USING GEDMATCH
Created March 2015

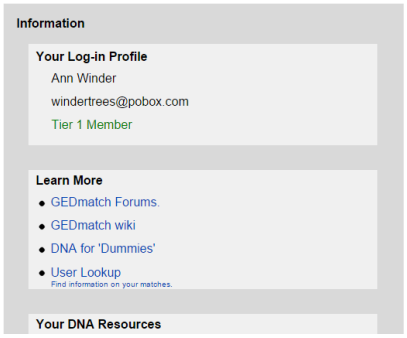
GEDmatch is a free, non-profit site that accepts raw autosomal data files from Ancestry, FTDNA, and 23andme. As such, it provides a large autosomal database that spans these three testing organizations. GEDmatch uses a slightly different algorithm for the comparison, so some additional matches may be available, as well as different views of the comparisons. GEDmatch is not affiliated with any of the testing companies.

For the Winder Wonderland DNA Project, the administrators ask that you let them upload your test results to GEDmatch, so that all of the samples in our project will be in one place. To do this, we will need your kit number and password. We promise to keep this information private. Also, if you would like to have your data uploaded under an alias, let us know and we will do so.

GEDmatch has several tools to help analyze your autosomal data, described below. You will have to register... it is free... at which point you will have access to any kits you have the number for, provided it has been uploaded to GEDmatch. GEDmatch kits are simply the same number the testing company gives you, prefixed with F for FTDNA, A for Ancestry, M for 23andme. You may also see P for phased (more later) and L for Lazarus (more later), both of which are interpolated data.

After your data has been uploaded, it may take several weeks for the site to fully process your data. But while waiting for the tools on the site to become available, you can do the one-to-one comparison to take a peek at preliminary matches. If the kits of promising looking matches that you found on FTDNA are not there, email the owners and suggest that they upload to GEDmatch. It's free!

GEDmatch Home Page



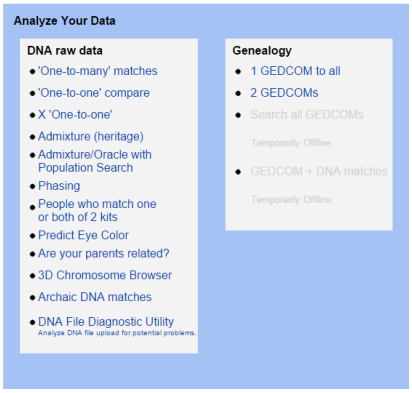
The upper left corner of your home page has **Information** about you and links to lots of helpful information. Check them out!

Note that I have a Tier 1 notation, because I have donated to the creators of the site and of the tools here. These are two fellows who do this work in their spare time and with their own money. They both have full-time jobs as well. These tools are important enough to me that I donate to keep them and their server going. I hope you will do the same! Simply hit the **Donate** button.

The **Your DNA Resources** section, under the **Information** box, will have a list of all the kits you administer. If you are a Winder Wonderland DNA Project member, and you have let the administrators upload your data, you won't have that list, but your kit number is the same as your FTDNA kit number with an F added to the beginning.

To the right of the Information box is the File Uploads box. If you are a Winder Wonderland DNA Project member, and you have let the administrators upload your data, you can ignore the upload raw data links.

On the right is a link to upload your gedcom. This is good to do, to help others decide if you are a potential match.

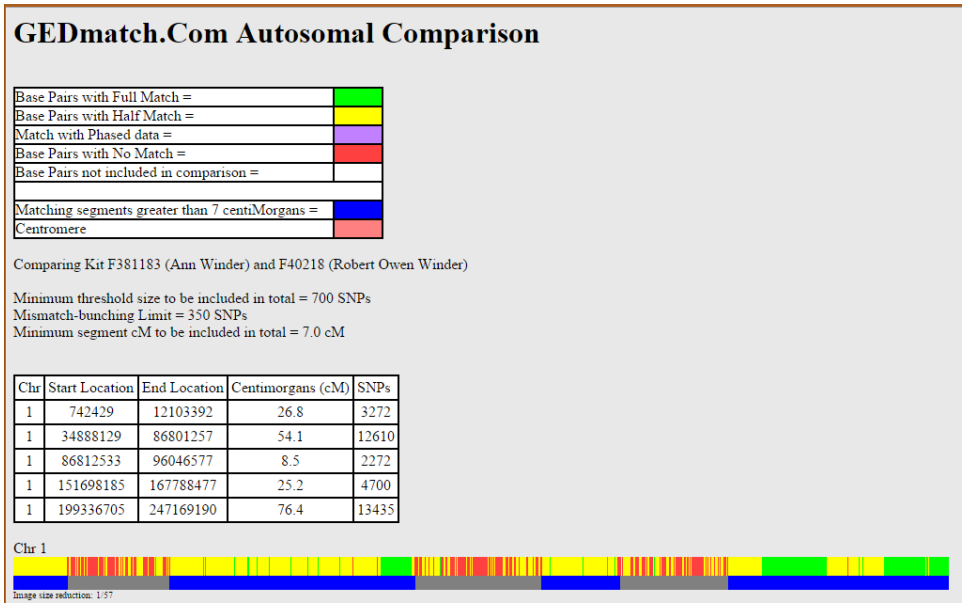


Under the Upload box is the Analyze Your Data box. These tools are available to all registered users, and are described, in order, below.

