
A Practical Application of **mtDNAManager** to Mitochondrial DNA Error Detection in Forensics

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DNA in Forensics 2008

mtDNAManager - forensic mtDNA database - Windows Internet Explorer

http://mtmanager.yonsei.ac.kr

mtDNAManager

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Password: Register

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About

Services

- Database
- Statistics
- Haplogroup
- My mtDNA

Help

- Query
- Sample
- Match

Mutation motifs

Recent updates

Contact us

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 for human mtDNA control region sequences. mtDNAManager is made free and open to all users and there is no login requirement. At the same time, mtDNAManager offers the option to store and match data with batch mode for registered users.

- [Access demo](#)

The aims of mtDNAManager are (i) to allow researchers to automatically estimate the mtDNA haplogroups of their own mtDNA sequences, (ii) to search high quality mtDNA databases generating reliable frequency estimates, and (iii) to collect and integrate publicly available high quality mtDNA control region sequence data.

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인터넷 100%

mtDNAManager's Open Database

Metapopulation	Subpopulation	No. of sequences	References
African	African	1148	Forensic Sci Commun (2002) 4 <i>Online</i>
	Kenyan	100	Int J Legal Med (2004) 118:294-306
	U.S. African	140	Forensic Sci Int: Genetics (2008) <i>in press</i>
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) 172:171-178
	German	313	Forensic Sci Int (2007) 172:218-224 Int J Legal Med (2006) 120:310-314
East Asian	Hungarian	416	Int J Legal Med (2007) 121:377-383
	East Asian	753	Forensic Sci Commun (2002) 4 <i>Online</i>
	Japanese	211	Int J Legal Med (2003) 117:218-225
Oceanian	Korean	593	Int J Legal Med (2006) 120:5-14
	-	-	-
Admixed	Hispanic	686	Forensic Sci Commun (2002) 4 <i>Online</i>
	Dubaian	249	Forensic Sci Int: Genetics (2008) 2(1):e9-10
	U.S. Hispanic	253	Forensic Sci Int: Genetics (2008) 2(2):e19-23 Forensic Sci Int: Genetics (2008) <i>in press</i>
	Venezuelan	100	Forensic Sci Int: Genetics (2008) <i>in press</i>
Total		7090	

Automatic haplogroup estimation

- Phased designation of haplogroups, i.e., **expected haplogroup** and **estimated haplogroup**, facilitates systematic error detection

Possess clear key diagnostic mutations

Sample List				Possess accompanying mutations for Expected HG			
Add	Edit	Delete	Import	Export	Print	Comments	Description
Sample ID	Expected HG	Estimated HG	rp 101-102-103-104-105-106-107-108-109-110-111-112-113-114-115-116-117-118-119-120-121-122-123-124-125-126-127-128-129-130-131-132-133-134-135-136-137-138-139-140-141-142-143-144-145-146-147-148-149-150-151-152-153-154-155-156-157-158-159-160-161-162-163-164-165-166-167-168-169-170-171-172-173-174-175-176-177-178-179-180-181-182-183-184-185-186-187-188-189-190-191-192-193-194-195-196-197-198-199-200-201-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-842-843-844-845-846-847-848-849-850-851-852-853-854-855-856-857-858-859-860-861-862-863-864-865-866-867-868-869-870-871-872-873-874-875-876-877-878-879-880-881-882-883-884-885-886-887-888-889-890-891-892-893-894-895-896-897-898-899-900-901-902-903-904-905-906-907-908-909-910-911-912-913-914-915-916-917-918-919-920-921-922-923-924-925-926-927-928-929-930-931-932-933-934-935-936-937-938-939-940-941-942-943-944-945-946-947-948-949-950-951-952-953-954-955-956-957-958-959-960-961-962-963-964-965-966-967-968-969-970-971-972-973-974-975-976-977-978-979-980-981-982-983-984-985-986-987-988-989-990-991-992-993-994-995-996-997-998-999-1000	rp 001-437	rp 430-576		
H105	T1	T1	16126 16163 16186 16189 16234 16519	73 195 263 309.1C 315.1C			T1
H106	T2	T2	16126 16163 16186 16189 16234 16519	73 195 263 309.1C 315.1C			T2
H1E1	H1a	H1a	16293 16311	143 195 263 309.1C 315.1C			H*
H1E2	H	H	16281 16519	263 315.1C			H*
H1E3	H	H	16083 16271 16519	263 309.1C 315.1C			H*
H1E4	H1b	H1b	16189 16256 16262 16519	263 309.1C 315.1C	523d 524d		H1b
H1E5	X2	X2	16134 16183C 16189 16223 16278 16519	73 195 263 309.1C 309.2C 315.1C			X2d
H1E6	J1c	J1c	16069 16126 16201 16265 16319	73 185 228 263 295 309.1C 315.1C	462 469 524.1A 524.2C		J1c
H1F1	H	H	16234 16283 16519	263 315.1C 315.2C			H*
H1F2	W	W	16223 16292 16295 16519	73 119 189 195 204 207 283 315.1C			W
H1F3	K1a	K1a	16222 16224 16311 16362 16519	73 114 263 309.1C 315.1C	497		K1a
H1F4	T1a	T1a	16126 16163 16186 16189 16234 16519	73 152 195 263 309.1C 315.1C			T1a
H1F5	H5	H5	16260 16304	263 309.1C 315.1C	456		H5
H1F6	U5a	U5a	16192 16256 16270 16300	73 143 263 315.1C			U5a1
H1O1	HVD	HVD	16153 16298	72 93 185 263 315.1C			HVD
H1O2	H	H	16311	263 309.1C 315.1C	523d 524d		H*
H1O3	H	H	16325 16519	263 309.1C 315.1C			H*
H1O4	H5	H5	16304	263 309.1C 309.2C 315.1C	456		H5
H1O5	T1	T1	16126 16163 16186 16189 16234 16519	73 195 263 315.1C			T1
H1O6	C	C	16083 16223 16234 16288 16298 16327 16518...	73 249d 263 309.1C 315.1C	489		C

