Running People Who Match 2 Kits Analysis on GEDmatch

(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 Gedmatch kit ID

Select People who match both, or 1 of 2 kits

Free Tools
One-To-Many - Limited Version
One-To-Many - Original Version
Relationship Probability
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.

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

Kit Number 1			
Kit Number 2			
cM threshold of larges 10	segment to qualify as	a match:	
cM threshold of total n or equal to largest seg	atching segments to o nent threshold.	qualify as a match.	Must be greater than
10			
Difference in generatic match. This may be use population such as Ash where both kits match estimated number of g highest cM to show as	ns results of 2 kits to o ful when kits being co kenazi. Otherwise, lea below the cM thresho enerations is above th a match, and the othe	common match to mpared are from ve as a high value ld, but the differer is value, will cause r kit to show as a n	disqualify it as a a highly admixed (default=99). In cases nce between their e the kit with the no-match.
99			
	DISPLAY RE	SULTS	

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

Kit 1: Kit 2: Found 269 mat 2 Submit Select	ches that match both kit t 3 or more from '√' colum	n, and click this button for addition	al display	and proce	ssing	options.			\searrow		
Toggle Select	Save ICW									1	
	SELECT ALL		T27 T9			Constations	1				
Match	~	Name	Shared	Largest	Gen	Shared	Largest	Gen	Difference	Ged/Wiki	Email
Τć		Denise A Sproed	3,580.8	281.5	1.0	122.6	30.4	3.4	2.4	GED Wiki	denisesproed@gmail.com
AC		Contraction and the	3,578.5	209.3	<mark>1.</mark> 0	46.1	27.7	4.1	3.1	GED	
Μ			3,570.2	275.8	1.0	46.3	40.2	4.1	3.1	GED Wiki	
M			0.460.7						2.4		
IVI			2,163.7	224.7	1.4	28.8	18.8	4.5	3.1		

Click to Select All in the box and then SUBMIT (if you click CTRL – Blue Hyperlink GED or WIKI, the tree will open on a new tab)

GEDmatch Visualization Options

Kits included Ti										
Chromosomes	& Segments Matrices GEDCc	om Lazarus List/C	SV Tag	Groups Edit	: Kit List	Clustering				
Lists and CSV Downloads										
List	Note	Speed vs Accuraccy	cM Value	Prevent Hard Breaks	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.			□ Prevent Hard Breaks		MATCH CSV FILE				
Matched Segment List	File contains matched segments for Primary Kit to other selected Kit numbers only.			□ Prevent Hard Breaks		PRIMARY MATCHED SEGMENT CSV				
Matrix Matched Segment List	File contains matched segments for selected kits to other selected kits only. 2	 Better Accuracy – Average Speed mode Best Accuracy – Slowest Speed mode 			3	MATRIX MATCHED SEGMENT CSV				

When the next screen opens, click on Visualization Options, next select the List/CSV tab and select Best Accuracy and click Matrix Matched Segment CSV. Then a file will generate and click on the HERE hyperlink to open the Excel

GEDmatch[®] Matrix CSV Generator

Comparison Finished (0 kits)

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:



- 3. Identify the Chromosome and segment where the first two match. Highlight that line.

 kit1 name1
 email1
 kit2
 name2
 email2
 cr
 cr

 T271542
 *D Mother Sproed
 denisesproed@gmail.com
 T#######
 *D Cousin Mickey Mouse
 denisesproed@gmail.com
 3
 63411
 20009298
 39.7
- 4. Copy the original tab onto a new Excel tab, filter the Chromosome you match (on example above it was Chromosome 3) and **sort** the target kits you started with by email2, name2, and name1

Sort							?	×
⁺ <u>A</u> dd	Level	<u>D</u> elete Level	Copy Level	<u>O</u> ptions		🗹 My	data ha	s <u>h</u> eaders
Column			Sort On		Order			
Sort by	email2	~	Cell Values	~	A to Z			~
Then by	name2	~	Cell Values	~	A to Z			~
Then by	name1	~	Cell Values	~	A to Z			~

- 5. Highlight the matches you both match at the overlapping regions of the same chromosome
- 6. Filter the tab by those you highlighted and copy those to a new tab called FOCUS
- 7. Return to the prior tab and resort all matches by Chromosome, Start, End positions.
- 8. Return to GEDmatch, click on the GEDCom tab and then Search then look through the trees for a common line

GEDmatch Visualization Options

Kits included T						
Chromosomes & Segments	Matrices	GEDCom	Lazarus	List/CSV	Tag Groups	Edit Kit List
GEDComs						
GEDCom				Acti	ion	
Find matching GEDComs					SEARCH	

9. Email the person with the analysis information starting with the strongest matches on FOCUS tab to yield a triangulated group of matches eventually