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Legend for accuracy ratings

Quality Rating	Red Content	Green Content	Blue Content	Signature Match	Genetic Distance	Signature Match	Genetic Distance
95	128	255	128	6 or more	6 or less	7 or more	7 or more
90	179	255	128	5	6 or less	6	7 or more
85	230	255	128	4	6 or less	5	7 or more
75	255	225	128	3	6 or less	4	7 or more
60	255	207	128	2	6 or less	3	7 or more
45	255	187	128			2	7 or more
30	255	168	128	1	6 or less		
20	255	148	128			1	7 or more
10	255	128	128	0	all		

This tree building methodology could be automated via developing a software tool that builds the attached chart. A robust functional specification has been created for consistent analysis and potential coding of this charting tool. This tool is now around 75 % completed and is written in C++.

If you have programming skills and are interested in the automation of this tree building methodology into a publicly available software tool, please give me call: Robert Casey at (512) 371-0579 (Austin, TX time zone).

Legend for Information contained for each tester:
First Field - FTDNA Kit number or YSEARCH ID
Second Field - Surname of the oldest proven ancestor
Third Field - Source of YSNP testing - NGS (Big Y or YElite), YSEQ (tested at YSEQ), L226 (L226 SNP pack), Z253 (older Z253 SNP Pack), Indiv (individually tested at FTDNA as well as many other older testing options such as NATGEO) and BLR (not YSNP tested but predicted L226 via binary logistic regression - the math that tracks YDNA testing).

All signatures are based only on the tested submissions. Signature matches and genetic distance are used to predict YSNP assignment.

Signature matches of predicted submissions are the number of mutations shared by the closest matching tested submission and the predicted submission. Genetic distance is the genetic distance between the closest tested submission and the predicted submission.

Note: Since the fastest mutating markers, CDYa/b are not included in this analysis, the signature matches and genetic distances have been lowered for accuracy ratings.

This analysis now predicts around 87 % of the known L226 submissions due to recent extensive testing via L226 SNP packs and Big Y testing.

Note: The “Quality Ratings” are currently only estimates and will be adjusted. If automated via coding, regression testing with and without tested information could adjust the ratings based on how well the model predicts vs. actual test results.

Note: The genetic distance adjustment for “Quality Ratings” will also need to be adjusted over time as well. Very high genetic distances will need to be filtered out.

Boxes that are light purple are YSNP boxes (that can also include YSTR mutations). Boxes that are blue-green are those testers that have been YSNP tested (if tested robustly enough, they are used for YSNP prediction of other testers not YSNP tested). Boxes with no color are YSTR only mutation boxes.

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Legend for
TMRCA estimates

For the first time (June, 2019), I have added TMRCA time estimates in two flavors: 1) YSNP based branches based on 60 years per YSNP mutation; 2) surname clusters (finding five surnames variants in any branch that are 50 % or more for the surname).

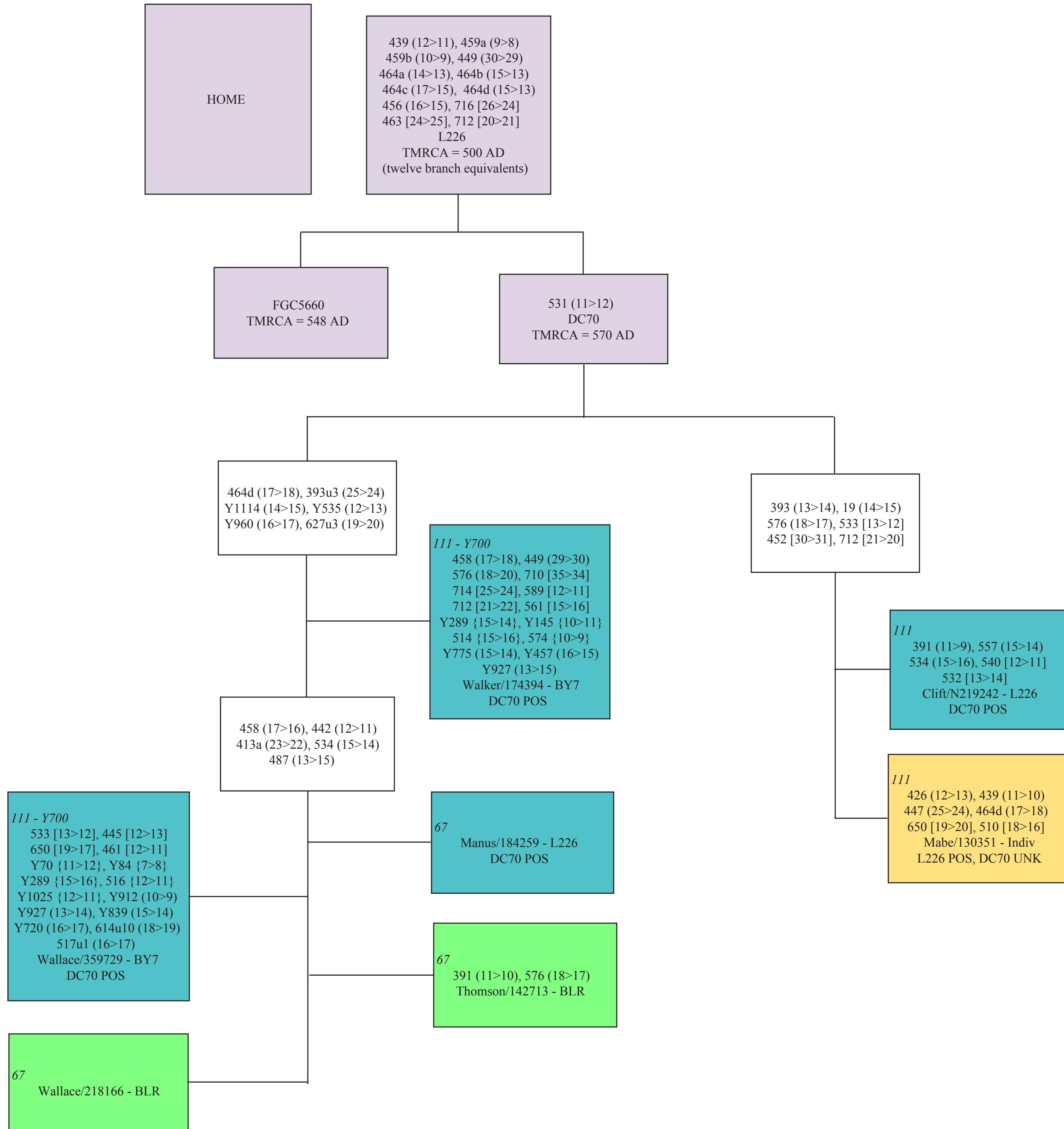
This first pass takes a very simplistic approach to surname clusters - you have at least five testers with the same surname to create a surname cluster and any YSTR or YSNP branch and must have over 50 % of testers with this surname. All reasonable surname variations are included. All YSNP branches below surname clusters revert back to 60 years per YSNP.

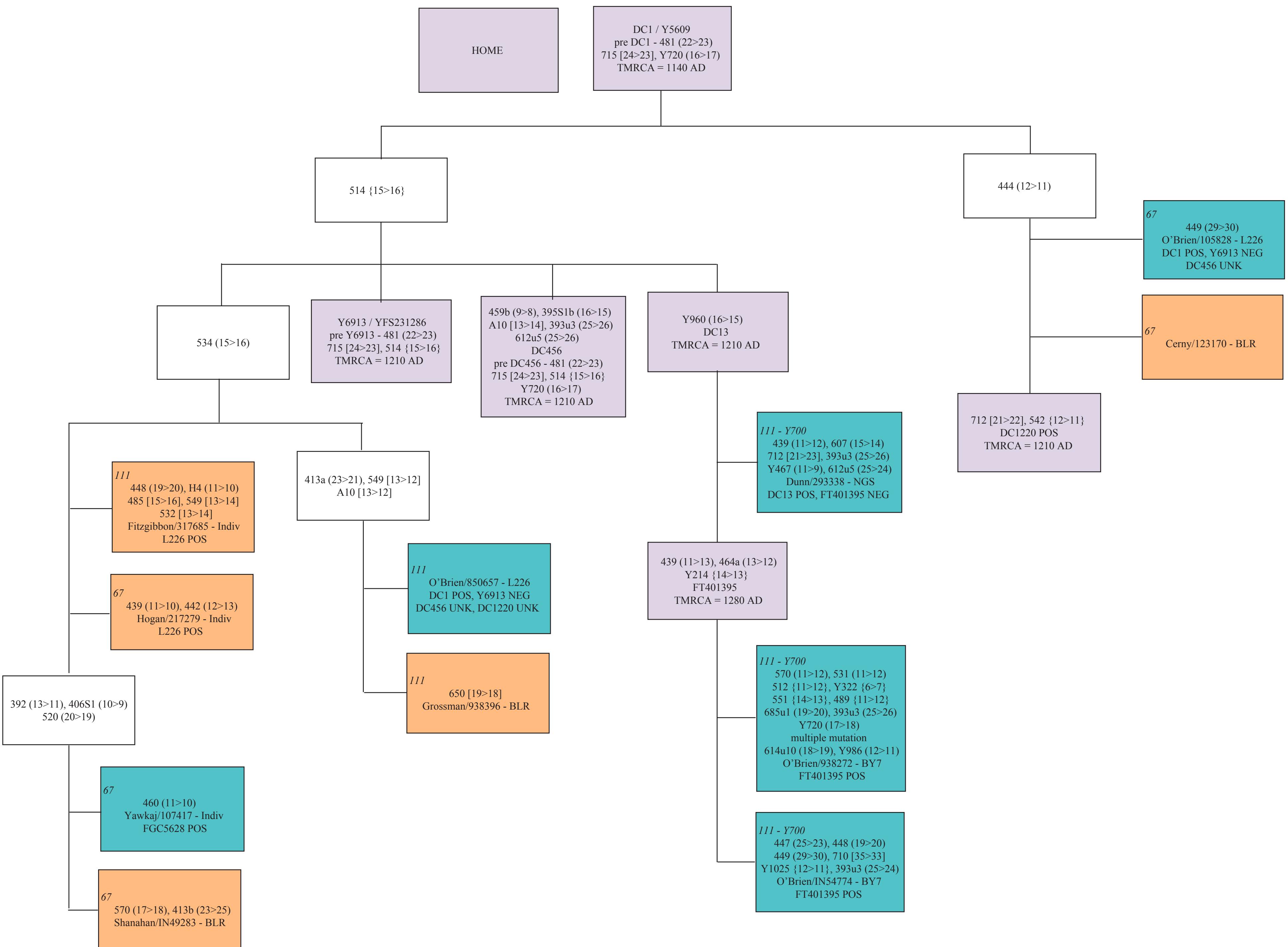
I also attempted my first pass on putting real dates vs. age of the events (years before present). I assumed that the average tester was born around 1960 and used the simplistic formula: Date = 1960 - (1500 - (YSNP level x 60)). Unfortunately, this results in L226 being 460 AD vs. 500 AD and may need some fine tuning in the future. Also, the estimate date for L226 continues to change as more L226 equivalents are converted to be branches just above L226.

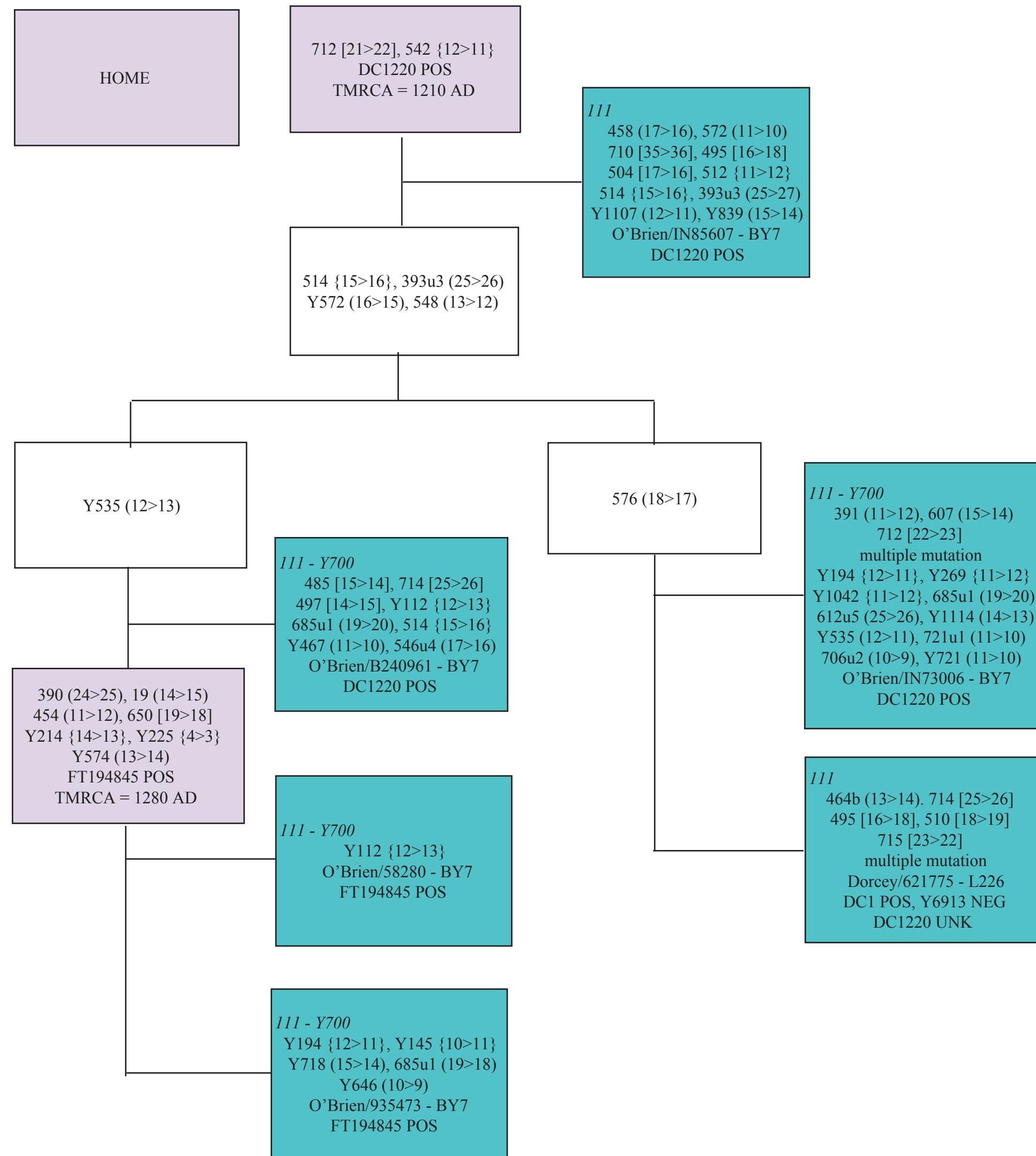
I have also been investigating variable dates on surname cluster dating (changing 1,000 AD to vary from 900 to 1100 AD based on two factors - percent of testers having the surname and allowing up to three surnames to allow for early prolific NPE lines).

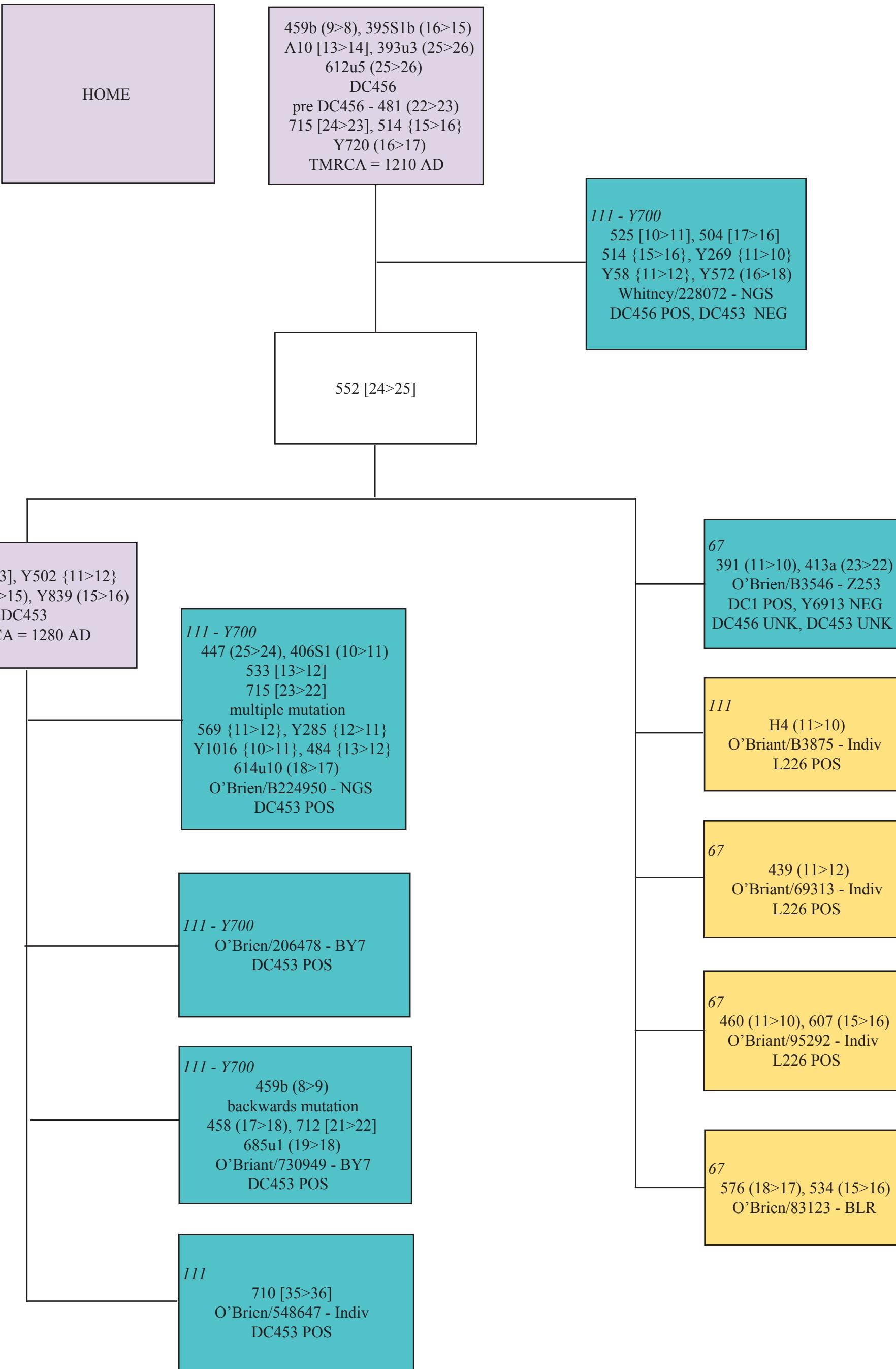
Also, I have experimented with YSTR branches for dating under the most recent YSNP levels and surname clusters. Unfortunately, the sample sizes are very small and the statistical variation is very large which will yield some very speculative dating.

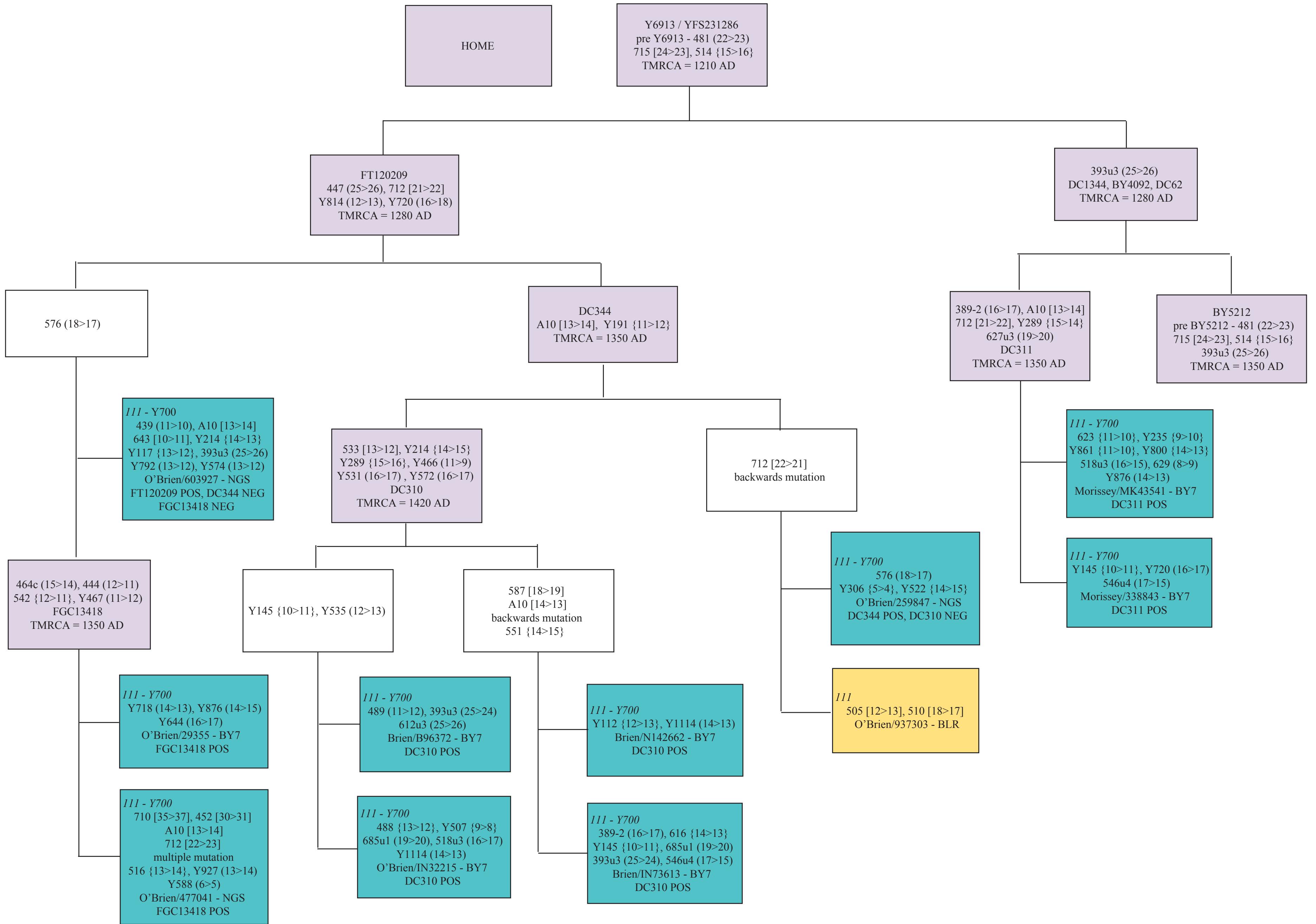
This more simplistic first pass is meant to get feedback on the base calculations. Future updates may fine tune the TMRCA estimate of surname clusters via tables and YSTR only TMRCA estimates may be added if I can figure out how to increase the reliability of these TMRCA estimates. I will not be constantly updating the TMRCA estimates as they would be very labor intensive to maintain.

