
mtDNAManager:

A Forensic Mitochondrial DNA Database Aimed at Supporting Data Quality Control and Generating Reliable Frequency Estimates

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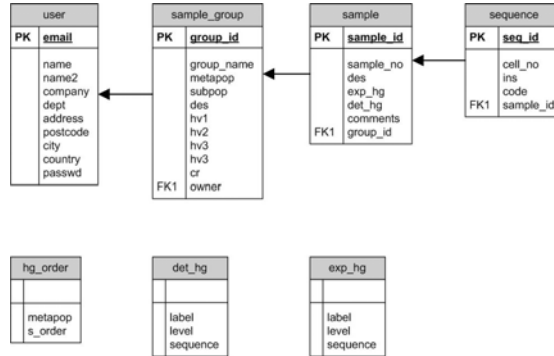
mtDNAManager (<http://mtmanager.yonsei.ac.kr>)

- The goal of mtDNAManager is to provide a web-based forensic mitochondrial DNA bioinformatics resource for supporting **data quality control** and generating **reliable frequency estimates** using a new approach based on haplogroup estimation and data comparison with the contents of a given database.
- mtDNAManager consists of previously reported **high quality mtDNA sequences**, and a set of **bioinformatics tools**, able to automatically characterize newly submitted data by **estimating its haplogroup according to the haplogroup-specific control region mutation motif**.



mtDNAManager structure

- The database is of relational type, designed and implemented using the multithreaded, multi-user **SQL database management system (DBMS), MySQL**.
- Web interfaces have all been implemented using Asynchronous JavaScript and XML (AJAX) technique based on **Javascript and PHP**.
- The system is optimized with **internet explorer v. 6.0 or more**.



mtDNAManager - forensic mtDNA database - Windows Internet Explorer

http://mtmanager.yonsei.ac.kr

mtDNAManager

E-mail: Login

Password: Register

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mtDNAManager: A forensic mitochondrial DNA database aimed at supporting data quality control and generating reliable frequency estimates

mtDNAManager provides a convenient web interface for analysis, query and storage of human mtDNA control region sequences. mtDNAManager is made available free of charge, but registration is required to store and manage data with batch mode.

- [Access demo](#)

The aims of mtDNAManager is (1) to allow researchers to automatically estimate mtDNA haplogroups of their own mtDNA sequences, (2) to generate reliable frequency estimates from high quality mtDNA databases, and (3) to collect and integrate high quality mtDNA control region sequence data publicly available.

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mtDNAManager Database

- The mtDNAManager's first release contains **4839 mtDNA control region sequences from FBI** and **593 Korean mtDNA control region sequences**. We will continue the effort to collect and integrate high quality mtDNA control region sequence data as much as possible.
- The mtDNAManager database will be extended as follows in the near future:

Metapopulation	Subpopulation	No. of sequences	References
African	African	1148	Forensic Sci Commun (2002) 4 <i>Online</i>
	Kenya	100	Int J Legal Med (2004) 118: 294-306
West Eurasian	Caucasian	1655	Forensic Sci Commun (2002) 4 <i>Online</i>
	Austrian	273	Forensic Sci Int (2007) 166: 164-175
	Finnish	200	Forensic Sci Int (2007) <i>In Press</i>
	German	313	Forensic Sci Int (2007) <i>In Press</i>
	Hungarian	416	Int J Legal Med (2007) <i>In Press</i>
	Rumanian	360	Ann Hum Genet (2007) <i>In Press</i>
East Asian	East Asian	753	Forensic Sci Commun (2002) 4 <i>Online</i>
	Japanese	211	Int J Legal Med (2003) 117:218-225
	Korean	593	Int J Legal Med (2006) 120:5-14
Oceanian	-	-	-
Admixed	Hispanic	686	Forensic Sci Commun (2002) 4 <i>Online</i>
Total		6708	

Database search

- By default but with an exchangeable setting, a **query system** retrieves sequences which **include the queried nucleotide polymorphisms** therein from a user-selected database.

