

G R O U P	ID	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D			
		Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y			
		S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S			
		5	5	3	3	5	5	6	4	4	5	4	4	4	5	5	4	4	5	4	4	4	5	4	6	5	4	5			
		3	7	9	9	9	3	4	7	0	1	2	1	1	5	9	3	9	3	5	4	8	2	4	1	6	8	7			
		1	8	5	5	0	7	1	2	6	1	5	3	3	7	4	6	0	4	0	4	1	0	6	7	8	7				
				S	S					S		a	b																		
				1	1					1																					
				a	b																										
2*	JT	11	9	15	16	8	10	10	8	10	10	12	21	21	16	10	12	12	16	8	12	25	20	13	12	11	13	11	11	12	12
2a	JN	11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	16	8	12	25	20	13	12	11	13	11	11	12	12
2a	TW2	11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	16	8	12	25	20	13	12	11	13	11	11	12	12
2a	TNS	11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	16	8	12	26	20	13	12	11	13	11	11	12	12
2c	SA	11	9	15	16	8	10	10	8	10	10	12	21	23	16	10	12	12	15	8	12	25	20	13	12	11	13	11	11	12	12
4*	JMc	11	9	15	16	8	10	10	8	10	10	12	23	24	16	10	12	12	14	8	13	24	20	13	12	11	13	11	11	12	12
4*	JM3	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	14	8	13	23	19	13	12	11	13	11	12	12	12
4*	MK	11	9	15	16	8	10	10	8	10	10	12	23	23	16	10	12	12	15	8	12	23	20	14	12	11	13	11	11	12	12
4*	MAE	12	9	15	16	8	10	10	8	10	10	12	21	22	16	10	12	12	15	8	10	22	20	14	12	11	13	11	11	12	12
4a	DS	11	9	14	16	8	10	10	8	10	11	12	23	23	16	10	12	12	15	8	12	23	21	13	12	11	13	11	11	13	12
4a	DH	11	9	14	16	8	10	10	8	10	11	12	23	23	16	10	12	12	16	8	12	23	21	13	12	11	13	11	11	13	12
4a	WE2	11	9	14	16	8	10	10	8	10	11	12	23	23	16	10	12	12	16	8	12	23	21	13	12	11	13	11	11	13	12
4b	SL	11	9	15	16	9	10	10	8	10	10	12	22	23	17	10	12	12	16	8	11	22	20	14	12	11	13	11	11	13	12
4*	McE	12	9	15	16	8	10	10	8	10	10	12	22	23	16	10	12	12	15	8	11	22	20	15	12	11	13	11	11	12	12
4c	WD	12	9	16	16	8	11	10	8	10	10	12	23	23	15	10	12	12	15	8	12	22	20	13	12	11	13	11	11	13	12
4c	PT	12	9	16	16	8	11	10	8	11	10	12	23	23	15	10	12	12	15	8	12	22	20	13	12	11	13	11	11	13	12
4c	RL2	12	9	16	16	8	11	10	8	10	10	12	23	23	15	10	12	12	15	8	12	22	20	13	12	11	13	11	11	13	12
5*	DR2	11	8	15	16	8	11	10	8	12	11	15	22	22	14	10	12	12	14	8	12	21	21	19	12	11	12	11	11	11	12
5a	WM	11	8	15	16	8	12	10	8	11	9	0	19	22	16	11	12	12	17	9	14	24	20	11	13	13	13	11	11	12	11
5a	HN	11	8	15	16	8	12	10	8	11	9	0	19	22	16	11	12	12	17	9	14	24	20	11	13	13	13	11	11	12	11

Have a look at the results. Remember that the men in Groups 1 and 2 (including the first nineteen men in the table above) are the men in the large, closely related group of Ewings. Except for CHY at DYS 534 = 15, SR at DYS 534 = 17, JL at DYS 557 = 17, JT at DYS 413b = 21 TNS at DYS 413a = 26 and SA at DYS 534 = 15, they all match one another perfectly on the additional 30 markers. The last time I edited this report, we had found few differences in this marker panel among Ewings in the closely related group and I was pessimistic that it was going to be of much help to us. Now, as you can see we have six off-modal markers in 19 haplotypes, and this makes me think that these markers might end up being more helpful than I thought. So far, we cannot get too worked up about having found a branch marker, because except for DYS 534 = 15, each of these off modal values has been found in only one man. And we cannot make much of the match between CHY and SA at DYS 534 because they differ at the defining marker for Group 2, DYS 391 on the 37-marker panel. Feel free to contact me if the logic of this statement eludes you and we can discuss it.

The situation is different for men who have not yet identified a closely related group. Any man who is looking for biological relatives by relying strictly on DNA results will benefit from testing as many markers as possible. This is even more important when the biological relatives may have a different surname. As I have often said, it is easier to disprove a relationship using DNA testing than it is to prove one, but most genetic genealogists will agree that it is highly likely that two men with close 67-marker matches have a common male ancestor within a genealogic timeframe.