If you are not already familiar with terms such as cM and SNP, I strongly suggest you visit The Beginner's Guide to Genetic Genealogy at https://sites.google.com/site/wheatonsurname/home.

One-to-one Compare

- Enter any two GEDmatch kit numbers to compare.
- This utility can be run with or without the bar graphs. The bar graphs represent the SNPs of each chromosome and are color coded: green for full match, yellow for half match, and red for no match. If you can find stretches of green and yellow, the match is looking good. In this case, where I am comparing myself to my brother, there is a long dark blue segment, indicating we are closely related.
- You will get a table for each of the 22 chromosomes, showing chromosome number, start position of the matching segment, end position of the matching segment, number of cMs in that segment, and the number of matching SNPs in the chromosome.



GEDmatch.Com Autosomal Comparison

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	

Comparing Kit F381183 (Ann Winder) and F40218 (Robert Owen Winder)

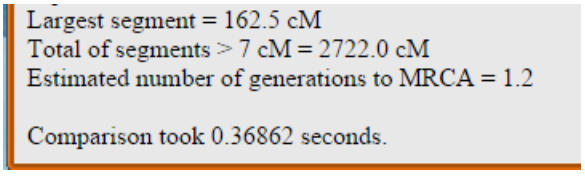
Minimum threshold size to be included in total = 700 SNPs
Mismatch-bunching Limit = 350 SNPs
Minimum segment cM to be included in total = 7.0 cM

Chr	Start Location	End Location	Centimorgans (cM)	SNPs
1	742429	12103392	26.8	3272
1	34888129	86801257	54.1	12610
1	86812533	96046577	8.5	2272
1	151698185	167788477	25.2	4700
1	199336705	247169190	76.4	13435

Chr 1

Image size reduction: 1/57

You can see that we match in several places, with the significant matches underlined in blue.



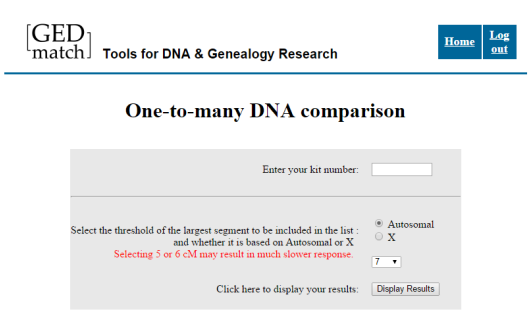
Largest segment = 162.5 cM
Total of segments > 7 cM = 2722.0 cM
Estimated number of generations to MRCA = 1.2

Comparison took 0.36862 seconds.

At the very bottom of the one-to-one compare output,

after the results for each of the 22 chromosomes, you can see the totals for your comparison. Note my brother is estimated as being 1.2 generations distant from me!

One-to-many compare



You can enter any kit number you want here, yours or any other you know about, but it must exist on GEDmatch!

7 cM is the shortest recommended matching chromosome segment to consider. The longer the segment, the more likely the match is due to there being an actual match rather than a random match.

Vocabulary lesson: Very short matching segments are likely to be Identical By State (IBS), which means false matches. True matches are called Identical By Descent (IBD), which means statistically significant matches. The longer the matching segment, measured in cMs, the more posiitive you can be that there is a common ancestor somewhere.

DNA matches to Kit F40218.

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
Click on 'A' for details on Autosomal comparison (Detail data may take up to a minute to process).
Click on 'X' for details on X-DNA comparison.

Select 2 or more from 'Select' column, and click this button for a Chromosome Browser comparison.
Chr-Browse

Select 2 or more from 'Select' column, and click this button for an Autosomal Matrix comparison.
A-Matrix

Select 2 or more from 'Select' column, and click this button for a Generations Matrix comparison.
Generations

Select 2 or more from 'Select' column, and click this button for an X-DNA Matrix comparison.
X-Matrix

* 'Adj cM' column has an adjustment applied to compensate for sex differences in X-Chromosome

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.

The top of the one-to-many results screen gives you many choices of what to do with your matches. But first, let's look at the list of matches GEDmatch found for you.

