

Supplementary Information for

Biparental Inheritance of Mitochondrial DNA in Humans

Shiyu Luo, C. Alexander Valencia, Jinglan Zhang, Ni-Chung Lee, Jesse Slone, Baoheng Gui, Xinjian Wang, Zhuo Li, Sarah Dell, Jenice Brown, Stella Maris Chen, Yin-Hsiu Chien, Wuh-Liang Hwu, Pi-Chuan Fan, Lee-Jun Wong, Paldeep S. Atwal, and Taosheng Huang

Corresponding author: Taosheng Huang

Email: Taosheng.Huang@cchmc.org

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Datasets S1 to S3

Sequence alignment

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Sequence	PT17 Haplogroup	Total Variants	Variants
II-40	U5b (U5b1d1c)	30	A73G, C150T , A263G, A750G, A1438G, A2179G, A2706G, T3197C , A4769G, C5437T , A5656G , C7028T, A7788G , G7912A , A8860G, G9477A , A11467G , G11719A, A12308G , G12372A , T13617C , T14182C , C14766T, A15326G, A15631G , T15721C , C16192T , C16218T , C16270T , C16320T Submit New Variants to Mitomap

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Fig. S1. The 30 SNPs in II-40's mtDNA (Family A) differing from the reference mtDNA haplogroup were predicted in Mitomaster. Haplogroup U5b (U5b1d1c)-related mtDNA variants are labeled in red rectangles.

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Sequence	PT17 Haplogroup	Total Variants	Variants
I-10	H1a (H1a1)	13	A73G , A263G, A750G, A1438G, G3010A , A4769G, T6365C , A8860G, G14198A, A15326G, A16162G , T16209C , T16519C Submit New Variants to Mitomap

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Fig. S2. The 13 SNPs in I-10's mtDNA (Family A) differing from the reference mtDNA haplogroup were predicted in Mitomaster. Haplogroup H1a (H1a1)-related mtDNA variants are labeled in red rectangles in addition to other defining SNPs (2706A, 7028C).

Sequence alignment

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Sequence	PT17 Haplogroup	Total Variants	Variants
I-1	R0a (R0a1)	19	T58C , C64T , A263G, A750G, A827G , A1438G, T2442C , A2706G, T3847C , A4769G, G6182A, C7028T, A8860G, C13188T , C14766T, A15326G, T16126C , C16291T, T16362C Submit New Variants to Mitomap

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Fig. S3. The 19 SNPs in I-1's mtDNA (Family A) differing from the reference mtDNA haplogroup were predicted in Mitomaster. Haplogroup R0a (R0a1)-related mtDNA variants are labeled in red rectangles.

Sequence alignment

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Sequence	PT17 Haplogroup	Total Variants	Variants
I-1	K1b (K1b2a)	34	A73G, T146C, T195C, A263G, A750G, T1189C, A1438G, A1811G, A2706G, A3480G, A4769G, G5913A, C7028T, A8860G, G9055A, A9058G, A9066C, T19698C, A10398G, A10550G, T11299C, A11467G, G11719A, A12308G, G12372A, T12738G, G12771A, C14167T, C14766T, T14798C, A15326G, T16224C, T16311C, T16519C Submit New Variants to Mitomap

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Fig. S4. The 34 SNPs in I-1's mtDNA (Family B) differing from the reference mtDNA haplogroup were predicted in Mitomaster. Haplogroup K1b (K1b2a)-related mtDNA variants are labeled in red rectangles.

Sequence alignment

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Sequence	PT17 Haplogroup	Total Variants	Variants
I-10	H (H)	9	A263G, A750G, A1438G, G1927A, G3531A, A4769G, A8860G, A15326G, T16519C Submit New Variants to Mitomap

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Fig. S5. The nine SNPs in I-10's mtDNA (Family B) differing from the reference mtDNA haplogroup were predicted in Mitomaster. Haplogroup H is defined by mtDNA genotype of 73A, 2706A, 7028C, 11719G and 14766C.