The screenshot displays the mtDNAManager search interface. Key elements include:

- Target database:** A dropdown menu set to 'FBI-Caucasian' (Forensic Sci Comm (2002) 4).
- Searching Option:** A text input field containing the sequence '16223 16290 16319 235'.
- Region:** Checkboxes for 'HV1', 'HV2', 'HV3', and 'Control Region', with 'HV1' and 'HV2' selected.
- Option:** A radio button for 'Include the queried nucleotide polymorphism' is selected, indicated by an arrow and the label 'Include option'.
- Searching Result:** A table with columns for 'Sample ID', 'Expected HG', 'Estimated HG', and 'Match Probability'. The table shows a match for sample 'np 16024-16569' with a match probability of 0.0042.
- Callout Box:** A red-bordered box at the bottom right states: 'Estimated mtDNA haplogroup affiliations using the bioinformatics resources of the mtDNAManager'.

Database search and statistics

- A query system of the mtDNAmanager also searches sequences which show a **match with the queried sequence data** from the database.

The screenshot shows the mtDNAmanager search interface. On the left, there is a 'Query' tab and a 'Home' tab. Below them, there are sections for 'Target Group' (Meta-population: West Eurasian, Name: FBI-Caucasian, Description: Forensic Sci Comm (2002)), 'Subpopulation' (Caucasian), and 'Description' (Forensic Sci Comm (2002) 4 (online)). There are checkboxes for 'HVI1', 'HVI2', 'HVI3', and 'Control Region'. A green arrow points to the 'FBI-Caucasian' target group with the label 'Target database'. In the center, the 'Searching Option' section shows the 'Sequence' as '16224 16311 73 146 152 263 315.1C'. There are checkboxes for 'HVI1', 'HVI2', 'HVI3', and 'Control Region'. A 'Match' radio button is selected. There are also checkboxes for 'Ignore heteroplasmic insertions in the poly C-stretches' and 'include the queried nucleotide polymorphism'. A green box labeled 'Match options' highlights these checkboxes. Below the search options are buttons for 'Search', 'Reset', and 'Frequency Estimates'. The 'Searching Result' section shows a table with columns: 'No. of Matched Samples', 'No. of Target Samples', and 'Match Probability'. The values are 8, 1655, and 0.0060 respectively. Below this is a table of search results with columns: 'Sample ID', 'Expected HG', 'Estimated HG', '16224-16589', 'np 001-437', and 'np 438-578'. A green arrow points to the 'Match Probability' column with the label 'Frequency estimates = (x+2)/(n+2)'. There are 'Export' and 'Print' buttons.

My mtDNA

- Upon registration, the mtDNAmanager provides web interfaces where **users can submit and store their own data with batch mode** and search sequences which show a match or include the queried nucleotide polymorphisms from their own database as well as the mtDNAmanager database.

The screenshot shows the mtDNAmanager sample manager interface. At the top, there is a 'Welcome, Colleague' message and 'Logout' and 'Change Profile' buttons. Below this is a table with columns: 'Sample ID', 'Description', 'Sequence ID', 'Expected HG', 'Estimated HG', '16224-16589', 'np 001-437', and 'np 438-578'. A green arrow points to the 'Batch mode' button with the label 'Import sequences with batch mode'. Below the table, there is a 'Batch input files' section with a table showing columns A, B, C, D, E. The table contains 4 rows of sample data. A green arrow points to the 'Export as an excel file' button with the label 'Export as an excel file'. There are also 'Add', 'Edit', 'Delete', 'Import', and 'Print' buttons at the top of the table.

Cross-match between data groups

- Upon registration, a match system permits **cross match of all sequence data between two selected groups** as well as retrieval of matched sequences for one of the data of a user-created data group from their own database or from the mtDNAManager database.

The screenshot displays the mtDNAManager web interface. On the left, the 'Working Group' is set to 'Demo-1' and the 'Target Group' is 'Demo-2'. The 'Cross-Match Information' section shows search parameters: Region 'HV1 HV2', Option 'ignore heteroplasmic insertions in the poly-C stretches', and Target Group 'Demo-1'. The 'Matched Sample List' table shows the following data:

