

# DNA Testing for Genealogy

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Mar 3, 2022

Bob Butler

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# DNA Tests for Genealogy

- now routine, and can be very effective

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- DNA Basics
- Autosomal DNA Tests
- Y chromosome Tests
- Mitochondrial Tests
- Segment Analysis
- Comparison of Testing Companies

# Human Cell DNA

## Nuclear and Mitochondrial



# Chomosomes and Base Pairs

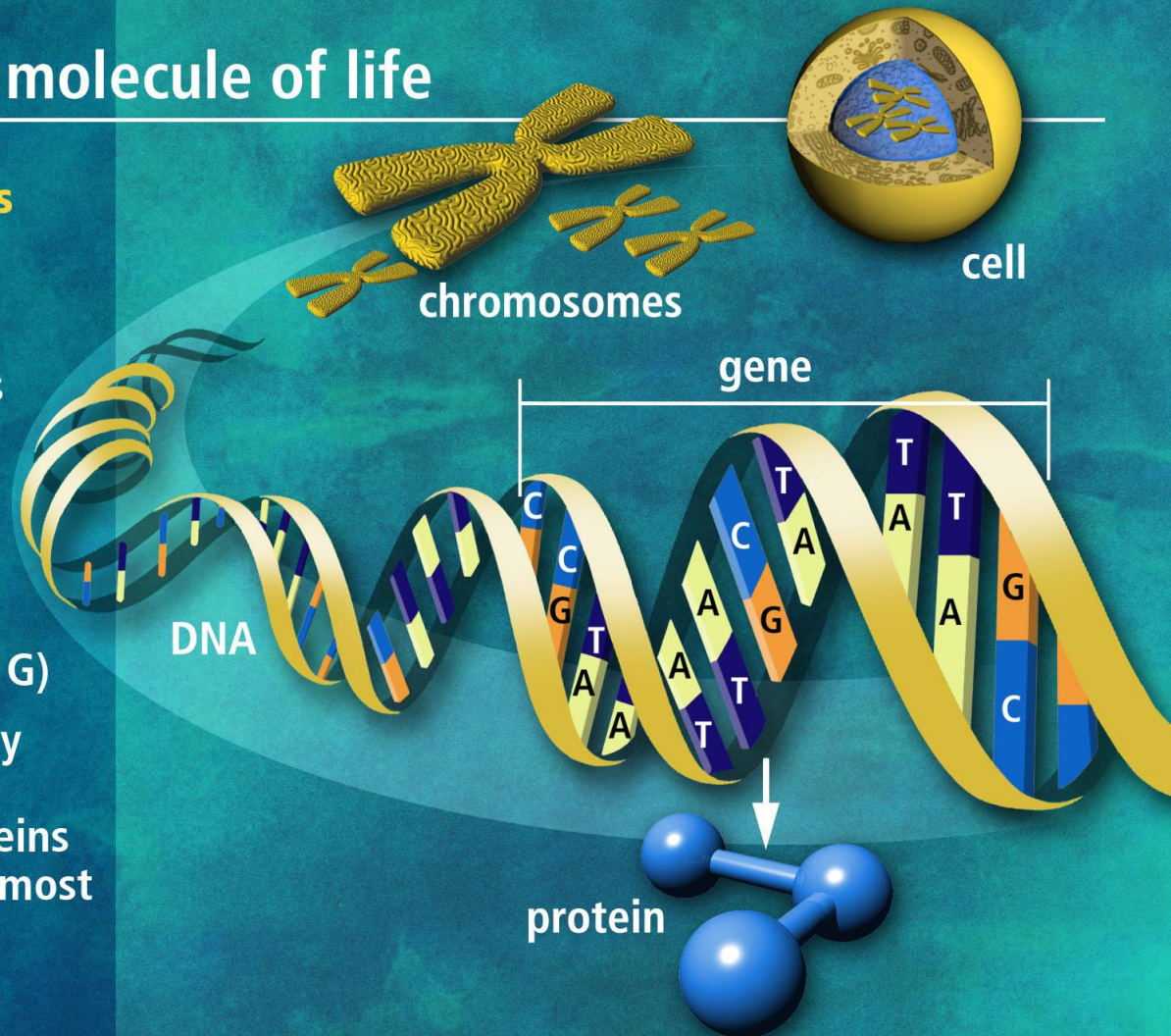
## Double Helix with Bases A,T,C,G

### **DNA** the molecule of life

#### Trillions of cells

Each cell:

- 46 human chromosomes
- 2 meters of DNA
- 3 billion DNA subunits (the bases: A, T, C, G)
- Approximately 30,000 genes code for proteins that perform most life functions



# Autosomal DNA Measurements

## SNPs (pronounced SNIPS)

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- Base pairs = Nucleotide pairs
  - » 3 billion for each set of 23 chromosomes
- Single Nucleotide Polymorphisms (SNPs)
  - » 10 million for each set of 23 chromosomes
  - » 0.33% of genome
- SNPs Measured for Genealogy Purposes
  - » 600 to 960 thousand for each set of 23 chromosomes
  - » 6 to 9.6% of SNPs.

# Sample Raw DNA Data

Both chromosomes measured at the same time.