Sequence alignment

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Sequence	PT17 Haplogroup	Total Variants	Variants
II-30	T2a (T2a1a)	34	A73G, A263G, G709A, A750G, A1438G, G1588A, A2706G, T2850C, T4216C, A4769G, A4917G, T7022C, C7028T, G8697A, A8860G, T10463C, A11251G, G11719A, A11812G, G13368A, T13965C, A14233G, A14687G, C14766T, G14905A, C15040T, A15326G, C15452A, A15607G, G15928A, T16126C, C16294T, C16296T, T16519C Submit New Variants to Mitomap

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Fig. S6. The 34 SNPs in II-30's mtDNA (Family B) differing from the reference mtDNA haplogroup were predicted in Mitomaster. Haplogroup T2a (T2a1a)-related mtDNA variants are labeled in red rectangle.

Sequence alignment

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Sequence	Predicted Haplogroup	Total Variants	Variants	
F3-GF-mitomaster.dna	K2b (K2b1a1a)	34	A73G, T146C, A263G, A750G, A1438G, A1811G, C2217T A2706G, A3480G, A4769G, G5231A, C7028T, A8860G, G9055A, T9698C, T9716C, A10550G, T11299C, A11467G, G11719A, C11869A, A12308G, G12372A, G13135A, A14037G C14167T, C14766T, T14798C, A15326G, C16222T, T16224C, C16270T, T16311C T16519C	Alignment Details

Fig. S7. The 34 SNPs in I-1's mtDNA (Family C) differing from the reference mtDNA haplogroup were predicted in Mitomaster. Haplogroup K2b (K2b1a1a)-related mtDNA variants are labeled in red rectangle.

Sequence alignment

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Sequence	Predicted Haplogroup	Total Variants	Variants	
F3-GM-mitomaster.dna	J2a (J2a1a1a2)	41	A73G, T146C, C150T T152C, T195C A215G, A263G, C295T, T319C, T489C, G513A, A750G, A1438G, T1850C, A2706G, A3447G, T4216C A4769G, C7028T, C7476T, G7789A A8860G, A10398G, A10499C, A11251G G11377A, G11719A, A11818G, A12612G G13708A, A13722G A14133G, C14766T, G15257A, A15326G, C15452A, C16069T, T16126C, G16145A T16231C, C16261T	Alignment Details

Fig. S8. The 41 SNPs in I-10's mtDNA (Family C) differing from the reference mtDNA haplogroup were predicted in Mitomaster. Haplogroup J2a (J2a1a1a2)-related mtDNA variants are labeled in red rectangle.

Sequence alignment

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Sequence	Predicted Haplogroup	Total Variants	Variants
F3-mother-mitomaster.dna	K2a (K2a7)	35	A73G, T146C , T152C , A263G, C315CC, CA514d, G709A , A750G, A1438G, A1811G , A2706G, A3480G , T4561C , A4769G, C7028T, G8292A, A8860G, G9055A , T9698C , T9716C, A10550G, T11299C , A11467G , G11719A, A12308G , C12346T , G12372A , C14167T, C14766T, T14798C , A15326G, A16066G, T16224C , T16311C , T16519C

[Alignment Details](#)

Fig. S9. The 35 SNPs in II-30's mtDNA (Family C) differing from the reference mtDNA haplogroup were predicted in Mitomaster. Haplogroup K2a (K2a7)-related mtDNA variants are labeled in red rectangle.

