GENETIC GENEALOGY

Account ID#: 1698950

RE: MATERNAL ANCESTRY DNA TEST REPORT

Please find enclosed the results of the mtDNA HVR1 and mtDNA HVR2 test which you have requested.

GENETIC GENEALOGY

DNA Test Results
HVR1, HVR2 Test Report

Print Date: January 20, 2015

Client Information

First Name:	Brian Nicholas	Account ID#	1698950
Last Name:	Rossiter	Profile ID#:	26364765

HVR1, HVR2 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.

HVR1 Sequence

```
16001  ATTCTAATTT AAACTATTCT CTGTTCTTTC ATGGGGAAGC AGATTTGGGT gCCACCCAAG TATTGACTCA CCCATCAACA ACCGCTATGT ATTTCGTACA
16101  TTACTGCCAG CCACCATGAA TATTGcACGG TACCATAAAT ACTTGACCAC CTGTAGTACA TAAAAACCCA ATCCACATCA AAACCCCCTC CCCATGCTTA
16201  CAAGCAAGTA CAGCAATCAA CCCTCAACTA TCACACATCA ACTGCAACTC CAAAGCCACC CCTCACCCAC TAGGATACCA ACAAACCTAC CCAtCtTTAA
16301  CAGcACATAG TACATAAAGC CATTTACCGT ACATAGCACA TTACAGTCAA ATCCCTTCTC GTCCCCATGG ATGACCCCCC TCAGATAGGG GTCCCTTGAC
16401  CACCATCCTC CGTGAAATCA ATATCCCGCA CAAGAGTGCT ACTCTCCTCG CTCCGGGCCC ATAACACTTG GGGGTAGCTA AAGTGAACTG TATCCGACAT
16501  CTGGTTCCTA CTTCAGGGcC ATAAAGCCTA AATAGCCCAC ACGTTCCCCT TAAATAAGAC ATCACGATG
```

HVR1 Qualified Cambridge Reference Sequence (rCRS) variations

Nucleotide Position	Region	Variant Type	Nucleotide Change
16051	HVR1	Substitution	A > G
16126	HVR1	Substitution	T > C
16294	HVR1	Substitution	C > T
16296	HVR1	Substitution	C > T
16304	HVR1	Substitution	T > C
16519	HVR1	Substitution	T > C

HVR2 Sequence

```
00001  GATCACAGGT CTATCACCCT ATTAACCACT CACGGGAGCT CTCCATGCAT TTGGTATTTT CGTCTGGGGG GTgTGCACGC GATAGCATTG CGAGACGCTG
00101  GAGCCGGAGC ACCCTATGTC GCAGTATCTG TCTTTGATTC CTGCCTCATC CTATTATTTA TCGCACCTAC GTTCAATATT ACAGGCGAAC ATACTTACTA
00201  AAGTGTGTTA ATTAATTAAT GCTTGTAGGA CATAATAATA ACAATTGAAT GTCTGCACAG CCgCTTTCCA CACAGACATC ATAACAAAAA ATTTCCACCA
00301  AACCCCCCC*T CCCCC*GCTTC TGGCCACAGC ACTTAAACAC ATCTCTGCCA AACCCCAAAA ACAAAGAACC CTAACACCAG CCTAACCAGA TTTCAAATTT
```

HVR2 Qualified Cambridge Reference Sequence (rCRS) variations

Nucleotide Position	Region	Variant Type	Nucleotide Change
73	HVR2	Substitution	A > G
263	HVR2	Substitution	A > G
309	HVR2	Insertion	C > CC
315	HVR2	Insertion	C > CC

mtDNA Haplogroup Prediction

The mtDNA consists of 3 regions: HVR1, HVR2 and Coding regions. Testing markers in all three regions of the mtDNA is required in order to conclusively confirm which mtDNA Haplogroup and mtDNA Subclade an individual belongs to. Testing only the HVR1 and HVR2 regions of the mtDNA can provide a prediction of the top 5 mtDNA Haplogroups that an individual most likely belong to. The

only way to conclusively confirm an individual's mtDNA Haplogroup and mtDNA Subclade is by testing markers in all three regions of the mtDNA.

