The Complete Guide to FamilyTreeDNA

Y-DNA, Mitochondrial, and Autosomal and X-DNA

By Roberta Estes

Color Page Supplement

To enhance your reading exerience, we have created this pdf for pages where color can better provide the distinctions the author is making.

You have our permission to print any of these pages to use with the book.

PAGES

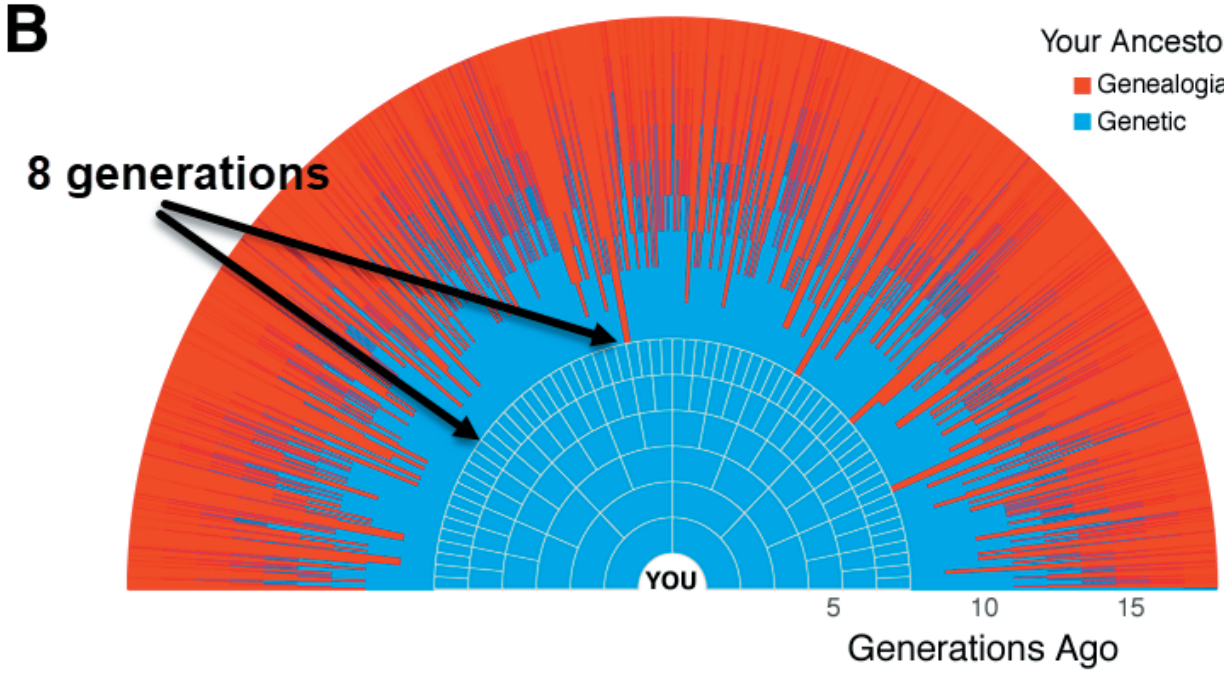


Figure 5. (A) You have an exponentially increasing number of genealogical ancestors, but a much smaller number of genetic ones. Your genealogical ancestors outnumber the world population less than 1,000 years ago. This is because most of your ancestors are duplicated in your family tree. (B) Most of your ancestors from 15 generations ago contributed no DNA to you, due to random genetic recombination, and finite space in the genome.

This figure created by Dr. Paul Maier at FamilyTreeDNA, from the *MyOrigins 3.0 White Paper*[13], illustrates that around seven or eight generations back in time, the amount of blue genetic contribution of a lineage starts to vary, then disappears entirely in some lines. Larger blocks or higher percentages of blue DNA indicate relationships closer in time, and smaller amounts of blue DNA indicate more distant ancestors. In other words, the DNA of the ancestors represented by red has disappeared in you, but they are still your ancestors. You just don't carry an individually discernible amount of the red ancestors' DNA today.

It's unlikely that you are completely missing DNA from one of your ancestors within the past six generations or so[14], but beyond that, it becomes increasingly likely that you inherited either no DNA from some ancestors or fragments too small to detect and be reported by DNA testing vendors as matches.

Translated, this means that autosomal DNA matching is most reliable in the closer and closest generations.

There is no documented occurrence of second cousins who don't match each other. 90% of third cousins match, and about 50% of fourth cousins. I wrote about that in the article, *Why Don't I Match My Cousin?*[15]

13 https://blog.familytreedna.com/wp-content/uploads/2021/08/myOrigins_3_WhitePaper.pdf

14 Assuming that they are in fact your ancestor.

15 https://dna-explained.com/2013/09/29/why-dont-i-match-my-cousin/

How Can I View My Matches' Marker Values?

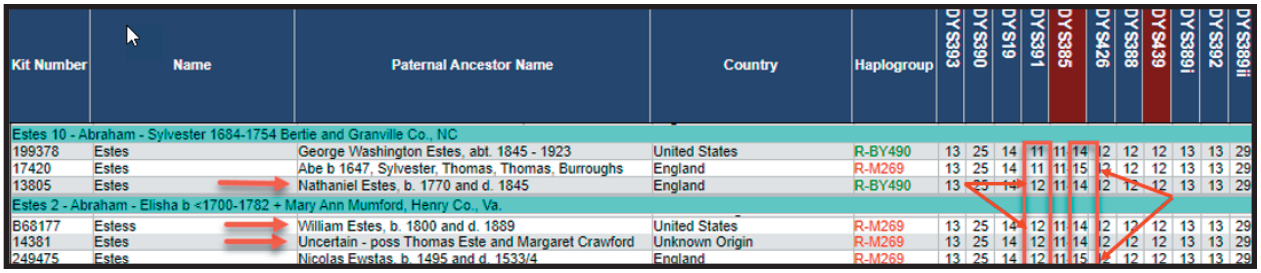
Genetic Distance tells you how closely you match, but it doesn't tell you the values of your markers when compared to each other.

For example, three men can match each other at a Genetic Distance of 1, and all 3 men mismatch each other on a different marker. On the other hand, you can mismatch two men at a distance of 1, and they match each other on the marker where they both mismatch you. They both are a GD of 1 to you, but they match each other exactly.

In order to sort men into family lines using STR markers, you need to know both how closely people match, and the values on mismatching markers.

You can't see other people's marker values on your match page, but you can if your matches have joined DNA projects.

Viewing the public Estes DNA Project[58], I can see all of the STR values of the men in the project from markers 1-111 on the Y-DNA Classic or Y-DNA Colorized Reports page. I'm only displaying a few of those values below.



Kit Number	Name	Paternal Ancestor Name	Country	Haplogroup	DYS393	DYS390	DYS19	DYS391	DYS385	DYS426	DYS388	DYS439	DYS389I	DYS392	DYS389II
Estes 10 - Abraham - Sylvester 1684-1754 Bertie and Granville Co., NC															
199378	Estes	George Washington Estes, abt. 1845 - 1923	United States	R-BY490	13	25	14	11	11 14	12	12	12	13	13	29
17420	Estes	Abe b 1647, Sylvester, Thomas, Thomas, Burroughs	England	R-M269	13	25	14	11	11 15	12	12	12	13	13	29
13805	Estes	Nathaniel Estes, b. 1770 and d. 1845	England	R-BY490	13	25	14	12	11 14	12	12	12	13	13	29
Estes 2 - Abraham - Elisha b <1700-1782 + Mary Ann Mumford, Henry Co., Va.															
B68177	Estess	William Estes, b. 1800 and d. 1889	United States	R-M269	13	25	14	12	11 14	12	12	12	13	13	29
14381	Estes	Uncertain - poss Thomas Este and Margaret Crawford	Unknown Origin	R-M269	13	25	14	12	11 14	12	12	12	13	13	29
249475	Estes	Nicolas Ewstas, b. 1495 and d. 1533/4	England	R-M269	13	25	14	12	11 15	12	12	12	13	13	29

As the volunteer project administrator, I've divided Estes testers into genealogical lines based on which son of Abraham, the immigrant, they descend from.

Let's use the values of two markers as an example.

All of the markers except DYS391 and the second value of DYS385, bracketed in red, match. Within the Estes family line, the matching marker values aren't of interest genealogically. The value is in the mismatching markers that will, hopefully, define lineages.

The testers mismatch on those two markers, so let's look for consistency between their values. Three men descend from Abraham's son, Sylvester, and three descend from his son, Elisha.

58 https://www.familytreedna.com/public/Estes?iframe=yresults

Earliest Known Ancestors and Trees

Don't forget about the Earliest Known Ancestor (EKA) field and country locations. In addition to individual matches and projects, the Discover™ tool, Globetrekker, the Time Tree, and the Group Time Tree all use this information.

Abraham - Abraham Jr. c 1697-1759 + Ann Watkins and Elizbaeth Jeeter, Caroline Co., Va.			
92743	Estes		Unknown Origin
45614	Estes		Unknown Origin
46167	Estes	Abraham Jr 1697-1759 m Ann Clark, Phillip bef 1720	Unknown Origin
43144	Estes	Abraham Jr 1697-1759 m Ann Clark, Phillip bef 1720	Unknown Origin
51909	Estes	Thomas Estes	United Kingdom
49592	Estes	Abraham Jr 1697-1759 m Ann Clark, Samuel b 1727	England
Abraham - Elisha b <1700-1782 + Mary Ann Mumford, Henry Co., Va.			
14495	Estes	Abraham b 1647, Elisha d 1782 m Mary Ann Mumford	England
19696	Estes	Henry Estes b 1874 in Orange Co Va	Unknown Origin

For men who don't know the identity of their Estes ancestor[61], the EKA field of their matches, or trees, or a combination of both, can indicate exactly where they need to search.

