Calculated on McGee using the following average mutation rates based on Marko Heinila.   FIDNAI - 37 Markers	Concretions to TMDCA	Coloulated on McCoo usin	aa tha fallaw	ina avaraga m	utation rates l	haaad on Mar	rka Hainila			
DNAH - 43 Markers   0.25%	Generations to TMRCA				utation rates i	based on Mar				
Probability of number of generations to MRCA   50%   16%   50%   84%   95%										
Probability of number of generations to MRCA         5%         16%         50%         84%         95%           Genetic Distance         DNAH (43 markers) mutation rate 0.25%         0         1         3         9         14           1         2         3         8         16         23           2         4         7         13         22         30           3         7         10         18         28         37           4         10         14         23         35         45           5         13         18         28         41         52           6         16         22         33         48         59           7         20         27         39         55         67           FTDNA (37 markers) mutation rate 0.36%           FTDNA (37 markers) mutation rate 0.36%           0         0         1         3         7         11           1         1         3         6         13         19           2         3         5         10         18         24           3         5         8         14         23 <t< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></t<>										
Section   Sect			Common - 3	32/34 Markers			0.24%			
0 0 1 3 9 14 1 2 3 8 16 23 2 4 7 13 22 30 3 7 10 18 28 37 4 10 14 23 35 45 5 13 18 28 41 52 6 16 22 33 48 59 7 20 27 39 55 67  FTDNA (37 markers) mutation rate 0.36% 0 0 1 3 7 11 1 1 3 6 13 19 2 3 5 8 14 23 30 4 9 11 19 28 36 5 10 15 23 34 42 6 13 18 27 39 49 7 17 22 32 45 55 8 20 26 37 51 61  Common (32 markers) mutation rate 0.24% 0 0 1 5 12 19 1 2 5 11 22 32 2 5 9 18 31 42 3 9 14 25 40 53 4 14 20 32 50 64 5 18 26 40 59 74		Probability of number of generations to MRCA	5%	16%	50%	84%	95%			
0 0 1 3 9 14 1 2 3 8 16 23 2 4 7 13 22 30 3 7 10 18 28 37 4 10 14 23 35 45 5 13 18 28 41 52 6 16 22 33 48 59 7 20 27 39 55 67  FTDNA (37 markers) mutation rate 0.36% 0 0 1 3 7 11 1 1 3 6 13 19 2 3 5 8 14 23 30 4 9 11 19 28 36 5 10 15 23 34 42 6 13 18 27 39 49 7 17 22 32 45 55 8 20 26 37 51 61  Common (32 markers) mutation rate 0.24% 0 0 1 5 12 19 1 2 5 11 22 32 2 5 9 18 31 42 3 9 14 25 40 53 4 14 20 32 50 64 5 18 26 40 59 74				DNAH (43 ma	rkers) mutat	ion rate 0.25	%			
1										
2 4 7 13 22 30 3 7 10 18 28 37 4 10 14 23 35 45 5 13 18 28 41 52 6 16 22 33 48 59 7 20 27 39 55 67  FTDNA (37 markers) mutation rate 0.36%				3						
3 7 10 18 28 37 4 10 14 23 35 45 5 13 18 28 41 52 6 16 22 33 48 59 7 20 27 39 55 67  FTDNA (37 markers) mutation rate 0.36% 0 0 1 3 7 11 1 1 3 6 13 19 2 3 5 10 18 24 3 5 8 14 23 30 4 9 11 19 28 36 5 10 15 23 34 42 6 13 18 27 39 49 7 17 22 32 45 55 8 20 26 37 51 61  Common (32 markers) mutation rate 0.24% 0 0 1 5 12 19 1 2 5 11 22 32 2 5 9 18 31 42 3 9 14 25 40 53 4 14 20 32 50 64 5 18 26 40 59 74		2								
