

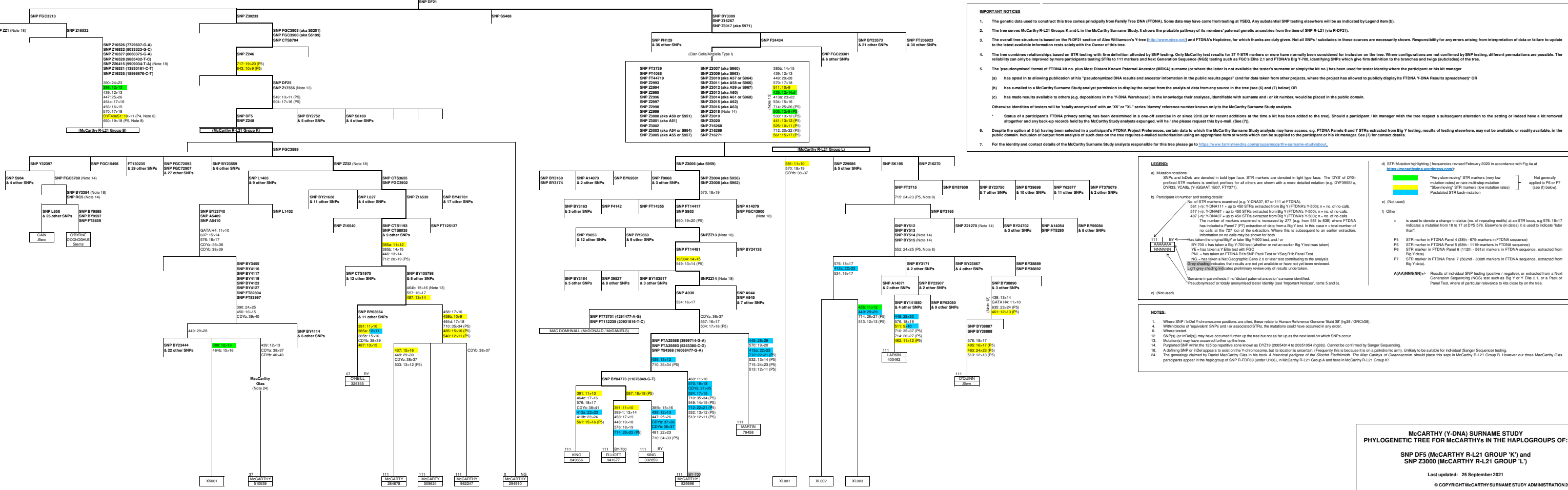
SNPs R-L21 and R-L49

SNP R-FGC3218 / S552

SNPs R-DF13 and R-CT5821 / Z542

STRs Estimated ancestral haplotype for R-DF13 (values at CDYs and DYS 533 uncertain)

FTDNA Panel		FTDNA Panel													FTDNA Panel (where applicable)													FTDNA Panel (where applicable)																		
1	393 390 390 394	391 391	390a 385a	385a 428	388 439	389-1 389-2	389-2	Value assumed													Value assumed													Value assumed												
	13 24 14 11	11 14	12 12	12 12	13 13	29																																								



IMPORTANT NOTICES

- The genetic data used to construct this tree comes principally from Family Tree DNA (FTDNA). Some data may have come from testing at YSEQ. Any substantial SNP testing elsewhere will be as indicated by Legend item (b).
- The tree serves McCarthy R-L21 Groups K and L in the McCarthy Surname Study. It shows the probable pathway of its members' paternal genetic ancestries from the time of SNP R-L21 (via R-DF21).
- The overall tree structure is based on the R-DF21 section of Alex Williamson's Y-tree (<http://www.ytree.com>) and FTDNA's Haplogroup, for which thanks are duly given. Not all SNPs' subclades in these sources are necessarily shown. Responsibility for any errors arising from interpretation of data or failure to update to the latest available information rests solely with the Owner of this tree.
- The tree combines relationships based on STR testing with firm definition afforded by SNP testing. Only McCarthy test results for 37 Y-STR markers or more have normally been considered for inclusion on the tree. Where configurations are not confirmed by SNP testing, different permutations are possible. The reliability can only be improved by more participants testing STRs to 111 markers and Next Generation Sequencing (NGS) testing such as FGC's Elite 2.1 and FTDNA's Big Y-700, identifying SNPs which give firm 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 identify where the participant or his kit manager
 - has opted in allowing 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) OR
 - has e-mailed to a McCarthy Surname Study analyst permission to display the output from the analysis of data from any source in the test (see (E) and (F) below) OR
 - has made results available to others (e.g. depositions in the "Y-DNA Warehouse") in the knowledge their analyses, identifiable with surname and / or kit number, would be placed in the public domain.
 Other identities of testers will be "totally anonymised" with an "XK" or "XL" series "dummy" reference number known only to the McCarthy Surname Study analysts.
- Status of a participant's FTDNA privacy setting has been determined in a one-off exercise in or since 2018 (or for recent additions at the time a kit has been added to the tree). Should a participant / kit manager wish the tree to respect a subsequent alteration to the setting or indeed have a kit removed altogether and any back-up records held by the McCarthy Study analysts expunged, will he / she please request this by e-mail. (See (7)).
- Despite the option at (5) (having been selected in a participant's FTDNA Privacy Preferences, certain data to which the McCarthy Surname Study analysts may have access, e.g. FTDNA Panels 6 & 7 STRs extracted from Big Y testing, results of testing elsewhere, may not be available, or readily available, in the public domain. Inclusion of output from analysis of such data on the tree requires e-mailed authorisation using an appropriate form of words which can be supplied to the participant or his kit manager. See (7) for contact details.
- For the identify and contact details of the McCarthy Surname Study analysts responsible for this tree please go to <https://www.familytreedna.com/groups/mccarthy-surname-study/about/>.