Brian Nicholas Rossiter has tested the HVR1 and HVR2 regions of his mtDNA and has not tested the Coding region. Based on the sequencing results of the mtDNA HVR1 and HVR2 regions, the top 5 predicted mtDNA haplogroups for Brian Nicholas Rossiter are as follows:

T (Medium prediction strength)
U (Weak prediction strength)
R (Weak prediction strength)
JT (Weak prediction strength)
H (Weak prediction strength)

Please note that HVR1 and HVR2 markers can only be used to generate a mtDNA Haplogroup prediction. The only way to conclusively confirm an individual's mtDNA Haplogroup and Subclade is by testing markers in all 3 regions: HVR1, HVR2 and Coding Regions.

Description of Brian Nicholas Rossiter's top predicted mtDNA Haplogroup: mtDNA Haplogroup T

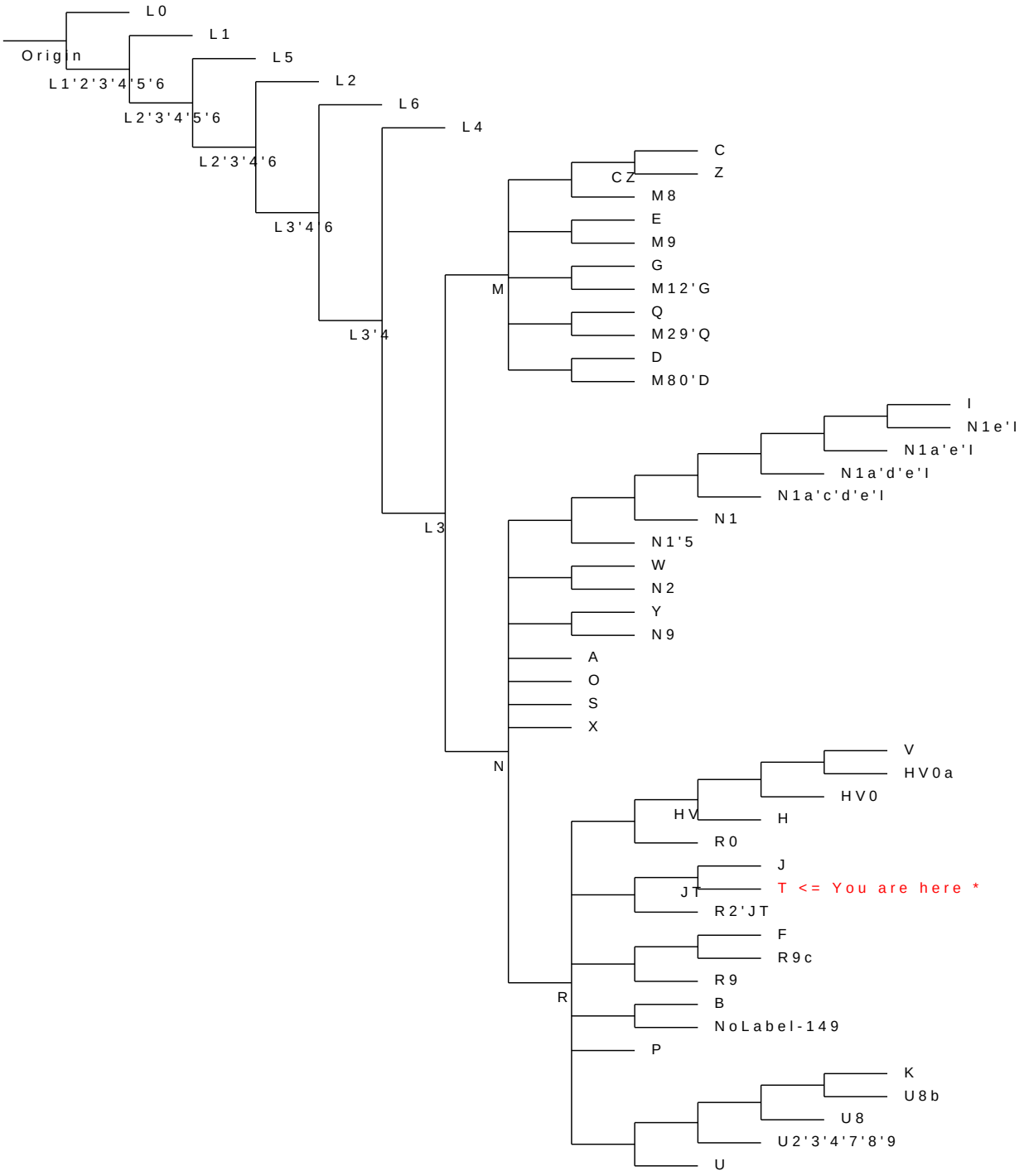
The woman who founded mtDNA Haplogroup T lived approximately 30,000 to 60,000 years ago in the Near East (Mesopotamia). Descendents of the mtDNA Haplogroup T line moved north and west into Eastern Europe approximately 10,000 years ago. Today, descendants of mtDNA Haplogroup T are found in highest concentrations 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.

