

Combining results from all tests

These are the steps to combine the results from all of your tests. One section is specifically for the situation where you can identify a paternal or maternal match, the rest applies to any situation. **Important note: File formats may change slightly please overlook this.**

Download files from dnagedcom.com

FTDNA files

There are 3 files to download; a chromosome browser file, a ICW file and a FF Match file. The FF Match file is mostly for reference.

Files must be cleaned up so that they can fit together and be treated in a similar manner.

1. Chromosome browser file

Clean up data by Clearing Content of first column this leaves a blank column. Add an F to this column for FTDNA

F	Natasha Marie Oberg	1	54538315	60138042	8.59	Natasha Marie Oberg
F	Diane Morgan	1	54879395	60138042	7.82	Diane Morgan
F	Doris Sullens	1	55980120	76505205	22.69	Doris Sullens

Delete the SNPs and ID columns - these are the two columns at the end

A	B	C	D	E	F	G	H
						SNP	Identifier
	Candace A	2	1.35E+08	1.37E+08	1.38	500	405122
	Candace A	3	65505873	67768689	3	500	405122
	Candace A	3	1.64E+08	1.68E+08	1.67	500	405122
	Candace A	6	57234857	65132087	1.82	500	405122
	Candace A	8	63011506	65832026	2.15	500	405122
	Candace A	8	70527808	72782585	2.41	500	405122

2. ICW file

No cleanup needed

23andme files

1. FIA file (indicate Profile name you want to use if there is more than one profile)

- Clean up data – First column contains names like this:
- **Diane Harman-Hoog vs Kenneth Wiley**
- Replace that string in the Find/Replace function by replacing Diane Harman-Hoog vs (the space after the vs is very important to include)
- This leaves Kenneth Wiley or whatever is after the vs in the original string.

Judith Scanlon vs JIM MYRTLE	2	206000000	215000000
Judith Scanlon vs JIM MYRTLE	2	232000000	236000000
Judith Scanlon vs JIM MYRTLE	10	4000000	31000000

Comparison
JIM MYRTLE
JIM MYRTLE

- Delete column with SNPs

Chromosc	Start point	End point	Genetic D	# SNPs
2	206000000	215000000	7.6	1725
2	232000000	236000000	8.3	1085
18	4000000	21000000	29.1	2922
X	3000000	13000000	20.5	1547

- Insert a first column, add a 23 here for all rows

Comparison
23 Judith Scanlon vs JIM MYRTLE
23 Judith Scanlon vs JIM MYRTLE
23 Judith Scanlon vs JIM MYRTLE

Get gedmatch data (if you have Ancestry test or matches from Ancestry who have uploaded there)

- Sort by Kit # to get all the accounts that start with A at the top (little arrow at top of column)

Kit Nb	Type	Triangulate
▼ ▲		
A892239	F2	<u>I</u>
M233934	V3	<u>I</u>
M140359	V3	<u>I</u>
FB2705	F2	<u>I</u>
M082115	V2	<u>I</u>
M221915	V3	<u>I</u>
F318732	F2	<u>I</u>
F28358	F2	<u>T</u>

Check box for each Autosomal match where the account starts with an A

Select 2 or more from 'Select' column, and click this button

Chr-Browse 

Select 2 or more from 'Select' column, and click this button

A-Matrix

Select 2 or more from 'Select' column, and click this button

Generations

Select 2 or more from 'Select' column, and click this button

X-Matrix

* 'Adj cM' column has an adjustment applied to compensat

Intensity of **GREEN background** indicates how recent (w

To qualify as a 'match' in the genealogical time frame, it must have BOTH. Results with the largest segment

Kit Nbr	Type	Triangulate	GEDCOM	List	Select	Se
▼ ▲						
A004420	F2	I	G G G	L	<input checked="" type="checkbox"/>	F
A004823	F2	I	G	L	<input checked="" type="checkbox"/>	M
A005023	F2	I		L	<input checked="" type="checkbox"/>	F
A006468	F2	I		L	<input checked="" type="checkbox"/>	F

