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Mitochondrial DNA Haplogroup Background Affects LHON, but Not Suspected LHON, in Chinese Patients

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Abstract

Recent studies have shown that mtDNA background could affect the clinical expression of Leber hereditary optic neuropathy (LHON). We analyzed the mitochondrial DNA (mtDNA) variation of 304 Chinese patients with m.11778G>A (sample #1) and of 843 suspected LHON patients who lack the three primary mutations (sample #2) to discern mtDNA haplogroup effect on disease onset. Haplogroup frequencies in the patient group was compared to frequencies in the general Han Chinese population ($n = 1,689$; sample #3). The overall matrilineal composition of the suspected LHON population resembles that of the general Han Chinese population, suggesting no association with mtDNA haplogroup. In contrast, analysis of these LHON patients confirms mtDNA haplogroup effect on LHON. Specifically, the LHON sample significantly differs from the general Han Chinese and suspected LHON populations by harboring an extremely lower frequency of haplogroup R9, in particular of its main sub-haplogroup F (#1 vs. #3, $P\text{-value} = 1.46 \times 10^{-17}$, OR = 0.051, 95% CI: 0.016–0.162; #1 vs. #2, $P\text{-value} = 4.44 \times 10^{-17}$, OR = 0.049, 95% CI: 0.015–0.154; in both cases, adjusted $P\text{-value} < 10^{-5}$) and higher frequencies of M7b (#1 vs. #3, adjusted $P\text{-value} = 0.001$ and #1 vs. #2, adjusted $P\text{-value} = 0.004$). Our result shows that mtDNA background affects LHON in Chinese patients with m.11778G>A but not suspected LHON. Haplogroup F has a protective effect against LHON, while M7b is a risk factor.

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Introduction

The three primary mutations (m.3460G>A in the *MT-ND1* gene, m.11778G>A in the *MT-ND4* gene, and m.14484T>C in the *MT-ND6* gene) on mitochondrial DNA (mtDNA) have been identified to be the essential factors for Leber hereditary optic neuropathy (LHON, OMIM 535000). It is estimated that over 95% of LHON patients have one of the three primary mutations [1–4]. Despite decades of extensive study on LHON, several enigmas remain unresolved. Previous studies suggested that incomplete penetrance and gender bias in the clinical expression of LHON were modulated by many factors, such as mtDNA background, nuclear genes and environmental factors [5–11].

By way of replicating the same findings in different and independent cohorts, it has been well established in European LHON patients that haplogroups J2, J1 and K increase the risk of blindness in patients with m.11778G>A, m.14484T>C and m.3460G>A, respectively, and haplogroup H is suggested to be a protective factor for LHON patients with m.11778G>A [5,12–14]. Our previous study of Chinese families with m.11778G>A

showed that haplogroup M7b1'2 could increase the risk of vision loss but haplogroup M8a might produce a protective effect [15]. However, frequencies of haplogroups M7b1'2 and M8a are not significantly altered in LHON pedigrees compared to the normal controls despite their apparent background effect on the penetrance [15]. This pattern is quite different from that of European patients, in which there is an internal consistency of the haplogroup association, namely, haplogroup J is present at an increased frequency in LHON families with m.11778G>A and m.14484T>C, and subdivisions of this haplogroup show increased penetrance [5]. Dissecting haplogroups in European LHON families have shown that the increased frequency of J was indeed due to an increased frequency of two specific nested sub-clades of J (one deriving from J1 and another deriving from J2) [5,14]. Insufficient sampling (limited statistical power), and/or potential population stratification may account for the lack of internal consistency in our observation [15].

Besides the LHON patients with the primary mutations, there are many suspected LHON patients expressing LHON clinical features but carrying none of the three primary mutations [16].

The exact pathogenic mechanism of these heterogeneous patients with suspected LHON has not been well examined. Rare pathogenic mutations, e.g. m.3635G>A, might account for the disease expression in a very small portion of these patients (Ref. [17,18] and references therein). The *MT-ND1* and *MT-ND6* genes were found to be mutational hotspots for LHON patients without the three primary mutations in European populations [19,20]. Similarly, we found that the *MT-ND1* and *MT-ND5* genes are mutational hotspots in Chinese suspected LHON patients with a family history but lacking the three primary mutations [21]. Whether there is an effect of mtDNA background on suspected LHON has not been tested so far.

In order to further verify the mtDNA haplogroup effect on LHON and to discern the potential effect of mtDNA background in cases of suspected LHON, we dissected the matrilineal pool of 304 LHON samples with m.11778G>A and 843 suspected LHON samples lacking the three primary mutations. We further sequenced four complete M7b mtDNA genomes and evaluated haplogroup-specific genetic variants that may be relevant for the haplogroup association with LHON. Our study provided an updated profile for the effect of mtDNA background on LHON in Chinese populations.

Materials and Methods

Ethics statement

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 Zhongshan Ophthalmic Center and the Kunming Institute of Zoology approved this study.

Patients

The patients received ophthalmological examinations at the Pediatric and Genetic Clinic of the Eye Hospital, Zhongshan Ophthalmic Center and/or local medical centers, and were categorized according to the expression of LHON clinical features (e.g. painless, acute or sub-acute vision deterioration without apparent reasons). LHON patients with primary mutation m.14484T>C or m.3460G>A were reported elsewhere [22,23] and were not discussed in this study. 175 LHON patients with m.11778G>A had a family history and were described in our previous study [15]; these patients were reanalyzed with the new samples in this study. LHON patients with both m.11778G>A and m.593T>C (n = 14) and suspected LHON patients with m.593T>C (n = 12) were discussed in a separate paper [24]. Patients without the three primary mutations of LHON were simply regarded as patients with suspected LHON, despite that this grouping included a very small proportion of LHON patients that were caused by other rare primary LHON mutations. Blood samples were collected from patients in vacuum tubes containing EDTA. For some cases, blood samples were collected on filtered papers.

Screening of primary LHON mutations, sequencing the mtDNA control region and complete genome

The PCR-single strand conformation polymorphism (PCR-SSCP) and allele specific PCR (AS-PCR) methods were jointly used to detect the three primary mutations as previously described [25]. The presence of the three primary mutations in the patients was independently screened in Kunming using method described by Bi et al. [26]. The mtDNA control region sequence of each patient was amplified by using primer pair (L15594: 5′-CG-CCTACACAATTCTCCGATC-3′ and H901: 5′-ACTTGGGT-TAATCGTGTGACC-3′) and the following PCR condition: one pre-denaturation cycle at 94°C for 5 min; 30 cycles at 94°C for 30 sec, 52°C for 30 sec, 72°C for 2 min; and one extension cycle at 72°C for 10 min. The PCR products were purified and sequenced by sequencing primers, which were used in our previous study [27], on a 3730 DNA analyzer (Applied Biosystems). Each sample was sequenced for an approximate 1.4 kb fragment (mtDNA regions 16033–16569 and 1–850; numbering according to the revised Cambridge reference sequence (rCRS) [28]) which cover the mtDNA control region, the *MT-TF* gene and part of the *MT-RNR1* gene. We determined the entire mtDNA sequences for four LHON patients (Fig. S1) belonging to haplogroup M7b1′2 using the same procedure and condition described in our previous study [27]. Novelty and potential pathogenicity for those non-synonymous private variants in these lineages were analyzed using the same method reported by Bandelt et al. [29].

mtDNA haplogroup classification and statistical analysis

The sequences were compared with the rCRS [28] and the variants in each mtDNA sequence were recorded and were further checked by using the MitoTool (www.mitotool.org) [30]. We classified each sample based on the haplogroup motifs that were identified according to the PhyloTree (http://www.phylotree.org; mtDNA tree Build 9, 20 Jun 2010) [31]. For samples which could not be unambiguously determined by the mtDNA control region sequence variants, PCR- restriction fragment length polymorphism (RFLP) analysis for specific coding region variant(s) was performed, e.g. a check of −5176*Alu*I was performed to confirm haplogroup D status.

We first compared the matrilineal composition of suspected LHON patients (n = 843) to 1,689 pooled Han Chinese mtDNAs from the general populations (Table S1), to discern the potential effect of mtDNA background on the onset of suspected LHON. Under the null hypothesis that the suspected LHON patients had a similar matrilineal composition as the pooled Han Chinese, the suspected LHON patients could be used as a second control group for comparison to the LHON patients. We then compared the newly obtained 304 LHON patients with m.11778G>A to the suspected LHON samples and the pooled Han Chinese samples, respectively, to discern the mtDNA haplogroup background effect on LHON and to verify the pattern as observed in our previous studies based on limited sample sizes [15]. We next pooled the newly obtained LHON patients (n = 304) with the reported LHON patients (n = 175; [15]). Combining these two different datasets provide more statistical power than the strategy of analyzing both data sets separately (Methods S1) [32].

Pearson's chi-square test with a one degree of freedom was used to assess the significance of the differences observed in haplogroup frequencies between cases and controls. The Fisher Exact test (two tailed) was applied to those cases with cell counts below five. A permutation test was used to address the issue of multiple testing in haplogroup association test; 100,000 permutations were used in all comparisons. The statistical package SPSS (version 15.0) and Stata v.8 (http://www.stata.com) were used for all the computations; adjusted *P*-values below 0.05 were considered to be statistically significant.

Results

Patient features

A total of 1,322 unrelated subjects collected from different provinces in China were enrolled in the current analysis based on the availability of DNA after the initial primary mutation

screening. These patients included 479 LHON patients with mutation m.11778G>A (including 175 samples reported in our previous study [15] and 304 samples newly sequenced) and 843 suspected LHON patients who expressed clinical features but did not harbor any of the three primary mutations. Only one out of 479 patients had the heteroplasmic mutation m.11778G>A. The overall frequency of patients with heteroplasmic mutation m.11778G>A was thus very low (0.21%; 1/479) in these Chinese patients based on the limitation of detection sensitivity of our approach. The mtDNA control region sequence variations for each patient are listed in the online Tables S2 and S3, and the sequences can be retrieved from GenBank under the Accession Numbers HM632037–HM632340 (for 304 LHON patients with m.11778G>A) and HM632341–HM633183 (for 843 suspected LHON patients).

mtDNA Haplogroup distribution in patients with suspected LHON

We first dissected the matrilineal genetic components in the suspected LHON (sample #2) and compared to the pooled Han

Chinese from the general populations (sample #3, $n = 1,689$). As shown in Table 1 and Fig. 1, the overall matrilineal composition of the 843 suspected LHON patients resembled that of the pooled Han Chinese. There was no statistically significant difference for any of the haplogroup classes between the two populations. Therefore, the suspected LHON sample, despite of its miscellaneous nature of the disease, could be used as the second independent control sample to compare with LHON patients with m.11778G>A in the subsequent analyses.

mtDNA Haplogroup distribution in LHON patients with m.11778G>A

To compare with the pattern that was reported in our previous studies based on limited number of patients [15], we treated the newly obtained 304 LHON patients as an independent sample (sample #1) and compared to the two control population groups. We found that haplogroups R9 (including its subhaplogroups F, F1, F1a) and M7b presented remarkable differences between the LHON patients and the controls after adjusting for multiple test (Tables 2 and 3). The LHON sample significantly differs from the

Table 1. Haplogroup frequencies and Pearson's chi-square test in 843 patients with suspected LHON and 1,689 Han Chinese from the general populations.

Haplogroup	Suspected LHON	Pooled Han Chinese[a]	P-value[b]	Adjusted P-value[c]	OR	95% CI
A	31	92	0.064	0.686	0.663	0.437–1.004
B4	126	196	0.021	0.314	1.339	1.052–1.703
B5	54	94	0.448	1.000	1.161	0.822–1.640
C	35	51	0.172	0.969	1.391	0.897–2.157
D4	115	252	0.423	1.000	0.901	0.710–1.143
D5	32	88	0.139	0.934	0.718	0.475–1.085
R9[d]	164	305	0.394	0.999	1.413	0.804–2.483
F	143	274	0.677	1.000	1.055	0.845–1.317
F1	99	193	0.229	0.991	1.175	0.903–1.530
F1a	71	132	0.281	0.997	1.165	0.882–1.541
F2	17	48	0.216	0.988	1.421	0.812–2.487
F2a	16	22	0.246	0.994	1.466	0.766–2.806
F3	12	15	0.216	0.988	1.612	0.751–3.458
F3a	12	13	0.117	0.887	1.862	0.846–4.098
F4	7	8	0.270	0.996	1.759	0.636–4.868
G	31	71	0.598	1.000	0.870	0.566–1.338
M10	14	35	0.579	1.000	0.798	0.427–1.492
M12	8	4	0.031	0.436	4.036	1.212–13.441
M7b	59	119	1.000	1.000	0.993	0.718–1.372
M7c	32	54	0.504	1.000	1.195	0.765–1.865
M8a	27	63	0.575	1.000	0.854	0.540–1.351
M9a	11	29	0.539	1.000	0.757	0.376–1.522
N9a	33	62	0.847	1.000	1.069	0.695–1.645
R11	5	10	1.000	1.000	1.002	0.341–2.940
Y	7	16	0.944	1.000	0.876	0.359–2.136
Z	21	50	0.585	1.000	0.837	0.500–1.404

[a]Pooled Han Chinese were from reported populations (see Table S1 for more information).
[b]Two tailed Fisher exact test was applied instead of a Pearson chi-square test in cases containing cell counts below five.
[c]Adjusted P-value: adjustment of P-values was carried out with a permutation-based approach; number of permutations = 100,000; OR (95% CI): Odds Ratio (95% Confidence Interval).
[d]Note that haplogroup F is a sub-haplogroup of haplogroup R9 and therefore the number of F mtDNAs are also included here.
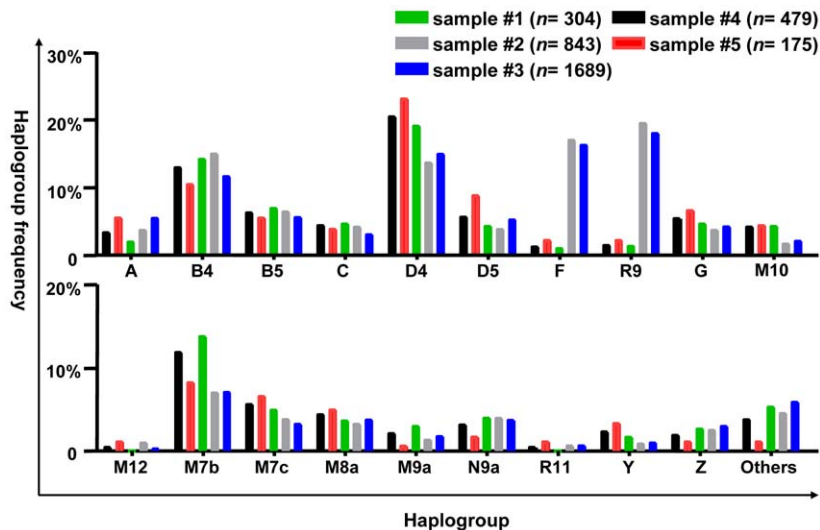doi:10.1371/journal.pone.0027750.t001

Figure 1. mtDNA haplogroup distribution frequency of different cohorts of LHON patients with m.11778G>A and control samples.
Detailed information for the newly sequenced LHON patients with m.11778G>A (sample #1, n = 304), reported LHON patients with m.11778G>A in our previous study (sample #5, n = 175; Ref. [15]), pooled LHON patients (sample #4, n = 479), suspected LHON patients (sample #2, n = 843) and the reported Han Chinese from the general populations (sample 3, n = 1,689; Table S1) are listed in Tables 2 and 3 and Tables S4, S5, S6, S7. Haplogroup R9 contains samples belonging to haplogroup F and its subhaplogroups. We lumped together all these haplogroups that occurred in less than five individuals per haplogroup as others.
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general Han Chinese and suspected LHON populations by harboring an extremely lower frequency of haplogroup R9 (#1 vs. #3, $P\text{-value} = 7.62 \times 10^{-19}$, OR = 0.061, 95% CI: 0.022–0.164; #1 vs. #2, $P\text{-value} = 5.19 \times 10^{-19}$, OR = 0.055, 95% CI: 0.020–0.150; in both cases, adjusted P-value $< 10^{-5}$), in particular of its main sub-haplogroup F (#1 vs. #3, $P\text{-value} = 1.46 \times 10^{-17}$, OR = 0.051, 95% CI: 0.016–0.162; #1 vs. #2, $P\text{-value} = 4.32 \times 10^{-17}$, OR = 0.049, 95% CI: 0.015–0.154; in both cases, adjusted P-value $< 10^{-5}$) and higher frequencies of M7b (#1 vs. #3, $P\text{-value} = 7.00 \times 10^{-5}$, adjusted P-value = 0.001 and #1 vs. #2, $P\text{-value} = 3.23 \times 10^{-4}$, adjusted P-value = 0.004). Distribution of the other haplogroups had no statistical difference between the two comparisons after adjustment of P-values.

We further pooled the newly analyzed LHON patients with the previously reported LHON patients [15] as one population for comparison, to increase the power of the statistical test [32]. The dissection of matrilineal genetic components in the enlarged LHON population [479 LHON patients with m.11778G>A (sample #4)] and comparison to the two control groups [suspected LHON (sample #2) and pooled Han Chinese from the general populations (sample #3)] revealed several interesting yet important features (Fig. 1 and Tables S4 and S5). First, haplogroups M7b (#4 vs. #3, adjusted P-value = 0.018; #4 vs. #2, adjusted P-value = 0.047) and possibly D4 (#4 vs. #3, adjusted P-value = 0.085; #4 vs. #2, adjusted P-value = 0.031) are both more prevalent in patients with LHON than in the general Han Chinese group. Most of LHON patients with m.11778G>A belonging to haplogroup M7b could be further classified into M7b1'2 (77.19%, 44/57). Second, haplogroup R9, and more specifically, its sub-haplogroup F has a strikingly lower frequency in LHON patients with m.11778G>A than in the other two control populations (#4 vs. #3, nominal $P\text{-value} = 1.999 \times 10^{-24}$, adjusted P-value $< 10^{-5}$; #4 vs. #2, nominal $P\text{-value} = 9.133 \times 10^{-23}$, adjusted P-value $< 10^{-5}$). This significance is still strongly maintained for several F sub-haplogroups (F, F1, F1a), as also indicated when analyzing the newly sequenced LHON

patients (Tables 2 and 3) and the reported LHON patients with m.11778G>A in our previous study (Ref. [15] and references therein) (Tables S6 and S7), separately.

Complete mtDNA tree for LHON patients belonging to haplogroup M7b1'2

In order to further evaluate the effect of the haplogroup-specific variants that account for the haplogroup association with LHON, we determined four M7b complete mtDNAs (GenBank accession numbers JN645818–JN645821), and analyzed these sequences with those from published sources [24]. Five private variants (including four non-synonymous and one rRNA variant) were found in the four patients, but none of these variants (with the exception of m.8999T>C [p.V158A]) were conserved according to the evolutionary analysis performed by the MitoTool web server (Table 4). Two of these private variants (m.13105A>G and m.14978A>G) were reported as haplogroup-specific variants for other haplogroups. Interestingly, m.6228C>T (p.L109F) in patient Le777 and m.13105A>G (p.I257V) in patient Le666 were previously reported in LHON patients belonging to haplogroup M7b1'2 [15]. We presented sequence variants in each mtDNA in a classification tree following our previous strategy [15] (Fig. 2). The newly determined M7b sequences indicated two novel clades within M7b1, which were defined by m.13105A>G and m.6228C>T, respectively. We counted the number of private variants that were located in the terminal branches of the phylogenetic tree in each of the 13 mitochondrial DNA encoding genes in 12 LHON patients sequenced in this study and our previous study [15], and compared to that of 69 reported complete mtDNAs from the general populations (refer to [21] and references therein). There was no difference regarding the occurrence of private non-synonymous (NS) and synonymous (S) substitutions between the LHON patients and controls from the general populations; note that the sample size was very limited and this result should be treated with caution (Table S8).

Table 2. Haplogroup frequencies and Pearson's chi-square test in 304 LHON patients with m.11778G>A and 843 patients with suspected LHON.

Haplogroup	LHON	Suspected LHON	P-value[a]	Adjusted P-value[b]	OR	95% CI
A	6	31	0.150	0.931	0.527	0.218–1.277
B4	43	126	0.735	1.000	0.938	0.645–1.363
B5	21	54	0.761	1.000	1.084	0.643–1.827
C	14	35	0.738	1.000	1.114	0.591–2.101
D4	58	115	0.023	0.304	1.493	1.055–2.112
D5	13	32	0.712	1.000	1.132	0.586–2.187
R9[c]	4	164	5.190×10^{-19}	$<10^{-5}$	0.055	0.020–0.150
F	3	143	4.319×10^{-17}	$<10^{-5}$	0.049	0.015–0.154
F1	2	99	1.003×10^{-11}	$<10^{-5}$	0.050	0.012–0.203
F1a	1	71	6.614×10^{-9}	$<10^{-5}$	0.036	0.005–0.259
F2	0	17	9.725×10^{-3}	0.141	0.731	0.706–0.757
F3	1	12	0.203	0.979	0.229	0.030–1.765
F3a	1	12	0.203	0.979	0.229	0.030–1.765
F4	0	7	0.200	0.977	0.733	0.708–0.759
G	14	31	0.475	1.000	1.265	0.663–2.411
M10	13	14	0.010	0.144	2.645	1.229–5.694
M12	0	8	0.119	0.872	0.733	0.708–0.759
M7b	42	59	3.233×10^{-4}	0.004	2.130	1.400–3.241
M7c	15	32	0.391	0.999	1.315	0.702–2.465
M8a	11	27	0.729	1.000	1.135	0.556–2.316
M9a	9	11	0.059	0.631	2.308	0.947–5.624
N9a	12	33	0.980	1.000	1.009	0.514–1.979
R11	0	5	0.333	0.999	0.734	0.709–0.760
Y	5	7	0.232	0.989	1.997	0.629–6.340
Z	8	21	0.894	1.000	1.058	0.464–2.414

[a]Two tailed Fisher exact test was applied instead a Pearson chi-square test in cases containing cell counts below five.
[b]Adjusted P-value: adjustment of P-values was carried out with a permutation-based approach; number of permutations = 100,000; OR (95% CI): Odds Ratio (95% Confidence Interval).
[c]Note that haplogroup F is a sub-haplogroup of haplogroup R9 and the number of F mtDNAs are also included here.
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Discussion

In recent years, many studies reported that mtDNA background affects the expression of human disorders [33–37], although some positive findings could respond to false positives [38]. Among these studies, LHON is probably the most extensively studied disease that has been reported to be modulated by mtDNA haplogroups [5,12–15]. In this study, we analyzed 479 unrelated LHON samples with m.11778G>A (including 175 LHON patients reported in our previous study [15] and 304 patients newly sequenced) and 843 suspected LHON patients without the three primary mutations, with the aim of primarily addressing the following questions: (1) does mtDNA haplogroup background contribute to the suspected LHON? (2) will the enlarged LHON patients with m.11778G>A discern the internal consistency of the haplogroup association of LHON penetrance? Dissecting the matrilineal components of the enlarged sample size of LHON patients with m.11778G>A and the suspected LHON patients did provide new insightful information to both questions.

In contrast to the pattern that was observed in the LHON patients with m.11778G>A [15], the overall matrilineal composition of the suspected LHON patients resembles that of the pooled Han Chinese, showing no evident effect from mtDNA background (Fig. 1 and Tables 1, 2, 3). This result was not surprising, as the suspected LHON cohort was quite heterogeneous and might be caused by nuclear gene defects, as well as, some rare mtDNA pathogenic mutations. Indeed, we analyzed some of these patients and identified mutations in the OPA1 gene, suggesting that these patients should be classified as autosomal dominant optic atrophy (ADOA; authors' unpublished data). Nonetheless, the suspected LHON population could be used as a suitable control population for the LHON patients carrying m.11778G>A. In addition, both LHON carriers and none carriers of m.11778G>A were collected in the same geographic origin, a fact that helps to prevent the undesirable effects of population stratification in inflating type I error.

A direct comparison of the frequencies of the matrilineal components between the LHON population and the suspected LHON population or between the LHON population and the pooled Han Chinese from the general populations yields meaningful information on the mtDNA background effect on LHON. Haplogroup M7b1′2, which was found to increase vision loss risk in the presence of m.11778G>A [15], had a significantly higher occurrence in LHON patients with this mutation than in patients with suspected LHON or in Han Chinese from the general populations (Tables 2 and 3 and Tables S4 and S5). This

Table 3. Haplogroup frequencies and Pearson's chi-square test in 304 LHON patients with m.11778G>A and 1,689 Han Chinese from general populations.

Haplogroup	LHON	Pooled Han Chinese[a]	P-value[b]	Adjusted P-value[c]	OR	95% CI
A	6	92	0.010	0.144	0.350	0.152–0.806
B4	43	196	0.210	0.981	1.255	0.880–1.790
B5	21	94	0.355	1.000	1.259	0.772–2.055
C	14	51	0.152	0.948	1.551	0.847–2.838
D4	58	252	0.065	0.673	1.344	0.980–1.844
D5	13	88	0.494	1.000	0.813	0.448–1.474
R9[d]	4	304	7.621×10^{-19}	$<10^{-5}$	0.061	0.022–0.164
F	3	274	1.461×10^{-17}	$<10^{-5}$	0.051	0.016–0.162
F1	2	193	2.822×10^{-12}	$<10^{-5}$	0.051	0.013–0.208
F1a	1	132	5.356×10^{-9}	$<10^{-5}$	0.039	0.005–0.280
F2	0	48	7.125×10^{-4}	0.012	0.844	0.828–0.860
F3	1	15	0.492	1.000	0.368	0.049–2.799
F3a	1	13	0.708	1.000	0.425	0.055–3.265
F4	0	8	0.616	1.000	0.847	0.831–0.863
G	14	71	0.750	1.000	1.100	0.612–1.978
M10	13	35	0.021	0.288	2.111	1.104–4.039
M12	0	4	1.000	1.000	0.847	0.831–0.863
M7b	42	119	6.669×10^{-5}	0.001	2.115	1.453–3.078
M7c	15	54	0.127	0.908	1.572	0.875–2.822
M8a	11	63	0.925	1.000	0.969	0.505–1.861
M9a	9	29	0.144	0.936	1.746	0.818–3.727
N9a	12	62	0.814	1.000	1.078	0.574–2.026
R11	0	10	0.376	1.000	0.847	0.831–0.863
Y	5	16	0.273	0.995	1.749	0.636–4.809
Z	8	50	0.754	1.000	0.886	0.416–1.888

[a]Pooled Han Chinese were from reported populations (see Table S1 for more information).
[b]Two tailed Fisher exact test was applied instead a Pearson chi-square test in cases containing cell counts below five.
[c]Adjusted P-value: adjustment of P-values was carried out with a permutation-based approach; number of permutations = 100,000; OR (95% CI): Odds Ratio (95% Confidence Interval).
[d]Note that haplogroup F is a sub-haplogroup of haplogroup R9 and the number of F mtDNAs are also included here.
doi:10.1371/journal.pone.0027750.t003

Table 4. Private non-synonymous and mt-rRNA variants in four Chinese LHON patients with m.11778G>A and a haplogroup status of M7b1'2.

