

Account ID#: GBUS92136

RE: MATERNAL ANCESTRY DNA TEST REPORT

Please find enclosed the results of the Maternal Ancestry DNA Test Report (mtDNA HVR1, HVR2 and Coding Region) which you have requested.

FamilyVault DNA Database Usage

Your mtDNA markers qualify for FamilyVault DNA database search and analysis features. The FamilyVault DNA Ancestry database allows you to:

- Search for potential family links
- Compare against indigenous populations from around the world
- Find out more about your ancient haplogroup and view the migration path your ancestors took out of Africa.
- Compare against famous people in history
- Store and share your DNA data, collaborate with family members and organize results from other members of your family

To use the FamilyVault DNA database, go to www.dnaaccess.com and login using the Email registered to this account and your selected password. You can change your email and password at any time after you login to your account online.

Step 1: Go to www.dnaaccess.com

Step 2: Click "Sign in to FamilyVault"

Step 3: Enter the email **nick.rossiter1@btinternet.com** and your selected password. Once you login, you can change the email and password at any time. Once your email has been changed, the email shown in this report will no longer be valid and you will need to use your new email to login.

Note:

Always keep the email in your FamilyVault account current.
FamilyVault database usage is free and optional.

**DNA Test Results
HVR1, HVR2, Coding Region Test Report**

Print Date: October 18, 2017

Client Information

First Name: Brian Account ID# GBUS92136
 Last Name: Rossiter Testee ID#: 26364765

HVR1, HVR2, Coding Region Profile Results

The following mtDNA profile for Brian Nicholas Rossiter has been obtained through Sanger Sequencing. mtDNA is passed down from mother to child along the direct maternal lineage. All individuals who have descended from the same maternal lineage as Brian Nicholas Rossiter are expected to have exactly the same mtDNA profile as Brian Nicholas Rossiter's profile shown below. If two individuals have different mtDNA profiles, it will conclusively confirm that they did not descend from the same maternal lineage, regardless of family legend.

HVR-1 Sequence			
16001	ATTCTAATTT	AAACTATTCT	CTGTTCTTTC
16101	TTACTGCCAG	CCACCATGAA	TATTGCACGG
16201	CAAGCAAGTA	CAGCAATCAA	CCCTCAACTA
16301	CAGCACATAG	TACATAAAGC	CATTTACCGT
16401	CACCATCCTC	CGTGAATCA	ATATCCCGCA
16501	CTGGTTCCTA	CTTCAGGGCC	ATAAAGCCTA

HVR-1 Qualified Cambridge Reference Sequence (rCRS) variations			
Nucleotide Position	Region	Variant Type	Nucleotide Change
16051	HVR-1	Substitution	A>G
16126	HVR-1	Substitution	T>C
16294	HVR-1	Substitution	C>T
16296	HVR-1	Substitution	C>T
16304	HVR-1	Substitution	T>C
16519	HVR-1	Substitution	T>C

HVR-2 Sequence			
00001	GATCACAGGT	CTATCACCT	ATTAACCACT
00101	GAGCCGGAGC	ACCCTATGTC	GCAGTATCTG
00201	AAGTGTGTTA	ATTAATTAAT	GCTTGAGGA
00301	AACCCCCCT	CCCCCGCTTC	TGGCCACAGC

HVR-2 Qualified Cambridge Reference Sequence (rCRS) variations			
Nucleotide Position	Region	Variant Type	Nucleotide Change
00073	HVR-2	Substitution	A>G
00263	HVR-2	Substitution	A>G
00309	HVR-2	Insertion	C>C*
00315	HVR-2	Insertion	C>C*

Coding Region Sequence			
00401	TATCTTTTGG	CGGTATGCAC	TTTTAACAGT
00501	CCATCCTACC	CAGCACACAC	ACACCGCTGC
00601	GCAATACACT	NNNAATGTTT	AGACGGGCTC

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14301 TTCAGCTTCC TACACTATTA AAGTTTACCA CAACACCAC CCCATCATA TCTTTTACC ACAGCACC AA TCCCTACTCC ATCGTAACC CCACTAAAAC
14401 ACTCACAAG ACCTCAACCC CTGACCCCCA TGCTCAGGA TACTCTCAA TAGCCATCCG TGTAGTATAT CCAAAGACAA CCATCATTC CCCTAAATTA
14501 ATTAAAAAA CTATTAACCC CATATAACCT CCCCCAAA TCAGAATAAT AACACACCC ACCACACCCG TAACAATCAA TACTAAACCT CATAAATAG
14601 GAGAAGGCTT AGAAGAAAAC CCCACAACCC CCTACTTAA ACCCAACTC AACACAAAACA AAGCATACAT CATTATTCTC GCACGGACTA CAACACGAC
14701 CAATGATATG AAAAACCATC GTTGATTTT AACTACAAGA ACACCAATGA CCCCATACG CAAAATTAAC CCCCTAATA AATTAATTA CCACTCATTC
14801 ATCGACACTC CCACCCCAT CAACATCTCC GCATGATCA ACTTGGCTC ACTCTCCGAG ACCTGCTGAC TCCTCCAAAT CACCAACAGA CTATTCCTAG
14901 CCTACACTA CTACCCAGC GCCTCAACCC CCTTTTCAAT AATCGCCAC ATCACTCGG ACGTAAATTA TGGCTGAAT ATCCGCTAG TTTACGCCAA
15001 TGGCGCTCA ATATTCTTTA TCTGCCTTT CTTACACATC GGGCGAGGCC TATATTACGG ATCATTTTCT TACTCAGAAA CCTGAAACAT CCGCAATTATC
15101 CTCTGCTTG CAACTATAGC AACAGCTTC ATAGGCTATG TCCTCCGCTG AGGCCAAATA TCATTTCTGAG GGGCCACAGT AATTACAAC TTACTATCCG
15201 CCATCCCAT AATTGGGACA GACCTAGTTC AATGAATCTG AGGAGGCTAC TCAGTAGACA GTCCACCCT CACAGATTC TTTAGCTTTC ACTTCATCTT

15301	GCCCTTCATT	ATTGCAGCCC	TAGCAGCACT	CCACCTCCTA	TTCTTGCAGC	AAACGGGATC	AAACAACCCC	CTAGGAATCA	CCTCCCATTG	CGATAAAATC
15401	ACCTTCACCC	CTTACTACAC	AATCAAAGAC	GCCCTCGGCT	TACTTCTCTT	CATTCTCTCC	TTAATGACAT	TAACACTATT	CTCACCAGAC	CTCCTAGGCG
15501	ACCCAGACAA	TTATACCTA	GCCAACCCCT	TAAACACCCC	TCCCCACATC	AAGCCCGAAT	GATATTTTCT	ATTTCGCCTAC	ACAATTCTCC	GATCCGTCCC
15601	TAACAAGCTA	GGAGGCGTCC	TTGCCCTATT	ACTATCCATC	CTCATCCTAG	CAATAATCCC	CATCCTCCAT	ATATCCAAAC	AACAAGCAT	AATATTTGCG
15701	CCACTAAGCC	AATCACTTTA	TTGACTCCTA	GCCGCAGACC	TCCTCATTCT	AACCTGAATC	GGAGGACAAC	CAGTAAGCTA	CCCTTTTACC	ATCATTGGAC
15801	AAGTAGCATC	CGTACTATA	TTCACAAACA	TCCTAATCCT	AATACCAACT	ATCTCCCTAA	TTGAAAACAA	AATACTCAA	TGGGCCTGTC	CTTGAGTAT
15901	AAACTAATAC	ACCACTCTTG	TAAACCGAAG	ATGAAAACCT	TTTTCCAAGG	ACAAATCAGA	GAAAAAGTCT	TTAACTCCAC	CATTAGCACC	CAAAGCTAAG

Coding Region Qualified Cambridge Reference Sequence (rCRS) variations

Nucleotide Position	Region	Variant Type	Nucleotide Change
00709	Coding Region	Substitution	G>A
00750	Coding Region	Substitution	A>G
00930	Coding Region	Substitution	G>A
01438	Coding Region	Substitution	A>G
01888	Coding Region	Substitution	G>A
02706	Coding Region	Substitution	A>G
04216	Coding Region	Substitution	T>C
04769	Coding Region	Substitution	A>G
04917	Coding Region	Substitution	A>G
05147	Coding Region	Substitution	G>A
07028	Coding Region	Substitution	C>T
08697	Coding Region	Substitution	G>A
08860	Coding Region	Substitution	A>G
11251	Coding Region	Substitution	A>G
11719	Coding Region	Substitution	G>A
11812	Coding Region	Substitution	A>G
13368	Coding Region	Substitution	G>A
14233	Coding Region	Substitution	A>G
14766	Coding Region	Substitution	C>T
14861	Coding Region	Substitution	G>A
14905	Coding Region	Substitution	G>A
15326	Coding Region	Substitution	A>G
15452	Coding Region	Substitution	C>A
15607	Coding Region	Substitution	A>G
15928	Coding Region	Substitution	G>A

mtDNA Haplogroup and Subclade

Brian Nicholas Rossiter has tested the HVR1, HVR2 and Coding regions of his mtDNA.

The results of Brian Nicholas Rossiter's mtDNA HVR1, HVR2 and Coding Region test show that he is positive for 35 mutations: 16051, 16126, 16294, 16296, 16304, 16519, 73, 263, 309, 315, 709, 750, 930, 1438, 1888, 2706, 4216, 4769, 4917, 5147, 7028, 8697, 8860, 11251, 11719, 11812, 13368, 14233, 14766, 14861, 14905, 15326, 15452, 15607, and 15928. These 35 mutations in Brian Nicholas Rossiter's mtDNA confirm that he is a descendant of mtDNA Haplogroup T, subclade T2b13a on his maternal line.

The woman who founded mtDNA Haplogroup T lived approximately 30,000 to 60,000 years ago in the Near East (Mesopotamia).

Descendants of the mtDNA Haplogroup T line moved north and west into Eastern Europe approximately 10,000 years ago. Today, descendants of mtDNA Haplogroup T are found in highest concentrations in Eastern Europe, Russia (Baltic Sea and Urals) and the Middle East. Notable historical figures who belonged to mtDNA Haplogroup T include Tsar Nicholas II of Russia and American outlaw Jesse James.