4 10 14 23 35 45 5 13 18 28 41 52 6 16 22 33 48 59 7 20 27 39 55 67  FTDNA (37 markers) mutation rate 0.36%  0 0 1 3 7 11 1 1 3 6 13 19 2 3 5 10 18 24 3 5 8 14 23 30 4 9 11 19 28 36 5 10 15 23 34 42 6 13 18 27 39 49 7 17 22 32 45 55 8 20 26 37 51 61  Common (32 markers) mutation rate 0.24% 0 0 1 5 12 19 1 2 5 11 22 32 2 5 9 18 31 42 3 9 14 25 40 53 4 14 20 32 50 64 5 18 26 40 59 74			7							
5 13 18 28 41 52 6 16 22 33 48 59 7 20 27 39 55 67  FTDNA (37 markers) mutation rate 0.36%  0 0 1 3 7 11 1 1 3 6 13 19 2 3 5 10 18 24 3 5 8 14 23 30 4 9 11 19 28 36 5 10 15 23 34 42 6 13 18 27 39 49 7 17 22 32 45 55 8 20 26 37 51 61  Common (32 markers) mutation rate 0.24%  0 0 1 5 12 19 1 2 5 11 22 32 2 5 9 18 31 42 3 9 14 25 40 53 4 14 20 32 50 44 5 18 26 40 59 74			10							
6 16 22 33 48 59 7 20 27 39 55 67  FTDNA (37 markers) mutation rate 0.36%  0 0 1 3 7 11 1 1 3 6 13 19 2 3 5 10 18 24 3 5 8 14 23 30 4 9 11 19 28 36 5 10 15 23 34 42 6 13 18 27 39 49 7 17 22 32 45 55 8 20 26 37 51 61  Common (32 markers) mutation rate 0.24%  0 0 1 5 12 19 1 2 5 11 22 32 2 5 9 18 31 42 3 9 14 25 40 59 74										
FTDNA (37 markers) mutation rate 0.36%    0		6	16	22	33	48	59			
FTDNA (37 markers) mutation rate 0.36%  0										
0 0 1 3 7 11 1 1 2 3 6 13 19 2 3 5 10 18 24 3 5 8 14 23 30 4 9 11 19 28 36 5 10 15 23 34 42 6 13 18 27 39 49 7 17 22 32 45 55 8 20 26 37 51 61  Common (32 markers) mutation rate 0.24%  0 0 1 5 12 19 1 2 5 11 22 32 2 5 9 18 31 42 3 9 14 25 40 53 4 14 20 32 50 64 5 18 26 40 59 74										
0 0 1 3 7 11 1 1 2 3 6 13 19 2 3 5 10 18 24 3 5 8 14 23 30 4 9 11 19 28 36 5 10 15 23 34 42 6 13 18 27 39 49 7 17 22 32 45 55 8 20 26 37 51 61  Common (32 markers) mutation rate 0.24%  0 0 1 5 12 19 1 2 5 11 22 32 2 5 9 18 31 42 3 9 14 25 40 53 4 14 20 32 50 64 5 18 26 40 59 74			F	FTDNA (37 ma	rkers) muta	ation rate 0.3	6%			
1 1 3 6 13 19 2 3 5 10 18 24 3 5 8 14 23 30 4 9 11 19 28 36 5 10 15 23 34 42 6 13 18 27 39 49 7 17 22 32 45 55 8 20 26 37 51 61  Common (32 markers) mutation rate 0.24% 0 0 1 5 12 19 1 2 5 11 22 32 2 5 9 18 31 42 3 9 14 25 40 53 4 14 20 32 50 64 5 18 26 40 59 74		0								
2 3 5 10 18 24 3 5 8 14 23 30 4 9 11 19 28 36 5 10 15 23 34 42 6 13 18 27 39 49 7 17 22 32 45 55 8 20 26 37 51 61  Common (32 markers) mutation rate 0.24% 0 0 1 5 12 19 1 2 5 11 22 32 2 5 9 18 31 42 3 9 14 25 40 53 4 14 20 32 50 64 5 18 26 40 59 74				3		13				
3 5 8 14 23 30 4 9 11 19 28 36 5 10 15 23 34 42 6 13 18 27 39 49 7 17 22 32 45 55 8 20 26 37 51 61 Common (32 markers) mutation rate 0.24% 0 0 1 5 12 19 1 2 5 11 22 32 2 5 9 18 31 42 3 9 14 25 40 53 4 14 20 32 50 64 5 18 26 40 59 74		2	3	5	10	18	24			
4 9 11 19 28 36 5 10 15 23 34 42 6 13 18 27 39 49 7 17 22 32 45 55 8 20 26 37 51 61 Common (32 markers) mutation rate 0.24% 0 0 1 5 12 19 1 2 5 11 22 32 2 5 9 18 31 42 3 9 14 25 40 53 4 14 20 32 50 64 5 18 26 40 59 74		3	5	8	14	23	30			
