

## mtDNA Haplogroup Specific Control Region Mutation Motifs

### African Haplogroup

Haplogroup	HV1	HV2	HV3 <i>etc.</i>
L0	(16129)-16187-16189-16223-16230-16311	247	
L0a	16129-16148-16172-16187-16188G-16189-16223-16230-16311-16320	93-185-189-236-247	523d-524d
L0a1	16129-16148-16168-16172-16187-16188G-16189-16223-16230-16311-16320	93-185-189-(236)-247	523d-524d
L0a1a	16129-16148-16168-16172-16187-16188G-16189-16223-16230-16311-16320	93-185-189-200-236-247	523d-524d
L0a1b	16129-16148-16168-16172-16187-16188G-16189-16223-16230-16278-16311-16320	93-95C-185-189-236-247	523d-524d
L0a2	@16129-16148-16172-16187-16188G-16189-16223-16230-16311-16320	93-152-189-236-247	64, 523d-524d
L0f	16169-16187-16189-16223-(16230)-16278-16311-16327	(146)-189-247	16368
L0k	16166C-16172-16187-16189-16214-16223-16230-16278-16291G-16311	146-189-195-247	
L0d	(16129)-(16187)-16189-16223-16230-16243-16311	247	
L1	(16187)-16189-16223-16278-16311	182-247	523d-524d
L1b	16126-(16187)-16189-16223-(16264)-16270-16278-16311	(182)-185T-(195)-247	357, 523d-524d
L1b1	16126-16187-16189-16223-16264-16270-16278-16293-16311	182-185T-195-247	357, 523d-524d
L1b1*	16126-16187-16189-16223-16264-16270-16278-@16293-16311	182-185T-195-247	357, 523d-524d
L1c	16129-16187-16189-16223-16278-16311	152-(182)-186A-189C-247(or 247d)-316	523d-524d
L1c1	16129-(16187)-16189-16223-16278-16293-16360	151-152-182-186A-189C-195-247(or 247d)-316	523d-524d
L1c2	16129-16187-16189-16223-16265C-(16278)-16286R-16294-16311-(16360)	(151)-152-182-186A-189C-195-198-247-297-316	16527, 523d-524d
L1c3a	16129-@16187-16189M-16215-(16223)-16278-16294-16311-16360	151-152-182-186A-189C-@195-247-316	523d-524d
L1c3b	16129-(16187)-16189-16223-16278-16293-16294-16311-16360	(151)-152-182-186A-189C-@195-247-316	523d-524d
L1c4	16129-16184-16187-16189-16223-16278-16294-16301-16311-16360	152-182-186A-189C-195-247-297-316	523d-524d
L5	16129-16148-16166-16189-16223-16278-16311	182-195-247	459.1C
L5a	16129-16148-16166-16189-16223-16278-16311-16355-16362	152-182-195-247	455.1T-459.1C
L5c	16111-16129-16148-16166-16189-16223-16254-16278-16360	195-247(or 247d)	459.1C-535
L2	16223-16278	146-152(or 150)-195	16390
L2a	16223-16278-16294	146-152-195	16390
L2a1	(16223)-16278-(16294)-16309	146-152-195	16390
L2a1a	16223-16278-16294-16309	146-152-195	16368-16390
L2a1a	16223-16278-16286-16294-16309	146-152-195	16390
L2a1b	16183C-16189-16223-16278-16290-16294-16309	146-152-195	16390
L2a1*	16189-16192-16223-16278-16294	146-152-195	16390
L2a2	16189-16223-16229-16278-16291-16294-16311	@146-152-195	16390

Haplogroup	HV1	HV2	HV3 etc.
L2b	16114A-16129-16213-16223-16278	146-150-152-182-195-198-204	16390
L2b1	16114A-(16129)-16213-16223-16278-16362	150-(152)-182-195-198-204	16390, 418
L2b2	16114A-16129-16213-16223-16274-16278	146-150-152-182-183-195-198-204	16390
L2c	16223-16278	93-146-150-152-182-(195)-325	16390, 523d-524d
L2c*	16223-16278	@93-150-152-182-195-325	16390, 523d-524d
L2c2	16223-16264-16278	93-146-150-152-182-195-325	16390, 523d-524d
L2d	16129-16189-16278-16300-16354	146-150-195	16390-16399, 456
L2e	16111A-16145-16184-16223-16239-16278-16355	146-182	16390-16399-16400, 479
L6	16048-16223-16224-16278	146-152-185C	
L4a	16223-16260-16311-16362	195-198	
L4b1	16179-16189-16223-16239-16311-16320-16362	150-199	
L4b2	16223-16293T-16311-16355-(16362)	146	16399
L3a	16223-16316	152	523d-524d
L3b	16124-16223-16278-(16362)		523d-524d
L3b1a	@16124-16223-16278-16362		523d-524d
L3b1b	16124-16223-(16278)-16362	152	523d-524d
L3b1*	16124-16223-16278-16311-16362		523d-524d
L3b2	16124-16189-16278-16362		16527, 523d-524d
L3c	16223-16311-16362	152-195	498, 1C-523d-524d
L3d	16124-16223	152	523d-524d
L3d1a	16124-16223-16319	152	523d-524d
L3d1c	16124-16166-16223	152	523d-524d
L3d1d	16124-16223-16256	152	16368, 523d-524d
L3d3	16111-16124-16223	152-199	523d-524d
L3d3	16124-16189-16223-16278-16304-16311	152	523d-524d
L3d4	16124-16223	152-189-195	523d-524d
L3e1	16223-16327	150-189-200	
L3e1a	16185-16223-16327	150-189-(200)	
L3e1b	16223-16325d-16327	150-189	
L3e1d	16176-16223-16327	150-152-189-200	
L3e2	16223-16320	150-195	
L3e2a	16223-16320	150-195-198	499
L3e2b	16172-16189-16223-16320	150-195	
L3e2b*	16172-16183C-16189-16223-16320	150-152-195	
L3e3	16223-16265T	150-195	523d-524d-573.pC
L3e4	16051-16223-16264	150	523d-524d
L3e5	16041-16223	150	398, 523d-524d
L3i1	16223-16153		
L3i2	16223-16260-16311	150-152-189	504
L3k	16223	235-150	494
L3x	16169	150	
L3x1	16169-16223-16278	150-204	
L3x2	16169-16195	150-249d	494
L3f	16209-16223		
L3f1b	16209-16223-16292-16311	189	
L3f1b1	16129-16209-16223-16292-16295-16311	189-200	
L3f2	16209-16223-16311		
L3f3	16176-16209-16223-16234	189-318	

Haplogroup	HV1	HV2	HV3 <i>etc.</i>
<i>L3h1a1</i>	16223-16311		<i>516</i>
<i>L3h1a2</i>	16223-16311	146	<i>16399</i>
<i>L3h1a2*</i>	16192-16223-16311	146	<i>16399</i>
<i>L3h1b</i>	16223-16256A-16311	189C-195	
<i>M1</i>	16129-16189-(16223)-16249-16311	195	<i>16519, 489</i>
<i>M1a1</i>	16129-16189-16223-(16249)-16311-16359	195	<i>16519, 489</i>
<i>M23</i>	16223-16263-16311	152-195-204	<i>16519, 417, 489-533</i>
<i>U6</i>	16172-16219		
<i>U6a</i>	16172-16219-16278		
<i>U6bd</i>	16172-16219-16311		
<i>U6c</i>	16169-16172-16189	150	<i>437, 523d-524d</i>

\*For each mtDNA haplogroup, 73, 263, 315.1 and insertions in the HV2 poly-C stretch were ignored; all mutations are transitions unless exact nucleotide is brought out, suffix "d" indicates deletion and "." + a number (or p) + suffix indicates insertion; mutation sites which have been found in the majority, but not all samples from a respective haplogroup are given in parentheses; prefix "@" indicates back mutation; mtDNA haplogroups which need mutation motif outside of HV1 and HV2 region to estimate their own haplogroups are shown in italics.

