

Tab. S1. Primers, PCR conditions and restriction enzymes used for RFLP analysis

HAPLOGROUP DIAGNOSTIC SITES				
Haplogroup	Restriction sites	Primers	Amplicon (bp)	Annealing temperature
A	+663HaeIII	L550 5'-TAACCCCATACCCCGAACCA H706 5'-GGTGAAGTCACTGGAACGGG	195	50
B	(CCCCCTCTA) deletion	L8215 5'-ACAGT TTCATGCCCA TCGTC H8297 5'-ATGCTAAGTTAGCTTTACAG	121	52
C	+13262 AluI	L13192 5'-GCTTAGGCGCTATCACCCTC H13384 5'-ATATCTTGTTTCATTGTTAAG	232	55
L1/L2	+3592HpaI	L3408 5'-CTAGGCTATATACTACTACGC H3701 5'-AGATTGTTTGGGCTACTGCTCGCAGTG	341	50
M	+10397AluI	L10290 5'-TCCTTTTACCCCTACCATGAG H10557 5'-TTCCTTCTAGGCATAGTAG	305	52
N	+10871MnII	L10765 5'-CTAAA CCTACTCCAA TGCTA H11009 5'-GATAGTGGTTCACTGGATAA	282	52
JT	-11251 Tsp509I	L11163 5'-CTT GGC TAT CAT CAC CCG H11402 5'-ACA TGG GCT TTA GGG AGT CA	276	52
HV	-14766MseI	L14640: 5'ACCCACAAACCCCACTACT H14837 5' AGGAGTGAGCCGAAGTTTCA	238	50
LAPS				
mtDNA marker	Restriction sites	Primers	Amplicon (bp)	Annealing temperature
150T	-147 FokI	L15: 5' CACCCTATTAACCACTCACG 3' H389: 5' CTGGTTAGGCTGGTGTAGG 3'	375	50
5178A	-5176AluI	L5170 5'-CTACTACTATCTCGCACCTG H5464 5'-GTAGGAGTAGCGTGGTAA	331	52
9055A	-9052HhaI	L8845 5'-CC TAGCCATGGC CATCC H9161 5'-GGCTTACTAGAAGTGTGAAAACGT	356	52
10398G	+10394DdeI	L10290 5'-TCCTTTTACCCCTACCATGAG H10557 5'-TTCCTTCTAGGCATAGTAG	305	52
16000A	+16000HinfI	L15996 5' CTCCACCATTAGCACCCAAAGC H16401 5' TGATTTACGGAGGATGGTG	446	60
16069T	-16065HinfI	L15996 5' CTCCACCATTAGCACCCAAAGC H16401 5' TGATTTACGGAGGATGGTG	446	60
16390A	+16389HinfI	L16310 5'-CCACCCTTAACAGTACATAG H16543 5'-ATGTCTTATTTAAGGGGAAC	272	48

Tab. S2. HVSI sequences, RFLP haplotypes and the haplogroups of Atenas samples. Sequence data in phylip format are available from the Authors upon request.