					Haplogroup		Autosomal				X-DNA				
Kit Nbr	Type	List	Select	Sex	Mt	Y	Details	Total cM	largest cM	Gen	Details	Total cM	largest cM	Name	Email
M201539	V3	L		M			A	35.5	28.5	4.3	X	0	0	Derek Doss	derekodoss@yahoo.com
M171613	V3	L		M	H6a1	I1	A	37.4	22.5	4.3	X	0	0	*NickGC	ngcart2011@gmail.com
M192329	V3	L		F			A	31.3	31.3	4.4	X	0	0	*janniel	chandlerslocket@gmail.com
A162150	F2	L		F	H1B1		A	31.3	31.3	4.4	X	0	0	*Janniel	chandlerslocket@gmail.com
A324651	F2	L		F	h1c1		A	31.1	31.1	4.4	X	0	0	Juliana Mabrey	

You can sort this table by any of the columns marked with small blue arrows in the first row.

- **Kit Number**
  - These are the kit numbers as assigned by GEDmatch.

- **Type**
  - F1 – FTDNA Affymetrix files
  - F1N – National Geographic Genographic Project files
  - F2 – FTDNA Illumina files
  - V2 – 23andMe “V2” files
  - V3 – 23andMe “V3” (Illumina) files
- **List**
  - This link will take you to the matches for that particular kit number. This is the same as running a one-to-many comparison using that person's kit number.
- **Select**
  - A check box to use when you wish to compare more than 2 individuals. After you check the kits you want included you choose the chromosome or matrix option in the top part of the output page seen above and described blow.
- **Sex**
  - This could be important when a male has X matches because we then know that the connection must be through his mother, as males only receive their X DNA from their mother.
- **Autosomal**
  - **Details**
    - This is the same as running a one-to-one comparison between the kit you entered and the kit on this line of output. This utility shows the start and end location of the matching segments and the length.
  - **Total cM**
    - All of the matching segment lengths added up.
  - **Largest cM**
    - Of all the matching segments, this is the length of the largest one.
  - **Gen**
    - The number of estimated generations going back to a common ancestor. As usual, this estimate is to be taken with a grain of salt. At least one grain.
- **X-DNA**
  - **Details**
    - Shows you exactly where you match this kit on the X chromosome
  - **Total cM**
    - All of the matching segment lengths added up. Segments are counted if they are at least as long as the minimum length specified.
  - **Largest cM**
    - Of all the matching segments, this is the length of the largest one.

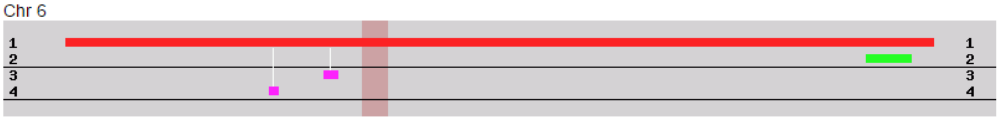
Chromosome Browser

- Run this from the **one-to-many compare** results page. You have specified a base kit to run the compare with, and this resulted in a list of kits that match in some way. Select at least 2 of these to compare with your base kit in the browser
- This displays a listing and a graph for each chromosome where the selected kits match.

Chr 6

Match ID	Type	Name	Matching segments on Chromosome 6	Overlap with previous match
1	F2	John H. Winder (F295619)	148878 - 170732528 (194.131 cM)	New Root
2	V3	*Becky (M813815)	157487691 - 166186209 (13.596 cM)	157487691 - 166186209
3	F2	Loren Winders (F320102)	50835899 - 53481730 (3.1233 cM)	Old Branch (1) , 50835899 - 53481730
4	F2	*bjmcd2 (A045159)	40056884 - 41729249 (3.5192 cM)	Old Branch (1) , 40056884 - 41729249

Chr 6



LEGEND

cM Range	color
> 100 cM	
50-100 cM	
20-50 cM	
10-20 cM	
5-10 cM	
< 5 cM	
Centromere	

Above is just one of the 22 charts on the chromosome browser results page. A legend appears with the results to chromosome 1 showing that unlike the FTDNA browser, here the colors indicate the strength of the match rather than the kit being matched. Each kit has a line on the graph. Here, we see kit 1 has a promising match to kit 2 and a very small match to kits 3 and 4.

The narrow white lines on the graph connecting the segments on kits 3 and 4 show that those kits match kit 1 but not kit 2

- **Chr #**
  - The chromosome being described in the following table
- **Match ID**
  - The number of the kit being matched. Kits do not retain their numbers across chromosomes.
- **Name**
  - The name the kit is registered under and the kit number
- **Matching Segments**
  - The locations on the chromosome where matches occur with the other kits
- **Overlap with previous match**
  - New Root: base segment
  - Old Branch: matches the kit specified. Old Branch (1) says that kit matches kit 1.

