SNPs R-L21, R-FGC3218, R-L459, R-Z260 and R-Z290

SNPs R-DF13, R-CTS8221/Z2542

STRs (See Legend note (a)). Estimated ancestral haplotype for R-DF13 (values at CDYa, DYS533 and DYS511 uncertain)

FTDNA Panel 1

393	390	19 / 394	391	385a	385b	426	388	439	389-1	392	389-2
13	**24**	**14**	**11**	**11**	**14**	**12**	**12**	**12**	**13**	**13**	**29**

FTDNA Panel 2

458	459a	459b	455	454	447	437	448	449	464a	464b	464c	464d
17	**9**	**10**	**11**	**11**	**25**	**15**	**19**	**29**	**15**	**15**	**17**	**17**

FTDNA Panel 3

	460	GATA H4	YCA IIa	YCA IIb	456	607	576	570	CDYa	CDYb	442	438
	11	**11**	**19**	**23**	**16**	**15**	**18**	**17**	**36/37**	**38**	**12**	**12**
Value assumed:									**36**			

FTDNA Panel 4

531	578	395S 1a	395S 1b	590	537	641	472	406S 1	511	425	413a	413b	557	594	436	490	534	450	444	481	520	446	617	568	487	572	640	492	565
11	**9**	**15**	**16**	**8**	**10**	**10**	**8**	**10**	**10**	**12**	**23**	**23**	**16**	**10**	**12**	**12**	**15**	**8**	**12**	**22**	**20**	**13**	**12**	**11**	**13**	**11**	**11**	**12**	**12**

FTDNA Panel 5

	710	485	632	495	540	714	716	717	505	556	549	589	522	494	533	636	575	638	462	452	445	GATA A10	463	441	GGA AT	525	712	593	650	532	715	504	513	561	552	726	635	587	643	497	510	434	461	435
	35	**15**	**9**	**16**	**12**	**25**	**26**	**19**	**12**	**11**	**13**	**12**	**11**	**9**	**12/13**	**12**	**10**	**11**	**11**	**30**	**12**	**13**	**24**	**13**	**10**	**10**	**20**	**15**	**19**	**13**	**24**	**17**	**12**	**15**	**24**	**12**	**23**	**18**	**10**	**14**	**17**	**9**	**12**	**11**
Value assumed:															**13**																													

Panel 6, extracted from Big Y test data (where applicable).

