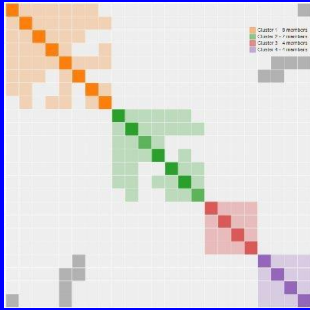




DNA
Special Interest
Group



Genetic Affairs

- Clusters & Segments

BIFHSGO – DNA SIG

June 5, 2021

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Clusters & Segments

Presentation Overview

- Total Match Clusters Demo & 8 Slides
- Segment Clusters 7
- DNA Pileups 6
- Triangulation & Final Clusters 4
- Genetic Affairs Summary 2

Match Cluster

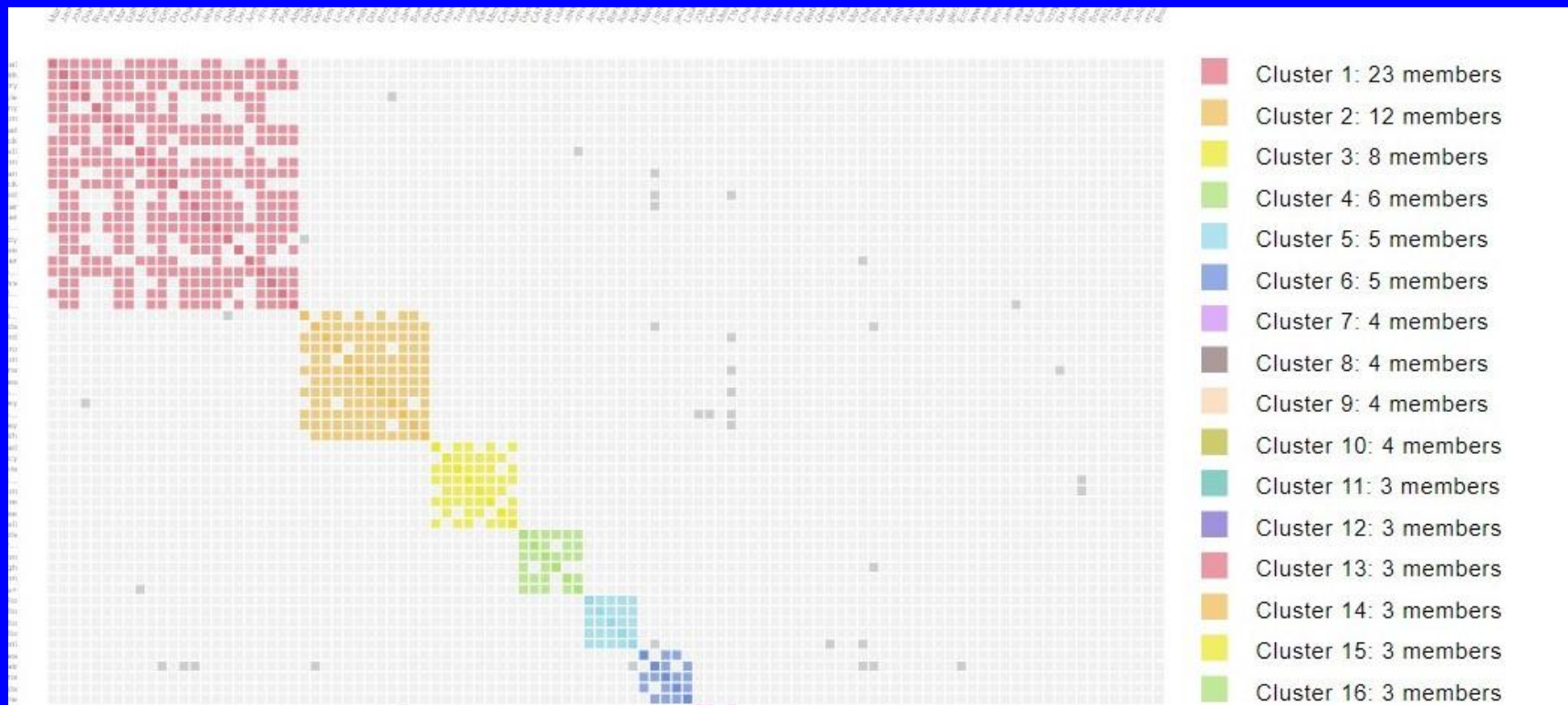
Cluster = Part of an Organized Match List

- Group People who match each other
- Probably a branch of your tree
- Clusters help focus further research

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

Genetic Affairs - MyHeritage

AutoCluster Sort Display & Cluster List 13



Name	total shared cM	Tree	Tree Person Count	Cluster
Mer [redacted]	32.22	https://www.myheritage.com/pedigree-tree-5	58	13
glen [redacted]	54.53	https://www.myheritage.com/pedigree-tree-3	106	13
Eric [redacted]	37.05	https://www.myheritage.com/pedigree-tree-5	73	13

