.355206	90.464	1,205,744
KOR01	RUS14	SPR	CAS	302.363284	3.690307	81.934	1,209,318
KOR01	RUS16	SPR	DOM	301.353825	4.193719	71.858	1,211,896
KOR01	RUS15	SPR	MUS	301.338993	3.807618	79.141	1,251,189
KOR01	JPN01	SPR	MUS	292.759767	3.854952	75.944	1,234,196
KOR01	RUS12	SPR	CAS	283.354964	3.969500	71.383	1,299,174
KOR01	UKR01	SPR	MUS	282.659803	4.591812	61.557	1,263,106
KOR01	RUS01	SPR	DOM	281.391093	2.736575	102.826	1,381,693
KOR01	RUS10	SPR	CAS	276.790413	4.808534	57.562	1,280,459
KOR01	CHN16	SPR	CAS	276.666438	3.977901	69.551	1,322,892
KOR01	JPN04	SPR	MUS	274.837000	3.721100	73.859	1,284,901
KOR01	CHN06	SPR	MUS	274.509997	3.142561	87.352	1,378,273
KOR01	CHN19	SPR	CAS	265.847011	3.842129	69.193	1,309,614
KOR01	CHN11	SPR	CAS	265.141524	3.193599	83.023	1,312,021
KOR01	CHN12	SPR	CAS	263.130116	3.325047	79.136	1,317,230
KOR01	CHN14	SPR	CAS	261.020522	2.808401	92.943	1,323,238
KOR01	CHN17	SPR	CAS	259.768770	2.678859	96.970	1,354,296
KOR01	CHN22	SPR	CAS	259.358460	2.885897	89.871	1,353,045
KOR01	CHN18	SPR	CAS	259.163846	2.757421	93.988	1,328,726
KOR01	TWN01	SPR	CAS	258.412129	2.868116	90.098	1,330,820
KOR01	VNM02	SPR	CAS	256.778279	2.600684	98.735	1,335,273
KOR01	VNM01	SPR	CAS	256.624380	2.627148	97.682	1,336,160
KOR01	PAK02	SPR	CAS	256.465442	2.671293	96.008	1,445,499
KOR01	PAK01	SPR	CAS	256.267916	2.649997	96.705	1,447,679
KOR01	IND04	SPR	CAS	256.225003	2.694874	95.079	1,337,921
KOR01	PAK04	SPR	CAS	256.179915	2.643836	96.897	1,336,928
KOR01	IND03	SPR	CAS	256.113078	2.679201	95.593	1,338,271
KOR01	IDN02	SPR	CAS	256.069440	2.645584	96.791	1,337,843
KOR01	LKA02	SPR	CAS	256.044460	2.676800	95.653	1,338,226
KOR01	IDN04	SPR	CAS	256.027382	2.666006	96.034	1,340,823
KOR01	BGD02	SPR	CAS	256.025077	2.688010	95.247	1,376,715
KOR01	IDN03	SPR	CAS	256.001285	2.658626	96.291	1,338,447
KOR01	PAK03	SPR	CAS	255.977409	2.665920	96.018	1,337,108

KOR01	IND07	SPR	CAS	255.905368	2.713007	94.325	1,445,808
KOR01	IND09	SPR	CAS	255.888398	2.685347	95.291	1,338,142
KOR01	IND02	SPR	CAS	255.867030	2.698938	94.803	1,338,370
KOR01	IND08	SPR	CAS	255.864202	2.711107	94.376	1,354,070
KOR01	IDN01	SPR	DOM	255.860232	2.685767	95.265	1,338,793
KOR01	LKA01	SPR	CAS	255.857166	2.722177	93.990	1,338,631
KOR01	IND05	SPR	CAS	255.855693	2.705717	94.561	1,338,575
KOR01	BGD01	SPR	CAS	255.849346	2.701047	94.722	1,376,822
KOR01	IND06	SPR	CAS	255.844890	2.652135	96.468	1,359,033
KOR01	IND01	SPR	CAS	255.697456	2.684907	95.235	1,375,022
KOR01	NPL01	SPR	NEP	252.535513	3.346145	75.471	1,346,946
KOR01	IRN01	SPR	DOM	252.527360	2.834481	89.091	1,356,009
KOR01	IRN04	SPR	DOM	252.480252	2.829403	89.234	1,356,263
KOR01	IRN03	SPR	DOM	252.472765	2.841816	88.842	1,356,292
KOR01	IRN02	SPR	DOM	252.463543	2.816941	89.623	1,356,158
KOR01	DEU04	SPR	DOM	252.401246	2.807629	89.898	1,357,654
KOR01	DEU03	SPR	DOM	252.377621	2.818519	89.543	1,357,609
KOR01	DEU05	SPR	DOM	252.367400	2.813410	89.702	1,357,456
KOR01	DEU06	SPR	DOM	252.354827	2.821163	89.451	1,357,550
KOR01	FRA02	SPR	DOM	252.350644	2.829214	89.195	1,357,107
KOR01	DEU02	SPR	DOM	252.348528	2.817383	89.568	1,357,825
KOR01	FRA04	SPR	DOM	252.345248	2.821838	89.426	1,357,053
KOR01	DEU01	SPR	DOM	252.344488	2.823176	89.383	1,357,611
KOR01	FRA01	SPR	DOM	252.336050	2.826375	89.279	1,357,381
KOR01	FRA03	SPR	DOM	252.317844	2.824172	89.342	1,357,164
KOR01	DEU07	SPR	DOM	252.316014	2.806105	89.917	1,357,995
KOR01	NPL02	SPR	NEP	247.071251	3.873355	63.787	1,360,717

Table 1-18 The f_4 statistics result of X chromosome. $f_4(\text{SPR, CAS; DOM, X})$ The f_4 statistics result of X chromosome. $f_4(\text{SPR, CAS; DOM, X})$

Pop1(W)	Pop2(X)	Pop3(Y)	Pop4(Z)	Pop4(Z) mtDNA Haplogroup	f_4 statistics	Standard Error	Z	BABA	ABBA	Number of SNPs that all population have data
SPR	IND04	DEU01	FRA01	DOM	-0.000043	0.000047	-0.899	1,652	1,780	3,005,216
SPR	IND04	DEU01	FRA02	DOM	-0.000815	0.002917	-0.279	50,914	53,364	3,005,216
SPR	IND04	DEU01	FRA03	DOM	0.000014	0.000052	0.262	2,589	2,548	3,005,216
SPR	IND04	DEU01	FRA04	DOM	0.000031	0.000052	0.589	1,878	1,786	3,005,216
SPR	IND04	DEU01	DEU02	DOM	0.000027	0.000045	0.614	1,918	1,836	3,005,216
SPR	IND04	DEU01	DEU03	DOM	0.000038	0.000051	0.750	2,645	2,531	3,005,216
SPR	IND04	DEU01	DEU04	DOM	0.000035	0.000045	0.773	2,082	1,977	3,005,216
SPR	IND04	DEU01	DEU05	DOM	0.000032	0.000037	0.858	1,751	1,656	3,005,216
SPR	IND04	DEU01	DEU06	DOM	0.000042	0.000048	0.869	2,024	1,898	3,005,216
SPR	IND04	DEU01	DEU07	DOM	0.000039	0.000044	0.905	2,632	2,514	3,005,216
SPR	IND04	DEU01	IRN01	DOM	0.000254	0.000248	1.023	18,157	17,394	3,005,216
SPR	IND04	DEU01	IRN02	DOM	0.000060	0.000054	1.119	2,786	2,604	3,005,216
SPR	IND04	DEU01	IRN03	DOM	0.000900	0.000580	1.553	44,251	41,545	3,005,216
SPR	IND04	DEU01	IRN04	DOM	0.000898	0.000577	1.556	44,284	41,586	3,005,216
SPR	IND04	DEU01	IRN05	CAS	0.000892	0.000571	1.564	44,277	41,595	3,005,216
SPR	IND04	DEU01	CZE01	MUS	0.000909	0.000580	1.568	44,256	41,524	3,005,216
SPR	IND04	DEU01	IRN06	MUS	0.000909	0.000580	1.568	44,281	41,548	3,005,216
SPR	IND04	DEU01	CZE02	MUS	0.000917	0.000583	1.573	44,315	41,560	3,005,216
SPR	IND04	DEU01	CZE03	MUS	0.000903	0.000573	1.577	44,309	41,595	3,005,216
SPR	IND04	DEU01	CZE04	MUS	0.000919	0.000580	1.584	44,303	41,541	3,005,216
SPR	IND04	DEU01	CZE05	MUS	0.000906	0.000571	1.587	44,255	41,532	3,005,216
SPR	IND04	DEU01	CZE06	MUS	0.000914	0.000575	1.588	44,289	41,544	3,005,216
SPR	IND04	DEU01	CZE07	MUS	0.000920	0.000576	1.595	44,346	41,583	3,005,216
SPR	IND04	DEU01	EST01	MUS	0.000917	0.000574	1.597	44,350	41,593	3,005,216
SPR	IND04	DEU01	RUS08	MUS	0.000925	0.000579	1.598	44,338	41,559	3,005,216
SPR	IND04	DEU01	RUS09	MUS	0.000913	0.000571	1.600	43,750	41,007	3,005,216
SPR	IND04	DEU01	RUS01	DOM	0.000907	0.000567	1.601	44,275	41,547	3,005,216
SPR	IND04	DEU01	UKR01	MUS	0.000909	0.000568	1.601	44,313	41,580	3,005,216
SPR	IND04	DEU01	RUS02	MUS	0.000909	0.000566	1.607	44,240	41,508	3,005,216
SPR	IND04	DEU01	RUS03	MUS	0.000904	0.000561	1.612	44,223	41,506	3,005,216
SPR	IND04	DEU01	RUS04	DOM	0.000908	0.000562	1.617	44,253	41,523	3,005,216
SPR	IND04	DEU01	RUS05	MUS	0.000909	0.000562	1.618	44,137	41,404	3,005,216
SPR	IND04	DEU01	RUS06	MUS	0.000930	0.000574	1.619	44,335	41,540	3,005,216
SPR	IND04	DEU01	RUS07	MUS	0.000937	0.000576	1.626	44,340	41,525	3,005,216
SPR	IND04	DEU01	RUS10	CAS	0.000932	0.000573	1.627	44,311	41,509	3,005,216
SPR	IND04	DEU01	RUS11	MUS	0.000931	0.000572	1.628	44,362	41,564	3,005,216
SPR	IND04	DEU01	RUS12	CAS	0.000933	0.000571	1.634	44,289	41,485	3,005,216
SPR	IND04	DEU01	RUS13	DOM	0.000920	0.000562	1.636	44,134	41,369	3,005,216
SPR	IND04	DEU01	RUS15	MUS	0.000933	0.000570	1.637	44,337	41,533	3,005,216
SPR	IND04	DEU01	RUS14	CAS	0.000937	0.000572	1.637	44,248	41,434	3,005,216
SPR	IND04	DEU01	RUS16	DOM	0.000932	0.000567	1.644	44,202	41,402	3,005,216
SPR	IND04	DEU01	RUS17	MUS	0.000948	0.000576	1.646	44,368	41,519	3,005,216
SPR	IND04	DEU01	KAZ01	MUS	0.000949	0.000574	1.653	44,385	41,531	3,005,216
SPR	IND04	DEU01	KAZ02	MUS	0.000931	0.000563	1.654	44,266	41,470	3,005,216
SPR	IND04	DEU01	KAZ03	MUS	0.000947	0.000573	1.654	44,322	41,475	3,005,216
SPR	IND04	DEU01	KAZ04	MUS	0.000935	0.000564	1.657	44,233	41,423	3,005,216
SPR	IND04	DEU01	KAZ05	MUS	0.000958	0.000575	1.666	44,374	41,495	3,005,216
SPR	IND04	DEU01	KOR01	MUS	0.000949	0.000568	1.671	44,313	41,461	3,005,216
SPR	IND04	DEU01	KOR02	MUS	0.000958	0.000571	1.678	44,356	41,476	3,005,216
SPR	IND04	DEU01	KOR03	MUS	0.000949	0.000563	1.685	44,275	41,424	3,005,216
SPR	IND04	DEU01	KOR04	MUS	0.000961	0.000567	1.694	44,261	41,374	3,005,216
SPR	IND04	DEU01	KOR05	MUS	0.000964	0.000569	1.694	44,358	41,460	3,005,216
SPR	IND04	DEU01	JPN01	MUS	0.000983	0.000572	1.717	44,332	41,379	3,005,216
SPR	IND04	DEU01	JPN02	MUS	0.000988	0.000574	1.722	44,409	41,439	3,005,216
SPR	IND04	DEU01	JPN03	MUS	0.000997	0.000575	1.734	44,182	41,185	3,005,216
SPR	IND04	DEU01	JPN04	MUS	0.000996	0.000572	1.739	44,407	41,414	3,005,216
SPR	IND04	DEU01	JPN05	MUS	0.000991	0.000561	1.766	44,348	41,370	3,005,216
SPR	IND04	DEU01	JPN06	MUS	0.001015	0.000558	1.818	44,361	41,311	3,005,216
SPR	IND04	DEU01	JPN07	MUS	0.001088	0.000590	1.843	44,476	41,206	3,005,216
SPR	IND04	DEU01	JPN08	MUS	0.000106	0.000057	1.857	4,365	4,048	3,005,216
SPR	IND04	DEU01	JPN09	MUS	0.000643	0.000335	1.921	24,626	22,693	3,005,216
SPR	IND04	DEU01	JPN10	MUS	0.000156	0.000079	1.964	4,400	3,931	3,005,216
SPR	IND04	DEU01	JPN11	MUS	0.001388	0.000692	2.006	45,120	40,949	3,005,216
SPR	IND04	DEU01	JPN12	MUS	0.001324	0.000625	2.117	44,969	40,991	3,005,216
SPR	IND04	DEU01	JPN13	CAS	0.000135	0.000060	2.254	4,243	3,837	3,005,216
SPR	IND04	DEU01	JPN14	MUS	0.001387	0.000603	2.301	44,868	40,699	3,005,216
SPR	IND04	DEU01	JPN15	CAS	0.001742	0.000712	2.445	45,639	40,405	3,005,216
SPR	IND04	DEU01	JPN16	CAS	0.000193	0.000072	2.663	4,325	3,745	3,005,216

SPR	IND04	DEU01	JPN17	CAS	0.001801	0.000676	2.665	45,990	40,579	3,005,216
SPR	IND04	DEU01	JPN18	CAS	0.001789	0.000644	2.776	44,326	38,951	3,005,216
SPR	IND04	DEU01	CHN01	MUS	0.001704	0.000601	2.833	45,612	40,493	3,005,216
SPR	IND04	DEU01	CHN02	MUS	0.002257	0.000707	3.191	46,851	40,067	3,005,216
SPR	IND04	DEU01	CHN03	MUS	0.002062	0.000643	3.207	46,338	40,142	3,005,216
SPR	IND04	DEU01	CHN04	MUS	0.002051	0.000630	3.256	46,087	39,923	3,005,216
SPR	IND04	DEU01	CHN05	MUS	0.002304	0.000686	3.360	46,658	39,733	3,005,216
SPR	IND04	DEU01	CHN06	MUS	0.001768	0.000524	3.373	45,777	40,465	3,005,216
SPR	IND04	DEU01	CHN07	MUS	0.001988	0.000587	3.388	46,191	40,217	3,005,216
SPR	IND04	DEU01	CHN08	MUS	0.003162	0.000884	3.578	48,247	38,744	3,005,216
SPR	IND04	DEU01	CHN09	MUS	0.002120	0.000592	3.579	46,268	39,896	3,005,216
SPR	IND04	DEU01	CHN10	MUS	0.002016	0.000536	3.764	46,264	40,205	3,005,216
SPR	IND04	DEU01	CHN11	CAS	0.002359	0.000623	3.785	46,902	39,813	3,005,216
SPR	IND04	DEU01	CHN12	CAS	0.002435	0.000640	3.805	46,762	39,444	3,005,216
SPR	IND04	DEU01	CHN13	MUS	0.007383	0.001740	4.242	59,310	37,122	3,005,216
SPR	IND04	DEU01	CHN14	CAS	0.005026	0.000826	6.084	51,671	36,567	3,005,216
SPR	IND04	DEU01	CHN15	MUS	0.006631	0.000993	6.678	54,039	34,110	3,005,216
SPR	IND04	DEU01	CHN16	CAS	0.006307	0.000913	6.908	50,410	31,455	3,005,216
SPR	IND04	DEU01	CHN17	CAS	0.005796	0.000747	7.759	52,525	35,107	3,005,216
SPR	IND04	DEU01	CHN18	CAS	0.008736	0.000732	11.941	58,512	32,257	3,005,216
SPR	IND04	DEU01	CHN19	CAS	0.009620	0.000739	13.022	60,143	31,232	3,005,216
SPR	IND04	DEU01	CHN20	CAS	0.007930	0.000579	13.697	56,863	33,031	3,005,216
SPR	IND04	DEU01	CHN21	CAS	0.015190	0.001098	13.839	72,442	26,793	3,005,216
SPR	IND04	DEU01	CHN22	CAS	0.009894	0.000710	13.931	60,658	30,925	3,005,216
SPR	IND04	DEU01	CHN23	MUS	0.010729	0.000714	15.017	59,533	27,290	3,005,216
SPR	IND04	DEU01	CHN24	MUS	0.010129	0.000639	15.858	61,100	30,659	3,005,216
SPR	IND04	DEU01	TWN01	CAS	0.010512	0.000647	16.249	60,274	28,684	3,005,216
SPR	IND04	DEU01	PAK01	CAS	0.010839	0.000612	17.713	62,406	29,832	3,005,216
SPR	IND04	DEU01	PAK02	CAS	0.011328	0.000618	18.338	63,709	29,667	3,005,216
SPR	IND04	DEU01	PAK03	CAS	0.010801	0.000589	18.349	62,195	29,736	3,005,216
SPR	IND04	DEU01	PAK04	CAS	0.010467	0.000568	18.425	61,723	30,267	3,005,216
SPR	IND04	DEU01	NPL01	NEP	0.011397	0.000618	18.431	64,207	29,957	3,005,216
SPR	IND04	DEU01	NPL02	NEP	0.011307	0.000612	18.462	63,722	29,741	3,005,216
SPR	IND04	DEU01	IND01	CAS	0.011324	0.000610	18.579	63,240	29,209	3,005,216
SPR	IND04	DEU01	IND02	CAS	0.010795	0.000579	18.649	62,129	29,689	3,005,216
SPR	IND04	DEU01	IND03	CAS	0.011144	0.000596	18.690	63,121	29,632	3,005,216
SPR	IND04	DEU01	IND05	CAS	0.011191	0.000596	18.775	63,107	29,476	3,005,216
SPR	IND04	DEU01	IND06	CAS	0.011496	0.000609	18.889	63,994	29,444	3,005,216
SPR	IND04	DEU01	IND07	CAS	0.010792	0.000570	18.921	62,553	30,119	3,005,216
SPR	IND04	DEU01	IND08	CAS	0.010927	0.000572	19.119	62,584	29,745	3,005,216
SPR	IND04	DEU01	IND09	CAS	0.011309	0.000584	19.381	63,570	29,584	3,005,216
SPR	IND04	DEU01	VNM01	CAS	0.012982	0.000669	19.406	67,034	28,021	3,005,216
SPR	IND04	DEU01	VNM02	CAS	0.011377	0.000577	19.731	64,026	29,837	3,005,216
SPR	IND04	DEU01	IDN01	DOM	0.010852	0.000546	19.868	62,695	30,082	3,005,216
SPR	IND04	DEU01	IDN02	CAS	0.011420	0.000568	20.114	63,540	29,222	3,005,216
SPR	IND04	DEU01	IDN03	CAS	0.011517	0.000567	20.323	63,637	29,026	3,005,216
SPR	IND04	DEU01	IDN04	CAS	0.011316	0.000553	20.456	63,791	29,784	3,005,216
SPR	IND04	DEU01	LKA01	CAS	0.011848	0.000576	20.564	64,840	29,235	3,005,216
SPR	IND04	DEU01	LKA02	CAS	0.012016	0.000513	23.411	64,684	28,575	3,005,216
SPR	IND04	DEU01	BGD01	CAS	0.014246	0.000506	28.170	70,206	27,395	3,005,216
SPR	IND04	DEU01	BGD02	CAS	0.039452	0.001011	39.022	130,683	12,122	3,005,216

Table 1-19 The f_4 statistics result of X chromosome. $f_4(\text{SPR, CAS; MUS, X})$ The f_4 statistics result of X chromosome. $f_4(\text{SPR, CAS; MUS, X})$

Pop1(W)	Pop2(X)	Pop3(Y)	Pop4(Z)	Pop4(Z) mtDNA Haplogroup	f_4 statistics	Standard Error	Z	BABA	ABBA	Number of SNPs that all population have data
SPR	IND04	KOR01	DEU06	DOM	-0.00094	0.000559	-1.684	41,494	44,320	3,005,216
SPR	IND04	KOR01	FRA04	DOM	-0.00088	0.000555	-1.593	41,617	44,274	3,005,216
SPR	IND04	KOR01	CHN06	MUS	-0.00064	0.000411	-1.568	26,039	27,973	3,005,216
SPR	IND04	KOR01	DEU01	DOM	-0.00090	0.000577	-1.556	41,586	44,284	3,005,216
SPR	IND04	KOR01	DEU05	DOM	-0.00087	0.000559	-1.551	41,602	44,208	3,005,216
SPR	IND04	KOR01	DEU03	DOM	-0.00086	0.000557	-1.549	41,614	44,206	3,005,216
SPR	IND04	KOR01	DEU07	DOM	-0.00087	0.000564	-1.544	41,723	44,339	3,005,216
SPR	IND04	KOR01	DEU02	DOM	-0.00086	0.000557	-1.537	41,651	44,223	3,005,216
SPR	IND04	KOR01	DEU04	DOM	-0.00087	0.000569	-1.523	41,617	44,220	3,005,216
SPR	IND04	KOR01	FRA02	DOM	-0.00086	0.000568	-1.511	41,639	44,219	3,005,216
SPR	IND04	KOR01	FRA03	DOM	-0.00086	0.000570	-1.508	41,679	44,263	3,005,216
SPR	IND04	KOR01	FRA01	DOM	-0.00084	0.000565	-1.481	41,699	44,216	3,005,216
SPR	IND04	KOR01	IRN03	DOM	-0.00079	0.000569	-1.393	41,634	44,015	3,005,216
SPR	IND04	KOR01	IRN02	DOM	-0.00076	0.000567	-1.344	41,738	44,030	3,005,216
SPR	IND04	KOR01	IRN04	DOM	-0.00074	0.000564	-1.316	41,655	43,884	3,005,216
SPR	IND04	KOR01	IRN01	DOM	-0.00071	0.000583	-1.208	41,750	43,869	3,005,216
SPR	IND04	KOR01	RUS01	DOM	-0.00026	0.000260	-0.980	21,214	21,980	3,005,216
SPR	IND04	KOR01	NPL02	NEP	-0.00171	0.002915	-0.588	49,403	54,550	3,005,216
SPR	IND04	KOR01	CHN09	MUS	-0.00001	0.000025	-0.217	823	839	3,005,216
SPR	IND04	KOR01	JPN10	MUS	0.00000	0.000028	0.096	353	345	3,005,216
SPR	IND04	KOR01	CZE05	MUS	0.00001	0.000048	0.137	1,810	1,791	3,005,216
SPR	IND04	KOR01	CZE06	MUS	0.00001	0.000052	0.218	1,790	1,756	3,005,216
SPR	IND04	KOR01	CZE07	MUS	0.00001	0.000051	0.226	1,802	1,768	3,005,216
SPR	IND04	KOR01	KAZ04	MUS	0.00001	0.000042	0.245	1,493	1,462	3,005,216
SPR	IND04	KOR01	CHN07	MUS	0.00001	0.000027	0.302	759	735	3,005,216
SPR	IND04	KOR01	EST01	MUS	0.00002	0.000048	0.306	2,174	2,130	3,005,216
SPR	IND04	KOR01	CHN08	MUS	0.00001	0.000031	0.313	808	779	3,005,216
SPR	IND04	KOR01	CHN24	MUS	0.00001	0.000016	0.328	622	606	3,005,216
SPR	IND04	KOR01	JPN13	CAS	0.00001	0.000028	0.404	348	315	3,005,216
SPR	IND04	KOR01	RUS09	MUS	0.00001	0.000025	0.445	959	925	3,005,216
SPR	IND04	KOR01	CZE03	MUS	0.00002	0.000047	0.467	1,889	1,823	3,005,216
SPR	IND04	KOR01	JPN14	MUS	0.00002	0.000029	0.557	376	328	3,005,216
SPR	IND04	KOR01	IRN06	MUS	0.00003	0.000058	0.566	1,913	1,815	3,005,216
SPR	IND04	KOR01	CHN02	MUS	0.00002	0.000032	0.600	1,562	1,504	3,005,216
SPR	IND04	KOR01	KAZ01	MUS	0.00003	0.000053	0.644	1,659	1,556	3,005,216
SPR	IND04	KOR01	CZE02	MUS	0.00004	0.000058	0.669	1,846	1,730	3,005,216
SPR	IND04	KOR01	JPN06	MUS	0.00002	0.000030	0.693	460	397	3,005,216
SPR	IND04	KOR01	RUS02	MUS	0.00004	0.000052	0.748	1,729	1,612	3,005,216
SPR	IND04	KOR01	CZE04	MUS	0.00003	0.000043	0.787	1,816	1,714	3,005,216
SPR	IND04	KOR01	RUS05	MUS	0.00004	0.000046	0.811	1,639	1,527	3,005,216
SPR	IND04	KOR01	KOR02	MUS	0.00001	0.000012	0.933	306	271	3,005,216
SPR	IND04	KOR01	CHN01	MUS	0.00004	0.000036	0.968	1,591	1,485	3,005,216
SPR	IND04	KOR01	KAZ02	MUS	0.00004	0.000036	0.988	1,436	1,330	3,005,216
SPR	IND04	KOR01	JPN08	MUS	0.00009	0.000086	1.081	743	464	3,005,216
SPR	IND04	KOR01	KOR05	MUS	0.00002	0.000017	1.096	289	231	3,005,216
SPR	IND04	KOR01	CZE01	MUS	0.00005	0.000047	1.101	1,736	1,582	3,005,216
SPR	IND04	KOR01	RUS04	DOM	0.00006	0.000056	1.119	1,761	1,571	3,005,216
SPR	IND04	KOR01	CHN15	MUS	0.00002	0.000019	1.168	743	677	3,005,216
SPR	IND04	KOR01	RUS08	MUS	0.00003	0.000026	1.217	857	760	3,005,216
SPR	IND04	KOR01	CHN23	MUS	0.00005	0.000041	1.246	1,744	1,592	3,005,216
SPR	IND04	KOR01	RUS06	MUS	0.00007	0.000051	1.310	1,768	1,568	3,005,216
SPR	IND04	KOR01	KOR03	MUS	0.00003	0.000019	1.407	352	271	3,005,216
SPR	IND04	KOR01	CHN13	MUS	0.00003	0.000023	1.420	812	713	3,005,216
SPR	IND04	KOR01	KAZ05	MUS	0.00005	0.000034	1.456	1,496	1,348	3,005,216
SPR	IND04	KOR01	CHN04	MUS	0.00006	0.000041	1.478	1,526	1,346	3,005,216
SPR	IND04	KOR01	KAZ03	MUS	0.00006	0.000040	1.519	1,551	1,369	3,005,216
SPR	IND04	KOR01	RUS11	MUS	0.00049	0.000310	1.579	3,606	2,133	3,005,216
SPR	IND04	KOR01	CHN03	MUS	0.00005	0.000033	1.585	1,585	1,430	3,005,216
SPR	IND04	KOR01	JPN03	MUS	0.00012	0.000068	1.711	1,038	687	3,005,216
SPR	IND04	KOR01	CHN10	MUS	0.00005	0.000029	1.750	861	711	3,005,216
SPR	IND04	KOR01	IRN05	CAS	0.00009	0.000048	1.773	2,122	1,867	3,005,216
SPR	IND04	KOR01	KOR04	MUS	0.00019	0.000104	1.834	1,489	916	3,005,216
SPR	IND04	KOR01	RUS14	CAS	0.00089	0.000478	1.863	8,084	5,407	3,005,216
SPR	IND04	KOR01	RUS07	MUS	0.00010	0.000050	2.005	1,878	1,579	3,005,216
SPR	IND04	KOR01	RUS17	MUS	0.00090	0.000450	2.008	6,340	3,627	3,005,216
SPR	IND04	KOR01	JPN05	MUS	0.00087	0.000432	2.014	4,409	1,795	3,005,216
SPR	IND04	KOR01	JPN11	MUS	0.00116	0.000571	2.038	6,296	2,798	3,005,216
SPR	IND04	KOR01	JPN15	CAS	0.00141	0.000665	2.115	7,162	2,936	3,005,216