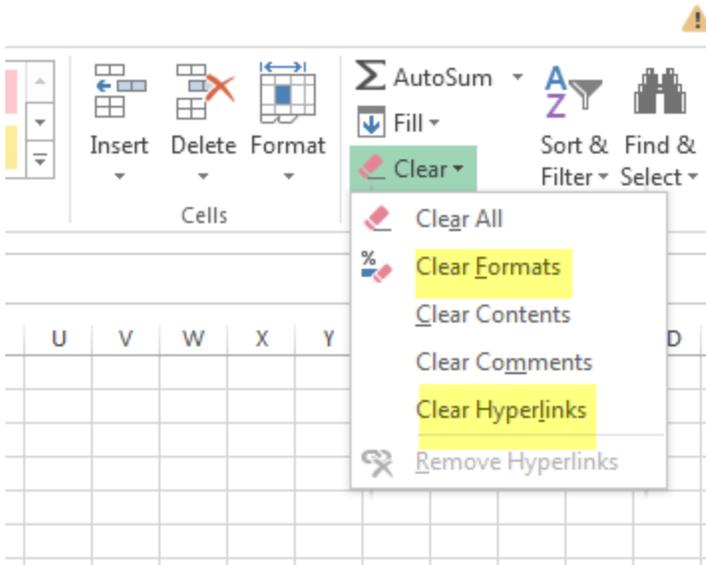
Compare Chromosomes (option at top) 

When comparisons come up, select table for each chromosome, paste into second column of new spreadsheet that will be for gedmatch downloads. In first column, you will paste number of that chromosome.

Paste next chromosome data below in the order of the number of the chromosome put chromosome number for each table you download in first column. You may need to use the Paste/Special Command, it depends on the version and kind of spreadsheet you are using

Continue until you have all chromosomes

- If you have Excel 2013 or greater then you can select the whole spreadsheet then click on Clear on the Home Bar and Clear the Formatting as well as the Hyperlinks



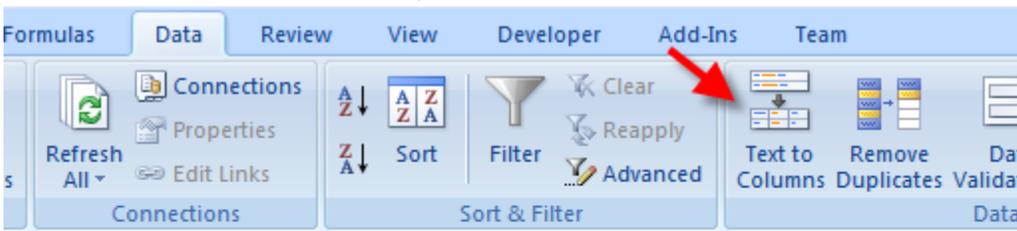
- If you have another spreadsheet check the Help function to see if you can do this.

Delete the last column of what you have downloaded from Gedmatch.

Select Column D, this has the starting and ending numbers for the segments and the cM for each segment. They need to be broken out into the correct columns. Example of two segments in this column below:

Match ID	Type	Name	Matching segments on Chromosome 13
1	F2	*wood box (A009408)	34093929 - 38860791 (7.5291 cM)
2	F2	*H. B. (A006156)	32685573 - 35150073 (3.0439 cM), 45409518 - 47229292 (3.148 cM)

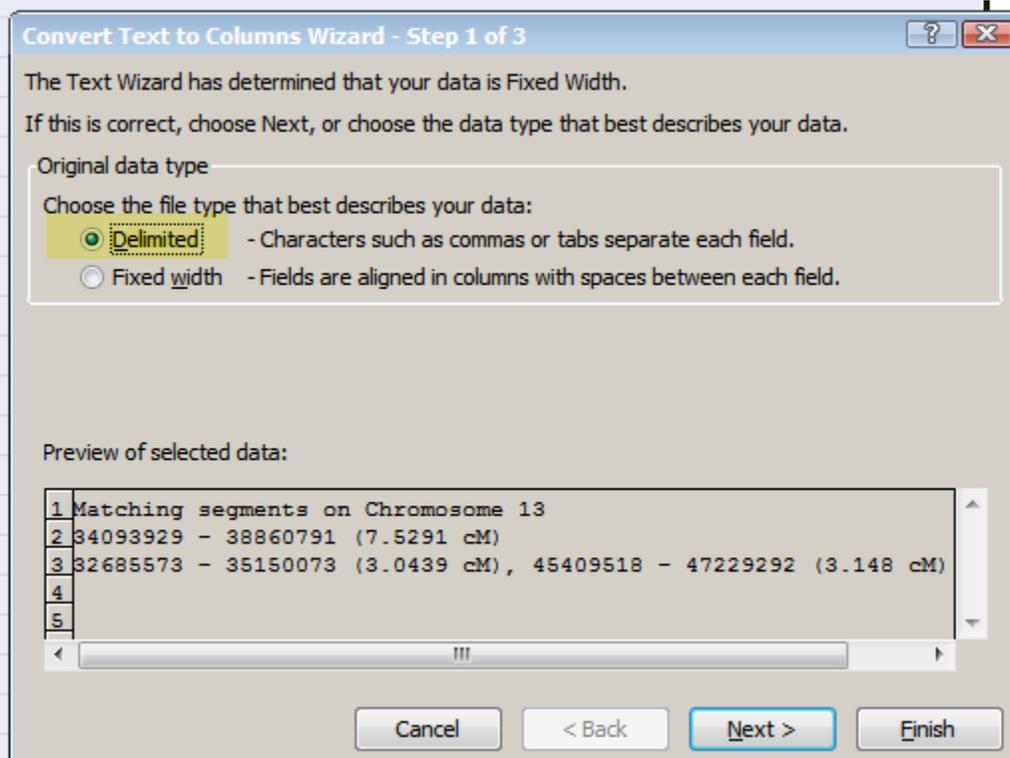
Use Text to Columns feature under Data in Excel. If you do not have this feature you can cut and paste the numbers into the columns,