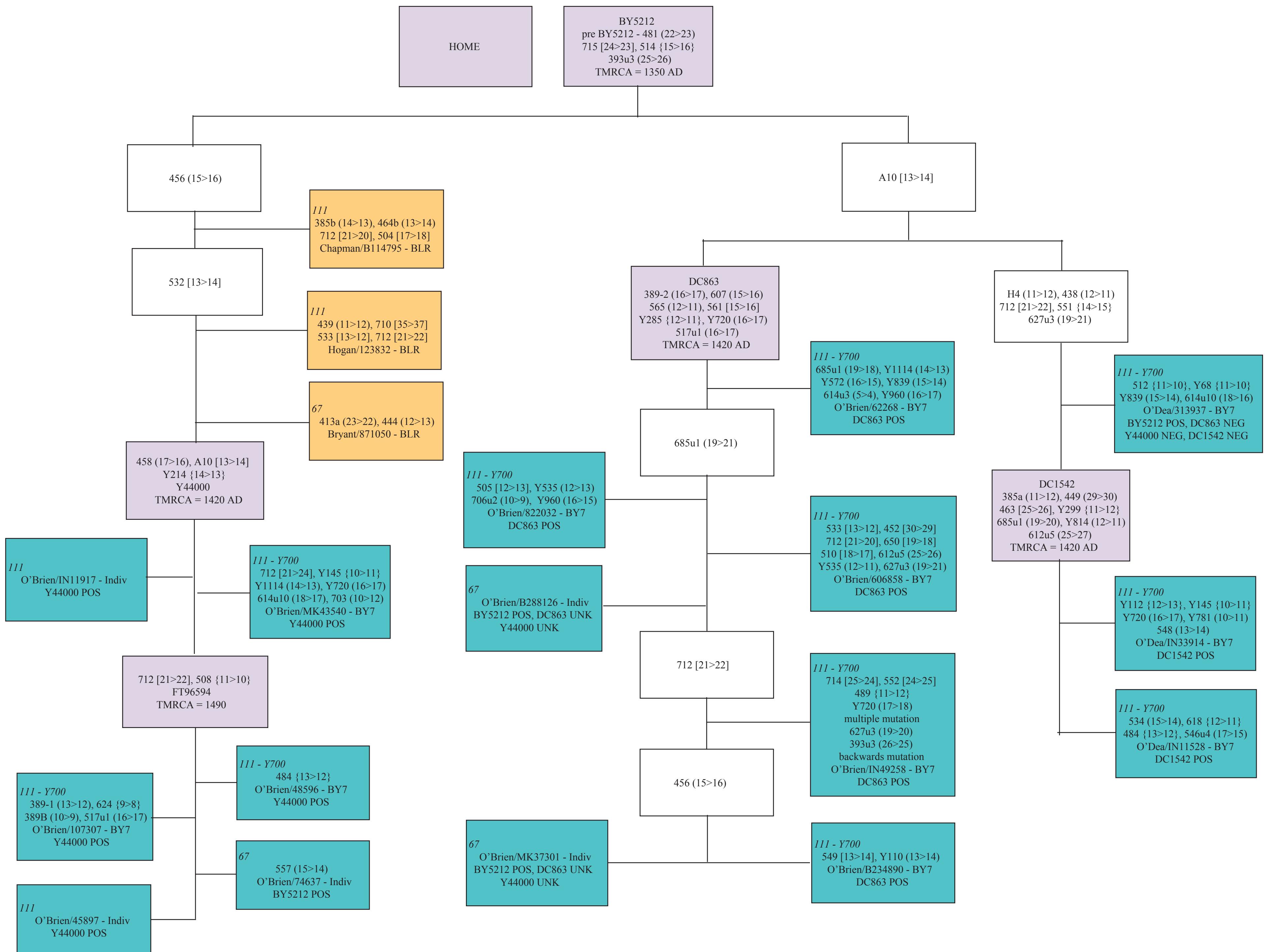


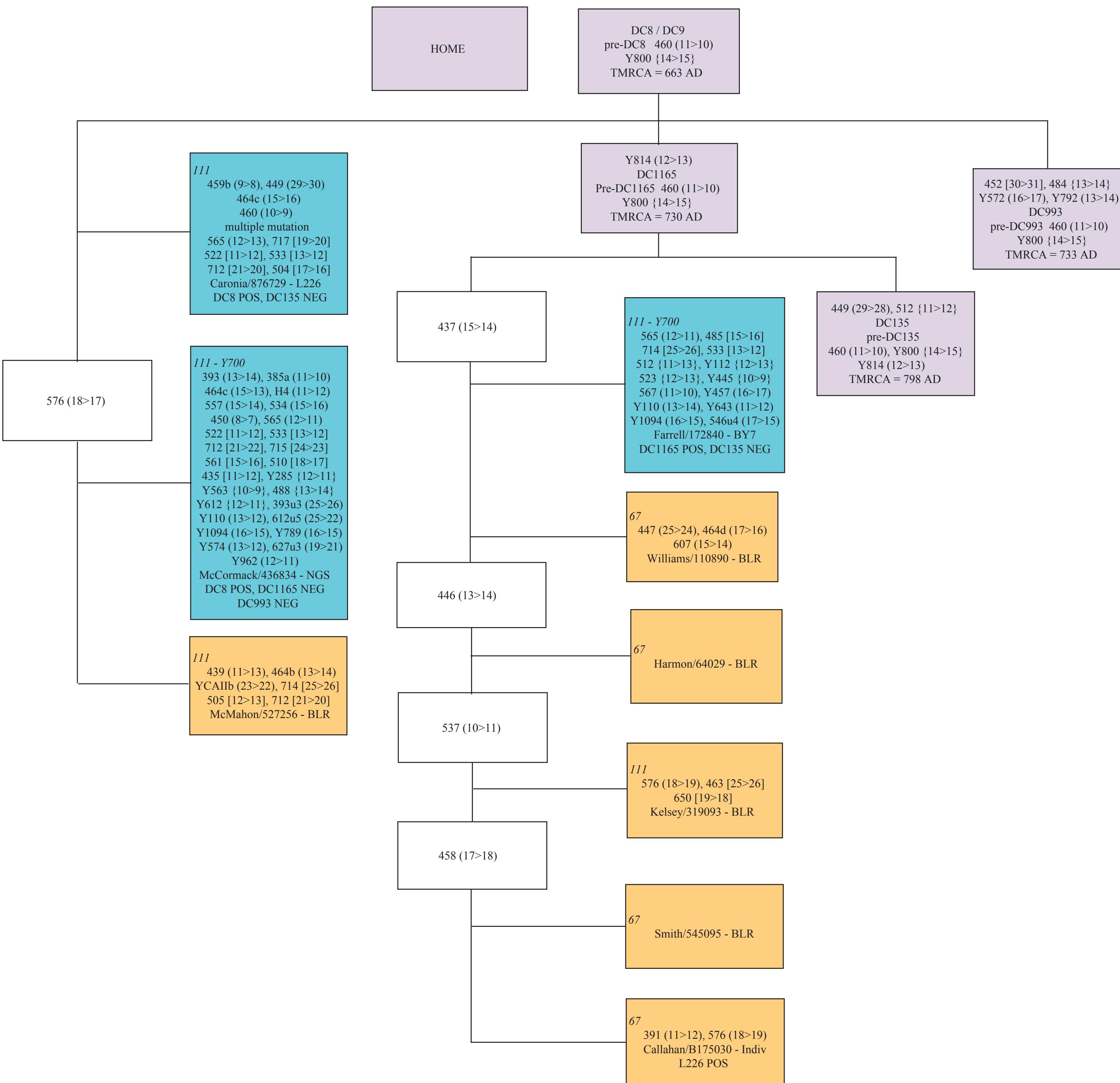


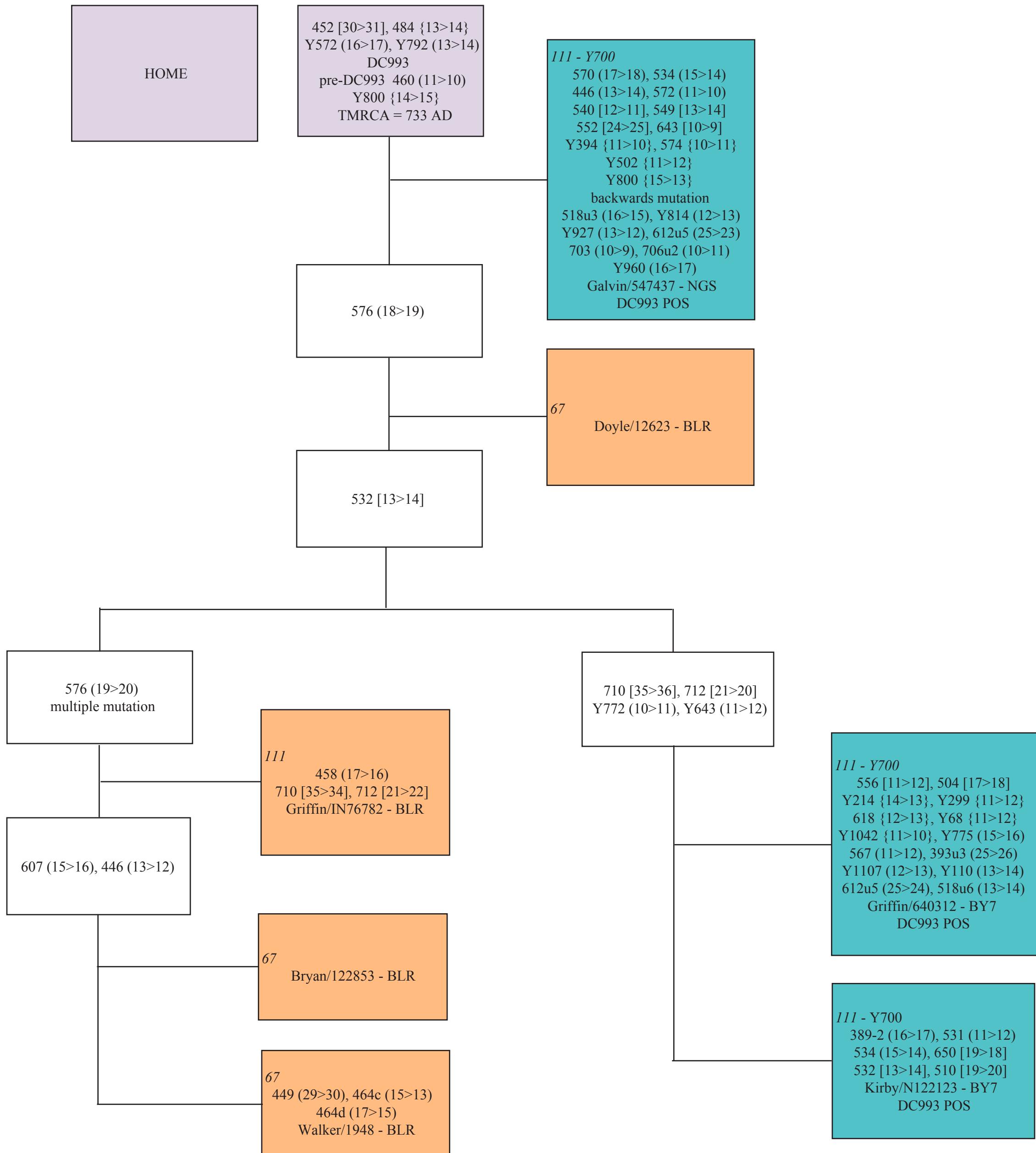


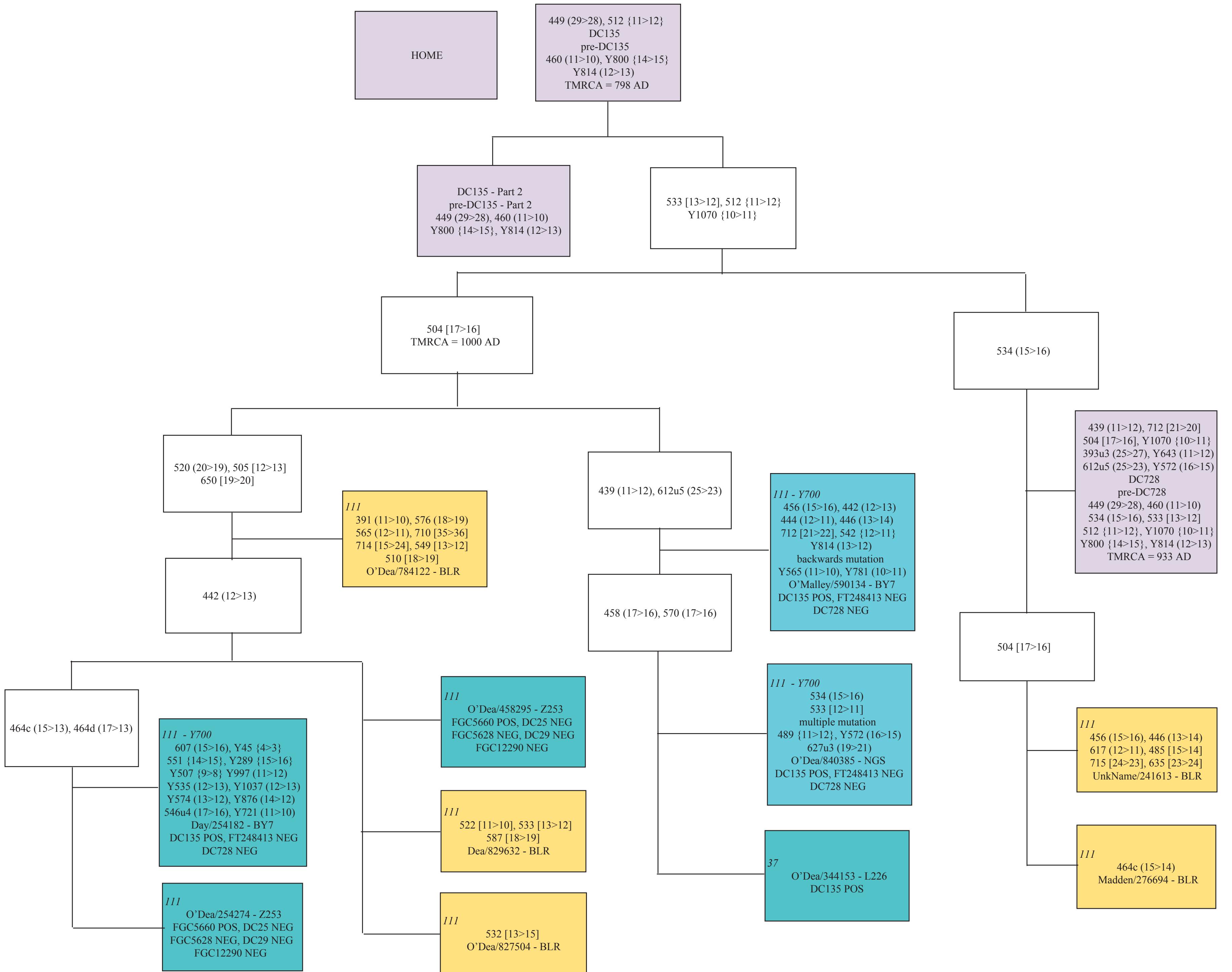


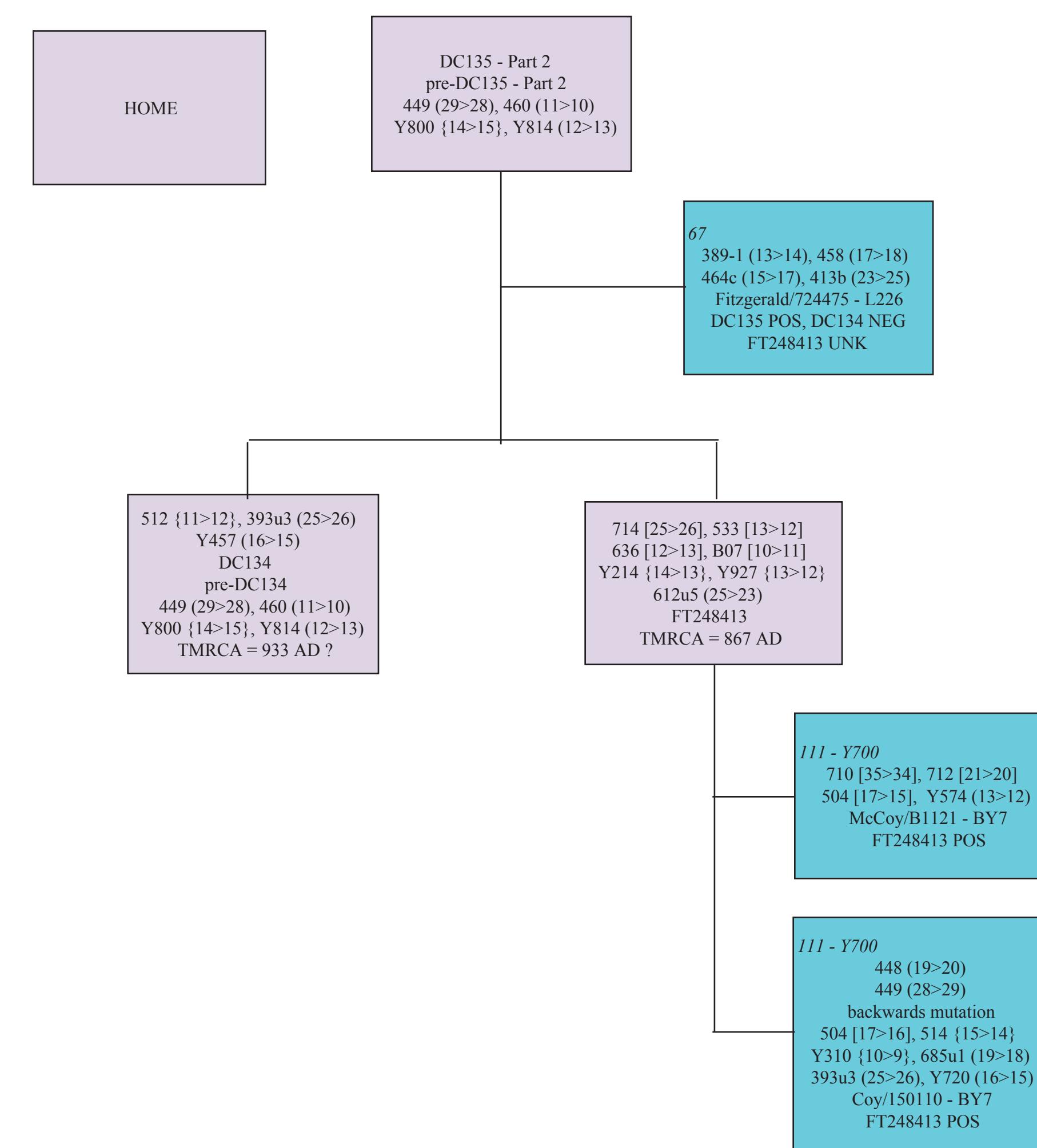


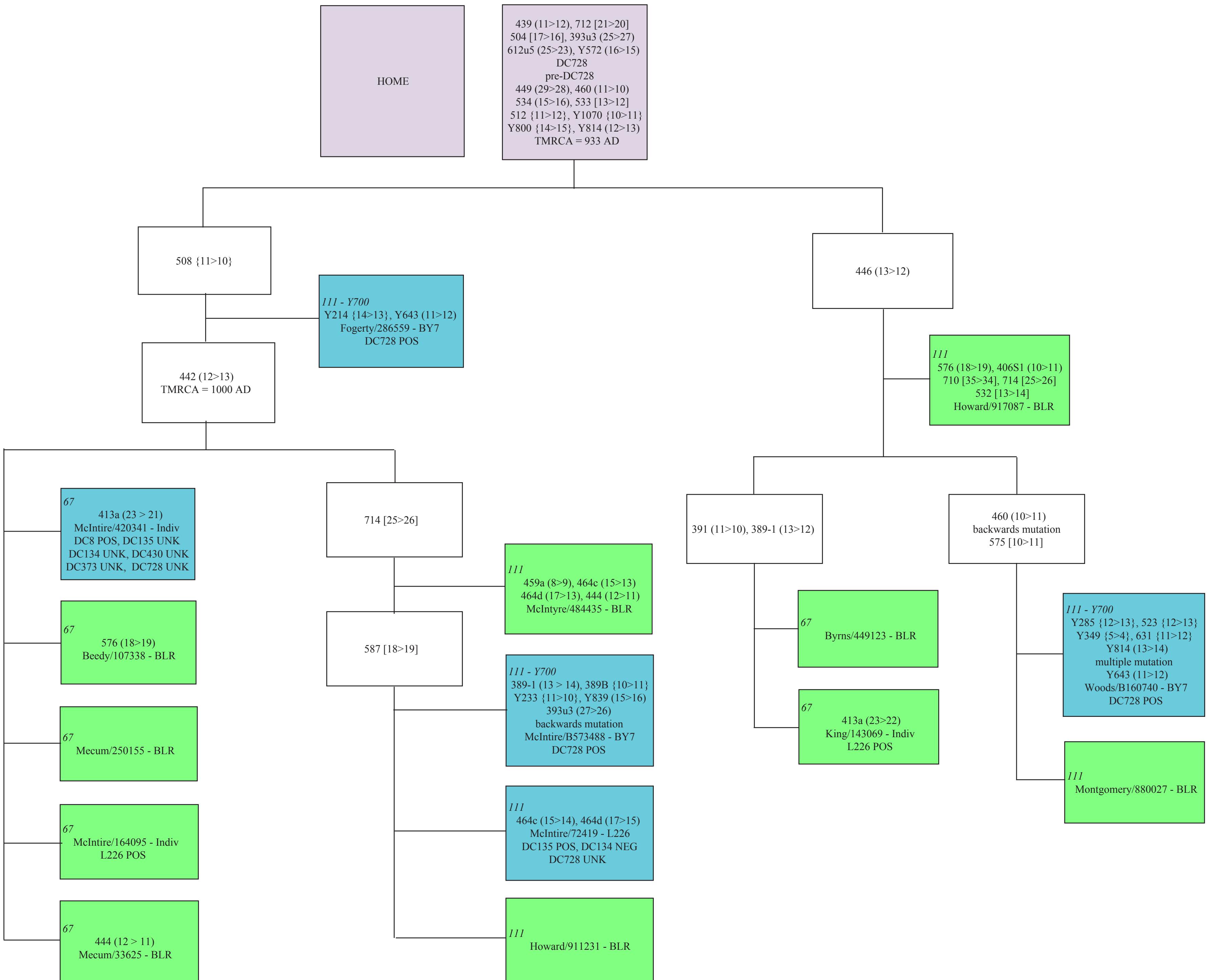


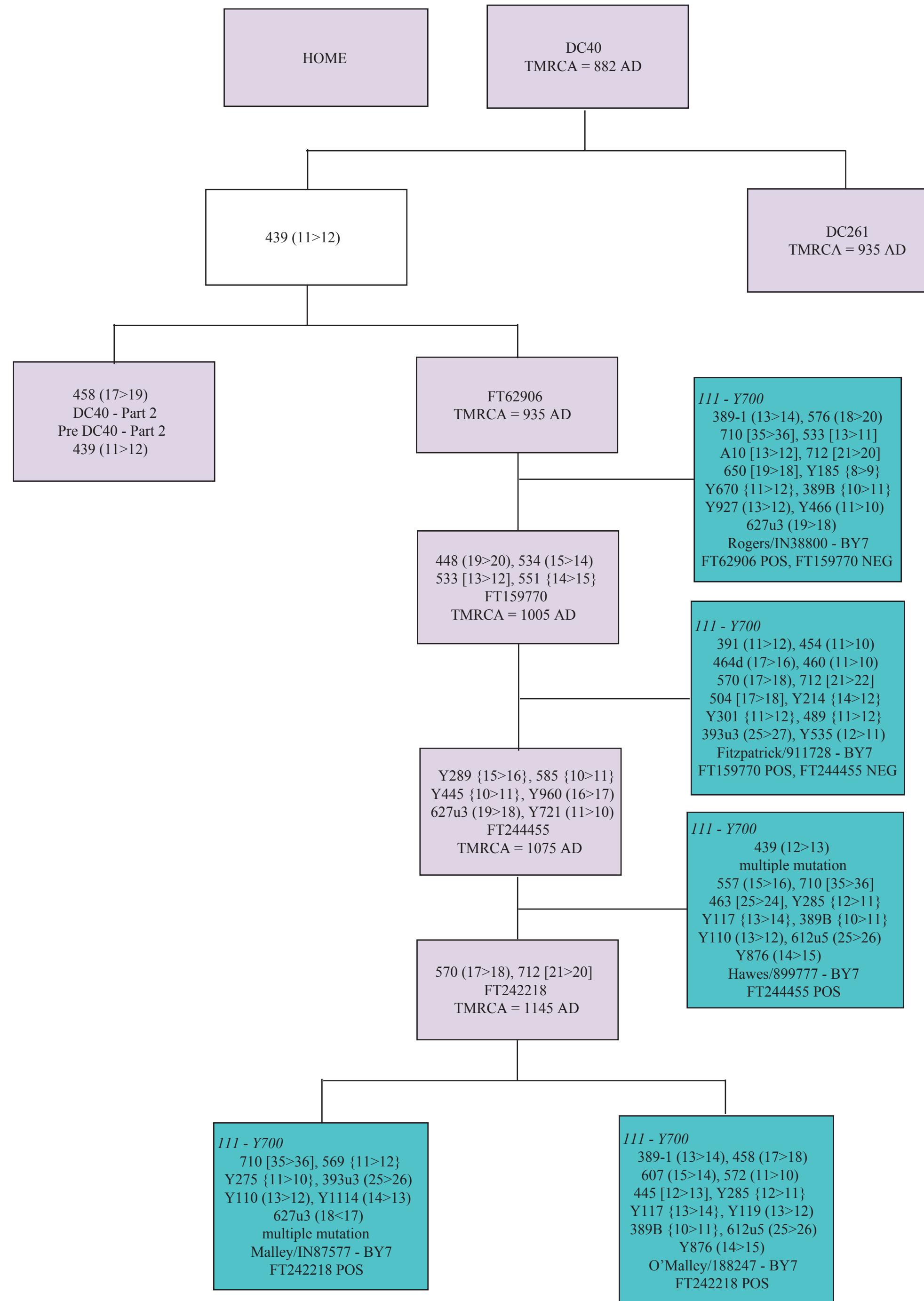


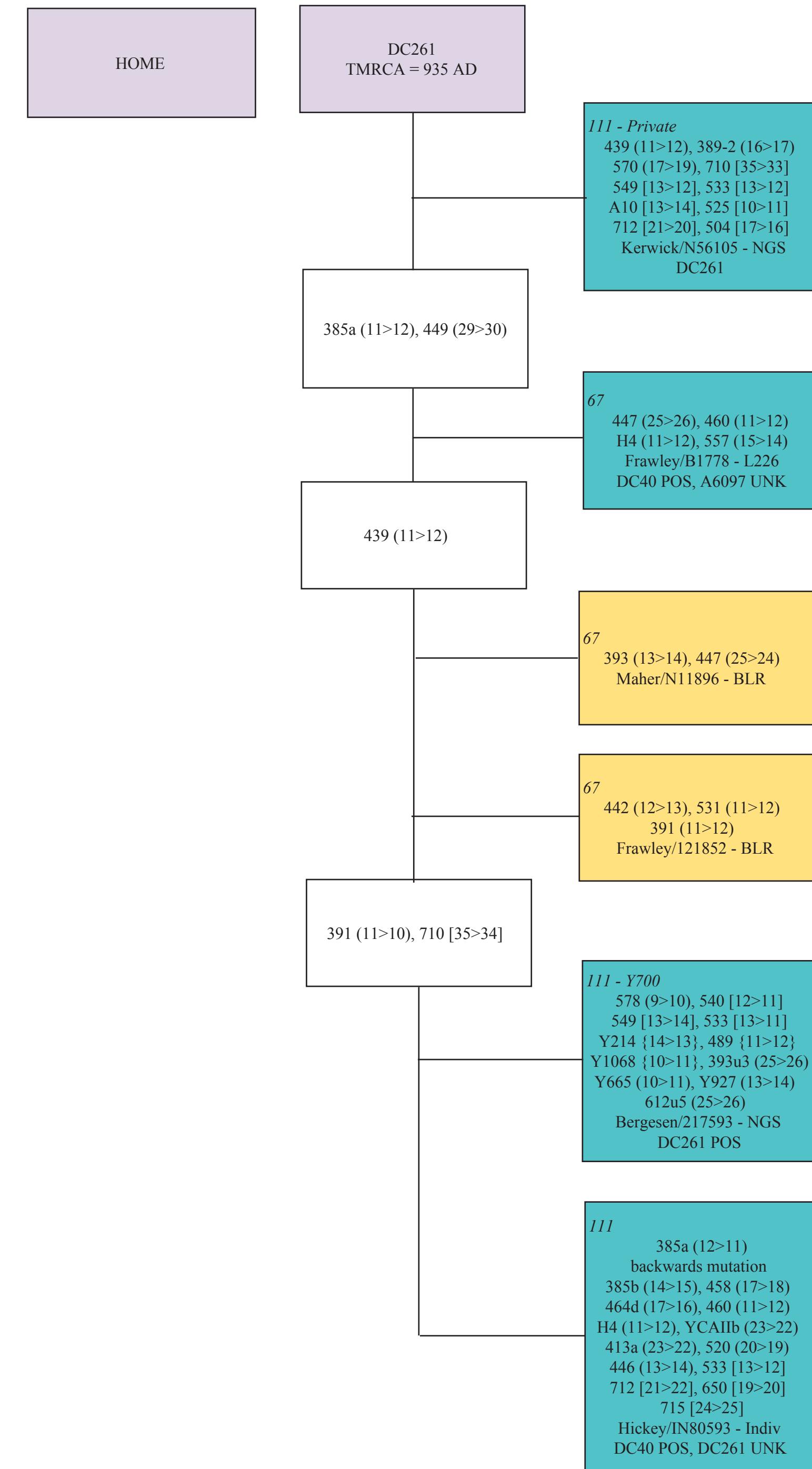


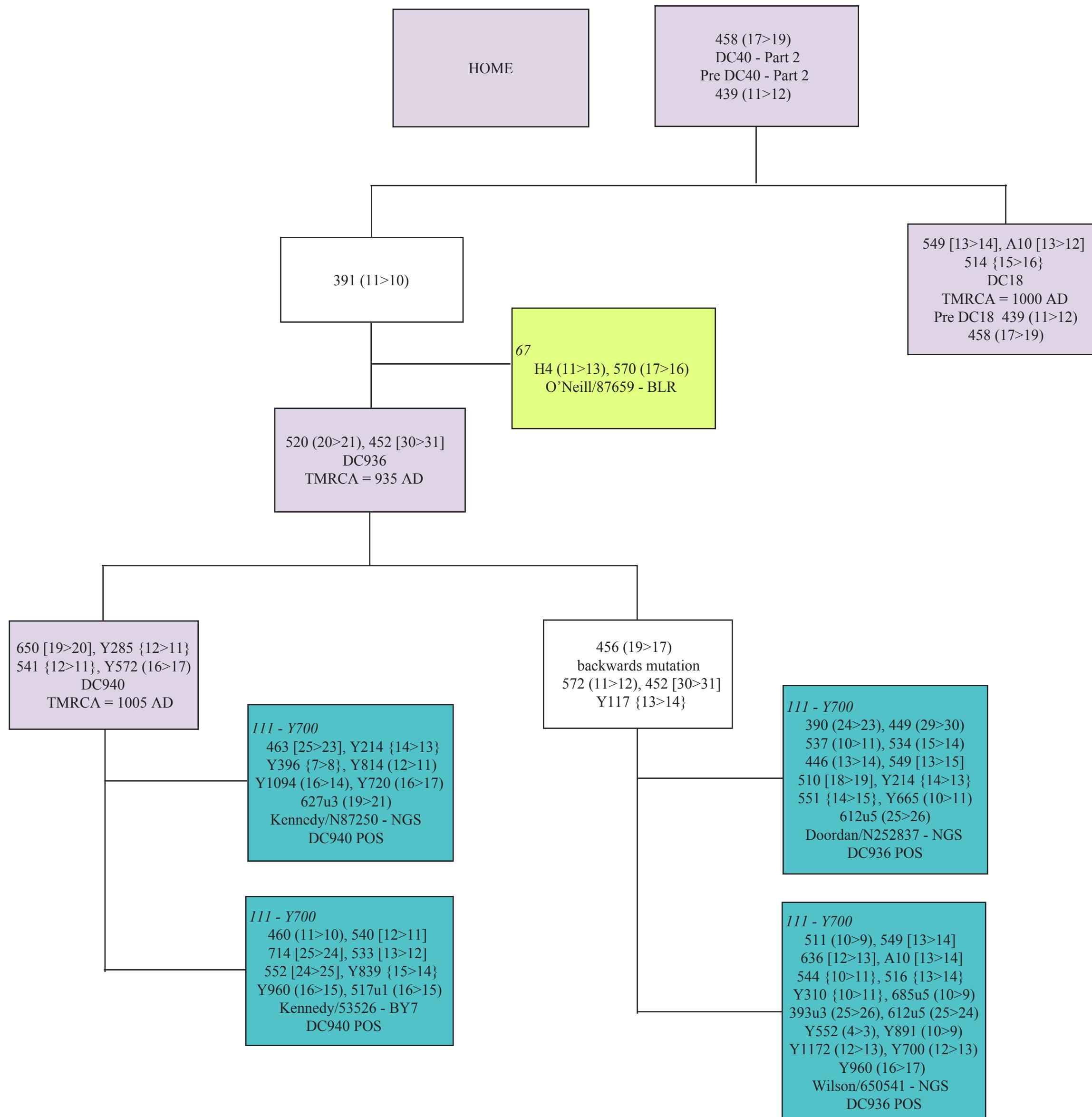


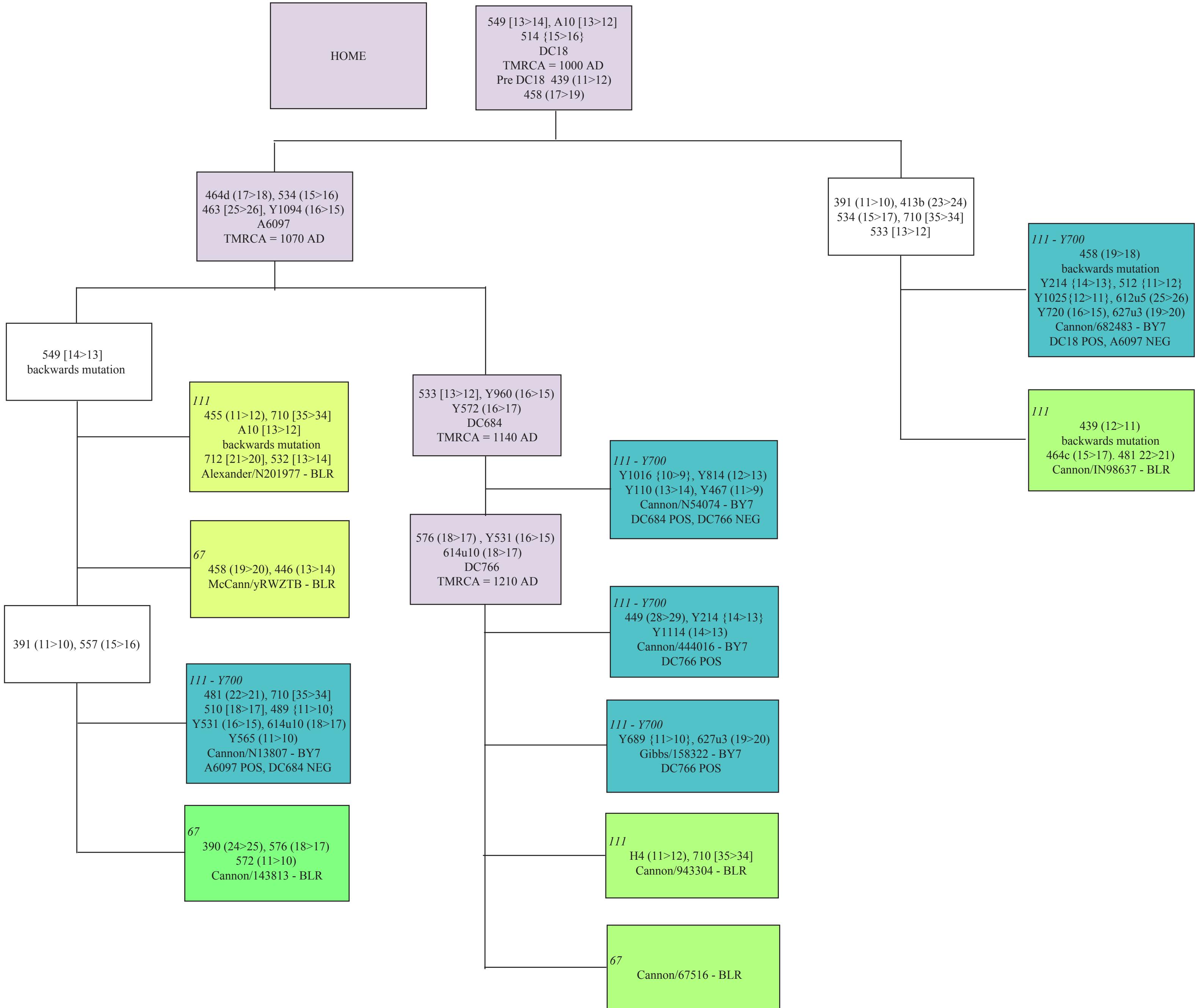


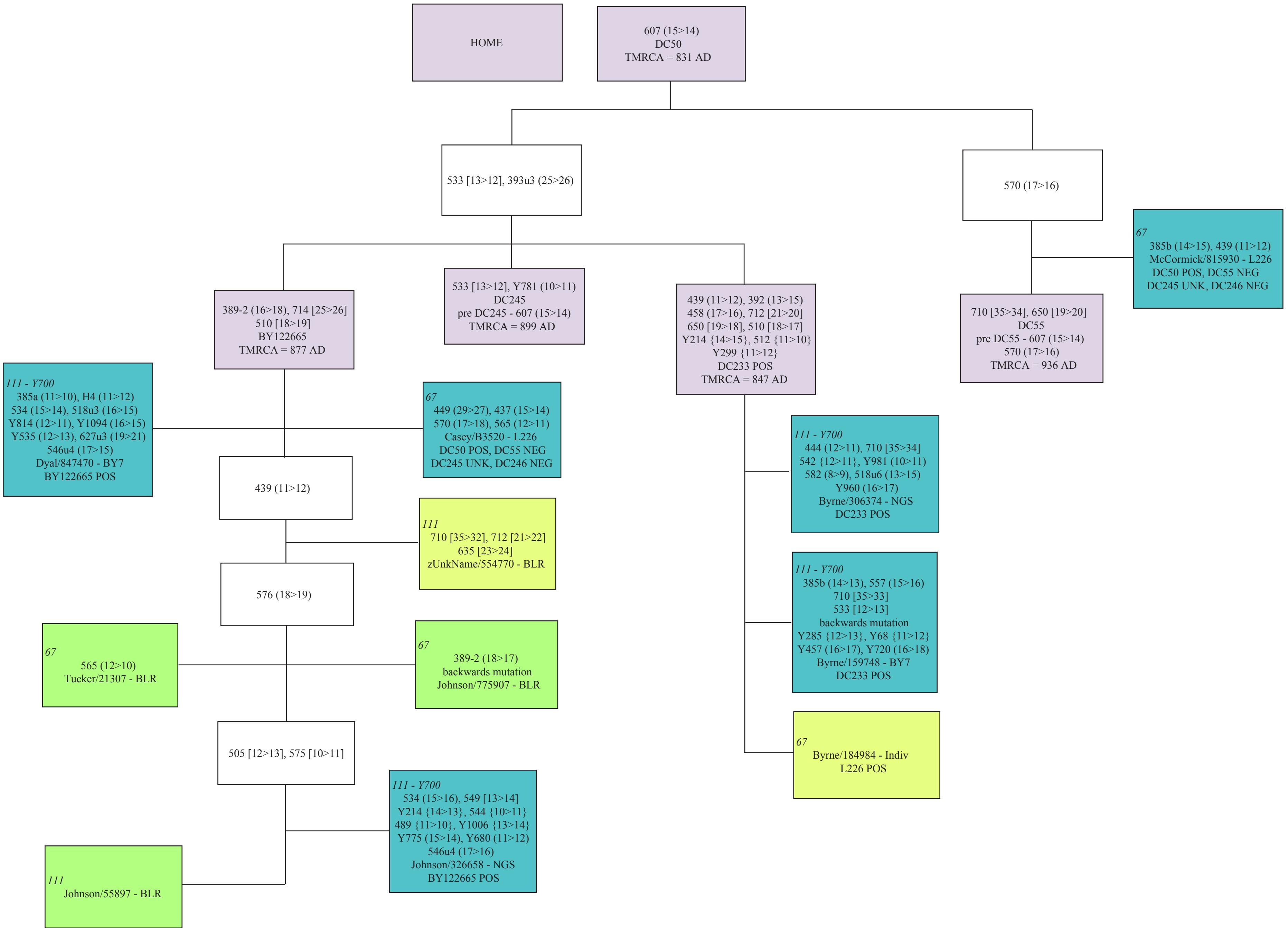


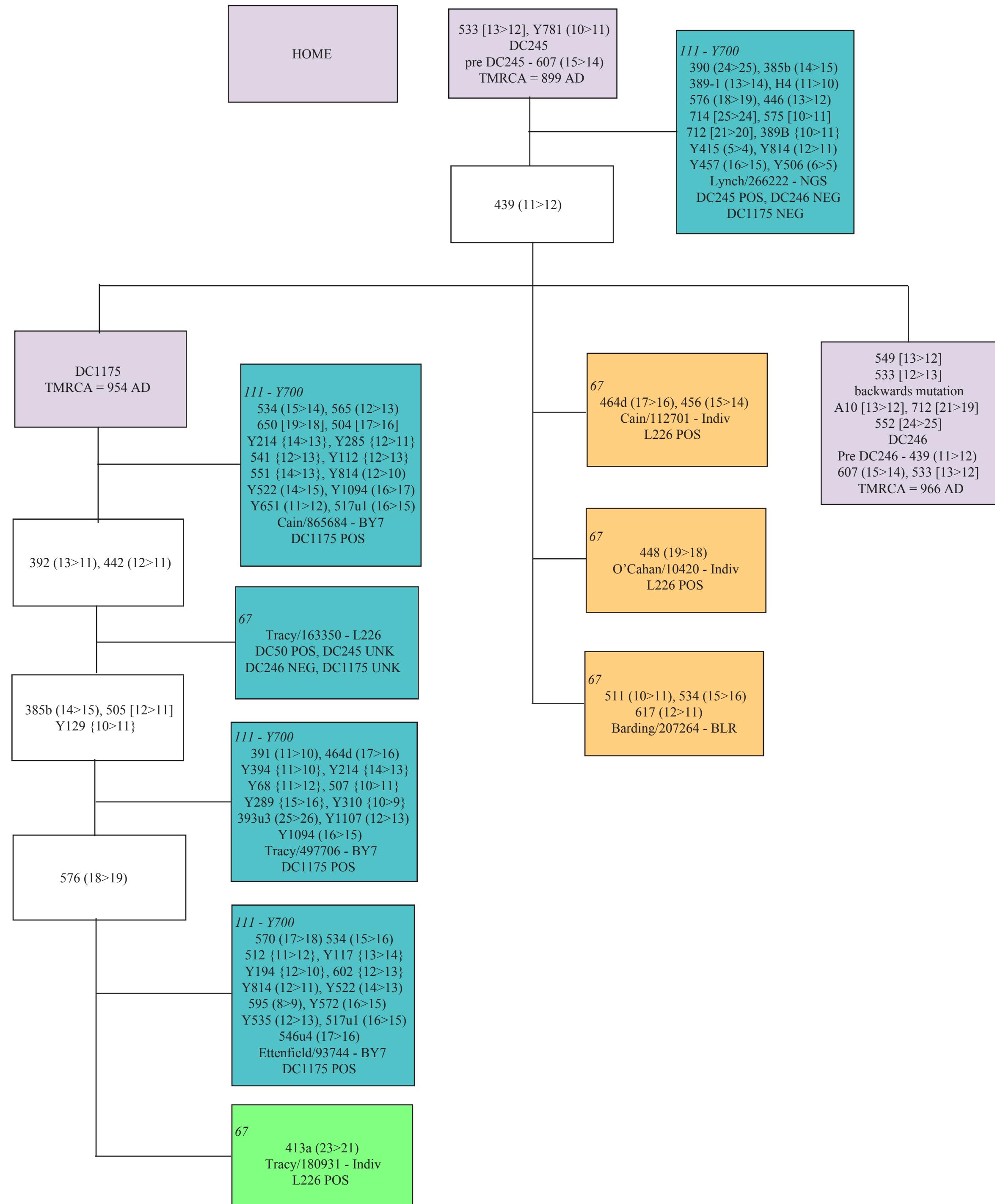


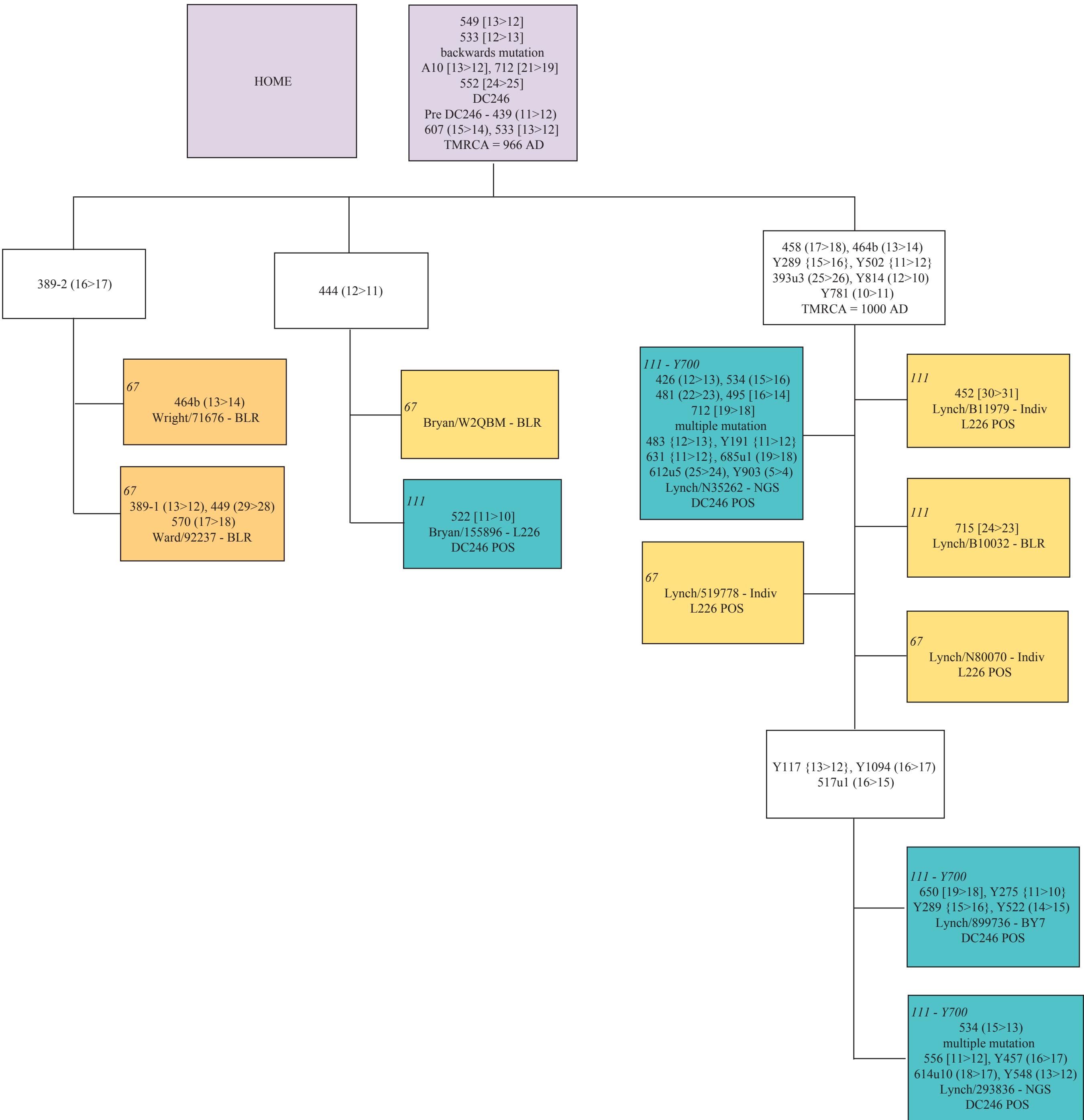


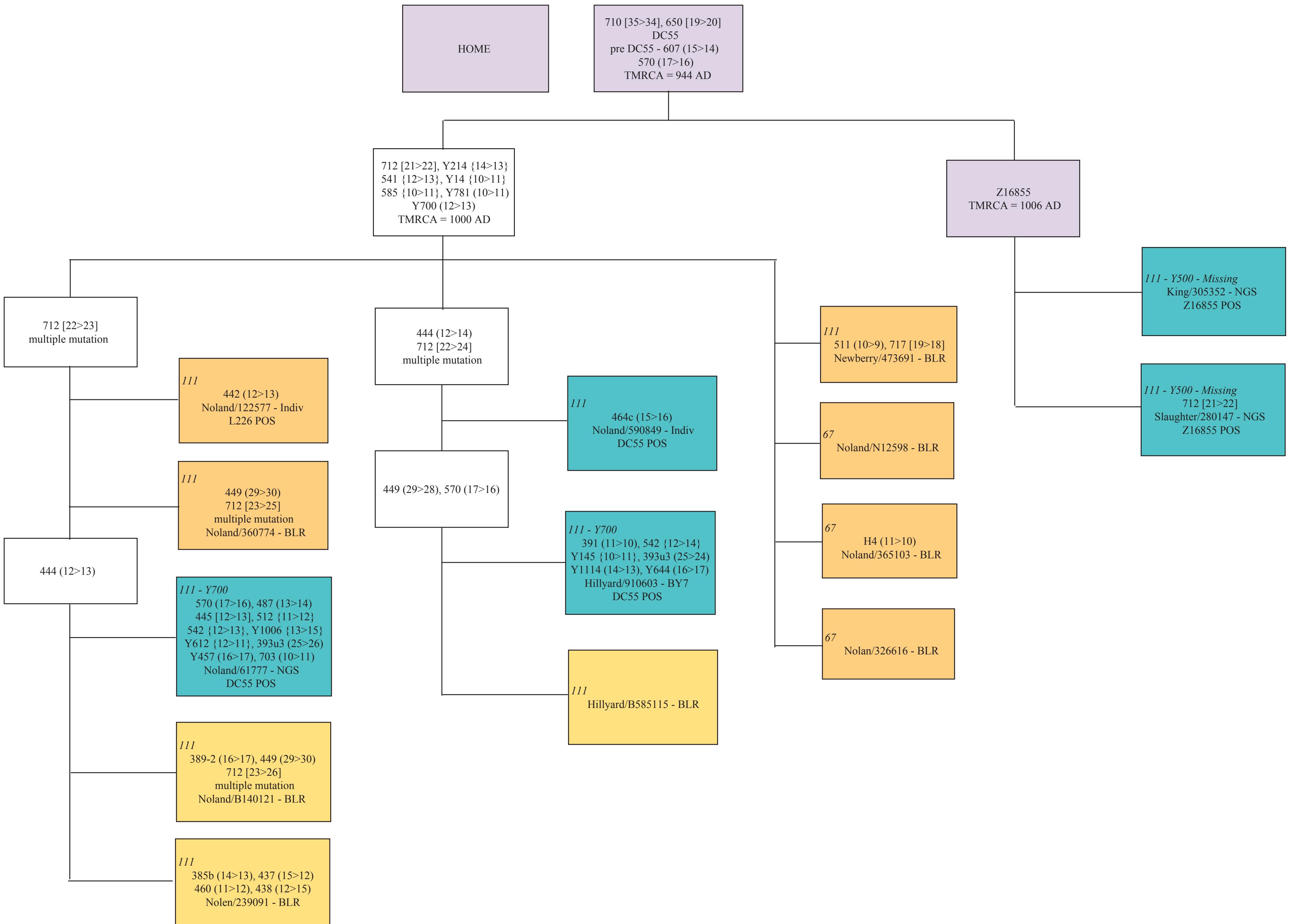


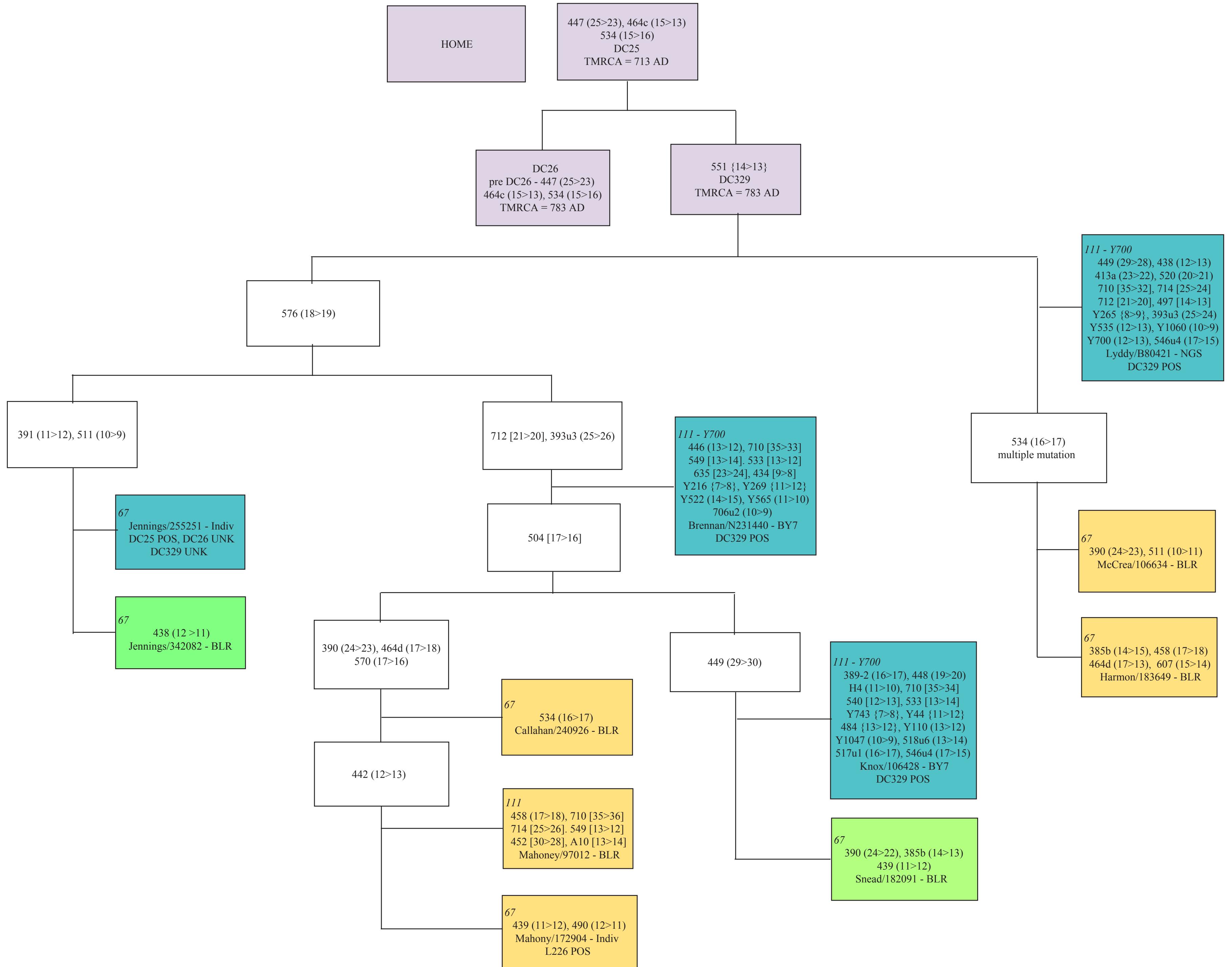


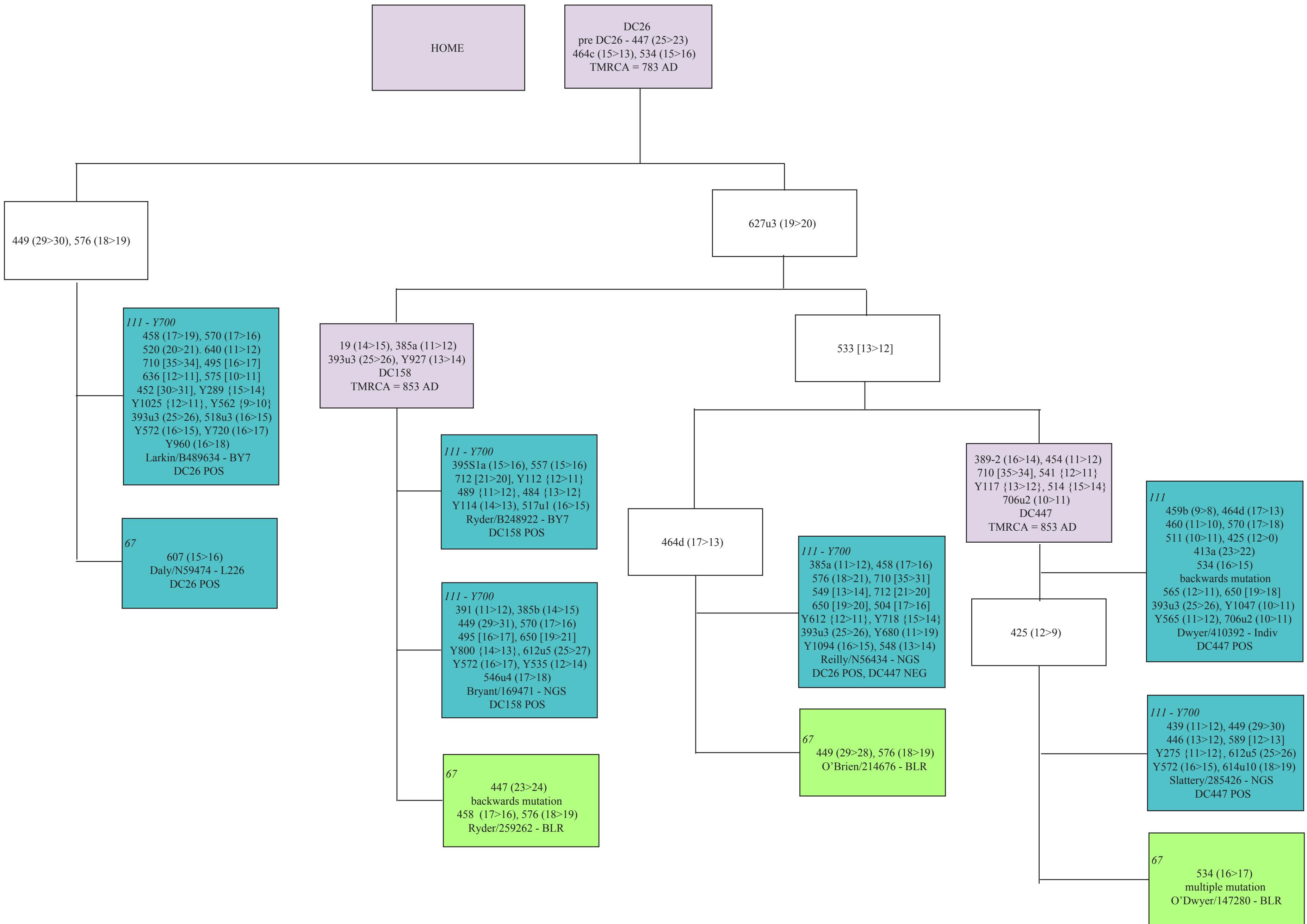


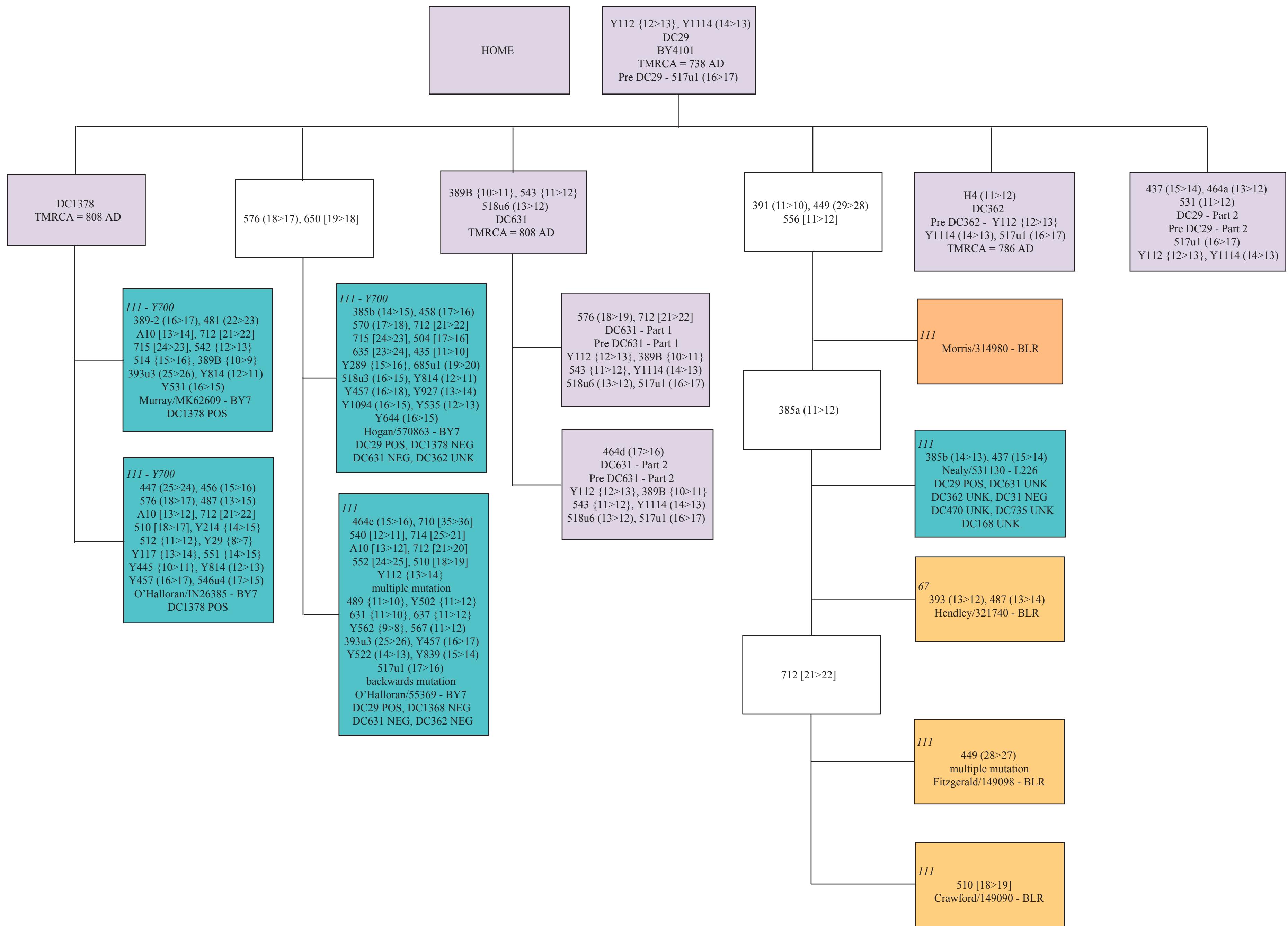