Autosomal Matrix

Autosomal DNA comparison matrix

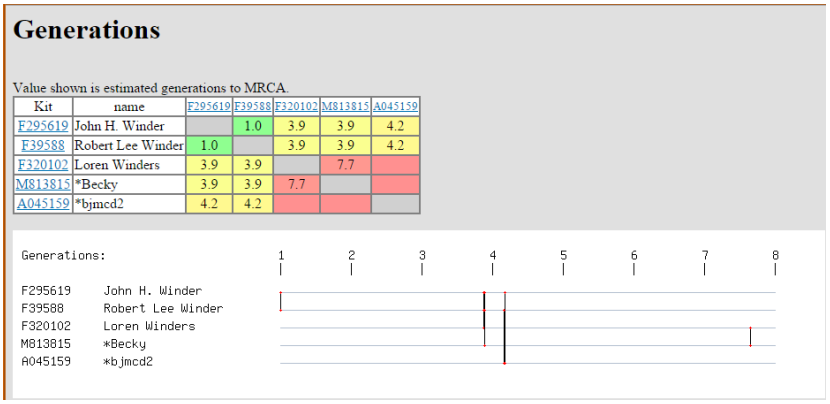
Value shown is cM total of matching segments over minimum threshold.

Kit	name	F295619	F39588	F320102	M813815	A045159
F295619	John H. Winder		3586.9	66.3	65.2	43.7
F39588	Robert Lee Winder	3586.9		66.3	65.5	44.5
F320102	Loren Winders	66.3	66.3		5.6	
M813815	*Becky	65.2	65.5	5.6		
A045159	*bjmcd2	43.7	44.5			

- Run this from the **one-to-many compare** results page. You have specified a base kit to run the compare with, and this resulted in a list of kits that match in some way. Select at least 2 of these to compare with your base kit in the autosomal matrix.
- Select several with large matching segments.
- There is no legend attached to this output.

Generations Matrix

This utility shows the estimated number of generations between any two kits.



Generations

Value shown is estimated generations to MRCA.

Kit	name	F295619	F39588	F320102	M813815	A045159
F295619	John H. Winder		1.0	3.9	3.9	4.2
F39588	Robert Lee Winder	1.0		3.9	3.9	4.2
F320102	Loren Winders	3.9	3.9		7.7	
M813815	*Becky	3.9	3.9	7.7		
A045159	*bjmcd2	4.2	4.2			

Generations: 1 2 3 4 5 6 7 8

F295619 John H. Winder
F39588 Robert Lee Winder
F320102 Loren Winders
M813815 *Becky
A045159 *bjmcd2

- Run this from the **one-to-many compare** results page. You have specified a base kit to run the compare with, and this resulted in a list of kits that match in some way. Select at least 2 of these to compare with your base kit in the autosomal matrix.

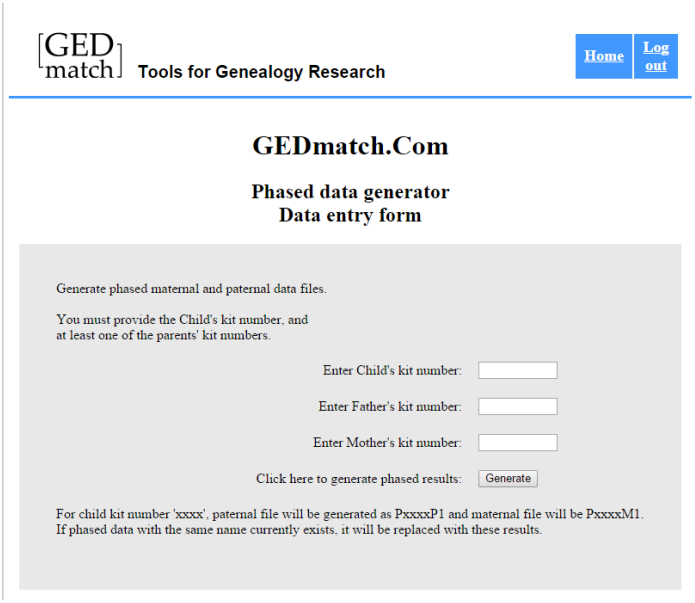
X-Matrix

This is the same as the autosomal compare matrix, except on the X chromosome.

Admixture (heritage) and **Oracle with Population Search**

This is where to find the pie charts showing estimated percentages of origins. This area of DNA testing for genealogy is still very much in its infancy. These tests work by comparing your results to reference samples gathered from around the world and results vary from one testing company to another. Play with these tools, but don't take them too seriously.

Phasing



GED match Tools for Genealogy Research

Home Log out

GEDmatch.Com

Phased data generator
Data entry form

Generate phased maternal and paternal data files.