## References

1. Salas A, Richards M, De la Fe T, Lareu MV, Sobrino B, Sanchez-Diz P, Macaulay V, Carracedo A. The making of the African mtDNA landscape. *Am J Hum Genet.* 2002;71(5):1082-111.
2. Salas A, Richards M, Lareu MV, Scozzari R, Coppa A, Torroni A, Macaulay V, Carracedo A. The African diaspora: mitochondrial DNA and the Atlantic slave trade. *Am J Hum Genet.* 2004;74(3):454-65.
3. Brandstatter A, Peterson CT, Irwin JA, Mpoke S, Koech DK, Parson W, Parsons TJ. Mitochondrial DNA control region sequences from Nairobi (Kenya): inferring phylogenetic parameters for the establishment of a forensic database. *Int J Legal Med.* 2004;118(5):294-306.
4. Kivisild T, Reidla M, Metspalu E, Rosa A, Brehm A, Pennarun E, Parik J, Geberhiwot T, Usanga E, Villems R. Ethiopian mitochondrial DNA heritage: tracking gene flow across and around the gate of tears. *Am J Hum Genet.* 2004;75(5):752-70.
5. Allard MW, Polanskey D, Miller K, Wilson MR, Monson KL, Budowle B. Characterization of human control region sequences of the African American SWGDAM forensic mtDNA data set. *Forensic Sci Int.* 2005;148(2-3):169-79.
6. Olivieri A, Achilli A, Pala M, Battaglia V, Fornarino S, Al-Zahery N, Scozzari R, Cruciani F, Behar DM, Dugoujon JM, Coudray C, Santachiara-Benerecetti AS, Semino O, Bandelt HJ, Torroni A. The mtDNA legacy of the Levantine early Upper Palaeolithic in Africa. *Science.* 2006;314(5806):1767-70.
7. Behar DM, Villems R, Soodyall H, Blue-Smith J, Pereira L, Metspalu E, Scozzari R, Makkani H, Tzur S, Comas D, Bertranpetit J, Quintana-Murci L, Tyler-Smith C, Wells RS, Rosset S; Genographic Consortium. The dawn of human matrilineal diversity. *Am J Hum Genet.* 2008;82(5):1130-40.
8. Ricaut FX, Razafindrazaka H, Cox MP, Dugoujon JM, Guitard E, Sambo C, Mormina M, Mirazon-Lahr M, Ludes B, Crubez E. A new deep branch of eurasian mtDNA macrohaplogroup M reveals additional complexity regarding the settlement of Madagascar. *BMC Genomics.* 2009;10(1):605.

**West Eurasian Haplogroup**

Haplogroup	HV1	HV2	HV3 <i>etc.</i>
R0a	16126-16362		64
R0a1a	16126-16355-16362	146	64
<i>pre-R0a2'3</i>	16126-16362		<u>60.IT-64</u>
HV0	16298	72	
HV1	16067		
HV2	16217	73-152	
HV4a	16221		
HV6	16172-16311		
HV7	16278-16311		16519
HV8	16311-16354		
HV9a	16311	131-152	
HV-14764	16319	143-152	
HV*	16223	235	523d-524d
HV*	16092-16278		
HV*	16129-16242-16356		
H		(73A)	
H1a	16162	73	16519
H1b	16189-16356		16519
H1f	16093-16189		16519
H1k	16189-16290		16519
<i>H1c</i>			16519, 477
H1c1	16263		16519, 477
<i>H1d</i>			16519, 456
H1o		267	16519, 485
H2a1	16354		
<i>H2a2a</i>	<i>rCRS</i>	<i>rCRS</i>	<i>rCRS</i>
H2a2b	16235-16291		
H2a3	16274		
H2b	16311	152	
H3a	16239G	152	
H5	16304		456
H36	16070	152	456
H6	16362	239	16482
H7*	16172-16173		16519
H8	16288-16362	146	
H9a	16168	152	
H10a	16114		
H11	16311	195	
H11a	16293-16311	195	
H12	16287	195	
H13a*	16218-16278	93	
H13a2	16148-16256-16319	189-193-249	
H14a	16256-16352		
<i>H15</i>			<u>55-57</u>
H20	16218-16328A		
H21	16192	186	
H22	16145-16227		
H27	16093-16129-16316		
H28		186A	
<i>H29</i>		93	<u>573.pC</u>
H30	16192	195	504
H31		146-195	
H38		235	
H39	16299		
T	16126-16294		16519
T1	16126-16163-16186-16189-16294		16519

Haplogroup	HV1	HV2	HV3 <i>etc.</i>
T1a	16126-16163-16186-16189-16294	152-195	16519
T1b	16126-16163-16189-16243-16294		16519
T2	16126-16294-16296		16519
T2b	16126-16294-16296-16304		16519
T2c	16126-16292-16294-(16296)		16519
T2d	16126-16294-16296	152	16519
T2e	16126-16153-16294-(16296)	150	16519
T2f	16126-16182C-16183C-16189-16294-16296-16298	195	16519
T2g	16126-16294-16296	200	16519
J	16069-16126	295	489
J1	16069-16126	295	462-489
J1b	16069-16126-16145-16222-16261	295	462-489
J1b1	16069-16126-16145-(16172)-16261	242-295	462-489
J1b2	16069-16126-16145-16261	271-295	462-489
J1b3	16069-16126-16145-16222-16235-16261-16271	295	462-489
J1b*	16069-@16126-16145-16261	151-152-295	462-489
J1c	16069-16126	(185)-(228)-295	462-489
J1c1	16069-16126	(185)-228-295	462-482-489
J1c2	16069-16126	185-188-295	462-489
J1c7	16069-16126-16261	(185)-(228)-295	462-489
J1c8	16069-16126-16319	185-228-295	462-489
J1d	16069-16126-16193	152-295	489
J2	16069-16126	150-195-295	489
J2a	16069-16126-16145-16231-16261	150-152-195-215-295	489
J2b	16069-16126-16193	150-(152)-295	489
U1	16249	285	
U1a	16189-16249	285	
U1a1	16189-16249	285	385, 523d-524d
U1b	16111-16249-16327	146-285	
U2	16051		
U2d	16051-16189-16234-16294	152-199-@263	16519, 471
U2e	16051-16129C-16189-(16362)	152-217	16519, 508
U3	16343	150	
U3a	16343	150	16390
U4/U9		195	499
U4	16356	195	16519, 499
U4a1	16134-16356	152-(195)	16519, 499
U4a2	(16356)	195-310	16519, 499
U4a3	16265-16356-16362	195-247	16519, 499-524.1A-524.2C
U4b1	16356	146-195	16519, 499
U4b2	16136-16356	195	16519, 499
U4c1	16179-16356	195	16519, 499
U9a	16051-16278	@195	499
U9b	16242	195	499-573.pC
U5	16270		
U5a	16256-16270		
U5a1	16256-16270		16399
U5a2	16256-16270		16526
U5b	16270	150	
U5b1b	16189-16270	150	
U5b1b1	16144-16189-16270	150	
U5b1b2	16189-16270	150-217	
U5b1c	16192-16311	150	

