



LEGEND (Generic for all McCarty trees; not all used on this tree).

a) Mutation notations
 SNPs and INDEs are denoted in bold type face. STR markers are denoted in light type face. The 'DYS' of DYS-prefixed STR markers is omitted; prefixes for all others are shown with a more detailed notation (e.g. DYS395a1a, DYS39, YCABA, Y-DGAAT 1807, FTY37).

b) Participant kit number and testing details:
 No. of STR markers examined (e.g. Y-DNA37, 67 or 111 at FTDNA).
 561 (n): Y-DNA11 + 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.
 487 (n): Y-DNA37 + up to 450 STRs extracted from Big Y (FTDNA's Y-500); n = no. of no-calls.
 838 (n) as 561 (n) but with up to 277 further STRs extracted from a Big Y-700 test.
 In this case n = total number of no-calls at the 727 loci examined in the Big Y-700 test.

c) STR Mutation highlighting (frequencies revised February 2020 in accordance with Fig 4a at <https://mcartydna.wordpress.com>)
 "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

d) Other
 is used to denote a change in status (e.g. of repeating motif) at an STR locus, e.g. 576: 18x17 indicates a mutation from 18 to 17 of 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 or Big Y-700 test data).
 P7 STR marker in FTDNA Panel 7 (562nd - 638th markers in FTDNA sequence, extracted from Big Y-700 test data).

AA|A|NNNN|N+/- Results of individual SNP testing (positive / negative), or extracted from a Next Generation Sequencing (NGS) test such as Big Y or Y-Elite 2.1, or a Pack or Panel Test, where of particular relevance to kits close by on the tree.

Surname in parentheses if no residual paternal ancestor's surname identified.
 "Pseudonymised" or totally anonymised tester identity (see 'Important Notices', items 5 and 6).

- IMPORTANT NOTICES**
- The genetic data used to construct this tree comes principally from Family Tree DNA (FTDNA). Data from testing at YSEQ may also be used.
 - The tree serves McCarty's in Haplogroup R-U152 and the McCarty Surname Study. It shows the probable pathway of its members' paternal genetic ancestries from the time of SNP R-U152. To provide such information, additional data has been mined from other projects displaying it in the public domain; in this respect, thanks are due to the haplotype owners and their project administrators for making their data available in the spirit of 'citizen science' for the mutual benefit of all concerned. Participant identities aside by the criteria of (b) below. Projects from which haplotypes have been taken include but are not limited to R-U152 and Subclades, Munster Irish Project and those pertinent to the following surnames or variants thereof: Combs, Noonan and Newman.
 - The overall tree structure is based on the pertinent sections of Alex Williamson's Y-tree (<http://www.ytree.net>) and FTDNA's Haplotree, for which thanks are duly given. Not all SNPs / subclades in these sources are necessarily shown and responsibility for any errors arising from interpretation of data or failure to update the information is mine alone.
 - The tree combines postulated relationships based on STR testing with information afforded by Big Y testing. Where configurations are not confirmed by SNP testing, different permutations are possible, particularly in the occurrence of more frequently occurring mutations such as those at DYS76, CDYb, DYS710 and DYS712. The postulation of back mutations is highlighted with blue background as indicated in Legend item (c). The reliability can only be improved by more participants testing STRs to 111 markers and Next Generation Sequencing (NGS) testing such as FGCs E2.1 and FTDNA's Big Y-700, identifies SNPs which give fine definition to the branches and twigs (subclades) of the tree.
 - The "pseudonymized" format of FTDNA kit no. plus Most Distant Known Paternal Ancestor (MDKA) surname (or where the latter is not available the tester's surname or simply the kit no.) has been used for tester identity where the participant:
 - has opted to allow publication of his "pseudonymized DNA results and ancestor information in the public results pages" (and for data taken from other projects, where the project has allowed to publicly display its FTDNA Y-DNA Results spreadsheet) AND/OR
 - has provided written permission for the incorporation in this tree of further data derived from analysis of files to which a McCarty Surname Study analyst has been given access (see also (b) below), or to which others have been given access in the knowledge they would place their analyses in the public domain (e.g. via the "DNA Warehouse").
 Otherwise identities of testers are "totally anonymised" with an 'XU152' series 'dummy' reference number the significance of which is and will remain known only to the McCarty Surname Study analysts who maintain this tree.
 - 'Guarded data' is that not shown on FTDNA's public results pages despite the option at 5 (a) having been selected in a participant's Project Preferences, or additional information derived from testing at YSeq. The former comprises FTDNA Panels 6 and 7 STRs (extracted from Big Y test data) and 'private' (aka participant-specific, individual or singleton) SNPs, although most of these SNPs may with a little ingenuity be identified from the publicly displayed Y-DNA SNP reports. Identification of such guarded data is only shown on the tree where the permission of 5 (b) above has been provided.
 - Should anyone wish his pseudonymised identity be reduced to a totally anonymised one, or his data completely removed from the tree and any back-up records I may hold, he is asked to contact me privately ([ndmccarty10\[at\]gmail\[dot\]com](mailto:ndmccarty10[at]gmail[dot]com)).
 - Each participant's status with respect to this option has been determined in a one-off exercise in November 2020. Should a participant amend his FTDNA privacy setting in respect of this data sharing option and this is not reflected in the tree will he please contact me as described at (7).
- N. McCarty

NOTES:

- Where SNP / InDel Y-chromosome positions are cited, these relate to Human Reference Genome 'Build 38' (hg38 / GRCh38).
- Within blocks of 'equivalent' SNPs and / or associated STRs, the mutations could have occurred in any order.
- Where tested / revealed.
- Mutation(s) may have occurred further up the tree.
- Purported SNP within the 125 bp repetitive zone known as DYI21 (20054914 to 20351056 (hg38)). Cannot be confirmed by Sanger Sequencing.
- A setting SNP or InDel appears to exist on the Y-chromosome, but its location is uncertain. Frequently this is because it is on a palindromic arm. Unlikely to be suitable for individual (Sanger Sequence) testing.

McCARTHY (Y-DNA) SURNAME STUDY
PHYLOGENETIC TREE FOR McCARTHY IN HAPLOGROUP R-U152
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