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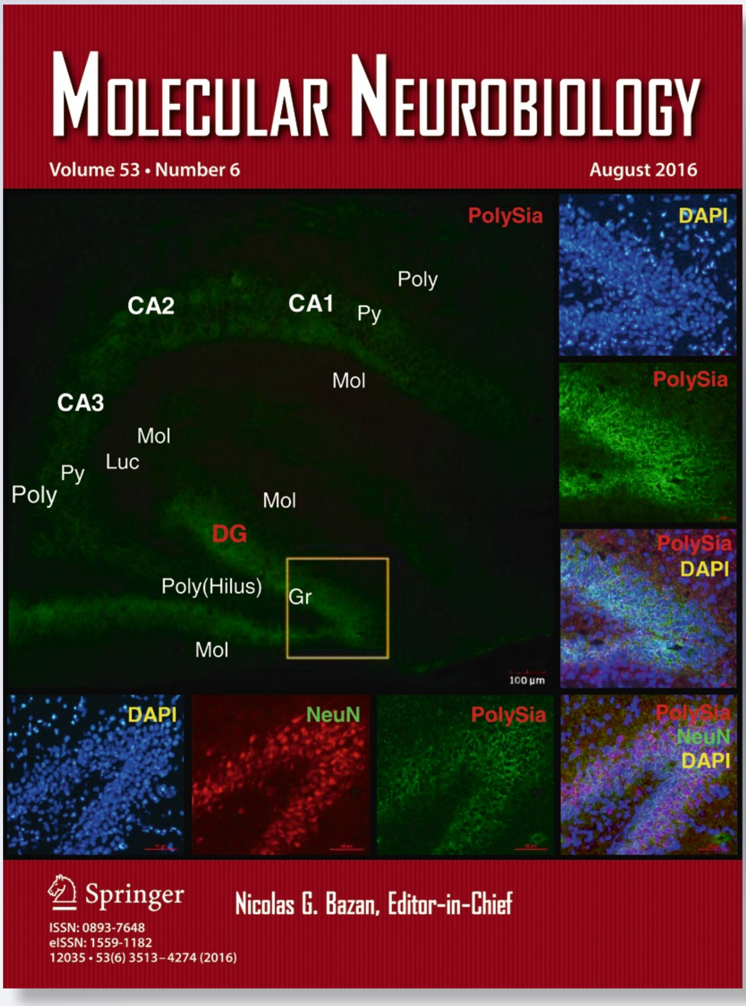
Molecular Neurobiology

ISSN 0893-7648
Volume 53
Number 6

Mol Neurobiol (2016) 53:3873-3881
DOI 10.1007/s12035-015-9323-y



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Mitochondrial DNA Haplogroup A Decreases the Risk of Drug Addiction but Conversely Increases the Risk of HIV-1 Infection in Chinese Addicts

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Received: 1 April 2015 / Accepted: 24 June 2015 / Published online: 11 July 2015

Abstract Drug addiction is one of the most serious social problems in the world today and addicts are always at a high risk of acquiring HIV infection. Mitochondrial impairment has been reported in both drug addicts and in HIV patients undergoing treatment. In this study, we aimed to investigate whether mitochondrial DNA (mtDNA) haplogroup could affect the risk of drug addiction and HIV-1 infection in Chinese. We analyzed mtDNA sequence variations of 577 Chinese intravenous drug addicts (289 with HIV-1 infection and 288 without) and compared with 2 control populations (n=362 and n=850). We quantified the viral load in HIV-1-infected patients with and without haplogroup A status and investigated the potential effect of haplogroup A defining variants m.4824A>G and m.8794C>T on the cellular reactive oxygen species (ROS) levels by using an allotopic expression assay. mtDNA haplogroup A had a protective effect against drug addiction but appeared to confer an increased risk of HIV infection in addicts. HIV-1-infected addicts with haplogroup A had a trend for a higher viral load, although the mean viral load was similar between carriers of haplogroup A and those with other haplogroup. Hela cells overexpressing allele m.8794 T showed significantly decreased ROS levels as compared to cells with the allele m.8794C (P=0.03). Our results suggested that mtDNA haplogroup A might protect against drug addiction but increase the risk of HIV-1 infection. The contradictory role of haplogroup A might be caused by an alteration in mitochondrial function due to a particular mtDNA ancestral variant.

Keywords Drug addiction · mtDNA haplogroup · HIV-1 infection · Chinese

Introduction

Drug addiction is a condition with a complex etiology and one of the most serious social problems in the world today. The condition causes damage to the central nervous system and leads to marked mental illness and behavioral abnormalities [1]. There is increasing evidence that suggests drug addiction is the result of both genetic and environmental factors [2–4]. Injecting drug users (IDUs), who abuse addictive drugs (such as heroin and other opioids) by intravenous injection, also have a very high risk of contracting human immunodeficiency virus (HIV) infection, which, if untreated, causes acquired immunodeficiency syndrome (AIDS) and progressive failure of the human immune system [5]. It is also to be

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A-Mei Zhang and Qiu-Xiang Hu contributed equally to this work.

Electronic supplementary material The online version of this article (doi:10.1007/s12035-015-9323-y) contains supplementary material, which is available to authorized users.

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noted that in the general population, there are some genetic factors which confer varying levels of resistance to HIV-1 infection and subsequent pathology [6, 7].

Mitochondria have a variety of important functions in the cell, such as energy production, antiviral innate immune signaling, and regulation of calcium [8–10]. Because the human brain needs a plentiful supply of energy to maintain neuronal structure and function, mitochondrial dysfunction (which can cause energy depletion, superoxide overproduction, metabolic imbalance, and disturbed signaling transmission) may be involved in many neurological disorders [11]. As a brain disease, the development of drug addiction may be accompanied by alterations in mitochondrial morphological structure and by other pathological changes, such as reduction in mtDNA copy number [12], and increased cell apoptosis mediated by a mitochondrial pathway [13]. Similarly, the antiviral role of mitochondria in human infectious diseases has been given more and more attention in recent years [14, 15]. Mitochondria are a common target of nucleoside analog reverse transcriptase inhibitor (NRTI) toxicity in multiple tissues during HIV treatment with NRTI antiretroviral drugs [16]. Overall, it appears that drug addiction and HIV treatment interact with mitochondria in many different ways.

Mitochondria have their own genetic molecule, mtDNA, which encodes 13 subunits of the oxidative phosphorylation complexes. The mitochondrial genetic background, or more simply termed, the mtDNA haplogroup described as a group of mtDNA lineages sharing a string of ancestral variants, has been linked to many diseases, such as Leber hereditary optic neuropathy [17, 18], leprosy [19], sepsis [20], and AIDS progression [21, 22]. However, a number of these studies had a high incidence of false positive associations due to various errors, and rigorous methodological and statistical standards in mtDNA genetic association studies should be performed to avoid any false positive associations between mtDNA variants and neurological diseases or between mtDNA variants and cancer (cf. [23–25]). We hypothesize that the inherited mtDNA haplogroup may affect the risk of drug addiction and the subsequent risk of acquiring HIV-1 infection. In this study, we have compared the distribution of the mtDNA haplogroups in IDUs, with and without HIV-1 infection, and subjects from the general populations of Yunnan Province of Southwest China, to investigate the potential effect of mtDNA haplogroup on drug addiction and HIV-1 infection. Our results showed that haplogroup A plays a protective role in drug addiction but also confers an increased genetic susceptibility to HIV-1 infection in the drug addicts who do belong to haplogroup A. The role of haplogroup A in drug addiction and HIV-1 infection might be caused by the ancient variant m.8794C>T which alters an amino acid in the mtDNA gene, *MT-ATP6*.

Materials and Methods

Subjects

The 577 IDUs (259 IDUs Dai Chinese and 318 IDUs Han Chinese; all addicted to heroin) and the 362 geographically and ethnically matched normal individuals (Control #1) were collected from Lincang and Dehong, Yunnan Province. The controls were adult individuals who had visited the local hospitals for physical examinations and were identified as not having drug addiction, nor HIV-1 infection. More than 95 % of IDUs (552/577) were males. Among them, 289 of the 577 IDUs were identified as being infected with HIV-1. The mean age of the IDUs was 32.1±7.7 years. All the subjects in this study were genetically unrelated. We also included a group of 850 healthy individuals from Yuxi, Yunnan Province [19] as another normal control population (Control #2). Written informed consents conforming to the tenets of the Declaration of Helsinki were obtained from each participant prior to the study. The institutional review boards of the Kunming Institute of Zoology approved this study.

mtDNA Sequencing and Haplogroup Classification

Genomic DNA was isolated from each whole blood sample by using Blood Genomic DNA Miniprep Kit (Axygen, USA). The mtDNA control region of each sample was amplified and directly sequenced according to the method described in our previous study [17, 18]. In brief, we identified sequence variations relative to the revised Cambridge Reference Sequence (rCRS) [26] and classified each individual by their respective haplogroup based on the control region information. The variants in each mtDNA sequence and haplogroup status were further checked by using the MitoTool (www.mitotool.org) [27]. We further genotyped m.5178C>A by using the RFLP approach (*Alu*I) to justify the predicted status of haplogroup D [17].

Quantification of the HIV-1 Viral Load

The HIV-1 viral load in the plasma of the IDUs was detected by using Quantitative Diagnostic Kit for Human Immunodeficiency Virus (HIV-1) RNA (RT-PCR-Fluorescent Probing) (QIAGEN, China) according to the manufacturer's instructions. Briefly, after viral RNA was extracted from plasma, a 25 μL reaction volume containing 7.5 μL of RNA extract was run in the 7500 Fast Real-Time PCR system (Applied Biosystems, USA). According to the manufacturer, results are recorded in copies/mL; one International Unit/mL is defined to be equivalent to 0.6 copies/mL. The lower detection limit of this quantitative method was 300 copies/mL (500 IU/mL). In further analysis, HIV-1 RNA was log10-transformed, making the lower detection limit 2.47 log10 copies/mL.

Allotopic Expression of Haplogroup A Defining Variants m.4824A>G and m.8794C>T

The pCMV/myc/mito vector with the wild-type MT-ND2 (nuclear-encoded) was a gift from Dr. Califano [28]. We cloned the fragment containing the *MT-ND2* gene from this vector together with the MTS^{COX10} fragment from the pCMV-Tag 4A-ATP6 vector into Ptango-zeo vector (Bio-Atom, China) by using *Bam*HI and *Not*I digestion. The plasmid with the wild type nuclear-encoded *MT-ATP6* gene in pCMV-Tag 4A vector (pCMV-Tag 4A-ATP6) was a kind gift from Dr. Corral-Debrinski [29]. The fragment containing the *MT-ATP6* gene and the mitochondrial targeting sequence (MTS) of the *COX10* gene (MTSCOX10) was sub-cloned into FUGW vector (Addgene, England, 14883). Vectors with the haplogroup A characteristic variants m.4824A>G and m.8794C>T were constructed by site-directed mutation method, following the same procedure described in our recent study [30]. We used primers F-A4824G (5′-CCAGAGGT TGCCCAAGGCACCCCTCTGACATC-3′)/R-A4824G (5′-GATGTCAGAGGGGTGCCTTGGGCAACCTCTGG-3′) to introduce variant m.4824A>G and 8794-F (5′-CTCGGACT CCTGCCTTACTCATTTACACCA-3′)/8794-R (5′-TGGT GTAAATGAGTAAGGCAGGAGTCCGAG-3′) to introduce m.8794C>T into the respective plasmids. Vectors with the wild-type m.4824A>G or m.8794C>T were transfected into Hela cells by using FuGENE HP (Roche, Switzerland, 06366236001) according to the manufacturer's instructions. After 48 h of transfection, the ROS level was assessed in the cell following the same approach as described in our previous study [31]. In brief, transfected Hela cells were incubated with 2 μM DCFH-DA probe (Sigma-Aldrich, USA, D6883) in PBS at 37 °C for 20 min, then washed with PBS and analyzed by using flow cytometry (BD, Vantage SE, USA) at 535 nm. Hela cells without any treatment were collected as reference controls.

Statistical Analysis

The association between the mtDNA haplogroups and drug addiction was evaluated by unconditional logistic regression model, with adjustment for gender, age, and age together with gender, respectively. Pearson's chi-square test and the Yates' correction for continuity with one degree of freedom were used to assess the significance of the differences of haplogroup frequencies between the IDUs, with and without HIV infection. Note that we have re-classified or grouped the sub-haplogroups in the subjects from Control #2 that were previously reported by Wang et al. [19] relative to the hierarchical mtDNA haplogroups of the IDUs. The Mann–Whitney test (two-tailed) was used to analyze the difference of viral load in HIV-1-infected IDUs, with and without haplogroup A status. Principal component analysis (PCA) was performed based on the mtDNA haplogroup distribution frequency in order to compare the overall clustering pattern of the analyzed populations, together with other reported Chinese general populations across China ([18] and the references therein) by using POPSTR software (http://harpending.humanevo.utah.edu/popstr/). mitPower (http://bioinformatics.cesga.es/mitpower/), a web-based tool to estimate the statistical power in mitochondrial disease studies, in particular with a consideration of different disease scenarios, variable sample sizes in cases and controls, and variable number of haplogroups and effect sizes [32], was used to evaluate whether the analyzed sample size is sufficient to uncover the interrelation between mtDNA haplogroup and the IDUs. To avoid any potential bias, we considered the mtDNA haplogroups occurring in over 1 % of the IDUs in the analysis and only adjusted *P* values, which were calculated by the Yates' correction for continuity, as below 0.05 were considered as statistically significant. For measurement of cellular ROS level, the assay was independently performed four times. The data was normalized to the control cells and were presented as mean values with standard errors. The difference between the 2 types of transfected cells was quantified by the Student's *t*-test. All statistical analysis was performed using the SPSS package (version 16.0).

Results

Statistical Power and Principal Component Analysis

We first calculated the statistical power of the sample size in this case–control study using mitPower [32]. The statistical power was 95.8 % and 99.5 % when we compared the IDUs with Control #1 and Control #2, respectively. After pooling the two control populations together as one population, the statistical power reached 99.9 %. These results suggested that the following analysis of the haplogroup distribution frequency between the IDUs and the control samples is statistically acceptable.

The mtDNA sequence variation and the haplogroup of each subject are listed in the supplementary Table S1 (for IDUs) and Table S2 (for controls). All these mtDNA sequences have been submitted to GenBank under accession numbers KF813118-KF813694 (for the 577 IDUs) and KF813695-KF814057 (for the 362 controls). We have restricted our comparison to those mtDNA haplogroups with a frequency of over 1 %, namely with a sample size of more than 5 IDUs; resulting in 16 haplogroups for which we compared the figures of IDUs and controls. The PC map based on the haplogroup frequencies showed that the IDUs and controls in this study were clustered together, which suggested that there was no population stratification between these samples (Fig. 1).

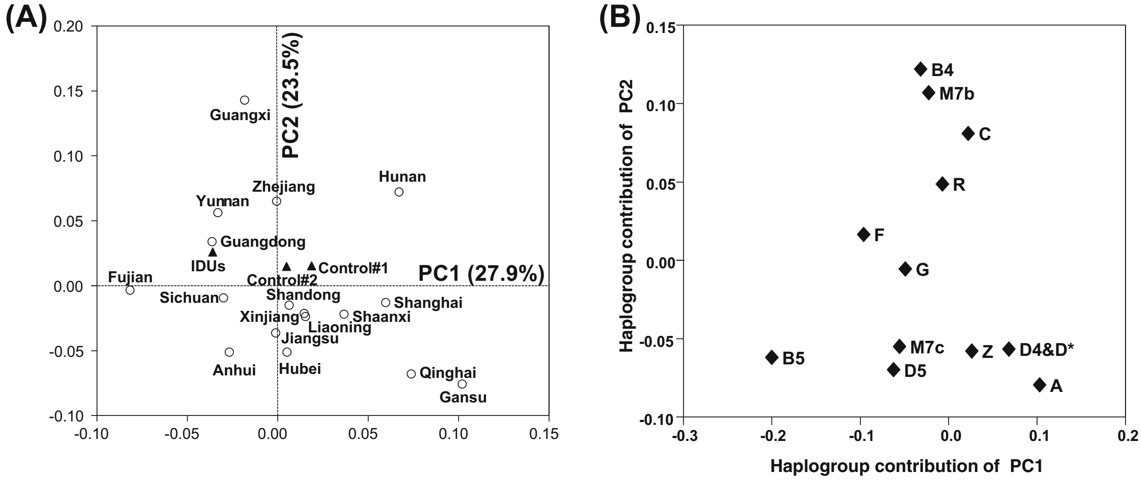

Fig. 1 Principal component analysis. Principal component analysis of injecting drug addicts (IDUs), control populations from Yunnan (Control #1 in this study and Control #2 in Wang et al. [19]), and reported Han Chinese populations across China. **a** PC map of Chinese regional populations based on the mtDNA haplogroup frequencies (>1 %). IDUs and two control populations were marked by *black triangles*, whereas the reported Han Chinese populations ([18] and references therein) were marked by *open circles*. **b** Plot of the haplogroup contribution to the first and second PCs

Haplogroup Distribution in IDUs and Controls

The mtDNA haplogroup distribution frequencies of the IDUs (n=577), Control #1 (n=362), and Control #2 (n=850) are listed in Table 1 and supplementary Table S3. When the IDUs were compared with Control #1, we found that haplogroup A offers a protective role against drug addiction after adjustment of age (adjusted P value=0.011) and gender (adjusted P value=0.009), respectively. But the significant difference disappeared when adjustment of age together with gender was considered.