AutoCluster on MyHeritage

<u>DNA Company</u>			<u>MyHeritage</u>	
User log onto			MyHeritage	
ID & Passwords provided to Genetic Affairs			No	
Clustering Parameters by			algorithm	
Typical min - max cM			30-400	
Results delivered by			email Zip file	
Visual Clustering			html file	
Printable Cluster List			Excel	
Link to Matches			Yes	
Link to Trees			Yes	
Input for DNA Painter			No	
Typical results: # matches			102	
Typical results: # clusters			19	

AutoCluster Comparison for 3 Vendors

<u>DNA Company</u>	<u>23&Me</u>	<u>FTDNA</u>	<u>MyHeritage</u>
User log onto	Genetic Affairs	Genetic Affairs	MyHeritage
ID & Passwords provided to GA	Yes	Yes	No
Clustering Parameters by	user	user	algorithm
Typical min - max cM	50-250 default	50-250 default	30-400
Results delivered by	email Zip file	email Zip file	email Zip file
Visual Clustering	html file	html file	html file
Printable Cluster List	Excel	Excel	Excel
Link to Matches	Yes	No	Yes
Link to Trees	No	Yes	Yes
Input for DNA Painter	Yes	Yes	No
Typical results: # matches	29	134	102
Typical results: # clusters	7	24	19

AutoCluster Comparison for 4 Vendors

<u>DNA Company</u>	<u>23&Me</u>	<u>FTDNA</u>	<u>MyHeritage</u>	<u>GEDmatch</u>
User log onto	Genetic Affairs	Genetic Affairs	MyHeritage	GEDmatch Tier 1
ID & Passwords provided to GA	Yes	Yes	No	No
Cost per run	US\$0.75	US\$0.75	no charge	no charge
Clustering Parameters by	user	user	algorithm	user
Typical min - max cM	50-250 default	50-250 default	30-400	25-250 test
Results delivered by	email Zip file	email Zip file	email Zip file	online / save html
Visual Clustering	html file	html file	html file	on-line
Printable Cluster List	Excel	Excel	Excel	screenshot/AutoTree
Link to Matches	Yes	No	Yes	Multi Kit Analysis
Link to Trees	No	Yes	Yes	Yes
Input for DNA Painter	Yes	Yes	No	Yes (to come)
Typical results: # matches	29	134	102	56
Typical results: # clusters	7	24	19	13

AutoCluster Comparison for 4 Vendors – More Options

<u>DNA Company</u>	<u>23&Me</u>	<u>FTDNA</u>	<u>MyHeritage</u>	<u>GEDmatch</u>
User log onto	Genetic Affairs	Genetic Affairs	MyHeritage	GEDmatch Tier 1
ID & Passwords provided to GA	Yes	Yes	No	No
Cost per run	US\$0.75	US\$0.75	no charge	no charge
Clustering Parameters by	user	user	algorithm	user
Typical min - max cM	50-250 default	50-250 default	30-400	25-250 test
Results delivered by	email Zip file	email Zip file	email Zip file	online / save html
Visual Clustering	html file	html file	html file	on-line
Printable Cluster List	Excel	Excel	Excel	screenshot/AutoTree
Link to Matches	Yes	No	Yes	Multi Kit Analysis
Link to Trees	No	Yes	Yes	Yes
Input for DNA Painter	Yes	Yes	No	Yes (to come)
Typical results: # matches	29	134	102	56
Typical results: # clusters	7	24	19	13
AutoTree	No	Yes	No	Yes
AutoSegment / ICW	Yes	Yes	No	No

Clustering with Manual Inputs

“Run AutoCluster with csv files”

Match Data can come from Ancestry, Living DNA, or anywhere.

Sample Match File & cM

Ver		359	maternal
Pet		278	
Leig		269	
RAI		246	
B.A		239	
Ella		102	paternal
Clif		195	
Lea		191	
Kat		184	
Sus		164	
CQ		157	
Tar		157	
J.K.		153	
Tar		152	
E.E		149	

Sample Shared Match File

Ver		Jan	
Ver		JRM	
Ver		She	
Mic		E.B	
ML		Ker	
Nar		Juli	
Nel		Dav	
Nel		ter	
Nel		ver	
Nel		j.k.	
Nel		a.w	
Llar		ver	
Llar		Kat	
Lor		Lin	
Lor		Der	