Origins and Distribution

Population studies have not yet been published for mtDNA Subclade T2b13a. However, population studies are available for the direct ancestors of mtDNA Subclade T2b13a. Population studies to date have found that the ancestors of T2b13a are found in the highest concentration in West Eurasian from Southern Germany. The percentage of each indigenous population which belong to mtDNA Subclade T2b13a is not yet available, however, the distribution of mtDNA Subclade T2b13a is as follows:

West Eurasian from Southern Germany > Murcia, Spain > Pas Valley, Northern Spain > North Europeans from Estonia and Sweden > Central Portugal > North Portugal > Ogliastra in Sardinia, Italy > Western Pomerania, Germany

Family Vault DNA Database Usage

The genetic sequence of Brian Nicholas Rossiter's mtDNA HVR1, HVR2 and Coding regions qualify for FamilyVault DNA database search and analysis features. The FamilyVault DNA Ancestry database allows you to:

- Search for potential family links
- Compare against indigenous populations from around the world
- Find out more about your haplogroup and view a map of your ancestor's ancient migration patterns
- Compare against famous people in history
- Store and share your DNA data, collaborate with family members and organize results from other members of your family

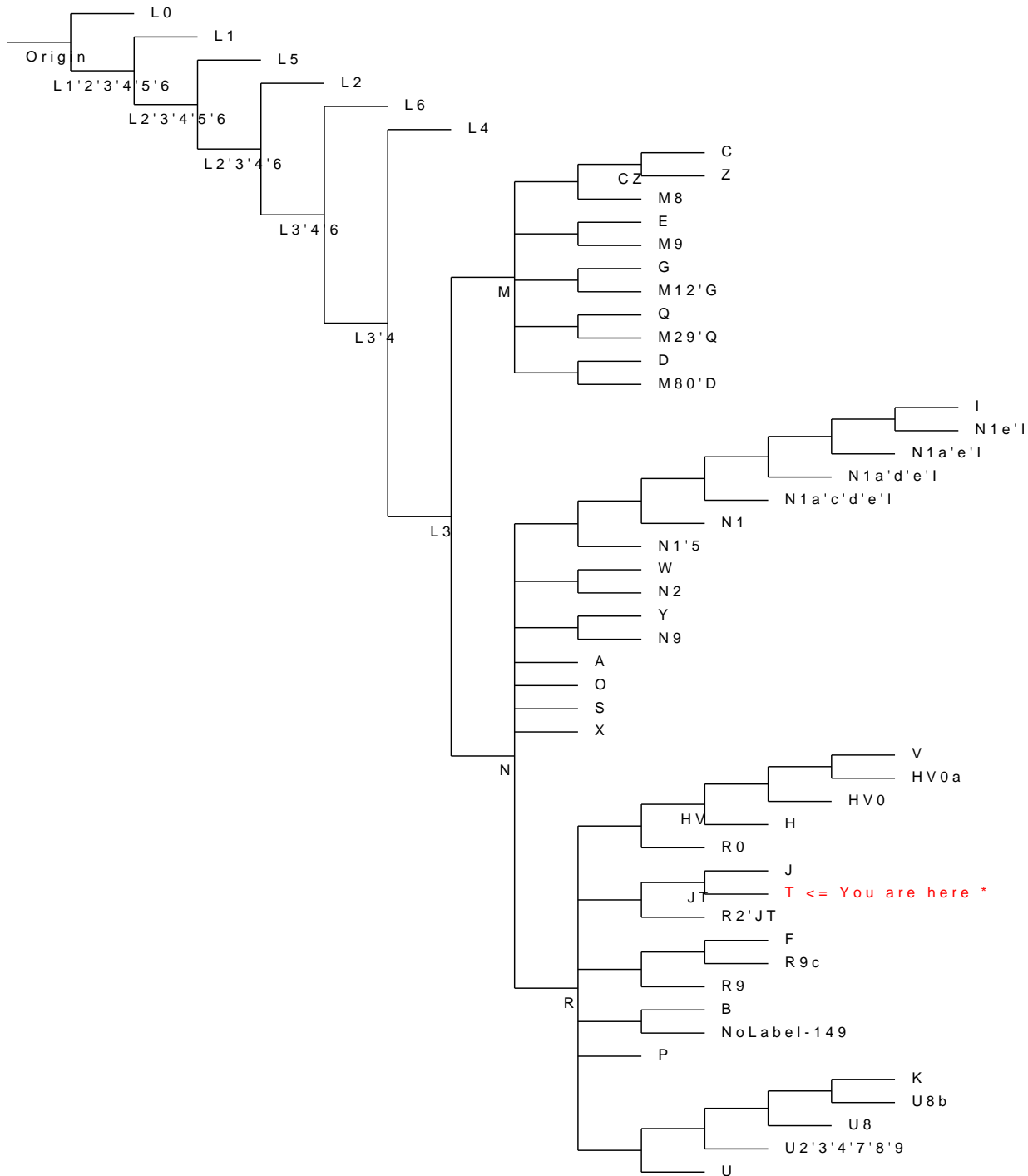
Refer to page 2 of this report for instructions on how to login to your account. After logging in to your account, follow these basic steps to begin searching:

1. To view which specific country or population group is the closest match to Brian Nicholas Rossiter's maternal lineage, click "DNA Ancestry", then select "Indigenous DNA".
2. To find potential relatives along Brian Nicholas Rossiter's direct maternal lineage, click "DNA Ancestry", then select "DNA Reunion" to view Brian Nicholas Rossiter's maternal line matches.
3. To view Brian Nicholas Rossiter's haplogroup and migration map, click "DNA Ancestry", then select "DNA Haplogroups".
4. To compare Brian Nicholas Rossiter's DNA markers against famous historical figures, click "DNA Ancestry", then select "Famous DNA".
5. To download additional copies of your report or to share your report with family members, click "My Results", then click on the PDF logo to download the report or click "Share" to share the report.

If you have any questions or require technical support, click "Help" and submit a ticket to our support team 24/7.

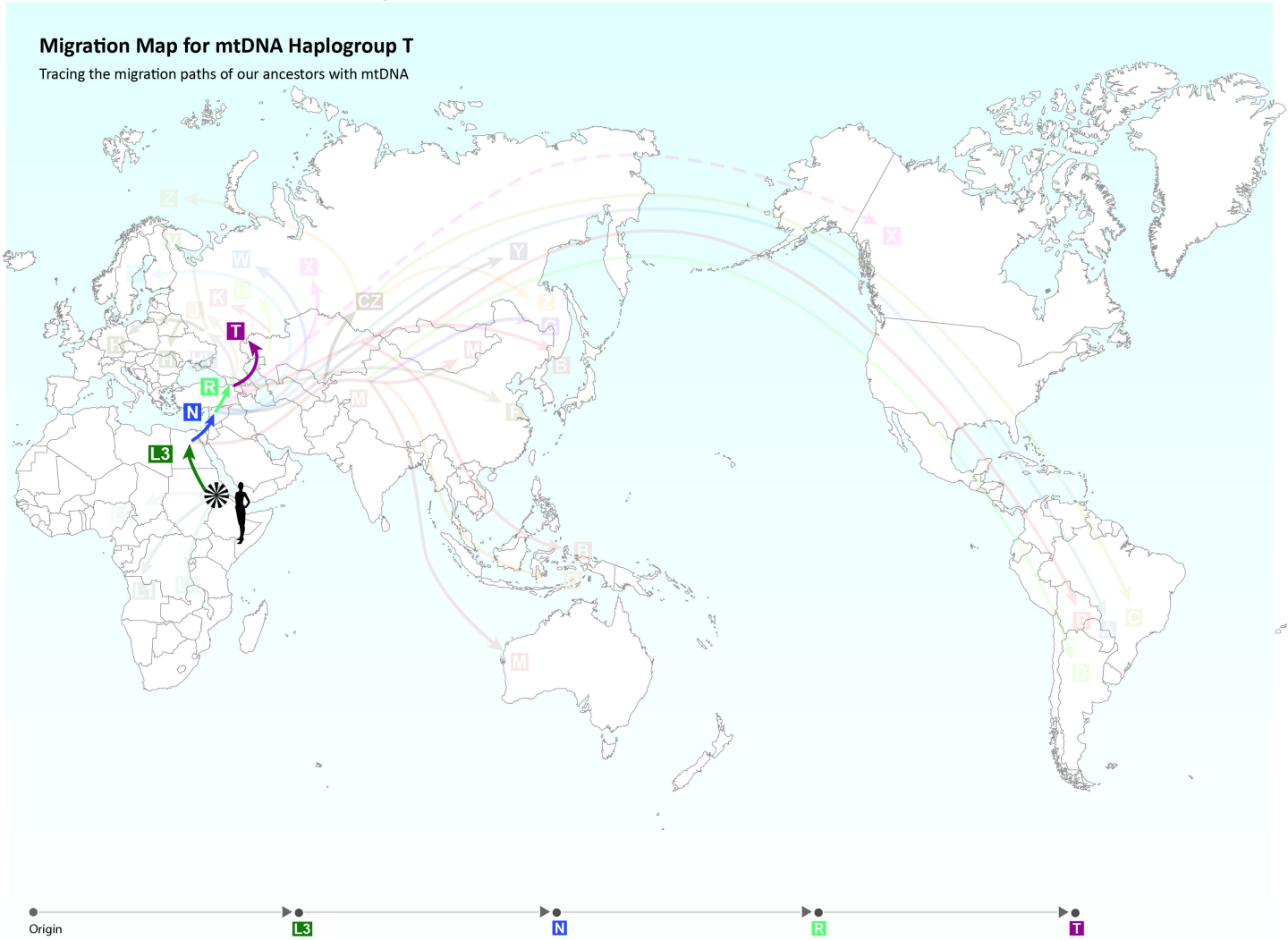
Appendix 1: mtDNA Phylogenetic Tree

The placement of mtDNA Haplogroup T in the mtDNA phylogenetic tree is as follows:



The major branches (mtDNA haplogroups) of the mtDNA phylogenetic tree are shown above. The origin of the tree represents the Mitochondrial Eve (MRCA), a name given by researchers to the most recent common matrilineal ancestor of all humans living today. The origin of the tree dates back approximately 100,000 to 250,000 years.