LEGEND:

a) Mutation notations
SNPs and indels are denoted in bold type face. STR markers are denoted in light type face. The DYS's of DYS-prefixed STR markers is omitted, prefixes for all others are shown with a more detailed notation (e.g. DYF3953.1a, DYF33, YCAII, Y-DNA17, Y-DNA18, Y-DNA19).

b) Participant ID number and testing details:
No. of STR markers examined (e.g. Y-DNA37, 67 or 111 at FTDNA).
501 (n): Y-DNA111 - up to 450 STRs extracted from Big Y (FTDNA's Y500); n = no. of no-calls.
517 (m): Y-DNA67 - up to 450 STRs extracted from Big Y (FTDNA's Y500); m = no. of no-calls.
487 (n): Y-DNA37 - up to 450 STRs extracted from Big Y (FTDNA's Y500); n = no. of no-calls.
The number of markers examined is increased by 277 (e.g. from 561 to 838) where FTDNA has included a Panel 7 (P7) extraction of data from a Big Y test. In this case n = total number of calls at the 727 loci of the extraction. Where this is subsequent to an earlier extraction, information on no-calls may be shown for both.
111 BY - has taken the original BigY or later Big Y 500 test, and/or BY 700 - has taken a Big Y 700 test (whether or not earlier Big Y test was taken)
P4/P5/P6/P7 - has taken an FTDNA R1a SNP Pack Test or YSEQ R1a Panel Test
NG - has taken a Nat Geographic Genie 2.0 or later test contributing to the analysis.
Grey shading indicates that results are not yet available or have not yet been reviewed.
Light grey shading indicates preliminary review only of results, underlines.
Surname in parenthesis is 'most distant paternal ancestor' surname identified.
"Pseudonymized" or totally anonymised testing (see "Important Notices", items 5 and 6).

c) (Not used)

d) STR Mutation highlighting (frequencies revised February 2020 in accordance with Fig 4a at <https://mccarthydna.wordpress.com/>):
Very slow moving STR markers (very low mutation rates) or rare multi-step mutation "Stepping" STR markers (low mutation rates)
Not generally applied to P6 or P7 (see (b) below).
Postulated STR back-mutation

e) (Not used)

f) Other
> is used to denote a change in status (no. of repeating motifs) at an STR locus, e.g. S76: 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 (389 - 679 markers in FTDNA sequence)
P5 STR marker in FTDNA Panel 5 (689 - 1119 markers in FTDNA sequence)
P6 STR marker in FTDNA Panel 6 (1129 - 5618 markers in FTDNA sequence, extracted from Big Y data)
P7 STR marker in FTDNA Panel 7 (5629 - 8388 markers in FTDNA sequence, extracted from Big Y data).

AAIAANNNNNN - 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 Flank or Panel Test, where of particular relevance to kits close by on the tree.

NOTES:

- Where SNP / indel Y chromosome positions are cited, these relate to Human Reference Genome "Build 38" (hg38) / GRCh38).
- Write blocks of "unrelated" SNPs and / or associated STRs, the mutations could have occurred in any order.
- Where tested.
- SNPs (in indels) may have occurred after the tree but not as far up the next level on which SNPs are confirmed.
- Mutations may have occurred further up the tree.
- Purported SNP within 125 bp repetitive zone known as DYF219 (2005494 to 20055154 (hg38)). Cannot be confirmed by Sanger Sequencing.
- A defining SNP for 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.
- The genealogy claimed by Daniel McCarthy Glas in his book *A Historical pedigree of the Slouch / Fiedlin / MacCarthy Glas* should place this sept in McCarthy R-L21 Group B. However our three MacCarthy Glas participants appear in the haplogroup of SNP R-FDR8 (under 01106), in McCarthy R-L21 Group A and hence in McCarthy R-L21 Group K.