SPR	IND04	KOR01	JPN16	CAS	0.00109	0.000511	2.135	5,915	2,640	3,005,216
SPR	IND04	KOR01	JPN12	MUS	0.00136	0.000610	2.229	6,817	2,732	3,005,216
SPR	IND04	KOR01	JPN18	CAS	0.00154	0.000658	2.335	7,323	2,703	3,005,216
SPR	IND04	KOR01	RUS03	MUS	0.00010	0.000041	2.394	1,655	1,361	3,005,216
SPR	IND04	KOR01	CHN21	CAS	0.00043	0.000172	2.483	3,582	2,302	3,005,216
SPR	IND04	KOR01	JPN09	MUS	0.00226	0.000911	2.487	10,812	4,007	3,005,216
SPR	IND04	KOR01	JPN07	MUS	0.00122	0.000489	2.502	6,005	2,332	3,005,216
SPR	IND04	KOR01	JPN17	CAS	0.00146	0.000574	2.544	7,995	3,603	3,005,216
SPR	IND04	KOR01	JPN02	MUS	0.00112	0.000439	2.548	6,249	2,889	3,005,216
SPR	IND04	KOR01	CHN05	MUS	0.00009	0.000033	2.754	1,411	1,139	3,005,216
SPR	IND04	KOR01	RUS16	DOM	0.00084	0.000298	2.833	9,210	6,675	3,005,216
SPR	IND04	KOR01	RUS15	MUS	0.00115	0.000397	2.909	9,178	5,712	3,005,216
SPR	IND04	KOR01	NPL01	NEP	0.00649	0.001933	3.355	58,267	38,777	3,005,216
SPR	IND04	KOR01	RUS13	DOM	0.00049	0.000139	3.522	5,055	3,584	3,005,216
SPR	IND04	KOR01	CHN20	CAS	0.00081	0.000214	3.758	7,296	4,874	3,005,216
SPR	IND04	KOR01	JPN01	MUS	0.00413	0.000826	4.996	24,230	11,825	3,005,216
SPR	IND04	KOR01	RUS10	CAS	0.00541	0.001070	5.056	35,886	19,628	3,005,216
SPR	IND04	KOR01	UKR01	MUS	0.00573	0.001071	5.351	31,631	14,400	3,005,216
SPR	IND04	KOR01	RUS12	CAS	0.00490	0.000823	5.953	29,862	15,142	3,005,216
SPR	IND04	KOR01	JPN04	MUS	0.00784	0.000943	8.313	42,816	19,259	3,005,216
SPR	IND04	KOR01	CHN16	CAS	0.00703	0.000731	9.625	39,988	18,855	3,005,216
SPR	IND04	KOR01	CHN19	CAS	0.00872	0.000857	10.174	51,034	24,821	3,005,216
SPR	IND04	KOR01	CHN11	CAS	0.00923	0.000888	10.400	52,351	24,609	3,005,216
SPR	IND04	KOR01	IDN02	CAS	0.00983	0.000905	10.861	60,188	30,642	3,005,216
SPR	IND04	KOR01	CHN12	CAS	0.00900	0.000823	10.936	53,433	26,398	3,005,216
SPR	IND04	KOR01	IDN01	DOM	0.00961	0.000843	11.408	60,040	31,148	3,005,216
SPR	IND04	KOR01	IND06	CAS	0.01060	0.000863	12.286	62,217	30,366	3,005,216
SPR	IND04	KOR01	IND09	CAS	0.01050	0.000849	12.369	62,003	30,451	3,005,216
SPR	IND04	KOR01	IND05	CAS	0.01043	0.000840	12.412	61,928	30,584	3,005,216
SPR	IND04	KOR01	CHN14	CAS	0.00957	0.000770	12.421	55,996	27,238	3,005,216
SPR	IND04	KOR01	CHN17	CAS	0.00994	0.000792	12.550	57,573	27,697	3,005,216
SPR	IND04	KOR01	IDN04	CAS	0.01025	0.000816	12.558	61,089	30,298	3,005,216
SPR	IND04	KOR01	PAK02	CAS	0.01429	0.001134	12.600	69,986	27,036	3,005,216
SPR	IND04	KOR01	TWN01	CAS	0.01003	0.000792	12.668	58,703	28,563	3,005,216
SPR	IND04	KOR01	IND01	CAS	0.01048	0.000827	12.675	62,091	30,600	3,005,216
SPR	IND04	KOR01	VNM02	CAS	0.00990	0.000778	12.717	59,683	29,941	3,005,216
SPR	IND04	KOR01	IDN03	CAS	0.01029	0.000808	12.745	61,212	30,279	3,005,216
SPR	IND04	KOR01	CHN18	CAS	0.00990	0.000767	12.897	58,088	28,352	3,005,216
SPR	IND04	KOR01	LKA01	CAS	0.01043	0.000807	12.927	61,808	30,475	3,005,216
SPR	IND04	KOR01	CHN22	CAS	0.00990	0.000762	12.995	57,820	28,058	3,005,216
SPR	IND04	KOR01	BGD02	CAS	0.01041	0.000793	13.130	61,502	30,219	3,005,216
SPR	IND04	KOR01	IND08	CAS	0.01052	0.000799	13.176	61,895	30,275	3,005,216
SPR	IND04	KOR01	VNM01	CAS	0.00995	0.000754	13.194	60,068	30,154	3,005,216
SPR	IND04	KOR01	BGD01	CAS	0.01041	0.000783	13.300	61,660	30,372	3,005,216
SPR	IND04	KOR01	IND07	CAS	0.01042	0.000773	13.484	61,590	30,281	3,005,216
SPR	IND04	KOR01	IND02	CAS	0.01095	0.000804	13.622	62,824	29,917	3,005,216
SPR	IND04	KOR01	PAK04	CAS	0.01208	0.000865	13.967	65,229	28,914	3,005,216
SPR	IND04	KOR01	LKA02	CAS	0.01062	0.000751	14.136	61,843	29,930	3,005,216
SPR	IND04	KOR01	PAK03	CAS	0.01112	0.000745	14.930	63,161	29,750	3,005,216
SPR	IND04	KOR01	PAK01	CAS	0.01335	0.000763	17.489	68,072	27,958	3,005,216
SPR	IND04	KOR01	IND03	CAS	0.03855	0.000938	41.085	128,464	12,601	3,005,216

Table 1-20 The f_4 statistics result of X chromosome. $f_4(\text{SPR}, \text{DOM}; \text{CAS}, \text{X})$ The f_4 statistics result of X chromosome. $f_4(\text{SPR}, \text{DOM}; \text{CAS}, \text{X})$

Pop1(W)	Pop2(X)	Pop3(Y)	Pop4(Z)	Pop4(Z) mtDNA Haplogroup	f_4 statistics	Standard Error	Z	BABA	ABBA	Number of SNPs that all population have data
SPR	DEU01	IND04	JPN02	MUS	-0.002738	0.000358	-7.647	31,978	40,205	3,005,216
SPR	DEU01	IND04	RUS08	MUS	-0.002981	0.000403	-7.392	32,582	41,540	3,005,216
SPR	DEU01	IND04	RUS09	MUS	-0.002973	0.000405	-7.341	32,647	41,580	3,005,216
SPR	DEU01	IND04	RUS17	MUS	-0.002671	0.000365	-7.322	32,553	40,579	3,005,216
SPR	DEU01	IND04	CHN09	MUS	-0.002991	0.000410	-7.293	32,606	41,595	3,005,216
SPR	DEU01	IND04	CHN10	MUS	-0.002982	0.000410	-7.274	32,559	41,519	3,005,216
SPR	DEU01	IND04	CHN15	MUS	-0.002996	0.000412	-7.269	32,580	41,583	3,005,216
SPR	DEU01	IND04	CHN13	MUS	-0.002988	0.000411	-7.263	32,586	41,564	3,005,216
SPR	DEU01	IND04	CHN24	MUS	-0.002986	0.000412	-7.253	32,620	41,595	3,005,216
SPR	DEU01	IND04	CHN07	MUS	-0.002964	0.000409	-7.251	32,624	41,532	3,005,216
SPR	DEU01	IND04	CHN02	MUS	-0.002993	0.000413	-7.246	32,598	41,593	3,005,216
SPR	DEU01	IND04	KAZ05	MUS	-0.002930	0.000405	-7.240	32,671	41,475	3,005,216
SPR	DEU01	IND04	CHN08	MUS	-0.002965	0.000410	-7.229	32,636	41,547	3,005,216
SPR	DEU01	IND04	KOR01	MUS	-0.002983	0.000413	-7.228	32,622	41,586	3,005,216
SPR	DEU01	IND04	CHN03	MUS	-0.002975	0.000412	-7.226	32,590	41,531	3,005,216
SPR	DEU01	IND04	KAZ02	MUS	-0.002921	0.000404	-7.222	32,707	41,485	3,005,216
SPR	DEU01	IND04	RUS02	MUS	-0.002959	0.000410	-7.219	32,633	41,525	3,005,216
SPR	DEU01	IND04	KAZ01	MUS	-0.002926	0.000405	-7.217	32,716	41,509	3,005,216
SPR	DEU01	IND04	KAZ03	MUS	-0.002936	0.000407	-7.215	32,652	41,476	3,005,216
SPR	DEU01	IND04	RUS05	MUS	-0.002858	0.000396	-7.215	32,834	41,423	3,005,216
SPR	DEU01	IND04	JPN11	MUS	-0.002687	0.000372	-7.215	32,066	40,142	3,005,216
SPR	DEU01	IND04	CHN04	MUS	-0.002961	0.000411	-7.209	32,596	41,495	3,005,216
SPR	DEU01	IND04	RUS04	DOM	-0.002851	0.000396	-7.200	32,806	41,374	3,005,216
SPR	DEU01	IND04	CHN05	MUS	-0.002942	0.000409	-7.188	32,597	41,439	3,005,216
SPR	DEU01	IND04	CHN01	MUS	-0.002963	0.000412	-7.187	32,630	41,533	3,005,216
SPR	DEU01	IND04	RUS06	MUS	-0.002948	0.000411	-7.178	32,600	41,460	3,005,216
SPR	DEU01	IND04	CHN23	MUS	-0.002880	0.000402	-7.168	32,769	41,424	3,005,216
SPR	DEU01	IND04	RUS03	MUS	-0.002922	0.000409	-7.148	32,632	41,414	3,005,216
SPR	DEU01	IND04	JPN07	MUS	-0.002540	0.000358	-7.105	32,262	39,896	3,005,216
SPR	DEU01	IND04	JPN14	MUS	-0.002962	0.000418	-7.093	32,643	41,544	3,005,216
SPR	DEU01	IND04	KOR05	MUS	-0.002967	0.000418	-7.089	32,645	41,560	3,005,216
SPR	DEU01	IND04	KOR03	MUS	-0.002971	0.000419	-7.086	32,631	41,559	3,005,216
SPR	DEU01	IND04	KOR02	MUS	-0.002963	0.000419	-7.077	32,645	41,548	3,005,216
SPR	DEU01	IND04	JPN06	MUS	-0.002961	0.000418	-7.077	32,642	41,541	3,005,216
SPR	DEU01	IND04	CZE01	MUS	-0.002923	0.000413	-7.074	32,677	41,461	3,005,216
SPR	DEU01	IND04	JPN13	CAS	-0.002952	0.000418	-7.068	32,653	41,524	3,005,216
SPR	DEU01	IND04	KOR04	MUS	-0.002845	0.000403	-7.061	32,655	41,206	3,005,216
SPR	DEU01	IND04	KAZ04	MUS	-0.002925	0.000414	-7.059	32,732	41,523	3,005,216
SPR	DEU01	IND04	JPN10	MUS	-0.002958	0.000420	-7.042	32,654	41,545	3,005,216
SPR	DEU01	IND04	RUS11	MUS	-0.002796	0.000400	-6.995	32,546	40,949	3,005,216
SPR	DEU01	IND04	IRN06	MUS	-0.002903	0.000416	-6.976	32,746	41,470	3,005,216
SPR	DEU01	IND04	IRN05	CAS	-0.002863	0.000412	-6.950	32,775	41,379	3,005,216
SPR	DEU01	IND04	JPN08	MUS	-0.002914	0.000422	-6.908	32,613	41,370	3,005,216
SPR	DEU01	IND04	JPN16	CAS	-0.002663	0.000386	-6.903	32,215	40,217	3,005,216
SPR	DEU01	IND04	JPN03	MUS	-0.002883	0.000418	-6.896	32,647	41,311	3,005,216
SPR	DEU01	IND04	CZE06	MUS	-0.002882	0.000429	-6.721	32,846	41,508	3,005,216
SPR	DEU01	IND04	JPN12	MUS	-0.002735	0.000407	-6.716	31,849	40,067	3,005,216
SPR	DEU01	IND04	JPN17	CAS	-0.002623	0.000391	-6.710	31,931	39,813	3,005,216
SPR	DEU01	IND04	CZE05	MUS	-0.002872	0.000429	-6.690	32,874	41,506	3,005,216
SPR	DEU01	IND04	CZE02	MUS	-0.002834	0.000427	-6.643	32,919	41,434	3,005,216
SPR	DEU01	IND04	JPN15	CAS	-0.002480	0.000376	-6.587	32,280	39,733	3,005,216
SPR	DEU01	IND04	CZE04	MUS	-0.002768	0.000425	-6.507	33,084	41,402	3,005,216
SPR	DEU01	IND04	CZE07	MUS	-0.002733	0.000424	-6.441	33,191	41,404	3,005,216
SPR	DEU01	IND04	CHN21	CAS	-0.002783	0.000436	-6.379	32,627	40,991	3,005,216
SPR	DEU01	IND04	JPN05	MUS	-0.002823	0.000446	-6.329	31,980	40,465	3,005,216
SPR	DEU01	IND04	RUS07	MUS	-0.002720	0.000436	-6.234	33,012	41,185	3,005,216
SPR	DEU01	IND04	JPN18	CAS	-0.002406	0.000389	-6.178	32,214	39,444	3,005,216
SPR	DEU01	IND04	JPN09	MUS	-0.002368	0.000388	-6.108	31,627	38,744	3,005,216
SPR	DEU01	IND04	CHN20	CAS	-0.002632	0.000454	-5.795	32,584	40,493	3,005,216
SPR	DEU01	IND04	RUS16	DOM	-0.002580	0.000451	-5.724	32,653	40,405	3,005,216
SPR	DEU01	IND04	JPN01	MUS	-0.002008	0.000352	-5.703	30,532	36,567	3,005,216
SPR	DEU01	IND04	CZE03	MUS	-0.002645	0.000468	-5.650	33,421	41,369	3,005,216
SPR	DEU01	IND04	RUS15	MUS	-0.002293	0.000497	-4.611	33,033	39,923	3,005,216
SPR	DEU01	IND04	NPL02	NEP	-0.008868	0.001992	-4.453	26,714	53,364	3,005,216
SPR	DEU01	IND04	RUS13	DOM	-0.002440	0.000552	-4.419	33,365	40,699	3,005,216
SPR	DEU01	IND04	JPN04	MUS	-0.001042	0.000252	-4.133	29,125	32,257	3,005,216
SPR	DEU01	IND04	CHN19	CAS	-0.000829	0.000203	-4.083	28,740	31,232	3,005,216
SPR	DEU01	IND04	CHN16	CAS	-0.000991	0.000244	-4.067	30,054	33,031	3,005,216

SPR	DEU01	IND04	EST01	MUS	-0.002264	0.000622	-3.639	34,204	41,007	3,005,216
SPR	DEU01	IND04	CHN11	CAS	-0.000705	0.000214	-3.302	28,540	30,659	3,005,216
SPR	DEU01	IND04	NPL01	NEP	-0.003204	0.001009	-3.174	27,492	37,122	3,005,216
SPR	DEU01	IND04	IND09	CAS	-0.000715	0.000231	-3.089	27,809	29,957	3,005,216
SPR	DEU01	IND04	IND01	CAS	-0.000674	0.000226	-2.981	27,812	29,837	3,005,216
SPR	DEU01	IND04	BGD02	CAS	-0.000610	0.000209	-2.916	27,908	29,741	3,005,216
SPR	DEU01	IND04	CHN12	CAS	-0.000729	0.000264	-2.757	28,735	30,925	3,005,216
SPR	DEU01	IND04	VNM01	CAS	-0.000641	0.000238	-2.697	28,156	30,082	3,005,216
SPR	DEU01	IND04	CHN14	CAS	-0.000579	0.000221	-2.621	28,527	30,267	3,005,216
SPR	DEU01	IND04	CHN18	CAS	-0.000609	0.000242	-2.513	28,290	30,119	3,005,216
SPR	DEU01	IND04	BGD01	CAS	-0.000545	0.000217	-2.508	27,947	29,584	3,005,216
SPR	DEU01	IND04	TWN01	CAS	-0.000498	0.000202	-2.460	28,249	29,745	3,005,216
SPR	DEU01	IND04	IND07	CAS	-0.000545	0.000224	-2.426	28,147	29,784	3,005,216
SPR	DEU01	IND04	CHN17	CAS	-0.000499	0.000210	-2.371	28,333	29,832	3,005,216
SPR	DEU01	IND04	IND02	CAS	-0.000547	0.000234	-2.339	27,590	29,235	3,005,216
SPR	DEU01	IND04	CHN22	CAS	-0.000411	0.000178	-2.310	28,502	29,736	3,005,216
SPR	DEU01	IND04	IND06	CAS	-0.000476	0.000213	-2.234	28,014	29,444	3,005,216
SPR	DEU01	IND04	IND05	CAS	-0.000490	0.000231	-2.121	28,195	29,667	3,005,216
SPR	DEU01	IND04	IDN04	CAS	-0.000506	0.000240	-2.109	28,111	29,632	3,005,216
SPR	DEU01	IND04	IDN03	CAS	-0.000433	0.000233	-1.860	28,176	29,476	3,005,216
SPR	DEU01	IND04	UKR01	MUS	-0.000935	0.000517	-1.810	31,300	34,110	3,005,216
SPR	DEU01	IND04	IND08	CAS	-0.000443	0.000253	-1.749	27,891	29,222	3,005,216
SPR	DEU01	IND04	LKA02	CAS	-0.000301	0.000207	-1.457	28,121	29,026	3,005,216
SPR	DEU01	IND04	PAK02	CAS	-0.000236	0.000177	-1.334	26,085	26,793	3,005,216
SPR	DEU01	IND04	VNM02	CAS	-0.000304	0.000284	-1.071	28,776	29,689	3,005,216
SPR	DEU01	IND04	PAK01	CAS	-0.000170	0.000191	-0.892	26,882	27,395	3,005,216
SPR	DEU01	IND04	PAK04	CAS	-0.000133	0.000211	-0.630	27,620	28,021	3,005,216
SPR	DEU01	IND04	PAK03	CAS	-0.000118	0.000192	-0.617	28,219	28,575	3,005,216
SPR	DEU01	IND04	RUS12	CAS	-0.000446	0.000831	-0.537	33,766	35,107	3,005,216
SPR	DEU01	IND04	RUS14	CAS	-0.000695	0.001872	-0.371	36,861	38,951	3,005,216
SPR	DEU01	IND04	IND03	CAS	-0.000020	0.000150	-0.132	12,063	12,122	3,005,216
SPR	DEU01	IND04	LKA01	CAS	0.000005	0.000475	0.010	29,222	29,209	3,005,216
SPR	DEU01	IND04	RUS10	CAS	0.003260	0.002367	1.377	41,252	31,455	3,005,216
SPR	DEU01	IND04	IDN01	DOM	0.001628	0.000866	1.879	33,576	28,684	3,005,216
SPR	DEU01	IND04	IDN02	CAS	0.003426	0.001761	1.946	37,587	27,290	3,005,216
SPR	DEU01	IND04	CHN06	MUS	0.031927	0.002314	13.800	113,343	17,394	3,005,216
SPR	DEU01	IND04	RUS01	DOM	0.022446	0.000550	40.845	90,148	22,693	3,005,216
SPR	DEU01	IND04	FRA01	DOM	0.050963	0.000914	55.753	155,759	2,604	3,005,216
SPR	DEU01	IND04	IRN01	DOM	0.045925	0.000817	56.197	141,761	3,745	3,005,216
SPR	DEU01	IND04	IRN03	DOM	0.045604	0.000770	59.228	141,097	4,048	3,005,216
SPR	DEU01	IND04	IRN02	DOM	0.045661	0.000767	59.536	141,059	3,837	3,005,216
SPR	DEU01	IND04	FRA03	DOM	0.051298	0.000846	60.623	156,693	2,531	3,005,216
SPR	DEU01	IND04	FRA04	DOM	0.051622	0.000847	60.920	157,683	2,548	3,005,216
SPR	DEU01	IND04	IRN04	DOM	0.045601	0.000746	61.106	140,971	3,931	3,005,216
SPR	DEU01	IND04	DEU07	DOM	0.054378	0.000880	61.765	165,253	1,836	3,005,216
SPR	DEU01	IND04	FRA02	DOM	0.051133	0.000814	62.825	156,180	2,514	3,005,216
SPR	DEU01	IND04	DEU04	DOM	0.055620	0.000847	65.681	168,805	1,656	3,005,216
SPR	DEU01	IND04	DEU02	DOM	0.054729	0.000832	65.745	166,369	1,898	3,005,216
SPR	DEU01	IND04	DEU03	DOM	0.054586	0.000803	67.993	166,021	1,977	3,005,216
SPR	DEU01	IND04	DEU06	DOM	0.055561	0.000799	69.579	168,755	1,780	3,005,216
SPR	DEU01	IND04	DEU05	DOM	0.055173	0.000786	70.164	167,593	1,786	3,005,216

Table 1-21 The f_4 statistics result of X chromosome. $f_4(\text{SPR}, \text{DOM}; \text{MUS}, \text{X})$ The f_4 statistics result of X chromosome. $f_4(\text{SPR}, \text{DOM}; \text{MUS}, \text{X})$

Pop1(W)	Pop2(X)	Pop3(Y)	Pop4(Z)	Pop4(Z) mtDNA Haplogroup	f_4 statistics	Standard Error	Z	BABA	ABBA	Number of SNPs that all population have data
SPR	DEU01	KOR01	NPL02	NEP	-0.005885	0.001991	-2.955	36,502	54,188	3,005,216
SPR	DEU01	KOR01	CHN15	MUS	-0.000013	0.000020	-0.644	660	699	3,005,216
SPR	DEU01	KOR01	CHN09	MUS	-0.000008	0.000028	-0.300	791	816	3,005,216
SPR	DEU01	KOR01	CHN24	MUS	-0.000004	0.000014	-0.264	601	612	3,005,216
SPR	DEU01	KOR01	CHN02	MUS	-0.000011	0.000043	-0.252	1,450	1,483	3,005,216
SPR	DEU01	KOR01	CHN13	MUS	-0.000005	0.000020	-0.248	744	759	3,005,216
SPR	DEU01	KOR01	NPL01	NEP	-0.000222	0.001188	-0.187	39,999	40,665	3,005,216
SPR	DEU01	KOR01	CHN10	MUS	0.000001	0.000026	0.044	769	766	3,005,216
SPR	DEU01	KOR01	RUS08	MUS	0.000002	0.000027	0.071	766	760	3,005,216
SPR	DEU01	KOR01	CHN03	MUS	0.000007	0.000042	0.173	1,467	1,445	3,005,216
SPR	DEU01	KOR01	RUS09	MUS	0.000010	0.000027	0.369	904	874	3,005,216
SPR	DEU01	KOR01	CHN01	MUS	0.000020	0.000042	0.480	1,493	1,433	3,005,216
SPR	DEU01	KOR01	CHN04	MUS	0.000022	0.000043	0.496	1,390	1,325	3,005,216
SPR	DEU01	KOR01	RUS02	MUS	0.000024	0.000039	0.608	1,631	1,560	3,005,216
SPR	DEU01	KOR01	CHN08	MUS	0.000017	0.000025	0.702	789	737	3,005,216
SPR	DEU01	KOR01	KOR03	MUS	0.000012	0.000016	0.747	299	262	3,005,216
SPR	DEU01	KOR01	CHN07	MUS	0.000018	0.000023	0.797	721	666	3,005,216
SPR	DEU01	KOR01	RUS06	MUS	0.000034	0.000039	0.880	1,636	1,533	3,005,216
SPR	DEU01	KOR01	CZE01	MUS	0.000060	0.000060	0.990	1,710	1,530	3,005,216
SPR	DEU01	KOR01	CHN05	MUS	0.000041	0.000041	0.998	1,319	1,197	3,005,216
SPR	DEU01	KOR01	KAZ01	MUS	0.000057	0.000054	1.056	1,658	1,488	3,005,216
SPR	DEU01	KOR01	KOR05	MUS	0.000016	0.000015	1.070	270	222	3,005,216
SPR	DEU01	KOR01	KAZ05	MUS	0.000053	0.000049	1.091	1,453	1,294	3,005,216
SPR	DEU01	KOR01	KAZ03	MUS	0.000047	0.000041	1.136	1,453	1,313	3,005,216
SPR	DEU01	KOR01	CZE06	MUS	0.000100	0.000087	1.158	1,913	1,611	3,005,216
SPR	DEU01	KOR01	JPN14	MUS	0.000021	0.000018	1.196	335	271	3,005,216
SPR	DEU01	KOR01	JPN06	MUS	0.000021	0.000017	1.232	416	352	3,005,216
SPR	DEU01	KOR01	CZE05	MUS	0.000111	0.000087	1.276	1,935	1,603	3,005,216
SPR	DEU01	KOR01	RUS14	CAS	0.002287	0.001778	1.286	11,168	4,293	3,005,216
SPR	DEU01	KOR01	JPN05	MUS	0.000159	0.000124	1.288	2,839	2,360	3,005,216
SPR	DEU01	KOR01	KAZ02	MUS	0.000062	0.000047	1.307	1,417	1,231	3,005,216
SPR	DEU01	KOR01	RUS05	MUS	0.000125	0.000094	1.331	1,744	1,369	3,005,216
SPR	DEU01	KOR01	JPN10	MUS	0.000024	0.000018	1.349	363	290	3,005,216
SPR	DEU01	KOR01	RUS04	DOM	0.000132	0.000093	1.416	1,852	1,456	3,005,216
SPR	DEU01	KOR01	KAZ04	MUS	0.000057	0.000039	1.461	1,470	1,298	3,005,216
SPR	DEU01	KOR01	RUS11	MUS	0.000186	0.000126	1.477	2,731	2,171	3,005,216
SPR	DEU01	KOR01	RUS07	MUS	0.000263	0.000173	1.521	2,187	1,396	3,005,216
SPR	DEU01	KOR01	JPN11	MUS	0.000295	0.000185	1.593	4,161	3,274	3,005,216
SPR	DEU01	KOR01	JPN03	MUS	0.000100	0.000062	1.609	905	605	3,005,216
SPR	DEU01	KOR01	RUS13	DOM	0.000542	0.000335	1.620	5,087	3,457	3,005,216
SPR	DEU01	KOR01	EST01	MUS	0.000719	0.000433	1.659	3,634	1,473	3,005,216
SPR	DEU01	KOR01	CHN23	MUS	0.000103	0.000062	1.661	1,776	1,468	3,005,216
SPR	DEU01	KOR01	JPN12	MUS	0.000248	0.000143	1.731	4,082	3,336	3,005,216
SPR	DEU01	KOR01	RUS17	MUS	0.000312	0.000180	1.731	4,741	3,803	3,005,216
SPR	DEU01	KOR01	CZE03	MUS	0.000338	0.000193	1.752	2,603	1,588	3,005,216
SPR	DEU01	KOR01	JPN13	CAS	0.000031	0.000017	1.770	344	252	3,005,216
SPR	DEU01	KOR01	JPN15	CAS	0.000503	0.000284	1.770	4,741	3,231	3,005,216
SPR	DEU01	KOR01	RUS03	MUS	0.000060	0.000033	1.807	1,535	1,354	3,005,216
SPR	DEU01	KOR01	KOR02	MUS	0.000020	0.000011	1.808	309	249	3,005,216
SPR	DEU01	KOR01	CHN21	CAS	0.000200	0.000110	1.811	2,767	2,167	3,005,216
SPR	DEU01	KOR01	KOR04	MUS	0.000137	0.000075	1.836	1,297	884	3,005,216
SPR	DEU01	KOR01	CZE02	MUS	0.000149	0.000081	1.849	1,996	1,548	3,005,216
SPR	DEU01	KOR01	IRN06	MUS	0.000080	0.000042	1.920	1,925	1,685	3,005,216
SPR	DEU01	KOR01	JPN08	MUS	0.000069	0.000036	1.926	643	436	3,005,216
SPR	DEU01	KOR01	CZE07	MUS	0.000250	0.000128	1.944	2,247	1,496	3,005,216
SPR	DEU01	KOR01	JPN18	CAS	0.000577	0.000293	1.966	4,785	3,051	3,005,216
SPR	DEU01	KOR01	IRN05	CAS	0.000120	0.000060	2.006	2,169	1,809	3,005,216
SPR	DEU01	KOR01	JPN09	MUS	0.000614	0.000298	2.059	6,737	4,891	3,005,216
SPR	DEU01	KOR01	CZE04	MUS	0.000215	0.000099	2.165	2,189	1,543	3,005,216
SPR	DEU01	KOR01	CHN20	CAS	0.000351	0.000150	2.341	5,950	4,895	3,005,216
SPR	DEU01	KOR01	JPN02	MUS	0.000245	0.000104	2.360	4,043	3,307	3,005,216
SPR	DEU01	KOR01	JPN17	CAS	0.000360	0.000153	2.360	5,170	4,087	3,005,216
SPR	DEU01	KOR01	RUS16	DOM	0.000403	0.000170	2.366	7,535	6,323	3,005,216
SPR	DEU01	KOR01	RUS15	MUS	0.000690	0.000290	2.381	7,741	5,667	3,005,216
SPR	DEU01	KOR01	JPN16	CAS	0.000320	0.000127	2.513	3,927	2,965	3,005,216
SPR	DEU01	KOR01	JPN07	MUS	0.000442	0.000176	2.519	3,954	2,625	3,005,216
SPR	DEU01	KOR01	RUS10	CAS	0.006243	0.002445	2.553	36,455	17,694	3,005,216
SPR	DEU01	KOR01	JPN01	MUS	0.000974	0.000317	3.076	16,270	13,341	3,005,216