Haplogroup	HV1	HV2	HV3 <i>etc.</i>
U5b2a1	16189-@16192-@16270-16325	150-152	
<i>U5b2a2</i>	16189-16192-16270	150	<u>16398</u>
U5b3	(16192)-16270-16304	150-(228)	
U5b3a	16192-16235-16270-16304	150	
U7	16318Y	152	<i>523d-524d</i>
U8a		282	
U8a1	16146-16342	282	
U8b	16189-16234		
K	16224-16311		<i>16519</i>
<i>K1a</i>	16224-16311		<i>16519, 497</i>
<i>K1a*</i>	16224-16234-16311		<i>16519, 497</i>
<i>K1a*</i>	16093-16224-16311		<i>16519, 497</i>
<i>K1a4b</i>	16224-16311	280G	<i>16519, 497</i>
<i>K1a6</i>	16224-16311		<i>16519-16527, 497</i>
<i>K1a9</i>	16093-16224-16311	195	<i>16519-16524, 497</i>
<i>K1a10</i>	16048-16224-16311	195	<i>16519, 497</i>
<i>K1a11</i>	16129-16224-16311	150-199	<i>16519, 16T, 497</i>
<i>K1b1a</i>	16224-16311-16319	152	<i>16519</i>
<i>K1b1c</i>	16224-16311	94	<i>16519</i>
<i>K1b2</i>	16224-16311	146-195	<i>16519, 524.1A-524.2C</i>
<i>K1c</i>	16224-16311	146-152	<i>16519, 498d</i>
<i>K1c2</i>	16224-16311-16320	146-152	<i>16519, 498d</i>
K2	16224-16311	146	<i>16519</i>
K2a	16224-16311	146-152	<i>16519</i>
K2b1	16224-16270-16311	146	<i>16519</i>
R1	16311	295A	<i>16519</i>
R2	16071	152	<i>16519</i>
I	16129-16223	199-204-250	<i>16391-16519</i>
I1	16129-16223-16311	199-204-250	<i>16391-16519, 455.1T-573.pC</i>
I1a	16129-16172-16223-16311	199-203-204-250	<i>16391-16519, (455.1T)-573.pC</i>
I2	16129-16223	152-199-204-207-250	<i>16391-16519, 573.pC</i>
I3	16129-16223	152-199-204-207-239-250	<i>16391-16519, 524.1A-524.2C-573.pC</i>
I4	16129-16223-16304	199-204-250	<i>16391-16519, 573.pC</i>
I5	16129-16148-16223	199-204-250	<i>16391-16519, 573.pC</i>
N1a	16147R-16172-16223-16248-16320-16355	(152)-199-204	<i>16519</i>
N1d	16223-16301-16356	199-204	<i>16519</i>
N1b	16145-16176R-16223		<i>16390-16519</i>
N1c	16201-16223-16265		
N2a	16153-16223	189-199	
W	16223-16292	189-195-204-207	<i>16519</i>
W1b	16223-16292	189-195-204-207-227	<i>16519</i>
W1c	16223-16292	119-189-195-204-207	<i>16519</i>
W1e	16223-16292-16295	189-195-204-207	<i>16519</i>
W3'5	16223-16292	189-194-195-204-207	<i>16519</i>
W4	16223-16292	143-189-194-195-196-204-207	<i>16519</i>
W5a	16223-16292-16362	189-194-195-204-207	<i>16519</i>
W6	16223-16292-16325	189-194-195-204-207	<i>16519</i>
X	16189-16278		<i>16519</i>
X1	16104-16189-@16278	146-153	<i>16519</i>
X3	16189-16278	146-153	<i>16519</i>
X3a	16126-16189-16278	146-153-256	<i>16519</i>

Haplogroup	HV1	HV2	HV3 <i>etc.</i>
X2	16189-16278	195	16519
X2a	16189-16213-16223-16278	153-195-200	16519
X2b	16189-16223-16278	(153)-195-225-226	16519
X2c	16183C-16189-16223-16255-16278	153-195-225-(227)	16519
X2e	16189A-16223-16278	153-195	16519
X2d	16189-16223-16278	@153-195-(204)-207	16519
X2f	16189-16223-16278	153-195-257	16519

## References

1. Macaulay V, Richards M, Hickey E, Vega E, Cruciani F, Guida V, Scozzari R, Bonne-Tamir B, Sykes B, Torroni A. The emerging tree of West Eurasian mtDNAs: a synthesis of control-region sequences and RFLPs. *Am J Hum Genet.* 1999;64(1):232-49.
2. Reidla M, Kivisild T, Metspalu E, Kaldma K, Tambets K, Tolk HV, Parik J, Loogväli EL, Derenko M, Malyarchuk B, Bermisheva M, Zhadanov S, Pennarun E, Gubina M, Golubenko M, Damba L, Fedorova S, Gusar V, Grechanina E, Mikerezi I, Moisan JP, Chaventré A, Khusnutdinova E, Osipova L, Stepanov V, Voevoda M, Achilli A, Rengo C, Rickards O, De Stefano GF, Papiha S, Beckman L, Janicijevic B, Rudan P, Anagnou N, Michalodimitrakis E, Koziel S, Usanga E, Geberhiwot T, Herrnstadt C, Howell N, Torroni A, Villems R. Origin and diffusion of mtDNA haplogroup X. *Am J Hum Genet.* 2003;73(5):1178-90.
3. Quintana-Murci L, Chaix R, Wells RS, Behar DM, Sayar H, Scozzari R, Rengo C, Al-Zahery N, Semino O, Santachiara-Benerecetti AS, Coppa A, Ayub Q, Mohyuddin A, Tyler-Smith C, Qasim Mehdi S, Torroni A, McElreavey K. Where west meets east: the complex mtDNA landscape of the southwest and Central Asian corridor. *Am J Hum Genet.* 2004;74(5):827-45.
4. Achilli A, Rengo C, Magri C, Battaglia V, Olivieri A, Scozzari R, Cruciani F, Zeviani M, Briem E, Carelli V, Moral P, Dugoujon JM, Roostalu U, Loogvali EL, Kivisild T, Bandelt HJ, Richards M, Villems R, Santachiara-Benerecetti AS, Semino O, Torroni A. The molecular dissection of mtDNA haplogroup H confirms that the Franco-Cantabrian glacial refuge was a major source for the European gene pool. *Am J Hum Genet.* 2004;75(5):910-8.
5. Palanichamy MG, Sun C, Agrawal S, Bandelt HJ, Kong QP, Khan F, Wang CY, Chaudhuri TK, Palla V, Zhang YP. Phylogeny of mitochondrial DNA macrohaplogroup N in India, based on complete sequencing: implications for the peopling of South Asia. *Am J Hum Genet.* 2004;75(6):966-78.
6. Achilli A, Rengo C, Battaglia V, Pala M, Olivieri A, Fornarino S, Magri C, Scozzari R, Babudri N, Santachiara-Benerecetti AS, Bandelt HJ, Semino O, Torroni A. Saami and Berbers--an unexpected mitochondrial DNA link. *Am J Hum Genet.* 2005;76(5):883-6.
7. Roostalu U, Kutuev I, Loogväli EL, Metspalu E, Tambets K, Reidla M, Khusnutdinova EK, Usanga E, Kivisild T, Villems R. Origin and expansion of haplogroup H, the dominant human mitochondrial DNA lineage in West Eurasia: the Near Eastern and Caucasian perspective. *Mol Biol Evol.* 2007;24(2):436-48.
8. Behar DM, Metspalu E, Kivisild T, Rosset S, Tzur S, Hadid Y, Yudkovsky G, Rosengarten D, Pereira L, Amorim A, Kutuev I, Gurwitz D, Bonne-Tamir B, Villems R, Skorecki K. Counting the founders: the matrilineal genetic ancestry of the Jewish Diaspora. *PLoS ONE.* 2008;3(4):e2062.
9. Malyarchuk BA, Perkova MA, Derenko MV, Vanecek T, Lazur J, Gomolcak P. Mitochondrial DNA variability in Slovaks, with application to the Roma origin. *Ann Hum Genet.* 2008;72(2):228-40.
10. Malyarchuk B, Grzybowski T, Derenko M, Perkova M, Vanecek T, Lazur J, Gomolcak P, Tsybovsky I. Mitochondrial DNA phylogeny in Eastern and Western Slavs. *Mol Biol Evol.* 2008;25(8):1651-8.
11. van Oven M, Kayser M. Updated comprehensive phylogenetic tree of global human mitochondrial DNA variation. *Hum Mutat.* 2009;30(2):e386-94. <http://www.phylotree.org>.
12. Alvarez-Iglesias V, Mosquera-Miguel A, Cerezo M, Quintáns B, Zarrabeitia MT, Cuscó I, Lareu MV, García O, Pérez-Jurado L, Carracedo A, Salas A. New population and phylogenetic features of the internal variation within mitochondrial DNA macro-haplogroup R0. *PLoS ONE.* 2009;4(4):e5112.
13. Logan J. A refined phylogeny for mtDNA haplogroup J. *Journal of Genetic Genealogy.* 2009;5(1):16-22.
14. Pala M, Achilli A, Olivieri A, Kashani BH, Perego UA, Sanna D, Metspalu E, Tambets K, Tamm E, Accetturo M, Carossa V, Lancioni H, Panara F, Zimmermann B, Huber G, Al-Zahery N, Brisighelli F, Woodward SR, Francalacci P, Parson W, Salas A, Behar DM, Villems R, Semino O, Bandelt HJ, Torroni A. Mitochondrial haplogroup U5b3: a distant echo of the epipaleolithic in Italy and the legacy of the early Sardinians. *Am J Hum Genet.* 2009;84(6):814-21.
15. Cerny V, Mulligan CJ, Fernandes V, Silva NM, Alshamali F, Non A, Harich N, Cherni L, El Gaaied AB, Al-Meerri A, Pereira L. Internal diversification of mitochondrial haplogroup R0a reveals post-Last Glacial Maximum demographic expansions in South Arabia. *Mol Biol Evol.* 2010; In press.