TIP: The EKA and the tester's tree may not contain the same information. Some people complete one or the other, but not both. Always check both.

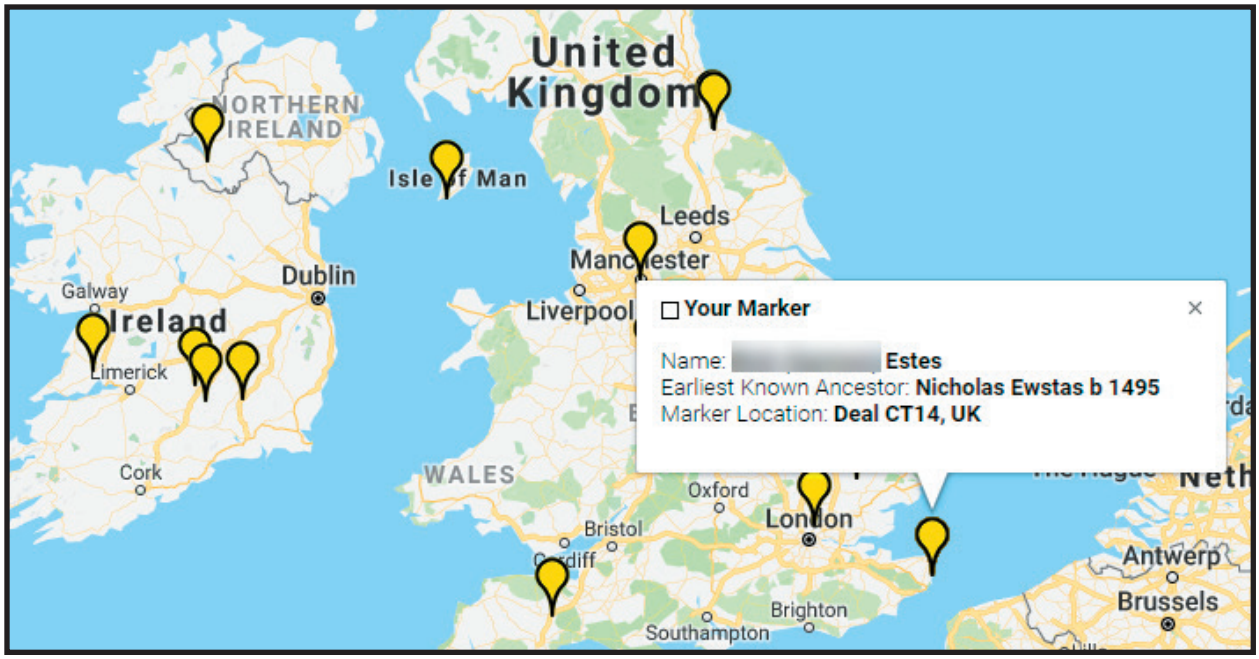
Of course, you can always email your matches and ask about their genealogy.

The EKA and trees are especially useful if a unique STR marker sequence or unique haplogroup defines their specific lineage.

Estes 2 - Abraham - Elisha b <1700-1782 + Mary Ann Mumford, Henry Co., Va.				
B8468	Estes	Robert Estes, b. 1475 and d. 1506	Engl...	R-P312
14495	Estes	abraham estes	England	R-DF49
19696	Estes	Henry Estes b 1874 in Orange Co Va	Unknown Origin	R-M269
201191	Estes		Unknown Origin	R-M269
235224	Estes		Unknown Origin	R-M269
14381	Estes	Uncertain - poss Thomas Este and Margaret Crawford	Unknown Origin	R-M269
29843	Coffey		Ireland	R-M269
244708	Estes	Nicholas Ewstas b 1495 Deal, Kent, England	England	R-BY490

Looking at the group for Elisha, son of Abraham, in the Estes DNA project, you can see that there are four haplogroups. R-M269 is colored red because it's predicted using STR results and not confirmed by SNP testing. The three haplogroups in green are more specific and are confirmed by SNP testing of some type. In this case, SNP testing could mean the purchase of one confirming SNP, an obsolete SNP-based test type that's no longer offered, a SNP Pack, or one of the Big Y tests. Now that the Big Y-700 test is available, we no longer recommend purchasing either individual SNPs or SNP Packs. Big Y test results are always the most specific and are automatically updated as new information is discovered.

61 https://dna-explained.com/2016/11/16/concepts-undocumented-adoptions-vs-untested-y-lines/



The pins are color-coded based on the number of mutations difference, or genetic distance. Exact matches, with a genetic distance of zero, are the closest.

Click on the name on the match list to "go to" their pin.

Of course, the first thing to ask is, "Who are the neighbors?" What might you have in common?

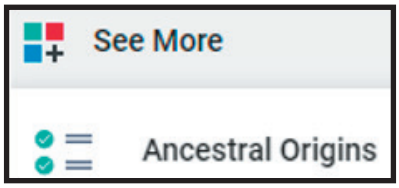
What other surnames do you match?

What history might be associated with those surnames?

Or locations?

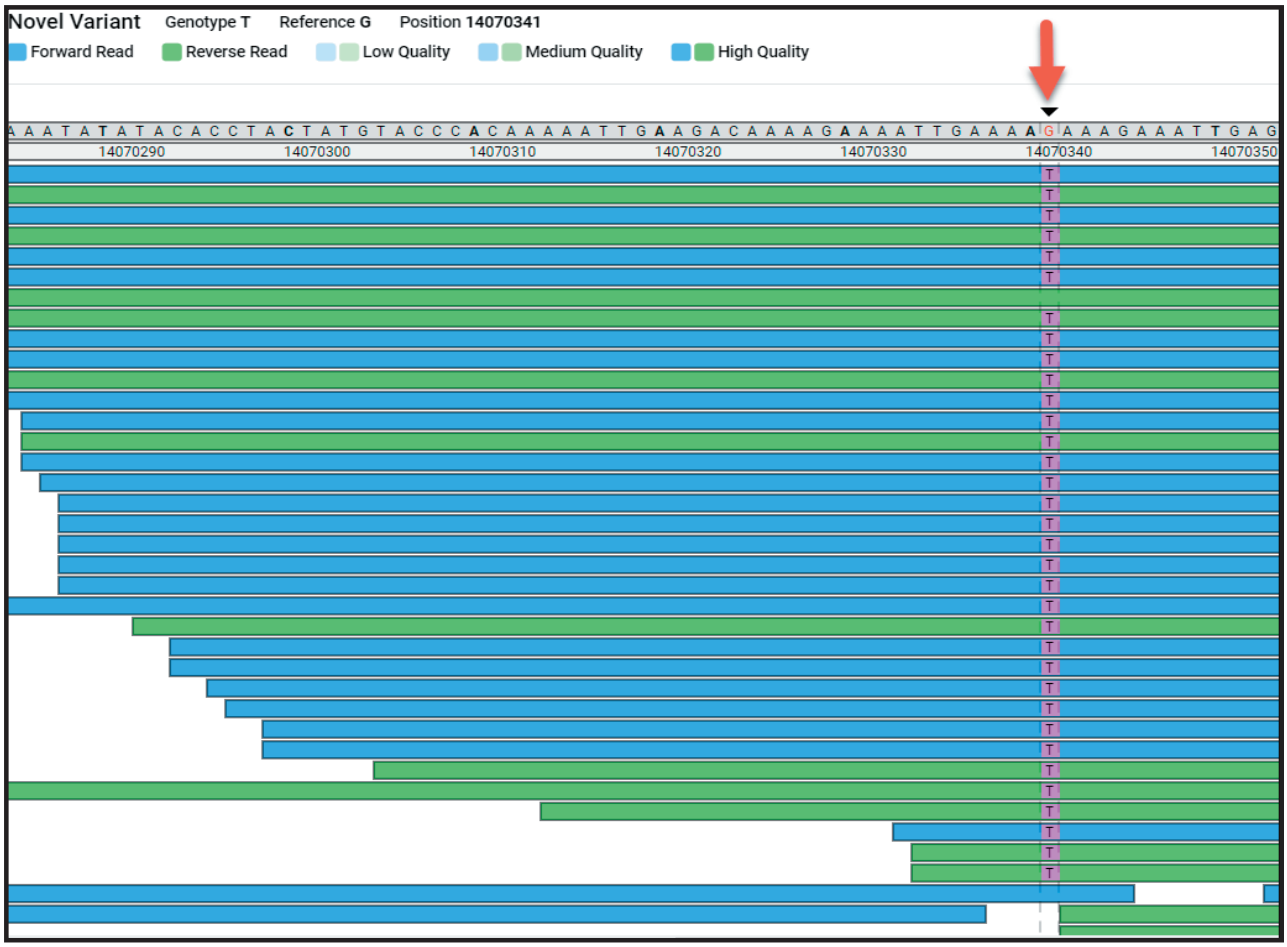
Next, let's see what kind of hints we can find in Ancestral Origins.

Ancestral Origins



FamilyTreeDNA compiles the location information provided by your matches about their ancestors.

For some people, the information is fairly vanilla, but for others, it can be informative, especially any comments.



The blue and green rows represent reads, or scans, of the chromosome. Blue rows indicate that the read was on a forward strand of DNA's double helix, and green rows indicate it was on a reverse strand of the helix. The darker the color of the bar, the better the quality of the read.

The reference value is shown in red text in the bar at the top, right beneath the black divot, which is a G in this case. Beneath the reference value, highlighted in bright pink, your value is displayed if it's different from G. In this case, the scan found a "T" 34 times, representing a very consistent, high-quality read for a value of T.