The difference of haplogroup A still existed when we compared the IDUs with Control #2 (adjusted P value=0.001 for age, and adjusted P value=0.019 for gender adjustment), also two more haplogroups showed a statistical difference between the two populations (haplogroup M7c, adjusted P value is 0.020, 0.023, and 0.031 for age, gender, and age together with gender, respectively; haplogroup Z, adjusted P value is 0.021, 0.027, and 0.045 for age, gender, and age together with gender, respectively). When we pooled the two control populations, the association of haplogroup A with drug addiction was even more robust (adjusted P value is 0.00038, 0.003, and 0.018 for age, gender, and age together with gender, respectively; supplementary Table S3).

As half of IDUs carried HIV-1 (n=289), we next compared the mtDNA haplogroup distributions in IDUs with and without HIV-1 (Table 2), to see whether the inheritance of the mtDNA haplogroup increased or decreased the risk of HIV-1 infection in IDUs. There was a statistical power of 78.8 % in these sub-grouped samples due to the limited number of individuals (289 IDUs with HIV-1 and 288 IDUs without HIV-1). Intriguingly, we found that haplogroup A had a higher frequency in IDUs with HIV-1 infection (6.23 %; 18/289) than in IDUs without HIV-1 infection (2.43 %; 7/288) (adjusted P value=0.042, OR=2.666, 95 % CI=1.096–6.485; Table 2) and predisposed to a 2.67-fold risk for HIV-1 infection in drug addicts.

Comparison of Viral Load in HIV-1 Infected IDUs with and without Haplogroup A Status

As mtDNA haplogroup A showed a protective effect on drug addiction but an increased risk of HIV-1 infection in IDUs, we conducted further tests to see whether this haplogroup influenced the viral load in HIV-1-infected IDUs. First, we screened the samples from the HIV-1 infected IDUs belonging to haplogroup A (n=14) and non-A (n=20) for their viral load, finding 7 IDUs who had undetectable viral load (<2.47 $\log_{10}$ copies/mL), but with only one belonging to haplogroup A. These observations suggested that haplogroup A might have a trend for a higher viral load. Next, we looked at only the IDUs who had shown a definite viral load and found that the mean viral load in HIV-1-infected IDUs with haplogroup A (n=13, mean value, 5.19 $\log_{10}$ copies/mL; range, <2.47–5.87 $\log_{10}$ copies/mL) was slightly higher than those belonging to other haplogroups (n=14, mean value, 4.86 log10 copies/mL; range, <2.47–5.5 log10 copies/mL) (Fig. 2). However, the overall difference was not statistically significant (P value=0.9034), possibly because of the limited number of samples considered by the analysis.

ROS Levels in Hela Cells Overexpressing Variants m.4824A>G and m.8794C>T

ROS Levels were detected at 48 hours after transfection. Hela cells overexpressing the *MT-ATP6* gene with allele m.8794 T

Table 1 Haplogroup frequencies in injecting drug addicts and normal controls from Yunnan, Southwest China

Haplogroup	IDUs (*n*=577) No. (%)	Control #1 (*n*=362) No. (%)	Control #2 (*n*=850) No. (%)	IDUs versus Control #1				IDUs versus Control #2		
				Adjusted *P* value[a]	Adjusted *P* value[b]	Adjusted *P* value[c]	Adjusted *P* value[d]	Adjusted *P* value[a]	Adjusted *P* value[b]	Adjusted *P* value[c]
A	25 (4.3)	36 (9.9)	80 (9.4)	0.011	0.009	0.075	0.124	0.001	0.019	0.062
B4	61 (10.6)	32 (8.8)	100 (11.8)	0.543	0.499	0.357	0.706	0.253	0.123	0.296
B5	44 (7.6)	20 (5.5)	43 (5.1)	0.668	0.603	0.47	0.529	0.386	0.546	0.688
C	26 (4.5)	21 (5.8)	45 (5.3)	0.153	0.127	0.151	0.306	0.374	0.974	0.96
D4	63 (10.9)	51 (14.1)	100 (11.8)	0.011	0.770	0.546	0.207	0.139	0.249	0.171
D5	16 (2.8)	8 (2.2)	28 (3.3)	0.829	0.645	0.739	0.445	0.284	0.218	0.121
F	121 (21.0)	62 (17.1)	154 (18.1)	Reference	Reference	Reference	Reference	Reference	Reference	Reference
G	31 (5.4)	19 (5.2)	53 (6.2)	0.522	0.982	0.979	0.756	0.312	0.606	0.568
M12	8 (1.4)	1 (0.3)	6 (0.7)	0.266	0.016	0.024	0.187	0.257	0.124	0.099
M71	6 (1.0)	3 (0.8)	9 (1.1)	0.712	0.616	0.393	0.876	0.717	0.761	0.753
M7b	39 (6.8)	20 (5.5)	39 (4.6)	0.891	0.364	0.321	0.863	0.631	0.441	0.638
M7c	14 (2.4)	1 (0.3)	8 (0.9)	0.368	0.247	0.292	0.75	0.020	0.023	0.031
N10	6 (1.0)	5 (1.4)	1 (0.1)	0.343	0.676	0.622	0.992	0.118	0.068	0.114
N21	7 (1.2)	2 (0.6)	9 (1.1)	0.740	0.463	0.603	0.266	0.834	0.824	0.719
R9	19 (3.3)	11 (3.0)	18 (2.1)	0.908	0.253	0.375	0.629	0.446	0.305	0.238
Z	6 (1.0)	8 (2.2)	24 (2.8)	0.253	0.085	0.221	0.296	0.021	0.027	0.045
Others [e]	85 (14.7)	62 (17.1)	133 (15.6)	0.218	0.151	0.369	0.304	0.114	0.301	0.263

Note: All data were calculated by using the unconditional logistic regression; the most popular haplogroup F was selected as the reference

[a] *P* value with an adjustment of age

[b] *P* value with an adjustment of gender

[c] *P* value with an adjustment of age and gender

[d] *P* value with an adjustment of nationality

[e] "Others" contains mtDNA haplogroups with a relatively low frequency (each is shared by less than 6 IDUs) and those individuals with unassigned haplogroup status, such as M*, N*, and R*

had an increased level of ROS compared with cells overexpressed allele m.8794C (*P*-value=0.037) (Fig. 3), suggesting that this ancient variant has an impact on mitochondrial function. We observed no difference between Hela cells overexpressing the *MT-ND2* gene with allele m.4824A and allele m.4824G.

Discussion

The mtDNA haplogroup background was formed during the peopling of modern humans across the world [33, 34] and evidence has steadily been accumulating to show that the maternal genetic background affects disease expression [18, 20, 35, 36], albeit there are also some potentially false positive reports (cf. [23–25]). In this study, we have attempted to show whether the mtDNA haplogroup of a person confers a genetic susceptibility to drug addiction and HIV-1 infection in Chinese individuals from Southwest China. We found that haplogroup A has a protective role against drug addiction but confers a genetic susceptibility to HIV-1 infection in the drug addicts with this haplogroup. This result was unexpected, especially considering the seemingly contradictory effects. Although the sample size analyzed in this study was of medium size, it had sufficient statistical power to discern a striking genetic effect. Unlike other haplogroups, the effect of haplogroup A was consistently robust when different control samples from Yunnan Province were considered. In addition, principal component analysis showed that the three populations (IDUs, Control #1, and Control #2) were clustered together (Fig. 1). Therefore, we do not think the current finding was caused by sampling bias or population substructure. We also found that HIV-1-infected IDUs belonging to haplogroup A showed a trend toward having a higher viral load and a lower frequency of undetectable viral load compared with those subjects belonging to other haplogroups; note that the pattern was based on the limited number of subjects available for analysis (Fig. 2). The seemingly conflicting role of haplogroup A (resistance to drug addiction and vulnerability to HIV-1 infection) may serve as a good example for a trade-off theory, in which evolution has shaped the matrilineal genetic background, carrying evolutionary changes that can lead

Table 2 Haplogroup frequencies in injecting drug addicts, with and without HIV-1 infection

Haplogroup	IDUs with HIV-1 (*n*=289) No. (%)	IDUs without HIV-1 (*n*=288) No. (%)	*P* value[a]	Adjusted *P* value[b]	OR (95 % CI)
A	18 (6.2)	7 (2.4)	0.025	0.042	2.666 (1.096–6.485)
B4	33 (11.4)	28 (9.7)	0.508	0.598	1.197 (0.703–2.038)
B5	22 (7.6)	22 (7.6)	0.990	0.885	0.996 (0.539–1.842)
C	12 (4.2)	14 (4.9)	0.682	0.834	0.848 (0.385–1.866)
D4	30 (10.4)	33 (11.5)	0.678	0.778	0.895 (0.530–1.511)
D5	5 (1.7)	11 (3.8)	0.126	0.202	0.443 (0.152–1.293)
F	64 (22.1)	57 (19.8)	0.487	0.554	1.153 (0.772–1.722)
G	16 (5.5)	15 (5.2)	0.861	0.992	1.067 (0.517–2.200)
M12	4 (1.4)	4 (1.4)	0.996	0.726	0.996 (0.249–4.023)
M71	1 (0.3)	5 (1.7)	0.100	0.217	0.197 (0.023–1.693)
M7b	15 (5.2)	24 (8.3)	0.133	0.181	0.602 (0.309–1.173)
M7c	6 (2.1)	8 (2.8)	0.584	0.782	0.742 (0.254–2.166)
N10	2 (0.7)	4 (1.4)	0.409	0.678	0.495 (0.090–2.723)
N21	6 (2.1)	1 (0.3)	0.058	0.129	6.085 (0.728–50.866)
R9	10 (3.5)	9 (3.1)	0.822	0.994	1.111 (0.445–2.776)
Z	3 (1.0)	3 (1.0)	0.997	0.685	0.997 (0.199–4.979)
Others[c]	42 (14.5)	43 (14.9)	0.893	0.987	0.969 (0.611–1.535)

[a] *P* value was calculated by Pearson's chi-square test

[b] Adjusted *P* value was calculated by the Yates' correction for continuity

[c] "Others" contains mtDNA haplogroups with a relatively low frequency (each is shared by less than 6 IDUs) and those individuals with unassigned haplogroup status, such as M*, N*, and R*

to an increase in fitness by raising resistance to drug addiction, while at the same time making the same group of people more susceptible to HIV-1 infection.

Indeed, when we checked the ancestral variations that define haplogroup A, we found two non-synonymous ancestral variants, m.4824A>G (p.T119A) and m.8794C>T (p.H90Y) [34], which are located in the *MT-ND2* gene and the *MT-ATP-6* gene, respectively. The ND2 protein is a component of the oxidative phosphorylation complex I which plays a very important role in the respiratory chain, and the non-synonymous variants, such as under consideration here, in the ND2 protein may lead to disorders [37, 38]. However, we found no change of ROS levels in the cells overexpressing either the ND2 protein bearing allele m.4824A or allele m.4824G (Fig. 3). This negative result could have been the result of suboptimal experimental conditions, due to a low level of allotopic expression and/or the importability of peptides into mitochondria caused by hydrophobicity of the expressed protein [39, 40]. Nonetheless, the membrane-spanning region prediction plot showed that m.4824A>G did not change the structure of the membrane-spanning region (Fig. 3). Taking all these results together, it seemed that m.4824A>G may not be the reason for the contradictory role of haplogroup A in drug addiction and HIV infection. The *MT-ATP6* gene encodes one of the components of Complex V and has been reported to be associated with diseases, such as LHON and cancer [17, 41]. In our study, variant m.8794C>T significantly increased cellular ROS levels and slightly changed the structure of the membrane-spanning region (Fig. 3). However, whether this

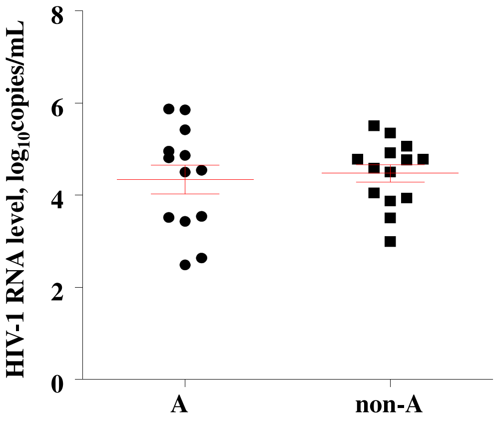

Fig. 2 Quantification of viral load in HIV-1 infected IDUs, with and without haplogroup A status. Each sample is represented by one *circle* (for HIV-1-infected IDU belonging to haplogroup A) or one *square* (for HIV-1-infected IDU not belonging to haplogroup A). The *middle line* in each group represents the mean number of the HIV-1 viral load, together with standard error of the group

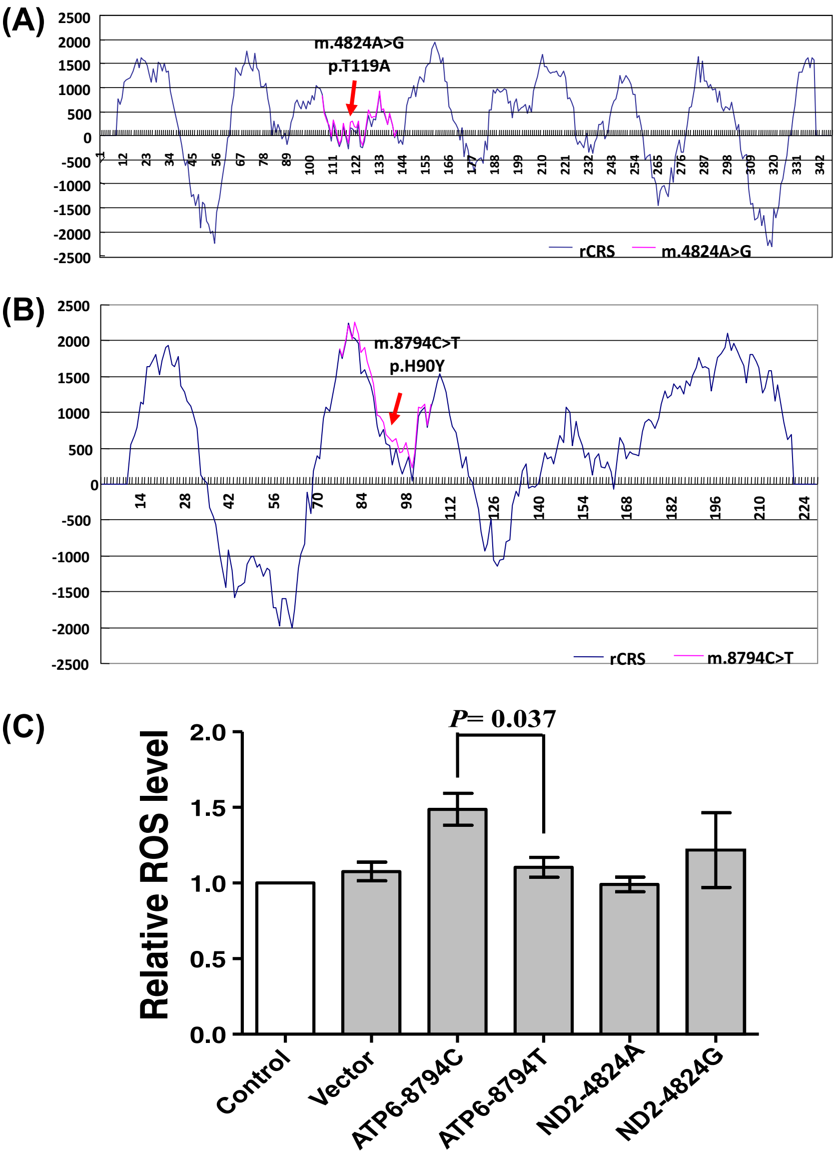

Fig. 3 Membrane-spanning region prediction plots and functional assessment of haplogroup A-specific variants. Membrane-spanning region prediction plots of the MT-ND2 and MT-ATP6 proteins bearing haplogroup A-specific variants and functional characterization of different alleles. The TMpred program (http://www.ch.embnet.org/software/TMPRED_form.html) was used to predict the membrane-spanning regions and their orientation. Variants m.4824A>G (p.T119A) did not change the structure of membrane-spanning region of MT-ND2 protein (**a**), whereas variant m.8794C>T (p.H90Y) slightly changed the structure of membrane-spanning region of MT-ATP6 protein (**b**). Cellular reactive oxygen species levels were quantified in Hela cells overexpressing haplogroup A-specific variants (**c**). Control: cells without any treatment; vector: cells transfected with empty vector; ATP-8794C and ATP-8794 T refer to cells transfected with the *MT-ATP6* gene with allele m.8794C and m.8794 T, respectively; ND2-4824A and ND2-4824G refer to cells transfected with the *MT-ND2* gene with allele m.4824A and m.4824G, respectively. Cells were incubated in PBS containing 0.5 μM DCFH-DA probe (Sigma-Aldrich) at 37 °C for 20 min, then were analyzed by flow cytometry at 535 nm. Data was presented as mean values±standard errors of multiple independent tests. Four independent tests were performed with consistent results

variant has led to the intriguing role of haplogroup A and how it has produced a complex effect were unclear. Therefore, a larger sample size and further functional verification are essential to confirm our results.

Besides haplogroup A, there were some other haplogroups (D4, Z, and M7c) that had a significant adjusted *P* value when we compared IDUs to the two control groups and the pooled control sample (Table 1 and supplementary Table S3). However, we did not observe a consistent pattern for haplogroups N10 and Z in the comparisons, and this would be better explained as being a sampling bias due to limited number of analyzed samples available instead of being a real association. Intriguingly, haplogroup M7c had a higher frequency in IDUs than in controls and increased the risk of drug addiction. This effect might be caused by the haplogroup-specific variant m.5442 T>C (p.F325L) [34]. Similar to m.4824A>G that defines haplogroup A, m.5442 T>C is located in the *MT-ND2* gene although it does not change the membrane-spanning region. Further analyses should be performed to validate the observed association and characterize the potential function of these haplogroup-defining variants.

