Exploring the genetic diversity of the Sephardic remnants in Northeast Portugal from autosomal data

Célia Carolina Martins Neto
Mestrado em Genética Forense
Departamento de Biologia
2013

Orientador
Luís Alvarez Fernandez, PhD, IPATIMUP

Dissertação de candidatura ao grau de mestre em Genética Forense submetida à Faculdade de Ciências da Universidade do Porto.

O presente trabalho foi desenvolvido no Instituto de Patologia e Imunologia Molecular da Universidade do Porto sob orientação do Doutor Luís Alvarez Fernandez.

Dissertation for applying to a Master's degree in Forensic Genetics, submitted to the Faculty of Sciences of the University of Porto.

The present work was developed at the Institute of Molecular Pathology and Immunology of the University of Porto under the scientific supervision of Luís Alvarez Fernandez, PhD.

AGRADECIMENTOS

O meu primeiro agradecimento, como não podia deixar de ser, é para o Luís. Por ter confiado em mim sem me conhecer, por ter apostado em mim, por se ter disposto a aturar-me, por ter sido incansável nas ideias, sugestões, melhoramentos, pela disponibilidade, pela transmissão de conhecimentos e, sobretudo, pelo companheirismo. ¡Gracias!

Agradeço imenso também ao Professor Amorim, por estar sempre disponível e por ter melhorado em muito o meu trabalho, com excelentes comentários e sugestões.

A Inês Nogueiro e o Rui Pereira foram, sem dúvida, duas das pessoas mais importantes neste trabalho, pelo apoio, pelo tempo, pela disponibilidade e pelo conhecimento que me transmitiram.

Quero agradecer também a todo o grupo de Genética Populacional, pela simpatia e apoio, em especial à Professora Maria João e à Cíntia porque, sempre que puderam, estiveram prontas a ajudar.

Por fim, mas em nada menos importante, ao Renato, principalmente pela amizade de sempre e pela companhia. Nem sempre melhorou o meu dia, mas esteve sempre lá, fosse um dia bom ou não.

Muito obrigado a todos os que, mencionados ou no anonimato, me ajudaram neste caminho de aprendizagem, para que pudesse chegar a este momento de realização, com a sensação de dever cumprido!

RESUMO

A palavra “Judeu” deriva de Judah, uma das doze Tribos de Israel, e pode estar associada a um seguidor do Judaísmo ou a um descendente de uma família judaica. Para se conhecer melhor este povo, há essencialmente dois fenómenos que devem ser percebidos: a Diáspora, e o Cripto-Judaísmo, sendo este definido como uma profissão secreta ao Judaísmo, enquanto que publicamente se professa outra religião.

Em Portugal, o achado arqueológico mais antigo que prova a presença de Judeus neste território data do século IV. Desde essa altura até ao século XIX, este povo viveu períodos de tolerância e períodos marcados por medidas de restrição e perseguições. Contudo, no distrito de Bragança, no Nordeste português, existe ainda uma pequena comunidade que tem vindo a preservar a sua cultura.

Populações judaicas têm vindo a ser estudadas à luz da genética desde o início do século XX, de forma a tentar resolver este complexo sistema de interações entre comunidades judaicas e as respectivas populações locais “acolhedoras”. Todavia, existe ainda uma grande falha no que toca à caracterização genética de populações judaicas na Península Ibérica, especialmente em relação a marcadores autossómicos.

Os nossos principais objectivos são combater esta limitação e aumentar o conhecimento existente sobre a origem, demografia e história destas populações, complementando os estudos de Nogueiro e colaboradores (2010) e Teixeira e colaboradores (2011), sobre marcadores de linhagem. Também pretendemos procurar diferenças entre esta população, outras populações judaicas, e os seus “vizinhos” não-judeus.

Os resultados obtidos com os marcadores de linhagem mostraram uma população capaz de manter um elevado nível de diversidade genética, com uma raíz no Médio Oriente. Estes resultados foram surpreendentes, uma vez que se esperaria o contrário de uma população isolada e pouco numerosa.

Com microssatélites autossómicos, a população de Bragança mostrou valores de diversidade muito próximos aos das suas populações vizinhas não-judaicas, a outras populações portuguesas e a outras comunidades judaicas espalhadas pelos países da Diáspora. Com marcadores de ancestralidade, esta população apresentou um comportamento mais similar à Europa do que a qualquer outro continente.

Uma vez que os marcadores de linhagem tinham mostrado uma subestruturação dentro desta população, nós tentamos obter o mesmo resultado para marcadores autossómicos. Contudo, encontramos apenas uma ausência da mesma, contrariamente ao esperado.

Comparando a nossa população de interesse com as suas populações vizinhas, concluímos não existirem diferenças genéticas. O próximo passo foi então perceber a relação entre esta comunidade e outras existentes em diferentes países da Diáspora. Todavia, o resultado voltou a ser uma ausência de diferenciação.

Fazendo o ponto da situação, sabíamos que a população judaica de Bragança apresentava um padrão normal de *outbreeding*, sem subestruturação e geneticamente muito próxima às populações não-judaicas vizinhas e a outras populações judaicas.

Queríamos então perceber a relação entre a nossa população de interesse e outras populações mundiais, especialmente a Europa e o Médio Oriente, analisando marcadores com uma reduzida taxa de mutação.

Embora a distinção entre Europa e Médio Oriente não fosse muito notável, a população judaica de Bragança apresentou um comportamento genético mais próximo à primeira que ao segundo.

Para terminar, é importante notar que, embora nenhuma das análises levadas a cabo por nós tenha sido capaz de detectar qualquer tipo de estruturação, é sabido que a população de Bragança não é assim tão homogénea, sendo isto comprovado com a análise a marcadores de linhagem. A solução passará então pelo aumento do número e capacidade de informação dos marcadores usados. Assim sendo, o uso de marcadores moleculares a um nível *genome-wide* pode ser de extrema importância na compreensão e avaliação das relações genéticas que envolvem comunidades judaicas.

Palavras-chave: Comunidade Judaica, autossomas, microssatélites, marcadores de ancestralidade, estruturação.

ABSTRACT

The word “Jew” derives from Judah, one of the twelve Tribes of Israel. It can define a follower of the Jewish faith, a descendent of a Jewish family or simply a person belonging to a certain ethnic group. There are essentially two phenomena that are important to understand in order to better know this people: the Diaspora, and the Crypto-Judaism, being the latter defined as the secret adherence to Judaism while publicly professing another faith.

In Portugal, the oldest archeological evidence found of Jewish presence dates back to the 4th century. From then to the 19th century, the Jewish communities in Portugal experienced tolerant periods, when the population proliferated, as well as others periods marked by restrictive measures and persecutions against Jews. However, in Bragança, Northeast Portugal, there is still a small community that preserves its culture.

Geneticists have been studying Jewish populations since the turn of the 20th century, in order to try to unravel what must be a complex system of interrelations among Jewish communities and non-Jewish hosts populations, but there is still a huge gap regarding the genetic characterization of Iberian Judaic populations, especially concerning autosomal markers.

Our aims are to offset this limitation and to increase the current knowledge about the origin and demographic history of these populations, complementing the studies conducted by Nogueiro and coworkers (2010) and Teixeira and coworkers (2011), based on mtDNA and ChrY lineage markers. We also pretend to seek for differences between this population, others Jewish population, and neighbor non-Jewish local populations.

The results obtained with lineage markers concur to show that the communities scattered over the Bragança district have succeeded in maintaining a high level of genetic diversity with a clear root in the Middle East. These findings are extremely surprising, as they show exactly the opposite of what is expected in isolated, small sized populations, namely a deep genetic diversity loss.

With autosomal microsatellites markers, we saw that regarding the major standard diversity indices, this community presented itself very similar to its non-Jewish Portuguese hosts (Bragança and Miranda), to other populations from Portugal, and to other Jewish communities from different Diaspora countries. With ancestry informative InDels, the behavior of this population is closer to Europe than to any other continent.

Once the lineage markers have shown a substructure within this community, we also wanted to prove that result with autosomal markers. However, an absence of sub-structuration was found, contrarily to what would be expected.

When we compared our population of interest with its long-term non-Jewish hosts, through several statistical analyses, we concluded that there are no differences between the Jewish community and its neighbors. The next step was to understand the relation between the Portuguese Jewish community and other Jewish populations from Diaspora countries. Nevertheless, an absence of differentiation between populations was also the result.

At this point, we already knew that our population of interest present itself as a normal outbreeding population, without within substructure, and very genetically close and similar to non-Jewish Portuguese and other Jewish populations.

Then, we wanted to understand its relation with other worldwide populations, especially with European and Middle Eastern ones, under the light of slow mutating markers.

Although the distinction between Europe and Middle East was not very clear, the Bragança Jewish population presented a genetic behavior much more similar to Europe than to Middle East.

Finally, it is important to note that, although none of our autosomal analyses was able to detect any kind of structure, we know that this population is not that homogenous, from previous results with lineage markers. The solution could be an increase of the number and informativeness of the markers. So, the use of genome-wide microsatellite markers would be of great importance in the understanding and evaluation of the genetic relationships involving Jewish communities.

Keywords: Jewish community, autosomes, microsatellites, ancestry informative marker, structure.

CONTENTS

FIGURES

TABLES

ABBREVIATIONS

µL	Microlitre
AIMs	Ancestry Informative Markers
AMOVA	Analysis of MOlecular VAriance
BCE	Before the Common Era
bp	Base pair
CE	Capillary Electrophoresis
CE	Common Era
Chr	Chromosome
CNVs	Copy Number Variants
DNA	DeoxyriboNucleic Acid
F_{ST}	Fixation Index
Gbp	Giga base pair
H_{exp}	Expected Heterozygosity
HGDP-CEPH	Human Genome Diversity Cell Line Panel
H_{obs}	Observed Heterozygosity
HWE	Hardy-Weinberg Equilibrium
i.e.	*id est*, that is
InDels	Insertion/Deletion Polymorphisms
Kbp	Kilo base pairs
Mbp	Mega base pair
ln	Natural logarithm
MCMC	Markov Chain Monte Carlo
MDS	MultiDimensional Scaling
mtDNA	Mitochondrial DNA
PCR	Polymerase Chain Reaction
SNPs	Single Nucleotide Polymorphisms
STRs	Short Tandem Repeats
T	Thymine
USA	United States of America
WMA	World Medical Association
α	*Alfa*, significance level for the p value

INTRODUCTION

1 The Jewish People

1.1 From Abraham to the 21st century

Jews were first known as Hebrews. Etymologically, this name derived from the term *ivri*, meaning Abraham in Hebrew. Abraham was the Jew's First Patriarch and the first to conceived the idea of a single, universal and immaterial God [1]. On the other hand, the etymon *Jew* derives from Judah, denomination of one of the two kingdoms split apart from the first unified Israelite Kingdom, emerged in the 11th century BCE [2-4].

According to the religious law, Jews are those whose mother was a Jew [5], with the exception of three male castes (Cohen, Levi and Israelite), in which "Jewishness" is determined by paternal descent [4]. However, today the word Jew ranges a variety of meanings, defining a follower of the Jewish faith, a descendant of a Jewish family, or simply a person belonging to a certain ethnic group – Jewish [4].

An essential phenomenon to understand the Jewish culture is the Diaspora. *Diaspora* is a Greek word that means dispersion, scattering. It is used to define the forced or encouraged dislocation of a big population mass, from one region to several distinct areas, and to identify any group that was exiled or resettled from their homeland [1, 4]. This Diaspora led to the dispersal of Jewish people from the Levant to many parts of the world (see Figure 1).

According to geographical dispersion, three main groups are recognized: Mizrahim, Ashkenazim, and Sephardim [4-6]. The Mizrahim group is composed by Middle Easterner or Oriental Jews living in contemporary Israel and Palestine, as well as in Iran, Iraq, Central Asia and the Arabian Peninsula. Ashkenazim Jews (from the Hebrew word for Germany) moved North of the Alps, probably from Italy. In the 12th and 13th centuries, Ashkenazim Jews were expelled from the Western European countries and were granted charters to settle in Poland and Lithuania [4, 5].

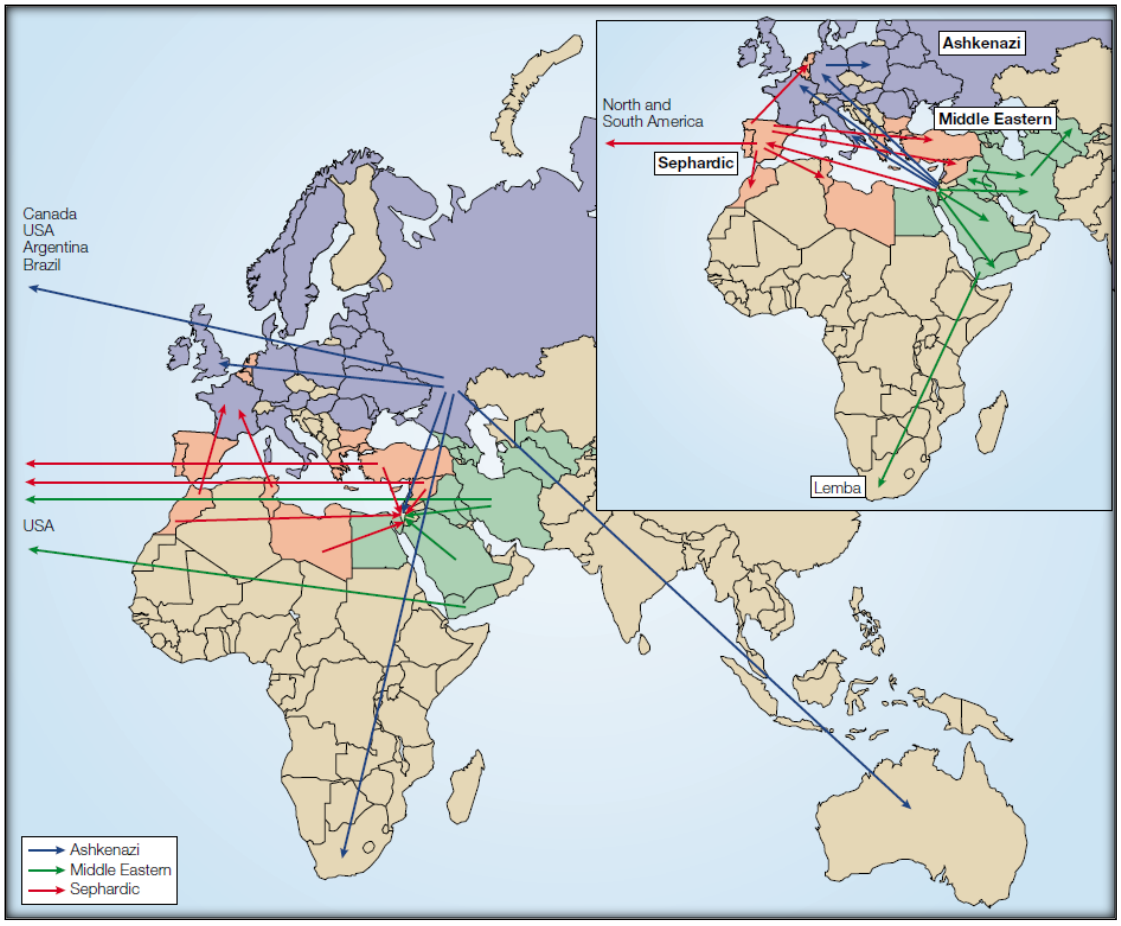

Figure 1. Destinies of the Jewish populations of the Diaspora. In blue, countries with Ashkenazi Jews populations. Countries with Sephardic Jews populations are in red, while countries with Middle Easterner Jews populations are in green. Arrows symbolize the movement of populations, according to the color of the population. The smaller figure shows the movements before the nineteenth century, while the main figure reports the Diaspora in the late nineteenth and early twentieth centuries. Adapted from Ostrer, 2001 [5].

Concerning the Sephardim group, it was only with Yohanan Ben Uziel, in the 1st century, while translating the Prophet's Book that *Sepharad* started to denominate the Iberian Peninsula, once until then *Sepharad* was used to denominate a far land. Therefore, the Jewish in the Peninsula were known as Sephardic Jews [1]. Nonetheless, most authors inaccurately refer to *Sepharad* only as Spain [4, 5, 7].

Sephardic Jews resided in Spain and Portugal, up to the Edict of Expulsion and the establishment of the Inquisition in these countries, in the late 15th century. As a consequence, they started a mass migration to North Africa (e.g., Morocco, Libya and Algeria), Italy, the Balkans, Turkey, Lebanon, Syria and the Americas [4, 5, 8-12].

Besides these three main groups, a fourth, Northern African Jews, can be considered, thanks to the wide range of the Roman Empire and the constant movements of this people. Nonetheless, there are also some other countries, such as Yemen, Ethiopia, India and China,

where Jewish communities can be found [8], and some with a big impact in Judaism, e.g., the Falasha Jews from Ethiopia and the Chinese Jews [4].

At the beginning of the 21st century, Jewry was comprised of about 13 million people, of whom 47% were of Ashkenazi, 30% of Sephardic and 23% of Oriental origin [4, 5]. This meant that one in about 510 people in the world was Jew [13] (see Figure 2).

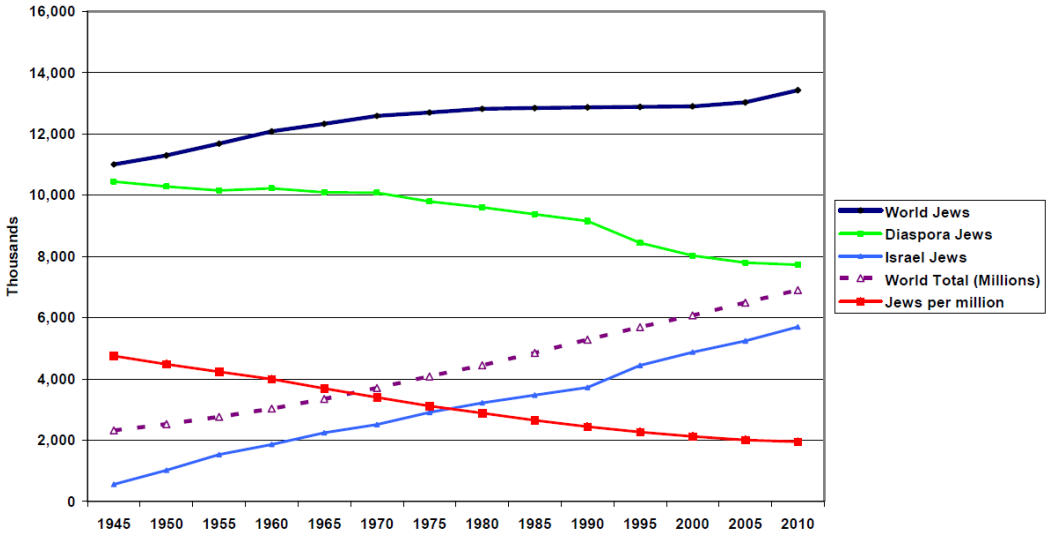

Figure 2. World total population and Jewish population worldwide distribution between 1945 and 2010. Adapted from DellaPergola, 2010 [13].

The increasing number of Jews in Israel and the decreasing number of Diaspora Jews prove the return of Jews to their ancestral homeland. This also brings forth the diminishing of the Diaspora range (eighty percent of the world Jewry lived in 2010 in only two countries: Israel and the USA) [13].

In Europe, the Jewish population was estimated in 1 455 900 in 2010, with a higher concentration in the Western part of the continent [13]. In Portugal, 3061 people assumed themselves as Jews, when answering the Census 2011, generating an average of 1 Jew per 3450 Portuguese inhabitants [14].

1.2 The Jews in the Iberian Peninsula

Archeological evidences prove the presence of Jews in the Iberian Peninsula since the 3rd century CE. In the specific case of Portugal, the earliest archeological evidence found was a tomb slab with a Latin inscription and a menorah – a seven armed chandelier, found in Mértola and dated from the 5th century (482 CE) [10, 15]. More recently, archeologists found a

tomb slab, in an excavation site in Silves, in South of Portugal, with the inscription *Yehel*, a Hebrew name (390 CE) [11].

Despite estimations made from the archeological record, the arrival of the Jewish communities to the Iberian Peninsula has not a specific date. However, their presence can also be tracked through cultural tradition records and other historic documents. Therefore, some authors believe the Israelites embarked on Phoenicians ships and arrived with them to Norhern Africa and Iberian Peninsula. Other historical events, such as the destruction of the First (586 BCE) and the Second Temples (70 CE), or the falling of the Kingdoms of Israel (622 BCE) and Judah (586 BCE), could also meant several migration waves out of Israel, to the Iberian Peninsula [1, 4, 6-8, 12].

At different times, Jews in the Iberian Peninsula suffered with persecution, expulsion and mandatory conversion. Although the first documented persecution against Jewish in the Iberian Peninsula occurred in 613, the burning of a synagogue in Mahon, Minorca Island, was the cause of the first mass conversion to Christianity in Hispania, in 5th century [1]. Because the alternative was their expulsion, the death penalty or the forced baptism, this persecution marks the beginning of Crypto-Judaism, i.e., the secret adherence to Judaism while publicly professing another religious faith. The Crypto-Jews attended to ceremonies in churches, but at home they continued practicing their Jewish rites, being at the same time Christians and Jews. A change was made in the family names, replacing the Hebrew for new Christian ones [12, 16-18].

After the Muslim establishment, between 720 and 1066, the Iberian Peninsula lived a period of tolerance called *convivencia*, during which Christians, Muslims and Jews lived together in peace, each one maintaining their religion. This led to a miscegenation process between indigenous people and the settlers [1, 7, 8].

With the Catholic kings, the life of Jews in Portugal had ups and downs, with some kings actually helping them to prosper, while others persecuted them [1, 12, 16, 19, 20].

Although Jews had been harassed since ever, the systematically persecution of Jews begun with the Catholic Kings of Spain in 1478 [12, 19]. On March 31st, 1492, the Spanish Edict of Expulsion was released, determining either the conversion or abandonment of all Jews and Moors within four months, under penalty of death and confiscation of property [16, 19, 20]. This caused a mass migration to Portugal, with numbers ranging between 600 families and 120 000 people, which represented about a tenth of the contemporary total Portuguese inhabitants [10, 12, 15, 21].

The Spanish pressure was felt in Portugal, and in December 1496, King Manuel I signed the Portuguese Edict of Expulsion. The order of expulsion in Iberian countries wasn´t new in

Europe. Before them, England expulsed Jews in 1290, and France in 1306, as well as several German cities [12, 16, 19, 20].

Nonetheless, in May of 1497, about 20 000 Jews, ready to exile, were baptized against their will [10, 16, 19, 20]. This episode marked not only the explosion of Crypto-Judaism but also the start of a new "group": *conversos* or *Cristãos-Novos*, i.e., New Christians, the ones who used to be Jews and were forcedly converted [12].

In 1506, a Jewish massacre killed thousands of *conversos* in Lisbon and the establishment of the Holy Office emerged as a solution to the imbalanced religious, socioeconomic and political structure of the country [12, 16, 19, 20, 22].

The Inquisition as it was, representing a court for faith defense, existed since the remote history of the Church but had its activity peak under the pontificate of Innocent III, in the 13th century. It combined ecclesiastical law, which imposed penalties such as excommunication or penitence, with civil law, which could impose the death penalty or confiscation of property. The bull establishing the Inquisition in Portugal was proclaimed in October 1536 under the reign of King João III. The judgments were made in public places with deaths by hanging or immolation and named *autos-de-fé*. The ones who escaped death penalty were convicted to a life sentence and usually sent to Angola, Brazil or other colonies. In 1624, there was, according to the calculations made by the Inquisition, 200 000 Jewish families, which is about a million people [10, 12, 15, 22].

The Inquisition and the distinction between Old and New-Christian ended in 1821, with the Pombaline discrimination law coming into effect, allowing a resurgence of Jewish communities all over the country [16, 20].

1.3 The Jews in Bragança

Bragança is a Portuguese district sited in the Northeastern extreme of the country, bordering with the Spanish provinces of Ourense, Zamora and Salamanca and it belongs to the Portuguese province of Trás-os-Montes e Alto Douro [23] (see Figure 3).

In 1065, when the Christian kingdom was divided, Bragança was part of County of Portucale that stretched from the Minho River to the Tejo River and was delimited by the Douro and Coa Rivers at East [1].

In 1187, King Sancho I granted the *Foral da Vila* to Bragança and ordered the reconstruction of the city walls. After several wars with the Spanish Kings, in 20th February of 1464, King Afonso V granted the *Foro de Cidade*, in sign of acknowledgement for the richness that the silk industry was bringing to the country [23-25]. At this point and according to

documentary evidences, there were already some Jewish communities established in Bragança, Chaves, Rio Livre, Mogadouro, Miranda do Douro, Vinhais, Alfândega da Fé, Vila Flor, Azinhoso, Bemposta, Mesão Frio, Moncorvo and Freixo de Espada à Cinta [19, 22].

Figure 3. Geographic representation of the Bragança district. Portugal is represented by the lighter grey area, with Bragança highlighted with a darker grey. This district is zoomed in (smaller square), showing the division within Bragança. The Spanish provinces that border with Bragança are highlighted by the darkest grey.

Thanks to its geographical location, when the Holly Office started to persecute the Spanish Jews, more than 33 000 entered in Portugal by the border in Bragança and Miranda do Douro. Some of these were made slaves but others established themselves as tanners, shoemakers and in the silk industry [10, 12, 15, 21, 24].

The Portuguese Holy Office reached Trás-os-Montes in 1582-1583, causing numerous accusations and arrests from the very beginning and reaching its peak in 1599. An example of these grim times is found in the village of Carção, where among 150 families, 130 people were arrested for Judaism [10, 12, 15, 22]. Until 1755, only in Bragança, 1601 citizens were prosecuted. The majority of these people was Jews with connections to the silk industry that run away to Paris, Bordeaux, Amsterdam and other European cities [24, 25].

The Israeli community of Bragança was founded in 1927 and in June 1928, the synagogue *Shaaré Pideon* was inaugurated, 431 years after the previous one. The fact that the first synagogue was built within the castle's walls suggests that this community was very important in the region [10, 12, 15, 21].

The period of tolerance to these communities was brief. Portugal was then under a dictatorship, which later demonstrated sympathy towards the Nazi Germany. So, in 1934, the community was dissolved and resumed to their previous clandestine traditions. A democratic regime was installed after 1974, and the opportunity for an open resurfacing occurred again. However, in contrast to the prominent case of Belmonte (Central Portugal), where the old Crypto-Jewish community assumed openly its faith and has built a synagogue and a cemetery, no such resurgence has been observed in Bragança - or indeed in the whole province of Trás-os-Montes [10, 15].

2 Population Genetics

According to the Oxford Dictionary, Population Genetics can be described as the study of the distribution of genes (alleles) in populations and the factors that change the frequency of genes and genotypes from generation to generation [26]. It comprises the study of the evolutionary forces that shape the differentiation between species and populations at a molecular level, learning their origin, phylogeny, genetic diversity and disease susceptibility, applied to Anthropology, Medicine or Forensic Science. In fact, Population and Forensic Genetics are inseparable, being the latter a scientific field focused on the genetic typing of biological samples for forensic purposes. When a DNA profile is obtained, it has to be compared with several databases for different populations. Those databases are only possible with Population Genetics studies [27].

It is then necessary to define what "population" means. In Forensic Genetics, a population can be described as a group of people sharing common ancestry [28]. Populations often have an ambiguous meaning, being irregularly defined on the basis of "race", geography, culture, religion, physical appearance or other criteria [29].

The genome of each individual is a temporary assemblage of DNA segments brought together for a single generation by a combination of chance, ancestry, recombination and natural selection. These segments have different histories because of recombination and can thus provide independent information about ancestry. The thousands of different genomic segments in any individual do not trace back to ancestors randomly spread around the globe; segment ancestry is constrained by population history [6, 30].

Population Genetics aims to understand the observed distribution of genetic variability and to infer histories of populations from genetic data. For this purpose, what really matter are the differences between sequences (variants). Differences can be summarized using statistics (such as allele frequencies or genetic distances) and used to quantify relationships among individuals or populations using clustering techniques [6].

Patterns of genetic diversity depend on one hand, on history, which includes demographic phenomena of migration, sub-structure and fluctuations in the population size, and on the other hand, of genetic factors such as mutation rates and selection [15]. So, the forces that affect gene frequencies in different populations include mutation, migration (gene flow), natural selection and random genetic drift [31].

The history of a population can led to its physical and/or cultural isolation. Usually, this kind of population is also genetically isolated, with allelic frequencies differing from other

populations [32]. Over time, isolated populations lose heterozygosity due to inbreeding because the gene selection pool is smaller and therefore, not as much shuffling of genes exists [31].

The understanding of this complex evolutionary process has in recent years, deserved particular interest, given its practical application in fields such as evolutionary genetics, medicine, etiology of human diseases, forensic studies, and genealogical reconstructions [15].

2.1 Molecular Markers

Population Genetics has been enhanced by the identification of millions of polymorphic markers that reside in close proximity to one another along the genome and that vary in their allele frequencies among populations. These discoveries have led to greater precision for estimates of genetic distances. The analyses have included deconvolution of ancestry for whole genomes or for segments of individual genomes and analyses of segmental sharing among individuals that provide greater accuracy for estimating their degree of relatedness [8].

Since it has been estimated that over 99.7% of the human genome is the same from individual to individual, regions that differ need to be found in the remaining 0.3% in order to tell people apart at the genetic level. This variation is caused by insertions or deletions, length polymorphisms and single nucleotide polymorphisms [28, 33].

The study of genetic variation, using DNA polymorphisms distributed throughout the genome, has allowed better understanding of the history and diversity of human populations as well as providing a system for the genetic identification of individuals [34]. DNA polymorphisms are usually defined as naturally occurring variants for which the most common allele as a frequency of no more than 99% [35].

The polymorphisms described until now can be separated into two groups, according to their mutation type and mechanism. Thus, one group includes multi-allelic markers, with moderate to high mutation rates (from 10^{-5} to 10^{-2}), and the other di-allelic markers, with low mutation rates (~$2.5x10^{-8}$). Another way to split these markers is, on one hand, the ones based on nucleotide substitutions (commonly called SNPs), and on the other hand the ones based on insertions and deletions of one or more nucleotides (InDels). InDels can in turn be divided into two groups: those with multiple alleles (multi-allelic) and those with only two alleles (di-allelic). Nearly all of multi-allelic InDels are based on tandem repeats and are known as microsatellites or STRs (Short Tandem Repeats). Di-allelic InDels are usually called simply InDels [33, 35, 36].

Initial studies of human genetic variation focused on Short Tandem Repeats (STRs) and Single Nucleotide Polymorphisms (SNPs). Only later, Copy Number Variants (CNVs) and

Insertion/Deletion Polymorphisms (InDels) were explored, unveiling previously unknown sources of genetic diversity that are likely to be important factors underlying inherited traits and diseases in humans [37].

Tandem Repeats Polymorphisms

There are many repeated DNA sequences scattered throughout the human genome. As these repeat sequences are typically located between genes, they can vary in size from person to person without impacting the genetic health of the individual [33].

Being the predominant type of polymorphisms used in human genetic studies since about 1990 [35], Microsatellites or Short Tandem Repeats (STRs) are polymorphic regions of DNA where alleles differ in size, ranging between 100 bp and 400 bp with a core unit of between 1 and 6 bp, and may be found surrounding the chromosomal centromere [28, 33, 38]. This variation between different alleles is caused by a difference in the number of repeat units that results in different lengths alleles and it is for this reason that tandem repeat polymorphisms are known as length polymorphisms [28, 38].

STRs are spread throughout the genome including the 22 autosomal chromosomes and the X and Y sex chromosomes and occur on average every 10 000 nucleotides, accounting for approximately 3% of the total human genome [28, 33].

Short tandem repeats are currently the most commonly analyzed genetic polymorphism in Forensic Genetics thanks to their easy amplification by polymerase chain reaction (PCR) without the problem of differential amplification [28, 33]. Besides, thanks to their very high mutation rates that produce very high levels of variation, these markers are universally used, allowing the establishment of well-structured national databases, simple methodologies and to evaluate relevant statistical parameters [15, 39]. Being co-dominant, neutrals and inherited in a Mendelian fashion are other advantages of microsatellites [40].

Microsatellites mutate at rates several orders of magnitude higher than that of bulk of DNA, with their own model, formulated by Levinson and Gutman, approximately 25 years ago [38, 40]. Replication slippage or slipped-strand mispairing refers to the out-of-register alignment of the two DNA strands following dissociation at the time when the DNA polymerase traverses the repetitive region. In unique eukaryotic sequences, the mutation rate is approximately 10^{-9} nucleotide per generation, while the mutation rate of microsatellites is in the order of $1x10^{-3}$ or $2x10^{-3}$. This range is explainable because the mutation rate differs between species, between loci and according to the allele size. In humans, the sex is also a variable affecting the mutation rate, once males mutate about five times as often as females because their number of mitotic germline cell divisions is higher [38].