SPR	DEU01	KOR01	RUS12	CAS	0.002536	0.000772	3.284	23,174	15,552	3,005,216
SPR	DEU01	KOR01	UKR01	MUS	0.002048	0.000592	3.459	21,985	15,831	3,005,216
SPR	DEU01	KOR01	IDN02	CAS	0.006409	0.001724	3.718	50,185	30,925	3,005,216
SPR	DEU01	KOR01	CHN12	CAS	0.002254	0.000489	4.610	35,934	29,160	3,005,216
SPR	DEU01	KOR01	IND09	CAS	0.002268	0.000470	4.831	40,709	33,893	3,005,216
SPR	DEU01	KOR01	CHN19	CAS	0.002154	0.000440	4.893	34,041	27,569	3,005,216
SPR	DEU01	KOR01	CHN18	CAS	0.002374	0.000485	4.894	38,721	31,586	3,005,216
SPR	DEU01	KOR01	IDN01	DOM	0.004610	0.000936	4.928	46,036	32,181	3,005,216
SPR	DEU01	KOR01	CHN14	CAS	0.002404	0.000487	4.940	37,579	30,355	3,005,216
SPR	DEU01	KOR01	CHN16	CAS	0.001992	0.000400	4.984	26,921	20,935	3,005,216
SPR	DEU01	KOR01	VNM01	CAS	0.002342	0.000466	5.020	40,343	33,306	3,005,216
SPR	DEU01	KOR01	CHN11	CAS	0.002278	0.000451	5.046	34,601	27,756	3,005,216
SPR	DEU01	KOR01	BGD01	CAS	0.002438	0.000473	5.156	41,012	33,685	3,005,216
SPR	DEU01	KOR01	JPN04	MUS	0.001941	0.000370	5.249	27,657	21,825	3,005,216
SPR	DEU01	KOR01	IND01	CAS	0.002309	0.000438	5.275	41,033	34,095	3,005,216
SPR	DEU01	KOR01	IDN04	CAS	0.002477	0.000467	5.301	40,937	33,495	3,005,216
SPR	DEU01	KOR01	VNM02	CAS	0.002679	0.000503	5.328	40,917	32,866	3,005,216
SPR	DEU01	KOR01	BGD02	CAS	0.002373	0.000444	5.350	40,775	33,644	3,005,216
SPR	DEU01	KOR01	IND06	CAS	0.002507	0.000467	5.373	41,308	33,774	3,005,216
SPR	DEU01	KOR01	TWN01	CAS	0.002485	0.000460	5.406	39,272	31,804	3,005,216
SPR	DEU01	KOR01	IND05	CAS	0.002493	0.000461	5.410	41,174	33,682	3,005,216
SPR	DEU01	KOR01	LKA01	CAS	0.002987	0.000545	5.481	42,333	33,356	3,005,216
SPR	DEU01	KOR01	IND02	CAS	0.002435	0.000441	5.519	41,163	33,844	3,005,216
SPR	DEU01	KOR01	IDN03	CAS	0.002550	0.000460	5.548	41,076	33,412	3,005,216
SPR	DEU01	KOR01	IND08	CAS	0.002540	0.000456	5.567	41,163	33,530	3,005,216
SPR	DEU01	KOR01	CHN17	CAS	0.002484	0.000440	5.647	38,330	30,866	3,005,216
SPR	DEU01	KOR01	CHN22	CAS	0.002572	0.000428	6.016	38,705	30,976	3,005,216
SPR	DEU01	KOR01	IND07	CAS	0.002438	0.000402	6.066	40,907	33,580	3,005,216
SPR	DEU01	KOR01	LKA02	CAS	0.002681	0.000434	6.172	41,226	33,168	3,005,216
SPR	DEU01	KOR01	PAK04	CAS	0.002849	0.000456	6.244	41,559	32,996	3,005,216
SPR	DEU01	KOR01	IND03	CAS	0.002963	0.000461	6.421	41,688	32,784	3,005,216
SPR	DEU01	KOR01	PAK02	CAS	0.002747	0.000417	6.590	41,042	32,787	3,005,216
SPR	DEU01	KOR01	PAK03	CAS	0.002864	0.000433	6.615	41,875	33,268	3,005,216
SPR	DEU01	KOR01	PAK01	CAS	0.002812	0.000407	6.913	41,176	32,725	3,005,216
SPR	DEU01	KOR01	IND04	CAS	0.002983	0.000413	7.228	41,586	32,622	3,005,216
SPR	DEU01	KOR01	CHN06	MUS	0.034910	0.002168	16.102	106,693	1,781	3,005,216
SPR	DEU01	KOR01	RUS01	DOM	0.025429	0.000532	47.807	78,690	2,271	3,005,216
SPR	DEU01	KOR01	IRN03	DOM	0.048587	0.000799	60.835	150,198	4,185	3,005,216
SPR	DEU01	KOR01	IRN01	DOM	0.048908	0.000796	61.434	150,876	3,897	3,005,216
SPR	DEU01	KOR01	IRN02	DOM	0.048644	0.000773	62.956	150,255	4,069	3,005,216
SPR	DEU01	KOR01	FRA04	DOM	0.054605	0.000863	63.282	166,732	2,633	3,005,216
SPR	DEU01	KOR01	FRA01	DOM	0.053946	0.000844	63.931	164,959	2,840	3,005,216
SPR	DEU01	KOR01	DEU07	DOM	0.057361	0.000888	64.569	174,359	1,977	3,005,216
SPR	DEU01	KOR01	IRN04	DOM	0.048583	0.000732	66.334	150,045	4,042	3,005,216
SPR	DEU01	KOR01	DEU04	DOM	0.058602	0.000880	66.608	177,742	1,630	3,005,216
SPR	DEU01	KOR01	DEU02	DOM	0.057711	0.000849	67.966	175,491	2,056	3,005,216
SPR	DEU01	KOR01	FRA03	DOM	0.054281	0.000783	69.319	165,865	2,740	3,005,216
SPR	DEU01	KOR01	DEU06	DOM	0.058544	0.000840	69.682	177,713	1,775	3,005,216
SPR	DEU01	KOR01	DEU05	DOM	0.058156	0.000822	70.720	176,646	1,875	3,005,216
SPR	DEU01	KOR01	FRA02	DOM	0.054116	0.000757	71.487	165,343	2,713	3,005,216
SPR	DEU01	KOR01	DEU03	DOM	0.057569	0.000720	80.010	175,079	2,072	3,005,216

Table 1-22 The f_4 statistics result of X chromosome. $f_4(\text{SPR, MUS; CAS, X})$ The f_4 statistics result of X chromosome. $f_4(\text{SPR, MUS; CAS, X})$

Pop1(W)	Pop2(X)	Pop3(Y)	Pop4(Z)	Pop4(Z) mtDNA Haplogroup	f_4 statistics	Standard Error	Z	BABA	ABBA	Number of SNPs that all population have data
SPR	KOR01	IND04	FRA03	DOM	-0.003907	0.000413	-9.462	32,522	44,263	3,005,216
SPR	KOR01	IND04	DEU07	DOM	-0.003909	0.000416	-9.387	32,592	44,339	3,005,216
SPR	KOR01	IND04	FRA01	DOM	-0.003889	0.000418	-9.313	32,529	44,216	3,005,216
SPR	KOR01	IND04	FRA04	DOM	-0.003880	0.000423	-9.161	32,614	44,274	3,005,216
SPR	KOR01	IND04	FRA02	DOM	-0.003874	0.000423	-9.154	32,576	44,219	3,005,216
SPR	KOR01	IND04	DEU06	DOM	-0.003870	0.000427	-9.068	32,689	44,320	3,005,216
SPR	KOR01	IND04	DEU04	DOM	-0.003824	0.000422	-9.056	32,729	44,220	3,005,216
SPR	KOR01	IND04	IRN04	DOM	-0.003745	0.000414	-9.055	32,631	43,884	3,005,216
SPR	KOR01	IND04	DEU02	DOM	-0.003876	0.000428	-9.048	32,573	44,223	3,005,216
SPR	KOR01	IND04	DEU01	DOM	-0.003881	0.000430	-9.027	32,622	44,284	3,005,216
SPR	KOR01	IND04	DEU05	DOM	-0.003858	0.000428	-9.019	32,615	44,208	3,005,216
SPR	KOR01	IND04	DEU03	DOM	-0.003847	0.000427	-9.007	32,644	44,206	3,005,216
SPR	KOR01	IND04	IRN01	DOM	-0.003698	0.000414	-8.935	32,757	43,869	3,005,216
SPR	KOR01	IND04	IRN02	DOM	-0.003761	0.000424	-8.862	32,726	44,030	3,005,216
SPR	KOR01	IND04	IRN03	DOM	-0.003752	0.000436	-8.607	32,739	44,015	3,005,216
SPR	KOR01	IND04	NPL02	NEP	-0.009154	0.002064	-4.434	27,041	54,550	3,005,216
SPR	KOR01	IND04	NPL01	NEP	-0.003689	0.001262	-2.924	27,689	38,777	3,005,216
SPR	KOR01	IND04	IND01	CAS	-0.000528	0.000231	-2.286	29,014	30,600	3,005,216
SPR	KOR01	IND04	BGD01	CAS	-0.000376	0.000207	-1.811	29,243	30,372	3,005,216
SPR	KOR01	IND04	IND08	CAS	-0.000361	0.000214	-1.688	29,191	30,275	3,005,216
SPR	KOR01	IND04	IND05	CAS	-0.000369	0.000224	-1.650	29,474	30,584	3,005,216
SPR	KOR01	IND04	IND06	CAS	-0.000380	0.000232	-1.637	29,224	30,366	3,005,216
SPR	KOR01	IND04	LKA01	CAS	-0.000368	0.000245	-1.500	29,370	30,475	3,005,216
SPR	KOR01	IND04	IND02	CAS	-0.000358	0.000240	-1.489	28,841	29,917	3,005,216
SPR	KOR01	IND04	IDN01	DOM	-0.000365	0.000253	-1.444	30,052	31,148	3,005,216
SPR	KOR01	IND04	IND07	CAS	-0.000320	0.000239	-1.340	29,321	30,281	3,005,216
SPR	KOR01	IND04	IND09	CAS	-0.000337	0.000270	-1.246	29,439	30,451	3,005,216
SPR	KOR01	IND04	IDN03	CAS	-0.000224	0.000182	-1.226	29,606	30,279	3,005,216
SPR	KOR01	IND04	IDN04	CAS	-0.000198	0.000181	-1.091	29,704	30,298	3,005,216
SPR	KOR01	IND04	PAK03	CAS	-0.000248	0.000244	-1.014	29,006	29,750	3,005,216
SPR	KOR01	IND04	BGD02	CAS	-0.000200	0.000217	-0.920	29,618	30,219	3,005,216
SPR	KOR01	IND04	LKA02	CAS	-0.000181	0.000211	-0.857	29,388	29,930	3,005,216
SPR	KOR01	IND04	IND03	CAS	-0.000112	0.000142	-0.786	12,265	12,601	3,005,216
SPR	KOR01	IND04	IDN02	CAS	-0.000156	0.000407	-0.382	30,175	30,642	3,005,216
SPR	KOR01	IND04	PAK04	CAS	-0.000045	0.000273	-0.165	28,778	28,914	3,005,216
SPR	KOR01	IND04	PAK01	CAS	0.000043	0.000197	0.218	28,087	27,958	3,005,216
SPR	KOR01	IND04	VNM01	CAS	0.000399	0.000413	0.967	31,354	30,154	3,005,216
SPR	KOR01	IND04	VNM02	CAS	0.000553	0.000559	0.990	31,604	29,941	3,005,216
SPR	KOR01	IND04	PAK02	CAS	0.000240	0.000173	1.391	27,759	27,036	3,005,216
SPR	KOR01	IND04	TWN01	CAS	0.002187	0.001032	2.119	35,136	28,563	3,005,216
SPR	KOR01	IND04	CHN18	CAS	0.002939	0.001185	2.479	37,184	28,352	3,005,216
SPR	KOR01	IND04	CHN22	CAS	0.003133	0.001066	2.939	37,475	28,058	3,005,216
SPR	KOR01	IND04	CHN12	CAS	0.006905	0.002256	3.061	47,149	26,398	3,005,216
SPR	KOR01	IND04	CHN17	CAS	0.003544	0.001110	3.193	38,347	27,697	3,005,216
SPR	KOR01	IND04	CHN14	CAS	0.004796	0.001390	3.450	41,649	27,238	3,005,216
SPR	KOR01	IND04	CHN11	CAS	0.008917	0.002407	3.704	51,405	24,609	3,005,216
SPR	KOR01	IND04	CHN19	CAS	0.009622	0.002369	4.062	53,737	24,821	3,005,216
SPR	KOR01	IND04	RUS10	CAS	0.020565	0.003708	5.546	81,432	19,628	3,005,216
SPR	KOR01	IND04	JPN04	MUS	0.018612	0.003182	5.849	75,192	19,259	3,005,216
SPR	KOR01	IND04	UKR01	MUS	0.026435	0.004237	6.239	93,842	14,400	3,005,216
SPR	KOR01	IND04	CHN16	CAS	0.020441	0.002490	8.209	80,286	18,855	3,005,216
SPR	KOR01	IND04	CHN06	MUS	0.018285	0.002199	8.316	82,924	27,973	3,005,216
SPR	KOR01	IND04	RUS12	CAS	0.027130	0.003060	8.866	96,673	15,142	3,005,216
SPR	KOR01	IND04	JPN01	MUS	0.036535	0.003467	10.539	121,620	11,825	3,005,216
SPR	KOR01	IND04	JPN09	MUS	0.050131	0.003393	14.773	154,660	4,007	3,005,216
SPR	KOR01	IND04	RUS14	CAS	0.046138	0.002753	16.760	144,062	5,407	3,005,216
SPR	KOR01	IND04	RUS16	DOM	0.045129	0.002437	18.515	142,296	6,675	3,005,216
SPR	KOR01	IND04	JPN15	CAS	0.053239	0.002701	19.712	162,931	2,936	3,005,216
SPR	KOR01	IND04	JPN17	CAS	0.052433	0.002528	20.743	161,175	3,603	3,005,216
SPR	KOR01	IND04	RUS15	MUS	0.045114	0.002115	21.328	141,289	5,712	3,005,216
SPR	KOR01	IND04	JPN18	CAS	0.053212	0.002486	21.403	162,615	2,703	3,005,216
SPR	KOR01	IND04	JPN16	CAS	0.054348	0.002444	22.233	165,967	2,640	3,005,216
SPR	KOR01	IND04	JPN12	MUS	0.053930	0.002403	22.446	164,805	2,732	3,005,216
SPR	KOR01	IND04	JPN11	MUS	0.054344	0.002126	25.559	166,113	2,798	3,005,216
SPR	KOR01	IND04	JPN07	MUS	0.054631	0.002112	25.871	166,509	2,332	3,005,216
SPR	KOR01	IND04	RUS17	MUS	0.048430	0.001832	26.435	149,170	3,627	3,005,216
SPR	KOR01	IND04	JPN05	MUS	0.055896	0.001885	29.661	169,775	1,795	3,005,216
SPR	KOR01	IND04	CHN20	CAS	0.047301	0.001559	30.334	147,024	4,874	3,005,216

SPR	KOR01	IND04	RUS11	MUS	0.051411	0.001588	32.371	156,633	2,133	3,005,216
SPR	KOR01	IND04	JPN02	MUS	0.054300	0.001560	34.799	166,072	2,889	3,005,216
SPR	KOR01	IND04	CHN21	CAS	0.054417	0.001445	37.651	165,837	2,302	3,005,216
SPR	KOR01	IND04	RUS13	DOM	0.049337	0.001281	38.506	151,852	3,584	3,005,216
SPR	KOR01	IND04	RUS01	DOM	0.025166	0.000563	44.723	97,610	21,980	3,005,216
SPR	KOR01	IND04	KOR04	MUS	0.058708	0.001056	55.599	177,347	916	3,005,216
SPR	KOR01	IND04	CHN02	MUS	0.052797	0.000817	64.593	160,172	1,504	3,005,216
SPR	KOR01	IND04	CHN03	MUS	0.052837	0.000801	65.992	160,215	1,430	3,005,216
SPR	KOR01	IND04	CHN01	MUS	0.052821	0.000799	66.098	160,225	1,485	3,005,216
SPR	KOR01	IND04	JPN03	MUS	0.059153	0.000850	69.629	178,454	687	3,005,216
SPR	KOR01	IND04	EST01	MUS	0.051688	0.000724	71.379	157,464	2,130	3,005,216
SPR	KOR01	IND04	CHN15	MUS	0.056400	0.000766	73.613	170,170	677	3,005,216
SPR	KOR01	IND04	CHN05	MUS	0.053593	0.000714	75.045	162,199	1,139	3,005,216
SPR	KOR01	IND04	KAZ04	MUS	0.052910	0.000703	75.216	160,467	1,462	3,005,216
SPR	KOR01	IND04	RUS03	MUS	0.052521	0.000696	75.497	159,198	1,361	3,005,216
SPR	KOR01	IND04	JPN08	MUS	0.059643	0.000786	75.897	179,703	464	3,005,216
SPR	KOR01	IND04	RUS09	MUS	0.055478	0.000727	76.354	167,650	925	3,005,216
SPR	KOR01	IND04	RUS07	MUS	0.052246	0.000678	77.005	158,590	1,579	3,005,216
SPR	KOR01	IND04	CHN09	MUS	0.055793	0.000722	77.293	168,510	839	3,005,216
SPR	KOR01	IND04	CZE05	MUS	0.052009	0.000673	77.325	158,088	1,791	3,005,216
SPR	KOR01	IND04	CZE03	MUS	0.051881	0.000668	77.657	157,737	1,823	3,005,216
SPR	KOR01	IND04	IRN06	MUS	0.051396	0.000662	77.663	156,271	1,815	3,005,216
SPR	KOR01	IND04	CHN07	MUS	0.056287	0.000723	77.801	169,889	735	3,005,216
SPR	KOR01	IND04	KAZ01	MUS	0.052360	0.000672	77.859	158,908	1,556	3,005,216
SPR	KOR01	IND04	CZE01	MUS	0.052139	0.000666	78.242	158,269	1,582	3,005,216
SPR	KOR01	IND04	CHN04	MUS	0.052935	0.000676	78.353	160,428	1,346	3,005,216
SPR	KOR01	IND04	RUS02	MUS	0.052258	0.000665	78.589	158,659	1,612	3,005,216
SPR	KOR01	IND04	CHN08	MUS	0.056266	0.000715	78.725	169,871	779	3,005,216
SPR	KOR01	IND04	CZE04	MUS	0.051987	0.000660	78.781	157,944	1,714	3,005,216
SPR	KOR01	IND04	CZE06	MUS	0.052160	0.000659	79.122	158,508	1,756	3,005,216
SPR	KOR01	IND04	RUS08	MUS	0.056150	0.000709	79.149	169,503	760	3,005,216
SPR	KOR01	IND04	CHN13	MUS	0.056300	0.000708	79.504	169,907	713	3,005,216
SPR	KOR01	IND04	IRN05	CAS	0.050906	0.000639	79.633	154,849	1,867	3,005,216
SPR	KOR01	IND04	CZE07	MUS	0.052057	0.000653	79.773	158,209	1,768	3,005,216
SPR	KOR01	IND04	CZE02	MUS	0.051940	0.000648	80.181	157,820	1,730	3,005,216
SPR	KOR01	IND04	JPN14	MUS	0.059945	0.000745	80.448	180,475	328	3,005,216
SPR	KOR01	IND04	CHN10	MUS	0.056009	0.000692	80.953	169,030	711	3,005,216
SPR	KOR01	IND04	KAZ02	MUS	0.053133	0.000656	81.026	161,007	1,330	3,005,216
SPR	KOR01	IND04	CHN23	MUS	0.052330	0.000641	81.577	158,854	1,592	3,005,216
SPR	KOR01	IND04	KAZ05	MUS	0.052945	0.000648	81.662	160,458	1,348	3,005,216
SPR	KOR01	IND04	KOR02	MUS	0.060157	0.000734	81.985	181,057	271	3,005,216
SPR	KOR01	IND04	JPN13	CAS	0.059950	0.000730	82.094	180,477	315	3,005,216
SPR	KOR01	IND04	KAZ03	MUS	0.053119	0.000647	82.098	161,004	1,369	3,005,216
SPR	KOR01	IND04	JPN06	MUS	0.059900	0.000725	82.583	180,409	397	3,005,216
SPR	KOR01	IND04	JPN10	MUS	0.059989	0.000714	84.010	180,626	345	3,005,216
SPR	KOR01	IND04	RUS06	MUS	0.052254	0.000622	84.029	158,602	1,568	3,005,216
SPR	KOR01	IND04	RUS05	MUS	0.052444	0.000618	84.926	159,132	1,527	3,005,216
SPR	KOR01	IND04	CHN24	MUS	0.057317	0.000672	85.348	172,856	606	3,005,216
SPR	KOR01	IND04	KOR03	MUS	0.060253	0.000698	86.322	181,343	271	3,005,216
SPR	KOR01	IND04	KOR05	MUS	0.060340	0.000698	86.440	181,566	231	3,005,216
SPR	KOR01	IND04	RUS04	DOM	0.052299	0.000602	86.915	158,740	1,571	3,005,216

Table 1-23 The f_4 statistics result of X chromosome. $f_4(\text{SPR}, \text{MUS}; \text{DOM}, \text{X})$ The f_4 statistics result of X chromosome. $f_4(\text{SPR}, \text{MUS}; \text{DOM}, \text{X})$

Pop1(W)	Pop2(X)	Pop3(Y)	Pop4(Z)	Pop4(Z) mtDNA Haplogroup	f_4 statistics	Standard Error	Z	BABA	ABBA	Number of SNPs that all population have data
SPR	KOR01	DEU01	JPN10	MUS	0.063870	0.000833	76.65	192,234	290	3,005,216
SPR	KOR01	DEU01	RUS04	DOM	0.056179	0.000735	76.43	170,287	1,456	3,005,216
SPR	KOR01	DEU01	JPN06	MUS	0.063780	0.000835	76.42	192,026	352	3,005,216
SPR	KOR01	DEU01	RUS05	MUS	0.056324	0.000753	74.82	170,636	1,369	3,005,216
SPR	KOR01	DEU01	KOR05	MUS	0.064221	0.000862	74.49	193,219	222	3,005,216
SPR	KOR01	DEU01	KOR02	MUS	0.064038	0.000863	74.19	192,696	249	3,005,216
SPR	KOR01	DEU01	JPN13	CAS	0.063830	0.000860	74.18	192,076	252	3,005,216
SPR	KOR01	DEU01	CHN24	MUS	0.061198	0.000831	73.68	184,524	612	3,005,216
SPR	KOR01	DEU01	JPN14	MUS	0.063825	0.000869	73.44	192,080	271	3,005,216
SPR	KOR01	DEU01	RUS06	MUS	0.056134	0.000767	73.18	170,229	1,533	3,005,216
SPR	KOR01	DEU01	KOR03	MUS	0.064133	0.000881	72.82	192,997	262	3,005,216
SPR	KOR01	DEU01	CZE02	MUS	0.055820	0.000773	72.24	169,300	1,548	3,005,216
SPR	KOR01	DEU01	CZE07	MUS	0.055937	0.000774	72.23	169,600	1,496	3,005,216
SPR	KOR01	DEU01	IRN06	MUS	0.055277	0.000771	71.68	167,804	1,685	3,005,216
SPR	KOR01	DEU01	CHN23	MUS	0.056210	0.000784	71.67	170,392	1,468	3,005,216
SPR	KOR01	DEU01	CZE01	MUS	0.056019	0.000784	71.46	169,880	1,530	3,005,216
SPR	KOR01	DEU01	KAZ03	MUS	0.057000	0.000800	71.29	172,610	1,313	3,005,216
SPR	KOR01	DEU01	CZE04	MUS	0.055867	0.000785	71.19	169,436	1,543	3,005,216
SPR	KOR01	DEU01	RUS02	MUS	0.056139	0.000789	71.16	170,269	1,560	3,005,216
SPR	KOR01	DEU01	CZE06	MUS	0.056041	0.000789	71.07	170,025	1,611	3,005,216
SPR	KOR01	DEU01	CZE05	MUS	0.055889	0.000788	70.92	169,562	1,603	3,005,216
SPR	KOR01	DEU01	KAZ02	MUS	0.057014	0.000808	70.53	172,570	1,231	3,005,216
SPR	KOR01	DEU01	RUS07	MUS	0.056127	0.000798	70.30	170,069	1,396	3,005,216
SPR	KOR01	DEU01	KAZ01	MUS	0.056240	0.000805	69.90	170,502	1,488	3,005,216
SPR	KOR01	DEU01	CHN10	MUS	0.059889	0.000857	69.88	180,746	766	3,005,216
SPR	KOR01	DEU01	KAZ05	MUS	0.056825	0.000814	69.80	172,066	1,294	3,005,216
SPR	KOR01	DEU01	CZE03	MUS	0.055762	0.000801	69.64	169,164	1,588	3,005,216
SPR	KOR01	DEU01	CHN04	MUS	0.056816	0.000818	69.47	172,069	1,325	3,005,216
SPR	KOR01	DEU01	IRN05	CAS	0.054786	0.000790	69.32	166,453	1,809	3,005,216
SPR	KOR01	DEU01	CHN13	MUS	0.060181	0.000881	68.33	181,615	759	3,005,216
SPR	KOR01	DEU01	CHN08	MUS	0.060147	0.000882	68.18	181,490	737	3,005,216
SPR	KOR01	DEU01	CHN07	MUS	0.060168	0.000886	67.87	181,482	666	3,005,216
SPR	KOR01	DEU01	EST01	MUS	0.055569	0.000822	67.60	168,470	1,473	3,005,216
SPR	KOR01	DEU01	RUS03	MUS	0.056402	0.000840	67.13	170,853	1,354	3,005,216
SPR	KOR01	DEU01	RUS08	MUS	0.060030	0.000898	66.87	181,164	760	3,005,216
SPR	KOR01	DEU01	CHN15	MUS	0.060280	0.000902	66.86	181,853	699	3,005,216
SPR	KOR01	DEU01	CHN09	MUS	0.059674	0.000894	66.75	180,149	816	3,005,216
SPR	KOR01	DEU01	RUS09	MUS	0.059359	0.000898	66.14	179,260	874	3,005,216
SPR	KOR01	DEU01	KAZ04	MUS	0.056790	0.000860	66.01	171,965	1,298	3,005,216
SPR	KOR01	DEU01	JPN08	MUS	0.063523	0.000966	65.76	191,337	436	3,005,216
SPR	KOR01	DEU01	CHN05	MUS	0.057474	0.000879	65.35	173,918	1,197	3,005,216
SPR	KOR01	DEU01	JPN03	MUS	0.063034	0.001024	61.57	190,035	605	3,005,216
SPR	KOR01	DEU01	CHN01	MUS	0.056702	0.000945	60.00	171,834	1,433	3,005,216
SPR	KOR01	DEU01	CHN03	MUS	0.056717	0.000953	59.52	171,893	1,445	3,005,216
SPR	KOR01	DEU01	CHN02	MUS	0.056678	0.000963	58.85	171,812	1,483	3,005,216
SPR	KOR01	DEU01	KOR04	MUS	0.062589	0.001113	56.23	188,976	884	3,005,216
SPR	KOR01	DEU01	RUS01	DOM	0.029047	0.000711	40.84	89,562	2,271	3,005,216
SPR	KOR01	DEU01	CHN21	CAS	0.058298	0.001472	39.60	177,364	2,167	3,005,216
SPR	KOR01	DEU01	RUS13	DOM	0.053217	0.001367	38.92	163,387	3,457	3,005,216
SPR	KOR01	DEU01	RUS11	MUS	0.055291	0.001531	36.12	168,333	2,171	3,005,216
SPR	KOR01	DEU01	JPN02	MUS	0.058181	0.001723	33.77	178,153	3,307	3,005,216
SPR	KOR01	DEU01	CHN20	CAS	0.051182	0.001650	31.03	158,706	4,895	3,005,216
SPR	KOR01	DEU01	JPN05	MUS	0.059777	0.002092	28.57	182,002	2,360	3,005,216
SPR	KOR01	DEU01	RUS17	MUS	0.052311	0.001852	28.25	161,008	3,803	3,005,216
SPR	KOR01	DEU01	JPN07	MUS	0.058511	0.002177	26.87	178,465	2,625	3,005,216
SPR	KOR01	DEU01	JPN11	MUS	0.058224	0.002210	26.35	178,251	3,274	3,005,216
SPR	KOR01	DEU01	JPN12	MUS	0.057811	0.002502	23.11	177,071	3,336	3,005,216
SPR	KOR01	DEU01	JPN16	CAS	0.058229	0.002558	22.76	177,955	2,965	3,005,216
SPR	KOR01	DEU01	RUS15	MUS	0.048995	0.002170	22.58	152,906	5,667	3,005,216
SPR	KOR01	DEU01	JPN18	CAS	0.057092	0.002639	21.63	174,625	3,051	3,005,216
SPR	KOR01	DEU01	RUS16	DOM	0.049009	0.002274	21.55	153,607	6,323	3,005,216
SPR	KOR01	DEU01	JPN17	CAS	0.056313	0.002646	21.28	173,321	4,087	3,005,216
SPR	KOR01	DEU01	JPN15	CAS	0.057120	0.002809	20.33	174,888	3,231	3,005,216
SPR	KOR01	DEU01	RUS14	CAS	0.050019	0.002913	17.17	154,611	4,293	3,005,216
SPR	KOR01	DEU01	JPN09	MUS	0.054011	0.003500	15.43	167,206	4,891	3,005,216
SPR	KOR01	DEU01	JPN01	MUS	0.040415	0.003527	11.46	134,798	13,341	3,005,216
SPR	KOR01	DEU01	RUS12	CAS	0.031010	0.003090	10.04	108,745	15,552	3,005,216

SPR	KOR01	DEU01	CHN06	MUS	0.022166	0.002219	9.99	68,393	1,781	3,005,216
SPR	KOR01	DEU01	CHN16	CAS	0.024322	0.002624	9.27	94,027	20,935	3,005,216
SPR	KOR01	DEU01	PAK02	CAS	0.004121	0.000453	9.10	45,171	32,787	3,005,216
SPR	KOR01	DEU01	IND04	CAS	0.003881	0.000430	9.03	44,284	32,622	3,005,216
SPR	KOR01	DEU01	PAK01	CAS	0.003923	0.000444	8.84	44,515	32,725	3,005,216
SPR	KOR01	DEU01	IDN01	DOM	0.003516	0.000416	8.45	42,746	32,181	3,005,216
SPR	KOR01	DEU01	IND03	CAS	0.003769	0.000446	8.45	44,109	32,784	3,005,216
SPR	KOR01	DEU01	IDN03	CAS	0.003657	0.000442	8.28	44,401	33,412	3,005,216
SPR	KOR01	DEU01	IDN04	CAS	0.003683	0.000459	8.02	44,562	33,495	3,005,216
SPR	KOR01	DEU01	IND02	CAS	0.003523	0.000439	8.02	44,430	33,844	3,005,216
SPR	KOR01	DEU01	LKA02	CAS	0.003700	0.000464	7.98	44,287	33,168	3,005,216
SPR	KOR01	DEU01	LKA01	CAS	0.003513	0.000442	7.95	43,913	33,356	3,005,216
SPR	KOR01	DEU01	IND07	CAS	0.003561	0.000452	7.89	44,281	33,580	3,005,216
SPR	KOR01	DEU01	PAK03	CAS	0.003633	0.000461	7.88	44,186	33,268	3,005,216
SPR	KOR01	DEU01	BGD02	CAS	0.003681	0.000479	7.69	44,705	33,644	3,005,216
SPR	KOR01	DEU01	IND05	CAS	0.003511	0.000457	7.68	44,234	33,682	3,005,216
SPR	KOR01	DEU01	BGD01	CAS	0.003505	0.000458	7.66	44,218	33,685	3,005,216
SPR	KOR01	DEU01	IND08	CAS	0.003520	0.000472	7.46	44,107	33,530	3,005,216
SPR	KOR01	DEU01	IND06	CAS	0.003500	0.000478	7.32	44,294	33,774	3,005,216
SPR	KOR01	DEU01	UKR01	MUS	0.030315	0.004213	7.20	106,935	15,831	3,005,216
SPR	KOR01	DEU01	PAK04	CAS	0.003835	0.000538	7.13	44,522	32,996	3,005,216
SPR	KOR01	DEU01	IND01	CAS	0.003353	0.000487	6.88	44,171	34,095	3,005,216
SPR	KOR01	DEU01	IND09	CAS	0.003544	0.000516	6.87	44,543	33,893	3,005,216
SPR	KOR01	DEU01	JPN04	MUS	0.022493	0.003370	6.67	89,420	21,825	3,005,216
SPR	KOR01	DEU01	VNM01	CAS	0.004280	0.000643	6.65	46,168	33,306	3,005,216
SPR	KOR01	DEU01	RUS10	CAS	0.024446	0.003726	6.56	91,160	17,694	3,005,216
SPR	KOR01	DEU01	IDN02	CAS	0.003725	0.000610	6.11	42,119	30,925	3,005,216
SPR	KOR01	DEU01	CHN17	CAS	0.007424	0.001294	5.74	53,177	30,866	3,005,216
SPR	KOR01	DEU01	VNM02	CAS	0.004434	0.000776	5.72	46,190	32,866	3,005,216
SPR	KOR01	DEU01	CHN19	CAS	0.013503	0.002407	5.61	68,147	27,569	3,005,216
SPR	KOR01	DEU01	CHN22	CAS	0.007014	0.001250	5.61	52,054	30,976	3,005,216
SPR	KOR01	DEU01	CHN14	CAS	0.008676	0.001574	5.51	56,428	30,355	3,005,216
SPR	KOR01	DEU01	CHN18	CAS	0.006819	0.001365	5.00	52,080	31,586	3,005,216
SPR	KOR01	DEU01	CHN11	CAS	0.012797	0.002580	4.96	66,214	27,756	3,005,216
SPR	KOR01	DEU01	TWN01	CAS	0.006068	0.001284	4.73	50,039	31,804	3,005,216
SPR	KOR01	DEU01	CHN12	CAS	0.010786	0.002291	4.71	61,573	29,160	3,005,216
SPR	KOR01	DEU01	IRN04	DOM	0.000136	0.000076	1.78	4,450	4,042	3,005,216
SPR	KOR01	DEU01	IRN01	DOM	0.000183	0.000118	1.55	4,446	3,897	3,005,216
SPR	KOR01	DEU01	IRN02	DOM	0.000119	0.000078	1.53	4,427	4,069	3,005,216
SPR	KOR01	DEU01	IRN03	DOM	0.000128	0.000105	1.22	4,570	4,185	3,005,216
SPR	KOR01	DEU01	DEU04	DOM	0.000057	0.000053	1.08	1,800	1,630	3,005,216
SPR	KOR01	DEU01	DEU03	DOM	0.000033	0.000067	0.50	2,171	2,072	3,005,216
SPR	KOR01	DEU01	DEU05	DOM	0.000023	0.000065	0.35	1,944	1,875	3,005,216
SPR	KOR01	DEU01	DEU06	DOM	0.000010	0.000054	0.19	1,806	1,775	3,005,216
SPR	KOR01	DEU01	NPL01	NEP	0.000191	0.001268	0.15	41,239	40,665	3,005,216
SPR	KOR01	DEU01	FRA02	DOM	0.000006	0.000067	0.09	2,732	2,713	3,005,216
SPR	KOR01	DEU01	DEU02	DOM	0.000004	0.000065	0.06	2,068	2,056	3,005,216
SPR	KOR01	DEU01	FRA04	DOM	0.000001	0.000074	0.01	2,635	2,633	3,005,216
SPR	KOR01	DEU01	FRA01	DOM	-0.000008	0.000078	-0.11	2,815	2,840	3,005,216
SPR	KOR01	DEU01	FRA03	DOM	-0.000027	0.000073	-0.36	2,660	2,740	3,005,216
SPR	KOR01	DEU01	DEU07	DOM	-0.000028	0.000055	-0.52	1,892	1,977	3,005,216
SPR	KOR01	DEU01	NPL02	NEP	-0.005273	0.002117	-2.49	38,341	54,188	3,005,216

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PART II: Whole-genome sequencing analysis of house mice (*Mus musculus*) captured in Madagascar

Introduction

House mice (*Mus musculus*) are small commensal mammals that spread worldwide along with human activities. They are thought to originate from the northern part of the Indian subcontinent (Boursot et al., 1993, 1996; Din et al., 1996) and to have experienced explosive population size growth after the initial colonization. Three major subspecies of house mice have been recognized so far (Didion and de Villena, 2013; Fujiwara et al., 2022): the southern Asian subspecies (*M. m. castaneus*: CAS), the northern Eurasian subspecies (*M. m. musculus*: MUS) and the western European subspecies (*M. m. domesticus*: DOM). Previous studies analyzing colonization patterns of house mice have provided insights into the history of human activity, such as migration, spread of agriculture and trading (Prager et al., 1998; Duplantier et al., 2002; Britton-Davidian et al., 2007; Searle et al., 2009a; Suzuki et al., 2013, 2015; Jing et al., 2014; Phifer-Rixey et al., 2018; Li et al., 2021; Fujiwara et al., 2022).

