The background of the slide features a series of overlapping, wavy, translucent lines in shades of green and blue. These lines create a sense of movement and depth, particularly on the left side where they are more densely packed and layered. The right side of the slide is a plain white background.

# The Mechanics of Finding your Family Using DNA

## Match Statistics



98% of your matches  
are related to you

~86% will be in  
4th-distant  
cousin range

~12% will be in  
2nd-3rd cousin  
range



DNA Results Comparison

Text results of the double helix composition of DNA showing individual RSID\* numbers

Section of Chromosome 1

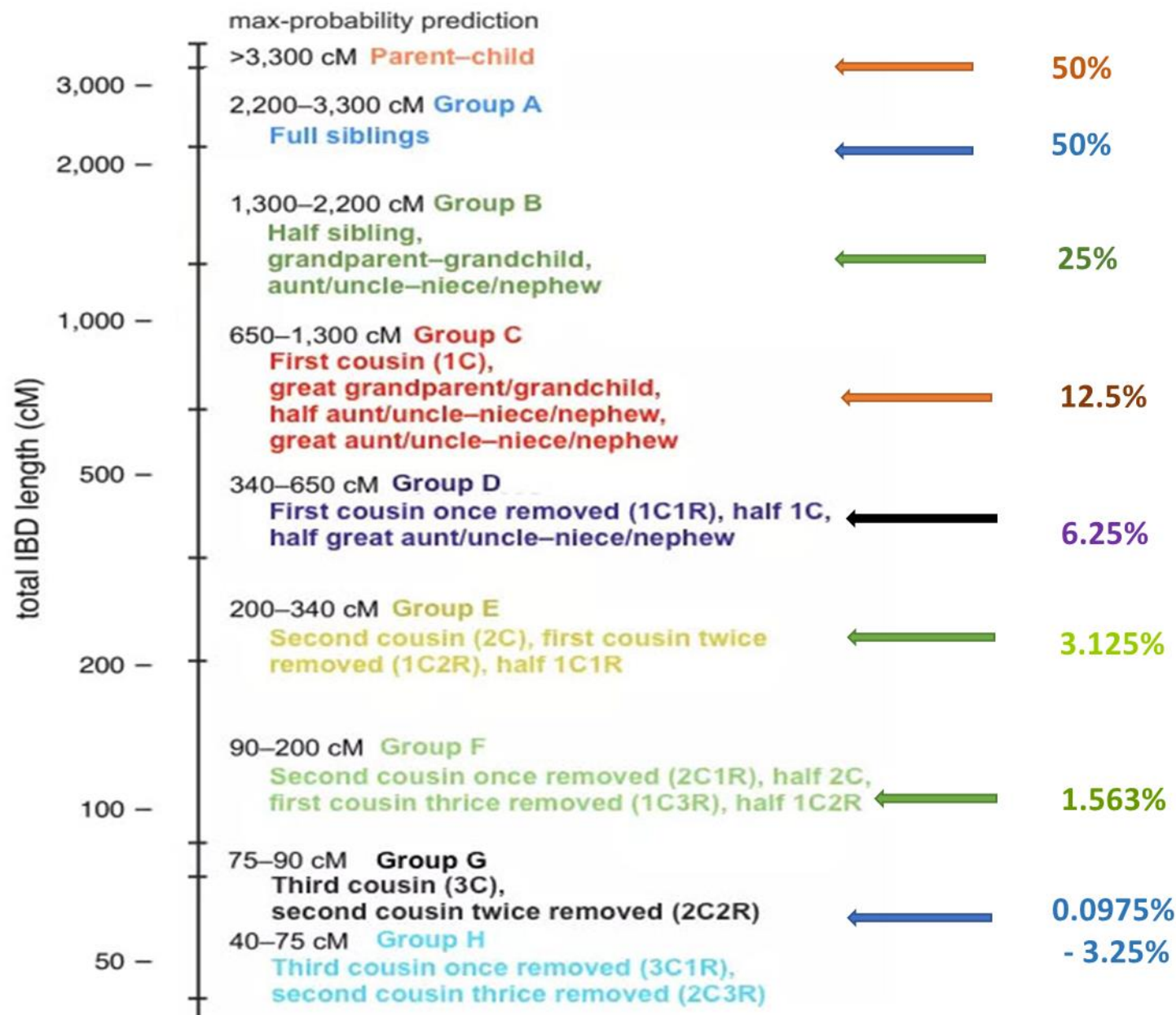
\*The **rs number** is an accession number used by researchers and databases to refer to specific SNPs. It stands for Reference SNP cluster ID. The **rsid** numbers are used for SNPs in diagnosing health and inherited traits.  
EX: Chr. 1 SNP rs28936694  
Is one of many associated with Glaucoma MYOC gene.

