The Day After…..

You Receive Results

Mark Moore
20170708

Definitions

DNA Segment - a block, chunk, piece, string of DNA on a chromosome, determined by a start location and an end location.

Recombination - the rearrangement of genetic material by crossing over in chromosomes.
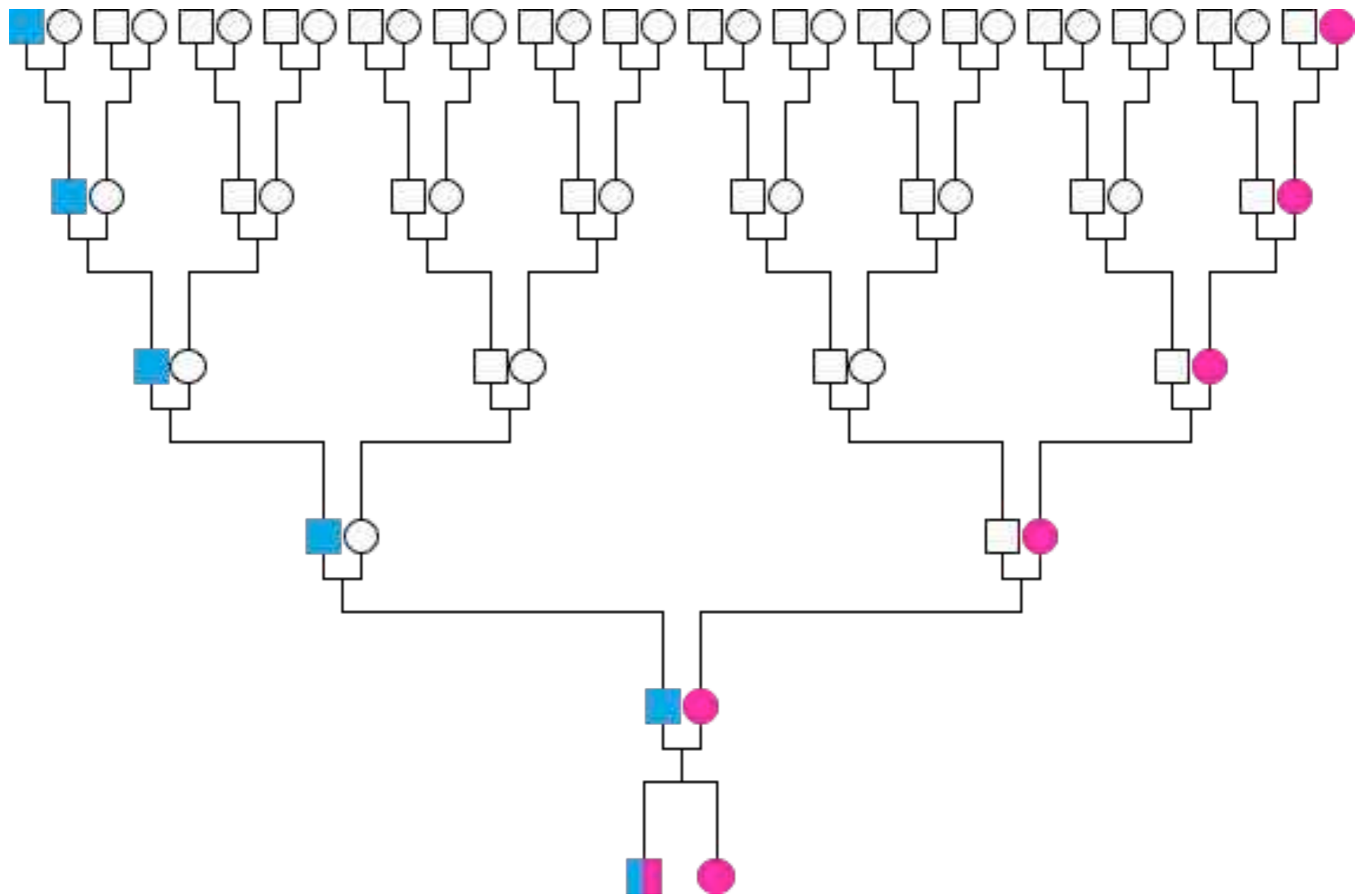
IBD - Identical by descent - inherited segments that are identical between two people

IBS - Identical by state - an algorithm error that falsely indicates two or more people have identical inherited segments

Phasing - the process of trying to determine which DNA came from the mother, and which came from the father

Triangulation - a term taken from surveying to describe a method of determining a common ancestor using data from three or more people

Half Identical Region (HIR) - matching of a DNA segment on one chromosome of a chromosome pair

Full test reports results for 16,569 bp

mtDNA

Control region or "d-loop"

125 rRNA

Cytochrome b

165 rRNA

NADH Dehydrogenase subunits

22 tRNA-encoding genes

13 protein-encoding regions

NADH Dehydrogenase subunits

NADH Dehdrogenase subunits

Cytochrome Oxidase subunits

ATP Synthase subunits

Cytochrome Oxidase subunits

www.isogg-org/wiki/Mitochondrial_DNA

If an exact match (genetic distance =0) then generally share a common ancestor in the last 22 generations
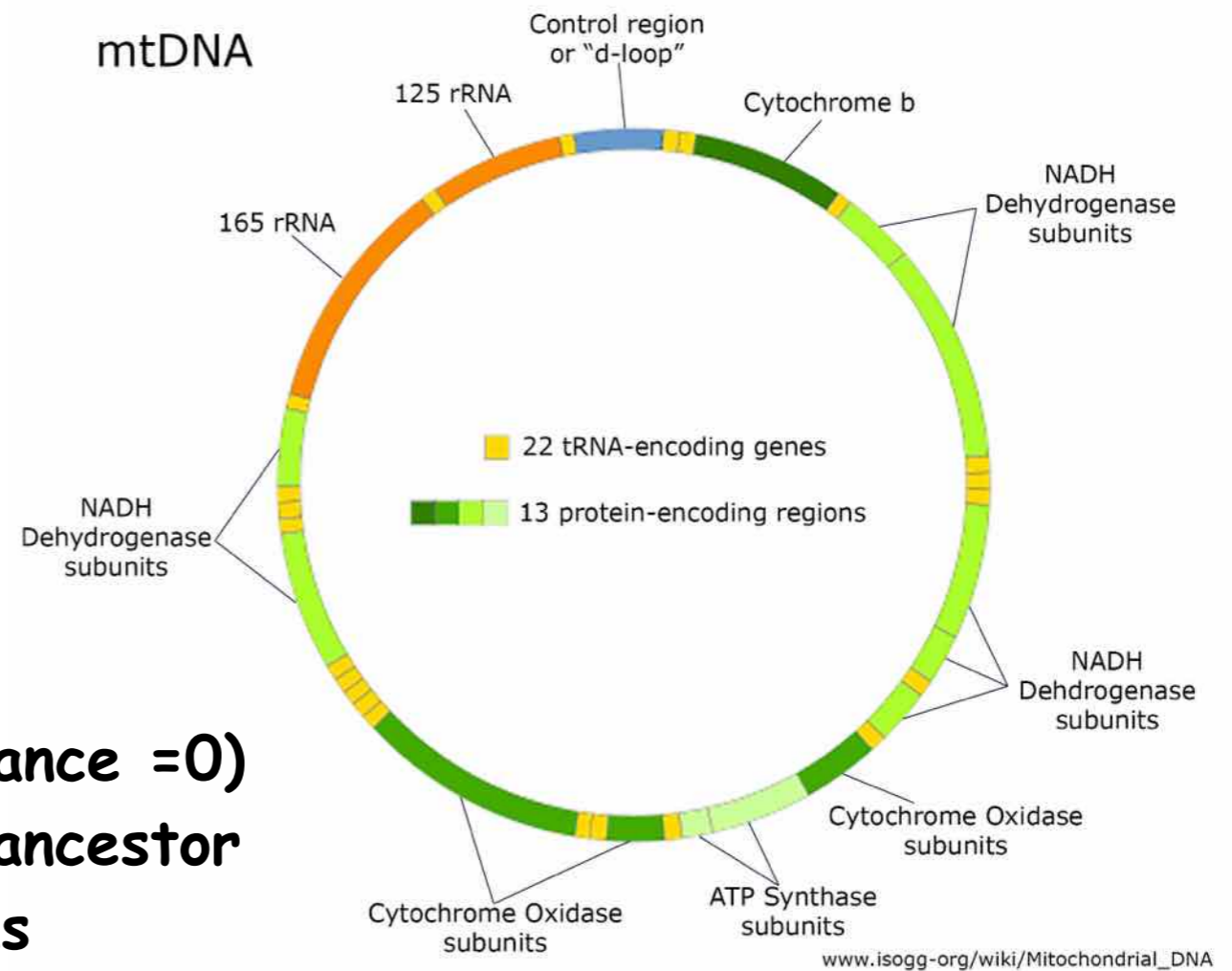
FTDNA conducts complete mtDNA test

23andMe tests "Selected branch defining SNPs"

Ancestry does not test mtDNA

Haplogroup is a genetic population group of people who share a common ancestor on the patrilineal or matrilineal lines

mtDNA - Results

Haplogroup - T2b24a

Your Origin

The mitochondrial haplogroup T is best characterized as a European lineage. With an origin in the Near East greater than 45,000 years ago, the major sub-lineages of haplogroup T entered Europe around the time of the Neolithic 10,000 years ago. Once in Europe, these sub-lineages underwent a dramatic expansion associated with the arrival of agriculture in Europe. Haplogroup T2 is one of the older sub-lineages and may have been present in Europe as early as the Late Upper Palaeolithic.

*Based on Build 17 from:

van Oven M, Kayser M. 2009. *Updated comprehensive phylogenetic tree of global human mitochondrial DNA variation*. Hum Mutat 30(2):E386-E394.

http://www.phylotree.org/ (Build 17)

USAGE POLICY: Use of the above Haplogroup description requires written permission from Gene by Gene.

Your Results

RSRS Values | rCRS Values

HVR1 DIFFERENCES FROM rCRS				
16126C	16294T	16296T	16304C	16519C

HVR2 DIFFERENCES FROM rCRS				
73G	263G	309.1C	315.1C	321C

CODING REGION DIFFERENCES FROM rCRS				
709A	750G	930A	1438G	1888A
2706G	4216C	4769G	4917G	5147A
5219T	5426C	7028T	8572A	8697A
8860G	10463C	11251G	11719A	11812G
13368A	14233G	14766T	14905A	15326G
15452A	15607G	15928A		

revised Cambridge Reference Sequence

38 differences

(CRS first published in 1981, corrected revised CRS published in 1999. Haplogroup H2a2a1)

6

Haplogroup - T2b24a

Your Origin

The mitochondrial haplogroup T is best characterized as a European lineage. With an origin in the Near East greater than 45,000 years ago, the major sub-lineages of haplogroup T entered Europe around the time of the Neolithic 10,000 years ago. Once in Europe, these sub-lineages underwent a dramatic expansion associated with the arrival of agriculture in Europe. Haplogroup T2 is one of the older sub-lineages and may have been present in Europe as early as the Late Upper Palaeolithic.

*Based on Build 17 from:

van Oven M, Kayser M. 2009. *Updated comprehensive phylogenetic tree of global human mitochondrial DNA variation.* Hum Mutat 30(2):E386-E394.

http://www.phylotree.org/ (Build 17)

USAGE POLICY: Use of the above Haplogroup description requires written permission from Gene by Gene.

Your Results

RSRS Values	rCRS Values

Extra Mutations	309.1C 315.1C 522.1A 522.2C C5219T C16296T
Missing Mutations	

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

HVR2 DIFFERENCES FROM RSRS				
C146T	C152T	C195T	A247G	309.1C
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	C5219T
T5426C	G7146A	T7256C	A7521G	T8468C
G8572A	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				

Reconstructed Sapiens Reference Sequence

71 differences

CeCe Moore
thinks there is a great upside to mtDNA testing

Currently FTDNA provides the most detailed haplogroup and subclade information
To get the same detail from 23andMe data use:

dna.jameslick.com/mthap/

Down load mtDNA data from 23andMe
Unzip data to produce a .txt file
go to James Lick website, choose the file and upload
and…

If you've tested your full mtDNA at FTDNA you can download it to
GenBank to increase a scientific database

mthap version 0.19b (2015-05-11); haplogroup data version PhyloTree Build 17 (2016-02-18)
raw data source genome_███████████████████████ t (51KB)

Found 2441 markers at 2440 positions covering 14.7% of mtDNA.

If you've tested at 23andMe and want more detailed information on your mtDNA haplogroup use dna.jameslick.com/mthap/

NOTICE: You appear to have uploaded a 23andme v3 raw data file which has 9 known unreliable markers that will be excluded from this analysis.

Markers found (shown as differences to rCRS):

HVR2: 73G 263G
CR: 709A 750G 930A 1438G 1888A 2706G 4216C 4769G 4917G 5147A 5426C 7028T 8697A 8860G 10463C 11251G 11719A 14233G 14766T 15326G 15452A 15607G 15928A
HVR1: 16126C 16304G (16519C)

IMPORTANT NOTE: The above marker list is almost certainly incomplete due to limitations of genotyping technology and is not comparable to mtDNA sequencing results. It should not be used with services or tools that expect sequencing results, such as mitosearch.