The current study has some limitations. First, we did not validate the current finding in independent validation populations because of lack of samples [24]. Following the strategy used in other studies [23, 42] and the suggestions proposed by Salas and Elson [24], we have attempted to limit the problem by using two control groups for comparison with the IDU group; a very useful method for the detection of potential population substructures leading to false positive findings [42]. We did not include a Bonferroni correction for all the comparisons, as this stringent test might miss a true association with a relatively weak genetic effect and the result always carries the risk of increasing the probability of type I error [43]. Indeed, the significant associations of mtDNA haplogroup with drug addiction or HIV-1 infection do not survive the Bonferroni correction or other corrections for multiple tests, e.g. false discovery rate. This suggests that our results should be received with caution and further validation using independent cohorts is needed. Nonetheless, the statistical power is very favorable to the conclusions and compensates for the stringency of the multiple test correction. Second, we did not have good clinical information for the IDUs with HIV-1 infection, and this prevented us from looking further into the possible effects of haplogroup, on gender and age on HIV-1 infection and AIDS progression. The quantification of viral load in HIV-1-infected IDUs, with and without haplogroup A, in this study was also restricted by the limited number of samples available for the test. Finally, we showed evidence that the haplogroup A characteristic variant m.8794C>T alters cellular ROS levels, but whether this effect has a role in the resistance to drug addiction and susceptibility to HIV-1 infection remains to be clarified.

Conclusion

In summary, we identified that the inheritance of mtDNA haplogroup A had a protective role in drug addiction but conferred a genetic susceptibility to HIV-1 infection in IDUs from Yunnan, Southwest China. These results are consistent with a trade-off theory of evolution, and the effect might be mediated by the ancient variant m.8794C>T, that along with other variants defines haplogroup A. Independent studies are necessary to validate our current findings.

Acknowledgments We thank all participants in this study. We thank Dr. Califano and Dr. Corral-Debrinski for sharing the plasmids and Miss Dandan Yu for the technical help. This study was supported by the National Natural Science Foundation of China (grant number 31171225), the Strategic Priority Research Program (B) of the Chinese Academy of Sciences (grant number XDB02020003), and the Ministry of Science and Technology of China (grant number 2011CB910900).

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Table S1. mtDNA sequence variations and haplogroup classification of 577 injecting drug addicts from Yunnan

Sample	Gender	HIV-1 infection *	Haplogroup	Region I (16000+)	Region II	5178 *Alu*I [a]
LC040	male	-	A	223 234 290 293C 319 519	73 152 235 263 309+C 315+C 523-524d 663 750	
YJ276	male	-	A	126 235 290 319 519	73 235 263 309+C 315+C 523-524d 663 750	
LC071	male	-	A4	223 290 319 362	73 151 152 235 263 315+C 663 750	
LC072	male	+	A4	172 223 231 290 319 362	73 151 152 200 235 263 315+C 523-524d 663 735 750	
LC103	male	+	A4	86 166d 223 290 319 362	73 152 200 235 263 315+C 523-524d 663 750	
LC120	male	-	A4	93 124 223 290 319 362	73 152 200 235 263 309+CC 315+C 523-524d 663 750	
LC331	male	+	A4	124 223 245 290 319 362	73 152 200 235 263 309+C 315+C 523-524d 663 750	
LC343	male	+	A4	124 223 290 319 362	73 152 200 207 235 263 305+C 315+C 523-524d 663 750	
LC348	male	+	A4	223 290 319 362	73 151 152 200 235 263 315+C 523-524d 663 735 750	
LC363	male	+	A4	223 290 311 319	64 73 146 235 263 309+C 315+C 523-524d 663 750	-
LC374	male	+	A4	223 290 311 319	64 73 146 235 263 309+C 315+C 523-524d 663 750	-
LC381	male	+	A4	214 223 274 290 319 362 527	73 152 235 263 309+C 315+C 523-524d 663 750	-
LC398	male	+	A4	124 223 290 319 362	73 152 200 235 263 309+C 315+C 523-524d 663 750	-
LC403	male	+	A4	124 223 290 319 362	73 152 200 235 263 309+C 315+C 523-524d 663 750	-
LC411	male	-	A4	223 290 311 319 362 519	73 152 234 235 263 309+C 315+C 663 729 750	
LC419	male	-	A4	223 234 290 293C 319 519	73 152 235 263 309+C 315+C 523-524d 571 663 750	
LC425	male	+	A4	124 223 290 319 362	73 152 200 235 263 309+C 315+C 523-524d 663 750	+
LC451	male	+	A4	184A 189 223 274 290 319 362 527	73 152 235 263 315+C 523-524d 663 750	
LC462	male	+	A4	93 129 145 223 290 319 362 519	73 152 235 263 315+C 523-524d 663 750	
LC468	male	+	A4	172 223 290 319 362 519	73 152 235 263 315+C 523-524d 663 750	
LCS19	male	+	A4	223 290 311 319	64 73 146 235 263 309+C 315+C 523-524d 663 750	
LCS21	male	+	A4	223 234 278 290 293C 319 519	73 152 235 263 315+C 523-524d 663 750	
LCS39	male	+	A4	124 223 290 319 362	73 152 200 235 263 309+C 315+C 523-524d 663 750	+

LCS54	male	+	A4	189 223 290 311 319	64 73 146 235 263 309+C 315+C 523-524d 663 750	
YJ023	male	-	A4	93 129 223 284 290 319 362 519	73 152 235 263 309+C 315+C 523-524d 663 750	
RL-066	male	-	B*	51 182C 183C 189 356 519 527	73 263 315+C 356+C 750	+
YL04	male	+	B*	51 183C 189 249 519	73 150 238 249d 263 309+C 315+C 523-524d 750	+
LC004	male	-	B4	108 182C 183C 189 217 362 519	73 263 309+CC 315+C 523-524d 750	
LC031	male	+	B4	183C 189 217 362 519	73 150 195 263 315+C 392 750	+
LC146	male	-	B4	68 182C 183C 189 217 261	73 263 309+CC 315+C 523-524d 750	
LC150	male	-	B4	108 182C 183C 189 217 234 319 362 519	73 263 309+CC 315+C 523-524d 750	
LC159	male	-	B4	129 182C 183C 189 217 519	73 263 309+CC 315+C 523-524d 750	
LC196	male	-	B4	182C 183C 189 217 299 519	73 189 193 198 204 263 309+CC 315+C 523-524d 709 750	
LC391	male	+	B4	108 182C 183C 189 217 234 362 519	73 263 309+C 315+C 523-524d 750	-
LC401	male	+	B4	168 183C 189 217 261 519	73 140 263 309+C 315+C 316 750 827	
LC407	male	-	B4	178 182C 183C 217 189	73 214 263 309d 315+C 368 709 750	
LC448	male	+	B4	93 182C 183C 188 189 193+C 214 217 261 519	73 146 263 309+C 315+C 523-524d 709 750	
LC458	male	-	B4	108 182C 183C 189 217 234 362 519	73 263 309+C 315+C 523-524d 750	
LC525	male	+	B4	108 182C 183C 189 217 362G 519	73 214 263 309+C 315+C 523-524d 750	
LCS59	male	+	B4	93 182C 183C 188 189 193+C 214 217 261 519	73 146 263 309+C 315+C 523-524d 709 750	
YJ069	male	-	B4	182C 183C 189 217 299 327 519	73 182 193 204 207 263 309+CC 315+C 523-524d 709 750	-
YJ240	male	-	B4	183C 189 217 223 519	73 200h 263 309+CC 315+C 573+5C 750 827	
LC143	male	-	B4a	93 182C 183C 189 217 243 261 519	73 146 263 309+C 315+C 523-524d 709 750	
YL03	male	+	B4a	167 182C 183C 189 217 218 261 519	73 146 152 263 315+C 350C 523-524d 709 750	
LC416	male	+	B4a1c	92 182C 183C 189 217 261 299 519	73 193 263 309+C 315+C 523-524d 709 750	
YL37	male	-	B4ac1	93 182C 183C 188 189 193+C 214 217 261 519	73 146 263 309+C 315+C 523-524d 709 750	
DH272	male	+	B4a'g	93 182C 183C 189 217 261 519	73 146 263 309+CC 315+C 523-524d 709 750	+
LC015	male	-	B4a'g	93 182C 183C 189 217 261 271 519	73 263 309+C 315+C 750	
LC060	male	-	B4a'g	182C 183C 189 217 240 261	73 263 309+CC 315+C 523-524d 750	

LC379	male	+	B4a'g	182C 183C 189 217 240 261	73 263 315+C 523-524d 750	-
LC399	male	+	B4a'g	182C 183C 189 217 261 519	73 146 263 307-309d 310 315+C 523-524d 709 750	-
LC436	male	+	B4a'g	93 182C 183C 189 217 261	73 263 315+C 750	
LC532	male	+	B4a'g	93 181C 182C 183C 189 213 217 261 519	73 263 309+C 315+C 523-524d 750	
YJ108	male	-	B4a'g	181C 182C 183C 189 213 217 261 292 519	61A 62 73 263 309+CC 315+C 523-524d 750	
YL30	male	+	B4a'g	93 182C 183C 189 217 261 519	73 146 263 309+CC 315+C 523-524d 709 750	
YL40	male	-	B4a'g	93 182C 183C 189 217 261 519	73 146 263 309+CC 315+C 523-524d 709 750	-
LC338	male	+	B4b1	136 183C 189 217 260 291A 325 519	73 263 309+C 315+C 499 523-524d 750 827	
LC361	male	+	B4b1	136 182C 183C 189 217 519	73 207 263 309+CCC 315+C 499 750 827	
DH277	male	+	B4c1	182C 183C 189 311 390 399 519	73 185 189 263 309+CC 315+C 523-524d 709 750	-
YJ010	male	-	B4c1	102 182C 183C 189 311 390 399 491 519	73 185 189 263 309+CC 315+C 709 750	
LC189	male	-	B4c1b	129 140 166 179 183C 189 217 257 274 335 519	73 150 195 263 315+C 709 750	
LC347	male	+	B4c1b	129 140 166 172 183C 189 217 256 274 335 519	73 150 263 309+CC 315+C 709 750	-
RL-074	male	+	B4c1b2	140 182C 183C 189 217 242A 274 335 519	73 146 150 263 315+C 456 523-524d 709 750	+
YL39	male	+	B4c1b2	140 182C 183C 189 217 242A 274 519	73 146 150 263 315+C 456 523-524d 709 750	
LC384	male	+	B4c1c	129 182C 183C 189 214 217 311 519	73 150 195 214 263 309+C 315+C 750	-
BS177	male	+	B4c2	147 183C 184A 189 217 219 235 519	73 263 269 309+C 315+C 523-524d 750	
LC173	male	-	B4c2	147 183C 184A 189 217 519	73 263 315+C 523-524d 750	-
LC190	male	-	B4c2	147 183C 184A 189 217 235 519	73 200 263 315+C 523-524d 750	
LC354	male	+	B4c2	147 183C 184A 189 217 235 399 400 519	73 263 315+C 750	+
RL-108	male	-	B4c2	147 183C 184A 189 217 235 519	73 146 263 309+C 315+C 750	
YJ167	male	-	B4c2	147 183C 184A 189 217 235 519	73 263 309+C 315+C 750	
YJ286	male	-	B4c2	147 183C 184A 189 217 235 519	73 263 309+C 315+C 523-524d 750	
YL31	male	-	B4c2	147 182+C 189 217 234 235 519	73 263 309+C 315+C 523-524d 750	
LC414	male	+	B4e	182C 183C 189 217 223 519	73 146 185 189 195 263 307-309d 315+C 513 750 827	-
LC422	male	+	B4e	182C 183C 189 217 223 519	73 146 185 189 195 215h 263 307-309d 315+C 513 750 827	-

LC507	male	+	B4e?	182C 183C 189 217 223 519	73 146 185 189 195 263 309+CC 315+C 513 750 827	
DH587	male	+	B4g	181C 182C 183C 189 213 217 261 292 519	61A 62 73 263 309+C 315+C 523-524d 750	
LC121	male	+	B4g	181C 182C 183C 189 213 217 261 265 292 519	73 263 279 309d 315+C 523-524d 750	
LC356	male	+	B4g	129 181C 182C 183C 189 213 217 261 292 519	61A 62 73 263 309+CC 315+C 523-524d 750	
LC366	male	+	B4g	181C 182C 183C 189 213 217 261 265 292 519	73 263 279 309d 315+C 523-524d 750	
RL-112	male	+	B4g	181C 182C 183C 189 213 217 261 292 362 519	61A 62 73 182 263 309+CC 315+C 523-524d 750	
YJ008	male	-	B4g	181C 182C 183C 189 213 217 261 292 362 519	61A 62 73 182 263 309+CC 315+C 523-524d 750	
YJ038	male	+	B4g	181C 182C 183C 189 213 217 235 261 292 519	61A 62 73 263 309+CC 315+C 523-524d 750	
YJ085	male	-	B4g	181C 182C 183C 189 213 217 261 292 362 519	61A 62 73 182 263 309+CC 315+C 523-524d 750	
YJ237	male	-	B4g	181C 182C 183C 189 213 217 261 292 362 519	61A 62 73 182 263 309+CC 315+C 523-524d 750	
YJ277	male	-	B4g	181C 182C 183C 189 213 217 261 292 362 519	61A 62 73 182 263 309+CC 315+C 471 523-524d 750	+
YL20	male	-	B4g	181C 182C 183C 189 213 217 261 292 362 519	61A 62 73 182 263 309+C 315+C 523-524d 750	
YY28	male	+	B4g	181C 182C 183C 189 213 217 261 292 362 519	61A 62 73 182 263 309+CC 315+C 471 523-524d 750	
RL-106	male	-	B5	140 183C 189 266A 519	73 210 263 309+C 315+C 523-524d 709 750	
DH345	male	+	B5a	140 183C 189 266A 519	73 152 210 263 309+CC 315+C 523-524d 709 750	
LC081	male	-	B5a	140 182C 183C 189 261 266A 519	73 152 210 263 315+C 523-524d 709 750	
LC083	male	-	B5a	140 183C 189 266A 519	73 146 210 263 309+CC 315+C 523-524d 709 750	
LC104	male	-	B5a	140 183C 189 266A 519	73 210 263 315+C 523-524d 593 709 750	
LC160	male	-	B5a	92 140 183C 189 266A 519	73 210 263 309+C 315+C 523-524d 709 750	
LC183	male	-	B5a	140 182C 183C 189 261 266A 325 519	73 146 152 210 263 309+CCC 315+C 523-524d 709 750	
LC333	male	+	B5a	140 183C 189 266A 519	73 210 263 309+C 315+C 523-524d 709 750	
LC350	male	+	B5a	182C 183C 189 266A 519	73 210 263 309+C 315+C 523-524d 709 750	
LC358	male	+	B5a	140 183C 189 266A 362 519	73 210 263 309+CC 315+C 523-524d 709 750	
LC388	male	+	B5a	140 183C 189 266A 519	73 210 263 315+C 523-524d 709 750	-
LC406	male	-	B5a	140 183C 189 266A 482 519	73 210 263 309+C 315+C 523-524d 709 750	
LC412	male	+	B5a	140 183C 189 266A 519	73 210 263 315+C 523-524d 709 750	

LC454	male	-	B5a	111A 140 187 189 256 266G 519	73 93 210 263 309+C 315+C 523-524d 709 750	
LC464	male	+	B5a	140 182C 183C 189 266A 362 519	73 210 263 309+C 315+C 502 523-524d 709 750	
LC508	male	-	B5a	140 183C 189 262 266A 519	64 73 146 210 263 309+C 315+C 523-524d 593 709 750	
LC531	male	+	B5a	129 140 183C 189 266A 519	73 210 263 315+C 523-524d 709 750	
LC537	male	+	B5a	140 183C 189 243 266A 293h 359 519	73 210 263 309+CC 315+C 523-524d 709 750	
LCS10	male	+	B5a	129 140 183C 189 266A 519	73 210 263 315+C 523-524d 709 750	
LCS50	male	-	B5a	111A 140 187 189 256 266G 519	73 93 210 263 309+C 315+C 523-524d 709 750	
RL-026	male	+	B5a	111 140 183C 189 234 243 463 519	73 103 131 204 263 309+C 315+C 523-524d 709 750	+
RL-100	male	+	B5a	140 183C 189 266A	73 210 263 309+C 315+C 523-524d 709 750	
RL-101	male	-	B5a	140 183C 189 266A 519	73 210 263 315+C 523-524d 709 750	
YJ034	male	+	B5a	140 182C 183C 189 266A 362 519	73 210 263 309+CC 315+C 523-524d 709 750	
YJ065	male	+	B5a	140 183C 189 266A 519	73 210 263 309+CC 315+C 523-524d 709 750	
YJ077	male	-	B5a	140 182C 183C 189 266A 519	73 210 263 309+C 315+C 523-524d 709 750	
YJ113	male	+	B5a	140 183C 189 266A 519	73 210 263 315+C 523-524d 709 750	
YJ126	male	-	B5a	140 183C 189 266A 519	73 210 263 309+CC 315+C 523-524d 709 750	
YJ156	male	-	B5a	140 183C 189 266A 311 355 519	73 210 263 309+C 315+C 523-524d 709 750	
YJ170	male	+	B5a	140 182C 183C 189 261 266A 519	73 152 210 263 309+CC 315+C 523-524d 709 750	
YJ234	male	-	B5a	140 183C 189 266A 519	73 210 263 309+CC 315+C 523-524d 709 750	
YJ245	male	+	B5a	140 183C 189 266A 519	73 210 263 315+C 523-524d 709 750	
YJ300	male	-	B5a	140 183C 189 266A 288 519	73 210 263 309+C 315+C 523-524d 709 750	
YL14	male	-	B5a	93 140 183C 189 260 266G 519	73 210 263 294 309+C 315+C 709 750	
YL15	male	-	B5a	140 182C 183C 189 266A 362 519	73 210 263 309+CC 315+C 523-524d 709 750	
YM04	male	+	B5a	140 182C 183C 189 266A 362 519	73 210 263 309+CC 315+C 523-524d 709 750	
LC453	male	-	B5a2	92 172 182C 183C 189 223 266 362	73 150 263 309+C 315+C 489 523-524d 750 752	
LC180	male	-	B5b	140 183C 189 243 355 519	73 103 263 309+C 315+C 523-524d 709 750	
LCS46	male	-	B5b	140 183C 189 243 311 519	73 103 204 263 315+C 523-524d 709 750	