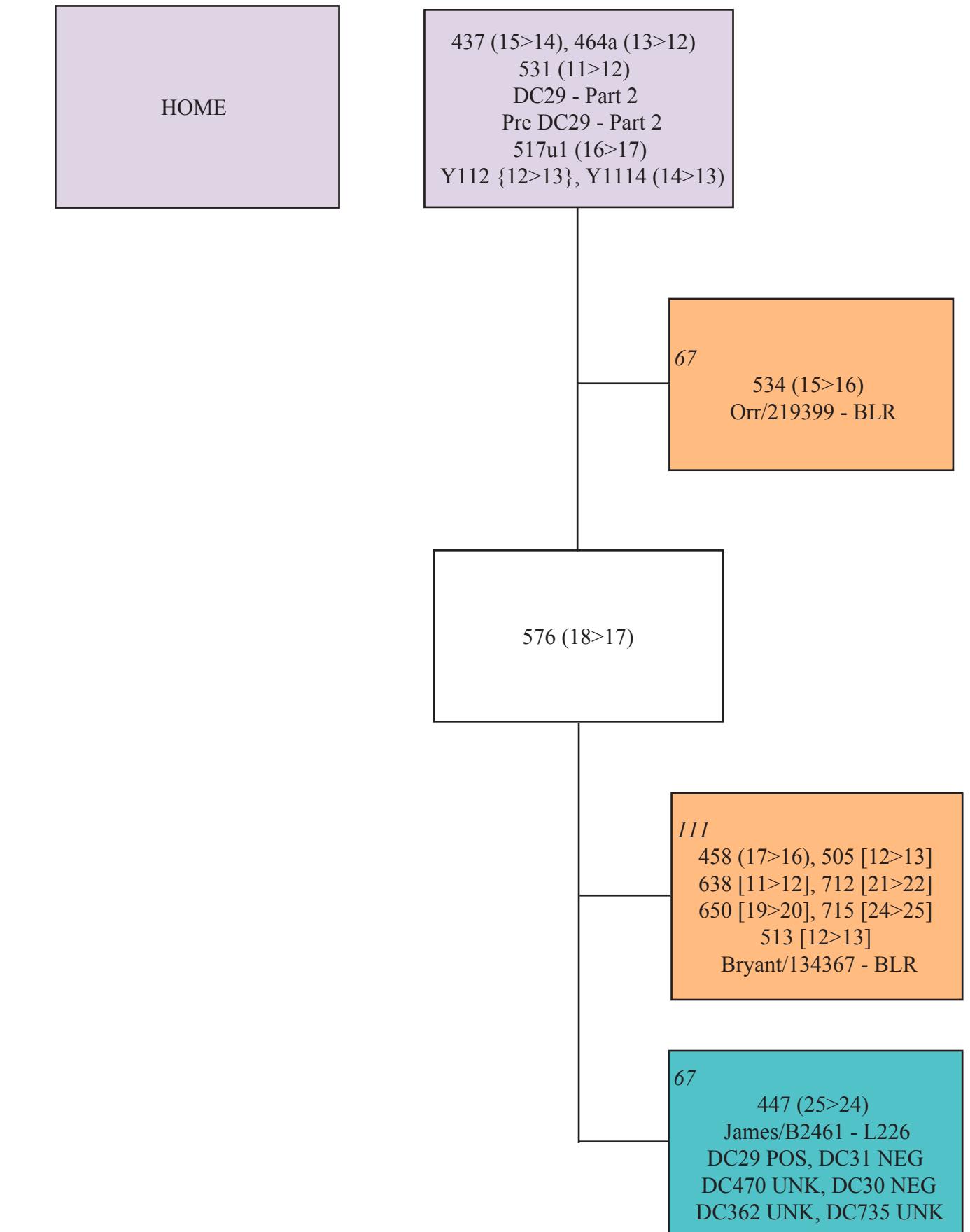


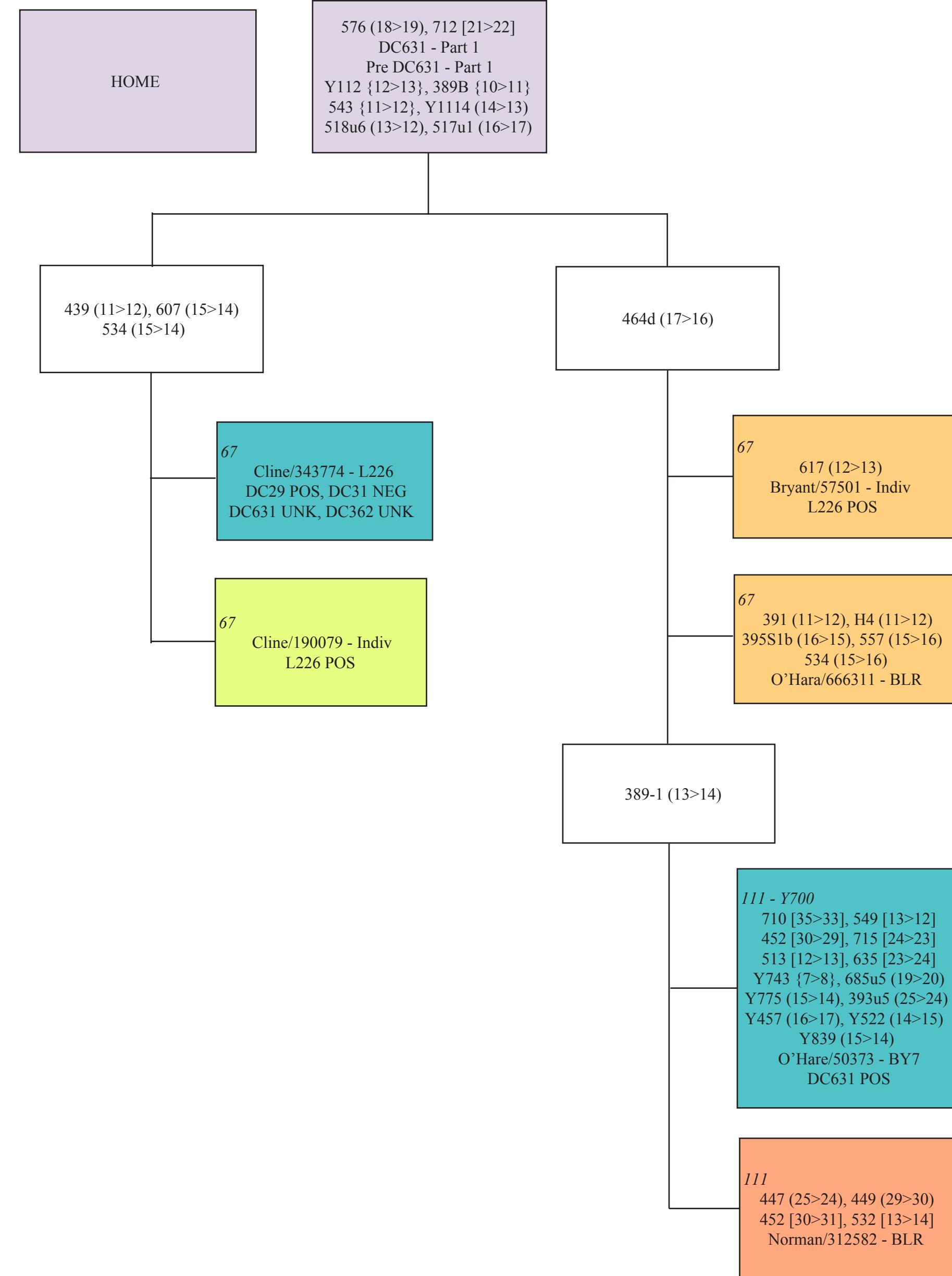


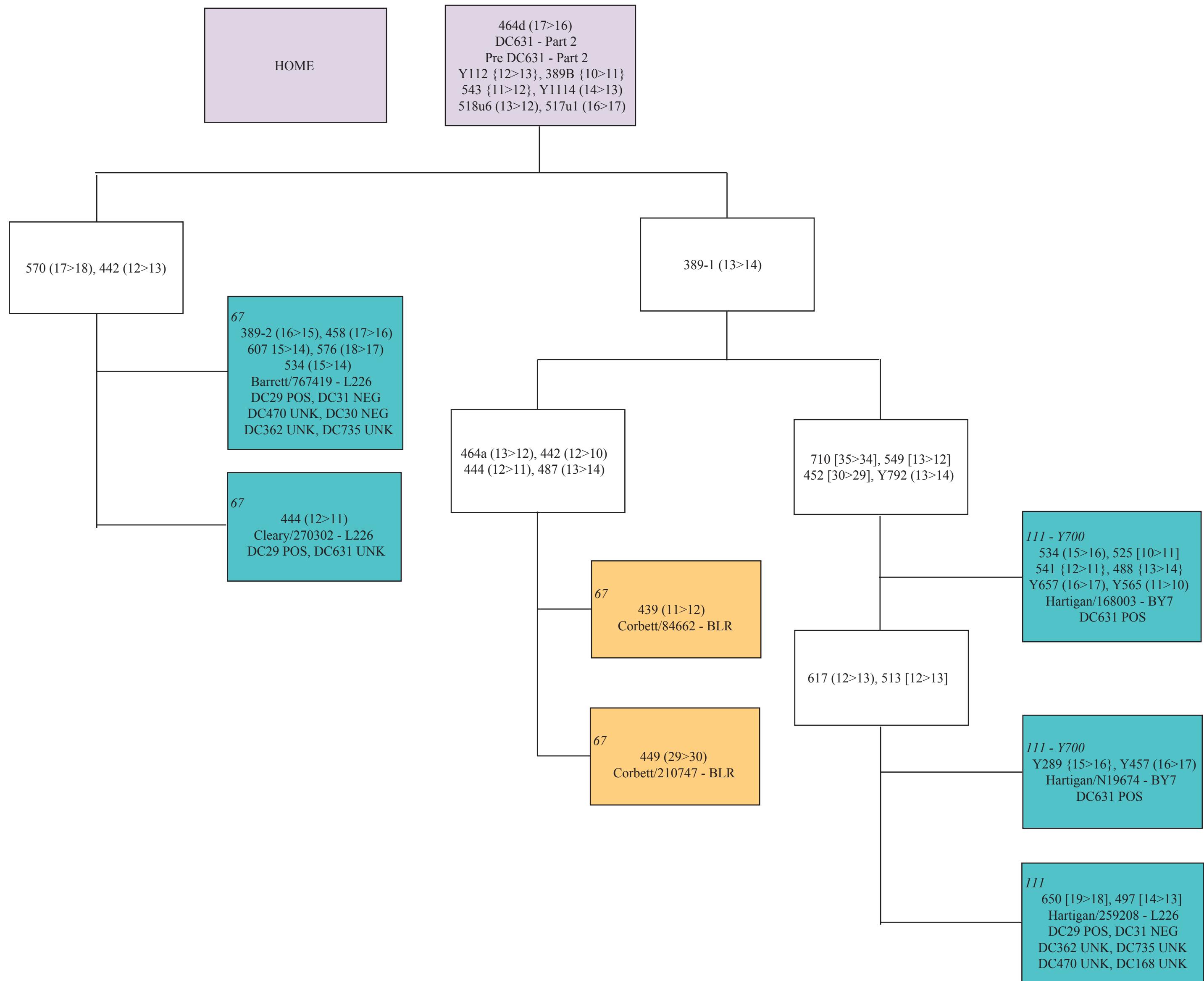


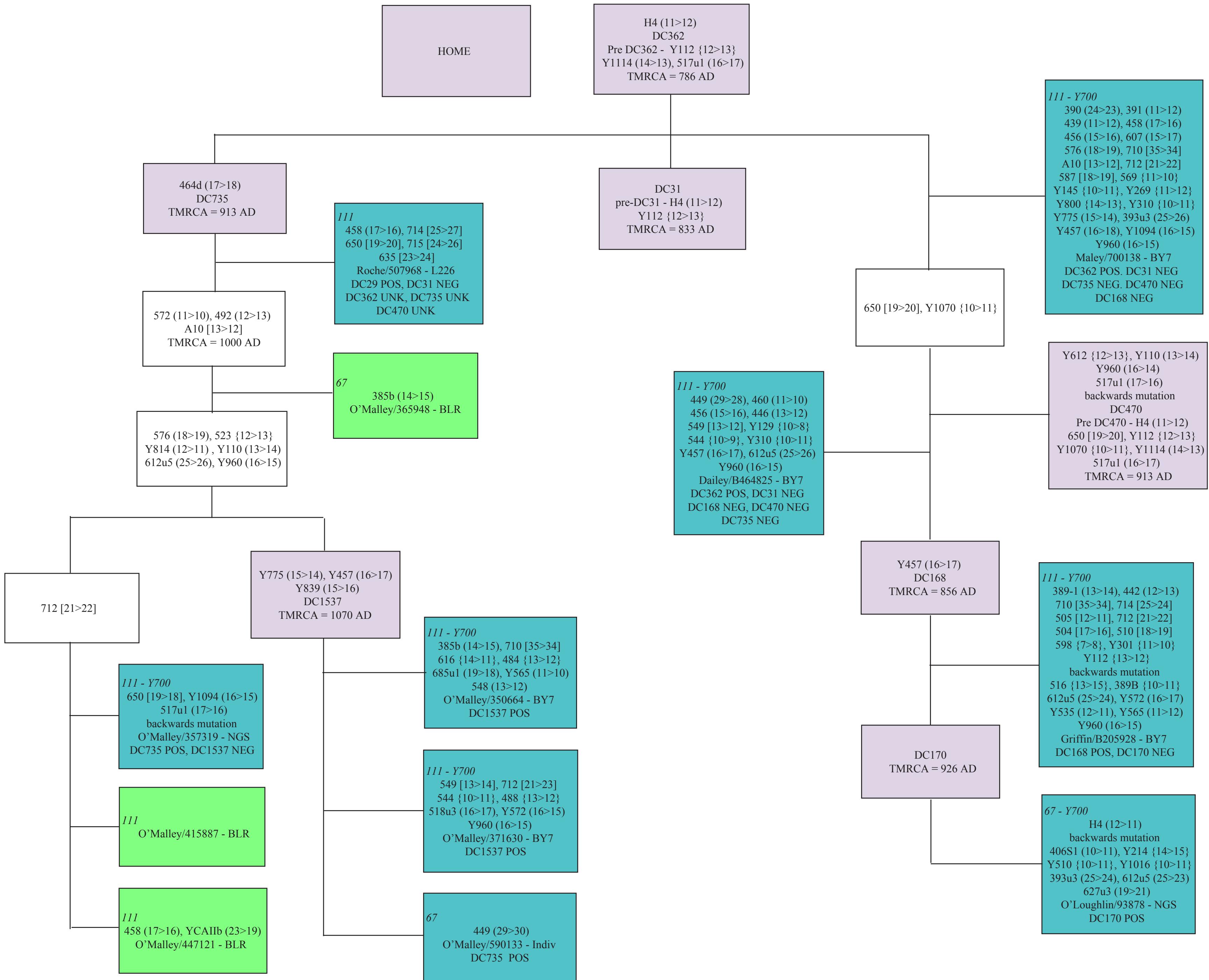


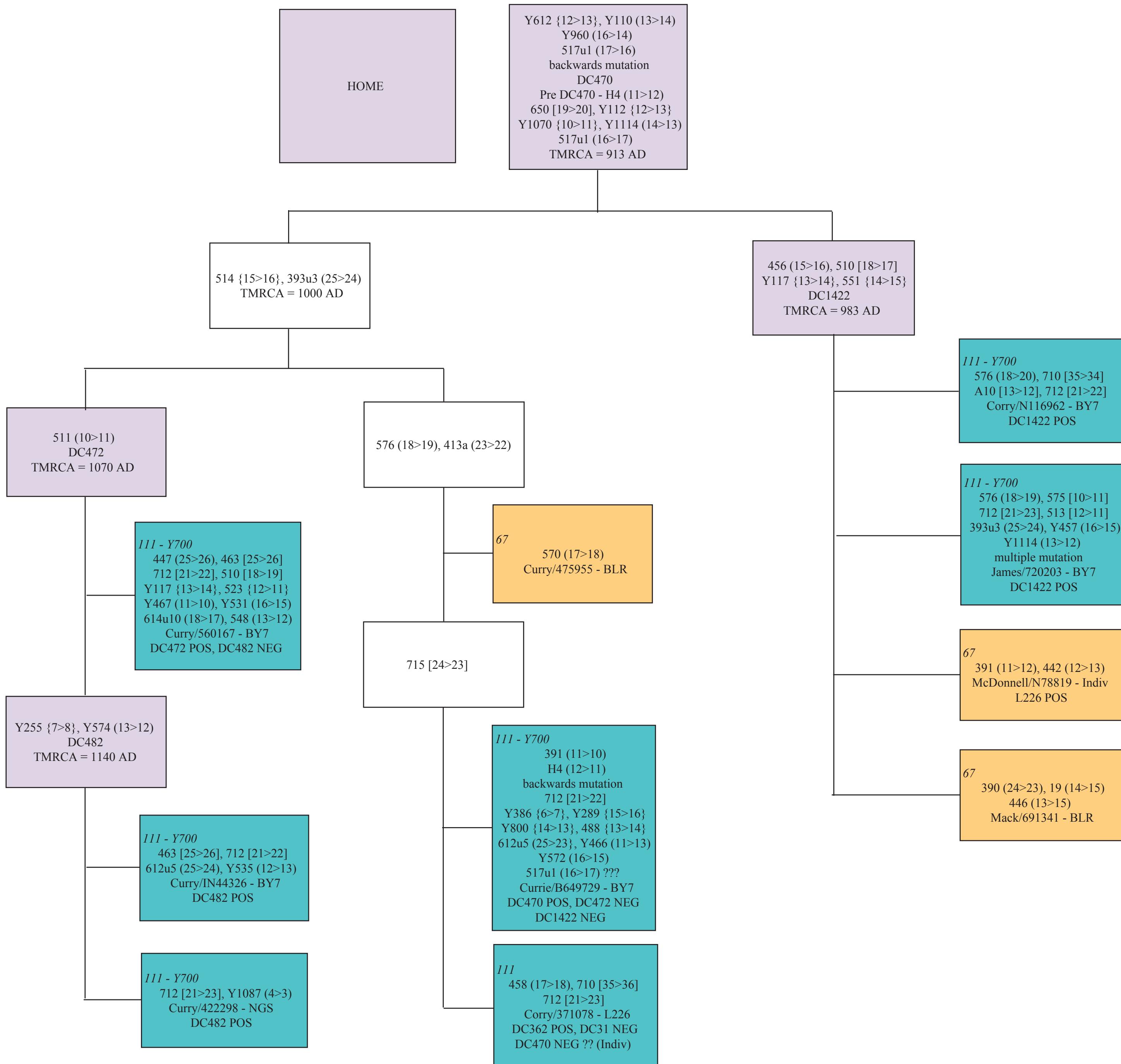


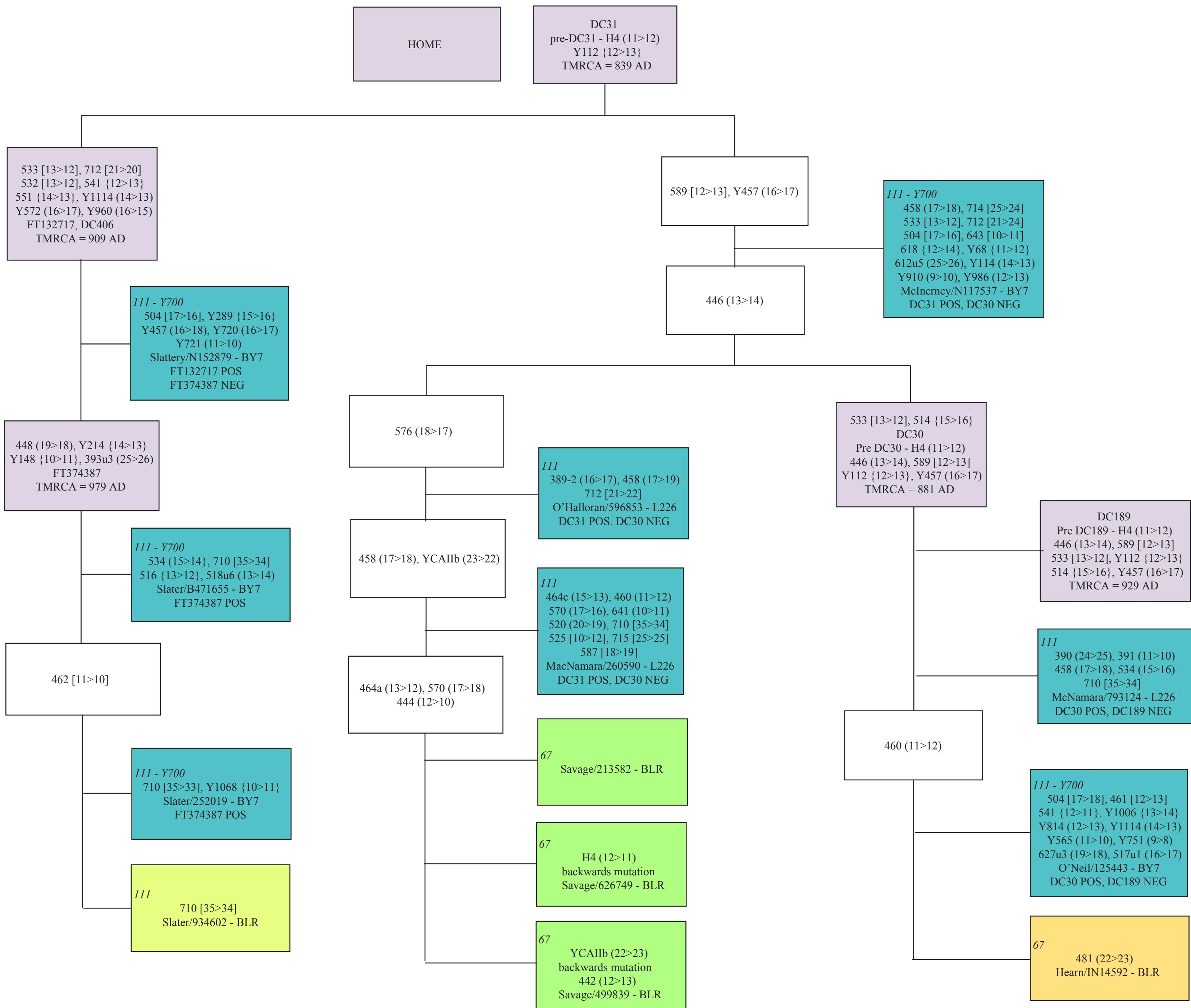


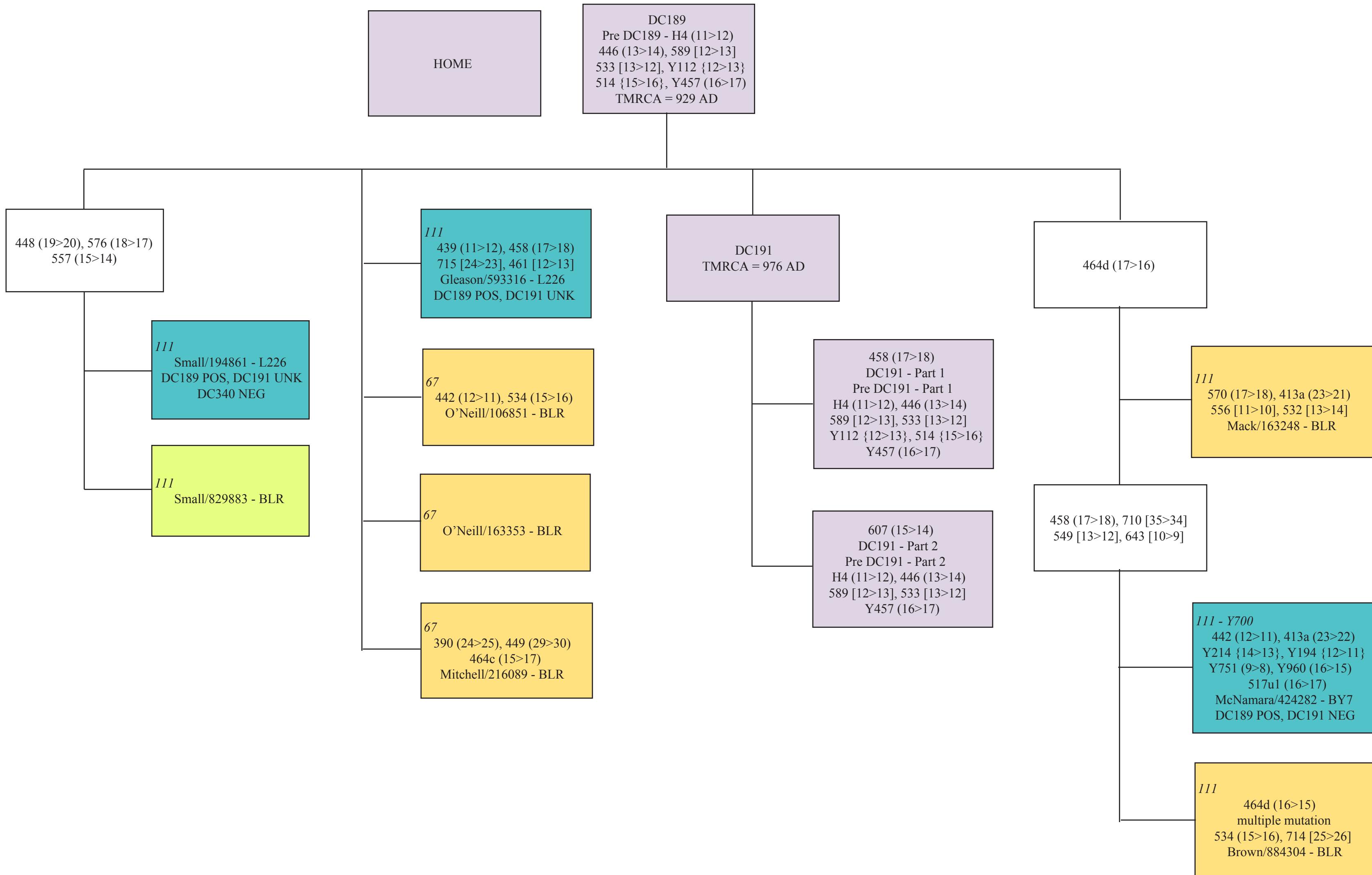


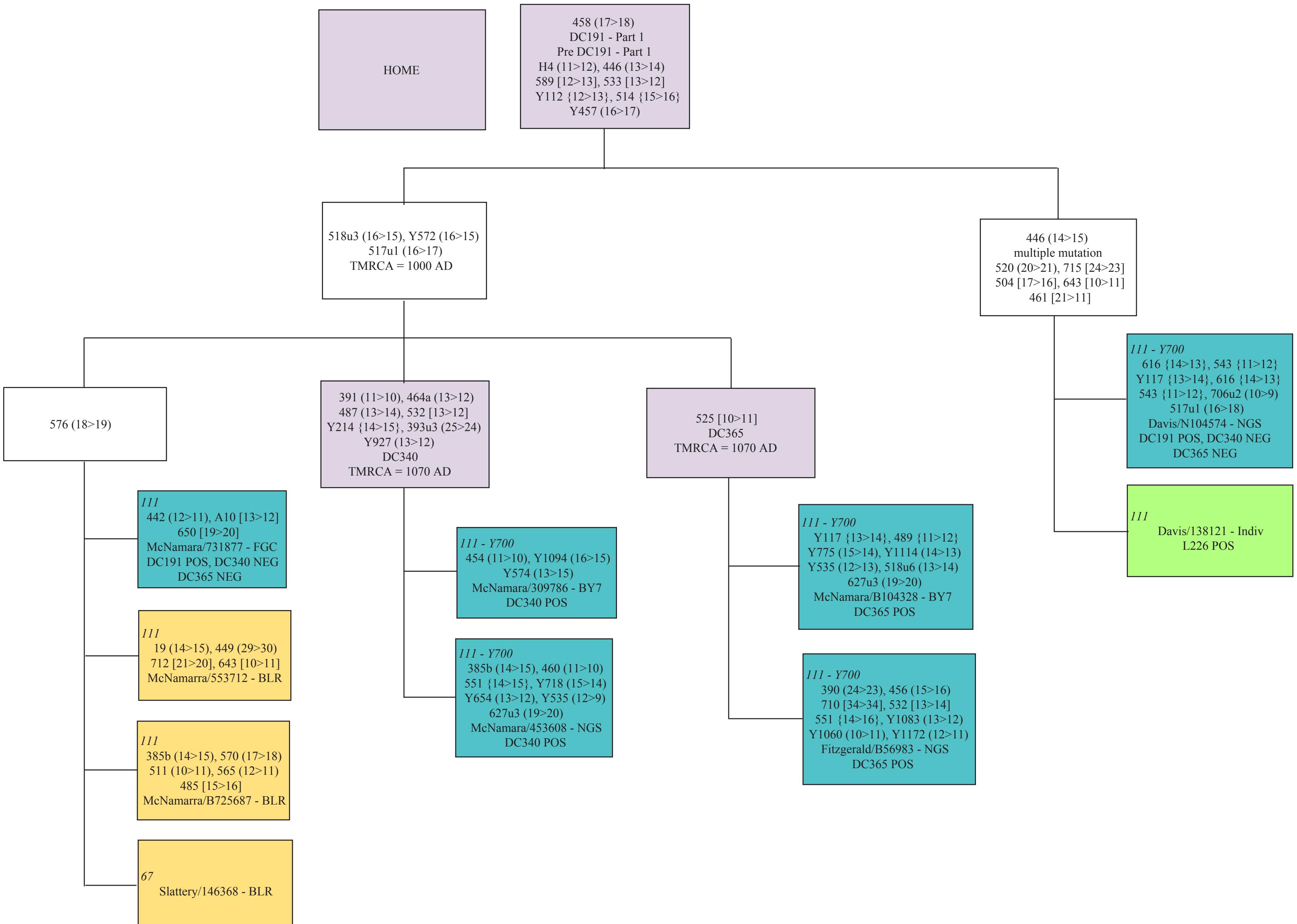


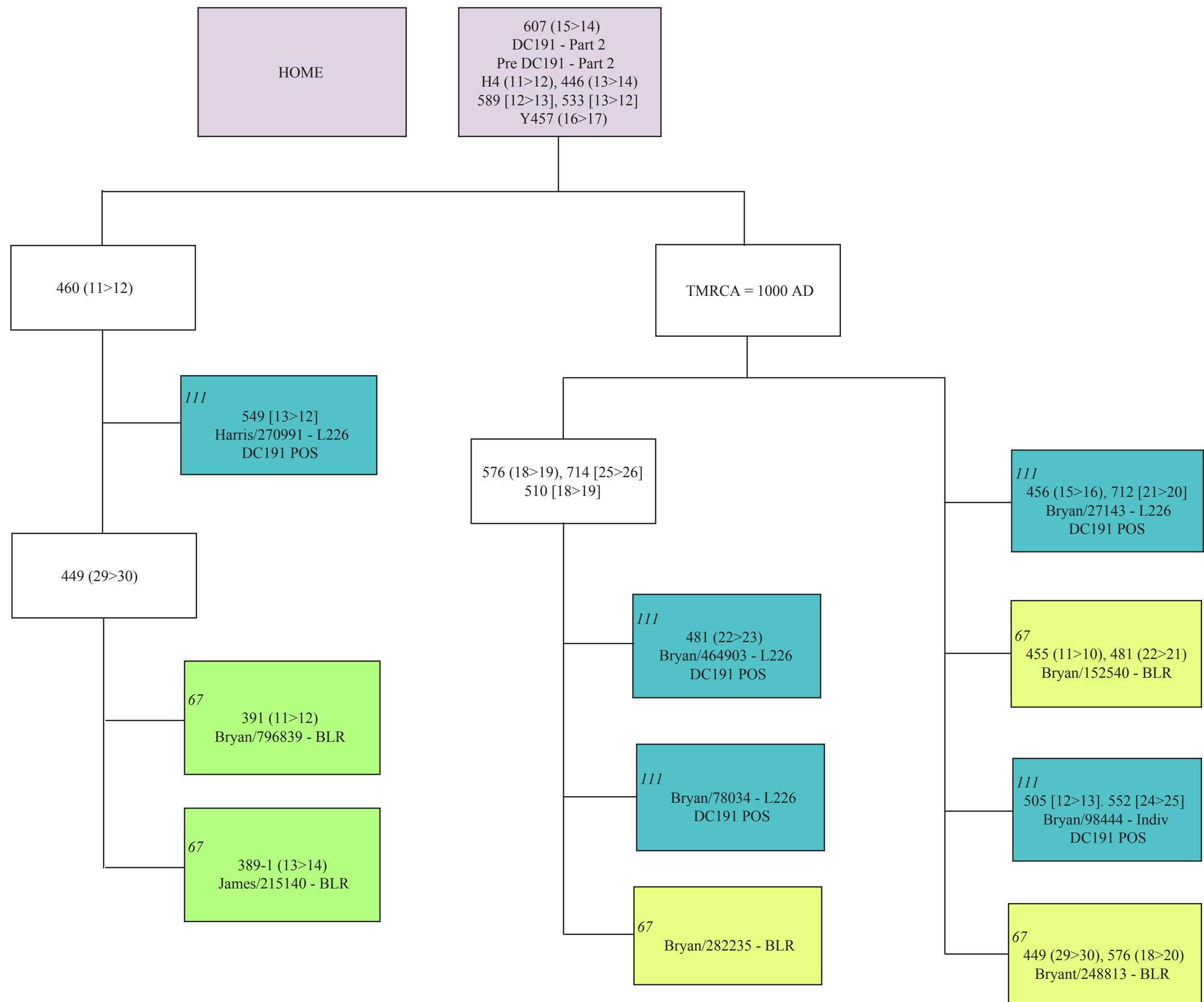


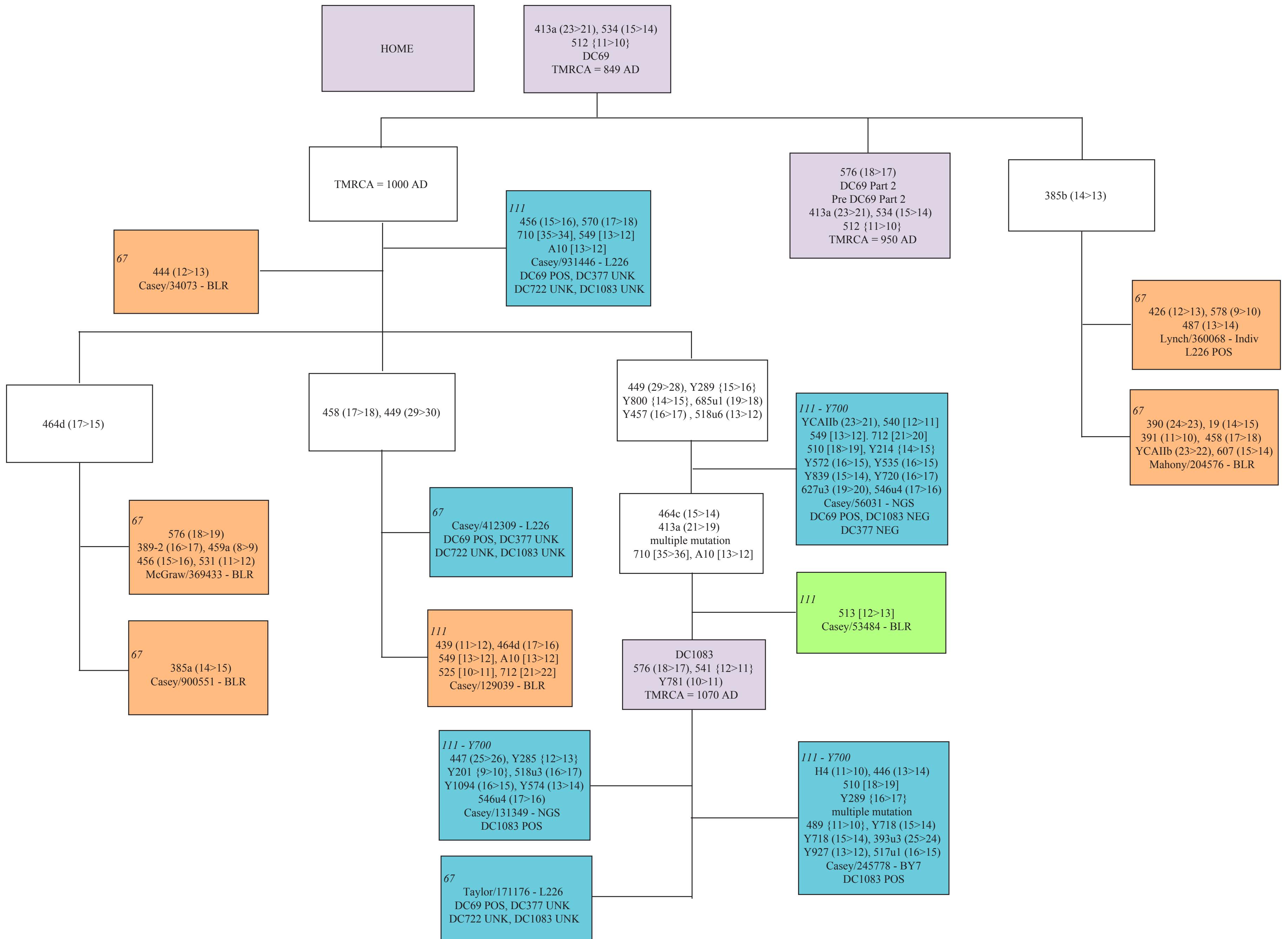


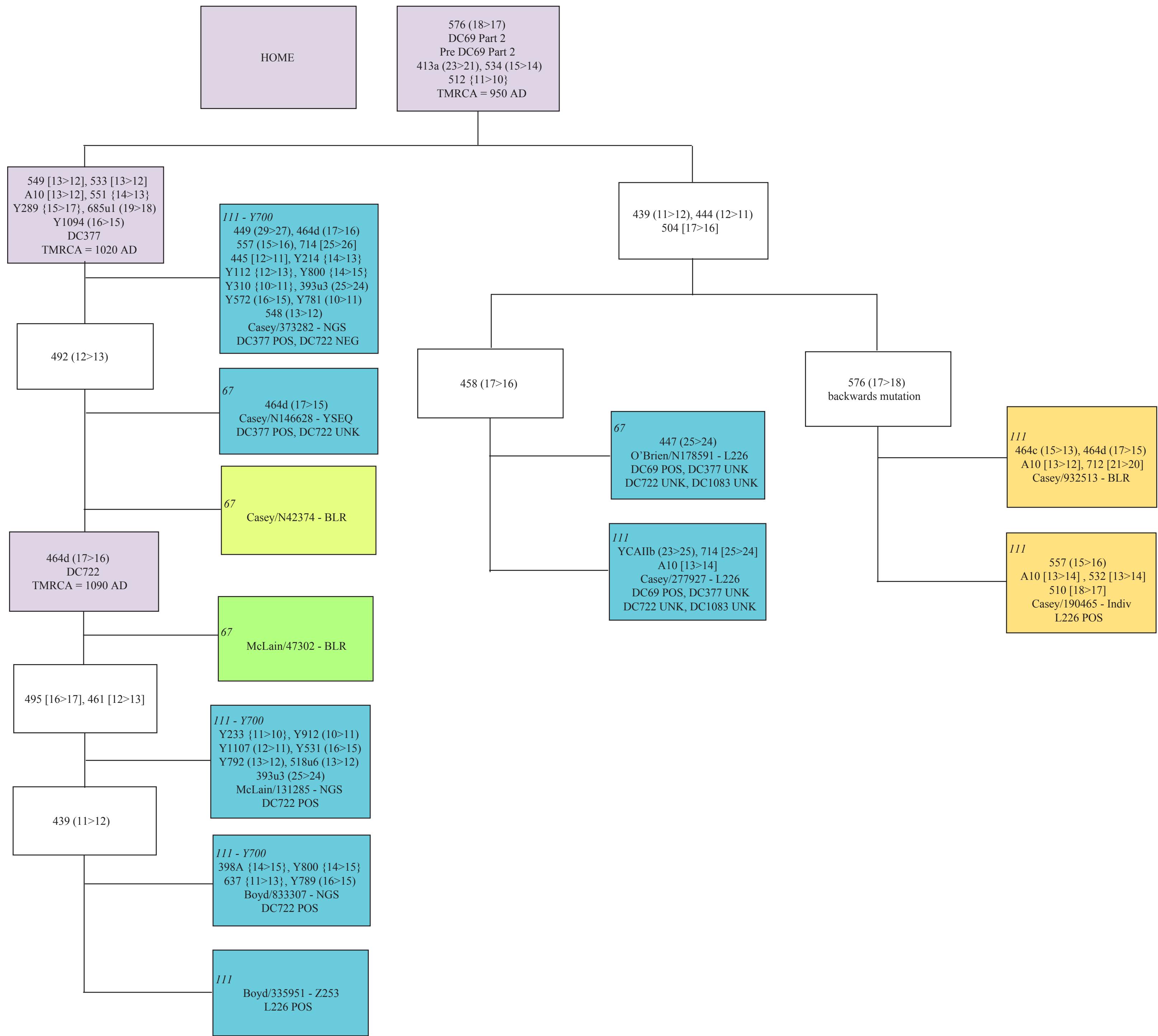


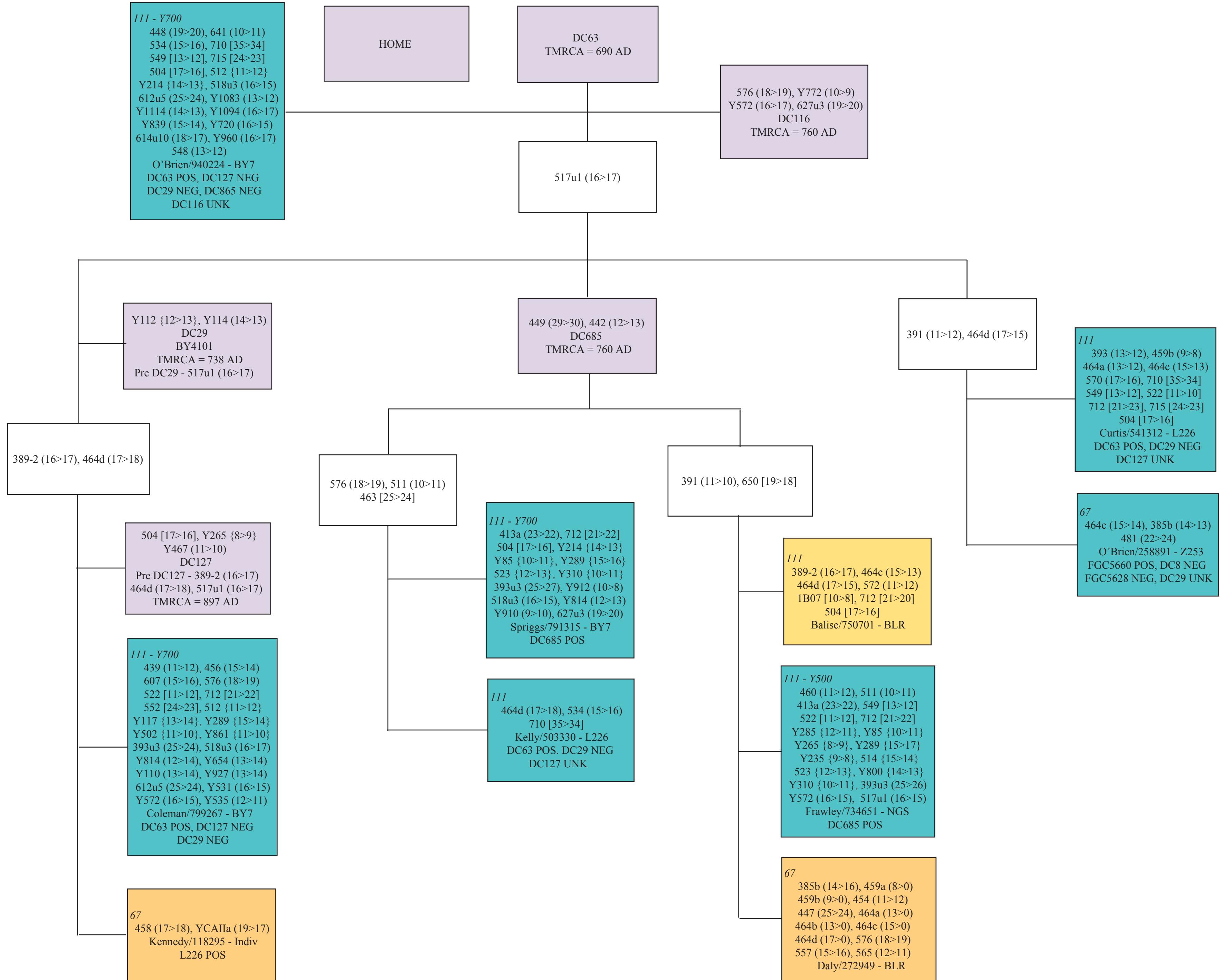


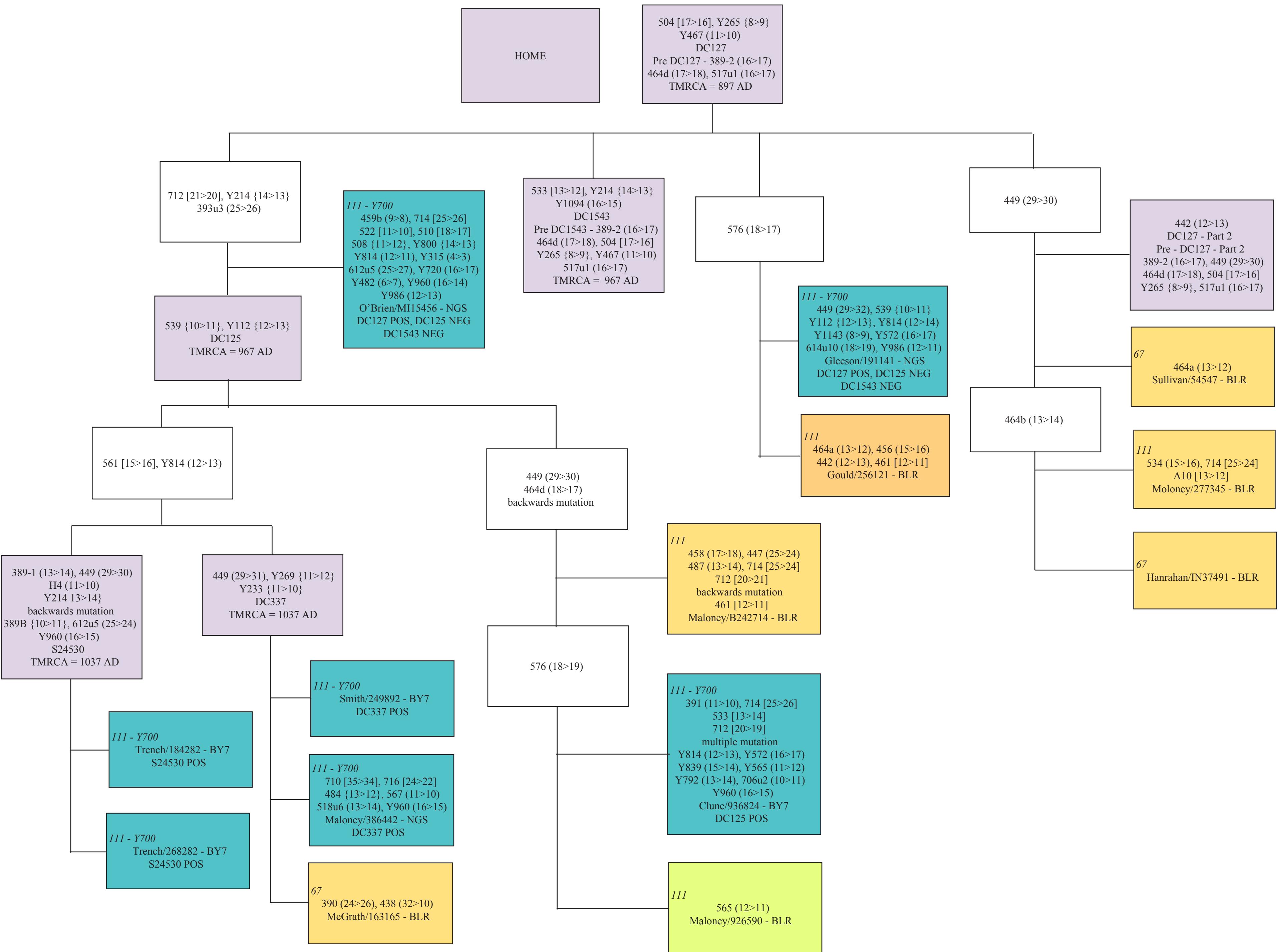


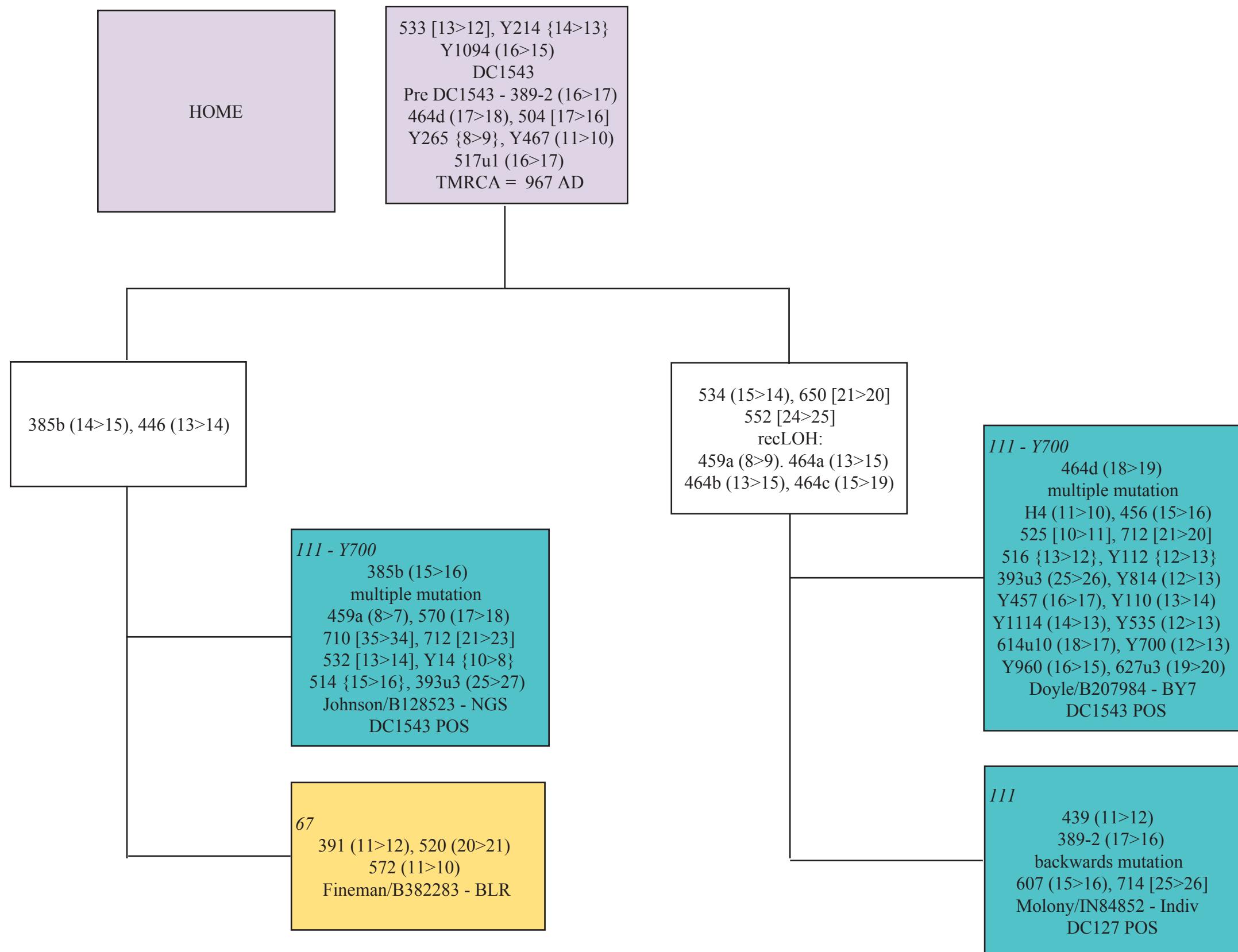


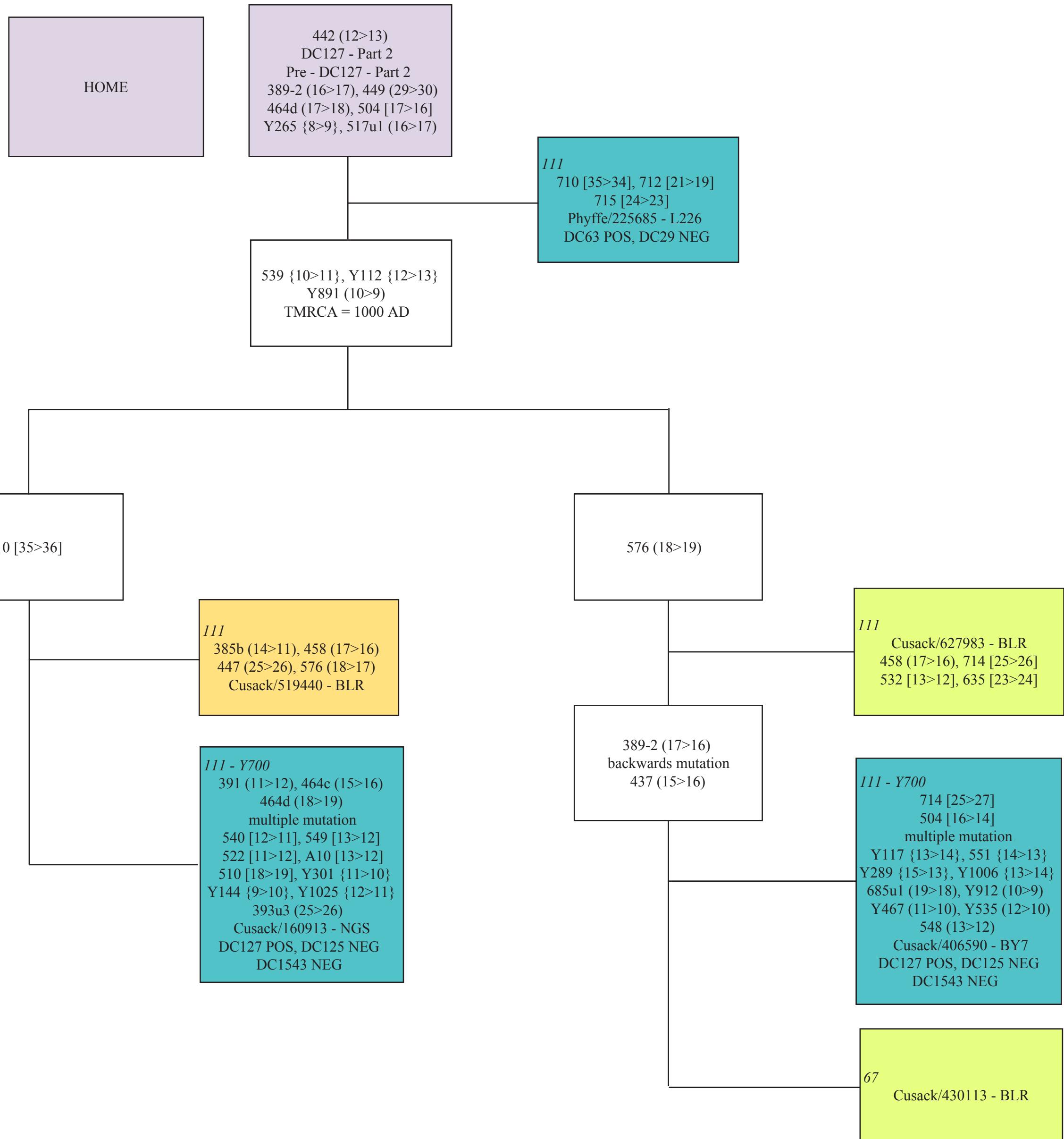


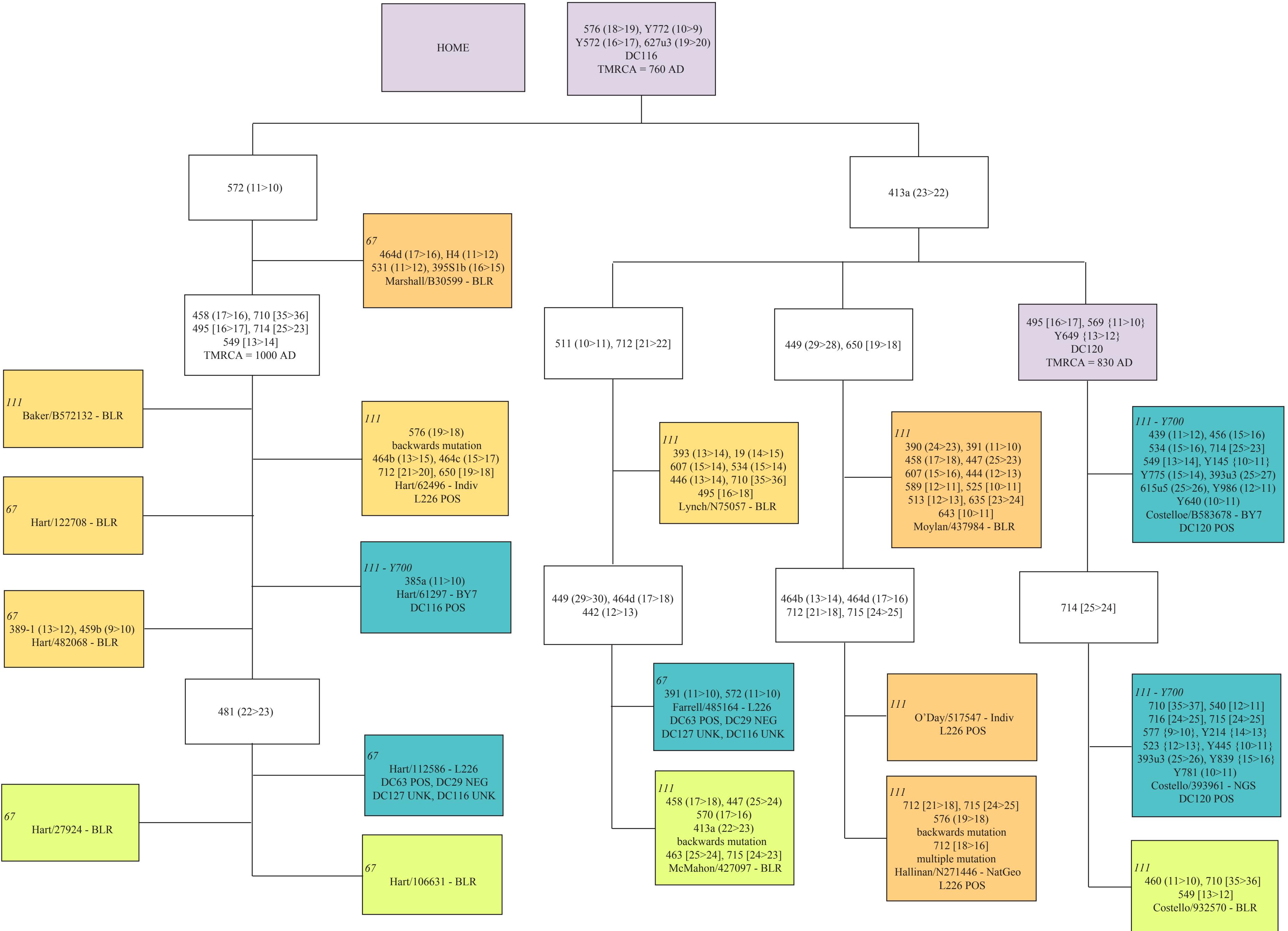


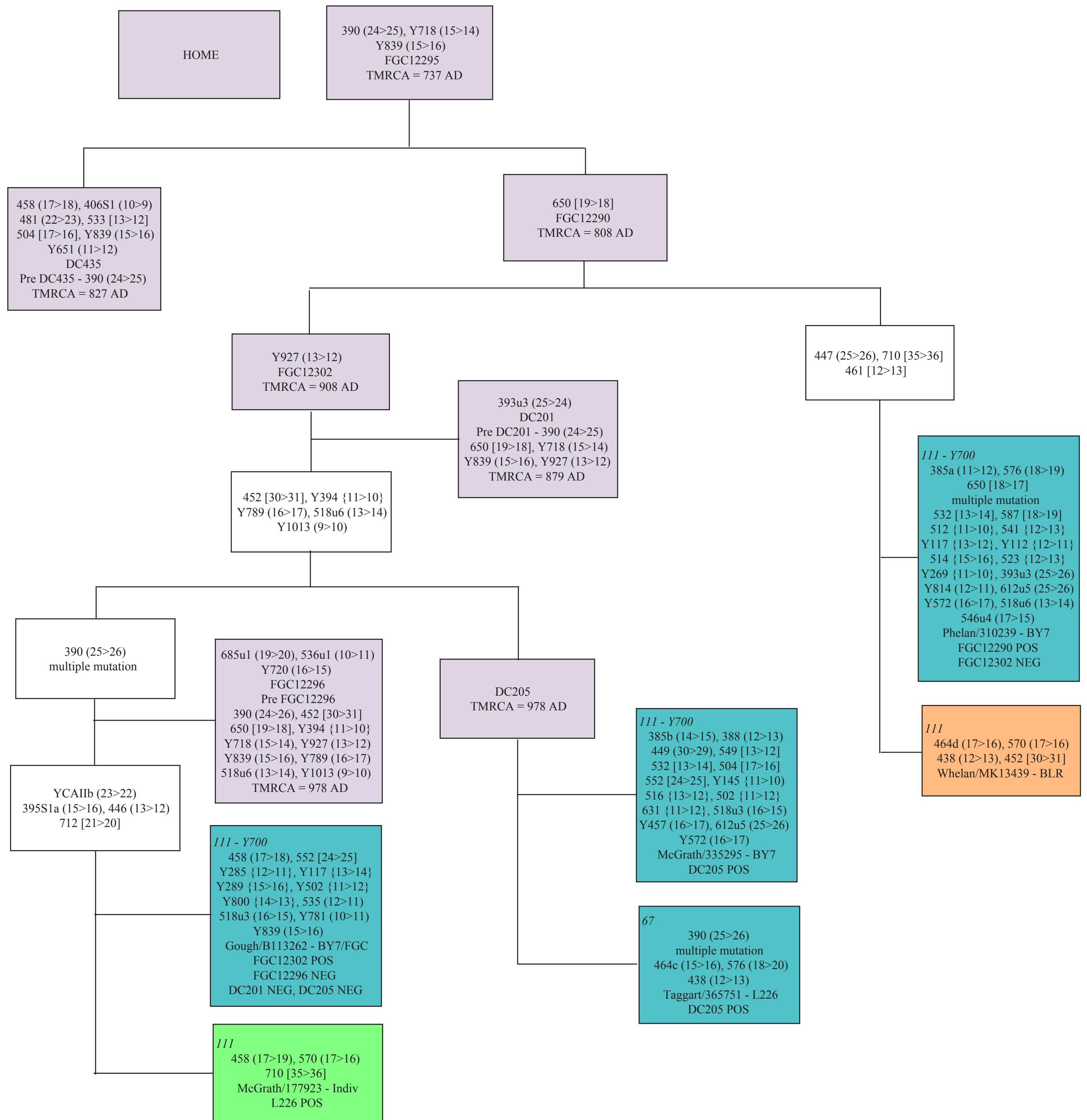