Best mtDNA Haplogroup Matches:

1) T2b24a

Defining Markers for haplogroup T2b24a:
HVR2: 73G 263G 321C
CR: 709A 750G 930A 1438G 1888A 2706G 4216C 4769G 4917G 5147A 5426C 7028T 8572A 8697A 8860G 10463C 11251G 11719A 11812G 13368A 14233G 14766T 14905A 15326G 15452A 15607G 15928A
HVR1: 16126C 16294T (16296T) 16304C

Marker path from rCRS to haplogroup T2b24a (plus extra markers):

H2a2a1(rCRS) ⇒ 263G ⇒ H2a2a ⇒ 8860G 15326G ⇒ H2a2 ⇒ 750G ⇒ H2a ⇒ 4769G ⇒ H2 ⇒ 1438G ⇒ H ⇒ 2706G 7028T ⇒ HV ⇒ 14766T ⇒ R0 ⇒

73G 11719A ⇒ R ⇒ 4216C ⇒ R2'JT ⇒ 11251G 15452A 16126C ⇒ JT ⇒ 709A 1888A 4917G 8697A 10463C 13368A 14905A 15607G 15928A 16294T ⇒ T ⇒ 11812G

14233G (16296T) ⇒ T2 ⇒ 930A 5147A 16304C ⇒ T2b ⇒ 321C ⇒ T2b24 ⇒ 5426C 8572A ⇒ T2b24a ⇒ (16519C)

Imperfect Match. Your results contained differences with this haplogroup:
Matches(26): 73G 263G 709A 750G 930A 1438G 1888A 2706G 4216C 4769G 4917G 5147A 5426C 7028T 8697A 8860G 10463C 11251G 11719A 14233G 14766T 15326G 15452A 15607G 15928A 16126C
Flips(1): 16304G
Extras(0): (16519C)
No-Calls(2): 11812G 13368A (16296T)
Untested(4): 321 8572 14905 16294

Y-DNA - Standard Y-STR Values

PANEL 1 (1-12) ℹ

Marker	DYS393	DYS390	DYS19 **	DYS391	DYS385	DYS426	DYS388	DYS439	DYS389I	DYS392	DYS389II ***
Value	14	24	13	10	15-16	11	12	10	12	11	30

PANEL 2 (13-25) ℹ

Marker	DYS458	DYS459	DYS455	DYS454	DYS447	DYS437	DYS448	DYS449	DYS464
Value	16	9-9	11	11	24	15	20	31	15-16-17-19

PANEL 3 (26-37) ℹ

Marker	DYS460	Y-GATA-H4	YCAII	DYS456	DYS607	DYS576	DYS570	CDY	DYS442	DYS438
Value	11	11	21-21	14	13	18	16	35-38	13	10

PANEL 4 (38-47) ℹ

Marker	DYS531	DYS578	DYF395S1	DYS590	DYS537	DYS641	DYS472	DYF406S1	DYS511
Value	10	8	15-15	8	11	10	8	10	9

PANEL 4 (48-60) ℹ

Marker	DYS425	DYS413	DYS557	DYS594	DYS436	DYS490	DYS534	DYS450	DYS444	DYS481	DYS520	DYS446
Value	0 *	21-23	16	11	12	12	15	7	12	24	17	13

PANEL 4 (61-67) ℹ

Marker	DYS617	DYS568	DYS487	DYS572	DYS640	DYS492	DYS565
Value	13	11	15	10	12	11	11
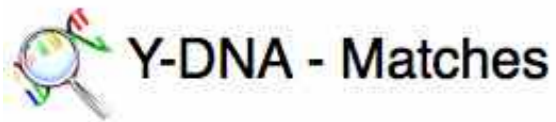
Y-DNA - Matches

FILTER MATCHES

Show Matches For: The Entire Database ⬍   Markers: 37 ⬍   Distance: All ⬍   Matches Per Page: 25 ⬍

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

37 MARKERS - 13 - MATCHES

Genetic Distance	Name	Earliest Known Ancestor	Y-DNA Haplogroup	Terminal SNP	Match Date ↑
0	🖥 TiP 📝 Y-DNA37		E-M35	M35	7/21/2010
0	🖥 TiP 📝 Y-DNA37		E-M35	M35	7/21/2010
0	🖥 TiP 📝 Y-DNA37		E-M35	M35	7/21/2010
1	🖥 TiP 📝 Y-DNA37		E-M35	M35	7/21/2010
1	🖥 TiP 📝 Y-DNA37		E-M35	M35	7/21/2010
1	🖥 TiP 📝 Y-DNA37		E-M35	M35	7/21/2010
2	🖥 TiP 📝 Y-DNA37		E-M35	M35	7/21/2010
2	🖥 TiP 📝 Y-DNA67 FF		E-PF1975	PF1975	7/21/2010
4	🖥 TiP 📝 Y-DNA37		E-M35	M35	7/21/2010

The match date is 7/21/2010 because that's when my test results were completed and matched these folks.

8 of 9 people had ▮▮▮▮▮▮▮▮▮▮▮▮ **as an email address**

Emailed and talked to ▮▮▮▮▮▮▮

▮▮▮▮ **surname was closest match genetic distance = 0, 37 marker test**

Found out about History and Genealogy of the ▮▮▮▮ **Family,**

    written in 1978 by ▮▮▮▮▮▮

Poling name probably got transcribed incorrectly for some people

Your Confirmed Haplogroup is E-Z830

Haplogroup E is an African lineage. It is currently believed that this haplogroup dispersed south from northern Africa with the Bantu agricultural expansion. E is also the most common lineage among African Americans. It is a diverse haplogroup with many branches and is found distributed throughout Africa today. It is also found at a very low frequency in North Africa and the Middle East.

| A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S | T |

| Tested Positive | Tested Negative | Presumed Positive | Test Available | Presumed Negative | Test in Progress |

| SK863 | E-SK863 |
| Z827 More... | E-Z827 |

E - Z827 SNP Pack
- Refine the geographic origins of your paternal line in 1 easy step! Learn more
- Get 150 SNPs related to Z827 for only $119.

$119

L19 More...	E-L19
M81 More...	E-M81
M183	E-M183
M165	E-M165
A5604 More...	E-A5604
A5603 More...	E-A5603
PF2477	E-PF2477
PF2546	E-PF2546
CTS12227 More...	E-CTS12227
MZ13 More...	E-MZ13
BY8902	E-BY8902
BY8905	E-BY8905
MZ11	E-MZ11
MZ12	E-MZ12
BY8940	E-BY8940
BY8950	E-BY8950
MZ39 More...	E-MZ39