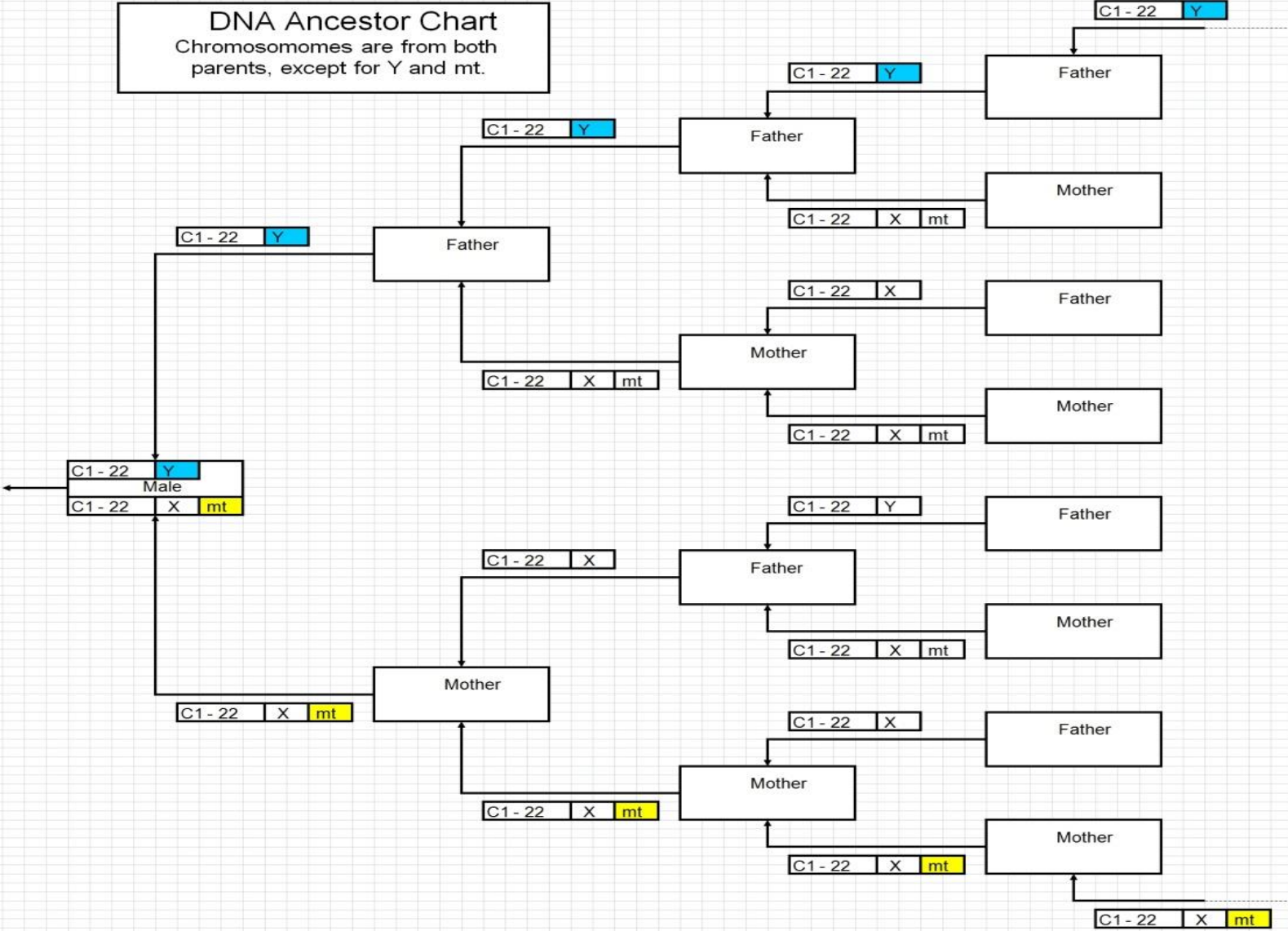
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```
# This data file generated by 23andMe at: Sat Jun 29 13:46:20 2013
# Each line corresponds to a single SNP. For each SNP, we provide its identifier
# (an rsid or an internal id), its location on the reference human genome, and the
# genotype call oriented with respect to the plus strand on the human reference sequence.
#
```

# rsid	chromosome	position	genotype
rs4477212	1	82154	AA
rs3094315	1	752566	AG
rs3131972	1	752721	AG
Rs12124819	1	776546	AG
Rs11240777	1	798959	AG
rs6681049	1	800007	CC
rs4970383	1	838555	AC

.... 960,000 rows of data. .... 24 MB

**DNA Ancestor Chart**  
 Chromosomes are from both parents, except for Y and mt.



# Autosomal DNA Tests

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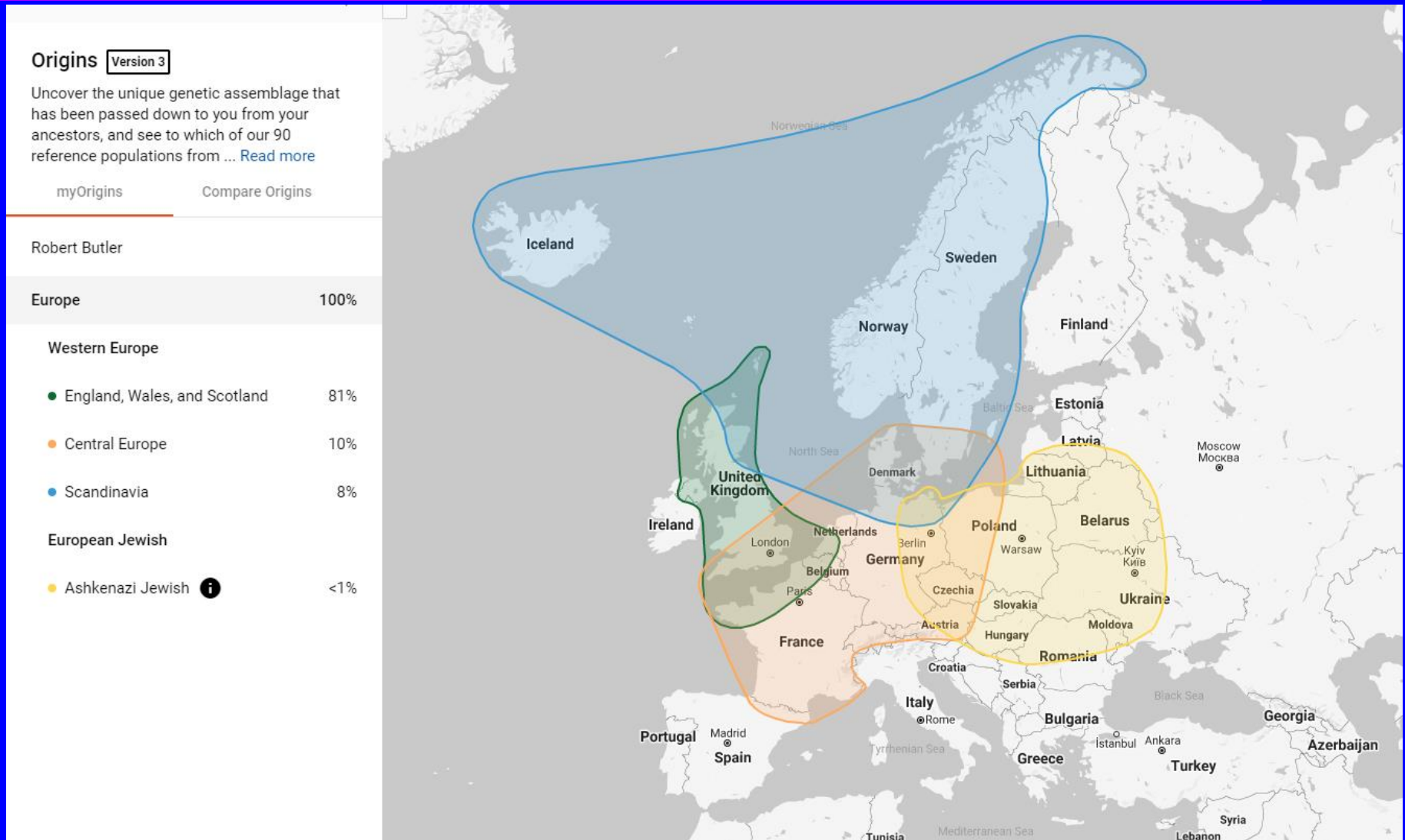
- Ethnicity Estimates – Conversation Piece
  - Deep Ancestry
  - Indefinite Conclusions
- DNA Matches – Practical Genealogy
  - Definite Matches with 3<sup>rd</sup> or 4<sup>th</sup> Cousins or closer
  - Identification of Common Ancestors Possible



# Autosomal Ethnicity Estimates

## Family Tree DNA

## Jan 2022



# Autosomal Ethnicity Estimates

Living DNA

More UK Detail



# Autosomal Ethnicity Estimates





- same person, different companies      Jan 2022

	Great Great Grandparents	
	Number	%
English	11	68.8
Scottish	2	12.5
Welsh	0	0
English Welsh & Scottish	13	81.3
Irish	2	12.5
Irish, Scottish & Welsh	4	25.0
Great Britain & Ireland	15	93.8
Northwest & Central Europe	1	6.3
German & Franch		
Scandinavian		
South & East Europe		
European Jewish		
<b>Total</b>	<b>16</b>	<b>100</b>

# Autosomal Ethnicity Estimates

- same person, 4 companies

Jan 2022

	Great Great Grandparents		 23andMe		 FamilyTreeDNA		 ancestryDNA			 MyHeritageDNA
	Number	%	2019	2021 & 2022	2019	2021 & 2022	2019	2021	2022	2019 - 2022
English	11	68.8					87	54	46	11.4
Scottish	2	12.5						30	39	0
Welsh	0	0						0	0	
English Welsh & Scottish	13	81.3				81		84	85	11.4
Irish	2	12.5				0		11	10	0
Irish, Scottish & Welsh	4	25.0					13	41	49	0
Great Britain & Ireland	15	93.8	67.5	81.3	69	81	100	95	95	11.4
Northwest & Central Europe	1	6.3	19.6	7.2	17	10.0	....	with English	....	88.6
German & Franch			7.5	2.5						
Scandinavian			3.7	7.5		8		5 Sweden	5 Swe+Den	0
South & East Europe			1.6	1.2	11					0
European Jewish						< 1				0
<b>Total</b>	<b>16</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>97</b>	<b>99</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>

# Marketplace - CBC

## Marketplace

## DNA Ancestry Tests

R.E. Butler

Following is a set of averages of the ethnicity estimates presented Jan 18.

Jan 19, 2019

Reported Areas	Expected	23&Me		Ancestry		FTDNA		My Heritage		Living DNA	
		Charlsie/Carly	Charlsie/Carly	Charlsie/Carly	Charlsie/Carly	Charlsie/Carly	Charlsie/Carly	Charlsie/Carly	Charlsie/Carly	Charlsie/Carly	Charlsie/Carly
Italian		38	37	27	29			3	3	40	24
Southeast Europe						43	40				
Iberian						6	8				
Europe South										4	3
Balkan & Greek		15	14	23	23			80	81		
<b>Total Southern Europe</b>	<b>Sicily</b>	<b>52</b>	<b>51</b>	<b>50</b>	<b>52</b>	<b>49</b>	<b>48</b>	<b>83</b>	<b>84</b>	<b>44</b>	<b>27</b>