STRs that are widely used in Forensic Genetics have either a four or five base-pair core-repeat motif (tetranucleotides and pentanucleotides, respectively) because longer repeats are less common in the human genome. Di- and trinucleotides show a higher stutter percentage (sometimes higher than the double); and it is easier to resolve closely spaced heterozygotes with size-based electrophoretic separations using tetranucleotides than using di- or trinucleotides [28, 33].

These markers can be classified as i) *simple repeats* – contain units of identical length and sequence; ii) *simple repeats with non-consensus repeats* – contain incomplete repeat units (e.g., microvariant: allele 9.3 at the TH01 locus – contains nine tetranucleotide repeats and one incomplete repeat because is missing a single adenine); iii) *compound repeats* – comprise two or more adjacent simple repeats; or iv) *complex repeats* – may contain several repeat blocks of variable unit length as well as variable intervening sequences [28, 33]. Complex repeats are more stable than simple repeats because the “interruptions” within the core sequence seem to stabilize the array [40].

STRs satisfy all the requirements for a forensic and/or population genetic marker: they are robust, leading to successful analysis of a wide range of biological material; the results generated in different laboratories are easily compared; they are highly discriminatory, especially when analyzing a large number of loci simultaneously (multiplexing); they are very sensitive, requiring only a few cells for a successful analysis; it is relatively cheap and easy to generate STR profiles; and there is a large number of STRs throughout the genome that do not appear to be under any selective pressure, i.e., to be neutral [28].

In a multiplex, STRs should have discrete and distinguishable alleles; a robust amplification; a high power of discrimination; an absence of genetic linkage with other loci being analyzed; low levels of artifact formation during the amplification; and the ability to be amplified as part of a multiplex PCR [28].

An essential feature of any STR used in forensic analysis is that the same biological material should give an identical profile regardless of the individual or laboratory that carries out the analysis. Without this standardization, compare results between laboratories and developments like national DNA databases would not be possible [28].

In addition to STR loci, the amelogenin locus which is present on the X and Y chromosomes has been incorporated into all commonly used STR multiplex kits. The amelogenin gene encodes for a protein that is a major component of tooth enamel matrix; there are two versions of the gene, the copy on the X chromosome has a 6 bp deletion and this length polymorphism allows the differentiation between the gene on the X and Y chromosomes [28].

Insertion and Deletion Polymorphisms

Insertion/deletion polymorphisms (InDels) are structural variations, more specifically length polymorphisms created by insertions or deletions of one or more nucleotides in the genome. They can be used as Ancestry Informative Markers (AIMs) or for Human Identification (HID) [33, 34, 37].

In this work, we will focus on AIM-InDels, once they can be used for ancestry affiliation, addressing the genetic structure of human populations and for estimating individual and global ancestry proportions in admixed populations [34, 41]. This is possible because AIM-InDels are markers whose allele frequency varies significantly between populations of distinct geographic origins [37, 41], and they work as slow mutating bi-allelic markers [39], being the two alleles simply classified as “long” or “short” [33].

AIMs are applied to Population Genetics studies mainly to analyze admixed populations by estimating admixture proportions both at the individual and population level. Also in the Forensic Genetics field, AIMs are of great interest, thanks to their potential to provide an intelligence tool in criminal investigations [37].

Di-allelic InDels become the choice genetic marker for many Population and Forensic Genetics studies due to their many advantages [29-31, 33, 35, 36]. Among them stand:

- Their small lengths, allowing an analysis through a simple PCR amplification and electrophoresis (e.g. standard dye-linked CE systems), also improving the amplification of degraded DNA and facilitating multiplexes and mixture detection;
- A widely spread distribution throughout the genome, at an average density of 1 InDel per 7.2 kbp of DNA (see Figure 4);
- A high percentage (between 16% and 25%) among all human DNA polymorphisms, consisting with the number from model organisms;
- An origination from a single mutation event which occurs at a low frequency and is subsequently stable (unlikely to present recurrent mutations) and do not present homoplasy;
- The genotyping of small InDels is relatively easy and inexpensive;
- Small InDels are also suitable for automation and analyses with high-throughput technologies; and
- The direct workflow minimizes manipulation, risks of contamination or samples mix-ups, and reduces to a minimum the number of variables affecting the end result.

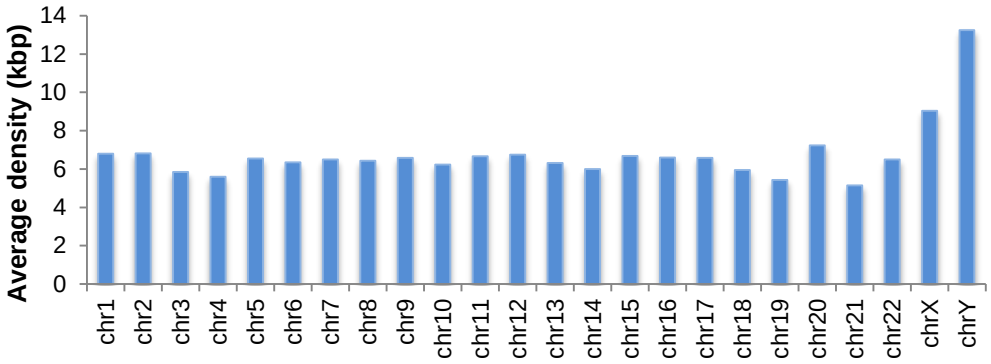

Figure 4. Genomic distribution of InDels by chromosome. Adapted from Mills et al. (2006) [42].

Although SNPs (Single Nucleotide Polymorphisms) are also widely used as bi-allelic AIMs, InDels overcome them because they don´t involve complex genotyping protocols, with more steps and implementation of new methods and expensive high throughput technologies. Besides, SNPs assays use large amplicon sizes, decreasing amplification success of degraded samples [43].

Using a 48 di-allelic autosomal InDels set, Pereira and coworkers (2012), managed to assign individuals as populations to continental ancestry and estimate ancestry proportions of different continental origins, as well as the different ancestors of a hybrid population. Assessing within-continent populations would require a much larger set. The random match probabilities of the set ranged in orders of magnitude from 10^{-14} to 10^{-15}, which is similar to about 13 STRs [33, 37].

Uniparental vs Biparental Genetic Systems

Both the biparentally inherited diploid genome (autosomes) and the uniparentally inherited haploid genome (maternally mitochondrial DNA (mtDNA) and paternally Y-chromosome (ChrY)), have been utilized with remarkable success to infer the ancestry of various populations [44].

Autosomal DNA genetic systems are shuffled with each generation because half of an individual's genetic information comes from his/her father and half from his/her mother. The genetic markers present in the ChrY and mtDNA represent "lineage markers". They are passed down from generation to generation without changing (except for mutational events). Maternal lineages can be traced with mtDNA sequence information while paternal lineages can be followed with ChrY markers [33] (see Figure 5).

The biparental and uniparental systems are inherently different, and each has advantages and disadvantages depending on the scientific hypothesis under consideration [44]. Human evolutionary or anthropological studies have typically focused on mtDNA or ChrY data, because the absence of recombination in these regions of the genome confer the power to construct hierarchical phylogenies with ease and fidelity, allowing researchers to infer past human behaviors and evolutionary events such as migrations, founder events, population bottlenecks or expansions, relative male and female contributions to an admixed population, marriage practices, and mode of transmission of languages. Nonetheless, their mode of inheritance limits their utility in providing information beyond the direct parental lineages [9, 44-50].

In contrast, the ubiquitous recombination characterizing the autosomes render attempts to draw unequivocal phylogenies most challenging, but these regions serve as a contemporary relic containing the broadest and most comprehensive record of genomic ancestral representation. Besides medical research, also Population and Forensic Genetics need autosomal data [9, 44-50].

Moreover, inferences gleaned from the autosomes, mtDNA and the ChrY can be concordant, complementary, or discordant with each other. Both in Forensic and Population Genetics, it's the individual that is analyzed. However, in Population Genetics, each individual is treated as belonging to a group and the analysis is done at a population level [44].

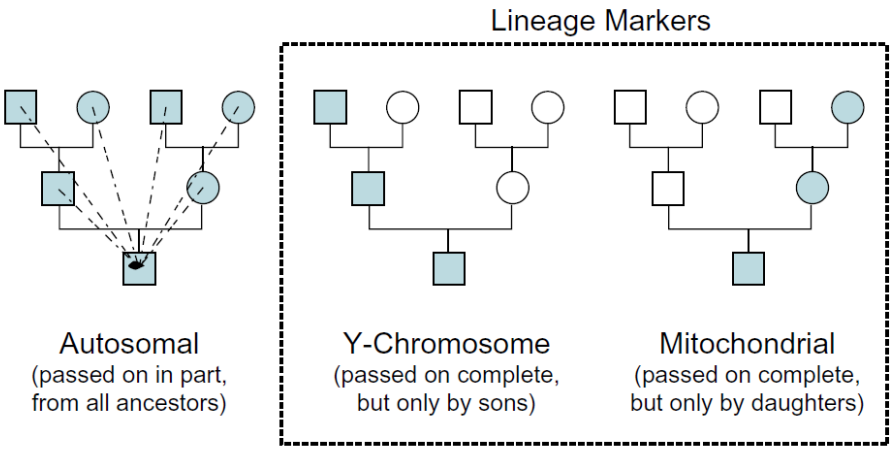

Figure 5. Illustration of inheritance patterns from recombining autosomal genetic markers and the lineage markers from the Y-chromosome and mitochondrial DNA. Adapted from Butler, 2011 [33].

2.2 Genetics Worldwide and Structured Populations

Although evidence of the impact of historical and/or cultural events can be gleaned from sources such as archeology, toponymy and linguistic elements, there is often debate about the weight of their corresponding demographic impact at a population level. Genetic analysis of modern populations can offer a more direct approach to recognize the impact of migrations and invasions in historical times, especially when source populations for migration are clearly differentiated from recipient populations [7].

There have been attempts to define populations genetically based on their racial identity or geographical location, and while it has been possible to classify individuals genetically into broad racial/geographic groupings, it has been shown that most genetic variation, around 85%, can be attributed to differences between individuals within a population. Differences between regions tend to be geographic gradients (clines), with gradual changes in allele frequencies [28].

Whether using a large set of microsatellites or di-allelic ancestry informative markers, it is possible to verify that the world population can be structured into five geographically defined clusters: America, Sub-Sahara Africa, East Asia, Oceania and a cluster composed of Europe, the Middle East and Central Asia [6, 29, 37, 47, 49]. World-level boundaries between major clusters mostly correspond to major physical barriers, such as oceans, mountain ranges or deserts, or to collections of linguistically similar populations [49].

If we look only to the European continent, it is possible to see a marked Northern-Southern division, with a clear separation of different ethnic and regional populations. Furthermore, although it was already said that Middle Eastern and European populations cluster together, this Northern-Southern separation allows to see that the Middle Eastern populations are more closely related to the Southern European group [47]. It is still noticeable a Southwest-Northeast cline, regarding the Middle Eastern contribution [46]. The desired commercial routs and trading posts across the Mediterranean Sea obligated several people, as Phoenicians and Romans, for instance, to conquer and establish themselves in the Mediterranean basin countries. The constant movement of people helped the spread of the Middle East genetic contribution to Southern European countries [51]. This contribution decreases with the distance from Middle East as it was demonstrated by autosomal microsatellites and biallelic DNA polymorphisms. The high Middle Eastern (and presumably Neolithic) proportion represents that half or more of the Europeans' genes descend from Neolithic ancestors who immigrated in Europe 10 000 years ago [46, 48, 52].

Within Europe, the Iberian Peninsula – often regarded as a source for Northward post-glacial expansions and a sphere of Neolithic influence from the Middle East - is of particular interest, because it has a complex recent history over the last two millennia, involving the long-

term residence of several different populations with very distinct geographical origins and their own particular cultural and religious characteristics, e.g., Celts, Phoenicians, Visigoths, Romans, North African Muslims and Sephardic Jews [7]. Genome-wide SNP data showed the Western half of the Iberian Peninsula to display the highest mean heterozygosity values in the continent, reflecting its history of population admixture [53]. Another genome-wide study supported the hypothesis that recent migrations from North Africa contributed substantially to the higher genetic diversity in Southwestern Europe. Besides, the haplotype sharing the authors observed between Europe and the Middle East followed a Southeast to Southwest gradient, whereas sharing between Europe and the Northern Africa followed the opposite pattern [54].

2.3 Genetics and the Jews

The Jewish community has been the focus of extensive genetic study over the past decades in an attempt to better understand the origins of this group [4].

Judaism is a mosaic of a culture, a religion, an ethnicity and a way of life. It is an identity that is not quite a nationality, but neither is it a simple ethnic or cultural phenomenon either. This unusual combination of characteristics, coupled with Jewish resistance over the centuries to assimilation and strong adherence to their religious faith, has contributed to the intense feelings of hatred, admiration, attraction, hostility and curiosity by the rest of the world [4].

First, researchers relied on linguistic, anthropological and archaeological evidences to try to solve the mystery of the origins of the Jewish people. But quickly the unique history of the Jews attracted DNA researchers attention [4].

The first question made to genetics was if an Ashkenazi and a Sephardic Cohanim shared a common ancestor as the oral tradition stated. After that, all kinds of questions started to arose, being the most important: do the genetic ancestry of contemporary Jewish populations demonstrate, to any degree, their supposed descent from the ancient Israelites of the Middle East? Or rather, do the DNA evidence indicate that Jews were simply a people who came to Europe during the Diaspora years, being mainly comprised of those descended from European ancestors? [4]

Several studies have supported genetic affinity among most Jewish populations, potentially due to shared Middle Eastern ancestry [50]. However, these ancestors represented a heterogeneous mix of Semitic and Mediterranean groups, even at their very beginning [4]. Other studies have also suggested similarity between Jewish and non-Jewish populations as a result of some level of gene flow among groups, generated by exogamy and incorporation

of local population members. It is this gene flow from host populations combined with genetic drift and possible local selection pressures that have led to detectable substructure among Jewish populations [9, 50].

Jewish genetics has been the subject of many studies in the field of archaeogenetics [44], and, as it happens in human evolutionary or anthropological studies, mtDNA and ChrY DNA have been the main focus, because the absence of recombination in these regions of the genome allows researchers to infer past human behaviors and evolutionary events [9].

Y-Chromosomal and Mitochondrial Data

On the other hand, ChrY and mtDNA studies of Jewish populations of Diaspora and their local host populations have, at times, provided conflicting results, but can be summarized as supporting the following: (i) almost all Jewish populations are derived from Middle Eastern ancestral populations; (ii) bottleneck events have had an effect on the gene pools of Jewish populations; (iii) local female contribution was significant in the establishment of certain Jewish populations; and (iv) local male contribution has been less significant for the establishment of most Jewish populations [9].

Studies of ChrY markers have provided opportunity to assess gene flow into Jewish populations from non-Jewish males [5]. Several ChrY studies have shown that different Jewish communities share a common origin in the Middle East, usually confirmed by the shared Cohen Modal Haplotype, although they can be quite heterogeneous as a consequence of genetic drift and different levels of admixture with their respective host populations [4, 10].

Regarding mtDNA, an unusual characteristic was found across almost all Jewish communities: the high frequency of particular mtDNA haplotypes within populations. This discovery suggested that an extreme female-specific founder effect had occurred in the genetic histories of most Jewish populations and that Jewish groups formed independently from each other around a small group of maternal founders [4].

In the end, both mitochondrial and ChrY studies anchor the origins of the Jews to the Middle East [5].

On a study conducted by Picornell and coworkers (2004), the authors analyzed mtDNA and ChrY markers from four Jewish populations: Ashkenazi, Sephardic, North African and Oriental. The data from mtDNA analysis showed that Jewish populations present a considerable differentiation between them, suggesting that each of the different Jewish communities formed independently around distinct groups of maternal founders and that subsequent gene flow from the host populations was limited on the female side. ChrY data

showed that all the Jewish populations grouped together, and presented a clear differentiation with respect to the non-Jewish populations [55, 56].

Taking into account only the ChrY of the Bragança Jewish population, Nogueiro and coworkers (2010) detected an ancestral genetic patrimony reflecting their origin in the Middle East, but also a smaller yet significant level of admixture with non-Jewish Iberian populations. The high haplotype diversity found also demonstrates that there were neither a low number of founders nor a high level of homogeneity of lineages [10]. On the other hand, for the same population but looking for mtDNA data, Teixeira and coworkers (2011) found some degree of admixture, similarly to other Diaspora Jewish populations, and the presence of a significant Middle East signature among this population [18].

Autosomal Data

Kopelman and coworkers (2009) undertook a genome-wide study with 678 autosomal microsatellites in several Jewish populations comparatively with Middle Eastern and European populations. The results obtained by them support the view that the Jewish populations largely share a common Middle Eastern ancestry and that over their history they have undergone varying degrees of admixture with non-Jewish populations of European descent. This is concluded because the Jewish populations had a high level of genetic similarity to each other, grouping together in several analyses. Moreover, these populations were also placed in an intermediate position in relation to the European and Middle Eastern populations, each clustering separately [50]. All these findings were also obtained by Behar and coworkers (2010), using SNPs [44].

Another note made by the authors was that Southern groups from Europe were placed closer to the Jewish populations than more northerly groups [50], also reported by Tian and coworkers (2009) [47]. Other genome-wide studies suggested not only a high degree of European admixture in Jewish European populations but also in Northern Africans, and that some non-Jewish populations from the Middle East as well as Southern European populations are the closest genetic neighbors to most Jewish groups [8, 50, 57].

The previous data, showing a close relationship between most contemporary Jews and non-Jewish populations from the Middle East and strong similarities between Jewish and their host neighbor populations, were reported as well by Behar and coworkers (2010). They still explain these similarities with large-scale introgressions, asymmetrical sex-biased gene flow, or religious and cultural diffusion. Their study further uncovers genetic structure that partitions most Jewish samples into three main subclusters, according to a split during the Diaspora, or an underappreciated contact between members of each cluster [44].

With a small set of microsatellites, Picornell and coworkers (2002) were not able to distinguish between four Jewish groups: Ashkenazi, Sephardic, North African and Oriental, or between them and other circum-Mediterranean populations [55, 56].

Tomàs and coworkers (2000) undertook a study very similar to ours, where they studied a Spanish Crypto-Jewish community, the Xuetas. This population lives in the Balearic Islands for a long time and they were also the targets of Inquisition. Because of this, the community has remained isolated and intermarriage with the host population did not take place until the middle of 20th century, consequently remaining a small and inbreeding population. When the authors compared it with other Jewish populations, they confirmed the Jewish origin and also a certain degree of admixture between the Xuetas and their gentile neighbors [58].

AIMS

There is still a huge gap regarding the genetic characterization of Iberian Judaic populations, especially concerning autosomal markers.

To offset this limitation, our strategy consist in genotyping a set of 15 STRs and a set of 46 InDels autosomal markers, in the available samples of the Bragança Jewish population, together with Portuguese samples of the same geographic area. This way we pretend to increase the current knowledge about the origin and demographic history of this population, complementing the studies conducted by Nogueiro and coworkers (2010) [10] and Teixeira and coworkers (2011) [18], based on mtDNA and ChrY lineage markers.

This new approach with autosomal markers aim to understand if:

- The population genetic history obtained agrees with that observed with the lineage markers;
- Once this population suffer from cultural isolation, it cause impoverishment of its genetic diversity;
- There was incorporation of genetic heritage of host population;
- There are differences between this population, others Jewish population and neighbor non-Jewish populations (Bragança and Miranda do Douro).

MATERIAL AND METHODS

1 Sampling Strategy and DNA Isolation

In this work two major sample sets were analyzed: one concerning the Jewish from Bragança, and another concerning a non-Jewish neighbor population.

The first set is composed by 53 unrelated self-designated Jewish individuals, native from five different municipalities of the Bragança district, in North-Eastern Portugal, namely Argoselo, Bragança, Carção, Mogadouro and Vilarinho dos Galegos (see Figure 3). This sample was previously genotyped for ChrY by Nogueiro and coworkers (2010) [10], and for the mtDNA by Teixeira and coworkers (2011) [18]. Total DNA was isolated from buccal cells collected on cytology brushes, using Blood and Cell Culture DNA Spin kit (GENOMED, GmbH, Germany) following the manufacturer's protocol, as referred by the authors in the materials and methods section [10, 18].

The second set is composed by 191 unrelated individuals: 86 native from Miranda do Douro municipality, and 105 native from other municipalities of the Bragança district. The sample from Miranda do Douro was previously genotyped for the ChrY by Marques (2011) [59], for the mtDNA by Mairal (2013) [60]and for the X chromosome by Pinto (2011) [61]. All blood samples were collected in the regional health centers and preserved in FTA™ cards (Whatman®, BioScienses). Total DNA was isolated according to the standard phenol-chloroform method [62] and the standard Chelex®-100TM (Biorad) protocol. Genotypes of 105 samples from the Bragança district were already available at the IPATIMUP genotype bank.

DNA sample donors were selected considering a combination of geographic and ethnographic/religious features. Sampling criteria was certificated for each individual through personal inquiries under strictly confidential circumstances, in order to avoid kinship for at least three generations, to define geographic origins and to confirm Jewish ancestry. Accordingly to the WMA Declaration of Helsinki, all samples were obtained under informed consent.

2 Genotyping

2.1 STRs

The DNA genotyping for the autosomal STR markers was performed using the AmpFlSTR® Identifiler PlusPCR Amplification Kit (Applied Biosystems). This kit contains primers for 15 autosomal loci (D2S1338, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D19S433, D21S11, FGA, TH01, TPOX, vWA and CSF1PO) and the amelogenin locus, for sex determination (see Supplementary Table 1).

DNA Amplification

PCR amplifications were done following manufacturer's specifications [63], adjusted for a final volume of 10 µL and under the conditions described in Table 1 and Table 2.

A positive control sample with a known genetic profile was included in each PCR run. The positive control used was the sample 9947A supplied with the kit.

Table 1. PCR reaction conditions for a single reaction of amplification with AmpFlSTR® Identifiler PlusPCR Amplification Kit.

PCR Reaction	
Reagents	**Volume per reaction (µL)**
Reaction Mix	4
Primer Mix	2
Water	3
DNA (±0,5-4 ng/µL)	1

Table 2. PCR program conditions for amplification with AmpFlSTR® Identifiler PlusPCR Amplification Kit, on a GeneAmp® PCR System 9700 Thermal Cycler.

		PCR Program	
		Temperature (ºC)	**Time**
Initial Denaturation		95 ºC	11 min
28 cycles	Denaturation	94 ºC	20 sec
	Annealing/Extension	59 ºC	3 min
Final Extension		60 ºC	10 min
Hold		4 ºC	∞

Fragment Detection

The PCR products obtained were prepared for subsequent analysis by adding 0.5 µL of the amplified product to 10 µL of a mix. This mix was prepared using 825 µL of Hi-Di™ Formamide (Applied Biosystems) and 15 µL of size standard GeneScan™ Liz 500®. An allelic ladder was also applied at this time, to help deduce the genotypes, under the same analyses conditions.

PCR products were then run on the ABI 3130xl Genetic Analyzer and the results analyzed through GeneMapper® ID Software v4.0. Figure 6 shows an electropherogram of a sample.

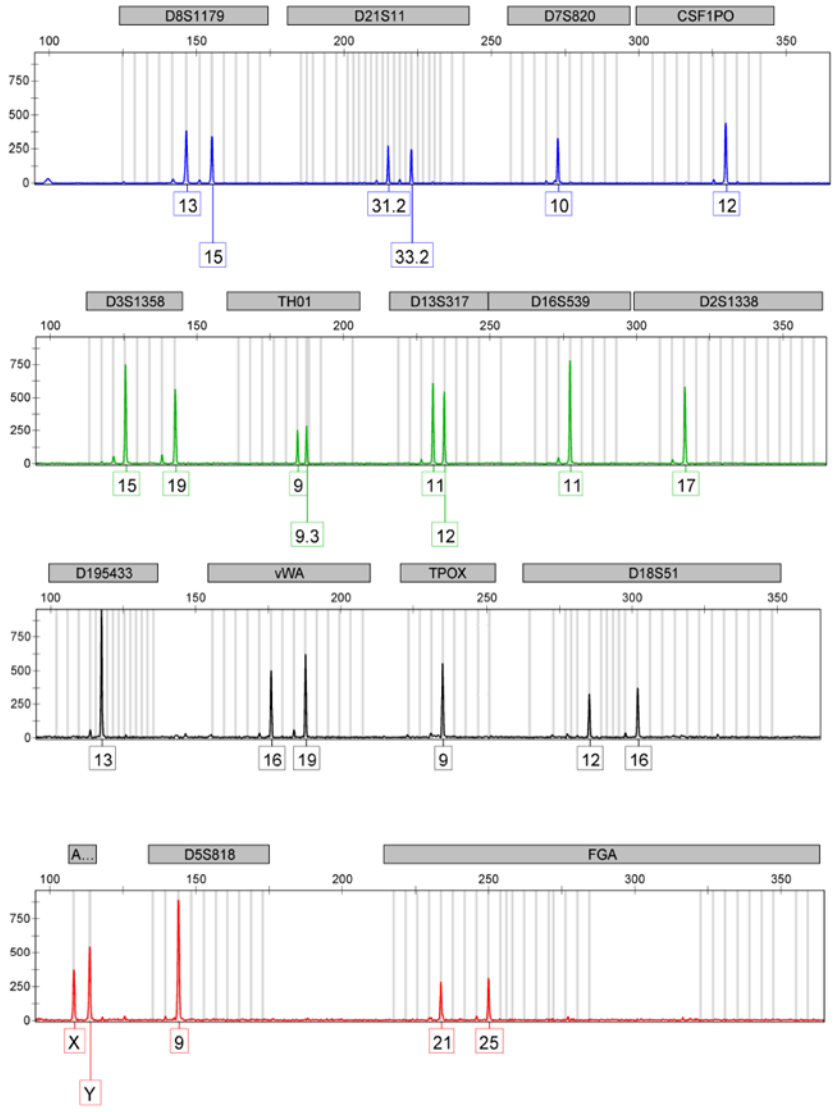

Figure 6. Electropherogram of a sample amplified with the AmpFlSTR® Identifiler PlusPCR Amplification Kit and analyzed with GeneMapper® ID Software v4.0.

2.2 InDels

All the work conducted using autosomal InDels was based on the study of Pereira and coworkers (2012) [37]. The 46 AIM-InDels used are fully described in Supplementary Table 2.

Although normally only two alleles by marker (coded 1 for the shorter and 2 for the longer) are considered, in this set there was two (MID-2264 and MID-360) that presented a third state, caused by a T deletion of the long allele (coded as 2-T) and by a T insertion on the short allele, respectively, as described by the multiplex authors' [37].

DNA Amplification

PCR reaction and amplification conditions are described in Table 3 and Table 4, according to Pereira and coworkers (2012) [37].

Table 3. PCR reaction conditions for a single reaction of amplification with InDels.

PCR Reaction	
Reagents	**Volume per reaction (µL)**
2x Qiagen Master Mix	5
10x Primer Mix	1
10x primer Mix reinforce	1
Water	2
DNA (±0,5-5 ng/µL)	1
Final Volume	10

Fragment Detection

The PCR products obtained were prepared for subsequent analysis by adding 1 µL of the amplified product to 10 µL of a mix. This mix was prepared using 1000 µL of Hi-Di™ Formamide and 30 µL of size standard GeneScan™ Liz 500®.

PCR products were then run on the ABI 3130 Genetic Analyzer and the results analyzed through GeneMapper® ID Software v4.0.

Table 4. PCR program conditions for amplification with InDels kit, on a GeneAmp® PCR System 9700 Thermal Cycler.

		PCR Program	
		Temperature (ºC)	**Time**
	Incubation	95 ºC	15 min
30 cycles	Denaturation	94 ºC	30 sec
	Annealing	60 ºC	90 sec
	Extension	72 ºC	45 sec
	Final Extension	72 ºC	60 min

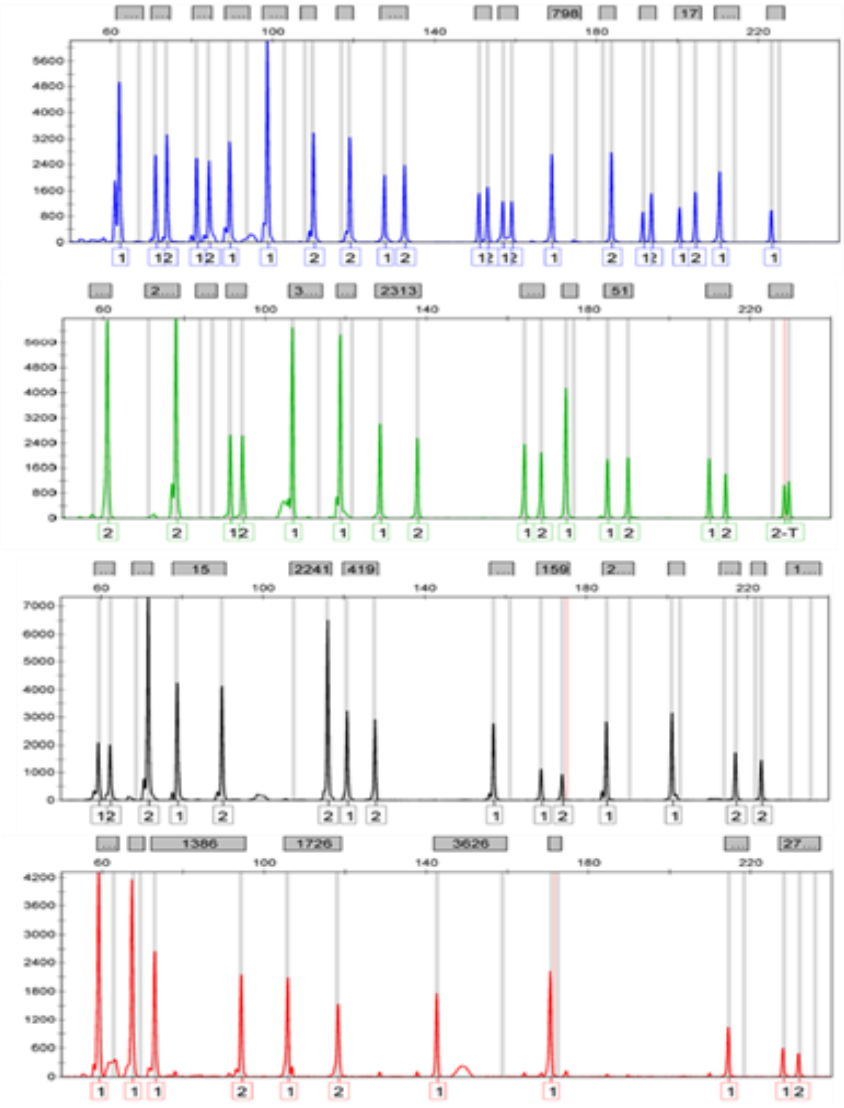

Figure 7. Electropherogram of a sample amplified with the InDels kit and analyzed with GeneMapper® ID Software v4.0.

3 Data Analysis

Data analyses were performed using genotypes from several populations worldwide. This set includes Jewish and non-Jewish populations typed for microsatellites or InDels. All populations used in all the performed analyses, as well as the corresponding number of samples, are shown in Table 5.

Table 5. Populations used in data analyses. For each population, it is also shown the markers used, its affiliation, the Jewish group, the number of samples and its availability.

Molecular Marker	Population Affiliation	Region/Origin	Group	No. of samples	Availability
STRs	Jewish	Bragança	Sephardic	53	---
		Sephardic	Sephardic	35	Picornell et al. [55, 64]
		Xuetas	Sephardic	102	Picornell et al. [55, 64]
		Libyan	Mediterranean	13	Picornell et al. [55, 64]
		Moroccan	Mediterranean	13	Picornell et al. [55, 64]
		Tunisian	Mediterranean	13	Picornell et al. [55, 64]
		Iranian	Middle Eastern	12	Picornell et al. [55, 64]
		Iraqi	Middle Eastern	13	Picornell et al. [55, 64]
		Ashkenazi	Northern European	25	Picornell et al. [55, 64]
		Total		279	
	Non-Jewish	Bragança		105	IPATIMUP
		Miranda do Douro		86	---
		Total		191	
InDels	Jewish	Bragança		52	---
	Non-Jewish	Africa		105	Pereira et al. [37]
		Europe		158	Pereira et al. [37]
		Middle East		159	Santos et al. [65]
		Central and South Asia		202	Santos et al. [65]
		East Asia		292	Pereira et al. [37]
		America		64	Pereira et al. [37]
		Oceania		28	Pereira et al. [37]
		Miranda do Douro		60	---
		Total		1057	

Using the Arlequin ver. 3.5.1.2 [66] software, we were able to estimate allelic frequencies, and observed and expected heterozygosities [67], for all populations considered with STRs, and only for Miranda and Bragança Jews for InDels.

Deviations from Hardy-Weinberg Equilibrium [68, 69], and pairwise linkage (Gametic Association) [70-72] were assessed using the web version of GenePop ver. 4.2 [73, 74]. In both

analyses, the Markov Chain parameters used were 10 000 steps of dememorization and 1000 batches, each one with 1000 iterations. These conditions were the same for all populations.