Sample	Haplogroup	Nucleotide variant (Amino acid change)	Gene	Conservation Index[a]	Reported[b] (population context)	Reported[b] (disease context)	Haplogroup specific variant[c]
Le95	M7b2	m.8999T>C (p.V158A)	MT-ATP6	1.000	Yes	No	No
		m.866A>G	MT-RNR1	0.256	Yes	No	No
Le666	M7b1	m.13105A>G (p.I257V)	MT-ND5	0.256	Yes	Yes	L5c, L3b, L3e2a, etc.
Le777	M7b1	m.6228C>T (p.L109F)	MT-CO1	0.140	Yes	Yes	No
Le978	M7b1'2'4	m.A14978G (p.I78V)	MT-CYB	0.651	Yes	Yes	C7a1

[a]The evolutionary conservation analysis was performed by comparing human mtDNA (GenBank accession no. J01415) to 43 different primate species by using the MitoTool (http://www.mitotool.org) [30]. A conservation index of 1 for certain variant means that this position is conserved in all species considered for comparison.
[b]Web and dataset based searches were performed on September 5, 2011, following the same strategy described in our previous study [29] (e.g. both 'G6249A mtDNA' and 'm.6249G>A mtDNA' were queried).
[c]The column "Haplogroup specific variant" refers to the presence of the corresponding variant in the world mtDNA phylogenetic tree displayed at http://www.phylotree.org/tree/main.htm (mtDNA tree Build 12; 20 Jul 2011) [31]. We listed the haplogroup name if it was characterized by the private variants identified in our newly generated M7b sequences.
doi:10.1371/journal.pone.0027750.t004
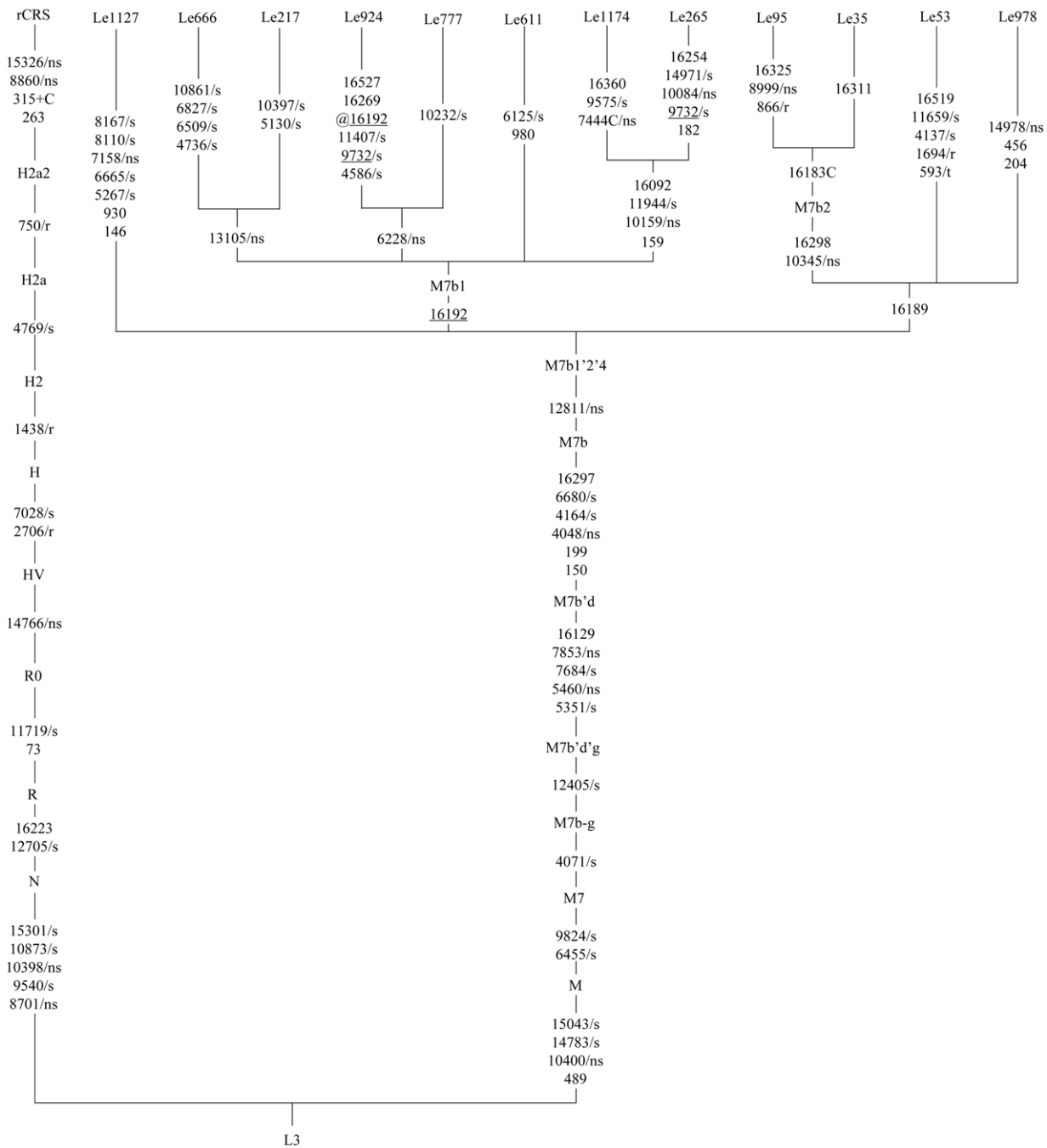
Figure 2. Classification tree of M7b complete mtDNA sequences, plus the revised Cambridge reference sequence (rCRS) [28]. Five Chinese LHON mtDNAs (including Le53 (GenBank accession number JF896798) which was reported in our recent study [24]) belonged to haplogroup M7b1′2 were analyzed. The length polymorphisms of the C-tracts in region 303–309 were not considered. Mutations on each uninterrupted branch segment are listed in an arbitrary order. Recurrent mutations are underlined. The synonymous and non-synonymous coding-region variants in each mtDNA are denoted by "/s" and "/ns", respectively. Variants in the rRNA genes and tRNA genes are denoted by "/r" and "/t", respectively.
doi:10.1371/journal.pone.0027750.g002

observation provides direct evidence for the internal consistency of association of haplogroup M7b1′2 with clinical expressions of LHON, as predicted by our previous study [15]. Note that in our previous study [15], the sample size for the control Han Chinese population was relatively small (n = 408) and this would bias the comparison for certain haplogroup. This defect had been corrected by including more Han Chinese samples from the general populations (n = 1,689) in the current analysis (Tables S6

and S7). As shown in Tables S2 and S3, most of the mtDNAs belonging to M7 and its subhaplogroups carry different control region profiles, indicating no close maternal relationship between these carriers; the different frequencies observed between cohorts are unlikely to be caused by close kinship. Analysis of the complete mtDNA sequence variation in those LHON patients belonging to M7b further supported our previous result that variant m.12811T>C would account for the haplogroup association with

LHON [15]. It seems that no other private variants would account for the overall increased risk for visual loss for pedigrees belonging to haplogroup M7b1′2.

On the other hand, haplogroup M8a was found to reduce the clinical penetrance of mutation m.11778G>A in Chinese families in our previous study [15]. However, even with increased sample size of LHON patients, there was no indication, as it was expected, of a reduced frequency of M8a in LHON patients relative to control populations.

Consistent with the previous observations [15], haplogroup D4 has a substantially higher frequency in the LHON patients (for 304 new patients, 58/304 = 19.08%; for pooled 479 patients, 98/479 = 20.50%) than in patients with suspected LHON (13.64%, 115/843) or in the pooled Han Chinese population (14.92%, 252/1689), though the adjusted P-value is not statistically significant (but marginal for pooled samples) between LHON patients and pooled Han Chinese. Because more than half of the LHON patients analyzed in this study were sporadic cases and we lacked the detailed clinical information for some families with self-reported disease history, we were unable to perform a correlation analysis to discern the effect of haplogroup D4 on the clinical expression of LHON. We failed to discern such an effect in our previous analysis for LHON families with m.11778G>A (Ref. [15] and references therein). Haplogroup D4 is defined by a string of non-synonymous variants (m.5178C>A in the *MT-ND2* gene and m.8414C>T in the *MT-ATP6* gene), synonymous variants (m.4883C>T in the *MT-ND2* gene, m.14668C>T in the *MT-ND6* gene) and one variant (m.3010G>A) in the *MT-RNR2* gene. It is most likely that the non-synonymous variants of haplogroup D4 might be responsible for the potentially functional effect. Indeed, variant m.5178C>A had been reported to be associated with a variety of human disorders [39] and longevity [40], despite the fact that there was controversy regarding its role in longevity [41], and the functional assay did not support the notion that this variant could alter mitochondrial matrix pH and intracellular calcium dynamics [42]. The exact role of haplogroup D4 in LHON needs further study.

Haplogroup F was very rare in the LHON patients (for 304 new patients, 3/304 = 0.99%; for pooled 479 patients, 6/479 = 1.25%), compared with its occurrence in the pooled Han Chinese from the general populations (274/1689 = 16.22%) and in the suspected LHON patients (143/843 = 16.96%). This result again confirmed the observation in our previous study [15] and a recent study in LHON patients from Thailand [10], in which an extremely low frequency of haplogroup F (including its subhaplogroups) was observed in LHON patients with m.11778G>A. Although the confounding effect of population stratification cannot be fully disregarded, the clear-cut different frequency of haplogroup F in two independent Chinese LHON patient cohorts (patients newly determined in this study and reported in our previous study [15]; Tables 2 and 3, Tables S6 and S7) with respect to the two independent control groups (suspected LHON patients plus the general Han Chinese) is so pronounced that it is reasonable to consider an alternative hypothesis that would involve haplogroup F as a protective factor in LHON patients. Because only six patients with m.11778G>A belong to haplogroup F in the LHON patients and half of them were sporadic, we could not estimate its potential effect on the clinical expression of LHON and analysis of the complete mtDNA sequence of some of these subjects yielded no insightful information [15]. Intriguingly, we also noticed a very low prevalence of F lineages (1.92%; 1/52) in LHON subjects with m.14484T>C in our recent study [23]. The exact reason for the extremely low frequency of F lineages in LHON patients with

m.11778G>A or m.14484T>C remains enigmatic. Notably, haplogroup F is one of the sub-clades of haplogroup R9, and R9 showed evidently lower frequency in LHON patients than in the two control samples (Tables 2 and 3, Tables S4, S5, S6, S7), so the ancient genetic variants of haplogroup R9 might contribute to the pathogenesis of LHON patients. Variant m.13928G>C was the only non-synonymous nucleotide change at the basal branch level of haplogroup R9 and caused serine to threonine at position 531 of the MT-ND5 protein, but this variant did not alter the hydrophobicity significantly and occurred multiple times in different populations and haplogroup backgrounds (cf. www. phylotree.org). Similar to mtDNA variant m.12811T>C which has been considered as the cause for the increased risk of M7b1′2 [15] and occurred in worldwide regions, the conservation and the hydrophobicity of m.13928G>C did not prove itself to be the possible pathogenic mutation, although recent studies showed that ancient variation may influence mtDNA replication and transcription [43] or contribute to cellular physiological changes in the presence of the primary mutations [44]. The deletion of adenine at position 249 is a characteristic variant of haplogroup F and other Asian haplogroups CZ, M31a1 and M36d1 [31]. Variant m.249delA was located in the mtTF1 binding site (MT-TFX or TFAM) which binds with mtTF and controls mtDNA transcription [45]. Some single base changes within this region have been identified to alter protein binding efficiency [43]. Whether m.249delA could affect the efficiency of mtDNA transcription remains unclear.

Population stratification could in part explain the results obtained in the present study. Monitoring population stratification is complex in mtDNA studies, but the use of two control groups, as performed in this study, helps to prevent its undesirable consequences in case-control studies. On the other hand, whether treating the newly analyzed 304 LHON patients with m.11778G>A and the reported LHON patients in our previous study [15] as independent samples, or pooled these new patients with the previously reported LHON patients [15] as an enlarged sample, we could get consistent findings for a lower frequency of the nested haplogroups R9, F, F1, and F1a. Therefore, we believe that different distribution frequencies of these haplogroups in LHON patients and control populations were biologically meaningful and might be shaped by the selection effect during the past.

One limitation of the current study is that we lacked detailed clinical information for these patients newly sequenced in this study (most of these patients were collected more than five years ago and there was no follow-up information), we could not perform a systematic estimation for LHON penetrance, disease severity and propensity to spontaneous recovery of visual acuity, as well as, their correlation with mtDNA genetic background. In future study, we will attempt to collect all detailed clinical data for each newly recruited patient and fulfill the task.

In summary, analysis of more newly collected LHON patients with m.11778G>A further supports the pattern that was observed in our previous studies [15], in that a significantly higher prevalence of haplogroups M7b and a strikingly low occurrence of haplogroup F have been confirmed. The higher frequency of M7b in patients with m.11778G>A than in control samples provides evidence for the internal consistency of association of haplogroup M7b1′2 with clinical expression of LHON. There was no evident effect of mtDNA background on Chinese patients with suspected LHON. Future studies could assist in providing further support to the present findings and provide new clues on the molecular mechanism by which a particular mtDNA background could influence clinical expression of LHON.

Supporting Information

Figure S1 Pedigree information for three Chinese LHON families with m.11778G>A that were sequenced for the entire mtDNA sequence. Patient Le95 was regarded as sporadic according to our definition for sporadic patient in our recent study [23]. Affected individuals are marked by filled symbols. The proband that was sequenced for the entire mtDNA sequence in each family was marked by an arrow. The probands in these families had been analyzed for the mtDNA control region sequence variation in our previous study [15].
(DOC)

Table S1 Information for the reported Han Chinese from the general populations.
(DOC)

Table S2 mtDNA sequence variation and haplogroup classification of 304 patients with LHON and m.11778G>A.
(XLS)

Table S3 mtDNA sequence variation and haplogroup classification of 843 patients with suspected LHON.
(XLS)

Table S4 Haplogroup frequencies and Pearson's chi-square test in 479 LHON patients with m.11778G>A and 843 patients with suspected LHON.
(DOC)

Table S5 Haplogroup frequencies and Pearson's chi-square test in 479 LHON patients with m.11778G>A and 1,689 Han Chinese from the general populations.
(DOC)

Table S6 Haplogroup frequencies and Pearson's chi-square test in 175 LHON patients with m.11778G>A and 843 patients with suspected LHON.
(DOC)

Table S7 Haplogroup frequencies and Pearson's chi-square test in 175 LHON patients with m.11778G>A and 1,689 Han Chinese from general populations.
(DOC)

Table S8 Comparison of the non-synonymous (NS) and synonymous (S) substitutions at the terminal branch level in the phylogenetic tree between 12 LHON patients belonging to haplogroup M7b1′2 and 69 reported Chinese complete mtDNAs from the general populations.
(DOC)

Methods S1 Supplementary methods for power calculations.
(DOC)

Author Contributions

Conceived and designed the experiments: Y-GY A-MZ QZ. Performed the experiments: A-MZ XJ RB. Analyzed the data: A-MZ RB AS Q-PK Y-GY. Contributed reagents/materials/analysis tools: QZ XJ SL XX PW XG. Wrote the paper: Y-GY A-MZ AS.

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Methods S1. Supplementary methods for power calculations

Power calculations were performed using the Quanto software [1], although this software was specifically designed for autosomal data; see comments in Salas et al. [2].

Statistical power of the test

Considering an average population minimum allele frequency (MAF) of 10%, the power to detect odds ratios as low as 1.5 for risk or protective haplogroups was above 80% in all the cases: a) 98% when considering suspected LHON patients vs. general Han Chinese, b) 84% when considering LHON patients vs. suspected LHON patients, and c) 91% for the comparisons between LHON patients vs. general Han Chinese.

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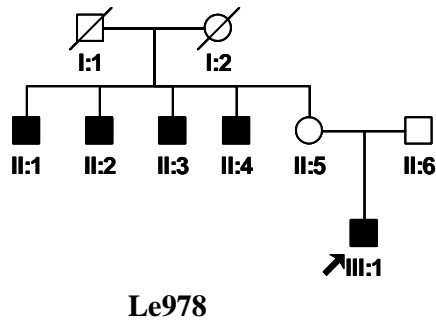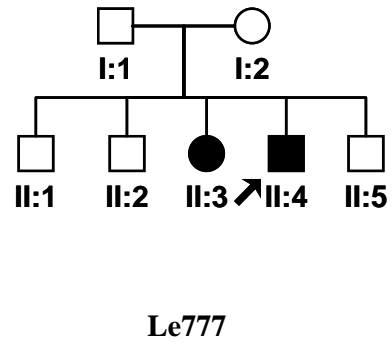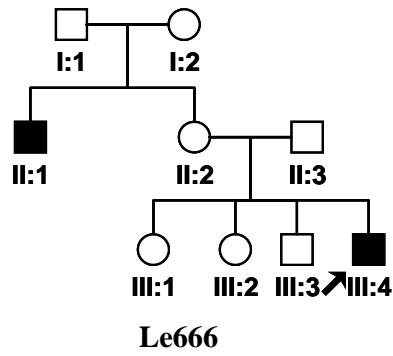
Le666

Le777

Le978

Figure S1 Pedigree information for three Chinese LHON families with m.11778G>A that were sequenced for the entire mtDNA sequence. Patient Le95 was regarded as sporadic according to our definition for sporadic patient in our recent study [23]. Affected individuals are marked by filled symbols. The proband that was sequenced for the entire mtDNA sequence in each family was marked by an arrow. The probands in these families had been analyzed for the mtDNA control region sequence variation in our previous study [15].

Table S1. Information for the reported Han Chinese from the general populations

Location	No. of samples	References
Shandong	126	1, 2
Hubei	42	2
Xinjiang	47	2
Yunnan	101	2, 4
Anhui	42	4
Fujian	54	4
Gansu	45	4
Guangxi	26	4
Hunan	16	4
Jiangsu	67	4
Jiangxi	23	4
Liaoning	102	4
Neimeng	45	4
Qinghai	44	4
Sichuan	70	4
Shanghai	56	4
Shanxi	53	4
Zhejiang	61	4
Guangdong	669	2, 3, 5, 6, 7
Total	1689	—

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Table S2. mtDNA sequence variation and haplogroup classification of 304 patients with LHON and m.11778G>A

Sample	Gender	Haplogroup	Sequenced region	Segment I (16000+)	Segment II	5176(*Alu* I)
Le209	M	A	16013-16569 and 1-908	93 195 223 230 290 319 362	73 152 235 263 309+CC 315+C 523-524d 663 750	
Le445	M	A	16010-16569 and 1-920	223 290 292A 319 362	73 152 199 235 263 298A 309+CC 315+C 523-524d 663 750	
Le1319	M	A	16006-16569 and 1-908	86 169 223 265 290 319 362	73 146 152 207 235 309+C 315+C 523-524d 663 750	
Le215	M	A	16012-16569 and 1-911	93 223 290 319 362	73 152 200 235 263 309+C 315+C 523-524d 663 750	
Le1045	M	A	16012-16569 and 1-909	168 172 223 290 319 362	73 151 152 200 235 263 309+CC 315+C 523-524d 663 750	
Le712	M	A5b	16060-16569 and 1-1131	126 235 290 319 519	73 235 263 309+CC 315+C 523-524d 663 750 961 1116	
Le308	M	B4	16011-16569 and 1-908	94 182C 183C 189 217	73 263 309+CC 315+C 466 523-524d 722 750	
Le744	M	B4	16013-16569 and 1-909	93 129 182C 183C 189 217	73 263 315+C 523-524d 750	
Le1626	M	B4	16010-16569 and 1-909	126 182C 183C 189 217 362 519	73 150 195 263 315+C 392 750	
Le23	M	B4	16012-16569 and 1-911	129 150 167 183C 189 217 234 519	73 152 263 315+C 556T 750 827	
Le1334	M	B4a	16012-16569 and 1-918	92 182C 183C 189 217 261 299 519	73 193 263 315+C 523-524d 709 750	
Le1464	M	B4a	16009-16569 and 1-909	168 182C 183C 189 217 256 258C 261 311 519	73 263 309+CC 315+C 356+C 523-524d 750	
Le970	F	B4a	16010-16569 and 1-905	182C 183C 189 217 219 261 286 519	73 146 263 309+CC 315+C 523-524d 750	
Le300	M	B4a	16008-16569 and 1-907	129 182C 183C 189 261 311 519	73 143 146 263 309 315+C 523-524d 750	
Le610	F	B4a	16010-16569 and 1-909	93 182C 183C 189 217 261 357 519	73 263 315+C 523-524d 750	
Le996	M	B4a	16012-16569 and 1-911	150 182C 183C 189 217 240 261	73 263 309+C 315+C 523-524d 750	
Le1169	M	B4a	16013-16569 and 1-908	182C 183C 189 217 231 240 261	73 263 309+C 315+C 750	
Le900	M	B4a	16011-16569 and 1-921	182C 183C 189 217 234 256 261 519	73 263 309+CC 315+C 523-524d 723 750	
Le528	M	B4a	16013-16569 and 1-921	168 182C 183C 189 217 258C 261 311 519	73 263 309+CC 315+C 523-524d 750	
Le1557	M	B4a	16027-16569 and 1-919	182C 183C 189 217 219 261 286 519	73 263 309+C 315+C 523-524d 750	
Le1589	M	B4a	16011-16569 and 1-911	93 182C 183C 189 217 261 390 519	73 263 309+CC 315+C 523-524d 750	
Le4	M	B4a1c	16009-16569 and 1-917	182C 183C 189 217 261 327 519	73 146 263 309dC 315+C 523-524d 709 750	
Le17	M	B4a1c	16010-16569 and 1-916	182C 183C 189 217 261 299 519	73 193 263 309+C 315+C 523-524d 709 750	
Le1347	M	B4b1	16013-16569 and 1-908	136 183C 189 217 309 354 519	73 207 263 309+C 315+C 499 750 827	
Le201	M	B4b1	16012-16569 and 1-910	136 183C 189 217 519	73 207 263 309+CC 315+C 499 523-524d 750 827	
Le936	M	B4b1	16017-16569 and 1-917	136 183C 189 217 519	73 152 207 263 309+CC 315+C 499 750 827	
Le1091	M	B4b1	16013-16569 and 1-898	136 183C 189 217 218 519	73 263 315+C 499 750 827	
Le7	M	B4b1	16012-16569 and 1-908	136 183C 189 217 218 239 248 519	73 152 263 315+C 499 750 827	
Le1082	M	B4b1	16031-16569 and 1-919	136 183C 189 217 218 352 519	73 263 309+CC 315+C 499 750 827	
Le602	M	B4b1	16015-16569 and 1-908	136 175 182C 183C 189 217 218 519	73 263 309+CC 315+C 499 750 827	
Le527	F	B4c1b	16022-16569 and 1-909	136 140 183C 189 217 249 265 274 291 335 519	73 150 263 315+C 709 750	
Le871	F	B4c1b	16013-16569 and 1-919	129 140 166 172 183C 189 217 274 293 335 519	73 150 199 263 315+C 709 750	
Le745	F	B4c1b	16041-16569 and 1-919	182C 183C 189 217 274 335 519	73 150 263 309+CC 315+C 709 750	
Le160	M	B4c1b	16012-16569 and 1-911	140 180 183C 189 217 274 319 335 519	73 150 263 309+C 315+C 709 750	
Le315	M	B4c1b	16012-16569 and 1-882	140 183C 189 217 274 335 519	73 150 152 263 309+C 315+C 709 750	
Le1224	M	B4c1b	16013-16569 and 1-908	129 140 166 183C 189 217 274 335 519	73 150 211 263 309+CC 315+C 709 750	
Le1421	M	B4c1b	16014-16569 and 1-921	126 140 183C 189 217 249 274 291 335 519	73 150 263 315+C 709 750	
Le1498	M	B4c1b	16032-16569 and 1-920	140 180 183C 189 217 274 319 335 519	73 150 263 309+CC 315+C 709 750	
Le1281	F	B4c1b	16012-16569 and 1-906	93 140 182C 183C 189 217 274 335 519	73 146 150 263 309+CC 315+C 709 750	
Le646	M	B4c1b	16013-16569 and 1-905	140 182C 183C 189 217 274 335 519	73 146 150 263 309+CC 315+C 709 750	

