

# Using Ancestry DNA and Third-Party Tools to Research Your Shared DNA Segments

**Walter Steets**

**Houston Genealogical Forum**

**DNA Interest Group**

**January 27, 2018**



# Today's agenda

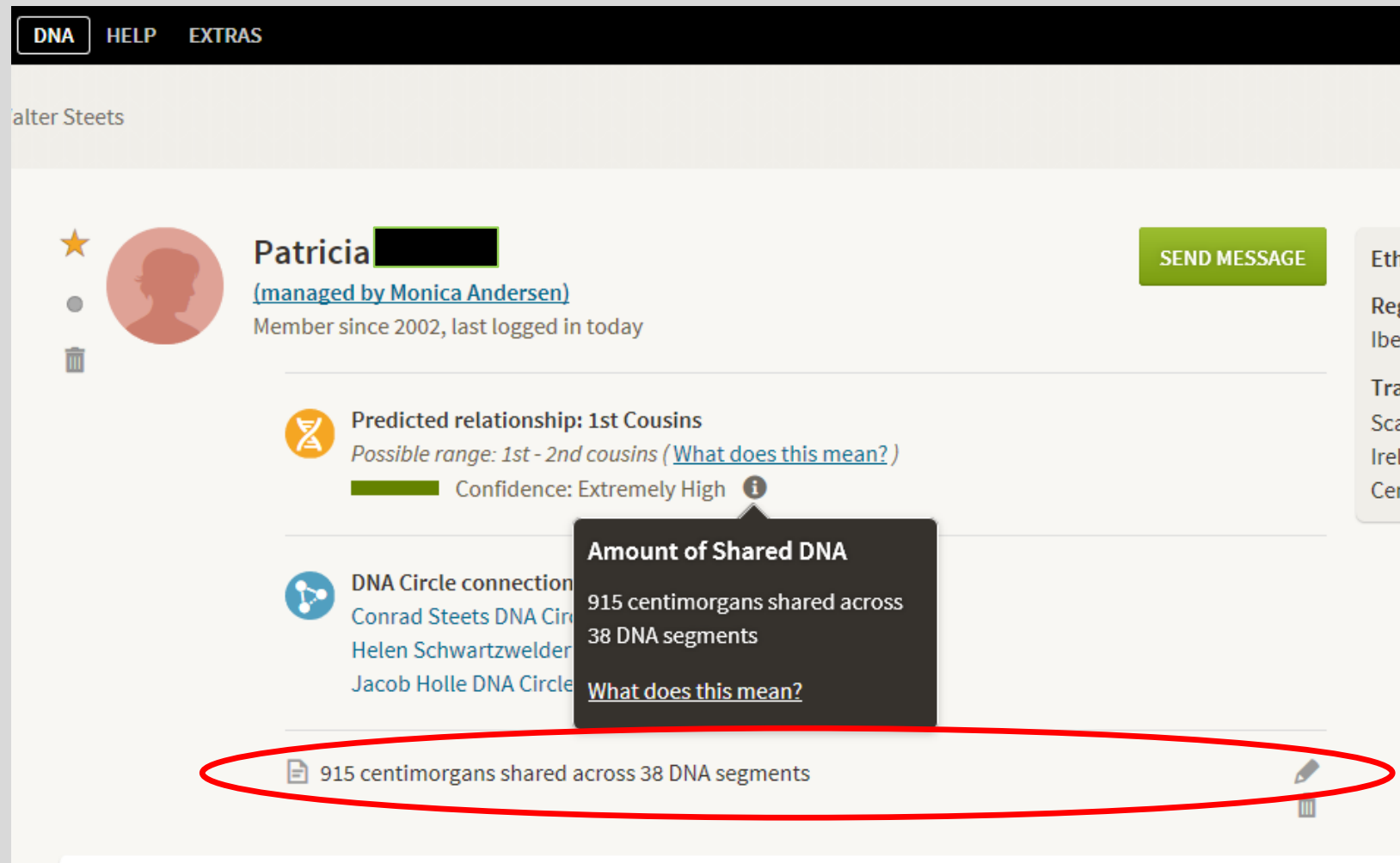
- Brief review of previous DIG session
- Displaying Ancestry Shared DNA using MedBetterDNA
- Downloading Raw DNA data from Ancestry
- Uploading Raw DNA data to GEDmatch
- GEDmatch tools
  - One-to-many
  - Matrices
  - Chromosome browser
  - One-to-one
- DNA Painter – Chromosome browser which displays phased chromosome data and labels for each segments
- Display of shared DNA and relationships using McGuire Diagrams