4 Types of DNA

mtDNA

atDNA

13

3GGP
4th cousins
~0.195%
~13.8cM

2GGP
3rd cousins
~0.781%
~53cM

G Grandparents
2nd cousins
~3.125%
~212cM

Grandparents
1st cousins
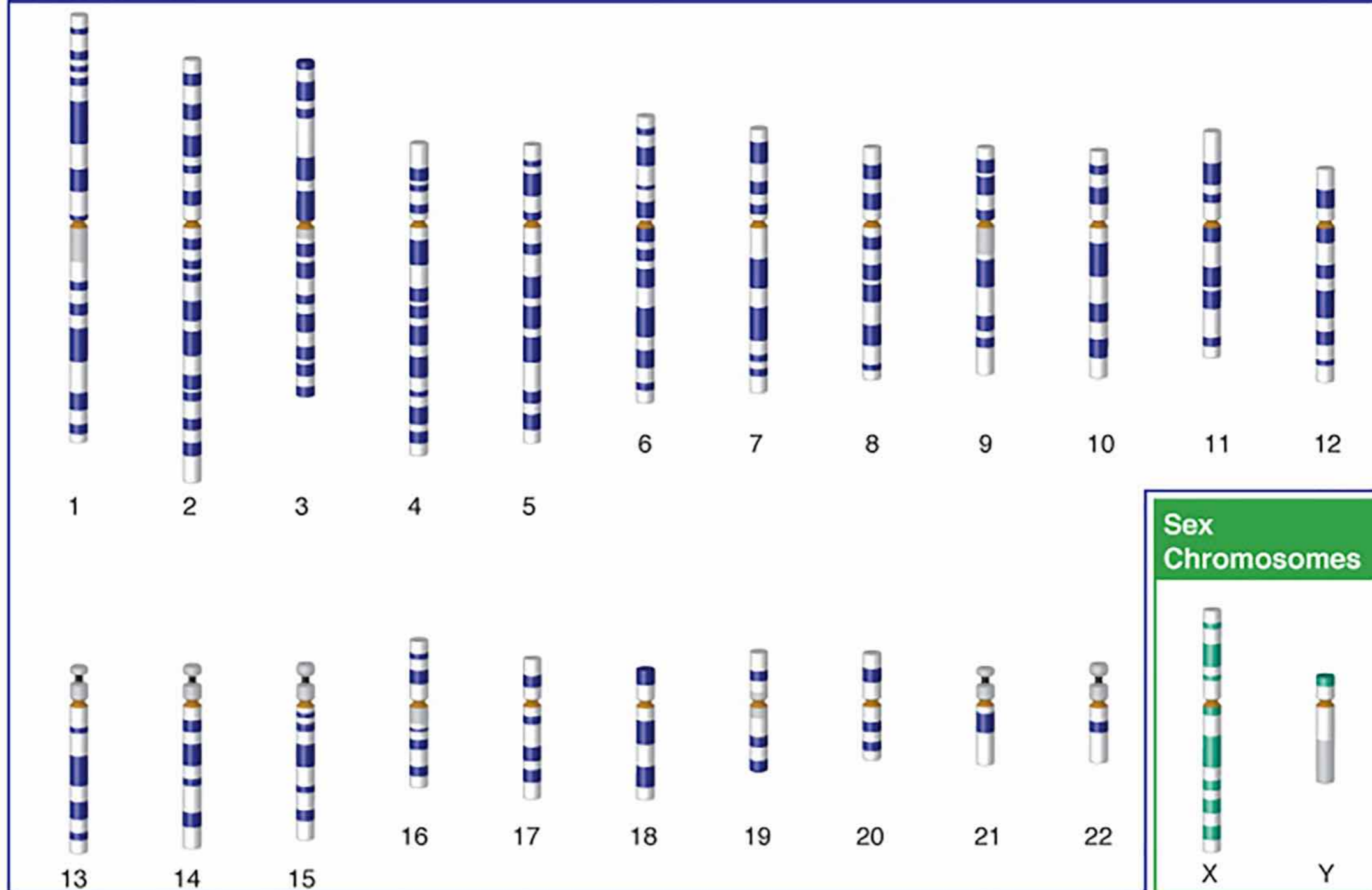~12.5%
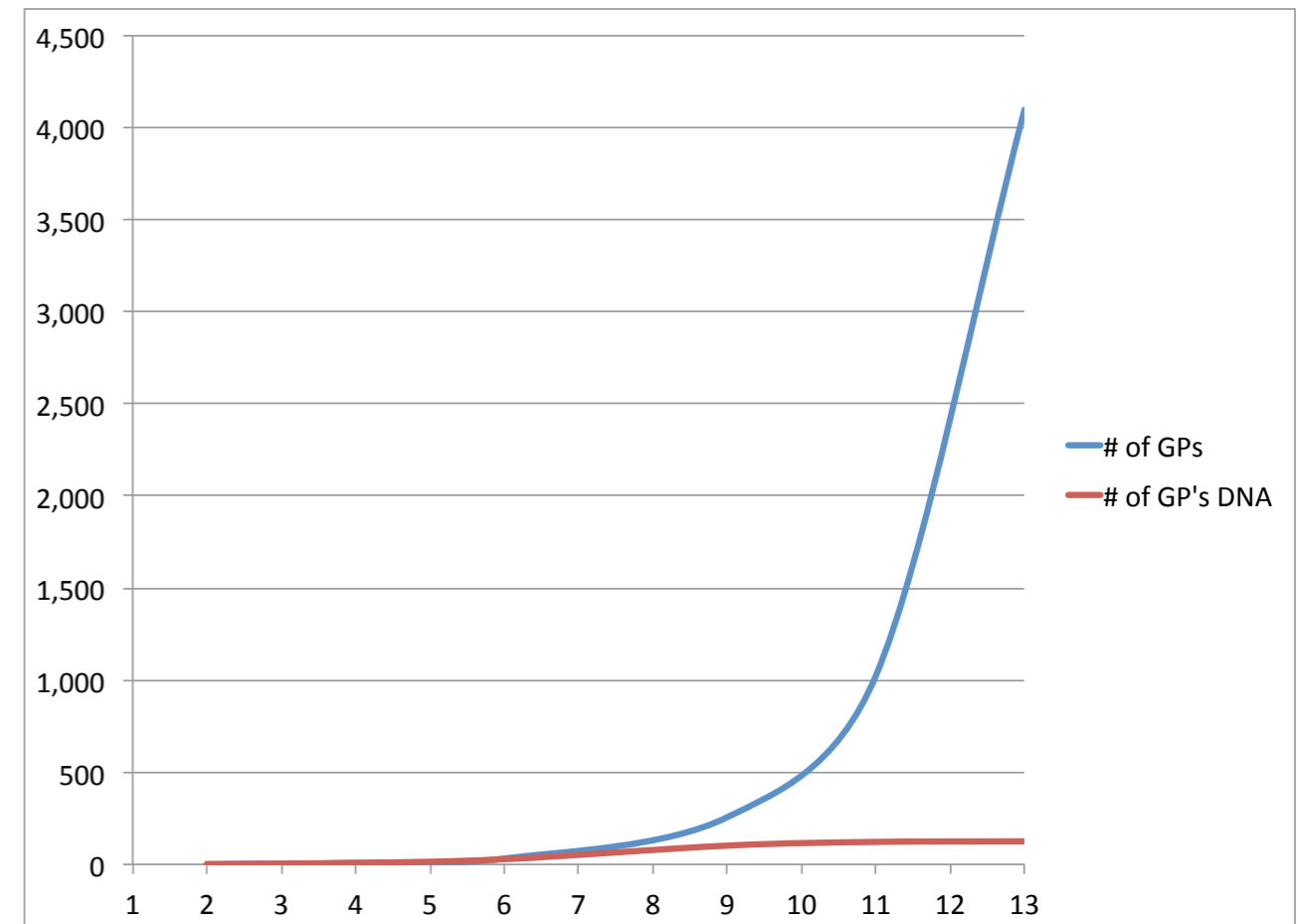~850cM
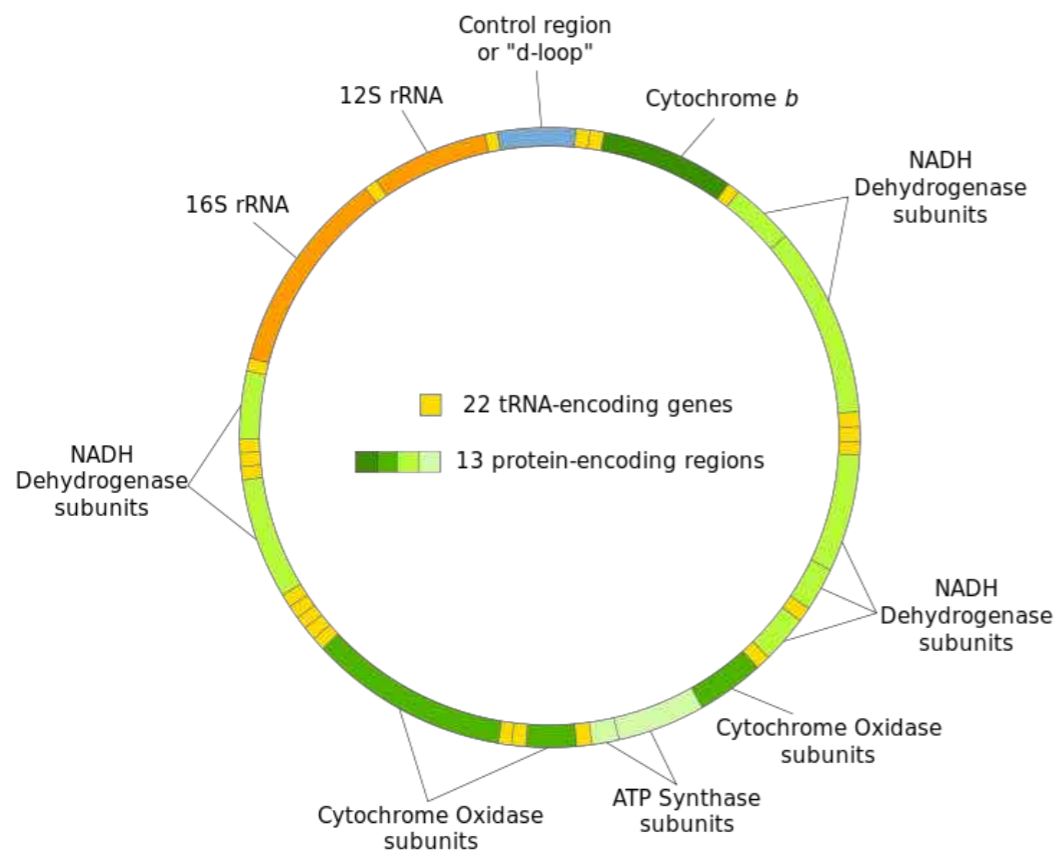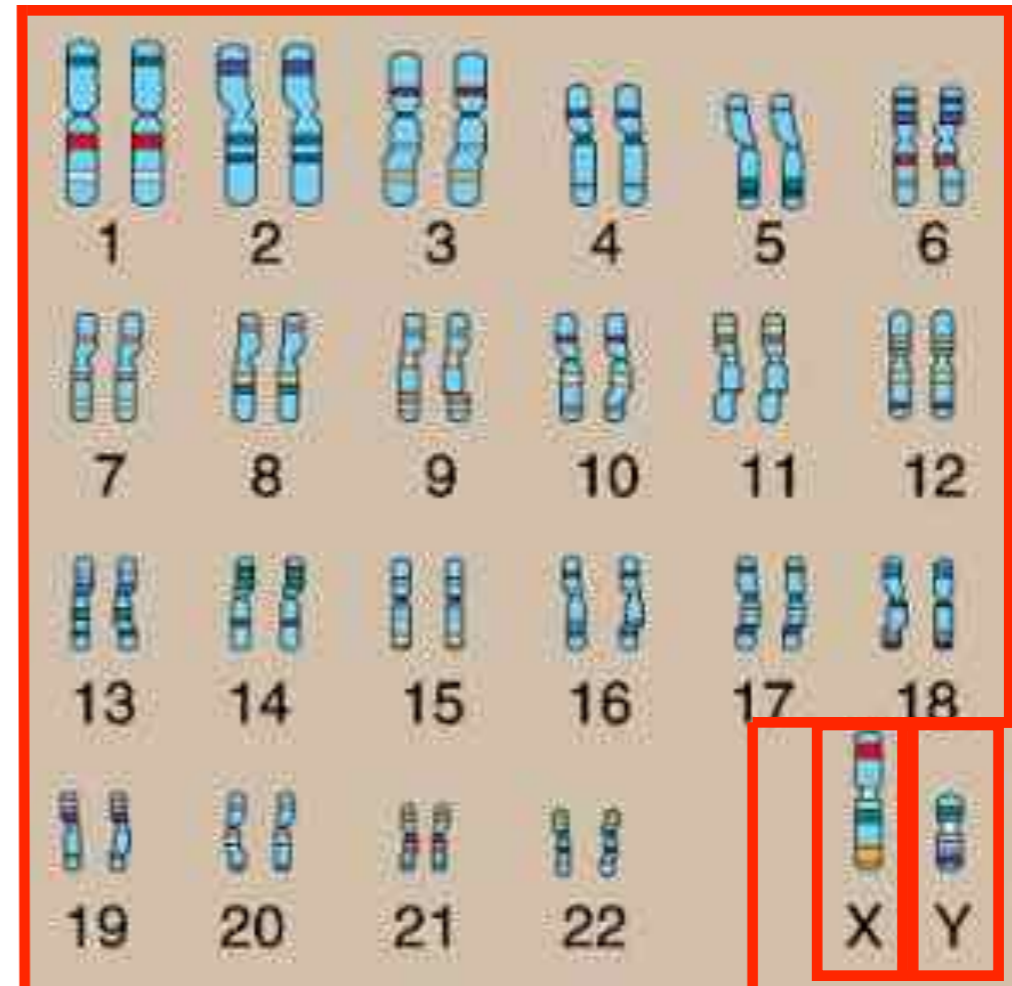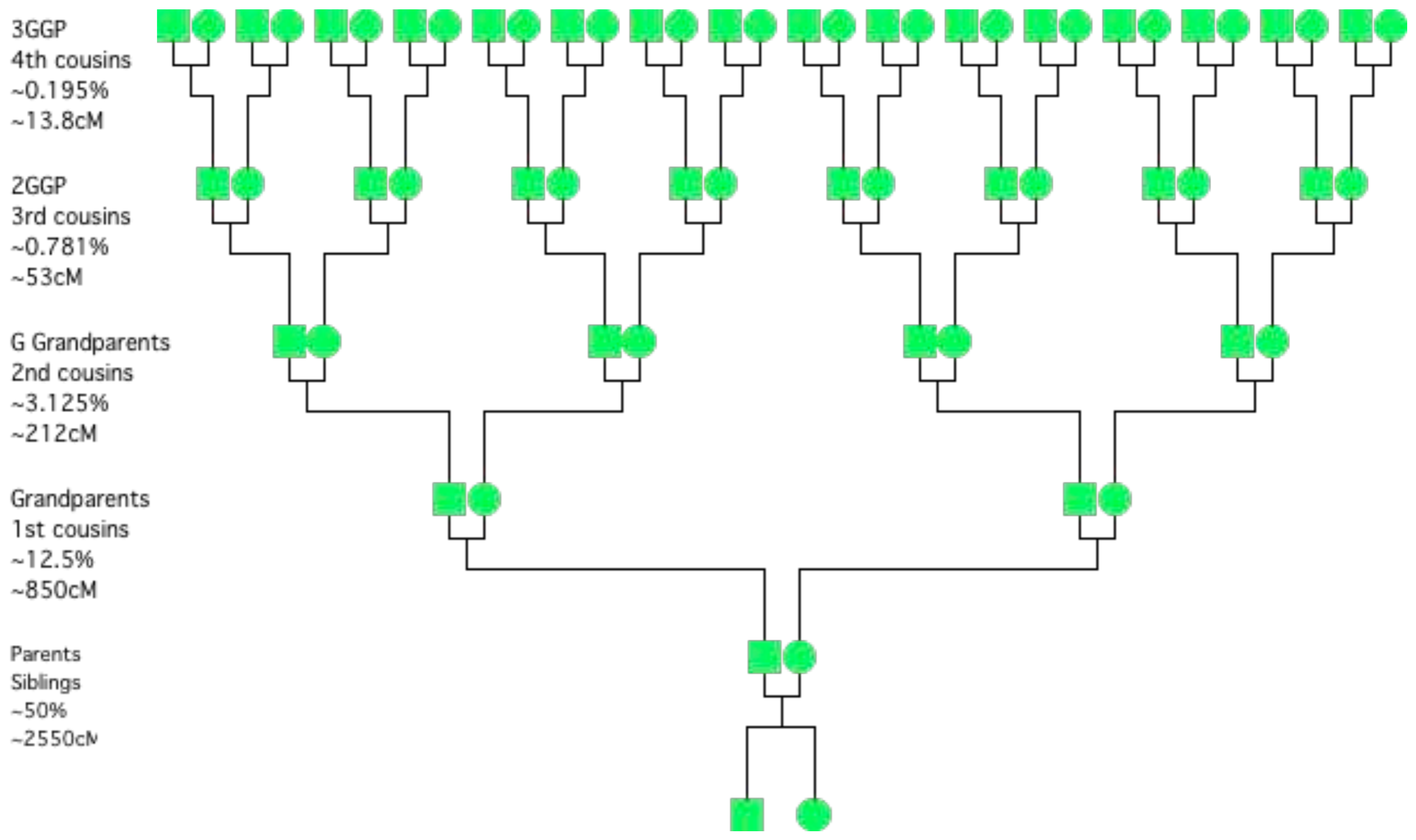
Parents
Siblings
~50%
~2550cM

Think
SEGMENTS
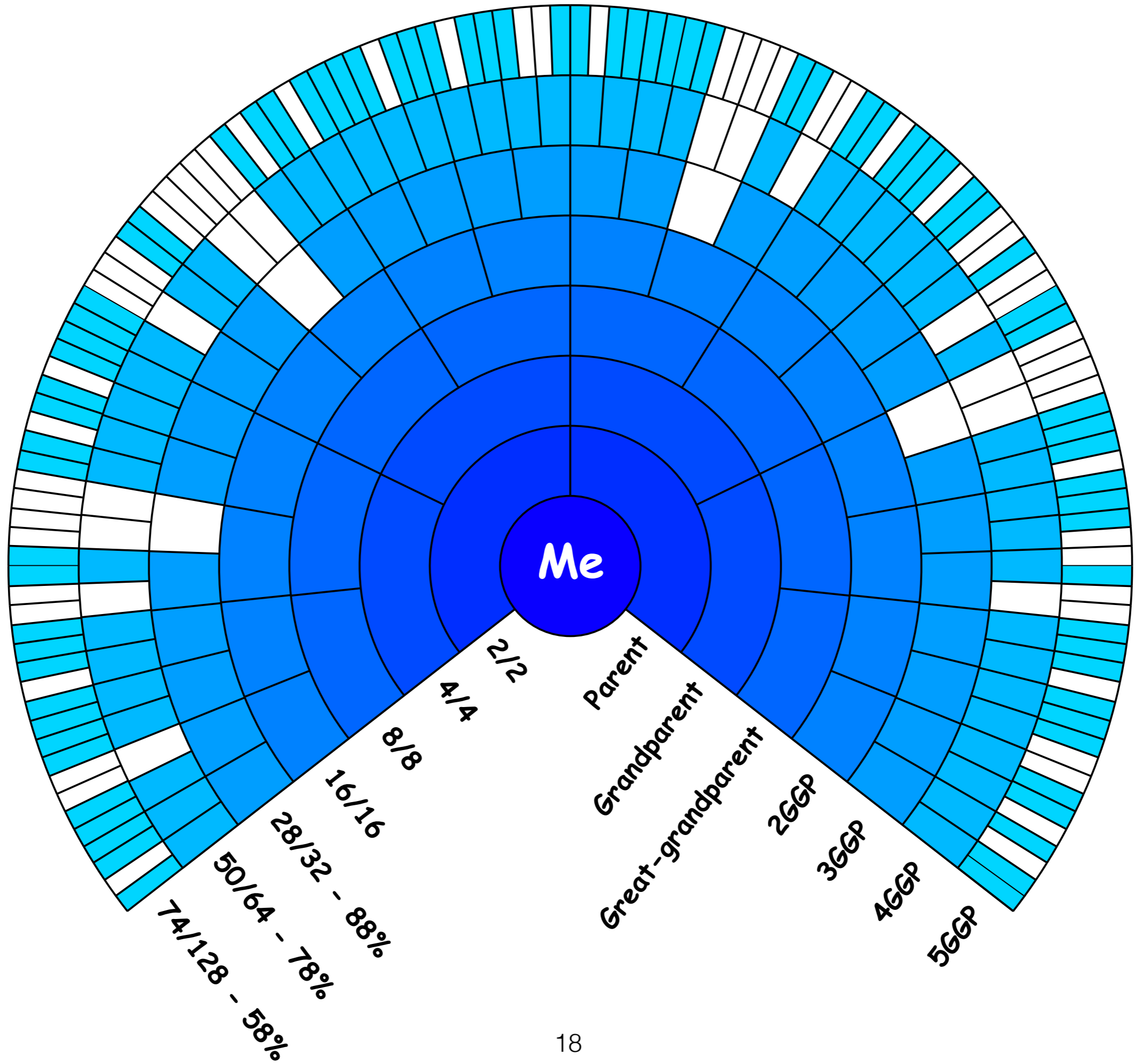
https://isogg.org/wiki/Autosomal_DNA