5 10 15 23 34 42 6 13 18 27 39 49 7 17 22 32 45 55 8 20 26 37 51 61  Common (32 markers) mutation rate 0.24%  0 0 1 5 12 19 1 2 5 11 22 32 1 2 5 9 18 31 42 3 9 14 25 40 53 4 14 20 32 50 64 5 18 26 40 59 74										
6 13 18 27 39 49 7 17 22 32 45 55 8 20 26 37 51 61  Common (32 markers) mutation rate 0.24%  0 0 1 5 12 19 1 2 5 11 22 32 2 5 9 18 31 42 3 9 14 25 40 53 4 14 20 32 50 64 5 18 26 40 59 74		5								
7 17 22 32 45 55 8 20 26 37 51 61										
Common (32 markers) mutation rate 0.24%       0     0     1     5     12     19       1     2     5     11     22     32       2     5     9     18     31     42       3     9     14     25     40     53       4     14     20     32     50     64       5     18     26     40     59     74										
0     0     1     5     12     19       1     2     5     11     22     32       2     5     9     18     31     42       3     9     14     25     40     53       4     14     20     32     50     64       5     18     26     40     59     74		8	20							
0     0     1     5     12     19       1     2     5     11     22     32       2     5     9     18     31     42       3     9     14     25     40     53       4     14     20     32     50     64       5     18     26     40     59     74										
0     0     1     5     12     19       1     2     5     11     22     32       2     5     9     18     31     42       3     9     14     25     40     53       4     14     20     32     50     64       5     18     26     40     59     74			C	Common (32 m	arkers) muta	ation rate 0.2	24%			
1     2     5     11     22     32       2     5     9     18     31     42       3     9     14     25     40     53       4     14     20     32     50     64       5     18     26     40     59     74		0								
2     5     9     18     31     42       3     9     14     25     40     53       4     14     20     32     50     64       5     18     26     40     59     74				5						
3 9 14 25 40 53 4 14 20 32 50 64 5 18 26 40 59 74		2		9	18					
5 18 26 40 59 74			9	14		40				
5 18 26 40 59 74		4	14	20	32	50	64			
		5	18							

f Mutations vs ability	Probability of x mutations	in 20 generations, i.e.	since circa 1250, usi	ng Ann Taylor's calculator:	
	37 markers @ average muta	ation rate of 0.36%			
		Mutations	Probability	Cumulative probability	
		0	7.0%	7.0%	
		1	18.6%	25.6%	
		2	24.9%	50.5%	
		3	22.0%	72.5%	
		4	14.6%	87.1%	
		5	7.8%	94.9%	
	Mean = 2.7 mutations				
	43 markers @ average muta	ation rate of 0.26%			
		Mutations	Probability	Cumulative probability	
		0	10.7%	10.7%	
		1	23.9%	34.6%	
		2	26.7%	61.3%	
		3	19.2%	80.5%	
		4	11.1%	91.6%	
		5	5.0%	96.6%	
	Mean = 2.2 mutations				

	Marker	FTDNA	Wikipedia	RogersDNA	Hawgood DNA	R1b Allele Frequency	Cheshire Clan Experience	Lancashire Clan	Other R1b Experience
Source		1	2	3	4	5			·