Have a look at the results on these markers for the men in Group 4. Remember that Group 4 consists of all the men in the project that are in Haplogroup R1b1b2, but not in its M222+ subclade. Look at Network Diagram—Overview: you can see that the men in Group 4 are at genetic distances from the Ewing modal on the order of 15 or 20 on the 37-marker panel. The men in Group 4* are not known to be related to one another or to the other men in the project. Groups 4a-4d are clusters of haplotypes

within Group 4. Groups 4c and 4d consist of men who are known on the basis of conventional genealogy to be related to the other men in their subgroup. Groups 4a and 4b also have some men known to be related, but also some who have similar enough DNA that we put them in these subgroups, even though that breaks our rule about how the groups are constituted, or at least bends it a little. But my point here is that in Group 4, the 67-marker upgrade seems to offer more information than it does in Groups 1 & 2.

Look now at Group 4a; it would help you to follow this if you also printed out the Group 4a Relationship Diagram and the Group 4 Results Table. JM, WR2 and WE2 are known to be related on the basis of their conventional genealogy. DH matches WE2 exactly on the 37-marker panel, so we think he might very well be in this same kindred. DS is not such a close match, though; he is genetic distance three from DH and WE2 on the 37-marker panel. But he matches them very closely on the additional 30 markers, differing at only one more marker, so that he is genetic distance four on the 67-marker panel. You can think about this in terms of percentages, if you like: 4/67 (6%) is closer than 3/37 (8%). Knowing the extra markers increases the likelihood of a close relationship in this case.

Look now at Group 4b. SL and ME are known third cousins. Their 37-marker panels match exactly except at CDYa, which is a notoriously rapidly mutating marker that can distinguish branches, but must be regarded with a somewhat jaundiced eye because it is more than usually subject to parallel and back mutations. PL is a Scottish man not known to be related to SL and ME. SL and ME do not know their immigrant ancestor. PA is genetic distance four on the 37-marker panel from ME and five from SL, so close enough to be in the same cluster, but not very close. McE is an American McEwen not known to be related to the others. On the 37-marker panel he is genetic distance 11 from SL and 14 from PA (including 2-step mutations at a few markers, but let's not get into that here). We tried including McE in Group 4b because all of these men appear to be in the so-called R1bSTR47-Scots cluster. But as you can see, on the additional 30 markers reported above, McE and SL differ at another six markers, which makes it hard to justify thinking about them being in the same cluster even. It is practically certain that ME would exactly match SL on these 30 markers, because they are third cousins, but we do not know what we would find if PA were tested for the additional markers. We might find that he is closer to SL and ME than we thought based on just 37 markers (as was the case with DS and the other two Group 4a men discussed in the paragraph above), or we might find that he is further.

Finally, look at Group 4c. PT and RL2 are known on the basis of their conventional genealogies to be sixth cousins of one another. They are genetic distance four from one another on the 37-marker panel, which is a little further than we would expect sixth cousins to be from one another, perhaps, but is not inconsistent with this relationship. (If the average mutation rate is .004, we would expect to find two mutations on average, and the odds that we would find exactly four are a little less than 10%.) But since they only have one additional difference in the additional 30 markers we are speaking about here, they are genetic distance five on the full 67-marker panel. [If we use the same mutation rate, we would expect four mutations on average, and the odds that we would find exactly five are about 14.5%. Or if you want to use the same "percentage method" that I spoke about above, 5/67 (7%) is closer than 4/37 (11%)]. As you can see, in this case studying more markers gave us a result a little closer to what we might have expected as an "average" result." This is not of any great interest to PT & RL2, who know their degree of relatedness because of the paper trail, but the example shows why a person who did not have a paper trail would want as many markers as possible. [Note that WD has also told me that he is a known relative of the other men in this group, but I have never received his conventional lineage and do not know exactly how he is related. His haplotype matches the modal for the three of them, and you can think of his results as being in some sense intermediate between the two of them.]

To Order or Upgrade to the 67-marker panel

We recommend that new members of the Ewing Surname Y-DNA Project start with the 37-marker panel, then upgrade to 67-markers depending on what the results of the 37-marker test reveal, but one could save a little money on the 67-marker panel by ordering it from the outset. If you want to join the Ewing Project by ordering the 67-marker test, go to our [Join Page](#), fill out the form, click **Y-DNA67** in the pull-down menu at the bottom of the page, click **Continue** and fill out the billing information. FtDNA will send you a sample collection kit.

If you are a member of the Ewing project and would like to upgrade to 67-markers, please go to your FtDNA personal page, click on **Order Tests & Upgrades** in the menu on the left-hand side of the page, then click on **Standard Orders**, and choose **Y-Refine37to67** on the pull-down menu at the bottom of the page. Then click **Continue** and fill out the billing information. It will not be necessary to submit another specimen, because FtDNA already has the one you submitted previously in storage. If you have trouble ordering the test or are not sure whether it will be an informative test for you, please send an email to david_ewing@clanewing.org and he will help you.