Matching segments on Chromosome 13

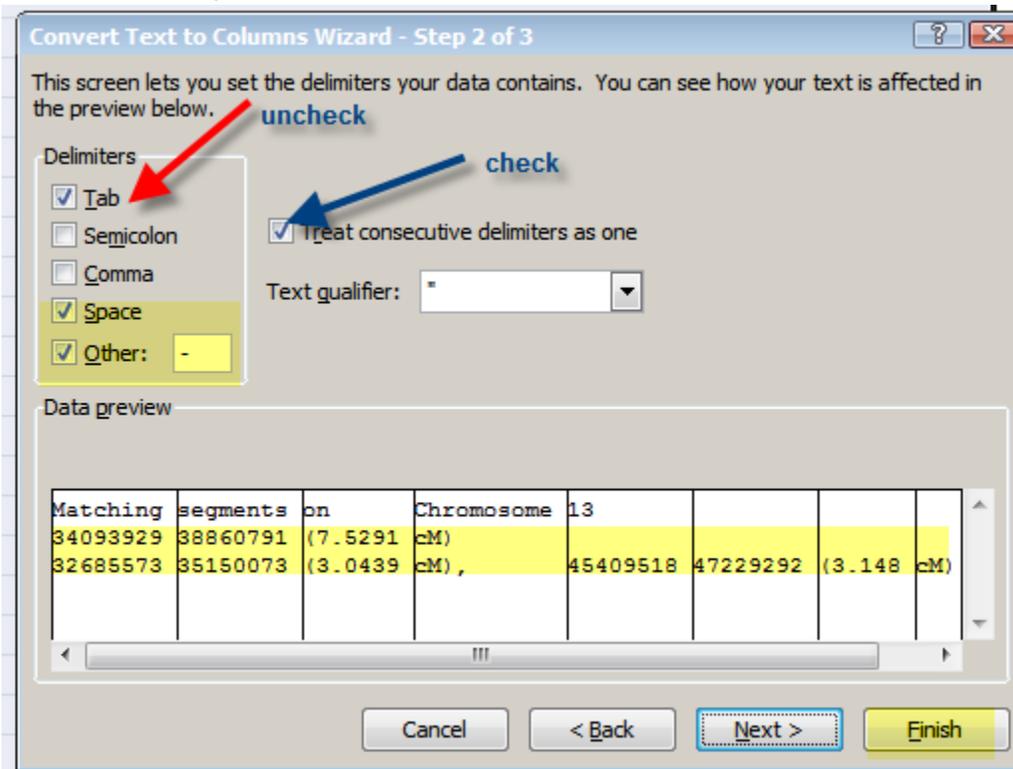
Formula Bar	D
	Matching segments on Chromosome 13
	34093929 - 38860791 (7.5291 cM)
	32685573 - 35150073 (3.0439 cM), 45409518 - 47229292 (3.148 cM)

In Text to Columns, chose that this is a Delimited File.



Then for the delimiters, UNCHECK the tab box, check the space box and put a - in the special character box and check that

Then check "treat consecutive delimiters as one". This means that space dash space is treated as one character/



Click on Finish

This is the result of that operation

C	D	E	F	G	H	I	J
Name	Matching	segments					
*wood_box (A009408)	34093929	38860791	(7.5291	cM)			
*H. B. (A006156)	32685573	35150073	(3.0439	cM),	45409518	47229292	(3.148 cM)

See how it split the numbers on either side of the dash?