LC371	male	+	B5b2	111 140 183C 189 234 242 243 463 519	73 103 131 263 309+C 315+C 523-524d 709 750	
LC535	male	+	B5b2	111 129 140 182C 183C 189 234 243 287 463 519	73 131 263 309+CC 315+C 523-524d 709 750	
LCS22	male	+	B5b2	111 140 183C 189 234 242 243 463 519	73 103 131 263 309+C 315+C 523-524d 709 750	
LCS73	male	+	B5b2	111 140 183C 189 234 243 463 519	73 103 131 146 204 207 263 309+CC 315+C 523-524d 709 750	+
YJ132	male	-	B5b2	111 140 182C 183C 189 234 243 463 519	73 103 131 204 263 315+C 523-524d 709 750	
LCS09	male	-	B6	93 179 182C 183C 189 297 342	73 150 263 309+CC 315+C 523-524d 750	
DH352	male	+	C	93 172 223 298 327 519	73 249d 263 315+C 489 750	
LC018	male	-	C	223 298 327 519	73 146 153 249d 263 309+C 315+C 489 750	
LC088	male	-	C	223 298 327 354 357 519	47 73 249d 263 309+C 315+C 489 523-524d 750	
LC131	male	-	C	189 223 298 319 327 519	73 249d 263 309+C 315+C 489 750	+
LC149	male	-	C	93 223 298 327 519	73 249d 263 315+C 466 489 750	
LC151	male	-	C	223 298 327 519	73 146 153 249d 263 309+C 315+C 489 750	
LC156	male	-	C	223 298 327 519	73 249d 263 309+C 315+C 460 463+C 489 750	
LC387	male	+	C	183C 189 223 298 327 357 519	73 249d 263 309+CC 315+C 489 750	-
LC435	male	+	C	189 223 298 327 357 519	73 249d 263 309+C 315+C 489 750	+
LC440	male	+	C	189 223 298 327 357 519	73 249d 263 309+C 315+C 489 750	
LC492	male	+	C	183C 189 223 298 327 357 519	73 249d 263 309+CC 315+C 489 750	
LC518	male	+	C	223 298 327 519	73 146 153 249d 263 309+C 315+C 489 750	
LCS31	male	+	C	223 298 327 519	73 249d 263 309+CC 315+C 489 750	
LCS51	male	+	C	223 298 327 519	73 249d 263 309+CC 315+C 489 750	
RL-063	male	-	C	189 223 298 319 327 519	73 249d 263 309+C 315+C 489 750	
YJ001	male	-	C	51 223 298 327 519	73 195 249d 263 315+C 489 750	
YJ100	male	+	C	189 223 298 327 357 519	73 249d 263 309+C 315+C 489 750	
YJ128	male	+	C	223 298 327 519	41 73 249d 263 309+CC 315+C 489 750	+
YJ199	male	-	C	172 223 298 327	73 146 249d 263 315+C 489 750	
YJ275	male	+	C	223 266 298 327 519	73 146 249d 263 315+C 489 750	

YL36	male	+	C	148 223 298 327 519	73 152 249d 263 315+C 449 489 750	
YJ003	male	-	C4a1	129 150 223 298 327 519	73 195 249d 263 309+CC 315+C 489 750	
LC056	male	-	C4b1	223 298 327 519	73 146 153 249d 263 309+C 315+C 489 750	
YJ176	male	-	C4b1	223 266 298 327 519	73 146 249d 263 315+C 489 750	+
YJ188	male	-	C4b1	223 266 298 327 519	73 146 249d 263 315+C 489 750	
LC163	male	-	C5	223 288 298 300 327 519	73 249d 263 315+C 489 595+C 750	
DH278	male	+	D4	223 362	73 263 309+C 315+C 489 750	
DH553	male	+	D4	93 223 274 362 519	73 263 298 315+C 489 750	
LC005	male	+	D4	92 147 189h 223 362 368	73 94 263 315+C 489 750	
LC053	male	-	D4	189 192 223 316 362	73 199 263 315+C 489 750	
LC082	male	-	D4	223 362	73 263 309+C 315+C 489 750	
LC089	male	-	D4	223 362	73 152 263 309+C 315+C 489 750	-
LC100	male	-	D4	201 223 362	73 152 263 309+C 315+C 489 750	
LC124	male	-	D4	223 362	73 152 263 309+C 315+C 489 750	-
LC158	male	-	D4	189 223 316 362	73 199 263 315+C 489 750	
LC186	male	-	D4	223 294 362	64 65A 73 195 237 263 315+C 489 501 523-524d 750	-
LC187	male	-	D4	174 223 311 362	73 152 263 309+C 315+C 489 507 750	
LC334	male	+	D4	223 362	56d 58A 71+G 73 151 152 263 309+C 315+C 489 750	
LC339	male	+	D4	223 259 298 299 362	73 263 315+C 489 508 750	
LC357	male	+	D4	189 223 362 519	73 150 195 263 309+C 315+C 489 523-524d 750	
LC362	male	+	D4	189 192 223 316 362	73 199 263 315+C 489 750	
LC375	male	+	D4	111 153 223 362 519	73 182 194 200 263 309+C 315+C 489 523-524d 750	
LC376	male	+	D4	92 223 362	73 94 263 315+C 489 750	-
LC392	male	+	D4	189 192 223 316 362	73 199 263 315+C 489 750	-
LC413	male	+	D4	86 223 362	73 263 315+C 489 750	
LC415	male	+	D4	223 362	73 152 263 309+C 315+C 489 750	

LC418	male	+	D4	223 362 519	73 194 263 315+C 489 523-524d 750	-
LC459	male	+	D4	129 223 362	73 263 309+C 315+C 489 750	
LC479	male	-	D4	223 274 294 362	73 207 263 309+C 315+C 489 750	
LC519	male	+	D4	86 92 362	73 94 263 315+C 489 750	
LC523	male	+	D4	111 153 223 362 519	73 182 194 200 263 309+C 315+C 489 523-524d 750	
LC528	male	-	D4	189 192 223 316 362 519	73 199 263 315+C 489 750	
LC529	male	+	D4	126 174 223 243 343 362	73 263 315+C 489 750	-
LCS02	male	+	D4	172 223 362	73 263 309+C 315+C 489 750	
LCS82	male	-	D4	92 223 362	73 94 263 315+C 489 750	
RL-073	male	+	D4	147 174 223 311 362	73 152 263 309+C 315+C 489 513 750	+
YJ093	male	+	D4	201 223 362	73 152 263 309+C 315+C 489 750	
YJ101	male	-	D4	124 223 362	73 152 200h 263 309+C 315+C 489 750	
YJ116	male	-	D4	223 254 274 362	73 263 298 309+C 315+C 489 750	
YJ129	male	-	D4	93 223 274 362 519	73 263 298 315+C 489 750	
YJ165	male	-	D4	223 266 311 325 362 519	73 263 309+C 315+C 489 750	
YJ180	male	-	D4	126 174 223 343 362	73 263 315+C 489 513 750	
YJ192	male	-	D4	223 301 362 519	73 152 263 309+C 315+C 489 750	
YJ221	male	-	D4	174 223 311 325 362	73 152 263 309+C 315+C 489 750	
YJ296	male	-	D4	223 362	73 263 309+C 315+C 489 750	+
YY31	male	+	D4	223 362	73 263 309+C 315+C 489 750	+
LC522	male	+	D4a	129 223 362	73 152 263 309+C 315+C 489 750	
LCS57	male	+	D4a	129 223 362	73 152 263 309+C 315+C 489 750	
LCS68	male	+	D4a	129 209 223 362 519	73 152 263 309+C 315+C 489 750	
YJ182	male	-	D4b1	185 189 223 232A 311 319 362	73 263 315+C 489 523-524d 750	-
YJ255	male	+	D4b1b	223 287 319 362	73 263 309+C 315+C 431 489 523-524d 750	
LC172	male	-	D4g1	145 223 278 362	73 263 309+C 315+C 489 573+4C 750	

RL-080	male	-	D4g2	223 274 362	73 263 298 309+C 315+C 489 750	
YJ104	male	-	D4g2	223 274 362 519	73 263 298 309+C 315+C 489 750	-
YJ256	male	-	D4g2	223 274 362	73 263 298 309+C 315+C 459d 466 489 750	
LC114	male	-	D4g2a	169 223 266 274 362	73 263 298 309+CC 315+C 489 750	
LC369	male	-	D4g2a	169 223 266 274 362	73 263 298 309+C 315+C 489 750	
RL-056	male	-	D4g2a	172 223 274 362 519	73 263 298 309+CC 315+C 489 750	+
YJ012	male	+	D4g2a	169 223 266 274 362	73 263 298 315+C 489 750	
YJ040	male	-	D4g2a	169 223 266 274 362	73 263 298 315+C 489 750	
YJ235	male	-	D4g2a	169 223 266 274 362	73 263 298 315+C 489 750	
LC025	male	-	D4h4a	174 223 262+C 311 362	73 152 263 315+C 489 750	
LC515	male	-	D4h4a	223 311 362	73 152 263 309+C 315+C 489 709 750	
YJ262	male	-	D4i	223 294 362	64 65A 73 195 237 263 309+C 315+C 489 501 750	
YL29	male	+	D4i	223 294 362	64 65A 73 195 237 263 309+C 315+C 489 501 750	
LC044	male	+	D4j	184 223 234 260 292 311 335 362	73 146 263 315+C 489 750	
LC126	male	+	D4j3	184 189 223 311 362	73 146 263 315+C 489 709 750	
LC429	male	+	D4j3	184 223 311 362	73 263 309+C 315+C 338 489 750	-
RL-114	male	-	D4q	223 256 304 311 362 519	73 200 263 315+C 489 750	
LC033	male	+	D5'6	189 362 519	73 263 315+C 489 750	
LC106	male	-	D5a	93 111 182C 183C 189 223 360 362	73 150 263 309+C 315+C 489 523-524d 750 752	
LCS53	male	-	D5a	93 111 145 182C 183C 189 223 360 362	73 150 263 489 309+CC 315+C 523-524d 573+C 750 752	
YY42	male	+	D5a	92 164 182C 183C 189 223 266 278 362	73 150 263 309+CC 315+C 489 523-524d 750 752	
LC136	male	-	D5a2	164 172 182C 183C 189 223 266 362	73 150 263 309+C 315+C 489 523-524d 750 752	
LC486	male	-	D5a2	92 164 172 182C 183C 189 223 243 266 319 362	73 150 263 309+C 315+C 489 523-524d 750 752	-
LCS16	male	-	D5a2	92 172 182C 183C 189 223 266 362	73 150 263 309+C 315+C 489 523-524d 750 752	
LC038	male	-	D5a2a	129 164 182C 183C 189 223 266 362	73 150 199 263 309+CC 315+C 489 523-524d 750 752	
LC378	male	+	D5a2a	92 164 172 182C 183C 189 223 266 287 362	73 150 263 315+C 489 523-524d 750 752	-

LC437	male	+	D5a2a	92 164 172 182C 183C 189 223 266 287 362	73 150 263 315+C 489 523-524d 750 752	+
YL07	male	+	D5a2a	92 164 182C 183C 189 223 266 278 362	73 150 263 309+C 315+C 489 523-524d 750 752	-
LC070	male	-	D5b	183C 189 223 357 362 519	73 150 263 309+C 315+C 456 489 681 750	
LCS27	male	-	D5b	182C 183C 189 223 362	73 150 152 263 309+C 315+C 456 489 681 750	
LCS63	male	+	D5b	172 189 223 355 362	73 150 263 309+CC 315+C 456 489 681 750	
YJ166	male	-	D5b	92 148 182C 183C 189 223 362 519	73 150 152 185 263 309+C 315+C 456 489 523-524d 681 750	
YJ230	male	-	D5b	182C 183C 189 223 311	73 150 263 309+CC 315+C 456 489 681 750	
YJ285	male	-	D5b	92 148 182C 183C 189 223 362 519	73 150 152 185 263 309+CC 315+C 456 489 523-524d 681 750	
YJ115	male	-	E1b	174 223 234 390 519	73 152 249d 263 279 309+C 315+C 489 750	
DH263	male	+	F	304 527	73 249d 263 315+C 709 750	
LC073	male	-	F	183C 189 243 304 519	73 249d 263 309+C 315+C 523-524d 750	
LC107	male	-	F	182C 183C 189 304	70 73 185 189 228 249d 263 309+CC 315+C 372 523-524d 573+5C 750	
LC385	male	+	F	183C 189 232A 249 304 362 519	73 152 153 249d 263 309+CC 315+C 523-524d 750	-
LC390	male	+	F	183C 189 274 304 519	73 208 249d 263 309+C 315+C 523-524d 709 750	-
LC402	male	-	F	183C 189 232A 249 304 311 360 519	73 249d 263 315+C 523-524d 750	-
LC524	male	+	F	183C 189 284 300 304 519	73 150 195 214 249d 263 309+C 315+C 523-524d 750	
RL-061	male	-	F	304 527	73 249d 263 315+C 709 750	+
RL-092	male	-	F	299 304	73 249d 263 309+CC 315+C 750	
RL-109	male	-	F	304	73 195 249d 263 315+C 750	
YJ061	male	-	F	183C 189 304 519	73 249d 263 309+C 315+C 523-524d 750	
YJ070	male	-	F	304	73 195 249d 263 315+C 750	
YL17	male	+	F	304 527	73 151 249d 263 315+C 709 750	
YY24	male	+	F	294 299 304	73 249d 263 309+C 315+C 750	
LCS36	male	+	F1	182C 183C 189 232A 249 304 519	73 152 249d 263 309+CC 315+C 523-524d 750	
DH319	male	+	F1a	129 172 304 519	73 249d 263 309+C 315+C 523-524d 750	

LC007	male	+	F1a	129 172 304 311 362 519	73 146 249d 263 315+C 523-524d 750	
LC032	male	-	F1a	129 172 304 519	73 249d 263 315+C 523-524d 750	+
LC041	male	-	F1a	129 172 304 519	73 152 249d 263 309+C 315+C 523-524d 573+C 750	
LC066	male	+	F1a	129 172 304 519	73 249d 263 309+C 315+C 523-524d 750	
LC067	male	-	F1a	129 172 304 311 362 519	73 146 152 249d 263 309+CC 315+C 521-524d 750	
LC085	male	-	F1a	129 172 187 304 519	73 249d 263 309+CC 315+C 523-524d 750	
LC095	male	-	F1a	86 129 172 189 304 519	73 150 249d 263 315+C 523-524d 750	
LC125	male	+	F1a	129 172 304 311 362 519	73 146 152 249d 263 309+CC 315+C 521-524d 681 750	-
LC140	male	+	F1a	172 304 519	73 249d 263 315+C 523-524d 750	
LC176	male	-	F1a	129 172 304 519	73 189 204 207 249d 263 309+C 315+C 523-524d 750	
LC184	male	-	F1a	129 172 304 519	73 249d 263 315+C 523-524d 750	
LC368	male	+	F1a	129 172 519	73 249d 263 315+C 523-524d 750	
LC372	male	+	F1a	129 172 304 519	73 249d 263 315+C 523-524d 750	
LC380	male	+	F1a	129 172 304 519	73 146 249d 263 309+C 315+C 523-524d 750	-
LC409	male	+	F1a	129 172 242 304 519	52 53 54C 71d 73 249d 263 309+C 315+C 318 523-524d 750	-
LC444	male	+	F1a	129 172 304 311 362 519	73 152 249d 263 309+CC 315+C 521-524d 750	
LC450	male	+	F1a	129 172 304 519	73 200 249d 263 315+C 523-524d 750	
LC488	male	+	F1a	129 172 304 519	73 249d 263 315+C 523-524d 750	
LC498	male	+	F1a	129 162 172 304 519	73 249d 263 315+C 523-524d 548 750	
LC520	male	+	F1a	129 172 304 519	73 249d 263 315+C 523-524d 750	
LC538	male	-	F1a	129 172 304 519	73 146 249d 263 309+C 315+C 523-524d 750	
LCS23	male	+	F1a	129 172 304 519	73 249d 263 315+C 523-524d 750	-
LCS34	male	-	F1a	129 162 172 292 304 519	73 152 195 249d 263 309+C 315+C 523-524d 750	
LCS64	male	+	F1a	129 172 242 304 519	73 52 53 54C 71d 73 249d 263 309+C 315+C 318 523-524d 750	
LCS67	male	+	F1a	129 172 304 311 519	73 146 249d 263 315+C 523-524d 750	
LCS72	male	+	F1a	129 172 304 519	73 249d 263 315+C 523-524d 750	-