Le1226	M	B4c1b	16012-16569 and 1-909	140 182C 183C 189 217 274 335 519	73 146 150 263 309+CC 315+C 709 750	
Le1588	M	B4c1c	16016-16569 and 1-911	182C 183C 189 217 261h 311 519	73 150 195 214 263 279 309+CC 315+C 750	
Le1232	F	B4c2	16010-16569 and 1-908	48 147 183C 184A 189 217 235 519	73 263 309+C 315+C 523-524d 750	
Le1225	M	B4c2	16012-16569 and 1-909	129 147 162 183C 184A 189 217 235 519	73 263 309+CC 315+C 750	
Le723	M	B4c2	16012-16569 and 1-909	129 147 162 183C 184A 189 217 235 519	73 263 309+C 315+C 750	+
Le1309	M	B4g	16007-16569 and 1-902	181C 182C 183C 189 213 217 261 292 301 519	61A 62 73 263 309+CC 315+C 523-524d 750	
Le325	M	B4g	16012-16569 and 1-918	181C 182C 183C 189 213 217 261 278 292 519	73 263 302C 309+C 315+C 455+T 523-524d 750	
Le1132	M	B4g	16013-16569 and 1-908	181C 182C 183C 189 213 217 261 292 519	73 263 309+CC 315+C 523-524d 750	
Le1539	M	B4g	16007-16569 and 1-909	95A 181C 182C 183C 189 213 217 261 274 292 301 519	61A 62 73 263 309+CC 315+C 523-524d 750	
Le1077	F	B5a	16013-16569 and 1-909	182C 183C 189 261 266A 519	73 152 210 263 309dC 315+C 523-524d 709 750	
Le1407	F	B5a	16009-16569 and 1-914	140 183C 189 262 266A 519	73 210 263 309+C 315+C 523-524d 593 709 750	
Le846	F	B5a	16010-16569 and 1-908	183C 189 260 266G 519	73 210 263 294 309+C 315+C 709 750	
Le16	M	B5a	16011-16569 and 1-908	140 183C 189 266A 519	73 210 263 309+CC 315+C 523-524d 709 750	
Le153	M	B5a	16024-16569 and 1-959	140 183C 189 266A 519	73 210 263 291+A 309+C 315+C 523-524d 709 750	
Le676	M	B5a	16013-16569 and 1-908	140 183C 189 266A 519	73 210 263 309+3C 315+C 523-524d 709 750	
Le955	M	B5a	16012-16569 and 1-906	140 183C 189 266A 519	73 210 263 309+CC 315+C 523-524d 709 750	
Le956	M	B5a	16013-16569 and 1-908	140 183C 189 266A 519	73 210 263 315+C 523-524d 709 750	
Le1125	M	B5a	16012-16569 and 1-908	182C 183C 189 266A 519	73 210 263 309+CC 315+C 523-524d 709 750	
Le1192	M	B5a	16013-16569 and 1-908	140 183C 189 262 266A 519	64 73 210 263 309+C 315+C 523-524d 593 709 750	
Le1272	M	B5a	16010-16569 and 1-909	93 140 183C 189 260 266G 519	73 210 263 294 309+C 315+C 709 750	
Le570	M	B5a	16012-16569 and 1-914	140 183C 189 266A 519	73 210 263 309+CC 315+C 523-524d 709 750	
Le915	M	B5a	16012-16569 and 1-798	140 183C 189 266A	73 210 263 315+C 523-524d 709 750	
Le501	M	B5a	16012-16569 and 1-909	140 183C 189 234 266A 519	73 150 210 263 309+CC 315+C 523-524d 709 750	
Le1393	M	B5a	16020-16569 and 1-919	140 183C 189 266A 519	73 210 263 309+CC 315+C 523-524d 709 750	
Le1050	M	B5a	16013-16569 and 1-904	93 140 183C 189 209 266A 304 361 399 519	73 152 153 204 210 249d 263 315+C 523-524d 709 750	
Le333	M	B5a	16043-16569 and 1-904	140 183C 189 260 266G 325 519	73 210 263 294 315+C 709 750	
Le1456	M	B5a	16017-16569 and 1-906	183C 189 260 266G 519	73 210 263 294 309+C 315+C 709 750	
Le750	F	B5a2a	16012-16569 and 1-909	140 187 189 256 266G 519	73 93 210 263 309+C 315+C 523-524d 709 750	
Le128	M	B5b	16017-16569 and 1-911	140 183C 189 243 519	73 204 207 263 315+C 523-524d 709 750	
Le1237	M	B5b2c	16012-16569 and 1-918	93 140 183C 189 234 243 463 519	73 94 103 131 263 309+C 315+C 481 523-524d 709 750	
Le866	M	C	16008-16569 and 1-908	51 223 298 327 519	73 188 204 249d 263 315+C 489 750	
Le625	M	C	16047-16569 and 1-945	223 298 327 519	73 146 151 152 249d 263 315+C 489 750 922	
Le1454	M	C	16032-16569 and 1-1013	223 243 298 327 519	73 146 204 249d 263 309+C 315+C 489 750	
Le695	M	C	16010-16569 and 1-920	93 223 298 319 327 519	73 146 249d 263 309+C 315+C 489 750	
Le1181	M	C	16013-16569 and 1-908	223 298 309 327 519	73 146 249d 263 315+C 489 750	
Le1450	M	C	16029-16569 and 1-915	189 223 298 327 519	73 146 249d 263 309+C 315+C 466 489 750	
Le1368	M	C4a	16020-16569 and 1-921	129 223 298 327 519	73 195 249d 263 309+C 315+C 489 750	
Le1378	F	C4a	16012-16569 and 1-908	223 298 327 354 357 519	73 249d 263 309+C 315+C 489 750	
Le109	M	C4a1	16017-16569 and 1-919	129 148 223 298 327 519	73 152 249d 263 315+C 449 489 750	
Le1151	M	C4a1	16013-16569 and 1-908	93 129 223 284 298 327 519	73 195 228T 249d 263 309+C 315+C 489 750	
Le661	M	C4a1	16009-16569 and 1-908	129 148 223 298 327 519	73 152 249d 263 315+C 449 489 750	
Le1447	M	C4a1	16016-16569 and 1-911	129 183C 189 223 298 327 519	73 249d 263 310d 489 750	
Le1547	M	C4a1	16013-16569 and 1-911	129 148 223 298 304 327 368 519	73 152 249d 263 309+CC 315+C 449 489 750	

Le1206	M	C5a	16013-16569 and 1-891	93 223 261 288 298 519	73 249d 263 315+C 489 595+C 750	
Le595	F	D4	16007-16569 and 1-902	93 223 362 519	73 194 263 315+C 489 523-524d 750	–
Le833	F	D4	16013-16569 and 1-901	223 243 362 519	73 194 263 315+C 489 523-524d 750	–
Le532	M	D4	16014-16569 and 1-906	223 362 519	73 194 263 315+C 489 523-524d 750	–
Le665	M	D4	16012-16569 and 1-907	223 362	73 263 315+C 489 750	–
Le301	M	D4	16012-16569 and 1-921	223 362	73 152 263 309+C 315+C 489 750	–
Le581	M	D4	16019-16569 and 1-899	189 192 223 316 362	73 263 309+C 315+C 489 750	–
Le311	M	D4	16012-16569 and 1-911	223 362	73 263 309+C 315+C 489 750	–
Le783	M	D4	16009-16569 and 1-900	214 223 311 362 519	73 195 200 263 309+C 315+C 489 750	–
Le840	M	D4	16013-16569 and 1-897	223 271 362 519	73 263 298 315+C 489 593 750	–
Le1590	M	D4	16013-16569 and 1-910	223 362 519	73 194 263 315+C 489 523-524d 750	–
Le429	M	D4	16012-16569 and 1-911	223 362	73 263 315+C 489 750	–
Le583	M	D4	16012-16569 and 1-908	92 223 311 362 390T	73 146 263 309+C 315+C 458A 489 750	–
Le684	M	D4	16012-16569 and 1-908	223 362	73 263 309+CC 315+C 489 750	–
Le1623	M	D4	16014-16569 and 1-921	223 286 362	73 146 263 315+C 489 750	–
Le1610	M	D4	16012-16569 and 1-918	169 223 266 274 362 465	73 263 298 309+CC 315+C 489 750	–
Le1282	M	D4	16014-16569 and 1-908	192 222 316 362	41 73 184 195 263 315+C 489 507 750	–
Le1167	M	D4	16022-16569 and 1-909	223 316 362	73 183 263 309+C 315+C 489 750	–
Le1221	M	D4	16013-16569 and 1-906	93 176 223 362	73 94 194 263 309+C 315+C 489 750	–
Le975	M	D4	16012-16569 and 1-911	223 362 519	73 194 263 315+C 489 523-524d 750	–
Le1424	M	D4	16017-16569 and 1-919	172 362 519	73 194 263 315+C 489 523-524d 750	–
Le1461	M	D4	16023-16569 and 1-909	95 223 362 519	73 195 263 309+C 315+C 489 750	–
Le999	M	D4	16013-16569 and 1-911	223 362	73 247 263 309+C 315+C 489 523-524d 750	–
Le962	M	D4	16010-16569 and 1-911	223 354 362	73 93 214 263 315+C 489 750	–
Le1427	M	D4	16017-16569 and 1-1034	92 223 362	73 94 263 309+C 315+C 489 750	
Le144	M	D4	16012-16569 and 1-916	223 362	73 263 309+C 315+C 489 750	–
Le630	M	D4	16047-16569 and 1-971	223 311 362 390	73 152 263 309+CC 315+C 489 513 750	
Le452	F	D4	16013-16569 and 1-915	223 362 519	73 150 194 205 263 315+C 489 523-524d 750	–
Le1061	M	D4	16014-16569 and 1-909	158 223 362 519	73 194 263 279 309+C 315+C 489 523-524d 750	–
Le1313	M	D4	16024-16569 and 1-918	223 362 519	73 153 194 263 315+C 340 489 523-524d 750	–
Le1617	F	D4	16017-16569 and 1-911	223 362 368	73 173 263 309+CC 315+C 489 499 524+AC 750	–
Le800	F	D4a	16010-16569 and 1-911	129 223 362 519	73 152 263 315+C 489 750	–
Le212	M	D4a	16014-16569 and 1-909	129 223 263 362 519	73 152 263 309+CC 315+C 489 507 750	–
Le792	M	D4a	16012-16569 and 1-914	93 129 223 270 274 311 362	73 152 196 263 309+C 315+C 489 750	–
Le649	M	D4a	16047-16569 and 1-970	93 129 172 223 362	73 152 263 309+C 315+C 489 750	
Le805	M	D4a1e	16012-16569 and 1-903	129 189 223 256 362 519	73 152 263 315+C 489 750	–
Le474	F	D4a3	16009-16569 and 1-919	51 129 223 249 362	73 152 263 315+C 489 750	–
Le233	M	D4a3	16012-16569 and 1-909	129 223 249 362	73 152 263 315+C 489 750	–
Le1092	M	D4a3	16009-16569 and 1-908	129 223 249 294 362	73 152 263 309+C 315+C 489 750	–
Le1040	M	D4a3	16015-16569 and 1-907	51 129 223 249 362	73 152 263 315+C 489 750	–
Le335	M	D4a3	16012-16569 and 1-906	223 249 362	73 152 263 309+C 315+C 489 750	–
Le863	M	D4a3	16020-16569 and 1-909	223 249 362	73 143 152 263 309+CC 315+C 489 750	–
Le8	M	D4a3	16013-16569 and 1-901	93 129 221 223 249 362	73 152 237 263 309+C 315+C 489 750	–

Le498	M	D4b1	16047-16569 and 1-917	129 173 223 319 362	73 263 309+CC 315+C 489 523-524d 750	
Le22	F	D4b1b	16007-16569 and 1-913	93 223 287 319 362	73 263 309+C 315+C 431 489 523-524d 750	–
Le280	F	D4c	16065-16569 and 1-885	223 245 362	73 194 263 309+C 315+C 489 750	
Le966	M	D4c	16013-16569 and 1-908	223 245 362	73 208 263 309+C 315+C 489 534 750	–
Le726M	M	D4e1a1	16007-16569 and 1-911	93 129 176 223 362	73 94 194 263 309+C 315+C 489 750	–
Le726	M	D4e1a1	16013-16569 and 1-915	93 129 176 223 362	73 94 194 263 309+C 315+C 489 750	–
Le1400	M	D4g2	16027-16569 and 1-910	223 274 362	73 263 298 309+C 315+C 489 546 549 750	–
Le1502	M	D4h	16001-16569 and 1-910	174 223 311 317 362	73 152 263 315+C 489 750	–
Le645	M	D4h1	16005-16569 and 1-908	174 223 362	73 263 315+C 489 750	–
Le261	M	D4h1	16012-16569 and 1-921	174 189 223 362	73 263 309+C 315+C 489 523-524d 750	–
Le910	M	D4h1	16009-16569 and 1-921	174 223 362	73 263 309+C 315+C 489 523-524d 750	–
Le1246	M	D4i	16011-16569 and 1-908	223 294 362	73 146 263 315+C 489 750	–
Le652	M	D4j3	16055-16569 and 1-943	184 311 362 519	73 194 263 315+C 489 523-524d 750	
Le6	M	D4k	16013-16569 and 1-904	192 223 298	73 195 263 309+CC 315+C 489 750	–
Le1029	M	D4k	16024-16569 and 1-911	192 223	73 195 263 309+C 315+C 489 750	–
Le1030	M	D4k	16012-16569 and 1-911	192 223	73 195 263 309+C 315+C 489 750	–
Le1080	M	D4k	16021-16569 and 1-904	192 223	73 185 195 263 315+C 489 750	
Le1487	M	D5a2	16028-16569 and 1-910	172 182C 183C 189 223 266 299 319 362	73 150 263 309+C 315+C 489 523-524d 750 752	
Le80	M	D5a2	16012-16569 and 1-918	92 164 182C 183C 189 223 266 362	73 150 263 309+C 315+C 489 523-524d 750 752	–
Le1369	M	D5a2	16012-16569 and 1-913	164 172 182C 183C 189 223 266 362	73 146 150 263 315+C 489 523-524d 750 752	–
Le1591	M	D5a2	16024-16569 and 1-858	92 164 182C 183C 189 223 266 362	73 150 263 309+CC 315+C 489 523-524d 750 752	–
Le1119	M	D5a2	16010-16569 and 1-908	92 182C 183C 189 223 266 362	73 150 152 263 315+C 489 523-524d 750 752	–
Le1190	F	D5b	16013-16569 and 1-906	183C 189 194C 195 223 362	73 146 150 263 309+CC 315+C 456 489 523-524d 681 750	–
Le1473	F	D5b	16009-16569 and 1-917	92 183C 189 223 311 317 362	73 150 263 315+C 456 489 681 750	–
Le244	M	D5b	16024-16569 and 1-911	183C 189 223 357 362 519	73 150 263 309+C 315+C 456 489 681 750	–
Le292	M	D5b	16012-16569 and 1-905	129 183C 189 223 362	73 146 150 263 309+C 315+C 456 489 681 750	–
Le887	M	D5b	16012-16569 and 1-908	189 223 362 519	73 150 263 309+C 315+C 456 489 681 750	–
Le1435	M	D5b	16009-16569 and 1-911	148 183C 189 223 362 519	73 150 152 185 188 263 309+CC 315+C 456 489 681 750	–
Le705	M	D5b	16066-16569 and 1-894	189 223 362 519	73 150 195 263 309+CC 315+C 456 489 681 750	
Le1331	F	D6a	16009-16569 and 1-913	189 223 274 362	73 263 309+CC 315+C 489 709 750	–
Le973	M	E	16014-16569 and 1-904	223 362 390 519	73 103 263 315+C 489 750	+
Le772	M	E	16012-16569 and 1-919	51 185 223 362 390	73 195 263 315+C 489 750	+
Le1268	F	F1a	16013-16569 and 1-907	172 201 304 362 519	73 200 249d 263 309+C 315+C 523-524d 750	
Le454	F	F1b	16012-16569 and 1-911	129 183C 189 217 232A 249 304 311 519	73 203 204 249d 263 309+C 315+C 523-524d 750	
Le425	M	F3a	16065-16569 and 1-937	93 260 298 355 362	73 207 249d 263 309+CC 315+C 524+AC 709 750	
Le275	F	G	16012-16569 and 1-920	223 362 463	73 263 309+CC 315+C 489 709 750	+
Le276	F	G	16012-16569 and 1-917	223 362 463	73 263 309+CC 315+C 489 709 750	+
Le830	M	G	16013-16569 and 1-907	214 223 362	73 152 263 309+C 315+C 489 709 750	+
Le40	M	G	16024-16569 and 1-882	111 223 362 519	73 189 263 315+C 489 532T 750	+
Le1307	M	G	16014-16569 and 1-921	93 223 311 362	73 152 263 309+C 315+C 489 709 750	+
Le872	M	G1a1	16012-16569 and 1-908	223 325 362 422 463 519	73 150 263 315+C 489 709 750	+
Le878	M	G1c	16012-16569 and 1-908	189 223 319 362 519	73 263 309+C 315+C 489 593 709 750	+
Le682	M	G1c	16009-16569 and 1-911	223 362 519	73 263 315+C 489 593 709 750	+

Le1561	M	G1c	16012-16569 and 1-911	223 284 295 297 362 519	73 146 207 263 309+CC 315+C 489 593 709 750	+
Le746	F	G3	16009-16569 and 1-913	93 223 274 362	73 152 204 263 315+C 489 709 750	+
Le142	F	G3	16012-16569 and 1-909	93 223 274 362	73 263 309+C 315+C 489 709 750	+
Le1444	M	G3	16019-16569 and 1-920	223 229 274 362	73 263 315+C 489 709 750	+
Le480	F	G3a	16015-16569 and 1-911	93 223 274 362	73 143 152 263 315+C 489 709 750	+
Le1177	M	G3a	16013-16569 and 1-908	223 274 362	73 143 152 153 263 309+C 315+C 489 709 750	+
Le1480	M	K1c	16027-16569 and 1-910	224 311 368 519	73 146 152 263 315+C 498d 750	
Le205	F	M10	16008-16569 and 1-909	193 223 311 357 497	73 146 263 309+C 315+C 489 523-524d 573+2C 709 750	
Le481	F	M10	16013-16569 and 1-873	129 223 311	73 263 309+C 315+C 489 573+5C 709 750	
Le1073	M	M10	16014-16569 and 1-870	129 223 311	73 263 309+CC 315+C 489 573+6C 709 750	
Le1486	M	M10	16007-16569 and 1-872	213h 223 256 311 399	73 263 309+C 315+C 489 573+4C 574C 709 750	
Le1544	M	M10	16027-16569 and 1-875	223 248 271 311 519	73 263 309+C 315+C 489 573+5C 709 750	
Le1489	M	M10a1	16007-16569 and 1-867	93 129 223 311 357 497	73 146 263 315+C 489 523-524d 573+3C 709 750	
Le855	M	M10a1	16006-16569 and 1-821	129 193 223 311 317 357 483 497	73 146 152 263 315+C 489 523-524d 573+4C 709 750	
Le431	M	M10a1	16014-16569 and 1-853	93 129 223 311 357 497	73 263 315+C 489 523-524d 573+5C 709 750	
Le352	M	M10a1	16013-16569 and 1-863	93 129 193 223 249 311 357 497 519	73 146 151 263 309+C 315+C 489 523-524d 573+4C 709 750	
Le587	M	M10a1	16001-16569 and 1-866	93 129 193 223 311 357 497	73 146 152 263 309+C 315+C 489 523-524d 573+4C 709 750	
Le1315	M	M10a1	16013-16569 and 1-873	93h 193 223 311 357 497	73 146 263 309+C 315+C 489 523-524d 573+3C 709 750	
Le330	M	M10a2	16019-16569 and 1-872	66 223 311	73 263 315+C 489 573+5C 709 750	
Le1153	M	M10a2	16013-16569 and 1-872	66 223 311	73 263 315+C 489 573+5C 709 750	
Le1492	M	M11	16013-16569 and 1-921	173 223	73 146 196 198 200 263 309+C 315+C 318 326 489 750	
Le1512	F	M11	16028-16569 and 1-911	93 175 223	73 195 198 215 263 309+C 315+C 318 326 489 750	
Le309	M	M11	16013-16569 and 1-908	196 223 261	73 200 215 263 309+CC 315+C 318 326 459+C 489 750	
Le520	M	M20	16012-16569 and 1-908	86 129 209 223 272 519	73 152 225 249d 263 315+C 316 489 523-524d 750	
Le1570	M	M20	16012-16569 and 1-909	86 129 209 213 223 272 519	73 152 225 249d 263 315+C 316 489 523-524d 750	
Le825	M	M33c	16008-16569 and 1-907	93 104 111 189 223 235 362 519	73 263 309+C 315+C 489 750	+
Le585	M	M7	16010-16569 and 1-914	173 223 362 519	73 146 189 199 263 315+C 489 523-524d 750	
Le1558	M	M73	16014-16569 and 1-907	166d 214 223 249 278	73 263 315+C 489 750	
Le1612	M	M74	16007-16569 and 1-894	223 274 311 362 381	63 64 66 73 146h 263 315+C 489 750	+
Le985	M	M7b	16017-16569 and 1-906	92 223 297	73 150 199 204 207 263 315+C 489 750	
Le960	M	M7b	16012-16569 and 1-914	223 297 327	73 150 199 204 263 309+C 315+C 489 750	
Le1555	M	M7b	16027-16569 and 1-921	172 223 297	73 150 199 203 204 263 315+C 489 750	
Le1059	M	M7b	16012-16569 and 1-909	38 129 220C 223 482 519	73 150 199 263 309+CC 315+C 489 750	
Le271	M	M7b	16009-16569 and 1-908	129 183C 189 223 297	73 150 199 204 263 309+C 315+C 374 456 489 750	
Le1088	M	M7b	16012-16569 and 1-908	129 189 223 248 297	73 150 199 204 207 263 309+C 315+C 489 750	
Le53	M	M7b	16012-16569 and 1-917	129 189 223 297 519	73 150 199 263 315+C 489 593 750	
Le1405	M	M7b	16015-16569 and 1-920	129 178 223 297 384h 519	73 150 159 199 263 309+C 315+C 489 750	
Le1099	M	M7b	16007-16569 and 1-907	129 178 223 297 519	73 150 159 199 263 309+C 315+C 489 750	
Le1478	M	M7b	16013-16569 and 1-909	223 297	73 150 199 204 263 309+C 315+C 489 750	
Le627	M	M7b	16016-16569 and 1-908	38 129 223 297	73 81 150 199 263 309+C 315+C 408A 489 750	
Le1404	M	M7b	16021-16569 and 1-866	129 189 223 297	73 150 199 263 309+C 315+C 489 567C 573+C 750	
Le1453	F	M7b1	16015-16569 and 1-908	92 129 192 223 254 297	73 150 159 182 199 263 315+C 489 750	
Le100	M	M7b1	16014-16569 and 1-919	129 192 223 297	73 150 199 263 309+C 315+C 489 750	

Le180	M	M7b1	16008-16569 and 1-920	129 192 223 297	73 150 199 263 309+C 315+C 489 750
Le25	M	M7b1	16007-16569 and 1-919	92 129 192 223 297	73 150 159 199 263 315+C 489 750
Le704	M	M7b1	16013-16569 and 1-910	129 192 207 223 297 319	73 146 150 199 263 309+C 315+C 489 750
Le1085	M	M7b1	16007-16569 and 1-909	129 192 223 297	73 150 182 199 263 309+C 315+C 459d 489 750
Le1110	M	M7b1	16013-16569 and 1-917	129 192 223 297	73 150 199 263 309+C 315+C 489 750
Le620	M	M7b1	16013-16569 and 1-908	129 192 223 297	73 150 199 204 263 309+C 315+C 489 750
Le1258	M	M7b1	16012-16569 and 1-919	92 129 192 223 297	73 150 159 199 263 315+C 489 750
Le134	M	M7b1	16007-16569 and 1-917	129 192 223 297	73 150 199 263 309+C 315+C 489 750
Le1157	M	M7b1	16008-16569 and 1-907	93 129 179 192 223 297	73 150 199 263 309+C 315+C 489 750
Le264	M	M7b1	16018-16569 and 1-907	129 192 223 297	73 150 199 263 309+CC 315+C 489 750
Le49	M	M7b1	16010-16569 and 1-914	129 192 223 297	73 150 199 263 309+CC 315+C 489 750
Le826	M	M7b1	16012-16569 and 1-908	129 192 223 297 519	73 150 199 263 315+C 489 750
Le1484	M	M7b1	16012-16569 and 1-909	129 192 223 291 297 299	73 150 263 315+C 489 523-524d 750
Le1603	M	M7b1	16016-16569 and 1-917	129 192 223 297	73 150 199 263 309+CC 315+C 489 750
Le1455	M	M7b1	16018-16569 and 1-915	129 192 223 297	73 150 199 263 309+CC 315+C 489 750
Le617	M	M7b1	16009-16569 and 1-921	129 188G 192 223 297	73 150 199 263 315+C 466 489 750
Le1394	M	M7b1	16013-16569 and 1-907	129 192 223 291 297 519	73 150 199 204 263 315+C 489 509 523-524d 750
Le1493	M	M7b1	16012-16569 and 1-913	129 192 223 297	73 150 199 263 309+CC 315+C 489 750
Le1481	M	M7b1	16009-16569 and 1-914	129 192 223 297 368	73 150 199 263 309+C 315+C 489 750
Le650	M	M7b1	16033-16569 and 1-850	129 192 223 297	73 150 199 263 309+C 315+C 332 489 513 750
Le1554	M	M7b1	16012-16569 and 1-916	129 192 223 297 355 519	73 150 199 263 309+CC 315+C 489 750
Le530	M	M7b1	16010-16569 and 1-860	129 192 223 297 362	73 150 195 199 263 309+C 315+C 489 750
Le1462	M	M7b1	16013-16569 and 1-905	129 192 223 297	73 150 199 263 309+C 315+C 489 750
Le1500	M	M7b1	16021-16569 and 1-921	129 192 223 297	73 150 199 263 315+C 489 750
Le790	M	M7b2	16007-16569 and 1-909	129 189 223 297 298	73 150 199 263 309+C 315+C 489 750
Le95	M	M7b2	16012-16569 and 1-921	129 183C 189 223 297 298 325	73 150 199 263 309+CC 315+C 489 750 866
Le778	M	M7b2	16012-16569 and 1-905	129 189 223 297 298	73 150 199 263 297h 315+C 489 750
Le1592	M	M7b3	16017-16569 and 1-911	86 240T 297 324 399	73 199 263 315+C 489 750
Le1602	F	M7c	16013-16569 and 1-914	223 278 295 519	73 146 199 263 309+CC 315+C 373 489 523-524d 750
Le769	F	M7c	16006-16569 and 1-909	223 293T 295 362 519	72 73 146 199 263 309+C 315+C 489 523-524d 750
Le761	M	M7c	16008-16569 and 1-920	223 295 519	73 146 199 263 309+C 315+C 489 523-524d 750
Le473	M	M7c	16069-16569 and 1-882	223 295 519	73 146 199 263 309+C 315+C 489 523-524d 573+3C 750
Le60	M	M7c	16009-16569 and 1-917	173 223 295 362 519	73 146 199 263 309+CC 315+C 489 523-524d 750
Le596	M	M7c	16018-16569 and 1-911	223 293 295 519	73 146 199 263 309+C 315+C 489 523-524d 750
Le447	M	M7c	16013-16569 and 1-921	75 223 293T 295 519	73 146 152 199 263 309+C 315+C 489 523-524d 750
Le1199	M	M7c	16013-16569 and 1-917	223 295 519	73 146 152 199 263 309+C 315+C 489 523-524d 750
Le1522	M	M7c	16008-16569 and 1-905	223 293T 295 362 519	72 73 146 199 263 309+C 315+C 489 523-524d 750
Le1144	M	M7c1b	16007-16569 and 1-909	38 223 294 295 335 519	73 146 199 263 309+C 315+C 489 523-524d 750
Le703	M	M7c1b	16013-16569 and 1-911	38 223 294 295 335 519	73 146 199 263 315+C 489 523-524d 750
Le1001	M	M7c3b	16017-16569 and 1-909	311 519	73 146A 199 204 263 309+C 315+C 489 523-524d 750
Le127	M	M7c3b	16005-16569 and 1-911	519	73 146A 199 263 309+C 315+C 489 523-524d 750
Le1158	M	M7c3b	16012-16569 and 1-908	519	73 146A 199 204 263 309+C 315+C 489 523-524d 750
Le1494	M	M7c3b	16013-16569 and 1-921	519	73 146A 199 204 263 309+C 315+C 489 523-524d 750