Madagascar is the fourth largest island in the world. It separated from the African continent and from the Indian subcontinent around 160 and 80 million years ago, respectively (Torsvik et al., 2000). The island is now about 300 km from the coastal line of the African continent at its shortest distance. Inferences from linguistic (Dahl, 1951, 1988; Adelaar, 1995), archaeological (Battistini and Verin, 1972; Dewar and Wright, 1993; Burney et al., 2004) and genetic (Hurles et al., 2005) evidence suggested that Malagasy people originate from both East

Africa and Southeast Asia (in particular, Borneo). When humans first arrived on Madagascar is still an open and controversial issue. Although previous archaeological evidence has suggested that the first human settlement on the island occurred 1,500–2,000 years ago (MacPhee and Burney, 1991; Burney et al., 2004; Gommery et al., 2011), recent excavations have provided evidence that humans became active on the island earlier than this (Dewar et al., 2013; Hansford et al., 2018; Douglass et al., 2019). More recently, studies using human genome data showed that ancient Malagasy people migrated from Borneo approximately 1,000–3,000 years ago and from the east coast of Africa around 700–1,500 years ago (Brucato et al., 2016; Pierron et al., 2017). A large commercial network connecting Asia and the Mediterranean Sea along the coastal regions of the Indian Ocean was established at least 1,000 years ago (Vérin and Wright, 1999), and traders from the Arabian Peninsula also sailed to the coast of Africa, including Madagascar (Allibert, 1988; Liszkowski, 2000).

Rodents have successfully colonized Madagascar, and there are at least 23 species of rodents currently inhabiting the island (Duplantier et al., 2002). After *Rattus rattus*, *M. musculus* is the second most common rodent found in human settlements throughout the island (Goodman, 1995). Duplantier et al. (2002) have reported that the tail of Madagascar house mice is as long as the head and body, which is a typical trait of DOM (Orsini et al., 1983). The Madagascar house mouse has therefore been thought to be a member of DOM (Boursot et al., 1993). In contrast, previous studies analyzing partial regions of mitochondrial genomes (control regions, the cytochrome *b* gene, and tRNAs) found that Madagascar house mice were genetically close to samples from Yemen, in the southern part of the Arabian Peninsula (Duplantier et al., 2002; Sakuma et al., 2016). The mtDNA analysis suggested that the Yemeni house mice form another potential subspecies, *M. m. gentilulus* (GEN), which is distinct from the other three major subspecies (Prager et al., 1998; Suzuki et al., 2013). The mtDNA sequences of Madagascar samples collected from different localities constituted a single cluster

with Yemeni samples (Duplantier et al., 2002; Sakuma et al., 2016). Suzuki et al. (2013) further compared the mitochondrial sequence of Yemeni GEN with those of other wild house mice and found that the mitochondrial lineage of the Yemeni GEN was in the most basal position to *M. musculus* among the other *M. musculus* subspecies. However, a study of microsatellite variation in the nuclear genome suggested that Madagascar mice are genetically close to CAS (Hardouin et al., 2015). These incongruences make the origin of Madagascar house mice highly controversial.

Previous studies on the genetic background of the house mouse in Madagascar are primarily based on mtDNA or limited nuclear genome analysis. To increase the resolution of genetic analyses, we performed high-quality whole-genome sequencing of five *M. musculus* samples captured in Madagascar and combined the data with a previously published worldwide house mouse genomic dataset (Harr et al., 2016; Fujiwara et al., 2022). We revealed the genetic features of these Madagascar wild house mice and estimated the divergence time between the continental and Madagascar samples. Our study provides insights into the prehistoric migration patterns of house mice and humans in Madagascar.

Results

Genetic diversity of Madagascar house mouse

We analyzed five whole-genome sequences of captured *M. musculus* from Madagascar that were partly analyzed in a previous study (Sakuma et al., 2016). These Madagascar samples were jointly genotyped with 128 publicly available samples, including seven *M. spretus* samples (Harr et al., 2016; Fujiwara et al., 2022). Table 2-1 presents a list of samples used in this study with sample IDs and approximate captured locations. The number of filtered SNVs in five Madagascar samples was 24,883,782 with an overall transition/transversion ratio of 2.10. The average per-sample nucleotide diversity (heterozygosity) of the Madagascar sample was 0.0031. The ratio of nonsynonymous to synonymous mutations in the CAS, DOM, MUS and Madagascar samples was calculated. Each subspecies showed a distinct distribution of the ratios. DOM, MUS and CAS showed high (0.3156–0.3301), intermediate (0.2955–0.3040) and low values (0.2842–0.2953), respectively. Madagascar samples showed a similar level of ratios to CAS (0.2865–0.2905). The histogram is shown in Figure 2-1. Table 2-2 presents the detailed results for each Madagascar sample.

The derived site frequency spectrum (DSFS) obtained from the Madagascar samples is shown in Figure 2-2 using *M. spretus* to polarize the direction of mutations. The sites were classified into synonymous, nonsynonymous and noncoding sites (Figure 2-2). The DSFS of Madagascar samples showed a deficiency of sites with low allele frequency, and an excess of sites with intermediate and high allele frequency. This pattern implies that the Madagascar populations underwent severe population decline. We also observed a slight excess of nonsynonymous polymorphisms compared with synonymous polymorphisms in the singleton class, indicating the segregation of slightly deleterious mutations in low frequency polymorphisms.

Population structure

To obtain an insight into the genetic features of Madagascar house mice, we first performed a principal component analysis (PCA) using 86,288,314 autosomal SNVs of 126 *M. musculus* samples (Figure 2-3). In the PCA plot, three clusters on the vertices of a triangle correspond to MUS, CAS and DOM genetic components, and individuals lying between the vertices should be inter-subspecies hybrid samples (Fujiwara et al., 2022). PC1 and PC2 represent the genetic differentiation between MUS and the others, and between DOM and the others, respectively. The Madagascar samples were positioned near the CAS cluster with a slightly admixed genetic component of DOM. There was little variation in PC scores among the Madagascar samples. The linkage disequilibrium (LD) pruned version of PCA was not considerably different from Figure 2-3 (Figure 2-4). We also performed ADMIXTURE analysis to estimate ancestral genetic components in the Madagascar samples (Figure 2-5), assuming three ($K = 3$) and four ($K = 4$) ancestral populations. In both results, the Madagascar samples were found to have a major CAS ancestry and a minor DOM ancestry.

Next, we constructed an autosomal genetic tree using the neighbor-joining method with the *M. spretus* samples as the outgroup (Figure 2-6). Only the samples that had a major subspecies component greater than 80% in the ADMIXTURE result ($K = 3$) were used in the phylogenetic analysis (see Methods for details). The Madagascar samples formed a single cluster within the CAS cluster. We also constructed a neighbor-net network (Figure 2-7), which had a similar pattern to the neighbor-joining tree, showing that the Madagascar samples are within the CAS cluster. To obtain a clearer picture, we used the outgroup f_3 statistics, $f_3(\text{MDG}, \text{X}; \text{SPR})$, where MDG, X and SPR represent Madagascar, non-Madagascar *M. musculus* and *M. spretus* samples, respectively. The results showed that individuals genetically close to the Madagascar samples (high f_3 values) were located around the coastal side of the South Asian regions and Indonesian islands (Figure 2-8).

We further investigated the pattern of genetic admixture in Madagascar samples using f_4 statistics. Following Fujiwara et al. (2022), we used Indian (IND03 and IND04) and German (DEU01–DEU07) samples as the reference populations for CAS and DOM, respectively. We computed $f_4(\text{SPR}, \text{CAS}; \text{DOM}, \text{MDG})$ and $f_4(\text{SPR}, \text{DOM}; \text{CAS}, \text{MDG})$, obtaining 0.0054 (Z-score: 52.43) and 0.0066 (Z-score: 26.25), respectively. In both cases, the f_4 statistics were significantly positive values, suggesting that the Madagascar samples were genetically closer to CAS than to DOM, but with a non-negligible amount of gene flow with DOM.

Mitochondrial lineage analysis

We investigated the genetic background of Madagascar samples using complete mitochondrial genomes. Phylogenetic trees based on maximum likelihood inference revealed that the five individuals from Madagascar formed a single cluster (Figure 2-9A, Figure 2-10). The Madagascar samples were situated in the most basal lineage of all *M. musculus* mitochondrial haplotypes, but bootstrap support was not sufficiently high (0.64, Figure 2-10). The time to the most recent common ancestor (tMRCA) of Madagascar mitochondrial lineages was estimated using the BEAST v1.8.4 software and we obtained the age of 3,100 years ago (Figure 2-9B).

Inference of past demographic history

Pairwise sequentially Markovian coalescent (PSMC) analysis was performed to infer the demographic history. All Madagascar samples showed almost the same effective population size trajectories over the past 1,000,000 years (Figure 2-11). The ancestral population of Madagascar samples showed a rapid increase from 300,000 to 200,000 years ago, peaked around 100,000 years ago, and has been slowly declining since then over the Last Glacial Period. PSMC plots for representative individuals of CAS and DOM are also shown in Figure 2-11. CAS and Madagascar populations showed similar population histories before

about 50,000 years ago. The CAS population exhibited a rapid decrease in effective population size after 50,000 years ago. The Madagascar samples also showed a similar decline, but with a slower rate than the CAS population. We also performed multiple sequentially Markovian coalescent (MSMC) analysis using Madagascar samples to analyze the relatively recent effective population size (Figure 2-12). The plot exhibits a historical bottleneck event for the Madagascar samples around 1,000–3,000 years ago.

Estimation of divergence time between populations

To estimate when the Madagascar samples diverged from the other populations, we performed a cross-population MSMC analysis. We evaluated cross coalescent rates between Madagascar samples and 13 other samples consisting of German DOM samples, Indian CAS samples and CAS samples from coastal and insular regions of the Indian Ocean. The latter refers to samples from India (Bhubaneswar, Hyderabad, Mysore), Bangladesh (Dhaka, Mymensingh), Sri Lanka (Colombo, Peradeniya) and Indonesia (Bali, Java). The divergence time between German DOM and Madagascar was approximately 225,000 years ago with a 95% confidence interval (CI) of 224,641–226,546. While an Indian CAS, which was sampled at an inland mountainous area, showed a divergence time of approximately 50,000 years ago (95% CI: 48,907–50,011) from Madagascar, the other CAS samples from the coastal and island regions of the Indian Ocean showed a much more recent (~4,000 years ago) divergence time from Madagascar samples (Figure 2-13). As a control, we performed the analysis for two samples from Bali and found that they did not show the signature of population divergence (Figure 2-14).

Discussion

The house mouse is an animal that has now colonized in a wide range of areas including remote islands. This creature has been living commensally with humans for at least 10,000 years (Cucchi et al., 2005) and is thought to have been introduced to islands, including Madagascar, by human activities over thousands or hundreds of years. Other than Madagascar, New Zealand (Searle et al., 2009a), Madeira (Gündüz et al., 2001) and the British Isles (Searle et al., 2009b) are known for their studies of the introduction of house mice to islands. In this study, we present genetic features of Madagascar house mice by comparing them with global samples and provide insights into how they have been introduced into and established on the island. However, we should make the caveat that this study was conducted using a limited number of samples captured in a small region of Madagascar, and these samples do not necessarily represent the entire Madagascar house mouse population. A large-scale sampling across the island would be desirable to draw a clearer picture in the future. We should also note that, although we showed population size trajectories inferred using PSMC and MSMC in Figure 2-11 and 2-12, apparent effective population size may change with many factors, such as population structure, migration and admixture, and may not reflect true effective population sizes (Mazet et al., 2016). Indeed, estimated effective population size (N_e) values should be viewed as the inverse of coalescent rate in a piecewise time.

Genetic background of the Madagascar wild house mouse samples

Previous studies have shown that wild *M. musculus* exhibit a very large effective population size and nucleotide diversity compared to humans. The Madagascar house mouse samples analyzed in this study also showed a higher nucleotide diversity (0.31%) than humans (0.08–0.12%) (Perry et al., 2012; Prado-Martinez et al., 2013; Arbiza et al., 2014). However, given that the Madagascar samples were clustered with CAS, whose nucleotide diversity is

around 0.74–0.79% (Geraldes et al., 2008; Phifer-Rixey et al., 2014; Harr et al., 2016), the relatively low nucleotide diversity of the Madagascar samples is probably related to the population bottleneck when they were brought to the island. The DSFS of Madagascar samples also agrees with the population bottleneck scenario. However, the ratios of nonsynonymous to synonymous mutations in Madagascar samples were comparable with those in CAS. The nonsynonymous/synonymous ratio is often interpreted as an indicator of the efficacy of natural selection against slightly deleterious mutations, because the effect of genetic drift should become stronger in small populations (Akashi et al., 2012). The observed pattern agrees with cases in humans and primates, where recent population size changes did not strongly affect the genetic load of individuals (Simons et al., 2014; Osada et al., 2015).

Based on the results of the PCA plot, ADMIXTURE, f_4 statistics, phylogenetic tree and phylogenetic network, we concluded that the nuclear genomes of Madagascar samples largely consisted of a CAS genetic component. This result is consistent with a previous microsatellite study (Hardouin et al., 2015). However, the analyses demonstrated that our Madagascar samples have experienced admixture events with DOM. A recent study of quantitative trait loci identified multiple regions causing hybrid male sterility in CAS and DOM hybrids (White et al., 2012). According to that study, a fairly high percentage of male individuals in the second-generation hybrids (F_2) exhibited phenotypes associated with infertility, indicating that gene introgression between CAS and DOM is difficult. Nevertheless, the Madagascar samples exhibit the genetic feature of CAS–DOM hybrids (DOM-like CAS), indicating that inter-subspecific hybridization is rare but possible.

Mitochondrial genome analysis indicated that the mitochondrial lineages of the Madagascar samples formed a monophyletic group with low nucleotide diversity and that these lineages have a recent origin, with a tMRCA of approximately 3,000 years ago. This pattern is consistent with the results of Duplantier et al. (2002), who analyzed samples from different

locations in Madagascar, except that Yemeni samples were also clustered with the Madagascar samples in Duplantier et al. (2002). The MSMC analysis showed that our Madagascar samples experienced a population bottleneck event about 1,000–3,000 years ago. These results suggest that *M. musculus* may have been first brought to the island of Madagascar during this period.

We showed that the mitochondrial lineage of Madagascar samples was placed in one of the most basal positions of the entire *M. musculus* species. However, the study by Duplantier et al. (2002), which analyzed 539 nucleotide sites in the D-loop of the mitochondrial genome, showed that the MUS clade was located at the basal position of all *M. musculus*. We created a phylogenetic tree with whole mitochondrial genomes and showed the mitochondrial genealogy with higher resolution than previous analyses, but the bootstrap value supporting the basal position was 0.64, which is still not sufficiently high to conclude with high confidence which mitochondrial lineage is the most basal.

Collectively, our study showed highly complex genetic features of the Madagascar samples. The nuclear genomes are mostly derived from CAS, but with a significant amount of admixture with DOM. In contrast, the mitochondrial lineage of Madagascar samples has diverged highly from both CAS and DOM lineages. These findings indicate that the genetic background of Madagascar house mice is unique among the other worldwide populations.

Divergence of Madagascar population from other CAS populations

We examined which CAS samples were closely related to the Madagascar samples. Although the neighbor-joining tree and neighbor-net network showed that the Madagascar samples clustered with Indian and Nepalese samples, f_3 statistics and MSMC analysis showed that the CAS samples in a wide range of the coastal and insular regions of the Indian Ocean are genetically closer to the Madagascar samples than the inland Indian samples. Considering that the inclusion of admixed samples to tree and network constructions potentially results in a

distorted pattern, we concluded that the results of f_3 statistics and MSMC were likely to be more reliable. In particular, the model of MSMC assumes that the coalescent time of genomic fragments between chromosomes differs across the genome and so the estimated divergence time should be more robust to gene flow and admixture events. The relatively recent divergence time (~4,000 years ago) between the Madagascar and the Indian Ocean coastal and insular populations suggests that the migration of the Madagascar population coincided with human activity in the Neolithic period.

Notably, there was a small but clear increase in the relative cross coalescent rate (rCCR) between the DOM–Madagascar populations around 50,000–70,000 years ago (Figure 2-13). This pattern is likely due to an admixture event between the ancestral population of German DOM and the Madagascar population. However, it should be noted that the peak timing (50,000–70,000 years ago) does not necessarily represent the actual timing of the admixture event. Since we used German DOM samples as representatives of DOM, if an unsampled or extinct DOM population was the source population, the peak timing would instead represent the divergence time between the ancestral population of German DOM and the unsampled/extinct DOM. Unfortunately, our dataset did not cover a large number of DOM samples, and we were not able to examine the timing of historical admixture events, if they existed.

Possible history of the Madagascar wild house mouse samples

The ancestors of present-day Malagasy people are thought to have dual origins on the Indonesian island of Borneo in Southeast Asia and on the east coast of Africa, and wild house mice are thought to have been introduced commensurately with the migration of these human ancestors who arrived on the island of Madagascar. Here, we would like to discuss the potential migration time and route of Madagascar house mice to the island.

First, we consider when the ancestors of the Madagascar house mouse were introduced onto the island. Although the rate of mitochondrial molecular evolution, nuclear genome mutation rate and generation time in wild house mice are controversial issues, and these assumptions make the estimated timing highly vulnerable, our analyses consistently indicate a strong population bottleneck around 1,000–3,000 years ago. Note that, in principle, population admixture would not create a spurious signal of a population bottleneck. However, the timing of the bottleneck is compatible with the generally accepted date of arrival in Madagascar of Austronesian-speaking peoples from the Indonesian Islands (BCE 300–CE 500) (Dewar and Wright, 1993; Burney et al., 2004; Hurles et al., 2005). Furthermore, cross-population MSMC analyses indicate that the divergence between the Madagascar samples and those from the coastal and insular areas of South and Southeast Asia surrounding the Indian Ocean occurred approximately 4,000 years ago. Since commensal animals, such as house mice, would not suddenly expand their population size without an appropriate type of human activity like agriculture, we suggest that the Madagascar house mice migrated to the island at the same time as or soon after the first Austronesian-speaking farmers arrived on the island.

Second, it is difficult to answer the question of where the ancestors of the Madagascar samples migrated from. Because our f_3 and MSMC analysis indicated that the Madagascar samples have genetic affinities with many samples from coastal and insular regions of the Indian Ocean, it would be difficult to precisely determine their origin. In addition, our samples did not cover Yemen, where previous mitochondrial studies have suggested an origin, or Borneo, where Austronesian-speaking peoples are supposed to have migrated from. The original homeland of the Madagascar samples therefore still remains an open question. Another interesting question is whether there were multiple introductions of house mice to Madagascar. Previous mitochondrial analyses of rats from multiple locations in Madagascar indicated that there is considerable genetic diversity within Madagascar, originating from multiple sites in

the Indian Ocean (Tollenaere et al., 2010). In this study, we show that Madagascar house mice possess both CAS and DOM genetic traits, which strongly supports the multiple origin scenario. If samples can be collected from multiple sites throughout Madagascar, a more definitive view of Madagascar house mice may be obtained in the future.

In summary, this study determined the whole-genome sequences of five Madagascar wild house mice and analyzed their genetic backgrounds. Until now, mice from Madagascar have been treated as DOM or GEN, but we showed that their genetic features are mostly derived from CAS with a non-negligible amount of introgression from DOM. In addition, mitochondrial and nuclear genome data indicated that they experienced a strong population bottleneck approximately 1,000–3,000 years ago, coinciding with the arrival of Austronesian farmers in Madagascar. In the future, mouse samples from the Middle East and Borneo, as well as more samples from across Madagascar, should clarify the in-depth genetic background and history of the Madagascar mouse population. Overall, we have revealed unique and highly complex genetic features of Madagascar house mice and provided insights into the evolutionary history of rodents that have successfully migrated to Madagascar, which has only been partially understood.

Material and Methods

Biological samples and genomic data

Five specimens of the Madagascar wild house mouse were collected in the Parc Botanique et Zoologique de Tsimbazaza, Madagascar and nearby areas, from which a partial mitochondrial genome and coat color-controlling gene were sequenced in the study of Sakuma et al. (2016). The other mitochondrial and nuclear genomic sequence data of *M. musculus* as well as the western Mediterranean mouse (*M. spretus*) were obtained from previous studies (Harr et al., 2016; Li et al., 2021; Fujiwara et al., 2022). These data were downloaded from the DDBJ (PRJDB11027) and the European Nucleotide Archive (PRJEB9450, PRJEB11742, PRJEB14167, PRJEB2176 and PRJEB11897). The reference complete mitochondrial sequence of *M. spretus* (NC_025952) was also used for the mitochondrial genome analysis. See Table 2-1 for detailed information on the samples used in this study.

Mapping genomic reads and variant calling

For the five Madagascar samples, 150-bp-length paired-end reads were sequenced using the DNBSEQ platform. The reads were quality checked using the FastQC v.0.11.9 tool (<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>). All cleaned reads were mapped to the house mouse reference genome sequence GRCm38 (mm10) using bwa-mem v.0.7.17-r1188 (Li and Durbin, 2009) algorithm with “-M” option and piped to the Samblaster v.0.1.26 (Faust and Hall, 2014) program with “-M” option to mark PCR-duplicated reads. For the data from Harr et al. (2016), we used samples that had greater than 20-fold median coverage. We used the GATK4 HaplotypeCaller (McKenna et al., 2010) function with “-ERC GVCF” to perform variant calls. The genomic variant call format (.gvcf) files of each sample were then merged to a jointly called genotype file using GATK4 GenomicDBImport and GenotypeGVCFs functions. We next conducted the GATK4 Variant Quality Score

Recalibration (VQSR) process, which applies the machine learning method to determine whether our raw variants are true or false positives. For VQSR, we downloaded the known single nucleotide variant (SNV) dataset of “mgp.v3.snps.rsIDdbSNPv137.vcf.gz” from the Sanger Institute web server (ftp://ftp-mouse.sanger.ac.uk/REL-1303-SNPs_Indels-GRCm38/) as a training dataset. Hard-filtered SNV data with parameters “QD < 2.0, FS > 60.0, MQ < 40.0, MQRankSum < -12.5, and ReadPosRankSum < -8.0” were also used as a training dataset. After VQSR, we used variants that passed within the 90% tranche (90% acceptance in all reliable training SNV datasets) for downstream analyses. The autosomal SNVs were then filtered using genomic mappability scores to restrict our analyses to non-repetitive regions. To calculate mappability scores of the reference genome sequence, we ran GenMap v.1.3.0 software (Pockrandt et al., 2020) with options “-K 30” and “-E 2” and used positions with the score of 1 (a 30-mer starting from a unique position in the genome, allowing for two mismatches) in downstream analyses. All samples were examined for kinship using KING v.2.2.6 software (Manichaikul et al., 2010) with the option “—kinship.” None of the samples from Madagascar showed a detectable kinship relationship. A total of 133 samples of mice, including five novel samples from Madagascar, were used in the following analyses.

Because the phenotypic records for sexes of Madagascar samples were not complete and may not be accurate, we determined the sexes of samples using the genomic sequence data. We calculated the read coverages on the sex chromosomes, and used the “depth” command of the samtools program to count the coverage of each sample in non-pseudoautosomal sites of the X and Y chromosomes that passed the mappability filter. The ratio of X to Y chromosome coverages exhibited a clear bimodal distribution, whose modes were 1.03–1.09 and 148.24–268.16. Three out of five samples were judged as males (Table 2-3). Synonymous and nonsynonymous SNVs were annotated with the house mouse gene annotation data version

GRCm38.101 (ftp://ftp.ensembl.org/pub/release-101/gtf/mus_musculus/) using the SnpEff and SnpSift programs (Cingolani et al., 2012a, 2012b).

Mitochondrial lineage analysis

The mitochondrial genome sequences of Madagascar samples were reconstructed by *de-novo* assembly software, Novoplasty v.4.2.1 (Dierckxsens et al., 2017), using the house mouse mitochondrial genome NC_005089 as a seed sequence. The mitochondrial sequences of all samples were aligned using MUSCLE (Edgar, 2004a, 2004b) implemented in MEGA7 (Kumar et al., 2016). All D-loop regions and gapped sites were removed, resulting in 16,038 bp length. To construct the maximum likelihood (ML) tree of mitochondrial genomes, we used IQ-TREE v.1.6.12 (Nguyen et al., 2015). The best substitution model, “TIM2+F+R3”, was selected using the ModelFinder (Kalyaanamoorthy et al., 2017) function implemented in IQ-TREE. Bootstrapping values were computed with 1,000 replications.

The divergence time among mitochondrial genomes was estimated using BEAST v1.8.4 (Drummond and Rambaut, 2007) with the HKY+G substitution and the strict clock models (Li et al., 2021). The Markov chain Monte Carlo simulation was run for 10 million steps including 10% burn-in steps, and samples were recorded for every 10,000 steps. Tracer v1.6 software (Rambaut et al., 2018) was used to assess the convergence of the chains and ensured effective sample size (ESS) values above 200 for most parameters. The trees were summarized using TreeAnnotator v1.8.4 software (<http://beast.community/treeannotator>) with the settings “Maximum clade credibility tree” and “Mean heights” and were displayed using FigTree v1.4.3 software (<http://tree.bio.ed.ac.uk/software/figtree/>). The time-dependent evolutionary rates of mtDNA (Ho et al., 2011) were considered as previously described (Li et al., 2021). Evolutionary rates of 2.4×10^{-8} substitutions/site/year and 1.1×10^{-7}

substitutions/site/year were used for the older (before 100,000 years ago) and younger divergences (after 20,000 years ago), respectively.

Population structure analysis of the Madagascar house mouse

We filtered our variant data to exclude indels and multiallelic SNVs using VCFtools. The filtered autosomal SNVs were then converted to a PLINK v.1.9 (Purcell et al., 2007) format. We polarized a mutation direction of each SNV using *M. spretus* as the outgroup species and calculated DSFS. In general practice, the SNVs in LD are excluded from population structure analysis. However, because the house mouse samples were genetically highly structured at the subspecies level, and excluding these SNVs would result in a very small number of SNVs for the downstream analysis, we performed PCA with and without LD pruning but presented the results without the LD pruning as primary results. PCA was performed using the smartpca program implemented in Eigensoft v.7.2.1 (Patterson et al., 2006) using the default parameter settings, except that we did not remove outlier samples automatically.

A neighbor-joining tree was reconstructed using a pairwise distance matrix generated from autosomal data (Saitou and Nei, 1987). Our previous study (Fujiwara et al., 2022) showed that samples with a high proportion of admixture may considerably distort the pattern of divergence among subspecies. In this study, we constructed phylogenetic trees using only those samples in which ancestry to a particular subspecies accounted for more than 80% in the ADMIXTURE analysis ($K = 3$). We computed all pairwise identity-by-state (IBS) distances using PRINK software with the “--distance square 1-ibs” option (Purcell et al., 2007). The tree was visualized using the Ape package in R (Paradis et al., 2004). Using the same samples, a Neighbor-Net tree (Bryant and Moulton, 2004) was computed using the phangorn package

(Schliep, 2011) with gdsfmt, SeqArray and SNPRelate packages (Zheng et al., 2012, 2017) in R.

We computed f_3 and f_4 statistics using AdmixTools v.7.0 (Patterson et al., 2012). The f_4 statistics were computed using the qpDstat program with “f4 mode” and “prints” options. The Indian CAS (IND03 and IND04) and German DOM (DEU01–DEU07) samples were used as reference populations. These samples showed the least amount of admixture with other subspecies based on the f_4 statistics in the previous study (Fujiwara et al., 2022). The configuration of the f_4 statistics is represented as $f_4(A, B; C, D)$, where A to D represent each population. The outgroup f_3 statistics were computed by the qp3pop program of AdmixTools using the “outgroupmode” option. In the outgroup f_3 -mode, the statistics of $f_3(A, B; C)$, where C represents an outgroup population, show the genetic drift from C to the common ancestor of A and B and represent the genetic relatedness between the population A and B.