LCS81	male	-	F1a	129 172 304 519	73 249d 263 309+C 315+C 523-524d 750	
RL-039	male	+	F1a	129 172 304 519	73 249d 263 315+C 523-524d 750	+
RL-079	male	-	F1a	129 172 304 519	73 249d 263 315+C 523-524d 750	
RL-105	male	-	F1a	129 172 304 519	73 109 189 207 249d 263 309+C 315+C 523-524d 750	
RL-115	male	-	F1a	129 172 304 519	73 249d 263 315+C 523-524d 750	
YJ072	male	-	F1a	129 172 304 519	73 249d 263 315+C 523-524d 750	+
YL38	male	+	F1a	129 172 304 519	73 249d 263 309+CC 315+C 750	
YY09	male	+	F1a	129 172 304 519	73 109 189 207 249d 263 309+C 315+C 523-524d 750	
YY15	male	+	F1a	129 172 304 519	73 189 207 249d 263 309+CC 315+C 523-524d 750	+
DH402	male	+	F1a1	129 162 172 304 519	73 249d 263 309+C 315+C 523-524d 750	-
DH630	male	+	F1a1	129 162 172 304 519	73 249d 263 315+C 523-524d 548 750	
LC051	male	+	F1a1	129 162 172 304 311 519	73 195 249d 263 309+C 315+C 523-524d 750	
LC175	male	-	F1a1	129 162 172 304 519	73 249d 263 315+C 523-524d 750	
LC191	male	-	F1a1	162 172 269 304 519	73 249d 263 315+C 523-524d 750	
LC377	male	+	F1a1	129 162 172 304 519	73 152 249d 263 309+C 315+C 523-524d 548 750	-
LC386	male	+	F1a1	129 162 172 304 371 519	73 249d 263 309+C 315+C 523-524d 750	-
LC404	male	-	F1a1	162 172 304 519	73 249d 263 315+C 523-524d	-
LC430	male	+	F1a1	129 162 172 304 519	73 249d 263 315+C 523-524d 750	-
LC439	male	+	F1a1	129 162 172 243 304 519	73 249d 263 315+C 523-524d 750	
LCS05	male	+	F1a1	129 162 172 243 304 519	73 249d 263 315+C 523-524d 750	
YJ002	male	-	F1a1	93 129 162 168 172 304 399 519	73 146 249d 263 309+C 315+C 523-524d 750	
YJ068	male	+	F1a1	129 172 291 304 519	73 189 204 207 249d 263 309+C 315+C 523-524d 750	+
YJ084	male	-	F1a1	129 162 172 304 399 519	73 249d 263 315+C 523-524d 750	+
YJ146	male	+	F1a1	129 172 304 519	73 249d 263 315+C 523-524d 750	
YJ181	male	-	F1a1	129 162 172 304 399 519	73 249d 263 315+C 523-524d 750	-
YJ252	male	-	F1a1	129 162 172 304 399 519	73 249d 263 315+C 523-524d 750	

YJ268	male	-	F1a1	129 162 172 304 399 519	73 249d 263 315+C 523-524d 750	-
YJ279	male	-	F1a1	129 162 172 304 311 399 519	73 152 249d 263 309+CC 315+C 523-524d 750	-
YL21	male	+	F1a1	129 140 162 172 189 304 519	73 94 249d 263 309+C 315+C 523-524d 750	
YY16	male	+	F1a1	93 129 162 168 172 304 399 519	73 146 249d 263 309+C 315+C 523-524d 750	
LC006	male	-	F1a1a	108 129 162 172 304 354 519	73 249d 263 315+C 523-524d 750	
LC019	male	-	F1a1a	108 129 162 172 304 354 519	73 249d 263 309+C 315+C 523-524d 750	
LC028	male	-	F1a1a	108 162 172 256 304 519	73 249d 263 309+C 315+C 523-524d 750	
LC030	male	-	F1a1a	108 162 172 256 304 519	73 249d 263 309+C 315+C 523-524d 750	
LC117	male	-	F1a1a	108 182C 183C 189 217 234 362 519	73 263 309+CC 315+C 523-524d 750	
LC123	male	-	F1a1a	83 108 162 172 295 304 519	73 152 249d 263 309+C 315+C 408A 523-524d 750	
LC138	male	+	F1a1a	129 162 172 304 519	73 94 249d 263 309+CC 315+C 523-524d 750	
LC342	male	+	F1a1a	108 129 162 172 227+A 304 354 519	73 249d 263 315+C 523-524d 750	
LC344	male	+	F1a1a	108 129 162 172 274 304 519	73 249d 263 309+C 315+C 523-524d 750	
LC383	male	+	F1a1a	108 129 162 172 304 354 519	73 249d 263 309+CC 315+C 523-524d 750	-
LC400	male	+	F1a1a	108 129 162 172 174 292 304 519	73 195 249d 263 309+C 315+C 523-524d 750	-
LC432	male	+	F1a1a	108 129 162 172 295 304 519	73 249d 263 309+CC 315+C 523-524d 750	-
LC481	male	-	F1a1a	108 162 172 256 304 519	73 249d 263 309+C 315+C 523-524d 750	
LCS07	male	+	F1a1a	108 129 162 172 227+A 304 354 519	73 249d 263 315+C 523-524d 750	
LCS08	male	+	F1a1a	108 129 162 172 304 519	73 249d 263 315+C 523-524d 750	
RL-076	male	-	F1a1a	108 129 162 172 295 304 311 519	73 249d 263 309+C 315+C 523-524d 750	
RL-102	male	-	F1a1a	108 162 172 295 304 362 519	73 152 249d 263 309+C 315+C 523-524d 750	
YJ149	male	-	F1a1a	108 129 162 172 270 304 519	73 249d 263 315+C 523-524d 750	
YJ160	male	+	F1a1a	108 129 162 169 172 304 519	73 146 249d 263 309+CC 315+C 523-524d 750	
YJ226	male	-	F1a1a	108 129 162 172 304	73 150 195 249d 263 315+C 523-524d 750	
YJ261	male	+	F1a1a	108 129 162 172 209 304 519	73 152 195 249d 263 309+CC 315+C 523-524d 750	
YL35	male	-	F1a1a	108 129 162 169 172 304 519	73 146 249d 263 309+C 315+C 523-524d 750	-

YL41	male	-	F1a1a	108 129 162 172 270 304 519	73 249d 263 315+C 523-524d 750	
LC167	male	-	F1b	182C 183C 189 232A 249 304 519	73 152 249d 263 309+C 315+C 523-524d 750	
LC024	male	-	F1b'd	183C 189 243 304 519	73 249d 263 315+C 523-524d 750	-
LC352	male	+	F1b'd	182C 183C 189 304 519	73 237 249d 263 309+CC 315+C 523-524d 750	
LC434	male	-	F1c	86 111 129 304 519	73 152 234 249d 263 309+C 315+C 523-524d 750	-
YJ022	male	-	F1c	111 129 266 304 519	73 152 249d 263 309+C 315+C 523-524d 750	+
YL32	male	+	F1c	111 129 304 519	73 152 234 249d 263 309+C 315+C 750	
LCS24	male	+	F1d	183C 189 300 304 519	73 146 150 195 198 215 249d 263 309+C 315+C 523-524d 750	
LCS76	male	+	F1d	183C 189 300 304 519	73 146 150 195 198 215 249d 263 309+C 315+C 523-524d 750	+
YJ102	male	-	F1d	189 284 291 304 519	73 146 249d 263 315+C 523-524d 750	
YJ243	male	-	F1d	183C 189 300 304 519	73 146 150 195 198 249d 263 309+CC 315+C 523-524d 750	
YL43	male	-	F1d	189 224 304 519	73 146 249d 263 309+CC 315+C 523-524d 750	
YM18	male	+	F1d	93 129 183C 189 519	73 146 249d 263 309+CC 315+C 523-524d 750	
LC500	male	+	F2a	185 266A 291 304 519	73 249d 263 315+C 747 750	
RL-019	male	+	F2a	92A 291 304	73 249d 263 315+C 750	+
YJ246	male	-	F2a	92A 170T 183C 189 291 304	73 249d 263 315+C 523-524d 750	
YL23	male	+	F2a	92A 183C 189 291 304 519	73 249d 263 309+CC 315+C 523-524d 750	
YL34	male	-	F2a	92A 189 291 304	73 249d 263 309+C 315+C 523-524d 750	-
DH405	male	+	F3a	260 298 355 362	73 249d 263 309+CC 315+C 709 750	
LC397	male	+	F3a	239 260 298 355 362 526	73 249d 263 309+CC 315+C 709 750	-
LCS79	male	-	F3a	260 298 355 362	73 204 207 249d 263 309+C 315+C 709 750	+
RL-012	male	+	F3a	260 298 355 362	73 207 249d 263 309+C 315+C 709 750	
RL-016	male	+	F3a	260 298 355 362	73 207 249d 263 309+C 315+C 709 750	
RL-091	male	-	F3a	260 298 355 362	73 207 249d 263 309+CC 315+C 709 750	
YJ260	male	-	F3a	260 298 355 362	73 207 249d 263 309+C 315+C 709 750	+
YL16	male	+	F3a	260 298 355 362	73 207 249d 263 309+C 315+C 709 750	

YM15	male	-	F3a	260 298 355 362	73 207 249d 263 309+C 315+C 709 750	
LC011	male	-	G	223 362	73 146 263 309+CC 315+C 489 709 750	
LC045	male	-	G	126 223 362 519	73 263 315+C 489 709 750	
LC059	male	-	G	153 183C 189 214 217 261	73 263 309+CC 315+C 489 709 750	
LC168	male	-	G	223 362	73 263 309+C 315+C 489 709 750	
LC174	male	-	G	51 209 223 362 519	73 153 263 315+C 489 573+5C 709 750	
LCS70	male	+	G	223 362	73 263 309+C 315+C 489 709 750	
YJ033	male	+	G	223 362	73 263 309+C 315+C 489 709 750	
YJ125	male	-	G	145 181 192 223 291 304 362 519	73 150 210 263 309+CC 315+C 489 709 750	
YJ297	male	-	G	223 362	73 263 309+C 315+C 489 709 750	
YJ298	male	-	G	223 362	73 263 309+CC 315+C 489 709 750	
LCS03	male	-	G1a2	184 223 290 362 519	73 263 315+C 489 709 750	
LC155	male	-	G1b	129 223 311	73 263 315+C 489 507 573+4C 709 750	
LC065	male	+	G1c	126 223 362 519	73 263 315+C 489 593 709 750	
LC079	male	-	G1c	126 223 362 519	73 263 315+C 489 593 709 750	
LC382	male	+	G1c	126 223 362 519	73 263 315+C 489 593 709 750	-
LCS17	male	+	G1c	192 223 362 519	73 263 315+C 489 593 709 750	
YJ264	male	-	G1c	126 223 362 519	63 73 263 315+C 489 593 709 750	
LC112	male	-	G2a	223 278 287 362	73 263 315+C 489 544A 709 750	
LC478	male	+	G2a	183C 189 223 278 362	73 260 263 315+C 489 709 750	
LC510	male	+	G2a	129 223 278 362	73 263 309+CC 315+C 489 709 750	
LC513	male	-	G2a	129 223 278 362	73 263 315+C 489 709 750	
LCS56	male	+	G2a	129 223 278 362	73 263 315+C 489 709 750	
LF017	male	-	G2a	223 278 362	73 152 263 309+C 315+C 489 573+2C 709 750	+
YL24	male	+	G2a	223 278 362	73 260 263 315+C 489 709 750	
LC503	male	+	G2a3	183C 189 223 278 362	73 260 263 315+C 489 709 750	

LC521	male	+	G2a3	183C 189 223 278 362	73 260 263 315+C 489 709 750	
LCS25	male	+	G2a3	183C 189 223 278 362	73 260 263 315+C 489 709 750	
LCS29	male	+	G2a3	183C 189 223 278 362	73 260 263 315+C 489 709 750	
YJ099	male	+	G3	223 274 362	73 195 263 309+C 315+C 489 709 750	
LC341	male	+	G3a	186 223 240 274 311G 362	73 143 152 195 263 309+C 315+C 489 709 750	
LC497	male	+	G3a1	215 223 274	16T 73 143 150 263 309+C 315+C 489 709 750	+
DH533	male	+	M*	223 304 344 362 381 519	73 263 309+CC 315+C 489 750	
LC428	male	+	M*	129 140 169 223 271	73 143 146 151 263 315+C 489 750	
LCS47	male	-	M*	129 140 169 223 271	73 143 146 151 263 315+C 489 750	
RL-042	male	+	M*	129 134 223 240 298 362	73 215 263 315+C 461 489 593 750	
RL-058	male	-	M*	223 258C 262+C 272 311 384 519	73 150 152 185 263 279 309+C 315+C 489 750	+
YJ043	male	+	M*	223 304 344 362 381 519	73 263 309+C 315+C 489 750	+
YJ073	male	-	M*	223 311 519	73 94 195 263 309+C 315+C 489 573+2C 709 750	-
DH504	male	+	M10	223 311 362 519	73 263 315+C 489 573+Cs 750	
YL10	male	-	M10	223 311 519	73 94 195 263 309+C 315+C 489 573+4C 709 750	
LC185	male	-	M10a1	93 129 193 223 311 357 497	73 146 263 309+C 315+C 489 523-524d 573+3C 709 750	
LC109	male	-	M11	223	73 198 200 215 263 315+C 318 326 489 709 750	
LC115	male	-	M11	223	73 146 198 215 263 315+C 318 326 489 739 750	
LC142	male	-	M11	86 223	73 198 200 215 263 309+C 315+C 318 326 489 750	
LC188	male	-	M11	CRS	73 198 200 215 263 315+C 318 326 489 750	-
LC064	male	-	M12	86 108 129 172 223 234 290 319	73 185 263 315+C 489 523-524d 750	
RL-071	male	+	M12	93 223 234 266 290 311	73 125 127 128 146 152 263 315+C 318 326 489 750	+
YJ171	male	-	M12a	172 183C 189 209 223 234 290 291 519	73 125 127 128 146 195 263 315+C 489 750	
YL19	male	-	M12a	129 223 234 290 362	73 125 127 128 263 295 309+C 315+C 318 489 513 523-524d 750	
LC469	male	+	M12a1	223 234 266 290 311	73 125 127 128 146 152 263 315+C 318 326 489 750	
LCS66	male	+	M12a1	223 234 266 290 311	73 125 127 128 146 152 263 315+C 318 326 489 750	

LCS80	male	+	M12a1	223 234 266 290 311	73 125 127 128 146 152 263 315+C 318 326 489 750	
LCS62	male	-	M12a1b	148 172 189 223 234 290 519	73 125 127 128 146 195 263 315+C 489 750	
YY04	male	+	M17a	48 129 209 223 325 519	73 159 182 199 263 315+C 489 750	
LC014	male	-	M20	86 129 209 223 272 519	73 146 152 225 249d 263 309+C 315+C 316 489 523-524d 750	
LC166	male	-	M20	86 129 209 223 272 519	73 152 225 249d 263 315+C 316 489 523-524d 750	
YJ009	male	-	M20	86 129 172 209 223 272 362 519	73 152 225 249d 263 309+C 310A 315+C 316 489 523-524d 750	
YJ194	male	-	M20	129 209 223 272 274 519	73 152 225 228 249d 263 315+C 316 489 523-524d 750	
LC012	male	-	M3	126 223 344 519	73 146 263 315+C 482 489 750	
LC169	male	-	M31a1	213 223 286 311 327 519	73 249d 263 309+C 315+C 489 750	-
YJ220	male	-	M31b	93 136 223 390	73 146 152 263 315+C 489 750 808	
YJ231	male	-	M31b	93 136 223	73 146 152 263 315+C 489 750 808	
LC157	male	-	M33b	223 324 362 519	73 263 315+C 489 676 750	
LC164	male	-	M33b	223 324 362 519	73 263 315+C 489 676 750	
LC195	male	-	M33b	223 324 362 519	73 263 315+C 489 676 750	-
LC530	male	+	M33b	172 223 324 362	73 152 183 195 263 309+CC 315+C 489 750	
YY39	male	+	M37a	220 223 274 311 519	73 151 152 235 263 309+C 315+C 523-524d 750	
LC457	male	+	M4	145 176 223 261 311 519	73 263 309+C 315+C 489 750	
LCS42	male	+	M4	145 176 223 261 311 519	73 263 309+C 315+C 489 750	
LC364	male	+	M49	223 234 519	73 257 263 315+C 489 750	
LC417	male	-	M49	223 234 519	73 257 263 315+C 489 750	-
LC517	male	+	M49	223 234 519	73 263 315+C 489 498d 750	
LCS04	male	+	M49	223 234 519	73 257 263 315+C 489 750	
RL-094	male	+	M49	223 234 519	73 263 315+C 489 750	
YL09	male	+	M6	223 258d 272 519	73 185h 263 315+C 489 750	
RL-062	male	-	M60b	93 223 266 357	73 189 263 309+C 315+C 489 523-524d 750	
LC052	male	-	M71	223 269 271 311	73 150 151 263 309+C 315+C 489 750	