You must provide the Child's kit number, and at least one of the parents' kit numbers.

Enter Child's kit number:
Enter Father's kit number:
Enter Mother's kit number:
Click here to generate phased results: Generate

For child kit number 'xxxx', paternal file will be generated as PxxxxP1 and maternal file will be PxxxxM1.
If phased data with the same name currently exists, it will be replaced with these results.

If at least one parent and his or her child tested, this tool will help show what was inherited from the parent. This is not an absolute, since the parents may have had a common ancestor.

Phasing is the process of trying to determine which DNA came from the mother, and which came from the father. The benefit of phasing is being able to identify which ancestor a segment was inherited from.

If you really want to know about this, see How Phasing Works .

GEDmatch.Com Phasing utility

Thanks to John S Walden for help in getting this utility on GEDmatch.

Child's Kit: F295619
Father's Kit: F39588
Processing without mother's kit.

Paternal kit number: PF295619P1

Maternal kit number: PF295619M1

Your phased Paternal and Maternal files have been generated.

One-to-one comparisons should be available immediately.
Please allow additional time for batch processing to complete before using One-to-many comparisons on these results.

Some other utilities may also require that batch processing be completed.

Phasing took 0.94951 seconds.

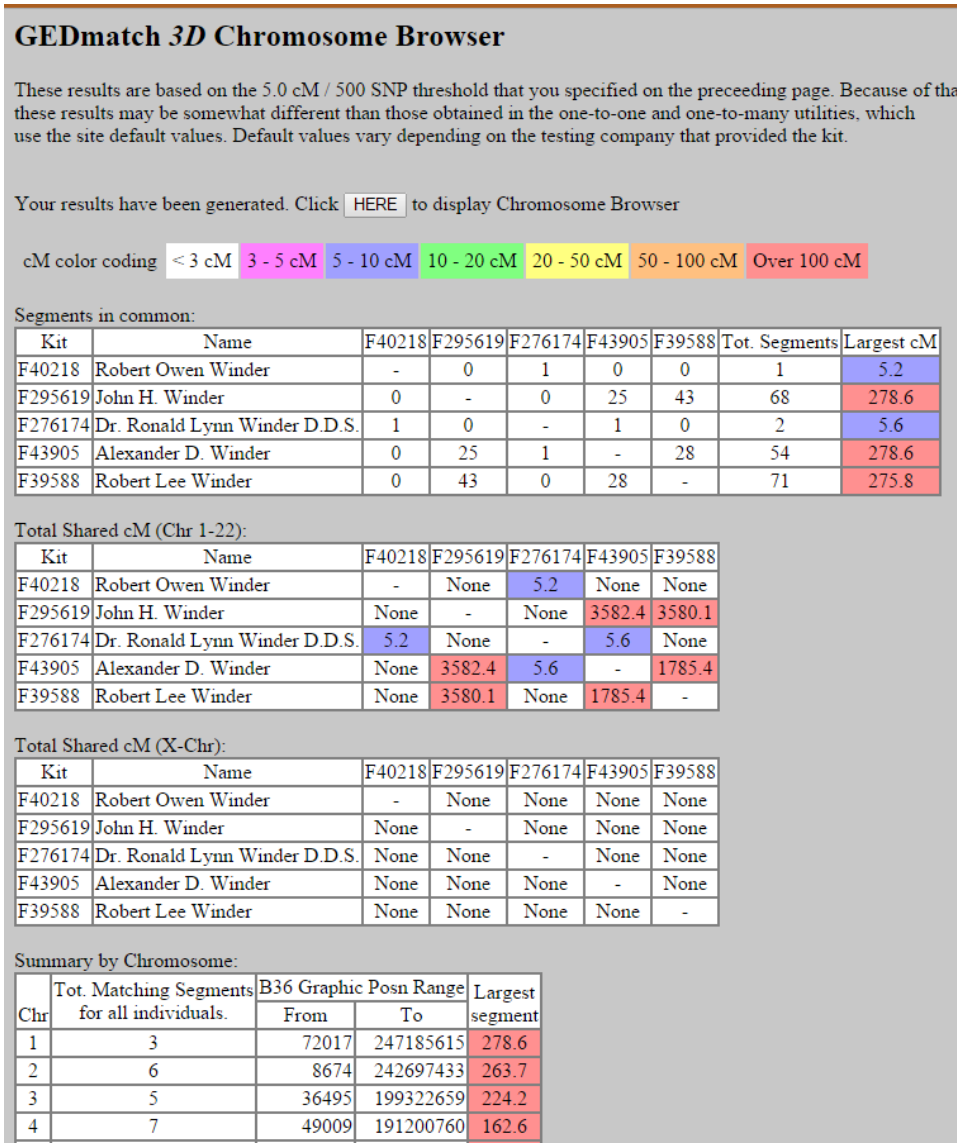
Finished.