Eastern European		28	25			36	35			3	2
Eastern Europe & Russia				39	38						
Broadly European		3	13							7	2
Northeast Europe										41	47
<b>Total East &amp; NE Europe</b>	<b>Ukraine</b>	<b>31</b>	<b>38</b>	<b>39</b>	<b>38</b>	<b>36</b>	<b>35</b>	<b>0</b>	<b>0</b>	<b>50</b>	<b>51</b>
North & West Europe								13	14	2	16
Baltic				9	9						
French&German		3									
Middle East						13	14	4	3		
Others		13	12	2	1	2	3			3	6
<b>Total</b>		<b>99</b>	<b>101</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>100</b>	<b>101</b>	<b>100</b>	<b>100</b>

# Autosomal DNA Tests

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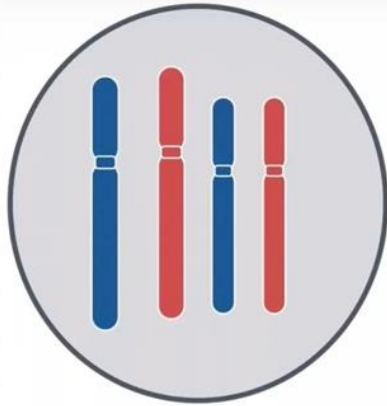
- DNA Matches – Practical Genealogy
  - Definite Matches with 3<sup>rd</sup> or 4<sup>th</sup> Cousins or closer
  - Identification of Common Ancestors Possible

# Autosomal DNA Inheritance

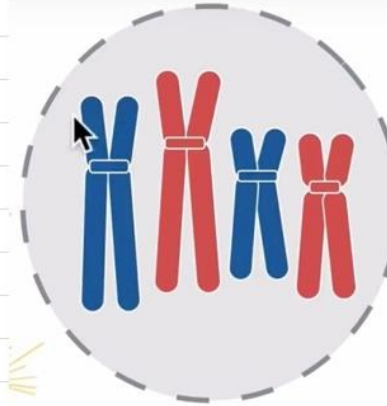
## Meiosis – Formation of Sperm & Egg

<https://www.youtube.com/watch?v=16enC385R0w>

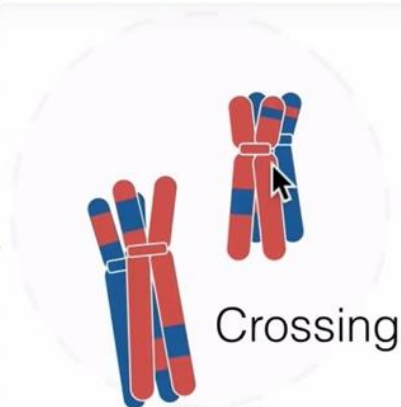
A. Two Copies of Each Chromosome



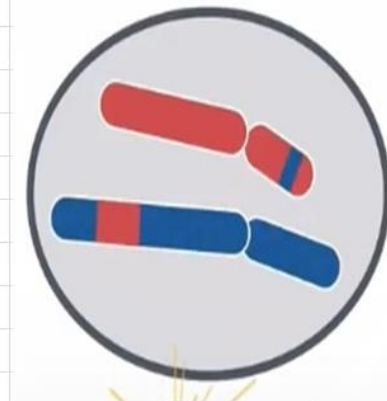
B. Chromosomes Duplicated



C. Chromosome Crossover

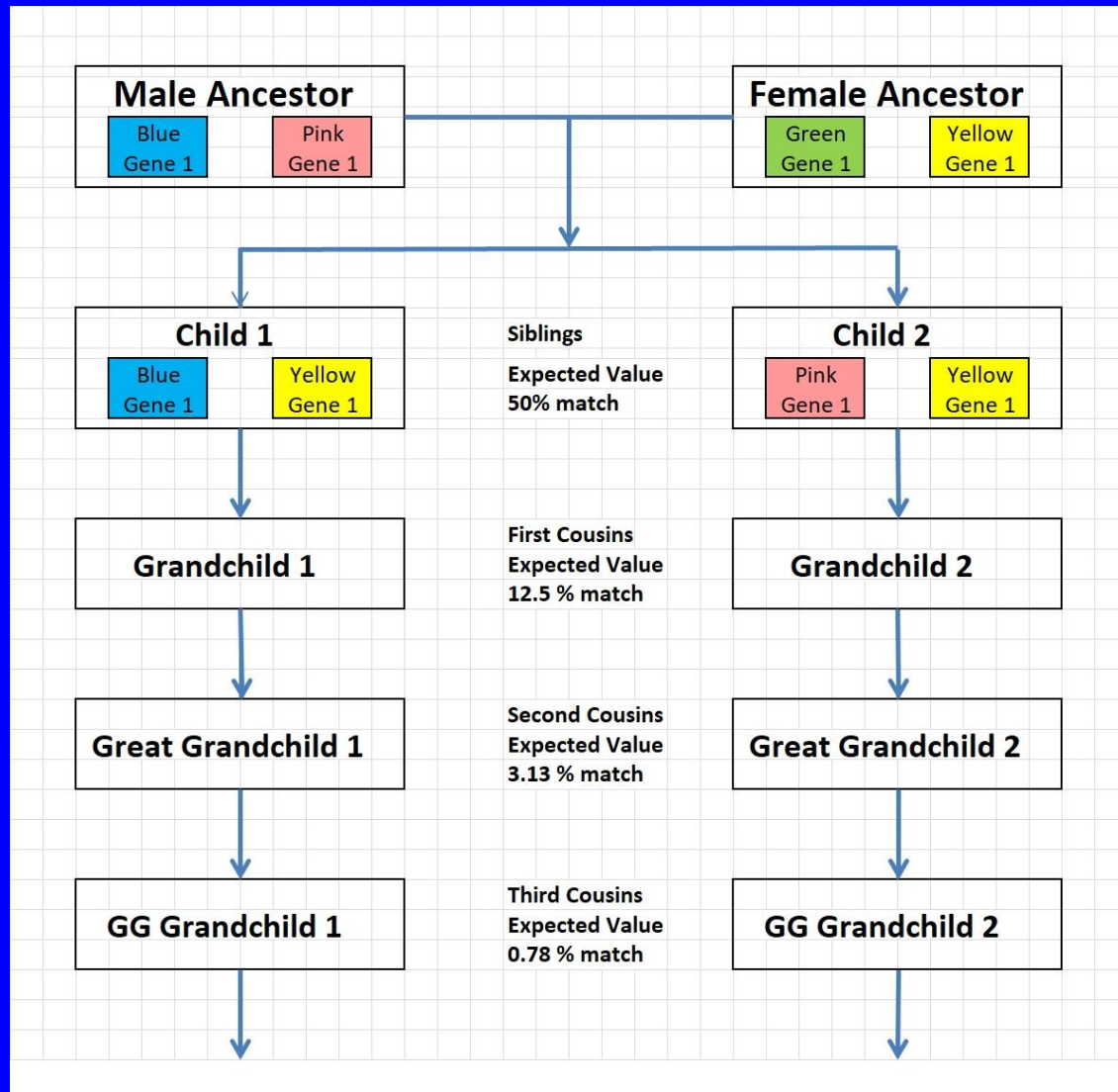


D. One of Four Sperm



# Autosomal DNA Inheritance

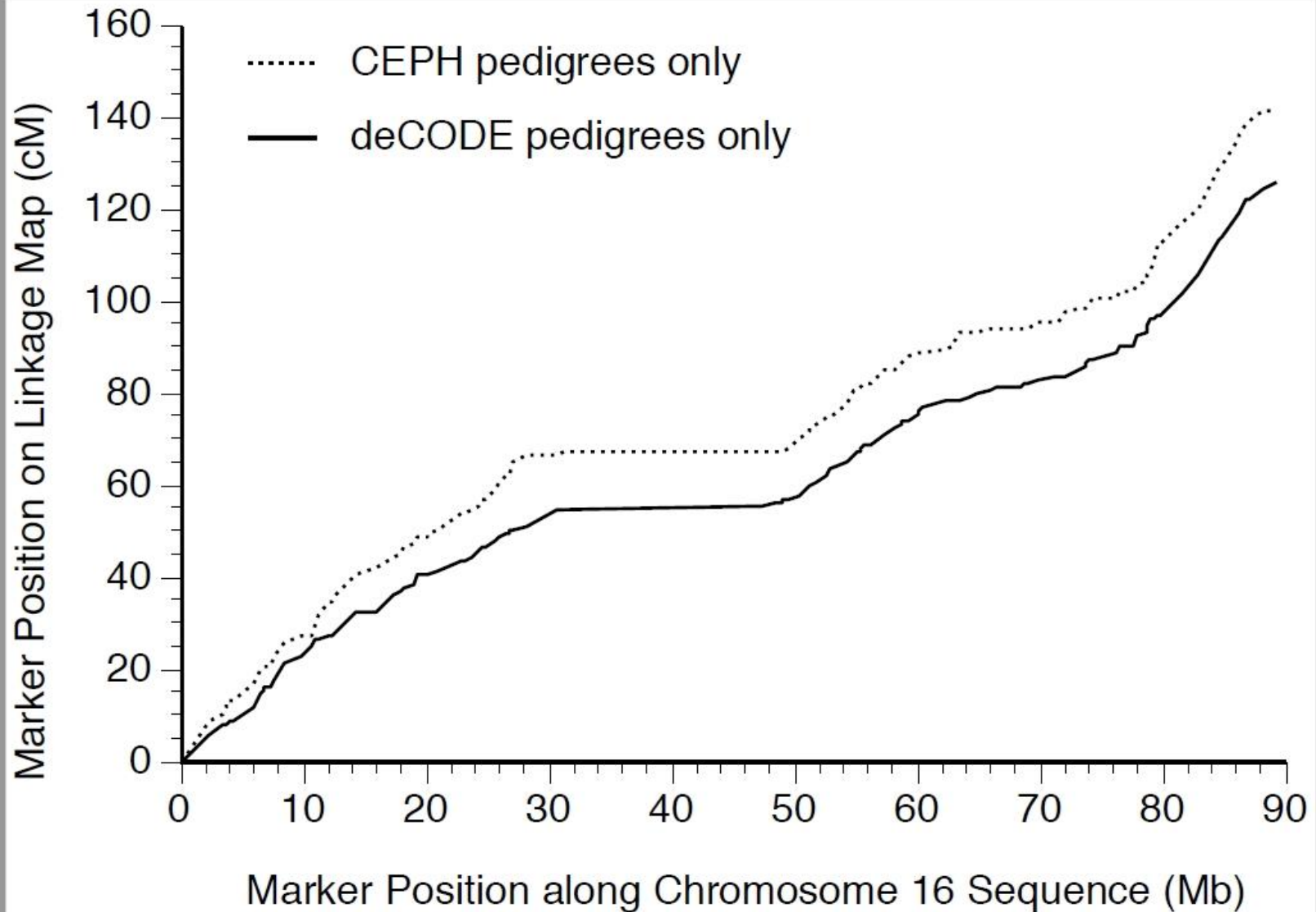
## Expected % Match vs Kinship





# Chromosome 16

## centiMorgans vs Base Pairs



# Autosomal DNA Matches

## centiMorgan Match vs Kinship

<b>Relationship</b>	<b>Expected Average DNA %</b>	<b>Expected Average DNA cM</b>	<b>Measured Average DNA cM *</b>	<b>Common Ancestors</b>	<b>Gens Back To Common Ancestors</b>	<b>Common Ancestor Possible Birth Year</b>
<b>Parent</b>	<b>50</b>	<b>3400</b>	<b>3487</b>			
<b>Sibling</b>	<b>50</b>	<b>3400</b>		<b>Parents</b>	<b>1</b>	<b>1940</b>
<b>Sibling (Excluding Doubles)</b>	<b>37.5</b>	<b>2550</b>	<b>2629</b>	<b>Parents</b>	<b>1</b>	<b>1940</b>
Nephew or Niece	25	1700	1750	Parents/Grandparents	1.5	
Uncle or Aunt	25	1700	1750	Parents/Grandparents	1.5	
<b>First Cousin</b>	<b>12.5</b>	<b>850</b>	<b>874</b>	<b>Grandparents</b>	<b>2</b>	<b>1910</b>
First Cousin once removed	6.25	425	439		2.5	
<b>Second Cousin</b>	<b>3.13</b>	<b>213</b>	<b>233</b>	<b>Great Grandparents</b>	<b>3</b>	<b>1880</b>
Second Cousin once removed	1.56	106	123		3.5	
<b>Third Cousin</b>	<b>0.78</b>	<b>53</b>	<b>74</b>	<b>GG Grandparents</b>	<b>4</b>	<b>1850</b>
Third Cousin once removed	0.39	27	48		4.5	
<b>Fourth Cousin</b>	<b>0.19</b>	<b>13</b>	<b>35</b>	<b>GGG Grands</b>	<b>5</b>	<b>1820</b>
Fourth Cousin once removed	0.1	7	28		5.5	
<b>Fifith Cousin</b>	<b>unreliable</b>	<b>3</b>	<b>25</b>	<b>GGGG Grandparents</b>	<b>6</b>	<b>1790</b>

\* Shared cM Project

# Shared cM Project - Blaine Bettinger

## Match Averages & Ranges v4.0

**New** Click on any relationship to view a histogram

[Read more about cousin relationships](#)

						Great-Great-Grandparent		GGGG Aunt / Uncle				
						Great-Great-Grandparent		GGG Aunt / Uncle				
Half GG-Aunt / Uncle 208 103 – 284	Great-Grandparent 887 485 – 1486						Great-Great-Aunt / Uncle 420 186 – 713	1C3R 117 25 – 238	2C3R 51 0 – 154		Other Relationships	