# DNA Data from Ancestry

## Obtaining the Shared DNA Data from an Ancestry Match Screen

- Go to a screen for one of your Shared Matches
- Click on the  icon following the Confidence: level
- The number of cM and segments will be displayed.
- Click on the  icon to open the notes box.
- Copy and paste the number of cM and segments into the notes box. The notes box may be viewed on the Shared Matches pages next to the match's name.
- You may also record the data in an Excel spreadsheet.






alter Steets



DNA HELP EXTRAS

Patricia [redacted] [SEND MESSAGE](#)

(managed by Monica Andersen)  
Member since 2002, last logged in today

 Predicted relationship: 1st Cousins  
Possible range: 1st - 2nd cousins ([What does this mean?](#))  
Confidence: Extremely High 

 DNA Circle connection  
Conrad Steets DNA Circle  
Helen Schwartzwelder  
Jacob Holle DNA Circle [What does this mean?](#)

 915 centimorgans shared across 38 DNA segments 



## MedBetterDNA

- Extension for Chrome web browser which only works with Chrome
- Can be installed from [Chrome Web Store](#) for free. Search for **MedBetterDNA**
- Without this extension, the Shared Matches page displays only single Notes
- With the extension, the Shared Matches webpage can display all Notes simultaneously
- The extension can also filter on Ancestry stars or on hashtags placed in notes.

**AncestryDNA Results for Walter Steets**

Sort by: Relationship | Date < 1 >

Filters HINTS NEW STARRED REGIONS SEARCH MATCHES

**IMMEDIATE FAMILY**

**1ST COUSIN**

**2ND COUSIN**

★ [charlese](#) 338 centimorgans shared across 20 DNA segments #maternal No family tree VIEW MATCH  
Possible range: 2nd - 3rd cousins ?  
Confidence: Extremely High ██████████  
Last logged in Jun 19, 2016

**3RD COUSIN**

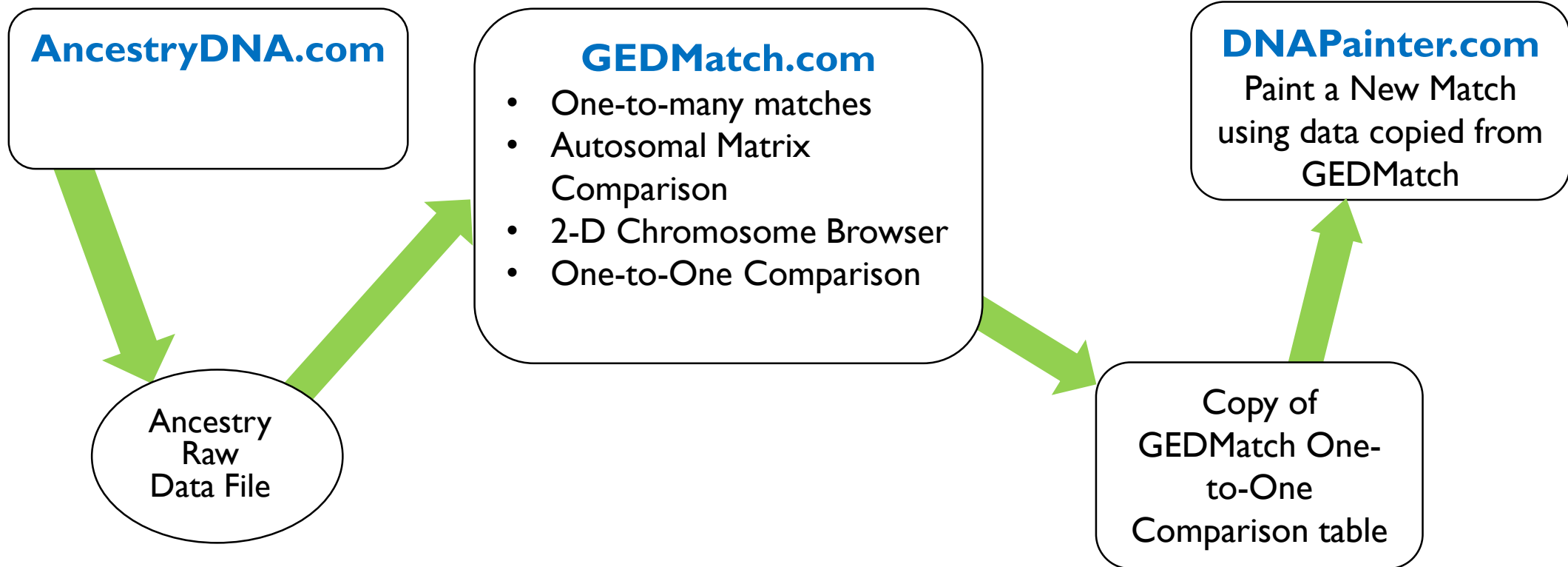
★ [thero](#) 168 centimorgans shared across 9 DNA segments #maternal daughter of Charle 2,328 people VIEW MATCH  
Possible range: 3rd - 4th cousins ?  
Confidence: Extremely High ██████████  
Last logged in 3 days ago

