# Autosomal DNA Tests – Part 2

Using Autosomal DNA to find your cousins

# Autosomal DNA – Part 1

- Basic genetics: DNA, mutations & SNPs
- The DNA testing process
- Compared the 3 companies
- Reviewed their 'Ethnicity Reports'

# SURVEY

Attended 'Autosomal DNA – Part 1'?

Have tested and received results?

Company used?

- FamilyTreeDNA?
- 23&Me?
- AncDNA?
- Tested at 2 DNA Co's? 3 DNA Co's?

# Goals

- What really is a match?
- Review of each company's tools
- Chromosome Browsers & Associated Tools
- The importance of 'Triangulated Groups'
- A comprehensive plan based on segment analysis
- Two Key '3d Party Tools'

# Part 1: Key Points

- DNA is passed down more unevenly for distant ancestors
- Eventually we receive no DNA from some ancestors
- atDNA testing limited to 5-6 generations (4th cousins)
- Siblings inherit varying segments of parental DNA
- DNA test can't tell which parent contributed which base in a pair*

( * unless you test at least one parent and do a bit of work)

# Matches

- **The more segments you share the closer you are to your match**
- **The more DNA you share in large segments the closer you are**
- **Shared segments are often measured in centiMorgans (cM)**

> *"A centiMorgan is equal to a 1% chance that a marker at one genetic locus on a chromosome will be separated from a marker at a second locus due to crossing over in a single generation"*

- **centiMorgans are statistical estimates of equal distance (genetically) from one point to another – 'DNA yardsticks'**

# Working with Cousins Who Match Your DNA

**Here is where the work begins**

**Matches displayed highest to lowest relationship (default)**

**Make it easy on your matches:**

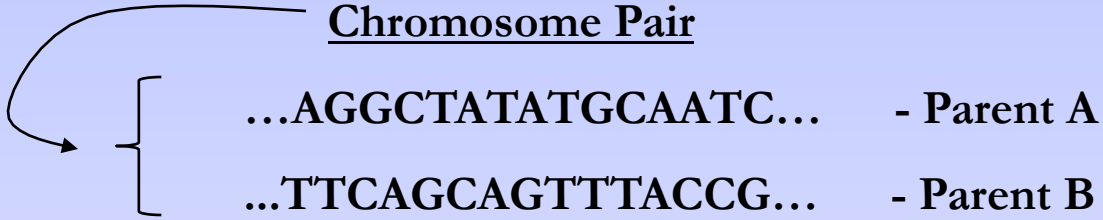
- **up-to-date email address**
- **oldest known paternal/maternal ancestor, date, location**
- **detailed list of ancestral surnames, dates, locations**
- **pedigree chart (GEDCOM or PDF) for them to use**

# What Is A Match?

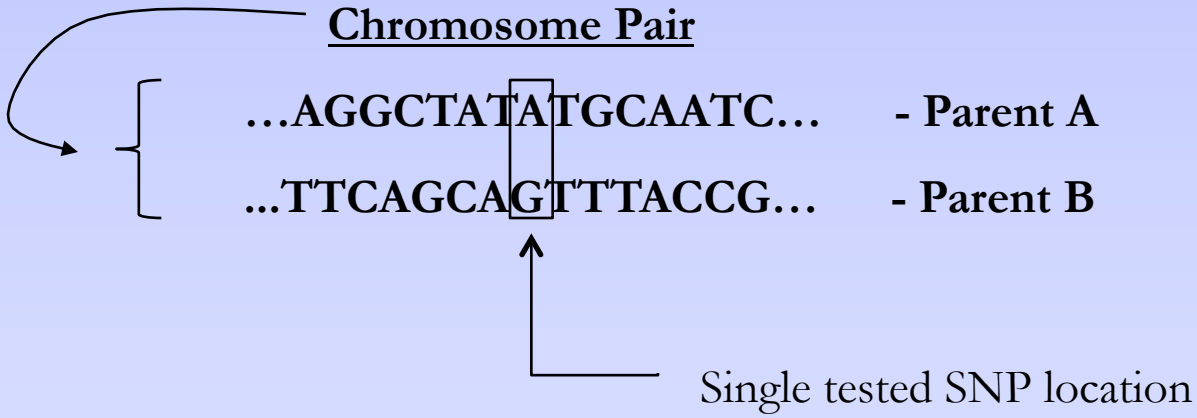
# What Is A Match?

**"A genetic match is another tester who has a run of identical SNPs long enough to exceed the testing companies threshold for relatedness."**

# What Is A Match?



# What Is A Match?



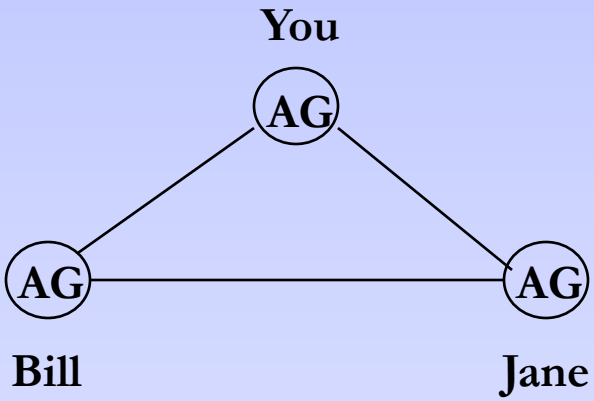
# What Is A Match?

**Your result = 'AG'**

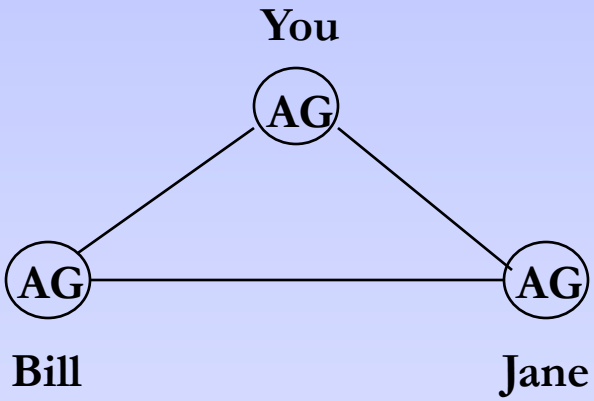
**Match 1 = Bill**

**Match 2 = Jane**

# What Is A Match?

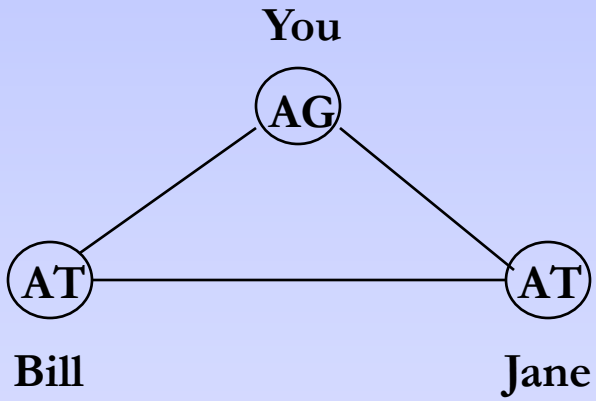


# What Is A Match?




You match with 'Full-Identical Regions' – both 'A' & 'G' in this case

# What Is A Match?




**You match with 'Half-Identical Regions' – either 'A' or 'G' ( 'A' in this case)**

**Most matches are Half-Identical Regions (HIR)**

# What Is A Match?

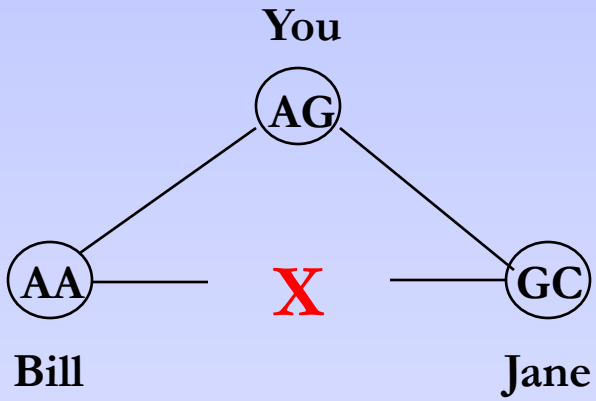
**You = 'AG'**

**Match 1 = Bill**

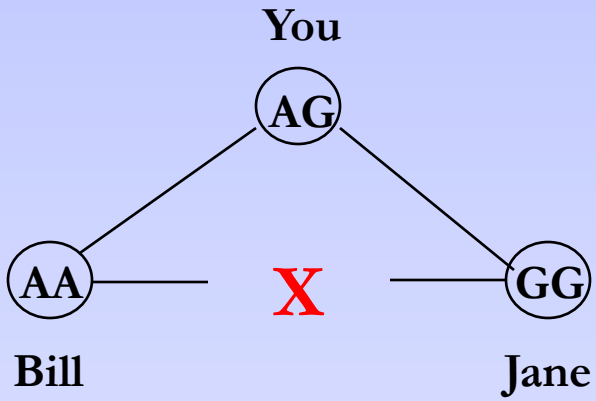
**Match 2 = Jane**

**KEY: initially you only know that Bill & Jane each match you – either with an A or G**

# What Is A Match?

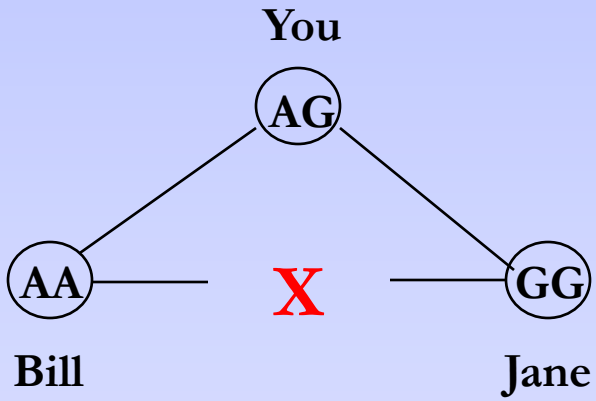


# What Is A Match?



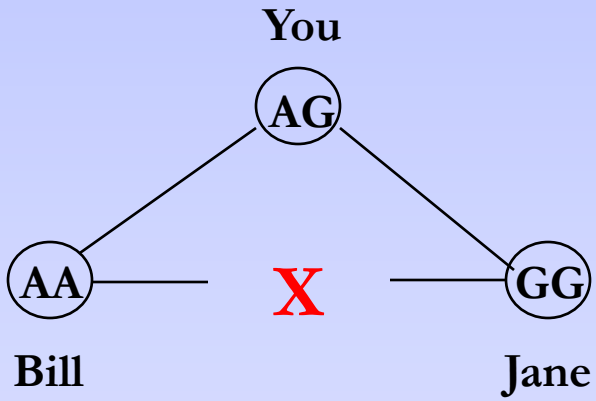

They match YOU but not each other

# What Is A Match?




**Which side of your family is Jane on ??**

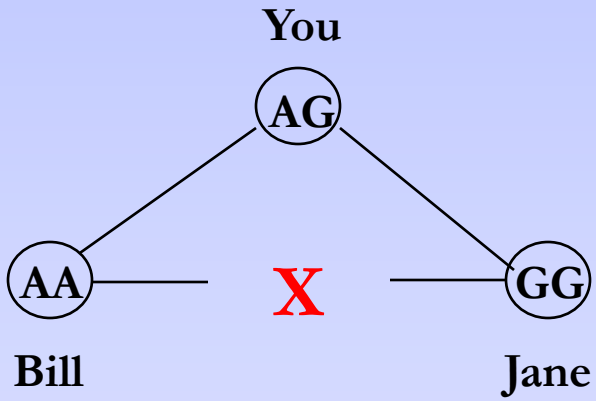
# What Is A Match?




**Option 1: Search Jane's tree & yours for common ancestor**

**(a lot of work for each & every match)**

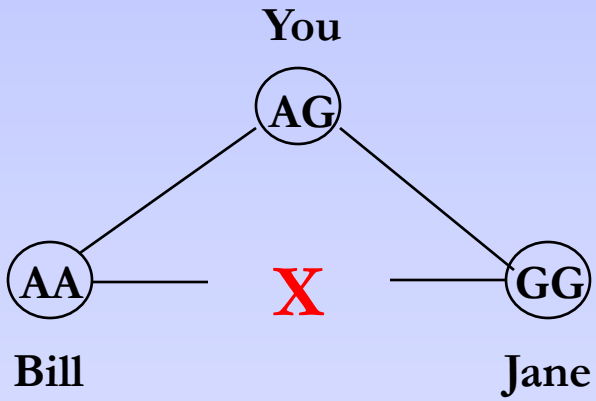
# What Is A Match?




## Option 1: Search Jane's tree & yours for common ancestor

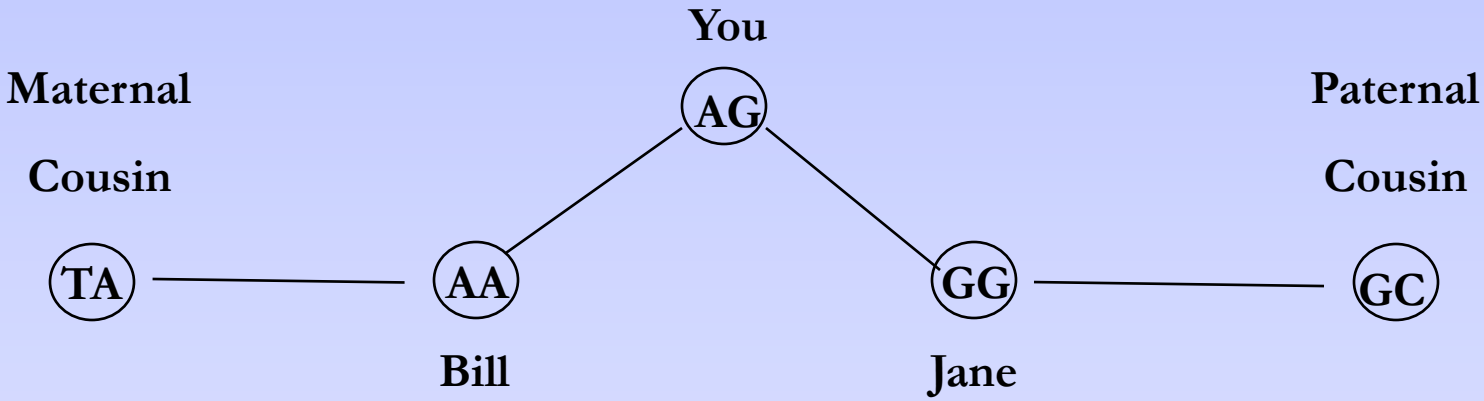
(If you found one would that be proof that's where DNA matched ?)

# What Is A Match?




Option 2: Test known cousins on both sides of your tree

# What Is A Match?




**Option 2: Test <u>known</u> relatives on both sides of your tree**

# Quick Overview of Each Company's Tools

# Common Information From Each Company

List of matches

Genealogy data – user dependent

Method to contact your matches

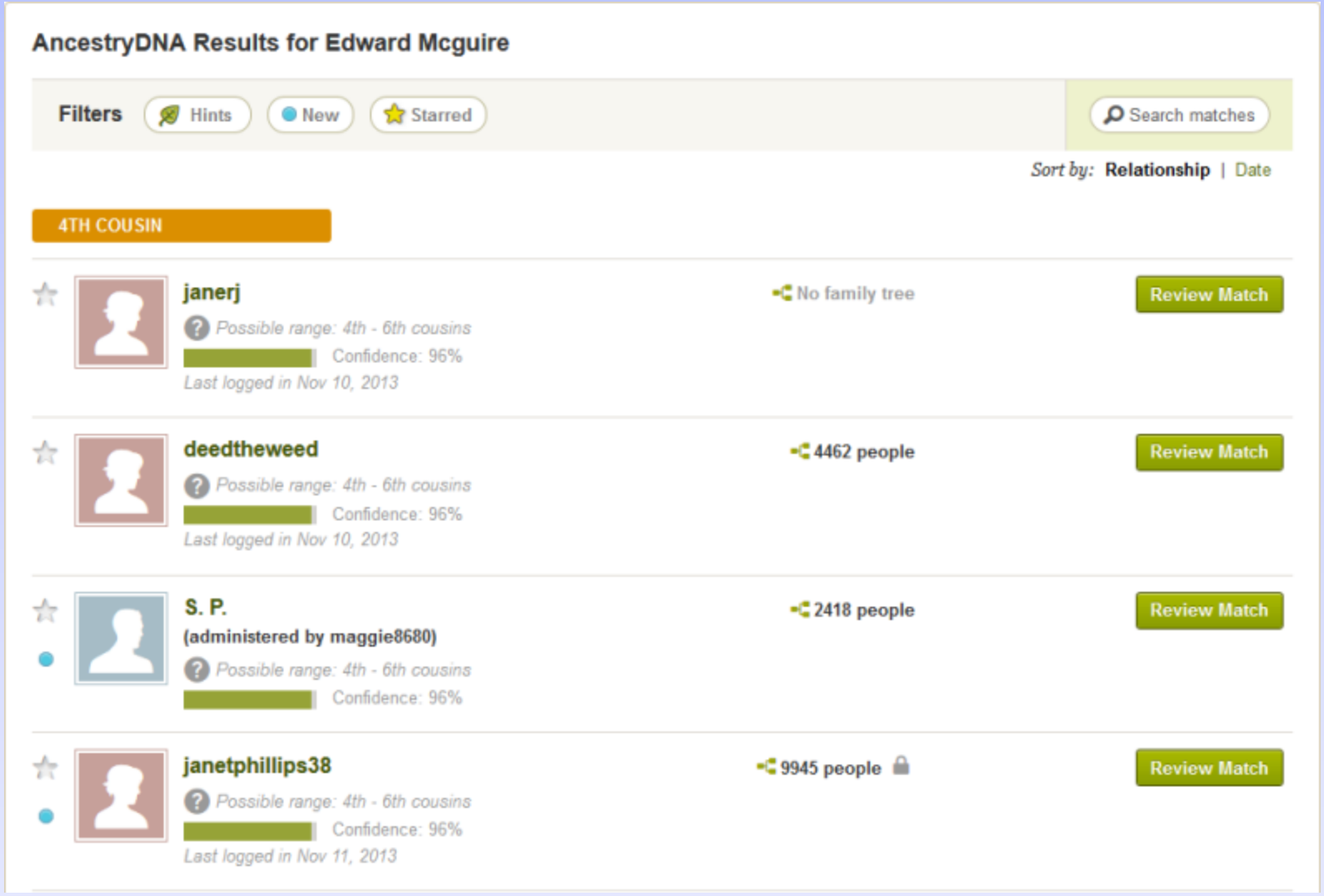
# AncestryDNA

List of matches

Genealogy data – user dependent

Method to contact your matches

# AncestryDNA Matches Page



# AncestryDNA

## 2012 – 4Q2014 Status

**Ancestry match threshold very low…often 10,000 matches**

**Minimal linkage between Ancestry Trees & AncestryDNA data**

**No tools to work with segment data (chromosome browser)**

**Little information on how Ancestry analyzed actual data**

# AncestryDNA

## 4Q2014 Upgrade

**Ancestry announces change to match-selection scheme**

**Far fewer matches – most appear to be better choices**

**DNA data & Tree data better coordinated – "DNA Circles"**

**No tools to work with segment data (chromosome browser)**

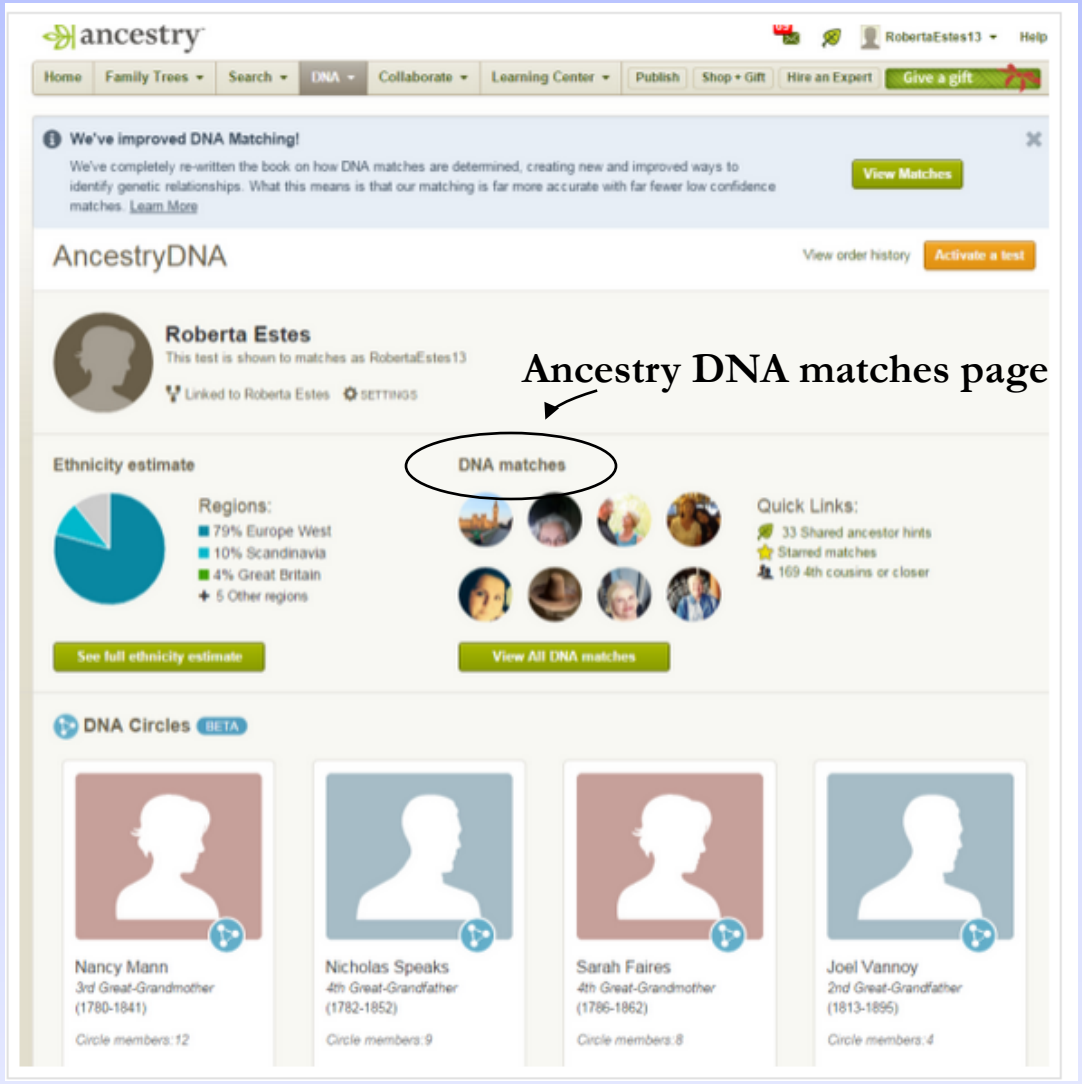
**Little information on how Ancestry determines DNA Circles**

| | Yesterday | Today | Shakey Leaves Yesterday | Shakey Leaves Today |
|---|---|---|---|---|
| **Total Matches** | 13,100 | 3,350 | | |
| | | | | |
| **2nd Cousins** | 1 – 99% confidence | 0 – shifted to third cousin | 0 | 0 |
| **3rd Cousins** | 10 | 8 – shifted to fourth cousins | 2 | 1 (shifted to 4th cousin) |
| **4th Cousins** | 243 | 161 | 10 | 14 |
| **Distant Cousins** | 12,846 | 3,181 | 36 | 18 |

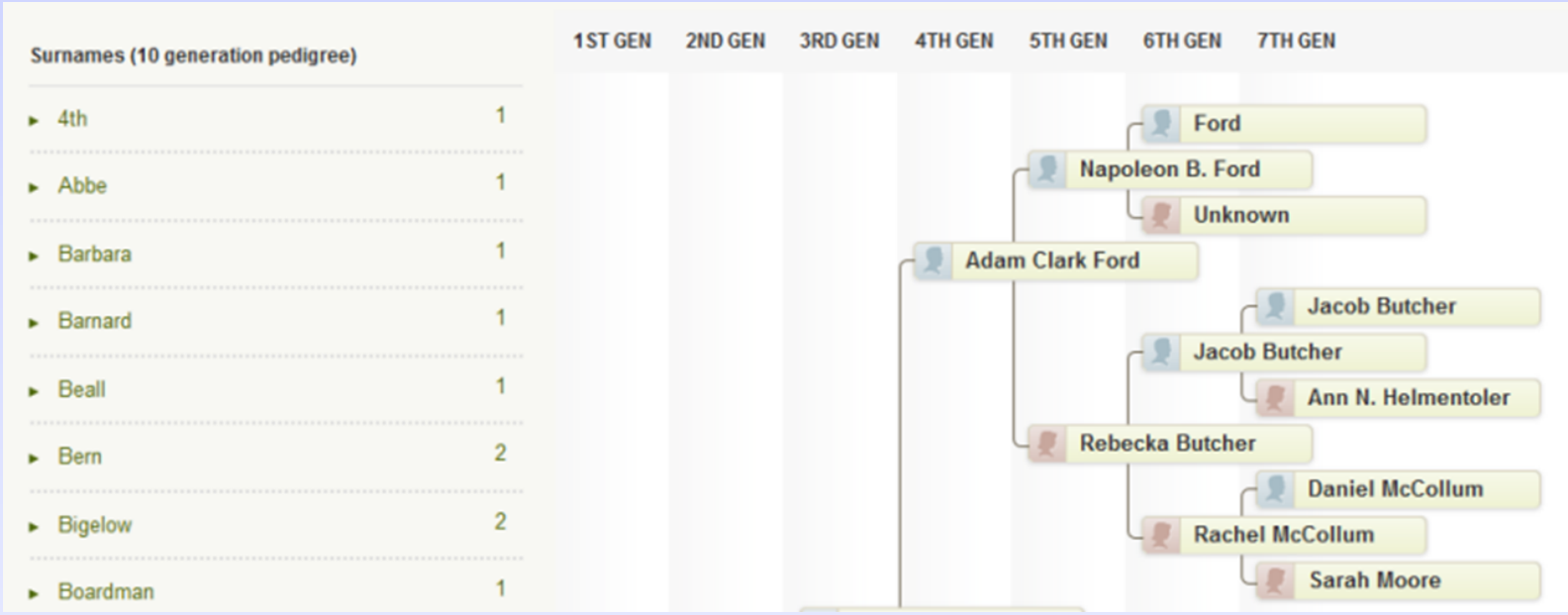
Source: Roberta Estes, http://dna-explained.com/category/ancestry-com/

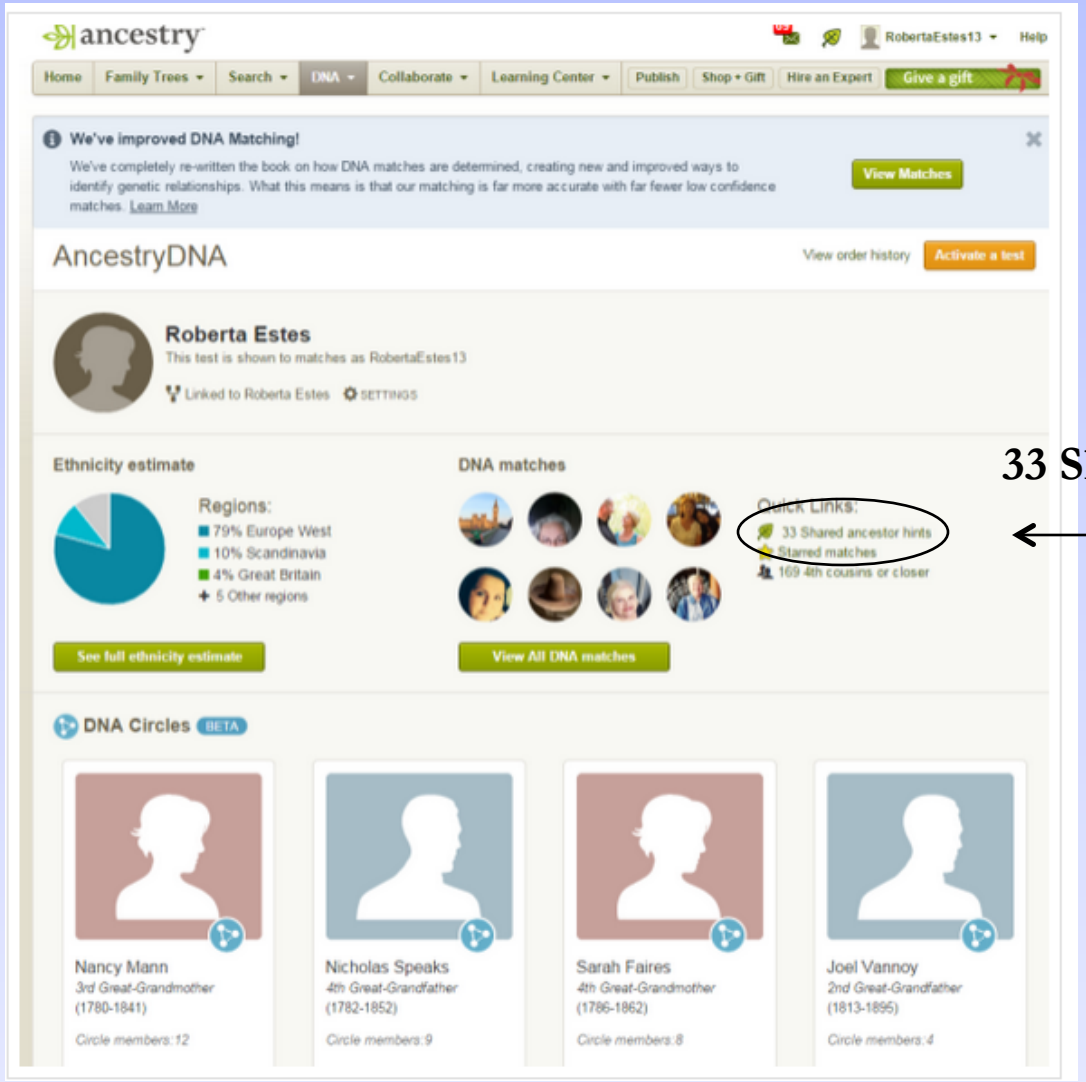
| Confidence Score | Details |
|---|---|
| Extremely High | **Approximate amount of sharing:** More than 30 centiMorgans<br>**Likelihood you and your match share a single recent common ancestor (within 5 or 6 generations):** Virtually 100%<br>**Description:** You and your match share enough DNA to prove that you're both descendants of a common ancestor (or couple)--and the connection is recent enough to be conclusive. |
| Very High | **Approximate amount of sharing:** 20-30 centiMorgans<br>**Likelihood you and your match share a single recent common ancestor (within 5 or 6 generations):** 99%<br>**Description:** You and your match share enough DNA that we are almost certain you're both descendants of a recent common ancestor (or couple). |
| High | **Approximate amount of sharing:** 12-20 centiMorgans<br>**Likelihood you and your match share a single recent common ancestor (within 5 or 6 generations):** 95%<br>**Description:** You and your match share enough DNA that it is likely you're both descendants of the same common ancestor or couple, but there's a small chance the common ancestor(s) are quite distant and difficult to identify. |
| Good | **Approximate amount of sharing:** 6-12 centiMorgans<br>**Likelihood you and your match share a single recent common ancestor (within 5 or 6 generations):** More than 50%<br>**Description:** You and your match share some DNA, probably from a recent common ancestor or couple, but the DNA may be from distant ancestors that are difficult to identify. |
| Moderate | **Approximate amount of sharing:** 6 centiMorgans or less<br>**Likelihood you and your match share a single recent common ancestor (within 5 or 6 generations):** 20-50%<br>**Description:** You and your match might share DNA because of a recent common ancestor or couple, share DNA from very distant ancestors, or you may not be related. |