Coding region haplogroups

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

Control Region Mutation motif for more than 400 mtDNA haplogroups

mtDNAManager

Query Home

About

Services

- Database
- Statistics
- Haplogroup
- My mtDNA

Help

- Query
- Sample
- Match
- Mutation motifs

Recent updates

Contact us

mtDNA Haplogroup Specific Control Region Mutation Motifs

African Haplogroup			
Haplogroup	HV1	HV2	HV3 etc.
L0a	16129-16148-16172-16187-16188G-16189-16223-16230-16311-16320	93-183-189-236-247	523a-524d
L0a1	16129-16148-16168-16172-16187-16188G-16189-16223-16230-16311-16320	93-183-189-(236)-247	523a-524d
L0a1a	16129-16148-16168-16172-16187-16188G-16189-16223-16230-16278-16311-16320	93-95C-183-189-236-247	523a-524d
L0a2	16129-16148-16172-16187-16188G-16189-16223-16230-16311-16320	93-152-189-236-247	523a-524d
L0d	(16129)-(16187)-16189-16223-16230-16243-16311	189-247	
L0f	16169-16187-16189-16223-(16230)-16278-16311-16327	189-247	1656b
L0g	16172-16187-16189-16200-16214-16223-16230-16278-16291G-16311	146-189-195-198-207-247	
L1b	16126-16187-16189-16223-16264-16270-16278-16311	183-185T-195-247	357, 523a-524d
L1b1	16126-16187-16189-16223-16264-16270-16278-16293-16311	(182)-185T-(195)-247	357, 523a-524d
L1c	(16129)-16189-(16223)-16278-16311	153-183-186A-189C-247(cc-247d)-316	523a-524d
L1c1	16129-16189-(16223)-16278-16293-16360	(151)-152-182-186A-189C-247(cc-247d)-316	523a-524d
L1c2	16129-16187-16189-(16223)-16265C-16278-16286G-16294-16311-16360	151-153-182-186A-189C-198-247-316	523a-524d

Database search using query

- Query system retrieves sequences which include the queried nucleotide polymorphisms from a user-selected database

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Sample Match Query Home

Target Group

- My mtDNA
- Open DB: West Eurasian

Name	Description
Austrian	Forensic Sci Int (2007) 160
FBI-Caucasian	Forensic Sci Comm (2002)
Finnish	Forensic Sci Int (2007) 172
German	Int J Legal Med (2006) 120
Hungarian	Int J Legal Med (2007) 121