The correction for multiple tests was performed according to Bonferroni in all the analyses [75]. The Bonferroni correction is used to reduce the chances of obtaining false-positive results when multiple tests are performed on a single set of data. This method consists of dividing the critical *p* value ($p>0.05$) by the number of comparisons being executed.

In order to study the genetic structure of all populations, Arlequin ver. 3.5.1.2 [66], GenAlEx ver. 6.501 [76] and Structure ver. 2.3.4 [77-80] were used. The first software computed pairwise F_{ST} distances, using the Slatkin's linearization [81], with 1000 permutations. With the purpose to have a graphic representation of these distances, a Principal Coordinates Analysis (PCoA) was computed using GenAlEx. PCoA is a multivariate technique that allows one to find and plot the major patterns within a multivariate data set. This process allows the major axes of variation to be located within a multidimensional data set. For them, each successive axis explains proportionately less of the total variation, such that when there are distinct groups, the first two axes will typically reveal most of the separation among them [76].

Still using Arlequin, we also assessed an Analysis of MOlecular VAriance (AMOVA) [82-84]. This analysis allowed the estimation of the percentage of genetic variation that was observed among groups, among populations within groups and within populations. For both markers, 10 100 permutations were done. To help in the choice of the best number of clusters and its components, we also used SAMOVA. This software implements an approach to define groups of populations that are geographically homogeneous and maximally differentiated from each other [85].

Then, to infer population structure, we used a Bayesian model-based clustering algorithm implemented in the Structure ver. 2.3.4 [77-80] software, available at http://pritch.bsd.uchicago.edu/structure.html. This software uses multilocus genotypes to infer the structure of each population and to estimate admixture proportions. It defines K clusters (where K has to be provided by the user), each of them being characterized by a set of allelic frequencies for each locus. The individuals are probabilistically grouped on the basis of their genotype without prior knowledge of their population affinities, and can have membership in multiple clusters, with membership coefficients summing to 1 across clusters. Three runs were performed for each K with the same run length of 10 000 burn-in and 10 000 Markov Chain Monte Carlo (MCMC) replications.

In all analyses, an ancestry model that assumes that the analyzed individuals may have inherited fractions of the genome from K different ancestral populations, i.e., without any prior information on the origin of samples was used. Also, allele frequencies were considered

correlated among populations. In the ancestral membership analyses, the option “updating allele frequencies using only individuals with PopFlag=1 data” was chosen.

CLUMPP permuted the Structure clusters output by the three independent runs for each K, so that they match up as closely as possible. Then, the results were graphically displayed by *distruct*. For each K, each color represents a different cluster and each vertical line represents a single individual. The proportion of each color within an individual signifies the fraction of ancestry derived from that color’s cluster.

At last, the best K was evaluated using the online software Structure Harvester ver. 0.6.93 [86], through the mean of estimated ln probability of data.

Besides all the software described above, we also test all populations with TESS ver.2.3 and GeneClass2 software. TESS is a computer program that implements a Bayesian clustering algorithm for spatial population genetic studies [87]. GeneClass2 is a software that computes various assignment criteria to assign or exclude reference populations as the origin of individuals, as well as of groups of individuals, on the basis of multilocus genotype data [88]. However, both these software did not add information to the results obtained by all the previously described analyses (data not shown).

RESULTS AND DISCUSSION

1 Allele Frequencies and Gene Diversity

1.1 STRs

Our first approach was to calculate standard diversity indices, in order to better know each of the considered populations and understand the relations among them.

The allelic frequencies for each STR marker corresponding to the samples of Miranda do Douro and Jews from Bragança are detailed in Supplementary Table 3.

Considering the allele composition in both populations, all loci revealed to be highly polymorphic and none of them was new, since all had been described previously.

A comparative analysis with the Portuguese populations (data not show) indicates that the most polymorphic locus is the D18S51. According to the accepted mutation model, the observed distribution of the 15 detected alleles at this locus was the expected (Figure 8).

Considering this allele distribution, the population from the Bragança district presented two private alleles (10 and 23), while the Jewish sample presented only one (24). This last population was the only one not showing the alleles 21 and 22.

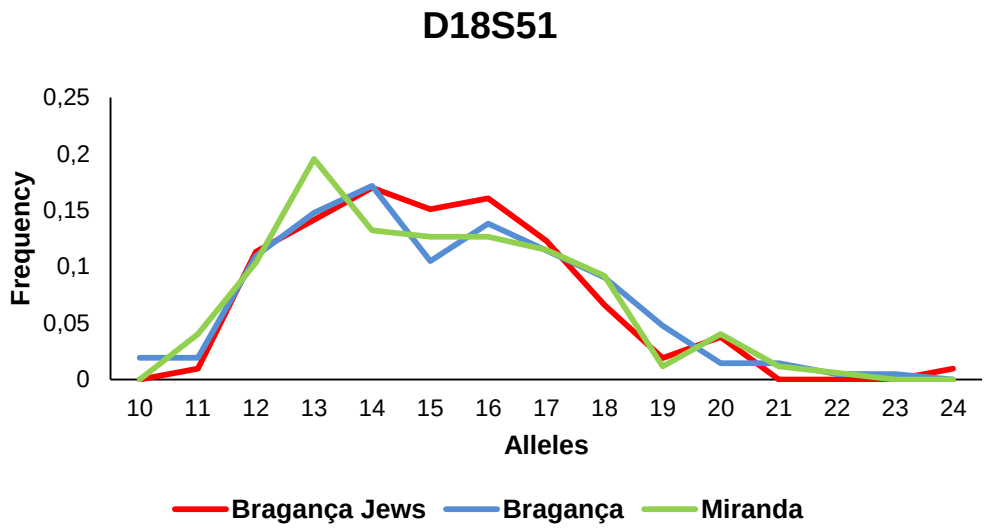

Figure 8. Graph showing the allele frequency distribution of the Portuguese populations at locus D18S51.

Looking to the allele frequency distribution at the same locus for all the considered populations, the shape of the graph obtained is slightly different (Figure 9). While all other populations present a distribution centered in allele 13, the Middle Eastern Jewish populations' distribution achieves its peak in the allele 16. In this case, the allele 23 continues to be exclusive to the Bragança district population, but the Ashkenazi population shares the allele 10. The allele 22 is also exclusive to both non-Jewish Portuguese populations. Regarding the allele 24, it was present only in the Portuguese Jewish and Sephardic (from Turkey) populations.

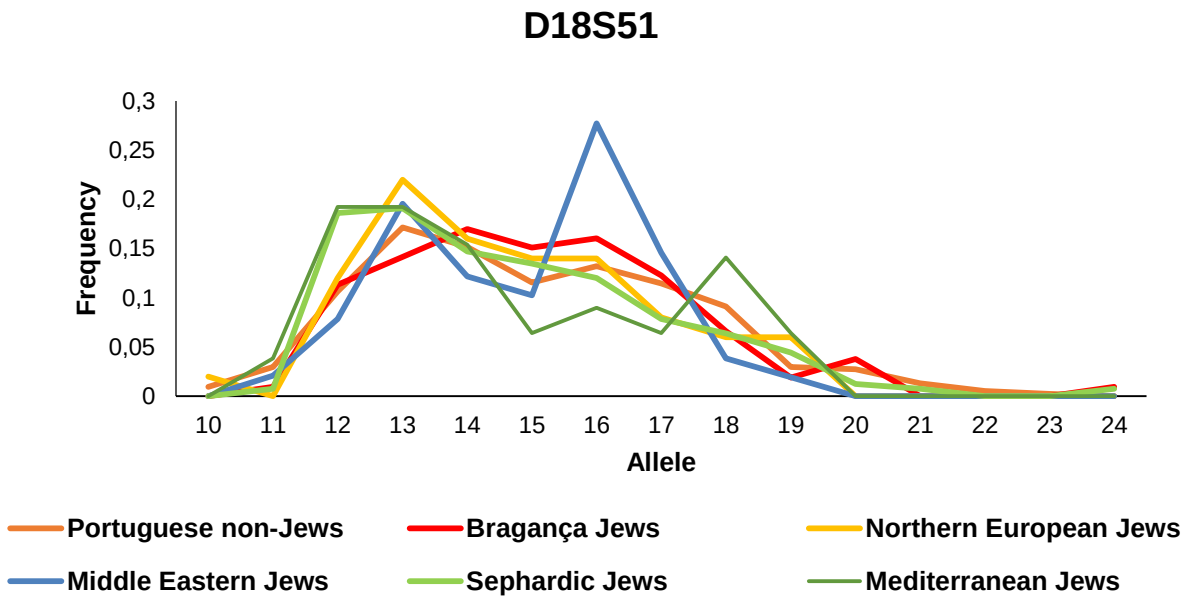

Figure 9. Graph showing the allele frequency distribution at locus D18S51 of all considered populations, grouped according to Table 5.

In relation to the gene diversity/heterozygosity, there are no differences among the considered groups. The observed and expected heterozygosities by locus in the analyzed populations are shown in Supplementary Table 4 and the mean heterozygosities for all populations are shown in Table 6.

All populations present values in the same range, being the more diverse the Moroccan Jewish population (0.81846 ± 0.03931) and the less diverse the Libyan Jews (0.76410 ± 0.06502). Some historical records can explain the diversity value observed in this last population on its relative isolation [89].

Although there are no major differences among groups, we see that the population with the lower observed heterozygosity is the Jewish from Bragança, while the one with the greater observed heterozygosity is the Ashkenazi Jews.

Comparing both heterozygosities computed for each population, it is clear that only two populations have an observed heterozygosity above the expected (the Tunisian and the Ashkenazi Jews).

When we compare our data from Portugal with published data for other Portuguese populations, we see that there are no big differences, either for the mean observed or expected heterozygosities. The mean values reported for Northern populations are respectively 0.78907 and 0.79247, in one study [90], and 0.79462 and 0.78518, in another [91]. Even if we look for the entire country, there are still no significant differences between the reported mean heterozygosities and the ones obtained by us [92, 93].

Table 6. Mean observed and expected heterozygosities for all populations.

		Mean Observed Heterozygosity	Mean Expected Heterozygosity
Portuguese non-Jews	Miranda	0.76877 ± 0.06279	0.79031 ± 0.06877
	Bragança	0.77714 ± 0.06665	0.79543 ± 0.05913
Sephardic Jews	Bragança Jews	0.72228 ± 0.09782	0.79299 ± 0.05969
	Sephardic	0.79841 ± 0.08272	0.80271 ± 0.03649
	Xuetas	0.80610 ± 0.07840	0.81074 ± 0.04616
Mediterranean Jews	Libyan	0.74359 ± 0.10879	0.76410 ± 0.06502
	Moroccan	0.76068 ± 0.10494	0.81846 ± 0.03931
	Tunisian	0.80342 ± 0.07789	0.79795 ± 0.05986
Middle Eastern Jews	Iranian	0.76852 ± 0.13029	0.80435 ± 0.05786
	Iraqi	0.76068 ± 0.11820	0.79795 ± 0.02070
Northern European Jews	Ashkenazi	0.82222 ± 0.03528	0.80154 ± 0.04677

1.2 InDels

After knowing a little more about the populations for microsatellites, we calculated the same indices using di-allelic InDels.

The allelic frequencies estimated in Miranda population and in the Jewish sample of Bragança for each marker are displayed in Supplementary Table 5.

Although normally only two alleles by marker are considered, there was two (MID-2264 and MID-360) that presented a third state, caused by a T deletion of the long allele and by a T insertion on the short allele, respectively, as described by the multiplex authors'. These third alleles seemed to be specific of European and African populations, respectively [37]. Once in our Jewish sample, only one marker (MID-2264) presented the third allele (as well as the population from Miranda), it suggests a closer ancestral relationship between Jews and Europeans than with Africans.

Two of the 46 InDels were monomorphic in the Jewish population (MID-1644 for allele 1 and MID-1802 for allele 2) and one in Miranda population (MID-3122 for allele 1). MID-1644 allele 1 showed a frequency of 0.953 in Europeans (and 0.94167 in Miranda), while in Africans, Americans and Asians its frequency was never greater than 0.25 [37]. Again, this may suggest, a shared ancestry between the Bragança Jews and other Europeans, more than with the other considered groups. The worldwide distribution of the other monomorphic allele's frequencies does not allow any more inferences.

Both observed and expected heterozygosities in the analyzed populations are shown in Supplementary Table 6. In the Bragança Jewish sample, observed heterozygosity ranged from 0.01923 (MID-3122 and MID-3072) to 0.63462 (MID-2264) while expected heterozygosity ranged from 0.01923 (MID-3122 and MID-3072) to 0.59466 (MID-2264). On the other hand, in the population from Miranda, observed heterozygosity ranged from 0.06667 (MID-593) to 0.55 (MID-2929) and expected heterozygosity from 0.06499 (MID-593) to 0.50994 (MID-2264).

2 Gametic Association

2.1 Hardy-Weinberg Equilibrium

STRs

In order to determine whether any difference between expected and observed heterozygosities is statistically significant, tests were computed. If that difference is not statistically significant, we conclude that the observed diploid genotypes are the product of a random union of gametes, i.e., are in Hardy-Weinberg Equilibrium. The tests results are shown in Supplementary Table 4.

Among all populations, only four (Miranda, Bragança Jews, Tunisian and Xuetas Jews) have loci deviated from the HWE.

However, since several tests were performed, the Bonferroni correction for multiple tests needed to be applied. Only the locus D21S11 in the Xuetas populations continued statistically significant, suggesting that there is a process acting to change the allele frequencies.

InDels

The same tests were computed using InDels data and the results obtained are shown in Supplementary Table 7. Concerning the Jewish population, three *p* values were statistically significant, i.e., below 0.05 (MID-2929, MID-128 and MID-2719). In the population from Miranda, no loci were deviated for HWE.

However, since several tests were performed, the Bonferroni correction for multiple tests was applied and none of the loci had a *p* value significant.

This absence of departures from Hardy-Weinberg Equilibrium was also reported by Pereira and coworkers (2012), when applying InDels to worldwide populations [37].

2.2 Pairwise linkage

STRs

Assuming the Hardy-Weinberg proportions of genotypes, all pairs of loci were then tested for the presence of significant association between them. For all populations, Supplementary Table 8 and Supplementary Table 9 show the *p* value for each pair tested, respectively for the Portuguese and for the non-Portuguese Jewish populations.

The *p* value of several pairs was found to be statistically significant in almost all populations. The only populations without any pair in association were Tunisian, Moroccan, Libyan and Iraqi Jews.

However, after applying the Bonferroni correction, among the Portuguese populations only Bragança still had pairs in association. In the other populations, all pairs of loci became independent, except three pairs in the Xuetas community (D7S820 – D8S1179, D8S1179 – FGA, and D18S51 – FGA).

InDels

For InDels markers, the next step was the same: test for association. Supplementary Table 10 shows the *p* value and the respective standard deviation for each pair of markers.

The Jewish population presented 37 pairs of loci with gametic association, while the population from Miranda showed 48 pairs in the same condition. However, after applying the Bonferroni correction, all loci showed independence, in both populations. No association between markers was also described for a worldwide population [37].

3 Genetic Structure

3.1 Within Bragança Jewish Population Level

STRs

After knowing a little more about the diversity indices in the Bragança Jewish population, we wanted to see how individuals relate genetically in this population.

So, a within population analysis was done to search for a substructure, with K ranging from 1 to 3. Figure 10 shows the membership proportions for different clusters within the Bragança Jewish population, assessed with Structure software, while Figure 11 shows the graph with the mean of estimated ln probability of the Structure output. In the latter figure, we can see that the best K, which is the less negative, is K=1. Therefore and contrarily to what would be expected from data previously obtained with uniparental markers [10, 18], the result presents no substructure, once each individual have nearly equal assignment values to each assumed population, giving the appearance that each individual is entirely and nearly equally admixed. This absence of individual or subgroup heterogeneity can be explained either by a historically recent but strong admixture process with the host population or a though slow paced homogenization for a quite extended period of time.

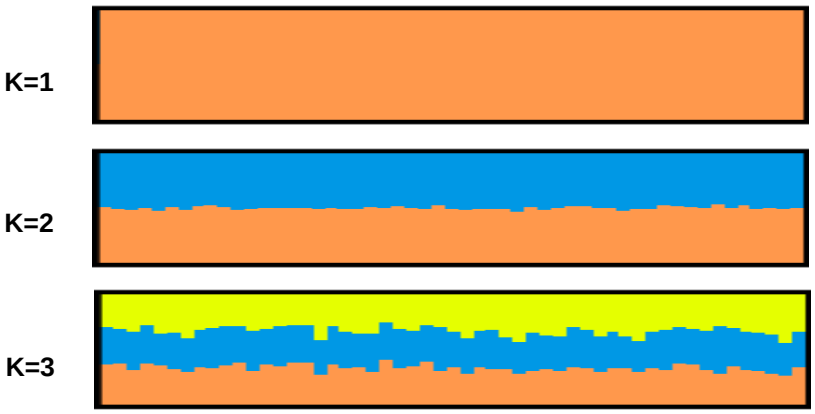

Figure 10. Jewish population structure, inferred with unsupervised clustering and performed using STRs data. The number of predefined clusters (K) is indicated to the left of each plot.

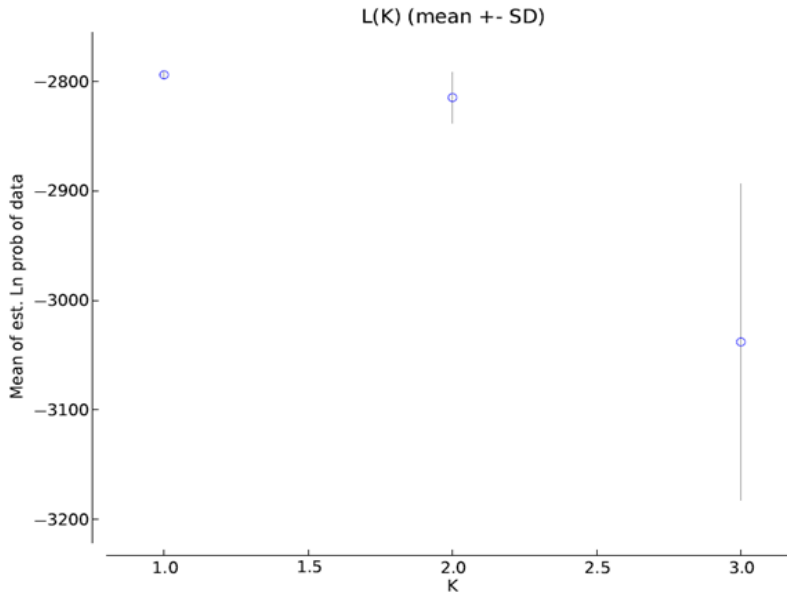

Figure 11. Graphic representation of the estimated ln probability.

Combination of STRs and InDels

To increase the power of the analysis, we combine microsatellite data with InDels in an intrapopulation analysis searching for substructure with the K ranging from 1 to 3.

Figure 12 shows the membership proportions for different clusters within the Bragança Jewish population, assessed with Structure software, while Figure 13 shows the graph with the mean of estimated ln probability of the Structure output. In the latter figure, we can see that the best K is K=1.

This result shows no difference when comparing to the result from STRs alone.

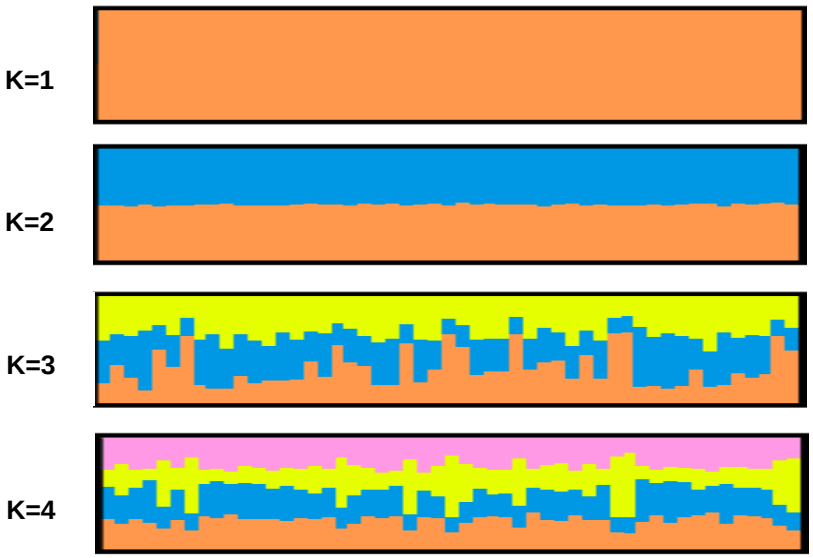

Figure 12. Jewish population structure, inferred with unsupervised clustering and performed using a combination of STRs and InDels data. The number of predefined clusters (K) is indicated to the left of each plot.

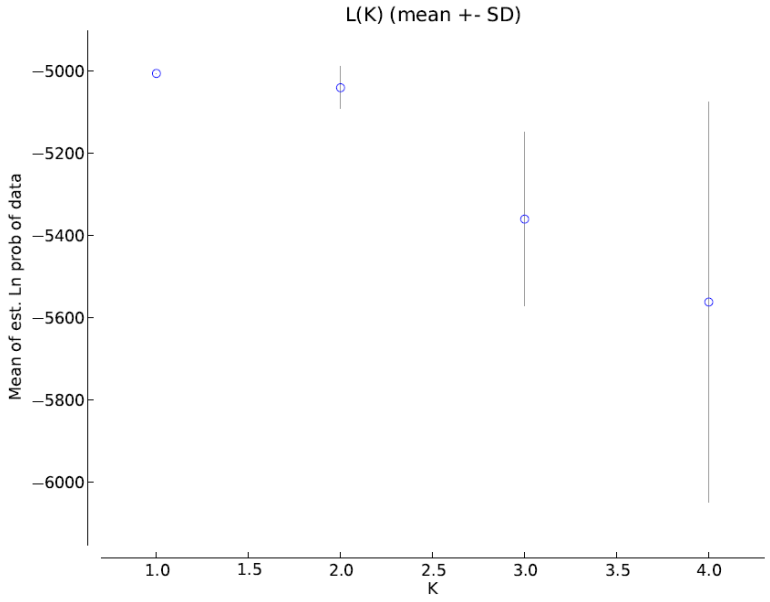

Figure 13. Graphic representation of the estimated ln probability.

It is also important to refer that we also computed an AMOVA in order to detect some differentiation within this population (data not shown). For that, we used the haplogroup data for the ChrY and the mtDNA [10, 18], once those markers had demonstrated a substructure within this population.

So, in the analysis for the ChrY haplogroup information, we created two groups: individuals with macrohaplogroups R* and I* (more common in the Iberian Peninsula) were put against the others. For the mtDNA information, a group was composed by individuals with macrohaplogroups H* and U5* (also common in the Iberian Peninsula), and all the others composed the other group. The last analysis consisted in a combination of both: individuals with both Iberian lineage haplogroups were put against the others.

Despite the previous results from Nogueiro and coworkers (2010) [10] and Teixeira and coworkers (2011) [18], in all these three analyses, no differentiation was detected within population for the autosomal microsatellite data.

3.2 Microgeographic Level (STRs)

Pairwise F_{ST} Distances

Once no major differentiation was found within the Jewish population, the next step was to analyze how this population relates to its non-Jewish Portuguese host populations.

The genetic distance between all Portuguese populations (Bragança, Miranda, and Bragança Jews) was measured through F_{ST} and the results are shown in Table 7. The distances ranged from 0.00097 (between Bragança and Miranda) to 0.00302 (between Miranda and Bragança Jews). Only the pair Miranda – Bragança Jews had a significant *p* value.

Thus, when we applied the Bonferroni correction, the distance between Miranda and the Jewish community became non-significant.

These findings suggest that there are no genetic differences between the Portuguese populations on test.

Table 7. Pairwise F_{ST} distances between Portuguese populations. All the statistical significant values are highlighted in bold. Those significant ($p<0.05$) are labeled with an asterisk.

	Bragança	Miranda
Miranda	0.00097	
Bragança Jews	0.00205	**0.00302***

To confirm these results, an AMOVA analysis was also computed (data not shown). From this test, we could conclude that the major differentiation is within populations and not among them. Even when Miranda and Bragança populations were group together against Bragança

Jews, attending a cultural/religious criterion, the AMOVA analysis showed greater differentiation inside groups than among them.

In a parallel analysis, we used a sample of 2124 Portuguese citizens from all parts of the country and computed the same analyses described above, excluding the Jewish population (data not shown). These analyses allowed us to conclude that there are no differences within the country, and that Bragança and Miranda are genetically undifferentiated from other Portuguese regions. With this, we assumed that these two populations could be considered a representation of the all country.

Structure Analysis

Understanding the previous results that demonstrate a very close relationship among the Portuguese populations analyzed, we looked for some kind of structure, under the light of different allele frequencies for each locus.

When we tried to cluster the considered populations with no a priori information and assuming different numbers of possible clusters with Structure software, we obtained

Figure 14 as an output, with K ranging from 1 to 5. Once again, the best K was evaluated by the ln probability (Figure 15).

From the Structure result, we see that all individuals, in all populations are assigned almost equally to each different cluster; there is no differentiation between populations and this is also supported by the ln probability graph, where the best K is 1, meaning that all the considered populations form one cluster. Besides, the wrong shape of the graph and the increasing standard deviation for each K do not support the presence of structured populations. Our population is as equal to the others as they are between them.

In conclusion, all Portuguese populations have the same genetic behave, making a differentiation difficult.

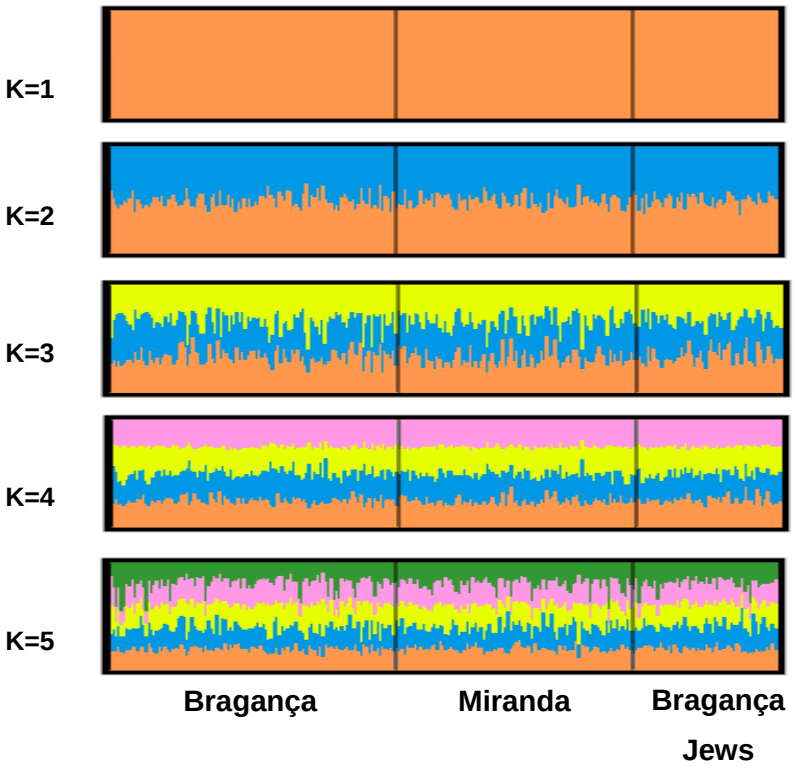

Figure 14. Population structure for Bragança, Miranda and Bragança Jewish populations, inferred with unsupervised clustering. The number of predefined clusters (K) is indicated to the left of each plot.

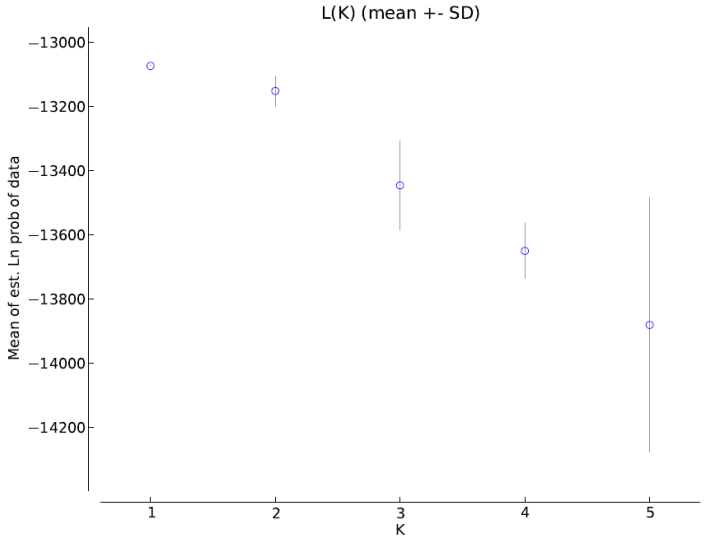

Figure 15. Graphic representation of the estimated ln probability.

3.3 Jewish Macrogeographic Level (STRs)

Pairwise F_{ST} Distances

At this point, we already knew how our population of interest behaves alone and in comparison with its Portuguese non-Jewish hosts. The next step was to see how it behaves when it is compared with other Jewish communities from different Diaspora countries.

First, we analyzed the genetic distance between all populations, through F_{ST} and the results are shown in Table 8. The distances ranged from 0.00032 (between Xuetas and Tunisian Jews) to 0.03703 (between Iranian and Libyan Jews). However, it should be noted that all the values are very small.

Among all pairs of populations, fourteen had a significant *p* value, which means that these fourteen pairs presented a *p* value lower than 0.05 (see Table 8). Four of these pairs had a *p* value equals to 0, so even after the Bonferroni correction was applied, they were still statistically significant. On the other hand, all the other pairs with a statistically significant *p* value became non-significant after the correction was applied.

In order to have a graphical representation of the previous data, we used compute a PCoA (Principal Coordinates Analysis, see Figure 16).

By the analysis of the figure, we can conclude that these populations cannot be separated into different clusters, not even if we consider the Diaspora groups. The Portuguese Jewish community is placed between the Northern European Ashkenazi, and the Mediterranean and Middle Eastern Jews.

Regarding the Iranian Jewish population, Atzmon and coworkers (2010) [57] have already described its smaller proximity with other Jewish populations. However, this finding was also applicable to the Iraqi populations, which was not found in our results.

Concerning the Balearic Island Jewish community, its more distant position in the graph can be explained by its geographic isolation, as well as by its previously reported endogamic "tradition" [58, 94].

The population from Libya is, among the Mediterranean, the most outlying, and as previously said, its genetic signature is more distinguishable, in agreement with its isolation [89].

The two populations from the Middle East are far apart one from another, contrarily of what would be expected.

Table 8. Pairwise F_{ST} distances between the Jewish populations. All the statistical significant values are highlighted in bold. Those significant (p<0.05) are labeled with an asterisk and those values that remain significant after the Bonferroni correction with two asterisks.

	Xuetas	Sephardic	Tunisian	Moroccan	Libyan	Iraqi	Iranian	Ashkenazi
Sephardic	**0.00810***							
Tunisian	-0.00032	-0.00687						
Moroccan	**0.00980***	-0.00104	-0.00988					
Libyan	**0.02136****	0.00961	-0.00609	0.00554				
Iraqi	0.00869	0.00614	-0.00846	-0.00165	-0.00908			
Iranian	**0.01751***	**0.02063***	0.00964	0.01513	**0.03703****	**0.02425***		
Ashkenazi	**0.01889****	0.00221	0.00717	0.00210	**0.01943***	0.00611	**0.02085***	
Bragança Jews	**0.00919****	0.00382	-0.00360	0.00359	**0.01398***	0.00559	**0.01909***	**0.00688***

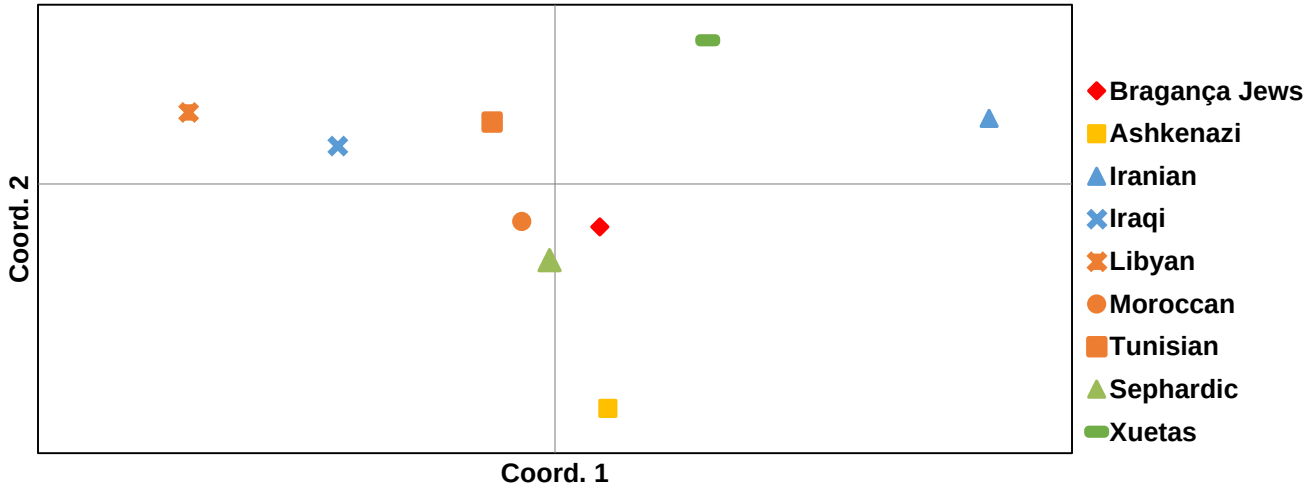

Figure 16. Principal Coordinates Analysis (PCoA) plot of all Jewish populations.