**Source: Blaine Bettinger, www.thegeneticgenealogist.com/2014/11/19/**


ancestry
RobertaEstes13
Help
Home
Family Trees
Search
DNA
Collaborate
Learning Center
Publish
Shop + Gift
Hire an Expert
Give a gift
We've improved DNA Matching!
We've completely re-written the book on how DNA matches are determined, creating new and improved ways to identify genetic relationships. What this means is that our matching is far more accurate with far fewer low confidence matches. Learn More
View Matches
AncestryDNA
View order history
Activate a test
Roberta Estes
This test is shown to matches as RobertaEstes13
Linked to Roberta Estes
SETTINGS
Ancestry DNA matches page
Ethnicity estimate
DNA matches
Regions:
79% Europe West
10% Scandinavia
4% Great Britain
5 Other regions
Quick Links:
33 Shared ancestor hints
Starred matches
169 4th cousins or closer
See full ethnicity estimate
View All DNA matches
DNA Circles
BETA
Nancy Mann
3rd Great-Grandmother
(1780-1841)
Circle members:12
Nicholas Speaks
4th Great-Grandfather
(1782-1852)
Circle members:9
Sarah Faires
4th Great-Grandmother
(1786-1862)
Circle members:8
Joel Vannoy
2nd Great-Grandfather
(1813-1895)
Circle members:4

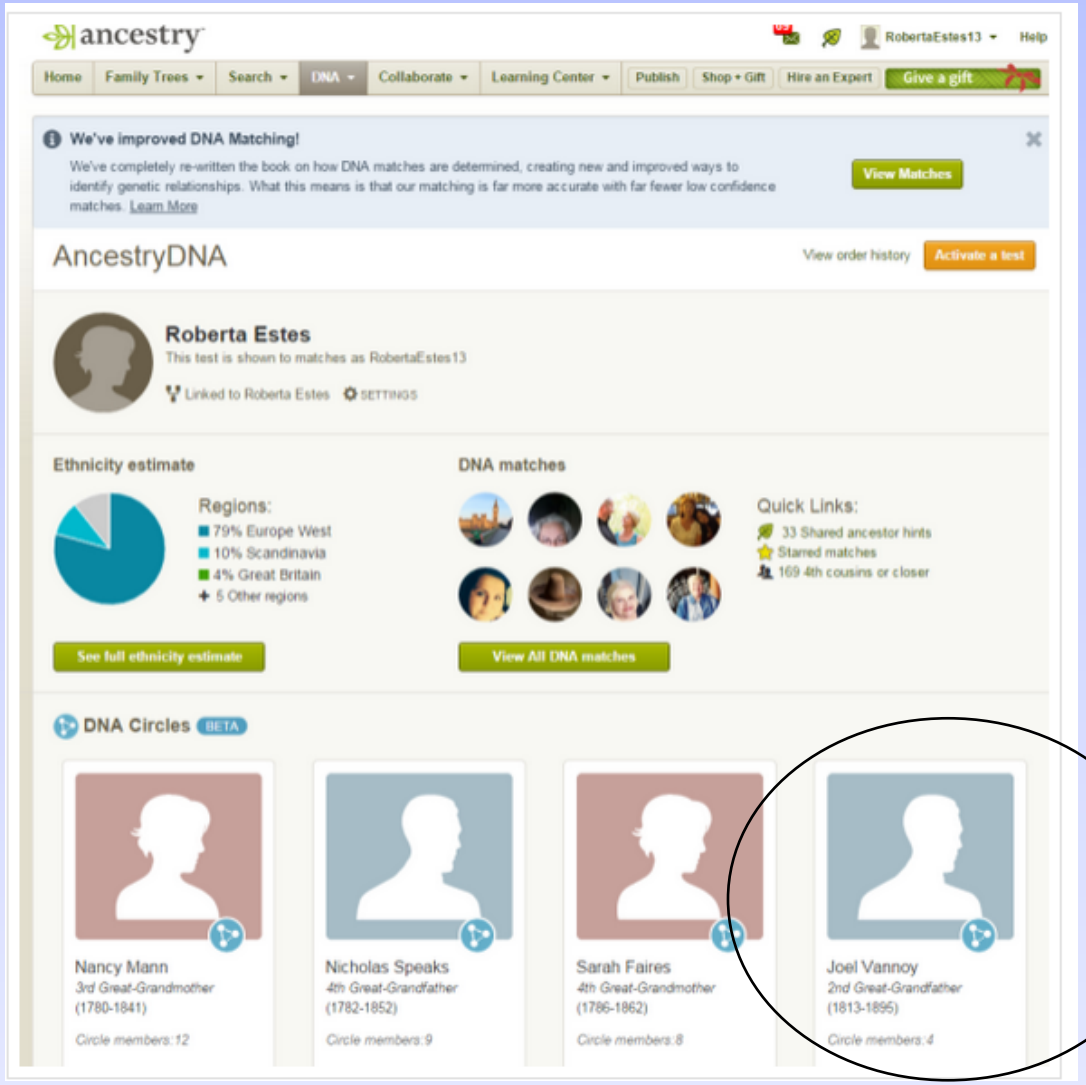
# AncestryDNA Matches Page




**33 Shared ancestors hints**


Shared Ancestor Hint
Joel Vannoy
2nd Great-Grandfather
&
Phebe Crumley
2nd Great-Grandmother
Elizabeth "Betty" Ann Vannoy
Great-Grandmother
William George Estes
Grandfather
William Sterling Estes
Father
Roberta Estes
Self
James H. Vannoy
Great-Grand uncle
James Abija Vannoy
1st Cousin (2x removed)
Everett Abija Vannoy
2nd Cousin (1x removed)
EHVannoy
3rd Cousin
SHARED SURNAMES
Direct ancestor surnames that appear in both EHVannoy's tree and Roberta Estes's tree
Anderson
Brown
Crumley
Faulkner
Gilkey
Hickerson
Lytle
Mason
McNiel
Mercer
Rash
Roberts
Shepherd
Vannoy
VanOy
Webb
1ST GEN
2ND GEN
3RD GEN
4TH GEN
5TH GEN
6TH GEN
7TH GEN
Daniel Vannoy
Elijah Vannoy
Sarah Hickerson
Joel Vannoy
William McNiel
Lois McNeil
Elizabeth Shepherd
James H. Vannoy




**DNA Circle for your ancestor**

# DNA Circles

**You must have a PUBLIC tree to be placed in a DNA Circle**

**You will share DNA with at least one other person in the DNA Circle, but you might not share with everyone in that circle. Those you don't share DNA with will share DNA with someone other than you in that circle**

**DNA Circles algorithm looks back 7 generations for a match, so the more complete your tree – the more likely you are to find a match**

**DNA Circles tool does require Ancestry subscription**

**About 50% of those with public trees will have at least one circle**

→ **DNA Circle is a potential team of researchers!**

Source: Blaine Bettinger, www.thegeneticgenealogist.com/2014/11/19/goodbye-false-positives-ancestrydna-updates-matching-algorithm/

# AncestryDNA

+ very easy to see 'proposed' common ancestor

+ improved value to matches list

+ DNA Circles identifies group to do joint research!

- many verified errors with chosen common ancestor

- many verified errors with DNA Circle results

- no segment analysis tools

- no understanding of how Ancestry is making calls

# 23andMe Analysis Tools

**23andMe has robust tools for segment analysis & triangulation**

**Tools are split into 3 areas of the site**

1. **Matches list is at – 'DNA Relatives'**

   (Home/DNA Relatives)

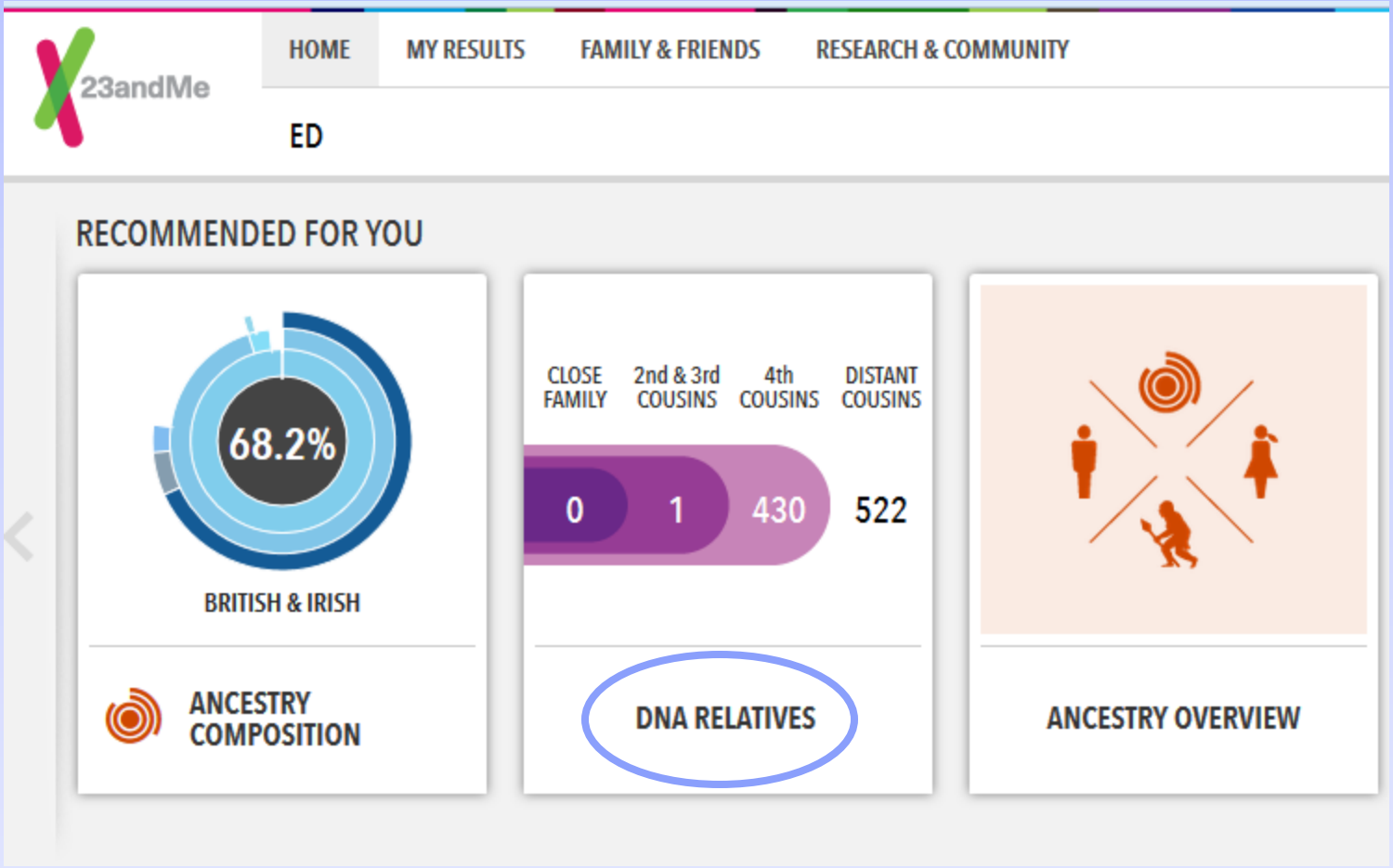
2. **Chromsome browser is at – 'Family Inheritance: Advanced'**

   (My Results/Ancestry Tools/ Family Inheritance: Advanced)

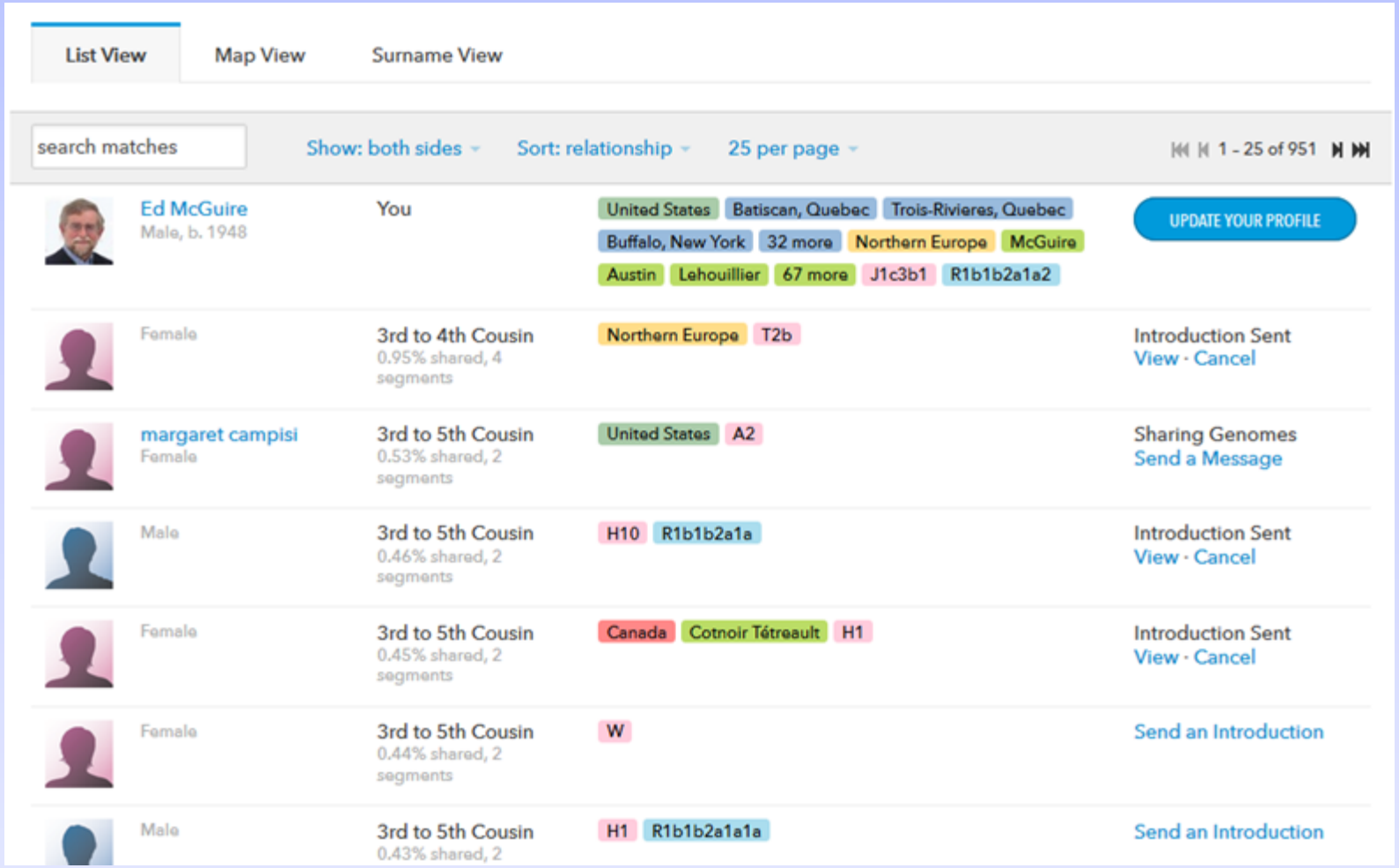
3. **Unique location tool – 'Countries of Ancestry'**

   (My Results/Ancestry Tools/ Countries of Ancestry)

**'Match' thresholds vary by tool (see Table 1 in your handout)**

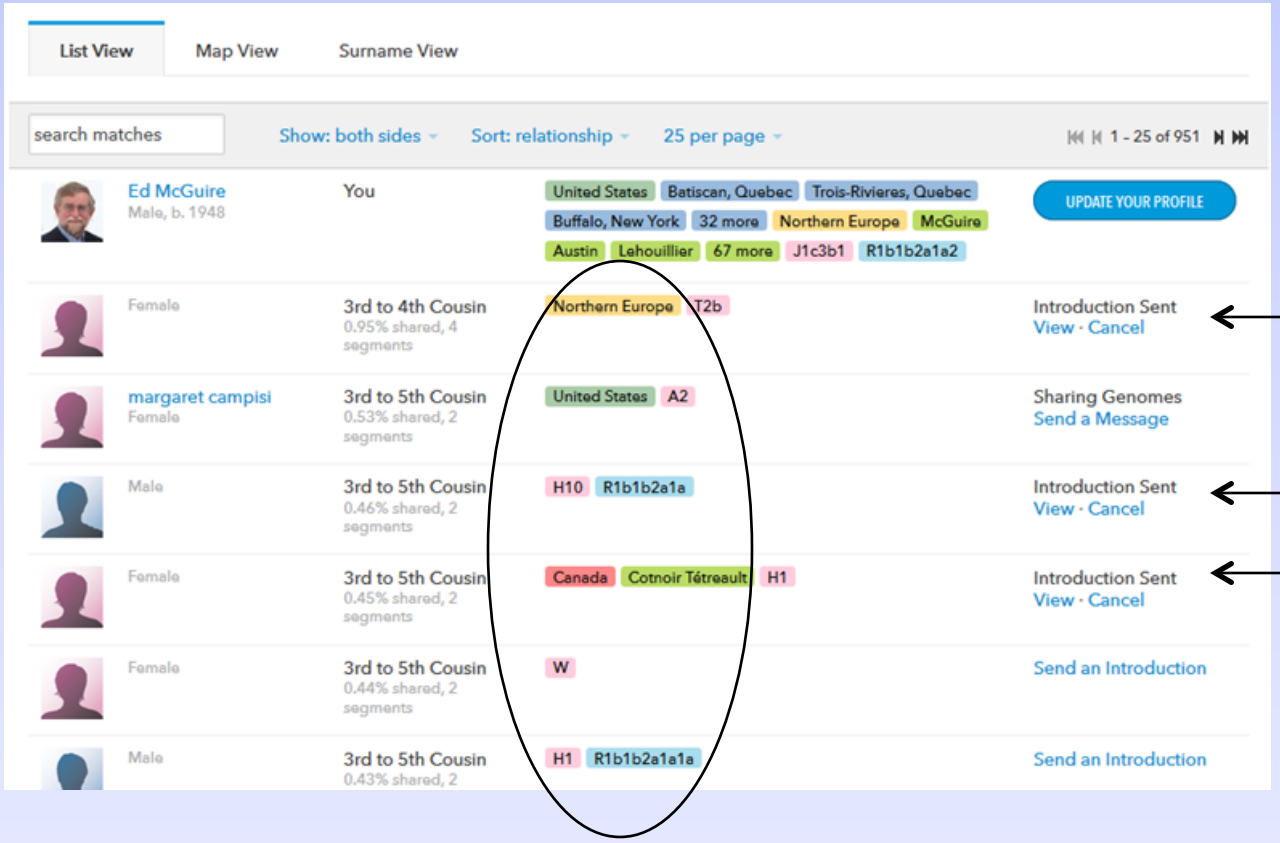

23andMe
HOME
MY RESULTS
FAMILY & FRIENDS
RESEARCH & COMMUNITY
ED
RECOMMENDED FOR YOU
68.2%
BRITISH & IRISH
ANCESTRY COMPOSITION
CLOSE FAMILY
2nd & 3rd COUSINS
4th COUSINS
DISTANT COUSINS
0
1
430
522
DNA RELATIVES
ANCESTRY OVERVIEW

# DNA Relatives Match List

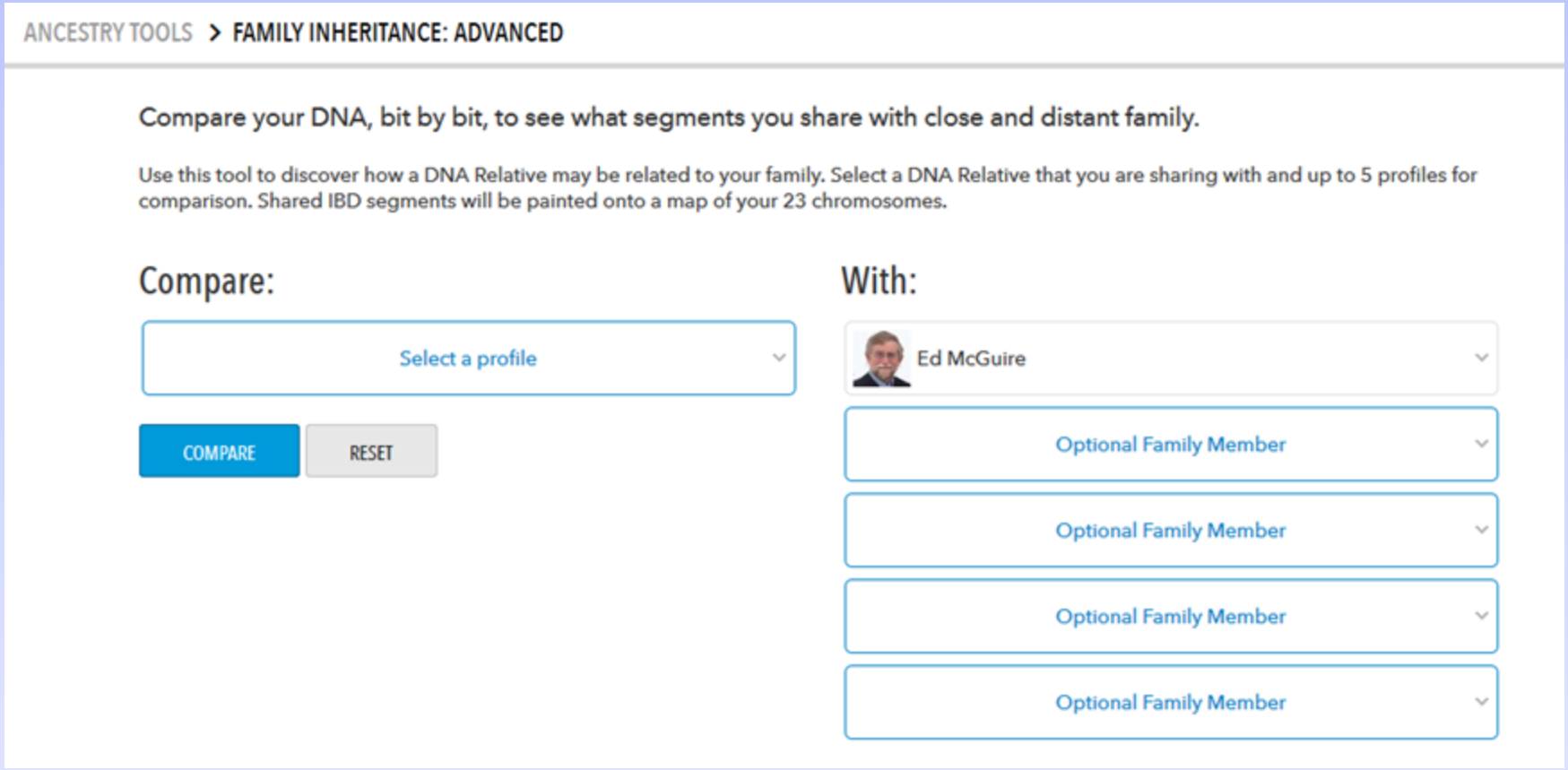


# DNA Relatives Match List

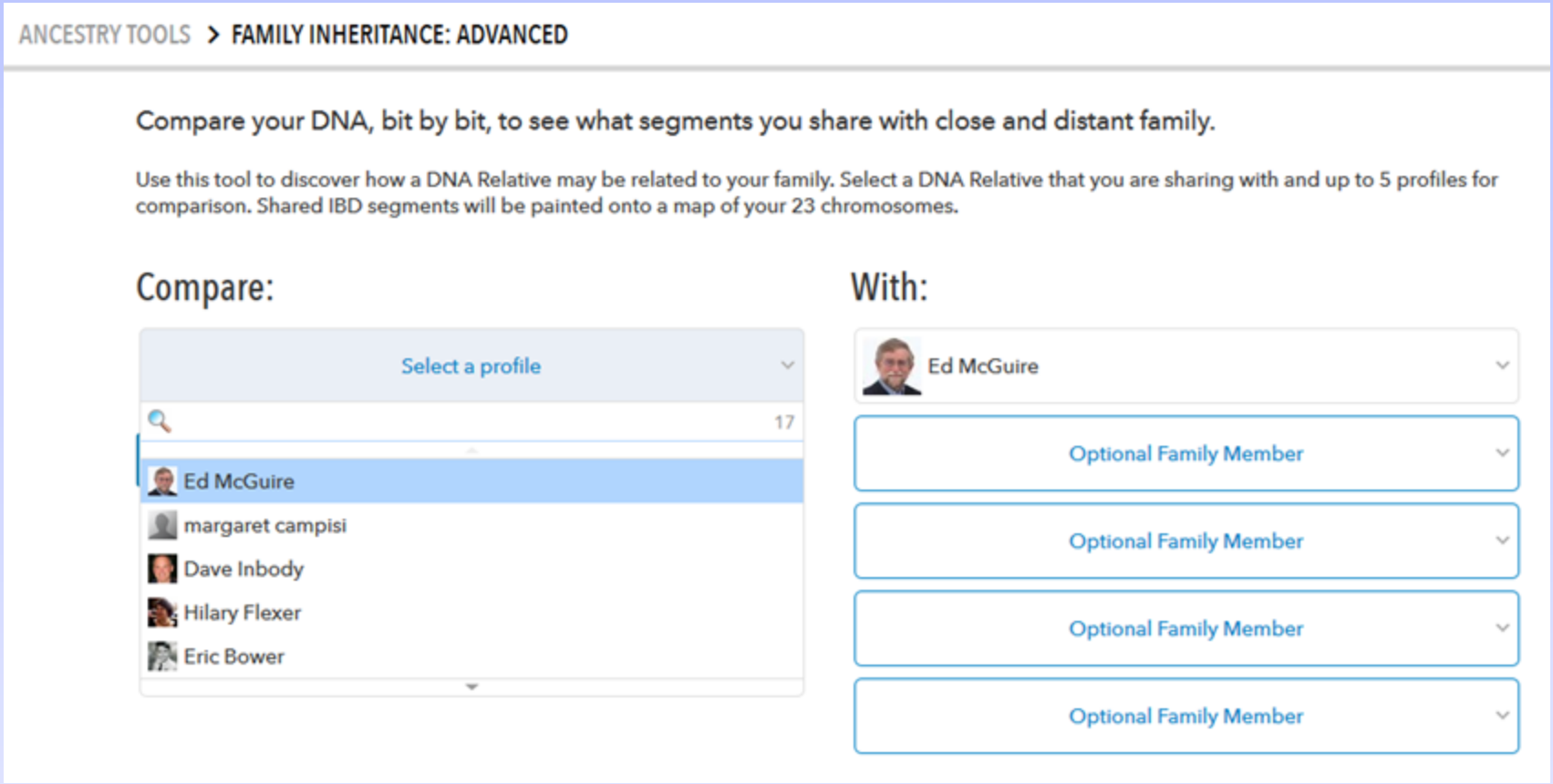
- You can see no data until you request 'sharing' & they accept
- Many testers not interested in genealogy