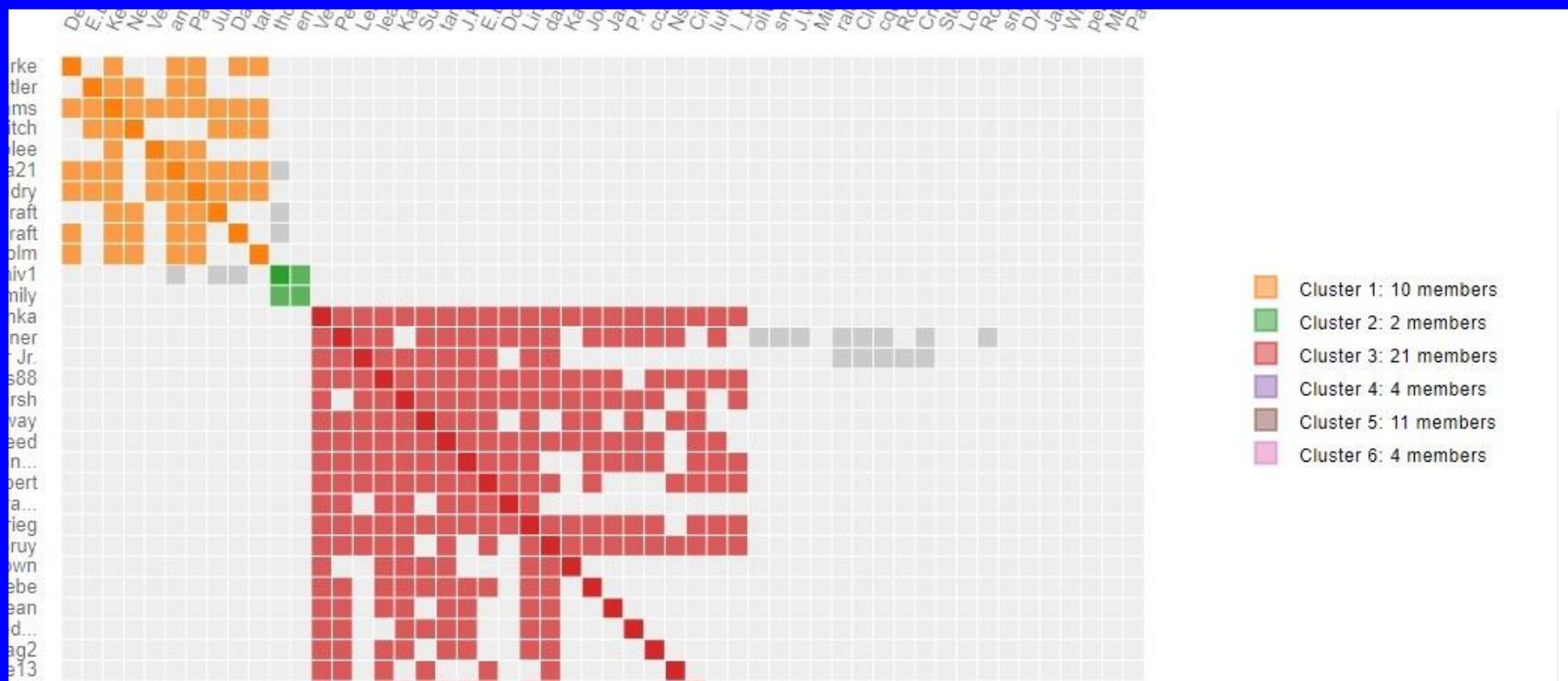
Clustering Ancestry Matches

“Ancestry DNA Match Table Maker”

Google Sheets for both Match Table and Shared Match Tables

Creator: Greg Clarke

Distributor: Family History Fanatics



Advantages of Segment Matches vs Total cM Matches

- Less likely to be false
- Less likely to be missed
- Can match people from different vendors
- Possible to deal with pile ups
- Step towards DNA Painting.

Finding Segment Matches

Family Tree DNA (Manual Search)

□ Method 1

- Family Finder - search for person of interest – ex: E. Hunt
- Chromo browser - ID segments – chromo 2, 175-212 Mbp
- Family Finder - search for shared matches with E. Hunt
- Chromo browser - ID shared matches with same segment.

□ Method 2

- Chromo browser - Download all segments (when not displaying)
- Read segment file into Excel – find person & ID segment
- Select correct chromosome
- Sort matches in order of segment start position.
- Select matching segments.

Finding Segment Matches

Family Tree DNA (Manual Display)

The screenshot displays the FamilyTreeDNA Chromosome Browser interface. The browser address bar shows the URL: <https://www.familytreedna.com/my/family-finder/chromosome-browser>. The page title is "myFTDNA - Chromosome Browser".

The interface is divided into two main sections: "Compare" on the left and "Shared DNA Segments" on the right.

Compare Section:

- Compare:** Robert Butler (YOU)
- With:** A list of 7 individuals is shown, with a light blue selection bar covering their names. The visible names are Eric 2nd, Fre 2nd, Ern 2nd, Rob 2nd, Par 2nd, Bra 2nd, and Mrs 3rd.
- Selected:** 7/7
- Clear All** button
- Update Selected Matches** button

Shared DNA Segments Section:

- Chromosome View:** The main display area showing DNA segments across chromosomes 2, 3, 4, and 5. Chromosomes 2, 3, and 4 show multiple horizontal bars representing shared segments, with some segments highlighted in various colors (blue, red, orange, yellow, dark blue).
- Detailed Segment Data:** A tab for viewing more information about the selected segments.

Match Popup:

A popup window is displayed over the shared DNA segments, showing details for a match:

- You and Mrs [Redacted]** (with a close button 'X')
- Genomic Position:** 174033151 - 204278384
- Shared cM:** 21.20
- SNPs:** 5984
- [View Segment Data](#)

Creating Segment Clusters With Genetic Affairs - FTDNA

- From Family Finder Page
 - Download all matches
- From Chromosome Browser
 - Download all segments (when not displaying)
- From Genetic Affairs
 - Run AutoSegment - for FTDNA
 - » Enter file names, min-max cM, overlap cM
 - » Pileup removal flag
- Segment Cluster results via email as zip files

Genetic Affairs - FTDNA

AutoSegment Cluster 8 11 matches

- Sort Display 46 clusters, too large.