16

Approximate odds that atDNA will be retained

Generation	# of grandparents	# of grandparents whose DNA you retain	% of grandparents represented in you DNA
4th (G Gp)	8	8	100%
6th (3G Gp)	32	28	88%
8th (5G Gp)	256	102	40%
10th (7G Gp)	1,024	122	12%
12th (9G Gp)	4,096	125	3%

Me

2/2
4/4
8/8
16/16
28/32 - 88%
50/64 - 78%
74/128 - 58%

Parent
Grandparent
Great-grandparent
2GGP
3GGP
4GGP
5GGP

18

Relationships Detected by Autosomal DNA Testing

Relationship level	%DNA shared	cMs range	Detected by testing	Notes
Parent/Child	50%	3400	100%	The percentage is exact, not an average
Siblings	50% (42%-58%)	2800-4000	100%	
Grandparent, grandchild, uncle/aunt, niece/nephew, half siblings	25% (18%-32%)	1200-2200	100%	Note that when the DNA testing companies predict a relationship, that they are predicting this information based on the shared DNA. They are not taking any paper documentation into account
1st cousins; GGP, GU or GA, half GA, half GU	12.5% (7.3%-13.8%)	500-950	> 99.9%	A half-aunt/uncle relationship is one where there is a half-sibling relationship between the parent and the aunt or uncle.
2nd cousins	3.13% (2.5%-5%)	170-340	> 99%	
3rd cousins	0.78% (0.3%-2.0%)	20-135	> 90%	
4th cousins	0.2% (0.0%-0.5%)	0-34	< 50%	Once a relationship is further than 4th cousin it becomes much more difficult to detect and differentiate the relationship based on the amount of shared DNA

International Society of Genetic Genealogists "Autosomal DNA Statistics" ISOGG Wiki
(http://www.isogg.org/wiki/Autosomal_DNA_statistics : accessed May 2014

% of cases

8C 7C 6C — .05 0.1 0.8 · 5C 3,4 · 4CIR 6,8 · 4C 13.7 · 3CIR 27.5 · 3C 55 · 2CIR 110 · 2C 220 · 1CIR 440 · 1C 880

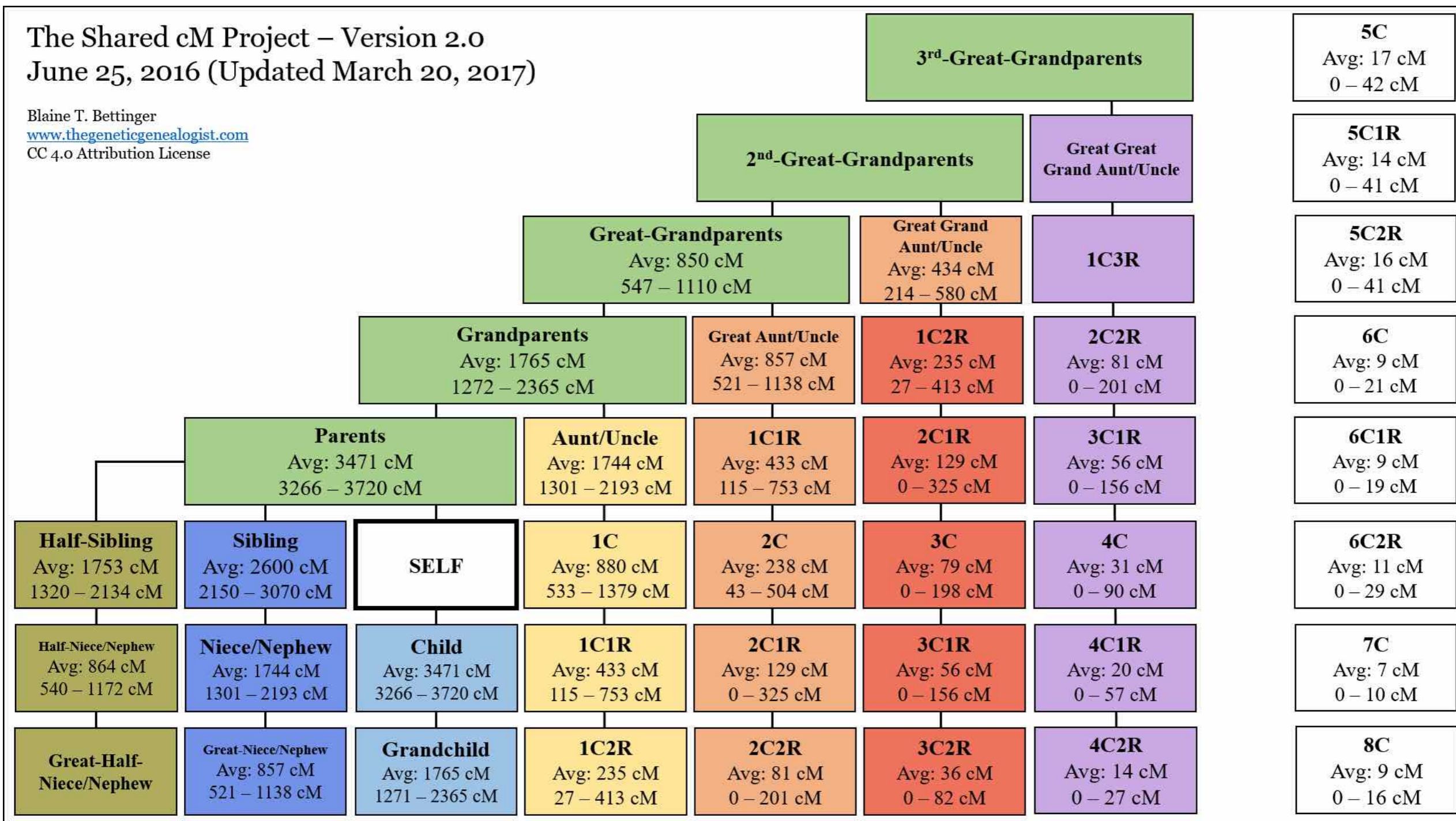cM (log scale)

1 · 7 · 10 · 100 · 1000
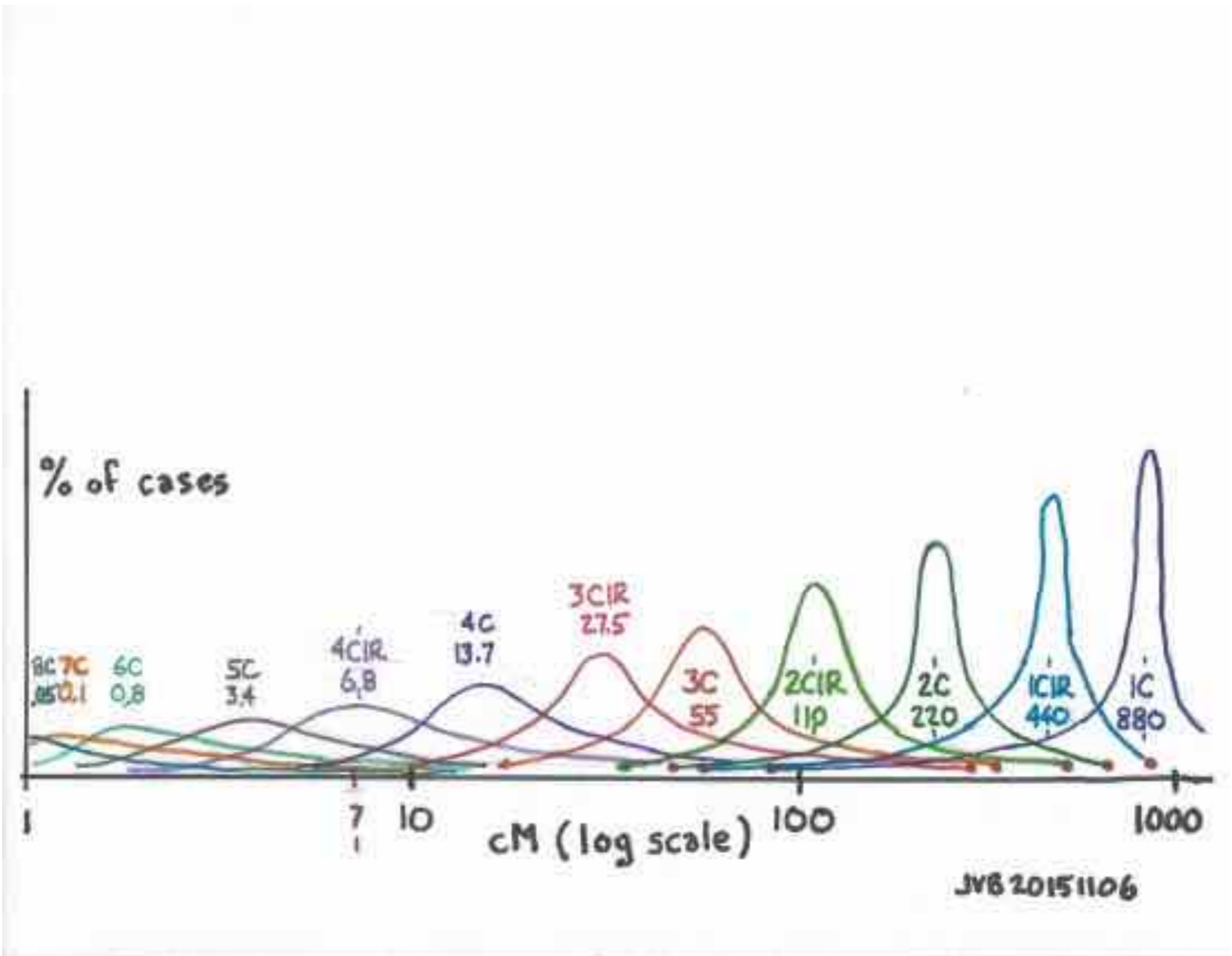
JVB 20151106

06B Segment-ology: Segment Size vs Cousinship Chart Needed; Jim Bartlett 2015-11-06
segementology.org

20

The Shared cM Project – Version 2.0
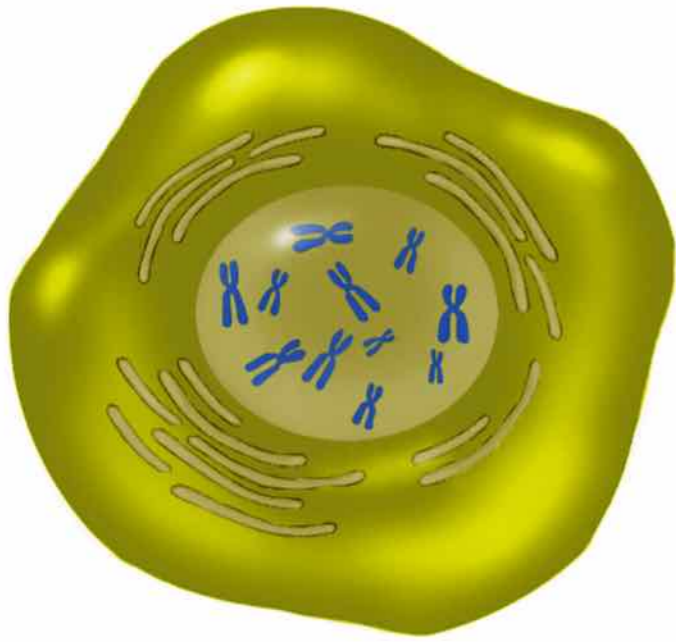**June 25, 2016 (Updated March 20, 2017)**