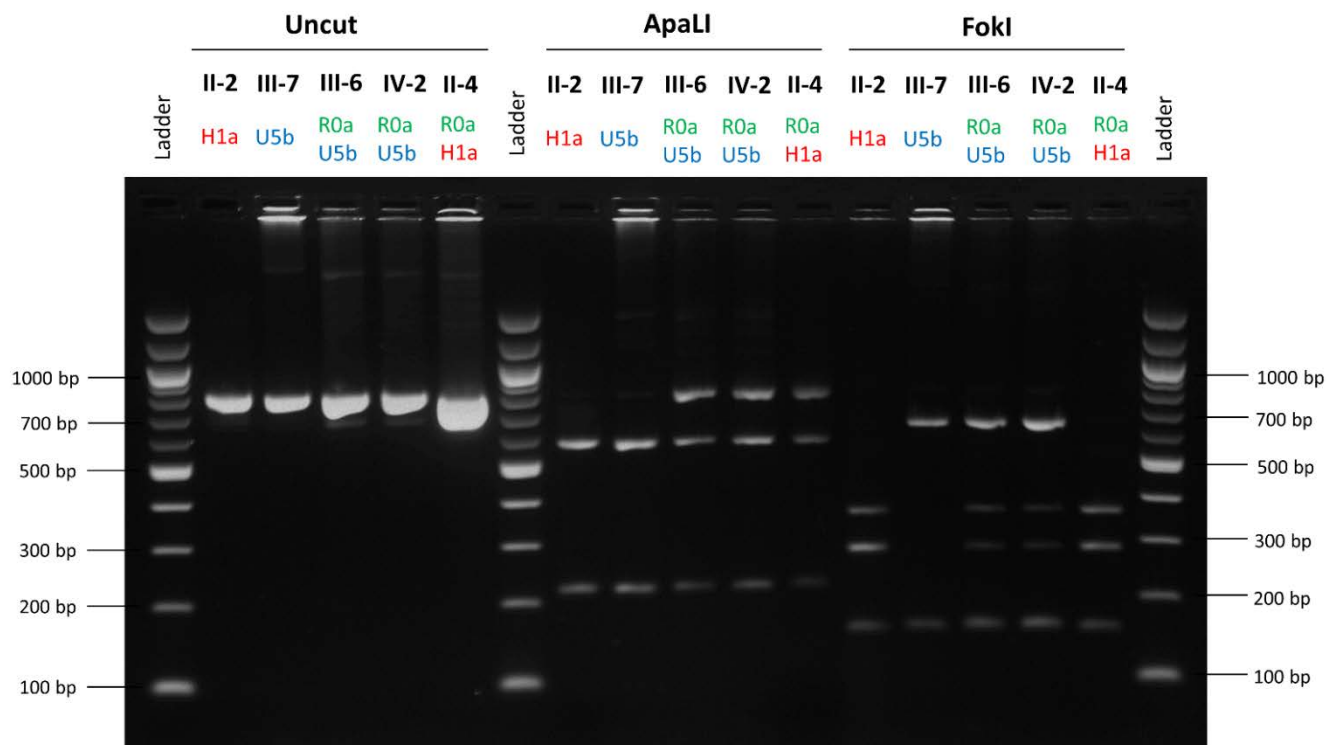


Fig. S10. RFLP analysis of selected members of Family A confirms the existence of the haplogroups detected by NGS. The haplogroups present in each individual are as indicated (“R0a” = R0a1, “H1a” = H1a1, and “U5b” = U5b1d1c). RFLP was performed on a 789 bp

PCR product covering positions 16426 to 626 in the human mitochondrial reference genome, which includes the hypervariable region HV2. The expected digest pattern for ApaLI is 789 bp for R0a1 and 572 bp and 217 bp for H1a1 and U5b1d1c. For FokI, the expected digest pattern is 632 bp and 157 bp for U5b1d1c and 355 bp, 277 bp, and 157 bp for R0a1 and H1a1.

Dataset S1. Comparison of mtDNA sequences of 11 family members in Family A. The mtDNA sequences were aligned with reference sequence- the human mitochondrial sequence reference NC_012920.1. SNPs were identified and submitted to MitoMaster for variant calls. All de novo SNPs were labeled with gray color and not included for analysis of mtDNA inheritance pattern in this family.

Dataset S2. Comparison of mtDNA sequences of five family members in Family B. The mtDNA sequences were aligned with reference sequence- the human mitochondrial sequence reference NC_012920.1. SNPs were identified and submitted to MitoMaster for variant calls.