Sample ID	Expected HG	Estimated HG	Sequence	Comments	Description
B001	B41c	B41c	H913C 16168 16211 16311 73 146 150 156 214 263 315 1C	30	B41c
B002	D40	D40	H223 16362 73 263 315 1C 466 466 1C	30	D4a
B003	G24J	G24J	H910 16223 16278 16282 16362 73 263 309 1C 309 2C 315 1C 466 524 1A	30	G24J
B004	D4b	D4b	H223 16362 73 162 263 309 1C 309 2C 315 1C 466 524 1A 524b	30	D4
B000	D41	D41	H164 16323 16311 16362 73 162 263 315 1C 466	30	D41

mtDNA haplogroup estimation

Sample ID	Expected HG	Estimated HG	np 10024-10569	np 001-437	np 438-570	Comments	Description
I1D5	T1	T1	10120 10162 10190 10109 16294 16519	73 195 263 309 1C 315 1C			T1
I1D6	T2	T2	16126 16204 16286 16519	73 160 200 263 315 1C			T2
I1E1	H11a	H11a	16293 16311	143 195 263 309 1C 315 1C			H*
I1E2	H	H	16291 16519	263 315 1C			H*
I1E3	H	H	16093 16271 16519	263 309 1C 315 1C			H*
I1E4	H11b	H11b	16189 16256 16362 16519	263 309 1C 315 1C	523d 524d		H11b
I1E5	X2	X2	16134 16163c 16189 16223 16278 16519	73 195 263 309 1C 309 2C 315 1C			X2d
I1E6	J1c	J1c	16069 16126 16201 16265 16319	73 185 226 263 295 309 1C 315 1C	462 480 524 1A 524 2C		J1c
I1F1	H	H	16234 16293 16519	263 315 1C 315 2C			H*
I1F2	W	W	16223 16282 16285 16519	73 119 188 195 204 207 263 315 1C			W
I1F3	K1a	K1a	16222 16224 16211 16262 16519	73 114 263 309 1C 315 1C	497		K1a
I1F4	T1a	T1a	16126 16163 16186 16109 16294 16519	73 152 195 263 309 1C 315 1C			T1a
I1F5	H5	H5	16260 16304	263 300 1C 315 1C	455		H5
I1F8	U5a	U5a	16102 16256 16270 16309	73 143 263 315 1C			U5a1
I1O1	HV0	HV0	16153 16298	72 93 195 263 315 1C			HV0
I1O2	H	H	16211	263 309 1C 315 1C	523d 524d		H*
I1O3	H	H	16225 16519	263 309 1C 315 1C			H*
I1O4	H5	H5	16304	263 309 1C 309 2C 315 1C	455		H5
I1O5	T1	T1	16126 16163 16186 16189 16294 16519	73 195 263 315 1C			T1
I1O6	C	C	16093 16223 16234 16288 16298 16327 16518	73 249d 263 309 1C 315 1C	489		C

Using the bioinformatics tools of mtDNAManager, **more than 98% of mtDNAs** of high quality datasets can be allocated to the same mtDNA haplogroups as those confirmed with the coding region SNP information.

mtDNAManager - forensic mtDNA database - Windows Internet Explorer

http://mtmanager.yonsei.ac.kr/info.php

mtDNAManager - forensic

http://mtmanager.yonsei.ac.kr/help/MutationMotif.pdf

http://mtmanager.yonsei.ac.kr/help/Mutatio...

Control Region Mutation motif for more than 350 mtDNA haplogroups

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mtDNA Haplogroup Specific Control Region Mutation Motifs

African Haplogroup

Haplogroup	HV1	HV2	HV3 etc.
L0a	16120-16148-16172-16187-16188G-16189-16223-16230-16311-16320	93-185-189-236-247	523d-524d
L0a1	16120-16148-16168-16172-16187-16188G-16189-16233-16290-16311-16320	93-185-189-(236)-247	523d-524d
L0a1a	16120-16148-16168-16172-16187-16188G-16189-16233-16290-16278-16311-16320	93-95C-185-189-236-247	523d-524d
L0a2	16120-16148-16172-16187-16188G-16189-16223-16230-16311-16320	93-152-189-236-247	523d-524d
L0d	(16120)-(16187)-16189-16223-16230-16243-16311	189-247	
L0f	16169-16187-16189-16223-(16230)-16278-16311-16327	189-247	16368
L0k	16172-16187-16189-16209-16214-16223-16230-16278-16291G-16311	146-189-195-198-207-247	
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
L1c	(16120)-(16189)-(16223)-16278-16311	132-182-186A-189C-247(or 247d)-316	523d-524d
L1c1	16120-16189-(16223)-16278-16293-16360	(151)-152-182-186A-189C-247(or 247d)-316	523d-524d
L1c2	16120-16187-16189-(16223)-16265C-16278-16286G-16294-16311-16360	151-152-182-186A-189C-198-247-316	523d-524d