Target database

Searching Option

Sequence: 16223 16290 16319 235

Region: HV1 HV2 HV3 Control Region

Option: Match Include option

ignore heteroplasmic insertions in the poly C-stretches

Maximum number of mismatched nucleotides: 0

include the queried nucleotide polymorphism

Search Reset Worldwide Frequency

Expected HG A Estimated HG A Comments

Searching Result

No. of Matched Samples	No. of Target Samples	Match Probability	Export	Print
5	1655	0.0042		
Sample ID	Expected HG	Estimated HG	np 16224-18588	np 001-437
GRC CAU 0003	A4a	A4a	18223 18248 18290 18319 18382	73 182 236 283 306 1C 316 1C np 438-578
USA CAU 0003	A2	A2	18111 18138 18172 18223 18290 18311 18316	73 148 183 236 283 316 1C 523a 524d
USA CAU 0005	A2	A2	18111 18223 18290 18319 18382	73 148 183 236 283 316 1C
USA CAU 0675	A2	A2	18111 18223 18290 18319 18382	73 148 189 236 283 308 1C 315 1C
USA CAU 0798	A2	A2	18111 18223 18290 18319 18382	73 148 183 236 283 308 1C 315 1C

Estimated mtDNA haplogroup affiliations using the bioinformatics resources of the mtDNAManager

mtDNA error detection

- Review the data by searching the database and estimating the most probable mtDNA haplogroups

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Target Group: My mtDNA, Open DB: West Eurasian

Sequence: 16226

Region: HV1 HV2 HV3 Control Region

Option: Match, Ignore heteroplasmic insertions in the poly C-stretches, Include the queried nucleotide polymorphism

Buttons: Search, Reset, Worldwide Frequency

Expected HG: T2b, Estimated HG: [blank]

No. of Matched Samples	No. of Target Samples	Match Probability
0	273	0.0073

Sample ID: np 001-437, np 438-576

T2b haplogroup-specific mutation motif : 16126-16294-16296-16304

mtDNA error detection

- Investigate the mutability of the site with potential error

mtDNAmanager

Welcome, Colleague
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Target Group: My mtDNA, Open DB: West Eurasian

Sequence: 16226

Region: HV1 HV2 HV3 Control Region

Option: Match, Ignore heteroplasmic insertions in the poly C-stretches, Include the queried nucleotide polymorphism

Buttons: Search, Reset, Worldwide Frequency

Expected HG: H, Estimated HG: H

No. of Matched Samples	No. of Target Samples	Match Probability
0	1655	0.0012

Sample ID: np 001-437, np 438-576

Group Information: Name: FBI-Caucasian, Metapopulation: West Eurasian, Subpopulation: Caucasian, Description: Forensic Sci Comm (2002) 4 Online, No. of Samples: 1655

mtDNA error detection

- Investigate the mutability of the site with potential error

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http://mtmanager.yonsei.ac.kr/sample/sample_search_req_print.php?group_id=255&Name=FBI-Caucasian&seq=16226&hvl=1&hvc=

Comments: **None of 7090 mtDNAs bears the 16226 mutation**

Population	Group Name	Description	No. of Matched Samples	No. of Population Samples	Match Probability
Admixed			0	1200	0.0016
Dubai, UAE	Dubai	FBI Genetic (2000) 2-6+10	0	249	0.0000
Hispanic	FBI-Hispanic	Forensic Sci Comm (2002) 4 Online	0	690	0.0029
U.S. Hispanic	US-Hispanic	FBI Genetic (2000) 2-4+18a2; FBI Genetic (2000) In Press	0	293	0.0078
Venezuelan	Venezuelan	FBI Genetic (2000) In Press	0	100	0.0190
African			0	1388	0.0014
African	FBI-African	Forensic Sci Comm (2002) 4 Online	0	1148	0.0017
African	US-African	FBI Genetic (2000) In Press	0	140	0.0141
American	Kiryan	Int J Legal Med (2004) 118 294-300	0	100	0.0190
East Asian			0	1587	0.0013
East Asian	FBI-Asian	Forensic Sci Comm (2002) 4 Online	0	793	0.0020
Japanese	Japanese	Int J Legal Med (2003) 117 218-226	0	211	0.0084
Korean	Korean-Torset	Int J Legal Med (2006) 120 8-14	0	893	0.0034
Oceanian			0	1 0000	0.0000
Oceanian	Oceanian	Coming Soon ...	0	0	1 0000
West Eurasian			0	2897	0.0007
Austrian	Austrian	Forensic Sci Int (2007) 166 164-176	0	273	0.0073
Caucasian	FBI-Caucasian	Forensic Sci Comm (2002) 4 Online	0	1666	0.0010
Finnish	Finnish	Forensic Sci Int (2007) 172 171-178	0	200	0.0098
German	German	Int J Legal Med (2005) 120 310-314; Forensic Sci Int (2007) 172 218-224	0	313	0.0083
Hungarian	Hungarian	Int J Legal Med (2007) 121 317-323	0	418	0.0048