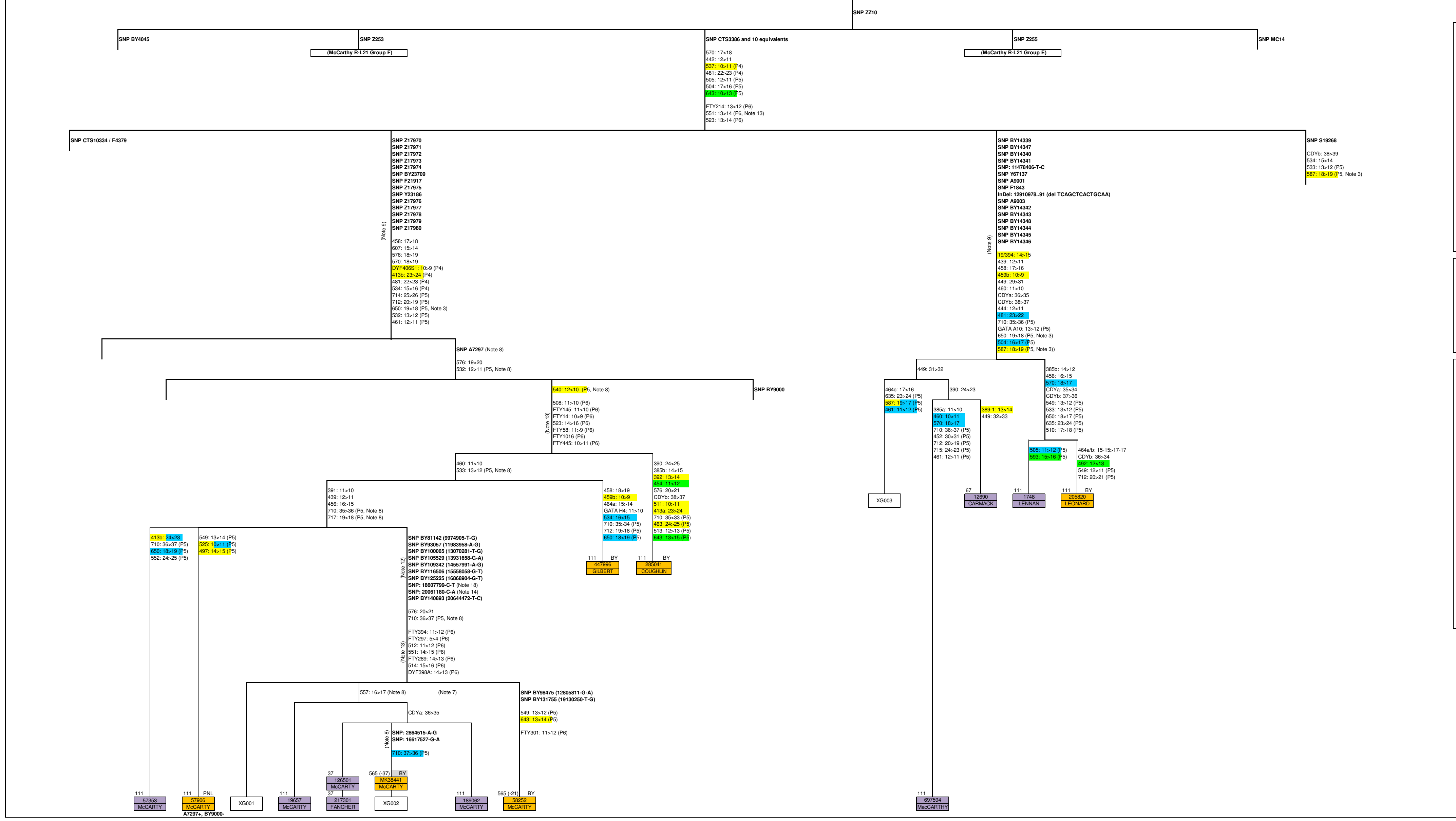
FTY 371	FTY 303	FTY 10	FTY 284	FTY 219	FTY 324	FTY 327	FTY 394	538	FTY 220	FTY 254	FTY 19	FTY 4	577	FTY 24	FTY 346	FTY 160	FTY 62	FTY 400	FTY 114	FTY 246	FTY 26	FTY 368	FTY 173	FTY 209	FTY 337	FTY 81	FTY 387	FTY 361	FTY 330	FTY 65	FTY 168	FTY 171	FTY 136	FTY 53	FTY 40	FTY 386	FTY 100	FTY 152	FTY 55	FTY 297	FTY 370	FTY 103	FTY 64	FTY 174	FTY 313	FTY 362	FTY 342	FTY 161	FTY 374	FTY 316	FTY 101	FTY 204	477	FTY 192	502	FTY 341	493	FTY 1	FTY 227	499	FTY 391	FTY 353	FTY 332	FTY 163	483	FTY 172	FTY 180	581	FTY 179	FTY 188	FTY 369	FTY 70	FTY 63	508	FTY 347	FTY 83	FTY 277	FTY 276	FTY 195	FTY 109	FTY 356	FTY 215	FTY 105	FTY 123	FTY 242	FTY 214	FTY 132	FTY 262	FTY 333	FTY 208	DYF 398B	FTY 43	FTY 166	FTY 13	FTY 11	584	608	FTY 95	FTY 151	FTY 388	FTY 256	580	FTY 234	FTY 268	FTY 139	FTY 27	FTY 75	512	FTY 329	FTY 320	FTY 7	FTY 247	FTY 211	474	FTY 39	FTY 376	FTY 37	FTY 373	475
5	**4**	**4**	**4**	**7**	**5**	**4**	**11**	**11**	**4**	**4**	**5**	**4**	**9**	**4**	**4**	**6**	**6**	**4**	**4**	**5**	**4**	**5**	**5**	**5**	**5**	**4**	**5**	**6**	**5**	**7**	**4**	**5**	**4**	**4**	**5**	**6**	**4**	**4**	**6**	**5**	**4**	**4**	**4**	**6**	**10**	**4**	**4**	**8**	**6**	**5**	**4**	**5**	**8**	**5**	**8**	**5**	**10**	**7**	**7**	**8**	**7**	**5**	**5**	**5**	**12**	**4**	**4**	**8**	**5**	**5**	**7**	**11**	**5**	**11**	**5**	**5**	**5**	**5**	**7**	**6**	**6**	**6**	**7**	**5**	**6**	**13**	**4**	**5**	**4**	**4**	**5**	**5**	**5**	**5**	**5**	**8**	**9**	**6**	**5**	**6**	**6**	**9**	**5**	**4**	**4**	**5**	**5**	**11**	**5**	**5**	**5**	**4**	**5**	**8**	**4**	**4**	**4**	**4**	**8**