Appendix 2: mtDNA Maternal Line Migration Map



Appendix 3: Population Distribution Frequency of mtDNA Haplogroup T2b13a in Europe

Population	% of Population belonging to T2b13a	% of Population belonging to T2b13	% of Population belonging to T2b	% of Population belonging to T2	% of Population belonging to T	Study Size	Reference
West Eurasian from Southern Germany	n/a	n/a	8%	11%	14%	100	Application of a quasi-median network analysis for the visualization of character conflicts to a population sample of mitochondrial DNA control region sequences from southern Germany (Ulm). Brandstätter A et al Int J Legal Med. 2006 Sep;120(5):310-4
Murcia, Spain	n/a	n/a	6.8%	9.1%	18.2%	44	Mitochondrial DNA and Y-chromosome structure at the Mediterranean and Atlantic façades of the Iberian Peninsula. Santos C et al Am J Hum Biol. 2014 Mar-Apr;26(2):130-41
Pas Valley, Northern Spain	n/a	n/a	6.56%	19.68%	19.68%	61	Variability of the entire mitochondrial DNA control region in a human isolate from the Pas Valley (northern Spain). Cardoso S et al J Forensic Sci. 2010 Sep;55(5):1196-201
North Europeans from Estonia and Sweden	n/a	n/a	6.3%	8.8%	8.8%	79	Evaluation of the 124-plex SNP typing microarray for forensic testing. Krjatskov K et al Forensic Sci Int Genet. 2009 Dec;4(1):43-8.
Central Portugal	n/a	n/a	5.6%	8.5%	19.2%	391	Mitochondrial DNA and Y-chromosome structure at the Mediterranean and Atlantic façades of the Iberian Peninsula. Santos C et al Am J Hum Biol. 2014 Mar-Apr;26(2):130-41
North Portugal	n/a	n/a	5.1%	7.2%	23%	470	Mitochondrial DNA and Y-chromosome structure at the Mediterranean and Atlantic façades of the Iberian Peninsula. Santos C et al Am J Hum Biol. 2014 Mar-Apr;26(2):130-41
Ogliastra in Sardinia, Italy	n/a	n/a	4.76%	9.52%	9.52%	63	High resolution analysis and phylogenetic network construction using complete mtDNA sequences in sardinian genetic isolates. Fraumene C et al Mol Biol Evol. 2006 Nov;23(11):2101-11. Epub 2006 Aug 10.
Western Pomerania, Germany	n/a	n/a	4.7%	4.7%	8.7%	300	Mitochondrial diversity of a northeast German population sample. Poetsch M et al Forensic Sci Int. 2003 Nov 26;137(2-3):125-32.
Sicily	n/a	n/a	4.53%	10.37%	16.83%	155	Human mitochondrial DNA variation in Southern Italy. Ottoni C et al Ann Hum Biol. 2009 Nov-Dec;36(6):785-811.
Galicia, Spain	n/a	n/a	4.3%	7.2%	17%	555	Mitochondrial DNA and Y-chromosome structure at the Mediterranean and Atlantic façades of the Iberian Peninsula. Santos C et al Am J Hum Biol. 2014 Mar-Apr;26(2):130-41
Vojvodina, Serbia	n/a	n/a	3.84%	5.76%	10.56%	104	Sequence polymorphism of the mitochondrial DNA control region in the population of Vojvodina Province, Serbia. Zgonjanin D et al Leg Med (Tokyo). 2010 Mar;12(2):104-7.
Catalonia, Spain	n/a	n/a	3.8%	7.3%	20.3%	469	Mitochondrial DNA and Y-chromosome structure at the Mediterranean and Atlantic façades of the Iberian Peninsula. Santos C et al Am J Hum Biol. 2014 Mar-Apr;26(2):130-41
Slovenia	n/a	n/a	3.8%	3.8%	5.8%	104	Mitochondrial DNA variability in Bosnians and Slovenians. Malyarchuk BA et al Ann Hum Genet. 2003 Sep;67(Pt 5):412-25.
Satakunta, Finland	n/a	n/a	3.57%	3.57%	3.57%	28	Finnish mitochondrial DNA HVS-I and HVS-II population data. Hedman M et al Forensic Sci Int. 2007 Oct 25;172(2-3):171-8. Epub 2007 Mar 2.
Varsinais-Suomi, Finland	n/a	n/a	3.45%	6.9%	10.35%	29	Finnish mitochondrial DNA HVS-I and HVS-II population data. Hedman M et al Forensic Sci Int. 2007 Oct 25;172(2-3):171-8. Epub 2007 Mar 2.
Italy	n/a	n/a	3.4%	6.4%	13%	395	Italian mitochondrial DNA database: results of a collaborative exercise and proficiency testing. Turchi C et al Int J Legal Med. 2008 May;122(3):199-204.
Basilicata, Italy	n/a	n/a	3.26%	7.62%	9.8%	92	Human mitochondrial DNA variation in Southern Italy. Ottoni C et al Ann Hum Biol. 2009 Nov-Dec;36(6):785-811.
Northern Central Italy	n/a	n/a	3.1%	9.6%	13.4%	384	Multiplex mtDNA coding region SNP assays for molecular dissection of haplogroups U/K and J/T. Grignani P et al Forensic Sci Int Genet. 2009 Dec;4(1):21-5.
Tatars in Buinsk	n/a	n/a	3.1%	4.7%	5.5%	126	Mitogenomic diversity in Tatars from the Volga-Ural region of Russia Malyarchuk B et al Mol Biol Evol. 2010 May 10.
Non-Ashkenazi Jews in Turkey	n/a	n/a	2.5%	9%	10.6%	123	Counting the founders: the matrilineal genetic ancestry of the Jewish Diaspora. Behar DM et al PLoS One. 2008 Apr 30;3(4):e2062.
Vasterbotten, Sweden	n/a	n/a	2.5%	5%	7.5%	40	Homogeneity in mitochondrial DNA control region sequences in Swedish subpopulations. Tillmar AO et al Int J Legal Med. 2010 Mar;124(2):91-8.
Gotland, Sweden	n/a	n/a	2.5%	2.5%	5%	40	Homogeneity in mitochondrial DNA control region sequences in Swedish subpopulations. Tillmar AO et al Int J Legal Med. 2010 Mar;124(2):91-8.
Varmland, Sweden	n/a	n/a	2.38%	4.76%	4.76%	42	Homogeneity in mitochondrial DNA control region sequences in Swedish subpopulations. Tillmar AO et al Int J Legal Med. 2010 Mar;124(2):91-8.
Macedonians in Republic of Macedonia	n/a	n/a	2.24%	4.48%	10.64%	179	Mitochondrial DNA control region population data from Macedonia. Zimmermann B et al Forensic Sci Int Genet. 2007 Dec;1(3-4):e4-9. Epub 2007 May 9.
South Portugal	n/a	n/a	2.2%	3.3%	8.8%	268	Mitochondrial DNA and Y-chromosome structure at the Mediterranean and Atlantic façades of the Iberian Peninsula. Santos C et al Am J Hum Biol. 2014 Mar-Apr;26(2):130-41
Valencia, Spain	n/a	n/a	2%	4.8%	8.8%	250	Mitochondrial DNA and Y-chromosome structure at the Mediterranean and Atlantic façades of the Iberian Peninsula. Santos C et al Am J Hum Biol. 2014 Mar-Apr;26(2):130-41
Dubrovnik, Croatia	n/a	n/a	1.65%	2.2%	2.2%	182	Influence of evolutionary forces and demographic processes on the genetic structure of three Croatian populations: a maternal perspective. Sarac J et al Ann Hum Biol. 2012 Mar;39(2):143-55.
Finland	n/a	n/a	1.55%	3.11%	5.7%	194	Finnish mitochondrial DNA HVS-I and HVS-II population data. Hedman M et al Forensic Sci Int. 2007 Oct 25;172(2-3):171-8. Epub 2007 Mar 2.

Mijet, Croatia	n/a	n/a	1.47%	1.47%	1.47%	68	Influence of evolutionary forces and demographic processes on the genetic structure of three Croatian populations: a maternal perspective. Sarac J et al Ann Hum Biol. 2012 Mar;39(2):143-55.
Non-Ashkenazi Jews in Bulgaria	n/a	n/a	1.4%	11.3%	12.7%	71	Counting the founders: the matrilineal genetic ancestry of the Jewish Diaspora. Behar DM et al PLoS One. 2008 Apr 30;3(4):e2062.
Bosians in Bosnia-Herzegovina	n/a	n/a	1.4%	1.4%	4.8%	144	Mitochondrial DNA variability in Bosnians and Slovenians. Malyarchuk BA et al Ann Hum Genet. 2003 Sep;67(Pt 5):412-25.
Basques in Northern Spain	n/a	n/a	0.94%	1.88%	1.88%	106	Mitochondrial DNA control region variation in an autochthonous Basque population sample from the Basque Country. Cardoso S et al Forensic Sci Int Genet. 2012 Jul;6(4):e106-8.
Ashkenazi Jews in Hungary	n/a	n/a	0.58%	0.58%	2.9%	173	Mitochondrial DNA control region variation in Ashkenazi Jews from Hungary. Brandstätter A et al Forensic Sci Int Genet. 2008 Jan;2(1):e4-6.
Denmark	n/a	n/a	0.5%	5.51%	8.51%	199	Mitochondrial DNA HV1 and HV2 variation in Danes. Mikkelsen M et al Forensic Sci Int Genet. 2010 Jul;4(4):e87-8.
Southeastern Cabo Verde Islands	n/a	n/a	0.5%	0.5%	0.5%	108	Mitochondrial portrait of the Cabo Verde archipelago: the Senegambian outpost of Atlantic slave trade. Brehm A et al Ann Hum Genet. 2002 Jan;66(Pt 1):49-60.
Lower Carniola, Slovenia	n/a	n/a	n/a	11.5%	24.8%	113	The maternal perspective for five Slovenian regions: The importance of regional sampling. Zupan A et al Ann Hum Biol. 2015 Jun 12:1-10.
Vallepietra, Italy	n/a	n/a	n/a	10.87%	39.13%	46	Traces of forgotten historical events in mountain communities in Central Italy: A genetic insight. Messina F et al Am J Hum Biol. 2015 Jul 8;27(4):508-19.
Volterra, Italy	n/a	n/a	n/a	10.5%	13.1%	114	Mitochondrial DNA variation of modern Tuscans supports the near eastern origin of Etruscans. Achilli A et al Am J Hum Genet. 2007 Apr;80(4):759-68.
Ostergötland/Jönköping, Sweden	n/a	n/a	n/a	10%	12.5%	40	Homogeneity in mitochondrial DNA control region sequences in Swedish subpopulations. Tillmar AO et al Int J Legal Med. 2010 Mar;124(2):91-8.
Prekmurje, Slovenia	n/a	n/a	n/a	9.8%	27%	82	The maternal perspective for five Slovenian regions: The importance of regional sampling. Zupan A et al Ann Hum Biol. 2015 Jun 12:1-10.
Calabria, Italy	n/a	n/a	n/a	9.47%	14.72%	95	Human mitochondrial DNA variation in Southern Italy. Ottoni C et al Ann Hum Biol. 2009 Nov-Dec;36(6):785-811.
Slovenia	n/a	n/a	n/a	8.7%	21.2%	402	The maternal perspective for five Slovenian regions: The importance of regional sampling. Zupan A et al Ann Hum Biol. 2015 Jun 12:1-10.
Styria, Slovenia	n/a	n/a	n/a	8.7%	23.2%	103	The maternal perspective for five Slovenian regions: The importance of regional sampling. Zupan A et al Ann Hum Biol. 2015 Jun 12:1-10.
North Portugal	n/a	n/a	n/a	8.33%	16.66%	84	Mitochondrial DNA affinities at the Atlantic fringe of Europe. González AM et al Am J Phys Anthropol. 2003 Apr;120(4):391-404.
Russia Ashkenazi Jews	n/a	n/a	n/a	8.2%	9.84%	61	The matrilineal ancestry of Ashkenazi Jewry: portrait of a recent founder event Behar DM et al Am J Hum Genet. 2006 Mar;78(3):487-97. Epub 2006 Jan 11.
Littoral region, Slovenia	n/a	n/a	n/a	8.2%	16.4%	49	The maternal perspective for five Slovenian regions: The importance of regional sampling. Zupan A et al Ann Hum Biol. 2015 Jun 12:1-10.
Murlo, Italy	n/a	n/a	n/a	8.1%	9.3%	86	Mitochondrial DNA variation of modern Tuscans supports the near eastern origin of Etruscans. Achilli A et al Am J Hum Genet. 2007 Apr;80(4):759-68.
Latvia	n/a	n/a	n/a	7.74%	9.42%	298	Mitochondrial DNA portrait of Latvians: towards the understanding of the genetic structure of Baltic-speaking populations. Pliss L et al Ann Hum Genet. 2006 Jul;70(Pt 4):439-58.
Austria/Hungary Ashkenazi Jews	n/a	n/a	n/a	7.4%	7.4%	27	The matrilineal ancestry of Ashkenazi Jewry: portrait of a recent founder event Behar DM et al Am J Hum Genet. 2006 Mar;78(3):487-97. Epub 2006 Jan 11.
Tuscany Casentino Valley, Italy	n/a	n/a	n/a	7.4%	10.7%	122	Mitochondrial DNA variation of modern Tuscans supports the near eastern origin of Etruscans. Achilli A et al Am J Hum Genet. 2007 Apr;80(4):759-68.
Eastern Azores Islands, Portugal	n/a	n/a	n/a	6%	8%	50	Genetic structure and origin of peopling in the Azores islands (Portugal): the view from mtDNA. Santos C et al Ann Hum Genet. 2003 Sep;67(Pt 5):433-56.
Saracinesco, Italy	n/a	n/a	n/a	5.71%	11.42%	35	Traces of forgotten historical events in mountain communities in Central Italy: A genetic insight. Messina F et al Am J Hum Biol. 2015 Jul 8;27(4):508-19.
Upper Carniola, Slovenia	n/a	n/a	n/a	5.5%	14.6%	55	The maternal perspective for five Slovenian regions: The importance of regional sampling. Zupan A et al Ann Hum Biol. 2015 Jun 12:1-10.
Modern Hungarian-speaking Seklers from Romanian Transylvania	n/a	n/a	n/a	5.5%	16.1%	75	Comparison of maternal lineage and biogeographic analyses of ancient and modern Hungarian populations. Tömöry G et al Am J Phys Anthropol. 2007 Nov;134(3):354-68.
Finistère, Morbihan, Normandy, Périgord-Limousin and Var, France	n/a	n/a	n/a	5.22%	11.08%	153	mtDNA polymorphisms in five French groups: importance of regional sampling. Dubut V et al Eur J Hum Genet. 2004 Apr;12(4):293-300.
Central Azores Islands, Portugal	n/a	n/a	n/a	5.01%	8.34%	60	Genetic structure and origin of peopling in the Azores islands (Portugal): the view from mtDNA. Santos C et al Ann Hum Genet. 2003 Sep;67(Pt 5):433-56.
Hungary	n/a	n/a	n/a	5%	9%	101	Comparison of maternal lineage and biogeographic analyses of ancient and modern Hungarian populations. Tömöry G et al Am J Phys Anthropol. 2007 Nov;134(3):354-68.
Finistère, Morbihan, Normandy, Périgord-Limousin and Var, France	n/a	n/a	n/a	4.91%	11.79%	203	mtDNA polymorphisms in five French groups: importance of regional sampling. Dubut V et al Eur J Hum Genet. 2004 Apr;12(4):293-300.