★ [pter](#) 157 centimorgans shared across 8 DNA segments #maternal No family tree VIEW MATCH  
Possible range: 3rd - 4th cousins ?  
Confidence: Extremely High ██████████  
Last logged in Sep 15, 2017

★ [B.S. \(managed by LindaColgin\)](#) 113 centimorgans shared across 6 DNA segments #maternal 1,949 people VIEW MATCH  
Possible range: 3rd - 4th cousins ?  
Confidence: Extremely High ██████████  
Last logged in yesterday



# DNA Data Transfer Process



# Download the DNA Raw Data File from Ancestry

- Last year Ancestry put in place new procedures
- The detailed procedure follows:
  - Login to Ancestry under the account of the person whose data you will be downloading and go to DNA Summary Page
  - Click on **SETTINGS** in the upper right corner of the screen
  - On the Test Settings web page, click on **Download Raw DNA Data**
  - In the Download Your Raw DNA Data pop-up window, enter your Ancestry account password, click in the box for the Ancestry agreement, and then click CONFIRM.
  - Find an new email from AncestryDNA and click on **Confirm Data Download** .
  - This should open the Download DNA Raw Data web page. Click on Download DNA Raw Data.
  - A pop-up box gives options to Open, Save, or Cancel the download. Click on Save and select a file directory in which to save the DNA download. You will have to know where to find the downloaded file in order to upload it into GEDMatch or another third-part tool.



# GEDMatch one-to-many Tool

Displays DNA kits matching a base kit. Comparable to Shared Matches in Ancestry.

- Kit Nbr – Identifier for DNA Raw data sets loaded into GEDMatch. First letter indicates testing company
- Select – allows matches to be selected for **chromosome** or **matrix** comparisons
- Details – clicking on **A** displays **one-to-one** list between base kit and A row kit
- Total cM – total shared cM
- Largest cM – length of single largest shared segment
- Gen – GEDMatches estimate of the number of generations between MRCA and match

