My Project Groups

You currently are not in any groups. Click here to search & join group projects.

- Join Projects
- myFTDNA Home
- myFTDNA Forum

My Account

- Contact Information
- User Preferences
- Order Tests & Upgrades
- Special Offers
- Order Certificates

My Maps

- Maps

Y-DNA

- Matches
- Haplotree
- Ancestral Origins
- DYS Values

mtDNA

- Matches
- Ancestral Origins
- Results

Tools

- Refer Friends & Family
- YSearch.org
- MitoSearch.org
- GEDCOM - Family Tree
- Genographic Project

mtDNA Results

Your Haplogroup and mutations relative to the Cambridge Reference Sequence (CRS) are shown below. A value of CRS indicates no mutations. High resolution (HVR2) results are shown only if you have requested the mtDNAPlus or mtDNA Refine test. If you ordered a Mega mtDNA the Coding Region (CR) will be displayed below.

As you go through your mtDNA results, we strongly encourage you to read the **mtDNA Results Tutorial** that we have put together in the form of frequently asked questions about mtDNA results.

Haplogroup - H

HVR1 differences from CRS	HVR2 differences from CRS		
16519C	93G	263G	315.1C

Copy and paste this table only to Excel or Word. You may need to adjust column widths in Excel after the paste operation.

- Download FASTA File - What is this link?
- Understanding your results. - (PDF, Requires Acrobat Reader)

H Specific mitochondrial haplogroups are typically found in different regions of the world, and this is due to unique population histories. In the process of spreading around the world, many populations—with their special mitochondrial haplogroups—became isolated, and specific haplogroups concentrated in geographic regions. Today, we have identified certain haplogroups that originated in Africa, Europe, Asia, the islands of the Pacific, the Americas, and even particular ethnic groups. Of course, haplogroups that are specific to one region are sometimes found in another, but this is due to recent migration.

Mitochondrial haplogroup H is a predominantly European haplogroup that originated outside of Europe before the last glacial maximum (LGM). It first expanded in the northern Near East and southern Caucasus between 33,000 and 26,000 years ago, and later migrations from Iberia suggest it reached Europe before the LGM. It has also spread to Siberia and Inner Asia. Today, about 40% of all mitochondrial lineages in Europe are classified as haplogroup H. More information about haplogroup H and its branches can be found here.

Cambridge Reference Sequence

The mitochondrion sequenced in 1981 became known as the Cambridge Reference Sequence (CRS) and has been used as a basis for comparison with your mtDNA. In other words, any place in your mtDNA where you have a difference from the CRS, is characterized as a mutation. if your results show no mutations at all, it means that your mtDNA matches the CRS. A mutation happens a) when a base replaces another base - for example a C (Cytosine) replaces an A (Adenine), b) when a base is no longer in that position and c) when a new base is inserted between the other bases without replacing any other. Those mutations are represented below according to the following color code:

a) Mutation at position: RED b) Mutation Deleted: ~~Strike~~ c) Mutation Inserted: Green

The CRS is displayed below and we indicate where your differences are using the above color coding system. Please note that when you see "ATTCTAATTT" under 16010, it actually means that 16001 has an "A" (Adenine), 16002 has a "T" (Thymine), 16003 has a "T" (Thymine), 16004 has a "C" (Cytosine) and so on. If your table of mutations above indicates you have a difference "192T," the second letter in the section under 16200 will be a red "C" meaning that the CRS letter at that place is a "C," whereas yours is the "T" reported in the chart above.

HVR1 REFERENCE SEQUENCE (STARTS AT: 16001)

16010	16020	16030	16040	16050	16060	16070	16080
ATTCTAATTT	AAACTATTCT	CTGTTCTTTC	ATGGGGAAGC	AGATTTGGGT	ACCACCCAAG	TATTGACTCA	CCCATCAACA
16090	16100	16110	16120	16130	16140	16150	16160
ACCGCTATGT	ATTTCGTACA	TTACTGCCAG	CCACCATGAA	TATTGTACGG	TACCATAAAT	ACTTGACCAC	CTGTAGTACA

16170	16180	16190	16200	16210	16220	16230	16240
TAAAAACCCA	ATCCACATCA	AAACCCCCTC	CCCATGCTTA	CAAGCAAGTA	CAGCAATCAA	CCCTCAACTA	TCACACATCA
16250	16260	16270	16280	16290	16300	16310	16320
ACTGCAACTC	CAAAGCCACC	CCTCACCCAC	TAGGATACCA	ACAAACCTAC	CCACCCTTAA	CAGTACATAG	TACATAAAGC
16330	16340	16350	16360	16370	16380	16390	16400
CATTTACCGT	ACATAGCACA	TTACAGTCAA	ATCCCTTCTC	GTCCCCATGG	ATGACCCCCC	TCAGATAGGG	GTCCCTTGAC
16410	16420	16430	16440	16450	16460	16470	16480
CACCATCCTC	CGTGAAATCA	ATATCCCGCA	CAAGAGTGCT	ACTCTCCTCG	CTCCGGGCCC	ATAACACTTG	GGGGTAGCTA
16490	16500	16510	16520	16530	16540	16550	16560
AAGTGAACTG	TATCCGACAT	CTGGTTCCTA	CTTCAGGGTC	ATAAAGCCTA	AATAGCCCAC	ACGTTCCCCT	TAAATAAGAC
16569							
ATCACGATG							

HVR2 REFERENCE SEQUENCE (STARTS AT: 1)

10	20	30	40	50	60	70	8
GATCACAGGT	CTATCACCCT	ATTAACCACT	CACGGGAGCT	CTCCATGCAT	TTGGTATTTT	CGTCTGGGGG	GTATGCACG
90	100	110	120	130	140	150	16
GATAGCATTG	CGAGACGCTG	GAGCCGGAGC	ACCCTATGTC	GCAGTATCTG	TCTTTGATTC	CTGCCTCATC	CTATTATTT
170	180	190	200	210	220	230	24
TCGCACCTAC	GTTCAATATT	ACAGGCGAAC	ATACTTACTA	AAGTGTGTTA	ATTAATTAAT	GCTTGTAGGA	CATAATAAT
250	260	270	280	290	300	310	32
ACAATTGAAT	GTCTGCACAG	CCACTTTCCA	CACAGACATC	ATAACAAAAA	ATTTCCACCA	AACCCCCCCT	CCCCCCGCTT
330	340	350	360	370	380	390	40
TGGCCACAGC	ACTTAAACAC	ATCTCTGCCA	AACCCCAAAA	ACAAAGAACC	CTAACACCAG	CCTAACCAGA	TTTCAAATT
410	420	430	440	450	460	470	48
TATCTTTTGG	CGGTATGCAC	TTTTAACAGT	CACCCCCCAA	CTAACACATT	ATTTTCCCCT	CCCACTCCCA	TACTACTAA
490	500	510	520	530	540	550	56
CTCATCAATA	CAACCCCCGC	CCATCCTACC	CAGCACACAC	ACACCGCTGC	TAACCCCATA	CCCCGAACCA	ACCAAACCC
570	580						
AAAGACACCC	CCCA						