

An experimental computer-generated Y-chromosomal phylogeny, leveraging public Geno 2.0 results and the current ISOGG tree

Chris Morley*

17th July 2013†

Abstract

The author of this report has created software to (i) facilitate the analysis of new Geno 2.0 data, and (ii) automate the preparation of a comprehensive draft Y-chromosomal phylogenetic tree incorporating publicly available Geno 2.0 Y-SNP data. The second item is presented in Part 2.

Author's note

Thank you for your interest in this project!

This report was first made public on 16 July 2013. Since then it has gone very mildly viral. I'd like to temper some of the excitement directed toward this initial version of my experimental Y-tree. Please do not discount the "experimental" nature of this tree. Some subclades proposed by my algorithm are known to be erroneous.

Stated another way, nobody should go out and get their linens embroidered with "M26→L707→YSC0000078" just because of what my experimental tree or predictor said.

The feedback I have received has been positive, encouraging and helpful. I will be the first to admit that further validation of this tree is needed. The computer-generated tree is too vast for one person to validate manually, so I will be working on a separate set of tools that will identify – as a last step in the tree-generation process – a (hopefully) short list of inconsistencies in the experimental tree. Each inconsistency will need to be manually investigated in order to determine its cause. One way or another, I think I will be able to improve my algorithm so that the number of inconsistencies is reduced. Those wishing to devote extensive time to manually validating my tree should probably wait until the next release.

These is another class of inconsistencies – a class containing inconsistencies only detectable by haplogroup specialists. The size of this class remains to be seen.

So yes, I have some ideas on how to further refine this process and address some of the outstanding issues. But I will not be able to immediately act on my ideas and release an updated tree. And I have no doubt that further flaws in this tree will surface.

All in all, please regard this experimental phylogeny as informative rather than authoritative. As I wrote in my announcement, it's not perfect, but it's a start.

ISOGG volunteers and Y-DNA project administrators: if you are asked to explain differences between this tree and the ISOGG one, you can save yourselves some time by directing people to read [this FAQ item](#).

An earlier version of this document is dated 16 July 2013. The differences between that version and this version are minor. The tree is exactly the same in both versions.

Chris Morley

1. The need for automation

1.1 Background

Genographic Project 2.0

The second phase of the Genographic Project [1] was announced in July 2012 [2, 3]. One facet of this project is wide-spectrum Y-SNP testing offered at an accessible price. The aggregation of these results will reinforce much of the existing Y-SNP phylogeny, while concurrently leading to the discovery of new branches and the slight repositioning of some existing branches.

*Morley Y-DNA Project Administrator; lead researcher, "Northwest England" cluster of R1a-L448. Contact: <http://www.MorleyDNA.com/contact>.

†An earlier version of this report, shaped as a proposal, was released for limited distribution on 5 July 2013.

The initial round of test results was released in December 2012 [4]. The Genographic Consortium is apparently preparing an updated Y-SNP phylogeny, but to the chagrin of genetic genealogy hobbyists it has not yet been released [5].

Manual analysis of this dataset is time-consuming. The vastness of the data is only one factor; there are several additional challenges to overcome before the data can be compared:

- the dataset is growing every day;
- the phylogenetic nomenclature is in perpetual flux;
- the publicly available Geno 2.0 Y-SNP data is decentralised;
- many Y-SNPs go by several names.

Even then, after monitoring the above, there are many more challenges at the comparison stage:

- the main source for publicly available Geno 2.0 data (various Family Tree DNA haplogroup project Y-SNP reports, for example, [6]) does not distinguish between negative calls and no-calls;
- some chip-tested SNPs are proving to be globally erratic [7];
- other chip-tested SNPs may be locally erratic (inconsistent results for an SNP may indicate an inadequate choice of primer, or the presence of additional nearby mutation(s) in one or more derived branches);
- some kits have had additional à la carte testing performed for SNPs not offered on the Geno 2.0 chip;
- a few SNPs have in some branches reverted to the ancestral state, potentially resulting in a false-negative call;
- some SNPs are recurrent, and it can be challenging to separate the multiple instances;
- it is not straightforward to determine where newly-discovered SNPs fit in relation to existing SNPs;
- existing phylogenies, against which comparisons are made, may place some SNPs erroneously, complicating the comparison procedure.

The members of the genetic genealogy community – the majority of them part-time volunteers – would therefore benefit greatly from the introduction of a robust tool to automate, standardise and centralise much of this analysis.

Depending on the cause of the “official” Geno 2.0-based phylogenetic tree’s publication delay, the Genographic Consortium may also benefit from the availability of such automation.

In light of the above challenges, this task is more complicated than it would initially appear. This report showcases the results from an initial attempt to tackle this problem.

Full-Y sequencing

Full Y-chromosomal sequencing will see growth over the next few years, soon supplanting chip-based wide-spectrum SNP testing as the test of choice for those seeking to extend the Y-chromosomal phylogenetic tree and determine their own position thereon. This technology will circumvent some of the chip-specific issues, but the corresponding increase in data will accelerate demand for automated analytical tools.

1.2 Prior Technology

Generally, the genetic genealogy volunteer community is quicker than the academic community to act on new phylogenetic discoveries. ISOGG’s Y-tree [8] can therefore be regarded as the most current phylogenetic authority. But as data volume increases, ISOGG’s volunteers will likely need help in order to keep pace with all the new developments. Many of these volunteers maintain separate, decentralised provisional trees for their own branches/haplogroups of interest. The level of detail varies between haplogroups.

The YCC phylogeny has not been updated since 2008 [9]. The Genographic Consortium’s awaited phylogeny is supposed to supersede this.

Thomas Krahn of Family Tree DNA maintains a draft Y tree [10]. It leads the ISOGG tree in some aspects, and lags behind in others. This too could probably benefit from increased automation.

FTDNA forum user Felix has just released *My Y-SNP Tree*, a free tool for comparing Y-SNPs against Thomas Krahn’s draft Y tree [11].

Ethio Helix has roughly classified some of the higher-level novel Geno 2.0 SNPs, using a non-fuzzy set theoretic approach [12].

Public raw Geno 2.0 data is scarce. Itaï Perez is analysing the Y-SNP facet of this raw Geno 2.0 data [13]. This will in particular be useful for external verification of FTDNA’s calling algorithm (applied during the Genographic-to-FTDNA transfer process).

The YFull service has recently classified 1000 Genomes project samples by terminal Y-SNP, using ISOGG tree 8.57 as the basis [14].

1.3 New Technology

Prior to preparing this report, the author developed a Y-SNP-based subclade predictor (now available at <http://ytree.MorleyDNA.com>), with the inputs being a person’s Y-SNP results. It suggests the person’s terminal subclade (or the closest parent subclade tested). This algorithm was able to correctly classify the Full Genomes Y-SNP demo results [15]. It also performed robustly when tested on Geno 2.0 data – either in the form of calls scored from a kit’s raw file, or in the form of calls reported in a public Family Tree DNA project after being transferred from the Genographic project.

The algorithm is most effective when using the ISOGG tree as a basis for classification.

Evidently, the Y-tree clade predictor performs better the more detailed the underlying phylogenetic tree is. And the refinement of a phylogenetic tree is greatly aided by the use of an accurate predictor and other analytical tools. The two pillars bootstrap each other.

To illustrate this, the author has used this Y-tree clade predictor (using the latest ISOGG tree as a basis for comparison) to classify over 1500 sets of publicly accessible Geno 2.0 Y-SNP calls. This information was then used as an input into another algorithm designed by the author – an algorithm developed to automate the construction of a phylogenetic Y-tree, while overcoming the challenges identified above. The technical details of this process will remain proprietary for the time being.

1.4 Data

ISOGG's latest Y-tree was used as a starting point. Off-tree SNPs identified by ISOGG as private or phylogenetically unreliable were not used as inputs. The algorithm used to develop these reports will include these SNPs in the output, if they show up in the available Geno data.

Over 1500 sets of Geno 2.0 positive calls (data transferred from the Genographic Project to Family Tree DNA) were used. These Geno 2.0 results were all collected from publicly accessible haplogroup and surname projects, including the haplogroup projects identified in the ISOGG wiki [16]. Coverage was skewed toward the most heavily-tested haplogroups.

User-provided earliest known ancestor information has been removed from this version of the phylogeny.

1.5 Results

The output of this automated tree-building process is presented in Section 2. See Table 1.1 for notation.

Symbol Class	Symbol	Description
SNPs	M343	Positions known to ISOGG [8]. If on a branch with available Geno results: then the available Geno 2.0 results are consistent with ISOGG's positioning [8].
	CTS3368	SNPs unplaced in ISOGG's tree – placement has been proposed by the phylogenetic algorithm.
	DF27	SNPs not Geno-tested (or excluded by FTDNA from the list of positive SNPs). Names and placement come from ISOGG's tree [8].
	L440	Expected by ISOGG to be at this location, but the Geno 2.0 data suggests otherwise. When observed high up in the Y-tree: FTDNA may have the ancestral and derived states backwards, leading to positive results being scored negative, and vice versa.
	CTS2526 ^R	The SNP is recurrent – it has been also placed elsewhere in this tree. Recurrent does not necessarily mean erratic.
	PAGE65 ^b	ISOGG [8] has identified this instance as a back-mutation.
Kits	N114522	Blue kit numbers link back to FTDNA project SNP reports; follow the link to see the kit's positive calls obtained from Geno testing, and the positive and negative results obtained from à la carte SNP testing. Surnames and user-provided descriptions of the earliest-known patrilineal ancestor have not been included in this version of the report.
	*	A kit with this superscript may belong to one of the non-Geno-tested sister clades. À la carte SNP testing of the non-Geno-tested sister clade's (or clades') defining SNP(s) will be necessary to definitively place this kit.
Clades	A1b1	A clade featuring Geno-tested SNPs.
	A0a	A clade that does <i>not</i> feature Geno-tested SNPs.
	-n	Represents a subclade new to ISOGG's tree, proposed by the author's phylogenetic algorithm. For example, R1b1-1 is proposed to be downstream of R1b1 (and upstream of R1b1a). Some of these new subclades, if terminal, may have already been deemed "private" by ISOGG.
	?	This branch does not feature any Geno-tested kits, and consequently its position in the new phylogeny is unconfirmed.
	△	The position of a subclade with this superscript cannot be fully resolved, because not all sister clades were Geno-tested, and none of the kits in this subclade have had the required non-Geno-tested SNPs tested à la carte.
Coverage statistics	(x/y)	y is the number of kits supposedly downstream of this SNP, and x is the number of these kits that are positive for the SNP. Some non-positive results could in fact be no-calls or back-mutations. If this SNP is situated on a branch untouched by Geno 2.0 testing then the figure (which would be 0/0) is omitted. It is also omitted for SNPs that were not Geno-tested and have no positive-testing downstream kits.