FTY 138	FTY 288	FTY 264	FTY 93	FTY 380	FTY 18	FTY 115	569	FTY 390	FTY 46	FTY 243	FTY 322	FTY 281	FTY 153	FTY 181	FTY 184	FTY 359	FTY 121	FTY 74	FTY 279	530	FTY 45	573	542	FTY 36	FTY 304	FTY 203	FTY 291	FTY 142	FTY 191	FTY 183	FTY 141	FTY 299	FTY 193	FTY 124	FTY 16	FTY 236	FTY 185	FTY 378	FTY 225	FTY 397	FTY 3	FTY 67	FTY 182	FTY 334	623	FTY 348	FTY 357	FTY 275	FTY 306	FTY 383	FTY 253	FTY 285	645	FTY 17	FTY 85	598	FTY 375	FTY 325	FTY 12	FTY 365	FTY 35	FTY 237	FTY 238	FTY 305	FTY 56	FTY 129	FTY 352	FTY 292	FTY 154	539	FTY 301	FTY 366	FTY 231	618	FTY 216	FTY 82	FTY 393	FTY 155	FTY 68	FTY 32	FTY 265	FTY 300	FTY 143	FTY 201	FTY 199	FTY 86	FTY 98	FTY 144	541	507	FTY 20	FTY 116	FTY 308	FTY 177	FTY 89	FTY 158	FTY 22	FTY 84	FTY 186	FTY 396	FTY 91	FTY 29	FTY 78	FTY 229	FTY 260	FTY 250	FTY 364	476	FTY 221	FTY 57	FTY 377	FTY 384	466	FTY 363	FTY 137	FTY 69	FTY 72	FTY 251	FTY 2
5	**6**	**6**	**4**	**4**	**4**	**5**	**11**	**4**	**6**	**6**	**6**	**4**	**4**	**4**	**4**	**5**	**6**	**6**	**4**	**9**	**4**	**10**	**12**	**4**	**5**	**5**	**8**	**6**	**11**	**6**	**5**	**11**	**5**	**6**	**6**	**5**	**8**	**4**	**4**	**4**	**6**	**4**	**4**	**5**	**11**	**7**	**5**	**11**	**5**	**5**	**4**	**12**	**8**	**6**	**10**	**7**	**5**	**4**	**4**	**5**	**5**	**8**	**4**	**6**	**7**	**10**	**4**	**6**	**4**	**10**	**11**	**4**	**5**	**12**	**7**	**4**	**5**	**6**	**11**	**6**	**8**	**5**	**4**	**8**	**5**	**5**	**5**	**9**	**12**	**10**	**6**	**6**	**6**	**8**	**4**	**6**	**4**	**7**	**4**	**7**	**5**	**8**	**5**	**6**	**5**	**7**	**4**	**11**	**5**	**6**	**4**	**5**	**7**	**4**	**4**	**4**	**7**	**5**	**4**

FTY 217	FTY 257	FTY 120	FTY 25	FTY 252	FTY 33	FTY 42	FTY 54	FTY 372	480	FTY 176	FTY 76	FTY 66	FTY 197	FTY 385	FTY 270	FTY 298	FTY 198	FTY 117	544	FTY 159	FTY 232	FTY 156	FTY 343	FTY 296	FTY 311	FTY 344	FTY 178	FTY 367	FTY 73	FTY 112	FTY 295	616	FTY 338	FTY 196	FTY 157	FTY 162	551	FTY 148	FTY 94	FTY 52	FTY 131	FTY 9	FTY 194	FTY 8	FTY 318	FTY 317	FTY 99	FTY 289	FTY 169	FTY 51	FTY 345	FTY 398	FTY 111	FTY 273	FTY 382	FTY 47	FTY 30	FTY 147	615	FTY 302	FTY 354	FTY 326	FTY 88	FTY 248	FTY 267	FTY 170	FTY 60	453	FTY 249	FTY 167	624	FTY 134	FTY 235	FTY 145	FTY 14	FTY 80	FTY 50	514	FTY 340	585	516	FTY 293	FTY 207	FTY 278	FTY 210	523	FTY 269	FTY 530	FTY 1156	FTY 1070	FTY 906	FTY 1004	FTY 331	FTY 31	FTY 226	FTY 335	583	FTY 339	FTY 113	FTY 280	FTY 255	FTY 59	620	FTY 349	FTY 130	FTY 119	DYF 398A	FTY 58	FTY 127	FTY 321	FTY 92	FTY 392	DYF 392	FTY 290	FTY 312	FTY 135	FTY 150	FTY 294	FTY 244
7	**6**	**5**	**6**	**9**	**5**	**5**	**6**	**8**	**8**	**6**	**6**	**6**	**4**	**4**	**6**	**4**	**10**	**13**	**10**	**6**	**6**	**4**	**6**	**5**	**5**	**5**	**4**	**4**	**5**	**13**	**5**	**14**	**4**	**5**	**8**	**6**	**13/14**	**10**	**7**	**5**	**5**	**6**	**12**	**4**	**6**	**7**	**6**	**14**	**4**	**5**	**6**	**5**	**5**	**6**	**5**	**5**	**5**	**5**	**8**	**10**	**11**	**4**	**4**	**9**	**11**	**7**	**4**	**11**	**4**	**5**	**9**	**10**	**9**	**11**	**10**	**5**	**4**	**15**	**5**	**10**	**13**	**5**	**4**	**7**	**7**	**13**	**11**	**10**	**4**	**10**	**5**	**4**	**6**	**5**	**4**	**4**	**8**	**4**	**6**	**4**	**7**	**5**	**8**	**5**	**4**	**8**	**14**	**11**	**4**	**7**	**5**	**8**	**8**	**4**	**7**	**5**	**9**	**5**	**6**