Dataset S3. Comparison of mtDNA sequences of five family members in Family C. The mtDNA sequences were aligned with reference sequence- the human mitochondrial sequence reference NC_012920.1. SNPs were identified and submitted to MitoMaster for variant calls.

Table S1. Alignment of a total of 46 differential mtDNA variants in family A

rCRS Position	Reference	Variant	I-1 ^(D)	I-10 ^(D) /II-2/III-3	II-1/II-3/II-4	II-40/III-7	III-6/IV-1/IV-2/IV-3
58	T	C	<u>C</u>	T	^{C/} T	T	^{C/} T
64	C	T	<u>T</u>	C	^T C	C	^T C
73	A	G	A	<u>G</u>	^{A/} G	G	^{A/} G
150	C	T	C	C	C	<u>T</u>	^{C/} T
263	A	G	G	G	G	G	G
750	A	G	G	G	G	G	G
827	A	G	<u>G</u>	A	^{G/} A	A	^{G/} A
1438	A	G	G	G	G	G	G
2179	A	G	A	A	A	G	^{A/} G
2442	T	C	<u>C</u>	T	^{C/} T	T	^{C/} T
2706	A	G	G	A	^{G/} A	G	G
3010	G	A	G	<u>A</u>	^{G/} A	G	G
3197	T	C	T	<u>T</u>	T	<u>C</u>	^T C
3847	T	C	<u>C</u>	T	^{C/} T	T	^{C/} T
4769	A	G	G	G	G	G	G
5437	C	T	C	C	C	<u>T</u>	^{C/} T
5656	A	G	A	A	A	<u>G</u>	^{A/} G
6182	G	A	A	G	^{A/} G	G	^{A/} G
6365	T	C	T	<u>C</u>	^T C	T	T
7028	C	T	T	C	^T C	T	T
7768	A	G	A	A	A	<u>G</u>	^{A/} G
7912	G	A	G	G	G	<u>A</u>	^{G/} A
8860	A	G	G	G	G	G	G
9477	G	A	G	G	G	<u>A</u>	^{G/} A
11467	A	G	A	A	A	<u>G</u>	^{A/} G
11719	G	A	G	G	G	A	^{G/} A
12308	A	G	A	A	A	<u>G</u>	^{A/} G
12372	G	A	G	G	G	<u>A</u>	^{G/} A
13188	C	T	<u>T</u>	C	^T C	C	^T C
13617	T	C	T	T	T	<u>C</u>	^T C
14182	T	C	T	T	T	<u>C</u>	^T C
14198	G	A	G	A	^{G/} A	G	G
14766	C	T	T	C	^T C	T	T
15326	A	G	G	G	G	G	G
15631	A	G	A	A	A	<u>G</u>	^{A/} G
15721	T	C	T	T	T	<u>C</u>	^T C
16126	T	C	<u>C</u>	T	^{C/} T	T	^{C/} T
16162	A	G	A	<u>G</u>	^{A/} G	A	A
16192	C	T	C	C	C	<u>T</u>	^{C/} T
16209	T	C	T	<u>C</u>	^T C	T	T
16218	C	T	C	C	C	<u>T</u>	^{C/} T
16270	C	T	C	C	C	<u>T</u>	^{C/} T
16291	C	T	T	C	^T C	C	^T C
16320	C	T	C	C	C	<u>T</u>	^{C/} T
16362	T	C	<u>C</u>	T	^{C/} T	T	^{C/} T
16519	T	C	T	C	^T C	T	T
Heteroplasmy %			100	100	^{40/} 60	100	^{40/} 60
Haplogroup			<u>R0a1</u>	<u>H1a1</u>	<u>R0a1/H1a1</u>	<u>U5b1d1c</u>	<u>R0a1/U5b1d1c</u>

Entries labeled (D) represent deduced mtDNA genotypes. Haplogroup related nucleotides have been underlined in the table.

