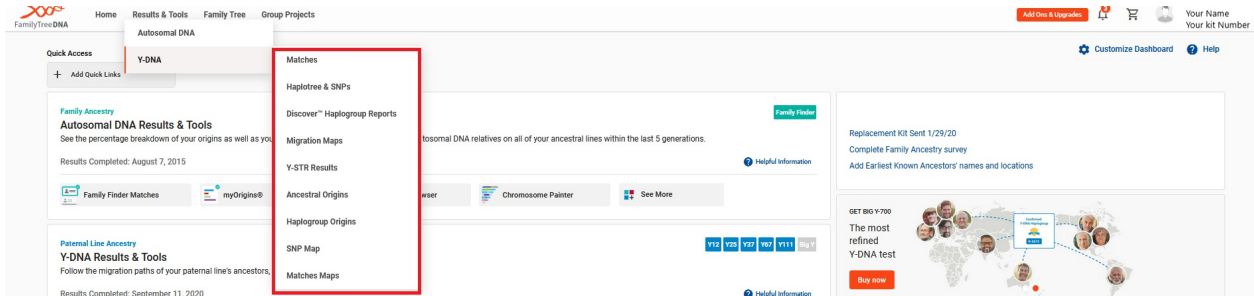


# The Y-DNA Results & Tools Menu

You probably entrusted your DNA to FTDNA in order to learn more about your ancestors; to fill out your family tree (as we say). But you may be among those who submit DNA for other reasons, especially to just find out where in the vast human tree you originated. This is not documentary genealogy – constructing and learning about your ancestors since 1500 – but going deeper into the human past. For those who are interested in their own recent family tree, deeper information may be seen through this menu. But if curiosity carries you back the long trek of human development, there is information on the FTDNA dashboard for you as well.

So, if you want to explore the full Y-DNA information, here we go. There are two ways to unlock this information, the easiest is to pull down the **Results & Tools** menu next to the **Home** button at the top of the screen. Pull it down, and choose **Y-DNA**. A second menu opens:



The top item on this sub-menu accesses your matches and will be treated in Step 1 as you proceed on the previous page.

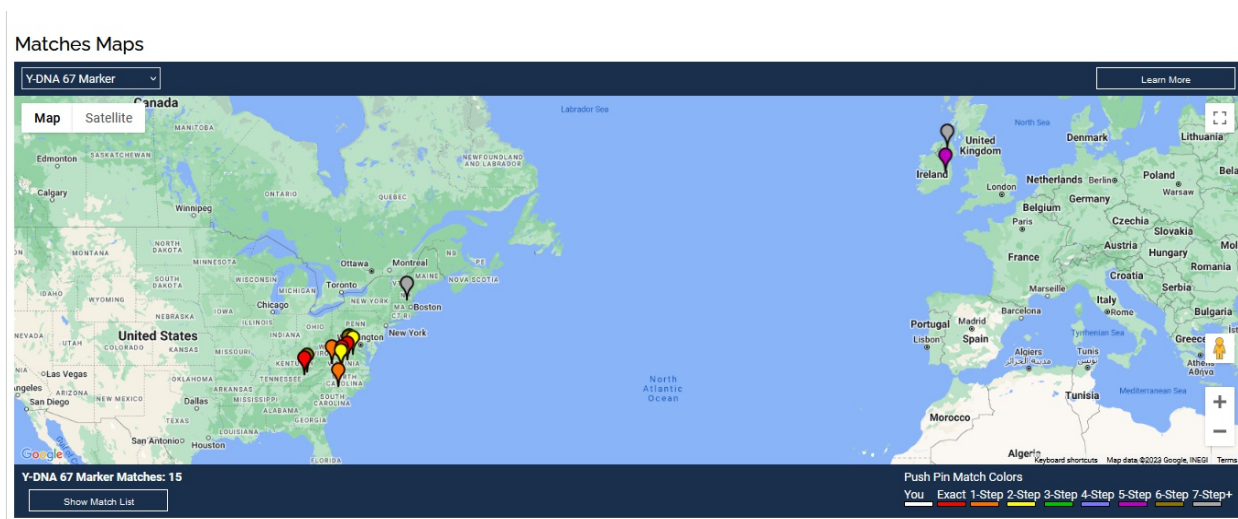
To explore the other items let's divide them into two groups: a group that drills down into your 37-111 marker Y-DNA results, and a group that gives you information on your distant ancestry.

## More on Your 37-111 Marker Results

First the former group: deeper information on your 37-111 marker test. The fifth item on this menu is vital to your identifying where in your Y-chromosome the mutation(s) that created genetic distance between you and your matches has occurred: **Y-STR Results**. Go ahead and open it. You will see a chart from three to five panels arranged in three to eleven rows with **Markers** and **Values** as cell titles. *Markers* are designated ranges on the Y-DNA genome on which mutations often occur from generation to generation. The *values* are the numbers of times a particular sequence repeats in that range. Generation-to-generation mutations on this marker will change the count of these sequences, thus providing a value. This is the way that mutations are mapped in STR (or "string") analysis. Thus, if you have a value of 25 on marker DYS390, it means that there is a DNA sequence tracked by FT-DNA's scientific analysis in range DYS390 that repeats 25 times. If during correspondence your match reports a value of 24 on DYS390, you have located the mutation on your Y-DNA that separates you from your match.

We recommend making a paper copy of these results. If you have enough knowledge of computing, it is also a good idea to make either a pdf or an image copy of this chart. When you reach out to your matches, this is the information that will help identify your genetic variation.