**South Asian (Indian) Haplogroup**

Haplogroup	HV1	HV2	HV3 <i>etc.</i>
<i>M*-489</i>	16223		<u>489</u>
M2	16223-16274-16319		16519, 447G-489
M2a1	16223-16270-16319-16352	204	16519, 447G-489
M2b	16169.1C-16189-16223-16274-16319-16320	152-182-195	16519, 447G-489-523d-524d
M3	16126-16223		482-489
M3c1	16183C-16189-16223-16294	152	16519, 482-489-523d-524d
M3c2	16126-16154-16223		16519, 482-489-523d-524d
M4	16145-16223-16261-16311		489
M5	16129-16223		16519, <u>489</u>
M5*	16129-16223-16230-16233-16304		16519, 489
M5a1	16129-16223-16291		16519, 489
<i>M6</i>	16223-16231-16362		<u>461-489</u>
M25	16223-16304		489
M18	16223-16318T	194-246	489
M38a	16223	189-246	16519, 489
M38bc	16223	195-246	16519, 489
M38de	16223	199-246	16519, 489-523d-524d
M30	16223	195A	489-523d-524d
<i>M30a</i>	16223	195A	489- <u>513</u> -523d-524d
M30b	16223	152-195A	489-523d-524d
M30c	16223	146-195A	489-523d-524d
M30e	16223-16234	152-195A	489-523d-524d
M31a1	16223-16311	249d	16519, 489
<i>M31a1</i>	16223-16311	200	16519, <u>489</u>
M31a2	16126-16145-16223	195	489
M31b	16126-16136-16223	152	489
M31c	16136-16223-16311	188-234-282	489
M32a	16223-16319-16344-16357	195-207	16526, 489
M32c	16086-16148-16223-16259-16278-16319		16399-16526, 489-523d-524d
M33a*	16223-16316	150-293	16519, 489
<i>M33a1</i>	16223-16294	195	16519, 489- <u>573.pC</u>
M33a2	16169-16172-16223		16519, 489
M33b	16223-16324-16362		16519, 489
M33c	16111-16223-16235-16362		16519, 489
M33d	16178-16223-16288	152-204-207	16519, 489-513
M34	16223-16249		489-569
M34a	16223-16249-16359	114	489-569
M34b	16051-16223-16249-16250		489-569
M35	16223	199	489
M35a	16093-16223	199	482-489
M35b	16223-16304	199-204	489
M35c	16145-16189-16223-16290		16381, 489
M36	16223	239	489
M37a	16223	151-152	489
M37e	16111-16189-16223-16295		489
<i>M39</i>	16223		<u>55.IT-65.IT-66T</u> , 489
<i>M40</i>	16223		<u>16463</u> , 489
M40a	16179-16223-16294	200	16463, 489
M41	16223-16327-16330		375, 489
M42a	16223-16287-16356		489
M42b	16189-16223	93-234	489



Haplogroup	HV1	HV2	HV3 etc.
M44	16223-16301	146	489
M45	16189-16223	146	489
M45a	16189-16223-16300	146-152	16519, 489
M48	16223-16225-16234	199	16390, 489
M49	16223-16234		16519, 489
M49ab	16153-16223-16234		16519, 489
M49d	16223-16234-16243		16519, 489
M52a	16223-16275-16327A		16390, 489-523d-524d-573.pC
M52b	16111-16192-16223	150	489
M53	16051-16183C-16189-16223-16316	240	390T, 489-523d-524d -572
M56	16223-16311		6L, 489
M57a	16111-16223-16311	152	489
M57b	16223-16311	146-189	489
M60a	16223-16284-16319		489-523d-524d
M60b	16223-16266-16357	189	489-523d-524d
M61	16223-16270-16362	152	16381, 489
M62	16223-16295	150	489
M62a	16147-16223-16295	146-150-310	489
M62b	16223-16260-16295	150-204	16519, 489
M63	16172-16192-16223	214	489
M64	16223-16263	152	16527, 489
M65	16223-16311		16519, 489-511
M65a	16223-16289		16519, 489-511
M65b	16223-16311	241	16519, 489-511
M66	16184-16223	195	16519, 489
M67	16075-16169-16223-16311	143	489
U2	16051		
U2a	16051-16206C		
U2b	16051	146	
U2c	16051-16234	152	
R5	16304		16524
R5a	16266-16304		16524
R5a1	16266-16304	93-200	16524, 523d-524d
R5a2	16304-16356	152	16524, 523d-524d
R6	16274-16362	195	
R6*	16093-16179-16227-16245-16274-16278-16362	195-246	
R6*	16129-16213-16362		
R7	16260-16261-16319-16362		
R8a1		195-198	
R8a2		185-189	
R8b		195	16390, 456
R30a*	16126-16181-16209		16519
R30a*		207	16519
R30b	16189-16298-16299	152-299d	16159, 373, 480
R30*	16129-16311	152-215	16497-16519, 373
R31a	16172-16304-16362	146-338	523d-524d
R31b	16051-16093-16189-16218-16291-16362	207-228-234	
N5	16111-16311		