Segment Cluster 8 - Chromosome 2				Segment Million Base Pairs		
Vendor	Match Name	Total cM	Start	End	Length	Seg cM
Total Matches = 11			170.9	215.1	44.2	
FTDNA	Fred	79	170.9	215.1	44.2	37.5
FTDNA	Ernie	67	170.9	212.4	41.5	35.5
FTDNA	Eric	51	174.8	212.4	37.6	29.7
FTDNA	Robe	66	174.4	205.5	31.1	22.1
FTDNA	Park	79	174.4	204.7	30.3	21.4
FTDNA	Bran	67	174.4	204.3	29.9	20.6
FTDNA	Davi	47	172.9	195.6	22.7	18.3
FTDNA	Kevin	41	174.4	197.5	23.1	17.0
FTDNA	Don	57	174.8	196.6	21.8	15.8
FTDNA	BAR	49	174.8	196.6	21.8	15.8
FTDNA	Kath	46	174.4	195.6	21.2	15.5

AutoSegment Cluster Comparison

<u>DNA Company</u>	<u>23&Me</u>	<u>FTDNA</u>	<u>MyHeritage</u>	<u>GEDmatch</u>
User log onto	23&Me	FTDNA	MyHeritage	GEDmatch T1
Cost per run	US\$0.75	US\$0.75	US\$0.75	US\$0.75
Download/Export Match File	aggregate data	Matches: CSV	Entire Matches	Run Segment Srch
Download/Export Segment File	(combined)	All Segments	shared segment	Run Triangulation
User log onto	Genetic Affairs	Genetic Affairs	Genetic Affairs	Genetic Affairs
Clustering Parameters by	user	user	user	user
Typical min - max cM	25-250 default	25-250 default	25-250 default	15-250 default
Typical segment overlap cM	15 default	15 default	15 default	9 default
Printable Cluster List	Excel	Excel	Excel	Excel
Link to Matches	Yes	email	Yes	email
Link to Trees	No	No	Yes	No
Input for DNA Painter	Yes	Yes	Yes	Yes
Typical results: # matches	262	253	195	497
Typical results: # clusters	43	46	43	92

Genetic Affairs – 4 Vendors Combined

Hybrid AutoSegment Cluster 13 47 matches

Match Cluster 109 - Segment Cluster 13 - Chromo 2			Segment Million Base Pairs			
Vendor	Match Name	Total cM	Start	End	Length	Seg cM
Total matches = 47			170.4	223.3	52.9	
MyHeritage	Amy	57	174.3	223.3	49.0	45.7
23andMe	Teel	54	174.5	223.2	48.7	45.2
FTDNA	Fred	79	171.2	215.4	44.2	38.2
23andMe	Udc	37	171.0	213.8	42.8	38.1
23andMe	Rod	36	170.4	212.9	42.5	37.1
FTDNA	Ernie	67	171.2	212.7	41.5	35.9
GEDmatch	A417	34	171.0	213.8	42.8	35.4
GEDmatch	A812	33	171.0	213.3	42.3	34.6
MyHeritage	glen	54	172.4	212.1	39.7	32.8
GEDmatch	A240	30	172.4	211.9	39.5	31.6
23andMe	Hun	36	175.1	212.9	37.8	30.3
MyHeritage	Eric	37	175.0	212.9	37.9	30.1
FTDNA	Eric	51	175.1	212.7	37.6	29.8
MyHeritage	Merc	32	174.3	206.7	32.4	25.2
23andMe	Mal	23	172.7	203.0	30.3	24.2
23andMe	Wal	22	174.2	205.7	31.5	23.9
MyHeritage	Mich	29	174.3	205.8	31.5	23.2

DNA Pileups

Segments with “excess” matches

- ❑ Pileups are segments that are so common that they cannot identify recent ancestors.
- ❑ Pileups are used by DNA Painter as a warning.
- ❑ Genetic Affairs has an option to eliminate matches that overlap a pileup by 3 cM
- ❑ There is a 5 cM pileup on Chromosome 2 that would eliminate the entire Hunt cluster.
- ❑ A different logic can be used so a 5 cM pileup does not eliminate a 30 cM match.