Correction of verified errors

	HV1 (16000+)	HV2
USA.CAU.000272	226-294-296-304	73-263-309.1C-315.1C
Corrected		
USA.CAU.000272	126-294-296-304	73-263-309.1C-315.1C

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Target Group: My mtDNA, Open DB: West Eurasian

Name: Austrian, Description: Forensic Sci Int (2007) 166

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

Sequence: 16126-16294-16296-16304-73-263-309.1C-315.1C

Search: [Search] [Reset] [Worldwide Frequency]

Expected HG: T2b, Estimated HG: T2b, Comments: Corrected USA.CAU.000272

Sample ID	Expected HG	Estimated HG	np 16024-16509	np 001-437	np 438-676
T2b	T2b	T2b	16120 16294 16296 16304 16519	73 195 263 309.1C 315.1C	
T2b	T2b	T2b	16120 16294 16296 16304 16302 16519	73 263 309.1C 315.1C	
T2b	T2b	T2b	16111 16120 16294 16296 16304 16311 16327	73 263 309.1C 315.1C	

T2b: 16126-16294-16296-16304

Correction of verified errors

	HV1 (16000+)	HV2	Haplogroup
USA.AFR.000074	126-187-189-223-264-270-278-311	73-143-146-152-195-263-264-315.1C	L1b1xL2a1
Corrected			
USA.AFR.000074	126-187-189-223-264-270-278-311	73-152-182-185T-189-195-247-263-315.1C-357	L1b1

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Target Group: African

Sequence: 73 143 146 152 195 263 264 315.1C

Region: HV1 HV2 HV3 Control Region

Option: Match

Ignore heteroplasmic insertions in the poly-C stretches

Maximum number of mismatched nucleotides: 1

Include the queried nucleotide polymorphism

Worldwide Frequency

Match options

Searching Result

Sample ID	Expected HG	Estimated HG	Match Probability
US.AFR-021	L2a1	L2a1	0.0054
US.AFR-022	L2a1	L2a1	
US.AFR-023	L2a1	L2a1	
US.AFR-024	L2a1	L2a1	
US.AFR-025	L2a1	L2a1	
US.AFR-026	L2a1	L2a1	
US.AFR-027	L2a1	L2a1	

Correction of verified errors

	HV1 (16000+)	HV2	Haplogroup
USA.AFR.000074	126-187-189-223-264-270-278-311	73-143-146-152-195-263-264-315.1C	L1b1xL2a1
Corrected			
USA.AFR.000074	126-187-189-223-264-270-278-311	73-152-182-185T-189-195-247-263-315.1C-357	L1b1

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Target Group: African

Sequence: 16126 16187 16189 16223 16264 16270 16278 16311 73 152 182 185T

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

Worldwide Frequency

Match options

Searching Result

Sample ID	Expected HG	Estimated HG	Match Probability
US.AFR-007	L1b1	L1b1	0.1098
US.AFR-007	L1b1	L1b1	
US.AFR-008	L1b1	L1b1	
US.AFR-008	L1b1	L1b1	
US.AFR-009	L1b1	L1b1	
US.AFR-009	L1b1	L1b1	
US.AFR-009	L1b1	L1b1	
US.AFR-100	L1b1	L1b1	

My mtDNA

- Upon registration, 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 open database

The screenshot shows the mtDNAmanager web interface. On the left, there is a 'Batch input files' section with a table containing sample information. A green arrow points from this section to the main 'Sample List' table. A red arrow points from the 'Sample List' table to an 'Export as an excel file' button.