Skaraborg, Sweden	n/a	n/a	n/a	4.88%	14.64%	41	Homogeneity in mitochondrial DNA control region sequences in Swedish subpopulations. Tillmar AO et al Int J Legal Med. 2010 Mar;124(2):91-8.
Azores, Portugal	n/a	n/a	n/a	4.78%	7.51%	146	Genetic structure and origin of peopling in the Azores islands (Portugal): the view from mtDNA. Santos C et al Ann Hum Genet. 2003 Sep;67(Pt 5):433-56.
Netherlands Ashkenazi Jews	n/a	n/a	n/a	4.76%	4.76%	21	The matrilineal ancestry of Ashkenazi Jewry: portrait of a recent founder event Behar DM et al Am J Hum Genet. 2006 Mar;78(3):487-97. Epub 2006 Jan 11.
Finistère, Morbihan, Normandy, Périgord-Limousin and Var, France	n/a	n/a	n/a	4.64%	10.44%	173	mtDNA polymorphisms in five French groups: importance of regional sampling. Dubut V et al Eur J Hum Genet. 2004 Apr;12(4):293-300.
Portugal	n/a	n/a	n/a	3.98%	8.64%	299	Mitochondrial DNA affinities at the Atlantic fringe of Europe. González AM et al Am J Phys Anthropol. 2003 Apr;120(4):391-404.
Ukraine Ashkenazi Jews	n/a	n/a	n/a	3.78%	5.67%	53	The matrilineal ancestry of Ashkenazi Jewry: portrait of a recent founder event Behar DM et al Am J Hum Genet. 2006 Mar;78(3):487-97. Epub 2006 Jan 11.
Savo, Finland	n/a	n/a	n/a	3.57%	7.14%	28	Finnish mitochondrial DNA HVS-I and HVS-II population data. Hedman M et al Forensic Sci Int. 2007 Oct 25;172(2-3):171-8. Epub 2007 Mar 2.
Ashkenazi Jews	n/a	n/a	n/a	3.38%	4.62%	568	The matrilineal ancestry of Ashkenazi Jewry: portrait of a recent founder event Behar DM et al Am J Hum Genet. 2006 Mar;78(3):487-97. Epub 2006 Jan 11.
Cappadocia, Turkey	n/a	n/a	n/a	3.37%	12.36%	89	Traces of forgotten historical events in mountain communities in Central Italy: A genetic insight. Messina F et al Am J Hum Biol. 2015 Jul 8;27(4):508-19.
Sephardic Jews	n/a	n/a	n/a	3.23%	6.46%	31	Mitochondrial DNA sequence variation in Jewish populations. Picornell A et al Int J Legal Med. 2006 Sep;120(5):271-81.
Romania Ashkenazi Jews	n/a	n/a	n/a	3.09%	3.09%	97	The matrilineal ancestry of Ashkenazi Jewry: portrait of a recent founder event Behar DM et al Am J Hum Genet. 2006 Mar;78(3):487-97. Epub 2006 Jan 11.
Bulgaria	n/a	n/a	n/a	3.06%	12.24%	196	Bulgarians vs the other European populations: a mitochondrial DNA perspective. Karachanak S et al Int J Legal Med. 2012 Jul;126(4):497-503.
Jenne, Italy	n/a	n/a	n/a	2.91%	5.82%	103	Traces of forgotten historical events in mountain communities in Central Italy: A genetic insight. Messina F et al Am J Hum Biol. 2015 Jul 8;27(4):508-19.
Western Azores Islands, Portugal	n/a	n/a	n/a	2.78%	5.56%	36	Genetic structure and origin of peopling in the Azores islands (Portugal): the view from mtDNA. Santos C et al Ann Hum Genet. 2003 Sep;67(Pt 5):433-56.
Blekinge and Kristianstad, Sweden	n/a	n/a	n/a	2.56%	5.12%	39	Homogeneity in mitochondrial DNA control region sequences in Swedish subpopulations. Tillmar AO et al Int J Legal Med. 2010 Mar;124(2):91-8.
Central Portugal	n/a	n/a	n/a	2.56%	5.12%	78	Mitochondrial DNA affinities at the Atlantic fringe of Europe. González AM et al Am J Phys Anthropol. 2003 Apr;120(4):391-404.
Pasiegos in Cantabria, Spain	n/a	n/a	n/a	2.44%	6.1%	82	Y chromosome and mitochondrial DNA characterization of Pasiegos, a human isolate from Cantabria (Spain). Maca-Meyer N et al Ann Hum Genet. 2003 Jul;67(Pt 4):329-39.
Galician in Canary Islands, Spain	n/a	n/a	n/a	2.33%	4.66%	43	Mitochondrial DNA affinities at the Atlantic fringe of Europe. González AM et al Am J Phys Anthropol. 2003 Apr;120(4):391-404.
Non-Pasiego and Non-Lebaniego Cantabrians in Cantabria, Spain	n/a	n/a	n/a	2.28%	4.56%	88	Y chromosome and mitochondrial DNA characterization of Pasiegos, a human isolate from Cantabria (Spain). Maca-Meyer N et al Ann Hum Genet. 2003 Jul;67(Pt 4):329-39.
Almeria, Spain	n/a	n/a	n/a	2.2%	4.4%	91	Mitochondrial DNA and Y-chromosome structure at the Mediterranean and Atlantic façades of the Iberian Peninsula. Santos C et al Am J Hum Biol. 2014 Mar-Apr;26(2):130-41.
Portuguese in South Portugal	n/a	n/a	n/a	2.19%	5.84%	137	Mitochondrial DNA affinities at the Atlantic fringe of Europe. González AM et al Am J Phys Anthropol. 2003 Apr;120(4):391-404.
Uppsala, Sweden	n/a	n/a	n/a	1.85%	5.55%	54	Homogeneity in mitochondrial DNA control region sequences in Swedish subpopulations. Tillmar AO et al Int J Legal Med. 2010 Mar;124(2):91-8.
Basques in Spain	n/a	n/a	n/a	1.8%	1.8%	55	Mitochondrial DNA haplogroup diversity in Basques: a reassessment based on HVI and HVII polymorphisms. Alfonso-Sánchez MA et al Am J Hum Biol. 2008 Mar-Apr;20(2):154-64.
Trevi nel Lazio, Italy	n/a	n/a	n/a	1.72%	24.12%	58	Traces of forgotten historical events in mountain communities in Central Italy: A genetic insight. Messina F et al Am J Hum Biol. 2015 Jul 8;27(4):508-19.
Oshevsk, Russia	n/a	n/a	n/a	1.33%	6.65%	75	Mitochondrial DNA variations in Russian and Belorussian populations. Belyaeva O et al Hum Biol. 2003 Oct;75(5):647-60.
Piglio, Italy	n/a	n/a	n/a	1.04%	6.24%	96	Traces of forgotten historical events in mountain communities in Central Italy: A genetic insight. Messina F et al Am J Hum Biol. 2015 Jul 8;27(4):508-19.
Austria	n/a	n/a	n/a	0.4%	13%	277	Rapid screening of mtDNA coding region SNPs for the identification of west European Caucasian haplogroups Brandstätter A et al Int J Legal Med (2003) 117 : 291-298.
Eastern Vlax Roma in Croatia	n/a	n/a	n/a	n/a	5.17%	232	The role of the Vlax Roma in shaping the European Romani maternal genetic history. Salihović MP et al Am J Phys Anthropol. 2011 Oct;146(2):262-70.
Northwestern Vlax Roma, Croatia	n/a	n/a	n/a	n/a	1.97%	152	The role of the Vlax Roma in shaping the European Romani maternal genetic history. Salihović MP et al Am J Phys Anthropol. 2011 Oct;146(2):262-70.
South Portugal	n/a	n/a	n/a	n/a	10.32%	58	Diversity of mtDNA lineages in Portugal: not a genetic edge of European variation. Pereira L et al Ann Hum Genet. 2000 Nov;64(Pt 6):491-506.
Central Portugal	n/a	n/a	n/a	n/a	10.8%	83	Diversity of mtDNA lineages in Portugal: not a genetic edge of European variation. Pereira L et al Ann Hum Genet. 2000 Nov;64(Pt 6):491-506.