Child				Mother											
	A	B	C	Alleles D		A	B	C	Alleles D	E	F	G	H	I	J
141	rs1153103	1	1415012	AA	141	rs1153103	1	1415012	AA						
142	rs1153105	1	1415099	CT	142	rs1153105	1	1415099	TT						
143	rs2862157	1	1418112	AA	143	rs2862157	1	1418112	AA						
144	rs819980	1	1425700	TT	144	rs819980	1	1425700	TT						
145	rs12021879	1	1439671	CC	145	rs12021879	1	1439671	CC						
146	rs6690515	1	1447325	GG	146	rs6690515	1	1447325	GG						
147	rs6669795	1	1450947	AA	147	rs6669795	1	1450947	AA						
148	rs10159041	1	1453921	--	148	rs10159041	1	1453921	TT						
149	rs3813216	1	1458567	--	149	rs3813216	1	1458567	--						
150	rs3737714	1	1458954	--	150	rs3737714	1	1458954	--						
151	rs12032637	1	1465382	AA	151	rs12032637	1	1465382	AA						
152	rs3118505	1	1472047	CC	152	rs3118505	1	1472047	CT						
153	rs9782908	1	1472201	CC	153	rs9782908	1	1472201	CC						
154	rs1571149	1	1474167	AG	154	rs1571149	1	1474167	AA						
155	rs7290	1	1477244	CT	155	rs7290	1	1477244	TT						
156	rs11807706	1	1477660	AA	156	rs11807706	1	1477660	AA						
157	rs3766180	1	1478153	CT	157	rs3766180	1	1478153	TT						
158	rs7533	1	1479333	--	158	rs7533	1	1479333	--						
159	rs2031709	1	1485984	CC	159	rs2031709	1	1485984	CC						
160	rs7531530	1	1489670	CT	160	rs7531530	1	1489670	CC						
161	rs880051	1	1493727	AG	161	rs880051	1	1493727	GG						
162	rs2296716	1	1497824	CT	162	rs2296716	1	1497824	CC						
163	rs9439468	1	1499298	AG	163	rs9439468	1	1499298	AA						
164	rs7519837	1	1510801	CC	164	rs7519837	1	1510801	CC						
165	rs6687029	1	1519068	AC	165	rs6687029	1	1519068	AC						
166	rs6604983	1	1521595	AA	166	rs6604983	1	1521595	AA						
167	rs28430872	1	1549605	CC	167	rs28430872	1	1549605	CC						
168	rs12748433	1	1559971	CT	168	rs12748433	1	1559971	TT						
169	rs28635343	1	1560103	CC	169	rs28635343	1	1560103	CC						
170	rs28464684	1	1566160	CT	170	rs28464684	1	1566160	CC						
171	rs28456011	1	1567206	GG	171	rs28456011	1	1567206	AG						
172	rs35154105	1	1598908	TT	172	rs35154105	1	1598908	TT						
173	rs28707307	1	1610809	AA	173	rs28707307	1	1610809	AA						
174	rs28487995	1	1619541	AG	174	rs28487995	1	1619541	AG						
175	rs35261312	1	1627987	CC	175	rs35261312	1	1627987	CC						
176	rs760925	1	1646574	GG	176	rs760925	1	1646574	GG						
177	rs909823	1	1647686	CC	177	rs909823	1	1647686	--						
178	rs3817856	1	1663831	CT	178	rs3817856	1	1663831	CC						
179	rs2294488	1	1664019	--	179	rs2294488	1	1664019	CC						
180	rs2294489	1	1664124	--	180	rs2294489	1	1664124	--						
181	rs1014988	1	1680219	--	181	rs1014988	1	1680219	--						
182	rs7407	1	1684472	TT	182	rs7407	1	1684472	TT						

Fully identical  
difference  
no match  
half-identical



# What Relationship, You Say?



Standard range of shared Centimorgans and the correlated relationships with estimated percentages of shared DNA.