LC353	male	+	M71	93 223 259 271	73 151 263 282 309+C 315+C 489 750	
YJ257	male	-	M71	94 223 271	73 151 263 309+C 315+C 489 518 750	
YJ263	male	-	M71	94h 223 271	73 151 263 309+C 315+C 489 518 750	
LC477	male	-	M71a1	223 269 271 311	73 150 151 263 315+C 489 750	
YJ293	male	-	M71b	223 260 264 271 519	73 151 263 309+C 315+C 489 524+2AC 750	-
LC026	male	+	M74b	223 246T 311 362 519	73 195 263 309+C 315+C 489 750	-
LC389	male	+	M75	51 68 182C 183C 189 223 311 399 482 519	73 143 146 150 152 263 309+C 315+C 489 523-524d 750	
LCS78	male	+	M75	51 68 182C 183C 189 223 311 399 482 519	73 143 146 150 152 263 309+C 315+C 489 750	+
LC506	male	-	M76a	124 146 183C 189 293C 325 362	73 146 234 263 309+C 315+C 489 513 523-524d 750	
LCS52	male	-	M76a	124 146 183C 189 293C 325 362	73 146 234 263 309+C 315+C 489 513 523-524d 750	
DH262	male	+	M7b	129 223 297	73 150 199 207 263 309+CC 315+C 489 750	
DH374	male	+	M7b	129 223 297	73 150 159h 199 263 309+C 315+C 489 750	
LC003	male	-	M7b	223 297	73 150 199 204 263 315+C 489 750	
LC046	male	-	M7b	129 189 223 297 519	73 150 199 263 309+C 315+C 489 593 750	
LC076	male	-	M7b	223 297 299	73 150 199 204 263 315+C 489 750	
LC102	male	-	M7b	223 290 297	73 150 189 199 204 263 315+C 489 750	
LC144	male	-	M7b	129 223 297 519	73 150 159 199 263 309+C 315+C 489 750	
LC162	male	-	M7b	223 297	66 73 150 199 204 263 309+C 315+C 489 750	
LC193	male	-	M7b	129 192 223 297	73 150 199 263 309+CC 315+C 489 750	
LC340	male	+	M7b	86 223 297	73 150 199 204 263 315+C 489 750	
LC370	male	+	M7b	129 183C 189 223 248 297	73 150 195 199 204 207 263 309+C 315+C 489 709 750	-
LC373	male	+	M7b	129 158 189 223 248 297	73 150 199 204 207 263 309+C 315+C 489 750	
LC420	male	+	M7b	129 192 223 297	73 146 150 195 199 263 309+CC 315+C 332 489 750	-
LC475	male	+	M7b	129 223 297	73 150 159 199 263 309+C 315+C 489 750	
LCS32	male	-	M7b	223 297	73 150 189 199 204 263 315+C 489 750	
LCS35	male	+	M7b	86 223 297	73 150 199 204 263 315+C 489 750	

LCS45	male	-	M7b	158 189 223 248 297	73 150 199 204 207 263 309+C 315+C 489 750	
LCS71	male	+	M7b	129 192 223 297 362 400	73 150 199 217 263 309+C 315+C 489 750	
LCS77	male	+	M7b	129 183C 189 223 248 297	73 150 195 199 204 207 263 309+CC 315+C 489 709 750	+
RL-028	male	-	M7b	129 192 223 297 301G 391 519	73 150 199 263 309+C 315+C 489 596 750	+
YJ064	male	-	M7b	129 223 297	73 150 159 199 263 315+C 489 750	
YJ067	male	-	M7b	223 297	73 150 199 204 263 309+C 315+C 489 750	+
YJ133	male	-	M7b	129 189 223 297	73 150 199 204 207 263 309+C 315+C 489 750	
YJ295	male	-	M7b	129 223 271 297	73 150 199 263 291+A 309+C 315+C 489 750	
YL02	male	-	M7b	129 223 297	73 150 159 199 263 315+C 489 750	-
YL05	male	+	M7b	171 223 297	73 150 199 204 263 315+C 489 750	
YY18	male	+	M7b	171 223 297	73 150 199 204 263 315+C 489 750	
LC074	male	+	M7b1	129 192 223 297	73 150 199 263 309+C 315+C 489 538 750	
LC090	male	-	M7b1	129 192 223 297	73 150 199 263 309+C 315+C 489 750	
LC108	male	-	M7b1	129 192 223 297	73 150 199 263 309+C 315+C 489 750	
LC113	male	-	M7b1	129 192 223 297	73 150 199 263 315+C 489 750	
LC137	male	+	M7b1	129 192 223 297	73 150 199 263 315+C 489 750	
LCS75	male	+	M7b1	129 189 192 223 297	73 150 199 204 207 263 315+C 489 750	+
YJ054	male	-	M7b1	129 192 223 297	73 150 199 207 263 309+C 315+C 489 750	+
YJ152	male	-	M7b1	129 189 192 223 297 519	73 150 199 263 309+C 315+C 489 593 750	
YJ211	male	-	M7b1	129 192 223 297	73 150 199 207 263 309+C 315+C 489 750	
YJ253	male	-	M7b1	129 192 223 297 357	73 150 199 263 309+C 315+C 489 750	
YL12	male	-	M7b1	129 192 223 297 519	73 150 263 309+C 315+C 489 750	
YJ213	male	-	M7b1'2	93 129 223 297 311	73 150 182 199 263 309+C 315+C 459d 489 750	
RL-075	male	+	M7b'd	129 147A 223 519	73 199 263 315+C 489 750	+
LC346	male	+	M7c	83 223 295 519	73 146 199 263 309+C 315+C 489 523-524d 750	-
LC495	male	+	M7c	223 278 295 519	73 146 199 263 309+C 315+C 489 523-524d 750	

LCS20	male	+	M7c	223 519	73 146 199 263 315+C 489 523-524d 750	
LCS37	male	+	M7c	223 519	73 146 199 263 315+C 489 523-524d 750	
RL-070	male	-	M7c	223 519	73 146 199 263 315+C 489 523-524d 750	-
YJ184	male	-	M7c	519	73 146A 199 204 263 309+C 315+C 489 523-524d 750	
YJ196	male	-	M7c	311 356 519	73 146A 199 263 315+C 489 523-524d 750	
YJ222	male	-	M7c	519	73 146A 199 204 263 309+C 315+C 489 523-524d 750	
YJ284	male	-	M7c	519	73 146A 199 263 315+C 489 523-524d 750	
YJ299	male	-	M7c	519	73 146A 199 204 263 309+C 315+C 489 523-524d 750	
YM20	male	+	M7c	181 519	73 146A 199 263 309+C 315+C 489 523-524d 750	
RL-003	male	-	M7c3	286 519	73 146A 199 204 263 309+C 315+C 489 523-524d 750	+
YJ011	male	-	M7c3	519	73 146A 199 263 315+C 489 523-524d 750	
LC349	male	+	M7c3b	519	73 146A 199 263 309+C 315+C 489 523-524d 750	
RL-011	male	-	M7c'e'f	86 223 278	73 146 263 315+C 489 750	
YJ236	male	+	M7c'e'f	93 193 223 519	73 146 152 263 309+C 315+C 489 750	
YJ267	male	+	M7c'e'f	223 243 344 519	73 146 263 309+C 315+C 356+C 489 501A 513 750 794	+
YL44	male	+	M7c'e'f	93 193 223 519	73 146 152 263 309+C 315+C 489 750	
DH271	male	+	M7e	172 223 311 519	73 146 263 309+C 315+C 489 523-524d 750	
RL-088	male	+	M7e	172 223 248 311 519	73 146 263 309+C 315+C 489 523-524d 750	-
YJ089	male	-	M7e	111 172 217 223 297 311 319 381	73 94 173 263 315+C 482 489 750	
LC367	male	+	M8a2	184 223 298 319	73 263 309d 310 315+C 489 750	
LCS14	male	+	M8a2	184 223 298 319	73 152 263 309+C 315+C 489 750	
LCS65	male	+	M8a2a	184 189 223 319 470 471 473	73 263 309+CC 315+C 489 750	
RL-077	male	+	M8a2a	184 189 223 298 311 319 390 468 470 471 473	73 146 263 309+C 315+C 489 750	
LCS11	male	-	M9	93 150 223 316 362	73 263 309+CC 315+C 489 524+AC 750	
LC476	male	+	M9a1a1a	223 234 316 362	73 263 309+C 315+C 489 523-524d 750	
LC058	male	+	M9a1b	158 223 234 362 519	73 150 152 153 263 315+C 489 750	

YJ131	male	-	M9a1b	223 234 294 362 519	73 150 152 153 263 315+C 489 750	
LCS43	male	-	M9b	42 51 209 223 362 519	73 153 263 315+C 489 573+4C 709 750	
LC483	male	-	N*	93 223 390 519	73 146 263 315+C 750	
LCS33	male	-	N*	93 223 390 519	73 146 263 315+C 750	
LC020	male	-	N10	51 86 169 172 183C 189 209 218 223 319 519	73 152 195 263 315+C	
LC039	male	-	N10	51 86 169 172 183C 189 209 218 223 319 519	73 152 195 263 315+C	
LC101	male	-	N10	172 223 234 258C 291A 298	73 150 199 263 309+C 315+C 504 523-524d	
LC105	male	-	N10	51 86 169 172 183C 189 209 218 223 319 519	73 152 195 263 315+C	
LC445	male	+	N10b	172 223 258C 291A 298	73 150 199 263 315+C	
LCS49	male	+	N10b	172 223 258C 291A 298	73 150 199 263 315+C	
LC527	male	+	N11a	145 189 223 355 519	73 195 240 263 315+C 523-524d 750 813	
DH275	male	+	N21	172 182 193 223 519	73 146 150 195 263 309+C 315+C 337d 750	
DH483	male	+	N21	182 193 223 519	73 150 195 263 309+C 315+C 337d 750	
LC170	male	-	N21	182 193 223 519	73 150 173 195 263 315+C 337d 750	
LC336	male	+	N21	182 184 193 223 260 519	73 150 195 263 315+C 337d 750	
LC405	male	+	N21	182 193 223 519	73 150 195 263 309+C 315+C 337d 750	-
LC427	male	+	N21	145 182 193 223 260 519	73 150 195 263 309+C 315+C 337d 750	-
LC463	male	+	N21	182 193 223 519	73 150 195 263 309+C 315+C 337d 750	
LC050	male	-	N9a	124 172 223 257A 261 304	73 150 152 263 309+CC 315+C 750	-
LC084	male	+	N9a	223 257A 261 292 519	73 150 263 309+C 315+C 750 827	
LC145	male	-	N9a	223 257A 261 519	73 150 259C 263 315+C 750	
LC165	male	-	R*	RCS	73 235 249d 263 315+C 523-524d 750	
LCS15	male	-	R*	108 182C 183C 189 217 234 362 519	73 263 309+C 315+C 523-524d 750	-
LCS38	male	-	R*	108 182C 183C 189 217 362G 519	73 152 263 309+C 315+C 523-524d 750	
LCS41	male	+	R*	108 182C 183C 189 217 234 362 519	73 263 309+C 315+C 523-524d 750	
LCS44	male	-	R*	108 182C 183C 189 217 362G 519	73 146 263 309+CC 315+C 523-524d 750	

LCS83	male	+	R*	108 182C 183C 189 217 362G 519	73 263 309+CC 315+C 523-524d	
YL18	male	-	R*	CDS	73 235 249d 263 315+C 750	
LC345	male	+	R11	182C 183C 189 311 390 519	73 185 189 195 234 263 309+C 315+C 709 750	-
LC408	male	+	R11	182C 183C 189 311 390 519	73 185 189 195 234 263 315+C 709 750	-
LCS18	male	+	R11	182C 183C 189 217 223 519	73 146 185 189 195 263 309+CC 315+C 513 750 827	
RL-081	male	-	R22	129 145 249 288 301 304 311 519	73 150 152 167A 263 315+C 329 523-524d 750	
YJ018	male	-	R5a	248 266 304 311 356 519 524	73 152 263 309+C 315+C 324 523-524d 750	
LCS60	male	+	R8a2	182C 183C 189 217 223 519	73 146 185 189 195 263 307-309d 315+C 513 523-524d 750 827	
LC337	male	+	R9	157 304 324	73 151 263 309+C 315+C 479 750	
LC394	male	+	R9	157 304 324	73 151 263 309+CC 315+C 479 750	
LC465	male	+	R9	93 148 157 304	73 151 263 309+C 315+C 374 479 750	-
LC485	male	-	R9	92 126 182 183C 189 304 390 519	73 195 249d 263 309+C 315+C 523-524d 750	
LCS12	male	-	R9	209 278 304 309 390	73 263 309+C 315+C 523-524d 750	
RL-085	male	-	R9b	93 192 304 309 390 519	73 152 263 309+C 315+C 523-524d 750	
YJ238	male	-	R9b	192 295 304 309 390 519	73 152 263 309+C 315+C 368h 523-524d 750	
YJ306	male	-	R9b	192 295 304 309 390 519	73 152 263 309+C 315+C 523-524d 750	
LC077	male	-	R9b1b	124 148 275 304 309 327 390 519	73 263 309+C 315+C 523-524d 750	
LC147	male	-	R9b1b	124 148 184 304 309 390 519	73 263 315+C 750	
LC360	male	+	R9b1b	124 148 184 304 309 390 519	73 263 315+C 750	+
LC393	male	+	R9b1b	124 148 275 304 309 327 390 519	73 263 309+C 315+C 523-524d 573+C 750	-
LC423	male	+	R9b1b	124 148 275 304 309 327 390 519	73 263 309+C 315+C 523-524d 750	
LC438	male	+	R9b1b	124 148 304 309 390 519	73 263 309+C 315+C 750	
LCS06	male	+	R9b1b	124 148 304 309 390 519	73 263 309+C 315+C 750	
LCS61	male	-	R9b1b	124 148 275 304 309 327 390 519	73 263 309+C 315+C 523-524d 750	
LCS69	male	+	R9b1b	124 148 184 304 309 390 519	73 263 315+C 750	-
RL-072	male	-	R9b1b	102 114 124 148 304 309 327 390 519	73 150 188T 263 309+C 315+C 750	+

LC424	male	+	R9c	157 256 305 304 335	73 236 249d 263 309+CC 315+C 750	
LC332	male	+	Y1	126 231 266 325 519	73 146 200 263 309+C 315+C 523-524d 750	
LC516	male	+	Y1	126 231 266 519	73 146 207 263 309+C 315+C 750	
LC110	male	-	Z	93 185 223 260 298	73 152 207 249d 263 309+C 315+C 489 750	
LC179	male	-	Z	185 223 242 260 298	73 143 152 249d 263 315+C 489 573+4C 750	
LC431	male	+	Z	129 185 188 189 223 260 298	73 152 249d 263 309+C 315+C 489 750	-
LC504	male	+	Z	260 298 355 362	73 207 249d 263 309+C 315+C 709 750	
RL-041	male	-	Z	185 223 260 298 319	73 143 152 249d 263 309+C 315+C 489 573+3C 750	
YY17	male	+	Z	185 223 260 298	73 152 249d 263 309+C 315+C 489 750	

* Patients with and without HIV-1 infection were marked by "+" and "-", respectively.

[a] When RFLP result was not available, items have been left blank. Haplogroup D is characterized by "-5178*Alu*I".

Table S2. mtDNA sequence variations and haplogroup classification of 362 healthy individuals from the general population in Yunnan

Sample	Haplogroup	Region I (16000+)	Region II	5178 *Alu*I [a]
DH-C150	A	93 126 155 223 234 290 319 519	73 152 235 263 309+C 315+C 523-524d 663	
DH-C280	A	93 129 223 284 290 319 362 519	73 152 235 263 309+C 315+C 523-524d	
DH-C068	A11	223 234 290 293C 319 519	73 152 235 263 309+C 315+C 523-524d	
DH-C075	A11	223 234 290 293C 319 519	73 152 235 263 309+C 315+C	
DH-C114	A11	51 223 234 290 293C 319 519	73 152 235 263 309+C 315+C 523-524d	
DH-C358	A11	223 234 290 293C 319 519	73 152 235 263 309+C 315+C 523-524d	
DH-C013	A4	124 223 290 319 362	73 152 200 235 263 309+C 315+C 523-524d	
DH-C046	A4	223 290 319 362	73 152 156 235 263 309+C 315+C 523-524d	
DH-C048	A4	223 235 290 311 319 362 519	73 152 199 234 235 263 309+C 315+C 523-524d	
DH-C055	A4	223 290 319 362	73 151 152 235 263 315+C 523-524d	
DH-C108	A4	223 290 319 362	73 152 235 309+C 315+C	
DH-C112	A4	93 172 223 234 290 319 362	73 152 207 235 309+C 315+C 523-524d	
DH-C120	A4	223 290 319 362	73 151 152 200 235 263 315+C 523-524d 663	
DH-C121	A4	124 223 245 290 300 319 362 519	73 152 200 235 263 309+C 315+C	
DH-C125	A4	124 223 290 319 362	73 152 200 235 263 309+C 315+C	
DH-C136	A4	223 290 319 362 519	73 151 152 200 235 263 309+C 315+C	
DH-C146	A4	223 284 290 319 362	73 152 235 263 309+C 315+C 523-524d	
DH-C151	A4	223 274 290 319 362 519 527	73 152 235 263 309+CC 315+C	
DH-C162	A4	223 290 319 362	73 151 152 200 235 263 315+C 523-524d 663	
DH-C177	A4	124 223 290 319 362	73 152 200 204 235 263 309+C 315+C	
DH-C184	A4	223 290 304 319 362	73 152 200 235 263 315+C 523-524d 663 750	
DH-C186	A4	223 290 319 362	73 152 235 263 315+C 523-524d	
DH-C199	A4	223 235 290 311 319 362 519 527	73 152 199 234 235 263 309+C 315+C 523-524d 573+4C	
DH-C203	A4	223 290 319 362 519	73 152 235 263 309+C 315+C	