## References

1. Metspalu M, Kivisild T, Metspalu E, Parik J, Hudjashov G, Kaldma K, Serk P, Karmin M, Behar DM, Gilbert MT, Endicott P, Mastana S, Papiha SS, Skorecki K, Torroni A, Villems R. Most of the extant mtDNA boundaries in south and southwest Asia were likely shaped during the initial settlement of Eurasia by anatomically modern humans. *BMC Genet.* 2004;5(1):26.
2. Palanichamy MG, Sun C, Agrawal S, Bandelt HJ, Kong QP, Khan F, Wang CY, Chaudhuri TK, Palla V, Zhang YP. Phylogeny of mitochondrial DNA macrohaplogroup N in India, based on complete sequencing: implications for the peopling of South Asia. *Am J Hum Genet.* 2004;75(6):966-78.
3. Sun C, Kong QP, Palanichamy MG, Agrawal S, Bandelt HJ, Yao YG, Khan F, Zhu CL, Chaudhuri TK, Zhang YP. The dazzling array of basal branches in the mtDNA macrohaplogroup M from India as inferred from complete genomes. *Mol Biol Evol.* 2006;23(3):683-90.
4. Thangaraj K, Chaubey G, Singh VK, Vanniarajan A, Thanseem I, Reddy AG, Singh L. In situ origin of deep rooting lineages of mitochondrial Macrohaplogroup 'M' in India. *BMC Genomics.* 2006;7:151.
5. Thanseem I, Thangaraj K, Chaubey G, Singh VK, Bhaskar LV, Reddy BM, Reddy AG, Singh L. Genetic affinities among the lower castes and tribal groups of India: inference from Y chromosome and mitochondrial DNA. *BMC Genet.* 2006;7:42.
6. Reddy BM, Langstieh BT, Kumar V, Nagaraja T, Reddy AN, Meka A, Reddy AG, Thangaraj K, Singh L. Austro-Asiatic tribes of Northeast India provide hitherto missing genetic link between South and Southeast Asia. *PLoS ONE.* 2007;2(11):e1141.
7. Chaubey G, Karmin M, Metspalu E, Metspalu M, Selvi-Rani D, Singh VK, Parik J, Solnik A, Naidu BP, Kumar A, Adarsh N, Mallick CB, Trivedi B, Prakash S, Reddy R, Shukla P, Bhagat S, Verma S, Vasnik S, Khan I, Barwa A, Sahoo D, Sharma A, Rashid M, Chandra V, Reddy AG, Torroni A, Foley RA, Thangaraj K, Singh L, Kivisild T, Villems R. Phylogeography of mtDNA haplogroup R7 in the Indian peninsula. *BMC Evol Biol.* 2008;8:227.
8. Kumar S, Padmanabham PB, Ravuri RR, Uttaravalli K, Koneru P, Mukherjee PA, Das B, Kotal M, Xaviour D, Saheb SY, Rao VR. The earliest settlers' antiquity and evolutionary history of Indian populations: evidence from M2 mtDNA lineage. *BMC Evol Biol.* 2008;8:230.
9. Fornarino S, Pala M, Battaglia V, Maranta R, Achilli A, Modiano G, Torroni A, Semino O, Santachiara-Benerecetti SA. Mitochondrial and Y-chromosome diversity of the Tharus (Nepal): a reservoir of genetic variation. *BMC Evol Biol.* 2009;9:154.
10. Kumar S, Ravuri RR, Koneru P, Urade BP, Sarkar BN, Chandrasekar A, Rao VR. Reconstructing Indian-Australian phylogenetic link. *BMC Evol Biol.* 2009;9:173.
11. Chandrasekar A, Kumar S, Sreenath J, Sarkar BN, Urade BP, Mallick S, Bandopadhyay SS, Barua P, Barik SS, Basu D, Kiran U, Gangopadhyay P, Sahani R, Prasad BV, Gangopadhyay S, Lakshmi GR, Ravuri RR, Padmaja K, Venugopal PN, Sharma MB, Rao VR. Updating phylogeny of mitochondrial DNA macrohaplogroup M in India: dispersal of modern human in South Asian corridor. *PLoS One.* 2009;4(10):e7447.
12. Zhao M, Kong QP, Wang HW, Peng MS, Xie XD, Wang WZ, Jiayang, Duan JG, Cai MC, Zhao SN, Cidanpingcuo, Tu YQ, Wu SF, Yao YG, Bandelt HJ, Zhang YP. Mitochondrial genome evidence reveals successful Late Paleolithic settlement on the Tibetan Plateau. *Proc Natl Acad Sci U S A.* 2009;106(50):21230-5.
13. Easwarkhanth M, Haque I, Ravesh Z, Romero IG, Meganathan PR, Dubey B, Khan FA, Chaubey G, Kivisild T, Tyler-Smith C, Singh L, Thangaraj K. Traces of sub-Saharan and Middle Eastern lineages in Indian Muslim populations. *Eur J Hum Genet.* 2010;18(3):354-63.

**East Asian Haplogroup**

Haplogroup	HV1	HV2	HV3 <i>etc.</i>
D4/G	16223-16362		489
D1	16223-16325-16362		489
D4a	16129-16223-16362	152	(16519), 489
D4a3	16129-16223-16249-16362	152	16519, 489
D4a4	16129-16223-16294-16362	152	16519, 489
D4b1	16223-16319-16362		489-523d-524d
D4b2a	16223-16355-16362	280	489-523d-524d
<i>D4b2a</i>	16223-16362	199	489-523d-524d
D4b2b	(16223)-16362	194	16519, 489-523d-524d
D4c	16245-16362		489
D4e1	16223-16362	94	489
D2	16129-16223-16271-16362		489
D4e*	16223-16256-16362		489
D4g1	16223-16278-16362		489-573.pC
D4g2	16223-16362	195-298	489
D4g2a	(16223)-16274-16362	298	489
D4h1	16174-16223-16362	146-183	489
D4h*	16174-16223-16311-16362	152	489
D4h3	16223-16301-16342-16362		489
D4i	16223-16294-16362		489
D4j1a	16068-16223-16362		489
D4j2	16223-16291-16362	152	489
D4j3	16184-16223-16311-16362		489
D4j*	16223-16293-16362		489
D4k	16192-16223-@16362	195	489
<i>D4l</i>	16223-16362		16368, 489
D4m1	16244-16362		489
D4m2	16042-16223-16362		489
D4n	16223-16355A-16362		489
D4o	16223-16290-16362	195	489
D4p	16223-16362	195-198	489
D4q	16223-16256-16362	200	489
D5	16189-16223-16362	150	489
D5a1	16182C-16183C-16189-16223-16362	150-309d	16390, 68, 489
D5a2	16182Y-16183C-16189-16223-16266-16362	150	489-523d-524d
D5a3	16182C-16183C-16189-16223-16360-16362	150	489
<i>D5b</i>	16189-16223-16362	150	456-489
D5b1a	16167-16189-16223-16362	150	456-489
D5b1b	16189-16216-16223-16362	150	16519, 456-489
D5c	16188.1C-16193.1C-16362	150-(151)-152	489
D5d	16148-16189-16223-16362	150	489
D6a	16189-16223-16274-16362	146	489
D6c	16189-16223-16311-16362	152	489
G1a1	16223-16325-16362	150	16519, 489
G1a2	16184-16223-16290-16362	150	489
G1a3	16184-16214-16223-16362	@150	489
<i>G1b</i>	16129-16223-@16362		16017, 489
G2a	16189-16223-16278-16362		489
G2a1	16223-16227-16278-(16362)		489
G2a2	16051-16150-16223-16278-16362		489
G2a3	(16189)-16223-16278-16362	260	489
G2a4	16204-16223-16278-16362	146-152	489
G2b	16172-16223-16362	@263	489
G2c	16093-16223-16278-16303-16311-16362		64, 489
G3a	16223-16274-(16362)	143-(152)	489