In this example, G is the reference value - the value in the reference genome- T is this person's genotype, which is a derived value, meaning it is different from the reference value.

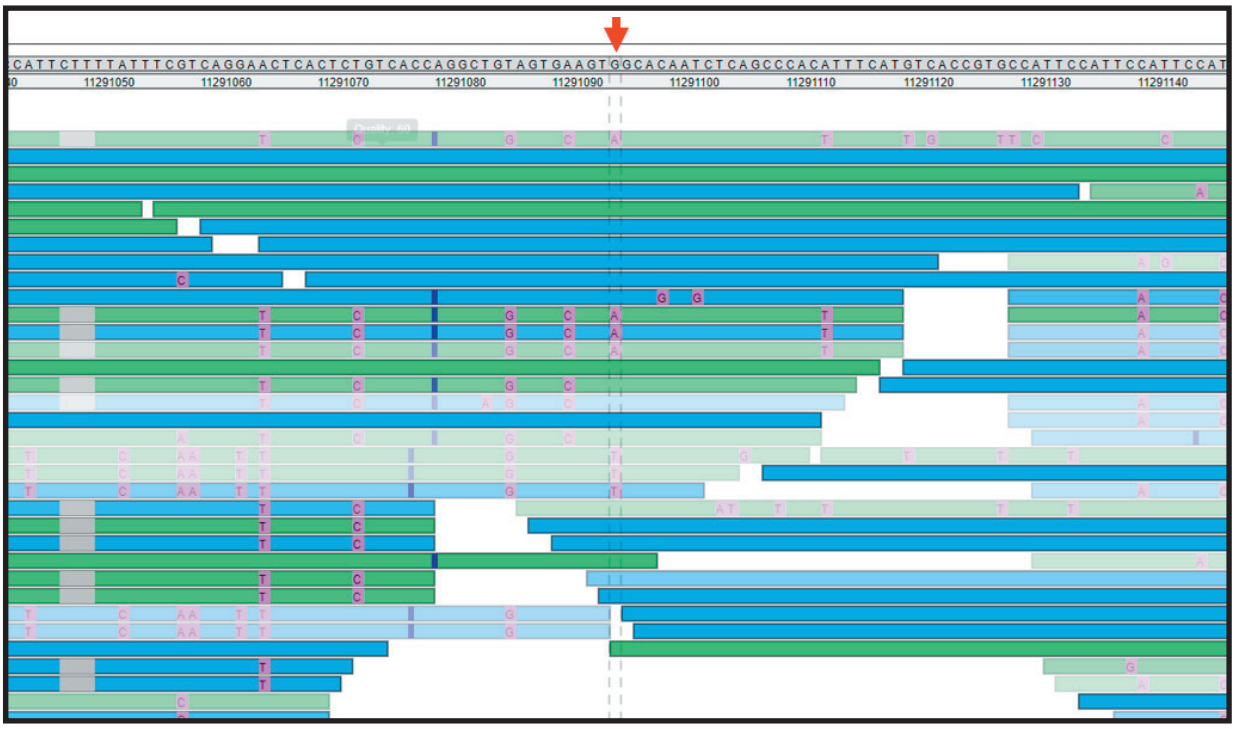
This is a very clean read, but some reads aren't consistent.

To be counted as an actual mutation, the mutated value must be found:

- In greater than five quality reads AND
- Not in a "messy" region

TIP: The Big Y test generally scans the Y chromosome at least 30 times, and often "as many times as it takes" to achieve a quality read.

What does a messy region look like? Great question.



Here's an example of a poor-quality read in a messy area. The values found are inconsistent. The reference value is G, but both an A and a T are found three times each. Furthermore, low-quality forward and reverse reads are lighter, indicating poor quality. Quality reads are darker. Additional indicators of a messy region are shown by the other scattered, random pink mutations in this region.

These scan anomalies are not and should not be counted as mutations when they occur under these circumstances. This is also why every private variant match is reviewed by the phylogeneticist during the naming process. [73]

Big Y Block Tree

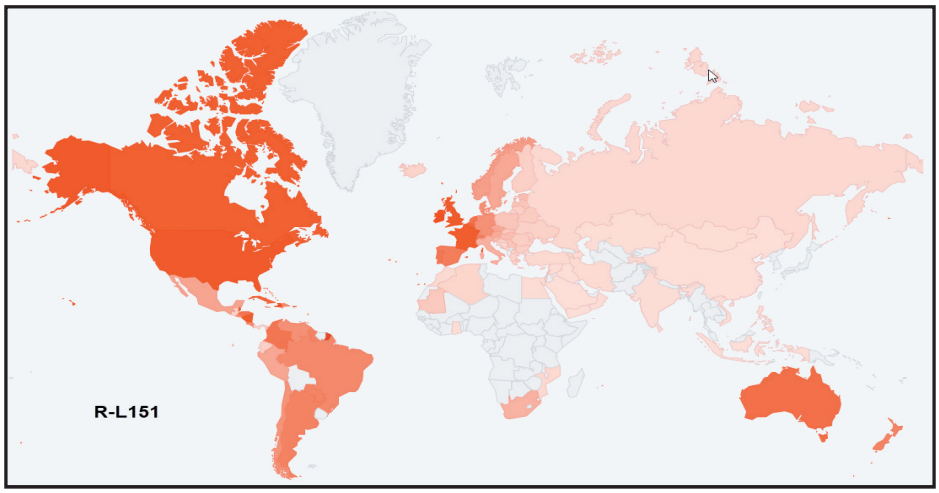
The Block Tree is a method of curating and displaying your Big Y matches on the haplotree to make it easier to visualize their positions in relation to each other.

Keep in mind that men who have not tested to the Big Y-700 level will also be displayed on the tree if they have taken the Big Y-500 and match within a genetic distance of 30 SNPs. If they were to upgrade to the Big Y-700, they might be placed on a more refined branch of the tree. The Big Y-500 lacks the granularity of the Big Y-700 and should be upgraded whenever possible.

73 https://blog.familytreedna.com/big-y-manual-review-lifetime-analysis/

Country Frequency

Country Frequency provides a heat map of the locations of the Earliest Known Ancestor for other testers whose end-of-line SNP is the haplogroup you're viewing.



Ancestors of people whose end-of-line SNP is R-L151 are found in most of the world, except for portions of Africa and a few other locations. R-L151 is not the most refined haplogroup possible. In other words, R-L151[84], which was born about 3000 BCE, or 5000 years ago, has more than 28,000 descendant haplogroups in more than 160 countries.

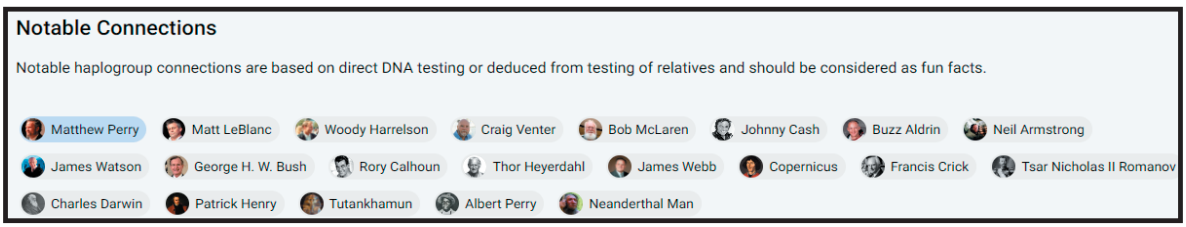
Keep in mind that these locations reflect migration and sometimes where testers are brick-walled, like the United States, not necessarily original locations.

Notable Connections

Notable Connections is a fun section that displays notable people who share the same or upstream haplogroups.

You could match actors, politicians, musicians, scientists, royal families, ancient kings like Tutankhamun, and even Neanderthal Man. New entries are added regularly in both this section and Ancient Connections, so check back often.

Big Y testers who access Discover™ through their account may have 20 or more Ancient and Notable Connections, but public users accessing Discover™ through the free public interface or Y-DNA testers who have not taken the Big Y test are limited to about 11 connections in each category.



84 https://discover.familytreedna.com/y-dna/R-L151/story

Globetrekker

For Big Y testers, Globetrekker is a unique animated map, following the path and development of your haplogroup beginning with Y-Adam, then out of Africa to the location where it is currently found outside of the Americas, Australia, New Zealand, and other areas colonized during the European expansion era. At present, only indigenous Native American haplogroups are displayed in the Americas.[85]

85 https://dna-explained.com/2023/08/04/globetrekker-a-new-feature-for-big-y-customers-from-familytreedna/

Terrain, elevation, sea level, currents, and even glaciation are taken into consideration when determining the most likely path for humans to have taken from place to place.

Globetrekker is a premium tool for Big Y testers only.

My white pin on this map is near the bottom, with the red arrow by the "y" in Germany.

- Exact matches are red pins
- Genetic distance of 1 is orange
- Genetic distance of 2 is yellow

In general, red pins are more relevant and more closely related to you than orange or yellow pins unless something unusual is involved, such as heteroplasmies[122] which might preclude matching or cause someone who would otherwise be a close match to appear as a more distant match.

In my case, my earliest known ancestor was found in Germany in 1621, but most of my exact matches, except for two, are found in either Sweden or Norway, conveying the message that her ancestors were found in Scandinavia. The question, of course, is when, how, and why did her maternal ancestor arrive in Germany? Evaluating the history of the region provided critical clues.

122 https://dna-explained.com/2021/06/10/what-is-a-heteroplasmy-and-why-do-i-care/

On your Chromosome Browser page, all 23 chromosomes, including the X chromosome, will be displayed, but for brevity, I'm showing only 4 chromosomes here.

The background light grey bands of each chromosome are "me."