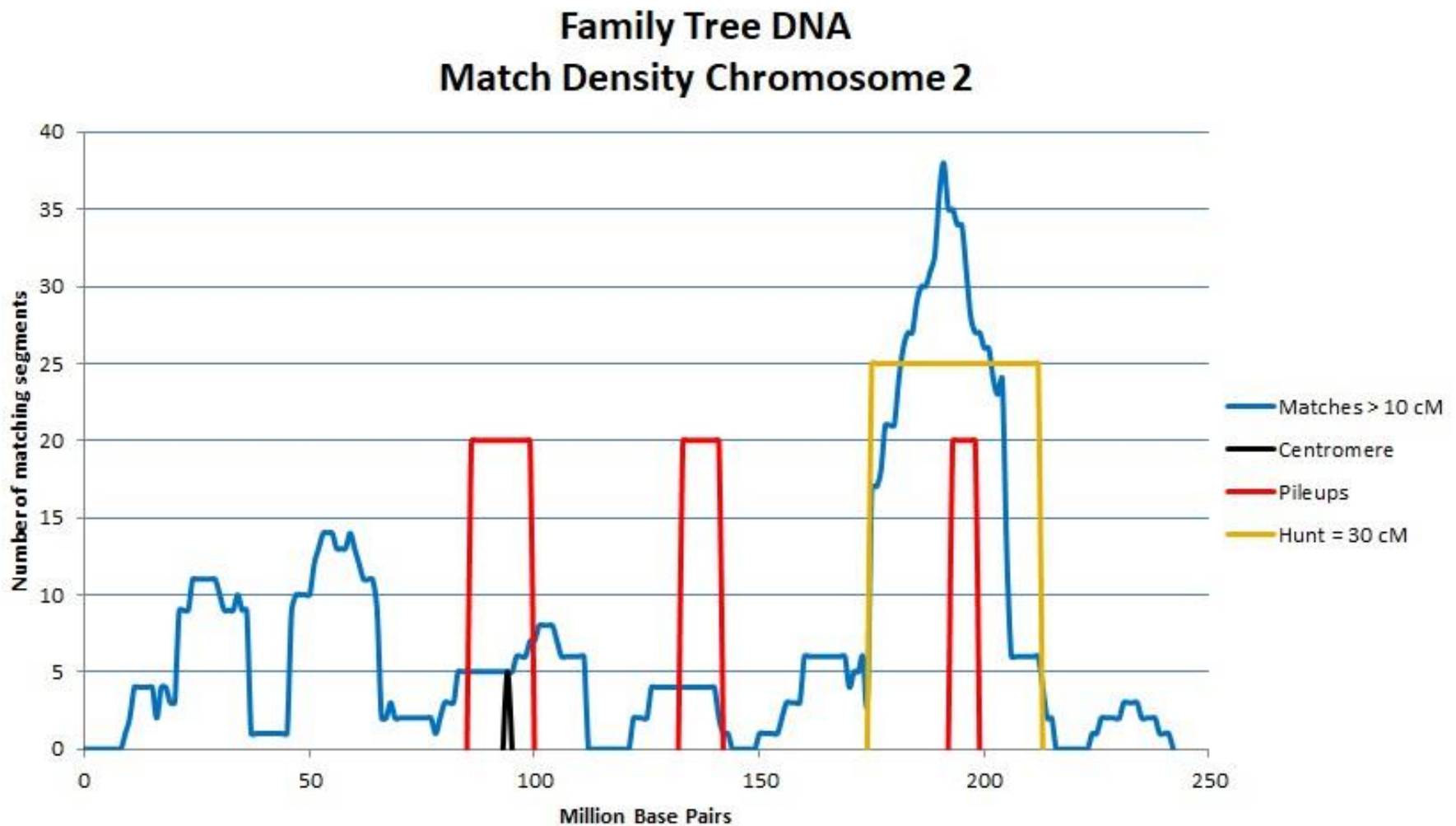
Pileups Reported by Hong Li Used by Genetic Affairs & DNA Painter

Chromosome	Starting position	Ending position	Genetic length (in cM)	Ratio of observed to expected IBD		
				GERMLINE Europe	GERMLINE Asia	ISCA Europe
chr9	38,293,483	72,605,261	8.15	39	13	10
chr8	10,428,647	13,469,693	7.96	38	26	2
chr21	16,344,186	19,375,168	6.91	22	15	2
chr10	44,555,093	53,240,188	7.58	22	21	2
chr22	16,051,881	25,095,451	20.82	22	22	3
chr2	85,304,243	99,558,013	6.53	21	21	2
chr1	118,434,520	153,401,108	9.95	19	33	47
chr15	20,060,673	25,145,260	10.46	15	20	42
chr17	77,186,666	78,417,478	5.66	11	7	0.1
chr15	27,115,823	30,295,750	9.29	9	3	3
chr17	59,518,083	64,970,531	6.23	9	4	4
chr2	132,695,025	141,442,636	9.16	7	0	4
chr16	19,393,068	24,031,556	6.18	6	2	5
chr2	192,352,906	198,110,229	5.04	4	2	4
Total	14 regions		119.92			