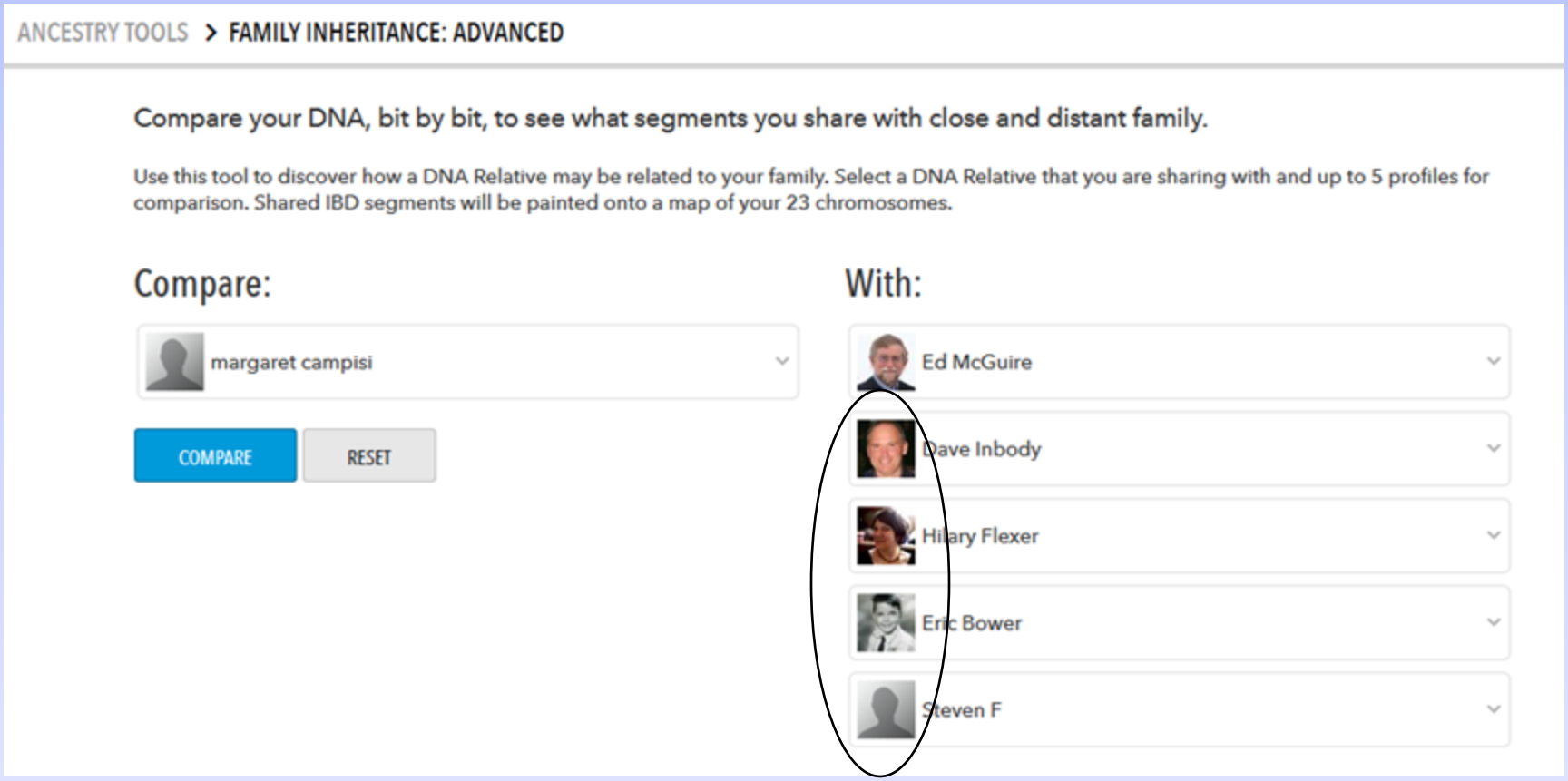
# Family Inheritance: Advanced



# Family Inheritance: Advanced



# Family Inheritance: Advanced

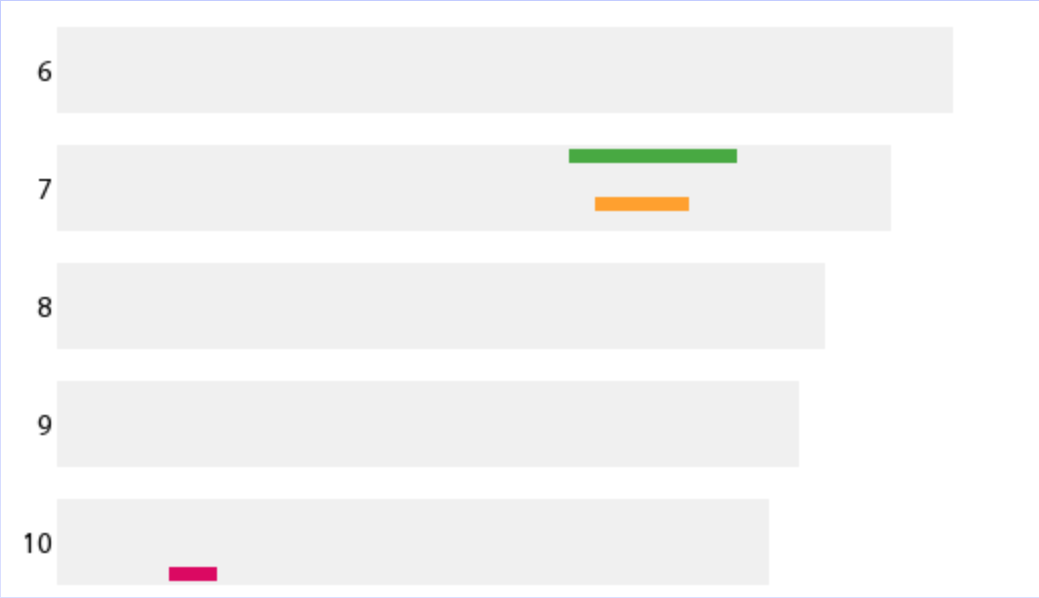


# Family Inheritance: Advanced

View in a table, or download table.

| Comparison | Half IBD | # segments |
|---|---|---|
| Ed McGuire vs. margaret campisi | 39 cM | 2 |
| Ed McGuire vs. Dave Inbody | 20 cM | 1 |
| Ed McGuire vs. Eric Bower | 16 cM | 1 |
| Ed McGuire vs. Lauren Brothers | 16 cM | 1 |
| Ed McGuire vs. Michael Marsh | 12 cM | 1 |

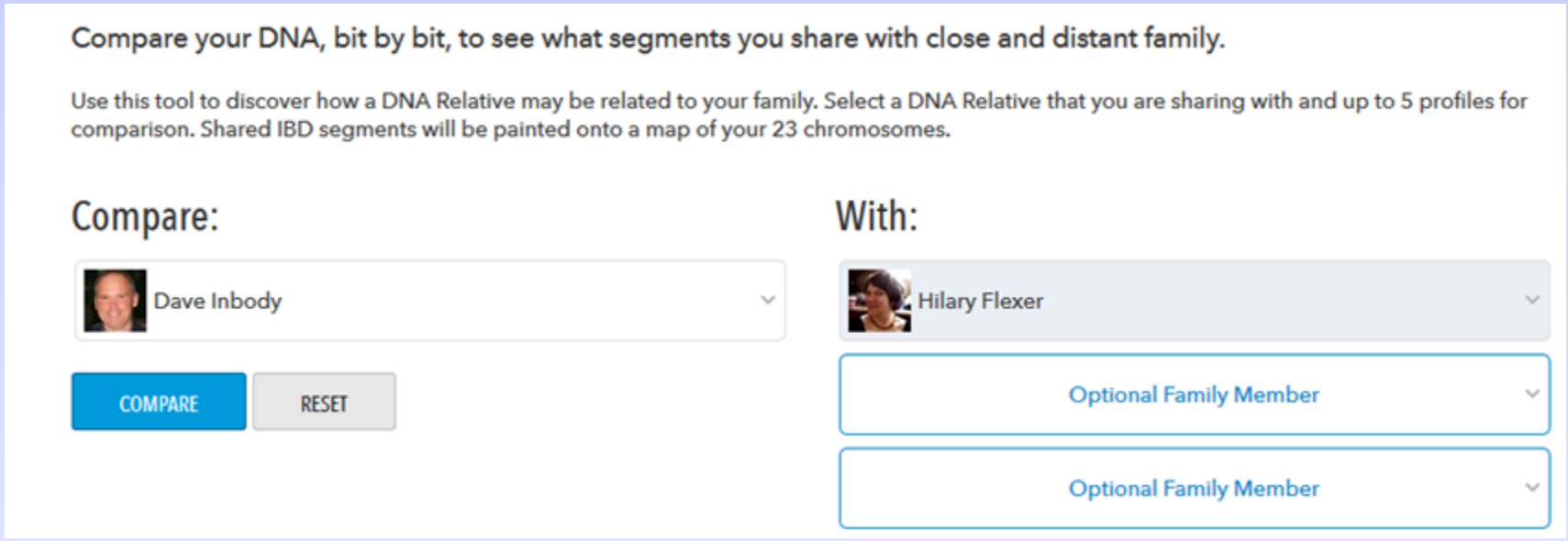
# Family Inheritance: Advanced




Margaret Campisi & Lauren Brothers overlap on CHR 7

# Family Inheritance: Advanced

- Unique feature allows you to compare matches against each other
- If they match you at same segment…do they match each other??



# Countries of Ancestry

- Testers must 'opt in' and add their grandparents' homeland
- You must 'opt in' to utilize this data
- If you match anyone in that DB – where their GPs all one country

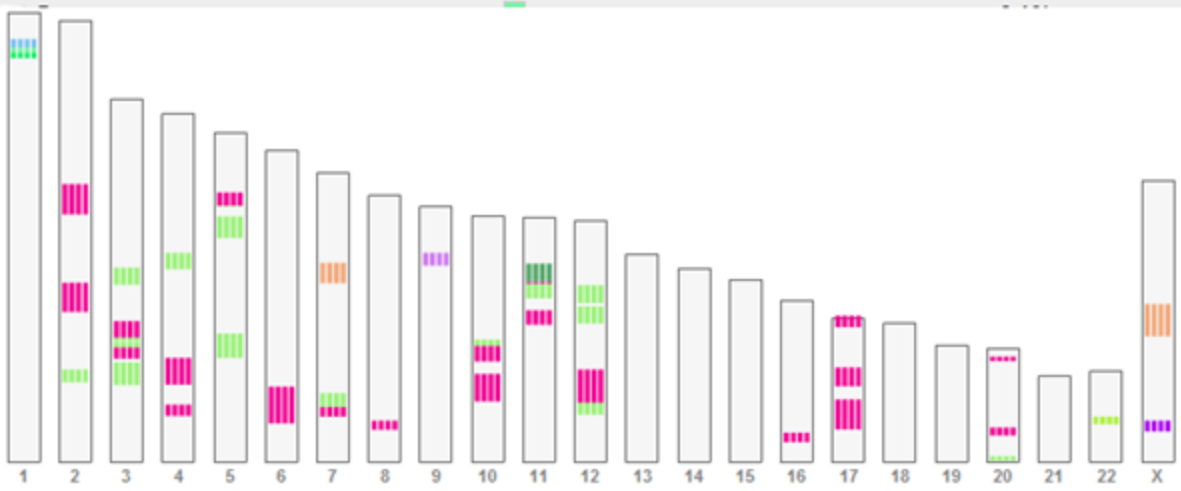
  → paints that DNA with ancestors homeland

Note: 5cM threshold here…lots more matches are available

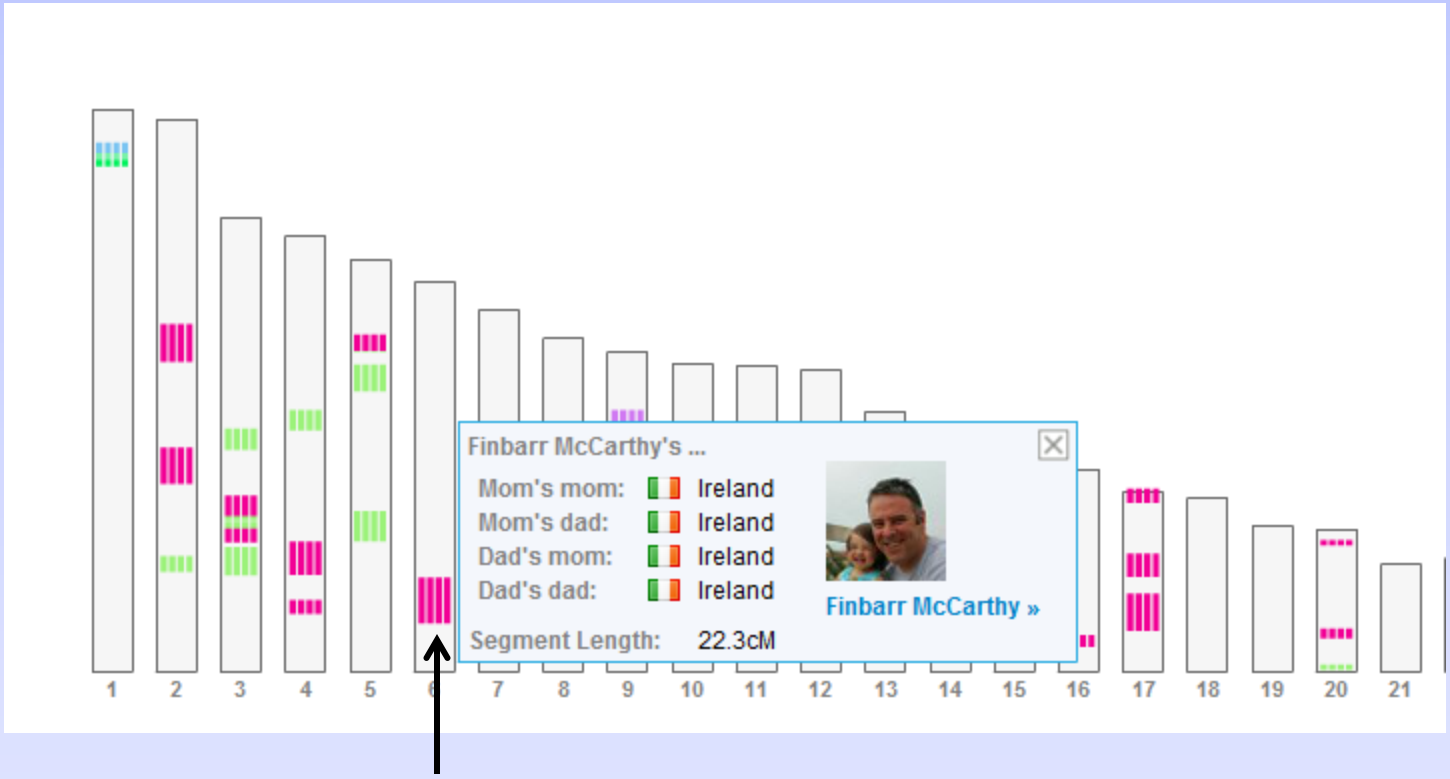
- Very helpful feature!!

# Countries of Ancestry

| Country | Color | Percent of Ed McGuire's Genome Covered |
|---|---|---|
| Ireland | | 3.6% |
| United Kingdom | | 2.3% |
| France | | 0.5% |
| Mexico | | 0.2% |
| Ukraine | | 0.1% |



# Countries of Ancestry



# Countries of Ancestry

Finbarr McCarthy

Health and Ancestry

You are not sharing with Finbarr McCarthy.

Why can't I invite this user to share genomes?

You have sent an invitation to Finbarr McCarthy to share genomes. Click here to cancel it.

SEND A MESSAGE

## Personal Information

**Sex:** Male

## Ancestry Information

**Birthplace:** Ireland

**Family Surnames:** McCarthy, Hamilton, Lanigan, O'Sullivan, Dunne, Fleming, Leary, McGrath, Killen

**Family Locations:** Cork, Bantry, Kilkenny, Tipperary, Ireland

# 23andMe

+ robust chromosome browser

+ ability to triangulate multiple matches to segment

+ allows comparison of matches to each other

+ COA tool matches testers homeland to DNA segments

- much lower response rates (but big user base)

- very difficult system for contacting matches

- focus remains mostly medical genetics

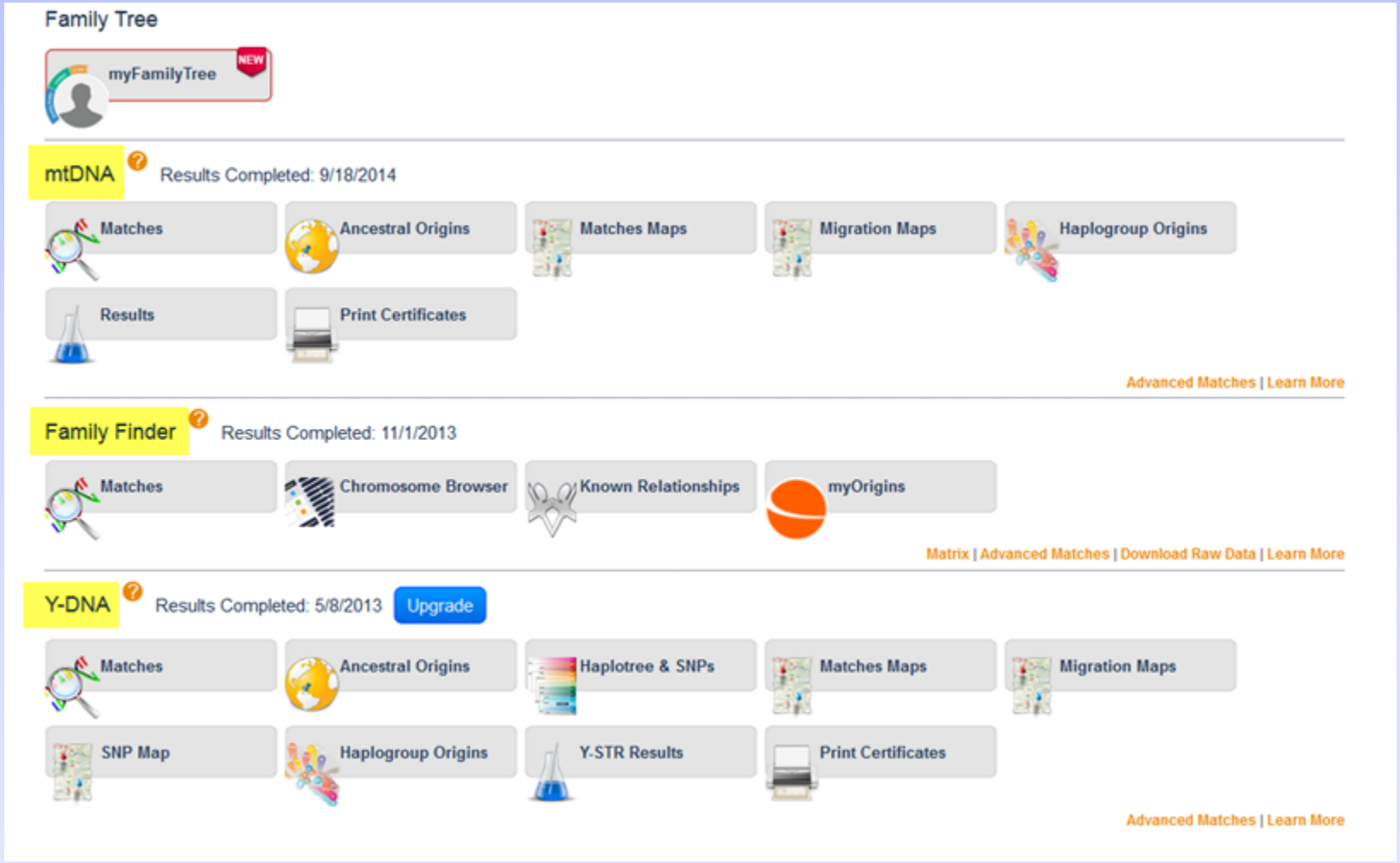
# FamilyTree DNA Analysis Tools

FTDNA has robust tools for segment analysis & triangulation

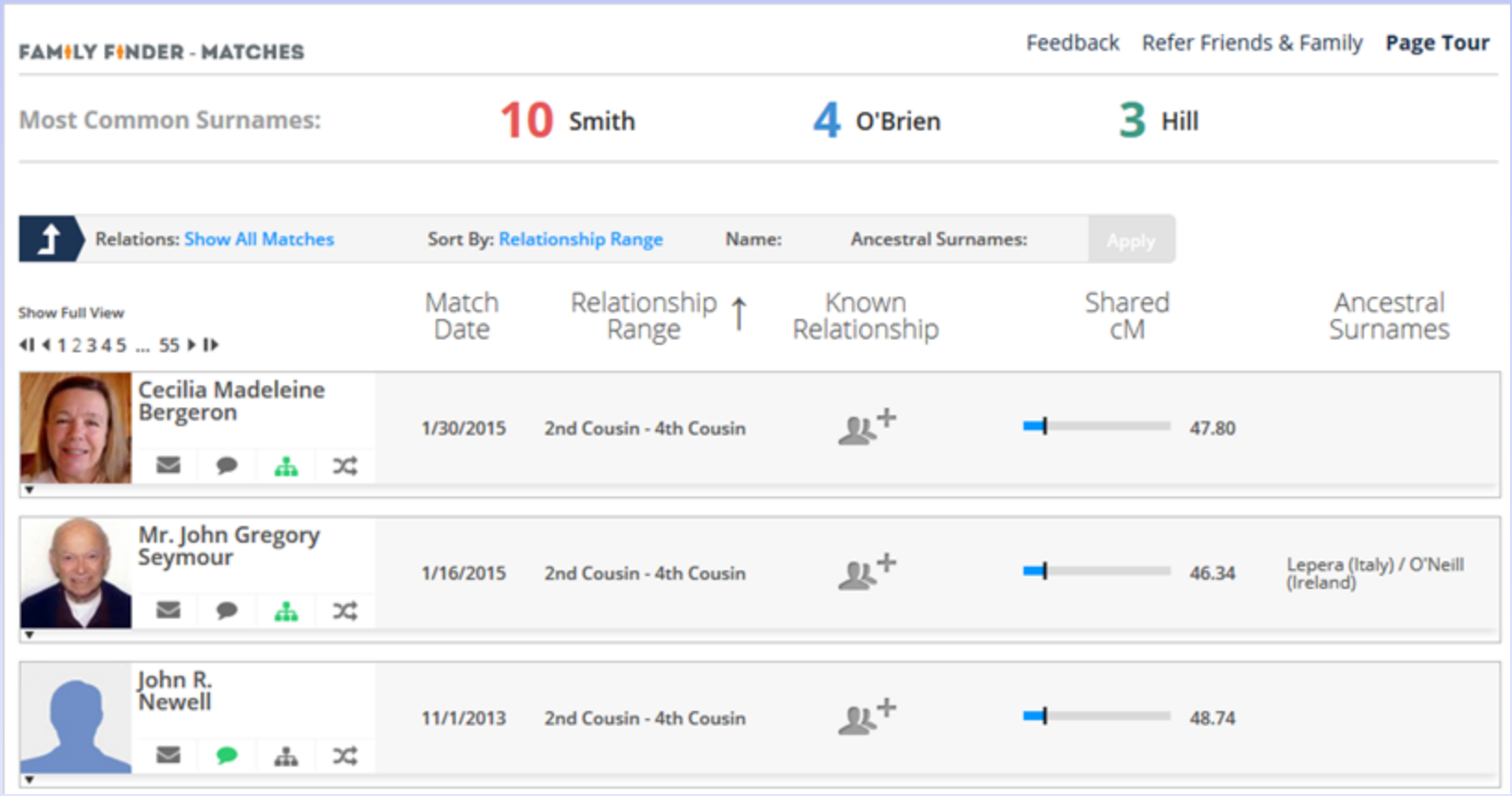
Tools are all located in one area

Site is well-organized

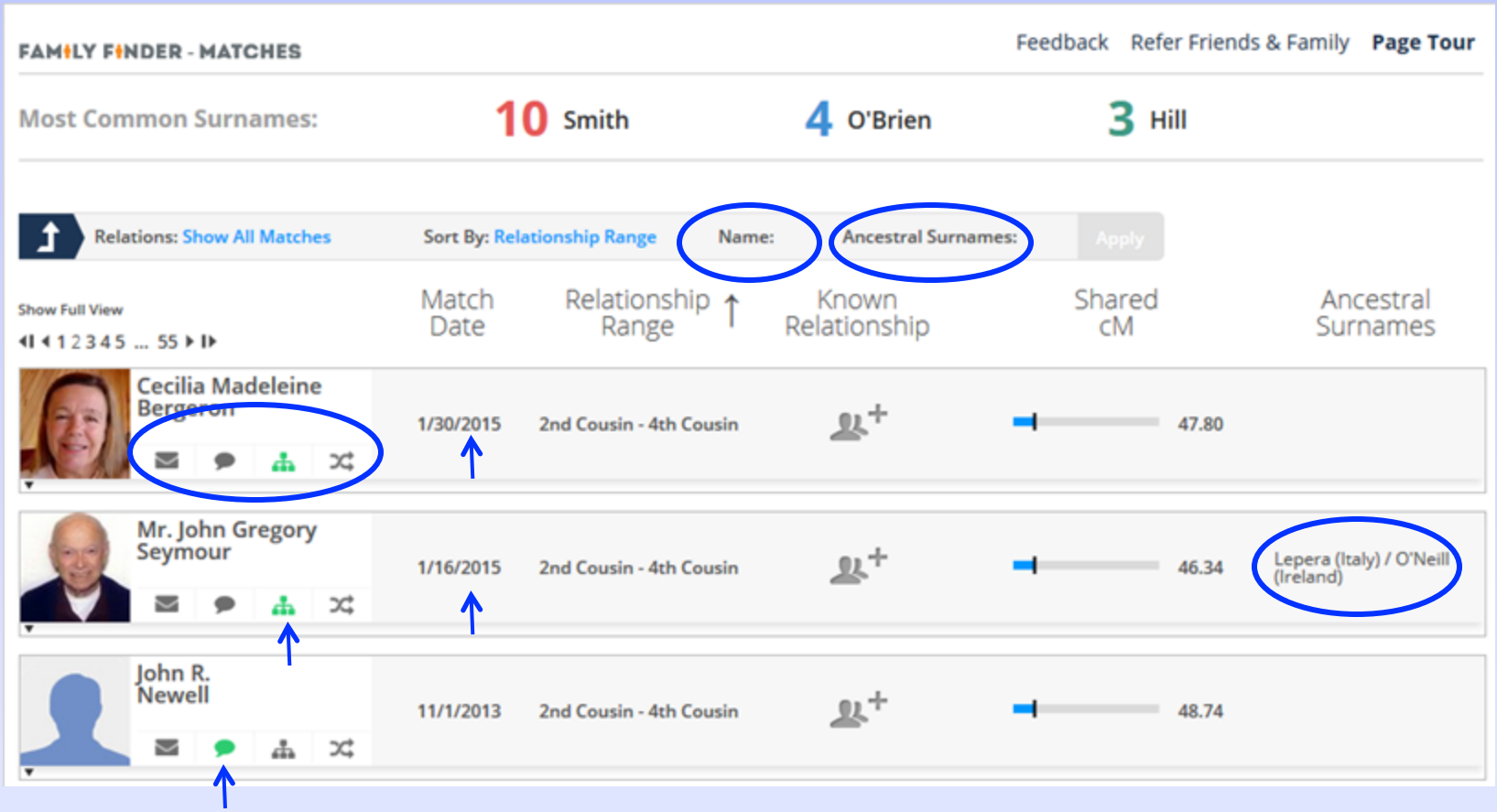
# FamilyTreeDNA Home Page



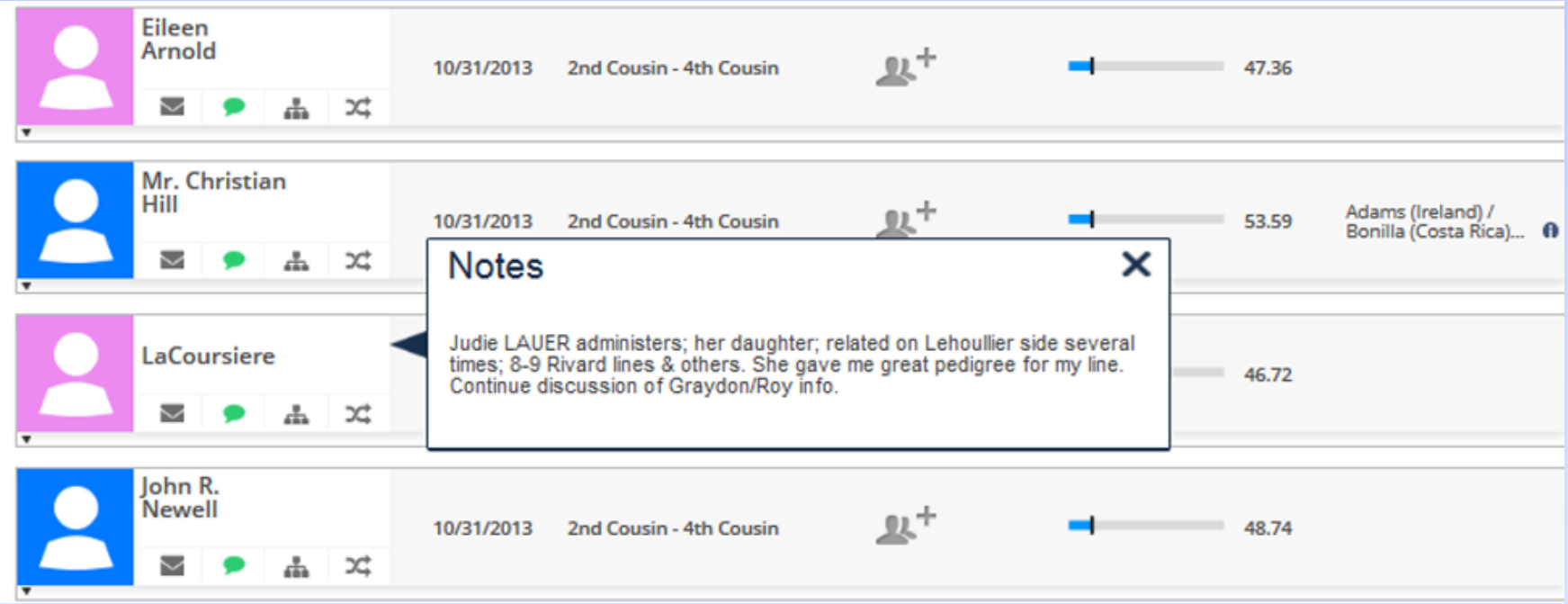
# FamilyTreeDNA 'FamilyFinder' Tool



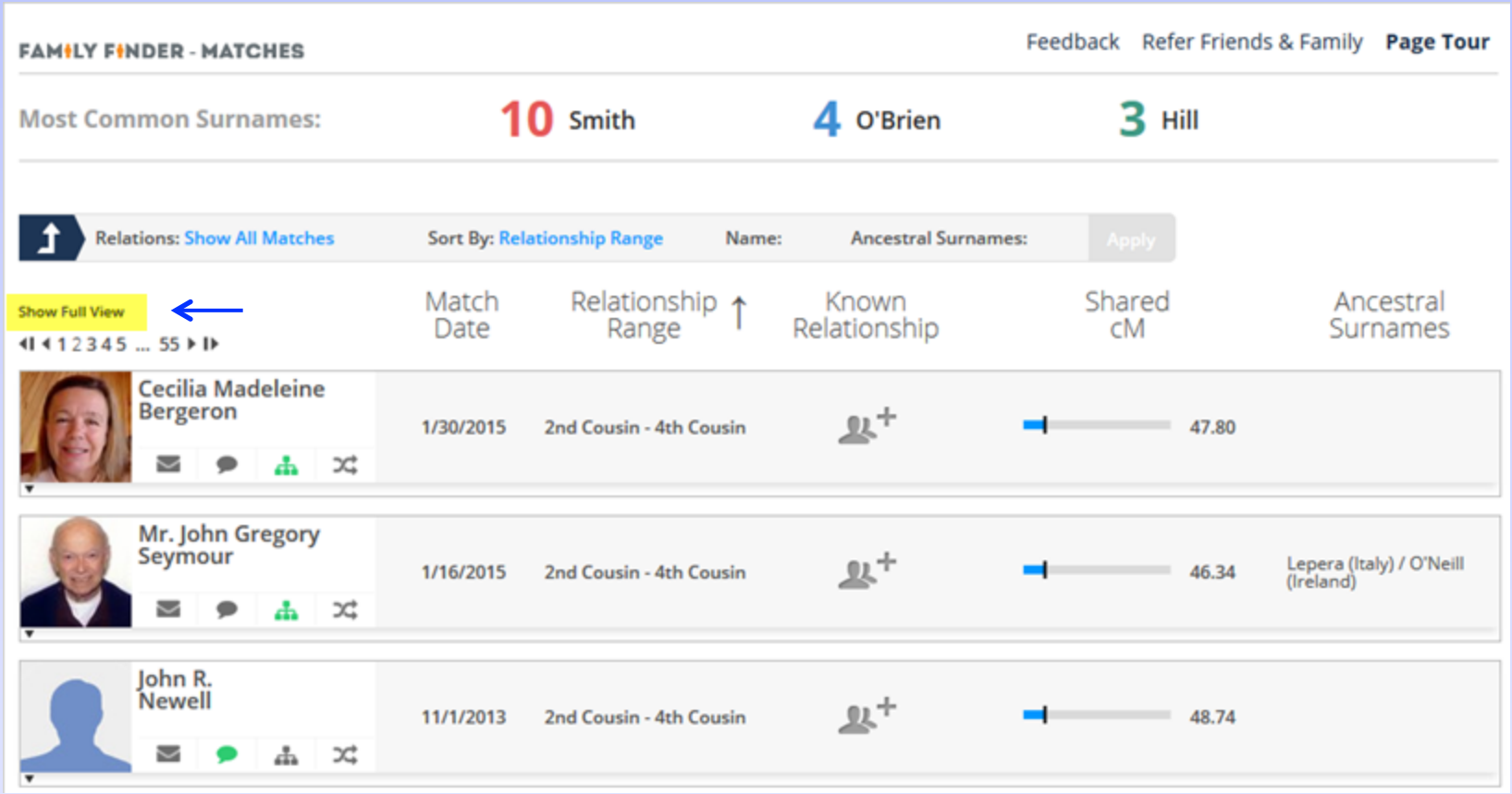
# FamilyTreeDNA 'FamilyFinder' Tool



# FT-DNA Matches Page

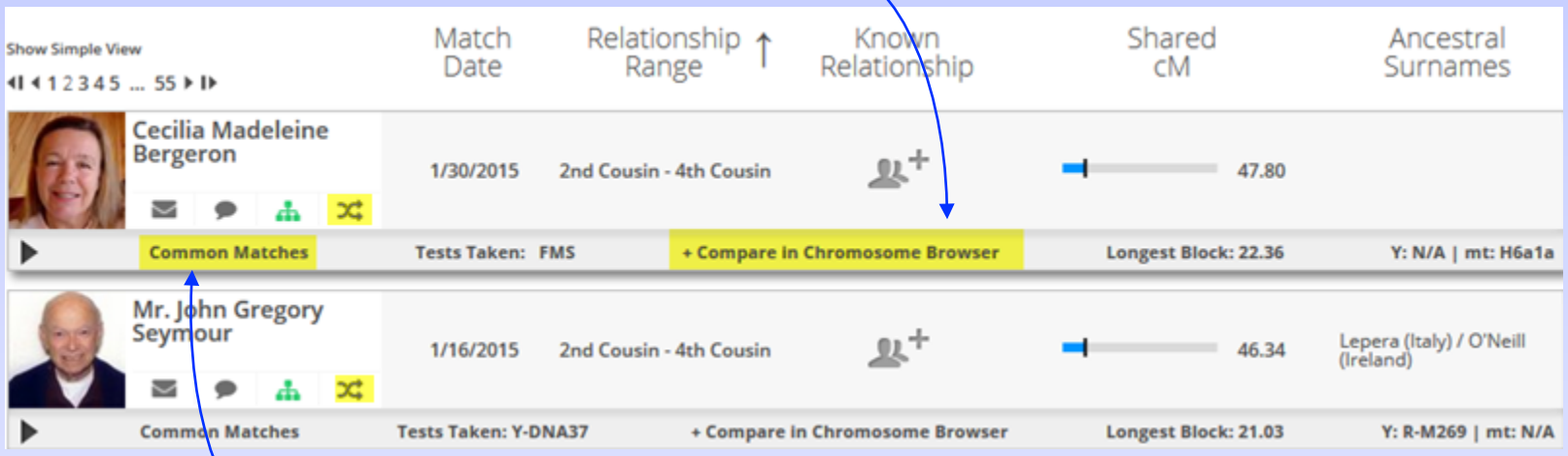


# FamilyTreeDNA 'FamilyFinder' Tool



# FamilyTreeDNA 'FamilyFinder' Tool

Chromosome Browser: visual layout of segments




In Common With (ICW) Tool: find all who match target cousin

# FamilyTreeDNA

+ robust chromosome browser

+ ability to triangulate multiple matches to segment

+ allows comparison of matches to each other

+ best response rates (but smaller user base)

