

Notes:

- Only test results for 27 markers or more for McCarthy (and surnames associated therewith) have been considered. For other surnames, qualification for inclusion is 111 STR markers with SNP testing beyond CTS466 or any of its equivalents. Some kits not meeting these requirements are included when of interest in relation to identifying kit. Please report any protocol errors to [mcclathr@me.com](mailto:mcclathr@me.com).
- Where SNP 1 (DdeI Y-chromosome positions are cited, these relate to Human Reference Genome Build 38 (hg38) (GRCh38).
- Some of these SNPs 1 (DdeIs) (as applicable) may have occurred on a higher branch of this tree, but not as high as the next level above which includes SNPs.
- Recurrent, but phylogenetically consistent as placed.
- It is likely that bases marked with this note within a lineage within a relative region of the Y-chromosome or, where very close together, participated in a MNP. In the latter case, it is most likely for SNP interpretation software to handle single base substitutions rather than complex mutations, they are treated relatively.
- With corresponding change in 389.2 (the allele count for which includes 389.1).
- This tree assumes CDYb = 37 and DYS712 = 21 for the ancestral Irish Type II haplogroup; they may however be 38 and 20 respectively, in which case appropriate adjustments should be made throughout the subsequent branches.
- Where tested revealed:
- Test on Watson.
- It appears that a subsequent 13-12 back mutation at DYS 442 occurred independently on many occasions, implying some instability with 13 at the marker.
- Where position location is given for these MacCarthys, it is Cluair Fehobair, it is Cluair Fehobair (Lewis and Harris).
- A second MacCarthy Cluair descendant has a very different haplogroup.
- Subject to verification for all surnames.
- There are several distinct O'Sullivan Irish Type II lineages, O'Sullivans and O'Sullivan Beane are also found in the R-DF211...J216568-P314.2 lineage of McCarthy R-L21 Group B.
- SNP within the 125 to 126 repeat zone known as DY219 (positions 2221880 to 2251294) (hg37). They are not shown on this tree unless of potential significance. Cannot be confirmed by Sangar Sequencing.
- Suspected SNP may be difficult or impossible to confirm by Sangar Sequencing. Note 18 may also apply.
- Position determined through divergence of James Kane and detailed investigation by Alex Williamson.
- A definitive SNP appears to exist on the Y-chromosome, but its location is uncertain.
- SNP occurs within a STR and may therefore be unreliable. May also be seen elsewhere but phylogenetically consistent where here as placed.
- Other configurations of this tree are also possible from human. Full participant testing to 111 STR markers and / or SNP testing is needed for resolution.
- Alternate configuration based on shared mutation at DYS19:394 possible.
- Note the phonic similarity among (Mc)Carthy, McCarney, Mooney, Moynihan and Minihan: if a back mutation in the Mooney's stem is assumed, the Mooney's become closer still to 557642 Moynihan.
- Could they ultimately be reported fairly history. Chromosome kit 493555 would be shown branching off the stem before the occurrence of mutations at DYS 578 and 532 and thus without the need to conjecture back mutations.
- Assignment to McCarthy McManagh is provisional and requires testing to 111 markers to confirm.
- SNP occurs at the junction of two homoplasies; may be difficult or impossible to confirm by Sangar Sequencing.
- Placement of this mutation subject to further investigation.
- Low quality NGS test result verified by Sangar Sequence Testing.
- Any of these FTDNA Panel 6 mutations (extracted from Big Y) could have occurred from the time of SNP FGC11134 up to the time indicated here.
- These SNPs appear to be shared with a participant we had as yet unidentified kit number.

