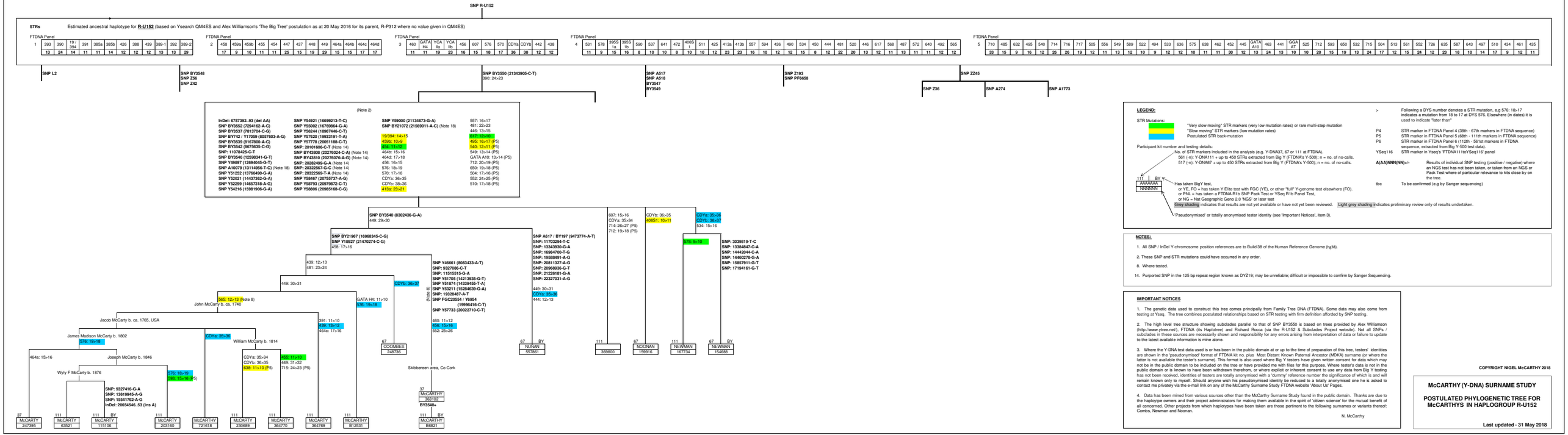

LEGEND:

STR Mutations:

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

Participant kit number and testing details:

No. of STR markers included in the analysis (e.g. Y-DNA37, 67 or 111 at FTDNA).
561 (-n): Y-DNA111 + up to 450 STRs extracted from Big Y (FTDNA's Y-500); n = no. of no-calls.
517 (-n): Y-DNA67 + up to 450 STRs extracted from Big Y (FTDNA's Y-500); n = no. of no-calls.

111 T BY
AAAAAAA
NNNNNN

Has taken BigY test.
or YE, FO = has taken Y Elite test with FGC (YE), or other "full" Y-genome test elsewhere (FO).
or PNL = has taken a FTDNA R1b SNP Pack Test or YSeq R1b Panel Test.
or NG = Nat Geographic Geno 2.0 'NGS' or later test

Grey shading indicates that results are not yet available or have not yet been reviewed. Light grey shading indicates preliminary review only of results undertaken.

'Pseudonymised' or totally anonymised tester identity (see 'Important Notices', item 3).

> Following a DYS number denotes a STR mutation, e.g 576: 18>17 indicates a mutation from 18 to 17 at DYS 576. Elsewhere (in dates) it is used to indicate 'later than"

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)
P6 STR marker in FTDNA Panel 6 (112th - 561st markers in FTDNA sequence, extracted from Big Y-500 test data).
YSeq116 STR marker in Yseq's 'FTDNA111toYSeq116' panel

A(AA)NNN(NN)+/- Results of individual SNP testing (positive / negative) where an NGS test has not been taken, or taken from an NGS or Pack Test where of particular relevance to kits close by on the tree.

tbc To be confirmed (e.g by Sanger sequencing)

NOTES:

1. All SNP / InDel Y-chromosome position references are to Build 38 of the Human Reference Genome (hg38).
2. These SNP and STR mutations could have occurred in any order.
8. Where tested.
14. Purported SNP in the 125 bp repeat region known as DYZ19; may be unreliable; difficult or impossible to confirm by Sanger Sequencing.

IMPORTANT NOTICES

1. The genetic data used to construct this tree comes principally from Family Tree DNA (FTDNA). Some data may also come from testing at Yseq. The tree combines postulated relationships based on STR testing with firm definition afforded by SNP testing.

2. The high level tree structure showing subclades parallel to that of SNP BY3550 is based on trees provided by Alex Williamson (http://www.ytree.net/), FTDNA (its Haplotree) and Richard Rocca (via the R-U152 & Subclades Project website). Not all SNPs / subclades in these sources are necessarily shown and responsibility for any errors arising from interpretation of data or failure to update to the latest available information is mine alone.

3. Where the Y-DNA test data used is or has been in the public domain at or up to the time of preparation of this tree, testers' identities are shown in the 'pseudonymised' format of FTDNA kit no. plus Most Distant Known Paternal Ancestor (MDKA) surname (or where the latter is not available the tester's surname). This format is also used where Big Y testers have given written consent for data which may not be in the public domain but have not provided me with files for this purpose. Where tester's data is not in the public domain or is known to have been withdrawn therefrom, or where explicit or inherent consent to use any data from Big Y testing has not been received, identities of testers are totally anonymised with a 'dummy' reference number the significance of which is and will remain known only to myself. Should anyone wish his pseudonymised identity be reduced to a totally anonymised one he is asked to contact me privately via the e-mail link on any of the McCarthy Surname Study FTDNA website 'About Us' Pages.

4. Data has been mined from various sources other than the McCarthy Surname Study found in the public domain. Thanks are due to the haplotype owners and their project administrators for making them available in the spirit of 'citizen science' for the mutual benefit of all concerned. Other projects from which haplotypes have been taken are those pertinent to the following surnames or variants thereof: Combs, Newman and Noonan.

N. McCarthy

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McCARTHY (Y-DNA) SURNAME STUDY

POSTULATED PHYLOGENETIC TREE FOR McCARTHYS IN HAPLOGROUP R-U152

Last updated - 31 May 2018