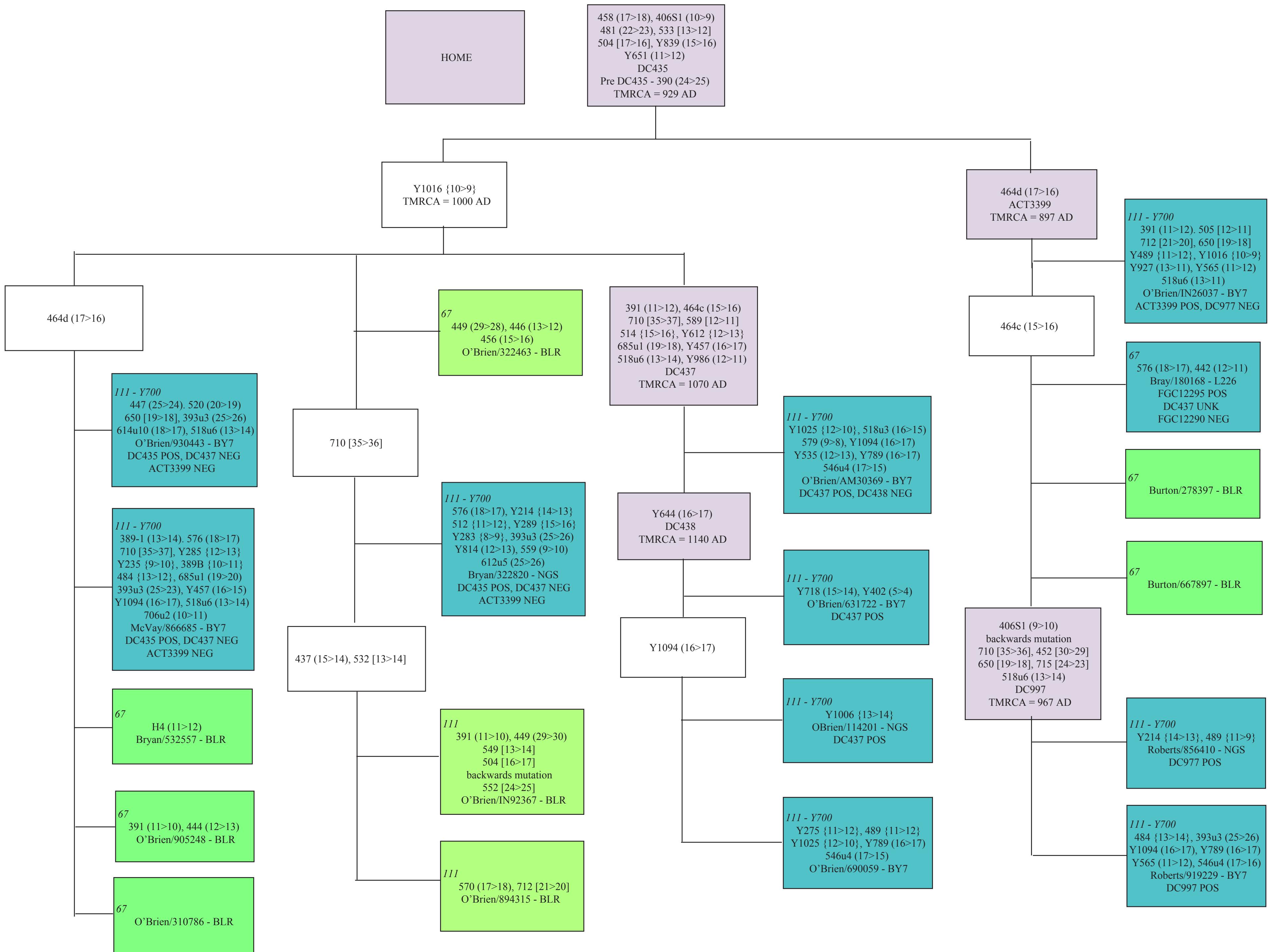


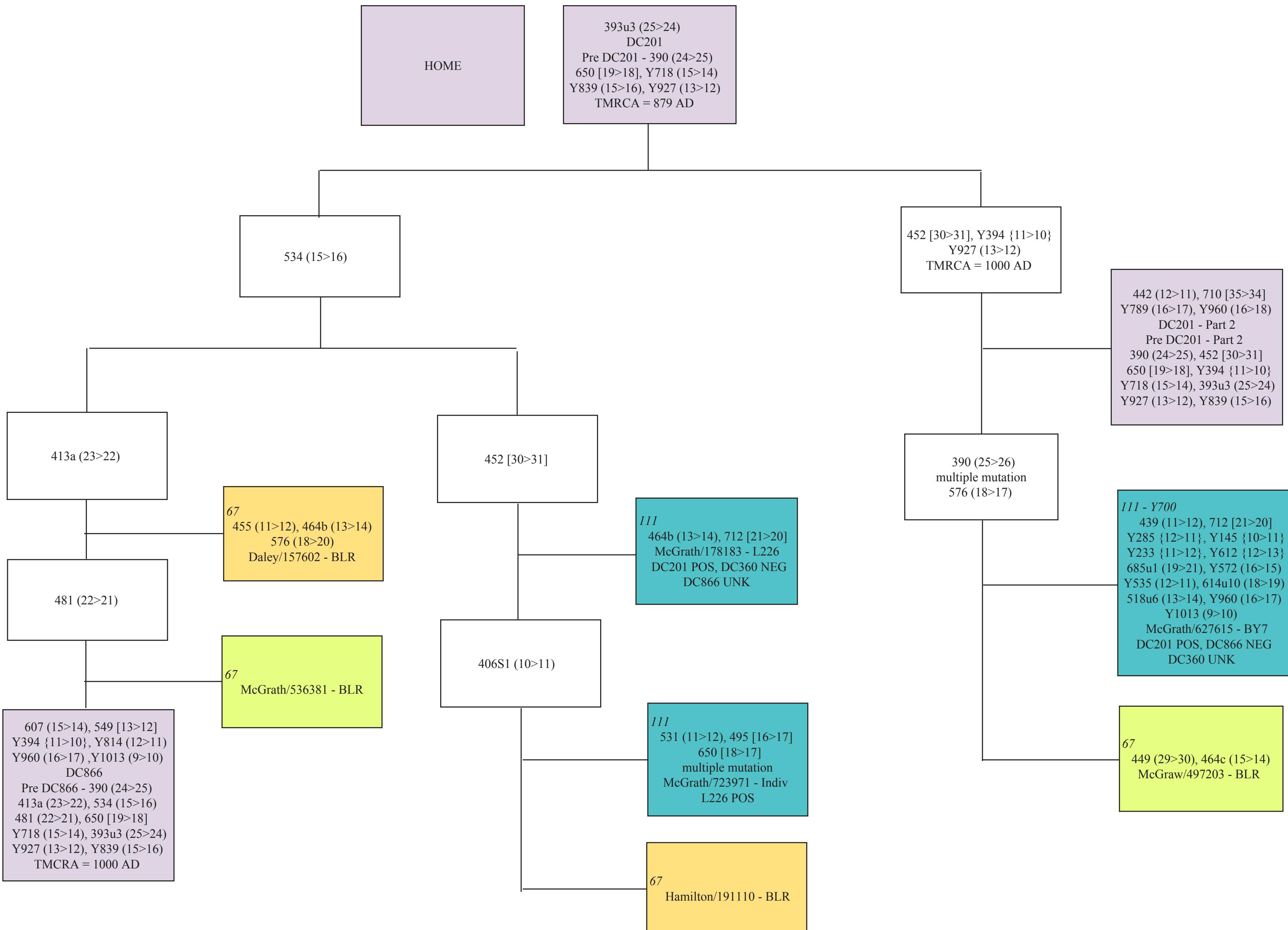


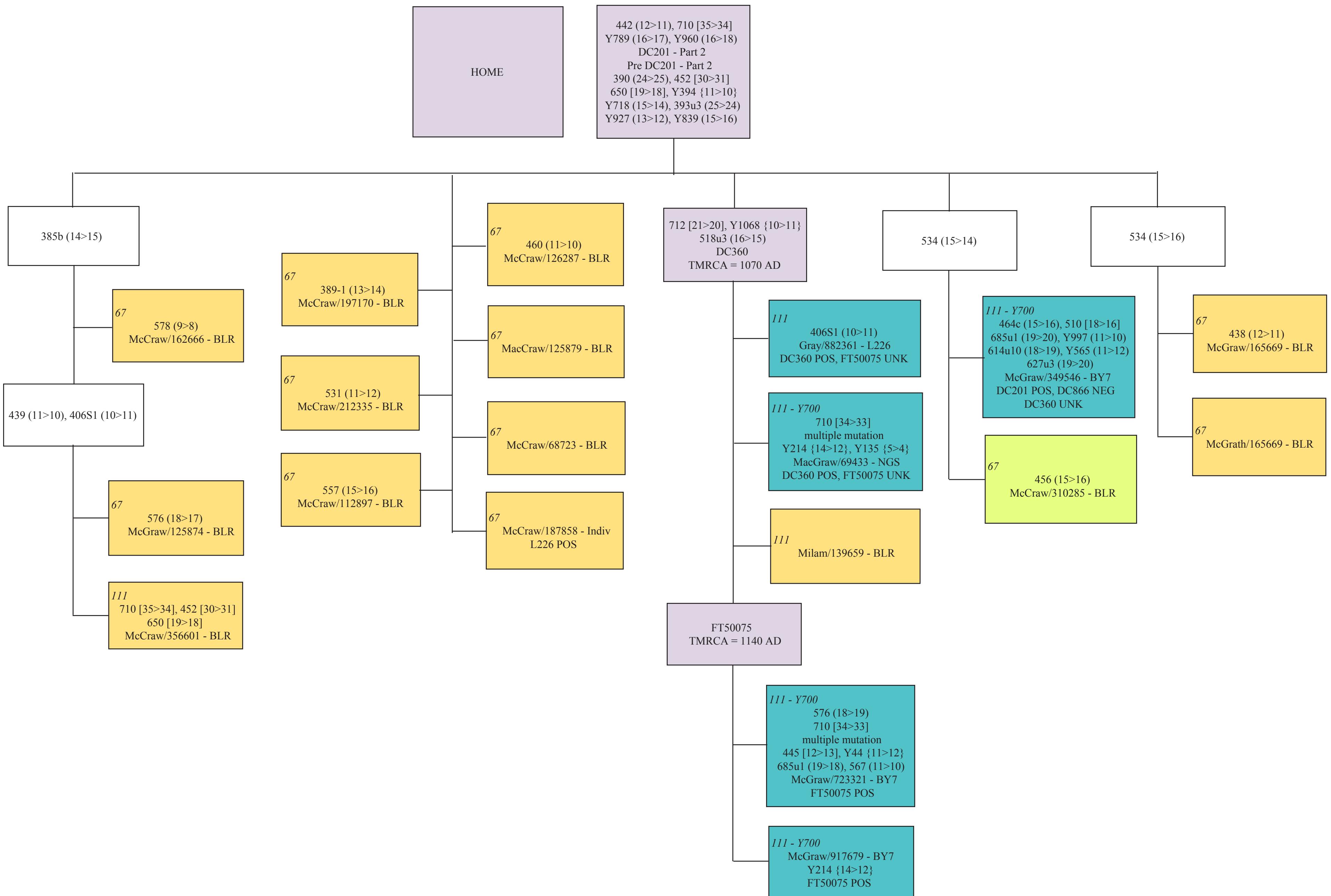


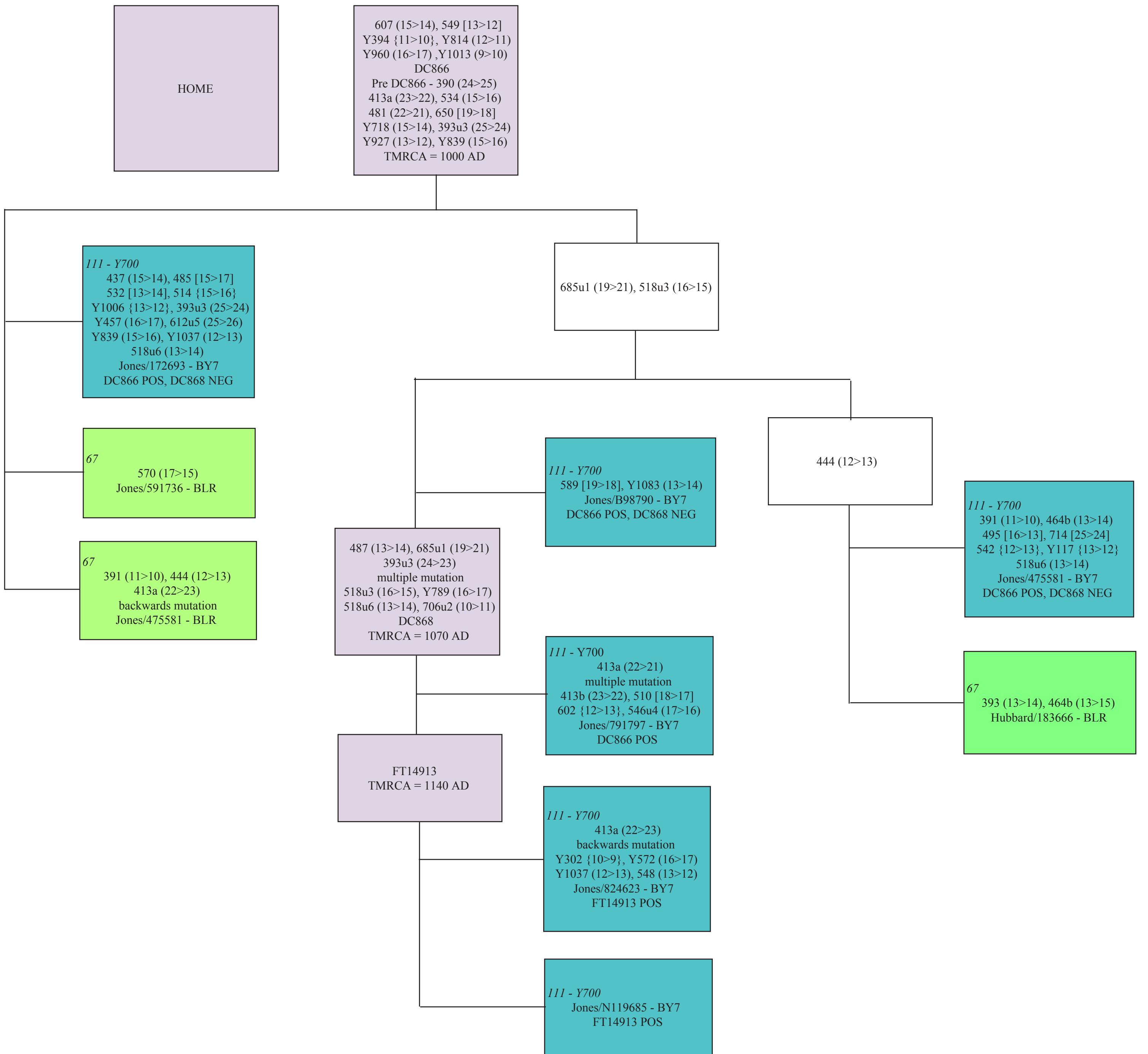


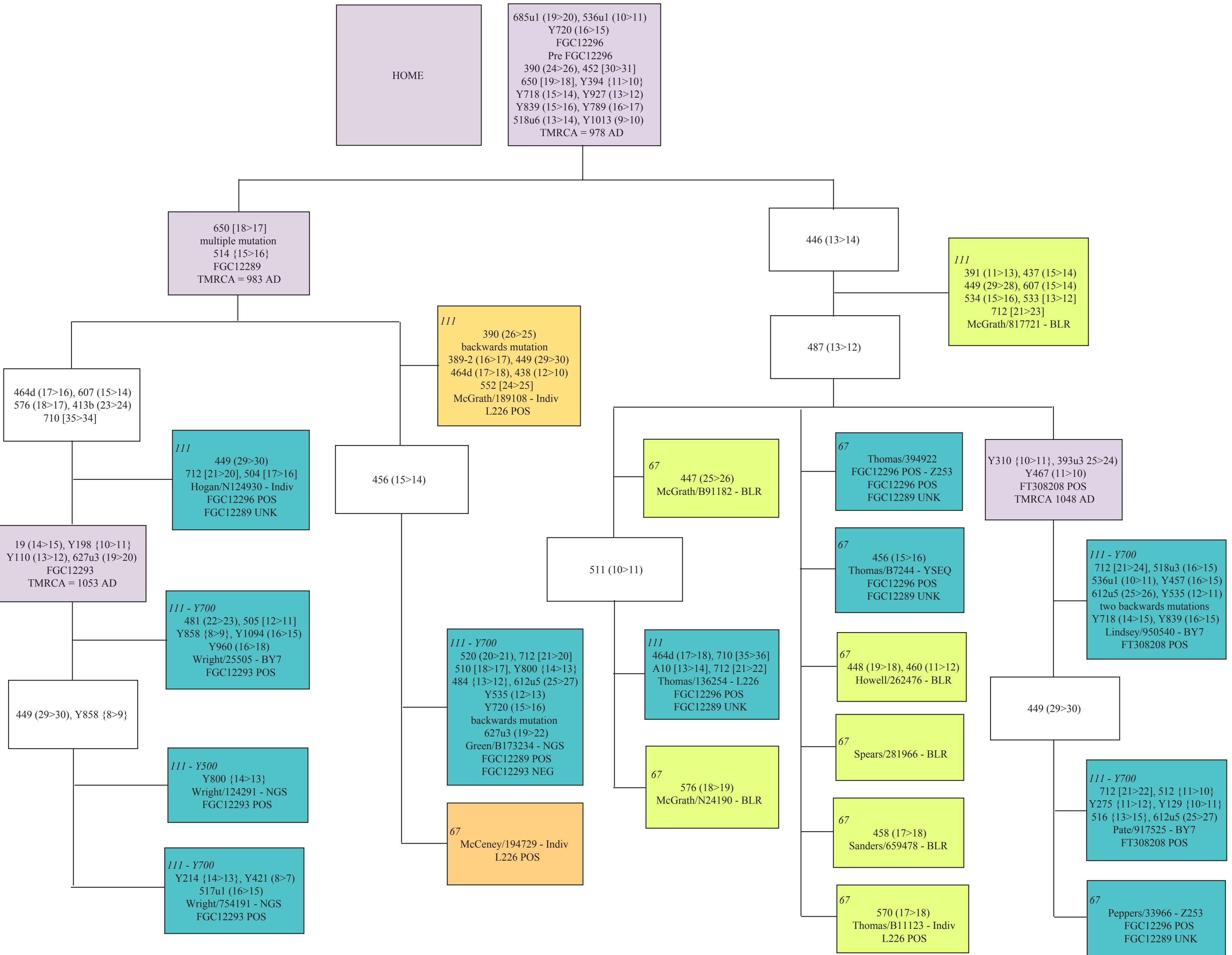


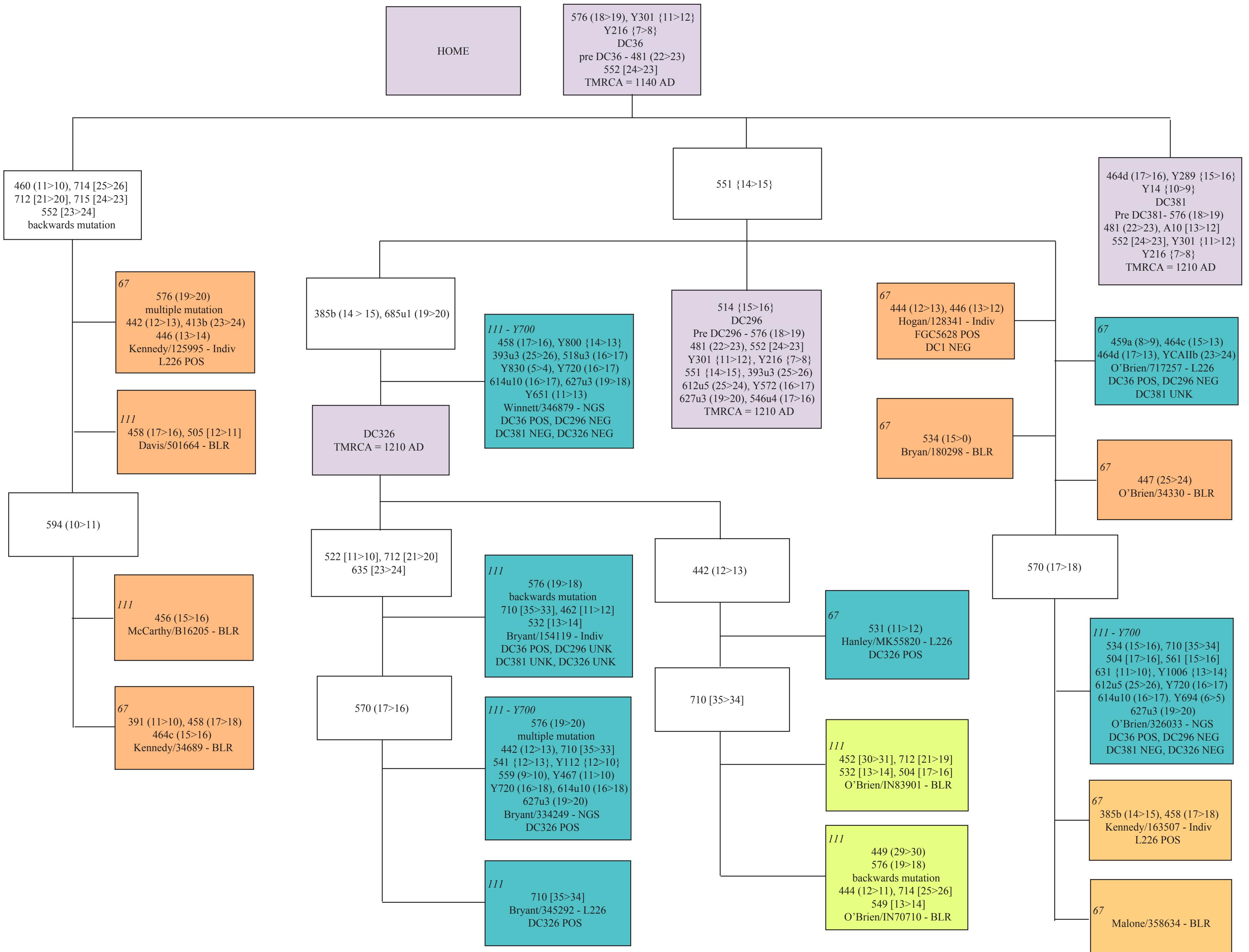


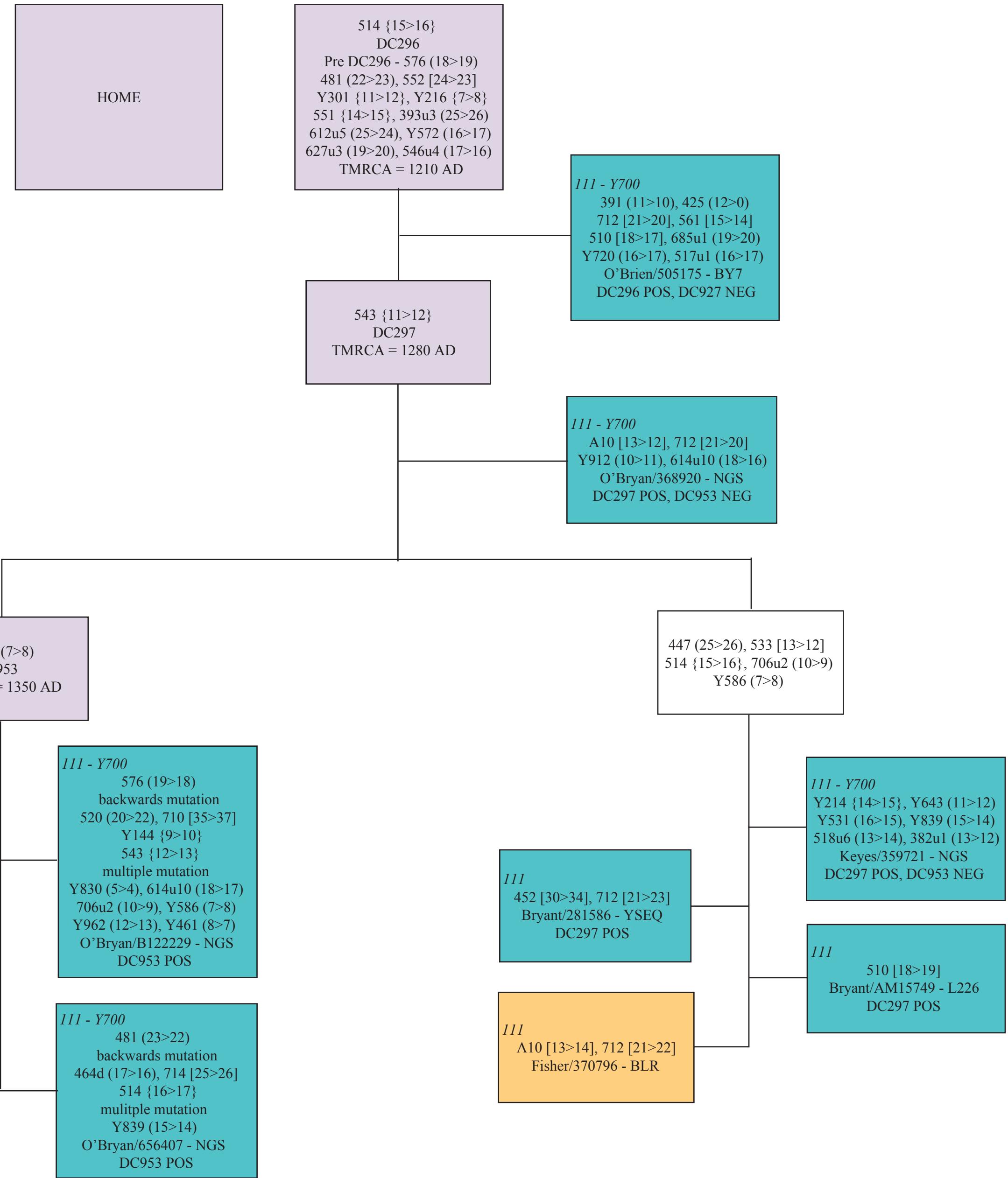


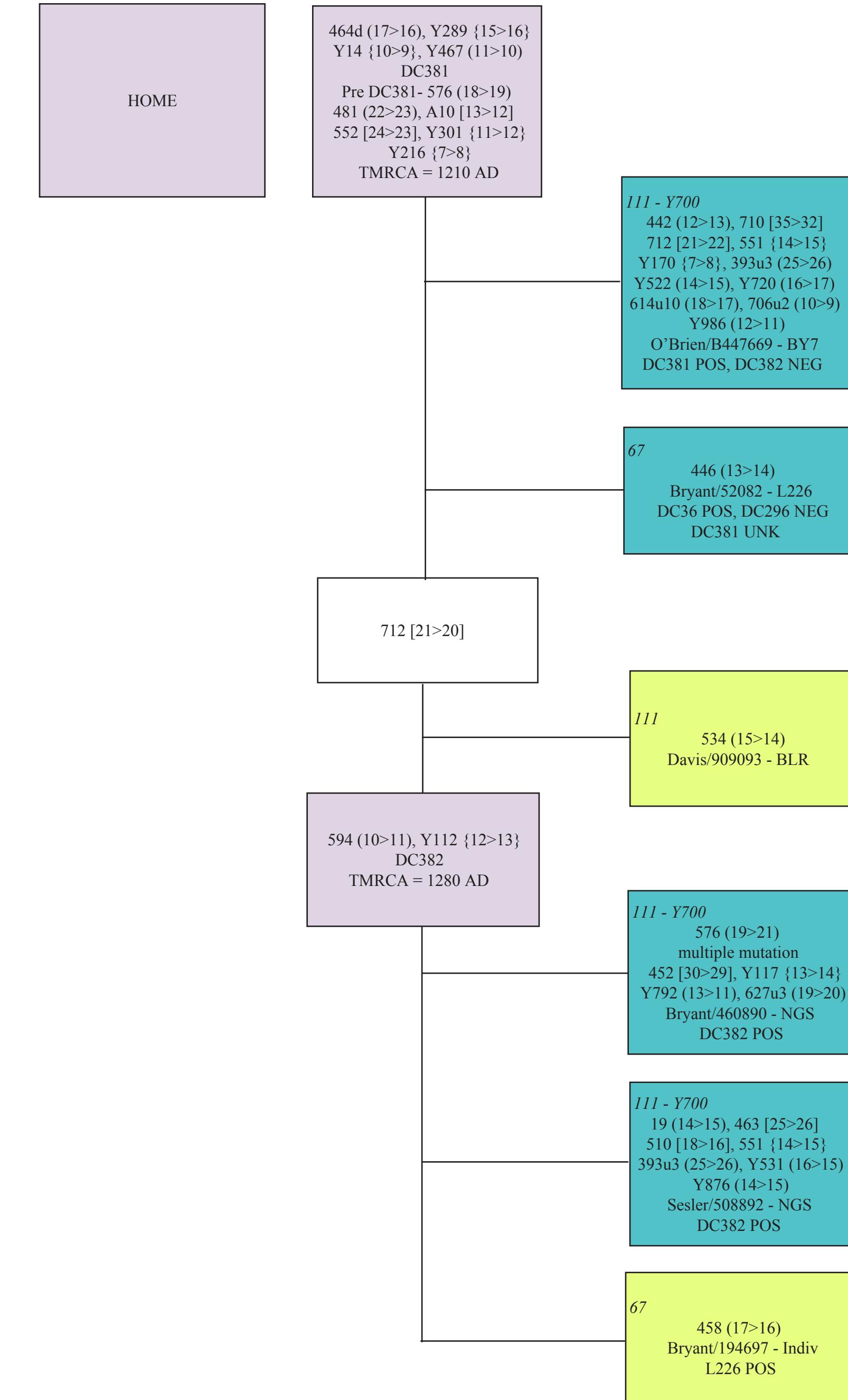


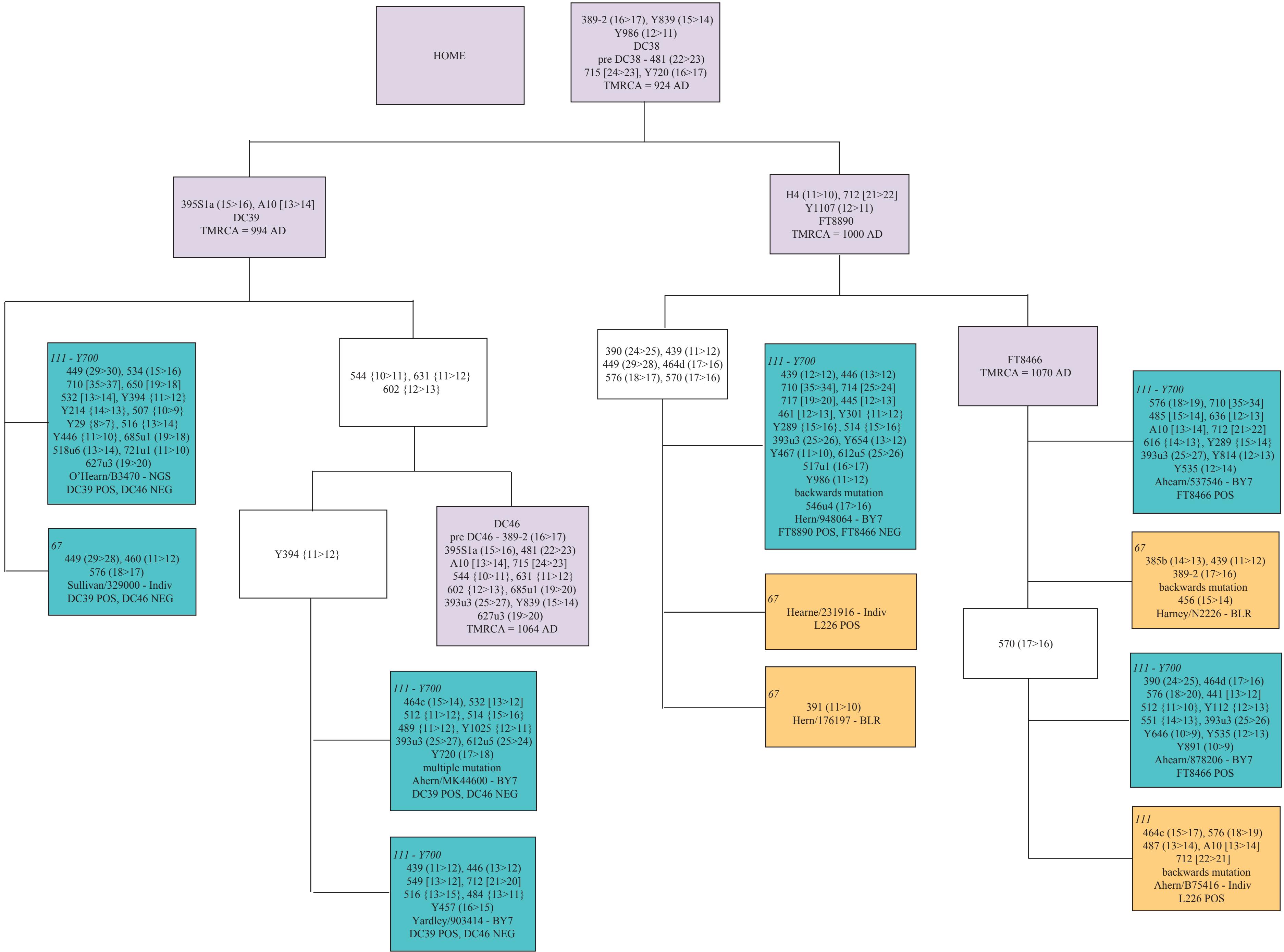












HOME

DC46
pre DC46 - 389-2 (16>17)
395S1a (15>16), 481 (22>23)
A10 [13>14], 715 [24>23]
544 {10>11}, 631 {11>12}
602 {12>13}, 685u1 (19>20)
393u3 (25>27), Y839 (15>14)
627u3 (19>20)
TMRCA = 1064 AD

III - Y700
531 (11>10), 710 [35>34]
616 {14>13}, Y535 (12>11)
Y1172 (12>11)
Colegrove/MK31083 - NGS
DC46 POS, DC47 NEG