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mtDNA data quality control

Sample List

Add Edit Delete Import Export Print

N9a1: 16129-16223-16257A-16261-150

Sample ID	Expected HG	Estimated HG	np 16024-16589	np 16092-16519	np 438-576	Comments
Demo-01	D4b1	D4b1	16223 162319 16362	73 152 263 309.1C 315.1C	489 523d 524d	
Demo-02	N9a1	N9a1	16129 16223 16257A 16261	73 152 263 309.1C 315.1C	489 523d 524d	
Demo-03	A5b	A5b	16126 16223 16235 16290 16319 16519	73 235 263 315.1C	489 523d 524d	
Demo-04	D4a3	D4a3	16129 16223 16249 16266 16304 16362 16519	73 152 263 309.1C 315.1C	489	
Demo-05	F1b	F1b	16129R 16182C 16183C 16189 16232A 16249 ...	73 152 249d 263 315.1C	523d 524d	16129R
Demo-06	A4	A4	16223 16290 16319 16362	73 146 152 200 235 263 309.1C 315.1C	523d 524d	
Demo-07	B5b	B5b	16140 16183C 16362	73 103 263 315.1C	523d 524d	
Demo-08	D4/G	D4/G	16223 16260 16292	73 146 263 309.1C 315.1C	489	
Demo-09	A5a	A5a	16187 16223 16290 16519	73 146 195 235 263 309.1C 309.2C 31...	523d 524d	
Demo-10	D4j1	D4j1	16184 16223 16311 16362	73 263 309.1C 315.1C	489	
Demo-11	M9a	M9a	16223 16234 16316 16362	73 263 315.1C	489	
Demo-12	B4c1a	B4c1a	16086 16183C 16362	73 263 309.1C 315.1C	523d 524d	
Demo-13	M7b2	M7b2	16129 16185	73 150 152 199 263 309.1C 315.1C	489 573.1C	
Demo-14	M7a	M7a	16223 16362	73 263 315.1C	489	16362T
Demo-15	M7a	M7a	16209 16223	73 263 309.1C 315.1C	489 523d 524d	
Demo-16	F1a1	F1a1	16129 16182 16172 16304 16519	64 73 249d 263 309.1C 315.1C	523d 524d	
Demo-17	F2*	F2*		73 195 200 235 249d 263 309.1C 315.1C...	459d	
Demo-18	G3a	G3a	16223 1627	73 143 152 204 263 315.1C	489	
Demo-19	A	A	16179 16223	73 235 263 309.1C 315.1C	523d 524d	
Demo-20			16086 16223	73 103 204 263 315.1C	489	

150?

16319 missed out?

A5a: 16187-16223-16290-16319-235-523d-524d

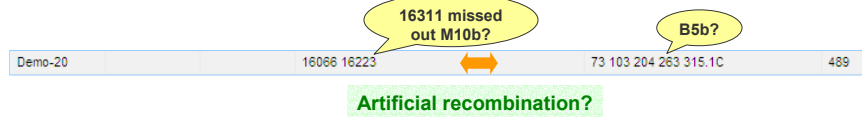
16362C?

16311 missed out M10b?

B5b?

Artificial recombination?

Detection of errors in mtDNA sequence



Sample ID	Expected HG	Estimated HG	Match Probability
K028	B5b	B5b	0.0289
K072	B5b	B5b	0.0289
K175	B5b	B5b	0.0289
K289	B5b	B5b	0.0289
K345	B5b	B5b	0.0289
K448	B5b	B5b	0.0289
K453	B5b	B5b	0.0289
K466	B5b	B5b	0.0289
K514	B5b	B5b	0.0289
K533	B5b	B5b	0.0289
K542	B5b	B5b	0.0289

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http://mtmanager.yonsei.ac.kr/info...

http://mtmanager.yonsei.ac.kr

mtDNAmanager

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- [Access demo](#) **Please click here to see the demo of personal data !**

The aims of mtDNAmanager is (1) to allow researchers to automatically estimate mtDNA haplogroups of their own mtDNA sequences, (2) to generate reliable frequency estimates from high quality mtDNA databases, and (3) to collect and integrate high quality mtDNA control region sequence data publicly available.