Demographic inference

Pairwise sequentially Markovian coalescent (PSMC) (Li and Durbin, 2011) analysis was performed for all five samples from Madagascar. To create the input file for PSMC, we used the “mpileup” command of samtools with the “-C 50, -O, -D 60, -d 10” option to obtain the consensus autosomal genome sequence with GRCm38 (mm10) as the reference genome. The PSMC was conducted using the options “-N25 -t15 -r5 -p ‘1*4+25*2+1*4+1*6’”. We performed 100 bootstrap replicates to show the CIs of piecewise estimated N_e . Generation time (g) was assumed to be 1 year (Bronson, 1979; Suzuki et al., 2004; Geraldine et al., 2008), considering mating in the wild environment, and the autosomal mutation rate (μ) was assumed to be 5.7×10^{-9} per site per generation (Milholland et al., 2017).

MSMC (Schiffels and Durbin, 2014) and its second version (MSMC2: <https://github.com/stschiff/msmc2>) (Malaspina et al., 2016; Schiffels and Wang, 2020) were

used to estimate N_e changes and population separation history. Phased haplotype sequences, which were inferred using ShapeIt4 software (Delaneau et al., 2019), were used as input data for MSMC/MSMC2. We performed phasing of 126 house mouse samples, excluding seven *M. spretus* samples. The “Mapping Data for G2F1 Based Coordinates” (Liu et al., 2014) from “Mouse Map Converter (<http://cgd.jax.org/mousemapconverter/>)” was downloaded and the recombination rates in the files were used for ShapeIt4 and MSMC/MSMC2. To estimate the population separation history, we used two haplotypes from each sample to calculate the rCCR for given population pairs (Schiffels and Durbin, 2014). The half value of rCCR (i.e., rCCR = 0.5) is assumed as the time when the two populations separated. For bootstrapping, the original input data were cut into blocks of 5 Mbp each, which were randomly sampled to create a 3-Gbp-length pseudo genome. A total of 20 pseudo genomes were used for the bootstrapping. To visualize the MSMC/MSMC2 results, we used the same g and μ as the PSMC analysis.

Figures and Legends

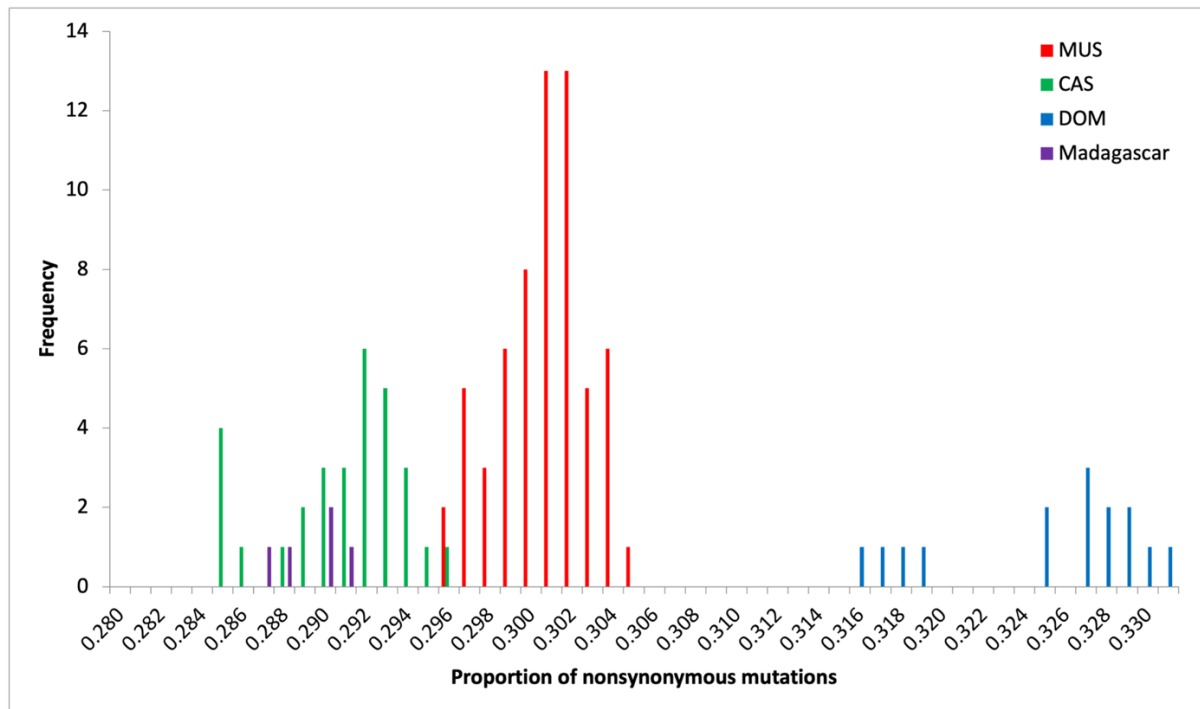


Figure 2-1 Histogram showing the ratio of nonsynonymous to synonymous mutations.

The histogram shows the proportion of nonsynonymous substitutions among the Madagascar sample and the major subspecies. Potential hybrid samples were excluded for plotting.

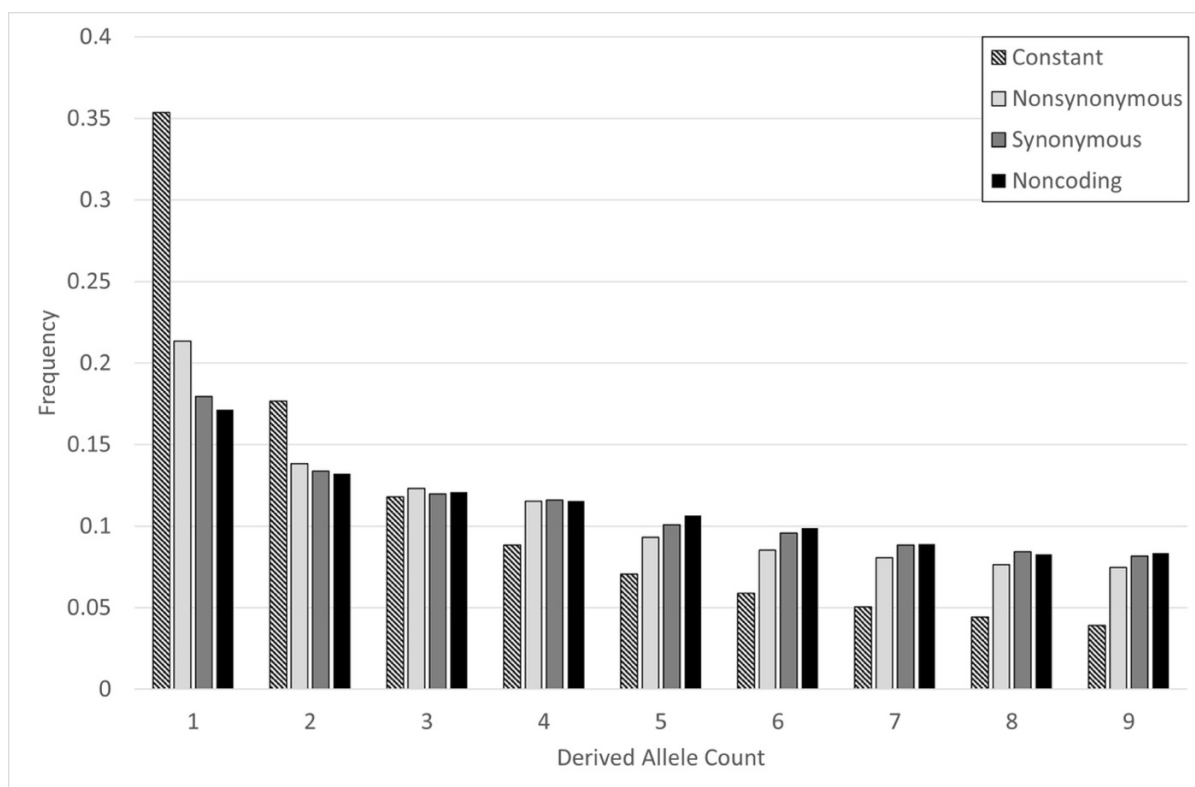


Figure 2-2 Derived allele frequency spectrum of five Madagascar samples.

Light gray, dark gray and black colors represent nonsynonymous, synonymous and noncoding, respectively. The neutral expected frequencies for constant population size are indicated by striped bars.

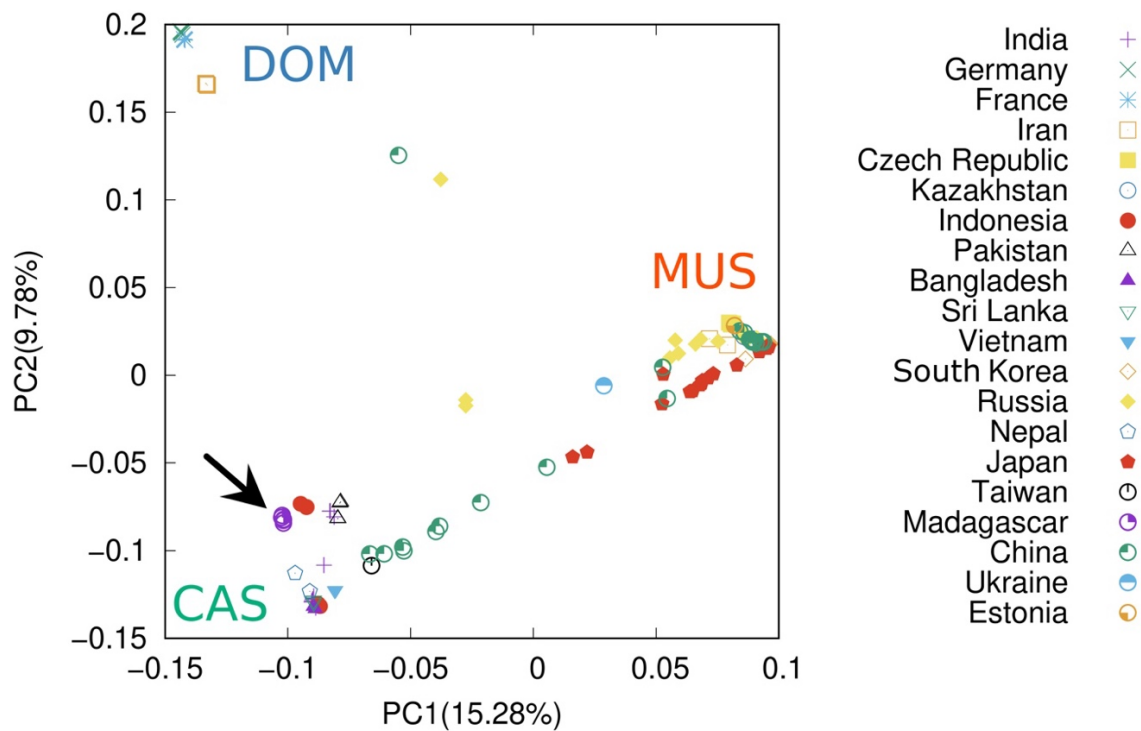


Figure 2-3 Principal component analysis plot of *M. musculus* using autosomal single nucleotide variants (SNVs).

The points in the figure represent the eigenvalues of individual samples collected from the countries shown on the right. The upper left, lower left and middle right vertices of the triangle represent *Mus musculus domesticus* (DOM), *M. m. castaneus* (CAS) and *M. m. musculus* (MUS) genetic components, respectively. The proportion of variance for each eigenvalue is shown in parentheses on the labels of the x-axis and y-axis. The arrow shows the position of the Madagascar samples.

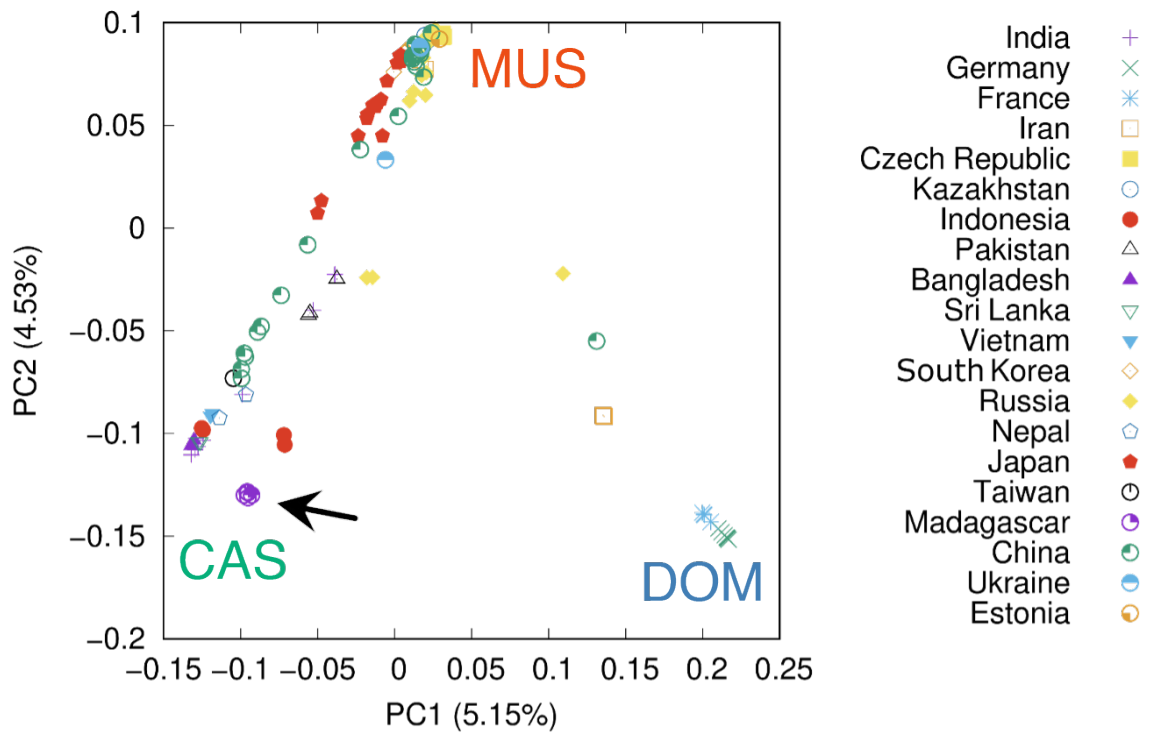


Figure 2-4 Principal component analysis plot of *M. musculus* using LD pruned autosomal single nucleotide variants (SNVs).

The points in the figure represent the eigenvalues of individual samples collected from the countries shown on the right. The lower right, lower left, and upper middle vertices of the triangle represent *Mus musculus domesticus* (DOM), *M. m. castaneus* (CAS), and *M. m. musculus* (MUS) genetic components, respectively. The proportion of variance for each eigenvalue is shown in parentheses on the labels of the x-axis and y-axis. The arrow shows the position of the Madagascar samples.

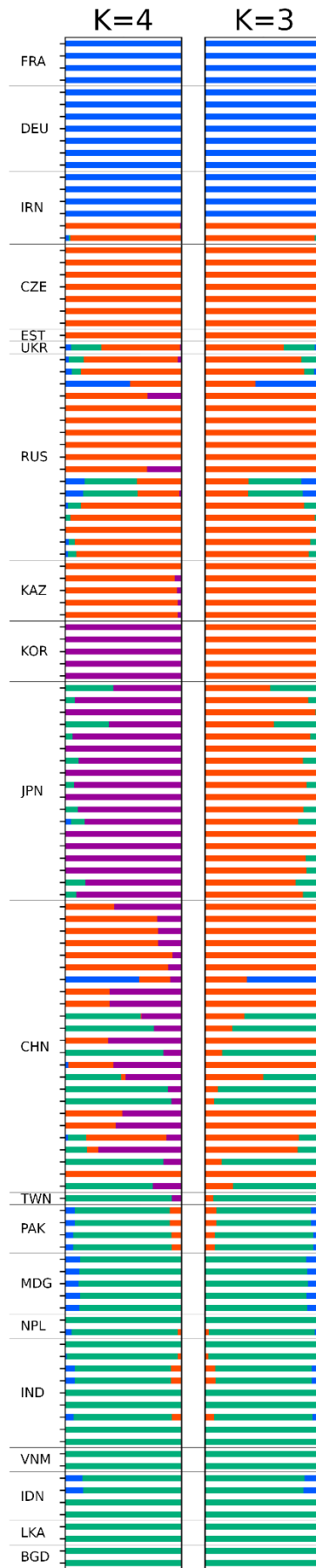


Figure 2-5 ADMIXTURE using autosomes from global and Madagascar samples.

The plot shows the proportion of estimated subspecies' genetic components. Results for cluster $K = 3$ and $K = 4$ are presented. Samples with the same country code are ordered according to sampling site from west to east and north to south.

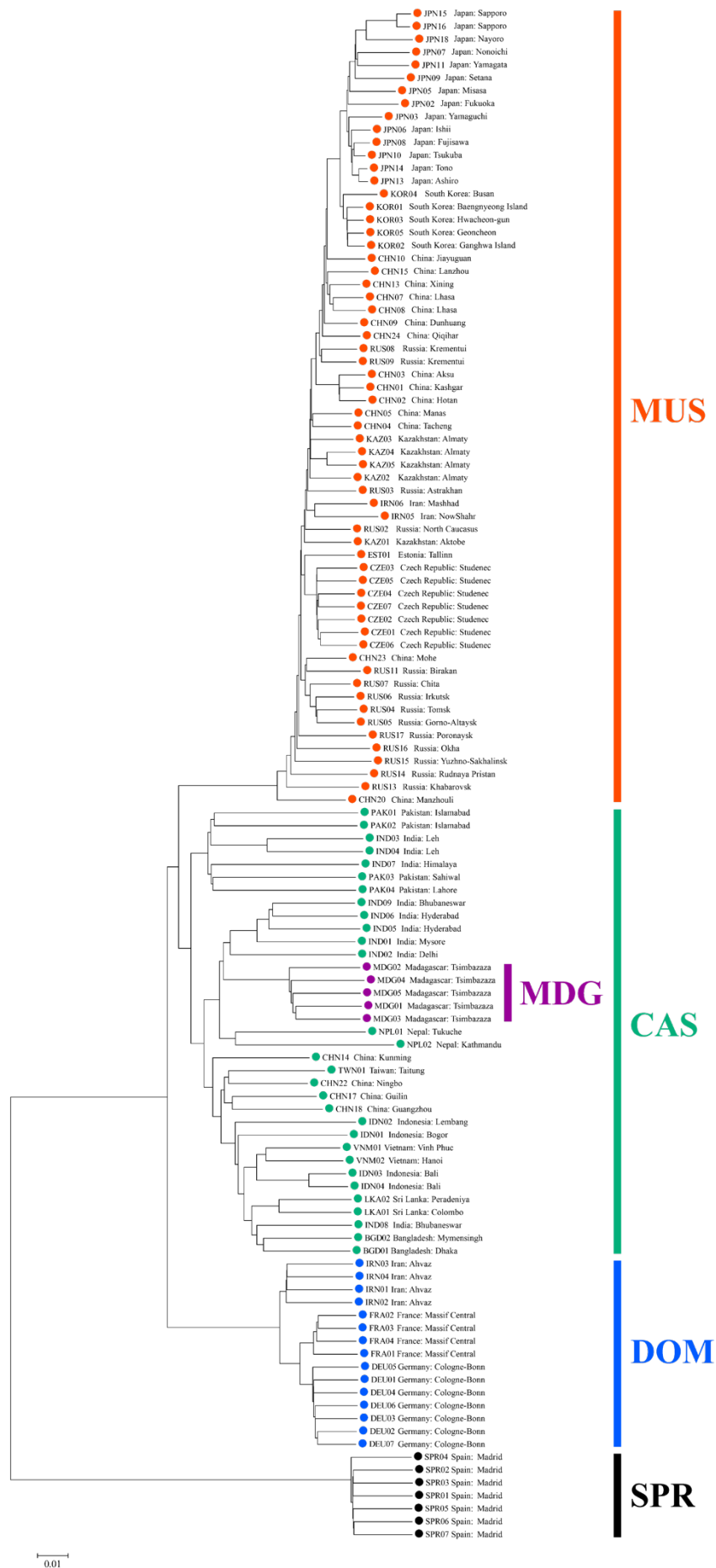


Figure 2-6 The neighbor-joining tree using pairwise genetic distances of *M. musculus*.

Neighbor-joining tree using pairwise genetic distances of *M. musculus*. The seven samples of *M. spretus* (SPR) were used as the outgroup. The color shows the subspecies: red (*M. m. musculus*: MUS), green (*M. m. castaneus*: CAS), blue (*M. m. domesticus*: DOM) and magenta (*M. musculus*: Madagascar (MDG)). Hybrid samples were excluded from tree construction. The scale shows the identity-by-state (IBS) distance.

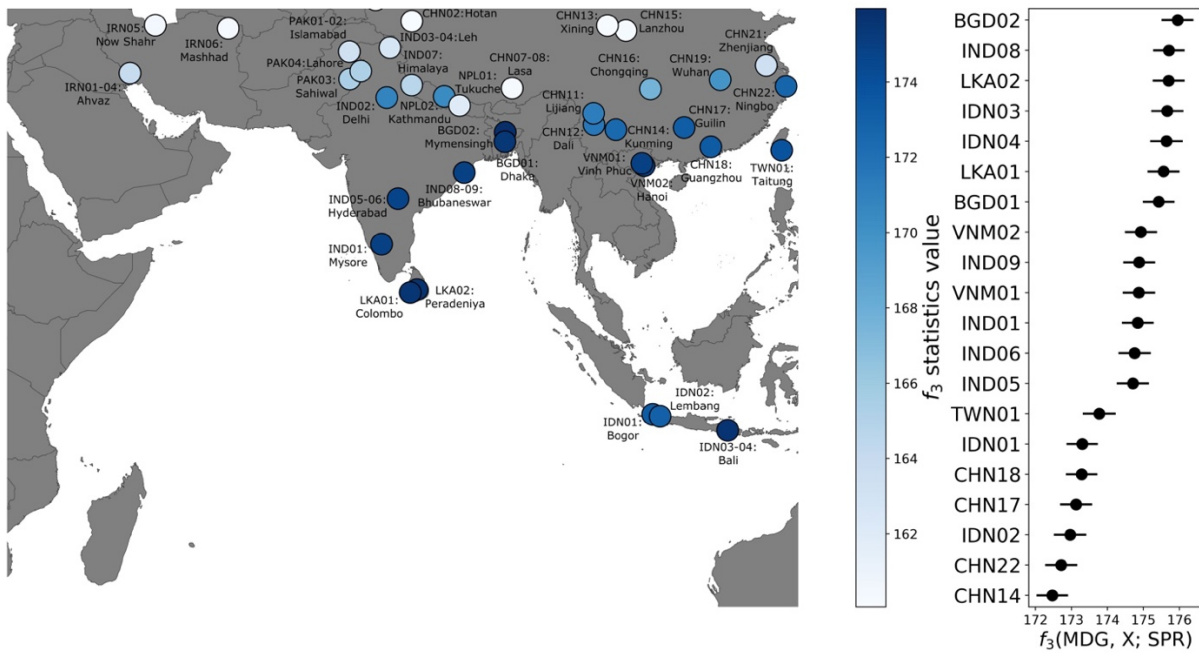


Figure 2-8 Outgroup f_3 (MDG, X; SPR) statistics.

The right plot shows the top 20 outgroup f_3 statistics values in which individuals of regional origin are genetically close to the Madagascar wild house mice. The horizontal line associated with each point indicates the standard error. Higher values indicate greater genetic closeness to the Madagascar house mice. The left world map shows the f_3 statistics value heat map focused on the South Asian region.

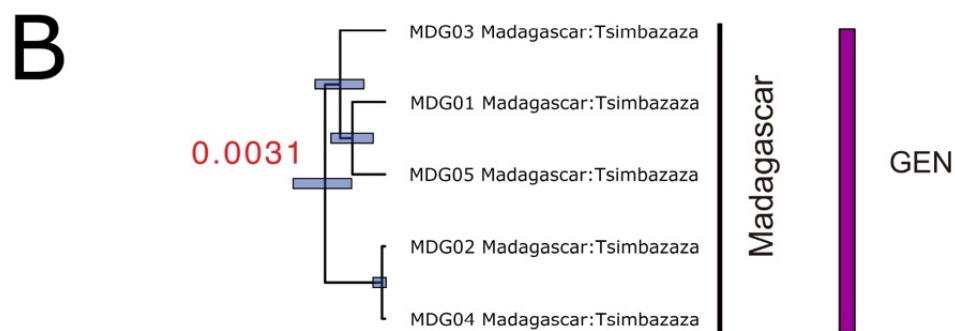
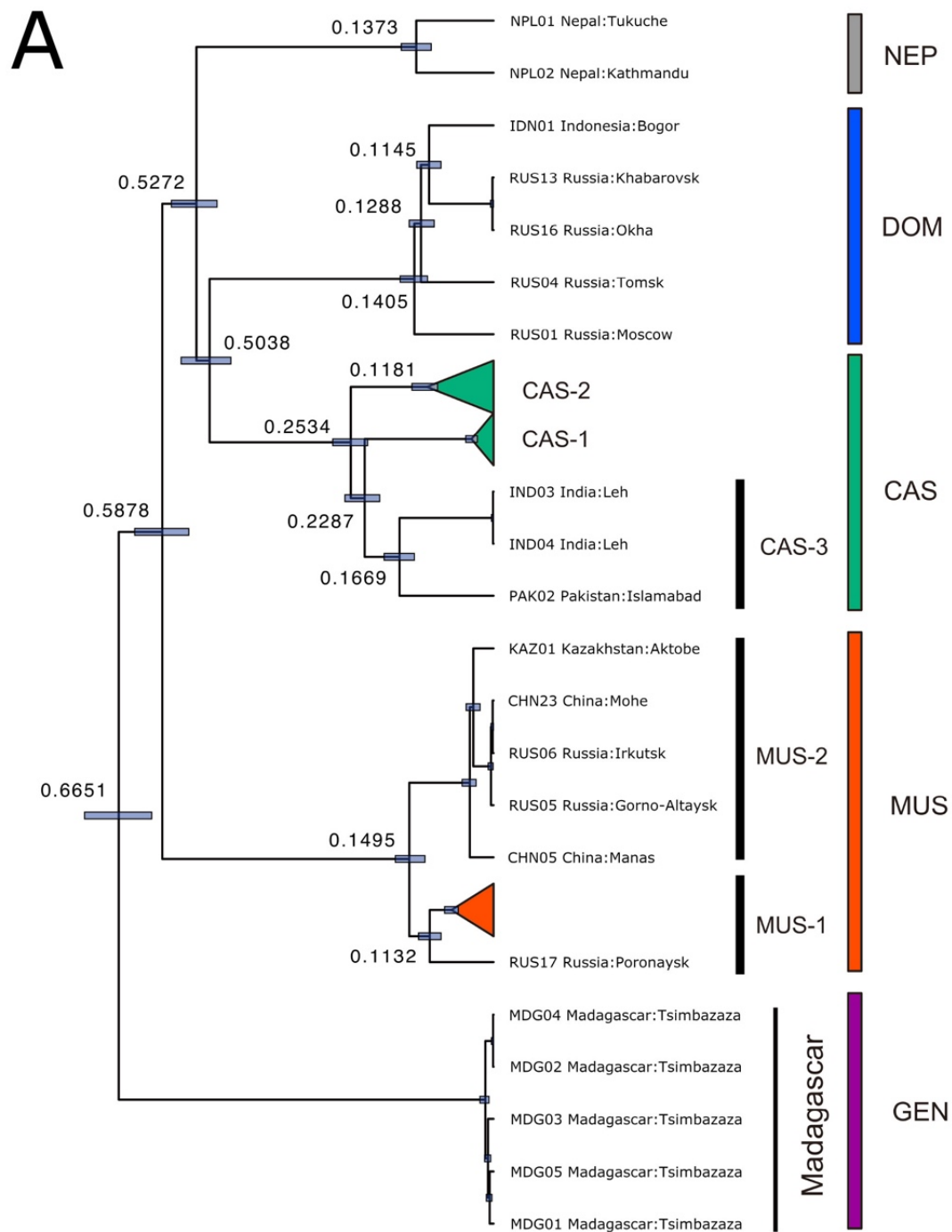


Figure 2-9 Phylogenetic tree of *M. musculus* entire mitochondrial genome sequences (15,000 bp) with a Bayesian-relaxed molecular clock.

Numbers represent the divergence time of haplotypes in million years, and the blue bars represent the 95% highest posterior density interval. (A) Divergence times of five haplogroups of *M. musculus* were estimated using a mutation rate of 2.4×10^{-8} substitutions/site/year. See Li et al. (2021) for the details of the subclades. (B) Given the time dependency of the mtDNA evolutionary rate, the mean time of the most recent common ancestor of the five haplotypes from Madagascar was estimated with a molecular clock of 1.1×10^{-7} substitutions/site/year.

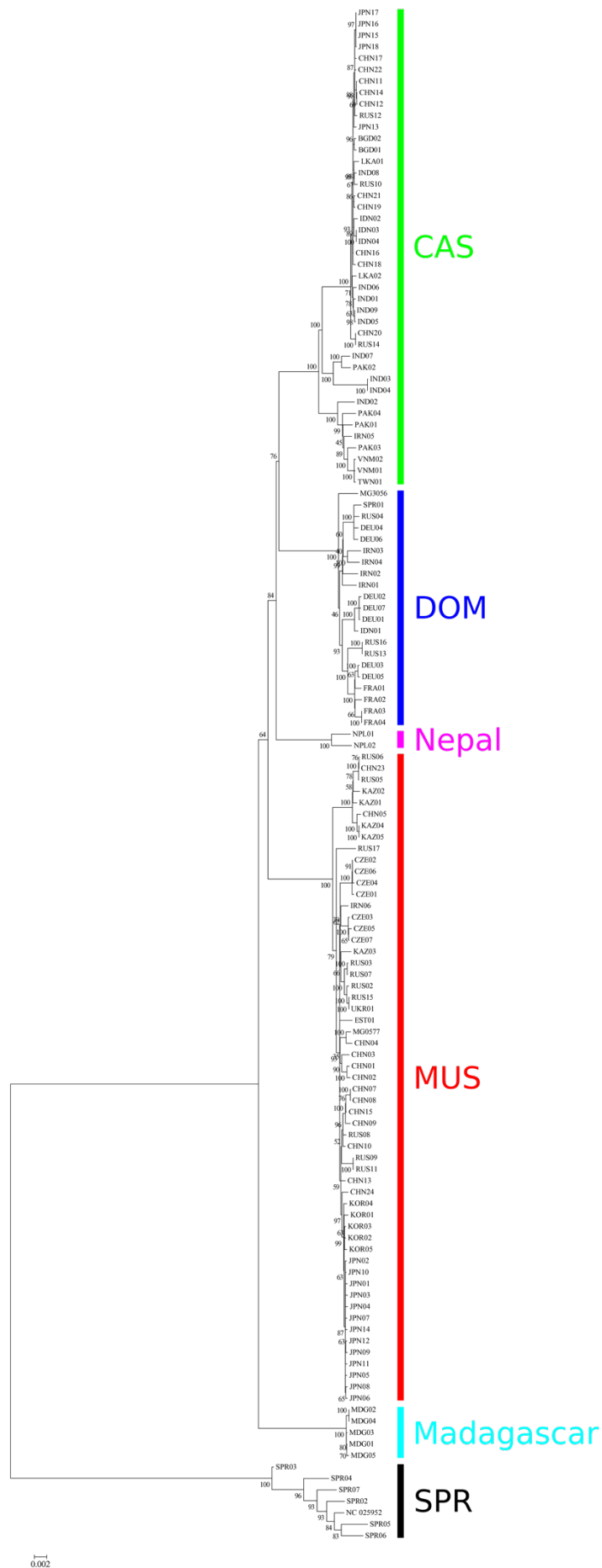


Figure 2-10 The maximum likelihood tree using mitochondrial genomes.