+ most open & efficient communications

- no tool to compare one match to another

- only identifies HIRs (23andMe can also do FIR)

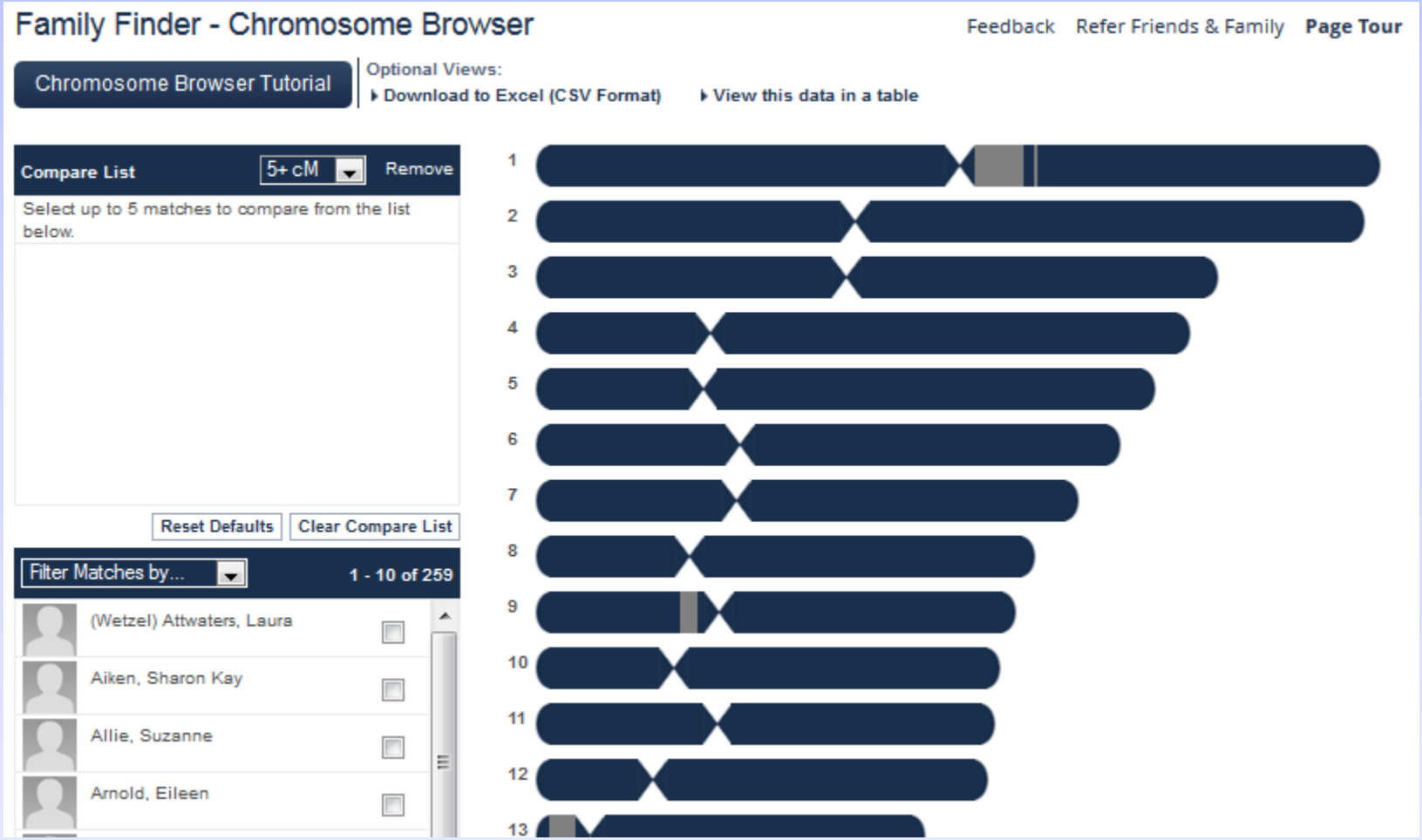
# Chromosome Browsers

# and

# Triangulation

# FT-DNA Chromosome Browser

## Blank Chromosome Map of my Aunt Rita



# FT-DNA Chromosome Browser

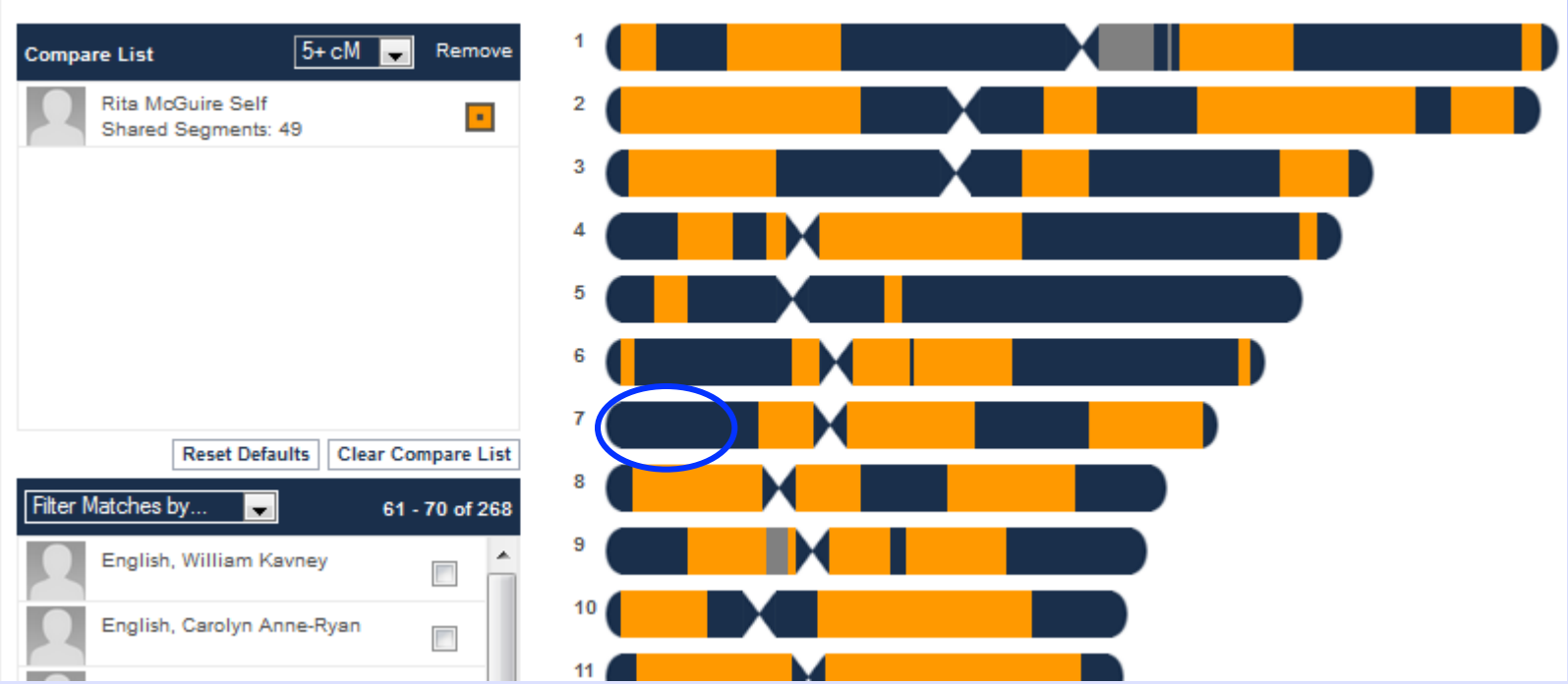
**Shared block of DNA between LaCoursie & Aunt Rita**

# FT-DNA Chromosome Browser

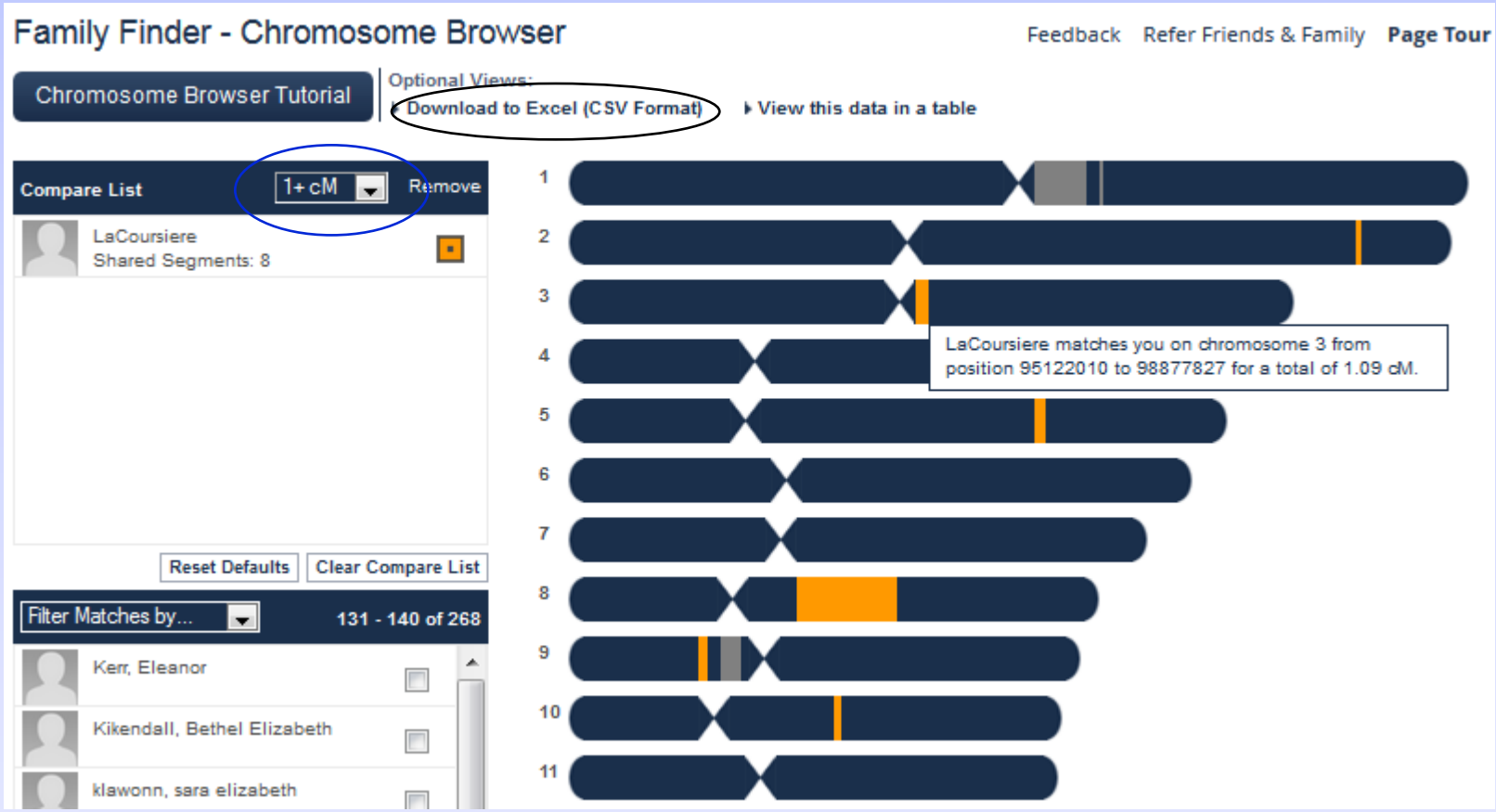
**Shared block of DNA between LaCoursie & Ed McGuire**