Table S2. Alignment of a total of 58 differential mtDNA variants in family B

rCRS Position	Reference	Variant	I-1 ^(D)	I-10 ^(D)	II-3	II-30/III-1/III-5	III-2
73	A	G	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>G</u>	<u>G</u>
146	T	C	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>T</u>	<u>C/T</u>
195	T	C	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>T</u>	<u>C/T</u>
263	A	G	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>
709	G	A	<u>G</u>	<u>G</u>	<u>G</u>	<u>A</u>	<u>G/A</u>
750	A	G	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>
1189	T	C	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>T</u>	<u>C/T</u>
1438	A	G	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>
1811	A	G	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>A</u>	<u>G/A</u>
1888	G	A	<u>G</u>	<u>G</u>	<u>G</u>	<u>A</u>	<u>G/A</u>
1927	G	A	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>G</u>	<u>G</u>
2706	A	G	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>G</u>	<u>G</u>
2850	T	C	<u>T</u>	<u>T</u>	<u>T</u>	<u>C</u>	<u>T/C</u>
3480	A	G	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>A</u>	<u>G/A</u>
3531	G	A	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>G</u>	<u>G</u>
4216	T	C	<u>T</u>	<u>T</u>	<u>T</u>	<u>C</u>	<u>T/C</u>
4769	A	G	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>
4917	A	G	<u>A</u>	<u>A</u>	<u>A</u>	<u>G</u>	<u>A/G</u>
5913	G	A	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>G</u>	<u>A/G</u>
7022	T	C	<u>T</u>	<u>T</u>	<u>T</u>	<u>C</u>	<u>T/C</u>
7028	C	T	<u>T</u>	<u>C</u>	<u>T/C</u>	<u>T</u>	<u>T</u>
8697	G	A	<u>G</u>	<u>G</u>	<u>G</u>	<u>A</u>	<u>G/A</u>
8860	A	G	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>
9055	G	A	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>G</u>	<u>A/G</u>
9058	A	G	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>A</u>	<u>G/A</u>
9066	A	C	<u>C</u>	<u>A</u>	<u>C/A</u>	<u>A</u>	<u>C/A</u>
9698	T	C	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>T</u>	<u>C/T</u>
10398	A	G	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>A</u>	<u>G/A</u>
10463	T	C	<u>T</u>	<u>T</u>	<u>T</u>	<u>C</u>	<u>T/C</u>
10550	A	G	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>A</u>	<u>G/A</u>
11251	A	G	<u>A</u>	<u>A</u>	<u>A</u>	<u>G</u>	<u>A/G</u>
11299	T	C	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>T</u>	<u>C/T</u>
11467	A	G	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>A</u>	<u>G/A</u>
11719	G	A	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>A</u>	<u>A</u>
11812	A	G	<u>A</u>	<u>A</u>	<u>A</u>	<u>G</u>	<u>A/G</u>
12308	A	G	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>A</u>	<u>G/A</u>
12372	G	A	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>G</u>	<u>A/G</u>
12738	T	G	<u>G</u>	<u>T</u>	<u>G/T</u>	<u>T</u>	<u>G/T</u>
12771	G	A	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>G</u>	<u>A/G</u>
13368	G	A	<u>G</u>	<u>G</u>	<u>G</u>	<u>A</u>	<u>G/A</u>
13965	T	C	<u>T</u>	<u>T</u>	<u>T</u>	<u>C</u>	<u>T/C</u>
14167	C	T	<u>T</u>	<u>C</u>	<u>T/C</u>	<u>C</u>	<u>T/C</u>
14233	A	G	<u>A</u>	<u>A</u>	<u>A</u>	<u>G</u>	<u>A/G</u>
14687	A	G	<u>A</u>	<u>A</u>	<u>A</u>	<u>G</u>	<u>A/G</u>
14766	C	T	<u>T</u>	<u>C</u>	<u>T/C</u>	<u>T</u>	<u>T</u>
14798	T	C	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>T</u>	<u>C/T</u>
14905	G	A	<u>G</u>	<u>G</u>	<u>G</u>	<u>A</u>	<u>G/A</u>
15040	C	T	<u>C</u>	<u>C</u>	<u>C</u>	<u>T</u>	<u>C/T</u>
15326	A	G	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>
15452	C	A	<u>C</u>	<u>C</u>	<u>C</u>	<u>A</u>	<u>C/A</u>
15607	A	G	<u>A</u>	<u>A</u>	<u>A</u>	<u>G</u>	<u>A/G</u>
15928	G	A	<u>G</u>	<u>G</u>	<u>G</u>	<u>A</u>	<u>G/A</u>
16126	T	C	<u>T</u>	<u>T</u>	<u>T</u>	<u>C</u>	<u>T/C</u>
16224	T	C	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>T</u>	<u>C/T</u>
16294	C	T	<u>C</u>	<u>C</u>	<u>C</u>	<u>T</u>	<u>C/T</u>
16296	C	T	<u>C</u>	<u>C</u>	<u>C</u>	<u>T</u>	<u>C/T</u>
16311	T	C	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>T</u>	<u>C/T</u>
16519	T	C	<u>C</u>	<u>C</u>	<u>C</u>	<u>C</u>	<u>C</u>
Heteroplasmy %			100	100	28/72	100	51/49
Haplogroup			<u>K1b2a</u>	<u>H</u>	<u>K1b2a/H</u>	<u>T2a1a</u>	<u>K1b2a/T2a1a</u>