Le1332	F	M7e	16012-16569 and 1-920	172 223 274 291 311 519	73 146 263 315+C 489 523-524d 750	+
Le26	M	M8a2	16015-16569 and 1-895	184 223 298 319	73 199 263 315+C 489 750	
Le806	M	M8a2	16013-16569 and 1-906	184 223 298 319	73 263 315+C 489 750	
Le1457	M	M8a2	16009-16569 and 1-908	184 223 298 319	73 215 263 309+CC 315+C 489 750	
Le845	M	M8a2	16012-16569 and 1-908	184 189 223 298 319 355 362 519	73 263 309+C 315+C 489 523-524d 750	
Le327	M	M8a2	16013-16569 and 1-918	93 184 189 223 294 298 319 355 362 519	73 263 309+C 315+C 489 523-524d 750	
Le1605	M	M8a2	16038-16569 and 1-914	134 184 223 298 319	73 263 309+C 315+C 489 750	
Le907	M	M8a2	16012-16569 and 1-921	184 223 249 298 319	73 234 263 309+C 315+C 489 750	
Le1338	M	M8a2	16012-16569 and 1-897	126 184 223 293 298 319	73 152 263 309+CC 315+C 489 750	
Le1415	M	M8a2	16008-16569 and 1-873	184 223 298 319	73 263 315+C 489 750	
Le1624	M	M8a2	16049-16569 and 1-921	184 223 298 311 319	73 152 263 309+C 315+C 489 750	
Le1616	F	M8a2a	16012-16569 and 1-924	184 189 223 298 319 470 471 473	73 263 315+C 489 750	
Le506	F	M9a	16007-16569 and 1-917	223 234 240 362 519	73 153 263 315+C 489 750	
Le417	M	M9a	16013-16569 and 1-916	223 234 240 311 362 519	73 153 263 315+C 489 750	
Le1584	M	M9a	16012-16569 and 1-910	223 234 248 265C 316 362	73 153 263 309+C 315+C 489 750	+
Le1373	M	M9a	16008-16569 and 1-909	223 234 311 316 362 526	73 153 263 309+CC 315+C 489 750	+
Le1485	M	M9a	16013-16569 and 1-921	158 234 362 519	73 150 152 153 263 309+C 315+C 489 750	+
Le1326	M	M9a	16014-16569 and 1-908	223 234 311 316 362 526	73 153 263 309+C 315+C 489 750	
Le1128	M	M9a	16009-16569 and 1-874	129 192 223 234 362	73 153 195 263 315+C 489 750	+
Le499	M	M9a	16012-16569 and 1-920	223 224 234 316 362	73 152 153 263 309+C 315+C 489 750	+
Le117	M	M9a	16014-16569 and 1-921	223 234 291 316 362	73 153 263 309+C 315+C 489 750	
Le428	M	N11a	16065-16569 and 1-919	145 183C 189 223 355 519	73 195 240 263 309+C 315+C 523-524d 750 813	
Le219	M	N9a	16019-16569 and 1-921	182C 183C 189 223 257A 261 286	73 150 263 309+CC 315+C 750	
Le446	M	N9a	16007-16569 and 1-914	223 257A 261 311 390	73 150 263 309+CC 315+C 524+2AC 750	
Le1363	M	N9a	16012-16569 and 1-907	223 257A 261 311	73 150 263 309+C 315+C 750	
Le1606	M	N9a	16013-16569 and 1-911	223 257A 261	73 150 263 315+C 750	
Le1581	M	N9a	16027-16569 and 1-917	223 257A 261 519	73 150 204 263 309+C 315+C 750	
Le143	M	N9a	16012-16569 and 1-908	51 93 223 257A 261	73 150 263 309+C 315+C 750	
Le756	M	N9a	16019-16569 and 1-911	172 189 223 257A 261	73 150 195 263 315+C 750	
Le267	M	N9a	16013-16569 and 1-920	51 86 172 223 257A 261 287	73 150 263 309+C 315+C 750	
Le451	F	N9a	16017-16569 and 1-918	172 223 257A 261 497	73 150 263 309+C 315+C 750	
Le734	F	N9a1	16012-16569 and 1-909	111 129 223 257A 261	73 150 263 315+C 750	
Le1499	M	N9a1	16028-16569 and 1-911	111 129 223 257A 261	73 150 263 309+CC 315+C 750	
Le990	M	N9a1	16014-16569 and 1-908	111 129 223 257A 261	73 150 263 309+C 315+C 750	
Le735	M	R9b1	16012-16569 and 1-908	192 304 309 390 519	73 263 315+C 523-524d 750	
Le768	M	X2	16013-16569 and 1-909	189 223 278 519	73 153 195 225 226 263 315+C 750	
Le240	M	Y	16012-16569 and 1-909	126 231 384 519	73 146 207 263 309+C 315+C 750	
Le2	M	Y1b	16013-16569 and 1-908	126 231 266 519	73 146 263 309+C 315+C 750	
Le304	M	Y1b	16043-16569 and 1-943	126 231 266 519	73 146 263 309+CC 315+C 750	
Le303	M	Y1b	16012-16569 and 1-911	126 231 266 519	73 146 263 309+CC 315+C 750	
Le495	M	Y2	16012-16569 and 1-909	93 126 231 265 311	73 263 309+C 315+C 482 750	
Le5	M	Z	16013-16569 and 1-873	171T 185 223 260 298 311	73 152 249d 263 315+C 489 750	
Le687	M	Z	16033-16569 and 1-895	185 189 223 260 298 380	73 131 152 249d 263 315+C 489 723 750	

Le1324	M	Z	16011-16569 and 1-918	185 209 223 260 298	73 143 152 199 204h 249d 263 309+C 315+C 489 750
Le449	M	Z	16010-16569 and 1-916	136 223 260 298 519	73 146 152 249d 263 309+CC 315+C 489 750
Le816	M	Z	16008-16569 and 1-908	185 223 260 298 302	73 151 152 249d 263 315+C 489 573+C 634 750
Le710	M	Z	16014-16569 and 1-921	185 223 260 298 302	73 151 152 249d 263 309+C 315+C 489 750
Le1412	M	Z	16010-16569 and 1-917	114Ah 185 223 260 298 519	73 151 152 249d 263 309+C 315+C 489 750
Le115	M	Z4	16008-16569 and 1-919	185 223 260 298 302	73 151 152 249d 263 309+C 315+C 489 750

Note – Sequence variation was scored relative to the revised Cambridge reference sequence (rCRS)[1]. Suffixes A, G, C and T indicate transversions, "h" indicates heteroplasmy, "d" and "+" indicate deletions and insertions, respectively. Indels (insertion and deletion) are recorded at the last possible site. "+" and "−" denote the absence and presence of the restriction site, respectively. "M" and "F" indicate male and female, respectively.

Supplementary Reference

1. Andrews RM, Kubacka I, Chinnery PF, Lightowlers RN, Turnbull DM, Howell N (1999) Reanalysis and revision of the Cambridge reference sequence for human mitochondrial DNA. Nat Genet 23:147

Table S3. mtDNA sequence variation and haplogroup classification of 843 patients with suspected LHON

Sample	Gender	Haplogroup	Sequenced region	Segment I (16000+)	Segment II	5176(*Alu* I)
Le1032	F	A	16012-16569 and 1-908	223 290 319 325 362	73 151 152 235 263 309+C 315+C 523-524d 663 750	
Le61	F	A	16008-16569 and 1-917	223 235 290 311 319 362 519	73 152 234 235 263 309+CC 315+C 523-524d 663 750	
Le94	F	A	16021-16569 and 1-914	223 235 290 311 319 362 519	73 152 234 235 263 309+C 315+C 523-524d 663 750	
Le169	F	A	16012-16569 and 1-914	223 290 319 362	73 152 204 207 235 309+C 315+C 523-524d 663 750	
Le1266	F	A	16009-16569 and 1-901	92 223 290 319 362	73 152 235 263 309+C 315+C 524+AC 663 750	
Le1439	F	A	16040-16569 and 1-883	223 235 290 311 319 362 519 527	73 152 199 234 235 259 263 309+C 315+C 523-524d 573+5C 663 750	
Le1020	M	A	16013-16569 and 1-908	196 223 290 311 319 362	73 152 235 263 309+C 315+C 523-524d 663 750	
Le171	M	A	16009-16569 and 1-911	223 261 290 319 362	73 152 182 235 263 309+CC 315+C 523-524d 663 750	
Le1186	M	A	16013-16569 and 1-908	223 290 292 319 356 362	73 152 235 315+C 523-524d 663 750	
Le179	M	A	16009-16569 and 1-909	223 290 319 362	73 152 188 235 309+C 315+C 523-524d 663 750	
Le1451	M	A	16021-16569 and 1-921	92 223 290 319 362	73 152 235 315+C 523-524d 663 750	
Le815	M	A	16013-16569 and 1-806	93 223 290 319 362	73 152 235 309+CC 315+C 513-514d 663 750	
Le844	M	A	16013-16569 and 1-819	223 235 290 311 319 362 519 527	73 152 199 234 235 263 309+C 315+C 523-524d 573+3C 663 750	
Le870	M	A	16012-16569 and 1-919	223 287 290 311 319 362 519	73 152 235 263 315+C 523-524d 663 750	
Le1318	M	A	16012-16569 and 1-909	179 223 290 311 319 362 519	73 152 235 263 315+C 663 750	
Le1036	M	A	16009-16569 and 1-921	93 157 223 290 319 362	73 152 195 235 263 309+C 315+C 523-524d 663 750	
Le1296	M	A	16031-16569 and 1-920	223 290 319 362	73 151 152 235 263 309+C 315+C 523-524d 663 735 750	
Le1553	M	A	16020-16569 and 1-914	223 290 319 362	73 152 207 235 309+CC 315+C 523-524d 663 750	
Le1043	M	A	16014-16569 and 1-908	172 223 290 319 362	73 152 207 235 309+C 315+C 523-524d 663 750	
Le31	F	A	16005-16569 and 1-899	166d 223 290 319 362	73 152 200 235 263 315+C 523-524d 663 750	
Le426	F	A	16012-16569 and 1-909	93 223 290 319 362	73 151 152 200 235 263 315+C 523-524d 663 735 750	
Le639	F	A	16013-16569 and 1-867	223 290 319 362	73 151 152 200 235 263 315+C 523-524d 663 735 750	
Le857(1)	F	A	16020-16569 and 1-908	223 290 319 362	73 151 152 200 235 263 309+C 315+C 523-524d 663 735 750	
Le93	M	A	16013-16569 and 1-911	126 223 290 319 362	73 152 200 235 263 315+C 523-524d 663 750	
Le1166	M	A	16007-16569 and 1-909	216 223 290 294 319 325 362	73 152 194 195 200 235 263 309+C 315+C 523-524d 663 750	
Le1527	M	A	16013-16569 and 1-919	216 223 290 294 319 362	73 152 195 200 235 263 309+C 315+C 523-524d 663 750	
Le455	M	A	16012-16569 and 1-914	223 263 290 319 362	73 152 200 207 235 315+C 523-524d 663 750	
Le1222	M	A11	16056-16569 and 1-914	223 234 290 293C 319 519 527	73 152 189 194 235 263 309+C 315+C 523-524d 663 750	
Le701	F	A5b	16006-16569 and 1-920	126 223 234 290 319 519	73 235 263 315+C 523-524d 663 750	
Le1483	F	A5b	16072-16569 and 1-917	126 223 234 290 319 519	73 235 263 309+C 315+C 523-524d 663 750	
Le466	M	A5b	16012-16569 and 1-909	126 223 235 290 319 519	73 152 235 263 315+C 523-524d 663 750	
Le1288	M	B	16012-16569 and 1-908	93 178 183C 189 311 519	73 263 309+CC 315+C 750	
Le1257	M	B	16006-16569 and 1-861	93 178 182C 183C 189 519	73 263 315+C 750	
Le1228	F	B	16013-16569 and 1-908	93 179 182C 183C 189	73 150 263 309+C 315+C 750	
Le293	F	B	16010-16569 and 1-910	93 183C 189 519	73 249d 263 309+C 315+C 523-524d 650 750	

Le73	M	B	16008-16569 and 1-911	93 178 182C 183C 189 519	64 73 152 263 309+CC 315+C 750
Le599	F	B4	16009-16569 and 1-904	183C 189 217	73 150 195 263 315+C 750
Le167	F	B4	16013-16569 and 1-906	183C 189 217 311	73 150 195 214 263 309+CC 315+C 750
Le407	F	B4	16013-16569 and 1-909	183C 189 217 311	73 150 195 214 263 309+C 315+C 750
Le632	M	B4	16012-16569 and 1-909	182C 183C 189 217 274 289 301 519	73 183 263 310d 374 523-524d 750
Le234	M	B4	16016-16569 and 1-909	92 182C 183C 189 217 274 289 301 519	73 183 263 310d 315+C 374 750
Le75	M	B4	16007-16569 and 1-911	92 183C 189 217 519	55 56 73 207 263 309+C 315+C 750 827
Le1067	F	B4	16012-16569 and 1-921	183C 189 217 519	73 150 263 315+C 556T 750 827
Le460	M	B4	16013-16569 and 1-873	183C 189 217 223 304 519	73 263 309+CC 315+C 573+4C 750 827
Le1028	M	B4	16012-16569 and 1-908	183C 189 217 519	73 152 263 309+CC 315+C 316 750 827
Le1016	M	B4	16016-16569 and 1-873	150 182C 183C 189 217 234 519	73 263 315+C 556T 750 827
Le742	M	B4a	16009-16569 and 1-908	182C 183C 189 217 261	73 263 310d 750
Le547	M	B4a	16013-16569 and 1-909	182C 183C 189 217 261 299 311 355 390 519	73 263 309+CC 315+C 750
Le1021	M	B4a	16012-16569 and 1-897	129 182C 183C 189 217 261 293 311	73 263 309dC 315+C 523-524d 750
Le439	F	B4a	16012-16569 and 1-905	182C 183C 189 217 261 519	73 146 195 263 309+CC 315+C 523-524d 750
Le384	M	B4a	16012-16569 and 1-908	182C 183C 189 217 223 261 519	73 146 263 309+C 315+C 523-524d 750
Le1263	M	B4a	16012-16569 and 1-911	168 182C 183C 189 217 261 311 519	73 146 263 309+C 315+C 523-524d 750
Le832	M	B4a	16010-16569 and 1-919	182C 183C 189 217 261 324 519	65G 73 263 309+C 315+C 523-524d 709 750
Le190	M	B4a	16013-16569 and 1-909	182C 183C 189 217 261 324 519	65G 73 263 309+3C 315+C 523-524d 709 750
Le943	F	B4a	16012-16569 and 1-901	182C 183C 189 217 261 399 519	73 263 309+C 315+C 523-524d 750
Le71	F	B4a	16012-16569 and 1-885	182C 183C 189 217 261	73 263 309+C 315+C 750
Le502	F	B4a	16011-16569 and 1-901	168 182C 183C 189 217 258C 261 311 519	73 263 309+C 315+C 356+C 523-524d 750
Le624	F	B4a	16012-16569 and 1-908	182C 183C 189 217 261 299 311 355 390 519	73 263 309+CC 315+C 750
Le707	F	B4a	16006-16569 and 1-909	182C 183C 189 217 261	73 195 263 315+C 523-524d 750
Le1250	F	B4a	16012-16569 and 1-908	129 182C 183C 189 261 519	73 263 309+CC 315+C 523-524d 750
Le1460	F	B4a	16017-16569 and 1-914	93 182C 183C 189 217 261 357 519	73 263 315+C 523-524d 750
Le1038	F	B4a	16007-16569 and 1-909	93 179 182C 183C 189 217 261 303 519	73 263 315+C 523-524d 750
Le1209	F	B4a	16009-16569 and 1-881	129 182C 183C 187A 189 261	73 227 263 315+C 328 523-524d 750
Le1271	F	B4a	16012-16569 and 1-882	93 182C 183C 189 217 261	73 263 309+C 315+C 750
Le483	F	B4a	16011-16569 and 1-916	129 182C 183C 189 261	73 263 309+CC 315+C 523-524d 750
Le571	M	B4a	16010-16569 and 1-909	182C 183C 189 217 240 261	73 204 263 310d 750
Le410	M	B4a	16014-16569 and 1-908	182C 183C 189 217 261 298 360 519	73 152 263 309+C 315+C 523-524d 750
Le361	M	B4a	16012-16569 and 1-908	182C 183C 189 217 240 260 261 519	73 263 309+CC 315+C 750
Le552	M	B4a	16009-16569 and 1-909	182C 183C 189 217 221 240 261	73 263 309+3C 315+C 750
Le861	M	B4a	16012-16569 and 1-908	93 182C 183C 189 217 261 290 357 519	73 263 315+C 523-524d 750
Le199	M	B4a	16007-16569 and 1-909	129 182C 183C 189 217 240 261	73 263 309+CC 315+C 750
Le564	M	B4a	16019-16569 and 1-903	182C 183C 189 217 221 240 261	73 263 309+CC 315+C 750
Le1060	M	B4a	16013-16569 and 1-873	93 182C 183C 189 217 261	73 263 315+C 750

Le1564	M	B4a	16012-16569 and 1-909	93 182C 183C 189 217 261	73 263 315+C 750	
Le802	M	B4a	16012-16569 and 1-873	182C 183C 189 217 234 261 519	73 263 309+C 315+C 523-524d 573+3C 750	
Le1227	M	B4a	16007-16569 and 1-898	129 182C 183C 189 217 261 354	73 263 308-309d 315+C 523-524d 750	
Le1302	M	B4a	16009-16569 and 1-911	181C 182C 183C 189 217 261 284	73 263 309+CC 315+C 523-524d 750	
Le1058	M	B4a	16007-16569 and 1-907	150 182C 183C 189 217 240 261	73 195 263 309+C 315+C 523-524d 750	
Le1095	M	B4a	16012-16569 and 1-908	86 129 182C 183C 189 217 261 519	73 263 309+CC 315+C 523-524d 750	
Le1619	M	B4a	16039-16569 and 1-917	182C 183C 189 217 240 261	73 263 309+CCC 315+C 750	
Le1604	M	B4a	16017-16569 and 1-906	168 182C 183C 189 217 261 311 327 519	73 263 308-309d 315+C 676 750	
Le1446	M	B4a	16023-16569 and 1-918	129 182C 183C 189 261 311	73 263 309+CC 315+C 523-524d 750	
Le1375	M	B4a	16014-16569 and 1-920	181C 182C 183C 189 213 217 261 362 519	73 189 263 309+C 315+C 523-524d 750	
Le1083	M	B4a	16011-16569 and 1-914	86 150 182C 183C 189 217 240 261	73 263 309+CC 315+C 523-524d 750	
Le1094	M	B4a	16013-16569 and 1-902	182C 183C 189 217 261 299 355 390 519	73 263 309+CC 315+C 750	
Le1335	M	B4a	16010-16569 and 1-910	168 182C 183C 189 217 258C 261 311 519	73 263 309+C 315+C 356+C 523-524d 750	
Le1406	M	B4a	16015-16569 and 1-911	182C 183C 189 217 221 240 261	73 263 307-309d 315+C 750	
Le633	M	B4a	16013-16569 and 1-917	182C 183C 189 217 261 362	73 263 309+C 315+C 523-524d 750	
Le1388	M	B4a	16012-16569 and 1-904	129 182C 183C 189 261 519	73 263 309+CC 315+C 523-524d 750	
Le1286	M	B4a1c	16013-16569 and 1-908	169h 182C 183C 189 217 261 299 519	73 193 263 309d 315+C 523-524d 709 750	
Le1374	F	B4b1	16014-16569 and 1-914	136 182C 183C 189 217 298 519	73 150 152 263 315+C 357 499 750 827	
Le355	M	B4b1	16012-16569 and 1-911	136 183C 189 217 519	73 146 263 309+C 315+C 499 750 827	
Le598	M	B4b1	16032-16569 and 1-908	136 183C 189 217 260 300 519	73 195 263 309+CC 315+C 499 523-524d 750 827	
Le291	M	B4b1	16012-16569 and 1-921	136 182C 183C 189 217 270 298 519	73 150 152 263 310d 499 750 827	
Le1576	M	B4b1	16009-16569 and 1-909	136 183C 189 217 260 519	73 263 309+CC 315+C 499 523-524d 750 827	
Le1390	M	B4b1	16017-16569 and 1-914	136 183C 189 217 260 519	73 263 309+C 315+C 499 523-524d 750 827	
Le775	M	B4b1	16009-16569 and 1-911	136 183C 189 217 260 287 325 519	73 263 315+C 499 523-524d 750 827	
Le33	M	B4b1	16035-16569 and 1-921	136 182C 183C 189 217 270 298 519	73 150 152 263 310d 499 750 827	
Le1563	M	B4b1	16009-16569 and 1-908	136 182C 183C 189 217 270 298 519	73 150 152 263 309-310d 499 750 827	
Le1458	M	B4b1	16012-16569 and 1-907	136 183C 189 217 260 325 519	73 263 315+C 499 523-524d 750 827	
Le797	M	B4b1	16009-16569 and 1-916	136 183C 189 217 260 287 325 519	73 263 315+C 499 523-524d 750 827	+
Le1160	M	B4b1	16012-16569 and 1-866	136 182C 183C 189 217 290A 293C 519	73 146 263 309+CC 315+C 499 750 827	
Le629	F	B4b1	16013-16569 and 1-907	136 183C 189 217 519	73 150 207 263 309+CC 315+C 408A 499 750 827	
Le505	F	B4b1	16012-16569 and 1-908	136 183C 189 217 519	73 150 207 263 309+CC 315+C 408A 499 750 827	
Le1548	F	B4b1	16012-16569 and 1-913	136 183C 189 217 258T 519	73 207 263 309+CC 315+C 499 523-524d 750 827	
Le282	M	B4b1	16012-16569 and 1-909	136 179 182C 183C 189 217 519	73 150 207 263 309+CC 315+C 499 750 827	
Le901	M	B4b1	16005-16569 and 1-908	93 136 183C 189 217 519	73 195 207 263 309+C 315+C 499 750 827	
Le717	M	B4b1	16012-16569 and 1-907	111 136 182C 183C 189 217 519	73 207 263 315+C 499 750 827	
Le91	M	B4b1	16013-16569 and 1-908	136 183C 189 217 519	73 146 152 207 263 309+C 315+C 499 750 827	
Le1131	M	B4b1	16012-16569 and 1-908	136 182C 183C 189 217 519	73 207 263 309+CC 315+C 499 523-524d 750 827	
Le1339	F	B4b1	16031-16569 and 1-919	136 154 183C 189 218 240 519	73 195 249d 263 309+CC 315+C 499 750 827	

Le1311	M	B4b1	16011-16569 and 1-908	38 136 183C 189 217 218 519	73 249d 263 309+C 315+C 499 750 827
Le1002	M	B4b1	16016-16569 and 1-908	51 136 183C 189 217 218 519	73 227 263 309+CC 315+C 499 636 750 827
Le1298	M	B4b1	16011-16569 and 1-917	136 147 183C 189 217 218 519	73 263 309+C 315+C 499 750 827
Le509	F	B4b1	16015-16569 and 1-908	136 183C 189 217 309 354 519	73 207 263 315+C 499 750 827
Le601	F	B4b1	16008-16569 and 1-908	136 183C 189 217 309 354 519	73 207 263 315+C 498 499 750 827
Le753	F	B4b1	16013-16569 and 1-909	136 183C 189 217 309 354 519	73 146 207 263 315+C 499 750 827
Le594	F	B4b1	16012-16569 and 1-906	136 183C 189 217 309 354 519	73 263 315+C 499 750 827
Le59	M	B4b1	16012-16569 and 1-878	136 183C 189 217 309 354 519	73 207 263 315+C 499 750 827
Le1529	M	B4b1a1	16013-16569 and 1-911	136 183C 189 217 284 519	73 199 202 207 263 309+C 315+C 499 750 827
Le906	F	B4c1b	16013-16569 and 1-909	140 183C 189 217 274 305T 335 519	73 195 263 309+C 315+C 709 750
Le1534	F	B4c1b	16010-16569 and 1-911	129 140 166 182C 183C 189 217 274 335 519	73 150 263 309+CC 315+C 709 750
Le989	F	B4c1b	16012-16569 and 1-915	129 140 166 183C 189 217 274 311 357 519 566	73 150 263 309+CC 315+C 573+2C 709 750
Le297	M	B4c1b	16013-16569 and 1-909	140 183C 189 217 266 274 335 342 519	73 150 263 309+C 315+C 709 750
Le1306	M	B4c1b	16012-16569 and 1-908	140 183C 189 217 274 519	73 150 185 188 263 291+A 309+CC 315+C 466 709 750
Le575	M	B4c1b	16013-16569 and 1-909	129 140 166 183C 189 217 274 335 519	73 150 195 263 309+C 315+C 709 750
Le1185	M	B4c1b	16008-16569 and 1-914	129 140 166 183C 189 217 274 519	73 150 263 309+CC 315+C 709 750
Le852	M	B4c1b	16013-16569 and 1-908	129 140 145 166 183C 189 217 274 335 519	73 150 263 309+C 315+C 709 750
Le961	M	B4c1b	16006-16569 and 1-905	136 140 183C 189 217 249 274 280 291 335 519	73 150 263 315+C 709 750
Le1428	M	B4c1b	16037-16569 and 1-1057	129 140 166 183C 189 217 274 311 357 519	73 150 263 309+C 315+C 709 750
Le959	M	B4c1b	16009-16569 and 1-909	136 140 183C 189 217 249 274 291 335 519	73 150 263 315+C 709 750
Le86	F	B4c1b	16008-16569 and 1-906	129 140 166 183C 189 217 274 335 519	73 146 150 195 263 309+CC 315+C 709 750
Le1546	F	B4c1b	16013-16569 and 1-911	129 140 166 183C 189 217 274 335 519	73 146 150 263 309+CC 315+C 709 750
Le491	F	B4c1b	16012-16569 and 1-908	51 140 182C 183C 189 217 274 335 519	73 146 150 189 195 263 309+CC 315+C 709 750
Le1164	F	B4c1b	16011-16569 and 1-899	37 129 140 166 183C 189 217 274h 335 519	73 146 150 263 315+C 709 750
Le10	M	B4c1b	16012-16569 and 1-911	134 140 182C 183C 189 217 242A 274 335 519	73 146 150 263 315+C 456 523-524d 709 750
Le1290	M	B4c1b	16010-16569 and 1-910	140 182C 183C 189 217 274 335 519	73 146 150 263 309+CC 315+C 709 750
Le656	M	B4c1b	16021-16569 and 1-907	140 182C 183C 189 217 274 311 335 519	73 146 150 195 263 309+C 315+C 709 750
Le1175	M	B4c1b	16011-16569 and 1-909	140 182C 183C 189 217 274 335 519	73 146 150 263 309+CC 315+C 709 750
Le477	M	B4c1b	16011-16569 and 1-908	140 183C 189 217 274 289 316 335 483 519	73 146 150 263 309+CC 315+C 709 750
Le409	F	B4c1b	16013-16569 and 1-910	129 138 140 166 183C 189 217 274 335 519	73 146 150 195 263 309+CC 315+C 709 750
Le681	M	B4c1b	16014-16569 and 1-904	93 140 182C 183C 189 217 274 311 335 519	73 146 150 263 309+C 315+C 709 750
Le360	M	B4c1b	16012-16569 and 1-908	129 140 145 166 183C 189 217 274 335 519	73 146 150 263 309+CC 315+C 709 750
Le702	M	B4c1b	16010-16569 and 1-909	129 140 145 166 183C 189 217 274 335 519	73 146 150 263 309+CC 315+C 709 750
Le606	M	B4c1c	16013-16569 and 1-920	182C 183C 189 217 311 526	73 150 195 214 263 279 309+C 315+C 750
Le1218	M	B4c2	16009-16569 and 1-874	147 183C 184A 189 217 235 260 293 519	73 263 309+C 315+C 523-524d 750
Le155	F	B4d1	16017-16569 and 1-906	172 183C 189 217 274 519	73 263 309+C 315+C 316 750 827
Le165	F	B4d1	16007-16569 and 1-917	182C 183C 189 217 519	73 263 309dC 315+C 316 750 827
Le1179	M	B4d1	16010-16569 and 1-908	183C 189 217 519	73 263 309+CC 315+C 316 750 827