DC47
TMRCA = 1134 AD

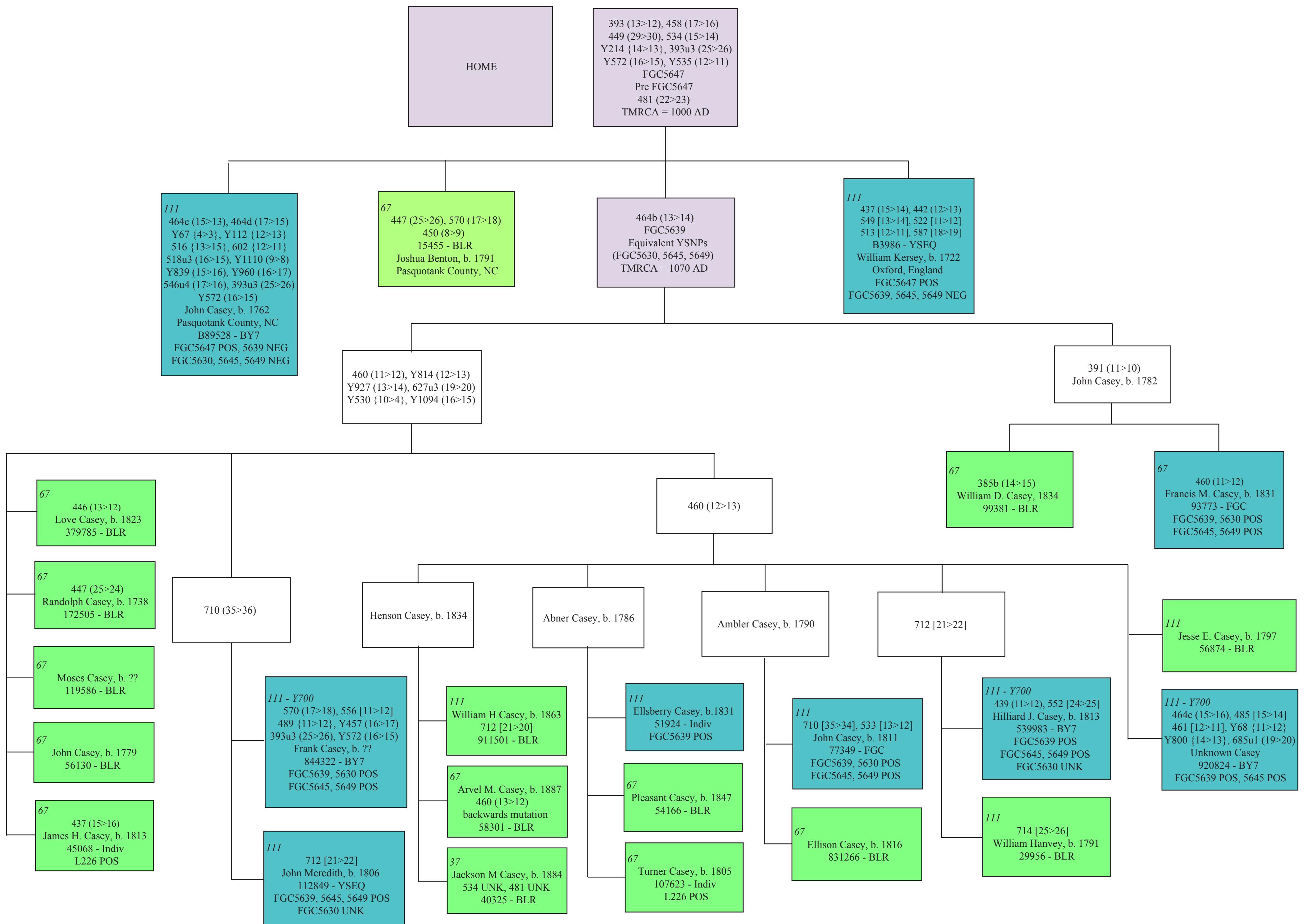
III - Y700
712 [21>22], 616 {14>12}
Peevy/111836 - NGS
DC47 POS

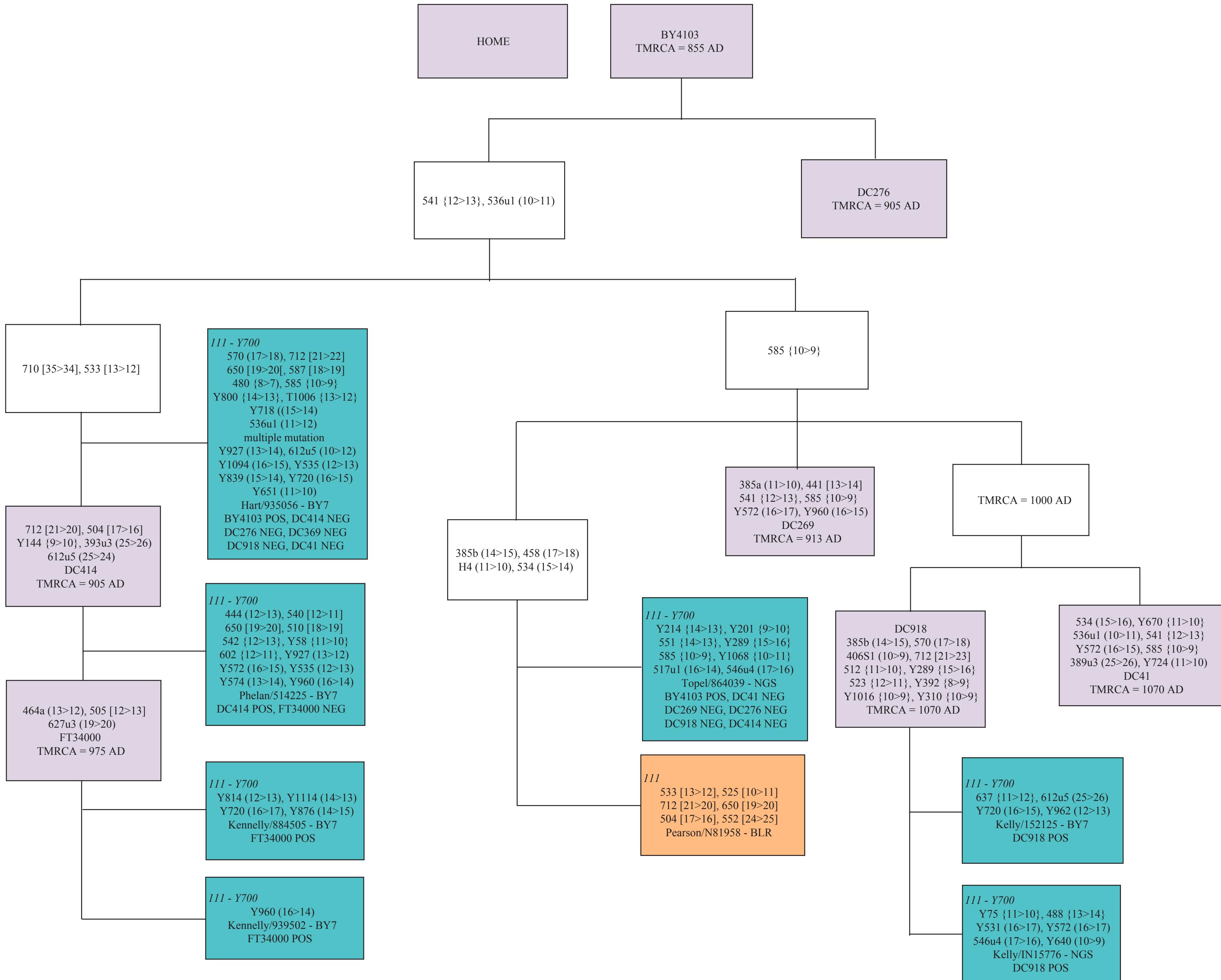
446 (13>12) , Y394 {11>12}

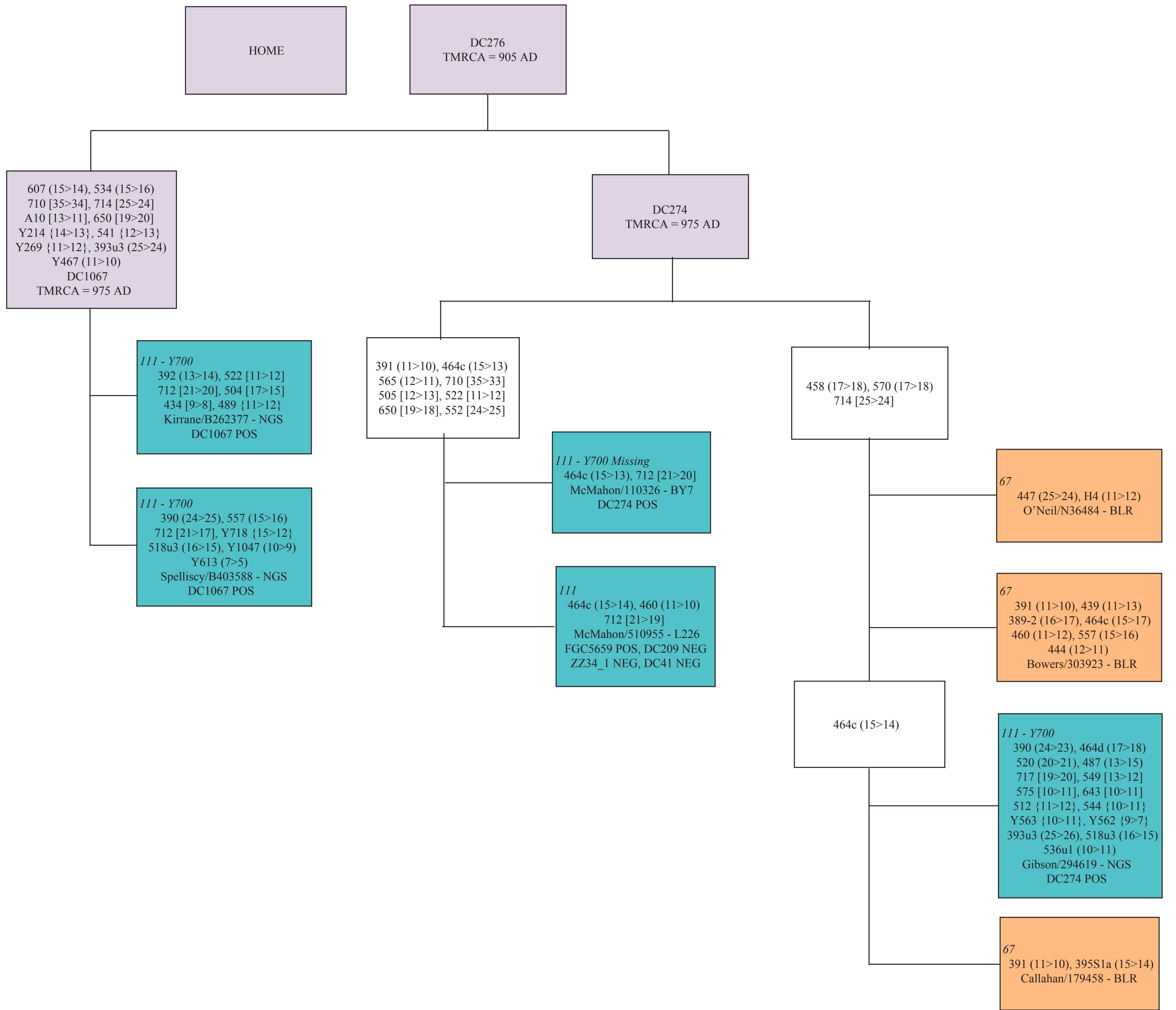
III - Y700
Y986 (12>11)
Brown/138720 - BY7
DC47 POS

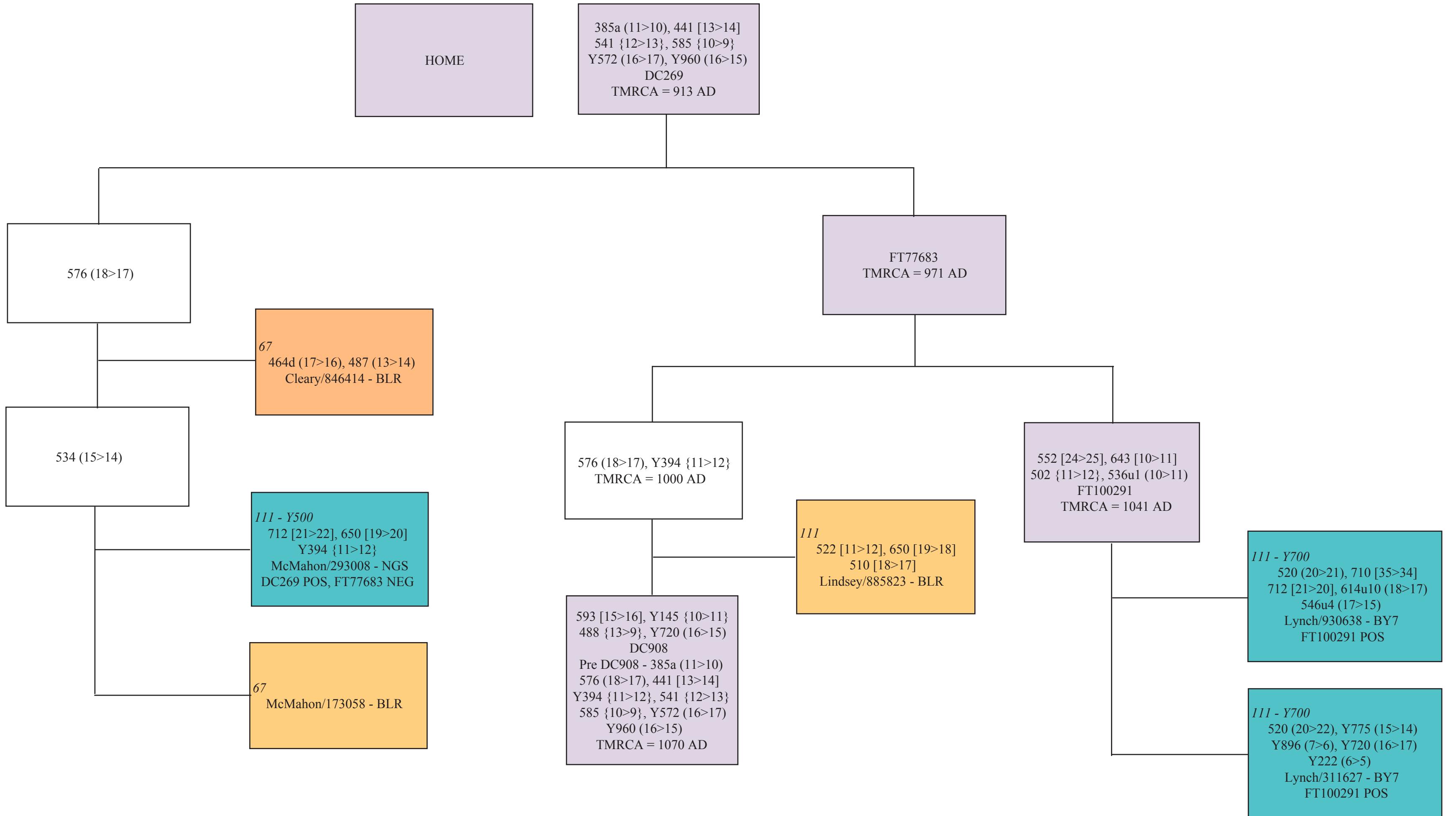
III - Y700
561 [15>16], Y145 {10>11}
Y233 {11>10}, Y665 (10>11)
Y565 (11>10)
Peavey/90545 - NGS
DC47 POS

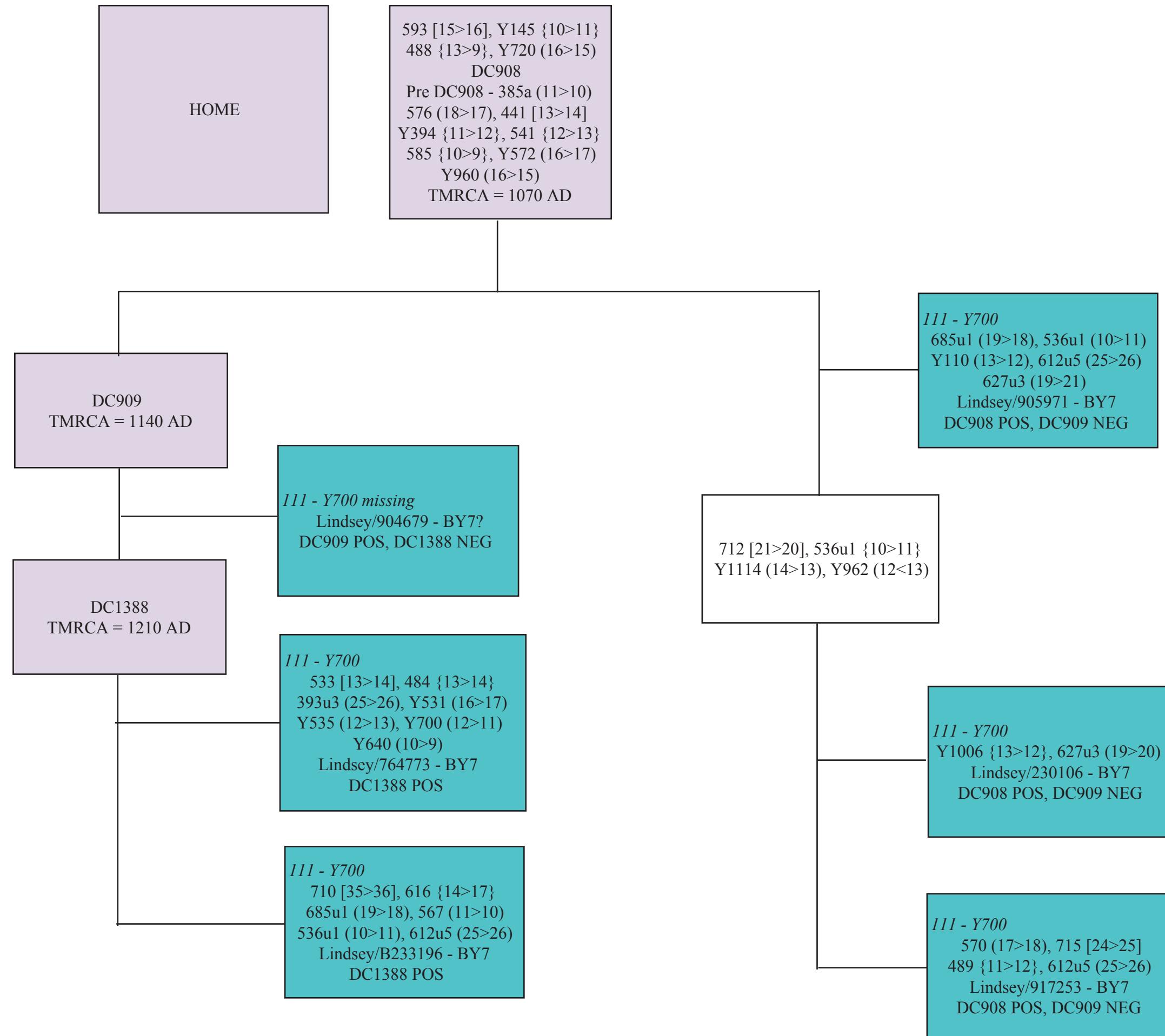
III - Y700
Y1042 {11>10}, Y1039 {5>4}
Y654 (13>12), Y1047 (10>11)
Brown/286386 - NGS
DC47 POS

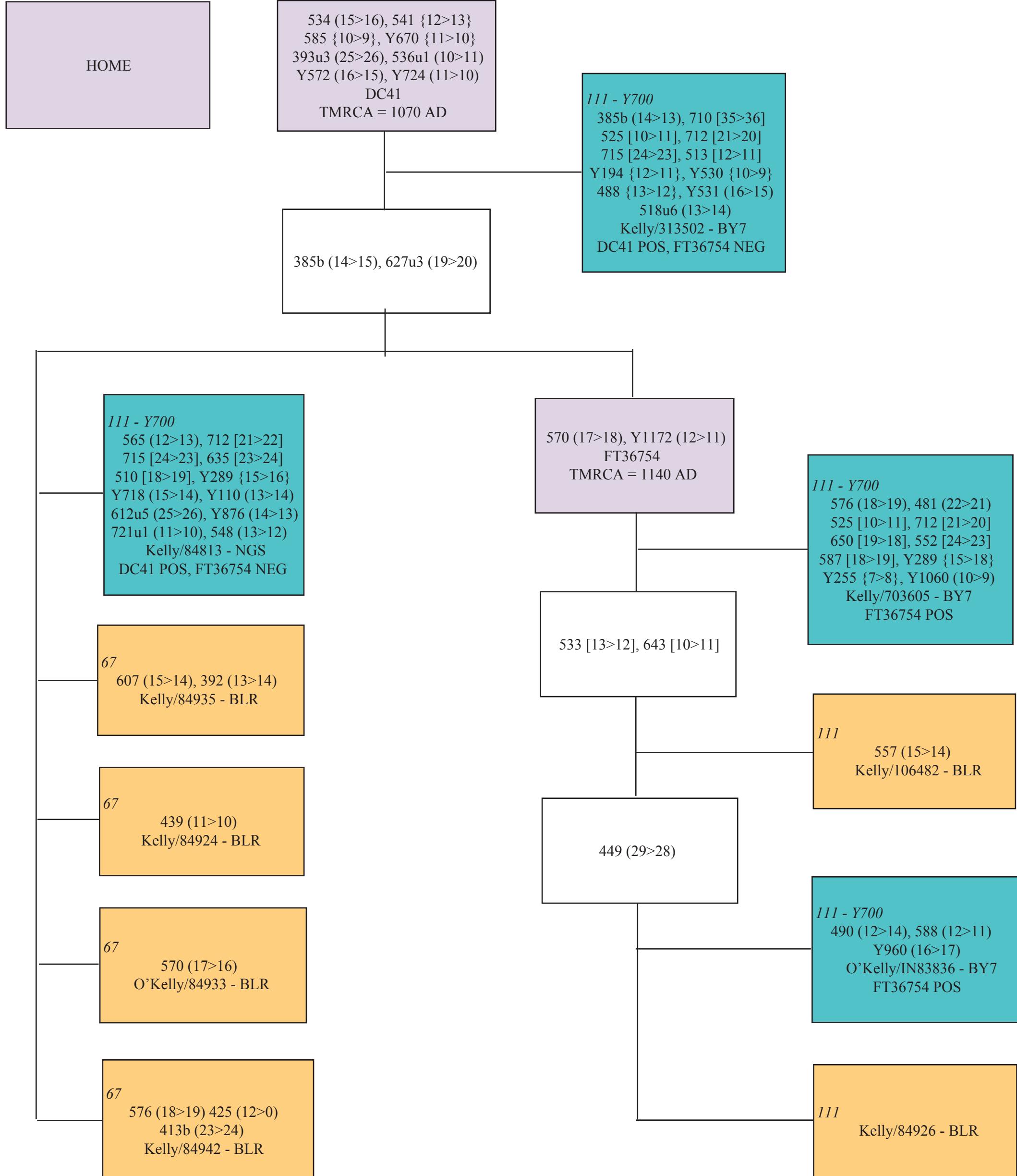


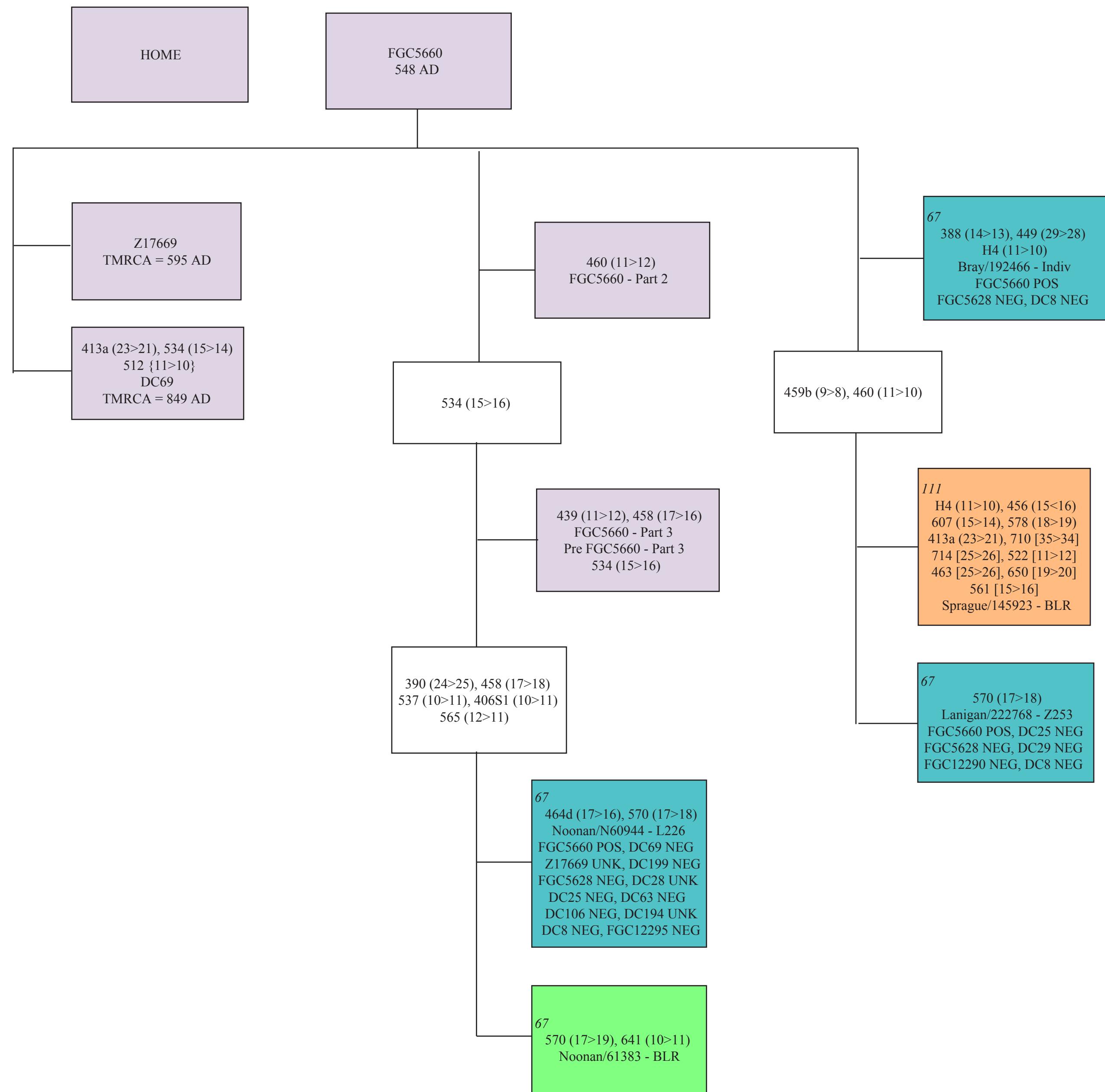


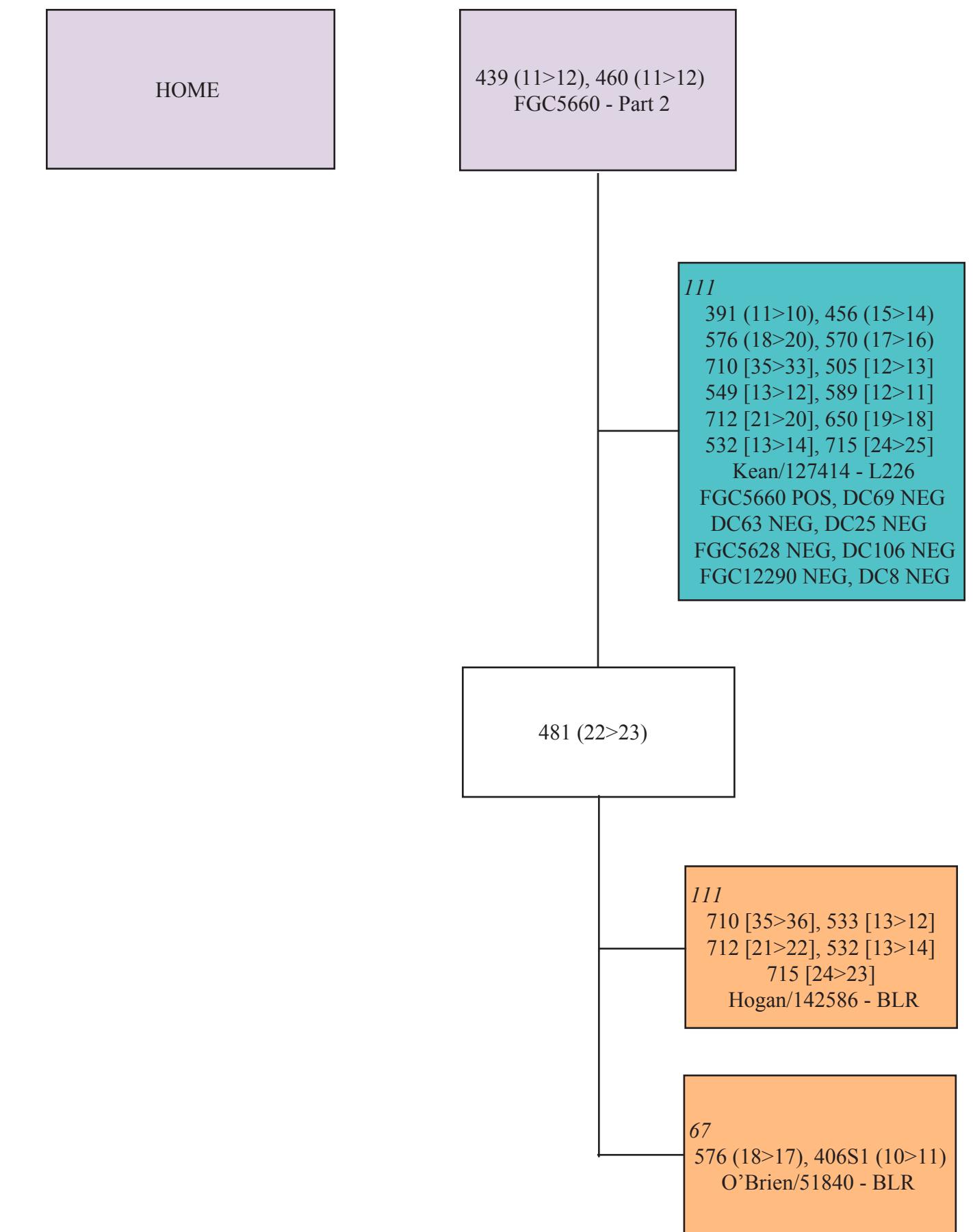












HOME

439 (11>12), 458 (17>16)
FGC5660 - Part 3
Pre FGC5660 - Part 3
534 (15>16)

67
447 (25>26), 460 (11>12)
456 (15>16)
Mahone/MK23915 - L226
FGC5660 POS, DC69 NEG
DC25 NEG, FGC5628 NEG
DC8 NEG, DC63 NEG
DC106 NEG
FGC12295 NEG

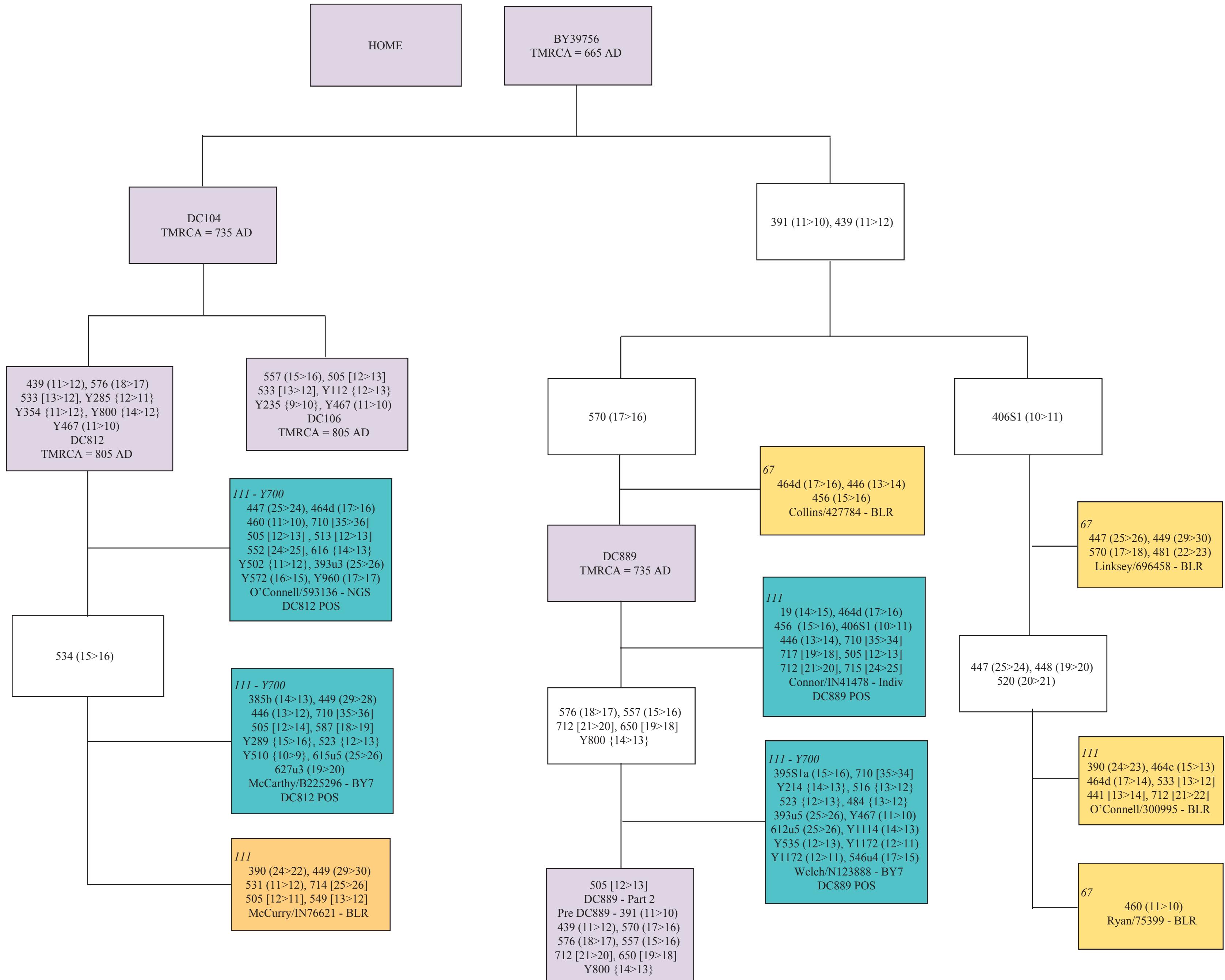
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449 (29>28)
Currell/489080 - BLR

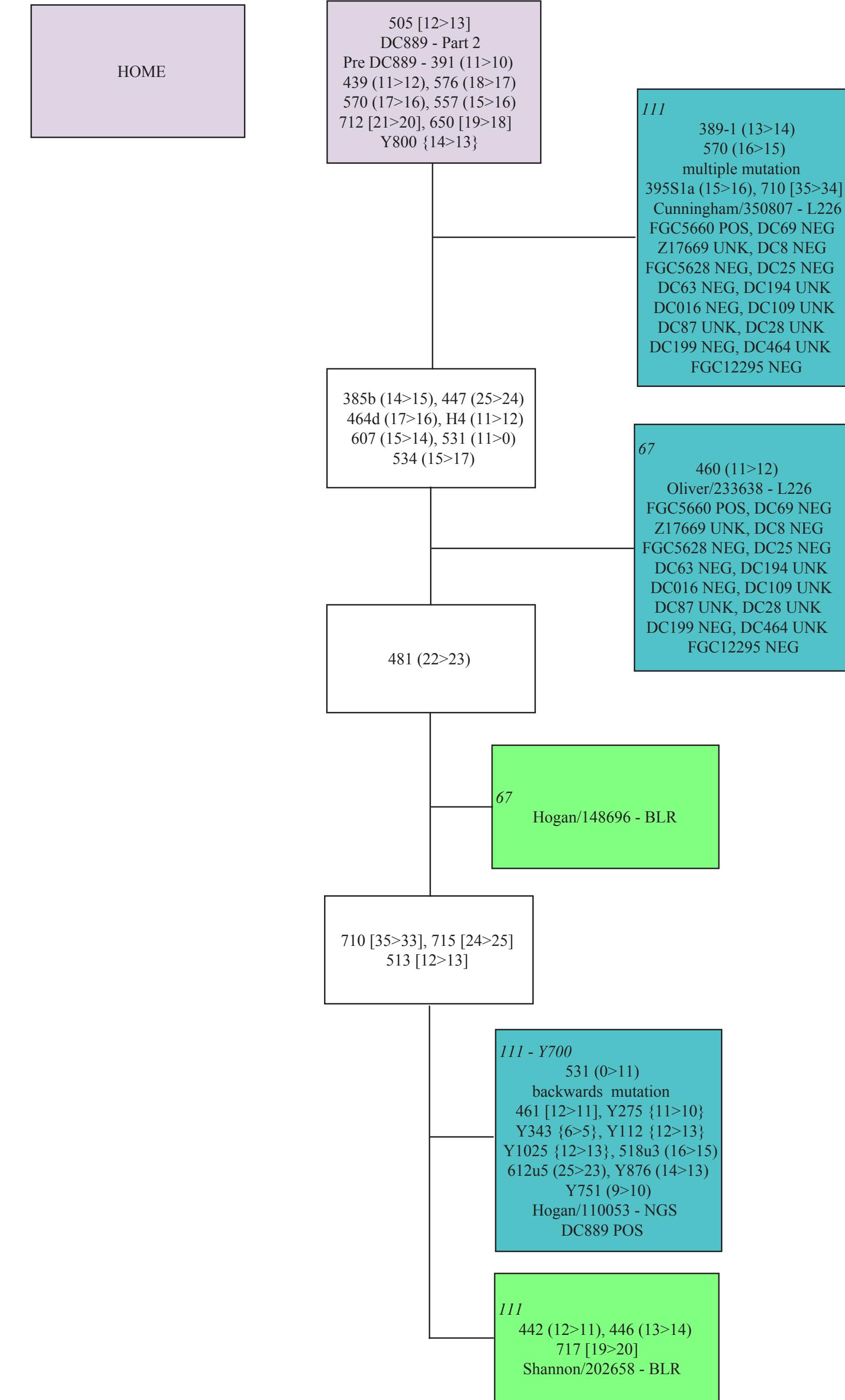
391 (11>10), 437 (15>16)
448 (19>20), H4 (11>10)
520 (20>21)

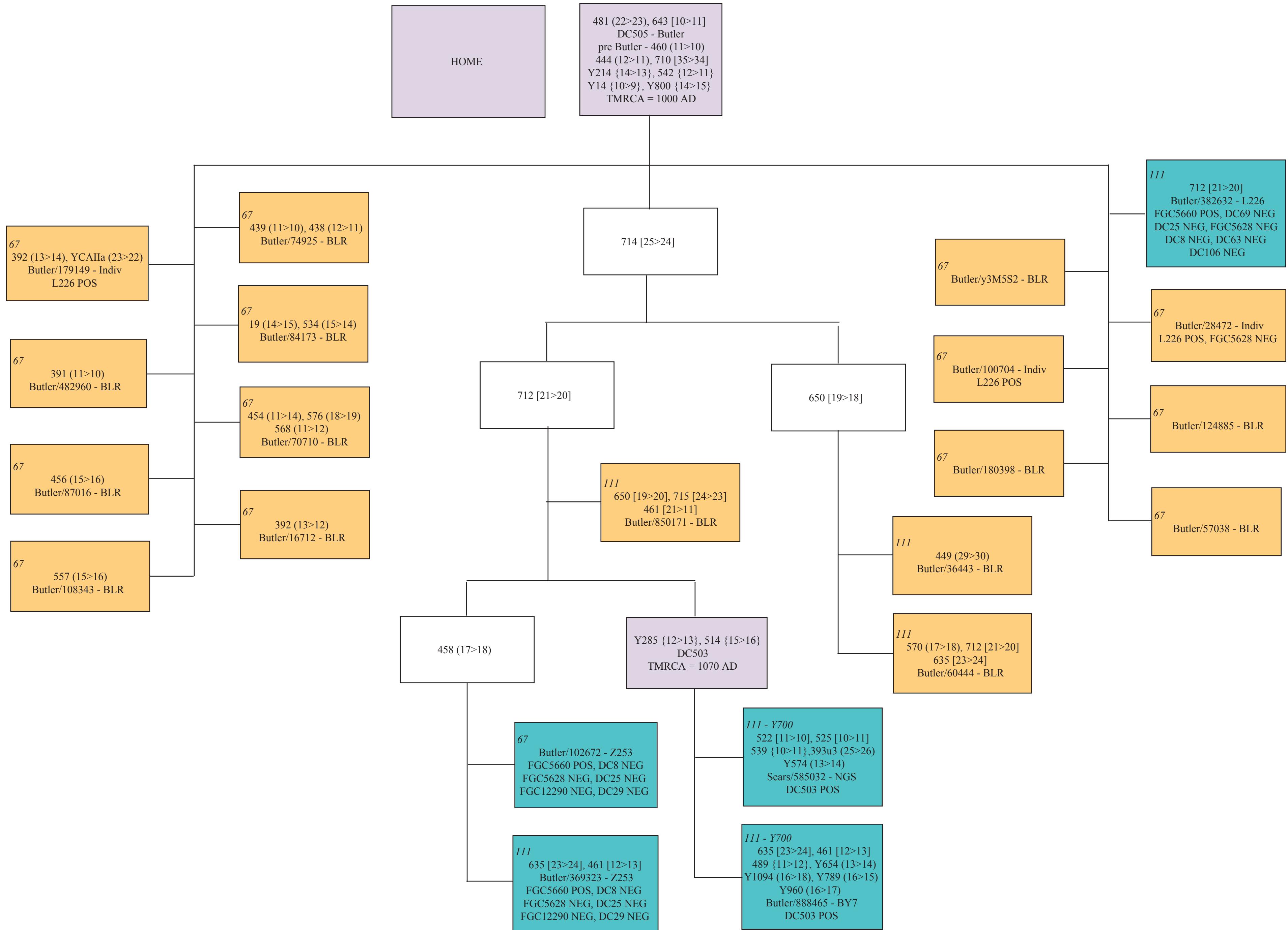
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607 (15>16)
Quillen/N76182 - BLR

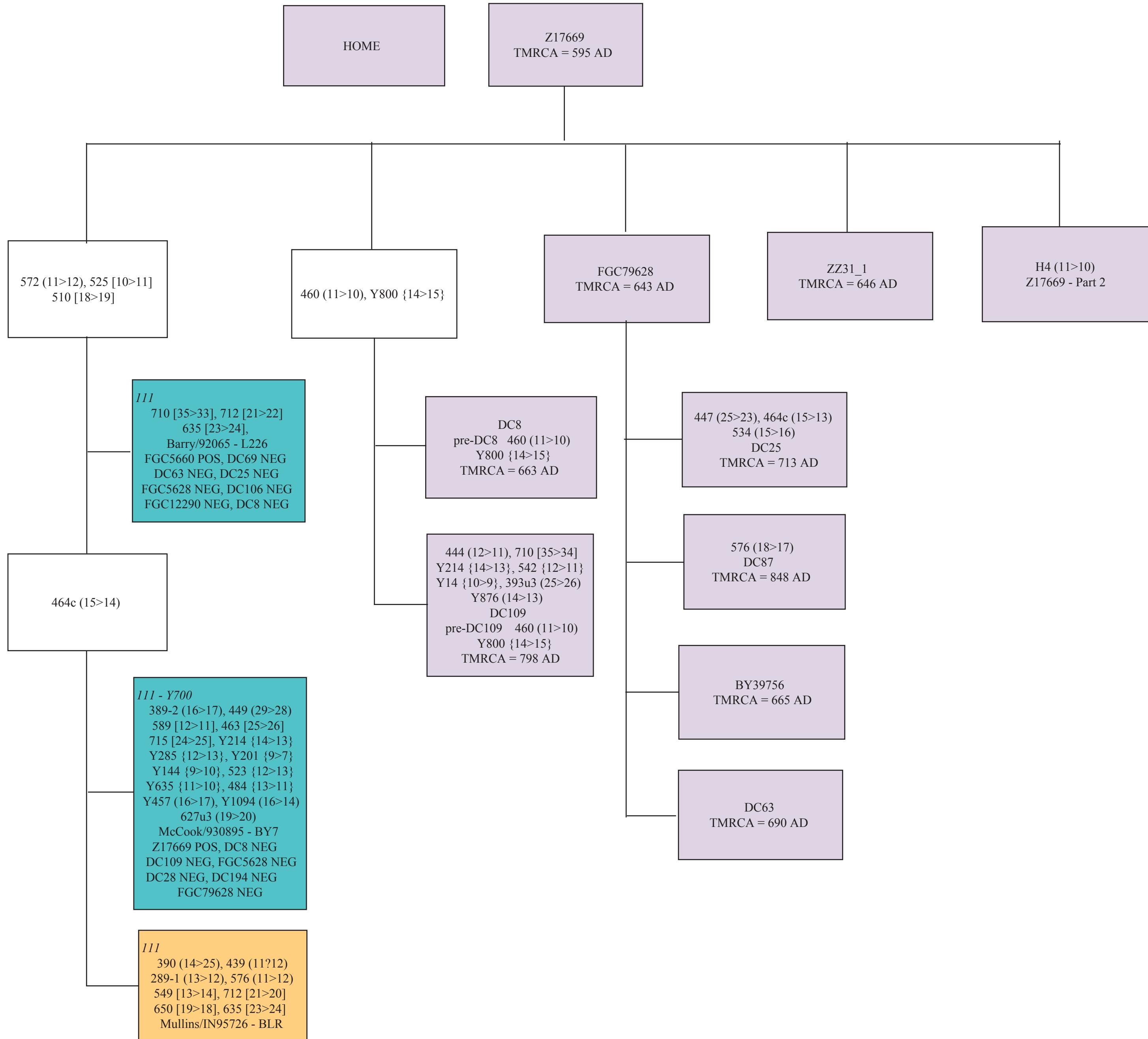
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534 (16>17)
Quillin/213063 - BLR