IMPORTANT NOTES

- The genetic data used to construct this tree comes principally from Family Tree DNA (FTDNA). Some data comes from testing at Full Genomes Corporation (FGC) or YSeq and occasionally the Personal Genome Project (PGP) or other sources as denoted just above the test kit number references (see Legend item 6).
- The tree was originally intended to serve R-L21 Group A in the McCarthy Surname Study and includes all Irish Type II McCarthys who have tested to 27 STR markers. It subsequently aimed also to include all members of the R1C-3466 Plus Project established to represent those with the Irish Type II haplogroup who had tested by, and of July 2017, STRs to 111 markers and / or SNPs beyond CTS466. Data published since July 2017 continues to be included but may not be exhaustive. Data has also been mined from other projects displaying it in the public domain. In this respect, thanks are due to the haplogroup owners and their project administrators for making their data available in the spirit of 'open science' for the mutual benefit of all concerned. Projects which haplogroups have been taken include but are not limited to Ireland's Kinship Project, Personal Genome Project (PGP), R-L21, Z20 and Subclade Project, R1C-3466 Irish Project, and those pertinent to the following surnames or variants thereof: Bean, Cockslogh, Cotter, Cronley, Daly, Donohoe, Ferguson, Gleason, Hayes, Healy, Killybeg, Lane, Leahy, Lindsay, Moon, Molyneux, O'Clawh, O'Donoghue, O'Keefe, O'Mahony, Patterson, Reagan, Shanahan, Sullivan.
- The high level tree structure is largely based on James Kane's work on the FGC11134 and Subclade Project, set up to cater for those who tested positive for SNP FGC11134 but negative for CTS466 and its many equivalents, and for which banks are still given. Not all SNPs / surnames in these sources are necessarily shown and responsibility for any errors arising from misrepresentation of data is taken to update to the latest available information in more scope.
- The tree continues postulated relationships based on STR testing with firm definition afforded by SNP 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 DY548, DY576, CDYab, DY974, DY9831 and DY512. The postulation of back mutations is highlighted with blue background as indicated in Legend item 6b. The reliability can only be improved by more participants testing STRs to 111 or 125 markers and Next Generation Sequencing (NGS) testing such as FGC's Elite 2.1 and FTDNA's Big Y-500, identifying SNPs which give firm definition to the branches and tags (subclades) of the tree.
- The 'pseudonymised' format of FTDNA kit no. plus Most Distant Known Paternal Ancestor (MDKA surname or where the latter is available is either the surname or simply the kit no.) was used for tester identity when the participant:
  - has opted in to sharing his data in the public viewing of FTDNA's Y-DNA results (and for data taken from other projects, where the project has allowed to publicly display its FTDNA Y-DNA Results spreadsheet);
  - has provided written permission for the incorporation in this tree of further data derived from analysis of files to which it has been given access"; or
  - to which others have been given access in the knowledge they would place their analysis in the public domain.
 Otherwise identities of testers are 'totally anonymised' with an 'X' series 'dummy' reference number the significance of which is and will remain known only to myself or my successor in maintaining this tree.
- 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 ([mcclathr@me.com](mailto:mcclathr@me.com) or 00353 87 2007484).

\*Each participant's status with respect to this option will have been determined in a one-off exercise at some time from 18 August 2018 onwards. Should he have subsequently amended this from 'Opt in to sharing' to 'Opt out of sharing', his information on FTDNA's Panel 6 and various SNP data extracted from a participant's Big Y-500 file to which I have, as a (Co-)Administrator, been given access, or additional information derived from testing at YSeq where the participant has registered with a kit or ID T1, for which I am the Administrator.

N. McCarthy

Position determined by one or more terminal (i.e. most recent shared) SNPs indicated. Postulated position based on STR mutations being similar to that of (any) other(s) who have tested the terminal SNP(s) shown and sometimes name similarity. Postulated position based on STR mutations being similar to that of (any) other(s) who have tested the terminal SNP(s) shown and sometimes name similarity).