4<sup>th</sup> Cousins share 0-90 cM or 0.0122%-0.195%

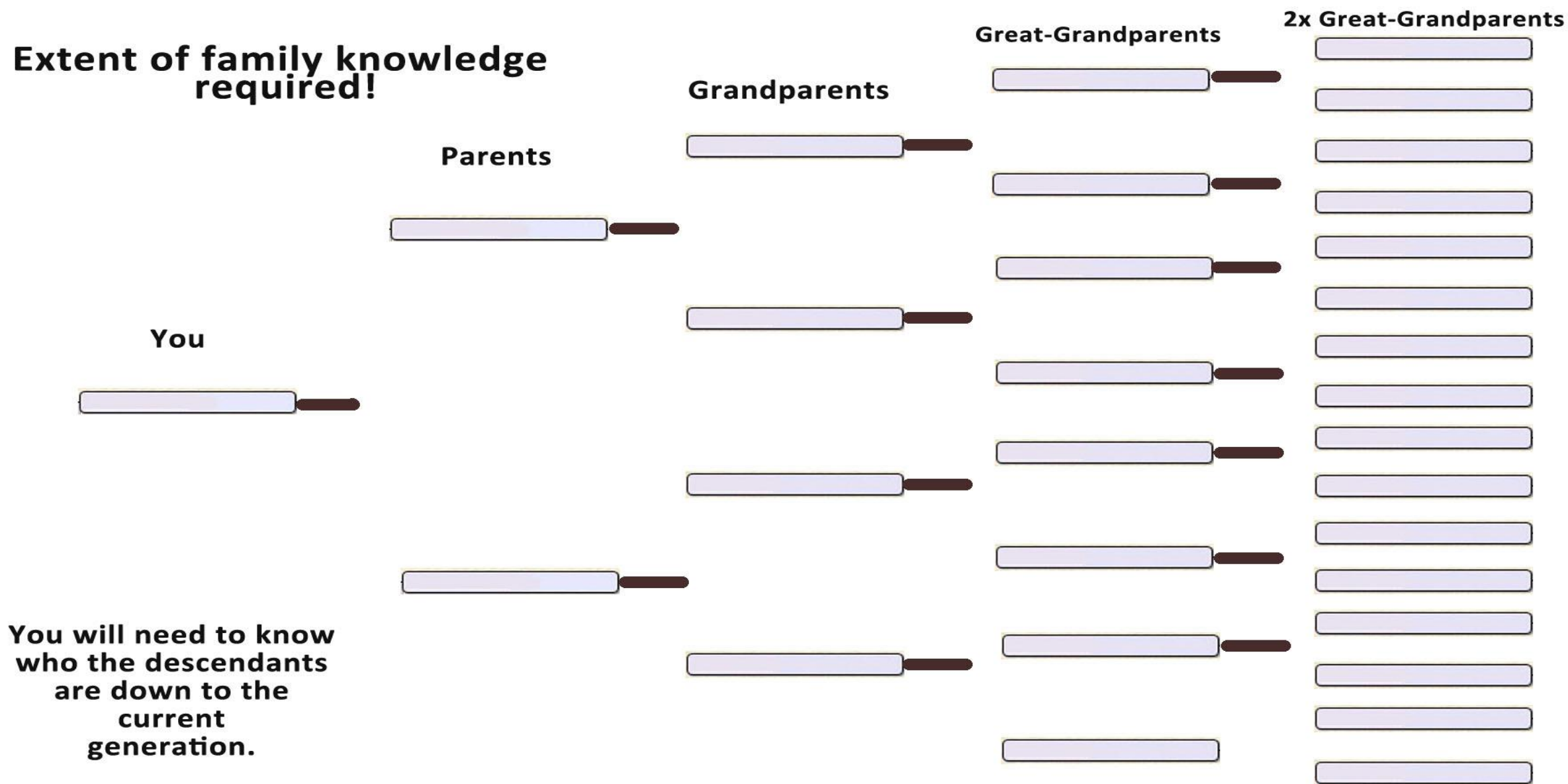
5<sup>th</sup> Cousins share 0-42 cM or 0.0061%-0.087%

6<sup>th</sup> Cousins share 0-29 cM or 0.0030%-0.043%

7<sup>th</sup> Cousins share 1-10 cM or 0.0015%-0.0215%

8<sup>th</sup> Cousins share 0-16 cM or 0.000725%-0.01075%

# Extent of family knowledge required!





# Leeds Method of Clustering Matches

37\_S\_Young\_Chrom\_Autoso\_20181230.xlsx - Excel

	A	B	C	D	E	F	G	H	I	J	K	L	M
1			HILL	BAKER	BODEKER	GREGORY							
2	BEATTY	M											
3	BOSWELL	M											
4	BRAND	M											
5	C.	M											
6	COBLEY	P		KNOWN									
7	COCKRIEL	M											
8	DOBLE												
9	HARRIS												
10	KENNEDY	M											
11	KENNEDY	M											
12	LADD	M-P											
13	LUKE												
14	MATHEWS	M											
15	MCDONALD	M											
16	PEACHEE	M											
17	PHARE	M-P	KNOWN										
18	ROOT-BOWMAN	M											
19	SCHUBERT	M											
20	SCHUBERT	M											
21	SCHUBERT	M											
22	SYNDER	M											
23	TRAVIS	M											
24	VANCE	M-P	KNOWN										
25	WEDDLE	M											
26	WEST	M											
27	WRIGHT	M											
28	MAYER												
29	SHERMAN												
30	BUTTERWORTH												
31	THORNTON												
32													

Names highlighted with deep yellow carry more than one match with another tester. Testers Phare and Synder are known to be related to the subject many times over.