Now select the columns with the numbers and replace first the “(“ and then the “)” in these columns to get rid of the parentheses.

Now get rid of the columns with cM in them,

This is the result

A	B	C	D	E	F	G	H	I
Match ID	Type	Name	Matching	segments				
1	F2	*wood_box A009408)	34093929	38860791	7.5291			
2	F2	*H. B. A006156)	32685573	35150073	3.0439	45409518	47229292	3.148

Now I prefer to format the numbers to make it easier to work with. Select the columns with the long numbers, one at a time, then right click on the column and Format Cells and then choose Numbers, 0 decimal points and use the comma to show 1000s.

Lastly, select the columns that have the shorter numbers (the cMs) and format those to 3 decimal points.

Name	Matching	segments				
*wood_box A009408)	34,093,929	38,860,791	7.53			
*H. B. A006156)	32,685,573	35,150,073	3.04	45,409,518	47,229,292	3.15

Sort the worksheet on column F largest to smallest.

Mark the row below the last row with 6 cMs in it

Below that line check the columns to the right for cM over 6.

Cut and paste the start, end and cM columns for any segments over 6 cM into columns D, E and F, If there is more than one set over 6 cM, insert a blank line below the name and then copy the name into the new row and add the additional start, end and cM into that row,

*bliese (A472571) 3,532,902 5,348,391 5.43 6,072,432 9,624,470

Becomes

*bliese (A472571) 6,072,432 9,624,470 8.60

And

Cheryl Ann) 28,165 29,226,407 58.06 29,502,984 88,668,978

Becomes

Cheryl Ann	148,878	32,045,016	53.84
Cheryl Ann	32,124,200	170,732,309	140.20

Go back to top of spreadsheet and adjust for any entries that have more than one segment over 6 cM. Make sure all segments over 6 cM are in column F.

Sort again on column F, largest to smallest.

Delete any rows where column F is below 6 cM.

Then once again sort on the chromosome column (B) and a second level for the start column (C)

Insert a new first column, enter A in the column for each row

	Chromosome	Matchname	Start	End	cM
A	13	*wood box A009408}	34,093,929	38,860,791	7.53
A	13	*H. B. A006156}	32,685,573	35,150,073	3.04
A	13	*H. B. A006156}	45,409,518	47,229,292	3.15

Combining the data

Start a combined spreadsheet

Paste all data with header row from your Chromosome Browser file in your combined spreadsheet

Paste all data from your FIA file into the spreadsheet- do not include header , Genetic Distance will be in the cM column

Paste all data from your Gedmatch sheet into the Combined Sheet

You will now have a large sheet of chromosome data from 3 sources

Adding ICW

Add ICW matrix, copy all names in set, paste this list of names in the set at the right hand side of the set and then click on cell to the right of the list and one cell above the top name you just pasted in. Then choose Paste Transpose from the Paste Options. This will paste a row of these names. (See Methodology for organizing chromosome data if this is not clear.

From FTDNA

Using the FTDNA ICW file download. Look up a person in the left column and if another person in the set is in the the second column next to this person's name, then add an X at the intersection in the matrix you just pasted in.

If the name is not in the FTDNA download, either because they have no ICW or because the test was in a different system, you might want to put a ? in the matrix.

From 23andme

There is a new feature at dnagedcom.com that lets you get the ICW matches for you and one person at a time. The screen will be changing soon as it is very cryptic at this time.

Right now, go to dnagedcom and sign in. You may not find it exactly the same as this example when you get there.

Go to the Download 23andme tab.

Enter the name and password of the person who is primary (this would usually be you).

Uncheck the AC file.

If there are multiple profiles on this account, enter the name of the profile you want as the persons whose results you want used.

In the bottom FIA Match blank use the name of the second person you want to check the ICW with.

CAUTION: the two fields – profile and FIA Match are case sensitive. Jones does not equal jones or JONES

WELCOME TO THE TOOLS SECTION FOR 23ANDME.

Email address:

Password:

Profile: - Leave blank for all or enter part of name to match

Run FIA: - Family Inheritance: Advanced - Will be run for all profiles

Run AC: - Ancestry Composition - Will be run for all profiles

Run AF: - Ancestry Finder - Only runs for the last profile in your account

FIA Match: - Enter value here if you want to run FIA against a match instead of your profile.