McCarthy (Y-DNA) SURNAME STUDY and R1b-CTS466 PLUS PROJECT

POSTULATED 'IRISH TYPE II' PHYLOGENETIC TREE FOR MCCARTHYS (McCarthy R-L21 GROUP 'A') AND VARIOUS OTHER SURNAMES

Sheet 1 of 13

N. McCarthy Last updated - 06 October 2018

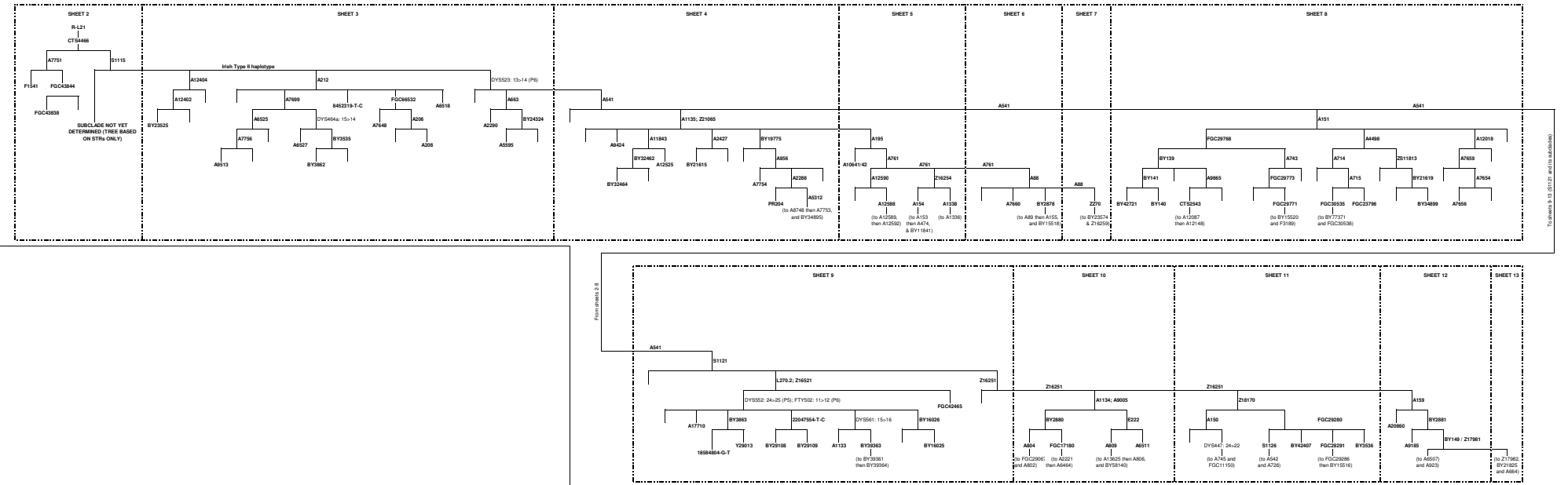
© COPYRIGHT NGEL MCCARTHY 2018

LEGEND:

- Mutation positions: SNPs and CDNs are denoted in light 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. DY365T.1A, DY93S, (Y)GGGAAAT: 807, (Y)T271).
- Participant kit number and testing details:
  - Number of STR markers included in the analysis (e.g. Y-DNA22, 22 or 111 at FTDNA).
  - 150, 155 STRs of FTDNA's Y-DNA11 test plus additional 14 markers comprising Yseq's FTDNA11 to Yseq117 panel. (T4 indicates later panel only tested).
  - 576 (or 410) Y-DNA11 + up to 450 STRs extracted from Big Y (FTDNA's Y-500), with n = no. of no-calls.
  - 571 (or 410) Y-DNA11 + up to 450 STRs extracted from Big Y (FTDNA's Y-500), with n = no. of no-calls.
  - 487 (or 410) Y-DNA11 + up to 450 STRs extracted from Big Y (FTDNA's Y-500), with n = no. of no-calls.
  - or Yeq or PGP's has taken Y-Ebe test with FGC (Yeq), or Personal Genome Project respectively.
  - has taken Big Y test.
  - or Yeq or PGP's has taken Y-Ebe test with FGC (Yeq), or Personal Genome Project respectively.
  - or P23AM - has a terminal SNP significant in a 23cm test.
  - or FGC - other 'N' genetic data obtained.
  - Grey shading indicates that results are not yet available or have not yet been reviewed.
  - Light grey shading indicates preliminary review only of surname identified.
- Validation of position on tree is indicated as follows:
  - Position determined by one or more terminal (i.e. most recent shared) SNPs indicated.
  - Postulated position based on STR mutations being similar to that of (any) other(s) who have tested the terminal SNP(s) shown and sometimes name similarity.
  - Postulated position based on STR mutations being similar to that of (any) other(s) who have tested the terminal SNP(s) shown and sometimes name similarity).