This tool results in two new kits, prefixed by P, representing the projected kits for the child's parents. The kit ending in P1 is the paternal projection, and the kit ending in M1 is the maternal projection.

People who match one or both of 2 kits

This tool finds kits that are in common with 2 kits, or that match one kit but not the other.

3D Chromosome Browser



GEDmatch *3D* Chromosome Browser

These results are based on the 5.0 cM / 500 SNP threshold that you specified on the preceeding page. Because of tha
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	F40218	F295619	F276174	F43905	F39588	Tot. Segments	Largest cM
F40218	Robert Owen Winder	-	0	1	0	0	1	5.2
F295619	John H. Winder	0	-	0	25	43	68	278.6
F276174	Dr. Ronald Lynn Winder D.D.S.	1	0	-	1	0	2	5.6
F43905	Alexander D. Winder	0	25	1	-	28	54	278.6
F39588	Robert Lee Winder	0	43	0	28	-	71	275.8

Total Shared cM (Chr 1-22):

Kit	Name	F40218	F295619	F276174	F43905	F39588
F40218	Robert Owen Winder	-	None	5.2	None	None
F295619	John H. Winder	None	-	None	3582.4	3580.1
F276174	Dr. Ronald Lynn Winder D.D.S.	5.2	None	-	5.6	None
F43905	Alexander D. Winder	None	3582.4	5.6	-	1785.4
F39588	Robert Lee Winder	None	3580.1	None	1785.4	-

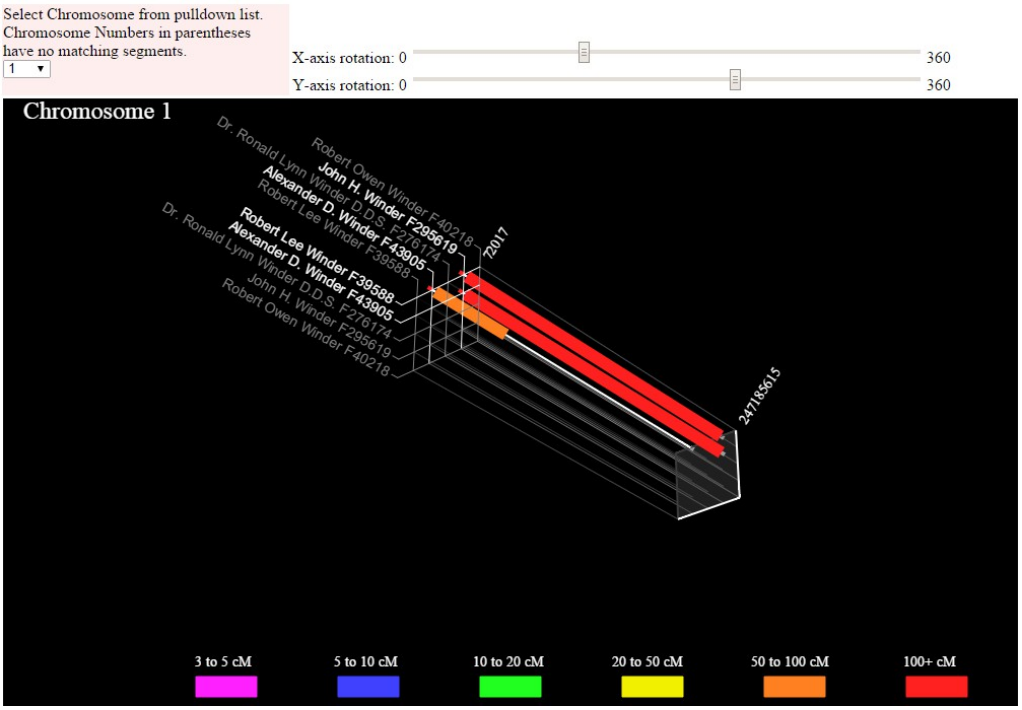
Total Shared cM (X-Chr):

Kit	Name	F40218	F295619	F276174	F43905	F39588
F40218	Robert Owen Winder	-	None	None	None	None
F295619	John H. Winder	None	-	None	None	None
F276174	Dr. Ronald Lynn Winder D.D.S.	None	None	-	None	None
F43905	Alexander D. Winder	None	None	None	-	None
F39588	Robert Lee Winder	None	None	None	None	-

Summary by Chromosome:

Chr	Tot. Matching Segments for all individuals.	B36 Graphic Posn Range From	B36 Graphic Posn Range To	Largest segment
1	3	72017	247185615	278.6
2	6	8674	242697433	263.7
3	5	36495	199322659	224.2
4	7	49009	191200760	162.6