Example: DNA matches to Kit M795 – Sharron

| Kit Nbr | Type | List              | Select                              | Sex | GED/WikiTree | Mt  | Y      | Details           | Total cM | largest cM | Gen | Details           | Total cM | largest cM | Name (* => alias) | Email |
|---------|------|-------------------|-------------------------------------|-----|--------------|-----|--------|-------------------|----------|------------|-----|-------------------|----------|------------|-------------------|-------|
|         |      | ▼ ▲               |                                     |     |              | ▼ ▲ | ▼ ▲    |                   | ▼        | ▼          | ▼ ▲ |                   | ▼        | ▼          | ▼ ▲               | ▼ ▲   |
| M3571   | V4   | <a href="#">L</a> | <input type="checkbox"/>            | M   |              | H   | G2a4   | <a href="#">A</a> | 3551.5   | 214.5      | 1.0 | <a href="#">X</a> | 194.6    | 119.4      | Sean Ne           |       |
| T7407   | F2   | <a href="#">L</a> | <input checked="" type="checkbox"/> | M   |              |     | R-M269 | <a href="#">A</a> | 1962     | 95.9       | 1.4 | <a href="#">X</a> | 62.5     | 36.7       | SD W              |       |
| T3693   | F2   | <a href="#">L</a> | <input checked="" type="checkbox"/> | M   |              |     |        | <a href="#">A</a> | 1736.3   | 123.5      | 1.5 | <a href="#">X</a> | 103.9    | 53.1       | Charles W N       |       |
| A9785   | F2   | <a href="#">L</a> | <input checked="" type="checkbox"/> | M   |              |     |        | <a href="#">A</a> | 1458.5   | 132.4      | 1.6 | <a href="#">X</a> | 98.8     | 53.1       | PR N              |       |
| A7516   | F2   | <a href="#">L</a> | <input checked="" type="checkbox"/> | M   |              |     |        | <a href="#">A</a> | 490.3    | 48.3       | 2.4 | <a href="#">X</a> | 141.6    | 92.7       | BC                |       |
| A1702   | F2   | <a href="#">L</a> | <input checked="" type="checkbox"/> | F   |              |     |        | <a href="#">A</a> | 420.6    | 43.7       | 2.5 | <a href="#">X</a> | 25       | 25         | CWW               |       |



## GEDMatch Autosomal Matrix Tool

- Displays the total amount of DNA shared between each pair of kits matching a base kit
- Relationships between matches may be estimated by referring to Shared cM Project data
- More useful than Ancestry Shared Matches. For example, maternal and paternal matches can be identified.
- A GEDMatch Tier I subscription (\$ 10./month) is required to display more than 5 rows and columns.

| Kit                    | name                   | <a href="#">M 3795</a> | <a href="#">T 407</a> | <a href="#">T 693</a> | <a href="#">A 785</a> | <a href="#">A 516</a> | <a href="#">A 702</a> | <a href="#">A 968</a> | <a href="#">A 928</a> | <a href="#">A 457</a> | <a href="#">T 445</a> |
|------------------------|------------------------|------------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|
| <a href="#">M 3795</a> | Sharron [redacted]     |                        | 1962.0                | 1736.2                | 1458.5                | 490.3                 | 420.6                 | 220.7                 | 131.7                 | 94.9                  | 68.9                  |
| <a href="#">T 407</a>  | SD W [redacted]        | 1962.0                 |                       |                       |                       | 761.0                 |                       | 351.7                 | 105.3                 |                       |                       |
| <a href="#">T 693</a>  | Charles W N [redacted] | 1736.2                 |                       |                       | 2742.5                |                       | 921.0                 |                       |                       | 247.9                 | 146.0                 |
| <a href="#">A 785</a>  | PR N [redacted]        | 1458.5                 |                       | 2742.5                |                       |                       | 1046.6                |                       |                       | 170.0                 | 122.1                 |
| <a href="#">A 516</a>  | BC [redacted]          | 490.3                  | 761.0                 |                       |                       |                       |                       | 3573.4                | 123.2                 |                       |                       |
| <a href="#">A 702</a>  | CWW [redacted]         | 420.6                  |                       | 921.0                 | 1046.6                |                       |                       |                       |                       | 269.9                 | 202.4                 |
| <a href="#">A 968</a>  | S [redacted]           | 220.7                  | 351.7                 |                       |                       | 3573.4                |                       |                       | 42.4                  |                       |                       |
| <a href="#">A 928</a>  | *nora [redacted]       | 131.7                  | 105.3                 |                       |                       | 123.2                 |                       | 42.4                  |                       | 5.3                   |                       |
| <a href="#">A 457</a>  | *GK [redacted]         | 94.9                   |                       | 247.9                 | 170.0                 |                       | 269.9                 |                       | 5.3                   |                       | 3584.9                |
| <a href="#">T 445</a>  | MK [redacted]          | 68.9                   |                       | 146.0                 | 122.1                 |                       | 202.4                 |                       |                       | 3584.9                |                       |





## GEDMatch One-to-One Comparison Tool

Provides detailed information for each DNA segment shared between two kits

- Chr – chromosome number
- Start Location – starting location in megabase pairs (Mb)
- End Location – end location in megabase pairs (Mb)
- Centimorgans – amount of shared DNA in cM
- SNPs – number of single nucleotide polymorphisms contained in segment

This data is copied and pasted into the DNAPainter chromosome browser.