Le605	M	B4d3	16009-16569 and 1-908	183d 186 189 217 234 519	73 151 152 197 263 315+C 546 750 827
Le1525	F	B4g	16010-16569 and 1-911	181C 182C 183C 189 213 217 261 292 519	61A 62 73 263 309+CCC 315+C 523-524d 750
Le770	F	B4g	16012-16569 and 1-921	181C 182C 183C 189 213 217 261 292 354 519	61A 62 73 263 309+CC 315+C 523-524d 750
Le934	F	B4g	16009-16569 and 1-909	86 181C 182C 183C 189 213 217 261 292 519	61A 62 73 263 315+C 523-524d 750
Le166	M	B4g	16013-16569 and 1-909	181C 182C 183C 189 213 217 261 292 519	73 263 309+C 315+C 523-524d 750
Le1345	M	B4g	16014-16569 and 1-908	153 181C 182C 183C 189 213 217 261 292 362 519	73 196 263 315+C 523-524d 750
Le994	M	B4g	16008-16569 and 1-909	181C 182C 183C 189 213 217 261 292 362 519	61A 62 73 263 309+3C 315+C 523-524d 750
Le847	M	B4g	16016-16569 and 1-908	181C 182C 183C 189 213 217 242 261 292 301 519	61A 62 73 150 263 308-309d 315+C 523-524d 750
Le1098	M	B4g	16009-16569 and 1-907	181C 182C 183C 189 213 217 261 292 519	61A 71d 73 263 309d 315+C 523-524d 750
Le1113	M	B4g	16009-16569 and 1-908	181C 182C 183C 189 213 217 261 292 519	61A 62 73 263 309+CC 315+C 523-524d 750
Le1293	M	B4g	16013-16569 and 1-909	153 181C 182C 183C 189 213 217 261 292 362 519	73 152 263 315+C 523-524d 750
Le1362	M	B4g	16007-16569 and 1-911	181C 182C 183C 189 213 217 261 292 519	73 263 309+CC 315+C 523-524d 750
Le673	M	B4g	16019-16569 and 1-1045	153 181C 182C 183C 189 213 217 261 292 362 519	73 263 309+CC 315+C 523-524d 750
Le893	F	B5	16012-16569 and 1-909	111 129 140 183C 184 189 243 463 519	73 131 263 315+C 523-524d 709 750
Le345	F	B5a	16013-16569 and 1-911	140 183C 189 209 266A 519	73 210 263 315+C 523-524d 709 750
Le58	F	B5a	16012-16569 and 1-909	140 182C 183C 189 261 266A 519	73 152 210 263 315+C 523-524d 709 750
Le1523	F	B5a	16005-16569 and 1-911	140 183C 189 266A 519	73 210 263 309+CC 315+C 523-524d 709 750
Le397	F	B5a	16016-16569 and 1-917	93 140 183C 189 260 266G 519	73 210 263 294 309+C 315+C 709 750
Le430	F	B5a	16012-16569 and 1-909	140 183C 189 266A 519	73 210 263 315+C 523-524d 709 750
Le1201	F	B5a	16012-16569 and 1-891	140 183C 189 262 266A 519	64 73 210 263 315+C 523-524d 593 709 750
Le132	F	B5a	16008-16569 and 1-909	140 189 266A 354 519	73 152 210 228 263 309+C 315+C 523-524d 709 750
Le850	F	B5a	16016-16569 and 1-905	140 183C 189 262 266A 519	73 210 263 315+C 523-524d 593 709 750
Le278	M	B5a	16012-16569 and 1-909	140 183C 189 266A	73 210 263 309+CC 315+C 523-524d 709 750
Le349	M	B5a	16012-16569 and 1-908	140 182C 183C 189 261 266A 519	73 146 152 210 263 315+C 523-524d 709 750
Le277	M	B5a	16012-16569 and 1-909	140 183C 189 266A 519	73 210 263 315+C 523-524d 709 750
Le62	M	B5a	16013-16569 and 1-897	140 183C 189 266A 519	73 146 210 263 309+CC 315+C 523-524d 709 750
Le378	M	B5a	16013-16569 and 1-908	140 183C 189 266A 519	73 210 263 309+CC 315+C 523-524d 709 750
Le178	M	B5a	16012-16569 and 1-909	140 183C 189 266A 482 519 525	73 210 263 309+CC 315+C 523-524d 709 750
Le765	M	B5a	16006-16569 and 1-909	140 183C 189 266A 519	73 146 210 263 309+CC 315+C 523-524d 709 750
Le663	M	B5a	16019-16569 and 1-909	140 183C 189 209 266A 519	73 210 263 315+C 523-524d 709 750
Le880	M	B5a	16014-16569 and 1-908	140 183C 189 266A 519	73 210 263 279 309+C 315+C 523-524d 709 750
Le1203	M	B5a	16012-16569 and 1-913	140 183C 189 266A 519	73 210 235 263 309+CC 315+C 523-524d 709 750
Le653	M	B5a	16012-16569 and 1-908	93 140 183C 189 260 266G 519	73 210 263 294 309+C 315+C 709 750
Le690	M	B5a	16007-16569 and 1-909	140 183C 189 266A 519	73 210 263 309+C 315+C 523-524d 593 709 750
Le1380	M	B5a	16012-16569 and 1-909	140 183C 189 266A 519	73 210 263 309+C 315+C 523-524d 648 709 750
Le637	M	B5a	16012-16569 and 1-908	114A 188 189 234 235 266A 327 519	73 210 263 309+C 315+C 523-524d 709 750
Le39	M	B5a	16008-16569 and 1-921	140 183C 189 266A 519	73 210 263 315+C 523-524d 709 750
Le1615	M	B5a	16021-16569 and 1-921	140 183C 189 218 266A 319 519	73 210 263 315+C 523-524d 709 750

Le1599	M	B5a	16013-16569 and 1-909	140 183C 189 266A 519	73 263 309+C 315+C 523-524d 709 750
Le1608	M	B5a	16024-16569 and 1-921	140 183C 189 266A 519	73 210 263 309+C 315+C 523-524d 709 750
Le1565	M	B5a	16010-16569 and 1-909	140 189 266A 311 519	73 263 315+C 523-524d 709 750
Le1044	M	B5a	16012-16569 and 1-906	93 140 183C 189 266A 361 399 519	73 152 153 204 210 263 309+CC 315+C 709 750
Le1348	M	B5a	16010-16569 and 1-908	92 140 183C 189 234 266A 519	73 210 263 315+C 523-524d 709 750
Le728	M	B5a	16009-16569 and 1-910	140 182C 183C 189 266A 519	73 210 263 315+C 523-524d 593 709 750
Le1204	M	B5a	16012-16569 and 1-889	140 183C 189 266A 519	73 210 263 315+C 523-524d 593 709 750
Le1090	M	B5a	16007-16569 and 1-917	140 183C 189 266A 482 519	73 210 263 309+C 315+C 523-524d 709 750
Le1537	M	B5a	16025-16569 and 1-921	140 182C 183C 189 266A	73 210 263 309+C 315+C 523-524d 709 750
Le1396	M	B5a	16013-16569 and 1-916	140 183C 189 261 266A 519	73 210 263 309+C 315+C 523-524d 709 750
Le1594	M	B5a	16015-16569 and 1-920	188 189 266A 287 318 519	73 200 210 263 315+C 523-524d 709 750
Le507	F	B5a2	16013-16569 and 1-908	140 187 189 266G 519	73 93 210 263 309+CC 315+C 375 523-524d 709 750
Le137	M	B5a2	16010-16569 and 1-911	140 187 189 256 266G 519	73 93 210 263 315+C 523-524d 709 750
Le986	M	B5a2	16014-16569 and 1-908	140 187 189 256 266G 519	73 93 210 263 315+C 523-524d 709 750
Le1046	M	B5a2	16008-16569 and 1-908	140 187 189 256 266A 519	73 93 210 257 263 315+C 523-524d 709 750
Le1163	M	B5a2	16013-16569 and 1-908	92 140 187 189 266A 519	73 93 146 210 263 315+C 523-524d 709 750
Le895	F	B5b	16012-16569 and 1-919	140 183C 189 243 519	73 103 189 203 204 263 309+C 315+C 523-524d 709 750
Le21	M	B5b	16008-16569 and 1-872	140 183C 189 194C 195 243 519	73 103 152 195 204 263 309+C 315+C 523-524d 573+4C 709 750
Le674	M	B5b	16014-16569 and 1-875	140 183C 189 194C 195 243 262 311 519	73 103 152 195 204 263 309+3C 315+C 523-524d 573+3C 709 750
Le1070	M	B5b	16013-16569 and 1-906	140 166 183C 189 243 519	73 103 152 195 204 263 309+CC 315+C 523-524d 573+3C 709 750 868
Le1572	M	B5b	16013-16569 and 1-902	140 183C 189 243 311 319 519	73 103 204 207 263 309+C 315+C 523-524d 709 750
Le569	M	B5b	16017-16569 and 1-908	140 154 183C 189 234 243 465 519	73 93 131 203 204 263 315+C 408A 523-524d 709 750
Le743	M	B5b	16017-16569 and 1-1042	93h 140 183C 189 243 519	73 204 263 309+C 315+C 523-524d 709 750
Le92	F	B5b2	16009-16569 and 1-908	111 140 183C 189 234 243 256 463 519	73 103 131 146 263 309+C 315+C 523-524d 709 750
Le1255	F	B5b2	16012-16569 and 1-915	111 140 182C 183C 189 209 234 243 304 463 519	73 103 131 263 309+CC 315+C 523-524d 709 750
Le1010	M	B5b2	16013-16569 and 1-907	111 140 183C 189 234 243 463 519	73 103 131 195 263 309+C 315+C 523-524d 709 750
Le1418	M	B5b2	16013-16569 and 1-873	111 140 183C 189 234 243 463 519	73 103 131 199 204 263 309+C 315+C 523-524d 573+5C 709 750
Le1567	M	B5b2b	16009-16569 and 1-909	111 140 183C 189 234 243 519	73 103 131 204 207 263 309+CCC 315+C 523-524d 709 750
Le963	F	B5b2c	16012-16569 and 1-908	129 189 234 243 463 519	73 93 263 309+C 315+C 481 523-524d 709 750
Le162	F	C	16013-16569 and 1-909	223 298 327 519	73 249d 263 309+CC 315+C 489 750
Le796	F	C	16006-16569 and 1-884	51 223 298 327 519	73 188 204 249d 263 315+C 489 750
Le500	F	C	16012-16569 amd 1-908	183C 189 223 298 327 519	73 249d 263 309+CC 315+C 489 750
Le37	F	C	16017-16569 and 1-914	93 172 223 298 327 519	73 249d 263 309+C 315+C 489 750
Le20	M	C	16008-16569 and 1-916	86 223 298 327	73 249d 263 315+C 489 750
Le533	M	C	16016-16569 and 1-908	298 327 519	73 249d 263 309+C 315+C 489 750
Le1491	M	C	16008-16569 and 1-908	183C 189 223 298 327 519 527	73 249d 263 309+CC 315+C 489 750
Le1596	M	C	16012-16569 and 1-914	213 223 286 311 327 519	73 249d 263 309+C 315+C 489 750
Le839	M	C	16012-16569 and 1-909	183C 189 223 298 327 519 527	73 249d 263 309+CC 315+C 489 750

Le1521	M	C	16014-16569 and 1-911	93 145 193 223 298 327 519	73 249d 263 309+C 315+C 489 750	
Le824	M	C	16008-16569 and 1-911	223 298 327	73 150 249d 263 309+CC 315+C 489 523-524d 750	
Le795	M	C	16007-16569 and 1-921	67 93 145 223 294 298 327 519	73 249d 263 309+CC 315+C 489 750	
Le1551	M	C	16014-16569 and 1-921	93 183C 189 223 298 327 519	73 249d 263 309+CC 315+C 489 750	
Le979	M	C	16009-16569 and 1-914	153 189 223 298 327 519	73 207 249d 263 315+C 489 750	
Le1585	M	C	16009-16569 and 1-919	183C 189 223 298 327 519	73 207 249d 263 309+CC 315+C 489 750	
Le371	M	C	16013-16569 and 1-909	223 298 327 519	44+C 73 249d 263 315+C 489 750	
Le578	F	C	16013-16569 and 1-908	223 298 327 519	73 146 249d 263 309+CC 315+C 489 750	
Le1417	F	C	16012-16569 and 1-909	223 298 327 519	73 146 249d 263 309+CC 315+C 489 750	
Le314	M	C	16012-16569 and 1-908	86 223 242 256 298 327 519	73 146 249d 263 315+C 489 720 750	
Le927	F	C4a	16015-16569 and 1-906	223 298 311 327 357 519	73 249d 263 310d 315+C 489 750	
Le609	M	C4a	16033-16569 and 1-911	223 298 318 327 357 519	73 195 249d 263 309+CC 315+C 489 634 750	
Le1253	M	C4a	16035-16569 and 1-921	189 223 247 298 327 357 519	47 73 249d 263 309+C 315+C 489 523-524d 750	
Le24	F	C4a1	16007-16569 and 1-919	129 183C 189 223 298 327 519	73 249d 263 309+C 315+C 489 750	
Le377	F	C4a1	16013-16569 and 1-907	129 148 223 298 327 519	73 152 249d 263 315+C 449 489 750	
Le118	M	C4a1	16013-16569 and 1-908	129 192 223 298 327 519	73 249d 263 315+C 489 750	
Le317	M	C4a1	16020-16569 and 1-909	129 148 223 298 327 519	73 152 249d 263 315+C 449 489 750	
Le295	M	C4a1	16009-16569 and 1-909	93 129 223 298 327 519	73 194 249d 263 309+C 315+C 489 750	
Le1382	M	C4a1	16012-16569 and 1-921	129 148 223 298 327 519	73 152 249d 263 315+C 449 489 750	
Le935	M	C4a1	16008-16569 and 1-908	129 223 298 327	73 249d 263 315+C 489 523-524d 750	
Le34	M	C4a1	16024-16569 and 1-921	93 129 223 298 519	73 195 228T 249d 263 309+CC 315+C 489 524+AC 750	
Le1504	M	C4a1	16017-16569 and 1-918	93 129 223 298 327 519	73 151 195 249d 263 309+C 315+C 489 495 750	
Le896	F	C4a2	16013-16569 and 1-919	171 223 298 300 327 344 357 519	47 73 152 183 249d 263 309+C 315+C 489 508 750	
Le112	F	C4a2	16007-16569 and 1-897	167 171 223 298 327 344 357	47 73 146 249d 263 315+C 489 750	
Le307	M	C5	16001-16569 and 1-917	86 223 230 274 288 298 327 519	73 249d 263 315+C 489 595+C 750	
Le81	M	C5a	16007-16569 and 1-921	93 129 223 261 288 298 519	73 249d 263 315+C 489 595+C 750	
Le1474	M	CZ	16013-16569 and 1-909	223 298	73 249d 263 309+C 315+C 489 523-524d 750	
Le467	F	D4	16012-16569 and 1-911	92 223 362	73 263 309+C 315+C 489 750	–
Le77	F	D4	16007-16569 and 1-921	292 362 519	73 263 315+C 489 523-524d 750	–
Le79	F	D4	16013-16569 and 1-911	292 362 519	73 263 315+C 489 523-524d 750	–
Le1256	F	D4	16012-16569 and 1-908	223 249 362	73 263 315+C 489 750	–
Le326	F	D4	16012-16569 and 1-908	362	73 152 195 263 309+C 315+C 489 750	–
Le424	F	D4	16014-16569 and 1-909	93 223 362	73 263 309+C 315+C 489 750	–
Le1274	F	D4	16012-16569 and 1-913	223 362	73 263 315+C 489 750	–
Le1562	F	D4	16012-16569 and 1-915	223 311h 316 362	73 183 263 315+C 489 750	–
Le755	F	D4	16008-16569 and 1-900	223 286 362	73 263 315+C 489 750	–
Le1236	F	D4	16012-16569 and 1-908	223 249 362	73 263 315+C 489 750	–
Le648	F	D4	16013-16569 and 1-907	218 223 362	73 263 309+C 315+C 489 750	–

Le1622	F	D4	16021-16569 and 1-911	223 355 362	73 152 195 199 263 309+CC 315+C 489 750	–
Le1482	F	D4	16009-16569 and 1-911	223 362	73 195 263 315+C 489 750	–
Le450	F	D4	16013-16569 and 1-907	223 362 519	73 194 263 315+C 489 523-524d 750	–
Le787	M	D4	16012-16569 and 1-869	223 362 519	73 263 315+C 489 523-524d 573+3C 750	–
Le101	M	D4	16006-16569 and 1-911	223 234 316 362	73 194 263 309+C 315+C 489 750	–
Le19	M	D4	16012-16569 and 1-911	223 249 362	73 263 315+C 489 750	–
Le194	M	D4	16019-16569 and 1-908	223 316 362	73 183 263 315+C 489 750	–
Le227	M	D4	16012-16569 and 1-908	223 225 261 362	73 146 263 315+C 489 750	–
Le328	M	D4	16018-16569 and 1-909	223 311 362	73 195 263 309+C 315+C 489 750	–
Le560	M	D4	16012-16569 and 1-908	223 249 362	73 153 263 309+CC 315+C 489 750	–
Le186	M	D4	16007-16569 and 1-918	86 124 223 362 519	73 194 263 309+C 315+C 489 523-524d 750	–
Le540	M	D4	16014-16569 and 1-875	192 222 316 362	41 73 184 195 263 309+C 315+C 489 507 750	–
Le1148	M	D4	16013-16569 and 1-907	188+CC 223 362	73 183 184 199 204 263 309+C 315+C 489 495 523-524d 750	–
Le323	M	D4	16014-16569 and 1-909	223 362	73 207 263 315+C 489 513 750	–
Le1465	M	D4	16015-16569 and 1-908	223 271 362 519	73 263 298 315+C 489 593 750	–
Le1049	M	D4	16008-16569 and 1-908	172 223 362 526T	73 150 263 315+C 489 750	–
Le1300	M	D4	16015-16569 and 1-920	223 362 519	73 194 263 315+C 489 523-524d 750	–
Le1171	M	D4	16010-16569 and 1-909	223 362	73 263 309+C 315+C 489 750	–
Le1180	M	D4	16013-16569 and 1-902	92 223 362 519	73 263 309+C 315+C 489 750	–
Le1305	M	D4	16014-16569 and 1-899	92 223 362 519	73 263 309+C 315+C 489 750	–
Le932	M	D4	16010-16569 and 1-909	223 271 293T 362	73 195 263 309+C 315+C 489 750	–
Le992	M	D4	16013-16569 and 1-908	111 223 362 519	73 194 195 263 309+C 315+C 489 523-524d 750	–
Le1372	M	D4	16012-16569 and 1-909	223 260 362	73 195 263 315+C 489 523-524d 709 750	–
Le619	M	D4	16012-16569 and 1-921	168 223 362	73 152 195 263 309+C 315+C 489 523-524d 750	–
Le146	M	D4	16007-16569 and 1-911	169 223 362	73 263 309+C 315+C 489 750	–
Le926	M	D4	16012-16569 and 1-909	223 362	73 152 263 309+C 315+C 489 750	–
Le1466	M	D4	16009-16569 and 1-902	223 362 519	73 194 263 315+C 489 523-524d 750	–
Le1238	M	D4	16012-16569 and 1-905	223 362	73 263 309+C 315+C 489 750	–
Le1287	M	D4	16012-16569 and 1-906	223 232A 274 295 362	73 185 204 263 298 309+C 315+C 489 523-524d 750	–
Le1443	M	D4	16017-16569 and 1-909	223 311 362 519	73 146 150 263 315+C 489 523-524d 750	–
Le1580	M	D4	16013-16569 and 1-911	172 223 362	73 263 309+C 315+C 489 629 750	–
Le68	M	D4	16033-16569 and 1-918	93 172 362 519	73 194 263 315+C 489 523-524d 750	–
Le1249	M	D4	16009-16569 and 1-881	223 362	73 94 146 263 309+CC 315+C 489 644 709 750	–
Le622	M	D4	16023-16569 and 1-921	223 311 362	73 195 263 309+C 315+C 489 750	–
Le1299	M	D4	16012-16569 and 1-906	223 362	73 263 315+C 489 750	–
Le1545	M	D4	16024-16569 and 1-909	223 278 311 362	73 195 263 309+C 315+C 489 750	–
Le1518	M	D4	16017-16569 and 1-910	93 223 362 519	73 194 263 315+C 489 523-524d 750	–
Le1475	M	D4	16012-16569 and 1-921	223 260 292 311 362	73 146 263 315+C 489 750	–

Le113	F	D4	16009-16569 and 1-911	223 362	73 263 298 309+C 315+C 489 709 750	–
Le298	M	D4	16012-16569 and 1-909	223 362 519	73 194 263 315+C 489 523-524d 750	–
Le758	M	D4	16007-16569 and 1-919	223 288 362 519	73 152 194 263 315+C 489 523-524d 750	–
Le260	M	D4	16021-16569 and 1-911	51 223 362 519	73 194 263 309+C 315+C 489 523-524d 750	–
Le1426	M	D4	16013-16569 and 1-783	223 362 519	73 194 263 315+C 489 523-524d 750	–
Le951	F	D4	16012-16569 and 1-908	223 362 519	73 150 194 263 315+C 489 523-524d 750	–
Le875	M	D4	16012-16569 and 1-911	223 362 519	73 150 194 263 309+C 315+C 489 523-524d 750	–
Le340	F	D4	16012-16569 and 1-919	86 223 362	73 263 309+C 315+C 489 750	–
Le1511	M	D4	16022-16569 and 1-921	86 192 223 271 316 362	73 184 263 309+C 315+C 489 750	–
Le1618	M	D4a	16015-16569 and 1-907	129 223 362	73 263 309+C 315+C 489 750	–
Le1165	F	D4a	16015-16569 and 1-913	93 129 223 263 311 362 519	73 152 263 315+C 489 750 792	–
Le890	F	D4a	16017-16569 and 1-909	129 223 311 362	73 152 263 309+C 315+C 489 750	–
Le1283	F	D4a	16013-16569 and 1-919	129 223 263 362 519	73 152 263 309+C 315+C 489 750	–
Le170	M	D4a	16009-16569 and 1-908	129 223 362 519	73 152 263 309+C 315+C 489 750	–
Le1133	M	D4a	16012-16569 and 1-909	129 223 362 519	73 152 263 315+C 489 750	–
Le136	M	D4a	16012-16569 and 1-905	129 223 362 519	73 152 263 315+C 489 750	–
Le138	M	D4a	16018-16569 and 1-911	129 183C 189 223 270 362 519	73 146 152 263 309+CC 315+C 489 523-524d 750	–
Le248	M	D4a	16006-16569 and 1-908	129 223 270 362 519	73 146 152 263 309+C 315+C 489 523-524d 750	–
Le468	M	D4a	16011-16569 and 1-907	129 223 263 362 519	73 152 263 309+C 315+C 489 507 750	–
Le1170	M	D4a	16012-16569 and 1-908	111 129 223 255 263 362 519	73 152 263 309+C 315+C 489 507 750	–
Le1154	M	D4a	16012-16569 and 1-908	129 223 362 519	73 152 263 309+C 315+C 489 750	–
Le56	M	D4a	16012-16569 and 1-920	129 153 223 362 519	73 152 263 309+CC 315+C 489 750	–
Le757	M	D4a	16012-16569 and 1-908	129 223 263 362 519	73 152 263 309+C 315+C 489 750	–
Le1381	M	D4a	16012-16569 and 1-914	129 223 362 519	73 152 263 309+C 315+C 489 750	–
Le55	F	D4a1e	16008-16569 and 1-856	129 223 256 299 362 519	73 152 263 315+C 489 723 750	–
Le376	F	D4a1e	16010-16569 and 1-897	129 223 256 362 519	73 152 263 315+C 489 750	–
Le1515	F	D4a3	16013-16569 and 1-909	129 223 249 311 362	73 152 263 309+C 315+C 489 750	–
Le1520	M	D4a3	16025-16569 and 1-918	129 223 249 362	73 152 263 315+C 489 750	–
Le711	M	D4a3	16009-16569 and 1-909	129 223 249 311 362 519	73 152 263 309+C 315+C 489 750	–
Le1423	M	D4a3	16018-16569 and 1-909	129 223 249 278 311 362	73 152 263 309+CC 315+C 489 524+AC 750	–
Le247	M	D4a3	16013-16569 and 1-908	129 223 249 362	73 146 152 196 263 309+C 315+C 489 750	–
Le1009	M	D4a3	16012-16569 and 1-908	93 129 223 249 362	73 152 263 309+CC 315+C 489 750	–
Le224	M	D4b1	16012-16569 and 1-917	185 189d 223 232A 319 362	73 263 315+C 489 523-524d 750	–
Le732	M	D4b1	16009-16569 and 1-908	185 186 189 223 232A 319 362	73 263 309+C 315+C 489 523-524d 750	–
Le794	M	D4b1	16012-16569 and 1-907	158 223 284 287 319	73 152 204 263 309+C 315+C 489 523-524d 750	–
Le1597	M	D4b1	16024-16569 and 1-919	185 189d 223 232A 319 362	73 263 309+C 315+C 489 523-524d 750	–
Le911	M	D4b1	16009-16569 and 1-921	223 239 243 319 362	73 152 263 309+C 315+C 489 523-524d 750	–
Le597	F	D4b1b	16017-16569 and 1-921	93 223 287 319 362 380	73 263 309+C 315+C 431 489 523-524d 750	–

