

Running People Who Match 2 Kits Analysis

(This is most effective when you are a Tier 1 Gedmatch supporter (donating \$10 in the month you are wanting to run the analysis).

Begin by selecting a Kit ID from your **One to Many Match list** to compare to your managed Gedmatch kit ID

Select **People who match both, or 1 of 2 kits**

DNA Applications:

- [One-To-Many Beta - give it a try](#)
- [One-To-Many DNA Comparison Result](#)
- [One-to-One Autosomal DNA Comparison](#)
- [One-to-One X-DNA Comparison](#)
- [Admixture \(heritage\)](#)
- [Admixture / Oracle with Population Search](#)
- [People who match both, or 1 of 2 kits](#)
- [DNA File Diagnostic Utility](#)
Analyze DNA file upload for potential problems.
- [Are your parents related?](#)
- [3-D Chromosome Browser](#)
- [Archaic DNA Matches](#)

Enter the two kits selected to compare, in the First and Second Kit number fields -accept the default settings and then DISPLAY RESULTS

GEDmatch

People who match both kits, or 1 of 2 kits

Enter first kit number:

Enter second kit number:

cM threshold of largest segment to qualify as a match:

cM threshold of total matching segments to qualify as a match. Must be greater than or equal to largest segment threshold.

Difference in generations results of 2 kits to common match to disqualify it as a match. This may be useful when kits being compared are from a highly admixed population such as Ashkenazi. Otherwise, leave as a high value (default=99). In cases where both kits match below the cM threshold, but the difference between their estimated number of generations is above this value, will cause the kit with the highest cM to show as a match, and the other kit to show as a no-match.

Click here to display your results:

The results show the matches to the two kits being compared:

GEDmatch®

People who match both kits, or 1 of 2 kits

Kit 1:

Kit 2:

Matches both kits

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

Match	✓	Name	T468293						Generations Difference	Email
			Shared	Largest	Gen	Shared	Largest	Gen		
T674236	<input type="checkbox"/>	Denise A Sproed	3586.7	281.5	1.0	19.3	19.3	4.8	3.8	denisesproed@gmail.com
	<input type="checkbox"/>		3584.7	224.2	1.0	19.3	19.3	4.8	3.8	
	<input type="checkbox"/>		3575.4	263.7	1.0	19.3	19.3	4.8	3.8	
	<input type="checkbox"/>		2522.6	167.2	1.3	19.0	19.0	4.8	3.5	

Click to select in the box and then SUBMIT at the top

Multi Kit Analysis

Manual Kit Selection/Entry

Tag Group Selection

Manual Kit Selection/Entry

Visualization Options

When the next screen opens, click on Visualization Options

Next select the List/CSV tab and lower the threshold to 5 and click Matrix Matched Segment CSV

GEDmatch Visualization Options

Kits included ---

Chromosomes & Segments

Matrices

GEDCom

Lazarus

List/CSV

Tag Groups

Edit Kit List

Clustering

Lists and CSV Downloads

List	Note	cM Value	Action
Kit number List	File contains selected Kit numbers only. No match data.		Kit Numbers CSV file
Match List	File contains total match data for selected Kit numbers only.	7 ▼	Match CSV file
Matched Segment List	File contains matched segments for Primary Kit to other selected Kit numbers only.	7 ▼	Primary Matched Segment CSV
Matrix Matched Segment List	File contains matched segments for selected kits to other selected kits only.	5 ▼	Matrix Matched Segment CSV

Then a file will generate and click on the HERE hyperlink to open the Excel

GEDmatch®

Matrix CSV Generator V0.1

Software Version Jun 26 2019 00:30:49

cM threshold= 5.0

overlap floor= 0

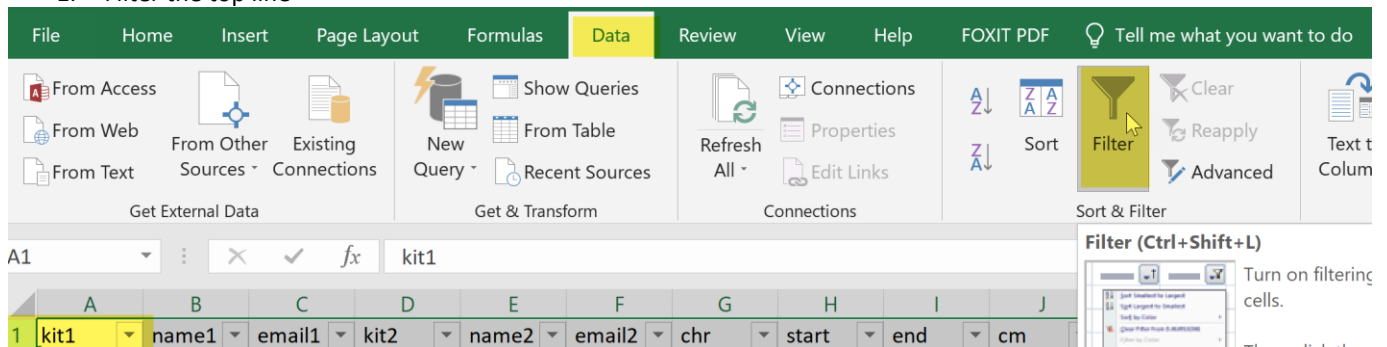
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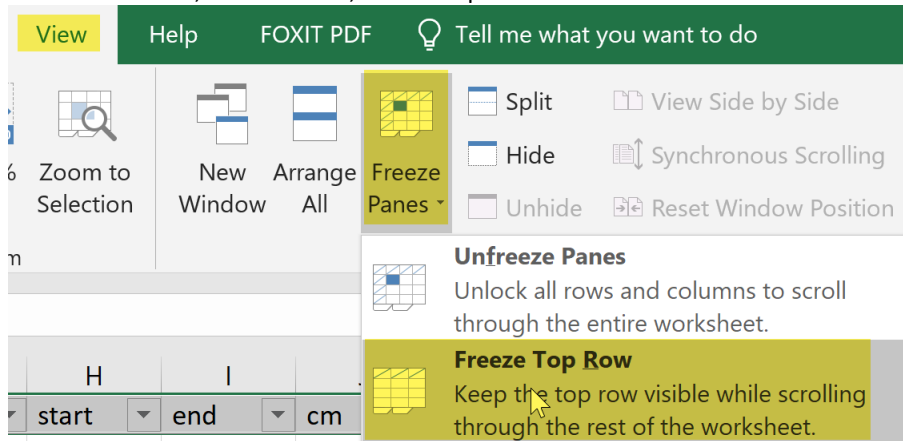
Click [HERE](#) to download segment match csv data to a comma-separated CSV file.

Once the excel file opens, the following analysis steps can be completed:

1. Filter the top line



2. Set view, Freeze Panes, Freeze Top Row



3. Identify the Chromosome and segment where the first two match. Highlight that line.
4. Remove the first, second & third cousin matches to each other (close, multi-line matches)
5. Sort by Chromosome, Start, End positions.
6. Click on the GEDCom tab and then Search then look through the trees for a common line

[Chromosomes & Segments](#) [Matrices](#) **[GEDCom](#)** [Lazarus](#) [List/CSV](#) [Tag Groups](#)

[Edit Kit List](#) [Clustering](#)

GEDComs

GEDCom

Action

Find matching GEDComs

[Search](#)

7. Filter the file for those who match on the same Chromosome overlapping
8. Email the person with the analysis information showing the likely group of triangulated matches.