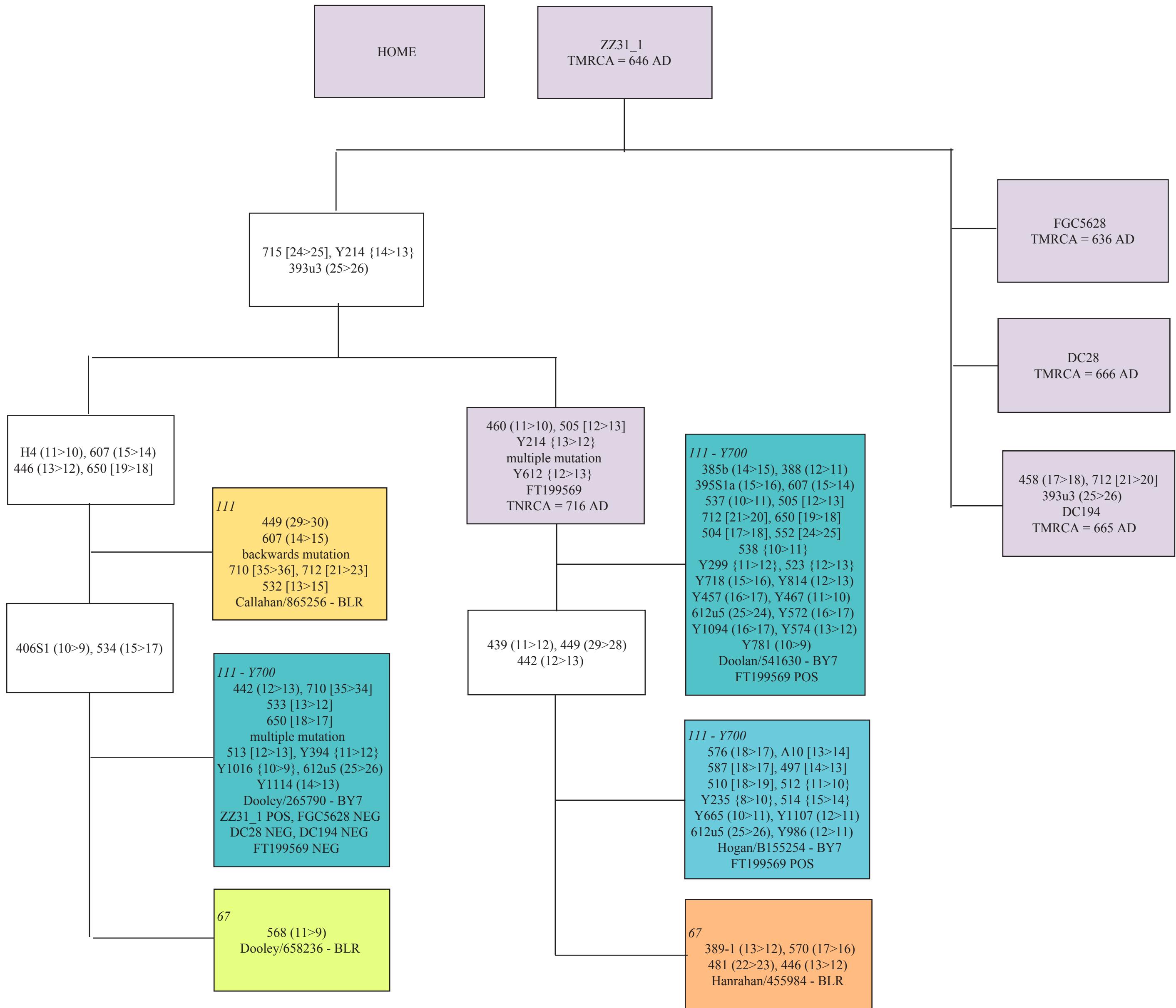
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442 (12>13)
Quillin/276166 - BLR