The area where every person matches me on that chromosome is shown on their own band of my chromosome. All 7 people are stacked up for each chromosome so I can see them side by side.

Viewing Chromosome 1, at the top, we see that Cheryl's match to me is shown first in band 1. On a color image, her matching DNA to me is blue. Her band of my chromosome shows the segment or segments where she matches me on Chromosome 1.

Other matches are stacked below in their own band of my Chromosome 1.

Her brother, Donald's match to me is shown on band 2.

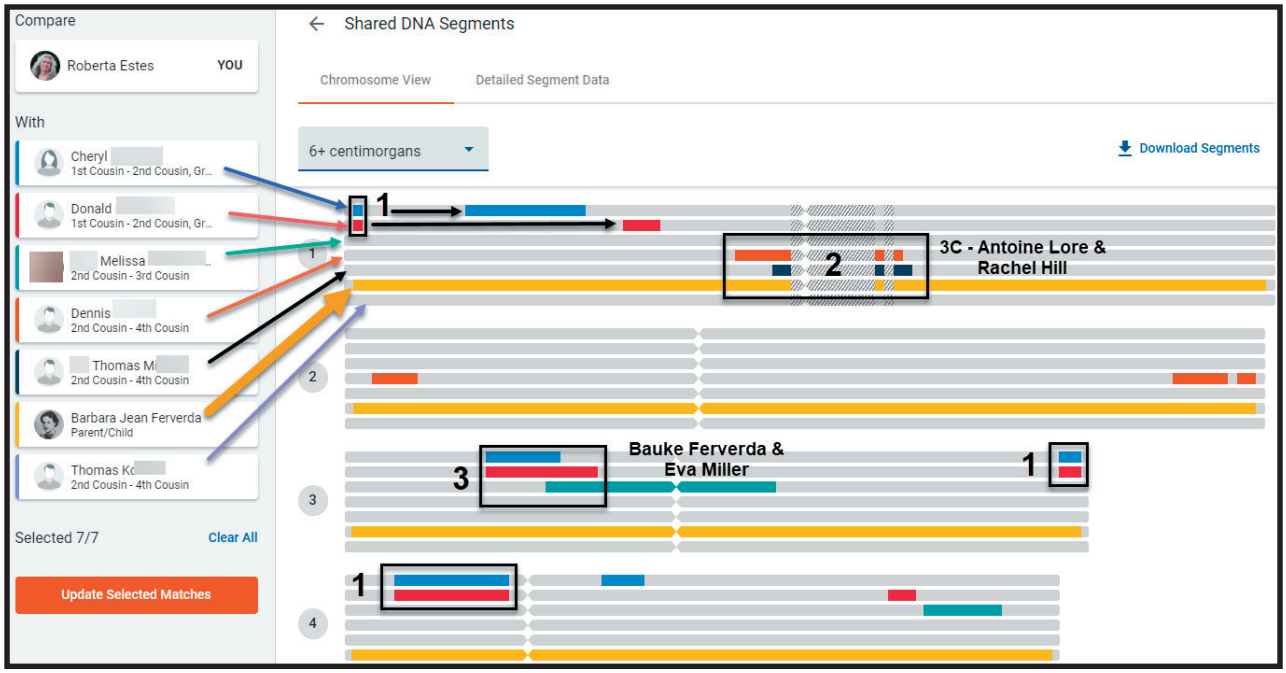
Melissa's match to me is shown on band 3. It's empty because Melissa does not match me on Chromosomes 1 or 2, but she does on Chromosomes 3 and 4.

Other matches have their own bands as well, with results colored to match their profile tab, at left. I've drawn arrows for each one.

Note my mother's, Barbara Jean Ferverda's larger (yellow) arrow in band 6. I match her on every segment of every chromosome. I received half of Mother's DNA, meaning some portion of her mother or father's segments at every location, so I will match her across every chromosome.

We don't know whether I received her mother's DNA or her father's DNA at any specific location. We need to determine which based on who else we both match at that location.

Based on the common ancestors of my matches, I know immediately that the segments of DNA where my mother and I match Cheryl, Donald, Melissa, and Thomas K. are from my mother's paternal line, and that the DNA where Mother and I match Dennis and Thomas M. (bands 4 and 5) are from my mother's maternal line.



I've numbered and boxed the areas we'll discuss.

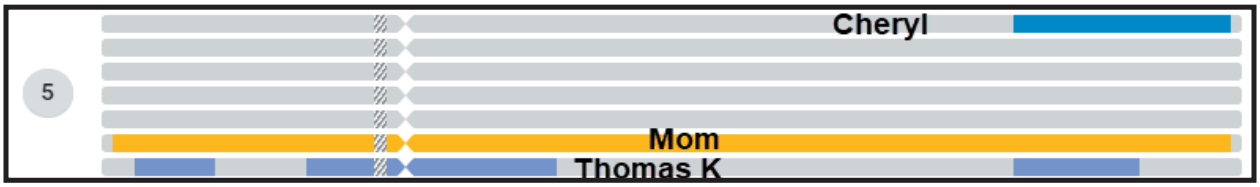
#1 – Cheryl and Donald are full siblings. I've included both of them to illustrate why it's important to test siblings. In three locations that are labeled "1," they both match me and mother on the same segments. We all inherited those segments of DNA from our common ancestors, Bauke Ferverda and Eva Miller. However, in other locations, as you can see on Chromosome 1 to the right of the "1" black box, Cheryl and Donald inherited different segments of DNA from their parents. Mother and I match Cheryl on one segment of DNA that Donald doesn't share, and vice versa.

Everyone who matches me, Mother, and Donald or Cheryl on those segments will have received those segments from our common known ancestor, through a common ancestor upstream who contributed them to all of us.

Given that each person triangulates for all matches involved on a specific segment, chances of false positive, invalid, or identical by chance matches are minimal, especially with larger segments over 10 cMs or so.

#2 – On Chromosome 1, further to the right, we see that Mother and I match both Dennis and Thomas M., who are both my third cousins, and both descend from Antoine Lore & Rachel Hill. Notice that this match spans the centromere[176] of the chromosome (hashed markings and white diamond) or the waist of the chromosome, where matching is not performed because of quality issues within that region, regardless of the vendor. However, due to the matching portions on both sides of the centromere, it's still counted as a valid, contiguous match.

#3 – Example three shows three cousins who don't match me on exactly the same segment, but do match on overlapping segments of DNA. In this case, Cheryl and Donald match each other on a significant portion of that segment, where they both match me. So do Donald and Melissa, but Melissa and Cheryl only overlap on a small portion. While they all match me, and by inference, mother, they don't all match each other on this entire segment.[177]



Thomas K. only matches me and Mother on Chromosome 5, but on three separate segments that, together, comprise over 70 cMs of shared DNA. He also matches Cheryl on the third segment on Chromosome 5, but Cheryl's match to me extends beyond that of Thomas's.

Our shared ancestors with Thomas K. descend through Evaline Louise Miller (1857-1939),[178] through her father, John David Miller (1812-1902),[179] and through his parents David Miller (1781-1851)[180] and Catharina Schaeffer (c1781-1826)[181].

Therefore, we know these shared segments descended from David Miller and Catharina Schaeffer to Mother and then to me. I love knowing which of my ancestors contributed my DNA segments.

176 https://help.familytreedna.com/hc/en-us/articles/4418230173967-Glossary-Terms-#c-0-2

177 As the Ferverda DNA Project administrator, I have access to the match lists of project members.

178 https://dna-explained.com/2019/06/22/evaline-louise-miller-ferverdas-will-estate-and-legacy-52-ancestors-243/

179 https://dna-explained.com/2016/07/04/john-david-miller-1812-1902-never-in-his-wildest-dreams-52-ancestors-125/

180 https://dna-explained.com/2016/07/17/david-miller-1781-1851-tamed-3-frontiers-52-ancestors-126/

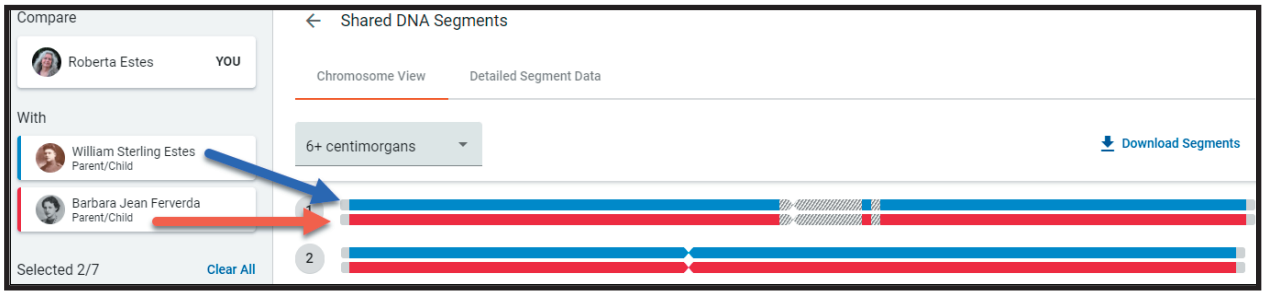
181 https://dna-explained.com/2016/07/24/catharina-schaeffer-c1775-c1826-and-the-invisible-hand-of-providence-52-ancestors-127/

Therefore, we know that anyone who matches me and my mother on the same segment is related through an ancestor on my mother's side. Based on who else matches on that same segment, and which of our ancestors that person descends from, we can assign that segment to a specific ancestor or ancestral couple.

However, in the situation where you don't know which side people are assigned to, meaning whether they match you through your mother or father's side, you have no assurance that two people matching you on the same segment are from the same side of your family.