# FT-DNA Chromosome Browser

## Chromosome Map of Shared DNA with my Aunt Rita

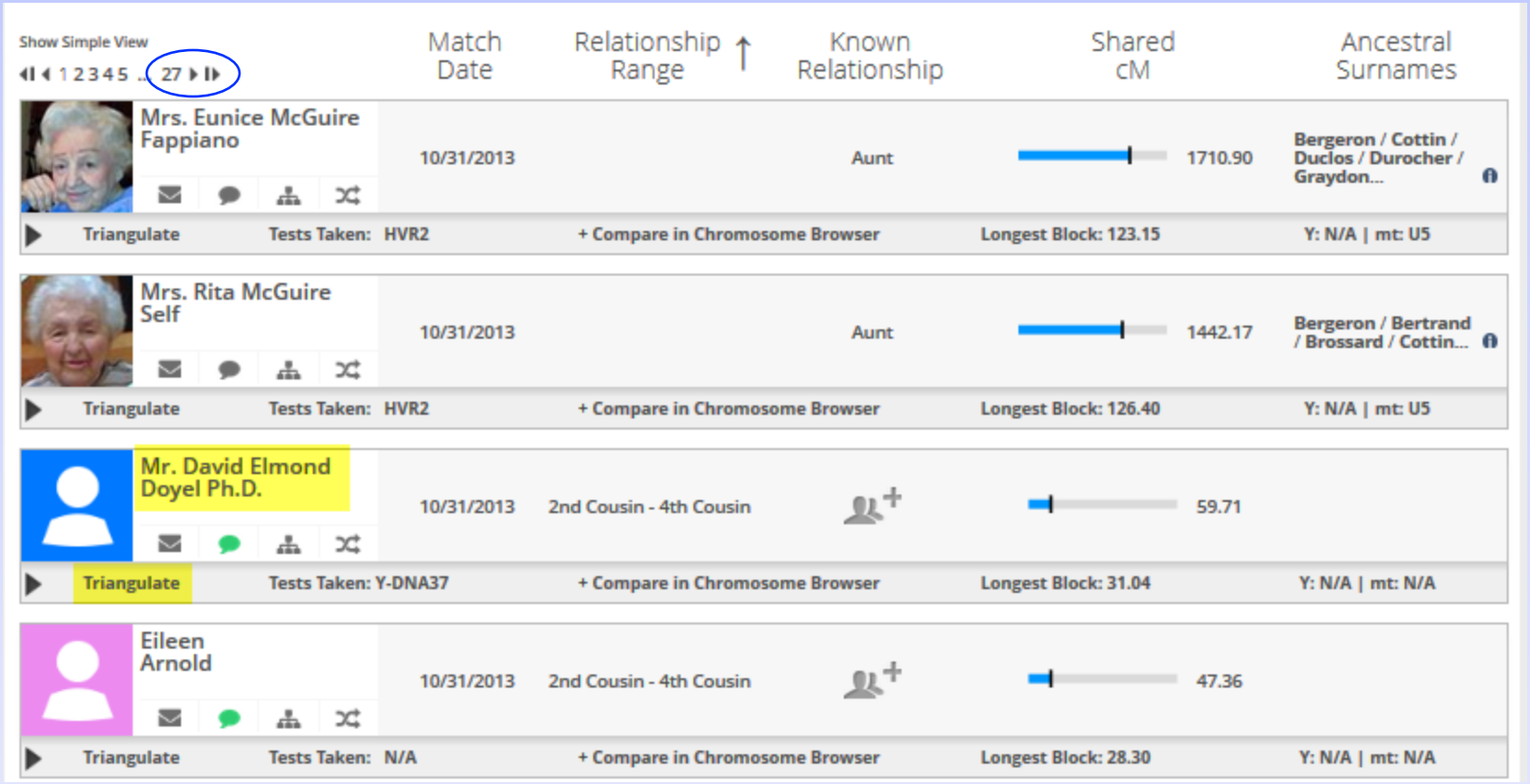


# FT-DNA Chromosome Browser

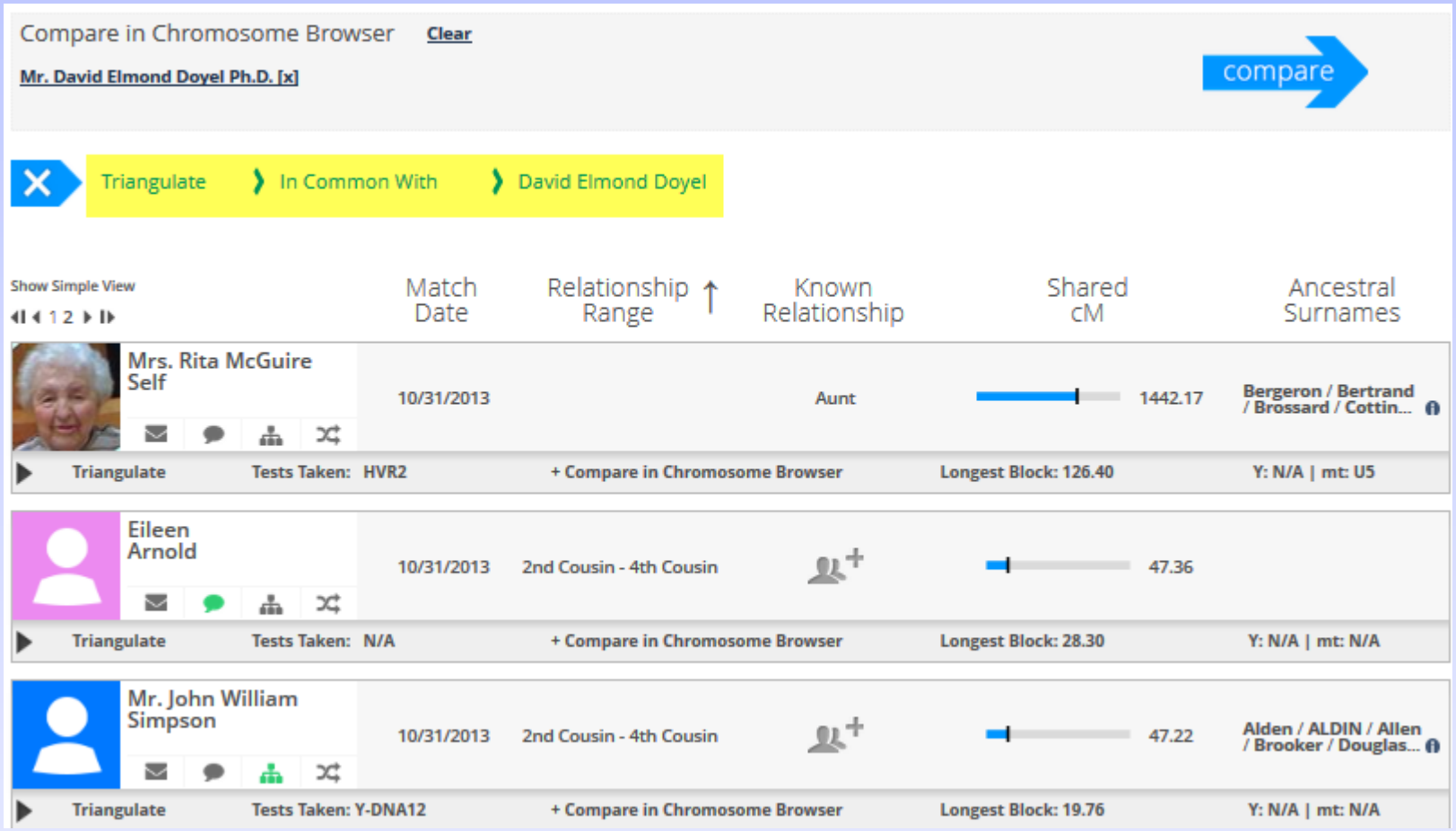


# Autosomal DNA Tools

## Using the 'In Common With' Tool

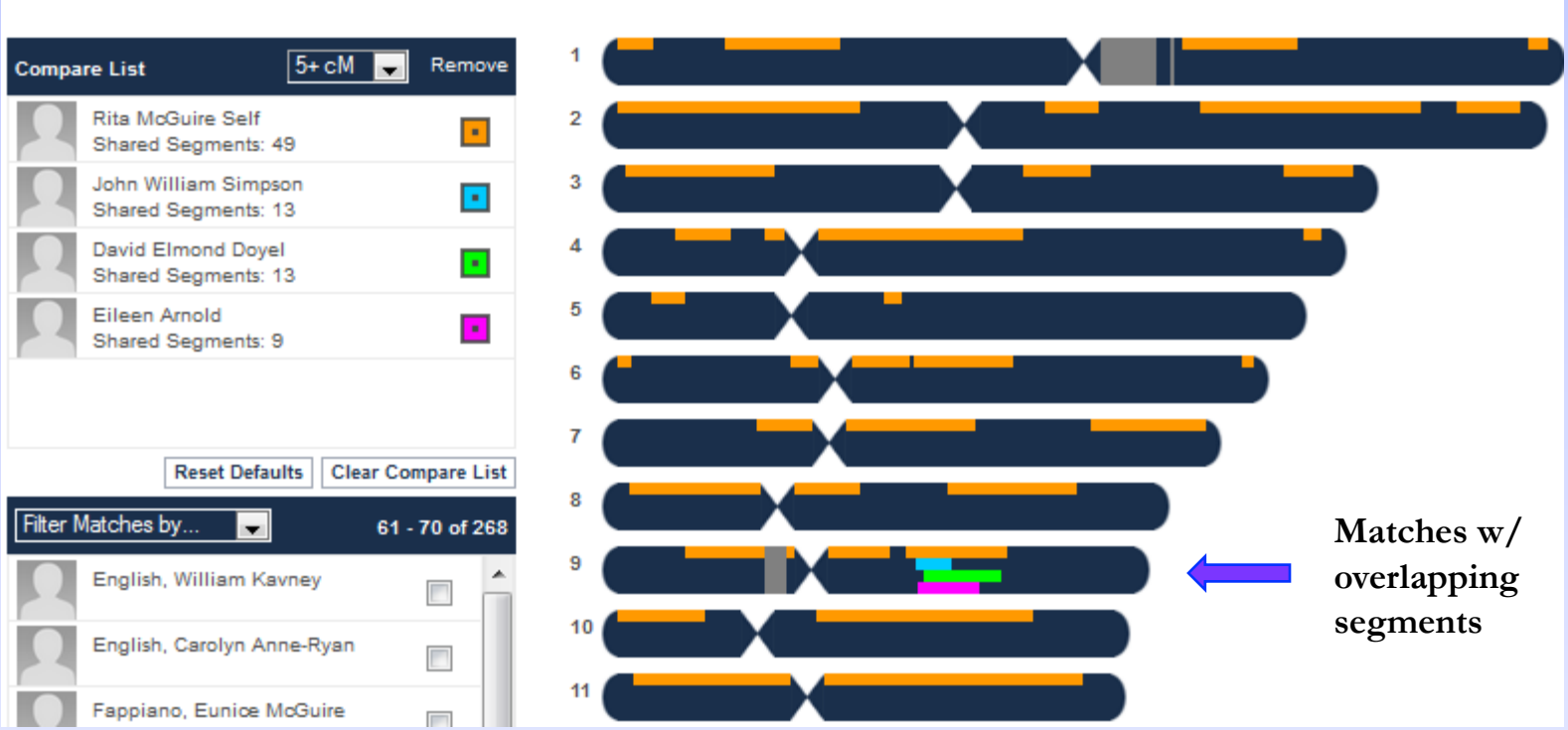


# Autosomal DNA Tools



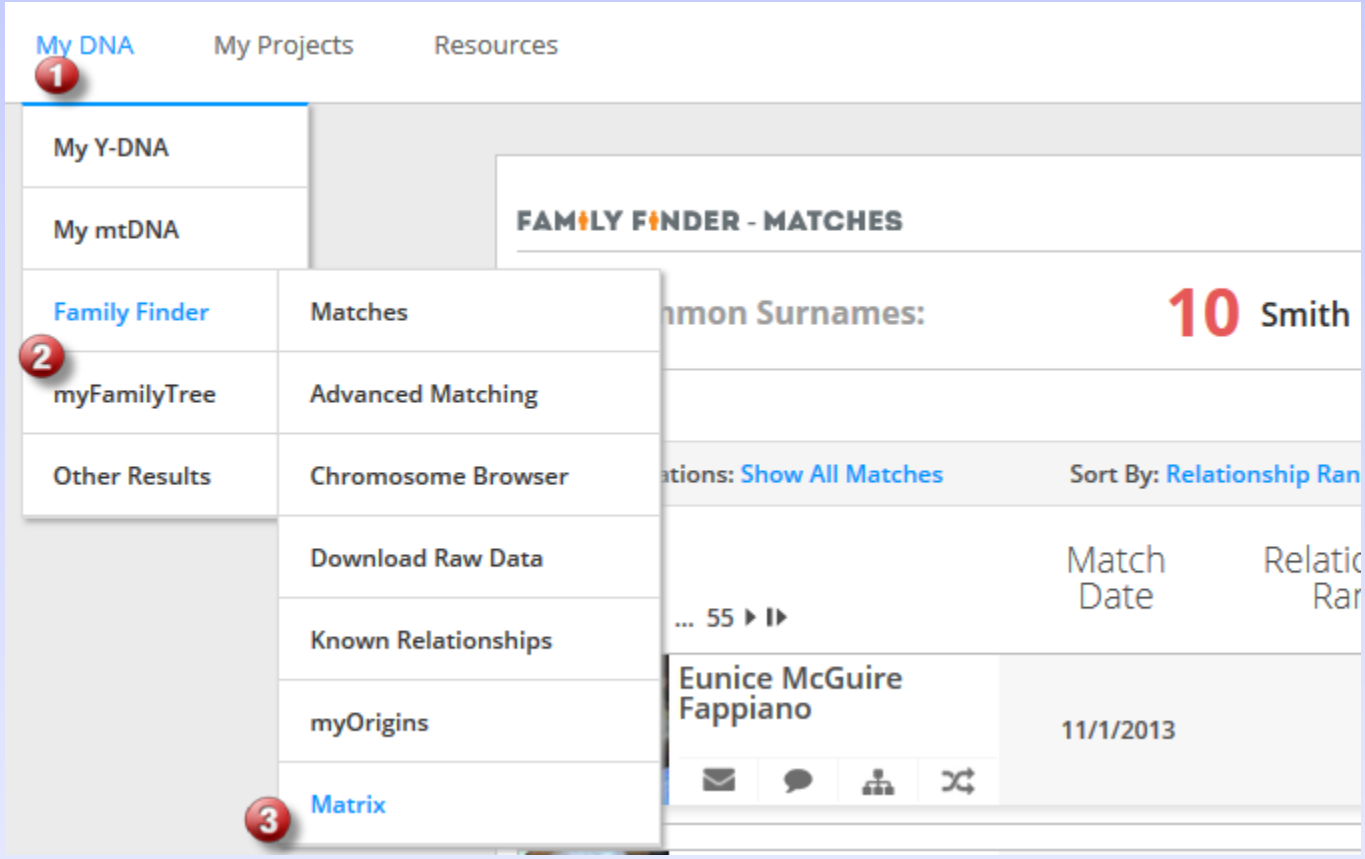
# FT-DNA Chromosome Browser

## Triangulation: People in common w/ McGuire & Doyel

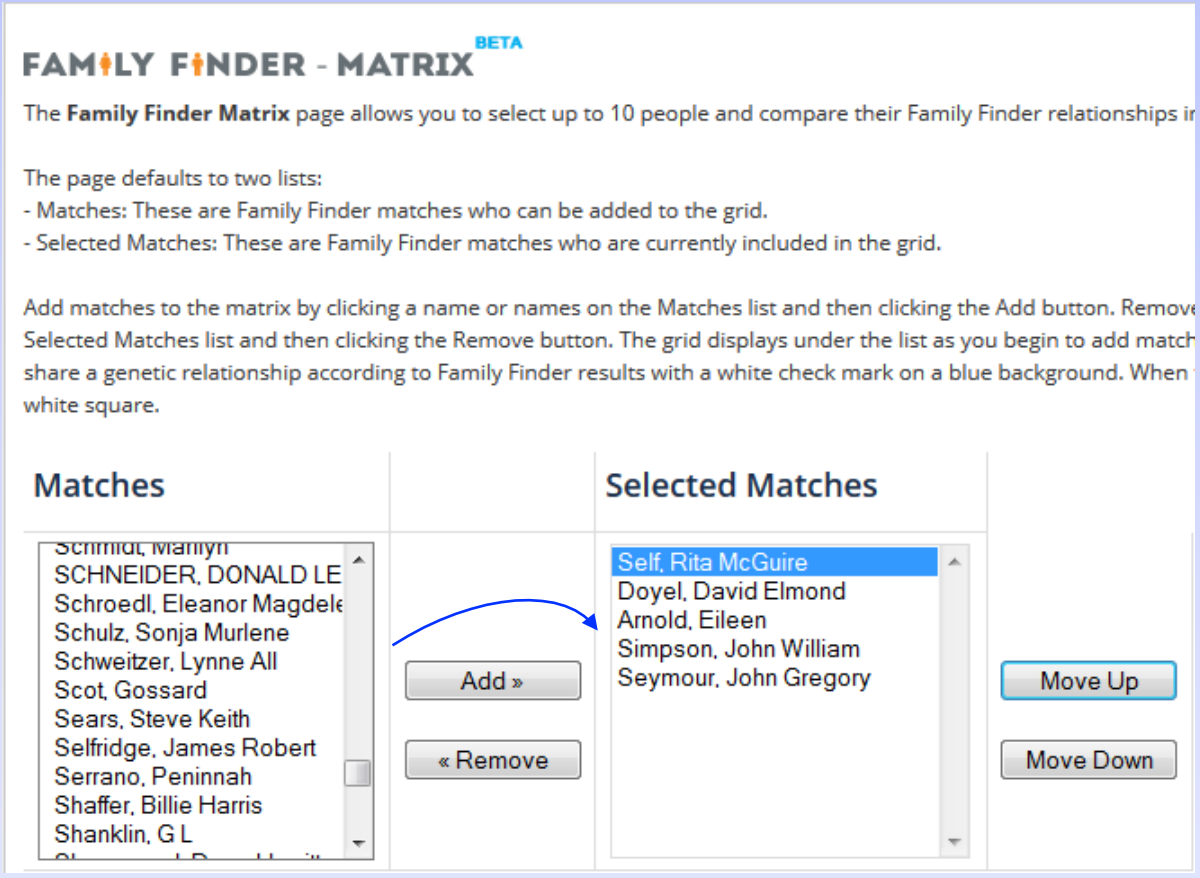


# FT-DNA Matrix Tool

**Run Matrix Tool on People in common w/ McGuire & Doyel**



# FT-DNA Matrix Tool



# FT-DNA Matrix Tool

Matrix Matches

| | Rita McGuire Self | David Elmond Doyel | Eileen Arnold | John Gregory Seymour | John William Simpson |
|---|---|---|---|---|---|
| Rita McGuire Self | | ✓ | ✓ | ✓ | ✓ |
| David Elmond Doyel | ✓ | | ✓ | ✓ | ✓ |
| Eileen Arnold | ✓ | ✓ | | ✓ | ✓ |
| John Gregory Seymour | ✓ | ✓ | ✓ | | ✓ |
| John William Simpson | ✓ | ✓ | ✓ | ✓ | |

✓ - This person is identified as a match.

# FT-DNA Matrix Tool

Matrix Matches

| | Rita McGuire Self | David Elmond Doyel | Eileen Arnold | John William Simpson | John Gregory Seymour | Eunice McGuire Fappiano |
|---|---|---|---|---|---|---|
| Rita McGuire Self | | ✓ | ✓ | ✓ | ✓ | ✓ |
| David Elmond Doyel | ✓ | | ✓ | ✓ | ✓ | |
| Eileen Arnold | ✓ | ✓ | | ✓ | ✓ | |
| John William Simpson | ✓ | ✓ | ✓ | | ✓ | |
| John Gregory Seymour | ✓ | ✓ | ✓ | ✓ | | |
| Eunice McGuire Fappiano | ✓ | | | | | |

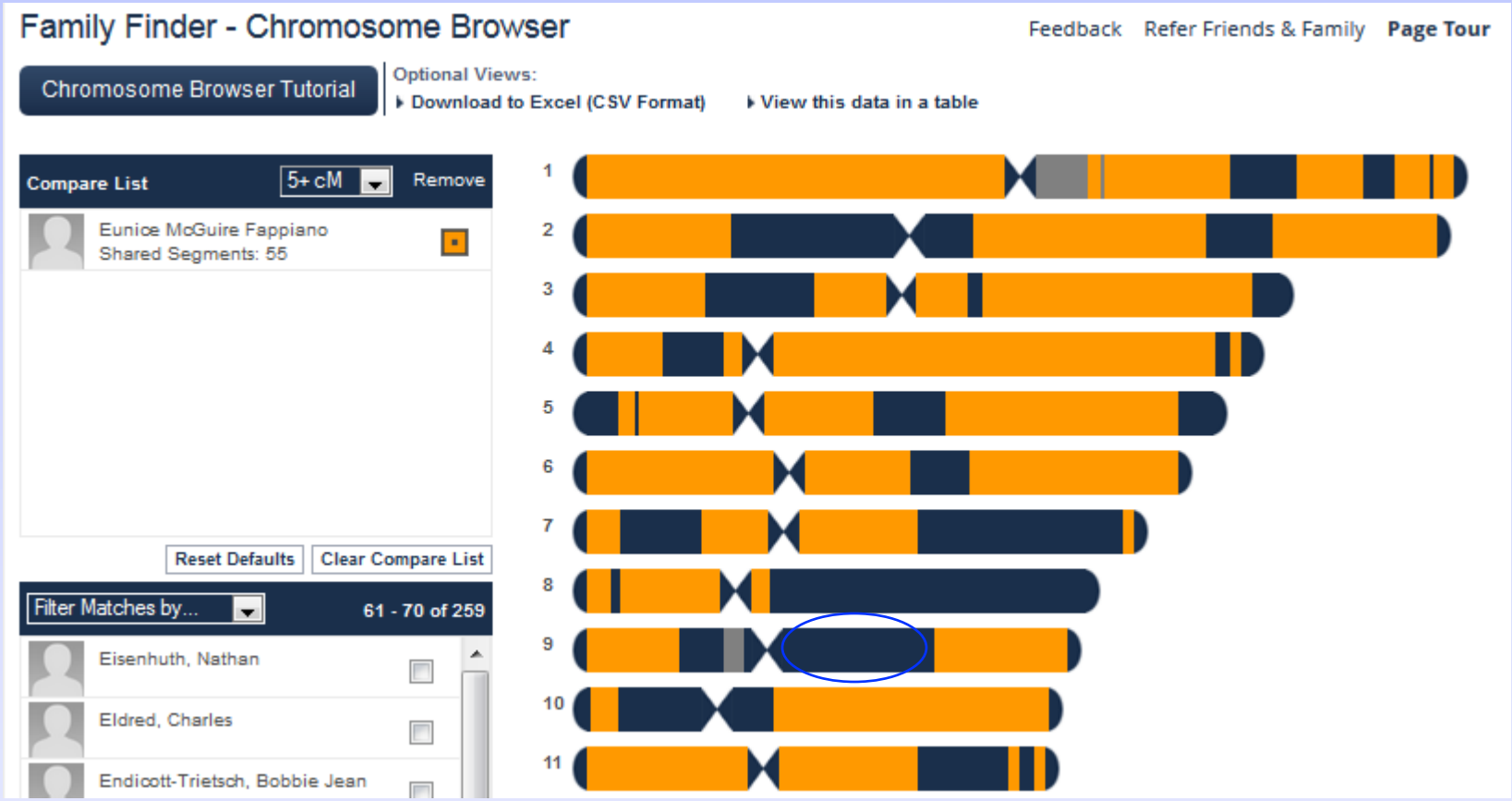
✓ - This person is identified as a match.

**Person can match another tester – but at another segment (rare)**

**Solution would be to compare matches to each other in browser (like 23andMe)**

# FT-DNA Chromosome Browser

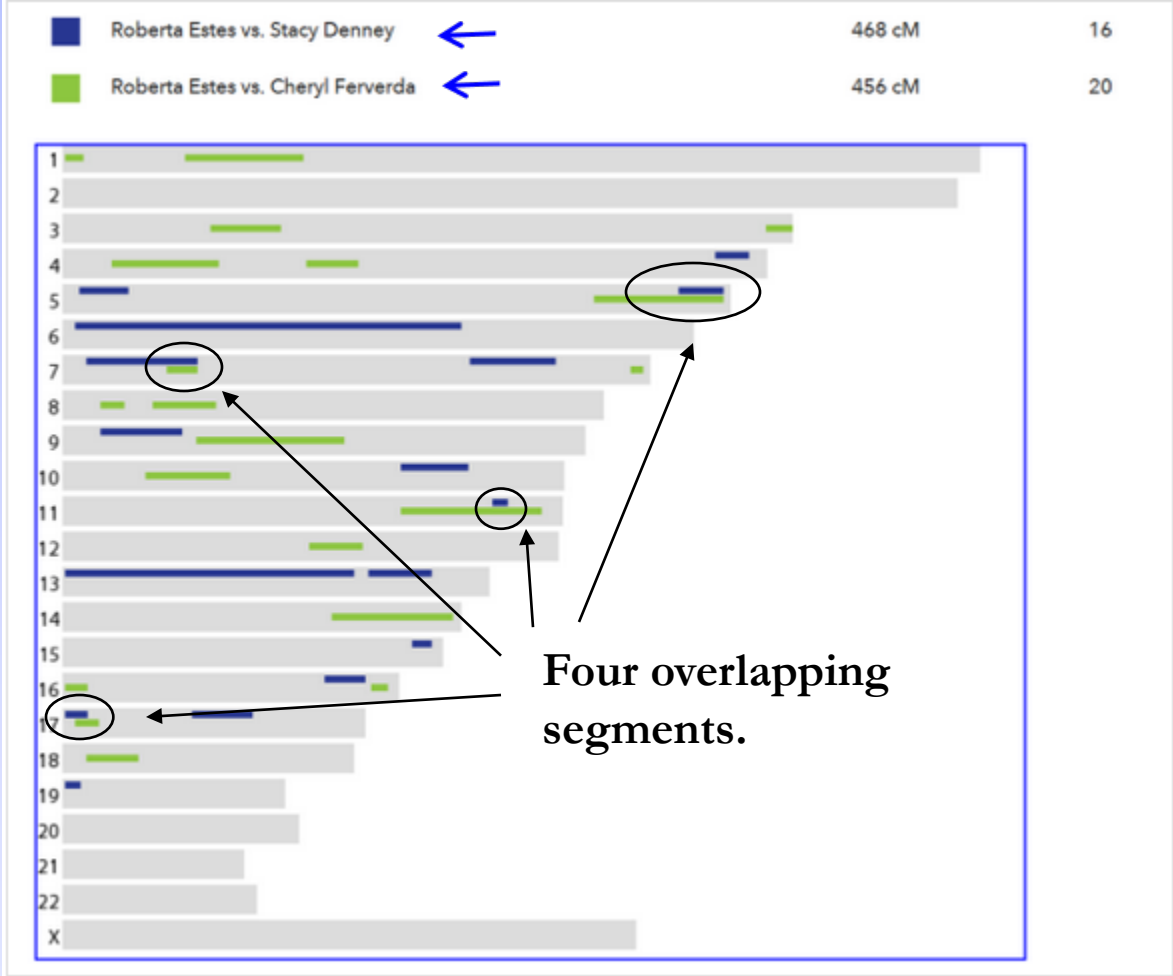
## Chromosome map for sisters Rita and Eunice



# FT-DNA Chromosome Browser

**Two Aunts don't share this segment on Chromosome 9**

## 23andMe Chromosome Browser for Roberta Estes

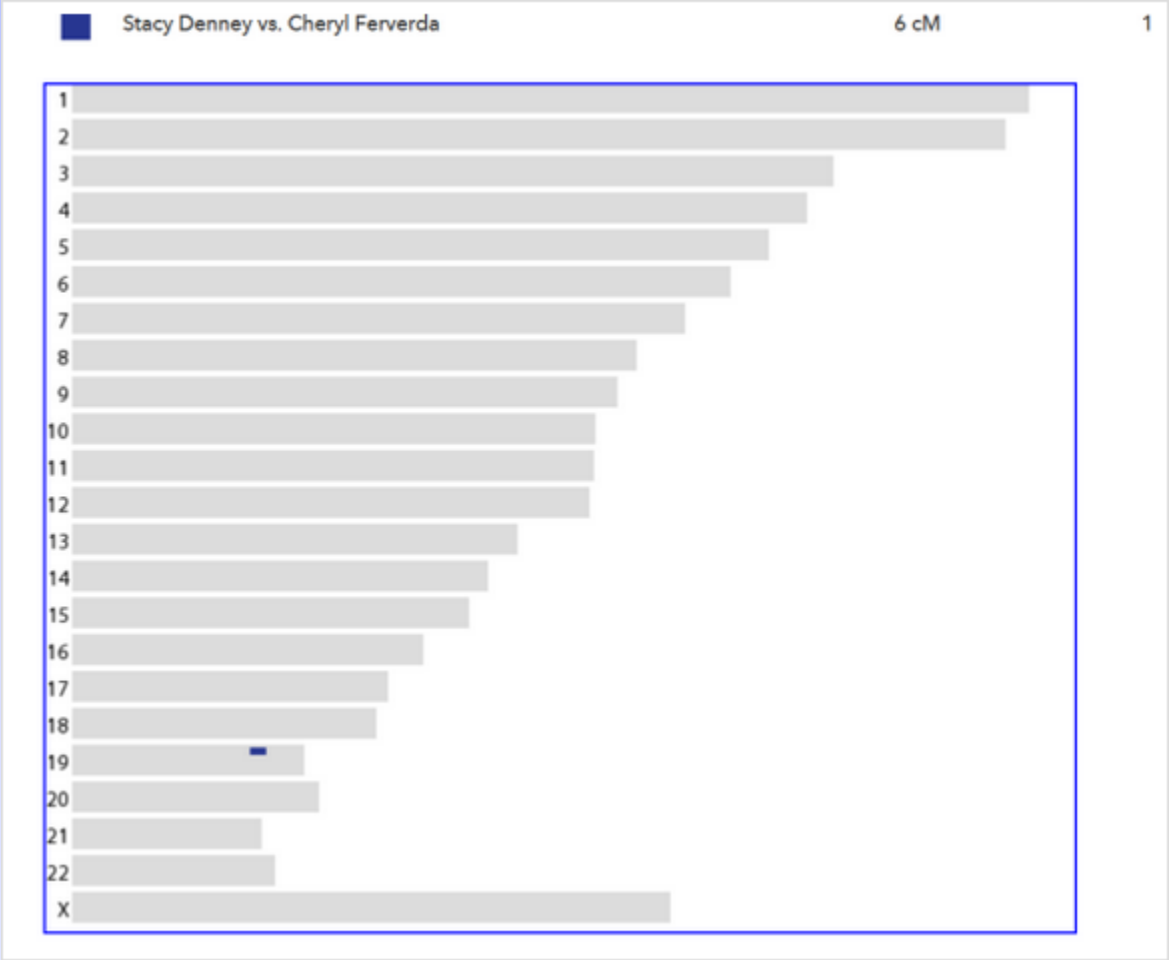



Source: http://dna-explained.com/2013/06/07/navigating-23andme-for-genealogy/

# Chromosome Browser – Inferring Matches

- data show Stacy & Cheryl share DNA w/ Roberta
- data imply Stacy & Cheryl share w/ each other in 4 places
- both have lines from Ohio in 1800s name Miller

# Stacy vs Cheryl – 4 matches disappear




Source: http://dna-explained.com/2013/06/07/navigating-23andme-for-genealogy/

# Chromosome Browser – Inferring Matches

- data show Stacy & Cheryl share DNA w/ Roberta
- data implies Stacy & Cheryl share w/ each other in 4 places
- both have lines from Ohio in 1800s name Miller

- but Stacy matches Roberta's dad; Cheryl matches Roberta's mom!

Remember: each chromosome pair has two sides

Net: matching on same chromosome not always conclusive

(P.S. – and AncestryDNA needs a chromosome browser!!)

# Triangulated Groups

# What is a Triangulated Group?

- Three or more testers who all match each other
- They overlap segments in Chromosome Browser
- All of the matches match each other - at that segment

# The Value in Finding Triangulated Groups

**Working on individual matches can lead to success but is very inefficient**

- **communication workload is higher than for groups**
- **you & your single match may not have records deep enough**
- **teams can divide tasks and keep each other motivated**
- **team has more chance someone has rec'd for 'Common Ancestor'**

**Finding several matches who all match each other at the same spot**

- **far more reliable DNA result than you and single match**
- **anomalies in data more likely to show up & be recognized**

# Key Steps in Finding Triangulated Groups

1. Develop organization system (logs and spreadsheet)
2. Contact matches – especially at 23andMe to 'share genomes'
3. Download match information & family tree data to spreadsheet
4. Locate multiple matches who appear to share common segments

# Key Steps in Finding Triangulated Groups

## 2. Arrange them by Chr + Start – End with this

| Rel | Co | KIT | MA | LN | em | Chr | Start poi | End poin | cMs | SNPs | TG | Czn | Surnames | Tree |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 23 | jvb | Jani | Sa | RF | 1 | 30.4 | 37.5 | 9.4 | | | | | |
| JGm | Gm | jvb | Alle | Wi | ma | 1 | 102.1 | 110.6 | 8.2 | 1,833 | | | | |
| D | 23 | jvb | Che | As | RF | 1 | 116.1 | 152.9 | 17.3 | 1,609 | | | 2gp=Norway | |
| | 23 | jvb | Cyn | Bra | RF | 1 | 242.4 | 245.8 | 8.2 | 759 | | | | |
| | 23 | jvb | Cat | Dv | RF | 4 | 28.3 | 36.3 | 7.6 | 1,228 | | 8C | SANFORD | http://t |
| | 23 | jvb | Luc | Co | hoF | 6 | 24.6 | 35.3 | 7.2 | | | | [4gp= UK,Can,Ger,Ire | |
| UGm | 23 | jvb | Der | Ril | der | 6 | 24.7 | 39.1 | 12.1 | 4,770 | | | | |
| ICW-0( | F37 | jvb | She | Sh | jea | 6 | 24.7 | 37.0 | 9.3 | 9,000 | | | [MOORE,OSBORN] | |
| U37 | F37 | jvb | ROI | Se | rlse | 6 | 24.7 | 39.3 | 12.2 | 9,700 | | | | |
| JGm | Gm | jvb | ( ) | | jess | 6 | 24.8 | 38.8 | 10.1 | 8,693 | | | | |
| D | 23 | jvb | Kev | Mc | RF | 6 | 24.9 | 37.3 | 9.5 | 4,173 | | | >[Ireland] | http://t |
| D | 23 | jvb | Mic | Mc | Mc | 6 | 24.9 | 36.7 | 8.3 | 3,995 | | | | http://t |
| | 23 | jvb | Mar | Ch | RF | 6 | 24.9 | 37.3 | 9.5 | 4,168 | | | [n cent WV | |
| UGm | Gm | jvb | Windia | | dia | 6 | 24.9 | 40.6 | 12.8 | 8,593 | | | | |
| | 23 | jvb | FleurDe | | Tro | 6 | 25.0 | 37.5 | 9.5 | | | | | |
| | 23 | jvb | Will | He | wh | 6 | 25.0 | 40.0 | 12.4 | | | 9C | DICKENSON? | |
| DR37 | F37 | jvb | Mar | Ro | gol | 6 | 25.1 | 36.4 | 8.3 | 8,700 | | | | |
| J37 | F37 | jvb | Kev | Mc | kev | 6 | 25.1 | 37.3 | 9.3 | 9,000 | | | | http://t |
| J37 | F37 | jvb | Cat | Fe | cth | 6 | 25.1 | 37.3 | 9.3 | 9,000 | | | [MOORE?] | FFTree |
| U37 | F37 | jvb | Jam | Gr | jgra | 6 | 25.1 | 39.3 | 12.1 | 9,600 | | | | |
| UGm | 23 | jvb | Fred | Ril | lize | 6 | 25.1 | 39.2 | 11.6 | 4,672 | | | | |
| U37 | F37 | jvb | Elsi | We | elsi | 6 | 25.4 | 37.7 | 9.8 | 9,000 | | | | |
| UGm | Gm | jvb | FEN | Mc | lov | 6 | 25.5 | 40.9 | 12.5 | 9,023 | | | | |
| J37 | F37 | jvb | Ste | Ay | ste | 6 | 25.6 | 37.3 | 9.2 | 8,800 | | | | |
| J37 | F37 | jvb | Tra | Jo | be | 6 | 26.1 | 37.3 | 9.0 | 8,600 | | | | |
| JGm | Gm | jvb | Jac | Sa | De | 7 | 83.3 | 94.8 | 8.7 | 2,504 | | | | |
| | 23 | jvb | Adr | Ellswo | | 7 | 83.3 | 105.5 | 18.1 | 4,029 | | | | |
| J37,BV | F37 | jvb | Lar | Ha | larr | 7 | 83.5 | 105.3 | 20.0 | 5,200 | | 5C-1 | HATHAWAY | |
| D | 23 | jvb | Oliv | Cli | olli | 8 | 111.2 | 126.9 | 15.9 | 3,111 | | | | |
| JA37,D | F37 | jvb | Glo | Fu | gfu | 8 | 111.5 | 124.3 | 14.0 | 2,693 | | 10C | OVERTON/GARDINER | |

jim4bartletts@verizon.net 240-475-7664

# Sorting Matches Into Correct Triangulated Groups

| KIT | MA | LN | em | Chr | Start po | End poir | cMs | SNPs | TG | Czn | Surnames |
|---|---|---|---|---|---|---|---|---|---|---|---|
| jvb | Luc | Co | noF | 6 | 24.6 | 35.3 | 7.2 | | A | | [4gp= UK,Can,Ger,Ire |
| jvb | Der | Ril | der | 6 | 24.7 | 39.1 | 12.1 | 4,770 | B | | |
| jvb | She | Sh | jea | 6 | 24.7 | 37.0 | 9.3 | 9,000 | A | | [MOORE,OSBORN] |
| jvb | ROI | Se | rlse | 6 | 24.7 | 39.3 | 12.2 | 9,700 | B | | |
| jvb | ( ) | | jess | 6 | 24.8 | 38.8 | 10.1 | 8,693 | A | | |
| jvb | Kev | Mc | RF | 6 | 24.9 | 37.3 | 9.5 | 4,173 | A | | >[Ireland] |
| jvb | Mic | Mc | Mc | 6 | 24.9 | 36.7 | 8.3 | 3,995 | A | | |
| jvb | Ma | Ch | RF | 6 | 24.9 | 37.3 | 9.5 | 4,168 | B | | [n cent WV |
| jvb | Windia | | dia | 6 | 24.9 | 40.6 | 12.8 | 8,593 | B | | |
| jvb | FleurDeTro | | | 6 | 25.0 | 37.5 | 9.5 | | IBS | | |
| jvb | Will | He | whe | 6 | 25.0 | 40.0 | 12.4 | | B | 9C | **DICKENSON?** |
| jvb | Ma | Ro | gol | 6 | 25.1 | 36.4 | 8.3 | 8,700 | A | | |
| jvb | Kev | Mc | kev | 6 | 25.1 | 37.3 | 9.3 | 9,000 | A | | |
| jvb | Cat | Fe | cth | 6 | 25.1 | 37.3 | 9.3 | 9,000 | A | | [MOORE?] |
| jvb | Jam | Gr | jgra | 6 | 25.1 | 39.3 | 12.1 | 9,600 | B | | |
| jvb | Fre | Ril | lize | 6 | 25.1 | 39.2 | 11.6 | 4,672 | B | | |

# Key Steps in Finding Triangulated Groups

1. Develop organization system (logs and spreadsheet)
2. Contact matches – especially at 23andMe to 'share genomes'
3. Download match information & family tree data to spreadsheet
4. Locate multiple matches who appear to share common segments
5. Investigate (chromosome browser, ICW, and confirm joint matches
6. Organize all rows (matches) by segments they share in common

# Sorting Matches Into Correct Triangulated Groups

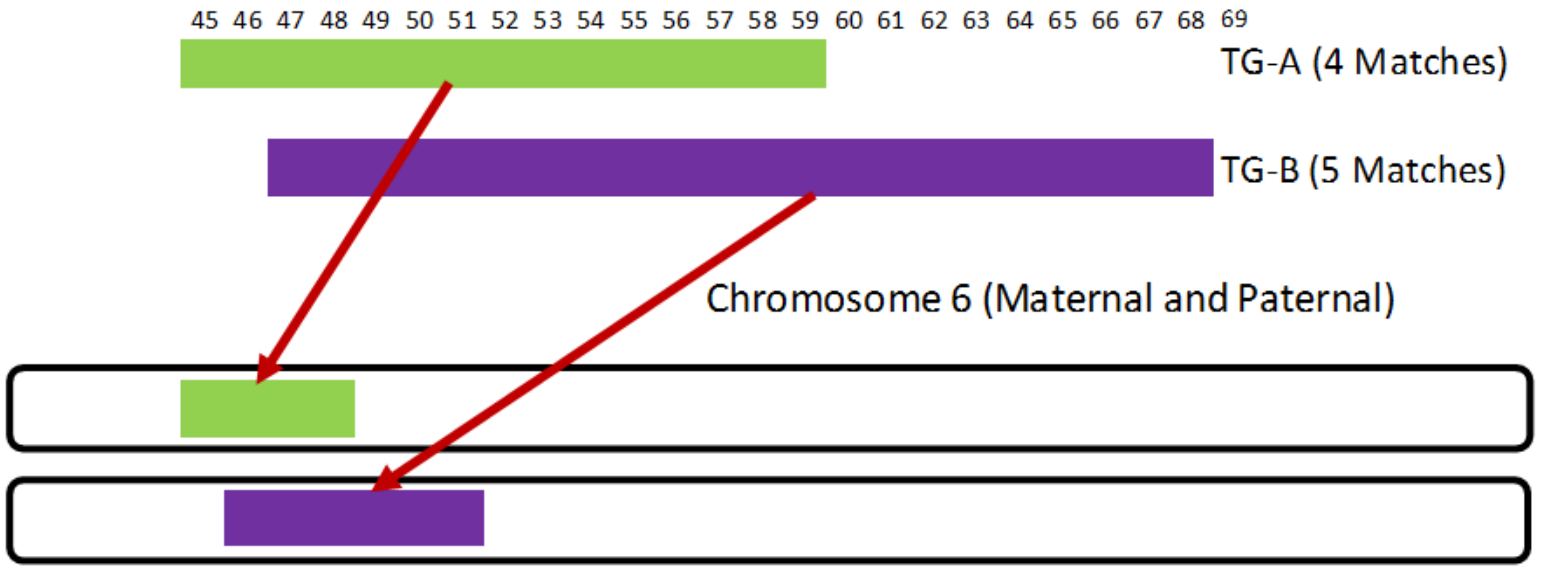
| KIT | MA | LN | em | Chr | Start po | End poin | cMs | SNPs | TG | Czn | Surnames |
|---|---|---|---|---|---|---|---|---|---|---|---|
| jvb | Luc | Co | noF | 6 | 24.6 | 35.3 | 7.2 | | A | | [4gp= UK, Can, Ger, Ire |
| jvb | She | Sh | jear | 6 | 24.7 | 37.0 | 9.3 | 9,000 | A | | [MOORE, OSBORN] |
| jvb | ( ) | | jess | 6 | 24.8 | 38.8 | 10.1 | 8,693 | A | | |
| jvb | Kev | Mc | RF | 6 | 24.9 | 37.3 | 9.5 | 4,173 | A | | >[Ireland] |
| jvb | Mic | Mc | Mc | 6 | 24.9 | 36.7 | 8.3 | 3,995 | A | | |
| jvb | Mar | Ro | gol | 6 | 25.1 | 36.4 | 8.3 | 8,700 | A | | |
| jvb | Kev | Mc | kev | 6 | 25.1 | 37.3 | 9.3 | 9,000 | A | | |
| jvb | Cat | Fe | cth | 6 | 25.1 | 37.3 | 9.3 | 9,000 | A | | [MOORE?] |
| jvb | Ste | Ayl | ste | 6 | 25.6 | 37.3 | 9.2 | 8,800 | A | | |
| jvb | Tra | Jol | kbe | 6 | 26.1 | 37.3 | 9.0 | 8,600 | A | 5C-1 | **HATHAWAY** |
| jvb | Der | Ril | den | 6 | 24.7 | 39.1 | 12.1 | 4,770 | B | | |
| jvb | RO | Se | rlse | 6 | 24.7 | 39.3 | 12.2 | 9,700 | B | | |
| jvb | Mar | Ch | RF | 6 | 24.9 | 37.3 | 9.5 | 4,168 | B | | [n cent WV |
| jvb | Windia | | dia | 6 | 24.9 | 40.6 | 12.8 | 8,593 | B | | |
| jvb | Will | He | wh | 6 | 25.0 | 40.0 | 12.4 | | B | 9C | **DICKENSON?** |
| jvb | Jam | Gr | jgra | 6 | 25.1 | 39.3 | 12.1 | 9,600 | B | | |
| jvb | Fre | Ril | lize | 6 | 25.1 | 39.2 | 11.6 | 4,672 | B | | |
| jvb | Elsi | We | elsi | 6 | 25.4 | 37.7 | 9.8 | 9,000 | B | | |
| jvb | FEM | Mc | love | 6 | 25.5 | 40.9 | 12.5 | 9,023 | B | | |
| jvb | FleurDeTro | | | 6 | 25.0 | 37.5 | 9.5 | | IBS | | |