Haplogroup	HV1	HV2	HV3 <i>etc.</i>
G3b1	16223-16274-16362	195	489
G4	16114A-16223-16362	191.1A	489
M7a	16209-16223		489
M7a1	16209-16223-16324		489-(523d-524d)
M7a2	16140-16209-16223	146	489
M7b	(16129)-16223-16297	150-199	489
M7b1	16129-16192-16223-16297	150-199	489
M7b2	16129-16189-16223-16297-16298	150-199	489
M7b4	@16129-16223-16297	150-199-204	489
M7b3	16086-@16223-16297-16324	199	489
M7d	16129-16152-16179-16192-16223	@199	489
M7c	16223	146-199	16519, 489-523d-524d
M7c1	16223-16295	(146)-199	16519, 489-523d-524d (or 513d-514d)
M7c3	@16223	146A-199	489-523d-524d
M8	16223-16298		489
M8a	16223-16298-16319		489
M8a1	16223-16298-16319-16311		489
M8a2	16184-16223-16298-16319		489
CZ	16223-16298	249d	489
C	(16223)-16298-16327	249d	16519, 489
C1	(16223)-(16298)-16325-16327	249d-290d-291d	16519, 489-523d-524d
C1a	16223-16298-16325-16327-16356	93-249d-290d-291d	16519, 489-523d-524d
C1b	(16223)-(16298)-16325-16327	249d-290d-291d	16519, 489-493-523d-524d
C1c	16223-16298-16325-16327	249d-290d-291d	16519, 489-@523d-@524d
C1d	16051-(16223)-(16298)-16325-16327	194-249d-290d-291d	16519, 489-523d-524d
C1d1c	16051-16188-16223-(16298)-16325-16327-16362	(194)-249d-290d-291d	16519, 489-523d-524d
C4a1	16129-16223-16298-16327	195-249d	16519, 489
C4a2'3'4	16223-16298-16327-16357	249d	16519, 489
C4b1/C7a	16223-16298-16327	146-249d	16519, 489
C5	16223-16288-16298-16327	249d	16519, 489
C5a	16223-16261-16288-16298-@16327	249d	16519, 489
C5b1	16148-16223-16288-16298-16327	249d	16519, 489
C7a1	16223-16298-16327	146-153-249d	16519, 489
pre-Z	16223-16260-16298	152-249d	489
Z	16185-16223-16260-16298	152-249d(or 247d)	489
Z*	16185-16223-16260-16294-16298	150-249d	489
M9a*	16223-16234-16362	153	489
M9a	16223-16234-16316-16362		489
M9d	16158-16223-16234-16362	150-152-153	16519, 489
M9c	16223-16234-16271-16362	153	489
M9b	16051-16209-16223-16362		489-573.pC
M10	16223-16311		489-573.pC
M10a	16129-16223-16311-16357		16497, 489 523d-524d-573.pC
M10b	16066-16223-16311		489-573.pC
M11	16223	215-318-326	489
M12	16223-16234-16290		489
M13a	16145-16188(or 16188d)-16223	152	489

Haplogroup	HV1	HV2	HV3 etc.
F	16304	249d	
F1ac	16129-16304	249d	16519, 523d-524d
F1a	16129-16172-16304	249d	16519, 523d-524d
F1a1	(16129)-16162-16172-(16304)	249d	(16519), 523d-524d
F1a2	@16129-16172-16304	249d	16465-16519, 523d-524d
F1a3	@16129-16172-16284-16304-16311	249d	16390-16519, 523d-524d
F1c	16111-16129-16304	152-249d	16519, 523d-524d
F1bde	(16183C)-16189-16304	249d	16519, 523d-524d
F1b	(16182C)-16183C-16189-16232A-16249-16304-16311	249d	(16519), 523d-524d
F1d	16189-16304	146-249d	16519, 523d-524d
F1e	16189-16304-16355	249d	16519, 523d-524d
F2*	@16304	235-249d	
F2a	16291-16304	249d	
F2b	16203-16304	249d	
F3	16298-@16304-16362	249d	
F3a	16298-@16304-16355-16362	249d	
F3b	16220C-16298-@16304-16362	249d	
F4a	16207-16304-16362	146-249d	16399
F4b	16218-16304-16311	249d	573.pC
B4	16183C-16189-16217		
B4a	16182C-16183C-16189-16217-16261		(16519), 523d-524d
B4a1a	16182C-16183C-16189-16217-16261	146	(16519), 523d-524d
B4a1b	16182C-16183C-16189-16217-16261-16288-16311		(16519), 523d-524d
B4g	16182C-16183C-16189-16217-16261-16292		16519, 523d-524d
B4b	16183C-16189-16217		16519, 499
B4b1	16136-16183C-16189-16217		16519, 499
B2a	16111-16183C-16189-16217		16483-16519, 499
B2c	16182C-16183C-16189-16217		16519, 499
B2f	16183C-16189-16217-(16298)	114G	16519, 499
B4d1	16183C-16189-16217	316	
B4d3	16183C-16185-16189d-16217-16234	(151)	16519, 546
B4c1a	16183C-16189-16217-16311		
B4c1b	16140-16183C-16189-16217-16274	150	
B4c1c	16183C-16189-16217-16311	150-195-214	
B4c2	16147-16184A-16189-16217-16235		
B4f	16168-16172-16183C-16189-16217-16249-16325	200	16390
B5	16140-16189		16519, 523d-524d
B5a	16140-16189-16266R	210	16519, 523d-524d
B5a2	16129-16140-16187-16189-16266R	93-210	16519, 523d-524d
B5b	16140-16183C-16189-16243		16519, 523d-524d (or 513d-514d)
B5b2	16111-16140-16183C-16189-16234-16243		(16463)-16519, 523d-524d
B5b3	16140-16183C-16189-16243-16256	103-189-199-203-204	16519, 523d-524d
R11	16183C-16189-16311	185-189	16519
A	16223-16290-16319	235	
A4	16223-16290-16319-16362	235	523d-524d
A2	16111-16223-16290-16319-(16362)	146-(235)	64, 523d-524d
A4a	16223-16249-16290-16319-16362	(235)	523d-524d
A4b	16189-16223-16290-16319-16362	235	523d-524d
A4c	16223-16290-16319-16362	200-235	523d-524d

Haplogroup	HV1	HV2	HV3 <i>etc.</i>
A4d	16223-16290-16319-16362	151-235	523d-524d
A5a	16187-16223-16290-16319	235	523d-524d
A5b	16126-(16223)-16235-16290-16319	235	
A5c	16129-16213-16223-16290-16319	152-235	@523d-@524d
A7	16051-16223-16290-16319	152-235	523d-524d
A8	16223-16242-16290-16319	146-152-(235)	64, 523d-524d
A11	16223-16290-16293C-16319	152-235	523d-524d
N9a	16223-16257A-16261	150	
N9a1	16111-16129-16223-16257A-16261	150	
N9a3	16129-16223-16257A-16261	150	
N9a2	16172-16223-16257A-16261	150	
<i>N9a2ab</i>	16172-16223-16257A-16261	150	<u>16497</u>
N9a4	16145-16172-16223-16245-16257A-(16261)	150	524.1A-524.2C
N9a5	16172-16189-16209-16223-16257A-16261	150	
N9a6	16223-16257A-16261-16292	150	
N9b	16183C-16189-16223		16519
<i>N9b1b</i>	16129-16183C-16189-16223		<u>16390-16519</u>
N9b1c	16183C-16189-16223	94	16519
N9b2	16183C-16189-16223-16294-16309		16519
Y	16126-16231		
Y1	16126-16231-16266	146	16519
Y2	16126-16231-16311		482