Remember, you have two copies of each chromosome, one from your mother and one from your father. I wrote about this in "*Concepts: Your Matches on the Same Segment are NOT Necessarily Related to Each Other*."[184]

Here's the best example I can possibly show you.



I've selected my father and my mother and **compared them to my chromosomes**. I match both of them on the entire length of every chromosome, of course, but that does not mean they match each other. They don't.

Remember, the chromosome browser is ALWAYS from the perspective of the tester.

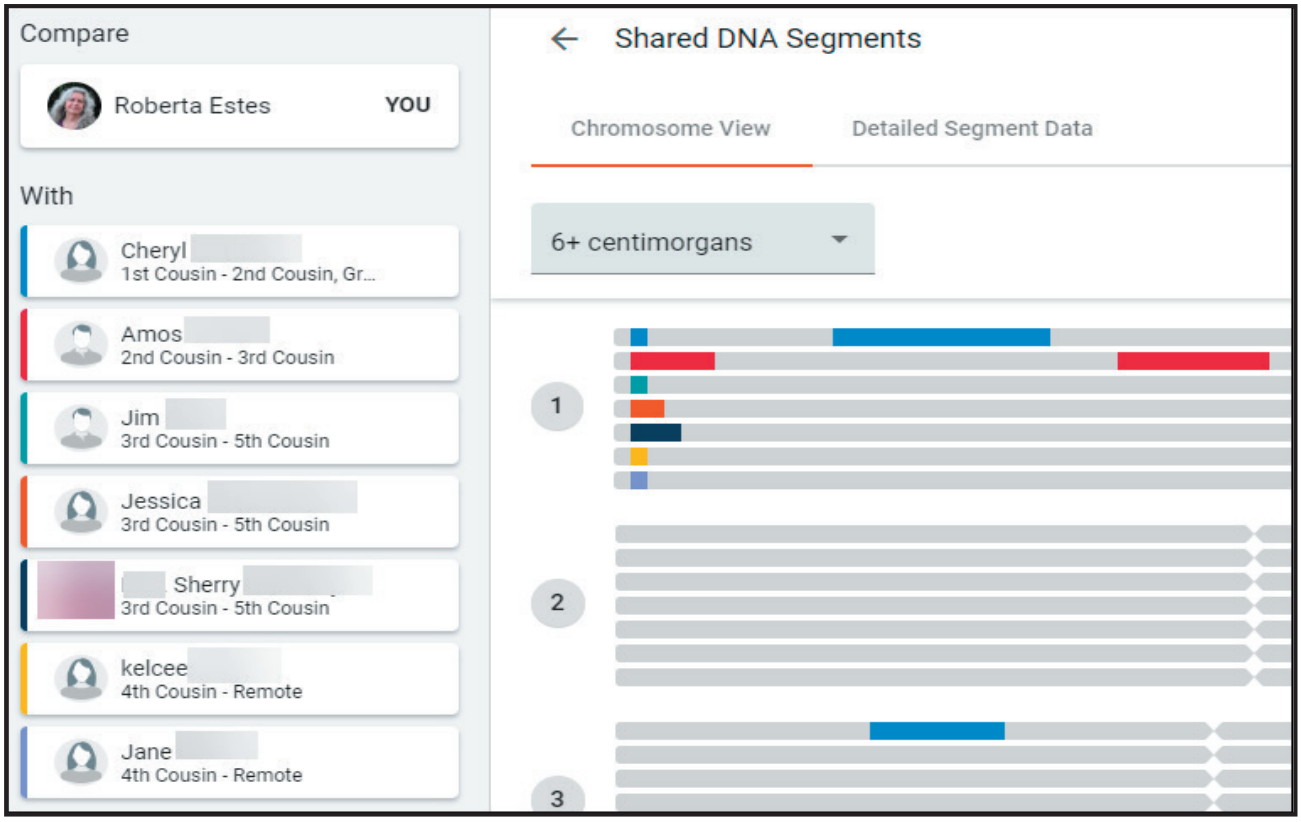
Now, let's say I'm an adoptee and don't have a DNA test for either parent nor do I know how I'm related to any of my matches.

Here are 7 people who match me at the beginning of Chromosome 1. You've already met Cheryl.

Are these people related to me on my mother's side, or my father's side, or are they identical by chance?[185]

184 https://dna-explained.com/2022/12/13/concepts-your-matches-on-the-same-segment-are-not-necessarily-related-to-each-other/

185 https://dna-explained.com/2016/03/10/concepts-identical-bydescent-state-population-and-chance/



In this example, no one is bucketed or assigned paternally or maternally, so these matches could be from either side, or neither side, meaning they are identical by chance.

There's no way to tell without additional information.

The best way is bucketing, but that's not always possible.

Identifying common ancestors is useful too, but remember that every segment has its own history. Just because you share a specific common ancestor with a match doesn't necessarily mean that ALL of your common segments are from that same ancestor, or that all matching segments are valid matches.

TIP: Identical start and end segment locations do NOT indicate a common ancestor. That's a common fallacy.

Notice that all of these matches begin at the same location, and several have the same end segment too.

Care to guess whether these segment matches are maternal or paternal?

In display order, these segments are attributed as follows:

- Cheryl – assigned and confirmed maternal side
- Amos – assigned and confirmed paternal side
- Jim – assigned and confirmed maternal

Match Name	Chr	Start Location	End Location	Centimorgans	Matching SNPs	Bucketed
James	1	725266	4744206	9.803617	1614	mother
Cheryl	1	725266	5764879	13.141793	2168	mother
Cody	1	725266	5777457	13.166938	2151	mother
Sherry	1	725266	10713765	21.004978	4053	father
William Sterling Estes	1	725266	249222527	284.03668	82095	**father**
Donald	1	725266	5764879	12.653017	1582	mother
Jim	1	725266	5922308	13.553952	1663	mother
Jessica	1	725266	7537500	15.894821	2141	father
Amos	1	725266	15050177	29.553602	4096	father
Barbara Jean Ferverda	1	725266	249218992	283.5479	56980	**mother**

I downloaded the entire Chromosome Browser Results spreadsheet and filtered/sorted the spreadsheet as described above so that all of my matches on Chromosome 1 begin with those who match me on the smallest-numbered start location, or the furthest left portion of the chromosome.

My matches are bucketed, so I colored my matches above accordingly to reflect which parent they match.

- My maternally bucketed match rows, including my mother, James, Cheryl, Cody, Donald, and Jim, are colored red, which show up as dark grey.
- My paternally bucketed matches, including my father, Sherry, Jessica, and Amos, are colored light blue, which show up as lighter grey

You have two options available for color-coding your matches to identify which people on the spreadsheet are assigned maternally, paternally, or both.

Option 1: Manually color code your spreadsheet rows

If you're only dealing with a few rows, or if you're not terribly comfortable with manipulating spreadsheets, you may just want to manually color a portion of your spreadsheet.

In the example above, I can do that easily by checking a match on the match list or the spreadsheet to determine how they are bucketed.

You can see that the first match, James, is maternally bucketed, and I've colored his row red.

If your parent has tested, even if you haven't uploaded a GEDCOM file or created a tree for bucketing, you can see if James matches you in common with one of your parents by using the "In Common With" filter. Color appropriately.

I removed the other columns on the Match Spreadsheet, above, leaving only the Full Name and the Matching Bucket. Your matches aren't in the same order between the two spreadsheets, which doesn't matter.

Full Name	Matching Bucket
Barbara Jean Ferverda	**Maternal**
James	Maternal
Cheryl	Maternal
Donald	Maternal
Cody	Maternal
Jim	Maternal
William Sterling Estes	**Paternal**
Sherry	Paternal
Jessica	Paternal
Amos	Paternal

Filter/Sort the "Matching Bucket" column, then color with the legend you want to represent each side. I selected red (maternal) and blue (paternal.)

Match Name	Matching Bucket	Chr	Start Location	End Location	Centimorgans	Matching SNPs	Bucketed
James		1	725266	4744206	9.803617	1614	mother
Cheryl		1	725266	5764879	13.141793	2168	mother
Cody		1	725266	5777457	13.166938	2151	mother
Sherry		1	725266	10713765	21.004978	4053	father
William Sterling Estes		**1**	**725266**	**249222527**	**284.03668**	**82095**	**father**
Donald		1	725266	5764879	12.653017	1582	mother
Jim		1	725266	5922308	13.553952	1663	mother
Jessica		1	725266	7537500	15.894821	2141	father
Amos		1	725266	15050177	29.553602	4096	father
Barbara Jean Ferverda		**1**	**725266**	**249218992**	**283.5479**	**56980**	**mother**

On your Segment Spreadsheet, above, which won't be colored yet, insert a column to the right of the Match Name column and title it, Matching Bucket.

Match Name	Matching Bucket	Ch	Start Locatic	End Locatic	Centimorgai	Matching SNP	Bucketed
Amos		1	725266	15050177	29.553602	4096	father
Amos	Paternal						
Barbara Jean Ferverda		**1**	**725266**	**249218992**	**283.5479**	**56980**	**mother**
Barbara Jean Ferverda	Maternal						
Cheryl		1	725266	5764879	13.141793	2168	mother
Cheryl	Maternal						
Cody		1	725266	5777457	13.166938	2151	mother
Cody	Maternal						
Donald		1	725266	5764879	12.653017	1582	mother
Donald	Maternal						
James		1	725266	4744206	9.803617	1614	mother
James	Maternal						
Jessica		1	725266	7537500	15.894821	2141	father
Jessica	Paternal						
Jim		1	725266	5922308	13.553952	1663	mother
Jim	Maternal						
Sherry		1	725266	10713765	21.004978	4053	father
Sherry	Paternal						
William Sterling Estes		**1**	**725266**	**249222527**	**284.03668**	**82095**	**father**
William Sterling Estes	Paternal						

Copy the colored Full Name column contents and the Matching Bucket contents from the Family Finder Matches Spreadsheet and paste them into the first two columns in the Chromosome Browser Results Spreadsheet as illustrated above, **BELOW the existing rows of data**. **Do not overwrite existing rows of data**.