Refer to the Population Distribution Frequency section of this report for the currently known distribution frequency of mtDNA Haplogroup T.

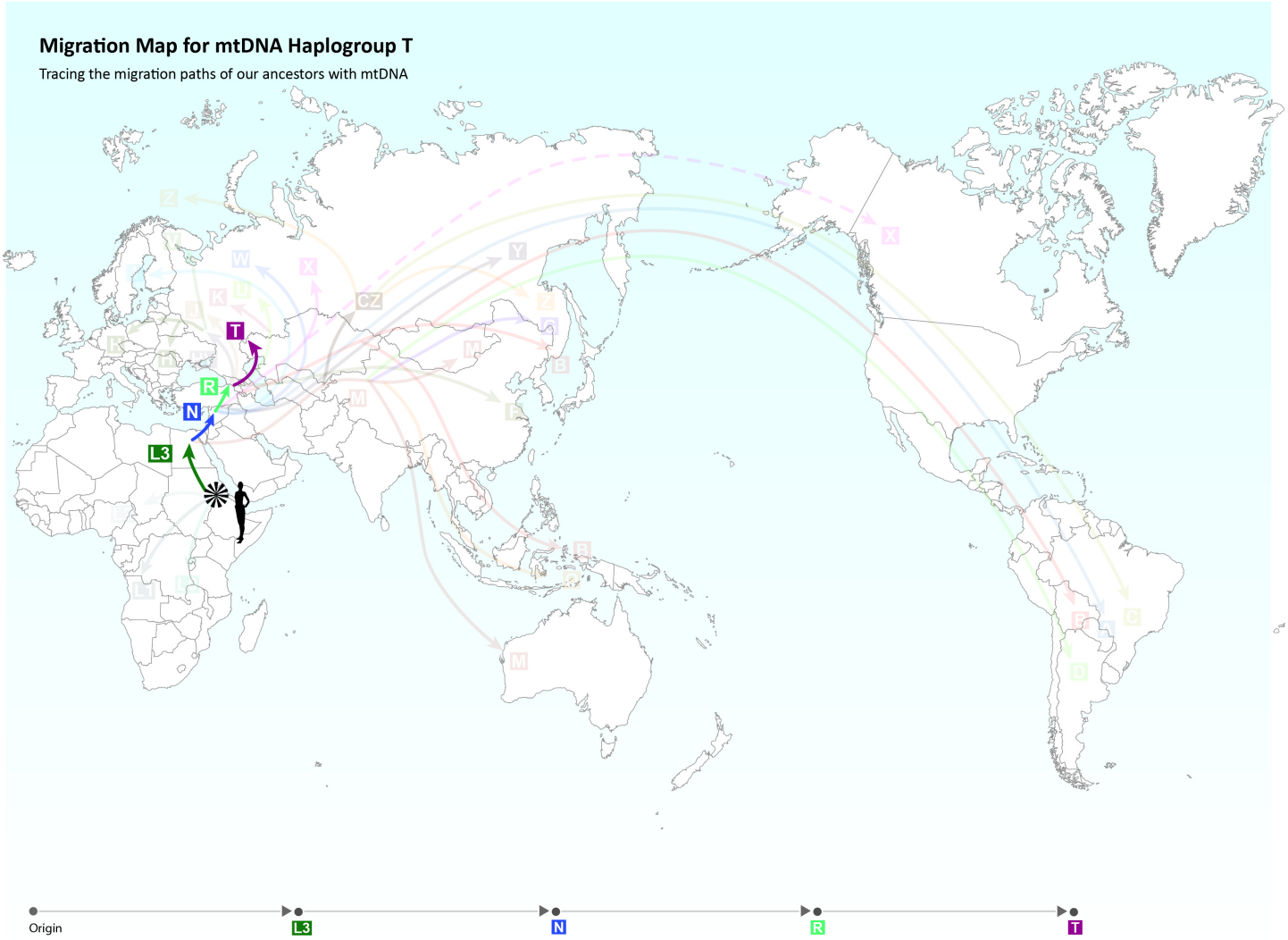
GENETIC GENEALOGY

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.



Population Distribution Frequency of mtDNA Haplogroup T in Europe

Population	% of Population belonging to T	Study Size	Reference
Maine et Loire - Maine-Anjou, France	14.56%	55	An mtDNA perspective of French genetic variation. Richard C et al
Hérault - Languedoc, France	14.13%	85	An mtDNA perspective of French genetic variation. Richard C et al
Austrians	12.6%	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.
Tuscany, Italy	10.4%	48	Classification of European mtDNAs From an Analysis of Three European Populations. Torroni A et al Genetics (1996) 144: 1835-50.
Czech population of Western Bohemia	9.5%	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.

Poles from the Pomerania-Kujawy region of northern Poland	9.4%	436	Mitochondrial DNA variability in Poles and Russians. Malyarchuk BA et al Ann Hum Genet. 2002 Jul;66(Pt 4):261-83.
Russians from three European regions of Russia (Stavropol region, Orel region, Saratov region)	9%	201	Mitochondrial DNA variability in Poles and Russians. Malyarchuk BA et al Ann Hum Genet. 2002 Jul;66(Pt 4):261-83.
Finland	6.1%	49	Classification of European mtDNAs From an Analysis of Three European Populations. Torroni A et al Genetics (1996) 144: 1835-50.
Finistère - Brittany, France	5.82%	120	An mtDNA perspective of French genetic variation. Richard C et al
Loire-Atlantique - Brittany, France	5.32%	75	An mtDNA perspective of French genetic variation. Richard C et al
Somme - Picardie, France	5.12%	78	An mtDNA perspective of French genetic variation. Richard C et al
Vendée - Poitou, France	5%	80	An mtDNA perspective of French genetic variation. Richard C et al