Blaine T. Bettinger
www.thegeneticgenealogist.com
CC 4.0 Attribution License

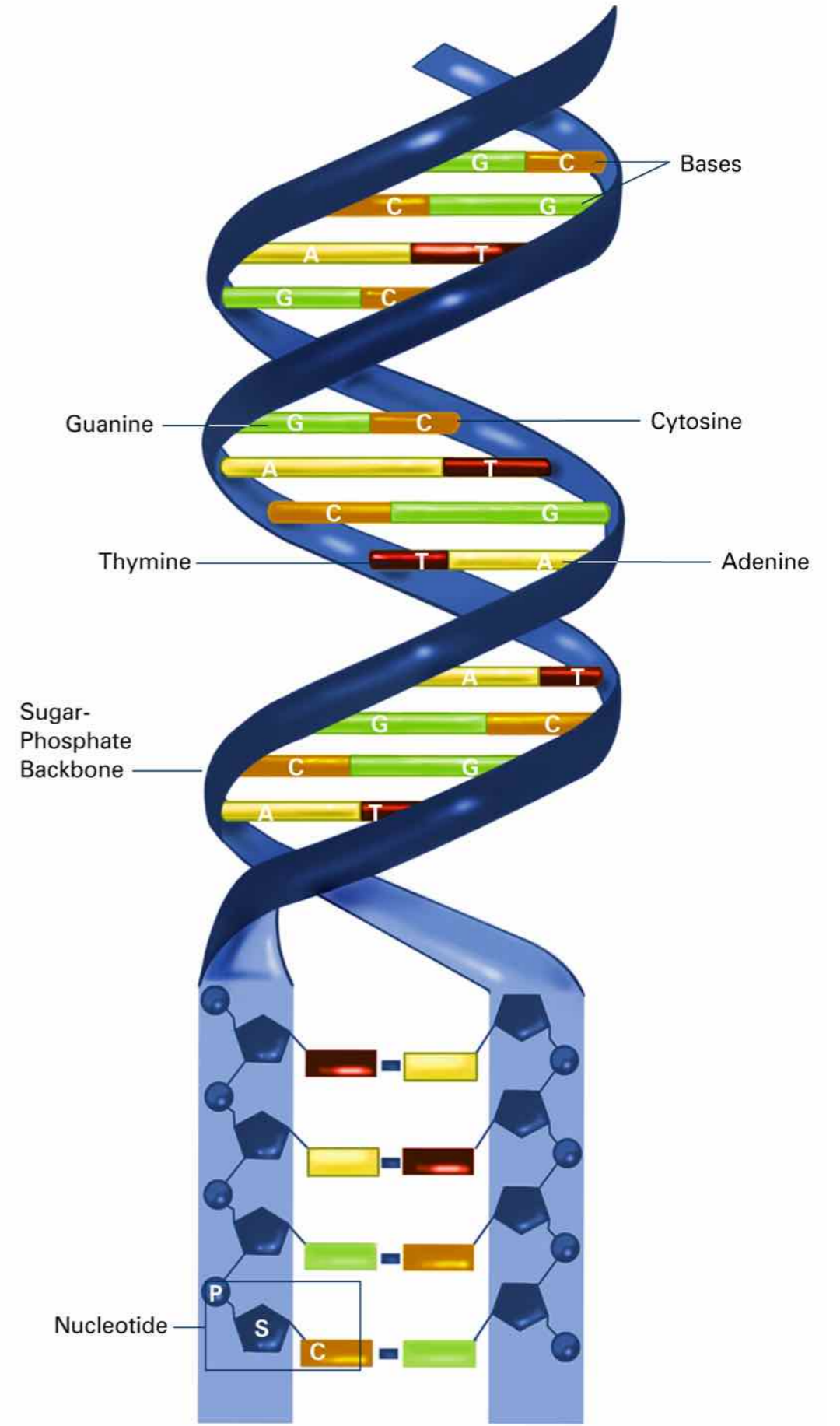|						3rd-Great-Grandparents	5C Avg: 17 cM 0 – 42 cM
					2nd-Great-Grandparents	Great Great Grand Aunt/Uncle	5C1R Avg: 14 cM 0 – 41 cM
				Great-Grandparents Avg: 850 cM 547 – 1110 cM	Great Grand Aunt/Uncle Avg: 434 cM 214 – 580 cM	1C3R	5C2R Avg: 16 cM 0 – 41 cM
			Grandparents Avg: 1765 cM 1272 – 2365 cM	Great Aunt/Uncle Avg: 857 cM 521 – 1138 cM	1C2R Avg: 235 cM 27 – 413 cM	2C2R Avg: 81 cM 0 – 201 cM	6C Avg: 9 cM 0 – 21 cM
		Parents Avg: 3471 cM 3266 – 3720 cM	Aunt/Uncle Avg: 1744 cM 1301 – 2193 cM	1C1R Avg: 433 cM 115 – 753 cM	2C1R Avg: 129 cM 0 – 325 cM	3C1R Avg: 56 cM 0 – 156 cM	6C1R Avg: 9 cM 0 – 19 cM
Half-Sibling Avg: 1753 cM 1320 – 2134 cM	Sibling Avg: 2600 cM 2150 – 3070 cM	SELF	1C Avg: 880 cM 533 – 1379 cM	2C Avg: 238 cM 43 – 504 cM	3C Avg: 79 cM 0 – 198 cM	4C Avg: 31 cM 0 – 90 cM	6C2R Avg: 11 cM 0 – 29 cM
Half-Niece/Nephew Avg: 864 cM 540 – 1172 cM	Niece/Nephew Avg: 1744 cM 1301 – 2193 cM	Child Avg: 3471 cM 3266 – 3720 cM	1C1R Avg: 433 cM 115 – 753 cM	2C1R Avg: 129 cM 0 – 325 cM	3C1R Avg: 56 cM 0 – 156 cM	4C1R Avg: 20 cM 0 – 57 cM	7C Avg: 7 cM 0 – 10 cM
Great-Half-Niece/Nephew	Great-Niece/Nephew Avg: 857 cM 521 – 1138 cM	Grandchild Avg: 1765 cM 1271 – 2365 cM	1C2R Avg: 235 cM 27 – 413 cM	2C2R Avg: 81 cM 0 – 201 cM	3C2R Avg: 36 cM 0 – 82 cM	4C2R Avg: 14 cM 0 – 27 cM	8C Avg: 9 cM 0 – 16 cM

https://isogg.org/wiki/Autosomal_DNA_statistics#Distribution_of_genealogical_relationships_for_given_amounts_of_shared_DNA

21

IBD (Identical by Descent) v IBS (Identical by State)

cM of Matching Segment	% IBD	% IBS
11 cM	>99%	<1%
10 cM	99%	1%
9 cM	80%	20%
8 cM	50%	50%
7 cM	30%	70%
6 cM	20%	80%
5 cM	5%	95%
4 cM	1%	99%

Chromosomes are made of
DNA - deoxyribonucleic acid

Bases

Guanine — Cytosine

Thymine — Adenine

Sugar-Phosphate Backbone

Nucleotide

P

S

C

Chromosome 9 Pair – unspiraled and flattened

3 locations out of approximately 32878 locations used on Chromosome 9 (36587 to 140186312)

Results are not necessarily in order from the "first" or "second" chromosome

Results are from same "side" of chromosome

	AC	TC	AG
	rs2243313 106660961	rs2230805 106663850	rs4149279 106667080

gene

Base Pair

ATG........TAA T C G A TAC.................ACT A.............C.............A

TAC........ATT A G C T ATG.................TGA T...............G..................T

gene

gene

ATG........TAA T C G A TAC.................ACT C.............T.............G

TAC........ATT A G C T ATG.................TGA G...............A..................C

Base Pair

gene
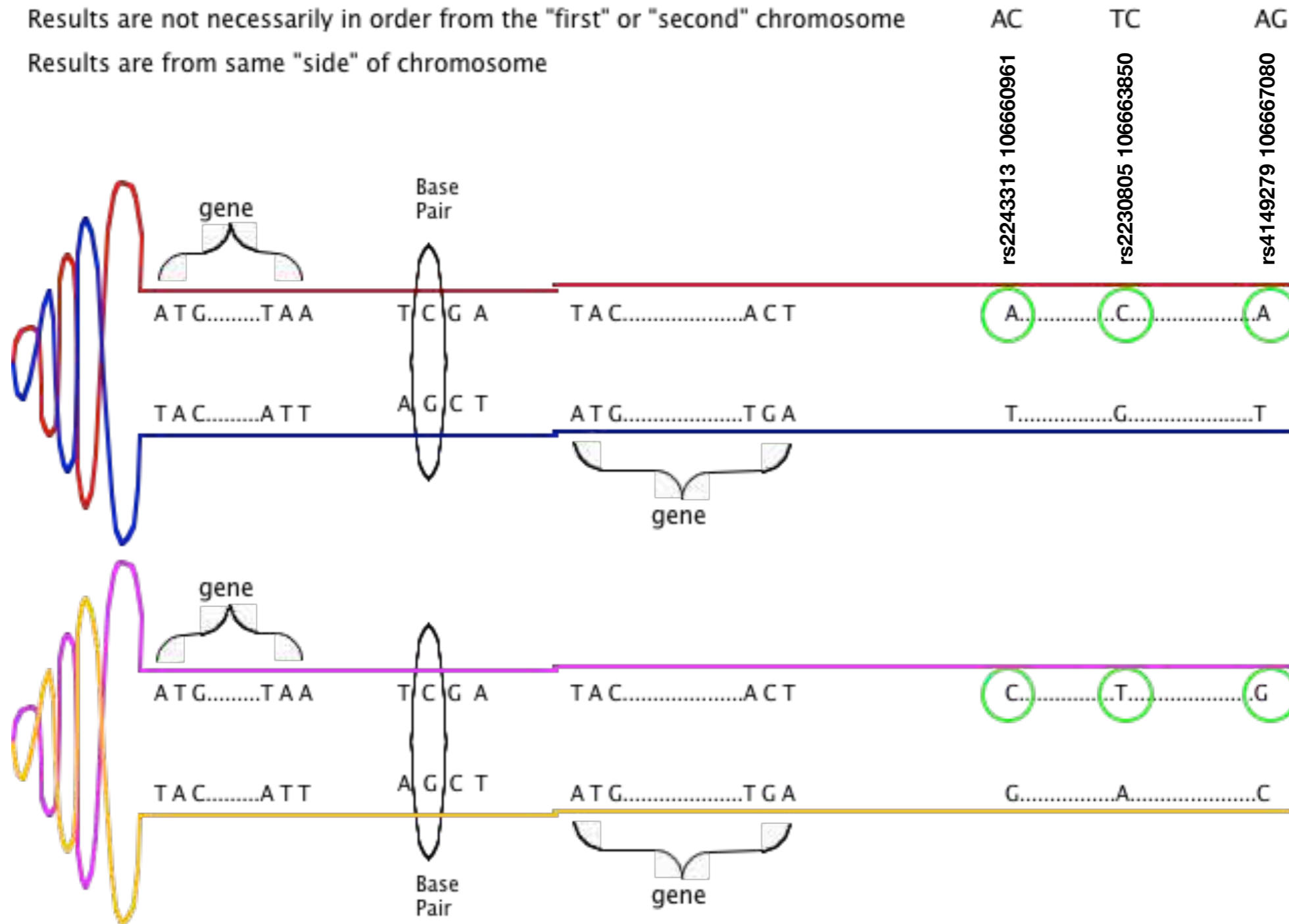
Approximately 3,000,000,000 base pairs across 46 chromosomes (23 pairs of chromosomes)

Not to Scale

24

How DNA is inherited

DAD

1	2
A	G
C	T
G	A
T	A
C	A
T	A
G	C

ME

1	2
A	C
C	G
G	A
T	C
A	G
A	A
C	C

MOM

1	2
C	T
G	C
A	T
C	T
G	A
A	T
G	C

from Blaine Bettinger

25

MRCA

Most Recent Common Ancestor

Originated when Y-chromosome & mitochondrial DNA testing were the only DNA tests available.
Both lead to a single individual as a common ancestor