Half 1C2R 125 16 – 269	Half Great-Aunt / Uncle 431 184 – 668	Grandparent 1754 984 – 2462				Great-Aunt / Uncle 850 330 – 1467	1C2R 221 33 – 471	2C2R 71 0 – 244	3C2R 36 0 – 166		6C 18 0 – 71	
Half 2C1R 66 0 – 190	Half 1C1R 224 62 – 469	Half Aunt / Uncle 871 492 – 1315	Parent 3485 2376 – 3720			Aunt / Uncle 1741 1201 – 2282	1C1R 433 102 – 980	2C1R 122 14 – 353	3C1R 48 0 – 192	4C1R 28 0 – 126	6C1R 15 0 – 56	
Half 3C 48 0 – 168	Half 2C 120 10 – 325	Half 1C 449 156 – 979	Half Sibling 1759 1160 – 2436	Sibling 2613 1613 – 3488	SELF	1C 866 396 – 1397	2C 229 41 – 592	3C 73 0 – 234	4C 35 0 – 139	5C 25 0 – 117	6C2R 13 0 – 45	
Half 3C1R 37 0 – 139	Half 2C1R 66 0 – 190	Half 1C1R 224 62 – 469	Half Niece / Nephew 871 492 – 1315	Niece / Nephew 1740 1201 – 2282	Child 3487 2376 – 3720	1C1R 433 102 – 980	2C1R 122 14 – 353	3C1R 48 0 – 192	4C1R 28 0 – 126	5C1R 21 0 – 80	7C 14 0 – 57	
Half 3C2R 27 0 – 78	Half 2C2R 48 0 – 144	Half 1C2R 125 16 – 269	Half Great-Niece / Nephew 431 184 – 668	Great-Niece / Nephew 850 330 – 1467	Grandchild 1754 984 – 2462	1C2R 221 33 – 471	2C2R 71 0 – 244	3C2R 36 0 – 166	4C2R 22 0 – 93	5C2R 18 0 – 65	7C1R 12 0 – 50	
Half 3C3R	Half 2C3R	Half 1C3R 60 0 – 120	Half GG-Niece / Nephew 208 103 – 284	Great-Great-Niece / Nephew 420 186 – 713	Great-Grandchild 887 485 – 1486	1C3R 117 25 – 238	2C3R 51 0 – 154	3C3R 27 0 – 98	4C3R 19 0 – 60	5C3R 13 0 – 30	8C 11 0 – 42	

# Autosomal DNA Matches

## 23andMe Match List

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Donald Bray

2nd Cousin

2.30% DNA shared, 8 segments



Dulcie Ommanny

2nd Cousin

2.22% DNA shared, 8 segments



effie whitmore

2nd Cousin, Once Removed

1.89% DNA shared, 9 segments



William Watt

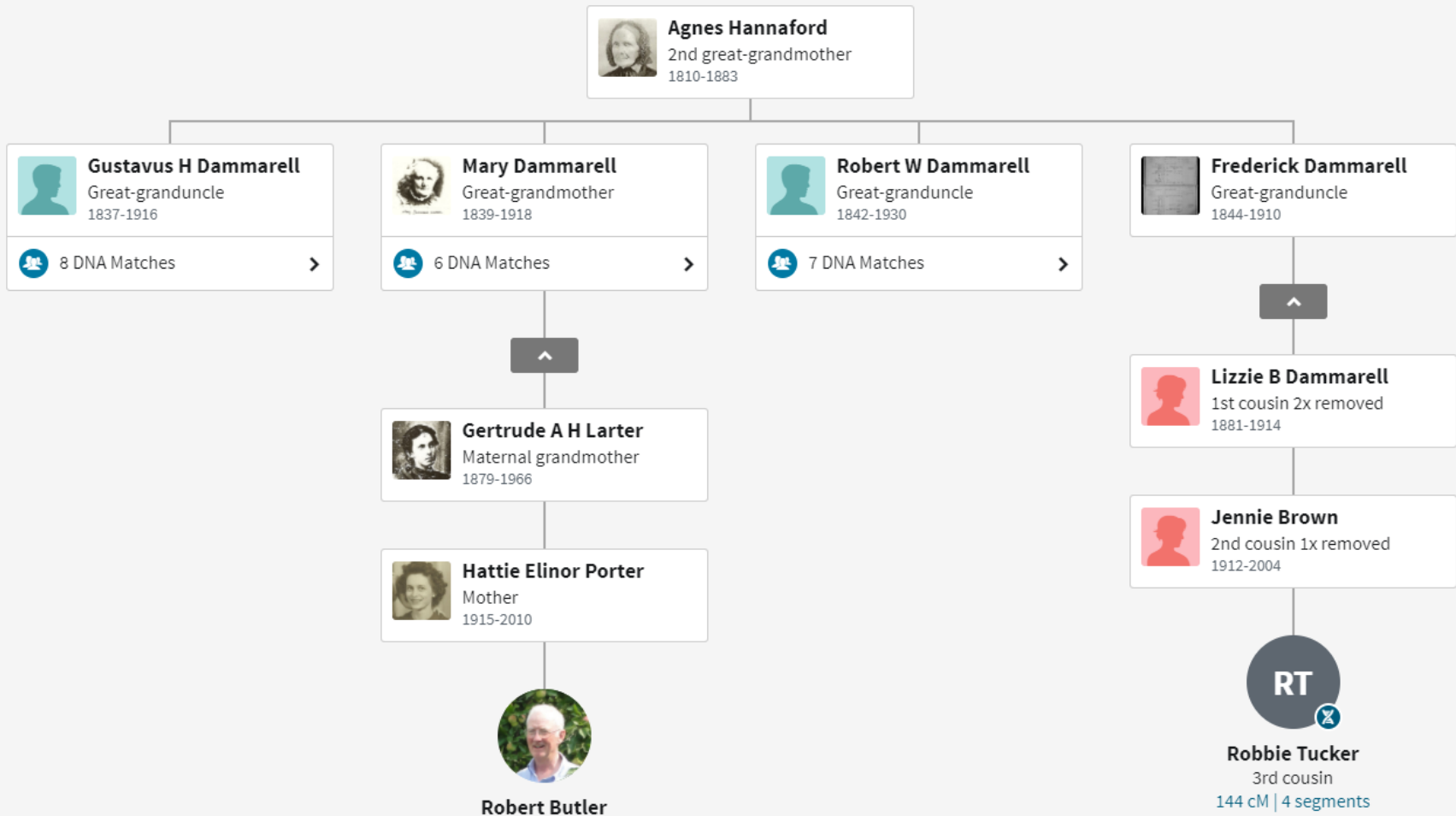
2nd Cousin, Once Removed

1.31% DNA shared, 5 segments

Invitation sent

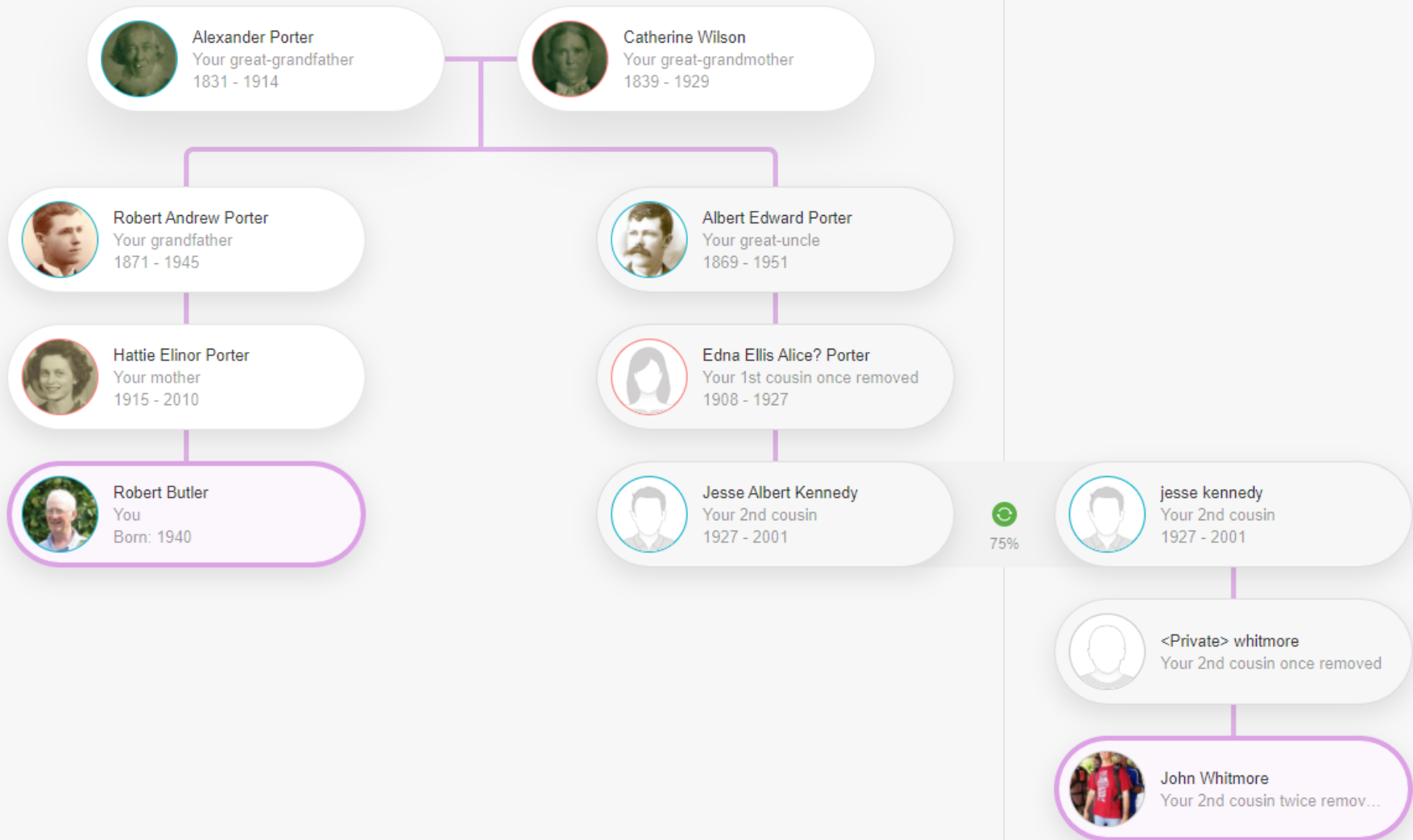
# Autosomal Matches - Ancestry

## Common Ancestors: ThruLines



# Autosomal Matches – My Heritage

## Common Ancestors: Theory of Family Relativity



# Match Clustering

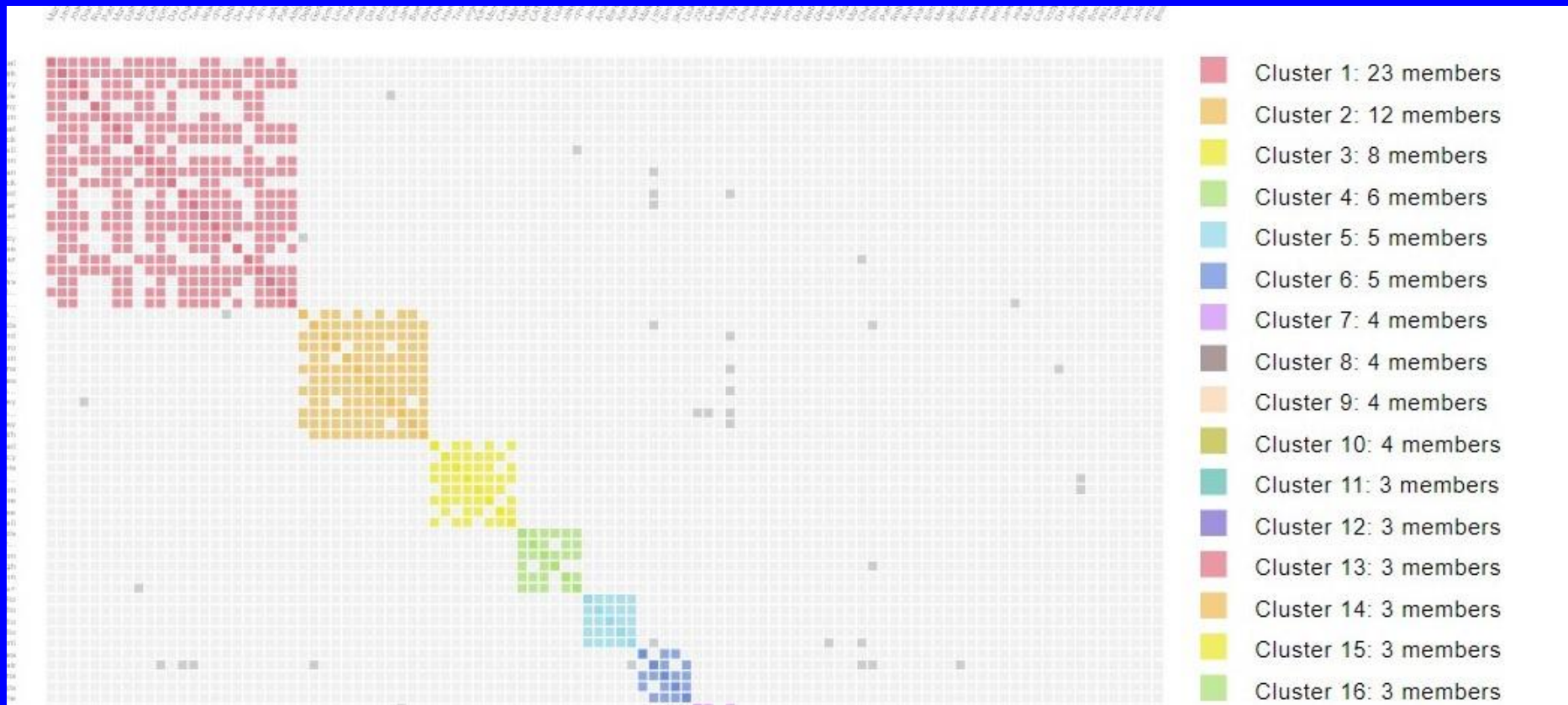
People who match each other – tree branch

## □ My Heritage – Genetic Affairs Example

My Heritage	Cluster 3								REB	
Name	Cheryl	Harry	Trish	Virginia	Karen	Michael	Carolyn	Marie	Total Shared cM	People in Tree
Cheryl	-		39	33		23		15	40.72	8
Harry		-	101	2438	29	47	38		53.46	86
Trish	39	101	-	82	15	33		53	70.92	
Virginia	33	2438	82	-	32	21	18	17	48.67	152
Karen		29	15	32	-	34	37		30.18	1
Michael	23	47	33	21	34	-		39	35.66	1
Carolyn		38		18	37		-	26	44.18	17
Marie	15		53	17		39	26	-	51.17	3

# Match Clustering

## My Heritage – Genetic Affairs Demo





# Match Clustering

People who match each other – tree branch






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- Genetic Affairs works with:
  - 23&Me      log on
  - FTDNA      log on
  - MyHeritage   built in (not adjustable)
  - GEDmatch   built in (adjustable )
  
- Genetic Affairs no longer allowed to work with Ancestry.      ( high computer load? )

# Autosomal DNA Matches

Jan 2022

- Same person (British & Irish), 5 Companies

					