AMOVA

In order to try to explain the genetic distances results, AMOVA was computed with Arlequin, using nine Jewish populations from different Diaspora countries. These populations were tested for two clustering combinations: “no cluster” and “by geographic region”.

The obtained results are shown in Table 9. For the “by geographic region” clustering, four groups were considered: Sephardic, composed by all considered Sephardic populations (namely Sephardic from Turkey, Xuetas, and the Jewish community of Bragança); Mediterranean, composed by Libyan, Moroccan and Tunisian; Middle Eastern, composed by the populations from Iran and Iraq; and Ashkenazi population (see Table 5).

Table 9. AMOVA results for two different grouping methods involving the Jewish populations.

	Percentage of variation	Fixation Indices	p value
No Grouping			
Among populations	0.92	0.00920	0.00000 ± 0.00000
Within populations	99.08		
Grouping by geographic region			
Among groups	0.30	0.00302	0.22000 ± 0.00387
Among populations within groups	0.73	0.00731	0.00020 ± 0.00014
Within populations	98.97	0.01031	0.00000 ± 0.00000

As expected, the major variation is within populations in both cases. When we test the populations without any group affiliation, we see that the variation among them is statistically significant, showing that the populations are different.

Then, when we group them according to its Diaspora group, only the *p* value for the “among groups” variation is non-significant, showing that this grouping strategy is not the more suitable. Even within groups, the populations are different.

Structure Analysis

Once we realized that some populations were more distant and maybe also more different than the others, we inferred some structure among the considered populations, through an

unsupervised analysis with Structure. The obtained results are showed in Figure 17and Figure 18 shows the mean ln probability.

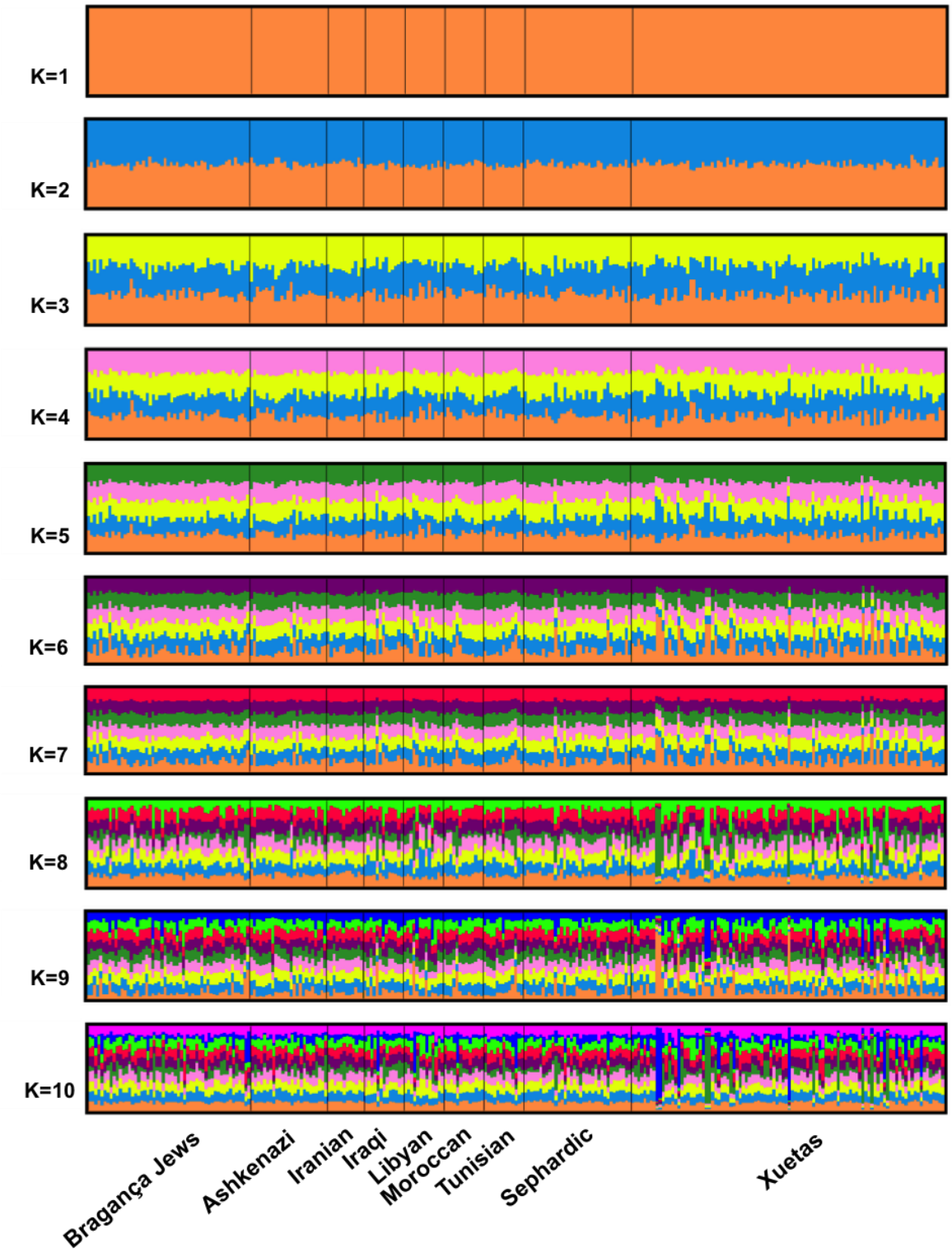

Figure 17. Population structure for all considered Jewish populations, inferred with unsupervised clustering. The number of predefined clusters (K) is indicated to the left of each plot.

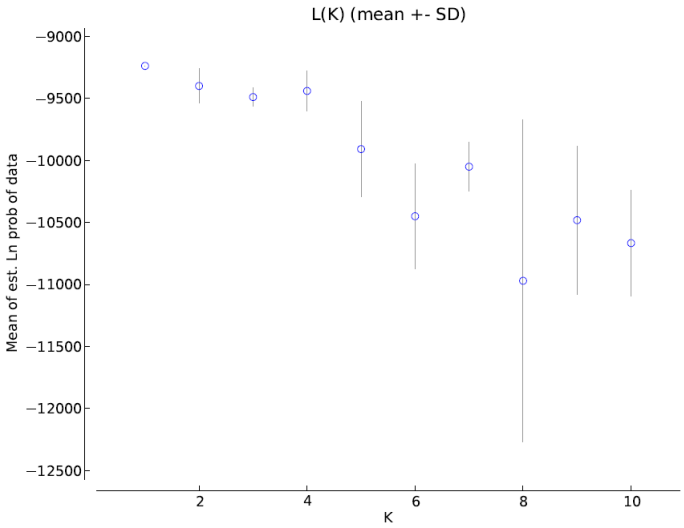

Figure 18. Graphic representation of the estimated ln probability.

From the Structure result, we see that all individuals are equally assigned, reflecting an absence of differentiation between populations. This is also supported by the ln probability graph, where the best K is 1, meaning that all populations can be grouped in only one cluster. So, all the populations are very similar to the each other, including our Jewish population from Bragança.

Although the F_{ST} analysis reflects some detachment among the populations, their distances were not able to generate a structure among them.

4 Ancestral Membership Analysis (InDels)

4.1 Pairwise F_{ST} Distances

As it has been said, the Bragança Jewish population was also typed with InDels. Once these slow mutating polymorphisms are used for ancestry affiliation, addressing the genetic structure of human populations and for estimating individual and global ancestry proportions in admixed populations, we used the collected data to inquire about the ancestry of this population. This analysis was possible thanks to different analyses in which we compared the population of interest with worldwide populations, in general, and its more likely parental populations.

The first step was to measure the genetic distances between the populations analyzed by us, and worldwide populations, separated by continent.

The genetic distances between all populations was measured through F_{ST} and the results are shown in Table 10.

The distances ranged from 0.00226 (between Europe and Miranda) to 0.44141 (between America and Africa).

Miranda is the closest to our population (F_{ST}=0.00373), although the distance to Europe is very similar (F_{ST}=0.00563), as expected. The distance between the Jewish population from Bragança and its other likely ancestral population, Middle East (F_{ST}=0.01332), is almost as bigger as between the two parental populations (F_{ST}=0.01450).

Besides the pair Europe-Miranda (p=0.06055 ± 0.00739), all pairs of populations were statistically significant, once their *p* value was lower than 0.05. The only pair with a significant *p* value different from 0 was Jewish-Miranda (p=0.03809 ± 0.0060). However, after the Bonferroni correction was applied, this pair became non-significant.

Table 10. Matrix of the F_{ST} genetic distances between all pairs of populations, obtained when using InDels. All the statistical significant values are highlighted in bold. Those significant (p<0.05) are labeled with an asterisk and those values that remain significant after the Bonferroni correction with two asterisks.

	Africa	Europe	East Asia	America	Oceania	Central and South Asia	Middle East	Bragança Jewish
Europe	**0.36241****							
East Asia	**0.39194****	**0.28249****						
America	**0.44141****	**0.29502****	**0.21931****					
Oceania	**0.37284****	**0.22317****	**0.22480****	**0.30818****				
Central and South Asia	**0.28916****	**0.03555****	**0.18108****	**0.19678****	**0.16731****			
Middle East	**0.29017****	**0.01450****	**0.25264****	**0.26557****	**0.17528****	**0.02705****		
Bragança Jewish	**0.36660****	**0.00563****	**0.28708****	**0.30190****	**0.23147****	**0.03097****	**0.01332****	
Miranda	**0.35348****	0.00226	**0.28938****	**0.29509****	**0.22841****	**0.03303****	**0.01156****	**0.00373***

These findings suggest that there are no genetic differences between Miranda and Europe, and Miranda and Jewish. Although very small, the distance between Europe and the Jewish population on test is significant. The distance between our population and the other possible parental population, Middle East, is also statistically significant, although bigger.

In conclusion, the distance between the Bragança Jewish population and both likely parental populations are statistically significant. The only population whose distance to Bragança Jews is non-significant, is Miranda do Douro.

To better visualize these results, Figure 19 shows a Principal Coordinates Analysis plot. Here, the previous conclusions are clearer: Europe, Miranda and Jewish populations created a tight cluster, almost overlapping, while American, African, East Asian and Oceanic populations are very distant from the cluster and from each other. Central and South Asian, and Middle Eastern populations are also apart from each other and from the small cluster, but still very close to it, allowing the view of a larger cluster.

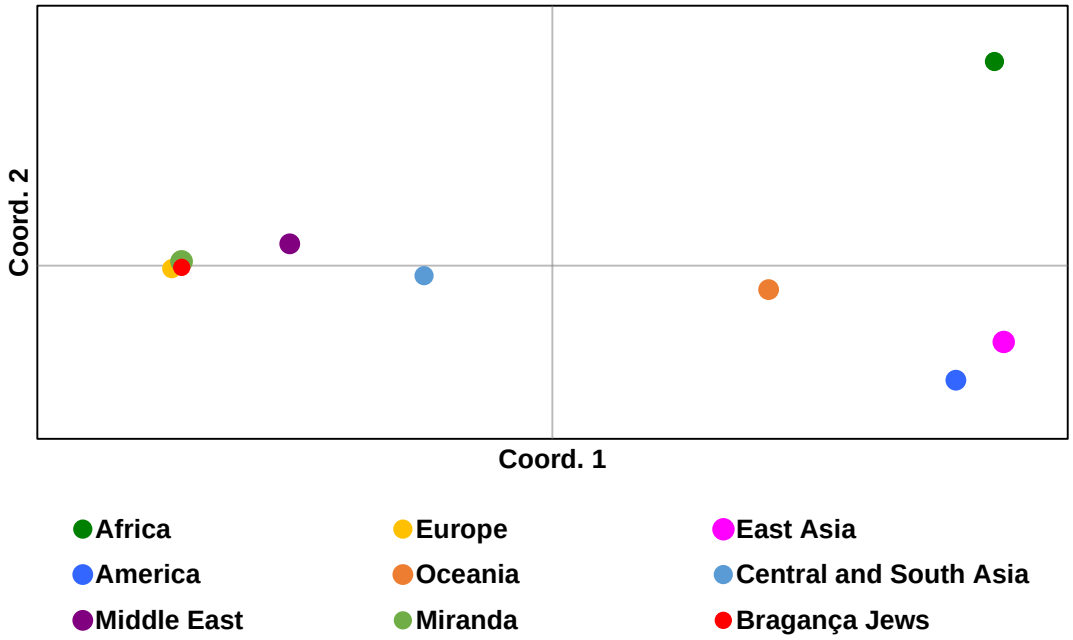

Figure 19. Principal Coordinates Analysis plot of worldwide populations.

Enlarging the section of the previous PCoA that contains the populations of interest (Middle East, Europe, and Bragança Jewish), we obtain Figure 20. In this figure, it is clear the distinction between the European and the Middle Eastern populations. It is also clear that the

Jewish population from Bragança is closer to the European than to the Middle Eastern population.

Although some authors refer Jewish populations sitting between Middle East and Europe [44, 50], our results differ. When doing a worldwide analysis, our Jewish population practically overlaps with Europe. When it is compared only with Europe and Middle East, it is closer the former than to the latter.

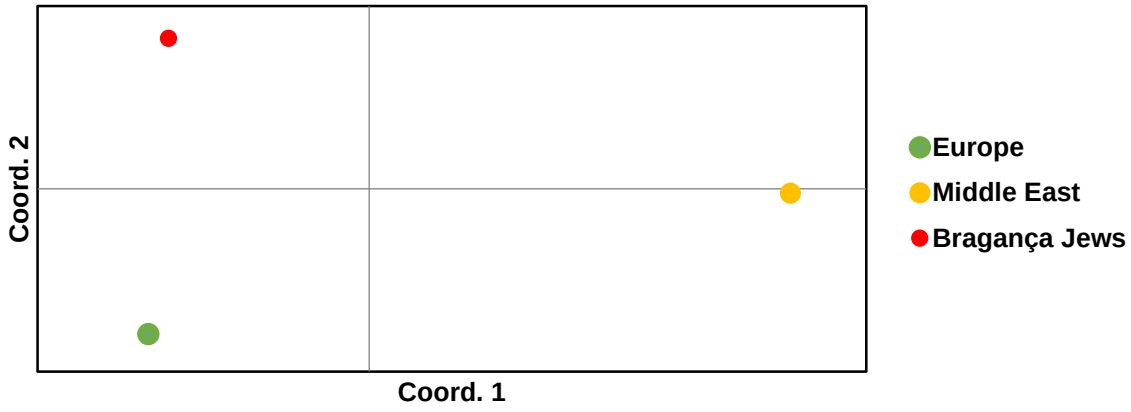

Figure 20. Principal Coordinates Analysis plot of possible parental populations for the Bragança Jewish community.

4.2 AMOVA

Using worldwide populations from HGDP-CEPH panels plus Miranda and Jewish from Bragança populations, we computed AMOVA considering different clustering combinations. In order to choose which clusters better enhance the differences, we used the SAMOVA software and the fixation indices obtained for each number of clusters are shown in Figure 21.

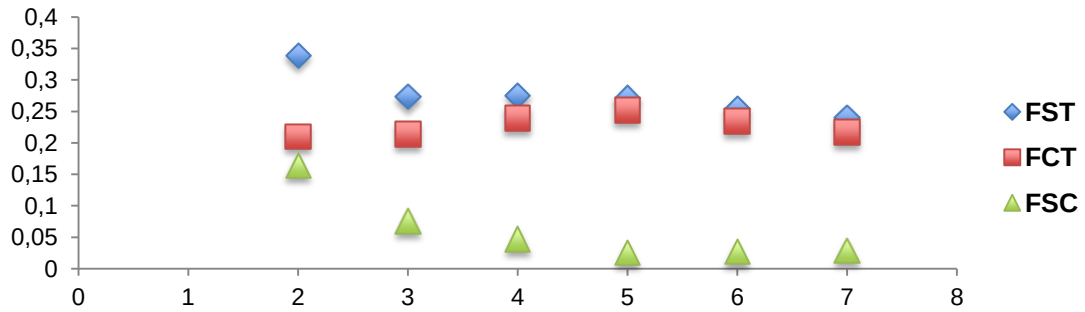

Figure 21. Graph showing the variation of the fixation Indices (F_{ST}, F_{CT}, and F_{SC}) for number of clusters considered.

Once we are trying to maximize the differences between groups, we want the greater F_{CT} with the smaller F_{SC}. So, the best number of cluster is 5 and the software split the populations into the following groups: group 1: Oceania; group 2: America; group 3: Africa; group 4: East Asia; and group 5: Europe, Miranda, Bragança Jews, Middle East, and Central and South Asia.

The next step was to perform an AMOVA test with no grouping strategy and with this one suggested by SAMOVA. The obtained results are shown in Table 11.

Table 11. AMOVA results for all the considered populations, when using InDels and testing for different clustering combinations.

	Percentage of variation	Fixation Indices	p value
No Grouping			
Among populations	20.81	0.20807	0.00000 ± 0.00000
Within populations	79.19		
Grouping by SAMOVA results			
Among groups	25.24	0.25242	0.00684 ± 0.00231
Among populations within groups	1.88	0.02520	0.00000 ± 0.00000
Within populations	72.87	0.27127	0.00000 ± 0.00000

As expected, the major variation is within populations in both cases. When we test the populations without any group affiliation, we see that the variation among them is statistically significant, showing that the populations are different.

Then, when we group them according to SAMOVA results, the variation within populations is still the greater but the variation among populations within groups is very low. Besides, the *p* value for the “among groups” variation is statistically significant, showing that this is a good grouping strategy. This result was expected, once the InDels set used was wittingly designed for an intercontinental differentiation [37].

In this separation, the Jewish population from Bragança is included in the European group, with Miranda, other European populations, and the Middle East.

4.3 Structure Analysis

Worldwide Analysis

At a worldwide analysis, we already knew that this set of markers was able to successfully separate up to 5 continents (Africa, Europe, East Asia, America, and Oceania) [37]. Nonetheless, we wanted to know to which region, Bragança Jewish and Miranda populations were more similar. We also wanted to incorporate in the analysis two more regions: Central and South Asia, and Middle East, a likely ancestral population of the Bragança Jews.

So, we used the software Structure to divide all these populations or groups of populations in clusters. Figure 22 represents the Structure results for a supervised analysis when InDels data was used and Figure 23 the ln probability that will help us to choose the best K, i.e., the number of clusters that better define our sample, in this case ranging from 1 to 10.

In the first figure, we see that as the K increases, the sample is divided in clusters. Looking for Figure 23, we see that the best K is K=6, because the respective ln is the less negative with the major variation before the plateau. Back to the Figure 22, for K=6, we can then differentiate 6 clusters: African, East Asian, American, Oceanic, Central and South Asian, and the last formed by European, Middle Eastern, Jewish from Bragança and Miranda populations.

The first four clusters are well defined. The distinction between Central and South Asia and the remaining populations is less clear, but still noticeable.

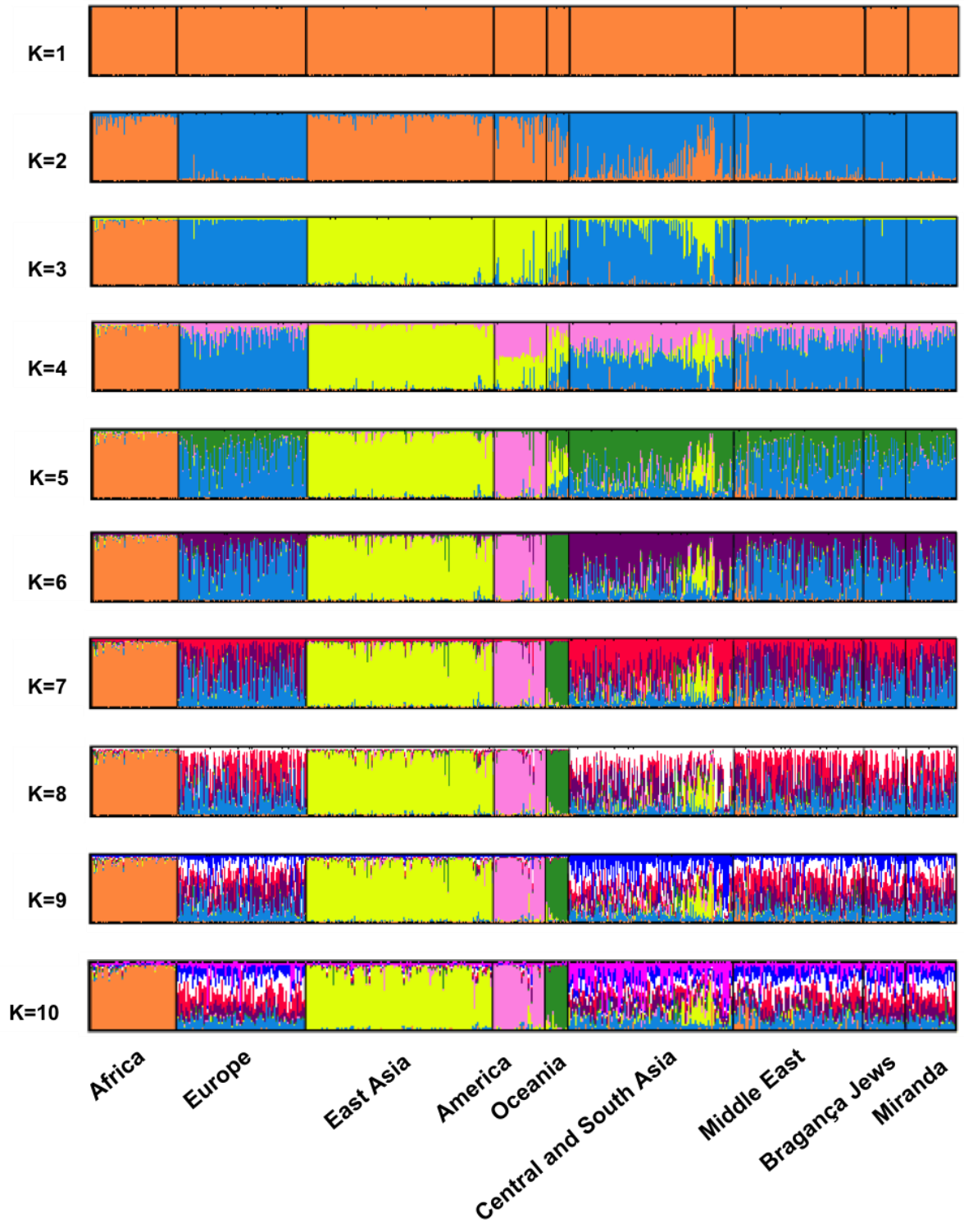

Figure 22. Ancestral membership proportions for worldwide populations, inferred with supervised clustering. The number of predefined clusters (K) is indicated to the left of each plot.

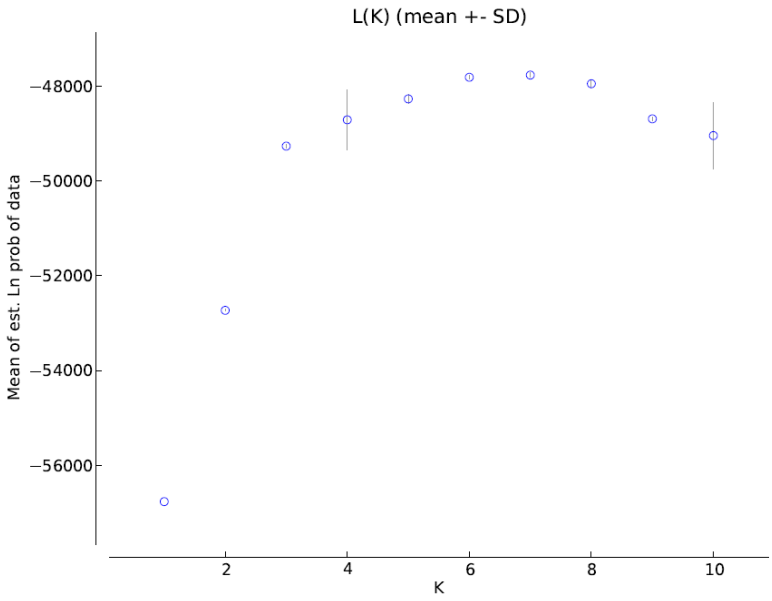

Figure 23. Graphic representation of the estimated ln probability.

In conclusion, the Bragança Jewish population falls in the same cluster as its non-Jewish neighbors and its more likely parental populations, Europe and Middle East.

Possible Parental Populations Analysis

Then, the last step was to compare only our population of interest with its possible parental populations: Europe and Middle East; or in other words, look for some kind of substructure within the European/Middle Eastern cluster previously mentioned. In this analysis, also supervised, we included Miranda too because is a European population and is geographically close to our Jewish population. Figure 24 shows the result from Structure with K between 1 and 5, while Figure 25 shows the graph of the ln probability.

From the Structure, we can conclude that, although it is not a clear differentiation between the two parental populations, a slight distinction is noticeable. From the ln probability graph, we see that the best K is K=2, which means that these four populations are better defined in two clusters. Looking for the K=2 result, we see that one cluster matches the European group, while the other matches the Middle Eastern group. Both the Miranda and the Jewish populations have a pattern much more similar to Europe than to Middle East. This fact is also supported by the distribution of the membership proportions by population in the two clusters (Table 12). The Jewish population has a distribution of admixture more similar to Europe. However, some shared Middle Eastern gene pool can be inferred.

The surprise is in the distribution of Miranda. Although the major percentage is for the same cluster as Europe, because it is smaller it becomes also very close to the Middle East.

In conclusion, we can affirm that, although not perfectly visible, our Jewish population is much more similar and closer to Europe, as the previous results from F_{ST} have shown.

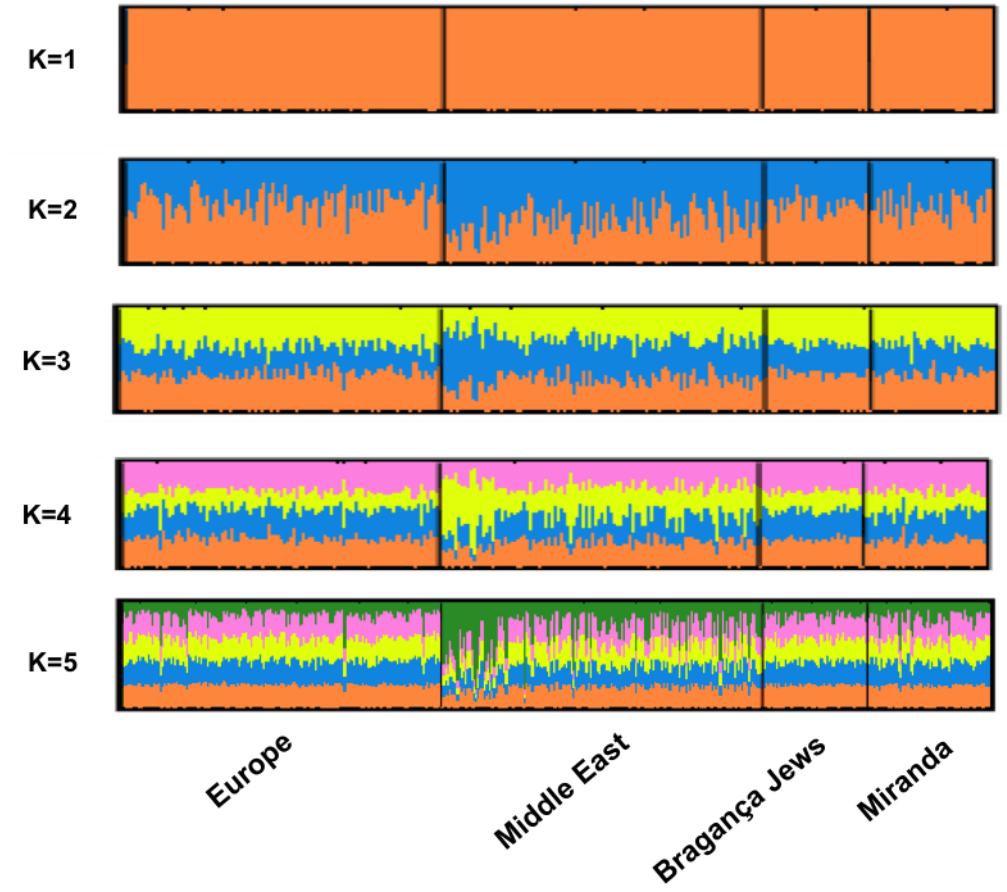

Figure 24. Ancestral membership proportions for the two possible parental populations, Bragança Jews and Miranda populations, inferred with supervised clustering. The number of predefined clusters (K) is indicated to the left of each plot.

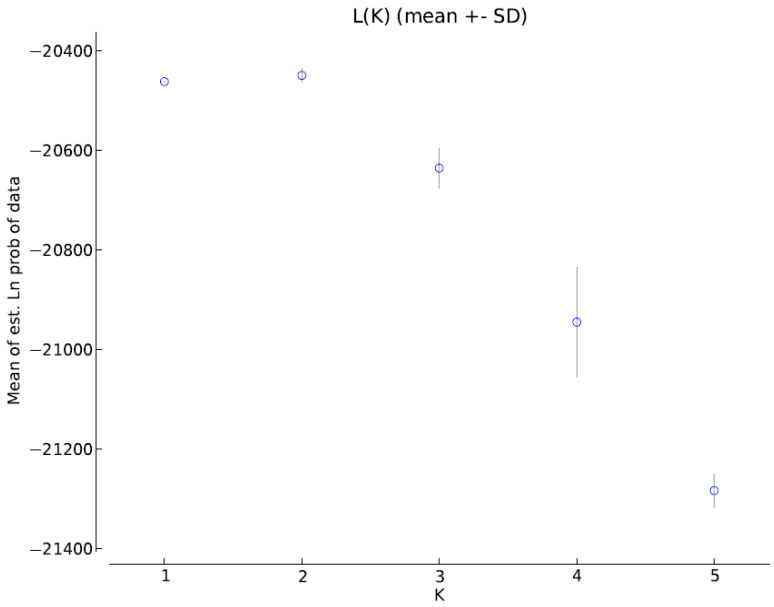

Figure 25. Graphic representation of the estimated ln probability.

Table 12. Table with membership proportions.

	Cluster 1	Cluster 2
Europe	0.602	0.398
Middle East	0.413	0.587
Jewish from Bragança	0.580	0.420
Miranda	0.551	0.449

CONCLUSION

The main focus of our study was the genetic characterization of the Bragança Jewish population. Regarding the major standard diversity indices, this community presented values very similar to its non-Jewish Portuguese hosts (Bragança and Miranda), as well as to other populations from Portugal. When we compared our population to other Jewish communities from different Diaspora countries, the results were the same; no major difference was found among them.

Using slow mutating di-allelic markers, we compared Bragança Jewish and Miranda populations to other worldwide populations. In both mentioned populations, the results for the diversity indices were more close to the European than to any others, suggesting a close relation between Europe and the two analyzed populations.

This similarity between our population formed by Bragança Jews and other populations was extremely surprising, as they show exactly the opposite of what is expected in isolated, small sized populations, namely a deep genetic diversity loss.

Then, after knowing a little more about all the populations considered in this study, we did a search for genetic structure, using a Bayesian model-based clustering algorithm. We started with a within Jewish population analysis, in order to look for some kind of substructure, as the lineage markers had previously shown. However, either with microsatellites data or with a combination of them with InDels markers, no substructure was detected. This absence of individual or subgroup heterogeneity can be explained either by a historically recent but strong admixture process with the host population or a though slow paced homogenization for a quite extended period of time. To clarify under which of these alternative modes was the admixture predominantly taking place, the study of linked markers (namely from the X-chromosome) should be undertaken.

Realizing that our sample genetically behaves as one population without substructure, we wanted to see its behavior with its long-term non-Jewish host populations, namely Bragança and Miranda do Douro. Using microsatellite data and through measuring the genetic distance between these populations, we found that the distances were very small, as expected, and statistically non-significant.

From these, when we used the Structure software to cluster the three populations, we already expected non-differentiation. And the result was exactly that: one is the number of clusters that better define these three populations. So, we can conclude that there are no differences between the Jewish community and its neighbors.

The next step was to understand the relation between the Portuguese Jewish community and other Jewish populations from Diaspora countries. From a genetic distances analysis we saw that the Tunisian and Moroccan Jews were the closest, while the Iranian Jews were the farthest. Atzmon and coworkers (2010) [57] have already described the Iranian Jewish population's smaller proximity with other Jewish populations.

However, the only statistically significant distance involving the Portuguese Jewish community was with the Xueta population. This can be explained by its geographic isolation, as well as by its previously reported endogamic "tradition" [58, 94].

