

A perfect 12 for 12 (or 25 for 25 or 37 for 37) marker match is known as genetic distance zero. In other words, the difference between the values for all the markers when one set is compared (subtracted) from the other set is zero. When one marker differs by the value of one and all of the remaining markers are identical, the genetic distance is said to be one. If two markers differ by one, and all the remaining markers are identical, then the genetic distance is two, and so on. In the same fashion, if the allele value of an individual marker for two participants differs by two, then that single marker accounts for a genetic distance of two.

So, to calculate the genetic distance between any two participants, you subtract the allele values for all the markers from one participant from the allele values of the other participant. The genetic distance for the two participants is then the sum of the absolute values of the differences for the markers. There are some adjustments to this straight forward calculation because of the markers being tested. For example marker number 10 (389-1) and marker number 12 (389-2) have now been shown to mutate in tandem; i.e. when a rare mutation occurs, both of these markers exhibit a change at the same time. Therefore, a different allele value for these two markers between two participants represents only a genetic distance of one, not two.

Genetic Distance is calculated the same way for the three different quantities of markers (12, 25 or 37); however, the meaning of the Genetic Distance calculation is different depending on the number of markers being evaluated. The following three tables explain the meaning of Genetic Distance for the results from 12, 25 and 37 marker tests.

12 - Marker Matches

DISTANCE	RELATEDNESS	EXPLANATION
0	Related	This represents a perfect 12 for 12 match which means you share a common male ancestor with a person who shares your Surname (or variant).
1	Probably Related	You share the same surname (or variant) with another male and you mismatch by only one 'point' on only one marker (or two tandem markers).
2	Probably Not Related	You share the same surname (or variant) but are off by 2 'points' or two locations out of twelve markers. It's possible that you are related when the 12-marker genetic distance calculation is 2, however, a more definitive test of at least 25 markers would be required
3	Not Related	Your genetic distance is too far off to be considered related, although a more definitive test is probably warranted to be sure.
4	Not Related	You are not related and the odds greatly favor that you have not shared a common male ancestor in more than 2,000 years.
5	Not Related	You are not related and the odds greatly favor that you have not shared a common male ancestor in more than 5,000 years.
> 5	Not Related	You are totally unrelated.

25 - Marker Matches

DISTANCE	RELATEDNESS	EXPLANATION
0	Related	This represents a perfect 25 for 25 match which means you share a common male ancestor with a person who shares your Surname (or variant).
1	Probably Related	You share the same surname (or variant) with another male and you mismatch by only one 'point' on only one marker (or two tandem markers). For most closely related and same surnamed individuals, the mismatched markers are usually either DYS 439 or DYS 385a or 385b from the first 12 markers, and DYS #s 458, 459a, 459b, 449, 464a-d in the markers from 13 to 25. These markers have shown themselves to move most rapidly. The probability of a close relationship is very high with a genetic

		distance of one.
2	Probably Not Related	You share the same surname (or variant) but mismatch by 2 'points' or two locations out of 25 markers tested. The probability of a close relationship is good, however, your results show multiple mutations; therefore, more time (generations) probably exists between you and the other same surnamed person than if you were separated by a genetic distance of one
3	Not Related	You share the same surname (or variant) but mismatch by 3 'points' or three locations out of 25 markers tested. If enough time (generations) has passed it is possible that you and the other distantly related family members' line each have had a mutation, or perhaps 2. The only way to prove that is to test additional family lines and find when the mutation(s) took place. In this case, it would be advantageous for you and the other possible distant cousin to be tested at the 37 marker level.
4	Not Related	Matching only 21 out of 25 markers is too far off to be considered related. Unlikely but vaguely possible that the rule for only possible related applies. It is important to determine what set of results most typifies 'most' members of the group you are 'close' to matching. You could be 21/25 with an individual, but 23/25 with the center (most common) of the group and your potential relatedness to him is through the center of the group.
5	Not Related	When you match only 20 out of 25 markers, even if the other person shares the same surname, you are not related and the odds greatly favor that you have not shared a common male ancestor with this other person in excess of 2,000 years.
6	Not Related	When you match only 19 out of 25 markers, even if the other person shares the same surname, you are not related and the odds greatly favor that you have not shared a common male ancestor with this other person in excess of 5,000 years.
> 6	Not Related	When your genetic distance is more than 6, you are totally unrelated to this person.