Table 1.1: Notation used in the novel draft Y phylogeny

1.6 Discussion

Owing to the automated nature of the process, it is straightforward for the author to issue revised computer-generated draft phylogenies, as new information becomes available.

The draft phylogenies resulting from this process will not replace the existing ISOGG tree. But they should help reduce the workload of ISOGG project administrators. It will not make their roles obsolete. Their judgement is still needed to decide which SNPs are worthy of inclusion in the ISOGG tree. Moreover, the algorithm will identify some SNPs with inconsistent information, requiring manual examination in order to place on the tree. The reports developed by the author will serve as a *guideline* for further ISOGG tree expansion; ISOGG will retain editorial control over its Y-tree.

The Genographic Consortium phylogenetic tree – whenever it is published – should be superior to the tree presented here. The Genographic Consortium has a vastly larger and more diverse dataset to work with, and consequently one would expect the resultant paper to contain numerous branches not included here. Additionally, the Genographic Consortium, having access to all the raw data, will know which non-positive calls are negatives and which are in fact no-calls, thereby simplifying the tree construction process. The Genographic Consortium's paper will likely be treated to pre-publication peer review. This will delay the delivery but ensure the quality of the final result. It remains to be seen whether/how/how frequently the Genographic Consortium will update its phylogenetic tree after its initial publication.

Outstanding issues for the experimental phylogeny:

- The *PAGE#* class of SNPs needs to be equated with the *PAGES0000#* class of SNPs.
- The downstream SNP coverage statistics for known backmutations need to be corrected.
- Future versions of the phylogenetic report will split the tree into sections.
- Non-Latin letters (from the user-submitted earliest known ancestor descriptions) typeset as question marks.
- For non-Geno-tested SNPs, the denominator in the coverage statistics should be the number of kits downstream that have had this SNP tested à la carte, instead of the total number of kits downstream.
- The author will release a separate automatically-generated report identifying discrepancies/gaps in the ISOGG data, suggesting potentially unreliable SNPs and listing SNPs whose positions need to be confirmed manually.
- See [this thread](#) for further issues.

1.7 Summary

There is present demand for tools that will automate the production and maintenance of a high-resolution Y-SNP phylogenetic tree. Demand will rise further. This report showcases the results from an initial attempt at tackling this problem.

1.8 References

- [1] Eran Elhaik, Elliott Greenspan, Sean Staats, Thomas Krahn, Chris Tyler-Smith, Yali Xue, et al., *The GenoChip: A New Tool for Genetic Anthropology*. *Genome Biol Evol*. 2013; 5(5): 1021–1031, <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3673633/>, 9 May 2013 (accessed 15 July 2013).
- [2] CeCe Moore, *National Geographic and Family Tree DNA Announce Geno 2.0*. Your Genetic Genealogist, <http://www.yourgeneticgenealogist.com/2012/07/national-geographic-and-family-tree-dna.html>, July 25 2012 (accessed 5 July 2013).
- [3] Roberta Estes, *National Geographic – Geno 2.0 Announcement – The Human Story*. DNAeXplained – Genetic Genealogy, <http://dna-explained.com/2012/07/25/national-geographic-gen-2-0-announcement-the-human-story/>, July 25 2012 (accessed 5 July 2013).
- [4] Roberta Estes, *Geno 2.0 Results – First Peek*. DNAeXplained – Genetic Genealogy, <http://dna-explained.com/2012/12/11/geno-2-0-results-first-peek/>, 11 December 2012 (accessed 5 July 2013).
- [5] eng.Molgen.org community, *Geno 2.0 Y-phylogeny*. A Genetic Genealogy Community: Y-DNA, Mt-DNA, Autosomal DNA (Molgen.org English Forums), <http://eng.molgen.org/viewtopic.php?f=4&t=1080>, 24 April 2013 (accessed 5 July 2013).
- [6] Łukasz Łapiński et al., *R1a1a and Subclades Y-DNA Project – Y-DNA SNP*. Family Tree DNA Y-Haplogroup Project, <http://www.familytreedna.com/public/r1a/default.aspx?section=ysnp>, 15 July 2013 (accessed 15 July 2013).
- [7] Itai Perez, *Re: [DNA] It's been a month, let's start complaining about Geno 2.0 transfer errors*. GENEALOGY-DNA-L Mailing List, <http://archiver.rootsweb.ancestry.com/th/read/GENEALOGY-DNA/2013-01/1358179571>, 14 January 2013 (accessed 5 July 2013).
- [8] International Society of Genetic Genealogy, *Y-DNA Haplogroup Tree 2013, Version: 8.61*. <http://www.isogg.org/tree/>, 16 July 2013 (accessed 16 July 2013).
- [9] The Y Chromosome Consortium, *Ytree (YCC2008)*. <http://ytree.ftdna.com/index.php?name=YCC2008&parent=root>, 2008 (accessed 5 July 2013).
- [10] Family Tree DNA (Thomas Krahn et. al.), *Ytree (Draft Phylogeny)*. <http://ytree.ftdna.com/>, 2013 (accessed 5 July 2013).
- [11] Felix, *My Y-SNP Tree*. Genetic Genealogy Tools: Open source software for genetic genealogy, <http://www.y-str.org/tools/my-y-snp-tree/>, 3 July 2013 (accessed 5 July 2013).
- [12] Ethio Helix, *Geno 2.0 YDNA SNP Pathways*. Ethio Helix Blog, <http://ethiohelix.blogspot.com/2013/03/geno-20-ydnapathways.html>, 24 April 2013 (accessed 5 July 2013).
- [13] Itai Perez, *Geno 2.0 Y-Chromosome Genome Comparison: Extending Y-DNA Haplogroup Knowledge via Collaboration*. <http://itai.perez.free.fr/GenoCompare/>, 5 June 2013 (accessed 5 July 2013).

- [14] YFull Y-Chr Sequence Interpretation Service, *YFull 1000 Genomes (Tree)*. <http://www.yfull.com/tree/>, 12 July 2013 (accessed 15 July 2013).
- [15] Full Genomes Corp., *Demo for product: "Comprehensive Y-Chromosome Sequencing"*. <https://fullgenomes.com/demo>, 2013 (accessed 5 July 2013).
- [16] International Society of Genetic Genealogy, *Y-DNA haplogroup projects*. ISOGG Wiki, http://www.isogg.org/wiki/Y-DNA_haplogroup_projects, 26 June 2013 (accessed 5 July 2013).

Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

2. Experimental computer-generated Y-SNP phylogeny

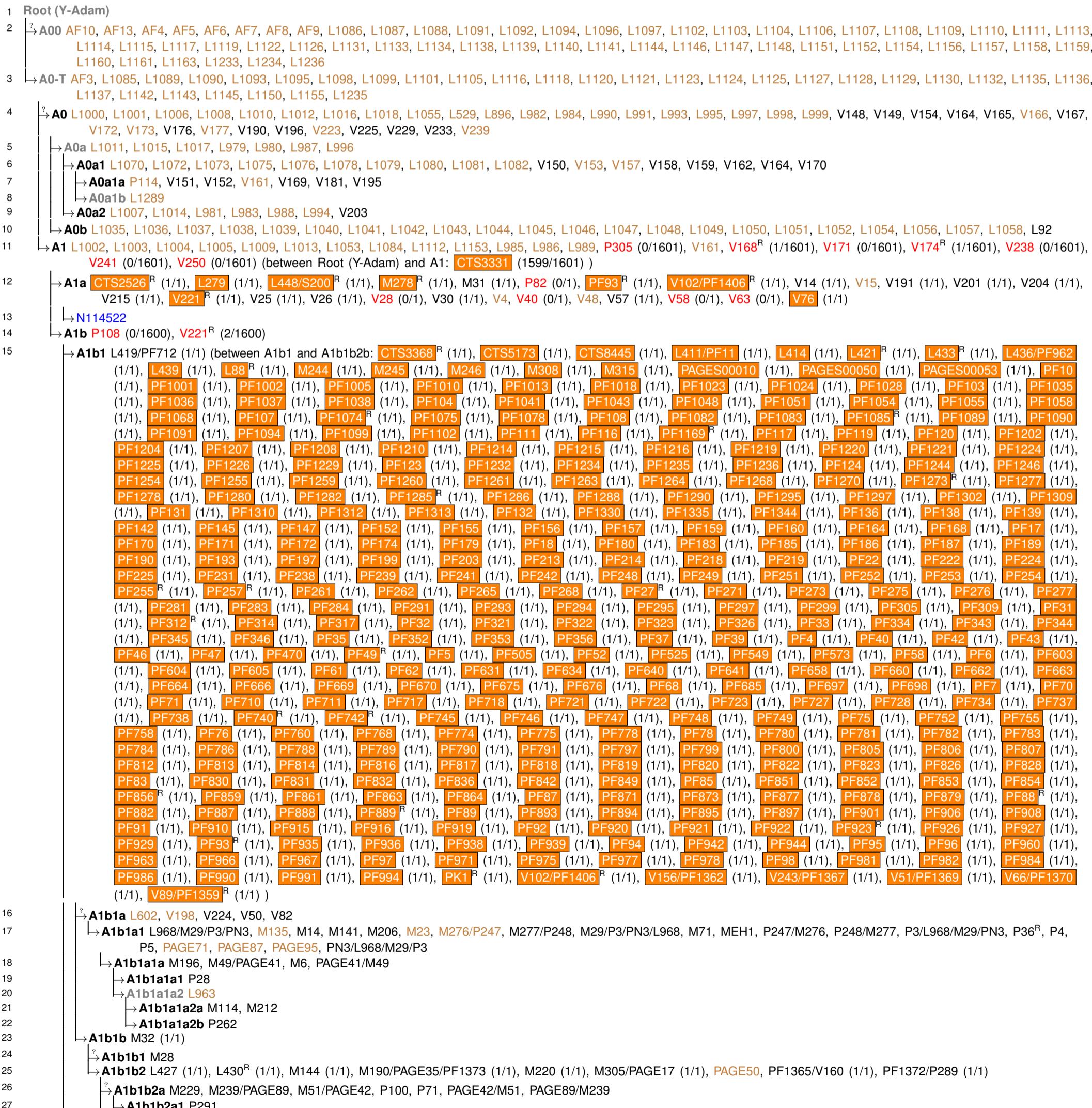
2.1 Experimental Y tree (automated)

Notice

This phylogeny uses ISOGG Y-DNA Haplogroup Tree version 8.61 (16 July 2013) [8] as a starting point.