North Portugal	n/a	n/a	n/a	n/a	11.11%	99	Diversity of mtDNA lineages in Portugal: not a genetic edge of European variation. Pereira L et al Ann Hum Genet. 2000 Nov;64(Pt 6):491-506.
Andalusia, Spain	n/a	n/a	n/a	n/a	10%	50	Mitochondrial DNA characterisation of European isolates: the Maragatos from Spain. Larruga JM et al Eur J Hum Genet. 2001 Sep;9(9):708-16.
Castile, Spain	n/a	n/a	n/a	n/a	7.89%	38	Mitochondrial DNA characterisation of European isolates: the Maragatos from Spain. Larruga JM et al Eur J Hum Genet. 2001 Sep;9(9):708-16.
Leonese in Iberian Peninsula	n/a	n/a	n/a	n/a	4.92%	61	Mitochondrial DNA characterisation of European isolates: the Maragatos from Spain. Larruga JM et al Eur J Hum Genet. 2001 Sep;9(9):708-16.
Maragatos in Astorga, Spain	n/a	n/a	n/a	n/a	4.08%	49	Mitochondrial DNA characterisation of European isolates: the Maragatos from Spain. Larruga JM et al Eur J Hum Genet. 2001 Sep;9(9):708-16.
Hvar, Croatia	n/a	n/a	n/a	n/a	13.91%	108	The evidence of mtDNA haplogroup F in a European population and its ethnohistoric implications. Tolk HV et al Eur J Hum Genet. 2001 Sep;9(9):717-23.
Northern Savo, Finland	n/a	n/a	n/a	n/a	1%	100	Evidence for mtDNA admixture between the Finns and the Saami. Meiniälä M et al Hum Hered. 2001;52(3):160-70.
Kainuu, Finland	n/a	n/a	n/a	n/a	0.96%	104	Evidence for mtDNA admixture between the Finns and the Saami. Meiniälä M et al Hum Hered. 2001;52(3):160-70.
Northern Ostrobothnia, Finland	n/a	n/a	n/a	n/a	8.08%	99	Evidence for mtDNA admixture between the Finns and the Saami. Meiniälä M et al Hum Hered. 2001;52(3):160-70.
Bashkiria, Russia	n/a	n/a	n/a	n/a	3.6%	83	Mitochondrial DNA variations in Russian and Belorussian populations. Belyaeva O et al Hum Biol. 2003 Oct;75(5):647-60.
Belorussians in Russia	n/a	n/a	n/a	n/a	6.53%	92	Mitochondrial DNA variations in Russian and Belorussian populations. Belyaeva O et al Hum Biol. 2003 Oct;75(5):647-60.
Morbihan, France	n/a	n/a	n/a	n/a	7.32%	41	An mtDNA perspective of French genetic variation. Richard C et al Ann Hum Biol. 2007 Jan-Feb;34(1):68-79.
Finistere, France	n/a	n/a	n/a	n/a	6.65%	120	An mtDNA perspective of French genetic variation. Richard C et al Ann Hum Biol. 2007 Jan-Feb;34(1):68-79.
Loire-Atlantique, France	n/a	n/a	n/a	n/a	6.65%	75	An mtDNA perspective of French genetic variation. Richard C et al Ann Hum Biol. 2007 Jan-Feb;34(1):68-79.
Pyrénées-Atlantiques, France	n/a	n/a	n/a	n/a	3.7%	81	An mtDNA perspective of French genetic variation. Richard C et al Ann Hum Biol. 2007 Jan-Feb;34(1):68-79.
Sarthe, France	n/a	n/a	n/a	n/a	8.34%	36	An mtDNA perspective of French genetic variation. Richard C et al Ann Hum Biol. 2007 Jan-Feb;34(1):68-79.
Maine et Loire, France	n/a	n/a	n/a	n/a	16.38%	55	An mtDNA perspective of French genetic variation. Richard C et al Ann Hum Biol. 2007 Jan-Feb;34(1):68-79.
Somme, France	n/a	n/a	n/a	n/a	12.81%	78	An mtDNA perspective of French genetic variation. Richard C et al Ann Hum Biol. 2007 Jan-Feb;34(1):68-79.
Hérault in Languedoc, France	n/a	n/a	n/a	n/a	15.31%	85	An mtDNA perspective of French genetic variation. Richard C et al Ann Hum Biol. 2007 Jan-Feb;34(1):68-79.
Calvados in France	n/a	n/a	n/a	n/a	2.17%	46	An mtDNA perspective of French genetic variation. Richard C et al Ann Hum Biol. 2007 Jan-Feb;34(1):68-79.
Vendée, France	n/a	n/a	n/a	n/a	5%	80	An mtDNA perspective of French genetic variation. Richard C et al Ann Hum Biol. 2007 Jan-Feb;34(1):68-79.
Lastovo, Croatia	n/a	n/a	n/a	n/a	3.92%	51	Influence of evolutionary forces and demographic processes on the genetic structure of three Croatian populations: a maternal perspective. Sarac J et al Ann Hum Biol. 2012 Mar;39(2):143-55.
Siwa Berbers in Tunisia	n/a	n/a	n/a	n/a	1.3%	77	The complex and diversified mitochondrial gene pool of Berber populations. Coudray C et al Ann Hum Genet. 2009 Mar;73(2):196-214. Epub 2008 Nov 27.
Pohjanmaa, Finland	n/a	n/a	n/a	n/a	3.45%	29	Finnish mitochondrial DNA HVS-I and HVS-II population data. Hedman M et al Forensic Sci Int. 2007 Oct 25;172(2-3):171-8. Epub 2007 Mar 2.
Karjala, Finland	n/a	n/a	n/a	n/a	3.33%	30	Finnish mitochondrial DNA HVS-I and HVS-II population data. Hedman M et al Forensic Sci Int. 2007 Oct 25;172(2-3):171-8. Epub 2007 Mar 2.
Slovenia	n/a	n/a	n/a	n/a	5.88%	102	Mitochondrial DNA variability in Bosnians and Slovenians. Malyarchuk BA et al Ann Hum Genet. 2003 Sep;67(Pt 5):412-25.
Bosnians in Bosnia-Herzegovina	n/a	n/a	n/a	n/a	4.91%	142	Mitochondrial DNA variability in Bosnians and Slovenians. Malyarchuk BA et al Ann Hum Genet. 2003 Sep;67(Pt 5):412-25.
Turgovzi Romani in Omurtag, Bulgaria	n/a	n/a	n/a	n/a	4%	25	Origins and divergence of the Roma (gypsies). Gresham D et al Am J Hum Genet. 2001 Dec;69(6):1314-31. Epub 2001 Nov 9.
Roma Gypsies from Northern Bulgaria in Kalderash	n/a	n/a	n/a	n/a	4.35%	23	Origins and divergence of the Roma (gypsies). Gresham D et al Am J Hum Genet. 2001 Dec;69(6):1314-31. Epub 2001 Nov 9.
Lom Romani in Lom, Bulgaria	n/a	n/a	n/a	n/a	2.33%	43	Origins and divergence of the Roma (gypsies). Gresham D et al Am J Hum Genet. 2001 Dec;69(6):1314-31. Epub 2001 Nov 9.
Monteni Romani in Balkan Mountain villages, Bulgaria	n/a	n/a	n/a	n/a	4.76%	42	Origins and divergence of the Roma (gypsies). Gresham D et al Am J Hum Genet. 2001 Dec;69(6):1314-31. Epub 2001 Nov 9.