	23 of 30 test results to d	late are haplogr	oup R1b (mo	stly R1b1a2).			7 x DNAH, 4 x FTDNA = 11	2 x DNAH, 6 x FTDNA = 8	8 x DNAH, 7 x FTDNA = 15
							= most common allele unless noted	= most common allele unless noted	= most common allele unless noted
Panel 1 (1-12)		0.250%	0.185%		0.211%				
	DYS393		0.076%	as Wikipedia	0.150%	13 = 92%, 12 = 2%, 14 = 5%	One mutation at 14	5 x 13, 3 x 14	1 x 12, 2 x 14
	DYS390		0.311%	do	0.340%	23 = 58%. 24 = 31%, 25= 7%, 22 = 3%	All at 24		4 x 25, 9 x 24, 1 x 22, 1 x 2
	DYS19		0.151%	do	0.230%	14 = 91%, 15 = 7%			4 x 15
	DYS391		0.265%	do	0.270%	11 = 67%, 10 = 28%, 12 = 5%	One mutation at 10	Three mutations at 10	4 x 10, 1 x 12
	DYS385		0.226%	do	0.320%	11-14=70% 11-15=14% 12-14 = 6%			2 x 12-14, 3 x 11-15, 3 x others
	DYS426		0.009%			12 = 98%			
	DYS388		0.222%		0.050%	12 = 98%			
	DYS439		0.477%	do		12 = 62%, 11 = 24%, 13 = 12%	One mutation at 111, one at 13	7 x 11, 1 x 12	6 x 11, 4 x 13
	DYS389i		0.186%	do	0.250%	13 = 83%, 14 = 12%, 12 = 4%		1 x 12, 1 x 14	2 x 12, 1 x 14
	DYS392		0.052%	do	0.140%	13 = 94%, 14 = 4%		7 x 14, 1 x 13	1 x 15
	DYS389ii		0.242%	do	0.280%	29 = 65%, 30 = 19%, 28 = 11%		1 x 28, 1 x 30	3 x 30., 2 x 28

	Marker	FTDNA	Wikipedia	RogersDNA	Hawgood DNA	R1b Allele Frequency	Cheshire Clan Experience	Lancashire Clan	Other R1b Experience
Source		1	2	3	4	5	•		
	23 of 30 test results to d	ate are haplogr	oup R1b (mo	stly R1b1a2).			7 x DNAH, 4 x FTDNA = 11	2 x DNAH, 6 x FTDNA = 8	8 x DNAH, 7 x FTDNA = 15
							= most common allele unless noted	= most common allele unless noted	= most common allele unless noted
Panel 2 (13-25)		0.300%	0.352%		0.363%				
	DYS458		0.814%	do	0.730%	17 = 51%, 16 = 20%, 18 = 20%, 19 = 6%	One mutation at 16, one at 18		2 x 16, 2 x 18, 1 x 19
	DYS459		0.132%	do	0.210%	9-10=82%, 9-9=16%	One mutation at 9-9		
	DYS455		0.016%	do	0.070%	11 = 98%			
	DYS454		0.016%	do	0.070%	11 = 98%			
	DYS447		0.264%	do	0.300%	25 = 54%, 24 = 31%, 26 = 11%		all 24	2 x 24
	DYS437		0.099%	do	0.170%	15 = 85%, 14 = 12%	AII = 14		2 x 14
	DYS448		0.135%	do	0.170%	19 = 90%, 18 = 5%, 20 = 5%			1 x 20
	DYS449		0.838%	do	0.880%	29 = 44%, 30 = 28%, 28 = 13%, 31 = 10%	All = 30	3 x 29, 4 x 30	7 x 29, 1 x 30, 2 x 28
	DYS464a		0.566%	do		15 = 83%, 14 = 12%, 16 = 3%		15-16-17-19 x 5, = 2% probability	2 x 14, 1 x 16
	DYS464b		0.566%	do	0.500%	15 = 70%, 16 = 26%		1 x 15, 6 x 16	4 x 16
	DYS464c		0.566%	do	0.500%	17 = 53%, 16 = 33%, 15 = 9%	9 x 16, 2 x 15	6 x 17, 1 x 16	5 x 15, 3 x 16, 5 x 17
	DYS464d		0.566%	do	0.550%	17 = 49%, 18 = 37%, 16 = 8%, 15 = 1%, 19 = 4%	All = 16	all 19	1 x 15, 2 x 16, 5 x 17, 3 x 18, 1 x 19

	Marker	FTDNA	Wikipedia	RogersDNA		R1b Allele Frequency	Cheshire Clan Experience	Lancashire Clan	Other R1b Experience
Source		1	2	3	4	5	•		·
	23 of 30 test results to o	date are haplogr	oup R1b (mo	stly R1b1a2).			7 x DNAH, 4 x FTDNA = 11	2 x DNAH, 6 x FTDNA = 8	8 x DNAH, 7 x FTDNA = 15
							= most common allele unless noted	= most common allele unless noted	= most common allele unless noted