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miDNAManager - forensic mtDNA database - Windows Internet Explorer

http://mtmanager.yonsei.ac.kr/sample_manager.php

Welcome, Colleague

A sample system

Group List	Sample List																																																																																																																																				
<table border="1"> <thead> <tr> <th>Name</th> <th>Description</th> </tr> </thead> <tbody> <tr> <td>Demo-1</td> <td>Demo Sequences</td> </tr> <tr> <td>Demo-2</td> <td>Demo Sequences</td> </tr> </tbody> </table>	Name	Description	Demo-1	Demo Sequences	Demo-2	Demo Sequences	<table border="1"> <thead> <tr> <th>Sample ID</th> <th>Expected HG</th> <th>Estimated HG</th> <th>np 16024-16569</th> <th>np 001-437</th> <th>np 438-576</th> </tr> </thead> <tbody> <tr> <td>K001</td> <td>D5a2</td> <td>D5a2</td> <td>16164 16172 16182T 16183C 16189 16223 162...</td> <td>73 150 263 309.1C 309.2C 315.1C</td> <td>489 523d 524d</td> </tr> <tr> <td>K002</td> <td>N9a1</td> <td>N9a1</td> <td>16111 16129 16223 16257A 16261 16298</td> <td>73 150 263 315.1C</td> <td></td> </tr> <tr> <td>K003</td> <td>D4/G</td> <td>D4/G</td> <td>16223 16224 16362 16519</td> <td>73 263 309.1C 315.1C</td> <td>489</td> </tr> <tr> <td>K004</td> <td>M7b2</td> <td>M7b2</td> <td>16129 16189 16223 16257 16297 16298</td> <td>73 150 199 263 315.1C</td> <td>489</td> </tr> <tr> <td>K005</td> <td>D5b</td> <td>D5b</td> <td>16189 16223 16362 16519</td> <td>73 146 150 252 263 309.1C 309.2C 31...</td> <td>489 489</td> </tr> <tr> <td>K006</td> <td>D4a</td> <td>D4a</td> <td>16086 16129 16223 16362 16519</td> <td>73 152 263 315.1C</td> <td>489</td> </tr> <tr> <td>K007</td> <td>M7b2</td> <td>M7b2</td> <td>16129 16189 16223 16242 16297 16298</td> <td>73 150 199 263 309.1C 315.1C</td> <td>489</td> </tr> <tr> <td>K008</td> <td>B5b</td> <td>B5b</td> <td>16140 16183C 16189 16243 16355 16519</td> <td>73 103 263 309.1C 309.2C 315.1C</td> <td>523d 524d</td> </tr> <tr> <td>K009</td> <td>M10b</td> <td>M10b</td> <td>16068 16223 16311</td> <td>73 263 315.1C</td> <td>489 573.1C 573.2C</td> </tr> <tr> <td>K010</td> <td>A4</td> <td>A4</td> <td>16223 16290 16319 16362</td> <td>73 200 235 263 309.1C 315.1C</td> <td>523d 524d 573.1C</td> </tr> <tr> <td>K011</td> <td>G2a1</td> <td>G2a1</td> <td>16183 16223 16227 16278 16362</td> <td>73 146 207 263 315.1C</td> <td>489</td> </tr> <tr> <td>K012</td> <td>M10a</td> <td>M10a</td> <td>16129 16148 16193 16223 16311 16357 16497</td> <td>73 146 152 263 309.1C 315.1C</td> <td>489 523d 524d 573.1C</td> </tr> <tr> <td>K013</td> <td>N9a1</td> <td>N9a1</td> <td>16111 16129 16223 16257A 16261</td> <td>73 150 195 263 309.1C 309.2C 315.1C</td> <td></td> </tr> <tr> <td>K014</td> <td>B4</td> <td>B4</td> <td>16182C 16183C 16189 16217 16295</td> <td>73 150 195 263 309.1C 315.1C</td> <td></td> </tr> <tr> <td>K015</td> <td>G1a1</td> <td>G1a1</td> <td>16075 16223 16325 16362 16519</td> <td>73 150 263 315.1C</td> <td>489</td> </tr> <tr> <td>K016</td> <td>B4b1</td> <td>B4b1</td> <td>16136 16175 16183C 16189 16217 16218 16519</td> <td>56d 58A 71.1G 73 263 309.1C 309.2C...</td> <td>489</td> </tr> <tr> <td>K017</td> <td>A5a</td> <td>A5a</td> <td>16187 16223 16290 16319</td> <td>73 235 263 315.1C</td> <td>523d 524d</td> </tr> <tr> <td>K018</td> <td>B4c1a</td> <td>B4c1a</td> <td>16183C 16189 16217 16311 16519</td> <td>73 263 309.1C 315.1C</td> <td></td> </tr> <tr> <td>K019</td> <td>N9a1</td> <td>N9a1</td> <td>16129 16223 16257A 16261</td> <td>73 150 263 309.1C 315.1C</td> <td></td> </tr> <tr> <td>K020</td> <td>M9a</td> <td>M9a</td> <td>16223 16234 16316 16362 16519</td> <td>73 263 309.1C 309.2C 315.1C</td> <td>489</td> </tr> </tbody> </table>	Sample ID	Expected HG	Estimated HG	np 16024-16569	np 001-437	np 438-576	K001	D5a2	D5a2	16164 16172 16182T 16183C 16189 16223 162...	73 150 263 309.1C 309.2C 315.1C	489 523d 524d	K002	N9a1	N9a1	16111 16129 16223 16257A 16261 16298	73 150 263 315.1C		K003	D4/G	D4/G	16223 16224 16362 16519	73 263 309.1C 315.1C	489	K004	M7b2	M7b2	16129 16189 16223 16257 16297 16298	73 150 199 263 315.1C	489	K005	D5b	D5b	16189 16223 16362 16519	73 146 150 252 263 309.1C 309.2C 31...	489 489	K006	D4a	D4a	16086 16129 16223 16362 16519	73 152 263 315.1C	489	K007	M7b2	M7b2	16129 16189 16223 16242 16297 16298	73 150 199 263 309.1C 315.1C	489	K008	B5b	B5b	16140 16183C 16189 16243 16355 16519	73 103 263 309.1C 309.2C 315.1C	523d 524d	K009	M10b	M10b	16068 16223 16311	73 263 315.1C	489 573.1C 573.2C	K010	A4	A4	16223 16290 16319 16362	73 200 235 263 309.1C 315.1C	523d 524d 573.1C	K011	G2a1	G2a1	16183 16223 16227 16278 16362	73 146 207 263 315.1C	489	K012	M10a	M10a	16129 16148 16193 16223 16311 16357 16497	73 146 152 263 309.1C 315.1C	489 523d 524d 573.1C	K013	N9a1	N9a1	16111 16129 16223 16257A 16261	73 150 195 263 309.1C 309.2C 315.1C		K014	B4	B4	16182C 16183C 16189 16217 16295	73 150 195 263 309.1C 315.1C		K015	G1a1	G1a1	16075 16223 16325 16362 16519	73 150 263 315.1C	489	K016	B4b1	B4b1	16136 16175 16183C 16189 16217 16218 16519	56d 58A 71.1G 73 263 309.1C 309.2C...	489	K017	A5a	A5a	16187 16223 16290 16319	73 235 263 315.1C	523d 524d	K018	B4c1a	B4c1a	16183C 16189 16217 16311 16519	73 263 309.1C 315.1C		K019	N9a1	N9a1	16129 16223 16257A 16261	73 150 263 309.1C 315.1C		K020	M9a	M9a	16223 16234 16316 16362 16519	73 263 309.1C 309.2C 315.1C	489