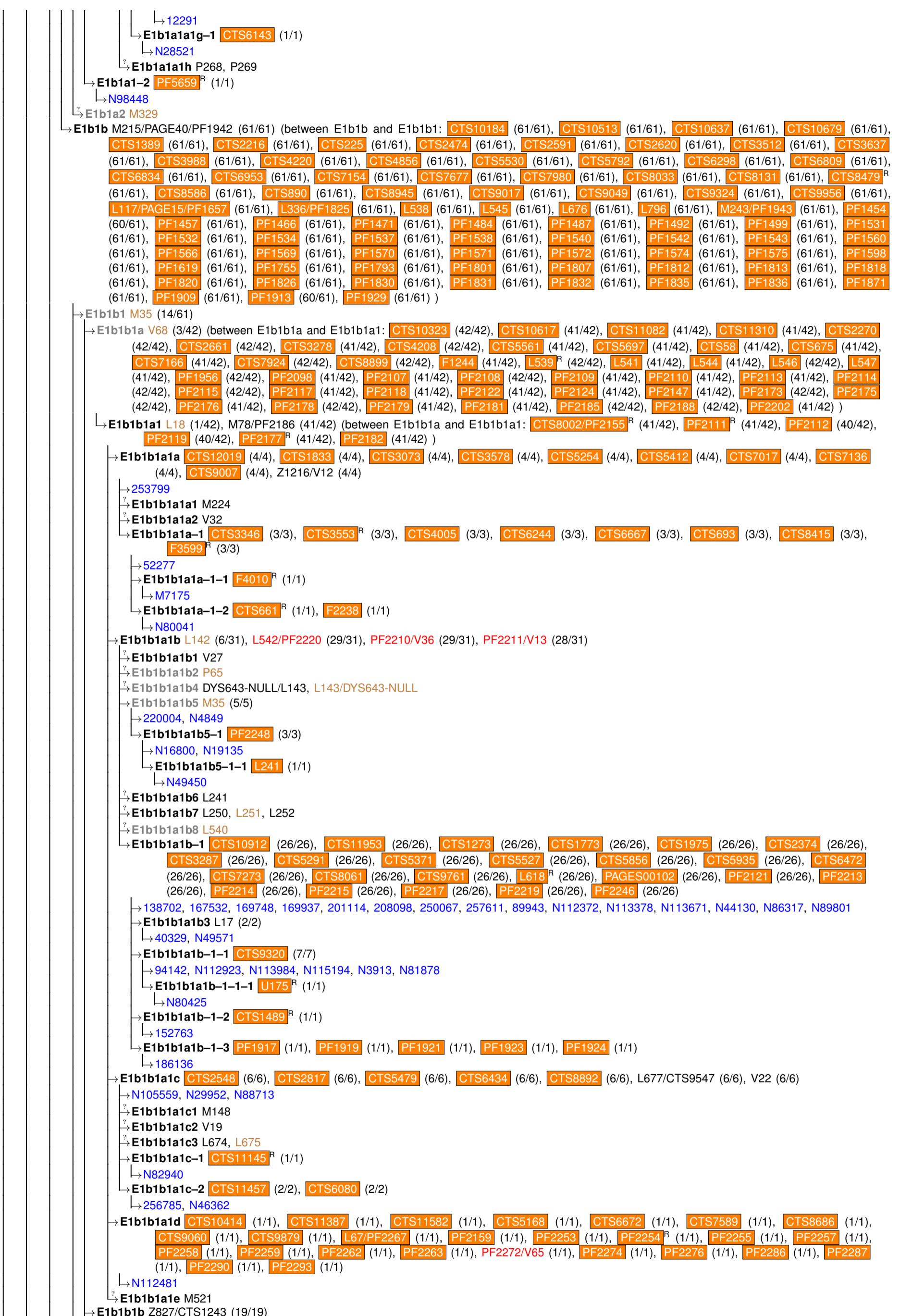
This is an experimental tree. Please do not base major SNP-purchasing decisions on this, yet. It needs to be looked over by some experts to ensure that there are no systematic errors. ISOGG does not sponsor or endorse this experimental tree.

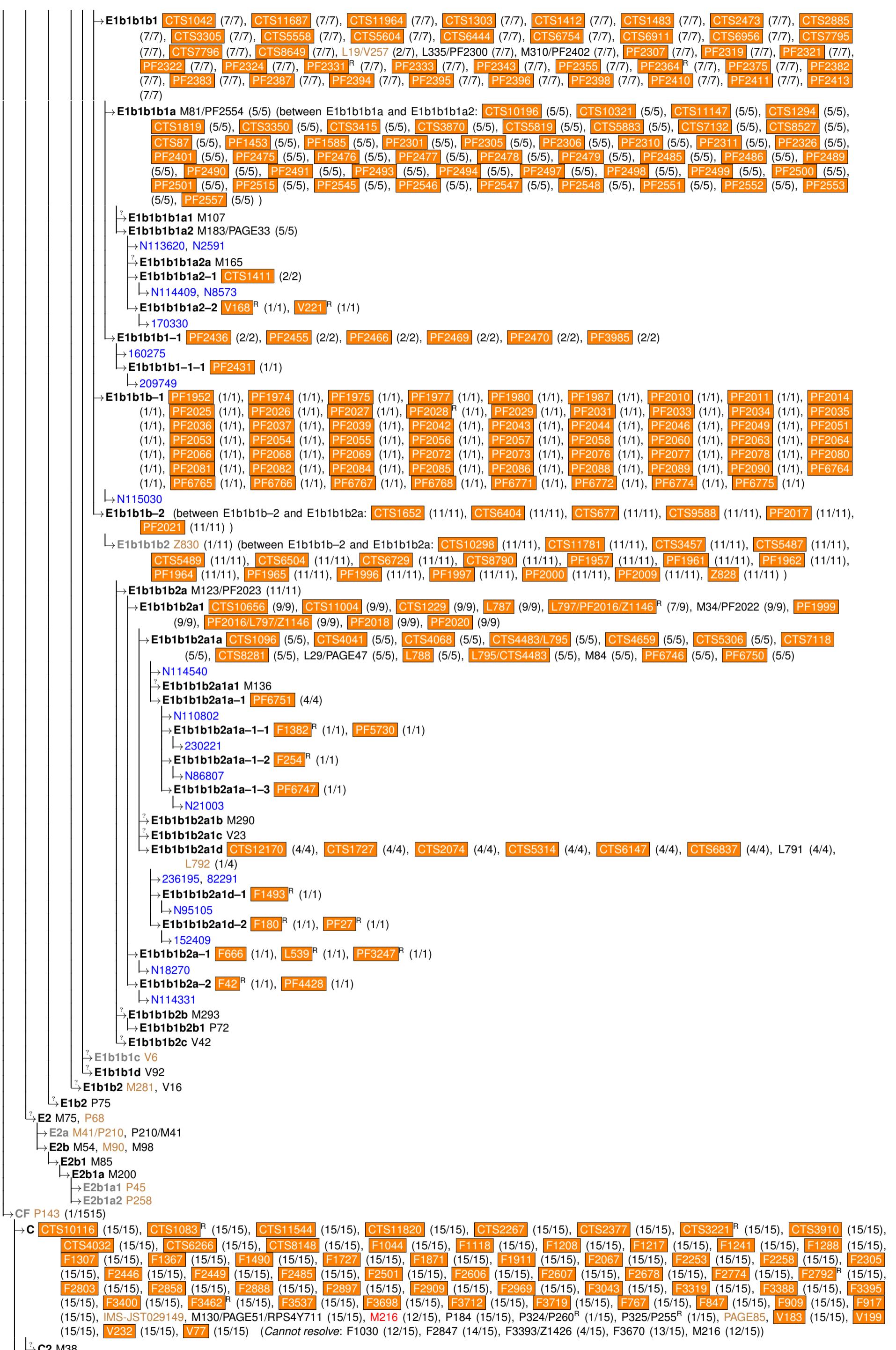
This tree is for personal, non-commercial use. It is to be distributed according to the Creative Commons Attribution-NonCommercial-NoDerivs 3.0 Unported license, with the additional condition that it may not be used in Y-subclade prediction software without the author's prior consent.