## References

1. Kivisild T, Tolk HV, Parik J, Wang Y, Papiha SS, Bandelt HJ, Villems R. The emerging limbs and twigs of the East Asian mtDNA tree. *Mol Biol Evol.* 2002;19(10):1737-51.
2. Kong QP, Yao YG, Sun C, Bandelt HJ, Zhu CL, Zhang YP. Phylogeny of east Asian mitochondrial DNA lineages inferred from complete sequences. *Am J Hum Genet.* 2003;73(3):671-6.
3. Kong QP, Yao YG, Liu M, Shen SP, Chen C, Zhu CL, Palanichamy MG, Zhang YP. Mitochondrial DNA sequence polymorphisms of five ethnic populations from northern China. *Hum Genet.* 2003;113(5):391-405.
4. Maruyama S, Minaguchi K, Saitou N. Sequence polymorphisms of the mitochondrial DNA control region and phylogenetic analysis of mtDNA lineages in the Japanese population. *Int J Legal Med.* 2003;117(4):218-25.
5. Yao YG, Kong QP, Wang CY, Zhu CL, Zhang YP. Different matrilineal contributions to genetic structure of ethnic groups in the silk road region in china. *Mol Biol Evol.* 2004;21(12):2265-80.
6. Tanaka M, Cabrera VM, Gonzalez AM, Larruga JM, Takeyasu T, Fuku N, Guo LJ, Hirose R, Fujita Y, Kurata M, Shinoda K, Umetsu K, Yamada Y, Oshida Y, Sato Y, Hattori N, Mizuno Y, Arai Y, Hirose N, Ohta S, Ogawa O, Tanaka Y, Kawamori R, Shamoto-Nagai M, Maruyama W, Shimokata H, Suzuki R, Shimodaira H. Mitochondrial genome variation in eastern Asia and the peopling of Japan. *Genome Res.* 2004;14(10A):1832-50.
7. Wen B, Li H, Gao S, Mao X, Gao Y, Li F, Zhang F, He Y, Dong Y, Zhang Y, Huang W, Jin J, Xiao C, Lu D, Chakraborty R, Su B, Deka R, Jin L. Genetic structure of Hmong-Mien speaking populations in East Asia as revealed by mtDNA lineages. *Mol Biol Evol.* 2005;22(3):725-34.
8. Kong QP, Bandelt HJ, Sun C, Yao YG, Salas A, Achilli A, Wang CY, Zhong L, Zhu CL, Wu SF, Torroni A, Zhang YP. Updating the East Asian mtDNA phylogeny: a prerequisite for the identification of pathogenic mutations. *Hum Mol Genet.* 2006;15(13):2076-86.
9. Lee HY, Yoo JE, Park MJ, Chung U, Kim CY, Shin KJ. East Asian mtDNA haplogroup determination in Koreans: haplogroup-level coding region SNP analysis and subhaplogroup-level control region sequence analysis. *Electrophoresis.* 2006;27(22):4408-18.
10. Tamm E, Kivisild T, Reidla M, Metspalu M, Smith DG, Mulligan CJ, Bravi CM, Rickards O, Martinez-Labarga C, Khusnutdinova EK, Fedorova SA, Golubenko MV, Stepanov VA, Gubina MA, Zhadanov SI, Ossipova LP, Damba L, Voevoda MI, Dipierri JE, Villems R, Malhi RS. Beringian standstill and spread of Native American founders. *PLoS ONE.* 2007;2(9):e829.
11. Derenko M, Malyarchuk B, Grzybowski T, Denisova G, Dambueva I, Perkova M, Dorzhu C, Luzina F, Lee HK, Vanecsek T, Villems R, Zakharov I. Phylogeographic analysis of mitochondrial DNA in northern asian populations. *Am J Hum Genet.* 2007;81(5):1025-41.
12. Achilli A, Perego UA, Bravi CM, Coble MD, Kong QP, Woodward SR, Salas A, Torroni A, Bandelt HJ. The phylogeny of the four pan-American MtDNA haplogroups: implications for evolutionary and disease studies. *PLoS ONE.* 2008;3(3):e1764.
13. Volodko NV, Starikovskaya EB, Mazunin IO, Eltsov NP, Naidenko PV, Wallace DC, Sukernik RI. Mitochondrial genome diversity in arctic Siberians, with particular reference to the evolutionary history of Beringia and Pleistocenic peopling of the Americas. *Am J Hum Genet.* 2008;82(5):1084-100.
14. Qin Z, Yang Y, Kang L, Yan S, Cho K, Cai X, Lu Y, Zheng H, Zhu D, Fei D, Li S, Jin L, Li H; and The Genographic Consortium. A mitochondrial revelation of early human migrations to the Tibetan Plateau before and after the last glacial maximum. *Am J Phys Anthropol.* 2010; In press.

**Southeast Asian Haplogroup**

Haplogroup	HV1	HV2	HV3 <i>etc.</i>
M7e	16172-16223-16311	146	489-523d-524d
<i>Elala</i>	16223-16291-16362		16390-16519, 489
<i>Ela2</i>	16223-16362		16390-16519, 373, 489
<i>E1b</i>	16223-16362	152	16390-16519, 489
<i>E1bl</i>	16223-16261-16362	152	16390-16519, 489
<i>E2</i>	16051-16223-16362	195	16390, 489
<i>E2*</i>	16051-16185-16223-16362	195	16390, 489
M13b1	(16093)-16129-16223-16263	207	16381-16519, 489
M13b2	16129-16172-16195-16270		489
M17a	16129-16209-16223-16325		489
M17b	16189-16209-16223		489
M17c	16209-16223-16304		489
M20	16129-16209-16223-16272	152-225-249d-316	16159, 489-523d-524d
M21a	(16093)-16129-16223-16256-16271-(16362)		489
M21b	16223-16239-16263-16325		16519, 489
M21c	16223-16242	200-204	16519, 489
M21d	16145-(16181)-16192-16223-16291-16304	210	489
M22	16223-16290-16304		489
M22*	16124-16179A-16223-16261		489-523d-524d
M46*	16223-16278	152	489
M46*	16223-16243-16262-16278-16311-16319	152	489-499- 524.1A-524.2C
M46*	16214A-16223-16278	152	489-523d-524d
M46*	16140-16172-16189-16223-16278	249	489-523d-524d
M47	16129-16166C-16189-16223-16287-16319		489
M50	16223-16263-16278		489
M50*	16166C-16223-16263-16309		489
M50*	16209-16223-16224-16263-16278-16319	146	489-523d-524d
M51	16223-16278	150	489
M51a1	16223-16278-16294	150	489
M51*	16189-16223-16278	150	489-523d-524d
M71	16223-16271	151	(16519), 489
M71a1	16223-16269-16271	150-151	16519, 489
M71a*	16129-16140-16223-16271	143-146	16519, 489
M71b	16223-16260-16264-16271	151	16159, 489-524.1A-524.2C
M72	16166d-16172-16214-16223		489
M73a	16184A-16223-16278		489
M73b	16223-16278-16354	199	489
M74	16223-16311-16362		16381, 489
M74a	16223-16311-16362		16381, 63-64-66-489
M75	16068-16183C-16189-16223	146-150	489
M76	16124-16189-16278-16293C-16362		489
M76*	16183C-16189-@16278-16293Y-16325-16362	146	489-513
M77	16129-16183C-16189-16213-16218-16223		489
M-4491	16217-16223-16319	94-173-204	16381, 482-489
F1a4	16129-16172-16294-16304-16362	152-249d	16519, 523d-524d
R9b1	16304-16309		16390-(16519)
R9b1a	16304-16309	183	16390-16519, 523d-524d
R9b1a1	16288-16304-16309	143-183	16390-16519, 523d-524d
R9b1b	16124-16148-16304-16309		16390-16519
R9b2	16304-16362		
R9c	16256-16304-16335		