Despite the statistically significant distances found, mostly involving the Xueta and Libyan populations, when a clustering algorithm was applied to these data, all individuals were equally assigned, reflecting an absence of differentiation between populations, evidenced by a K=1 as the best one to define this group of Jewish communities.

At this point, we already knew that our population of interest presents itself as a normal outbreeding population, without within substructure, and very genetically close and similar to non-Jewish Portuguese and other Jewish populations.

Then, we wanted to understand its relation with other worldwide populations, especially with European and Middle Eastern ones, under the light of slow mutating markers. The two mentioned populations had a special interest for us once they could be considered as the better candidates for parental populations.

Looking to the genetic distances, the close relation between the Bragança Jewish, the Miranda and the European populations is clear, either with F_{ST} distances or in the PCoA graph. In the latter, it is possible to see a close position between this cluster and the Middle Eastern group of populations. This result was not expected because the literature reports an equidistant position between the Jewish populations, and Europe and Middle East [44, 50].

A Principal Coordinates Analysis assessed only with the two ancestral populations and the Bragança Jewish community showed the Jewish populations much more closer to Europe than to Middle East.

Under a Structure analysis, the previously mentioned result was also achieved, although with less clarity. The distinction between Europe and Middle East was less clear, but present. This is due to the set of InDels used, once it was designed to improve differentiation among the 5 major continents only. Nevertheless, the Bragança Jewish population presented an admixture pattern much more similar to Europe than to Middle East.

Finally, it is important to note that, although none of our autosomal analyses was able to detect any kind of structure, we know that this population is not that homogenous, from previous results with lineage markers. They found that 41% of the mtDNA variation [18] and 53% of the ChrY variation [10] were of Middle East origin, producing an average of 47% in the gene

pool of this population. Considering that autosomes have an effective population size four times greater than the lineage markers, we expect than that this population presents 11.75% of autosomal Middle Eastern introgression. Since the human genome has about 3.2 Gbp [95] , it would represent a total amount of 378 Mbp of Middle Eastern ancestry per individual in the Bragança Jewish population's gene pool. Important to refer that these expected length are most likely fragmented.

Interestingly, the F_{ST} distance found between the Bragança Jews and the Portugal population with autosomal markers was four times greater than the one found for the ChrY markers [10].

In a sample with low levels of differentiation, the ability to detect substructure increases with the amount of data available, resulting both from the number and informativeness of the sample as well as from the number and informativeness of the markers. Increasing the number of autosomal markers used in Population Genetic studies has the potential to provide more detailed information that may help to resolve the population structure of Jewish populations and their historical neighbors [9, 50, 89]. So, the use of genome-wide microsatellite markers would be of great importance in the understanding and evaluation of the genetic relationships involving Jewish communities.

REFERENCES

[1] Steinhardt I: Raízes dos Judeus em Portugal: Entre Godos e Sarracenos. Lisboa: Nova Vega, 2012.

[2] Barnavi É: História Universal dos Judeus: Lisboa Contexto, 1992.

[3] Rodrigues MA: Judeus in Enciclopédia Luso-Brasileira de Cultura. Verbo, 1971.

[4] Levy-Coffman E: A Mosaic of People: The Jewish Story and the Reassessment of DNA Evidence. Journal of Genetic Genealogy 2005, 1:12-33.

[5] Ostrer H: A Genetic Profile of Contemporary Jewish Populations. Nature Reviews 2001, 2:891-7.

[6] Colonna V, Pagani L, Xue Y, Tyler-Smith C: A World in a Grain of Sand: Human History from Genetic Data. Genome Biology 2011, 12:234.

[7] Adams SM, Bosch E, Balaresque PL, Ballereau SJ, Lee AC, Arroyo E, López-Parra AM, Aler M, Grifo MSG, Brion M, Carracedo Á, Lavinha J, Martínez-Jarreta B, Quintana-Murci L, Picornell A, Ramon M, Skorecki K, Behar DM, Calafell F, Jobling MA: The Genetic Legacy of Religious Diversity and Intolerance: Paternal Lineages of Christians, Jews, and Muslims in the Iberian Peninsula. American Journal of Human Genetics 2008, 83:725-36.

[8] Ostrer H, Skorecki K: The Population Genetics of the Jewish People. Human genetics 2013, 132:119-27.

[9] Listman JB, Hasin D, Kranzler HR, Malison RT, Mutirangura A, Sughondhabirom A, Aharonovich E, Spivak B, Gelernter J: Identification of Population Substructure among Jews using STR Markers and Dependence on Reference Populations Included. BMC genetics 2010, 11:48.

[10] Nogueiro I, Manco L, Gomes V, Amorim A, Gusmão L: Phylogeographic Analysis of Paternal Lineages in NE Portuguese Jewish Communities. American journal of physical anthropology 2010, 141:373-81.

[11] Graen D: Oldest Jewish Archaeological Evidence on the Iberian Peninsula: Sensational Discovery by Archaeologists of Jena University at a Portuguese Excavation Site. Friedrich-Schiller Universitat Jena, 2012.

[12] Azevedo JLd: História dos Cristãos-Novos Portugueses: Clássica Editora, 1989.

[13] DellaPergola S: World Jewish Population, 2010. Current Jewish Population Reports. Edited by Bank BINAJD. University of Connecticut, 2010.

[14] INE: Censos 2011 Resultados Definitivos - Portugal. Lisboa: Instituto Nacional de Estatística, 2012.

[15] Nogueiro I, Gusmão L, Amorim A: Crypto-Jews From Trás-os-Montes, Portugal: A History Told By The Y Chromosome. HaLapid: Society for Crypto Judaic Studies, 2009.

[16] Martins J: Portugal e os Judeus: Nova Vega Limitada, 2006.

[17] Wilke CL: História dos Judeus Portugueses: Edições 70, 2009.

[18] Teixeira JC, Nogueiro I, Goios A, Gusmão L, Amorim A, Alvarez L: Mitochondrial DNA-Control Region Sequence Variation in the NE Portuguese Jewish Community. Forensic Science International: Genetics Supplement Series 2011, 3:e51-e2.

[19] Pignatelli M: A Comunidade Israelita de Lisboa: o Passado e o Presente na Construção da Etnicidade dos Judeus de Lisboa: Universidade Técnica de Lisboa, 2000.

[20] Canelo DA: The Last Crypto-Jews of Portugal: IJS, 1990.

[21] Garcia MA: Os Judeus de Belmonte: Os Caminhos da Memória: Universidade Nova de Lisboa, 1993.

[22] Azevedo EM: Cristãos Novos no Nordeste Transmontano: Asociación Caminos de Cervantes y Sefarad, 1994.

[23] Selections RsD: Enciclopédia Geográfica. Edited by Selections RsD. Reader's Digest Selections, 1989.

[24] Fernandes A: O Meu Nome é Bragança. Bragança, 2010.

[25] Lima A, Menéndez JA: Bragança, um olhar sobre a História, 2004.

[26] Cammack R, Attwood TK, Campbell PN, Parish JH, Smith AD, Stirling JL, Vella F: Oxford Dictionary of Biochemistry and Molecular Biology: Revised Edition. Oxford Dictionary. Edited by Editors TG. Oxford University Press, 2006.

[27] Teixeira J: Phylogeographic Analysis of Maternal Lineages in the Potuguese Jewish Community. Departamento de Biologia. Porto: Faculdade de Ciências da Universidade do Porto, 2011.

[28] Goodwin W, Linacre A, Hadi S: An Introduction to Forensic Genetics: John Wiley & Sons, 2007.

[29] Bastos-Rodrigues L, Pimenta JR, Pena SDJ: The Genetic Structure of Human Populations Studied through Short Insertion-Deletion Polymorphisms. Annals of human genetics 2006, 70:658-65.

[30] Barbujani G, Colonna V: Human genome diversity: frequently asked questions. Trends in Genetics 2010, 26:285-95.

[31] Butler JM: Forensic DNA Typing: Elsevier Academic Press, 2005.

[32] Sheffield VC, Stone EM, Carmi R: Use of Isolated Inbred Human Populations for Identification of Disease Genes. Trends in Genetics 1998, 14:391-6.

[33] Butler JM: Advanced Topics in Forensic DNA Typing: Methodology: Elsevier, 2011.

[34] Pereira R, Phillips C, Alves C, Amorim A, Carracedo Á, Gusmao L: A New Multiplex for Human Identification using Insertion/Deletion Polymorphisms. Electrophoresis 2009, 30:3682-90.

[35] Weber JL, David D, Heil J, Fan Y, Zhao C, Marth G: Human Diallelic Insertion/Deletion Polymorphisms. American Journal of Human Biology 2002, 71:854:62.

[36] Agrafioti I, Stumpf MPH: SNPSTR: a database of compound microsatellite-SNP markers. Nucleic Acids Research 2007, 35:D71-D5.

[37] Pereira R, Phillips C, Pinto N, Santos C, Santos SEBd, Amorim A, Carracedo Á, Gusmão L: Straightforward Inference of Ancestry and Admixture Proportions through Ancestry-Informative Insertion Deletion Multiplexing. PloS one 2012, 7:e29684.

[38] Ellegren H: Microsatellite Mutation in the Germline: Implications for Evolutionary Inference. TIG 2000, 16:551-7.

[39] Manta F, Caiafa A, Pereira R, Silva D, Amorim A, Carvalho EF, Gusmao L: Indel Markers: Genetic Diversity of 38 Polymorphisms in Brazilian Populations and Application in a Paternity Investigation with Post Mortem Material. Forensic science international Genetics 2012, 6:658-61.

[40] Jarne P, Lagoda PJL: Microsatellites, from Molecules to Populations and Back. Tree 1996, 11:424-9.

[41] Santos NPC, Ribeiro-Rodrigues EM, Ribeiro-Dos-Santos ÂKC, Pereira R, Gusmão L, Amorim A, Guerreiro JF, Zago MA, Matte C, Hutz MH, Santos SEB: Assessing Individual Interethnic Admixture and Population Substructure using a 48-Insertion-Deletion (INSEL) Ancestry-Informative Marker (AIM) Panel. Human mutation 2010, 31:184-90.

[42] Mills RE, Luttig CT, Larkins CE, Beauchamp A, Tsui C, Pittard WS, Devine SE: An Initial Map of Insertion and Deletion (INDEL) Variation in the Human Genome. Genome research 2006, 16:1182-90.

[43] Pereira R, Phillips C, Alves C, Amorim A, Carracedo Á, Gusmão L: Insertion/Deletion Polymorphisms: A Multiplex Assay and Forensic Applications. Forensic Science International: Genetics Supplement Series 2009, 2:513-5.

[44] Behar DM, Yunusbayev B, Metspalu M, Metspalu E, Rosset S, Parik J, Rootsi S, Chaubey G, Kutuev I, Yudkovsky G, Khusnutdinova EK, Balanovsky O, Semino O, Pereira L, Comas D, Gurwitz D, Bonne-Tamir B, Parfitt T, Hammer MF, Skorecki K, Villems R: The Genome-Wide Structure of the Jewish People. Nature 2010, 466:238-42.

[45] Rosenberg NA, Mahajan S, Ramachandran S, Zhao C, Pritchard JK, Feldman MW: Clines, Clusters, and the Effect of Study Design on the Inference of Human Population Structure. PLoS genetics 2005, 1:e70.

[46] Belle EMS, Landry P-A, Barbujani G: Origins and Evolution of the Europeans' Genome: Evidence from Multiple Microsatellite Loci. Proceedings Biological sciences / The Royal Society 2006, 273:1595-602.

[47] Tian C, Kosoy R, Nassir R, Lee A, Villoslada P, Klareskog L, Hammarstrom L, Henri-JeanGarchon, Pulver AE, Ransom M, Gregersen P, Seldin MF: European Population Genetic Substructure: Further Definition of Ancestry Informative Markers for Distinguishing among Diverse European Ethnic Groups. Molecular Medicine 2009, 15:371-83.

[48] Seldin MF, Shigeta R, Villoslada P, Selmi C, Tuomilehto J, Silva G, Belmont JW, Klareskog L, Gregersen PK: European Population Substructure: Clustering of Northern and Southern Populations. PLoS genetics 2006, 2:1339-51.

[49] Rosenberg NA, Pritchard JK, Weber JL, Cann HM, Kidd KK, Zhivotovsky LA, Feldman MW: Genetic Structure of Human Populations. Science 2002, 298:2381-4.

[50] Kopelman NM, Stone L, Wang C, Gefel D, Feldman MW, Hillel J, Rosenberg NA: Genomic Microsatellites Identify Shared Jewish Ancestry Intermediate between Middle Eastern and European Populations. BMC genetics 2009, 10:80.

[51] Bosch E, Calafell F, Comas D, Oefner PJ, Underhill PA, Bertranpetit J: High-Resolution Analysis of Human Y-Chromosome Variation Shows a Sharp Discontinuity and Limited Gene Flow between Northwestern Africa and the Iberian Peninsula. The American Journal of Human Genetics 2001, 68:1019-29.

[52] Barbujani G, Bertorelle G: Genetics and the Population History of Europe. PNAS 2001, 98:22-5.

[53] Lao O, Lu TT, Nothnagel M, Junge O, Freitag-Wolf S, Caliebe A, Balascakova M, Bertranpetit J, Bindoff LA, Comas D, Holmlund G, Kouvatsi A, Macek M, Mollet I, Parson W, Palo J, Ploski R, Sajantila A, Tagliabracci A, Gether U, Werge T, Rivadeneira F, Hofman A, Uitterlinden AG, Gieger C, Wichmann H-E, Rüther A, Schreiber S, Becker C, Nürnberg P, Nelson MR, Krawczak M, Kayser M: Correlation between Genetic and Geographic Structure in Europe. Current Biology 2008, 18:1241-8.

[54] Botigue LR, Henn BM, Gravel S, Maples BK, Gignoux CR, Corona E, Atzmon G, Burns E, Ostrer H, Flores C, Bertranpetit J, Comas D, Bustamante CD: Gene flow from North Africa contributes to differential human genetic diversity in southern Europe. Proceedings of the National Academy of Sciences of the United States of America 2013, 110:11791-6.

[55] Picornell A, Tomás C, Jiménez G, Castro JA, Ramon MM: Jewish Population Genetic Data in 20 Polymorphic Loci. Forensic Science International 2002, 125:52-8.

[56] Picornell A, Giménez P, Jiménez G, Castro JA, Ramon MM: Maternal and Paternal Contributions in Jewish Populations. International Congress Series 2004, 1261:383-5.

[57] Atzmon G, Hao L, Pe'er I, Velez C, Pearlman A, Palamara PF, Morrow B, Friedman E, Oddoux C, Burns E, Ostrer H: Abraham's Children in the Genome Era: Major Jewish Diaspora Populations Comprise Distinct Genetic Clusters with Shared Middle Eastern Ancestry. American Journal of Human Genetics 2010, 86:850-9.

[58] Tomàs C, Picornell A, Castro JA, Ramon MM, Gusmão L, Lareu MV, Carracedo Á: Genetic Variability at nine STR loci in the Chueta (Majorcan Jews) and the Balearic Populations Investigated by a Single Multiplex Reaction. International Journal of Legal Medicine 2000, 113:263-7.

[59] Marques S: Leonese Dialects in Portugal: Linguistic-Genetic Relationships through Y Chromosome Analysis. Departamento de Biologia. FCUP: Universidade do Porto, 2012.

[60] Mairal Q, Santos C, Silva M, Marques SL, Ramos A, Aluja MP, Amorim A, Prata MJ, Alvarez L: Linguistic isolates in Portugal: Insights from the mitochondrial DNA pattern. Forensic science international Genetics.

[61] Pinto J: Leonese Dialects in the Portuguese-Spanish border: A Population Genetic Study through the Analysis of X-Chromosomal Markers. Departamento de Biologia. FCUP: Universidade do Porto, 2011.

[62] Sambrook J, Fritsch EF, Maniatis T: Molecular Cloning: A Laboratory Manual. New York: Cold Spring Harbor Laboratory Press, 1989.

[63] Biosystems A: AmpFlSTR® Identifiler® Plus: PCR Amplification Kit. Life Technologies Corporatipon, 2012.

[64] Picornell A, Tomás C, Castro JA, Ramon MM: STR Data for 13 Loci from Jewish Populations. International Congress Series 2003, 1239:109-12.

[65] Santos C: Unpublished Data. University of Santiago de Compostela, 2013.

[66] Excoffier L, Lischer HEL: Arlequin suite ver 3.5: A new series of Programs to Perform Population Genetics Analyses under Linux and Windows. Molecular Ecology Resources 2010, 10:564-7.

[67] Nei M: Molecular Evolutionary Genetics: Columbia University Press, 1987.

[68] Guo SW, Thompson EA: Performing the Exact test of Hardy-Weinberg Proportion for Multiple Alleles. Biometrics 1992, 48:361-72.

[69] Levene H: On a Matching Problem Arising in Genetics. Annals of Mathematical Statistics 1949, 20:91-4.

[70] Slatkin M: Linkage Disequilibrium in Growing and Stable Populations. Genetics 1994:331-6.

[71] Slatkin M, Excoffier L: Testing for Linkage Disequilibrium in Genotypic Data using the EM Algorithm. Heredity 1996:377-83.

[72] Lewontin RC, Kojima K-I: The Evolutionary Dynamics of Complex Polymorphisms. Evolution 1960, 14:450-72.

[73] Raymond M, Rousset F: GENEPOP (Version 1.2): Population Genetics Software for Exact Tests and Ecumenicism. Journal of Heredity 1995, 86:248-9.

[74] Rousset F: Genepop007: a Complete re-Implementation of the Genepop Software for Windows and Linux. Molecular Ecology Resources 2008, 8:103-6.

[75] Bonferroni CE: Teoria Statistica delle Classi e Calcolo delle Probabilità. R Istituto Superiore di Scienze Economiche e Commerciali di Firenze 1936. pp. 3-62.

[76] Peakall R, Smouse PE: GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research—an update. Bioinformatics 2012, 28:2537-9.

[77] Pritchard JK, Stephens M, Donnelly P: Inference of Population Structure Using Multilocus Genotype Data. Genetics Society of America 2000, 155:945–59.

[78] Falush D, Stephens M, Pritchard JK: Inference of Population Structure Using Multilocus Genotype Data: Linked Loci and Correlated Allele Frequencies. Genetics Society of America 2003, 164:1567–87.

[79] Falush D, Stephens M, Pritchard JK: Inference of Population Structure using Multilocus Genotype Data: Dominant Markers and Null Alleles. Molecular Ecology Notes 2007.

[80] Hubisz MJ, Falush D, Stephens M, Pritchard JK: Inferring Weak Population Structure with the Assistance of Sample Group Information. Molecular Ecology Resources 2009, 9:1322-32.

[81] Slatkin M: A Measure of Population Subdivision Based on Microsatellite Allele Frequencies. Genetics 1995, 139:457-62.

[82] Weir BS, Cockerham CC: Estimating F-statistics for the Analysis of Population Structure. Evolution 1984, 38:1358-70.

[83] Weir BS: Genetic Data Analysis II: Methods for Discrete Population Genetic Data: Sinauer Assoc., Inc., 1996.

[84] Excoffier L, Smouse P, Quattro J: Analysis of Molecular Variance Inferred from Metric Distances among DNA Haplotypes: Application to Human Mitochondrial DNA Restriction Data. Genetics 1992, 131:479-91.

[85] Dupanloup I, Schneider S, Excoffier L: A simulated annealing approach to define the genetic structure of populations. Molecular Ecology 2002, 11:2571-81.

[86] Earl DA, vonHoldt BM: STRUCTURE HARVESTER: A Website and Program for Visualizing STRUCTURE Output and Implementing the Evanno Method. Conservation Genetics Resources 2012, 4:359-61.

[87] Durand E, Chen C, Françoies O: TESS version 2.3 - Reference Manual. 2009.

[88] Piry S, Alapetite A, Cornuet JM, Paetkau D, Baudouin L, Estoup A: GENECLASS2: a software for genetic assignment and first-generation migrant detection. The Journal of heredity 2004, 95:536-9.

[89] Rosenberg NA, Woolf E, Pritchard JK, Schaap T, Gefel D, Shpirer I, Lavi U, Bonné-Tamir B, Hillel J, Feldman MW: Distinctive genetic signatures in the Libyan Jews. Proceedings of the National Academy of Sciences 2001, 98:858-63.

[90] Amorim A, Alves C, Gusmão L, Pereira L: Extended Northern Portuguese Database on 21 Autosomal STRs used in Genetic Identification. International Congress Series 2006, 1288:364-6.

[91] Pinheiro MF, Cainé L, Pontes L, Abrantes D, Lima G, Pereira MJ, Rezende P: Allele Frequencies of Sixteen STRs in the Population of Northern Portugal. Forensic Science International 2005, 148:221-3.

[92] Vieira-Silva C, Cruz C, Ribeiro T, Espinheira R: South Portugal Population Genetic Analysis with 17 Loci STRs. International Congress Series 2006, 1288:367-8.

[93] Lopes V, Serra A, Gamero J, Sampaio L, Balsa F, Oliveira C, Batista L, Corte-Real F, Vieira DN, Vide MC, Anjos MJ, Carvalho M: Allelic Frequency Distribution of 17 STRs from Identifiler and PowerPlex-16 in Central Portugal area and the Azores Archipelago. Forensic science international Genetics 2009, 4:e1-7.

[94] Ramon M, Picornell A, Castro JA: Human Populations of the Balearic Islands: the Case of Chuetas and Ibizans. Contributions to Science 2008, 4:85-91.

[95] NCBI.

APPENDIX

Supplementary Table 1. Loci present in AmpFISTR® Identifiler Plus PCR Amplification kit, Applied Biosystems, with their respective chromosomal location, physical position, category and repeat motif, and allele range. Adapted from Butler, 2011 [33].

Locus	Chromosomal location	Physical position	Category and repeat motif	Allele range
D2S1338	2q35	Chr 2, 218 879 Mb	Compound TGCC/TTCC	10 to 31
D3S1358	3p21.31	Chr 3, 45 582 Mb	Compound TCTA/TCTG	6 to 26
D5S818	5q23.2	Chr 5, 123 111 Mb	Simple AGAT	4 to 29
D7S820	7q21.11	Chr 7, 83 789 Mb	Simple GATA	5 to 16
D8S1179	8q24.13	Chr 8, 125.907 Mb	Compound TCTA/TCTG	6 to 20
D13S317	13q31.1	Chr 13, 82 692 Mb	Simple TATC	5 to 17
D16S539	16q24.1	Chr 16, 86 386 Mb	Simple GATA	4 to 17
D18S51	18q21.33	Chr 18, 60 949 Mb	Simple AGAA	5.3 to 40
D19S433	19q12	Chr 19, 30 416 Mb	Compound AAGG/TAGG	5.2 to 20
D21S11	21q21.1	Chr 21, 20 554 Mb	Complex TCTA/TCTG	12 to 43.2
FGA	4q31.3 Alpha fibrinogen, 3rd intron	Chr 4, 155 509 Mb	Compound CTTT/TTCC	12.2 to 51.2
TH01	11p15.5 Tyrosine hydroxylase, 1st intron	Chr 11, 2.192 Mb	Simple TCAT	3 to 14
TPOX	2p25.3 Thyroid peroxidase, 10th intron	Chr 2, 1 493 Mb	Simple AATG	4 to 16
vWA	12p13.31 von Willebrand Factor, 40th intron	Chr 12, 6 093 Mb	Compound TCTA/TCTG	10 to 25
CSF1PO	5q33.1 c-fms proto-oncogene, 6th intron	Chr 5, 149 455 Mb	Simple AGAT	5 to 17

Supplementary Table 2. Characterization of the 46 AIM-InDels used. Extracted from Pereira et al. (2012) [37].

MID	rs number	Chromosome	Position (bp)	Allele described in dbSNP
MID-1470	rs2307666	11	64729920	-/GTTAC
MID-777	rs1610863	16	6551830	-/GAA
MID-196	rs16635	6	99789775	-/CAT
MID-881	rs1610965	5	79746093	-/ACTT
MID-3122	rs35451359	18	45110983	-/ATCT
MID-548	rs140837	6	3708909	-/CT
MID-659	rs1160893	2	224794577	-/CT
MID-2011	rs2308203	2	109401291	-/CTAGA
MID-2929	rs33974167	8	87813725	-/TA
MID-593	rs1160852	6	137345857	-/TT
MID-798	rs1610884	5	56122323	-/GGGAAA
MID-1193	rs2067280	5	89818959	-/AT
MID-1871	rs2308067	7	127291541	-/TT
MID-17	rs4183	3	3192524	-/TAAC
MID-2538	rs3054057	15	86010538	-/AACA
MID-1644	rs2307840	1	36099090	-/GT
MID-3854	rs60612424	6	84017514	-/TCTA
MID-2275	rs3033053	14	42554496	-/TCAGCAG
MID-94	rs16384	22	42045009	-/AAC
MID-3072	rs34611875	18	67623917	-/GCCCCCA
MID-772	rs1610859	5	128317275	-/TAG
MID-2313	rs3045215	1	234740917	-/ATTATAACT
MID-297	rs25621	6	139858158	-/TTCT
MID-1636	rs23077832	1	55590789	-/AA
MID-51	rs16343	4	17635560	-/TTTAT
MID-2431	rs3031979	8	73501951	-/ATTG
MID-2264	rs34122827	13	63778778	-/AAGT
MID-2256	rs133052	22	41042364	-/CAT
MID-128	rs6490	12	108127168	-/ATT
MID-15	rs4181	2	42577803	-/AAATACACAC
MID-2241	rs3030826	6	67176774	-/GTCCAATA
MID-419	rs140708	6	170720016	-/AATGGCA
MID-943	rs1611026	5	82545545	-/TGAT
MID-159	rs16438	20	25278470	-/CCCCA
MID-2005	rs2308161	10	69800909	-/AACAAT
MID-250	rs16687	7	83887882	-/CA
MID-1802	rs2307998	5	7814345	-/GGA
MID-1607	rs2307803	3	108981031	-/TG
MID-1734	rs2307930	6	84476378	-/CCAT
MID-406	rs25630	6	14734341	-/AG
MID-1386	rs2307582	1	247768775	-/AAACTATTCATTTTTCACCCT
MID-1726	rs2307922	1	39896964	-/CAAGAACTATAAT/ CACTATCTATTAT
MID-3626	rs11267926	15	45526069	-/AATATAATTTCTCCA
MID-360	rs25584	12	112145217	-/AA
MID-1603	rs2307799	5	70828427	-/TTGT
MID-2719	rs34541393	20	30701405	-/AACT

Supplementary Table 3. Allele frequencies by locus for Bragança Jews, Bragança and Miranda populations.

STR locus	Allele	Frequency		
		Bragança Jews	Bragança	Miranda
D2S1338				
	16	0.06604	0.04286	0.03448
	17	0.26415	0.30000	0.27011
	18	0.09434	0.09048	0.05747
	19	0.13208	0.08571	0.13793
	20	0.15094	0.15238	0.14943
	21	0.02830	0.02381	0.04023
	22	0.02830	0.03810	0.04023
	23	0.08491	0.07143	0.04598
	24	0.13208	0.12857	0.09770
	25	0.00943	0.05714	0.08621
	26	0.00943	0.00476	0.02874
	27	-	0.00476	0.01149
D3S1358				
	13	-	0.00476	-
	14	0.07547	0.10952	0.10345
	15	0.27358	0.30476	0.29885
	16	0.29245	0.23810	0.24138
	17	0.22642	0.17143	0.20115
	18	0.08491	0.15714	0.14368
	19	0.04717	0.01429	0.01149
D5S818				
	7	-	0.00476	-
	9	0.04717	0.01429	0.06322
	10	0.04717	0.08095	0.05747
	11	0.32075	0.34762	0.39080
	12	0.42453	0.40476	0.35632
	13	0.15094	0.14762	0.12644
	14	0.00943	-	-
	22	-	-	0.00575
D7S820				
	7	-	0.01905	0.00575
	8	0.14151	0.12381	0.18391
	9	0.13208	0.11429	0.13218
	10	0.27358	0.27143	0.25287
	11	0.27358	0.28095	0.28736
	12	0.14151	0.16190	0.11494
	13	0.03774	0.02857	0.01724
	14	-	-	0.00575
D8S1179				

	8	0.01887	-	0.00575
	9	-	0.00476	-
	10	0.10377	0.10952	0.06322
	11	0.11321	0.05714	0.09770
	12	0.10377	0.16190	0.13218
	13	0.33019	0.30000	0.36207
	14	0.05660	0.22381	0.20690
	15	0.23585	0.11429	0.09770
	16	0.03774	0.02381	0.03448
	17	-	0.00476	-
D13S317				
	8	0.09434	0.12381	0.09884
	9	0.10377	0.06667	0.06395
	10	0.03774	0.06190	0.03488
	11	0.34906	0.30952	0.37209
	12	0.25472	0.23810	0.26744
	13	0.08491	0.16190	0.09302
	14	0.07547	0.03333	0.06977
	15	-	0.00476	-
D16S539				
	8	0.00943	0.02381	0.04598
	9	0.09434	0.07619	0.16667
	10	0.05660	0.09048	0.09770
	11	0.44340	0.35714	0.23563
	12	0.25472	0.21905	0.27011
	13	0.12264	0.20000	0.14368
	14	0.01887	0.02857	0.03448
	15	-	0.00476	0.00575
D18S51				
	10	-	0.01905	-
	11	0.00943	0.01905	0.04023
	12	0.11321	0.10952	0.10345
	13	0.14151	0.14762	0.19540
	14	0.16981	0.17143	0.13218
	15	0.15094	0.10476	0.12644
	16	0.16038	0.13810	0.12644
	17	0.12264	0.11429	0.11494
	18	0.06604	0.09048	0.09195
	19	0.01887	0.04762	0.01149
	20	0.03774	0.01429	0.04023
	21	-	0.01429	0.01149
	22	-	0.00476	0.00575
	23	-	0.00476	-
	24	0.00943	-	-
D19S433				

	10	-	-	0.01163
	11	-	0.00952	0.02907
	12	0.11765	0.04762	0.15116
	12.2	-	0.00952	0.00581
	13	0.2451	0.29524	0.24419
	13.2	0.0098	0.01905	0.01162
	14	0.19608	0.29524	0.21512
	14.2	0.01961	0.02381	0.00581
	15	0.17647	0.15714	0.18605
	15.2	0.11765	0.04762	0.06395
	16	0.04902	0.04286	0.0407
	16.2	0.06863	0.03333	0.02907
	17	-	0.00476	0.00581
	17.2	-	0.01429	-
D21S11				
	24.2	-	0.00476	-
	25	-	-	0.01156
	27	-	0.03810	0.01734
	28	0.19811	0.10000	0.12139
	29	0.18868	0.16667	0.23121
	30	0.21698	0.26190	0.30636
	30.2	0.05660	0.05238	0.01156
	31	0.04717	0.09048	0.06936
	31.2	0.14151	0.11429	0.10983
	32	0.00943	0.03810	0.00578
	32.2	0.08491	0.10000	0.09249
	33.2	0.05660	0.02857	0.01734
	34.2	-	-	0.00578
	36	-	0.00476	-
FGA				
	18	-	0.01905	0.01163
	19	0.06604	0.08571	0.09884
	20	0.17925	0.12381	0.16860
	21	0.18868	0.21429	0.20930
	22	0.24528	0.15238	0.14535
	22.2	-	0.00952	-
	22.3	-	-	0.00581
	23	0.05660	0.17619	0.12791
	24	0.12264	0.12381	0.12791
	25	0.07547	0.05238	0.07558
	26	0.01887	0.03810	0.02326
	27	0.04717	-	0.00581
	44.2	-	0.00476	-
TH01				
	5	0.00943	-	-

	6	0.24528	0.22857	0.24138
	7	0.05660	0.13333	0.12069
	8	0.16038	0.17619	0.12644
	9	0.22642	0.20952	0.25862
	9.3	0.28302	0.23333	0.21839
	10	0.01887	0.01905	0.03448
TPOX				
	7	-	-	0.00578
	8	0.46226	0.48095	0.54335
	9	0.13208	0.12857	0.10983
	10	0.11321	0.10000	0.08671
	11	0.26415	0.27143	0.24277
	12	0.02830	0.01429	0.01156
	13	-	0.00476	-
vWA				
	13	-	-	0.01149
	14	0.06604	0.10952	0.09195
	15	0.14151	0.14286	0.13218
	16	0.24528	0.29048	0.22414
	17	0.22642	0.22857	0.28736
	18	0.21698	0.17143	0.15517
	19	0.04717	0.05238	0.09195
	20	0.05660	0.00476	0.00575
CSF1PO				
	7	-	0.00476	-
	8	-	0.00476	-
	9	0.04717	0.03333	0.01744
	10	0.26415	0.24762	0.25000
	11	0.22642	0.31429	0.36628
	12	0.37736	0.29524	0.33140
	13	0.07547	0.08095	0.03488
	14	0.00943	0.01429	-
	15	-	0.00476	-

Supplementary Table 4. Observed and expected heterozygosities, and *p* value for the Hardy-Weinberg Equilibrium by locus and by population.