Your Chromosome Browser Results spreadsheet is already sorted by chromosome size.

Next, filter/sort by Match Name.

Match Name	Matching Bucket	Chr	Start Location	End Location	Centimorgans	Matching SNPs	Bucketed
James		1	725266	4744206	9.803617	1614	mother
Cheryl		1	725266	5764879	13.141793	2168	mother
Cody		1	725266	5777457	13.166938	2151	mother
Sherry		1	725266	10713765	21.004978	4053	father
William Sterling Estes		**1**	**725266**	**249222527**	**284.03668**	**82095**	**father**
Donald		1	725266	5764879	12.653017	1582	mother
Jim		1	725266	5922308	13.553952	1663	mother
Jessica		1	725266	7537500	15.894821	2141	father
Amos		1	725266	15050177	29.553602	4096	father
Barbara Jean Ferverda		**1**	**725266**	**249218992**	**283.5479**	**56980**	**mother**
Barbara Jean Ferverda	Maternal						
Cheryl	Maternal						
Donald	Maternal						
Cody	Maternal						
Jim	Maternal						
William Sterling Estes	Paternal						
Sherry	Paternal						
Jessica	Paternal						
Amos	Paternal						

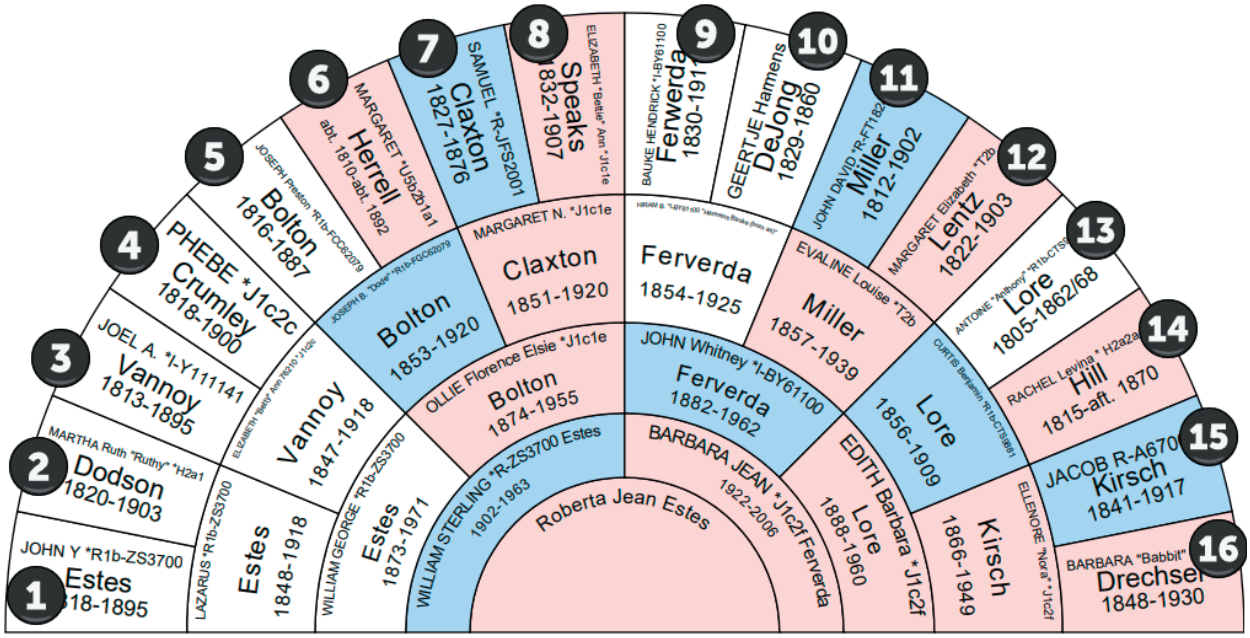
This unique X chromosome inheritance path provides us with a fourth very useful type of DNA for genealogy. X-matching is included with your Family Finder test.

The X chromosome, even though it is autosomal in nature, meaning it recombines and divides, is really its own distinct tool that is not equivalent to autosomal matching in the way we're accustomed. We need to learn about the message it's delivering and how to interpret X matches.

FamilyTreeDNA is currently the only vendor[192] that utilizes X chromosome matching, which is another good reason to encourage your matches at other vendors to upload their results to FamilyTreeDNA for free matching.

TIP: The X chromosome is not the same as mitochondrial DNA, but people often confuse the two.[193]

My X Chromosome Family Tree



Roberta's 4-Generation X-Chromosome Fan Chart

This fan chart[194] of my family tree colorizes the X chromosome inheritance path. In this chart, males are colored blue and females pink, but the salient point is that I can inherit some portion of (or all of) a copy of my X chromosome from the colorized ancestors, and only those ancestors.

Because males don't inherit an X chromosome from their fathers, they CANNOT inherit any portion of an X chromosome from their fathers' ancestors.

Looking at my chart, you see that, as a female, I inherited an X chromosome from both of my parents, but my father only inherited an X chromosome from his mother.

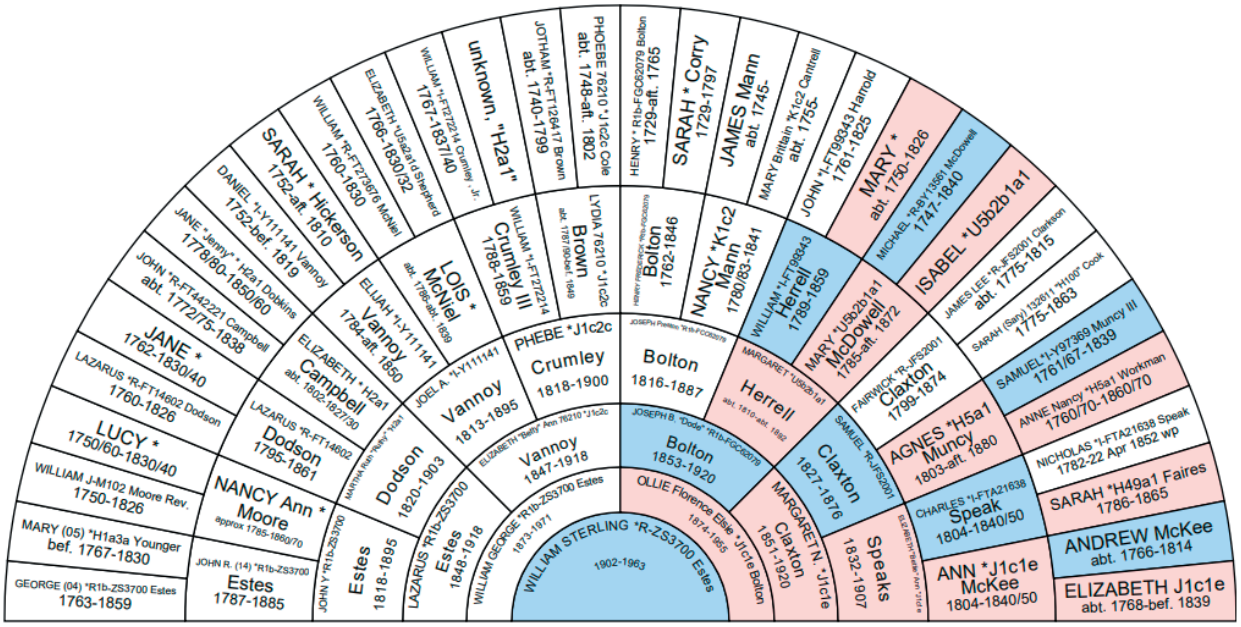
192 23andMe provided X-DNA segment information prior to their data exposure.

193 https://dna-explained.com/2017/07/26/x-matching-and-mitochondrial-dna-is-not-the-same-thing/

194 https://dna-explained.com/2017/02/07/using-x-and-mitochondrial-dna-charts-by-charting-companion/

Men don't inherit an X chromosome from their fathers. Therefore, I didn't inherit an X chromosome from any of the people whose positions in the chart don't have any color.

X matching for females eliminates 50%, or 8 of 16 4th-generation matches shown on previous page.



Male 5-Generation X-DNA Fan Chart

I know positively that I inherited my paternal grandmother, Ollie Bolton's entire X chromosome, because hers is the only X chromosome my father, as shown in his fan chart above, had to give me.

X matching for males eliminates 75%, or 24 of 32 possible 5th-generation ancestors, displayed above.

Tip: Sometimes, men appear to have X matches on their father's side, but this is impossible. Those matches must be identical by chance, or somehow related in an unknown way on their mother's side.

On my mother's side, I inherited an X chromosome from my mother, which is some combination of the X chromosomes from her father and mother. It's also possible that I inherited all of my maternal grandmother's or maternal grandfather's X chromosome, meaning they did not recombine during meiosis.

X chromosome matching and analysis is different due to:

- The unique inheritance pattern, meaning fewer recombination events occurred.
- The fact that X-DNA is not inherited from several lines.
- The X chromosome contains fewer SNPs, referred to as SNP density, so less possible locations to match as compared to the other chromosomes.

X-DNA potentially reaches back further in time than autosomal DNA on the other chromosomes at the same generational level, so you may have inherited the DNA of an ancestor on the X chromosome that you did not on other chromosomes. X-DNA represents a golden opportunity to match in a different way.

Using X-DNA

Let's say that I have a 30 cM X match with a male.