# Key Steps in Finding Triangulated Groups

1. Develop organization system (logs and spreadsheet)
2. Contact matches – especially at 23andMe to 'share genomes'
3. Download match information & family tree data to spreadsheet
4. Locate multiple matches who appear to share common segments
5. Investigate (chromosome browser, ICW, and confirm joint matches
6. Organize all rows (matches) by segments they share in common
7. Use know relatives to determine which side of your tree (mom vs dad)
8. Use TG as team of experts to chase down Common Ancestor
9. Assign that segment to the Common Ancestor

# Sorting Matches Into Correct Triangulated Groups

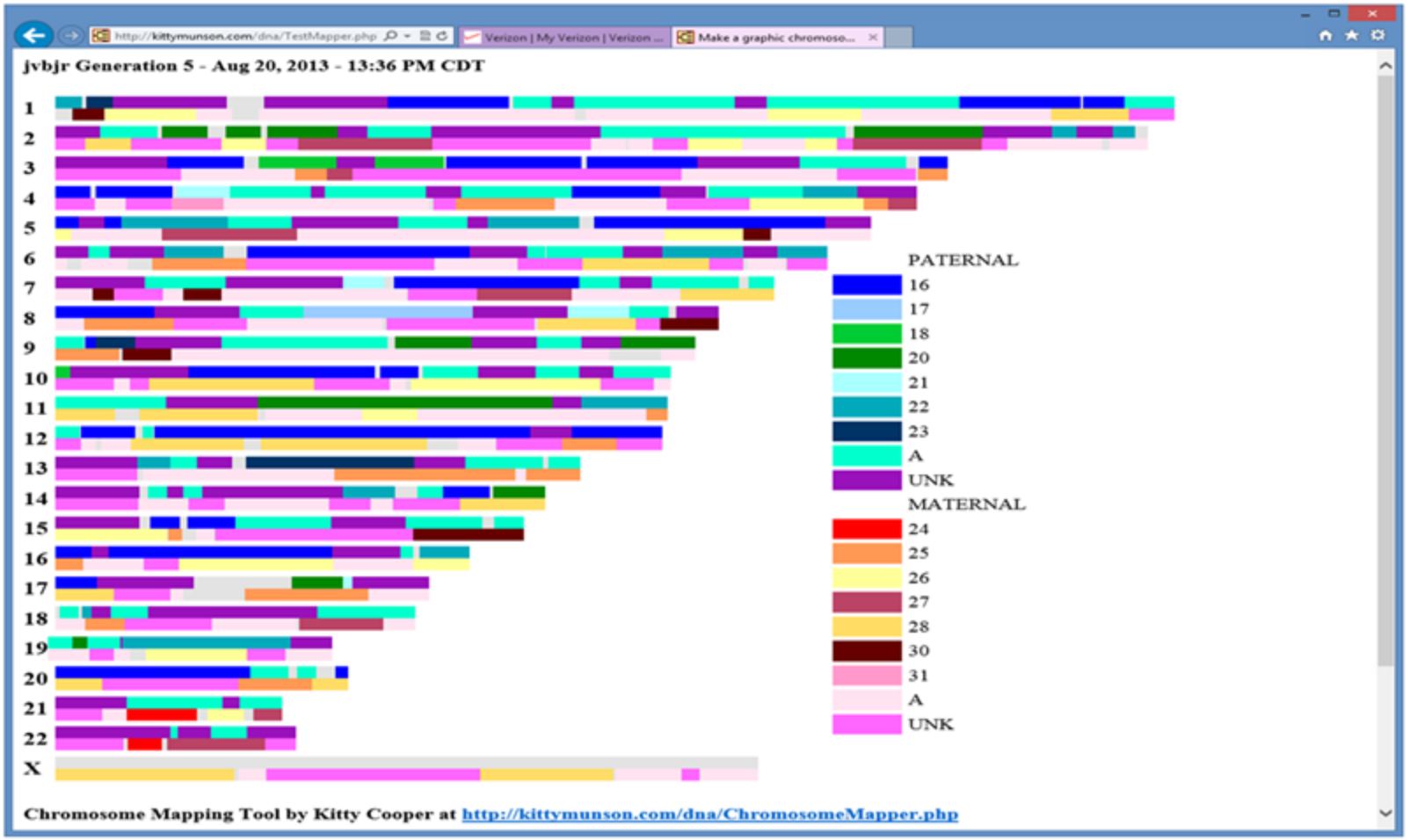
-Individual Match Segments rolled up into TG Segments
-Two overlapping TGs, each with Matches
-Each TG is a part of a different Chromosome 6
-Each TG comes from a different Common Ancestor




jim4bartletts@verizon.net 240-475-7664

# The Final Goal – Chromosome Map of Your Ancestors

## Phase 5 – Chromosome Mapping – about 40%



# Two Key 3rd Party Tools

**GEDmatch**

**Autosomal DNA Segment Analyzer**

# GEDmatch

**Location:** http://v2.gedmatch.com/login1.php

## One to Many Report

| | | | | | Haplogroup | | Autosomal | | | | X-DNA | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Kit Nbr | Type | List | Select | Sex | Mt | Y | Details | Total cM | largest cM | Gen | Details | Total cM | largest cM |
| M181251 | V4 | L | | M | u5 | r1b1b2 | A | 3587.1 | 281.5 | 1 | X | 196 | 196 |
| A710015 | F2 | L | | M | J | R1b1a2 | A | 3585.8 | 214.5 | 1 | X | 186.8 | 97.7 |
| F294401 | F2 | L | | F | U5 | | A | 1843.9 | 126.8 | 1.5 | X | 0 | 0 |
| F294399 | F2 | L | | F | U5 | | A | 1523.3 | 126.6 | 1.6 | X | 0 | 0 |
| F261918 | F2 | L | | M | U5 | I-M223 | A | 1559.7 | 111.5 | 1.6 | X | 67.8 | 67.8 |
| A373877 | F2 | L | | F | | | A | 49.4 | 15.9 | 4.1 | X | 3.7 | 3.7 |
| A413529 | F2 | L | | F | | | A | 46.3 | 12.3 | 4.1 | X | 0 | 0 |
| F296954 | F2 | L | | F | | | A | 41.8 | 13.6 | 4.2 | X | 0 | 0 |
| A962374 | F2 | L | | F | | | A | 44.7 | 13.1 | 4.2 | X | 0 | 0 |
| FB4683 | F2 | L | | F | H7 | | A | 43.9 | 10.8 | 4.2 | X | 0 | 0 |
| F325072 | F2 | L | | F | | | A | 40.2 | 10.7 | 4.2 | X | 0 | 0 |
| F285837 | F2 | L | | M | | I-M253 | A | 40.9 | 10.6 | 4.2 | X | 0 | 0 |
| A973047 | F2 | L | | M | | | A | 35.3 | 21.6 | 4.3 | X | 0 | 0 |
| A615370 | F2 | L | | F | | | A | 36 | 21.2 | 4.3 | X | 0 | 0 |

# GEDmatch

## One to One Report

| | |
|---|---|
| Kit Number 1: | F267073 |
| Kit Number 2: | A373877 |
| Show graphic bar for each Chromosome? | ○ Yes ◉ No |
| For compressed graphic, enter width in pixels ( zero or blank for expanded graphic, default=1000 ) | 1000 |
| SNP count minimum threshold to be considered a matching segment (Leave blank for default value = 700) | |
| Minimum segment cM size to be included in total: (Leave blank for default value = 7) | |

# GEDmatch

## One to One Report

### GEDmatch.Com Autosomal Comparison

Comparing Kit F267073 (*ebmvt) and A373877 (*jmstevens)

Minimum threshold size to be included in total = 700 SNPs
Mismatch-bunching Limit = 350 SNPs
Minimum segment cM to be included in total = 7.0 cM

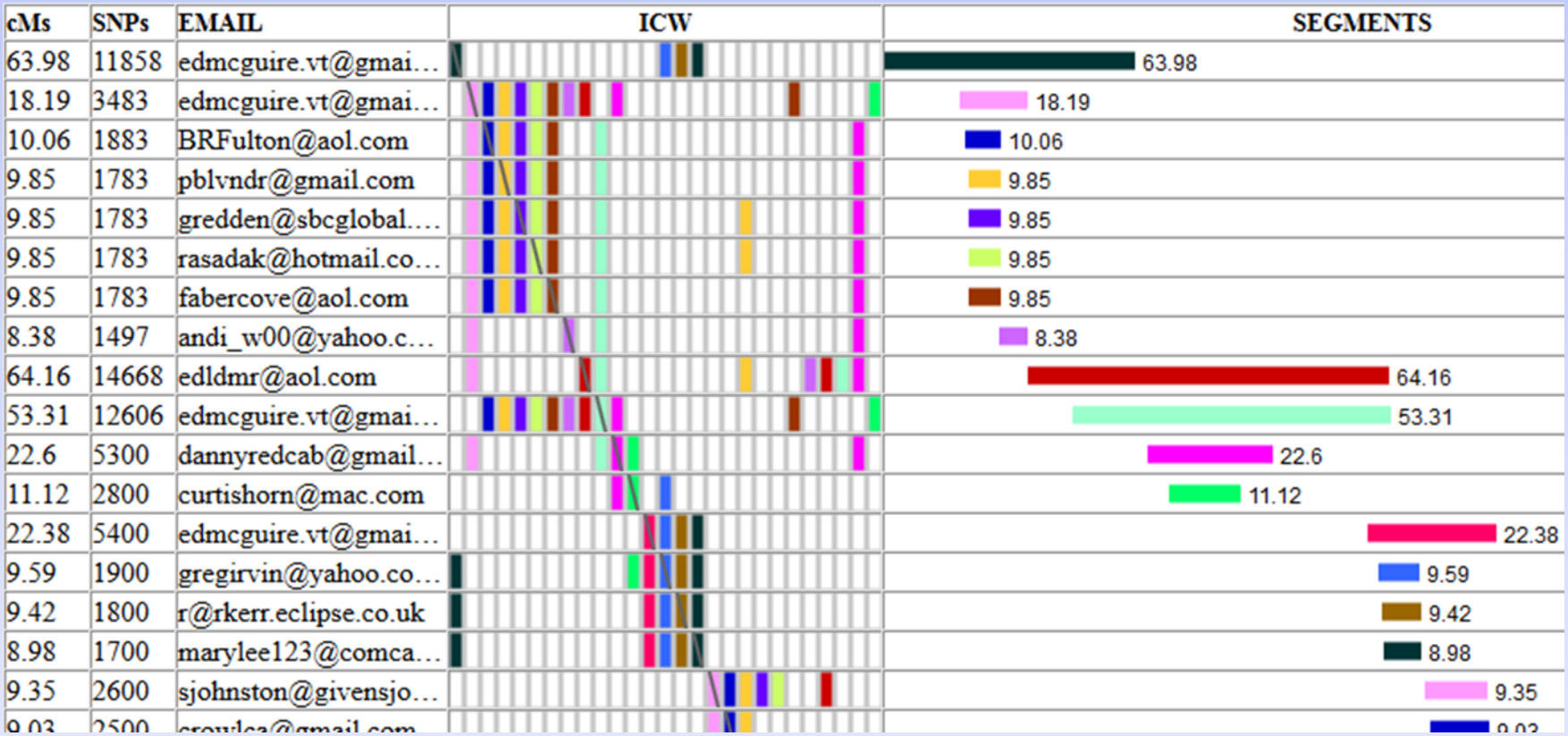
| Chr | Start Location | End Location | Centimorgans (cM) | SNPs |
|---|---|---|---|---|
| 12 | 12063116 | 21813381 | 15.9 | 2992 |

Largest segment = 15.9 cM
Total of segments > 7 cM = 15.9 cM
Estimated number of generations to MRCA = 4.9

Comparison took 0.16551 seconds.

# Autosomal DNA Segment Analyser (ADSA) Tool

**Location:** http://www.dnagedcom.com/



| cMs | SNPs | EMAIL | ICW | SEGMENTS |
|---|---|---|---|---|
| 63.98 | 11858 | edmcguire.vt@gmai… | | 63.98 |
| 18.19 | 3483 | edmcguire.vt@gmai… | | 18.19 |
| 10.06 | 1883 | BRFulton@aol.com | | 10.06 |
| 9.85 | 1783 | pblvndr@gmail.com | | 9.85 |
| 9.85 | 1783 | gredden@sbcglobal.… | | 9.85 |
| 9.85 | 1783 | rasadak@hotmail.co… | | 9.85 |
| 9.85 | 1783 | fabercove@aol.com | | 9.85 |
| 8.38 | 1497 | andi_w00@yahoo.c… | | 8.38 |
| 64.16 | 14668 | edldmr@aol.com | | 64.16 |
| 53.31 | 12606 | edmcguire.vt@gmai… | | 53.31 |
| 22.6 | 5300 | dannyredcab@gmail… | | 22.6 |
| 11.12 | 2800 | curtishorn@mac.com | | 11.12 |
| 22.38 | 5400 | edmcguire.vt@gmai… | | 22.38 |
| 9.59 | 1900 | gregirvin@yahoo.co… | | 9.59 |
| 9.42 | 1800 | r@rkerr.eclipse.co.uk | | 9.42 |
| 8.98 | 1700 | marylee123@comca… | | 8.98 |
| 9.35 | 2600 | sjohnston@givensjo… | | 9.35 |
| 9.03 | 2500 | crowlca@gmail.com | | 9.03 |

# Tuesday, 24 March – DNA Special Interest Group

**(6:30 – 8:00 PM)**

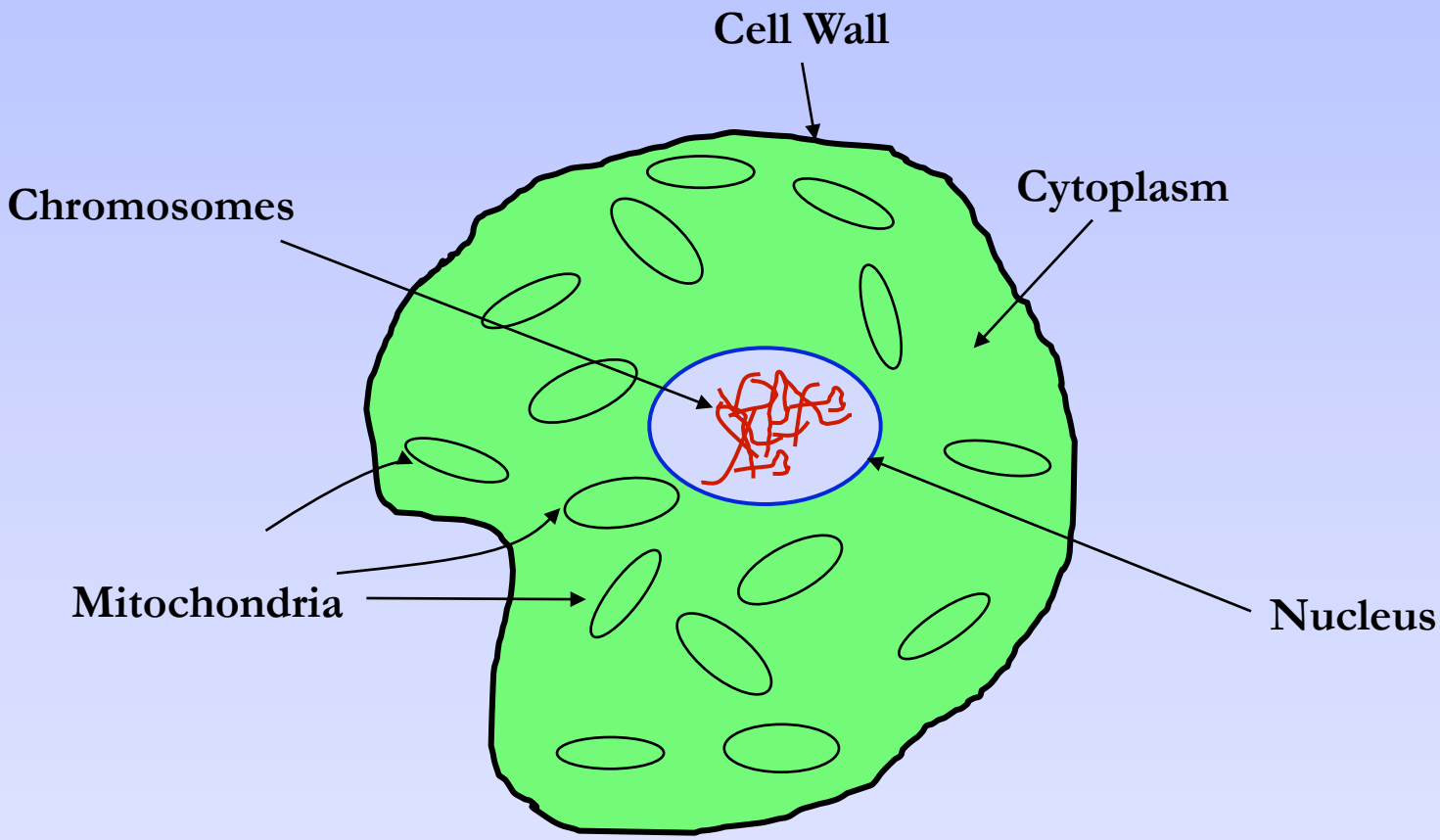
**Layout of GEDmatch tools**

**Where to get instructions for uploading data**

**Demonstrations using the tool**

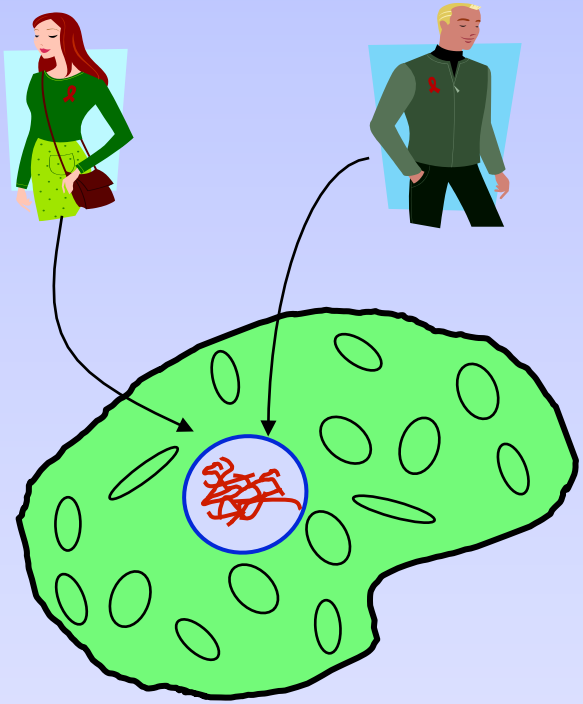
# Thank You

# Any Questions?




Hominid Cell

# Parental Contributions to Autosomal DNA



# Each Cell's 23 Chromosome Pairs

**Karyogram of Human Male Cell**

Source: *Wikipedia.org (en.wikipeida.org/wiki/Karyotype)*

# Variation in the Inheritance of Autosomal DNA

# Random Assortment of Chromosomes

| 1 | 2 | 3 | 4 | 5 |
|---|---|---|---|---|
| M | M | M | M | M |
| D | D | D | D | D |

| 1 | 2 | 3 | 4 | 5 |
|---|---|---|---|---|
| M | M | M | M | M |
| D | D | D | D | D |

Gramma = Adams

Grampa = Jones

Gramma =Meyer

Grampa = Provost

(Simplified example with 5 chromosome pairs instead of full 22 pairs)

# Random Assortment of Chromosomes

| 1 | 2 | 3 | 4 | 5 |
|---|---|---|---|---|
| M | M | M | M | M |
| D | D | D | D | D |

| 1 | 2 | 3 | 4 | 5 |
|---|---|---|---|---|
| M | M | M | M | M |
| D | D | D | D | D |

Gramma = Adams

Grampa = Jones

Gramma =Meyer

Grampa = Provost

| CHR 1 | CHR 2 | CHR 3 | CHR 4 | CHR 5 |
|---|---|---|---|---|
| Meyer | Adams | Meyer | Jones | Provost |
| Jones | Meyer | Adams | Provost | Jones |

(Mom: $2^5 = 32$ possibilities) & (Dad: $2^5 = 32$ possibilities) → 32 x 32 = 1024

# Random Assortment of Chromosomes

| 1 | 2 | 3 | 4 | 5 |
|---|---|---|---|---|
| M | M | M | M | M |
| D | D | D | D | D |

| 1 | 2 | 3 | 4 | 5 |
|---|---|---|---|---|
| M | M | M | M | M |
| D | D | D | D | D |

Gramma = Adams

Grampa = Jones

Gramma =Meyer

Grampa = Provost

| CHR 1 | CHR 2 | CHR 3 | CHR 4 | CHR 5 |
|---|---|---|---|---|
| Meyer | Adams | Meyer | Jones | Provost |
| Jones | Meyer | Adams | Provost | Jones |

$(2^5 = 32 \text{ possibilities})^2$

$(2^{22} = 4M+ \text{ possibilities})^2$

# Autosomal DNA and Recombination

Thomas Hunt Morgan's illustration of crossing over (1916)

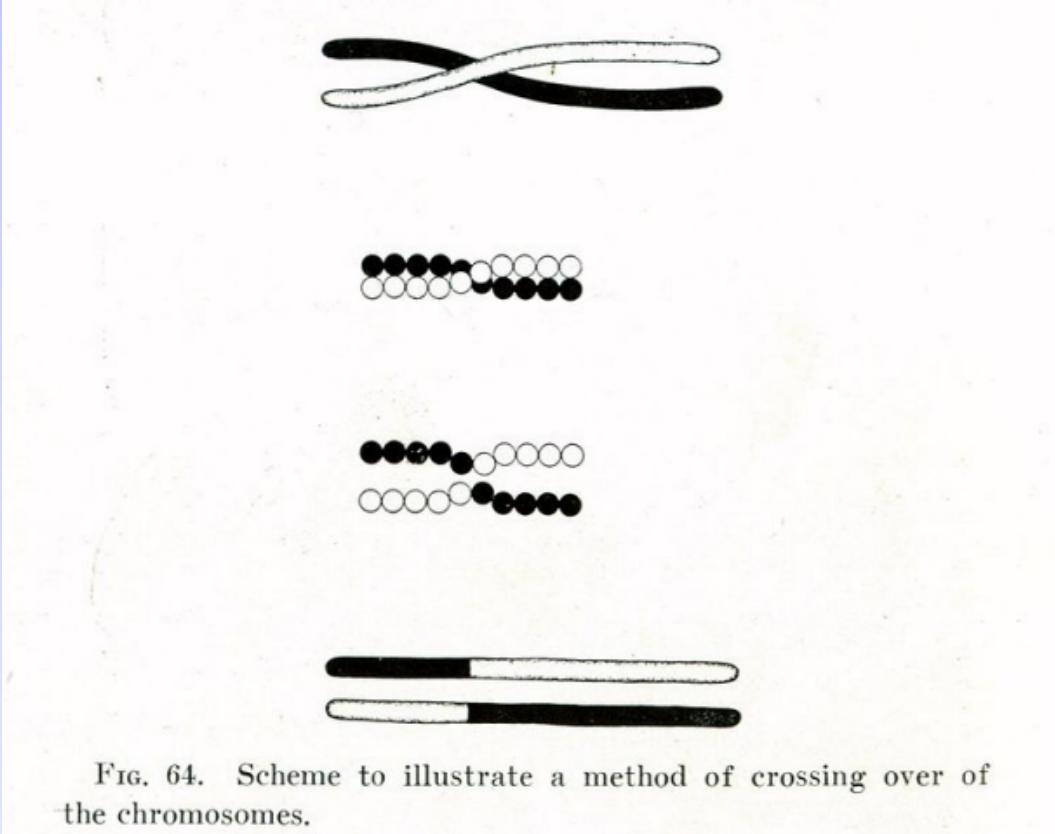


FIG. 64. Scheme to illustrate a method of crossing over of the chromosomes.

http://en.wikipedia.org/wiki/File:Morgan_crossover_1.jpg

# Autosomal DNA and Recombination

Thomas Hunt Morgan's illustration of crossing over (1916)

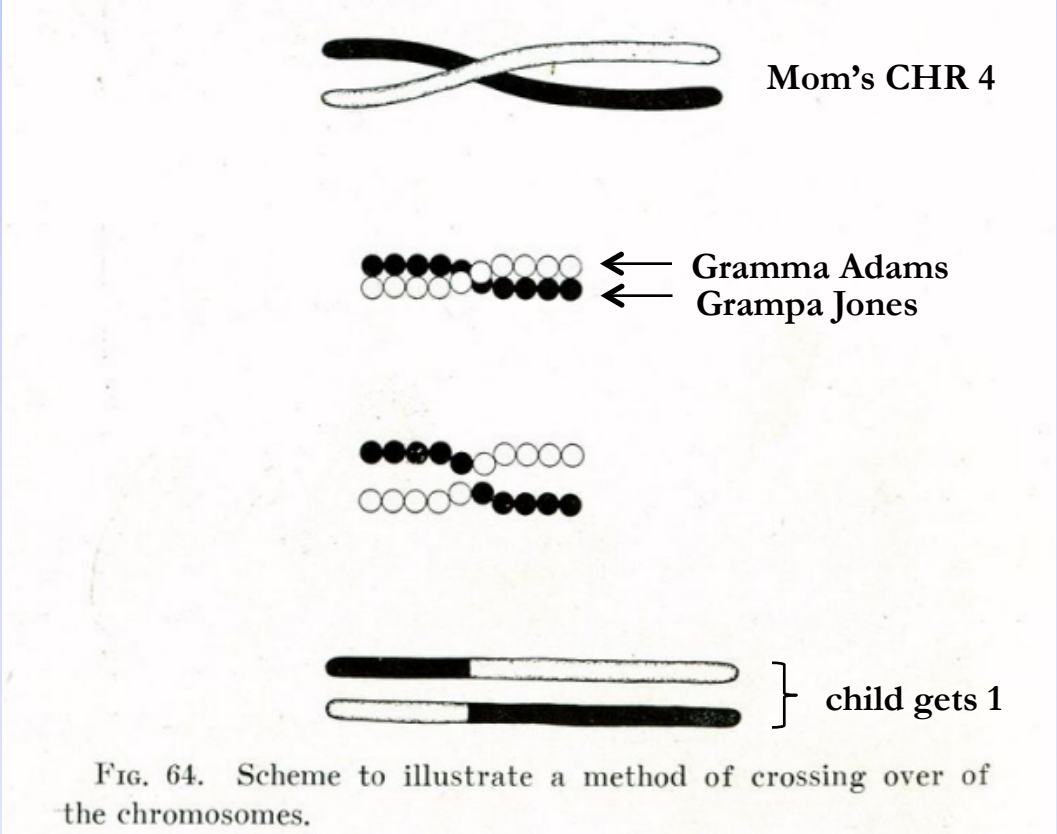



FIG. 64. Scheme to illustrate a method of crossing over of the chromosomes.

http://en.wikipedia.org/wiki/File:Morgan_crossover_1.jpg

# What Do We Inherit?

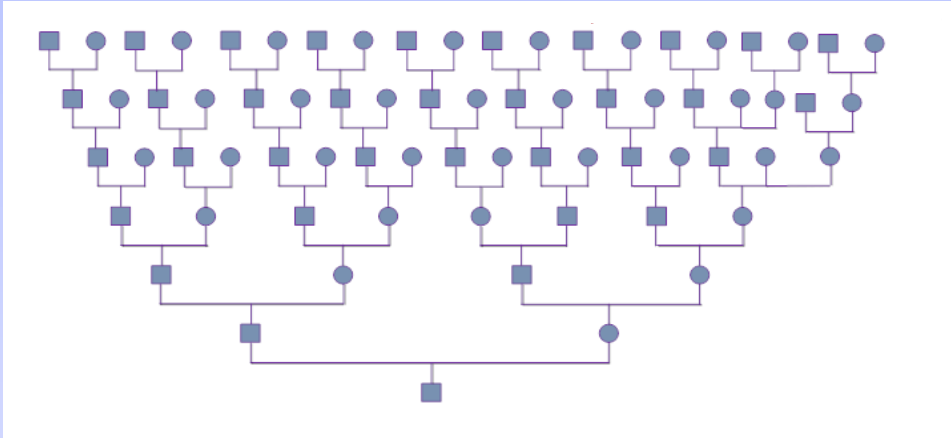
- 2 parents have total of 44 chromsome pairs
- 4 grandparents have total of 88 pairs
- 1 child only has room for 22 pairs

We must have less and less DNA from older ancestors

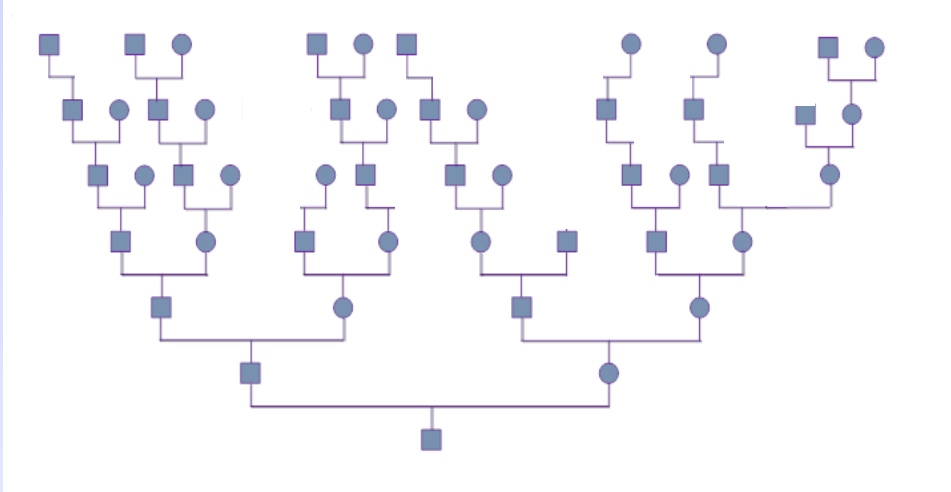
NET: Our oldest ancestors start to disappear from our genetic tree !!