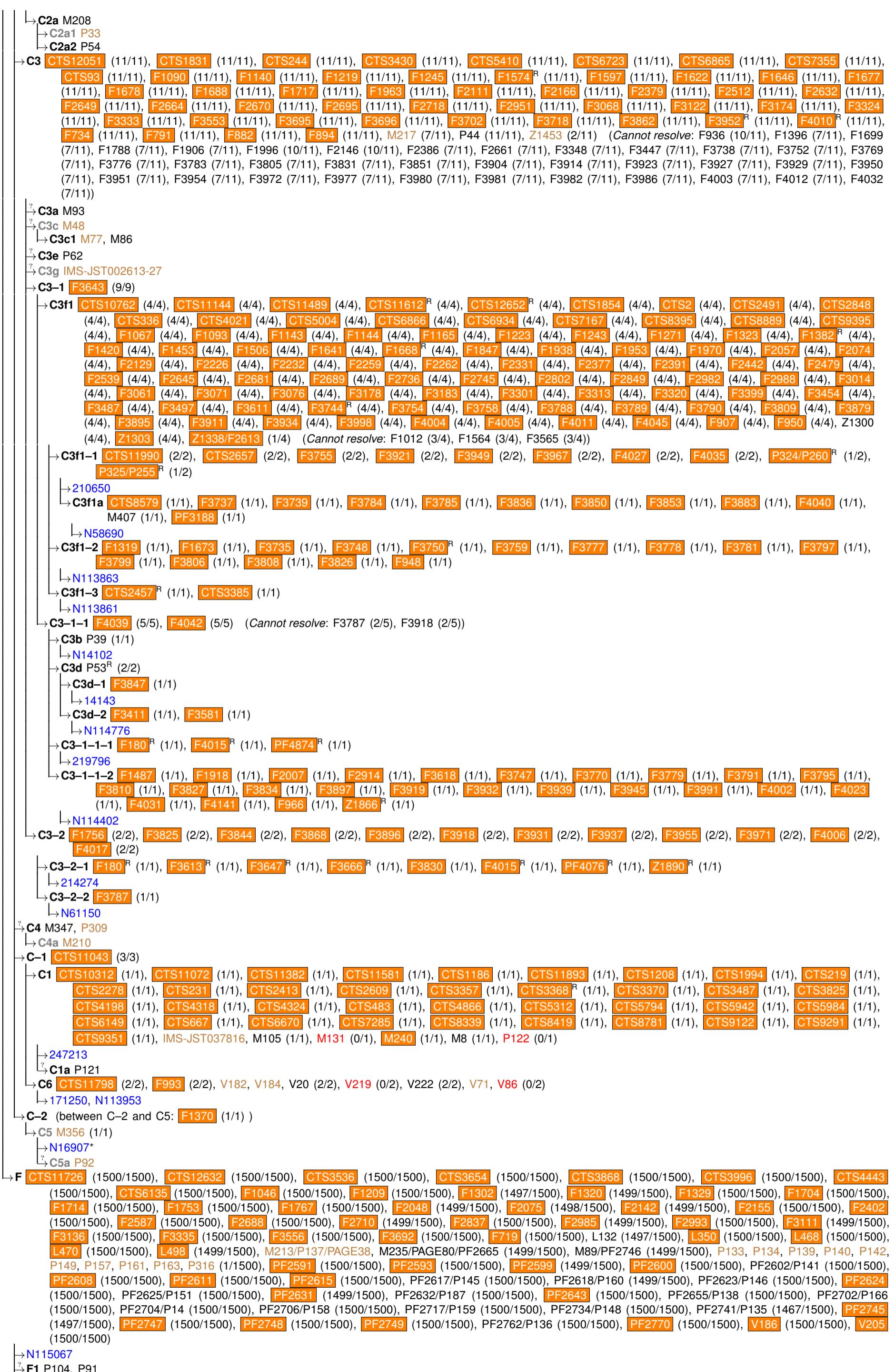




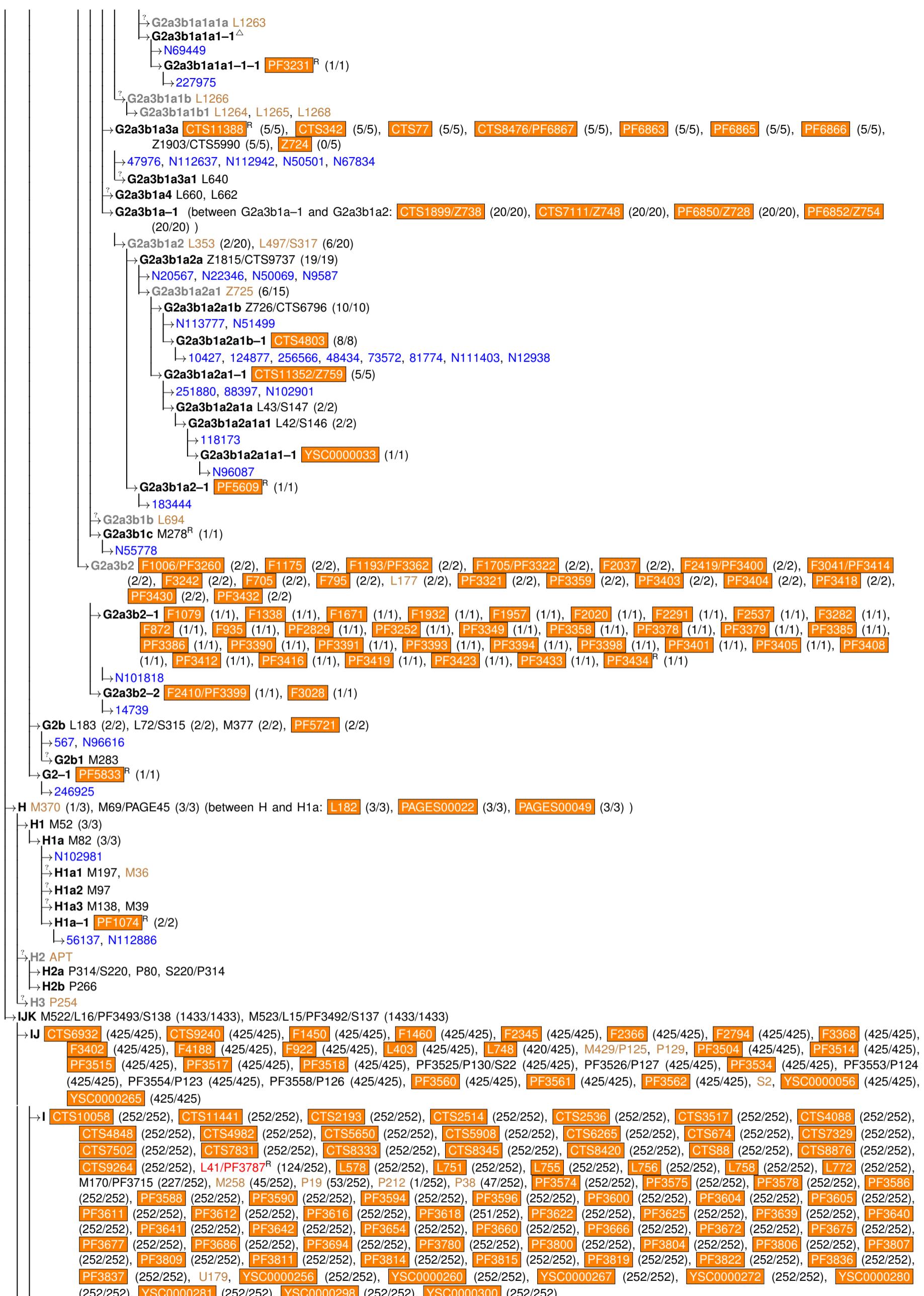


Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

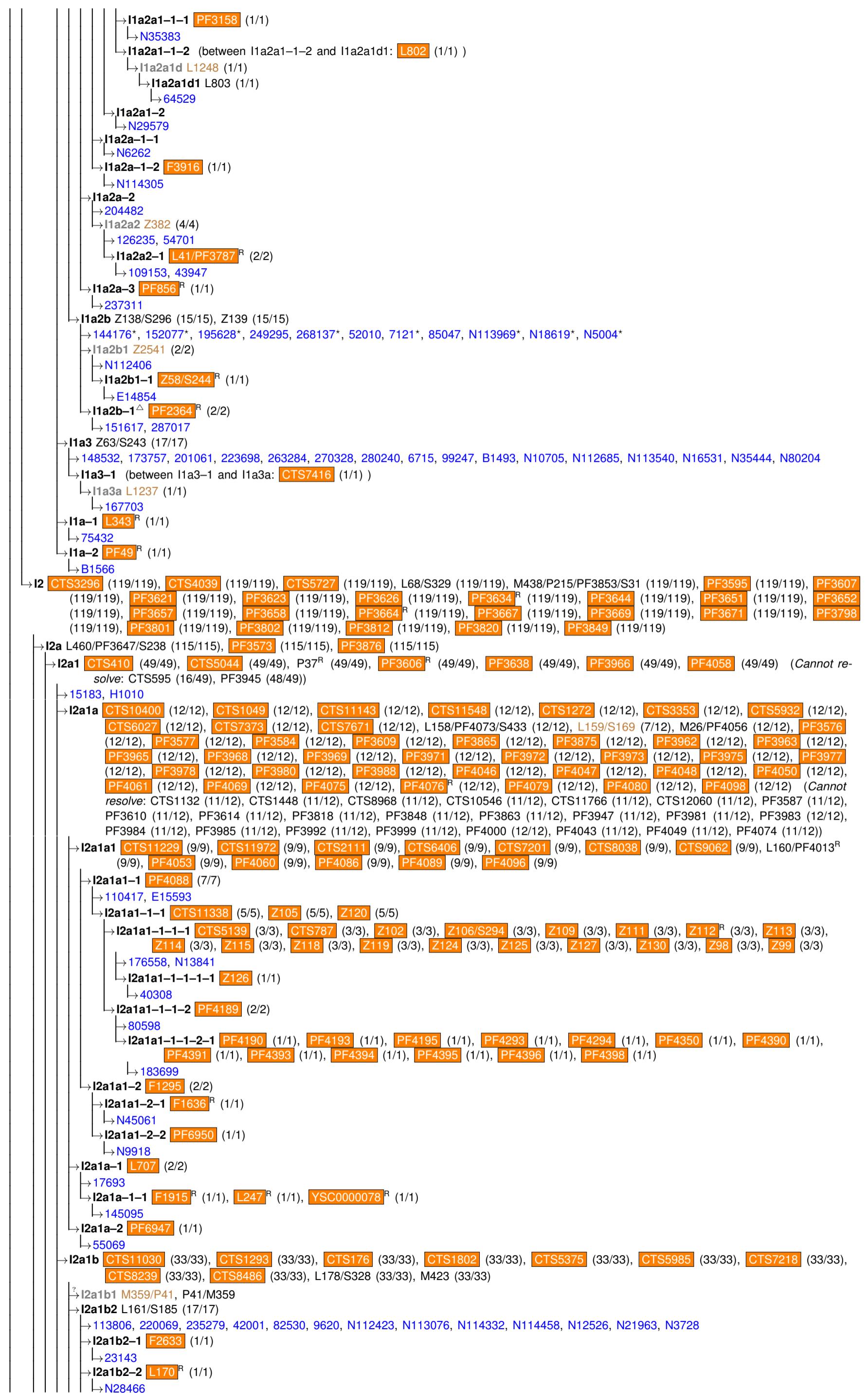
Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