Panel 3 (26-37)		0.710%	0.936%		0.930%	1			
	DNAH present		0.279%		0.300%				
	FTDNA Specific		1.857%		1.812%				
	DYS460		0.402%	do	0.340%	11 = 74%, 10 = 21%			3 x 10,
	Y-GATA-H4		0.208%	do	0.320%	11 = 68%, 10 = 26%, 12 = 5%			1 x 12
	YCAlla		0.123%	do	0.160%	19 = 95%, 20 = 1%			2 x 20
	YCAIIb		0.123%	do	0.160%	23 = 81%, 22 = 9%, 24 = 6%			2 x 22, 1 x 24
	DYS456		0.735%	do	0.540%	16 = 41%, 15 = 33%, 17 = 21%	8 x 16, 3 x 15	1 x 17	6 x 15, 1 x 17
	DYS607*		0.411%	do	0.390%	15 = 70%, 14 = 21% 16 = 7%			1 x 14, 1 x 16
	DYS576*		1.022%	do	0.860%	17 = 41%, 18 = 29%, 19 = 10%, 16 = 16%	1 x 17, 4 x 18	2 x 17, 2 x18, 1 x 19	1 x 18, 1 x 20, 1 x 21
	DYS570*		0.790%	do	0.750%	17 = 56%, 18 = 23%, 16 = 12%, 19 = 7%		1 x 17, 1 x 18	1 x 16, 2 x 20
	CDYa*		3.531%	do		36 = 30%, 35 = 14%, 34 = 4%, 37 = 29%, 38 = 16%	1 x 34, 3 x 35, 1 x 36	3 x 37, 2 x 38	1 x 34, 2 x 38
	CDYb*		3.531%	do		38 = 31%, 39 = 32%, 36 = 7%	. , ,	2 x 38, 3 x 39	2 x 36, 1 x 37
	DYS442		0.324%	do	0.500%	12 = 70%, 13 = 15 %, 11 = 12%	One mutation at 11	all 13	3 x 11, 2 x 13
	DYS438		0.035%	do	0.080%	12 = 93%, 10 = <1%	1 x 10		

	Marker	FTDNA	Wikipedia	RogersDNA		R1b Allele Frequency	Cheshire Clan Experience	Lancashire Clan	Other R1b Experience
Source		1	2	3	4	5			
	23 of 30 test results to dat	te are haplog	roup R1b (mo:	stly R1b1a2).			7 x DNAH, 4 x FTDNA = 11		8 x DNAH, 7 x FTDNA = 15
							= most common allele unless noted	= most common allele unless noted	= most common allele unless noted
		* = FTDNA s	pecific						
DNAH Specific				0.237%					
	DYS441			0.132%			all 13	2 x 13	all 13
	DYS444			0.321%	0.290%	12 = 78%, 11 = 8%, 13 = 13%	3 x 11, 3 x 12, 2 x 13	2 x 12	8 x 12, 1 x 11, 1 x 13
	DYS445			0.296%	0.260%		all 12	2 x 12	all 12
	DYS446			0.095%	0.310%	13 = 79%, 12 = 8%, 14 = 11%	12, 1 mutation at 13	2 x 14	7 x 13, 1 x 14
	DYS452			0.314%	0.330%		all 30	2 x 30	7 x 30, 1 x 31
	DYS461			0.233%			all 12	2 x 12	7 x 12 1 x 13
	DYS462			0.053%	0.150%		all 11	2 x 11	7 x 11, 1 x 12
	DYS463			0.162%	0.190%		all 24	2 x 24	all 24
	DYS635			0.492%	0.340%		all 22	2 x 23	6 x 23, 1 x 24, 1 x 25
	GATA A10			0.379%	0.340%		all 13	2 x 13	6 x 13, 1 x 14, 1 x 12
	GATA 1B			0.130%			all 10	2 x 10	7 x 10, 1 x 11
Overall		My Rates	FTDNA + R	Wiki + R	RogersDNA	Hawgood DNA	Heinila	Burgarella + Heilina infill	lain McD
	FTDNA - 37 Markers	0.36%	0.417%	0.487%	0.487%	0.498%	0.358	% 0.352%	0.428%
	DNAH - 43 Markers	0.25%	0.222%	0.220%	0.220%	0.238%	0.247	% 0.255%	0.300%
	Common - 32/34 Markers	0.24%	0.277%	0.273%	0.273%	0.292%	0.241	% 0.235%	0.322%
	FTDNA 25	0.25%					0.242	% 0.252%	0.315%
	FTDNA 67	0.26%					0.258	% 0.258%	0.326%
	FTDNA 111	0.26%					0.259	% 0.272%	0.308%
	FTDNA + is FTDNA panel	s 1 and 2 plu	s RogersDNA	values					
	Hawwod DNA uses values	s from Roger	sDNA where n	nissing from H	awgood DNA				
Sources				gi-bin/ystrmuta					
				/List_of_Y-STF					
			-	/geddna/mutat					
				.co.uk/str%20d	data.html				
	5	U106 Project	t at FTDNA ar	nd Yahoo					