Batch input files

A	B	C	D	E
1. Sample	Description	np 16024-16589		np 436-576
2. USA-MF0050	afghan	16183C 16086T	730 1622 2630 308 1C 315 1C	
3. JAIT CAU024	Chauhan	2630 315 1C		489
4. CHN-ADN037	Asian	16223T 16362C	730 146C 2630 315 1C	489C

Sample List

Sample ID	Expected HG	Estimated HG	np 16024-16589	np 436-576	Comments
Demo-01	D4b1	D4b1	16223 16319 16362	489 523d 524d	
Demo-02	N9a1		16129 16223 16257A 16281	73 152 263 309.1C 315.1C	
Demo-03	A5b	A5b	16126 16223 16235 16290 16319 16519	73 235 263 315.1C	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 16...	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		16187 16223 16290 16519	73 146 195 235 263 309.1C 309.2C 31...	523d 524d
Demo-10	D4j1	D4j1	16184 16223 16311 16362	73 203 263 315.1C	489
Demo-11	M9a	M9a	16223 16234 16316 16362	73 263 309.1C 315.1C	489
Demo-12	B4c1a	B4c1a	16086 16183C 16...	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		16223 16362T	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....	459d
Demo-18	G3a	G3a	16223 1627	73 143 152 204 263 315	489
Demo-19	A	A	16179 16223 16...	73 235 263 309.1C 315	523d 524d
Demo-20			16086 16223	73 103 204 263 315.1C	489

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 436-576	Comments
Demo-01	D4b1	D4b1	16223 16319 16362	489 523d 524d	
Demo-02	N9a1		16129 16223 16257A 16281	73 152 263 309.1C 315.1C	150?
Demo-03	A5b	A5b	16126 16223 16235 16290 16319 16519	73 235 263 315.1C	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 16...	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		16187 16223 16290 16519	73 146 195 235 263 309.1C 309.2C 31...	523d 524d
Demo-10	D4j1	D4j1	16184 16223 16311 16362	73 203 263 315.1C	489
Demo-11	M9a	M9a	16223 16234 16316 16362	73 263 309.1C 315.1C	489
Demo-12	B4c1a	B4c1a	16086 16183C 16...	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		16223 16362T	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....	459d
Demo-18	G3a	G3a	16223 1627	73 143 152 204 263 315	489
Demo-19	A	A	16179 16223 16...	73 235 263 309.1C 315	523d 524d
Demo-20			16086 16223	73 103 204 263 315.1C	489

Artificial recombination?

miDNAManager - forensic mtDNA database - Windows Internet Explorer

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

http://mtmanager.yonsei.ac.kr

miDNAManager

E-mail: Login

Password: Register

Query Home

About

Services

- Database
- Statistics
- Haplogroup
- My mtDNA

Help

- Query
- Sample
- Match

Mutation motifs

Recent updates

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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 for human mtDNA control region sequences. mtDNAManager is made free and open to all users and there is no login requirement. At the same time, mtDNAManager offers the option to store and match data with batch mode for registered users.

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

The aims of mtDNAManager are (i) to allow researchers to automatically estimate the mtDNA haplogroups of their own mtDNA sequences, (ii) to search high quality mtDNA databases generating reliable frequency estimates, and (iii) to collect and integrate publicly available high quality mtDNA control region sequence data.

YONSEI UNIVERSITY

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miDNAManager - forensic mtDNA database - Windows Internet Explorer