<b>Number of Customers</b>	12 million	1.4 million	19 million	5.2 million	1.2 million
<b>Minimum Match (about 50% false) cM</b>	5	7	7	8	7
<b>Total Matches reported</b>	1509 <sup>*1</sup>	5,004	23,980	11,234	> 10,000
<b>Matches (mostly true) 20 cM or more</b>	1501	284	1,334	1,339	346
<b>Quality Matches (most useful) 35 to 600 cM <sup>*2</sup></b>	150	22	266	96	36
<b>Matches with known common ancestors</b>	21 <sup>*3</sup>	5 <sup>*3</sup>	61 <sup>*3</sup>	13 <sup>*4</sup>	11 <sup>*6</sup>
<b>Matches common ancestor hints or trees</b>	n/a	n/a	> 140 Thrulines	16 ToFR + many SM <sup>*5</sup>	
<b>Shared Matches</b>	Yes	Yes	Yes	Yes	Yes
<b>Match Size between Shared Matches</b>	Yes	No	No	Yes	Yes
<b>Conventional Genealogy</b>	No	No	Yes	Yes	No
<b>Ongoing Subscription Cost for effective match identification</b>	No	No	Yes	Yes	No
<b>* Notes</b>	1. Limited to 1509 matches 2. QM used by Family History Fanatics 3. Trees by Ancestry Matches & Thrulines		4. Mainly Theory of Family Relativity 5. Smart Matches not all common ancestors 6. Most matches from Ancestry test data		

# Y DNA Test

## - Family Tree DNA

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- ❑ Uses same sample as autosomal test
- ❑ Measurement of Y chromosome “Stutters”
- ❑ Analysis of STRs - Short Tandem Repeats
  - for example GATC – GATC .... 13 times
- ❑ Matches – low probability – uses STRs
- ❑ Deep Ancestry – Archeology – uses SNPs

# Y DNA Tests

## STR Measurements

### Y-DNA - Standard Y-STR Values

#### PANEL 1 (1-12) ⓘ

Marker	DYS393	DYS390	DYS19 **	DYS391	DYS385	DYS426	DYS388	DYS439	DYS389I	DYS392	DYS389II ***
Value	13	25	15	11	11-14	12	12	12	14	13	31

#### PANEL 2 (13-25) ⓘ

Marker	DYS458	DYS459	DYS455	DYS454	DYS447	DYS437	DYS448	DYS449	DYS464
Value	17	9-10	11	11	25	15	19	30	14-15-17-17

#### PANEL 3 (26-37) ⓘ

Marker	DYS460	Y-GATA-H4	YCAII	DYS456	DYS607	DYS576	DYS570	CDY	DYS442	DYS438
Value	10	10	19-23	16	15	18	17	36-38	12	12

# Y DNA Tests

## STR Matches

### Y-DNA - Matches



#### FILTER MATCHES

Show Matches For:  Markers:  Distance:  Matches Per Page:

Display Only Matches With Big Y:

Last Name Starts With:  (Optional) New Since:  [Run Report](#)

#### 37 MARKERS - 2 - MATCHES

Genetic Distance ↑	Big Y STR Differences	Name	Earliest Known Ancestor	Y-DNA Haplogroup
4		<a href="#">Mr. Gerald Louis Lane</a>    Y-DNA67	Lewis Charpel Lane, 2/14/1863-12/8/1942	R-M269
4		<a href="#">Mr. Ralph Andrew Goff</a>    Y-DNA67		R-M269

# Y DNA Tests

## STR Generations to Common Ancestors

### Y-DNA TiP Report

In comparing Y-DNA 37 marker results, the probability that **Mr. Gerald Louis Lane** and **Robert Ewart Butler** shared a common ancestor within the last...

COMPARISON CHART	
Generations	Percentage
2	2.36%
4	13.33%
6	31.16%
8	50.25%
10	66.63%
12	78.89%
14	87.25%
16	92.58%
18	95.81%
20	97.69%

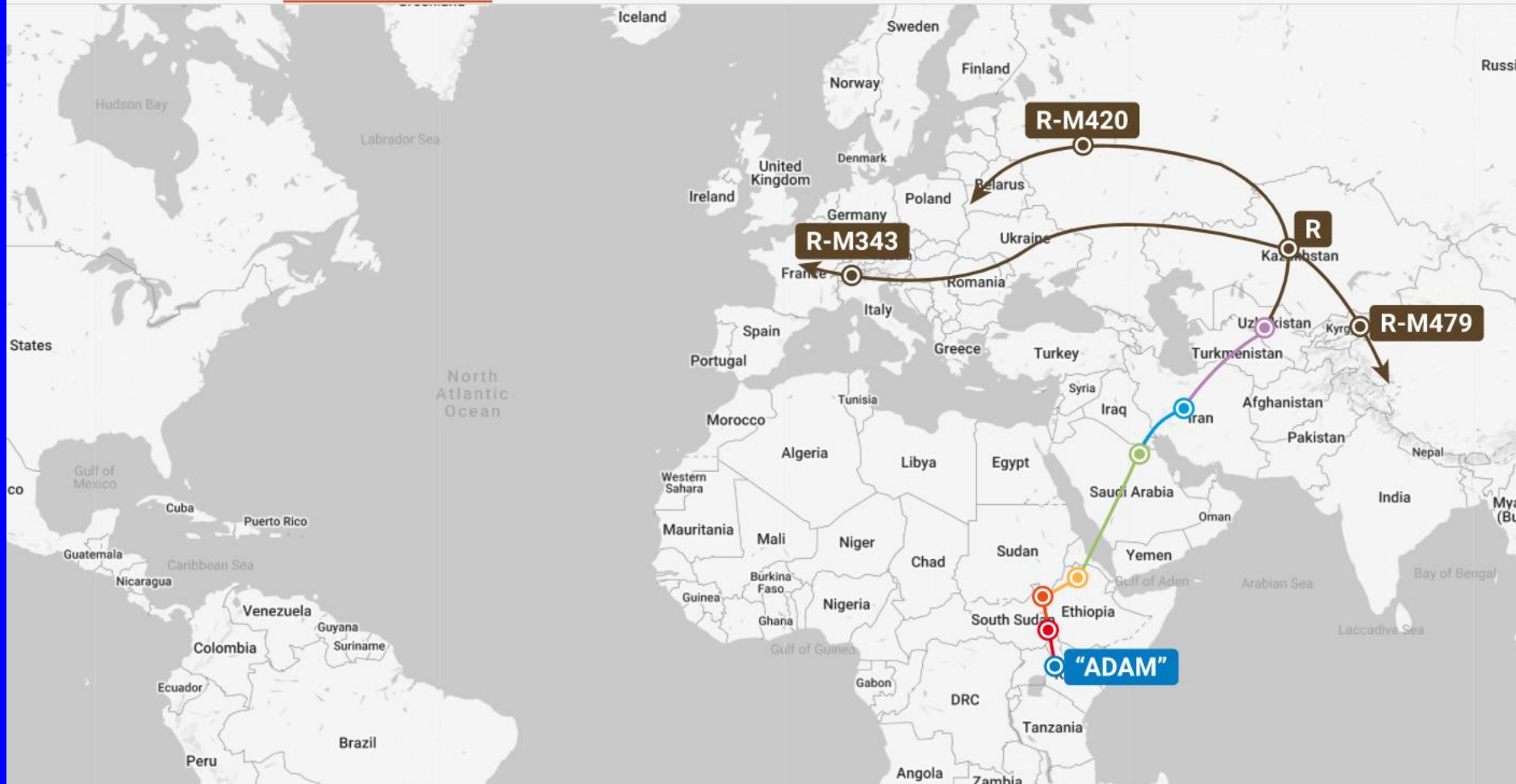
# Y DNA Tests

## SNP Haplogroup & Migration - Archealogy

Y-DNA Haplogroup

Your Migration Map

All Migration Maps



# Mitochondrial DNA Tests

## - Family Tree DNA

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- ❑ Uses same sample as autosomal test
- ❑ Measurement of Mitochondrial SNPs
  - HVR1+HVR2 Sequence (2 \* ~ 600 SNPs)