Entries labeled (D) represent deduced mtDNA genotypes. Haplogroup related nucleotides have been underlined in the table.

Table S3. Alignment of a total of 68 differential mtDNA variants in family C

rCRS Position	Reference	Variant	I-1 ^(D)	I-10 ^(D)	II-3	II-30	III-6/III-7/IV-1	rCRS Position	Reference	Variant	I-1 ^(D)	I-10 ^(D)	II-3	II-30	III-6/III-7/IV-1
73	A	G	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	10550	A	G	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>G</u>	<u>G</u>
146	T	C	<u>C</u>	<u>C</u>	<u>C</u>	<u>C</u>	<u>C</u>	11251	A	G	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>A</u>	<u>A</u>
150	C	T	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>C</u>	<u>C</u>	11299	T	C	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>C</u>	<u>C</u>
152	T	C	<u>T</u>	<u>C</u>	<u>T/C</u>	<u>C</u>	<u>T/C</u>	11377	G	A	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>G</u>	<u>G</u>
195	T	C	<u>T</u>	<u>C</u>	<u>T/C</u>	<u>T</u>	<u>T</u>	11467	A	G	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>G</u>	<u>G</u>
215	A	G	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>A</u>	<u>A</u>	11719	G	A	<u>A</u>	<u>A</u>	<u>A</u>	<u>A</u>	<u>A</u>
263	A	G	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	11818	A	G	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>A</u>	<u>A</u>
295	C	T	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>C</u>	<u>C</u>	11869	C	A	<u>A</u>	<u>C</u>	<u>A/C</u>	<u>C</u>	<u>A/C</u>
319	T	C	<u>T</u>	<u>C</u>	<u>T/C</u>	<u>T</u>	<u>T</u>	12308	A	G	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>G</u>	<u>G</u>
489	T	C	<u>T</u>	<u>C</u>	<u>T/C</u>	<u>T</u>	<u>T</u>	12346	C	T	<u>C</u>	<u>C</u>	<u>C</u>	<u>T</u>	<u>C/T</u>
513	G	A	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>G</u>	<u>G</u>	12372	G	A	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>A</u>	<u>A</u>
709	G	A	<u>G</u>	<u>G</u>	<u>G</u>	<u>A</u>	<u>G/A</u>	12612	A	G	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>A</u>	<u>A</u>
750	A	G	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	13135	G	A	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>G</u>	<u>A/G</u>
1438	A	G	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	13708	G	A	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>G</u>	<u>G</u>
1811	A	G	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>G</u>	<u>G</u>	13722	A	G	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>A</u>	<u>A</u>
1850	T	C	<u>T</u>	<u>C</u>	<u>T/C</u>	<u>T</u>	<u>T</u>	14037	A	G	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>A</u>	<u>G/A</u>
2217	C	T	<u>T</u>	<u>C</u>	<u>T/C</u>	<u>C</u>	<u>T/C</u>	14133	A	G	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>A</u>	<u>A</u>