Comparing Kit M795 (Sharron ) and T407 (SD)

| Chr | Start Location | End Location | Centimorgans (cM) | SNPs  |
|-----|----------------|--------------|-------------------|-------|
| 1   | 10,571,810     | 34,393,357   | 39.5              | 2,824 |
| 1   | 57,132,516     | 65,091,102   | 12.1              | 1,038 |
| 1   | 95,607,476     | 179,560,671  | 64.3              | 6,132 |
| 1   | 235,112,783    | 247,141,305  | 28.1              | 1,750 |
| 2   | 8,674          | 19,415,870   | 39.7              | 2,645 |
| 2   | 43,152,887     | 132,985,731  | 77.7              | 7,894 |
| 2   | 135,002,918    | 169,796,597  | 27.6              | 3,001 |
| 3   | 38,411         | 6,394,564    | 19.1              | 1,237 |
| 3   | 71,730,598     | 136,075,130  | 47.6              | 4,995 |
| 3   | 146,038,973    | 190,878,374  | 51.4              | 4,290 |

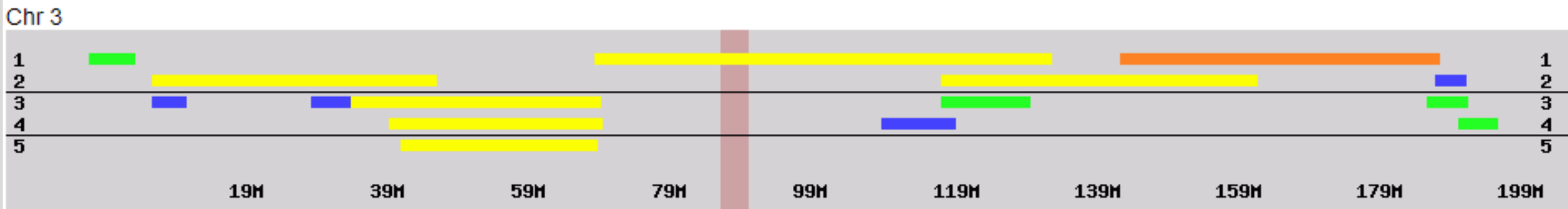


# GEDMatch Chromosome Browser

- Displays positions of shared segments on each chromosome pair by kit
- GEDMatch chromosome browser doesn't distinguish between maternal and paternal matches –i.e. phased data
- Work-around for displaying phased data would be to identify paternal and maternal matches in Matrix Tool and select only maternal or paternal matches to be displayed in One-to-many Tool.

Chr 3

| Match ID | Type | Name                                       | Matching segments on Chromosome 3   | Overlap with previous match  |
|----------|------|--|---|--|
| 1        | F2   | SD W [redacted]<br>(T [redacted] 407)      | 38411 - 6439294 (19.2518 cM), 71730598 - 136089933 (47.6947 cM),<br>146038973 - 190996741 (51.734 cM)   | New Root   |
| 2        | F2   | Charles W [redacted]<br>(T [redacted] 693) | 9095004 - 49029696 (43.5865 cM), 120594452 - 165099574 (40.938 cM),<br>190528181 - 194675489 (9.403 cM)   | 120594452 - 136089933, 146038973 - 165099574,<br>190528181 - 190996741   |
| 3        | F2   | PR N [redacted]<br>(A [redacted] 785)      | 9095004 - 13793386 (7.0949 cM), 31458491 - 37010073 (5.4022 cM),<br>37067047 - 72437744 (37.2007 cM), 120594452 - 132974671 (10.688 cM),<br>189325415 - 194910475 (13.068 cM) | 9095004 - 13793386, 31458491 - 37010073,<br>37067047 - 49029696, 120594452 - 132974671,<br>190528181 - 194675489 |
| 4        | F2   | CWW [redacted]<br>(A [redacted] 702)       | 42530528 - 72454412 (32.6238 cM), 112085416 - 122470457 (9.604 cM),<br>193776447 - 199228595 (12.132 cM)  | 42530528 - 72437744, 120594452 - 122470457,<br>193776447 - 194910475   |
| 5        | F2   | BC [redacted]<br>(A [redacted] 516)        | 44109583 - 71928942 (29.9846 cM)  | 44109583 - 71928942  |