			Obs.Het.	**Exp.Het.**	**HWE**
Portugal	Bragança	D2S1338	0.80000	0.84648	0.1553
		D3S1358	0.82857	0.78788	0.2320
		D5S818	0.65714	0.69004	0.4037
		D7S820	0.80952	0.79540	0.7721
		D8S1179	0.81905	0.80861	0.2491
		D13S317	0.79048	0.80036	0.5534

			Obs.Het.	Exp.Het.	HWE
		D16S539	0.75238	0.77275	0.9431
		D18S51	0.89524	0.88631	0.4750
		D195433	0.74286	0.79594	0.3764
		D21S11	0.80000	0.85997	0.0705
		FGA	0.86667	0.86124	0.6071
		TH01	0.75238	0.80406	0.8736
		TPOX	0.68571	0.67145	0.2881
		vWA	0.77143	0.80264	0.9562
		CSF1PO	0.68571	0.74837	0.1566
	Miranda	D2S1338	0.75862	0.86287	0.3090
		D3S1358	0.81609	0.78500	0.4379
		D5S818	0.74713	0.70102	0.6896
		D7S820	0.73563	0.79317	0.1972
		D8S1179	0.83908	0.78885	0.0963
		D13S317	0.80233	0.76588	0.8034
		D16S539	0.74713	0.81490	0.1127
		D18S51	0.85057	0.88154	0.2335
		D195433	0.74118	0.83442	**0.0057***
		D21S11	0.81395	0.81631	**0.0469***
		FGA	0.83721	0.86271	0.4505
		TH01	0.77011	0.80905	0.3436
		TPOX	0.60465	0.62972	0.4939
		vWA	0.75862	0.81324	0.1425
		CSF1PO	0.70930	0.69604	0.2089
	Bragança Jews	D2S1338	0.69811	0.85840	0.0930
		D3S1358	0.69811	0.78059	0.2341
		D5S818	0.69811	0.69614	0.2833
		D7S820	0.81132	0.79892	0.8928
		D8S1179	0.75472	0.80359	0.2897
		D13S317	0.66038	0.78670	0.1168
		D16S539	0.64151	0.71770	0.1521
		D18S51	0.86792	0.87673	0.6271
		D195433	0.60784	0.84333	**0.0039***
		D21S11	0.81132	0.85013	0.5487
		FGA	0.90566	0.84924	0.7104
		TH01	0.71698	0.78652	0.7027
		TPOX	0.62264	0.69200	0.0547
		vWA	0.77358	0.81941	0.2122
		CSF1PO	0.56604	0.73549	**0.0138***
Mediterranean Jews	Libyan	D3S1358	0.84615	0.73538	0.5795
		D5S818	0.61538	0.76000	0.1960
		D7S820	0.69231	0.66154	0.8360
		D8S1179	0.69231	0.81538	0.0861
		D13S317	0.61538	0.75692	0.5380

			Obs.Het.	Exp.Het.	HWE
		D18S51	0.92308	0.88000	0.9504
		D21S11	0.76923	0.75385	0.4518
		FGA	0.69231	0.81231	0.4961
		vWA	0.84615	0.70154	0.5761
	Moroccan	D3S1358	0.69231	0.84923	0.2734
		D5S818	0.69231	0.75692	0.8289
		D7S820	0.53846	0.80923	0.0599
		D8S1179	0.84615	0.81538	0.8680
		D13S317	0.76923	0.83385	0.6772
		D18S51	0.84615	0.88000	0.1708
		D21S11	0.76923	0.79077	0.5746
		FGA	0.84615	0.85231	0.5645
		vWA	0.84615	0.77846	1.0000
	Tunisian	D3S1358	0.76923	0.73538	0.8552
		D5S818	0.84615	0.75692	0.9470
		D7S820	0.69231	0.79692	0.5728
		D8S1179	0.84615	0.71385	0.9314
		D13S317	0.69231	0.76308	0.2206
		D18S51	0.76923	0.88000	0.2020
		D21S11	0.92308	0.86462	0.8958
		FGA	0.84615	0.85538	0.8130
		vWA	0.84615	0.81538	**0.0284***
	Sephardic (from Turkey)	D3S1358	0.77143	0.76190	0.6232
		D5S818	0.80000	0.75611	0.2010
		D7S820	0.80000	0.79255	0.3911
		D8S1179	0.71429	0.80414	0.0529
		D13S317	0.64706	0.77656	0.0952
		D18S51	0.85294	0.84241	0.5077
		D21S11	0.88571	0.83520	0.8483
		FGA	0.91429	0.86046	0.3190
		vWA	0.80000	0.79503	0.7774
	Xuetas	D3S1358	0.74510	0.77770	0.7377
		D5S818	0.76471	0.77736	0.6549
		D7S820	0.84314	0.79059	0.3245
		D8S1179	0.85294	0.83845	0.0575
		D13S317	0.69608	0.72762	0.4602
		D18S51	0.88235	0.87323	0.0556
		D21S11	0.71569	0.82677	**0.0033***
		FGA	0.92157	0.85956	0.4301
		vWA	0.83333	0.82536	0.1649
Northern European Jews	Ashkenazi	D3S1358	0.84000	0.80327	0.6050
		D5S818	0.76000	0.70776	0.2888
		D7S820	0.88000	0.83673	0.4613
		D8S1179	0.84000	0.80980	0.9853
		D13S317	0.80000	0.80980	0.1481

			Obs.Het.	Exp.Het.	HWE
		D18S51	0.84000	0.87592	0.3815
		D21S11	0.80000	0.76408	0.4270
		FGA	0.80000	0.81714	0.5290
		vWA	0.84000	0.78939	0.5842
Middle Eastern Jews	Iranian	D3S1358	0.58333	0.74275	0.4443
		D5S818	0.66667	0.75725	0.7791
		D7S820	0.83333	0.74638	0.4735
		D8S1179	0.83333	0.82971	0.9088
		D13S317	0.75000	0.76449	0.6995
		D18S51	0.83333	0.84058	0.3026
		D21S11	0.91667	0.90580	0.3601
		FGA	0.91667	0.86232	0.2574
		vWA	0.58333	0.78986	0.2982
	Iraqi	D3S1358	0.76923	0.77231	0.1033
		D5S818	0.61538	0.76615	0.8070
		D7S820	0.76923	0.81231	0.3021
		D8S1179	0.61538	0.80000	0.2053
		D13S317	0.84615	0.79385	0.2945
		D18S51	0.69231	0.78769	0.5369
		D21S11	0.92308	0.82462	0.9975
		FGA	0.92308	0.82462	0.8789
		vWA	0.69231	0.80000	0.2508

Supplementary Table 5. Allele frequencies for the Jewish and Miranda populations typed with InDels.

InDel locus	Allele	Frequency	
		Bragança Jews	Miranda
MID-1470	1	0.56731	0.61864
	2	0.43269	0.38136
MID-777	1	0.40385	0.30833
	2	0.59615	0.69167
MID-196	1	0.48077	0.50833
	2	0.51923	0.49167
MID-881	1	0.875	0.86667
	2	0.125	0.13333
MID-3122	1	0.99038	1
	2	0.0096154	-
MID-548	1	0.096154	0.2
	2	0.90385	0.8
MID-659	1	0.18269	0.11667
	2	0.81731	0.88333

InDel locus	Allele	Frequency	
		Bragança Jews	Miranda
MID-2011	1	0.84615	0.75
	2	0.15385	0.25
MID-2929	1	0.75962	0.59167
	2	0.24038	0.40833
MID-593	1	0.028846	0.033333
	2	0.97115	0.96667
MID-798	1	0.68269	0.625
	2	0.31731	0.375
MID-1193	1	0.19231	0.1
	2	0.80769	0.9
MID-1871	1	0.22115	0.24167
	2	0.77885	0.75833
MID-17	1	0.24038	0.28333
	2	0.75962	0.71667
MID-2538	1	0.39423	0.41667
	2	0.60577	0.58333
MID-1644	1	1	0.94167
	2	-	0.058333
MID-3854	1	0.038462	0.125
	2	0.96154	0.875
MID-2275	1	0.096154	0.10833
	2	0.90385	0.89167
MID-94	1	0.25962	0.25424
	2	0.74038	0.74576
MID-3072	1	0.99038	0.91667
	2	0.0096154	0.083333
MID-772	1	0.97115	0.91667
	2	0.028846	0.083333
MID-2313	1	0.26923	0.25833
	2	0.73077	0.74167
MID-297	1	0.75	0.8
	2	0.25	0.2
MID-1636	1	0.75962	0.73333
	2	0.24038	0.26667
MID-51	1	0.68269	0.60833
	2	0.31731	0.39167
MID-2431	1	0.096154	0.091667
	2	0.90385	0.90833
MID-2264	1	0.44231	0.58333
	2	0.45192	0.39167
	2-T	0.10577	0.025

InDel locus	Allele	Frequency	
		Bragança Jews	Miranda
MID-2256	1	0.17308	0.29167
	2	0.82692	0.70833
MID-128	1	0.46154	0.475
	2	0.53846	0.525
MID-15	1	0.46154	0.425
	2	0.53846	0.575
MID-2241	1	0.23077	0.21667
	2	0.76923	0.78333
MID-419	1	0.83654	0.84167
	2	0.16346	0.15833
MID-943	1	0.75962	0.775
	2	0.24038	0.225
MID-159	1	0.54808	0.50833
	2	0.45192	0.49167
MID-2005	1	0.56731	0.64167
	2	0.43269	0.35833
MID-250	1	0.74038	0.69167
	2	0.25962	0.30833
MID-1802	1	-	0.058333
	2	1	0.94167
MID-1607	1	0.18627	0.19167
	2	0.81373	0.80833
MID-1734	1	0.82692	0.75833
	2	0.17308	0.24167
MID-406	1	0.65385	0.73333
	2	0.34615	0.26667
MID-1386	1	0.16346	0.225
	2	0.83654	0.775
MID-1726	1	0.65385	0.75833
	2	0.34615	0.24167
MID-3626	1	0.77885	0.675
	2	0.22115	0.325
MID-360	1	0.81731	0.86667
	2	0.18269	0.13333
MID-1603	1	0.43269	0.39167
	2	0.56731	0.60833
MID-2719	1	0.32692	0.275
	2	0.67308	0.725

Supplementary Table 6. Expected and Observed Heterozygosities for Bragança Jewish and Miranda populations with InDels.

Locus	Bragança Jewish		Miranda	
	Observed Heterozygosity	Expected Heterozygosity	Observed Heterozygosity	Expected Heterozygosity
MID-1470	0.44231	0.49571	0.49153	0.47588
MID-777	0.61538	0.48618	0.41667	0.43011
MID-196	0.57692	0.50411	0.48333	0.50406
MID-881	0.21154	0.22087	0.26667	0.23305
MID-3122	0.01923	0.01923	This locus is monomorphic	
MID-548	0.15385	0.17550	0.40000	0.32269
MID-659	0.28846	0.30153	0.20000	0.20784
MID-2011	0.19231	0.26288	0.43333	0.37815
MID-2929	0.25000	0.36875	0.55000	0.48725
MID-593	0.05769	0.05657	0.06667	0.06499
MID-798	0.44231	0.43745	0.35000	0.47269
MID-1193	0.26923	0.31367	0.20000	0.18151
MID-1871	0.32692	0.34783	0.31667	0.36961
MID-17	0.36538	0.36875	0.46667	0.40952
MID-2538	0.48077	0.48226	0.50000	0.49020
MID-1644	This locus is monomorphic		0.08333	0.11078
MID-3854	0.07692	0.07468	0.21667	0.22059
MID-2275	0.15385	0.17550	0.18333	0.19482
MID-94	0.36538	0.38816	0.30508	0.38244
MID-3072	0.01923	0.01923	0.16667	0.15406
MID-772	0.05769	0.05657	0.16667	0.15406
MID-2313	0.38462	0.39731	0.35000	0.38641
MID-297	0.38462	0.37864	0.23333	0.32269
MID-1636	0.36538	0.36875	0.33333	0.39440
MID-51	0.48077	0.43745	0.51667	0.48053
MID-2431	0.15385	0.17550	0.18333	0.16793
MID-2264	0.63462	0.59466	0.48333	0.50994
MID-2256	0.26923	0.28902	0.48333	0.41667
MID-128	0.34615	0.50187	0.48333	0.50294
MID-15	0.61538	0.50187	0.48333	0.49286
MID-2241	0.38462	0.35848	0.36667	0.34230
MID-419	0.28846	0.27614	0.28333	0.26877
MID-943	0.36538	0.36875	0.41667	0.35168
MID-159	0.44231	0.50019	0.45000	0.50406
MID-2005	0.55769	0.49571	0.45000	0.46373
MID-250	0.36538	0.38816	0.41667	0.43011
MID-1802	This locus is monomorphic		0.08333	0.11078
MID-1607	0.33333	0.30615	0.31667	0.31246
MID-1734	0.34615	0.28902	0.41667	0.36961
MID-406	0.42308	0.45706	0.30000	0.39440
MID-1386	0.28846	0.27614	0.31667	0.35168
MID-1726	0.46154	0.45706	0.35000	0.36961
MID-3626	0.40385	0.34783	0.51667	0.44244

Locus	Bragança Jewish		Miranda	
	Observed Heterozygosity	Expected Heterozygosity	Observed Heterozygosity	Expected Heterozygosity
MID-360	0.36538	0.30153	0.26667	0.23305
MID-1603	0.48077	0.49571	0.35000	0.48053
MID-2719	0.30769	0.44436	0.41667	0.40210
Mean	0.33668	0.34006	0.34511	0.34991
s.d.	0.15790	0.14555	0.12965	0.12663

Supplementary Table 7. P value for the Hardy-Weinberg Equilibrium for the BragançaJewish and Miranda populations with InDels.

Locus	Bragança Jews	Miranda
MID-1470	0,5726	1
MID-777	0,0823	1
MID-196	0,4033	0,6119
MID-881	0,5746	0,5807
MID-3122	No information	No information
MID-548	0,3798	0,4283
MID-659	0,6643	1
MID-2011	0,0808	0,4821
MID-2929	0,0492	0,5967
MID-593	1	1
MID-798	1	0,0568
MID-1193	0,3668	1
MID-1871	0,6925	0,4878
MID-17	1	0,5163
MID-2538	1	0,7942
MID-1644	No information	0,1701
MID-3854	1	1
MID-2275	0,3791	0,5165
MID-94	0,7219	0,1655
MID-3072	No information	1
MID-772	1	1
MID-2313	1	0,7398
MID-397	1	0,105
MID-1636	1	0,507
MID-51	0,535	0,5967
MID-2431	0,3788	1
MID-2264	0,3936	1
MID-2256	0,6329	0,3483
MID-128	0,0286	0,6116
MID-15	0,1602	1

Locus	Bragança Jews	Miranda
MID-2241	0,7119	0,7158
MID-419	1	1
MID-943	1	0,154
MID-159	0,4163	0,4468
MID-2005	0,4054	1
MID-250	0,7222	0,7604
MID-1802	No information	0,1685
MID-1607	1	1
MID-1734	0,3256	0,4806
MID-406	0,7579	0,0944
MID-1386	1	0,4413
MID-1726	1	1
MID-3626	0,4189	0,2435
MID-360	0,1818	0,5795
MID-1603	1	0,054
MID-2719	0,0317	1

Supplementary Table 8. *p* values for all pairs of loci tested for pairwise association, on the Portuguese populations. All the statistical significant values are highlighted in bold. Those significant ($p<0.05$) are labeled with an asterisk and those values that remain significant after the Bonferroni correction with two asterisks.

		Bragança	Miranda	Bragança Jews
D2S1338	D3S1358	0.43212	0.649119	0.710914
D2S1338	D5S818	0.632599	0.120230	0.36392
D3S1358	D5S818	0.272304	0.227182	0.598836
D2S1338	D7S820	0.145939	0.495068	0.766963
D3S1358	D7S820	0.381711	0.836433	0.701548
D5S818	D7S820	0.21865	0.094014	0.622006
D2S1338	D8S1179	0.267891	0.064279	0.362877
D3S1358	D8S1179	0.762304	**0.042749***	0.994947
D5S818	D8S1179	0.537019	0.064734	0.926179
D7S820	D8S1179	**0.001119***	0.491524	0.122276
D2S1338	D13S317	**0.001475***	0.161348	0.075712
D3S1358	D13S317	0.8903	0.078457	0.291965
D5S818	D13S317	0.196585	0.366916	0.414491
D7S820	D13S317	0.294841	0.783760	0.489698
D8S1179	D13S317	**0.048809***	**0.025153***	0.621651
D2S1338	D16S539	**0.000269***	0.089069	0.897275
D3S1358	D16S539	0.372189	0.178582	0.208235
D5S818	D16S539	0.685158	0.239718	0.35783
D7S820	D16S539	**0.036771***	0.194696	0.081006
D8S1179	D16S539	0.674637	0.280024	0.2214
D13S317	D16S539	0.074298	0.092760	0.91227

		Bragança	Miranda	Bragança Jews
D2S1338	D18S51	0.072637	0.393229	0.058103
D3S1358	D18S51	0.92695	0.587378	0.137327
D5S818	D18S51	0.097359	0.409353	0.713757
D7S820	D18S51	**0.000866***	0.116521	0.668196
D8S1179	D18S51	**0.013611***	0.873845	0.379617
D13S317	D18S51	0.84494	0.261530	0.714362
D16S539	D18S51	0.75613	**0.030232***	0.945152
D2S1338	D195433	0.135019	0.198022	**0.021815***
D3S1358	D195433	**0.026508***	0.113144	0.274264
D5S818	D195433	0.184036	0.658886	0.059746
D7S820	D195433	0.603589	0.136472	0.987095
D8S1179	D195433	0.31958	**0.009887***	0.114466
D13S317	D195433	0.223397	0.290420	**0.01011***
D16S539	D195433	0.102791	0.067771	0.579323
D18S51	D195433	0.527297	0.187792	1
D2S1338	D21S11	**0.012247***	0.159913	0.789184
D3S1358	D21S11	0.068072	0.777195	0.483037
D5S818	D21S11	0.375196	0.747793	0.395155
D7S820	D21S11	0.11239	0.324864	0.966526
D8S1179	D21S11	0.565808	0.056680	0.957995
D13S317	D21S11	0.132758	0.438501	**0.041442***
D16S539	D21S11	0.101039	0.356592	0.589186
D18S51	D21S11	0.145623	0.182923	1
D195433	D21S11	0.742114	0.395269	0.611208
D2S1338	FGA	0.062928	0.308895	0.526066
D3S1358	FGA	0.519038	**0.036949***	0.422899
D5S818	FGA	0.409667	0.729386	0.649382
D7S820	FGA	**0.011486***	0.062589	0.497855
D8S1179	FGA	**0.027292***	0.209498	0.055072
D13S317	FGA	0.104371	0.962724	0.58367
D16S539	FGA	0.297184	**0.031494***	0.055437
D18S51	FGA	**0****	0.167375	0.164431
D195433	FGA	0.268097	0.123202	0.899538
D21S11	FGA	0.06142	0.909142	1
D2S1338	TH01	**0.027845***	0.754828	0.280884
D3S1358	TH01	0.687264	0.911237	0.319984
D5S818	TH01	0.411825	0.748190	0.672628
D7S820	TH01	0.220731	0.723052	0.261988
D8S1179	TH01	0.261129	0.237305	0.784106
D13S317	TH01	0.11468	0.855170	0.453194
D16S539	TH01	0.316057	**0.018028***	0.626718
D18S51	TH01	0.349508	0.203116	0.940269
D195433	TH01	0.145545	0.304177	0.990636

		Bragança	Miranda	Bragança Jews
D21S11	TH01	0.123397	0.148395	0.230699
FGA	TH01	0.480368	0.054386	0.747798
D2S1338	TPOX	0.462242	0.352407	0.340766
D3S1358	TPOX	0.753736	0.636666	0.462053
D5S818	TPOX	0.600169	0.273849	0.060744
D7S820	TPOX	0.372289	0.311074	0.291435
D8S1179	TPOX	0.638159	0.577700	0.255739
D13S317	TPOX	0.314695	0.556035	0.436906
D16S539	TPOX	0.241893	0.814867	0.826436
D18S51	TPOX	0.574682	0.183322	0.843457
D195433	TPOX	**0.02902***	0.595349	0.903295
D21S11	TPOX	0.456521	0.616610	0.7349
FGA	TPOX	0.35209	0.288775	0.436441
TH01	TPOX	0.577901	0.089324	**0.020087***
D2S1338	vWA	**0.001258***	0.325016	0.927669
D3S1358	vWA	0.733524	0.323239	0.324481
D5S818	vWA	0.344651	0.059120	0.243528
D7S820	vWA	0.228456	0.203295	0.675991
D8S1179	vWA	0.13064	**0.008704***	0.611641
D13S317	vWA	0.165248	0.312988	0.998414
D16S539	vWA	0.0696	0.149731	0.989285
D18S51	vWA	0.096731	0.623932	0.295383
D195433	vWA	**0.016754***	0.783058	0.232857
D21S11	vWA	**0.000594***	0.494852	0.939773
FGA	vWA	0.06989	**0.040419***	0.821289
TH01	vWA	0.154068	0.062420	0.362883
TPOX	vWA	0.398015	0.451070	0.727643
D2S1338	CSF1PO	0.174754	0.416716	0.651705
D3S1358	CSF1PO	0.744665	0.059942	0.720401
D5S818	CSF1PO	0.392194	0.362380	0.207173
D7S820	CSF1PO	**0.020232***	0.533462	0.571988
D8S1179	CSF1PO	0.973075	**0.040728***	0.852373
D13S317	CSF1PO	0.359554	0.052763	0.634412
D16S539	CSF1PO	0.286229	0.642628	**0.022842***
D18S51	CSF1PO	0.310108	0.468410	0.260934
D195433	CSF1PO	**0.023245***	0.895396	0.590771
D21S11	CSF1PO	0.444334	0.871654	0.921673
FGA	CSF1PO	0.11708	0.404050	0.326363
TH01	CSF1PO	0.834499	0.509363	0.063342
TPOX	CSF1PO	0.521687	0.939500	0.95632
vWA	CSF1PO	0.121343	0.101152	0.797828

Supplementary Table 9. *p* values for all pairs of loci tested for the pairwise association, on all non-Portuguese populations. All the statistical significant values are highlighted in bold. Those significant ($p<0.05$) are labeled with an asterisk and those values that remain significant after the Bonferroni correction with two asterisks.

		Xuetas	Tunisian	Sephardic	Moroccan	Libyan	Iraqi	Iranian	Ashkenazi
D3S1358	D5S818	0.102066	1	0.785227	1	0.611287	1	1	0.614267
D3S1358	D7S820	0.433906	0.404671	0.190897	1	0.835349	1	1	0.651625
D5S818	D7S820	0.102038	0.32138	0.558863	1	1	1	0.425255	0.417641
D3S1358	D8S1179	**0.017359***	0.656911	0.981125	1	0.554267	0.431887	1	1
D5S818	D8S1179	0.191974	0.564777	0.385052	0.168867	1	1	1	0.719735
D7S820	D8S1179	**0****	0.357177	0.085347	0.15077	0.520109	1	1	1
D3S1358	D13S317	0.217517	0.620641	0.6157	1	1	0.213575	0.278596	0.372258
D5S818	D13S317	0.119379	1	0.340042	1	1	1	1	0.894272
D7S820	D13S317	0.209241	0.332123	0.311194	1	0.520042	1	1	0.285326
D8S1179	D13S317	0.262502	0.571765	0.589226	1	1	1	1	0.264133
D3S1358	D18S51	**0.014782***	1	0.265463	1	0.141539	0.436585	0.268629	0.393738
D5S818	D18S51	0.381909	1	0.101335	1	1	1	0.231046	0.766203
D7S820	D18S51	0.22877	1	0.079403	0.131973	1	1	0.42048	0.352759
D8S1179	D18S51	0.066213	1	0.649296	1	1	0.213446	1	0.338931
D13S317	D18S51	0.484246	1	0.29761	1	1	1	1	1
D3S1358	D21S11	**0.02863***	0.203752	**0.033271***	1	0.689037	0.226442	1	1
D5S818	D21S11	0.238871	1	0.25173	1	1	1	1	0.994805
D7S820	D21S11	**0.030145***	0.09568	0.874543	1	0.183018	1	**0.010263***	0.763365
D8S1179	D21S11	0.054073	1	0.102725	1	0.37877	1	1	0.336175
D13S317	D21S11	0.059947	1	0.214034	1	1	1	1	0.861441
D18S51	D21S11	0.062667	1	0.304083	0.165753	1	1	1	1
D3S1358	FGA	**0.033978***	0.241855	0.618257	1	0.384338	1	0.284236	0.662346
D5S818	FGA	0.118726	1	0.324183	1	0.227424	0.163798	1	0.713001
D7S820	FGA	**0.037086***	1	**0.005787***	1	1	1	1	**0.036686***
D8S1179	FGA	**0.000965****	1	0.051499	1	1	0.204102	1	0.554331

		Xuetas	Tunisian	Sephardic	Moroccan	Libyan	Iraqi	Iranian	Ashkenazi
D13S317	FGA	**0.029543***	1	0.564909	1	1	1	1	0.674533
D18S51	FGA	**0****	1	0.705706	1	1	1	0.237136	1
D21S11	FGA	0.592384	1	0.71093	1	0.251957	1	1	0.744732
D3S1358	vWA	**0.025152***	0.278121	0.140487	1	0.911711	1	0.214841	1
D5S818	vWA	0.125089	0.188294	0.964967	1	0.679866	1	1	0.321226
D7S820	vWA	0.320347	1	0.825883	1	0.418437	1	1	0.70074
D8S1179	vWA	0.403833	0.709007	0.787467	1	1	1	1	0.691577
D13S317	vWA	0.17955	1	0.479338	1	1	1	0.152813	0.132608
D18S51	vWA	0.227246	0.251136	0.856061	0.1477	1	1	1	0.098277
D21S11	vWA	0.286614	1	0.85651	0.191368	1	1	1	1
FGA	vWA	0.164837	1	0.55321	0.131338	0.41072	1	1	0.692093

Supplementary Table 10. *p* value for the pairwise association between the two Portuguese populations with InDels. All the statistical significant values are highlighted in bold. Those significant ($p<0.05$) are labeled with an asterisk and those values that remain significant after the Bonferroni correction with two asterisks.

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-1470	MID-777	0,74991	0,001194	0,859387	0,00086
MID-1470	MID-196	0,255752	0,001567	0,889116	0,000786
MID-777	MID-196	0,073202	0,000905	0,785712	0,001262
MID-1470	MID-881	0,671023	0,001554	0,327826	0,001278
MID-777	MID-881	0,20236	0,001503	0,623237	0,001171
MID-196	MID-881	0,842829	0,001107	0,137486	0,001005
MID-1470	MID-3122	1	0	No contingency	
MID-777	MID-3122	1	0	No contingency	
MID-196	MID-3122	1	0	No contingency	
MID-881	MID-3122	1	0	No contingency	
MID-1470	MID-548	0,044169	0,000794	0,350015	0,002031
MID-777	MID-548	0,144682	0,001406	0,465045	0,002198
MID-196	MID-548	0,331725	0,001731	0,526388	0,002061
MID-881	MID-548	0,785187	0,00141	0,144827	0,001356
MID-3122	MID-548	1	0	No contingency	
MID-1470	MID-659	0,019698	0,000506	0,163592	0,001631
MID-777	MID-659	0,06714	0,000932	0,952495	0,000526
MID-196	MID-659	0,514463	0,001907	0,422759	0,002064
MID-881	MID-659	1	0	1	0
MID-3122	MID-659	1	0	No contingency	
MID-548	MID-659	0,296724	0,001882	0,161609	0,001882
MID-1470	MID-2011	0,884957	0,000682	0,779929	0,001277
MID-777	MID-2011	0,430283	0,001577	0,123957	0,001467
MID-196	MID-2011	0,626653	0,001348	0,696062	0,001509
MID-881	MID-2011	0,086521	0,001058	0,407451	0,001562
MID-3122	MID-2011	1	0	No contingency	
MID-548	MID-2011	0,823272	0,001182	0,762309	0,001618
MID-659	MID-2011	0,005202	0,000207	0,496824	0,002286
MID-1470	MID-2929	0,625098	0,001443	0,708774	0,001418
MID-777	MID-2929	0,261725	0,001537	0,518848	0,001679
MID-196	MID-2929	0,365121	0,0016	0,481118	0,001815
MID-881	MID-2929	0,303535	0,001855	0,917513	0,00042
MID-3122	MID-2929	1	0	No contingency	
MID-548	MID-2929	0,013958	0,000393	0,216937	0,001878
MID-659	MID-2929	0,653883	0,001596	0,875611	0,000959
MID-2011	MID-2929	0,846077	0,00093	0,363194	0,001993
MID-1470	MID-593	0,793968	0,000581	0,843239	0,000532
MID-777	MID-593	1	0	0,098616	0,000706
MID-196	MID-593	0,838783	0,000574	0,262848	0,00092
MID-881	MID-593	0,61033	0,001027	1	0

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-3122	MID-593	1	0	No contingency	
MID-548	MID-593	1	0	0,673689	0,001023
MID-659	MID-593	0,426959	0,001152	1	0
MID-2011	MID-593	1	0	0,239587	0,001087
MID-2929	MID-593	1	0	0,726379	0,000737
MID-1470	MID-798	0,242056	0,001522	0,228166	0,001555
MID-777	MID-798	0,352484	0,001716	0,045571	0,000758
MID-196	MID-798	1	0	0,951801	0,000477
MID-881	MID-798	1	0	0,742756	0,000971
MID-3122	MID-798	1	0	No contingency	
MID-548	MID-798	0,145991	0,001344	0,521206	0,002213
MID-659	MID-798	0,178998	0,001423	0,306667	0,002043
MID-2011	MID-798	0,898303	0,000769	0,297805	0,00196
MID-2929	MID-798	0,622214	0,001604	0,662516	0,001587
MID-593	MID-798	0,438391	0,001092	0,679428	0,000784
MID-1470	MID-1193	0,451325	0,001742	0,912775	0,000417
MID-777	MID-1193	0,390297	0,001666	0,406602	0,001224
MID-196	MID-1193	0,540451	0,001594	0,69543	0,000986
MID-881	MID-1193	0,298036	0,001801	0,442941	0,000833
MID-3122	MID-1193	0,058374	0,00051	No contingency	
MID-548	MID-1193	0,73618	0,0014	0,784203	0,000977
MID-659	MID-1193	0,141215	0,001361	0,749183	0,000978
MID-2011	MID-1193	0,909867	0,000691	1	0
MID-2929	MID-1193	0,6343	0,001437	0,087592	0,000751
MID-593	MID-1193	0,478386	0,0011	0,584034	0,000454
MID-798	MID-1193	0,412225	0,001675	0,694743	0,000999
MID-1470	MID-1871	0,17761	0,001495	0,666327	0,001524
MID-777	MID-1871	0,867607	0,000945	0,658856	0,001622
MID-196	MID-1871	0,102293	0,001174	0,697264	0,001403
MID-881	MID-1871	0,624912	0,001536	0,023571	0,000434
MID-3122	MID-1871	0,386178	0,001222	No contingency	
MID-548	MID-1871	0,456173	0,001829	0,717095	0,001654
MID-659	MID-1871	0,674967	0,001443	0,543667	0,001838
MID-2011	MID-1871	0,73708	0,00133	0,869195	0,000995
MID-2929	MID-1871	0,524528	0,001631	0,709944	0,00136
MID-593	MID-1871	0,618435	0,000976	0,733687	0,00092
MID-798	MID-1871	0,871349	0,00096	0,551287	0,001633
MID-1193	MID-1871	0,912217	0,000715	0,329387	0,001287
MID-1470	MID-17	0,917723	0,000622	0,79593	0,001203
MID-777	MID-17	0,076787	0,000946	0,17232	0,001497
MID-196	MID-17	0,184755	0,001579	0,417235	0,001828
MID-881	MID-17	0,827969	0,001093	0,477408	0,001383