Value assumed (551): **13**

FTY 48	FTY 282	489	FTY 272	FTY 239	FTY 258	FTY 49	574	FTY 41	FTY 905	FTY 1103	FTY 502	FTY 743	FTY 443	FTY 670	FTY 883	631	FTY 1042	FTY 510	389B	FTY 512	FTY 837	642	FTY 407	FTY 935	FTY 563	FTY 1016	FTY 1091	FTY 1049	FTY 1155	602	FTY 587	FTY 635	FTY 904	543	FTY 1148	FTY 861	FTY 742	FTY 433	FTY 1039	FTY 71	FTY 259	FTY 108	FTY 336	FTY 44	FTY 233	FTY 274	FTY 34	FTY 942	FTY 1068	FTY 945	FTY 1051	FTY 658	FTY 625	FTY 800	FTY 818	FTY 971	FTY 509	FTY 1025	FTY 835	FTY 984	637	FTY 832	FTY 689	FTY 998	FTY 520	FTY 445	FTY 809	FTY 428	FTY 562	FTY 897	FTY 1064	FTY 1088	FTY 1052	DYF 405	FTY 310	FTY 189	488	FTY 283	FTY 28	FTY 578	484	FTY 858	FTY 596	FTY 915	FTY 446	FTY 452	FTY 1006	FTY 612	FTY 507
4	**6**	**11**	**5**	**4**	**6**	**4**	**10**	**6**	**6**	**4**	**11**	**7**	**6**	**11**	**4**	**11**	**11**	**10**	**10**	**5**	**5**	**9**	**4**	**4**	**10**	**10**	**4**	**8**	**5**	**12**	**5**	**11**	**4**	**11**	**4**	**11**	**4**	**5**	**5**	**4**	**5**	**5**	**5**	**11**	**11**	**6**	**5**	**5**	**10**	**4**	**5**	**7**	**4**	**14**	**5**	**4**	**4**	**12**	**4**	**5**	**11**	**4**	**11**	**8**	**6**	**10**	**5**	**9**	**9**	**5**	**7**	**4**	**7**	**6**	**10**	**5**	**13**	**8**	**7**	**4**	**13**	**8**	**4**	**4**	**11**	**4**	**13**	**12**	**9**



LEGEND:

a) Mutation notations
SNPs and InDels 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. DYF395S1a, DYR33, YCAIIb, (Y-)GGAAT 1B07, FTY371).

b) Participant kit number and testing details:

111 | BY
AAAAAAA
NNNNNN

- No. of STR markers included in the analysis (e.g. Y-DNA37, 67 or 111 at FTDNA).
  - 125: All STRs of FTDNA' s Y-DNA111 test plus additional 14 markers comprising Yseq's 'FTDNA111 to YSeq116' panel. ('14' indicates latter panel only tested).
  - 575 (-n): As '125' + up to 450 STRs extracted from Big Y (FTDNA's Y-500); n = no. of no-calls
  - 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.
  - 487 (-n): Y-DNA37 + up to 450 STRs extracted from Big Y (FTDNA's Y-500); n = no. of no-calls.
- Has taken BigY test,
  - or YE or PGP = has taken Y Elite test with FGC (YE), or Personal Genome Project respectively
  - 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
  - or 23&Me = has a terminal SNP identified in a 23andMe test.
  - or FO = other "full" Y-genome test elsewhere.
  - 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' (below), items 5 and 6).