  - Full Match Sequence FMS (~16,000 SNPs)
- ❑ Comparison to Reference Sequences
- ❑ Matches – low probability – uses SNP differences
- ❑ Deep Ancestry – Archeology - uses SNPs



# Mitochondrial DNA Measurements - Comparison to References

Your Results

RSRS Values

rCRS Values

Extra Mutations

T199C 315.1C 522.1A 522.2C T16075C C16296T

Missing Mutations

HVR1 DIFFERENCES FROM RSRS				
T16075C	T16126C	A16129G	T16187C	C16189T
T16223C	G16230A	T16278C	C16294T	C16296T
T16304C	C16311T			

HVR2 DIFFERENCES FROM RSRS				
C146T	C152T	C195T	T199C	A247G
315.1C	T321C	522.1A	522.2C	

CODING REGION DIFFERENCES FROM RSRS				
G709A	A769G	A825t	G930A	A1018G
G1888A	A2758G	C2885T	T3594C	G4104A
T4216C	T4312C	A4917G	G5147A	G7146A
T7256C	A7521G	T8468C	T8655C	G8697A
G8701A	C9540T	G10398A	T10463C	T10664C
A10688G	C10810T	C10873T	C10915T	A11251G
A11812G	A11914G	T12705C	G13105A	G13276A
G13368A	T13506C	T13650C	A14233G	G14905A
C15452a	A15607G	G15928A		

# Mitochondrial DNA Matches

## mtDNA - Matches

### FILTER MATCHES

Show Matches For:  Regions:  Matches Per Page:

Last Name Starts With:  (Optional) New Since:

### HVR1, HVR2, CODING REGIONS - 79 MATCHES

Page: 1 2 3 4 of 4

Genetic Distance	Name		Earliest Known Ancestor	mtDNA Haplogroup	Match Date
1	Una Shirley Lillian Mansfield	FMS FF	Elizabeth Butcher b.1775	T2b24	12/17/2020
1	Bo Sällström	FMS		T2b24	12/17/2020
1	Lotta Mathilda Rutgersson	FMS FF		T2b24	12/17/2020
1	Jeremy Wiseman	FMS		T2b24	12/17/2020
1	Thomas Allen Wozny	FMS FF		T2b24	12/17/2020
1	Roberta Regnery	FMS FF	Elizabeth Bunny, b. 1665 and d.1721	T2b24	12/17/2020

# Mitochondrial DNA

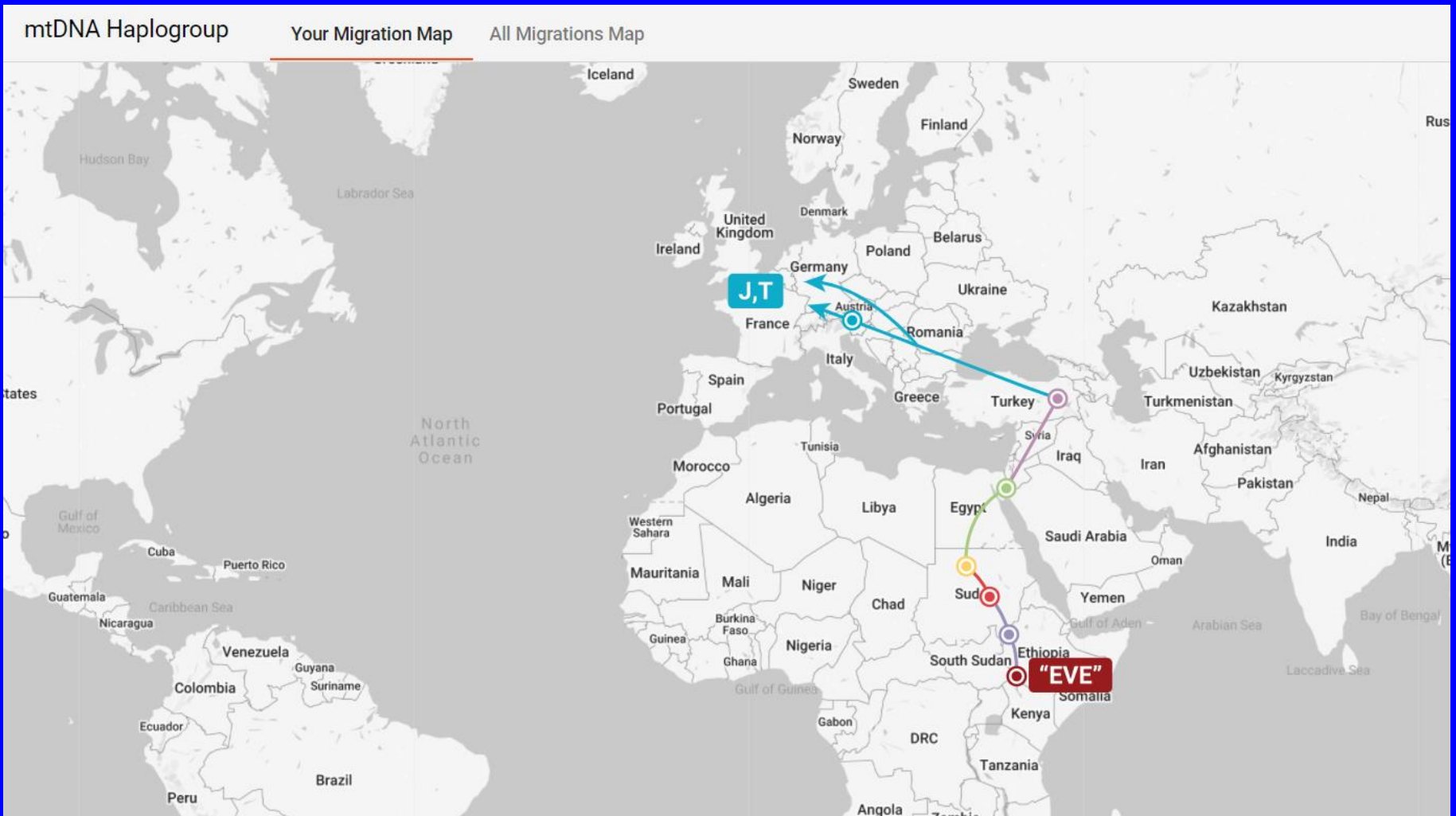
## Common Ancestor Probabilities

Testing Level	Matching Level	Generations to Common Ancestor	
		50% Confidence Interval	95% Confidence Interval
mtDNA	HVR1	52 (about 1,300 years)	NA*
mtDNA Plus	HVR1 & HVR2	28 (about 700 years)	NA*
mtFull Sequence	HVR1, HVR2, & Coding Region	5 (about 125 years)	22 (about 550 years)

\*The range of generations to a common ancestor at this level is too broad to calculate a 95%

□ mtFull Sequence Match      90%      16 gens ( ~ 400 years)

# Mitochondrial DNA Migration – Deep Ancestry - Archeology



# Genealogy Research Stages

## Increasing Efforts, Complexity & Results

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- I. Conventional Genealogy - Gen 101
  - Sources & Data Bases
- II. DNA Genealogy - Gen 201
  - DNA Testing & Common Ancestors
  - Confirmation of Conventional Research
  - Larger Trees – Wider and Deeper
- III. DNA Segment Analysis - Gen 301
  - Larger Trees – Wider and Deeper

# Finding Segment Matches Chromosome Browser

The screenshot displays the myFTDNA Chromosome Browser interface. The browser window title is "myFTDNA - Chromosome Brows" and the URL is "https://www.familytreedna.com/my/family-finder/chromosome-browser".

**Compare Section:**

- Selected: Robert Butler (YOU)
- With: Eric 2nd, Fred 2nd, Erni 2nd, Rob 2nd, Par 2nd, Bra 2nd, Mrs 3rd (all selected)
- Selected 7/7, Clear All
- Update Selected Matches

**Shared DNA Segments Section:**

- Chromosome View / Detailed Segment Data