The substitution model (TIM2+F+R3) was determined by the best fit model of ModelFinder implemented in IQ-TREE. The colored line and captions correspond to the mitochondrial genome clades of *Mus musculus*. The numbers exhibit the results of the bootstrap resampling with 1000 replications.

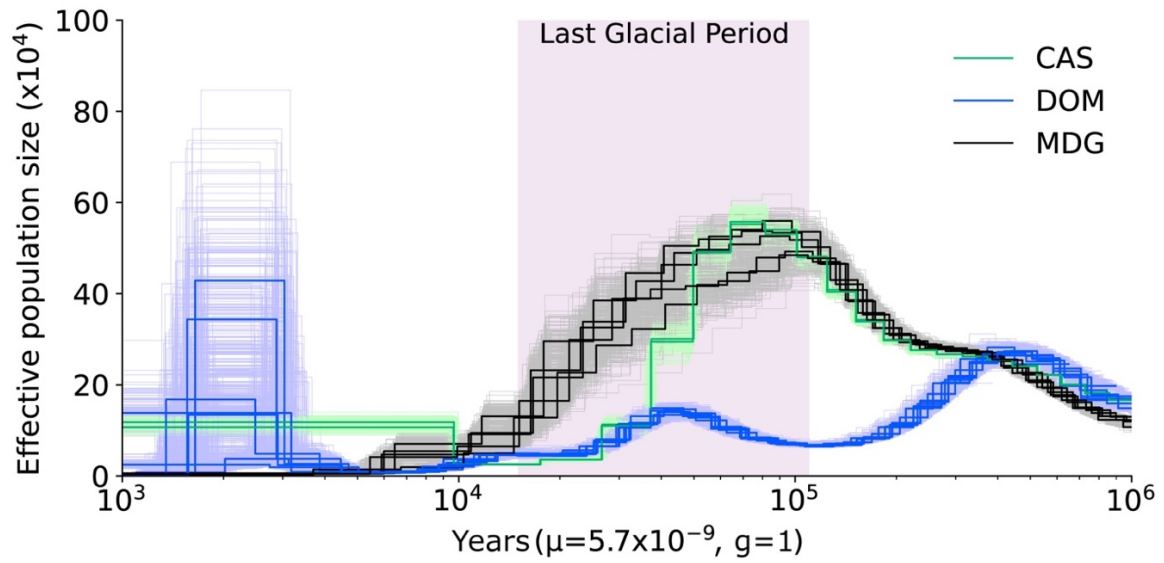


Figure 2-11 The PSMC plot of *M. musculus* from Madagascar.

Green, blue and black lines represent the inferred effective population size transition of CAS, DOM and Madagascar (MDG) mouse populations, respectively. The x-axis represents years before the present, scaled by $g = 1$ and $\mu = 5.7 \times 10^{-9}$, and the y-axis represents the number of the inferred effective population size. Lines with lighter colors represent 100 replications of the bootstrapping results.

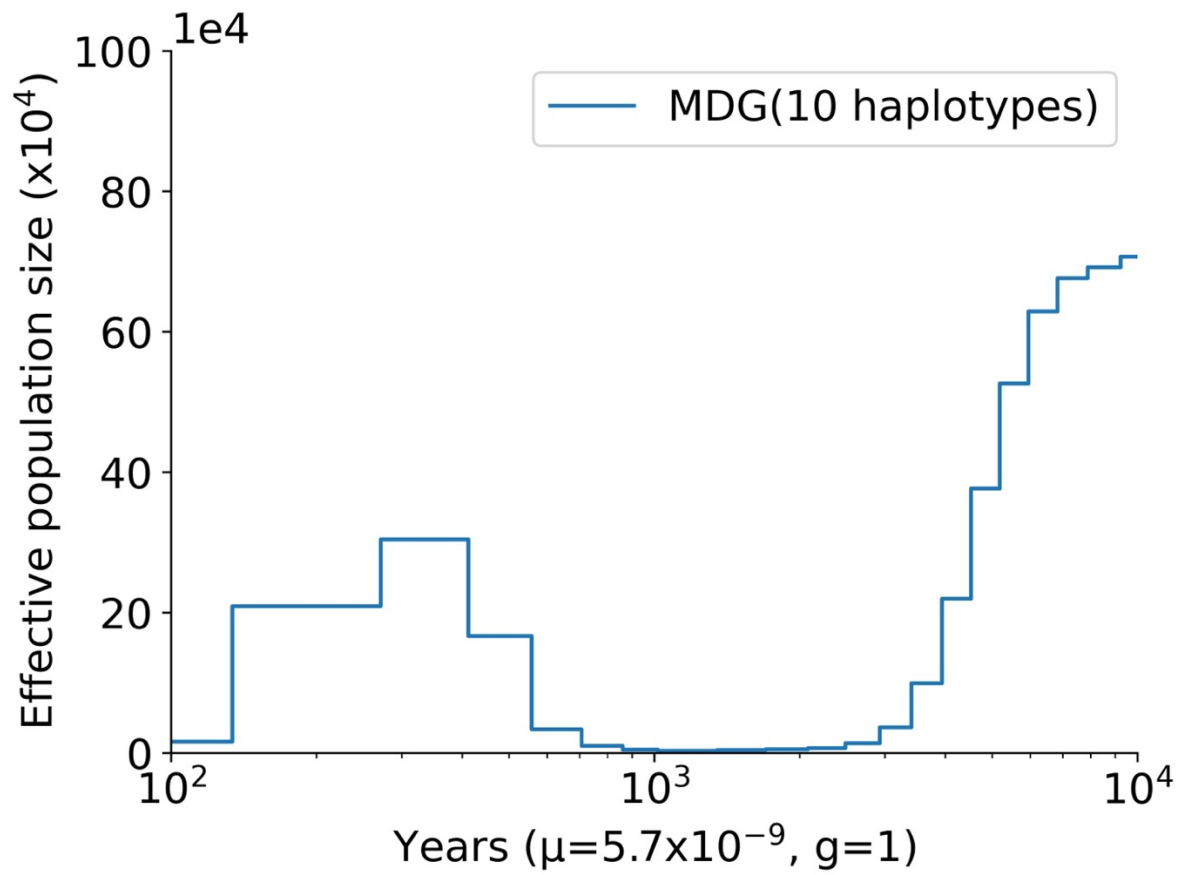


Figure 2-12 MSMC plot of five Madagascar samples using 10 haplotypes.

The x-axis represents years before the present, scaled by $g = 1$ and $\mu = 5.7 \times 10^{-9}$. The y-axis represents the inferred effective population size of Madagascar house mice.

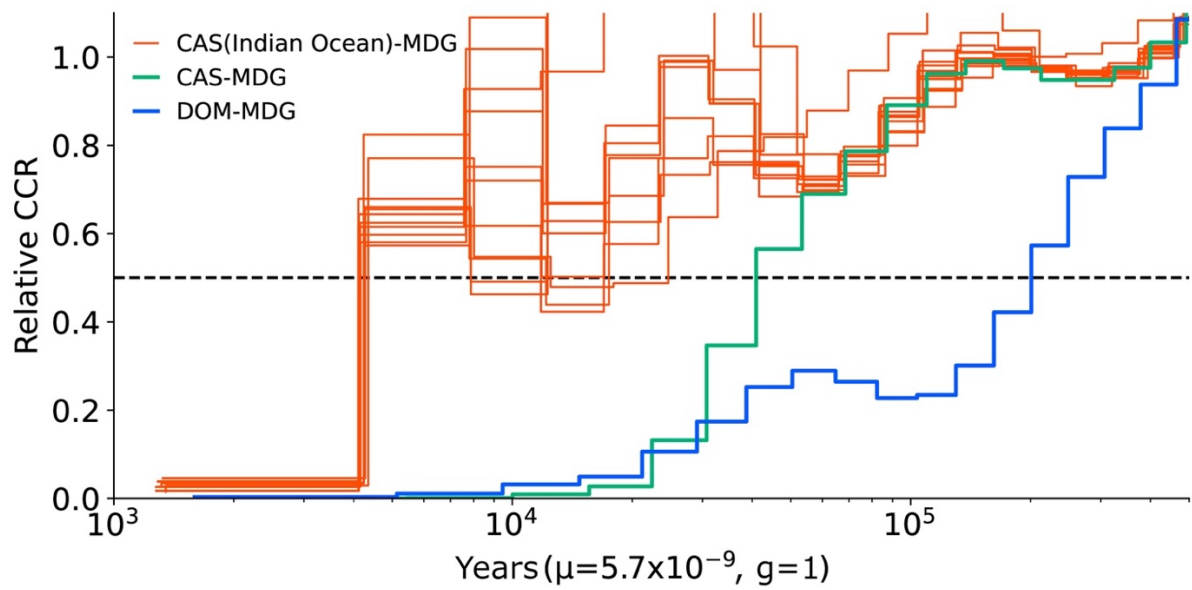


Figure 2-13 Relative cross coalescent rate (rCCR) between the CAS (Indian Ocean)-MDG, CAS-MDG and DOM-MDG inter-populations.

Relative cross coalescent rate (rCCR) between the CAS (Indian Ocean)-MDG, CAS-MDG and DOM-MDG inter-populations. The x-axis represents years before the present, scaled by $g = 1$ and $\mu = 5.7 \times 10^{-9}$. The rCCR value of 0.5 is assumed heuristically as the time when the two populations separated.

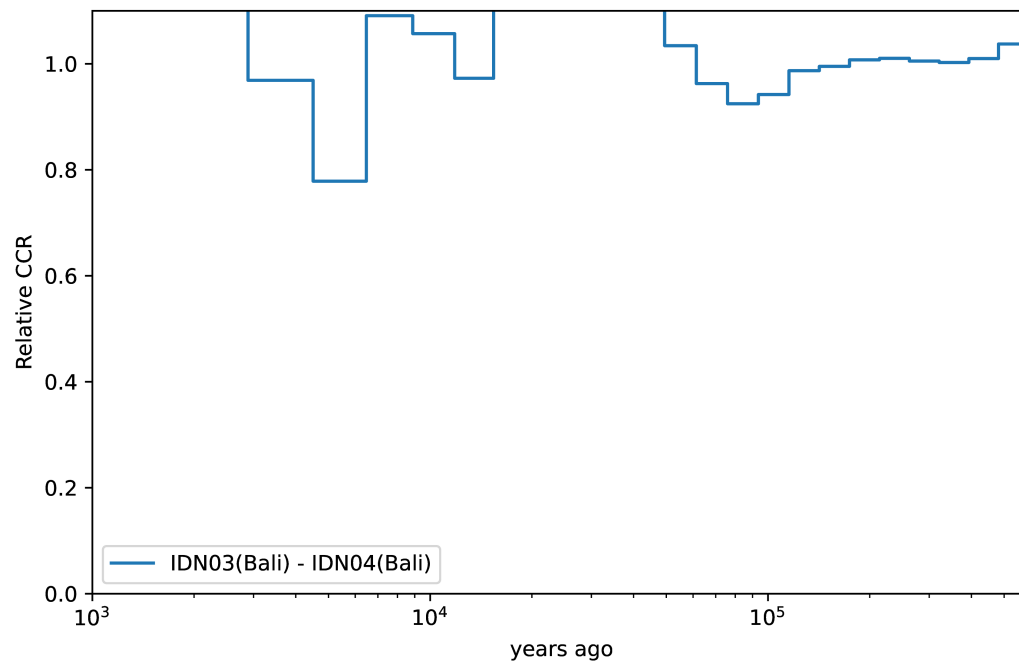


Figure 2-14 The rCCR plot of two Bali, Indonesia samples as control.

If the two samples were divergent, the rCCR should show less than 0.5, but since these two samples are from the same population, they do not show such a trend.

Tables

Table 2-1 Sample list of whole genome sequencing data of wild house mouse used in this study.

Sample list of whole genome sequencing data of wild house mouse used in this study.						
Sample Code	Sample ID	mtDNA Haplogroup	Location	**Latitude	**Longitude	Reference
BGD01	HI0373	CAS	Bangladesh: Dhaka	23.702000	90.366944	Fujiwara et al. 2022, Li et al. 2021
BGD02	HI0347	CAS	Bangladesh: Mymensingh	24.753889	90.403056	Fujiwara et al. 2022, Li et al. 2021
CHN01	MG0686	MUS	China: Kashgar	39.468100	75.993800	Fujiwara et al. 2022, Li et al. 2021
CHN02	MG0747	MUS	China: Hotan	37.100000	80.016667	Fujiwara et al. 2022, Li et al. 2021
CHN03	MG0608	MUS	China: Aksu	41.185000	80.290400	Fujiwara et al. 2022, Li et al. 2021
CHN04	MG0611	MUS	China: Tacheng	46.751700	82.986900	Fujiwara et al. 2022, Li et al. 2021
CHN05	MG0597	MUS	China: Manas	44.300000	86.216667	Fujiwara et al. 2022, Li et al. 2021
CHN06	MG0577	MUS	China: Urumqi	43.800000	87.583333	Fujiwara et al. 2022, Li et al. 2021
CHN07	MG0716	MUS	China: Lhasa	29.653400	91.171900	Fujiwara et al. 2022, Li et al. 2021
CHN08	MG0721	MUS	China: Lhasa	29.653400	91.171900	Fujiwara et al. 2022, Li et al. 2021
CHN09	MG0871	MUS	China: Dunhuang	40.142100	94.661900	Fujiwara et al. 2022, Li et al. 2021
CHN10	MG5086	MUS	China: Jiayuguan	39.773200	98.288200	Fujiwara et al. 2022, Li et al. 2021
CHN11	MG0917	CAS	China: Lijiang	26.855200	100.225900	Fujiwara et al. 2022, Li et al. 2021
CHN12	MG0797	CAS	China: Dali	25.606500	100.267600	Fujiwara et al. 2022, Li et al. 2021
CHN13	MG0565	MUS	China: Xining	36.616667	101.766667	Fujiwara et al. 2022, Li et al. 2021
CHN14	MG0529	CAS	China: Kunming	25.046400	102.709400	Fujiwara et al. 2022, Li et al. 2021
CHN15	MG0507	MUS	China: Lanzhou	36.060600	103.826800	Fujiwara et al. 2022, Li et al. 2021
CHN16	MG0709	CAS	China: Chongqing	29.563700	106.550400	Fujiwara et al. 2022, Li et al. 2021
CHN17	MG0501	CAS	China: Guilin	25.275000	110.296000	Fujiwara et al. 2022, Li et al. 2021
CHN18	MG0504	CAS	China: Guangzhou	23.132000	113.266000	Fujiwara et al. 2022, Li et al. 2021
CHN19	MG0908	CAS	China: Wuhan	30.593400	114.304600	Fujiwara et al. 2022, Li et al. 2021
CHN20	MG0863	CAS	China: Manzhouli	49.598000	117.379000	Fujiwara et al. 2022, Li et al. 2021
CHN21	MG0713	CAS	China: Zhenjiang	32.188000	119.424000	Fujiwara et al. 2022, Li et al. 2021
CHN22	MG0795	CAS	China: Ningbo	29.860300	121.624500	Fujiwara et al. 2022, Li et al. 2021
CHN23	MG0631	MUS	China: Mohe	52.972000	122.539000	Fujiwara et al. 2022, Li et al. 2021
CHN24	MG0992	MUS	China: Qiqihar	47.354900	123.918200	Fujiwara et al. 2022, Li et al. 2021
CZE01	ERS957497	MUS	Czech Republic: Studenec	see Harr et al. 2016		Harr et al. 2016
CZE02	ERS957498	MUS	Czech Republic: Studenec	see Harr et al. 2016		Harr et al. 2016
CZE03	ERS957499	MUS	Czech Republic: Studenec	see Harr et al. 2016		Harr et al. 2016
CZE04	ERS957500	MUS	Czech Republic: Studenec	see Harr et al. 2016		Harr et al. 2016
CZE05	ERS957501	MUS	Czech Republic: Studenec	see Harr et al. 2016		Harr et al. 2016
CZE06	ERS957502	MUS	Czech Republic: Studenec	see Harr et al. 2016		Harr et al. 2016
CZE07	ERS957503	MUS	Czech Republic: Studenec	see Harr et al. 2016		Harr et al. 2016
DEU01	ERS739373	DOM	Germany: Cologne-Bonn	see Harr et al. 2016		Harr et al. 2016
DEU02	ERS739374	DOM	Germany: Cologne-Bonn	see Harr et al. 2016		Harr et al. 2016
DEU03	ERS739375	DOM	Germany: Cologne-Bonn	see Harr et al. 2016		Harr et al. 2016
DEU04	ERS739376	DOM	Germany: Cologne-Bonn	see Harr et al. 2016		Harr et al. 2016
DEU05	ERS739377	DOM	Germany: Cologne-Bonn	see Harr et al. 2016		Harr et al. 2016
DEU06	ERS739378	DOM	Germany: Cologne-Bonn	see Harr et al. 2016		Harr et al. 2016
DEU07	ERS739379	DOM	Germany: Cologne-Bonn	see Harr et al. 2016		Harr et al. 2016
EST01	MG3044	MUS	Estonia: Tallinn	59.437222	24.745278	Fujiwara et al. 2022, Li et al. 2021
FRA01	ERS739382	DOM	France: Massif Central	see Harr et al. 2016		Harr et al. 2016
FRA02	ERS739385	DOM	France: Massif Central	see Harr et al. 2016		Harr et al. 2016
FRA03	ERS739386	DOM	France: Massif Central	see Harr et al. 2016		Harr et al. 2016
FRA04	ERS739388	DOM	France: Massif Central	see Harr et al. 2016		Harr et al. 2016
IDN01	HI0112	DOM	Indonesia: Bogor	-6.600000	106.800000	Fujiwara et al. 2022, Li et al. 2021
IDN02	HI0134	CAS	Indonesia: Lombok	-6.817000	107.617000	Fujiwara et al. 2022, Li et al. 2021
IDN03	HI0115	CAS	Indonesia: Bali	-8.369167	115.138333	Fujiwara et al. 2022, Li et al. 2021
IDN04	HI0116	CAS	Indonesia: Bali	-8.369167	115.138333	Fujiwara et al. 2022, Li et al. 2021
IND01	HI0274	CAS	India: Mysore	12.308611	76.653056	Fujiwara et al. 2022, Li et al. 2021
IND02	HI0185	CAS	India: Delhi	28.610000	77.230000	Fujiwara et al. 2022, Li et al. 2021
IND03	HI0159	CAS	India: Leh	34.160000	77.580000	Fujiwara et al. 2022, Li et al. 2021
IND04	HI0161	CAS	India: Leh	34.160000	77.580000	Fujiwara et al. 2022, Li et al. 2021
IND05	HI0328	CAS	India: Hyderabad	17.370000	78.480000	Fujiwara et al. 2022, Li et al. 2021
IND06	HI0329	CAS	India: Hyderabad	17.370000	78.480000	Fujiwara et al. 2022, Li et al. 2021
IND07	ERS003044	CAS	India: Himalaya	see Harr et al. 2016		Harr et al. 2016
IND08	HI0313	CAS	India: Bhubaneswar	20.270000	85.840000	Fujiwara et al. 2022, Li et al. 2021
IND09	HI0321	CAS	India: Bhubaneswar	20.270000	85.840000	Fujiwara et al. 2022, Li et al. 2021
IRN01	ERS739389	DOM	Iran: Ahvaz	see Harr et al. 2016		Harr et al. 2016
IRN02	ERS739393	DOM	Iran: Ahvaz	see Harr et al. 2016		Harr et al. 2016
IRN03	ERS739395	DOM	Iran: Ahvaz	see Harr et al. 2016		Harr et al. 2016
IRN04	ERS739396	DOM	Iran: Ahvaz	see Harr et al. 2016		Harr et al. 2016
IRN05	MG5135	CAS	Iran: Now Shahr	36.648889	51.496111	Fujiwara et al. 2022, Li et al. 2021
IRN06	MG0417	MUS	Iran: Mashhad	36.300000	59.600000	Fujiwara et al. 2022, Li et al. 2021
JPN01	HS2788	MUS	Japan: Okinawa Island	26.212444	127.680917	Fujiwara et al. 2022, Li et al. 2021

JPN02	HS4272	MUS	Japan: Fukuoka	33.590139	130.401722	Fujiwara et al. 2022, Li et al. 2021
JPN03	HS4273	MUS	Japan: Yamaguchi	34.178028	131.473778	Fujiwara et al. 2022, Li et al. 2021
JPN04	HS4411	MUS	Japan: Oda	35.192083	132.499361	Fujiwara et al. 2022, Li et al. 2021
JPN05	HS4097	MUS	Japan: Misasa	35.408444	133.861778	Fujiwara et al. 2022, Li et al. 2021
JPN06	HS4120	MUS	Japan: Ishii	34.074167	134.440556	Fujiwara et al. 2022, Li et al. 2021
JPN07	HS2815	MUS	Japan: Nonoichi	36.519417	136.609778	Fujiwara et al. 2022, Li et al. 2021
JPN08	HS4056	MUS	Japan: Fujisawa	35.338833	139.491111	Fujiwara et al. 2022, Li et al. 2021
JPN09	HS4271	MUS	Japan: Setana	42.417111	139.883028	Fujiwara et al. 2022, Li et al. 2021
JPN10	HS4169	MUS	Japan: Tsukuba	36.083472	140.076444	Fujiwara et al. 2022, Li et al. 2021
JPN11	HS3534	MUS	Japan: Yamagata	38.255417	140.339611	Fujiwara et al. 2022, Li et al. 2021
JPN12	HS2323	MUS	Japan: Hakodate	41.768667	140.728917	Fujiwara et al. 2022, Li et al. 2021
JPN13	MG0230	CAS	Japan: Ashiro	40.101389	141.052028	Fujiwara et al. 2022, Li et al. 2021
JPN14	HS3538	MUS	Japan: Tono	39.702083	141.154500	Fujiwara et al. 2022, Li et al. 2021
JPN15	MG0296	CAS	Japan: Sapporo	43.121917	141.245833	Fujiwara et al. 2022, Li et al. 2021
JPN16	MG0297	CAS	Japan: Sapporo	43.121917	141.245833	Fujiwara et al. 2022, Li et al. 2021
JPN17	HS2445	CAS	Japan: Takikawa	43.557833	141.910417	Fujiwara et al. 2022, Li et al. 2021
JPN18	HS2326	CAS	Japan: Nayoro	44.355833	142.463333	Fujiwara et al. 2022, Li et al. 2021
KAZ01	HS1464	MUS	Kazakhstan: Aktobe	50.283333	57.166667	Fujiwara et al. 2022, Li et al. 2021
KAZ02	ERS957504	MUS	Kazakhstan: Almaty	see Harr et al. 2016		Harr et al. 2016
KAZ03	ERS957506	MUS	Kazakhstan: Almaty	see Harr et al. 2016		Harr et al. 2016
KAZ04	ERS957508	MUS	Kazakhstan: Almaty	see Harr et al. 2016		Harr et al. 2016
KAZ05	ERS957510	MUS	Kazakhstan: Almaty	see Harr et al. 2016		Harr et al. 2016
KOR01	HS0682	MUS	South Korea: Baengnyeong Island	37.966667	124.650000	Fujiwara et al. 2022, Li et al. 2021
KOR02	HS4238	MUS	South Korea: Ganghwa Island	37.700000	126.433333	Fujiwara et al. 2022, Li et al. 2021
KOR03	HS4233	MUS	South Korea: Hwacheon-gun	38.107500	127.714444	Fujiwara et al. 2022, Li et al. 2021
KOR04	MG0444	MUS	South Korea: Busan	35.100000	129.033333	Fujiwara et al. 2022, Li et al. 2021
KOR05	HS1368	MUS	South Korea: Geoncheon	35.837686	129.045187	Fujiwara et al. 2022, Li et al. 2021
LKA01	HI0488	CAS	Sri Lanka: Colombo	6.934444	79.842778	Fujiwara et al. 2022, Li et al. 2021
LKA02	HI0484	CAS	Sri Lanka: Peradeniya	7.266667	80.600000	Fujiwara et al. 2022, Li et al. 2021
MDG01	HS5555	GEN	Madagascar: Tsimbazaza	-18.93	47.526111	Fujiwara et al. 2022, Li et al. 2021
MDG02	HS5558	GEN	Madagascar: Tsimbazaza	-18.93	47.526111	Fujiwara et al. 2022, Li et al. 2021
MDG03	HS5559	GEN	Madagascar: Tsimbazaza	-18.93	47.526111	Fujiwara et al. 2022, Li et al. 2021
MDG04	HS5560	GEN	Madagascar: Tsimbazaza	-18.93	47.526111	Fujiwara et al. 2022, Li et al. 2021
MDG05	HS5561	GEN	Madagascar: Tsimbazaza	-18.93	47.526111	Fujiwara et al. 2022, Li et al. 2021
NPL01	HS1467	NEP	Nepal: Tukuhe	28.740000	83.620000	Fujiwara et al. 2022, Li et al. 2021
NPL02	HS1523	NEP	Nepal: Kathmandu	27.717200	85.324000	Fujiwara et al. 2022, Li et al. 2021
PAK01	HI0173	CAS	Pakistan: Islamabad	33.716667	73.066667	Fujiwara et al. 2022, Li et al. 2021
PAK02	HI0175	CAS	Pakistan: Islamabad	33.716667	73.066667	Fujiwara et al. 2022, Li et al. 2021
PAK03	HI0261	CAS	Pakistan: Sahiwal	30.661111	73.108333	Fujiwara et al. 2022, Li et al. 2021
PAK04	HI0264	CAS	Pakistan: Lahore	31.549722	74.343611	Fujiwara et al. 2022, Li et al. 2021
RUS01	MG3056	DOM	Russia: Moscow	55.755833	37.617222	Fujiwara et al. 2022, Li et al. 2021
RUS02	MG3010	MUS	Russia: North Caucasus	43.711400	44.806100	Fujiwara et al. 2022, Li et al. 2021
RUS03	HS3612	MUS	Russia: Astrakhan	46.350000	48.050000	Fujiwara et al. 2022, Li et al. 2021
RUS04	HS3604	DOM	Russia: Tomsk	56.500000	84.966667	Fujiwara et al. 2022, Li et al. 2021
RUS05	HS3605	MUS	Russia: Gorno-Altaysk	51.950000	85.966667	Fujiwara et al. 2022, Li et al. 2021
RUS06	HS3608	MUS	Russia: Irkutsk	52.283333	104.283333	Fujiwara et al. 2022, Li et al. 2021
RUS07	MG3012	MUS	Russia: Chita	52.050000	113.466667	Fujiwara et al. 2022, Li et al. 2021
RUS08	MG3007	MUS	Russia: Krementui	50.155148	115.906841	Fujiwara et al. 2022, Li et al. 2021
RUS09	MG3008	MUS	Russia: Krementui	50.155148	115.906841	Fujiwara et al. 2022, Li et al. 2021
RUS10	HS1411	CAS	Russia: Khasan	42.428333	130.645556	Fujiwara et al. 2022, Li et al. 2021
RUS11	MG3026	MUS	Russia: Birakan	49.000833	131.720000	Fujiwara et al. 2022, Li et al. 2021
RUS12	MG3025	CAS	Russia: Vladivostok	43.133333	131.900000	Fujiwara et al. 2022, Li et al. 2021
RUS13	MG3037	DOM	Russia: Khabarovsk	48.483333	135.083333	Fujiwara et al. 2022, Li et al. 2021
RUS14	MG3018	CAS	Russia: Rudnaya Pristan	44.358611	135.810278	Fujiwara et al. 2022, Li et al. 2021
RUS15	MG3048	MUS	Russia: Yuzhno-Sakhalinsk	46.966667	142.733333	Fujiwara et al. 2022, Li et al. 2021
RUS16	HS3607	DOM	Russia: Okha	53.583333	142.933333	Fujiwara et al. 2022, Li et al. 2021
RUS17	MG3045	MUS	Russia: Poronaysk	49.216667	143.116667	Fujiwara et al. 2022, Li et al. 2021
SPR01	ERS957512	<i>Mus spretus</i>	Spain: Madrid	see Harr et al. 2016		Harr et al. 2016
SPR02	ERS957513	<i>Mus spretus</i>	Spain: Madrid	see Harr et al. 2016		Harr et al. 2016
SPR03	ERS957514	<i>Mus spretus</i>	Spain: Madrid	see Harr et al. 2016		Harr et al. 2016
SPR04	ERS957515	<i>Mus spretus</i>	Spain: Madrid	see Harr et al. 2016		Harr et al. 2016
SPR05	ERS957516	<i>Mus spretus</i>	Spain: Madrid	see Harr et al. 2016		Harr et al. 2016
SPR06	ERS957517	<i>Mus spretus</i>	Spain: Madrid	see Harr et al. 2016		Harr et al. 2016
SPR07	ERS957519	<i>Mus spretus</i>	Spain: Madrid	see Harr et al. 2016		Harr et al. 2016
TWN01	HS2400	CAS	Taiwan: Taitung	22.758333	121.144444	Fujiwara et al. 2022, Li et al. 2021
UKR01	MG3066	MUS	Ukraine: Donetsk	48.002778	37.805278	Fujiwara et al. 2022, Li et al. 2021
VNM01	HI0505	CAS	Viet Nam: Vinh Phuc	21.300000	105.600000	Fujiwara et al. 2022, Li et al. 2021
VNM02	HI0520	CAS	Viet Nam: Hanoi	21.028472	105.854167	Fujiwara et al. 2022, Li et al. 2021

*Fujiwara, K. et al. (2022) Insights into *Mus musculus* Population Structure across Eurasia Revealed by Whole-Genome Analysis, *Genome Biol. Evol.* 14, evac068,

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*Li, Y. et al. (2021) House mouse *Mus musculus* dispersal in East Eurasia inferred from 98 newly determined complete mitochondrial genome sequences. *Heredity* 126, 132–147.

**Latitude and longitude are not absolute points of sample collection, but rather approximate locations.

Table 2-2 Basic statistics of Malagasy house mouse samples

Basic statistics of Malagasy house mouse samples

Sample code	Sample ID	Location	mtDNA haplogroup	Median coverage	Ts/Tv	Per-sample nucleotide diversity	Nonsynonymous	Synonymous	Nonsynonymous /Synonymous
MDG01	HS5555	Madagascar: Tsimbazaza	GEN	26.0	2.107	0.003091476	85684	209312	0.40936019
MDG02	HS5558	Madagascar: Tsimbazaza	GEN	27.0	2.099	0.003602944	88291	216901	0.407056676
MDG03	HS5559	Madagascar: Tsimbazaza	GEN	27.0	2.104	0.003338113	85936	214002	0.401566341
MDG04	HS5560	Madagascar: Tsimbazaza	GEN	27.0	2.107	0.002250803	81478	199493	0.408425358
MDG05	HS5561	Madagascar: Tsimbazaza	GEN	26.0	2.104	0.003375003	87030	215782	0.403323725

Table 2-3 Sex of the collected sample by computing the depth of the sex chromosomes.