The lowest item on the Y-DNA pull down menu is **Matches Maps**. Select this and it opens a world map with pins geographically locating the **Paternal Earliest Known Ancestor** as reported by your Y-DNA matches. Note that this information is **not** a product of Y-DNA analysis alone, it starts there but is only as good as the self reporting by your matches. Nevertheless, a cluster of these pins has significance. In a crude way it provides information. For example, look at the following:



Note this map is generated with 67 marker results (upper left hand corner). For this person 15 matches reported their **Paternal Earliest Known Ancestor**. They were clustered in Virginia with a smaller group in northeast Tennessee and in Upstate South Carolina. Note also that a small group are in Ireland. That tells us something about this person’s origins during the genealogical period.

Play around with this map. You can reveal matches with the button in the lower left hand corner and change from 37 to 67 to 111 tests in the upper left hand corner. The button in the upper right hand corner will provide further explanation.

Another expression of this information is found in the menu choice **Ancestral Origins**, this time generated by counting the reports of your matches. Perusing this list will also show some clusters that point you toward your genealogical origins. Again remember that it is not a scientific report only, but a list generated from self-reporting.

That concludes the deeper material available for your correspondence with your matches if you have taken the tests up to 111 marker.

## Where do you fit in the Human Tree?

The other group of markers provide your long term view back into the history of humanity.

Haplogroups are groupings of the human family far into the past. You will notice, for example, that most of the matches for the person who is serving as our example in illustrating the dashboard are on the matches list as Y Haplogroup R-M269. This is a common haplogroup for Daltons. Select **Discover Haplogroup Reports** from the Y-DNA pull down menu and you will open a history of this haplogroup. Explore this report. It answers most of your questions about your deep origins. Note particularly the menu on the left of this page. It will allow you to dig even deeper in these more distant origins (before the genealogical period c1500). There is a whole lot of fun information from exploring this menu.

(Do note that FT-DNA developed this page as a stimulus for you to purchase the BigY-700 upgrade. There are several places on this and other haplogroup pages where you can indicate your desire to make this purchase. More on that in the next topic in this guide.)

The Y-DNA pull down menu selection **Migration Maps** is a simplified depiction of the ancient route of those from your haplogroup.

The rest of the choices on this menu – **Haplogroups & SNPs**, **Haplogroup Origins**, and **SNP map** – will become more useful to those who have purchased the BigY-700 test.

## Difference between STR and SNP Analysis: A note on the BigY-700 test.

Two distinct frameworks now compete when analyzing Y-DNA results. They are referred to easily as “string” (STR) or “snip” (SNP) results. At a very general level the former are counts of sequences of DNA that repeat at particular locations on the Y chromosome; the latter reads the content of a particular location on the Y chromosome. Strings are more likely to detect mutations within a few generations; mutations appear in snips far less frequently across generations. Thus the two differ on the number and speed of mutations they identify across generations, giving each a unique power.

Which is best to use for our work? To answer that question we should first introduce time scale and ranges of time in ancestral research. The time scale for ancestry or family history research is often divided into three ranges:

- the genealogical range, roughly the last 10-12 generations, back to approximately the year 1500. This is a rough estimate of the era when documents are available to support genealogical research;
- at the other extreme the deep origins range which traces back to the dawn of humanity and follows the path of your DNA pattern as it evolves in the thousands of years since;

- and an intermediate range, say 500 to 1000 years ago or about from the year 1000-1500 C.E., before written records are generally available but after European history has begun.

Of course, our Family Group project is focused within genealogical time: the years since 1500. An effective Y-DNA testing program must satisfy two criteria to contribute to our Family Group project: (1) the generation-to-generation mutations must be detected frequently enough to allow the sorting of members into different family sub-groups within genealogical time, and (2) enough matching males must report test results to allow the sub-groups to emerge from comparing tests.

STR tests are superior on both criteria for the genealogical time frame. STR mutations appear between generations with enough frequency within that time frame to permit sorting of families. In contrast, mutations appear in SNP tests at a much slower rate, making them less powerful in the genealogical time frame.

In addition, however, STR tests have the virtue of being less expensive. This permits us to more easily attract a larger number of males to provide test results permitting sub-groups to more easily emerge. When we recommend upgrades (to 67 or 111 markers) to enhance results, they will not be so economically burdensome. Developing sub-groups with SNP tests still requires the requisite number of males to purchase SNP tests, and FTDNA's Big Y-700 that includes the SNP test simply remains too expensive to generate that number of test takers that make our results more robust.

We should also mention that the genealogical range of 10-12 generations aligns with the reliability range for STR tests for Y-DNA. Although STR tests do have some weaknesses such as some chance of a reverse-mutation (mutating back to the original value, thus making the mutation invisible), overall greater frequency of mutation outweighs those weaknesses for our questions. SNP tests are appropriate for answering questions about ancient origins and may be superior to STR tests when we begin to research beyond the 10-12 generation horizon.

But a further word on the BigY-700 and SNP tests. Two factors in their favor.

First, some day we will move beyond the focus of our current Family Group, to relate the Irish Daltons to the English Daltons, or to investigate how our members who do not seem to be matches today relate to those of us who are. At that point we may need to move to SNP tests because we will be focused on an earlier time.

Second, as more and more people from our group purchase the BigY-700, just as with the STR-oriented project, more robust results in sorting out families of Daltons will emerge. The haplogroup will become more differentiated. So far, we have more robust results from STR tests. But your purchase of the BigY-700 now may assist in our family group project in the future. Wait too long to contribute and we may not be able to add your Y-DNA. So it is an investment in the future.

For a fuller explanation of STR and SNP tests, we recommend this explanation of DNA research by Blaine Bettinger