- Chromosomes 2, 3, 4, and 5 are shown with shared segments highlighted in various colors (blue, red, orange, yellow, dark blue).

**Match Popup:**

- Title: You and Mrs [redacted]
- Close button: X
- Genomic Position: 174033151 - 204278384
- Shared cM: 21.20
- SNPs: 5984
- View Segment Data

# Chromosome Mapping

## DNA Painter



# Segment Cluster after Pileup Removal and after Triangulation Check

Match Cluster 109 - Segment Cluster 13 - Chromo 2				Segment Million Base Pairs			Adjusted for Pileups	
Vendor	Match Name	Total cM	Start	End	Length	Seg cM	Length	Seg cM
Paternal TG	Total matches = 47		170.4	223.3	52.9			
Maternal TG	Pile Up Segment		192.4	198.1	5.7	5.0		
MyHeritage	Amy	57	174.3	223.3	49.0	45.7	43.3	40.7
23andMe	Tee	54	174.5	223.2	48.7	45.2	43.0	40.2
FTDNA	Fred	79	171.2	215.4	44.2	38.2	38.5	33.2
23andMe	Udc	37	171.0	213.8	42.8	38.1	37.1	33.1
23andMe	Rod	36	170.4	212.9	42.5	37.1	36.8	32.1
FTDNA	Ernie	67	171.2	212.7	41.5	35.9	35.8	30.9
GEDmatch	A41	34	171.0	213.8	42.8	35.4	37.1	30.4
GEDmatch	A81	33	171.0	213.3	42.3	34.6	36.6	29.6
MyHeritage	glen	54	172.4	212.1	39.7	32.8	34.0	27.8
GEDmatch	A24	30	172.4	211.9	39.5	31.6	33.8	26.6
23andMe	Hun	36	175.1	212.9	37.8	30.3	32.1	25.3
MyHeritage	Eric	37	175.0	212.9	37.9	30.1	32.2	25.1
FTDNA	Eric	51	175.1	212.7	37.6	29.8	31.9	24.8
MyHeritage	Mer	32	174.3	206.7	32.4	25.2	26.7	20.2
23andMe	Mal	23	172.7	203.0	30.3	24.2	24.6	19.2
23andMe	Wal	22	174.2	205.7	31.5	23.9	25.8	18.9
MyHeritage	Mich	29	174.3	205.8	31.5	23.2	25.8	18.2



# Genetic Genealogy Web Sites

## Family History Fanatics Rating

<https://youtube.com/watch?v=DiZmj-9yybo&feature=share>

Weighting				0.3	0.15	0.2	0.15	0.2	
	Database Size	QM/M	Genealogy Activity	Effective Size	Effective QM	Triangulation	Transfer	X-factor	Total Score
MyHeritage	6	16.3	0.55	3.3	8.97	2	1	2	3.28
GEDmatch	1.75	14.3	0.62	1.1	8.87	3	2	3	3.16
Ancestry	20	15.6	0.4	5.2	6.24	0	0	1	2.70
Family Tree DNA	1.75	19.4	0.55	1.0	10.67	1	1	2	2.64
23andMe	12	16	0.25	3.0	4.00	2	0	2	2.30
LivingDNA	0.75	26.7	0.25	0.2	6.68	0	2	0	1.36
				1.56	1.6005	0.6	0.3	0.6	

- M = Database size – millions of tests
- QM = Quality Matches 35 to 600 cM
- Genealogical Activity – See website – partly related to trees.
- X-factor related to tools
- Results based on Arbitrary Parameters and Factors.

# Genetic Genealogy Web Sites

## Rating Based on Common Ancestors Identified

- Match data for REB – Canadian of English, Scottish & Irish Descent
- Match identification based on Family Tree with 4200 people
- No testing at GEDmatch. Included for comparison of results
- Common Ancestors Identified mainly dependent on Quality Matches

	Data Base	Total	Matches	Quality	QM/M	Trees > 25 people				Common
	Size M	Matches	>20 cM	Matches	per million	Number	Trees/QM	Hints	Hints/QM	Ancestors
				35-600 cM			%		%	Confirmed
Ancestry	20	24062	1337	266	13.3	101	38	64	24	61
MyHeritage	6	11234	1339	96	16.0	41	43	9	9	13
23&Me	12	1512	1500	150	12.5	0	0			21
FTDNA	1.75	5004	284	22	12.6					5
LivingDNA	0.75	pending			0					
GEDmatch	1.75	?	346	36	20.6					11

# DNA Testing Companies

Feb 2022

[https://isogg.org/wiki/Autosomal\\_DNA\\_testing\\_comparison\\_chart](https://isogg.org/wiki/Autosomal_DNA_testing_comparison_chart)