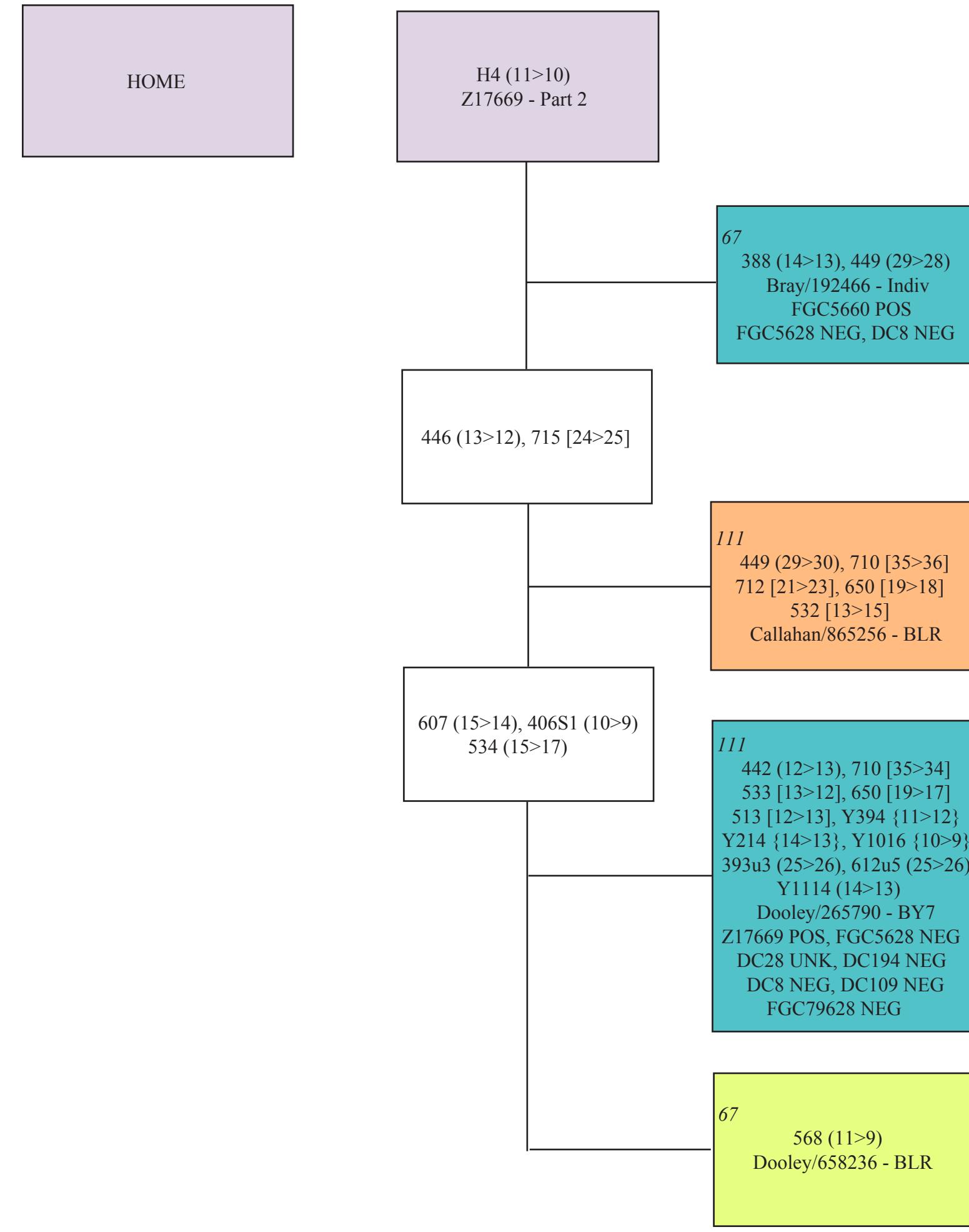


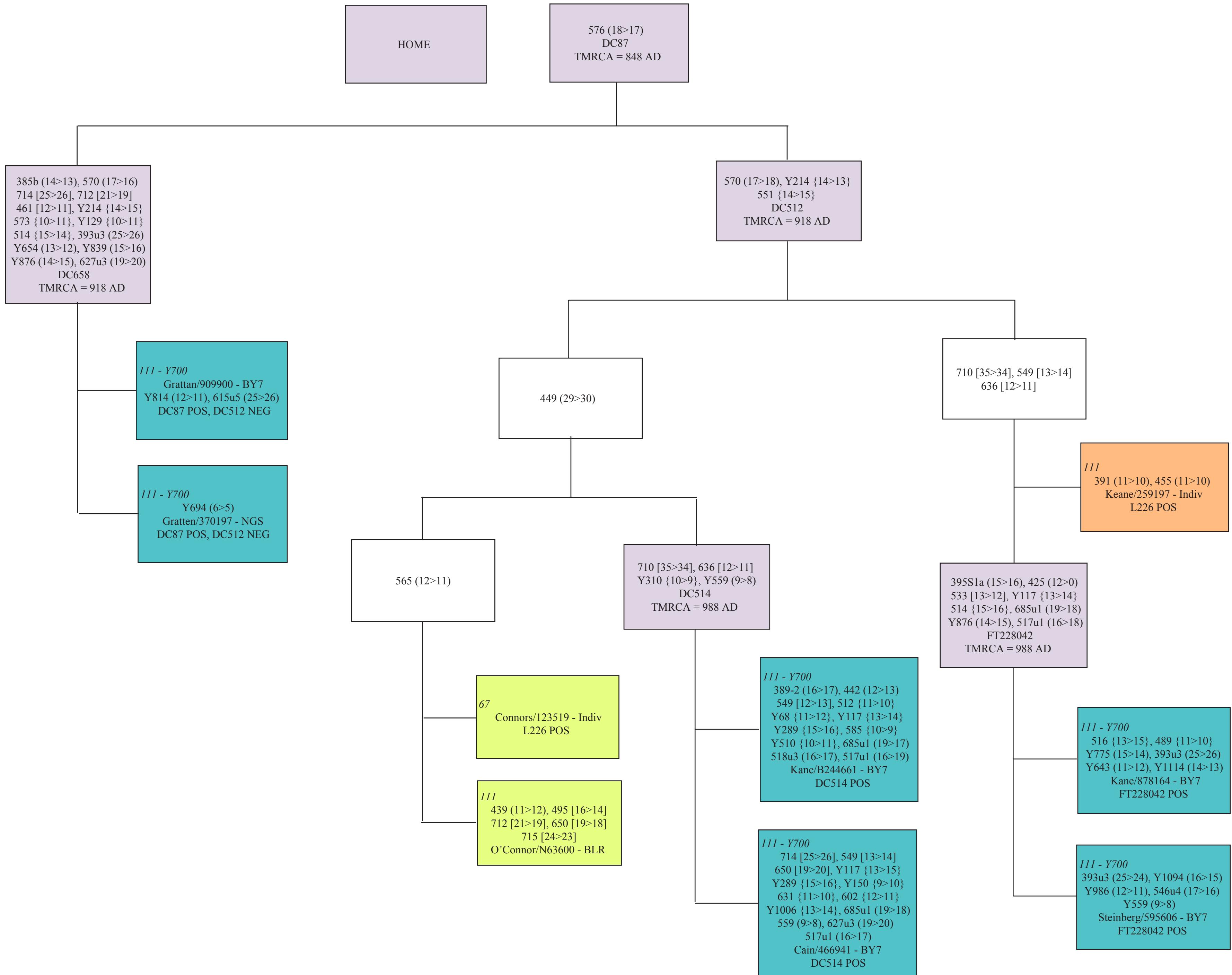


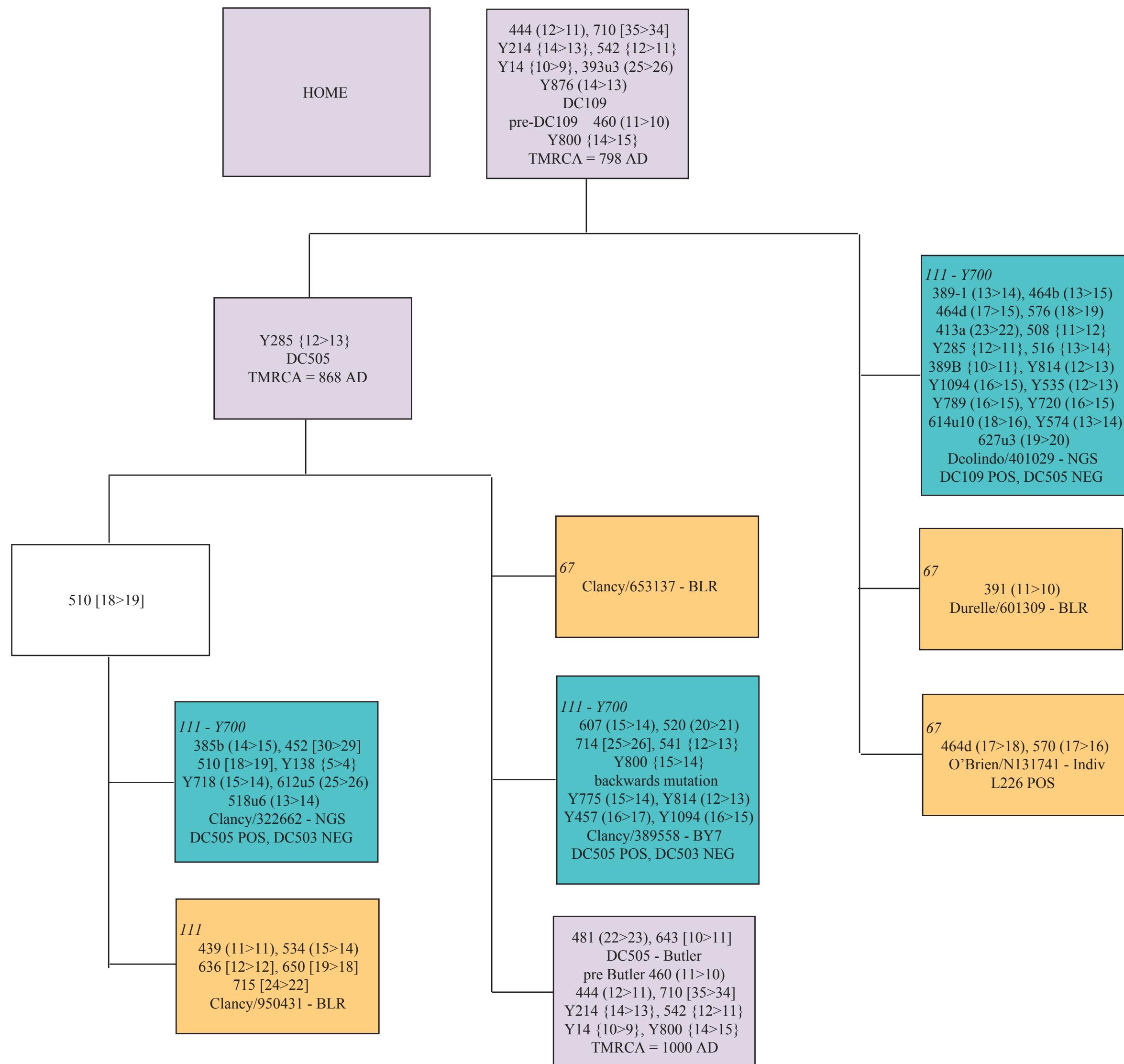


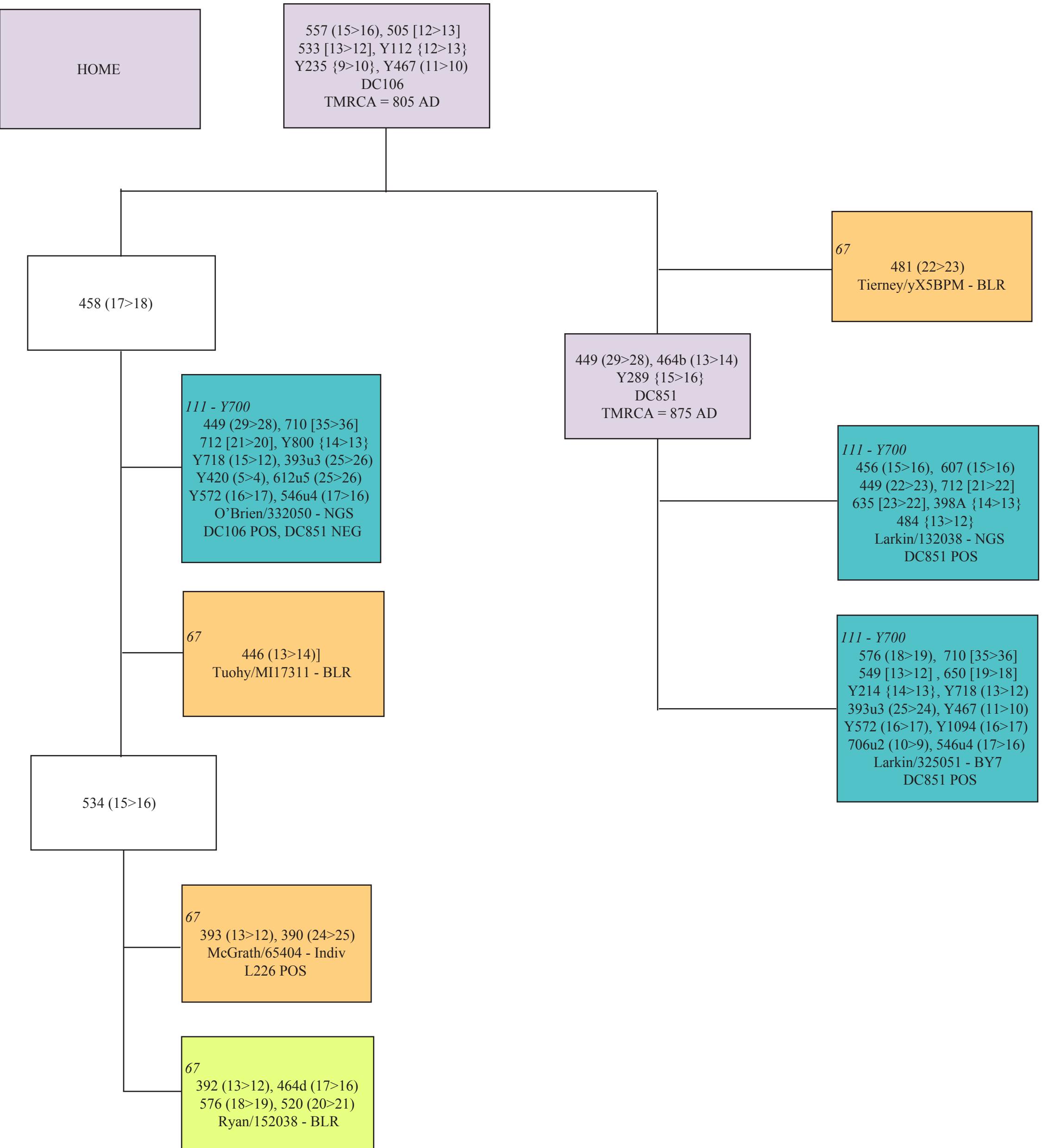


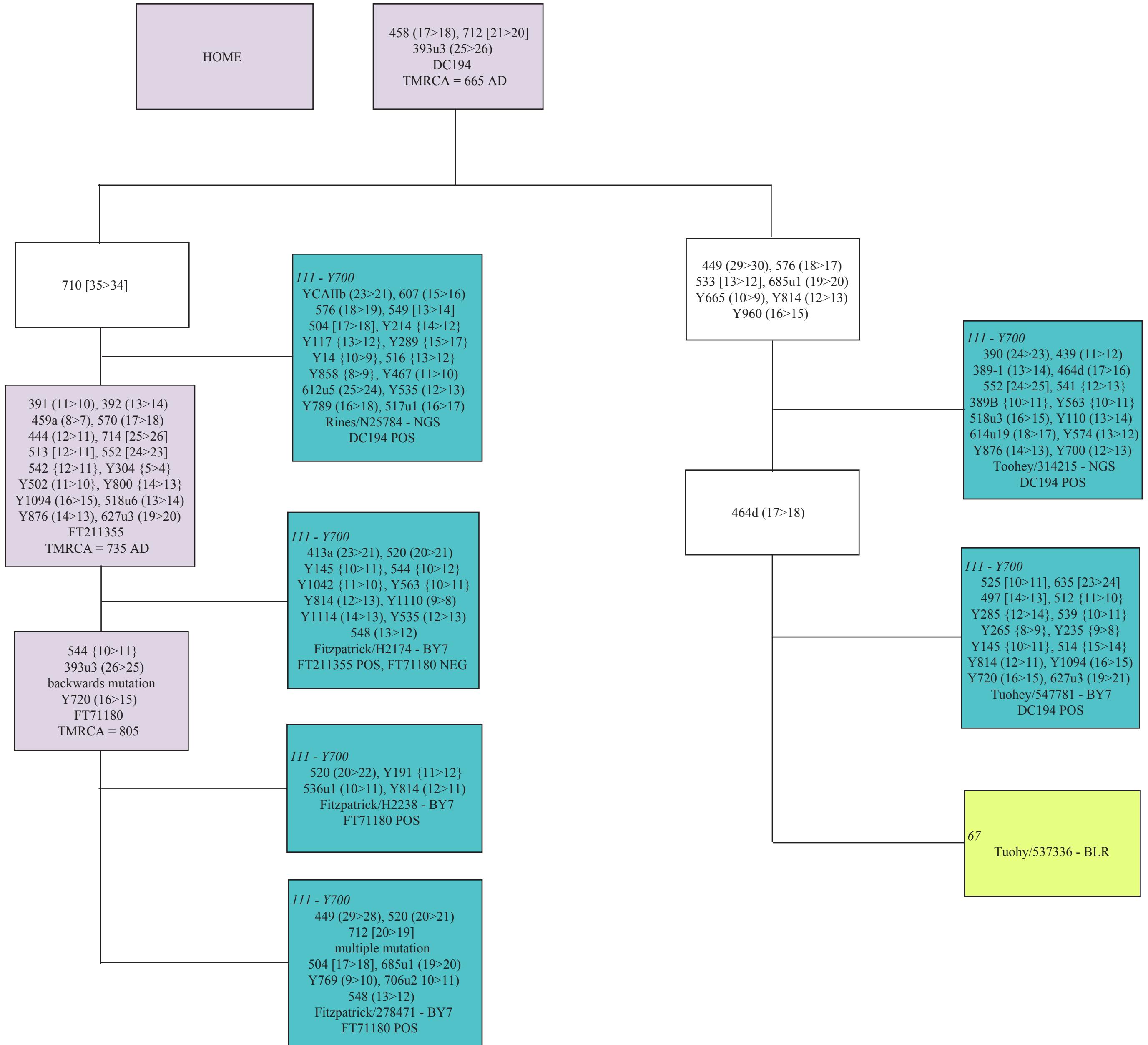


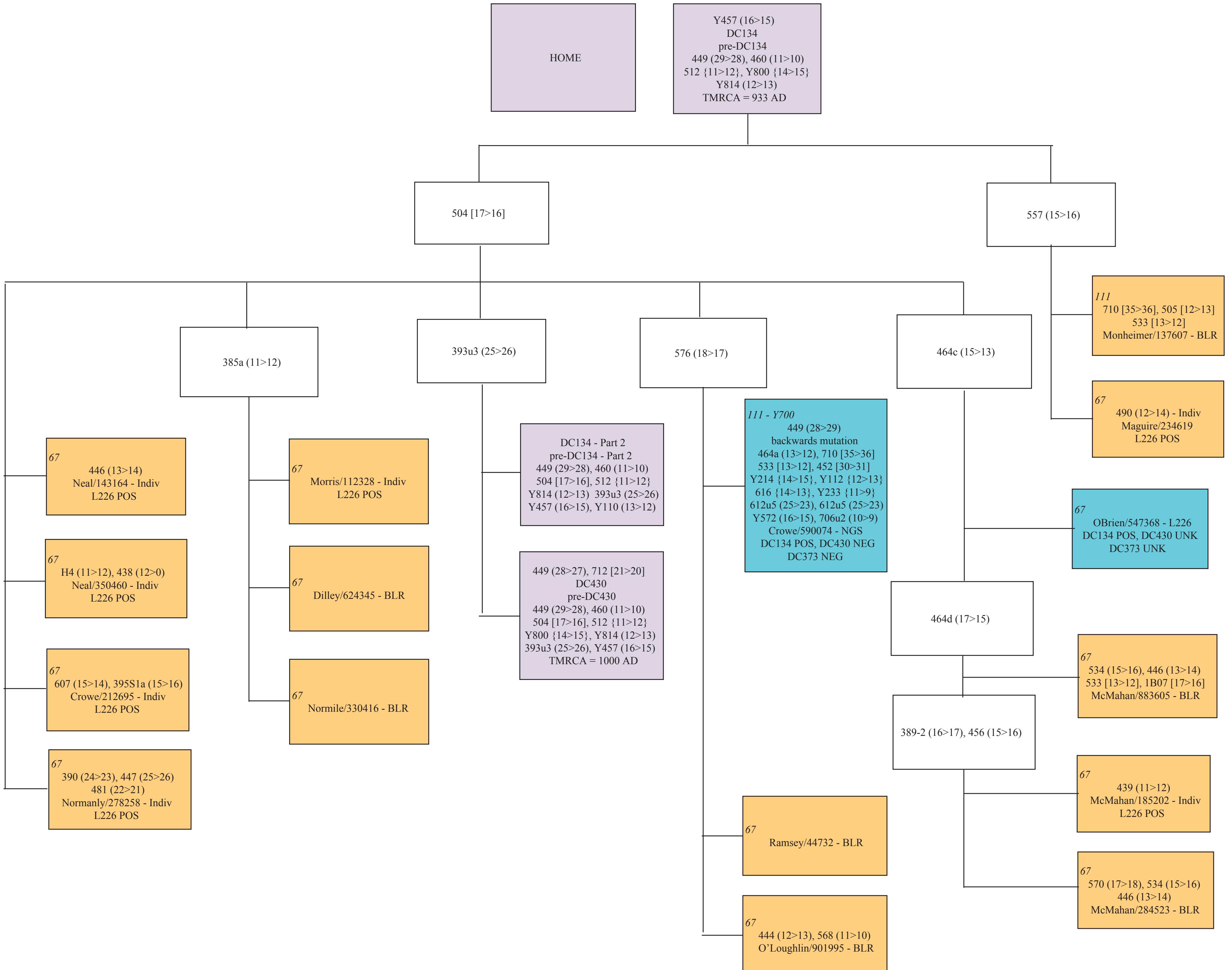


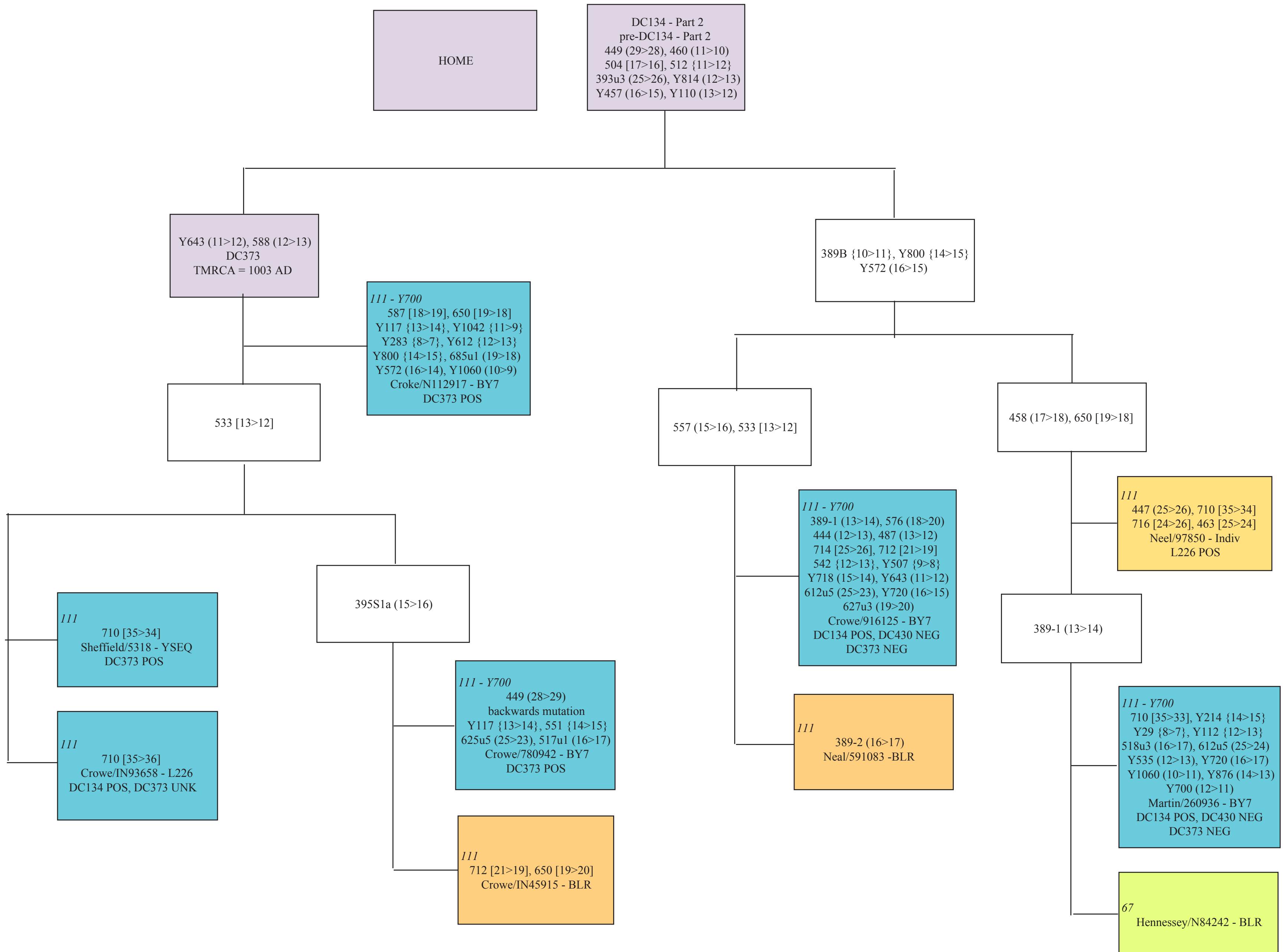


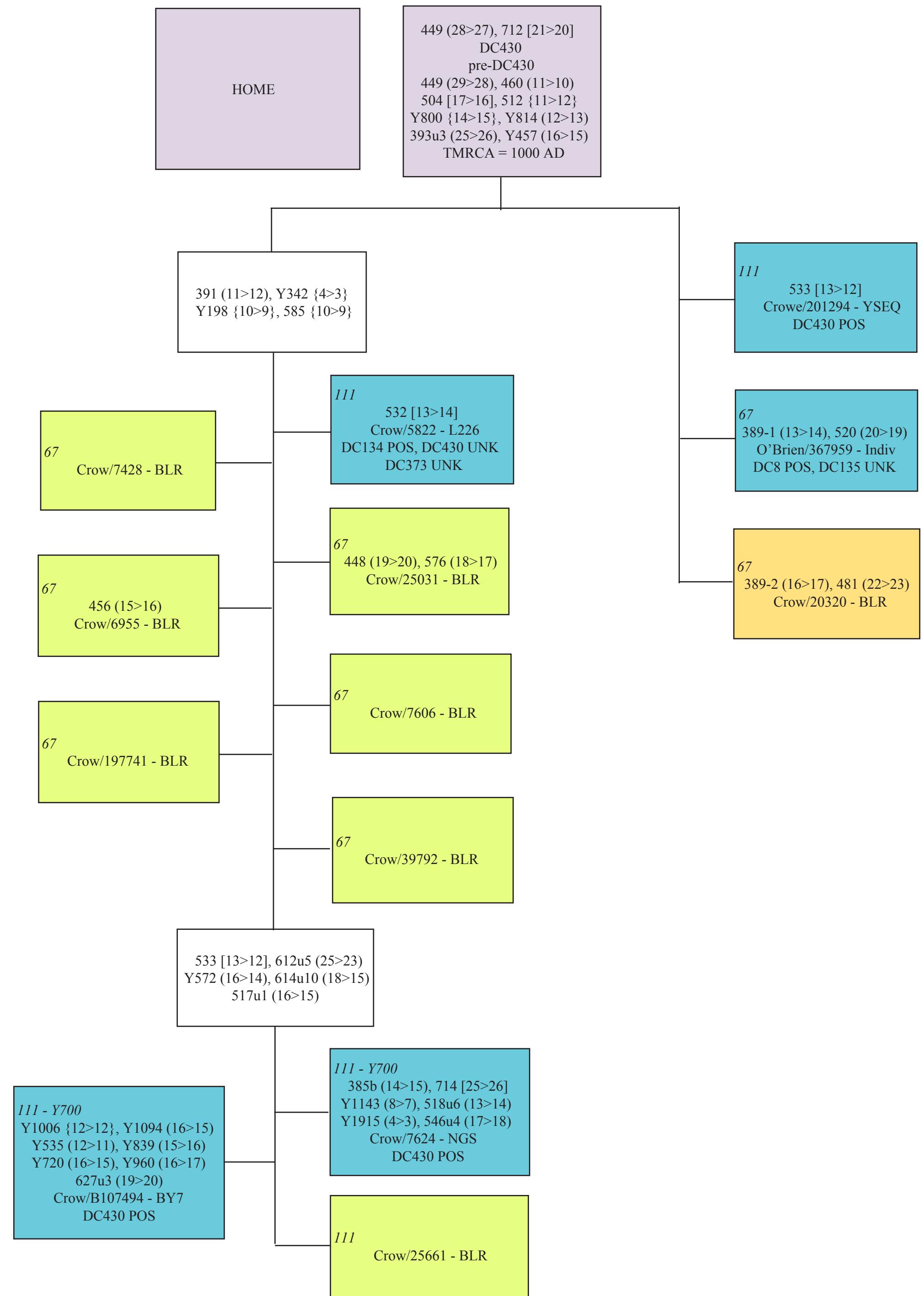


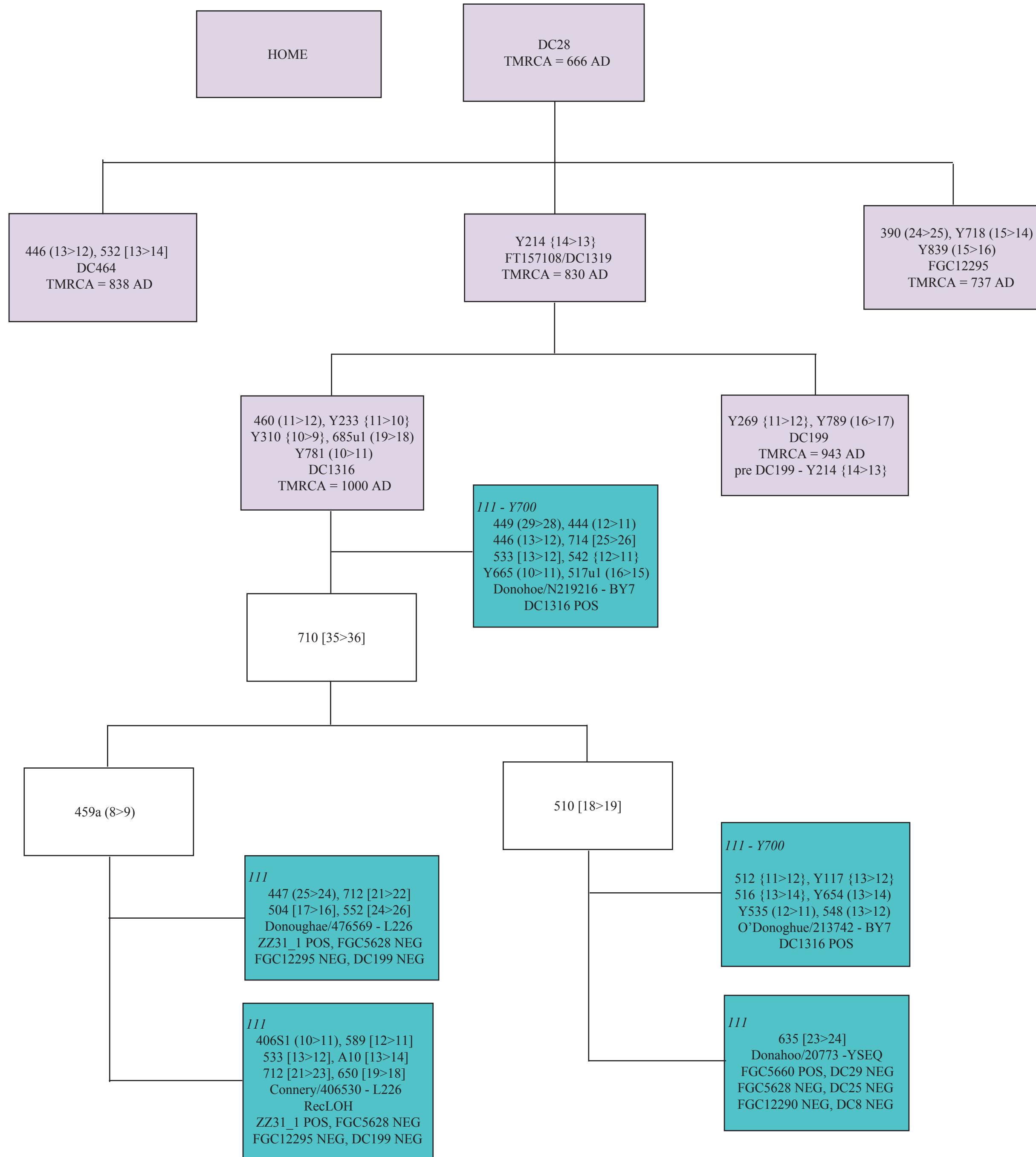


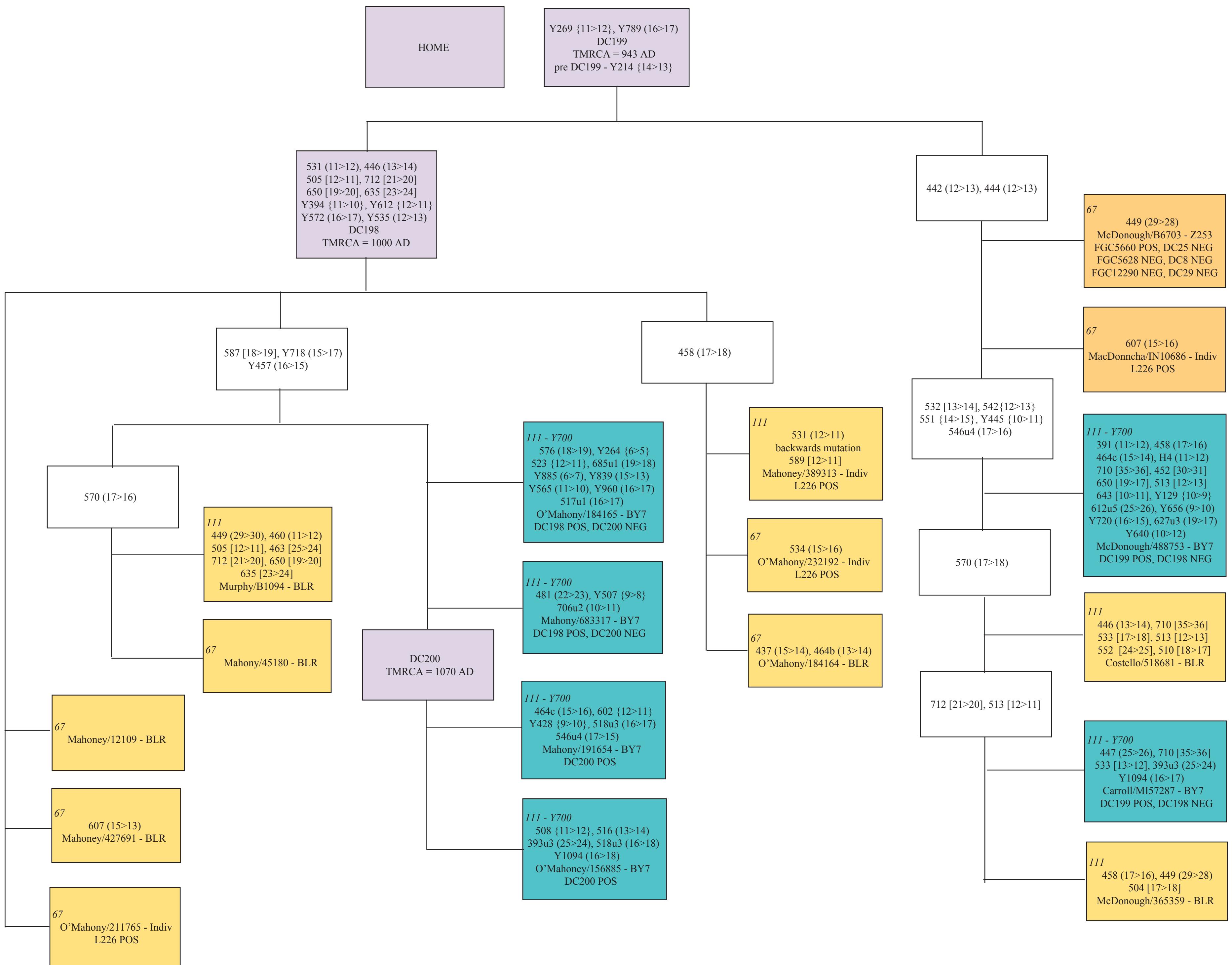


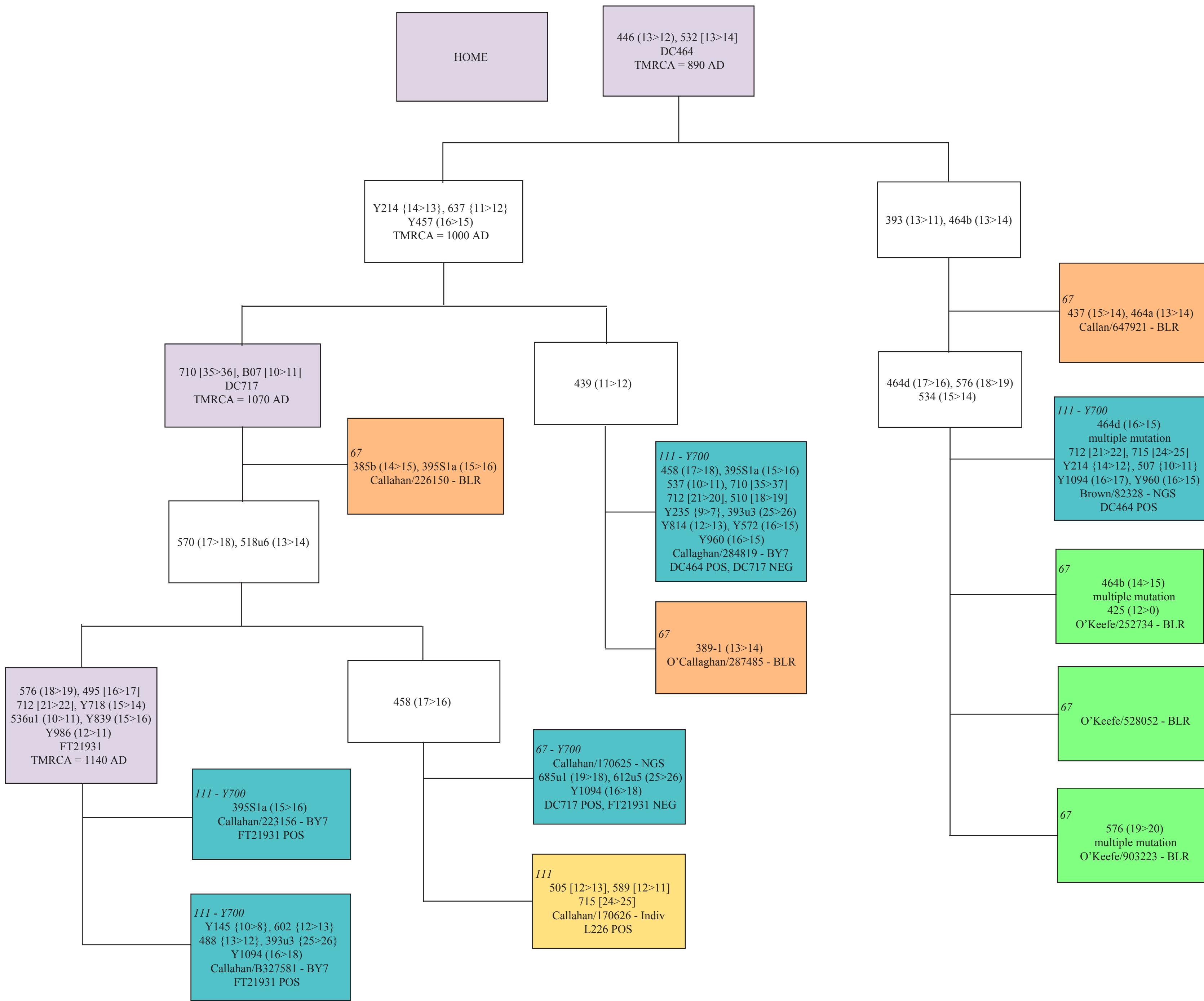


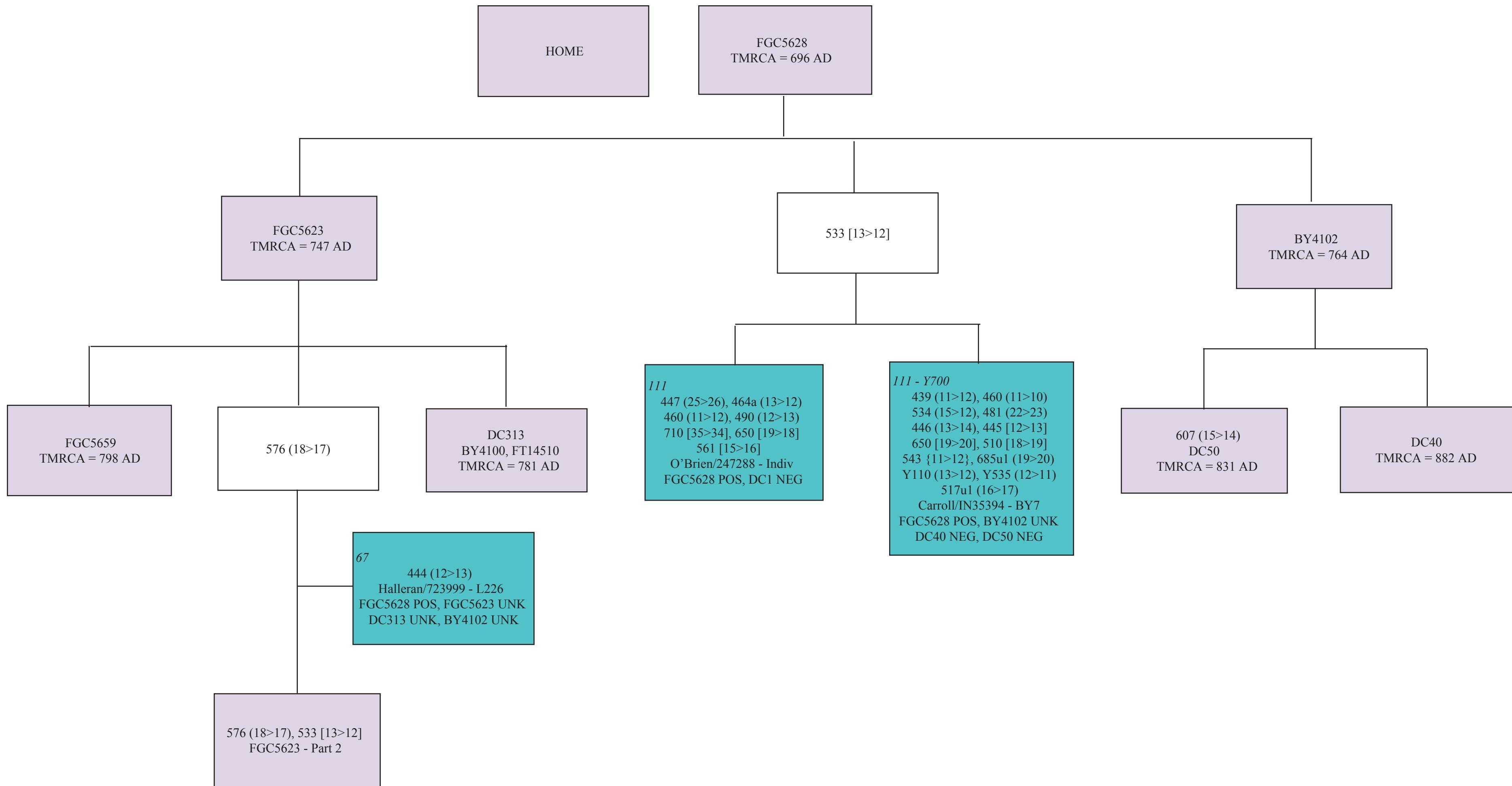


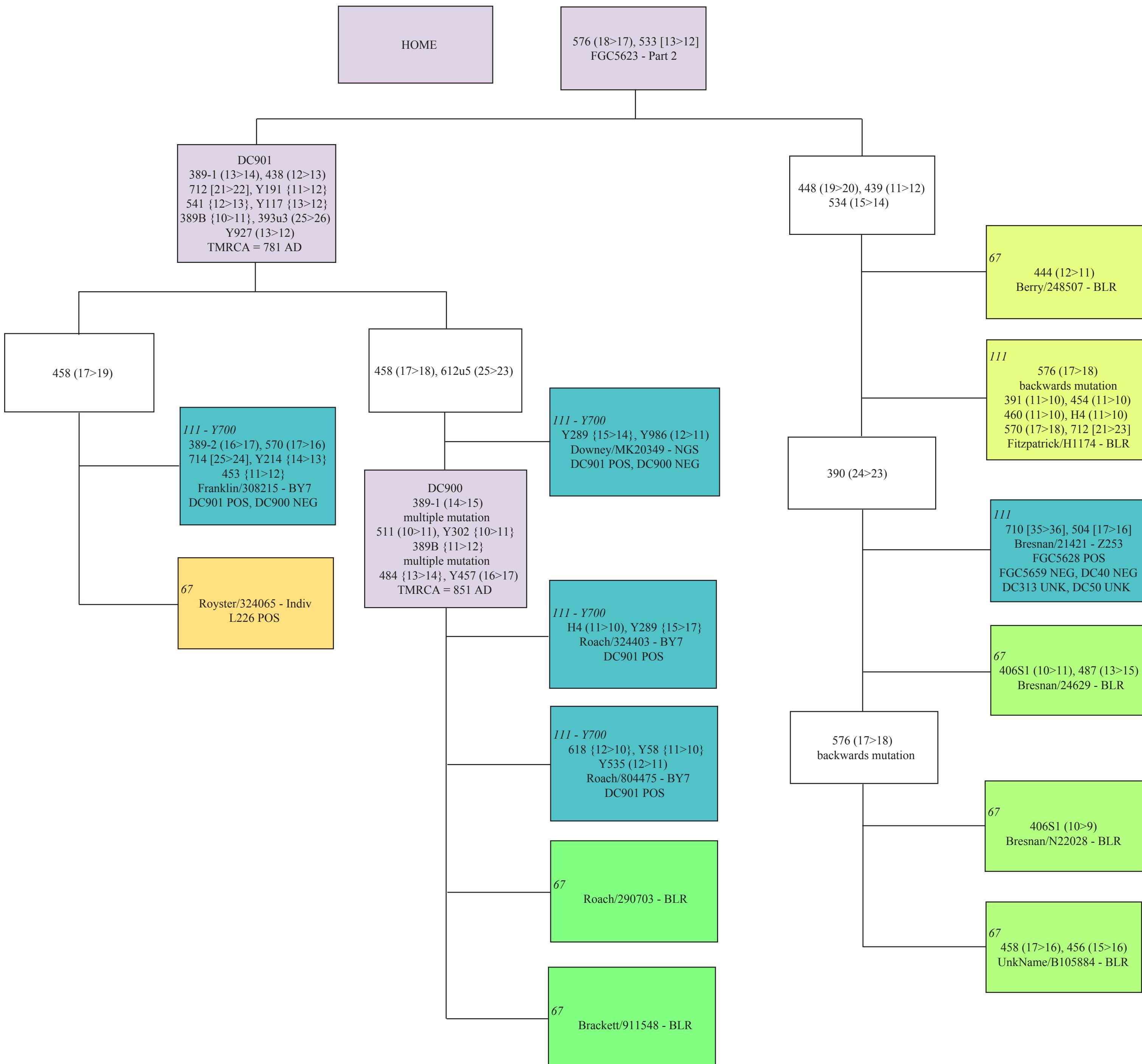


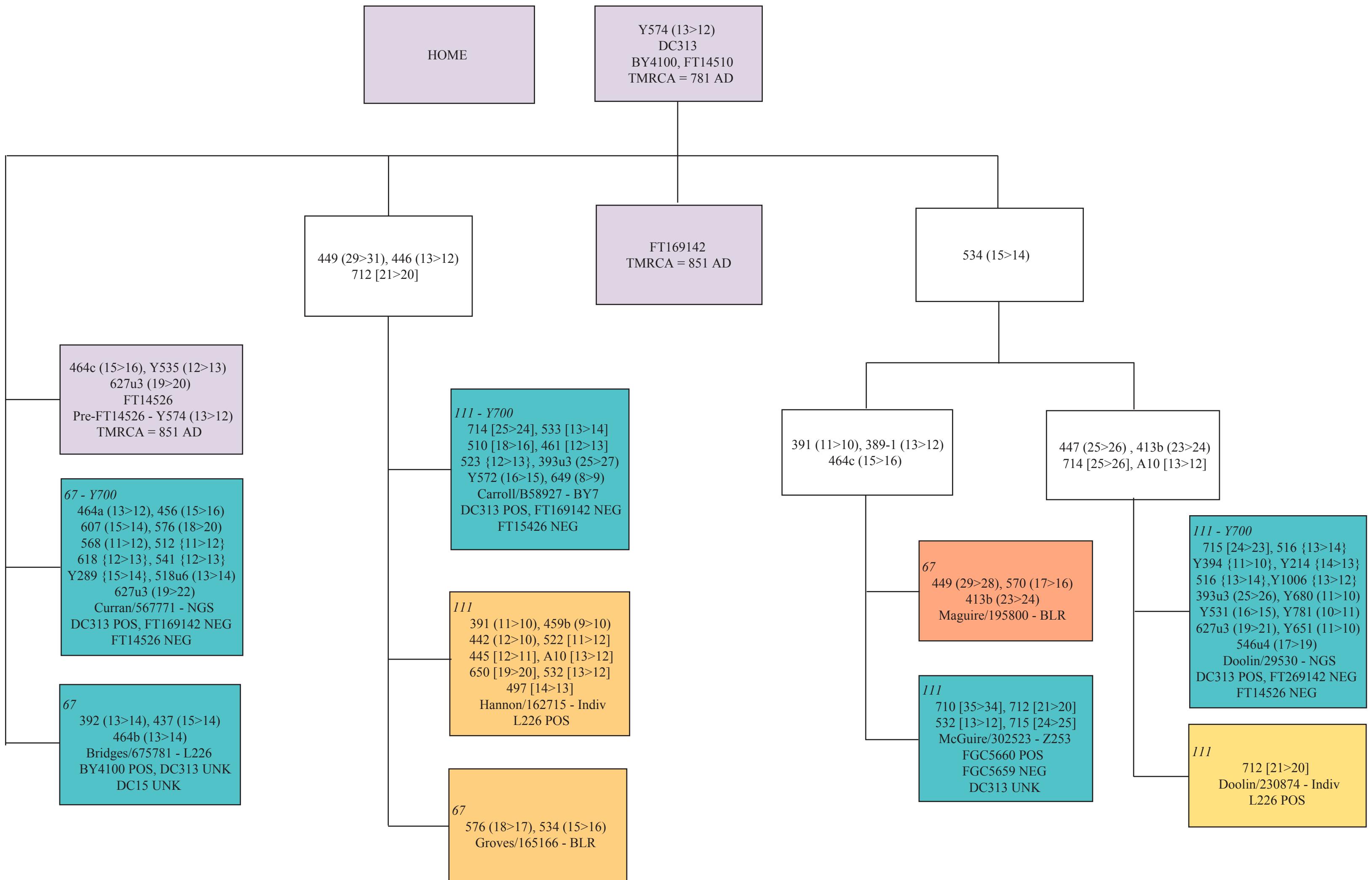


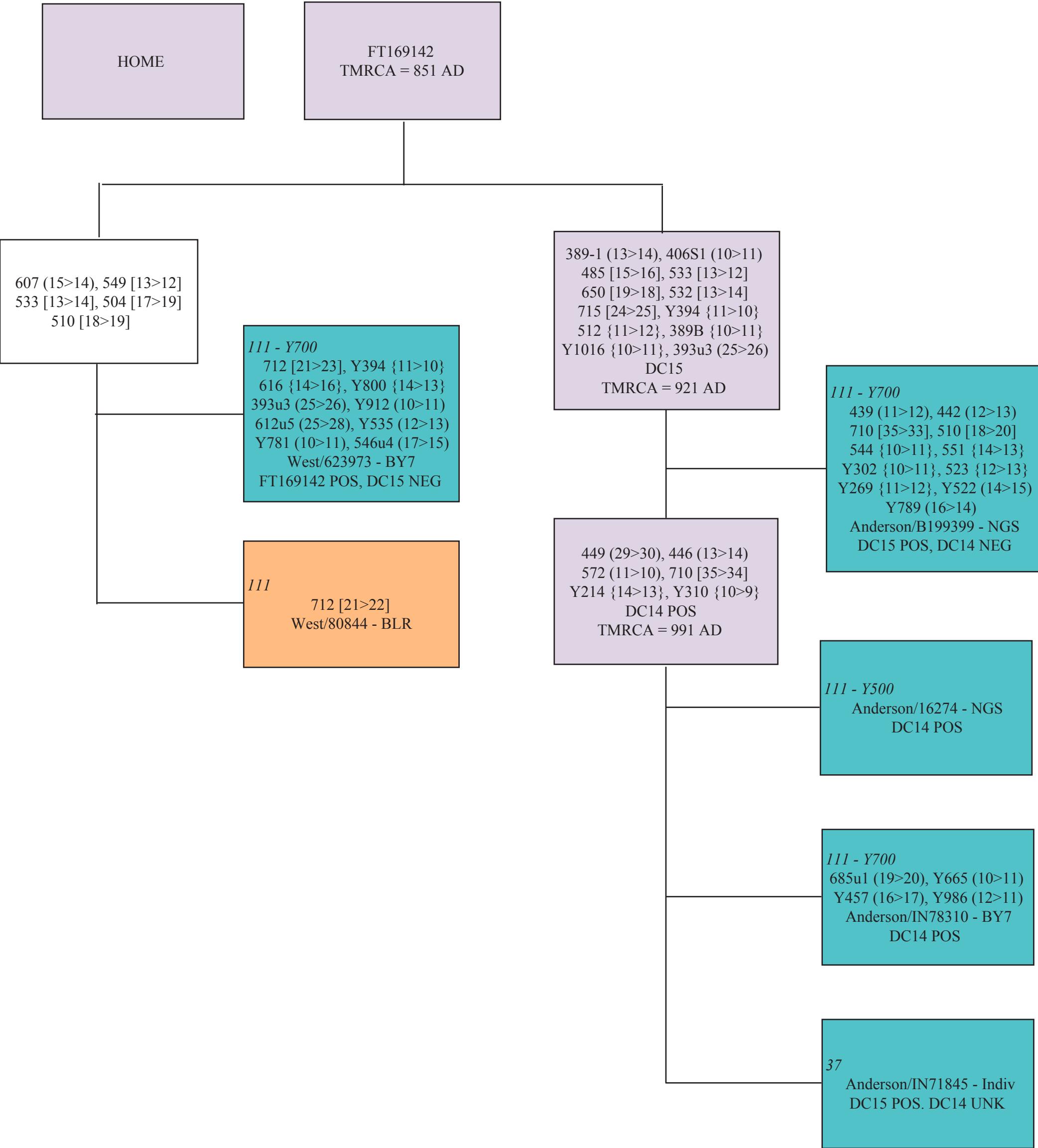


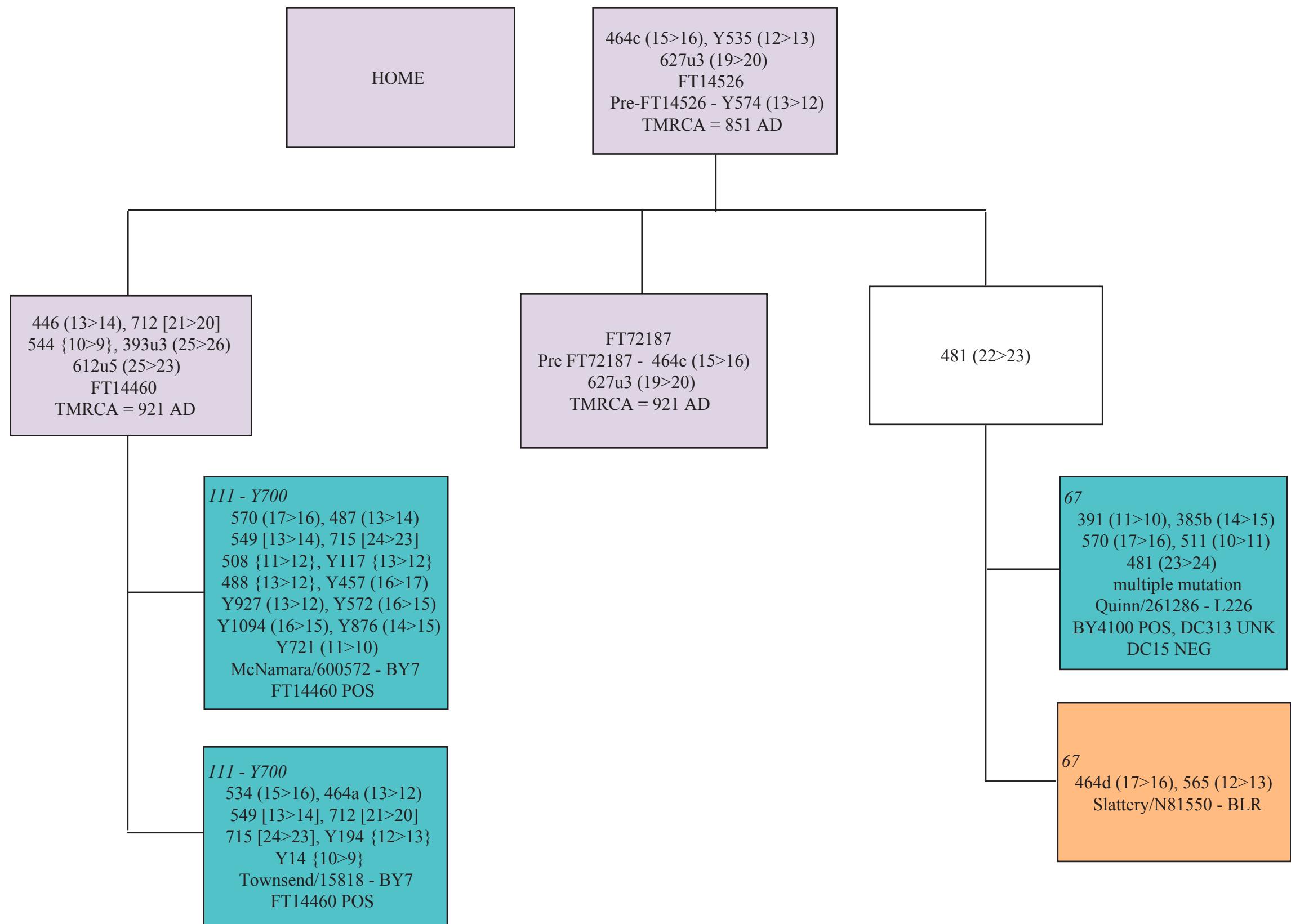


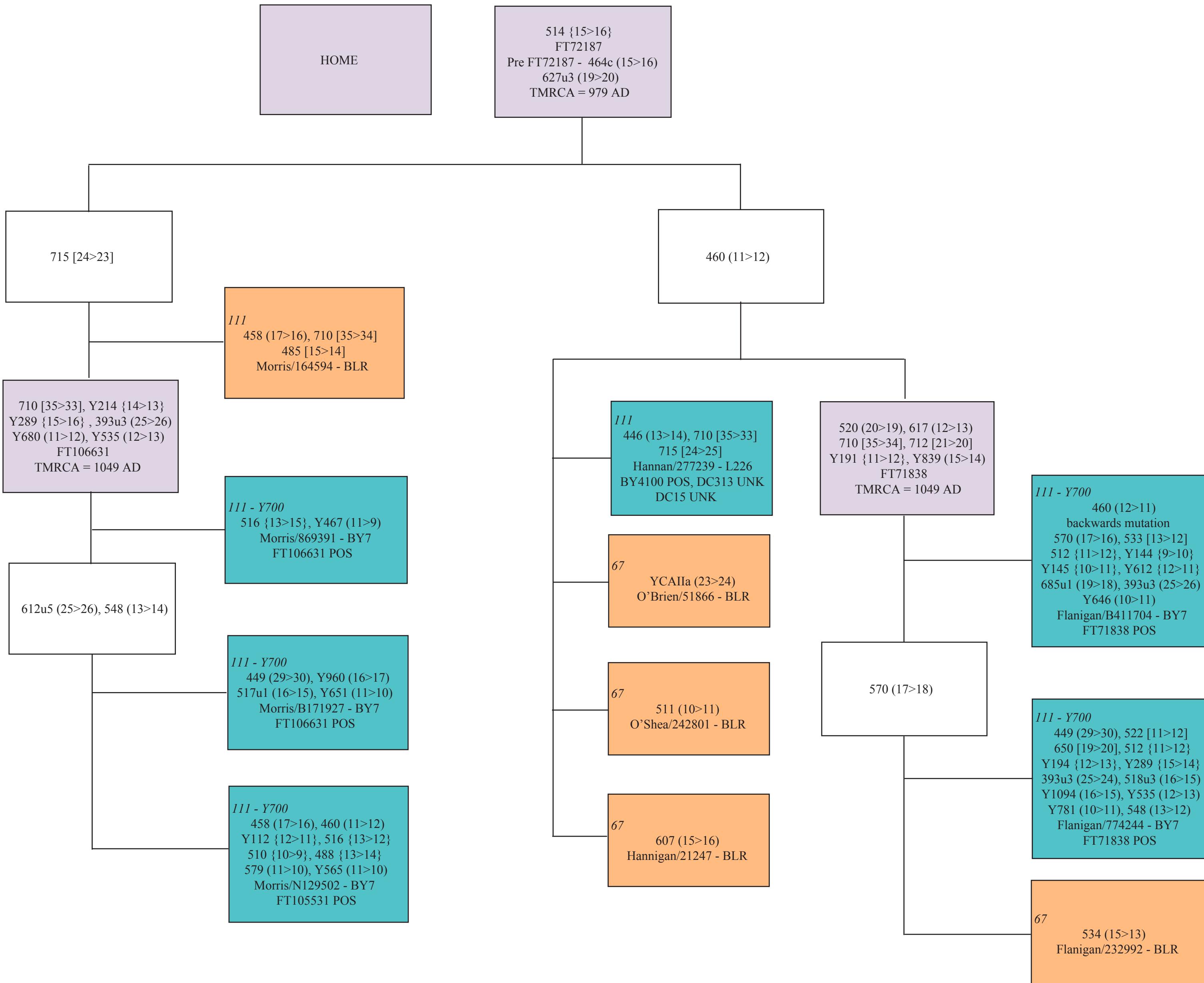


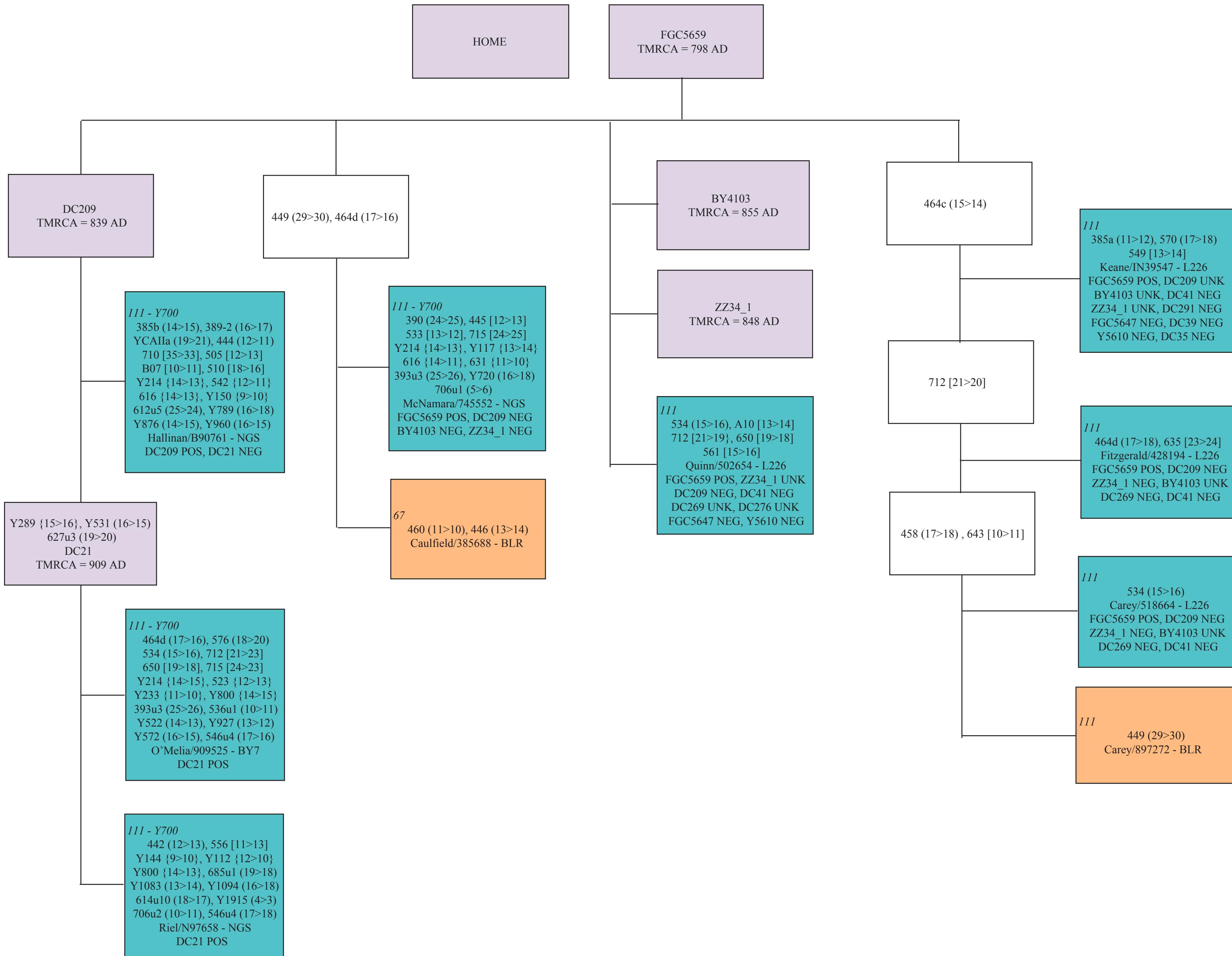


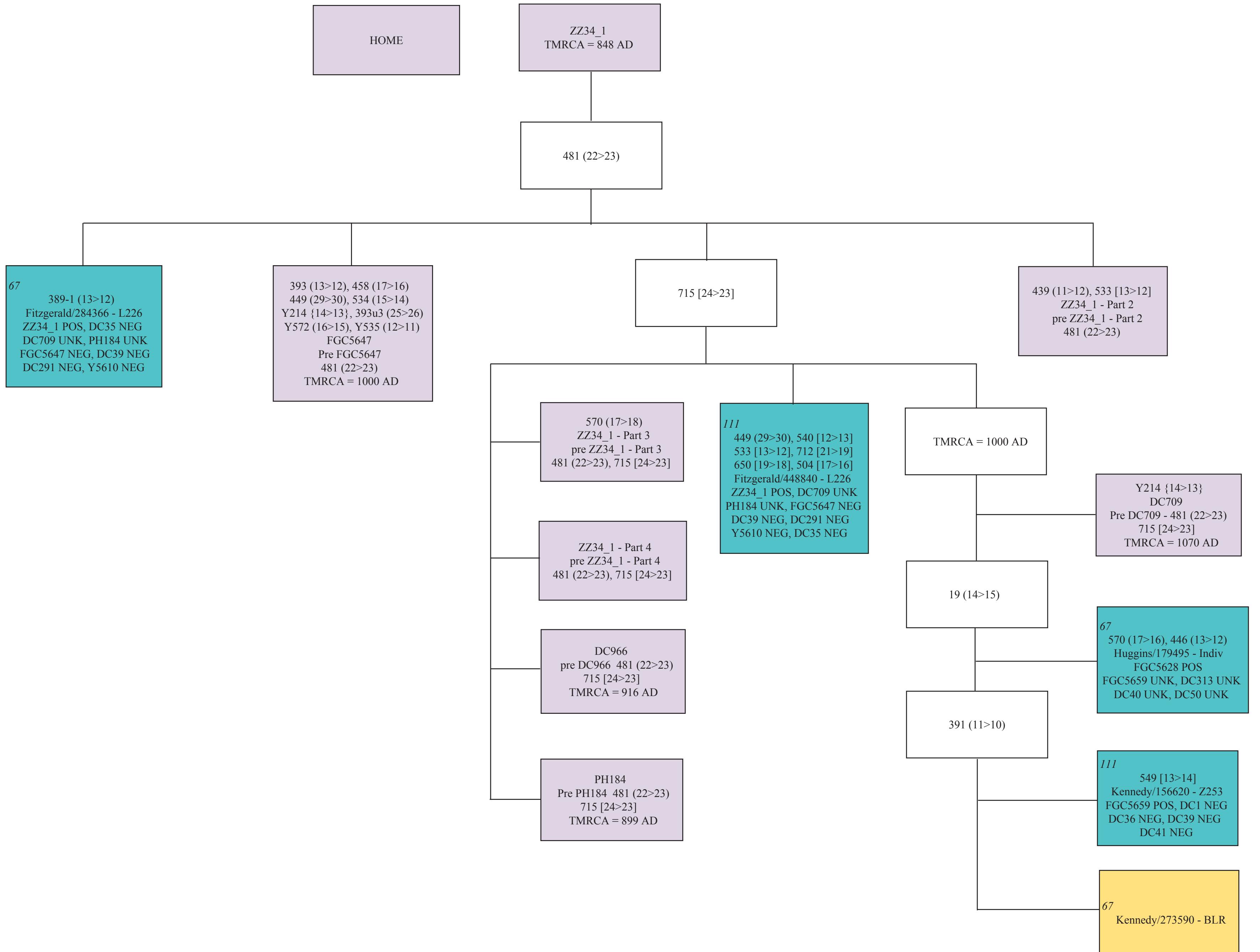


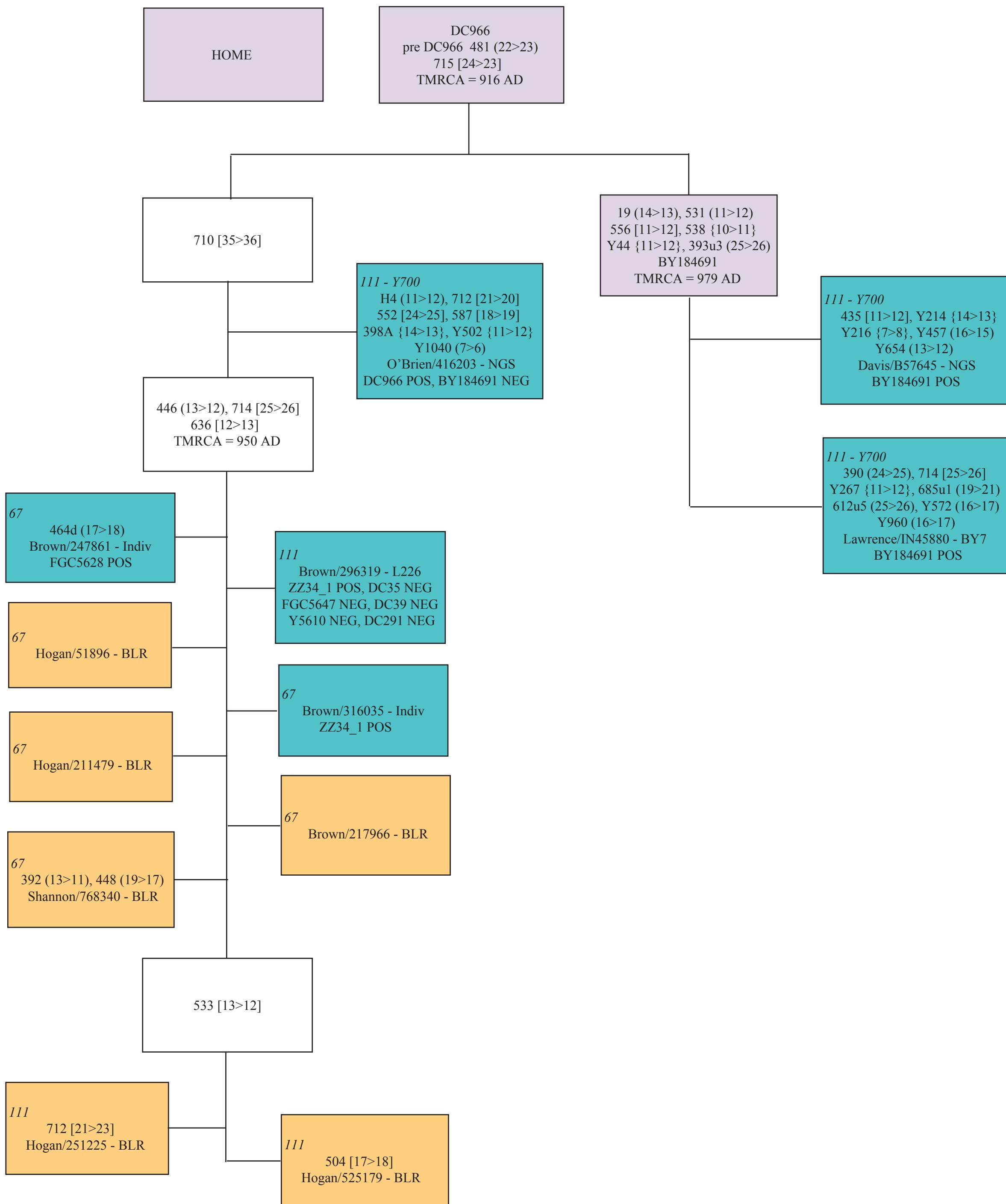












HOME

439 (11>12), 533 [13>12]
ZZ34_1 - Part 2
pre ZZ34_1 - Part 2
481 (22>23)

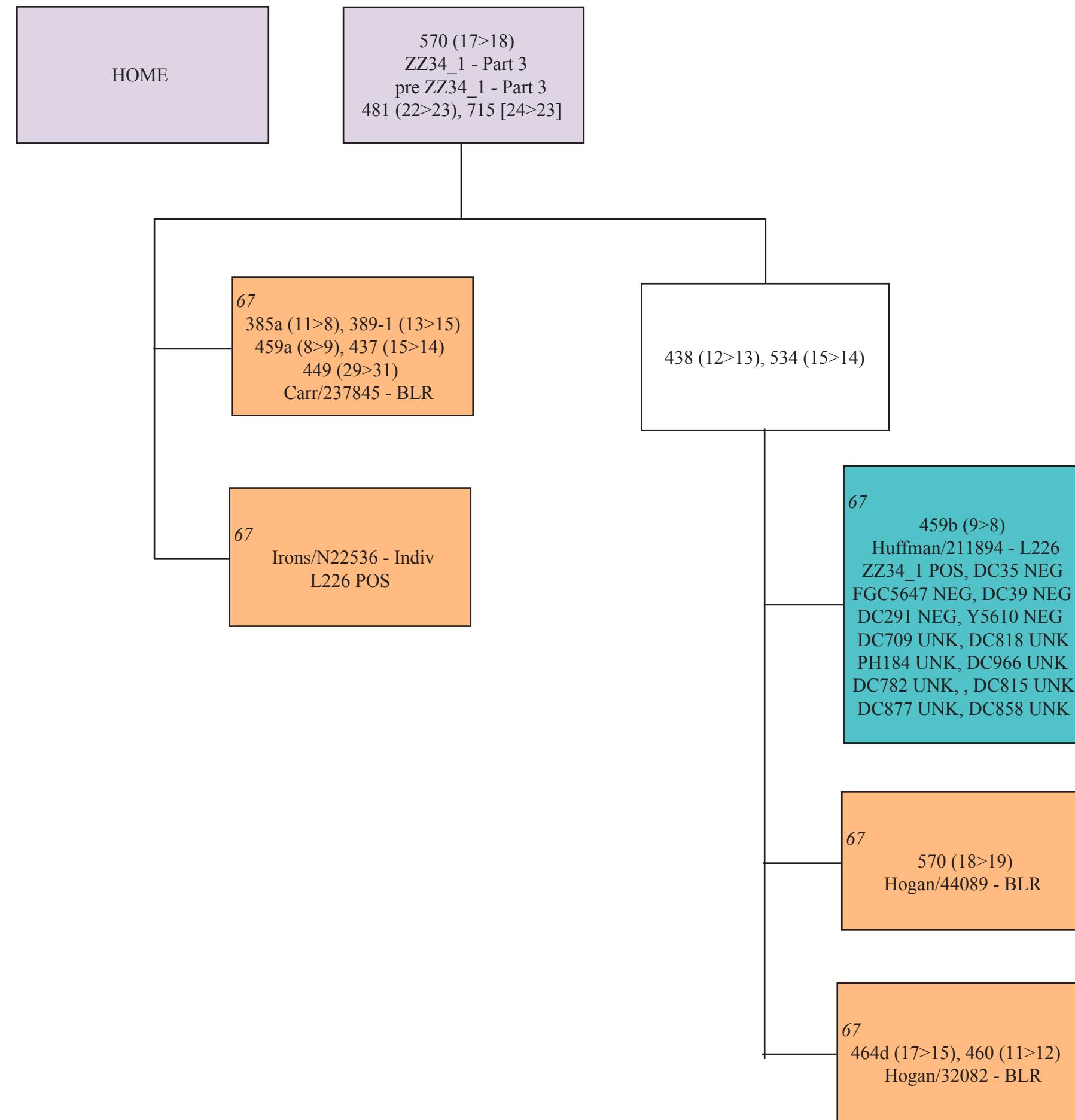
67
449 (29>28)
Fitzgerald/183282 - Indiv
L226 POS

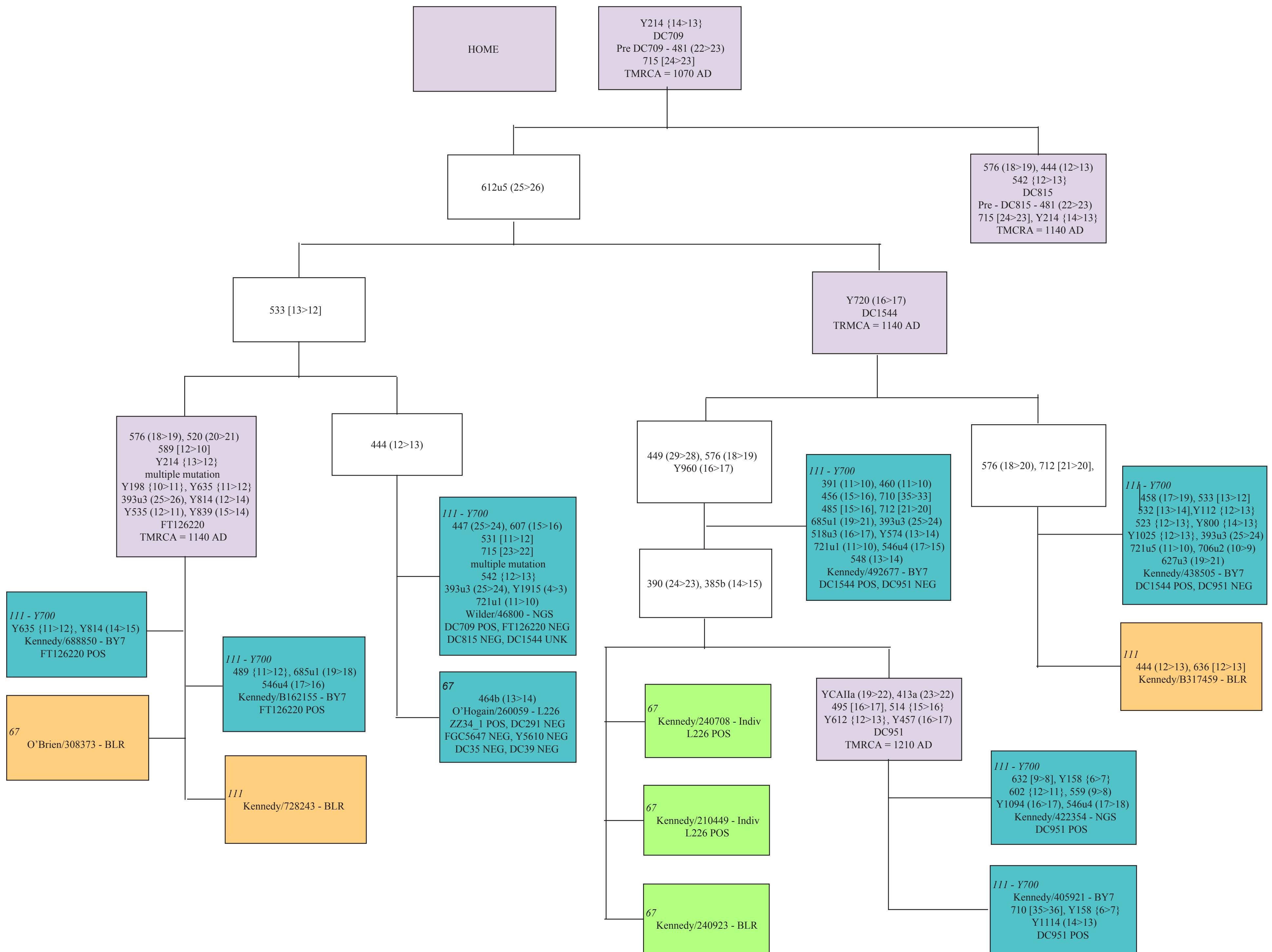
67
YCAIIb (23>22)
Graham/27276 - Indiv
L226 POS

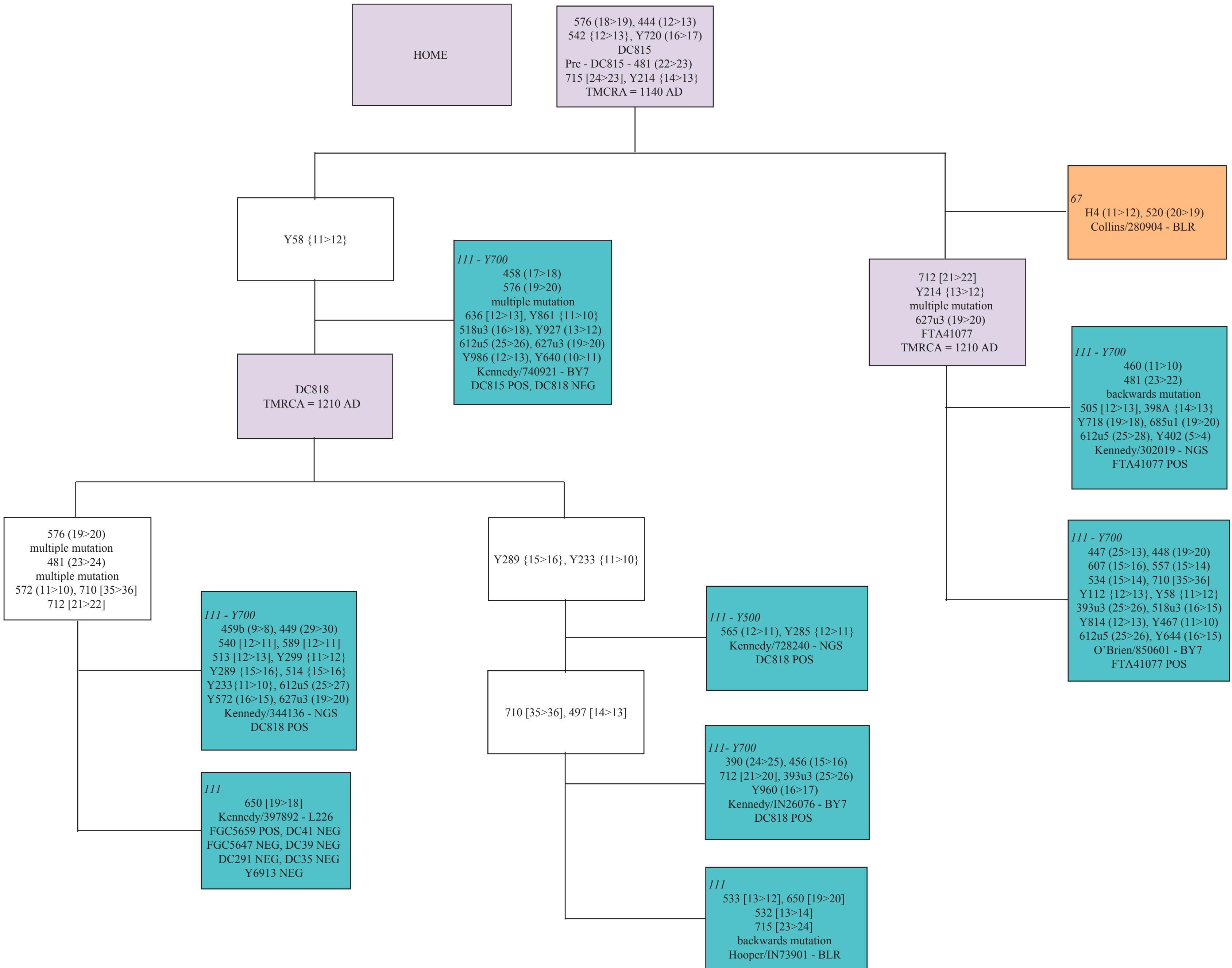
712 [21>22], 532 [13>14]

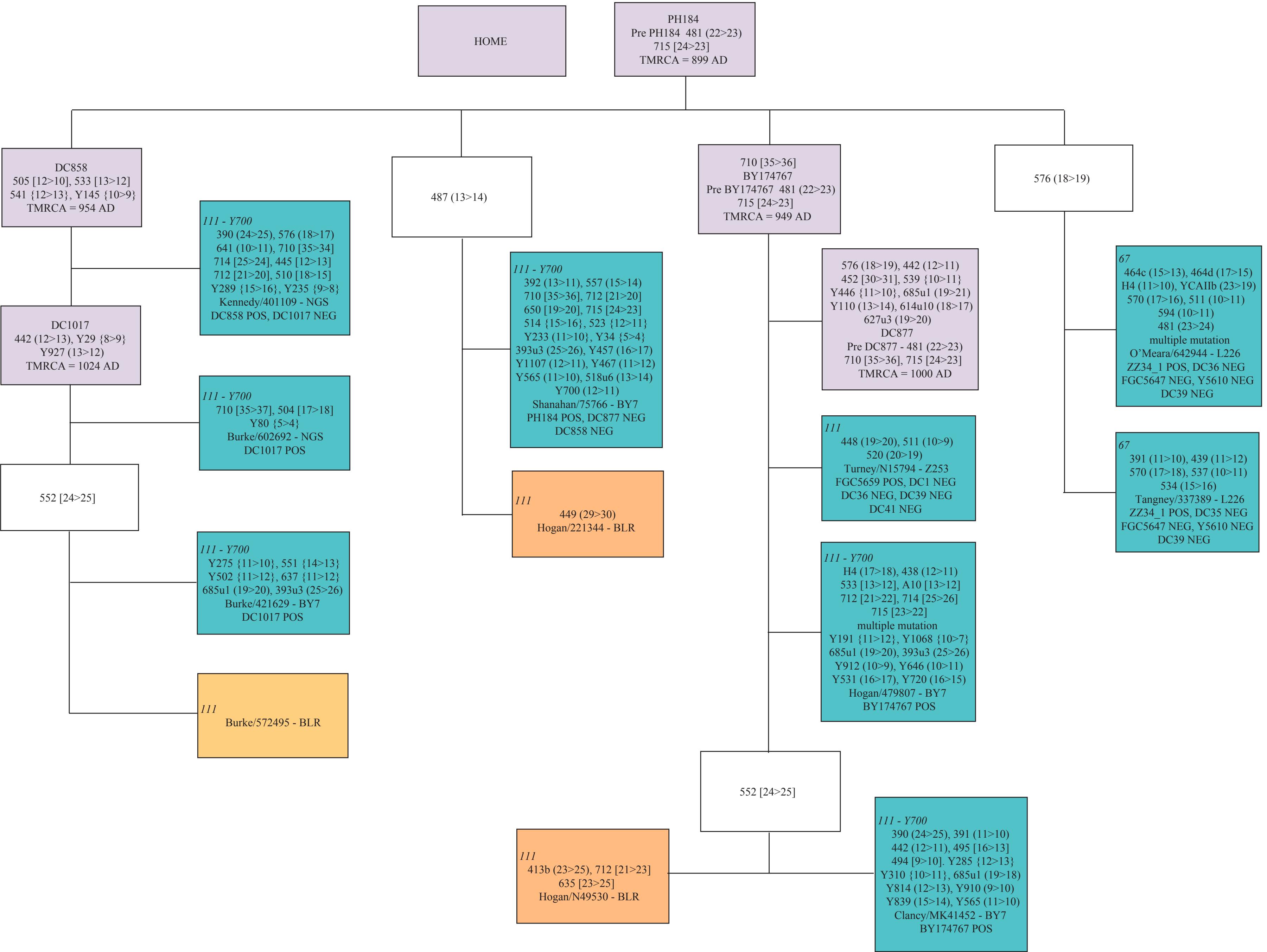
111
714 [25>24], 715 [24>23]
Graham/583951 - L226
ZZ34_1 POS, DC35 NEG
DC709 UNK, PH184 UNK
FGC5647 NEG, DC39 NEG
DC291 NEG, Y5610 NEG