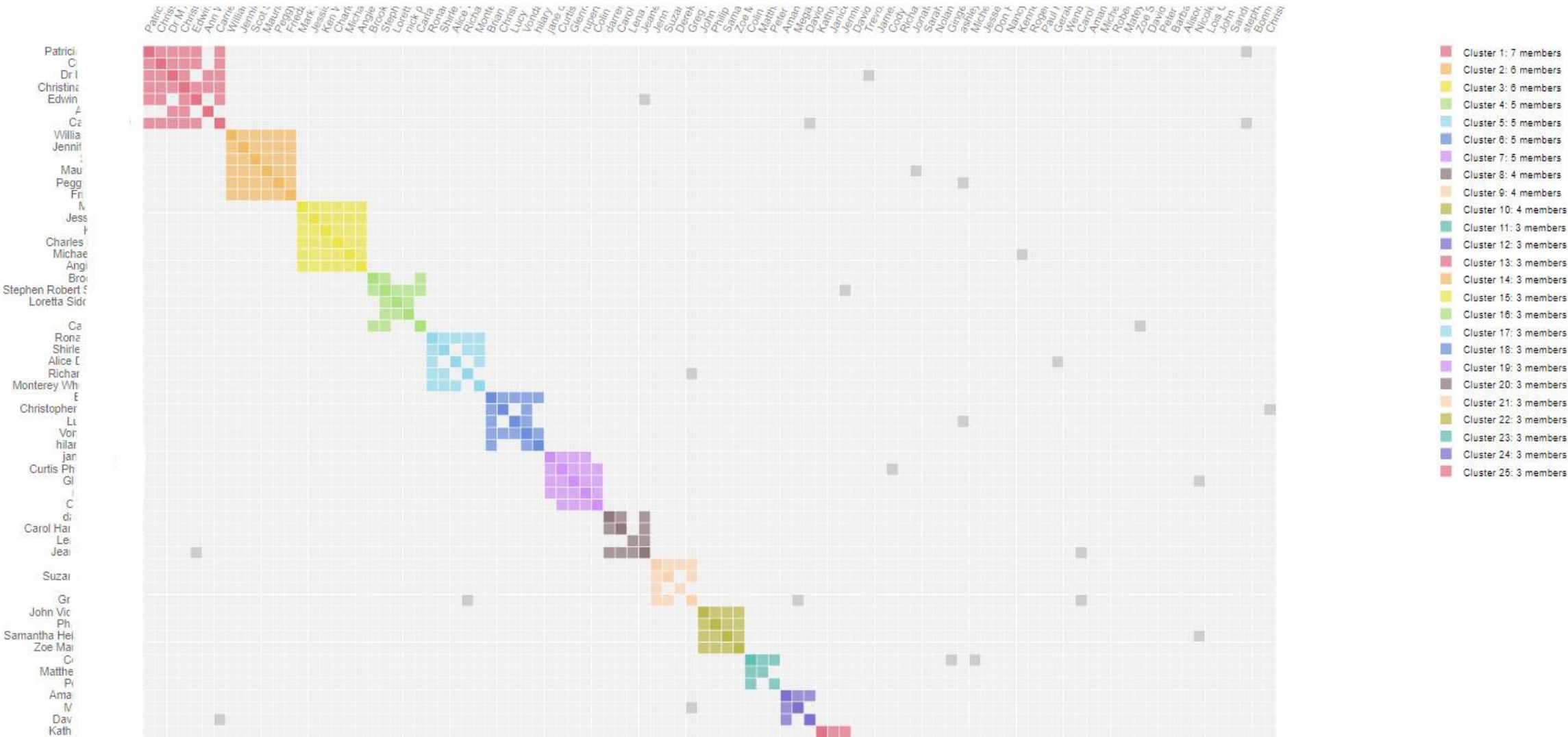
Note the matches that show “KNOWN” in the coloured box. Any other matches that match those people will likely share the same set or one of the same set of great-grandparents.

Note the matches for which I have no known surnames.