Sex of the collected sample by computing the depth of the sex chromosomes.

Sample Code	Sample ID	Chromosome X Total Depth	Chromosome Y Total Depth	Chromosome X (Normalized)	Chromosome Y (Normalized)	X/Y ratio	Sex
MDG01	HS5555	1,659,509,030	15,751,830	18.324	17.654	1.038	M
MDG02	HS5558	3,180,178,155	116,836	35.114	0.131	268.160	F
MDG03	HS5559	1,704,627,115	15,290,145	18.822	17.136	1.098	M
MDG04	HS5560	1,686,612,760	15,456,122	18.623	17.323	1.075	M
MDG05	HS5561	3,089,337,937	205,312	34.111	0.230	148.242	F

Reference

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PART III: Revealing migration and admixture patterns of wild house mice from East Asia

Introduction

House mouse (*Mus musculus*) is one of the most widespread creatures of all rodents, with habitat in all continents over the world including East Asia. This small rodent is commensal to humans and has spread to the world with human activities such as migration, the spread of agriculture, and trading (Britton-Davidian et al., 2007; Duplantier et al., 2002; Fujiwara et al., 2022b; Jing et al., 2014; Li et al., 2021; Phifer-Rixey et al., 2018; Prager et al., 1998; Searle et al., 2009a, 2009b; Suzuki et al., 2013, 2015). Recent studies of mitochondrial, nuclear genes, and genomes have recognized three major subspecies (Boursot et al. 1993; Didion and de Villena 2013; Geraldès et al. 2008, 2011; Moriwaki et al. 1986; Phifer-Rixey et al. 2014; White et al. 2009; Yang et al. 2007; Yonekawa et al. 1980, 1981) *M. m. castaneus* (CAS), *M. m. domesticus* (DOM), and *M. m. musculus* (MUS), that diverged in ancient 200–500kya (Boursot et al. 1996; Bonhomme and Searle 2012; Fujiwara et al. 2022; Geraldès et al. 2008, 2011; Phifer-Rixey et al. 2020; Salcedo et al. 2007; Suzuki et al. 2004). The origin of the house mouse is thought to be the northern part of the Indian subcontinent (Boursot et al. 1993; Din et al. 1996), but hybridization through secondary contact between subspecies has been observed during the process of dispersal throughout the world (e.g. Božíková et al. 2005; Din et al. 1996; Dod et al. 1993, 2005; Geraldès et al. 2008; Jing et al. 2014; Jones et al. 2010; Macholan et al. 2007; Prager et al. 1993; Sage et al. 1993; Teeter et al. 2008, 2010; Terashima et al. 2006; Yonekawa et al. 2012;). In East Asia, hybridization through secondary contact is thought to be ongoing in the Japanese archipelago and central China (Fujiwara et al. 2022a). An interesting phenomenon regarding the hybrids of house mice is the

presence of asymmetric hybrid incompatibility among subspecies. Previous studies with wild-derived strains of house mice revealed relatively strong hybrid incompatibility between CAS and DOM (White et al., 2012) and between DOM and MUS (Janousek et al. 2012; Vyskočilová et al. 2009; White et al. 2011), but not specifically between CAS and MUS.

Of the three major subspecies of house mice, CAS and MUS are widely recognized as inhabiting East Asia. In East Asia and its surrounding areas, MUS is distributed in northern China, Russian Far East, and Korea, while CAS is distributed in southern China and Taiwan. In the Japanese archipelago, another subspecies, *M. m. molossinus*, has long been recognized to inhabit. However, recent studies have revealed that *M. m. molossinus* is a hybrid of *M. m. musculus* and *M. m. castaneus* through genetic analysis (Takada et al. 2013, Sakai et al. 2005, Yonekawa et al. 1980, Yonekawa et al. 1988). Recent genome-wide studies have revealed that most wild Japanese house mice have a genetic background of MUS (Fujiwara et al. 2022a). In China, mitochondrial and microsatellite analyses identified subspecies of MUS and CAS in northern and southern China, respectively (Jing et al. 2014). The Yangtze River basin is the boundary between the two subspecies, and the area surrounding this region is considered to be a hybrid zone (Din et al. 1996, Jing et al. 2014). According to the previous study, MUS has been derived from an ancestral population from Middle Asia region that migrated to China via Kazakhstan through the Taklamakan Desert (Jing et al. 2014, Suzuki et al. 2015), while CAS has been derived from an ancestral population from Indo-Pakistan region which migrated to China via Southeast Asia (Jing et al. 2014, Li et al. 2021). However, in contrast, a study using a genome-wide dataset showed that even samples from southern China had a small genetic component of MUS, suggesting a wider hybrid zone than previously considered (Fujiwara et al. 2022a).

In the Japanese archipelago, the mitochondrial haplogroup shows a different trend from the genetic trends in mainland China; CAS mainly distributes in the northern part of the Japanese

archipelago (Hokkaido and Tohoku region), whilst MUS is observed in the southern part of the Japanese archipelago (Kanto, Chubu, Kansai, Chugoku, Shikoku, and Kyushu) (Kuwayama et al. 2017, Li et al. 2021). By analyzing full-length mitochondrial sequences of wild *M. musculus* samples collected from a wide range of regions in East Asia, previous studies have suggested that the CAS was first introduced to the Japanese archipelago from southern China and migrated northward towards Hokkaido, and then MUS is considered to have migrated from the Korean Peninsula to the Japanese archipelago at the same time that paddy rice cultivation was introduced to the Japanese archipelago (Kuwayama et al. 2017, Li et al. 2021).

In this study, we analyzed 138 whole-genome sequences of *M. musculus* including newly sequenced East Asian house mice from China, Japan, Korea, and surrounding regions. By contrasting autosomal loci with the population differentiation patterns of mitochondria and Y chromosomes, we inferred the evolutionary history of two East Asian subspecies populations. The results of each analysis showed incongruent trends and results, revealing the complexity of the study of wild house mice. This study focuses on the evolutionary history of *M. musculus* in East Asia and provides new insights into how secondary contact mediated by human activity has shaped the genetic traits of the commensal animal.

Results

Autosomal genetic variation in East Asia

In this study, we have determined an additional 37 *M. musculus* whole genome sequences mainly collected from East Asia. The updated version of the principal component analysis using autosomal SNVs is shown in Figure 3-1. Overall trends are similar to our previous analysis, however, resolution in China, Japan, and South Korea is increased. Based on the PC1 score (difference between MUS and CAS genetic elements), a CAS-MUS ratio plot for autosomal genetic diversity for the Japanese archipelago samples showed the following trends as shown in Figure 3-2. In Figure 3-2, the CAS-like signal is stronger in the Sea of Japan side samples than Pacific Ocean side samples.

Mitochondrial genetic variation in East Asia

We obtained whole mitochondrial sequences of 37 additional *M. musculus* samples and created a maximum likelihood phylogenetic tree using all 170 samples with previous global samples for comparison (Figure 3-3). The mitochondrial analysis also included mitochondrial reference sequences for *M. spretus* (NC_205952) and *M. musculus* (NC_005089). In Figure 3-3, each clade represents a mitochondrial haplogroup, and Figure 3-4 illustrates the mitochondrial haplogroup for each sample on the world map. In China, it can be seen that the MUS-type and CAS-type haplogroups are separated by the Yangtze River. In Japan, MUS-type haplogroups are generally observed, but CAS-type haplogroups are also found in Hokkaido and Tohoku. This result is consistent with previous studies and was confirmed in this analysis. CAS-type haplogroups have also been found in the Russian Far East, and in addition, DOM-type haplogroups have been found in some port towns.

Y chromosome genetic variation in East Asia

In our previous analysis (Fujiwara et al. 2022a, 2022b), we did not mention about Y chromosome, because we had not sequenced the whole genome of a sufficient number of males. At this time, however, the male sample has been increased to a total of 79 samples and, including 24 publicly available data, 103 male samples are available for analysis. We filtered this Y chromosome data according to the Materials and Methods section, and then constructed a maximum likelihood phylogenetic tree (Figure 3-5). In Figure 3-5, the tree topology among the subspecies is similar to the mitochondrial results, showing that CAS and DOM are sister clades and MUS is the outer clade. As shown in Figure 3-4 for mitochondria, we plotted the haplotypes of the Y chromosome on a world map based on the clades of the phylogenetic tree (Figure 3-6). In East Asia, the diversity observed in mitochondria is not observed in the Y chromosome, which is almost entirely MUS-type. We further used BEAST to estimate the divergence age. Since the mutation rate of the Y chromosome was not known, we used two methods. The first method is to calculate the divergence timing of *M. musculus* and *M. spretus* as a calibration point at 1 million years, and the second method is to use the mutation rate (5.7×10^{-9} mutations per bp) of germline cells (Milholland et al. 2017) for the prior parameter (Figure 3-7). For Figure 3-7, clade I corresponds to Europe and Russia, clade II to Central Asia, clade III to southern China, clade IV to northern China, and clade V to northern China, Korea, and Japan, respectively. In Clade V, which includes samples from the Japanese archipelago, only three samples from Saga, Misasa, and Fukuoka are separated from the other Japanese samples, and samples from Chuncheon, Hwacheon, Baengnyeong Is., and Gyeongju in South Korea are located between these separated Japanese samples.

Discussion

House mice are thought to be commensal animals and closely related to human activity. In this study, we attempted to analyze East Asian house mice from multiple perspectives: autosomes, mitochondria, and Y chromosomes. Previous mitochondrial studies have suggested the existence of mice with both CAS-type and MUS-type mitochondria in China (Jing et al. 2014), with the MUS-type migrating northward from Central Asia via a northern route, and the CAS-type migrating northward from Southeast Asia. The CAS-type was thought to have migrated northward from Southeast Asia. They inhabit the area bordered by the Yangtze River, and the border area has been considered to be a hybrid zone. On the other hand, mice with MUS-type and CAS-type mitochondria have been observed in the Japanese archipelago. Previous studies have suggested that the habitats of the two species are reversed in the Japanese archipelago (Kuwayama et al. 2017, Li et al. 2021, Terashima et al. 2006), with the South Asian subspecies (CAS-type) inhabiting Hokkaido and Tohoku, and the North Eurasian subspecies (MUS-type) inhabiting Honshu, Shikoku, and Kyushu. This reversal of subspecies distribution in the Japanese Islands is thought to be due to the difference in the timing of the introduction of the CAS-type and MUS-type into the Japanese Islands. The CAS-type was introduced to the Japanese Islands from China about 3,500 years ago, and it is thought that the CAS-type migrated northward and extended its habitat to Hokkaido and Tohoku. The MUS-type was introduced from the Korean Peninsula about 2,700 years ago, along with paddy rice cultivation, and spread throughout the Japanese archipelago, but did not spread to Hokkaido and the Tohoku region. Interestingly, the CAS-type is also found in the Russian Far East. These CAS-type samples are very old (about 8800 years ago) based on the divergence estimation of previous studies (Li et al. 2021).

In our study, we evaluated autosomal CAS and MUS types in the Japanese archipelago. In contrast to previous mitochondrial results, our results showed a CAS-type signal on the Sea

of Japan side and a MUS-type signal on the Pacific side (Figure 3-2). One possible reason for the discrepancy between mitochondrial haplogroups and autosomal subspecies in the Japanese archipelago is the influence of human maritime trade. Considering the results of the mitochondrial analysis, the first CAS-type house mice introduced into Hokkaido and Tohoku were boarded during maritime trade on the Sea of Japan side, and subsequently mixed with house mice from other cities on the Sea of Japan side. It is possible that this led to an increase in the ratio of CAS genetic elements in the autosomal genome of individual mice on the Sea of Japan coast. The mitochondrial results support the CAS-type of the first Japanese wild house mouse because there are individuals with an old lineage of CAS-type mitochondrial haplogroups in the Russian Far East. Considering those individuals in the Far East region, the CAS type once existed in this Far East region for about 8,800 years ago and the Japanese Islands for about 3,500 years ago, and then the MUS type migrated to the Japanese Islands and spread throughout the archipelago (Li et al. 2021). However, it is thought that the CAS type in Hokkaido and Tohoku spread to other cities on the Sea of Japan side due to subsequent maritime trade.

The Y chromosome showed results that are very difficult to interpret. Based on the Y chromosome data used in this study, the relationship among the three subspecies in the maximum likelihood phylogenetic tree shows almost the same topology as the results of the mitochondrial maximum likelihood phylogenetic tree (Figure 3-5). The three subspecies appear to have three branches, but subtly DOM and CAS have a sister clade, with the MUS type located on the outer side. Interestingly, however, all individuals that were CAS-type in the phylogenetic analysis of East Asian mitochondria are dominated by the MUS-type (Figure 3-6). Considering the hypothesis that the Chinese CAS type migrated northward via Southeast Asia and the CAS type migrated to the Japanese archipelago and migrated as far north as Hokkaido, the complete dominance of the MUS type in this East Asian region is very strange.

There are two possible explanations for the dominance of the MUS-type Y chromosome in East Asia. The first possibility is that MUS males have a large migratory range. Since it is difficult for house mice to cross rivers and oceans by themselves, many MUS-type males may board ships and move to other locations. This may have led to the spread of the Y chromosome from northern China to southern China, and also to the spread of the Y chromosome throughout the Japanese archipelago. The second possibility is that some kind of natural selection is at work in the reproduction of MUS-type males. It is undeniable that natural selection is at work in our East Asian data set, in that all of them show MUS-type Y chromosomes. For example, it may be possible that natural selection occurs through molecular mechanisms in reproductive behavior (e.g., MUS-type sperm outcompete sperm of other subspecies types). Since there are now many experimental strains of wild-derived house mice, we expect that the results will become clearer in the future through verification using these experimental strains. The results of the Y chromosome divergence time estimation using BEAST indicate that the common ancestor of the Japanese sample is approximately 4,200 to 8,500 years before, which is considerably older than both the mitochondrial divergence time estimates of approximately 3,500 years ago for the CAS type and approximately 2,700 years ago for the MUS type. However, it cannot be denied that this Y-chromosome age estimate may be completely different from the historical fact because the mutation rate is unknown.

Material and Methods

Genomic samples

In this study, we have determined whole genome sequence of new 37 *Mus musculus* samples collected mostly in East Asia. The detail list of newly determined samples is shown in Table 3-1. This new dataset includes samples from China, Indonesia, Japan, Myanmar, Philippines, Russia, South Korea. For comparison, we also combined global sample dataset what we have used in previous study (Fujiwara et al. 2022a, 2022b, and Harr et al. 2016). We obtained whole genome data of *Mus spretus* from Harr et al. 2016 for outgroup samples of *Mus musculus*. In this study, we analyze 170 *M. musculus* and *M. spretus* samples in total (163 samples out of 170 are *M. musculus*). For mitochondrial analysis, we downloaded NC_205952 and NC_005089 as reference mitochondrial sequence of *M. spretus* and *M. musculus*, respectively.

Mapping and genotype calling

The whole genome sequence of 37 additional East Asian sample has been sequenced by the DNBSEQ platform with a paired-end 150 bp length. The detail methodology about quality check, mapping reads, and genotype calling is same as our previous study (Fujiwara et al. 2022a, 2022b). The sexes of additional 37 samples are also determined by counting mapped reads to sex chromosomes as same strategy that we performed in previous study (Fujiwara et al. 2022a, 2022b). The determined sexes of our samples are also shown in Table 3-1.

Autosome re-sequencing analysis

As we demonstrated in previous study (Fujiwara et al. 2022a, 2022b), we performed principal component analysis of 163 *M. musculus* samples including 37 newly determined samples. For reasons indicated in our previous study, linkage disequilibrium (LD) was not filtered in our dataset in this study. Principal component analysis was demonstrated using

smartpca from Eigensoft software with default parameters except that outliers were not excluded.

Mitochondrial genome assembly analysis

The complete mitochondrial sequence of all additional 37 samples were *de novo* assembled by GetOrganelle software (Jin et al. 2020) with maximum extension rounds to 10 and kmer settings to 21,45,65,85,105,127. All assembled complete mitochondrial genomes were checked by Bandage software (Wick et al. 2015) to verify whether properly circularized or not. The phylogenetic tree based on maximum likelihood method is constructed by IQ-TREE software (Nguyen et al. 2015) with 1000 replicates bootstrapping. All D-Loop regions and gapped sites were removed. Before constructing phylogenetic tree, we performed ModelFinder software (Kalyaanamoorthy et al. 2017) implemented in IQ-TREE to determine which substitution model fits the real data. According to ModelFinder, “TIM2+F+R3” was chosen as best-fit substitution model by Bayesian Information Criterion.

Y chromosome re-sequencing analysis

In this study, we also re-sequenced Y chromosome using raw read data obtained by whole genome sequencing. The list of male samples that used for re-sequence is shown in Table 3-2. We downloaded NC_000087.7 (GRCm38) for reference sequence of Y chromosome. Raw reads were mapped to the reference Y chromosome sequence using bwa-mem with “-M” option (Li and Durbin, 2009). The samblaster software with “-M” option was piped to determine PCR duplicated reads (Faust and Hall, 2014). The SNVs and Indels were called by GATK4 (McKenna et al., 2010) HaplotypeCaller with “-ERC GVCF” option to obtain genomic variant calling files (gVCF). All sample gVCF were then genotyped by GATK4 GenotypeGVCF with “-all-sites” option. To calculate mappability scores of Y chromosome, we performed GenMap software with “-K 30” and “-E 2” options. For downstream analysis, we filtered out the positions which does not have mappability score with 1. Since the Y chromosome of the house

mouse has a short arm (Yp) and a long arm (Yq) (McLaren et al. 1988), and the chromosome on the long arm is a repeat of the gene encoded on the short arm, we analyzed only the short arm of this Y chromosome (the first 3.4 Mb length). We also excluded SNP positions that were determined to be "LowQual" by the GATK4 HaplotypeCaller and those with read depths of 3 or less. To facilitate downstream analysis, the obtained VCF files of the Y chromosome were converted to Fasta and Nexus files. The maximum likelihood phylogenetic tree of Y chromosome is constructed by IQ-TREE software (Nguyen et al. 2015) with 1000 replicates of bootstrapping. As we performed on mitochondrial analysis, the ModelFinder (Kalyaanamoorthy et al. 2017) implemented in IQ-TREE was computed to determine best-fit substitution model for our Y chromosome dataset. According to ModelFinder, "GTR+F+I+G4" was chosen as best-fit substitution model by Akaike Information Criterion. For estimating divergence dates of Y chromosome, we performed BEAST2 software (Bouckaert et al. 2019) with "GTR+F+G4" substitution and strict clock models. Markov chain Monte Carlo simulations were run for 10 million steps, including 10% burn-in steps, and samples were recorded for every 10,000 steps. We confirmed with Tracer software (Rambaut et al. 2018) that the BEAST2 simulation chain results were convergent, and the effective sample size (ESS) values were above 200 for all parameters. All simulated trees were summarized by TreeAnnotator software implemented in BEAST2 with "Maximum clade credibility tree" and "Mean heights" options.

Figures and Legends

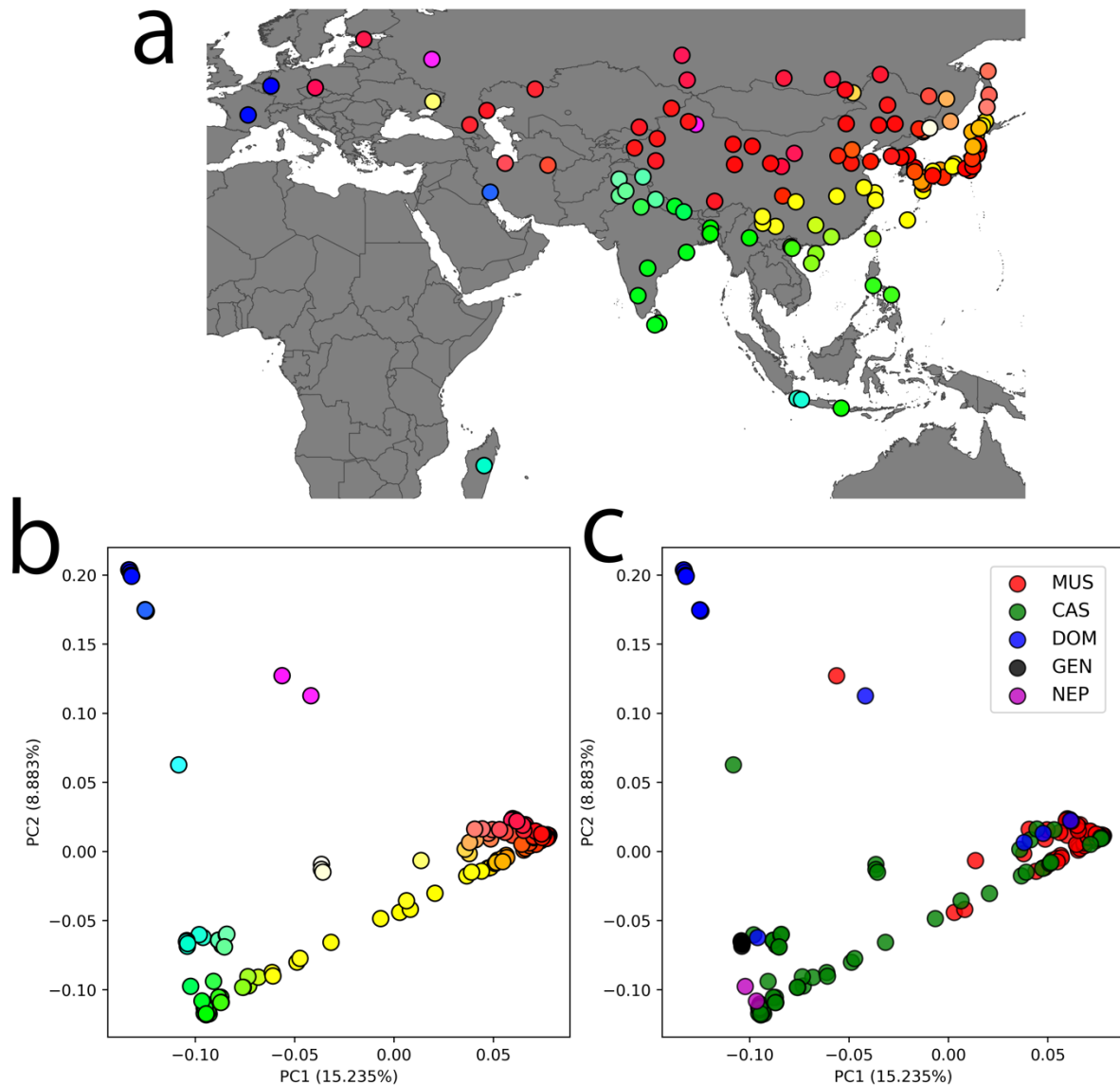


Figure 3-1 Updated PCA results for wild house mice with additional new samples from East Asia.

(a) Geographical map of sampling locations. Circles represent each individual, and the assigned color is the same as that in panel (b). (b) PCA plot of wild house mice produced using autosomal SNVs. The x and y axes represent PC1 and PC2, respectively. Circles are colored according to “Maxwell’s color triangle,” assigning three vertices to the RGB colors. Red, green, and blue color intensities correspond to the MUS, CAS, and DOM genetic components, respectively. The proportion of variance for each PC is shown in parentheses on the axis label.

(c) PCA plot of wild house mice produced using autosomal SNVs labeled with the mitochondrial genome haplogroup of each sample. NEP represents the mitochondrial haplogroup of Nepalese origin. The proportion of variance for each PC is shown in parentheses on the axis label.

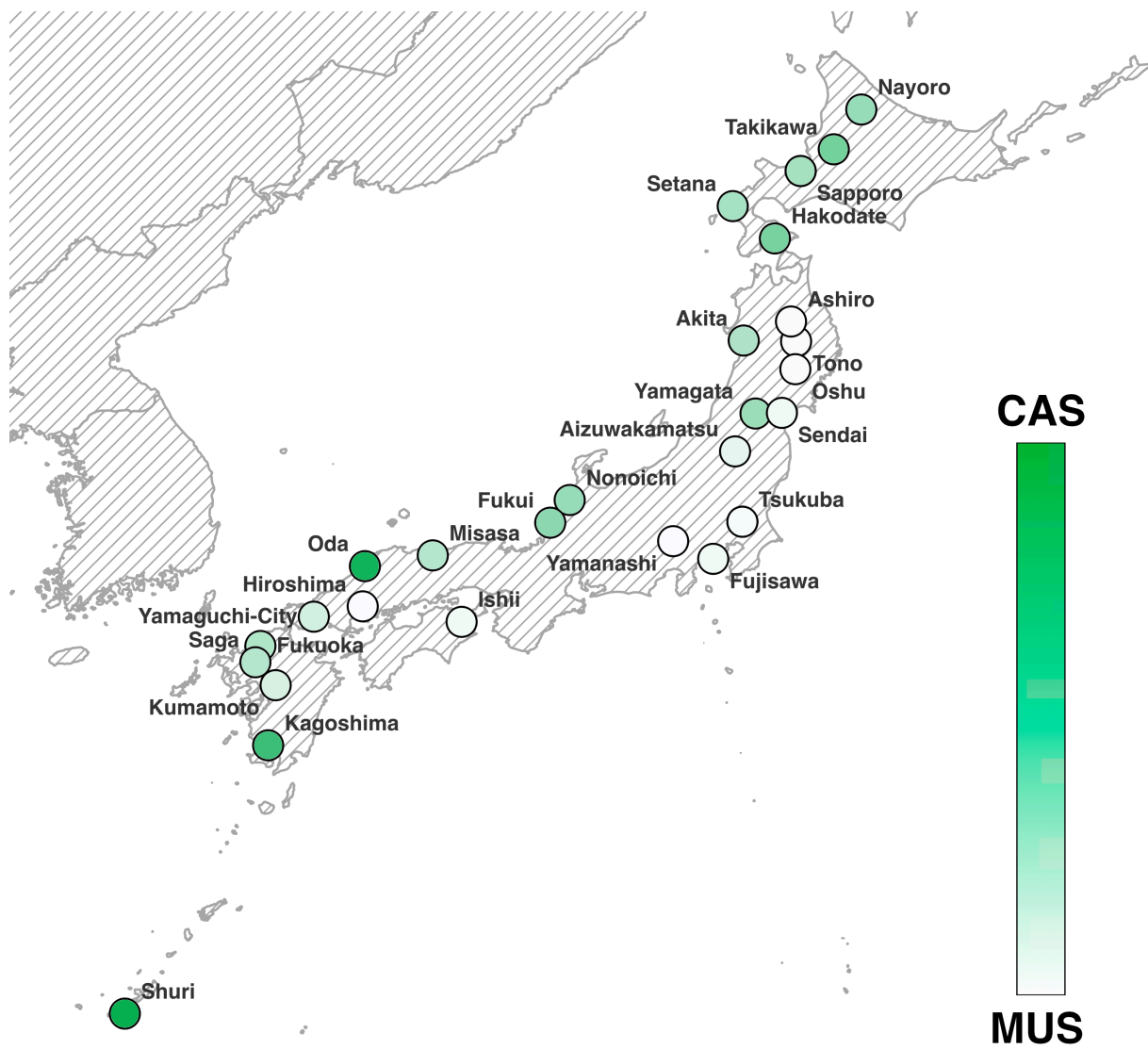
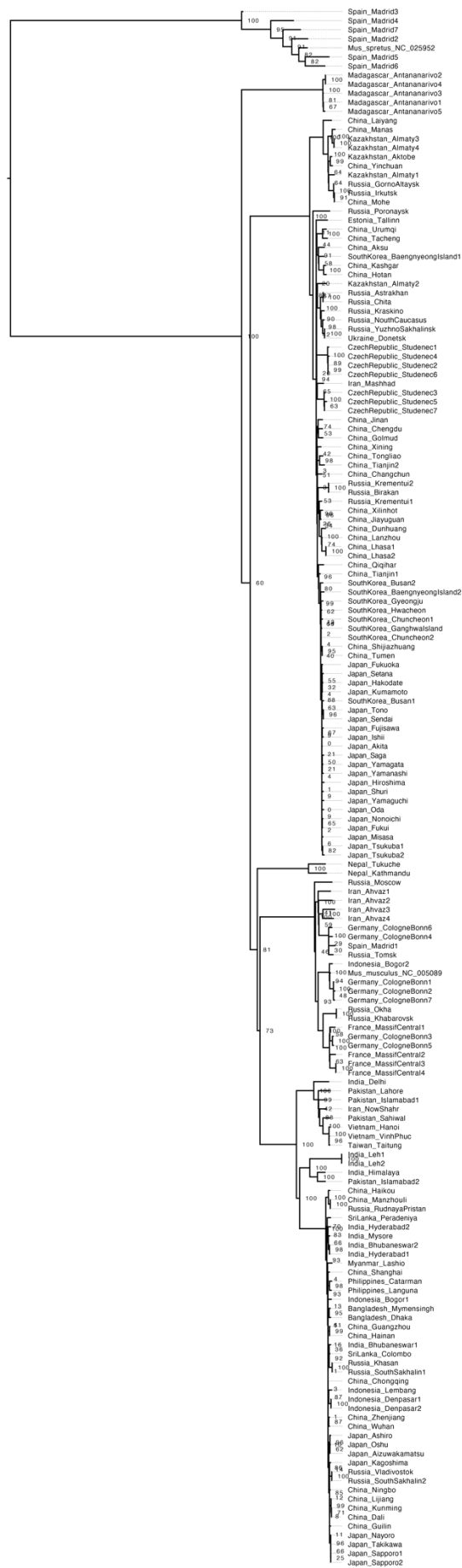


Figure 3-2 CAS type ratio in the Japanese Islands.

Each circle indicates the location where the house mouse sample was collected. The color in the circle represents the ratio of CAS-type genomic elements in that genome.



SPR
GEN

MUS

NEP

DOM

CAS

0.02

Figure 3-3 The updated maximum likelihood tree using mitochondrial genomes with additional new samples from East Asia.

The substitution model (TIM2+F+R3) was determined by the best fit model of ModelFinder implemented in IQ-TREE. The colored line and captions correspond to the mitochondrial genome clades of *Mus musculus*. The numbers exhibit the results of the bootstrap resampling with 1000 replications.