atDNA testing may determine the
most recent common couple or ancestor<u>s</u>

IBD
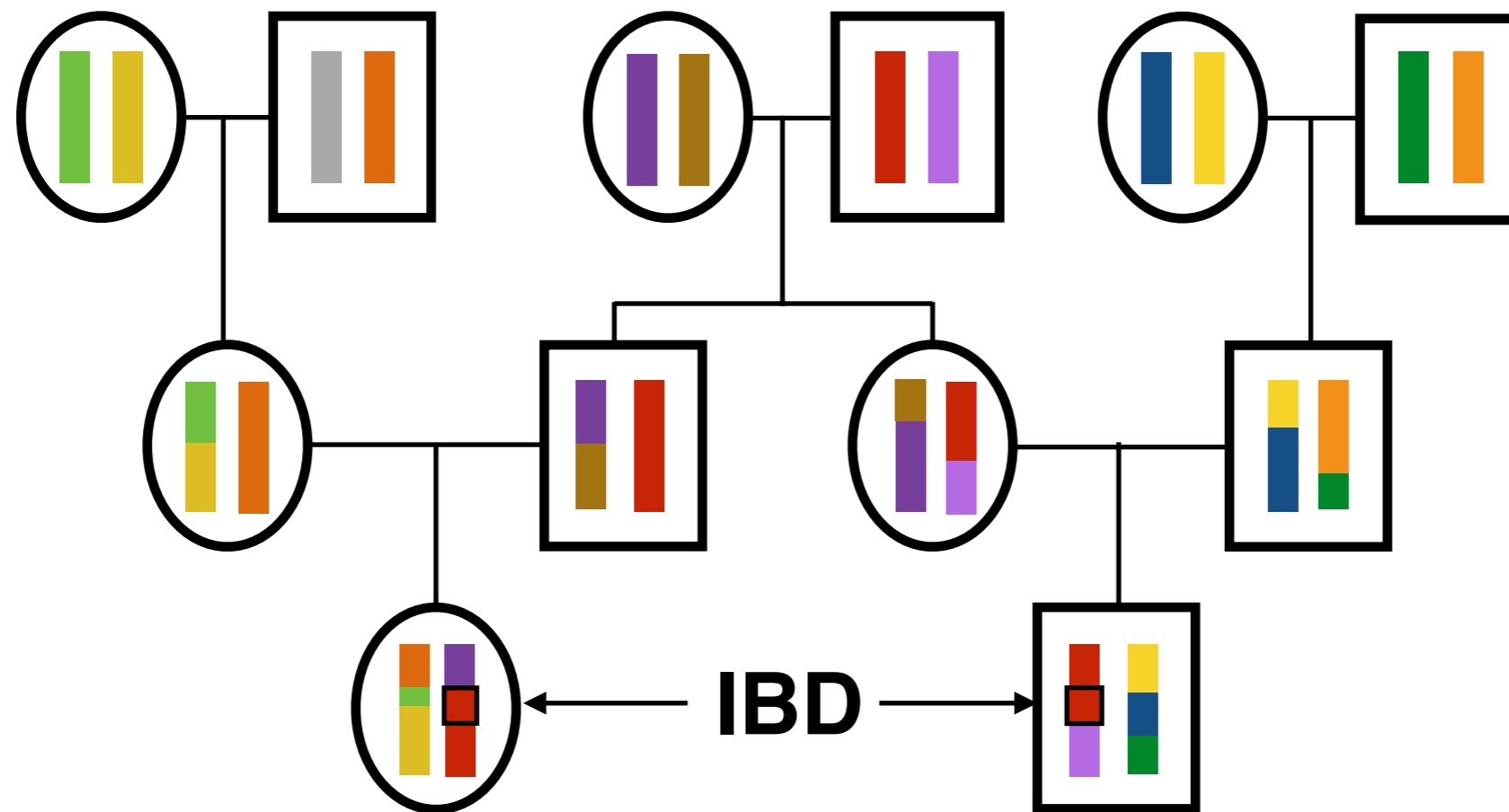
Crossover Recombination in Autosomes and X chromosomes
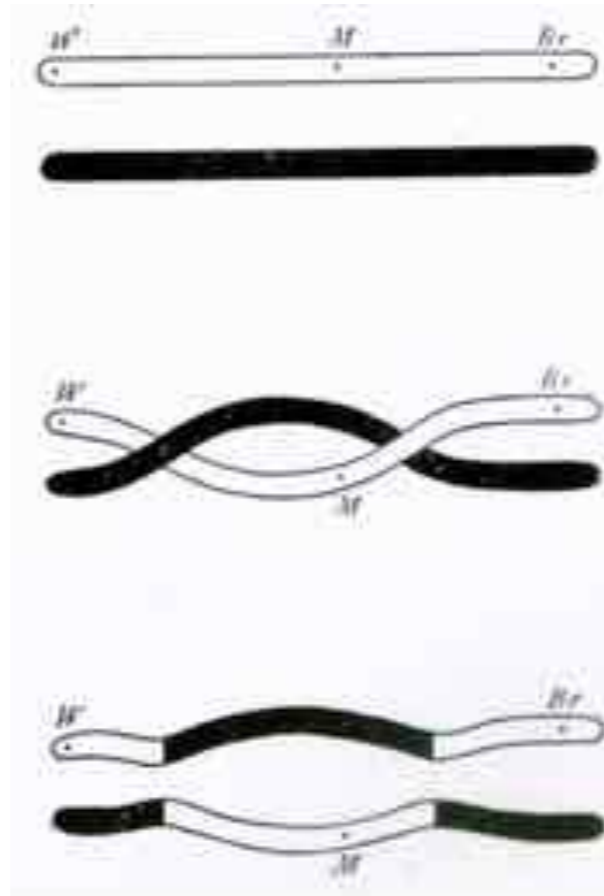
Only the homologous chromosomes that pair up from each parent engage in crossover recombination like this. In a female, two Xs pair up and behave like the other chromosomes (the autosomes). The X chromosome and the Y chromosome line up but only exchange minimal information, mostly at the tips. For our purposes, the X does not mix when passed through a male to a daughter. Almost the entire chromosome remains intact i.e. the A-C-G-T... sequence remains the same in a male.

However, it is not dormant. The X still contributes important genes to every male.

Segments of DNA Example
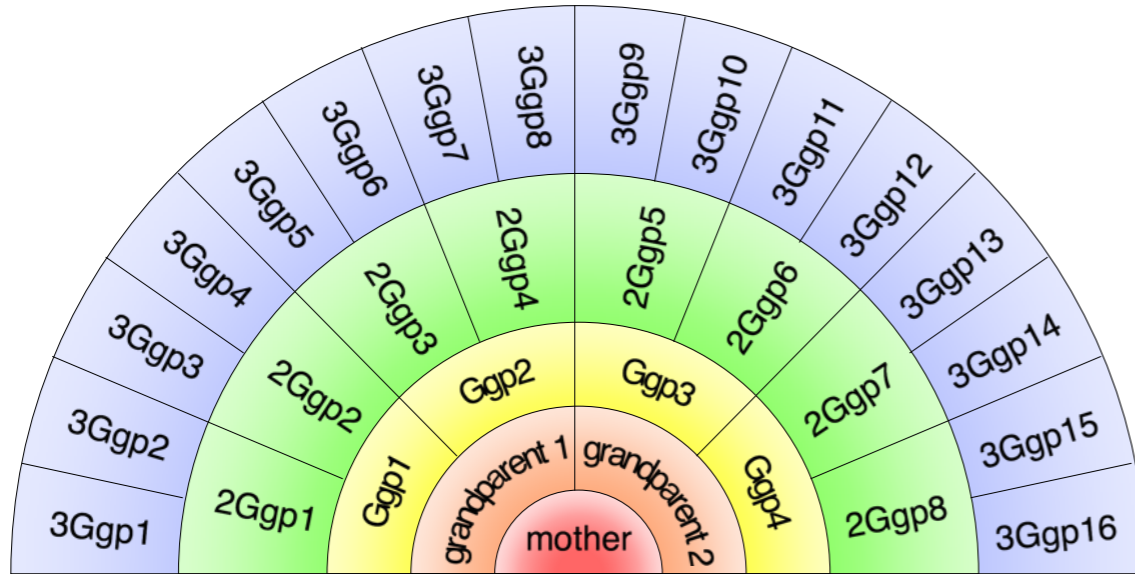
3rd Ggp level	3Ggp1	3Ggp2	3Ggp6	3Ggp7	3Ggp10	3Ggp11	3Ggp12	3Ggp16	3Ggp6

2nd Ggp level	2Ggp1	2Ggp3	2Ggp4	2Ggp5	2Ggp6	2Ggp8	2Ggp3

Ggp level	Ggp1	Ggp2	Ggp3	Ggp4	Ggp2

gp level	grandparent 1	grandparent 2	grandparent 1

Chromosome 11 Pair	mother
	father

Confidence Level ↑
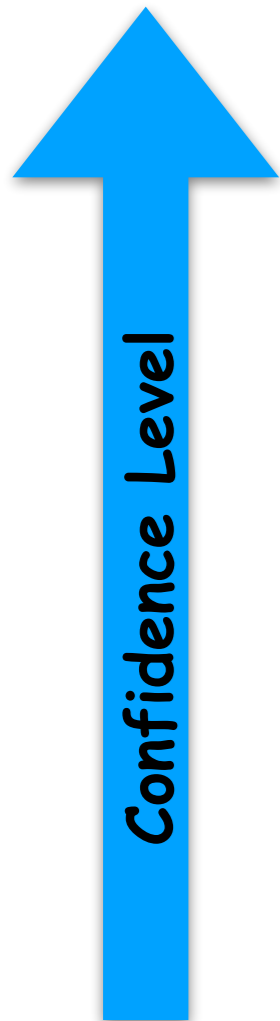
TRIANGULATION GROUP

- Overlapping segment of DNA confirmed to be shared by three or more people

Available at:

- All GEDmatch Matches
- Limited 23andMe Matches

PSEUDO-TRIANGULATION GROUP

- Apparent overlapping segment of DNA shared by three or more people who are ICW
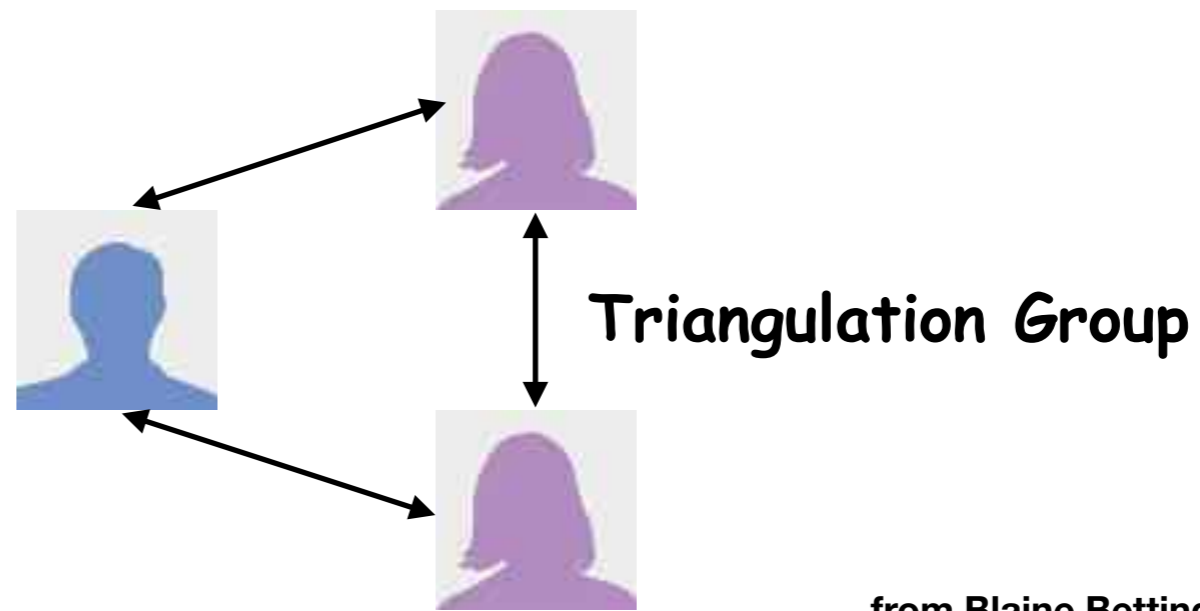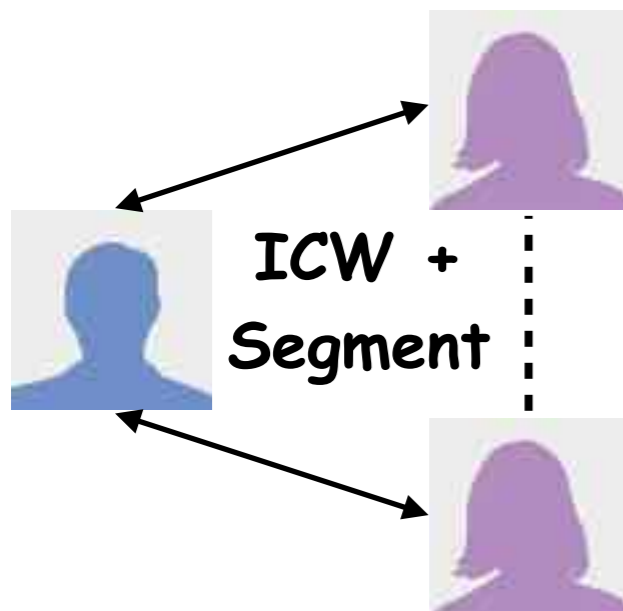
Available at:

- FTDNA Matches
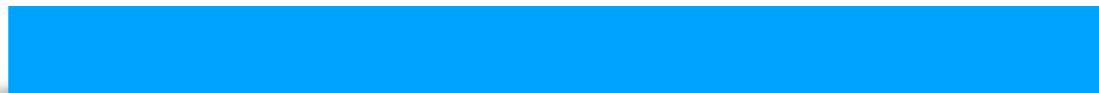- Family Finder Matrix is an ICW tool

SHARED MATCHES GROUP

- Three or more people who are ICW

Available at:

- AncestryDNA Matches

ICW + Segment

Triangulation Group

from Blaine Bettinger, Ph.D., J.D.

	GEDmatch			23andMe			FTDNA		
Chr	Beg	End	cM	Beg	End	cM	Beg	End	cM
1	14,995,446	17,424,530	4.3981				163,867,733	165,401,957	1.59
3							122,057,936	124,537,709	2.67
4	27,323,664	35,681,228	7.0264	27,872,339	34,731,789	6.73	27,422,488	34,709,899	6.89
4	38,665,016	44,094,607	7.9129	39,258,771	44,130,266	5.91	38,906,166	43,505,495	5.76
4	90,343,677	130,664,282	29.9410	90,238,073	130,230,383	31.53	88,986,032	130,595,838	33.91
5	86,762,783	91,820,476	3.964				87,182,083	90,937,093	2.07
6	44,745,858	47,000,610	3.2957				29,609,493	33,749,934	4.55
7							57,492,724	66,609,369	2.23
9	16,667,221	18,656,780	3.5543				16,685,690	18,414,272	2.47
10							19,600,058	20,916,620	1.84
12							32,965,070	39,161,962	2.23
15							40,899,345	43,796,695	1.76
16							65,173,037	67,852,271	3.3

Jim Bartlett suggests using a single spreadsheet with segments >7cM
GEDmatch reflects data uploaded from FTDNA for

People   DNA

DNA Relatives

Find and connect with genetic relatives to learn about relationships, shared ancestors and family history. View overlapping segments to find common ancestors.

Sort by | Strength of Relationship ⌄ | | Showing 1260 out of 1260 relatives

	Name	Strength of Relationship	Sharing
☆ JM	Female	50.0% shared, 24 segments	●
☆ AM	Female	31.2% shared, 29 segments	**Sharing** ●
☆ AL	Female	13.2% shared, 35 segments	●
☆ SM	Male	1.90% shared, 8 segments	**Not Sharing** ●
☆ IM	Male	d Cousin / 1.54% shared, 6 segments	**Pending** ●
☆	Female	ousin / 0.47% shared, 3 segments	**Open Sharing** ●
☆ CR	Female	ousin / 0.47% shared, 3 segments	●

1 2 3 4 ... 51 Next >

Filters   Update DNA Relatives profile

Search keywords

Name, relation, or location   🔍

Reset

Notifications ⓘ   ⌄

Relationship ⓘ   ⌃

Closest   3   4   5   6   7+

Download aggregate data ⓘ

23andMe eliminates segments <5cM
Can sort to remove everything <10cM

32

HOME   REPORTS   **TOOLS**   RESEARCH

People   **DNA**

Compare your DNA with close and distant relatives

Identical or overlapping DNA segments indicate a common ancestor and can help identify relationships across multiple relatives. Learn more about how to use this tool.