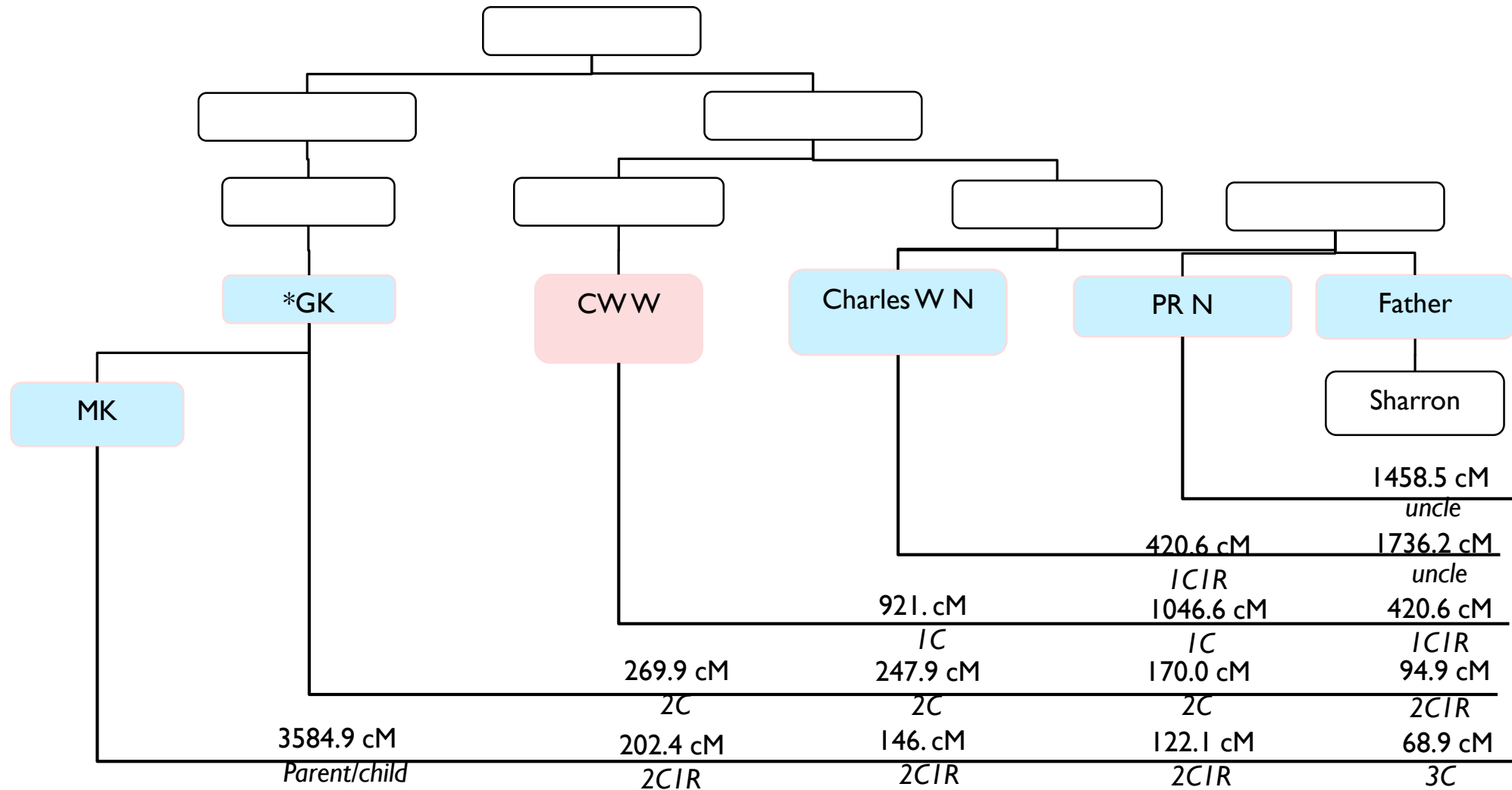


# DNA Painter

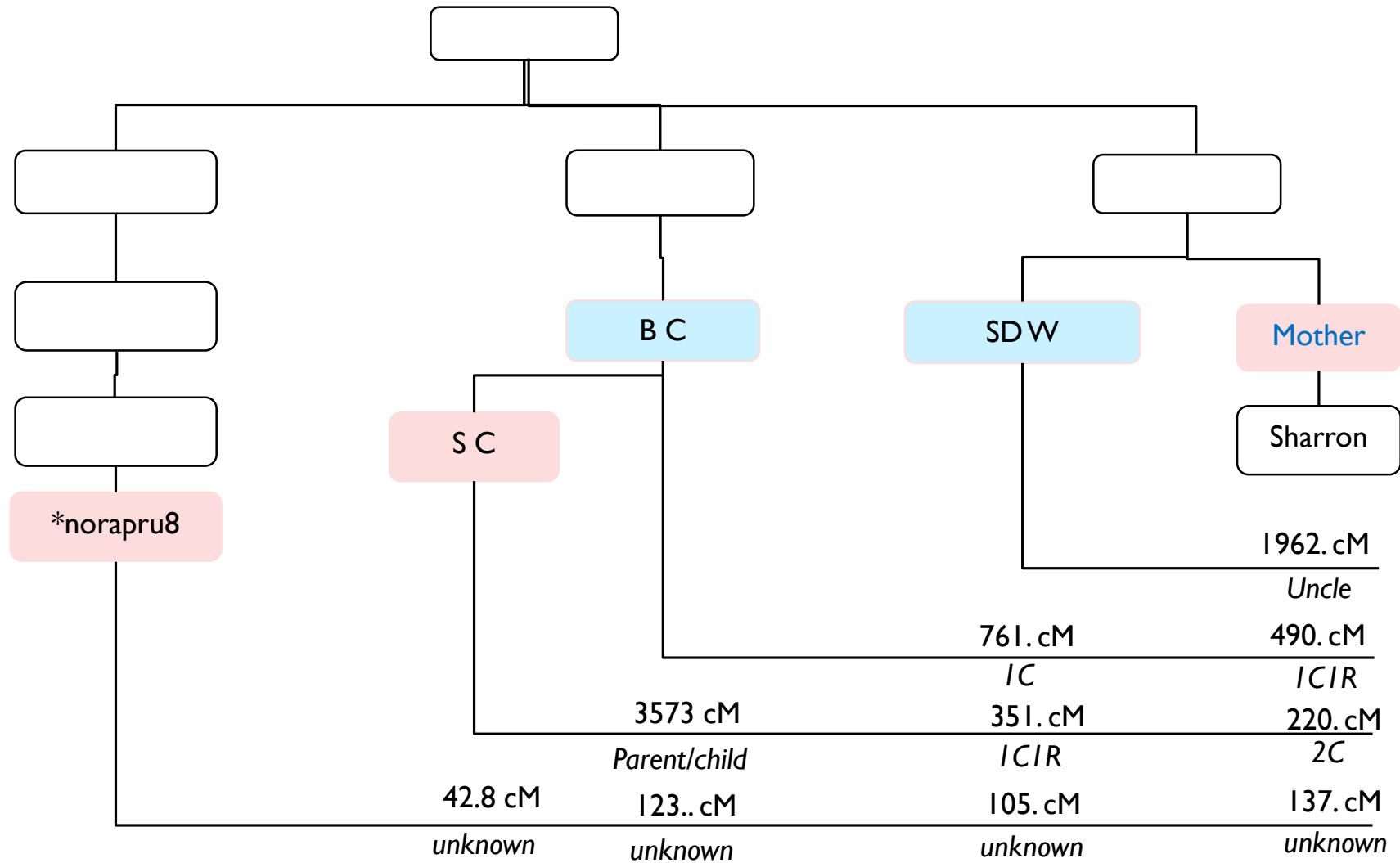
- DNA Painter allows you to display phased and labeled shared DNA segment data.
- Individual segments may be labeled by MRCA ancestor – may help to identify unknown matches



# McGuire Method Diagram: Sharron's Paternal Matches



# McGuire Method Diagram: Sharron's Maternal Matches



# Questions ?