- STR Mutation frequencies:
  - Very slow moving STR markers (very low mutation rates) or very rare multi-step mutation (slow moving STR markers (low mutation rates)). Not yet applied to PS.
  - Slow moving STR markers (low mutation rates). Not yet applied to PS.
  - Postulated STR back-mutation.
- Other:
  - is used to denote a change in state (the allele, or no. of repeating motifs) at an STR locus, e.g. 576: 1b-17 indicates a mutation from 18 to 17 repeating motifs at DYS 576. Dash/dashes (indicates) is used to indicate 'late test'.
  - P4 STR marker in FTDNA Panel 4 (8th - 87th markers in FTDNA sequence).
  - PS STR marker in FTDNA Panel 5 (89th - 119th markers in FTDNA sequence).
  - PS STR marker in FTDNA Panel 6 (120th - 565th markers in FTDNA sequence), extracted from Big Y-500 test data.
  - \*Yseq116 STR marker in Yseq's FTDNA11 to Yseq117 panel.
- ALAN/BROOKIN: Results of individual SNP testing (positive / negative) where an NGS test has not been taken, or claim from NGS or PGP Test where of particular relevance to kits close by on the tree.
- DC: Test confirmed (e.g. by Sangar sequencing).
- NT: Not tested, or 'not' where tested.

LAYOUT OF THIS DOCUMENT (BY MAJOR SUBCLADES)



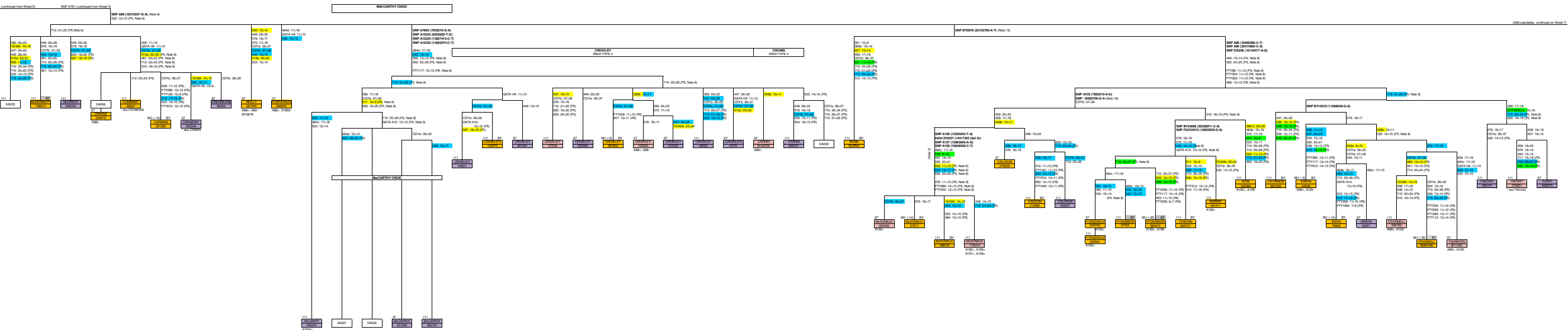






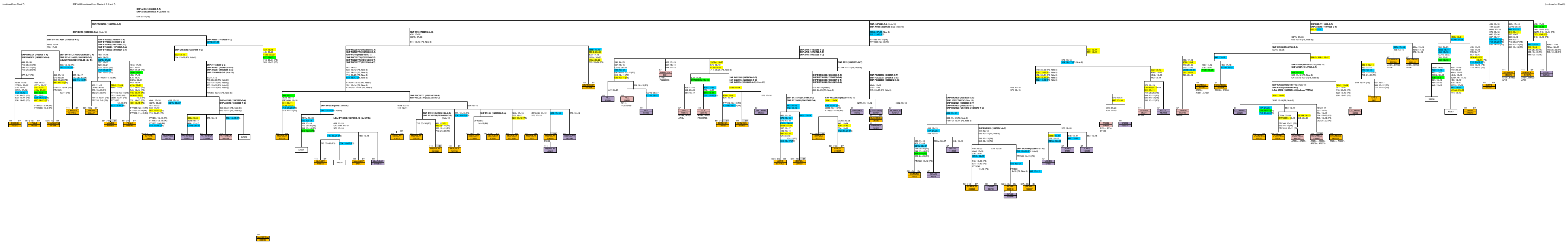


continued from Sheet 5 SMP A76) continued from Sheet 4 and 5) (M8) continues continued on Sheet 7)