doi:10.1371/journal.pgen.1004144.t003

Match Density Plot

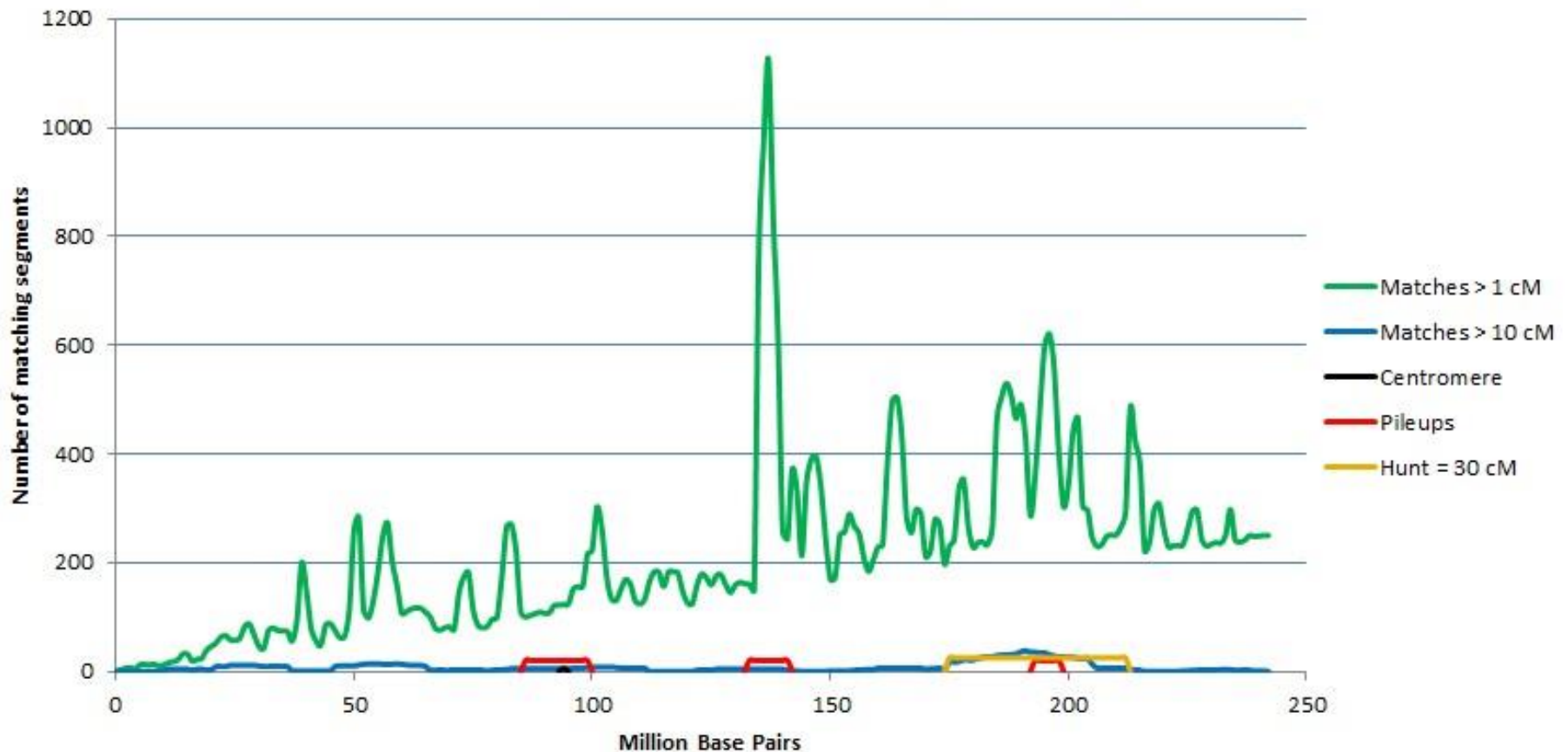
Match Length vs Pileup Length



Match Density Plot

Matches including 1 cM segments

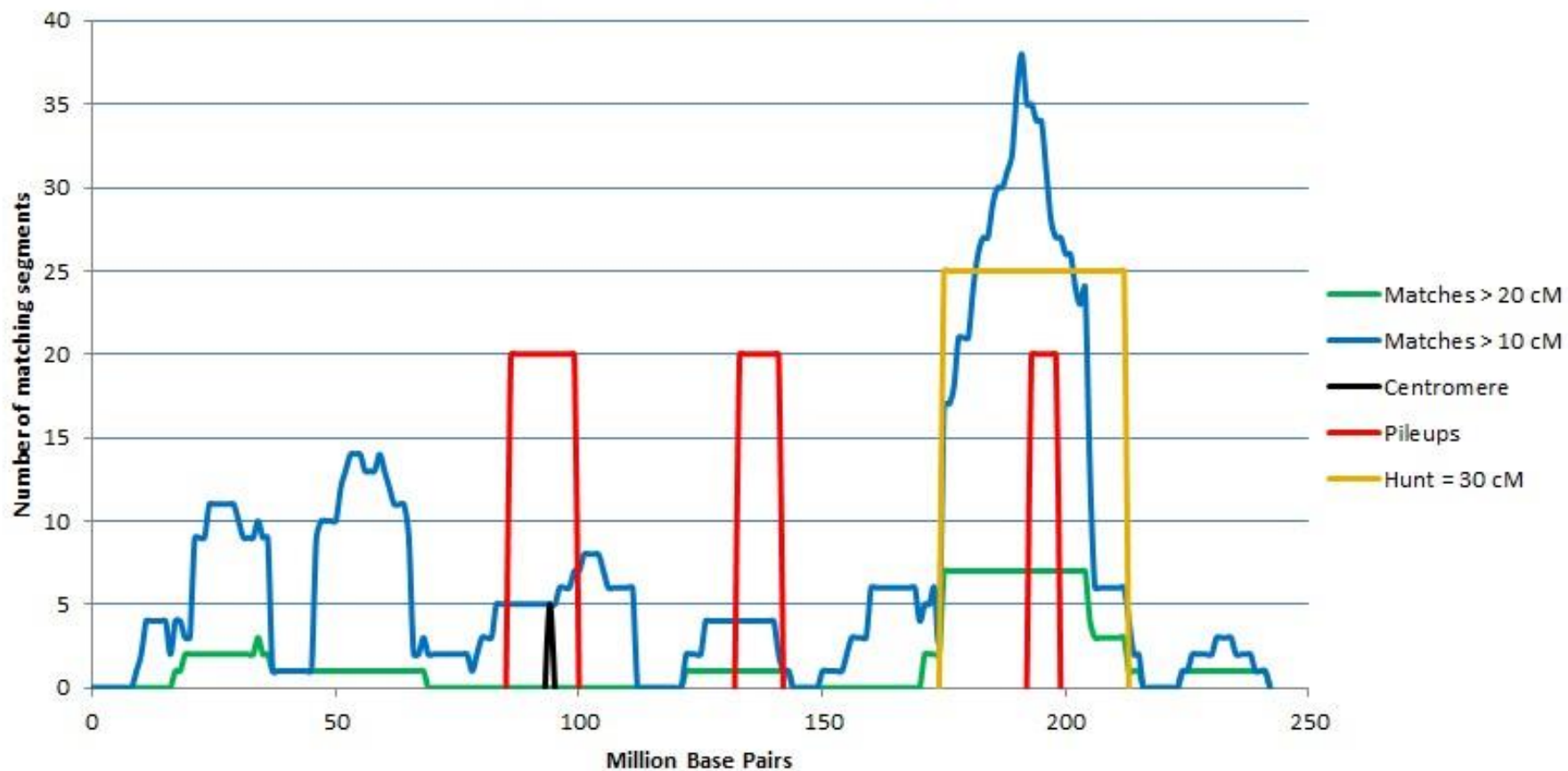
Family Tree DNA
Match Density Chromosome 2 using 1 cM segments