Please be VERY PATIENT when you hit the button. This can take 30 minutes to an hour. When it is complete, a Zip file will be downloaded

Be careful to enter the data like this, otherwise it may take several hours to run.

To get data after program has run

Click on Members tab. Then Files

The screenshot shows the website's navigation bar with the 'Members' tab highlighted. A dropdown menu is visible, containing two options: 'View Files' (highlighted in green) and 'Change Password'.

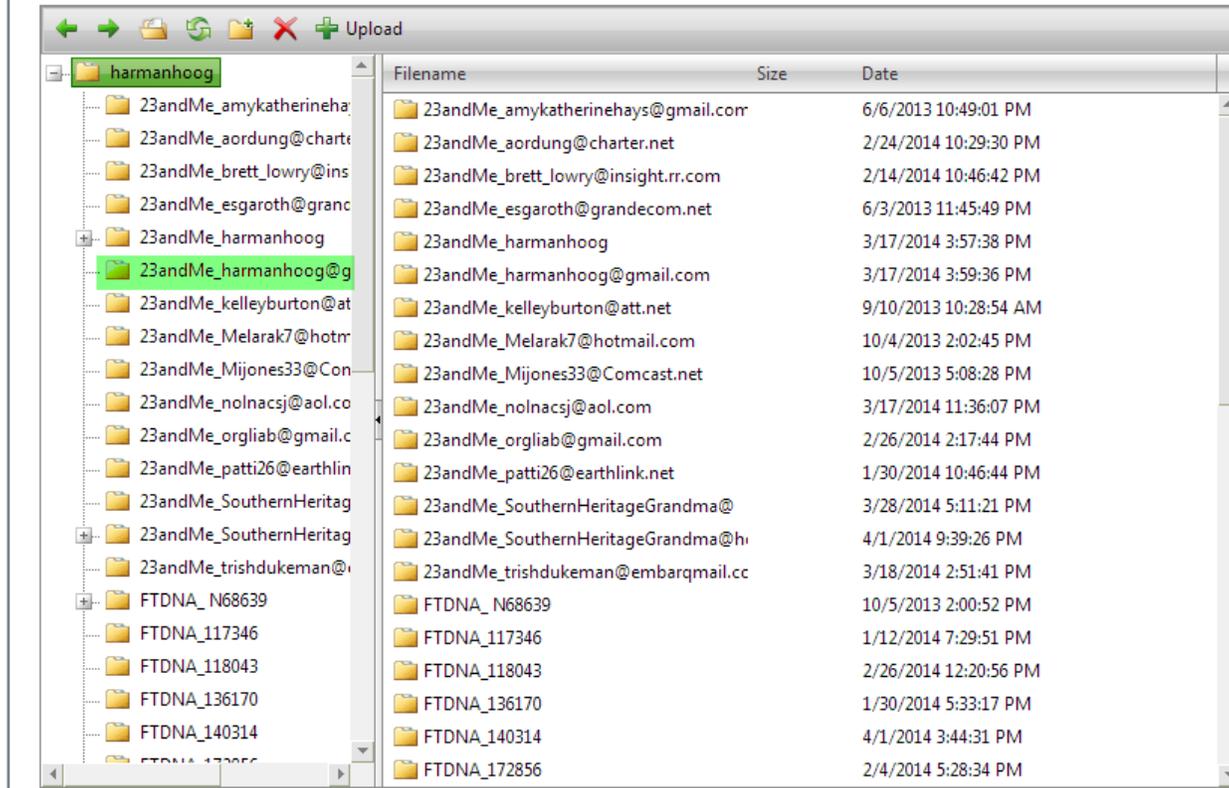
Click on the login name that appears on list on left part of that screen

DNAGEDCOM Welcome harmanhoog! [Log Out](#)