Le1543	M	D4c	16013-16569 and 1-909	223 245 362 368	73 263 315+C 489 750	–
Le798	M	D4c	16009-16569 and 1-909	223 245 362	73 263 309+C 315+C 489 534 545 750	–
Le402	M	D4e1a	16009-16569 and 1-909	223 362	73 94 263 309+C 315+C 489 750	–
Le418	M	D4e1a	16018-16569 and 1-911	92 223 362	73 94 263 315+C 489 750	–
Le993	M	D4e1a1	16015-16569 and 1-919	176 223 362	73 94 189 194 263 309+C 315+C 489 750	–
Le226	F	D4e1a2	16009-16569 and 1-909	42 223 291 362	73 94 214 263 309+C 315+C 455+T 489 750	–
Le1488	M	D4e1a2	16008-16569 and 1-908	92 223 362	73 94 214 263 315+C 489 750	–
Le274	M	D4e1a2	16011-16569 and 1-884	92 223 311 362	73 94 214 263 309+C 315+C 489 750	–
Le1071	M	D4g2	16007-16569 and 1-908	223 362 519	73 195 207 263 298 315+C 489 750	–
Le1294	M	D4g2a	16013-16569 and 1-875	223 259A 274 362 519	73 263 298 309+C 315+C 489 573+3C 750	–
Le200	M	D4g2a	16008-16569 and 1-914	169 223 266 274 327h 362	73 263 298 309+CC 315+C 489 750	–
Le864	M	D4g2a1a	16027-16569 and 1-1000	223 274 362	73 263 298 309+C 315+C 489 546 750	–
Le1292	F	D4h1	16012-16569 and 1-858	174 179 223 362	73 131 263 315+C 489 750	–
Le99	F	D4h1	16012-16569 and 1-909	174 362 566	73 263 309+CC 315+C 489 750	–
Le593	F	D4h1	16014-16569 and 1-908	48 174 223 343 362	73 152 263 309+C 315+C 489 750	–
Le948	M	D4h1	16015-16569 and 1-863	93 174 223 362	73 189 263 309+C 315+C 489 573+3C 750	–
Le1097	M	D4i	16013-16569 and 1-908	111 129 223 229 294 362	73 263 309+CC 315+C 489 523-524d 750	–
Le822	F	D4j3	16012-16569 and 1-908	184 223 311 362	73 263 309+C 315+C 489 750	–
Le1376	F	D4j3	16016-16569 and 1-916	184 223 311 362	73 195 263 315+C 489 750	–
Le159	F	D4j3	16007-16569 and 1-917	184 223 311 362 519	73 263 309+C 315+C 489 750	–
Le827	M	D4j3	16017-16569 and 1-911	184 223 288 311 362	73 263 309+C 315+C 489 750	–
Le888	M	D4j3	16012-16569 and 1-921	184 223 311 362	73 263 309+C 315+C 489 722 750	–
Le920	M	D4j3	16013-16569 and 1-911	184 223 311 362	73 263 315+C 489 750	–
Le283	M	D4k	16012-16569 and 1-909	192 223	73 195 263 309+C 315+C 489 750	–
Le749	M	D4k	16010-16569 and 1-914	192 223	73 150 185 195 263 309+C 315+C 489 750	–
Le29	F	D4m2	16008-16569 and 1-914	42 223 362	73 247 263 309+C 315+C 489 523-524d 750	–
Le557	M	D4n	16014-16569 and 1-906	223 325 355A 362	73 195 263 315+C 489 750	–
Le1360	M	D4q	16013-16569 and 1-908	223 256 311 362 519	73 200 234 263 315+C 489 750	–
Le1004	F	D5a	16011-16569 and 1-919	182C 183C 189 223 360 362	73 150 263 309+CC 315+C 489 750 752	–
Le736	M	D5a	16012-16569 and 1-911	111 182C 183C 189 223 360 362	73 150 263 309+CC 315+C 489 523-524d 750 752	–
Le799	F	D5a2	16009-16569 and 1-913	51 172 182C 183C 189 223 266 362	73 150 263 309+C 315+C 489 523-524d 750 752	–
Le857(2)	F	D5a2	16012-16569 and 1-918	164 172 182C 183C 189 223 362	73 150 152 200 263 315+CC 489 523-524d 750 752	–
Le658	M	D5a2	16006-16569 and 1-909	164 172 182C 183C 189 223 259 362	73 150 263 309+C 315+C 489 523-524d 750 752	–
Le1526	M	D5a2	16012-16569 and 1-909	153 164 172 182C 183C 189 223 259 362	73 150 263 315+C 489 523-524d 750 752	–
Le803	F	D5a2a	16006-16569 and 1-909	92 164 167 172 182C 183C 189 223 266 293 362	73 150 263 315+C 489 493 523-524d 750 752	–
Le1611	F	D5a2a	16011-16569 and 1-921	92 164 182C 183C 189 223 266 362	73 150 263 309+C 315+C 489 523-524d 750 752	–
Le462	M	D5a2a	16012-16569 and 1-908	164 182C 183C 189 223 266 362	73 150 195 207 263 309+CC 315+C 489 523-524d 750 752	–
Le1134	M	D5a2a	16011-16569 and 1-918	92 164 167 172 182C 183C 189 223 266 293 362	73 150 263 315+C 489 523-524d 750 752	–

Le950	M	D5a2a	16012-16569 and 1-909	92 164 167 172 182C 183C 189 223 224 266 362	73 150 263 315+C 489 523-524d 750 752	–
Le1614	M	D5a2a	16025-16569 and 1-917	164 172 182C 183C 189 223 266 311 362	73 150 263 309+C 315+C 489 523-524d 750 752	–
Le773	M	D5a2a	16009-16569 and 1-911	92 164 182C 183C 189 223 266 362	73 150 152 263 309+C 315+C 489 523-524d 750 752	–
Le48	M	D5a2a	16012-16569 and 1-896	86 92 164 182C 183C 185 189d 223 266 362	73 150 263 315+C 489 523-524d 750 752	–
Le1510	F	D5b	16034-16569 and 1-911	182C 183C 189 223 362	73 150 263 309+CC 315+C 456 489 681 750 865	–
Le1006	F	D5b	16012-16569 and 1-908	182C 183C 189 223 362	73 150 263 309+CC 315+C 456 489 681 750	–
Le733	F	D5b	16012-16569 and 1-916	148 182C 183C 189 223 362 519	73 150 152 263 315+C 456 489 523-524d 681 750	–
Le1212	F	D5b	16012-16569 and 1-910	189 223 362 519	73 150 263 309+C 315+C 456 489 681 750	–
Le1072	F	D5b	16012-16569 and 1-908	189 223 362 519	73 150 263 309+CC 315+C 456 489 681 750	–
Le1536	F	D5b	16025-16569 and 1-909	86 189 223 292 362	73 146 150 263 309+C 315+C 456 489 681 750	–
Le83	M	D5b	16009-16569 and 1-911	183C 189 194C 195 223 362	73 146 150 263 309+CC 315+C 456 489 523-524d 681 750	–
Le42	M	D5b	16009-16569 and 1-910	148 182C 183C 189 223 362 519	73 150 152 263 309+CC 315+C 456 489 523-524d 681 750	–
Le50	M	D5b	16008-16569 and 1-919	148 179 183C 189 223 362 519	73 150 152 185 195 263 309+C 315+C 456 489 523-524d 681 750	–
Le188	M	D5b	16012-16569 and 1-919	182C 183C 189 223 362	73 150 263 309+C 315+C 456 489 681 750	–
Le320	M	D5b	16013-16569 and 1-908	189 223 291 362 519	73 150 309+CC 315+C 456 489 524+AC 681 750	–
Le294	M	D5b	16012-16569 and 1-911	182C 183C 189 223 362	73 150 263 309+CC 315+C 456 489 524+AC 681 750	–
Le1217	M	D5b	16013-16569 and 1-909	148 179 183C 189 223 362 519	73 150 152 185 195 263 315+C 456 489 523-524d 681 750	–
Le1301	M	D5b	16013-16569 and 1-909	189 223 362 519	73 150 309+C 315+C 456 489 681 711 750	–
Le914	M	D5c	16022-16569 and 1-901	51 189 223 319 362 390	73 146 150 151 152 263 309+CC 315+C 489 750	–
Le995	M	D5c	16007-16569 and 1-909	189 190 193+2C 290 362 390 519	73 146 150 151 152 182 195 217 263 315+C 489 524+AC 750	–
Le1124	M	D5c	16008-16569 and 1-909	51 189 223 320 362 390	73 146 150 151 152 263 309+C 315+C 489 750	–
Le859	F	D5c	16012-16569 and 1-909	189 190 193+2C 223 311 316 362	73 150 151 152 263 309+CC 315+C 489 750	–
Le1330	M	D6a	16010-16569 and 1-908	189 192 223 274 362	73 263 309+C 315+C 489 709 750	–
Le1280	F	D6c	16019-16569 and 1-907	184 189 223 311 362	73 146 152 263 315+C 489 709 750	–
Le114	M	D6c	16008-16569 and 1-921	183C 189 223 311 362	73 152 239 263 309+C 315+C 489 709 750	–
Le1352	M	D6c	16013-16569 and 1-908	172 189 223 240C 311 362	16T 73 152 263 309+C 315+C 489 709 750	–
Le1291	F	F	16009-16569 and 1-917	209 304	73 249d 263 309+C 315+C 750	
Le1505	F	F	16043-16569 and 1-909	304 527	73 125G 189 249d 263 309+C 315+C 750	
Le1559	F	F	16011-16569 and 1-873	304 311	73 249d 263 309+CC 315+C 523-524dh 750	
Le916	M	F	16012-16569 and 1-908	192 304 527	73 249d 263 315+C 709 750	
Le831	M	F	16007-16569 and 1-908	304	73 249d 263 309+C 315+C 606 750	
Le1138	M	F	16012-16569 and 1-909	167 221 304 519	73 152 195 249d 263 275 309+C 315+C 750	
Le982	M	F	16013-16569 and 1-909	221 304 519	73 152 195 249d 263 275 309+C 315+C 750	
Le1047	M	F	16008-16569 and 1-908	304 311	73 152 249d 263 309+CC 315+C 750	
Le161	M	F1	16013-16569 and 1-906	129 189 203 304 519	73 249d 263 315+C 750	
Le379	F	F1a	16009-16569 and 1-910	129 172 304 519	73 249d 263 309+C 315+C 521-524d 750	
Le27	F	F1a	16007-16569 and 1-920	129 172 304 519	73 249d 263 315+C 523-524d 750	
Le272	F	F1a	16020-16569 and 1-874	172 218 304 311	73 249d 263 315+C 573+4C 750	

Le139	F	F1a	16014-16569 and 1-909	129 172 294 304 362 519	73 152 249d 263 309+C 315+C 521-524d 750
Le1075	F	F1a	16012-16569 and 1-887	129 172 304 519	73 249d 263 315+C 523-524d 750
Le1025	F	F1a	16012-16569 and 1-909	172 274 304 519	73 249d 263 309+C 315+C 523-524d 750
Le679	F	F1a	16008-16569 and 1-920	129 172 304 519	73 249d 263 309+C 315+C 521-524d 750
Le1403	F	F1a	16019-16569 and 1-908	172 209 304 519	73 200 249d 263 309+CC 315+C 523-524dh 750
Le1264	F	F1a	16013-16569 and 1-911	129 172 304 519	53 54C 73 249d 263 309+C 315+C 318 523-524d 750
Le435	F	F1a	16012-16569 and 1-908	75 172 304 519	73 249d 263 315+C 523-524d 750
Le1262	F	F1a	16012-16569 and 1-907	86 129 172 183C 189 304 519	73 249d 263 315+C 523-524d 750
Le1433	F	F1a	16014-16569 and 1-909	129 172 304 519	73 249d 263 309+C 315+C 521-524d 750
Le1370	F	F1a	16014-16569 and 1-906	129 172 183C 189 304 519	73 152 249d 263 309+CC 315+C 523-524d 750
Le1317	F	F1a	16013-16569 and 1-908	51 129 172 304 311 497 519	73 152 249d 263 315+C 523-524d 750
Le337	M	F1a	16012-16569 and 1-908	129 172 304 519	73 249d 263 315+C 523-524d 750
Le475	M	F1a	16007-16569 and 1-901	129 172 304 519	73 152 249d 263 309+CC 315+C 523-524d 573+C 750
Le65	M	F1a	16008-16569 and 1-917	129 172 304 519	73 249d 263 309+C 315+C 466 521-524d 750
Le329	M	F1a	16013-16569 and 1-908	129 172 304 519	73 249d 263 315+C 523-524d 750
Le461	M	F1a	16012-16569 and 1-908	129 172 304 519	73 249d 263 315+C 523-524d 750
Le339	M	F1a	16008-16569 and 1-869	129 172 304 519	73 234h 249d 263 315+C 523-524d 750
Le72	M	F1a	16009-16569 and 1-911	129 172 304 519	52 53 54T 71d 73 249d 263 309+C 315+C 318 523-524d 750
Le1583	M	F1a	16009-16569 and 1-919	129 172 304 399 519	73 249d 263 309+C 315+C 523-524d 750
Le1041	M	F1a	16013-16569 and 1-908	129 172 295 304 519	73 249d 263 315+C 523-524d 750
Le1310	M	F1a	16012-16569 and 1-909	172 304 519	73 189h 249d 263 315+C 482h 523-524d 750
Le14	M	F1a	16011-16569 and 1-873	129 172 304 519	73 146 249d 263 309+C 315+C 523-524d 750
Le140	M	F1a	16012-16569 and 1-911	129 172 304 311 362 519	73 152 249d 263 309+CC 315+C 521-524d 750
Le957	M	F1a	16007-16569 and 1-908	129 172 304 519	73 249d 263 309+CC 315+C 521-524d 750
Le1533	M	F1a	16013-16569 and 1-910	129 172 304 519	73 249d 263 315+C 523-524d 750
Le1496	M	F1a	16012-16569 and 1-920	86 129 172 189 304 519	73 249d 263 315+C 523-524d 750
Le1353	M	F1a	16012-16569 and 1-902	129 172 304 519	52 53 54C 73 249d 263 309+CC 315+C 318 523-524d 750
Le1051	M	F1a	16021-16569 and 1-909	129 172 304 519	73 152 249d 263 315+C 523-524d 709 750
Le1391	M	F1a	16013-16569 and 1-921	172 189 245 304 519	73 249d 263 309+C 315+C 523-524d 750
Le543	M	F1a	16013-16569 and 1-908	172 274 304 519	73 249d 263 309+C 315+C 523-524d 750
Le1598	M	F1a	16007-16569 and 1-908	171 172 274 304 362 519	73 249d 263 309+CC 315+C 523-524d 750
Le183	F	F1a1	16012-16569 and 1-908	129 162 172 243 304 519	73 151 249d 263 315+C 509 523-524d 750
Le408	F	F1a1	16010-16569 and 1-908	129 162 172 304 399 519	73 152 249d 263 315+C 523-524d 750
Le667	F	F1a1	16009-16569 and 1-902	129 162 172 304 519	64 73 249d 263 309+C 315+C 523-524d 750
Le1422	F	F1a1	16013-16569 and 1-908	129 162 172 304 519	73 249d 263 309+C 315+C 523-524d 750
Le472	F	F1a1	16010-16569 and 1-908	129 162 172 304 497	73 249d 263 315+C 523-524d 750
Le344	M	F1a1	16013-16569 and 1-909	129 162 172 304 362 399 519	73 249d 263 315+C 523-524d 750
Le793	M	F1a1	16007-16569 and 1-921	129 162 172 304 399 519	73 249d 263 315+C 523-524d 750

Le1240	M	F1a1	16009-16569 and 1-905	129 162 172 223 304 399 519	73 249d 263 309+C 315+C 523-524d 750
Le1303	M	F1a1	16011-16569 and 1-898	129 162 172 304 362 399 519	73 152 249d 263 315+C 523-524d 750
Le566	M	F1a1	16017-16569 and 1-908	129 162 172 304 399 519	73 249d 263 315+C 523-524d 750
Le1141	M	F1a1	16009-16569 and 1-908	129 162 172 304 311 519	73 200 249d 263 315+C 523-524d 750
Le984	M	F1a1	16010-16569 and 1-904	129 162 172 304 335 519	73 249d 251 263 315+C 523-524d 750
Le130	M	F1a1	16013-16569 and 1-908	129 162 172 304 399 519	73 200 249d 263 309+C 315+C 523-524d 750
Le1413	M	F1a1	16013-16569 and 1-908	129 162 172 304 399 519	73 249d 263 309+C 315+C 523-524d 750
Le1582	M	F1a1	16007-16569 and 1-909	129 162 172 287 304 399 519	73 249d 263 315+C 523-524d 750
Le849	M	F1a1	16012-16569 and 1-901	129 162 172 304 497 519	73 195 207 249d 263 309+C 315+C 523-524d 750
Le1162	M	F1a1	16013-16569 and 1-909	129 162 172 304 399 519	73 249d 263 315+C 523-524d 750
Le1314	M	F1a1	16012-16569 and 1-872	129 162 172 304 399 519	73 146 249d 263 309+C 315+C 523-524d 750
Le1076	F	F1a1a	16008-16569 and 1-908	108 129 162 172 304 519	73 150 249d 263 309+C 315+C 523-524d 750
Le350	F	F1a1a	16019-16569 and 1-908	108 129 162 172 304 519	73 150 195 249d 263 309+C 315+C 523-524d 750
Le411	F	F1a1a	16012-16569 and 1-909	108 129 162 172 304 519	73 150 249d 263 315+C 523-524d 750
Le1437	F	F1a1a	16009-16569 and 1-921	108 129 162 172 304 519	73 249d 263 309+C 315+C 523-524d 750
Le76	M	F1a1a	16011-16569 and 1-921	108 162 172 304 519	73 150 195 249d 263 309+C 315+C 523-524d 750
Le103	M	F1a1a	16006-16569 and 1-920	108 129 162 172 214 304 519	73 249d 263 315+C 523-524d 750
Le434	M	F1a1a	16010-16569 and 1-909	108 129 162 172 304 519	73 249d 263 309+C 315+C 523-524d 750
Le722	M	F1a1a	16010-16569 and 1-910	108 129 162 172 201 304 311 519	73 150 249d 263 315+C 523-524d 750
Le193	M	F1a1a	16013-16569 and 1-911	108 129 162 172 201 303 304 311 519	73 150 249d 263 315+C 523-524d 750
Le1277	M	F1a1a	16012-16569 and 1-909	108 129 162 172 390 519	73 249d 263 315+C 523-524d 750
Le388	M	F1a1a	16007-16569 and 1-911	108 129 162 172 304 519	73 249d 263 315+C 523-524d 750
Le1593	M	F1a1a	16012-16569 and 1-917	108 129 162 172 304 519	73 150 249d 263 315+C 523-524d 750
Le1471	M	F1a1a	16012-16569 and 1-909	108 129 162 172 304 519	73 195 249d 263 309+C 315+C 523-524d 750
Le1035	M	F1a1a	16012-16569 and 1-918	108 129 162 172 189 304 519	73 189 249d 263 315+C 523-524d 750
Le1223	M	F1a1a	16016-16569 and 1-892	108 129 162 172 304 519	73 150 249d 263 315+C 523-524d 750
Le828	F	F1a1c	16013-16569 and 1-911	162 172 304 519	73 249d 263 309+C 315+C 523-524d 548 750
Le1276	F	F1a1c	16013-16569 and 1-909	129 162 172 304 519	73 249d 263 309+C 315+C 523-524d 548 750
Le1540	M	F1a1c	16006-16569 and 1-909	86 129 162 172 304 519	73 249d 263 315+C 523-524d 548 750
Le1524	M	F1a2	16016-16569 and 1-909	172 304 465 519	73 249d 263 309+C 315+C 521-524d 750
Le211	M	F1a'c	16013-16569 and 1-908	129 189 304 519	73 152 249d 263 309+CC 315+C 750
Le347	M	F1a'c	16010-16569 and 1-908	129 304 362 519	73 152 249d 263 309+C 315+C 523-524d 750
Le1490	M	F1a'c	16012-16569 and 1-920	129 304 362 519	73 152 249d 263 309+CC 315+C 523-524d 750
Le801	M	F1b	16012-16569 and 1-917	183C 189 232A 249 304 311 519	73 249d 263 309+C 315+C 523-524d 750
Le729	M	F1b	16013-16569 and 1-910	134 183C 189 232A 249 304 519	73 152 249d 263 315+C 523-524d 573 750
Le694	M	F1b1a	16009-16569 and 1-910	129 182C 183C 189 232A 249 304 311 344 519	73 152 249d 263 309+CC 315+C 523-524d 750
Le30	F	F1b'd'e	16007-16569 and 1-911	182C 183C 189 249 300 304 519	73 150 195 249d 263 309+C 315+C 523-524d 750
Le239	F	F1b'd'e	16012-16569 and 1-917	183C 189 223 304 519	73 249d 263 309+C 315+C 709 750

Le348	F	F1b'd'e	16009-16569 and 1-913	183C 189 304	73 249d 263 309+C 315+C 750 761
Le401	F	F1b'd'e	16009-16569 and 1-910	153 183C 189 278 300 304 357 519	73 249d 263 309+CC 315+C 523-524d 750
Le1531	F	F1b'd'e	16008-16569 and 1-914	183C 189 304 519	73 249d 263 309+CC 315+C 750
Le899	F	F1b'd'e	16019-16569 and 1-1017	93 183C 189 304 519	73 249d 263 309+C 315+C 523-524d 750
Le441	M	F1b'd'e	16012-16569 and 1-920	153 183C 189 278 300 304 357 519	73 249d 263 309+CC 315+C 523-524d 750
Le129	M	F1b'd'e	16013-16569 and 1-920	93 183C 189 304 519	73 152 249d 263 309+CC 315+C 523-524d 750
Le372	M	F1b'd'e	16018-16569 and 1-909	183C 189 304 519	73 249d 263 309+C 315+C 709 750
Le123	F	F1c	16009-16569 and 1-918	111 129 266 304 519	73 152 249d 263 309+C 315+C 523-524d 750
Le940	F	F1c	16014-16569 and 1-907	111 129 304 519	73 152 249d 263 315+C 523-524d 750
Le721	F	F1c	16021-16569 and 1-873	111 129 266 304 519	73 152 249d 263 309+C 315+C 523-524d 709 750
Le621	F	F1c	16017-16569 and 1-911	51 129 266 304 519	73 152 249d 263 309+C 315+C 523-524d 709 750
Le516	F	F1c	16013-16569 and 1-908	111 129 266 304 519	73 152 249d 263 309+C 315+C 523-524d 709 750
Le126	M	F1c	16013-16569 and 1-914	93 111 192 249 263 298 355 362 390	97 100-105d 207 249d 263 309+CC 315+C 709 750
Le881	F	F1d	16017-16569 and 1-905	189 304 519	73 146 249d 263 309+C 315+C 523-524d 750
Le1467	F	F1d	16010-16569 and 1-920	187 189 207 304 519	73 146 249d 263 291d 309+CC 315+C 750
Le981	M	F1d	16013-16569 and 1-906	189 304 519	73 146 249d 263 309+CC 315+C 523-524d 750
Le331	M	F1d	16012-16569 and 1-913	183C 189 278 304 357 465 519	73 146 151 249d 263 309+C 315+C 523-524d 750
Le1595	M	F1d	16010-16569 and 1-920	92A 189 291 304	73 146 249d 263 309+C 315+C 523-524d 750
Le1408	M	F1d	16013-16569 and 1-909	189 284 304	73 146 195h 249d 263 309+C 315+C 523-524d 750
Le354	F	F2	16007-16569 and 1-906	CRS	73 235 249d 263 315+C 750
Le1420	M	F2a	16017-16569 and 1-921	92Ah 291 304 311h	73 249d 263 309+CC 315+C 523-524d 750
Le1398	M	F2a	16024-16569 and 1-908	291 304	73 249d 263 315+C 750
Le341	F	F2a	16020-16569 and 1-907	92A 189 291 304 519	73 249d 263 309+C 315+C 523-524d 750
Le781	M	F2a	16013-16569 and 1-909	92A 189 291 304	73 249d 263 309+CC 315+C 523-524d 750
Le419	F	F2a	16014-16569 and 1-909	92A 278 291 304	73 249d 263 309+C 315+C 523-524d 750
Le443	F	F2a	16013-16569 and 1-921	92A 291 304	73 199 249d 263 309+C 315+C 523-524d 750
Le964	F	F2a	16032-16569 and 1-1039	92A 291 304	73 249d 263 315+C 523-524d 750 1005
Le640	M	F2a	16012-16569 and 1-909	92A 291 304	73 210 249d 263 309+CC 315+C 523-524d 736 750
Le1172	M	F2a	16012-16569 and 1-909	203 291 304 519	73 195 249d 263 309+CC 315+C 750
Le87	M	F2a	16009-16569 and 1-894	92A 291 304	73 249d 263 309+C 315+C 523-524d 750
Le1008	M	F2a	16058-16569 and 1-906	92A 168 291 304 311	73 249d 263 315+C 523-524d 750
Le184	M	F2a	16008-16569 and 1-910	92A 291 304	73 249d 263 309+C 315+C 523-524d 750
Le438	M	F2a	16013-16569 and 1-909	86 203 274 291 304 519	73 249d 263 315+C 750
Le45	M	F2a	16007-16569 and 1-911	167 203 304 318 519	73 182 249d 263 315+C 750
Le1416	M	F2a	16013-16569 and 1-909	92A 291 304 311	73 249d 263 309+CC 315+C 523-524d 750
Le1384	M	F2a	16007-16569 and 1-909	92A 192 291 304	73 195 249d 263 315+C 523-524d 750
Le810	F	F3a	16006-16569 and 1-911	260 298 355 362	73 207 249d 263 309+CC 315+C 709 750
Le1383	F	F3a	16012-16569 and 1-921	260 298 355 356 362 526	73 207 249d 263 309+C 315+C 709 750