French Ashkenazi Jews	n/a	n/a	n/a	n/a	4.26%	47	The matrilineal ancestry of Ashkenazi Jewry: portrait of a recent founder event Behar DM et al Am J Hum Genet. 2006 Mar;78(3):487-97. Epub 2006 Jan 11.
Chelha-speaking Jerbian Berbers in Jerba Island	n/a	n/a	n/a	n/a	15.4%	26	Islands inside an island: reproductive isolates on Jerba island Loueslati BY et al Am J Hum Biol. 2006 Jan;18(1):149-53
Jerbian Arabs in Jerba Island	n/a	n/a	n/a	n/a	25.01%	24	Islands inside an island: reproductive isolates on Jerba island Loueslati BY et al Am J Hum Biol. 2006 Jan;18(1):149-53
Finland	n/a	n/a	n/a	n/a	1.7%	403	Traces of early Eurasians in the Mansi of northwest Siberia revealed by mitochondrial DNA analysis. Derbeneva OA et al Am J Hum Genet. 2002 Apr;70(4):1009-14. Epub 2002 Feb 13.
Saami	n/a	n/a	n/a	n/a	n/a	176	Traces of early Eurasians in the Mansi of northwest Siberia revealed by mitochondrial DNA analysis. Derbeneva OA et al Am J Hum Genet. 2002 Apr;70(4):1009-14. Epub 2002 Feb 13.
Mansi in Russia	n/a	n/a	n/a	n/a	10.3%	98	Traces of early Eurasians in the Mansi of northwest Siberia revealed by mitochondrial DNA analysis. Derbeneva OA et al Am J Hum Genet. 2002 Apr;70(4):1009-14. Epub 2002 Feb 13.
Mansi in Northern Sos'va River and Lyamin River Basin	n/a	n/a	n/a	n/a	15.4%	39	Traces of early Eurasians in the Mansi of northwest Siberia revealed by mitochondrial DNA analysis. Derbeneva OA et al Am J Hum Genet. 2002 Apr;70(4):1009-14. Epub 2002 Feb 13.
Mansi in Konda River, Russia	n/a	n/a	n/a	n/a	6.8%	59	Traces of early Eurasians in the Mansi of northwest Siberia revealed by mitochondrial DNA analysis. Derbeneva OA et al Am J Hum Genet. 2002 Apr;70(4):1009-14. Epub 2002 Feb 13.
Poland	n/a	n/a	n/a	n/a	11.5%	436	Russian Old Believers: genetic consequences of their persecution and exile, as shown by mitochondrial DNA evidence. Rubinstein S et al Hum Biol. 2008 Jun;80(3):203-37.
Slovenia	n/a	n/a	n/a	n/a	5.8%	104	Russian Old Believers: genetic consequences of their persecution and exile, as shown by mitochondrial DNA evidence. Rubinstein S et al Hum Biol. 2008 Jun;80(3):203-37.
Bosnians	n/a	n/a	n/a	n/a	4.9%	144	Russian Old Believers: genetic consequences of their persecution and exile, as shown by mitochondrial DNA evidence. Rubinstein S et al Hum Biol. 2008 Jun;80(3):203-37.
Russians in Eastern Europe	n/a	n/a	n/a	n/a	10.9%	201	Russian Old Believers: genetic consequences of their persecution and exile, as shown by mitochondrial DNA evidence. Rubinstein S et al Hum Biol. 2008 Jun;80(3):203-37.
Ancient Norwegians	n/a	n/a	n/a	n/a	2.33%	43	Mitochondrial DNA variation in the Viking age population of Norway. Krzewińska M et al Philos Trans R Soc Lond B Biol Sci. 2015 Jan 19;370(1660):20130384.
Norway	n/a	n/a	n/a	n/a	8.47%	838	Mitochondrial DNA variation in the Viking age population of Norway. Krzewińska M et al Philos Trans R Soc Lond B Biol Sci. 2015 Jan 19;370(1660):20130384.
Jenne, Italy	n/a	n/a	n/a	n/a	4.62%	65	Traces of forgotten historical events in mountain communities in Central Italy: A genetic insight. Messina F et al Am J Hum Biol. 2015 Jul 8;27(4):508-19.
Vallepietra, Italy	n/a	n/a	n/a	n/a	11.11%	18	Traces of forgotten historical events in mountain communities in Central Italy: A genetic insight. Messina F et al Am J Hum Biol. 2015 Jul 8;27(4):508-19.
Trevi nel Lazio, Italy	n/a	n/a	n/a	n/a	n/a	23	Traces of forgotten historical events in mountain communities in Central Italy: A genetic insight. Messina F et al Am J Hum Biol. 2015 Jul 8;27(4):508-19.
Saracinesco, Italy	n/a	n/a	n/a	n/a	7.69%	13	Traces of forgotten historical events in mountain communities in Central Italy: A genetic insight. Messina F et al Am J Hum Biol. 2015 Jul 8;27(4):508-19.
Piglio, Italy	n/a	n/a	n/a	n/a	n/a	47	Traces of forgotten historical events in mountain communities in Central Italy: A genetic insight. Messina F et al Am J Hum Biol. 2015 Jul 8;27(4):508-19.
Filettino, Italy	n/a	n/a	n/a	n/a	11.76%	17	Traces of forgotten historical events in mountain communities in Central Italy: A genetic insight. Messina F et al Am J Hum Biol. 2015 Jul 8;27(4):508-19.
Cappadocia, Turkey	n/a	n/a	n/a	n/a	9.26%	54	Traces of forgotten historical events in mountain communities in Central Italy: A genetic insight. Messina F et al Am J Hum Biol. 2015 Jul 8;27(4):508-19.
Filettino, Italy	n/a	n/a	n/a	n/a	16.28%	43	Traces of forgotten historical events in mountain communities in Central Italy: A genetic insight. Messina F et al Am J Hum Biol. 2015 Jul 8;27(4):508-19.
Latvia	n/a	n/a	n/a	n/a	8.8%	114	Ancient DNA reveals lack of continuity between neolithic hunter-gatherers and contemporary Scandinavians. Malmström H et al Curr Biol. 2009 Nov 3;19(20):1758-62.
Lithuania	n/a	n/a	n/a	n/a	10.4%	163	Ancient DNA reveals lack of continuity between neolithic hunter-gatherers and contemporary Scandinavians. Malmström H et al Curr Biol. 2009 Nov 3;19(20):1758-62.
Estonia	n/a	n/a	n/a	n/a	13.7%	117	Ancient DNA reveals lack of continuity between neolithic hunter-gatherers and contemporary Scandinavians. Malmström H et al Curr Biol. 2009 Nov 3;19(20):1758-62.
Saami	n/a	n/a	n/a	n/a	n/a	37	Ancient DNA reveals lack of continuity between neolithic hunter-gatherers and contemporary Scandinavians. Malmström H et al Curr Biol. 2009 Nov 3;19(20):1758-62.
Sweden	n/a	n/a	n/a	n/a	7.6%	290	Ancient DNA reveals lack of continuity between neolithic hunter-gatherers and contemporary Scandinavians. Malmström H et al Curr Biol. 2009 Nov 3;19(20):1758-62.
Tatars in Aznakaevo	n/a	n/a	n/a	n/a	8.4%	71	Mitogenomic diversity in Tatars from the Volga-Ural region of Russia Malyarchuk B et al Mol Biol Evol. 2010 May 10.
Slovenia	n/a	n/a	n/a	n/a	5.8%	104	Mitochondrial DNA variability in the Czech population, with application to the ethnic history of Slavs. Malyarchuk BA et al Hum Biol. 2006 Dec;78(6):681-96.
Bosnians	n/a	n/a	n/a	n/a	4.9%	144	Mitochondrial DNA variability in the Czech population, with application to the ethnic history of Slavs. Malyarchuk BA et al Hum Biol. 2006 Dec;78(6):681-96.
Czech in Western Bohemia, Czech Republic	n/a	n/a	n/a	n/a	12.3%	179	Mitochondrial DNA variability in the Czech population, with application to the ethnic history of Slavs. Malyarchuk BA et al Hum Biol. 2006 Dec;78(6):681-96.

Russians from three European regions of Russia (Stavropol region, Orel region, Saratov region)	n/a	n/a	n/a	n/a	11%	201	Mitochondrial DNA variability in Poles and Russians. Malyarchuk BA et al Ann Hum Genet. 2002 Jul;66(Pt 4):261-83.
Poles from the Pomerania-Kujawy region of Northern Poland	n/a	n/a	n/a	n/a	11.5%	436	Mitochondrial DNA variability in Poles and Russians. Malyarchuk BA et al Ann Hum Genet. 2002 Jul;66(Pt 4):261-83.
Northwestern Cabo Verde Islands	n/a	n/a	n/a	n/a	n/a	184	Mitochondrial portrait of the Cabo Verde archipelago: the Senegambian outpost of Atlantic slave trade. Brehm A et al Ann Hum Genet. 2002 Jan;66(Pt 1):49-60.
Belmonte Jews (Non-Ashkenazi) in Portugal	n/a	n/a	n/a	n/a	n/a	30	Counting the founders: the matrilineal genetic ancestry of the Jewish Diaspora. Behar DM et al PLoS One. 2008 Apr 30;3(4):e2062.
Tuscany, Italy	n/a	n/a	n/a	n/a	10.4%	48	Classification of European mtDNAs From an Analysis of Three European Populations. Torroni A et al Genetics. 1996 Dec;144(4):1835-50.
Sweden	n/a	n/a	n/a	n/a	21.6%	37	Classification of European mtDNAs From an Analysis of Three European Populations. Torroni A et al Genetics. 1996 Dec;144(4):1835-50.
Finland	n/a	n/a	n/a	n/a	6.1%	49	Classification of European mtDNAs From an Analysis of Three European Populations. Torroni A et al Genetics. 1996 Dec;144(4):1835-50.

Appendix 3: Population Distribution Frequency of mtDNA Haplogroup T2b13a in Middle East & Central Asia

Population	% of Population belonging to T2b13a	% of Population belonging to T2b13	% of Population belonging to T2b	% of Population belonging to T2	% of Population belonging to T	Study Size	Reference
Bedouins (Non-Jewish)	n/a	n/a	1.8%	8.7%	12.1%	58	Counting the founders: the matrilineal genetic ancestry of the Jewish Diaspora. Behar DM et al PLoS One. 2008 Apr 30;3(4):e2062.
Non-Ashkenazi Jews in Iran	n/a	n/a	1.2%	18.3%	20.7%	82	Counting the founders: the matrilineal genetic ancestry of the Jewish Diaspora. Behar DM et al PLoS One. 2008 Apr 30;3(4):e2062.
Druze in Israel	n/a	n/a	0.6%	0.6%	7.3%	311	The Druze: a population genetic refugium of the Near East. Shlush LI et al PLoS One. 2008 May 7;3(5):e2105.
Non-Ashkenazi Jews in Iraq	n/a	n/a	n/a	20%	21.5%	135	Counting the founders: the matrilineal genetic ancestry of the Jewish Diaspora. Behar DM et al PLoS One. 2008 Apr 30;3(4):e2062.
Non-Ashkenazi Jews in Georgia	n/a	n/a	n/a	9.5%	9.5%	74	Counting the founders: the matrilineal genetic ancestry of the Jewish Diaspora. Behar DM et al PLoS One. 2008 Apr 30;3(4):e2062.
Non-Ashkenazi Jews in Azerbaijan	n/a	n/a	n/a	8.6%	8.6%	58	Counting the founders: the matrilineal genetic ancestry of the Jewish Diaspora. Behar DM et al PLoS One. 2008 Apr 30;3(4):e2062.
Oriental Jews	n/a	n/a	n/a	4.35%	8.7%	23	Mitochondrial DNA sequence variation in Jewish populations. Picornell A et al Int J Legal Med. 2006 Sep;120(5):271-81.
Non-Ashkenazi Jews in Yemen	n/a	n/a	n/a	0.8%	1.6%	119	Counting the founders: the matrilineal genetic ancestry of the Jewish Diaspora. Behar DM et al PLoS One. 2008 Apr 30;3(4):e2062.
Yemenite in Yemen	n/a	n/a	n/a	0.7%	9.84%	142	Mitochondrial DNA reveals distinct evolutionary histories for Jewish populations in Yemen and Ethiopia. Non AL et al Am J Phys Anthropol. 2011 Jan;144(1):1-10.
Shugnan in Tajikistan and High Pamirs	n/a	n/a	n/a	n/a	2.27%	44	Where west meets east: the complex mtDNA landscape of the southwest and Central Asian corridor. Quintana-Murci L et al Am J Hum Genet. 2004 May;74(5):827-45. Epub 2004 Apr 7.Click here to read
Kurds in Turkmenistan	n/a	n/a	n/a	n/a	18.75%	32	Where west meets east: the complex mtDNA landscape of the southwest and Central Asian corridor. Quintana-Murci L et al Am J Hum Genet. 2004 May;74(5):827-45. Epub 2004 Apr 7.Click here to read
Turkmenistan	n/a	n/a	n/a	n/a	7.32%	41	Where west meets east: the complex mtDNA landscape of the southwest and Central Asian corridor. Quintana-Murci L et al Am J Hum Genet. 2004 May;74(5):827-45. Epub 2004 Apr 7.Click here to read
Uzbek in Surkhandarya, Uzbekistan	n/a	n/a	n/a	n/a	4.76%	42	Where west meets east: the complex mtDNA landscape of the southwest and Central Asian corridor. Quintana-Murci L et al Am J Hum Genet. 2004 May;74(5):827-45. Epub 2004 Apr 7.Click here to read
Mazandarian in Northern Iran and Southwestern Caspian Sea Area	n/a	n/a	n/a	n/a	14.28%	21	Where west meets east: the complex mtDNA landscape of the southwest and Central Asian corridor. Quintana-Murci L et al Am J Hum Genet. 2004 May;74(5):827-45. Epub 2004 Apr 7.Click here to read
Gilaki in Northern Iran and Southwestern Caspian Sea Area	n/a	n/a	n/a	n/a	16.21%	37	Where west meets east: the complex mtDNA landscape of the southwest and Central Asian corridor. Quintana-Murci L et al Am J Hum Genet. 2004 May;74(5):827-45. Epub 2004 Apr 7.Click here to read
Turkish in Eastern and Western Azerbaijan	n/a	n/a	n/a	n/a	15%	40	Where west meets east: the complex mtDNA landscape of the southwest and Central Asian corridor. Quintana-Murci L et al Am J Hum Genet. 2004 May;74(5):827-45. Epub 2004 Apr 7.Click here to read
Persian in Central and Southern Central Iran	n/a	n/a	n/a	n/a	9.52%	42	Where west meets east: the complex mtDNA landscape of the southwest and Central Asian corridor. Quintana-Murci L et al Am J Hum Genet. 2004 May;74(5):827-45. Epub 2004 Apr 7.Click here to read