Solvenians in Slovenia	4.9%	102	Mitochondrial DNA variability in Bosnians and Slovenians. Malyarchuk BA et al Ann Hum Genet. 2003 Sep;67(Pt 5):412-25.
Slovenians	4.8%	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.
Monteni Romani in Balkan Mountain villages, Bulgaria	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.Click here to read
Lebaniegos in Cantabria, Spain	4.17%	72	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.
Pasiegos in Cantabria, Spain	3.66%	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.
Portuguese in North Portugal	3.57%	84	Mitochondrial DNA affinities at the Atlantic fringe of Europe. González AM et al Am J Phys Anthropol. 2003 Apr;120(4):391-404.
Bosnians in Bosnia-Herzegovina	3.51%	142	Mitochondrial DNA variability in Bosnians and Slovenians. Malyarchuk BA et al Ann Hum Genet. 2003 Sep;67(Pt 5):412-25.
Bosnians	3.5%	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.
French, France (Finistère, Morbihan, Normandy, Périgord-Limousin, Var)	3.43%	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.Click here to read
Azores in Central Azores Islands, Portugal	3.33%	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.
Calabria, Italy	3.15%	95	Human mitochondrial DNA variation in Southern Italy. Ottoni C et al
French, France (Finistère, Morbihan, Normandy, Périgord-Limousin, Var)	2.9%	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.Click here to read
Italians	2.9%	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.
Tatars in Aznakaevo	2.8%	71	Mitogenomic diversity in Tatars from the Volga-Ural region of Russia Malyarchuk B et al Mol Biol Evol. 2010 May 10. [Epub ahead of print]
Northeast Germany (Western Pomerania)	2.7%	300	Mitochondrial diversity of a northeast German population sample. Poetsch M et al Forensic Sci Int. 2003 Nov 26;137(2-3):125-32.