Le786	F	F3a	16017-16569 and 1-908	260 274 298 355 362	73 207 249d 263 309+CC 315+C 709 750	
Le1197	F	F3a	16012-16569 and 1-904	260 298 355 362	73 207 249d 263 309+C 315+C 709 750	
Le904	M	F3a	16012-16569 and 1-897	260 298 311 355 362	73 249d 263 315+C 709 750	
Le1066	M	F3a	16012-16569 and 1-907	260 298 355 362	73 207 249d 263 309+C 315+C 709 750	
Le43	M	F3a	16012-16569 and 1-797	260 298 355 362	73 207 249d 263 315+C 709 750	
Le572	M	F3a	16016-16569 and 1-907	260 298 311 355 362	73 249d 263 309+CC 315+C 709 750	
Le1573	M	F3a	16012-16569 and 1-911	260 298 355 362	73 204 207 249d 263 309+C 315+C 385 709 750	
Le1397	M	F3a	16018-16569 and 1-920	93 111 192 249 263 298 355 362 390	73 207 249d 263 309+CC 315+C 709 750	
Le1577	M	F3a	16008-16569 and 1-910	260 298 355 362	73 207 249d 263 309+C 315+C 709 750	
Le1506	M	F3a	16012-16569 and 1-909	93 260 298 355 362	73 207 249d 263 315+C 709 750	+
Le82	F	F4a	16012-16569 and 1-909	207 304 399	73 146 152 249d 263 281 309+CC 315+C 750	
Le939	F	F4a	16010-16569 and 1-920	126 181 207 274 304 362 399	73 146 200 249d 251 263 309+CC 315+C 317A 750	
Le512	M	F4a	16010-16569 and 1-908	207 304 399	73 146 152 249d 263 281 315+C 538T 750	
Le1239	M	F4a	16014-16569 and 1-910	207 304 399	73 146 152 249d 263 281 309+C 315+C 374 709 750	
Le1267	M	F4a	16012-16569 and 1-909	207 304 399	73 146 152 204 207 249d 263 281 315+C 750 869	
Le1325	F	F4a1	16009-16569 and 1-909	207 304 362 399 497	73 146 152 249d 263 315+C 750	
Le613	M	F4a1	16008-16569 and 1-907	207 304 360 362 399 497	73 146 152 207 249d 263 309+C 315+C 709 750	
Le1442	F	G	16015-16569 and 1-914	223 287 362	73 263 297 309+CC 315+C 489 709 750	+
Le1265	M	G	16008-16569 and 1-917	172 223 362	73 315+C 489 709 750	+
Le1568	M	G	16009-16569 and 1-909	111 129 223 300 362 497 519	73 150 263 309+CC 315+C 489 523-524d 750	+
Le1273	M	G1a1	16012-16569 and 1-909	223 325 362 390 519	73 150 263 309+C 315+C 489 709 750	+
Le1308	M	G1a1	16010-16569 and 1-872	75 223 325 362 519	73 150 263 315+C 489 709 750 827	+
Le15(1)	F	G1c	16012-16569 and 1-906	223 362 519	73 263 309+C 315+C 489 593 709 750	+
Le433	F	G1c	16007-16569 and 1-908	92 223 362 519	73 263 315+C 489 593 709 750	+
Le207	F	G2a	16017-16569 and 1-909	223 227 272 274 278 319 362 519	73 152 198 263 282 309+C 315+C 489 523-524d 709 750	+
Le1194	F	G2a	16011-16569 and 1-921	209 223 227 278 304 362 519	73 263 309+C 315+C 489 709 750	+
Le1323	F	G2a	16010-16569 and 1-910	223 278 362	73 263 315+C 489 507 709 750	+
Le561	F	G2a	16012-16569 and 1-921	189 223 278 362	73 185 263 309+C 315+C 489 709 750	+
Le1155	F	G2a	16011-16569 and 1-921	145 223 233 278 362	73 263 309+CC 315+C 489 709 750	+
Le1477	F	G2a	16013-16569 and 1-873	223 227 278 362	73 152 263 315+C 489 573+5C 709 750	+
Le1575	F	G2a	16012-16569 and 1-911	223 227 278 362	73 146 263 309+C 315+C 489 709 750	+
Le589	M	G2a	16012-16569 and 1-903	129 223 278 362	73 263 315+CC 489 709 750	+
Le829	M	G2a	16012-16569 and 1-921	223 227 278 304 362	73 146 263 309+C 315+C 489 709 750	+
Le788	M	G2a	16016-16569 and 1-908	223 278 362	73 263 309+C 315+C 489 507 709 750	+
Le1340	M	G2a	16011-16569 and 1-910	223 227 278 362 519	73 152 263 315+C 489 523-524d 709 711 750	+
Le1063	M	G2a	16012-16569 and 1-908	172 223 227 272 278 319 362 519	73 152 263 309+C 315+C 489 709 750	+
Le635	M	G2a	16009-16569 and 1-908	93 223 227 278 304 362	73 309+CC 315+C 489 709 750	+
Le1230	M	G2a	16008-16569 and 1-899	172 223 227 272 278 319 362 519	73 152 215 263 309+C 315+C 489 709 750	+

Le608	M	G2a	16023-16569 and 1-1031	169 223 227 278 362 519	73 152 263 315+C 489 523-524d 709 711 750	+
Le1513	M	G2a1c	16027-16569 and 1-911	183C 189 194 195 223 227 278 362 519	73 214 263 315+C 489 709 750	+
Le668	M	G2a1d	16009-16569 and 1-895	192 223 278 362	73 260 263 315+C 489 709 750	+
Le1556	M	G2b	16024-16569 and 1-918	172 223 362	73 315+C 489 709 750	+
Le157	F	G3	16014-16569 and 1-917	223 274 311 362	73 263 309+C 315+C 489 709 750	+
Le490	F	G3a	16017-16569 and 1-908	223 274 357 380 519	73 143 234 263 315+C 489 709 750	+
Le324	F	G3a	16008-16569 and 1-909	129 223 274 311 362	73 84 143 263 315+C 489 709 750	+
Le809	M	G3a	16009-16569 and 1-909	129 223 274 311 362	9 73 143 263 315+C 489 709 750	+
Le1468	M	G3a1	16012-16569 and 1-915	215 223 274	16T 73 143 150 263 315+C 489 709 750	+
Le1176	M	G4	16012-16569 and 1-908	93 114A 189 215 223 362 519	73 191+A 194 204 263 309+C 315+C 489 709 750	+
Le1105	M	H2a2	16008-16569 and 1-918	287 519	263 315+C 750	
Le321	F	H6	16012-16569 and 1-909	129 362	239 263 309+CC 315+C 750	+
Le493	F	M*	16012-16569 and 1-908	95 223 278 295 519	73 199 262 263 315+C 489 523-524d 709 750	
Le1566	F	M*	16014-16569 and 1-908	129 148 232 287 311 327A	64 73 93 189 200 263 309+C 315+C 485 489 750	
Le41	M	M*	16006-16569 and 1-911	183C 189 300 304 311 519	73 150 195 249d 263 309+C 315+C 489 523-524d 750	
Le1401	M	M*	16019-16569 and 1-921	189 223 319	73 236 263 309+C 315+C 489 750	
Le1033	F	M*	16012-16569 and 1-911	68 183C 189 223 292 311 519	73 146 150 152 263 310d 489 523-524d 750	
Le1289	F	M*	16012-16569 and 1-908	223 311 355 362	73 152 263 315+C 489 750	+
Le774	M	M*	16008-16569 and 1-909	126 182C 183C 189 223 278	73 150 189 263 308-309d 315+C 316 438 489 750	
Le518	F	M*	16009-16569 and 1-909	126 223 304 344 362 381 519	73 263 309+C 315+C 489 750	+
Le1385	M	M*	16022-16569 and 1-913	223 304 344 362 381 519	73 263 309+C 315+C 489 750	
Le149	M	M10	16013-16569 and 1-874	129 223 311	73 263 315+C 489 573+4C 709 750	
Le236	M	M10	16007-16569 and 1-881	129 223 311	73 263 309+C 315+C 489 573+4C 709 750	
Le862	M	M10	16010-16569 and 1-875	93 129 223 311	73 263 309+C 315+C 489 573+5C 709 750	
Le573	M	M10	16013-16569 and 1-865	223 256 299 311	73 263 315+C 489 573+5C 709 750	
Le121	M	M10	16012-16569 and 1-862	129 223 311	73 152 215 263 309+C 315+C 489 573+5C 709 750	
Le1535	M	M10	16007-16569 and 1-850	129 223 311	73 152 263 309+C 315+C 489 573+5C 709 750	
Le1503	M	M10	16008-16569 and 1-851	129 223 311	73 263 309+C 315+C 489 573+4C 709 750	
Le398	M	M10a1	16008-16569 and 1-873	93 129 223 311 357 497	73 143 263 315+C 489 523-524d 573+4C 709 750	
Le680	M	M10a1	16013-16569 and 1-873	129 223 293C 311 357 465 497	73 263 309+C 315+C 489 523-524d 573+4C 709 750	
Le660	M	M10a1	16012-16569 and 1-873	129 193 223 311 357 497 519	73 146 152 263 309+C 315+C 489 523-524d 573+4C 709 750	
Le471	M	M10a1	16007-16569 and 1-850	129 193 223 311 357 497	73 146 263 315+C 489 523-524d 573+3C 709 750	
Le1156	M	M10a1	16023-16569 and 1-871	93 129 223 311 357 497	73 146 263 315+C 489 523-524d 573+5C 709 750	
Le133	F	M10a2	16013-16569 and 1-873	66 92 223 311	73 150 263 315+C 489 573+4C 709 750	
Le1102	M	M10a2	16013-16569 and 1-873	66 223 311	73 263 315+C 489 573+4C 709 750	
Le64	F	M11	16011-16569 and 1-921	223	73 198 215 263 309+C 315+C 318 326 489 750	
Le1476	F	M11	16013-16569 and 1-908	129 223 398 488	73 200 215 263 315+C 318 326 489 633 750	
Le776	M	M11	16009-16569 and 1-916	172 223 295 519	73 200 215 263 309+C 315+C 318 326 471 489 750	

Le1069	M	M12a	16007-16569 and 1-906	93 223 290 519	73 125 127 128 150 194 263 315+C 318 489 750	
Le972	F	M12a	16009-16569 and 1-908	86 223 234 290 362	73 125 127 128 263 315+C 318 489 513-514d 750	+
Le1586	F	M12a	16031-16569 and 1-920	223 234 287 290 362	73 125 127 128 263 309+C 315+C 318 489 513-514d 750	
Le1431	F	M12a	16013-16569 and 1-908	172 223 234 290 311	73 125 127 128 150 263 309+C 315+C 489 750	
Le253	M	M12a	16010-16569 and 1-909	223 234 290 362	73 125 127 128 263 295 309+C 315+C 318 489 513-514d 750	+
Le1409	M	M12a	16009-16569 and 1-917	183C 189 223 234 290 362	73 125 127 128 263 309+C 315+C 318 489 513-514d 750	+
Le1434	M	M12a	16015-16569 and 1-921	223 234 290 362	73 125 127 128 263 295 309+C 315+C 318 489 513-514d 750	
Le1193	M	M12a	16012-16569 and 1-908	189 223 234 290 362	73 125 127 128 263 309+C 315+C 318 489 513-514d 750	
Le1517	M	M33c	16016-16569 and 1-909	111 223 235 362 519	73 263 309+C 315+C 489 750	+
Le1106	F	M71	16013-16569 and 1-921	223 269 271 368	73 150 151 263 309+C 315+C 489 750	
Le484	F	M71	16013-16569 and 1-908	223 269 271	73 150 151 263 315+C 489 750	
Le1024	F	M71	16012-16569 and 1-909	223 271	73 151 263 309+C 315+C 489 518 750	
Le116	F	M74	16016-16569 and 1-909	223 274 311 362 381	63 64 66 73 146 263 315+C 489 750	+
Le544	F	M74	16009-16569 and 1-919	223 274 311 362 381	63 64 66 73 263 315+C 489 750	+
Le938	M	M74	16021-16569 and 1-919	223 274 311 362 381	63 64 66 73 263 315+C 489 750	+
Le496	F	M7a	16016-16569 and 1-911	209 223 311 362 519	73 152 263 309+C 315+C 489 750	
Le412	F	M7b	16010-16569 and 1-911	150 223 297 311 327	73 150 199 204 263 309+CC 315+C 489 750	
Le689	F	M7b	16007-16569 and 1-911	223 297	73 150 199 204 263 315+C 489 523-524d 750	
Le968	F	M7b	16011-16569 and 1-908	223 297	73 199 204 263 315+C 489 750	
Le390	F	M7b	16009-16569 and 1-909	223 297	73 199 204 263 309+C 315+C 489 750	
Le122	M	M7b	16023-16569 and 1-911	223 297	73 150 151 199 204 207 263 315+C 489 750	
Le147	M	M7b	16008-16569 and 1-918	223 297	73 150 199 204 263 309+CC 315+C 489 750	
Le131	M	M7b	16023-16569 and 1-911	223 297	73 150 152 199 204 263 309+C 315+C 489 750	
Le346	M	M7b	16013-16569 and 1-911	223 297	73 150 199 204 263 309+C 315+C 489 750	
Le791	M	M7b	16012-16569 and 1-911	223 297	73 150 152 199 204 263 309+C 315+C 489 750	
Le12	M	M7b	16008-16569 and 1-907	223 297 327	73 150 199 204 263 315+C 489 523-524d 750	
Le1210	M	M7b	16007-16569 and 1-911	223 297	73 150 199 204 263 309+C 315+C 489 750	
Le1234	M	M7b	16009-16569 and 1-909	86 223 297	73 150 199 204 263 309+C 315+C 489 750	
Le386	M	M7b	16012-16569 and 1-911	93 223 274 297	73 150 199 204 263 309+C 315+C 489 750	
Le1425	M	M7b	16014-16569 and 1-908	223 297 300	73 150 199 204 249d 263 309+C 315+C 489 750	
Le1621	M	M7b	16009-16569 and 1-914	223 297	73 150 199 204 263 309+CC 315+C 489 750	
Le1402	M	M7b	16013-16569 and 1-909	93 223 297	73 150 199 204 263 271 309+CC 315+C 489 750	
Le1395	M	M7b	16017-16569 and 1-921	223 297	73 150 199 204 263 309+CC 315+C 489 750	
Le517	F	M7b	16012-16569 and 1-908	129 223 297	73 150 199 263 309+C 315+C 489 750	
Le933	F	M7b	16012-16569 and 1-908	129 189 297 319 519	73 150 199 263 309+C 315+C 489 593 750	
Le1459	F	M7b	16017-16569 and 1-918	129 183C 189 223 248 297 300	73 150 199 204 207 263 315+C 489 750	
Le651	F	M7b	16012-16569 and 1-909	129 140 189 223 248 297	73 150 188 199 204 207 263 315+C 489 750	
Le192	M	M7b	16014-16569 and 1-918	38 129 220C 223 297	73 150 199 263 309+C 315+C 489 523-524d 750	

Le313	M	M7b	16009-16569 and 1-909	129 223 269T 297 519	73 150 199 263 309+C 315+C 489 750
Le1438	M	M7b	16017-16569 and 1-914	129 223 297	73 150 199 263 309+CC 315+C 489 750
Le958	M	M7b	16013-16569 and 1-909	129 223 271 297	73 150 199 202 263 309+CC 315+C 489 750
Le925	M	M7b	16014-16569 and 1-901	129 183C 189 223 248 297	73 150 152 199 204 207 263 315+C 489 750
Le1549	M	M7b	16008-16569 and 1-909	129 189 223 297	73 146 150 199 204 263 309+C 315+C 456 489 750
Le305	M	M7b	16012-16569 and 1-908	129 223 297	73 150 152 199 204 263 309+C 315+C 489 750
Le3	F	M7b1	16012-16569 and 1-921	129 192 223 297	73 150 199 263 309+C 315+C 489 750
Le1259	F	M7b1	16013-16569 and 1-892	129 192 223 297	73 150 183 199 263 315+C 466 489 750
Le1448	F	M7b1	16007-16569 and 1-918	129 192 217 223 297	73 150 199 263 309+CC 315+C 489 750
Le672	F	M7b1	16011-16569 and 1-919	129 192 223 297 497	73 150 199 263 309+C 315+C 489 750
Le949	F	M7b1	16012-16569 and 1-908	129 189 192 223 297 519	73 150 199 263 309+C 315+C 489 593 750
Le600	F	M7b1	16012-16569 and 1-907	129 192 223 297	73 150 199 263 309+C 315+C 489 750
Le279	F	M7b1	16014-16569 and 1-909	129 192 223 297 519	73 150 199 263 315+C 489 750
Le834	F	M7b1	16013-16569 and 1-907	192 223 297	73 131 150 199 263 309+CC 315+C 489 750
Le1410	F	M7b1	16024-16569 and 1-913	129 189 192+T 223 297 384	73 150 199 214 263 309+C 315+C 489 750
Le1216	F	M7b1	16012-16569 and 1-921	129 192 223 297	73 143 150 152 263 309+C 315+C 408A 489 750
Le1601	F	M7b1	16015-16569 and 1-911	129 192 223 297 422	73 150 182 199 263 315+C 459d 489 750
Le111	F	M7b1	16008-16569 and 1-917	129 192 223 297	73 150 199 263 315+C 489 524+AC 750
Le257	M	M7b1	16007-16569 and 1-908	129 192 223 297	73 150 263 309+C 315+C 489 523-524d 750
Le263	M	M7b1	16009-16569 and 1-909	114 129 192 223 297 519	73 150 199 263 315+C 489 750
Le287	M	M7b1	16007-16569 and 1-909	129 192 223 297	73 150 199 263 315+C 489 750
Le521	M	M7b1	16009-16569 and 1-874	129 192 223 297	73 150 199 263 309+C 315+C 489 750
Le1087	M	M7b1	16012-16569 and 1-904	129 192 223 297	73 150 199 263 309+CC 315+C 489 709 750
Le1182	M	M7b1	16014-16569 and 1-921	95 129 192 223 297	73 150 199 263 309+C 315+C 489 750
Le885	M	M7b1	16011-16569 and 1-909	129 192 223 297	73 150 199 263 309+C 315+C 489 750
Le38	M	M7b1	16012-16569 and 1-919	129 192 223 297 519	73 150 199 263 309+C 315+C 489 750
Le1183	M	M7b1	16013-16569 and 1-908	129 192 223 297	73 150 199 263 315+C 450 489 750
Le383	M	M7b1	16012-16569 and 1-908	129 192 297	73 150 199 263 309+C 315+C 489 750
Le838	M	M7b1	16015-16569 and 1-915	129 192 223 297	73 150 199 263 309+CC 315+C 489 750
Le1387	M	M7b1	16017-16569 and 1-921	129 192 223 297	73 150 199 263 309+CC 315+C 489 750
Le1152	M	M7b1	16009-16569 and 1-908	129 192 223 297	73 150 199 263 309+C 315+C 489 750
Le1312	M	M7b1	16013-16569 and 1-897	129 192 223 297	73 150 199 263 309+C 315+C 489 750
Le636	M	M7b1	16018-16569 and 1-906	144 189 192 223 297 519	73 150 199 263 315+C 489 593 750
Le709	M	M7b1	16006-16569 and 1-909	129 189 192 223 278 297 519	73 150 199 263 315+C 489 593 750
Le486	F	M7b2	16012-16569 and 1-909	129 189 223 297 298d	73 150 199 263 309+C 315+C 489 750
Le36	M	M7b2	16005-16569 and 1-911	129 189 223 297 298	73 150 199 263 309+CC 315+C 489 750
Le437	F	M7b3	16012-16569 and 1-897	86 129 297 324 497 519	73 199 263 315+C 489 750
Le242	M	M7c	16017-16569 and 1-917	51 223 295 304 390 519	73 199 263 309+C 315+C 489 523-524d 750

Le456	F	M7c	16009-16569 and 1-921	192 223 224 519	73 146 152 195 198 199 263 309+CC 315+C 489 750	+
Le52	F	M7c	16012-16569 and 1-921	223 519	73 146 199 263 315+C 489 523-524d 750	
Le96	F	M7c	16009-16569 and 1-908	223 362 519	73 146 199 263 315+C 489 523-524d 750	
Le1039	M	M7c	16013-16569 and 1-909	93 223 519	73 146 199 204 263 309+C 315+C 489 523-524d 750	
Le1241	M	M7c	16013-16569 and 1-872	75 223 293T 295 519	73 146 152 199 263 309+C 315+C 489 523-524d 750	
Le479	M	M7c	16009-16569 and 1-911	223 295 304 519	73 199 263 309+C 315+C 489 523-524d 750	
Le453	M	M7c	16017-16569 and 1-908	189 223 278 519	73 146 199 263 309+C 315+C 338 489 523-524d 750	
Le1358	M	M7c	16009-16569 and 1-914	223 295 304 311 519	73 199 263 315+C 489 523-524d 750	
Le1392	F	M7c	16013-16569 and 1-913	223 295 519	73 146 199 204 263 315+C 489 523-524d 750	
Le1571	F	M7c	16020-16569 and 1-910	223 295 304 311 519	73 199 263 309+CC 315+C 489 523-524d 750	
Le1445	F	M7c	16015-16569 and 1-921	223 295 519	73 146 199 263 309+C 315+C 489 523-524d 750	
Le1389	M	M7c	16022-16569 and 1-867	223 293T 295	72 73 146 199 263 309+CC 315+C 489 523-524d 750	
Le1541	M	M7c	16016-16569 and 1-910	223 293T 295	72 73 146 199 263 309+CC 315+C 489 523-524d 750	
Le1609	M	M7c	16012-16569 and 1-907	223 295 519 527	73 146 152 199 263 315+C 489 523-524d 750	
Le588	F	M7c	16010-16569 and 1-890	75 223 293T 295 519	73 146 152 263 309+C 315+C 489 523-524d 750	
Le693	F	M7c	16009-16569 and 1-909	75 209 223 293T 295 519	73 146 152 198 199 263 309+CC 315+C 489 523-524d 750	
Le389	F	M7c	16012-16569 and 1-909	75 223 293T 295 519	73 146 152 199 263 309+C 315+C 489 523-524d 750	
Le32	M	M7c	16007-16569 and 1-917	223 295 311 519	73 146 152 199 206A 263 315+C 489 523-524d 750	
Le225	M	M7c	16013-16569 and 1-909	75 223 293T 295 519	73 146 152 199 263 309+CC 315+C 489 523-524d 750	
Le718	M	M7c	16008-16569 and 1-914	93 223 295 297 519	73 146 152 199 263 315+C 489 523-524d 750	
Le725	M	M7c	16013-16569 and 1-921	209 223 295 519	73 146 199 263 309+C 315+C 489 523-524d 750	
Le1245	M	M7c	16013-16569 and 1-893	223 295 362 519	73 146 152 199 263 309+C 315+C 489 523-524d 750	
Le504	M	M7c	16013-16569 and 1-897	294 295 319 519	73 146 199 263 315+C 489 523-524d 750	
Le1122	M	M7c	16009-16569 and 1-908	189 223 278 295 355 519	73 146 199 263 309+C 315+C 489 523-524d 750	
Le908	M	M7c	16007-16569 and 1-920	295 319 519	73 146 199 263 309+C 315+C 489 523-524d 750	
Le883	M	M7c	16014-16569 and 1-908	295 319 519	73 146 199 263 315+C 489 523-524d 750	
Le403	F	M7c3	16012-16569 and 1-909	519	73 146A 199 263 309+C 315+C 489 523-524d 750	
Le1109	F	M7c3	16008-16569 and 1-908	519	73 146A 152 199 263 309+C 315+C 489 523-524d 750	
Le902	M	M7c3	16016-16569 and 1-907	248 519	73 146A 199 204 207 263 309+C 315+C 489 523-524d 750	
Le135	M	M7c3	16008-16569 and 1-909	148 278 519	73 146A 199 263 309+C 315+C 489 523-524d 750	
Le1419	M	M7c3	16013-16569 and 1-907	519	73 146A 199 263 309+C 315+C 489 523-524d 750	
Le432	M	M8a2	16016-16569 and 1-907	184 223 298 319	73 263 315+C 489 750	
Le231	F	M8a2	16010-16569 and 1-909	184 223 291 298 319	73 263 315+C 489 750	
Le685	F	M8a2	16009-16569 and 1-911	184 223 298 311 319	73 263 309+CC 315+C 489 574 750	
Le848	F	M8a2	16013-16569 and 1-901	184 223 293C 298 319 519	73 152 263 309+C 315+C 489 750	
Le1432	F	M8a2	16012-16569 and 1-914	184 223 293C 298 319 519	73 152 263 309+C 315+C 489 750	
Le110	M	M8a2	16011-16569 and 1-919	184 223 298 319	73 263 315+C 489 750	
Le1015	M	M8a2	16012-16569 and 1-908	184 223 298 319	73 152 263 309+C 315+C 489 750	