DH-C208	A4	223 290 293C 319 519	73 152 235 263 309+C 315+C 523-524d
DH-C213	A4	223 274 290 319 362 519 527	73 152 235 263 309+C 315+C 523-524d 663
DH-C216	A4	223 290 319 362	73 151 152 200 235 263 315+C 523-524d 663
DH-C226	A4	223 235 290 311 319 362 519 527	73 152 199 234 235 263 309+C 315+C 523-524d
DH-C234	A4	223 290 319 362	73 152 235 309+C 315+C 523-524d 663
DH-C235	A4	93 223 290 319 362	73 151 152 200 235 263 315+C 523-524d 663
DH-C256	A4	223 290 319 325 362	41 73 152 235 263 315+C 523-524d 663
DH-C257	A4	209 223 290 319 362	73 152 156 235 263 315+C 523-524d 663
DH-C289	A4	93 223 290 319 362 519	73 152 235 263 309+C 315+C 449 523-524d 663
DH-C383	A4	223 290 319 362	73 152 235 309+CC 315+C 523-524d 663 750
DH-C393	A4	223 234 290 293C 319 519	73 151 152 235 263 309+C 315+C 523-524d
DH-C109	A5b1	93 126 223 234 235 290 319 519	73 152 235 263 315+C 523-524d 663 750
DH-C100	B*	93 169 182C 183C 189 261 357 519	73 263 309+CC 315+C
DH-C242	B*	126 183C 189 231 264h 266 519	73 263 309+CC 315+C
DH-C244	B*	51 182C 183C 189 220 222 519	73 263 309+CC 315+C 750
DH-C005	B4	93 183C 189 217 234 519	73 263 315+C
DH-C006	B4	183C 189 217 223 519	73 263 309+C 315+C
DH-C016	B4	183C 189 217 234 249 519	73 263 309+C 315+C 556T
DH-C023	B4	182C 183C 189 217 240 261	73 263 309+CC 315+C 523-524d 750
DH-C054	B4	183C 189 217 234 519	73 263 309+CC 315+C 750 827
DH-C070	B4	108 182C 183C 189 217 362 519	73 263 309+CC 315+C
DH-C077	B4	182C 183C 189 217 223 519	73C 185 189 194 195 198 263 309+C 315+C 513 750
DH-C191	B4	182C 183C 189 217 240 261	73 263 309+CC 315+C 523-524d 750
DH-C218	B4	108 182C 183C 189 217 362A 519	73 263 309+C 315+C 523-524d 750
DH-C237	B4	182C 183C 189 217 240 261	73 263 309+CC 315+C 523-524d
DH-C243	B4	182C 183C 189 217 311 362 519	73 263 315+C 523-524d 750

DH-C247	B4	93 183d 186 189 217 519	73 152 263 309+C 315+C 316
DH-C339	B4	182C 183C 189 217 261	73 263 309+CC 315+C 523-524d 750
DH-C381	B4	182C 183C 189 217 311	73 263 315+C 368
DH-C388	B4	150 182C 183C 189 217 261	73 263 309+CC 315+C 523-524d 750
DH-C278	B4a	169 182C 183C 189 217 240 261	73 263 309+CC 315+C 523-524d 750
DH-C397	B4a	167 182C 183C 189 217 261 519	73 146 152 263 315+C 350C 523-524d
DH-C404	B4a	168 182C 183C 189 217 261 311 519	73 182 185 263 309+CC 315+C 523-524d 750
DH-C197	B4a4	92 182C 183C 189 217 261 299 519	73 193 263 309+C 315+C 523-524d
DH-C091	B4b1a	136 183C 189 217 309 354 519	73 204 207 263 315+C 499
DH-C110	B4b1a	136 183C 189 217 519	73 150 207 263 315+C 499
DH-C022	B4c1b	140 183C 189 217 249 274 335 519	73 150 152 263 315+C
DH-C061	B4c1b	129 140 148 166 183C 189 217 274 311 357 519 566	73 150 263 309+CC 315+C 709 750
DH-C086	B4c2	147 183C 184A 189 217 235 519	73 263 309+C 315+C 523-524d
DH-C097	B4c2	147 183C 184A 189 217 235 519	73 263 309+C 315+C 523-524d 750
DH-C281	B4c2	147 183C 184A 189 217 235 519	73 263 315+C 507
DH-C377	B4c2	147 162 183C 184A 189 217 235 519	73 263 309+C 315+C
DH-C045	B4g	181C 182C 183C 189 213 217 261 292 312 519	61A 62 73 152 263 309+CC 315+C
DH-C238	B4g	181C 182C 183C 189 213 217 261 292 294 519	73 263 309d 315+C 523-524d
DH-C277	B4g	181C 182C 183C 189 213 217 261 292 519	61A 62 73 263 315+C 523-524d 750
DH-C314	B4g	181C 182C 183C 189 213 217 261 292 519	61A 62 73 263 309+C 315+C 523-524d 750
DH-C392	B4g	181C 182C 183C 189 213 217 242 261 292 301 519	61A 62 73 183 263 310d 523-524d 750
DH-C020	B5a	140 183C 189 266A 519	73 93 210 263 309+C 315+C
DH-C127	B5a	140 189 266A 519	73 210 263 309+C 315+C 523-524d
DH-C133	B5a	140 183C 189 266A 519	73 210 263 309+C 315+C 523-524d 709 750
DH-C145	B5a	140 182C 183C 189 266A 362 519	73 210 263 309+CC 315+C 523-524d 709 750
DH-C157	B5a	140 183C 189 266A 519	73 210 263 309+CC 315+C

DH-C225	B5a	140 183C 189 266A 519	73 146 210 263 315+C 523-524d 709 750
DH-C230	B5a	140 182C 183C 189 261 266A 519	73 152 210 309+CC 315+C 523-524d 709 750
DH-C246	B5a	140 182C 183C 189 266A 362 519	73 143 210 228 263 309+C 315+C 523-524d
DH-C321	B5a	140 183C 189 266A 519	73 210 263 309+C 315+C 523-524d
DH-C351	B5a	182C 183C 189 266A 519	73 210 263 309+C 315+C 523-524d 709 750
DH-C361	B5a	140 182C 183C 189 266A 519	73 152 210 263 309+CC 315+C 455+T 523-524d 709 750
DH-C379	B5a	140 183C 189 266A 519	73 210 263 309+C 315+C 523-524d
DH-C148	B5a1d	129 140 173 182C 183C 189 261 266A 519	73 152 249d 210 263 309+CC 315+C 456 523-524d 709 750
DH-C248	B5a1d	129 140 182C 183C 189 261 266A 519	73 152 210 309+CC 315+C 523-524d 709 750
DH-C173	B5a2a	140 187 189 256 266G 362 519	73 93 210 263 315+C 523-524d
DH-C352	B5a2a	140 187 189 256 266G 519	73 93 210 263 315+C 523-524d 709 750
DH-C212	B5b	140 183C 189 243 311 355 519	73 103 263 309+C 315+C 523-524d
DH-C241	B5b2	111 140 183C 189 234 243 463 519	73 103 150 263 315+C 481 523-524d
DH-C107	B5b2a	111 140 182C 183C 189 234 243 463 519	73 103 131 143 204 228 263 309+C 315+C 523-524d
DH-C219	B5b2a	111 129 140 183C 189 234 243 463 519	73 103 131 150 152 263 309+CC 315+C
DH-C012	B6a	93 179 182C 183C 189	73 150 263 309+CC 315+C 750
DH-C072	B6a	93 124 179 182C 183C 189 243	73 150 263 315+C
DH-C117	B6a	93 179 182C 183C 189 266 342	73 150 263 309+CC 315+C
DH-C004	C	223 298 327 519	73 146 153 249d 263 309+C 315+C 489
DH-C019	C	223 298 327 354 357 519	47 73 249d 263 315+C 489 523-524d 750
DH-C028	C	223 298 327 519	73 249d 263 315+C 489
DH-C037	C	223 266 298 327 519	73 146 249d 263 315+C 489
DH-C073	C	189 223 298 327 519	73 249d 263 309+C 315+C 489
DH-C129	C	189 223 261 298 327 519	73 249d 263 309+C 315+C 489
DH-C193	C	223 298 327 354 357 519	47 73 249d 263 309+C 315+C 489 523-524d
DH-C295	C	223 298 327 519	73 249d 263 309+C 315+C 489

DH-C316	C	189 223 298 327 519	73 207 249d 263 309+C 315+C 489	
DH-C350	C	92 189 223 288 298 327 355 519	73 249d 263 309+C 315+C 489 529h 750	
DH-C359	C	223 298 311 327 357 519	73 249d 263 310d 489 750	
DH-C400	C	189 223 298 327 519	73 249d 263 309+C 315+C 489	
DH-C401	C	223 298 327 519	41 73 249d 263 309+CC 315+C 489	
DH-C033	C4	183C 189 223 239 298 327 357 519	73 200 249d 263 309+CC 315+C 372	
DH-C128	C4	183C 189 223 239 298 327 357 519	73 200 249d 263 309+C 315+C 372 489	
DH-C368	C4	183C 189 223 239 298 327 357 519	73 200 249d 263 309+C 315+C 372 489 750	
DH-C273	C4a5	129 192 223 298 311 327 519	73 249d 263 309+C 315+C 489	
DH-C333	C4a5	129 192 223 298 311 327 519	73 195 249d 263 309+C 315+C 489	
DH-C372	C4a5	129 192 223 298 311 327 519	73 249d 263 309+C 315+C 489	
DH-C376	C5d1	93 169 223 288 298 327 390 519	73 249d 263 309+C 315+C 489	
DH-C399	C7a1d	86 223 242 256 298 327 390 519	73 146 249d 263 315+C 489	
DH-C011	D4	223 362 519	73 263 315+C 489 523-524d 750	-
DH-C017	D4	223 362 526	73 146 263 309+CC 315+C 489	-
DH-C026	D4	223 249 362 519	73 263 315+C 489	-
DH-C035	D4	172 174 223 293 311 362	73 152 263 309+C 315+C 489	-
DH-C038	D4	223 294 362	64 65A 73 195 237 263 309+C 315+C 489 501	-
DH-C043	D4	174 223 311 325 362	73 152 263 309+C 315+C 489	-
DH-C053	D4	223 259 298 299 362	73 263 315+C 489	-
DH-C059	D4	362 519	73 152 194 263 315+C 489 523-524d 750	-
DH-C078	D4	174 223 311 320 362	73 152 263 315+C 489	-
DH-C094	D4	223 294 362	73 146 263 315+C 489	-
DH-C098	D4	174 223 286 362	73 263 315+C 489	-
DH-C101	D4	172 174 223 311 325 362	73 152 263 309+C 315+C 489	-
DH-C116	D4	93 223 232 290 362	73 195 198 263 315+C 489	-

DH-C141	D4	93 223 362	73 263 309+C 315+C 489	-
DH-C168	D4	223 362 519	73 199 263 309+C 315+C	-
DH-C169	D4	184 213 223 311 362	73 263 309+C 315+C 338 489	-
DH-C171	D4	86 223 362	73 263 309+C 315+C 489	-
DH-C176	D4	223 362 519	73 199 263 309+C 315+C 489	-
DH-C180	D4	223 355A 362	73 150 154 263 309+C 315+C 489	-
DH-C188	D4	223 320 362 519	73 199 263 309+C 315+C 489	-
DH-C192	D4	223 362 519	73 263 315+C 489 523-524d	-
DH-C200	D4	187 223 271 362 519	73 199 263 309+C 315+C 489	-
DH-C204	D4	223 362 519	73 194 263 315+C 489 523-524d	-
DH-C209	D4	256 274 311 362 519	73 200 263 315+C 489	-
DH-C215	D4	193 223 362	73 199 263 315+C 489	-
DH-C220	D4	114A 223 362	73 152 263 309+C 315+C 489	-
DH-C222	D4	92 223 362	73 94 146 263 309+C 315+C 489	-
DH-C223	D4	223 362 519	73 194 263 315+C 489	-
DH-C231	D4	223 362	73 152 195 263 309+CC 315+C 489	-
DH-C236	D4	93 187 223 271 362 519	73 199 263 315+C 489	-
DH-C245	D4	93 223 294 362	64 65A 73 195 237 263 315+C 489 501 750	-
DH-C282	D4	172 174 223 311 362	73 263 309+C 315+C 489	-
DH-C283	D4	223 294 362	64 65A 73 195 237 263 309+C 315+C 489 501	-
DH-C299	D4	126 174 223 343 362	73 263 309+C 315+C	-
DH-C318	D4	126 174 223 343 362	73 263 315+C 489	-
DH-C323	D4	126 174 223 343 362	73 263 315+C 489 513	-
DH-C330	D4	223 243 362	73 263 309+C 315+C 489 523-524d 750	-
DH-C331	D4	192 223	73 195 263 309+C 315+C 489	-
DH-C337	D4	223 362 519	73 194 263 315+C 489	-

DH-C353	D4	223 362 519	73 199 263 309+C 315+C 489 750 813	-
DH-C360	D4	223 259 298 299 362	73 263 315+C 489	-
DH-C385	D4	223 249 362	73 263 309+C 315+C 489	-
DH-C394	D4	223 362 526	73 146 200 263 309+CC 315+C	-
DH-C179	D4a	129 223 270 362 519	73 146 152 263 309+C 315+C 489	-
DH-C345	D4c	93 189 223 245 362	73 263 315+C 489 534 750	-
DH-C217	D4g2	223 274 362 519	73 263 298 315+C 489	-
DH-C380	D4g2	223 274 362 519	73 263 298 309+C 315+C 489 524+AC 710 750	-
DH-C152	D4g2a	172 223 274 362	73 263 298 315+C 489	-
DH-C340	D4g2a	183C 189 223 274 362 519	73 263 298 308-310d 315+C 316 489 750	-
DH-C346	D4q	223 256 311 362 519	73 200 263 315+C 489 750	-
DH-C354	D4q	223 256 274 311 362 519	73 200 263 315+C 489	-
DH-C051	D5	104 153 164 182C 183C 189 223 266 362	73 150 243 263 315+C 489 523-524d	-
DH-C287	D5a2	164 172 182C 183C 189 223 259 362	73 150 263 309+C 315+C 489 523-524d	-
DH-C123	D5a2a1	92 164 167 182C 183C 189 223 266 362 519	73 150 195 263 309+CC 315+C 489 523-524d 750	-
DH-C254	D5a2a1	92 164 167 172 182C 183C 189 223 266 293 362	73 150 263 309+C 315+C 489 523-524d	-
DH-C251	D5a3	93 111 182C 183C 189 223 360 362	73 150 263 309+C 315+C 489 523-524d	-
DH-C040	D5b	182C 183C 189 223 362	73 150 263 309d 315+C 456 489	-
DH-C195	D5b	164 167 182C 183C 189 223 245 362 519	73 150 195 263 309d 315+C 489 523-524d	-
DH-C214	D5b	183C 189 223 362 519	73 150 152 263 309+CC 315+C 456 489	-
DH-C140	D6c	183C 189 223 311 362	73 152 204 228T 263 315+C 489 523-524d	-
DH-C274	E1b	37 223 234 362 390 519	73 152 249d 263 309+C 315+C 489	+
DH-C285	E1b	156 223 234 261 390 519	73 152 249d 263 279 309+CC 315+C 489	+
DH-C384	E1b	174 223 234 390 519	73 152 249d 263 279 309+C 315+C 489	+
DH-C044	F	182C 183C 189 304	70 73 185 189 249d 263 309+CC 315+C 372 381 523-524d 573+Cs	

DH-C074	F	182C 183C 189 304 519	73 237 249d 263 309+CC 315+C 523-524d 750
DH-C087	F	93 183C 189 304 519	73 249d 263 315+C 523-524d
DH-C105	F	86 182C 183C 189 304 519	73 150 237 249d 263 309+CC 315+C
DH-C132	F	183C 189 278 304 357 519	73 186 249d 263 309+C 315+C 523-524d
DH-C144	F	182C 183C 189 304 519	73 249d 263 309+CC 315+C
DH-C172	F	183C 189 304 519	73 249d 263 309+CC 315+C 523-524d 750
DH-C185	F	182C 183C 189 304 519	73 249d 263 309+CC 315+C 523-524d
DH-C293	F	182C 183C 189 304 519	73 249d 263 309+C 315+C 523-524d 750
DH-C201	F1a	129 154 172 304 519	73 249d 263 315+C 523-524d
DH-C064	F1a1	129 162 172 304 311 519	73 249d 263 315+C 523-524d 750
DH-C085	F1a1	129 172 304 519	73 152 249d 263 315+C 523-524d
DH-C093	F1a1	129 162 172 189 304 519	73 94 249d 263 309+CC 315+C 523-524d
DH-C122	F1a1	129 162 172 304 497 519	73 234 249d 263 315+C
DH-C155	F1a1	129 162 172 304 311 519	73 249d 263 315+C 464 523-524d
DH-C165	F1a1	129 172 304 519	73 249d 263 309+C 315+C
DH-C178	F1a1	129 172 304 519	73 249d 263 315+C
DH-C190	F1a1	129 162 172 189 304 519	73 249d 263 309+C 315+C 523-524d
DH-C211	F1a1	129 172 304 519	73 195 249d 263 315+C 513 523-524d 750
DH-C224	F1a1	93 129 162 172 304 399 519	73 249d 263 309+C 315+C 523-524d
DH-C255	F1a1	129 172 304 320 519	73 249d 263 309+CC 315+C 523-524d
DH-C288	F1a1	129 172 189 304 519	73 249d 263 315+C 523-524d
DH-C294	F1a1	129 172 304 519	73 249d 263 315+C 523-524d 750
DH-C300	F1a1	129 172 304 519	73 249d 263 309+CC 315+C 523-524d
DH-C320	F1a1	129 162 172 261 304 519	73 195 249d 263 315+C 523-524d 593
DH-C322	F1a1	129 172 304 519	53 54C 73 249d 263 309+CC 315+C 318 385 523-524d
DH-C341	F1a1	129 162 172 287 304 399 519	73 249d 263 315+C 523-524d