Match Density Plot

Matches minimum 20 cM

Family Tree DNA
Match Density Chromosome 2 using 20 cM segments



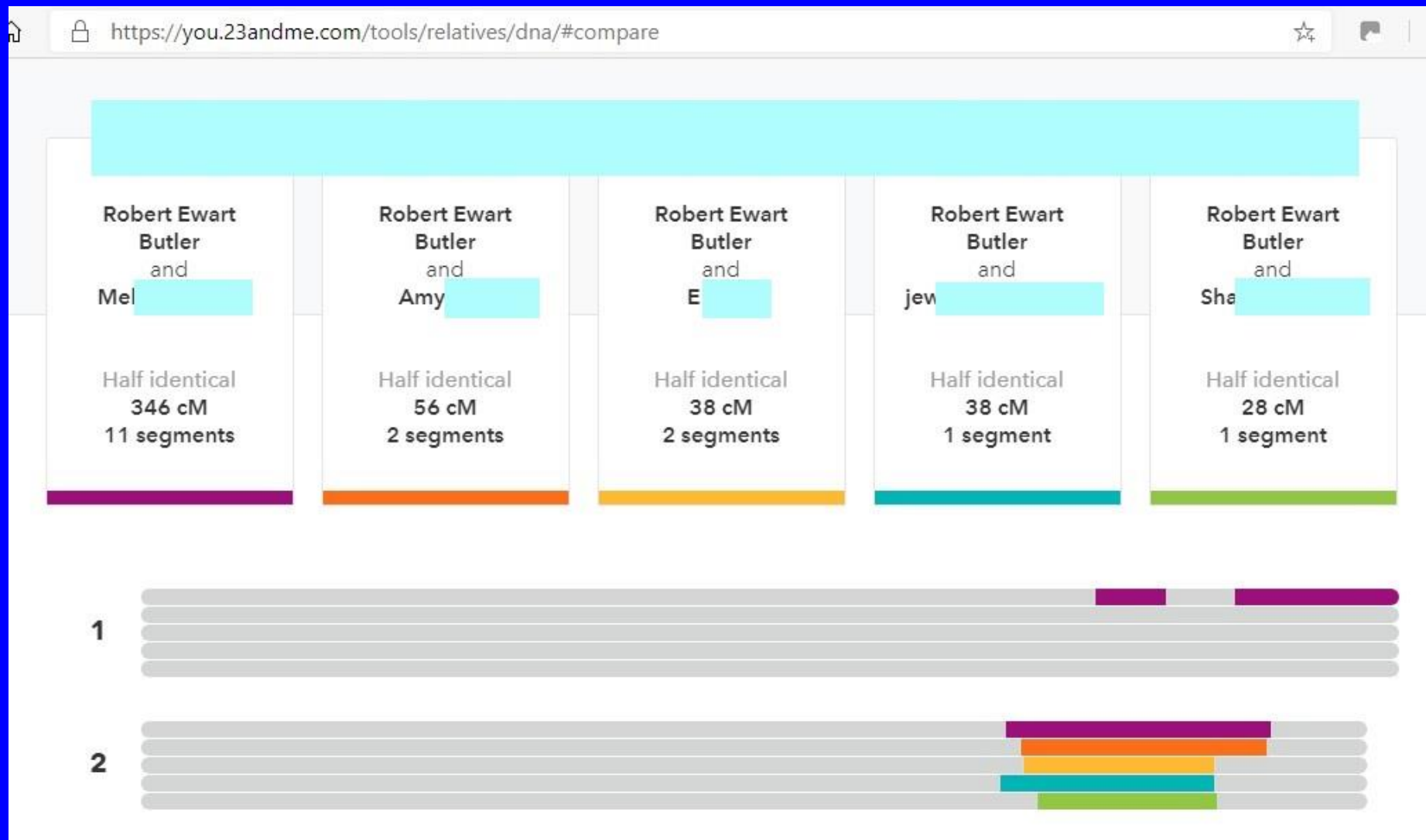
Segment Cluster after Pileup Removal

Net useful segment = total segment – pileup

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
Total matches = 47			170.4	223.3	52.9			
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	Roc	36	170.4	212.9	42.5	37.1	36.8	32.1
FTDNA	Erni	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	Hur	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	Wa	22	174.2	205.7	31.5	23.9	25.8	18.9
MyHeritage	Micl	29	174.3	205.8	31.5	23.2	25.8	18.2

Segment Matches

Paternal & Maternal Combined



Triangulated Matches

Paternal & Maternal Separated (23&Me)

You and Amy may have Relatives in Common
 Finding common relatives can help you piece together your family story.

Relative in common		You	Amy	Shared DNA
Mel		1st Cousin, Twice Removed (4.64%)	4th Cousin (0.63%)	Yes
Step		3rd Cousin (1.71%)	4th Cousin (0.33%)	No
Tho		3rd Cousin (1.48%)	5th Cousin (0.09%)	No
Chr		3rd Cousin (1.46%)	4th Cousin (0.44%)	No

You and E may have Relatives in Common
 Finding common relatives can help you piece together your family story.

Relative in common		You	E	Shared DNA
J S		4th Cousin (0.42%)	4th Cousin (0.36%)	Share to see
Geo		4th Cousin (0.39%)	5th Cousin (0.10%)	No
René		4th Cousin (0.38%)	Distant Cousin (0.09%)	No
Shav		4th Cousin (0.38%)	4th Cousin (0.72%)	Yes

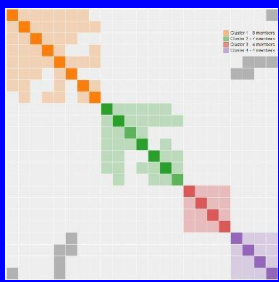
Segment Cluster after Pileup Removal and after Triangulation Check

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

Total cM Cluster of Ancestry Matches

Manual Group Cluster & Google Sheets Formatting

Highlighted names also on segment clusters.				
Name/Manager	Total cM	People in Tree	Notes	
B.eile	42 cM	Public 12		
Julia	40 cM	Private 56		
Glori	37 cM	No Trees		
Diane	33 cM	Public 47	Common ancestor	John Wilson & Jane Hunt