37 - Marker Matches		
DISTANCE	RELATEDNESS	EXPLANATION
0	Very Tightly Related	This represents a perfect 37 for 37 match. Your perfect match means you share a common male ancestor with a person who shares your surname (or variant). Your relatedness is extremely close with the common ancestor predicted, 50% of the time, in 5 generations or less and with a 90% probability within 16 generations. Very few people achieve this close level of a match. All confidence levels are well within the time frame that surnames were adopted in Western Europe.

1	Tightly Related	This represents a 36 out of 37 match. In this case, when you should share the same surname (or a variant) with another male and you mismatch by only one 'point' at only one marker you are tightly related. It's most likely that you matched 24/25 or 25/25 on a previous Y-DNA test and your mismatch will be found within DYS 576, 570, CDYa or CDYb. Very few people achieve this close level of a match. Your mismatch is within the range of most well established surname lineages in Western Europe.
2	Related	In this case, if you share the same surname (or a variant) with another male and you mismatch by only two 'points' for a 35 for 37 match you are related. It's most likely that you matched 24/25 or 25/25 on previous Y-DNA tests and your mismatch will be found within DYS 439 or DYS 385A, 385B, 389-1 and 389-2, from the first panel of 12 markers, or from within the second panel at DYS #'s 458, 459a, 459b, 449, or within 464a-d. If you matched exactly on previous tests you probably have a mismatch at DYS 576, 570, CDYa or CDYb in this panel of markers. Your mismatch is likely within the range of most well established surname lineages in Western Europe.
3	Related	In this case, if you share the same surname (or a variant) with another male and you mismatch by three 'points' --a 34 for 37 match you are related. Because of the volatility within some of the markers this result is slightly tighter than being 11/12 or 23/25 and it's most likely that you matched 24/25 or 25/25 on previous Y-DNA tests. Your mismatch will most often be found within DYS 439 or DYS 385A, 385B, 389-1 and 389-2 from the first panel of 12 markers, or within the second panel: DYS #'s 458, 459a, 459b, 449, or within 464a-d. If you matched exactly on the previous tests you probably have a mismatch at DYS 576, 570, CDYa or CDYb in the newest panel of markers. Your mismatch is likely within the range of most well established surname lineages in Western Europe
4	Probably Related	In this case, if you share the same surname (or a variant) with another male and you mismatch by four 'points', a 33/37 match you are probably related. Because of the volatility within some of the markers this is about the same as being 11/12 and it's most likely that you matched 23/25 or 24/25 on previous Y-DNA tests. If you matched exactly on previous tests you probably have a mismatch at DYS 576, 570, CDYa or CDYb in the newest panel of markers. If several or many generations have passed it is likely that these two lines are related through other family members. That would require that each line had passed a mutation and one person would have experienced at least 2 mutations. The only way to confirm is to test additional family lines and find where the mutations took place. Only by testing additional family members can you find the person in between each of you...this 'in between' becomes essential for you to find, and without him the possibility of a match exists, but further evidence must be pursued. If you test additional individuals you will most likely find that their DNA falls in-between the persons who are 4 apart.

		demonstrating relatedness within this family cluster or Haplotype.
5	Only Possibly Related	In this case, if you share the same surname (or a variant) with another male and you mismatch by five 'points', a 32/37 match you may be related. It is most likely that you did not match 12/12 or 24/25 or 25/25 in previous Y-DNA tests. If several or many generations have passed it is possible that these two men are related through other family members. That would require that each line had experienced separate mutations and one person would have experienced at least 2 mutations. The only way to confirm or deny is to test additional family lines and find where the mutation took place. Only by testing additional family members can you find the person in between each of you...this 'in-betweener' becomes essential for you to find, and without him only the possibility of a match exists, further evidence should be pursued. If you test additional individuals you must find the person whose DNA results falls in-between the persons that are 5 apart demonstrating relatedness within this family cluster or Haplotype.
6	Not Related	The 31 out of 37 match is too far off to be considered related, unless you can find an "in-betweener" as for determining 'Only Possibly Related,' above. It is important to determine what set of results most typifies the largest number members of the group you are 'close' to matching. You may be 31/37 with an individual, but 34/37 with the center of the group, and your potential relatedness to him is through the center of the group.
> 6	Not Related	In this case, for 30 out of 37 are worse, you are not related and the odds greatly favor that you have not shared a common male ancestor with this person within thousands of years. You are probably even in different Haplogroups on the Phylogenetic tree of Homo Sapiens.