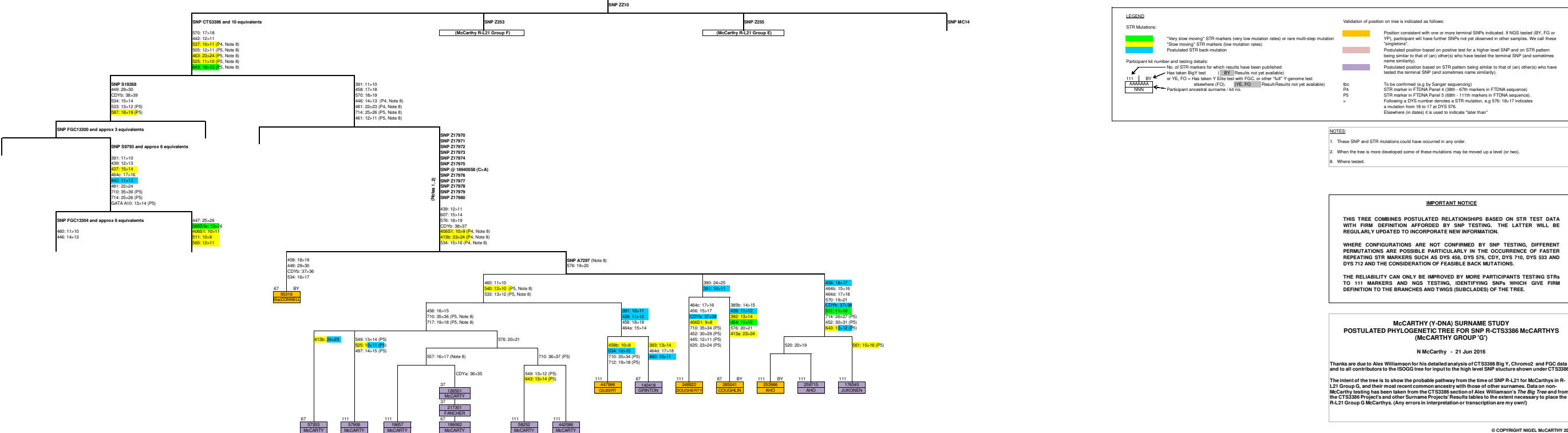


R-L21
|
R-DF13

FTDNA Panel																				FTDNA Panel										FTDNA Panel										FTDNA Panel										FTDNA Panel																																																																		
Estimated ancestral haplotype for R-DF13 (values at CDYs and DYS 533 uncertain)																																																																																																																				
1	393	390	197	391	395c	395d	425	388	439	390-1	392	399-2	2	456	456a	456b	455	454	447	437	448	449	464a	464b	464c	464d	3	460	GATA	YCA	YCA	456	607	576	570	CDYc	CDYs	442	438	4	531	576	395b	395b	590	590	537	641	472	400b	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	595	5	710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	438	462	452	445	GATA	463	441	GGA	425	712	593	650	532	715	594	513	561	552	726	635	587	643	497	510	434	461	435
	13	24	14	11	11	14	12	12	12	13	13	20		17	9	10	11	11	25	15	19	29	15	15	17	17		11	11	19	29	16	15	18	17	36/37	38	12	12		11	9	15	16	8	10	10	8	10	10	10	12	22	23	16	10	12	12	15	8	12	22	20	13	12	11	13	11	11	12	12		35	15	9	16	12	25	26	19	12	11	13	12	11	9	12/13	12	10	11	11	30	12	GATA	463	441	GGA	425	712	593	650	532	715	594	513	561	552	726	635	587	643	497	510	434	461	435
																				Value assumed: 36																				Value assumed: 13																																																																												



LEGEND

STR Mutations:

- Green box: "Very slow moving" STR markers (very low mutation rates) or rare multi-step mutation
- Blue box: "Slow moving" STR markers (low mutation rates)
- Yellow box: Postulated STR back-mutation
- Purple box: Postulated position based on STR pattern being similar to that of (an) other(s) who have tested the terminal SNP (and sometimes name similarity).

Participant kit number and testing details:

Participant kit number and testing details: No. of STR markers for which results have been published (e.g. by Sanger sequencing) or VE, FO = Has taken Y-DNA test with FGC, or other "big Y" genome test elsewhere (FO), (VE, FO) (Result Results not yet available)

Participant ancestral surname / kit no.

Validation of position on tree is indicated as follows:

- Yellow box: Position consistent with one or more terminal SNPs indicated. If NGS tested (BY, FG or YP), participant will have further SNPs not yet observed in other samples. We call these "Singletons".
- Purple box: Postulated position based on STR pattern being similar to that of (an) other(s) who have tested the terminal SNP (and sometimes name similarity).
- Purple box: Postulated position based on STR pattern being similar to that of (an) other(s) who have tested the terminal SNP (and sometimes name similarity).

To be confirmed (e.g. by Sanger sequencing)
 STR marker in FTDNA Panel 4 (388b - 637b) markers in FTDNA sequence)
 STR marker in FTDNA Panel 5 (688b - 1111b) markers in FTDNA sequence)
 Following a DYS number denotes a STR mutation, e.g. 576: 16b-17 indicates a mutation from 16 to 17 at DYS 576.
 Elsewhere (in dates) it is used to indicate "later than"

- NOTES:**
- These SNP and STR mutations could have occurred in any order.
 - When the tree is more developed some of these mutations may be moved up a level (or two).
 - Where tested.

IMPORTANT NOTICE

THIS TREE COMBINES POSTULATED RELATIONSHIPS BASED ON STR TEST DATA WITH FIRM DEFINITION AFFORDED BY SNP TESTING. THE LATTER WILL BE REGULARLY UPDATED TO INCORPORATE NEW INFORMATION.

WHERE CONFIGURATIONS ARE NOT CONFIRMED BY SNP TESTING, DIFFERENT PERMUTATIONS ARE POSSIBLE PARTICULARLY IN THE OCCURRENCE OF FASTER REPEATING STR MARKERS SUCH AS DYS 458, DYS 576, CDY, DYS 710, DYS 533 AND DYS 712 AND THE CONSIDERATION OF FEASIBLE BACK MUTATIONS.

THE RELIABILITY CAN ONLY BE IMPROVED BY MORE PARTICIPANTS TESTING STRs TO 111 MARKERS AND NGS TESTING, IDENTIFYING SNPs WHICH GIVE FIRM DEFINITION TO THE BRANCHES AND TWIGS (SUBCLADES) OF THE TREE.

MCCARTHY (Y-DNA) SURNAME STUDY
POSTULATED PHYLOGENETIC TREE FOR SNP R-CTS3386 MCCARTHYS (McCarthy Group 'G')

N. McCarthy - 21 Jun 2016

Thanks are due to Alex Williamson for his detailed analysis of CTS3386 Big Y, Chromo2 and FGC data and to all contributors to the BIGG tree for input to the high level SNP structure shown under CTS3386.

The intent of the tree is to show the probable pathway from the time of SNP R-L21 for McCarthys in R-L21 Group G, and their most recent common ancestry with those of other surnames. Data on non-McCarthy testing has been taken from the CTS3386 section of Alex Williamson's The Big Y tree and from the CTS3386 Projects and other Surname Projects Results tables to the extent necessary to place the R-L21 Group G McCarthys. (Any errors in interpretation or transcription are my own)