modern Hungarian-speaking Seklers from Romanian Transylvania	2.7%	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.
French, France (Finistère, Morbihan, Normandy, Périgord-Limousin, Var)	2.6%	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.Click here to read
Sicily, Italy	2.58%	155	Human mitochondrial DNA variation in Southern Italy. Ottoni C et al
Morbihan - Brittany, France	2.44%	41	An mtDNA perspective of French genetic variation. Richard C et al
Bashkiria, Russia	2.4%	83	Mitochondrial DNA variations in Russian and Belorussian populations. Belyaeva O et al
Lom Romani in Lom, Bulgaria	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.Click here to read
Belorussians in Russia	2.18%	92	Mitochondrial DNA variations in Russian and Belorussian populations. Belyaeva O et al
Roma (Gypsies) from Bulgaria, Spain and Lithuania	2.18%	275	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.Click here to read
Calvados - Normandy, France	2.17%	46	An mtDNA perspective of French genetic variation. Richard C et al
Azores (Portugal) in the Atlantic Ocean	2.05%	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.
Bosians in Bosnia-Herzegovina	2%	144	Mitochondrial DNA variability in Bosnians and Slovenians. Malyarchuk BA et al Ann Hum Genet. 2003 Sep;67(Pt 5):412-25.
Hungarians	2%	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.
Portuguese in Portugal	1.66%	299	Mitochondrial DNA affinities at the Atlantic fringe of Europe. González AM et al Am J Phys Anthropol. 2003 Apr;120(4):391-404.
Portuguese in Central Portugal	1.28%	78	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	1.14%	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.
Macedonians in Republic of Macedonia	1.12%	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.
Slovenians in Slovenia	1%	104	Mitochondrial DNA variability in Bosnians and Slovenians. Malyarchuk BA et al Ann Hum Genet. 2003 Sep;67(Pt 5):412-25.
Vojvodina , Serbia	0.96%	104	Sequence polymorphism of the mitochondrial DNA control region in the population of Vojvodina Province, Serbia. Zgonjanin D et al
Portuguese in South Portugal	0.73%	137	Mitochondrial DNA affinities at the Atlantic fringe of Europe. González AM et al Am J Phys Anthropol. 2003 Apr;120(4):391-404.
Finns in Finland	0.52%	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.
Tatars in Buinsk	0%	126	Mitogenomic diversity in Tatars from the Volga-Ural region of Russia Malyarchuk B et al Mol Biol Evol. 2010 May 10. [Epub ahead of print]
Northern-central Italians	0%	384	Multiplex mtDNA coding region SNP assays for molecular dissection of haplogroups U/K and J/T. Grignani P et al Forensic Science International: Genetics, In Press, Corrected Proof, Available online 6 May 2009.

Population Distribution Frequency of mtDNA Haplogroup T in Middle East & Central Asia

Population	% of Population belonging to T	Study Size	Reference
Turkish in Eastern and Western Azerbaijian	12.5%	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	7.14%	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
Persians	4.9%	82	Phylogeographic analysis of mitochondrial DNA in northern Asian populations. Derenko M et al Am J Hum Genet. 2007 Nov;81(5):1025-41.
Uzbek, Uzbekistan (Surkhandarya)	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
Yemenite in Yemen	4.22%	142	Mitochondrial DNA reveals distinct evolutionary histories for Jewish populations in Yemen and Ethiopia. Non AL et al
Kurdish in Turkmenistan	3.13%	64	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
Shugnan in Tajikistan and High Pamirs	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
Oriental Jews	2.17%	46	Mitochondrial DNA sequence variation in Jewish populations. Picornell A et al
Druze in Israel	1.9%	311	The Druze: a population genetic refugium of the Near East. Shlush LI et al PLoS One. 2008 May 7;3(5):e2105.
Southwest and Central Asians (Iran, Pakistan, Azerbaijan, India, Uzbekistan, Turkmenistan, Tajikistan)	1.42%	1404	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
Turkmen in Turkmenistan	1.22%	82	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