# What Do We Inherit?

Genealogical Tree



Genetic Tree



# What Do We Inherit?

- Parents have total of 44 chromsome pairs (12 billion bases)
- Grandparents have total of 88 pairs (24 billion bases)
- Children only have room for 22 pairs (6 billion bases)

We must have less and less DNA from older ancestors

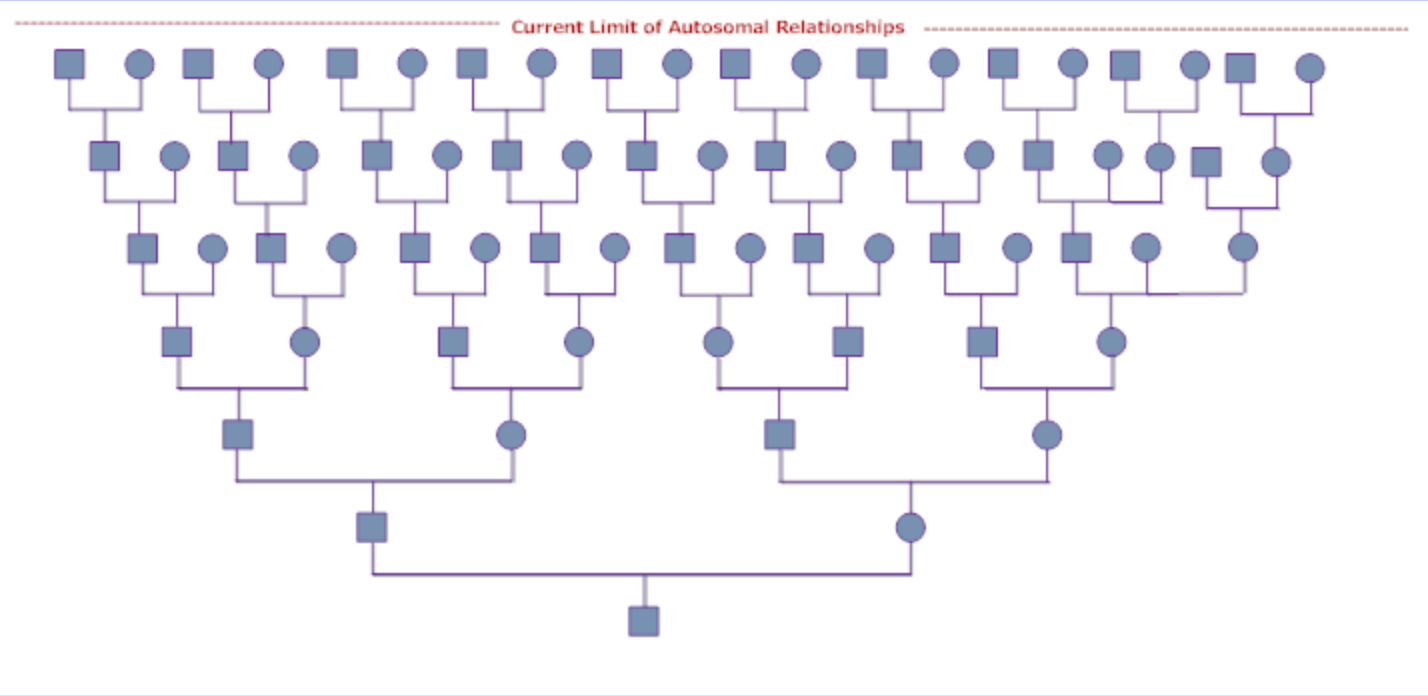
NET: Our oldest ancestors start to disappear from our genetic tree !!

BUT: Due to recombination random pieces from distant ancestors can persist

(i.e. – we occasionally get 21 cM segment from 10$^{th}$ GG parent)

# Autosomal DNA Testing Finds More Relationships

## Limitation Is 5 to 6 Generations



# GEDMatch Table With Anyone Who Uploads Data

| | | | | | | | Haplogroup | | Autosomal | | | | X-DNA | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Kit Nbr | Type | Triangulate | GEDCOM | List | Select | Sex | Mt | Y | Details | Total cM | largest cM | Gen | Details | Total cM | largest cM | Name |
| A710015 | F2 | T | | L | | M | J | R1b1a2 | A | 3585.8 | 214.5 | 1 | X | 186.8 | 97.7 | *mcgvtedw |
| F294401 | F2 | T | | L | | F | U5 | | A | 1843.9 | 126.8 | 1.5 | X | 0 | 0 | *emfct |
| F294399 | F2 | T | | L | | F | U5 | | A | 1523.3 | 126.6 | 1.6 | X | 0 | 0 | *rmsct |
| A373877 | F2 | T | | L | | F | | | A | 49.4 | 15.9 | 4.1 | X | 3.7 | 3.7 | *jmstevens |
| A413529 | F2 | T | | L | | F | | | A | 46.3 | 12.3 | 4.1 | X | 0 | 0 | Mary Jo Hiestand |
| F296954 | F2 | T | | L | | F | | | A | 41.8 | 13.6 | 4.2 | X | 0 | 0 | Erin Elizabeth Rodriguez |
| A962374 | F2 | T | | L | | F | | | A | 44.7 | 13.1 | 4.2 | X | 0 | 0 | G E |
| FB4683 | F2 | T | | L | | F | H7 | | A | 43.9 | 10.8 | 4.2 | X | 0 | 0 | *"Duffy" |
| F325072 | F2 | T | | L | | F | | | A | 40.2 | 10.7 | 4.2 | X | 0 | 0 | *RBailey |
| F285837 | F2 | T | | L | | M | | I-M253 | A | 40.9 | 10.6 | 4.2 | X | 0 | 0 | Dan Matthews |
| A973047 | F2 | T | | L | | M | | | A | 35.3 | 21.6 | 4.3 | X | 0 | 0 | *K.A. through Melissa |
| A615370 | F2 | T | | L | | F | | | A | 36 | 21.2 | 4.3 | X | 0 | 0 | *WendyW |
| F227166 | F2 | T | G | L | | M | | R1b1a2 | A | 37.7 | 13.3 | 4.3 | X | 0 | 0 | *ROBERTS Uncle |
| F31300 | F2 | T | | L | | M | H7 | R-L2 | A | 34.6 | 10.7 | 4.3 | X | 0 | 0 | *Jacques |
| A141470 | F2 | T | | L | | M | | | A | 35.8 | 10.5 | 4.3 | X | 0 | 0 | Kenneth Wood |
| A602490 | F2 | T | | L | | F | | | A | 30.6 | 23.5 | 4.4 | X | 0 | 0 | Alison June Moore |
| M203920 | V3 | T | | L | | F | T2e | | A | 33.1 | 15.9 | 4.4 | X | 3.7 | 3.7 | Julia Stevens |
| M195557 | V3 | T | | L | | F | T2e | | A | 33.1 | 15.9 | 4.4 | X | 3.7 | 3.7 | Julia Stevens |
| F252553 | F2 | T | | L | | M | | | A | 33 | 13 | 4.4 | X | 0 | 0 | phil whitelock |
| F293138 | F2 | T | | L | | U | K | R1b1a2 (R-M269) | A | 30.8 | 12.5 | 4.4 | X | 0 | 0 | *Susan Whalen |
| F103192 | F2 | T | | L | | F | H1am1 | | A | 32 | 10.5 | 4.4 | X | 3.2 | 3.2 | Dora Smith |
| A738433 | F2 | T | | L | | M | H5a1 | R1b1b2a1a2d | A | 29.7 | 23 | 4.5 | X | 0 | 0 | Dave Inbody |
| M070626 | V3 | T | | L | | F | | | A | 27.6 | 21.2 | 4.5 | X | 0 | 0 | *WendyW |

# Autosomal DNA Analyzer (ADSA)

**CHROMOSOME 1**
**34 matching segments**
**Longest is 104.33 cMs**

| MATCH NAME | START | END | cMs | SNPs | EMAIL | ICW | SEGMENTS |
|---|---|---|---|---|---|---|---|
| Eunice McGuire Fapp… | 72017 | 10595681 | 19.2 | 2986 | edldmr@aol.com | | 19.2 |
| Rita McGuire Self | 72017 | 10595681 | 19.2 | 2986 | edmcguire.vt@gmai… | | 19.2 |
| Glen Austin | 72017 | 11839927 | 21.92 | 3375 | edmcguire.vt@gmai… | | 21.92 |
| Eunice McGuire Fapp… | 19695400 | 29684992 | 11.33 | 2600 | edldmr@aol.com | | 11.33 |
| Glen Austin | 28147571 | 61623798 | 36.88 | 8565 | edmcguire.vt@gmai… | | 36.88 |
| Rita McGuire Self | 29685855 | 59716284 | 33.41 | 7665 | edmcguire.vt@gmai… | | 33.41 |
| Jacqueline Tessier Car… | 30017434 | 36632339 | 8.26 | 1800 | jckeller2@gmail.com | | 8.26 |
| Thomas Alexander G… | 63922287 | 70824008 | 7.9 | 1800 | tmrgull@msn.com | | 7.9 |
| Dee Fennell | 67855642 | 80089390 | 9.24 | 2800 | Smarsh34@cinci.rr.… | | 9.24 |
| Robert F. McCoy | 67855642 | 81490003 | 10.72 | 3200 | rfmccoy@verizon.net | | 10.72 |
| Aaron M Summer | 76790866 | 86724394 | 9.49 | 2700 | aaronmsummer@g… | | 9.49 |
| Lynn Leonard | 78384318 | 93047038 | 15.02 | 3797 | lynn@brassringfarm… | | 15.02 |
| Eunice McGuire Fapp… | 94298211 | 149505675 | 29.5 | 8024 | edldmr@aol.com | | 29.5 |
| Glen Austin | 100779165 | 175552623 | 54.43 | 13321 | edmcguire.vt@gmai… | | 54.43 |
| Victor Stanley Dunn | 103128353 | 112374032 | 10.21 | 2400 | victor.dunn@virgini… | | 10.21 |
| Tommy McManus | 103927079 | 110902085 | 7.88 | 1700 | tomarn@warwick.net | | 7.88 |
| Karen Jean Horton | 103927079 | 111711482 | 8.8 | 2000 | egrdn@aol.com | | 8.8 |
| Gail Lynne Lyons | 103927079 | 113537116 | 11.18 | 2600 | rodngail.lyons@yah… | | 11.18 |
| Robert McNichols | 106616587 | 114104489 | 9.6 | 2200 | kay-stanton@cfl.rr.c… | | 9.6 |
| Bruce Murduck | 108087714 | 114399681 | 7.95 | 1900 | murduck@one-nam… | | 7.95 |
| Teresa Jenkins | 112676556 | 148683537 | 10.54 | 2524 | tlj137@yahoo.com | | 10.54 |

# Autosomal DNA Analyzer (ADSA)

| cMs | SNPs | EMAIL | ICW | SEGMENTS |
|---|---|---|---|---|
| 63.98 | 11858 | edmcguire.vt@gmai… | | 63.98 |
| 18.19 | 3483 | edmcguire.vt@gmai… | | 18.19 |
| 10.06 | 1883 | BRFulton@aol.com | | 10.06 |
| 9.85 | 1783 | pblvndr@gmail.com | | 9.85 |
| 9.85 | 1783 | gredden@sbcglobal.… | | 9.85 |
| 9.85 | 1783 | rasadak@hotmail.co… | | 9.85 |
| 9.85 | 1783 | fabercove@aol.com | | 9.85 |
| 8.38 | 1497 | andi_w00@yahoo.c… | | 8.38 |
| 64.16 | 14668 | edldmr@aol.com | | 64.16 |
| 53.31 | 12606 | edmcguire.vt@gmai… | | 53.31 |
| 22.6 | 5300 | dannyredcab@gmail… | | 22.6 |
| 11.12 | 2800 | curtishorn@mac.com | | 11.12 |
| 22.38 | 5400 | edmcguire.vt@gmai… | | 22.38 |
| 9.59 | 1900 | gregirvin@yahoo.co… | | 9.59 |
| 9.42 | 1800 | r@rkerr.eclipse.co.uk | | 9.42 |
| 8.98 | 1700 | marylee123@comca… | | 8.98 |
| 9.35 | 2600 | sjohnston@givensjo… | | 9.35 |
| 9.03 | 2500 | crowlca@gmail.com | | 9.03 |

# Thomas Hunt Morgan's illustration of crossing over (1916)

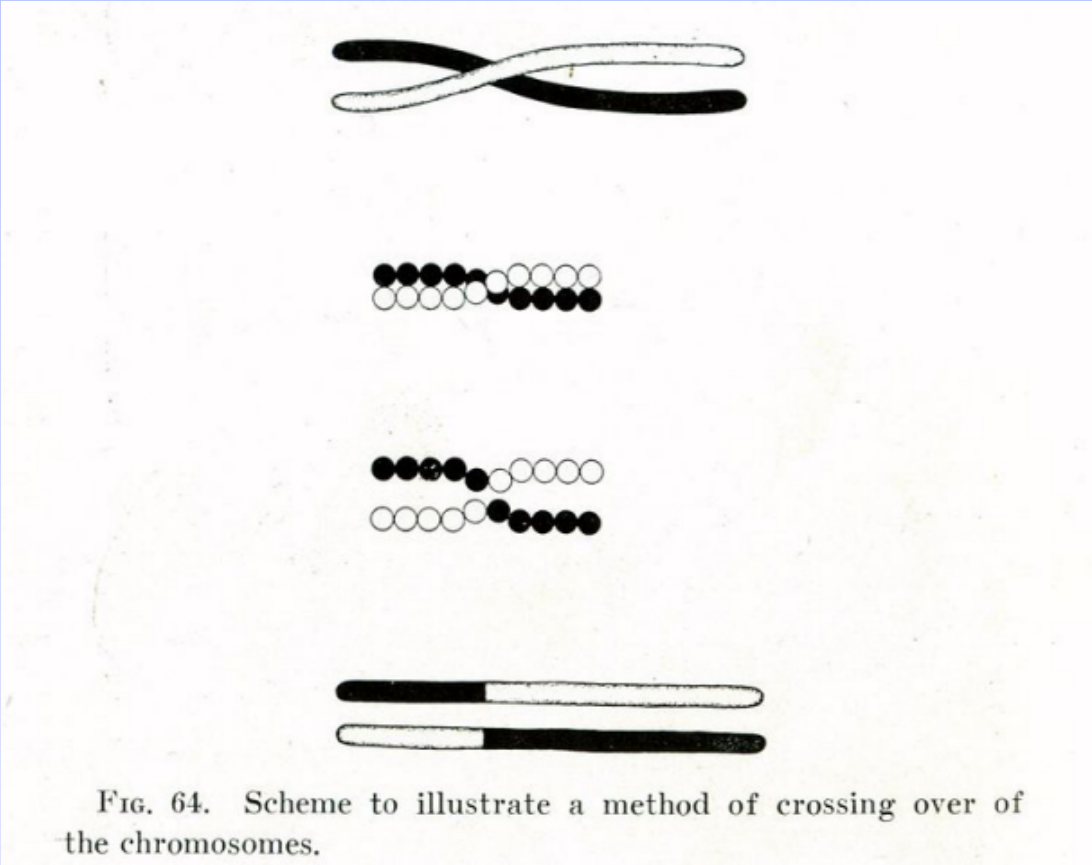


FIG. 64. Scheme to illustrate a method of crossing over of the chromosomes.

Source: Wikipedia.org

http://en.wikipedia.org/wiki/File:Morgan_crossover_1.jpg

# Special Interest Groups

| Interest Group | Week of the Month |
|---|---|
| Scottish | 1st Tuesday (6:30 pm) |
| Quebec Research | 2nd Tuesday (6:30 pm) |
| Irish | 3rd Tuesday (6:30 pm) |
| Genetic Genealogy | 4th Tuesday (6:30 pm) |

# AutosomalDNA Testing Recommentations

My top choice is FamilyTreeDNA (in my opinion)

If looking for African-American cousins & origins – AncestryDNA

If not intending to ever work with segment data - AncestryDNA

If also doing medical testing – 23andMe

If mainly interested in ethnicity percentages – 23andMe

If adoptee / unknown parentage – need to test with all three

If someone in your family tested w/ company A – you might follow lead

# Autosomal Test Results

You can search for those common ancestors in a **bigger** pond!!

ancestryDNA

FamilyTreeDNA
HISTORY UNEARTHED DAILY

23andMe

→ GEDmatch

# GEDMatch Table With Anyone Who Uploads Data

| | | | | | | | Haplogroup | | Autosomal | | | | X-DNA | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Kit Nbr | Type | Triangulate | GEDCOM | List | Select | Sex | Mt | Y | Details | Total cM | largest cM | Gen | Details | Total cM | largest cM | Name |
| A710015 | F2 | T | | L | | M | J | R1b1a2 | A | 3585.8 | 214.5 | 1 | X | 186.8 | 97.7 | *mcgvtedw |
| F294401 | F2 | T | | L | | F | U5 | | A | 1843.9 | 126.8 | 1.5 | X | 0 | 0 | *emfct |
| F294399 | F2 | T | | L | | F | U5 | | A | 1523.3 | 126.6 | 1.6 | X | 0 | 0 | *rmsct |
| A373877 | F2 | T | | L | | F | | | A | 49.4 | 15.9 | 4.1 | X | 3.7 | 3.7 | *jmstevens |
| A413529 | F2 | T | | L | | F | | | A | 46.3 | 12.3 | 4.1 | X | 0 | 0 | Mary Jo Hiestand |
| F296954 | F2 | T | | L | | F | | | A | 41.8 | 13.6 | 4.2 | X | 0 | 0 | Erin Elizabeth Rodriguez |
| A962374 | F2 | T | | L | | F | | | A | 44.7 | 13.1 | 4.2 | X | 0 | 0 | G E |
| FB4683 | F2 | T | | L | | F | H7 | | A | 43.9 | 10.8 | 4.2 | X | 0 | 0 | *"Duffy" |
| F325072 | F2 | T | | L | | F | | | A | 40.2 | 10.7 | 4.2 | X | 0 | 0 | *RBailey |
| F285837 | F2 | T | | L | | M | | I-M253 | A | 40.9 | 10.6 | 4.2 | X | 0 | 0 | Dan Matthews |
| A973047 | F2 | T | | L | | M | | | A | 35.3 | 21.6 | 4.3 | X | 0 | 0 | *K.A. through Melissa |
| A615370 | F2 | T | | L | | F | | | A | 36 | 21.2 | 4.3 | X | 0 | 0 | *WendyW |
| F227166 | F2 | T | G | L | | M | | R1b1a2 | A | 37.7 | 13.3 | 4.3 | X | 0 | 0 | *ROBERTS Uncle |
| F31300 | F2 | T | | L | | M | H7 | R-L2 | A | 34.6 | 10.7 | 4.3 | X | 0 | 0 | *Jacques |
| A141470 | F2 | T | | L | | M | | | A | 35.8 | 10.5 | 4.3 | X | 0 | 0 | Kenneth Wood |
| A602490 | F2 | T | | L | | F | | | A | 30.6 | 23.5 | 4.4 | X | 0 | 0 | Alison June Moore |
| M203920 | V3 | T | | L | | F | T2e | | A | 33.1 | 15.9 | 4.4 | X | 3.7 | 3.7 | Julia Stevens |
| M195557 | V3 | T | | L | | F | T2e | | A | 33.1 | 15.9 | 4.4 | X | 3.7 | 3.7 | Julia Stevens |
| F252553 | F2 | T | | L | | M | | | A | 33 | 13 | 4.4 | X | 0 | 0 | phil whitelock |
| F293138 | F2 | T | | L | | U | K | R1b1a2 (R-M269) | A | 30.8 | 12.5 | 4.4 | X | 0 | 0 | *Susan Whalen |
| F103192 | F2 | T | | L | | F | H1am1 | | A | 32 | 10.5 | 4.4 | X | 3.2 | 3.2 | Dora Smith |
| A738433 | F2 | T | | L | | M | H5a1 | R1b1b2a1a2d | A | 29.7 | 23 | 4.5 | X | 0 | 0 | Dave Inbody |
| M070626 | V3 | T | | L | | F | | | A | 27.6 | 21.2 | 4.5 | X | 0 | 0 | *WendyW |

# Genetic Genealogy At Our Library

## 4th Tuesday is 'DNA Night' for members

- DNA forum for discussions, questions and answers
- A focus on tools, tips and deeper understanding of the technology

"We're Here To Help"

# Don't Forget!

- Use our online forum on DNA testing (in Members Only area)
- Best books on genetic genealogy on sale here
- NEW: DNA testing laminated guides (6 topics)
- Big selection of other genealogy books & laminate guides

  - we do take credit cards & cash & checks

- Memberships ($30)

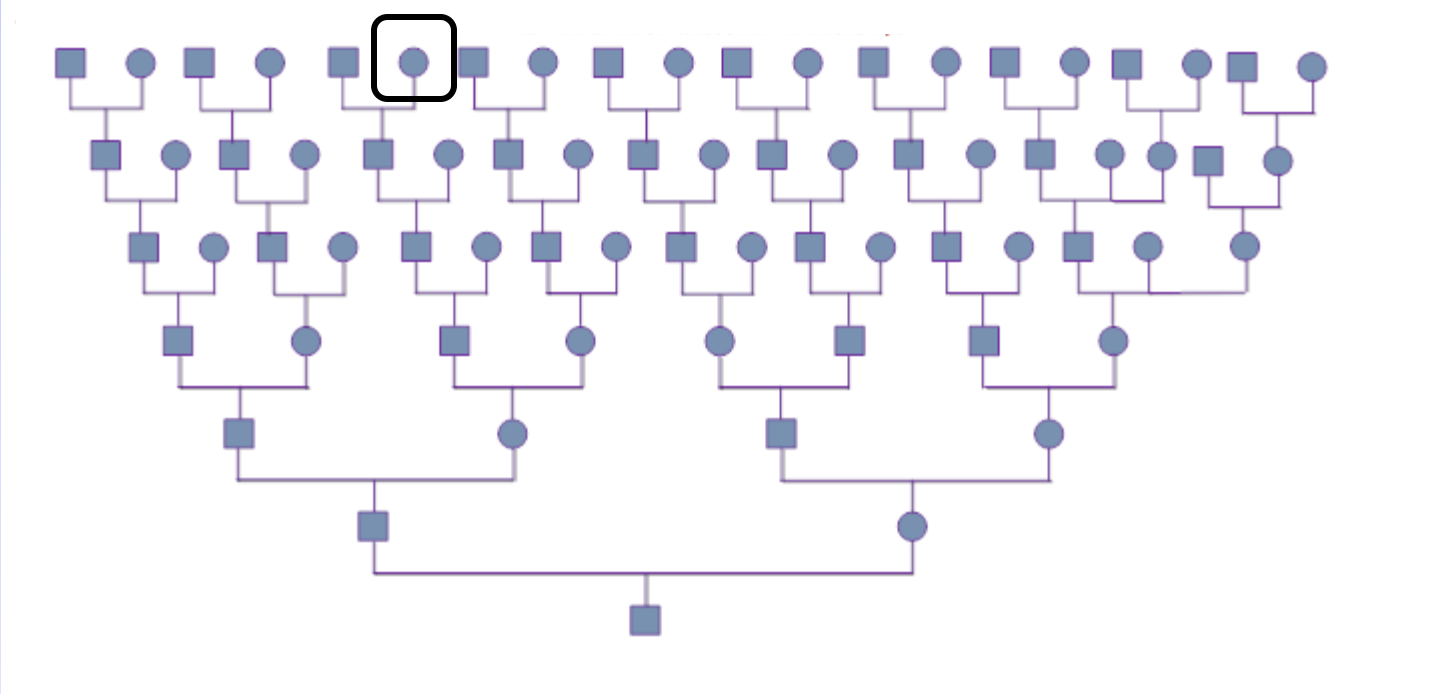
# Thank You!

# Questions?

# How Do Our DNA Tests & Genealogies Work Together ?

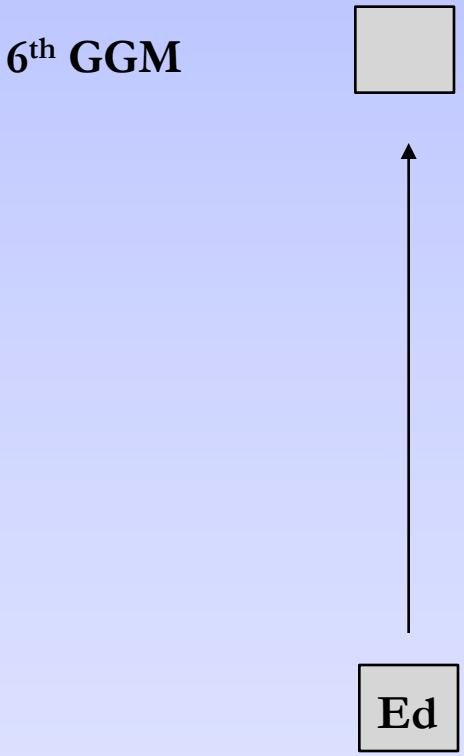
# How Your DNA Tests & Genealogies Work Together