# AutoClusters

For: L      Kit: FT-B4B

Order DNA Matches by: **Cluster**





Total number of DNA Matches: 96

Min threshold: 25 cM

Max threshold: 350 cM

Shared DNA Matches min threshold: 10 cM

## AutoClusters Information

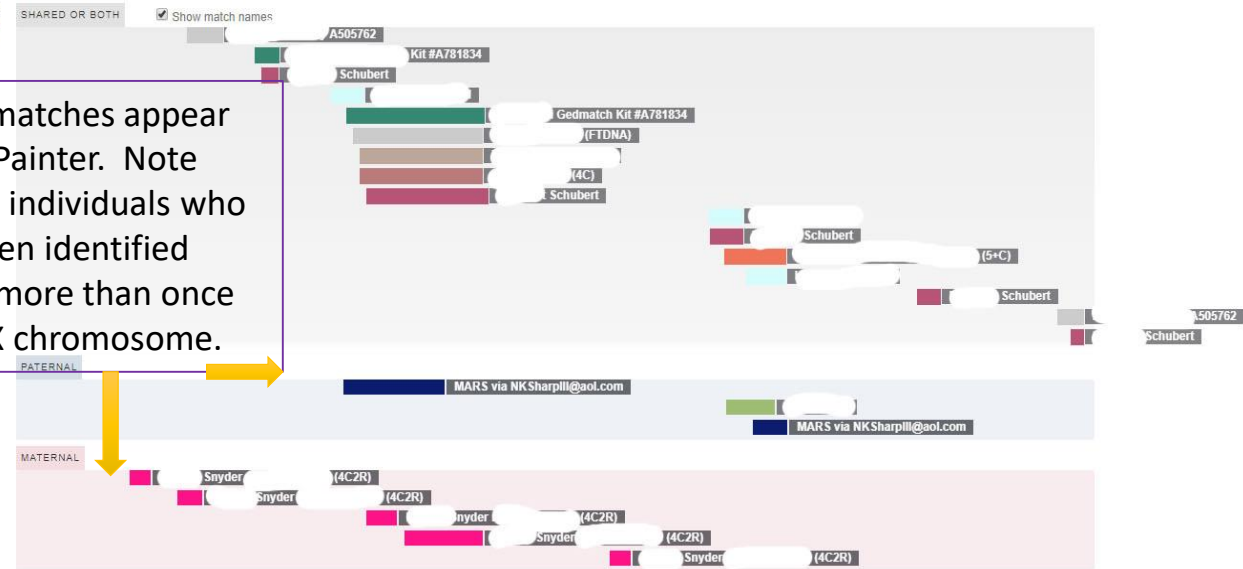
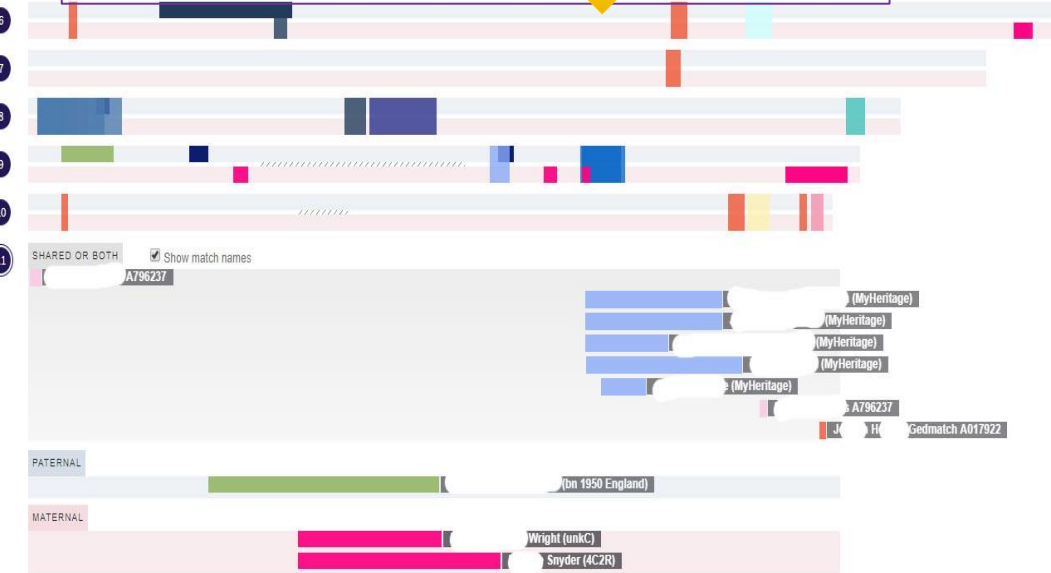
Name	cM	Largest cM	Segments	ICW	Cluster	Tree	Notes
<input type="text" value="Search"/>	<input type="text" value="Min cM"/>	<input type="text" value="Min Largest cM"/>	<input type="text" value="Min Segmer"/>	<input type="text" value="Min #"/>	<input type="text" value="Search for"/>		<input type="text" value="Search for notes"/>
▼ Cluster 1 (7 people)							
<a href="#">Patrici</a>	26.6	26.6	1	6	1	<a href="#">9</a>	
<a href="#">Chr</a>	26.9	26.9	1	5	1	<a href="#">1782</a>	
<a href="#">Dr M A</a>	25.7	25.7	1	5	1		
<a href="#">Christina</a>	26.1	26.1	1	7	1	<a href="#">50</a>	
<a href="#">Edwin</a>	27.9	20.6	2	3	1	<a href="#">4</a>	
<a href="#">Ann</a>	26.1	11.1	3	1	1	<a href="#">1</a>	
<a href="#">Carrie</a>	39.7	39.7	1	7	1	<a href="#">25</a>	
▼ Cluster 2 (6 people)							
<a href="#">William</a>	36	23	3	6	2	<a href="#">5</a>	
<a href="#">Jennifer</a>	25.2	25.2	1	4	2	<a href="#">52</a>	
<a href="#">Scol</a>	28.2	28.2	1	5	2		
<a href="#">Maurice</a>	25.8	13.3	3	5	2	<a href="#">1609</a>	
<a href="#">Peggy</a>	25.5	25.5	1	4	2	<a href="#">1</a>	
<a href="#">Frieda</a>	29.1	29.1	1	4	2	<a href="#">1956</a>	
▼ Cluster 3 (6 people)							
<a href="#">Mark</a>	27.5	27.5	1	5	3		
<a href="#">Jessica</a>	27.9	21.9	2	6	3	<a href="#">212</a>	
<a href="#">Ken</a>	27.1	27.1	1	6	3	<a href="#">837</a>	
<a href="#">Charles</a>	33	26.2	2	4	3	<a href="#">6</a>	
<a href="#">Michael I</a>	39	24.4	3	6	3	<a href="#">2</a>	
<a href="#">Angie</a>	27.3	18.8	2	4	3	<a href="#">65</a>	
▼ Cluster 4 (5 people)							
<a href="#">Brooke</a>	33	11.1	4	2	4	<a href="#">20</a>	
<a href="#">Stephen</a>	27.5	12.3	3	5	4	<a href="#">58</a>	
<a href="#">Loretta</a>	32	10.6	4	1	4	<a href="#">280</a>	
<a href="#">nick</a>	27.8	8.4	4	1	4	<a href="#">20</a>	