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Sample ID	Expected HG	Estimated HG	np 16024-16569	np 001-437	np 438-576																																																																																																																																
K001	D5a2	D5a2	16164 16172 16182T 16183C 16189 16223 162...	73 150 263 309.1C 309.2C 315.1C	489 523d 524d																																																																																																																																
K002	N9a1	N9a1	16111 16129 16223 16257A 16261 16298	73 150 263 315.1C																																																																																																																																	
K003	D4/G	D4/G	16223 16224 16362 16519	73 263 309.1C 315.1C	489																																																																																																																																
K004	M7b2	M7b2	16129 16189 16223 16257 16297 16298	73 150 199 263 315.1C	489																																																																																																																																
K005	D5b	D5b	16189 16223 16362 16519	73 146 150 252 263 309.1C 309.2C 31...	489 489																																																																																																																																
K006	D4a	D4a	16086 16129 16223 16362 16519	73 152 263 315.1C	489																																																																																																																																
K007	M7b2	M7b2	16129 16189 16223 16242 16297 16298	73 150 199 263 309.1C 315.1C	489																																																																																																																																
K008	B5b	B5b	16140 16183C 16189 16243 16355 16519	73 103 263 309.1C 309.2C 315.1C	523d 524d																																																																																																																																
K009	M10b	M10b	16068 16223 16311	73 263 315.1C	489 573.1C 573.2C																																																																																																																																
K010	A4	A4	16223 16290 16319 16362	73 200 235 263 309.1C 315.1C	523d 524d 573.1C																																																																																																																																
K011	G2a1	G2a1	16183 16223 16227 16278 16362	73 146 207 263 315.1C	489																																																																																																																																
K012	M10a	M10a	16129 16148 16193 16223 16311 16357 16497	73 146 152 263 309.1C 315.1C	489 523d 524d 573.1C																																																																																																																																
K013	N9a1	N9a1	16111 16129 16223 16257A 16261	73 150 195 263 309.1C 309.2C 315.1C																																																																																																																																	
K014	B4	B4	16182C 16183C 16189 16217 16295	73 150 195 263 309.1C 315.1C																																																																																																																																	
K015	G1a1	G1a1	16075 16223 16325 16362 16519	73 150 263 315.1C	489																																																																																																																																
K016	B4b1	B4b1	16136 16175 16183C 16189 16217 16218 16519	56d 58A 71.1G 73 263 309.1C 309.2C...	489																																																																																																																																
K017	A5a	A5a	16187 16223 16290 16319	73 235 263 315.1C	523d 524d																																																																																																																																
K018	B4c1a	B4c1a	16183C 16189 16217 16311 16519	73 263 309.1C 315.1C																																																																																																																																	
K019	N9a1	N9a1	16129 16223 16257A 16261	73 150 263 309.1C 315.1C																																																																																																																																	
K020	M9a	M9a	16223 16234 16316 16362 16519	73 263 309.1C 309.2C 315.1C	489																																																																																																																																