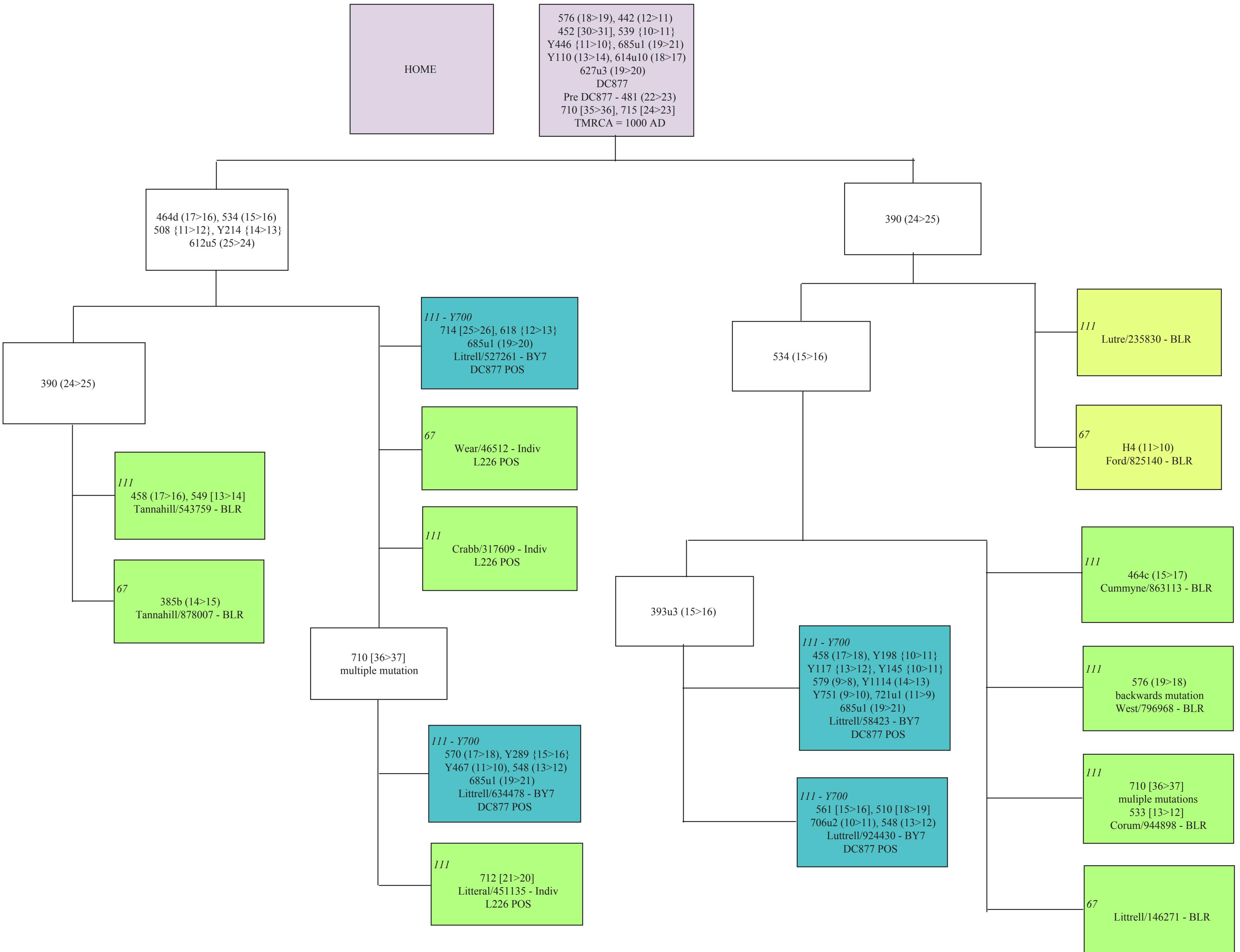
111
710 [35>36]
Graham/196734 - BLR

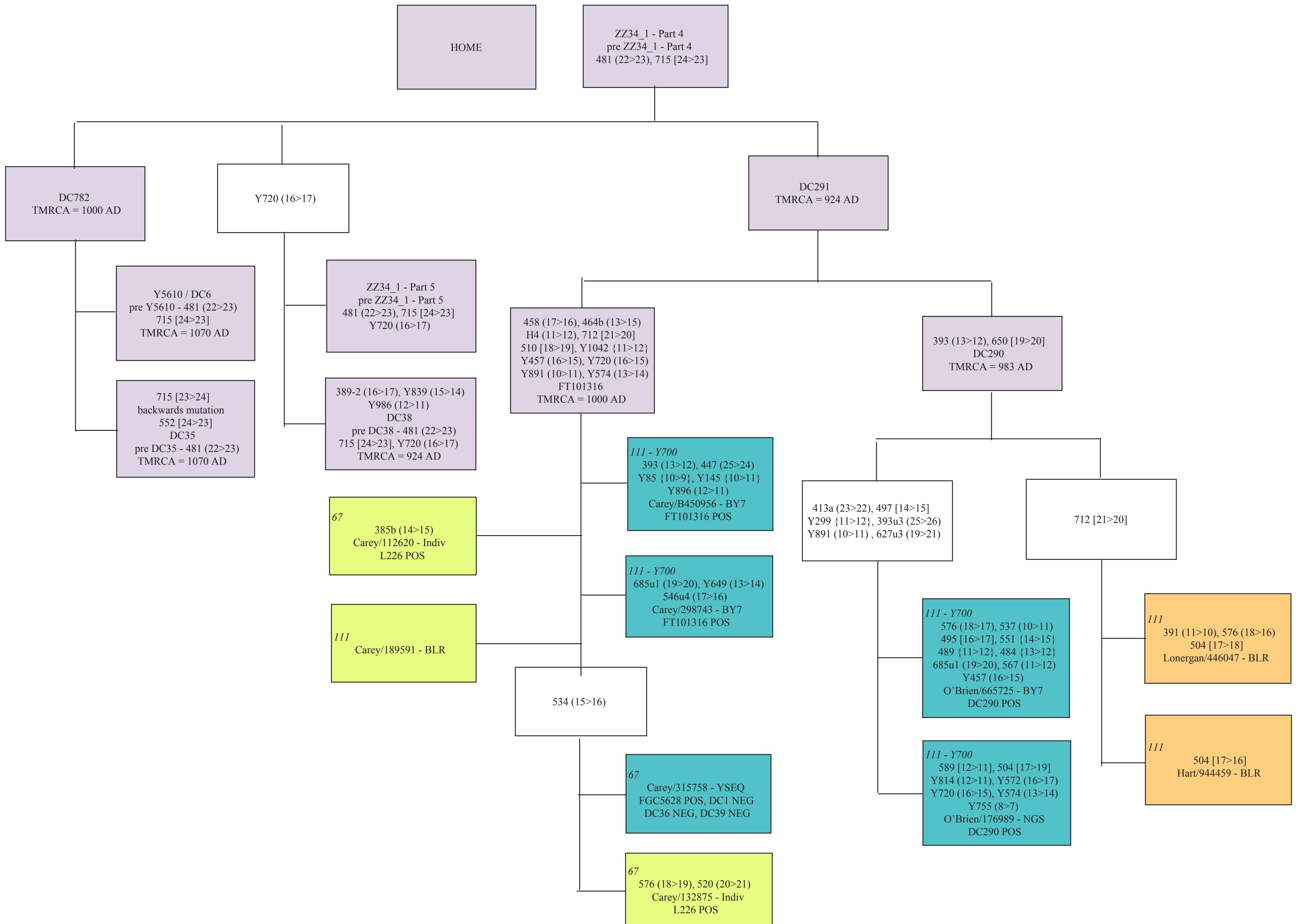


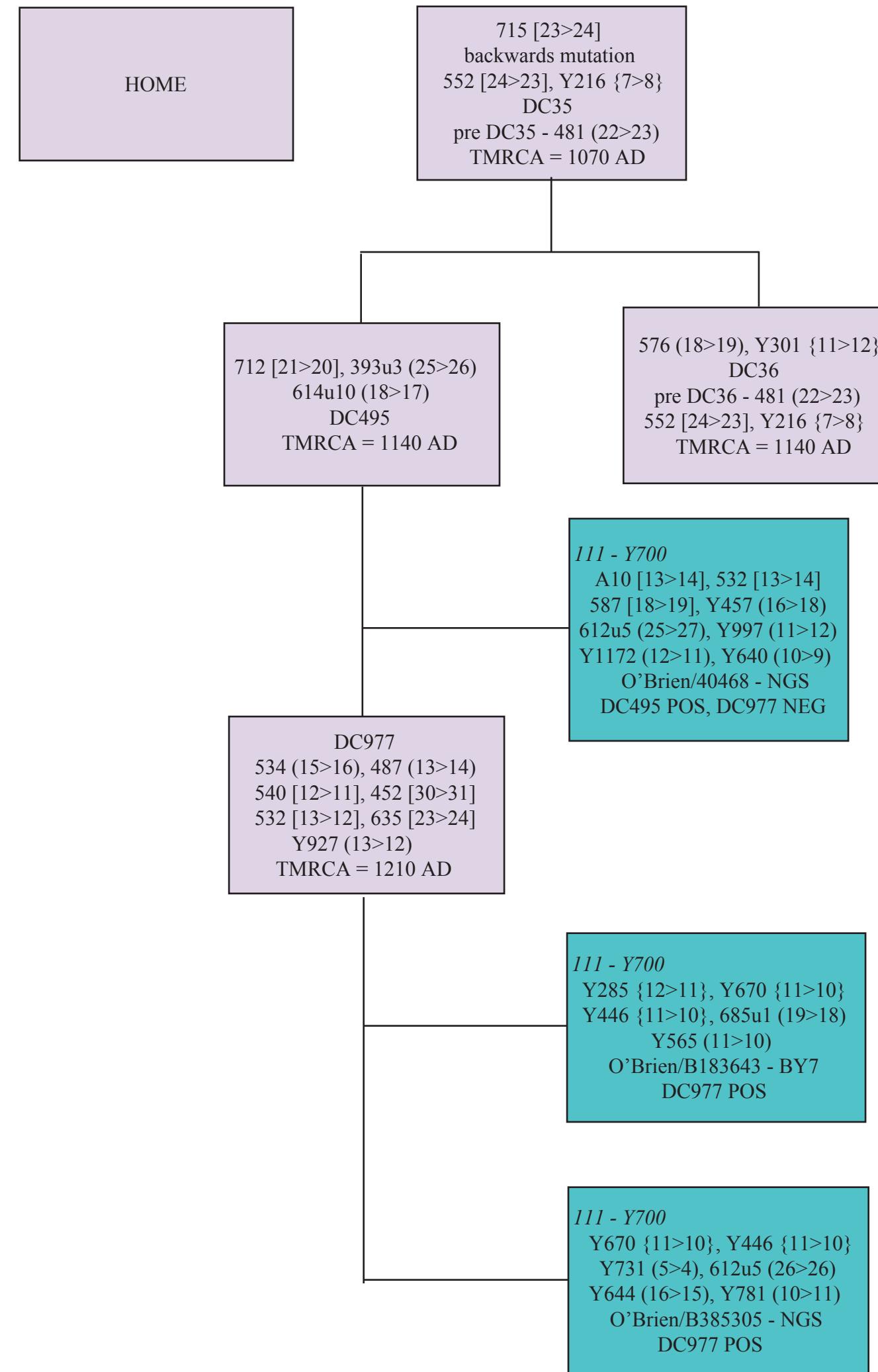


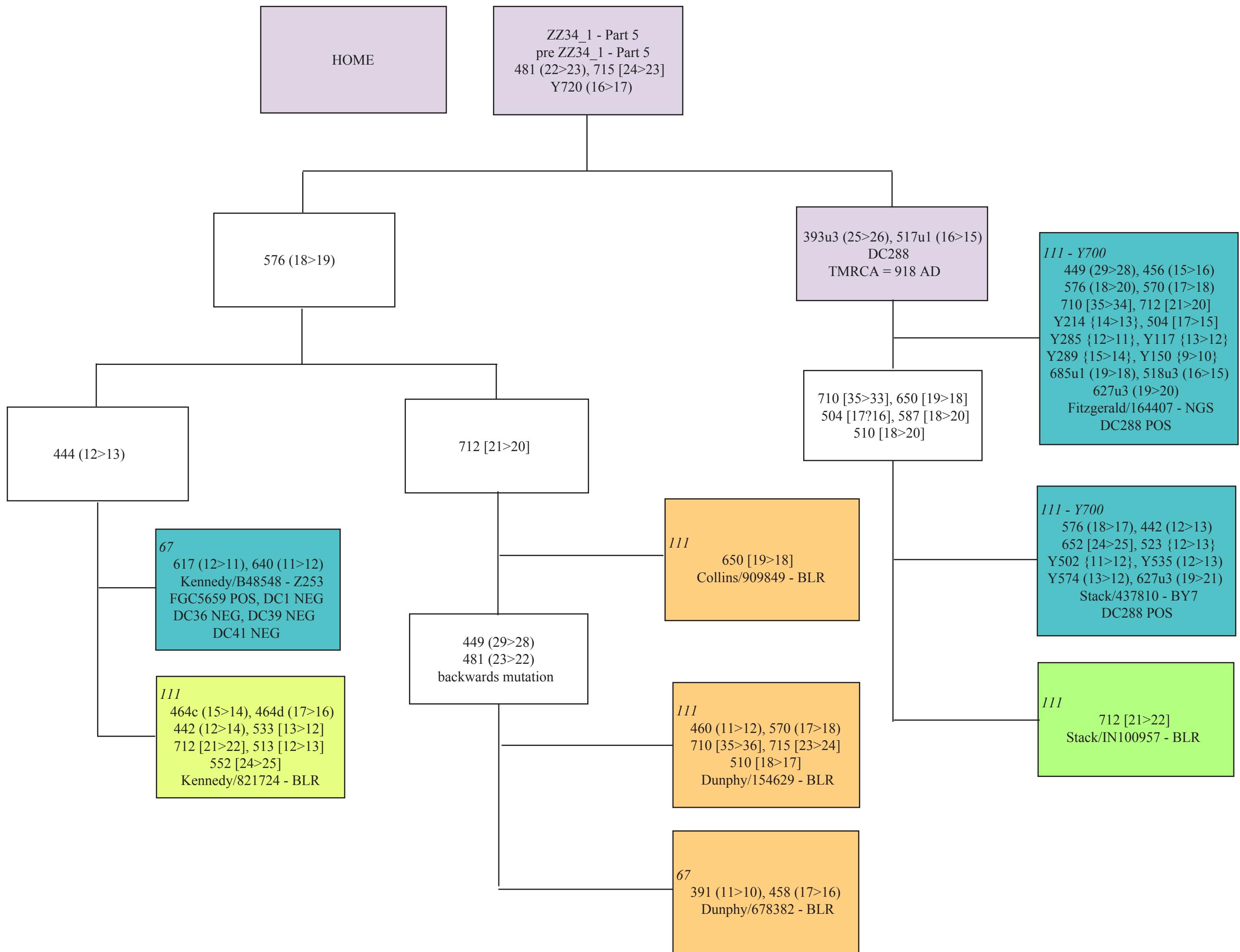


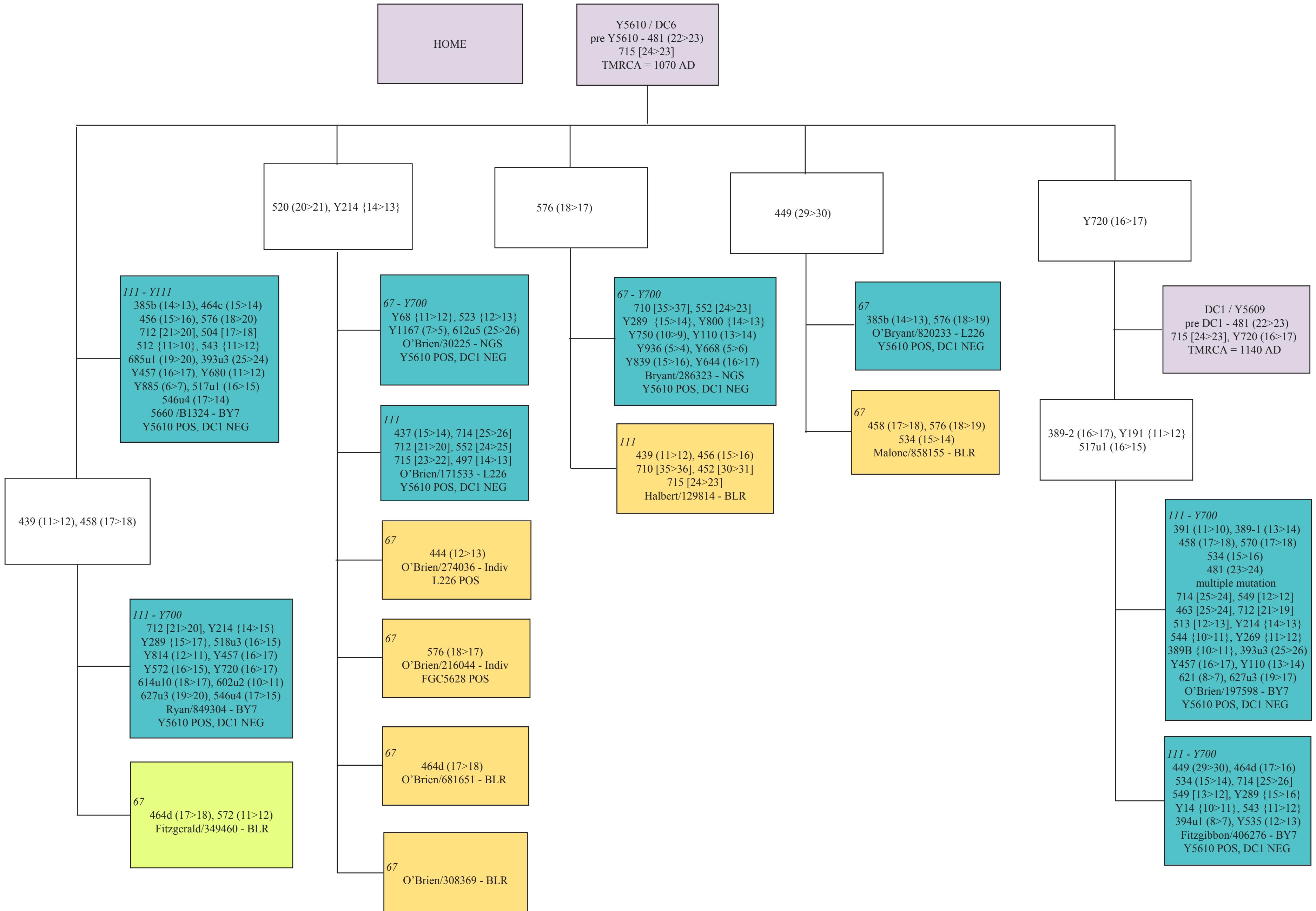


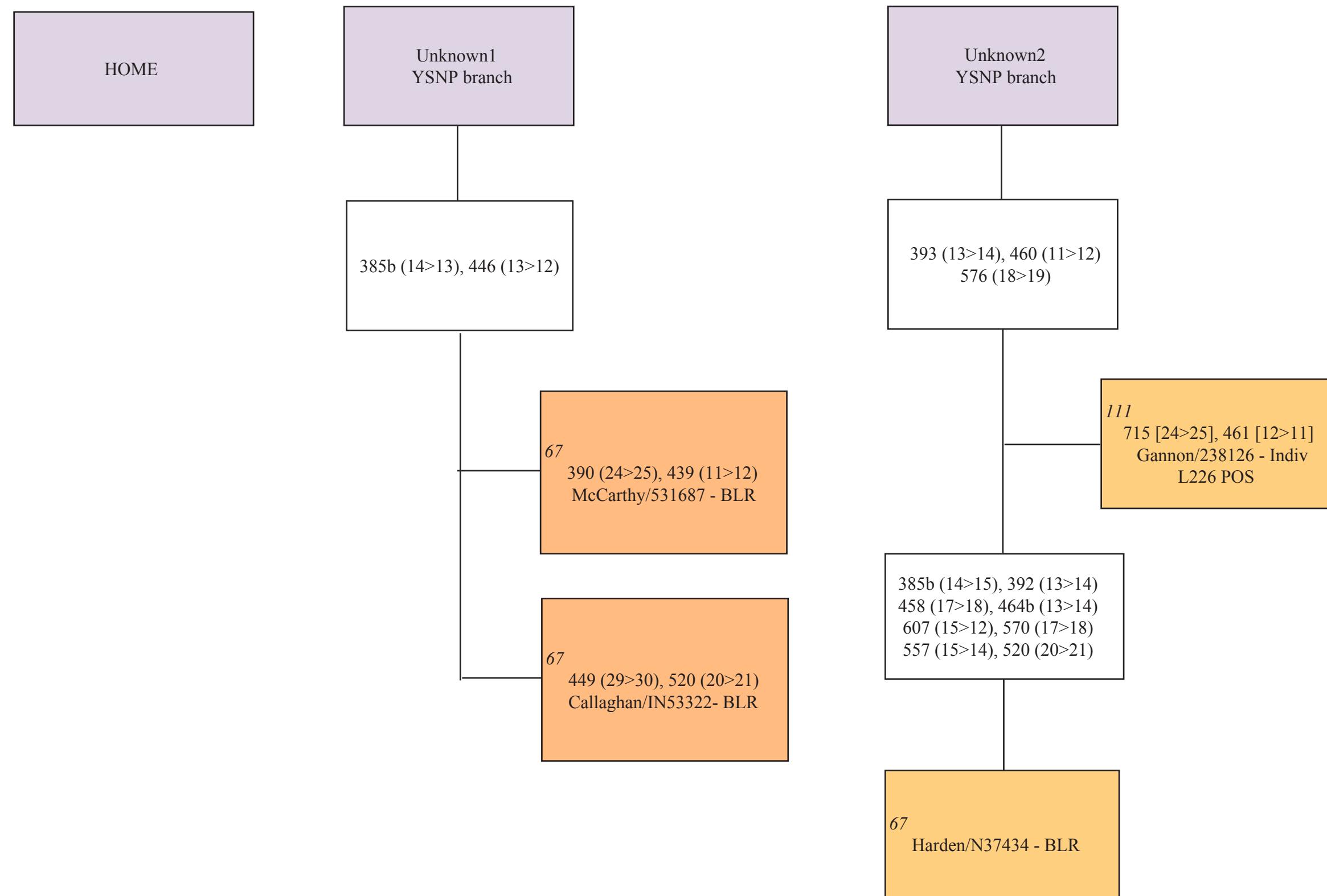


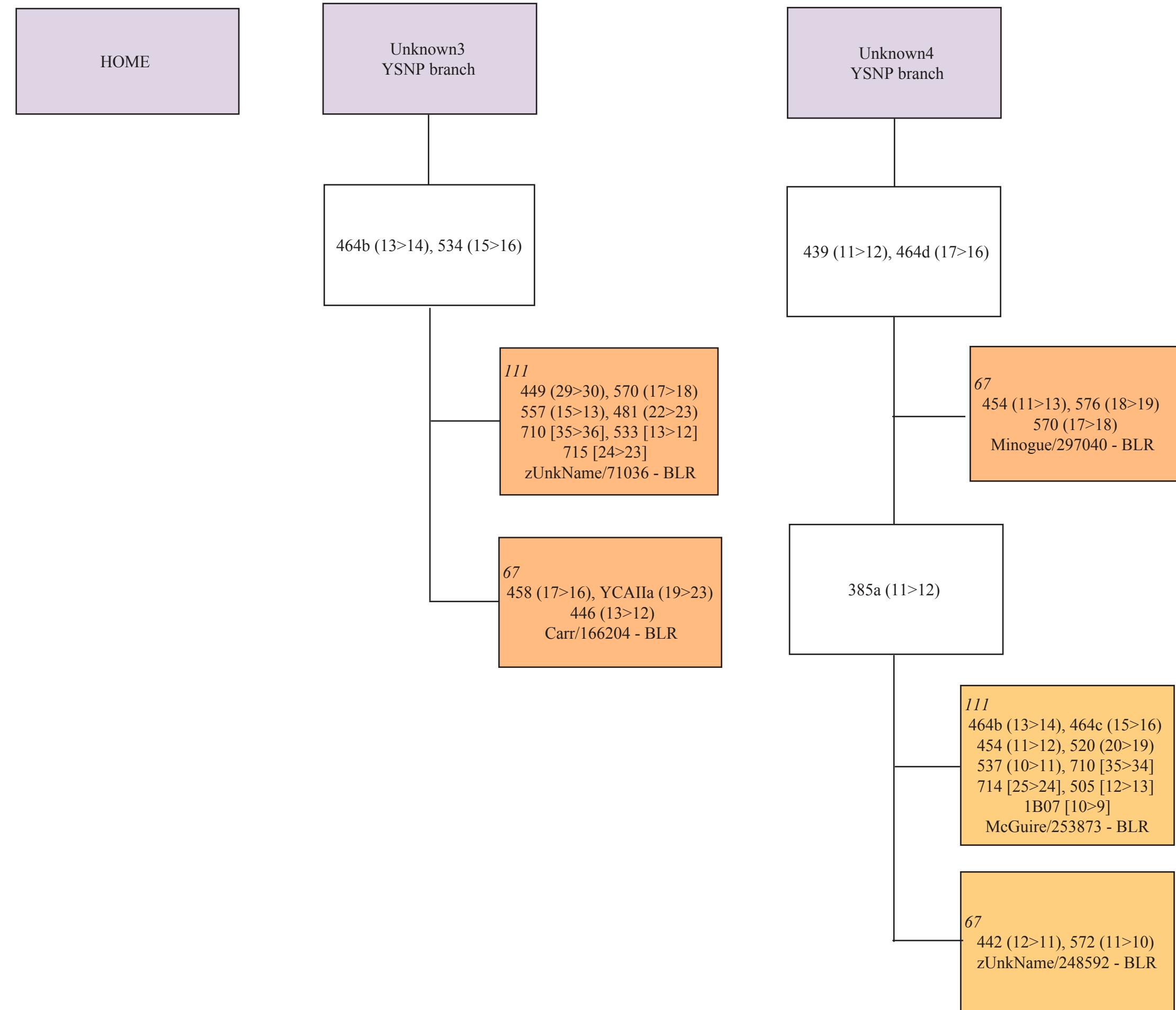


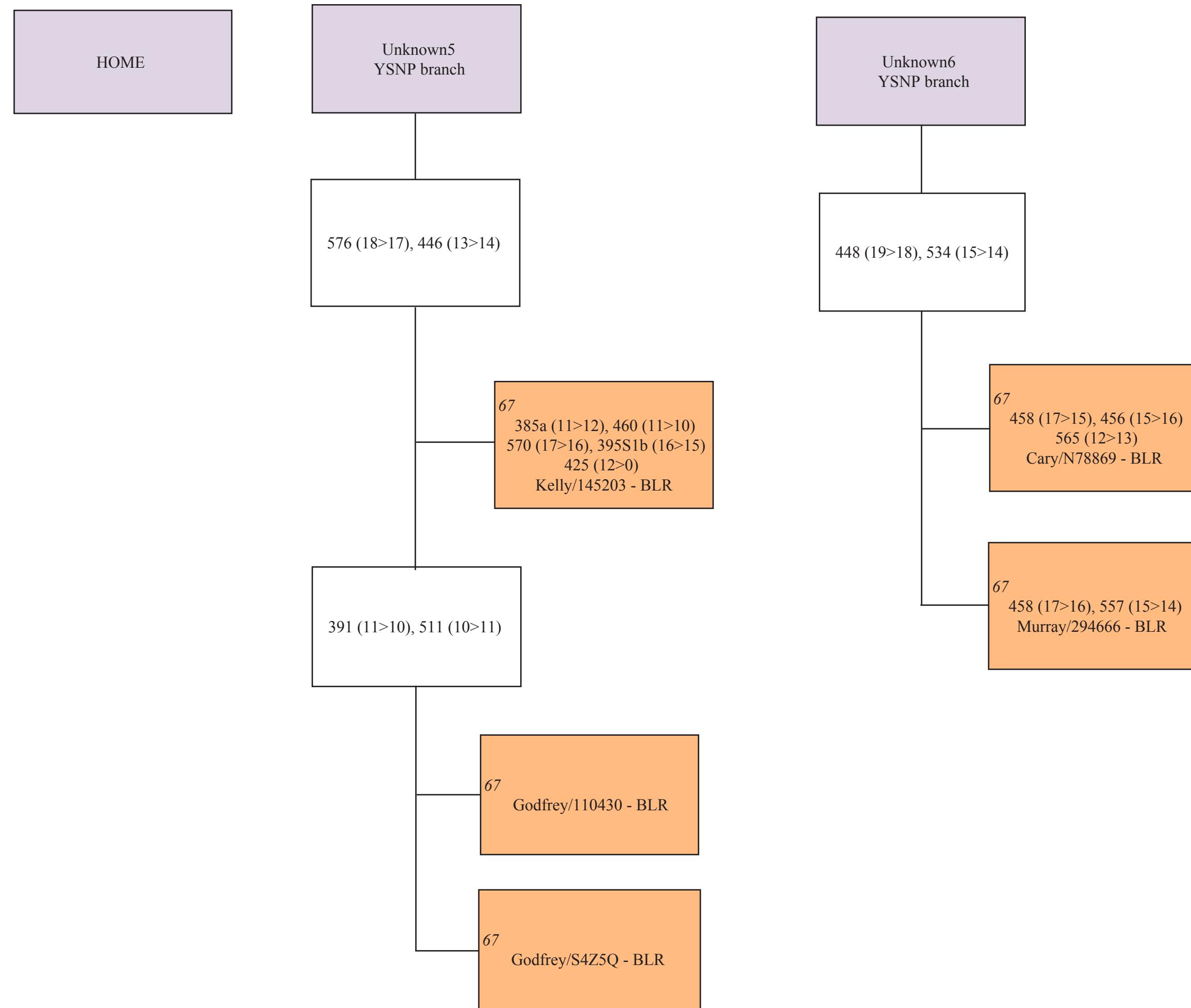


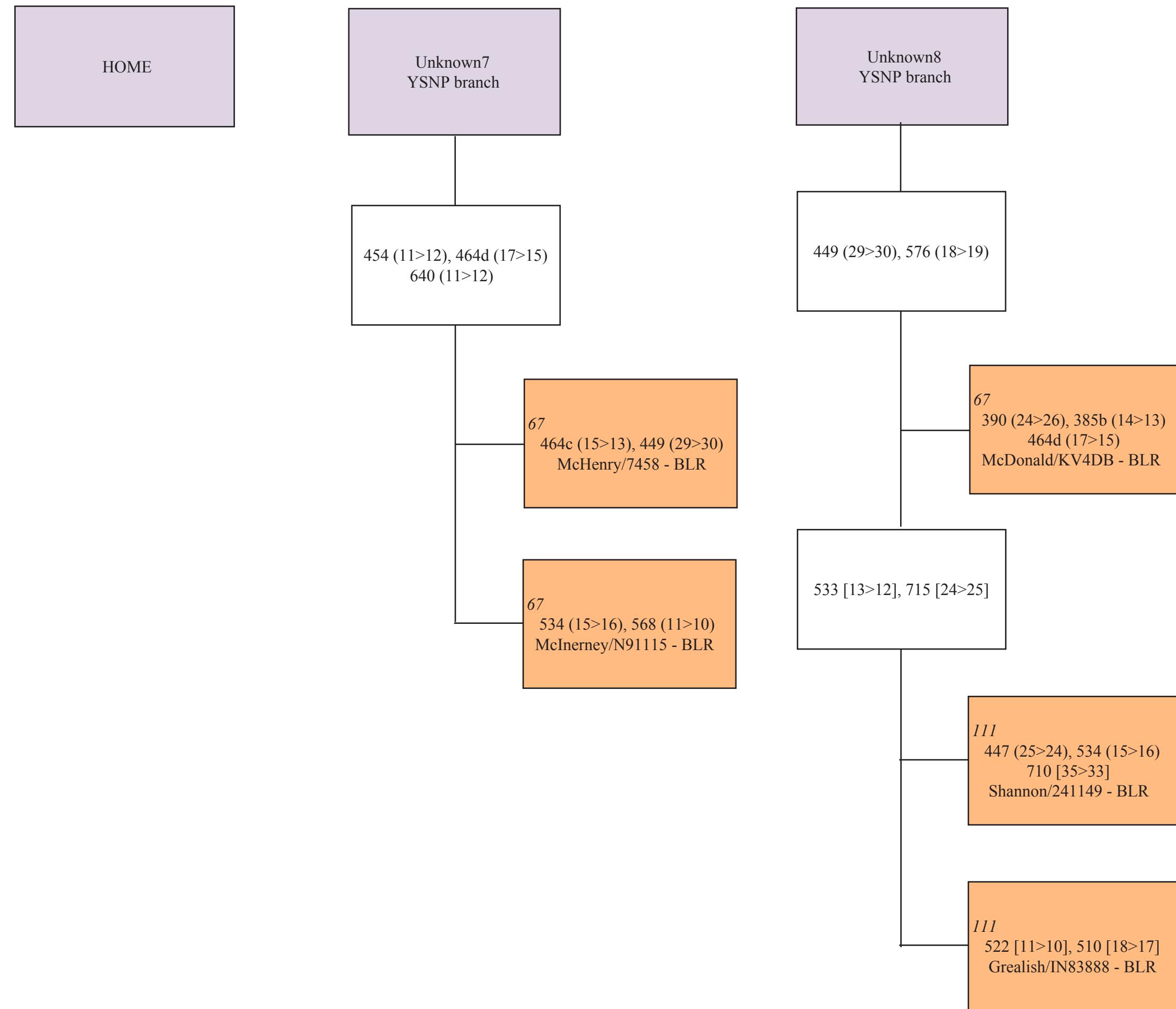


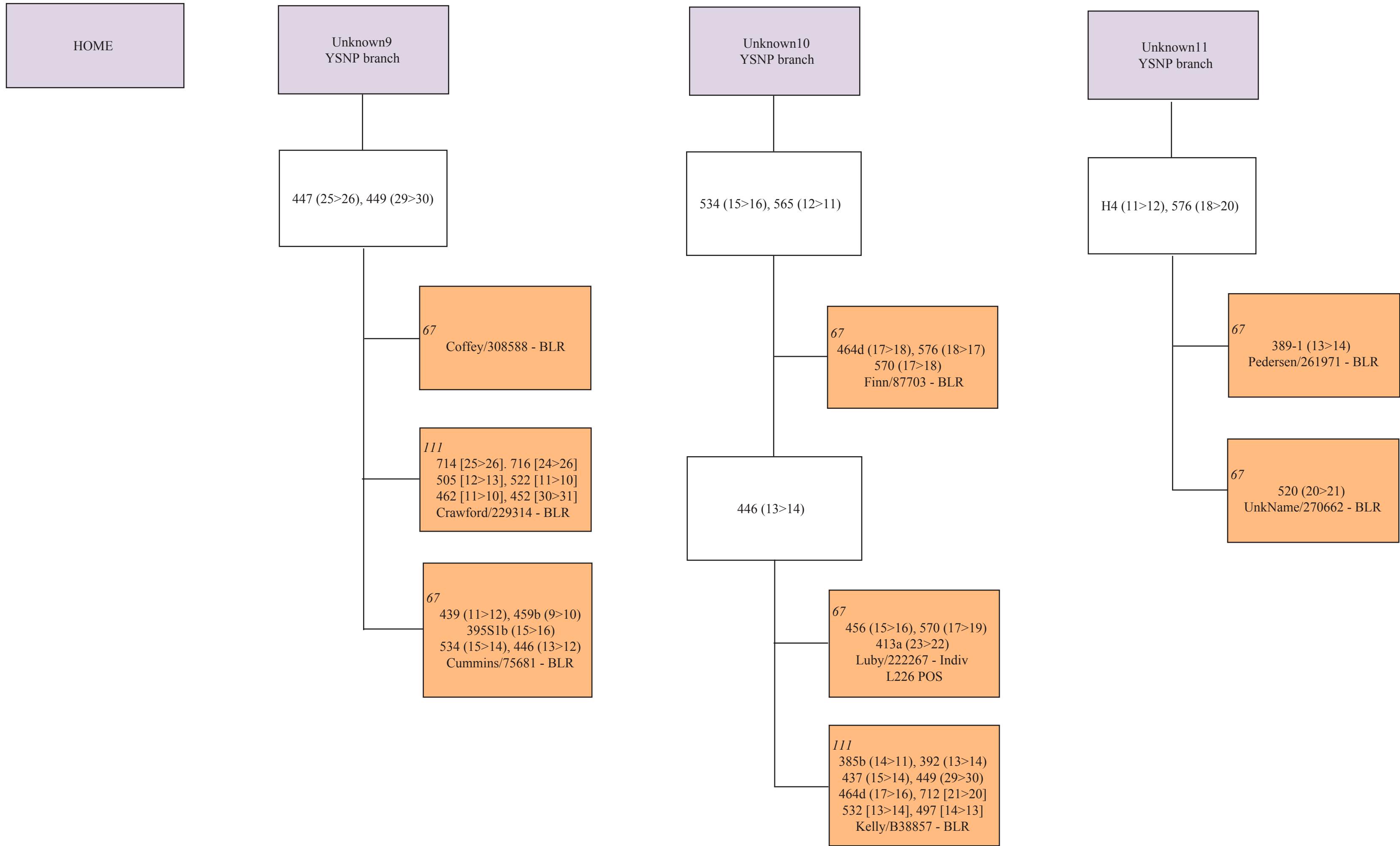


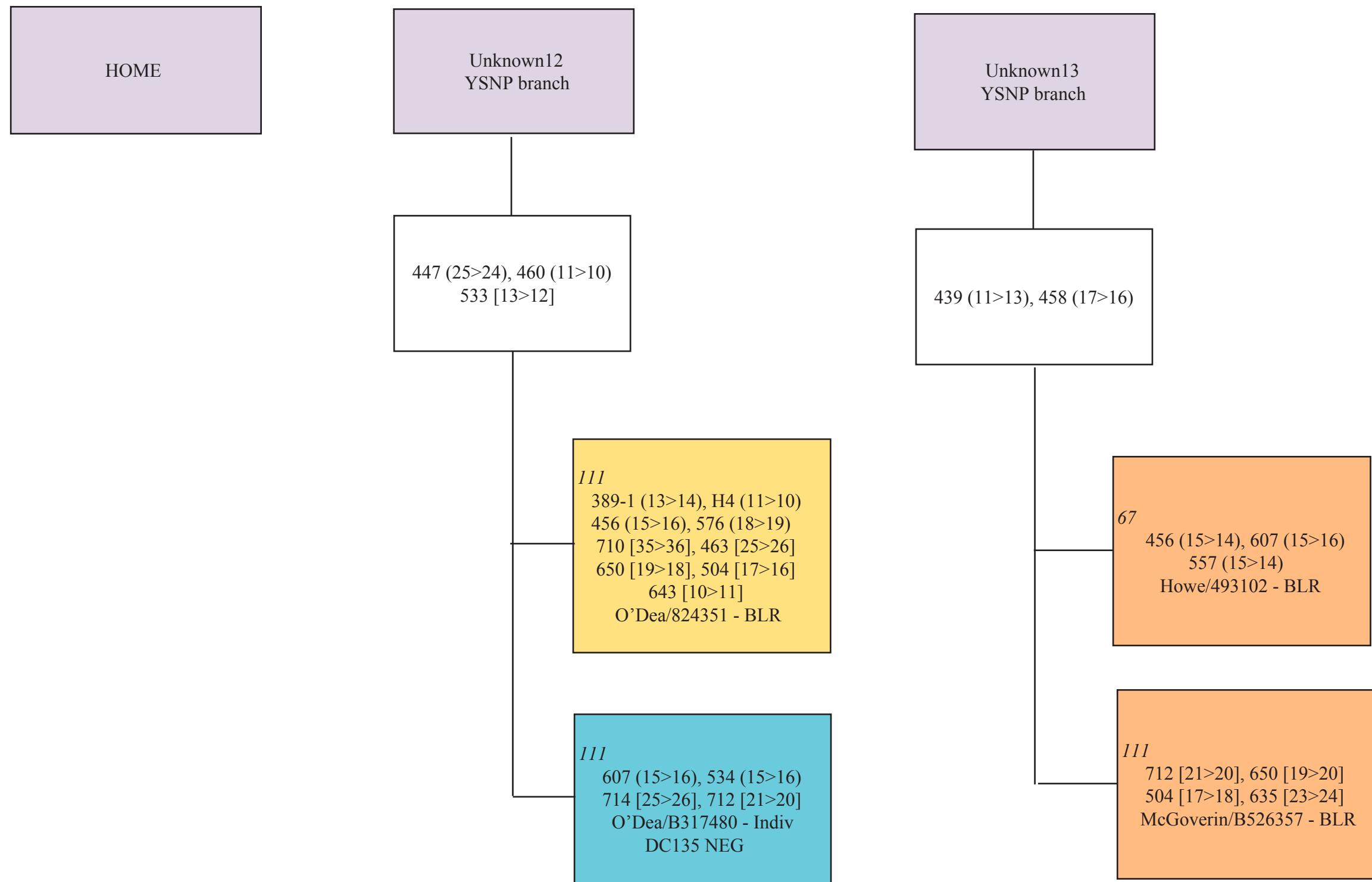






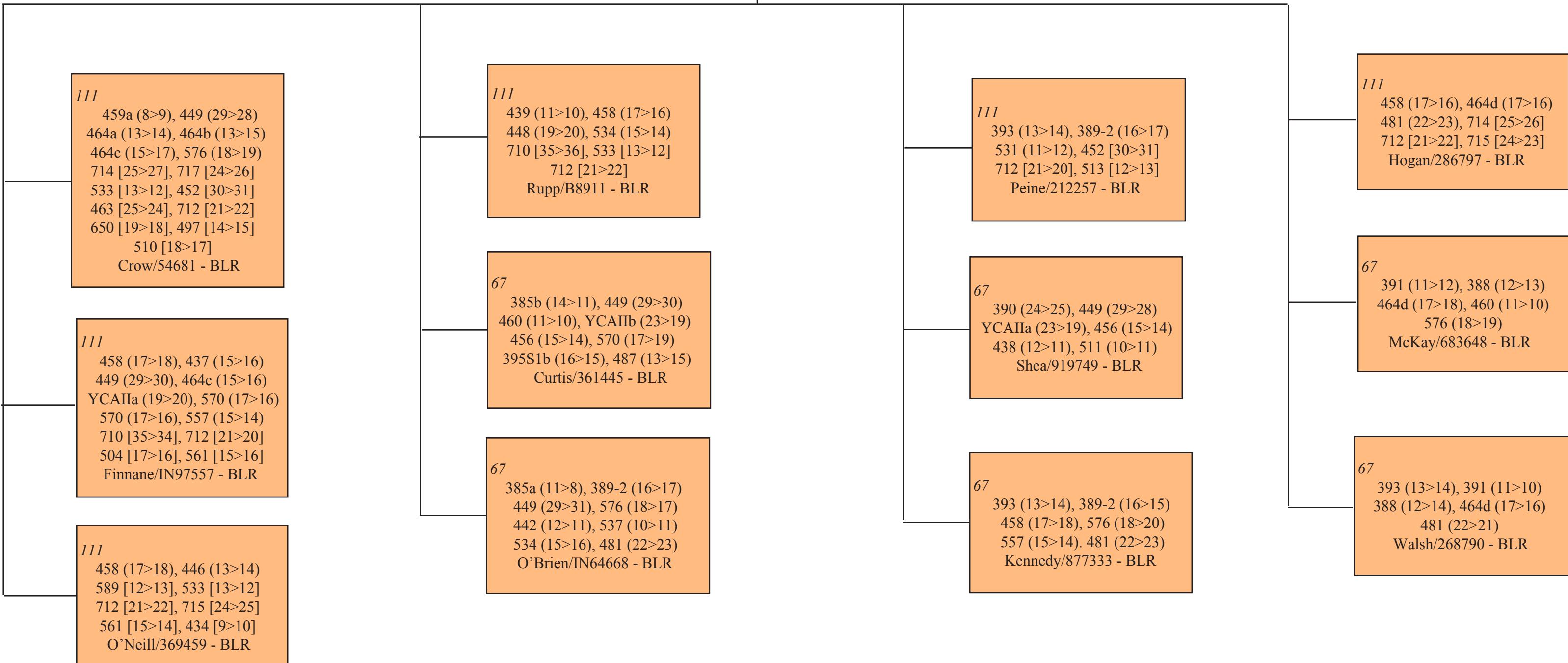






HOME

Testers with no
shared signatures
(larger signatures)



HOME

Testers with no
shared signatures
(smaller signatures)