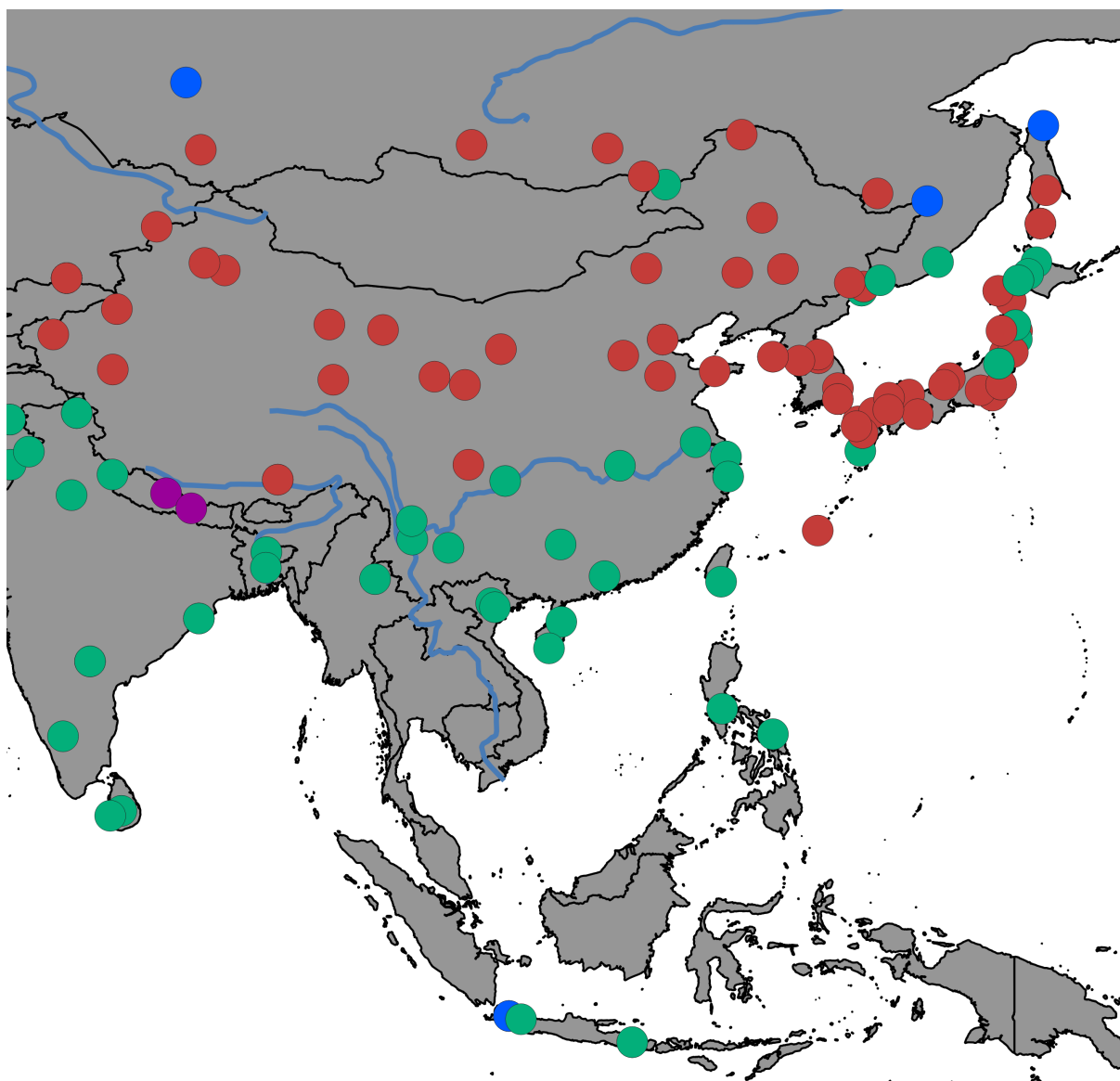
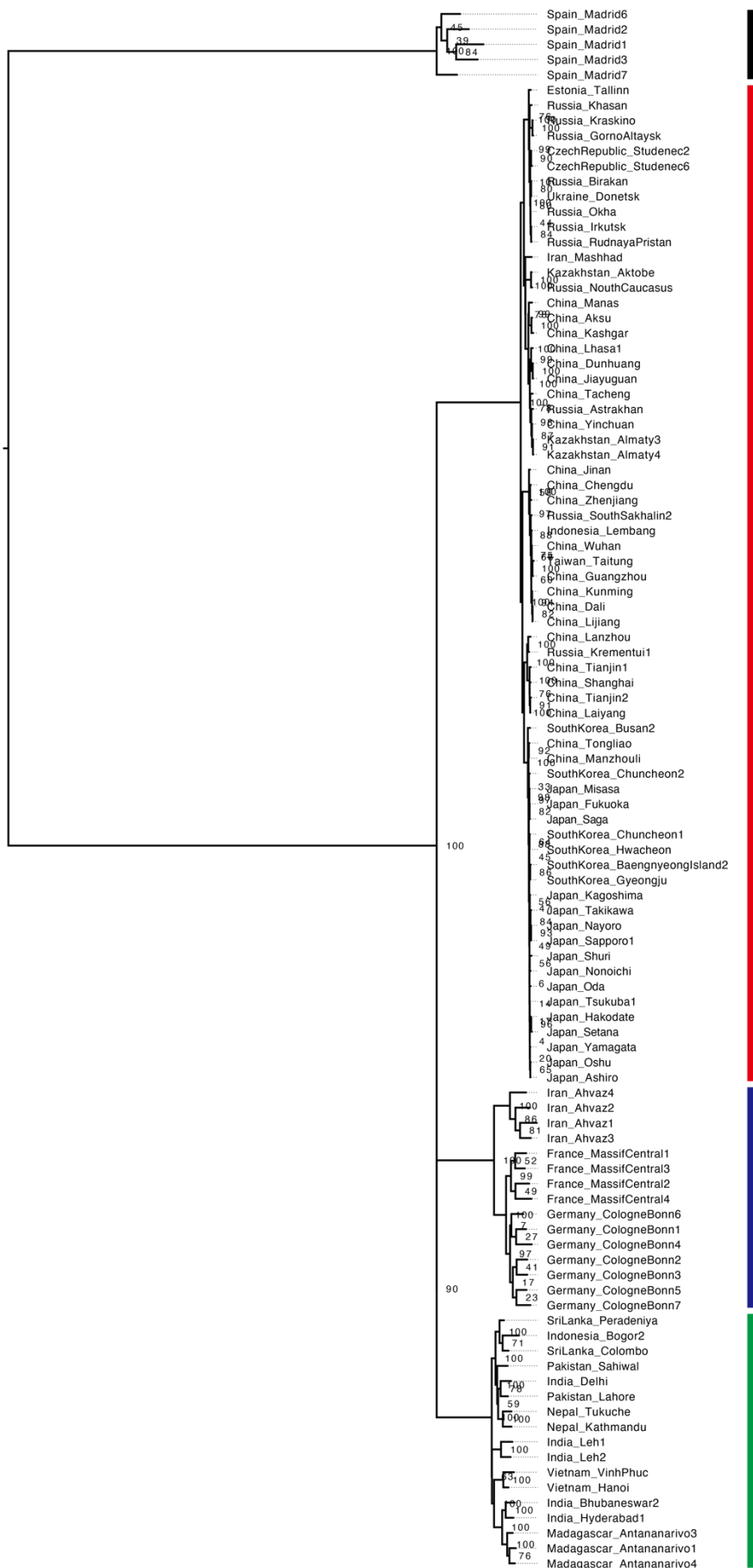


Figure 3-4 Geographical map of mitochondrial haplogroups in East Asia.

Each circle indicates the location where the house mouse sample was collected. The color of circles indicates the mitochondrial haplogroup: MUS (red), CAS (green), DOM (blue), and NEP (purple).



SPR

MUS

DOM

CAS

0.003

Figure 3-5 The maximum likelihood tree using Y chromosome genomes.

The substitution model (GTR+F+I+G4) was determined by the best fit model of ModelFinder implemented in IQ-TREE. The colored line and captions correspond to the Y chromosome genome clades of *Mus musculus*. The numbers exhibit the results of the bootstrap resampling with 1000 replications.

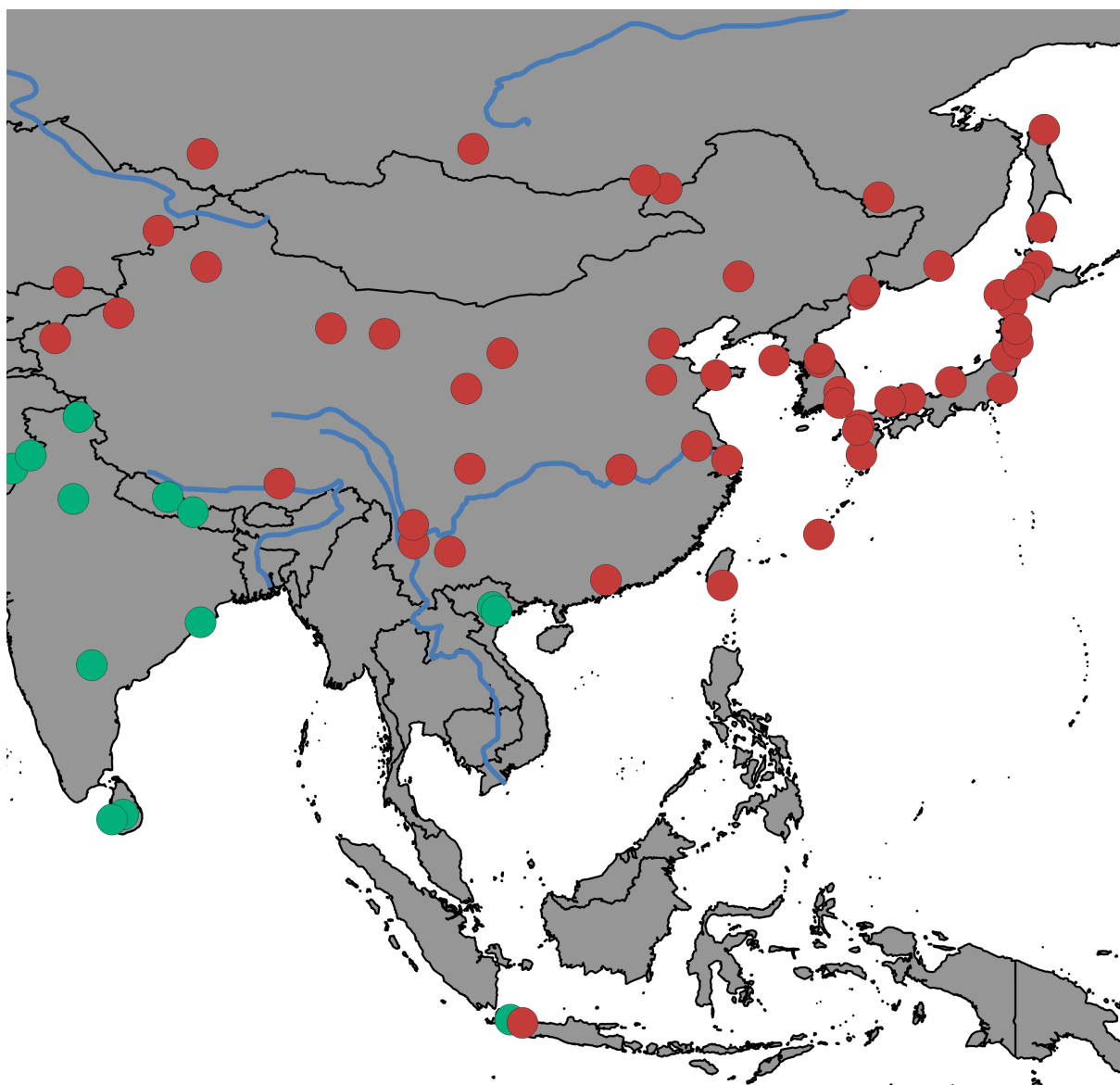


Figure 3-6 Geographical map of Y chromosome subspecies in East Asia.

Each circle indicates the location where the house mouse sample was collected. The color of circles indicates the Y chromosome subspecies: MUS (red), CAS (green), DOM (blue).

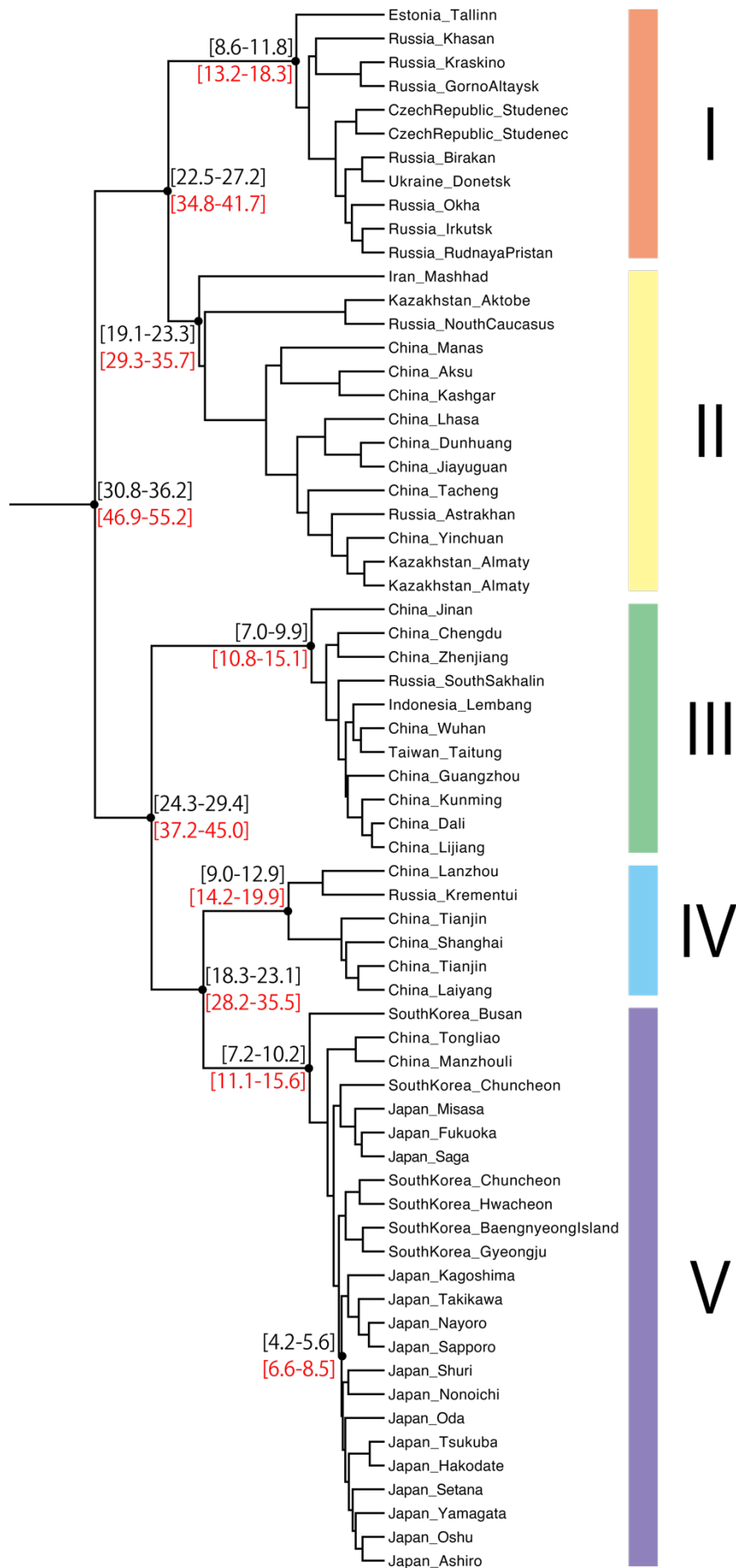


Figure 3-7 Y chromosome phylogenetic tree of *M. m. musculus* and estimated divergence dates.

The node with black dot corresponds to the time to most recent common ancestors (kilo years ago: kya) of the clade (brackets indicate the 95% highest posterior density: black color (calibrated *M. spretus* and *M. musculus* divergence as 1 million years) and red color (5.7 x 10⁻⁹ mutations per bp as prior)).

Tables

Table 3-1 List of additional *Mus musculus* samples mainly collected in East Asia.

List of additional <i>Mus musculus</i> samples mainly collected in East Asia.							
SampleID	Place	mtDNA Haplogroups	Sex	*Latitude	*Longitude	Median Coverage	Mean Coverage
HI0111	Indonesia:Bogor, Java	CAS	female	-6.6	106.8	31.0X	29.0X
HI0196	Philippines:Catarmen	CAS	female	12.45	124.65	31.0X	28.7X
HI0410	Korea:Chuncheon	MUS	male	37.866667	127.733333	25.0X	23.4X
HI0447	Philippines:Languna, Putho town, L.B.	CAS	female	14.17	121.22	26.0X	24.4X
HI0468	Korea:Udu-dong, Chuncheon	MUS	male	37.866667	127.733333	25.0X	23.7X
HS1413	Russia:Kraskino	MUS	male	42.711194	130.787056	28.0X	25.7X
HS3540	Korea:Busan	MUS	female	35.1	129.033333	33.0X	30.8X
HS3603	Japan:Kagoshima	CAS	male	31.596806	130.557139	32.0X	29.7X
HS3721	Myanmar:Lashio	CAS	female	22.933333	97.75	33.0X	30.6X
HS5817	Japan:Fukui	MUS	female	36.064056	136.219583	33.0X	30.6X
HS5821	Japan:Kumamoto	MUS	female	32.803	130.707861	30.0X	27.8X
HS5822	Japan:Yamanashi	MUS	female	35.693444	138.686889	29.0X	26.6X
HS6021	Japan:Saga	MUS	male	33.2635	130.300833	23.0X	21.4X
HS6022	Japan:Oshu	CAS	male	39.144472	141.139139	26.0X	24.0X
HS6023	Japan:Sendai	MUS	female	38.268222	140.869417	25.0X	23.3X
HS6025	Japan:Hiroshima	MUS	female	34.38525	132.455306	27.0X	24.7X
HS6026	Japan:Tsukuba	MUS	female	36.083472	140.076444	24.0X	22.1X
MG0294	China:Changchun	MUS	female	43.897	125.326	31.0X	29.0X
MG0295	China:Chengdu	MUS	male	30.66	104.063333	31.0X	29.1X
MG0439	China:Shanghai	CAS	male	31.228611	121.474722	32.0X	29.9X
MG0488	Japan:Aizuwakamatsu	CAS	female	37.49483	139.92975	32.0X	30.1X
MG0490	Japan:Akita	MUS	female	39.719889	140.102583	25.0X	23.4X
MG0682	Korea:BaengnyeongIsland	MUS	female	37.966667	124.65	30.0X	28.7X
MG0690	China:Yinchuan	MUS	male	38.472	106.2589	26.0X	24.4X
MG0710	China:Haikou, Hainan	CAS	female	20.042778	110.341667	27.0X	25.3X
MG0711	China:Sanya, Hainan	CAS	female	18.2529	109.5117	27.0X	24.8X
MG0783	China:Jinan	MUS	male	36.6702	117.0207	26.0X	24.6X
MG0810	China:Tongliao	MUS	male	43.654	122.243	32.0X	30.0X
MG0826	China:Tianjin	MUS	male	39.123611	117.198056	26.0X	24.1X
MG0869	China:Golmud	MUS	female	36.4072	94.9283	26.0X	24.0X
MG2021	China:Tianjin	MUS	male	39.123611	117.198056	26.0X	23.9X
MG2024	China:Shijiazhuang	MUS	female	38.0377	114.5304	26.0X	24.0X
MG2026	China:Tumen	MUS	female	42.966667	129.85	27.0X	24.6X
MG2030	China:Xilinhot	MUS	female	43.9334	116.086	26.0X	24.4X
MG2031	China:Laiyang	MUS	male	36.975833	120.713611	27.0X	24.6X
MG3046	Russia:SouthSakhalin	CAS	female	46.966667	142.733333	30.0X	29.1X
MG3047	Russia:SouthSakhalin	CAS	male	46.966667	142.733333	30.0X	28.9X

*Latitude and longitude are not absolute points of sample collection, but rather approximate locations.

Table 3-2 List of samples used for Y chromosome analysis.

List of samples used for Y chromosome analysis.

SampleID	Place	mtDNA Haplogroups	*Latitude	*Longitude	Median Coverage	Mean Coverage
ERS739373	Germany:Cologne-Bonn	DOM	50.865833	7.142778	22.0X	20.6X
ERS739374	Germany:Cologne-Bonn	DOM	50.865833	7.142778	22.0X	21.1X
ERS739375	Germany:Cologne-Bonn	DOM	50.865833	7.142778	23.0X	22.1X
ERS739376	Germany:Cologne-Bonn	DOM	50.865833	7.142778	23.0X	21.5X
ERS739377	Germany:Cologne-Bonn	DOM	50.865833	7.142778	20.0X	18.5X
ERS739378	Germany:Cologne-Bonn	DOM	50.865833	7.142778	21.0X	19.5X
ERS739379	Germany:Cologne-Bonn	DOM	50.865833	7.142778	20.0X	19.2X
ERS739382	France:Massif Central	DOM	45.528333	2.814167	21.0X	19.7X
ERS739385	France:Massif Central	DOM	45.528333	2.814167	20.0X	18.6X
ERS739386	France:Massif Central	DOM	45.528333	2.814167	21.0X	20.1X
ERS739388	France:Massif Central	DOM	45.528333	2.814167	22.0X	20.3X
ERS739389	Iran:Ahvaz	DOM	31.320278	48.669167	23.0X	21.6X
ERS739393	Iran:Ahvaz	DOM	31.320278	48.669167	23.0X	21.8X
ERS739395	Iran:Ahvaz	DOM	31.320278	48.669167	23.0X	22.1X
ERS739396	Iran:Ahvaz	DOM	31.320278	48.669167	22.0X	20.3X
ERS957498	Czech Republic:Studenec	MUS	50.55	15.533333	25.0X	22.7X
ERS957502	Czech Republic:Studenec	MUS	50.55	15.533333	24.0X	22.0X
ERS957508	Kazakhstan:Almaty	MUS	43.2775	76.895833	25.0X	22.7X
ERS957510	Kazakhstan:Almaty	MUS	43.2775	76.895833	26.0X	23.7X
ERS957512	Spain:Madrid	DOM	40.41677	-3.70379	22.0X	20.9X
ERS957513	Spain:Madrid	SPR	40.41677	-3.70379	27.0X	24.4X
ERS957514	Spain:Madrid	SPR	40.41677	-3.70379	25.0X	23.1X
ERS957517	Spain:Madrid	SPR	40.41677	-3.70379	25.0X	22.7X
ERS957519	Spain:Madrid	SPR	40.41677	-3.70379	24.0X	22.2X
HI0112	Indonesia:Bogor, Java	DOM	-6.6	106.8	25.0X	23.7X
HI0134	Indonesia:Lembang, Java	CAS	-6.817	107.617	29.0X	27.4X
HI0159	India:Leh	CAS	34.16	77.58	31.0X	28.3X
HI0161	India:Leh	CAS	34.16	77.58	29.0X	27.1X
HI0185	India:Delhi	CAS	28.61	77.23	30.0X	27.5X
HI0261	Pakistan:Sahiwal	CAS	30.661111	73.108333	33.0X	30.3X
HI0264	Pakistan:Lahore	CAS	31.549722	74.343611	34.0X	31.8X
HI0321	India:Bhubaneswar	CAS	20.27	85.84	30.0X	27.1X
HI0328	India:Hyderabad	CAS	17.37	78.48	29.0X	26.8X
HI0410	South Korea:Chuncheon	MUS	37.866667	127.733333	25.0X	23.4X
HI0468	South Korea:Udu-dong, Chuncheon	MUS	37.866667	127.733333	25.0X	23.7X
HI0484	Sri Lanka:Peradeniya	CAS	7.266667	80.6	33.0X	30.2X
HI0488	Sri Lanka:Colombo	CAS	6.934444	79.842778	32.0X	28.9X
HI0505	Vietnam:Vinh Phuc	CAS	21.3	105.6	29.0X	26.8X
HI0520	Vietnam:Hanoi	CAS	21.028472	105.854167	32.0X	29.6X
HS0682	South Korea:Baengnyeong Island	MUS	37.966667	124.65	28.0X	25.9X
HS1368	South Korea:Gyeongju	MUS	35.8376859	129.0451866	28.0X	25.8X
HS1411	Russia:Khasan	CAS	42.428333	130.645556	30.0X	27.6X
HS1413	Russia:Kraskino	MUS	42.711194	130.787056	28.0X	25.7X
HS1464	Kazakhstan:Aktobe	MUS	50.283333	57.166667	31.0X	28.6X
HS1467	Nepal:Tukuche	NEP	28.74	83.62	32.0X	29.6X
HS1523	Nepal:Kathmandu	NEP	27.7172	85.324	32.0X	29.3X
HS2323	Japan:Hakodate	MUS	41.768667	140.728917	31.0X	28.7X
HS2326	Japan:Nayoro	CAS	44.355833	142.463333	30.0X	27.9X
HS2400	Taiwan:Taitung	CAS	22.758333	121.144444	31.0X	28.6X
HS2445	Japan:Takikawa	CAS	43.557833	141.910417	30.0X	28.0X
HS2788	Japan:Shuri	MUS	26.212444	127.680917	32.0X	29.5X
HS2815	Japan:Nonoichi	MUS	36.519417	136.609778	32.0X	29.1X
HS3534	Japan:Yamagata	MUS	38.255417	140.339611	29.0X	26.3X
HS3603	Japan:Kagoshima	CAS	31.596806	130.557139	32.0X	29.7X
HS3605	Russia:Gorno-Altaysk	MUS	51.95	85.966667	33.0X	29.9X
HS3607	Russia:Okha	DOM	53.583333	142.933333	33.0X	30.3X
HS3608	Russia:Irkutsk	MUS	52.283333	104.283333	32.0X	29.2X
HS3612	Russia:Astrakhan	MUS	46.35	48.05	31.0X	28.8X
HS4097	Japan:Misasa	MUS	35.408444	133.861778	29.0X	26.7X
HS4169	Japan:Tsukuba	MUS	36.083472	140.076444	30.0X	27.5X
HS4233	South Korea:Hwacheon	MUS	38.1075	127.714444	31.0X	28.5X
HS4271	Japan:Setana	MUS	42.417111	139.883028	26.0X	24.5X
HS4272	Japan:Fukuoka	MUS	33.590139	130.401722	30.0X	28.1X
HS4411	Japan:Oda	MUS	35.192083	132.499361	31.0X	28.4X
HS5555	Madagascar:Antananarivo	GEN	-18.933333	47.516667	26.0X	24.4X
HS5559	Madagascar:Antananarivo	GEN	-18.933333	47.516667	27.0X	25.1X
HS5560	Madagascar:Antananarivo	GEN	-18.933333	47.516667	27.0X	24.9X
HS6021	Japan:Saga	MUS	33.2635	130.300833	23.0X	21.4X
HS6022	Japan:Oshu	CAS	39.144472	141.139139	26.0X	24.0X
MG0230	Japan:Ashiro	CAS	40.101389	141.052028	31.0X	29.4X

MG0295	China:Chengdu	MUS	30.66	104.063333	31.0X	29.1X
MG0296	Japan:Sapporo	CAS	43.121917	141.245833	29.0X	27.0X
MG0417	Iran:Mashhad	MUS	36.3	59.6	30.0X	27.3X
MG0439	China:Shanghai	CAS	31.228611	121.474722	32.0X	29.9X
MG0444	South Korea:Busan	MUS	35.1	129.033333	30.0X	28.3X
MG0504	China:Guangzhou	CAS	23.132	113.266	30.0X	28.2X
MG0507	China:Lanzhou	MUS	36.0606	103.8268	29.0X	26.9X
MG0529	China:Kunming	CAS	25.0464	102.7094	32.0X	29.4X
MG0597	China:Manas	MUS	44.3	86.216667	32.0X	29.4X
MG0608	China:Aksu	MUS	41.185	80.2904	32.0X	29.3X
MG0611	China:Tacheng	MUS	46.7517	82.9869	28.0X	25.8X
MG0686	China:Kashgar	MUS	39.4681	75.9938	30.0X	27.4X
MG0690	China:Yinchuan	MUS	38.472	106.2589	26.0X	24.4X
MG0713	China:Zhenjiang	CAS	32.188	119.424	32.0X	29.1X
MG0716	China:Lhasa	MUS	29.6534	91.1719	29.0X	27.3X
MG0783	China:Jinan	MUS	36.6702	117.0207	26.0X	24.6X
MG0797	China:Dali	CAS	25.6065	100.2676	32.0X	29.5X
MG0810	China:Tongliao	MUS	43.654	122.243	32.0X	30.0X
MG0826	China:Tianjin	MUS	39.123611	117.198056	26.0X	24.1X
MG0863	China:Manzhouli	CAS	49.598	117.379	32.0X	29.2X
MG0871	China:Dunhuang	MUS	40.1421	94.6619	29.0X	26.8X
MG0908	China:Wuhan	CAS	30.5934	114.3046	29.0X	26.7X
MG0917	China:Lijiang	CAS	26.8552	100.2259	29.0X	26.7X
MG2021	China:Tianjin	MUS	39.123611	117.198056	26.0X	23.9X
MG2031	China:Laiyang	MUS	36.975833	120.713611	27.0X	24.6X
MG3007	Russia:Krementui	MUS	50.155148	115.906841	34.0X	32.0X
MG3010	Russia:Nouth Caucasus	MUS	43.7114	44.8061	28.0X	26.3X
MG3018	Russia:Rudnaya Pristan	CAS	44.358611	135.810278	31.0X	28.5X
MG3026	Russia:Birakan	MUS	49.000833	131.72	31.0X	29.2X
MG3044	Estonia:Tallinn	MUS	59.437222	24.745278	29.0X	27.2X
MG3047	Russia:South Sakhalin	CAS	46.966667	142.733333	30.0X	28.9X
MG3066	Ukraine:Donetsk	MUS	48.002778	37.805278	30.0X	27.6X
MG5086	China:Jiayuguan	MUS	39.7732	98.2882	29.0X	27.0X

*Latitude and longitude are not absolute points of sample collection, but rather approximate locations.

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Conclusion

In this study, I have determined the whole genome of wild house mice collected worldwide, mainly from Eurasia. House mice are commensal animal that is strictly related to human activity. Until now, mostly mitochondria and a limited number of genetic regions have been studied in wild house mice, to tell the history of the species. In my first analysis, I sequenced the whole genome sequence of about 100 wild house mice as a genetic resource and demonstrated the genetic relationship between the three major subspecies of mice, confirming that MUS and CAS are genetically close and that they diverged about 180,000 years ago. The second analysis provided insight into the dispersal and migration patterns of humans and mice, using Madagascar as an example. The subspecies of the Madagascar house mouse, which had not been previously identified, was shown to be genetically DOM-like CAS. The house mouse is thought to have been introduced to Madagascar about 3,000 years ago, suggesting a close relationship with the history of human introductions to the Madagascar island. The third analysis suggested that hybrids of MUS and CAS are very widely distributed and diverse in East Asia, especially in China and Japan, and showed a different trend in the Japanese archipelago from previous mitochondrial studies. The mitochondrial and Y chromosome results suggest that the Y chromosome of MUS is highly predominant in East Asia, whereas mitochondria are diverse in north and south China and north and south Japan.

For prospects, it will be possible to estimate the global spread of house mice by collecting samples from a more wide area or by analyzing multiple samples collected at one specific point. Since the spread of house mice is closely related to human agriculture, the future analysis may allow us to unravel human history from a different perspective than direct human studies. It is also possible that the worldwide distribution of house mice is influenced by natural

selection specific to each region. In future studies, we would like to clarify the effects of natural selection that exist only in certain regions of the world, such as the Japanese archipelago.