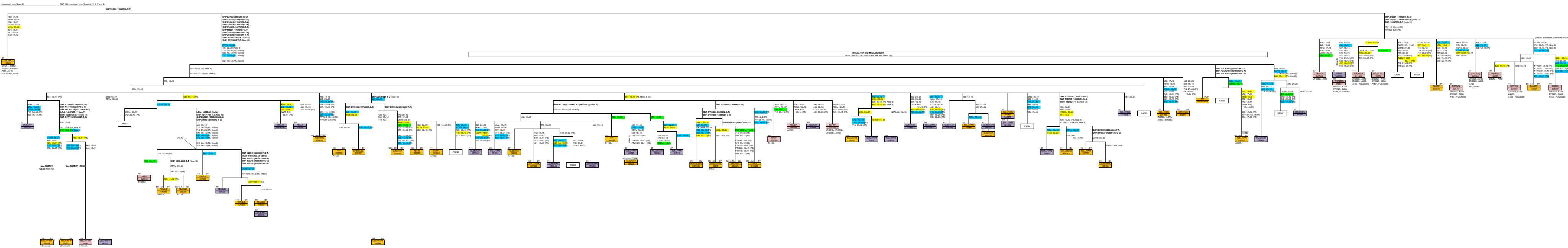




McCauley (New 15) R20: T15-1  
 Fox (New 15) R20: T15-1  
 O'Donnell (New 15) R20: T15-1

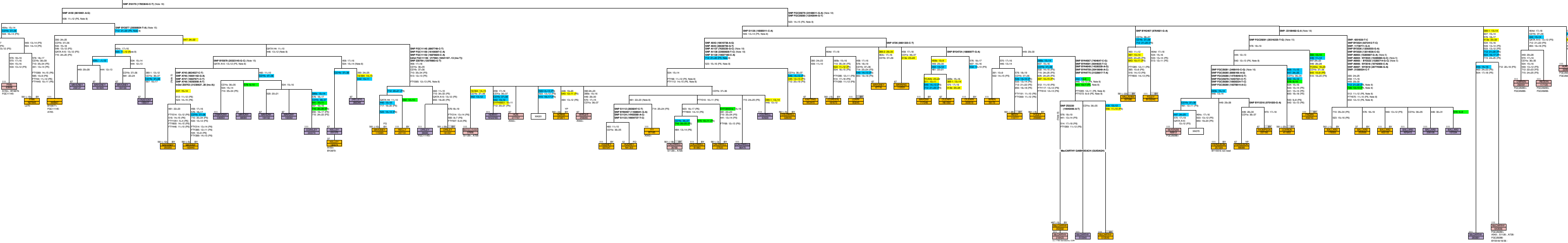






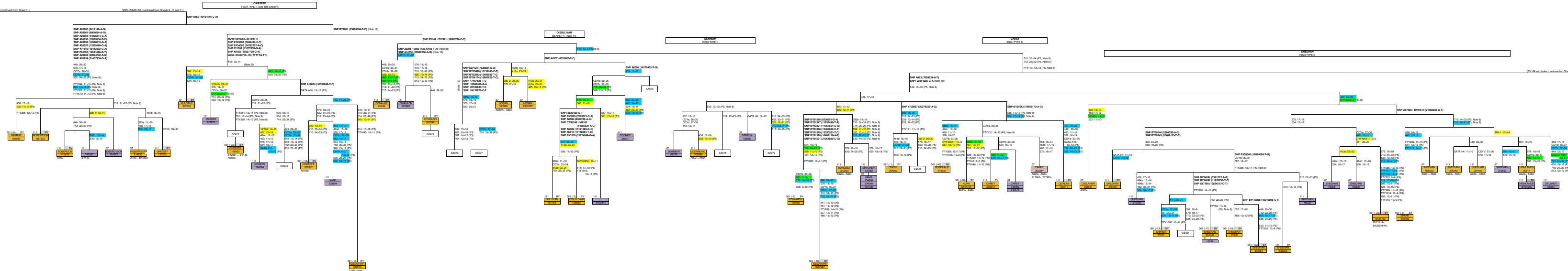


(continued from Sheet 10)      SNP 21057/152 (continued from Sheet 8 and 10)      (Y2281) subclade (continued on Sheet 12)



(continued from Sheet 10)      SNP 21057/152 (continued from Sheet 8 and 10)      (Y2281) subclade (continued on Sheet 12)

(continued from Sheet 11)



(IRISH) surnames, continued on Sheet 13