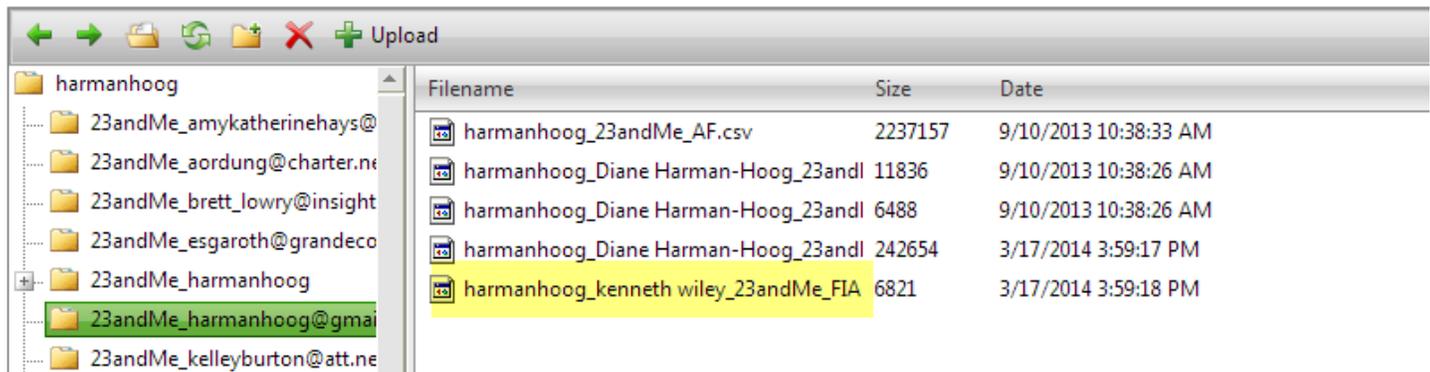
[Home](#) [Information](#) [Family Tree DNA](#) [23andMe](#) [Autosomal Tools](#) [Gedcom Tools](#) [Members](#) [User Accounts](#)

Select Folder on left and then double click on the file to download.

If you see a building folder, that means your files are still downloading to that folder. If that folder is very old and nothing is in it, you can delete that folder and try again. Please be patient! The system has to access the DNA companies server a lot to gather the information and depending on that this can take several hours. Running another download at the same time will cause your data to get locked up and you may need to wait several hours for it to get cleared and unlocked.



Open the file on the right that has the list of files for the user. The file should have both names in it as well as FIA.



We are looking at alternative methods of doing that.

From Gedmatch

Triangle candidates with *New Gedmatch Triangulation Tool*

Combining ICWs

You can use the FTDNA ICW file as your main ICW file, then you can paste other ICW into the file.

You need to make an adjustment to your data.

If John is ICW with Mary, you need to add 2 rows to the ICW file.

One has John in the first column and Mary in the second column

The second row would have Mary in the first column and John in the second column.

If Patsy has 11 ICW, then you would add 22 rows. 11 rows have Patsy in column 1 and the list of her ICW in column 2

Then you put Patsy in 11 rows in column 2 and her matches opposite her in column 1.

If you have some one that is tested at more than one system, by making sure that the name appears the same for all tests as it does in the FTDNA test, then the ICW from FTDNA will also run against all of them.

Frank Martinez is his name in FTDNA

Frank W Martinez is his name in 23andme

Change the 23andme name to Frank instead of Frank W.

Run Kworks or Jworks

Use your two combined files, the chromosome data file and the ICW file and run Jworks or Kworks. The programs are available on <http://dnaged.com> under the tab Autosomal tools. Be sure to read the directions.

Identifying maternal and paternal

If you know anything about one side or the other that might identify your matches as maternal or paternal you can now separate your matches into one side or the other

If one side is Irish –Dutch and the other side Italian for example. Check the countries of ancestry report on 23andme for the least common of these (probably in this case Italian. Then look to see which of these are in the original FIA report. Check to find one of them who seems to be in common with other Italians through the process described above. Assume this is from the Italian side of the family. You will fast find out if you are wrong, If it is paternal then color the rows with this person and their ICW matches blue. You will be expanding on this.

The idea is that some people tested in more than one system. If they are paternal in one, they will be paternal in the other and everyone they are ICW within each system is also paternal. You can keep rolling that on by looking for the ICW to the first people that were ICW, etc.

You may find a few people that seem to violate this. I color their row purple for unsure

If you know one side, then so much the better. Start by looking for those ICW with someone you know is on the other side. Color them appropriately.

The variation on this is that if you have a half sibling, then run an ICW list on FTW or on 23andme for each of you.

Color code the list for one of your sources to red text. Extract the name list. Combine the :red text list and the black text list. Sort on name. Those names that show as both red and black are common ancestors between you. The ones that are only red or only black are only ICW with one of the two half siblings. Color appropriately and then look for the same name in the other systems results and also in ICW matches to your ICW matches.

This process picks up speed as you get more and more people filled in.

After you do this, save the worksheet and make a copy. Then delete all matches from the copy for the side you are not interested in.

Precede by