Southwest and Central Asia (Iran, Pakistan, Azerbaijan, India, Uzbekistan, Turkmenistan, Tajikistan)	n/a	n/a	n/a	n/a	6.64%	702	Where west meets east: the complex mtDNA landscape of the southwest and Central Asian corridor. Quintana-Murci L et al Am J Hum Genet. 2004 May;74(5):827-45. Epub 2004 Apr 7. Click here to read
Yemeni in Kuwait	n/a	n/a	n/a	n/a	0.87%	115	Ethiopian mitochondrial DNA heritage: tracking gene flow across and around the gate of tears. Kivisild T et al Am J Hum Genet. 2004 Nov;75(5):752-70. Epub 2004 Sep 27.
Yemeni in East of Sana'a, Yemen	n/a	n/a	n/a	n/a	5%	40	Regional differences in the distribution of the sub-Saharan, West Eurasian, and South Asian mtDNA lineages in Yemen. Cerný V et al Am J Phys Anthropol. 2008 Jun;136(2):128-37.
Yemeni in North of Sana'a, Yemen	n/a	n/a	n/a	n/a	5.72%	35	Regional differences in the distribution of the sub-Saharan, West Eurasian, and South Asian mtDNA lineages in Yemen. Cerný V et al Am J Phys Anthropol. 2008 Jun;136(2):128-37.
Yemeni in West of Sana'a, Yemen	n/a	n/a	n/a	n/a	4.48%	67	Regional differences in the distribution of the sub-Saharan, West Eurasian, and South Asian mtDNA lineages in Yemen. Cerný V et al Am J Phys Anthropol. 2008 Jun;136(2):128-37.
Yemeni in South of Sana'a, Yemen	n/a	n/a	n/a	n/a	13.96%	43	Regional differences in the distribution of the sub-Saharan, West Eurasian, and South Asian mtDNA lineages in Yemen. Cerný V et al Am J Phys Anthropol. 2008 Jun;136(2):128-37.
Yemenis	n/a	n/a	n/a	n/a	8.64%	185	Regional differences in the distribution of the sub-Saharan, West Eurasian, and South Asian mtDNA lineages in Yemen. Cerný V et al Am J Phys Anthropol. 2008 Jun;136(2):128-37.
Indian Tamils in Sri Lanka	n/a	n/a	n/a	n/a	n/a	22	A study of genetic polymorphisms in mitochondrial DNA hypervariable regions I and II of the five major ethnic groups and Vedda population in Sri Lanka. Ranasinghe R et al Leg Med (Tokyo). 2015 May 27.
Muslims in Sri Lanka	n/a	n/a	n/a	n/a	n/a	30	A study of genetic polymorphisms in mitochondrial DNA hypervariable regions I and II of the five major ethnic groups and Vedda population in Sri Lanka. Ranasinghe R et al Leg Med (Tokyo). 2015 May 27.
Vedda in Sri Lanka	n/a	n/a	n/a	n/a	n/a	30	A study of genetic polymorphisms in mitochondrial DNA hypervariable regions I and II of the five major ethnic groups and Vedda population in Sri Lanka. Ranasinghe R et al Leg Med (Tokyo). 2015 May 27.
Malay in Sri Lanka	n/a	n/a	n/a	n/a	n/a	30	A study of genetic polymorphisms in mitochondrial DNA hypervariable regions I and II of the five major ethnic groups and Vedda population in Sri Lanka. Ranasinghe R et al Leg Med (Tokyo). 2015 May 27.
Sinhalese in Sri Lanka	n/a	n/a	n/a	n/a	1.7%	60	A study of genetic polymorphisms in mitochondrial DNA hypervariable regions I and II of the five major ethnic groups and Vedda population in Sri Lanka. Ranasinghe R et al Leg Med (Tokyo). 2015 May 27.
Yemenis	n/a	n/a	n/a	n/a	0.9%	115	Ethiopian mitochondrial DNA heritage: tracking gene flow across and around the gate of tears. Kivisild T et al Am J Hum Genet. 2004 Nov;75(5):752-70. Epub 2004 Sep 27.
Tajikstan	n/a	n/a	n/a	n/a	2.3%	44	Phylogeographic analysis of mitochondrial DNA in northern Asian populations. Derenko M et al Am J Hum Genet. 2007 Nov;81(5):1025-41.
Kurds	n/a	n/a	n/a	n/a	12%	25	Phylogeographic analysis of mitochondrial DNA in northern Asian populations. Derenko M et al Am J Hum Genet. 2007 Nov;81(5):1025-41.
Persians	n/a	n/a	n/a	n/a	13.4%	82	Phylogeographic analysis of mitochondrial DNA in northern Asian populations. Derenko M et al Am J Hum Genet. 2007 Nov;81(5):1025-41.
Druze (Non-Jewish)	n/a	n/a	n/a	n/a	1.3%	77	Counting the founders: the matrilineal genetic ancestry of the Jewish Diaspora. Behar DM et al PLoS One. 2008 Apr 30;3(4):e2062.

Background Information for mtDNA Testing

Mitochondrial DNA (mtDNA) is DNA which is found in the mitochondria of human cells. Both males and females have mtDNA so both males and females can take the mtDNA test, but only females will pass their mtDNA down to the next generation. The strict **matrilineal** inheritance pattern of mtDNA means that your **mtDNA profile** is unique to your **Maternal lineage** and shared by all people who descended from the same **matrilineal ancestral lineage** as you. Testing your mtDNA allows you to trace your **direct Maternal ancestry** (your mother's, mother's, mother's.... maternal line).

mtDNA is a circular loop of DNA that is approximately 16,569 base pairs in length, consisting of **3 regions: HVR1, HVR2, and Coding Regions**. The Coding region is approximately 30x larger than the HVR1 and HVR2 regions. All three regions contain markers which are important for ancestral analysis.

mtDNA Testing

The mtDNA test uses a technique called Sanger Sequencing to read the entire sequence of DNA in each region of the mtDNA tested. The **HVR1 test** sequences approximately 500 base pairs of DNA ranging from positions 16000 to 16569 in the HVR1 region of your mtDNA; the **HVR2 test** sequences approximately 400 base pairs of DNA ranging from positions 1 to 400 in the HVR2 region of your mtDNA; and the **Coding region test** sequences approximately 15,600 base pairs of DNA ranging from positions 400 to 16000 in the Coding region of your mtDNA. The three regions together (HVR1, HVR2 and Coding Regions) represent your entire mtDNA and when all three regions of your mtDNA are tested, it is considered a mtDNA "Full Sequencing" test.

You can choose to test all 3 regions of your mtDNA (mtDNA full sequencing) or you can test only a few regions at a time, starting with the HVR1 region. If you choose to test all 3 regions, you will receive a reading on all 16,569 base pairs of your mtDNA. The DNA sequence for each region tested is provided to you in your mtDNA test report. Your mtDNA sequencing results are also compared to a reference sequence called "rCRS" (revised Cambridge Reference Sequence) and all of the positions within your mtDNA which differ from rCRS are listed in your report.

Your unique mtDNA sequence result is known as your **mtDNA profile**. Individuals share the same mtDNA profile if their mtDNA sequences are an exact match to each other. Since mtDNA is passed down from mother to child along the direct maternal lineage, individuals who have descended from the same maternal lineage are expected to have exactly the same or very similar mtDNA profiles. If two individuals have different mtDNA profiles, it would conclusively confirm that they did not descend from the same maternal lineage, regardless of family legend.

If two individuals have a perfect match at their HVR1 and HVR2 regions, further comparison of the much larger Coding region can provide a higher stringency comparison and further resolution.

mtDNA Haplogroups

DNA studies have shown that all people living today can trace their ancestry back to common roots in Africa approximately 100,000 to 300,000 years ago. Over time, man eventually journeyed out of Africa, and in many waves of migrations which spanned tens of thousands of years, eventually populated the rest of the world. During these ancient journeys, small mutations called "SNPs" occurred randomly in their DNA. Each SNP acts as a "time-and-date stamp" which allows us to understand the approximate time and location in the journey our ancestors were when the SNP first occurred. Once a SNP occurs, it is passed down to all future generations and serves as a marker which allows us to approximate where our ancestors were at specific timepoints every few thousand years along the ancient migration route out of Africa. Today, our Y-DNA and mtDNA contains a rich collection of SNP markers, passed down to us from our ancient ancestors over thousands of years. Y-DNA SNPs are used for tracing paternal ancestry and mtDNA SNPs are used for tracing maternal ancestry.

Using SNP markers found in our mtDNA, all people living today can be plotted onto a Maternal tree of mankind called the "**mtDNA Phylogenetic Tree**". The main branches of the tree are called "**mtDNA Haplogroups**". The finer sub-branches of the tree are called "**mtDNA Subclades**".

mtDNA Haplogroups are associated with different regions of the world

mtDNA Haplogroups are ancient family groups dating back tens of thousand of years. Each mtDNA Haplogroup is associated with a specific migration path leading to specific regions of the world, so once you know which mtDNA Haplogroup you belong to, you will

know the general geographical location of the world your Maternal ancestors came from, i.e. Asia, Europe, Americas (Native American), Africa, Middle East, Australia, etc.

Refer to the following table to view a summary of the major mtDNA Haplogroups found in different regions of the world.

Region	Major mtDNA Haplogroups found in region specified
Native Americans	A, B, C, D, X
Oceanic and Aboriginal Australians	O, P, Q, R, S
East Asian	A, B, C, D, E, F, G, M, Y, Z
South Asian (i.e. India)	G, M, W
Europe and Middle East	CZ, H, HV, HV0, I, J, JT, K, R0, T, U, V, W, X
Diverse	N, R
African	L0, L1, L2, L3, L4, L5, L6

Haplogroups pertain to ancient ancestry dating back tens of thousands of years and will not provide any information regarding recent ancestry such as what happened in the last few hundred years.

mtDNA Haplogroups can be further classified into finer sub-branches called "Subclades". Knowing your Subclade can often provide further geographical localization of your ancestry if published research on the geographical distribution of the Subclade is available.

mtDNA Haplogroup and Subclade Determination

Your mtDNA contains three regions: HVR1, HVR2 and Coding Regions. Testing **only the HVR1 and HVR2 regions** of your mtDNA, allows you to **predict the top five mtDNA Haplogroups** which you most likely belong to. Testing **all three regions** of your mtDNA (HVR1, HVR2 and Coding Regions) is required in order to conclusively **confirm which mtDNA Haplogroup** you belong to. It will also confirm your mtDNA Subclade.

