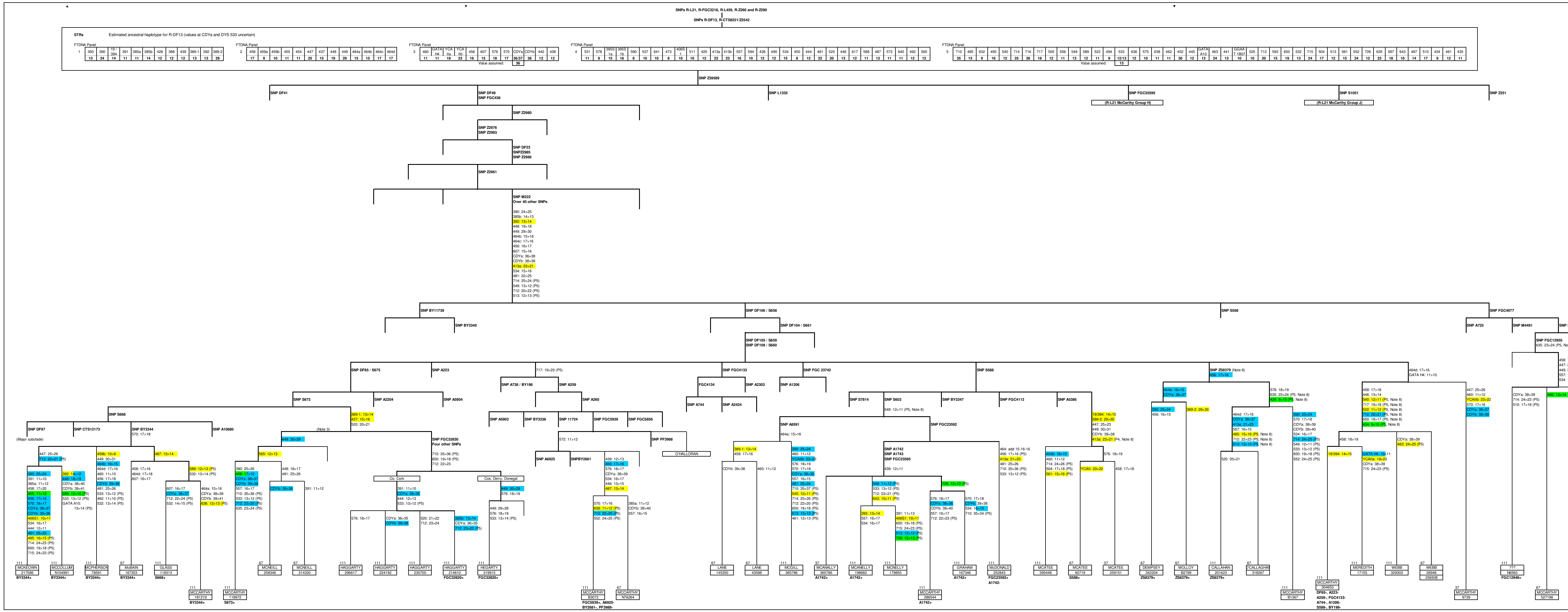

McCARTHY (Y-DNA) SURNAME STUDY
POSTULATED PHYLOGENETIC TREE FOR SNP R-M222 McCARTHYS
(McCARTHY R-L21 GROUP 'C')

N McCarthy 30 December 2016

This tree combines postulated relationships based on STR testing with firm definition afforded by SNP testing. Thanks are due to Alex Williamson for his detailed analysis of R-DF49 NGS data (Big Y and FGC) .

The intent of the tree is to show the probable pathway from the time of SNP R-L21 for McCarthys in Group C, and their most recent common ancestry with those of other surnames. The overall structure of the tree has been taken from ISOGG's master tree, the DF49 section of Alex Williamson's *The Big Tree* and FTDNA's *haplotree* at various times and is subject to ongoing updating. STR data for specific haplotypes has been taken from publicly available spreadsheets pertaining to the appropriate surname projects or the R-M222 Project. Any errors in interpretation or transcription are my own!

The sets of STR mutations associated with the various subclades are subject to amendment (moving up or down the tree, and /or postulation of further back-mutations) as more data becomes available.

LEGEND

STR Mutations:

- (green) "Very slow moving" STR markers (very low mutation rates) or rare multi-step mutation
- (yellow) "Slow moving" STR markers (low mutation rates)
- (blue) Postulated STR back-mutation

Participant kit number and testing details:

111 | BY — AAAAAAA / NNN

- No. of STR markers for which results have been published
- Has taken BigY test (BY Results not yet available)
- or YE, FO = Has taken Y Elite test with FGC, or other "full" Y-genome test elsewhere (FO). (YE, FO Results not yet available)
- Participant ancestral surname / kit no.

tbc	To be confirmed (e.g by Sanger sequencing)
P4	STR marker in FTDNA Panel 4 (38th - 67th markers in FTDNA sequence)
P5	STR marker in FTDNA Panel 5 (68th - 111th markers in FTDNA sequence).

NOTES:

1. These SNP and STR mutations could have occurred in any order.
2. When the tree is more developed some of these STR mutations may be moved up a level (or two).
3. This branch could be positive for some or all of FGC32820 and its equivalents.
8. Where tested.
16. Suspected SNP may be difficult or impossible to confirm by Sanger Sequencing. Note 18 may also apply.
18. A defining SNP appears to exist on the Y-chromosome, but its location is uncertain.

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