Compare

MM

With

Select another relative to compare with.

Compare

Search or select DNA Relatives and Friends
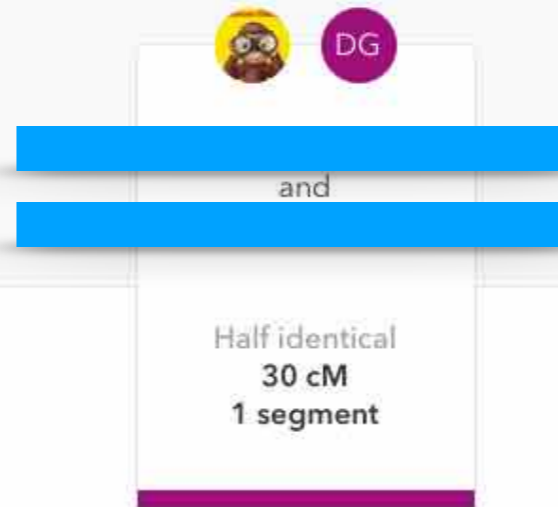
First and/or last name   🔍

2S

3S

AL   AM

Download of 23andMe Aggregate Data

	Display Name	Surname	Chr	Start	End	cMs	Sharing Status
1							
152			4	70,765,416	88,304,358	16.6	OPEN_SHARING
153			4	73,067,627	90,116,432	16.5	OPEN_SHARING
154			4	89,316,509	128,167,093	31.5	OPEN_SHARING
155			4	89,323,214	111,765,413	18.2	OPEN_SHARING
156			4	89,420,956	128,688,803	31.5	OPEN_SHARING
157			4	90,238,073	130,230,383	31.5	SHARED
158			4	95,706,285	124,297,449	23.3	OPEN_SHARING
159			4	96,581,831	128,167,093	25.1	OPEN_SHARING
160			4	101,906,493	128,167,093	21.4	OPEN_SHARING
161			4	105,106,136	116,411,907	10.7	OPEN_SHARING
162			4	109,417,821	128,688,803	16.1	OPEN_SHARING
163			4	109,448,161	128,688,803	16.1	OPEN_SHARING
164			4	109,474,255	128,167,093	16.0	OPEN_SHARING
165			4	131,641,319	142,065,531	10.5	OPEN_SHARING

935 segments >5cM

730 segments >10cM

Now comparing DNA segments.
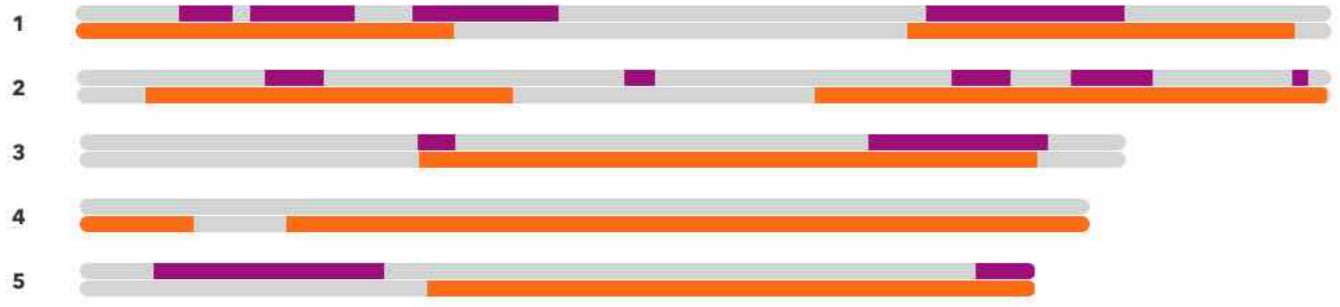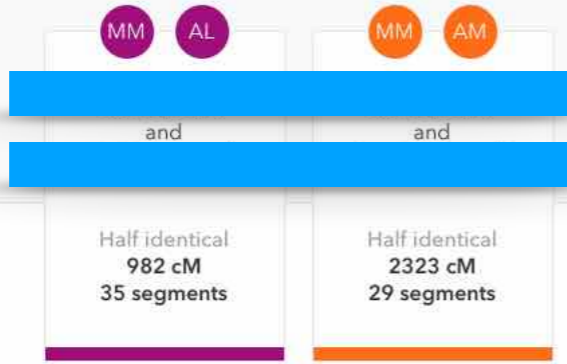
Select different relatives or friends to compare.

and

Half identical
30 cM
1 segment

But is this overlap on the same chromosome?

1
2
3
4

34

Family Finder - Matches

Search name or ancestral surnames [🔍]

Advanced Search

🖥 Chromosome Browser | = In Common With | ≠ Not In Common With | Reset Filter

1-30 of 2684 « ‹ › » Page 1 / 90 Go

	All (2684)	👤 Paternal (0)	👤 Maternal (0)	👫 Both (0)	

	Name	Match Date	Relationship Range	Shared Centimorgans	Longest Block	X-Match	Linked Relationship	Ancestral Surnames	➕
☐		02/03/2016	1st Cousin - 3rd Cousin	268	60		👥⁺		
☐		06/21/2015	2nd Cousin - 4th Cousin	100	60		👥⁺		
☐		12/07/2016	2nd Cousin - 4th Cousin	95	63		👥⁺		
☐		03/11/2016	2nd Cousin - 4th Cousin	88	39		👥⁺		
☐		04/16/2017	2nd Cousin - 4th Cousin	59	22		👥⁺		
☐		12/29/2011	3rd Cousin - 5th Cousin	59	13		👥⁺		

Download Matches: CSV Excel

Download Filtered Matches: CSV Excel

1-30 of 2684 « ‹ › » Page 1 / 90 Go

This is not the data you want!

Family Finder - Matches

Most Common Surnames: **30 Smith** **20 williams** **18 Jones**

Search name or ancestral surnames

Advanced Search

Chromosome Browser | = In Common With | ≠ Not In Common With | Reset Filter

1-30 of 48 « ‹ › » Page 1 / 2 Go

| | All (48) | Paternal (0) | Maternal (0) | Both (0) |

Name	Match Date	Relationship Range	Shared Centimorgans	Longest Block	X-Match	Linked Relationship	Ancestral Surnames	➕
	06/21/2015	2nd Cousin - 4th Cousin	100	60				
	07/06/2015	2nd Cousin - 4th Cousin	78	45				
	05/15/2016	2nd Cousin - 4th Cousin	53	32				
	10/03/2014	5th Cousin - Remote Cousin	53	10	X-Match			
	12/20/2013	3rd Cousin - 5th Cousin	52	13				
	12/16/2014	3rd Cousin - 5th Cousin	51	13				

Family Finder - Chromosome Browser

Feedback   Refer Friends & Family   **Page Tour**

Chromosome Browser Tutorial

Optional Views:
▸ Download to Excel (CSV Format)   ▸ View this data in a table ▸ Download All Matches to Excel (CSV Format)

This link downloads segment data for all FTDNA matches

Compare List | 5+ cM | Remove

1
2
3
4
5
6

37

	A	B	C	D	E	F	G	H
1	NAME	MATCHNAME	Chr	Start	End	cMs	SNPs	
344			4	75182448	84466080	9.81	1957	
345			4	75808538	84883367	9.95	1957	
346			4	88986032	130595838	33.91	8300	
347			4	89423117	106484130	12.91	3300	
348			4	89423117	104621016	12.11	3000	
349			4	89423117	103058031	10.71	2700	
350			4	89423117	103058031	10.71	2700	
351			4	89872280	130251569	31.64	7900	
352			4	89872280	122535192	26.08	6400	
353			4	89872280	108074785	13.45	3500	
354			4	89872280	108074785	13.45	3500	
355			4	89872280	106484130	12.03	3200	
356			4	89872280	102452008	9.55	2500	
357			4	95925308	113502251	14.55	3500	
358			4	95925308	112351238	13.6	3300	
359			4	95925308	111846805	13.24	3200	
360			4	96346892	110803736	11.02	2800	
361			4	96346892	110803736	11.02	2800	

29725 segments

1612 segments >9.5cM

Use Matrix to determine if matches are on the same chromosome

	NAME	MATCHNAME	Chr	Start	End	cMs	SNPs	
344			4	75182448	84466080	9.81	1957	
345			4	75808538	84883367	9.95	1957	
346			4	88986032	130595838	33.91	8300	
347			4	89423117	106484130	12.91	3300	
348			4	89423117	104621016	12.11	3000	
349			4	89423117	103058031	10.71	2700	
350			4	89423117	103058031	10.71	2700	
351			4	89872280	130251569	31.64	7900	
352			4	89872280	122535192	26.08	6400	
353			4	89872280	108074785	13.45	3500	
354			4	89872280	108074785	13.45	3500	
355			4	89872280	106484130	12.03	3200	
356			4	89872280	102452008	9.55	2500	
357			4	95925308	113502251	14.55	3500	
358			4	95925308	112351238	13.6	3300	
359			4	95925308	111846805	13.24	3200	
360			4	96346892	110803736	11.02	2800	
361			4	96346892	110803736	11.02	2800	

Matrix Matches

One person doesn't match

or……?

- This person is identified as a match.

Don't Use GEDmatch if:

You or your relatives want
privacy for your
genealogical DNA results

Use GEDmatch if:

You have relatives who:

- want to use a free site

- have tested with different companies and you want data all in one spot, or

- have tested at Ancestry and you want to be able to use tools,

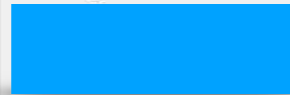- want to find other matches who are relatives.

You want to make the most of your genetic DNA information and want to use:

- use a robust set of tools not found together anywhere else, or

- start triangulation groups (TG) to find every common ancestor for every TG, and/or

- use spreadsheets to help analyze TGs

Information
+14

Your Log-in Profile

[blue redacted box]

Tier 1 Member

Tier 1 Paid Until 2017-07-21
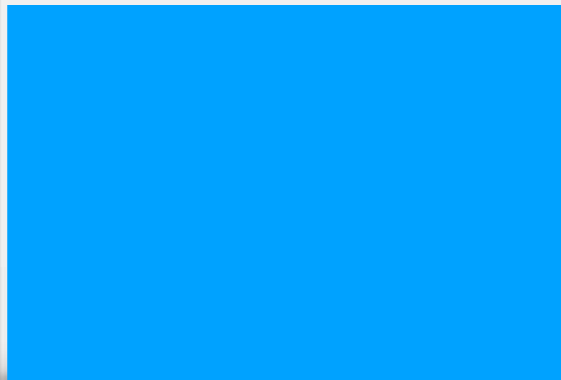
View/Change your profile (password, email, groups)

Server IP: 172.31.38.221

Learn More

- Using GEDmatch
  For new GEDmatch users
- GEDmatch Forums.
- GEDmatch wiki
- GEDmatch® FAQ page
- DNA for 'Dummies'
- User Lookup
  Find information on your matches.
- Site Policy Statement
- New Profile Management Features
- New One to Many Features

Your DNA Resources

[blue redacted box]

EDIT or DELETE your DNA resource profiles.

Your GEDCOM Resources

[blue redacted box]
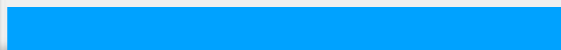
Click on the GEDCOM number above to go to the individual detail page for the point person. To change the point person, or to create a link between a DNA kit and a person in your GEDcom: Go to their individual detail page in the online tree and at the bottom of that page there is a box for linking a DNA kit to that GEDCOM, or for changing the point person.

Click HERE to manage other GEDCOM resource details.

File Uploads

Raw DNA file Uploads

- Generic Upload *FAST*
- 23andMe *fast* & easy
  Do NOT open or un-zip raw
  DNA data files before uploading.

Genealogy - Family Trees

- GEDCOM
  genealogy Upload
- GEDCOM
  genealogy Upload
  Fast Beta version

Analyze Your Data

DNA raw data

- 'One-to-many' matches
  Information: Disappeared kits recovery information
- Action: 'One-to-many' recovery no account email matches
- 'One-to-one' compare
- X 'One-to-one'
- Admixture (heritage)
- Admixture/Oracle with Population Search
- Phasing
- People who match one or both of 2 kits Updated
- Predict Eye Color
- Are your parents related?
- 3D Chromosome Browser
- Archaic DNA matches
- Multiple Kit Analysis NEW
- DNA File Diagnostic Utility
  Analyze DNA file upload for potential problems.

Genealogy

- 1 GEDCOM to all
- 2 GEDCOMs
- Search all GEDCOMs Revised
- GEDCOM + DNA matches

Tier 1 Utilities
These additional utilities are available to members of GEDmatch® Tier 1.

DNA Raw Data

- 'One-to-many' matches New Version!
- Matching Segment Search
  Find other kits with segments that match yours.
- Relationship Tree projection
- Lazarus
  Create surrogate kits to represent close ancestors.
- Triangulation
  Identify and confirm triangulation groups (TG) from your matches.
- Triangulation Groups BETA
  Triangulation Groups - Expanded
- 'My Evil Twin' Phasing BETA
  The DNA you did NOT inherit

DNA matches to Kit ▓▓▓▓▓

Mark Moore

These matches are calculated from DNA raw data files submitted by users.
Results are based on the default parameters for the GEDmatch Autosomal comparison software.
These results are for comparison only and will likely be somewhat different than those shown by your testing company.

Default parameters (and results) may change periodically based on feedback from users, and from new research results.