HG ^a		HVSI ^b	RFLPs ^c
A	HL007	111 223 290 319 362	663G 10871C
A	HL013	111 223 290 319 362	663G 10871C
A	HL018	111 223 290 319 362	663G 10871C
A	HL035	111 223 290 319 362	663G 10871C
A	HL039	111 223 290 319 362	663G 10871C
A	HL052	111 223 290 319 362	663G 10871C
A	HL054	111 223 290 319 362	663G 10871C
A	HL058	111 223 290 319 362	663G 10871C
A	HL064	111 223 290 319 362	663G 10871C
A	HL069	111 223 290 319 362	663G 10871C
A	HL082	111 223 290 319 362	663G 10871C
A	HL089	111 223 290 319 362	663G 10871C
A	HL091	111 223 290 319 362	663G 10871C
A	HL107	111 223 290 319 362	663G 10871C
A	HL122	111 223 290 319 362	663G 10871C
A	HL141	111 223 290 319 362	663G 10871C
A	HL145	111 223 290 319 362	663G 10871C
A	HL150	111 223 290 319 362	663G 10871C
A	HL151	111 223 290 319 362	663G 10871C
A	HL110	111 223 290 319 362	663G 10871C
A	HL032	085 111 223 290 319 362	663G 10871C
A	HL031	111 136 223 290 319 362	663G 10871C
A	HL002	111 136 223 290 319 324 362	663G 10871C
A	HL026	111 136 223 290 319 324 362	663G 10871C
A	HL028	111 136 223 290 319 324 362	663G 10871C
A	HL053	111 136 223 290 319 324 362	663G 10871C
A	HL072	111 136 223 290 319 324 362	663G 10871C
A	HL120	111 136 223 290 311 319 362	663G 10871C
A	HL073	111 136 223 290 311 319 327 362	663G 10871C
A	HL084	111 136 223 290 311 319 327 362	663G 10871C
A	HL029	111 175 185 290 319 362	663G 10871C
A	HL094	111 175 185 290 319 362	663G 10871C
A	HL105	111 175 290 300 319 362	663G 10871C
A	HL033	111 223 224 290 300 319 325 362	663G 10871C
A	HL043	111 223 224 290 300 319 325 362	663G 10871C
A	HL075	111 220 223 290 299 319 362	663G 10871C
A	HL079	111 223 290 299 319 362	663G 10871C
A	HL152	111 223 290 299 319 362	663G 10871C
A	HL080	92 111 185 215 223 290 319 362	663G 10871C
A	HL062	111 172 187 223 290 319 362	663G 10871C
A	HL003	111 187 189 223 290 319 352 362	663G 10871C
A	HL009	111 187 189 223 290 319 352 362	663G 10871C
A	HL010	111 187 189 223 290 319 352 362	663G 10871C
A	HL017	111 187 189 223 290 319 352 362	663G 10871C
A	HL022	111 187 189 223 290 319 352 362	663G 10871C
A	HL024	111 187 189 223 290 319 352 362	663G 10871C
A	HL034	111 187 189 223 290 319 352 362	663G 10871C
A	HL050	111 187 189 223 290 319 352 362	663G 10871C
A	HL055	111 187 189 223 290 319 352 362	663G 10871C
A	HL081	111 187 189 223 290 319 352 362	663G 10871C
A	HL085	111 187 189 223 290 319 352 362	663G 10871C
A	HL103	111 187 189 223 290 319 352 362	663G 10871C
A	HL117	111 187 189 223 290 319 352 362	663G 10871C
A	HL124	111 187 189 223 290 319 352 362	663G 10871C
A	HL134	111 187 189 223 290 319 352 362	663G 10871C
A	HL138	111 187 189 223 290 319 352 362	663G 10871C
A	HL148	111 187 189 223 290 319 352 362	663G 10871C