Group Information

Name: Demo-1
 Metapopulation: East Asian
 Subpopulation: Korean
 Description: Demo Sequences
 HV1:
 HV2:
 HV3:
 Control Region:
 No. of Samples: 593

miDNAManager - forensic mtDNA database - Windows Internet Explorer

http://mtmanager.yonsei.ac.kr/group.php#

Welcome, Colleague

A match system

Working Group	Working Sample																																																						
<table border="1"> <thead> <tr> <th>Name</th> <th>Description</th> </tr> </thead> <tbody> <tr> <td>Demo-1</td> <td>Demo Sequences</td> </tr> <tr> <td>Demo-2</td> <td>Demo Sequences</td> </tr> </tbody> </table>	Name	Description	Demo-1	Demo Sequences	Demo-2	Demo Sequences	<table border="1"> <thead> <tr> <th>Sample ID</th> <th>Expected HG</th> <th>Estimated HG</th> <th>np 16024-16569</th> <th>np 001-437</th> <th>np 438-576</th> </tr> </thead> <tbody> <tr> <td>K008</td> <td>B5b</td> <td>B5b</td> <td>16140 16183C 16189 16243 16355 16519</td> <td>73 103 263 309.1C 309.2C 315.1C</td> <td>523d 524d</td> </tr> <tr> <td>K009</td> <td>M10b</td> <td>M10b</td> <td>16068 16223 16311</td> <td>73 263 315.1C</td> <td>489 573.1C 573.2C</td> </tr> <tr> <td>K010</td> <td>A4</td> <td>A4</td> <td>16223 16290 16319 16362</td> <td>73 200 235 263 309.1C 315.1C</td> <td>523d 524d 573.1C</td> </tr> <tr> <td>K011</td> <td>G2a1</td> <td>G2a1</td> <td>16183 16223 16227 16278 16362</td> <td>73 146 207 263 315.1C</td> <td>489</td> </tr> <tr> <td>K012</td> <td>M10a</td> <td>M10a</td> <td>16129 16148 16193 16223 16311 16357 16497</td> <td>73 146 152 263 309.1C 315.1C</td> <td>489 523d 524d 573.1C</td> </tr> <tr> <td>K013</td> <td>N9a1</td> <td>N9a1</td> <td>16111 16129 16223 16257A 16261</td> <td>73 150 195 263 309.1C 309.2C 315.1C</td> <td></td> </tr> <tr> <td>K014</td> <td>B4</td> <td>B4</td> <td>16182C 16183C 16189 16217 16295</td> <td>73 150 195 263 309.1C 315.1C</td> <td></td> </tr> </tbody> </table>	Sample ID	Expected HG	Estimated HG	np 16024-16569	np 001-437	np 438-576	K008	B5b	B5b	16140 16183C 16189 16243 16355 16519	73 103 263 309.1C 309.2C 315.1C	523d 524d	K009	M10b	M10b	16068 16223 16311	73 263 315.1C	489 573.1C 573.2C	K010	A4	A4	16223 16290 16319 16362	73 200 235 263 309.1C 315.1C	523d 524d 573.1C	K011	G2a1	G2a1	16183 16223 16227 16278 16362	73 146 207 263 315.1C	489	K012	M10a	M10a	16129 16148 16193 16223 16311 16357 16497	73 146 152 263 309.1C 315.1C	489 523d 524d 573.1C	K013	N9a1	N9a1	16111 16129 16223 16257A 16261	73 150 195 263 309.1C 309.2C 315.1C		K014	B4	B4	16182C 16183C 16189 16217 16295	73 150 195 263 309.1C 315.1C	
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Matching Option