++++++++++++++++++++++

Click on 'L' for list of matches for that person (May take up to 5 minutes to process)
Click on 'A' for details on Autosomal comparison.
Click on 'X' for details on X-DNA comparison.

Select 3 or more from 'Select' column, and click this button for additional display and processing options.
Submit

Intensity of **GREEN background** indicates how recent (within last 30 days) a match is.

To qualify as a 'match' in the genealogical time frame, results must have a largest Autosomal segment that has at least 700 SNPs and be at least 7 cM.
It must have BOTH. Results with the largest segment less than 7 cM are highlighted in pink.
In general, the results shown below use thresholds LESS than 7cM / 700 SNPs.
PLEASE verify any result shown on this list with the one-to-one comparison tool before assuming any match is real.
To check the number of SNPs, click on the 'A' on the same line to view the one-to-one comparison detail.

Please DO NOT send emails to anyone on this list without first using the one-to-one utility to verify that it is a legitimate match.
DO NOT create mass mailing lists from these results.

						Haplogroup			Autosomal				X-DNA				
Kit Nbr	Type	List	Select	Sex	GED/WikiTree	Mt	Y	Details	Total cM	largest cM	Gen	Details	Total cM	largest cM	Name	Email
▼ ▲						▼ ▲	▼ ▲		▼	▼	▼ ▲		▼	▼	▼ ▲	▼ ▲
	V4	L	☐	F				A	3587.1	263.7	1.0	X	196	196		
	V4	L	☐	F		X2e		A	2385.4	159.8	1.3	X	0	0		
	V4	L	☑	F		T2b		A	990.1	124.4	1.9	X	48.1	48.1		
	F2	L	☑	M			R-M269	A	296.6	59.5	2.8	X	0	0		
	F2	L	☐	F				A	89.6	43.7	3.7	X	0	0		
	F2	L	☐	F	GED			A	72.2	50.4	3.8	X	0	0		
	V4	L	☐	F	GED	H1		A	62.7	48.8	3.9	X	0	0		
	F2	L	☐	F				A	61.6	49.4	3.9	X	0	0		
	F2	L	☐	M			R-M269	A	61.3	37.4	3.9	X	0	0		
	F2	L	☐	F				A	56	27.7	4.0	X	0	0		
	F2	L	☐	M		T2b4-T152C!	I-M170	A	53.6	31.0	4.0	X	0	0		
	F2	L	☐	M	GED			A	51.8	23.8	4.1	X	0	0		
	F2	L	☑	M			J2a	A	49.8	37.4	4.1	X	0	0		
	F2	L	☐	F				A	49.6	49.6	4.1	X	0	0		

[GED match]

Tools for DNA and Genealogy Research   Learn More ⌄   File uploads ⌄   Analyze Your Data ⌄   Tier 1 Utilities ⌄   Profile Managment ⌄   Home   Log out

GEDmatch Visualization Options

Kits included ---

Chromosome Browsers   Matrices   GEDCom   List/CSV   Tag Groups

2-D and 3-D Chromosome Browsers

Browser	Note	Parameter	Value	Action
2-D Chromosome Browser				Chr-Browse
3-D Chromosome Browser		cM threshold min=3cM	5	3D Chr-Browse

GEDmatch.com, tools for DNA and genealogy research - Website and contents © 2011-2017 by GEDmatch, Inc.

GEDmatch *3D* Chromosome Browser(3)

These results are based on the 5.0 cM / 500 SNP threshold that you specified on the preceeding page. Because of that, these results may be somewhat different than those obtained in the one-to-one and one-to-many utilities, which use the site default values. Default values vary depending on the testing company that provided the kit.

Your results have been generated. Click [HERE] to display Chromosome Browser

cM color coding < 3 cM 3 - 5 cM 5 - 10 cM 10 - 20 cM 20 - 50 cM 50 - 100 cM Over 100 cM

Segments in common:

Kit	Name					Tot. Segments	Largest cM
		-	38	14	2	54	89.0
		38	-	6	3	47	89.0
		14	6	-	2	22	59.5
		2	3	2	-	7	38.3

Total Shared cM (Chr 1-22):

Kit	Name				
		-	989.9	291.3	49.8
		989.9	-	173.6	62.3
		291.3	173.6	-	10.8
		49.8	62.3	10.8	-

Total Shared cM (X-Chr):

Kit	Name	T484500	M547847	T810768	A762159
		-	48.1	None	None
		48.1	-	None	None
		None	None	-	None
		None	None	None	-

45

Segment Details:

Kit1		Kit2			Build 36		
Kit Nbr.	Name	Kit Nbr.	Name	Chr	From	To	cM
				1	20262909	31180643	13.7
				1	34236038	55285583	21.2
				1	66540717	96665243	26.8
				1	167089071	206618991	37.6
				2	36065216	47881969	14.6
				2	105219264	112139659	5.8
				2	169297944	182212528	14.5
				2	192173843	208457176	14.0
				2	234900214	238445056	7.2
				2	4372315	10584486	16.9
				3	150549688	184683062	31.6
				3	64227843	71604184	9.2
				3	124376943	151337702	30.0
				4	125713954	133922718	5.6
				4	186396439	191140682	13.0
				5	169294588	180623543	26.2
				5	14089509	57980586	40.5
				5	13681954	77855837	59.5
				5	10558585	56778019	44.5
				6	85179320	139853382	51.6
				6	150878	3644702	11.0
				6	12537848	42454532	36.9
				7	142009763	158763730	35.1
				7	117457890	131495652	12.5
				7	42432789	141724336	89.0
				7	140018	7152277	11.2
				7	120751201	132349786	12.8

One-to-many DNA comparison for kit [____] filter by ⊙ autosomal ○ X with this offset [0 ⇕] with this limit [500 ⇕] and cm size [10 ⇕] [Search] [Tips]

[Select all]

matches 1:501

[Visualization Options]

						Haplogroup		Autosomal			X-DNA	
Select ❓	Kit ⇕	Name ⇕	Email ❓ ⇕	GED❓ WikiTree ⇕ ❓	Age(days) ⇕ ❓	Type ⇕	Sex ⇕	Mt ⇕	Y ⇕	Total ⇕ cM	Largest ⇕	Gen ⇕	Total ⇕ cM	La
☐					488	V4	F			3587.1	263.7	1.00	196.0	
☐					543	V4	F	X2e		2385.4	159.8	1.30	0.0	
☑					532	V4	F	T2b		990.1	124.4	1.90	48.1	
☑					490	F2	M		R-M269	296.6	59.5	2.80	0.0	
☐					1065	F2	F			89.6	43.7	3.70	0.0	
☐				GED	747	F2	F			72.2	50.4	3.80	0.0	
☐				GED	563	V4	F	H1		62.7	48.8	3.90	0.0	
☐					271	F2	F			61.6	49.4	3.90	0.0	
☐					91	F2	M		R-M269	61.3	37.4	3.94	0.0	
☐					254	F2	M	T2b4-T152C!	I-M170	53.6	31.0	4.00	0.0	
☐					49	F2	F			56.0	27.7	4.00	0.0	
☐				GED	133	F2	M			51.8	23.8	4.06	0.0	
☐					59	F2	F			49.6	49.6	4.09	0.0	
☑					365	F2	M		J2a	49.8	37.4	4.10	0.0	
☐					292	F2	F			49.4	29.7	4.10	0.0	
☐					452	F2	M			47.8	23.2	4.10	0.0	
☐				GED	1197	F2	M			47.1	41.1	4.10	0.0	
☐				GED	1197	F2	M			46.5	41.1	4.10	0.0	
☐					92	F2	F			47.3	37.4	4.12	0.0	
☐				GED	2192	F2	M	H23	R1b1b2a1a	44.9	29.9	4.20	0.0	
☐				GED	920	F2	F			44.9	39.9	4.20	0.0	
☑					350	F2	M			44.2	44.2	4.20	0.0	
☑					444	F2	F			42.8	28.8	4.20	0.0	
☐					333	F2	F			41.8	32.7	4.20	0.0	

GEDmatch Visualization Options

Kits included ---

| Chromosome Browsers | Matrices | GEDCom | List/CSV | Tag Groups |

2-D and 3-D Chromosome Browsers

Browser	Note	Parameter	Value	Action
2-D Chromosome Browser				Chr-Browse
3-D Chromosome Browser		cM threshold min=3cM	5	3D Chr-Browse

GEDmatch Visualization Options

Kits included ---

| Chromosome Browsers | Matrices | GEDCom | List/CSV | Tag Groups |

Lists and CSV Downloads

List	Note	Action
Matching Segment List		Segment CSV file
Match List		Match CSV file

GEDmatch Triangulation Groups

This utility groups your triangulated matches together.

Using a phased kit may produce more accurate results.

GEDmatch Kit Number:

Max number of kits to read: 600

Minimum segment cM size:
(Min segment SNP size defaults to 50 x cM)
Suggested values are 7cM for phased kit
or 15 cM for unphased kit.   15

Upper cM limit of matches to use:
Higher values include close relatives.   1500

Triangulate

GEDmatch DNA Segment Search

This utility allows you to find other kits with matching chromosome segments.

Kit Number:	▮▮▮▮▮
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)	☐
Show graphic bar for Chromosome?	⦿ Yes ◯ No

Submit

GEDmatch Segment Triangulation

This utility finds people who match you with your top matches as shown in the one-to-many results and below the upper threshold limit that you specify. It then compares those matches against each other. Results can be sorted by chromosome and position, or by kit number, chromosome and position, and then displayed in tabular and graphical format for each matching segment larger than 5cM. Close relatives can be excluded from results by specifying an upper segment threshold limit. All kits must have completed batch processing to be included in results.

GEDmatch Kit Number:	▮▮▮▮▮
Upper Segment Threshold Limit:	3000 ⬍ cM
Display Options:	◯ Show results sorted by chromosome, segment start position ◯ Show results sorted by kit_number, chromosome, segment start position ⦿ Show results sorted both ways

Triangulate

GEDmatch Triangulation Groups

This utility groups your triangulated matches together.

Using a phased kit may produce more accurate results.

GEDmatch Kit Number:	▮▮▮▮▮
Max number of kits to read:	600 ⬍
Minimum segment cM size: (Min segment SNP size defaults to 50 x cM) Suggested values are 7cM for phased kit or 15 cM for unphased kit.	15
Upper cM limit of matches to use: Higher values include close relatives.	1500 ⬍

Triangulate

DNA Triangulation means three Matches have segments which match each other at the same location. Example: Amy has a shared segment with Bill, who has a shared segment with Carl, who has a shared segment with Amy; and all these shared segments are at the same location on the same chromosome [often abbreviated A=B=C=A]

50

Matching Segments

	A	B	C	D	E	F	G	H	I
543		4	78,380,244	88,675,465	10.1	1,921		F	
544		4	89,247,502	103,504,728	11.3	1,582		M	
545		4	89,280,934	112,508,107	19.3	4,216		F	
546		4	89,286,550	106,987,190	13.5	1,449		F	
547		4	89,286,550	106,613,829	13.3	3,120		F	
548		4	89,455,759	102,793,390	10.5	2,516		F	
549		4	89,458,516	129,463,901	30.5	7,288		M	
550		4	89,458,516	122,734,984	26.6	3,589		F	
551		4	90,342,690	108,270,949	12.7	3,181		F	
552		4	90,342,690	108,065,243	12.6	1,385		F	
553		4	90,343,677	130,664,282	29.9	7,729		M	
554		4	95,579,369	113,540,002	15.2	3,342		U	
555		4	95,643,249	113,044,431	14.7	3,233		U	
556		4	95,643,249	113,044,431	14.7	3,237		U	
557		4	96,120,504	110,693,770	11.6	1,157		F	
558		4	96,307,872	110,448,166	11.2	2,557		M	
559		4	96,325,345	110,884,079	11.7	1,498		M	
560		4	96,345,294	120,292,033	19.7	2,593		M	
561		4	99,640,764	117,625,676	15.8	3,374		F	
562		4	99,640,764	116,729,054	15.3	3,292		F	
563		4	99,644,376	116,729,054	15.3	3,256		M	
564		4	101,713,880	113,536,924	10.4	2,095		F	
565		4	103,559,533	122,438,683	15.4	3,530		F	
566		4	106,685,577	118,500,818	10.9	2,152		F	

Old Triangulation

	A	B	C	D	E	F	G	H	I	J
760	4							71,155,785	83,867,610	11.6
761	4							71,155,785	85,089,596	13.7
762	4							71,155,785	90,010,098	18.8
763	4							71,155,785	85,372,476	14.1
764	4							89,458,516	112,513,069	19
765	4							89,458,516	122,310,999	26.3
766	4							96,342,284	120,054,596	19.6
767	4							99,630,806	117,627,442	15.8
768	4							90,345,213	122,310,999	24.8
769	4							89,458,516	122,484,896	26.4
770	13							26,423,790	35,354,084	17.4
771	13							26,423,790	35,354,084	17.4

Triangulation Beta

	A	B	C	D	E	F	G	H	I	J	K
123		C08					3	10194158	29459514	24.9	10264
124		C08					3	10319111	23768626	18	7099
125	C08	C09					3	11655970	29459514	22.2	9327
126	C08	C09					3	11485568	24881862	17	7090
127		D35					4	89458516	129474048	30.5	16005
128		D35					4	89279775	122310999	26.6	13211
129		D35					4	89198553	112513069	19.4	9469
130	D35	D38					4	96342284	120054596	19.6	9459
131	D35	D40					4	103373027	122577494	15.6	7574
132		F34					6	46263367	104385108	36.1	22623
133		F34					6	55498834	97396706	24.2	15651
134		F34					6	56114802	97495811	23.8	15439