I know immediately that our most recent common ancestor is on his mother's side.

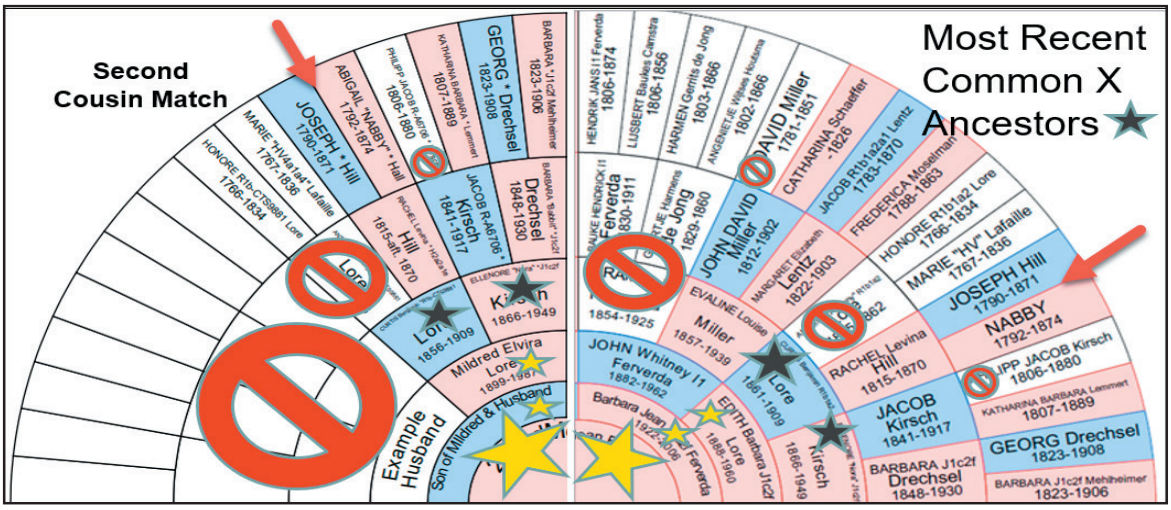
I know, based on my fan chart, which ancestral lines are eliminated in my tree. I've immediately narrowed the ancestors from 16 to 5 on his side and 16 to 8 on my side.

Two matching males is even easier because you know immediately that the common ancestor must be on both of their mother's sides, with only 5 candidate lines each at the great-great-grandparent generation.

Female-to-female matches are slightly more complex, but there are still 8 immediately eliminated lines each.

In this match with a female second cousin, I was able to identify who she was via our common ancestor based on the X chromosome path. Below, I'm showing the relevant halves of her chart (paternal), and mine (maternal), side by side.

I added blockers on her chart and mine too.



As it turns out, we both inherited most of our X chromosomes from our great-grandparents, marked above with the black stars.

Several lines are blocked, and my grandfather's X chromosome is not a possibility because the common ancestor is my maternal grandmother's parents. My grandfather is not one of my cousin's ancestors.

Having identified this match as my closest relative (other than my mother) to descend on my mother's maternal side, I was able to map that portion of my X chromosome to my great-grandparents Nora Kirsch[200] and Curtis Benjamin Lore[201], then through his mother to her parents Joseph Hill[202] and Nabby Hall[203] through additional matches.

200 https://dna-explained.com/2015/10/05/nora-kirsch-1866-1949-quilter-extraordinaire-52-ancestors-92/

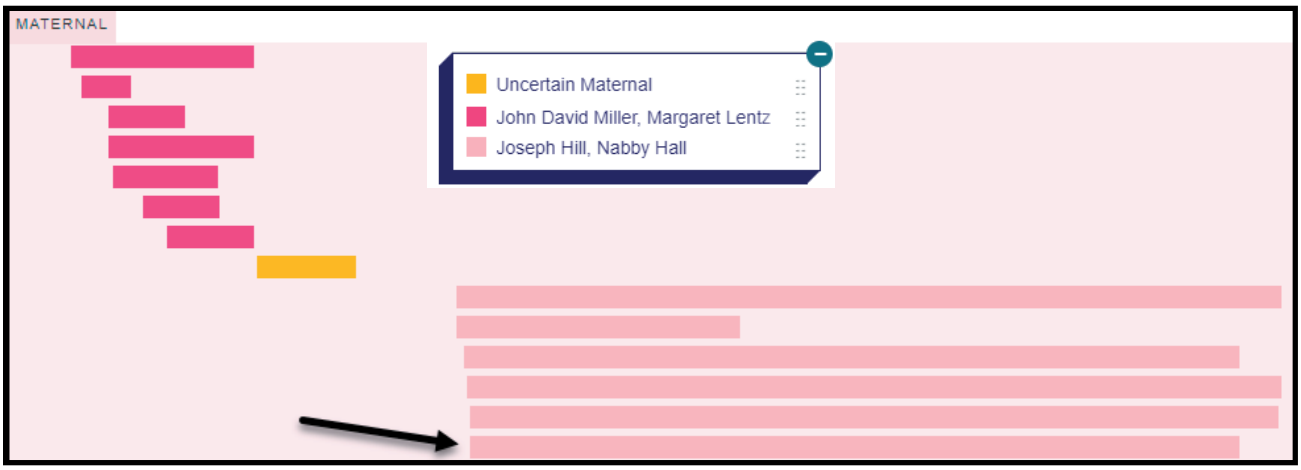
201 https://dna-explained.com/2021/04/25/curtis-lore-white-plague-times-two-52-ancestors-329/

202 https://dna-explained.com/2016/03/21/joseph-hill-1790-1871-the-second-joseph-shinglemaker-52-ancestors-116/

203 https://dna-explained.com/2016/03/27/abigail-nabby-hall-1792-1874-pioneer-settler-in-little-fort-52-ancestors-117/

My X Chromosome at DNA Painter

I paint my DNA segments for all my chromosomes at DNAPainter,[204] which provides me with a central tracking mechanism that is visual in nature and allows me to combine matches from multiple vendors who provide segment information.



Here's my maternal X chromosome and how I utilized chromosome painting to push the identification of the ancestors whose X chromosome I inherited back an additional two generations.

Using that initial X chromosome match with my second cousin, shown by the arrow at the bottom, I mapped a large segment of my maternal X chromosome to my maternal great-grandparents.

By viewing the trees of subsequent X maternal matches, I was then able to push those common segments, shown painted directly above that match with the same color, back another two generations, to Joseph Hill (1790-1871) and Nabby Hall (1792-1874.) I was able to do that based on the fact that other matches descend from Joseph and Nabby through different children, meaning we all triangulate on that segment.[205]

I received no known X-DNA from my great-grandmother, Nora Kirsch, although a small portion of my X chromosome is still unassigned and "Uncertain."

I received a small portion of my maternal X chromosome, in magenta, at left, from my maternal great-great-grandparents, John David Miller (1812-1902)[206] and Margaret Lentz (1822-1903)[207].

The X chromosome is a powerful tool and can reach far back in time.

TIP: In some cases, the X, and other chromosomes, can be inherited intact from one grandparent. I could have inherited my mother's entire copy of her mother's, or her father's X chromosome based on random recombination, or not. As it turns out, I didn't, and I know that because I've mapped my chromosomes to identify my ancestors.

204 https://dna-explained.com/2019/10/14/dnapainter-instructions-and-resources/

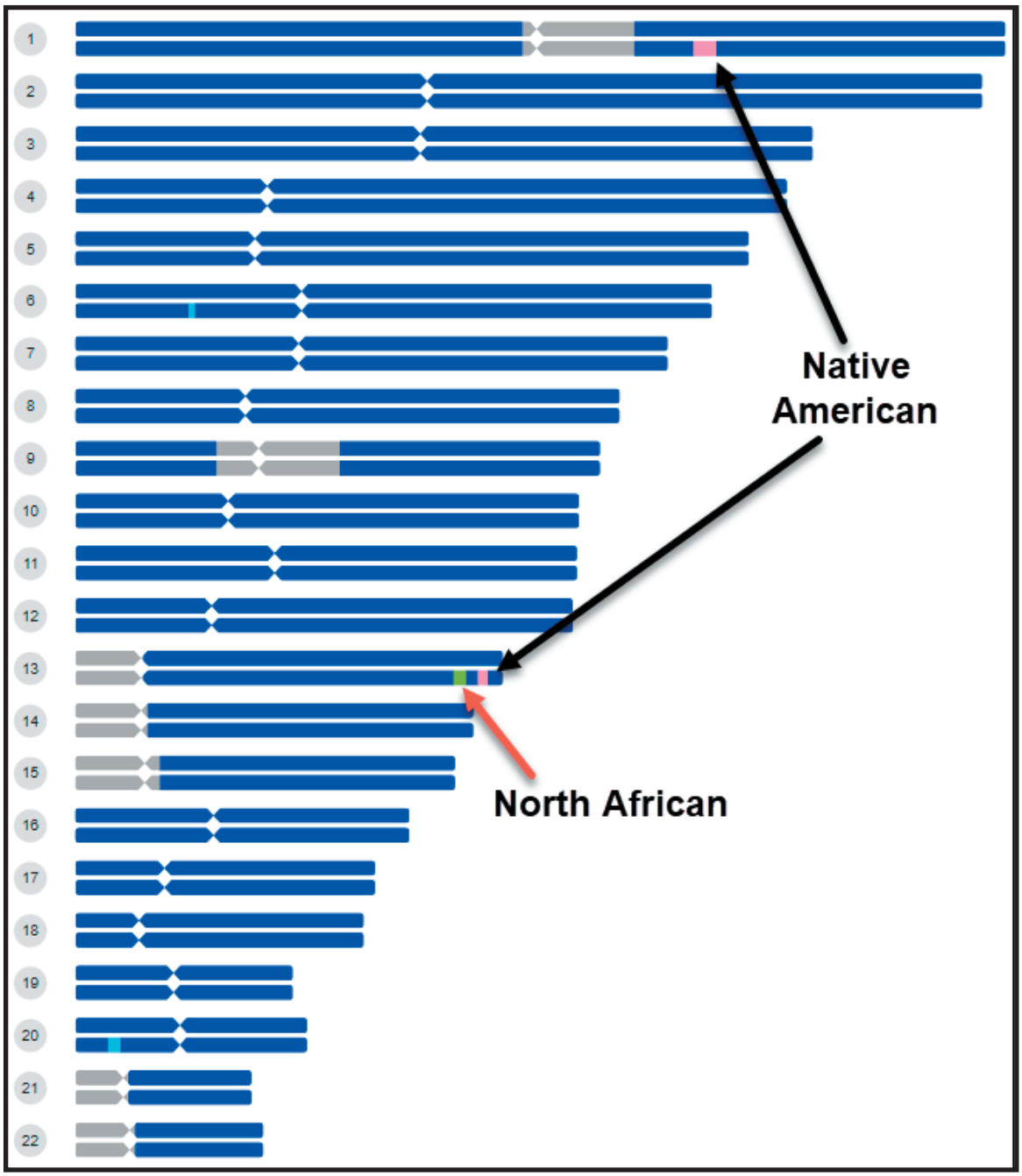
205 https://dna-explained.com/2020/04/01/triangulation-in-action-at-dnapainter/