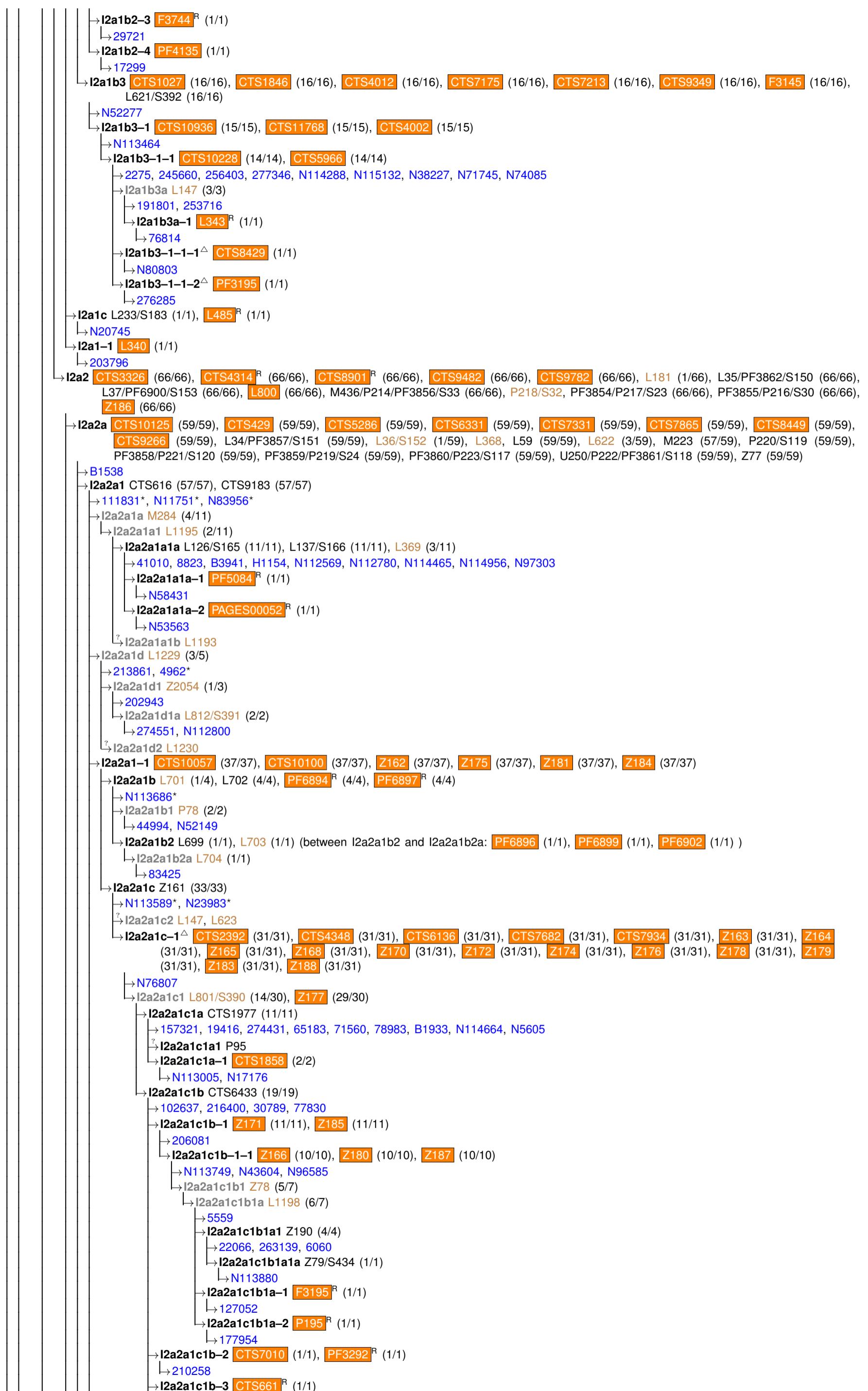




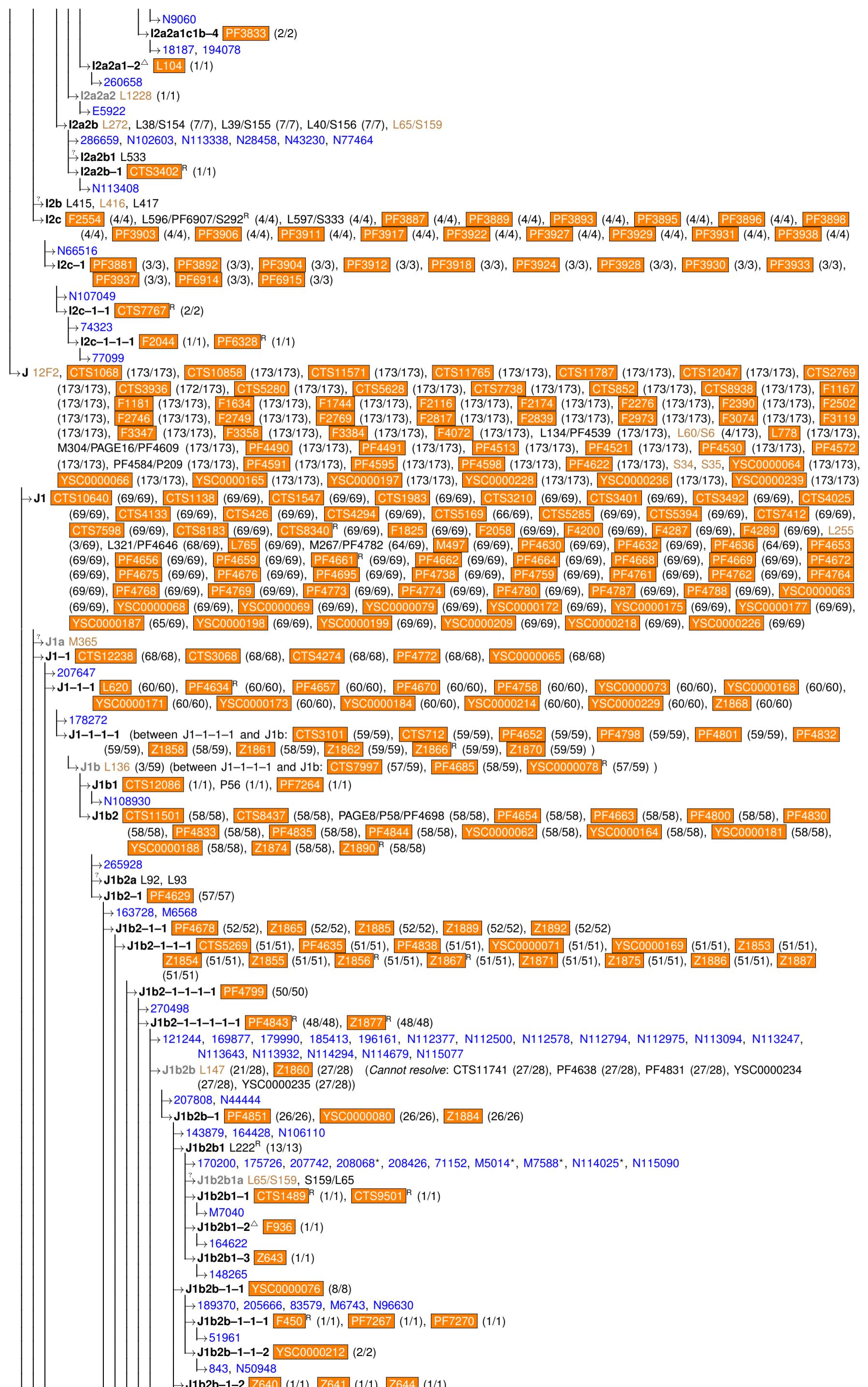
Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

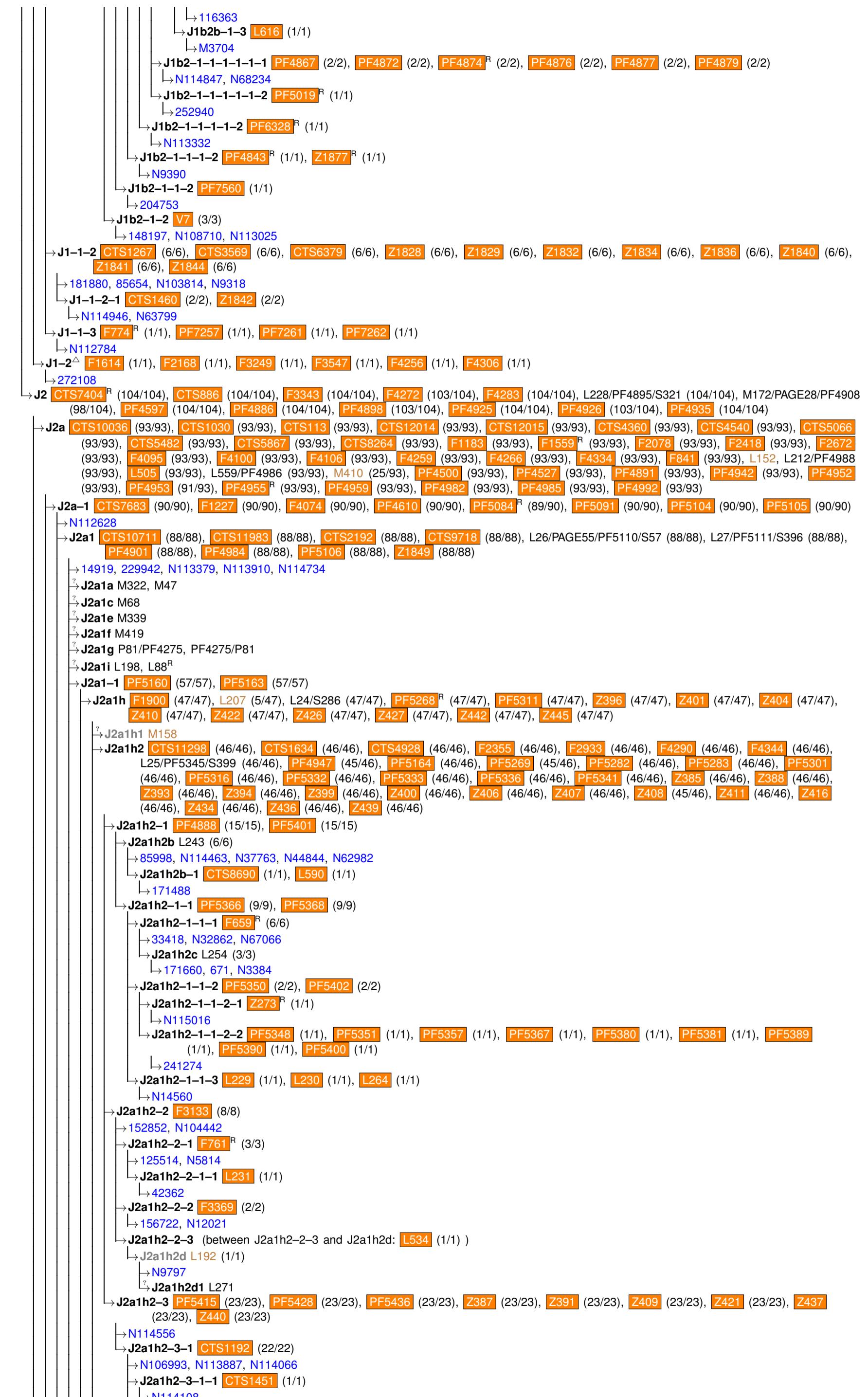
Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

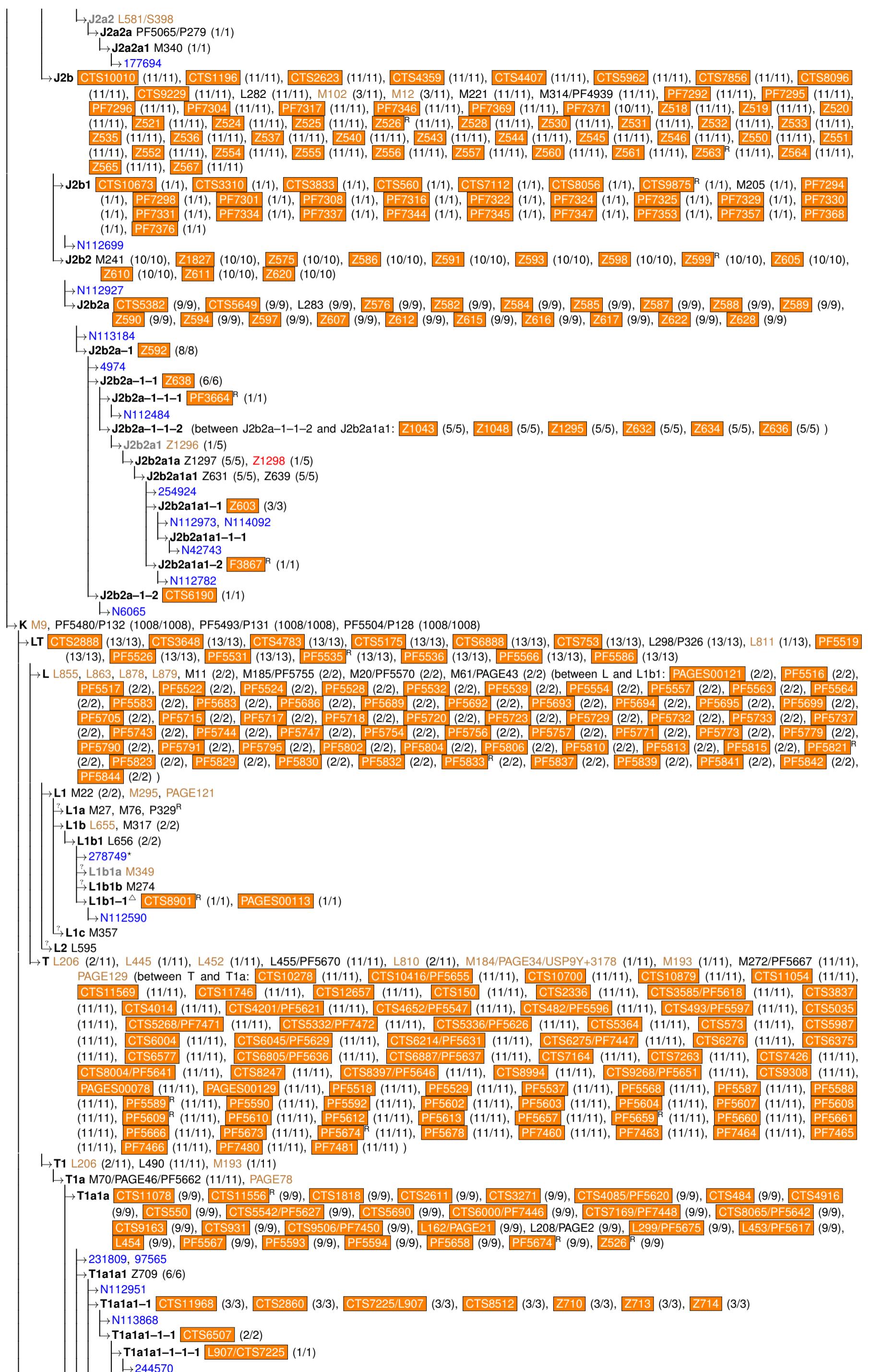
Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.