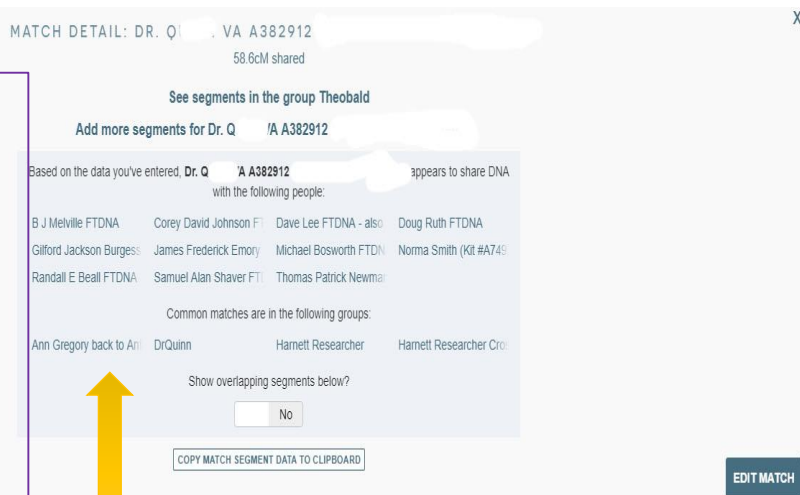
Colours over both Paternal and Maternal lines indicate an unknown match.

# DNA PAINTER

How X-matches appear in DNA Painter. Note that the individuals who have been identified appear more than once on the X chromosome.

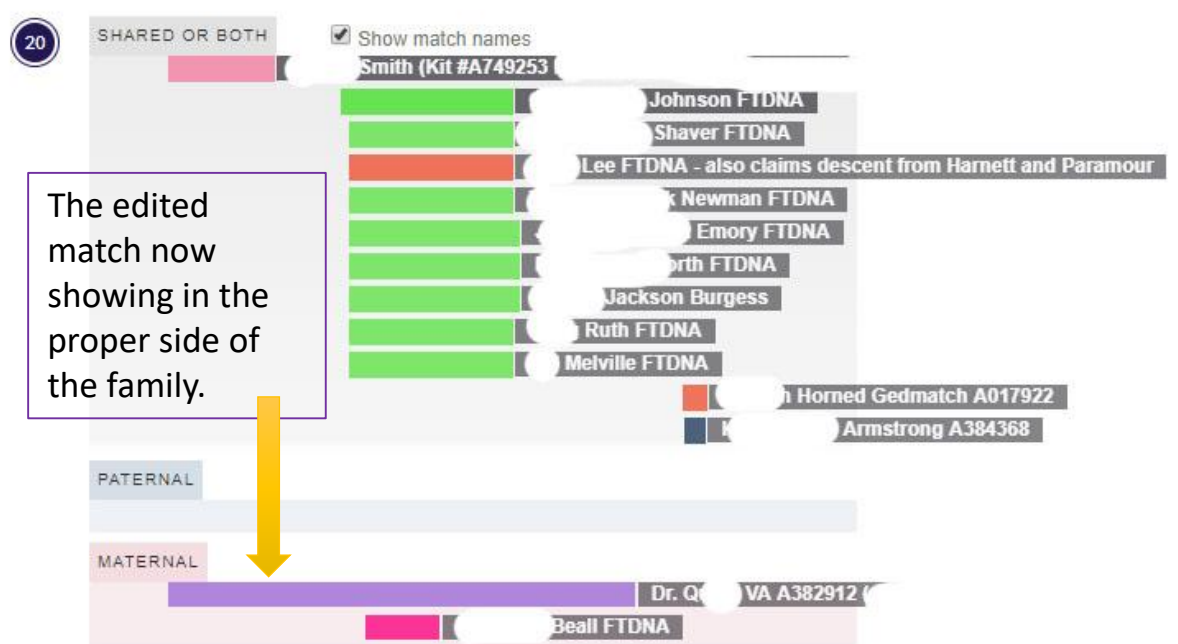


Once a match is identified as descending from a specific ancestor the unknown match can be edited to attach to the proper group.



Note the suggested possible matches to the match being edited. Something to think about!

The edited match now showing in the proper side of the family.



# Prediction of the MRCA of Mr. D. W.

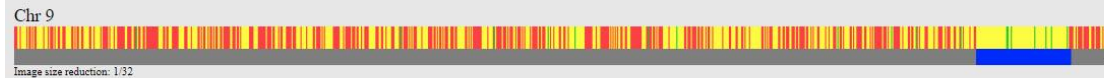
I corresponded with Mr. D. W.  
over 10 years ago regarding a  
possible relationship involving  
his illegitimate ancestor. The  
DNA results actually supported  
our earlier genealogical  
research.