Dave	31 cM	Unlinked		
judyS	29 cM	Public 65		
Kath	28 cM	Public 70	Common ancestor	Frances Harper ??
Shar	28 cM	Private 11	Common ancestor	Frances Harper ??
joan	26 cM	Private 1,229	Common ancestor	John Wilson & Jane Hunt
Danie	26 cM			
hunt	25 cM	Private 3,656		
jrske	24 cM	Public 167		
Dore	24 cM	Public 633		
Mary	23 cM	Unlinked		
Amb	22 cM	Public 2,340	Common ancestor	Frances Harper ??
betty	22 cM	Public 116		
Fred	21 cM	Public 2	Common ancestor	Frances Harper ??



Genetic Affairs

Main Programs

Websites



Show websites

Show registered FamilyTreeDNA and 23andme websites



Register a new website

Register a new FamilyTreeDNA or 23andme website using your login credentials

AutoCluster analyses



Run AutoCluster

Run AutoCluster analysis for FamilyTreeDNA or 23andme profiles. Select the website and profile to start the AutoCluster analysis.



Run AutoTree

Run AutoTree analysis for FamilyTreeDNA profiles. Select the FTDNA profile to start the AutoTree analysis.

AutoSegment analyses



Run AutoSegment

Run AutoSegment analysis using locally downloaded DNA segments from MyHeritage, FTDNA, 23andme or GEDmatch



Run hybrid AutoSegment

Run a hybrid AutoSegment analysis and combine DNA segments from MyHeritage, FTDNA, 23andme or GEDmatch profiles

Genetic Affairs Summary

Primary Functionality - Sorting Matches

- ❑ Clustering based on Total cM or Segment matches
- ❑ Costs

<u>DNA Company</u>		<u>23&Me</u>	<u>FTDNA</u>	<u>MyHeritage</u>	<u>GEDmatch</u>	<u>Ancestry CSV</u>
AutoCluster,	\$/run	US\$0.75	US\$0.75	0	0	US\$0.50
AutoSegment,	\$/run	US\$0.75	US\$0.75	US\$0.75	US\$0.75	-
Hybrid AutoSegment for # of vendors:			2	3	4	-
	\$/run		US\$1.00	US\$1.25	US\$1.50	-

- ❑ All segment programs provide input to DNA Painter.
- ❑ Present pileup removal logic not recommended
- ❑ Triangulation needed for segment matches
 - Some development is underway

Clusters & Segments



Questions ?