## I. Conventional Genealogy - Gen 101

Records, billions				27	16
Ongoing Subscription Cost Cdn \$/year				260	269-389
REB Rating				9/10	7/10

## II. DNA Genealogy - Gen 201

Number of Customers	12 million	1.4 million	19 million	4.5 million
Autosomal DNA Test & Shipping Cost	CDN \$149	CDN \$115	CDN \$149	CDN \$139
Y DNA & mtDNA Tests (extra costs)		Yes		
Personal Ancestry/Ethnicity (ISOGG Rating)	7/10	3.5/10	5/10	5/10
DNA Genealogy (REB Rating - Brit & Irish)	5/10	5/10	9/10	7/10

## III. DNA Segment Analysis - Gen 301

Match & Segment Lists	Yes	Yes	No	Yes
Chromosome Browser	Yes	Yes	No	Yes
Triangulation	Yes	Partial	No	Yes
DNA Segment Analysis Rating	7/10	6/10	0/10	8/10

Main Reason to Choose	Health & Trait Report	Y & mt Tests	Best Trees & Matching	Good Overall
	Personal Ancestry	Projects		Good Tools

# Genetic Non-Discrimination Act

Bill S-201    Royal Assent May 2017

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This enactment prohibits any person from requiring an individual to undergo a genetic test or disclose the results of a genetic test as a condition of providing goods or services to, entering into or continuing a contract or agreement with, or offering specific conditions in a contract or agreement with, the individual.

# BIFHSGO Pending Presentation

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The British Isles Family History Society of Greater Ottawa  
is planning to host:

“DNA & Genealogy – The DNA of Cornwall”

by  
Dr. Joe Flood

Tentatively late April

# Backups

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# Chromosomes, Base Pairs, Genes & SNPs measured



# Shared cM Project

## 3<sup>rd</sup> Cousin Once Removed Histogram

The Shared cM Project – Version 3.0 (August 2017)

Relationship

#

Min

Average

Max

Histogram

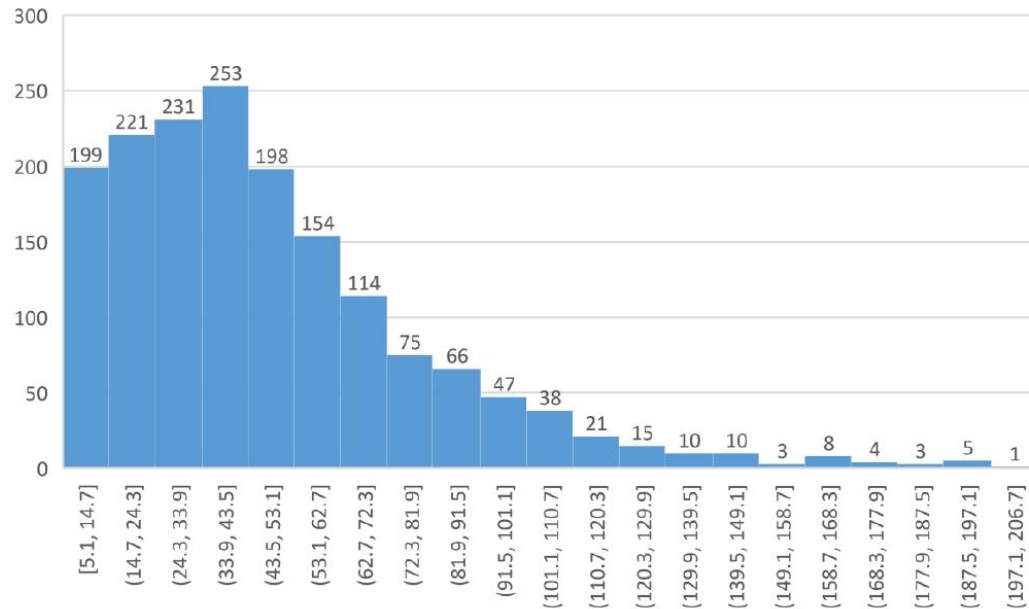
3C1R  
(Cluster #8)

1736

0

48

173





# King Richard III ?

## Mitochondrial DNA – U of Leicester

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The DNA results showed a perfect whole-mitochondrial genome match between Skeleton 1 of the Greyfriars site and Michael Ibsen and a single base difference (mutation) with Wendy Duldig. This was not at all unexpected given the number of generations between them and is consistent with all three of them being related in the genealogical time span.

# King Richard III ?

## Y Chromosome - U of Leicester

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Genealogical information showed that all five living male-line relatives of Richard III were descended from Henry Somerset, the 5th Duke of Beaufort and the Y chromosome data for four out of the five male-line relatives showed a match consistent with them being related as expected.

However, one of the five had a very different Y chromosome type indicating that a false-paternity had occurred within the last few generations. The Y chromosome type of the Skeleton 1 did not match any of the living male-line relatives showing that a false-paternity event (or events) had also occurred somewhere in the 19 generations between Richard III and Henry Somerset, 5th Duke of Beaufort.