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

miDNAManager

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A sample system

Sample Match Query Home

Group List

Add Edit Delete

Name Description

Demo-African FSI: Genetics (2008) in Pres

Demo-Asian ULM (2006) 120-5-14

Demo-Casework Skeletal Remains of Korean

Demo-European EMPOP

Demo-Hispanic FSI: Genetics (2008) in Pres

Sample List

Add Edit Delete Import Export Print

Sample ID	Expected HG	Estimated HG	np 16024-16569	np 001-437	np 438-576
AUT0500000	K1a	K1a	16224 16287 16311 16519	73 263 309.1C 315.1C	497
AUT0500001	H	H	16519	235 263 309.1C 309.2C 315.1C	
AUT0500002	H	H	16037 16188A 16519	263 309.1C 309.2C 315.1C	524.1A 524.2C
AUT0500003	J1c	J1c	16069 16126 16324 16366 16390 16519	73 185 188 228 263 295 309.1C 315.1C	462 489 523d 524
AUT0500004	J1c	J1c	16069 16126 16261	73 185 189 228 263 295 309.1C 315.1C	462 489
AUT0500005	H	H		263 315.1C 340	523d 524d
AUT0500006	K	K	16093 16224 16311 16319 16463 16519	73 151 152 199 263 309.1C 315.1C	524.1A 524.2C
AUT0500007	U5b2*	U5b2*	16189 16192 16270 16396	73 150 263 315.1C	
AUT0500008			16248 16519	73 187T 263 315.1C	523d 524d
AUT0500009	H	H	16519	189 263 315.1C	
AUT0500010	H1c1	H1c1	16093 16263 16311 16390 16519	263 315.1C	477
AUT0500011	H5	H5	16304	146 195 263 309.1C 315.1C	456
AUT0500012	U4	U4	16179 16266 16356 16519	73 150 195 263 309.1C 315.1C	499 524.1A 524.2C
AUT0500013	H1c	H1c		263 309.1C 315.1C	477
AUT0500014	H1c	H1c	16519	263 315.1C	477
AUT0500015	H	H	16183C 16189 16519	263 309.1C 309.2C 315.1C	
AUT0500016	X2b	X2b	16182C 16183C 16189 16223 16278 16519	73 152 153 189 195 225 226 263 315...	
AUT0500017	U5b2*	U5b2*	16189 16192 16270 16396	73 150 263 315.1C	
AUT0500018	H1b	H1b	16189 16356 16362 16519	263 309.1C 315.1C	523d 524d
AUT0500019	T1	T1	16126 16163 16186 16189 16294 16519	73 195 263 309.1C 315.1C	

Group Information

Name Demo-European

Metapopulation West Eurasian

Subpopulation Austrian

Description EMPOP

HV1

HV2

HV3

Control Region

No. of Samples 273

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

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miDNAManager - forensic mtDNA database - Windows Internet Explorer

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

miDNAManager - forensic mtDNA database

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A match system

Sample Match Query Home

Working Sample

Name	Description	Sample ID	Expected HG	Estimated HG	np 16024-16569	np 001-437	np 438-576
Demo-African	FSI: Genetics (2008) In Pres	B001	B4c1c	B4c1c	16183C 16189 16217 16311	73 146 150 195 214 263 315.1C	489 499.1C
Demo-Asian	ULM (2006) 120.5-14	B002	D4/G	D4/G	16223 16362	73 263 315.1C	489 524.1A 524.2
Demo-Case-work	Skeletal Remains of Korean	B003	G2a3	G2a3	16189 16223 16278 16292 16362	73 260 263 309.1C 309.2C 315.1C	489 523d 524d
Demo-European	EMPOP	B004	D4/G	D4/G	16223 16362	73 152 263 309.1C 309.2C 315.1C	489
Demo-Hispanic	FSI: Genetics (2008) In Pres	B005	D4j1	D4j1	16184 16223 16311 16362	73 152 263 315.1C	489
		B006	D5a1	D5a1	16182C 16183C 16189 16223 16362	68 73 150 263 309d 315.1C	489
		B007	D4/G	D4/G	16223 16362	73 263 309.1C 315.1C	489 523d 524d

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 Worldwide Frequency

Matching Result

No. of Matched Samples	No. of Target Samples	Match Probability
1	593	0.0050

Export Print

Sample ID	Expected HG	Estimated HG	np 16024-16569	np 001-437	np 438-576
K371	B4c1c	B4c1c	16183C 16189 16217 16311	73 146 150 195 214 263 315.1C	

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

miDNAManager - forensic mtDNA database

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A query system

Sample Match Query Home

Target Group

My mtDNA

Open DB: African

Name Description

Demo-African FSI: Genetics (2008) In Pres

Demo-Asian ULM (2006) 120.5-14

Demo-Case-work Skeletal Remains of Korean

Demo-European EMPOP

Demo-Hispanic FSI: Genetics (2008) In Pres

Searching Option

Sequence 16187 235

Region HV1 HV2 HV3 Control Region

Match

Option Ignore heteroplasmic insertions in the poly C-stretches

Maximum number of mismatched nucleotides 0

Include the queried nucleotide polymorphism

Search Reset Worldwide Frequency

Expected HG A5a Estimated HG H Comments

Searching Result

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

Export Print

Group Information

Name Demo-Asian

Metapopulation East Asian

Subpopulation Korean

Description ULM (2006) 120.5-14

HV1

HV2

HV3

Control Region

No. of Samples 593

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	16096 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

Concluding remarks

- The mtDNAManager provides systematic routines for **error detection** and strategies for screening database by enabling researchers to **automatically estimate the most probable haplogroups** and search the high-quality database.
- 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>)



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