## GEDmatch.Com Autosomal Comparison - V2.1.1(c)

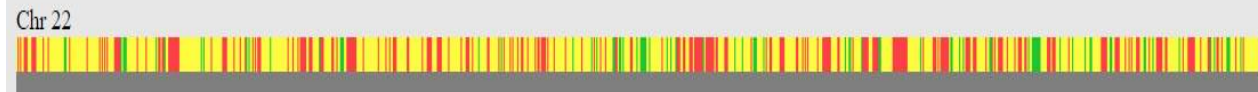
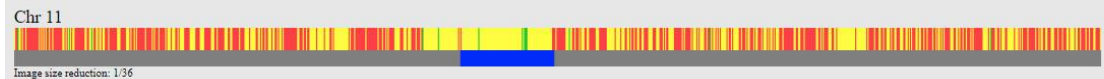
Base Pairs with Full Match =	
Base Pairs with Half Match =	
Match with Phased data =	
Base Pairs with No Match =	
Base Pairs not included in comparison =	
Matching segments greater than 7 centiMorgans =	
Centromere	



Chr	Start Location	End Location	Centimorgans (cM)	SNPs
9	125,937,079	136,282,174	18.2	2,679



Chr	Start Location	End Location	Centimorgans (cM)	SNPs
11	56,198,401	68,923,712	9.7	2,966



Largest segment = 18.2 cM  
Total of segments > 7 cM = 27.9 cM  
2 matching segments  
Estimated number of generations to MRCA = 4.5

674543 SNPs used for this comparison.

**Actual distance to MRCA 6 generations. Not the predicted 4.5. The predicted distance of 4.5 generations could not determine that there were multiple lines of ancestry shared by Mr. D. W. and myself based on the number of shared centimorgans.**



# Prediction of the MRCA of L. S.

## GEDmatch.Com Autosomal Comparison - V2.1.1(c)

Comparing Kit T-

and A

Minimum threshold size to be included in total = 500 SNPs

Mismatch-bunching Limit = 250 SNPs

Minimum segment cM to be included in total = 7.0 cM

Chr	Start Location	End Location	Centimorgans (cM)	SNPs
11	44,621,551	78,589,080	22.7	3,037

Largest segment = 22.7 cM

Total of segments > 7 cM = 22.7 cM

1 matching segments

Estimated number of generations to MRCA = 4.7



403394 SNPs used for this comparison.

Comparison took 0.26383 seconds.

Ver: Apr 23 2017 21:26:52

Actual distance to MRCA for L.S. is 8 generations! Only traditional genealogical research proved the kinship connection.

**Ms. L.S. is unknown to me. However, her match on Chromosome 11 overlayed and was larger than the match of Mr. D. W. on that same chromosome of 56,298,401-68,913,712. Ms. L. S. had an extensive tree online and I was able to fill in the missing generations and make the match.**

