(BACK)

mthap version 0.19c (2023-08-15); haplogroup data version PhyloTree Build 17 (2016-02-18) +mods
raw data source ManuSporny-genome.txt (23MB)

Found 2708 markers at 2558 positions covering 15.4% of mtDNA.

NOTICE: You appear to have uploaded a 23andme v3 raw data file which has 9 known unreliable markers that will be excluded from this analysis.

Markers found (shown as differences to rCRS):

HVR2: 73G 263G 461T 489C
CR: 750G 1438G 2706G 3537G 4769G 5082C 5301G 7028T 8563G 8701G 8860G 9540C 10398G 10400T 10640C 10873C 11719A 12705T 14766T 14783C 15043A 15301A 15326G
HVR1: 16111T 16223T 16231C 16320T 16362C (16519C)

IMPORTANT NOTE: The above marker list is almost certainly incomplete due to limitations of genotyping technology and is not comparable to mtDNA sequencing results. It should not be used with services or tools that expect sequencing results, such as mitosearch.

Best mtDNA Haplogroup Matches:

1) M6a

Defining Markers for haplogroup M6a:
HVR2: 73G 263G 461T 489C
CR: 750G 1438G 2706G 3537G 4769G 5082C 5301G 5558G 7028T 8701G 8860G 9540C 10398G 10400T 10640C 10873C 11719A 12705T 14128G 14766T 14783C 15043A 15301A 15326G
HVR1: 16223T 16231C 16362C

Marker path from rCRS to haplogroup M6a (plus extra markers):
H2a2a1(rCRS) ⇨ 263G ⇨ H2a2a ⇨ 8860G 15326G ⇨ H2a2 ⇨ 750G ⇨ H2a ⇨ 4769G ⇨ H2 ⇨ 1438G ⇨ H ⇨ 2706G 7028T ⇨ HV ⇨ 14766T ⇨ R0 ⇨ 73G 11719A ⇨ R ⇨ 12705T 16223T ⇨ N ⇨ 8701G 9540C 10398G 10873C 15301A ⇨ L3 ⇨ 489C 10400T 14783C 15043A ⇨ M ⇨ 461T 5301G 5558G 10640C 14128G 16362C ⇨ M6 ⇨ 3537G 5082C 16231C ⇨ M6a ⇨ 8563G 16111T 16320T (16519C)

Imperfect Match. Your results contained differences with this haplogroup:
Matches(29): 73G 263G 461T 489C 750G 1438G 2706G 3537G 4769G 5082C 5301G 7028T 8701G 8860G 9540C 10398G 10400T 10640C 10873C 11719A 12705T 14766T 14783C 15043A 15301A 15326G 16223T 16231C 16362C
Extras(3): 8563G 16111T 16320T (16519C)
No-Calls(1): 14128G
Untested(1): 5558

2) M6a1

Defining Markers for haplogroup M6a1:
HVR2: 73G 263G 461T 489C
CR: 750G 1438G 2706G 3486T 3537G 4769G 5082C 5301G 5558G 7028T 8701G 8860G 9329A 9540C 10398G 10400T 10640C 10873C 11719A 12705T 13966G 14128G 14766T 14783C 15043A 15301A 15326G
HVR1: 16223T 16231C 16362C

Marker path from rCRS to haplogroup M6a1 (plus extra markers):
H2a2a1(rCRS) ⇨ 263G ⇨ H2a2a ⇨ 8860G 15326G ⇨ H2a2 ⇨ 750G ⇨ H2a ⇨ 4769G ⇨ H2 ⇨ 1438G ⇨ H ⇨ 2706G 7028T ⇨ HV ⇨ 14766T ⇨ R0 ⇨ 73G 11719A ⇨ R ⇨ 12705T 16223T ⇨ N ⇨ 8701G 9540C 10398G 10873C 15301A ⇨ L3 ⇨ 489C 10400T 14783C 15043A ⇨ M ⇨ 461T 5301G 5558G 10640C 14128G 16362C ⇨ M6 ⇨ 3537G 5082C 16231C ⇨ M6a ⇨ 3486T 9329A 13966G ⇨ M6a1 ⇨ 8563G 16111T 16320T (16519C)

Imperfect Match. Your results contained differences with this haplogroup:
Matches(29): 73G 263G 461T 489C 750G 1438G 2706G 3537G 4769G 5082C 5301G 7028T 8701G 8860G 9540C 10398G 10400T 10640C 10873C 11719A 12705T 14766T 14783C 15043A 15301A 15326G 16223T 16231C 16362C
Mismatches(2): 9329G 13966A
Extras(3): 8563G 16111T 16320T (16519C)
No-Calls(1): 14128G
Untested(2): 3486 5558

3) M6

Defining Markers for haplogroup M6:
HVR2: 73G 263G 461T 489C
CR: 750G 1438G 2706G 4769G 5301G 5558G 7028T 8701G 8860G 9540C 10398G 10400T 10640C 10873C 11719A 12705T 14128G 14766T 14783C 15043A 15301A 15326G
HVR1: 16223T 16362C

Marker path from rCRS to haplogroup M6 (plus extra markers):
H2a2a1(rCRS) ⇨ 263G ⇨ H2a2a ⇨ 8860G 15326G ⇨ H2a2 ⇨ 750G ⇨ H2a ⇨ 4769G ⇨ H2 ⇨ 1438G ⇨ H ⇨ 2706G 7028T ⇨ HV ⇨ 14766T ⇨ R0 ⇨ 73G 11719A ⇨ R ⇨ 12705T 16223T ⇨ N ⇨ 8701G 9540C 10398G 10873C 15301A ⇨ L3 ⇨ 489C 10400T 14783C 15043A ⇨ M ⇨ 461T 5301G 5558G 10640C 14128G 16362C ⇨ M6 ⇨ 3537G 5082C 8563G 16111T 16231C 16320T (16519C)

Imperfect Match. Your results contained differences with this haplogroup:
Matches(26): 73G 263G 461T 489C 750G 1438G 2706G 4769G 5301G 7028T 8701G 8860G 9540C 10398G 10400T 10640C 10873C 11719A 12705T 14766T 14783C 15043A 15301A 15326G 16223T 16362C
Extras(6): 3537G 5082C 8563G 16111T 16231C 16320T (16519C)
No-Calls(1): 14128G
Untested(1): 5558

Need help?

First, please check the Frequently Asked Questions for guidance on how to read this report. If you still have questions, there is a discussion about mthap on eng.molgen.org. You can also email your questions to me at james.lick@jameslick.com. So that I can best help you, please include a copy of the complete mthap report and/or your mtDNA data file in your email.