**Hundreds of Ancestors with Thousands of Living Descendants**



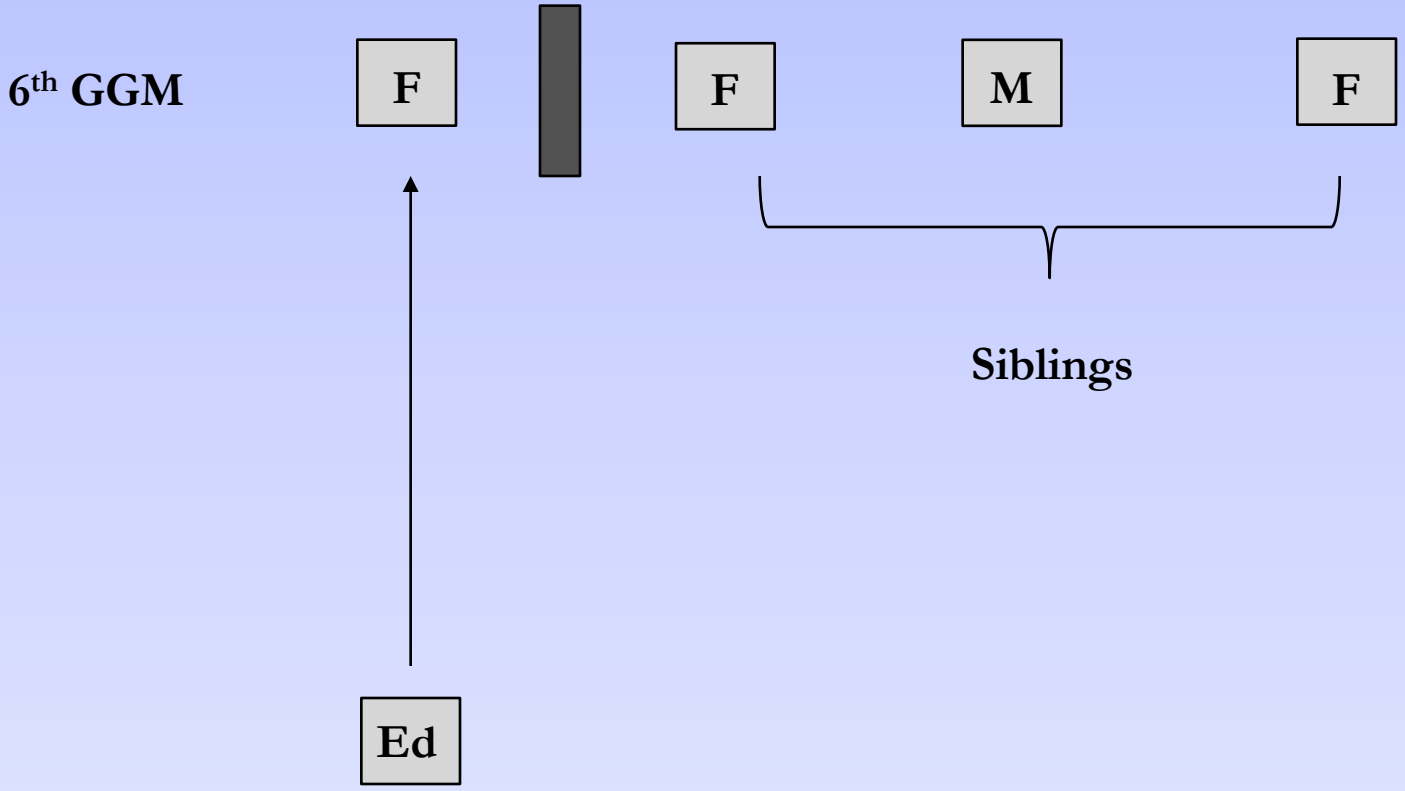
**Traditional Genealogy**

# How Your DNA Tests & Genealogies Work Together

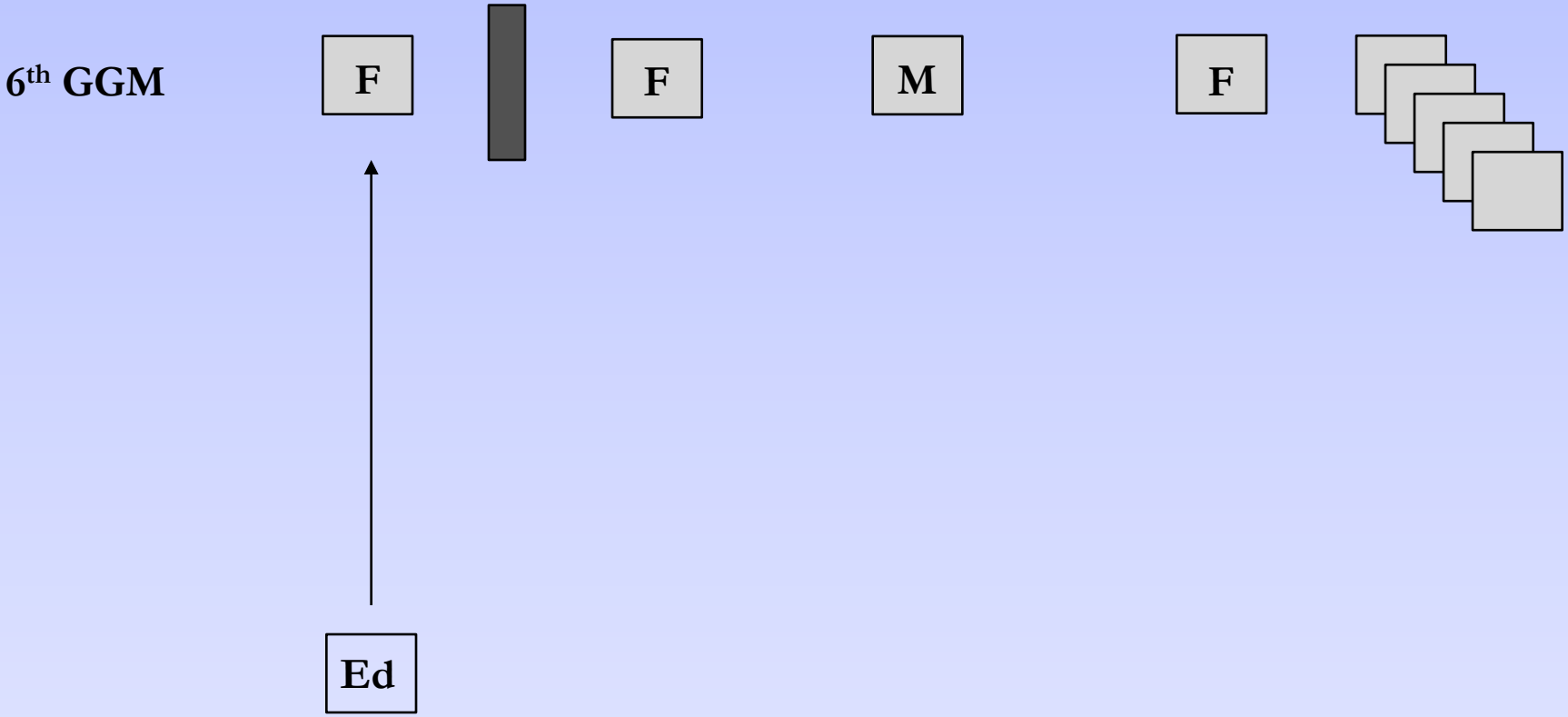



Traditional Genealogy

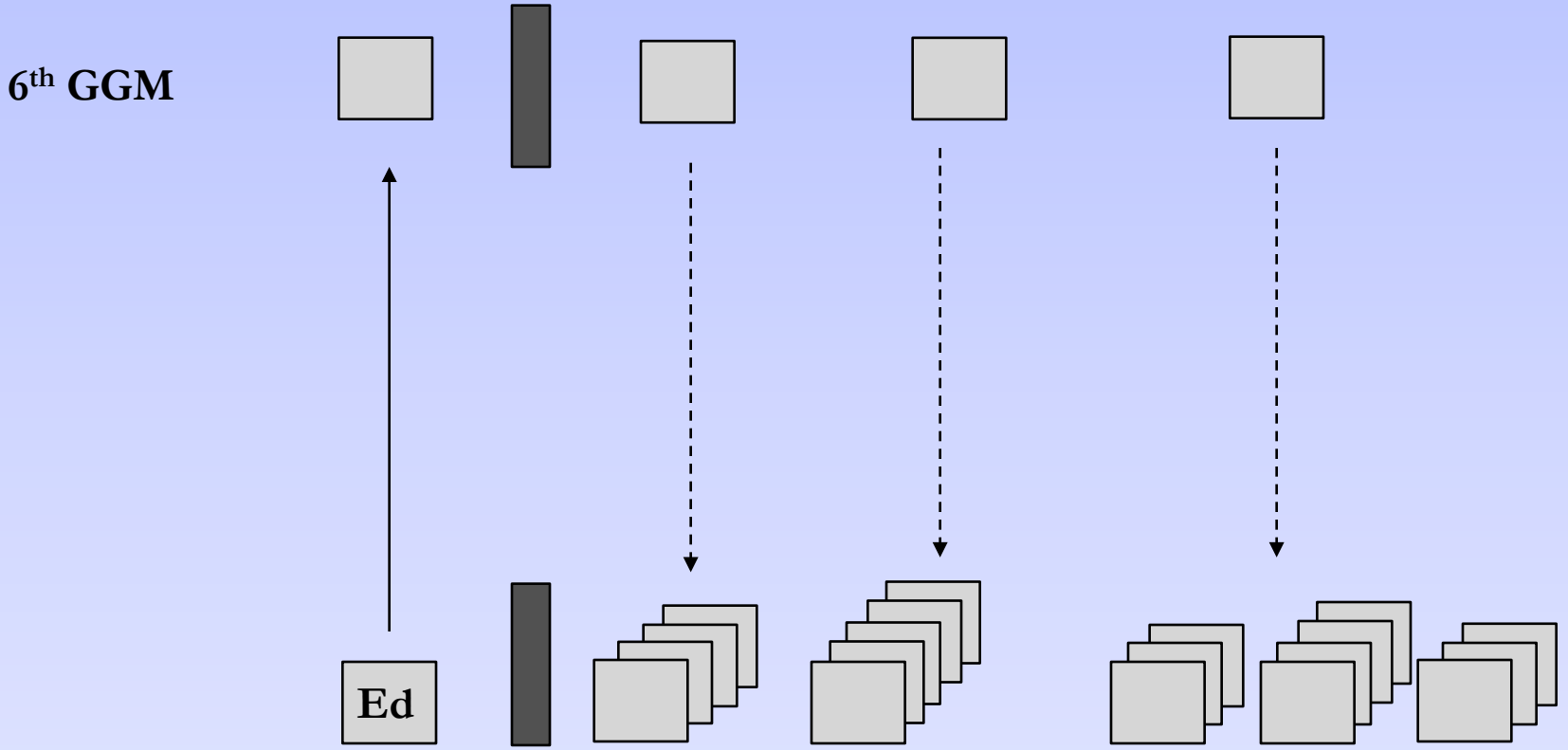
# How Your DNA Tests & Genealogies Work Together



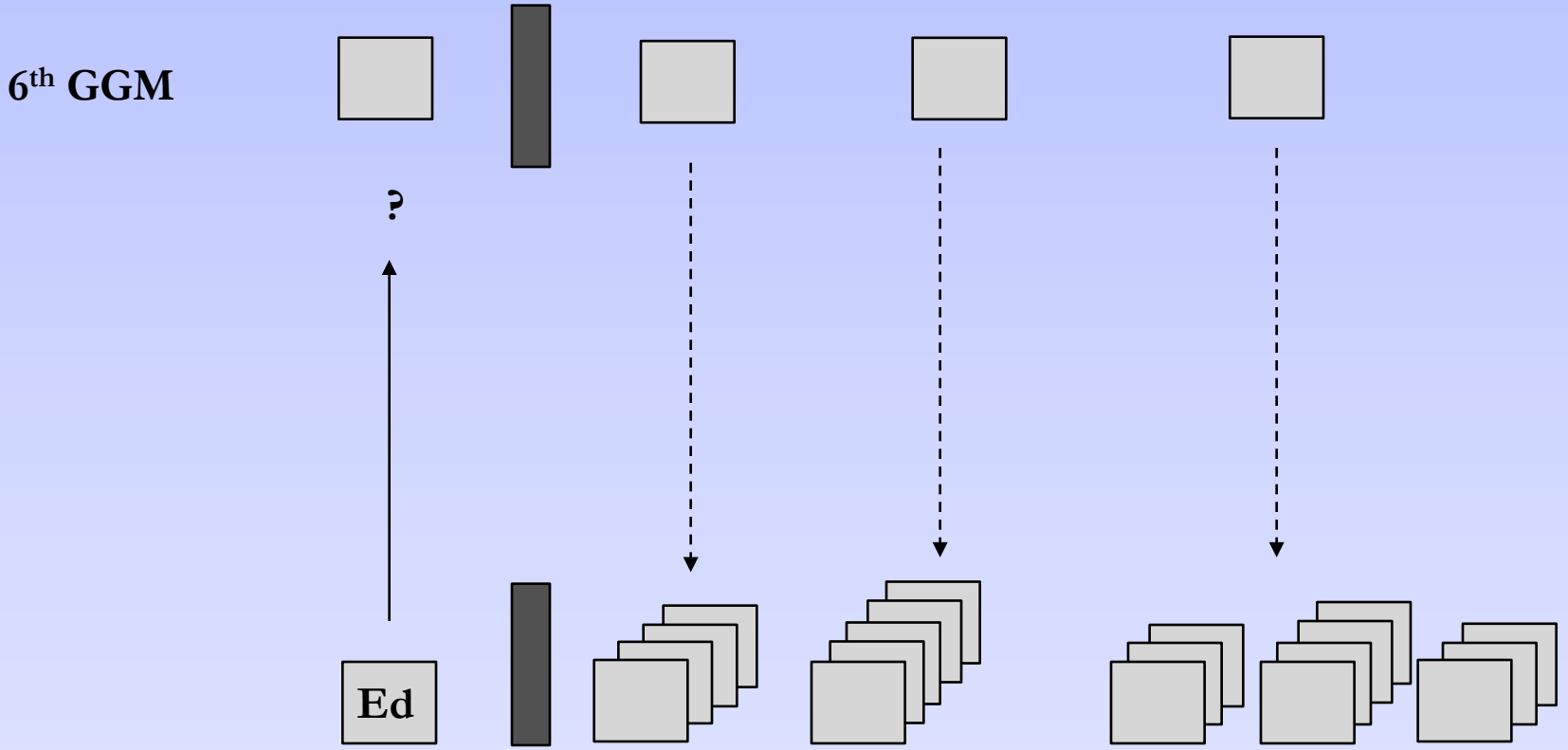
# How Your DNA Tests & Genealogies Work Together



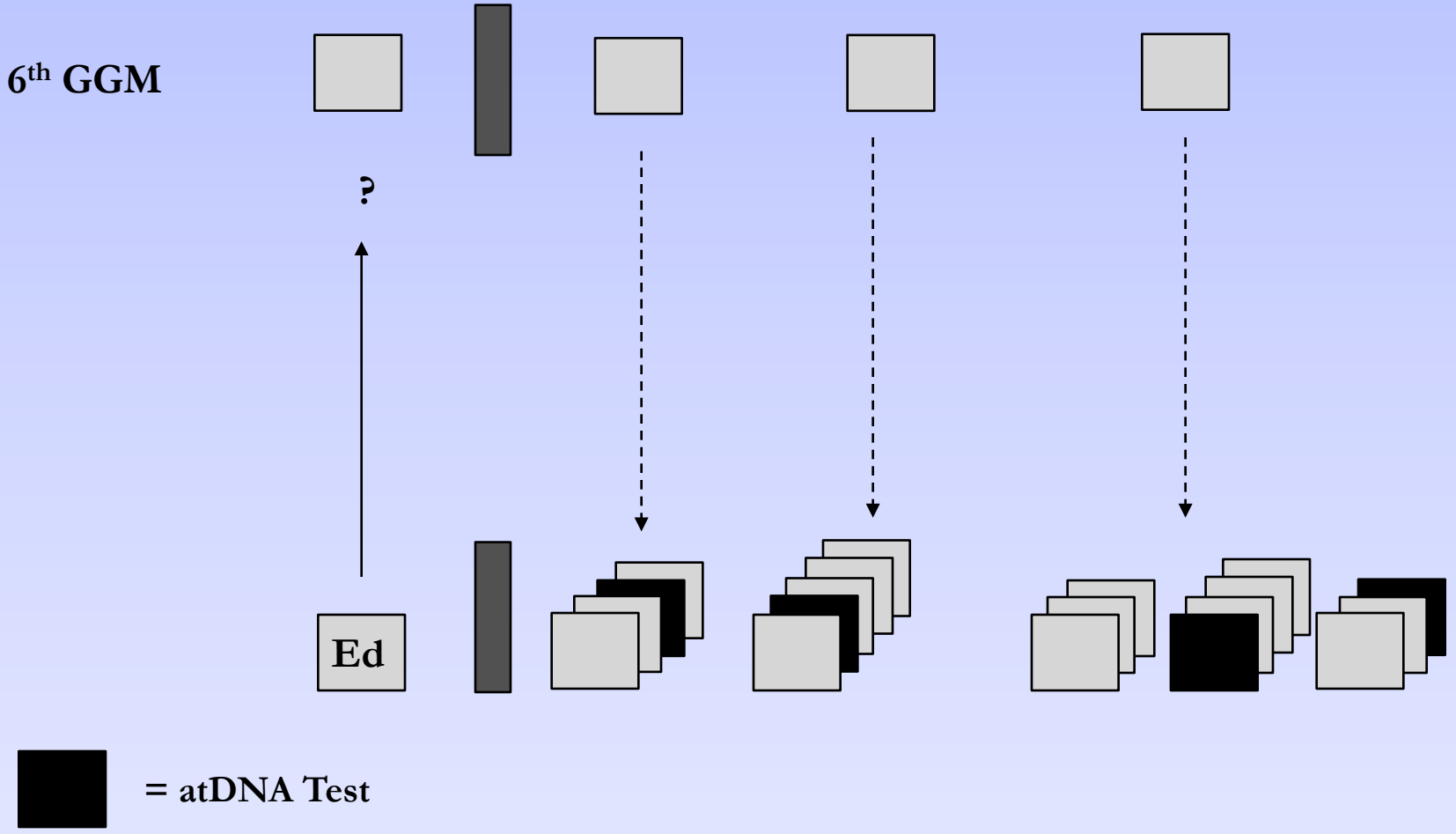
# How Your DNA Tests & Genealogies Work Together



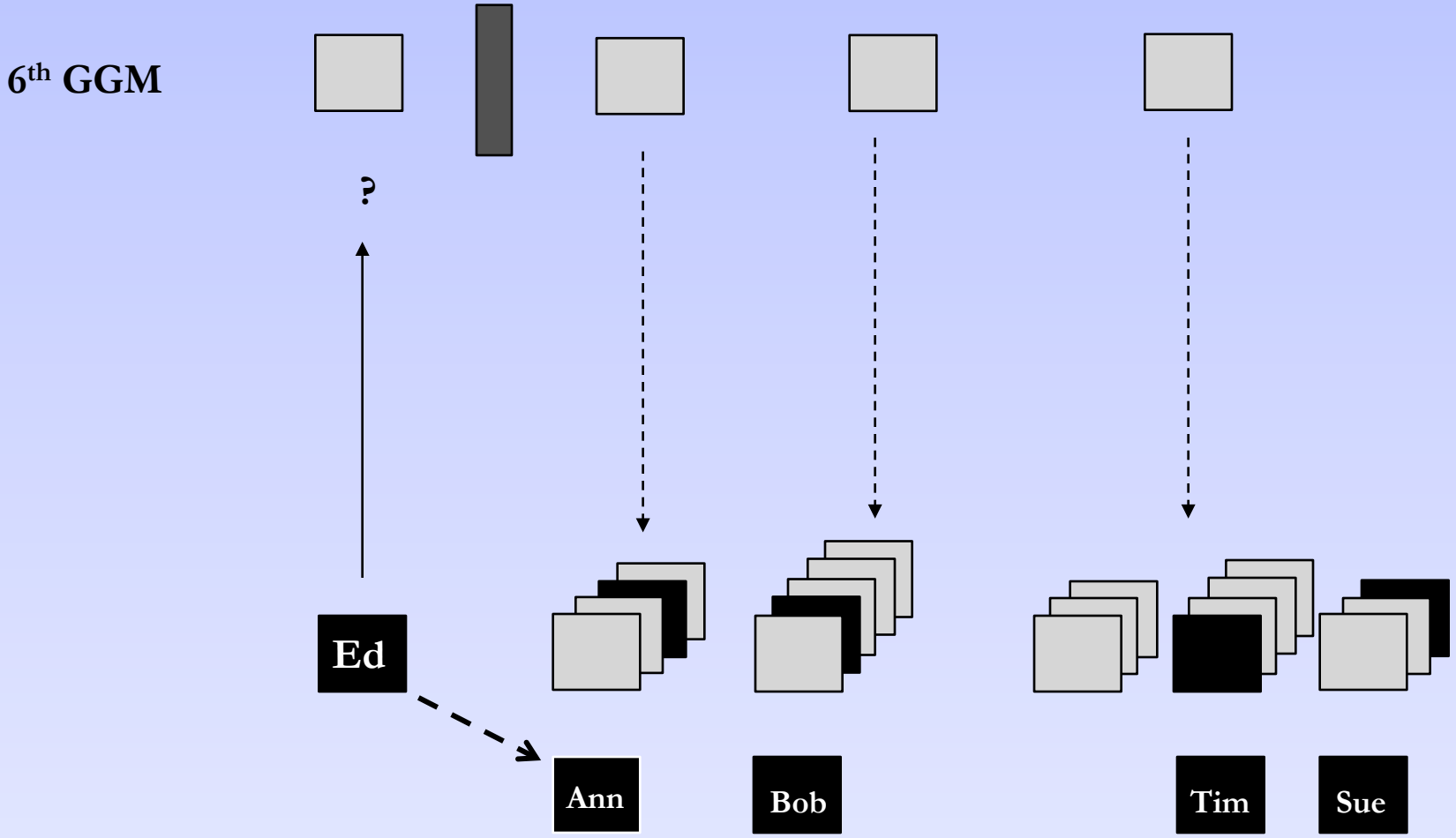
# Genealogy – it's all about finding family



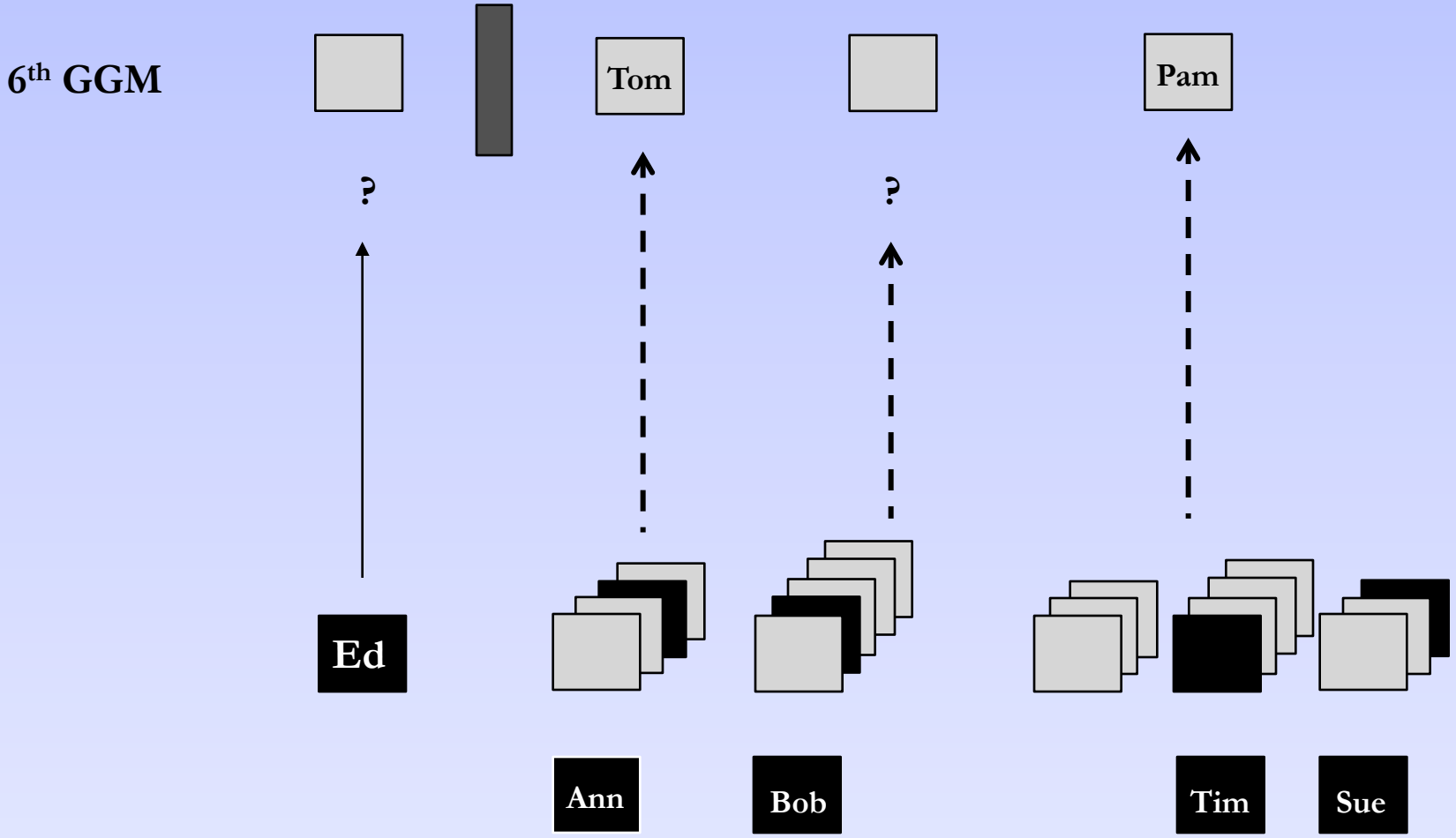
# Genealogy – it's all about finding family



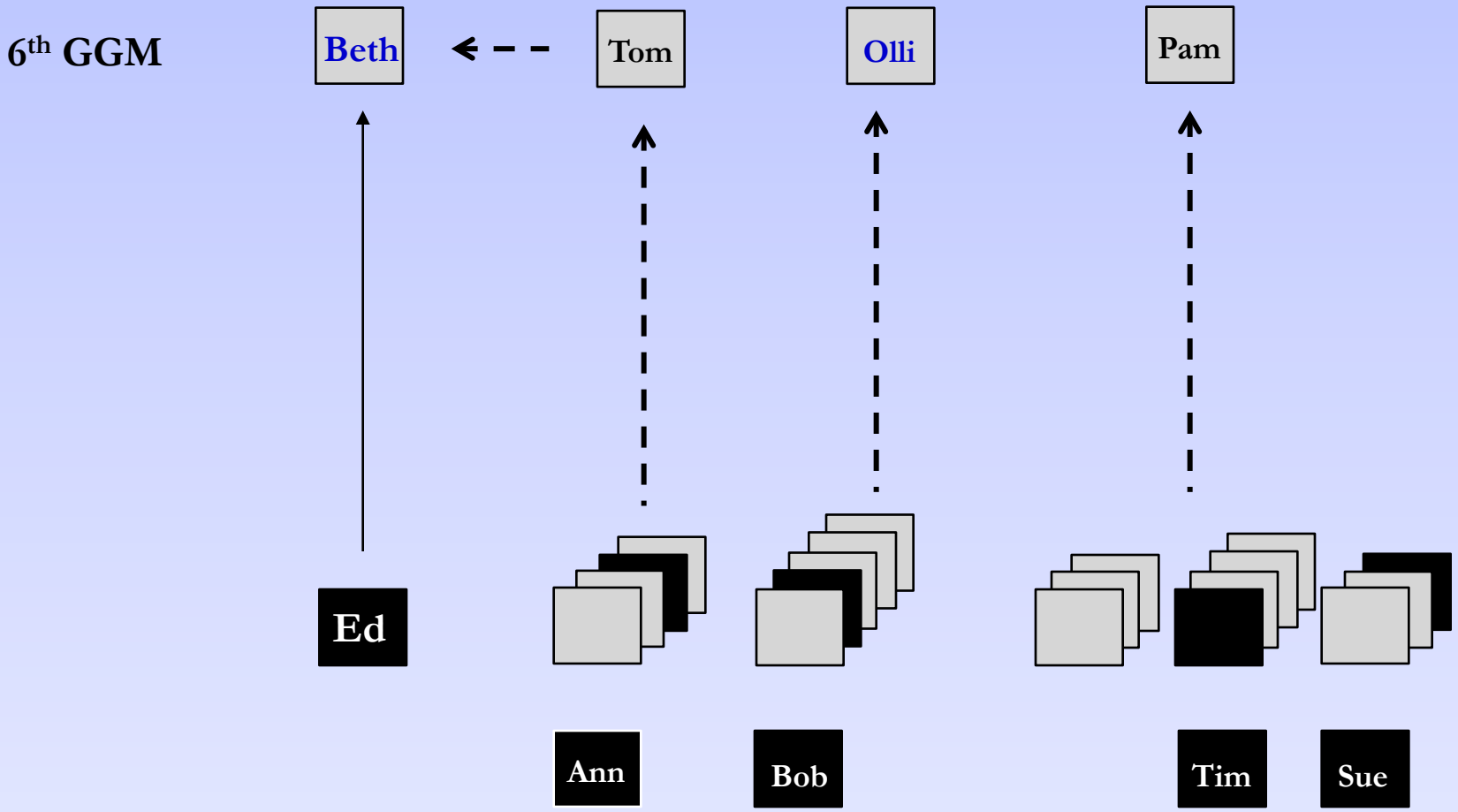
# Genealogy – it's all about finding family



# Genealogy – it's all about finding family



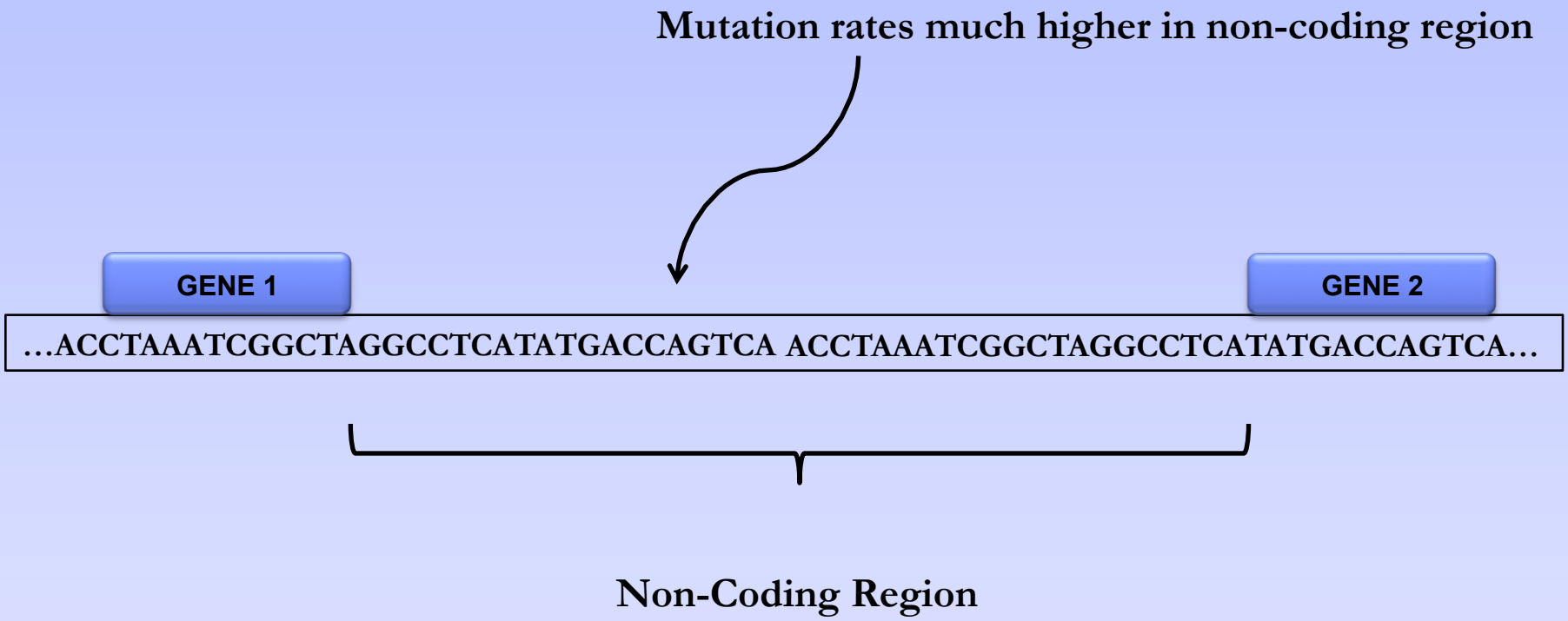
# Genealogy – it's all about finding family

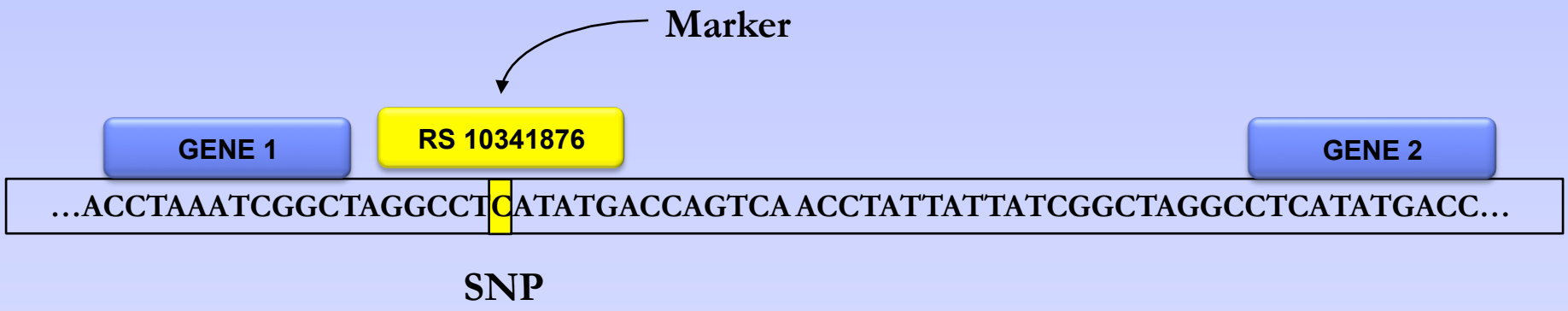


Humans have about 20,000 genes

Genes comprise 1.5% of our DNA


Non-Coding Region


Mutation rates much higher in non-coding region
GENE 1
GENE 2
…ACCTAAATCGGCTAGGCCTCATATGACCAGTCA ACCTAAATCGGCTAGGCCTCATATGACCAGTCA…
Non-Coding Region




A ‘marker’ is a location where we already know mutations have occurred in the past.

# FT-DNA Matches Page

**Ed McGuire** <edmcguire.vt@gmail.com> Nov 4 (11 days ago)

to ddoyel

Dear David:

I recently obtained results from Family Tree DNA and found that I share about 60 cM of DNA with you, placing us possibly in the range of 2d to 4th cousins. I was hoping to compare surnames and ancestral origins if you were willing to do that.

My surnames are with my data on the Family Tree DNA website. My eight great-grandparents' origins are as follows:

McGuire: County Limerick, Ireland
Roche: County Kilkenny, Ireland
O'Donnell: County Donegal, Ireland
Lehouillier: Batiscan, Champlain County, Quebec
Austin: Hampshire, England
Lynn: Northumberland, England
Hodges: Northumberland, England
Pasbach: Nassau, Germany

Sincerely,