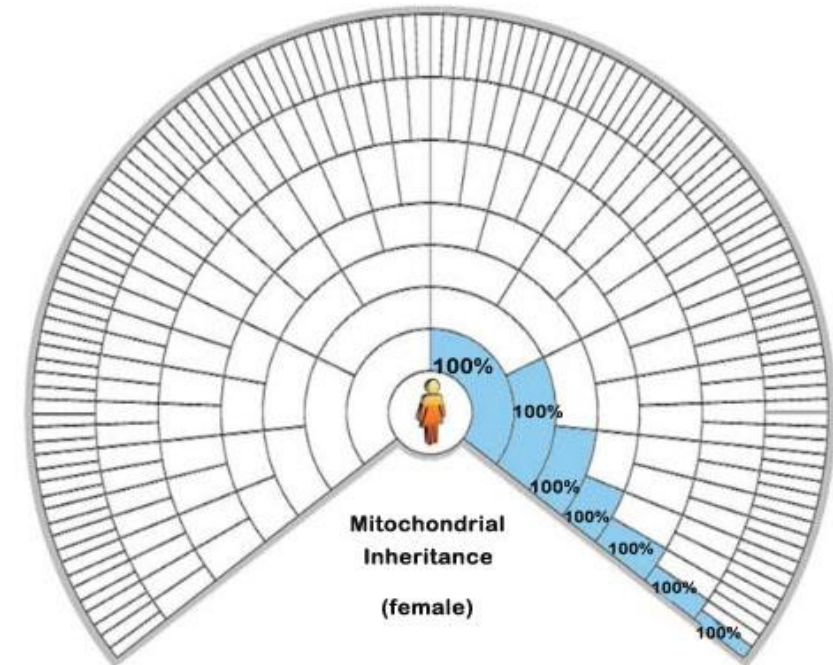
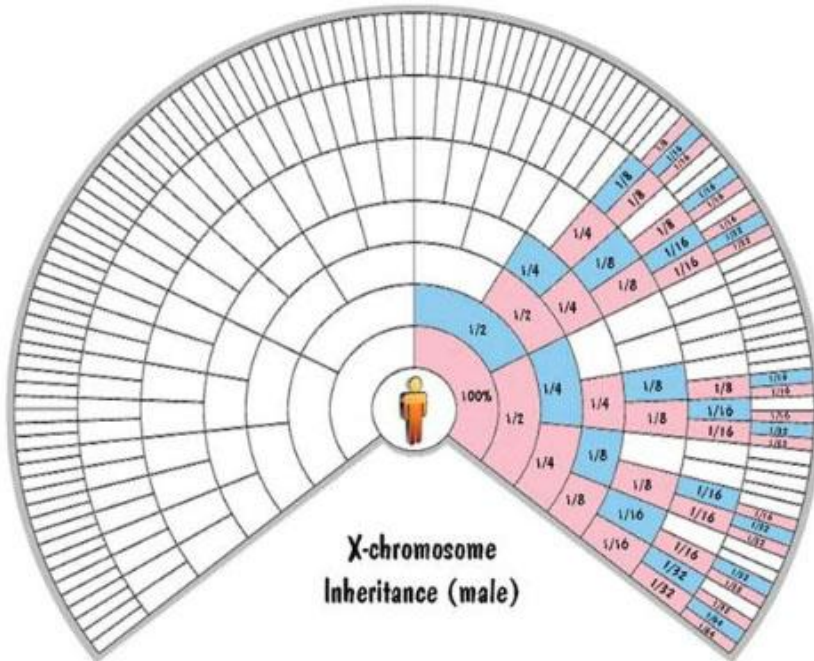
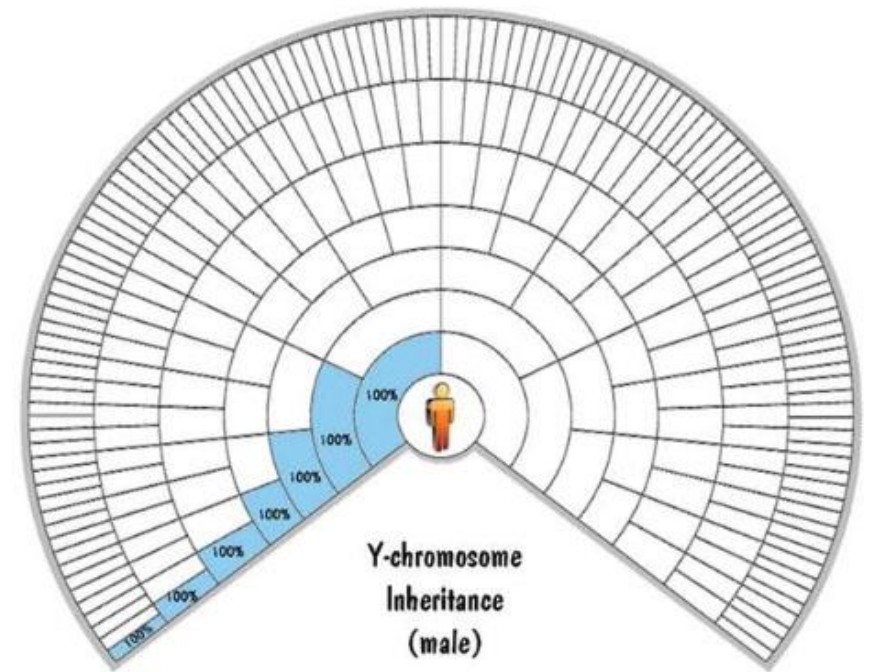
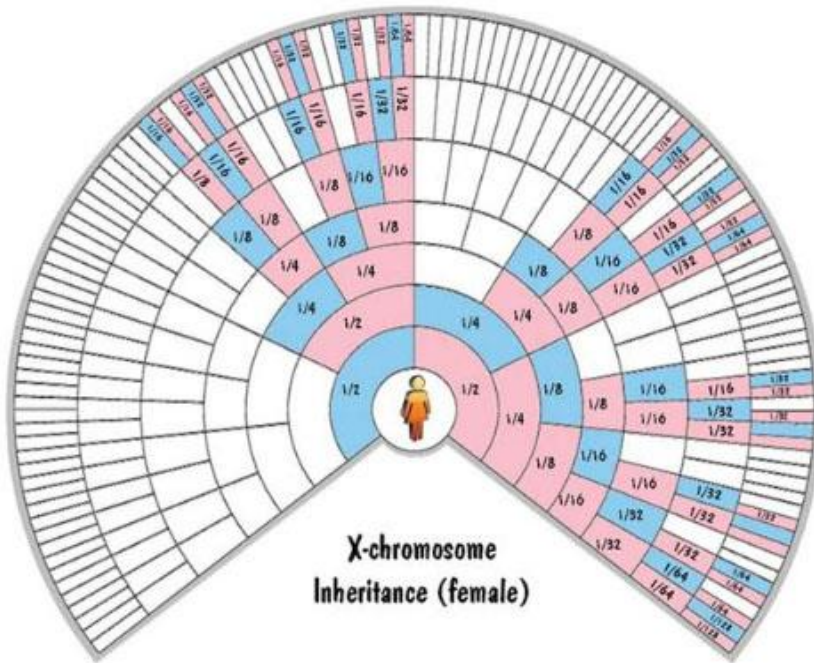
# X Matches

**23andMe** X-DNA can be viewed in the 23andMe chromosome browser or downloaded, but only for those matches who choose to share genomes with you. The raw data can be transferred to GEDmatch for comparison with other kits in the GEDmatch database.

**AncestryDNA** does not provide or show any X-DNA information, so X-chromosome information can only be accessed by transferring a copy of the **raw data to FTDNA or GEDmatch** for analysis.

**MyHeritage** DNA does not yet show X-matches, but they announced at their Nov 2018 Live Conference that X-matches would be coming in future. You can upload a copy of your MyHeritage DNA **raw data to FTDNA or GEDmatch** for X analysis.

**Living DNA** does not yet report on X-matches, but will likely do so in the future when all their matching and features have been fully implemented. FTDNA does not accept Living DNA results.







# Thank you!

Contact Info:

Email: [info@ancestrysolutions.com](mailto:info@ancestrysolutions.com)

Phone: 289-273-6590