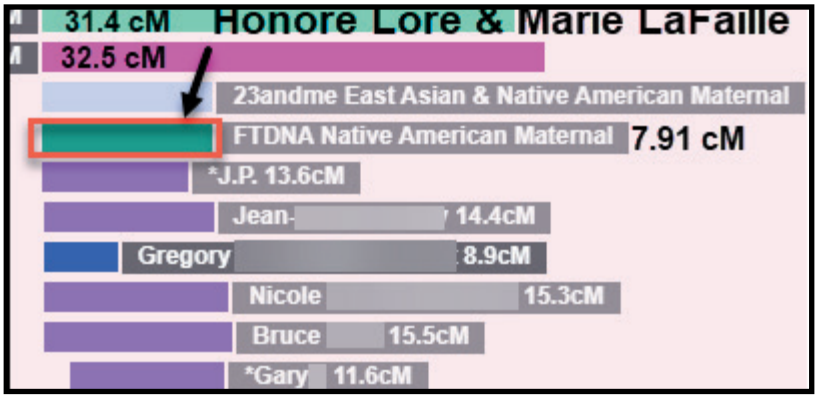
206 https://dna-explained.com/2016/07/04/john-david-miller-1812-1902-never-in-his-wildest-dreams-52-ancestors-125/

207 https://dna-explained.com/2016/06/27/margaret-lentz-1822-1903-the-seasons-and-the-sundays-52-ancestors-124/

Chromosome Painter - Ethnicity Chromosome Painting

I love this feature. The Chromosome Painter literally paints your population segments on your chromosomes.





On the relevant portion of my Chromosome 1, above, you can see that:

- I've renamed the segment FTDNA Native American Maternal, so I know exactly where it came from.
- 23andMe also found the same Native segment, which tends to confirm smaller cM population amounts.
- I have several matches to testers on the same area of my mother's chromosome.

The different colors correspond to different ancestors in the same lineage.

Honoré Lore/Lord and Marie LaFaille are my 6th-generation ancestors.

The other matching people share common ancestors with me in closer generations. Several matches span the entire Native segment. Two, however, at the top, match on a larger segment. The top match descends from Honoré and Marie, and the second match that's just slightly larger descends from one generation closer in time.

Each of these people should have (at least) this portion of their DNA assigned as Native American. If you only match on one segment with someone, and it's your Native segment, you know there's a common Native ancestor involved, and they contributed this segment to you both. You can confirm that you and your match share Native American ethnicity by using the Compare Origins feature.

What About Confirming Evidence?

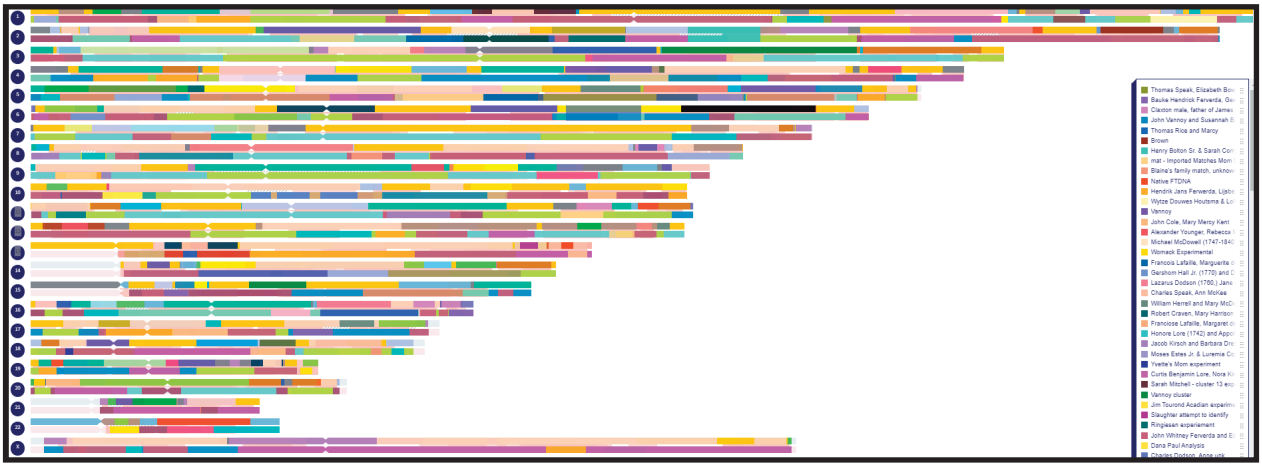
Now, of course, we need to ask if we have any documentary evidence or proof that the Native American designation is accurate.

As it turns out, we do. In historical records, a record from a priest to his bishop reports that Philippe Mius d'Azy[225], an Acadian settler, had two Amerindian wives.[226] Honoré Lord's[227] paternal grandmother is the granddaughter of Philippe Mius d'Azy with his first Native wife.

225 https://www.wikitree.com/wiki/Mius-24

226 https://www.wikitree.com/wiki/Mi'kmaq-17

227 https://dna-explained.com/2023/04/02/honorius-lord-1768-1834-catholic-church-records-illuminate-migration-along-the-richelieu-river-52-ancestors-393/



DNAPainter

I've mentioned DNAPainter several times in specific sections of this book, but I'd like to explain why I use DNAPainter extensively to paint:

- Segments from matches whose common ancestors I can identify at vendors who provide segment location information for your matches; FamilyTreeDNA, MyHeritage, 23andMe[244] and GEDmatch.
- Ethnicity/population segments from both FamilyTreeDNA and 23andMe, who provide segment address information for ethnicity segments.

DNAPainter allows users to paint segments by associating them with specific ancestors, or ancestral couples. Initially, you'll only be able to identify a common ancestral couple, until you match with someone who descends from the next generation further back in time, which allows you to identify which person of the pair contributed that particular segment.

John David	and	Elizabeth	
	|		\
Hiram and Eva			Ira
|			|
John and Edith			Everett
/		\	|
Jane & Don's parent		Mom	child
|	\	|	|
Jane	Don	Me	Bill

Let's look at an easy example.

244 Currently not available at 23andMe..

Let's say I match my first cousin, Jane, and her brother, Don, on a particular segment. I know that segment descended to all three of us from our common grandparents, John and Edith.

Who contributed that segment, or parts of that segment to our grandparents? Which grandparent gave that segment to us, or, is it a combination of segments from both grandparents?

Next, I match Bill on that same segment, and so do Jane and Don. We know that Jane, Don, and I are all related to Bill through the ancestor who contributed that segment to all four of us. But Bill doesn't descend from our grandparents so that common ancestor has to be further back than John and Edith.

Bill descends from my great-great-grandparents, John David and Elizabeth, through their son, Ira. Therefore, we know that our shared segment with Bill descends from John David and Elizabeth through their son Hiram through their son John's two children to Jane, Don and me.

In this example from DNAPainter, the two bottom segments are the painted segments from Jane and Don. Our most recent ancestors are our grandparents, John and Edith.

The next two segments from the bottom are the same segments, attributed to Hiram and Eva. The top three segments are the three segments from Jane, Don, and Bill. We know this segment, represented by several matches, descends from John David and Elizabeth, based on the match between me, Jane, Don (and others) with Bill on this segment. It's our match with Bill that cements **where** this segment originated, because we all share the entire segment **and** those ancestors, both.

As I continue to evaluate each of my matches for our common ancestors, eventually, I'll find another person who matches me, Jane, Don, and Bill on that segment, or a significant portion of that segment (generally 7 cMs or larger), and they will descend from the parents or grandparents of John David or Elizabeth. Then I'll have pushed my knowledge of where this segment originated back another generation or two.

That's how we "push segments back in time," associating those segments with specific ancestors through our matches with testers.

Before DNAPainter, genetic genealogists maintained a massive spreadsheet where we formed triangulation groups of people. Now we don't need to do that anymore, because we can paint those segments at DNAPainter, where they are stored and displayed visually by ancestor on each one of our chromosomes. Triangulation groups are formed automatically and visually.

Once we associate a particular segment with the most distant ancestor in the lineage, then we know that all matches downstream who share that segment descend from that ancestral couple.