Frequently Asked Questions

Will it tell me if I am Native American?

Yes, Y-DNA testing will allow you to find out if you may be Native American on your direct Paternal line and mtDNA DNA testing will allow you to find out if you may be Native American on your direct Maternal line.

If you are Native American on your **Paternal lineage**, your **Y-DNA test results** will show that you belong to **Y-DNA Haplogroup Q or C**. If your Y-DNA Haplogroup is NOT Q or C, it means that you are NOT Native American on your direct Paternal lineage.

If you are Native American on your **Maternal lineage**, your **mtDNA test results** will show that you belong to one of the known mtDNA Haplogroups that are found in Asians and Native Americans. Native Americans belong to **mtDNA Haplogroups A, B, C, D and X**. Cherokees belong mainly to groups B and C. If your mtDNA Haplogroup is NOT one of known Native American Haplogroups listed above, it means that you are NOT Native American on your direct Maternal lineage.

Please remember that your Y-DNA traces your Paternal line (father's father's father's.... line) and your mtDNA traces your Maternal line (mother's mother's mother's.... line). If your native ancestry is on a different line, such as your mother's father's line or your father's mother's line, you will not be able to trace that line using your own Y-DNA or mtDNA.

Will it tell me if I have Jewish Ancestry?

While there is no "Jewish" gene which is only found in Jews, there are certain Haplogroups that are strongly associated with individuals of Jewish descent.

The mtDNA Haplogroups most commonly found in Ashkenazi Jews are K (31.9%), H (20.4%), N (10.1%), J (8.1%), HV (5.8%), U (5.8%)

and T (4.8%).

The most common Y-DNA Haplogroups found in Jews are J (38%), R1b (30.7%), E (20.4%), G (9.7%), R1a (7.5%), Q (5.2%).

Together, Y-DNA Haplogroups J and E make up almost 60% of all Jews. In particular, Y-DNA Haplogroup J1 is strongly associated with Cohanim Jews. The Cohanim modal haplotype, which is strongly associated with Cohanim ancestry is as follows:

DYS393 = 12 DYS390 = 23 DYS19 = 14 DYS391 = 10 DYS388 = 16 DYS392 = 11

The "Cohanim Modal Haplotype" is found in 45% to 70% of Cohanim Jews.

Am I African? Doesn't everyone come from Africa?

DNA studies have shown that everyone originated from Africa over 150,000 years ago, but not all families stayed in Africa. Even though everyone originated from Africa, many ancient family groups "Haplogroups" migrated out of Africa to populate different parts of the world. The DNA test will tell you which Haplogroup you belong to. Your Haplogroup is associated with a specific region of the world, and not necessarily Africa. Only groups which stayed in Africa are Africans, and Africans belong to Haplogroups that are found mainly in Africa.

How can I find out about % ancestry?

Due to the manner in which Y-DNA and mtDNA are inherited, they can only trace the direct Paternal line or the direct Maternal line and cannot provide percentage of mixed ancestry from other lines.

The only marker that is inherited from multiple lines is Autosomal DNA. A person's Autosomal DNA is scrambled DNA from multiple lines so the information provided cannot pinpoint the ancestry a specific lineage. It can only provide a % of the overall mixture.

Can DNA ancestry testing tell me a date or specific city?

No. That is impossible. No DNA test can do that. There are no DNA markers that are specific to an exact date or city.

Can mtDNA tell me a specific country or race?

mtDNA testing can tell you which "Haplogroup" you belong to. Due to admixture, there are no DNA types which are exclusive to only one country. However, there are DNA types which are found in greater frequency in a certain country. Once you find out which Haplogroup and Subclade you belong to, you can find out which countries have the highest concentration of people with your genetic type.

Can mtDNA give me names?

No. mtDNA can be used to search for names of matches, but it cannot give you a name.

Will it tell me the general region of the world my ancestors came from?

Yes. When you test your mtDNA, you will find out which Haplogroup you belong to. Different Haplogroups are found specifically in different regions of the world.

Which line will mtDNA trace?

Maternal line (mother's mother's mother's..... line).

Surprises or lack of surprises with results?

Examples of some common types of questions:

I am European but my test results show that I am Native American/Asian, why?

I know I am European and the test shows that I am European, I didn't learn anything I didn't already know.

I am African American but my results show that I am South Asian, why?

Family legend indicates that I am Native American but my results indicate European, why?

DNA testing will give you the truth about your ancestry. For some, it will confirm what you already know or suspect. For others, it will bring completely surprising and shocking results that contradict what was previously known, and yet for others, it will confirm or reject family legends. The laboratory has absolutely no control over what your results will be, but it can guarantee that the test will show you

what you really are, regardless of whether the results are a surprise, shock, disappointment, or confirmation.



Certificate of mtDNA HVR1 Testing

This is to certify that

Brian Nicholas Rossiter

has sequenced the HVR1 region of his mtDNA. The following mtDNA profile has been obtained through mtDNA sequencing analysis.

HVR-1 Sequence										
16001	ATTCTAATTT	AACTATTCT	CTGTTCTTTC	ATGGGGAAGC	AGATTTGGGT	GCCACCCAAG	TATTGACTCA	CCCATCAACA	ACCGCTATGT	ATTCGTACA
16101	TACTGCCAG	CCACCATGAA	TATTGCACGG	TACCATAAAT	ACTTGACCAC	CTGTAGTACA	TAAAAACCCA	ATCCACATCA	AAACCCCTC	CCCATGCTTA
16201	CAAGCAAGTA	CAGCAATCAA	CCCTCAACTA	TCACACATCA	ACTGCAACTC	CAAAGCCACC	CCTCACCCAC	TAGGATACCA	ACAAACCTAC	CCATCTTTAA
16301	CAGCACATAG	TACATAAAGC	CATTTACCGT	ACATAGCACA	TTACAGTCAA	ATCCCTTCTC	GTCCCATGG	ATGACCCCC	TCAGATAGGG	GTCCCTTGAC
16401	CACCATCCTC	CGTGAAATCA	ATATCCCGCA	CAAGAGTGCT	ACTCTCCTCG	CTCCGGGCC	ATAACTTG	GGGGTAGTA	AAGTGAAGT	TATCCGACAT
16501	CTGGTTCCTA	CTTCAGGGCC	ATAAAGCCTA	AATAGCCAC	ACGTTCCCT	TAAATAAGAC	ATCACGATG			
HVR-1 Qualified Cambridge Reference Sequence (rCRS) variations										
Nucleotide Position		Region			Variant Type		Nucleotide Change			
16051 A>G, 16126 T>C, 16294 C>T, 16296 C>T, 16304 T>C, 16519 T>C										

Individuals share the same mtDNA haplotype if their mtDNA profiles are an exact match to each other. Individuals who have descended from the same maternal lineage will have exactly the same mtDNA profile. If two individuals have completely different mtDNA profiles, it will conclusively confirm that they did not descend from the same maternal lineage, regardless of written family history.



Certificate of mtDNA HVR2 Testing

This is to certify that

Brian Nicholas Rossiter

has sequenced the HVR2 region of his mtDNA. The following mtDNA profile has been obtained through mtDNA sequencing analysis.

HVR-2 Sequence										
00001	GATCACAGGT	CTATCACCT	ATTAACCACT	CACGGGAGCT	CTCCATGCAT	TTGGTATTTT	CGTCTGGGGG	GTGTGCACGC	GATAGCATTG	CGAGACGCTG
00101	GAGCCGGAGC	ACCCTATGTC	GCAGTATCTG	TCTTTGATTG	CTGCCTCATC	CTATTATTTA	TCGCACCTAC	GTTCAATATT	ACAGGCGAAC	ATACTTACTA
00201	AAGTGTGTTA	ATTAATTAAT	GCTTGTAGGA	CATAATAATA	ACAATTGAAT	GTCTGCACAG	CGCTTTTCCA	CACAGACATC	ATAACAAAAA	ATTTCCACCA
00301	AACCCCCCT	CCCCCGCTTC	TGGCCACAGC	ACTTAAACAC	ATCTCTGCCA	AACCCCAAAA	ACAAAGAACC	CTAACACCAG	CCTAACCCAGA	TTTCAAATTT
HVR-2 Qualified Cambridge Reference Sequence (rCRS) variations										
Nucleotide Position		Region			Variant Type		Nucleotide Change			
73 A>G, 263 A>G, 309 C>C*, 315 C>C*										

Individuals share the same mtDNA haplotype if their mtDNA profiles are an exact match to each other. Individuals who have descended from the same maternal lineage will have exactly the same mtDNA profile. If two individuals have completely different mtDNA profiles, it will conclusively confirm that they did not descend from the same maternal lineage, regardless of written family history.



Certificate of mtDNA Coding Region Sequencing

This is to certify that

Brian Nicholas Bossert

has sequenced the Coding Region of his mtDNA. The following mtDNA profile has been obtained through mtDNA sequencing analysis.

Coding Region Sequence

Nucleotide Position	Region	Variant Type	Nucleotide Change
709 G>A, 750 A>G, 930 G>A, 1438 A>G, 1888 G>A, 2706 A>G, 4216 T>C, 4769 A>G, 4917 A>G, 5147 G>A, 7028 C>T, 8697 G>A, 8860 A>G, 11251 A>G, 11719 G>A, 11812 A>G, 13368 G>A, 14233 A>G, 14766 C>T, 14861 G>A, 14905 G>A, 15326 A>G, 15452 C>A, 15607 A>G, 15928 G>A			

Coding Region Qualified Cambridge Reference Sequence (rCRS) variations

Nucleotide Position	Region	Variant Type	Nucleotide Change
709 G>A, 750 A>G, 930 G>A, 1438 A>G, 1888 G>A, 2706 A>G, 4216 T>C, 4769 A>G, 4917 A>G, 5147 G>A, 7028 C>T, 8697 G>A, 8860 A>G, 11251 A>G, 11719 G>A, 11812 A>G, 13368 G>A, 14233 A>G, 14766 C>T, 14861 G>A, 14905 G>A, 15326 A>G, 15452 C>A, 15607 A>G, 15928 G>A			

Individuals share the same mtDNA haplotype if their mtDNA profiles are an exact match to each other. Individuals who have descended from the same maternal lineage will have exactly the same mtDNA profile. If two individuals have completely different mtDNA profiles, it will conclusively confirm that they did not descend from the same maternal lineage, regardless of written family history.