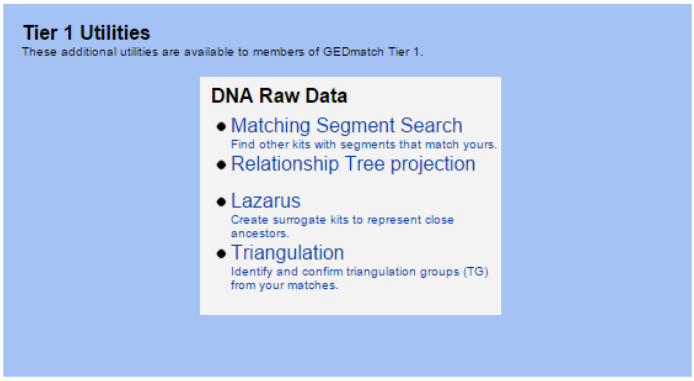
This browser produces a color coded matrix of which kit matches another.



This is the 3D part, where it shows the relationships between the kits you specify.

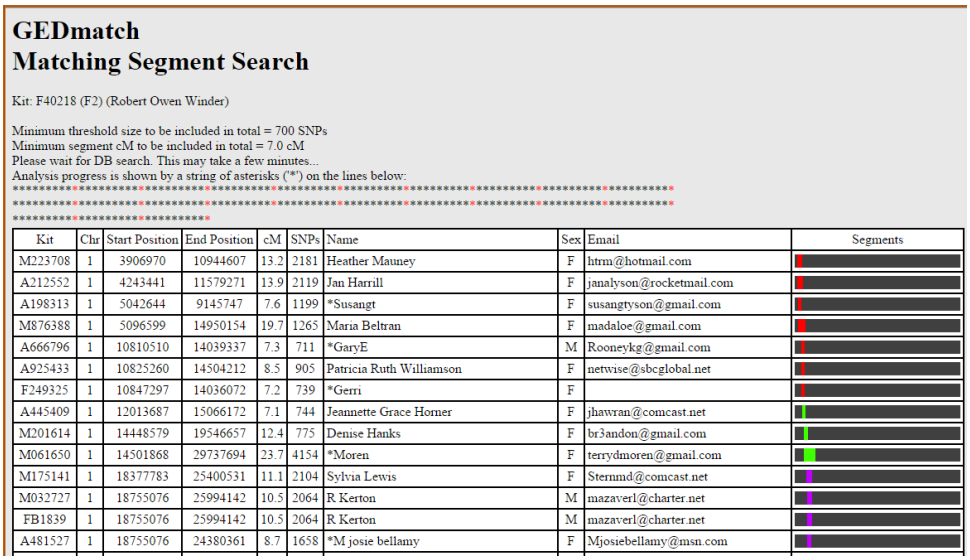
This is a picture of three generations: father, son, grandson plus another person in the project that has very little match.

TIER 1 TOOLS



These tools are available only to those who donate to the GEDmatch cause.

Matching Segment Search



GEDmatch
Matching Segment Search

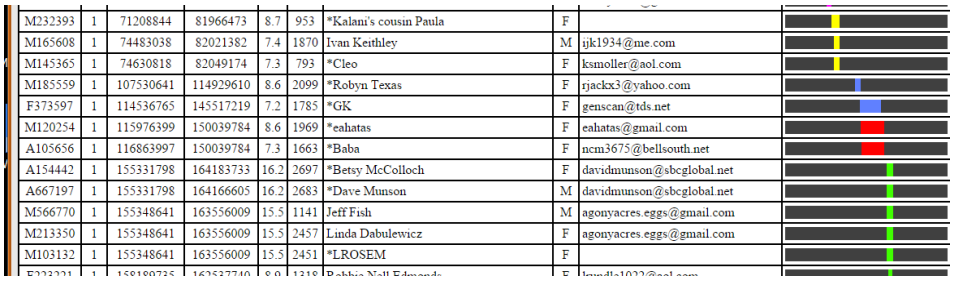
Kit: F40218 (F2) (Robert Owen Winder)

Minimum threshold size to be included in total = 700 SNPs
Minimum segment cM to be included in total = 7.0 cM
Please wait for DB search. This may take a few minutes...
Analysis progress is shown by a string of asterisks ("*") on the lines below:

Kit	Chr	Start Position	End Position	cM	SNPs	Name	Sex	Email	Segments
M223708	1	3906970	10944607	13.2	2181	Heather Mauney	F	htrm@hotmail.com	
A212552	1	4243441	11579271	13.9	2119	Jan Harrill	F	janalyson@rocketmail.com	
A198313	1	5042644	9145747	7.6	1199	*Susangt	F	susangtyson@gmail.com	
M876388	1	5096599	14950154	19.7	1265	Maria Beltran	F	madaloe@gmail.com	
A666796	1	10810510	14039337	7.3	711	*GaryE	M	Rooneykg@gmail.com	
A925433	1	10825260	14504212	8.5	905	Patricia Ruth Williamson	F	netwise@sbcglobal.net	
F249325	1	10847297	14036072	7.2	739	*Gerri	F		
A445409	1	12013687	15066172	7.1	744	Jeannette Grace Horner	F	jhawran@comcast.net	
M201614	1	14448579	19546657	12.4	775	Denise Hanks	F	br3andon@gmail.com	
M061650	1	14501868	29737694	23.7	4154	*Moren	F	terrydmoren@gmail.com	
M175141	1	18377783	25400531	11.1	2104	Sylvia Lewis	F	Sternmd@comcast.net	
M032727	1	18755076	25994142	10.5	2064	R Kerton	M	mazaver1@charter.net	
FB1839	1	18755076	25994142	10.5	2064	R Kerton	M	mazaver1@charter.net	
A481527	1	18755076	24380361	8.7	1658	*M josie bellamy	F	Mjosiebellamy@msn.com	

This tools searches the GEDmatch database for those kits that match the one you specify. This can take quite a while! When it finishes, you hopefully have some brand new hints for who to contact.

The results chart is very long, showing matches stacked for locations progressively along each chromosome



M232393	1	71208844	81966473	8.7	953	*Kalani's cousin Paula	F	
M165608	1	74483038	82021382	7.4	1870	Ivan Keithley	M	ijk1934@me.com
M145365	1	74630818	82049174	7.3	793	*Cleo	F	ksmoller@aol.com
M185559	1	107530641	114929610	8.6	2099	*Robyn Texas	F	rjackx3@yahoo.com
F373597	1	114536765	145517219	7.2	1785	*GK	F	genscan@tds.net
M120254	1	115976399	150039784	8.6	1969	*eahatas	F	eahatas@gmail.com
A105656	1	116863997	150039784	7.3	1663	*Baba	F	ncm3675@bellsouth.net
A154442	1	155331798	164183733	16.2	2697	*Betsy McColloch	F	davidmunson@sbcglobal.net
A667197	1	155331798	164166605	16.2	2683	*Dave Munson	M	davidmunson@sbcglobal.net
M566770	1	155348641	163556009	15.5	1141	Jeff Fish	M	agonyacres.eggs@gmail.com
M213350	1	155348641	163556009	15.5	2457	Linda Dabulewicz	F	agonyacres.eggs@gmail.com
M103132	1	155348641	163556009	15.5	2451	*LROSEM	F	

Scroll down until you find stacked segments of a larger length. The more kits stacked, the longer the segments, the more likely you have ancestors in common.

Relationship Tree projection

This utility calculates probable relationship paths based on Autosomal and X-DNA Genetic Distances. It is experimental, and the results should not be considered absolute. This application only works properly for 2 kits with a non-zero cM result for X.

Lazarus

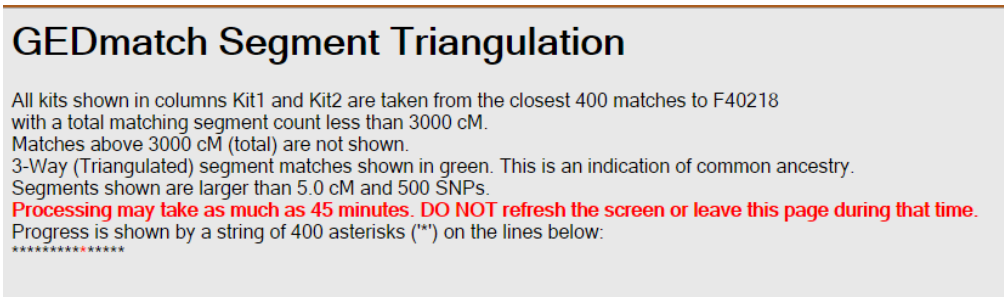
Generate 'pseudo-DNA kits' based on segments in common with your matches. These 'pseudo-DNA kits' can then be used as a surrogate for a common ancestor in other tests on this site. Segments are included for every combination where a match occurs between a kit in group1 and group2. The resulting are combined to create the final kit. It may be useful to save copies of the next page results, for future reference.

This tool requires

- the kit number for the target (the one you are trying to project parent kits for)
- at least one kit number for descendants of that target
- at least one other kit number of brother/sister, parents and cousins.

Since we do not have a set of tests to fit this set of criteria, I could not produce a sample output. Later!

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.

This process takes a long time! If you can run this tool in the wee hours of the night, it will run faster.

The output of this tool looks similar to that of the Matching Segment Search tool. Again, scroll down to find long, stacked segments to find contacts with possible common ancestry.

To find out more about this technique, visit DNAeXplained.