DH-C375	F1a1	129 172 519	73 249d 263 309+C 315+C
DH-C034	F1a1a	108 129 162 172 304 519	73 150 195 249d 263 309+C 315+C 523-524d 750
DH-C079	F1a1a	108 129 162 172 304	73 150 195 249d 263 315+C 523-524d
DH-C147	F1a1a	108 129 162 172 239 304 519	73 150 249d 263 315+C 523-524d
DH-C196	F1a1a	108 129 162 172 189 209 274 304 519	73 150 207 249d 263 309+C 315+C 523-524d
DH-C206	F1a1a	108 129 162 172 295 304 519	73 249d 263 315+C 523-524d
DH-C290	F1a1a	108 129 162 172 304 354 519	73 249d 263 309+C 315+C 523-524d
DH-C062	F1a1c	129 162 172 304 519	73 150 249d 263 315+C 523-524d 548
DH-C382	F1a1c	129 162 172 304 519	73 249d 263 315+C 523-524d 548
DH-C071	F1b	182C 183C 189 232A 249 304 519	73 152 249d 263 309+CC 315+C 523-524d 750
DH-C118	F1b	183C 189 232A 249 304 362 519	73 152 249d 263 309+C 315+C 523-524d
DH-C158	F1b	182C 183C 189 232A 249 304 519	73 152 249d 263 309+CC 315+C
DH-C229	F1b	182C 183C 189 232A 249 304 519	73 152 249d 263 309+CC 315+C 523-524d 750
DH-C315	F1b	183C 189 232A 249 304 311 519	73 249d 263 309+CC 315+C 523-524d 750
DH-C336	F1b	182C 183C 189 232A 249 304 519	73 152 249d 263 309+C 315+C 523-524d 750
DH-C342	F1b	182C 183C 189 232A 304 519	73 152 189 249d 263 309+CCC 315+C 523-524d 573+C 750
DH-C344	F1b	111 183C 189 232A 249 304 311 519	73 204 249d 263 315+C 523-524d
DH-C348	F1b	182C 183C 189 232A 249 304 519	73 152 249d 263 308+T 309+C 315+C 523-524d 750
DH-C357	F1b	145 183C 189 232A 249 304 362 519	73 152 249d 263 309+C 315+C 523-524d 750
DH-C160	F1c	111 129 304 311h 519	73 152 234 249d 263 309+CC 315+C
DH-C001	F1c1	92 111 129 304 519	73 152 234 249d 263 309+C 315+C
DH-C130	F1c1	92 111 129 304 519	73 152 234 249d 263 309+C 315+C 523-524d 750
DH-C181	F1c1	92 111 129 304 519	73 152 234 249d 263 309+C 315+C 523-524d
DH-C239	F1c1	92 111 129 304 519	73 152 234 249d 263 309+C 315+C 523-524d
DH-C202	F1c1a	111 129 266 304 519	73 152 249d 263 309+CC 315+C
DH-C104	F1d	183C 189 304 519	73 146 249d 263 315+C 523-524d

DH-C227	F2	185 266A 291 304 519	73 249d 263 315+C 747 750	
DH-C065	F2b1	92A 170T 183T 189 291 304	73 249d 263 315+C 517 523-524d 750	
DH-C081	F2b1	92A 170T 183T 189 291 304	73 249d 263 309+CC 315+C 517 523-524d	
DH-C332	F2b1	92A 183C 189 291 304 519	73 249d 263 309+C 315+C 523-524d	
DH-C395	F2b1	92A 170T 183T 189 291 304	73 249d 263 315+C 517 523-524d	
DH-C403	F2b1	92A 93 124 291 304	73 249d 263 309+C 315+C 523-524d	
DH-C253	F3a1	260 298 355 362	73 207 249d 263 309+CC 315+C	
DH-C327	F3b	220C 227 298 362	73 152 249d 263 309+CC 315+C	
DH-C063	F4a	126 140 189 207 304 362 399	73 146 249d 263 309+C 315+C 317A 750	
DH-C030	G	93 129 223 278 362	73 263 309+C 315+C 489	+
DH-C047	G	223 249 362	73 227T 263 309+C 315+C 489	-
DH-C126	G	223 362 519	73 263 309+C 315+C 489	+
DH-C221	G	172 217 223 319 381	73 94 152 173 263 315+C 373 482 489	+
DH-C056	G1c	126 223 362 519	73 263 315+C 489 593 709	+
DH-C378	G1c	126 223 362 519	73 263 489	+
DH-C402	G1c	126 223 362 519	73 263 315+C 489 593	+
DH-C039	G2a	129 223 278 292 362 519	52 73 263 309+C 315+C 489	+
DH-C090	G2a	189 223 227 234 278 362 519	73 263 315+C 455+TT 489	+
DH-C095	G2a	207 223 278 362	73 152 263 309+C 315+C 489	+
DH-C139	G2a	189 223 278 362	73 263 309+C 315+C 489	+
DH-C154	G2a	129 223 278 360 362	73 263 309+C 315+C 489	+
DH-C207	G2a	189 194 195 223 227 278 362 519	73 263 315+C 489	+
DH-C374	G2a	93 223 278 362 519	73 151 152 263 315+C 489	+
DH-C080	G3	223 274 319 362 519	73 228 263 309+CC 315+C	+
DH-C089	G3	166 223 274 362	73 146 263 309+C 315+C 489	+
DH-C252	G3	223 227 274 278 362 519	73 263 309+C 315+C 489 523-524d 709 750	+

DH-C334	G3	166 223 274 362	73 146 263 315+C 489 709	+
DH-C003	G3a2	186 223 240 274 311G 362	73 143 152 195 263 315+C 489 709 750	+
DH-C021	M*	188+C 193+C 293C 296+C 390 519	73 146 150 151 152 182 217 263 315+C 489 523-524d 750	
DH-C041	M*	69 136 217 223 319 381	73 94 173 204 263 315+C 482 489	
DH-C166	M*	223 519	73 146 152 199 263 309+C 315+C 489 523-524d	
DH-C398	M*	223 381 390	73 150 263 309+C 315+C 489	
DH-C066	M10a1a	93 193 223 311 357 497	73 146 263 315+C 489 523-524d	
DH-C103	M10a1a2	93 129 193 223 311 357 497 519	73 146 152 263 315+C 489 523-524d 569+TCCC	
DH-C135	M10a1a2	129 193 223 311 357 497 519	73 146 226 263 309+CC 315+C 489 523-524d	
DH-C156	M12a	93 129 172 182C 183C 189 223 234 290 519	73 125 127 128 146 152 195 263 309+CC 315+C 489	
DH-C142	M20	129 209 223 272 519	73 152 225 249d 263 309+C 315+C 316 489	
DH-C297	M20	129 209 223 272 519	73 152 189 195 225 249d 263 315+C 316 489 523-524d	
DH-C175	M21a	129 223 256 526	73 263 309+C 315+C 489	
DH-C329	M25	93 188 189 192 223 304 519	73 263 315+C 489	
DH-C149	M30c	51 223 320 357	73 146 195 207 263 309+C 315+C 356+C 489	
DH-C082	M33b	223 324 362 519	73 263 315+C	+
DH-C124	M33c	111 129 189 223 362 519	73 200 263 315+C 489 750	
DH-C335	M33c	111 223 362 519	73 263 315+C 489 523-524d	
DH-C032	M5a1	75 93 129 223 240 291 519	73 146 152 263 315+C 472 489 750	
DH-C029	M60a	223 284 319 519	73 263 315+C 489 523-524d 709 750	
DH-C261	M61	216 223 270 362 381 519	3 73 152 263 309+CC 315+C 489	
DH-C205	M7	223 320	73 146 207 263 309+CC 315+C 356+C 489	
DH-C076	M71	93 223 271	73 151 263 309+C 315+C 489 518	
DH-C088	M71b	174 223 260 264 271 519	73 151 263 309+CC 315+C 489 524+2AC	
DH-C324	M71b	223 260 264 271 519	73 151 263 309+CC 315+C 489	
DH-C111	M74	223 311 362	73 195 263 309+CC 315+C 385	+

DH-C189	M74	223 311 362	73 195 263 309+CC 315+C	+
DH-C276	M74	223 311 362	73 243 263 309+C 315+C 489	+
DH-C366	M74	223 311 362 519	73 263 315+C 489 573+C	+
DH-C042	M74a	223 274 311 362 381	63? 66T 67 73 263 315+C 489	
DH-C250	M74a	223 274 311 362 381	63 64 66 73 146 263 315+C 489	
DH-C113	M75	68 126 182C 183C 189 223 325 519	73 146 150 152 195 263 309+CC 315+C	
DH-C362	M75	51 68 182C 183C 189 223 311 399 519	73 143 146 150 152 263 315+C 489	
DH-C007	M7b	129 183C 189 217 223 519	73 150 199 263 315+C 489	
DH-C008	M7b	129 189 192+T 223 297	73 150 199 263 309+CC 315+C 489	
DH-C018	M7b	129 183C 189 223 297 468	73 150 199 204 263 309+CC 315+C 456 489 750	
DH-C025	M7b	129 192 223 297 519	73 150 263 309+C 315+C 489	
DH-C036	M7b	129 192 223 297 519	73 150 263 309+C 315+C 489	
DH-C057	M7b	129 223 297	73 150 159 199 263 315+C 489 750	
DH-C096	M7b	129 223 297 390	73 150 159 199 263 309+C 315+C 489 750	
DH-C115	M7b	129 192 223 297 519	73 150 263 309+CC 315+C 489 750	
DH-C134	M7b	129 192 223 234 297	73 150 199 263 309+C 315+C 489	
DH-C164	M7b	129 192 223 297	73 150 182 199 263 315+C 459d 489	
DH-C228	M7b	223 297 301	73 150 199 204 263 309+C 315+C 489	
DH-C260	M7b	129 192 223 289 297	73 150 182 199 263 315+C 459d 489	
DH-C279	M7b	129 192 223 297 311	73 150 152 182 199 263 309+C 315+C 489	
DH-C286	M7b	129 223 297 483	73 150 159 199 263 309+C 315+C 489	
DH-C319	M7b	129 189 192+T 223 297 519	73 150 199 263 309+CC 315+C	
DH-C325	M7b	129 189 192 223 297	73 150 199 204 207 263 315+C 489 750	
DH-C373	M7b	171 223 297	73 150 199 204 263 315+C 489	
DH-C296	M7b1	92 129 192 223 297	73 150 159 199 263 315+C 489	
DH-C083	M7b8	129 189 223 297	73 150 199 204 263 309+C 315+C 456 489	

DH-C084	M7b8	129 189 223 297	73 150 199 204 263 309+C 315+C 456 489	
DH-C258	M7c	129 519	73 146 199 263 315+C 489 523-524d	
DH-C058	M7c'e'f	75 129 223 240 258C 519	73 146 152 263 309+CC 315+C 472 489 750	
DH-C198	M7c'e'f	93 193 223 519	73 146 152 263 309+C 315+C 489	
DH-C259	M7c'e'f	93 223 390 519	73 146 263 315+C	
DH-C363	M7c'e'f	75 129 223 240	73 146 152 263 309+C 315+C 472 489 750	
DH-C014	M8a	223 298 319	73 263 309+C 315+C 489 523-524d 709 750	
DH-C284	M9a1b	213 223 234 311 362 519	73 150 152 153 263 309+C 315+C 489	+
DH-C387	M9a1b	223 224 234 316 362	73 152 153 263 309+C 315+C 489	+
DH-C159	M9a1b1	158 223 234 362 519	73 150 152 153 263 315+C 489 524+AC	+
DH-C183	M9a1b1	158 223 234 362 519	73 150 152 153 207 263 309+C 315+C 489	+
DH-C194	M9a1b1	158 223 234 362 519	73 150 152 153 207 263 315+C 489	+
DH-C233	M9a1b1	158 223 234 362 519	73 150 152 153 207 263 315+C 489	+
DH-C275	M9a1b1	158 223 234 362 519	73 150 152 153 207 263 309+C 315+C 489	+
DH-C060	M9a5	223 234 356 362	73 150 153 263 309+C 315+C 385 489	+
DH-C092	M9a5	223 234 356 362	73 150 153 263 309+C 315+C 385 489	+
DH-C390	M9b	51 209 223 362 519	73 153 263 315+C 489	+
DH-C298	N*	519	73 249d 263 315+C 518	
DH-C119	N10a	172 183C 189 223 362	73 185 189 263 285 315+C	
DH-C161	N10a	172 183C 189 223 293T 362	73 185 189 263 309+CC 315+C	
DH-C182	N10a	172 183C 189 223 362	73 185 189 263 285 309+CC 315+C	
DH-C210	N10a	172 183C 189 223 362	73 185 189 263 285 309+C 315+C	
DH-C137	N10b	69 172 223 278 291A 298 362 399	73 150 199 263 309+C 315+C	
DH-C343	N21	93 182 193 223 297 519	73 143 150 195 263 315+C 337d	
DH-C389	N21	182 193 223 260 519	73 150 195 263 315+C 337d	
DH-C170	N5	111 311	152 263 309+CC 315+C	

DH-C153	N9a	86 223 257A 261 311	73 150 263 309+C 315+C
DH-C138	N9a1	111 129 223 248 257A 261	73 150 263 309+C 315+C
DH-C009	N9a1	111 129 189 223 257A 261	73 150 263 309+C 315+C
DH-C102	N9a1	111 129 223 257A 261	73 150 263 309+C 315+C 513 709 750
DH-C163	N9a1	111 129 186 223 257A 261	73 150 263 309+C 315+C
DH-C391	R11	129 183C 189 352 355 519	73 150 152 185 189 263 309+CC 315+C 573+4C
DH-C338	R22	169 249 265C 288 291 304 519	58+C 73 152 199 263 309+C 315+C 329
DH-C349	R22	169 249 265C 288 291 304 519	73 152 199 263 309+C 315+C 329
DH-C015	R9	182C 183C 189 304 519	73 237 249d 263 309+CC 315+C 523-524d 750
DH-C067	R9	93 157 304	73 151 263 309+C 315+C 374 479
DH-C396	R9b	304 362 519	73 263 315+C
DH-C002	R9b1	192 295 304 309 390 519	73 152 263 309+C 315+C
DH-C050	R9b1a	192 259 288 304 309 390 519	73 143 183 263 309+C 315+C 523-524d 573+Cs
DH-C106	R9b1a	192 259 288 304 309 390 519	73 143 183 263 309+C 315+C 523-524d
DH-C031	R9b1b	124 148 184 304 309 390 519	73 263 309+C 315+C
DH-C249	R9b1b	124 148 275 304 309 327 390 519	73 152 263 309+C 315+C 523-524d
DH-C355	R9b1b	124 148 304 309 390 519	73 263 309+CC 315+C 750
DH-C266	R9c	183C 189 304 519	73 152 249d 263 309+CC 315+C 523-524d 750
DH-C167	R9c1	157 304 324	73 151 263 309+C 315+C 479
DH-C131	Z	185 223 260 298	73 152 207 249d 263 309+C 315+C 489 750
DH-C143	Z	185 223 260 298	73 152 249d 263 315+C 489 513
DH-C174	Z	185 223 260 298	73 152 153 249d 263 309+C 315+C 489 513
DH-C187	Z	148 223 260 298	73 210 249d 263 309+C 315+C 489
DH-C232	Z	129 185 188 223 260 298	73 152 194 249d 263 315+C 489
DH-C369	Z	185 223 260 298 519	73 152 249d 263 315+C 489
DH-C386	Z	185 223 298	73 152 207 249d 263 309+C 315+C 489

DH-C347	Z3a	93 185 223 260 293 298 357		73 152 207 249d 263 309+C 315+C 489

[a] When RFLP result was not available, items have been left blank. Haplogroup D is characterized by “-5178*Alu*I”.

Table S3. Haplogroup frequencies in injecting drug addicts and pooled normal controls

Haplogroup	IDUs (n= 577) No. (%)	Pooled Han[a] (n= 1212) No. (%)	IDUs versus Control #1 Adjusted *P*-value[b]	Adjusted *P*-value[c]	Adjusted *P*-value[d]
A	25 (4.3)	116 (9.6)	0.00038	0.003	0.018
B4	61 (10.6)	132 (10.9)	0.228	0.111	0.195
B5	44 (7.6)	63 (5.2)	0.425	0.509	0.605
C	26 (4.5)	66 (5.4)	0.251	0.728	0.732
D4	63 (10.9)	151 (12.5)	0.035	0.283	0.163
D5	16 (2.8)	36 (3.0)	0.366	0.251	0.141
F	121 (21.0)	216 (17.8)	reference	reference	reference
G	31 (5.4)	72 (5.9)	0.294	0.708	0.613
M12	8 (1.4)	7 (0.6)	0.137	0.065	0.052
M71	6 (1.0)	12 (1.0)	0.797	0.978	0.954
M7b	39 (6.8)	59 (4.9)	0.776	0.664	0.852
M7c	14 (2.4)	9 (0.7)	0.022	0.01	0.013
N10	6 (1.0)	6 (0.5)	0.479	0.142	0.214
N21	7 (1.2)	11 (0.9)	0.684	0.8	0.734
R9	19 (3.3)	29 (2.4)	0.814	0.719	0.749
Z	6 (1.0)	32 (2.6)	0.030	0.016	0.033
Others[e]	85 (14.7)	195 (16.1)	0.063	0.221	0.226

[a] Pooled control population contains the normal control in this study (N= 362) and the control population reported in our previous study (N= 850; Wang et al. 2012).

[b] *P*-value with an adjustment of age.

[c] *P*-value with an adjustment of gender.

[d] *P*-value with an adjustment of age and gender.

[e] "Others" contains mtDNA haplogroups with a relatively low frequency (each is shared by less than 6 IDUs) and those individuals with unassigned haplogroup status, such as M*, N*, R*.