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-3122	MID-17	1	0	No contingency	
MID-548	MID-17	0,882428	0,000914	0,090319	0,001232
MID-659	MID-17	0,747016	0,001263	1	0
MID-2011	MID-17	0,835741	0,001069	0,072369	0,001084
MID-2929	MID-17	0,443663	0,001837	0,920162	0,000678
MID-593	MID-17	1	0	0,689527	0,00101
MID-798	MID-17	0,43275	0,001691	0,662796	0,00156
MID-1193	MID-17	0,91844	0,000688	0,42328	0,001295
MID-1871	MID-17	0,957644	0,000479	1	0
MID-1470	MID-2538	0,670572	0,001561	0,809064	0,001131
MID-777	MID-2538	0,195882	0,001396	0,587893	0,001733
MID-196	MID-2538	0,111372	0,001153	0,182793	0,001454
MID-881	MID-2538	1	0	0,219746	0,00124
MID-3122	MID-2538	0,519762	0,001102	No contingency	
MID-548	MID-2538	0,402449	0,001726	0,444488	0,002094
MID-659	MID-2538	0,137076	0,001309	0,956339	0,00053
MID-2011	MID-2538	0,549424	0,001495	0,371109	0,001934
MID-2929	MID-2538	0,527886	0,001661	0,473386	0,001747
MID-593	MID-2538	0,376364	0,001033	0,546648	0,00101
MID-798	MID-2538	0,396872	0,001735	0,514202	0,001735
MID-1193	MID-2538	0,64187	0,001513	0,396377	0,001239
MID-1871	MID-2538	0,246886	0,001557	0,747517	0,001269
MID-17	MID-2538	0,764102	0,001364	0,823405	0,001072
MID-1470	MID-1644	No contingency		0,488819	0,00166
MID-777	MID-1644	No contingency		0,87804	0,000818
MID-196	MID-1644	No contingency		1	0
MID-881	MID-1644	No contingency		0,694964	0,000979
MID-3122	MID-1644	No contingency		No contingency	
MID-548	MID-1644	No contingency		0,308097	0,002109
MID-659	MID-1644	No contingency		0,704741	0,001758
MID-2011	MID-1644	No contingency		0,137151	0,001353
MID-2929	MID-1644	No contingency		0,537872	0,001521
MID-593	MID-1644	No contingency		0,350483	0,001423
MID-798	MID-1644	No contingency		0,260295	0,001489
MID-1193	MID-1644	No contingency		0,497343	0,00109
MID-1871	MID-1644	No contingency		0,793766	0,001299
MID-17	MID-1644	No contingency		0,633679	0,00184
MID-2538	MID-1644	No contingency		1	0
MID-1470	MID-3854	0,588447	0,000877	0,034393	0,000844
MID-777	MID-3854	1	0	0,348839	0,00172
MID-196	MID-3854	1	0	0,756176	0,001482
MID-881	MID-3854	1	0	0,790905	0,00091
MID-3122	MID-3854	1	0	No contingency	

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-548	MID-3854	1	0	1	0
MID-659	MID-3854	0,637491	0,001069	0,055722	0,001074
MID-2011	MID-3854	1	0	0,908275	0,000792
MID-2929	MID-3854	0,258211	0,00096	0,805134	0,001229
MID-593	MID-3854	0,216298	0,00065	1	0
MID-798	MID-3854	0,742117	0,000849	0,629651	0,001736
MID-1193	MID-3854	1	0	0,533572	0,001376
MID-1871	MID-3854	1	0	0,580821	0,001826
MID-17	MID-3854	1	0	0,483183	0,002035
MID-2538	MID-3854	0,704549	0,000724	0,011672	0,000415
MID-1644	MID-3854	No contingency		0,445874	0,001975
MID-1470	MID-2275	0,424363	0,001815	0,209267	0,001648
MID-777	MID-2275	0,750527	0,001272	0,038606	0,000821
MID-196	MID-2275	0,93543	0,000612	0,103244	0,001307
MID-881	MID-2275	0,091266	0,00108	1	0
MID-3122	MID-2275	1	0	No contingency	
MID-548	MID-2275	0,718213	0,001798	0,663943	0,00194
MID-659	MID-2275	0,851244	0,001226	0,438795	0,001977
MID-2011	MID-2275	0,125648	0,001155	0,427496	0,002297
MID-2929	MID-2275	0,009371	0,000368	0,140203	0,001339
MID-593	MID-2275	0,672551	0,001095	0,609262	0,000992
MID-798	MID-2275	0,624854	0,00146	0,367395	0,001837
MID-1193	MID-2275	0,328037	0,00192	0,206772	0,001052
MID-1871	MID-2275	0,552732	0,001887	0,406455	0,0018
MID-17	MID-2275	0,580475	0,001823	0,219225	0,001848
MID-2538	MID-2275	0,108537	0,001223	0,584092	0,001791
MID-1644	MID-2275	No contingency		1	0
MID-3854	MID-2275	0,634327	0,001004	1	0
MID-1470	MID-94	0,097566	0,0011	0,029736	0,000583
MID-777	MID-94	0,895001	0,00081	0,111727	0,001226
MID-196	MID-94	0,017026	0,000436	0,839303	0,00109
MID-881	MID-94	0,576847	0,001662	1	0
MID-3122	MID-94	1	0	No contingency	
MID-548	MID-94	0,657361	0,001555	0,085725	0,001217
MID-659	MID-94	0,82573	0,001034	0,009351	0,000415
MID-2011	MID-94	0,791228	0,001094	0,503915	0,001801
MID-2929	MID-94	0,353817	0,001694	0,151803	0,001311
MID-593	MID-94	0,650334	0,000979	0,858941	0,000519
MID-798	MID-94	0,882125	0,000811	0,971836	0,000335
MID-1193	MID-94	0,661953	0,001423	0,70261	0,000949
MID-1871	MID-94	0,815282	0,001132	0,271899	0,001666
MID-17	MID-94	0,007686	0,000289	0,432338	0,001907

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-2538	MID-94	0,050115	0,000776	0,54987	0,001664
MID-1644	MID-94	No contingency		0,429381	0,001736
MID-3854	MID-94	0,373666	0,00121	0,011223	0,000435
MID-2275	MID-94	0,742693	0,001322	1	0
MID-1470	MID-3072	0,557099	0,000996	0,036762	0,000515
MID-777	MID-3072	1	0	0,205085	0,001124
MID-196	MID-3072	1	0	0,673469	0,000986
MID-881	MID-3072	0,231108	0,00123	0,102718	0,000608
MID-3122	MID-3072	1	0	No contingency	
MID-548	MID-3072	1	0	0,770167	0,000991
MID-659	MID-3072	1	0	0,730306	0,001011
MID-2011	MID-3072	1	0	0,815919	0,000821
MID-2929	MID-3072	1	0	0,294131	0,001086
MID-593	MID-3072	1	0	1	0
MID-798	MID-3072	1	0	0,55471	0,001116
MID-1193	MID-3072	0,328016	0,001216	0,371651	0,000848
MID-1871	MID-3072	1	0	0,037485	0,000536
MID-17	MID-3072	1	0	0,590525	0,001031
MID-2538	MID-3072	1	0	0,64753	0,001031
MID-1644	MID-3072	No contingency		1	0
MID-3854	MID-3072	1	0	0,728739	0,001023
MID-2275	MID-3072	1	0	0,481612	0,001445
MID-94	MID-3072	0,439812	0,001198	1	0
MID-1470	MID-772	0,302246	0,000974	0,772643	0,000771
MID-777	MID-772	1	0	0,528095	0,000987
MID-196	MID-772	0,404358	0,000884	0,805737	0,00068
MID-881	MID-772	0,61117	0,000995	0,427097	0,000785
MID-3122	MID-772	1	0	No contingency	
MID-548	MID-772	0,672575	0,001065	0,773793	0,000967
MID-659	MID-772	1	0	0,143028	0,001001
MID-2011	MID-772	0,665026	0,000893	0,477689	0,001321
MID-2929	MID-772	0,57197	0,000858	0,487272	0,001092
MID-593	MID-772	1	0	1	0
MID-798	MID-772	1	0	0,731283	0,000898
MID-1193	MID-772	0,182602	0,000923	1	0
MID-1871	MID-772	0,346182	0,001193	0,372245	0,001316
MID-17	MID-772	1	0	0,902211	0,000462
MID-2538	MID-772	0,267795	0,000971	0,708083	0,000924
MID-1644	MID-772	No contingency		0,648474	0,000917
MID-3854	MID-772	1	0	0,117819	0,000981
MID-2275	MID-772	1	0	0,265109	0,001156
MID-94	MID-772	0,651605	0,001008	0,111068	0,000863
MID-3072	MID-772	1	0	0,20335	0,000654

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-1470	MID-2313	0,577381	0,001573	0,857469	0,000858
MID-777	MID-2313	1	0	0,136475	0,001238
MID-196	MID-2313	0,612992	0,001505	0,199553	0,001531
MID-881	MID-2313	0,241641	0,001821	0,901647	0,000498
MID-3122	MID-2313	1	0	No contingency	
MID-548	MID-2313	0,879269	0,000961	0,343613	0,002189
MID-659	MID-2313	1	0	0,673982	0,001596
MID-2011	MID-2313	0,416637	0,001761	0,9393	0,000604
MID-2929	MID-2313	0,43062	0,001775	0,160394	0,001422
MID-593	MID-2313	0,658385	0,001022	1	0
MID-798	MID-2313	0,946845	0,000522	0,598316	0,00159
MID-1193	MID-2313	0,180112	0,00136	0,789854	0,000774
MID-1871	MID-2313	0,462881	0,001654	0,69922	0,001519
MID-17	MID-2313	0,64996	0,001607	0,71401	0,001496
MID-2538	MID-2313	0,503901	0,001742	0,688994	0,00147
MID-1644	MID-2313	No contingency		0,81303	0,00114
MID-3854	MID-2313	1	0	0,18397	0,001581
MID-2275	MID-2313	0,165335	0,001412	0,10537	0,001232
MID-94	MID-2313	0,690639	0,001601	0,366351	0,001795
MID-3072	MID-2313	1	0	0,438929	0,001065
MID-772	MID-2313	0,658012	0,000996	0,876232	0,000502
MID-1470	MID-397	0,71658	0,001377	0,805167	0,001037
MID-777	MID-397	0,727734	0,00143	0,87602	0,000824
MID-196	MID-397	0,336441	0,001728	0,054422	0,000833
MID-881	MID-397	0,555476	0,001724	0,178012	0,001063
MID-3122	MID-397	1	0	No contingency	
MID-548	MID-397	0,37114	0,001932	0,273308	0,001843
MID-659	MID-397	0,332735	0,001741	1	0
MID-2011	MID-397	0,20083	0,001476	0,04921	0,000883
MID-2929	MID-397	0,596062	0,001657	0,283597	0,001626
MID-593	MID-397	0,633956	0,001043	1	0
MID-798	MID-397	0,636352	0,001569	0,460444	0,001755
MID-1193	MID-397	1	0	0,576107	0,001063
MID-1871	MID-397	0,351485	0,001742	0,322551	0,00171
MID-17	MID-397	0,925595	0,000665	0,860194	0,000967
MID-2538	MID-397	0,475051	0,001727	0,295526	0,001663
MID-1644	MID-397	No contingency		0,037136	0,000615
MID-3854	MID-397	0,171961	0,001056	1	0
MID-2275	MID-397	0,072606	0,001015	0,194486	0,001699
MID-94	MID-397	0,887487	0,000929	0,748321	0,001285
MID-3072	MID-397	1	0	0,619261	0,000771
MID-772	MID-397	0,6311	0,001018	0,667481	0,000785

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-2313	MID-397	0,339683	0,001755	0,324218	0,001728
MID-1470	MID-1636	0,014233	0,000413	0,701585	0,001448
MID-777	MID-1636	0,565054	0,001639	0,024564	0,000541
MID-196	MID-1636	0,246128	0,001625	0,628128	0,001545
MID-881	MID-1636	0,180758	0,001518	0,366094	0,001054
MID-3122	MID-1636	0,422019	0,00123	No contingency	
MID-548	MID-1636	0,441025	0,001965	0,22471	0,001774
MID-659	MID-1636	0,063272	0,001006	0,336175	0,001969
MID-2011	MID-1636	0,205367	0,001482	0,4876	0,001839
MID-2929	MID-1636	1	0	0,150921	0,001385
MID-593	MID-1636	1	0	0,152824	0,000891
MID-798	MID-1636	0,66586	0,001694	0,674557	0,001491
MID-1193	MID-1636	0,359409	0,001701	0,055654	0,000617
MID-1871	MID-1636	0,585139	0,001645	1	0
MID-17	MID-1636	0,122375	0,001311	1	0
MID-2538	MID-1636	0,795762	0,001216	0,95138	0,000439
MID-1644	MID-1636	No contingency		1	0
MID-3854	MID-1636	0,002146	0,00009	0,451948	0,001851
MID-2275	MID-1636	0,778146	0,001431	0,226974	0,001753
MID-94	MID-1636	0,582372	0,001692	0,116226	0,00119
MID-3072	MID-1636	1	0	0,086056	0,000774
MID-772	MID-1636	0,626824	0,000977	0,451172	0,001254
MID-2313	MID-1636	0,887944	0,000909	0,888421	0,000816
MID-397	MID-1636	0,487192	0,001722	0,5222	0,001724
MID-1470	MID-51	0,289672	0,001661	0,389963	0,001776
MID-777	MID-51	0,433673	0,001638	0,393108	0,00187
MID-196	MID-51	0,589586	0,001579	0,714698	0,001494
MID-881	MID-51	0,426478	0,001829	1	0
MID-3122	MID-51	1	0	No contingency	
MID-548	MID-51	0,78885	0,001179	0,283065	0,002007
MID-659	MID-51	0,42997	0,001769	0,150896	0,001385
MID-2011	MID-51	0,008335	0,000312	0,725323	0,001393
MID-2929	MID-51	0,841222	0,000984	0,664806	0,00154
MID-593	MID-51	0,297445	0,001105	1	0
MID-798	MID-51	0,941298	0,000566	0,911452	0,000736
MID-1193	MID-51	0,424608	0,001794	1	0
MID-1871	MID-51	0,566449	0,001676	0,173923	0,001424
MID-17	MID-51	0,591734	0,001709	0,058118	0,000923
MID-2538	MID-51	0,104768	0,001158	0,566506	0,001634
MID-1644	MID-51	No contingency		0,754662	0,00118
MID-3854	MID-51	0,420753	0,00123	0,66021	0,001677
MID-2275	MID-51	1	0	0,486915	0,001827
MID-94	MID-51	0,630347	0,001685	0,846136	0,000878

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-3072	MID-51	0,516057	0,001093	0,359559	0,001129
MID-772	MID-51	1	0	1	0
MID-2313	MID-51	0,759229	0,001298	0,005982	0,000273
MID-397	MID-51	0,014055	0,000393	0,66478	0,001469
MID-1636	MID-51	0,649733	0,001568	0,83469	0,000993
MID-1470	MID-2431	0,579694	0,001602	0,520789	0,001157
MID-777	MID-2431	0,05069	0,000815	0,643477	0,000997
MID-196	MID-2431	0,863756	0,000968	0,298945	0,001226
MID-881	MID-2431	1	0	0,713761	0,000526
MID-3122	MID-2431	1	0	No contingency	
MID-548	MID-2431	0,720686	0,001752	0,206138	0,001175
MID-659	MID-2431	0,392332	0,001958	0,750825	0,001035
MID-2011	MID-2431	0,172082	0,001472	0,335936	0,001483
MID-2929	MID-2431	0,075586	0,001015	0,431062	0,00111
MID-593	MID-2431	1	0	1	0
MID-798	MID-2431	0,215735	0,001611	1	0
MID-1193	MID-2431	0,736983	0,001392	1	0
MID-1871	MID-2431	0,588909	0,001842	0,700204	0,000843
MID-17	MID-2431	0,503474	0,001825	0,247825	0,001308
MID-2538	MID-2431	0,166654	0,001467	0,313361	0,001229
MID-1644	MID-2431	No contingency		0,649132	0,000955
MID-3854	MID-2431	1	0	0,417136	0,001305
MID-2275	MID-2431	1	0	0,548934	0,001249
MID-94	MID-2431	0,744563	0,001264	0,202646	0,001132
MID-3072	MID-2431	1	0	1	0
MID-772	MID-2431	0,673444	0,001042	1	0
MID-2313	MID-2431	0,035311	0,000718	0,592872	0,001102
MID-397	MID-2431	0,937653	0,000616	0,199853	0,001045
MID-1636	MID-2431	0,579089	0,001702	0,447039	0,001157
MID-51	MID-2431	0,836556	0,001028	0,237514	0,000996
MID-1470	MID-2264	0,080438	0,001411	0,260603	0,002372
MID-777	MID-2264	0,953955	0,000736	0,996003	0,000161
MID-196	MID-2264	0,625222	0,002357	0,813887	0,001654
MID-881	MID-2264	0,175105	0,002344	0,885295	0,000884
MID-3122	MID-2264	0,195564	0,001602	No contingency	
MID-548	MID-2264	0,964003	0,000782	0,55821	0,002822
MID-659	MID-2264	0,680973	0,002501	0,152443	0,002093
MID-2011	MID-2264	0,131538	0,001826	0,653283	0,002417
MID-2929	MID-2264	0,511063	0,002581	0,23296	0,002312
MID-593	MID-2264	0,145229	0,001473	0,420778	0,001799
MID-798	MID-2264	0,206896	0,002211	0,300916	0,002598
MID-1193	MID-2264	0,381217	0,002729	0,310083	0,001776

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-1871	MID-2264	0,652783	0,002401	0,491139	0,00259
MID-17	MID-2264	0,465523	0,002908	0,241019	0,00248
MID-2538	MID-2264	0,483555	0,002597	0,108685	0,001799
MID-1644	MID-2264	No contingency		0,533155	0,002657
MID-3854	MID-2264	0,136412	0,001359	0,944424	0,000947
MID-2275	MID-2264	0,866272	0,001675	0,143102	0,002054
MID-94	MID-2264	0,127246	0,001805	0,959822	0,000655
MID-3072	MID-2264	1	0	0,137485	0,001261
MID-772	MID-2264	0,416137	0,001859	0,876007	0,000948
MID-2313	MID-2264	0,749821	0,002132	0,723058	0,001974
MID-397	MID-2264	0,965757	0,000673	0,562348	0,00253
MID-1636	MID-2264	0,2046	0,002239	0,638487	0,002272
MID-51	MID-2264	0,994821	0,000198	0,726314	0,002048
MID-2431	MID-2264	0,825955	0,001909	0,87993	0,000927
MID-1470	MID-2256	0,506908	0,001787	0,050707	0,000908
MID-777	MID-2256	0,87165	0,000924	0,574274	0,001815
MID-196	MID-2256	0,050559	0,000767	0,204571	0,001692
MID-881	MID-2256	0,929401	0,000663	0,18958	0,001263
MID-3122	MID-2256	0,038553	0,000412	No contingency	
MID-548	MID-2256	0,646586	0,001889	0,378862	0,001935
MID-659	MID-2256	0,529758	0,001899	0,901388	0,000823
MID-2011	MID-2256	0,58186	0,001704	0,100954	0,001216
MID-2929	MID-2256	0,883476	0,000827	0,635504	0,001647
MID-593	MID-2256	0,277049	0,001285	0,685097	0,000957
MID-798	MID-2256	0,71649	0,0013	0,212709	0,00164
MID-1193	MID-2256	0,052509	0,000897	1	0
MID-1871	MID-2256	0,086608	0,001127	0,030677	0,000624
MID-17	MID-2256	0,530931	0,001727	0,389251	0,001781
MID-2538	MID-2256	0,480872	0,001749	0,547111	0,001729
MID-1644	MID-2256	No contingency		1	0
MID-3854	MID-2256	0,630793	0,001091	0,548211	0,00196
MID-2275	MID-2256	0,333416	0,0018	0,746591	0,00135
MID-94	MID-2256	0,098294	0,001245	0,370519	0,001942
MID-3072	MID-2256	0,307289	0,00121	0,465083	0,001423
MID-772	MID-2256	0,276197	0,001298	0,425817	0,001358
MID-2313	MID-2256	0,159902	0,001416	0,360385	0,001838
MID-397	MID-2256	0,576657	0,001701	0,923252	0,000678
MID-1636	MID-2256	0,847768	0,000941	0,343576	0,001907
MID-51	MID-2256	0,848664	0,001036	0,672152	0,00162
MID-2431	MID-2256	0,093609	0,001057	0,599088	0,00106
MID-2264	MID-2256	0,263824	0,0026	0,273369	0,002573
MID-1470	MID-128	0,450094	0,001898	0,243763	0,001507
MID-777	MID-128	0,321452	0,001625	0,843928	0,001042

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-196	MID-128	0,411107	0,001821	0,122821	0,001248
MID-881	MID-128	0,105528	0,001343	0,927851	0,000395
MID-3122	MID-128	1	0	No contingency	
MID-548	MID-128	0,583815	0,001675	0,645235	0,00193
MID-659	MID-128	1	0	0,587873	0,001853
MID-2011	MID-128	0,34426	0,001601	0,357441	0,001964
MID-2929	MID-128	0,531473	0,001669	0,811634	0,001137
MID-593	MID-128	0,497238	0,000962	0,584095	0,000907
MID-798	MID-128	0,255217	0,001566	0,336833	0,001898
MID-1193	MID-128	0,937942	0,000533	0,360215	0,001245
MID-1871	MID-128	0,163758	0,001321	0,360156	0,001707
MID-17	MID-128	0,575319	0,001611	0,292856	0,001892
MID-2538	MID-128	0,574101	0,00169	0,63586	0,001733
MID-1644	MID-128	No contingency		0,344325	0,001518
MID-3854	MID-128	0,829748	0,000576	0,431626	0,002058
MID-2275	MID-128	0,439241	0,001817	0,027833	0,000646
MID-94	MID-128	0,650497	0,001452	0,121937	0,00118
MID-3072	MID-128	0,287722	0,000845	1	0
MID-772	MID-128	0,62708	0,00084	0,720648	0,000862
MID-2313	MID-128	0,238899	0,001691	0,456907	0,001786
MID-397	MID-128	0,365292	0,001821	0,014993	0,000388
MID-1636	MID-128	0,189441	0,001478	0,594723	0,001619
MID-51	MID-128	0,474296	0,001666	0,748697	0,001412
MID-2431	MID-128	0,356853	0,001825	0,911117	0,000418
MID-2264	MID-128	0,316896	0,002407	0,581779	0,002508
MID-2256	MID-128	0,856707	0,000938	0,363065	0,001817
MID-1470	MID-15	0,645609	0,001564	0,253887	0,001652
MID-777	MID-15	0,063326	0,000821	0,344513	0,001839
MID-196	MID-15	0,807132	0,001074	0,812962	0,001183
MID-881	MID-15	0,636424	0,001648	0,226941	0,001198
MID-3122	MID-15	1	0	No contingency	
MID-548	MID-15	0,190932	0,001391	0,402469	0,002318
MID-659	MID-15	0,569254	0,001744	0,889194	0,000931
MID-2011	MID-15	0,35174	0,001609	0,838412	0,001017
MID-2929	MID-15	0,884096	0,000737	0,43676	0,001758
MID-593	MID-15	0,731724	0,000761	0,700597	0,000732
MID-798	MID-15	0,715952	0,00132	0,808232	0,001187
MID-1193	MID-15	0,586097	0,001526	0,440495	0,001317
MID-1871	MID-15	0,57892	0,001568	0,871442	0,000861
MID-17	MID-15	0,651786	0,001515	0,025814	0,00059
MID-2538	MID-15	0,745813	0,001277	0,728495	0,00138
MID-1644	MID-15	No contingency		0,681738	0,001335

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-3854	MID-15	1	0	0,264948	0,001903
MID-2275	MID-15	0,570414	0,001669	1	0
MID-94	MID-15	0,811878	0,001026	0,292484	0,001648
MID-3072	MID-15	1	0	0,57905	0,001154
MID-772	MID-15	1	0	0,62444	0,001039
MID-2313	MID-15	0,153904	0,001332	0,603548	0,001658
MID-397	MID-15	0,566365	0,001708	0,172433	0,001388
MID-1636	MID-15	0,392018	0,001827	0,76478	0,001233
MID-51	MID-15	0,927579	0,000541	0,424035	0,001796
MID-2431	MID-15	0,913443	0,000743	0,548453	0,001197
MID-2264	MID-15	0,942063	0,000859	0,642878	0,002362
MID-2256	MID-15	0,348692	0,001723	0,304818	0,001824
MID-128	MID-15	0,496543	0,001729	0,073497	0,000936
MID-1470	MID-2241	1	0	0,084227	0,001171
MID-777	MID-2241	0,36455	0,001796	0,450448	0,00177
MID-196	MID-2241	0,455442	0,001882	0,548295	0,00196
MID-881	MID-2241	0,674837	0,001714	0,342993	0,001536
MID-3122	MID-2241	1	0	No contingency	
MID-548	MID-2241	0,389227	0,001992	0,42464	0,002107
MID-659	MID-2241	0,362863	0,001855	0,015608	0,0004
MID-2011	MID-2241	0,80543	0,001215	0,775268	0,001286
MID-2929	MID-2241	0,898882	0,000788	0,936194	0,000619
MID-593	MID-2241	0,349524	0,001203	0,701032	0,00101
MID-798	MID-2241	0,963386	0,000457	0,726445	0,001372
MID-1193	MID-2241	0,278228	0,00175	0,514172	0,001346
MID-1871	MID-2241	0,211034	0,001559	0,133583	0,001252
MID-17	MID-2241	0,718363	0,001365	0,702546	0,001446
MID-2538	MID-2241	0,326231	0,001943	0,688176	0,001459
MID-1644	MID-2241	No contingency		0,679826	0,001855
MID-3854	MID-2241	0,694432	0,000957	0,732254	0,001658
MID-2275	MID-2241	0,769874	0,001483	0,749738	0,001627
MID-94	MID-2241	0,489601	0,001737	0,432022	0,001874
MID-3072	MID-2241	0,038623	0,000411	0,080969	0,000792
MID-772	MID-2241	1	0	0,402817	0,0015
MID-2313	MID-2241	0,689379	0,001437	0,675356	0,001489
MID-397	MID-2241	0,245856	0,001523	0,835602	0,00109
MID-1636	MID-2241	0,797576	0,001182	0,912077	0,000733
MID-51	MID-2241	0,892933	0,000887	0,020688	0,000556
MID-2431	MID-2241	1	0	1	0
MID-2264	MID-2241	0,930381	0,001118	0,68467	0,002377
MID-2256	MID-2241	0,296708	0,001767	0,753324	0,001346
MID-128	MID-2241	0,63069	0,001668	0,914145	0,000729
MID-15	MID-2241	0,184482	0,001524	0,888439	0,000827

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-1470	MID-419	0,28356	0,002052	0,335564	0,001951
MID-777	MID-419	0,386015	0,001787	0,73055	0,001687
MID-196	MID-419	0,604211	0,001779	0,199681	0,001886
MID-881	MID-419	0,080947	0,001193	0,494737	0,001453
MID-3122	MID-419	1	0	No contingency	
MID-548	MID-419	0,054818	0,000821	0,42189	0,002214
MID-659	MID-419	0,802665	0,001263	0,722317	0,001865
MID-2011	MID-419	0,171056	0,001351	0,062842	0,001015
MID-2929	MID-419	0,366398	0,00183	0,592648	0,001843
MID-593	MID-419	1	0	0,599442	0,001132
MID-798	MID-419	0,196728	0,001633	0,367857	0,00211
MID-1193	MID-419	0,532647	0,001809	1	0
MID-1871	MID-419	0,049023	0,000875	0,100587	0,001326
MID-17	MID-419	0,557011	0,001728	0,481999	0,002122
MID-2538	MID-419	0,445154	0,001988	0,434175	0,002111
MID-1644	MID-419	No contingency		0,759307	0,001645
MID-3854	MID-419	0,359344	0,00122	0,38528	0,00204
MID-2275	MID-419	1	0	0,586685	0,002165
MID-94	MID-419	0,258058	0,001723	0,61332	0,001778
MID-3072	MID-419	1	0	0,378634	0,001341
MID-772	MID-419	1	0	0,374387	0,001355
MID-2313	MID-419	0,153191	0,001596	0,22111	0,001689
MID-397	MID-419	0,318907	0,002091	0,729452	0,001642
MID-1636	MID-419	0,535859	0,00185	0,232629	0,001727
MID-51	MID-419	0,123246	0,001389	0,581091	0,001932
MID-2431	MID-419	0,038113	0,000675	1	0
MID-2264	MID-419	0,292479	0,002795	0,398477	0,002987
MID-2256	MID-419	0,705445	0,001629	0,101462	0,001385
MID-128	MID-419	0,021936	0,000653	0,013471	0,000495
MID-15	MID-419	0,515913	0,001872	0,453516	0,00208
MID-2241	MID-419	0,79881	0,001251	0,841076	0,001109
MID-1470	MID-943	0,369961	0,0017	0,365106	0,002263
MID-777	MID-943	0,421607	0,001886	0,529229	0,002127
MID-196	MID-943	0,063395	0,000871	0,011326	0,000499
MID-881	MID-943	0,933547	0,000627	0,144856	0,001194
MID-3122	MID-943	1	0	No contingency	
MID-548	MID-943	0,389589	0,001955	0,404965	0,002795
MID-659	MID-943	0,458634	0,001754	0,894721	0,000998
MID-2011	MID-943	0,890305	0,000805	0,480531	0,001748
MID-2929	MID-943	0,029472	0,000606	0,602955	0,002105
MID-593	MID-943	0,318262	0,001194	0,649343	0,001038
MID-798	MID-943	0,066402	0,000928	0,775055	0,001477

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-1193	MID-943	0,12076	0,001253	0,787455	0,000986
MID-1871	MID-943	0,166704	0,001415	0,012146	0,000421
MID-17	MID-943	0,21071	0,001518	0,333747	0,00186
MID-2538	MID-943	0,255734	0,001606	0,793042	0,00144
MID-1644	MID-943	No contingency		0,123678	0,001424
MID-3854	MID-943	0,724943	0,000903	0,800313	0,001542
MID-2275	MID-943	0,293109	0,001899	0,016758	0,000481
MID-94	MID-943	0,011582	0,000378	0,578474	0,002002
MID-3072	MID-943	1	0	0,778336	0,000964
MID-772	MID-943	0,626329	0,001016	1	0
MID-2313	MID-943	0,824284	0,00121	0,113579	0,001428
MID-397	MID-943	0,868554	0,000932	1	0
MID-1636	MID-943	0,284776	0,001579	1	0
MID-51	MID-943	0,947219	0,00056	0,351446	0,002144
MID-2431	MID-943	0,509753	0,001837	1	0
MID-2264	MID-943	0,640087	0,002496	0,454076	0,002955
MID-2256	MID-943	0,784972	0,001121	0,278421	0,001844
MID-128	MID-943	0,338411	0,001828	0,466183	0,002304
MID-15	MID-943	0,363109	0,001885	0,37321	0,002332
MID-2241	MID-943	0,497721	0,001856	0,50443	0,001921
MID-419	MID-943	0,578978	0,001815	0,764918	0,001825
MID-1470	MID-159	0,324753	0,001738	0,166469	0,001383
MID-777	MID-159	0,218983	0,001497	0,816761	0,001141
MID-196	MID-159	0,268747	0,001521	0,558701	0,001848
MID-881	MID-159	0,657848	0,00165	0,693735	0,001044
MID-3122	MID-159	0,557532	0,001038	No contingency	
MID-548	MID-159	0,465751	0,001794	0,694169	0,001834
MID-659	MID-159	0,794372	0,001171	0,829676	0,001124
MID-2011	MID-159	0,219212	0,001453	0,44472	0,002034
MID-2929	MID-159	0,515014	0,001573	0,645971	0,001691
MID-593	MID-159	0,787082	0,000614	1	0
MID-798	MID-159	0,735724	0,001342	0,471666	0,002006
MID-1193	MID-159	0,793574	0,001028	0,910649	0,000418
MID-1871	MID-159	0,747458	0,001279	0,956969	0,000442
MID-17	MID-159	0,091785	0,001105	0,493244	0,001855
MID-2538	MID-159	0,387403	0,001766	0,305673	0,001934
MID-1644	MID-159	No contingency		0,813964	0,001125
MID-3854	MID-159	0,669969	0,000804	1	0
MID-2275	MID-159	0,374301	0,001766	0,581984	0,001853
MID-94	MID-159	0,720687	0,001346	0,432534	0,001776
MID-3072	MID-159	0,556725	0,000982	0,612357	0,001082
MID-772	MID-159	0,593693	0,000863	0,903274	0,000462
MID-2313	MID-159	0,260097	0,001639	0,602247	0,001537

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-397	MID-159	0,411225	0,001729	0,602802	0,001497
MID-1636	MID-159	0,246037	0,001651	0,957807	0,000438
MID-51	MID-159	0,899254	0,000706	0,438116	0,001822
MID-2431	MID-159	0,244888	0,001704	0,771766	0,000755
MID-2264	MID-159	0,161143	0,001966	0,888465	0,001257
MID-2256	MID-159	0,855301	0,000922	0,696293	0,001496
MID-128	MID-159	0,694986	0,00154	0,938098	0,000575
MID-15	MID-159	0,537266	0,001654	0,88475	0,000857
MID-2241	MID-159	0,770776	0,001296	0,728993	0,001473
MID-419	MID-159	0,166871	0,001685	0,893021	0,000912
MID-943	MID-159	0,181382	0,001514	0,659034	0,001937
MID-1470	MID-2005	0,741995	0,001321	0,548228	0,001649
MID-777	MID-2005	0,958255	0,000405	0,402569	0,001925
MID-196	MID-2005	0,916236	0,000657	0,189726	0,001435
MID-881	MID-2005	0,849415	0,001011	0,916324	0,000435
MID-3122	MID-2005	1	0	No contingency	
MID-548	MID-2005	1	0	0,687418	0,001831
MID-659	MID-2005	0,722285	0,00136	0,215648	0,001736
MID-2011	MID-2005	0,242416	0,001504	0,105674	0,001385
MID-2929	MID-2005	0,3355	0,001661	0,967798	0,000359
MID-593	MID-2005	0,421182	0,000963	0,14029	0,000747
MID-798	MID-2005	0,126941	0,001245	0,635604	0,001627
MID-1193	MID-2005	0,308314	0,00166	1	0
MID-1871	MID-2005	0,920537	0,000615	0,553554	0,001825
MID-17	MID-2005	0,777771	0,001112	0,553168	0,00182
MID-2538	MID-2005	0,438402	0,001673	0,526101	0,00169
MID-1644	MID-2005	No contingency		0,409999	0,001664
MID-3854	MID-2005	0,526611	0,000842	0,023366	0,000661
MID-2275	MID-2005	1	0	0,207583	0,001624
MID-94	MID-2005	0,417528	0,001693	0,079201	0,001015
MID-3072	MID-2005	0,442615	0,001193	0,425863	0,001109
MID-772	MID-2005	0,00248	0,000109	0,696126	0,000962
MID-2313	MID-2005	0,142051	0,001313	0,978733	0,000258
MID-397	MID-2005	0,40222	0,001771	0,514894	0,001793
MID-1636	MID-2005	0,143278	0,001297	0,011019	0,000354
MID-51	MID-2005	0,287154	0,001679	0,608017	0,001608
MID-2431	MID-2005	0,097427	0,001157	0,365048	0,001152
MID-2264	MID-2005	0,730574	0,002042	0,765985	0,001959
MID-2256	MID-2005	0,841241	0,000954	0,27942	0,001734
MID-128	MID-2005	0,209186	0,001531	0,438231	0,001832
MID-15	MID-2005	0,742722	0,00123	0,923653	0,000643
MID-2241	MID-2005	0,284286	0,001829	0,752052	0,001283