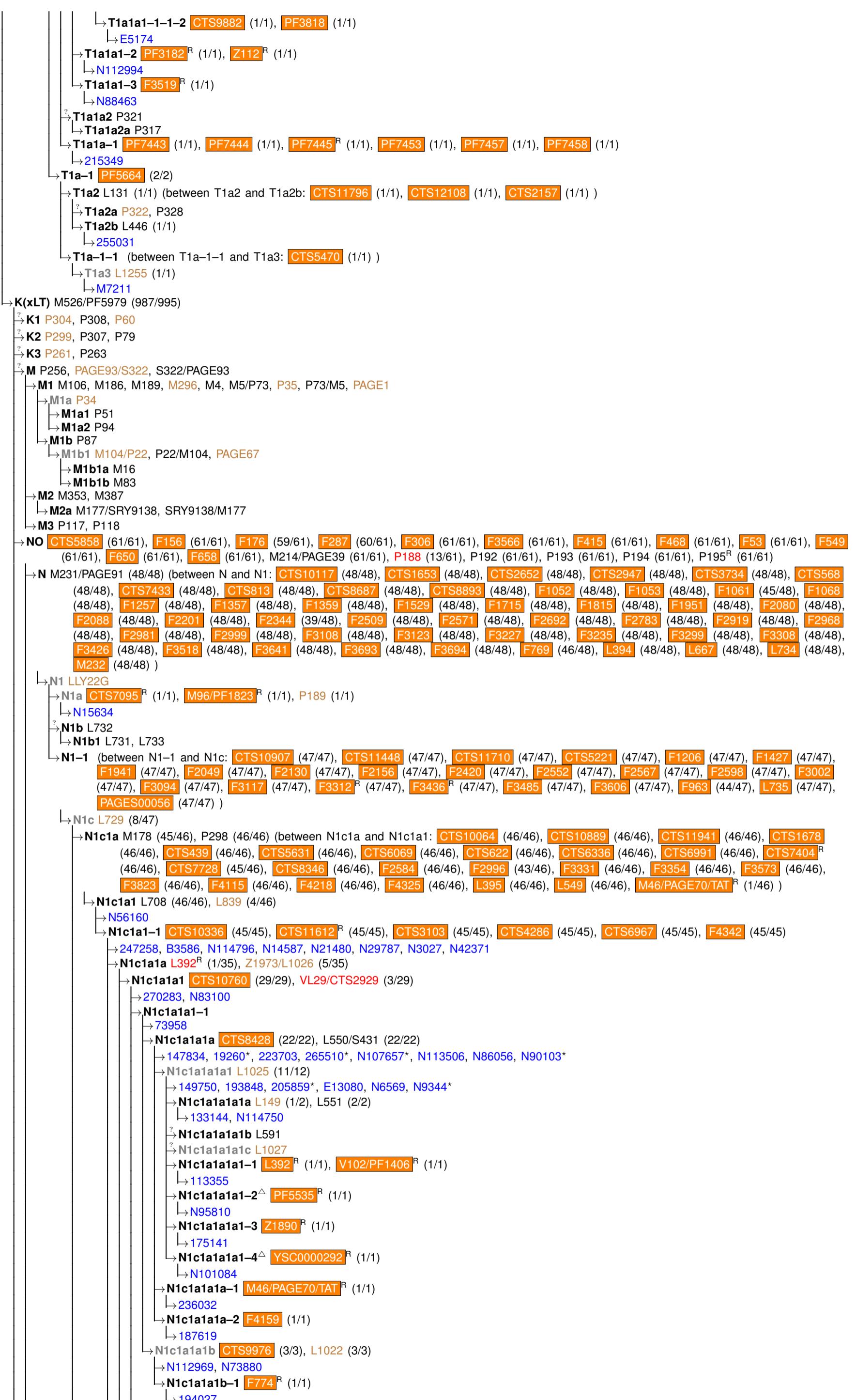
Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

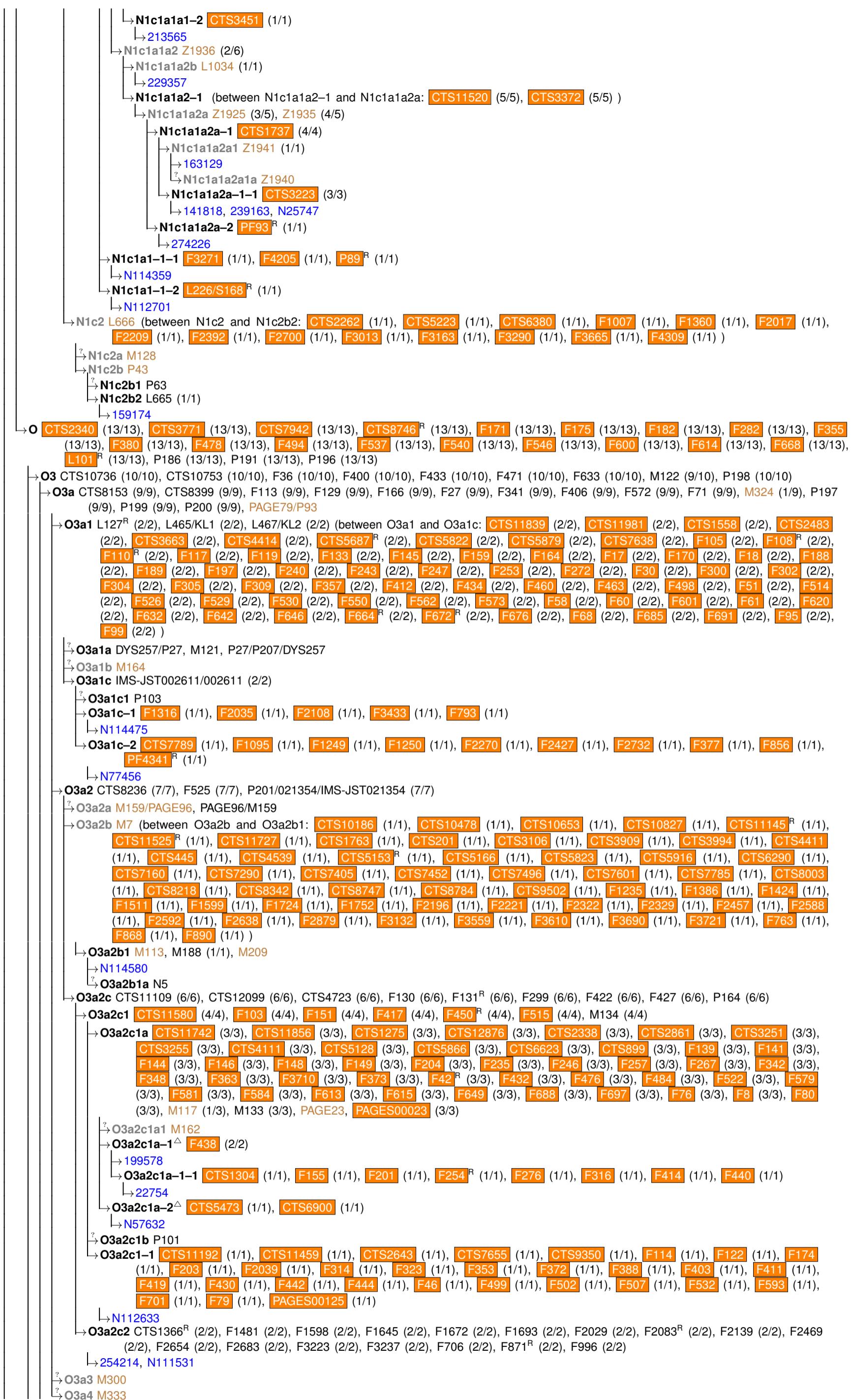
Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