Le459	M	M8a2	16017-16569 and 1-908	134 184 189 223 298 319	73 195 263 309+C 315+C 489 750	
Le971	M	M8a2	16007-16569 and 1-911	184 223 298 319	73 263 315+C 489 750	
Le1463	M	M8a2	16017-16569 and 1-914	134 184 223 298 319	73 263 309+C 315+C 489 750	
Le1495	M	M8a2	16012-16569 and 1-908	184 223 298 319	73 263 315+C 489 750	
Le1399	M	M8a2	16013-16569 and 1-908	184 223 290 298 319	73 152 263 315+C 489 750	
Le1068	M	M8a2	16009-16569 and 1-909	184 223 293 298 319 519	73 152 263 309+C 315+C 489 750	
Le1587	M	M8a2	16011-16569 and 1-915	184 223 298 311 319	73 263 315+C 489 709 750	
Le1019	M	M8a2	16007-16569 and 1-917	184 223 293C 298 319 519	73 152 263 309+C 315+C 489 750	
Le591	M	M8a2	16013-16569 and 1-1045	184 223 260 298 319	73 152 263 315+C 489 750	
Le415	F	M8a2a	16010-16569 and 1-909	93h 184 189 223 265 298 311 319 390 468 470 471 473	73 146 195 263 309+C 315+C 489 750	
Le150	F	M8a2a	16008-16569 and 1-917	184 189 223 298 319 468 470 471 473	73 152 195 263 309+CC 315+C 489 750	
Le1062	F	M8a2a	16012-16569 and 1-911	184 189 223 278 298 319 470 471 473	73 152 263 315+C 489 750	
Le741	F	M8a2a	16018-16569 and 1-909	184 189 223 298 319 470 471 473	73 263 315+C 489 750	
Le164	M	M8a2a	16007-16569 and 1-914	177 184 189 223 298 311 319 390 468 470 471 473	73 263 309+C 315+C 489 750	
Le9	M	M8a2a	16009-16569 and 1-910	124 184 189 223 298 311 319 390 443 468 470 471 473	73 263 309+C 315+C 489 750	
Le148	M	M8a2a	16013-16569 and 1-915	184 189 223 298 311 319 390 468 470 471 473	73 263 309+C 315+C 489 750	
Le748	M	M8a2a	16009-16569 and 1-908	184 189 223 298 319 468 470 471 473	73 152 189 263 315+C 489 750	
Le1371	M	M8a2a	16017-16569 and 1-913	184 185 186 189 223 298 319 470 471 473 476T	73 263 309+C 315+C 489 750	
Le1279	M	M8a2a	16013-16569 and 1-909	184 189 223 298 319 470 471 473	73 152 263 315+C 489 750	
Le919	M	M8a2a	16013-16569 and 1-921	184 189 223 298 319 470 471 473	73 195 263 309+C 315+C 489 750 827	
Le259	F	M9a	16012-16569 and 1-911	158 223 234 362 519	73 150 152 153 263 315+C 489 750	
Le513	F	M9a	16017-16569 and 1-911	223 234 291 316 362	73 153 263 309+C 315+C 489 750	
Le270	M	M9a	16012-16569 and 1-908	93 160 223 234 316 357	73 263 315+C 459+C 489 750	
Le391	M	M9a	16007-16569 and 1-897	93 160 223 234 316 357	73 263 315+C 489 750	
Le683	M	M9a	16018-16569 and 1-874	223 234 316 362	73 153 199 263 315+C 455+T 460 463+6C 489 750	
Le882	M	M9a	16013-16569 and 1-906	223 234 291 316 362	73 153 263 309+C 315+C 489 750	
Le946	M	M9a	16012-16569 and 1-909	51 223 234 362	73 153 195 263 309+C 315+C 489 750	
Le1034	M	M9a	16007-16569 and 1-918	145 154 223 234 316	73 153 263 315+C 489 523-524d 750	
Le626	F	M9a	16023-16569 and 1-908	93 160 223 234 316 357	73 263 315+C 489 750	
Le1411	M	M9a	16010-16569 and 1-909	169 223 234 316 362	73 263 309+CC 315+C 489 750	+
Le1084	M	M9a	16014-16569 and 1-906	223 234 249 291 316 356 362	73 153 260 263 272 309+C 315+C 489 702h 750	
Le582	M	M9b	16012-16569 and 1-873	51 209 223 294 362 519	73 153 263 315+C 489 573+4C 750	
Le470	M	N10	16012-16569 and 1-906	69 172 223 278 291A 362	73 150 152 199 263 315+C 709	
Le713	M	N10	16004-16569 and 1-919	69 172 223 278 291A 298 362	73 150 152 199 263 315+C 709	
Le628	F	N9a	16013-16569 and 1-873	184 223 257A 261	73 150 263 315+C 573+5C 709 750	
Le641	F	N9a	16012-16569 and 1-908	223 257A 261 311	73 150 263 309+CC 315+C 573+C 750	
Le929	F	N9a	16012-16569 and 1-908	223 257A 261	73 150 263 309+CC 315+C 750	
Le1137	F	N9a	16012-16569 and 1-906	183C 189 223 257A 261	73 150 263 315+C 574 750	

Le1089	F	N9a	16012-16569 and 1-906	223 257A 261	73 150 263 315+C 750
Le351	M	N9a	16012-16569 and 1-909	223 257A 261 311	73 150 263 309+C 315+C 573+C 709 750
Le168	M	N9a	16012-16569 and 1-911	157 189 223 257A 261	73 150 204 263 315+C 750
Le843	M	N9a	16012-16569 and 1-906	223 257A 261 311	73 150 263 309+C 315+C 750
Le897	M	N9a	16012-16569 and 1-902	223 257A 261 311	73 150 263 309+C 315+C 750
Le837	M	N9a	16013-16569 and 1-909	183C 189 223 257A 261 311	73 143 150 263 309+CC 315+C 750
Le842	M	N9a	16012-16569 and 1-909	223 257A 261 311	73 150 263 309+C 315+C 750
Le1248	M	N9a	16015-16569 and 1-907	129 223 257A 261	73 150 263 309+C 315+C 750
Le1112	M	N9a	16013-16569 and 1-909	111 182C 183C 189 223 257A 261	73 150 263 315+C 750
Le1516	M	N9a	16007-16569 and 1-909	223 257A 261 311 390	73 150 195 263 309+C 315+C 750
Le1538	M	N9a	16013-16569 and 1-908	93 223 257A 519	73 150 152 263 309+C 315+C 750
Le1147	M	N9a	16010-16569 and 1-907	223 257A 261 362 519	73 150 263 309+C 315+C 750
Le1377	M	N9a	16012-16569 and 1-913	173 223 257A 324	73 150 183 263 309+C 315+C 524+AC 750
Le1613	M	N9a	16038-16569 and 1-911	162 223 257A 261 264 362	73 150 151 263 309+C 315+C 750
Le1173	M	N9a	16013-16569 and 1-1075	189 223 257A 355	73 150 204 207 263 309+C 315+C 750
Le1254	M	N9a	16012-16569 and 1-919	223 257A 261 311	73 150 263 309+CC 315+C 750
Le281	F	N9a	16008-16569 and 1-908	129 223 257A 261 304	73 150 263 309+CC 315+C 750
Le1178	F	N9a	16012-16569 and 1-908	129 223 257A 261	73 150 263 309+C 315+C 750
Le909	M	N9a	16007-16569 and 1-909	129 223 248 257A 261	73 150 263 315+C 750
Le1386	M	N9a	16012-16569 and 1-919	129 223 257A 261 311 519	73 150 263 309+CC 315+C 750
Le1508	M	N9a	16016-16569 and 1-921	93 129 223 257A 260 261	73 150 263 309+C 315+C 373 750
Le1316	M	N9a	16012-16569 and 1-911	172 223 257A 261	73 150 263 309+C 315+C 750
Le208	M	N9a	16016-16569 and 1-909	172 223 257A 261	73 150 263 309+CC 315+C 750
Le923	F	N9a1	16008-16569 and 1-908	111 129 189 223 257A 261 265T 274 519	73 150 263 309+C 315+C 750
Le751	M	N9a1	16013-16569 and 1-914	111 129 223 257A 261	73 150 195 263 309+CC 315+C 750
Le1086	M	N9a1	16013-16569 and 1-908	111 129 223 257A 261	73 146h 150 263 309+C 315+C 750
Le1552	M	N9a1	16012-16569 and 1-918	108 111 129 223 257A 261	73 150 263 315+C 523-524d 750
Le1275	M	N9a4	16012-16569 and 1-898	145 172 223 245 257A 261	73 150 263 309+CC 315+C 524+2AC 750
Le1000	F	N9a6a	16010-16569 and 1-904	223 257A 261 292 294 362 519	73 150 263 309+C 315+C 750
Le1161	F	R*	16012-16569 and 1-911	231 519	73 146 263 309+C 315+C 750
Le634	F	R*	16007-16569 and 1-914	93 231 519	73 146 263 309+CC 315+C 750
Le574	F	R11	16010-16569 and 1-908	182C 183C 189 311 390 399 519	73 185 189 215 263 309+CC 315+C 524+AC 709 750
Le1252	F	R11	16010-16569 and 1-886	140 183C 189 304 311 365 519	73 185 189 263 309+CC 315+C 533 709 750
Le1472	F	R11	16013-16569 and 1-910	182C 183C 189 266 311 519	73 185 189 207 263 315+C 523-524d 709 750
Le120	M	R11	16012-16569 and 1-909	182C 183C 189 311 390 399 519	73 185 189 263 315+C 709 750
Le368	M	R11	16005-16569 and 1-910	92 145 182C 183C 189 311 390 519	73 185 189 263 309+C 315+C 709 750
Le15(2)	F	R9	16008-16569 and 1-921	93 157 304	73 151 263 309+C 315+C 479 750
Le1260	F	R9	16013-16569 and 1-909	93 157 304 399	73 143 146 151 263 309+CC 315+C 479 750

Le677	F	R9	16008-16569 and 1-909	157 304 324	73 263 309+C 315+C 479 750
Le312	M	R9	16016-16569 and 1-909	304 362 519	73 263 309+C 315+C 750
Le720	M	R9	16016-16569 and 1-902	93 157 304	73 151 263 309+C 315+C 479 634 750
Le1579	M	R9	16012-16569 and 1-914	157 304	73 151 263 309+C 315+C 479 750
Le1470	M	R9	16014-16569 and 1-920	304 362 519	73 263 309+CC 315+C 750
Le1243	M	R9	16012-16569 and 1-909	157 304	73 151 263 315+C 750
Le1542	M	R9	16013-16569 and 1-909	157 304 324	73 151 195 263 309+C 315+C 479 750
Le63	F	R9b	16008-16569 and 1-919	93 172 192 304 309 390 519	73 152 263 309+C 315+C 750
Le760	F	R9b	16009-16569 and 1-898	304 309 390 519	73 183 263 315+C 523-524d 750
Le654	F	R9b	16012-16569 and 1-921	192 304 309 390 519	73 152 263 309+C 315+C 523-524d 750
Le503	F	R9b	16012-16569 and 1-921	209 304 309 390	73 263 309+C 315+C 523-524d 750
Le469	M	R9b	16013-16569 and 1-906	304 309 390 519	73 183 263 315+C 523-524d 750
Le523	M	R9b	16009-16569 and 1-906	192 304 309 390 519	73 152 263 309+CC 315+C 523-524d 750
Le808	M	R9b	16010-16569 and 1-909	192 209 304 309 390 519	73 151 152 263 309+C 315+C 523-524d 750
Le299	M	R9b	16012-16569 and 1-914	148 304 390	73 263 309+C 315+C 709 750
Le44	M	R9b	16009-16569 and 1-907	189 304 309 390 519	73 152 263 309+C 315+C 523-524d 750
Le1189	M	R9b	16017-16569 and 1-908	145 192 243 304 309 390 519	73 183 263 309+CC 315+C 523-524d 750
Le1436	M	R9b	16023-16569 and 1-921	91 124 148 304 309 390 519	73 263 309+C 315+C 524+AC 750
Le1574	M	R9b	16014-16569 and 1-910	124 148 304 309 355 390 519	73 263 309+C 315+C 750
Le1100	M	U2e1	16017-16569 and 1-921	51 129C 154 248 362 391 519	73 152 217 263 315+C 340 508 750
Le284	M	Y1	16008-16569 and 1-921	126 231 266 278 519	73 146 207 263 309+CC 315+C 750
Le1479	M	Y1	16012-16569 and 1-906	126 172 231 266 399 519	73 143 146 263 266 309+C 315+C 750
Le1242	M	Y1	16012-16569 and 1-921	126 192 231 266 287 519	73 146 151 207 263 309+C 315+C 750
Le1055	M	Y1	16013-16569 and 1-908	126 176 231 266 399 519	73 146 263 309+C 315+C 750
Le195	M	Y1	16013-16569 and 1-911	126 231 266 362 519	73 146 150 263 309+C 315+C 750
Le448	M	Y2	16014-16569 and 1-908	126 231 311	73 263 315+C 482 523-524d 644 750
Le241	M	Y2	16012-16569 and 1-916	126 231 311	73 152 199 263 309+C 315+C 482 523-524d 750
Le57	F	Z	16006-16569 and 1-921	129 185 223 260 298	73 151 152 249d 263 309+C 315+C 489 750
Le739	F	Z	16013-16569 and 1-916	108 185 223 260 298	73 152 249d 263 309+C 315+C 489 750
Le102	M	Z	16013-16569 and 1-909	185 223 260 298 311 519	73 152 249d 263 309+C 315+C 489 709 750
Le817	M	Z	16012-16569 and 1-909	185 223 260 294 298	73 249d 263 315+C 489 750
Le1569	M	Z	16016-16569 and 1-911	185 223 260 298	73 152 214 249d 263 315+C 489 709 750
Le98	M	Z	16007-16569 and 1-910	185 223 260 298 311 519	73 152 249d 263 309+C 315+C 489 709 750
Le213	M	Z	16020-16569 and 1-916	136 185 223 260 274 298	73 152 249d 263 309+CC 315+C 489 750
Le252	M	Z	16010-16569 and 1-909	185 223 260 298	73 152 214 249d 263 315+C 417 489 709 750
Le254	M	Z	16012-16569 and 1-909	185 223 260 298	73 152 249d 263 309+CC 315+C 489 750
Le551	M	Z	16016-16569 and 1-905	185 223 260 298 519	73 152 249d 263 309+C 315+C 489 709 750
Le404	M	Z	16012-16569 and 1-916	185 223 260 298	73 152 214 249d 263 309+CC 315+C 489 709 750

Le536	M	Z	16007-16569 and 1-909	185 223 260 298 302	73 151 152 249d 263 309+C 315+C 489 750
Le69	M	Z	16017-16569 and 1-874	185 223 260 298	73 152 214 249d 263 315+C 489 709 750
Le945	M	Z	16009-16569 and 1-908	51 185 223 260 298	73 249d 263 315+C 489 750
Le476	M	Z	16013-16569 and 1-908	185 223 260 298 302	73 151 152 249d 263 309+C 315+C 489 750
Le1078	M	Z	16012-16569 and 1-907	136 223 260 298	73 146 152 183 249d 263 315+C 489 750
Le1198	M	Z	16012-16569 and 1-906	136 210 223 260 298 527	73 152 249d 263 309+C 315+C 489 750
Le511	M	Z	16013-16569 and 1-911	185 223 260 298	73 152 249d 263 309+C 315+C 489 723 750
Le1469	M	Z	16014-16569 and 1-908	185 223 260 298 519	73 152 249d 263 309+C 315+C 489 709 750
Le1056	M	Z	16014-16569 and 1-908	185 223 260 298 302	73 151 152 249d 263 315+C 489 750
Le1509	M	Z	16009-16569 and 1-908	185 223 260 298 302 362	73 151 152 249d 263 309+C 315+C 489 750

Note – Sequence variation was scored relative to the revised Cambridge reference sequence (rCRS) [1]. Suffixes A, G, C and T indicate transversions, "h" indicates heteroplasmy, "d" and "+" indicate deletions and insertions, respectively. Indels (insertion and deletion) are recorded at the last possible site. "+" and "－" denote the absence and presence of the restriction site, respectively. "M" and "F" indicate male and female, respectively.

Supplementary Reference

1. Andrews RM, Kubacka I, Chinnery PF, Lightowlers RN, Turnbull DM, Howell N (1999) Reanalysis and revision of the Cambridge reference sequence for human mitochondrial DNA. Nat Genet 23:147

Table S4. Haplogroup frequencies and Pearson's chi-square test in 479 LHON patients with m.11778G>A and 843 patients with suspected LHON

Haplogroup	LHON	Suspected LHON	P-value [a]	Adjusted P-value [b]	OR	95% CI
A	16	31	0.870	1.000	0.905	0.490-1.673
B4	62	126	0.357	1.000	0.846	0.610-1.173
B5	30	54	1.000	1.000	0.976	0.616-1.548
C	21	35	0.953	1.000	1.059	0.609-1.840
D4	98	115	0.002	0.031	1.628	1.210-2.190
D5	27	32	0.156	0.956	1.514	0.896-2.559
R9 [c]	7	164	3.276×10^{-26}	$<10^{-5}$	0.082	0.011-0.611
F	6	143	9.133×10^{-23}	$<10^{-5}$	0.062	0.027-0.142
F1	4	99	1.111×10^{-15}	$<10^{-5}$	0.064	0.023-0.175
F1a	2	71	3.096×10^{-13}	$<10^{-5}$	0.074	0.027-0.203
F2	1	17	0.006	0.092	0.102	0.013-0.766
F3	1	12	0.031	0.418	0.145	0.019-0.118
F3a	1	12	0.031	0.418	0.145	0.019-1.118
F4	0	7	0.046	0.553	0.636	0.610-0.662
G	26	31	0.172	0.962	1.503	0.882-2.564
M10	20	14	0.009	0.136	2.580	1.291-5.157
M12	2	8	0.344	1.000	0.438	0.093-2.069
M7b	57	59	0.003	0.047	1.795	1.224-2.632
M7c	27	32	0.156	0.946	1.514	0.896-2.559
M8a	20	27	0.359	0.999	1.317	0.730-2.374
M9a	10	11	0.387	1.000	1.613	0.680-3.826
N9a	15	33	0.563	1.000	0.793	0.426-1.476
R11	2	5	1.000	1.000	0.703	0.136-3.636
Y	11	7	0.050	0.590	2.807	1.081-7.290
Z	10	21	0.641	1.000	0.835	0.390-1.787

[a] Two tailed Fisher exact test was applied instead a Pearson chi-square test in cases containing cell counts below five

[b] Adjusted P-value: adjustment of P-values was carried out with a permutation-based approach; number of permutations = 100,000; OR (95% CI): Odds Ratio (95% Confidence Interval)

[c] Note that haplogroup F is a sub-haplogroup of haplogroup R9 and the number of F mtDNAs are also included here

Table S5. Haplogroup frequencies and Pearson's chi-square test in 479 LHON patients with m.11778G>A and 1,689 Han Chinese from the general populations

Haplogroup	LHON	Pooled Han Chinese [a]	P-value [b]	Adjusted P-value [c]	OR	95% CI
A	16	92	0.080	0.772	0.600	0.349-1.030
B4	62	196	0.472	1.000	1.133	0.834-1.537
B5	30	94	0.639	1.000	1.134	0.742-1.733
C	21	51	0.185	0.972	1.473	0.877-2.474
D4	98	252	0.005	0.085	1.467	1.132-1.901
D5	27	88	0.801	1.000	1.087	0.697-1.694
R9 [d]	7	305	5.807×10^{-27}	$<10^{-5}$	0.067	0.032-0.143
F	6	274	1.999×10^{-24}	$<10^{-5}$	0.066	0.029-0.148
F1	4	193	1.118×10^{-14}	$<10^{-5}$	0.075	0.028-0.204
F1a	2	132	1.318×10^{-12}	$<10^{-5}$	0.086	0.032-0.234
F2	1	48	0.001	0.018	0.072	0.010-0.519
F3	1	15	0.125	0.908	0.234	0.031-1.772
F3a	1	13	0.178	0.969	0.270	0.035-2.067
F4	0	8	0.131	0.921	0.778	0.761-0.796
G	26	71	0.308	1.000	1.308	0.825-2.074
M10	20	35	0.016	0.246	2.059	1.177-3.601
M12	2	4	0.619	1.000	1.766	0.323-9.672
M7b	57	119	0.001	0.018	1.782	1.277-2.487
M7c	27	54	0.019	0.273	1.809	1.126-2.904
M8a	20	63	0.654	1.000	1.125	0.673-1.880
M9a	10	29	0.731	1.000	1.220	0.591-2.523
N9a	15	62	0.672	1.000	0.848	0.478-1.505
R11	2	10	1.000	1.000	0.704	0.154-3.224
Y	11	16	0.034	0.453	2.458	1.133-5.332
Z	10	50	0.304	0.995	0.700	0.352-1.389

[a] Pooled Han Chinese were from reported populations (see supplementary Table 1 for more information).

[b] Two tailed Fisher exact test was applied instead a Pearson chi-square test in cases containing cell counts below five

[c] Adjusted P-value: adjustment of P-values was carried out with a permutation-based approach; number of permutations = 100,000; OR (95% CI): Odds Ratio (95% Confidence Interval)

[d] Note that haplogroup F is a sub-haplogroup of haplogroup R9 and the number of F mtDNAs are also included here

Table S6. Haplogroup frequencies and Pearson's chi-square test in 175 LHON patients with m.11778G>A and 843 patients with suspected LHON

Haplogroup	LHON [a]	Suspected LHON	P-value [b]	Adjusted P-value [c]	OR	95% CI
A	10	31	0.212	0.992	1.587	0.763-3.301
B4	19	126	0.159	0.845	0.693	0.415-1.157
B5	9	54	0.528	0.100	0.792	0.384-1.636
C	7	35	0.927	0.100	0.962	0.420-2.202
D4	40	115	0.002	0.016	1.876	1.252-2.809
D5	14	32	0.015	0.053	2.204	1.150-4.223
R9 [d]	3	164	1.678×10^{-11}	$<10^{-5}$	0.072	0.023-0.229
F	3	143	1.838×10^{-9}	$<10^{-5}$	0.085	0.027-0.271
F1	2	99	1.064×10^{-6}	$<10^{-5}$	0.087	0.021-0.357
F1a	1	71	2.731×10^{-5}	$<10^{-5}$	0.062	0.009-0.453
F2	1	17	0.339	0.981	0.279	0.037-2.112
F3	0	12	0.238	0.904	0.826	0.803-0.850
F3a	0	12	0.238	0.904	0.826	0.803-0.850
F4	0	7	0.611	0.100	0.827	0.804-0.851
G	12	31	0.057	0.699	1.928	0.970-3.834
M10	7	14	0.048	0.263	2.467	0.981-6.206
M12	2	8	0.685	0.100	1.207	0.254-5.732
M7b	15	59	0.466	1.000	1.246	0.689-2.251
M7c	12	32	0.070	0.762	1.866	0.941-3.699
M8a	9	27	0.206	0.990	1.639	0.757-3.548
M9a	1	11	0.703	0.100	0.435	0.056-3.389
N9a	3	33	0.181	0.952	0.428	0.130-1.412
R11	2	5	0.345	0.999	1.938	0.373-10.069
Y	6	7	0.005	0.092	4.240	1.407-12.775
Z	2	21	0.404	1.000	0.453	0.105-1.948

[a] The LHON patients were from our previous study [1]. Note that Le251 was wrongly classified in that study and was corrected as haplogroup Z in the current analysis.

[b] Two tailed Fisher exact test was applied instead a Pearson chi-square test in cases containing cell counts below five

[c] Adjusted P-value: adjustment of P-values was carried out with a permutation-based approach; number of permutations = 100,000; OR (95% CI): Odds Ratio (95% Confidence Interval)

[d] Note that haplogroup F is a sub-haplogroup of haplogroup R9 and the number of F mtDNAs are also included here

Supplementary reference

1. Ji Y, Zhang A-M, Jia X, Zhang Y-P, Xiao X, et al. (2008) Mitochondrial DNA haplogroups M7b1'2 and M8a affect clinical expression of leber hereditary optic neuropathy in Chinese families with the m.11778G>A mutation. Am J Hum Genet 83:760-768

Table S7. Haplogroup frequencies and Pearson's chi-square test in 175 LHON patients with m.11778G>A and 1,689 Han Chinese from general populations

Haplogroup	LHON [a]	Pooled Han Chinese [b]	P-value [c]	Adjusted P-value [d]	OR	95% CI
A	10	92	0.882	1.000	1.052	0.537-2.060
B4	19	196	0.768	1.000	0.928	0.563-1.528
B5	9	94	0.816	1.000	0.920	0.456-1.857
C	7	51	0.477	1.000	1.338	0.598-2.996
D4	40	252	0.006	0.043	1.690	1.158-2.464
D5	14	88	0.122	0.470	1.582	0.880-2.845
R9 [e]	3	304	6.462×10^{-11}	$<10^{-5}$	0.079	0.025-0.251
F	3	274	1.993×10^{-9}	$<10^{-5}$	0.090	0.029-0.284
F1	2	193	7.694×10^{-7}	$<10^{-5}$	0.090	0.022-0.364
F1a	1	132	3.642×10^{-5}	$<10^{-5}$	0.068	0.009-0.488
F2	1	48	0.081	0.708	0.196	0.027-1.432
F3	0	15	0.387	0.999	0.905	0.892-0.919
F3a	0	13	0.625	1.000	0.905	0.892-0.919
F4	0	8	1.000	1.000	0.906	0.893-0.919
G	12	71	0.105	0.890	1.678	0.891-3.158
M10	7	35	0.102	0.485	1.969	0.861-4.502
M12	2	4	0.102	0.808	4.870	0.886-26.781
M7b	15	119	0.457	1.000	1.237	0.706-2.168
M7c	12	54	0.013	0.219	2.229	1.168-4.252
M8a	9	63	0.356	1.000	1.399	0.684-2.865
M9a	1	29	0.355	0.998	0.329	0.045-2.430
N9a	3	62	0.275	0.965	0.458	0.142-1.474
R11	2	10	0.313	0.997	1.941	0.422-8.931
Y	6	16	0.004	0.059	3.712	1.434-9.613
Z	2	50	0.227	0.979	0.379	0.091-1.571

[a] The LHON patients were from our previous study [1]. Note that Le251 was wrongly classified in that study and was corrected as haplogroup Z in the current analysis.

[b] Pooled Han Chinese were from reported populations (see supplementary Table 1 for more information)

[c] Two tailed Fisher exact test was applied instead a Pearson chi-square test in cases containing cell counts below five

[d] Adjusted P-value: adjustment of P-values was carried out with a permutation-based approach; number of permutations = 100,000; OR (95% CI): Odds Ratio (95% Confidence Interval)

[e] Note that haplogroup F is a sub-haplogroup of haplogroup R9 and the number of F mtDNAs are also included here

Supplementary reference

1. Ji Y, Zhang A-M, Jia X, Zhang Y-P, Xiao X, et al. (2008) Mitochondrial DNA haplogroups M7b1'2 and M8a affect clinical expression of leber hereditary optic neuropathy in Chinese families with the m.11778G>A mutation. Am J Hum Genet 83:760-768

Table S8. Comparison of the non-synonymous (NS) and synonymous (S) substitutions at the terminal branch level in the phylogenetic tree between 12 LHON patients belonging to haplogroup M7b1'2 and 69 reported Chinese complete mtDNAs from the general populations

Gene	General population (n=69)[a]		LHON patients (n=12)		P [d]
	NS [b]	S [c]	NS [b]	S [c]	
MT-ND1	8	11	0	1	1.000
MT-ND2	4	6	0	4	0.251
MT-CO1	7	7	4	4	1.000
MT-CO2	2	5	0	2	1.000
MT-ATP8	1	4	0	0	-
MT-ATP6	11	2	1	0	1.000
MT-CO3	6	3	0	3	0.182
MT-ND3	1	1	3	2	1.000
MT-ND4L	0	6	0	0	-
MT-ND4	1	14	0	5	1.000
MT-ND5	7	19	2	0	0.095
MT-ND6	0	8	0	0	-
MT-CYB	5	9	1	1	1.000
Total	53	95	11	22	0.843

[a] Data from our previous study [c.f. Ref 1 and references therein].

[b] NS refers to the number of non-synonymous substitutions.

[c] S refers to the number of synonymous substitutions.

[d] P values were determined by the Fisher's exact test.

Supplementary reference

1. Zou Y, Jia X, Zhang A-M, Wang W-Z, Li S, et al. (2010) The MT-ND1 and MT-ND5 genes are mutational hotspots for Chinese families with clinical features of LHON but lacking the three primary mutations. Biochem Biophys Res Commun 399: 179-185