2706	A	G	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	14167	C	T	<u>T</u>	<u>C</u>	<u>T/C</u>	<u>T</u>	<u>T</u>
3447	A	G	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>A</u>	<u>A</u>	14766	C	T	<u>T</u>	<u>T</u>	<u>T</u>	<u>T</u>	<u>T</u>
3480	A	G	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>G</u>	<u>G</u>	14798	T	C	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>C</u>	<u>C</u>
4216	T	C	<u>T</u>	<u>C</u>	<u>T/C</u>	<u>T</u>	<u>T</u>	15257	G	A	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>G</u>	<u>G</u>
4561	T	C	<u>T</u>	<u>T</u>	<u>T</u>	<u>C</u>	<u>T/C</u>	15326	A	G	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>
4769	A	G	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	15452	C	A	<u>C</u>	<u>A</u>	<u>C/A</u>	<u>C</u>	<u>C</u>
5231	G	A	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>G</u>	<u>A/G</u>	16066	A	G	<u>A</u>	<u>A</u>	<u>A</u>	<u>G</u>	<u>A/G</u>
7028	C	T	<u>T</u>	<u>T</u>	<u>T</u>	<u>T</u>	<u>T</u>	16069	C	T	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>C</u>	<u>C</u>
7476	C	T	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>C</u>	<u>C</u>	16126	T	C	<u>T</u>	<u>C</u>	<u>T/C</u>	<u>T</u>	<u>T</u>
7789	G	A	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>G</u>	<u>G</u>	16145	G	A	<u>G</u>	<u>A</u>	<u>G/A</u>	<u>G</u>	<u>G</u>
8292	G	A	<u>G</u>	<u>G</u>	<u>G</u>	<u>A</u>	<u>G/A</u>	16222	C	T	<u>T</u>	<u>C</u>	<u>T/C</u>	<u>C</u>	<u>T/C</u>
8860	A	G	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	<u>G</u>	16224	T	C	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>C</u>	<u>C</u>
9055	G	A	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>A</u>	<u>A</u>	16231	T	C	<u>T</u>	<u>C</u>	<u>T/C</u>	<u>T</u>	<u>T</u>
9698	T	C	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>C</u>	<u>C</u>	16261	C	T	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>C</u>	<u>C</u>
9716	T	C	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>C</u>	<u>C</u>	16270	C	T	<u>T</u>	<u>C</u>	<u>T/C</u>	<u>C</u>	<u>T/C</u>
10398	A	G	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>A</u>	<u>A</u>	16311	T	C	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>C</u>	<u>C</u>
10499	A	G	<u>A</u>	<u>G</u>	<u>A/G</u>	<u>A</u>	<u>A</u>	16519	T	C	<u>C</u>	<u>T</u>	<u>C/T</u>	<u>C</u>	<u>C</u>
Heteroplasmy %			100	100	70/30	100	76/24	Heteroplasmy %			100	100	70/30	100	76/24
Haplogroup			<u>K2b1a1a</u>	<u>J2a1a1a2</u>	<u>K2b1a1a/J2a1a1a2</u>	<u>K2a7</u>	<u>K2b1a1a/K2a7</u>	Haplogroup			<u>K2b1a1a</u>	<u>J2a1a1a2</u>	<u>K2b1a1a/J2a1a1a2</u>	<u>K2a7</u>	<u>K2b1a1a/K2a7</u>

Entries labeled (D) represent deduced mtDNA genotypes. Haplogroup related nucleotides have been underlined in the table.