Region: HV1 HV2 HV3 Control Region

Option: Ignore heteroplasmic insertions in the poly C-stretches

Maximum number of mismatched nucleotides: 0

[Match] [Match All] [Frequency Estimates]

Matching Result

No. of Matched Samples	No. of Target Samples	Match Probability
1	101	0.0291

[Export] [Print]

Sample ID	Expected HG	Estimated HG	np 16024-16569	np 001-437	np 438-576
B019	B4	B4	16182C 16183C 16189 16217 16295	73 150 195 263 309.1C 309.2C 309.2C...	

A query system

Searching Option

Sequence: 16187 235

Region: HV1 HV2 HV3 Control Region

Option: Match Ignore heteroplasmic insertions in the poly C-stretches

Maximum number of mismatched nucleotides: 0

Include the queried nucleotide polymorphism

Expected HG: A5a Estimated HG: H Comments:

Searching Result

No. of Matched Samples	No. of Target Samples	Match Probability
19	593	0.0353

Sample ID	Expected HG	Estimated HG	np 16024-16569	np 001-437	np 438-576
K017	A5a	A5a	16187 16223 16290 16319	73 235 263 315.1C	523d 524d
K122	A5a	A5a	16187 16223 16290 16319	73 235 263 309.1C 315.1C	523d 524d
K178	A5a	A5a	16187 16189 16223 16290 16319	73 235 263 309.1C 315.1C	523d 524d
K184	A5a	A5a	16187 16223 16290 16296 16319	73 235 263 309.1C 315.1C	523d 524d
K191	A5a	A5a	16187 16223 16290 16319 16519	73 146 195 235 263 309.1C 309.2C 31...	523d 524d
K216	A5a	A5a	16187 16192 16223 16270 16290 16319	73 235 263 309.1C 315.1C	523d 524d
K222	A5a	A5a	16187 16223 16290 16319	73 235 263 309.1C 315.1C	523d 524d
K263	A5a	A5a	16086 16187 16223 16290 16319	73 235 263 309.1C 315.1C	523d 524d
K271	A5a	A5a	16187 16223 16290 16319 16519	73 195 235 263 309.1C 309.2C 315.1C	523d 524d
K308	A5a	A5a	16187 16223 16290 16319	73 235 263 315.1C	523d 524d
K382	A5a	A5a	16187 16223 16290 16319	73 235 263 315.1C	523d 524d
K366	A5a	A5a	16187 16215 16223 16290 16319	73 235 263 309.1C 315.1C	523d 524d

Concluding remarks

- The mtDNAManager is a forensic mitochondrial DNA database aimed at **supporting data quality control** and **generating reliable frequency estimates** using an approach based on haplogroup estimation and data comparison.
- The **mtDNAManager** provides a **convenient web interface** for analysis, query and storage of human mtDNA control region sequences.
- For comments, bug reports, suggestions for improvement, please contact us through the website (<http://mtmanager.yonsei.ac.kr>).