DNA Database Usage

Your mtDNA markers qualify for DNA database search and analysis features. The 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
- 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 DNA database, go to www.genebase.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.genebase.com

Step 2: Click "Login"

Step 3: Enter the email **nick.rossiter1@btinternet.com** and your selected password. If you had not previously registered an email to your account, a temporary non-functioning system email will be assigned to you. 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 account current.
Database usage is free and optional.

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 contain 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.

GENETIC GENEALOGY

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.

HVR1 Sequence

```
16001  ATTCTAATTT AAACTATTCT CTGTTCTTTC ATGGGGAAGC AGATTTGGGT gCCACCCAAG TATTGACTCA CCCATCAACA ACCGCTATGT ATTTCGTACA
16101  TTACTGCCAG CCACCATGAA TATTGcACGG TACCATAAAT ACTTGACCAC CTGTAGTACA TAAAAACCCA ATCCACATCA AAACCCCCTC CCCATGCTTA
16201  CAAGCAAGTA CAGCAATCAA CCCTCAACTA TCACACATCA ACTGCAACTC CAAAGCCACC CCTCACCCAC TAGGATACCA ACAAACCTAC CCAtCtTTAA
16301  CAGcACATAG TACATAAAGC CATTTACCGT ACATAGCACA TTACAGTCAA ATCCCTTCTC GTCCCCATGG ATGACCCCCC TCAGATAGGG GTCCCTTGAC
16401  CACCATCCTC CGTGAAATCA ATATCCCGCA CAAGAGTGCT ACTCTCCTCG CTCCGGGCCC ATAACACTTG GGGGTAGCTA AAGTGAACTG TATCCGACAT
16501  CTGGTTCCTA CTTCAGGGcC ATAAAGCCTA AATAGCCCAC ACGTTCCCCT TAAATAAGAC ATCACGATG
```

HVR1 Qualified Cambridge Reference Sequence (rCRS) variations

Nucleotide Position	Region	Variant Type	Nucleotide Change
16051	HVR1	Substitution	A > G
16126	HVR1	Substitution	T > C
16294	HVR1	Substitution	C > T
16296	HVR1	Substitution	C > T
16304	HVR1	Substitution	T > C
16519	HVR1	Substitution	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.

GENETIC GENEALOGY

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.

HVR2 Sequence			
00001 GATCACAGGT CTATCACCCT ATTAACCACT CACGGGAGCT CTCCATGCAT TTGGTATTTT CGTCTGGGGG GT**g**TGCACGC GATAGCATTG CGAGACGCTG 00101 GAGCCGGAGC ACCCTATGTC GCAGTATCTG TCTTTGATTC CTGCCTCATC CTATTATTTA TCGCACCTAC GTTCAATATT ACAGGCGAAC ATACTTACTA 00201 AAGTGTGTTA ATTAATTAAT GCTTGTAGGA CATAATAATA ACAATTGAAT GTCTGCACAG CC**g**CTTTCCA CACAGACATC ATAACAAAAA ATTTCCACCA 00301 AACCCCCCC*****T CCCCC*****GCTTC TGGCCACAGC ACTTAAACAC ATCTCTGCCA AACCCCAAAA ACAAAGAACC CTAACACCAG CCTAACCAGA TTTCAAATTT			
HVR2 Qualified Cambridge Reference Sequence (rCRS) variations			
Nucleotide Position	**Region**	**Variant Type**	**Nucleotide Change**
73	HVR2	Substitution	A > G
263	HVR2	Substitution	A > G
309	HVR2	Insertion	C > CC
315	HVR2	Insertion	C > CC

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.