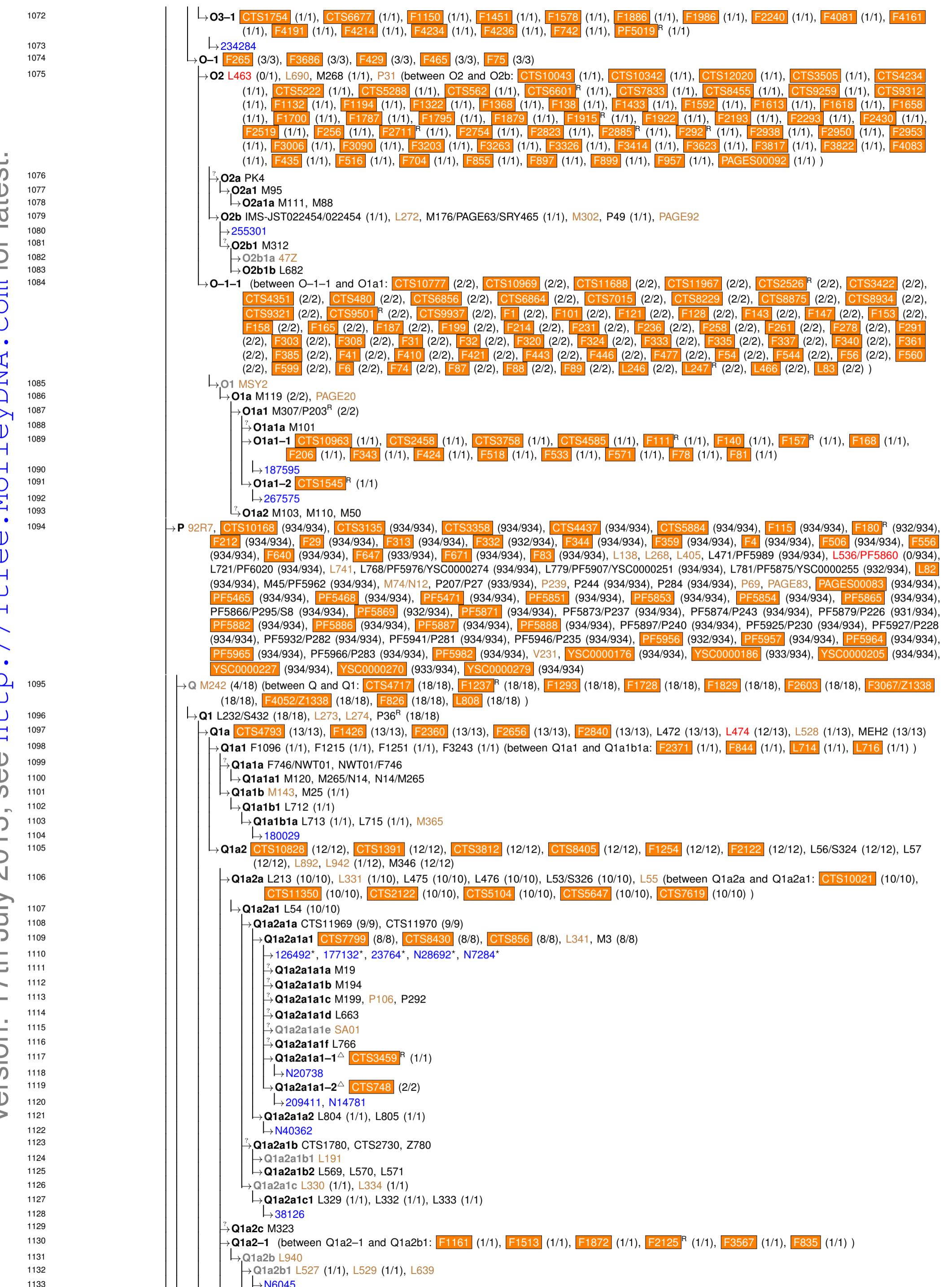
Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

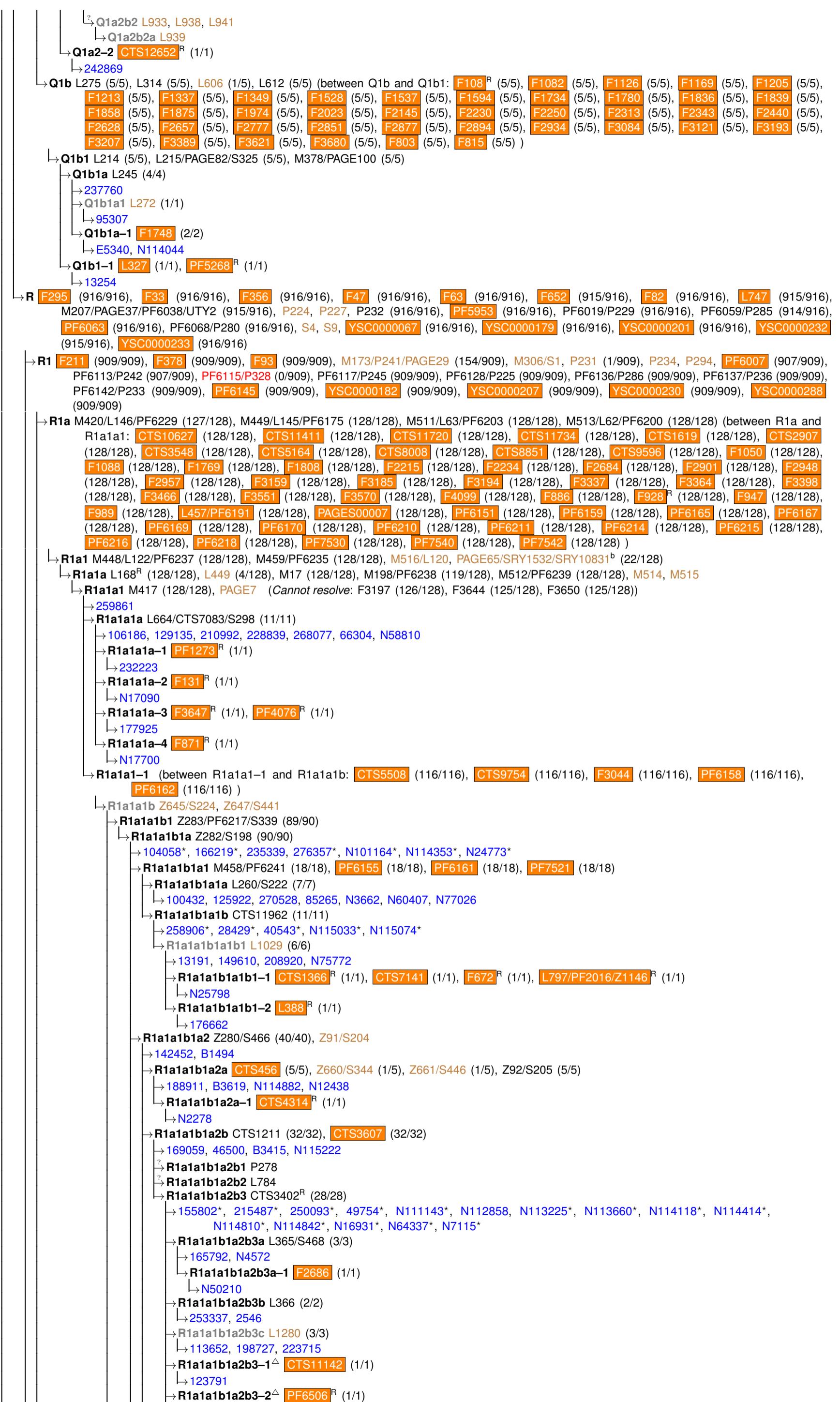
Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

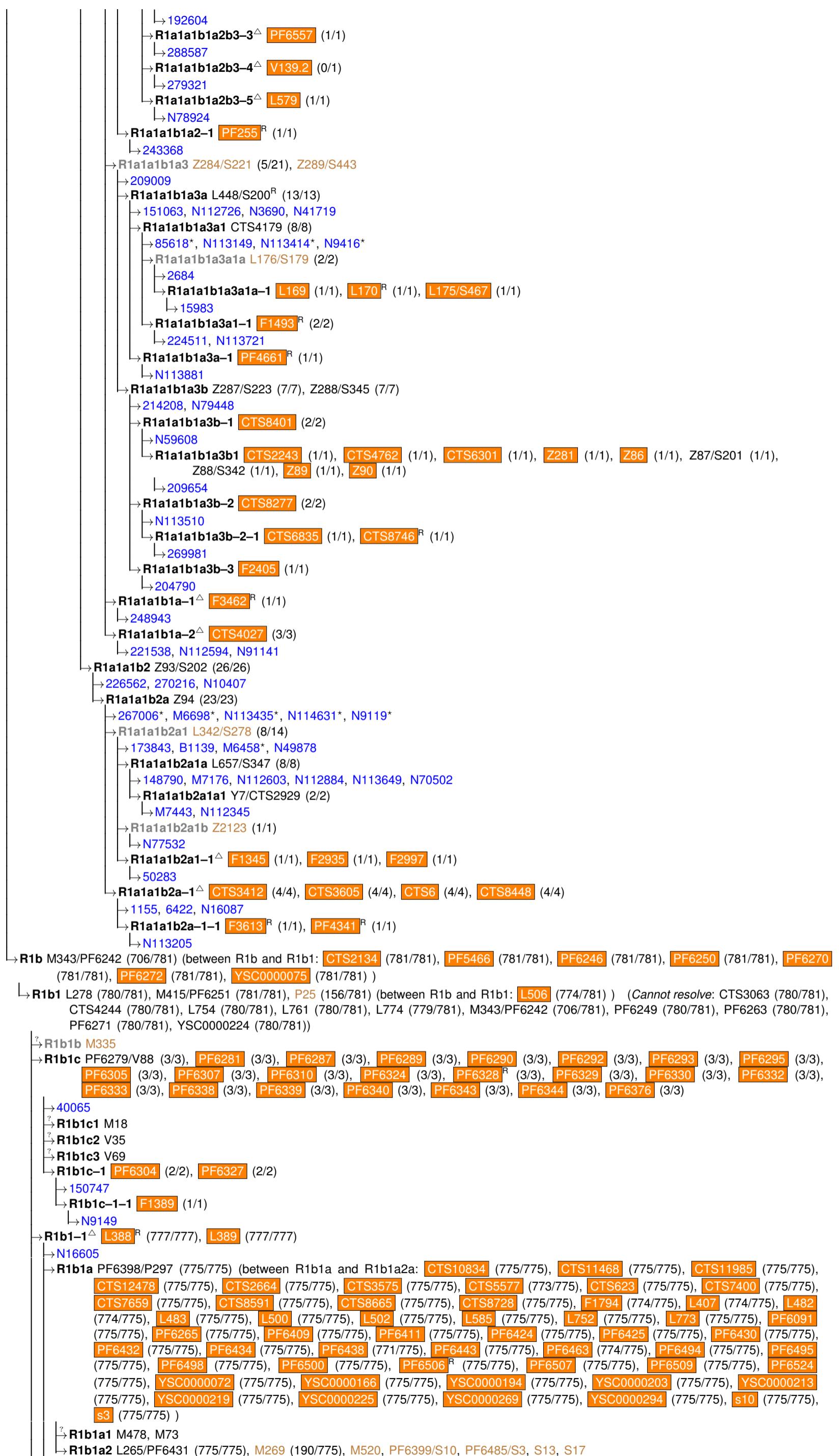
Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.



Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

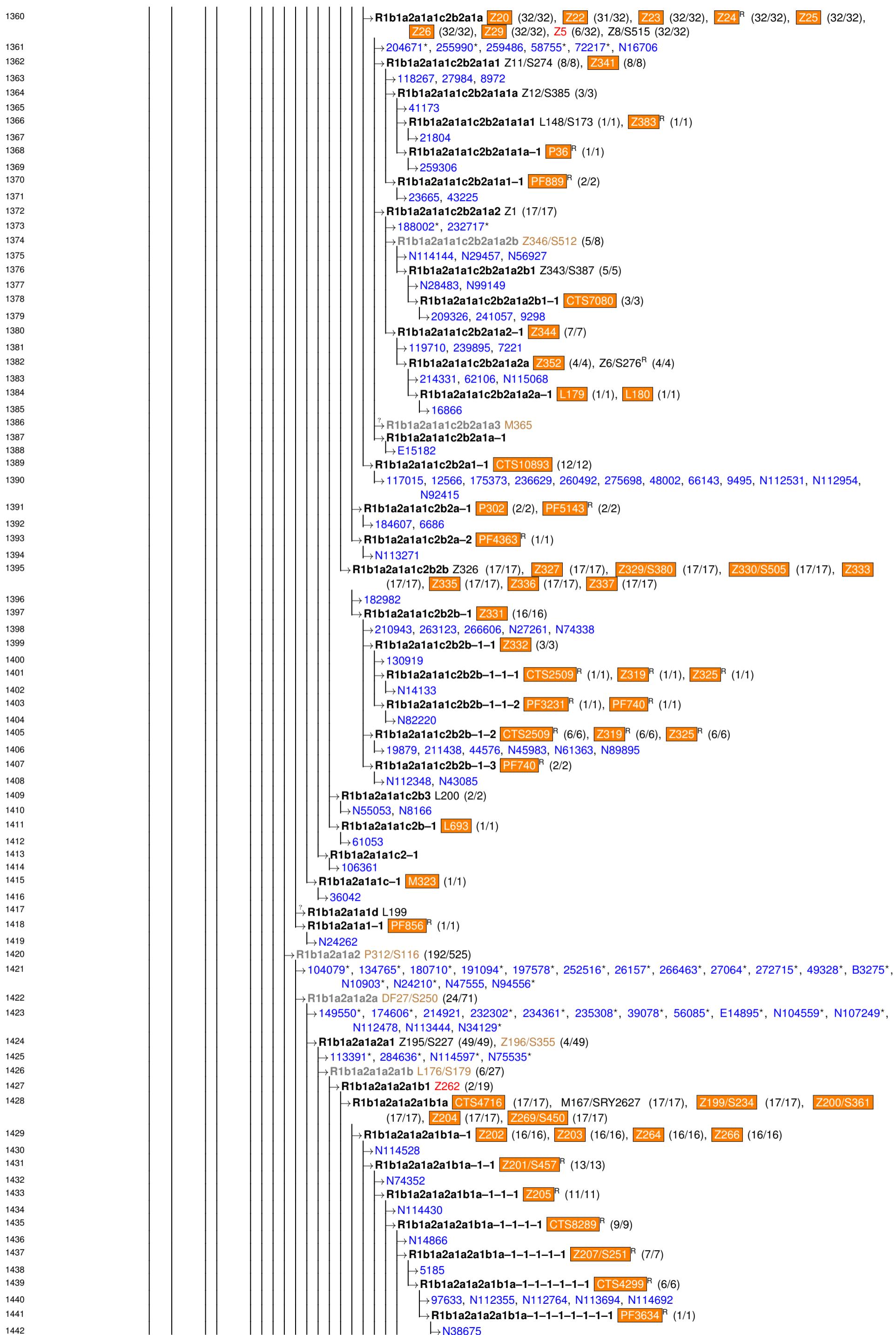
Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

1278
 1279
 1280
 1281
 1282
 1283
 1284
 1285
 1286
 1287
 1288
 1289
 1290
 1291
 1292
 1293
 1294
 1295
 1296
 1297
 1298
 1299
 1300
 1301
 1302
 1303
 1304
 1305
 1306
 1307
 1308
 1309
 1310
 1311
 1312
 1313
 1314
 1315
 1316
 1317
 1318
 1319
 1320
 1321
 1322
 1323
 1324
 1325
 1326
 1327
 1328
 1329
 1330
 1331
 1332
 1333
 1334
 1335
 1336
 1337
 1338
 1339
 1340
 1341
 1342
 1343
 1344
 1345
 1346
 1347
 1348
 1349
 1350
 1351
 1352
 1353
 1354
 1355
 1356
 1357
 1358
 1359

↳ **R1b1a2a** L150/PF6274 (775/775), **L23/PF6534/S141** (771/775), **L49/S349** (37/775)
 ↳ **R1b1a2a-1** **L478** (764/771), **PF6404** (770/771)
 ↳ **26483, N10795, N112959, N113118, N114022, N53795, N79525, N81217, N9475**
 ↳ **R1b1a2a1** M412/L51/PF6536/S167 (751/752)
 ↳ **R1b1a2a1a** L11/PF6539/S127 (749/749), L151/PF6542 (749/749), L52/PF6541 (748/749), PF6546/P310/S129 (748/749),
YSC0000082 (749/749), **YSC0000191** (749/749)
 ↳ **109950, 144416, 160165, 16296, 202807, 214080, 221617, 222323, 246984, 248663, 249898, 277935, 281393, 4354,**
B3027, B3630, N108633, N112350, N112469, N112805, N112880, N112890, N112979, N113270, N113291,
N113369, N114363, N114735, N24160, N29401, N45113, N91624, N93389
 ↳ **R1b1a2a1a1** M405/S21/U106 (163/181)
 ↳ **121519, 181203, 246919, 284914, N103013, N52462, N59802, N82860**
 ↳ **R1b1a2a1a1a** L217 (1/1)
 ↳ **23545**
 ↳ **R1b1a2a1a1b** Z18/S493 (20/20), **Z19^R** (4/20) (between R1b1a2a1a1b and R1b1a2a1a1b1: **Z16/S261** (20/20))
 ↳ **R1b1a2a1a1b1** Z14 (20/20)
 ↳ **147657*, N113223*, N115161, N17100*, N31052*, N44777, N61825, N65375*, N85364***
 ↳ **R1b1a2a1a1b1a** **Z372/S375** (6/8)
 ↳ **122883, 174347, N113653**
 ↳ **R1b1a2a1a1b1a1** L257/S186 (2/2)
 ↳ **N113458**
 ↳ **R1b1a2a1a1b1a1-1** **CTS11525^R** (1/1)
 ↳ **B3023**
 ↳ **R1b1a2a1a1b1a-1** **Z19^R** (2/2)
 ↳ **N14340, N37019**
 ↳ **R1b1a2a1a1b1a-2** **CTS10855^R** (1/1)
 ↳ **50394**
 ↳ **R1b1a2a1a1b1-1[△]** **L618^R** (1/1), **L797/PF2016/Z1146^R** (1/1), **Z454^R** (1/1)
 ↳ **N114052**
 ↳ **R1b1a2a1a1b1-2[△]** **F2125^R** (1/1)
 ↳ **N114742**
 ↳ **R1b1a2a1a1b1-3[△]** **CTS904** (1/1), **PF257^R** (1/1)
 ↳ **N83001**
 ↳ **R1b1a2a1a1c** Z381/S263 (151/151)
 ↳ **246302, 251733, 275871**
 ↳ **R1b1a2a1a1c1** Z156/S264 (41/41)
 ↳ **104866, 111203, 65132, 90791, B3197, N10078**
 ↳ **R1b1a2a1a1c1a** **Z305/S376** (10/31), Z306 (31/31), **Z307** (30/31)
 ↳ **202349**
 ↳ **R1b1a2a1a1c1a-1**
 ↳ **175525, 179381, 197037, 222086, 239336, 263108, 5010, 75848, 75884, E2541, H1112, N112415,**
N112502, N112833, N113250, N113640, N114348, N115206, N17289, N35071, N46336, N74756
 ↳ **R1b1a2a1a1c1a1** L1/DYS439-NULL/S26 (3/3)
 ↳ **14179, 176669, 57020**
 ↳ **R1b1a2a1a1c1a2** P89^R (1/1), **PF4142** (1/1)
 ↳ **1196**
 ↳ **R1b1a2a1a1c1a-1-1** **F2735^R** (1/1)
 ↳ **N6918**
 ↳ **R1b1a2a1a1c1a-1-2** **Z243** (1/1)
 ↳ **178396**
 ↳ **R1b1a2a1a1c1a-1-3** **CTS7550** (1/1)
 ↳ **B2570**
 ↳ **R1b1a2a1a1c1a-1-4** (between R1b1a2a1a1c1a-1-4 and R1b1a2a1a1c1a3: **L127^R** (1/1))
 ↳ **R1b1a2a1a1c1a3** **L128** (1/1)
 ↳ **5962**
 ↳ **R1b1a2a1a1c1-1** **CTS11337** (2/2)
 ↳ **252157**
 ↳ **R1b1a2a1a1c1-1-1** **L247^R** (1/1)
 ↳ **N115135**
 ↳ **R1b1a2a1a1c1-2** **F3024** (1/1)
 ↳ **176334**
 ↳ **R1b1a2a1a1c1-3** **F1668^R** (1/1)
 ↳ **230038**
 ↳ **R1b1a2a1a1c2** **Z301** (5/106)
 ↳ **R1b1a2a1a1c2a** M467/S29/U198 (6/6)
 ↳ **142323, 48449, B3389, N112992, N114583, N58648**
 ↳ **R1b1a2a1a1c2b** **L48/S162** (61/99)
 ↳ **182162, 212083, N80434**
 ↳ **R1b1a2a1a1c2b1** L47/S170 (19/19)
 ↳ **243843*, 42015*, N112928*, N113113*, N2146*, N64724***
 ↳ **R1b1a2a1a1c2b1a** L163/S352 (5/5), L44/S171 (5/5)
 ↳ **202816**
 ↳ **R1b1a2a1a1c2b1a1** **L46/S172** (2/3)
 ↳ **R1b1a2a1a1c2b1a1a** L164/S502 (2/3), **L237** (2/3), **L45/S353** (2/3), **L477** (2/3), **L493** (2/3) (Can-
 not resolve: L45/S353 (2/3), L46/S172 (2/3), L164/S502 (2/3), L237 (2/3), L477 (2/3), L493
 (2/3), L525 (2/3))
 ↳ **368, N109633, N39678**
 ↳ **R1b1a2a1a1c2b1a-1** **PF2062** (1/1)
 ↳ **1502**
 ↳ **R1b1a2a1a1c2b1b** **Z159** (7/7), **Z160** (7/7), **Z350** (7/7)
 ↳ **14584, 169807, 230445, 70092, 92584, N113456, N6478**
 ↳ **R1b1a2a1a1c2b1-1[△]** **CTS3553^R** (1/1)
 ↳ **N112671**
 ↳ **R1b1a2a1a1c2b2** **Z10** (5/74), **Z28** (74/74), **Z348** (74/74), Z9/S268 (74/74) (Cannot resolve: Z10 (5/74),
 Z334 (18/74), Z347 (18/74))
 ↳ **11104, 235324, 29149, N114572, N47495**
 ↳ **R1b1a2a1a1c2b2a** Z2 (52/52), **Z30** (52/52)
 ↳ **115148, 146664, 46804**
 ↳ **R1b1a2a1a1c2b2a1** **Z31** (46/46), Z7/S272 (46/46)
 ↳ **B3144, N81828**

Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779

Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.

Version: 17th July 2013; see <http://Ytree.MorleyDNA.com> for latest.