A	HL065	111 223 290 319 360 362	663G 10871C
A	HL076	111 223 290 319 360 362	663G 10871C
A	HL093	111 223 253 290 319 360 362	663G 10871C
A	HL100	111 209 223 290 319 360 362	663G 10871C
A	HL144	111 209 223 290 319 360 362	663G 10871C 150T
A	HL129	111 150 223 290 319 360 362	663G 10871C
A	HL139	111 150 223 290 319 360 362	663G 10871C
A	HL011	111 223 290 319 360 362 381	663G 10871C
A	HL066	111 223 290 319 360 362 381	663G 10871C
A	HL099	111 223 290 319 360 362 381	663G 10871C
A	HL101	111 223 290 319 360 362 381	663G 10871C 150T
A	HL102	111 223 290 319 360 362 381	663G 10871C
A	HL127	111 223 290 292 319 356 362	663G 10871C
A	HL135	111 223 290 292 319 356 362	663G 10871C
A	HL106	111 169 223 319 362	663G 10871C
B	HL014	183C 189 217	9bpDel 10871C
B	HL019	183C 189 217	9bpDel 10871C
B	HL023	183C 189 217	9bpDel 10871C
B	HL036	183C 189 217	9bpDel 10871C
B	HL037	183C 189 217	9bpDel 10871C
B	HL038	183C 189 217	9bpDel 10871C
B	HL045	183C 189 217	9bpDel 10871C
B	HL048	183C 189 217	9bpDel 10871C
B	HL056	183C 189 217	9bpDel 10871C
B	HL059	183C 189 217	9bpDel 10871C
B	HL070	183C 189 217	9bpDel 10871C
B	HL077	183C 189 217	9bpDel 10871C
B	HL078	183C 189 217	9bpDel 10871C
B	HL086	183C 189 217	9bpDel 10871C
B	HL087	183C 189 217	9bpDel 10871C
B	HL088	183C 189 217	9bpDel 10871C
B	HL090	183C 189 217	9bpDel 10871C
B	HL104	183C 189 217	9bpDel 10871C
B	HL111	183C 189 217	9bpDel 10871C
B	HL113	183C 189 217	9bpDel 10871C
B	HL114	183C 189 217	9bpDel 10871C
B	HL116	183C 189 217	9bpDel 10871C
B	HL118	183C 189 217	9bpDel 10871C
B	HL128	183C 189 217	9bpDel 10871C
B	HL131	183C 189 217	9bpDel 10871C 5178A
B	HL137	183C 189 217	9bpDel 10871C
B	HL001	183C 189 201 217	9bpDel 10871C
B	HL012	168 183C 189 217	9bpDel 10871C
B	HL046	183C 189 217 278	9bpDel 10871C
B	HL049	183C 189 217 311 362	9bpDel 10871C
B	HL071	183C 189 217 362	9bpDel 10871C
B	HL126	183C 189 217 362	9bpDel 10871C
B	HL051	051 086 183C 189 217	9bpDel 10871C
B	HL097	183C 189 217	9bpDel 10871C
B	HL098	183C 189 217 344	9bpDel 10871C
B	HL142	114 168 183C 189 217	9bpDel 10871C 5178A
B	HL149	183C 189 217 335	9bpDel 10871C
B	HL004	182C 183C 189 217	9bpDel 10871C
B	HL005	182C 183C 189 217	9bpDel 10871C
B	HL006	182C 183C 189 217	9bpDel 10871C
B	HL015	182C 183C 189 217	9bpDel 10871C
B	HL020	182C 183C 189 217	9bpDel 10871C
B	HL027	182C 183C 189 217	9bpDel 10871C
B	HL041	182C 183C 189 217	9bpDel 10871C
B	HL074	182C 183C 189 217	9bpDel 10871C
B	HL083	182C 183C 189 217	9bpDel 10871C

B	HL109	182C 183C 189 217	9bpDel 10871C
B	HL112	182C 183C 189 217	9bpDel 10871C
B	HL125	182C 183C 189 217	9bpDel 10871C
B	HL133	182C 183C 189 217	9bpDel 10871C
B	HL136	182C 183C 189 217	9bpDel 10871C
B	HL025	093 175 182C 183C 189 217	9bpDel 10871C
B	HL067	182C 183C 189 217	9bpDel 10871C
B	HL030	182C 183C 189 217 298	9bpDel 10871C
B	HL008	131 182C 183C 189 217 298	9bpDel 10871C
B	HL115	182C 183C 189 217 298	9bpDel 10871C
B	HL123	182C 183C 189 217 298	9bpDel 10871C
B	HL092	183C 189 217	9bpDel 10871C
C	HL016	298 325 327	13263G 10398G
C	HL096	129 189 223 298 325 327	13263G 10398G
D	HL047	183C 189 223 325 362	5178A 10398G
D	HL108	183C 189 223 325 362	5178A 10398G 9bpDel
D	HL130	183C 189 223 325 362	5178A 10398G
H	HL021	CRS	10871C 14766C
H	HL042	CRS	10871C 14766C
H	HL044	CRS	10871C 14766C
H	HL060	CRS	10871C 14766C
H	HL063	CRS	10871C 14766C
H	HL068	CRS	10871C 14766C
H	HL119	CRS	10871C 14766C
H	HL132	CRS	10871C 14766C
H	HL147	CRS	10871C 14766C
H1b	HL121	129 182C 183C 189 355 356 362	10871C 14766C
H1b	HL140	129 182C 183C 189 355 356 362	10871C 14766C
H1b	HL143	129 182C 183C 189 355 356 362	10871C 14766C 5178A
J	HL040	069 126 145 231 261	10871C 11251G 150T 10398G 16069T
J	HL057	069 126	10871C 11251G 10398G 16069T
J	HL061	069 126	10871C 11251G 10398G 16069T
J	HL146	069 126	10871C 11251G 10398G 16069T
L4g	HL095	086 129 169 172 189 192 223 261 278 293 311 360	150T 10398G

a: haplogroup assignments

b: mtDNA HVSI sequences. Mutation sites are -16000.

c: status of binary markers outside and inside mtDNA coding region. Polymorphisms associated with unusual longevity (LAPs) are highlighted in bold