Haplogroup	HV1	HV2	HV3 <i>etc.</i>
R9e	16157-16304	151	479
B6	16093-16179-16189	150	
B6	16051-16093-16183C-16189-16220		16519, 356.1C
B6*	16051-16183C-16189		16519, 356.1C
B*	16129-16183C-16189-16352-16355	150-152-185-189	573.pC
R21	16168-16295-16304	146-152-199-249	
R22	16249-16288-16304	329	
R23	16256-16290		16465
R24	16051-16185-16189-16324	146	
N10a	16172-16183C-16189-16223-16362	185-189	(523d-524d)
N10b	16069-16172-(16223)-16278-16291A-16298-16362	150-199	
N11	16355	195	16519
N11a	16189-16355	195	16519, 523d-524d
N21	16193-(16223)	150-195-337d	16519
N22	16168-(16223)-16249		
N*	16223-16263-16274-16311-16343		

#### References

1. Macaulay V, Hill C, Achilli A, Rengo C, Clarke D, Meehan W, Blackburn J, Semino O, Scozzari R, Cruciani F, Taha A, Shaari NK, Raja JM, Ismail P, Zainuddin Z, Goodwin W, Bulbeck D, Bandelt HJ, Oppenheimer S, Torroni A, Richards M. Single, rapid coastal settlement of Asia revealed by analysis of complete mitochondrial genomes. *Science*. 2005;308(5724):1034-6.
2. Hill C, Soares P, Mormina M, Macaulay V, Meehan W, Blackburn J, Clarke D, Raja JM, Ismail P, Bulbeck D, Oppenheimer S, Richards M. Phylogeography and ethnogenesis of aboriginal Southeast Asians. *Mol Biol Evol*. 2006;23(12):2480-91.
3. Hill C, Soares P, Mormina M, Macaulay V, Clarke D, Blumbach PB, Vizuete-Forster M, Forster P, Bulbeck D, Oppenheimer S, Richards M. A mitochondrial stratigraphy for island Southeast Asia. *Am J Hum Genet*. 2007;80(1):29-43.
4. Soares P, Trejaut JA, Loo JH, Hill C, Mormina M, Lee CL, Chen YM, Hudjashov G, Forster P, Macaulay V, Bulbeck D, Oppenheimer S, Lin M, Richards MB. Climate change and postglacial human dispersals in Southeast Asia. *Mol Biol Evol*. 2008;25(6):1209-18.
5. Dancause KN, Chan CW, Arunotai NH, Lum JK. Origins of the Moken Sea Gypsies inferred from mitochondrial hypervariable region and whole genome sequences. *J Hum Genet*. 2009;54(2):86-93.
6. Zimmermann B, Bodner M, Amory S, Fendt L, Röck A, Horst D, Horst B, Sanguansermsri T, Parson W, Brandstätter A. Forensic and phylogeographic characterization of mtDNA lineages from northern Thailand (Chiang Mai). *Int J Legal Med*. 2009;123(6):495-501.
7. Tabbada KA, Trejaut J, Loo JH, Chen YM, Lin M, Mirazón-Lahr M, Kivisild T, De Ungria MC. Philippine mitochondrial DNA diversity: a populated viaduct between Taiwan and Indonesia? *Mol Biol Evol*. 2010;27(1):21-31.
8. Peng MS, Quang HH, Dang KP, Trieu AV, Wang HW, Yao YG, Kong QP, Zhang YP. Tracing the Austronesian footprint in mainland Southeast Asia: A perspective from mitochondrial DNA. *Mol Biol Evol*. 2010; 27(10):2417-30.
9. Kong QP, Sun C, Wang HW, Zhao M, Wang WZ, Zhong L, Hao XD, Pan H, Wang SY, Cheng YT, Zhu CL, Wu SF, Liu LN, Jin JQ, Yao YG, Zhang YP. Large-scale mtDNA screening reveals a surprising matrilineal complexity in East Asia and its implications to the peopling of the region. *Mol Biol Evol*. 2010; In press.

**Oceanian Haplogroup**

Haplogroup	HV1	HV2	HV3 <i>etc.</i>
M27a	16048-16077T-16172-16223-16311-16320	195-234	489-537
M27b	16209-(16223)-16299	152	16390, 489
M27c	16223-16301-16304	146-186	489
M28	16148-16223-16362	152-195	16468, 489
M28a	16086-16129-16148-16223-16362	152-195	16468, 489
M28b	16148-16223-16362	94-152-195-204	16468, 489
M29	16189-16223-16311	151-152-211	464-489-513
M29a	16189-16223-16311	151-152-211-310	464-489-513
M29b	16189-16223-16294-16311	151-152-211	464-489-513
Q	16129-16223-16241-16311		489
Q1	16129-16144-16148-(16223)-16241-16265C-16311-16343	89-(92)-146	489
Q2	16066-16129-16223-16241-@16311	195-228T	489
Q3	16129-16223-16241-16311	143	489
P1	16176-16266-16357	212	
P2	16188-16278-16357	103-143	16497
P3		127-128	573.pC
P4a	16319	152	507-517
P4b	16274-16291		
P6	16311-16362		
S1	16075		
S3	16140-16187-16189-16287-16311	151-152-195	63-64-66
O	16213		
O1	16213-16303-16362	152	509

**References**

1. Friedlaender J, Schurr T, Gentz F, Koki G, Friedlaender F, Horvat G, Babb P, Cerchio S, Kaestle F, Schanfield M, Deka R, Yanagihara R, Merriwether DA. Expanding Southwest Pacific mitochondrial haplogroups P and Q. *Mol Biol Evol.* 2005;22(6):1506-17.
2. Merriwether DA, Hodgson JA, Friedlaender FR, Allaby R, Cerchio S, Koki G, Friedlaender JS. Ancient mitochondrial M haplogroups identified in the Southwest Pacific. *Proc Natl Acad Sci U S A.* 2005;102(37):13034-9.
3. Pierson MJ, Martinez-Arias R, Holland BR, Gemmell NJ, Hurles ME, Penny D. Deciphering past human population movements in Oceania: provably optimal trees of 127 mtDNA genomes. *Mol Biol Evol.* 2006;23(10):1966-75.
4. Friedlaender JS, Friedlaender FR, Hodgson JA, Stoltz M, Koki G, Horvat G, Zhadanov S, Schurr TG, Merriwether DA. Melanesian mtDNA complexity. *PLoS ONE.* 2007;2(2):e248.
5. Hudjashov G, Kivisild T, Underhill PA, Endicott P, Sanchez JJ, Lin AA, Shen P, Oefner P, Renfrew C, Villems R, Forster P. Revealing the prehistoric settlement of Australia by Y chromosome and mtDNA analysis. *Proc Natl Acad Sci U S A.* 2007;104(21):8726-30.

\*Update list: See “Recent updates” on <http://mtmanager.yonsei.ac.kr>

October 2 – 3, 2011  
September 27 - 30, 2010  
June 25 - 26, 2010  
June 19 - 22, 2010  
March 22 - 23, 2010  
March 1, 2010  
January 6 - 9, 2010  
November 26 - 28, 2009  
November 16 - 17, 2009  
October 27 - 28, 2009  
October 7 - 12, 2009  
September 5 - 7, 2009  
July 10 - 13, 2009  
June 21 - 22, 2009  
June 12 - 14, 2009  
May 19, 2009  
April 6-7, 2009  
February 1 - 9, 2009  
July 20, 2008  
May 3, 2008  
April 23 - 26, 2008  
October 30, 2007  
October 18, 2007  
September 9, 2007