c) Validation of position on tree is indicated as follows:
- (orange) Position determined by one or more terminal (i.e. most recent shared) SNPs indicated.
- (pink) Postulated position based on positive test for a higher level SNP and STR mutations being similar to that of (an) other(s) who have tested the terminal SNP(s) shown (and sometimes name similarity).
- (purple) Postulated position based on STR mutations being similar to that of (an) other(s) who have tested the terminal SNP(s) shown (and sometimes name similarity).

d) STR Mutation frequencies:
- (green) Very slow moving' STR markers (very low mutation rates) or very rare multi-step mutation
- (yellow) Slow moving' STR markers (low mutation rates)
- (Not yet applied to P6)
- (blue) Postulated STR back-mutation

e) Other
- \> is used to denote a change in status (the allele, or no. of repeating motifs) at an STR locus, e.g. 576: 18>17 indicates a mutation from 18 to 17 repaeting motifs 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. Where SNP / InDel Y-chromosome positions are cited, these relate to Human Reference Genome 'Build 38' (hg38 / GRCh38).
3. DYS 587: 18>19 could have occurred in an ancestor common to the SNP blocks headed by BY14339 and S19268. Also, DYS 650: 19>18 could have occurred in an ancestor common to the SNP blocks headed by BY14339 and Z17970, but these two possibilities are mutually exclusive.
7. Several different tree structures are possible in this region based on permutations for the mutation(s) at DYS 710.
8. Where tested.
9. Within groups of 'equivalent' SNPs and / or associated STRs, the mutations could have occurred in any order.
12. Some of these SNPs likely occurred higher up the tree, but not as early as the next level up on which SNPs are listed.
13. Some of these Panel 6 STR mutations likely occurred higher up the tree, but not as early as the next level up on which Panel 6 STR mutations are listed.
14. Purported SNP in the 125 bp repeat region known as DYZ19; may be unreliable and difficult or impossible to confirm by Sanger Sequencing.
18. A defining 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.

IMPORTANT NOTICES

1. **The genetic data used to construct this tree comes from Family Tree DNA (FTDNA).**
2. **The tree is intended to serve 'R-L21 Group G' in the McCarthy Surname Study and show the probable pathway of its members' genetic ancestries from the time of SNP R-L21 (via R-CTS3386), along with their most recent common ancestry shared with those of other surnames. 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 haploytpe owners and their project administrators for making their data available in the spirit of 'citizen science' for the mutual benefit of all concerned. Projects from which haplotypes and terminal SNPs have been taken include but are not limited to McCarty SC Edgfield, R1b-CTS3386 and Munster Irish.**
3. **The overall tree structure is based on the R-ZZ10>CTS3386 section 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 to the latest available information is mine alone.**
4. **The tree combines 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 DYS458, DYS576, CDYa/b, DYS710, DYS533 and DYS712. The postulation of back mutations is highlighted with blue background as indicated in Legend item (d). The reliability can only be improved by more participants testing STRs to 111 or 125 markers and Next Generation Sequence (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 twigs (subclades) of the tree.**
5. **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 or simply the kit no.) has been used for tester identity where the participant**

   (a) has opted in to sharing his data in the public viewing of FTDNA's Y-DNA results (and data taken from other projects, where the project has allowed to publicly display its FTDNA Y-DNA Results spreadsheet).*

   (b) has provided, where applicable, written permission for the incorporation in this tree of 'guarded' data not covered by (a) or to which others have been given access in the knowledge they would place their analyses in the public domain.**

   Otherwise identities of testers are 'totally anonymised' with an 'XG' series 'dummy' reference number the significance of which is and will remain known only to myself or my successor in maintaining this tree.
6. **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 (mccarthygenATtiscaliDOTcoDOTuk).**

* **Each participant's status with respect to this option will have been determined in a one-off exercise on 26 July 2018. Should he have subsequently amended this from 'Opt in to sharing' to 'Opt out of sharing', he will please contact me as described at (6).**

** **e.g. STR information on FTDNA's Panel 6 and various SNP data extracted from a participant's Big Y-500 files to which I have, as a (Co-)Administrator, been given access.**

N. McCarthy

McCARTHY (Y-DNA) SURNAME STUDY

POSTULATED PHYLOGENETIC TREE FOR SNP R-CTS3386
M(a)cCARTHYS (McCARTHY R-L21 GROUP 'G')

N McCarthy 14 August 2018

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