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-419	MID-2005	0,222975	0,001798	0,224359	0,001799
MID-943	MID-2005	0,374869	0,001764	0,012266	0,000469
MID-159	MID-2005	0,362942	0,001708	0,047055	0,000716
MID-1470	MID-250	0,560301	0,00163	0,386613	0,001854
MID-777	MID-250	0,105225	0,001134	0,585335	0,001776
MID-196	MID-250	0,658369	0,001508	0,463059	0,001686
MID-881	MID-250	1	0	0,183979	0,001101
MID-3122	MID-250	1	0	No contingency	
MID-548	MID-250	1	0	0,005357	0,000299
MID-659	MID-250	0,7777	0,001238	0,013545	0,000506
MID-2011	MID-250	0,514261	0,001687	0,850267	0,001052
MID-2929	MID-250	0,435823	0,001878	0,729049	0,001291
MID-593	MID-250	0,160801	0,000826	1	0
MID-798	MID-250	0,140724	0,00127	0,648514	0,001521
MID-1193	MID-250	0,314555	0,001753	0,715572	0,000908
MID-1871	MID-250	0,184699	0,00147	0,379505	0,001824
MID-17	MID-250	0,38844	0,001716	0,496822	0,001765
MID-2538	MID-250	0,398629	0,001809	0,717541	0,0013
MID-1644	MID-250	No contingency		0,15629	0,00143
MID-3854	MID-250	0,141653	0,000867	1	0
MID-2275	MID-250	0,18	0,001486	0,446915	0,001824
MID-94	MID-250	0,232244	0,001587	0,799256	0,001096
MID-3072	MID-250	1	0	0,452713	0,000977
MID-772	MID-250	0,425352	0,001135	0,385784	0,001071
MID-2313	MID-250	0,253396	0,001585	0,961487	0,000375
MID-397	MID-250	0,167446	0,001426	0,966614	0,000346
MID-1636	MID-250	0,429194	0,001748	0,625831	0,001635
MID-51	MID-250	0,152346	0,001326	0,28207	0,001695
MID-2431	MID-250	0,162887	0,001386	0,645477	0,000969
MID-2264	MID-250	0,793434	0,001834	0,868064	0,001339
MID-2256	MID-250	0,347306	0,001637	0,832294	0,001182
MID-128	MID-250	0,377662	0,001633	0,168566	0,001434
MID-15	MID-250	0,210573	0,00157	0,511053	0,001785
MID-2241	MID-250	0,1607	0,001481	0,026894	0,000668
MID-419	MID-250	0,631992	0,001699	1	0
MID-943	MID-250	0,166592	0,001414	0,44205	0,002147
MID-159	MID-250	0,865852	0,000828	0,336672	0,001722
MID-2005	MID-250	0,958894	0,000394	0,626512	0,001608
MID-1470	MID-1802	No contingency		0,805499	0,001013
MID-777	MID-1802	No contingency		0,389103	0,001769
MID-196	MID-1802	No contingency		0,426947	0,00161
MID-881	MID-1802	No contingency		0,696611	0,000996
MID-3122	MID-1802	No contingency		No contingency	

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-548	MID-1802	No contingency		0,195046	0,001736
MID-659	MID-1802	No contingency		1	0
MID-2011	MID-1802	No contingency		0,500713	0,002034
MID-2929	MID-1802	No contingency		0,111942	0,001125
MID-593	MID-1802	No contingency		1	0
MID-798	MID-1802	No contingency		0,348636	0,001635
MID-1193	MID-1802	No contingency		0,217332	0,001082
MID-1871	MID-1802	No contingency		0,314685	0,001796
MID-17	MID-1802	No contingency		0,453146	0,001917
MID-2538	MID-1802	No contingency		0,709498	0,00135
MID-1644	MID-1802	No contingency		0,737853	0,0017
MID-3854	MID-1802	No contingency		0,260469	0,001952
MID-2275	MID-1802	No contingency		1	0
MID-94	MID-1802	No contingency		0,850118	0,000961
MID-3072	MID-1802	No contingency		0,191074	0,000985
MID-772	MID-1802	No contingency		0,64656	0,000947
MID-2313	MID-1802	No contingency		0,753621	0,00139
MID-397	MID-1802	No contingency		0,744354	0,001451
MID-1636	MID-1802	No contingency		0,648379	0,001764
MID-51	MID-1802	No contingency		0,755571	0,001166
MID-2431	MID-1802	No contingency		1	0
MID-2264	MID-1802	No contingency		0,250891	0,002539
MID-2256	MID-1802	No contingency		1	0
MID-128	MID-1802	No contingency		0,760239	0,001234
MID-15	MID-1802	No contingency		0,680807	0,001301
MID-2241	MID-1802	No contingency		0,68074	0,00188
MID-419	MID-1802	No contingency		0,301476	0,002095
MID-943	MID-1802	No contingency		0,823387	0,00132
MID-159	MID-1802	No contingency		0,771426	0,001251
MID-2005	MID-1802	No contingency		1	0
MID-250	MID-1802	No contingency		0,778812	0,001119
MID-1470	MID-1607	0,07478	0,001233	0,169124	0,001588
MID-777	MID-1607	0,623933	0,001827	0,233094	0,00172
MID-196	MID-1607	0,475505	0,001953	0,595588	0,001747
MID-881	MID-1607	0,859429	0,001195	0,611807	0,00117
MID-3122	MID-1607	1	0	No contingency	
MID-548	MID-1607	0,111831	0,001325	0,763191	0,001453
MID-659	MID-1607	1	0	0,12484	0,001488
MID-2011	MID-1607	0,680858	0,00161	0,874497	0,000938
MID-2929	MID-1607	0,10351	0,001259	0,543611	0,001901
MID-593	MID-1607	0,031803	0,000312	1	0
MID-798	MID-1607	0,780344	0,001402	0,565946	0,001642

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-1193	MID-1607	1	0	0,490266	0,001364
MID-1871	MID-1607	0,704651	0,00148	0,297156	0,001779
MID-17	MID-1607	0,363572	0,001917	0,442272	0,001666
MID-2538	MID-1607	0,734029	0,001598	1	0
MID-1644	MID-1607	No contingency		0,452364	0,001818
MID-3854	MID-1607	1	0	0,131348	0,001498
MID-2275	MID-1607	0,500437	0,001926	0,77363	0,001561
MID-94	MID-1607	0,896764	0,000947	0,044083	0,000836
MID-3072	MID-1607	0,353183	0,001212	0,340397	0,001539
MID-772	MID-1607	0,065034	0,000683	0,608183	0,001329
MID-2313	MID-1607	0,165751	0,001643	0,295269	0,001829
MID-397	MID-1607	0,315382	0,00201	0,59753	0,001855
MID-1636	MID-1607	0,591985	0,001789	0,234222	0,001646
MID-51	MID-1607	0,953055	0,000518	0,694136	0,001548
MID-2431	MID-1607	1	0	0,17614	0,001205
MID-2264	MID-1607	0,490085	0,002928	0,443127	0,002816
MID-2256	MID-1607	0,7406	0,001373	0,674599	0,001449
MID-128	MID-1607	0,780156	0,001417	0,648127	0,00158
MID-15	MID-1607	0,074967	0,001098	0,552611	0,001749
MID-2241	MID-1607	1	0	0,338084	0,001947
MID-419	MID-1607	0,698103	0,00179	0,602962	0,001899
MID-943	MID-1607	1	0	0,691169	0,001747
MID-159	MID-1607	0,168343	0,001694	0,093476	0,001225
MID-2005	MID-1607	0,167122	0,00163	0,321328	0,001843
MID-250	MID-1607	0,045699	0,000917	0,523134	0,001833
MID-1802	MID-1607	No contingency		0,358429	0,00197
MID-1470	MID-1734	0,393346	0,001397	0,336384	0,001972
MID-777	MID-1734	0,505228	0,001324	0,706973	0,001352
MID-196	MID-1734	0,444642	0,001375	0,469371	0,001945
MID-881	MID-1734	1	0	0,143001	0,001118
MID-3122	MID-1734	0,346167	0,000594	No contingency	
MID-548	MID-1734	0,625468	0,001197	0,634557	0,001772
MID-659	MID-1734	0,067833	0,000729	0,466005	0,002406
MID-2011	MID-1734	1	0	0,134654	0,001325
MID-2929	MID-1734	0,758124	0,000887	0,198942	0,001748
MID-593	MID-1734	1	0	0,241528	0,001109
MID-798	MID-1734	0,698429	0,00099	0,017926	0,000552
MID-1193	MID-1734	0,572437	0,001206	0,118608	0,001032
MID-1871	MID-1734	0,482464	0,001102	0,750532	0,001342
MID-17	MID-1734	0,584707	0,00107	0,658649	0,001569
MID-2538	MID-1734	0,048922	0,000576	0,224372	0,001857
MID-1644	MID-1734	No contingency		0,121382	0,001313
MID-3854	MID-1734	1	0	0,407935	0,00236

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-2275	MID-1734	0,62725	0,001194	0,862262	0,001084
MID-94	MID-1734	0,598529	0,001271	0,812591	0,001137
MID-3072	MID-1734	1	0	0,567725	0,001346
MID-772	MID-1734	1	0	0,161331	0,00123
MID-2313	MID-1734	0,748185	0,000971	0,77019	0,001328
MID-397	MID-1734	0,144626	0,001053	0,169662	0,001521
MID-1636	MID-1734	0,533859	0,001173	0,827182	0,0011
MID-51	MID-1734	0,905208	0,000485	0,954394	0,000504
MID-2431	MID-1734	0,395559	0,001228	1	0
MID-2264	MID-1734	0,132264	0,001373	0,452124	0,00274
MID-2256	MID-1734	0,178273	0,001056	0,438492	0,001853
MID-128	MID-1734	0,410687	0,001424	0,192402	0,001717
MID-15	MID-1734	0,189507	0,001146	0,678834	0,001522
MID-2241	MID-1734	1	0	0,057548	0,00098
MID-419	MID-1734	1	0	0,718165	0,001727
MID-943	MID-1734	0,421147	0,001216	0,7952	0,0014
MID-159	MID-1734	1	0	0,207533	0,001769
MID-2005	MID-1734	0,246478	0,001347	0,42134	0,001965
MID-250	MID-1734	0,404254	0,001224	0,09954	0,001281
MID-1802	MID-1734	No contingency		0,09792	0,001274
MID-1607	MID-1734	0,152607	0,001359	0,59629	0,001696
MID-1470	MID-406	0,237512	0,00153	0,875598	0,000788
MID-777	MID-406	0,469508	0,001824	0,73041	0,001355
MID-196	MID-406	0,225624	0,001534	0,486932	0,001722
MID-881	MID-406	0,955112	0,000496	0,623278	0,001237
MID-3122	MID-406	0,558725	0,001036	No contingency	
MID-548	MID-406	1	0	0,761243	0,001509
MID-659	MID-406	0,439694	0,001858	0,007393	0,000334
MID-2011	MID-406	0,150512	0,001293	0,015443	0,00047
MID-2929	MID-406	0,481441	0,00178	0,3247	0,001773
MID-593	MID-406	0,193025	0,00081	0,053933	0,000534
MID-798	MID-406	0,878887	0,000735	0,008548	0,000301
MID-1193	MID-406	0,337022	0,001657	1	0
MID-1871	MID-406	0,591565	0,001693	0,615609	0,001552
MID-17	MID-406	1	0	0,173726	0,001523
MID-2538	MID-406	0,762387	0,001176	0,780471	0,001189
MID-1644	MID-406	No contingency		0,294468	0,001567
MID-3854	MID-406	0,855934	0,000521	0,242659	0,001806
MID-2275	MID-406	1	0	0,754372	0,001459
MID-94	MID-406	0,956315	0,000431	0,164943	0,001378
MID-3072	MID-406	0,558803	0,001045	0,386753	0,00114
MID-772	MID-406	1	0	0,403625	0,001114

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-2313	MID-406	0,725914	0,001331	0,11756	0,001255
MID-397	MID-406	0,284525	0,001622	0,462704	0,001777
MID-1636	MID-406	0,275699	0,001635	0,015678	0,000433
MID-51	MID-406	0,40031	0,001814	0,92722	0,000613
MID-2431	MID-406	0,684032	0,001495	0,579974	0,001079
MID-2264	MID-406	0,619114	0,002393	0,81787	0,001619
MID-2256	MID-406	0,473144	0,001772	0,452566	0,00196
MID-128	MID-406	0,86921	0,000915	0,361446	0,001653
MID-15	MID-406	0,367148	0,001655	0,15386	0,00143
MID-2241	MID-406	0,167967	0,001545	0,258506	0,001912
MID-419	MID-406	0,412114	0,00206	0,529943	0,001907
MID-943	MID-406	0,479174	0,001709	0,550504	0,002036
MID-159	MID-406	0,325088	0,001686	0,102594	0,001125
MID-2005	MID-406	0,848115	0,000954	0,907678	0,000673
MID-250	MID-406	0,545657	0,001734	0,074229	0,000981
MID-1802	MID-406	No contingency		0,84264	0,000987
MID-1607	MID-406	0,772562	0,001408	0,971698	0,000354
MID-1734	MID-406	1	0	0,128018	0,001439
MID-1470	MID-1386	0,877906	0,00096	0,774792	0,001249
MID-777	MID-1386	0,412299	0,00183	0,274522	0,001629
MID-196	MID-1386	0,711746	0,00158	0,924866	0,000594
MID-881	MID-1386	0,077739	0,001176	0,718211	0,000861
MID-3122	MID-1386	1	0	No contingency	
MID-548	MID-1386	0,270082	0,001964	1	0
MID-659	MID-1386	0,072723	0,000969	0,862822	0,001044
MID-2011	MID-1386	0,173414	0,001414	0,782853	0,001342
MID-2929	MID-1386	0,291514	0,001903	0,441144	0,001715
MID-593	MID-1386	0,571955	0,001036	0,687565	0,000998
MID-798	MID-1386	0,916297	0,000738	0,129958	0,001277
MID-1193	MID-1386	0,530846	0,00178	0,085694	0,000796
MID-1871	MID-1386	0,867607	0,001039	0,452362	0,001754
MID-17	MID-1386	1	0	0,745794	0,001337
MID-2538	MID-1386	0,040608	0,000845	0,886986	0,00073
MID-1644	MID-1386	No contingency		0,44043	0,001872
MID-3854	MID-1386	0,143916	0,001031	0,861947	0,001054
MID-2275	MID-1386	0,181004	0,001618	0,923116	0,000713
MID-94	MID-1386	0,841801	0,001139	0,707221	0,001355
MID-3072	MID-1386	1	0	0,281686	0,001156
MID-772	MID-1386	1	0	0,166137	0,001042
MID-2313	MID-1386	0,614855	0,001787	0,046712	0,000761
MID-397	MID-1386	0,936417	0,000653	0,802154	0,001133
MID-1636	MID-1386	0,308344	0,001953	0,374255	0,001676
MID-51	MID-1386	0,452793	0,001879	0,130799	0,001213

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-2431	MID-1386	0,118047	0,001445	0,242733	0,001313
MID-2264	MID-1386	0,13587	0,002161	0,316978	0,002572
MID-2256	MID-1386	0,224596	0,001844	0,810387	0,001163
MID-128	MID-1386	0,430484	0,002135	0,733506	0,001236
MID-15	MID-1386	0,946045	0,000568	0,439584	0,001767
MID-2241	MID-1386	1	0	0,555649	0,001878
MID-419	MID-1386	1	0	0,594244	0,001857
MID-943	MID-1386	0,472333	0,001836	1	0
MID-159	MID-1386	0,651609	0,001683	0,164655	0,001385
MID-2005	MID-1386	0,072521	0,001042	0,730363	0,001435
MID-250	MID-1386	0,098931	0,001228	0,818416	0,001153
MID-1802	MID-1386	No contingency		0,166218	0,001246
MID-1607	MID-1386	0,387211	0,002302	0,303505	0,001776
MID-1734	MID-1386	0,388799	0,001317	0,910261	0,000727
MID-406	MID-1386	0,580384	0,001899	0,859256	0,00097
MID-1470	MID-1726	0,008745	0,000281	0,862759	0,000945
MID-777	MID-1726	0,222001	0,001529	0,808531	0,001143
MID-196	MID-1726	0,475455	0,001681	0,099097	0,001178
MID-881	MID-1726	0,381176	0,0018	0,047017	0,000629
MID-3122	MID-1726	0,539331	0,001085	No contingency	
MID-548	MID-1726	1	0	0,378017	0,002039
MID-659	MID-1726	0,829864	0,001137	0,34717	0,002017
MID-2011	MID-1726	0,951054	0,000472	0,074341	0,001042
MID-2929	MID-1726	0,320971	0,001608	0,589212	0,001706
MID-593	MID-1726	1	0	1	0
MID-798	MID-1726	0,893299	0,000716	0,102388	0,001154
MID-1193	MID-1726	0,486851	0,001677	0,702488	0,000818
MID-1871	MID-1726	0,455544	0,001735	0,12354	0,001224
MID-17	MID-1726	0,058144	0,000885	0,895934	0,000833
MID-2538	MID-1726	0,08065	0,000958	0,711087	0,001379
MID-1644	MID-1726	No contingency		1	0
MID-3854	MID-1726	0,030108	0,000422	0,028436	0,000658
MID-2275	MID-1726	0,680184	0,001424	0,462393	0,001939
MID-94	MID-1726	0,832082	0,001046	0,264632	0,001588
MID-3072	MID-1726	1	0	0,204517	0,001132
MID-772	MID-1726	0,582502	0,000933	0,708137	0,000763
MID-2313	MID-1726	0,26314	0,001597	0,283118	0,001746
MID-397	MID-1726	0,210965	0,001536	0,123351	0,001261
MID-1636	MID-1726	0,207529	0,001505	0,096163	0,001074
MID-51	MID-1726	0,578516	0,001794	0,11266	0,00118
MID-2431	MID-1726	0,746158	0,001321	0,324445	0,001175
MID-2264	MID-1726	0,519248	0,002601	0,752716	0,001981

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-2256	MID-1726	1	0	0,15446	0,001449
MID-128	MID-1726	0,455528	0,001722	0,211762	0,001594
MID-15	MID-1726	0,665137	0,001365	0,855619	0,000934
MID-2241	MID-1726	0,639303	0,001503	0,967982	0,000425
MID-419	MID-1726	0,371844	0,001923	0,398247	0,001923
MID-943	MID-1726	0,324045	0,001579	0,332079	0,002159
MID-159	MID-1726	0,047042	0,000737	0,556357	0,001724
MID-2005	MID-1726	0,071782	0,000929	0,338539	0,001828
MID-250	MID-1726	0,871862	0,000876	0,28808	0,001711
MID-1802	MID-1726	No contingency		1	0
MID-1607	MID-1726	0,742417	0,001478	0,60421	0,001683
MID-1734	MID-1726	0,178595	0,001094	0,507244	0,001818
MID-406	MID-1726	1	0	0,057665	0,000839
MID-1386	MID-1726	0,787451	0,001281	0,699486	0,001474
MID-1470	MID-3626	0,253484	0,002087	0,907971	0,000691
MID-777	MID-3626	0,064179	0,001025	0,634854	0,001728
MID-196	MID-3626	0,955923	0,000516	0,726385	0,001311
MID-881	MID-3626	0,884422	0,001023	0,210832	0,001174
MID-3122	MID-3626	1	0	No contingency	
MID-548	MID-3626	0,858921	0,001204	0,688266	0,001837
MID-659	MID-3626	0,504569	0,001995	0,891948	0,000847
MID-2011	MID-3626	0,020272	0,000575	0,844451	0,001172
MID-2929	MID-3626	1	0	0,055777	0,000886
MID-593	MID-3626	1	0	0,036019	0,000483
MID-798	MID-3626	0,288585	0,001947	0,267581	0,001704
MID-1193	MID-3626	0,136406	0,001406	0,149941	0,001098
MID-1871	MID-3626	0,742216	0,001648	0,177525	0,001425
MID-17	MID-3626	0,077535	0,001018	0,045683	0,000753
MID-2538	MID-3626	0,055004	0,001061	0,794688	0,001245
MID-1644	MID-3626	No contingency		0,818552	0,001201
MID-3854	MID-3626	0,199488	0,001076	0,525502	0,001788
MID-2275	MID-3626	0,857085	0,001229	0,05908	0,000984
MID-94	MID-3626	0,26401	0,001718	0,930555	0,000646
MID-3072	MID-3626	0,421145	0,001234	1	0
MID-772	MID-3626	0,116987	0,000884	0,402715	0,001172
MID-2313	MID-3626	0,760199	0,001545	0,050902	0,000803
MID-397	MID-3626	0,33722	0,00199	0,037991	0,000669
MID-1636	MID-3626	0,382287	0,001849	0,38093	0,001713
MID-51	MID-3626	0,746223	0,001653	0,385912	0,001754
MID-2431	MID-3626	0,625512	0,001944	0,650802	0,000841
MID-2264	MID-3626	1	0	0,052946	0,001146
MID-2256	MID-3626	0,724815	0,001463	0,971679	0,000368
MID-128	MID-3626	0,096146	0,001426	0,237115	0,001606

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-15	MID-3626	0,868722	0,001052	0,853778	0,000987
MID-2241	MID-3626	0,779036	0,001405	0,363229	0,001858
MID-419	MID-3626	0,34832	0,002151	0,467674	0,001888
MID-943	MID-3626	0,39537	0,001903	0,853256	0,001085
MID-159	MID-3626	0,721086	0,001627	0,146291	0,001347
MID-2005	MID-3626	0,115778	0,001395	0,823081	0,00108
MID-250	MID-3626	0,862125	0,001074	0,973223	0,000309
MID-1802	MID-3626	No contingency		0,570809	0,001747
MID-1607	MID-3626	0,645154	0,002092	0,335347	0,001798
MID-1734	MID-3626	0,349189	0,001594	0,648097	0,0016
MID-406	MID-3626	0,687759	0,00179	0,968114	0,000334
MID-1386	MID-3626	0,493251	0,002148	0,648967	0,001657
MID-1726	MID-3626	0,238995	0,00184	0,152065	0,001332
MID-1470	MID-360	0,353254	0,001383	0,230552	0,001172
MID-777	MID-360	0,070371	0,000662	0,6888	0,00111
MID-196	MID-360	0,148542	0,001039	0,741492	0,001028
MID-881	MID-360	1	0	1	0
MID-3122	MID-360	0,364878	0,0006	No contingency	
MID-548	MID-360	0,171393	0,001237	0,517835	0,001481
MID-659	MID-360	0,691196	0,00098	0,180127	0,00129
MID-2011	MID-360	0,535891	0,001233	0,184575	0,0013
MID-2929	MID-360	0,396498	0,00128	0,600957	0,001168
MID-593	MID-360	1	0	0,564205	0,000528
MID-798	MID-360	0,014918	0,000343	0,631533	0,001147
MID-1193	MID-360	0,694104	0,000938	1	0
MID-1871	MID-360	0,235421	0,00118	0,656239	0,001022
MID-17	MID-360	0,593504	0,001345	0,661449	0,000869
MID-2538	MID-360	0,030851	0,00047	0,185399	0,001112
MID-1644	MID-360	No contingency		0,253299	0,001148
MID-3854	MID-360	0,284048	0,000635	0,121575	0,001156
MID-2275	MID-360	0,806523	0,000743	0,584054	0,001314
MID-94	MID-360	0,909063	0,00049	0,002741	0,000128
MID-3072	MID-360	0,365422	0,000579	0,726625	0,000554
MID-772	MID-360	1	0	1	0
MID-2313	MID-360	0,049117	0,000646	0,155263	0,001051
MID-397	MID-360	0,894636	0,000524	0,391148	0,001104
MID-1636	MID-360	0,030686	0,000487	0,080625	0,000903
MID-51	MID-360	0,834464	0,00069	0,371019	0,001348
MID-2431	MID-360	0,175366	0,001201	0,262039	0,000871
MID-2264	MID-360	0,557959	0,001762	0,641316	0,001602
MID-2256	MID-360	1	0	0,234404	0,001372
MID-128	MID-360	0,302579	0,001391	0,175294	0,001075

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-15	MID-360	0,198099	0,001134	0,725287	0,001007
MID-2241	MID-360	0,286067	0,001401	0,822706	0,000743
MID-419	MID-360	0,151763	0,001293	0,260285	0,001265
MID-943	MID-360	0,650885	0,001067	0,830061	0,000873
MID-159	MID-360	0,022735	0,000437	0,386559	0,001371
MID-2005	MID-360	0,530445	0,001239	0,051735	0,000622
MID-250	MID-360	1	0	0,833007	0,00071
MID-1802	MID-360	No contingency		1	0
MID-1607	MID-360	0,852752	0,000744	0,032381	0,000542
MID-1734	MID-360	0,380345	0,001073	0,752525	0,00082
MID-406	MID-360	0,457844	0,001305	0,274789	0,00116
MID-1386	MID-360	0,847133	0,000725	1	0
MID-1726	MID-360	0,122299	0,000899	0,201327	0,001195
MID-3626	MID-360	0,853846	0,000722	0,283539	0,001175
MID-1470	MID-1603	0,93347	0,000541	0,84804	0,001044
MID-777	MID-1603	0,609086	0,001483	0,424532	0,001813
MID-196	MID-1603	0,100829	0,001036	0,523493	0,001855
MID-881	MID-1603	0,87711	0,000938	0,076556	0,000764
MID-3122	MID-1603	1	0	No contingency	
MID-548	MID-1603	0,805184	0,001191	0,908122	0,000874
MID-659	MID-1603	0,892908	0,000811	0,651923	0,001658
MID-2011	MID-1603	0,317725	0,00154	0,691521	0,001526
MID-2929	MID-1603	0,160148	0,001261	0,412592	0,001871
MID-593	MID-1603	0,424097	0,001048	0,261659	0,000971
MID-798	MID-1603	0,022122	0,000511	0,538005	0,001865
MID-1193	MID-1603	0,912337	0,000632	0,835621	0,000648
MID-1871	MID-1603	0,403514	0,00168	0,009879	0,000316
MID-17	MID-1603	0,36773	0,001653	0,096057	0,001187
MID-2538	MID-1603	0,975978	0,000287	0,105361	0,001195
MID-1644	MID-1603	No contingency		0,337031	0,001692
MID-3854	MID-1603	0,171457	0,000827	0,778984	0,001378
MID-2275	MID-1603	1	0	0,459578	0,001942
MID-94	MID-1603	0,109366	0,00115	0,243379	0,001527
MID-3072	MID-1603	1	0	0,740639	0,000865
MID-772	MID-1603	0,807541	0,000572	0,294272	0,001136
MID-2313	MID-1603	0,656303	0,00147	0,564664	0,00174
MID-397	MID-1603	0,888918	0,000743	0,68358	0,001385
MID-1636	MID-1603	0,986547	0,000199	0,082149	0,000982
MID-51	MID-1603	0,878143	0,000753	0,328209	0,001726
MID-2431	MID-1603	0,195525	0,001416	0,622703	0,001094
MID-2264	MID-1603	0,180113	0,002018	0,428343	0,002723
MID-2256	MID-1603	0,230248	0,001615	0,652293	0,001581
MID-128	MID-1603	0,592089	0,001701	0,06354	0,000911

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-15	MID-1603	1	0	0,138744	0,001343
MID-2241	MID-1603	0,375747	0,001852	0,76034	0,001378
MID-419	MID-1603	0,928618	0,000671	0,076442	0,00124
MID-943	MID-1603	0,177867	0,001464	0,954314	0,00053
MID-159	MID-1603	0,295411	0,001694	0,651631	0,001662
MID-2005	MID-1603	0,335717	0,001654	0,856611	0,000989
MID-250	MID-1603	0,206504	0,001484	0,101825	0,001124
MID-1802	MID-1603	No contingency		0,02178	0,00056
MID-1607	MID-1603	0,030955	0,000729	0,739269	0,001378
MID-1734	MID-1603	0,32054	0,001365	0,122583	0,001451
MID-406	MID-1603	0,991984	0,00014	0,197452	0,00146
MID-1386	MID-1603	0,691229	0,001638	0,504823	0,001727
MID-1726	MID-1603	0,475988	0,001767	0,501152	0,001715
MID-3626	MID-1603	0,711482	0,001742	0,397435	0,0018
MID-360	MID-1603	0,804348	0,000839	1	0
MID-1470	MID-2719	0,740656	0,001385	0,28343	0,001635
MID-777	MID-2719	0,820891	0,000962	0,640209	0,00176
MID-196	MID-2719	0,961956	0,000353	0,967892	0,000368
MID-881	MID-2719	0,702589	0,001539	0,441449	0,001136
MID-3122	MID-2719	1	0	No contingency	
MID-548	MID-2719	0,88696	0,000866	0,445629	0,002191
MID-659	MID-2719	0,695193	0,001419	0,842918	0,001138
MID-2011	MID-2719	0,6898	0,001337	0,821542	0,001209
MID-2929	MID-2719	0,558117	0,001566	0,332812	0,001768
MID-593	MID-2719	0,148319	0,000879	1	0
MID-798	MID-2719	0,117049	0,001186	0,083013	0,001084
MID-1193	MID-2719	0,368772	0,001695	0,539122	0,001017
MID-1871	MID-2719	0,242279	0,001687	0,128274	0,001263
MID-17	MID-2719	0,582171	0,001576	0,385434	0,001822
MID-2538	MID-2719	0,924135	0,00065	0,136013	0,001353
MID-1644	MID-2719	No contingency		0,170771	0,001513
MID-3854	MID-2719	0,531983	0,000834	0,598088	0,0017
MID-2275	MID-2719	0,272046	0,001688	0,939914	0,000633
MID-94	MID-2719	0,880255	0,00079	0,988333	0,000181
MID-3072	MID-2719	1	0	0,08938	0,000904
MID-772	MID-2719	0,423978	0,000996	0,261633	0,001227
MID-2313	MID-2719	0,024732	0,000533	0,145308	0,001319
MID-397	MID-2719	0,127482	0,001288	0,807229	0,001132
MID-1636	MID-2719	0,433219	0,001734	0,642499	0,001706
MID-51	MID-2719	0,905119	0,000674	0,126298	0,001264
MID-2431	MID-2719	0,444438	0,001721	0,88756	0,000484
MID-2264	MID-2719	0,697169	0,002139	0,476136	0,002674

Locus#1	Locus#2	Bragança Jewish		Miranda	
		p value	s.d.	p value	s.d.
MID-2256	MID-2719	0,304722	0,001754	0,241908	0,00168
MID-128	MID-2719	0,865685	0,000901	0,682948	0,001477
MID-15	MID-2719	0,641018	0,00145	0,511651	0,001791
MID-2241	MID-2719	0,801372	0,001162	0,272081	0,001772
MID-419	MID-2719	0,188473	0,00176	0,320548	0,001847
MID-943	MID-2719	0,100004	0,001101	0,498919	0,002252
MID-159	MID-2719	0,726445	0,001451	0,037699	0,00069
MID-2005	MID-2719	0,320573	0,001623	0,411611	0,001971
MID-250	MID-2719	0,623092	0,001643	0,106198	0,001171
MID-1802	MID-2719	No contingency		0,567888	0,001821
MID-1607	MID-2719	0,030435	0,000689	0,786596	0,001266
MID-1734	MID-2719	0,270068	0,001312	0,393815	0,001911
MID-406	MID-2719	0,73413	0,001299	0,130692	0,001354
MID-1386	MID-2719	0,511465	0,001912	0,460118	0,001682
MID-1726	MID-2719	0,894186	0,000697	0,271668	0,001744
MID-3626	MID-2719	0,748732	0,001491	0,452888	0,001929
MID-360	MID-2719	0,267505	0,001338	0,806751	0,000787
MID-1603	MID-2719	0,913819	0,000655	0,410808	0,001779